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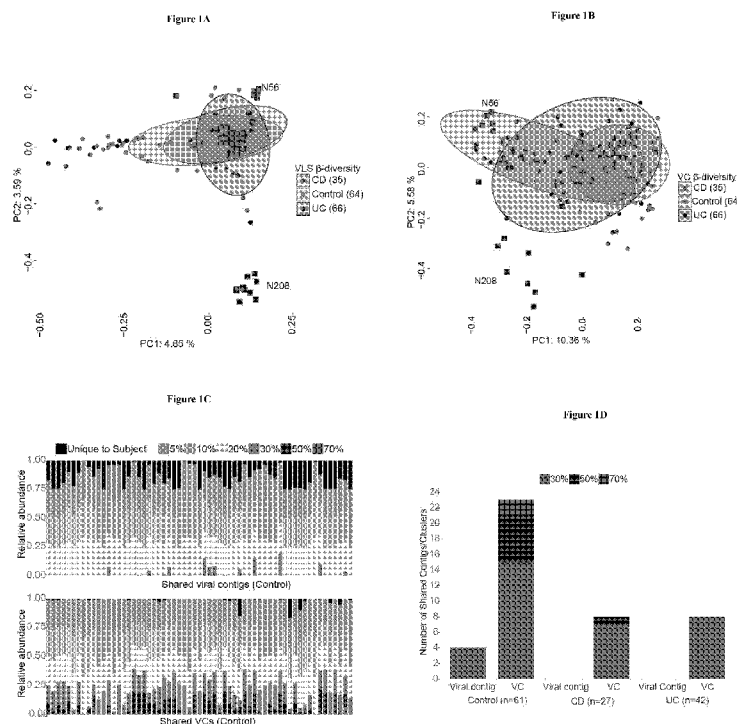
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(54) Title: MATERIALS AND METHODS FOR ASSESSING VIROME AND MICROBIOME MATTER



(57) Abstract: A method is described of analyzing the microbiome, including the virome, of a patient. Viral marker clusters for diagnosing inflammatory bowel disease, Crohn's disease and ulcerative colitis are identified from such analysis. Methods of diagnosis and treatment of dysbiosis and various disorders, such as inflammatory bowel disease, Crohn's disease and ulcerative colitis, are also included.

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MATERIALS AND METHODS FOR ASSESSING VIROME AND MICROBIOME MATTER

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to United States Provisional Application Serial Number 62/861,807, filed on 14 June 2019, United States Provisional Application Serial Number 62/861,818, filed on 14 June 2019, United States Provisional Application Serial Number 62/861,776, filed on 14 June 2019, and United States Provisional Application Serial Number 62/861,746, filed on 14 June 2019. The disclosure of each of the aforementioned applications is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention, in some aspects, relates to a method of analyzing the microbiome, e.g., virome, of a patient. The present invention, in some aspects, also relates to methods of diagnosing and treating dysbiosis of the microbiome, and various disorders that include infections and inflammatory disorders.

BACKGROUND

[0003] The virome is likely to be one of the major forces shaping the human gut microbiome, but is perhaps its least understood component. The virome is dominated by phages, such as bacteriophages, which play vital roles in many microbial communities by driving diversity, facilitating nutrient turnover (Weitz et al., 2015. *ISME J*, 9, 1352-64) and facilitating horizontal gene transfer (Canchaya et al., 2003. *Current opinion in microbiology*, 6, 417-424). High throughput sequencing has revealed the enormous diversity of the viral fraction of microbial ecosystems. Understanding the role of bacteriophages in microbial community structure can provide for more understanding and/or control of the alterations in human gut microbiome composition and diversity associated with many diseases, including Inflammatory Bowel Disease (IBD) (Gevers et al., 2014. *Cell Host Microbe*, 15, 382-392; Halfvarson et al., 2017. *Nat Microbiol*, 2, 17004), obesity (Le Chatelier et al., 2013. *Nature*, 500, 541-6) and diabetes (Forslund et al., 2015. *Nature*, 528, 262-266).

[0004] Many gut bacteria (and potential phage hosts) remain difficult to culture (Forster et al., 2019. *Nat Biotechnol*, 37, 186-192). This places a heavy reliance on metagenomic sequencing and bioinformatic approaches. However, a lack of universal marker genes (similar to 16S rRNA for the bacteriome) and a subsequent lack of taxonomic information due to poorly populated databases (Krishnamurthy and Wang, 2017. *Virus Res*, 239, 136-142) means that database-independent analysis of the virome must be carried out at the level of metagenomic assembly or individual viral genome. Early sequencing studies using 454 technology first described the novelty and diversity of the human gut virome (Minot et al., 2011. *Genome Res*, 21, 1616-25), but were only able to identify 2% of reads and with limits in sequencing depth, the true diversity and composition was not revealed. Improvements in sequencing technologies have allowed the virome to be analyzed in unprecedented detail with studies sequencing up to 50 million reads per sample (Zuo et al., 2019. Gut mucosal virome alterations in ulcerative colitis. *Gut*) and have confirmed that the virome is incredibly diverse, that the majority do not align to known sequences in databases (viral dark matter) (Roux et al., 2015b. Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. *Elife*, 4), and that composition is highly unique to individuals (Reyes et al., 2010, *Nature*, 466, 334-8).

[0005] Inflammatory Bowel Disease, including Crohn's disease (CD) and ulcerative colitis (UC), is a chronic disorder of the intestinal tract resulting in periods of flare (active) and remission (inactive) disease. IBD has been associated with alterations in the human gut microbiome which include decreased diversity and reduced abundance of the *Firmicutes* and *Bacteroides*. There is tentative evidence that the gut virome plays a role in IBD (Norman et al., 2015. *Cell*, 160, 447-60; Zuo et al., 2019. *Gut*; Fernandes et al., 2019. *J Pediatr Gastroenterol Nutr*, 68, 30-36) where IBD is associated with a decreased overall virome diversity and abundance and an increased abundance of the family *Caudovirales*. Because only a small fraction of gut virome are classified at the family level, let alone classified genomically, nearly all of this research has been conducted on a fraction of the virome, with a current benchmark study using about 15% of the data (Norman et al., 2015. *Cell*, 160, 447-60). This hampers the identification of virome disease biomarkers and means that any link between virome, bacteriome and disease status remains elusive.

[0006] Analysis of the whole gut virome using metagenomic assembly is also challenging. At this level of resolution, the virome exhibits enormous diversity and interpersonal variation, obscuring patterns in the virome across individuals and cohorts.

[0007] Accordingly, there is a need for improved systems and methods to identify markers for IBD in the gut virome.

SUMMARY OF THE INVENTION

[0008] In one aspect, a method is provided for identifying a plurality of viral marker clusters for determining the presence of inflammatory bowel disease (IBD) using viral genome sequences, the method comprising:

- obtaining a first dataset representing a first plurality of viral genome sequences derived from gastrointestinal (GI) microbiota samples of a healthy cohort;

- obtaining a second dataset representing a second plurality of viral genome sequences derived from GI microbiota samples of a cohort diagnosed with IBD;

- creating a first plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group viral genome sequences of the first dataset, each viral cluster in the first plurality of viral clusters comprising one or more viral genome sequences derived from the healthy cohort;

- creating a second plurality of viral clusters by using protein clustering to group like proteins derived from the second dataset and by using protein homology to group viral genome sequences of the second dataset, each viral cluster in the second plurality of viral clusters comprising one or more viral genome sequences derived from the cohort diagnosed with IBD; and

- identifying a plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters.

[0009] In some embodiments, at least a portion of the first plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database, and

- at least a portion of the second plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database.

[0010] In some embodiments, a totality of the first plurality and second plurality of viral genome sequences are each unassociated with a viral taxonomic category derived from a viral genome database.

[0011] In some embodiments, the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises using machine learning to identify the plurality of marker clusters.

[0012] In some embodiments, the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises identifying the plurality of marker clusters unassociated with a known taxon.

[0013] In some embodiments, each of the viral clusters in the plurality of marker clusters respectively represent an unidentified taxon of higher rank than a strain and of lower rank than a family.

[0014] In some embodiments, the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises performing beta diversity analysis on the first plurality of viral clusters and the second plurality of viral clusters.

[0015] In some embodiments, performing the beta diversity analysis comprises performing a scaling and ordination technique selected from a group consisting of principal coordinates analysis (PCoA), principal components analysis (PCA), non-metric multidimensional scaling (NMDS), canonical correspondence analysis (CCA), and redundancy analysis (RDA).

[0016] In some embodiments, the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises calculating differential abundance of viral clusters in the first plurality of viral clusters and the second plurality of viral clusters.

[0017] In some embodiments, the healthy cohort and the cohort diagnosed with IBD are each human cohorts.

[0018] In some embodiments, the methods described above further comprise:

associating a first data subset of the second dataset with a first sub-cohort diagnosed with IBD and Crohn's disease (CD);

associating a second data subset of the second dataset with a second sub-cohort diagnosed with IBD and ulcerative colitis (UC);

associating a first subset of viral clusters of the second plurality of viral clusters with the first sub-cohort;

associating a second subset of viral clusters of the second plurality of viral clusters with the second sub-cohort; and

identifying a first subset of marker clusters of the plurality of marker clusters and a second subset of marker clusters of the plurality of marker clusters by comparing the first subset of viral clusters to the second subset of viral clusters.

[0019] In some embodiments, the above methods further comprise:

representing the viral genome sequences in the first dataset each respectively as a first viral contig of a protein sequence; and

representing the viral genome sequences in the second dataset each respectively as a second viral contig of a protein sequence.

[0020] In some embodiments, of the above methods,

the first dataset further represents a first plurality of identified viral genome sequences derived from the healthy cohort,

the second dataset further represents a second plurality of identified viral genome sequences derived from the cohort diagnosed with IBD, and

the method further comprises:

creating a first plurality of reference viral clusters using protein clustering to group like proteins and protein homology to group identified viral genome sequences of the first plurality of identified viral genome sequences;

creating a second plurality of reference viral clusters using protein clustering to group like proteins and protein homology to group identified viral genome sequences of the second plurality of identified viral genome sequences; and

wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters further comprises identifying the plurality of marker clusters by comparing a combination of the first plurality of viral clusters and the first plurality of reference viral clusters to a combination of the second plurality of viral clusters and the second plurality of reference viral clusters.

[0021] In some embodiments, of the above methods,

the first plurality of identified viral genome sequences are associated with a viral taxonomic category present in a viral genome database, and

the second plurality of identified viral genome sequences are associated with a viral taxonomic category present in a viral genome database.

[0022] In one aspect, a method for determining the presence of inflammatory bowel disease (IBD) in a subject is provided, the method comprising:

obtaining an individual viral dataset representing a plurality of viral genome sequences derived from a GI microbiota sample obtained from the subject;

creating a plurality of subject viral clusters using protein clustering to group like proteins derived from the individual viral dataset and by using protein homology to group unidentified viral genome sequences of the individual viral dataset, each viral cluster in the plurality of subject viral clusters comprising one or more viral genome sequences derived from the subject;

obtaining a plurality of marker clusters indicative of the presence or absence of IBD; and

comparing the plurality of subject viral clusters to the plurality of marker clusters.

[0023] In some embodiments, at least a portion of the plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database. In some embodiments, a totality of the plurality of viral genome sequences are each unassociated with a viral taxonomic category derived from a viral genome database. In some embodiments, at least a portion of the plurality of marker clusters are unassociated with a viral taxonomic category derived from a viral genome database.

[0024] In some embodiments, the above methods further comprise determining the presence of IBD in the subject based at least in part on the comparison of the plurality of subject viral clusters to the plurality of marker clusters. In some embodiments, the marker clusters comprise one or more viral clusters from taxa Siphoviridae, Myoviridae, Podoviridae, CrAss-like, or Microviridae. In some embodiments, the plurality of marker clusters comprises one or more viral clusters selected from vc2, vc6, vc7, vc13, vc14, vc15, vc17, vc19, vc21, vc22, vc23, vc24, vc25, vc28, vc29, vc36, vc37, vc38, vc39, vc40, vc42, vc45, vc48, vc53, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc75, vc76, vc77, vc78, vc79, vc80, vc82, vc84, vc85, vc86, vc88, vc89, vc91, vc92, vc94, vc95, vc96, vc97, vc98, vc99, vc101, vc102, vc103, vc104, vc108, vc109, vc112, vc113, vc115, vc117, vc118, vc122, vc123, vc124, vc130, vc132, vc136, vc138, vc142, vc143, vc152, vc154, vc155, vc160, vc161, vc175, vc178, vc181, vc190, vc193, vc205, vc209, vc216, vc218, vc225, vc232, vc263, vc264, vc281, vc284, vc298, vc320, vc411, vc413, vc420, vc456, and vc467. In some embodiments, an increased

abundance of one or more viral clusters selected from vc2, vc13, vc14, vc15, vc17, vc21, vc22, vc36, vc40, vc48, vc53, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc77, vc78, vc79, vc80, vc85, vc88, vc89, vc91, vc94, vc95, vc97, vc102, vc108, vc113, vc115, vc117, vc118, vc122, vc123, vc130, vc132, vc142, vc152, vc155, vc160, vc161, vc175, vc178, vc181, vc205, vc218, vc232, vc263, vc264, vc281, vc298, vc413, and vc420 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of IBD in the subject. In some embodiments, an increased abundance of one or more viral clusters selected from vc15, vc66, vc71, vc73, vc77, vc78, vc79, vc80, vc91, vc94, vc108, vc113, vc117, vc118, vc132, vc142, vc155, vc160, vc178, vc232, vc264, vc281, vc298, and vc420 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

[0025] In some embodiments, an increased abundance of one or more viral clusters selected from vc28 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject. In some embodiments, an increased abundance of one or more viral clusters selected from vc2, vc17, vc21, vc22, vc53, vc70, vc74, vc85, vc88, vc89, vc115, vc122, vc123, vc130, vc152, vc161, vc175, vc181, vc205, vc218, vc263, and vc413 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject. In some embodiments, an increased abundance of viral cluster vc2 in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject. In some embodiments, an increased abundance of one or more viral clusters selected from vc38, vc46, vc48, vc54, vc57, vc62, vc64, vc69, vc71, vc108, vc111, vc114, vc115, vc128, vc159, vc162, vc215, vc220, vc242, vc340, vc374, and vc392 in the subject sample as compared to a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject. In some embodiments, an increased abundance of one or more viral clusters selected from vc16, vc119, and vc163 in the subject sample as compared to a patient with a flare-up of ulcerative colitis (UC) is indicative of the presence of UC in remission in the subject.

[0026] In some embodiments, a decreased abundance of one or more viral clusters selected from vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216,

vc225, vc284, vc320, vc411, vc456, and vc467 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of IBD in the subject. In some embodiments, a decreased abundance of one or more viral clusters selected from vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject. In some embodiments, a decreased abundance of one or more viral clusters selected from vc7, vc25, vc47, and vc64 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject. In some embodiments, a decreased abundance of vc98 and/or vc103 viral cluster in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

[0027] In some embodiments, obtaining the dataset(s) is performed by sequencing VLP DNA isolated from GI microbiota sample(s).

[0028] In some embodiments, the method further comprises:

obtaining an individual bacteriome dataset representing bacterial sequences derived from the GI microbiota sample obtained from the subject; and

evaluating the individual bacteriome dataset for the presence of bacterial taxa associated with IBD.

[0029] In a specific embodiment, the method further comprises determining the presence of IBD in the subject based at least in part on the comparison of the individual bacteriome dataset to at least one of a healthy control and a control diagnosed with IBD.

[0030] In some embodiments, the bacterial taxa associated with IBD comprise one or more bacterial genera selected from *Clostridium XIVa*, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, *Flavonifractor*, *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Dorea*, *Roseburia*, *Odoribacter*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In a specific embodiment, an increased abundance of one or more bacterial genera selected from *Clostridium XIVa*, *Blautia*,

Veillonella, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, and *Flavonifractor* in the subject sample as compared to a healthy control is indicative of the presence of IBD in the subject. In a specific embodiment, an increased abundance of one or more bacterial genera selected from *Clostridium XIVa*, *Blautia*, *Megasphaera*, and *Fusobacterium* in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

[0031] In some embodiments, an increased abundance of one or more bacterial species selected from *Bacteroides fragilis* and *Ruminococcus gnavus* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject. In some embodiments, an increased abundance of *Ruminococcus gnavus* in the subject sample as compared to a control sample from a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject. In some embodiments, an increased abundance of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes* in the subject sample as compared to a control sample from a patient with a flare-up of ulcerative colitis (UC) in remission is indicative of the presence of UC in remission in the subject. In some embodiments, an increased abundance of bacterial genus *Flavonifractor* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

[0032] In some embodiments, a decreased abundance of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* in the subject sample as compared to a healthy control is indicative of the presence of IBD in the subject. In some embodiments, a decreased abundance of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject. In some embodiments, a decreased abundance of bacterial genus *Akkermansia* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject. In some embodiments, obtaining the individual bacteriome dataset is

performed by sequencing 16S rDNA or a V region of 16S rDNA in the GI microbiota sample.

In a specific embodiment, the V region is V4 region.

[0033] In some embodiments, the GI microbiota sample is a fecal sample. In some embodiments, the subject is human.

[0034] In various embodiments of the above methods, the method further comprises administering an IBD treatment to the subject. In various embodiments, the method further comprises administering to the subject additional diagnostic tests for IBD, CD and/or UC. In various embodiments, the method further comprises enrolling the subject in a clinical trial.

[0035] In various embodiments of the above methods, comparing the plurality of subject viral clusters to the plurality of marker clusters comprises:

- identifying common clusters present in the plurality of subject viral clusters and the plurality of marker clusters;

- determining relative abundance of members within each common cluster in the plurality of subject viral clusters;

- associating a correlation value with each common cluster in the plurality of marker clusters;
- and

- comparing the relative abundance of members within each common cluster in the plurality of subject viral clusters to the correlation value of each common cluster in the plurality of marker clusters.

[0036] In one aspect a kit is provided for determining the presence of inflammatory bowel disease (IBD) in a subject, the kit comprising:

- a device to:

- receive a first dataset representing a plurality of unidentified viral genome sequences derived from a GI microbiota sample obtained from the subject;

- receive a second dataset representing a plurality of viral genome IBD marker clusters;

- create a plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group unidentified viral genome sequences of the plurality of unidentified viral genome sequences, each viral cluster in the plurality of viral clusters comprising one or more unidentified viral genome sequences of the plurality of unidentified genome sequences; and

- compare the first plurality of viral clusters to the second dataset; and

determine the presence of IBD based at least in part on the comparison of the plurality of viral clusters to the second dataset.

[0037] In some embodiments, the device is further configured to:

receive a third dataset representing bacteria from the GI microbiota sample obtained from the subject;

evaluate the third dataset for the purpose of IBD diagnosis; and

determine the presence of IBD based at least in part on the evaluation of the third database.

[0038] In some embodiments of the above kits, the GI microbiota sample is one or more of group consisting a fecal sample, a cecal sample, an ileal sample, and a colonic microbiota sample. In some embodiments, the IBD is ulcerative colitis (UC). In some embodiments, the IBD is Crohn's disease (CD). In some embodiments, the subject is human.

[0039] In another aspect is provided a system comprising:

one or more processors;

a memory in communication with the one or more processors and storing instructions thereon that, when executed by the one or more processors, are configured to cause the system to:

receive a first dataset representing a first plurality of viral genome sequences derived from a healthy cohort;

receive a second dataset representing a second plurality of viral genome sequences derived from a cohort diagnosed with IBD;

create a first plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group viral genome sequences of the first dataset, each viral cluster in the first plurality of viral clusters comprising one or more viral genome sequences derived from the healthy cohort;

create a second plurality of viral clusters by using protein clustering to group like proteins derived from the second dataset and by using protein homology to group viral genome sequences of the second dataset, each viral cluster in the second plurality of viral clusters comprising one or more viral genome sequences derived from the cohort diagnosed with IBD; and

identify a plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters.

[0040] In one aspect a method is provided for preventing and/or treating inflammatory bowel disease (IBD) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467. In some embodiments, the method further comprises administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In a specific embodiment, the probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia*.

[0041] In another aspect a method is provided for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

[0042] In another aspect is provided a method for preventing and/or treating Crohn's disease (CD) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284. In some embodiments, the method further comprises administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Ruminococcus*,

Methanobrevibacter, Clostridium IV, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Bifidobacterium, Oscillibacter, Flavonifractor, Dorea, Roseburia, and Odoribacter or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In a specific embodiment, the probiotic composition comprises one or more bacterial strains from the genus selected from Ruminococcus, Methanobrevibacter, Clostridium IV, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Bifidobacterium, Oscillibacter, Flavonifractor, Dorea, Roseburia, and Odoribacter.

[0043] In another aspect is provided a method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

[0044] In another aspect is provided a for preventing and/or treating ulcerative colitis (UC) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster vc98 and/or vc103. In some embodiments, the method further comprises administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of the bacterial genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus. In a specific embodiment, the probiotic composition comprises one or more bacterial strains from the genus *Akkermansia*.

[0045] In another aspect is provided a method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

[0046] In another aspect is provided a method for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*,

Catenibacterium, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In a specific embodiment, the probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia*.

[0047] In another aspect is provided a method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In a specific embodiment, the probiotic composition comprises one or more bacterial strains from the genus selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter*.

[0048] In another aspect, a method is provided for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of the genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus. In a specific embodiment, the probiotic composition comprises one or more bacterial strains from the genus *Akkermansia*.

[0049] In some embodiments of the above aspects, the V region is V4 region.

[0050] In another aspect is provided a method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s)

stimulates growth and/or activity of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes*.

[0051] In another aspect a method is provided for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic comprising one or more of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes*.

[0052] In various embodiments of the above aspects, the subject is human.

BRIEF DESCRIPTION OF THE DRAWINGS

[0053] **Figures 1A-1D** demonstrate a comparison of commonality pre and post clustering of viral contigs. PCoA of Spearman distances using pre-clustering (viral contigs) (**Figure 1A**) and post-clustering viral cluster (VC) count tables (**Figure 1B**). **Figure 1C** shows the relative abundance of viral contigs (top) and VCs (bottom) for control subjects at varying thresholds of commonality across subjects. **Figure 1D** depicts the number of viral contigs/VCs shared between 30%, 50% and 70% of subjects in each cohort.

[0054] **Figures 2A-2D** show the virome composition comparison of the IBD cohorts to controls. **Figure 2A** depicts PCoA using Spearman distances. **Figure 2B** depicts alpha diversity (observed VCs) with p-values from wilcoxon tests. **Figure 2C** shows volcano plots of differential abundance results from DeSeq2 between controls and CD. **Figure 2D** shows volcano plots of differential abundance results from DeSeq2 between control and UC. All points above the dotted line are significant.

[0055] **Figures 3A-3D** show the bacterial compositional comparison of the IBD cohorts and controls. **Figure 3A** depicts PCoA using unweighted UniFrac distances. **Figure 3B** is a plot showing alpha diversity (Chao1 diversity) with p-values from wilcoxon tests. **Figure 3C** shows differential abundance results from DeSeq2 between controls and CD. **Figure 3D** shows differential abundance results from DeSeq2 between control and UC. All points above the dotted line are significant.

[0056] **Figures 4A-4B** show the drivers of PCoA separation for the virome (spearman distances; **Figure 4A**) and 16S unweighted UniFrac (**Figure 4B**). VC and RSV abundances were correlated, using spearman correlations, with PC axis 1 and 2. Only significant correlations with a rho of greater than 0.35 or -0.35 were graphed for the virome or $\pm .5$ for the 16S (or a

maximum of the top 6 for each quadrant). Grey arrows indicate unclassified VCs/RSVs. The length of the arrow represents the degree of correlation to the PC axes.

[0057] **Figures 5A-5F** demonstrate the investigation of differences in viromes and 16S between subjects in UC flare and UC remission. Beta diversity for viromes (using Spearman distances; **Figure 5A**) and 16S (unweighted UniFrac; **Figure 5B**) are shown. VCs and RSV abundance were correlated with PC axis 1 and 2. Only significant correlations with a rho of greater than ± 0.35 were graphed for the virome or $\pm .5$ (or top 6 for each quadrant) for the 16S. Grey arrows indicate unclassified VCs/RSVs. The length of the arrow represents the degree of correlation to the PC axes. Alpha diversity is shown in **Figure 5C** for VC (Observed VCs and Shannon), and in **Figure 5D** for 16S (Chao1 and Shannon diversity), differential abundance results using DeSeq2 between UU flare are shown in **Figure 5E**, along with remission for VCs (**Figure 5E**) and 16S (**Figure 5F**). All points above the dotted line are significant.

[0058] **Figures 6A-6D** show the classification between healthy controls and patients with IBD using VC and 16S composition. The top 20 importance factors are shown for each models for VCs (**Figure 6A**), 16S (**Figure 6B**), VCs and 16S combined (**Figure 6C**). The shades of grey of the bars correspond to differential abundance between groups; text to the right of the bar are the classifications and/or the bacterial annotation to CRISPR protospacers. **Figure 6D** shows the ROC curve analysis for each of the 3 models including the % accuracy.

[0059] **Figure 7A** depicts a VC PCoA using Spearman distances comparing the 3 cohorts CD, UC and controls. **Figure 7B** shows distances between points in each cohort for the VC spearman PCoA. **Figure 7C** shows 16S PCoA using unweighted UniFrac distances comparing the 3 cohorts. **Figure 7D** is a boxplot showing distances between points in each cohort for the 16S unweighted UniFrac PCoA. P-values for boxplots are from wilcoxon tests.

[0060] **Figures 8A-8F** show the alpha diversity of patients with IBD versus healthy controls. Shown are Observed VCs (**Figure 8A**), Shannon diversity of VCs (**Figure 8B**), Chao1 diversity of 16S counts (**Figure 8C**), and Shannon diversity of 16S counts (**Figure 8D**). P-values for boxplots are from wilcoxon tests. **Figure 8E** shows Spearman correlations between observed VC counts and observed bacterial species counts. **Figure 8F** shows Shannon diversity of VCs and 16S counts.

[0061] **Figures 9A-9B** show the alpha diversity of observed VLPs for any VCs classified as Caudovirales tested for disease groups and controls (**Figure 9A**) and disease groups/states and controls (**Figure 9B**). P-values for boxplots are from wilcoxon tests.

[0062] **Figures 10A-10B** show the read alignment for samples in each cohort to VCs classified as lysogenic (**Figure 10A**) and non-lysogenic (**Figure 10B**). P-values for boxplots are from wilcoxon tests.

[0063] **Figure 11** depicts a Procrustes plot of the Virome PCoA using Spearman distances and the 16S PCoA with unweighted UniFrac. Lines connect samples from the same subject.

[0064] **Figure 12** depicts a Procrustes plot of the Virome PCoA using Spearman distances and the 16S PCoA with unweighted UniFrac. Lines connect samples from the same subject.

[0065] **Figure 13A** shows the Spearman correlation between estimated viral load and observed VCs. **Figure 13B** shows viral load plotted per subject with points colored using various intensities of grey by disease status

[0066] **Figure 14** depicts a network plot of CRISPR protospacers to the 20 most relevant VCs (10 key and additional important VCs from machine learning). Clusters and CRISPR protospacers are colored using various intensities of grey according to differential abundance using DeSeq2.

[0067] **Figures 15A-15J** show images of the 10 key drivers in the separation of IBD and controls. Annotations are using pVOGs.

[0068] **Figure 16** is a block diagram illustrating a system or device for identifying virome marker clusters according to aspects of the present invention.

[0069] **Figure 17** is a block diagram illustrating a system or device for detecting health or disease in a subject based at least in part on virome marker clusters according to aspects of the present invention.

DETAILED DESCRIPTION

[0070] It is an object of the present invention to meet the above-stated needs. Generally, this disclosure provides a framework for analyzing viromes across cohorts and demonstrates the presence of significant IBD signals in the virome, which could have value in the development of biomarkers and therapeutics into the future.

[0071] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0072] As used herein, the term “bacteria” encompasses both prokaryotic organisms and archaea present in mammalian microbiota.

[0073] The term “microbiota” is used herein to refer to microorganisms (e.g., bacteria, archaea, fungi, protozoa) and viruses (e.g., phages and eukaryotic viruses) present in a host animal or human (e.g., in the gastrointestinal tract, skin, oral cavity, vagina, etc.). Microbiota exerts a significant influence on health and well-being of the host. Viruses present in microbiota are separately described as “virobiota”. The term “microbiome” refers to the collective genes of all organisms comprising the microbiota.

[0074] The term “virome” is used herein to refer to include viruses, virus-like particles (VLPs), and molecules that closely resemble viruses but may or may not be infectious and may or may not include viral genetic material. The “virome” can include the “virobiota” but is not limited to the “virobiota”.

[0075] A “microbiota sample” it is meant a sample that contains a microbiota from a particular source. A “GI microbiota sample” is from the gastro-intestinal tract, and may include a fecal microbiota sample. Microbiota samples may comprise all of the components present in the microbiota.

[0076] The term “gastrointestinal (GI) microbiota” is used to refer to microorganisms (e.g., bacteria, fungi, unicellular parasites) and viruses (e.g., phages and eukaryotic viruses) in the digestive tract.

[0077] As used herein, the term “dysbiosis” refers to a microbial imbalance on or inside the body. Dysbiosis can result from, e.g., antibiotic exposure as well as other causes, e.g., infections with pathogens including viruses, bacteria and eukaryotic parasites. Dysbiosis can also result from unknown causes, or causes that are not yet known. The term “consequences of dysbiosis” refers to various disorders associates with dysbiosis. For example, dysbiosis in the GI tract has been reported to be associated with a wide variety of illnesses, such as, e.g., irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), chronic fatigue syndrome, obesity, rheumatoid arthritis, ankylosing spondylitis, bacterial vaginosis, colitis, small intestinal cancer, colorectal cancer, metabolic syndrome, cardiovascular disease, Crohn's disease, infectious

gastroenteritis, non-infectious gastroenteritis, food allergy, Celiac disease, gastrointestinal graft versus host disease, pouchitis, intestinal failure, short bowel syndrome, antibiotics-associated diarrhea, etc.

[0078] The term “restoring normal microbiota” is used herein to refer to restoring microbiota of a subject to the level of bioactivity and diversity of corresponding microbiota of a healthy subject. This may also be considered as normalizing the microbiota, populating the microbiota, populating normal microbiota, preventing the onset of dysbiosis, or augmenting the growth of at least one type of virus in a subject.

[0079] Specific changes in microbiota discussed herein can be detected using various methods, including without limitation quantitative PCR (qPCR) or high-throughput sequencing methods which detect over- and under-represented genes in the total bacterial population (e.g., 454-sequencing for community analysis; screening of microbial 16S ribosomal RNAs (16S rRNA), etc.), or transcriptomic or proteomic studies that identify lost or gained microbial transcripts or proteins within total bacterial populations. See, e.g., U.S. Patent Publication No. 2010/0074872; Eckburg et al., *Science*, 2005, 308:1635-8; Costello et al., *Science*, 2009, 326:1694-7; Grice et al., *Science*, 2009, 324:1190-2; Li et al., *Nature*, 2010, 464: 59-65; Bjursell et al., *Journal of Biological Chemistry*, 2006, 281:36269-36279; Mahowald et al., *PNAS*, 2009, 14:5859-5864; Wikoff et al., *PNAS*, 2009, 10:3698-3703.

[0080] Various exemplary ways of amplifying and sequencing of nucleic acids from microbiota samples includes, but is not limited to: solid-phase PCR involving bridge amplification of DNA fragments of the biological samples on a substrate with oligo adapters, wherein amplification involves primers having a forward index sequence (e.g., Illumina forward index for MiSeq/NextSeq/HiSeq platforms) or a reverse index sequence (e.g., Illumina reverse index for MiSeq/NextSeq/HiSeq platforms), a forward barcode sequence or a reverse barcode sequence, a transposase sequence (e.g., corresponding to a transposase binding site for MiSeq/NextSeq/HiSeq platforms), a linker, an additional random base, and a sequence for targeting a specific target region (e.g., 16S region, 18S region, ITS region). Illumina sequencing (e.g., with a HiSeq platform, with a MiSeq platform, with a NextSeq platform, etc.) may be used as part of a sequencing-by-synthesis technique.

[0081] As used herein, the terms “a microbiota disease” and “disease of a microbiota” refer to a change in the composition of a microbiota, including without limitation very small changes in a

relative abundance of one or more organisms within the microbiota as compared to a healthy control. Microbiota diseases can result from, e.g., infections with pathogens including viruses, bacteria and eukaryotic parasites, antibiotic exposure as well as other causes. Exemplary microbiota diseases in the GI tract include, but are not limited to, irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), chronic fatigue syndrome, obesity, rheumatoid arthritis, ankylosing spondylitis, colitis, small intestinal cancer, colorectal cancer, metabolic syndrome, cardiovascular disease, Crohn's disease, gastroenteritis, food allergy, Celiac disease, gastrointestinal graft versus host disease, pouchitis, intestinal failure, short bowel syndrome, diarrhea, etc.

[0082] As used herein, the term “probiotic” refers to a substantially pure bacteria (i.e., a single isolate, of, e.g., live bacterial cells, conditionally lethal bacterial cells, inactivated bacterial cells, killed bacterial cells, spores, recombinant carrier strains), or a mixture of desired bacteria, bacteria components or bacterial extract, or bacterially-derived products (natural or synthetic bacterially-derived products such as, e.g., bacterial antigens or metabolic products) and may also include any additional components that can be administered to a mammal. Such compositions are also referred to herein as a “bacterial inoculant.”

[0083] As used herein, the term “prebiotic” refers to an agent that increases the number and/or activity of one or more desired bacteria, enhancing their growth. Non-limiting examples of prebiotics useful in the methods of the present disclosure include fructooligosaccharides (e.g., oligofructose, inulin, inulin-type fructans), galactooligosaccharides, human milk oligosaccharides (HMO), Lacto-N-neotetraose, D-Tagatose, xylo-oligosaccharides (XOS), arabinoxylan-oligosaccharides (AXOS), N-acetylglucosamine, N-acetylgalactosamine, glucose, other five- and six-carbon sugars (such as arabinose, maltose, lactose, sucrose, cellobiose, etc.), amino acids, alcohols, resistant starch (RS), and mixtures thereof. See, e.g., Ramirez-Farias et al., *Br J Nutr* (2008) 4:1-10; Pool-Zobel and Sauer, *J Nutr* (2007), 137:2580S-2584S. The prebiotic may be effective to fully, or partially, restore normal microbiota.

[0084] As used herein, the term “viral cluster” or “VC” refers to a set of contigs that fit certain criteria described herein, which are in turn grouped together based on protein homology profiles.

[0085] As used herein, the term “stimulate” when used in connection with growth and/or activity of bacteria encompasses the term “enhance”.

[0086] The terms “treat” or “treatment” of a state, disorder or condition include: (1) preventing, delaying, or reducing the incidence and/or likelihood of the appearance of at least one clinical or sub-clinical symptom of the state, disorder or condition developing in a subject that may be afflicted with or predisposed to the state, disorder or condition but does not yet experience or display clinical or subclinical symptoms of the state, disorder or condition; or (2) inhibiting the state, disorder or condition, i.e., arresting, reducing or delaying the development of the disease or a relapse thereof (in case of maintenance treatment) or at least one clinical or sub-clinical symptom thereof; or (3) relieving the disease, i.e., causing regression of the state, disorder or condition or at least one of its clinical or sub-clinical symptoms. The benefit to a subject to be treated is either statistically significant or at least perceptible to the patient or to the physician.

[0087] The terms “patient”, “individual”, “subject”, “mammal”, and “animal” are used interchangeably herein and refer to mammals, including, without limitation, human and veterinary animals (e.g., cats, dogs, cows, horses, sheep, pigs, etc.) and experimental animal models. In a preferred embodiment, the subject is a human.

[0088] As used herein, the term “therapeutically effective amount” refers to the amount of a compound, composition, particle, organism (e.g., a probiotic or a microbiota transplant), etc. that, when administered to a subject for treating (e.g., preventing or ameliorating) a state, disorder or condition, is sufficient to effect such treatment. The “therapeutically effective amount” will vary depending, e.g., on the agent being administered as well as the disease severity, age, weight, and physical conditions and responsiveness of the subject to be treated. The terms “therapeutically effective amount” and “effective amount” are used interchangeably.

[0089] As used herein, the term “acceptable” with reference to excipients, diluents, and carriers refers to molecular entities and compositions that are generally regarded as physiologically tolerable.

[0090] The term “carrier” refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water or aqueous solution saline solutions and aqueous dextrose and glycerol solutions are preferably employed as carriers, particularly for injectable solutions. Alternatively, the carrier can be a solid dosage form carrier, including but

not limited to one or more of a binder (for compressed pills), a glidant, an encapsulating agent, a flavorant, and a colorant. Suitable pharmaceutical carriers are described in “Remington’s Pharmaceutical Sciences” by E.W. Martin.

[0091] The term “about” or “approximately” means within a statistically meaningful range of a value. Such a range can be within an order of magnitude, preferably within 50%, more preferably within 20%, still more preferably within 10%, and even more preferably within 5% of a given value or range. The allowable variation encompassed by the term “about” or “approximately” depends on the particular system under study, and can be readily appreciated by one of ordinary skill in the art.

[0092] The terms “a,” “an,” and “the” do not denote a limitation of quantity, but rather denote the presence of “at least one” of the referenced item.

[0093] The practice of the present invention employs, unless otherwise indicated, conventional techniques of statistical analysis, molecular biology (including recombinant techniques), microbiology, cell biology, and biochemistry, which are within the skill of the art. Such tools and techniques are described in detail in e.g., Sambrook et al. (2001) *Molecular Cloning: A Laboratory Manual*. 3rd ed. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York; Ausubel et al. eds. (2005) *Current Protocols in Molecular Biology*. John Wiley and Sons, Inc.: Hoboken, NJ; Bonifacino et al. eds. (2005) *Current Protocols in Cell Biology*. John Wiley and Sons, Inc.: Hoboken, NJ; Coligan et al. eds. (2005) *Current Protocols in Immunology*, John Wiley and Sons, Inc.: Hoboken, NJ; Coico et al. eds. (2005) *Current Protocols in Microbiology*, John Wiley and Sons, Inc.: Hoboken, NJ; Coligan et al. eds. (2005) *Current Protocols in Protein Science*, John Wiley and Sons, Inc.: Hoboken, NJ; and Enna et al. eds. (2005) *Current Protocols in Pharmacology*, John Wiley and Sons, Inc.: Hoboken, NJ. Additional techniques are explained, e.g., in U.S. Patent No. 7,912,698 and U.S. Patent Appl. Pub. Nos. 2011/0202322 and 2011/0307437.

[0094] The term “computing system” is intended to include stand alone machines or devices and/or a combination of machines, components, modules, systems, servers, processors, memory, detectors, user interfaces, computing device interfaces, network interfaces, hardware elements, software elements, firmware elements, and other computer-related units. By way of example, but not limitation, a computing system can include one or more of a general-purpose computer, a special-purpose computer, a processor, a portable electronic device, a portable electronic medical

instrument, a stationary or semi-stationary electronic medical instrument, or other electronic data processing apparatus.

[0095] The term “database” as referred to herein is intended to include a collection of indexed data stored on a computer readable medium. By way of example and not limitation, data in the database can include numerical values, textual values, computational representation of physical objects (including living, non-living, organic, non-organic objects, and combinations thereof), computational representation of physical phenomena, categorical classification. Various data can be linked together or otherwise indexed. By way of example and not limitation, data in the database can be represented as an indexed matrix.

[0096] The term “dataset” as referred to herein is intended to include information that can be provided to a computing system in a computer readable format.

[0097] The terms “component,” “module,” “system,” “server,” “processor,” “memory,” and the like are intended to include one or more computer-related units, such as but not limited to hardware, firmware, a combination of hardware and software, software, or software in execution. For example, a component may be, but is not limited to being, a process running on a processor, an object, an executable, a thread of execution, a program, and/or a computer. By way of illustration, both an application running on a computing device and the computing device can be a component. One or more components can reside within a process and/or thread of execution and a component may be localized on one computer and/or distributed between two or more computers. In addition, these components can execute from various computer readable media having various data structures stored thereon. The components may communicate by way of local and/or remote processes such as in accordance with a signal having one or more data packets, such as data from one component interacting with another component in a local system, distributed system, and/or across a network such as the Internet with other systems by way of the signal.

[0098] Some implementations of the disclosed technology will be described more fully with reference to the accompanying drawings. This disclosed technology may, however, be embodied in many different forms and should not be construed as limited to the implementations set forth herein. The components described hereinafter as making up various elements of the disclosed technology are intended to be illustrative and not restrictive.

[0099] It is also to be understood that the mention of one or more method steps does not preclude the presence of additional method steps or intervening method steps between those steps expressly identified. Similarly, it is also to be understood that the mention of one or more components in a device or system does not preclude the presence of additional components or intervening components between those components expressly identified.

[00100] Certain embodiments and implementations of the disclosed technology are described above with reference to block and flow diagrams of systems and methods and/or computer program products according to example embodiments or implementations of the disclosed technology. It will be understood that one or more blocks of the block diagrams and flow diagrams, and combinations of blocks in the block diagrams and flow diagrams, respectively, can be implemented by computer-executable program instructions. Likewise, some blocks of the block diagrams and flow diagrams may not necessarily need to be performed in the order presented, may be repeated, or may not necessarily need to be performed at all, according to some embodiments or implementations of the disclosed technology.

[00101] These computer-executable program instructions may be loaded onto a computing system such as a general-purpose computer, a special-purpose computer, a processor, or other programmable data processing apparatus to produce a machine, such that the instructions that execute on the computer, processor, or other programmable data processing apparatus create means for implementing one or more functions specified in the flow diagram block or blocks. These computer program instructions may also be stored in a computer-readable memory that can direct a computer or other programmable data processing apparatus to function in a manner, such that the instructions stored in the computer-readable memory produce an article of manufacture including instruction means that implement one or more functions specified in the flow diagram block or blocks.

[00102] As an example, embodiments or implementations of the disclosed technology may provide for a computer program product, including a computer-usable medium having a computer-readable program code or program instructions embodied therein, said computer-readable program code adapted to be executed to implement one or more functions specified in the flow diagram block or blocks. Likewise, the computer program instructions may be loaded onto a computer or other programmable data processing apparatus to cause a series of operational elements or steps to be performed on the computer or other programmable apparatus

to produce a computer-implemented process such that the instructions that execute on the computer or other programmable apparatus provide elements or steps for implementing the functions specified in the flow diagram block or blocks.

[00103] Accordingly, blocks of the block diagrams and flow diagrams support combinations of means for performing the specified functions, combinations of elements or steps for performing the specified functions, and program instruction means for performing the specified functions. It will also be understood that each block of the block diagrams and flow diagrams, and combinations of blocks in the block diagrams and flow diagrams, can be implemented by special-purpose, hardware-based computer systems that perform the specified functions, elements or steps, or combinations of special-purpose hardware and computer instructions.

[00104] In some embodiments presented herein, IBD markers can be identified using unidentified viral genome sequences derived from a cohort of healthy subjects and a cohort of subjects diagnosed with IBD. Individuals in each cohort can be human. The viral genome sequences can be unidentified in that they are not taxonomically classified in a viral genome database. The viral genome sequences can be unidentified in that they are considered “viral dark matter” as described herein and would otherwise be understood by a person of ordinary skill in the art. The viral genome sequences can be unidentified at the order level, at the family level, strain level, or any intervening level. The viral genome sequences can be unidentified in that they are classified taxonomically, at some level, in a viral genome database, however, the viral genome sequences have not been compared to the classification database. Viral genome sequences can include sequenced VLPs, molecules that closely resemble viruses, but are non-infectious because they contain no viral genetic material. Viral genome sequences can be derived from gastrointestinal (GI) microbiota samples provided from individuals in each cohort. Metagenomic assembly can be performed on the samples using short reads to resolve viral genomes. The reads can subsequently be aligned to determine abundance, or count of members in each viral genome. The resolved viral genomes can include unidentified viral genome sequences. To the extent that resolved viral genomes can be identified, the IBD markers can also be identified using the identified viral genomes.

[00105] In some embodiments of the various methods presented herein, IBD markers can be identified using unidentified viral genome sequences derived from a cohort of healthy subjects and a cohort of subjects diagnosed with IBD. Protein clustering and protein homology can be

performed on the whole virome, including the unidentified viral genome sequences, from each cohort, resulting in viral clusters. A viral cluster can each include one or more unidentified viral genome sequences. The viral clusters can each respectively be associated with the cohort of healthy subjects, the cohort of subjects diagnosed with IBD, or both cohorts. IBD markers can be identified by comparing viral clusters associated with the healthy cohort to viral clusters associated with the cohort diagnosed with IBD. The IBD markers can thereby be identified without relying on categorization of viral genome sequences in a database. In some embodiments, viral clusters associated with IBD can further be associated with one or both of a sub-cohort diagnosed with Crohn's disease (CD) and a sub-cohort diagnosed with ulcerative colitis (UC).

[00106] The viral genome sequences can be represented as datasets that are readable by a computational device or system. For instance, the viral genome sequences can be represented as viral contigs. Each viral genome sequence can be represented in whole or in part. Each viral genome sequence can be represented with resolution at the strain level.

[00107] Each dataset can be associated with a cohort and/or sub-cohort. The datasets collectively can include a significant number of viral genome sequence reads within the GI microbiota samples provided from the individuals. In some embodiments, the dataset is performed by sequencing VLP DNA isolated from GI microbiota sample(s). The VLP DNA may be isolated from GI microbiota samples and prepared by any of the various methods of preparing DNA known in the art, such as those described in Thurber R.V. et al., 2009, Laboratory procedures to generate viral metagenomes. *Nat Protoc* 4:470–483; Reyes, A., et al., 2010, Viruses in the faecal microbiota of monozygotic twins and their mothers. *Nature* 466:334–338; and Minot S. et al., 2011, The human gut virome: inter-individual variation and dynamic response to diet. *Genome Res* 21:1616–1625, each of which is incorporated by reference herein in its entirety. The datasets collectively can include a number of viral genome sequence reads within the GI microbiota samples. The reads per sample can include the ranges of 15% to 97%, 25% to 97%, 50% to 97%, 60% to 97%, 70% to 97%, 80% to 97%, and 90% to 97%.

[00108] The viral genome sequences can be represented as protein sequences. Alternatively, the viral genome sequences can be represented as a sequence from which protein sequences or protein content can be derived (e.g. genetic sequence).

[00109] Protein clustering and protein homology can be performed on the whole virome, including the unidentified viral genome sequences, from each cohort, resulting in viral clusters. To the extent that the whole virome includes identified viral genome sequences, the identified viral genome sequences can be included in the protein clustering and protein homology analysis. Proteins can be derived from each dataset based on the viral genome sequences. The proteins can be organized into protein clusters (PCs) using Markov cluster (MCL)-based protein families, transitive clustering (TransClust), spectral clustering of protein sequences (SCPS), High-Fidelity clustering of protein sequences (HiFix) or other appropriate technique. Additional clustering techniques are described in Bernardes et al., BMC Bioinformatics (2015) 16:34 “Evaluation and improvements of clustering algorithms for detecting remote homologous protein families”, incorporated by reference herein.

[00110] To determine protein homology viral genome sequences, or protein sequences derived therefrom can be evaluated pairwise such that each pair is given a similarity score based on the shared protein content between the sequences within the pair. Viral clusters can be determined based on the similarity scores.

[00111] A viral cluster can include one or more unidentified viral genome sequences. A viral cluster can be completely populated by unidentified viral genome sequences. A viral cluster can be unassociated with a known taxon. A viral cluster can represent an unidentified taxon of higher rank than a strain and of lower rank than a family.

[00112] The viral clusters can each respectively be associated with the cohort of healthy subjects, the cohort of subjects diagnosed with IBD, or both cohorts. Or, said another way, a collection of viral clusters associated with the healthy cohort can be created such that each viral cluster in the collection includes at least one viral genome derived from the healthy cohort, and another collection of viral clusters associated with the cohort diagnosed with IBD can be created such that this collection of viral clusters includes at least one viral genome derived from the cohort diagnosed with IBD.

[00113] IBD markers can be identified by comparing viral clusters associated with the healthy cohort to viral clusters associated with the cohort diagnosed with IBD. The IBD markers can thereby be identified without relying on categorization of viral genome sequences in a database.

[00114] Viral clusters associated with IBD can further be associated with one or both of a sub-cohort diagnosed with Crohn's disease (CD) and a sub-cohort diagnosed with ulcerative colitis (UC).

[00115] IBD markers can be defined as a viral cluster that is prevalent in at least one cohort and/or sub-cohort and minimal or absent in at least one other cohort or sub-cohort. In other words, the IBD markers can include viral clusters that are found predominantly in the healthy cohort and not in the IBD cohort and viral clusters that are found predominantly in the IBD cohort and not in the healthy cohort.

[00116] When the IBD cohort is further sub-divided into CD and UC, the IBD markers can include viral clusters that are found predominantly in the CD cohort and not the UC cohort and vice-versa, regardless of whether the same viral clusters are predominant in both the healthy and IBD cohorts. IBD marker clusters can be identified by comparing the viral clusters associated with the CD sub-cohort to the UC sub-cohort. Within the total collection of IBD marker clusters, the IBD marker clusters can include a first subset of IBD marker clusters that are viral clusters more prevalently found in subjects diagnosed with CD compared to UC and a second subset of IBD marker clusters that are viral clusters more prevalently found in subjects diagnosed with UC compared to CD.

[00117] The IBD markers can include viral clusters that contain no identified viral sequences. An IBD marker can be unassociated with a known taxon. An IBD marker cluster can represent an unidentified taxon of higher rank than a strain and of lower rank than a family.

[00118] To the extent that the whole virome includes identified viral genome sequences, the identified viral genome sequences can be included in the protein clustering and protein homology analysis. A viral cluster including an identified viral genome sequence can represent an unidentified taxon of higher rank than a strain and of lower rank than a family. A viral cluster including an identified viral genome sequence can be associated with one or more cohorts and/or sub-cohorts. Identified viral genome sequences can be clustered by protein clustering and protein homology to create reference viral clusters. Reference viral clusters can be associated with one or more cohorts and/or sub-cohorts. Identification of IBD marker clusters can include comparing reference viral clusters associated with the healthy cohort to reference viral clusters associated with the cohort diagnosed with IBD. Similarly, IBD marker clusters can include comparing reference viral clusters associated with CD with reference viral clusters associated with UC.

[00119] To the extent that the whole virome includes identified viral genome sequences, the IBD markers can include viral clusters that contain at least one identified viral sequence. An IBD marker cluster containing an identified viral sequence can include an unidentified grouping of viral sequences. An IBD marker cluster can be an unidentified grouping of viral sequences, optionally comprising an identified viral sequence. An IBD marker cluster containing an identified viral sequence can represent an identified taxon.

[00120] Identification of the IBD markers as described above can be performed on a computing system having one or more processors and a memory with instructions thereon that can be performed by the processor(s). The computing system can receive datasets associated with each cohort and/or sub-cohort that each respectively include unidentified viral genome sequences. The viral genome sequences can be represented as a viral contig or other suitable computer-readable format. The computing system can create viral clusters for each dataset associated with each cohort and/or sub-cohort. Clustering can use a protein clustering algorithm to group like proteins and a protein homology algorithm to group viral genome sequences, including unidentified viral genome sequences, into viral clusters. Viral clusters can be compared across cohorts and/or sub-cohorts to identify marker clusters. Marker clusters can represent clusters highly represented in at least one cohort and/or sub-cohort that is also marginally represented in at least one other cohort and/or sub-cohort.

[00121] Identification of the marker clusters can be performed using machine learning. The datasets can include an association for each viral cluster to a known variable, the known variable being the health state of the patient (healthy, IBD diagnosis, and optionally CD diagnosis and/or UC diagnosis). For each health state, the system can determine a correlated set of viral clusters from the total set of viral clusters. Viral clusters having a strong correlation to the presence or absence of a given health state can be identified as viral clusters.

[00122] Identification of the marker clusters can be performed using a beta diversity analysis on the viral clusters. A count table can be created by summing the counts of the viral genomic sequences (potentially represented as viral contigs) in each viral cluster. The count table can be subjected to an ordination method to determine beta diversity. The beta diversity analysis can be performed through principal coordinates analysis (PCoA), principal components analysis (PCA), non-metric multidimensional scaling (NMDS), canonical correspondence analysis (CCA), redundancy analysis (RDA), and/or other suitable technique.

[00123] Identification of the marker clusters can be performed using a calculation of differential abundance of viral clusters across cohorts and/or sub-cohorts. The calculation can be executed using a test or software package such as available through DESeq2, t-test, Wilcoxon rank-sum test, edgeR package, metagenomieSeq package, ANCOM package, and/or other suitable technique, algorithm, or software package.

[00124] Figure 16 is block diagram illustrating an example system 100 for identifying IBD marker clusters. The system 100 can include a non-transient memory 120 with executable instructions thereon to perform methods for identifying IBD marker clusters as described herein, a processor 130 in communication with the memory 120 capable of receiving and executing the instructions from the memory 120, to identify IBD marker clusters, and an output interface 140 capable of outputting a representation of the IBD marker clusters identified by the processor 130. The system can be in communication with a data store 110 on which cohort datasets are stored. The processor 130 can be configured to receive the datasets from the datastore 110, receive instructions from the memory 120, compute IBD marker clusters by performing operations on the datasets according to the executable instructions, and provide a representation of the IBD marker clusters to the output interface 140. The representation of the IBD marker clusters can be a computer-readable representation and/or a human user interface. Preferably, output interface 140 can provide a means for conveying a computer readable representation of the IBD marker clusters to a digital storage medium such that the IBD marker clusters can be accessed by an IBD diagnosis device such as an example IBD diagnosis device as described herein. The system 100 can be contained within a singular device, potentially even a singular semiconductor chip (e.g. system on a chip), or can be distributed across multiple devices at multiple geographical locations as would be understood by a person of ordinary skill in the art. For instance, the data store 110 can be provided by a data server at a location remote to the processor 130 via a network (e.g. internet), and the processor 130 can be located on a computing device remote from the memory 120 and the executable instructions can be transmitted from through a network (e.g. internet) to the processor.

[00125] In various embodiments, a subject can be diagnosed with IBD by analyzing unidentified viral genome sequences derived from the subject. Viral genome sequences can be obtained from the subject through a fecal sample or other means. The viral genome sequences can be derived from a GI microbiota sample obtained from the subject. The viral genome

sequences can include unidentified viral genome sequences. The viral genome sequences can be represented as a subject dataset. The subject dataset can be in a computer readable format. The analysis can include clustering the viral genome sequences from the subject, including the unidentified viral genome sequences obtained from the patient. Clustering of the subject's viral genome sequences can be carried out similar to as described above. The collection of viral clusters created based on the subject's viral genome sequences can be compared to IBD markers. The IBD markers can be identified through analysis of a healthy cohort and a cohort diagnosed with IBD similar to as described above. The subject can be diagnosed with IBD based on analysis and comparison of viral genome sequences alone. Alternatively, bacteria derived from the subject can be analyzed for the purpose of IBD diagnosis of the subject and analysis of the viral genome sequences can be performed in conjunction such that the combination of bacterial and viral analysis can be used to diagnose the subject with IBD.

[00126] The marker clusters may comprise one or more viral clusters from taxa *Siphoviridae*, *Myoviridae*, *Podoviridae*, CrAss-like, or *Microviridae*. The marker clusters may comprise viral clusters from *Siphoviridae*. The marker clusters may comprise viral clusters from *Myoviridae*. The marker clusters may comprise viral clusters from *Podoviridae*. The marker clusters may comprise CrAss-like viral clusters. The marker clusters may comprise viral clusters from *Microviridae*.

[00127] The marker clusters may comprise one or more of the following exemplary viral clusters: vc2, vc6, vc7, vc13, vc14, vc15, vc17, vc19, vc21, vc22, vc23, vc24, vc25, vc28, vc29, vc36, vc37, vc38, vc39, vc40, vc42, vc45, vc48, vc53, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc75, vc76, vc77, vc78, vc79, vc80, vc82, vc84, vc85, vc86, vc88, vc89, vc91, vc92, vc94, vc95, vc96, vc97, vc98, vc99, vc101, vc102, vc103, vc104, vc108, vc109, vc112, vc113, vc115, vc117, vc118, vc122, vc123, vc124, vc130, vc132, vc136, vc138, vc142, vc143, vc152, vc154, vc155, vc160, vc161, vc175, vc178, vc181, vc190, vc193, vc205, vc209, vc216, vc218, vc225, vc232, vc263, vc264, vc281, vc284, vc298, vc320, vc411, vc413, vc420, vc456, and vc467. Alternatively, vc5, vc9, vc10 may be used as marker clusters.

[00128] In various embodiments, an increased abundance of one or more of the following marker clusters in the subject sample, as compared to that of a sample from a healthy patient or control, is indicative of the presence of IBD in the subject: vc2, vc13, vc14, vc15, vc17, vc21, vc22, vc36, vc40, vc48, vc53, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc77, vc78, vc79, vc80,

vc85, vc88, vc89, vc91, vc94, vc95, vc97, vc102, vc108, vc113, vc115, vc117, vc118, vc122, vc123, vc130, vc132, vc142, vc152, vc155, vc160, vc161, vc175, vc178, vc181, vc205, vc218, vc232, vc263, vc264, vc281, vc298, vc413, and vc420. The abundance may be increased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00129] In various embodiments, an increased abundance of one or more of the following marker clusters in the subject sample, as compared to that of a sample from a healthy patient or control, is indicative of the presence of Crohn's Disease (CD) in the subject: vc15, vc66, vc71, vc73, vc77, vc78, vc79, vc80, vc91, vc94, vc108, vc113, vc117, vc118, vc132, vc142, vc155, vc160, vc178, vc232, vc264, vc281, vc298, and vc420. In some embodiments, an increased abundance of one or more viral clusters selected from vc28 in the subject sample as compared to a healthy control is indicative of the presence of CD in the subject. In these embodiments, the abundance may be increased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00130] In various embodiments, an increased abundance of one or more of the following marker clusters in the subject sample, as compared to that of a sample from a healthy patient or control, is indicative of the presence of ulcerative colitis (UC) in the subject: vc2, vc17, vc21, vc22, vc53, vc70, vc74, vc85, vc88, vc89, vc115, vc122, vc123, vc130, vc152, vc161, vc175, vc181, vc205, vc218, vc263, and vc413. In some embodiments, an increased abundance of viral cluster vc2 in the subject sample as compared to a healthy control is indicative of the presence of UC in the subject. In some embodiments, an increased abundance of one or more viral clusters selected from vc38 vc46, vc48, vc54, vc57, vc62, vc64, vc69, vc71, vc108, vc111, vc114, vc115, vc128, vc159, vc162, vc215, vc220, vc242, vc340, vc374, and vc392 in the subject sample as compared to a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject. In some embodiments, an increased abundance of one or more viral clusters selected from vc16, vc119, and vc163 in the subject sample as compared to a

patient with a flare-up of ulcerative colitis (UC) is indicative of the presence of UC in remission in the subject. In these embodiments, the abundance may be increased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00131] In various embodiments, a decreased abundance of one or more of the following marker clusters in the subject sample, as compared to that of a sample from a healthy patient or control, is indicative of the presence of IBD in the subject: vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467. In some embodiments, a decreased abundance of one or more viral clusters selected from vc7, vc25, vc47, and vc64 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject. The abundance may be decreased 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00132] In various embodiments, a decreased abundance of one or more of the following marker clusters in the subject sample, as compared to that of a sample from a healthy patient or control, is indicative of the presence of Crohn's Disease (CD) in the subject: vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284. The abundance may be decreased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00133] In various embodiments, an increased abundance of vc98 and/or vc103 in the subject sample, as compared to that of a sample from a healthy patient or control, is indicative of the presence of ulcerative colitis (UC) in the subject. The abundance may be increased by 10-99%,

10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00134] The dataset may be prepared by sequencing VLP DNA isolated from GI microbiota sample(s). A fourth dataset may be obtained that represents bacterial sequences derived from the GI microbiota sample obtained from the subject, with the fourth dataset for the presence of bacterial taxa associated with IBD. The fourth dataset may be obtained by sequencing 16S rDNA or a V region (*e.g.*, V4 region) of 16S rDNA in the GI microbiota sample. The presence of IBD in the subject may be determined based at least in part on the comparison of the fourth dataset to at least one of a healthy control and a control diagnosed with IBD.

[00135] In various embodiments, the GI microbiota sample is a fecal sample. In various embodiments, the GI microbiota sample is a cecal sample. In various embodiments, the GI microbiota sample is an ileal sample. In various embodiments, the GI microbiota sample is a colonic microbiota sample. In various embodiments, microbiota from other sites can be used, such as oral microbiota samples, nasal microbiota samples, skin microbiota samples, and vaginal microbiota samples.

[00136] In various embodiments, the subject is human.

[00137] The methods may further comprise administering an IBD treatment to the subject. IBD treatments include conventional treatments such as mesalamine, steroids, immunomodulators, and dietary modification. IBD treatments may also comprise administration of compositions comprising viruses and bacteria, as described below.

[00138] Also provided is a method for preventing and/or treating IBD in a subject. An effective amount of one or more viruses from any of the following viral clusters is administered: vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467. The method may further comprise administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*,

Methanobrevibacter, Clostridium IV, Faecalibacterium, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Howardella, Bifidobacterium, Oscillibacter, Parabacteroides, Flavonifractor, Blautia, Dorea, Roseburia, Odoribacter, Catenibacterium, and Akkermansia or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium, Ruminococcus, Coprococcus, Methanobrevibacter, Clostridium IV, Faecalibacterium, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Howardella, Bifidobacterium, Oscillibacter, Parabacteroides, Flavonifractor, Blautia, Dorea, Roseburia, Odoribacter, Catenibacterium, and Akkermansia*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00139] Also provided is a method for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39. The method may further comprise administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Catenibacterium, Ruminococcus, Coprococcus, Methanobrevibacter, Clostridium IV, Faecalibacterium, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Howardella, Bifidobacterium, Oscillibacter, Parabacteroides, Flavonifractor, Blautia, Dorea, Roseburia, Odoribacter, Catenibacterium, and Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium, Ruminococcus, Coprococcus, Methanobrevibacter, Clostridium IV, Faecalibacterium, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Howardella, Bifidobacterium, Oscillibacter, Parabacteroides, Flavonifractor, Blautia, Dorea, Roseburia, Odoribacter, Catenibacterium, and Akkermansia*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00140] Also provided is a method for preventing and/or treating CD in a subject. An effective amount of one or more viruses from any of the following viral clusters is administered: vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284.

[00141] Also provided is a method for preventing and/or treating CD in a subject in need thereof. An effective amount of one or more viruses from any of the following viral clusters is administered: vc10, vc23, and vc39. The method may further comprise administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00142] Also provided is a method for preventing and/or treating UC in a subject in need thereof. An effective amount of one or more viruses from any of the following viral clusters is administered: vc10, vc23, and vc39. The method may further comprise administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*,

Ruminococcus2, Alistipes, Sporobacter, Bifidobacterium, Oscillibacter, Flavonifractor, Dorea, Roseburia, and Odoribacter. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00143] Also provided is a method for preventing and/or treating UC in a subject. An effective amount of a virus from a viral cluster vc98 and/or vc103 is administered. The method may further comprise administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof. The composition stimulates growth and/or activity in the GI microbiota of the subject of the bacterial genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus *Akkermansia*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00144] Also provided is a method for preventing and/or treating IBD in a subject in need thereof. An effective amount of a probiotic or a prebiotic composition or a combination thereof is administered to the subject. The composition stimulates growth and/or activity of one or more bacterial genera selected from *Catenibacterium, Ruminococcus, Coprococcus, Methanobrevibacter, Clostridium IV, Faecalibacterium, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Howardella, Bifidobacterium, Oscillibacter, Parabacteroides, Flavonifractor, Blautia, Dorea, Roseburia, Odoribacter, Catenibacterium, and Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium, Ruminococcus, Coprococcus, Methanobrevibacter, Clostridium IV, Faecalibacterium, Barnesiella, Dialister, Ruminococcus2, Alistipes, Sporobacter, Howardella, Bifidobacterium, Oscillibacter, Parabacteroides, Flavonifractor, Blautia, Dorea, Roseburia, Odoribacter, Catenibacterium, and Akkermansia*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00145] Also provided is a method for preventing and/or treating CD in a subject in need thereof. An effective amount of a probiotic or a prebiotic composition or a combination thereof is

administered to the subject. The composition stimulates growth and/or activity of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00146] Also provided is a method for preventing and/or treating UC in a subject in need thereof. An effective amount of a probiotic or a prebiotic composition or a combination thereof is administered to the subject. The composition stimulates growth and/or activity of the genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus. In some embodiments, the probiotic composition comprises one or more bacterial strains from the genus *Akkermansia*. The prebiotic or probiotic composition may be effective to fully, or partially, restore normal microbiota.

[00147] Any of the above methods may further comprise administering to the subject additional diagnostic tests for IBD, CD and/or UC.

[00148] Any of the above methods may further comprise enrolling the subject in a clinical trial.

[00149] Bacterial taxa associated with IBD may comprise one or more of the following bacterial genera: *Clostridium XIVa*, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, *Flavonifractor*, *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Dorea*, *Roseburia*, *Odoribacter*, and *Akkermansia*. Bacterial taxa associated with IBD may comprise a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

[00150] An increased abundance of one or more of the following bacterial genera in the subject sample as compared to a healthy control may be indicative of the presence of IBD in the subject: *Clostridium XIVa*, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, and *Flavonifractor*. The abundance may be increased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00151] An increased abundance of one or more of the following bacterial genera in the subject sample as compared to a healthy control may be indicative of the presence of Crohn's Disease (CD) in the subject: *Clostridium XIVa*, *Blautia*, *Megasphaera*, and *Fusobacterium*. The abundance may be increased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

An increased abundance of the bacterial genus *Flavonifractor* in the subject sample as compared to a healthy control may be indicative of the presence of ulcerative colitis (UC) in the subject.

An increased abundance of one or more bacterial species selected from *Bacteroides fragilis* and *Ruminococcus gnavus* in the subject sample as compared to a healthy control may be indicative of the presence of UC in the subject. An increased abundance of *Ruminococcus gnavus* in the subject sample as compared to a control sample from a patient with UC in remission may be indicative of the presence of a flare-up of UC in the subject. An increased abundance of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes* in the subject sample as compared to a control sample from a patient with a flare-up of UC in remission may be indicative of the presence of UC in remission in the subject. The abundance may be increased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00152] A decreased abundance of one or more of the following bacterial genera in the subject sample as compared to a healthy control may be indicative of the presence of IBD in the subject: *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia*. The abundance may be decreased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00153] A decreased abundance of one or more of the following bacterial genera in the subject sample as compared to a healthy control may be indicative of the presence of Crohn's Disease (CD) in the subject: *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter*. The abundance may be decreased by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00154] A decreased abundance, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold, of the bacterial genus *Akkermansia* in the subject sample as compared to a healthy control may be indicative of the presence of ulcerative colitis (UC) in the subject.

[00155] The analysis of the collection of the viral clusters created based on the subject's viral genome sequences can include identifying common clusters present in both the collection of viral clusters associated with the subject and present in the collection of marker clusters. For each common cluster, a relative abundance of members within that cluster found in the subject's GI microbiota sample can be determined. For each common cluster, a correlation value can be

associated with each common cluster in the collection of marker clusters. The comparison of the viral clusters derived from the subject to the marker clusters can include comparing the relative abundance of members within each common cluster associated with the patient to the correlation value of each common cluster in the collection of marker clusters.

[00156] In some embodiments, the subject can be diagnosed with Crohn's disease if there is a decrease in the abundance of a virus of a viral taxon listed in Table 13 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00157] In some embodiments, the subject can be diagnosed with ulcerative colitis if there is a decrease in the abundance of a virus of a viral taxon listed in Table 14 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00158] In some embodiments, the subject can be diagnosed with Crohn's disease if there is an increase in the abundance of a virus of a viral taxon listed in Table 15 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00159] In some embodiments, the subject can be diagnosed with ulcerative colitis if there is an increase in the abundance of a virus of a viral taxon listed in Table 16 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by

about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00160] In some embodiments, the subject can be diagnosed with Crohn's disease if there is an increase in the abundance of bacteria of a bacterial taxon listed in Table 15 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00161] In some embodiments, the subject can be diagnosed with ulcerative colitis if there is an increase in the abundance of bacteria of a bacterial taxon listed in Table 16 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00162] In some embodiments, the subject can be diagnosed with Crohn's disease if there is an increase in the abundance of bacteria of a bacterial taxon listed in Table 17 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00163] In some embodiments, the subject can be diagnosed with ulcerative colitis if there is an increase in the abundance of bacteria of a bacterial taxon listed in Table 18 in the subject as compared to a reference amount of the abundance of the virus in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00164] In some embodiments, the subject can be diagnosed with IBD (e.g., Crohn's disease or ulcerative colitis) if in the subject the abundance of one or more viruses in vc23 is reduced as compared the abundance of the same one or more viruses in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00165] In some embodiments, the subject can be diagnosed with IBD (e.g., Crohn's disease or ulcerative colitis) if in the subject the abundance of one or more viruses in vc39 is reduced as compared the abundance of the same one or more viruses in one or more healthy subjects, e.g., by 10-99%, 10-20%, 20-30%, 30-50%, 40-60%, 50-70%, 60-80%, 70-90%, 80-100%, 90-110%, 100-150%, 120-170%, 150-200%, by two-fold to 1,000-fold, about two-fold, by about three-fold, by about four-fold, by about five-fold, by about 10-fold, by about 20-fold, by about 50-fold, by about 100-fold, by about 200-fold, by about 500-fold, or by about 1,000-fold.

[00166] In some embodiments, the subject can be diagnosed with IBD (e.g., Crohn's disease or ulcerative colitis) if in the subject the abundance of one or more viruses in vc10 is reduced as compared the abundance of the same one or more viruses in one or more healthy subjects.

[00167] In various embodiments, a kit for determining the presence of IBD in a subject can include a device to receive viral genome sequences, including unidentified viral genome sequences, from an individual subject and diagnose the subject for IBD based at least in part on the virome marker clusters. The viral genome sequences can be derived from a GI microbiota sample provided by the subject. The GI microbiota sample can be a fecal sample. The GI microbiota sample can be a cecal sample. The GI microbiota sample can be an ileal sample. The GI microbiota sample can be a colonic microbiota sample. In various embodiments, microbiota from other sites can be used, such as oral microbiota samples, nasal microbiota samples, skin microbiota samples, and vaginal microbiota samples.

[00168] Diagnosis can include clustering the received viral genome sequences and comparing the subject's viral genome clusters to the marker clusters. The viral genome sequences can be clustered by protein clustering and protein homology as described herein. The device can also analyse bacteria from the subject for the purpose of IBD diagnosis. The bacteria can be derived from the same GI microbiota sample provided by the subject used to obtain the viral genome

sequences or a separate GI microbiota sample. The subject can be diagnosed for IBD based on the analysis of the bacteria and/or the analysis of the viral genome sequences. The IBD diagnosis can include a diagnosis for ulcerative colitis and/or Crohn's disease.

[00169] Figure 17 is a block diagram illustration of a system or device 200 (referred to herein for simplicity as "device") that be used as part of a kit for detecting IBD or health in a subject. The device 200 can include a dataset input module 210 configured to receive a dataset derived from a GI microbiota sample of a subject, a clustering module 220 configured to determine viral genome sequences within the subject's dataset and cluster the viral genome sequences into viral clusters, a marker cluster input module 230 configured to receive an input that is based on IBD marker clusters, a cluster comparison module 240 that is configured to compare the subject's viral clusters to the input representation of the marker clusters, and an output interface 250 configured to provide an indication of health or disease based on the comparison of the subject's viral clusters to the representation of the marker clusters. The modules 210, 220, 230, 240 can be implemented by a computing system in hardware and/or software according to the principles described herein and as would be appreciated and understood by a person of ordinary skill in the art.

[00170] The dataset input module, when implemented at least in part by hardware, can include a wired or wireless receiver capable of receiving an electronic signal representative of the subject's dataset. The clustering module 220, when implemented at least in part of hardware, can include a processor in communication with a memory with instructions thereon to create viral clusters based on and/or associated with the subject's dataset according the the principles described herein. The marker cluster input module 230, when implemented at least in part by hardware, can include a wired or wireless receiver capable of receiving an electronic signal representative of IBD marker clusters. Additionally, or alternatively, the marker cluster input module 230 can include a memory store with a representation of the IBD marker clusters stored thereon. The cluster comparison module 240, when implemented at least in part by hardware, can include memory with instructions thereon to compare the subject's viral clusters to the IBD marker clusters and provide as an output and indication of health or disease. The output interface 250, when implemented at least in part by hardware, can include a wired or wireless transmitter configured to transmit an electronic signal representative of the indication nfo health or disease. Additionally, or alternatively, the output interface 250 can include a user interface configured to

provide an auditory, visual, or other sensory indication to a user that can be interpreted as an indication of health or disease.

[00171] In one aspect, the disclosure provides a method for treating dysbiosis in the gastrointestinal tract of a subject (e.g., human) in need thereof, said method comprising administering to said subject a therapeutically effective amount of any of the viruses described herein. In some embodiments, the virus is from any viral taxon listed in Table 13. In some embodiments, the virus is from any viral taxon listed in Table 14.

[00172] In one aspect, the disclosure provides a method for treating dysbiosis in the gastrointestinal tract of a subject (e.g., human) in need thereof, said method comprising administering to said subject a therapeutically effective amount of an inhibitor of, or an agent that specifically targets, any of the viruses described herein. In some embodiments, the virus is from any viral taxon listed in Table 11. In some embodiments, the virus is from any viral taxon listed in Table 12.

[00173] In one aspect, the disclosure provides a method for treating dysbiosis in the gastrointestinal tract of a subject (e.g., human) in need thereof, said method comprising administering to said subject a therapeutically effective amount of any of the bacteria described herein. In some embodiments, the bacteria is from any bacterial taxon listed in Table 17. In some embodiments, the bacteria is from any bacterial taxon listed in Table 18.

[00174] In one aspect, the disclosure provides a method for treating dysbiosis in the gastrointestinal tract of a subject (e.g., human) in need thereof, said method comprising administering to said subject a therapeutically effective amount of an inhibitor of, or agent that specifically targets, any of the bacteria described herein. In some embodiments, the bacteria is from any bacterial taxon listed in Table 15. In some embodiments, the bacteria is from any bacterial taxon listed in Table 16.

[00175] In another aspect, the disclosure provides a method for treating a gastrointestinal (GI) disorder in a subject (e.g., human) in need thereof, said method comprising administering to said subject a therapeutically effective amount of any of the virus compositions described herein. Non-limiting examples of encompassed GI disorders include, e.g., inflammatory bowel disease (IBD), ulcerative colitis, Crohn's disease, irritable bowel syndrome (IBS), infectious gastroenteritis, non-infectious gastroenteritis, food allergy, and gastrointestinal graft versus host disease.

[00176] The disclosure also provides pharmaceutical compositions comprising the viruses and/or bacteria of the disclosure. The compositions disclosed herein can be formulated into a variety of forms and administered by a number of different means. Non-limiting examples of useful routes of delivery include oral, topical, rectal, mucosal, sublingual, nasal, intravenous, subcutaneous, and via naso/oro-gastric gavage. The active agent may be systemic after administration or may be localized by the use of regional administration, intramural administration, or use of an implant that acts to retain the active dose at the site of implantation. The active agent, vector, virus, bacteriophage, particle, or a bacterial inoculant can be mixed with a carrier and (for easier delivery to the digestive tract) applied to liquid or solid food, or feed or to drinking water. The carrier material should be non-toxic to the virus/bacteriophage/bacteria and the subject/patient. Non-limiting examples of formulations useful in the methods of the present disclosure include oral capsules and saline suspensions for use in feeding tubes, transmission via nasogastric tube, or enema. If live virus, bacteriophage or bacteria are used, the carrier should preferably contain an ingredient that promotes viability of the virus/bacteriophage/bacteria during storage. The formulation can include added ingredients to improve palatability, improve shelf-life, impart nutritional benefits, and the like. If a reproducible and measured dose is desired, the formulation can be administered by a rumen cannula. In certain embodiments, the formulation used in the methods of the disclosure further comprises a buffering agent. Examples of useful buffering agents include saline, sodium bicarbonate, milk, yogurt, infant formula, and other dairy products.

[00177] Bacteria-containing formulations may also comprise one or more prebiotics which promote growth and/or immunomodulatory activity of the bacteria in the formulation. While it is possible to use a compound, vector, virus, bacteriophage, particle, or a bacterial inoculant of the present disclosure for therapy as is, it may be preferable to administer it in a pharmaceutical formulation, e.g., in admixture with a suitable pharmaceutical excipient, diluent or carrier selected with regard to the intended route of administration and standard pharmaceutical practice. The excipient, diluent and/or carrier must be “acceptable” in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. Acceptable excipients, diluents, and carriers for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington: The Science and Practice of Pharmacy. Lippincott Williams & Wilkins (A.R. Gennaro edit. 2005). The choice of

pharmaceutical excipient, diluent, and carrier can be selected with regard to the intended route of administration and standard pharmaceutical practice. Although there are no physical limitations to delivery of the formulations of the present disclosure, oral delivery is preferred for delivery to the digestive tract because of its ease and convenience, and because oral formulations readily accommodate additional mixtures, such as milk, yogurt, and infant formula.

[00178] Oral delivery may also include the use of nanoparticles that can be targeted, e.g., to the GI tract of the subject, such as those described in Yun et al., *Adv Drug Deliv Rev.* 2013, 65(6):822-832 (e.g., mucoadhesive nanoparticles, negatively charged carboxylate- or sulfate-modified particles, etc.). Non-limiting examples of other methods of targeting delivery of compositions to the GI tract are discussed in U.S. Pat. Appl. Pub. No. 2013/0149339 and references cited therein (e.g., pH sensitive compositions [such as, e.g., enteric polymers which release their contents when the pH becomes alkaline after the enteric polymers pass through the stomach], compositions for delaying the release [e.g., compositions which use hydrogel as a shell or a material which coats the active substance with, e.g., in vivo degradable polymers, gradually hydrolyzable polymers, gradually water-soluble polymers, and/or enzyme degradable polymers], bioadhesive compositions which specifically adhere to the colonic mucosal membrane, compositions into which a protease inhibitor is incorporated, a carrier system being specifically decomposed by an enzyme present in the colon).

[00179] For oral administration, the active ingredient(s) can be administered in solid dosage forms, such as capsules, tablets, and powders, or in liquid dosage forms, such as elixirs, syrups, and suspensions. A capsule typically comprises a core material comprising a bacterial composition and a shell wall that encapsulates the core material. In some embodiments, the core material comprises at least one of a solid, a liquid, and an emulsion. In other embodiments, the shell wall material comprises at least one of a soft gelatin, a hard gelatin, and a polymer. Suitable polymers include, but are not limited to: cellulosic polymers such as hydroxypropyl cellulose, hydroxyethyl cellulose, hydroxypropyl methyl cellulose (HPMC), methyl cellulose, ethyl cellulose, cellulose acetate, cellulose acetate phthalate, cellulose acetate trimellitate, hydroxypropylmethyl cellulose phthalate, hydroxypropylmethyl cellulose succinate and carboxymethylcellulose sodium; acrylic acid polymers and copolymers, such as those formed from acrylic acid, methacrylic acid, methyl acrylate, ammonio methacrylate, ethyl acrylate, methyl methacrylate and/or ethyl methacrylate (e.g., those copolymers sold under the trade name

“Eudragit”); vinyl polymers and copolymers such as polyvinyl pyrrolidone, polyvinyl acetate, polyvinylacetate phthalate, vinylacetate crotonic acid copolymer, and ethylene-vinyl acetate copolymers; and shellac (purified lac). In yet other embodiments, at least one polymer functions as taste-masking agents.

[00180] The active component(s) can be encapsulated in gelatin capsules together with inactive ingredients and powdered carriers, such as glucose, lactose, sucrose, mannitol, starch, cellulose or cellulose derivatives, magnesium stearate, stearic acid, sodium saccharin, talcum, magnesium carbonate. Examples of additional inactive ingredients that may be added to provide desirable color, taste, stability, buffering capacity, dispersion or other known desirable features are red iron oxide, silica gel, sodium lauryl sulfate, titanium dioxide, and edible white ink. Similar diluents can be used to make compressed tablets. Both tablets and capsules can be manufactured as sustained release products to provide for continuous release of medication over a period of hours. Compressed tablets can be sugar coated or film coated to mask any unpleasant taste and protect the tablet from the atmosphere, or enteric-coated for selective disintegration in the gastrointestinal tract. Liquid dosage forms for oral administration can contain coloring and flavoring to increase patient acceptance.

[00181] Formulations suitable for parenteral administration include aqueous and nonaqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and nonaqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives.

[00182] Alternatively, powders or granules embodying the bacterial and viral compositions disclosed herein can be incorporated into a food product. In some embodiments, the food product is a drink for oral administration. Non-limiting examples of a suitable drink include fruit juice, a fruit drink, an artificially flavored drink, an artificially sweetened drink, a carbonated beverage, a sports drink, a liquid dairy product, a shake, an alcoholic beverage, a caffeinated beverage, infant formula and so forth. Other suitable means for oral administration include aqueous and nonaqueous solutions, emulsions, suspensions and solutions and/or suspensions reconstituted from non-effervescent granules, containing at least one of suitable solvents, preservatives, emulsifying agents, suspending agents, diluents, sweeteners, coloring agents, and flavoring agents. The food product can be a solid foodstuff. Suitable examples of a solid foodstuff include

without limitation a food bar, a snack bar, a cookie, a brownie, a muffin, a cracker, an ice cream bar, a frozen yogurt bar, and the like.

[00183] In other embodiments, the bacterial and viral compositions disclosed herein are incorporated into a therapeutic food. In some embodiments, the therapeutic food is a ready-to-use food that optionally contains some or all essential macronutrients and micronutrients. In another embodiment, the compositions disclosed herein are incorporated into a supplementary food that is designed to be blended into an existing meal. In one embodiment, the supplemental food contains some or all essential macronutrients and micronutrients. In another embodiment, the bacterial compositions disclosed herein are blended with or added to an existing food to fortify the food's protein nutrition. Examples include food staples (grain, salt, sugar, cooking oil, margarine), beverages (coffee, tea, soda, beer, liquor, sports drinks), snacks, sweets and other foods.

[00184] The useful dosages of the compositions and formulations of the disclosure will vary widely, depending upon the nature of the disease, the patient's medical history, the frequency of administration, the manner of administration, the clearance of the agent from the host, and the like. The initial dose may be larger, followed by smaller maintenance doses. The dose may be administered as infrequently as weekly or biweekly, or fractionated into smaller doses and administered daily, semi-weekly, etc., to maintain an effective dosage level.

Additional Embodiments:

1. A method for identifying a plurality of viral marker clusters for determining the presence of inflammatory bowel disease (IBD) using viral genome sequences, the method comprising:

obtaining a first dataset representing a first plurality of viral genome sequences derived from gastrointestinal (GI) microbiota samples of a healthy cohort;

obtaining a second dataset representing a second plurality of viral genome sequences derived from GI microbiota samples of a cohort diagnosed with IBD;

creating a first plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group viral genome sequences of the first dataset, each viral cluster in the first plurality of viral clusters comprising one or more viral genome sequences derived from the healthy cohort;

creating a second plurality of viral clusters by using protein clustering to group like proteins derived from the second dataset and by using protein homology to group viral genome sequences of the second dataset, each viral cluster in the second plurality of viral clusters comprising one or more viral genome sequences derived from the cohort diagnosed with IBD; and

identifying a plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters.

2. The method of embodiment 1,

wherein at least a portion of the first plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database, and

wherein at least a portion of the second plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database.

3. The method of embodiments 1 or 2, wherein a totality of the first plurality and second plurality of viral genome sequences are each unassociated with a viral taxonomic category derived from a viral genome database.

4. The method of any one of embodiments 1-3, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises using machine learning to identify the plurality of marker clusters.

5. The method of any one of embodiments 1-4, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises identifying the plurality of marker clusters unassociated with a known taxon.

6. The method of any one of embodiments 1-5, wherein each of the viral clusters in the plurality of marker clusters respectively represent an unidentified taxon of higher rank than a strain and of lower rank than a family.

7. The method of any one of embodiments 1-6, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral

clusters comprises performing beta diversity analysis on the first plurality of viral clusters and the second plurality of viral clusters.

8. The method of embodiment 7, wherein performing the beta diversity analysis comprises performing a scaling and ordination technique selected from a group consisting of principal coordinates analysis (PCoA), principal components analysis (PCA), non-metric multidimensional scaling (NMDS), canonical correspondence analysis (CCA), and redundancy analysis (RDA).

9. The method of any one of embodiments 1-8, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises calculating differential abundance of viral clusters in the first plurality of viral clusters and the second plurality of viral clusters.

10. The method of any one of embodiments 1-9, wherein the healthy cohort and the cohort diagnosed with IBD are each human cohorts.

11. The method of any one of embodiments 1-10, further comprising:

associating a first data subset of the second dataset with a first sub-cohort diagnosed with IBD and Crohn's disease (CD);

associating a second data subset of the second dataset with a second sub-cohort diagnosed with IBD and ulcerative colitis (UC);

associating a first subset of viral clusters of the second plurality of viral clusters with the first sub-cohort;

associating a second subset of viral clusters of the second plurality of viral clusters with the second sub-cohort; and

identifying a first subset of marker clusters of the plurality of marker clusters and a second subset of marker clusters of the plurality of marker clusters by comparing the first subset of viral clusters to the second subset of viral clusters.

12. The method of any one of embodiments 1-11, further comprising:
 - representing the viral genome sequences in the first dataset each respectively as a first viral contig of a protein sequence; and
 - representing the viral genome sequences in the second dataset each respectively as a second viral contig of a protein sequence.
13. The method of any one of embodiments 1-12,
 - wherein the first dataset further represents a first plurality of identified viral genome sequences derived from the healthy cohort,
 - wherein the second dataset further represents a second plurality of identified viral genome sequences derived from the cohort diagnosed with IBD, and
 - wherein the method further comprises:
 - creating a first plurality of reference viral clusters using protein clustering to group like proteins and protein homology to group identified viral genome sequences of the first plurality of identified viral genome sequences;
 - creating a second plurality of reference viral clusters using protein clustering to group like proteins and protein homology to group identified viral genome sequences of the second plurality of identified viral genome sequences; and
 - wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters further comprises identifying the plurality of marker clusters by comparing a combination of the first plurality of viral clusters and the first plurality of reference viral clusters to a combination of the second plurality of viral clusters and the second plurality of reference viral clusters.
14. The method of embodiment 13,
 - wherein the first plurality of identified viral genome sequences are associated with a viral taxonomic category present in a viral genome database, and
 - wherein the second plurality of identified viral genome sequences are associated with a viral taxonomic category present in a viral genome database.

15. A method for determining the presence of inflammatory bowel disease (IBD) in a subject, the method comprising:
- obtaining an individual viral dataset representing a plurality of viral genome sequences derived from a GI microbiota sample obtained from the subject;
 - creating a plurality of subject viral clusters using protein clustering to group like proteins derived from the individual viral dataset and by using protein homology to group unidentified viral genome sequences of the individual viral dataset, each viral cluster in the plurality of subject viral clusters comprising one or more viral genome sequences derived from the subject;
 - obtaining a plurality of marker clusters indicative of the presence or absence of IBD; and
 - comparing the plurality of subject viral clusters to the plurality of marker clusters.
16. The method of embodiment 15, wherein at least a portion of the plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database.
17. The method of embodiments 15 or 16, wherein a totality of the plurality of viral genome sequences are each unassociated with a viral taxonomic category derived from a viral genome database.
18. The method of any one of embodiments 15-17, wherein at least a portion of the plurality of marker clusters are unassociated with a viral taxonomic category derived from a viral genome database.
19. The method of any one of embodiments 15-18, further comprising determining the presence of IBD in the subject based at least in part on the comparison of the plurality of subject viral clusters to the plurality of marker clusters.
20. The method of any one of embodiments 15-19, wherein the marker clusters comprise one or more viral clusters from taxa Siphoviridae, Myoviridae, Podoviridae, CrAss-like, or Microviridae.

21. The method of any one of embodiments 15-20, wherein the plurality of marker clusters comprises one or more viral clusters selected from vc2, vc6, vc7, vc13, vc14, vc15, vc17, vc19, vc21, vc22, vc23, vc24, vc25, vc28, vc29, vc36, vc37, vc38, vc39, vc40, vc42, vc45, vc48, vc53, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc75, vc76, vc77, vc78, vc79, vc80, vc82, vc84, vc85, vc86, vc88, vc89, vc91, vc92, vc94, vc95, vc96, vc97, vc98, vc99, vc101, vc102, vc103, vc104, vc108, vc109, vc112, vc113, vc115, vc117, vc118, vc122, vc123, vc124, vc130, vc132, vc136, vc138, vc142, vc143, vc152, vc154, vc155, vc160, vc161, vc175, vc178, vc181, vc190, vc193, vc205, vc209, vc216, vc218, vc225, vc232, vc263, vc264, vc281, vc284, vc298, vc320, vc411, vc413, vc420, vc456, and vc467.

22. The method of embodiments 15-21, wherein an increased abundance of one or more viral clusters selected from vc2, vc13, vc14, vc15, vc17, vc21, vc22, vc36, vc40, vc48, vc53, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc77, vc78, vc79, vc80, vc85, vc88, vc89, vc91, vc94, vc95, vc97, vc102, vc108, vc113, vc115, vc117, vc118, vc122, vc123, vc130, vc132, vc142, vc152, vc155, vc160, vc161, vc175, vc178, vc181, vc205, vc218, vc232, vc263, vc264, vc281, vc298, vc413, and vc420 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of IBD in the subject.

23. The method of embodiment 22, wherein an increased abundance of one or more viral clusters selected from vc15, vc66, vc71, vc73, vc77, vc78, vc79, vc80, vc91, vc94, vc108, vc113, vc117, vc118, vc132, vc142, vc155, vc160, vc178, vc232, vc264, vc281, vc298, and vc420 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

24. The method of embodiment 22, wherein an increased abundance of one or more viral clusters selected from vc28 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

25. The method of embodiment 22, wherein an increased abundance of one or more viral clusters selected from vc2, vc17, vc21, vc22, vc53, vc70, vc74, vc85, vc88, vc89, vc115, vc122, vc123, vc130, vc152, vc161, vc175, vc181, vc205, vc218, vc263, and vc413 in the plurality of

subject viral clusters as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

26. The method of embodiment 22, wherein an increased abundance of viral cluster vc2 in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

27. The method of any one of embodiments 15-21, wherein an increased abundance of one or more viral clusters selected from vc38, vc46, vc48, vc54, vc57, vc62, vc64, vc69, vc71, vc108, vc111, vc114, vc115, vc128, vc159, vc162, vc215, vc220, vc242, vc340, vc374, and vc392 in the subject sample as compared to a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject.

28. The method of any one of embodiments 15-21, wherein an increased abundance of one or more viral clusters selected from vc16, vc119, and vc163 in the subject sample as compared to a patient with a flare-up of ulcerative colitis (UC) is indicative of the presence of UC in remission in the subject.

29. The method of any one of embodiments 15-21, wherein a decreased abundance of one or more viral clusters selected from vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of IBD in the subject.

30. The method of embodiment 29, wherein a decreased abundance of one or more viral clusters selected from vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

31. The method of embodiment 29, wherein a decreased abundance of one or more viral clusters selected from vc7, vc25, vc47, and vc64 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.
32. The method of embodiment 29, wherein a decreased abundance of vc98 and/or vc103 viral cluster in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.
33. The method of any one of embodiments 15-32, wherein obtaining the dataset(s) is performed by sequencing VLP DNA isolated from GI microbiota sample(s).
34. The method of any one of embodiments 15-33, further comprising:
obtaining an individual bacteriome dataset representing bacterial sequences derived from the GI microbiota sample obtained from the subject; and
evaluating the individual bacteriome dataset for the presence of bacterial taxa associated with IBD.
35. The method of embodiment 34, further comprising determining the presence of IBD in the subject based at least in part on the comparison of the individual bacteriome dataset to at least one of a healthy control and a control diagnosed with IBD.
36. The method of embodiment 34 or embodiment 35, wherein the bacterial taxa associated with IBD comprise one or more bacterial genera selected from *Clostridium XIVa*, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, *Flavonifractor*, *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Dorea*, *Roseburia*, *Odoribacter*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

37. The method of embodiment 36, wherein an increased abundance of one or more bacterial genera selected from *Clostridium XI*_{Va}, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, and *Flavonifractor* in the subject sample as compared to a healthy control is indicative of the presence of IBD in the subject.

38. The method of embodiment 37, wherein an increased abundance of one or more bacterial genera selected from *Clostridium XI*_{Va}, *Blautia*, *Megasphaera*, and *Fusobacterium* in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

39. The method of embodiment 34 or embodiment 35, wherein an increased abundance of one or more bacterial species selected from *Bacteroides fragilis* and *Ruminococcus gnavus* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

40. The method of embodiment 34 or embodiment 35, wherein an increased abundance of *Ruminococcus gnavus* in the subject sample as compared to a control sample from a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject.

41. The method of embodiment 34 or embodiment 35, wherein an increased abundance of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes* in the subject sample as compared to a control sample from a patient with a flare-up of ulcerative colitis (UC) in remission is indicative of the presence of UC in remission in the subject.

42. The method of embodiment 37, wherein an increased abundance of bacterial genus *Flavonifractor* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

43. The method of embodiment 36, wherein a decreased abundance of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*,

Clostridium IV, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* in the subject sample as compared to a healthy control is indicative of the presence of IBD in the subject.

44. The method of embodiment 43, wherein a decreased abundance of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

45. The method of embodiment 43, wherein a decreased abundance of bacterial genus *Akkermansia* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

46. The method of any one of embodiments 34-45, wherein obtaining the individual bacteriome dataset is performed by sequencing 16S rDNA or a V region of 16S rDNA in the GI microbiota sample.

47. The method of embodiment 46, wherein the V region is V4 region.

48. The method of any one of embodiments 15-47, wherein the GI microbiota sample is a fecal sample, a cecal sample, an ileal sample, or a colonic microbiota sample.

49. The method of any one of embodiments 15-48, wherein the subject is human.

50. The method of any one of embodiments 15-49, further comprising administering an IBD treatment to the subject.

51. The method of any one of embodiments 15-50, further comprising administering to the subject additional diagnostic tests for IBD, CD and/or UC.

52. The method of any one of embodiments 15-51, further comprising enrolling the subject in a clinical trial.

53. The method of any one of embodiments 15-52, wherein comparing the plurality of subject viral clusters to the plurality of marker clusters comprises:

identifying common clusters present in the plurality of subject viral clusters and the plurality of marker clusters;

determining relative abundance of members within each common cluster in the plurality of subject viral clusters;

associating a correlation value with each common cluster in the plurality of marker clusters; and

comparing the relative abundance of members within each common cluster in the plurality of subject viral clusters to the correlation value of each common cluster in the plurality of marker clusters.

54. A kit for determining the presence of inflammatory bowel disease (IBD) in a subject comprising:

a device to:

receive a first dataset representing a plurality of unidentified viral genome sequences derived from a GI microbiota sample obtained from the subject;

receive a second dataset representing a plurality of viral genome IBD marker clusters;

create a plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group unidentified viral genome sequences of the plurality of unidentified viral genome sequences, each viral cluster in the plurality of viral clusters comprising one or more unidentified viral genome sequences of the plurality of unidentified genome sequences; and

compare the first plurality of viral clusters to the second dataset; and

determine the presence of IBD based at least in part on the comparison of the plurality of viral clusters to the second dataset.

55. The kit of embodiment 54, wherein the device is further configured to:
receive a third dataset representing bacteria from the GI microbiota sample obtained from the subject;
evaluate the third dataset for the purpose of IBD diagnosis; and
determine the presence of IBD based at least in part on the evaluation of the third database.
56. The kit of embodiment 54 or 55, wherein the GI microbiota sample is one or more of group consisting a fecal sample, a cecal sample, an ileal sample, and a colonic microbiota sample.
57. The kit of any of embodiments 54-56, wherein the IBD is ulcerative colitis (UC).
58. The kit of any of embodiments 54-56, wherein the IBD is Crohn's disease (CD).
59. The kit of any one of embodiments 54-58, wherein the subject is human.
60. A system comprising:
one or more processors;
a memory in communication with the one or more processors and storing instructions thereon that, when executed by the one or more processors, are configured to cause the system to:
receive a first dataset representing a first plurality of viral genome sequences derived from a healthy cohort;
receive a second dataset representing a second plurality of viral genome sequences derived from a cohort diagnosed with IBD;
create a first plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group viral genome sequences of the first dataset, each viral cluster in the first plurality of viral clusters comprising one or more viral genome sequences derived from the healthy cohort;
create a second plurality of viral clusters by using protein clustering to group like proteins derived from the second dataset and by using protein homology to group viral genome sequences of the second dataset, each viral cluster in the second plurality of viral

clusters comprising one or more viral genome sequences derived from the cohort diagnosed with IBD; and

identify a plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters.

61. A method for preventing and/or treating inflammatory bowel disease (IBD) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467.

62. A method for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

63. A method for preventing and/or treating Crohn's disease (CD) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284.

64. A method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

65. A method for preventing and/or treating ulcerative colitis (UC) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster vc98 and/or vc103.

66. A method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

67. The method of embodiment 61, further comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

68. The method of embodiment 63, further comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

69. The method of embodiment 65, further comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of the bacterial genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus.

70. A method for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

71. A method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

72. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of the genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus.

73. The method of embodiment 67 or embodiment 70, wherein said probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*,

Oscillibacter, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia*.

74. The method of embodiment 68 or embodiment 71, wherein said probiotic composition comprises one or more bacterial strains from the genus selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter*.

75. The method of embodiment 69 or embodiment 72, wherein said probiotic composition comprises one or more bacterial strains from the genus *Akkermansia*.

76. The method of any one of embodiments 67-75, wherein the V region is V4 region.

77. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes*.

78. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic comprising one or more of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes*.

79. The method of any one of embodiments 61-78, wherein the subject is human.

EXAMPLES

[00185] The present invention is also described and demonstrated by way of the following examples. However, the use of these and other examples anywhere in the specification is illustrative only and in no way limits the scope and meaning of the invention or of any exemplified term. Likewise, the invention is not limited to any particular preferred embodiments described here. Indeed, many modifications and variations of the invention may be apparent to those skilled in the art upon reading this specification, and such variations can be made without

departing from the invention in spirit or in scope. The invention is therefore to be limited only by the terms of the appended claims along with the full scope of equivalents to which those claims are entitled.

[00186] As an illustration of the principles described above, an analysis the whole-virome of a published keystone IBD virome cohort is presented herein. Using protein-based clustering of viral sequences, example methods applied according to the present invention are demonstrated to overcome high levels of inter-individual variation in the gut virome and reveal compositional changes within the gut virome in subjects with IBD. Virome changes are shown to reflect alterations in bacterial composition. Viromes of individuals with Crohn's disease can be characterized by increased numbers of temperate phage sequences. No substantial change is observed in viral alpha diversity across cohorts. Incorporating both the bacteriome and virome composition is demonstrated to offered more accurate classification of subjects as healthy or diseased compared to classification based on the bacteriome alone.

[00187] An analysis of a keystone dataset consisting of subjects with CD, UC and healthy controls is presented herein. This analysis overcomes strain-level resolution using protein homology and MCL to create higher taxonomic ranks and reveals hitherto unseen compositional patterns across the virome in health and disease. The analysis includes up to 97% of reads per sample ($78.55 \pm 18.79\%$ (mean $\pm$ SD)), rather than the 15% used in a prior publication also relying on the same keystone dataset(Norman et al., 2015, which is incorporated herein by reference in its entirety). As demonstrated in the presently illustrated analysis, it is possible to identify patterns across individuals and cohorts. Alterations in the virome were observed and potential disease biomarkers were identified for further characterization. This disclosure shows that virome alterations mimic that of the bacteriome and offers an improved method for classifying IBD patients from healthy subjects.

[00188] Without wishing to be bound by theory, the described approach provides insight into the viral dark matter in human health and disease. The methods also allow cohort comparisons and overcome problems associated with the high level of inter-individual variation. By identifying sequences which are associated with health and disease, this approach provides a framework for identifying novel virome biomarkers and targets for further wet-lab characterization.

[00189] It has been previously reported that the human gut virome exhibits high levels of inter-individual variation (Reyes et al., 2010. *Nature*, 466, 334-8) which is exacerbated by the need to analyze the virome at an assembly level which leads to strain level analysis. Unlike 16S analysis performed on bacteria, which is assessed at higher taxonomic ranks such as family and genus, viral and phage taxonomy does not have a similar defined structure which makes comparisons of cohorts very difficult. Strain level resolution hampers cohort comparisons due to a lack of commonality amongst in samples in the dataset which masks compositional patterns occurring at higher taxonomic ranks. The analysis presented here originally utilized vOTUs (viral contigs made non-redundant at 90% identity over 90% of the length), but this level of resolution masked shared signals across cohorts. This was overcome by clustering viral genomes based on their protein content using vContact2 (Bolduc et al., 2017. vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect Archaea and Bacteria. *PeerJ*, 5, e3243) to create a higher, protein based, taxonomic rank. This revealed shared virome features while retaining relevant biological signals across the cohort (as seen by VCs across subjects), increased the variation explained in the beta diversity (increased eigenvalues) and decreased the abundance of unique viral VCs per subject across the dataset. Viral clustering also enabled the detection of a core virome in healthy subjects, consisting of eight VCs across 50% of the cohort. This proved to be a key differentiator between health and disease throughout the analysis. Many of these core VCs were differentially abundant in health and disease and were primary drivers of PCoA separation and machine learning predictions. Without wishing to be bound by theory, the method can allow for improved comparisons of cohorts for a multitude of disease conditions and body sites by enabling the analysis of the whole virome with a reduction of the level of uniqueness at strain level; differently abundant VCs across cohorts can themselves be viral marker clusters or can lead to the identification of viral marker clusters that can be used to classify individual subject samples as indicative of health or disease.

[00190] In beta diversity analysis, IBD subjects shifted significantly away from healthy controls thus providing evidence of compositional differences in the gut viromes. Drivers of these separations were associated with *Myoviridae* and *Siphoviridae* in IBD and *Microviridae* and crAss-like phages in healthy subjects. This was also reflected in differential abundance analysis with many VCs classified as *Myoviridae* and *Siphoviridae* significantly increased in subjects with IBD. No differences were found between the alpha diversity of the subjects with IBD and

healthy controls, a finding contradictory to previous publications (Zuo et al., 2019. *Gut*), including previous analysis of this dataset (Norman et al., 2015. *Cell*, 160, 447-60). These findings may reflect the limited scope of database dependent analysis methods and that changes in these subsets of the viral community are not reflected in the virome as a whole. The findings presented here also suggest that although the composition of the virome is altered in subjects with disease the number of viruses remains consistent. The alpha diversity of VCs was assessed with a classification in the order *Caudovirales* to replicate the work of Norman et al., (2015. *Cell*, 160, 447-60). Results were in agreement in that an increase in *Caudovirales* diversity in the CD cohort was observed, however no significance for UC versus controls was observed when analyzing the total virome. This could reflect a more global change with abundant lytic phage being replaced with temperate phage in IBD environments. It was speculated that a more stressful environment for the bacteria could result in lysogenic phage being released. This stress would also result in a decreased bacterial alpha diversity in IBD which was also observed here. In terms of beta diversity subjects with IBD had the smallest distances between points which could also be attributed to the low diversity. The incorporation of ϕ Q33, a lactococcal phage not native to the human gut, at known concentrations allowed for the quantification of the total bacteriophage loads in the fecal samples. Interestingly, viral load was inversely proportional to observed VCs suggesting that dominance of particular viruses rather than an expansion of many could be responsible for a higher viral load.

[00191] This study provides new evidence of a correlation between alterations in the whole human gut virome to IBD. As previously reported the genus *Faecalibacterium* (Lopez-Siles et al., 2015. *Appl Environ Microbiol*, 81, 7582-92; Lopez-Siles et al., 2018. *Front Cell Infect Microbiol*, 8, 281; Gevers et al., 2014. *Cell Host Microbe*, 15, 382-392; Pascal et al., 2017. *Gut*, 66, 813-822; Machiels et al., 2014. *Gut*, 63, 1275-83) was depleted in IBD cohorts along with *Ruminococcaceae* (Gevers et al., 2014). Furthermore, it was found many differentially abundant taxa in agreement with the literature including *Fusobacterium* (Pascal et al., 2017, Strauss et al., 2011. *Inflamm Bowel Dis*, 17, 1971-8; Gevers et al., 2014), *Veillonella* (Gevers et al., 2014) and *Ruminococcus gnavus* (Joossens et al., 2011. *Gut*, 60, 631-7; Willing et al., 2010. *Gastroenterology*, 139, 1844-1854 e1) which correlated towards the shift in beta diversity as previously found in subjects with IBD. The trends observed in both alpha and beta diversity are also in agreement with previous reports (Halfvarson et al., 2017. *Nat Microbiol*, 2, 17004;

Manichanh et al., 2006. *Gut*, 55, 205-11; Dicksved et al., 2008. *ISME J*, 2, 716-27; Pascal et al., 2017. *Gut*, 66, 813-822) and the previous analysis of this dataset (Norman et al., 2015. *Cell*, 160, 447-60), thus providing validity to the cohort tested and the methods. Although it is not possible from a cross-sectional study to know whether the virome alters the bacteriome or *vice-versa*, the datasets complement each other. The beta diversity trends were observed in both datasets and this was confirmed through Procrustes analysis. Although 16S showed improved accuracy in classifying subjects with IBD from controls, the addition of the virome improved upon this classification to over 94% area under the curve and to over 85% accuracy. All subjects with IBD were correctly classified, proving further evidence that the gut bacteriome and virome are truly altered in IBD disease, such that the gut bacteriome and virome are potential avenues for any of diagnosis, therapeutics and correction.

[00192] A common trend observed in the present virome analysis is the increased severity in the virome alteration of CD patients in comparison to UC, a finding replicated in the 16S. In PCoA, CD is located further from the healthy controls while subjects with CD are also the least stable cohort. There were also a greater number of differentially abundant clusters between healthy and CD compared to healthy and UC. Subjects with CD also had more differentially abundant RSVs than UC versus controls in the bacteriome, together with being located furthest from controls on the PCoA. This CD cohort had the least beta stability which may also be linked to having the lowest diversity. Interestingly, CD had a significantly higher diversity of *Caudovirales* and an increased number of reads aligned to lysogenic VCs when compared to healthy controls. Furthermore, when differentiating cohorts using machine learning, many of the top 20 importance factors were differentially abundant between CD and controls for both virome and 16S models.

[00193] In light of the findings of this study two potential scenarios were proposed to describe the host-bacteriome-virome interaction in IBD and particular CD. One hypothesis is that oxidative stress in the gut during inflammation (Rigottier-Gois, 2013. *ISME J*, 7, 1256-61) creates a more stressful living environment for the bacteria which lyse and release lysogenic phage, also resulting in decreased bacterial diversity. These lysogenic phage are then detected in virome analysis as seen in this study and previously reported (Norman et al., 2015. *Cell*, 160, 447-60, Zuo et al., 2019. Gut mucosal virome alterations in ulcerative colitis. *Gut*). Secondly, although less probable, an event causing more lysogenic induction would result in increased

bacterial lysis, therefore a decreased bacterial alpha diversity, and more lysogenic phage being detected. Currently it is not possible to pinpoint the precise mechanism of action, however it is clear that there are specific compositional differences in the viromes of subjects with IBD.

[00194] Examining the interaction of virome composition and disease state in UC in greater detail revealed more subtle changes than that seen between health and disease. This finding, in conjunction with the overall comparison between UC, CD and healthy controls, suggests the virome is not only less perturbed between healthy and UC, but also between flare and remission. This may reflect the disease severity of UC relative to CD or that they may interact with the host in different ways. Differences in disease locations, severity and risk factors such as the potential paradoxical relationship between CD and UC with smoking (Berkowitz et al., 2018. *Front Immunol*, 9, 74) have previously alluded to differences in disease etiologies. It is possible that the virome composition does not alter significantly between disease states to the same extent as disease versus healthy. However, disease status was not tested in a CD cohort which may be more fruitful as the difference in CD were more exaggerated.

[00195] Those of ordinary skill in the art can envision additional steps and methods for analysis. Increased sample sizes, particularly for disease state, may increase the ability to detect any potential alterations between flare and remission. Inclusion of one or more of food frequency questionnaires, medical history details, and medication history (Maier et al., 2018. *Nature*, 555, 623-628) may provide for improved analysis of the microbiota. Addition of metadata, such as that including household controls, can assist in the statistical analysis and can allow the exploration of environmental effects. Other DNA amplification steps besides MDA amplification, which has a known bias towards *Microviridae* (Parras-Molto et al., 2018. *Microbiome*, 6, 119), can be undertaken. More modern methods such as the accel-NGS prep kit may remove the need for amplification and may provide for more reliable indication of diversity (Roux et al., 2016. Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. *PeerJ*, 4, e2777).

[00196] This study provides a detailed analysis of whole virome composition comparing CD/UC and healthy controls data. It also represents a detailed study of the unidentified majority of the virome in human disease and provides insights, paving the way for better understanding of the human virome as a whole. This analysis shows that analysis of the dark matter can be used to detect accurate profiles of the human gut virome. Although it is not yet possible to conclude if

the bacteriome shapes the virome or *vice-versa*, they do correlate with each other, as shown by Procrustes analysis, and can assist in the classification of subjects with IBD from healthy controls. This analysis provides a method for the comparison of whole viromes across cohorts in diseases other than IBD, which will give further insights into how a fuller understanding of the role of the microbiome in health and disease can be beneficial.

[00197]

Datasets

[00198] A publicly available dataset which was generated on human gut virome composition associated with IBD (Norman et al., 2015) was utilized. The dataset was analyzed with a novel whole-virome analysis protocol that provided novel insights into compositional changes of the virome, and any potential role of such changes in IBD. The dataset (Norman dataset) comprised 165 virome samples from 130 subjects, more specifically 61 healthy controls, 27 subjects with Crohn's disease (CD), and 42 subjects with ulcerative colitis (UC). Of these, six samples were known to be collected during CD flare, eight in CD remission, 13 in UC flare, and 20 in UC remission. To build upon these findings, a second dataset (Simponi dataset) was generated that consisted of longitudinal samples from 40 subjects with UC. These samples included 82 samples from periods of flare and 31 samples from periods of remission, allowing for the investigation of the impact of disease status on gut virome composition. 16S rRNA gene sequencing data was also obtained and performed for 149 (Normal dataset) and 109 (Simponi dataset) samples.

Protein-based clustering can overcome virome individuality and allow cohort comparisons

[00199] In order to compare the viromes of subjects with IBD to healthy controls, the overall composition was initially investigated at a viral contig level through PCoA of beta diversity (**Figure 1A**). The viral contigs represent individual viral genomes (whole or part), and therefore the resolution is at the strain level. This level of resolution was reflected in the extremely high levels of individuality amongst subjects at an assembly level. It was also observed in beta diversity as individuals were the primary drivers of separation with longitudinal samples grouping together. This individual specificity masked compositional differences of the virome. Each of the cohorts (control, CD and UC) showed little divergence with overlapping ellipses, while PC-axes 1 and 2 described very little of the variation in the dataset (4.85% and 3.59%).

[00200] To overcome this high interpersonal variation, investigation of disease specific compositional changes in the virome a lower taxonomic resolution (i.e. a higher taxonomic rank) was developed. This was achieved by clustering viral contigs based on protein similarities and MCL using vContact2 (see methods). The viral contigs clustered into 472 Viral Clusters (VCs) of >2 members with 2,382 singletons remaining. (Singletons are henceforward referred to as a VC with one member.) The resulting VCs formed a new count table and so a VC-based PCoA was produced (**Figure 1B**).

[00201] Samples largely grouped per condition with noticeable increases in the eigenvalues to 10.36% and 5.58% variation explained for PC-axes 1 and 2 respectively. However, it should be noted that samples with true deviation from the main cohort (such as subjects N208 and N56) remained distinctive, suggesting that the clustering process retains true compositional differences. To further determine if the use of clustering decreased the masking effect of intra-individuality, the viral contig and VC relative abundances were plotted for control subjects and colored by the percent abundance of shared viral contigs/clusters across the remainder of the control cohort (**Figure 1C**). The relative abundance of viral contigs unique to each subject was 14% ($\pm 8\%$) on average while an abundance of only 1.7% ($\pm 4\%$) on average per subject was shared across 30% the healthy control cohort. There were no individual viral contigs shared across greater than 50% of the cohort. In contrast, clustering reduced the mean abundance of clusters unique to the subject to 1.3% ($\pm 3\%$), while there was a mean abundance of 15% ($\pm 6\%$) per subject shared across 30% of the cohort, 7.1% ($\pm 6.6\%$) across 50% and 0.7% ($\pm 1.4\%$) across 70%. A total of eight VCs were now shared across 30% of CD and UC cohorts where previously no viral contigs had been found (**Figure 1D**). Therefore the use of clustering resulted in increased commonality across the dataset and therefore allowed for the comparison of viromes between cohorts.

Analysis of viral clusters reveals IBD specific alterations in the gut virome

[00202] PCoA beta diversity analysis using Spearman distances found CD relapse and remission located furthest from controls (p-value: 0.0023 and 0.0032, respectively) followed by UC relapse/remission (p-values: 0.002/0.0023) (**Figure 2A**). Small variations were observed in the disease state of each condition but were not significant although this may be due to small sample sizes. PCoA without the division of disease status showed CD and UC beta diversity

significantly differed from healthy controls (p-values: 0.0002 and 0.0002; **Figure 7A**). The healthy cohort was also the least diverse across subjects, followed by UC, having the smallest pairwise distances between points (**Figure 7B**). This level of commonality was also reflected when comparing the number of clusters shared across each cohort as previously addressed (**Figure 1D**). There was an observable core virome (defined as presence across >50% of subjects) in the healthy cohort with two VCs (vc2 and vc7) shared across >70% of subjects and six (vc1, vc10, vc23, vc25, vc32, vc39) across >50%. The majority of these VCs were unclassified (i.e. did not cluster with known viral genomes) with the exception of vc1, classified as *Siphoviridae*, and vc10 which is a crAss-like phage. In contrast, core VC's were not found across UC subjects and just one core VC (vc32 unclassified) was found across CD subjects.

[00203] To assess the impact of whole virome analysis, *Caudovirales* and overall viral alpha diversity were assessed as these had been found to be different across cohorts using database dependent methods in the original analysis. Alpha diversity was calculated for each sample using the VC count tables. There were no significant differences across the cohorts and disease states for each disease (**Figure 2B**). Differences between the IBD conditions and healthy controls were compared using an additional diversity measurement (Shannon diversity) but no significance was found (**Figures 8A-8B**). The alpha diversity of any VCs assigned to *Caudovirales* families was also compared (**Figures 9A-9B**) and significance was found for CD (increased) versus healthy only.

[00204] DeSeq2 analysis revealed a number of classifiable VCs, including two crAss-like phages and two *Microviridae*, at significantly increased abundances in healthy controls compared to CD (**Figure 2C**) and UC (**Figure 2D**). vc19 and vc320 (crAss-like phages) were absent from all CD and only vc320 was in one subject with UC, but other clusters classified as crAss-like phages were present. Conversely VCs classified as *Siphoviridae* (nine for CD, eight for UC) and *Myoviridae* (one for CD, two for UC) were increased in CD and UC versus controls. However, many of the most differentially abundant clusters were taxonomically unassigned and were therefore classed as being a part of the “viral dark matter”. 49 VCs were increased in control samples relative to CD with 86 differentially abundant in total. 25 VCs were increased in control samples relative to UC with 59 differentially abundant in total. All DeSeq2 results are found in **Table 1** (control vs CD) and **Table 2** (control vs UC). Interestingly, 30 of the 37 VCs (81%) increased in CD compared to controls and 28 of the 34 (82%) for UC versus controls were

categorized as lysogenic. This was just 32% and 24% for VC increased in CD and UC, respectively. Further investigation into the presence of lysogenic VC abundance in each cohort indicated that CD subjects have significantly more reads aligned to lysogenic VCs than healthy controls (**Figures 10A-10B**).

The bacteriome also differs between patients with IBD and controls

[00205] Bacteriome data was compared to previously published studies to verify this dataset is not an outlier. Beta diversity (unweighted UniFrac) showed CD (relapse/remission) samples grouping furthest from controls (p-value: 0.0065, 0.0332) followed by UC (relapse/remission) (p-value: 0.018, 0.001) (**Figure 3A**), which was reflected in the virome composition.

Interestingly, and in contrast to the virome, the control bacteriome contained the largest variation amongst samples with CD having the smallest distances between points (**Figures 7C-7D**).

[00206] Decreased alpha diversity was observed (Chao1 diversity) in the IBD cohorts versus healthy controls with the largest differences observed in CD flare (p-value: 0.012) and remission (p-value: 0.018) along with UC Flare (p-value: 0.051) (**Figure 3B**). Due to the small sample sizes this analysis was also repeated without the division of disease status and using various metrics (**Figures 8C-8D**). For both Chao1 diversity and Shannon diversity, the healthy cohort was significantly higher than both IBD cohorts, while UC was also significantly increased when compared to CD (0.001).

[00207] A large number of taxa were found differentially abundant between control and CD (**Figure 3C**) and control versus UC (**Figure 3D**). A total of 113 taxa were decreased in CD versus controls while just 17 were increased. Similarly, 69 were increased in control vs UC and only 21 significantly increased in UC. Many of the taxa increased in controls versus both IBD cohorts were of the phyla *Firmicutes* and included the genera *Faecalibacterium* and the families *Ruminococcaceae* and *Clostridiales*. The most differentially abundant RSVs increased in CD versus controls included *Fusobacterium* and *Veillonella*, while the most increased in UC versus controls were *Clostridium sensu stricto* and *Lachnospiraceae* (DeSeq2 results are listed in **Table 3** (control vs CD) and **Table 4** (control vs UC)).

Correlations between PCoA and abundance counts reveal key drivers of gut microbiome composition

[00208] The drivers of significant shifts in beta diversity were assessed through correlations between PC coordinates and the VCs (for the virome) and RSVs (for the bacteriome). There were 25 VCs significantly correlated to PC-axes 1 and/or 2 (**Figure 4A**). Dependent upon the correlation coefficient, the associations could further be broken down into four quadrants. In quadrant 1 (top left), towards subjects with IBD, there were 18 significantly correlated and comprised of eight *Siphoviridae*, two *Myoviridae*, two Heterogeneous and six unclassified (**Table 5**). Quadrant 3 (bottom left) one *Myoviridae* and 1 unclassified VC were significantly correlated towards subjects with IBD. VCs classed as *Microviridae* and crAss-like phages were significantly correlated towards the healthy controls (quadrant 4, bottom right), while there were also two unclassified VCs.

[00209] There were 76 RSVs significantly correlated towards controls (quadrant 1) for the beta diversity of 16S composition (**Figure 4B**). The correlations with the highest correlation coefficient (rho values) included RSVs with taxonomic assignments to *Firmicutes*, *Ruminococcaceae* and *Alistipes*. Quadrant 3 correlations, also towards controls, contained 46 RSVs including *Alistipes indistinctus* and *Clostridiales*. For Quadrant 4, towards IBD subjects, four RSVs were significantly correlated including *Ruminococcus gnaves* and *Flavonifractor plautii* (**Table 6**).

[00210] The relationship between the virome and 16S composition was investigated through Procrustes analysis (**Figures 10A and 10B**). There was a significant positive correlation with an observed correlation coefficient of 0.7143 (p-value of 0.001). However, VC alpha diversity did not significantly correlate with observed bacterial species (**Figure 8E**), although there was significant weak correlation with Shannon diversity (p-value: 0.038, rho: 0.194) (**Figure 8F**).

Alterations in virome composition are less distinct between UC activity states

[00211] Differences in disease states (flare and remission) were investigated using a second cohort of 40 subjects with ulcerative colitis, sampled longitudinally resulting in 113 virome and 109 16S samples. Beta diversity analysis of virome composition using VCs (**Figure 5A**) did not show significant separation between flare and remission (p-value: 0.17). However, unclassified viral cluster vc40 was found to be significant (**Table 7**). In 16S analysis, the shift between flare

and remission in beta diversity was not significant (p-value: 0.022) and there were 14 RSVs correlated to PC-axes 1 or 2 (**Figure 5B, Table 8**). RSVs towards the shift in UC remission (quadrant 1) included *Faecalibacterium prausnitzii*, *Dorea longicatena* and *Coprococcus comes*. An RSV classified as *Ruminococcus gnavus* was the only RSV which correlated towards UC flare. The virome and 16S were correlated using Procrustes analysis and there was a significant positive correlation, in agreement with previous results, with an observed correlation coefficient of 0.906 (p-value of 0.001) (**Figure 12**).

[00212] Although the median alpha diversity was higher in the virome for UC flare (**Figure 5C**) and UC remission for the 16S (**Figure 5D**), these values were not significant when assessed using both Chao1 and Shannon diversity, again in agreement with the previous analysis. Viral load was estimated through spiking with a known concentration of lactococcal ϕ Q33 phage and was found to be negatively correlated with viral alpha diversity (ρ : -0.415, p-value: 0.009) (**Figure 13A**). Viral diversity was also investigated over time and in relation to disease status (**Figure 13B**) and although there were fluctuations in the time series there was no observable trend with disease status and a comparison resulted no significant differences (p-value: 0.383).

[00213] Two crAss-like phages were increased in subjects in remission when compared to flare along with 2 *Siphoviridae*, 1 *Microviridae* and 7 unclassified phage (**Figure 5E, Table 9**). Conversely there were 39 VCs increased in flare. These included two *Anelloviridae*, one *Myoviridae*, ten *Siphoviridae* and 24 unclassified. *Bacteroides* and *Dialister* were the only RSVs increased in remission while seven RSVs were increased in flare including *Enterococcus*, *Prevotella* and *Streptococcus* (**Figure 5F, Table 10**).

Virome composition aids the classification between Health and Disease

[00214] The ability of the virome and 16S composition to differentiate between patients with IBD and healthy controls was tested through the use of machine learning. Sample sizes were increased by combining UC and CD samples to form a composite IBD cohort. The virome alone (**Figure 6A**) yielded an accuracy of 0.769 (p-value of 0.032) with four of the top five contributors (vc39, vc23, vc38 and vc45) being increased in controls versus both IBD states. All five of these clusters were unclassified but two had CRISPR protospacer alignments to *Lachnospiraceae* and *Parabacteroides* while the remaining two had hits to *Bacteroides*. The 16S alone had a greater predictive power than the virome (accuracy: 0.824, p-value: 0.008) with an

RSV classified as *Ruminococcaceae* contributing the largest gain followed by a *Clostridiales* and *Odoribacter splanchnicus* (**Figure 6B**). The virome and the 16S were combined and the predictive power measured (**Figure 6C**). The accuracy increased to 0.853 (p-value: 0.0026) with the virome contributing to five of the top 20 most important features. Of these, 4 had CRISPR protospacers to bacteria including the order *Clostridiales*, the family *Lachnospiraceae*, genus *Pseudoflavonifractor*, *Clostridium* and *Johnsonella* along with *Fusobacterium* and *Bacteroides* (**Figure 14**). Differences between CD and healthy proved to be the main predictors of disease with 11 VCs/RSVs being decreased in CD and one increased when compared to controls.

[00215] ROC curve analysis was performed as a second measure of accuracy of each model (**Figure 6D**). The AUC (area under the curve) of the virome alone was 78.31%, a decrease compared to 16S AUC which yielded an AUC of 89.72%. However, the virome and 16S combined had the largest AUC with 94.79%, predicting all 16 patients with IBD as IBD and only misclassifying five controls as IBD.

Key VCs revealed by the analysis of IBD viromes

[00216] Through various approaches of virome analysis ten key VCs consistently emerged (**Figures 15A-15J**). A key VC was defined as any which was core in one cohort and largely absent from another and/or significantly correlated in the PCoA axes and differentially abundant between the cohorts. vc23, vc39 and vc10 were present in the healthy core and largely absent from the subjects with CD (7, 14 and 26% respectively) and UC (12, 14 and 40% respectively). These three VCs were all in the top seven importance factors in the machine learning while vc39 and vc23 were in the top two. vc23, although unclassified, contained CRISPR protospacers to *Parabacteroides*, while vc39, also unclassified, had hits to undefined *Lachnospiraceae*. C10, a crAss-like phage, did not feature any CRISPR protospacer alignments.

[00217] The remaining 7 key VCs (vc17, vc13, vc5, vc15, vc9, vc22 and vc101) were all significantly correlated to the PC-axes and were at significantly increased abundance in UC and/or CD compared to healthy controls, with the exception of vc101 which was increased in control and UC versus CD. vc13, vc15, vc17, all classified as *Siphoviridae*, had CRISPR protospacer hits to a number of genus of the *Firmicutes*, including *Blautia*, *Coprobacillus*, *Pentoiphilus*, *Ruminococcus*, *Enterococcus*, *Lactobacillus*, *Streptococcus* and *Clostridium* (**Figure 14**). vc5, vc9, vc22, classified as *Myoviridae*, contained CRISPR protospacers to

Firmicutes genera *Clostridium*, *Coprobacillus*, *Enterococcus*, *Lactobacillus*, *Johnsonella*, *Roseburia*, *Ruminococcus*, *Veillonella* and *Flavonifractor* along with the Proteobacteria *Parasutterella* (**Figure 14**). Finally, vc101, a *Microviridae*, did not have any CRISPR protospacer alignments.

[00218] The key VCs were shown to be effective as marker clusters for classifying individual subject GI microbiota datasets within the larger dataset as either diseased or healthy.

[00219] Below are the methods used in the Examples described above.

STAR Methods / Data Download

Original Norman et al., cohort

[00220] Raw sequencing reads (virome and 16S) for the Norman et al., 2015 cohort were downloaded using a link in the original publication (Norman et al., 2015. *Cell*, 160, 447-60).

Simponi cohort

To build upon these findings, the Simponi cohort, consisting of longitudinal samples from 40 subjects with UC, including 82 samples from periods of flare and 31 samples from periods of remission, was processed and analyzed. The processing included extraction of fecal VLP DNA, library preparation and sequencing. Processing also included extraction of fecal DNA, library preparation and 16S sequencing. Q33 spiking was also performed.

Bioinformatic viral processing

[00222] The samples described in Norman et al. were used. Raw sequence (2,199,754 ± 983,529) quality was assessed using FASTQC and filtered using Trimmomatic using the following parameters: SLIDINGWINDOW: 4:20, MINLEN: 60 HEADCROP 15; CROP 225. Human reads were removed using Kraken (v.0.10.5) (Wood and Salzberg, 2014. *Genome Biol*, 15, R46) and version 38 of the human genome, which resulted in a mean of 1,130,518 ± 436,424 sequences per sample. SPAdes meta (Nurk et al., 2017. *Genome Res*, 27, 824-834) was utilized to assemble the reads into contigs per sample accurately (Sutton et al., 2019. *Microbiome*, 7, 12) which were subsequently pooled and retained if longer than 1kb. Redundancy was removed with 90% identity over 90% of the length (of the shorter) retaining the longest contig in each case. Bacterial contamination was removed by using an extensive set of inclusion criteria to select

viral sequences only. Briefly, contigs were required to be: 1) VirSorter (Roux et al., 2015a. VirSorter: mining viral signal from microbial genomic data. *PeerJ*, 3, e985) positive, 2) circular, 3) a minimum of 2 pVogs with at least 3 per 1kb (Grazziotin et al., 2017. *Nucleic Acids Res*, 45, D491-D498), 4) alignment to an in-house crAssphage database (threshold: $1e^{-10}$) (Guerin et al., 2018. *Cell Host Microbe*, 24, 653-664 e6), 5) greater than 3kb with no hits to the nt database (vx.y) (threshold: $1e^{-10}$), 6) hits to viral RefSeq database (threshold: $1e^{-10}$) (v.89), and less than 3 ribosomal proteins as predicted using the COG database (Tatusov et al., 2000. *Nucleic Acids Res*, 28, 33-6).

[00223] Quality reads were subsequently aligned to the reference set of viral sequences ($n = 7,605$) using bowtie2. Using SAMTools, a count table was generated and finally a 75% breadth of coverage filter was employed to predict spurious bowtie2 alignments. Any viral sequences which did not feature a recruited read coverage of at least 1 over 75% of the total sequence length were set to 0. The final set of viral contigs was 7,582.

Clustering and Taxonomy

[00224] Protein sequences were predicted using Prodigal (Hyatt et al., 2010. *BMC Bioinformatics*, 11, 119) ($n=121,021$) and subsequently clustered using vContact2 (Bolduc et al., 2017. vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect Archaea and Bacteria. *PeerJ*, 5, e3243) using a pc-inflation and vc-inflation of 1.5 with all other parameters set to default. This resulted in 472 viral clusters of >2 members and 2,382 singletons, hereby referred to as a viral cluster (VC) with one member. A cluster count table was generated by summing all the counts from the previous table in each cluster. Taxonomic classification was assigned to a cluster using vContact2 and a custom database of viral genomes formed from the concatenation of the taxonomically classified portion of the NCBI's Viral RefSeq (v.89) and the JGI's IMG-VR (downloaded 9 January 2019). The resulting clusters were classified to family level based on the presence of reference genomes within. Clusters containing genomes from multiple families, were termed "heterogeneous", and may arise from disagreement between protein based phylogeny and current taxonomic classification discussed further by Bolduc *et al.* CRISPR protospacers were predicted from the human microbiome project bacterial reference genomes (VERSION/REF) using PILRCR (Edgar, 2007). These were aligned to VLS using blastn (-task "blastn-short") and formatted with blastn_formatter. (The top alignments with an

evaluate score $<1e-5$ to each VLS was retained in each case). A VC was deemed lysogenic if it contained VLS with alignments to PVOGs featuring annotated integrase genes or site specific recombinase genes.

Simponi

[00225] The same processing as described above was performed for the Simponi cohort where $2,523,262 \pm 1,289,619$ raw reads were quality filtered (Trimmomatic: SLIDINGWINDOW: 4:20, MINLEN: 60 HEADCROP 15; CROP 135 (fwd), 120 (rev)) and assembled yielding 8,089 viral contigs in the final count table which lead to 484 clusters of > 2 members and 4,521 of one member.

Bioinformatic 16S processing

[00226] The samples described in Norman et al. were used. Read quality was assessed on the raw reads ($68,146 \pm 32,196$) using FastQC before and after quality filtering using Trimmomatic; HEADCROP:15 CROP:235 SLIDINGWINDOW:4:20 MINLEN:30. The trimmed reads of the Norman *et al.* 16S dataset were then processed using DADA2 (Callahan et al., 2016. *Nat Methods*, 13, 581-3) (v1.10.1). To do this, reads were quality filtered further (truncLen=230, maxEE=1.4, truncQ=11), before dereplication and *de novo* chimera removal (method = "consensus"). 16S reads published in this study were processed using the same method (truncLen=c(180,100), maxEE=1.4, truncQ=2) and the resulting sequence tables of both datasets merged in DADA2. Chimeras were removed *de novo* from the combined datasets (method="consensus"), followed by a round of reference based chimera removal using UCHIME (Edgar et al., 2011. *Bioinformatics*, 27, 2194-200) (v4.2) against the ChimeraSlayer Gold database. Resulting non-chimeric RSVs were sorted by length, with all RSVs having a minimum length of 200 bp and a maximum of 260bp retained. The final count table resulted in a mean of $41,060 \pm 17,131$ counts per sample. Classification of retained RSVs was achieved using mothur (Schloss et al., 2009. *Appl Environ Microbiol*, 75, 7537-41) (v1.38.0, bootstrap ≥ 80), while SPINGO (Allard et al., 2015. *BMC Bioinformatics*, 16, 324) (v1.3, bootstrap ≥ 0.8 , similarity ≥ 0.5) was used for species level classification. The RDP v11.4 database was used in both instances.

Simponi

[00227] The same methods as above were employed to process the 16S raw data from the Simponi cohort. There were $382,602 \pm 181,911$ raw reads. The following Trimmomatic parameters were applied: HEADCROP:20 SLIDINGWINDOW:4:20 CROP:210 MINLEN:50, resulting in a mean of $76,619 \pm 40,278$ counts in the final count table per sample after being subjected to the bioinformatics pipeline.

Data Analysis and Statistics

[00228] All statistics and figure generation were performed in R (v.3.5.1). Alpha and beta diversity was calculated using phyloseq (v.1.26) while differential abundance was with DeSeq2 (v.1.22.1). Correlations were using the spearman method, an Adonis from the vegan library (v.2.5-3) was utilized to investigate for significance in the beta diversity while Procrustes coordinates and significance was generating using procuste and procuste.randtest from the vegan library. Significance was defined as less than 0.05 and all adjustments (where required) was using the Benjamini-hochberg method. For all statistical tests, one sample was chosen at random per subject. All figures were generated using ggplot2 (v.3.1.0). Machine learning was carried out in R using the XgBoost package (0.71.2). In each case, the model was trained on 70% of the data and results refer to the remaining 30% of the data which tested the model. Parameters were optimized for each model. ROC curves and accuracy were performed using the R library RORC (v.1.0-7). Contig figures were generated using GView (vx.y).

Data Availability

[00229] Accession numbers for downloading the original raw sequences used in Norman et al. can be found in Norman et al., 2015.

[00230] Below are the tables referenced in the Examples described above.

[00231] The abbreviations in the table are described as follows:

[00232] “DeSeq2” refers to software for estimating variance-mean dependence in count data from high-throughput sequencing assays, and for testing differential expression based on a model using the negative binomial distribution. See, Love MI, Huber W, Anders S (2014). “Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2.” *Genome Biology*, 15, 550.

[00233] “lfcSE” refers to the logfoldchangeStandard Error calculation performed by DeSeq2.

[00234] “stat” refers to the Wald statistic calculation performed by DeSeq2.

[00235] The “p-value” ranges from zero to one and indicates the probability of finding such values from a given null (H0) hypothesis.

[00236] The “p_{adj}” value is the p-value adjusted for multiple testing using the Benjamini-Hochberg method.

[00237] The remaining values, e.g., for “RSV”, “Control Mean”, “Control Median”, “Control Present”, “CD Mean”, “CD Median”, “CD Present”, “UC Mean”, “UC Median”, “UC Present”, “logfdr”, “Domain”, and “Classification”, “pc1” and “pc2”, refer to the control, Crohn’s disease, and ulcerative colitis samples or are understood by those of ordinary skill who work with DeSeq2.

[00238] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims. It is further to be understood that all values are approximate and are provided for description.

[00239] Patents, patent applications, publications, product descriptions, and protocols are cited throughout this application, the disclosures of which are incorporated herein by reference in their entireties for all purposes.

Table 1. DeSeq2 results of VC counts comparing Healthy controls to CD

VC	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
vc1	6539.36	0.65	1.15	0.56	5.74E-01	6.13E-01	4.41E-03
vc10	156782.86	0.19	1.57	0.12	9.05E-01	9.13E-01	1.10E-01
vc100	0.95	3.97	3.14	1.26	2.06E-01	2.87E-01	2.90E-06
vc101	1999.09	-9.87	2.24	-4.41	1.05E-05	2.99E-05	3.43E-02
vc102	5.65	24.12	3.14	7.68	1.58E-14	6.82E-14	0.00E+00
vc103	513.71	-4.85	3.13	-1.55	1.21E-01	2.04E-01	3.15E-03
vc104	256.01	-28.17	3.15	-8.93	4.10E-19	4.30E-18	4.34E-04
vc105	5.51	-5.66	3.15	-1.80	7.26E-02	1.49E-01	2.23E-04
vc106	2.91	-4.74	3.15	-1.50	1.33E-01	2.13E-01	1.10E-05
vc108	394.10	30.00	3.14	9.56	1.22E-21	2.97E-20	0.00E+00
vc109	10.39	-23.81	3.15	-7.55	4.37E-14	1.50E-13	1.15E-04
vc11	450.89	-2.63	2.01	-1.31	1.91E-01	2.78E-01	1.88E-03
vc111	1.77	-4.03	3.16	-1.28	2.02E-01	2.84E-01	1.42E-05
vc112	1678.85	-30.00	3.15	-9.52	1.81E-21	3.17E-20	1.49E-02
vc113	4.26	23.72	3.14	7.56	4.18E-14	1.46E-13	0.00E+00
vc114	3.12	-4.84	3.15	-1.54	1.25E-01	2.06E-01	5.85E-05
vc117	4.65	23.85	3.14	7.60	3.08E-14	1.17E-13	7.94E-07
vc118	13.13	25.23	3.14	8.04	9.32E-16	5.26E-15	4.93E-05
vc12	56520.69	-2.82	1.73	-1.63	1.04E-01	1.84E-01	4.22E-02
vc120	12.65	5.13	3.13	1.64	1.02E-01	1.84E-01	2.17E-06
vc124	51.33	-25.98	3.15	-8.24	1.74E-16	1.12E-15	4.70E-04
vc125	1.60	4.72	3.14	1.50	1.33E-01	2.13E-01	0.00E+00
vc126	1.78	4.87	3.14	1.55	1.21E-01	2.04E-01	1.73E-05
vc127	620.07	-4.12	1.78	-2.31	2.07E-02	5.17E-02	7.11E-04
vc128	0.48	2.97	3.15	0.95	3.44E-01	4.12E-01	0.00E+00
vc129	2.92	5.59	3.14	1.78	7.51E-02	1.53E-01	1.46E-06
vc13	421.13	6.52	2.29	2.85	4.44E-03	1.19E-02	9.30E-05
vc132	18.65	25.77	3.14	8.21	2.25E-16	1.38E-15	0.00E+00

vc135	3.56	5.87	3.14	1.87	6.14E-02	1.31E-01	0.00E+00
vc136	236.32	-29.86	3.15	-9.47	2.79E-21	4.10E-20	1.90E-02
vc138	31.88	-23.87	3.15	-7.57	3.75E-14	1.33E-13	4.23E-03
vc139	0.50	3.03	3.15	0.96	3.35E-01	4.07E-01	1.18E-05
vc14	696.72	9.92	2.78	3.57	3.59E-04	1.01E-03	1.12E-05
vc142	139.29	28.58	3.14	9.10	8.64E-20	1.06E-18	0.00E+00
vc143	19.68	-24.67	3.15	-7.82	5.16E-15	2.37E-14	3.11E-04
vc145	1.04	-3.29	3.16	-1.04	2.97E-01	3.78E-01	1.12E-05
vc146	2.10	5.11	3.14	1.63	1.04E-01	1.84E-01	0.00E+00
vc147	2.87	5.56	3.14	1.77	7.64E-02	1.53E-01	0.00E+00
vc148	1.53	-3.82	3.16	-1.21	2.26E-01	3.07E-01	5.49E-04
vc15	324.45	8.04	3.13	2.57	1.02E-02	2.64E-02	7.98E-05
vc151	0.53	3.12	3.15	0.99	3.22E-01	3.99E-01	0.00E+00
vc153	2.04	5.07	3.14	1.61	1.07E-01	1.86E-01	0.00E+00
vc154	23.05	-24.88	3.11	-7.99	1.37E-15	7.55E-15	1.03E-04
vc155	4298.96	30.00	3.14	9.56	1.22E-21	2.97E-20	1.20E-05
vc159	1.40	-3.70	3.16	-1.17	2.41E-01	3.20E-01	4.51E-05
vc16	870.41	-4.51	1.94	-2.32	2.02E-02	5.10E-02	2.82E-03
vc160	9.45	23.97	3.14	7.64	2.26E-14	9.55E-14	5.88E-06
vc165	6.63	-5.93	3.15	-1.88	6.02E-02	1.30E-01	5.28E-05
vc17	1007.16	3.41	2.54	1.34	1.80E-01	2.70E-01	1.32E-04
vc172	2.42	5.31	3.14	1.69	9.06E-02	1.76E-01	0.00E+00
vc177	0.92	-3.12	3.16	-0.99	3.24E-01	3.99E-01	1.74E-05
vc178	9.46	24.84	3.14	7.91	2.54E-15	1.27E-14	0.00E+00
vc18	348.79	-0.33	2.28	-0.15	8.83E-01	8.96E-01	1.79E-03
vc182	2.72	-4.64	3.15	-1.47	1.41E-01	2.21E-01	1.77E-05
vc183	2.02	-4.21	3.15	-1.34	1.82E-01	2.70E-01	3.91E-05
vc189	1.11	-3.39	3.16	-1.07	2.83E-01	3.65E-01	6.77E-05
vc19	2317.61	-30.00	2.60	-11.54	8.18E-31	9.00E-29	1.37E-02
vc190	27.11	-23.74	3.15	-7.53	5.08E-14	1.72E-13	4.54E-03
vc193	27.83	-25.15	3.15	-7.98	1.51E-15	8.12E-15	1.04E-03
vc194	1.69	-3.96	3.16	-1.26	2.09E-01	2.89E-01	2.71E-05
vc198	3.26	5.75	3.14	1.83	6.72E-02	1.41E-01	0.00E+00

vc2	8885.70	-0.33	1.05	-0.31	7.55E-01	7.79E-01	6.24E-03
vc20	200.38	2.29	1.93	1.18	2.37E-01	3.17E-01	4.72E-04
vc200	8.55	-6.29	3.15	-2.00	4.59E-02	1.06E-01	1.09E-04
vc206	4.26	-5.29	3.15	-1.68	9.35E-02	1.76E-01	1.48E-04
vc209	188.25	-27.76	3.15	-8.81	1.29E-18	1.24E-17	3.07E-03
vc21	1114.11	1.70	2.29	0.74	4.59E-01	5.10E-01	4.20E-04
vc210	3.92	-5.17	3.15	-1.64	1.01E-01	1.84E-01	2.53E-04
vc212	0.53	-2.40	3.16	-0.76	4.47E-01	4.99E-01	2.39E-05
vc216	15.22	-24.35	3.15	-7.72	1.15E-14	5.05E-14	1.24E-04
vc217	0.66	-2.68	3.16	-0.85	3.97E-01	4.55E-01	5.39E-06
vc218	4.65	23.85	3.14	7.60	3.08E-14	1.17E-13	4.52E-04
vc22	111.81	3.69	3.13	1.18	2.38E-01	3.17E-01	1.60E-04
vc220	1.30	-3.60	3.16	-1.14	2.54E-01	3.33E-01	7.53E-06
vc225	53.87	-26.05	2.37	-10.98	4.90E-28	2.69E-26	7.34E-05
vc23	28061.85	-8.45	1.70	-4.97	6.87E-07	2.02E-06	3.14E-02
vc232	4.86	23.91	3.14	7.61	2.65E-14	1.04E-13	5.05E-06
vc238	1.09	4.17	3.14	1.33	1.84E-01	2.72E-01	0.00E+00
vc24	364.08	-29.99	3.15	-9.51	1.85E-21	3.17E-20	3.89E-03
vc240	7.86	-6.17	3.15	-1.96	5.03E-02	1.15E-01	9.95E-03
vc241	0.40	-2.07	3.16	-0.66	5.12E-01	5.55E-01	6.65E-05
vc244	1.57	4.69	3.14	1.49	1.35E-01	2.15E-01	1.15E-06
vc25	7350.79	-8.26	1.41	-5.84	5.35E-09	1.66E-08	2.59E-02
vc251	6.43	-5.88	3.15	-1.87	6.21E-02	1.31E-01	1.50E-04
vc259	1.83	-4.06	3.16	-1.29	1.98E-01	2.83E-01	4.91E-06
vc26	132.79	-5.62	2.81	-2.00	4.57E-02	1.06E-01	4.09E-04
vc262	1.94	-4.16	3.16	-1.32	1.88E-01	2.75E-01	9.55E-05
vc264	7.04	24.42	3.14	7.78	7.28E-15	3.27E-14	0.00E+00
vc266	0.66	-2.68	3.16	-0.85	3.96E-01	4.55E-01	1.44E-05
vc267	0.99	4.03	3.14	1.28	1.99E-01	2.83E-01	0.00E+00
vc268	2.27	5.22	3.14	1.66	9.63E-02	1.77E-01	0.00E+00
vc269	1.91	4.97	3.14	1.58	1.13E-01	1.95E-01	0.00E+00
vc27	722.98	5.65	2.69	2.10	3.57E-02	8.62E-02	2.61E-04
vc270	0.97	4.00	3.14	1.27	2.03E-01	2.84E-01	0.00E+00

vc276	0.40	2.71	3.15	0.86	3.89E-01	4.51E-01	0.00E+00
vc28	258.08	8.87	3.13	2.83	4.60E-03	1.22E-02	1.70E-04
vc281	8.03	24.61	3.14	7.84	4.56E-15	2.14E-14	0.00E+00
vc282	0.95	-3.17	3.16	-1.00	3.16E-01	3.99E-01	8.50E-06
vc284	199.95	-27.81	3.15	-8.82	1.13E-18	1.13E-17	2.17E-03
vc29	38.21	-28.31	3.15	-8.98	2.74E-19	3.02E-18	5.42E-04
vc298	5.00	23.94	3.14	7.62	2.45E-14	1.00E-13	0.00E+00
vc3	3018.37	-1.10	1.51	-0.73	4.67E-01	5.13E-01	1.36E-02
vc30	2226.55	1.56	1.80	0.87	3.86E-01	4.51E-01	8.32E-03
vc31	277.93	0.59	2.48	0.24	8.11E-01	8.34E-01	1.05E-04
vc311	7.03	-6.01	3.15	-1.91	5.66E-02	1.23E-01	1.78E-04
vc32	161155.85	-1.82	1.34	-1.35	1.76E-01	2.67E-01	9.77E-02
vc320	27.36	-24.71	3.15	-7.84	4.58E-15	2.14E-14	2.44E-04
vc33	4663.51	-4.38	2.26	-1.94	5.26E-02	1.18E-01	1.95E-02
vc330	1.23	4.34	3.14	1.38	1.67E-01	2.58E-01	0.00E+00
vc34	16.26	-0.71	3.13	-0.23	8.20E-01	8.39E-01	4.35E-04
vc345	7.59	-6.12	3.15	-1.94	5.22E-02	1.18E-01	1.51E-03
vc346	0.57	-2.49	3.16	-0.79	4.30E-01	4.88E-01	5.55E-06
vc35	34.31	5.20	3.13	1.66	9.65E-02	1.77E-01	8.72E-06
vc36	180.86	28.97	3.14	9.23	2.72E-20	3.75E-19	5.79E-05
vc37	3494.98	-12.92	2.08	-6.21	5.14E-10	1.64E-09	8.83E-03
vc38	71955.23	-5.61	1.76	-3.18	1.45E-03	3.98E-03	7.59E-02
vc384	4.28	-5.30	3.15	-1.68	9.31E-02	1.76E-01	9.56E-05
vc39	30825.66	-9.01	1.58	-5.70	1.21E-08	3.68E-08	3.28E-02
vc396	0.49	3.00	3.15	0.95	3.40E-01	4.10E-01	0.00E+00
vc398	0.41	-2.10	3.16	-0.67	5.06E-01	5.51E-01	6.37E-06
vc4	2541.03	-1.00	1.73	-0.58	5.64E-01	6.08E-01	9.81E-03
vc40	20.64	25.83	3.14	8.23	1.88E-16	1.18E-15	1.65E-05
vc404	1.14	-3.42	3.16	-1.08	2.79E-01	3.61E-01	1.56E-05
vc41	450.71	-1.71	2.23	-0.77	4.44E-01	4.98E-01	1.59E-03
vc411	9.31	-23.65	3.15	-7.50	6.36E-14	2.12E-13	5.95E-05
vc414	3.51	-5.01	3.15	-1.59	1.12E-01	1.94E-01	4.98E-05
vc42	1404.53	-15.94	2.36	-6.76	1.38E-11	4.47E-11	1.64E-02

vc420	13.51	25.33	3.14	8.07	7.12E-16	4.12E-15	0.00E+00
vc421	1.16	4.26	3.14	1.36	1.75E-01	2.67E-01	0.00E+00
vc43	14.76	-1.41	3.13	-0.45	6.53E-01	6.84E-01	8.31E-05
vc44	7.43	-1.67	3.13	-0.53	5.93E-01	6.30E-01	1.09E-04
vc45	17753.18	-11.38	2.07	-5.49	4.05E-08	1.22E-07	2.44E-02
vc455	5.56	-5.67	3.15	-1.80	7.20E-02	1.49E-01	5.56E-03
vc456	73.88	-26.48	3.15	-8.40	4.46E-17	3.27E-16	9.28E-03
vc46	583.50	-1.75	3.08	-0.57	5.69E-01	6.11E-01	3.02E-03
vc462	0.49	-2.31	3.16	-0.73	4.65E-01	5.13E-01	4.59E-05
vc467	11.44	-23.93	3.15	-7.59	3.19E-14	1.18E-13	5.11E-05
vc47	8187.95	-4.12	2.14	-1.93	5.35E-02	1.18E-01	2.64E-02
vc48	22.76	25.41	3.14	8.09	5.76E-16	3.42E-15	1.87E-06
vc49	239.58	4.03	3.13	1.29	1.97E-01	2.83E-01	2.62E-04
vc5	1058.05	2.44	2.14	1.14	2.54E-01	3.33E-01	2.38E-04
vc50	1391.38	-3.44	2.26	-1.52	1.28E-01	2.09E-01	2.15E-02
vc51	2.53	-0.65	3.14	-0.21	8.36E-01	8.51E-01	2.21E-05
vc52	85.04	1.47	3.13	0.47	6.38E-01	6.72E-01	3.22E-04
vc55	335.45	-29.99	3.15	-9.51	1.87E-21	3.17E-20	5.29E-04
vc56	3430.30	-16.87	2.30	-7.33	2.22E-13	7.30E-13	1.10E-02
vc57	887.79	1.20	2.30	0.52	6.01E-01	6.36E-01	1.75E-03
vc58	30.66	-24.74	3.15	-7.85	4.29E-15	2.10E-14	1.47E-04
vc59	31798.33	-3.30	2.04	-1.62	1.06E-01	1.86E-01	3.05E-02
vc6	935.51	-4.40	1.58	-2.78	5.40E-03	1.41E-02	2.58E-03
vc60	3456.88	-8.71	3.00	-2.91	3.66E-03	9.93E-03	2.31E-02
vc61	2621.85	-10.44	1.75	-5.95	2.63E-09	8.27E-09	2.78E-02
vc62	6440.69	-30.00	2.68	-11.20	4.12E-29	3.02E-27	2.26E-02
vc63	35.73	2.66	2.70	0.99	3.25E-01	3.99E-01	9.26E-06
vc64	1352.90	-10.25	2.23	-4.59	4.47E-06	1.30E-05	9.36E-03
vc65	1206.32	0.77	2.42	0.32	7.49E-01	7.78E-01	4.51E-03
vc66	79.87	27.59	3.14	8.79	1.50E-18	1.38E-17	0.00E+00
vc67	653.20	4.06	3.13	1.30	1.94E-01	2.81E-01	1.24E-03
vc68	34.60	26.66	3.14	8.49	2.04E-17	1.60E-16	0.00E+00
vc69	4.61	23.83	3.14	7.59	3.22E-14	1.18E-13	5.51E-06

vc7	26124.14	-3.63	1.07	-3.40	6.72E-04	1.87E-03	2.65E-02
vc71	372.25	29.91	3.14	9.53	1.60E-21	3.17E-20	0.00E+00
vc72	3576.10	-4.71	2.30	-2.05	4.06E-02	9.70E-02	6.60E-03
vc73	716.14	30.00	3.14	9.56	1.22E-21	2.97E-20	0.00E+00
vc74	4.06	6.06	3.14	1.93	5.35E-02	1.18E-01	3.04E-05
vc75	174.66	-27.66	3.15	-8.77	1.73E-18	1.52E-17	1.22E-03
vc76	15247.19	-11.97	2.27	-5.27	1.33E-07	3.95E-07	3.13E-02
vc77	62.04	7.33	3.13	2.34	1.93E-02	4.94E-02	2.83E-06
vc78	1992.78	30.00	3.14	9.56	1.22E-21	2.97E-20	0.00E+00
vc79	1677.48	30.00	3.14	9.56	1.22E-21	2.97E-20	2.20E-07
vc8	84.47	2.84	3.13	0.91	3.64E-01	4.33E-01	6.59E-04
vc80	117.18	28.36	3.14	9.04	1.64E-19	1.89E-18	7.73E-05
vc82	976.72	-30.00	2.45	-12.26	1.41E-34	3.11E-32	6.51E-03
vc83	2.13	-4.29	3.15	-1.36	1.74E-01	2.67E-01	5.52E-05
vc84	57.86	-25.07	3.15	-7.95	1.85E-15	9.47E-15	8.13E-04
vc86	142.94	-27.29	3.15	-8.66	4.88E-18	4.13E-17	1.58E-03
vc89	87.97	-24.75	2.93	-8.45	3.02E-17	2.29E-16	6.18E-04
vc9	566.19	3.44	2.05	1.68	9.28E-02	1.76E-01	5.12E-04
vc90	28.05	0.24	3.13	0.08	9.40E-01	9.44E-01	1.68E-04
vc91	26.88	26.30	3.14	8.38	5.44E-17	3.86E-16	0.00E+00
vc92	98.59	-26.88	3.15	-8.52	1.53E-17	1.25E-16	1.03E-03
vc93	1460.42	2.88	2.40	1.20	2.30E-01	3.10E-01	7.74E-03
vc94	352.42	29.83	3.14	9.50	2.07E-21	3.25E-20	7.72E-05
vc95	9.31	23.78	3.14	7.57	3.64E-14	1.31E-13	0.00E+00
vc96	63.13	-26.17	3.15	-8.30	1.03E-16	6.89E-16	3.81E-03
vc97	4.96	23.94	3.14	7.62	2.46E-14	1.00E-13	8.86E-06
vc98	39.52	-2.43	3.13	-0.78	4.37E-01	4.93E-01	5.72E-04
vc99	26.56	-25.08	3.15	-7.95	1.80E-15	9.43E-15	6.61E-04
ERR843914_NODE _16_length_6283_c ov_8.28276	25.05	26.20	3.14	8.35	7.03E-17	4.83E-16	0.00E+00

ERR843915_NODE _154_length_2010_ cov_4.02353	1.05	-3.31	3.16	-1.05	2.95E-01	3.77E-01	3.20E-05
ERR843919_NODE _191_length_1400_ cov_918.941	13.25	-6.93	3.15	-2.20	2.81E-02	6.94E-02	2.57E-04
ERR843935_NODE _218_length_4332_ cov_7.12789	0.41	2.75	3.15	0.87	3.83E-01	4.50E-01	0.00E+00
ERR843935_NODE _232_length_4192_ cov_6.65289	0.48	2.97	3.15	0.95	3.44E-01	4.12E-01	0.00E+00
ERR843935_NODE _238_length_4127_ cov_5.06827	0.50	3.03	3.15	0.96	3.35E-01	4.07E-01	0.00E+00
ERR843946_NODE _45_length_1458_c ov_4.15182	1235.51	0.11	2.06	0.05	9.58E-01	9.58E-01	8.70E-04
ERR843946_NODE _47_length_1356_c ov_2.56341	192.14	-27.39	2.99	-9.16	5.15E-20	6.66E-19	3.05E-04
ERR843947_NODE _105_length_2913_ cov_3.96046	0.68	-2.72	3.16	-0.86	3.89E-01	4.51E-01	5.62E-05
ERR843963_NODE _174_length_1845_ cov_2.26592	3.34	-4.94	3.15	-1.57	1.17E-01	2.00E-01	1.23E-05
ERR843979_NODE _219_length_1216_ cov_4.18002	11.16	-6.68	3.15	-2.12	3.42E-02	8.36E-02	1.52E-04
ERR843988_NODE _62_length_10972_ cov_9.45644	2.26	5.22	3.14	1.66	9.67E-02	1.77E-01	0.00E+00

ERR843988_NODE _73_length_9057_c ov_16.1537	1.49	4.62	3.14	1.47	1.42E-01	2.21E-01	0.00E+00
ERR843988_NODE _80_length_8423_c ov_12.4432	1.56	4.68	3.14	1.49	1.36E-01	2.15E-01	0.00E+00
ERR844000_NODE _71_length_3167_c ov_8.44248	3.80	2.47	3.13	0.79	4.31E-01	4.88E-01	3.85E-06
ERR844003_NODE _349_length_2477_ cov_210.188	1.12	4.21	3.14	1.34	1.80E-01	2.70E-01	9.27E-07
ERR844016_NODE _70_length_2504_c ov_3.02817	8.67	-6.31	3.15	-2.00	4.53E-02	1.06E-01	1.62E-02
ERR844020_NODE _23_length_5895_c ov_16607.2	5.06	-5.54	3.15	-1.76	7.90E-02	1.57E-01	6.32E-03
ERR844022_NODE _79_length_1766_c ov_77.1251	12.08	-24.01	3.15	-7.61	2.65E-14	1.04E-13	1.63E-04
ERR844023_NODE _9_length_8998_co v_27.7459	3.03	-4.80	3.15	-1.52	1.28E-01	2.09E-01	1.58E-05
ERR844037_NODE _58_length_2663_c ov_4.82094	4.45	-5.35	3.15	-1.70	8.95E-02	1.76E-01	1.86E-04
ERR844046_NODE _166_length_3009_ cov_5.21733	0.41	-2.10	3.16	-0.67	5.06E-01	5.51E-01	2.77E-06
ERR844052_NODE _165_length_1995_ cov_41.0737	1.64	1.31	3.14	0.42	6.77E-01	7.06E-01	5.28E-06

ERR844055_NODE _66_length_9897_c ov_19.7659	1.74	4.84	3.14	1.54	1.23E-01	2.05E-01	0.00E+00
ERR844060_NODE _618_length_1268_ cov_8.21764	0.70	3.52	3.14	1.12	2.63E-01	3.42E-01	0.00E+00
ERR844060_NODE _80_length_8504_c ov_80.3276	2.86	5.56	3.14	1.77	7.67E-02	1.53E-01	0.00E+00
ERR844064_NODE _208_length_1069_ cov_3.91519	0.91	-3.11	3.16	-0.99	3.25E-01	3.99E-01	1.97E-05
ERR844068_NODE _63_length_1995_c ov_3.36959	0.94	-3.15	3.16	-1.00	3.19E-01	3.99E-01	3.20E-05
ERR844071_NODE _56_length_5651_c ov_21.5981	41.96	3.60	2.95	1.22	2.21E-01	3.02E-01	9.03E-05
ERR844071_NODE _90_length_4634_c ov_7.16903	0.75	-2.85	3.16	-0.90	3.67E-01	4.34E-01	1.11E-05
ERR844076_NODE _61_length_2246_c ov_31.8508	1.61	-3.88	3.16	-1.23	2.18E-01	3.00E-01	1.50E-04
ERR844079_NODE _60_length_1568_c ov_369.693	4.33	-5.31	3.15	-1.68	9.21E-02	1.76E-01	6.21E-05
VC	Control Median	Control Present (n=61)	CD Mean	CD Median	CD Present (n=27)	logfdr	Classificatio n
vc1	4.90E-04	37	7.76E-03	4.30E-04	17	0.21	Siphoviridae
vc10	9.22E-03	36	1.22E-01	0	7	0.04	CrAss-like
vc100	0	2	1.36E-05	0	3	0.54	Unclassified

vc101	0	17	1.29E-05	0	3	4.52	Microviridae
vc102	0	0	2.90E-04	0	2	13.17	Heterogeneous
vc103	0	8	2.55E-04	0	3	0.69	Siphoviridae
vc104	0	9	0.00E+00	0	0	17.37	Unclassified
vc105	0	3	0.00E+00	0	0	0.83	Unclassified
vc106	0	3	5.31E-06	0	2	0.67	Unclassified
vc108	0	0	4.67E-02	0	4	19.53	Heterogeneous
vc109	0	3	2.21E-05	0	1	12.82	Unclassified
vc11	0	16	6.15E-04	0	7	0.56	Siphoviridae
vc111	0	3	1.94E-05	0	2	0.55	Siphoviridae
vc112	0	12	9.55E-07	0	1	19.50	Unclassified
vc113	0	0	8.83E-05	0	4	12.84	Siphoviridae
vc114	0	4	1.74E-04	0	2	0.69	Unclassified
vc117	0	1	6.95E-04	0	3	12.93	Unclassified
vc118	0	1	6.46E-04	0	2	14.28	Unclassified
vc12	3.91E-05	31	2.26E-02	0	6	0.74	CrAss-like
vc120	0	3	4.13E-04	0	2	0.74	Unclassified
vc124	0	5	1.42E-03	0	1	14.95	Unclassified
vc125	0	0	1.22E-04	0	2	0.67	Unclassified
vc126	0	1	3.28E-05	0	2	0.69	Unclassified
vc127	0	24	6.28E-04	0	3	1.29	Unclassified
vc128	0	0	2.19E-05	0	3	0.39	Unclassified
vc129	0	1	4.08E-04	0	3	0.82	Unclassified
vc13	0	8	1.17E-02	0	10	1.92	Siphoviridae
vc132	0	0	6.11E-03	0	6	14.86	Unclassified
vc135	0	0	7.91E-04	0	2	0.88	Unclassified
vc136	0	11	0.00E+00	0	0	19.39	Unclassified
vc138	0	7	7.13E-04	0	1	12.88	Unclassified
vc139	0	1	1.14E-05	0	3	0.39	Unclassified
vc14	0	2	1.14E-02	0	10	2.99	Siphoviridae
vc142	0	0	6.55E-04	0	5	17.98	Unclassified

vc143	0	3	0.00E+00	0	0	13.63	Unclassified
vc145	0	2	2.38E-05	0	1	0.42	Unclassified
vc146	0	0	7.20E-05	0	3	0.74	Unclassified
vc147	0	0	6.83E-05	0	3	0.81	Unclassified
vc148	0	2	2.80E-06	0	1	0.51	Unclassified
vc15	0	5	2.71E-02	0	7	1.58	Siphoviridae
vc151	0	0	1.19E-04	0	3	0.40	Unclassified
vc153	0	0	1.63E-04	0	3	0.73	Siphoviridae
vc154	0	9	2.08E-05	0	2	14.12	Unclassified
vc155	0	3	3.91E-02	0	2	19.53	Unclassified
vc159	0	2	0.00E+00	0	0	0.50	Unclassified
vc16	0	20	1.19E-03	0	5	1.29	Siphoviridae
vc160	0	2	1.08E-03	0	3	13.02	Unclassified
vc165	0	5	0.00E+00	0	0	0.89	Unclassified
vc17	0	6	5.55E-03	0	10	0.57	Siphoviridae
vc172	0	0	2.59E-04	0	3	0.75	Siphoviridae
vc177	0	5	0.00E+00	0	0	0.40	Unclassified
vc178	0	0	3.12E-04	0	2	13.90	Unclassified
vc18	0	12	5.71E-03	0	7	0.05	Siphoviridae
vc182	0	3	0.00E+00	0	0	0.66	Unclassified
vc183	0	2	0.00E+00	0	0	0.57	Unclassified
vc189	0	3	0.00E+00	0	0	0.44	Unclassified
vc19	0	15	0.00E+00	0	0	28.05	CrAss-like
vc190	0	5	0.00E+00	0	0	12.76	Unclassified
vc193	0	4	0.00E+00	0	0	14.09	Unclassified
vc194	0	3	0.00E+00	0	0	0.54	Unclassified
vc198	0	0	9.51E-04	0	2	0.85	Siphoviridae
vc2	9.04E-04	47	4.95E-03	0	13	0.11	Podoviridae
vc20	0	15	2.52E-03	0	8	0.50	Siphoviridae
vc200	0	4	0.00E+00	0	0	0.97	Unclassified
vc206	0	2	0.00E+00	0	0	0.75	Unclassified
vc209	0	5	0.00E+00	0	0	16.91	Unclassified
vc21	0	12	2.43E-03	0	8	0.29	Siphoviridae

vc210	0	3	0.00E+00	0	0	0.74	Unclassified
vc212	0	3	0.00E+00	0	0	0.30	Unclassified
vc216	0	4	0.00E+00	0	0	13.30	Unclassified
vc217	0	4	0.00E+00	0	0	0.34	Unclassified
vc218	0	1	4.94E-04	0	2	12.93	Unclassified
vc22	0	5	5.04E-03	0	4	0.50	Myoviridae
vc220	0	2	0.00E+00	0	0	0.48	Unclassified
vc225	0	13	3.68E-06	0	1	25.57	Unclassified
vc23	1.26E-04	32	7.28E-03	0	2	5.70	Unclassified
vc232	0	1	2.88E-04	0	2	12.98	Unclassified
vc238	0	0	6.75E-05	0	3	0.57	Unclassified
vc24	0	8	0.00E+00	0	0	19.50	Unclassified
vc240	0	2	9.37E-07	0	1	0.94	Unclassified
vc241	0	2	0.00E+00	0	0	0.26	Myoviridae
vc244	0	1	3.82E-04	0	2	0.67	Unclassified
vc25	6.78E-05	36	3.97E-03	0	4	7.78	Unclassified
vc251	0	4	0.00E+00	0	0	0.88	Unclassified
vc259	0	4	5.61E-06	0	2	0.55	Genomoviridae
vc26	0	12	5.75E-05	0	2	0.97	Unclassified
vc262	0	2	0.00E+00	0	0	0.56	Unclassified
vc264	0	0	1.06E-04	0	2	13.49	Unclassified
vc266	0	6	1.69E-05	0	1	0.34	Unclassified
vc267	0	0	2.74E-05	0	3	0.55	Unclassified
vc268	0	0	6.26E-05	0	3	0.75	Unclassified
vc269	0	0	1.30E-04	0	3	0.71	Unclassified
vc27	0	7	3.81E-03	0	7	1.06	Heterogeneous
vc270	0	0	9.28E-05	0	3	0.55	Unclassified
vc276	0	0	7.17E-06	0	2	0.35	Unclassified
vc28	0	3	3.41E-03	0	6	1.91	Siphoviridae
vc281	0	0	2.41E-04	0	2	13.67	Unclassified
vc282	0	3	0.00E+00	0	0	0.40	CrAss-like

vc284	0	6	0.00E+00	0	0	16.95	Unclassified
vc29	0	6	2.10E-05	0	2	17.52	Siphoviridae
vc298	0	0	2.10E-03	0	2	13.00	Unclassified
vc3	0	27	5.29E-03	0	12	0.29	Siphoviridae
vc30	0	23	2.82E-02	0	8	0.35	Microviridae
vc31	0	7	2.26E-04	0	9	0.08	Siphoviridae
vc311	0	2	0.00E+00	0	0	0.91	Unclassified
vc32	6.79E-05	41	6.81E-02	5.30E-05	17	0.57	Unclassified
vc320	0	6	0.00E+00	0	0	13.67	CrAss-like
vc33	0	17	2.03E-02	0	5	0.93	Siphoviridae
vc330	0	0	8.22E-05	0	2	0.59	Unclassified
vc34	0	5	7.59E-05	0	6	0.08	Unclassified
vc345	0	2	0.00E+00	0	0	0.93	Unclassified
vc346	0	2	0.00E+00	0	0	0.31	Unclassified
vc35	0	3	2.31E-03	0	5	0.75	Unclassified
vc36	0	1	1.35E-02	0	5	18.43	Heterogeneous
vc37	0	20	5.38E-06	0	2	8.79	Unclassified
vc38	4.89E-05	31	1.08E-02	0	5	2.40	Unclassified
vc384	0	2	0.00E+00	0	0	0.75	Unclassified
vc39	1.76E-04	34	1.83E-02	0	4	7.43	Unclassified
vc396	0	0	1.02E-05	0	2	0.39	Unclassified
vc398	0	3	0.00E+00	0	0	0.26	Unclassified
vc4	0	26	8.18E-03	0	6	0.22	Unclassified
vc40	0	2	3.88E-03	0	6	14.93	Siphoviridae
vc404	0	2	5.07E-05	0	1	0.44	Unclassified
vc41	0	17	8.36E-03	0	3	0.30	Podoviridae
vc411	0	2	0.00E+00	0	0	12.67	Unclassified
vc414	0	2	0.00E+00	0	0	0.71	Unclassified
vc42	0	16	4.41E-03	0	2	10.35	Unclassified
vc420	0	0	6.45E-05	0	4	14.38	Unclassified
vc421	0	0	3.95E-05	0	3	0.57	Unclassified
vc43	0	6	2.77E-05	0	3	0.17	Siphoviridae

vc44	0	7	5.27E-06	0	3	0.20	Heterogeneous
vc45	0	23	6.13E-05	0	1	6.91	Unclassified
vc455	0	2	0.00E+00	0	0	0.83	Unclassified
vc456	0	3	0.00E+00	0	0	15.49	Unclassified
vc46	0	12	1.39E-02	0	4	0.21	Siphoviridae
vc462	0	2	0.00E+00	0	0	0.29	Unclassified
vc467	0	2	0.00E+00	0	0	12.93	Unclassified
vc47	0	19	4.76E-02	0	6	0.93	Unclassified
vc48	0	1	1.13E-03	0	6	14.47	Siphoviridae
vc49	0	4	1.16E-02	0	6	0.55	Unclassified
vc5	0	13	1.40E-03	0	9	0.48	Myoviridae
vc50	0	16	4.45E-03	0	5	0.68	Unclassified
vc51	0	3	2.56E-05	0	3	0.07	Siphoviridae
vc52	0	3	8.29E-04	0	5	0.17	Unclassified
vc55	0	7	3.34E-03	0	1	19.50	Unclassified
vc56	0	17	2.48E-06	0	1	12.14	Unclassified
vc57	0	14	1.07E-03	0	6	0.20	Unclassified
vc58	0	7	1.27E-05	0	1	13.68	Unclassified
vc59	0	24	1.93E-02	0	5	0.73	Unclassified
vc6	0	28	1.16E-02	0	4	1.85	Unclassified
vc60	0	13	3.43E-02	0	2	2.00	Unclassified
vc61	0	26	4.48E-06	0	3	8.08	Unclassified
vc62	0	15	0.00E+00	0	0	26.52	Unclassified
vc63	0	6	8.50E-05	0	5	0.40	Unclassified
vc64	0	17	3.62E-03	0	2	4.89	Unclassified
vc65	0	15	9.93E-03	0	4	0.11	Unclassified
vc66	0	0	1.93E-03	0	4	16.86	Myoviridae
vc67	0	11	1.08E-02	0	5	0.55	Myoviridae
vc68	0	0	2.80E-03	0	4	15.79	Siphoviridae
vc69	0	2	5.81E-05	0	4	12.93	Unclassified
vc7	2.57E-03	50	1.75E-02	0	11	2.73	Microviridae

vc71	0	0	2.85E-03	0	6	19.50	Heterogeneous
vc72	0	16	4.25E-03	0	5	1.01	Unclassified
vc73	0	0	1.65E-02	0	5	19.53	Unclassified
vc74	0	3	1.06E-04	0	2	0.93	Unclassified
vc75	0	8	2.10E-03	0	1	16.82	Unclassified
vc76	0	19	2.95E-05	0	2	6.40	Unclassified
vc77	0	2	1.07E-03	0	6	1.31	Unclassified
vc78	0	0	4.96E-03	0	5	19.53	Heterogeneous
vc79	0	1	4.09E-02	0	3	19.53	Heterogeneous
vc8	0	6	5.74E-03	0	3	0.36	Siphoviridae
vc80	0	3	2.87E-03	0	2	17.72	Unclassified
vc82	0	16	3.29E-06	0	1	31.51	Unclassified
vc83	0	3	3.62E-05	0	1	0.57	Unclassified
vc84	0	6	4.19E-03	0	1	14.02	Unclassified
vc86	0	7	7.90E-05	0	2	16.38	Unclassified
vc89	0	12	2.48E-02	0	2	15.64	Unclassified
vc9	0	11	3.39E-02	0	11	0.75	Myoviridae
vc90	0	6	3.98E-04	0	2	0.02	Unclassified
vc91	0	0	1.81E-03	0	5	15.41	Siphoviridae
vc92	0	6	0.00E+00	0	0	15.90	Unclassified
vc93	0	13	4.20E-02	0	6	0.51	Unclassified
vc94	0	1	7.76E-03	0	4	19.49	Unclassified
vc95	0	0	9.58E-05	0	5	12.88	Unclassified
vc96	0	7	2.39E-06	0	1	15.16	Podoviridae
vc97	0	1	4.50E-05	0	4	13.00	Unclassified
vc98	0	3	2.60E-03	0	3	0.31	Siphoviridae
vc99	0	7	6.69E-05	0	1	14.03	Myoviridae
ERR843914_NODE _16_length_6283_c ov_8.28276	0	0	4.52E-04	0	3	15.32	Unclassified

ERR843915_NODE _154_length_2010_ cov_4.02353	0	3	0.00E+00	0	0	0.42	CrAss-like
ERR843919_NODE _191_length_1400_ cov_918.941	0	5	0.00E+00	0	0	1.16	Unclassified
ERR843935_NODE _218_length_4332_ cov_7.12789	0	0	7.78E-06	0	2	0.35	Unclassified
ERR843935_NODE _232_length_4192_ cov_6.65289	0	0	8.48E-06	0	2	0.39	Unclassified
ERR843935_NODE _238_length_4127_ cov_5.06827	0	0	4.48E-06	0	2	0.39	Podoviridae
ERR843946_NODE _45_length_1458_c ov_4.15182	0	19	1.02E-03	0	5	0.02	Unclassified
ERR843946_NODE _47_length_1356_c ov_2.56341	0	10	1.71E-04	0	1	18.18	Unclassified
ERR843947_NODE _105_length_2913_ cov_3.96046	0	2	0.00E+00	0	0	0.35	Unclassified
ERR843963_NODE _174_length_1845_ cov_2.26592	0	4	0.00E+00	0	0	0.70	Unclassified
ERR843979_NODE _219_length_1216_ cov_4.18002	0	6	0.00E+00	0	0	1.08	Unclassified
ERR843988_NODE _62_length_10972_ cov_9.45644	0	0	7.07E-05	0	3	0.75	Unclassified

ERR843988_NODE _73_length_9057_c ov_16.1537	0	0	5.28E-05	0	2	0.66	Unclassified
ERR843988_NODE _80_length_8423_c ov_12.4432	0	0	6.48E-05	0	3	0.67	Unclassified
ERR844000_NODE _71_length_3167_c ov_8.44248	0	4	1.33E-04	0	3	0.31	Unclassified
ERR844003_NODE _349_length_2477_ cov_210.188	0	1	3.67E-05	0	2	0.57	Anelloviridae
ERR844016_NODE _70_length_2504_c ov_3.02817	0	6	5.23E-07	0	1	0.97	Smacoviridae
ERR844020_NODE _23_length_5895_c ov_16607.2	0	3	0.00E+00	0	0	0.81	Unclassified
ERR844022_NODE _79_length_1766_c ov_77.1251	0	3	7.92E-04	0	1	12.98	Unclassified
ERR844023_NODE _9_length_8998_co v_27.7459	0	3	1.52E-03	0	1	0.68	Unclassified
ERR844037_NODE _58_length_2663_c ov_4.82094	0	5	4.70E-05	0	1	0.75	CrAss-like
ERR844046_NODE _166_length_3009_ cov_5.21733	0	2	0.00E+00	0	0	0.26	Unclassified
ERR844052_NODE _165_length_1995_ cov_41.0737	0	2	2.50E-05	0	3	0.15	Anelloviridae

ERR844055_NODE _66_length_9897_c ov_19.7659	0	0	5.54E-05	0	2	0.69	Unclassified
ERR844060_NODE _618_length_1268_ cov_8.21764	0	0	4.82E-05	0	2	0.47	Unclassified
ERR844060_NODE _80_length_8504_c ov_80.3276	0	0	7.05E-05	0	2	0.81	Unclassified
ERR844064_NODE _208_length_1069_ cov_3.91519	0	3	0.00E+00	0	0	0.40	Unclassified
ERR844068_NODE _63_length_1995_c ov_3.36959	0	3	0.00E+00	0	0	0.40	CrAss-like
ERR844071_NODE _56_length_5651_c ov_21.5981	0	8	8.94E-03	0	6	0.52	Unclassified
ERR844071_NODE _90_length_4634_c ov_7.16903	0	3	0.00E+00	0	0	0.36	Unclassified
ERR844076_NODE _61_length_2246_c ov_31.8508	0	3	0.00E+00	0	0	0.52	Genomovirid ac
ERR844079_NODE _60_length_1568_c ov_369.693	0	4	0.00E+00	0	0	0.75	Unclassified

Table 2. DeSeq2 results of VC counts comparing Healthy controls to UC

VC	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
vc1	4142.91	0.09	0.95	0.10	9.21E-01	9.45E-01	4.41E-03

vc10	119827.86	-0.73	1.29	-0.56	5.74E-01	7.10E-01	1.10E-01
vc101	1671.17	-6.25	1.98	-3.15	1.64E-03	5.15E-03	3.43E-02
vc102	6.12	23.89	2.95	8.10	5.30E-16	1.93E-15	0.00E+00
vc103	419.64	-28.57	2.95	-9.68	3.79E-22	1.19E-20	3.15E-03
vc104	213.28	-4.78	2.94	-1.63	1.03E-01	1.76E-01	4.34E-04
vc105	7.34	-0.19	2.94	-0.06	9.49E-01	9.64E-01	2.23E-04
vc106	5.87	0.53	2.94	0.18	8.58E-01	9.24E-01	1.10E-05
vc109	12.76	-0.52	2.94	-0.18	8.59E-01	9.24E-01	1.15E-04
vc11	952.42	1.45	1.65	0.88	3.80E-01	5.19E-01	1.88E-03
vc111	3.61	1.07	2.94	0.36	7.16E-01	8.51E-01	1.42E-05
vc112	1327.36	-8.66	2.94	-2.95	3.19E-03	9.64E-03	1.49E-02
vc114	3.95	-0.39	2.94	-0.13	8.94E-01	9.32E-01	5.85E-05
vc115	10.91	24.70	2.95	8.38	5.38E-17	2.88E-16	0.00E+00
vc118	25.58	25.89	2.95	8.78	1.57E-18	1.24E-17	4.93E-05
vc119	3.32	5.45	2.95	1.85	6.48E-02	1.28E-01	6.29E-06
vc12	48096.69	-2.46	1.64	-1.49	1.35E-01	2.17E-01	4.22E-02
vc122	14.81	24.46	2.95	8.30	1.06E-16	5.05E-16	7.56E-07
vc123	11.34	24.75	2.95	8.40	4.61E-17	2.67E-16	5.15E-07
vc124	86.19	0.59	2.94	0.20	8.41E-01	9.17E-01	4.70E-04
vc127	698.93	-0.92	1.62	-0.57	5.70E-01	7.10E-01	7.11E-04
vc128	2.94	5.27	2.95	1.79	7.41E-02	1.36E-01	0.00E+00
vc13	194.30	5.00	2.13	2.35	1.88E-02	4.99E-02	9.30E-05
vc130	6.21	23.91	2.95	8.11	5.01E-16	1.87E-15	0.00E+00
vc136	1795.49	3.71	2.94	1.26	2.06E-01	3.03E-01	1.90E-02
vc138	20.32	-25.36	2.95	-8.59	8.88E-18	5.81E-17	4.23E-03
vc14	152.69	7.35	2.40	3.06	2.19E-03	6.75E-03	1.12E-05
vc143	16.33	-25.05	2.95	-8.49	2.16E-17	1.30E-16	3.11E-04
vc15	248.48	5.13	2.39	2.15	3.15E-02	7.98E-02	7.98E-05
vc152	5.49	23.35	2.95	7.92	2.36E-15	8.23E-15	0.00E+00
vc154	17.71	-3.85	2.70	-1.43	1.54E-01	2.37E-01	1.03E-04
vc16	1090.27	-0.46	1.68	-0.28	7.82E-01	8.72E-01	2.82E-03
vc161	154.96	28.06	2.95	9.52	1.70E-21	3.81E-20	2.53E-04
vc165	6.02	-5.82	2.95	-1.97	4.86E-02	1.06E-01	5.28E-05

vc17	2241.59	9.58	1.87	5.13	2.84E-07	9.50E-07	1.32E-04
vc175	17.12	25.33	2.95	8.59	8.45E-18	5.77E-17	1.82E-05
vc18	540.95	1.87	1.96	0.95	3.40E-01	4.72E-01	1.79E-03
vc181	29.12	26.04	2.95	8.84	9.96E-19	8.69E-18	1.82E-05
vc19	2419.21	-0.71	2.41	-0.29	7.68E-01	8.72E-01	1.37E-02
vc190	23.53	-3.90	2.94	-1.33	1.85E-01	2.79E-01	4.54E-03
vc193	24.87	-25.64	2.95	-8.68	3.89E-18	2.91E-17	1.04E-03
vc2	69904.25	4.11	0.90	4.58	4.69E-06	1.53E-05	6.24E-03
vc20	86.78	-0.10	1.88	-0.05	9.58E-01	9.64E-01	4.72E-04
vc200	5.90	-5.80	2.95	-1.96	4.97E-02	1.07E-01	1.09E-04
vc205	9.81	24.55	2.95	8.33	8.17E-17	4.06E-16	6.57E-04
vc206	3.53	-5.06	2.95	-1.71	8.69E-02	1.52E-01	1.48E-04
vc209	156.68	-28.13	2.95	-9.53	1.61E-21	3.81E-20	3.07E-03
vc21	1939.29	5.22	1.94	2.69	7.06E-03	1.98E-02	4.20E-04
vc210	2.73	-4.69	2.95	-1.59	1.13E-01	1.86E-01	2.53E-04
vc216	12.82	-24.73	2.95	-8.38	5.51E-17	2.88E-16	1.24E-04
vc218	297.96	29.33	2.95	9.95	2.48E-23	1.95E-21	4.52E-04
vc22	699.64	6.24	2.45	2.54	1.10E-02	3.02E-02	1.60E-04
vc225	43.57	-26.40	2.16	-12.20	3.29E-34	5.16E-32	7.34E-05
vc23	25280.09	-4.70	1.60	-2.94	3.29E-03	9.73E-03	3.14E-02
vc24	301.99	-28.80	2.95	-9.75	1.77E-22	9.27E-21	3.89E-03
vc240	6.52	-5.94	2.95	-2.01	4.43E-02	1.03E-01	9.95E-03
vc25	6865.77	-2.24	1.26	-1.78	7.45E-02	1.36E-01	2.59E-02
vc251	5.33	-5.65	2.95	-1.91	5.57E-02	1.14E-01	1.50E-04
vc26	158.56	-0.50	1.86	-0.27	7.89E-01	8.72E-01	4.09E-04
vc263	8.50	24.35	2.95	8.26	1.45E-16	6.33E-16	0.00E+00
vc27	120.64	2.42	2.94	0.82	4.10E-01	5.46E-01	2.61E-04
vc28	10.91	3.81	2.90	1.31	1.90E-01	2.81E-01	1.70E-04
vc284	178.71	-3.06	2.94	-1.04	2.98E-01	4.21E-01	2.17E-03
vc29	36.43	-2.20	2.94	-0.75	4.53E-01	5.88E-01	5.42E-04
vc3	3496.39	-0.15	1.35	-0.11	9.09E-01	9.39E-01	1.36E-02
vc30	2689.19	1.77	1.44	1.23	2.19E-01	3.19E-01	8.32E-03
vc31	95.00	2.01	2.50	0.81	4.21E-01	5.55E-01	1.05E-04

vc311	5.83	-5.78	2.95	-1.96	5.03E-02	1.07E-01	1.78E-04
vc32	151345.36	-0.59	1.17	-0.50	6.16E-01	7.55E-01	9.77E-02
vc320	22.73	-25.50	2.95	-8.64	5.84E-18	4.17E-17	2.44E-04
vc33	4587.21	-1.67	1.92	-0.87	3.87E-01	5.22E-01	1.95E-02
vc34	441.36	5.38	2.94	1.83	6.68E-02	1.30E-01	4.35E-04
vc345	6.29	-5.89	2.95	-1.99	4.61E-02	1.05E-01	1.51E-03
vc35	10.16	2.91	2.94	0.99	3.22E-01	4.51E-01	8.72E-06
vc36	73.96	26.05	2.95	8.84	9.57E-19	8.69E-18	5.79E-05
vc37	2060.00	0.21	1.63	0.13	8.97E-01	9.32E-01	8.83E-03
vc38	55886.73	-7.47	1.37	-5.46	4.80E-08	1.64E-07	7.59E-02
vc384	3.55	-5.06	2.95	-1.71	8.65E-02	1.52E-01	9.56E-05
vc39	21658.16	-4.28	1.52	-2.81	4.89E-03	1.40E-02	3.28E-02
vc4	1902.84	-2.78	1.49	-1.87	6.20E-02	1.25E-01	9.81E-03
vc40	67.92	27.22	2.81	9.70	3.01E-22	1.18E-20	1.65E-05
vc41	1139.84	-4.56	2.02	-2.25	2.43E-02	6.35E-02	1.59E-03
vc411	8.61	-24.19	2.95	-8.19	2.61E-16	1.05E-15	5.95E-05
vc413	11.22	24.74	2.95	8.39	4.76E-17	2.67E-16	0.00E+00
vc414	3.25	-4.94	2.95	-1.67	9.48E-02	1.63E-01	4.98E-05
vc42	44680.99	2.39	2.12	1.13	2.59E-01	3.69E-01	1.64E-02
vc43	20.06	0.40	2.94	0.14	8.91E-01	9.32E-01	8.31E-05
vc44	47.99	3.37	2.36	1.43	1.53E-01	2.37E-01	1.09E-04
vc45	16407.27	-2.67	1.82	-1.46	1.43E-01	2.25E-01	2.44E-02
vc455	4.61	-5.44	2.95	-1.84	6.54E-02	1.28E-01	5.56E-03
vc456	43.38	-26.39	2.95	-8.94	3.92E-19	4.39E-18	9.28E-03
vc46	458.93	-1.93	2.77	-0.70	4.86E-01	6.15E-01	3.02E-03
vc467	9.53	-24.33	2.95	-8.24	1.76E-16	7.47E-16	5.11E-05
vc47	10014.57	-0.57	1.97	-0.29	7.72E-01	8.72E-01	2.64E-02
vc48	33.21	26.25	2.95	8.91	5.25E-19	5.15E-18	1.87E-06
vc49	75.84	1.13	2.94	0.39	7.00E-01	8.39E-01	2.62E-04
vc5	290.90	1.86	1.62	1.15	2.52E-01	3.63E-01	2.38E-04
vc50	2774.70	1.13	1.62	0.70	4.86E-01	6.15E-01	2.15E-02
vc51	17.37	3.87	2.94	1.32	1.88E-01	2.81E-01	2.21E-05
vc52	45.72	-1.79	2.94	-0.61	5.42E-01	6.81E-01	3.22E-04

vc53	63.85	27.17	2.95	9.22	2.99E-20	4.27E-19	0.00E+00
vc54	2.94	5.27	2.95	1.79	7.41E-02	1.36E-01	1.10E-03
vc55	94.39	-27.46	2.95	-9.30	1.39E-20	2.43E-19	5.29E-04
vc56	3843.55	0.55	1.99	0.28	7.82E-01	8.72E-01	1.10E-02
vc57	479.00	-1.04	2.34	-0.45	6.56E-01	7.98E-01	1.75E-03
vc58	57.76	0.89	2.94	0.30	7.63E-01	8.72E-01	1.47E-04
vc59	26462.18	-2.96	1.53	-1.93	5.31E-02	1.11E-01	3.05E-02
vc6	1448.24	-1.18	1.37	-0.86	3.89E-01	5.22E-01	2.58E-03
vc60	5615.46	0.59	2.64	0.22	8.23E-01	9.03E-01	2.31E-02
vc61	2467.61	-2.64	1.63	-1.62	1.06E-01	1.78E-01	2.78E-02
vc62	4633.31	-8.83	2.35	-3.75	1.77E-04	5.68E-04	2.26E-02
vc63	2.79	0.16	2.94	0.05	9.57E-01	9.64E-01	9.26E-06
vc64	1154.06	-4.36	1.98	-2.20	2.81E-02	7.23E-02	9.36E-03
vc65	3633.65	-0.27	2.05	-0.13	8.95E-01	9.32E-01	4.51E-03
vc67	58.09	-6.16	2.94	-2.09	3.63E-02	8.76E-02	1.24E-03
vc68	116.97	27.38	2.95	9.29	1.57E-20	2.46E-19	0.00E+00
vc69	8.00	23.39	2.95	7.93	2.12E-15	7.56E-15	5.51E-06
vc7	28204.78	-0.75	0.95	-0.80	4.26E-01	5.58E-01	2.65E-02
vc70	7.00	24.08	2.95	8.17	3.16E-16	1.24E-15	4.09E-05
vc72	2848.53	0.28	1.83	0.15	8.77E-01	9.32E-01	6.60E-03
vc74	7.64	24.20	2.95	8.21	2.22E-16	9.19E-16	3.04E-05
vc75	152.29	-27.78	2.95	-9.41	5.04E-21	9.90E-20	1.22E-03
vc76	13263.32	-4.57	1.80	-2.53	1.13E-02	3.05E-02	3.13E-02
vc78	5.34	6.13	2.95	2.08	3.76E-02	8.95E-02	0.00E+00
vc79	3.84	5.65	2.95	1.92	5.53E-02	1.14E-01	2.20E-07
vc8	22.49	-0.80	2.94	-0.27	7.86E-01	8.72E-01	6.59E-04
vc82	9036.86	3.89	1.97	1.98	4.79E-02	1.06E-01	6.51E-03
vc83	2.42	-0.89	2.94	-0.30	7.63E-01	8.72E-01	5.52E-05
vc84	40.51	-26.30	2.95	-8.91	5.17E-19	5.15E-18	8.13E-04
vc85	8.53	24.35	2.95	8.26	1.45E-16	6.33E-16	2.53E-06
vc86	97.44	-5.26	2.94	-1.79	7.32E-02	1.36E-01	1.58E-03
vc88	9.78	24.55	2.95	8.33	8.27E-17	4.06E-16	2.82E-06
vc89	4380.97	7.11	2.52	2.82	4.80E-03	1.40E-02	6.18E-04

vc9	413.00	2.56	1.75	1.46	1.43E-01	2.25E-01	5.12E-04
vc90	20.54	-1.01	2.94	-0.34	7.32E-01	8.64E-01	1.68E-04
vc92	491.13	2.60	2.76	0.94	3.47E-01	4.78E-01	1.03E-03
vc93	314.03	-3.37	2.18	-1.54	1.22E-01	1.98E-01	7.74E-03
vc94	2.61	5.09	2.95	1.73	8.40E-02	1.50E-01	7.72E-05
vc95	6.54	23.98	2.95	8.13	4.12E-16	1.58E-15	0.00E+00
vc96	52.28	-26.65	2.95	-9.03	1.80E-19	2.35E-18	3.81E-03
vc97	38.99	26.48	2.95	8.98	2.60E-19	3.14E-18	8.86E-06
vc98	31.05	-25.94	2.95	-8.79	1.56E-18	1.24E-17	5.72E-04
vc99	178.02	1.27	2.94	0.43	6.65E-01	8.03E-01	6.61E-04
ERR843919_NODE_ 191_length_1400_co v_918.941	8.29	-6.29	2.95	-2.13	3.32E-02	8.29E-02	2.57E-04
ERR843942_NODE_ 149_length_2376_co v_469.01	4.43	5.86	2.95	1.99	4.69E-02	1.05E-01	0.00E+00
ERR843946_NODE_ 45_length_1458_cov _4.15182	708.44	-0.08	1.99	-0.04	9.68E-01	9.68E-01	8.70E-04
ERR843946_NODE_ 47_length_1356_cov _2.56341	182.90	-1.94	2.67	-0.73	4.67E-01	6.01E-01	3.05E-04
ERR843979_NODE_ 219_length_1216_co v_4.18002	8.09	-6.25	2.95	-2.12	3.43E-02	8.41E-02	1.52E-04
ERR844000_NODE_ 71_length_3167_cov _8.44248	58.52	5.06	2.52	2.01	4.44E-02	1.03E-01	3.85E-06
ERR844016_NODE_ 70_length_2504_cov _3.02817	7.19	-3.93	2.95	-1.33	1.82E-01	2.78E-01	1.62E-02

ERR844020_NODE_ 23_length_5895_cov_ _16607.2	4.20	-5.31	2.95	-1.80	7.24E-02	1.36E-01	6.32E-03
ERR844022_NODE_ 79_length_1766_cov_ _77.1251	10.02	-24.40	2.95	-8.26	1.43E-16	6.33E-16	1.63E-04
ERR844023_NODE_ 9_length_8998_cov_ 27.7459	2.52	-4.57	2.95	-1.55	1.22E-01	1.98E-01	1.58E-05
ERR844037_NODE_ 58_length_2663_cov_ _4.82094	3.71	-5.13	2.95	-1.74	8.26E-02	1.49E-01	1.86E-04
ERR844071_NODE_ 56_length_5651_cov_ _21.5981	33.46	0.67	2.39	0.28	7.79E-01	8.72E-01	9.03E-05
ERR844074_NODE_ 15_length_11407_co v_10.5426	18.32	25.15	2.95	8.53	1.45E-17	9.11E-17	2.12E-04
ERR844079_NODE_ 60_length_1568_cov_ _369.693	2.75	-4.70	2.95	-1.59	1.12E-01	1.86E-01	6.21E-05
VC	Control Median	Control Present (n=61)	UC Mean	UC Median	UC Present (n=42)	logfdr	Classificatio n
vc1	4.90E-04	37	1.08E-02	6.04E-04	27	0.02	Siphoviridae
vc10	9.22E-03	36	5.89E-02	0	17	0.15	CrAss-like
vc101	0	17	2.31E-04	0	6	2.29	Microviridae
vc102	0	0	1.87E-04	0	5	14.71	Heterogeneous
vc103	0	8	2.07E-06	0	1	19.92	Siphoviridae
vc104	0	9	6.67E-04	0	2	0.75	Unclassified
vc105	0	3	1.96E-04	0	4	0.02	Unclassified
vc106	0	3	5.66E-05	0	4	0.03	Unclassified

vc109	0	3	1.49E-04	0	4	0.03	Unclassified
vc11	0	16	7.62E-03	0	15	0.29	Siphoviridae
vc111	0	3	1.07E-05	0	3	0.07	Siphoviridae
vc112	0	12	1.14E-04	0	2	2.02	Unclassified
vc114	0	4	3.45E-05	0	4	0.03	Unclassified
vc115	0	0	9.23E-05	0	2	15.54	Siphoviridae
vc118	0	1	5.45E-04	0	4	16.91	Unclassified
vc119	0	1	9.37E-05	0	3	0.89	Myoviridae
vc12	3.91E-05	31	2.32E-02	0	7	0.66	CrAss-like
vc122	0	1	8.49E-03	0	2	15.30	Unclassified
vc123	0	1	4.35E-04	0	4	15.57	Unclassified
vc124	0	5	7.17E-03	0	4	0.04	Unclassified
vc127	0	24	1.03E-03	0	7	0.15	Unclassified
vc128	0	0	3.35E-05	0	3	0.87	Unclassified
vc13	0	8	6.73E-03	0	13	1.30	Siphoviridae
vc130	0	0	9.84E-05	0	4	14.73	Podoviridae
vc136	0	11	2.59E-02	0	4	0.52	Unclassified
vc138	0	7	1.81E-04	0	1	16.24	Unclassified
vc14	0	2	1.24E-03	0	13	2.17	Siphoviridae
vc143	0	3	1.70E-06	0	1	15.89	Unclassified
vc15	0	5	8.60E-04	0	11	1.10	Siphoviridae
vc152	0	0	4.55E-05	0	4	14.08	Unclassified
vc154	0	9	9.12E-05	0	3	0.63	Unclassified
vc16	0	20	1.55E-02	0	11	0.06	Siphoviridae
vc161	0	2	3.02E-03	0	4	19.42	Unclassified
vc165	0	5	0.00E+00	0	0	0.98	Unclassified
vc17	0	6	1.66E-02	0	16	6.02	Siphoviridae
vc175	0	1	1.14E-04	0	4	16.24	Unclassified
vc18	0	12	4.40E-03	0	11	0.33	Siphoviridae
vc181	0	2	3.70E-04	0	5	17.06	Unclassified
vc19	0	15	8.29E-03	0	5	0.06	CrAss-like
vc190	0	5	1.89E-05	0	2	0.55	Unclassified
vc193	0	4	0.00E+00	0	0	16.54	Unclassified

vc2	9.04E-04	47	9.54E-02	5.67E-04	28	4.81	Podoviridae
vc20	0	15	2.71E-04	0	7	0.02	Siphoviridae
vc200	0	4	0.00E+00	0	0	0.97	Unclassified
vc205	0	1	8.47E-04	0	2	15.39	Unclassified
vc206	0	2	0.00E+00	0	0	0.82	Unclassified
vc209	0	5	0.00E+00	0	0	19.42	Unclassified
vc21	0	12	2.12E-02	0	12	1.70	Siphoviridae
vc210	0	3	2.67E-05	0	1	0.73	Unclassified
vc216	0	4	0.00E+00	0	0	15.54	Unclassified
vc218	0	1	4.46E-03	0	6	20.71	Unclassified
vc22	0	5	1.13E-02	0	13	1.52	Myoviridae
vc225	0	13	0.00E+00	0	0	31.29	Unclassified
vc23	1.26E-04	32	8.83E-03	0	5	2.01	Unclassified
vc24	0	8	1.72E-04	0	2	20.03	Unclassified
vc240	0	2	0.00E+00	0	0	0.99	Unclassified
vc25	6.78E-05	36	2.35E-02	0	13	0.87	Unclassified
vc251	0	4	0.00E+00	0	0	0.94	Unclassified
vc26	0	12	4.58E-04	0	11	0.06	Unclassified
vc263	0	0	4.85E-04	0	2	15.20	Unclassified
vc27	0	7	1.65E-03	0	4	0.26	Heterogeneous
vc28	0	3	1.09E-03	0	7	0.55	Siphoviridae
vc284	0	6	1.60E-04	0	3	0.38	Unclassified
vc29	0	6	8.03E-05	0	5	0.23	Siphoviridae
vc3	0	27	6.81E-03	0	17	0.03	Siphoviridae
vc30	0	23	4.10E-02	0	17	0.50	Microviridae
vc31	0	7	8.00E-03	0	11	0.26	Siphoviridae
vc311	0	2	0.00E+00	0	0	0.97	Unclassified
vc32	6.79E-05	41	7.84E-02	6.36E-05	25	0.12	Unclassified
vc320	0	6	2.08E-06	0	1	16.38	CrAss-like
vc33	0	17	5.82E-03	0	10	0.28	Siphoviridae
vc34	0	5	9.66E-03	0	8	0.89	Unclassified
vc345	0	2	0.00E+00	0	0	0.98	Unclassified

vc35	0	3	9.75E-05	0	4	0.35	Unclassified
vc36	0	1	8.40E-03	0	5	17.06	Heterogeneous
vc37	0	20	1.17E-02	0	14	0.03	Unclassified
vc38	4.89E-05	31	3.12E-03	0	15	6.79	Unclassified
vc384	0	2	0.00E+00	0	0	0.82	Unclassified
vc39	1.76E-04	34	1.32E-02	0	6	1.86	Unclassified
vc4	0	26	1.16E-03	0	10	0.90	Unclassified
vc40	0	2	5.86E-04	0	8	19.93	Siphoviridae
vc41	0	17	1.36E-04	0	5	1.20	Podoviridae
vc411	0	2	0.00E+00	0	0	14.98	Unclassified
vc413	0	0	1.54E-04	0	2	15.57	Unclassified
vc414	0	2	0.00E+00	0	0	0.79	Unclassified
vc42	0	16	6.32E-02	0	10	0.43	Unclassified
vc43	0	6	1.58E-04	0	7	0.03	Siphoviridae
vc44	0	7	5.72E-04	0	10	0.63	Heterogeneous
vc45	0	23	9.85E-03	0	8	0.65	Unclassified
vc455	0	2	0.00E+00	0	0	0.89	Unclassified
vc456	0	3	0.00E+00	0	0	17.36	Unclassified
vc46	0	12	3.55E-04	0	5	0.21	Siphoviridae
vc467	0	2	0.00E+00	0	0	15.13	Unclassified
vc47	0	19	3.09E-02	0	9	0.06	Unclassified
vc48	0	1	4.97E-04	0	7	17.29	Siphoviridae
vc49	0	4	7.55E-04	0	4	0.08	Unclassified
vc5	0	13	2.12E-03	0	16	0.44	Myoviridae
vc50	0	16	2.26E-02	0	19	0.21	Unclassified
vc51	0	3	2.90E-04	0	6	0.55	Siphoviridae
vc52	0	3	9.70E-05	0	6	0.17	Unclassified
vc53	0	0	1.67E-03	0	6	18.37	Myoviridae
vc54	0	1	4.26E-04	0	5	0.87	Siphoviridae
vc55	0	7	0.00E+00	0	0	18.61	Unclassified
vc56	0	17	2.74E-02	0	9	0.06	Unclassified

vc57	0	14	5.26E-03	0	6	0.10	Unclassified
vc58	0	7	6.48E-04	0	6	0.06	Unclassified
vc59	0	24	1.16E-02	0	17	0.95	Unclassified
vc6	0	28	7.95E-04	0	12	0.28	Unclassified
vc60	0	13	3.26E-02	0	7	0.04	Unclassified
vc61	0	26	1.03E-02	0	8	0.75	Unclassified
vc62	0	15	6.88E-03	0	4	3.25	Unclassified
vc63	0	6	1.67E-05	0	5	0.02	Unclassified
vc64	0	17	4.89E-03	0	6	1.14	Unclassified
vc65	0	15	2.97E-03	0	9	0.03	Unclassified
vc67	0	11	1.01E-04	0	2	1.06	Myoviridae
vc68	0	0	1.04E-02	0	6	18.61	Siphoviridae
vc69	0	2	1.38E-04	0	7	14.12	Unclassified
vc7	2.57E-03	50	1.13E-02	5.56E-05	21	0.25	Microviridae
vc70	0	3	5.77E-05	0	4	14.91	Unclassified
vc72	0	16	9.80E-03	0	13	0.03	Unclassified
vc74	0	3	6.65E-05	0	4	15.04	Unclassified
vc75	0	8	1.56E-05	0	1	19.00	Unclassified
vc76	0	19	3.02E-02	0	12	1.52	Unclassified
vc78	0	0	3.83E-05	0	4	1.05	Heterogeneous
vc79	0	1	1.32E-04	0	3	0.94	Heterogeneous
vc8	0	6	2.07E-03	0	4	0.06	Siphoviridae
vc82	0	16	2.60E-02	0	11	0.98	Unclassified
vc83	0	3	3.62E-05	0	5	0.06	Unclassified
vc84	0	6	1.73E-05	0	1	17.29	Unclassified
vc85	0	1	4.74E-04	0	5	15.20	Unclassified
vc86	0	7	1.33E-04	0	5	0.87	Unclassified
vc88	0	3	4.80E-04	0	4	15.39	Unclassified
vc89	0	12	2.88E-02	0	8	1.86	Unclassified
vc9	0	11	5.78E-04	0	15	0.65	Myoviridae
vc90	0	6	8.58E-05	0	3	0.06	Unclassified

vc92	0	6	6.06E-03	0	8	0.32	Unclassified
vc93	0	13	1.70E-02	0	8	0.70	Unclassified
vc94	0	1	1.01E-04	0	2	0.82	Unclassified
vc95	0	0	1.88E-04	0	3	14.80	Unclassified
vc96	0	7	1.92E-04	0	1	17.63	Podoviridae
vc97	0	1	8.30E-04	0	5	17.50	Unclassified
vc98	0	3	3.50E-06	0	2	16.91	Siphoviridae
vc99	0	7	2.22E-03	0	2	0.10	Myoviridae
ERR843919_NODE_ 191_length_1400_co v_918.941	0	5	7.55E-05	0	2	1.08	Unclassified
ERR843942_NODE_ 149_length_2376_co v_469.01	0	0	2.50E-04	0	2	0.98	Anelloviridae
ERR843946_NODE_ 45_length_1458_cov _4.15182	0	19	5.41E-04	0	4	0.01	Unclassified
ERR843946_NODE_ 47_length_1356_cov _2.56341	0	10	1.28E-04	0	4	0.22	Unclassified
ERR843979_NODE_ 219_length_1216_co v_4.18002	0	6	1.48E-04	0	1	1.08	Unclassified
ERR844000_NODE_ 71_length_3167_cov _8.44248	0	4	9.38E-05	0	8	0.99	Unclassified
ERR844016_NODE_ 70_length_2504_cov _3.02817	0	6	2.23E-06	0	3	0.56	Smacoviridae
ERR844020_NODE_ 23_length_5895_cov _16607.2	0	3	0.00E+00	0	0	0.87	Unclassified

ERR844022_NODE_ 79_length_1766_cov_ _77.1251	0	3	6.42E-04	0	2	15.20	Unclassified
ERR844023_NODE_ 9_length_8998_cov_ 27.7459	0	3	0.00E+00	0	0	0.70	Unclassified
ERR844037_NODE_ 58_length_2663_cov_ _4.82094	0	5	0.00E+00	0	0	0.83	CrAss-like
ERR844071_NODE_ 56_length_5651_cov_ _21.5981	0	8	7.47E-05	0	8	0.06	Unclassified
ERR844074_NODE_ 15_length_11407_co v_10.5426	0	1	8.90E-04	0	3	16.04	Unclassified
ERR844079_NODE_ 60_length_1568_cov_ _369.693	0	4	4.90E-05	0	1	0.73	Unclassified

Table 3. DeSeq2 results of 16S RVS counts comparing Healthy controls to CD

RSV	Base Mean	log2Fold Change	lfcSE	stat	p-value	padj
Seq_0000375	25.46	-25.06	1.55	-16.15	1.14E-58	6.27E-56
Seq_0000528	30.69	-25.32	1.82	-13.95	3.30E-44	9.08E-42
Seq_0000466	17.27	-24.52	1.83	-13.37	8.51E-41	1.56E-38
Seq_0000756	16.12	-24.44	1.92	-12.75	3.30E-37	4.54E-35
Seq_0000643	20.08	-24.74	1.95	-12.71	5.07E-37	5.58E-35
Seq_0000534	23.19	-24.93	2.14	-11.67	1.71E-31	1.57E-29
Seq_0000373	41.84	-25.40	2.30	-11.05	2.23E-28	1.75E-26
Seq_0000797	13.97	-24.20	2.20	-11.01	3.45E-28	2.37E-26
Seq_0000284	12.35	-24.04	2.20	-10.94	7.39E-28	4.52E-26
Seq_0000988	9.77	-23.75	2.18	-10.89	1.33E-27	7.33E-26

Seq_0000201	118.61	-25.85	2.39	-10.81	3.10E-27	1.42E-25
Seq_0000360	27.34	-24.40	2.26	-10.82	2.86E-27	1.42E-25
Seq_0000206	30.31	-25.30	2.38	-10.61	2.67E-26	1.13E-24
Seq_0000395	10.83	-23.90	2.28	-10.46	1.25E-25	4.92E-24
Seq_0000827	8.52	-23.60	2.27	-10.42	2.05E-25	7.51E-24
Seq_0000937	10.86	-23.89	2.30	-10.40	2.53E-25	8.69E-24
Seq_0000272	53.22	-26.08	2.57	-10.17	2.81E-24	9.11E-23
Seq_0000309	21.42	23.99	2.40	9.99	1.77E-23	5.42E-22
Seq_0000299	81.89	-25.88	2.60	-9.94	2.76E-23	7.73E-22
Seq_0000835	14.28	-24.28	2.44	-9.94	2.81E-23	7.73E-22
Seq_0000644	17.31	-23.35	2.46	-9.48	2.53E-21	6.63E-20
Seq_0000863	14.09	-24.26	2.58	-9.40	5.22E-21	1.31E-19
Seq_0000697	9.07	24.19	2.66	9.10	8.85E-20	2.12E-18
Seq_0000440	18.56	-24.63	2.76	-8.92	4.56E-19	1.04E-17
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Seq_0000421	16.22	-24.46	3.01	-8.13	4.23E-16	8.95E-15
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Seq_0000551	10.30	-23.83	3.01	-7.92	2.34E-15	4.02E-14
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Seq_0000063	273.13	-10.24	1.51	-6.79	1.09E-11	1.76E-10
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Seq_0000144	125.14	-8.00	1.30	-6.15	7.83E-10	1.20E-08
Seq_0000265	54.28	-6.27	1.06	-5.89	3.86E-09	5.58E-08
Seq_0000364	27.67	-7.80	1.32	-5.89	3.79E-09	5.58E-08
Seq_0000852	11.35	-6.51	1.12	-5.79	6.97E-09	9.82E-08
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Seq_0000338	32.39	-5.56	1.05	-5.31	1.08E-07	1.38E-06

Seq_0000166	164.81	-9.46	1.87	-5.06	4.28E-07	5.36E-06
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Seq_0000508	19.27	-7.28	1.57	-4.65	3.36E-06	4.02E-05
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Seq_0000158	136.19	-4.60	1.02	-4.50	6.78E-06	7.61E-05
Seq_0000609	12.97	-5.86	1.30	-4.50	6.95E-06	7.64E-05
Seq_0000107	78.33	-6.01	1.37	-4.40	1.07E-05	1.15E-04
Seq_0000271	48.96	-5.80	1.33	-4.36	1.30E-05	1.37E-04
Seq_0000215	51.34	-4.70	1.09	-4.33	1.52E-05	1.58E-04
Seq_0000199	109.35	-6.23	1.44	-4.32	1.59E-05	1.59E-04
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Seq_0000482	18.72	-5.23	1.22	-4.28	1.88E-05	1.84E-04
Seq_0000131	210.63	-8.01	1.89	-4.23	2.31E-05	2.19E-04
Seq_0000242	110.57	-7.20	1.70	-4.24	2.28E-05	2.19E-04
Seq_0000391	17.11	-5.75	1.39	-4.15	3.36E-05	3.14E-04
Seq_0000731	8.68	-3.47	0.85	-4.11	4.01E-05	3.67E-04
Seq_0000976	6.87	-5.79	1.42	-4.07	4.74E-05	4.27E-04
Seq_0000274	36.93	-6.58	1.64	-4.00	6.30E-05	5.59E-04
Seq_0000193	73.77	-5.48	1.37	-3.99	6.62E-05	5.78E-04
Seq_0000237	67.82	-5.77	1.47	-3.92	8.79E-05	7.55E-04
Seq_0000383	34.04	-6.06	1.57	-3.85	1.20E-04	1.02E-03
Seq_0000113	284.81	-5.93	1.55	-3.82	1.33E-04	1.08E-03
Seq_0000684	12.31	-6.63	1.73	-3.83	1.30E-04	1.08E-03
Seq_0000983	7.28	-5.87	1.54	-3.82	1.33E-04	1.08E-03
Seq_0000119	92.31	5.16	1.36	3.79	1.49E-04	1.19E-03
Seq_0000501	13.33	-8.32	2.21	-3.77	1.65E-04	1.30E-03
Seq_0000032	662.52	-3.14	0.84	-3.76	1.70E-04	1.32E-03
Seq_0000231	66.58	6.66	1.79	3.72	1.96E-04	1.49E-03
Seq_0000326	42.47	-5.25	1.42	-3.71	2.11E-04	1.59E-03
Seq_0000151	141.57	-5.97	1.63	-3.66	2.50E-04	1.86E-03
Seq_0000734	4.65	-5.23	1.44	-3.63	2.83E-04	2.08E-03
Seq_0000489	17.24	-2.88	0.79	-3.63	2.88E-04	2.09E-03

Seq_0000192	99.34	-7.00	1.94	-3.61	3.01E-04	2.15E-03
Seq_0000867	7.90	-5.99	1.68	-3.57	3.62E-04	2.55E-03
Seq_0000089	39.67	7.49	2.12	3.54	4.04E-04	2.81E-03
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Seq_0001029	5.77	-5.54	1.59	-3.49	4.79E-04	3.17E-03
Seq_0001143	8.20	-6.04	1.77	-3.42	6.23E-04	4.08E-03
Seq_0000454	9.93	-4.98	1.46	-3.41	6.51E-04	4.21E-03
Seq_0000014	1389.04	-2.54	0.77	-3.29	1.00E-03	6.40E-03
Seq_0000571	11.69	-4.72	1.44	-3.28	1.03E-03	6.48E-03
Seq_0000425	25.15	-2.90	0.89	-3.25	1.15E-03	7.17E-03
Seq_0000491	21.96	-3.98	1.23	-3.25	1.17E-03	7.23E-03
Seq_0000020	1160.28	-3.09	0.95	-3.24	1.19E-03	7.24E-03
Seq_0000229	6.49	6.62	2.05	3.24	1.20E-03	7.28E-03
Seq_0000628	7.78	-5.97	1.85	-3.23	1.22E-03	7.30E-03
Seq_0000784	8.69	-3.69	1.15	-3.22	1.26E-03	7.48E-03
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Seq_0000869	10.70	-4.03	1.29	-3.12	1.79E-03	1.04E-02
Seq_0000890	11.49	-5.54	1.79	-3.10	1.94E-03	1.11E-02
Seq_0000132	44.71	6.66	2.18	3.06	2.24E-03	1.27E-02
Seq_0001313	5.45	-5.45	1.82	-3.00	2.71E-03	1.52E-02
Seq_0001256	4.31	-5.12	1.71	-2.99	2.76E-03	1.53E-02
Seq_0000275	61.96	-5.59	1.88	-2.97	2.96E-03	1.63E-02
Seq_0000701	5.63	-5.50	1.91	-2.88	4.00E-03	2.16E-02
Seq_0000850	6.91	-5.80	2.01	-2.88	3.99E-03	2.16E-02
Seq_0000134	144.37	-2.67	0.93	-2.87	4.16E-03	2.22E-02
Seq_0000439	36.15	-3.91	1.38	-2.83	4.60E-03	2.43E-02
Seq_0000179	95.95	-2.61	0.93	-2.81	4.89E-03	2.56E-02
Seq_0000196	29.94	4.97	1.79	2.78	5.38E-03	2.79E-02
Seq_0001253	5.46	-4.37	1.57	-2.78	5.49E-03	2.82E-02
Seq_0000122	125.65	2.59	0.94	2.76	5.69E-03	2.90E-02
Seq_0000418	37.66	-5.51	2.00	-2.75	5.90E-03	2.98E-02

Seq_0000170	91.46	-2.99	1.09	-2.74	6.10E-03	3.05E-02
Seq_0000236	20.28	2.01	0.74	2.72	6.59E-03	3.27E-02
Seq_0000103	160.44	-2.85	1.06	-2.70	6.95E-03	3.41E-02
Seq_0000479	6.51	-5.71	2.13	-2.68	7.44E-03	3.62E-02
Seq_0001013	6.02	-5.60	2.12	-2.64	8.26E-03	3.98E-02
Seq_0001395	4.67	-5.23	1.99	-2.63	8.42E-03	4.03E-02
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Seq_0001335	3.11	-4.19	1.61	-2.61	9.14E-03	4.26E-02
Seq_0001169	4.33	-5.12	1.97	-2.59	9.47E-03	4.37E-02
Seq_0000153	22.40	3.73	1.44	2.59	9.61E-03	4.40E-02
Seq_0000287	44.46	-2.20	0.85	-2.59	9.71E-03	4.41E-02
Seq_0000961	6.91	-5.80	2.25	-2.58	9.83E-03	4.43E-02
Seq_0000599	21.09	-3.55	1.38	-2.57	1.02E-02	4.56E-02
Seq_0000768	10.56	-3.78	1.48	-2.56	1.05E-02	4.63E-02
Seq_0001372	4.10	-5.04	1.97	-2.56	1.05E-02	4.63E-02
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Seq_0000101	15.77	7.59	3.00	2.53	1.13E-02	4.86E-02
Seq_0001057	5.54	-4.03	1.59	-2.53	1.14E-02	4.87E-02
Seq_0001748	2.58	-4.38	1.73	-2.52	1.16E-02	4.90E-02
Seq_0000323	49.13	-3.38	1.34	-2.51	1.19E-02	5.00E-02
Seq_0001280	4.68	-5.24	2.08	-2.51	1.20E-02	5.00E-02
Seq_0000344	22.41	-4.34	1.75	-2.48	1.31E-02	5.41E-02
Seq_0000824	7.35	-5.89	2.38	-2.48	1.32E-02	5.41E-02
Seq_0000209	31.68	-3.22	1.30	-2.47	1.34E-02	5.46E-02
Seq_0000993	5.64	-5.50	2.23	-2.47	1.37E-02	5.52E-02
Seq_0000622	22.51	-6.20	2.52	-2.46	1.38E-02	5.55E-02
Seq_0000324	35.99	-3.42	1.40	-2.45	1.43E-02	5.71E-02
Seq_0001177	5.71	-5.19	2.13	-2.44	1.47E-02	5.81E-02
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Seq_0001663	1.71	-3.79	1.61	-2.35	1.87E-02	7.26E-02

Seq_0000080	146.66	-1.98	0.85	-2.32	2.02E-02	7.78E-02
Seq_0000635	9.48	-6.25	2.70	-2.32	2.04E-02	7.79E-02
Seq_0000799	5.15	-5.37	2.34	-2.29	2.18E-02	8.27E-02
Seq_0000606	8.78	-6.14	2.68	-2.29	2.21E-02	8.33E-02
Seq_0000303	5.80	6.80	3.00	2.27	2.33E-02	8.66E-02
Seq_0001034	4.87	-5.29	2.33	-2.27	2.33E-02	8.66E-02
Seq_0000185	68.22	-3.20	1.42	-2.25	2.42E-02	8.93E-02
Seq_0001037	4.71	-5.24	2.33	-2.25	2.45E-02	9.00E-02
Seq_0000465	12.15	-2.03	0.90	-2.24	2.52E-02	9.17E-02
Seq_0000280	62.09	-2.18	0.98	-2.22	2.61E-02	9.40E-02
Seq_0001125	4.23	-3.72	1.67	-2.22	2.62E-02	9.40E-02
Seq_0000560	10.23	-2.77	1.26	-2.20	2.79E-02	9.91E-02
Seq_0001948	2.32	-4.22	1.92	-2.20	2.79E-02	9.91E-02
Seq_0000006	1604.41	-1.79	0.82	-2.18	2.89E-02	1.02E-01
Seq_0000021	857.82	-2.28	1.04	-2.18	2.91E-02	1.02E-01
Seq_0000554	6.93	-5.80	2.66	-2.18	2.92E-02	1.02E-01
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Seq_0000191	15.03	-4.48	2.09	-2.14	3.26E-02	1.11E-01
Seq_0000163	116.22	-1.76	0.82	-2.13	3.30E-02	1.12E-01
Seq_0001283	2.94	-4.56	2.15	-2.12	3.40E-02	1.15E-01
Seq_0001637	2.37	-4.26	2.01	-2.11	3.46E-02	1.16E-01
Seq_0000041	304.26	-2.78	1.32	-2.10	3.55E-02	1.18E-01
Seq_0000065	287.56	-1.58	0.76	-2.09	3.62E-02	1.19E-01
Seq_0000128	77.34	2.17	1.04	2.10	3.61E-02	1.19E-01
Seq_0001614	2.80	-4.50	2.15	-2.09	3.66E-02	1.20E-01
Seq_0000443	6.01	3.51	1.69	2.08	3.78E-02	1.23E-01
Seq_0000298	4.86	6.21	3.00	2.07	3.84E-02	1.24E-01
Seq_0001133	5.49	-5.47	2.64	-2.07	3.86E-02	1.24E-01
Seq_0000325	19.42	-3.90	1.89	-2.06	3.93E-02	1.25E-01
Seq_0000514	11.39	-4.66	2.26	-2.06	3.94E-02	1.25E-01
Seq_0001679	2.19	-4.14	2.01	-2.06	3.90E-02	1.25E-01
Seq_0000203	25.80	-2.38	1.16	-2.05	4.01E-02	1.26E-01

Seq_0000160	22.23	2.03	0.99	2.05	4.07E-02	1.27E-01
Seq_0001848	2.14	-4.10	2.01	-2.05	4.07E-02	1.27E-01
Seq_0000820	6.65	-5.74	2.82	-2.03	4.19E-02	1.30E-01
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Seq_0000698	6.51	-5.71	2.83	-2.02	4.36E-02	1.32E-01
Seq_0000129	131.06	-1.39	0.69	-2.01	4.45E-02	1.34E-01
Seq_0000427	7.74	-5.96	3.01	-1.98	4.75E-02	1.41E-01
Seq_0001329	3.54	-4.83	2.44	-1.98	4.73E-02	1.41E-01
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Seq_0001517	2.76	-4.47	2.28	-1.97	4.94E-02	1.44E-01
Seq_0000047	160.28	1.66	0.86	1.93	5.33E-02	1.54E-01
Seq_0000057	236.29	1.70	0.88	1.93	5.37E-02	1.54E-01
Seq_0000184	83.23	-1.34	0.69	-1.93	5.38E-02	1.54E-01
Seq_0000436	22.17	-4.51	2.34	-1.93	5.40E-02	1.54E-01
Seq_0000924	5.35	-5.43	2.81	-1.93	5.37E-02	1.54E-01
Seq_0000736	10.63	-3.56	1.85	-1.92	5.45E-02	1.54E-01
Seq_0001968	2.04	-4.04	2.11	-1.92	5.52E-02	1.56E-01
Seq_0001127	4.61	-2.61	1.36	-1.91	5.62E-02	1.58E-01
Seq_0002016	1.23	-3.31	1.74	-1.91	5.67E-02	1.58E-01
Seq_0000412	19.94	-3.36	1.77	-1.90	5.76E-02	1.60E-01
Seq_0001425	2.38	-4.26	2.26	-1.89	5.91E-02	1.63E-01
Seq_0001493	2.40	-4.27	2.27	-1.89	5.92E-02	1.63E-01
Seq_0000618	9.18	-3.39	1.80	-1.88	6.03E-02	1.65E-01
Seq_0000497	16.14	-1.78	0.95	-1.87	6.09E-02	1.66E-01
Seq_0001693	2.76	-4.48	2.41	-1.86	6.32E-02	1.71E-01
Seq_0000633	4.49	-5.18	2.79	-1.85	6.38E-02	1.72E-01
Seq_0001370	2.24	-4.18	2.25	-1.85	6.40E-02	1.72E-01
Seq_0000402	24.29	-2.40	1.31	-1.84	6.62E-02	1.77E-01
Seq_0001366	2.13	-4.10	2.24	-1.83	6.77E-02	1.80E-01
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Seq_0001332	2.57	-4.37	2.41	-1.82	6.95E-02	1.83E-01
Seq_0000741	11.03	-2.66	1.47	-1.80	7.14E-02	1.87E-01
Seq_0000269	30.25	1.86	1.03	1.80	7.22E-02	1.88E-01
Seq_0000515	5.25	-5.40	3.01	-1.80	7.26E-02	1.88E-01
Seq_0000819	2.34	4.67	2.62	1.78	7.50E-02	1.94E-01
Seq_0000100	76.27	1.08	0.61	1.77	7.72E-02	1.98E-01
Seq_0000378	4.88	-5.30	3.01	-1.76	7.84E-02	2.00E-01
Seq_0000665	2.49	4.35	2.48	1.75	7.99E-02	2.03E-01
Seq_0001707	2.26	-4.19	2.39	-1.75	8.00E-02	2.03E-01
Seq_0000995	1.41	3.04	1.75	1.74	8.21E-02	2.07E-01
Seq_0001500	2.21	-4.16	2.39	-1.74	8.23E-02	2.07E-01
Seq_0000085	210.98	-1.90	1.10	-1.73	8.41E-02	2.07E-01
Seq_0000210	65.04	-2.58	1.50	-1.73	8.41E-02	2.07E-01
Seq_0000435	4.61	-5.21	3.01	-1.73	8.31E-02	2.07E-01
Seq_0001659	1.82	-3.87	2.24	-1.73	8.34E-02	2.07E-01
Seq_0000772	2.35	5.16	3.00	1.72	8.53E-02	2.09E-01
Seq_0001787	2.60	-4.39	2.56	-1.71	8.68E-02	2.12E-01
Seq_0000918	4.33	-5.12	3.01	-1.70	8.86E-02	2.16E-01
Seq_0000208	21.56	5.06	2.99	1.69	9.02E-02	2.17E-01
Seq_0001348	1.67	-3.75	2.21	-1.69	9.03E-02	2.17E-01
Seq_0001596	2.52	-4.34	2.56	-1.69	9.01E-02	2.17E-01
Seq_0000749	4.14	-5.06	3.01	-1.68	9.26E-02	2.21E-01
Seq_0000689	4.01	4.07	2.43	1.68	9.30E-02	2.22E-01
Seq_0000037	143.43	1.94	1.16	1.67	9.53E-02	2.26E-01
Seq_0000387	4.98	-4.98	3.01	-1.66	9.76E-02	2.28E-01
Seq_0000871	2.91	-4.08	2.46	-1.66	9.74E-02	2.28E-01
Seq_0002087	1.33	-3.42	2.06	-1.66	9.73E-02	2.28E-01
Seq_0000015	97.98	-2.54	1.54	-1.65	9.93E-02	2.31E-01
Seq_0000367	2.27	-4.19	2.55	-1.65	9.96E-02	2.31E-01
Seq_0001130	2.31	-2.38	1.46	-1.63	1.02E-01	2.36E-01
Seq_0000445	9.76	-3.10	1.90	-1.63	1.03E-01	2.38E-01
Seq_0001115	2.38	4.88	3.00	1.63	1.04E-01	2.38E-01
Seq_0000411	20.14	-1.39	0.86	-1.62	1.06E-01	2.41E-01

Seq_0000962	4.33	3.38	2.10	1.61	1.07E-01	2.44E-01
Seq_0000187	11.88	3.07	1.91	1.60	1.09E-01	2.46E-01
Seq_0000505	15.76	-1.97	1.23	-1.60	1.09E-01	2.46E-01
Seq_0000873	2.06	-4.05	2.53	-1.60	1.09E-01	2.46E-01
Seq_0000281	54.66	-1.74	1.10	-1.58	1.14E-01	2.54E-01
Seq_0001919	1.65	-3.73	2.36	-1.58	1.14E-01	2.54E-01
Seq_0000176	1.65	4.65	2.96	1.57	1.16E-01	2.56E-01
Seq_0002312	1.17	-3.24	2.06	-1.57	1.16E-01	2.56E-01
Seq_0001413	1.91	-3.94	2.53	-1.56	1.18E-01	2.61E-01
Seq_0000424	3.21	-4.69	3.01	-1.56	1.19E-01	2.61E-01
Seq_0000079	86.73	3.14	2.04	1.54	1.22E-01	2.66E-01
Seq_0002516	0.97	-2.97	1.92	-1.54	1.22E-01	2.66E-01
Seq_0000329	3.08	-4.63	3.01	-1.54	1.24E-01	2.67E-01
Seq_0000477	3.08	-4.63	3.01	-1.54	1.24E-01	2.67E-01
Seq_0000777	2.23	-4.17	2.72	-1.53	1.25E-01	2.68E-01
Seq_0002671	0.84	-2.76	1.80	-1.53	1.25E-01	2.68E-01
Seq_0000738	4.94	-4.59	3.01	-1.53	1.27E-01	2.71E-01
Seq_0001454	2.16	-4.12	2.71	-1.52	1.28E-01	2.71E-01
Seq_0000810	2.91	-4.55	3.01	-1.51	1.31E-01	2.76E-01
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Seq_0000471	2.77	-4.48	3.01	-1.49	1.37E-01	2.87E-01
Seq_0000094	94.64	2.09	1.42	1.47	1.40E-01	2.92E-01
Seq_0000718	2.69	-4.43	3.01	-1.47	1.41E-01	2.92E-01
Seq_0002236	1.15	-3.22	2.18	-1.48	1.40E-01	2.92E-01
Seq_0000380	11.27	-4.40	3.00	-1.47	1.42E-01	2.94E-01
Seq_0000722	6.64	-2.97	2.03	-1.47	1.43E-01	2.94E-01
Seq_0002225	1.58	-3.67	2.50	-1.46	1.43E-01	2.94E-01
Seq_0000082	132.65	-1.41	0.97	-1.45	1.46E-01	2.98E-01
Seq_0002127	1.54	-3.63	2.50	-1.45	1.47E-01	2.99E-01
Seq_0000488	2.53	-4.35	3.01	-1.44	1.49E-01	3.02E-01
Seq_0000474	2.26	-4.18	2.90	-1.44	1.49E-01	3.02E-01
Seq_0000487	4.66	-4.33	3.01	-1.44	1.50E-01	3.02E-01
Seq_0002126	1.81	-3.86	2.69	-1.44	1.51E-01	3.03E-01

Seq_0000241	2.44	-4.29	3.01	-1.43	1.54E-01	3.07E-01
Seq_0000670	2.43	-4.29	3.01	-1.43	1.54E-01	3.07E-01
Seq_0000023	725.16	1.38	0.97	1.42	1.55E-01	3.08E-01
Seq_0002197	1.42	-3.51	2.49	-1.41	1.59E-01	3.14E-01
Seq_0000989	1.69	-3.77	2.68	-1.41	1.60E-01	3.15E-01
Seq_0000866	4.20	-2.89	2.07	-1.40	1.62E-01	3.16E-01
Seq_0000876	2.30	-4.21	3.01	-1.40	1.62E-01	3.16E-01
Seq_0000907	1.18	4.19	3.00	1.39	1.63E-01	3.18E-01
Seq_0000308	2.39	-3.80	2.74	-1.39	1.66E-01	3.19E-01
Seq_0000525	2.25	-4.18	3.01	-1.39	1.65E-01	3.19E-01
Seq_0000592	1.78	4.17	3.00	1.39	1.65E-01	3.19E-01
Seq_0001975	1.36	-3.45	2.49	-1.39	1.66E-01	3.19E-01
Seq_0001819	1.95	-3.97	2.89	-1.38	1.69E-01	3.24E-01
Seq_0000097	2.30	2.42	1.78	1.36	1.74E-01	3.29E-01
Seq_0000106	155.18	-1.57	1.15	-1.36	1.74E-01	3.29E-01
Seq_0000108	118.35	0.87	0.65	1.34	1.80E-01	3.29E-01
Seq_0000150	2.70	3.68	2.73	1.35	1.78E-01	3.29E-01
Seq_0000213	67.23	-1.80	1.34	-1.34	1.80E-01	3.29E-01
Seq_0000248	43.80	-0.91	0.68	-1.35	1.76E-01	3.29E-01
Seq_0000558	2.09	-4.07	3.01	-1.35	1.76E-01	3.29E-01
Seq_0000610	0.90	3.18	2.37	1.34	1.79E-01	3.29E-01
Seq_0000662	3.43	-4.04	3.01	-1.34	1.79E-01	3.29E-01
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Seq_0000729	2.05	-4.05	3.01	-1.34	1.79E-01	3.29E-01
Seq_0001104	3.16	-4.07	3.01	-1.35	1.76E-01	3.29E-01
Seq_0001558	1.27	-3.36	2.48	-1.36	1.75E-01	3.29E-01
Seq_0000227	29.22	2.95	2.21	1.33	1.82E-01	3.32E-01
Seq_0000143	123.68	-1.47	1.12	-1.31	1.89E-01	3.40E-01
Seq_0000680	1.93	-3.96	3.01	-1.31	1.89E-01	3.40E-01
Seq_0001195	1.41	-3.50	2.67	-1.31	1.89E-01	3.40E-01
Seq_0001222	3.14	-2.55	1.94	-1.31	1.89E-01	3.40E-01
Seq_0001243	1.73	-3.80	2.88	-1.32	1.87E-01	3.40E-01
Seq_0000555	0.97	3.93	3.00	1.31	1.91E-01	3.42E-01

Seq_0001059	1.87	-3.91	3.01	-1.30	1.93E-01	3.43E-01
Seq_0001081	1.88	-3.92	3.01	-1.30	1.93E-01	3.43E-01
Seq_0001458	1.88	-3.92	3.01	-1.30	1.93E-01	3.43E-01
Seq_0002209	1.36	-3.45	2.66	-1.30	1.94E-01	3.43E-01
Seq_0000624	0.93	3.88	3.00	1.29	1.97E-01	3.47E-01
Seq_0000653	1.99	-3.29	2.56	-1.28	1.99E-01	3.50E-01
Seq_0000498	1.77	-3.83	3.01	-1.27	2.03E-01	3.52E-01
Seq_0000748	8.48	3.00	2.35	1.27	2.02E-01	3.52E-01
Seq_0001301	3.52	-1.65	1.30	-1.27	2.04E-01	3.52E-01
Seq_0001520	1.76	-3.82	3.01	-1.27	2.04E-01	3.52E-01
Seq_0001634	1.78	-3.84	3.01	-1.28	2.02E-01	3.52E-01
Seq_0001646	0.83	-2.74	2.14	-1.28	2.01E-01	3.52E-01
Seq_0000145	96.75	-1.84	1.46	-1.26	2.09E-01	3.55E-01
Seq_0000417	7.95	-1.55	1.23	-1.26	2.09E-01	3.55E-01
Seq_0000468	29.34	-1.44	1.15	-1.26	2.08E-01	3.55E-01
Seq_0000547	3.06	-3.78	3.01	-1.26	2.09E-01	3.55E-01
Seq_0000872	9.95	-2.01	1.60	-1.26	2.08E-01	3.55E-01
Seq_0001924	1.05	-3.08	2.47	-1.25	2.12E-01	3.59E-01
Seq_0002013	1.04	-3.07	2.46	-1.25	2.13E-01	3.59E-01
Seq_0000300	26.23	-2.75	2.22	-1.24	2.17E-01	3.60E-01
Seq_0000616	1.64	-3.72	3.01	-1.24	2.16E-01	3.60E-01
Seq_0001294	1.45	-3.54	2.86	-1.24	2.16E-01	3.60E-01
Seq_0001943	1.43	-3.52	2.85	-1.23	2.17E-01	3.60E-01
Seq_0002558	0.88	-2.82	2.28	-1.24	2.16E-01	3.60E-01
Seq_0000225	101.95	2.16	1.76	1.23	2.19E-01	3.64E-01
Seq_0002455	0.99	-2.99	2.45	-1.22	2.22E-01	3.67E-01
Seq_0000800	9.10	-2.15	1.77	-1.22	2.23E-01	3.67E-01
Seq_0002693	0.75	-2.59	2.13	-1.22	2.24E-01	3.67E-01
Seq_0001097	1.56	-3.65	3.01	-1.21	2.25E-01	3.69E-01
Seq_0000098	24.29	1.65	1.37	1.21	2.28E-01	3.71E-01
Seq_0001451	1.54	-3.63	3.01	-1.21	2.28E-01	3.71E-01
Seq_0000603	1.52	-3.62	3.01	-1.20	2.30E-01	3.72E-01
Seq_0001210	1.52	-3.62	3.01	-1.20	2.30E-01	3.72E-01

Seq_0001208	1.51	-3.60	3.01	-1.20	2.32E-01	3.74E-01
Seq_0000347	15.68	-2.47	2.07	-1.19	2.33E-01	3.75E-01
Seq_0000580	0.73	3.56	3.01	1.19	2.36E-01	3.75E-01
Seq_0000713	1.48	-3.57	3.01	-1.19	2.36E-01	3.75E-01
Seq_0001431	2.09	-3.24	2.74	-1.18	2.37E-01	3.75E-01
Seq_0002395	0.93	-2.90	2.45	-1.18	2.36E-01	3.75E-01
Seq_0002643	0.93	-2.91	2.45	-1.19	2.35E-01	3.75E-01
Seq_0000838	1.46	-3.55	3.01	-1.18	2.38E-01	3.76E-01
Seq_0001086	1.45	-3.55	3.01	-1.18	2.39E-01	3.76E-01
Seq_0001317	2.00	-3.01	2.57	-1.17	2.41E-01	3.79E-01
Seq_0000173	1.42	-3.51	3.01	-1.17	2.43E-01	3.80E-01
Seq_0000793	1.42	-3.51	3.01	-1.17	2.43E-01	3.80E-01
Seq_0000847	1.23	-3.31	2.84	-1.16	2.44E-01	3.80E-01
Seq_0000061	303.97	-0.95	0.82	-1.16	2.47E-01	3.83E-01
Seq_0000226	41.90	2.31	2.02	1.15	2.51E-01	3.90E-01
Seq_0000076	220.44	-1.36	1.19	-1.14	2.55E-01	3.90E-01
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Seq_0000437	1.16	-3.22	2.83	-1.14	2.56E-01	3.90E-01
Seq_0000955	1.32	-3.40	3.01	-1.13	2.58E-01	3.90E-01
Seq_0001058	2.16	-2.37	2.08	-1.14	2.54E-01	3.90E-01
Seq_0001296	0.83	2.90	2.56	1.13	2.58E-01	3.90E-01
Seq_0001827	1.14	-3.19	2.83	-1.13	2.58E-01	3.90E-01
Seq_0002669	0.84	-2.76	2.44	-1.13	2.58E-01	3.90E-01
Seq_0002770	0.74	-2.57	2.27	-1.14	2.56E-01	3.90E-01
Seq_0001365	1.30	-3.39	3.01	-1.13	2.60E-01	3.92E-01
Seq_0000420	10.71	-2.71	2.42	-1.12	2.62E-01	3.93E-01
Seq_0000087	2.30	-3.36	3.01	-1.12	2.64E-01	3.96E-01
Seq_0000169	34.58	-1.77	1.60	-1.11	2.69E-01	4.02E-01
Seq_0002144	0.91	-2.88	2.61	-1.10	2.71E-01	4.04E-01
Seq_0000699	1.22	-3.30	3.01	-1.09	2.74E-01	4.07E-01
Seq_0001259	0.90	-2.85	2.61	-1.09	2.75E-01	4.07E-01
Seq_0000279	22.83	1.04	0.97	1.08	2.79E-01	4.11E-01
Seq_0001326	1.20	-3.27	3.01	-1.09	2.78E-01	4.11E-01

Seq_0002822	1.19	-3.26	3.01	-1.08	2.79E-01	4.11E-01
Seq_0001378	1.19	-3.25	3.01	-1.08	2.81E-01	4.11E-01
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Seq_0000054	311.03	1.69	1.59	1.06	2.89E-01	4.17E-01
Seq_0000164	84.46	1.90	1.79	1.06	2.88E-01	4.17E-01
Seq_0000282	31.50	-1.10	1.04	-1.06	2.91E-01	4.17E-01
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Seq_0001237	1.13	-3.18	3.01	-1.06	2.91E-01	4.17E-01
Seq_0001529	0.94	2.17	2.04	1.06	2.87E-01	4.17E-01
Seq_0001998	1.12	-3.18	3.01	-1.05	2.92E-01	4.17E-01
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Seq_0000832	2.37	-3.13	3.01	-1.04	2.98E-01	4.23E-01
Seq_0000294	10.81	1.60	1.54	1.04	3.00E-01	4.25E-01
Seq_0001434	1.18	-2.59	2.50	-1.04	3.00E-01	4.25E-01
Seq_0001764	1.66	-1.73	1.68	-1.03	3.01E-01	4.25E-01
Seq_0002464	0.92	-2.88	2.80	-1.03	3.04E-01	4.28E-01
Seq_0001336	1.04	-3.07	3.01	-1.02	3.08E-01	4.32E-01
Seq_0001477	1.02	-3.03	3.01	-1.00	3.15E-01	4.41E-01
Seq_0001200	3.51	-1.51	1.52	-1.00	3.19E-01	4.46E-01
Seq_0001592	0.99	-2.99	3.01	-0.99	3.21E-01	4.47E-01
Seq_0000582	0.98	-2.98	3.01	-0.99	3.23E-01	4.48E-01
Seq_0000675	9.26	1.57	1.59	0.99	3.23E-01	4.48E-01
Seq_0000111	94.92	-0.97	0.98	-0.98	3.25E-01	4.48E-01
Seq_0001419	0.97	-2.97	3.01	-0.98	3.25E-01	4.48E-01
Seq_0000732	6.01	-1.29	1.32	-0.98	3.28E-01	4.51E-01
Seq_0000933	0.95	-2.93	3.01	-0.97	3.31E-01	4.51E-01
Seq_0001675	1.19	-2.16	2.22	-0.98	3.29E-01	4.51E-01
Seq_0002183	0.93	-2.40	2.46	-0.97	3.31E-01	4.51E-01
Seq_0000398	30.67	1.49	1.53	0.97	3.33E-01	4.52E-01
Seq_0000579	1.94	-2.91	3.01	-0.97	3.33E-01	4.52E-01
Seq_0000802	0.93	-2.91	3.01	-0.97	3.34E-01	4.52E-01

Seq_0001540	0.80	-2.69	2.79	-0.97	3.35E-01	4.52E-01
Seq_0000389	0.91	-2.87	3.01	-0.95	3.41E-01	4.55E-01
Seq_0000632	0.90	-2.85	3.01	-0.95	3.44E-01	4.55E-01
Seq_0000929	1.27	-2.86	3.01	-0.95	3.42E-01	4.55E-01
Seq_0001095	0.90	-2.85	3.01	-0.95	3.44E-01	4.55E-01
Seq_0001226	0.90	-2.86	3.01	-0.95	3.43E-01	4.55E-01
Seq_0001475	0.91	-2.87	3.01	-0.95	3.41E-01	4.55E-01
Seq_0001765	0.91	-2.88	3.01	-0.96	3.39E-01	4.55E-01
Seq_0002405	0.77	2.88	3.01	0.96	3.39E-01	4.55E-01
Seq_0002292	0.87	-2.82	3.01	-0.94	3.49E-01	4.62E-01
Seq_0000270	56.32	1.10	1.18	0.93	3.52E-01	4.63E-01
Seq_0000846	0.86	-2.80	3.01	-0.93	3.52E-01	4.63E-01
Seq_0000432	0.86	-2.80	3.01	-0.93	3.53E-01	4.64E-01
Seq_0000130	165.65	-0.80	0.87	-0.92	3.57E-01	4.66E-01
Seq_0001322	0.99	-2.60	2.83	-0.92	3.57E-01	4.66E-01
Seq_0002593	0.79	-1.99	2.16	-0.92	3.56E-01	4.66E-01
Seq_0001721	0.85	-2.77	3.01	-0.92	3.59E-01	4.66E-01
Seq_0002128	0.82	-2.72	3.00	-0.91	3.65E-01	4.73E-01
Seq_0000968	0.82	-2.73	3.01	-0.90	3.66E-01	4.73E-01
Seq_0000949	0.79	-2.66	3.01	-0.88	3.77E-01	4.85E-01
Seq_0000963	0.79	-2.66	3.01	-0.88	3.76E-01	4.85E-01
Seq_0001685	0.78	-2.66	3.01	-0.88	3.78E-01	4.86E-01
Seq_0000311	22.27	-1.38	1.59	-0.87	3.87E-01	4.96E-01
Seq_0000795	0.75	-2.59	3.01	-0.86	3.90E-01	4.98E-01
Seq_0001261	1.90	2.07	2.42	0.86	3.92E-01	4.98E-01
Seq_0001512	1.09	-2.58	3.01	-0.86	3.91E-01	4.98E-01
Seq_0001605	0.75	-2.58	3.01	-0.86	3.92E-01	4.98E-01
Seq_0002119	0.73	-2.56	2.99	-0.85	3.93E-01	4.98E-01
Seq_0000042	496.22	-0.63	0.75	-0.84	3.99E-01	4.99E-01
Seq_0000332	2.54	2.53	2.99	0.84	3.99E-01	4.99E-01
Seq_0000739	0.73	-2.56	3.01	-0.85	3.96E-01	4.99E-01
Seq_0000823	4.72	-1.63	1.93	-0.85	3.98E-01	4.99E-01
Seq_0001225	0.73	-2.55	3.01	-0.85	3.97E-01	4.99E-01

Seq_0001674	0.73	-2.55	2.99	-0.85	3.95E-01	4.99E-01
Seq_0000052	16.88	2.50	2.98	0.84	4.03E-01	5.02E-01
Seq_0000370	32.83	-0.78	0.93	-0.84	4.03E-01	5.02E-01
Seq_0001269	3.53	-1.60	1.98	-0.81	4.19E-01	5.19E-01
Seq_0001409	2.11	-1.70	2.10	-0.81	4.19E-01	5.19E-01
Seq_0002645	0.83	-1.95	2.46	-0.79	4.27E-01	5.28E-01
Seq_0000073	213.21	-1.00	1.29	-0.78	4.36E-01	5.37E-01
Seq_0000400	32.23	1.69	2.18	0.77	4.39E-01	5.37E-01
Seq_0000499	0.94	-2.19	2.82	-0.78	4.37E-01	5.37E-01
Seq_0000585	8.01	2.05	2.65	0.77	4.40E-01	5.37E-01
Seq_0001878	0.73	-1.89	2.44	-0.77	4.39E-01	5.37E-01
Seq_0000093	154.05	-0.73	0.96	-0.77	4.43E-01	5.40E-01
Seq_0000343	27.76	-1.03	1.35	-0.76	4.45E-01	5.42E-01
Seq_0000496	17.81	-1.90	2.52	-0.75	4.52E-01	5.48E-01
Seq_0001286	1.40	-2.25	3.01	-0.75	4.54E-01	5.50E-01
Seq_0002351	0.78	-1.52	2.04	-0.74	4.57E-01	5.52E-01
Seq_0000394	25.75	-1.08	1.46	-0.74	4.60E-01	5.55E-01
Seq_0000044	688.02	1.13	1.55	0.73	4.64E-01	5.57E-01
Seq_0002105	0.82	-1.80	2.46	-0.73	4.63E-01	5.57E-01
Seq_0001254	1.06	-2.20	3.01	-0.73	4.65E-01	5.57E-01
Seq_0000716	1.51	-1.75	2.57	-0.68	4.95E-01	5.92E-01
Seq_0000565	2.02	2.00	3.00	0.67	5.03E-01	6.01E-01
Seq_0000448	14.52	-0.76	1.15	-0.66	5.09E-01	6.06E-01
Seq_0000450	33.96	-0.73	1.13	-0.65	5.17E-01	6.13E-01
Seq_0000470	6.61	0.92	1.42	0.65	5.17E-01	6.13E-01
Seq_0000171	103.66	-0.55	0.86	-0.63	5.27E-01	6.22E-01
Seq_0000874	0.75	-1.91	3.01	-0.63	5.26E-01	6.22E-01
Seq_0001014	5.49	-0.61	0.96	-0.63	5.29E-01	6.23E-01
Seq_0000195	2.06	1.88	2.99	0.63	5.31E-01	6.23E-01
Seq_0000105	251.48	-0.75	1.22	-0.62	5.35E-01	6.28E-01
Seq_0000230	22.69	-0.81	1.31	-0.61	5.39E-01	6.29E-01
Seq_0000314	9.59	1.15	1.87	0.62	5.38E-01	6.29E-01
Seq_0000674	10.44	1.20	2.04	0.59	5.58E-01	6.50E-01

Seq_0000340	7.66	1.72	2.99	0.57	5.66E-01	6.56E-01
Seq_0000755	1.14	1.72	3.00	0.57	5.66E-01	6.56E-01
Seq_0000840	0.90	-1.13	1.98	-0.57	5.68E-01	6.57E-01
Seq_0000285	2.59	1.68	2.99	0.56	5.74E-01	6.64E-01
Seq_0000181	37.86	0.81	1.46	0.56	5.77E-01	6.65E-01
Seq_0001660	1.21	-1.67	3.01	-0.56	5.78E-01	6.65E-01
Seq_0000522	8.86	-0.50	0.90	-0.55	5.80E-01	6.66E-01
Seq_0000062	282.98	-0.37	0.67	-0.55	5.83E-01	6.68E-01
Seq_0000349	9.84	0.79	1.51	0.52	6.01E-01	6.87E-01
Seq_0000254	1.99	-1.55	3.00	-0.52	6.05E-01	6.90E-01
Seq_0000217	0.73	-1.47	3.01	-0.49	6.25E-01	7.08E-01
Seq_0000232	42.11	-0.56	1.14	-0.49	6.24E-01	7.08E-01
Seq_0000694	11.60	-0.57	1.16	-0.49	6.22E-01	7.08E-01
Seq_0002661	0.74	-1.26	2.62	-0.48	6.31E-01	7.14E-01
Seq_0000202	9.75	-1.23	2.73	-0.45	6.53E-01	7.36E-01
Seq_0001019	1.27	-0.91	2.03	-0.45	6.53E-01	7.36E-01
Seq_0002747	0.81	-1.23	2.83	-0.43	6.64E-01	7.47E-01
Seq_0000008	2033.43	-0.21	0.49	-0.43	6.69E-01	7.50E-01
Seq_0000067	169.94	0.57	1.34	0.43	6.70E-01	7.51E-01
Seq_0000842	4.35	0.74	1.75	0.42	6.73E-01	7.52E-01
Seq_0000967	1.03	1.25	3.02	0.41	6.80E-01	7.59E-01
Seq_0000112	148.02	-0.49	1.22	-0.40	6.87E-01	7.64E-01
Seq_0000090	94.45	0.31	0.77	0.40	6.90E-01	7.67E-01
Seq_0000095	230.58	-0.31	0.83	-0.37	7.12E-01	7.88E-01
Seq_0000257	80.22	-0.37	1.00	-0.37	7.11E-01	7.88E-01
Seq_0001044	0.91	1.10	3.02	0.37	7.15E-01	7.90E-01
Seq_0000773	5.52	-0.56	1.60	-0.35	7.26E-01	8.00E-01
Seq_0000050	434.44	-0.40	1.15	-0.35	7.29E-01	8.01E-01
Seq_0000692	7.67	0.82	2.41	0.34	7.33E-01	8.04E-01
Seq_0000556	2.28	0.78	2.36	0.33	7.42E-01	8.13E-01
Seq_0000069	170.01	0.34	1.06	0.32	7.48E-01	8.18E-01
Seq_0000321	1.20	-0.96	3.01	-0.32	7.51E-01	8.20E-01
Seq_0000124	105.75	-0.42	1.35	-0.31	7.57E-01	8.20E-01

Seq_0000156	94.07	0.38	1.22	0.31	7.56E-01	8.20E-01
Seq_0000197	58.37	0.29	0.94	0.31	7.56E-01	8.20E-01
Seq_0000570	3.29	0.92	2.99	0.31	7.57E-01	8.20E-01
Seq_0000429	9.34	0.51	1.67	0.31	7.59E-01	8.21E-01
Seq_0000588	3.40	0.71	2.43	0.29	7.71E-01	8.31E-01
Seq_0002607	0.84	-0.54	1.86	-0.29	7.73E-01	8.32E-01
Seq_0000449	2.88	0.71	2.53	0.28	7.78E-01	8.35E-01
Seq_0000688	9.96	0.33	1.18	0.28	7.79E-01	8.35E-01
Seq_0000066	71.61	-0.29	1.06	-0.27	7.84E-01	8.37E-01
Seq_0000415	9.69	-0.56	2.04	-0.28	7.83E-01	8.37E-01
Seq_0001624	2.17	-0.49	1.92	-0.25	7.99E-01	8.52E-01
Seq_0000702	8.11	-0.41	1.72	-0.24	8.13E-01	8.65E-01
Seq_0001869	1.25	-0.47	2.02	-0.23	8.16E-01	8.67E-01
Seq_0000077	129.75	-0.21	0.98	-0.22	8.29E-01	8.75E-01
Seq_0000293	47.50	-0.21	0.95	-0.22	8.29E-01	8.75E-01
Seq_0000737	1.77	-0.54	2.46	-0.22	8.28E-01	8.75E-01
Seq_0000821	9.04	0.36	1.66	0.21	8.30E-01	8.75E-01
Seq_0000022	246.30	-0.16	0.82	-0.20	8.42E-01	8.84E-01
Seq_0000039	365.68	-0.12	0.61	-0.20	8.41E-01	8.84E-01
Seq_0000222	48.69	-0.36	2.00	-0.18	8.56E-01	8.97E-01
Seq_0000138	99.05	-0.22	1.24	-0.17	8.62E-01	9.01E-01
Seq_0000212	92.09	-0.15	0.91	-0.16	8.72E-01	9.09E-01
Seq_0000940	6.02	-0.23	1.45	-0.16	8.72E-01	9.09E-01
Seq_0000476	10.92	0.31	1.99	0.16	8.76E-01	9.11E-01
Seq_0000172	46.76	0.15	1.05	0.15	8.83E-01	9.17E-01
Seq_0001066	1.25	0.34	2.40	0.14	8.88E-01	9.20E-01
Seq_0000404	1.53	-0.41	3.00	-0.14	8.91E-01	9.21E-01
Seq_0000137	190.01	-0.16	1.23	-0.13	8.98E-01	9.26E-01
Seq_0001532	1.70	-0.23	1.97	-0.12	9.05E-01	9.33E-01
Seq_0000543	20.01	-0.15	1.41	-0.11	9.13E-01	9.37E-01
Seq_0001792	1.35	0.19	1.75	0.11	9.13E-01	9.37E-01
Seq_0000703	0.72	0.29	2.94	0.10	9.21E-01	9.44E-01
Seq_0000190	59.55	0.18	1.85	0.10	9.23E-01	9.44E-01

Seq_0001204	2.02	-0.07	1.35	-0.06	9.56E-01	9.73E-01	
Seq_0002507	0.73	-0.17	3.01	-0.06	9.54E-01	9.73E-01	
Seq_0000363	7.27	-0.06	1.71	-0.04	9.70E-01	9.84E-01	
Seq_0000386	14.28	0.05	1.37	0.04	9.71E-01	9.84E-01	
Seq_0000625	7.73	-0.10	2.99	-0.03	9.73E-01	9.84E-01	
Seq_0000788	1.05	0.09	2.70	0.03	9.72E-01	9.84E-01	
Seq_0001417	0.93	0.07	2.47	0.03	9.76E-01	9.85E-01	
Seq_0000045	445.21	0.02	0.67	0.02	9.80E-01	9.87E-01	
Seq_0000072	120.96	0.02	1.27	0.02	9.85E-01	9.87E-01	
Seq_0000941	1.09	0.05	3.00	0.02	9.86E-01	9.87E-01	
Seq_0001075	1.45	-0.03	1.53	-0.02	9.82E-01	9.87E-01	
Seq_0000007	1494.26	0.00	0.77	0.01	9.96E-01	9.96E-01	
RSV	Control Mean	Control Median	Control Present (n=47)	CD Mean	CD Median	CD Present (n=28)	logfdr
Seq_0000375	2.45E-03	0	20	0	0	0	55.20
Seq_0000528	1.17E-03	0	16	0	0	0	41.04
Seq_0000466	5.98E-04	0	15	0	0	0	37.81
Seq_0000756	4.98E-04	0	14	0	0	0	34.34
Seq_0000643	6.50E-04	0	14	0	0	0	34.25
Seq_0000534	7.86E-04	0	12	0	0	0	28.80
Seq_0000373	1.42E-03	0	11	0	0	0	25.76
Seq_0000797	6.18E-04	0	11	0	0	0	25.62
Seq_0000284	2.60E-03	0	13	0	0	0	25.35
Seq_0000988	3.28E-04	0	11	0	0	0	25.14
Seq_0000201	4.30E-03	0	11	7.64E-04	0	1	24.85
Seq_0000360	1.18E-03	0	11	0	0	0	24.85
Seq_0000206	2.19E-03	0	11	0	0	0	23.95
Seq_0000395	7.61E-04	0	11	0	0	0	23.31
Seq_0000827	3.85E-04	0	10	6.49E-05	0	1	23.12
Seq_0000937	3.83E-04	0	10	0	0	0	23.06

Seq_0000272	1.82E-03	0	9	2.01E-05	0	1	22.04
Seq_0000309	4.27E-06	0	1	3.03E-03	0	9	21.27
Seq_0000299	2.62E-03	0	9	0	0	0	21.11
Seq_0000835	4.80E-04	0	9	0	0	0	21.11
Seq_0000644	7.06E-04	0	9	6.52E-05	0	1	19.18
Seq_0000863	5.30E-04	0	8	0	0	0	18.88
Seq_0000697	2.92E-05	0	1	1.16E-03	0	6	17.67
Seq_0000440	1.31E-03	0	8	0	0	0	16.98
Seq_0000167	0.00E+00	0	0	1.61E-03	0	6	16.83
Seq_0000421	1.48E-03	0	6	0	0	0	14.05
Seq_0000959	0.00E+00	0	0	1.01E-03	0	4	13.94
Seq_0000407	1.54E-04	0	2	2.07E-03	0	4	13.73
Seq_0000446	1.81E-03	0	7	0	0	0	13.73
Seq_0000243	2.07E-03	0	7	0	0	0	13.48
Seq_0000268	2.22E-03	0	5	0	0	0	13.48
Seq_0000551	3.62E-04	0	6	0	0	0	13.40
Seq_0000423	7.67E-06	0	1	5.50E-03	0	4	11.77
Seq_0000063	9.90E-03	0	23	1.44E-05	0	2	9.75
Seq_0000152	3.95E-03	1.06E-03	29	4.14E-05	0	3	7.93
Seq_0000144	4.80E-03	9.32E-04	27	5.66E-04	0	1	7.92
Seq_0000265	2.03E-03	1.61E-03	31	3.03E-04	0	2	7.25
Seq_0000364	9.79E-04	1.12E-04	24	0	0	0	7.25
Seq_0000852	3.96E-04	2.56E-04	27	0	0	0	7.01
Seq_0000333	1.77E-03	1.08E-04	24	5.38E-04	0	1	6.55
Seq_0000758	5.49E-04	9.69E-05	24	0	0	0	6.06
Seq_0000081	5.61E-03	0	18	4.00E-04	0	1	5.92
Seq_0000338	1.28E-03	6.91E-04	31	4.25E-05	0	2	5.86
Seq_0000166	5.76E-03	0	16	1.83E-05	0	2	5.27
Seq_0000312	2.30E-03	0	20	6.86E-05	0	2	4.70
Seq_0000508	7.41E-04	0	19	0	0	0	4.40
Seq_0000091	6.91E-03	4.96E-03	32	3.15E-04	0	6	4.39
Seq_0000327	2.34E-03	0	11	2.23E-06	0	1	4.27
Seq_0000158	5.35E-03	1.47E-03	36	2.10E-04	0	4	4.12

Seq_0000609	4.72E-04	0	23	7.25E-06	0	1	4.12
Seq_0000107	4.16E-03	3.59E-04	25	5.34E-03	0	2	3.94
Seq_0000271	1.72E-03	2.04E-04	24	2.17E-04	0	3	3.86
Seq_0000215	1.88E-03	4.98E-04	32	4.86E-04	0	3	3.80
Seq_0000199	4.61E-03	0	22	8.04E-05	0	4	3.80
Seq_0000573	5.31E-04	0	18	0	0	0	3.80
Seq_0000482	9.51E-04	2.51E-04	26	3.99E-05	0	1	3.73
Seq_0000131	7.46E-03	0	17	3.19E-05	0	1	3.66
Seq_0000242	4.00E-03	0	19	4.05E-04	0	2	3.66
Seq_0000391	6.70E-04	0	22	1.38E-05	0	1	3.50
Seq_0000731	3.14E-04	2.52E-04	36	3.44E-05	0	2	3.43
Seq_0000976	2.29E-04	0	20	5.11E-05	0	1	3.37
Seq_0000274	2.07E-03	0	19	2.08E-05	0	1	3.25
Seq_0000193	2.63E-03	1.80E-04	25	5.72E-05	0	2	3.24
Seq_0000237	2.33E-03	0	22	6.68E-04	0	3	3.12
Seq_0000383	1.18E-03	0	19	2.43E-05	0	2	2.99
Seq_0000113	1.07E-02	0	23	1.87E-04	0	3	2.97
Seq_0000684	4.66E-04	0	16	0	0	0	2.97
Seq_0000983	2.56E-04	0	18	0	0	0	2.97
Seq_0000119	1.47E-04	0	14	1.03E-02	3.92E-04	15	2.93
Seq_0000501	4.54E-04	0	10	9.79E-04	0	2	2.89
Seq_0000032	2.14E-02	9.37E-03	41	1.00E-02	8.85E-05	15	2.88
Seq_0000231	4.63E-05	0	4	5.12E-03	0	13	2.83
Seq_0000326	1.45E-03	0	22	2.57E-04	0	3	2.80
Seq_0000151	4.92E-03	0	19	6.37E-03	0	4	2.73
Seq_0000734	1.81E-04	0	19	0	0	0	2.68
Seq_0000489	7.20E-04	3.94E-04	39	2.01E-04	0	5	2.68
Seq_0000192	3.92E-03	0	15	1.62E-04	0	2	2.67
Seq_0000867	3.43E-04	0	16	0	0	0	2.59
Seq_0000089	7.28E-03	0	5	1.75E-02	0	10	2.55
Seq_0000786	3.59E-04	0	15	2.55E-05	0	1	2.54
Seq_0000355	9.19E-04	5.98E-04	30	1.22E-04	0	4	2.53
Seq_0000127	8.95E-04	0	15	1.56E-02	1.12E-03	16	2.52

Seq_0001029	1.96E-04	0	17	0	0	0	2.50
Seq_0001143	2.78E-04	0	15	0	0	0	2.39
Seq_0000454	1.26E-03	0	19	1.43E-04	0	2	2.38
Seq_0000014	4.58E-02	2.55E-02	44	1.03E-02	3.30E-04	16	2.19
Seq_0000571	4.78E-04	0	21	4.72E-05	0	1	2.19
Seq_0000425	8.27E-04	5.99E-04	35	1.77E-04	0	6	2.14
Seq_0000491	7.89E-04	3.91E-04	27	7.89E-05	0	1	2.14
Seq_0000020	3.86E-02	1.49E-02	39	5.63E-03	0	12	2.14
Seq_0000229	3.36E-05	0	1	5.35E-04	0	10	2.14
Seq_0000628	3.00E-04	0	14	0	0	0	2.14
Seq_0000784	3.23E-04	1.35E-04	26	2.86E-05	0	2	2.13
Seq_0000078	5.09E-03	9.55E-04	31	5.87E-04	0	9	2.04
Seq_0000869	3.95E-04	0	23	1.89E-05	0	2	1.98
Seq_0000890	4.95E-04	0	15	6.57E-06	0	1	1.95
Seq_0000132	5.49E-05	0	5	8.57E-03	0	9	1.90
Seq_0001313	2.62E-04	0	14	0	0	0	1.82
Seq_0001256	1.60E-04	0	15	0	0	0	1.81
Seq_0000275	2.38E-03	0	15	4.81E-05	0	2	1.79
Seq_0000701	1.94E-04	0	13	0	0	0	1.67
Seq_0000850	2.60E-04	0	12	0	0	0	1.67
Seq_0000134	4.73E-03	3.00E-03	38	3.52E-03	0	7	1.65
Seq_0000439	1.36E-03	2.87E-04	24	6.23E-05	0	2	1.61
Seq_0000179	3.48E-03	1.66E-03	39	8.53E-04	0	6	1.59
Seq_0000196	5.23E-05	0	8	1.06E-02	0	10	1.55
Seq_0001253	2.06E-04	0	16	1.08E-05	0	2	1.55
Seq_0000122	1.57E-03	0	23	9.35E-03	4.77E-03	22	1.54
Seq_0000418	1.44E-03	0	13	2.56E-05	0	2	1.53
Seq_0000170	3.33E-03	1.61E-03	32	6.76E-04	0	5	1.52
Seq_0000236	1.21E-03	1.14E-04	28	1.36E-03	4.57E-04	21	1.49
Seq_0000103	5.56E-03	2.75E-03	36	1.06E-03	0	5	1.47
Seq_0000479	4.30E-04	0	12	0	0	0	1.44
Seq_0001013	2.00E-04	0	11	0	0	0	1.40
Seq_0001395	2.47E-04	0	12	0	0	0	1.39

Seq_0000519	3.67E-04	0	9	2.81E-04	0	2	1.38
Seq_0000486	1.00E-03	0	11	1.60E-04	0	2	1.37
Seq_0001335	1.15E-04	0	15	3.31E-06	0	1	1.37
Seq_0001169	1.67E-04	0	12	0	0	0	1.36
Seq_0000153	8.74E-05	0	14	1.59E-03	0	10	1.36
Seq_0000287	1.52E-03	1.43E-03	37	4.64E-04	0	8	1.36
Seq_0000961	2.79E-04	0	10	2.55E-05	0	1	1.35
Seq_0000599	7.55E-04	1.67E-04	24	1.60E-04	0	1	1.34
Seq_0000768	3.92E-04	0	20	4.03E-05	0	1	1.33
Seq_0001372	1.31E-04	0	12	0	0	0	1.33
Seq_0000664	4.94E-04	0	22	6.80E-05	0	1	1.32
Seq_0000833	3.20E-04	0	8	6.93E-06	0	1	1.32
Seq_0000101	1.80E-06	0	1	2.19E-02	0	3	1.31
Seq_0001057	2.24E-04	0	17	1.55E-05	0	1	1.31
Seq_0001748	9.56E-05	0	14	0	0	0	1.31
Seq_0000323	1.66E-03	0	23	2.72E-04	0	5	1.30
Seq_0001280	1.63E-04	0	11	0	0	0	1.30
Seq_0000344	8.42E-04	0	16	3.49E-05	0	2	1.27
Seq_0000824	2.45E-04	0	9	0	0	0	1.27
Seq_0000209	1.07E-03	3.17E-04	25	8.80E-05	0	3	1.26
Seq_0000993	3.37E-04	0	11	0	0	0	1.26
Seq_0000622	9.98E-04	0	8	1.28E-05	0	1	1.26
Seq_0000324	1.19E-03	0	22	1.38E-04	0	4	1.24
Seq_0001177	2.35E-04	0	10	2.23E-06	0	1	1.24
Seq_0000334	1.43E-03	0	23	1.26E-04	0	3	1.19
Seq_0001657	8.61E-05	0	13	0	0	0	1.14
Seq_0001663	6.43E-05	0	15	0	0	0	1.14
Seq_0000080	5.17E-03	2.04E-03	43	1.86E-03	0	8	1.11
Seq_0000635	8.98E-04	0	8	1.32E-04	0	1	1.11
Seq_0000799	1.69E-04	0	9	0	0	0	1.08
Seq_0000606	3.40E-04	0	7	0	0	0	1.08
Seq_0000303	5.06E-06	0	1	4.31E-03	0	3	1.06
Seq_0001034	1.64E-04	0	9	0	0	0	1.06

Seq_0000185	2.71E-03	0	22	9.53E-04	0	6	1.05
Seq_0001037	1.76E-04	0	9	0	0	0	1.05
Seq_0000465	3.99E-04	2.54E-04	33	2.88E-04	0	6	1.04
Seq_0000280	2.02E-03	1.29E-03	36	6.39E-04	0	5	1.03
Seq_0001125	2.36E-04	0	15	2.44E-04	0	2	1.03
Seq_0000560	5.72E-04	0	22	1.90E-04	0	5	1.00
Seq_0001948	8.88E-05	0	12	0	0	0	1.00
Seq_0000006	5.14E-02	3.82E-02	44	1.61E-02	0	13	0.99
Seq_0000021	2.86E-02	1.72E-02	38	8.90E-03	0	8	0.99
Seq_0000554	4.53E-04	0	8	3.60E-04	0	1	0.99
Seq_0000541	3.63E-04	0	9	0	0	0	0.98
Seq_0001146	1.87E-04	0	11	7.44E-06	0	1	0.97
Seq_0000191	1.95E-03	0	13	2.12E-05	0	2	0.95
Seq_0000163	3.62E-03	1.91E-03	37	1.69E-03	0	13	0.95
Seq_0001283	1.35E-04	0	10	0	0	0	0.94
Seq_0001637	9.23E-05	0	11	0	0	0	0.93
Seq_0000041	2.22E-02	8.60E-05	28	1.60E-02	0	8	0.93
Seq_0000065	9.35E-03	7.97E-03	43	5.32E-03	0	12	0.92
Seq_0000128	1.98E-03	6.45E-04	25	2.61E-02	3.74E-04	16	0.92
Seq_0001614	1.03E-04	0	10	0	0	0	0.92
Seq_0000443	5.57E-05	0	5	5.65E-04	0	11	0.91
Seq_0000298	0.00E+00	0	0	1.44E-02	0	3	0.91
Seq_0001133	3.49E-04	0	8	0	0	0	0.91
Seq_0000325	6.63E-04	0	15	1.29E-03	0	2	0.90
Seq_0000514	4.12E-04	0	10	1.74E-05	0	1	0.90
Seq_0001679	7.92E-05	0	11	0	0	0	0.90
Seq_0000203	3.24E-03	2.43E-04	28	5.18E-04	0	5	0.90
Seq_0000160	2.46E-04	3.88E-05	25	3.76E-03	9.20E-05	14	0.90
Seq_0001848	8.78E-05	0	11	0	0	0	0.90
Seq_0000820	2.58E-04	0	6	0	0	0	0.89
Seq_0000223	2.80E-03	0	9	1.70E-04	0	2	0.89
Seq_0000509	1.08E-03	0	7	0	0	0	0.89
Seq_0000259	1.06E-03	0	8	1.07E-03	0	2	0.88

Seq_0000698	5.39E-04	0	7	0	0	0	0.88
Seq_0000129	3.98E-03	3.43E-03	42	2.62E-03	9.70E-05	14	0.87
Seq_0000427	1.27E-03	0	5	4.08E-04	0	1	0.85
Seq_0001329	1.30E-04	0	8	0	0	0	0.85
Seq_0000104	5.59E-03	0	22	1.09E-03	0	6	0.85
Seq_0001151	2.02E-04	0	11	9.27E-06	0	1	0.85
Seq_0001517	9.39E-05	0	9	0	0	0	0.84
Seq_0000047	6.05E-03	3.18E-04	32	3.02E-02	3.73E-03	22	0.81
Seq_0000057	3.61E-03	1.31E-04	25	1.46E-02	7.38E-03	27	0.81
Seq_0000184	2.68E-03	1.33E-03	42	1.90E-03	1.45E-04	14	0.81
Seq_0000436	8.12E-04	0	9	3.94E-05	0	2	0.81
Seq_0000924	3.49E-04	0	7	0	0	0	0.81
Seq_0000736	3.45E-04	0	13	4.02E-04	0	4	0.81
Seq_0001968	6.86E-05	0	10	0	0	0	0.81
Seq_0001127	1.80E-04	0	20	2.45E-05	0	2	0.80
Seq_0002016	4.36E-05	0	13	0	0	0	0.80
Seq_0000412	7.44E-04	0	16	4.40E-04	0	2	0.80
Seq_0001425	9.55E-05	0	9	0	0	0	0.79
Seq_0001493	9.88E-05	0	9	0	0	0	0.79
Seq_0000618	3.20E-04	0	14	1.08E-04	0	3	0.78
Seq_0000497	4.73E-04	1.74E-04	29	2.42E-04	0	10	0.78
Seq_0001693	1.06E-04	0	8	0	0	0	0.77
Seq_0000633	7.29E-04	0	7	0	0	0	0.77
Seq_0001370	8.14E-05	0	9	0	0	0	0.77
Seq_0000402	7.10E-04	0	23	2.64E-04	0	5	0.75
Seq_0001366	8.34E-05	0	9	0	0	0	0.75
Seq_0002129	4.68E-05	0	12	0	0	0	0.74
Seq_0001332	8.36E-05	0	8	0	0	0	0.74
Seq_0000741	3.84E-04	0	21	5.13E-05	0	1	0.73
Seq_0000269	4.98E-04	0	15	2.26E-03	5.40E-04	23	0.73
Seq_0000515	4.73E-04	0	7	3.89E-04	0	1	0.73
Seq_0000819	1.70E-05	0	2	5.75E-04	0	6	0.71
Seq_0000100	1.45E-03	7.67E-04	42	4.69E-03	1.91E-03	20	0.70

Seq_0000378	1.75E-03	0	7	0	0	0	0.70
Seq_0000665	5.09E-06	0	2	6.70E-04	0	6	0.69
Seq_0001707	9.40E-05	0	8	0	0	0	0.69
Seq_0000995	9.06E-06	0	6	7.40E-04	0	8	0.68
Seq_0001500	7.18E-05	0	8	0	0	0	0.68
Seq_0000085	8.04E-03	2.39E-03	35	2.78E-03	0	6	0.68
Seq_0000210	2.31E-03	0	21	4.79E-04	0	5	0.68
Seq_0000435	1.46E-03	0	5	1.21E-04	0	1	0.68
Seq_0001659	5.84E-05	0	9	0	0	0	0.68
Seq_0000772	1.75E-04	0	2	8.22E-04	0	3	0.68
Seq_0001787	8.15E-05	0	7	0	0	0	0.67
Seq_0000918	5.04E-04	0	4	0	0	0	0.67
Seq_0000208	1.83E-04	0	6	9.20E-03	0	2	0.66
Seq_0001348	6.97E-05	0	9	0	0	0	0.66
Seq_0001596	1.15E-04	0	7	0	0	0	0.66
Seq_0000749	6.46E-04	0	7	2.50E-04	0	1	0.65
Seq_0000689	1.24E-05	0	2	4.40E-04	0	6	0.65
Seq_0000037	2.26E-03	0	23	8.84E-03	1.92E-04	16	0.65
Seq_0000387	1.51E-03	0	4	1.26E-04	0	2	0.64
Seq_0000871	2.18E-04	0	8	6.19E-06	0	2	0.64
Seq_0002087	5.21E-05	0	10	0	0	0	0.64
Seq_0000015	9.67E-03	0	19	6.26E-03	0	9	0.64
Seq_0000367	3.30E-04	0	9	5.72E-04	0	2	0.64
Seq_0001130	8.09E-05	0	16	6.25E-05	0	4	0.63
Seq_0000445	7.14E-04	0	14	1.00E-04	0	2	0.62
Seq_0001115	1.86E-06	0	1	7.81E-04	0	3	0.62
Seq_0000411	6.76E-04	3.17E-04	27	3.38E-04	2.18E-04	16	0.62
Seq_0000962	3.63E-05	0	3	4.40E-04	0	8	0.61
Seq_0000187	6.58E-05	0	4	8.27E-04	0	11	0.61
Seq_0000505	5.32E-04	1.72E-04	26	1.73E-04	0	3	0.61
Seq_0000873	1.58E-04	0	8	0	0	0	0.61
Seq_0000281	1.70E-03	1.02E-03	28	7.53E-04	0	8	0.59
Seq_0001919	5.40E-05	0	8	0	0	0	0.59

Seq_0000176	0.00E+00	0	0	2.80E-04	0	5	0.59
Seq_0002312	5.13E-05	0	10	0	0	0	0.59
Seq_0001413	6.39E-05	0	7	0	0	0	0.58
Seq_0000424	8.19E-04	0	4	0	0	0	0.58
Seq_0000079	1.59E-03	0	10	1.34E-02	0	9	0.57
Seq_0002516	3.51E-05	0	11	0	0	0	0.57
Seq_0000329	7.48E-04	0	7	0	0	0	0.57
Seq_0000477	6.21E-04	0	6	0	0	0	0.57
Seq_0000777	4.06E-04	0	7	2.92E-04	0	1	0.57
Seq_0002671	2.84E-05	0	12	0	0	0	0.57
Seq_0000738	8.03E-04	0	6	3.19E-05	0	1	0.57
Seq_0001454	1.49E-04	0	7	0	0	0	0.57
Seq_0000810	4.77E-04	0	5	0	0	0	0.56
Seq_0000649	7.58E-04	0	5	0	0	0	0.54
Seq_0000471	6.10E-04	0	5	0	0	0	0.54
Seq_0000094	1.26E-03	0	20	5.80E-03	0	9	0.53
Seq_0000718	3.83E-04	0	5	7.23E-05	0	1	0.53
Seq_0002236	3.98E-05	0	9	0	0	0	0.53
Seq_0000380	1.76E-03	0	7	1.91E-05	0	1	0.53
Seq_0000722	2.45E-04	0	12	2.86E-05	0	1	0.53
Seq_0002225	6.12E-05	0	7	0	0	0	0.53
Seq_0000082	4.24E-03	1.64E-03	35	2.22E-03	0	11	0.53
Seq_0002127	6.18E-05	0	7	0	0	0	0.52
Seq_0000488	3.09E-04	0	5	1.02E-03	0	1	0.52
Seq_0000474	2.96E-04	0	6	6.94E-05	0	1	0.52
Seq_0000487	1.22E-03	0	4	3.83E-05	0	1	0.52
Seq_0002126	7.75E-05	0	6	0	0	0	0.52
Seq_0000241	1.86E-03	0	6	0	0	0	0.51
Seq_0000670	2.15E-03	0	4	0	0	0	0.51
Seq_0000023	1.02E-02	4.93E-03	36	3.57E-02	2.11E-04	14	0.51
Seq_0002197	5.19E-05	0	7	0	0	0	0.50
Seq_0000989	1.38E-04	0	6	7.23E-05	0	1	0.50
Seq_0000866	2.85E-04	0	12	2.95E-04	0	2	0.50

Seq_0000876	6.07E-04	0	5	3.51E-04	0	2	0.50
Seq_0000907	8.86E-05	0	2	4.27E-04	0	2	0.50
Seq_0000308	4.03E-04	0	7	5.55E-06	0	1	0.50
Seq_0000525	2.24E-04	0	5	0	0	0	0.50
Seq_0000592	4.61E-06	0	1	5.64E-04	0	3	0.50
Seq_0001975	5.10E-05	0	7	0	0	0	0.50
Seq_0001819	8.64E-05	0	6	0	0	0	0.49
Seq_0000097	2.14E-05	0	8	3.13E-03	0	8	0.48
Seq_0000106	4.64E-03	1.89E-03	31	1.88E-03	0	7	0.48
Seq_0000108	2.15E-03	6.55E-04	39	4.28E-03	1.46E-03	26	0.48
Seq_0000150	1.07E-05	0	4	7.39E-04	0	3	0.48
Seq_0000213	1.93E-03	6.88E-04	25	6.96E-04	0	5	0.48
Seq_0000248	1.45E-03	8.80E-04	42	1.16E-03	5.00E-05	14	0.48
Seq_0000558	4.34E-04	0	6	0	0	0	0.48
Seq_0000610	1.07E-06	0	1	4.66E-05	0	6	0.48
Seq_0000662	4.16E-04	0	6	1.09E-05	0	1	0.48
Seq_0000667	4.39E-04	0	3	0	0	0	0.48
Seq_0000729	3.47E-04	0	6	1.25E-03	0	1	0.48
Seq_0001104	2.32E-04	0	5	8.66E-06	0	1	0.48
Seq_0001558	4.37E-05	0	7	4.36E-05	0	1	0.48
Seq_0000227	2.79E-03	0	8	4.62E-03	0	7	0.48
Seq_0000143	3.99E-03	1.47E-03	32	1.52E-03	0	7	0.47
Seq_0000680	6.23E-04	0	4	0	0	0	0.47
Seq_0001195	2.28E-04	0	8	1.91E-05	0	1	0.47
Seq_0001222	1.59E-04	0	11	4.81E-05	0	4	0.47
Seq_0001243	1.52E-04	0	6	0	0	0	0.47
Seq_0000555	0.00E+00	0	0	3.61E-04	0	4	0.47
Seq_0001059	1.10E-04	0	5	0	0	0	0.46
Seq_0001081	3.26E-04	0	5	0	0	0	0.46
Seq_0001458	1.39E-04	0	4	0	0	0	0.46
Seq_0002209	4.72E-05	0	6	0	0	0	0.46
Seq_0000624	0.00E+00	0	0	5.33E-04	0	2	0.46
Seq_0000653	9.60E-05	0	7	2.28E-05	0	2	0.46

Seq_0000498	6.04E-04	0	3	1.57E-05	0	1	0.45
Seq_0000748	6.49E-04	0	6	1.16E-03	0	5	0.45
Seq_0001301	1.10E-04	0	19	5.24E-05	0	4	0.45
Seq_0001520	8.97E-05	0	4	4.89E-05	0	1	0.45
Seq_0001634	1.32E-04	0	4	0	0	0	0.45
Seq_0001646	2.94E-05	0	9	1.22E-04	0	1	0.45
Seq_0000145	3.11E-03	0	21	1.43E-03	0	7	0.45
Seq_0000417	3.29E-04	0	21	1.34E-04	0	6	0.45
Seq_0000468	1.01E-03	8.16E-04	28	3.62E-04	0	5	0.45
Seq_0000547	8.93E-04	0	4	3.19E-05	0	1	0.45
Seq_0000872	3.05E-04	0	17	1.68E-04	0	3	0.45
Seq_0001924	6.00E-05	0	8	0	0	0	0.45
Seq_0002013	6.42E-05	0	8	0	0	0	0.45
Seq_0000300	1.23E-03	0	9	4.53E-04	0	5	0.44
Seq_0000616	3.40E-04	0	6	0	0	0	0.44
Seq_0001294	2.00E-04	0	6	0	0	0	0.44
Seq_0001943	8.51E-05	0	6	0	0	0	0.44
Seq_0002558	3.21E-05	0	8	0	0	0	0.44
Seq_0000225	1.10E-03	0	12	7.54E-03	0	10	0.44
Seq_0002455	3.47E-05	0	7	0	0	0	0.44
Seq_0000800	2.90E-04	0	16	1.11E-04	0	1	0.44
Seq_0002693	3.06E-05	0	9	0	0	0	0.43
Seq_0001097	1.10E-04	0	5	0	0	0	0.43
Seq_0000098	1.23E-03	0	12	1.57E-03	2.05E-04	15	0.43
Seq_0001451	2.01E-04	0	4	0	0	0	0.43
Seq_0000603	4.26E-04	0	4	0	0	0	0.43
Seq_0001210	2.08E-04	0	4	2.28E-04	0	1	0.43
Seq_0001208	2.51E-04	0	4	0	0	0	0.43
Seq_0000347	5.93E-04	0	13	1.15E-04	0	1	0.43
Seq_0000580	0.00E+00	0	0	5.74E-04	0	2	0.43
Seq_0000713	4.61E-04	0	4	0	0	0	0.43
Seq_0001431	1.64E-04	0	6	6.80E-06	0	1	0.43
Seq_0002395	3.71E-05	0	7	0	0	0	0.43

Seq_0002643	3.65E-05	0	7	0	0	0	0.43
Seq_0000838	6.84E-04	0	5	0	0	0	0.43
Seq_0001086	2.66E-04	0	5	0	0	0	0.42
Seq_0001317	1.14E-04	0	7	6.74E-06	0	1	0.42
Seq_0000173	1.02E-03	0	5	0	0	0	0.42
Seq_0000793	4.40E-04	0	4	0	0	0	0.42
Seq_0000847	6.01E-05	0	6	0	0	0	0.42
Seq_0000061	8.23E-03	5.15E-03	41	9.29E-03	7.83E-05	14	0.42
Seq_0000226	4.20E-04	0	7	2.78E-03	0	9	0.41
Seq_0000076	7.42E-03	1.45E-03	28	4.99E-03	0	10	0.41
Seq_0000305	1.56E-03	0	19	5.17E-04	0	3	0.41
Seq_0000437	1.18E-03	0	10	0	0	0	0.41
Seq_0000955	3.88E-04	0	3	0	0	0	0.41
Seq_0001058	7.24E-05	0	9	1.25E-05	0	2	0.41
Seq_0001296	5.14E-06	0	1	5.71E-05	0	5	0.41
Seq_0001827	4.49E-05	0	5	0	0	0	0.41
Seq_0002669	2.89E-05	0	7	0	0	0	0.41
Seq_0002770	2.47E-05	0	8	0	0	0	0.41
Seq_0001365	6.92E-05	0	5	0	0	0	0.41
Seq_0000420	1.10E-03	0	10	3.03E-04	0	3	0.41
Seq_0000087	6.16E-04	0	4	7.83E-06	0	1	0.40
Seq_0000169	2.11E-03	0	16	6.62E-04	0	7	0.40
Seq_0002144	3.19E-05	0	6	0	0	0	0.39
Seq_0000699	8.50E-04	0	2	0	0	0	0.39
Seq_0001259	1.22E-04	0	8	0	0	0	0.39
Seq_0000279	4.15E-04	8.56E-05	26	2.30E-03	1.37E-04	15	0.39
Seq_0001326	2.50E-04	0	5	0	0	0	0.39
Seq_0002822	6.08E-05	0	3	0	0	0	0.39
Seq_0001378	2.99E-04	0	5	0	0	0	0.39
Seq_0000946	3.36E-04	0	2	0	0	0	0.39
Seq_0001706	1.09E-04	0	5	1.00E-04	0	1	0.39
Seq_0001319	1.67E-04	0	6	8.76E-05	0	1	0.38
Seq_0000054	3.91E-03	0	17	2.32E-02	0	10	0.38

Seq_0000164	1.07E-03	0	7	6.34E-03	2.52E-04	14	0.38
Seq_0000282	1.07E-03	9.03E-04	30	2.13E-03	0	7	0.38
Seq_0000652	2.55E-04	0	3	1.25E-03	0	5	0.38
Seq_0001237	2.35E-04	0	2	3.88E-05	0	1	0.38
Seq_0001529	1.16E-05	0	4	5.23E-05	0	6	0.38
Seq_0001998	6.46E-05	0	4	0	0	0	0.38
Seq_0000060	6.82E-03	0	16	1.96E-03	0	11	0.37
Seq_0000832	3.86E-04	0	2	9.39E-06	0	3	0.37
Seq_0000294	1.55E-04	0	11	8.09E-04	0	10	0.37
Seq_0001434	1.50E-04	0	8	6.81E-06	0	1	0.37
Seq_0001764	5.17E-05	0	13	2.05E-05	0	2	0.37
Seq_0002464	2.98E-05	0	5	0	0	0	0.37
Seq_0001336	2.04E-04	0	5	0	0	0	0.36
Seq_0001477	1.43E-04	0	3	0	0	0	0.36
Seq_0001200	1.18E-04	0	15	5.67E-05	0	4	0.35
Seq_0001592	7.11E-05	0	4	0	0	0	0.35
Seq_0000582	9.99E-04	0	4	0	0	0	0.35
Seq_0000675	1.46E-04	0	11	3.83E-04	0	9	0.35
Seq_0000111	2.80E-03	6.63E-04	32	2.05E-03	0	13	0.35
Seq_0001419	5.25E-05	0	4	1.64E-04	0	1	0.35
Seq_0000732	2.25E-04	0	19	1.57E-04	0	5	0.35
Seq_0000933	6.01E-04	0	4	0	0	0	0.35
Seq_0001675	3.78E-05	0	8	4.73E-05	0	2	0.35
Seq_0002183	3.02E-05	0	6	4.98E-06	0	1	0.35
Seq_0000398	4.08E-04	0	14	1.98E-03	0	10	0.34
Seq_0000579	9.13E-04	0	3	3.19E-05	0	1	0.34
Seq_0000802	1.29E-04	0	5	0	0	0	0.34
Seq_0001540	1.10E-04	0	7	0	0	0	0.34
Seq_0000389	1.41E-04	0	3	0	0	0	0.34
Seq_0000632	5.50E-04	0	4	0	0	0	0.34
Seq_0000929	7.61E-04	0	2	1.28E-05	0	1	0.34
Seq_0001095	3.46E-04	0	4	0	0	0	0.34
Seq_0001226	1.23E-04	0	6	0	0	0	0.34

Seq_0001475	7.69E-05	0	3	0	0	0	0.34
Seq_0001765	7.65E-05	0	5	0	0	0	0.34
Seq_0002405	4.63E-06	0	1	9.84E-05	0	3	0.34
Seq_0002292	2.73E-05	0	4	0	0	0	0.34
Seq_0000270	1.03E-03	1.76E-04	28	2.71E-03	0	8	0.33
Seq_0000846	4.09E-05	0	5	7.89E-05	0	2	0.33
Seq_0000432	1.94E-03	0	4	0	0	0	0.33
Seq_0000130	4.67E-03	2.21E-03	42	2.90E-03	0	9	0.33
Seq_0001322	3.55E-04	0	6	7.48E-06	0	1	0.33
Seq_0002593	2.52E-05	0	8	4.13E-06	0	1	0.33
Seq_0001721	7.91E-05	0	5	0	0	0	0.33
Seq_0002128	5.66E-05	0	4	0	0	0	0.33
Seq_0000968	1.46E-04	0	2	1.38E-04	0	1	0.32
Seq_0000949	1.79E-04	0	3	0	0	0	0.31
Seq_0000963	8.28E-05	0	3	0	0	0	0.31
Seq_0001685	1.12E-04	0	5	0	0	0	0.31
Seq_0000311	7.56E-04	0	19	4.10E-04	0	3	0.30
Seq_0000795	6.36E-04	0	3	0	0	0	0.30
Seq_0001261	2.02E-05	0	4	1.14E-04	0	4	0.30
Seq_0001512	2.06E-04	0	5	1.28E-05	0	1	0.30
Seq_0001605	1.04E-04	0	2	0	0	0	0.30
Seq_0002119	6.17E-05	0	5	0	0	0	0.30
Seq_0000042	1.34E-02	1.10E-02	44	1.11E-02	3.38E-04	15	0.30
Seq_0000332	7.26E-04	0	4	7.71E-05	0	2	0.30
Seq_0000739	1.54E-04	0	5	0	0	0	0.30
Seq_0000823	1.60E-04	0	11	4.84E-05	0	3	0.30
Seq_0001225	1.72E-04	0	3	0	0	0	0.30
Seq_0001674	1.10E-04	0	6	0	0	0	0.30
Seq_0000052	1.04E-03	0	7	8.15E-03	0	3	0.30
Seq_0000370	1.01E-03	6.95E-04	34	8.73E-04	0	8	0.30
Seq_0001269	1.16E-04	0	11	3.82E-05	0	2	0.28
Seq_0001409	9.95E-05	0	10	2.67E-05	0	2	0.28
Seq_0002645	2.62E-05	0	6	3.66E-06	0	1	0.28

Seq_0000073	7.15E-03	6.07E-04	26	4.22E-03	0	9	0.27
Seq_0000400	4.46E-04	0	7	2.28E-03	0	7	0.27
Seq_0000499	4.69E-05	0	5	1.32E-04	0	3	0.27
Seq_0000585	8.64E-05	0	3	4.04E-04	0	5	0.27
Seq_0001878	2.47E-05	0	6	3.05E-06	0	1	0.27
Seq_0000093	4.45E-03	1.55E-03	36	6.77E-03	0	10	0.27
Seq_0000343	8.01E-04	1.78E-04	25	4.38E-04	0	3	0.27
Seq_0000496	5.67E-04	0	8	1.01E-04	0	2	0.26
Seq_0001286	2.11E-04	0	5	1.23E-05	0	1	0.26
Seq_0002351	2.59E-05	0	8	6.69E-06	0	2	0.26
Seq_0000394	7.58E-04	0	21	5.66E-04	0	4	0.26
Seq_0000044	1.81E-02	0	20	2.22E-02	0	10	0.25
Seq_0002105	3.14E-05	0	6	4.58E-05	0	2	0.25
Seq_0001254	2.17E-04	0	3	7.24E-06	0	2	0.25
Seq_0000716	1.41E-04	0	8	1.69E-04	0	2	0.23
Seq_0000565	3.26E-05	0	3	3.73E-04	0	3	0.22
Seq_0000448	4.19E-04	0	20	3.14E-04	0	12	0.22
Seq_0000450	1.08E-03	6.19E-04	29	7.97E-04	0	6	0.21
Seq_0000470	2.16E-04	0	17	4.19E-03	0	8	0.21
Seq_0000171	2.83E-03	1.79E-03	38	2.66E-03	0	11	0.21
Seq_0000874	5.13E-05	0	4	1.01E-04	0	2	0.21
Seq_0001014	1.52E-04	8.85E-05	25	1.44E-04	0	9	0.21
Seq_0000195	8.19E-04	0	3	5.75E-03	0	5	0.21
Seq_0000105	9.35E-03	1.14E-03	27	6.45E-03	0	11	0.20
Seq_0000230	1.11E-03	0	20	4.21E-03	0	9	0.20
Seq_0000314	1.98E-04	0	9	1.54E-03	0	8	0.20
Seq_0000674	1.56E-04	0	10	4.90E-04	0	4	0.19
Seq_0000340	3.17E-04	0	5	2.19E-03	0	4	0.18
Seq_0000755	5.16E-05	0	2	2.22E-04	0	4	0.18
Seq_0000840	2.49E-05	0	8	1.03E-05	0	3	0.18
Seq_0000285	2.94E-03	0	5	2.35E-04	0	2	0.18
Seq_0000181	6.98E-04	0	19	2.29E-03	0	7	0.18
Seq_0001660	7.72E-05	0	3	9.15E-05	0	2	0.18

Seq_0000522	2.57E-04	1.30E-04	29	2.44E-04	0	10	0.18
Seq_0000062	7.09E-03	4.17E-03	43	7.45E-03	3.02E-03	18	0.18
Seq_0000349	7.81E-04	0	13	7.77E-04	0	9	0.16
Seq_0000254	2.65E-04	0	5	4.62E-04	0	3	0.16
Seq_0000217	9.07E-04	0	5	1.21E-05	0	1	0.15
Seq_0000232	1.12E-03	7.87E-04	27	1.13E-03	0	8	0.15
Seq_0000694	2.90E-04	1.90E-04	27	1.78E-04	0	4	0.15
Seq_0002661	2.69E-05	0	5	7.58E-06	0	1	0.15
Seq_0000202	1.73E-03	0	8	7.21E-03	0	4	0.13
Seq_0001019	8.18E-05	0	9	9.45E-05	0	3	0.13
Seq_0002747	2.67E-05	0	4	8.27E-06	0	1	0.13
Seq_0000008	4.93E-02	2.22E-02	46	7.04E-02	3.34E-02	28	0.12
Seq_0000067	3.07E-03	0	23	8.44E-03	0	10	0.12
Seq_0000842	8.49E-05	0	10	1.96E-04	0	6	0.12
Seq_0000967	3.47E-04	0	1	5.74E-05	0	1	0.12
Seq_0000112	3.75E-03	1.77E-03	30	3.18E-03	0	6	0.12
Seq_0000090	2.14E-03	5.01E-04	32	4.28E-03	1.34E-03	23	0.12
Seq_0000095	5.96E-03	4.07E-03	42	6.25E-03	0	12	0.10
Seq_0000257	2.31E-03	9.89E-04	36	1.89E-03	0	7	0.10
Seq_0001044	3.03E-04	0	1	5.10E-05	0	1	0.10
Seq_0000773	1.42E-04	0	15	2.57E-04	0	5	0.10
Seq_0000050	9.97E-03	5.76E-04	32	1.26E-02	0	12	0.10
Seq_0000692	2.16E-04	0	6	4.04E-04	0	4	0.09
Seq_0000556	1.20E-04	0	8	3.09E-04	0	4	0.09
Seq_0000069	3.74E-03	1.69E-03	34	6.74E-03	0	9	0.09
Seq_0000321	8.46E-05	0	3	3.59E-03	0	3	0.09
Seq_0000124	3.04E-03	1.20E-03	25	3.58E-03	0	6	0.09
Seq_0000156	2.02E-03	8.72E-04	26	6.46E-03	0	9	0.09
Seq_0000197	1.25E-03	7.59E-04	34	2.46E-03	0	10	0.09
Seq_0000570	1.97E-04	0	4	1.37E-03	0	2	0.09
Seq_0000429	2.01E-04	0	13	3.35E-04	0	6	0.09
Seq_0000588	1.06E-04	0	7	1.21E-03	0	4	0.08
Seq_0002607	2.39E-05	0	10	1.98E-05	0	2	0.08

Seq_0000449	3.70E-04	0	7	5.49E-04	0	4	0.08
Seq_0000688	2.23E-04	0	21	3.39E-04	0	9	0.08
Seq_0000066	1.84E-03	2.36E-04	28	1.82E-03	0	13	0.08
Seq_0000415	2.45E-04	0	10	1.79E-04	0	4	0.08
Seq_0001624	5.35E-05	0	10	7.98E-05	0	3	0.07
Seq_0000702	2.78E-04	0	12	9.47E-04	0	7	0.06
Seq_0001869	4.38E-05	0	7	2.76E-05	0	4	0.06
Seq_0000077	2.97E-03	8.58E-04	33	3.72E-03	0	13	0.06
Seq_0000293	1.27E-03	2.55E-04	34	1.66E-03	0	10	0.06
Seq_0000737	1.22E-04	0	8	2.08E-04	0	3	0.06
Seq_0000821	1.88E-04	0	12	5.03E-04	0	7	0.06
Seq_0000022	6.43E-03	3.81E-03	37	2.84E-02	3.27E-04	19	0.05
Seq_0000039	8.88E-03	6.40E-03	43	1.24E-02	3.05E-03	23	0.05
Seq_0000222	1.21E-03	0	12	1.81E-03	0	5	0.05
Seq_0000138	2.46E-03	1.28E-03	25	3.33E-03	0	9	0.05
Seq_0000212	2.53E-03	9.71E-04	36	4.30E-03	0	11	0.04
Seq_0000940	1.51E-04	0	16	4.84E-04	0	6	0.04
Seq_0000476	2.57E-04	0	11	3.53E-04	0	4	0.04
Seq_0000172	1.07E-03	7.00E-04	33	1.39E-03	0	6	0.04
Seq_0001066	4.17E-05	0	5	5.59E-05	0	3	0.04
Seq_0000404	1.53E-03	0	4	9.83E-04	0	2	0.04
Seq_0000137	5.48E-03	6.82E-05	25	6.43E-03	0	12	0.03
Seq_0001532	4.03E-05	0	8	4.50E-05	0	4	0.03
Seq_0000543	6.14E-04	0	18	9.67E-04	0	8	0.03
Seq_0001792	3.50E-05	0	8	8.65E-05	0	6	0.03
Seq_0000703	3.54E-06	0	2	2.62E-03	0	3	0.03
Seq_0000190	3.57E-03	0	13	2.19E-03	0	7	0.03
Seq_0001204	5.09E-05	0	15	6.14E-05	0	6	0.01
Seq_0002507	1.95E-05	0	3	4.62E-05	0	2	0.01
Seq_0000363	1.49E-04	0	12	7.38E-04	0	6	0.01
Seq_0000386	5.36E-04	0	14	6.77E-04	0	12	0.01
Seq_0000625	4.16E-04	0	3	5.62E-04	0	4	0.01
Seq_0000788	4.47E-05	0	5	4.97E-04	0	3	0.01

Seq_0001417	1.66E-05	0	5	2.12E-05	0	2	0.01
Seq_0000045	1.06E-02	7.83E-03	43	1.36E-02	3.05E-03	19	0.01
Seq_0000072	2.72E-03	9.67E-05	24	5.69E-03	0	10	0.01
Seq_0000941	1.06E-04	0	3	4.95E-05	0	2	0.01
Seq_0001075	3.90E-05	0	11	5.31E-05	0	6	0.01
Seq_0000007	3.64E-02	1.82E-02	42	4.76E-02	4.18E-03	20	0.00
RSV	Domain	Phylum	Class	Order	Family	Genus	
Seq_0000375	Archaea	Euryarchaeota	Methanobacteriia	Methanobacteriales	Methanobacteriaceae	Methanobrevibacter	
Seq_0000528	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000466	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000756	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000643	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	
Seq_0000534	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000373	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus	
Seq_0000797	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	
Seq_0000284	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	
Seq_0000988	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000201	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	
Seq_0000360	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella	
Seq_0000206	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000395	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2	

Seq_0000827	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000937	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000272	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000309	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000299	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Catenibacterium
Seq_0000835	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000644	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000863	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000697	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000440	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000167	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000421	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000959	Bacteria	Fusobacteriia	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium
Seq_0000407	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000446	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000243	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000268	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified

Seq_0000551	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000423	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000063	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000152	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000144	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000265	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000364	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000852	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000333	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000758	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000081	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000338	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000166	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000312	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000508	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Sporobacter
Seq_0000091	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0000327	Bacteria	Firmicutes	Erysipelotrichi a	Erysipelotrich ales	Erysipelotrichac eae	Erysipelotrichaceae _unclassified
Seq_0000158	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Ruminococcaceae_ unclassified
Seq_0000609	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_unclas sified
Seq_0000107	Bacteria	Actinobact eria	Actinobacteria	Bifidobacterial es	Bifidobacteriace ae	Bifidobacterium
Seq_0000271	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Ruminococcaceae_ unclassified
Seq_0000215	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Oscillibacter
Seq_0000199	Bacteria	Firmicutes	Firmicutes_un classified	Firmicutes_un classified	Firmicutes_uncl assified	Firmicutes_unclassi fied
Seq_0000573	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_u nclassified
Seq_0000482	Bacteria	Bacteroidet es	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000131	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000242	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_unclas sified
Seq_0000391	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Clostridium_IV
Seq_0000731	Bacteria	Bacteria_u nclassified	Bacteria_uncla ssified	Bacteria_uncla ssified	Bacteria_unclass ified	Bacteria_unclassifie d
Seq_0000976	Bacteria	Actinobact eria	Actinobacteria	Actinobacteria _unclassified	Actinobacteria_u nclassified	Actinobacteria_uncl assified
Seq_0000274	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_unclas sified
Seq_0000193	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Ruminococcaceae_ unclassified
Seq_0000237	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcacea e	Clostridium_IV

Seq_0000383	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000113	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000684	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000983	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000119	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000501	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000032	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000231	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000326	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000151	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000734	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000489	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Odoribacter
Seq_0000192	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000867	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000089	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000786	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000355	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0000127	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001029	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor
Seq_0001143	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Howardella
Seq_0000454	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000014	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000571	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000425	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000491	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000020	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000229	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000628	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000784	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000078	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000869	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000890	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000132	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0001313	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0001256	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0000275	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000701	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000850	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000134	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000439	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000179	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000196	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0001253	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000122	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000418	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000170	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000236	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000103	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000479	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001013	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0001395	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0000519	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000486	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0001335	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001169	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000153	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000287	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000961	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000599	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000768	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001372	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000664	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000833	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000101	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacteriaceae_unclassified
Seq_0001057	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001748	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0000323	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001280	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000344	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
Seq_0000824	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000209	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000993	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000622	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio
Seq_0000324	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001177	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000334	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001657	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001663	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000080	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcaceae_unclassified
Seq_0000635	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000799	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000606	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
Seq_0000303	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0001034	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000185	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001037	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000465	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0000280	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0001125	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000560	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0001948	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000006	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000021	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000554	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000541	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001146	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000191	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000163	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001283	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricoccus
Seq_0001637	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000041	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_0000065	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000128	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0001614	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000443	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes

Seq_0000298	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0001133	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000325	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000514	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001679	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000203	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Seq_0000160	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Pasteurellaceae_unclassified
Seq_0001848	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000820	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000223	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000509	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000259	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0000698	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000129	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000427	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001329	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000104	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus

Seq_0001151	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001517	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000047	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia/Shigella
Seq_0000057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000184	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000436	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000924	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000736	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001968	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001127	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0002016	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000412	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001425	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001493	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000618	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000497	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001693	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia

Seq_0000633	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001370	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000402	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0001366	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0002129	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001332	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000741	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000269	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVIII
Seq_0000515	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcus
Seq_0000819	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000100	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor
Seq_0000378	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000665	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Pediococcus
Seq_0001707	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000995	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XI	Gemella
Seq_0001500	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000085	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Seq_0000210	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000435	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001659	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000772	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001787	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Enterorhabdus
Seq_0000918	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000208	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	Burkholderiales_unclassified
Seq_0001348	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001596	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000749	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000689	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000037	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000387	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000871	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0002087	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000015	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000367	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0001130	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000445	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001115	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000411	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000962	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000187	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus
Seq_0000505	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000873	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000281	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001919	Bacteria	Firmicutes	Clostridia	Clostridia_unclassified	Clostridia_unclassified	Clostridia_unclassified
Seq_0000176	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0002312	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001413	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000424	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000079	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcus
Seq_0002516	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000329	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000477	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0000777	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
Seq_0002671	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000738	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001454	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000810	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XIII	Mogibacterium
Seq_0000649	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0000471	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000094	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000718	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0002236	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000380	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000722	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002225	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000082	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0002127	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000488	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides

Seq_0000474	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0000487	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcaceae_unclassified
Seq_0002126	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000241	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000670	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000023	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0002197	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000989	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0000866	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000876	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000907	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000308	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000525	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000592	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0001975	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001819	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000097	Bacteria	Fusobacteriia	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium

Seq_0000106	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000108	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000150	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000213	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000248	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000558	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000610	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Solobacterium
Seq_0000662	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000667	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000729	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001104	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001558	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Pseudoflavonifractor
Seq_0000227	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000143	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000680	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001195	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001222	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Coprobaillus
Seq_0001243	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000555	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0001059	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001081	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0001458	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0002209	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000624	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000653	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000498	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000748	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001301	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0001520	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001634	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001646	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000145	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000417	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000468	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000547	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000872	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0001924	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0002013	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000300	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000616	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001294	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001943	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0002558	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000225	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002455	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Holdemania
Seq_0000800	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002693	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001097	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000098	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001451	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000603	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001210	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001208	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Seq_0000347	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000580	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000713	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001431	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0002395	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0002643	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000838	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001086	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001317	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000173	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000793	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000847	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000061	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000226	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000076	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000305	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000437	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000955	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0001058	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001296	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0001827	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002669	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Oxalobacteraceae_unclassified
Seq_0002770	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001365	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000420	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000087	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000169	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0002144	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000699	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0001259	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000279	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001326	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Peptococcus
Seq_0002822	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001378	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	Burkholderiales_unclassified
Seq_0000946	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium

Seq_0001706	Bacteria	Proteobacteria	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified
Seq_0001319	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0000054	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000164	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000282	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000652	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001237	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0001529	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0001998	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000060	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000832	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000294	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001434	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Porphyromonadaceae_unclassified
Seq_0001764	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0002464	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001336	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001477	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001200	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0001592	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000582	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000675	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000111	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0001419	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000732	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000933	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001675	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Butyricimonas
Seq_0002183	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000398	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000579	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000802	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001540	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000389	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000632	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000929	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001095	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus

Seq_0001226	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001475	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001765	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Allisonella
Seq_0002405	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0002292	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Butyricimonas
Seq_0000270	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Parasutterella
Seq_0000846	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000432	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000130	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001322	Bacteria	Proteobacteria	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified
Seq_0002593	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001721	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002128	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000968	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000949	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000963	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001685	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000311	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0000795	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001261	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Pseudoflavonifractor
Seq_0001512	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001605	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0002119	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000042	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000332	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000739	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000823	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001225	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0001674	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000052	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000370	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001269	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001409	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0002645	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000073	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000400	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa

Seq_0000499	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000585	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001878	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000093	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000343	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000496	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001286	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0002351	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Gordonibacter
Seq_0000394	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000044	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0002105	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001254	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000716	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000565	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000448	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVIII
Seq_0000450	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
Seq_0000470	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Seq_0000171	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000874	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001014	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000195	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacteriaceae_unclassified
Seq_0000105	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000230	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Clostridium_XI
Seq_0000314	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000674	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000340	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000755	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000840	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000285	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_0000181	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001660	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000522	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000062	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000349	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000254	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000217	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia

Seq_0000232	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000694	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0002661	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000202	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0001019	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0002747	Bacteria	Cyanobacteria/Chloroplast	Chloroplast	Chloroplast	Streptophyta	Streptophyta_unclassified
Seq_0000008	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000067	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000842	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000967	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000112	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000090	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Clostridium_XI
Seq_0000095	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000257	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001044	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0000773	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000050	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000692	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000556	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0000069	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000321	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000124	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000156	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000197	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000570	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000429	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000588	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0002607	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000449	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000688	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Holdemania
Seq_0000066	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium_sensu_stricto
Seq_0000415	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001624	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000702	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001869	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000077	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0000293	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000737	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000821	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000022	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000039	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0000222	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000138	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0000212	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000940	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000476	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Seq_0000172	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001066	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lactonifactor
Seq_0000404	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000137	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Phascolarctobacterium
Seq_0001532	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000543	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001792	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Allobaculum
Seq_0000703	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000190	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0001204	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified

Seq_0002507	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000363	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000386	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000625	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000788	Bacteria	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Coprobacillus
Seq_0001417	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter
Seq_0000045	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000072	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000941	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0001075	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Seq_0000007	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Table 4. DeSeq2 results of 16S RVS counts comparing Healthy controls to UC

RSV	Base Mean	log2Fold Change	lfcSE	stat	p-value	padj
Seq_0000242	103.66	-27.10	1.63	-16.65	3.08E-62	1.23E-59
Seq_0000383	31.31	-24.74	1.54	-16.09	2.94E-58	5.87E-56
Seq_0000528	29.03	-25.81	1.72	-14.98	9.75E-51	1.30E-48
Seq_0000890	10.86	-24.46	1.73	-14.17	1.35E-45	1.35E-43
Seq_0000756	15.14	-24.93	1.83	-13.66	1.81E-42	1.44E-40
Seq_0000643	18.70	-23.81	1.85	-12.87	6.56E-38	4.36E-36
Seq_0000284	11.50	-24.56	2.10	-11.72	1.05E-31	5.99E-30
Seq_0000988	9.03	-24.24	2.08	-11.65	2.37E-31	1.18E-29

Seq_0000299	75.39	-27.11	2.47	-10.96	6.01E-28	2.66E-26
Seq_0000835	13.17	-24.74	2.33	-10.61	2.81E-26	1.12E-24
Seq_0000229	28.74	25.45	2.46	10.33	5.23E-25	1.90E-23
Seq_0000863	12.91	-23.26	2.46	-9.44	3.81E-21	1.27E-19
Seq_0000496	9.38	-24.30	2.59	-9.40	5.71E-21	1.75E-19
Seq_0000446	24.83	-25.62	2.84	-9.03	1.66E-19	4.74E-18
Seq_0000607	5.80	23.21	2.65	8.77	1.83E-18	4.87E-17
Seq_0000421	15.52	-24.98	2.92	-8.57	1.08E-17	2.69E-16
Seq_0000041	269.40	-8.55	1.03	-8.28	1.27E-16	2.97E-15
Seq_0000113	263.73	-9.62	1.29	-7.43	1.09E-13	2.42E-12
Seq_0000131	189.38	-11.22	1.74	-6.44	1.19E-10	2.49E-09
Seq_0000100	141.09	2.10	0.50	4.23	2.29E-05	4.57E-04
Seq_0000199	103.75	-5.67	1.39	-4.07	4.80E-05	9.12E-04
Seq_0000160	45.94	3.02	0.76	3.97	7.28E-05	1.32E-03
Seq_0001143	7.48	-6.25	1.68	-3.72	2.03E-04	3.52E-03
Seq_0000644	16.36	-8.20	2.25	-3.64	2.69E-04	4.48E-03
Seq_0000797	13.75	-7.36	2.03	-3.63	2.83E-04	4.52E-03
Seq_0000758	14.21	-4.04	1.27	-3.19	1.42E-03	2.18E-02
Seq_0000119	33.16	3.23	1.03	3.13	1.72E-03	2.49E-02
Seq_0000734	4.59	-4.21	1.35	-3.12	1.78E-03	2.49E-02
Seq_0000037	306.26	3.00	0.96	3.12	1.81E-03	2.49E-02
Seq_0000937	10.41	-6.54	2.12	-3.08	2.05E-03	2.73E-02
Seq_0000132	23.91	5.41	1.82	2.98	2.93E-03	3.77E-02
Seq_0001013	5.58	-5.82	2.03	-2.87	4.07E-03	4.95E-02
Seq_0000280	58.21	-2.33	0.81	-2.87	4.10E-03	4.95E-02
Seq_0000098	73.20	3.32	1.18	2.82	4.80E-03	5.64E-02
Seq_0000032	634.15	-2.78	0.99	-2.81	4.97E-03	5.66E-02
Seq_0000191	13.78	-5.76	2.07	-2.79	5.34E-03	5.92E-02
Seq_0000158	140.71	-2.43	0.89	-2.74	6.08E-03	6.56E-02
Seq_0000804	5.82	5.78	2.12	2.72	6.52E-03	6.84E-02
Seq_0000993	5.28	-5.75	2.14	-2.69	7.19E-03	7.36E-02
Seq_0000850	6.58	-5.05	1.89	-2.67	7.62E-03	7.60E-02
Seq_0000825	5.15	5.54	2.10	2.63	8.47E-03	8.24E-02

Seq_0000153	19.74	3.16	1.21	2.61	9.03E-03	8.58E-02
Seq_0000375	24.94	-3.76	1.46	-2.58	9.91E-03	9.19E-02
Seq_0000293	34.05	-2.39	0.93	-2.56	1.04E-02	9.41E-02
Seq_0000057	173.26	2.37	0.93	2.55	1.07E-02	9.44E-02
Seq_0000257	58.91	-2.28	0.90	-2.55	1.09E-02	9.44E-02
Seq_0000786	9.60	-4.11	1.62	-2.54	1.11E-02	9.44E-02
Seq_0000852	12.09	-2.48	0.98	-2.53	1.15E-02	9.58E-02
Seq_0000635	8.93	-6.50	2.58	-2.52	1.19E-02	9.66E-02
Seq_0001125	3.97	-3.87	1.57	-2.47	1.37E-02	1.09E-01
Seq_0000976	7.23	-2.85	1.17	-2.44	1.48E-02	1.16E-01
Seq_0000236	22.44	1.92	0.80	2.39	1.68E-02	1.29E-01
Seq_0000333	48.25	-3.01	1.26	-2.38	1.74E-02	1.29E-01
Seq_0001948	2.16	-4.19	1.76	-2.38	1.75E-02	1.29E-01
Seq_0000687	4.92	5.86	2.47	2.37	1.79E-02	1.30E-01
Seq_0000200	9.67	6.83	2.91	2.34	1.91E-02	1.34E-01
Seq_0000212	66.72	-2.02	0.87	-2.34	1.94E-02	1.34E-01
Seq_0000468	25.27	-2.56	1.10	-2.34	1.95E-02	1.34E-01
Seq_0000065	291.55	-1.38	0.59	-2.33	1.99E-02	1.35E-01
Seq_0000290	9.62	6.63	2.91	2.28	2.28E-02	1.52E-01
Seq_0001133	5.33	-5.76	2.54	-2.27	2.34E-02	1.53E-01
Seq_0000202	7.19	-6.19	2.74	-2.26	2.39E-02	1.54E-01
Seq_0000223	6.87	-6.13	2.72	-2.25	2.45E-02	1.55E-01
Seq_0001313	5.53	-3.73	1.70	-2.20	2.79E-02	1.68E-01
Seq_0000698	6.19	-5.98	2.72	-2.20	2.79E-02	1.68E-01
Seq_0001253	5.52	-3.13	1.43	-2.20	2.81E-02	1.68E-01
Seq_0000171	84.58	-1.73	0.79	-2.19	2.82E-02	1.68E-01
Seq_0000184	83.99	-1.25	0.58	-2.17	2.97E-02	1.74E-01
Seq_0000380	10.62	-5.72	2.65	-2.16	3.10E-02	1.76E-01
Seq_0000015	1962.96	2.98	1.38	2.15	3.12E-02	1.76E-01
Seq_0000749	5.58	-5.83	2.71	-2.15	3.13E-02	1.76E-01
Seq_0000571	12.07	-2.85	1.34	-2.12	3.42E-02	1.87E-01
Seq_0000429	28.75	2.64	1.26	2.10	3.57E-02	1.87E-01
Seq_0000551	6.71	-6.09	2.90	-2.10	3.58E-02	1.87E-01

Seq_0000924	4.98	-5.66	2.70	-2.10	3.61E-02	1.87E-01
Seq_0001637	2.33	-3.75	1.79	-2.09	3.67E-02	1.87E-01
Seq_0000137	128.59	-2.70	1.29	-2.09	3.67E-02	1.87E-01
Seq_0000364	29.70	-2.33	1.12	-2.09	3.69E-02	1.87E-01
Seq_0000201	111.90	-4.78	2.29	-2.09	3.69E-02	1.87E-01
Seq_0000614	2.78	4.29	2.09	2.06	3.98E-02	1.98E-01
Seq_0000869	11.19	-2.43	1.19	-2.05	4.07E-02	1.98E-01
Seq_0001127	4.59	-2.49	1.22	-2.03	4.20E-02	1.98E-01
Seq_0000722	6.10	-3.78	1.86	-2.03	4.22E-02	1.98E-01
Seq_0001693	2.56	-4.70	2.32	-2.03	4.25E-02	1.98E-01
Seq_0001150	5.22	4.63	2.29	2.02	4.30E-02	1.98E-01
Seq_0000633	4.26	-5.43	2.69	-2.02	4.30E-02	1.98E-01
Seq_0001177	5.43	-4.24	2.10	-2.02	4.34E-02	1.98E-01
Seq_0000052	425.67	4.28	2.12	2.02	4.37E-02	1.98E-01
Seq_0000768	10.64	-2.72	1.36	-2.00	4.51E-02	2.02E-01
Seq_0000378	4.68	-5.42	2.71	-2.00	4.57E-02	2.03E-01
Seq_0001493	2.31	-4.15	2.08	-1.99	4.62E-02	2.03E-01
Seq_0001526	2.12	3.82	1.95	1.96	5.05E-02	2.18E-01
Seq_0000130	151.68	-1.32	0.68	-1.95	5.14E-02	2.18E-01
Seq_0000519	10.44	-4.29	2.20	-1.95	5.14E-02	2.18E-01
Seq_0001707	2.18	-4.47	2.31	-1.94	5.28E-02	2.21E-01
Seq_0000179	102.90	-1.57	0.81	-1.93	5.33E-02	2.21E-01
Seq_0000312	62.33	-2.95	1.53	-1.93	5.37E-02	2.21E-01
Seq_0000694	9.37	-1.87	0.98	-1.91	5.60E-02	2.25E-01
Seq_0000387	4.67	-5.57	2.92	-1.91	5.63E-02	2.25E-01
Seq_0000443	7.84	3.61	1.89	1.91	5.63E-02	2.25E-01
Seq_0000367	3.40	-4.06	2.15	-1.89	5.92E-02	2.33E-01
Seq_0000275	61.38	-3.29	1.75	-1.88	5.95E-02	2.33E-01
Seq_0000882	2.20	4.34	2.31	1.88	6.00E-02	2.33E-01
Seq_0000738	4.29	-5.45	2.92	-1.87	6.19E-02	2.38E-01
Seq_0000918	4.18	-5.41	2.92	-1.85	6.37E-02	2.42E-01
Seq_0000450	28.63	-1.78	0.96	-1.85	6.43E-02	2.42E-01
Seq_0001218	2.13	4.44	2.43	1.83	6.77E-02	2.50E-01

Seq_0001657	2.35	-3.17	1.74	-1.83	6.79E-02	2.50E-01
Seq_0000696	2.80	4.77	2.63	1.82	6.93E-02	2.50E-01
Seq_0000265	61.15	-1.96	1.08	-1.81	6.98E-02	2.50E-01
Seq_0000871	2.71	-4.78	2.65	-1.80	7.11E-02	2.50E-01
Seq_0000327	75.30	-4.10	2.27	-1.80	7.11E-02	2.50E-01
Seq_0001019	5.89	2.70	1.50	1.80	7.14E-02	2.50E-01
Seq_0000269	36.36	1.96	1.09	1.80	7.15E-02	2.50E-01
Seq_0000435	4.54	-5.21	2.92	-1.79	7.42E-02	2.56E-01
Seq_0001222	4.39	-2.81	1.58	-1.78	7.47E-02	2.56E-01
Seq_0000534	23.24	-3.64	2.04	-1.78	7.51E-02	2.56E-01
Seq_0000833	9.02	-3.91	2.20	-1.78	7.56E-02	2.56E-01
Seq_0000876	3.48	-5.14	2.92	-1.76	7.79E-02	2.61E-01
Seq_0001262	3.47	3.79	2.16	1.76	7.84E-02	2.61E-01
Seq_0000188	4.38	5.10	2.91	1.75	8.01E-02	2.64E-01
Seq_0000329	3.00	-4.93	2.84	-1.74	8.23E-02	2.69E-01
Seq_0000349	24.52	2.41	1.40	1.72	8.45E-02	2.74E-01
Seq_0000281	54.22	-1.68	0.98	-1.72	8.63E-02	2.78E-01
Seq_0000187	3.06	3.85	2.26	1.70	8.88E-02	2.82E-01
Seq_0000872	9.25	-2.48	1.46	-1.70	8.95E-02	2.82E-01
Seq_0000274	38.87	-2.56	1.51	-1.69	9.07E-02	2.82E-01
Seq_0000170	100.29	-1.56	0.92	-1.69	9.09E-02	2.82E-01
Seq_0000424	2.99	-4.92	2.92	-1.69	9.16E-02	2.82E-01
Seq_0001395	4.92	-2.98	1.78	-1.67	9.48E-02	2.82E-01
Seq_0001104	2.87	-4.86	2.92	-1.67	9.56E-02	2.82E-01
Seq_0000662	2.86	-4.86	2.92	-1.67	9.57E-02	2.82E-01
Seq_0000491	24.23	-1.75	1.05	-1.66	9.65E-02	2.82E-01
Seq_0000172	77.04	1.27	0.76	1.66	9.74E-02	2.82E-01
Seq_0000515	2.81	-4.84	2.92	-1.66	9.75E-02	2.82E-01
Seq_0000477	3.00	-4.44	2.68	-1.66	9.76E-02	2.82E-01
Seq_0000487	4.36	-4.83	2.92	-1.66	9.77E-02	2.82E-01
Seq_0000440	18.12	-4.37	2.64	-1.66	9.79E-02	2.82E-01
Seq_0000628	8.01	-3.05	1.84	-1.65	9.81E-02	2.82E-01
Seq_0000810	2.70	-4.78	2.92	-1.64	1.02E-01	2.89E-01

Seq_0000122	83.76	1.48	0.90	1.63	1.03E-01	2.90E-01
Seq_0000020	1361.56	-1.31	0.81	-1.62	1.06E-01	2.97E-01
Seq_0000069	272.09	1.27	0.79	1.61	1.06E-01	2.97E-01
Seq_0001370	2.22	-3.23	2.01	-1.60	1.09E-01	2.99E-01
Seq_0000649	2.51	-4.67	2.92	-1.60	1.09E-01	2.99E-01
Seq_0000471	2.48	-4.65	2.92	-1.59	1.11E-01	2.99E-01
Seq_0000090	137.54	1.06	0.66	1.59	1.11E-01	2.99E-01
Seq_0000279	31.82	1.58	0.99	1.59	1.11E-01	2.99E-01
Seq_0001248	2.13	4.64	2.92	1.59	1.12E-01	2.99E-01
Seq_0001335	3.26	-2.51	1.58	-1.59	1.12E-01	2.99E-01
Seq_0000488	2.40	-4.61	2.92	-1.58	1.14E-01	3.02E-01
Seq_0000241	2.34	-4.57	2.92	-1.57	1.17E-01	3.08E-01
Seq_0000112	121.93	-1.61	1.04	-1.54	1.24E-01	3.23E-01
Seq_0000151	148.13	-2.33	1.53	-1.52	1.28E-01	3.30E-01
Seq_0000670	2.14	-4.44	2.92	-1.52	1.28E-01	3.30E-01
Seq_0000108	129.82	0.85	0.57	1.51	1.32E-01	3.36E-01
Seq_0000525	2.07	-4.40	2.92	-1.51	1.32E-01	3.36E-01
Seq_0000622	22.94	-3.35	2.25	-1.49	1.36E-01	3.42E-01
Seq_0001280	4.77	-2.89	1.94	-1.49	1.36E-01	3.42E-01
Seq_0000370	30.22	-1.22	0.83	-1.48	1.39E-01	3.48E-01
Seq_0000547	2.44	-4.29	2.92	-1.47	1.41E-01	3.49E-01
Seq_0000185	70.02	-2.11	1.44	-1.47	1.43E-01	3.49E-01
Seq_0000573	16.13	-2.05	1.40	-1.47	1.43E-01	3.49E-01
Seq_0000664	16.06	-1.86	1.27	-1.46	1.44E-01	3.49E-01
Seq_0001329	3.55	-3.35	2.31	-1.45	1.47E-01	3.54E-01
Seq_0000755	9.66	2.95	2.03	1.45	1.47E-01	3.54E-01
Seq_0000323	53.94	-1.65	1.14	-1.44	1.49E-01	3.57E-01
Seq_0000799	5.18	-2.93	2.05	-1.43	1.53E-01	3.58E-01
Seq_0000181	58.96	1.55	1.08	1.43	1.54E-01	3.58E-01
Seq_0000989	9.20	2.49	1.74	1.42	1.54E-01	3.58E-01
Seq_0000454	11.06	-1.99	1.40	-1.42	1.55E-01	3.58E-01
Seq_0000066	82.37	1.24	0.87	1.42	1.55E-01	3.58E-01
Seq_0000784	10.23	-1.48	1.04	-1.42	1.56E-01	3.58E-01

Seq_0000832	2.19	-4.14	2.92	-1.42	1.56E-01	3.58E-01
Seq_0000163	128.72	-1.03	0.73	-1.41	1.59E-01	3.62E-01
Seq_0000599	23.17	-1.69	1.22	-1.39	1.64E-01	3.72E-01
Seq_0000067	285.97	1.56	1.14	1.37	1.71E-01	3.87E-01
Seq_0000962	2.97	2.44	1.79	1.36	1.74E-01	3.90E-01
Seq_0000014	1698.99	-0.82	0.61	-1.35	1.77E-01	3.94E-01
Seq_0000731	11.00	-0.95	0.70	-1.35	1.78E-01	3.95E-01
Seq_0000268	10.34	-3.90	2.91	-1.34	1.80E-01	3.96E-01
Seq_0001748	2.86	-2.19	1.66	-1.32	1.85E-01	4.05E-01
Seq_0000363	14.00	2.08	1.57	1.32	1.87E-01	4.05E-01
Seq_0000085	239.61	-1.17	0.89	-1.32	1.87E-01	4.05E-01
Seq_0000373	41.94	-3.05	2.33	-1.31	1.90E-01	4.08E-01
Seq_0000499	7.65	2.63	2.01	1.31	1.91E-01	4.08E-01
Seq_0000418	39.84	-2.51	1.93	-1.30	1.92E-01	4.08E-01
Seq_0001146	5.95	-2.59	1.98	-1.30	1.92E-01	4.08E-01
Seq_0001787	2.65	-2.96	2.28	-1.30	1.94E-01	4.10E-01
Seq_0000930	4.63	2.63	2.04	1.29	1.97E-01	4.12E-01
Seq_0000800	9.19	-1.89	1.46	-1.29	1.97E-01	4.12E-01
Seq_0000210	68.14	-1.84	1.44	-1.28	2.01E-01	4.16E-01
Seq_0000047	134.88	0.98	0.76	1.28	2.02E-01	4.16E-01
Seq_0000023	699.89	1.02	0.80	1.27	2.04E-01	4.16E-01
Seq_0000213	68.18	-1.49	1.18	-1.27	2.04E-01	4.16E-01
Seq_0000847	8.07	2.20	1.73	1.27	2.04E-01	4.16E-01
Seq_0000063	304.77	-2.01	1.59	-1.26	2.07E-01	4.19E-01
Seq_0000008	1921.35	-0.58	0.46	-1.26	2.08E-01	4.19E-01
Seq_0000684	14.06	-2.02	1.63	-1.24	2.14E-01	4.28E-01
Seq_0000827	9.31	-2.45	1.97	-1.24	2.15E-01	4.28E-01
Seq_0000543	15.42	-1.58	1.28	-1.23	2.19E-01	4.32E-01
Seq_0000334	48.27	-1.43	1.16	-1.23	2.20E-01	4.32E-01
Seq_0000486	8.26	-2.51	2.05	-1.23	2.20E-01	4.32E-01
Seq_0000505	16.87	-1.31	1.07	-1.22	2.21E-01	4.32E-01
Seq_0000145	100.18	-1.50	1.24	-1.22	2.24E-01	4.35E-01
Seq_0001204	4.17	1.53	1.26	1.21	2.25E-01	4.35E-01

Seq_0000522	14.94	0.97	0.80	1.20	2.29E-01	4.42E-01
Seq_0000169	68.77	1.69	1.41	1.20	2.32E-01	4.44E-01
Seq_0001057	6.27	-1.71	1.43	-1.19	2.33E-01	4.44E-01
Seq_0000355	32.48	-1.08	0.90	-1.19	2.34E-01	4.44E-01
Seq_0000653	10.88	2.02	1.71	1.19	2.35E-01	4.45E-01
Seq_0000741	12.24	-1.33	1.12	-1.18	2.37E-01	4.46E-01
Seq_0000192	110.49	-2.13	1.81	-1.18	2.40E-01	4.49E-01
Seq_0001029	6.89	-1.56	1.35	-1.16	2.45E-01	4.56E-01
Seq_0000425	31.28	-0.87	0.75	-1.16	2.47E-01	4.56E-01
Seq_0000094	79.35	1.47	1.27	1.16	2.47E-01	4.56E-01
Seq_0000439	40.63	-1.59	1.38	-1.15	2.49E-01	4.56E-01
Seq_0000338	41.40	-1.08	0.93	-1.15	2.49E-01	4.56E-01
Seq_0000254	32.53	2.35	2.06	1.14	2.52E-01	4.56E-01
Seq_0000215	64.31	-1.11	0.97	-1.14	2.53E-01	4.56E-01
Seq_0000476	6.94	-2.05	1.79	-1.14	2.53E-01	4.56E-01
Seq_0000588	13.25	2.14	1.88	1.14	2.54E-01	4.56E-01
Seq_0000143	130.65	-1.10	0.97	-1.14	2.56E-01	4.56E-01
Seq_0000042	496.08	-0.73	0.64	-1.14	2.56E-01	4.56E-01
Seq_0000842	2.38	-2.19	1.95	-1.12	2.61E-01	4.61E-01
Seq_0000983	8.50	-1.54	1.37	-1.12	2.62E-01	4.61E-01
Seq_0000466	19.43	-1.93	1.72	-1.12	2.62E-01	4.61E-01
Seq_0000324	40.04	-1.57	1.41	-1.11	2.67E-01	4.65E-01
Seq_0000427	7.60	-3.23	2.91	-1.11	2.67E-01	4.65E-01
Seq_0001256	4.97	-1.84	1.68	-1.10	2.72E-01	4.71E-01
Seq_0000196	5.20	1.75	1.61	1.09	2.77E-01	4.78E-01
Seq_0001169	4.89	-1.81	1.67	-1.09	2.78E-01	4.78E-01
Seq_0000039	491.77	0.60	0.56	1.08	2.79E-01	4.78E-01
Seq_0001614	3.15	-1.89	1.76	-1.07	2.82E-01	4.82E-01
Seq_0000509	7.10	-2.74	2.57	-1.06	2.88E-01	4.88E-01
Seq_0000231	5.40	2.42	2.28	1.06	2.89E-01	4.88E-01
Seq_0000144	157.61	-1.17	1.11	-1.05	2.92E-01	4.92E-01
Seq_0000227	21.21	2.01	1.93	1.04	2.96E-01	4.97E-01
Seq_0000152	74.41	-1.16	1.12	-1.04	2.99E-01	4.99E-01

Seq_0000874	3.00	2.16	2.09	1.03	3.02E-01	5.02E-01
Seq_0000273	3.34	2.96	2.91	1.02	3.09E-01	5.11E-01
Seq_0000824	7.98	-2.25	2.24	-1.01	3.14E-01	5.18E-01
Seq_0000308	15.50	2.84	2.83	1.00	3.16E-01	5.19E-01
Seq_0000489	22.11	-0.73	0.74	-0.99	3.21E-01	5.22E-01
Seq_0000105	234.03	-1.16	1.16	-0.99	3.21E-01	5.22E-01
Seq_0000022	222.34	-0.71	0.72	-0.98	3.25E-01	5.28E-01
Seq_0000226	38.85	1.83	1.88	0.98	3.29E-01	5.30E-01
Seq_0000045	393.96	-0.64	0.66	-0.97	3.30E-01	5.30E-01
Seq_0000078	199.16	-0.90	0.93	-0.97	3.34E-01	5.35E-01
Seq_0000197	46.60	-0.75	0.79	-0.95	3.44E-01	5.49E-01
Seq_0001372	4.83	-1.71	1.82	-0.94	3.47E-01	5.50E-01
Seq_0000508	23.91	-1.29	1.38	-0.94	3.48E-01	5.50E-01
Seq_0000314	8.86	1.48	1.58	0.94	3.50E-01	5.50E-01
Seq_0000688	7.42	-0.94	1.01	-0.93	3.50E-01	5.50E-01
Seq_0000777	2.44	-2.36	2.57	-0.92	3.58E-01	5.61E-01
Seq_0000230	40.54	0.95	1.05	0.91	3.62E-01	5.64E-01
Seq_0000448	26.31	0.95	1.05	0.90	3.67E-01	5.69E-01
Seq_0000044	382.45	-1.25	1.39	-0.90	3.71E-01	5.69E-01
Seq_0000272	60.15	-1.92	2.14	-0.90	3.71E-01	5.69E-01
Seq_0000050	383.84	-0.94	1.05	-0.90	3.71E-01	5.69E-01
Seq_0000325	22.65	-1.50	1.70	-0.88	3.76E-01	5.75E-01
Seq_0001596	2.92	-1.95	2.21	-0.88	3.78E-01	5.76E-01
Seq_0001431	2.34	-2.13	2.43	-0.88	3.80E-01	5.76E-01
Seq_0000271	62.27	-1.05	1.20	-0.87	3.83E-01	5.77E-01
Seq_0000077	186.26	0.70	0.81	0.87	3.84E-01	5.77E-01
Seq_0000343	27.72	-1.06	1.22	-0.87	3.85E-01	5.77E-01
Seq_0000134	185.95	-0.64	0.74	-0.86	3.87E-01	5.78E-01
Seq_0001014	5.41	-0.83	0.96	-0.86	3.88E-01	5.78E-01
Seq_0000093	157.85	-0.73	0.85	-0.86	3.93E-01	5.82E-01
Seq_0001679	2.61	-1.58	1.90	-0.83	4.05E-01	5.97E-01
Seq_0000470	8.02	-0.93	1.11	-0.83	4.06E-01	5.97E-01
Seq_0000546	3.23	2.41	2.91	0.83	4.07E-01	5.97E-01

Seq_0000394	25.62	-1.14	1.38	-0.82	4.10E-01	5.98E-01
Seq_0000054	275.29	1.15	1.40	0.82	4.12E-01	5.98E-01
Seq_0000420	10.84	-1.98	2.41	-0.82	4.12E-01	5.98E-01
Seq_0000866	4.84	-1.42	1.76	-0.81	4.18E-01	6.04E-01
Seq_0000474	2.55	-2.07	2.59	-0.80	4.24E-01	6.10E-01
Seq_0000748	4.86	1.68	2.17	0.77	4.41E-01	6.33E-01
Seq_0000243	12.04	-2.17	2.83	-0.77	4.43E-01	6.34E-01
Seq_0000076	244.48	-0.80	1.05	-0.76	4.49E-01	6.36E-01
Seq_0000736	12.17	-1.28	1.69	-0.76	4.49E-01	6.36E-01
Seq_0000618	10.88	-1.30	1.73	-0.76	4.50E-01	6.36E-01
Seq_0000287	56.67	-0.58	0.77	-0.75	4.55E-01	6.39E-01
Seq_0000395	31.13	1.32	1.79	0.74	4.59E-01	6.39E-01
Seq_0000203	32.47	-0.67	0.91	-0.74	4.60E-01	6.39E-01
Seq_0000270	53.61	0.71	0.96	0.74	4.61E-01	6.39E-01
Seq_0000138	147.03	0.79	1.07	0.74	4.62E-01	6.39E-01
Seq_0000305	40.35	-1.15	1.56	-0.74	4.62E-01	6.39E-01
Seq_0001301	4.03	-0.85	1.16	-0.73	4.64E-01	6.39E-01
Seq_0000675	7.99	0.94	1.29	0.73	4.66E-01	6.39E-01
Seq_0001646	2.11	1.09	1.50	0.73	4.68E-01	6.39E-01
Seq_0000129	159.65	-0.42	0.58	-0.73	4.68E-01	6.39E-01
Seq_0000103	214.10	-0.56	0.77	-0.72	4.69E-01	6.39E-01
Seq_0001635	2.21	1.80	2.56	0.70	4.83E-01	6.53E-01
Seq_0001295	3.28	1.57	2.23	0.70	4.84E-01	6.53E-01
Seq_0000128	85.85	0.63	0.90	0.70	4.85E-01	6.53E-01
Seq_0000560	13.14	-0.75	1.10	-0.68	4.94E-01	6.64E-01
Seq_0000737	3.69	-1.45	2.15	-0.67	5.01E-01	6.71E-01
Seq_0000104	197.64	-0.93	1.42	-0.65	5.13E-01	6.84E-01
Seq_0000941	7.07	1.40	2.14	0.65	5.14E-01	6.84E-01
Seq_0000095	232.34	-0.42	0.65	-0.64	5.20E-01	6.89E-01
Seq_0000060	256.70	-0.80	1.25	-0.64	5.23E-01	6.90E-01
Seq_0000062	293.96	-0.33	0.52	-0.64	5.24E-01	6.90E-01
Seq_0000222	42.35	-1.01	1.62	-0.63	5.30E-01	6.96E-01
Seq_0000449	26.70	1.19	1.91	0.62	5.33E-01	6.97E-01

Seq_0000237	92.55	-0.81	1.32	-0.62	5.38E-01	7.02E-01
Seq_0001425	3.06	-1.24	2.02	-0.61	5.41E-01	7.03E-01
Seq_0000073	231.40	-0.72	1.18	-0.61	5.44E-01	7.05E-01
Seq_0001283	3.86	-1.09	1.80	-0.60	5.46E-01	7.05E-01
Seq_0000166	129.48	-1.08	1.79	-0.60	5.48E-01	7.05E-01
Seq_0001151	6.62	-1.17	1.95	-0.60	5.50E-01	7.06E-01
Seq_0000359	5.82	-1.71	2.90	-0.59	5.56E-01	7.10E-01
Seq_0001332	3.19	-1.25	2.13	-0.59	5.57E-01	7.10E-01
Seq_0000940	5.32	-0.86	1.47	-0.58	5.59E-01	7.10E-01
Seq_0000360	34.37	-1.20	2.09	-0.58	5.64E-01	7.14E-01
Seq_0000326	59.51	-0.67	1.17	-0.57	5.67E-01	7.14E-01
Seq_0000106	185.65	-0.52	0.92	-0.57	5.68E-01	7.14E-01
Seq_0000311	40.99	0.79	1.40	0.57	5.72E-01	7.14E-01
Seq_0001483	3.85	1.28	2.27	0.56	5.73E-01	7.14E-01
Seq_0001034	5.90	-1.25	2.22	-0.56	5.74E-01	7.14E-01
Seq_0000609	18.36	-0.63	1.12	-0.56	5.75E-01	7.14E-01
Seq_0000692	9.22	0.95	1.71	0.56	5.78E-01	7.14E-01
Seq_0000091	263.32	-0.58	1.04	-0.56	5.78E-01	7.14E-01
Seq_0001517	3.60	-1.03	1.87	-0.55	5.83E-01	7.18E-01
Seq_0000482	26.46	-0.59	1.10	-0.54	5.90E-01	7.20E-01
Seq_0000823	9.25	0.86	1.60	0.54	5.90E-01	7.20E-01
Seq_0000347	33.66	0.91	1.69	0.53	5.93E-01	7.20E-01
Seq_0000225	24.81	0.76	1.42	0.53	5.94E-01	7.20E-01
Seq_0000732	6.87	-0.62	1.16	-0.53	5.94E-01	7.20E-01
Seq_0000436	28.04	-1.13	2.15	-0.53	5.98E-01	7.23E-01
Seq_0000412	25.87	-0.79	1.52	-0.52	6.02E-01	7.26E-01
Seq_0000193	102.59	-0.69	1.35	-0.51	6.11E-01	7.34E-01
Seq_0000961	9.55	-0.92	1.85	-0.50	6.20E-01	7.43E-01
Seq_0000867	11.29	-0.70	1.42	-0.49	6.22E-01	7.43E-01
Seq_0000127	45.04	0.61	1.28	0.48	6.32E-01	7.52E-01
Seq_0000556	8.96	0.84	1.79	0.47	6.39E-01	7.59E-01
Seq_0001269	4.12	-0.85	1.90	-0.45	6.55E-01	7.74E-01
Seq_0000344	48.60	0.75	1.68	0.45	6.56E-01	7.74E-01

Seq_0000111	109.99	-0.44	1.00	-0.44	6.61E-01	7.77E-01
Seq_0000417	9.59	-0.51	1.18	-0.44	6.62E-01	7.77E-01
Seq_0001130	3.06	-0.59	1.36	-0.43	6.68E-01	7.79E-01
Seq_0000021	1188.88	-0.30	0.70	-0.43	6.68E-01	7.79E-01
Seq_0001059	2.35	-1.16	2.76	-0.42	6.73E-01	7.81E-01
Seq_0000156	103.18	0.48	1.13	0.42	6.73E-01	7.81E-01
Seq_0000209	59.27	0.48	1.17	0.41	6.79E-01	7.85E-01
Seq_0000554	9.15	-1.02	2.52	-0.41	6.85E-01	7.89E-01
Seq_0000282	38.30	-0.34	0.86	-0.40	6.92E-01	7.93E-01
Seq_0000802	2.29	1.03	2.60	0.40	6.92E-01	7.93E-01
Seq_0000206	42.20	-0.89	2.29	-0.39	6.96E-01	7.94E-01
Seq_0000087	5.69	1.13	2.90	0.39	6.97E-01	7.94E-01
Seq_0000391	24.95	-0.50	1.35	-0.37	7.09E-01	8.04E-01
Seq_0000820	8.83	-0.78	2.09	-0.37	7.10E-01	8.04E-01
Seq_0000402	32.62	-0.40	1.12	-0.35	7.23E-01	8.17E-01
Seq_0000465	16.62	-0.27	0.79	-0.35	7.28E-01	8.21E-01
Seq_0000716	7.11	0.66	1.98	0.34	7.37E-01	8.28E-01
Seq_0001663	2.60	-0.43	1.33	-0.33	7.44E-01	8.34E-01
Seq_0001558	2.60	0.56	1.83	0.31	7.58E-01	8.47E-01
Seq_0000479	9.29	-0.59	1.94	-0.30	7.61E-01	8.48E-01
Seq_0000232	55.97	0.30	1.01	0.30	7.63E-01	8.48E-01
Seq_0001317	2.67	-0.69	2.34	-0.29	7.69E-01	8.52E-01
Seq_0000248	59.00	0.16	0.55	0.28	7.76E-01	8.57E-01
Seq_0000913	8.65	0.68	2.40	0.28	7.78E-01	8.58E-01
Seq_0000404	2.47	0.76	2.78	0.28	7.83E-01	8.61E-01
Seq_0000606	8.09	-0.71	2.64	-0.27	7.86E-01	8.62E-01
Seq_0000541	4.02	-0.61	2.29	-0.27	7.89E-01	8.63E-01
Seq_0000415	13.71	0.48	1.83	0.26	7.93E-01	8.65E-01
Seq_0000501	19.62	-0.57	2.20	-0.26	7.96E-01	8.65E-01
Seq_0001366	3.13	-0.52	2.04	-0.25	7.99E-01	8.66E-01
Seq_0000702	5.12	-0.38	1.64	-0.23	8.18E-01	8.84E-01
Seq_0000411	26.83	-0.15	0.69	-0.22	8.28E-01	8.92E-01
Seq_0001037	7.18	-0.39	1.82	-0.21	8.32E-01	8.92E-01

Seq_0000080	226.20	0.12	0.57	0.21	8.32E-01	8.92E-01	
Seq_0000294	7.20	0.34	1.68	0.20	8.41E-01	8.97E-01	
Seq_0000081	295.46	0.28	1.42	0.20	8.43E-01	8.97E-01	
Seq_0000079	20.73	-0.37	1.90	-0.20	8.44E-01	8.97E-01	
Seq_0000164	13.33	0.46	2.34	0.19	8.46E-01	8.97E-01	
Seq_0000514	17.17	-0.38	2.10	-0.18	8.55E-01	9.03E-01	
Seq_0000082	195.62	0.14	0.75	0.18	8.55E-01	9.03E-01	
Seq_0000072	135.44	0.19	1.07	0.18	8.60E-01	9.05E-01	
Seq_0000259	11.62	-0.42	2.56	-0.17	8.68E-01	9.12E-01	
Seq_0000190	29.29	-0.30	1.87	-0.16	8.73E-01	9.14E-01	
Seq_0000773	7.17	0.20	1.36	0.15	8.84E-01	9.23E-01	
Seq_0000300	43.27	0.22	1.68	0.13	8.97E-01	9.34E-01	
Seq_0000701	9.17	-0.21	1.79	-0.12	9.05E-01	9.41E-01	
Seq_0001058	3.70	0.19	1.73	0.11	9.10E-01	9.44E-01	
Seq_0000400	19.55	0.18	1.96	0.09	9.26E-01	9.57E-01	
Seq_0000674	7.77	0.18	2.00	0.09	9.28E-01	9.57E-01	
Seq_0000445	16.26	0.15	1.86	0.08	9.35E-01	9.60E-01	
Seq_0000124	118.65	-0.08	0.99	-0.08	9.39E-01	9.60E-01	
Seq_0000398	19.44	0.10	1.34	0.07	9.41E-01	9.60E-01	
Seq_0000616	2.83	0.18	2.49	0.07	9.42E-01	9.60E-01	
Seq_0000386	15.43	0.09	1.21	0.07	9.43E-01	9.60E-01	
Seq_0000006	2273.56	-0.03	0.59	-0.05	9.56E-01	9.71E-01	
Seq_0000007	1577.35	0.03	0.60	0.05	9.59E-01	9.71E-01	
Seq_0001200	4.96	-0.06	1.33	-0.05	9.62E-01	9.72E-01	
Seq_0000107	182.72	-0.03	1.09	-0.03	9.75E-01	9.82E-01	
Seq_0000061	388.62	-0.02	0.75	-0.03	9.77E-01	9.82E-01	
Seq_0000497	23.36	-0.02	0.87	-0.02	9.85E-01	9.87E-01	
Seq_0000821	8.60	0.01	1.40	0.01	9.93E-01	9.93E-01	
RSV	Control Mean	Control Median	Control Present (n=47)	UC Mean	UC Median	UC Pres ent (n=3 9)	logfdr

Seq_0000242	4.00E-03	0	19	0	0	0	58.91
Seq_0000383	1.18E-03	0	19	0	0	0	55.23
Seq_0000528	1.17E-03	0	16	1.49E-05	0	1	47.89
Seq_0000890	4.95E-04	0	15	2.75E-05	0	1	42.87
Seq_0000756	4.98E-04	0	14	0	0	0	39.84
Seq_0000643	6.50E-04	0	14	0	0	0	35.36
Seq_0000284	2.60E-03	0	13	1.82E-04	0	1	29.22
Seq_0000988	3.28E-04	0	11	1.27E-05	0	1	28.93
Seq_0000299	2.62E-03	0	9	2.24E-04	0	1	25.57
Seq_0000835	4.80E-04	0	9	0	0	0	23.95
Seq_0000229	3.36E-05	0	1	3.60E-03	0	9	22.72
Seq_0000863	5.30E-04	0	8	0	0	0	18.90
Seq_0000496	5.67E-04	0	8	7.27E-04	0	1	18.76
Seq_0000446	1.81E-03	0	7	0	0	0	17.32
Seq_0000607	0	0	0	8.72E-04	0	7	16.31
Seq_0000421	1.48E-03	0	6	9.85E-05	0	2	15.57
Seq_0000041	2.22E-02	8.60E-05	28	1.72E-04	0	14	14.53

Seq_0000113	1.07E-02	0	23	7.16E-04	0	6	11.62
Seq_0000131	7.46E-03	0	17	8.06E-04	0	2	8.60
Seq_0000100	1.45E-03	7.67E-04	42	6.98E-03	2.12E-03	37	3.34
Seq_0000199	4.61E-03	0	22	9.91E-04	0	5	3.04
Seq_0000160	2.46E-04	3.88E-05	25	2.09E-03	3.47E-04	30	2.88
Seq_0001143	2.78E-04	0	15	0	0	0	2.45
Seq_0000644	7.06E-04	0	9	2.04E-06	0	1	2.35
Seq_0000797	6.18E-04	0	11	1.65E-05	0	2	2.34
Seq_0000758	5.49E-04	9.69E-05	24	3.82E-05	0	2	1.66
Seq_0000119	1.47E-04	0	14	1.65E-03	2.60E-04	24	1.60
Seq_0000734	1.81E-04	0	19	4.57E-04	0	3	1.60
Seq_0000037	2.26E-03	0	23	1.41E-02	1.65E-03	27	1.60
Seq_0000937	3.83E-04	0	10	4.08E-06	0	1	1.56
Seq_0000132	5.49E-05	0	5	4.50E-03	0	13	1.42
Seq_0001013	2.00E-04	0	11	3.94E-05	0	1	1.31
Seq_0000280	2.02E-03	1.29E-03	36	9.85E-04	0	14	1.31

Seq_0000098	1.23E-03	0	12	8.28E-03	3.36E-04	23	1.25
Seq_0000032	2.14E-02	9.37E-03	41	4.72E-03	0	8	1.25
Seq_0000191	1.95E-03	0	13	7.99E-04	0	3	1.23
Seq_0000158	5.35E-03	1.47E-03	36	1.40E-03	0	15	1.18
Seq_0000804	2.81E-05	0	2	4.75E-04	0	9	1.16
Seq_0000993	3.37E-04	0	11	1.27E-05	0	1	1.13
Seq_0000850	2.60E-04	0	12	7.89E-05	0	2	1.12
Seq_0000825	5.79E-06	0	1	8.94E-04	0	10	1.08
Seq_0000153	8.74E-05	0	14	3.33E-03	0	16	1.07
Seq_0000375	2.45E-03	0	20	2.05E-04	0	4	1.04
Seq_0000293	1.27E-03	2.55E-04	34	1.16E-03	0	9	1.03
Seq_0000057	3.61E-03	1.31E-04	25	9.97E-03	8.69E-04	25	1.03
Seq_0000257	2.31E-03	9.89E-04	36	4.81E-04	0	10	1.03
Seq_0000786	3.59E-04	0	15	1.90E-05	0	3	1.03
Seq_0000852	3.96E-04	2.56E-04	27	7.27E-05	0	9	1.02
Seq_0000635	8.98E-04	0	8	7.43E-05	0	1	1.02

Seq_0001125	2.36E-04	0	15	9.98E-06	0	2	0.96
Seq_0000976	2.29E-04	0	20	3.71E-05	0	8	0.94
Seq_0000236	1.21E-03	1.14E-04	28	2.88E-03	1.70E-04	22	0.89
Seq_0000333	1.77E-03	1.08E-04	24	2.09E-04	0	7	0.89
Seq_0001948	8.88E-05	0	12	3.92E-06	0	1	0.89
Seq_0000687	0	0	0	3.77E-04	0	7	0.89
Seq_0000200	9.24E-05	0	1	3.53E-03	0	4	0.87
Seq_0000212	2.53E-03	9.71E-04	36	6.03E-04	0	13	0.87
Seq_0000468	1.01E-03	8.16E-04	28	1.73E-04	0	6	0.87
Seq_0000065	9.35E-03	7.97E-03	43	4.06E-03	2.88E-03	25	0.87
Seq_0000290	1.04E-04	0	2	2.92E-03	0	4	0.82
Seq_0001133	3.49E-04	0	8	0	0	0	0.82
Seq_0000202	1.73E-03	0	8	8.54E-05	0	1	0.81
Seq_0000223	2.80E-03	0	9	7.34E-05	0	1	0.81
Seq_0001313	2.62E-04	0	14	1.46E-05	0	2	0.77
Seq_0000698	5.39E-04	0	7	1.30E-04	0	1	0.77
Seq_0001253	2.06E-04	0	16	2.23E-05	0	5	0.77

Seq_0000171	2.83E-03	1.79E-03	38	1.06E-03	0	15	0.77
Seq_0000184	2.68E-03	1.33E-03	42	1.46E-03	2.95E-04	27	0.76
Seq_0000380	1.76E-03	0	7	1.46E-04	0	3	0.75
Seq_0000015	9.67E-03	0	19	6.46E-02	6.94E-05	21	0.75
Seq_0000749	6.46E-04	0	7	0	0	0	0.75
Seq_0000571	4.78E-04	0	21	6.51E-05	0	4	0.73
Seq_0000429	2.01E-04	0	13	1.82E-03	0	17	0.73
Seq_0000551	3.62E-04	0	6	3.33E-04	0	1	0.73
Seq_0000924	3.49E-04	0	7	2.53E-05	0	1	0.73
Seq_0001637	9.23E-05	0	11	6.67E-06	0	2	0.73
Seq_0000137	5.48E-03	6.82E-05	25	9.89E-04	0	8	0.73
Seq_0000364	9.79E-04	1.12E-04	24	2.19E-04	0	11	0.73
Seq_0000201	4.30E-03	0	11	1.47E-04	0	2	0.73
Seq_0000614	1.84E-05	0	3	1.99E-03	0	9	0.70
Seq_0000869	3.95E-04	0	23	9.60E-05	0	6	0.70
Seq_0001127	1.80E-04	0	20	2.89E-05	0	5	0.70

Seq_0000722	2.45E-04	0	12	1.05E-04	0	3	0.70
Seq_0001693	1.06E-04	0	8	0	0	0	0.70
Seq_0001150	2.46E-05	0	2	2.85E-04	0	8	0.70
Seq_0000633	7.29E-04	0	7	3.49E-05	0	1	0.70
Seq_0001177	2.35E-04	0	10	4.10E-05	0	2	0.70
Seq_0000052	1.04E-03	0	7	2.07E-02	0	10	0.70
Seq_0000768	3.92E-04	0	20	5.23E-05	0	4	0.69
Seq_0000378	1.75E-03	0	7	1.14E-06	0	1	0.69
Seq_0001493	9.88E-05	0	9	6.67E-05	0	3	0.69
Seq_0001526	5.05E-06	0	2	1.77E-04	0	9	0.66
Seq_0000130	4.67E-03	2.21E-03	42	2.05E-03	5.67E-04	23	0.66
Seq_0000519	3.67E-04	0	9	1.72E-04	0	3	0.66
Seq_0001707	9.40E-05	0	8	0	0	0	0.66
Seq_0000179	3.48E-03	1.66E-03	39	9.75E-04	0	16	0.66
Seq_0000312	2.30E-03	0	20	2.97E-04	0	5	0.66
Seq_0000694	2.90E-04	1.90E-04	27	2.12E-04	0	9	0.65

Seq_0000387	1.51E-03	0	4	0	0	0	0.65
Seq_0000443	5.57E-05	0	5	4.88E-04	0	9	0.65
Seq_0000367	3.30E-04	0	9	7.39E-06	0	2	0.63
Seq_0000275	2.38E-03	0	15	2.16E-04	0	5	0.63
Seq_0000882	3.14E-06	0	2	1.01E-03	0	7	0.63
Seq_0000738	8.03E-04	0	6	0	0	0	0.62
Seq_0000918	5.04E-04	0	4	0	0	0	0.62
Seq_0000450	1.08E-03	6.19E-04	29	3.48E-04	0	12	0.62
Seq_0001218	1.41E-06	0	1	4.79E-04	0	7	0.60
Seq_0001657	8.61E-05	0	13	8.17E-06	0	1	0.60
Seq_0000696	1.84E-06	0	1	6.00E-04	0	6	0.60
Seq_0000265	2.03E-03	1.61E-03	31	5.26E-04	0	7	0.60
Seq_0000871	2.18E-04	0	8	3.86E-05	0	1	0.60
Seq_0000327	2.34E-03	0	11	2.98E-04	0	3	0.60
Seq_0001019	8.18E-05	0	9	3.74E-04	0	11	0.60
Seq_0000269	4.98E-04	0	15	1.95E-03	1.04E-04	23	0.60

Seq_0000435	1.46E-03	0	5	4.55E-06	0	1	0.59
Seq_0001222	1.59E-04	0	11	3.10E-05	0	7	0.59
Seq_0000534	7.86E-04	0	12	6.02E-05	0	2	0.59
Seq_0000833	3.20E-04	0	8	2.45E-05	0	3	0.59
Seq_0000876	6.07E-04	0	5	6.16E-05	0	1	0.58
Seq_0001262	1.38E-05	0	3	1.91E-04	0	7	0.58
Seq_0000188	3.37E-06	0	2	1.79E-02	0	3	0.58
Seq_0000329	7.48E-04	0	7	7.24E-04	0	3	0.57
Seq_0000349	7.81E-04	0	13	1.78E-03	0	13	0.56
Seq_0000281	1.70E-03	1.02E-03	28	5.95E-04	0	14	0.56
Seq_0000187	6.58E-05	0	4	7.54E-04	0	8	0.55
Seq_0000872	3.05E-04	0	17	9.29E-05	0	5	0.55
Seq_0000274	2.07E-03	0	19	5.26E-04	0	6	0.55
Seq_0000170	3.33E-03	1.61E-03	32	1.21E-03	0	15	0.55
Seq_0000424	8.19E-04	0	4	6.24E-06	0	1	0.55
Seq_0001395	2.47E-04	0	12	2.62E-05	0	3	0.55

Seq_0001104	2.32E-04	0	5	0	0	0	0.55
Seq_0000662	4.16E-04	0	6	1.57E-04	0	1	0.55
Seq_0000491	7.89E-04	3.91E-04	27	2.21E-04	0	9	0.55
Seq_0000172	1.07E-03	7.00E-04	33	3.20E-03	8.60E-04	23	0.55
Seq_0000515	4.73E-04	0	7	6.39E-04	0	3	0.55
Seq_0000477	6.21E-04	0	6	5.66E-04	0	3	0.55
Seq_0000487	1.22E-03	0	4	4.04E-04	0	4	0.55
Seq_0000440	1.31E-03	0	8	2.08E-04	0	2	0.55
Seq_0000628	3.00E-04	0	14	1.27E-04	0	2	0.55
Seq_0000810	4.77E-04	0	5	1.38E-05	0	1	0.54
Seq_0000122	1.57E-03	0	23	4.15E-03	1.02E-03	26	0.54
Seq_0000020	3.86E-02	1.49E-02	39	1.99E-02	3.12E-04	25	0.53
Seq_0000069	3.74E-03	1.69E-03	34	9.41E-03	1.58E-03	26	0.53
Seq_0001370	8.14E-05	0	9	3.30E-05	0	3	0.52
Seq_0000649	7.58E-04	0	5	0	0	0	0.52
Seq_0000471	6.10E-04	0	5	0	0	0	0.52

Seq_0000090	2.14E-03	5.01E-04	32	5.36E-03	1.91E-03	34	0.52
Seq_0000279	4.15E-04	8.56E-05	26	1.85E-03	0	16	0.52
Seq_0001248	0	0	0	6.96E-04	0	4	0.52
Seq_0001335	1.15E-04	0	15	2.03E-05	0	2	0.52
Seq_0000488	3.09E-04	0	5	7.55E-04	0	3	0.52
Seq_0000241	1.86E-03	0	6	8.70E-04	0	2	0.51
Seq_0000112	3.75E-03	1.77E-03	30	1.97E-03	0	12	0.49
Seq_0000151	4.92E-03	0	19	1.49E-03	0	8	0.48
Seq_0000670	2.15E-03	0	4	0	0	0	0.48
Seq_0000108	2.15E-03	6.55E-04	39	5.44E-03	1.25E-03	36	0.47
Seq_0000525	2.24E-04	0	5	1.17E-03	0	1	0.47
Seq_0000622	9.98E-04	0	8	9.06E-05	0	4	0.47
Seq_0001280	1.63E-04	0	11	2.68E-05	0	2	0.47
Seq_0000370	1.01E-03	6.95E-04	34	4.34E-04	0	14	0.46
Seq_0000547	8.93E-04	0	4	4.55E-06	0	1	0.46
Seq_0000185	2.71E-03	0	22	5.99E-04	0	6	0.46
Seq_0000573	5.31E-04	0	18	4.23E-04	0	7	0.46

Seq_0000664	4.94E-04	0	22	1.57E-04	0	6	0.46
Seq_0001329	1.30E-04	0	8	9.36E-06	0	1	0.45
Seq_0000755	5.16E-05	0	2	5.81E-04	0	11	0.45
Seq_0000323	1.66E-03	0	23	7.83E-04	0	13	0.45
Seq_0000799	1.69E-04	0	9	2.97E-05	0	3	0.45
Seq_0000181	6.98E-04	0	19	2.45E-03	1.62E-04	20	0.45
Seq_0000989	1.38E-04	0	6	5.00E-04	0	11	0.45
Seq_0000454	1.26E-03	0	19	1.01E-04	0	5	0.45
Seq_0000066	1.84E-03	2.36E-04	28	1.58E-02	4.05E-04	24	0.45
Seq_0000784	3.23E-04	1.35E-04	26	1.33E-04	0	8	0.45
Seq_0000832	3.86E-04	0	2	4.05E-06	0	2	0.45
Seq_0000163	3.62E-03	1.91E-03	37	2.12E-03	5.90E-04	22	0.44
Seq_0000599	7.55E-04	1.67E-04	24	3.55E-04	0	7	0.43
Seq_0000067	3.07E-03	0	23	1.07E-02	0	19	0.41
Seq_0000962	3.63E-05	0	3	2.01E-04	0	11	0.41
Seq_0000014	4.58E-02	2.55E-02	44	3.22E-02	8.37E-03	31	0.40

Seq_0000731	3.14E-04	2.52E-04	36	1.91E-04	0	15	0.40
Seq_0000268	2.22E-03	0	5	4.97E-04	0	2	0.40
Seq_0001748	9.56E-05	0	14	2.90E-05	0	2	0.39
Seq_0000363	1.49E-04	0	12	2.69E-03	0	10	0.39
Seq_0000085	8.04E-03	2.39E-03	35	3.86E-03	0	18	0.39
Seq_0000373	1.42E-03	0	11	1.91E-04	0	1	0.39
Seq_0000499	4.69E-05	0	5	3.81E-04	0	8	0.39
Seq_0000418	1.44E-03	0	13	4.44E-04	0	4	0.39
Seq_0001146	1.87E-04	0	11	3.30E-05	0	2	0.39
Seq_0001787	8.15E-05	0	7	1.03E-05	0	2	0.39
Seq_0000930	6.54E-05	0	3	2.23E-04	0	9	0.38
Seq_0000800	2.90E-04	0	16	6.66E-05	0	6	0.38
Seq_0000210	2.31E-03	0	21	5.69E-04	0	7	0.38
Seq_0000047	6.05E-03	3.18E-04	32	5.13E-03	6.55E-04	31	0.38
Seq_0000023	1.02E-02	4.93E-03	36	2.44E-02	9.24E-03	25	0.38
Seq_0000213	1.93E-03	6.88E-04	25	7.46E-04	0	11	0.38

Seq_0000847	6.01E-05	0	6	3.72E-04	0	11	0.38
Seq_0000063	9.90E-03	0	23	2.41E-03	0	5	0.38
Seq_0000008	4.93E-02	2.22E-02	46	4.16E-02	2.49E-02	37	0.38
Seq_0000684	4.66E-04	0	16	1.19E-04	0	4	0.37
Seq_0000827	3.85E-04	0	10	1.37E-04	0	4	0.37
Seq_0000543	6.14E-04	0	18	2.37E-04	0	10	0.36
Seq_0000334	1.43E-03	0	23	6.49E-04	0	12	0.36
Seq_0000486	1.00E-03	0	11	1.04E-04	0	4	0.36
Seq_0000505	5.32E-04	1.72E-04	26	2.93E-04	0	9	0.36
Seq_0000145	3.11E-03	0	21	1.33E-03	0	14	0.36
Seq_0001204	5.09E-05	0	15	1.69E-04	0	10	0.36
Seq_0000522	2.57E-04	1.30E-04	29	5.14E-04	0	19	0.35
Seq_0000169	2.11E-03	0	16	5.37E-03	0	13	0.35
Seq_0001057	2.24E-04	0	17	7.95E-05	0	5	0.35
Seq_0000355	9.19E-04	5.98E-04	30	5.45E-04	0	15	0.35
Seq_0000653	9.60E-05	0	7	6.22E-04	0	11	0.35

Seq_0000741	3.84E-04	0	21	1.60E-04	0	11	0.35
Seq_0000192	3.92E-03	0	15	9.64E-04	0	6	0.35
Seq_0001029	1.96E-04	0	17	9.53E-05	0	7	0.34
Seq_0000425	8.27E-04	5.99E-04	35	5.98E-04	0	18	0.34
Seq_0000094	1.26E-03	0	20	6.53E-03	0	14	0.34
Seq_0000439	1.36E-03	2.87E-04	24	5.29E-04	0	4	0.34
Seq_0000338	1.28E-03	6.91E-04	31	5.92E-04	0	13	0.34
Seq_0000254	2.65E-04	0	5	2.12E-03	0	10	0.34
Seq_0000215	1.88E-03	4.98E-04	32	9.50E-04	0	13	0.34
Seq_0000476	2.57E-04	0	11	3.04E-04	0	6	0.34
Seq_0000588	1.06E-04	0	7	5.62E-04	0	9	0.34
Seq_0000143	3.99E-03	1.47E-03	32	2.11E-03	0	15	0.34
Seq_0000042	1.34E-02	1.10E-02	44	9.68E-03	3.06E-03	24	0.34
Seq_0000842	8.49E-05	0	10	2.57E-05	0	2	0.34
Seq_0000983	2.56E-04	0	18	9.45E-05	0	6	0.34
Seq_0000466	5.98E-04	0	15	1.83E-04	0	4	0.34

Seq_0000324	1.19E-03	0	22	3.97E-04	0	5	0.33
Seq_0000427	1.27E-03	0	5	1.53E-04	0	2	0.33
Seq_0001256	1.60E-04	0	15	4.55E-05	0	2	0.33
Seq_0000196	5.23E-05	0	8	2.21E-04	0	10	0.32
Seq_0001169	1.67E-04	0	12	4.25E-05	0	5	0.32
Seq_0000039	8.88E-03	6.40E-03	43	1.59E-02	8.46E-03	31	0.32
Seq_0001614	1.03E-04	0	10	2.38E-05	0	5	0.32
Seq_0000509	1.08E-03	0	7	1.66E-04	0	3	0.31
Seq_0000231	4.63E-05	0	4	2.35E-04	0	6	0.31
Seq_0000144	4.80E-03	9.32E-04	27	2.96E-03	0	14	0.31
Seq_0000227	2.79E-03	0	8	1.38E-03	0	9	0.30
Seq_0000152	3.95E-03	1.06E-03	29	9.04E-04	0	9	0.30
Seq_0000874	5.13E-05	0	4	1.04E-03	0	9	0.30
Seq_0000273	1.07E-04	0	3	6.59E-04	0	3	0.29
Seq_0000824	2.45E-04	0	9	5.03E-05	0	2	0.29
Seq_0000308	4.03E-04	0	7	2.85E-03	0	4	0.29

Seq_0000489	7.20E-04	3.94E-04	39	4.44E-04	0	14	0.28
Seq_0000105	9.35E-03	1.14E-03	27	4.07E-03	0	13	0.28
Seq_0000022	6.43E-03	3.81E-03	37	4.24E-03	3.90E-04	27	0.28
Seq_0000226	4.20E-04	0	7	1.49E-03	0	11	0.28
Seq_0000045	1.06E-02	7.83E-03	43	7.00E-03	1.50E-03	25	0.28
Seq_0000078	5.09E-03	9.55E-04	31	3.01E-03	7.17E-05	21	0.27
Seq_0000197	1.25E-03	7.59E-04	34	9.65E-04	0	19	0.26
Seq_0001372	1.31E-04	0	12	6.87E-05	0	3	0.26
Seq_0000508	7.41E-04	0	19	3.26E-04	0	8	0.26
Seq_0000314	1.98E-04	0	9	1.99E-03	0	13	0.26
Seq_0000688	2.23E-04	0	21	1.53E-04	0	14	0.26
Seq_0000777	4.06E-04	0	7	1.49E-04	0	2	0.25
Seq_0000230	1.11E-03	0	20	1.44E-03	2.07E-04	20	0.25
Seq_0000448	4.19E-04	0	20	1.32E-03	0	18	0.24
Seq_0000044	1.81E-02	0	20	6.96E-03	0	13	0.24
Seq_0000272	1.82E-03	0	9	5.77E-04	0	6	0.24

Seq_0000050	9.97E-03	5.76E-04	32	9.35E-03	0	16	0.24
Seq_0000325	6.63E-04	0	15	1.24E-03	0	6	0.24
Seq_0001596	1.15E-04	0	7	7.10E-05	0	4	0.24
Seq_0001431	1.64E-04	0	6	1.90E-05	0	3	0.24
Seq_0000271	1.72E-03	2.04E-04	24	1.47E-03	0	11	0.24
Seq_0000077	2.97E-03	8.58E-04	33	6.23E-03	4.86E-04	26	0.24
Seq_0000343	8.01E-04	1.78E-04	25	4.01E-04	0	7	0.24
Seq_0000134	4.73E-03	3.00E-03	38	4.24E-03	8.11E-04	22	0.24
Seq_0001014	1.52E-04	8.85E-05	25	1.08E-04	0	10	0.24
Seq_0000093	4.45E-03	1.55E-03	36	3.20E-03	0	18	0.23
Seq_0001679	7.92E-05	0	11	3.35E-05	0	2	0.22
Seq_0000470	2.16E-04	0	17	5.31E-04	0	15	0.22
Seq_0000546	1.35E-04	0	3	6.58E-04	0	4	0.22
Seq_0000394	7.58E-04	0	21	4.01E-04	0	6	0.22
Seq_0000054	3.91E-03	0	17	8.71E-03	0	15	0.22
Seq_0000420	1.10E-03	0	10	3.80E-04	0	4	0.22

Seq_0000866	2.85E-04	0	12	1.65E-04	0	7	0.22
Seq_0000474	2.96E-04	0	6	2.49E-04	0	4	0.21
Seq_0000748	6.49E-04	0	6	2.63E-04	0	6	0.20
Seq_0000243	2.07E-03	0	7	8.45E-04	0	3	0.20
Seq_0000076	7.42E-03	1.45E-03	28	4.55E-03	0	17	0.20
Seq_0000736	3.45E-04	0	13	2.39E-04	0	6	0.20
Seq_0000618	3.20E-04	0	14	1.43E-04	0	4	0.20
Seq_0000287	1.52E-03	1.43E-03	37	1.11E-03	0	16	0.19
Seq_0000395	7.61E-04	0	11	1.04E-03	0	9	0.19
Seq_0000203	3.24E-03	2.43E-04	28	8.48E-04	0	18	0.19
Seq_0000270	1.03E-03	1.76E-04	28	2.77E-03	0	18	0.19
Seq_0000138	2.46E-03	1.28E-03	25	4.89E-03	0	17	0.19
Seq_0000305	1.56E-03	0	19	9.13E-04	0	5	0.19
Seq_0001301	1.10E-04	0	19	6.71E-05	0	8	0.19
Seq_0000675	1.46E-04	0	11	3.52E-04	0	15	0.19
Seq_0001646	2.94E-05	0	9	9.04E-05	0	9	0.19

Seq_0000129	3.98E-03	3.43E-03	42	3.87E-03	2.03E-03	26	0.19
Seq_0000103	5.56E-03	2.75E-03	36	4.69E-03	1.67E-03	24	0.19
Seq_0001635	1.82E-05	0	2	8.12E-05	0	5	0.18
Seq_0001295	5.74E-05	0	5	1.20E-04	0	6	0.18
Seq_0000128	1.98E-03	6.45E-04	25	3.30E-03	8.76E-04	24	0.18
Seq_0000560	5.72E-04	0	22	2.35E-04	0	12	0.18
Seq_0000737	1.22E-04	0	8	1.09E-04	0	4	0.17
Seq_0000104	5.59E-03	0	22	2.78E-03	0	9	0.16
Seq_0000941	1.06E-04	0	3	3.81E-04	0	9	0.16
Seq_0000095	5.96E-03	4.07E-03	42	4.71E-03	9.45E-04	27	0.16
Seq_0000060	6.82E-03	0	16	4.73E-03	2.13E-04	23	0.16
Seq_0000062	7.09E-03	4.17E-03	43	7.37E-03	5.02E-03	32	0.16
Seq_0000222	1.21E-03	0	12	3.52E-03	0	11	0.16
Seq_0000449	3.70E-04	0	7	1.24E-03	0	10	0.16
Seq_0000237	2.33E-03	0	22	1.67E-03	0	11	0.15
Seq_0001425	9.55E-05	0	9	3.66E-05	0	3	0.15

Seq_0000073	7.15E-03	6.07E-04	26	3.60E-03	0	14	0.15
Seq_0001283	1.35E-04	0	10	4.80E-05	0	5	0.15
Seq_0000166	5.76E-03	0	16	1.42E-03	0	6	0.15
Seq_0001151	2.02E-04	0	11	8.76E-05	0	3	0.15
Seq_0000359	1.53E-03	0	5	7.93E-04	0	4	0.15
Seq_0001332	8.36E-05	0	8	4.05E-05	0	3	0.15
Seq_0000940	1.51E-04	0	16	9.70E-05	0	5	0.15
Seq_0000360	1.18E-03	0	11	1.19E-03	0	5	0.15
Seq_0000326	1.45E-03	0	22	1.32E-03	0	14	0.15
Seq_0000106	4.64E-03	1.89E-03	31	5.52E-03	2.05E-04	20	0.15
Seq_0000311	7.56E-04	0	19	1.31E-03	0	9	0.15
Seq_0001483	4.66E-05	0	4	1.63E-04	0	6	0.15
Seq_0001034	1.64E-04	0	9	2.10E-04	0	3	0.15
Seq_0000609	4.72E-04	0	23	3.23E-04	0	11	0.15
Seq_0000692	2.16E-04	0	6	3.80E-04	0	12	0.15
Seq_0000091	6.91E-03	4.96E-03	32	4.89E-03	0	14	0.15

Seq_0001517	9.39E-05	0	9	5.10E-05	0	5	0.14
Seq_0000482	9.51E-04	2.51E-04	26	5.91E-04	0	10	0.14
Seq_0000823	1.60E-04	0	11	3.00E-04	0	9	0.14
Seq_0000347	5.93E-04	0	13	8.83E-04	0	8	0.14
Seq_0000225	1.10E-03	0	12	1.17E-03	0	14	0.14
Seq_0000732	2.25E-04	0	19	1.45E-04	0	10	0.14
Seq_0000436	8.12E-04	0	9	3.90E-04	0	5	0.14
Seq_0000412	7.44E-04	0	16	4.95E-04	0	8	0.14
Seq_0000193	2.63E-03	1.80E-04	25	1.63E-03	0	7	0.13
Seq_0000961	2.79E-04	0	10	1.54E-04	0	6	0.13
Seq_0000867	3.43E-04	0	16	2.16E-04	0	8	0.13
Seq_0000127	8.95E-04	0	15	2.09E-03	0	17	0.12
Seq_0000556	1.20E-04	0	8	9.60E-04	0	10	0.12
Seq_0001269	1.16E-04	0	11	7.59E-05	0	3	0.11
Seq_0000344	8.42E-04	0	16	2.10E-03	0	6	0.11
Seq_0000111	2.80E-03	6.63E-04	32	2.86E-03	0	14	0.11

Seq_0000417	3.29E-04	0	21	7.65E-04	0	9	0.11
Seq_0001130	8.09E-05	0	16	1.20E-04	0	7	0.11
Seq_0000021	2.86E-02	1.72E-02	38	2.76E-02	8.61E-03	31	0.11
Seq_0001059	1.10E-04	0	5	1.31E-04	0	4	0.11
Seq_0000156	2.02E-03	8.72E-04	26	3.93E-03	0	13	0.11
Seq_0000209	1.07E-03	3.17E-04	25	1.75E-03	0	11	0.10
Seq_0000554	4.53E-04	0	8	9.12E-04	0	4	0.10
Seq_0000282	1.07E-03	9.03E-04	30	8.67E-04	0	17	0.10
Seq_0000802	1.29E-04	0	5	6.54E-04	0	4	0.10
Seq_0000206	2.19E-03	0	11	9.74E-04	0	4	0.10
Seq_0000087	6.16E-04	0	4	2.98E-03	0	3	0.10
Seq_0000391	6.70E-04	0	22	5.16E-04	0	6	0.09
Seq_0000820	2.58E-04	0	6	1.51E-04	0	7	0.09
Seq_0000402	7.10E-04	0	23	6.81E-04	0	13	0.09
Seq_0000465	3.99E-04	2.54E-04	33	4.15E-04	0	16	0.09
Seq_0000716	1.41E-04	0	8	2.10E-04	0	6	0.08

Seq_0001663	6.43E-05	0	15	5.70E-05	0	7	0.08
Seq_0001558	4.37E-05	0	7	6.44E-05	0	7	0.07
Seq_0000479	4.30E-04	0	12	1.27E-03	0	6	0.07
Seq_0000232	1.12E-03	7.87E-04	27	1.93E-03	0	15	0.07
Seq_0001317	1.14E-04	0	7	4.55E-05	0	3	0.07
Seq_0000248	1.45E-03	8.80E-04	42	2.04E-03	8.17E-04	28	0.07
Seq_0000913	1.56E-04	0	4	3.12E-04	0	6	0.07
Seq_0000404	1.53E-03	0	4	2.48E-04	0	5	0.07
Seq_0000606	3.40E-04	0	7	7.00E-04	0	3	0.06
Seq_0000541	3.63E-04	0	9	6.58E-04	0	4	0.06
Seq_0000415	2.45E-04	0	10	1.24E-03	0	8	0.06
Seq_0000501	4.54E-04	0	10	5.01E-04	0	3	0.06
Seq_0001366	8.34E-05	0	9	9.91E-05	0	4	0.06
Seq_0000702	2.78E-04	0	12	1.17E-04	0	7	0.05
Seq_0000411	6.76E-04	3.17E-04	27	7.00E-04	6.72E-04	28	0.05
Seq_0001037	1.76E-04	0	9	1.53E-04	0	7	0.05

Seq_0000080	5.17E-03	2.04E-03	43	7.14E-03	1.72E-03	34	0.05
Seq_0000294	1.55E-04	0	11	1.19E-03	0	8	0.05
Seq_0000081	5.61E-03	0	18	7.51E-03	0	14	0.05
Seq_0000079	1.59E-03	0	10	2.11E-03	0	10	0.05
Seq_0000164	1.07E-03	0	7	7.89E-04	0	6	0.05
Seq_0000514	4.12E-04	0	10	9.89E-04	0	5	0.04
Seq_0000082	4.24E-03	1.64E-03	35	1.45E-02	1.51E-03	27	0.04
Seq_0000072	2.72E-03	9.67E-05	24	6.92E-03	0	19	0.04
Seq_0000259	1.06E-03	0	8	1.02E-03	0	4	0.04
Seq_0000190	3.57E-03	0	13	1.73E-03	0	7	0.04
Seq_0000773	1.42E-04	0	15	1.77E-04	0	9	0.03
Seq_0000300	1.23E-03	0	9	2.93E-03	0	13	0.03
Seq_0000701	1.94E-04	0	13	4.63E-04	0	5	0.03
Seq_0001058	7.24E-05	0	9	9.35E-05	0	7	0.03
Seq_0000400	4.46E-04	0	7	5.94E-04	0	9	0.02
Seq_0000674	1.56E-04	0	10	4.16E-04	0	5	0.02

Seq_0000445	7.14E-04	0	14	4.35E-04	0	4	0.02
Seq_0000124	3.04E-03	1.20E-03	25	3.61E-03	3.39E-04	20	0.02
Seq_0000398	4.08E-04	0	14	6.53E-04	0	14	0.02
Seq_0000616	3.40E-04	0	6	5.94E-04	0	6	0.02
Seq_0000386	5.36E-04	0	14	6.78E-04	0	17	0.02
Seq_0000006	5.14E-02	3.82E-02	44	5.88E-02	4.21E-02	30	0.01
Seq_0000007	3.64E-02	1.82E-02	42	4.43E-02	2.41E-02	34	0.01
Seq_0001200	1.18E-04	0	15	1.60E-04	0	9	0.01
Seq_0000107	4.16E-03	3.59E-04	25	4.10E-03	0	18	0.01
Seq_0000061	8.23E-03	5.15E-03	41	1.29E-02	5.58E-04	22	0.01
Seq_0000497	4.73E-04	1.74E-04	29	6.61E-04	0	18	0.01
Seq_0000821	1.88E-04	0	12	2.65E-04	0	12	0.00
RSV	Domain	Phylum	Class	Order	Family	Genus	
Seq_0000242	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified	
Seq_0000383	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	
Seq_0000528	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified	
Seq_0000890	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified	

Seq_0000756	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000643	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000284	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000988	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000299	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Catenibacterium
Seq_0000835	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000229	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000863	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000496	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000446	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000607	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000421	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000041	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_0000113	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000131	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000100	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor
Seq_0000199	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000160	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Pasteurellaceae_unclassified
Seq_0001143	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Howardella

Seq_0000644	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000797	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000758	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000119	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000734	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000037	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000937	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000132	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0001013	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000280	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000098	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000032	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000191	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000158	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000804	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000993	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000850	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0000825	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000153	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000375	Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobrevibacter
Seq_0000293	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000257	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000786	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000852	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000635	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0001125	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000976	Bacteria	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	Actinobacteria_unclassified
Seq_0000236	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000333	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001948	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000687	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000200	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Alloprevotella
Seq_0000212	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000468	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000065	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000290	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megamonas
Seq_0001133	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000202	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000223	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001313	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000698	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001253	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000171	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000184	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000380	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000015	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000749	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000571	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000429	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000551	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000924	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified

Seq_0001637	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000137	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Phascolarctobacterium
Seq_0000364	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000201	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000614	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000869	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001127	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000722	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001693	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0001150	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000633	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001177	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000052	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000768	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000378	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0001493	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001526	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified

Seq_0000130	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000519	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001707	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000179	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000312	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000694	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000387	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000443	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0000367	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000275	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000882	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Anaerococcus
Seq_0000738	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000918	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000450	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
Seq_0001218	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0001657	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000696	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcus
Seq_0000265	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000871	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0000327	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0001019	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0000269	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVI II
Seq_0000435	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001222	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Coprobacillus
Seq_0000534	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000833	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000876	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001262	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Peptoniphilus
Seq_0000188	Bacteria	Fusobacteriia	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium
Seq_0000329	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000349	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000281	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000187	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus
Seq_0000872	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000274	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000170	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia

Seq_0000424	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001395	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0001104	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000662	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000491	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000172	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000515	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcus
Seq_0000477	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000487	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcaceae_unclassified
Seq_0000440	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000628	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000810	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XIII	Mogibacterium
Seq_0000122	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000020	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000069	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0001370	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000649	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified

Seq_0000471	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000090	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Clostridium_XI
Seq_0000279	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001248	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Parvimonas
Seq_0001335	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000488	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000241	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000112	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000151	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000670	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000108	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000525	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000622	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio
Seq_0001280	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000370	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000547	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000185	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000573	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000664	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0001329	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000755	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000323	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000799	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000181	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000989	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0000454	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000066	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000784	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000832	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000163	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000599	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000067	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000962	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000014	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000731	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000268	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified

Seq_0001748	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0000363	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000085	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000373	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000499	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000418	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001146	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001787	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Enterorhabdus
Seq_0000930	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000800	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000210	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000047	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia/Shigella
Seq_0000023	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000213	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000847	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000063	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000008	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000684	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified

Seq_0000827	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000543	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000334	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000486	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000505	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000145	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001204	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000522	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000169	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0001057	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000355	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000653	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000741	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000192	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001029	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor
Seq_0000425	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000094	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000439	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000338	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000254	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000215	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000476	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Seq_0000588	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0000143	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000042	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000842	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000983	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000466	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000324	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000427	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001256	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000196	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0001169	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000039	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0001614	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0000509	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000231	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000144	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000227	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000152	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000874	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000273	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0000824	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000308	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000489	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Odoribacter
Seq_0000105	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000022	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000226	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000045	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000078	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000197	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001372	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000508	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Sporobacter

Seq_0000314	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000688	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Holdemania
Seq_0000777	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
Seq_0000230	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Clostridium_XI
Seq_0000448	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVII
Seq_0000044	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000272	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000050	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000325	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001596	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0001431	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000271	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000077	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000343	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000134	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0001014	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000093	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Seq_0001679	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000470	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Seq_0000546	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0000394	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000054	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000420	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000866	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000474	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0000748	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000243	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000076	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000736	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000618	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000287	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000395	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000203	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Seq_0000270	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Parasutterella
Seq_0000138	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0000305	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides

Seq_0001301	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000675	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0001646	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000129	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000103	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0001635	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001295	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000128	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000560	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000737	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000104	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000941	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000095	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000060	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000062	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000222	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000449	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000237	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0001425	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000073	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia

Seq_0001283	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricicoccus
Seq_0000166	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001151	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000359	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001332	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000940	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000360	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0000326	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000106	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000311	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001483	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0001034	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000609	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000692	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000091	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001517	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000482	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000823	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000347	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus

Seq_0000225	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000732	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000436	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000412	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000193	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000961	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000867	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000127	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000556	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001269	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000344	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
Seq_0000111	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000417	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001130	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000021	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0001059	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000156	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000209	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000554	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Seq_0000282	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000802	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000206	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000087	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000391	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000820	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000402	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000465	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0000716	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0001663	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001558	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Pseudoflavonifractor
Seq_0000479	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000232	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001317	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000248	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000913	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000404	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000606	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum

Seq_0000541	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000415	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000501	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001366	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000702	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000411	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001037	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000080	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcaceae_unclassified
Seq_0000294	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000081	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000079	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcus
Seq_0000164	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000514	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000082	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0000072	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000259	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0000190	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium

Seq_0000773	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000300	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000701	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001058	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000400	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000674	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000445	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000124	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000398	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000616	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000386	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000006	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000007	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001200	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000107	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000061	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000497	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0000821	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
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Table 5. Spearman correlations between VC counts and PC-axes 1 and 2 from Spearman distances

VC	pc1 p-value	pc1 rho	pc1 p-values adjusted	pc2 p-value	pc2 p-values adjusted	pc1 rho	pc2 rho	Quad- rant	Classificatio n
vc17	2.39E-10	-0.62	3.76E-07	5.15E-01	9.60E-01	-0.62	0.07	Q1	Siphoviridae
vc13	1.90E-08	-0.56	1.50E-05	8.34E-01	9.87E-01	-0.56	0.02	Q1	Siphoviridae
vc34	4.09E-08	-0.55	2.15E-05	3.40E-01	8.97E-01	-0.55	0.10	Q1	Unclassified
vc5	1.12E-07	-0.54	3.53E-05	3.00E-01	8.97E-01	-0.54	0.11	Q1	Myoviridae
vc15	1.91E-07	-0.53	5.01E-05	1.83E-02	8.97E-01	-0.53	0.26	Q1	Siphoviridae
vc9	4.97E-07	-0.51	1.12E-04	2.77E-01	8.97E-01	-0.51	0.12	Q1	Myoviridae
vc3	1.26E-06	-0.50	2.47E-04	6.67E-01	9.60E-01	-0.50	0.05	Q1	Siphoviridae
vc48	6.52E-05	-0.42	9.56E-03	2.22E-01	8.97E-01	-0.42	0.13	Q1	Siphoviridae
vc21	6.68E-05	-0.42	9.56E-03	1.24E-01	8.97E-01	-0.42	0.17	Q1	Siphoviridae
vc36	7.65E-05	-0.42	1.00E-02	1.59E-02	8.97E-01	-0.42	0.26	Q1	Heterogeneous
vc49	9.30E-05	-0.41	1.13E-02	8.58E-01	1	-0.41	0.02	Q1	Unclassified
vc18	1.80E-04	-0.40	1.82E-02	6.28E-01	9.60E-01	-0.40	0.05	Q1	Siphoviridae
vc27	1.85E-04	-0.39	1.82E-02	4.56E-01	9.47E-01	-0.39	0.08	Q1	Heterogeneous
vc14	2.70E-04	-0.39	2.50E-02	3.86E-01	8.97E-01	-0.39	0.10	Q1	Siphoviridae
vc11	3.05E-04	-0.38	2.67E-02	1.39E-01	8.97E-01	-0.38	0.16	Q1	Unclassified
vc94	3.99E-04	-0.38	3.31E-02	3.84E-01	8.97E-01	-0.38	0.10	Q1	Unclassified
vc114	5.82E-04	-0.37	4.54E-02	6.43E-01	9.60E-01	-0.37	0.05	Q1	Unclassified
vc73	6.06E-04	-0.36	4.54E-02	6.62E-02	8.97E-01	-0.36	0.20	Q1	Unclassified
vc1	9.74E-08	-0.54	3.53E-05	5.73E-01	9.60E-01	-0.54	-0.06	Q3	Unclassified
vc22	1.45E-05	-0.45	2.54E-03	8.35E-01	9.88E-01	-0.45	-0.02	Q3	Myoviridae
vc101	8.44E-02	0.19	3.02E-01	9.75E-08	1.41E-04	0.19	-0.54	Q4	Unclassified
ERR8439 46_NOD E_47_len	4.81E-02	0.22	3.02E-01	9.37E-05	3.69E-02	0.22	-0.41	Q4	Unclassified

gth_1356 _cov_2.5 6341									
vc10	1.59E-02	0.26	3.02E-01	4.12E-07	2.16E-04	0.26	-0.52	Q4	Unclassified
ERR8439 46_NOD E_45_len gth_1458 _cov_4.1 5182	6.76E-03	0.29	2.73E-01	1.79E-07	1.41E-04	0.29	-0.53	Q4	Unclassified
vc7	1.82E-04	0.40	1.82E-02	1.11E-01	8.97E-01	0.40	-0.17	Q4	Microviridae

Table 6. Spearman correlations between RSV counts and PC-axes 1 and 2 from unweighted UniFrac distances

RSV	pc1 p- values	pc1 p- value adjusted	pc2 p- values	pc2 p-value adjusted	pc1 rho	pc2 rho	Qua d	Genus	Species
Seq_000344 7	1.98E- 03	4.66E- 02	0.22	0.53	-0.37	0.15	Q1	Ruminococcac eae_unclassifi ed	Unclassified
Seq_000145 8	1.85E- 03	4.46E- 02	0.09	0.52	-0.37	0.21	Q1	Ruminococcus	Ruminococcus _champanellen sis
Seq_000051 9	1.54E- 03	3.80E- 02	0.78	0.90	-0.37	0.03	Q1	Clostridiales_ unclassified	Unclassified
Seq_000001 5	1.39E- 03	3.51E- 02	0.02	0.52	-0.38	0.27	Q1	Prevotella	Prevotella_cop ri
Seq_000150 0	1.28E- 03	3.30E- 02	0.29	0.62	-0.38	0.13	Q1	Clostridiales_ unclassified	Unclassified
Seq_000222 5	1.25E- 03	3.24E- 02	0.11	0.52	-0.38	0.19	Q1	Clostridiales_ unclassified	Unclassified

Seq_0001787	1.13E-03	3.00E-02	0.30	0.64	-0.38	0.13	Q1	Enterorhabdus	Unclassified
Seq_0001097	9.75E-04	2.65E-02	0.07	0.52	-0.39	0.22	Q1	Bacteria_unclassified	Unclassified
Seq_0001256	9.58E-04	2.62E-02	0.40	0.69	-0.39	0.10	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0002127	9.48E-04	2.62E-02	0.62	0.82	-0.39	0.06	Q1	Firmicutes_unclassified	Unclassified
Seq_0002881	9.37E-04	2.61E-02	0.50	0.77	-0.39	0.08	Q1	Clostridiales_unclassified	Unclassified
Seq_0003070	8.75E-04	2.49E-02	0.04	0.52	-0.39	0.25	Q1	Bacteria_unclassified	Unclassified
Seq_0002144	7.93E-04	2.30E-02	0.20	0.52	-0.39	0.16	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0001058	7.81E-04	2.29E-02	0.87	0.94	-0.40	0.02	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0002395	7.73E-04	2.28E-02	0.75	0.89	-0.40	0.04	Q1	Firmicutes_unclassified	Unclassified
Seq_0001413	6.95E-04	2.09E-02	0.44	0.72	-0.40	0.09	Q1	Bacteria_unclassified	Unclassified
Seq_0001133	6.69E-04	2.05E-02	0.99	1	-0.40	0.00	Q1	Clostridiales_unclassified	Unclassified
Seq_0000052	6.66E-04	2.05E-02	0.00	0.37	-0.40	0.35	Q1	Prevotella	Prevotella_copri
Seq_0002358	6.32E-04	1.98E-02	0.02	0.52	-0.40	0.29	Q1	Victivallis	Victivallis_vadensis
Seq_0000477	5.69E-04	1.84E-02	0.19	0.52	-0.40	0.16	Q1	Clostridiales_unclassified	Unclassified
Seq_0002806	5.53E-04	1.81E-02	0.70	0.87	-0.41	0.05	Q1	Firmicutes_unclassified	Unclassified

Seq_0001975	5.40E-04	1.79E-02	0.41	0.70	-0.41	0.10	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0001943	5.28E-04	1.77E-02	0.05	0.52	-0.41	0.24	Q1	Firmicutes_unclassified	Unclassified
Seq_0002644	4.72E-04	1.62E-02	0.54	0.80	-0.41	0.08	Q1	Clostridiales_unclassified	Unclassified
Seq_0003169	4.62E-04	1.60E-02	0.11	0.52	-0.41	0.20	Q1	Clostridiales_unclassified	Unclassified
Seq_0000768	4.39E-04	1.54E-02	0.82	0.92	-0.41	0.03	Q1	Lachnospiraceae_unclassified	Unclassified
Seq_0000799	4.24E-04	1.50E-02	0.34	0.66	-0.41	0.12	Q1	Alistipes	Alistipes_senegalensis
Seq_0000436	3.97E-04	1.46E-02	0.16	0.52	-0.41	0.17	Q1	Bacteria_unclassified	Unclassified
Seq_0001283	3.83E-04	1.46E-02	0.02	0.52	-0.42	0.28	Q1	Butyrivibrio	Eubacterium_desmolans
Seq_0001104	3.61E-04	1.39E-02	0.04	0.52	-0.42	0.25	Q1	Clostridiales_unclassified	Unclassified
Seq_0000440	3.25E-04	1.30E-02	0.47	0.75	-0.42	0.09	Q1	Clostridium_IV	Eubacterium_siraeum
Seq_0001614	3.20E-04	1.30E-02	0.08	0.52	-0.42	0.21	Q1	Clostridiales_unclassified	Unclassified
Seq_0001366	3.19E-04	1.30E-02	0.63	0.83	-0.42	0.06	Q1	Firmicutes_unclassified	Unclassified
Seq_0000741	3.18E-04	1.30E-02	0.16	0.52	-0.42	0.17	Q1	Clostridiales_unclassified	Unclassified
Seq_0000215	2.71E-04	1.16E-02	0.64	0.84	-0.43	0.06	Q1	Oscillibacter	Oscillospira_guilliermondii
Seq_0000380	2.23E-04	1.03E-02	0.01	0.52	-0.43	0.30	Q1	Clostridiales_unclassified	Unclassified

Seq_0002368	2.16E-04	1.03E-02	0.05	0.52	-0.43	0.24	Q1	Bacteria_unclassified	Unclassified
Seq_0001431	2.06E-04	1.00E-02	0.06	0.52	-0.43	0.23	Q1	Bacteria_unclassified	Unclassified
Seq_0000223	2.00E-04	9.88E-03	0.85	0.93	-0.43	0.02	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0001370	1.77E-04	9.03E-03	0.90	0.96	-0.44	0.02	Q1	Clostridiales_unclassified	Unclassified
Seq_0000824	1.49E-04	7.88E-03	0.30	0.63	-0.44	0.13	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0001195	1.38E-04	7.48E-03	0.09	0.52	-0.44	0.21	Q1	Firmicutes_unclassified	Unclassified
Seq_0000085	1.21E-04	7.03E-03	0.85	0.93	-0.45	0.02	Q1	Bacteroides	Bacteroides_caccae
Seq_0000199	1.14E-04	6.73E-03	0.96	0.99	-0.45	0.01	Q1	Firmicutes_unclassified	Unclassified
Seq_0002126	1.14E-04	6.73E-03	0.01	0.52	-0.45	0.30	Q1	Bacteria_unclassified	Unclassified
Seq_0000988	1.11E-04	6.73E-03	0.47	0.75	-0.45	0.09	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0002497	8.98E-05	5.88E-03	0.03	0.52	-0.45	0.26	Q1	Victivallis	Victivallis_vadensis
Seq_0001364	7.09E-05	5.21E-03	0.02	0.52	-0.46	0.28	Q1	Clostridiales_unclassified	Unclassified
Seq_0001146	6.68E-05	5.03E-03	0.14	0.52	-0.46	0.18	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000797	5.74E-05	4.55E-03	0.30	0.63	-0.46	0.13	Q1	Firmicutes_unclassified	Unclassified

Seq_0000850	4.69E-05	3.97E-03	0.46	0.73	-0.47	0.09	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000756	3.72E-05	3.40E-03	0.76	0.89	-0.48	0.04	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000609	2.57E-05	2.42E-03	0.63	0.83	-0.48	0.06	Q1	Clostridiales_unclassified	Unclassified
Seq_0001313	2.53E-05	2.42E-03	0.95	0.99	-0.48	0.01	Q1	Alistipes	Alistipes_indistinctus
Seq_0002671	2.03E-05	2.11E-03	0.67	0.85	-0.49	0.05	Q1	Firmicutes_unclassified	Unclassified
Seq_0000479	1.60E-05	1.72E-03	0.83	0.92	-0.49	0.03	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000063	1.53E-05	1.70E-03	0.31	0.64	-0.50	0.12	Q1	Clostridiales_unclassified	Unclassified
Seq_0000694	1.52E-05	1.70E-03	0.49	0.75	-0.50	0.09	Q1	Blautia	Unclassified
Seq_0001348	1.30E-05	1.57E-03	0.02	0.52	-0.50	0.27	Q1	Clostridiales_unclassified	Unclassified
Seq_0001872	1.10E-05	1.44E-03	0.55	0.80	-0.50	0.07	Q1	Firmicutes_unclassified	Unclassified
Seq_0001517	1.07E-05	1.44E-03	0.25	0.59	-0.50	0.14	Q1	Clostridiales_unclassified	Unclassified
Seq_0000375	8.78E-06	1.30E-03	0.57	0.80	-0.51	0.07	Q1	Methanobrevibacter	Methanobrevibacter_smithii
Seq_0000873	7.26E-06	1.21E-03	0.03	0.52	-0.51	0.26	Q1	Ruminococcaceae_unclassified	Flavonifractor_plautii
Seq_0000491	3.13E-06	5.55E-04	0.62	0.83	-0.53	0.06	Q1	Lachnospiraceae_unclassified	Unclassified

Seq_000191	1.74E-06	3.27E-04	0.01	0.52	-0.54	0.31	Q1	Clostridia_unclassified	Unclassified
Seq_000083	9.81E-07	1.97E-04	0.01	0.52	-0.55	0.32	Q1	Firmicutes_unclassified	Unclassified
Seq_0000113	9.05E-07	1.97E-04	0.81	0.91	-0.55	0.03	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000786	6.90E-07	1.79E-04	0.21	0.53	-0.56	0.15	Q1	Clostridiales_unclassified	Unclassified
Seq_0000937	5.51E-07	1.66E-04	0.06	0.52	-0.56	0.22	Q1	Bacteria_unclassified	Unclassified
Seq_0000274	4.67E-07	1.56E-04	0.57	0.80	-0.56	0.07	Q1	Clostridiales_unclassified	Unclassified
Seq_0000191	3.26E-07	1.23E-04	0.02	0.52	-0.57	0.28	Q1	Clostridiales_unclassified	Unclassified
Seq_0000628	2.04E-07	8.77E-05	0.27	0.60	-0.58	0.13	Q1	Bacteria_unclassified	Unclassified
Seq_0000275	1.75E-07	8.77E-05	0.24	0.57	-0.58	0.14	Q1	Firmicutes_unclassified	Unclassified
Seq_0000383	4.33E-09	4.35E-06	0.34	0.66	-0.64	0.12	Q1	Firmicutes_unclassified	Unclassified
Seq_0000193	2.45E-14	3.68E-11	0.54	0.80	-0.76	0.07	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000152	6.23E-15	1.88E-11	0.83	0.92	-0.77	0.03	Q1	Ruminococcaceae_unclassified	Unclassified
Seq_0000122	1.03E-04	6.48E-03	0.84	0.92	0.45	0.02	Q2	Clostridium_IVa	Unclassified
Seq_0000449	8.92E-04	2.51E-02	0.26	0.60	0.39	0.14	Q2	Lachnospiraceae_unclassified	Unclassified

Seq_0000443	1.75E-03	4.24E-02	0.60	0.82	0.37	0.06	Q2	Anaerostipes	Unclassified
Seq_0000236	1.75E-03	4.24E-02	0.91	0.97	0.37	0.01	Q2	Bacteria_unclassified	Clostridium_innocuum
Seq_0000367	2.02E-03	4.72E-02	0.74	0.88	-0.37	-0.04	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0001226	1.97E-03	4.66E-02	0.88	0.94	-0.37	-0.02	Q3	Clostridiales_unclassified	Unclassified
Seq_0000437	1.88E-03	4.50E-02	0.33	0.66	-0.37	-0.12	Q3	Clostridiales_unclassified	Unclassified
Seq_0000355	1.47E-03	3.65E-02	0.04	0.52	-0.38	-0.25	Q3	Clostridiales_unclassified	Eubacterium_venteriosum
Seq_0000890	1.46E-03	3.65E-02	0.63	0.83	-0.38	-0.06	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0001425	1.23E-03	3.23E-02	0.71	0.88	-0.38	-0.04	Q3	Bacteria_unclassified	Unclassified
Seq_0000731	1.12E-03	2.99E-02	0.01	0.52	-0.38	-0.33	Q3	Bacteria_unclassified	Unclassified
Seq_0000465	8.52E-04	2.44E-02	0.04	0.52	-0.39	-0.24	Q3	Collinsella	Collinsella_aerofaciens
Seq_0000078	7.16E-04	2.13E-02	0.15	0.52	-0.40	-0.18	Q3	Ruminococcus	Unclassified
Seq_0000237	6.75E-04	2.05E-02	0.10	0.52	-0.40	-0.20	Q3	Clostridium_IV	Eubacterium_siraeum
Seq_0000684	6.33E-04	1.98E-02	0.06	0.52	-0.40	-0.23	Q3	Bacteria_unclassified	Unclassified
Seq_0000571	5.88E-04	1.89E-02	0.20	0.52	-0.40	-0.15	Q3	Alistipes	Alistipes_indistinctus
Seq_0000983	5.22E-04	1.77E-02	0.56	0.80	-0.41	-0.07	Q3	Lachnospiraceae_unclassified	Unclassified

Seq_0000734	4.22E-04	1.50E-02	0.32	0.64	-0.41	-0.12	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0002312	4.12E-04	1.49E-02	0.88	0.94	-0.41	-0.02	Q3	Ruminococcaceae_unclassified	Unclassified
Seq_0000534	3.92E-04	1.46E-02	0.66	0.85	-0.41	-0.05	Q3	Ruminococcaceae_unclassified	Unclassified
Seq_0000852	3.92E-04	1.46E-02	0.24	0.57	-0.41	-0.14	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0000541	3.55E-04	1.39E-02	0.95	0.99	-0.42	-0.01	Q3	Ruminococcaceae_unclassified	Unclassified
Seq_0000210	3.31E-04	1.31E-02	0.36	0.66	-0.42	-0.11	Q3	Clostridiales_unclassified	Unclassified
Seq_0000287	3.20E-04	1.30E-02	0.42	0.71	-0.42	-0.10	Q3	Coprococcus	Coprococcus_catus
Seq_0001127	2.68E-04	1.16E-02	0.11	0.52	-0.43	-0.20	Q3	Clostridiales_unclassified	Unclassified
Seq_0000466	2.49E-04	1.10E-02	0.37	0.67	-0.43	-0.11	Q3	Ruminococcaceae_unclassified	Unclassified
Seq_0000573	2.41E-04	1.08E-02	0.74	0.89	-0.43	-0.04	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0000333	2.39E-04	1.08E-02	0.56	0.80	-0.43	-0.07	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0001637	2.23E-04	1.03E-02	0.77	0.89	-0.43	-0.04	Q3	Ruminococcaceae_unclassified	Unclassified

Seq_0000021	1.82E-04	9.13E-03	0.30	0.63	-0.44	-0.13	Q3	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000334	1.61E-04	8.36E-03	0.55	0.80	-0.44	-0.07	Q3	Firmicutes_unclassified	Unclassified
Seq_0000425	1.39E-04	7.48E-03	0.02	0.52	-0.44	-0.28	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0000020	1.29E-04	7.17E-03	0.01	0.52	-0.44	-0.30	Q3	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0000701	1.28E-04	7.17E-03	0.93	0.97	-0.44	-0.01	Q3	Firmicutes_unclassified	Unclassified
Seq_0001657	9.52E-05	6.10E-03	0.51	0.78	-0.45	-0.08	Q3	Firmicutes_unclassified	Unclassified
Seq_0000784	8.96E-05	5.88E-03	0.06	0.52	-0.45	-0.23	Q3	Clostridiales_unclassified	Unclassified
Seq_0000284	8.43E-05	5.77E-03	0.92	0.97	-0.46	-0.01	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0001372	8.40E-05	5.77E-03	0.90	0.96	-0.46	-0.02	Q3	Ruminococcaceae_unclassified	Unclassified
Seq_0001663	8.39E-05	5.77E-03	0.40	0.69	-0.46	-0.10	Q3	Bacteria_unclassified	Unclassified
Seq_0000961	6.67E-05	5.03E-03	0.63	0.83	-0.46	-0.06	Q3	Ruminococcaceae_unclassified	Unclassified
Seq_0000338	4.88E-05	3.97E-03	0.07	0.52	-0.47	-0.22	Q3	Alistipes	Unclassified
Seq_0000976	4.77E-05	3.97E-03	0.00	0.49	-0.47	-0.34	Q3	Actinobacteria_unclassified	Unclassified
Seq_0000242	4.17E-05	3.69E-03	0.59	0.81	-0.47	-0.07	Q3	Clostridiales_unclassified	Unclassified

Seq_0000103	2.57E-05	2.42E-03	0.11	0.52	-0.48	-0.19	Q3	Alistipes	Alistipes_putredinis
Seq_0001253	1.18E-05	1.48E-03	0.75	0.89	-0.50	-0.04	Q3	Alistipes	Alistipes_indistinctus
Seq_0000265	9.10E-06	1.30E-03	0.00	0.38	-0.51	-0.35	Q3	Lachnospiraceae_unclassified	Unclassified
Seq_0001029	8.45E-06	1.30E-03	0.65	0.84	-0.51	-0.06	Q3	Flavonifractor	Flavonifractor_plautii
Seq_0000664	9.35E-07	1.97E-04	0.40	0.68	-0.55	-0.10	Q3	Blautia	Unclassified
Seq_0000091	1.39E-07	8.38E-05	0.92	0.97	-0.58	-0.01	Q3	Clostridiales_unclassified	Unclassified
Seq_0000364	4.64E-08	3.49E-05	0.94	0.99	-0.60	-0.01	Q3	Alistipes	Unclassified
Seq_0000057	7.13E-07	1.79E-04	0.92	0.97	0.56	-0.01	Q4	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0000008	1.04E-03	2.79E-02	0.42	0.71	0.39	-0.10	Q4	Blautia	Unclassified
Seq_0000100	1.33E-03	3.40E-02	0.81	0.91	0.38	-0.03	Q4	Flavonifractor	Flavonifractor_plautii

Table 7. Spearman correlations between VC counts and PC-axes 1 and 2 from Spearman distances

VC	pc1 p-value	pc1 rho	pc1 p-value adjusted	pc2 p-value	pc2 rho	pc2 p-value adjusted	Classification
vc100	0.02	-0.37	0.64	0.14	0.24	0.97	Unclassified
vc102	0.57	-0.09	0.80	0.06	0.30	0.97	Unclassified
vc103	0.03	0.34	0.64	0.10	0.27	0.97	Unclassified
vc104	0.46	-0.12	0.74	0.42	0.13	0.97	Siphoviridae
vc106	0.31	-0.16	0.66	0.32	0.16	0.97	Unclassified

vc107	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc109	0.60	-0.09	0.82	0.64	0.08	0.97	Siphoviridae
vc11	0.13	-0.24	0.64	0.89	-0.02	0.97	Heterogeneous
vc112	0.45	0.12	0.72	0.12	-0.25	0.97	Genomoviridae
vc113	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
vc114	0.77	-0.05	0.94	0.64	0.08	0.97	Unclassified
vc115	0.16	-0.23	0.64	0.59	0.09	0.97	Unclassified
vc116	0.14	-0.24	0.64	0.21	-0.20	0.97	Myoviridae
vc117	0.29	0.17	0.66	0.71	0.06	0.97	Siphoviridae
vc119	0.53	-0.10	0.80	0.26	0.18	0.97	Unclassified
vc12	0.05	0.31	0.64	0.04	0.32	0.97	Unclassified
vc120	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc121	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc122	0.08	-0.28	0.64	0.63	-0.08	0.97	Unclassified
vc123	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc124	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
vc126	0.86	0.03	0.94	0.65	-0.07	0.97	Unclassified
vc127	0.83	-0.03	0.94	0.97	-0.01	0.97	Siphoviridae
vc128	0.80	-0.04	0.94	0.14	-0.24	0.97	Unclassified
vc129	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc13	0.89	0.02	0.94	0.09	0.28	0.97	Unclassified
vc130	0.02	-0.36	0.64	0.61	-0.08	0.97	Unclassified
vc131	0.84	-0.03	0.94	0.96	-0.01	0.97	Siphoviridae
vc132	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
vc133	0.42	-0.13	0.68	0.21	-0.20	0.97	Papillomaviridae
vc134	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc135	0.77	-0.05	0.94	0.95	-0.01	0.97	Unclassified
vc136	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc137	0.34	-0.15	0.66	0.85	-0.03	0.97	Myoviridae
vc138	0.08	-0.28	0.64	0.63	-0.08	0.97	Unclassified
vc14	0.79	0.04	0.94	0.84	0.03	0.97	Siphoviridae
vc140	0.56	0.09	0.80	0.07	0.29	0.97	Unclassified

vc141	0.37	0.15	0.66	0.10	0.27	0.97	Unclassified
vc144	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc145	0.05	-0.31	0.64	0.02	0.38	0.97	Microviridae
vc146	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc148	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc149	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc15	0.59	0.09	0.82	0.66	0.07	0.97	Unclassified
vc150	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc151	0.66	-0.07	0.89	0.08	-0.28	0.97	Unclassified
vc153	0.84	-0.03	0.94	0.96	-0.01	0.97	Unclassified
vc154	0.46	0.12	0.73	0.85	0.03	0.97	Heterogeneous
vc155	0.37	0.15	0.66	0.70	0.06	0.97	Myoviridae
vc157	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc158	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
vc159	0.12	-0.25	0.64	0.83	0.04	0.97	Unclassified
vc16	0.56	-0.10	0.80	0.89	-0.02	0.97	Unclassified
vc160	0.39	-0.14	0.68	0.74	0.05	0.97	Unclassified
vc161	0.19	0.21	0.64	0.36	-0.15	0.97	Podoviridae
vc162	0.45	-0.12	0.72	0.15	-0.23	0.97	Unclassified
vc163	0.19	0.21	0.64	0.69	0.06	0.97	Unclassified
vc164	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc167	0.90	0.02	0.94	0.90	-0.02	0.97	Heterogeneous
vc168	0.49	-0.11	0.76	0.80	0.04	0.97	Siphoviridae
vc169	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified
vc17	0.22	0.20	0.64	0.25	0.18	0.97	Microviridae
vc170	0.48	0.11	0.76	0.09	-0.27	0.97	Unclassified
vc171	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
vc173	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
vc174	0.47	0.12	0.74	0.86	0.03	0.97	Unclassified
vc175	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc176	0.83	-0.03	0.94	0.97	-0.01	0.97	Podoviridae
vc177	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc179	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

vc18	0.32	0.16	0.66	0.23	0.20	0.97	Unclassified
vc180	0.15	-0.23	0.64	0.31	-0.17	0.97	Unclassified
vc181	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc182	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc183	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc184	0.82	-0.04	0.94	0.96	0.01	0.97	Unclassified
vc185	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc186	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc187	0.49	-0.11	0.76	0.80	0.04	0.97	Unclassified
vc189	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc19	0.45	0.12	0.72	0.01	0.42	0.97	Siphoviridae
vc190	0.05	-0.31	0.64	0.26	-0.18	0.97	Unclassified
vc191	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc192	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc193	0.61	-0.08	0.84	0.05	0.32	0.97	Unclassified
vc194	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc195	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
vc196	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
vc197	0.81	0.04	0.94	0.44	0.13	0.97	Unclassified
vc199	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc2	0.20	-0.21	0.64	0.03	0.34	0.97	Unclassified
vc20	0.67	-0.07	0.91	0.42	0.13	0.97	Unclassified
vc200	0.79	-0.04	0.94	0.49	0.11	0.97	Siphoviridae
vc201	0.37	-0.14	0.66	0.41	0.13	0.97	Unclassified
vc202	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc205	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified
vc206	0.44	0.13	0.71	0.17	0.22	0.97	Unclassified
vc207	0.49	-0.11	0.76	0.80	0.04	0.97	Unclassified
vc209	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
vc21	0.01	-0.40	0.64	0.15	0.23	0.97	Unclassified
vc210	0.47	0.12	0.74	0.86	0.03	0.97	Unclassified
vc211	0.55	0.10	0.80	0.14	0.24	0.97	Unclassified
vc213	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified

vc215	0.83	0.04	0.94	0.34	0.16	0.97	Unclassified
vc219	0.28	0.17	0.64	0.52	-0.10	0.97	Siphoviridae
vc22	0.42	0.13	0.68	0.44	0.13	0.97	Unclassified
vc220	0.07	-0.29	0.64	0.74	-0.05	0.97	Unclassified
vc221	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc222	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc223	0.83	-0.03	0.94	0.97	-0.01	0.97	Siphoviridae
vc224	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc225	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc226	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc228	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc229	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc23	0.51	0.11	0.79	0.52	0.10	0.97	Heterogeneous
vc230	0.37	-0.15	0.66	0.84	0.03	0.97	Siphoviridae
vc231	0.08	-0.28	0.64	0.63	-0.08	0.97	Unclassified
vc232	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc233	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc234	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc235	0.44	-0.13	0.71	0.67	-0.07	0.97	Unclassified
vc236	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc237	0.37	-0.15	0.66	0.42	0.13	0.97	Siphoviridae
vc238	0.12	-0.25	0.64	0.83	0.04	0.97	Unclassified
vc239	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc24	0.56	-0.10	0.80	0.27	0.18	0.97	Unclassified
vc240	0.12	-0.25	0.64	0.79	0.04	0.97	Unclassified
vc242	0.82	-0.04	0.94	0.96	0.01	0.97	Unclassified
vc243	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc244	0.82	-0.04	0.94	0.96	0.01	0.97	Unclassified
vc245	0.49	-0.11	0.76	0.80	0.04	0.97	Unclassified
vc246	0.70	-0.06	0.93	0.07	0.29	0.97	Unclassified
vc247	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc25	0.75	-0.05	0.94	0.42	-0.13	0.97	Microviridae
vc250	0.29	0.17	0.66	0.71	0.06	0.97	Unclassified

vc251	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc252	0.21	-0.20	0.64	0.67	-0.07	0.97	Unclassified
vc254	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
vc255	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc256	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc260	0.71	-0.06	0.94	0.51	0.11	0.97	Unclassified
vc261	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc262	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc268	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc269	0.59	-0.09	0.82	0.06	-0.30	0.97	Unclassified
vc27	0.82	-0.04	0.94	0.09	-0.27	0.97	Heterogeneous
vc272	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc274	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc275	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified
vc277	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
vc279	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc28	0.49	0.11	0.77	0.01	0.41	0.97	Myoviridae
vc280	0.18	-0.22	0.64	0.16	-0.23	0.97	Inoviridae
vc283	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
vc284	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
vc285	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc286	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc287	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc288	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc289	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc29	0.00	0.60	0.07	0.36	-0.15	0.97	Unclassified
vc290	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc292	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc293	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc296	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc297	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc298	0.52	0.11	0.79	0.24	-0.19	0.97	Unclassified
vc299	0.64	0.08	0.87	0.11	-0.26	0.97	Unclassified

vc3	0.79	0.04	0.94	0.08	-0.28	0.97	Siphoviridae
vc301	0.87	0.03	0.94	0.83	0.03	0.97	Unclassified
vc306	0.82	-0.04	0.94	0.96	0.01	0.97	Unclassified
vc31	0.55	0.10	0.80	0.03	0.34	0.97	Microviridae
vc310	0.07	-0.29	0.64	0.61	-0.08	0.97	Unclassified
vc312	0.83	0.03	0.94	0.73	-0.06	0.97	Unclassified
vc313	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
vc314	0.17	-0.22	0.64	0.33	-0.16	0.97	Unclassified
vc315	0.55	-0.10	0.80	0.51	-0.11	0.97	Unclassified
vc32	0.53	-0.10	0.80	0.74	-0.05	0.97	Siphoviridae
vc320	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
vc323	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
vc324	0.62	0.08	0.85	0.40	0.14	0.97	Unclassified
vc325	0.72	0.06	0.94	0.66	-0.07	0.97	Unclassified
vc328	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
vc329	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
vc33	0.40	0.14	0.68	0.56	0.10	0.97	Siphoviridae
vc330	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
vc332	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
vc334	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc335	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc338	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc34	0.12	-0.25	0.64	0.59	0.09	0.97	Siphoviridae
vc340	0.22	-0.20	0.64	0.73	-0.06	0.97	Unclassified
vc341	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc342	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
vc343	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc344	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc345	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
vc347	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc349	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc35	0.79	0.04	0.94	0.25	0.19	0.97	Siphoviridae
vc350	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

vc351	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc352	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc353	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc354	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc355	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc356	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc357	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc358	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc359	0.31	-0.17	0.66	0.72	-0.06	0.97	Unclassified
vc36	0.01	0.40	0.64	0.25	-0.18	0.97	Heterogeneous
vc360	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc361	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc362	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc363	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc364	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc365	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc366	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc37	0.04	0.33	0.64	0.02	0.37	0.97	Unclassified
vc373	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc374	0.05	-0.31	0.64	0.64	0.08	0.97	Unclassified
vc375	0.28	-0.18	0.64	0.93	0.01	0.97	Unclassified
vc378	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc379	0.47	0.12	0.74	0.86	0.03	0.97	Unclassified
vc38	0.70	0.06	0.93	0.47	-0.12	0.97	Unclassified
vc380	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc381	0.49	-0.11	0.76	0.80	0.04	0.97	Unclassified
vc383	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc384	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
vc387	0.82	-0.04	0.94	0.96	0.01	0.97	Unclassified
vc388	0.37	-0.14	0.66	0.41	0.13	0.97	Unclassified
vc389	0.61	-0.08	0.85	0.32	-0.16	0.97	Unclassified
vc39	0.18	-0.22	0.64	0.48	0.11	0.97	Unclassified
vc390	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

vc391	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc392	0.45	-0.12	0.72	0.81	-0.04	0.97	Unclassified
vc393	0.49	-0.11	0.76	0.80	0.04	0.97	Unclassified
vc394	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc395	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc399	0.64	0.08	0.87	0.11	-0.26	0.97	Unclassified
vc40	0.81	-0.04	0.94	0.00	-0.72	0.00	Unclassified
vc400	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc401	0.42	-0.13	0.68	0.21	-0.20	0.97	Siphoviridae
vc403	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
vc405	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc406	0.53	0.10	0.80	0.43	0.13	0.97	Unclassified
vc41	0.53	-0.10	0.80	0.88	0.03	0.97	Siphoviridae
vc410	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
vc411	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc412	0.49	-0.11	0.76	0.80	0.04	0.97	Unclassified
vc415	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc416	0.03	0.34	0.64	0.26	-0.18	0.97	Unclassified
vc417	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
vc418	0.83	-0.03	0.94	0.97	-0.01	0.97	Heterogeneous
vc419	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc42	0.72	0.06	0.94	0.53	0.10	0.97	Siphoviridae
vc420	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc421	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc422	0.82	0.04	0.94	0.95	0.01	0.97	Unclassified
vc423	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc424	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc425	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc426	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
vc427	0.21	-0.20	0.64	0.72	0.06	0.97	Siphoviridae
vc428	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc429	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc43	0.56	-0.09	0.80	0.41	0.13	0.97	Siphoviridae

vc430	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc431	0.83	-0.03	0.94	0.42	0.13	0.97	Myoviridae
vc432	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
vc433	0.79	-0.04	0.94	0.49	0.11	0.97	Unclassified
vc437	0.72	-0.06	0.94	0.50	0.11	0.97	Unclassified
vc44	0.02	-0.36	0.64	0.21	0.20	0.97	Unclassified
vc442	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
vc443	0.70	-0.06	0.93	0.07	0.29	0.97	Unclassified
vc444	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
vc445	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc446	0.28	0.17	0.64	0.52	-0.10	0.97	Unclassified
vc447	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
vc45	0.86	-0.03	0.94	0.62	0.08	0.97	Podoviridae
vc454	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc455	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
vc458	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
vc46	0.31	-0.17	0.66	0.72	-0.06	0.97	Unclassified
vc461	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc462	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
vc464	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc465	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
vc47	0.18	-0.22	0.64	0.32	-0.16	0.97	Siphoviridae
vc473	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc474	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc475	0.03	-0.34	0.64	0.04	0.33	0.97	Unclassified
vc477	0.03	-0.35	0.64	0.18	0.22	0.97	Unclassified
vc478	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
vc479	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
vc48	0.69	-0.07	0.93	0.79	-0.04	0.97	Unclassified
vc484	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
vc49	0.62	0.08	0.86	0.04	-0.32	0.97	Unclassified
vc5	0.37	-0.14	0.66	0.60	0.09	0.97	Myoviridae
vc50	0.49	0.11	0.76	0.39	0.14	0.97	Siphoviridae

vc51	0.57	-0.09	0.80	0.50	0.11	0.97	Siphoviridae
vc53	0.51	0.11	0.79	0.52	0.10	0.97	Siphoviridae
vc54	0.25	0.18	0.64	0.08	-0.28	0.97	Unclassified
vc57	0.04	-0.33	0.64	0.53	0.10	0.97	Unclassified
vc58	0.38	0.14	0.67	0.45	-0.12	0.97	Anelloviridae
vc59	0.81	-0.04	0.94	0.52	-0.10	0.97	Siphoviridae
vc6	0.09	-0.28	0.64	0.69	0.06	0.97	Myoviridae
vc60	0.34	-0.16	0.66	0.28	0.17	0.97	Unclassified
vc61	0.18	0.22	0.64	0.53	0.10	0.97	Unclassified
vc62	0.07	-0.29	0.64	0.70	0.06	0.97	Unclassified
vc63	0.27	-0.18	0.64	0.35	0.15	0.97	Unclassified
vc64	0.06	-0.30	0.64	0.59	0.09	0.97	Unclassified
vc67	0.38	-0.14	0.68	0.49	0.11	0.97	Siphoviridae
vc68	0.20	-0.21	0.64	0.96	-0.01	0.97	Unclassified
vc69	0.08	-0.28	0.64	0.44	0.13	0.97	Unclassified
vc7	0.36	-0.15	0.66	0.29	0.17	0.97	Unclassified
vc70	0.73	-0.06	0.94	0.37	0.14	0.97	Unclassified
vc71	0.07	-0.29	0.64	0.57	0.09	0.97	Unclassified
vc72	0.85	0.03	0.94	0.43	0.13	0.97	Siphoviridae
vc75	0.37	-0.15	0.66	0.01	0.39	0.97	Unclassified
vc76	0.10	0.26	0.64	0.37	0.14	0.97	Unclassified
vc77	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
vc78	0.26	-0.18	0.64	0.67	0.07	0.97	Unclassified
vc79	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc8	0.69	-0.06	0.93	0.52	0.10	0.97	Heterogeneous
vc80	0.38	-0.14	0.68	0.68	0.07	0.97	Unclassified
vc81	0.90	0.02	0.94	0.54	0.10	0.97	Siphoviridae
vc82	0.16	-0.23	0.64	0.29	-0.17	0.97	Unclassified
vc84	0.08	-0.28	0.64	0.63	-0.08	0.97	Unclassified
vc86	0.89	-0.02	0.94	0.07	-0.29	0.97	Siphoviridae
vc87	0.62	-0.08	0.85	0.10	0.26	0.97	Unclassified
vc88	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
vc89	0.01	-0.39	0.64	0.11	0.26	0.97	Unclassified

vc90	0.05	-0.31	0.64	0.56	0.09	0.97	Unclassified
vc91	0.82	0.04	0.94	0.66	0.07	0.97	Myoviridae
vc92	0.85	-0.03	0.94	0.64	0.08	0.97	Siphoviridae
vc93	0.42	-0.13	0.68	0.25	-0.19	0.97	Anelloviridae
vc94	0.21	-0.20	0.64	0.64	-0.08	0.97	Siphoviridae
vc95	0.21	-0.20	0.64	0.64	-0.08	0.97	Myoviridae
vc96	0.86	-0.03	0.94	0.20	0.21	0.97	Unclassified
vc97	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
vc98	0.07	-0.29	0.64	0.20	0.21	0.97	Unclassified
vc99	0.79	-0.04	0.94	0.64	0.08	0.97	Unclassified
NG_14253_10_lib223967_5684_N ODE_106_length_1773_cov_2.135 62	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_133_length_1428_cov_2.388 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_15_length_14642_cov_4.648 52	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_150_length_1218_cov_2.061 05	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_153_length_1190_cov_2.545 37	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_160_length_1088_cov_1.683 45	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_174_length_1023_cov_1.689 05	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_20_length_8323_cov_3.7702	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae

NG_14253_10_lib223967_5684_N ODE_69_length_2674_cov_2.3432 6	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_75_length_2498_cov_4.2865 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_82_length_2272_cov_6.7456	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_10_lib223967_5684_N ODE_97_length_1933_cov_2.1389 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_119_length_1340_cov_1 7.4093	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_128_length_1257_cov_6 9.515	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_154_length_1043_cov_1 6.1164	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_55_length_3229_cov_2. 26402	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_57_length_3110_cov_2. 7892	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_62_length_2842_cov_2. 21493	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_11xxx_lib223957_568 4_NODE_78_length_2080_cov_2. 17185	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_14_lib223986_5684_N ODE_103_length_1089_cov_2.680 85	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_14_lib223986_5684_N ODE_106_length_1079_cov_2.408 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_14_lib223986_5684_N ODE_47_length_2593_cov_2.4751 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_14_lib223986_5684_N ODE_60_length_1834_cov_2.7425 5	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_14_lib223986_5684_N ODE_88_length_1259_cov_2.3895 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_15_lib223937_5684_N ODE_42_length_1144_cov_1.7089 1	0.90	-0.02	0.94	0.42	-0.13	0.97	Unclassified
NG_14253_15_lib223937_5684_N ODE_45_length_1035_cov_1.8010 2	0.90	-0.02	0.94	0.42	-0.13	0.97	Unclassified
NG_14253_16_lib223966_5684_N ODE_103_length_4483_cov_2.230 13	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_106_length_4423_cov_4.200 09	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_108_length_4283_cov_2.667 93	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_111_length_4117_cov_3.315 85	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_16_lib223966_5684_N ODE_121_length_3902_cov_2.461 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_124_length_3769_cov_3.929 99	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_13_length_60022_cov_10.95 79	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_130_length_3582_cov_2.288 91	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_132_length_3512_cov_2.025 17	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_134_length_3415_cov_2.247 32	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_141_length_3283_cov_2.297 09	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_143_length_3269_cov_2.752 33	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_14253_16_lib223966_5684_N ODE_144_length_3261_cov_2.627 89	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_145_length_3220_cov_2.200 32	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_150_length_3108_cov_6.905 01	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_16_lib223966_5684_N ODE_151_length_3079_cov_2.406 08	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_152_length_3034_cov_2.242 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_153_length_3021_cov_2.623 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_162_length_2860_cov_2.702 32	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_19_length_41370_cov_9.159 09	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_231_length_2161_cov_2.792 5	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_26_length_23987_cov_7.286 65	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_27_length_22812_cov_5.572 22	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_30_length_19379_cov_4.328 56	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_332_length_1638_cov_2.610 23	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_382_length_1481_cov_41.28 05	0.02	-0.36	0.64	0.14	0.24	0.97	Unclassified

NG_14253_16_lib223966_5684_N ODE_46_length_11230_cov_3.904 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_48_length_11003_cov_2.837 69	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_54_length_8947_cov_3.4787 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_57_length_8266_cov_3.5099 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_58_length_7553_cov_3.2099 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_59_length_7442_cov_3.6248 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_62_length_7137_cov_4.9295 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_63_length_7014_cov_3.2302 1	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_14253_16_lib223966_5684_N ODE_75_length_6132_cov_3.7755 5	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_77_length_6110_cov_3.7993 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_85_length_5533_cov_3.9043 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_16_lib223966_5684_N ODE_97_length_4826_cov_2.8775 9	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_16_lib223966_5684_N ODE_99_length_4684_cov_2.5279 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_101_length_3426_cov_2.306 44	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_103_length_3284_cov_2.674 82	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_104_length_3246_cov_3.760 58	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_105_length_3246_cov_2.479 79	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_109_length_3076_cov_2.812 64	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_111_length_3045_cov_1.781 27	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_112_length_3018_cov_2.827 54	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_187_length_1923_cov_2.152 03	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_228_length_1633_cov_1.643 85	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_19_lib223950_5684_N ODE_23_length_15366_cov_5.078 57	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_26_length_15118_cov_4.838 48	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_280_length_1324_cov_1.363 28	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_357_length_1102_cov_1.481 38	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_39_length_8027_cov_2.7765 9	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_43_length_7576_cov_3.0545 1	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_51_length_6466_cov_2.8621 1	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_63_length_5380_cov_3.8103 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_66_length_5297_cov_244.09	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_75_length_4552_cov_4.0338	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_78_length_4462_cov_3.2164 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_19_lib223950_5684_N ODE_79_length_4364_cov_2.8626 1	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_81_length_4334_cov_97.323 2	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_83_length_4250_cov_137.45 2	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_19_lib223950_5684_N ODE_84_length_4234_cov_1.8916	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_85_length_4152_cov_3.1552 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_88_length_3888_cov_1.9900 9	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_94_length_3627_cov_2.2631 6	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_95_length_3550_cov_2.8944 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_19_lib223950_5684_N ODE_96_length_3546_cov_2.2291 6	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_20_lib223970_5684_N ODE_42_length_5833_cov_5.3158 5	0.24	-0.19	0.64	0.20	-0.21	0.97	Unclassified
NG_14253_20_lib223970_5684_N ODE_58_length_4111_cov_2.4107 5	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified

NG_14253_20_lib223970_5684_N ODE_70_length_3269_cov_30.552	0.77	0.05	0.94	0.58	-0.09	0.97	Unclassified
NG_14253_21_lib223968_5684_N ODE_113_length_2410_cov_2.578 77	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_123_length_2226_cov_2.269 92	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_185_length_1458_cov_2.621 53	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_33_length_6650_cov_110.89 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_45_length_6336_cov_3.4566 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_56_length_5509_cov_5.2744 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_64_length_4813_cov_2.5458 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_75_length_3823_cov_3.0968 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_79_length_3693_cov_4.6484 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_83_length_3416_cov_2.1068 1	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_21_lib223968_5684_N ODE_94_length_3064_cov_2.0658	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_21_lib223968_5684_N ODE_95_length_3058_cov_1.9883 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_23_lib223975_5684_N ODE_108_length_1393_cov_1.607 62	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_111_length_1350_cov_1.293 44	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_112_length_1345_cov_2.125 58	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_124_length_1247_cov_2.666 11	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_132_length_1176_cov_1.596 79	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_136_length_1156_cov_1.445 05	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_140_length_1130_cov_2.072 56	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_142_length_1117_cov_1.590 4	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_143_length_1115_cov_1.925 47	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified

NG_14253_23_lib223975_5684_N ODE_151_length_1066_cov_1.614 24	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_159_length_1020_cov_1.900 52	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_161_length_1007_cov_2.184 87	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_27_length_5508_cov_2.9952 3	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_33_length_4917_cov_5.7527 8	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_50_length_3216_cov_1.8937	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_52_length_3098_cov_1.7190 3	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_56_length_3032_cov_2.9694 3	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_59_length_2973_cov_2.8831 4	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_61_length_2866_cov_2.4823 9	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_67_length_2369_cov_2.1197 1	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified

NG_14253_23_lib223975_5684_N ODE_78_length_2007_cov_2.3278 7	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_23_lib223975_5684_N ODE_96_length_1561_cov_2.0152 7	0.47	0.12	0.74	0.21	0.20	0.97	Unclassified
NG_14253_26_lib223959_5684_N ODE_102_length_5995_cov_3.431 65	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_12_length_31620_cov_6.405 26	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_124_length_4932_cov_2.958 58	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_125_length_4841_cov_3.876 93	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_126_length_4811_cov_2.452 27	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_127_length_4754_cov_2.866 57	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14253_26_lib223959_5684_N ODE_128_length_4641_cov_5.698 65	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_130_length_4637_cov_3.845 48	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_133_length_4337_cov_2.806 63	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_26_lib223959_5684_N ODE_135_length_4299_cov_259.4 16	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_136_length_4270_cov_2.569 16	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_141_length_4066_cov_2.845 43	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14253_26_lib223959_5684_N ODE_146_length_4029_cov_2.438 85	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14253_26_lib223959_5684_N ODE_148_length_3925_cov_2.426 36	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_150_length_3847_cov_2.764 24	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14253_26_lib223959_5684_N ODE_151_length_3840_cov_2.320 48	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_152_length_3828_cov_3.169 89	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_153_length_3822_cov_2.586 67	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_154_length_3791_cov_3.085 12	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_162_length_3366_cov_14.00 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_26_lib223959_5684_N ODE_163_length_3366_cov_2.551 19	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_169_length_3267_cov_44.54 95	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified
NG_14253_26_lib223959_5684_N ODE_171_length_3235_cov_2.951 26	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_176_length_3174_cov_1.942 61	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_178_length_3144_cov_2.054 06	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_179_length_3138_cov_2.511 51	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_181_length_3118_cov_2.149 85	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_185_length_3044_cov_15.49 85	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_252_length_2319_cov_6.255 3	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_26_lib223959_5684_N ODE_254_length_2312_cov_2.739 92	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_300_length_1971_cov_2.263 57	0.00	-0.44	0.64	0.28	0.17	0.97	Unclassified

NG_14253_26_lib223959_5684_N ODE_332_length_1763_cov_2.597 78	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_40_length_14086_cov_3.406 1	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_62_length_10411_cov_4.019 41	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_65_length_10103_cov_4.934 32	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_69_length_9023_cov_7.3466 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_75_length_7949_cov_4.9784 6	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_77_length_7821_cov_6.4589 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_78_length_7802_cov_3.7240 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_79_length_7635_cov_2.5014 5	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_26_lib223959_5684_N ODE_90_length_6769_cov_4.2296 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_27_lib223932_5684_N ODE_20_length_6484_cov_3.0472 9	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified

NG_14253_27_lib223932_5684_N ODE_36_length_4505_cov_82.769 9	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified
NG_14253_27_lib223932_5684_N ODE_60_length_2102_cov_3.2481 7	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified
NG_14253_27_lib223932_5684_N ODE_7_length_11704_cov_4.3500 6	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified
NG_14253_27_lib223932_5684_N ODE_75_length_1608_cov_2.4501	0.13	0.24	0.64	0.47	-0.12	0.97	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_105_length_3715_cov_5 .72158	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_106_length_3587_cov_1 1.5153	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_107_length_3566_cov_4 .19361	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_110_length_3405_cov_2 .49224	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_120_length_3149_cov_2 .61829	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_122_length_3111_cov_6 .79516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_123_length_3079_cov_9 .61045	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_28xxx_lib223971_568 4_NODE_125_length_3037_cov_3 .29041	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_17_length_17366_cov_6 .02455	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_18_length_17304_cov_4 .56838	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_28_length_12229_cov_4 .23903	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_30_length_11563_cov_6 .14694	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_32_length_11222_cov_8 .36348	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_33_length_11169_cov_1 2.5539	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_35_length_10396_cov_3 .86887	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_38_length_9663_cov_2. 89051	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_40_length_8960_cov_4. 89377	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_46_length_8121_cov_4. 07042	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_28xxx_lib223971_568 4_NODE_48_length_7888_cov_3. 07711	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_51_length_7617_cov_3. 78815	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_54_length_7245_cov_3. 77441	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_55_length_6978_cov_16 .5997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_56_length_6901_cov_5. 3941	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_67_length_5781_cov_3. 14705	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_68_length_5758_cov_22 .1154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_69_length_5743_cov_2. 93126	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_71_length_5710_cov_11 .9019	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_72_length_5684_cov_7. 65305	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_74_length_5504_cov_3. 41053	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_28xxx_lib223971_568 4_NODE_79_length_5391_cov_8. 00375	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_81_length_5291_cov_3. 03266	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_28xxx_lib223971_568 4_NODE_82_length_5247_cov_4. 27119	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_89_length_4872_cov_8. 73801	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_93_length_4667_cov_3. 12251	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_94_length_4604_cov_2. 83469	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_95_length_4421_cov_26 4.015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_96_length_4339_cov_3. 10481	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_98_length_4272_cov_21 5.509	0.33	-0.16	0.66	0.13	-0.24	0.97	Unclassified
NG_14253_28xxx_lib223971_568 4_NODE_99_length_4237_cov_3. 31636	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_29xxx_lib223979_568 4_NODE_11_length_6180_cov_3. 77649	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified

NG_14253_29xxx_lib223979_568 4_NODE_14_length_5812_cov_74 .9104	0.18	-0.22	0.64	0.16	-0.23	0.97	Microviridae
NG_14253_29xxx_lib223979_568 4_NODE_17_length_5328_cov_4. 5953	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified
NG_14253_29xxx_lib223979_568 4_NODE_21_length_4141_cov_2. 65345	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified
NG_14253_29xxx_lib223979_568 4_NODE_37_length_3278_cov_10 .0729	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified
NG_14253_29xxx_lib223979_568 4_NODE_40_length_3061_cov_6. 94544	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified
NG_14253_29xxx_lib223979_568 4_NODE_7_length_17306_cov_7. 02411	0.18	-0.22	0.64	0.16	-0.23	0.97	Unclassified
NG_14253_3_lib223926_5684_N ODE_18_length_7765_cov_20.135 7	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_14253_3_lib223926_5684_N ODE_22_length_7039_cov_2.9269 8	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_3_lib223926_5684_N ODE_28_length_6463_cov_377.61 1	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_14253_3_lib223926_5684_N ODE_50_length_3888_cov_2.6769 5	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_103_length_2446_cov_6 .77959	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_30xxx_lib223945_568 4_NODE_124_length_1781_cov_8 .3372	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_140_length_1417_cov_8 .39574	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_148_length_1275_cov_4 .20164	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_163_length_1118_cov_4 6.73	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_169_length_1052_cov_1 .65998	0.48	-0.11	0.76	0.77	-0.05	0.97	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_18_length_4865_cov_3. 74387	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_26_length_3866_cov_40 0.222	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_32_length_3365_cov_99 .9873	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_43_length_3051_cov_7. 18725	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_30xxx_lib223945_568 4_NODE_84_length_2647_cov_16 .2064	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_32_lib223948_5684_N ODE_30_length_3288_cov_2.7896 7	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_33_lib223940_5684_N ODE_164_length_1317_cov_2.698 1	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_181_length_1261_cov_2.199 83	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_184_length_1250_cov_2.002 51	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_216_length_1122_cov_2.157 45	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_221_length_1108_cov_1.979 11	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_239_length_1042_cov_2.097 26	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_242_length_1033_cov_2.674 85	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_245_length_1027_cov_1.408 44	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_34_length_6036_cov_8.1106 8	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_43_length_4882_cov_3.1760 9	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_33_lib223940_5684_N ODE_50_length_4258_cov_2.9103	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified

NG_14253_33_lib223940_5684_N ODE_68_length_2758_cov_4.0573 4	0.58	-0.09	0.80	0.52	0.10	0.97	Unclassified
NG_14253_34xxx_lib223976_568 4_NODE_30_length_3042_cov_2. 67057	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_34xxx_lib223976_568 4_NODE_94_length_1080_cov_1. 98732	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_100_length_5854_cov_7 .53526	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_102_length_5840_cov_7 6.5839	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_105_length_5691_cov_5 .3852	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_110_length_5497_cov_5 .41419	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_111_length_5483_cov_5 .18294	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_114_length_5403_cov_3 .36219	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_118_length_5242_cov_9 1.0023	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_120_length_5193_cov_2 .75107	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae

NG_14253_35xxx_lib223952_568 4_NODE_122_length_5039_cov_8 .30762	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_126_length_4991_cov_2 .15154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_127_length_4967_cov_1 1.0731	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_128_length_4949_cov_2 5.5787	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_137_length_4715_cov_5 .49657	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_140_length_4614_cov_5 .89647	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_143_length_4491_cov_4 .18417	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_146_length_4469_cov_3 .85387	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_157_length_4287_cov_3 .77457	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_165_length_4158_cov_2 .83817	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_168_length_4075_cov_2 .59279	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_35xxx_lib223952_568 4_NODE_173_length_3985_cov_2 .10891	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_176_length_3960_cov_4 .21076	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_178_length_3957_cov_3 .02178	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_179_length_3948_cov_2 .28179	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_181_length_3915_cov_4 .18083	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_185_length_3835_cov_2 .17804	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_186_length_3834_cov_3 .22784	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_187_length_3813_cov_1 .79431	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_188_length_3773_cov_2 .59548	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_193_length_3697_cov_4 .45826	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_197_length_3571_cov_1 .75256	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_35xxx_lib223952_568 4_NODE_204_length_3518_cov_2 .32515	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_206_length_3487_cov_2 .03293	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_210_length_3414_cov_2 .65377	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_213_length_3369_cov_2 .59505	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_217_length_3336_cov_3 .70527	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_218_length_3327_cov_5 0.6314	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_22_length_14292_cov_6 .99761	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_220_length_3287_cov_2 .5133	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_221_length_3283_cov_2 .67348	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_227_length_3207_cov_3 .4099	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_228_length_3172_cov_2 .5239	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_35xxx_lib223952_568 4_NODE_232_length_3149_cov_4 .28054	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_233_length_3145_cov_2 .90194	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_236_length_3094_cov_1 .65449	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_242_length_3078_cov_2 .79061	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_28_length_12198_cov_1 5.4893	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_359_length_2244_cov_3 .44724	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_422_length_2025_cov_6 .40964	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_45_length_9747_cov_3. 45821	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_47_length_9732_cov_6. 48186	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_49_length_9452_cov_5. 78642	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_51_length_9056_cov_3. 12976	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_35xxx_lib223952_568 4_NODE_66_length_7584_cov_2. 79041	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_75_length_7070_cov_11 .5695	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_79_length_6632_cov_5. 71157	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_81_length_6529_cov_5. 17006	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_87_length_6289_cov_4. 60523	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_93_length_6171_cov_2. 82178	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_94_length_6164_cov_3. 85186	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_95_length_6096_cov_3. 92634	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_35xxx_lib223952_568 4_NODE_96_length_6030_cov_4. 76653	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_36_lib223946_5684_N ODE_23_length_6015_cov_3.2555 4	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified
NG_14253_36_lib223946_5684_N ODE_30_length_4375_cov_5.0363 4	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified

NG_14253_36_lib223946_5684_N ODE_35_length_4010_cov_2.9512	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified
NG_14253_36_lib223946_5684_N ODE_37_length_3725_cov_5.4583 1	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_107_length_4826_cov_3 .05345	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_113_length_4144_cov_3 .15432	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_116_length_3995_cov_4 .78046	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_117_length_3958_cov_2 .773	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_118_length_3810_cov_3 .40879	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_121_length_3755_cov_2 .53027	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_37xxx_lib223930_568 4_NODE_122_length_3752_cov_2 .43982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_126_length_3555_cov_2 .95429	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_127_length_3553_cov_3 .3582	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_37xxx_lib223930_568 4_NODE_131_length_3504_cov_2 .19165	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_135_length_3451_cov_2 .0742	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_137_length_3412_cov_2 .88889	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_139_length_3358_cov_2 .6267	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_141_length_3354_cov_2 .26705	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_148_length_3174_cov_2 .64636	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_37xxx_lib223930_568 4_NODE_149_length_3169_cov_2 .76397	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_150_length_3151_cov_2 .48902	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_155_length_3051_cov_2 .48598	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_163_length_3012_cov_2 .46804	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_164_length_3000_cov_5 7.1025	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_37xxx_lib223930_568 4_NODE_182_length_2899_cov_2 0.2901	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_216_length_2635_cov_1 .78643	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_37xxx_lib223930_568 4_NODE_24_length_18983_cov_4 .66589	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_265_length_2239_cov_2 .02656	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_279_length_2109_cov_1 .63583	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_28_length_16924_cov_7 5.4837	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_291_length_1908_cov_2 .82083	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14253_37xxx_lib223930_568 4_NODE_317_length_1669_cov_2 .32342	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_37xxx_lib223930_568 4_NODE_337_length_1539_cov_1 .72978	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_37xxx_lib223930_568 4_NODE_386_length_1308_cov_2 .37191	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_401_length_1256_cov_1 .91424	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_37xxx_lib223930_568 4_NODE_425_length_1168_cov_3 .04492	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_37xxx_lib223930_568 4_NODE_439_length_1146_cov_1 .47388	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_44_length_11396_cov_4 04.508	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_452_length_1092_cov_1 .72324	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_51_length_9665_cov_5. 21322	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_64_length_7492_cov_2. 82789	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_65_length_7195_cov_3. 41835	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_75_length_6495_cov_3. 00031	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_96_length_5391_cov_2. 73894	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_37xxx_lib223930_568 4_NODE_99_length_5275_cov_5. 5523	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14253_39_lib223923_5684_N ODE_23_length_4795_cov_8.1706 8	0.21	0.20	0.64	0.28	-0.17	0.97	Unclassified

NG_14253_39_lib223923_5684_N ODE_28_length_3595_cov_6.2635 6	0.21	0.20	0.64	0.28	-0.17	0.97	Unclassified
NG_14253_39_lib223923_5684_N ODE_29_length_3375_cov_3.0286 1	0.21	0.20	0.64	0.28	-0.17	0.97	Unclassified
NG_14253_39_lib223923_5684_N ODE_30_length_3169_cov_5.5796 4	0.21	0.20	0.64	0.28	-0.17	0.97	Unclassified
NG_14253_40_lib223961_5684_N ODE_23_length_4199_cov_2.7934 4	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_40_lib223961_5684_N ODE_27_length_3837_cov_10.488 4	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14253_40_lib223961_5684_N ODE_32_length_3192_cov_2.1016 9	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_42_lib223934_5684_N ODE_18_length_8552_cov_5.1179 2	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
NG_14253_42_lib223934_5684_N ODE_19_length_7250_cov_3.6236 3	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
NG_14253_42_lib223934_5684_N ODE_37_length_3108_cov_2.4510 3	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
NG_14253_42_lib223934_5684_N ODE_39_length_3060_cov_2.9198	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified
NG_14253_42_lib223934_5684_N ODE_44_length_2602_cov_2.8307 8	0.77	-0.05	0.94	0.70	-0.06	0.97	Unclassified

NG_14253_45_lib223921_5684_N ODE_18_length_3466_cov_27.505 1	0.33	-0.16	0.66	0.13	-0.24	0.97	Unclassified
NG_14253_45_lib223921_5684_N ODE_19_length_3330_cov_7.0882 4	0.33	-0.16	0.66	0.13	-0.24	0.97	Unclassified
NG_14253_45_lib223921_5684_N ODE_23_length_2614_cov_2.2778 4	0.33	-0.16	0.66	0.13	-0.24	0.97	Unclassified
NG_14253_47_lib223969_5684_N ODE_17_length_6810_cov_2.3871 2	0.97	0.01	0.97	0.37	0.15	0.97	Unclassified
NG_14253_47_lib223969_5684_N ODE_23_length_6096_cov_3.3557 4	0.97	0.01	0.97	0.37	0.15	0.97	Unclassified
NG_14253_47_lib223969_5684_N ODE_36_length_3850_cov_113.13 1	0.72	-0.06	0.94	0.27	0.18	0.97	Unclassified
NG_14253_47_lib223969_5684_N ODE_38_length_3100_cov_1.8633 8	0.97	0.01	0.97	0.37	0.15	0.97	Unclassified
NG_14253_48_lib223938_5684_N ODE_125_length_1614_cov_7.159 08	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_48_lib223938_5684_N ODE_131_length_1571_cov_2.060 03	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_48_lib223938_5684_N ODE_140_length_1492_cov_2.537 93	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_48_lib223938_5684_N ODE_166_length_1334_cov_2.757 62	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified

NG_14253_48_lib223938_5684_N ODE_190_length_1223_cov_1.983 73	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_48_lib223938_5684_N ODE_20_length_7403_cov_3.8958 9	0.97	0.01	0.97	0.37	0.15	0.97	Unclassified
NG_14253_48_lib223938_5684_N ODE_34_length_5728_cov_3.0176 3	0.97	0.01	0.97	0.37	0.15	0.97	Unclassified
NG_14253_48_lib223938_5684_N ODE_54_length_3844_cov_2.8601 2	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_48_lib223938_5684_N ODE_72_length_2688_cov_2.7500 9	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_12_length_15255_cov_5 .04724	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_14_length_12462_cov_8 .50093	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_15_length_10052_cov_1 7.212	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_23_length_8437_cov_8. 01467	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_238_length_1323_cov_1 .8194	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_26_length_7301_cov_3. 75918	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_49xxx_lib223928_568 4_NODE_260_length_1219_cov_1 .93385	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_28_length_6958_cov_3. 0607	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_281_length_1169_cov_4 .43357	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_289_length_1147_cov_1 .70971	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_41_length_5852_cov_3. 29101	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_45_length_5510_cov_97 .345	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_50_length_4785_cov_3. 19302	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_52_length_4652_cov_4. 17359	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_56_length_4406_cov_16 .4125	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_62_length_4070_cov_2. 7589	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_65_length_3981_cov_2. 77789	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_49xxx_lib223928_568 4_NODE_69_length_3929_cov_23 .9404	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_75_length_3430_cov_3. 02252	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_76_length_3412_cov_2. 76318	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_77_length_3400_cov_16 .8185	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_78_length_3372_cov_3. 17727	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_8_length_22447_cov_5. 37152	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_49xxx_lib223928_568 4_NODE_86_length_3241_cov_3. 04143	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_50xxx_lib223925_568 4_NODE_104_length_2290_cov_3 .1396	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
NG_14253_50xxx_lib223925_568 4_NODE_122_length_1841_cov_2 .35834	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
NG_14253_50xxx_lib223925_568 4_NODE_169_length_1319_cov_1 8.9525	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
NG_14253_50xxx_lib223925_568 4_NODE_187_length_1222_cov_2 .61183	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified

NG_14253_50xxx_lib223925_5684_NODE_72_length_3518_cov_6.66214	0.91	0.02	0.95	0.48	0.12	0.97	Unclassified
NG_14253_50xxx_lib223925_5684_NODE_79_length_3022_cov_157.914	0.23	0.20	0.64	0.05	0.31	0.97	Unclassified
NG_14253_50xxx_lib223925_5684_NODE_83_length_2879_cov_2.98336	0.70	0.06	0.93	0.28	0.17	0.97	Unclassified
NG_14253_51_lib223983_5684_NODE_30_length_4811_cov_75.0753	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_51_lib223983_5684_NODE_36_length_3859_cov_2.2642	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_51_lib223983_5684_NODE_48_length_2733_cov_1.62024	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_52_lib223941_5684_NODE_111_length_1333_cov_3.1471	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_52_lib223941_5684_NODE_46_length_3149_cov_2.13348	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_52_lib223941_5684_NODE_54_length_2771_cov_2.74853	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_52_lib223941_5684_NODE_75_length_2092_cov_3.13255	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_54_lib223955_5684_NODE_28_length_4990_cov_3.49929	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified

NG_14253_54_lib223955_5684_N ODE_32_length_4552_cov_3.0591 5	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_33_length_4494_cov_10.632 3	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_41_length_3786_cov_2.6732 8	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_42_length_3715_cov_2.5202 2	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_43_length_3684_cov_2.9537 1	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_46_length_3218_cov_2.135	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_48_length_3118_cov_2.4985 3	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_54_lib223955_5684_N ODE_55_length_2525_cov_2.3558 7	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_14_length_11844_cov_1 0.8574	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_15_length_11292_cov_5 .19151	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_20_length_8815_cov_4. 13938	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_56xxx_lib223972_568 4_NODE_21_length_8342_cov_4. 34512	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_25_length_7669_cov_4. 54571	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_31_length_6121_cov_4. 11012	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_40_length_5171_cov_11 27.18	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_41_length_4474_cov_11 94.45	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_50_length_3056_cov_2. 58547	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_7_length_21192_cov_23 .2746	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_56xxx_lib223972_568 4_NODE_96_length_1559_cov_5. 7254	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_7xxx_lib223922_5684 _NODE_141_length_1231_cov_1. 93793	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14253_7xxx_lib223922_5684 _NODE_167_length_1045_cov_1. 45051	0.04	-0.33	0.64	0.70	0.06	0.97	Unclassified
NG_14253_7xxx_lib223922_5684 _NODE_42_length_4117_cov_3.5 1551	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14253_7xxx_lib223922_5684_NODE_48_length_3809_cov_4.48855	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_7xxx_lib223922_5684_NODE_49_length_3436_cov_17.7965	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_7xxx_lib223922_5684_NODE_50_length_3372_cov_2.59512	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14253_7xxx_lib223922_5684_NODE_53_length_3162_cov_677.887	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
NG_14253_7xxx_lib223922_5684_NODE_94_length_1807_cov_2.37785	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
NG_14253_8_lib223960_5684_NODE_65_length_1169_cov_1.92819	0.01	-0.40	0.64	0.09	0.27	0.97	Unclassified
NG_14253_8_lib223960_5684_NODE_86_length_1006_cov_1.63617	0.02	-0.37	0.64	0.03	0.34	0.97	Unclassified
NG_14253_9_lib223974_5684_NODE_116_length_1822_cov_74.0453	0.70	-0.06	0.93	0.18	-0.22	0.97	Circoviridae
NG_14253_9_lib223974_5684_NODE_65_length_3796_cov_26.8583	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
NG_14253_9_lib223974_5684_NODE_71_length_3600_cov_3.50945	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
NG_14253_9_lib223974_5684_NODE_84_length_3045_cov_2.4087	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified

NG_14253_9_lib223974_5684_N ODE_89_length_2656_cov_6.4951 9	0.89	-0.02	0.94	0.07	-0.29	0.97	Unclassified
NG_14571_100xxx_NODE_103_1 ength_5593_cov_3.132	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_104_1 ength_5570_cov_4.38422	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_105_1 ength_5559_cov_31.9993	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_106_1 ength_5505_cov_8.30018	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_100xxx_NODE_109_1 ength_5417_cov_5.36815	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_110_1 ength_5371_cov_4.78386	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_113_1 ength_5173_cov_3.22157	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_115_1 ength_5047_cov_2.73077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_116_1 ength_5036_cov_3.17687	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_118_1 ength_4939_cov_6.32535	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_119_1 ength_4923_cov_14.8846	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_100xxx_NODE_123_1 ength_4839_cov_3.83821	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_124_1 ength_4834_cov_8.72379	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_125_1 ength_4810_cov_2.72787	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_100xxx_NODE_129_1 ength_4755_cov_3.58766	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_100xxx_NODE_130_1 ength_4691_cov_2.27157	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_132_1 ength_4629_cov_2.92151	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_133_1 ength_4622_cov_2.60258	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_136_1 ength_4510_cov_8.01639	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_137_1 ength_4492_cov_2.80911	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_138_1 ength_4471_cov_12.4287	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_14_le ngth_18388_cov_19.1191	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_141_1 ength_4408_cov_3.91661	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_144_1 ength_4321_cov_4.02907	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_15_le ngth_18374_cov_54.2111	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_153_1 ength_4148_cov_2.7872	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_156_1 ength_3986_cov_2.62834	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_157_1 ength_3946_cov_4.97661	0.26	-0.18	0.64	0.54	-0.10	0.97	Unclassified
NG_14571_100xxx_NODE_158_1 ength_3918_cov_12.4165	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_159_1 ength_3902_cov_4.47388	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_160_1 ength_3887_cov_3.28862	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_100xxx_NODE_162_1 ength_3848_cov_2.58265	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_163_1 ength_3837_cov_2.49921	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_165_1 ength_3818_cov_2.86022	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_17_le ngth_16315_cov_11.9609	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_170_1 ength_3661_cov_3.73405	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_100xxx_NODE_173_1 ength_3599_cov_4.27991	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_175_1 ength_3552_cov_3.18359	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_183_1 ength_3354_cov_2.99606	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_184_1 ength_3327_cov_3.83771	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_187_1 ength_3307_cov_3.21771	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_19_le ngth_14465_cov_8.01325	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_193_1 ength_3227_cov_8.36538	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_196_1 ength_3177_cov_1.96957	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_198_1 ength_3162_cov_3.77148	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_202_1 ength_3090_cov_4.28501	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_25_le ngth_12590_cov_6.09158	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_100xxx_NODE_291_1 ength_2329_cov_3.17018	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_299_1 ength_2251_cov_4.01184	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_3_len gth_28977_cov_18.5951	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_36_le ngth_10664_cov_4.99039	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_4_len gth_26817_cov_41.5298	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_45_le ngth_9545_cov_5.50674	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_49_le ngth_9119_cov_6.06388	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_50_le ngth_9046_cov_6.55189	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_51_le ngth_8905_cov_4.51469	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_56_le ngth_8486_cov_5.6055	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_6_len gth_24189_cov_5.0496	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_60_le ngth_8037_cov_5.34415	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_64_le ngth_7672_cov_9.66483	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_65_le ngth_7657_cov_3.86951	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_68_le ngth_7530_cov_4.22127	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_100xxx_NODE_7_len gth_22416_cov_5.67515	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_100xxx_NODE_72_length_7362_cov_11.0289	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_100xxx_NODE_76_length_6945_cov_2.582	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_100xxx_NODE_78_length_6870_cov_22.3351	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_100xxx_NODE_84_length_6452_cov_7.98859	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_100xxx_NODE_9_length_20656_cov_23.7757	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_100xxx_NODE_92_length_6148_cov_35.1036	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_100xxx_NODE_96_length_6031_cov_5.15395	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_110_length_9412_cov_2.64235	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_118_length_8879_cov_4.30338	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_12_length_23189_cov_5.09761	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_121_length_8841_cov_5.06636	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_132_length_8241_cov_3.20779	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_142_length_7644_cov_4.6491	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_148_length_7342_cov_5.42761	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_151_length_7197_cov_3.50756	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_101xxx_NODE_152_length_7171_cov_6.36425	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_101xxx_NODE_153_1 ength_7102_cov_9.97247	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_185_1 ength_5972_cov_4.289	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_190_1 ength_5872_cov_3.33161	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_210_1 ength_5441_cov_2.82733	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_226_1 ength_4989_cov_2.84131	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_275_1 ength_4158_cov_12.7736	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_292_1 ength_3885_cov_3.3141	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_305_1 ength_3708_cov_3.24364	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_312_1 ength_3611_cov_2.62823	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_314_1 ength_3599_cov_304.299	0.52	-0.10	0.79	0.37	-0.15	0.97	Unclassified
NG_14571_101xxx_NODE_322_1 ength_3517_cov_2.53813	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_323_1 ength_3495_cov_2.98517	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_324_1 ength_3477_cov_11.0123	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_326_1 ength_3456_cov_2.66833	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_344_1 ength_3339_cov_3.09227	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_352_1 ength_3235_cov_2.4022	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_101xxx_NODE_361_1 ength_3133_cov_3.46914	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_363_1 ength_3074_cov_2.78668	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_373_1 ength_2990_cov_4.22487	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_41_le ngth_15437_cov_7.17254	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_43_le ngth_14924_cov_6.24265	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_44_le ngth_14585_cov_3.98713	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_49_le ngth_13929_cov_10.6224	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_71_le ngth_12302_cov_7.1059	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_82_le ngth_11182_cov_11.0823	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_84_le ngth_11117_cov_4.30962	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_101xxx_NODE_89_le ngth_10791_cov_5.5516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_14571_101xxx_NODE_98_le ngth_10033_cov_8.15865	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_102xxx_NODE_10_le ngth_29520_cov_37.4209	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_1005_ length_1970_cov_7.1624	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_102_1 ength_11982_cov_4.20667	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_1098_ length_1745_cov_2.60237	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_1133_ length_1676_cov_5.11474	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_117_1 ength_11338_cov_22.7856	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_121_1 ength_11152_cov_4.44625	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_1219_ length_1532_cov_2.29452	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_1249_ length_1484_cov_1.77327	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_134_1 ength_10682_cov_8.51397	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_140_1 ength_10495_cov_4.58784	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_141_1 ength_10478_cov_6.98849	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_156_1 ength_9975_cov_4.6249	0.21	-0.20	0.64	0.64	-0.08	0.97	Podoviridae
NG_14571_102xxx_NODE_16_le ngth_24568_cov_128.171	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_1606_ length_1126_cov_1.66947	0.21	-0.20	0.64	0.64	-0.08	0.97	Siphoviridae
NG_14571_102xxx_NODE_161_1 ength_9814_cov_17.0206	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_164_1 ength_9738_cov_4.21254	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_168_1 ength_9689_cov_16.5752	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_169_1 ength_9679_cov_63.2905	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_184_1 ength_9341_cov_7.61221	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_185_1 ength_9334_cov_4.59694	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_186_1 ength_9333_cov_6.14723	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_192_1 ength_9135_cov_8.92291	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_195_1 ength_9066_cov_13.0897	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_20_1e ngth_22453_cov_16.0563	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_202_1 ength_8848_cov_9.24201	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_204_1 ength_8729_cov_13.2218	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_206_1 ength_8695_cov_12.8231	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_207_1 ength_8680_cov_47.2391	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_215_1 ength_8472_cov_11.8407	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_222_1 ength_8305_cov_4.74667	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_227_1 ength_8235_cov_34.9154	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_233_1 ength_8093_cov_26.5508	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_236_1 ength_8068_cov_7.43592	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_238_1 ength_8045_cov_8.48085	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_239_1 ength_8042_cov_17.0861	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_241_1 ength_7953_cov_4.45632	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_244_1 ength_7868_cov_105.123	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_250_1 ength_7771_cov_5.82932	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_252_1 ength_7715_cov_4.57937	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_253_1 ength_7714_cov_8.24142	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_256_1 ength_7621_cov_3.65927	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_26_le ngth_20704_cov_24.1199	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_261_1 ength_7494_cov_9.50262	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_262_1 ength_7485_cov_36.4841	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_265_1 ength_7466_cov_5.91904	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_270_1 ength_7401_cov_4.02233	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_272_1 ength_7366_cov_507.391	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_273_1 ength_7349_cov_1206.16	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_275_1 ength_7317_cov_3.95346	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_276_1 ength_7311_cov_4.08104	0.21	-0.20	0.64	0.64	-0.08	0.97	Myoviridae
NG_14571_102xxx_NODE_277_1 ength_7304_cov_4.6852	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_279_1 ength_7243_cov_13.2927	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_283_1 ength_7183_cov_5.27413	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_289_1 ength_7111_cov_45.3125	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_296_1 ength_6959_cov_11.0087	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_299_1 ength_6923_cov_3.29295	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_301_1 ength_6899_cov_88.5935	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_307_1 ength_6825_cov_51.5371	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_311_1 ength_6805_cov_5.99185	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_312_1 ength_6780_cov_21.8513	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_314_1 ength_6750_cov_3.48783	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_317_1 ength_6639_cov_3.98223	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_319_1 ength_6623_cov_9.67677	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_324_1 ength_6554_cov_3.5767	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_33_1e ngth_19178_cov_101.203	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_332_1 ength_6403_cov_2.96928	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_333_1 ength_6402_cov_40.2485	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_335_1 ength_6399_cov_1002.21	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_336_1 ength_6345_cov_5.1194	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_340_1 ength_6301_cov_5.66795	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_342_1 ength_6266_cov_309.931	0.21	-0.20	0.64	0.64	-0.08	0.97	Siphoviridae
NG_14571_102xxx_NODE_343_1 ength_6259_cov_3.16731	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_359_1 ength_6076_cov_8.8658	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_36_le ngth_18568_cov_17.3419	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_365_1 ength_5992_cov_10.695	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_372_1 ength_5890_cov_11.8773	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_374_1 ength_5881_cov_2.53948	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_375_1 ength_5856_cov_9.92346	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_376_1 ength_5855_cov_8.33741	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_380_1 ength_5827_cov_13.9037	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_382_1 ength_5776_cov_816.685	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_388_1 ength_5730_cov_3.37938	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_392_1 ength_5663_cov_2.45685	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_397_1 ength_5554_cov_3.93908	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_398_1 ength_5545_cov_6.12004	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_399_1 ength_5545_cov_2.82605	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_408_1 ength_5479_cov_12.4216	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_418_1 ength_5378_cov_24.6153	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_422_1 ength_5333_cov_4.81148	0.21	-0.20	0.64	0.64	-0.08	0.97	Siphoviridae
NG_14571_102xxx_NODE_425_1 ength_5297_cov_244.562	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_44_le ngth_16560_cov_45.7796	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_445_1 ength_5097_cov_3.46807	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_451_1 ength_5074_cov_3.18111	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_455_1 ength_5053_cov_3.36234	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_457_1 ength_5009_cov_3.16875	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_459_1 ength_4987_cov_5.46878	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_461_1 ength_4972_cov_2.90055	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_462_1 ength_4961_cov_37.3671	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_467_1 ength_4900_cov_41.902	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_469_1 ength_4889_cov_4.6717	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_470_1 ength_4878_cov_35.9326	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_472_1 ength_4864_cov_7.21647	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_473_1 ength_4863_cov_13.4282	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_475_1 ength_4848_cov_2.83705	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_477_1 ength_4832_cov_223.995	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_480_1 ength_4771_cov_4.28075	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_483_1 ength_4721_cov_3.17381	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_485_1 ength_4717_cov_2.70206	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_486_1 ength_4711_cov_4.72337	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_488_1 ength_4681_cov_3.09879	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_495_1 ength_4606_cov_2.59262	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_497_1 ength_4590_cov_3.00948	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_498_1 ength_4587_cov_29.9823	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_499_1 ength_4579_cov_47.076	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_502_1 ength_4534_cov_2.77897	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_504_1 ength_4510_cov_4.67924	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_505_1 ength_4508_cov_9.76286	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_510_1 ength_4475_cov_2.75995	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_511_1 ength_4467_cov_3.47461	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_512_1 ength_4465_cov_8.87868	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_513_1 ength_4455_cov_2.98659	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_515_1 ength_4451_cov_9.9313	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_525_1 ength_4370_cov_706.683	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_528_1 ength_4352_cov_3.66977	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_532_1 ength_4315_cov_3.98052	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_54_le ngth_15592_cov_44.7747	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_542_1 ength_4253_cov_6.86208	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_545_1 ength_4240_cov_2.98853	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_549_1 ength_4175_cov_38.9893	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_550_1 ength_4173_cov_3.09059	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_553_1 ength_4163_cov_12.795	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_555_1 ength_4138_cov_4.04433	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_560_1 ength_4115_cov_3.1197	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_561_1 ength_4111_cov_6.13856	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_563_1 ength_4103_cov_99.8701	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_567_1 ength_4077_cov_5.77623	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_568_1 ength_4066_cov_11.6183	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_57_le ngth_15437_cov_5.80878	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_573_1 ength_4021_cov_124.804	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_574_1 ength_4016_cov_3.61336	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_575_1 ength_4003_cov_7.17148	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_576_1 ength_4003_cov_2.43313	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_579_1 ength_3997_cov_3.08676	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_580_1 ength_3977_cov_5.57828	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_582_1 ength_3961_cov_3.92652	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_586_1 ength_3949_cov_51.0207	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_593_1 ength_3873_cov_3.75327	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_601_1 ength_3855_cov_3.48421	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_602_1 ength_3837_cov_2.47541	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_603_1 ength_3836_cov_9.75165	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_605_1 ength_3829_cov_3.47509	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_608_1 ength_3810_cov_2.87244	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_61_le ngth_15123_cov_8.53869	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_610_1 ength_3801_cov_49.0635	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_613_1 ength_3793_cov_13.5482	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_615_1 ength_3789_cov_26.7287	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_618_1 ength_3782_cov_3.85887	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_623_1 ength_3724_cov_2.74898	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_626_1 ength_3706_cov_2.16845	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_629_1 ength_3694_cov_4.5856	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_631_1 ength_3691_cov_7.022	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_632_1 ength_3689_cov_3.36764	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_633_1 ength_3663_cov_2.77578	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_634_1 ength_3661_cov_1984.1	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_639_1 ength_3630_cov_8.4358	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_641_1 ength_3618_cov_13.7019	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_648_1 ength_3577_cov_58.0997	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_649_1 ength_3575_cov_96.7625	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_65_le ngth_14899_cov_13.1913	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_653_1 ength_3545_cov_2.86762	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_656_1 ength_3535_cov_3.5431	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_66_le ngth_14481_cov_24.3941	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_662_1 ength_3486_cov_2300.35	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_67_le ngth_14121_cov_416.413	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_670_1 ength_3409_cov_26.1553	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_672_1 ength_3400_cov_6.41256	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_676_1 ength_3375_cov_7.20633	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_681_1 ength_3365_cov_7.69124	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_683_1 ength_3341_cov_19.3302	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_688_1 ength_3314_cov_19.1933	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_689_1 ength_3312_cov_16.5732	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_690_1 ength_3311_cov_3.22574	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_691_1 ength_3308_cov_3.10729	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_696_1 ength_3257_cov_2.26921	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_699_1 ength_3250_cov_101.286	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_700_1 ength_3234_cov_3.19064	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_709_1 ength_3200_cov_3.46804	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_71_1e ngth_13951_cov_6.78282	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_710_1 ength_3174_cov_43.604	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_711_1 ength_3174_cov_11.9054	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_719_1 ength_3148_cov_2.38733	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_721_1 ength_3142_cov_2.67638	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_724_1 ength_3126_cov_3.09769	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_726_1 ength_3115_cov_40.6873	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_727_1 ength_3112_cov_3.27969	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_102xxx_NODE_729_1 ength_3094_cov_24.922	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_730_1 ength_3091_cov_2.72332	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_732_1 ength_3077_cov_54.4854	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_736_1 ength_3052_cov_3.05539	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_739_1 ength_3040_cov_1.96214	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_741_1 ength_3032_cov_3.04434	0.21	-0.20	0.64	0.64	-0.08	0.97	Myoviridae
NG_14571_102xxx_NODE_745_1 ength_3016_cov_3.99865	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_75_le ngth_13768_cov_89.278	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_76_le ngth_13553_cov_4.99511	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_79_le ngth_13434_cov_13.1656	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_85_le ngth_12953_cov_6.16274	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_87_le ngth_12735_cov_7.93651	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_90_le ngth_12583_cov_10.1446	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_92_le ngth_12479_cov_57.796	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_95_le ngth_12414_cov_12.7335	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_102xxx_NODE_98_le ngth_12302_cov_5.30889	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_103_NODE_17_length_4169_cov_2.76811	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_103_NODE_22_length_2923_cov_36.2664	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_103_NODE_6_length_6182_cov_4.22164	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_101_1_length_3838_cov_2.55036	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_102_1_length_3781_cov_112.233	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_105_1_length_3723_cov_3.12541	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_106_1_length_3699_cov_2.42179	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_111_1_length_3495_cov_3.47442	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_112_1_length_3442_cov_3.20933	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_113_1_length_3339_cov_1.85871	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_119_1_length_3160_cov_2.89308	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_121_1_length_3058_cov_3.77223	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_123_1_length_3014_cov_2.43731	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_138_1_length_2649_cov_2.97147	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_139_1_length_2622_cov_2.46864	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_104xxx_NODE_156_1_length_2333_cov_3.70325	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_104xxx_NODE_161_1 ength_2296_cov_2.98527	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_197_1 ength_1800_cov_2.91519	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_20_le ngth_14634_cov_4.25098	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_104xxx_NODE_22_le ngth_13349_cov_9.15729	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_26_le ngth_13030_cov_5.13279	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_28_le ngth_12767_cov_4.26046	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_104xxx_NODE_32_le ngth_11429_cov_16.1241	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_331_1 ength_1118_cov_1.95014	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_378_1 ength_1032_cov_2.66121	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_387_1 ength_1016_cov_1.31634	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_51_le ngth_7080_cov_3.25082	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_59_le ngth_6147_cov_4.31238	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_68_le ngth_5210_cov_4.46363	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_69_le ngth_5187_cov_2.79638	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_70_le ngth_5065_cov_2.92156	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_76_le ngth_4802_cov_2.97535	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_104xxx_NODE_80_le ngth_4633_cov_3.2879	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_81_le ngth_4509_cov_4.79165	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_82_le ngth_4491_cov_2.94364	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_84_le ngth_4376_cov_2.62023	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_88_le ngth_4235_cov_4.78971	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_90_le ngth_4141_cov_2.02276	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_104xxx_NODE_95_le ngth_3939_cov_972.235	0.84	0.03	0.94	0.46	-0.12	0.97	Anelloviridae
NG_14571_104xxx_NODE_96_le ngth_3923_cov_2.10341	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_104xxx_NODE_97_le ngth_3904_cov_2.8979	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_101_1 ength_10886_cov_4.94137	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_106xxx_NODE_102_1 ength_10880_cov_3.87492	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_112_1 ength_9995_cov_2.48785	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_12_le ngth_30495_cov_9.62316	0.03	-0.34	0.64	0.89	-0.02	0.97	Unclassified
NG_14571_106xxx_NODE_122_1 ength_9286_cov_5.15578	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_126_1 ength_9124_cov_11.2924	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_133_1 ength_8762_cov_3.76996	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_106xxx_NODE_134_1 ength_8686_cov_2.87522	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_136_1 ength_8493_cov_3.39844	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_138_1 ength_8450_cov_4.876	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_140_1 ength_8355_cov_3.43229	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_141_1 ength_8297_cov_3.80066	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
NG_14571_106xxx_NODE_159_1 ength_7457_cov_3.79506	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_167_1 ength_7233_cov_4.56562	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_174_1 ength_7074_cov_2.76749	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_176_1 ength_7062_cov_3.98145	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_181_1 ength_6888_cov_3.982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_185_1 ength_6723_cov_13.1168	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_187_1 ength_6692_cov_3.6738	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_106xxx_NODE_198_1 ength_6317_cov_3.47557	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_206_1 ength_6084_cov_3.02919	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_217_1 ength_5635_cov_2.99032	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_218_1 ength_5625_cov_3.21544	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_106xxx_NODE_225_1 ength_5525_cov_4.07294	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_226_1 ength_5502_cov_3.34735	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_232_1 ength_5414_cov_2.93226	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_106xxx_NODE_241_1 ength_5257_cov_3.40292	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_250_1 ength_5083_cov_3.37092	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_255_1 ength_5001_cov_99.9147	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_259_1 ength_4973_cov_2.70313	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_260_1 ength_4956_cov_4.65946	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_106xxx_NODE_266_1 ength_4907_cov_4.47197	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_289_1 ength_4471_cov_4.14085	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_291_1 ength_4406_cov_2.5254	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_106xxx_NODE_293_1 ength_4374_cov_2.76684	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_294_1 ength_4366_cov_3.10926	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_300_1 ength_4314_cov_4.12421	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_302_1 ength_4295_cov_2.90236	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_305_1 ength_4242_cov_3.78624	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_106xxx_NODE_31_length_20289_cov_5.6621	0.03	-0.34	0.64	0.86	-0.03	0.97	Unclassified
NG_14571_106xxx_NODE_313_length_4130_cov_3.10012	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_106xxx_NODE_314_length_4126_cov_3.53623	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_318_length_4090_cov_3.20074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_323_length_3977_cov_11.9643	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_330_length_3907_cov_2.64953	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_334_length_3868_cov_3.48466	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_335_length_3854_cov_3.30034	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_336_length_3850_cov_2.85481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_338_length_3802_cov_2.96237	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_344_length_3757_cov_3.46542	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_345_length_3752_cov_1.86692	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_347_length_3742_cov_2.87985	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_35_length_17949_cov_3.77646	0.12	-0.25	0.64	0.83	0.04	0.97	Unclassified
NG_14571_106xxx_NODE_351_length_3705_cov_2.75205	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_106xxx_NODE_361_length_3622_cov_3.35268	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_106xxx_NODE_365_1 ength_3606_cov_2.82625	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_370_1 ength_3571_cov_3.407	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_376_1 ength_3469_cov_2.92824	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_377_1 ength_3458_cov_2.92918	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_38_1e ngth_17535_cov_5.10303	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_382_1 ength_3406_cov_2.41212	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_384_1 ength_3388_cov_2.10861	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_385_1 ength_3386_cov_2.81807	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_391_1 ength_3334_cov_2.59134	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_393_1 ength_3318_cov_2.60435	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_394_1 ength_3302_cov_2.75793	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_396_1 ength_3232_cov_2.13157	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_400_1 ength_3213_cov_2.79734	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_402_1 ength_3208_cov_3.10276	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_404_1 ength_3185_cov_3.24601	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_406_1 ength_3169_cov_2.28356	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_106xxx_NODE_411_1 ength_3111_cov_3.18357	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_415_1 ength_3099_cov_2.07983	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_417_1 ength_3087_cov_2.55343	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_428_1 ength_3021_cov_2.20128	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_432_1 ength_3008_cov_2.0657	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_49_le ngth_15930_cov_4.72913	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_59_le ngth_14981_cov_4.3167	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_60_le ngth_14888_cov_5.54797	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_61_le ngth_14829_cov_4.14762	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_647_1 ength_2124_cov_2.23925	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_73_le ngth_13619_cov_7.86405	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_74_le ngth_13574_cov_4.08455	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_106xxx_NODE_869_1 ength_1642_cov_2.54127	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_880_1 ength_1615_cov_2.08077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_91_le ngth_11893_cov_4.33443	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_106xxx_NODE_93_le ngth_11579_cov_4.53783	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_108xxx_NODE_103_1 ength_5482_cov_4.04846	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_105_1 ength_5453_cov_7.51704	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_109_1 ength_5439_cov_12.237	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_113_1 ength_5308_cov_6.51837	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_114_1 ength_5296_cov_2.99351	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_115_1 ength_5280_cov_3.1022	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_116_1 ength_5264_cov_2.26512	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_118_1 ength_5051_cov_2.35929	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_119_1 ength_5022_cov_2.2426	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_121_1 ength_4900_cov_2.79567	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_122_1 ength_4889_cov_4.28031	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_123_1 ength_4879_cov_2.95937	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_125_1 ength_4858_cov_3.73225	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_128_1 ength_4796_cov_3.09682	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_129_1 ength_4758_cov_3.78971	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_130_1 ength_4725_cov_4.98201	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_108xxx_NODE_133_1 ength_4547_cov_2.10975	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_134_1 ength_4545_cov_2.24321	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_135_1 ength_4520_cov_2.89295	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_139_1 ength_4401_cov_6.68983	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_140_1 ength_4376_cov_2.03309	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_144_1 ength_4302_cov_3.87167	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_145_1 ength_4299_cov_2.33742	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_148_1 ength_4208_cov_3.28172	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_154_1 ength_4142_cov_3.07585	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_157_1 ength_4068_cov_2.31099	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_161_1 ength_3928_cov_2.71443	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_162_1 ength_3924_cov_3.00362	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_165_1 ength_3883_cov_3.03579	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_166_1 ength_3771_cov_3.831	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_168_1 ength_3727_cov_2.88344	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_169_1 ength_3715_cov_7.12131	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_108xxx_NODE_171_1 ength_3579_cov_3.96737	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_173_1 ength_3513_cov_2.92568	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_174_1 ength_3491_cov_2.36816	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_177_1 ength_3474_cov_3.06347	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_179_1 ength_3467_cov_3.98095	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_180_1 ength_3450_cov_2.69161	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_182_1 ength_3411_cov_2.89839	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_184_1 ength_3385_cov_2.62432	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_186_1 ength_3370_cov_2.93756	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_187_1 ength_3361_cov_5.02571	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_188_1 ength_3347_cov_2.07625	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_189_1 ength_3311_cov_2.71376	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_190_1 ength_3295_cov_2.14383	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_192_1 ength_3288_cov_3.02413	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_195_1 ength_3203_cov_8.7068	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_196_1 ength_3193_cov_2.30051	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_108xxx_NODE_197_1 ength_3152_cov_5.00904	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_20_le ngth_18359_cov_5.9257	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_202_1 ength_3041_cov_2.58573	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_203_1 ength_3040_cov_3.24255	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_204_1 ength_3008_cov_2.43278	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_211_1 ength_2886_cov_2.05263	0.90	0.02	0.94	0.90	-0.02	0.97	Podoviridae
NG_14571_108xxx_NODE_22_le ngth_16063_cov_7.73445	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_27_le ngth_14184_cov_5.48694	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_29_le ngth_13858_cov_6.41998	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_31_le ngth_13163_cov_4.23932	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_35_le ngth_11368_cov_4.26271	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_37_le ngth_11215_cov_15.9995	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_41_le ngth_10568_cov_3.73585	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_47_le ngth_9890_cov_3.51957	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_470_1 ength_1498_cov_2.94317	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_49_le ngth_9589_cov_5.91808	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_108xxx_NODE_53_le ngth_8858_cov_2.71146	0.95	-0.01	0.97	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_56_le ngth_8264_cov_3.21189	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_57_le ngth_8151_cov_6.71146	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_62_le ngth_7705_cov_4.96884	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_64_le ngth_7462_cov_4.68651	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_65_le ngth_7365_cov_4.04966	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_66_le ngth_7329_cov_3.56283	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_67_le ngth_7215_cov_3.53045	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_68_le ngth_7103_cov_10.7076	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_69_le ngth_7009_cov_5.51251	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_70_le ngth_6974_cov_3.09134	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_75_le ngth_6649_cov_2.63603	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_78_le ngth_6373_cov_2.48465	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_80_le ngth_6234_cov_97.5647	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_82_le ngth_6195_cov_7.49072	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_83_le ngth_6171_cov_3.99003	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified

NG_14571_108xxx_NODE_91_le ngth_5851_cov_5.04141	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_92_le ngth_5816_cov_3.82885	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_93_le ngth_5815_cov_6.475	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_94_le ngth_5790_cov_3.74333	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_96_le ngth_5668_cov_5.47123	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_97_le ngth_5648_cov_5.29394	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_108xxx_NODE_98_le ngth_5598_cov_2.56197	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_109xxx_NODE_13_le ngth_4136_cov_3.07106	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_14_le ngth_4064_cov_2.61886	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_15_le ngth_3977_cov_5.16395	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_18_le ngth_3733_cov_2.67863	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_19_le ngth_3732_cov_3.04705	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_20_le ngth_3620_cov_3.23142	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_24_le ngth_3303_cov_2.6795	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_109xxx_NODE_7_len gth_7142_cov_11.968	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_105_l ength_6204_cov_3.34754	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_110xxx_NODE_106_1 ength_6077_cov_4.00947	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_109_1 ength_5964_cov_4.7822	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_110xxx_NODE_110_1 ength_5841_cov_7.83287	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_112_1 ength_5788_cov_2.76365	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_118_1 ength_5397_cov_8.50917	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_122_1 ength_5345_cov_3.56786	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_123_1 ength_5335_cov_13.5765	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_139_1 ength_4764_cov_3.16946	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_144_1 ength_4704_cov_3.0527	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_145_1 ength_4699_cov_3.14729	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_146_1 ength_4679_cov_2.77595	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_147_1 ength_4665_cov_3.82321	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_149_1 ength_4610_cov_5.66498	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_150_1 ength_4603_cov_3.6372	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_16_le ngth_17491_cov_12.6586	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_162_1 ength_4315_cov_4.22535	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_110xxx_NODE_163_1 ength_4307_cov_6.2246	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_167_1 ength_4083_cov_8.22865	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_169_1 ength_3970_cov_2.53282	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_171_1 ength_3961_cov_4.21966	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_172_1 ength_3907_cov_21.5722	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_185_1 ength_3556_cov_3.21565	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_190_1 ength_3444_cov_4.69608	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_191_1 ength_3372_cov_2.16581	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_192_1 ength_3371_cov_7.00754	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_195_1 ength_3313_cov_4.81522	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_205_1 ength_3101_cov_7.05515	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_207_1 ength_3063_cov_13.7443	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_208_1 ength_3048_cov_2.08052	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_209_1 ength_3032_cov_2.59657	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_214_1 ength_3000_cov_41.0537	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_110xxx_NODE_22_le ngth_14842_cov_14.2558	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_110xxx_NODE_223_1 ength_2852_cov_2.95316	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_231_1 ength_2751_cov_2.1684	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_24_1e ngth_14212_cov_14.7584	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_241_1 ength_2649_cov_13.5251	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_251_1 ength_2543_cov_13.0426	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_110xxx_NODE_260_1 ength_2424_cov_4.33347	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_266_1 ength_2358_cov_29.7091	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_274_1 ength_2238_cov_3.91113	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_280_1 ength_2195_cov_9.53645	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_327_1 ength_1865_cov_3.20331	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_33_1e ngth_12948_cov_20.9446	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_333_1 ength_1838_cov_3.553	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_14571_110xxx_NODE_338_1 ength_1826_cov_4.39526	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_36_1e ngth_12552_cov_8.82468	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_386_1 ength_1522_cov_4.75665	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_110xxx_NODE_39_1e ngth_12076_cov_8.04833	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_110xxx_NODE_41_le ngth_11711_cov_15.7438	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_457_1 ength_1289_cov_4.44489	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_46_le ngth_11272_cov_13.8546	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_48_le ngth_10784_cov_7.67676	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_49_le ngth_10532_cov_4.75126	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_110xxx_NODE_51_le ngth_10347_cov_4.59716	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_513_1 ength_1147_cov_1.94597	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_52_le ngth_9963_cov_7.29663	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_53_le ngth_9844_cov_9.48034	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_546_1 ength_1096_cov_1.60231	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_110xxx_NODE_57_le ngth_9514_cov_3.44825	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_59_le ngth_9362_cov_5.64489	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_65_le ngth_9021_cov_3.75006	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_66_le ngth_8920_cov_5.08438	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_67_le ngth_8713_cov_6.39293	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_68_le ngth_8685_cov_5.48633	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_110xxx_NODE_71_le ngth_8462_cov_6.11609	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_75_le ngth_7892_cov_12.3765	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_77_le ngth_7658_cov_4.06997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_78_le ngth_7597_cov_19.153	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_79_le ngth_7531_cov_2.90262	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_84_le ngth_7148_cov_3.19244	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_85_le ngth_7118_cov_22.8761	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_87_le ngth_6936_cov_4.69423	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_92_le ngth_6693_cov_127.188	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_110xxx_NODE_94_le ngth_6681_cov_3.45035	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_111xxx_NODE_100_1 ength_4384_cov_2.46385	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_105_1 ength_4332_cov_5.09516	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_108_1 ength_4316_cov_2.52664	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_109_1 ength_4315_cov_3.01197	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_110_1 ength_4252_cov_3.44532	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_112_1 ength_4064_cov_2.66775	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified

NG_14571_111xxx_NODE_115_1 ength_3941_cov_3.4475	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_120_1 ength_3791_cov_2.97725	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_121_1 ength_3764_cov_3.19439	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_130_1 ength_3498_cov_3.60325	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_133_1 ength_3281_cov_3.9752	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_140_1 ength_3121_cov_2.40476	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_142_1 ength_3104_cov_3.00295	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_147_1 ength_2988_cov_2.74224	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_149_1 ength_2916_cov_3.65397	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_157_1 ength_2694_cov_1.7571	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_164_1 ength_2625_cov_2.76226	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_165_1 ength_2603_cov_2.34655	0.37	0.15	0.66	0.70	0.06	0.97	Myoviridae
NG_14571_111xxx_NODE_190_1 ength_2196_cov_2.0808	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
NG_14571_111xxx_NODE_201_1 ength_2046_cov_3.56303	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_202_1 ength_2044_cov_2.45199	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_212_1 ength_1949_cov_1.99789	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified

NG_14571_111xxx_NODE_216_1 ength_1914_cov_1.60409	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_223_1 ength_1877_cov_2.56861	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_258_1 ength_1595_cov_2.98766	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_274_1 ength_1493_cov_2.33449	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_275_1 ength_1491_cov_2.27855	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_323_1 ength_1264_cov_48.7717	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_36_le ngth_11168_cov_4.95652	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_38_le ngth_10930_cov_6.97885	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_40_le ngth_10710_cov_83.0364	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_42_le ngth_10514_cov_26.6812	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
NG_14571_111xxx_NODE_46_le ngth_9857_cov_2.55703	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_49_le ngth_9785_cov_9.45725	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_57_le ngth_7543_cov_28.4419	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_61_le ngth_6874_cov_15.591	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_64_le ngth_6612_cov_3.10142	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_65_le ngth_6530_cov_5.25714	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified

NG_14571_111xxx_NODE_68_le ngth_6221_cov_4.53438	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_70_le ngth_5952_cov_3.79057	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_82_le ngth_5350_cov_2.60113	0.37	0.15	0.66	0.70	0.06	0.97	Siphoviridae
NG_14571_111xxx_NODE_85_le ngth_5194_cov_2.97315	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_86_le ngth_5151_cov_4.10204	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_89_le ngth_4900_cov_3.75975	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_91_le ngth_4790_cov_3.7962	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_93_le ngth_4684_cov_2.33247	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_111xxx_NODE_96_le ngth_4603_cov_6.10466	0.37	0.15	0.66	0.70	0.06	0.97	Unclassified
NG_14571_112xxx_NODE_12_le ngth_12423_cov_8.16389	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_13_le ngth_12252_cov_32.3354	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_15_le ngth_10020_cov_4.36207	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_208_1 ength_1591_cov_2.58398	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_26_le ngth_8323_cov_3.55757	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_27_le ngth_8177_cov_12.9331	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_28_le ngth_8159_cov_15.537	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_112xxx_NODE_30_le ngth_7378_cov_7.60467	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_31_le ngth_7270_cov_7.62176	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_33_le ngth_7109_cov_4.92557	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_40_le ngth_6520_cov_26.0759	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_41_le ngth_6514_cov_8.81623	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_42_le ngth_6336_cov_5.18946	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_45_le ngth_6103_cov_10.8649	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_47_le ngth_6012_cov_12.278	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_48_le ngth_5727_cov_4.22144	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_50_le ngth_5456_cov_5.28069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_53_le ngth_5414_cov_2.32245	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_54_le ngth_5257_cov_4.04344	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_56_le ngth_5087_cov_2.85135	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_57_le ngth_4950_cov_5.47967	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_58_le ngth_4819_cov_6.03547	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_112xxx_NODE_59_le ngth_4619_cov_2.4209	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_60_le ngth_4560_cov_2.95871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_61_le ngth_4515_cov_4.54238	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_62_le ngth_4461_cov_7.34226	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_64_le ngth_4366_cov_6.43934	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_65_le ngth_4243_cov_3.60649	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_14571_112xxx_NODE_7_len gth_13476_cov_18.6178	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_76_le ngth_3682_cov_12.8445	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_77_le ngth_3681_cov_2.36128	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_79_le ngth_3634_cov_3.97765	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_8_len gth_13435_cov_22.0042	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_80_le ngth_3613_cov_14.0141	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_81_le ngth_3570_cov_7.19659	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_82_le ngth_3515_cov_3.19133	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_85_le ngth_3442_cov_63.2749	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_112xxx_NODE_86_le ngth_3437_cov_4.51538	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_112xxx_NODE_87_length_3383_cov_3.564	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_89_length_3353_cov_6.4815	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_9_length_13373_cov_15.6596	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_92_length_3235_cov_12.4173	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_93_length_3216_cov_26.3521	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_95_length_3166_cov_5.59081	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_97_length_3036_cov_3.7531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_112xxx_NODE_98_length_3032_cov_2.90124	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_100_length_3235_cov_2.26195	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_102_length_3211_cov_2.95976	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_160_length_1624_cov_1.76482	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_17_length_13190_cov_3.87387	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_18_length_12879_cov_5.54585	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_20_length_12691_cov_5.02817	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_22_length_11975_cov_5.5922	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_23_length_11966_cov_6.36387	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_113xxx_NODE_29_le ngth_10851_cov_5.10902	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_113xxx_NODE_30_le ngth_10601_cov_11.9933	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_31_le ngth_10205_cov_4.39103	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_32_le ngth_9918_cov_5.50978	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_34_le ngth_9459_cov_11.8273	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_35_le ngth_9050_cov_5.27482	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_42_le ngth_7664_cov_2.83322	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_45_le ngth_7491_cov_3.84266	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_46_le ngth_7481_cov_2.78225	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_48_le ngth_7404_cov_12.6473	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_49_le ngth_7160_cov_17.7382	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_52_le ngth_6937_cov_3.57614	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_53_le ngth_6914_cov_3.40968	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_55_le ngth_6892_cov_4.82931	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_57_le ngth_6659_cov_3.92671	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_113xxx_NODE_58_le ngth_6545_cov_4.79291	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_113xxx_NODE_6_length_23773_cov_13.695	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_64_length_5814_cov_6.54957	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_66_length_5742_cov_2.68771	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_67_length_5700_cov_3.34589	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_70_length_5421_cov_3.57175	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_71_length_5305_cov_4.864	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_72_length_5243_cov_3.05204	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_79_length_4479_cov_3.54317	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_82_length_4249_cov_5.17883	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_84_length_4104_cov_2.91899	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_86_length_4021_cov_4.78265	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_91_length_3546_cov_3.26898	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_96_length_3348_cov_2.21439	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_113xxx_NODE_97_length_3343_cov_4.95833	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_114xxx_NODE_100_length_5618_cov_5.08341	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_101_length_5598_cov_4.68248	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified

NG_14571_114xxx_NODE_102_1 ength_5575_cov_2.9779	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_110_1 ength_5374_cov_4.70822	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_113_1 ength_5339_cov_3.14667	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_115_1 ength_5322_cov_10.1675	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_118_1 ength_5148_cov_2.58669	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_123_1 ength_4961_cov_3.1488	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_124_1 ength_4914_cov_3.18646	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_125_1 ength_4870_cov_4.00208	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_130_1 ength_4679_cov_2.0891	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_131_1 ength_4648_cov_3.79578	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_135_1 ength_4462_cov_4.94441	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_139_1 ength_4332_cov_3.09376	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_143_1 ength_4235_cov_3.25574	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_145_1 ength_4232_cov_2.71989	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_150_1 ength_4153_cov_3.42435	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_152_1 ength_4125_cov_3.12088	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified

NG_14571_114xxx_NODE_153_1 ength_4098_cov_2.83379	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_154_1 ength_4072_cov_2.38611	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_156_1 ength_4054_cov_3.28632	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_162_1 ength_3873_cov_3.55946	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_163_1 ength_3862_cov_2.67218	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_168_1 ength_3764_cov_5.33621	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_169_1 ength_3762_cov_7.31427	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_170_1 ength_3755_cov_3.47027	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_171_1 ength_3754_cov_3.29413	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_172_1 ength_3704_cov_19.1261	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_174_1 ength_3683_cov_3.25441	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_177_1 ength_3672_cov_3.67625	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_178_1 ength_3653_cov_27.1048	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_179_1 ength_3641_cov_2.75042	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_180_1 ength_3635_cov_3.09246	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_183_1 ength_3535_cov_2.26494	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified

NG_14571_114xxx_NODE_184_1 ength_3534_cov_2.81518	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_186_1 ength_3488_cov_3.77775	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_188_1 ength_3450_cov_2.64212	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_189_1 ength_3430_cov_5.72859	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_19_le ngth_16625_cov_10.7639	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_191_1 ength_3417_cov_2.94795	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_192_1 ength_3359_cov_3.09715	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_193_1 ength_3354_cov_4.00818	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_195_1 ength_3300_cov_3.28382	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_197_1 ength_3268_cov_3.14597	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_198_1 ength_3265_cov_6.60498	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_200_1 ength_3250_cov_205.382	0.14	-0.24	0.64	0.49	-0.11	0.97	Unclassified
NG_14571_114xxx_NODE_203_1 ength_3197_cov_13.4338	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_208_1 ength_3142_cov_2.51409	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_21_le ngth_14789_cov_5.1073	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_214_1 ength_3050_cov_2.93356	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified

NG_14571_114xxx_NODE_219_1 ength_3004_cov_4.46185	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_23_le ngth_14213_cov_3.96603	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_30_le ngth_11555_cov_6.83557	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_308_1 ength_2320_cov_3.81854	0.80	-0.04	0.94	0.43	-0.13	0.97	Anelloviridae
NG_14571_114xxx_NODE_32_le ngth_11368_cov_4.23628	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_34_le ngth_10645_cov_7.73966	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_39_le ngth_9668_cov_5.32383	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_443_1 ength_1713_cov_1.54403	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_451_1 ength_1687_cov_1.84375	0.28	-0.17	0.64	0.64	0.08	0.97	Podoviridae
NG_14571_114xxx_NODE_55_le ngth_8372_cov_3.94241	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_57_le ngth_8236_cov_8.08679	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_61_le ngth_8024_cov_5.49667	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_62_le ngth_7874_cov_3.38253	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_68_le ngth_6984_cov_4.60644	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_69_le ngth_6942_cov_6.05895	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_70_le ngth_6934_cov_4.17866	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified

NG_14571_114xxx_NODE_73_le ngth_6794_cov_5.71628	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_75_le ngth_6740_cov_3.34608	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_77_le ngth_6630_cov_5.77475	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_78_le ngth_6626_cov_4.06446	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_79_le ngth_6526_cov_3.93896	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_80_le ngth_6511_cov_8.10905	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_81_le ngth_6488_cov_3.10586	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_83_le ngth_6452_cov_2.77724	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_86_le ngth_6159_cov_5.30406	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_91_le ngth_5942_cov_4.72567	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_92_le ngth_5800_cov_4.84543	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_93_le ngth_5799_cov_3.47476	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_96_le ngth_5738_cov_2.12476	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_114xxx_NODE_98_le ngth_5656_cov_5.00678	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified
NG_14571_115xxx_NODE_102_1 ength_3089_cov_3.55636	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_20_le ngth_13281_cov_5.24777	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_115xxx_NODE_25_le ngth_12436_cov_5.05218	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_30_le ngth_11465_cov_12.5263	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_33_le ngth_10993_cov_12.1964	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_34_le ngth_10825_cov_9.92386	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_37_le ngth_9569_cov_11.9501	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_39_le ngth_8987_cov_15.5883	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_42_le ngth_8566_cov_4.57455	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_43_le ngth_7962_cov_6.12761	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_46_le ngth_7305_cov_9.36069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_48_le ngth_7081_cov_6.72972	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_55_le ngth_6305_cov_2.9168	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_56_le ngth_6271_cov_5.03057	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_71_le ngth_5186_cov_3.22686	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_76_le ngth_4481_cov_7.8545	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_79_le ngth_4428_cov_3.18295	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_115xxx_NODE_82_le ngth_4099_cov_3.14021	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_115xxx_NODE_89_length_3800_cov_4.13298	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_115xxx_NODE_91_length_3696_cov_56.4194	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_115xxx_NODE_92_length_3684_cov_2.62607	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_115xxx_NODE_94_length_3353_cov_4.31383	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_115xxx_NODE_95_length_3335_cov_2.33018	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_115xxx_NODE_97_length_3193_cov_2.39898	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_115xxx_NODE_99_length_3164_cov_3.04085	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_117_NODE_28_length_11453_cov_4.32321	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_117_NODE_30_length_8057_cov_9.4174	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_117_NODE_61_length_4618_cov_3.26912	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_117_NODE_64_length_4307_cov_3.41322	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_117_NODE_80_length_3387_cov_2.85834	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_117_NODE_82_length_3266_cov_2.66833	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_117_NODE_83_length_3218_cov_2.25545	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_14571_118_NODE_14_length_5512_cov_3.05094	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_118_NODE_16_length_5053_cov_2.63806	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_118_NODE_20_length_2725_cov_3.3824	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_119xxx_NODE_10_length_25408_cov_6.42882	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_100_1_length_7029_cov_4.66418	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_103_1_length_6935_cov_5.52151	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_104_1_length_6884_cov_8.28218	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_105_1_length_6838_cov_7.91125	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_108_1_length_6788_cov_6.92099	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_11_length_23885_cov_7.33068	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_110_1_length_6754_cov_3.17764	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_113_1_length_6520_cov_6.53766	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_115_1_length_6469_cov_3.39367	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_116_1_length_6382_cov_8.89436	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_117_1_length_6332_cov_13.7758	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_118_1_length_6327_cov_7.00415	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_121_1_length_6302_cov_3.02257	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_124_1_length_6211_cov_3.30621	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_125_1 ength_6145_cov_6.43629	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_127_1 ength_5803_cov_7.80063	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_128_1 ength_5778_cov_2.68408	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_129_1 ength_5757_cov_3.79533	0.42	-0.13	0.68	0.57	0.09	0.97	Siphoviridae
NG_14571_119xxx_NODE_137_1 ength_5552_cov_5.76278	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_138_1 ength_5533_cov_2.90581	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_139_1 ength_5530_cov_6.02922	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_140_1 ength_5493_cov_12.02	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_141_1 ength_5483_cov_3.18976	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_142_1 ength_5481_cov_9.12864	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_145_1 ength_5432_cov_3.03757	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_150_1 ength_5269_cov_4.43709	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_151_1 ength_5245_cov_3.92582	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_152_1 ength_5226_cov_22.9745	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_155_1 ength_5160_cov_4.86151	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_156_1 ength_5103_cov_2.87242	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_159_1 ength_5044_cov_9.01223	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_163_1 ength_4913_cov_7.22108	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_165_1 ength_4878_cov_4.74456	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_166_1 ength_4860_cov_11.6857	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_169_1 ength_4793_cov_3.33643	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_171_1 ength_4753_cov_6.89102	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_172_1 ength_4731_cov_3.50599	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_174_1 ength_4715_cov_2.62103	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_175_1 ength_4702_cov_2.89542	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_18_le ngth_17888_cov_9.94645	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_180_1 ength_4647_cov_100.985	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_183_1 ength_4575_cov_3.82212	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_190_1 ength_4439_cov_6.24042	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_191_1 ength_4391_cov_25.0044	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_194_1 ength_4329_cov_2.58704	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_195_1 ength_4287_cov_16.1056	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_196_1 ength_4269_cov_3.11343	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_198_1 ength_4234_cov_2.74563	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_199_1 ength_4227_cov_3.03571	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_200_1 ength_4199_cov_8.90203	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_201_1 ength_4149_cov_2.25256	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_203_1 ength_4118_cov_3.40217	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_204_1 ength_4086_cov_5.51526	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_206_1 ength_4065_cov_5.29102	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_208_1 ength_4031_cov_3.78546	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_209_1 ength_4006_cov_12.1716	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_210_1 ength_4006_cov_3.99393	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_213_1 ength_3913_cov_2.19725	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_214_1 ength_3902_cov_2.732	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_215_1 ength_3898_cov_8.04892	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_218_1 ength_3856_cov_4.49592	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_220_1 ength_3810_cov_2.23728	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_221_1 ength_3787_cov_2.84003	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_222_1 ength_3757_cov_2.47272	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_224_1 ength_3704_cov_2.21814	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_227_1 ength_3655_cov_3.075	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_233_1 ength_3478_cov_2.6506	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_234_1 ength_3442_cov_2.24565	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_236_1 ength_3353_cov_3.63766	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_237_1 ength_3345_cov_3.98997	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_241_1 ength_3328_cov_3.26673	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_245_1 ength_3287_cov_3.3948	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_246_1 ength_3287_cov_2.60922	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_250_1 ength_3254_cov_2.66052	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_251_1 ength_3234_cov_2.48474	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_252_1 ength_3233_cov_2.91221	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_253_1 ength_3232_cov_3.88071	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_255_1 ength_3213_cov_3.58874	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_258_1 ength_3175_cov_4.38686	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_259_1 ength_3139_cov_2.53696	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_261_1 ength_3128_cov_4.32379	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_263_1 ength_3070_cov_27.1615	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_266_1 ength_3041_cov_5.56731	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_267_1 ength_3014_cov_3.10818	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_273_1 ength_2971_cov_2.30418	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_29_le ngth_14703_cov_20.927	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_291_1 ength_2783_cov_2.42302	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_30_le ngth_14232_cov_10.7928	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_319_1 ength_2472_cov_3.6326	0.83	-0.03	0.94	0.97	-0.01	0.97	Podoviridae
NG_14571_119xxx_NODE_32_le ngth_13357_cov_7.99451	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_33_le ngth_13305_cov_4.14015	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_34_le ngth_13159_cov_5.33814	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_361_1 ength_2175_cov_410.478	0.90	0.02	0.94	0.01	-0.39	0.97	Unclassified
NG_14571_119xxx_NODE_37_le ngth_12500_cov_6.04885	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_38_le ngth_12439_cov_7.80669	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_391_1 ength_2015_cov_7.25612	0.83	-0.03	0.94	0.97	-0.01	0.97	Siphoviridae
NG_14571_119xxx_NODE_47_le ngth_10789_cov_5.57909	0.83	-0.03	0.94	0.97	-0.01	0.97	Siphoviridae
NG_14571_119xxx_NODE_507_1 ength_1590_cov_2.80261	0.54	-0.10	0.80	0.49	-0.11	0.97	Unclassified
NG_14571_119xxx_NODE_52_le ngth_10399_cov_3.98695	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_53_le ngth_10068_cov_4.57415	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_55_le ngth_9962_cov_4.5484	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_564_1 ength_1435_cov_2.12681	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_57_le ngth_9786_cov_5.48248	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_63_le ngth_9261_cov_5.15186	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_64_le ngth_9206_cov_10.0157	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_66_le ngth_9059_cov_6.26866	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_67_le ngth_9034_cov_13.1651	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_68_le ngth_9006_cov_3.25148	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_73_le ngth_8574_cov_8.43468	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_75_le ngth_8290_cov_2.38203	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified

NG_14571_119xxx_NODE_76_le ngth_8287_cov_6.92408	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_82_le ngth_7990_cov_10.7487	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_86_le ngth_7795_cov_3.66124	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_90_le ngth_7464_cov_3.55757	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_91_le ngth_7365_cov_13.6995	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_93_le ngth_7334_cov_4.51999	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_94_le ngth_7261_cov_7.52026	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_98_le ngth_7048_cov_4.47934	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_119xxx_NODE_99_le ngth_7037_cov_3.43498	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_14571_57_NODE_108_length _7501_cov_6.23449	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_113_length _7129_cov_4.96256	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_115_length _7094_cov_3.05782	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_124_length _6738_cov_49.6401	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_126_length _6673_cov_6.35585	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_136_length _6376_cov_2.95349	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_137_length _6225_cov_2.0752	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified

NG_14571_57_NODE_138_length _6211_cov_26.4282	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_141_length _6151_cov_4.72703	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_15_length 18166_cov_6.16979	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_150_length _5896_cov_3.98836	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_151_length _5866_cov_5.3989	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_152_length _5852_cov_8.1123	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_153_length _5832_cov_7.73723	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_154_length _5781_cov_5.61334	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_157_length _5734_cov_9.24987	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_161_length _5619_cov_3.97035	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_166_length _5429_cov_18.5573	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_170_length _5342_cov_2.67921	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_171_length _5319_cov_7.41318	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_173_length _5297_cov_12.9397	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_176_length _5205_cov_4.2099	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_178_length _5163_cov_3.00587	0.16	-0.23	0.64	0.36	0.15	0.97	Unclassified

NG_14571_57_NODE_182_length _5108_cov_3.03701	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_184_length _5071_cov_4.03768	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_189_length _4969_cov_7.63411	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_194_length _4735_cov_2.23718	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_196_length _4694_cov_2.35439	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_198_length _4650_cov_3.37802	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_205_length _4522_cov_3.37609	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_211_length _4288_cov_2.53059	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_213_length _4248_cov_2.9089	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_214_length _4248_cov_2.59909	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_22_length _15912_cov_7.63467	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_225_length _3886_cov_5.59854	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_226_length _3884_cov_3.31079	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_228_length _3874_cov_54.4407	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_23_length _15874_cov_8.72874	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_234_length _3740_cov_3.55495	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified

NG_14571_57_NODE_236_length _3705_cov_2.58658	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_237_length _3676_cov_3.71591	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_238_length _3652_cov_20.3456	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_240_length _3631_cov_2.74916	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_244_length _3507_cov_8.13123	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_246_length _3505_cov_6.83333	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_25_length _14485_cov_6.35003	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_251_length _3422_cov_3.89159	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_252_length _3419_cov_17.8124	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_253_length _3363_cov_2.28416	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_254_length _3331_cov_3.65995	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_26_length _14307_cov_6.50926	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_260_length _3228_cov_3.2827	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_261_length _3208_cov_4.26705	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_265_length _3181_cov_3.15067	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_266_length _3178_cov_2.71214	0.37	-0.15	0.66	0.42	0.13	0.97	Siphoviridae

NG_14571_57_NODE_268_length_3137_cov_10.8894	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_271_length_3078_cov_3.49818	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_272_length_3065_cov_3.03821	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_28_length_13964_cov_14.7814	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_289_length_2893_cov_4.16385	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_301_length_2794_cov_5.00767	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_31_length_13509_cov_7.04043	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_316_length_2653_cov_2.85874	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_353_length_2439_cov_2.46141	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_357_length_2410_cov_2.33546	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_390_length_2197_cov_1.99066	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_57_NODE_392_length_2187_cov_2.47842	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_435_length_1974_cov_2.53205	0.37	-0.15	0.66	0.42	0.13	0.97	Myoviridae
NG_14571_57_NODE_442_length_1958_cov_2.15081	0.37	-0.15	0.66	0.42	0.13	0.97	Myoviridae
NG_14571_57_NODE_449_length_1938_cov_1.90653	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_48_length_12210_cov_10.0764	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified

NG_14571_57_NODE_496_length_1761_cov_2.55862	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_503_length_1734_cov_2.43121	0.37	-0.15	0.66	0.42	0.13	0.97	Myoviridae
NG_14571_57_NODE_511_length_1709_cov_2.09069	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_52_length_12030_cov_5.35591	0.37	-0.15	0.66	0.42	0.13	0.97	Myoviridae
NG_14571_57_NODE_53_length_11923_cov_4.96099	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_544_length_1622_cov_1.49394	0.37	-0.15	0.66	0.42	0.13	0.97	Myoviridae
NG_14571_57_NODE_548_length_1596_cov_1.76184	0.12	-0.25	0.64	0.83	0.04	0.97	Unclassified
NG_14571_57_NODE_575_length_1530_cov_2.70847	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_64_length_10400_cov_5.26457	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_648_length_1353_cov_2.22034	0.37	-0.15	0.66	0.42	0.13	0.97	Siphoviridae
NG_14571_57_NODE_65_length_10353_cov_3.5134	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_68_length_9796_cov_106.523	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_70_length_9440_cov_5.28279	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_71_length_9343_cov_4.67926	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_75_length_9124_cov_5.91697	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_76_length_9051_cov_5.42908	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified

NG_14571_57_NODE_760_length_ _1193_cov_2.30316	0.59	0.09	0.82	0.55	0.10	0.97	Unclassified
NG_14571_57_NODE_77_length_ 9046_cov_6.74819	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_79_length_ 8917_cov_3.79316	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_82_length_ 8610_cov_2.82653	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_86_length_ 8467_cov_6.43046	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_57_NODE_97_length_ 7939_cov_3.50989	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_58_NODE_120_length_ _2357_cov_3.01173	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_126_length_ _2300_cov_10.2285	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_128_length_ _2294_cov_2.31577	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
NG_14571_58_NODE_13_length_ 30504_cov_5.48084	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_169_length_ _1806_cov_3.17875	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_171_length_ _1798_cov_3.03213	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
NG_14571_58_NODE_18_length_ 22503_cov_4.65338	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
NG_14571_58_NODE_189_length_ _1651_cov_2.58083	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_21_length_ 16114_cov_6.34454	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
NG_14571_58_NODE_212_length_ _1455_cov_2.78357	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified

NG_14571_58_NODE_215_length_ _1428_cov_2.25419	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_260_length_ _1172_cov_2.12355	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_28_length_ 11190_cov_5.60539	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_290_length_ _1056_cov_4.34965	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_293_length_ _1053_cov_5.28056	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_34_length_ 10109_cov_3.3696	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_36_length_ 8520_cov_15.8174	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_50_length_ 5461_cov_3.79671	0.07	-0.29	0.64	0.51	-0.11	0.97	Microviridae
NG_14571_58_NODE_52_length_ 5015_cov_2.98468	0.97	-0.01	0.97	0.47	0.12	0.97	Siphoviridae
NG_14571_58_NODE_57_length_ 4555_cov_36.3422	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_61_length_ 4382_cov_3.39265	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
NG_14571_58_NODE_64_length_ 3989_cov_2.47077	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_65_length_ 3864_cov_2.64505	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_66_length_ 3709_cov_3.38834	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_74_length_ 3268_cov_4.85839	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_75_length_ 3261_cov_11.874	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified

NG_14571_58_NODE_76_length_ 3252_cov_29.33	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_58_NODE_93_length_ 2907_cov_2.06872	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
NG_14571_59_NODE_110_length_ _1887_cov_2.92413	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_155_length_ _1292_cov_1.97413	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_164_length_ _1257_cov_1.79451	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_189_length_ _1076_cov_2.05093	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_29_length_ 7761_cov_5.238	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_33_length_ 6878_cov_35.0097	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_59_NODE_35_length_ 6734_cov_4.7025	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_36_length_ 6579_cov_3.07189	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_54_length_ 4077_cov_10.3794	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_55_length_ 4014_cov_6.91942	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_59_length_ 3781_cov_3.12077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_61_length_ 3764_cov_4.06498	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_64_length_ 3379_cov_2.69615	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_65_length_ 3364_cov_10.4358	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_59_NODE_66_length_ 3321_cov_2.08206	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_73_length_ 2950_cov_2.24145	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_80_length_ 2681_cov_2.54075	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Geminiviridae
NG_14571_59_NODE_82_length_ 2648_cov_2.29117	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_83_length_ 2626_cov_2.59238	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_59_NODE_86_length_ 2531_cov_2.35945	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_59_NODE_87_length_ 2507_cov_1.92945	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_93_length_ 2288_cov_2.34438	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_59_NODE_95_length_ 2273_cov_46.5505	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_61_NODE_11_length_ 3041_cov_1.93938	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_101_length_ _3827_cov_3.02306	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_102_length_ _3736_cov_2.95327	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_108_length_ _3545_cov_3.73784	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_110_length_ _3431_cov_2.57613	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_111_length_ _3428_cov_1.93893	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_112_length_ _3364_cov_30.4811	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_64_NODE_116_length_ _3184_cov_11491.1	0.91	-0.02	0.94	0.14	-0.24	0.97	Unclassified
NG_14571_64_NODE_230_length_ _1446_cov_1.85047	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_26_length_ 14029_cov_6.08008	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_27_length_ 13930_cov_4.74321	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_38_length_ 9729_cov_6.36531	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_44_length_ 9026_cov_9.43451	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_45_length_ 8892_cov_6.49847	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_51_length_ 7521_cov_27.0687	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_52_length_ 7127_cov_4.70786	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_57_length_ 6541_cov_4.02112	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_58_length_ 6317_cov_2.70297	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_60_length_ 6192_cov_20.4282	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_61_length_ 6057_cov_3.06231	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_69_length_ 5471_cov_1536.61	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_71_length_ 5339_cov_3.18641	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_74_length_ 5189_cov_3.44196	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_64_NODE_78_length_ 4953_cov_2.58289	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_81_length_ 4812_cov_3.05781	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_83_length_ 4788_cov_3.36869	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_90_length_ 4337_cov_3.89421	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_94_length_ 4066_cov_4.11219	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_64_NODE_96_length_ 3978_cov_4.07851	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_98_length_ 3930_cov_2.40181	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_64_NODE_99_length_ 3929_cov_2.44063	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_65_NODE_110_length_ _1939_cov_1.51168	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_15_length_ 29016_cov_5.50799	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_199_length_ _1109_cov_2.56357	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_211_length_ _1034_cov_2.44842	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_22_length_ 14692_cov_34.4036	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_35_length_ 8133_cov_4.82199	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_36_length_ 7535_cov_28.208	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_41_length_ 6636_cov_3.37244	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified

NG_14571_65_NODE_53_length_ 5865_cov_4.79639	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_55_length_ 5791_cov_2.96077	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_57_length_ 5691_cov_3.91608	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_64_length_ 5116_cov_3.22466	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_68_length_ 4303_cov_6.99341	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_71_length_ 4054_cov_2.3916	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_74_length_ 3855_cov_2.44395	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_76_length_ 3772_cov_3.09066	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_77_length_ 3591_cov_2.2483	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_78_length_ 3550_cov_3.40887	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_79_length_ 3506_cov_2.04665	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_81_length_ 3425_cov_1.67448	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_82_length_ 3362_cov_2.32114	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_83_length_ 3194_cov_13.7225	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_65_NODE_94_length_ 2468_cov_34.0406	0.42	0.13	0.68	0.25	0.19	0.97	Unclassified
NG_14571_67xxx_NODE_106_le ngth_4390_cov_5.73195	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified

NG_14571_67xxx_NODE_107_le ngth_4386_cov_3.14477	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_111_le ngth_4185_cov_2.96271	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_113_le ngth_4091_cov_6.78642	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_115_le ngth_3975_cov_2.99464	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_118_le ngth_3896_cov_5.35355	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_119_le ngth_3880_cov_2.56366	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_12_le ngth_23271_cov_8.65998	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_123_le ngth_3817_cov_2.22461	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_129_le ngth_3594_cov_3.31817	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_130_le ngth_3583_cov_3.13634	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_131_le ngth_3547_cov_2.41982	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_132_le ngth_3435_cov_2.56154	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_134_le ngth_3380_cov_6.70737	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_139_le ngth_3280_cov_3.51907	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_141_le ngth_3213_cov_2.71913	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_142_le ngth_3186_cov_2.20632	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified

NG_14571_67xxx_NODE_144_le ngth_3178_cov_3.09638	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_147_le ngth_3128_cov_2.34331	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_148_le ngth_3112_cov_564.5	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_151_le ngth_3054_cov_2.3918	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_152_le ngth_3052_cov_2.43346	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_153_le ngth_3007_cov_11.6687	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_166_le ngth_2732_cov_2.18715	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_184_le ngth_2343_cov_3.60577	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_20_len gth_19310_cov_7.54313	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_204_le ngth_2023_cov_2.4436	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_23_len gth_17441_cov_6.87956	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_26_len gth_16931_cov_8.18701	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_27_len gth_16823_cov_4.54449	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_28_len gth_16776_cov_8.46558	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_30_len gth_14458_cov_8.80955	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_33_len gth_13797_cov_5.48246	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified

NG_14571_67xxx_NODE_34_len gth_13476_cov_6.59303	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_36_len gth_12586_cov_4.46333	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_42_len gth_11455_cov_5.21447	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_424_le ngth_1064_cov_2.21011	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_43_len gth_11452_cov_5.60744	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_44_len gth_11397_cov_4.10307	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_47_len gth_11197_cov_6.48743	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_49_len gth_10882_cov_4.21723	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_51_len gth_10075_cov_9.2982	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_52_len gth_9370_cov_9.78755	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_61_len gth_8564_cov_4.66118	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_65_len gth_7770_cov_3.80089	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_66_len gth_7585_cov_6.89495	0.58	0.09	0.80	0.90	0.02	0.97	Siphoviridae
NG_14571_67xxx_NODE_67_len gth_7542_cov_5.60104	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_68_len gth_7143_cov_3.77074	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_69_len gth_7131_cov_7.85585	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified

NG_14571_67xxx_NODE_70_len gth_6909_cov_10.5155	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_73_len gth_6771_cov_2.67749	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_75_len gth_6719_cov_12.1253	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_76_len gth_6587_cov_2.91228	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_77_len gth_6575_cov_5.02945	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_78_len gth_6493_cov_4.33877	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_8_len h_28422_cov_8.18472	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_84_len gth_5816_cov_3.29056	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_87_len gth_5752_cov_6.94734	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_88_len gth_5749_cov_6.79101	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_95_len gth_5247_cov_3.85555	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_96_len gth_5208_cov_4.54395	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_67xxx_NODE_99_len gth_4781_cov_8.03745	0.58	0.09	0.80	0.90	0.02	0.97	Unclassified
NG_14571_69xxx_NODE_100_le ngth_19747_cov_12.342	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_1033_1 ength_2748_cov_2.79577	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_1049_1 ength_2685_cov_14.6696	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_119_le ngth_18188_cov_3.75512	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_128_le ngth_17713_cov_4.04576	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_131_le ngth_17620_cov_96.5016	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_1336_l ength_1879_cov_2.68202	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_14571_69xxx_NODE_136_le ngth_16888_cov_7.09475	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_140_le ngth_16805_cov_9.74985	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_143_le ngth_16722_cov_3.50219	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_146_le ngth_16434_cov_33.1982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_148_le ngth_16418_cov_9.30355	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_149_le ngth_16413_cov_7.25345	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_160_le ngth_15719_cov_10.871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_164_le ngth_15376_cov_161.794	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_168_le ngth_15090_cov_3.42221	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_172_le ngth_14718_cov_4.91502	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_173_le ngth_14620_cov_9.24277	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_176_le ngth_14373_cov_11.4341	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae

NG_14571_69xxx_NODE_18_length_42441_cov_32.2334	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_180_length_14180_cov_4.71993	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_187_length_14023_cov_6.64483	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_1875_length_1241_cov_1.83221	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
NG_14571_69xxx_NODE_188_length_13987_cov_8.91028	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_190_length_13951_cov_3.40594	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_1902_length_1223_cov_2.23801	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_197_length_13686_cov_23.3722	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_2005_length_1154_cov_2.14559	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_204_length_13514_cov_5.55457	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_206_length_13458_cov_5.26957	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_208_length_13417_cov_8.9197	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_211_length_13185_cov_10.5893	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_212_length_13139_cov_6.12787	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_215_length_12930_cov_299.369	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_229_length_12645_cov_3.81334	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_69xxx_NODE_23_length_39970_cov_10.0355	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_230_length_12559_cov_9.86692	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_237_length_12285_cov_10.2092	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_241_length_12098_cov_5.76758	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_243_length_12034_cov_4.04007	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_247_length_11856_cov_14.239	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_250_length_11591_cov_12.1207	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_251_length_11591_cov_3.10298	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_258_length_11339_cov_10.7031	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_260_length_11198_cov_9.23459	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_261_length_11178_cov_83.2805	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_264_length_11059_cov_6.17157	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_269_length_10986_cov_7.1063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_273_length_10861_cov_4.02082	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_277_length_10743_cov_5.20865	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_278_length_10718_cov_4.63659	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_69xxx_NODE_28_length_36772_cov_43.1957	0.05	-0.31	0.64	0.64	0.08	0.97	Unclassified
NG_14571_69xxx_NODE_280_length_10705_cov_7.26545	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_289_length_10406_cov_121.074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_293_length_10347_cov_7.21551	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_297_length_10318_cov_9.97437	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Myoviridae
NG_14571_69xxx_NODE_302_length_10149_cov_3.96493	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_306_length_9996_cov_654.302	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_308_length_9948_cov_9.29769	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_310_length_9902_cov_4.2027	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_315_length_9767_cov_15.6953	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_316_length_9753_cov_7.75407	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_318_length_9727_cov_4.8322	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_326_length_9522_cov_16.0922	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_330_length_9493_cov_4.90496	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_331_length_9463_cov_6.88542	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_335_length_9261_cov_19.2174	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_69xxx_NODE_337_le ngth_9194_cov_17.2592	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_351_le ngth_9037_cov_8.71743	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_361_le ngth_8746_cov_6.25417	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_363_le ngth_8704_cov_3.38166	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_364_le ngth_8701_cov_10.1624	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_367_le ngth_8682_cov_3.07001	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_368_le ngth_8644_cov_13.5218	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_374_le ngth_8479_cov_6.90171	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_375_le ngth_8475_cov_10.805	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_380_le ngth_8408_cov_3.01772	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_381_le ngth_8404_cov_3.51994	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_385_le ngth_8338_cov_2.72099	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_391_le ngth_8204_cov_289.269	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_394_le ngth_8176_cov_14.0857	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_395_le ngth_8126_cov_9.90497	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_397_le ngth_8084_cov_5.33043	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified

NG_14571_69xxx_NODE_398_le ngth_8071_cov_44.2393	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_399_le ngth_8036_cov_52.829	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_400_le ngth_7995_cov_7.78262	0.97	0.01	0.97	0.37	0.15	0.97	Unclassified
NG_14571_69xxx_NODE_405_le ngth_7833_cov_7.65197	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_406_le ngth_7820_cov_4.6774	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_409_le ngth_7714_cov_4.41859	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_411_le ngth_7664_cov_18.9842	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_414_le ngth_7636_cov_6.62155	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_418_le ngth_7592_cov_19.1923	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_419_le ngth_7590_cov_5.66503	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_421_le ngth_7582_cov_5.04212	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_422_le ngth_7575_cov_3.30452	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_423_le ngth_7572_cov_438.719	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_426_le ngth_7544_cov_183.203	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_427_le ngth_7521_cov_6.47335	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_428_le ngth_7510_cov_6.29658	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_43_len ngth_30848_cov_8.89222	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_430_le ngth_7473_cov_3.66972	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_431_le ngth_7461_cov_9.01944	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_433_le ngth_7421_cov_8.68626	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_436_le ngth_7344_cov_3.15146	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_438_le ngth_7333_cov_5.04685	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_441_le ngth_7253_cov_6.02598	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_444_le ngth_7220_cov_4.74724	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_452_le ngth_7119_cov_4.48967	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_453_le ngth_7114_cov_7.95849	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_454_le ngth_7105_cov_3.08837	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_458_le ngth_7064_cov_146.755	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_460_le ngth_7040_cov_3.94817	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_461_le ngth_7022_cov_6.62739	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_465_le ngth_6946_cov_4.99391	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_466_le ngth_6915_cov_3.08776	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_468_le ngth_6878_cov_4.41917	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_470_le ngth_6863_cov_2.49383	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_471_le ngth_6839_cov_6.1763	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_474_le ngth_6774_cov_4.79268	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_475_le ngth_6774_cov_4.61378	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_481_le ngth_6666_cov_5.07185	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_482_le ngth_6645_cov_27.5505	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_483_le ngth_6641_cov_3.15229	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_487_le ngth_6624_cov_3.50069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_490_le ngth_6621_cov_4.11209	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_494_le ngth_6562_cov_5.8915	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_499_le ngth_6512_cov_9.75971	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_500_le ngth_6500_cov_2.4405	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_504_le ngth_6457_cov_2.97063	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_505_le ngth_6452_cov_3.96514	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_511_le ngth_6346_cov_232.749	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_512_le ngth_6329_cov_5.51084	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
NG_14571_69xxx_NODE_515_le ngth_6290_cov_4.71981	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_517_le ngth_6265_cov_226.592	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_519_le ngth_6247_cov_15.2414	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_52_le ngth_26765_cov_5.34167	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_520_le ngth_6224_cov_3.17993	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_521_le ngth_6200_cov_2.69178	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_522_le ngth_6187_cov_3.33366	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_524_le ngth_6179_cov_8.12884	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_527_le ngth_6151_cov_55.3264	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_529_le ngth_6087_cov_304.054	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_530_le ngth_6079_cov_4.06059	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_533_le ngth_6070_cov_6.05187	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_536_le ngth_6014_cov_3.12485	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_539_le ngth_5961_cov_16.0173	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_541_le ngth_5951_cov_17.8789	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_543_le ngth_5925_cov_11.4768	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_546_le ngth_5817_cov_2.94915	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_547_le ngth_5798_cov_634.651	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_549_le ngth_5759_cov_6.34099	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_551_le ngth_5734_cov_303.805	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_554_le ngth_5703_cov_3.95662	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_557_le ngth_5676_cov_3.46896	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_558_le ngth_5674_cov_24.6015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_559_le ngth_5670_cov_4.93909	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_69xxx_NODE_561_le ngth_5641_cov_2.8788	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_562_le ngth_5630_cov_17.1894	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_57_len gth_25528_cov_5.30742	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_576_le ngth_5494_cov_2.72256	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_577_le ngth_5479_cov_4.51235	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_578_le ngth_5473_cov_3.83924	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_584_le ngth_5429_cov_6.02121	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_585_le ngth_5429_cov_3.70357	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_587_le ngth_5424_cov_2.60179	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_588_le ngth_5415_cov_3.43134	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_591_le ngth_5404_cov_6.41503	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_594_le ngth_5379_cov_3.3349	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_595_le ngth_5369_cov_4.38276	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_596_le ngth_5362_cov_16.1751	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_597_le ngth_5339_cov_2.63607	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_599_le ngth_5317_cov_2.38388	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_603_le ngth_5273_cov_3.57857	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_604_le ngth_5247_cov_122.835	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_605_le ngth_5229_cov_2.27348	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_607_le ngth_5212_cov_5.12197	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_608_le ngth_5207_cov_6.4736	0.28	-0.17	0.64	0.64	0.08	0.97	Unclassified

NG_14571_69xxx_NODE_609_le ngth_5194_cov_8.30804	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_610_le ngth_5186_cov_53.2444	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_611_le ngth_5183_cov_5.27984	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_612_le ngth_5176_cov_5.28037	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_613_le ngth_5170_cov_2.61271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_615_le ngth_5154_cov_2.99843	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_618_le ngth_5131_cov_4.27128	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_621_le ngth_5099_cov_2.32772	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_625_le ngth_5072_cov_43.9031	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_626_le ngth_5069_cov_3.1775	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_627_le ngth_5065_cov_3.58782	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_628_le ngth_5063_cov_2.67252	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_629_le ngth_5058_cov_58.271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_630_le ngth_5057_cov_8.08497	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_632_le ngth_5027_cov_4.5541	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_633_le ngth_5027_cov_3.04525	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_636_le ngth_5012_cov_4.73795	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_637_le ngth_5003_cov_2.65137	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_639_le ngth_4987_cov_6.20012	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_642_le ngth_4936_cov_7.14198	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_644_le ngth_4919_cov_3.12644	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_645_le ngth_4916_cov_4.1907	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_650_le ngth_4855_cov_2.51042	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_654_le ngth_4822_cov_3.45312	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_655_le ngth_4813_cov_5.43989	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_661_le ngth_4736_cov_3.49498	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_662_le ngth_4721_cov_7.69546	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_664_le ngth_4716_cov_2.52371	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_667_le ngth_4671_cov_5.68523	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_669_le ngth_4643_cov_3.11181	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_670_le ngth_4642_cov_22.1951	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_671_le ngth_4642_cov_6.87835	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_674_le ngth_4609_cov_9.28898	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_675_le ngth_4593_cov_3.68532	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_681_le ngth_4542_cov_181.955	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_684_le ngth_4515_cov_24.9516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_685_le ngth_4514_cov_5.1549	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_686_le ngth_4508_cov_2.13182	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_69_le ngth_23556_cov_14.2143	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_692_le ngth_4432_cov_17.1001	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_693_le ngth_4416_cov_2.87159	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_694_le ngth_4400_cov_16.186	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_695_le ngth_4390_cov_2.14233	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_696_le ngth_4389_cov_7.20651	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_702_le ngth_4344_cov_5.51014	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_705_le ngth_4311_cov_3.84657	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_708_le ngth_4262_cov_2.87663	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_71_le ngth_22982_cov_7.38134	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_712_le ngth_4231_cov_2.87189	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_714_le ngth_4222_cov_4.67219	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_725_le ngth_4169_cov_2.01799	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_730_le ngth_4119_cov_4.56029	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_731_le ngth_4073_cov_2.44301	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_732_le ngth_4057_cov_7.75162	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_74_le ngth_22631_cov_350.354	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_741_le ngth_3980_cov_16.3027	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_742_le ngth_3980_cov_6.18013	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_744_le ngth_3962_cov_2.61275	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_748_le ngth_3952_cov_5.48601	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_751_le ngth_3935_cov_2.66701	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_752_le ngth_3929_cov_4.12416	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_753_le ngth_3928_cov_4.18151	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_754_le ngth_3927_cov_2.88068	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_757_le ngth_3882_cov_2.70159	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_759_le ngth_3868_cov_1.95253	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_761_le ngth_3851_cov_3.15174	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_763_le ngth_3836_cov_3.44724	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_764_le ngth_3831_cov_29.5344	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_771_le ngth_3793_cov_3.7603	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_772_le ngth_3782_cov_3.57741	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_773_le ngth_3782_cov_2.19292	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_774_le ngth_3779_cov_3.56982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_775_le ngth_3777_cov_3.10398	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_776_le ngth_3768_cov_4.57231	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_778_le ngth_3757_cov_26.1723	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_78_len gth_22354_cov_6.01233	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_783_le ngth_3746_cov_57.256	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_785_le ngth_3739_cov_2.10668	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_788_le ngth_3725_cov_2.73924	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_790_le ngth_3714_cov_2.54222	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_795_le ngth_3677_cov_54.3067	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_798_le ngth_3665_cov_3.01856	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_799_le ngth_3664_cov_2.33666	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_808_le ngth_3626_cov_2.43853	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_809_le ngth_3621_cov_3.80426	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_810_le ngth_3616_cov_3.85285	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_811_le ngth_3616_cov_2.48666	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_816_le ngth_3592_cov_5.31891	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_818_le ngth_3590_cov_2.29307	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_819_le ngth_3583_cov_4.83532	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_821_le ngth_3567_cov_10.8995	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_824_le ngth_3543_cov_5.27552	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_825_le ngth_3541_cov_2.56196	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_826_le ngth_3539_cov_210.73	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_831_le ngth_3506_cov_2.65749	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_832_le ngth_3504_cov_3.66628	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_833_le ngth_3503_cov_3.84598	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_839_le ngth_3465_cov_2.5217	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_84_le ngth_21596_cov_9.5743	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_841_le ngth_3447_cov_2.94575	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_843_le ngth_3446_cov_3.42229	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_844_le ngth_3435_cov_445.243	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_846_le ngth_3431_cov_32.6822	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_847_le ngth_3431_cov_2.0705	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_850_le ngth_3420_cov_3.45141	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_851_le ngth_3419_cov_3.12931	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_852_le ngth_3417_cov_2.1279	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_856_le ngth_3387_cov_34.6474	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_857_le ngth_3374_cov_2.76981	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_860_le ngth_3363_cov_2.74123	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_861_le ngth_3359_cov_2.1132	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_862_le ngth_3357_cov_2.71502	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_863_le ngth_3352_cov_4.18077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_865_le ngth_3350_cov_3.15417	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_866_le ngth_3342_cov_1.83267	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_867_le ngth_3341_cov_3.63877	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_869_le ngth_3325_cov_2.38777	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_874_le ngth_3294_cov_3.94041	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_877_le ngth_3261_cov_2.79164	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_882_le ngth_3243_cov_2.76317	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_883_le ngth_3240_cov_3.39278	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_885_le ngth_3237_cov_2.89566	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_894_le ngth_3203_cov_2.02668	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_896_le ngth_3200_cov_2.35803	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_897_le ngth_3195_cov_3.47006	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_898_le ngth_3192_cov_3.77271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_899_le ngth_3182_cov_3.33483	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_905_le ngth_3161_cov_7.88249	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_908_le ngth_3145_cov_2.87508	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_909_le ngth_3142_cov_4.52996	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_91_le ngth_20845_cov_6.10154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_912_le ngth_3126_cov_3.08629	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_913_le ngth_3125_cov_8.6342	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_915_le ngth_3119_cov_2.11847	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_916_le ngth_3111_cov_2.81872	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_69xxx_NODE_917_le ngth_3104_cov_3.50148	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_918_le ngth_3102_cov_3.44733	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_919_le ngth_3099_cov_2.6475	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_69xxx_NODE_922_le ngth_3092_cov_2.5647	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_926_le ngth_3070_cov_3.12272	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_69xxx_NODE_929_le ngth_3053_cov_3.3429	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_930_le ngth_3052_cov_15.9231	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_932_le ngth_3047_cov_2.53777	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_69xxx_NODE_933_le ngth_3039_cov_2.59517	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_69xxx_NODE_936_length_3033_cov_18.4486	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_937_length_3032_cov_26.3409	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_939_length_3027_cov_2.86406	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_941_length_3014_cov_7.60595	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_942_length_3012_cov_2.03585	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_943_length_3008_cov_3.12462	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_946_length_3005_cov_2.83119	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_69xxx_NODE_948_length_3001_cov_3.08113	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_96_length_20003_cov_3.50236	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_97_length_19944_cov_7.99201	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_69xxx_NODE_986_length_2905_cov_2.72386	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_71_NODE_18_length_4846_cov_2.41954	0.11	0.26	0.64	0.97	0.01	0.97	Unclassified
NG_14571_71_NODE_19_length_4685_cov_3.19719	0.11	0.26	0.64	0.97	0.01	0.97	Unclassified
NG_14571_71_NODE_36_length_1747_cov_1.70863	0.11	0.26	0.64	0.97	0.01	0.97	Unclassified
NG_14571_74xxx_NODE_21_length_3284_cov_2.50418	0.25	0.19	0.64	0.09	0.27	0.97	Unclassified
NG_14571_75_NODE_34_length_4041_cov_4.15329	0.25	0.19	0.64	0.09	0.27	0.97	Unclassified

NG_14571_75_NODE_39_length_3165_cov_3.23698	0.25	0.19	0.64	0.09	0.27	0.97	Unclassified
NG_14571_75_NODE_70_length_1553_cov_2.3745	0.18	0.22	0.64	0.03	0.34	0.97	Unclassified
NG_14571_76xxx_NODE_12_length_8395_cov_24.7432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_13_length_7503_cov_4.6199	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_27_length_5117_cov_15.6922	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_28_length_5002_cov_2.77481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_29_length_4729_cov_3.00407	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_30_length_4677_cov_2.65837	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_31_length_4559_cov_2.22536	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_32_length_4431_cov_3.55622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_35_length_4264_cov_2.53599	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_36_length_4253_cov_4.97975	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_38_length_4158_cov_3.68462	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_41_length_3474_cov_6.71951	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_42_length_3401_cov_3.76778	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_76xxx_NODE_44_length_3161_cov_15.7946	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_76xxx_NODE_48_len gth_3001_cov_2.8778	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_76xxx_NODE_6_lengt h_13579_cov_4.71926	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_76xxx_NODE_7_lengt h_13331_cov_5.00339	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_76xxx_NODE_86_len gth_1754_cov_2.97116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_76xxx_NODE_9_lengt h_12538_cov_6.97004	0.64	0.08	0.87	0.11	-0.26	0.97	Unclassified
NG_14571_77xxx_NODE_11_len gth_5722_cov_4.0187	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_110_le ngth_1092_cov_1.81581	0.94	0.01	0.97	0.03	-0.34	0.97	Unclassified
NG_14571_77xxx_NODE_122_le ngth_1022_cov_2.51189	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_15_len gth_5426_cov_198.06	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_28_len gth_3144_cov_2.81742	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_30_len gth_3057_cov_1.83711	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_4_lengt h_8421_cov_5.32871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_45_len gth_2264_cov_5.19149	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Anelloviridae
NG_14571_77xxx_NODE_5_lengt h_8289_cov_4.72941	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_77xxx_NODE_9_lengt h_6401_cov_2.89159	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_79_NODE_41_length_ 2447_cov_2.32776	0.12	0.25	0.64	0.05	0.31	0.97	Unclassified

NG_14571_81xxx_NODE_151_len ngth_1350_cov_2.29884	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_160_len ngth_1310_cov_2.31155	0.52	0.10	0.79	0.77	0.05	0.97	Myoviridae
NG_14571_81xxx_NODE_17_len gth_10866_cov_4.11137	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_180_len ngth_1185_cov_1.70265	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_21_len gth_7890_cov_4.83331	0.65	-0.08	0.88	0.89	-0.02	0.97	Myoviridae
NG_14571_81xxx_NODE_212_len ngth_1044_cov_1.72093	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_24_len gth_6355_cov_8.35841	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_29_len gth_5568_cov_2.80337	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_30_len gth_5562_cov_2.53859	0.52	0.10	0.79	0.77	0.05	0.97	Myoviridae
NG_14571_81xxx_NODE_31_len gth_5546_cov_3.75851	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_33_len gth_5395_cov_2.86311	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_34_len gth_5339_cov_8.51911	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_43_len gth_3939_cov_2.98429	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_52_len gth_3540_cov_2.45968	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_53_len gth_3410_cov_2.72638	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_55_len gth_3334_cov_2.56725	0.22	-0.20	0.64	0.20	0.20	0.97	Unclassified

NG_14571_81xxx_NODE_56_len gth_3222_cov_3.35175	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_61_len gth_2835_cov_2.37842	0.69	-0.06	0.93	0.91	-0.02	0.97	Myoviridae
NG_14571_81xxx_NODE_65_len gth_2668_cov_2.23574	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_7_lengt h_32195_cov_137.094	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_81xxx_NODE_81_len gth_2266_cov_2.47354	0.52	0.10	0.79	0.77	0.05	0.97	Unclassified
NG_14571_82xxx_NODE_101_le ngth_10232_cov_12.219	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_1019_l ength_1280_cov_1.81714	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_103_le ngth_10150_cov_12.8631	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_105_le ngth_10052_cov_9.54916	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_106_le ngth_10004_cov_13.5711	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_107_le ngth_9969_cov_125.535	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_108_le ngth_9801_cov_5.04771	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_1083_l ength_1204_cov_1.48738	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_109_le ngth_9693_cov_26.8809	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_11_len gth_34893_cov_28.249	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_113_le ngth_9316_cov_4.36573	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_115_le ngth_9112_cov_9.55007	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_116_le ngth_9012_cov_4.33828	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_118_le ngth_8960_cov_5.11567	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_1218_l ength_1064_cov_1.77899	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_82xxx_NODE_123_le ngth_8714_cov_9.55873	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_125_le ngth_8627_cov_6.49487	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_127_le ngth_8467_cov_10.3483	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_131_le ngth_8269_cov_7.50292	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_132_le ngth_8219_cov_8.41303	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_133_le ngth_8214_cov_3.51591	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_134_le ngth_8178_cov_38.356	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_137_le ngth_8030_cov_3.81229	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_138_le ngth_8022_cov_4.575	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_140_le ngth_7992_cov_4.98879	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_141_le ngth_7943_cov_11.5261	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_145_le ngth_7837_cov_4.92367	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_147_le ngth_7775_cov_11.2234	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_148_le ngth_7734_cov_6.85089	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_149_le ngth_7667_cov_5.21479	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_154_le ngth_7464_cov_6.90808	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_155_le ngth_7464_cov_4.07113	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_160_le ngth_7329_cov_7.70759	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_161_le ngth_7317_cov_5.36381	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_162_le ngth_7241_cov_4.39146	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_164_le ngth_7139_cov_6.94241	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_165_le ngth_7085_cov_5.94708	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_166_le ngth_7071_cov_31.0589	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_167_le ngth_7070_cov_33.4509	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_170_le ngth_6981_cov_4.25224	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_172_le ngth_6964_cov_39.6193	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_173_le ngth_6874_cov_3.10632	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_174_le ngth_6835_cov_7.32891	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_177_le ngth_6806_cov_7.12576	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_178_le ngth_6804_cov_3.65358	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_181_le ngth_6700_cov_15.9211	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_182_le ngth_6651_cov_7.87796	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_82xxx_NODE_183_le ngth_6646_cov_5.62145	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_186_le ngth_6603_cov_4.58674	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_188_le ngth_6509_cov_3.5736	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_190_le ngth_6493_cov_11.0014	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_192_le ngth_6468_cov_5.36582	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_195_le ngth_6454_cov_60.4208	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_197_le ngth_6431_cov_3.98494	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_198_le ngth_6423_cov_17.3373	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_203_le ngth_6369_cov_5.05179	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_207_le ngth_6314_cov_4.15546	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_210_le ngth_6244_cov_10.1813	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_211_le ngth_6239_cov_10.4895	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_216_length_6131_cov_6.82423	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_219_length_6077_cov_3.56526	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_228_length_5873_cov_4.07013	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_229_length_5850_cov_9.37118	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_23_length_21703_cov_4.29111	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_82xxx_NODE_233_length_5753_cov_7.57617	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_238_length_5687_cov_5.14613	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_24_length_21013_cov_8.35175	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_242_length_5612_cov_3.79971	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_243_length_5610_cov_7.91683	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_246_length_5587_cov_39.5766	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_247_length_5583_cov_11.2317	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_251_length_5546_cov_9.43325	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_252_length_5544_cov_10.9525	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_260_length_5414_cov_4.23922	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_261_length_5390_cov_21.7829	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_82xxx_NODE_263_le ngth_5346_cov_3.69741	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_264_le ngth_5337_cov_4.8404	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_270_le ngth_5300_cov_4.74318	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_272_le ngth_5290_cov_4.11442	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_277_le ngth_5189_cov_3.24309	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_280_le ngth_5061_cov_3.70875	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_285_le ngth_5003_cov_4.27107	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_287_le ngth_4978_cov_5.15742	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_288_le ngth_4909_cov_4.11537	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_290_le ngth_4877_cov_4.62609	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_293_le ngth_4836_cov_4.10228	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_294_le ngth_4831_cov_4.04941	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_295_le ngth_4828_cov_6.69642	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_296_le ngth_4826_cov_4.22322	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_298_le ngth_4805_cov_3.40379	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_301_le ngth_4746_cov_11.2156	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_303_le ngth_4701_cov_7.03932	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_304_le ngth_4697_cov_2.43753	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_305_le ngth_4695_cov_2.61272	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_31_len gth_18313_cov_6.52514	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_310_le ngth_4658_cov_20.4523	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_311_le ngth_4621_cov_2.31559	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_312_le ngth_4604_cov_4.14926	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_313_le ngth_4590_cov_10.9427	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_317_le ngth_4542_cov_6.42746	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_318_le ngth_4518_cov_2.21331	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_320_le ngth_4493_cov_3.37584	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_325_le ngth_4436_cov_3.14106	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_33_len gth_18072_cov_17.0051	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_330_le ngth_4382_cov_3.34181	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_333_le ngth_4370_cov_3.73048	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_334_le ngth_4353_cov_3.48837	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_335_le ngth_4351_cov_37.2284	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_336_le ngth_4349_cov_23.2769	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_337_le ngth_4281_cov_2.58992	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_34_le ngth_18065_cov_11.2668	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_340_le ngth_4250_cov_2.65578	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_342_le ngth_4221_cov_13.596	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_346_le ngth_4193_cov_3.49831	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_348_le ngth_4170_cov_3.53487	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_351_le ngth_4060_cov_22.2694	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_358_le ngth_4024_cov_3.42908	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_364_le ngth_3915_cov_6.5796	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_369_le ngth_3889_cov_4.4614	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_370_le ngth_3889_cov_4.0313	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_372_le ngth_3869_cov_4.12559	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_377_le ngth_3814_cov_12.5009	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_379_le ngth_3803_cov_3.12967	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_383_le ngth_3759_cov_3.34233	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_391_le ngth_3681_cov_1.96773	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_392_le ngth_3679_cov_35.7395	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_394_le ngth_3640_cov_4.37322	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_40_len gth_16970_cov_7.58191	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_402_le ngth_3602_cov_3.32168	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_411_le ngth_3522_cov_6.74733	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_416_le ngth_3507_cov_5.03592	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_418_le ngth_3485_cov_3.64752	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_422_le ngth_3423_cov_3.48872	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_424_le ngth_3400_cov_2.61136	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_425_le ngth_3399_cov_3.55443	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_82xxx_NODE_426_le ngth_3396_cov_10.6277	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_427_le ngth_3378_cov_2.87902	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_429_le ngth_3366_cov_6.16672	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_43_len gth_16865_cov_9.47329	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_433_le ngth_3328_cov_34.4788	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_436_le ngth_3312_cov_2.57783	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_440_le ngth_3279_cov_3.77605	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_441_le ngth_3278_cov_24.0341	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_445_le ngth_3207_cov_5.50349	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_446_le ngth_3203_cov_2.94663	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_447_le ngth_3187_cov_43.3771	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_82xxx_NODE_448_le ngth_3185_cov_3.43802	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_453_le ngth_3155_cov_4.11194	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_454_le ngth_3151_cov_3.62661	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_455_le ngth_3147_cov_3.11805	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_457_le ngth_3134_cov_4.19162	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_461_le ngth_15580_cov_14.8844	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_462_le ngth_3110_cov_10.8295	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_465_le ngth_3086_cov_3.52029	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_467_le ngth_3080_cov_2.4919	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_469_length_3074_cov_4.58132	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_47_length_15393_cov_58.8798	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_470_length_3067_cov_2.99768	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_471_length_3056_cov_3.60447	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_475_length_3025_cov_2.21785	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_476_length_3014_cov_2.13214	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_50_length_15100_cov_14.1315	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_526_length_2662_cov_2.85002	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_53_length_14663_cov_20.5088	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_54_length_14613_cov_12.6218	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_56_length_14251_cov_9.91484	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_82xxx_NODE_575_length_2380_cov_3.66452	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_63_length_13832_cov_5.60739	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_64_length_13742_cov_124.822	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_65_length_13653_cov_11.0451	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_68_length_12953_cov_7.78532	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_82xxx_NODE_71_len gth_12647_cov_96.8883	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_73_len gth_12538_cov_14.7015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_762_le ngth_1702_cov_18.6503	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_77_len gth_12049_cov_5.23528	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_82_len gth_11388_cov_7.81197	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_83_len gth_11384_cov_4.95684	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_85_len gth_11076_cov_5.3271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_852_le ngth_1515_cov_1.83219	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_86_len gth_11009_cov_4.00266	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_88_len gth_10981_cov_13.2799	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_89_len gth_10807_cov_9.66536	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_90_len gth_10747_cov_9.27591	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_92_len gth_10665_cov_7.27097	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_93_len gth_10661_cov_4.30634	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_95_len gth_10612_cov_6.80506	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_82xxx_NODE_967_le ngth_1343_cov_1.92158	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_82xxx_NODE_971_length_1339_cov_52.4276	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_98_length_10476_cov_7.54592	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_82xxx_NODE_99_length_10428_cov_4.31437	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_83xxx_NODE_30_length_8675_cov_4.15847	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_83xxx_NODE_31_length_8603_cov_4.50515	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_83xxx_NODE_64_length_4035_cov_57.0045	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_83xxx_NODE_67_length_3875_cov_17.2783	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_83xxx_NODE_72_length_3572_cov_2.53682	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_84_NODE_22_length_5992_cov_2.87081	0.28	0.17	0.64	0.52	-0.10	0.97	Unclassified
NG_14571_84_NODE_42_length_3809_cov_2.87587	0.28	0.17	0.64	0.52	-0.10	0.97	Unclassified
NG_14571_85xxx_NODE_104_length_3923_cov_3.44984	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_85xxx_NODE_107_length_3739_cov_3.50054	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_85xxx_NODE_109_length_3724_cov_3.13192	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_85xxx_NODE_111_length_3529_cov_3.81318	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_85xxx_NODE_113_length_3418_cov_1.8769	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_85xxx_NODE_118_length_3271_cov_2.34391	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_85xxx_NODE_128_le ngth_2934_cov_2.91212	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_143_le ngth_2412_cov_1.92321	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_85xxx_NODE_145_le ngth_2354_cov_3.67464	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_146_le ngth_2341_cov_6.77559	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_153_le ngth_2266_cov_1.89959	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_175_le ngth_2020_cov_2.23206	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_199_le ngth_1709_cov_1.5127	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_243_le ngth_1401_cov_2.68871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_85xxx_NODE_259_le ngth_1321_cov_2.42654	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_85xxx_NODE_271_le ngth_1251_cov_1.70903	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_335_le ngth_1051_cov_2.59538	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_349_le ngth_1022_cov_1.5243	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_42_len gth_11773_cov_8.95264	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_44_len gth_11111_cov_4.64942	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_50_len gth_10382_cov_8.73855	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_52_len gth_9913_cov_3.37604	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_85xxx_NODE_58_len gth_8413_cov_4.16906	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_61_len gth_8229_cov_6.39552	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_65_len gth_7458_cov_4.08105	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_70_len gth_6776_cov_3.45068	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_72_len gth_6720_cov_5.28162	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_76_len gth_6119_cov_3.40881	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_80_len gth_5786_cov_24.6727	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_85xxx_NODE_84_len gth_5498_cov_6.7077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_89_len gth_4898_cov_3.32975	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_91_len gth_4728_cov_2.7156	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_92_len gth_4725_cov_56.0073	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_93_len gth_4640_cov_2.86521	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_94_len gth_4601_cov_74.3159	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_85xxx_NODE_95_len gth_4462_cov_3.01271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_98_len gth_4326_cov_2.64645	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_85xxx_NODE_99_len gth_4217_cov_3.40437	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_86xxx_NODE_127_len ngth_1871_cov_1.77919	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_146_len ngth_1650_cov_2.92727	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_158_len ngth_1538_cov_2.6116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_20_len gth_8663_cov_16.3711	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_21_len gth_8324_cov_8.37078	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_22_len gth_7926_cov_3.76416	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_27_len gth_7529_cov_5.36259	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_31_len gth_6405_cov_6.78724	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_40_len gth_5187_cov_26.6269	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_42_len gth_5024_cov_3.47595	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_43_len gth_4882_cov_2.94054	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_44_len gth_4850_cov_2.28342	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_47_len gth_4470_cov_4.66614	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_86xxx_NODE_48_len gth_4380_cov_9.07098	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_54_len gth_3925_cov_2.75504	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_57_len gth_3799_cov_2.18803	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_86xxx_NODE_62_len gth_3589_cov_3.52547	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_14571_86xxx_NODE_65_len gth_3385_cov_2.26607	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_67_len gth_3310_cov_2.8129	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_68_len gth_3299_cov_2.80425	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_69_len gth_3270_cov_2.77667	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_72_len gth_3236_cov_10.3467	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_73_len gth_3235_cov_2.93679	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_76_len gth_3155_cov_3.23613	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_86xxx_NODE_78_len gth_3022_cov_3.5541	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_87xxx_NODE_13_len gth_8065_cov_3.55381	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_87xxx_NODE_26_len gth_4527_cov_3.17531	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_87xxx_NODE_32_len gth_3526_cov_2.23768	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_87xxx_NODE_46_len gth_2747_cov_6.10327	0.64	-0.08	0.87	0.83	0.03	0.97	Unclassified
NG_14571_89_NODE_101_length _5403_cov_14.3018	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_105_length _5313_cov_3.43077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_106_length _5300_cov_2.88713	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_89_NODE_107_length _5261_cov_3.62735	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_108_length _5149_cov_4.19297	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_109_length _5104_cov_59.7643	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_111_length _5010_cov_7.68052	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_114_length _4933_cov_3.93419	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_116_length _4872_cov_4.0328	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_117_length _4846_cov_3.2799	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_118_length _4757_cov_6.59124	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_122_length _4547_cov_4.01514	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_124_length _4392_cov_3.78326	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_126_length _4260_cov_2.81094	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_128_length _4153_cov_26.4922	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_134_length _3993_cov_2.90528	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_135_length _3942_cov_4.23437	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_136_length _3939_cov_2.61509	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_139_length _3923_cov_2.09488	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_89_NODE_140_length _3911_cov_59.3791	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_142_length _3811_cov_3.67758	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_144_length _3800_cov_3.0737	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_146_length _3749_cov_31.5555	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_149_length _3554_cov_2425.04	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_152_length _3465_cov_13.3487	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_153_length _3459_cov_2.31904	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_154_length _3440_cov_3.78405	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_155_length _3438_cov_2.34112	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_158_length _3370_cov_2.44977	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_159_length _3349_cov_6.2544	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_16_length _20510_cov_38.459	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_160_length _3270_cov_16.8781	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_161_length _3235_cov_6.33145	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_162_length _3223_cov_2.28157	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_89_NODE_163_length _3221_cov_2.88471	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_89_NODE_165_length_3205_cov_2.43778	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_166_length_3204_cov_4.80216	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_167_length_3157_cov_2.38717	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_168_length_3149_cov_23.2088	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_170_length_3133_cov_2.49805	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_174_length_3075_cov_2.25232	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_178_length_3047_cov_3.8877	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_18_length_19601_cov_391.95	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_20_length_17851_cov_17.0069	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_218_length_2347_cov_2.80148	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_22_length_17040_cov_6.17733	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_227_length_2213_cov_32.0181	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_269_length_1700_cov_1.93495	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_29_length_13124_cov_7.48718	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_31_length_13086_cov_9.73624	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_33_length_12479_cov_60.2349	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae

NG_14571_89_NODE_34_length_12356_cov_6.26421	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_36_length_12020_cov_26.2874	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_39_length_11482_cov_6.83583	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_398_length_1035_cov_2.94796	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_4_length_35208_cov_14.1072	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_40_length_11176_cov_7.72035	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_43_length_10608_cov_21.3894	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_45_length_10123_cov_14.4299	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_49_length_9265_cov_52.3717	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_52_length_8964_cov_3.61028	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_53_length_8719_cov_25.7383	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_54_length_8214_cov_10.9746	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_55_length_8166_cov_10.6949	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_58_length_8032_cov_7.92854	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_60_length_7967_cov_60.8333	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_63_length_7827_cov_4.25875	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_89_NODE_66_length_7524_cov_15.9068	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_68_length_7498_cov_6.27959	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_73_length_7233_cov_4.94316	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_8_length_26366_cov_7.09361	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_81_length_6620_cov_3.42133	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_82_length_6606_cov_4.59686	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_85_length_6401_cov_105.32	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_86_length_6391_cov_6.27494	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_87_length_6378_cov_2.90068	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_89_length_6226_cov_6.32102	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_94_length_5768_cov_5.17311	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_95_length_5711_cov_4.97595	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_97_length_5574_cov_2.69444	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_98_length_5509_cov_10.7763	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_89_NODE_99_length_5500_cov_4.61194	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_90xxx_NODE_103_length_4763_cov_5.83645	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_90xxx_NODE_113_le ngth_4288_cov_2.88235	0.21	-0.20	0.64	0.64	-0.08	0.97	Unclassified
NG_14571_90xxx_NODE_127_le ngth_3886_cov_3.49595	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_90xxx_NODE_128_le ngth_3871_cov_2.74319	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_90xxx_NODE_134_le ngth_3700_cov_3.0321	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_90xxx_NODE_149_le ngth_3377_cov_4.34076	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_90xxx_NODE_186_le ngth_2784_cov_2.53499	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_90xxx_NODE_289_le ngth_1911_cov_2.16379	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_90xxx_NODE_511_le ngth_1347_cov_2.89861	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_14571_90xxx_NODE_86_len gth_5359_cov_6.96192	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_100_le ngth_7312_cov_5.10349	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_101_le ngth_7270_cov_7.01982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_102_le ngth_7152_cov_36.8791	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_109_le ngth_6791_cov_3.41271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_110_le ngth_6787_cov_8.97683	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_112_le ngth_6710_cov_39.7289	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_113_le ngth_6608_cov_7.00382	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_91xxx_NODE_123_le ngth_6114_cov_6.06734	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_127_le ngth_5987_cov_3.33227	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_128_le ngth_5874_cov_2.55405	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_13_le ngth_39687_cov_62.4301	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_131_le ngth_5742_cov_2.70072	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_137_le ngth_5400_cov_2.85351	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_138_le ngth_5372_cov_6.39703	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_141_le ngth_5026_cov_5.00382	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_143_le ngth_4938_cov_12.3696	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_144_le ngth_4930_cov_3.08021	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_146_le ngth_4873_cov_8.80884	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_150_le ngth_4775_cov_23.6761	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_151_le ngth_4713_cov_2.85444	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_152_le ngth_4672_cov_2.35954	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_157_le ngth_4383_cov_52.8371	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_158_le ngth_4295_cov_2.8592	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_91xxx_NODE_159_le ngth_4266_cov_2.83116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_162_le ngth_4135_cov_3.01838	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_163_le ngth_4059_cov_3.35015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_164_le ngth_3965_cov_182.31	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_166_le ngth_3847_cov_2.73075	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_167_le ngth_3817_cov_18.1986	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_170_le ngth_3766_cov_2.22501	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_172_le ngth_3722_cov_3.71884	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_173_le ngth_3706_cov_5.30816	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_174_le ngth_3677_cov_4.74406	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_177_le ngth_3575_cov_2.46392	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_178_le ngth_3548_cov_2.6095	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_183_le ngth_3442_cov_17.5282	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_184_le ngth_3431_cov_3.58649	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_185_le ngth_3420_cov_14.4639	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_187_le ngth_3385_cov_2.74745	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_91xxx_NODE_188_le ngth_3350_cov_9.25159	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_189_le ngth_3343_cov_4.28345	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_190_le ngth_3319_cov_3.13603	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_191_le ngth_3310_cov_2.45284	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_195_le ngth_3233_cov_2.07048	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_196_le ngth_3219_cov_6.40676	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_197_le ngth_3153_cov_2.34958	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_198_le ngth_3151_cov_64.313	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_199_le ngth_3119_cov_2.79439	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_200_le ngth_3112_cov_3.32908	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_202_le ngth_3097_cov_2.13018	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_203_le ngth_3085_cov_15.33	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_204_le ngth_3085_cov_2.30264	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_205_le ngth_3077_cov_2.58173	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_208_le ngth_3050_cov_2.37362	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_217_le ngth_2841_cov_2.38478	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_91xxx_NODE_222_length_2776_cov_2.63359	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_258_length_2289_cov_1.95613	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_91xxx_NODE_26_length_20899_cov_4.23196	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_91xxx_NODE_311_length_1865_cov_1.6989	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_91xxx_NODE_315_length_1852_cov_2.43517	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_323_length_1782_cov_1.8095	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_338_length_1695_cov_2.57317	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_34_length_16761_cov_122.181	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_35_length_16530_cov_27.34	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_36_length_16450_cov_4.00647	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_373_length_1456_cov_3.33333	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_46_length_14183_cov_5.15027	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_49_length_13254_cov_8.97932	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_50_length_13188_cov_14.2565	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_53_length_12975_cov_4.35201	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_91xxx_NODE_54_length_12958_cov_110.097	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_91xxx_NODE_6_lengt h_43156_cov_13.2864	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_14571_91xxx_NODE_61_len gth_11957_cov_4.69501	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_68_len gth_10667_cov_5.96787	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_69_len gth_10405_cov_8.48106	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_71_len gth_10166_cov_8.54792	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_74_len gth_9957_cov_37.6588	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_76_len gth_9834_cov_7.48216	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_77_len gth_9630_cov_8.34883	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_78_len gth_9598_cov_6.65619	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_81_len gth_9235_cov_49.8069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_83_len gth_9170_cov_6.85815	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_84_len gth_9152_cov_3.62229	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
NG_14571_91xxx_NODE_85_len gth_8887_cov_12.8632	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_86_len gth_8773_cov_4.43462	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_87_len gth_8751_cov_4.56279	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_89_len gth_8497_cov_24.4271	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_91xxx_NODE_90_len gth_8425_cov_6.18172	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_92_len gth_8339_cov_7.97079	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_93_len gth_8260_cov_12.8191	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_94_len gth_8052_cov_262.957	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_96_len gth_7712_cov_9.53206	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_97_len gth_7533_cov_3.81706	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_91xxx_NODE_98_len gth_7502_cov_3.61206	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_92xxx_NODE_101_le ngth_6147_cov_40.9375	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_102_le ngth_6065_cov_76.3652	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_103_le ngth_5982_cov_5.60182	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_105_le ngth_5927_cov_4.4346	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_108_le ngth_5755_cov_18.5072	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_111_len gth_16373_cov_1262.61	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_111_le ngth_5646_cov_4.31479	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_119_le ngth_5439_cov_99.9361	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_120_le ngth_5425_cov_586.669	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified

NG_14571_92xxx_NODE_121_le ngth_5414_cov_7.16925	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_122_le ngth_5369_cov_14.7542	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_123_le ngth_5338_cov_3.06511	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_125_le ngth_5280_cov_46.3267	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_127_le ngth_5104_cov_41.3268	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_131_le ngth_4897_cov_1850.21	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_132_le ngth_4839_cov_65.7329	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_133_le ngth_4800_cov_136.294	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_135_le ngth_4764_cov_3.268	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_138_le ngth_4695_cov_41.3931	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_140_le ngth_4592_cov_41.7858	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_141_le ngth_4552_cov_298.822	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_145_le ngth_4476_cov_10.399	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_155_le ngth_4062_cov_11.3127	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_156_le ngth_4024_cov_3.17813	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_158_le ngth_3924_cov_2.79607	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified

NG_14571_92xxx_NODE_163_le ngth_3829_cov_176.209	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_164_le ngth_3790_cov_3.53681	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_165_le ngth_3755_cov_9.17108	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_168_le ngth_3649_cov_3.47273	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_169_le ngth_3622_cov_3.82562	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_170_le ngth_3612_cov_10.2426	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_172_le ngth_3588_cov_81.3753	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_173_le ngth_3585_cov_6.19037	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_174_le ngth_3583_cov_4.14399	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_178_le ngth_3521_cov_4.8468	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_182_le ngth_3422_cov_327.29	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_183_le ngth_3415_cov_2.34881	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_184_le ngth_3413_cov_472.097	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_187_le ngth_3322_cov_3.03275	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_19_len gth_14782_cov_92.7323	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_193_le ngth_3165_cov_2.83119	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified

NG_14571_92xxx_NODE_194_len ngth_3135_cov_83.3	0.08	-0.28	0.64	0.63	-0.08	0.97	Unclassified
NG_14571_92xxx_NODE_20_len gth_14587_cov_70.2764	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_200_len ngth_3005_cov_9.74339	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_26_len gth_13273_cov_196.039	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_30_len gth_12576_cov_79.8995	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_34_len gth_11611_cov_3.48962	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_35_len gth_11571_cov_6.05662	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_40_len gth_11029_cov_44.2385	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_45_len gth_10420_cov_179.014	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_46_len gth_10412_cov_7.12658	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_51_len gth_9892_cov_1406.17	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_52_len gth_9865_cov_18.6397	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_55_len gth_9540_cov_549.264	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_58_len gth_9197_cov_8.34752	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_59_len gth_9139_cov_1689.27	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_60_len gth_9120_cov_15.1455	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified

NG_14571_92xxx_NODE_61_len gth_9097_cov_215.138	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_63_len gth_9067_cov_41.0887	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_64_len gth_9055_cov_135.875	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_65_len gth_9030_cov_6.18897	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_67_len gth_8932_cov_5.87991	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_7_lengt h_19941_cov_868.128	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_70_len gth_8783_cov_92.0182	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_71_len gth_8635_cov_22.7608	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_74_len gth_8534_cov_64.2187	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_76_len gth_8407_cov_956.097	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_77_len gth_8343_cov_10.1228	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_78_len gth_8291_cov_5.52416	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_79_len gth_8183_cov_14.2478	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_80_len gth_8141_cov_762.032	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_84_len gth_7837_cov_15.38	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_89_len gth_7614_cov_405.519	0.08	-0.28	0.64	0.63	-0.08	0.97	Unclassified

NG_14571_92xxx_NODE_9_lengt h_17964_cov_34.5539	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_92xxx_NODE_97_len gth_6550_cov_64.7216	0.25	-0.19	0.64	0.83	-0.03	0.97	Unclassified
NG_14571_93xxx_NODE_100_le ngth_10711_cov_109.982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1000_1 ength_3413_cov_6.22662	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1001_1 ength_3411_cov_4.52235	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1003_1 ength_3397_cov_2.57121	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1004_1 ength_3395_cov_30.1922	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1005_1 ength_3392_cov_10.6874	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1006_1 ength_3389_cov_106.58	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1007_1 ength_3380_cov_3.46406	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1008_1 ength_3378_cov_86.7942	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1009_1 ength_3373_cov_1.55907	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1011_1 ength_3372_cov_5.46066	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1012_1 ength_3372_cov_3.4697	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1013_1 ength_3372_cov_2.92765	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1014_1 ength_3371_cov_4.44481	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_1016_1 ength_3368_cov_11.0244	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1017_1 ength_3367_cov_73.3367	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1018_1 ength_3366_cov_2.14014	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_102_le ngth_10612_cov_12.1996	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1020_1 ength_3363_cov_3.84492	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1021_1 ength_3361_cov_6.57139	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1023_1 ength_3347_cov_6.42254	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1024_1 ength_3345_cov_3.55289	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1028_1 ength_3339_cov_28.3331	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1029_1 ength_3339_cov_3.49574	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1030_1 ength_3321_cov_8.16901	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1031_1 ength_3321_cov_5.29026	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1032_1 ength_3321_cov_3.44795	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1033_1 ength_3309_cov_8.14843	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1037_1 ength_3301_cov_3.60608	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1038_1 ength_3295_cov_52.5988	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_104_length_10499_cov_58.374	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1041_length_3280_cov_5.0862	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1043_length_3275_cov_4.77826	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1044_length_3270_cov_77.3456	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1045_length_3270_cov_10.2367	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1046_length_3267_cov_3.82908	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1047_length_3266_cov_85.1788	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1048_length_3263_cov_10.3547	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1049_length_3259_cov_2.58084	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_105_length_10473_cov_97.113	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1050_length_3257_cov_31.2936	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1052_length_3248_cov_4.59474	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1055_length_3246_cov_12.4071	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1056_length_3244_cov_3.10536	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1057_length_3234_cov_7.75181	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1058_length_3231_cov_6.99559	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_1059_1 ength_3224_cov_14.7889	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_106_1e ngth_10454_cov_215.885	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1063_1 ength_3214_cov_5.38207	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1064_1 ength_3213_cov_3.46802	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1065_1 ength_3210_cov_6.59357	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1066_1 ength_3206_cov_2.65122	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1067_1 ength_3202_cov_76.3391	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1069_1 ength_3195_cov_4.16561	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_107_1e ngth_10431_cov_107.261	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1070_1 ength_3187_cov_2.1871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1071_1 ength_3186_cov_18.8272	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1073_1 ength_3185_cov_8.75272	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_14571_93xxx_NODE_1075_1 ength_3183_cov_3.27653	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1076_1 ength_3180_cov_2.38592	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1078_1 ength_3178_cov_5.91483	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1079_1 ength_3178_cov_5.10983	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_108_1 ength_10376_cov_8.4424	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1080_1 ength_3177_cov_7.48943	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1081_1 ength_3158_cov_40.1643	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1082_1 ength_3143_cov_34.7215	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1083_1 ength_3139_cov_7.63424	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1084_1 ength_3134_cov_17.6974	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1085_1 ength_3124_cov_2.85782	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1086_1 ength_3113_cov_5.60595	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1087_1 ength_3111_cov_2.76571	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1088_1 ength_3108_cov_6.18506	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1089_1 ength_3107_cov_6.09338	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1090_1 ength_3104_cov_34.1778	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1092_1 ength_3094_cov_12.7516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1093_1 ength_3089_cov_665.469	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1095_1 ength_3082_cov_3.47836	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1097_1 ength_3080_cov_11.8207	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_1098_1 ength_3079_cov_29.752	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1099_1 ength_3077_cov_3.01191	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_110_1e ngth_10336_cov_49.2109	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1100_1 ength_3076_cov_29.3635	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1101_1 ength_3074_cov_39.6933	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1102_1 ength_3072_cov_382.612	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1106_1 ength_3061_cov_2.1477	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1107_1 ength_3057_cov_2.9437	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1108_1 ength_3056_cov_46.8914	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1109_1 ength_3053_cov_179.333	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_111_1e ngth_10325_cov_12.0481	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1110_1 ength_3050_cov_3.49015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1112_1 ength_3046_cov_19.2989	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1115_1 ength_3042_cov_6.22297	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1116_1 ength_3042_cov_3.076	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1118_1 ength_3040_cov_2.21139	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_1119_1 ength_3036_cov_3.3737	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_112_le ngth_10287_cov_3.70964	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1120_1 ength_3031_cov_2.33703	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1121_1 ength_3026_cov_10.5695	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1122_1 ength_3018_cov_2.0162	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1123_1 ength_3014_cov_6.84792	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1124_1 ength_3011_cov_3.51827	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1125_1 ength_3009_cov_7.73009	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1126_1 ength_3004_cov_18.6775	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_114_le ngth_10181_cov_35.0833	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_115_le ngth_10142_cov_20.5841	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_117_le ngth_10048_cov_9.30101	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_119_le ngth_10010_cov_157.742	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_12_len gth_18984_cov_48.5357	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_120_le ngth_9999_cov_27.5343	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_121_le ngth_9986_cov_133.641	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_122_le ngth_9971_cov_124.766	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_123_le ngth_9949_cov_11.067	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_124_le ngth_9936_cov_5.40381	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_125_le ngth_9887_cov_35.8448	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_126_le ngth_9834_cov_14.4083	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1264_l ength_2643_cov_3.04946	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_128_le ngth_9782_cov_13.9967	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_129_le ngth_9772_cov_33.7908	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_130_le ngth_9714_cov_42.311	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1307_l ength_2542_cov_2.19381	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_131_le ngth_9712_cov_7.40686	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_132_le ngth_9683_cov_61.8232	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_133_le ngth_9656_cov_38.2178	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1333_l ength_2467_cov_2.3749	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_134_le ngth_9655_cov_14.4567	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_136_le ngth_9595_cov_4.77945	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_1361_le ngth_2402_cov_3.58117	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_138_le ngth_9560_cov_25.1322	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_140_le ngth_9542_cov_34.0078	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_141_le ngth_9541_cov_9.55018	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_142_le ngth_9541_cov_6.74004	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_143_le ngth_9524_cov_6.26159	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_144_le ngth_9509_cov_4.94077	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_145_le ngth_9460_cov_74.5117	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_146_le ngth_9452_cov_29.1979	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_147_le ngth_9443_cov_5.56966	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_148_le ngth_9433_cov_47.9555	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_149_le ngth_9414_cov_10.9515	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_150_le ngth_9397_cov_32.5643	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_153_le ngth_9369_cov_10.4491	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_154_le ngth_9236_cov_40.7505	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_155_le ngth_9216_cov_10.6834	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_156_length_9163_cov_5.73485	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_157_length_9098_cov_158.081	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_158_length_9090_cov_10.0307	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1594_length_2003_cov_2.35832	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_93xxx_NODE_160_length_9036_cov_18.8497	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_162_length_9005_cov_39.1369	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_163_length_9005_cov_8.0124	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_164_length_8987_cov_204.021	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_165_length_8987_cov_12.3839	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_167_length_8923_cov_19.021	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_168_length_8914_cov_6.45062	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_169_length_8891_cov_15.1959	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_17_length_18044_cov_25.2174	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_171_length_8869_cov_32.7333	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_173_length_8834_cov_13.6992	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_174_length_8823_cov_37.4487	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_175_length_8794_cov_25.2799	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_176_length_8793_cov_16.8497	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_177_length_8769_cov_22.2629	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1777_length_1710_cov_8.59879	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_14571_93xxx_NODE_179_length_8747_cov_51.1928	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_18_length_17662_cov_21.9375	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_180_length_8740_cov_6.22994	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_182_length_8734_cov_16.6935	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_183_length_8676_cov_99.6764	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_184_length_8674_cov_15.5289	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_185_length_8649_cov_9.55562	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_186_length_8619_cov_36.5819	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_1869_length_1605_cov_2.75935	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_187_length_8617_cov_6.64751	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_188_length_8603_cov_11.1311	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_189_length_8577_cov_25.8161	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_1891_1 ength_1576_cov_2.6522	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_190_le ngth_8566_cov_12.9982	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_193_le ngth_8528_cov_10.8054	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_195_le ngth_8480_cov_143.297	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_1956_1 ength_1506_cov_2.16402	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_196_le ngth_8473_cov_6.12746	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_197_le ngth_8432_cov_14.1997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_198_le ngth_8423_cov_10.8289	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_199_le ngth_8421_cov_15.1396	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_200_le ngth_8392_cov_103.397	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_201_le ngth_8382_cov_108.863	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_202_le ngth_8370_cov_4.36332	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_205_le ngth_8336_cov_8.459	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_2065_1 ength_1420_cov_2.82418	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_207_le ngth_8321_cov_6.30583	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_208_le ngth_8306_cov_38.2139	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_209_length_8288_cov_61.7731	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_21_length_17068_cov_197.428	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_211_length_8276_cov_23.2921	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_214_length_8189_cov_4.75559	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_217_length_8155_cov_9.89753	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_218_length_8140_cov_4.51973	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_219_length_8136_cov_5.01968	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_22_length_16978_cov_106.05	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_220_length_8134_cov_14.1386	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_221_length_8130_cov_3.71319	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_222_length_8129_cov_5.8811	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_2228_length_1270_cov_1.69877	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_224_length_8111_cov_13.8396	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_225_length_8094_cov_149.596	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_226_length_8083_cov_3.84106	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_227_length_8077_cov_43.2473	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_228_length_8049_cov_32.7367	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_229_length_8028_cov_7.83519	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_23_length_16910_cov_12.5512	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_230_length_8026_cov_7.54347	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_231_length_8019_cov_9.72903	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_232_length_8014_cov_7.06785	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_233_length_8012_cov_20.9795	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_234_length_7973_cov_5.72847	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_235_length_7960_cov_103.522	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_236_length_7955_cov_69.92	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_237_length_7951_cov_26.3823	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_238_length_7932_cov_12.328	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_239_length_7914_cov_10.4856	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_24_length_16758_cov_10.5815	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_240_length_7908_cov_61.1142	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_242_length_7901_cov_12.888	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_243_le ngth_7888_cov_9.06753	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_244_le ngth_7888_cov_5.50504	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_245_le ngth_7877_cov_24.6516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_247_le ngth_7846_cov_106.973	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_248_le ngth_7843_cov_42.2169	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_249_le ngth_7836_cov_4.97314	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_25_le ngth_16592_cov_10.3565	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_250_le ngth_7822_cov_9.17742	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_251_le ngth_7819_cov_5.50116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_252_le ngth_7812_cov_10.0727	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_253_le ngth_7801_cov_7.65169	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_254_le ngth_7788_cov_5.72081	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_256_le ngth_7743_cov_10.4493	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_257_le ngth_7725_cov_12.6258	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_258_le ngth_7725_cov_4.46949	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_259_le ngth_7720_cov_29.4581	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_26_len ngth_16454_cov_6.17275	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_260_le ngth_7711_cov_7.22962	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_261_le ngth_7711_cov_6.22871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_263_le ngth_7700_cov_65.8595	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_264_le ngth_7694_cov_7.30501	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_265_le ngth_7693_cov_11.483	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_269_le ngth_7579_cov_26.5518	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_27_len ngth_16274_cov_7.4869	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_270_le ngth_7577_cov_37.0284	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_272_le ngth_7517_cov_41.4244	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_273_le ngth_7506_cov_7.34103	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_274_le ngth_7504_cov_14.9211	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_275_le ngth_7496_cov_7.1997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_276_le ngth_7495_cov_32.9272	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_277_le ngth_7492_cov_21.8849	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_278_le ngth_7482_cov_3.42453	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_279_length_7469_cov_13.1244	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_28_length_16069_cov_43.3905	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_281_length_7439_cov_24.0444	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_284_length_7415_cov_25.8561	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_285_length_7408_cov_18.4432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_286_length_7375_cov_109.221	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_287_length_7367_cov_101.947	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_288_length_7363_cov_143.72	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_29_length_15985_cov_4.62429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_290_length_7342_cov_16.7435	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_291_length_7313_cov_69.4267	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_292_length_7303_cov_158.019	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_294_length_7297_cov_5.80061	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_295_length_7288_cov_28.811	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_296_length_7287_cov_4.97608	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_299_length_7273_cov_154.65	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_300_le ngth_7273_cov_8.01441	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_302_le ngth_7239_cov_24.4471	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_303_le ngth_7230_cov_10.2404	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_304_le ngth_7215_cov_7.02835	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_305_le ngth_7199_cov_154.283	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_306_le ngth_7194_cov_6.26516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_307_le ngth_7181_cov_8.02554	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_308_le ngth_7164_cov_22.4289	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_309_le ngth_7164_cov_8.35687	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_311_le ngth_15869_cov_14.6512	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_311_le ngth_7152_cov_4.474	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_313_le ngth_7135_cov_43.8661	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_314_le ngth_7115_cov_12.2907	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_315_le ngth_7100_cov_123.27	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_316_le ngth_7083_cov_7.4587	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_318_le ngth_7057_cov_9.10026	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_319_le ngth_7046_cov_197.565	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_32_le ngth_15688_cov_163.797	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_320_le ngth_7015_cov_6.4329	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_321_le ngth_7006_cov_7.35333	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_322_le ngth_7001_cov_48.8383	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_324_le ngth_6990_cov_3.82177	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_325_le ngth_6988_cov_12.9429	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_326_le ngth_6977_cov_10.0392	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_327_le ngth_6975_cov_5.44104	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_328_le ngth_6972_cov_4.53694	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_329_le ngth_6971_cov_4.13664	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_330_le ngth_6956_cov_83.2514	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_332_le ngth_6906_cov_14.0588	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_333_le ngth_6902_cov_4.73945	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_334_le ngth_6872_cov_35.1512	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_335_le ngth_6871_cov_12.364	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_336_le ngth_6847_cov_3.38369	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_337_le ngth_6830_cov_25.2034	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_340_le ngth_6823_cov_5.02911	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_341_le ngth_6806_cov_7.64657	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_342_le ngth_6772_cov_21.8246	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_343_le ngth_6770_cov_10.631	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_344_le ngth_6770_cov_8.06478	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_345_le ngth_6765_cov_5.40522	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_347_le ngth_6753_cov_152.075	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_348_le ngth_6726_cov_15.0806	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_349_le ngth_6711_cov_3.17293	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_350_le ngth_6697_cov_81.3359	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_351_le ngth_6678_cov_6.9689	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_352_le ngth_6664_cov_10.6033	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_353_le ngth_6659_cov_10.4211	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_354_le ngth_6657_cov_20.947	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_355_le ngth_6653_cov_4.89179	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_356_le ngth_6645_cov_15.3448	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_357_le ngth_6642_cov_32.1167	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_358_le ngth_6635_cov_15.8384	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_36_len gth_14934_cov_84.6968	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_360_le ngth_6625_cov_10.6409	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_362_le ngth_6614_cov_4.37811	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_363_le ngth_6609_cov_18.3479	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_365_le ngth_6575_cov_5.59847	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_367_le ngth_6516_cov_54.5149	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_368_le ngth_6506_cov_7.43435	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_369_le ngth_6502_cov_10.492	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_371_le ngth_6474_cov_150.716	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_372_le ngth_6463_cov_5.75125	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_375_le ngth_6412_cov_98.7832	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_376_le ngth_6412_cov_9.78119	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_378_length_6396_cov_31.6904	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_379_length_6387_cov_273.735	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_38_length_14832_cov_122.255	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_380_length_6380_cov_9.08933	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_381_length_6379_cov_36.6622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_383_length_6360_cov_27.1892	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_384_length_6344_cov_4.1606	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_385_length_6338_cov_4.31736	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_387_length_6323_cov_10.9375	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_388_length_6317_cov_3.0955	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_39_length_14311_cov_128.752	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_390_length_6308_cov_60.2551	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_391_length_6298_cov_23.0961	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_392_length_6287_cov_20.7914	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_393_length_6278_cov_77.8919	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_394_length_6278_cov_6.67909	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_395_le ngth_6275_cov_5.55209	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_396_le ngth_6273_cov_11.5495	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_397_le ngth_6266_cov_3.86443	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_399_le ngth_6263_cov_9.98776	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_401_le ngth_14133_cov_7.30608	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_400_le ngth_6260_cov_16.1028	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_401_le ngth_6251_cov_8.9001	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_402_le ngth_6248_cov_5.42532	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_403_le ngth_6247_cov_4.47481	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_406_le ngth_6242_cov_94.0936	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_409_le ngth_6178_cov_6.19974	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_411_le ngth_14120_cov_22.5892	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_411_le ngth_6144_cov_5.77024	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_412_le ngth_6141_cov_5.31975	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_413_le ngth_6077_cov_11.1133	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_414_le ngth_6067_cov_4.88124	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_415_le ngth_6065_cov_70.116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_416_le ngth_6048_cov_5.4869	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_418_le ngth_6043_cov_3.72345	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_419_le ngth_6032_cov_9.0783	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_421_le ngth_6013_cov_9.51225	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_422_le ngth_6009_cov_5.03446	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_423_le ngth_6002_cov_5.0486	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_424_le ngth_5990_cov_188.654	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_425_le ngth_5990_cov_5.18602	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_427_le ngth_5988_cov_6.26648	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_428_le ngth_5986_cov_10.9369	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_429_le ngth_5985_cov_11.4705	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_43_1en gth_14062_cov_173.035	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_431_le ngth_5954_cov_6.86133	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_432_le ngth_5947_cov_11.4516	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_433_le ngth_5945_cov_210.001	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_435_le ngth_5924_cov_6.36616	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_436_le ngth_5917_cov_39.1213	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_438_le ngth_5906_cov_29.0689	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_441_le ngth_5888_cov_13.3069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_442_le ngth_5884_cov_6.3263	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_444_le ngth_5872_cov_8.36067	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_446_le ngth_5855_cov_44.1997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_449_le ngth_5837_cov_83.4474	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_451_le ngth_13809_cov_127.997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_450_le ngth_5814_cov_4.45546	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_452_le ngth_5813_cov_10.7362	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_453_le ngth_5813_cov_6.9571	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_454_le ngth_5811_cov_4.31202	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_456_le ngth_5795_cov_7.97091	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_458_le ngth_5787_cov_65.6586	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_459_le ngth_5781_cov_5.22022	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_460_le ngth_5770_cov_62.0469	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_461_le ngth_5763_cov_8.01016	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_462_le ngth_5753_cov_123.761	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_466_le ngth_5733_cov_30.7193	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_467_le ngth_5733_cov_27.4033	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_468_le ngth_5719_cov_5.65731	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_47_len gth_13647_cov_18.9127	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_471_le ngth_5710_cov_127.997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_472_le ngth_5709_cov_57.6265	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_473_le ngth_5704_cov_50.045	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_474_le ngth_5700_cov_2.76085	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_475_le ngth_5698_cov_33.6307	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_476_le ngth_5687_cov_5.04705	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_477_le ngth_5686_cov_27.9586	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_478_le ngth_5685_cov_96.6286	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_480_le ngth_5663_cov_3.39354	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_481_le ngth_5651_cov_3.68263	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_482_le ngth_5648_cov_4.78795	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_483_le ngth_5646_cov_7.58934	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_484_le ngth_5642_cov_2.71738	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_485_le ngth_5634_cov_102.9	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_486_le ngth_5632_cov_6.68173	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_487_le ngth_5632_cov_3.32275	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_488_le ngth_5626_cov_7.57745	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_489_le ngth_5617_cov_71.9561	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_490_le ngth_5616_cov_4.40514	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_491_le ngth_5616_cov_3.45675	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_492_le ngth_5615_cov_4.1304	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_493_le ngth_5607_cov_34.2759	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_494_le ngth_5604_cov_3.22004	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_495_le ngth_5595_cov_49.7458	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_496_le ngth_5571_cov_58.4215	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_497_le ngth_5553_cov_21.3398	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_498_le ngth_5538_cov_6.43863	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_499_le ngth_5535_cov_13.9465	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_500_le ngth_13342_cov_206.682	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_503_le ngth_5527_cov_23.2449	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_505_le ngth_5517_cov_19.1093	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_507_le ngth_5499_cov_4.991	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_509_le ngth_5485_cov_403.837	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_511_le ngth_5456_cov_16.5738	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_516_le ngth_5445_cov_5.04119	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_518_le ngth_5433_cov_4.2341	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_519_le ngth_5427_cov_114.563	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_520_le ngth_5425_cov_384.428	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_521_le ngth_5420_cov_9.46822	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_523_le ngth_5406_cov_52.9116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_523_le ngth_5402_cov_27.1846	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_524_le ngth_5399_cov_10.2156	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_525_le ngth_5397_cov_8.22052	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_526_le ngth_5383_cov_12.1111	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_527_le ngth_5377_cov_5.29444	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_528_le ngth_5375_cov_4.09887	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_530_le ngth_5370_cov_268.43	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_531_le ngth_5369_cov_20.6998	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_532_le ngth_5369_cov_14.098	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_533_le ngth_5365_cov_22.7913	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_534_le ngth_5355_cov_4.88491	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_535_le ngth_5344_cov_21.5436	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_537_le ngth_5320_cov_25.3823	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_538_le ngth_5320_cov_6.51453	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_539_le ngth_5313_cov_4.7887	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_54_len gth_13134_cov_6.41387	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_540_le ngth_5305_cov_3.88762	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_541_le ngth_5298_cov_41.6168	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_542_le ngth_5289_cov_5.85059	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_544_le ngth_5281_cov_4.18102	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_545_le ngth_5279_cov_12.3497	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_546_le ngth_5263_cov_6.41935	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_547_le ngth_5259_cov_9.95292	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_548_le ngth_5257_cov_5.23587	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_549_le ngth_5250_cov_5.02618	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_551_le ngth_13062_cov_16.3595	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_550_le ngth_5246_cov_6.42015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_551_le ngth_5243_cov_4.30031	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_552_le ngth_5241_cov_4.96452	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_553_le ngth_5238_cov_59.1462	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_554_le ngth_5220_cov_8.99419	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_555_le ngth_5211_cov_5.21043	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_556_le ngth_5210_cov_108.066	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_557_le ngth_5204_cov_4.18042	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_558_le ngth_5189_cov_4.48929	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_559_le ngth_5183_cov_5.43857	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_56_len gth_13017_cov_150.934	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_561_le ngth_5180_cov_3.69561	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_562_le ngth_5178_cov_4.36463	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_563_le ngth_5160_cov_2.75357	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_564_le ngth_5150_cov_13.6312	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_565_le ngth_5150_cov_7.90186	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_567_le ngth_5132_cov_5.39374	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_568_le ngth_5127_cov_5.3748	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_569_le ngth_5121_cov_36.075	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_57_len gth_12943_cov_29.7244	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_571_le ngth_5118_cov_12.1132	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_572_le ngth_5110_cov_30.2558	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_573_le ngth_5110_cov_7.5723	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_575_le ngth_5101_cov_9.63199	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_578_le ngth_5096_cov_10.8756	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_579_le ngth_5093_cov_14.9758	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_58_le ngth_12844_cov_118.811	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_580_le ngth_5091_cov_4.53674	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_581_le ngth_5089_cov_37.5528	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_582_le ngth_5066_cov_3.18878	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_583_le ngth_5065_cov_22.9545	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_584_le ngth_5063_cov_49.5172	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_585_le ngth_5052_cov_5.71043	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_586_le ngth_5051_cov_4.99339	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_587_le ngth_5049_cov_3.18382	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_589_le ngth_5045_cov_7.35686	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_59_le ngth_12829_cov_146.099	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_590_le ngth_5041_cov_49.0177	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_591_le ngth_5040_cov_43.0646	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_592_le ngth_5036_cov_5.49307	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_593_le ngth_5035_cov_3.65261	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_596_le ngth_5029_cov_2.93627	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_597_le ngth_5020_cov_6.44733	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_598_le ngth_5006_cov_9.44678	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_599_le ngth_5001_cov_76.4618	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_600_le ngth_4997_cov_84.1696	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_602_le ngth_4988_cov_7.57248	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_603_le ngth_4984_cov_17.662	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_606_le ngth_4966_cov_24.3026	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_607_le ngth_4954_cov_6.7326	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_608_le ngth_4951_cov_19.9728	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_610_le ngth_4942_cov_53.1297	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_611_le ngth_4935_cov_17.6137	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_612_le ngth_4928_cov_12.4254	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_614_le ngth_4893_cov_395.269	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_615_le ngth_4887_cov_3.06519	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_616_le ngth_4872_cov_5.11231	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_617_le ngth_4867_cov_30.4007	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_619_le ngth_4850_cov_5.02086	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_620_le ngth_4849_cov_13.3317	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_621_le ngth_4846_cov_4.77332	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_622_le ngth_4845_cov_8.21336	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_623_le ngth_4843_cov_3.11069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_624_le ngth_4842_cov_12.4176	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_626_le ngth_4836_cov_2.70571	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_627_le ngth_4835_cov_9.80669	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_628_le ngth_4834_cov_4.16573	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_629_le ngth_4818_cov_3.13584	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_63_len gth_12566_cov_28.454	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_632_le ngth_4808_cov_3.89964	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_633_le ngth_4806_cov_5.02021	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_634_le ngth_4805_cov_6.42716	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_635_le ngth_4799_cov_6.36762	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_637_le ngth_4795_cov_4.49831	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_638_le ngth_4793_cov_36.8795	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_639_le ngth_4790_cov_7.4226	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_640_le ngth_4785_cov_27.9556	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_643_le ngth_4761_cov_4.78389	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_645_le ngth_4746_cov_24.1149	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_646_le ngth_4745_cov_10.9842	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_648_le ngth_4742_cov_6.76125	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_649_le ngth_4731_cov_3.33618	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_65_len gth_12453_cov_8.33296	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_650_le ngth_4730_cov_23.3037	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_652_le ngth_4729_cov_3.93261	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_653_le ngth_4725_cov_4.52099	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_654_le ngth_4721_cov_6.79318	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_656_length_4710_cov_4.02707	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_659_length_4704_cov_7.40955	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_66_length_12382_cov_43.157	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_660_length_4702_cov_20.7762	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_661_length_4702_cov_12.7334	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_662_length_4702_cov_7.70992	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_663_length_4685_cov_3.78251	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_664_length_4683_cov_2.2366	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_667_length_4656_cov_5.48946	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_668_length_4649_cov_48.2723	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_669_length_4648_cov_38.7396	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_67_length_12336_cov_4.32856	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_671_length_4640_cov_9.4458	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_673_length_4632_cov_69.246	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_675_length_4613_cov_19.4105	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_676_length_4602_cov_16.8498	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_14571_93xxx_NODE_677_le ngth_4597_cov_99.8443	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_678_le ngth_4595_cov_10.0857	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_679_le ngth_4592_cov_2.98633	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_68_le ngth_12272_cov_11.7256	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_680_le ngth_4589_cov_9.77525	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_681_le ngth_4587_cov_8.89585	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_683_le ngth_4567_cov_169.537	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_685_le ngth_4566_cov_6.93239	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_686_le ngth_4565_cov_9.83215	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_687_le ngth_4565_cov_4.16896	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_688_le ngth_4560_cov_2.43973	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_689_le ngth_4558_cov_7.70087	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_690_le ngth_4558_cov_7.57562	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_691_le ngth_4556_cov_3.12531	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_692_le ngth_4550_cov_6.00467	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_693_le ngth_4544_cov_14.38	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_694_le ngth_4541_cov_30.8179	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_695_le ngth_4535_cov_280.673	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_696_le ngth_4526_cov_14.8309	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_697_le ngth_4525_cov_13.1402	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_699_le ngth_4524_cov_4.41018	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_70_len gth_12186_cov_53.755	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_700_le ngth_4523_cov_7.33774	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_701_le ngth_4521_cov_3.93753	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_702_le ngth_4515_cov_7.75762	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_703_le ngth_4505_cov_150.01	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_704_le ngth_4505_cov_12.2796	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_705_le ngth_4502_cov_3.46863	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_706_le ngth_4497_cov_5.26069	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_707_le ngth_4494_cov_7.65488	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_709_le ngth_4484_cov_6.60759	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_71_len gth_12180_cov_44.868	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_710_le ngth_4484_cov_3.3678	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_711_le ngth_4481_cov_7.84727	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_712_le ngth_4474_cov_3.98529	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_713_le ngth_4456_cov_8.90048	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_715_le ngth_4448_cov_7.13613	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_718_le ngth_4442_cov_6.80146	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_720_le ngth_4436_cov_2.53892	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_721_le ngth_4432_cov_9.23943	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_722_le ngth_4422_cov_7.90451	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_723_le ngth_4415_cov_8.7945	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_727_le ngth_4385_cov_15.4344	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_728_le ngth_4385_cov_7.73464	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_729_le ngth_4381_cov_13.1313	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_73_len gth_11938_cov_86.7626	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_730_le ngth_4380_cov_10.4368	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_731_le ngth_4375_cov_5.08611	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_732_le ngth_4363_cov_18.9554	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_733_le ngth_4358_cov_59.3793	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_734_le ngth_4358_cov_6.35533	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_735_le ngth_4354_cov_2.73064	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_736_le ngth_4353_cov_15.3104	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_737_le ngth_4349_cov_7.5503	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_74_le ngth_11815_cov_61.3682	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_740_le ngth_4337_cov_3.49556	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_741_le ngth_4336_cov_14.1343	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_742_le ngth_4334_cov_6.2545	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_744_le ngth_4321_cov_22.1414	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_745_le ngth_4319_cov_24.3841	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_746_le ngth_4318_cov_19.1612	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_747_le ngth_4318_cov_4.61647	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_749_le ngth_4302_cov_73.2863	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_750_le ngth_4301_cov_19.6517	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_751_le ngth_4291_cov_3.38503	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_752_le ngth_4281_cov_67.0315	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_753_le ngth_4281_cov_8.1486	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_754_le ngth_4276_cov_4.32101	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_755_le ngth_4274_cov_4.74188	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_757_le ngth_4258_cov_423.492	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_758_le ngth_4257_cov_4.75964	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_759_le ngth_4250_cov_5.08725	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_76_len gth_11793_cov_7.45885	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_761_le ngth_4244_cov_4.11482	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_762_le ngth_4228_cov_32.8828	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_763_le ngth_4219_cov_15.1455	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_764_le ngth_4214_cov_4.04112	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_765_le ngth_4213_cov_464.66	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_766_le ngth_4201_cov_2.69006	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_767_le ngth_4195_cov_5.69928	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_768_le ngth_4191_cov_14.3786	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_769_le ngth_4186_cov_3.93198	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_77_le ngth_11768_cov_123.262	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_770_le ngth_4180_cov_135.136	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_772_le ngth_4174_cov_8.32678	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_775_le ngth_4156_cov_5.93636	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_776_le ngth_4155_cov_143.533	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_777_le ngth_4153_cov_489.51	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_778_le ngth_4148_cov_43.2551	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_779_le ngth_4145_cov_11.8403	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_780_le ngth_4138_cov_45.7088	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_781_le ngth_4138_cov_31.4154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_782_le ngth_4134_cov_23.8247	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_783_le ngth_4134_cov_3.07306	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_784_le ngth_4130_cov_2.64074	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_785_le ngth_4126_cov_79.1606	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_786_le ngth_4121_cov_5.25111	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_790_le ngth_4114_cov_5.92781	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_793_le ngth_4102_cov_2.32518	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_794_le ngth_4100_cov_3.54635	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_796_le ngth_4094_cov_9.19411	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_797_le ngth_4093_cov_181.969	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_799_le ngth_4081_cov_85.7668	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_8_lengt h_21735_cov_21.367	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_800_le ngth_4081_cov_3.67586	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_801_le ngth_4080_cov_6.2636	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_802_le ngth_4079_cov_4.77435	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_804_le ngth_4074_cov_2.67753	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_805_le ngth_4064_cov_90.2834	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_806_le ngth_4057_cov_2.34939	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_807_le ngth_4056_cov_42.8268	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_808_le ngth_4051_cov_75.8594	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_810_le ngth_4051_cov_5.03529	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_811_le ngth_4050_cov_2.81477	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_814_le ngth_4035_cov_21.006	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_815_le ngth_4035_cov_9.72538	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_816_le ngth_4024_cov_13.0877	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_817_le ngth_4019_cov_125.694	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_818_le ngth_4016_cov_74.2461	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_819_le ngth_4016_cov_17.4873	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_82_len gth_11475_cov_82.2828	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_820_le ngth_4013_cov_3.20566	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_821_le ngth_4004_cov_141.396	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_823_le ngth_3990_cov_2.59466	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_824_le ngth_3989_cov_6.99441	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_826_le ngth_3974_cov_2.08701	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_827_le ngth_3972_cov_23.1527	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_828_le ngth_3970_cov_5.93997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_83_len ngth_11465_cov_12.4677	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_830_le ngth_3959_cov_62.7641	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_831_le ngth_3951_cov_8.22305	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_832_le ngth_3949_cov_26.8737	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_834_le ngth_3946_cov_4.86662	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_835_le ngth_3939_cov_9.48919	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_836_le ngth_3936_cov_10.6905	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_838_le ngth_3934_cov_10.2024	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_839_le ngth_3933_cov_3.58871	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_840_le ngth_3930_cov_6.10839	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_841_le ngth_3930_cov_2.77935	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_843_le ngth_3903_cov_5.342	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_845_le ngth_3899_cov_5.04448	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_846_le ngth_3899_cov_4.84105	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_847_le ngth_3890_cov_20.0154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_850_le ngth_3879_cov_4.2249	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_852_le ngth_3877_cov_4.90921	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_853_le ngth_3872_cov_7.14593	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_854_le ngth_3871_cov_50.3912	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_855_le ngth_3870_cov_15.1455	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_857_le ngth_3866_cov_43.062	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_858_le ngth_3865_cov_17.7874	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_859_le ngth_3862_cov_4.69714	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_86_1en gth_11247_cov_11.6879	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_860_le ngth_3857_cov_4.42925	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_862_le ngth_3832_cov_3.29733	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_864_le ngth_3830_cov_3.95444	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_865_le ngth_3826_cov_7.28534	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_866_le ngth_3815_cov_51.8287	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_867_le ngth_3810_cov_4.76751	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_87_1en gth_11223_cov_8.28071	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_872_le ngth_3785_cov_3.57158	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_873_le ngth_3773_cov_111.004	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_874_le ngth_3769_cov_9.39338	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_875_le ngth_3768_cov_87.7285	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_877_le ngth_3763_cov_117.901	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_878_le ngth_3752_cov_21.3949	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_879_le ngth_3746_cov_35.8659	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_880_le ngth_3742_cov_39.3683	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_881_le ngth_3742_cov_5.47437	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_882_le ngth_3740_cov_20.7091	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_883_le ngth_3738_cov_7.00264	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_884_le ngth_3734_cov_4.97662	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_885_le ngth_3732_cov_5.6731	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_888_le ngth_3719_cov_44.5977	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_889_le ngth_3718_cov_5.67158	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_891_le ngth_3710_cov_3.97921	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_892_le ngth_3703_cov_5.68613	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_893_le ngth_3703_cov_2.50466	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_14571_93xxx_NODE_895_le ngth_3698_cov_25.8345	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_896_le ngth_3695_cov_23.111	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_897_le ngth_3689_cov_9.88608	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_898_le ngth_3681_cov_19.7038	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_899_le ngth_3679_cov_6.22158	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_90_le ngth_11129_cov_8.08064	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_900_le ngth_3670_cov_3.66362	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_903_le ngth_3665_cov_7.73934	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_904_le ngth_3663_cov_11.3196	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_905_le ngth_3661_cov_3.62119	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_906_le ngth_3652_cov_46.6486	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_907_le ngth_3652_cov_3.22991	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_909_le ngth_3646_cov_2.81314	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_91_le ngth_11039_cov_6.21185	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_910_le ngth_3645_cov_565.659	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_913_le ngth_3635_cov_4.11508	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_914_le ngth_3633_cov_80.0011	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_915_le ngth_3633_cov_8.40414	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_916_le ngth_3632_cov_3.20883	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_917_le ngth_3629_cov_37.1642	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_918_le ngth_3625_cov_319.136	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_919_le ngth_3624_cov_63.5677	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_92_le ngth_11027_cov_14.7065	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_920_le ngth_3624_cov_21.1952	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_921_le ngth_3622_cov_5.31343	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_922_le ngth_3621_cov_8.90746	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_923_le ngth_3618_cov_117.955	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_924_le ngth_3616_cov_11.3451	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_926_le ngth_3613_cov_9.49972	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_927_le ngth_3609_cov_2.8534	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_928_le ngth_3608_cov_6.43062	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_929_le ngth_3606_cov_11.0969	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_93_le ngth_10979_cov_6.42292	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_932_le ngth_3604_cov_3.90758	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_933_le ngth_3600_cov_10.5253	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_934_le ngth_3598_cov_3.42901	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_935_le ngth_3596_cov_3.99972	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_936_le ngth_3596_cov_3.88788	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_937_le ngth_3592_cov_3.09302	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_939_le ngth_3582_cov_28.4003	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_940_le ngth_3568_cov_2.58867	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_941_le ngth_3562_cov_16.8557	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_942_le ngth_3562_cov_9.52352	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_943_le ngth_3557_cov_7.36636	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_944_le ngth_3548_cov_2.42628	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_946_le ngth_3546_cov_3.9682	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_947_le ngth_3542_cov_24.5105	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_948_le ngth_3542_cov_11.8056	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_95_le ngth_10922_cov_88.2839	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_950_le ngth_3537_cov_3.33515	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_951_le ngth_3530_cov_3.36978	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_952_le ngth_3525_cov_3.81239	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_953_le ngth_3524_cov_2.85154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_954_le ngth_3523_cov_7.12543	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_955_le ngth_3520_cov_40.2274	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_956_le ngth_3519_cov_5.81611	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_957_le ngth_3517_cov_6.74552	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_958_le ngth_3515_cov_224.563	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_96_le ngth_10821_cov_58.7557	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_960_le ngth_3513_cov_2.98988	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_961_le ngth_3511_cov_2.37963	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_962_le ngth_3510_cov_13.3453	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_963_le ngth_3500_cov_31.5901	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_964_le ngth_3498_cov_8.72164	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_965_le ngth_3496_cov_3.38913	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_967_le ngth_3492_cov_17.2787	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_969_le ngth_3489_cov_10.8888	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_970_le ngth_3485_cov_3.90146	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_971_le ngth_3484_cov_9.32167	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_976_le ngth_3478_cov_9.86912	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_977_le ngth_3477_cov_13.5523	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_98_le ngth_10750_cov_22.9598	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_980_le ngth_3475_cov_41.9681	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_981_le ngth_3470_cov_10.4123	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_983_le ngth_3467_cov_4.47479	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_984_le ngth_3461_cov_5.48121	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_985_le ngth_3458_cov_5.09139	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_986_le ngth_3454_cov_33.5152	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_93xxx_NODE_987_le ngth_3448_cov_3.6148	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_14571_93xxx_NODE_988_length_3447_cov_11.6601	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_989_length_3446_cov_14.3312	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_99_length_10721_cov_47.0481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_991_length_3432_cov_2.74889	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_992_length_3430_cov_3.44948	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_993_length_3429_cov_56.602	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_996_length_3420_cov_20.2678	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_997_length_3419_cov_5.36801	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_998_length_3417_cov_66.5205	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_93xxx_NODE_999_length_3413_cov_34.3374	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_94_NODE_19_length_14591_cov_9.83661	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_94_NODE_192_length_1131_cov_2.21654	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_94_NODE_50_length_5637_cov_2.51487	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_94_NODE_71_length_4020_cov_35.5881	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_96_NODE_100_length_6326_cov_5.40073	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_105_length_6165_cov_3.15745	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified

NG_14571_96_NODE_109_length _6016_cov_2.81496	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_113_length _5914_cov_258.003	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_116_length _5849_cov_2.91169	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_138_length _4789_cov_3.19983	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_141_length _4669_cov_3.37581	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_142_length _4667_cov_2.47121	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_144_length _4535_cov_5.28862	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_157_length _4306_cov_2.0127	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_159_length _4183_cov_3.35296	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_162_length _4117_cov_2.61349	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_170_length _3893_cov_2.90803	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_173_length _3842_cov_2.62002	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_179_length _3660_cov_3.28655	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_181_length _3648_cov_2.30615	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_182_length _3633_cov_3.33706	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_184_length _3603_cov_2.49352	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified

NG_14571_96_NODE_185_length_3576_cov_2.41039	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_189_length_3389_cov_11.0684	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_192_length_3283_cov_3.17193	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_195_length_3227_cov_2.42907	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_196_length_3213_cov_2.23591	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_200_length_3179_cov_3.83451	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_201_length_3158_cov_2.17693	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_206_length_3112_cov_2.48152	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_210_length_3053_cov_2.30821	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_49_length_12961_cov_2.7559	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_50_length_12723_cov_5.24629	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_53_length_12359_cov_3.32266	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_56_length_11168_cov_3.99055	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_57_length_10711_cov_2.70045	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_63_length_9514_cov_3.87388	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_79_length_7850_cov_4.67146	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified

NG_14571_96_NODE_80_length_7791_cov_3.08273	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_86_length_7242_cov_3.52038	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_92_length_6858_cov_3.67941	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_93_length_6656_cov_2.64081	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_94_length_6514_cov_2.64809	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_96_NODE_99_length_6336_cov_4.24646	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_14571_98xxx_NODE_108_length_3832_cov_6.50622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_109_length_3785_cov_3.74638	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_113_length_3684_cov_2.50014	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_128_length_3325_cov_2.53731	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_131_length_3259_cov_13.7903	0.11	-0.26	0.64	0.58	0.09	0.97	Unclassified
NG_14571_98xxx_NODE_138_length_3110_cov_2.53257	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_139_length_3106_cov_17.0252	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_140_length_3101_cov_2.79481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
NG_14571_98xxx_NODE_153_length_2843_cov_3.02977	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_178_length_2531_cov_1.50929	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae

NG_14571_98xxx_NODE_204_length_2342_cov_3.19545	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
NG_14571_98xxx_NODE_316_length_1756_cov_1.87419	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_37_length_8595_cov_4.72447	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_386_length_1493_cov_2.97497	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
NG_14571_98xxx_NODE_447_length_1325_cov_2.71811	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_46_length_7482_cov_5.19779	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_516_length_1204_cov_1.75457	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_52_length_6729_cov_4.87234	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_582_length_1114_cov_1.60246	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_87_length_4513_cov_3.07402	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_98xxx_NODE_88_length_4508_cov_34.5414	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_14571_99xxx_NODE_28_length_4028_cov_3.03197	0.11	-0.26	0.64	0.58	0.09	0.97	Siphoviridae
NG_14571_99xxx_NODE_39_length_2588_cov_2.40189	0.11	-0.26	0.64	0.58	0.09	0.97	Siphoviridae
NG_14571_99xxx_NODE_40_length_2548_cov_2.95708	0.11	-0.26	0.64	0.58	0.09	0.97	Unclassified
NG_14571_99xxx_NODE_53_length_2018_cov_2.42792	0.11	-0.26	0.64	0.58	0.09	0.97	Unclassified
NG_14571_99xxx_NODE_75_length_1599_cov_2.04404	0.11	-0.26	0.64	0.58	0.09	0.97	Siphoviridae

NG_14571_99xxx_NODE_88_len gth_1372_cov_2.32422	0.11	-0.26	0.64	0.58	0.09	0.97	Unclassified
NG_14571_99xxx_NODE_90_len gth_1321_cov_2.26461	0.11	-0.26	0.64	0.58	0.09	0.97	Unclassified
NG_14571_Simponi_NODE_107_1 ength_1511_cov_2.38187	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_124_1 ength_1350_cov_1.77297	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_13_le ngth_14792_cov_7.56287	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_164_1 ength_1072_cov_1.84366	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_29_le ngth_7436_cov_2.54681	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_45_le ngth_4857_cov_2.37047	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_54_le ngth_3874_cov_2.3713	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_58_le ngth_3369_cov_2.57634	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_59_le ngth_3317_cov_2.71306	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_62_le ngth_3199_cov_2.01972	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_64_le ngth_3035_cov_2.85168	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_14571_Simponi_NODE_66_le ngth_3008_cov_2.38605	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_1 02_length_2441_cov_1.83906	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_1 4_length_19342_cov_6.38809	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified

NG_15813_1_lib254060_NODE_1 7_length_12802_cov_4.3753	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_1 87_length_1354_cov_1.67667	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_2 0_length_10479_cov_3.65627	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_2 2_length_9355_cov_3.59559	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_2 3_length_8757_cov_3.52666	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_2 5_length_7702_cov_2.99501	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_3 7_length_6407_cov_3.97103	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_4 3_length_5702_cov_3.14362	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_4 6_length_5566_cov_161.186	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_1_lib254060_NODE_5 6_length_4824_cov_3.72279	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_5 8_length_4765_cov_2.97728	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_6 0_length_4733_cov_19.6554	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_6 1_length_4464_cov_1.91041	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_6 3_length_4398_cov_19.0228	0.16	0.23	0.64	0.33	-0.16	0.97	Circoviridae
NG_15813_1_lib254060_NODE_6 4_length_4398_cov_5.58232	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_7 0_length_3851_cov_3.25079	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_1_lib254060_NODE_7 1_length_3746_cov_2.69846	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_7 5_length_3684_cov_3.97796	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_7 6_length_3679_cov_1.78228	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_8 0_length_3466_cov_2.58106	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_8 6_length_3071_cov_2.56432	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_8 7_length_2937_cov_3.4431	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_9 6_length_2553_cov_2.45092	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_1_lib254060_NODE_9 9_length_2478_cov_15.1176	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Anelloviridae
NG_15813_116_lib254048_NODE _114_length_6263_cov_3.15126	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _115_length_6250_cov_6.99903	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _119_length_5997_cov_4.78997	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _122_length_5953_cov_3.46372	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _123_length_5951_cov_5.5	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_15813_116_lib254048_NODE _126_length_5856_cov_3.11274	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _131_length_5738_cov_3.94387	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _133_length_5636_cov_3.56854	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified

NG_15813_116_lib254048_NODE _137_length_5481_cov_2.56045	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _142_length_5449_cov_2.51835	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _149_length_5371_cov_2.92645	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _161_length_4943_cov_14.7502	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _166_length_4774_cov_3.09218	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _167_length_4762_cov_3.13469	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _168_length_4759_cov_2.55548	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _176_length_4574_cov_2.83049	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _182_length_4371_cov_2.68026	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _199_length_4079_cov_2.42744	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _201_length_4010_cov_2.24627	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _207_length_3875_cov_1.65105	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _209_length_3847_cov_6.21783	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _211_length_3829_cov_4.75464	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _212_length_3797_cov_2.69341	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _213_length_3789_cov_4.3744	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_116_lib254048_NODE _214_length_3747_cov_1.90466	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _215_length_3734_cov_3.39712	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _219_length_3680_cov_2.71641	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _224_length_3624_cov_3.37966	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _227_length_3613_cov_2.64306	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _235_length_3440_cov_2.72555	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _236_length_3439_cov_2.26891	0.37	-0.15	0.66	0.42	0.13	0.97	Unclassified
NG_15813_116_lib254048_NODE _237_length_3375_cov_3.68614	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _238_length_3363_cov_2.20919	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _239_length_3361_cov_2.25862	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _240_length_3350_cov_2.48346	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _242_length_3305_cov_3.85938	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _243_length_3298_cov_2.82424	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_15813_116_lib254048_NODE _244_length_3296_cov_2.61894	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _245_length_3280_cov_3.44806	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
NG_15813_116_lib254048_NODE _246_length_3277_cov_1.98448	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_116_lib254048_NODE _247_length_3265_cov_1.95981	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _251_length_3231_cov_2.61209	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _253_length_3182_cov_9.97474	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _256_length_3151_cov_2.0814	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _258_length_3129_cov_3.17404	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _259_length_3120_cov_3.07374	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _261_length_3118_cov_2.30149	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _263_length_3092_cov_3.61475	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _266_length_3044_cov_1.65105	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _268_length_3003_cov_2.15536	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _275_length_2942_cov_2.47177	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _316_length_2598_cov_2.82068	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _328_length_2514_cov_2.38552	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _36_length_18834_cov_4.1599	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _453_length_1820_cov_3.53973	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_116_lib254048_NODE _460_length_1783_cov_1.81192	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_116_lib254048_NODE_473_length_1737_cov_1.90606	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
NG_15813_116_lib254048_NODE_494_length_1672_cov_1.69017	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_52_length_12796_cov_4.78903	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_526_length_1582_cov_2.48461	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_586_length_1419_cov_1.86364	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_67_length_9954_cov_4.60208	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_694_length_1246_cov_2.5508	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_70_length_9475_cov_3.69713	0.33	0.16	0.66	0.33	0.16	0.97	Unclassified
NG_15813_116_lib254048_NODE_73_length_9058_cov_4.23381	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_78_length_8341_cov_3.16715	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_79_length_8338_cov_4.09405	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_790_length_1100_cov_1.51579	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_86_length_7761_cov_3.06488	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_116_lib254048_NODE_94_length_6930_cov_2.92916	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_12_lib254055_NODE_120_length_1318_cov_2.39272	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_163_length_1046_cov_2.84864	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified

NG_15813_12_lib254055_NODE_ 19_length_9600_cov_3.30581	0.83	0.03	0.94	0.25	-0.19	0.97	Podoviridae
NG_15813_12_lib254055_NODE_ 20_length_7980_cov_3.88328	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_ 38_length_5230_cov_6.08329	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_ 49_length_4388_cov_4.61805	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_ 60_length_3221_cov_3.08181	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_ 61_length_3101_cov_6.73342	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_ 77_length_2218_cov_2.07582	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_12_lib254055_NODE_ 9_length_25769_cov_6.81936	0.83	0.03	0.94	0.25	-0.19	0.97	Unclassified
NG_15813_120_lib254062_NODE_ _101_length_7737_cov_8.91877	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_ _104_length_7487_cov_4.75821	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_ _108_length_7304_cov_6.44986	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_ _112_length_7048_cov_5.89547	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_ _116_length_6926_cov_12.6654	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_15813_120_lib254062_NODE_ _118_length_6861_cov_7.39186	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_ _119_length_6833_cov_44.2569	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_ _120_length_6820_cov_4.24848	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_120_lib254062_NODE _121_length_6742_cov_5.86197	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _125_length_6683_cov_6.23642	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _127_length_6616_cov_4.97836	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _140_length_6199_cov_4.27783	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _145_length_5832_cov_3.00796	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_15813_120_lib254062_NODE _146_length_5813_cov_5.06148	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _151_length_5752_cov_6.462	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _153_length_5722_cov_7.50856	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _154_length_5722_cov_4.86924	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _157_length_5563_cov_5.29684	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _158_length_5549_cov_2.95177	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _159_length_5532_cov_12.7086	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _162_length_5504_cov_11.6697	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _166_length_5444_cov_50.2641	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _173_length_5279_cov_3.31585	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _174_length_5275_cov_4.48736	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_120_lib254062_NODE _177_length_5173_cov_2.94939	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _18_length_17962_cov_13.5063	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _188_length_5037_cov_6.99037	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _192_length_4935_cov_4.78074	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _199_length_4755_cov_4.74149	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _20_length_17183_cov_6.16371	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Heterogeneous
NG_15813_120_lib254062_NODE _204_length_4677_cov_3.65015	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _208_length_4560_cov_4.47969	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _209_length_4511_cov_16.5	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _211_length_4450_cov_3.23413	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _215_length_4424_cov_3.26848	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _216_length_4422_cov_2.23471	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _22_length_15793_cov_7.74508	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _223_length_4240_cov_4.19618	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _227_length_4156_cov_3.98366	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _230_length_4123_cov_5.0204	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_120_lib254062_NODE _236_length_3983_cov_3.42872	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _238_length_3965_cov_9.59795	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _247_length_3778_cov_3.57239	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _248_length_3774_cov_4.18957	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _257_length_3657_cov_3.16685	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _259_length_3636_cov_5.38202	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _260_length_3612_cov_5.17262	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_15813_120_lib254062_NODE _264_length_3570_cov_5.34538	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _266_length_3570_cov_3.38122	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _267_length_3520_cov_3.57489	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_15813_120_lib254062_NODE _268_length_3514_cov_2.7161	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _270_length_3495_cov_3.66308	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_15813_120_lib254062_NODE _271_length_3492_cov_13.8135	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _277_length_3407_cov_352.357	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _283_length_3332_cov_17.3702	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _285_length_3300_cov_2.40154	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_120_lib254062_NODE _286_length_3297_cov_4.47409	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _287_length_3293_cov_4.39314	0.90	0.02	0.94	0.90	-0.02	0.97	Unclassified
NG_15813_120_lib254062_NODE _288_length_3290_cov_4.40247	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _29_length_15121_cov_6.09399	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_15813_120_lib254062_NODE _291_length_3255_cov_2.80656	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _294_length_3187_cov_1.97605	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _297_length_3165_cov_6.07556	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _300_length_3143_cov_6.06444	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _306_length_3100_cov_3.22036	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _31_length_14330_cov_8.16259	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _310_length_3062_cov_29.7938	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _314_length_3052_cov_2.46547	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _316_length_3022_cov_2.99663	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _318_length_3018_cov_2.02599	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _33_length_13780_cov_17.6364	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _343_length_2826_cov_2.53086	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_120_lib254062_NODE _35_length_13118_cov_13.5739	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _38_length_12849_cov_22.2155	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _39_length_12777_cov_6.83988	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _405_length_2432_cov_2.12116	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _43_length_12371_cov_5.47093	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _46_length_12062_cov_44.1975	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _461_length_2127_cov_2.27944	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
NG_15813_120_lib254062_NODE _468_length_2098_cov_1.73813	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _47_length_11609_cov_36.3734	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _485_length_1984_cov_5.96112	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _532_length_1830_cov_7.91718	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _57_length_10702_cov_11.9816	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _58_length_10627_cov_12.8103	0.83	-0.03	0.94	0.97	-0.01	0.97	Unclassified
NG_15813_120_lib254062_NODE _59_length_10567_cov_10.0276	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _64_length_10087_cov_48.1583	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_120_lib254062_NODE _67_length_9741_cov_10.2936	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_120_lib254062_NODE_71_length_9602_cov_4.75961	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_15813_120_lib254062_NODE_75_length_9202_cov_9.71586	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_77_length_9103_cov_5.67672	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_79_length_9016_cov_7.15545	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_82_length_8858_cov_6.35624	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_86_length_8618_cov_13.3927	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_87_length_8535_cov_6.59163	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_875_length_1190_cov_1.72159	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_120_lib254062_NODE_94_length_8110_cov_7.31049	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_2_lib254051_NODE_113_length_1245_cov_2.48571	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_2_lib254051_NODE_19_length_10705_cov_3.32526	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_2_lib254051_NODE_50_length_4337_cov_2.6483	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_2_lib254051_NODE_54_length_3903_cov_2.61227	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_2_lib254051_NODE_61_length_3160_cov_2.48631	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_2_lib254051_NODE_63_length_3017_cov_2.05976	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_25_lib254053_NODE_119_length_1884_cov_7.93603	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_15813_25_lib254053_NODE_16_length_13946_cov_20.2001	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_194_length_1329_cov_7.36499	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_263_length_1056_cov_9.51349	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_4_length_50835_cov_33.9372	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_46_length_4468_cov_2.5579	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_57_length_3805_cov_868.795	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_60_length_3651_cov_2.00695	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_66_length_3260_cov_3.04867	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_67_length_3248_cov_2.77263	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_71_length_3093_cov_3.70474	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_25_lib254053_NODE_89_length_2365_cov_4.50823	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anelloviridae
NG_15813_38_lib254052_NODE_149_length_1594_cov_2.1501	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_38_lib254052_NODE_17_length_5178_cov_19.0217	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Microviridae
NG_15813_38_lib254052_NODE_27_length_3830_cov_2792.06	0.16	0.23	0.64	0.33	-0.16	0.97	Unclassified
NG_15813_38_lib254052_NODE_29_length_3789_cov_776.797	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_38_lib254052_NODE_53_length_3013_cov_92.9212	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_15813_38_lib254052_NODE_84_length_2835_cov_183.888	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_4_lib254020_NODE_25_length_3769_cov_228.286	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_4_lib254020_NODE_31_length_3281_cov_7.0155	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_4_lib254020_NODE_33_length_3122_cov_22.343	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_4_lib254020_NODE_53_length_2021_cov_2.15463	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_41_lib254054_NODE_24_length_4469_cov_2.57363	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_41_lib254054_NODE_25_length_4240_cov_2.34432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_41_lib254054_NODE_33_length_3153_cov_3.08263	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_41_lib254054_NODE_34_length_3006_cov_2.15656	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_44_lib254059_NODE_24_length_3876_cov_2.79063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_44_lib254059_NODE_28_length_3645_cov_3.89192	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_44_lib254059_NODE_46_length_2017_cov_2.1998	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_44_lib254059_NODE_5_length_11898_cov_4.35574	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_44_lib254059_NODE_7_length_9936_cov_3.06986	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_44_lib254059_NODE_9_length_8104_cov_5.03404	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_53_lib254058_NODE_122_length_1935_cov_2.15957	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_15813_53_lib254058_NODE_33_length_7501_cov_6.02297	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_53_lib254058_NODE_43_length_5913_cov_3.74479	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_53_lib254058_NODE_49_length_5401_cov_2.61878	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_15813_53_lib254058_NODE_53_length_4534_cov_3.13374	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_53_lib254058_NODE_57_length_4124_cov_2.80413	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_53_lib254058_NODE_61_length_3631_cov_2.74916	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_53_lib254058_NODE_64_length_3550_cov_1.95966	0.18	0.22	0.64	0.11	0.26	0.97	Unclassified
NG_15813_53_lib254058_NODE_69_length_3272_cov_2.42928	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_6_lib254061_NODE_102_length_8761_cov_4.16632	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_107_length_7544_cov_3.64762	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_108_length_7448_cov_2.61004	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_113_length_7082_cov_4.39761	0.42	-0.13	0.68	0.21	-0.20	0.97	Siphoviridae
NG_15813_6_lib254061_NODE_114_length_6760_cov_3.01193	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_116_length_6712_cov_3.3072	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_120_length_6266_cov_4.07712	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_123_length_6185_cov_2.80962	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified

NG_15813_6_lib254061_NODE_1 30_length_5635_cov_8.59928	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 31_length_5620_cov_2.17071	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 32_length_5562_cov_2.83512	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 37_length_5200_cov_3.1794	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 38_length_5155_cov_24.8196	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 46_length_4690_cov_2.74973	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 47_length_4573_cov_3.10071	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 50_length_4284_cov_2.34051	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 51_length_4242_cov_2.4502	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 52_length_4237_cov_3.36944	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 56_length_4130_cov_2.85939	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 61_length_3856_cov_2.39384	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 64_length_3707_cov_3.06353	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 68_length_3546_cov_3.35463	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 71_length_3468_cov_2.66979	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 74_length_3365_cov_2.49789	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified

NG_15813_6_lib254061_NODE_1 75_length_3357_cov_2.75893	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 79_length_3231_cov_2.21883	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 82_length_3184_cov_2.47779	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 83_length_3182_cov_2.27311	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 84_length_3165_cov_2.47621	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 86_length_3116_cov_1.99706	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 87_length_3071_cov_682.234	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 89_length_3010_cov_2.67682	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_1 96_length_2856_cov_2.25634	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_2 06_length_2767_cov_49.8396	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_2 17_length_2622_cov_70.3487	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_3 6_length_42100_cov_19.868	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_4 02_length_1378_cov_1.90098	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_4 74_length_1216_cov_29.6581	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_5 1_length_26835_cov_7.78633	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_5 7_length_22465_cov_6.58652	0.42	-0.13	0.68	0.21	-0.20	0.97	Siphoviridae

NG_15813_6_lib254061_NODE_5 96_length_1047_cov_4.02419	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_6 0_length_19677_cov_22.916	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_6 12_length_1026_cov_2.4861	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_6 4_length_18208_cov_4.88112	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_6 9_length_16436_cov_4.78353	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_9 1_length_9906_cov_6.58779	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_9 6_length_9481_cov_5.80437	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_9 7_length_9371_cov_6.00869	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_6_lib254061_NODE_9 8_length_8900_cov_6.16608	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_15813_95_lib254056_NODE_ 102_length_4180_cov_2.75273	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_ 116_length_3459_cov_2.02526	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_ 136_length_2785_cov_3.84139	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_ 182_length_1848_cov_1.74233	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_ 235_length_1311_cov_65.7858	0.16	-0.23	0.64	0.18	0.22	0.97	Unclassified
NG_15813_95_lib254056_NODE_ 47_length_10830_cov_4.54747	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_ 63_length_7345_cov_3.98176	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

NG_15813_95_lib254056_NODE_75_length_5653_cov_2.9498	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_80_length_5388_cov_3.27152	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_84_length_5092_cov_3.58348	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_86_length_5071_cov_3.40032	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_94_length_4782_cov_3.59573	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_15813_95_lib254056_NODE_97_length_4497_cov_2.75304	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_18_lib261984_NODE_102_length_3491_cov_3.03347	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_107_length_3345_cov_3.84498	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_118_length_3105_cov_2.74459	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_121_length_3012_cov_3.06053	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_134_length_2815_cov_2.51014	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_19_length_23539_cov_6.78624	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_194_length_1975_cov_2.09375	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_40_length_8616_cov_9.82175	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_56_length_5245_cov_2.85992	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_58_length_5051_cov_6.13771	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified

NG_16262_18_lib261984_NODE_65_length_4742_cov_2.04822	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_70_length_4688_cov_3.04986	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_71_length_4631_cov_3.43073	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_72_length_4624_cov_2.71153	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_79_length_4200_cov_3.8152	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_80_length_4124_cov_3.28754	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_81_length_4117_cov_2.38897	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_83_length_4047_cov_2.27129	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_84_length_4024_cov_3.17989	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_95_length_3801_cov_3.25227	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_98_length_3585_cov_4.75524	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_18_lib261984_NODE_99_length_3545_cov_3.20229	0.13	-0.24	0.64	0.13	0.24	0.97	Unclassified
NG_16262_24_lib261981_NODE_11_length_1609_cov_1.69305	0.70	-0.06	0.93	0.18	-0.22	0.97	Unclassified
NG_16262_31_lib261986_NODE_101_length_4323_cov_3.31724	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_103_length_4248_cov_3.70212	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_107_length_4108_cov_4.62077	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_31_lib261986_NODE_109_length_3860_cov_3.35059	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_110_length_3858_cov_3.95188	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_111_length_3583_cov_2.70748	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_112_length_3559_cov_3.76884	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_113_length_3559_cov_2.91296	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_120_length_3313_cov_2.3674	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_124_length_3183_cov_3.23689	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_128_length_3075_cov_3.09735	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_129_length_3058_cov_2.88045	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_156_length_2489_cov_2.40509	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
NG_16262_31_lib261986_NODE_174_length_2065_cov_1.70746	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_19_length_20988_cov_4.71289	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_195_length_1740_cov_2.62849	0.42	-0.13	0.68	0.21	-0.20	0.97	Unclassified
NG_16262_31_lib261986_NODE_20_length_19638_cov_5.84936	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_242_length_1385_cov_2.99699	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_25_length_16148_cov_5.76251	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_31_lib261986_NODE_295_length_1034_cov_1.81307	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_30_length_14778_cov_4.55023	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_31_length_14748_cov_3.6695	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_34_length_13708_cov_5.96243	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_35_length_13132_cov_3.27216	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_36_length_12358_cov_3.9388	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_37_length_12331_cov_5.1806	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_39_length_12181_cov_4.09965	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_40_length_11971_cov_3.97415	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_42_length_11675_cov_5.80671	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_43_length_11606_cov_4.57536	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_49_length_9153_cov_3.99341	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_54_length_7706_cov_3.44609	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_55_length_7694_cov_3.45202	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_59_length_7334_cov_4.29661	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_65_length_6402_cov_3.34237	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_31_lib261986_NODE_68_length_6236_cov_3.17343	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_69_length_6221_cov_3.79841	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_70_length_6221_cov_3.48005	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_73_length_6150_cov_3.1936	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_74_length_6143_cov_3.01626	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_77_length_5958_cov_3.39675	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_84_length_5219_cov_3.48277	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_87_length_5030_cov_4.49628	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_88_length_4990_cov_2.33394	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_90_length_4826_cov_2.88325	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_91_length_4790_cov_3.58965	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_93_length_4700_cov_3.58385	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_96_length_4574_cov_3.18411	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_31_lib261986_NODE_97_length_4560_cov_3.89678	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_5_lib261985_NODE_41_length_2077_cov_4.75371	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_5_lib261985_NODE_44_length_1721_cov_6.40816	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_100_length_20820_cov_9.15507	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_101_length_20423_cov_6.68092	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_1024_length_2186_cov_2.92257	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_103_length_20119_cov_8.53843	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_107_length_19440_cov_5.76678	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_108_length_19348_cov_12.9518	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_109_length_19228_cov_8.98472	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_1096_length_2050_cov_2.51479	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_111_length_18698_cov_10.903	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_113_length_18481_cov_8.92163	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_114_length_18377_cov_9.59486	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_115_length_18353_cov_18.8881	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_117_length_17908_cov_9.05904	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_119_length_17798_cov_13.8619	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_121_length_17689_cov_10.3205	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_122_length_17523_cov_11.1381	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_124_length_17422_cov_11.5252	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_1240_length_1822_cov_2.26259	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
NG_16262_55_lib261982_NODE_126_length_17370_cov_9.44597	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_129_length_16985_cov_13.8637	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_130_length_16970_cov_20.7087	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_131_length_16908_cov_8.79203	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_133_length_16558_cov_7.52669	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_134_length_16327_cov_5.00928	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_136_length_16079_cov_12.1678	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_137_length_16014_cov_5.58074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_139_length_15925_cov_9.75236	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_144_length_15282_cov_8.45295	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_145_length_15173_cov_7.7964	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_146_length_15120_cov_7.36442	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_148_length_15040_cov_4.97598	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_149_length_14963_cov_9.91213	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_150_length_14861_cov_7.08476	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_151_length_14808_cov_7.41483	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_153_length_14759_cov_5.74415	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_1539_length_1521_cov_2.64393	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_154_length_14669_cov_3.73779	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_155_length_14641_cov_5.92088	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_156_length_14459_cov_8.17391	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_158_length_14349_cov_9.14754	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_159_length_14146_cov_5.91328	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_160_length_14014_cov_5.48406	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_161_length_13886_cov_5.52447	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_162_length_13882_cov_4.3287	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_164_length_13609_cov_3.89376	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_165_length_13498_cov_5.37685	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_166_length_13491_cov_6.43086	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_167_length_13484_cov_8.49743	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_168_length_13466_cov_3.30251	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
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NG_16262_55_lib261982_NODE_172_length_13022_cov_5.7162	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_174_length_12811_cov_6.21057	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_176_length_12796_cov_8.53795	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_177_length_12724_cov_5.44123	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_179_length_12462_cov_7.60063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_181_length_12410_cov_4.81878	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_182_length_12394_cov_6.50101	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_183_length_12387_cov_5.01898	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_185_length_12288_cov_5.03401	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_186_length_12248_cov_10.5073	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_187_length_12246_cov_5.73144	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_189_length_12176_cov_5.12944	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_190_length_12172_cov_7.18684	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_192_length_12010_cov_4.35759	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_1936_length_1261_cov_2.42537	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_194_length_11858_cov_6.08489	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_195_length_11722_cov_6.43413	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_197_length_11470_cov_18.5086	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_198_length_11439_cov_6.86929	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_199_length_11322_cov_6.24967	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_200_length_11200_cov_6.00646	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_201_length_11131_cov_3.94854	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_202_length_11087_cov_3.99211	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_205_length_11016_cov_5.29596	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_206_length_10954_cov_5.00128	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_207_length_10866_cov_8.17713	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_208_length_10652_cov_4.93309	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_209_length_10651_cov_4.81172	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_2095_length_1196_cov_1.76687	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_211_length_10568_cov_4.80139	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
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NG_16262_55_lib261982_NODE_215_length_10392_cov_5.67186	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_216_length_10365_cov_5.61746	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_217_length_10332_cov_5.18332	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_218_length_10330_cov_11.8411	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_220_length_10304_cov_10.1509	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_221_length_10299_cov_8.88891	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_223_length_10276_cov_5.06095	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_225_length_10145_cov_4.44252	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_226_length_10141_cov_6.04422	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_227_length_10077_cov_6.73119	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_229_length_10046_cov_5.34151	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_230_length_10041_cov_3.98107	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_231_length_9879_cov_4.59619	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_232_length_9878_cov_5.51379	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_233_length_9870_cov_7.05736	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_235_length_9838_cov_7.92426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_236_length_9831_cov_6.57263	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_239_length_9687_cov_9.45183	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_241_length_9682_cov_5.87036	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_243_length_9620_cov_5.05436	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_246_length_9502_cov_5.02043	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_247_length_9479_cov_6.41543	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_248_length_9464_cov_4.19386	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_249_length_9439_cov_4.4367	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_252_length_9409_cov_4.66132	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_253_length_9393_cov_4.67905	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_254_length_9373_cov_5.74104	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_255_length_9316_cov_4.77454	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_257_length_9268_cov_3.87822	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_258_length_9267_cov_11.831	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_259_length_9234_cov_4.34775	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_260_length_9133_cov_6.95726	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_261_length_9078_cov_5.70863	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_262_length_9041_cov_5.2495	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_263_length_9009_cov_4.64932	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_264_length_8977_cov_4.48487	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_266_length_8942_cov_6.06133	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_268_length_8903_cov_3.82007	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_269_length_8897_cov_6.0751	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_270_length_8870_cov_5.9519	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_271_length_8862_cov_4.39457	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_272_length_8850_cov_4.09574	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_273_length_8732_cov_4.41385	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_274_length_8726_cov_8.2265	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_275_length_8698_cov_5.92792	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_276_length_8695_cov_5.02315	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_277_length_8669_cov_9.39389	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_278_length_8662_cov_5.71314	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_282_length_8543_cov_2.77521	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_284_length_8417_cov_5.02942	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_285_length_8415_cov_7.57943	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_286_length_8365_cov_3.29134	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_287_length_8342_cov_4.2189	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_289_length_8293_cov_5.32993	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_290_length_8289_cov_5.41778	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_291_length_8287_cov_6.40172	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_292_length_8253_cov_4.30873	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_293_length_8221_cov_5.27382	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_295_length_8115_cov_4.2897	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_296_length_8032_cov_3.64022	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_297_length_8000_cov_6.96488	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_298_length_7987_cov_9.4386	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_299_length_7970_cov_3.60076	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_300_length_7966_cov_7.55151	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_301_length_7954_cov_6.88366	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_304_length_7857_cov_4.24686	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_305_length_7844_cov_4.47914	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_306_length_7804_cov_4.24777	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_308_length_7778_cov_4.12715	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_309_length_7773_cov_4.98031	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_310_length_7773_cov_3.22998	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_311_length_7707_cov_4.35089	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_312_length_7698_cov_4.40024	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_313_length_7694_cov_5.26705	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_314_length_7689_cov_4.34504	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_315_length_7654_cov_4.68509	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_316_length_7642_cov_3.99328	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
NG_16262_55_lib261982_NODE_317_length_7628_cov_3.50231	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_318_length_7625_cov_4.55363	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_319_length_7622_cov_3.20074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_320_length_7589_cov_6.0661	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_321_length_7577_cov_4.26868	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_322_length_7569_cov_4.25286	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_324_length_7488_cov_15.1726	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_325_length_7446_cov_3.65674	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_326_length_7429_cov_5.30892	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_327_length_7375_cov_3.05219	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_328_length_7355_cov_3.64904	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_330_length_7346_cov_3.20998	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_332_length_7178_cov_5.88839	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_333_length_7176_cov_6.66423	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_334_length_7157_cov_4.74796	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_335_length_7156_cov_3.80341	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_336_length_7137_cov_3.34807	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_339_length_7045_cov_3.51416	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_340_length_7031_cov_3.54014	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_341_length_6991_cov_4.30479	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_342_length_6972_cov_7.52118	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_343_length_6854_cov_3.82027	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_344_length_6847_cov_9.33598	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_345_length_6846_cov_3.26064	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_346_length_6827_cov_6.04843	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_348_length_6789_cov_4.79789	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_349_length_6784_cov_3.77055	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_350_length_6782_cov_3.23175	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_351_length_6776_cov_3.88335	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_352_length_6771_cov_5.63431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_354_length_6720_cov_3.47172	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_355_length_6687_cov_4.45009	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_356_length_6686_cov_4.55663	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_357_length_6654_cov_5.58797	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_359_length_6616_cov_4.68511	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_361_length_6603_cov_2.95281	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_362_length_6588_cov_4.11358	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_365_length_6568_cov_3.68248	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_366_length_6556_cov_3.72989	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_368_length_6528_cov_3.65858	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_369_length_6493_cov_4.05825	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_370_length_6489_cov_6.89074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_371_length_6487_cov_5.2245	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_372_length_6463_cov_46.8892	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_373_length_6462_cov_3.09318	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_375_length_6415_cov_3.60833	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_376_length_6397_cov_8.10643	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_377_length_6395_cov_3.22539	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_378_length_6359_cov_3.89356	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae

NG_16262_55_lib261982_NODE_379_length_6329_cov_6.25709	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_380_length_6296_cov_4.17529	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_381_length_6265_cov_4.88422	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_384_length_6200_cov_6.55834	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_385_length_6198_cov_3.53264	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_387_length_6167_cov_5.13465	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_388_length_6140_cov_4.01611	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_393_length_6008_cov_3.34	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_394_length_6004_cov_4.80366	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_395_length_5974_cov_4.07974	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_396_length_5940_cov_4.39949	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_397_length_5925_cov_3.00818	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_398_length_5923_cov_4.2304	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_401_length_5856_cov_6.10464	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_402_length_5847_cov_4.31233	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_404_length_5798_cov_3.70207	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_405_length_5789_cov_4.61981	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_406_length_5786_cov_5.96981	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_408_length_5744_cov_5.44894	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_409_length_5711_cov_4.24204	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_410_length_5711_cov_3.37836	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_411_length_5708_cov_3.4992	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_412_length_5702_cov_3.38268	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_413_length_5700_cov_3.57857	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_414_length_5677_cov_5.33796	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_415_length_5672_cov_4.41214	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_416_length_5666_cov_4.23472	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_419_length_5626_cov_4.72824	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_420_length_5603_cov_6.11229	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_421_length_5588_cov_4.57708	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_423_length_5559_cov_5.18368	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_424_length_5551_cov_4.08788	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_425_length_5536_cov_3.91772	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_426_length_5524_cov_5.17535	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_428_length_5524_cov_3.52587	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_429_length_5517_cov_3.66917	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_430_length_5507_cov_6.75037	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_431_length_5505_cov_2.49394	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_432_length_5485_cov_4.21436	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_434_length_5472_cov_4.9317	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_435_length_5468_cov_11.2512	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_436_length_5463_cov_4.54826	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_439_length_5420_cov_4.77279	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_440_length_5413_cov_3.74804	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_441_length_5404_cov_4.01309	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_442_length_5397_cov_3.77761	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_444_length_5307_cov_4.33778	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_447_length_5286_cov_4.32135	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_448_length_5273_cov_3.4496	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_449_length_5214_cov_4.24598	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_450_length_5173_cov_3.33919	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_452_length_5153_cov_3.84778	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_453_length_5139_cov_3.88906	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_454_length_5108_cov_2.5563	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_455_length_5101_cov_3.98692	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_457_length_5086_cov_2.97595	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_458_length_5081_cov_3.09948	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_459_length_5079_cov_3.71298	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_461_length_5019_cov_3.12893	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_463_length_4999_cov_9.28621	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_464_length_4969_cov_3.9711	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_465_length_4934_cov_3.2935	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_469_length_4901_cov_4.50165	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_470_length_4897_cov_2.91264	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_471_length_4888_cov_3.24829	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_472_length_4866_cov_2.58512	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_474_length_4862_cov_3.07489	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_475_length_4861_cov_3.76966	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_476_length_4842_cov_2.77355	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_477_length_4833_cov_4.15802	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_479_length_4778_cov_2.8719	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_480_length_4777_cov_3.39983	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_482_length_4763_cov_4.524	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_484_length_4745_cov_4.10981	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_485_length_4741_cov_2.75181	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_486_length_4738_cov_3.18642	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_487_length_4734_cov_6.8754	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_488_length_4702_cov_2.44696	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_490_length_4697_cov_3.75183	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_491_length_4690_cov_2.64531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

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NG_16262_55_lib261982_NODE_493_length_4649_cov_3.19221	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_494_length_4619_cov_3.58677	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_495_length_4616_cov_3.61171	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_496_length_4606_cov_4.20897	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_497_length_4566_cov_4.31656	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_498_length_4562_cov_3.16863	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_499_length_4548_cov_4.99555	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_500_length_4532_cov_3.153	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_501_length_4529_cov_2.45619	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_502_length_4525_cov_7.33691	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_504_length_4459_cov_3.82879	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_505_length_4457_cov_2.91413	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_508_length_4422_cov_3.07236	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_510_length_4415_cov_3.0328	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_511_length_4405_cov_3.6508	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_512_length_4398_cov_4.15657	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
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NG_16262_55_lib261982_NODE_514_length_4392_cov_3.88886	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_515_length_4390_cov_7.7391	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_519_length_4346_cov_5.354	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_520_length_4346_cov_3.68236	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_521_length_4344_cov_5.43833	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_522_length_4342_cov_3.57686	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_523_length_4322_cov_4.29224	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_524_length_4320_cov_3.11161	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_525_length_4300_cov_3.67986	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_526_length_4292_cov_3.83951	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_527_length_4289_cov_2.84388	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_529_length_4279_cov_3.22704	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_530_length_4273_cov_4.5441	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_531_length_4255_cov_3.72619	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_532_length_4255_cov_3.34619	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_533_length_4253_cov_2.83945	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_534_length_4235_cov_3.42608	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_535_length_4208_cov_3.67421	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_536_length_4205_cov_2.61928	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_538_length_4188_cov_3.15582	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_540_length_4173_cov_2.56144	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_541_length_4159_cov_4.06238	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_542_length_4154_cov_3.05855	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_543_length_4148_cov_3.80357	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_546_length_4131_cov_3.37365	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_547_length_4125_cov_4.05995	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_548_length_4124_cov_5.25362	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_549_length_4094_cov_2.48576	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_550_length_4085_cov_4.09479	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_551_length_4071_cov_4.31076	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_552_length_4069_cov_4.84205	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_554_length_4049_cov_2.9667	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_555_length_4034_cov_5.40337	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_556_length_4028_cov_3.78882	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_557_length_4024_cov_3.37113	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_558_length_4016_cov_2.91997	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_559_length_4014_cov_3.09144	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_560_length_4012_cov_3.35001	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
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NG_16262_55_lib261982_NODE_562_length_4008_cov_2.9188	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_564_length_3996_cov_4.99822	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_565_length_3984_cov_2.93459	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_566_length_3981_cov_7.82603	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_567_length_3980_cov_5.08382	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_568_length_3979_cov_3.62156	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_569_length_3956_cov_2.78518	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

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NG_16262_55_lib261982_NODE_570_length_3923_cov_2.8803	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_571_length_3915_cov_2.65984	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_572_length_3915_cov_2.22953	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_573_length_3910_cov_3.4677	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_575_length_3899_cov_3.34599	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_576_length_3890_cov_3.36584	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_577_length_3878_cov_3.95998	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_578_length_3863_cov_2.61345	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_58_length_33444_cov_15.8077	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_580_length_3852_cov_4.12536	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_583_length_3815_cov_4.44947	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_584_length_3814_cov_4.38095	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_585_length_3806_cov_4.21328	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_586_length_3785_cov_4.44826	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
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NG_16262_55_lib261982_NODE_589_length_3777_cov_3.53896	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_59_length_32107_cov_14.1981	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_590_length_3777_cov_2.20634	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_592_length_3773_cov_4.16326	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_594_length_3763_cov_4.08522	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_595_length_3759_cov_2.62257	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_596_length_3741_cov_2.75393	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_597_length_3737_cov_3.22243	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_60_length_31855_cov_7.86704	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_600_length_3722_cov_2.41996	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_601_length_3719_cov_3.57915	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_602_length_3717_cov_4.71873	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_603_length_3715_cov_5.07514	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_604_length_3709_cov_3.82594	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_606_length_3706_cov_3.41359	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_607_length_3696_cov_2.87586	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_608_length_3696_cov_2.8039	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_609_length_3694_cov_3.78511	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_610_length_3681_cov_4.07722	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_611_length_3677_cov_4.09856	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_613_length_3675_cov_3.90276	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_614_length_3673_cov_3.06025	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_616_length_3658_cov_2.83403	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_618_length_3651_cov_2.84399	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_619_length_3650_cov_2.58414	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_620_length_3641_cov_3.0304	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_621_length_3641_cov_2.2903	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_622_length_3613_cov_2.95165	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_623_length_3613_cov_2.84767	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_625_length_3607_cov_2.86092	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_626_length_3599_cov_3.28499	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_627_length_3595_cov_2.50254	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_628_length_3590_cov_4.64074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_629_length_3589_cov_3.80928	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_630_length_3562_cov_4.93442	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_631_length_3550_cov_2.61602	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_632_length_3548_cov_2.92098	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_633_length_3546_cov_2.67459	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_636_length_3512_cov_3.53486	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_637_length_3503_cov_5.85557	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_638_length_3501_cov_3.62565	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_641_length_3491_cov_2.66531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_642_length_3485_cov_3.70408	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_643_length_3477_cov_3.02601	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_644_length_3477_cov_2.3986	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_645_length_3471_cov_3.37412	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_646_length_3466_cov_3.41249	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_649_length_3452_cov_2.42567	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_650_length_3448_cov_4.18155	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_651_length_3445_cov_4.52271	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_652_length_3439_cov_2.74911	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_653_length_3436_cov_4.14818	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_654_length_3423_cov_2.87886	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_656_length_3401_cov_6.65631	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_657_length_3398_cov_3.51361	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_658_length_3397_cov_3.13824	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_66_length_28755_cov_12.4277	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_660_length_3382_cov_3.54043	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_661_length_3365_cov_2.95952	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_664_length_3331_cov_2.78541	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_665_length_3330_cov_2.67511	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_666_length_3329_cov_2.57086	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_667_length_3324_cov_2.7721	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_668_length_3322_cov_2.28466	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_669_length_3298_cov_2.79494	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_670_length_3295_cov_2.83272	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_671_length_3294_cov_2.83637	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_672_length_3293_cov_3.18283	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_673_length_3279_cov_3.43641	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_674_length_3279_cov_2.41098	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_675_length_3271_cov_3.7245	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_676_length_3257_cov_5.28201	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_678_length_3247_cov_2.48622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_679_length_3233_cov_3.28918	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_68_length_27700_cov_6.36394	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_680_length_3232_cov_3.27258	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_681_length_3226_cov_2.91138	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_682_length_3222_cov_2.976	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_683_length_3215_cov_3.3807	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_684_length_3214_cov_3.59671	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_685_length_3207_cov_4.36199	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_686_length_3205_cov_3.09714	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_687_length_3203_cov_2.96792	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_688_length_3203_cov_2.13914	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_689_length_3193_cov_4.35883	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_690_length_3193_cov_4.07584	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_691_length_3189_cov_5.12476	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_693_length_3173_cov_2.60487	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_694_length_3164_cov_2.88067	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_695_length_3153_cov_2.80052	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_697_length_3143_cov_4.25	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_698_length_3143_cov_3.29534	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_70_length_26277_cov_27.7581	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_700_length_3141_cov_4.13286	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_701_length_3138_cov_3.13396	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_702_length_3138_cov_2.02043	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_703_length_3133_cov_3.87102	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_704_length_3132_cov_4.72246	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_706_length_3123_cov_3.29596	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_707_length_3119_cov_3.70463	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_708_length_3119_cov_3.19648	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_709_length_3117_cov_3.32789	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_710_length_3115_cov_3.39804	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_712_length_3112_cov_2.8649	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_713_length_3107_cov_3.03145	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_714_length_3099_cov_3.95466	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_715_length_3098_cov_2.67006	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_717_length_3090_cov_2.16343	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_718_length_3085_cov_3.76469	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_719_length_3080_cov_2.99868	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_720_length_3079_cov_3.44478	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_721_length_3074_cov_3.56741	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_722_length_3063_cov_3.23737	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_723_length_3061_cov_2.99135	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_724_length_3053_cov_1.60607	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_725_length_3045_cov_3.44147	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_726_length_3044_cov_5.55604	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_727_length_3044_cov_2.26531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_728_length_3038_cov_2.57962	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_729_length_3036_cov_4.0681	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_73_length_26047_cov_19.4892	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_730_length_3036_cov_2.85475	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_731_length_3035_cov_3.32114	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_732_length_3029_cov_2.59381	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_733_length_3028_cov_3.69324	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_734_length_3020_cov_2.91872	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_735_length_3011_cov_2.53857	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_737_length_3006_cov_8.11115	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_738_length_3006_cov_2.3287	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_74_length_25989_cov_9.70348	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_740_length_3002_cov_3.13811	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_78_length_24879_cov_6.15465	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_81_length_24154_cov_10.9593	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_82_length_23914_cov_10.8155	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_83_length_23862_cov_12.4976	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_86_length_23311_cov_8.20352	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_87_length_23261_cov_14.1494	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_88_length_23256_cov_9.56217	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_90_length_23073_cov_6.27839	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_92_length_22788_cov_6.45467	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_949_length_2340_cov_2.67133	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_95_length_22039_cov_13.9261	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_97_length_21483_cov_10.6483	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_972_length_2293_cov_1.83199	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_55_lib261982_NODE_98_length_21457_cov_5.19054	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_55_lib261982_NODE_99_length_21091_cov_6.70531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_101_length_8716_cov_11.9064	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_102_length_8538_cov_9.8042	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_105_length_8221_cov_8.08842	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_106_length_8193_cov_4.56316	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_107_length_8138_cov_4.64283	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_114_length_7375_cov_42.3699	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_115_length_7204_cov_2.98937	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_116_length_7177_cov_6.78124	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_118_length_7026_cov_5.103	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_120_length_6908_cov_36.919	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_124_length_6521_cov_4.04114	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_126_length_6240_cov_5.86516	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_127_length_6054_cov_6.72745	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_130_length_5986_cov_4.1192	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_66_lib261987_NODE_132_length_5908_cov_10.4481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Myoviridae
NG_16262_66_lib261987_NODE_133_length_5900_cov_3.90813	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_138_length_5540_cov_22.7125	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_140_length_5526_cov_20.9249	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_141_length_5487_cov_19.185	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_143_length_4960_cov_20.5498	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_144_length_4937_cov_3.2456	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_146_length_4817_cov_57.6415	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_147_length_4749_cov_22.66	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_151_length_4529_cov_600.981	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_153_length_4442_cov_16.0875	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_154_length_4429_cov_4.86854	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_155_length_4384_cov_19.0843	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_164_length_4170_cov_2.77181	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_167_length_4127_cov_4.81803	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_168_length_4123_cov_3.47173	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_66_lib261987_NODE_169_length_4094_cov_2.73756	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_170_length_3940_cov_5.087	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_171_length_3773_cov_2.97795	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_177_length_3556_cov_3.82919	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_18_length_35870_cov_10.6011	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_181_length_3482_cov_3.41815	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_182_length_3458_cov_6.0382	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_183_length_3430_cov_3.02193	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_185_length_3407_cov_3.00388	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_186_length_3369_cov_2.76011	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_187_length_3280_cov_2.91814	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_19_length_35380_cov_10.1936	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_190_length_3226_cov_3.96941	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_191_length_3187_cov_3.36111	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_193_length_3161_cov_11.6584	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_194_length_3131_cov_3.48602	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_66_lib261987_NODE_197_length_3035_cov_3.61174	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_198_length_3003_cov_9.19233	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_20_length_33912_cov_20.9586	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_22_length_33531_cov_32.1376	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_239_length_2123_cov_3.50774	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_299_length_1504_cov_3.53968	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_32_length_25469_cov_14.897	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_339_length_1267_cov_1.48762	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_400_length_1051_cov_1.07731	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_46_length_19825_cov_43.5628	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_47_length_19809_cov_12.8866	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_48_length_19460_cov_27.0266	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_5_length_59879_cov_30.7188	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_52_length_18428_cov_8.77739	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_60_length_14394_cov_41.8356	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_61_length_14279_cov_6.69783	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

NG_16262_66_lib261987_NODE_68_length_13229_cov_10.0155	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_69_length_13116_cov_5.97956	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_71_length_12947_cov_17.2695	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_75_length_12678_cov_4.52222	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_76_length_12662_cov_19.573	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_82_length_11173_cov_5.15506	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_83_length_10909_cov_4.77649	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_84_length_10890_cov_104.149	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_86_length_10847_cov_6.6174	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_87_length_10756_cov_8.0828	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_89_length_10526_cov_4.97794	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_90_length_10423_cov_4.50945	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_91_length_10125_cov_3.80308	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
NG_16262_66_lib261987_NODE_96_length_9324_cov_15.1078	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc1	0.91	0.02	0.95	0.77	-0.05	0.97	Podoviridae
vc10	0.90	0.02	0.94	0.22	0.20	0.97	Unclassified
vc101	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

vc105	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
vc108	0.76	-0.05	0.94	0.99	0.00	0.99	Unclassified
vc110	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
vc111	0.98	0.00	0.98	0.20	0.21	0.97	Unclassified
vc118	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
vc125	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
vc139	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
vc142	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
vc143	0.11	0.25	0.64	1.00	0.00	1.00	Siphoviridae
vc147	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc152	0.98	0.00	0.98	0.52	-0.10	0.97	Myoviridae
vc156	1.00	0.00	1.00	0.26	0.18	0.97	Siphoviridae
vc165	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
vc166	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc172	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc178	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
vc188	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
vc198	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc203	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc204	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc208	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

vc212	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc214	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Myoviridae
vc216	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc217	0.14	0.24	0.64	0.98	0.00	0.99	Unclassified
vc218	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc227	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc241	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
vc248	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc249	0.97	-0.01	0.97	0.47	0.12	0.97	Siphoviridae
vc253	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc257	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
vc258	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
vc259	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
vc26	0.97	-0.01	0.98	0.80	0.04	0.97	Myoviridae
vc263	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc264	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc265	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc266	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc267	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

vc270	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc271	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc273	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc276	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Siphoviridae
vc278	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc281	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc282	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc291	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc294	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc295	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc30	0.93	0.02	0.96	0.51	-0.11	0.97	Unclassified
vc300	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc302	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc303	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc304	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc305	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc307	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified

vc308	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc309	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc311	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc316	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc317	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Polyomavirida e
vc318	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Siphoviridae
vc319	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc321	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc322	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc326	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc327	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc331	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc333	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc336	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc337	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc339	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

vc346	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc348	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
vc367	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc368	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc369	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
vc370	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc371	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc372	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc376	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc377	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc382	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc385	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc386	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc396	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc397	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc398	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc4	0.91	0.02	0.95	0.73	0.06	0.97	Siphoviridae
vc402	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

vc404	0.93	0.01	0.96	0.56	-0.09	0.97	Siphoviridae
vc407	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc408	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc409	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc413	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc414	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
vc434	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
vc435	0.97	-0.01	0.97	0.47	0.12	0.97	Unclassified
vc436	0.97	-0.01	0.97	0.47	0.12	0.97	Myoviridae
vc438	0.97	-0.01	0.97	0.47	0.12	0.97	Siphoviridae
vc439	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc440	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Podoviridae
vc441	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc448	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc449	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc450	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc451	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc452	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc453	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

vc456	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc457	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc459	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc460	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc463	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc466	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc467	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc468	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc469	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc470	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc471	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc472	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc476	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc480	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc481	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified
vc482	#N/A	#N/ A	#N/A	#N/A	#N/ A	#N/A	Unclassified

vc483	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Unclassified
vc52	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Podoviridae
vc55	0.75	0.05	0.94	0.97	0.01	0.98	Podoviridae
vc56	0.97	-0.01	0.97	0.53	0.10	0.97	Heterogeneous
vc65	0.91	0.02	0.94	0.65	-0.07	0.97	Unclassified
vc66	0.93	-0.01	0.97	0.77	-0.05	0.97	Podoviridae
vc73	0.34	0.15	0.66	1.00	0.00	1.00	Unclassified
vc74	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
vc83	0.09	-0.27	0.64	0.99	0.00	0.99	Unclassified
vc85	0.98	0.00	0.98	0.52	-0.10	0.97	Siphoviridae
vc9	0.91	-0.02	0.94	0.90	0.02	0.97	Siphoviridae

Table 8. Spearman correlations between RSV counts and PC-axes 1 and 2 from unweighted UniFrac distances

RSV	pc1 p-value	pc1 rho	pc1 p-value adjusted	pc2 p-value	pc2 rho	pc2 p-value adjusted	Genus	Species
Seq_0000296	3.88E-03	-0.46	0.17	2.10E-06	0.69	2.90E-03	Clostridiales_unclassified	Unclassified
Seq_0000155	9.00E-04	-0.52	0.07	3.37E-05	0.63	1.41E-02	Coprococcus	Coprococcus_comes
Seq_0000070	6.38E-03	-0.44	0.22	5.75E-05	0.61	1.41E-02	Lachnospiraceae_unclassified	Unclassified
Seq_0000012	2.31E-02	-0.37	0.37	5.18E-05	0.61	1.41E-02	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000075	3.09E-02	-0.36	0.38	4.67E-05	0.62	1.41E-02	Ruminococcus2	Ruminococcus_torques

Seq_0000034	3.42E-01	-0.16	0.58	6.10E-05	0.61	1.41E-02	Anaerostipes	Anaerostipes_hadrus
Seq_0000049	2.29E-03	-0.49	0.13	1.82E-04	0.58	3.60E-02	Dorea	Dorea_longicatena
Seq_0000013	2.14E-01	0.21	0.47	6.34E-04	- 0.54	1.10E-01	Escherichia/Shigella	Unclassified
Seq_0000083	1.21E-02	-0.41	0.29	8.34E-04	- 0.53	1.28E-01	Methanobrevibacter	Methanobrevibacter_smithii
Seq_0000683	5.94E-01	-0.09	0.76	9.43E-04	- 0.52	1.31E-01	Ralstonia	Unclassified
Seq_0000017	4.22E-08	0.76	0.00	3.03E-03	- 0.47	2.54E-01	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0000182	2.42E-02	-0.37	0.37	3.12E-03	- 0.47	2.54E-01	Chlorophyta_unclassified	Unclassified
Seq_0000291	2.42E-02	-0.37	0.37	3.12E-03	- 0.47	2.54E-01	Acidiphilium	Unclassified
Seq_0000307	2.42E-02	-0.37	0.37	3.12E-03	- 0.47	2.54E-01	Bacteria_unclassified	Unclassified
Seq_0001118	2.42E-02	-0.37	0.37	3.12E-03	- 0.47	2.54E-01	Bacteroidales_unclassified	Unclassified
Seq_0000004	9.78E-02	-0.28	0.44	2.75E-03	0.48	2.54E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000604	2.99E-01	-0.18	0.54	2.16E-03	0.49	2.54E-01	Clostridiales_unclassified	Eubacterium_ventriosum
Seq_0000117	9.42E-01	-0.01	0.96	3.51E-03	0.47	2.70E-01	Anaerostipes	Anaerostipes_hadrus
Seq_0000310	1.08E-02	-0.41	0.29	4.16E-03	0.46	3.03E-01	Clostridiales_unclassified	Eubacterium_hallii
Seq_0000403	1.82E-01	-0.22	0.47	4.51E-03	0.46	3.12E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0000120	1.23E-02	-0.41	0.29	6.44E-03	0.44	4.24E-01	Clostridiales_unclassified	Eubacterium_hallii
Seq_0000009	2.63E-02	-0.37	0.37	8.18E-03	0.43	4.53E-01	Collinsella	Collinsella_aerofaciens

Seq_0000483	4.11E-02	0.34	0.42	7.81E-03	- 0.43	4.53E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000467	1.10E-01	-0.27	0.44	8.02E-03	0.43	4.53E-01	Ruminococcaceae_ unclassified	Faecalibacterium_ prausnitzii
Seq_0000931	2.14E-01	-0.21	0.47	7.35E-03	0.43	4.53E-01	Dorea	Dorea_longicatena
Seq_0000216	2.27E-02	-0.37	0.37	8.92E-03	0.42	4.56E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001818	3.98E-02	-0.34	0.42	8.98E-03	0.42	4.56E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000735	9.45E-02	-0.28	0.44	9.56E-03	0.42	4.56E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000559	1.33E-01	-0.25	0.45	9.52E-03	0.42	4.56E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001753	2.74E-01	-0.18	0.52	1.05E-02	0.42	4.83E-01	Firmicutes_unclassi fied	Unclassified
Seq_0000174	5.66E-01	-0.10	0.75	1.10E-02	0.41	4.91E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001138	8.58E-03	-0.43	0.26	1.16E-02	0.41	4.96E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000377	1.91E-01	0.22	0.47	1.18E-02	- 0.41	4.96E-01	Lactobacillales_unc lassified	Unclassified
Seq_0000453	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Leptospirillum	Leptospirillum_fer riphilum
Seq_0000681	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Gammaproteobacte ria_unclassified	Unclassified
Seq_0000750	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Acidithiobacillus	Unclassified
Seq_0000964	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Acidithiobacillus	Acidithiobacillus_ ferrooxidans
Seq_0001020	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Bacteria_unclassifi ed	Cyanidium_caldari um
Seq_0001341	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Alicyclobacillus	Unclassified

Seq_0001594	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Acidithiobacillus	Acidithiobacillus_ ferrooxidans
Seq_0001800	1.20E-01	-0.26	0.45	1.66E-02	- 0.39	5.23E-01	Acidobacterium_un classified	Acidobacterium_c apsulatum
Seq_0002322	1.28E-01	-0.25	0.45	1.64E-02	- 0.39	5.23E-01	Alicyclobacillus	Unclassified
Seq_0003146	1.28E-01	-0.25	0.45	1.64E-02	- 0.39	5.23E-01	Ferroplasma	Unclassified
Seq_0000851	2.43E-01	-0.20	0.49	1.38E-02	0.40	5.23E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001310	1.16E-01	0.26	0.45	1.75E-02	- 0.39	5.37E-01	Rhizobiales_unclas sified	Unclassified
Seq_0000549	5.23E-02	-0.32	0.44	2.05E-02	0.38	6.05E-01	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0000657	6.33E-02	-0.31	0.44	2.03E-02	- 0.38	6.05E-01	Akkermansia	Akkermansia_muc iniphila
Seq_0000433	7.24E-07	-0.71	0.00	5.31E-02	0.32	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001534	2.45E-04	-0.57	0.05	3.19E-02	0.35	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000720	3.22E-04	-0.56	0.06	1.26E-01	0.26	6.18E-01	Bacteroides	Unclassified
Seq_0000228	3.96E-04	-0.55	0.06	6.13E-02	0.31	6.18E-01	Dorea	Dorea_formicigen erans
Seq_0000026	5.20E-04	-0.54	0.06	4.62E-02	0.33	6.18E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0000771	6.02E-04	-0.54	0.06	3.71E-02	0.34	6.18E-01	Bacteria_unclassifi ed	Unclassified
Seq_0000651	9.46E-04	-0.52	0.07	1.32E-01	0.25	6.18E-01	Odoribacter	Odoribacter_splan chnicus
Seq_0000251	1.20E-03	0.51	0.08	8.33E-02	- 0.29	6.18E-01	Blautia	Unclassified
Seq_0001235	1.75E-03	-0.50	0.11	2.60E-02	0.37	6.18E-01	Alistipes	Unclassified

Seq_0000397	2.03E-03	-0.49	0.12	7.59E-02	0.30	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0000396	2.53E-03	-0.48	0.14	6.95E-02	0.30	6.18E-01	Clostridium_sensu_stricto	Unclassified
Seq_0001012	2.61E-03	0.48	0.14	2.74E-02	-0.36	6.18E-01	Clostridium_XIVa	Clostridium_nexile
Seq_0000189	3.35E-03	0.47	0.16	2.24E-02	-0.37	6.18E-01	Clostridium_XIVa	Clostridium_nexile
Seq_0000040	4.46E-03	-0.46	0.18	1.46E-01	0.24	6.18E-01	Blautia	Ruminococcus_obesum
Seq_0000252	5.09E-03	-0.45	0.19	5.34E-02	0.32	6.18E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000253	5.93E-03	0.44	0.22	5.66E-02	-0.32	6.18E-01	Lactobacillus	Unclassified
Seq_0001194	6.86E-03	0.44	0.22	5.84E-02	-0.31	6.18E-01	Pediococcus	Unclassified
Seq_0000356	9.17E-03	-0.42	0.28	9.05E-02	-0.28	6.18E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0000033	1.17E-02	-0.41	0.29	9.30E-02	0.28	6.18E-01	Blautia	Blautia_luti
Seq_0001023	1.18E-02	-0.41	0.29	4.88E-02	-0.33	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0002064	1.05E-02	-0.42	0.29	2.70E-02	0.36	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000401	1.33E-02	-0.40	0.31	9.76E-02	0.28	6.18E-01	Subdoligranulum	Unclassified
Seq_0000016	1.37E-02	0.40	0.31	3.78E-02	-0.34	6.18E-01	Pediococcus	Unclassified
Seq_0000381	1.50E-02	-0.40	0.33	1.05E-01	-0.27	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0000691	1.64E-02	-0.39	0.34	1.07E-01	0.27	6.18E-01	Alistipes	Unclassified
Seq_0000035	1.84E-02	-0.39	0.37	1.40E-01	0.25	6.18E-01	Erysipelotrichaceae_unclassified	Unclassified
Seq_0000043	2.32E-02	-0.37	0.37	1.60E-01	0.24	6.18E-01	Roseburia	Eubacterium_rectale

Seq_0000214	2.37E-02	-0.37	0.37	5.81E-02	- 0.31	6.18E-01	Akkermansia	Akkermansia_muciniphila
Seq_0000247	2.81E-02	0.36	0.37	2.92E-02	- 0.36	6.18E-01	Dorea	Clostridium_hylemonae
Seq_0000267	1.98E-02	0.38	0.37	3.70E-02	- 0.34	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000548	2.25E-02	-0.37	0.37	2.50E-02	0.37	6.18E-01	Roseburia	Unclassified
Seq_0000648	3.01E-02	0.36	0.37	1.62E-01	- 0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001135	2.90E-02	0.36	0.37	1.61E-01	- 0.24	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001788	2.94E-02	-0.36	0.37	4.97E-02	- 0.32	6.18E-01	Firmicutes_unclassified	Unclassified
Seq_0002443	2.91E-02	-0.36	0.37	8.57E-02	0.29	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002805	3.01E-02	0.36	0.37	1.62E-01	- 0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003928	2.71E-02	-0.36	0.37	5.38E-02	- 0.32	6.18E-01	Firmicutes_unclassified	Unclassified
Seq_0000186	3.27E-02	-0.35	0.38	1.46E-01	0.24	6.18E-01	Firmicutes_unclassified	Eubacterium_biforme
Seq_0003067	3.49E-02	-0.35	0.40	1.20E-01	- 0.26	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001155	3.59E-02	-0.35	0.40	1.28E-01	- 0.25	6.18E-01	Collinsella	Unclassified
Seq_0001580	3.59E-02	-0.35	0.40	1.28E-01	- 0.25	6.18E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0002208	3.59E-02	-0.35	0.40	1.28E-01	- 0.25	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0000002	3.73E-02	-0.34	0.40	1.37E-01	0.25	6.18E-01	Bifidobacterium	Unclassified
Seq_0000053	3.81E-02	-0.34	0.41	3.62E-02	0.35	6.18E-01	Blautia	Blautia_faecis
Seq_0001560	4.14E-02	-0.34	0.42	5.80E-02	- 0.31	6.18E-01	Bacteroidales_unclassified	Unclassified

Seq_0001941	4.14E-02	-0.34	0.42	5.80E-02	- 0.31	6.18E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0002021	4.14E-02	-0.34	0.42	5.80E-02	- 0.31	6.18E-01	Bacteria_unclassifi ed	Unclassified
Seq_0002959	4.14E-02	-0.34	0.42	5.80E-02	- 0.31	6.18E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0003210	4.14E-02	-0.34	0.42	5.80E-02	- 0.31	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000561	4.35E-02	-0.33	0.42	4.82E-02	0.33	6.18E-01	Blautia	Unclassified
Seq_0001511	4.33E-02	-0.33	0.42	4.80E-02	0.33	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0003258	4.26E-02	-0.34	0.42	1.12E-01	- 0.27	6.18E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0000030	4.83E-02	-0.33	0.44	5.36E-02	0.32	6.18E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001279	4.94E-02	-0.33	0.44	4.89E-02	- 0.33	6.18E-01	Bacteria_unclassifi ed	Unclassified
Seq_0001611	4.87E-02	-0.33	0.44	4.44E-02	0.33	6.18E-01	Bacteria_unclassifi ed	Unclassified
Seq_0000148	6.59E-02	0.31	0.44	4.77E-02	- 0.33	6.18E-01	Clostridium_XVIII	Clostridium_ramo sum
Seq_0000159	6.67E-02	-0.30	0.44	5.84E-02	0.31	6.18E-01	Ruminococcus2	Unclassified
Seq_0000183	6.43E-02	-0.31	0.44	2.68E-02	0.36	6.18E-01	Ruminococcaceae_ unclassified	Gemmiger_formic ilis
Seq_0000204	9.15E-02	0.28	0.44	1.47E-01	- 0.24	6.18E-01	Flavonifractor	Flavonifractor_pla utii
Seq_0000319	9.15E-02	-0.28	0.44	9.38E-02	0.28	6.18E-01	Bacteroides	Bacteroides_cacca e
Seq_0000337	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Prevotellaceae_uncl assified	Unclassified
Seq_0000506	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Mogibacterium	Unclassified
Seq_0000637	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Prevotellaceae_uncl assified	Unclassified

Seq_0000645	6.18E-02	-0.31	0.44	1.09E-01	0.27	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000646	9.26E-02	0.28	0.44	3.00E-02	- 0.36	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000655	5.03E-02	0.32	0.44	1.25E-01	- 0.26	6.18E-01	Lactobacillus	Unclassified
Seq_0000715	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteroidetes_unclassified	Unclassified
Seq_0000855	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Alistipes	Unclassified
Seq_0001009	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Methanobrevibacter	Methanobrevibacter_woesei
Seq_0001068	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteroidetes_unclassified	Unclassified
Seq_0001212	7.48E-02	-0.30	0.44	1.35E-01	0.25	6.18E-01	Ruminococcaceae_unclassified	Flavonifractor_plautii
Seq_0001231	8.84E-02	0.28	0.44	7.49E-02	- 0.30	6.18E-01	Blautia	Unclassified
Seq_0001289	1.04E-01	-0.27	0.44	1.52E-01	0.24	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001427	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Phenylobacterium	Unclassified
Seq_0001498	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Sutterella	Unclassified
Seq_0001503	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Collinsella	Unclassified
Seq_0001567	7.96E-02	-0.29	0.44	8.97E-02	0.28	6.18E-01	Firmicutes_unclassified	Unclassified
Seq_0001705	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Chitinophagaceae_unclassified	Unclassified
Seq_0001745	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteria_unclassified	Unclassified

Seq_0001749	5.95E-02	0.31	0.44	5.85E-02	- 0.31	6.18E-01	Rothia	Rothia_dentocario sa
Seq_0001760	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Slackia	Slackia_euolifaci ens
Seq_0002234	8.26E-02	-0.29	0.44	6.39E-02	- 0.31	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002364	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Collinsella	Collinsella_aerofa ciens
Seq_0002437	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002533	9.05E-02	-0.28	0.44	1.16E-01	0.26	6.18E-01	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0002566	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002619	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002758	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002761	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Lactobacillus	Unclassified
Seq_0002924	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Candidatus_Saccha ribacteria_unclassif ied	Unclassified
Seq_0003018	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0003088	7.20E-02	-0.30	0.44	1.54E-01	0.24	6.18E-01	Butyricicoccus	Eubacterium_des molans
Seq_0003161	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0003194	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0003209	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Lachnospiraceae_u nclassified	Unclassified

Seq_0003260	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Enterorhabdus	Unclassified
Seq_0003269	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Anaerostipes	Anaerostipes_butyraticus
Seq_0003340	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003423	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003657	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003677	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0003898	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003932	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Barnesiella	Barnesiella_intestinalis
Seq_0003971	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Firmicutes_unclassified	Unclassified
Seq_0003972	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0004204	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004265	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0004412	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0004614	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0004858	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Pediococcus	Pediococcus_parvulus
Seq_0004859	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteria_unclassified	Unclassified

Seq_0005174	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0005175	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Oscillibacter	Unclassified
Seq_0005176	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0005446	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteroides	Unclassified
Seq_0005665	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0006488	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0006489	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Acidobacterium_unclassified	Acidobacterium_capsulatum
Seq_0007249	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0007292	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Firmicutes_unclassified	Unclassified
Seq_0007293	1.12E-01	-0.27	0.44	1.36E-01	- 0.25	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0000245	1.18E-01	0.26	0.45	9.47E-02	- 0.28	6.18E-01	Enterococcus	Unclassified
Seq_0001084	1.20E-01	-0.26	0.45	2.94E-02	0.36	6.18E-01	Blautia	Unclassified
Seq_0000025	1.24E-01	-0.26	0.45	1.45E-01	- 0.24	6.18E-01	Bacteroides	Bacteroides_fragilis
Seq_0000238	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Bacteroidales_unclassified	Unclassified
Seq_0001355	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0001604	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Prevotellaceae_unclassified	Unclassified
Seq_0002425	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Burkholderiales_unclassified	Unclassified

Seq_0002897	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Bacteroidales_unclassified	Unclassified
Seq_0003380	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Lactobacillus	Lactobacillus_iners
Seq_0003679	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Collinsella	Collinsella_tanaka ei
Seq_0003712	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0004252	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Collinsella	Unclassified
Seq_0006447	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Phenylobacterium	Unclassified
Seq_0006448	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0006450	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Acidocella	Unclassified
Seq_0007257	1.36E-01	-0.25	0.45	1.12E-01	- 0.27	6.18E-01	Thermoplasmatales_unclassified	Unclassified
Seq_0000335	1.68E-01	-0.23	0.47	5.52E-02	0.32	6.18E-01	Ruminococcus	Ruminococcus_cal lidus
Seq_0000368	1.77E-01	0.23	0.47	5.37E-02	- 0.32	6.18E-01	Streptococcus	Unclassified
Seq_0000385	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Clostridium_sensu_stricto	Clostridium_parap utrificum
Seq_0000416	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Lachnospiraceae_unclassified	Ruminococcus_gn avus
Seq_0000419	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Peptostreptococcaceae_unclassified	Clostridium_rumin antium
Seq_0000441	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Peptostreptococcaceae_unclassified	Clostridium_rumin antium
Seq_0000442	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Lachnospiraceae_unclassified	Ruminococcus_gn avus

Seq_0000458	1.53E-01	0.24	0.47	1.21E-01	0.26	6.18E-01	Clostridium_XVIII	Clostridium_spiroforme
Seq_0000475	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0000517	1.87E-01	0.22	0.47	1.39E-01	- 0.25	6.18E-01	Bacteria_unclassified	Clostridium_innocuum
Seq_0000671	1.89E-01	-0.22	0.47	8.25E-02	0.29	6.18E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0000807	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0000979	1.70E-01	-0.23	0.47	2.42E-02	0.37	6.18E-01	Clostridium_XIVb	Clostridium_lactatifermentans
Seq_0001036	1.67E-01	-0.23	0.47	1.04E-01	0.27	6.18E-01	Bacteroides	Unclassified
Seq_0001040	1.68E-01	-0.23	0.47	5.74E-02	0.32	6.18E-01	Blautia	Unclassified
Seq_0001096	1.77E-01	-0.23	0.47	1.46E-01	0.24	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0001187	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Enterobacteriaceae_unclassified	Unclassified
Seq_0001523	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0001740	1.94E-01	0.22	0.47	5.48E-02	- 0.32	6.18E-01	Actinomyces	Actinomyces_graevenitzii
Seq_0001897	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Atopobium	Atopobium_parvulum
Seq_0001974	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0002086	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Streptococcus	Unclassified
Seq_0002363	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Clostridium_sensu_stricto	Unclassified
Seq_0002435	2.21E-01	-0.21	0.47	1.55E-01	- 0.24	6.18E-01	Ruminococcaceae_unclassified	Unclassified

Seq_0002529	2.21E-01	-0.21	0.47	1.55E-01	- 0.24	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0002575	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Actinomyces	Unclassified
Seq_0002576	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Clostridium_sensu_stricto	Unclassified
Seq_0002714	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Leptotrichia	Unclassified
Seq_0002913	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0002925	2.21E-01	-0.21	0.47	1.55E-01	- 0.24	6.18E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002936	2.02E-01	0.21	0.47	1.47E-01	- 0.24	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0002939	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Candidatus_Saccharibacteria_unclassified	Unclassified
Seq_0003126	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Rothia	Rothia_mucilaginosa
Seq_0003254	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Prevotella	Unclassified
Seq_0003355	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Solobacterium	Solobacterium_mooresii
Seq_0003459	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Prevotella	Prevotella_melaninogenica
Seq_0003463	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Howardella	Unclassified
Seq_0003790	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Eubacterium	Eubacterium_brahy
Seq_0003891	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Abiotrophia	Abiotrophia_defectiva
Seq_0003892	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified

Seq_0004062	2.21E-01	-0.21	0.47	1.55E-01	- 0.24	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004714	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Candidatus_Saccha ribacteria_unclassif ied	Unclassified
Seq_0004994	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Fusobacterium	Unclassified
Seq_0005400	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Firmicutes_unclassi fied	Unclassified
Seq_0005625	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Prevotella	Prevotella_nanceie nsis
Seq_0006066	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Prevotella	Prevotella_pallens
Seq_0006420	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Odoribacter	Odoribacter_splan chnicus
Seq_0007228	2.28E-01	0.20	0.47	1.63E-01	- 0.23	6.18E-01	Verrucomicrobia_u nclassified	Unclassified
Seq_0000581	2.47E-01	-0.20	0.50	2.70E-02	0.36	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000304	2.64E-01	0.19	0.51	1.19E-01	- 0.26	6.18E-01	Blautia	Unclassified
Seq_0000510	2.73E-01	-0.18	0.52	1.28E-01	0.25	6.18E-01	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0000266	2.78E-01	0.18	0.52	6.94E-02	- 0.30	6.18E-01	Streptococcus	Unclassified
Seq_0001239	2.86E-01	-0.18	0.54	7.12E-02	0.30	6.18E-01	Anaerostipes	Anaerostipes_hadr us
Seq_0001642	3.06E-01	-0.17	0.54	3.49E-02	- 0.35	6.18E-01	Ralstonia	Unclassified
Seq_0001833	3.23E-01	0.17	0.56	8.00E-02	0.29	6.18E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001144	3.25E-01	0.17	0.57	4.67E-02	- 0.33	6.18E-01	Streptococcus	Unclassified

Seq_0000239	3.27E-01	-0.17	0.57	1.37E-01	0.25	6.18E-01	Sutterella	Sutterella_stercoricanis
Seq_0003097	3.32E-01	0.16	0.57	1.06E-01	- 0.27	6.18E-01	Lachnospiraceae_unclassified	Clostridium_hathewayi
Seq_0003251	3.32E-01	-0.16	0.57	1.18E-01	0.26	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0000055	3.40E-01	0.16	0.58	4.27E-02	- 0.33	6.18E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0000361	3.52E-01	-0.16	0.58	6.43E-02	0.31	6.18E-01	Clostridiales_unclassified	Eubacterium_eligens
Seq_0001736	3.49E-01	-0.16	0.58	5.37E-02	- 0.32	6.18E-01	Oscillibacter	Unclassified
Seq_0000005	3.63E-01	-0.15	0.59	3.17E-02	0.35	6.18E-01	Blautia	Unclassified
Seq_0000118	3.64E-01	-0.15	0.60	8.39E-02	- 0.29	6.18E-01	Bacteroides	Bacteroides_coprocola
Seq_0000457	3.71E-01	-0.15	0.60	8.60E-02	0.29	6.18E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000372	3.87E-01	-0.15	0.62	9.18E-02	- 0.28	6.18E-01	Actinomyces	Actinomyces_odontolyticus
Seq_0000405	4.10E-01	0.14	0.63	9.40E-02	- 0.28	6.18E-01	Prevotella	Prevotella_copri
Seq_0000849	4.11E-01	-0.14	0.63	1.36E-01	0.25	6.18E-01	Clostridiales_unclassified	Eubacterium_coprostanoligenes
Seq_0000708	4.28E-01	-0.13	0.65	7.28E-02	0.30	6.18E-01	Lactococcus	Lactococcus_lactis
Seq_0001844	4.29E-01	-0.13	0.66	1.49E-01	0.24	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003554	4.69E-01	-0.12	0.67	2.98E-02	0.36	6.18E-01	Roseburia	Unclassified
Seq_0003708	4.69E-01	-0.12	0.67	2.98E-02	0.36	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0000038	4.77E-01	-0.12	0.68	7.33E-02	- 0.30	6.18E-01	Akkermansia	Akkermansia_muciniphila
Seq_0000595	4.80E-01	-0.12	0.69	1.03E-01	0.27	6.18E-01	Prevotella	Prevotella_stercoraria

Seq_0000277	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Lactobacillaceae_u nclassified	Unclassified
Seq_0000352	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000865	5.14E-01	-0.11	0.70	1.27E-01	- 0.26	6.18E-01	Streptococcus	Streptococcus_mutans
Seq_0001110	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001199	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Clostridium_XVIII	Unclassified
Seq_0001268	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Enterococcus	Unclassified
Seq_0001654	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Lactobacillales_unc lassified	Unclassified
Seq_0002311	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Leptospirillum	Leptospirillum_ferriphilum
Seq_0002426	5.12E-01	-0.11	0.70	2.46E-02	0.37	6.18E-01	Lachnospiraceae_u nclassified	Eubacterium_ramus
Seq_0003178	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Clostridium_XVIII	Clostridium_ramosum
Seq_0003522	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Mycobacterium	Unclassified
Seq_0004758	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Ruminococcaceae_u nclassified	Unclassified
Seq_0005049	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Desulfovibrio	Unclassified
Seq_0005192	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Enterococcaceae_u nclassified	Unclassified
Seq_0005464	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Bacteroides	Bacteroides_fragilis
Seq_0006543	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Cloacibacterium	Unclassified

Seq_0006544	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Bifidobacteriaceae_ unclassified	Unclassified
Seq_0006545	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0006546	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0007353	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Akkermansia	Akkermansia_muc iniphila
Seq_0007355	5.20E-01	-0.11	0.70	9.21E-02	- 0.28	6.18E-01	Sphingomonadacea e_unclassified	Unclassified
Seq_0001303	5.41E-01	-0.10	0.73	8.89E-02	0.28	6.18E-01	Bacteria_unclassifi ed	Unclassified
Seq_0002066	5.55E-01	0.10	0.74	7.18E-02	- 0.30	6.18E-01	Corynebacterium	Corynebacterium_ durum
Seq_0000331	5.67E-01	0.10	0.75	1.44E-01	- 0.25	6.18E-01	Eggerthella	Eggerthella_lenta
Seq_0000464	5.81E-01	-0.09	0.75	4.94E-02	- 0.33	6.18E-01	Subdoligranulum	Unclassified
Seq_0000535	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0001260	5.64E-01	0.10	0.75	4.11E-02	0.34	6.18E-01	Bifidobacterium	Unclassified
Seq_0001515	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Enterobacteriaceae _unclassified	Unclassified
Seq_0001583	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001859	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002223	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Streptococcus	Unclassified
Seq_0002414	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002486	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Clostridiales_uncla ssified	Eubacterium_elige ns

Seq_0002858	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0003337	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Erysipelotrichaceae_unclassified	Unclassified
Seq_0003556	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Blautia	Unclassified
Seq_0003710	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Clostridium_XIVb	Unclassified
Seq_0003894	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Acinetobacter	Unclassified
Seq_0005157	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0005431	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0005651	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Pseudoflavonifractor	Pseudoflavonifractor_capillosus
Seq_0006089	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0006090	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0006091	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0007256	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Alistipes	Unclassified
Seq_0007369	5.81E-01	-0.09	0.75	1.12E-01	0.27	6.18E-01	Oscillibacter	Unclassified
Seq_0000086	5.83E-01	-0.09	0.75	2.89E-02	-0.36	6.18E-01	Enterococcus	Unclassified
Seq_0001772	6.03E-01	-0.09	0.77	8.33E-02	0.29	6.18E-01	Peptoniphilus	Unclassified
Seq_0000157	6.08E-01	0.09	0.78	3.23E-02	0.35	6.18E-01	Lactococcus	Unclassified
Seq_0001888	6.18E-01	0.08	0.78	6.11E-02	-0.31	6.18E-01	Lactobacillus	Lactobacillus_rhamnosus
Seq_0000744	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Dorea	Dorea_longicatena
Seq_0000818	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Clostridia_unclassified	Eubacterium_coprostanoligenes
Seq_0001003	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Blautia	Blautia_luti
Seq_0001016	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Prevotella	Prevotella_stercorae

Seq_0001168	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Dorea	Dorea_longicatena
Seq_0001601	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Roseburia	Eubacterium_rectale
Seq_0001609	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001874	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Roseburia	Eubacterium_rectale
Seq_0002150	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002541	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002542	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0002712	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Firmicutes_unclassified	Unclassified
Seq_0002971	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003037	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Ruminococcus2	Unclassified
Seq_0003192	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Leuconostoc	Unclassified
Seq_0003621	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Lactobacillus	Unclassified
Seq_0004828	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Flavonifractor	Flavonifractor_plautii
Seq_0005392	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Clostridiales_unclassified	Unclassified
Seq_0006405	6.46E-01	-0.08	0.79	1.63E-01	0.23	6.18E-01	Rothia	Rothia_dentocariosa
Seq_0001487	6.63E-01	0.07	0.81	2.48E-02	-0.37	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0002946	6.67E-01	0.07	0.82	2.49E-02	-0.37	6.18E-01	Oribacterium	Oribacterium_sinus
Seq_0000051	6.87E-01	0.07	0.84	1.46E-01	-0.24	6.18E-01	Pasteurellaceae_unclassified	Unclassified

Seq_0000154	7.02E-01	-0.07	0.85	1.37E-01	- 0.25	6.18E-01	Megasphaera	Unclassified
Seq_0000194	7.01E-01	0.07	0.85	1.43E-01	- 0.25	6.18E-01	Lactobacillus	Unclassified
Seq_0001106	7.01E-01	0.07	0.85	2.90E-02	0.36	6.18E-01	Prevotella	Prevotella_copri
Seq_0001527	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Butyricimonas	Unclassified
Seq_0001846	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Coprococcus	Coprococcus_com es
Seq_0002565	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Oscillibacter	Unclassified
Seq_0003526	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Butyricimonas	Unclassified
Seq_0003592	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Butyricimonas	Unclassified
Seq_0003654	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004132	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Bacteroidales_uncl assified	Unclassified
Seq_0004863	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Oscillibacter	Unclassified
Seq_0006496	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Corynebacterium	Corynebacterium_ durum
Seq_0006497	7.14E-01	-0.06	0.85	1.36E-01	0.25	6.18E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000518	7.79E-01	-0.05	0.88	9.69E-02	- 0.28	6.18E-01	Megamonas	Unclassified
Seq_0000576	7.63E-01	-0.05	0.88	4.70E-02	- 0.33	6.18E-01	Streptococcus	Unclassified
Seq_0002241	7.67E-01	-0.05	0.88	4.34E-02	- 0.33	6.18E-01	Clostridium_XIVa	Unclassified
Seq_0000899	8.48E-01	0.03	0.93	6.05E-02	- 0.31	6.18E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000175	8.71E-01	0.03	0.94	1.56E-01	- 0.24	6.18E-01	Turicibacter	Turicibacter_sang uinis
Seq_0001862	8.81E-01	0.03	0.95	4.26E-02	0.34	6.18E-01	Ruminococcaceae_ unclassified	Unclassified

Seq_0000502	9.26E-01	-0.02	0.95	1.39E-01	0.25	6.18E-01	Ruminococcus2	Ruminococcus_torques
Seq_0000843	8.98E-01	0.02	0.95	7.06E-02	- 0.30	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001757	9.23E-01	-0.02	0.95	4.59E-02	0.33	6.18E-01	Gordonibacter	Gordonibacter_pamelaeae
Seq_0002519	9.52E-01	0.01	0.97	1.47E-01	- 0.24	6.18E-01	Oscillibacter	Unclassified
Seq_0000350	9.63E-01	0.01	0.98	6.83E-02	- 0.30	6.18E-01	Clostridium_sensu_stricto	Unclassified
Seq_0000647	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Bacteria_unclassified	Unclassified
Seq_0000690	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Prevotella	Prevotella_copri
Seq_0000966	9.98E-01	0.00	1.00	5.96E-02	0.31	6.18E-01	Roseburia	Roseburia_hominis
Seq_0001801	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Prevotella	Prevotella_stercoraria
Seq_0002709	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Clostridiales_unclassified	Eubacterium_hallii
Seq_0002818	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Blautia	Blautia_luti
Seq_0002948	9.97E-01	0.00	1.00	6.77E-02	- 0.30	6.18E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003043	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Blautia	Unclassified
Seq_0003090	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Blautia	Unclassified
Seq_0006519	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Bifidobacterium	Unclassified
Seq_0007337	1.00E+00	0.00	1.00	9.21E-02	0.28	6.18E-01	Prevotella	Prevotella_copri
Seq_0000943	6.59E-01	-0.08	0.81	1.64E-01	0.23	6.21E-01	Proteobacteria_unclassified	Unclassified
Seq_0000410	9.13E-04	-0.52	0.07	1.82E-01	0.22	6.24E-01	Roseburia	Roseburia_inulinivorans
Seq_0000785	8.83E-04	-0.52	0.07	1.76E-01	0.23	6.24E-01	Blautia	Unclassified
Seq_0000792	2.69E-02	0.36	0.37	1.86E-01	- 0.22	6.24E-01	Actinomyces	Actinomyces_odontolyticus

Seq_0001995	3.02E-02	-0.36	0.37	1.76E-01	0.23	6.24E-01	Lachnospiraceae_unclassified	Clostridium_glycyrrhizinilyticum
Seq_0000288	1.07E-01	0.27	0.44	1.94E-01	- 0.22	6.24E-01	Clostridium_XIVb	Clostridium_lactatifermentans
Seq_0000829	6.86E-02	-0.30	0.44	1.95E-01	- 0.22	6.24E-01	Citrobacter	Unclassified
Seq_0002255	5.97E-02	-0.31	0.44	1.83E-01	0.22	6.24E-01	Blautia	Unclassified
Seq_0004009	1.11E-01	-0.27	0.44	1.79E-01	0.23	6.24E-01	Clostridiales_unclassified	Unclassified
Seq_0000019	1.55E-01	-0.24	0.47	1.86E-01	- 0.22	6.24E-01	Prevotella	Prevotella_copri
Seq_0001682	1.53E-01	-0.24	0.47	1.84E-01	0.22	6.24E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004615	2.44E-01	-0.20	0.49	1.68E-01	- 0.23	6.24E-01	Bacteria_unclassified	Unclassified
Seq_0000704	2.47E-01	-0.20	0.50	1.94E-01	0.22	6.24E-01	Barnesiella	Barnesiella_intestinihominis
Seq_0001683	2.89E-01	-0.18	0.54	1.89E-01	- 0.22	6.24E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000712	3.06E-01	0.17	0.54	1.95E-01	- 0.22	6.24E-01	Morganella	Unclassified
Seq_0001667	3.25E-01	-0.17	0.57	1.85E-01	0.22	6.24E-01	Blautia	Unclassified
Seq_0003256	3.36E-01	-0.16	0.58	1.76E-01	- 0.23	6.24E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000390	3.41E-01	-0.16	0.58	1.71E-01	0.23	6.24E-01	Clostridiales_unclassified	Eubacterium_eligens
Seq_0000135	3.74E-01	-0.15	0.60	1.90E-01	- 0.22	6.24E-01	Megasphaera	Unclassified
Seq_0001433	3.86E-01	0.15	0.62	1.82E-01	0.22	6.24E-01	Erysipelotrichaceae_unclassified	Eubacterium_doliculum
Seq_0001688	4.14E-01	0.14	0.64	1.77E-01	- 0.23	6.24E-01	Staphylococcus	Unclassified

Seq_0001062	4.24E-01	-0.14	0.65	1.89E-01	- 0.22	6.24E-01	Bacteroides	Bacteroides_fragilis
Seq_0000114	5.54E-01	0.10	0.74	1.80E-01	- 0.23	6.24E-01	Clostridium_sensu_stricto	Unclassified
Seq_0001028	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Bifidobacterium	Unclassified
Seq_0001178	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Clostridiales_unclassified	Unclassified
Seq_0001352	5.81E-01	-0.09	0.75	1.92E-01	- 0.22	6.24E-01	Clostridium_XIVb	Unclassified
Seq_0001545	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001977	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Blautia	Unclassified
Seq_0001989	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Prevotella	Prevotella_copri
Seq_0002067	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Bacteroides	Bacteroides_vulgatus
Seq_0002689	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Blautia	Unclassified
Seq_0002690	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Dialister	Dialister_invisus
Seq_0002733	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Clostridia_unclassified	Unclassified
Seq_0002857	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Erysipelotrichaceae_unclassified	Unclassified
Seq_0002986	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Gordonibacter	Gordonibacter_pamelaeae
Seq_0003064	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Holdemania	Holdemania_filiformis
Seq_0004494	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Flavonifractor	Flavonifractor_plautii
Seq_0006417	5.81E-01	0.09	0.75	1.94E-01	0.22	6.24E-01	Clostridiales_unclassified	Unclassified
Seq_0002713	6.76E-01	-0.07	0.82	1.77E-01	0.23	6.24E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000246	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Bacteroides	Bacteroides_vulgatus

Seq_0000597	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Dialister	Unclassified
Seq_0000620	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Bacteroides	Bacteroides_vulga tus
Seq_0000806	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Parasutterella	Parasutterella_excr ementihominis
Seq_0000848	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Megasphaera	Unclassified
Seq_0000886	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Megasphaera	Unclassified
Seq_0000927	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001147	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Escherichia/Shigell a	Unclassified
Seq_0001161	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Acinetobacter	Unclassified
Seq_0001252	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001400	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0001959	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002213	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Bacteroides	Unclassified
Seq_0002235	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Acidaminococcus	Acidaminococcus_ fermentans
Seq_0002989	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Acinetobacter	Unclassified
Seq_0003127	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Enhydrobacter	Unclassified
Seq_0003525	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Chryseobacterium	Chryseobacterium_ hominis

Seq_0003751	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Bacteria_unclassified	Unclassified
Seq_0004065	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Clostridium_XIVa	Unclassified
Seq_0004188	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004411	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Odoribacter	Odoribacter_splanchnicus
Seq_0004523	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Acinetobacter	Unclassified
Seq_0006121	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Firmicutes_unclassified	Unclassified
Seq_0006123	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0006124	9.27E-01	0.02	0.95	1.94E-01	- 0.22	6.24E-01	Methylobacterium	Unclassified
Seq_0000001	9.35E-01	0.01	0.96	1.72E-01	0.23	6.24E-01	Bifidobacterium	Unclassified
Seq_0000640	9.74E-01	-0.01	0.98	1.85E-01	0.22	6.24E-01	Clostridium_IV	Clostridium_leptum
Seq_0003888	9.74E-01	0.01	0.98	1.87E-01	0.22	6.24E-01	Ruminococcaceae_unclassified	Clostridium_leptum
Seq_0001850	4.82E-01	-0.12	0.69	1.98E-01	- 0.22	6.33E-01	Anaerostipes	Anaerostipes_butylicus
Seq_0000276	6.27E-03	-0.44	0.22	2.16E-01	0.21	6.34E-01	Clostridium_XI	Unclassified
Seq_0000472	9.38E-03	0.42	0.28	2.09E-01	- 0.21	6.34E-01	Gemella	Unclassified
Seq_0000142	1.12E-02	-0.41	0.29	2.29E-01	0.20	6.34E-01	Clostridium_XI	Clostridium_bartlettii
Seq_0002055	1.64E-02	0.39	0.34	2.56E-01	- 0.19	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000661	1.78E-02	-0.39	0.36	2.63E-01	0.19	6.34E-01	Coprococcus	Coprococcus_eutactus

Seq_0001346	1.78E-02	-0.39	0.36	2.63E-01	0.19	6.34E-01	Coprococcus	Coprococcus_euta ctus
Seq_0000115	2.29E-02	-0.37	0.37	1.99E-01	0.22	6.34E-01	Bacteroides	Bacteroides_sterco ris
Seq_0000177	2.19E-02	-0.38	0.37	2.63E-01	0.19	6.34E-01	Bacteroides	Bacteroides_massi liensis
Seq_0000536	2.11E-02	-0.38	0.37	2.09E-01	- 0.21	6.34E-01	Bacteroidales_uncl assified	Unclassified
Seq_0002143	1.94E-02	-0.38	0.37	2.02E-01	- 0.21	6.34E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0000557	3.86E-02	-0.34	0.41	2.48E-01	0.19	6.34E-01	Ruminococcus2	Ruminococcus_lac taris
Seq_0000589	4.85E-02	0.33	0.44	2.04E-01	- 0.21	6.34E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000781	4.85E-02	0.33	0.44	2.04E-01	- 0.21	6.34E-01	Bacteria_unclassifi ed	Eubacterium_dolic hum
Seq_0000233	7.31E-02	0.30	0.44	2.66E-01	- 0.19	6.34E-01	Lactobacillus	Unclassified
Seq_0000503	9.03E-02	-0.28	0.44	2.22E-01	- 0.21	6.34E-01	Erysipelotrichaceae _unclassified	Eubacterium_cylin droides
Seq_0000615	7.92E-02	-0.29	0.44	2.22E-01	0.21	6.34E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000677	9.69E-02	-0.28	0.44	2.42E-01	- 0.20	6.34E-01	Subdoligranulum	Unclassified
Seq_0000679	5.57E-02	-0.32	0.44	2.32E-01	0.20	6.34E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000909	8.71E-02	-0.29	0.44	2.40E-01	- 0.20	6.34E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001088	1.05E-01	-0.27	0.44	2.47E-01	- 0.20	6.34E-01	Bacteria_unclassifi ed	Unclassified
Seq_0001905	8.68E-02	0.29	0.44	2.42E-01	- 0.20	6.34E-01	Ruminococcaceae_ unclassified	Faecalibacterium_ prausnitzii

Seq_0002193	1.10E-01	-0.27	0.44	2.58E-01	0.19	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002613	1.11E-01	-0.27	0.44	2.17E-01	-0.21	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004246	5.14E-02	-0.32	0.44	2.18E-01	0.21	6.34E-01	Firmicutes_unclassified	Unclassified
Seq_0000318	1.15E-01	-0.26	0.45	2.34E-01	-0.20	6.34E-01	Ruminococcus2	Ruminococcus_torques
Seq_0000814	1.20E-01	-0.26	0.45	2.14E-01	0.21	6.34E-01	Parabacteroides	Parabacteroides_merdae
Seq_0000123	1.86E-01	-0.22	0.47	2.08E-01	-0.21	6.34E-01	Bifidobacterium	Unclassified
Seq_0000180	1.45E-01	-0.24	0.47	2.33E-01	0.20	6.34E-01	Ruminococcus	Unclassified
Seq_0000260	1.52E-01	0.24	0.47	2.35E-01	-0.20	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000262	1.63E-01	0.23	0.47	2.28E-01	-0.20	6.34E-01	Prevotella	Prevotella_copri
Seq_0000320	2.28E-01	-0.20	0.47	2.67E-01	-0.19	6.34E-01	Prevotella	Unclassified
Seq_0000322	1.63E-01	0.23	0.47	2.28E-01	-0.20	6.34E-01	Prevotella	Prevotella_copri
Seq_0000408	1.63E-01	0.23	0.47	2.28E-01	-0.20	6.34E-01	Lactobacillus	Unclassified
Seq_0000636	1.63E-01	0.23	0.47	2.28E-01	-0.20	6.34E-01	Pediococcus	Unclassified
Seq_0000723	2.28E-01	-0.20	0.47	2.67E-01	-0.19	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0000787	1.63E-01	0.23	0.47	2.28E-01	-0.20	6.34E-01	Lactobacillus	Unclassified
Seq_0000881	2.28E-01	-0.20	0.47	2.67E-01	-0.19	6.34E-01	Lactobacillus	Unclassified
Seq_0000888	1.63E-01	0.23	0.47	2.28E-01	-0.20	6.34E-01	Escherichia/Shigella	Unclassified

Seq_0000950	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Lactobacillus	Unclassified
Seq_0000960	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Lactobacillus	Unclassified
Seq_0001145	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0001148	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Sutterella	Sutterella_wadsworthensis
Seq_0001215	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bacteroidetes_unclassified	Unclassified
Seq_0001258	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Eubacteriaceae_unclassified	Eubacterium_limosum
Seq_0001281	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001300	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0001351	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0001730	1.60E-01	-0.24	0.47	2.38E-01	0.20	6.34E-01	Collinsella	Collinsella_aerofaciens
Seq_0001743	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Rothia	Rothia_mucilaginosa
Seq_0001937	1.63E-01	-0.23	0.47	2.26E-01	0.20	6.34E-01	Actinobacteria_unclassified	Unclassified
Seq_0002030	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002189	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Lactobacillales_unclassified	Unclassified
Seq_0002330	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Morganella	Unclassified
Seq_0002452	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Olsenella	Unclassified

Seq_0002488	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Lactobacillus	Unclassified
Seq_0002626	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Lactobacillus	Unclassified
Seq_0002678	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Clostridium_XI	Unclassified
Seq_0002745	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Firmicutes_unclassified	Unclassified
Seq_0002759	2.19E-01	-0.21	0.47	2.45E-01	0.20	6.34E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002988	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Psychrobacter	Unclassified
Seq_0003017	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Olsenella	Unclassified
Seq_0003229	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0003298	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Catenibacterium	Catenibacterium_mitsuokai
Seq_0003341	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Catenibacterium	Catenibacterium_mitsuokai
Seq_0003359	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Firmicutes_unclassified	Unclassified
Seq_0003361	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Pasteurellaceae_unclassified	Unclassified
Seq_0003425	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Firmicutes_unclassified	Unclassified
Seq_0003466	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0003715	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0003821	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bacteria_unclassified	Unclassified

Seq_0003931	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0003974	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Lactobacillus	Lactobacillus_kali xensis
Seq_0004064	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0004343	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Shinella	Unclassified
Seq_0004521	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Firmicutes_unclassi fied	Unclassified
Seq_0004608	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0004757	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Enterococcus	Unclassified
Seq_0004860	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Rhizobium	Rhizobium_giardi nii
Seq_0004861	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bacteria_unclassifi ed	Unclassified
Seq_0005031	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bacteria_unclassifi ed	Unclassified
Seq_0005179	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Clostridium_sensu_ stricto	Unclassified
Seq_0005180	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Lactobacillus	Unclassified
Seq_0005449	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Clostridium_XIVa	Unclassified
Seq_0005457	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Lactobacillus	Lactobacillus_inte stinalis
Seq_0005667	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Rhodobacteraceae_ unclassified	Unclassified
Seq_0005668	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Ruminococcaceae_ unclassified	Faecalibacterium_ prausnitzii

Seq_0005669	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0006117	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Pedobacter	Unclassified
Seq_0006118	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bosea	Unclassified
Seq_0006492	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0006493	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Comamonadaceae_ unclassified	Unclassified
Seq_0006494	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Clostridiales_uncla ssified	Unclassified
Seq_0006523	1.63E-01	0.23	0.47	2.28E-01	- 0.20	6.34E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0007297	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Clostridiales_uncla ssified	Unclassified
Seq_0007298	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Bifidobacteriaceae_ unclassified	Unclassified
Seq_0007299	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Chlamydiales_uncl assified	Unclassified
Seq_0007300	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Clostridiales_uncla ssified	Unclassified
Seq_0007301	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Pseudomonas	Unclassified
Seq_0007302	2.28E-01	-0.20	0.47	2.67E-01	- 0.19	6.34E-01	Proteobacteria_uncl assified	Unclassified
Seq_0000885	2.41E-01	-0.20	0.49	2.29E-01	0.20	6.34E-01	Lactobacillus	Lactobacillus_delb rueckii
Seq_0001868	3.40E-01	0.16	0.58	2.26E-01	- 0.20	6.34E-01	Lactobacillus	Unclassified
Seq_0001051	3.43E-01	-0.16	0.58	2.54E-01	- 0.19	6.34E-01	Bacteria_unclassifi ed	Unclassified

Seq_0001284	3.66E-01	-0.15	0.60	2.65E-01	- 0.19	6.34E-01	Eubacterium	Unclassified
Seq_0002527	3.70E-01	-0.15	0.60	2.48E-01	- 0.19	6.34E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000240	3.77E-01	0.15	0.61	2.59E-01	- 0.19	6.34E-01	Veillonella	Unclassified
Seq_0000393	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Catenibacterium	Catenibacterium_ mitsuokai
Seq_0000564	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Ruminococcus	Ruminococcus_cal lidus
Seq_0000656	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Anaerostipes	Anaerostipes_hadr us
Seq_0000714	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001018	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Clostridiales_uncla ssified	Eubacterium_copr ostanoligenes
Seq_0001093	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Streptococcus	Unclassified
Seq_0001299	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Anaerostipes	Anaerostipes_hadr us
Seq_0001579	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Barnesiella	Barnesiella_intesti nihominis
Seq_0001954	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0002044	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Catenibacterium	Catenibacterium_ mitsuokai
Seq_0002095	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Prevotellaceae_uncl assified	Unclassified
Seq_0002099	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Dorea	Dorea_formicigen erans
Seq_0002171	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0002218	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Bacteroides	Bacteroides_copro philus

Seq_0002305	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Clostridiales_unclassified	Unclassified
Seq_0002319	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Catenibacterium	Catenibacterium_mitsuokai
Seq_0002348	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Clostridium_sensu_stricto	Clostridium_disporicum
Seq_0002735	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Catenibacterium	Catenibacterium_mitsuokai
Seq_0002775	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Bacteroides	Bacteroides_uniformis
Seq_0002893	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Streptococcus	Unclassified
Seq_0003101	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Prevotella	Unclassified
Seq_0003128	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Firmicutes_unclassified	Unclassified
Seq_0003267	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Clostridium_IV	Unclassified
Seq_0003358	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0003560	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Clostridiales_unclassified	Unclassified
Seq_0004260	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Clostridiales_unclassified	Unclassified
Seq_0004406	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004588	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004589	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Streptococcus	Unclassified
Seq_0004708	4.07E-01	0.14	0.63	2.67E-01	0.19	6.34E-01	Streptococcus	Streptococcus_mutans
Seq_0005164	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0005437	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Odoribacter	Odoribacter_splanchnicus

Seq_0006096	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Bacteroidetes_unclassified	Unclassified
Seq_0006097	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Prevotella	Prevotella_ruminicola
Seq_0007270	4.07E-01	-0.14	0.63	2.28E-01	0.20	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0004990	5.38E-01	-0.10	0.73	2.15E-01	-0.21	6.34E-01	Bacteria_unclassified	Unclassified
Seq_0000753	6.16E-01	-0.09	0.78	2.15E-01	0.21	6.34E-01	Paraprevotella	Paraprevotella_clara
Seq_0000456	7.79E-01	0.05	0.88	2.54E-01	0.19	6.34E-01	Bacteria_unclassified	Eubacterium_cylindroides
Seq_0000409	8.54E-01	0.03	0.93	2.52E-01	0.19	6.34E-01	Bacteroides	Bacteroides_ovatus
Seq_0000354	8.62E-01	0.03	0.93	2.23E-01	0.21	6.34E-01	Prevotella	Prevotella_copri
Seq_0001411	9.41E-01	-0.01	0.96	2.04E-01	0.21	6.34E-01	Bacteroidales_unclassified	Unclassified
Seq_0001180	9.60E-01	-0.01	0.97	2.62E-01	-0.19	6.34E-01	Prevotella	Prevotella_copri
Seq_0001373	9.60E-01	-0.01	0.97	2.62E-01	-0.19	6.34E-01	Bacteroidetes_unclassified	Unclassified
Seq_0002612	9.60E-01	-0.01	0.97	2.62E-01	-0.19	6.34E-01	Clostridium_XIVa	Unclassified
Seq_0001602	9.87E-01	0.00	1.00	2.29E-01	-0.20	6.34E-01	Clostridiales_unclassified	Unclassified
Seq_0000139	2.00E-02	-0.38	0.37	2.73E-01	-0.19	6.45E-01	Paraprevotella	Paraprevotella_clara
Seq_0000868	2.00E-02	-0.38	0.37	2.73E-01	-0.19	6.45E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002194	1.17E-01	-0.26	0.45	2.74E-01	0.18	6.45E-01	Olsenella	Unclassified
Seq_0000003	2.27E-01	-0.20	0.47	2.73E-01	0.18	6.45E-01	Bacteroides	Bacteroides_vulgatus
Seq_0000527	1.48E-01	-0.24	0.47	2.73E-01	0.18	6.45E-01	Oscillibacter	Unclassified

Seq_0000469	8.81E-01	-0.03	0.95	2.74E-01	0.18	6.45E-01	Ruminococcaceae_unclassified	Eubacterium_coprostanoligenes
Seq_0001129	9.02E-01	-0.02	0.95	2.76E-01	-0.18	6.48E-01	Bacteroides	Bacteroides_plebeius
Seq_0000566	1.20E-02	0.41	0.29	2.81E-01	-0.18	6.57E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000126	7.34E-01	-0.06	0.87	2.81E-01	-0.18	6.57E-01	Bifidobacterium	Bifidobacterium_dentium
Seq_0002288	9.78E-01	0.00	0.99	2.83E-01	-0.18	6.60E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000064	5.70E-05	-0.61	0.02	3.04E-01	-0.17	6.65E-01	Ruminococcus	Ruminococcus_bromii
Seq_0000452	4.45E-03	-0.46	0.18	2.89E-01	0.18	6.65E-01	Bacteroides	Bacteroides_uniformis
Seq_0000880	7.87E-03	-0.43	0.25	2.97E-01	0.18	6.65E-01	Clostridiales_unclassified	Unclassified
Seq_0000382	3.18E-02	0.35	0.38	3.03E-01	-0.17	6.65E-01	Clostridium_XIVa	Unclassified
Seq_0000601	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000719	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000997	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Lactobacillales_unclassified	Lactobacillus_alvei
Seq_0001039	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Pediococcus	Unclassified
Seq_0001205	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Blautia	Blautia_faecis
Seq_0001224	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001628	9.21E-02	0.28	0.44	3.10E-01	-0.17	6.65E-01	Lachnospiraceae_unclassified	Unclassified

Seq_0002057	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002257	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0002916	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Lactobacillaceae_u nclassified	Unclassified
Seq_0003656	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Clostridium_XIVb	Unclassified
Seq_0003827	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0003976	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0004268	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Bacteria_unclassifi ed	Clostridium_innoc uum
Seq_0004624	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Blautia	Blautia_faecis
Seq_0005466	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Dialister	Dialister_invisus
Seq_0006160	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Lachnospiraceae_u nclassified	Ruminococcus_gn avus
Seq_0007356	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Blautia	Unclassified
Seq_0007357	9.21E-02	0.28	0.44	3.10E-01	- 0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001444	1.16E-01	-0.26	0.45	2.88E-01	- 0.18	6.65E-01	Firmicutes_unclassi fied	Unclassified
Seq_0002716	1.35E-01	-0.25	0.45	3.02E-01	0.17	6.65E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000136	2.05E-01	-0.21	0.47	3.07E-01	0.17	6.65E-01	Bacteroides	Unclassified
Seq_0001116	1.58E-01	-0.24	0.47	3.00E-01	0.18	6.65E-01	Blautia	Unclassified
Seq_0000511	2.50E-01	-0.19	0.50	2.91E-01	0.18	6.65E-01	Prevotella	Prevotella_copri
Seq_0001163	2.74E-01	0.18	0.52	2.94E-01	- 0.18	6.65E-01	Lactobacillus	Unclassified

Seq_0000256	6.18E-01	0.08	0.78	2.93E-01	- 0.18	6.65E-01	Bifidobacterium	Unclassified
Seq_0000513	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Lactobacillus	Lactobacillus_rum inis
Seq_0001160	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Burkholderiales_un classified	Unclassified
Seq_0001264	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Clostridium_XI	Clostridium_glyco licum
Seq_0001398	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Roseburia	Roseburia_intestin alis
Seq_0001559	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Clostridium_XI	Unclassified
Seq_0002604	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002624	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0003825	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004266	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Oscillibacter	Unclassified
Seq_0005670	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Clostridiales_uncla ssified	Unclassified
Seq_0005672	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0006503	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Clostridiales_uncla ssified	Unclassified
Seq_0006504	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Bifidobacterium	Unclassified
Seq_0006505	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0006506	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Bacteria_unclassifi ed	Unclassified
Seq_0006508	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0007315	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Bacteria_unclassifi ed	Unclassified

Seq_0007316	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Bifidobacterium	Unclassified
Seq_0007317	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Clostridiales_uncla ssified	Unclassified
Seq_0007318	7.83E-01	-0.05	0.88	3.10E-01	0.17	6.65E-01	Bacteria_unclassifi ed	Unclassified
Seq_0001339	8.02E-01	-0.04	0.90	2.89E-01	- 0.18	6.65E-01	Bacteria_unclassifi ed	Unclassified
Seq_0000358	7.21E-01	-0.06	0.86	3.11E-01	0.17	6.68E-01	Prevotella	Prevotella_copri
Seq_0003122	2.67E-02	-0.36	0.37	3.13E-01	0.17	6.70E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000462	4.54E-01	0.13	0.66	3.14E-01	- 0.17	6.72E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002233	1.55E-01	-0.24	0.47	3.14E-01	0.17	6.72E-01	Collinsella	Collinsella_aerofa ciens
Seq_0000521	3.74E-01	-0.15	0.60	3.22E-01	0.17	6.86E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001484	4.63E-01	-0.12	0.67	3.23E-01	0.17	6.88E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000984	4.66E-01	-0.12	0.67	3.26E-01	- 0.17	6.93E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0000219	4.07E-04	-0.55	0.06	3.40E-01	- 0.16	6.93E-01	Alistipes	Alistipes_putredini s
Seq_0000428	4.77E-03	-0.45	0.18	3.38E-01	0.16	6.93E-01	Coprococcus	Coprococcus_euta ctus
Seq_0000018	1.54E-02	-0.40	0.33	3.27E-01	0.17	6.93E-01	Bifidobacterium	Unclassified
Seq_0000459	4.91E-02	0.33	0.44	3.49E-01	- 0.16	6.93E-01	Lactobacillus	Unclassified
Seq_0001432	5.75E-02	0.32	0.44	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000048	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Bifidobacterium	Unclassified
Seq_0000295	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Veillonella	Veillonella_ratti

Seq_0000663	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0000693	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Ruminococcus_gn avus
Seq_0001045	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001188	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001227	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001362	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Enterococcus	Unclassified
Seq_0001533	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001548	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Proteus	Unclassified
Seq_0001715	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Erysipelotrichaceae _unclassified	Unclassified
Seq_0001719	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Erysipelotrichaceae _unclassified	Unclassified
Seq_0001807	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001963	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002135	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Clostridium_XIVa	Clostridium_symb iosum
Seq_0002285	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Bacteria_unclassifi ed	Unclassified
Seq_0002303	1.78E-01	-0.23	0.47	3.52E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002832	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified

Seq_0002991	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002992	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Blautia	Unclassified
Seq_0003823	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Blautia	Unclassified
Seq_0003904	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0004269	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Alloprevotella	Unclassified
Seq_0004270	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Prevotella	Prevotella_stercor ea
Seq_0004870	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Ruminococcaceae_u nclassified	Clostridium_meth ylpentosum
Seq_0006540	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Prevotella	Prevotella_stercor ea
Seq_0006541	1.94E-01	0.22	0.47	3.56E-01	- 0.16	6.93E-01	Desulfovibrio	Desulfovibrio_pig er
Seq_0000460	2.74E-01	-0.18	0.52	3.41E-01	- 0.16	6.93E-01	Parasutterella	Parasutterella_excr ementihominis
Seq_0004747	2.74E-01	-0.18	0.52	3.41E-01	- 0.16	6.93E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001958	2.84E-01	-0.18	0.53	3.38E-01	0.16	6.93E-01	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0000046	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Enterobacteriaceae _unclassified	Unclassified
Seq_0000261	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Bacteroides	Bacteroides_vulga tus
Seq_0000550	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0000801	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Faecalibacterium	Faecalibacterium_ prausnitzii

Seq_0000859	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Enterobacteriaceae_unclassified	Unclassified
Seq_0001535	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Butyricicoccus	Butyricicoccus_pullicaeorum
Seq_0003162	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Blautia	Unclassified
Seq_0003275	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Enterobacteriaceae_unclassified	Unclassified
Seq_0004421	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Clostridium_sensu_stricto	Unclassified
Seq_0004529	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Alloprevotella	Alloprevotella_rav
Seq_0006140	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0006141	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Clostridiales_unclassified	Unclassified
Seq_0006522	3.56E-01	-0.16	0.58	3.56E-01	0.16	6.93E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000028	4.46E-01	-0.13	0.66	3.29E-01	-0.17	6.93E-01	Turicibacter	Turicibacter_sanguinis
Seq_0001033	5.36E-01	-0.11	0.72	3.57E-01	-0.16	6.93E-01	Bacteroides	Bacteroides_ovatus
Seq_0000572	5.48E-01	0.10	0.74	3.55E-01	-0.16	6.93E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001890	5.69E-01	-0.10	0.75	3.36E-01	-0.16	6.93E-01	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0001439	6.43E-01	-0.08	0.79	3.35E-01	0.16	6.93E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000778	6.80E-01	-0.07	0.83	3.36E-01	-0.16	6.93E-01	Bifidobacterium	Unclassified
Seq_0000058	7.57E-01	0.05	0.88	3.47E-01	0.16	6.93E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003496	7.57E-01	0.05	0.88	3.47E-01	0.16	6.93E-01	Lachnospiraceae_unclassified	Unclassified

Seq_0000301	8.79E-01	-0.03	0.95	3.34E-01	- 0.16	6.93E-01	Veillonella	Veillonella_dispar
Seq_0000926	9.29E-01	0.02	0.95	3.57E-01	0.16	6.93E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000056	9.49E-01	0.01	0.97	3.50E-01	0.16	6.93E-01	Dialister	Dialister_invisus
Seq_0000975	9.71E-01	-0.01	0.98	3.36E-01	0.16	6.93E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000666	9.74E-01	-0.01	0.98	3.48E-01	- 0.16	6.93E-01	Lactobacillus	Unclassified
Seq_0000568	3.62E-01	0.15	0.59	3.59E-01	- 0.16	6.97E-01	Escherichia/Shigella	Unclassified
Seq_0004248	1.64E-01	-0.23	0.47	3.64E-01	- 0.15	7.05E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001384	1.25E-02	-0.41	0.29	3.66E-01	0.15	7.07E-01	Clostridium_XIVa	Unclassified
Seq_0000029	1.82E-01	-0.22	0.47	3.65E-01	0.15	7.07E-01	Prevotellaceae_unclassified	Unclassified
Seq_0001725	4.45E-01	-0.13	0.66	3.70E-01	- 0.15	7.14E-01	Blautia	Blautia_glucerasea
Seq_0003034	3.93E-01	-0.14	0.63	3.74E-01	0.15	7.20E-01	Bacteria_unclassified	Unclassified
Seq_0000915	3.70E-01	-0.15	0.60	3.76E-01	0.15	7.23E-01	Oscillibacter	Unclassified
Seq_0000544	4.42E-01	0.13	0.66	3.76E-01	- 0.15	7.24E-01	Sutterella	Sutterella_wadsworthensis
Seq_0000780	1.06E-02	-0.42	0.29	3.86E-01	0.15	7.31E-01	Bacteria_unclassified	Unclassified
Seq_0001910	6.66E-02	-0.30	0.44	4.03E-01	0.14	7.31E-01	Firmicutes_unclassified	Unclassified
Seq_0002377	6.66E-02	-0.30	0.44	4.03E-01	0.14	7.31E-01	Alistipes	Unclassified
Seq_0002736	8.20E-02	-0.29	0.44	3.91E-01	0.15	7.31E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000165	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Prevotella	Prevotella_buccae

Seq_0000263	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Prevotella	Prevotella_oris
Seq_0000278	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Prevotella	Prevotella_oris
Seq_0000342	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Prevotella	Prevotella_oris
Seq_0001179	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Blautia	Unclassified
Seq_0001391	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Capnocytophaga	Unclassified
Seq_0001399	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Clostridium_sensu_ stricto	Unclassified
Seq_0001542	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Oscillibacter	Oscillibacter_valer icigenes
Seq_0001569	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002207	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sang uinis
Seq_0002262	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Clostridium_sensu_ stricto	Unclassified
Seq_0002336	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Clostridium_sensu_ stricto	Unclassified
Seq_0002707	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sang uinis
Seq_0002744	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sang uinis
Seq_0003255	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sang uinis
Seq_0003442	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Prevotella	Prevotella_dentico la
Seq_0003622	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sang uinis

Seq_0004054	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Firmicutes_unclassified	Unclassified
Seq_0004327	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sanguinis
Seq_0004390	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Unclassified
Seq_0004595	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Turicibacter	Turicibacter_sanguinis
Seq_0006067	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Blautia	Unclassified
Seq_0007362	1.36E-01	0.25	0.45	4.07E-01	- 0.14	7.31E-01	Clostridium_XIVa	Unclassified
Seq_0002512	2.09E-01	0.21	0.47	4.03E-01	- 0.14	7.31E-01	Mogibacterium	Unclassified
Seq_0001164	7.98E-01	-0.04	0.89	4.03E-01	- 0.14	7.31E-01	Mannheimia	Unclassified
Seq_0000987	8.53E-01	0.03	0.93	3.85E-01	0.15	7.31E-01	Clostridiales_unclassified	Eubacterium_eligens
Seq_0001324	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Acidaminococcus	Acidaminococcus_fermentans
Seq_0001722	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Porphyromonas	Porphyromonas_asaccharolytica
Seq_0002170	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Acidaminococcus	Acidaminococcus_fermentans
Seq_0002873	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Catenibacterium	Catenibacterium_mitsuokai
Seq_0002910	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003089	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0003318	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Roseburia	Eubacterium_rectale

Seq_0003582	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Bacteria_unclassified	Unclassified
Seq_0003752	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0003817	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Olsenella	Unclassified
Seq_0004007	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Bacteroidetes_unclassified	Unclassified
Seq_0004323	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0005394	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0005395	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Haemophilus	Unclassified
Seq_0005615	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0005616	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0006051	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Dialister	Dialister_pneumointes
Seq_0007217	8.54E-01	-0.03	0.93	4.07E-01	0.14	7.31E-01	Bifidobacterium	Unclassified
Seq_0001834	9.44E-01	-0.01	0.97	4.03E-01	0.14	7.31E-01	Clostridiales_unclassified	Eubacterium_ventriosum
Seq_0001423	9.52E-01	-0.01	0.97	4.05E-01	-0.14	7.31E-01	Lachnospiraceae_unclassified	Clostridium_scindens
Seq_0000099	1.55E-01	-0.24	0.47	4.08E-01	0.14	7.32E-01	Roseburia	Roseburia_faecis
Seq_0000765	1.59E-01	0.24	0.47	4.09E-01	-0.14	7.32E-01	Veillonella	Unclassified
Seq_0000362	2.69E-01	-0.19	0.51	4.09E-01	0.14	7.32E-01	Mogibacterium	Unclassified
Seq_0000815	5.83E-01	-0.09	0.75	4.09E-01	-0.14	7.32E-01	Prevotella	Prevotella_copri
Seq_0001198	9.15E-01	-0.02	0.95	4.12E-01	0.14	7.35E-01	Blautia	Unclassified
Seq_0000463	3.67E-02	0.34	0.40	4.14E-01	-0.14	7.38E-01	Lachnospiraceae_unclassified	Unclassified

Seq_0002075	2.95E-01	-0.18	0.54	4.21E-01	0.14	7.50E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000538	3.09E-01	-0.17	0.54	4.26E-01	- 0.13	7.53E-01	Collinsella	Collinsella_tanaka ei
Seq_0001539	3.09E-01	-0.17	0.54	4.26E-01	- 0.13	7.53E-01	Clostridiales_unclassified	Unclassified
Seq_0001794	3.09E-01	-0.17	0.54	4.26E-01	- 0.13	7.53E-01	Ruminococcaceae_unclassified	Intestinimonas_but yriciproducens
Seq_0002185	3.09E-01	-0.17	0.54	4.26E-01	- 0.13	7.53E-01	Clostridiales_unclassified	Unclassified
Seq_0002462	3.09E-01	-0.17	0.54	4.26E-01	- 0.13	7.53E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004060	3.09E-01	-0.17	0.54	4.26E-01	- 0.13	7.53E-01	Clostridiales_unclassified	Unclassified
Seq_0002181	3.32E-01	-0.16	0.57	4.30E-01	- 0.13	7.59E-01	Ruminococcaceae_unclassified	Faecalibacterium_ prausnitzii
Seq_0002760	3.32E-01	-0.16	0.57	4.30E-01	- 0.13	7.59E-01	Firmicutes_unclassified	Unclassified
Seq_0000991	2.87E-01	0.18	0.54	4.33E-01	- 0.13	7.62E-01	Actinomyces	Unclassified
Seq_0002172	3.46E-02	-0.35	0.40	4.41E-01	- 0.13	7.74E-01	Firmicutes_unclassified	Unclassified
Seq_0002035	3.68E-01	-0.15	0.60	4.41E-01	0.13	7.74E-01	Olsenella	Unclassified
Seq_0002856	3.40E-02	-0.35	0.39	4.42E-01	0.13	7.75E-01	Alistipes	Alistipes_indistinctus
Seq_0000011	9.07E-02	0.28	0.44	4.55E-01	0.13	7.76E-01	Streptococcus	Unclassified
Seq_0000431	6.00E-02	-0.31	0.44	4.52E-01	- 0.13	7.76E-01	Dialister	Unclassified
Seq_0000889	9.31E-02	-0.28	0.44	4.53E-01	- 0.13	7.76E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001782	2.26E-01	0.20	0.47	4.47E-01	- 0.13	7.76E-01	Actinomyces	Actinomyces_lingnae

Seq_0000938	2.59E-01	-0.19	0.51	4.55E-01	- 0.13	7.76E-01	Bacteria_unclassified	Eubacterium_cylindroides
Seq_0000728	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000783	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Dialister	Unclassified
Seq_0000910	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Sutterella	Sutterella_stercoricanis
Seq_0000917	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Erysipelotrichaceae_unclassified	Streptococcus_pleomorphicus
Seq_0001050	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Lactobacillus	Unclassified
Seq_0001137	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Lactobacillus	Unclassified
Seq_0001321	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001462	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001876	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Bacteria_unclassified	Eubacterium_cylindroides
Seq_0002817	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Megamonas	Unclassified
Seq_0003100	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003408	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004745	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Bacteria_unclassified	Unclassified
Seq_0005181	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0006119	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Bacteria_unclassified	Unclassified

Seq_0007303	3.10E-01	0.17	0.54	4.61E-01	- 0.12	7.76E-01	Firmicutes_unclassified	Unclassified
Seq_0000351	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Veillonella	Unclassified
Seq_0000659	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001052	8.36E-01	-0.04	0.93	4.47E-01	- 0.13	7.76E-01	Clostridiales_unclassified	Unclassified
Seq_0001394	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001543	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Lactococcus	Unclassified
Seq_0001557	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Coprococcus	Unclassified
Seq_0001587	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Anaerostipes	Anaerostipes_hadrus
Seq_0002224	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002342	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Erysipelotrichaceae_unclassified	Unclassified
Seq_0005451	8.54E-01	0.03	0.93	4.61E-01	0.12	7.76E-01	Atopobium	Atopobium_parvulum
Seq_0003123	8.84E-01	-0.02	0.95	4.47E-01	0.13	7.76E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003788	8.84E-01	-0.02	0.95	4.47E-01	0.13	7.76E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000794	9.06E-01	-0.02	0.95	4.54E-01	0.13	7.76E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002254	3.58E-03	-0.47	0.17	4.64E-01	0.12	7.80E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0003035	5.67E-01	0.10	0.75	4.67E-01	0.12	7.83E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000532	4.91E-04	-0.54	0.06	5.04E-01	0.11	7.84E-01	Slackia	Slackia_isoflavoni convertens
Seq_0004012	1.09E-02	-0.41	0.29	5.03E-01	0.11	7.84E-01	Clostridiales_unclassified	Unclassified

Seq_0000024	2.63E-02	-0.37	0.37	4.79E-01	- 0.12	7.84E-01	Peptostreptococcaceae_unclassified	Unclassified
Seq_0000341	2.44E-02	-0.37	0.37	4.71E-01	- 0.12	7.84E-01	Clostridium_IV	Unclassified
Seq_0001334	2.43E-02	-0.37	0.37	4.91E-01	0.12	7.84E-01	Alistipes	Alistipes_massiliensis
Seq_0000973	3.94E-02	0.34	0.42	4.86E-01	- 0.12	7.84E-01	Clostridiales_unclassified	Unclassified
Seq_0003650	4.47E-02	-0.33	0.42	4.97E-01	- 0.12	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0000524	6.11E-02	-0.31	0.44	4.98E-01	0.11	7.84E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001338	7.70E-02	-0.29	0.44	5.01E-01	0.11	7.84E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002153	5.59E-02	-0.32	0.44	5.05E-01	- 0.11	7.84E-01	Clostridiales_unclassified	Unclassified
Seq_0001763	1.21E-01	0.26	0.45	4.91E-01	- 0.12	7.84E-01	Lactobacillus	Lactobacillus_agilis
Seq_0002077	1.24E-01	-0.26	0.45	4.69E-01	0.12	7.84E-01	Ruminococcaceae_unclassified	Oscillospira_guilliermondii
Seq_0000313	2.07E-01	-0.21	0.47	4.69E-01	0.12	7.84E-01	Clostridiales_unclassified	Unclassified
Seq_0000330	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Prevotella	Prevotella_copri
Seq_0000371	1.92E-01	0.22	0.47	5.12E-01	- 0.11	7.84E-01	Clostridium_XIVa	Clostridium_symbiosum
Seq_0000500	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Alloprevotella	Unclassified
Seq_0000587	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Pseudoramibacter	Pseudoramibacter_alactolyticus
Seq_0000725	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Erysipelotrichaceae_unclassified	Eubacterium_biforme
Seq_0000898	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Ruminococcaceae_unclassified	Eubacterium_coprostanoligenes

Seq_0000996	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001047	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Bifidobacterium	Unclassified
Seq_0001048	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Blautia	Blautia_luti
Seq_0001099	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Bacteroides	Bacteroides_intestinalis
Seq_0001490	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Erysipelotrichaceae_unclassified	Eubacterium_biforme
Seq_0001643	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Erysipelotrichaceae_unclassified	Eubacterium_biforme
Seq_0001720	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_unclassified	Unclassified
Seq_0001841	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0001901	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Peptostreptococcaceae_unclassified	Unclassified
Seq_0001980	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Paraprevotella	Paraprevotella_clara
Seq_0001997	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridium_XI	Unclassified
Seq_0002008	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0002115	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0002123	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Catenibacterium	Catenibacterium_mitsuokai
Seq_0002297	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Bacteroidetes_unclassified	Unclassified
Seq_0002389	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Bacteroidales_unclassified	Coprobacter_fastidiosus

Seq_0002415	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Prevotella	Prevotella_copri
Seq_0002487	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002504	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0002530	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Bifidobacterium	Bifidobacterium_bifidum
Seq_0002588	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Alloscardovia	Alloscardovia_omnicolens
Seq_0002605	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002691	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0003041	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Blautia	Ruminococcus_obeseum
Seq_0003338	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_unclassified	Unclassified
Seq_0003379	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0003495	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Clostridiales_unclassified	Unclassified
Seq_0003524	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Bacteria_unclassified	Unclassified
Seq_0003586	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0003627	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Bacteria_unclassified	Unclassified
Seq_0003681	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0003822	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Ruminococcaceae_unclassified	Unclassified

Seq_0003927	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0003970	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Ruminococcaceae_ unclassified	Flavonifractor_pla utii
Seq_0004066	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Mitsuokella	Mitsuokella_multa cida
Seq_0004126	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004127	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004128	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004205	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Bacteria_unclassifi ed	Unclassified
Seq_0004206	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Bilophila	Bilophila_wadswor rthia
Seq_0004340	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Bifidobacterium	Unclassified
Seq_0004341	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0004415	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004515	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Betaproteobacteria_ unclassified	Unclassified
Seq_0004517	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0004524	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Gordonibacter	Gordonibacter_pa melaeae
Seq_0004616	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0004850	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified

Seq_0004851	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0005020	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0005021	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0005162	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridium_XIVa	Unclassified
Seq_0005163	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Bacteria_unclassifi ed	Unclassified
Seq_0005434	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Butyricicoccus	Unclassified
Seq_0005436	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Ruminococcaceae_ unclassified	Flavonifractor_pla utii
Seq_0005452	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Bacteria_unclassifi ed	Unclassified
Seq_0006095	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Clostridiales_uncla ssified	Unclassified
Seq_0006459	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0006460	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Butyricimonas	Unclassified
Seq_0006461	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Parabacteroides	Parabacteroides_jo hnsonii
Seq_0006498	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0006499	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Ruminococcaceae_ unclassified	Eubacterium_sirae um
Seq_0007269	1.94E-01	-0.22	0.47	5.20E-01	- 0.11	7.84E-01	Alistipes	Unclassified
Seq_0007308	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Ruminococcaceae_ unclassified	Unclassified

Seq_0007374	1.63E-01	-0.23	0.47	5.20E-01	0.11	7.84E-01	Firmicutes_unclassified	Unclassified
Seq_0001744	3.22E-01	0.17	0.56	4.83E-01	- 0.12	7.84E-01	Finegoldia	Finegoldia_magna
Seq_0002743	4.43E-01	0.13	0.66	4.94E-01	0.12	7.84E-01	Blautia	Unclassified
Seq_0000673	4.88E-01	0.12	0.69	4.96E-01	0.12	7.84E-01	Peptoniphilus	Unclassified
Seq_0000264	5.45E-01	0.10	0.73	4.87E-01	- 0.12	7.84E-01	Prevotella	Prevotella_stercor ea
Seq_0001345	5.50E-01	0.10	0.74	4.89E-01	0.12	7.84E-01	Bacteria_unclassified	Unclassified
Seq_0001467	6.75E-01	-0.07	0.82	5.14E-01	0.11	7.84E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0001285	7.75E-01	-0.05	0.88	5.14E-01	- 0.11	7.84E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001173	8.43E-01	0.03	0.93	5.14E-01	- 0.11	7.84E-01	Ruminococcaceae_unclassified	Eubacterium_des molans
Seq_0000161	4.40E-02	0.33	0.42	5.21E-01	0.11	7.85E-01	Streptococcus	Unclassified
Seq_0001369	5.70E-02	-0.32	0.44	5.21E-01	0.11	7.85E-01	Barnesiella	Barnesiella_intesti nihominis
Seq_0003793	2.39E-01	-0.20	0.49	5.26E-01	0.11	7.91E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000084	3.12E-02	-0.35	0.38	5.29E-01	- 0.11	7.95E-01	Catenibacterium	Catenibacterium_ mitsuokai
Seq_0001347	3.45E-01	-0.16	0.58	5.35E-01	0.11	8.03E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000198	4.20E-05	-0.62	0.02	5.37E-01	0.10	8.06E-01	Bacteroides	Unclassified
Seq_0001521	6.75E-01	-0.07	0.82	5.40E-01	0.10	8.09E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001448	2.95E-03	-0.48	0.15	5.55E-01	- 0.10	8.13E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000490	2.98E-02	-0.36	0.37	5.81E-01	- 0.09	8.13E-01	Bacteria_unclassified	Unclassified

Seq_0000808	2.98E-02	-0.36	0.37	5.81E-01	- 0.09	8.13E-01	Desulfovibrio	Unclassified
Seq_0003716	2.98E-02	-0.36	0.37	5.81E-01	- 0.09	8.13E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0000036	3.20E-02	-0.35	0.38	5.72E-01	0.10	8.13E-01	Bifidobacterium	Bifidobacterium_b ifidum
Seq_0000249	4.94E-02	-0.33	0.44	5.47E-01	0.10	8.13E-01	Ruminococcus	Ruminococcus_br omii
Seq_0001024	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001025	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XIVa	Clostridium_alde nense
Seq_0001094	1.12E-01	0.27	0.44	5.57E-01	- 0.10	8.13E-01	Anaerostipes	Unclassified
Seq_0001309	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XIVa	Clostridium_hathe wayi
Seq_0001387	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Ruminococcus	Ruminococcus_ch ampanellensis
Seq_0001502	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001927	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002113	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Blautia	Unclassified
Seq_0002148	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XI	Unclassified
Seq_0002201	5.41E-02	-0.32	0.44	5.79E-01	- 0.09	8.13E-01	Slackia	Slackia_equolifaci ens
Seq_0002242	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Peptostreptococcac eae_unclassified	Clostridium_rumin antium
Seq_0002286	1.12E-01	0.27	0.44	5.57E-01	- 0.10	8.13E-01	Lachnospiraceae_u nclassified	Unclassified

Seq_0002320	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Blautia	Unclassified
Seq_0002754	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XIVa	Unclassified
Seq_0003036	1.04E-01	0.27	0.44	5.50E-01	- 0.10	8.13E-01	Clostridium_XIVa	Unclassified
Seq_0003062	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0003189	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XIVa	Clostridium_hathe wayi
Seq_0003419	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XIVa	Clostridium_orotic um
Seq_0003489	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Erysipelotrichaceae _unclassified	Eubacterium_dolic hum
Seq_0003516	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XI	Clostridium_bartle ttii
Seq_0003648	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Coprobacillus	Coprobacillus_cat eniformis
Seq_0004115	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Clostridium_XIVa	Unclassified
Seq_0004181	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Robinsoniella	Robinsoniella_peo riensis
Seq_0004183	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0004321	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Lachnospiraceae_u nclassified	Ruminococcus_gn avus
Seq_0004989	1.12E-01	0.27	0.44	5.81E-01	- 0.09	8.13E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0000789	1.45E-01	-0.24	0.47	5.59E-01	- 0.10	8.13E-01	Barnesiella	Barnesiella_intesti nihominis
Seq_0001112	2.13E-01	0.21	0.47	5.61E-01	0.10	8.13E-01	Sutterella	Sutterella_stercori canis
Seq_0001488	2.25E-01	-0.20	0.47	5.81E-01	0.09	8.13E-01	Butyricimonas	Unclassified

Seq_0001578	2.12E-01	-0.21	0.47	5.71E-01	0.10	8.13E-01	Clostridiales_unclassified	Unclassified
Seq_0002799	1.50E-01	-0.24	0.47	5.80E-01	-0.09	8.13E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000430	2.62E-01	-0.19	0.51	5.64E-01	-0.10	8.13E-01	Veillonella	Unclassified
Seq_0000140	3.04E-01	-0.17	0.54	5.69E-01	-0.10	8.13E-01	Weissella	Unclassified
Seq_0000533	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Prevotella	Prevotella_copri
Seq_0000552	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Prevotella	Prevotella_copri
Seq_0000766	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Prevotella	Unclassified
Seq_0000767	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Clostridiales_unclassified	Unclassified
Seq_0001055	3.04E-01	-0.17	0.54	5.69E-01	-0.10	8.13E-01	Lactobacillaceae_unclassified	Unclassified
Seq_0001142	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Dialister	Unclassified
Seq_0001621	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002137	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Prevotella	Prevotella_stercor
Seq_0002746	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002829	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Clostridium_XIVa	Unclassified
Seq_0002990	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Prevotella	Prevotella_stercor
Seq_0003428	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Blautia	Unclassified
Seq_0003655	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Allisonella	Allisonella_histaminiformans
Seq_0003764	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0003765	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Clostridia_unclassified	Unclassified

Seq_0003933	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0005186	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Prevotella	Prevotella_copri
Seq_0005682	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Clostridiales_uncla ssified	Unclassified
Seq_0006136	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0007333	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0007334	3.10E-01	-0.17	0.54	5.81E-01	0.09	8.13E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0000316	5.00E-01	-0.11	0.70	5.80E-01	- 0.09	8.13E-01	Prevotella	Prevotella_copri
Seq_0000710	7.52E-01	0.05	0.88	5.76E-01	0.09	8.13E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001507	8.70E-01	-0.03	0.94	5.57E-01	0.10	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001940	8.90E-01	0.02	0.95	5.54E-01	- 0.10	8.13E-01	Parvimonas	Parvimonas_micra
Seq_0003818	8.90E-01	0.02	0.95	5.54E-01	- 0.10	8.13E-01	Clostridium_XVIII	Clostridium_ramo sum
Seq_0001021	9.32E-01	0.01	0.96	5.47E-01	0.10	8.13E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001214	8.00E-02	0.29	0.44	5.83E-01	- 0.09	8.14E-01	Ruminococcaceae_ unclassified	Eubacterium_des molans
Seq_0001241	1.33E-01	-0.25	0.45	5.83E-01	- 0.09	8.14E-01	Ruminococcus	Unclassified
Seq_0000244	1.56E-01	-0.24	0.47	5.84E-01	0.09	8.14E-01	Acidaminococcacea e_unclassified	Phascolarctobacter ium_succinatutens
Seq_0000059	6.33E-01	0.08	0.79	5.85E-01	- 0.09	8.15E-01	Prevotella	Prevotella_copri
Seq_0001695	1.11E-01	-0.27	0.44	6.05E-01	0.09	8.41E-01	Ruminococcaceae_ unclassified	Unclassified

Seq_0000168	4.86E-01	-0.12	0.69	6.06E-01	- 0.09	8.43E-01	Collinsella	Collinsella_tanaka ei
Seq_0001650	2.69E-01	-0.19	0.51	6.08E-01	- 0.09	8.44E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0002937	6.83E-03	-0.44	0.22	6.28E-01	0.08	8.52E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0003124	6.83E-03	-0.44	0.22	6.28E-01	0.08	8.52E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0002301	3.01E-02	-0.36	0.37	6.36E-01	- 0.08	8.52E-01	Ruminococcaceae_ unclassified	Faecalibacterium_ prausnitzii
Seq_0004342	2.49E-02	-0.37	0.37	6.36E-01	0.08	8.52E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000031	1.23E-01	-0.26	0.45	6.37E-01	- 0.08	8.52E-01	Clostridium_sensu stricto	Clostridium_dispo ricum
Seq_0000951	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Dialister	Unclassified
Seq_0001330	2.63E-01	0.19	0.51	6.36E-01	- 0.08	8.52E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001450	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Prevotella	Prevotella_copri
Seq_0001619	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001669	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Paraprevotella	Paraprevotella_cla ra
Seq_0002470	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0002914	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Ruminococcus	Unclassified
Seq_0002974	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Sporobacter	Unclassified
Seq_0003760	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Butyricimonas	Butyricimonas_vir osa
Seq_0004263	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Bacteria_unclassifi ed	Unclassified
Seq_0004520	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Prevotella	Prevotella_copri
Seq_0004609	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Collinsella	Collinsella_aerofa ciens

Seq_0005024	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Prevotella	Prevotella_copri
Seq_0005025	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Collinsella	Collinsella_aerofaciens
Seq_0005026	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Clostridiales_unclassified	Unclassified
Seq_0005027	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Bacteria_unclassified	Unclassified
Seq_0005660	2.67E-01	-0.19	0.51	6.46E-01	0.08	8.52E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001191	3.11E-01	0.17	0.54	6.16E-01	-0.09	8.52E-01	Parvimonas	Parvimonas_micra
Seq_0000493	4.93E-01	-0.12	0.70	6.35E-01	0.08	8.52E-01	Blautia	Blautia_faecis
Seq_0000774	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Anaerostipes	Anaerostipes_hadrus
Seq_0000958	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Oscillibacter	Unclassified
Seq_0001077	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Peptostreptococcus	Peptostreptococcus_stomatis
Seq_0001083	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Peptostreptococcaceae_unclassified	Unclassified
Seq_0001923	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002328	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Clostridium_sensu_stricto	Clostridium_butyricum
Seq_0002444	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002786	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Bacteria_unclassified	Unclassified
Seq_0002819	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Bacteria_unclassified	Unclassified
Seq_0003125	9.27E-01	-0.02	0.95	6.46E-01	-0.08	8.52E-01	Pseudoflavonifractor	Pseudoflavonifractor_capillosus

Seq_0003232	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Paraprevotella	Paraprevotella_cla ra
Seq_0003632	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Bifidobacterium	Unclassified
Seq_0003718	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Bacteria_unclassifi ed	Unclassified
Seq_0003796	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0003887	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Blautia	Unclassified
Seq_0003975	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Bacteria_unclassifi ed	Unclassified
Seq_0004053	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Clostridium_IV	Unclassified
Seq_0004347	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Bacteria_unclassifi ed	Unclassified
Seq_0004623	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Catenibacterium	Catenibacterium_ mitsuokai
Seq_0004759	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Firmicutes_unclassi fied	Unclassified
Seq_0004871	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0005193	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0005465	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Clostridium_XIVa	Unclassified
Seq_0006548	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0007379	9.27E-01	-0.02	0.95	6.46E-01	- 0.08	8.52E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002243	9.32E-01	0.01	0.96	6.22E-01	0.08	8.52E-01	Prevotella	Prevotella_copri
Seq_0000348	9.50E-01	-0.01	0.97	6.20E-01	0.08	8.52E-01	Collinsella	Unclassified

Seq_0002168	9.58E-01	-0.01	0.97	6.31E-01	0.08	8.52E-01	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0000844	2.96E-02	0.36	0.37	6.49E-01	- 0.08	8.53E-01	Clostridium_XIVa	Unclassified
Seq_0001946	5.45E-01	-0.10	0.73	6.49E-01	- 0.08	8.53E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0004185	5.45E-01	-0.10	0.73	6.49E-01	- 0.08	8.53E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000660	8.16E-01	-0.04	0.91	6.49E-01	- 0.08	8.53E-01	Enterobacteriaceae_unclassified	Unclassified
Seq_0000831	3.06E-02	0.36	0.37	6.51E-01	- 0.08	8.55E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000218	1.40E-02	-0.40	0.31	6.55E-01	0.08	8.57E-01	Dialister	Dialister_succinatiphilus
Seq_0000706	2.41E-02	-0.37	0.37	6.54E-01	0.08	8.57E-01	Clostridium_IV	Eubacterium_siracum
Seq_0000092	4.09E-01	-0.14	0.63	6.54E-01	0.08	8.57E-01	Lactobacillus	Unclassified
Seq_0003252	4.81E-01	0.12	0.69	6.55E-01	0.08	8.57E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002230	4.32E-01	-0.13	0.66	6.56E-01	0.08	8.58E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000998	9.12E-01	-0.02	0.95	6.58E-01	- 0.08	8.59E-01	Clostridium_XIVa	Clostridium_glycyrrhizinilyticum
Seq_0000141	3.31E-01	-0.16	0.57	6.60E-01	- 0.07	8.60E-01	Lactobacillus	Unclassified
Seq_0001909	5.03E-01	-0.11	0.70	6.59E-01	0.08	8.60E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001459	8.45E-01	0.03	0.93	6.64E-01	- 0.07	8.65E-01	Megasphaera	Unclassified
Seq_0006108	9.39E-02	-0.28	0.44	6.67E-01	- 0.07	8.67E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002413	7.05E-04	-0.53	0.07	6.85E-01	0.07	8.73E-01	Clostridiales_unclassified	Unclassified

Seq_0001670	3.70E-02	-0.34	0.40	6.78E-01	0.07	8.73E-01	Howardella	Howardella_ureilytica
Seq_0001666	4.30E-02	0.33	0.42	7.05E-01	- 0.06	8.73E-01	Butyricicoccus	Eubacterium_desmolans
Seq_0000353	1.05E-01	-0.27	0.44	6.81E-01	- 0.07	8.73E-01	Prevotella	Unclassified
Seq_0002544	5.16E-02	-0.32	0.44	6.85E-01	0.07	8.73E-01	Firmicutes_unclassified	Unclassified
Seq_0002874	1.29E-01	0.25	0.45	6.91E-01	- 0.07	8.73E-01	Clostridiales_unclassified	Unclassified
Seq_0001806	1.39E-01	-0.25	0.46	7.12E-01	- 0.06	8.73E-01	Firmicutes_unclassified	Unclassified
Seq_0000317	2.12E-01	0.21	0.47	7.11E-01	- 0.06	8.73E-01	Blautia	Unclassified
Seq_0001079	1.75E-01	-0.23	0.47	7.06E-01	- 0.06	8.73E-01	Clostridiales_unclassified	Unclassified
Seq_0002522	2.11E-01	-0.21	0.47	7.04E-01	0.06	8.73E-01	Acinetobacter	Unclassified
Seq_0002876	2.11E-01	-0.21	0.47	7.04E-01	0.06	8.73E-01	Bacteria_unclassified	Unclassified
Seq_0000071	2.37E-01	-0.20	0.49	7.11E-01	- 0.06	8.73E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000346	2.99E-01	0.18	0.54	6.85E-01	0.07	8.73E-01	Anaerococcus	Anaerococcus_vaginalis
Seq_0001353	4.19E-01	-0.14	0.64	6.96E-01	- 0.07	8.73E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001221	4.89E-01	-0.12	0.69	7.04E-01	0.06	8.73E-01	Prevotella	Prevotella_bivia
Seq_0002846	5.60E-01	-0.10	0.75	6.75E-01	- 0.07	8.73E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0000668	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Moraxella	Unclassified
Seq_0001644	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Firmicutes_unclassified	Clostridium_innocuum
Seq_0001789	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Barnesiella	Barnesiella_intestinihominis

Seq_0002317	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0004200	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Clostridiales_unclassified	Unclassified
Seq_0004339	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Firmicutes_unclassified	Clostridium_innocuum
Seq_0004744	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Lactococcus	Unclassified
Seq_0004849	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Streptococcus	Unclassified
Seq_0005160	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0005161	6.46E-01	0.08	0.79	7.14E-01	0.06	8.73E-01	Lactococcus	Unclassified
Seq_0000444	7.30E-01	0.06	0.86	7.09E-01	0.06	8.73E-01	Paraprevotella	Paraprevotella_clara
Seq_0000221	7.60E-01	-0.05	0.88	6.82E-01	-0.07	8.73E-01	Alistipes	Unclassified
Seq_0000286	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Fusobacterium	Fusobacterium_equinum
Seq_0000297	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Bacteroides	Bacteroides_vulgatus
Seq_0000328	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Peptostreptococcus	Peptostreptococcus_anaerobius
Seq_0000724	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Fusobacterium	Fusobacterium_equinum
Seq_0001102	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Fusobacterium	Fusobacterium_nucleatum
Seq_0001182	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Prevotella	Prevotella_bivia
Seq_0001193	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Dialister	Dialister_pneumointes
Seq_0001703	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Roseburia	Eubacterium_rectale
Seq_0001913	7.83E-01	0.05	0.88	7.14E-01	-0.06	8.73E-01	Roseburia	Eubacterium_rectale

Seq_0003099	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Clostridiales_uncla ssified	Eubacterium_ventr iosum
Seq_0003377	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0003517	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Dialister	Dialister_invisus
Seq_0003555	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Bacteria_unclassifi ed	Unclassified
Seq_0003675	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Clostridium_XIVb	Clostridium_lactat ifermentans
Seq_0003711	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Gardnerella	Gardnerella_vagin alis
Seq_0003791	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Ruminococcaceae_ unclassified	Intestinimonas_but yriciproducens
Seq_0003917	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Murdochiella	Murdochiella_asac charolytica
Seq_0004050	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Bacteria_unclassifi ed	Eubacterium_cylin droides
Seq_0004830	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0004996	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Prevotellaceae_uncl assified	Prevotella_copri
Seq_0004997	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Clostridiales_uncla ssified	Unclassified
Seq_0005129	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Ruminococcus2	Unclassified
Seq_0005404	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Prevotella	Prevotella_corpori s
Seq_0005405	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0005406	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Prevotella	Unclassified

Seq_0005626	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Anaerococcus	Anaerococcus_obe siensis
Seq_0005627	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Lactobacillus	Lactobacillus_jens enii
Seq_0006069	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Barnesiella	Barnesiella_intesti nihominis
Seq_0006070	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Leptotrichia	Unclassified
Seq_0006423	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Blautia	Unclassified
Seq_0007232	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0007233	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0007234	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Ruminococcaceae_ unclassified	Eubacterium_des molans
Seq_0007235	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Clostridiales_uncla ssified	Unclassified
Seq_0007237	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Bacteroidetes_uncl assified	Unclassified
Seq_0007238	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Firmicutes_unclassi fied	Clostridium_innoc uum
Seq_0007239	7.83E-01	0.05	0.88	7.14E-01	- 0.06	8.73E-01	Bacteroidetes_uncl assified	Unclassified
Seq_0000220	9.52E-01	-0.01	0.97	7.11E-01	- 0.06	8.73E-01	Bacteroides	Bacteroides_copro cola
Seq_0002375	9.61E-01	-0.01	0.97	6.90E-01	- 0.07	8.73E-01	Lachnospiraceae_u nclassified	Clostridium_glycy rrhizinilyticum
Seq_0001278	1.22E-01	-0.26	0.45	7.19E-01	0.06	8.79E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002154	1.22E-01	-0.26	0.45	7.19E-01	0.06	8.79E-01	Collinsella	Collinsella_aerofa ciens

Seq_0002410	4.85E-01	0.12	0.69	7.25E-01	- 0.06	8.84E-01	Clostridium_sensu_ stricto	Clostridium_cadav eris
Seq_0000894	6.60E-01	-0.07	0.81	7.25E-01	- 0.06	8.84E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0000619	2.13E-02	-0.38	0.37	7.30E-01	- 0.06	8.89E-01	Clostridiales_uncla ssified	Unclassified
Seq_0003179	8.59E-01	-0.03	0.93	7.30E-01	- 0.06	8.89E-01	Blautia	Blautia_hydrogeno trophica
Seq_0000292	7.97E-04	-0.53	0.07	7.33E-01	- 0.06	8.92E-01	Bacteroides	Unclassified
Seq_0001030	4.34E-02	-0.33	0.42	7.36E-01	0.06	8.94E-01	Bacteria_unclassifi ed	Unclassified
Seq_0001320	2.24E-01	-0.20	0.47	7.40E-01	0.06	8.97E-01	Oscillibacter	Unclassified
Seq_0002069	7.41E-01	-0.06	0.88	7.40E-01	- 0.06	8.97E-01	Anaerofustis	Anaerofustis_sterc orihominis
Seq_0000654	8.23E-01	-0.04	0.92	7.41E-01	0.06	8.98E-01	Blautia	Blautia_hydrogeno trophica
Seq_0001446	9.69E-01	-0.01	0.98	7.41E-01	- 0.06	8.98E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0003177	9.26E-01	-0.02	0.95	7.44E-01	- 0.06	9.00E-01	Coriobacteriaceae_ unclassified	Unclassified
Seq_0001576	4.24E-03	-0.46	0.18	7.46E-01	0.06	9.01E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001415	6.44E-01	0.08	0.79	7.46E-01	- 0.06	9.01E-01	Clostridiales_uncla ssified	Eubacterium_halli
Seq_0001973	1.23E-02	-0.41	0.29	7.50E-01	- 0.05	9.05E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0002480	5.79E-01	0.09	0.75	7.52E-01	0.05	9.06E-01	Streptococcus	Unclassified
Seq_0000074	9.21E-01	-0.02	0.95	7.55E-01	0.05	9.09E-01	Parasutterella	Parasutterella_excr ementihominis
Seq_0000537	2.10E-04	-0.57	0.05	7.63E-01	0.05	9.10E-01	Coprococcus	Coprococcus_catu s

Seq_0000948	2.47E-02	-0.37	0.37	7.75E-01	0.05	9.10E-01	Ruminococcaceae_unclassified	Eubacterium_desmolans
Seq_0000812	4.62E-02	0.33	0.43	7.72E-01	- 0.05	9.10E-01	Streptococcus	Unclassified
Seq_0000224	3.69E-01	-0.15	0.60	7.68E-01	- 0.05	9.10E-01	Roseburia	Unclassified
Seq_0000109	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Sarcina	Sarcina_ventriculi
Seq_0000211	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Prevotella	Prevotella_stercor ea
Seq_0000539	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Prevotella	Prevotella_copri
Seq_0000754	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Betaproteobacteria_unclassified	Unclassified
Seq_0001272	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0001847	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Dorea	Dorea_longicatena
Seq_0002411	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Lactobacillus	Unclassified
Seq_0002803	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Prevotella	Prevotella_copri
Seq_0003069	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Veillonellaceae_unclassified	Pectinatus_cerevisi iiphilus
Seq_0003103	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Faecalibacterium	Faecalibacterium_p rausnitzii
Seq_0003198	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0003212	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Coriobacteriaceae_unclassified	Unclassified
Seq_0003343	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Veillonellaceae_unclassified	Pectinatus_cerevisi iiphilus
Seq_0003631	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Clostridiales_uncla ssified	Unclassified
Seq_0006524	4.61E-01	0.12	0.66	7.83E-01	0.05	9.10E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002082	4.91E-01	0.12	0.70	7.57E-01	- 0.05	9.10E-01	Rothia	Rothia_mucilagino sa

Seq_0000234	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Blautia	Unclassified
Seq_0001054	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001085	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Blautia	Blautia_luti
Seq_0001238	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Blautia	Unclassified
Seq_0001640	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0002139	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Gordonibacter	Gordonibacter_pa melaeae
Seq_0002174	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Clostridiales_uncla ssified	Unclassified
Seq_0002450	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Streptococcus	Unclassified
Seq_0002495	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0002520	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Clostridium_IV	Unclassified
Seq_0002614	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Clostridiales_uncla ssified	Eubacterium_hallii
Seq_0002896	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Blautia	Blautia_glucerasea
Seq_0003753	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Bifidobacterium	Unclassified
Seq_0003962	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Clostridium_XIVa	Clostridium_glycy rrhizinilyticum
Seq_0004184	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004389	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Blautia	Unclassified

Seq_0004710	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Erysipelotrichaceae_unclassified	Eubacterium_bifforme
Seq_0006053	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Alistipes	Alistipes_indistinctus
Seq_0007359	5.20E-01	0.11	0.70	7.83E-01	- 0.05	9.10E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002149	6.30E-01	0.08	0.79	7.81E-01	0.05	9.10E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000102	8.67E-01	0.03	0.94	7.71E-01	0.05	9.10E-01	Prevotella	Unclassified
Seq_0000125	8.76E-01	0.03	0.95	7.76E-01	- 0.05	9.10E-01	Enterobacteriaceae_unclassified	Unclassified
Seq_0000121	6.86E-04	-0.53	0.07	7.86E-01	- 0.05	9.13E-01	Bacteroidetes_unclassified	Unclassified
Seq_0001128	4.76E-03	-0.45	0.18	7.98E-01	- 0.04	9.25E-01	Firmicutes_unclassified	Unclassified
Seq_0001972	3.90E-01	-0.15	0.63	7.98E-01	0.04	9.25E-01	Clostridium_IV	Clostridium_leptum
Seq_0000757	6.18E-01	-0.08	0.78	8.01E-01	0.04	9.27E-01	Bifidobacterium	Unclassified
Seq_0001440	6.18E-01	-0.08	0.78	8.01E-01	0.04	9.27E-01	Collinsella	Collinsella_aerofaciens
Seq_0001374	5.12E-02	0.32	0.44	8.04E-01	- 0.04	9.28E-01	Firmicutes_unclassified	Unclassified
Seq_0002587	2.08E-01	-0.21	0.47	8.04E-01	0.04	9.28E-01	Gordonibacter	Gordonibacter_pamelaee
Seq_0001778	2.38E-01	-0.20	0.49	8.06E-01	0.04	9.31E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000096	6.56E-01	-0.08	0.81	8.08E-01	0.04	9.32E-01	Erysipelotrichaceae_unclassified	Eubacterium_bifforme
Seq_0000088	4.97E-02	-0.33	0.44	8.13E-01	0.04	9.37E-01	Bacteroides	Unclassified
Seq_0002090	3.30E-02	0.35	0.38	8.40E-01	- 0.03	9.41E-01	Clostridium_XVIII	Unclassified
Seq_0002400	8.67E-02	-0.29	0.44	8.40E-01	- 0.03	9.41E-01	Clostridiales_unclassified	Unclassified

Seq_0000760	2.47E-01	0.20	0.50	8.47E-01	0.03	9.41E-01	Eggerthella	Eggerthella_lenta
Seq_0003317	2.51E-01	-0.19	0.51	8.17E-01	0.04	9.41E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000877	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Bifidobacterium	Unclassified
Seq_0000985	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Blautia	Unclassified
Seq_0001120	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Lactobacillus	Unclassified
Seq_0001282	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Collinsella	Collinsella_aerofaciens
Seq_0001316	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Clostridium_XVIII	Clostridium_saccharogumia
Seq_0001497	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Peptostreptococcaceae_unclassified	Unclassified
Seq_0001837	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Dorea	Dorea_formicigerans
Seq_0003129	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Clostridium_XVIII	Clostridium_saccharogumia
Seq_0003493	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Clostridiales_unclassified	Unclassified
Seq_0003590	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Clostridium_XVIII	Unclassified
Seq_0004528	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Blautia	Blautia_luti
Seq_0005042	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Bifidobacteriaceae_unclassified	Unclassified
Seq_0005188	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Bifidobacteriaceae_unclassified	Unclassified
Seq_0005456	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Gemella	Unclassified
Seq_0006138	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Methanosphaera	Methanosphaera_cuniculi
Seq_0006139	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Blautia	Unclassified
Seq_0006520	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0007338	2.67E-01	0.19	0.51	8.54E-01	0.03	9.41E-01	Lachnospiraceae_unclassified	Unclassified

Seq_0000207	3.67E-01	-0.15	0.60	8.51E-01	- 0.03	9.41E-01	Bilophila	Bilophila_wadsworthia
Seq_0000611	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Bacteroides	Bacteroides_cellulosilyticus
Seq_0000631	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Ruminococcus	Ruminococcus_bromii
Seq_0001201	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Blautia	Ruminococcus_obesum
Seq_0001232	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0001418	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Clostridiales_unclassified	Eubacterium_hallii
Seq_0001541	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Bacteroides	Unclassified
Seq_0001747	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002056	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Bacteroides	Unclassified
Seq_0002424	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Butyricimonas	Butyricimonas_viridosa
Seq_0002434	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0002637	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Streptococcus	Unclassified
Seq_0002656	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Blautia	Unclassified
Seq_0002706	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Ruminococcus	Unclassified
Seq_0002732	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Ruminococcaceae_unclassified	Unclassified
Seq_0002797	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_unclassified	Unclassified

Seq_0003061	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Asaccharobacter	Unclassified
Seq_0003253	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0003920	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0003964	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Bacteroidetes_uncl assified	Unclassified
Seq_0004116	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Parabacteroides	Unclassified
Seq_0004117	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004180	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0004182	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Alistipes	Alistipes_indistinc tus
Seq_0004245	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004247	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Porphyromonadace ae_unclassified	Parabacteroides_di stasonis
Seq_0004491	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Blautia	Unclassified
Seq_0004829	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0005617	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0005618	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0006056	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0007218	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Clostridiales_uncla ssified	Unclassified

Seq_0007360	4.61E-01	-0.12	0.66	8.54E-01	- 0.03	9.41E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001385	4.82E-01	0.12	0.69	8.34E-01	- 0.04	9.41E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000878	2.92E-03	-0.48	0.15	8.57E-01	- 0.03	9.43E-01	Burkholderiales_un classified	Unclassified
Seq_0003889	6.30E-02	-0.31	0.44	8.59E-01	- 0.03	9.44E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000934	5.86E-01	0.09	0.75	8.62E-01	0.03	9.47E-01	Prevotella	Prevotella_copri
Seq_0002212	2.73E-01	0.19	0.52	8.67E-01	- 0.03	9.52E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0000542	2.19E-02	-0.38	0.37	8.71E-01	- 0.03	9.55E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0000740	1.36E-01	-0.25	0.45	8.74E-01	0.03	9.57E-01	Prevotellaceae_uncl assified	Unclassified
Seq_0001774	3.02E-01	-0.17	0.54	8.76E-01	0.03	9.59E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0000494	2.62E-02	-0.37	0.37	8.78E-01	0.03	9.60E-01	Bacteroides	Bacteroides_ovatu s
Seq_0001265	2.26E-01	-0.20	0.47	8.81E-01	0.03	9.63E-01	Bacteria_unclassifi ed	Unclassified
Seq_0001673	2.26E-01	-0.20	0.47	8.81E-01	0.03	9.63E-01	Olsenella	Olsenella_uli
Seq_0000205	5.45E-01	-0.10	0.73	8.86E-01	0.02	9.67E-01	Alistipes	Unclassified
Seq_0001464	3.65E-01	0.15	0.60	8.92E-01	- 0.02	9.73E-01	Peptoniphilus	Unclassified
Seq_0000392	4.34E-05	-0.62	0.02	9.10E-01	- 0.02	9.76E-01	Enterorhabdus	Unclassified
Seq_0000414	4.44E-02	-0.33	0.42	8.97E-01	0.02	9.76E-01	Dialister	Dialister_succinati philus
Seq_0000068	1.02E-01	-0.27	0.44	9.01E-01	0.02	9.76E-01	Firmicutes_unclassi fied	Eubacterium_bifor me
Seq_0001582	6.53E-02	-0.31	0.44	9.25E-01	- 0.02	9.76E-01	Ruminococcaceae_ unclassified	Unclassified

Seq_0004317	2.57E-01	0.19	0.51	9.01E-01	- 0.02	9.76E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000010	2.82E-01	-0.18	0.53	9.08E-01	- 0.02	9.76E-01	Prevotella	Prevotella_copri
Seq_0000600	3.13E-01	0.17	0.55	9.04E-01	- 0.02	9.76E-01	Blautia	Unclassified
Seq_0000133	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Allobaculum	Allobaculum_sterc oricanis
Seq_0000529	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Lachnospiraceae_u nclassified	Ruminococcus_gn avus
Seq_0000906	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Bacteroides	Bacteroides_egger thii
Seq_0000990	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0001203	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Allobaculum	Unclassified
Seq_0001593	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Bacteroides	Bacteroides_egger thii
Seq_0001636	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Clostridiales_uncla ssified	Unclassified
Seq_0001737	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001996	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0002034	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Ruminococcaceae_ unclassified	Unclassified
Seq_0002911	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Clostridiales_uncla ssified	Unclassified
Seq_0003191	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Butyricicoccus	Unclassified
Seq_0003420	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Blautia	Unclassified
Seq_0003581	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Blautia	Blautia_glucerasea
Seq_0003583	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004052	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Prevotella	Unclassified

Seq_0005125	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0006054	3.56E-01	0.16	0.58	9.27E-01	0.02	9.76E-01	Clostridiales_unclassified	Unclassified
Seq_0002677	4.44E-01	-0.13	0.66	9.26E-01	0.02	9.76E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000339	5.61E-01	-0.10	0.75	9.11E-01	-0.02	9.76E-01	Firmicutes_unclassified	Eubacterium_biforme
Seq_0000235	6.11E-01	-0.09	0.78	9.09E-01	-0.02	9.76E-01	Acidaminococcus	Acidaminococcus_fermentans
Seq_0000413	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Bacteroides	Bacteroides_salyersiae
Seq_0000485	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Bilophila	Bilophila_wadsworthia
Seq_0001041	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Clostridium_IV	Unclassified
Seq_0001233	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Bacteroides	Bacteroides_vulgatus
Seq_0001672	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Bacteroidetes_unclassified	Unclassified
Seq_0001857	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Porphyromonas	Unclassified
Seq_0002004	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Actinomyces	Unclassified
Seq_0002232	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002894	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Peptoniphilus	Peptoniphilus_lacrimalis
Seq_0002938	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Varibaculum	Varibaculum_cambriense
Seq_0003965	7.14E-01	0.06	0.85	9.27E-01	-0.02	9.76E-01	Blautia	Unclassified

Seq_0003966	7.14E-01	0.06	0.85	9.27E-01	- 0.02	9.76E-01	Clostridiales_uncla ssified	Unclassified
Seq_0004186	7.14E-01	0.06	0.85	9.27E-01	- 0.02	9.76E-01	Clostridium_sensu_ stricto	Unclassified
Seq_0005396	7.14E-01	0.06	0.85	9.27E-01	- 0.02	9.76E-01	Parabacteroides	Parabacteroides_m erdae
Seq_0006057	7.14E-01	0.06	0.85	9.27E-01	- 0.02	9.76E-01	Clostridium_XIVa	Unclassified
Seq_0006406	7.14E-01	0.06	0.85	9.27E-01	- 0.02	9.76E-01	Roseburia	Unclassified
Seq_0007361	7.14E-01	0.06	0.85	9.27E-01	- 0.02	9.76E-01	Clostridiales_uncla ssified	Unclassified
Seq_0000928	5.85E-01	0.09	0.75	9.30E-01	- 0.02	9.78E-01	Enterobacteriaceae _unclassified	Unclassified
Seq_0004527	4.18E-01	-0.14	0.64	9.32E-01	0.01	9.80E-01	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0002572	1.68E-01	-0.23	0.47	9.41E-01	- 0.01	9.87E-01	Clostridium_XIVa	Unclassified
Seq_0003814	1.68E-01	-0.23	0.47	9.41E-01	- 0.01	9.87E-01	Butyricimonas	Butyricimonas_vir osa
Seq_0000315	2.42E-01	-0.20	0.49	9.39E-01	0.01	9.87E-01	Alistipes	Alistipes_finegoldi i
Seq_0000743	1.96E-01	0.22	0.47	9.46E-01	- 0.01	9.91E-01	Lachnospiraceae_u nclassified	Unclassified
Seq_0001358	7.27E-01	0.06	0.86	9.46E-01	0.01	9.91E-01	Erysipelotrichaceae _unclassified	Unclassified
Seq_0000879	3.01E-01	-0.17	0.54	9.48E-01	- 0.01	9.93E-01	Blautia	Unclassified
Seq_0001042	3.34E-01	-0.16	0.58	9.49E-01	- 0.01	9.93E-01	Clostridium_XIVa	Unclassified
Seq_0001092	2.91E-02	-0.36	0.37	9.53E-01	- 0.01	9.95E-01	Firmicutes_unclassi fied	Unclassified

Seq_0000146	1.58E-01	-0.24	0.47	9.56E-01	0.01	9.95E-01	Phascolarctobacterium	Phascolarctobacterium_faecium
Seq_0000623	2.08E-01	0.21	0.47	9.55E-01	- 0.01	9.95E-01	Eggerthella	Eggerthella_lenta
Seq_0003407	1.54E-01	-0.24	0.47	9.55E-01	- 0.01	9.95E-01	Collinsella	Unclassified
Seq_0001471	6.09E-01	-0.09	0.78	9.53E-01	- 0.01	9.95E-01	Allisonella	Allisonella_histaminiformans
Seq_0003336	9.77E-01	0.00	0.99	9.55E-01	0.01	9.95E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000900	4.62E-01	0.12	0.67	9.57E-01	- 0.01	9.96E-01	Lachnospiraceae_unclassified	Unclassified
Seq_0000676	2.56E-02	-0.37	0.37	9.67E-01	- 0.01	1	Peptococcus	Peptococcus_niger
Seq_0000492	9.21E-02	-0.28	0.44	1	0.00	1	Prevotella	Unclassified
Seq_0001564	9.21E-02	-0.28	0.44	1	0.00	1	Ruminococcaceae_unclassified	Unclassified
Seq_0001758	9.21E-02	-0.28	0.44	1	0.00	1	Clostridium_XIVa	Unclassified
Seq_0001783	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0001861	9.21E-02	-0.28	0.44	1	0.00	1	Ruminococcaceae_unclassified	Unclassified
Seq_0002023	9.21E-02	-0.28	0.44	1	0.00	1	Ruminococcus	Ruminococcus_albus
Seq_0002036	9.21E-02	-0.28	0.44	1	0.00	1	Clostridiales_unclassified	Unclassified
Seq_0002092	9.21E-02	-0.28	0.44	1	0.00	1	Pasteurellaceae_unclassified	Aggregatibacter_jeikei
Seq_0002401	6.62E-02	-0.31	0.44	9.87E-01	0.00	1	Ruminococcaceae_unclassified	Unclassified
Seq_0002438	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified

Seq_0002454	9.21E-02	-0.28	0.44	1	0.00	1	Clostridiales_unclassified	Eubacterium_coprostanoligenes
Seq_0002476	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0002478	9.21E-02	-0.28	0.44	1	0.00	1	Coprococcus	Coprococcus_eutactus
Seq_0002692	9.21E-02	-0.28	0.44	1	0.00	1	Butyricimonas	Butyricimonas_viridosa
Seq_0002879	9.21E-02	-0.28	0.44	1	0.00	1	Roseburia	Roseburia_inulinivorans
Seq_0002960	9.21E-02	-0.28	0.44	1	0.00	1	Desulfovibrio	Desulfovibrio_piger
Seq_0003021	9.21E-02	-0.28	0.44	1	0.00	1	Bacteroides	Bacteroides_coprophilus
Seq_0003068	9.21E-02	-0.28	0.44	1	0.00	1	Roseburia	Eubacterium_rectale
Seq_0003261	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Butyrivibrio_crossotus
Seq_0003339	9.21E-02	-0.28	0.44	1	0.00	1	Clostridiales_unclassified	Unclassified
Seq_0003383	9.21E-02	-0.28	0.44	1	0.00	1	Bacteria_unclassified	Unclassified
Seq_0003427	9.21E-02	-0.28	0.44	1	0.00	1	Bacteria_unclassified	Unclassified
Seq_0003593	9.21E-02	-0.28	0.44	1	0.00	1	Firmicutes_unclassified	Unclassified
Seq_0003757	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Butyrivibrio_crossotus
Seq_0003763	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0003819	9.21E-02	-0.28	0.44	1	0.00	1	Ruminococcus	Unclassified
Seq_0003899	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Bacteroides_pectinophilus

Seq_0004209	9.21E-02	-0.28	0.44	1	0.00	1	Bacteria_unclassified	Unclassified
Seq_0004210	9.21E-02	-0.28	0.44	1	0.00	1	Clostridiales_unclassified	Unclassified
Seq_0004344	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0004416	9.21E-02	-0.28	0.44	1	0.00	1	Bacteroides	Unclassified
Seq_0004525	9.21E-02	-0.28	0.44	1	0.00	1	Ruminococcaceae_unclassified	Unclassified
Seq_0004754	9.21E-02	-0.28	0.44	1	0.00	1	Bacteria_unclassified	Unclassified
Seq_0004755	9.21E-02	-0.28	0.44	1	0.00	1	Bacteroides	Bacteroides_coprophilus
Seq_0004865	9.21E-02	-0.28	0.44	1	0.00	1	Firmicutes_unclassified	Unclassified
Seq_0005036	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0005182	9.21E-02	-0.28	0.44	1	0.00	1	Firmicutes_unclassified	Unclassified
Seq_0005183	9.21E-02	-0.28	0.44	1	0.00	1	Bacteria_unclassified	Unclassified
Seq_0005673	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0006130	9.21E-02	-0.28	0.44	1	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0007320	9.21E-02	-0.28	0.44	1	0.00	1	Bacteria_unclassified	Unclassified
Seq_0007322	9.21E-02	-0.28	0.44	1	0.00	1	Firmicutes_unclassified	Unclassified
Seq_0007323	9.21E-02	-0.28	0.44	1	0.00	1	Clostridiales_unclassified	Unclassified
Seq_0003559	1.19E-01	-0.26	0.45	9.94E-01	0.00	1	Oscillibacter	Unclassified

Seq_0000905	1.40E-01	-0.25	0.46	9.83E-01	0.00	1	Catenibacterium	Catenibacterium_mitsuokai
Seq_0000936	2.04E-01	-0.21	0.47	9.67E-01	-0.01	1	Ruminococcus2	Unclassified
Seq_0005455	4.39E-01	-0.13	0.66	9.63E-01	0.01	1	Lachnospiraceae_unclassified	Unclassified
Seq_0000027	4.96E-01	0.12	0.70	9.86E-01	0.00	1	Streptococcus	Unclassified
Seq_0000149	5.19E-01	0.11	0.70	9.63E-01	-0.01	1	Acidaminococcus	Unclassified
Seq_0000626	5.31E-01	0.11	0.72	9.94E-01	0.00	1	Bacteroides	Bacteroides_plebeius
Seq_0000366	5.38E-01	0.10	0.73	9.72E-01	0.01	1	Lactobacillus	Unclassified
Seq_0000705	6.62E-01	0.07	0.81	9.63E-01	-0.01	1	Lactobacillus	Unclassified
Seq_0003709	7.39E-01	0.06	0.87	9.90E-01	0.00	1	Lachnospiraceae_unclassified	Unclassified
Seq_0000110	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0000116	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0000250	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0000258	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Subdoligranulum	Unclassified
Seq_0000306	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0000345	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Peptoclostridium_difficile
Seq_0000357	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Proteus	Unclassified
Seq_0000369	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified

Seq_0000426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_neonatale
Seq_0000478	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0000481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0000562	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0000574	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiaceae_1_unclassified	Unclassified
Seq_0000575	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulgaris
Seq_0000590	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0000591	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Clostridium_hathewayi
Seq_0000617	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0000630	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0000642	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pasteurellaceae_unclassified	Unclassified
Seq_0000685	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0000730	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Moraxella	Moraxella_lincolnii
Seq_0000746	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0000747	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Escherichia/Shigella	Unclassified
Seq_0000763	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_disiens

Seq_0000764	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Sutterella_stercoricanis
Seq_0000769	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0000770	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Unclassified
Seq_0000816	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Eubacterium_coprostanoligenes
Seq_0000826	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0000836	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Unclassified
Seq_0000845	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0000860	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0000862	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0000875	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0000883	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0000904	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Escherichia/Shigella	Escherichia/Shigella_coli
Seq_0000922	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Cronobacter	Unclassified
Seq_0000923	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacter	Unclassified
Seq_0000932	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Sutterella_stercoricanis
Seq_0000939	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_timoneensis

Seq_0000952	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0000969	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0000978	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_faecis
Seq_0000980	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pediococcus	Unclassified
Seq_0000999	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_luti
Seq_0001001	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0001004	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0001005	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0001006	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001007	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_disporicum
Seq_0001049	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0001063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0001080	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcus2	Ruminococcus_torques
Seq_0001089	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_oralis
Seq_0001107	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Collinsella_aerofaciens
Seq_0001114	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified

Seq_0001117	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Leuconostoc	Unclassified
Seq_0001119	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0001122	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0001132	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Unclassified
Seq_0001136	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pasteurellaceae_unclassified	Unclassified
Seq_0001139	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0001162	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Weissella	Unclassified
Seq_0001176	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acidaminococcaceae_unclassified	Unclassified
Seq_0001181	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Unclassified
Seq_0001186	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pasteurellaceae_unclassified	Unclassified
Seq_0001246	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiaceae_1_unclassified	Unclassified
Seq_0001250	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0001267	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonella	Unclassified
Seq_0001271	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Burkholderia	Unclassified
Seq_0001307	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sarcina	Sarcina_ventriculi
Seq_0001314	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified

Seq_0001325	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0001327	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Collinsella_aerofaciens
Seq_0001331	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0001340	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001342	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Streptococcus_massiliensis
Seq_0001350	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_hallii
Seq_0001354	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_buccalis
Seq_0001381	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Fusobacterium_nucleatum
Seq_0001383	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0001397	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_faecis
Seq_0001402	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Sutterella_wadsworthensis
Seq_0001404	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_hallii
Seq_0001416	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0001421	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_timonensis
Seq_0001437	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerostipes	Anaerostipes_butylicus
Seq_0001438	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parvimonas	Parvimonas_micra

Seq_0001442	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0001449	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0001461	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Megamonas	Unclassified
Seq_0001470	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Clostridium_hylemonae
Seq_0001474	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0001479	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0001485	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricoccus	Butyricoccus_pullicaeorum
Seq_0001491	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0001496	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0001499	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiaceae_1_unclassified	Unclassified
Seq_0001516	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0001531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0001556	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Fusobacterium_nucleatum
Seq_0001565	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0001568	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0001581	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii

Seq_0001586	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0001588	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coprococcus	Coprococcus_eutactus
Seq_0001603	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_eligens
Seq_0001610	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Asaccharobacter	Unclassified
Seq_0001615	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_faecis
Seq_0001622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pasteurellaceae_unclassified	Unclassified
Seq_0001623	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0001626	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Clostridium_symbiosum
Seq_0001633	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001641	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001645	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0001656	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0001658	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0001665	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulgatus
Seq_0001677	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0001678	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii

Seq_0001689	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0001700	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_shahii
Seq_0001709	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0001733	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0001739	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001759	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0001766	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001773	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Fusobacterium_equinum
Seq_0001779	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0001790	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001797	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0001798	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0001840	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sarcina	Sarcina_ventriculi
Seq_0001845	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Unclassified
Seq_0001851	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0001852	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified

Seq_0001863	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0001866	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Unclassified
Seq_0001867	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Eubacterium_rectale
Seq_0001875	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Methylobacterium	Unclassified
Seq_0001879	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0001892	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0001915	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Fusobacterium_equinum
Seq_0001917	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Eubacterium_rectale
Seq_0001921	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0001928	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001934	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0001962	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_luti
Seq_0001965	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0001981	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Lactobacillus_reuteri
Seq_0001985	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0001988	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerostipes	Anaerostipes_hadrus

Seq_0001993	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0001994	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0002011	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Megasphaera	Unclassified
Seq_0002020	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Phenylobacterium	Unclassified
Seq_0002022	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Unclassified
Seq_0002045	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0002051	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonella	Unclassified
Seq_0002058	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0002059	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcus	Peptostreptococcus_anerobius
Seq_0002062	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0002063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0002068	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Desulfovibrio	Desulfovibrio_piger
Seq_0002070	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Escherichia/Shigella	Unclassified
Seq_0002073	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0002076	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0002078	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcaceae_unclassified	Unclassified

Seq_0002081	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Ruminococcus_ob eum
Seq_0002091	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0002093	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Haemophilus	Unclassified
Seq_0002094	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Betaproteobacteria_ unclassified	Unclassified
Seq_0002096	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Escherichia/Shigell a	Unclassified
Seq_0002100	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0002101	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_sterco ris
Seq_0002107	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0002122	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parabacteroides	Parabacteroides_di stasonis
Seq_0002124	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Eubacterium_ramu lus
Seq_0002125	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Ruminococcus_gn avus
Seq_0002136	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0002140	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassifi ed	Unclassified
Seq_0002156	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_unifor mis
Seq_0002160	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0002161	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Unclassified

Seq_0002169	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonella	Unclassified
Seq_0002190	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0002195	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Flavobacteriaceae_unclassified	Unclassified
Seq_0002196	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillales_unclassified	Unclassified
Seq_0002202	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0002217	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0002231	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Clostridium_bartlettii
Seq_0002238	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_neonatale
Seq_0002244	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Eubacterium_rectale
Seq_0002256	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0002270	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0002277	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Barnesiella_intestinalis
Seq_0002278	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0002287	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0002295	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acidaminococcaceae_unclassified	Phascolarctobacterium_succinatutens
Seq_0002296	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Fusobacterium_nucleatum

Seq_0002298	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Lactobacillus_ruminis
Seq_0002300	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0002302	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002304	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Peptoclostridium_difficile
Seq_0002316	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0002323	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_faecis
Seq_0002326	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0002329	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Unclassified
Seq_0002341	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0002349	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Bifidobacterium_bifidum
Seq_0002361	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Holdemania	Holdemania_filiformis
Seq_0002374	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0002399	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0002412	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Capnocytophaga	Unclassified
Seq_0002427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0002436	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pseudomonas	Unclassified

Seq_0002442	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Clostridium_hathe wayi
Seq_0002451	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_ unclassified	Unclassified
Seq_0002453	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0002469	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Comamonadaceae_ unclassified	Unclassified
Seq_0002477	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_ unclassified	Unclassified
Seq_0002481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_uncl assified	Unclassified
Seq_0002484	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_ unclassified	Unclassified
Seq_0002485	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0002496	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Lactobacillus_reut eri
Seq_0002502	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Eubacterium_halli
Seq_0002503	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_uncl assified	Unclassified
Seq_0002511	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parasutterella	Parasutterella_excr ementihominis
Seq_0002513	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0002521	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0002528	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0002534	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_ stricto	Unclassified

Seq_0002543	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0002564	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Providencia	Unclassified
Seq_0002574	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcaceae_unclassified	Unclassified
Seq_0002577	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0002606	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0002615	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Eubacterium	Unclassified
Seq_0002616	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parvimonas	Parvimonas_micra
Seq_0002617	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Oscillibacter	Unclassified
Seq_0002618	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Eubacterium_ramu
Seq_0002625	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Intestinimonas_but
Seq_0002638	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_bergens
Seq_0002639	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Clostridium_hiran
Seq_0002640	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0002641	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acidobacterium_unclassified	Acidobacterium_c
Seq_0002654	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coprobacillus	Coprobacillus_cat
Seq_0002655	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Clostridium_alden

Seq_0002657	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0002666	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerostipes	Anaerostipes_hadrus
Seq_0002667	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Unclassified
Seq_0002668	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Barnesiella_intestinihominis
Seq_0002679	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coprococcus	Coprococcus_comes
Seq_0002708	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Streptococcus_pleomorphus
Seq_0002715	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0002731	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0002734	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Eubacterium_biforme
Seq_0002752	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_bivia
Seq_0002753	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptoniphilus	Peptoniphilus_coxii
Seq_0002756	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_disporicum
Seq_0002757	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonellaceae_unclassified	Unclassified
Seq_0002776	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0002785	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0002787	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillales_unclassified	Unclassified

Seq_0002798	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0002800	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Unclassified
Seq_0002802	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_disporicum
Seq_0002813	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_formicigerans
Seq_0002814	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0002815	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Wautersiella	Wautersiella_falsenii
Seq_0002816	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Lactobacillus_ruminis
Seq_0002830	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0002831	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_formicigerans
Seq_0002847	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0002859	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterococcus	Unclassified
Seq_0002860	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Leuconostoc	Unclassified
Seq_0002875	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0002877	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptoniphilus	Unclassified
Seq_0002878	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_viriosa
Seq_0002895	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Unclassified

Seq_0002912	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVb	Clostridium_lactat ifermentans
Seq_0002915	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_multisa ccharivorax
Seq_0002926	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0002927	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_ stricto	Unclassified
Seq_0002935	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0002940	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Unclassified
Seq_0002943	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alloprevotella	Alloprevotella_rav a
Seq_0002944	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sphingomonas	Unclassified
Seq_0002945	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0002947	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiaceae_1_u nclassified	Unclassified
Seq_0002955	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0002956	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Eikenella	Eikenella_corrode ns
Seq_0002957	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Clostridium_hyle monae
Seq_0002958	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Eubacterium_ventr iosum
Seq_0002961	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Weissella	Weissella_minor
Seq_0002970	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricicoccus	Butyricicoccus_pu llicaecorum

Seq_0002972	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0002973	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dialister	Dialister_propionificaciens
Seq_0002987	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Eubacterium_rectale
Seq_0003001	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_indistinctus
Seq_0003016	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVb	Clostridium_lactatifermentans
Seq_0003019	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Barnesiella_intestinihominis
Seq_0003022	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcus2	Unclassified
Seq_0003038	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Porphyromonadaceae_unclassified	Unclassified
Seq_0003039	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003040	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0003042	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0003063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0003065	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_stercoris
Seq_0003066	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptophyta_unclassified	Unclassified
Seq_0003098	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Megasphaera	Megasphaera_microaerophilum
Seq_0003102	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcus2	Unclassified

Seq_0003141	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003142	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003143	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Unclassified
Seq_0003144	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0003145	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0003180	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003190	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003195	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Proteobacteria_unclassified	Unclassified
Seq_0003196	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Unclassified
Seq_0003228	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0003230	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcus2	Ruminococcus_torques
Seq_0003231	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0003257	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptoniphilus	Peptoniphilus_duerdenii
Seq_0003259	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Mogibacterium	Unclassified
Seq_0003268	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Stenotrophomonas	Unclassified
Seq_0003270	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified

Seq_0003271	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Unclassified
Seq_0003272	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Vibrio	Unclassified
Seq_0003273	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Moraxella	Unclassified
Seq_0003274	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0003291	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dialister	Unclassified
Seq_0003292	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0003293	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0003295	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Leuconostoc	Unclassified
Seq_0003296	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0003297	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003335	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Clostridium_innocuum
Seq_0003354	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Unclassified
Seq_0003357	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0003374	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bilophila	Bilophila_wadsworthia
Seq_0003376	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003378	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_clarus

Seq_0003381	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0003402	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_hallii
Seq_0003403	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactonifactor	Lactonifactor_longoviformis
Seq_0003404	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_eligens
Seq_0003405	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dialister	Dialister_invisus
Seq_0003406	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Proteobacteria_unclassified	Unclassified
Seq_0003409	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003410	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Eubacterium_rectale
Seq_0003421	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillales_unclassified	Unclassified
Seq_0003422	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003424	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Sutterella_stercoricanis
Seq_0003426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulgatus
Seq_0003441	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Coprobacillus_cateniiformis
Seq_0003443	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0003444	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003445	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Lactobacillus_coleohominis

Seq_0003446	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Unclassified
Seq_0003460	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parasutterella	Parasutterella_secunda
Seq_0003461	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0003462	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_IV	Unclassified
Seq_0003464	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Desulfovibrio	Desulfovibrio_fairfieldensis
Seq_0003488	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0003491	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Clostridium_ruminantium
Seq_0003492	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003494	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_hallii
Seq_0003518	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Oribacterium	Oribacterium_sinus
Seq_0003519	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003520	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0003521	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Deltaproteobacteria_unclassified	Unclassified
Seq_0003523	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0003529	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0003551	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified

Seq_0003552	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0003553	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0003557	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Catenibacterium	Catenibacterium_mitsuokai
Seq_0003558	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XVIII	Unclassified
Seq_0003561	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Clostridium_nexile
Seq_0003562	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0003580	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003587	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Leuconostoc	Unclassified
Seq_0003588	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Eubacterium_tarantellae
Seq_0003589	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0003594	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0003623	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Odoribacter	Odoribacter_splanchnicus
Seq_0003624	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003625	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Proteobacteria_unclassified	Unclassified
Seq_0003626	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0003630	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified

Seq_0003649	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003651	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Eubacterium_tenu
Seq_0003652	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Unclassified
Seq_0003653	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0003673	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0003676	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Unclassified
Seq_0003678	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003680	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0003682	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Atopobium	Atopobium_parvulum
Seq_0003705	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Rubritalea	Unclassified
Seq_0003706	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XVIII	Unclassified
Seq_0003707	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Clostridium_hylemonae
Seq_0003713	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Halomonas	Unclassified
Seq_0003714	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0003717	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerostipes	Anaerostipes_hadrus
Seq_0003747	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerotruncus	Anaerotruncus_colihominis

Seq_0003748	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Eubacterium_dolicum
Seq_0003749	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Clostridium_innocuum
Seq_0003750	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003754	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0003755	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coprococcus	Unclassified
Seq_0003756	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Burkholderiales_unclassified	Unclassified
Seq_0003758	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_plebeius
Seq_0003759	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0003761	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0003762	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0003766	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003789	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_disporicum
Seq_0003792	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parabacteroides	Parabacteroides_johnsonii
Seq_0003794	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0003795	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonellaceae_unclassified	Unclassified
Seq_0003813	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified

Seq_0003815	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Christensenella_m inuta
Seq_0003816	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0003820	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Unclassified
Seq_0003826	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Faecalibacterium_ prausnitzii
Seq_0003854	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Gordonibacter	Unclassified
Seq_0003855	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003856	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Clostridium_glyco licum
Seq_0003857	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonella	Unclassified
Seq_0003858	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0003890	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0003893	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0003896	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0003901	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_ prausnitzii
Seq_0003902	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Unclassified
Seq_0003918	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bradyrhizobium	Unclassified
Seq_0003919	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Collinsella_aerofa ciens

Seq_0003921	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcaeae_unclassified	Clostridium_ruminantium
Seq_0003923	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Desulfovibrionales_unclassified	Unclassified
Seq_0003924	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Candidatus_Saccharibacteria_unclassified	Unclassified
Seq_0003926	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0003929	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_IV	Eubacterium_siraeum
Seq_0003930	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0003960	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerostipes	Unclassified
Seq_0003961	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_indistinctus
Seq_0003963	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_viridosa
Seq_0003967	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiaceae_1_unclassified	Unclassified
Seq_0003968	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Neisseria	Unclassified
Seq_0003969	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Akkermansia	Akkermansia_muciniphila
Seq_0004003	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Stenotrophomonas	Unclassified
Seq_0004004	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dialister	Unclassified
Seq_0004005	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Eubacterium_desmolans
Seq_0004006	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Intestinimonas_butyrificiproducens

Seq_0004008	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerococcus	Anaerococcus_murdochii
Seq_0004010	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0004011	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004013	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004014	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridia_unclassified	Unclassified
Seq_0004015	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0004047	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Arthrobacter	Unclassified
Seq_0004048	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Methylobacterium	Methylobacterium_jeotgali
Seq_0004049	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Clostridium_leptum
Seq_0004051	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004056	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Cloacibacterium	Unclassified
Seq_0004057	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Neisseriaceae_unclassified	Uruburuella_suis
Seq_0004058	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Porphyromonas	Porphyromonas_accharolytica
Seq_0004059	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Akkermansia	Akkermansia_muciniphila
Seq_0004061	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnoanaerobaculum	Lachnoanaerobaculum_umeaense

Seq_0004069	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Unclassified
Seq_0004113	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coprobacillus	Coprobacillus_cat eniformis
Seq_0004114	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassifi ed	Unclassified
Seq_0004118	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004119	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0004121	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004122	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Micrococcaceae_un classified	Unclassified
Seq_0004123	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sphingomonas	Unclassified
Seq_0004124	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_vir osa
Seq_0004125	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004129	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassi fied	Unclassified
Seq_0004131	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVb	Clostridium_lactat ifermentans
Seq_0004135	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004136	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillales_unc lassified	Unclassified
Seq_0004176	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XVIII	Clostridium_spirof orme
Seq_0004177	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Varibaculum	Varibaculum_cam briense

Seq_0004178	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Succinivibrio	Succinivibrio_dextrinosolvens
Seq_0004179	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004187	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004189	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Christensenella_minuta
Seq_0004190	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Flavonifractor_plautii
Seq_0004191	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0004193	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0004194	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Mucispirillum	Mucispirillum_schaedleri
Seq_0004195	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0004196	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004197	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_stercoris
Seq_0004199	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004201	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004202	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0004203	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0004239	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Eubacterium_doliculum

Seq_0004240	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004241	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004243	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Zoogloea	Unclassified
Seq_0004244	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0004249	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Peptoclostridium_difficile
Seq_0004253	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0004254	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0004256	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004257	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004261	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0004262	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonellaceae_unclassified	Unclassified
Seq_0004264	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0004271	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacillus	Unclassified
Seq_0004315	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0004316	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0004318	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pediococcus	Unclassified

Seq_0004319	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0004322	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004324	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulga tus
Seq_0004325	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_IV	Clostridium_leptu m
Seq_0004326	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004328	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerococcus	Anaerococcus_hyd rogenalis
Seq_0004332	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0004333	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Rhodococcus	Unclassified
Seq_0004334	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blastococcus	Unclassified
Seq_0004335	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0004336	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0004338	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Hallella	Unclassified
Seq_0004346	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_nordii
Seq_0004383	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004384	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bosea	Unclassified
Seq_0004385	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Leuconostoc	Unclassified

Seq_0004387	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004388	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Collinsella_aerofaciens
Seq_0004392	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004393	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0004394	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004395	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0004396	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Blautia_faecis
Seq_0004398	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004399	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Gammaproteobacteria_unclassified	Unclassified
Seq_0004402	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Peptococcus_niger
Seq_0004403	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Catenibacterium	Catenibacterium_mitsuokai
Seq_0004405	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Collinsella	Collinsella_aerofaciens
Seq_0004407	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0004408	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XI	Unclassified
Seq_0004409	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alloprevotella	Unclassified
Seq_0004410	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified

Seq_0004413	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Actinomyces_georgiae
Seq_0004417	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004418	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_virgosa
Seq_0004485	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Nocardioideae	Unclassified
Seq_0004486	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Ruminococcus_gnavus
Seq_0004487	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0004488	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004489	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0004490	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Anaerofustis	Anaerofustis_stercorihominis
Seq_0004492	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004493	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Campylobacter	Unclassified
Seq_0004495	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004496	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricicoccus	Butyricicoccus_pullicaeorum
Seq_0004497	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004498	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004499	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Cloacibacillus	Cloacibacillus_porcorum

Seq_0004500	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004502	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Paraprevotella	Paraprevotella clara
Seq_0004503	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomycetales_unclassified	Unclassified
Seq_0004504	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Burkholderiales_unclassified	Unclassified
Seq_0004505	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0004506	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0004508	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004509	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcus2	Ruminococcus torques
Seq_0004513	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004514	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Unclassified
Seq_0004516	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004518	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella buccalis
Seq_0004519	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0004522	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Subdoligranulum	Unclassified
Seq_0004583	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004584	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Nocardioides	Unclassified

Seq_0004585	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Paraprevotella	Paraprevotella_xylaniphila
Seq_0004586	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004587	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Clostridium_oroticum
Seq_0004590	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Subdoligranulum	Subdoligranulum_variabile
Seq_0004592	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_viriosa
Seq_0004593	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Clostridium_ruminantium
Seq_0004596	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Streptococcus_agalactiae
Seq_0004597	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Eubacterium	Unclassified
Seq_0004598	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004599	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiaceae_1_unclassified	Unclassified
Seq_0004601	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004602	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004603	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004604	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_viriosa
Seq_0004605	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004606	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified

Seq_0004607	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillales_unclassified	Unclassified
Seq_0004610	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004611	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0004612	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Lactonifactor_longoviformis
Seq_0004613	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004617	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0004699	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Oscillibacter	Unclassified
Seq_0004700	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004702	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Barnesiella_intestinihominis
Seq_0004703	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_sensu_stricto	Clostridium_neonatale
Seq_0004705	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0004706	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Sutterella_stercoricanis
Seq_0004707	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_salyersiae
Seq_0004709	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Lactobacillus_sanfranciscensis
Seq_0004711	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Flavonifractor_plautii

Seq_0004712	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_fluxus
Seq_0004713	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004715	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pediococcus	Unclassified
Seq_0004716	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parasutterella	Parasutterella_secunda
Seq_0004717	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0004718	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_luti
Seq_0004719	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004721	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Methylobacterium	Unclassified
Seq_0004724	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004725	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Chloroplast_unclassified	Unclassified
Seq_0004726	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Paraprevotella	Paraprevotella_clara
Seq_0004728	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0004729	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptostreptococcaceae_unclassified	Clostridium_ruminantium
Seq_0004730	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0004731	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Anaerostipes_hadrus
Seq_0004732	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Rhizobium	Unclassified

Seq_0004734	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0004737	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Akkermansia	Akkermansia_muciniphila
Seq_0004738	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004739	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_bivia
Seq_0004742	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_ventriosum
Seq_0004746	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified
Seq_0004748	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Mitsuokella	Mitsuokella_multacida
Seq_0004749	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Clostridium_innocuum
Seq_0004750	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004751	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004752	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0004818	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0004819	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0004820	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Atopobium	Atopobium_rimae
Seq_0004821	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0004823	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified

Seq_0004824	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0004825	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alphaproteobacteri a_unclassified	Unclassified
Seq_0004826	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004827	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_indistinc tus
Seq_0004831	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_uncl assified	Coprobacter_fastid iosus
Seq_0004832	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0004835	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Unclassified
Seq_0004836	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassi fied	Unclassified
Seq_0004837	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0004839	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassifi ed	Unclassified
Seq_0004840	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Veillonellaceae_un classified	Unclassified
Seq_0004842	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0004843	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0004844	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bradyrhizobium	Unclassified
Seq_0004847	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_copri
Seq_0004852	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassifi ed	Unclassified

Seq_0004853	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0004854	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0004855	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0004857	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Eubacterium_desmolans
Seq_0004862	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0004866	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Howardella	Howardella_ureilytica
Seq_0004867	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Olsenella	Unclassified
Seq_0004985	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Atopobium	Atopobium_rimae
Seq_0004986	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_viriosa
Seq_0004987	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulgatus
Seq_0004991	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0004993	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0004998	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Oscillibacter	Unclassified
Seq_0005000	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_indistinctus
Seq_0005001	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005002	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified

Seq_0005003	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_pallens
Seq_0005004	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Fusicatenibacter_saccharivorans
Seq_0005005	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005006	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005007	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005008	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005009	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005010	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Gp7_unclassified	Unclassified
Seq_0005012	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005013	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Catenibacterium	Unclassified
Seq_0005014	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Moryella	Moryella_indoligenes
Seq_0005015	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0005017	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Victivallis	Victivallis_vadensis
Seq_0005018	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005019	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0005022	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified

Seq_0005023	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_indistinctus
Seq_0005028	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005029	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0005030	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0005037	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Clostridium_innocuum
Seq_0005038	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005043	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacteriaceae_unclassified	Unclassified
Seq_0005044	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Neisseria	Unclassified
Seq_0005045	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0005047	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridia_unclassified	Unclassified
Seq_0005048	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005120	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005121	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0005122	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_IV	Unclassified
Seq_0005123	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Micrococcaceae_unclassified	Unclassified
Seq_0005124	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulgatus

Seq_0005126	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0005130	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005131	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0005134	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Catenibacterium	Catenibacterium_mitsuokai
Seq_0005135	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005137	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Betaproteobacteria_unclassified	Unclassified
Seq_0005139	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005140	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillaceae_unclassified	Lactobacillus_agilis
Seq_0005141	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XVIII	Clostridium_sporforme
Seq_0005142	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_stercoraria
Seq_0005143	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sphingobacteriaceae_unclassified	Unclassified
Seq_0005146	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005149	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005150	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Propionibacterium	Unclassified
Seq_0005151	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0005152	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified

Seq_0005155	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005156	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005158	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Unclassified
Seq_0005159	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005165	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005166	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005167	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Cloacibacterium	Unclassified
Seq_0005168	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005169	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0005170	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0005171	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Eubacterium	Eubacterium_infirmum
Seq_0005172	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005173	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_III	Unclassified
Seq_0005177	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Unclassified
Seq_0005184	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005189	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillus	Unclassified

Seq_0005190	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005379	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Eubacterium_desmolans
Seq_0005380	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005381	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005383	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005385	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005386	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Barnesiella	Barnesiella_intestinihominis
Seq_0005387	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005388	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005389	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005390	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005391	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactococcus	Lactococcus_lactis
Seq_0005393	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Clostridium_innocuum
Seq_0005397	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005398	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Turicibacter	Turicibacter_sanguinis
Seq_0005399	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Megasphaera	Megasphaera_microaerophilum

Seq_0005407	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Actinomyces_odontolyticus
Seq_0005408	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0005410	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005413	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sphingopyxis	Unclassified
Seq_0005414	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0005416	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005417	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Brevibacterium	Brevibacterium_yomogidense
Seq_0005418	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sphingomonadaceae_unclassified	Unclassified
Seq_0005419	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005420	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005421	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Porphyromonas	Porphyromonas_somerae
Seq_0005422	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Anaerostipes_hadrus
Seq_0005423	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005424	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005425	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acidaminococcus	Unclassified
Seq_0005429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified

Seq_0005439	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005440	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0005441	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0005444	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0005445	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dialister	Dialister_invisus
Seq_0005450	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Corynebacterium_durum
Seq_0005453	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005458	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Megasphaera	Unclassified
Seq_0005459	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005460	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0005461	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005463	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pediococcus	Unclassified
Seq_0005599	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_IV	Clostridium_leptum
Seq_0005600	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptoniphilus	Peptoniphilus_assa- ccharolyticus
Seq_0005601	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005602	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified

Seq_0005603	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0005604	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomycetales_unclassified	Unclassified
Seq_0005605	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005607	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005608	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Nocardiodaceae_unclassified	Unclassified
Seq_0005610	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005611	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005613	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_timoneensis
Seq_0005614	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_buccalis
Seq_0005619	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005620	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pasteurellaceae_unclassified	Unclassified
Seq_0005621	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Peptoniphilus	Unclassified
Seq_0005622	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_pyruvivorans
Seq_0005623	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sarcina	Sarcina_ventriculi
Seq_0005624	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Thermomonas	Thermomonas_hydrothermalis
Seq_0005628	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parabacteroides	Parabacteroides_merdae

Seq_0005630	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Vibrio	Vibrio_cholerae
Seq_0005631	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0005632	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0005633	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Thauera	Unclassified
Seq_0005635	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Unclassified
Seq_0005636	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0005638	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dolosigranulum	Dolosigranulum_p igrum
Seq_0005641	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclasi fied	Unclassified
Seq_0005642	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Phyllobacteriaceae_ unclassified	Mesorhizobium_lo ti
Seq_0005643	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_uncla ssified	Unclassified
Seq_0005645	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotella	Prevotella_stercor ea
Seq_0005647	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_ unclassified	Faecalibacterium_ prausnitzii
Seq_0005648	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_ unclassified	Unclassified
Seq_0005649	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_ unclassified	Flavonifractor_pla utii
Seq_0005653	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_ unclassified	Gordonibacter_pa melaeae
Seq_0005655	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacteriaceae_ unclassified	Unclassified

Seq_0005656	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0005657	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Oscillospira_guilliermondii
Seq_0005658	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Unclassified
Seq_0005659	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterella	Sutterella_stercoricanis
Seq_0005661	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0005662	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005663	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0005664	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactococcus	Unclassified
Seq_0005674	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0005675	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0005676	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005677	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Streptococcus_pleomorphic
Seq_0005683	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0005684	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactobacillales_unclassified	Unclassified
Seq_0005686	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0005688	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified

Seq_0005689	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0006036	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0006037	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006039	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bilophila	Bilophila_wadsworthia
Seq_0006040	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alloprevotella	Unclassified
Seq_0006041	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parvimonas	Parvimonas_micra
Seq_0006042	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Unclassified
Seq_0006043	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006044	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0006045	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006046	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0006049	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Atopobium	Atopobium_parvulum
Seq_0006050	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Porphyromonas	Porphyromonas_bennonis
Seq_0006058	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Novosphingobium	Unclassified
Seq_0006060	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006061	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Akkermansia	Akkermansia_muciniphila

Seq_0006063	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006064	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_vulgatus
Seq_0006065	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Odoribacter	Odoribacter_splanchnicus
Seq_0006072	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sutterellaceae_unclassified	Unclassified
Seq_0006073	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006074	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006075	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006076	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006077	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006079	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0006080	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006081	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0006082	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptomyces	Unclassified
Seq_0006083	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Paraprevotella	Paraprevotella_xylaniphila
Seq_0006084	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0006086	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified

Seq_0006087	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Blautia_faecis
Seq_0006088	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006092	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006098	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0006099	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Faecalibacterium	Faecalibacterium_prausnitzii
Seq_0006100	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0006101	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroides	Bacteroides_eggerthii
Seq_0006102	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Unclassified
Seq_0006103	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Candidatus_Saccharibacteria_unclassified	Unclassified
Seq_0006104	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Brevundimonas	Unclassified
Seq_0006105	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pasteurellaceae_unclassified	Unclassified
Seq_0006106	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Xanthomonadaceae_unclassified	Unclassified
Seq_0006109	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Prevotellaceae_unclassified	Unclassified
Seq_0006110	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Corynebacterium	Corynebacterium_durum
Seq_0006112	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006113	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Unclassified

Seq_0006114	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Unclassified
Seq_0006120	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006131	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006133	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Mitsuokella	Mitsuokella_jalaludinii
Seq_0006142	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Micrococcaceae_unclassified	Unclassified
Seq_0006143	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0006153	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Fusobacterium	Fusobacterium_periodonticum
Seq_0006154	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006156	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Pediococcus	Unclassified
Seq_0006389	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006390	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Candidatus_Saccharibacteria_unclassified	Unclassified
Seq_0006391	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006394	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006395	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptophyta_unclassified	Unclassified
Seq_0006396	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006397	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Fusicatenibacter_saccharivorans

Seq_0006398	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Unclassified
Seq_0006399	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0006400	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Dorea	Dorea_longicatena
Seq_0006401	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006402	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Solobacterium	Solobacterium_morei
Seq_0006407	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Actinomyces_odontolyticus
Seq_0006408	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0006409	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006411	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Porphyromonas	Porphyromonas_bennonis
Seq_0006413	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Actinomyces	Unclassified
Seq_0006414	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006415	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Eikenella	Eikenella_corrodens
Seq_0006416	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006418	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acidobacterium_unclassified	Acidobacterium_capsulatum
Seq_0006419	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006425	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified

Seq_0006426	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Allisonella	Allisonella_histaminiformans
Seq_0006427	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006429	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Alistipes_indistinctus
Seq_0006431	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006432	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Neisseriaceae_unclassified	Uruburuella_suis
Seq_0006433	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006434	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006435	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Paraprevotella	Paraprevotella clara
Seq_0006436	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006437	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVb	Clostridium_lactatifermentans
Seq_0006439	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006440	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006441	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006442	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006443	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0006444	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified

Seq_0006445	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006451	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006452	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006454	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0006457	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0006462	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006466	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006467	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVa	Unclassified
Seq_0006468	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parvimonas	Parvimonas_micra
Seq_0006469	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Atopobium	Atopobium_rimae
Seq_0006470	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006471	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0006472	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Hymenobacter	Unclassified
Seq_0006473	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006474	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006475	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified

Seq_0006476	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Cyanidium_caldarium
Seq_0006477	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Burkholderia	Unclassified
Seq_0006478	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Eggerthia	Eggerthia_catenaformis
Seq_0006479	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acinetobacter	Unclassified
Seq_0006481	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006482	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006483	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Mogibacterium	Mogibacterium_timidum
Seq_0006484	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006485	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006486	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006487	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006490	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0006509	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0006510	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Streptococcus	Unclassified
Seq_0006511	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006513	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified

Seq_0006514	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0006525	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Unclassified
Seq_0006526	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Enterobacteriaceae_unclassified	Unclassified
Seq_0006527	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006529	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Acidaminococcaceae_unclassified	Unclassified
Seq_0006530	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0006531	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Burkholderiales_unclassified	Unclassified
Seq_0006534	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Stomatobaculum_longum
Seq_0006536	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0006537	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Eubacterium_doliculum
Seq_0006538	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lactococcus	Lactococcus_lactis
Seq_0007198	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Butyricimonas	Butyricimonas_viriosa
Seq_0007201	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007205	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Capnocytophaga	Capnocytophaga_sputigena
Seq_0007206	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007207	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified

Seq_0007211	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Phascolarctobacterium	Phascolarctobacterium_faecium
Seq_0007212	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007213	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0007214	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridium_XIVb	Unclassified
Seq_0007215	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Erysipelotrichaceae_unclassified	Unclassified
Seq_0007219	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bradyrhizobium	Unclassified
Seq_0007220	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007221	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alloprevotella	Unclassified
Seq_0007223	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007224	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0007226	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Phocaeicola	Phocaeicola_abscessus
Seq_0007227	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Polyangiaceae_unclassified	Unclassified
Seq_0007241	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Paraprevotella	Unclassified
Seq_0007242	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007243	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0007244	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified

Seq_0007245	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Eubacterium_ventriosum
Seq_0007247	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0007248	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007250	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Parabacteroides	Parabacteroides_distasonis
Seq_0007252	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007254	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007259	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Sphingomonas	Unclassified
Seq_0007262	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified
Seq_0007264	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Porphyromonadaceae_unclassified	Coprobacter_fastidiosus
Seq_0007266	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007267	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0007268	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007272	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidales_unclassified	Unclassified
Seq_0007273	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacterium	Bifidobacterium_bifidum
Seq_0007275	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Alistipes	Unclassified
Seq_0007276	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Roseburia	Unclassified

Seq_0007277	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007279	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0007280	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Akkermansia	Akkermansia_muciniphila
Seq_0007281	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0007283	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Firmicutes_unclassified	Unclassified
Seq_0007284	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Faecalibacterium_prausnitzii
Seq_0007285	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Cyanobacteria_unclassified	Unclassified
Seq_0007287	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007288	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Solobacterium	Unclassified
Seq_0007291	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Campylobacter	Unclassified
Seq_0007296	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007306	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007324	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Ruminococcaceae_unclassified	Unclassified
Seq_0007325	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007327	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007339	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified

Seq_0007341	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Blautia	Unclassified
Seq_0007342	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Cardiobacterium	Cardiobacterium_valvarum
Seq_0007344	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Campylobacter	Campylobacter_gracilis
Seq_0007345	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Coriobacteriaceae_unclassified	Unclassified
Seq_0007347	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007348	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Candidatus_Saccharibacteria_unclassified	Unclassified
Seq_0007349	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteroidetes_unclassified	Unclassified
Seq_0007352	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007363	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007364	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007365	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007366	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bacteria_unclassified	Unclassified
Seq_0007367	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified
Seq_0007368	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Rhodobacteraceae_unclassified	Unclassified
Seq_0007370	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_unclassified	Unclassified
Seq_0007372	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Clostridiales_unclassified	Unclassified

Seq_0007373	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Mitsuokella	Mitsuokella_multa cida
Seq_0007376	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacteriaceae_ unclassified	Unclassified
Seq_0007377	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Bifidobacteriaceae_ unclassified	Unclassified
Seq_0007378	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	Lachnospiraceae_u nclassified	Eubacterium_ramu lus

Table 9. DeSeq2 results of VC counts comparing UC Flare to UC Remission

VC	Base Mean	log2Fold Change	lfcSE	stat	p-value	padj	UC Flare Mean
vc1	11409.68	1.76	1.59	1.10	2.70E-01	4.24E-01	2.23E-02
vc10	299130.97	-1.86	1.77	-1.05	2.92E-01	4.48E-01	5.77E-02
vc100	9.72	-0.93	2.92	-0.32	7.50E-01	8.67E-01	8.11E-05
vc103	985.71	0.29	2.92	0.10	9.21E-01	9.44E-01	3.82E-02
vc104	4.96	-6.02	2.95	-2.04	4.13E-02	9.35E-02	0
vc106	649.38	-6.75	2.92	-2.31	2.07E-02	4.92E-02	5.59E-05
vc108	10.80	22.34	2.96	7.55	4.50E-14	1.33E-13	1.12E-04
vc109	15.99	22.89	2.96	7.73	1.07E-14	4.14E-14	1.17E-02
vc11	41.60	0.68	2.92	0.23	8.16E-01	8.79E-01	4.04E-04
vc111	77.05	25.08	2.96	8.47	2.39E-17	2.89E-16	1.39E-03
vc112	9.99	-0.64	2.92	-0.22	8.28E-01	8.79E-01	7.13E-04
vc114	24.13	23.46	2.96	7.93	2.28E-15	1.15E-14	4.74E-04
vc115	16.84	22.88	2.96	7.73	1.09E-14	4.14E-14	2.34E-04
vc119	7.94	-23.61	2.95	-8.00	1.21E-15	7.74E-15	2.66E-06
vc12	6785.99	-1.47	2.63	-0.56	5.76E-01	7.18E-01	3.55E-03
vc122	5.76	5.72	2.96	1.93	5.33E-02	1.12E-01	8.47E-05
vc126	344.60	3.22	2.92	1.10	2.70E-01	4.24E-01	3.73E-02
vc128	41.10	24.21	2.96	8.18	2.90E-16	2.35E-15	1.21E-03
vc13	1074.32	-4.38	2.90	-1.51	1.31E-01	2.23E-01	1.54E-04
vc130	242.98	-0.17	2.60	-0.06	9.49E-01	9.57E-01	6.29E-04
vc138	5.74	5.72	2.96	1.93	5.36E-02	1.12E-01	3.20E-04

vc14	35.46	3.34	2.92	1.14	2.53E-01	4.07E-01	1.55E-04
vc143	211.65	26.50	2.96	8.95	3.52E-19	7.09E-18	7.92E-03
vc145	113.92	-27.29	2.95	-9.25	2.15E-20	6.51E-19	4.20E-06
vc15	66334.13	-2.44	1.74	-1.40	1.61E-01	2.67E-01	5.74E-02
vc159	59.06	24.17	2.96	8.16	3.23E-16	2.35E-15	5.88E-04
vc16	200.92	-28.07	2.95	-9.52	1.76E-21	1.07E-19	1.61E-02
vc162	25.06	23.52	2.96	7.94	1.96E-15	1.03E-14	7.42E-03
vc163	15.59	-24.58	2.95	-8.33	7.90E-17	7.96E-16	0
vc168	8.17	6.23	2.96	2.10	3.55E-02	8.27E-02	1.69E-03
vc17	1870.83	1.34	2.07	0.65	5.17E-01	6.80E-01	2.46E-03
vc18	3303.13	1.57	2.50	0.63	5.31E-01	6.82E-01	4.19E-02
vc19	755.08	-8.20	2.38	-3.44	5.83E-04	1.44E-03	2.81E-05
vc193	8.09	-23.52	2.95	-7.97	1.58E-15	9.09E-15	0
vc2	1077.04	-1.31	1.77	-0.74	4.58E-01	6.23E-01	1.37E-03
vc20	31.85	1.04	2.92	0.36	7.22E-01	8.56E-01	4.77E-04
vc207	3.18	4.87	2.96	1.64	1.01E-01	1.79E-01	8.72E-05
vc21	27065.92	0.52	2.35	0.22	8.25E-01	8.79E-01	6.64E-02
vc215	39.77	24.16	2.96	8.16	3.30E-16	2.35E-15	1.12E-02
vc22	166.11	2.13	2.92	0.73	4.65E-01	6.25E-01	1.11E-03
vc220	16.81	22.51	2.96	7.60	2.86E-14	9.12E-14	6.92E-03
vc23	13.03	22.60	2.96	7.63	2.27E-14	7.41E-14	6.62E-03
vc231	3.76	5.11	2.96	1.72	8.48E-02	1.58E-01	4.92E-05
vc24	305.40	-1.52	2.47	-0.62	5.38E-01	6.82E-01	1.75E-04
vc242	11.15	22.39	2.96	7.56	4.00E-14	1.21E-13	2.80E-04
vc25	5223.84	-2.26	2.31	-0.98	3.29E-01	4.97E-01	6.23E-03
vc26	3.18	4.87	2.96	1.64	1.01E-01	1.79E-01	1.19E-04
vc27	285.47	-0.98	2.92	-0.34	7.36E-01	8.65E-01	5.44E-03
vc28	180.21	-1.26	2.92	-0.43	6.66E-01	8.14E-01	6.13E-03
vc29	22795.50	-1.61	1.95	-0.82	4.10E-01	5.89E-01	3.44E-02
vc3	165.76	0.44	2.92	0.15	8.79E-01	9.12E-01	1.71E-02
vc30	16038.58	2.10	2.24	0.94	3.48E-01	5.19E-01	7.64E-02
vc31	432.02	-4.25	2.73	-1.56	1.20E-01	2.07E-01	1.64E-03
vc32	182.05	-27.92	2.95	-9.47	2.91E-21	1.17E-19	1.96E-04

vc33	10.20	21.44	2.96	7.24	4.42E-13	1.14E-12	5.40E-05
vc34	21.09	2.43	2.92	0.83	4.05E-01	5.89E-01	2.15E-04
vc340	9.75	22.20	2.96	7.50	6.57E-14	1.81E-13	5.11E-04
vc35	27.64	23.65	2.96	7.99	1.35E-15	8.18E-15	1.78E-03
vc359	4.44	5.34	2.96	1.80	7.12E-02	1.44E-01	6.61E-05
vc36	31.05	-1.93	2.91	-0.66	5.08E-01	6.75E-01	8.93E-06
vc37	394.61	0.80	2.80	0.28	7.76E-01	8.77E-01	2.42E-03
vc374	22.03	21.76	2.96	7.35	1.99E-13	5.23E-13	1.21E-03
vc38	200.79	25.30	2.96	8.55	1.25E-17	1.90E-16	3.43E-02
vc39	7.54	1.79	2.93	0.61	5.41E-01	6.82E-01	1.40E-04
vc392	11.73	21.00	2.96	7.09	1.31E-12	3.30E-12	6.28E-04
vc4	835.24	0.73	2.30	0.32	7.52E-01	8.67E-01	8.96E-03
vc40	5971.67	3.33	2.26	1.48	1.40E-01	2.36E-01	6.69E-02
vc41	29.47	0.73	2.92	0.25	8.03E-01	8.79E-01	4.48E-04
vc416	4.84	-5.99	2.95	-2.03	4.25E-02	9.35E-02	4.34E-05
vc42	9.90	22.22	2.96	7.50	6.21E-14	1.75E-13	6.13E-03
vc43	17.01	22.97	2.96	7.76	8.50E-15	3.55E-14	7.02E-04
vc45	5.66	5.70	2.96	1.92	5.44E-02	1.12E-01	2.67E-03
vc46	19.02	23.13	2.96	7.81	5.60E-15	2.51E-14	1.08E-03
vc48	16.54	22.29	2.96	7.53	5.12E-14	1.48E-13	1.72E-04
vc5	199.94	1.14	2.87	0.40	6.90E-01	8.27E-01	5.15E-04
vc50	34.35	1.27	2.92	0.44	6.63E-01	8.14E-01	4.87E-04
vc51	13.08	-3.20	2.92	-1.09	2.74E-01	4.25E-01	7.07E-05
vc53	6.57	5.91	2.96	2.00	4.60E-02	9.93E-02	4.38E-04
vc54	1220.79	28.67	2.96	9.69	3.45E-22	4.17E-20	4.25E-03
vc55	326.18	-2.17	2.92	-0.74	4.57E-01	6.23E-01	1.08E-02
vc56	153.38	26.05	2.96	8.80	1.38E-18	2.38E-17	5.72E-03
vc57	15.84	22.87	2.96	7.72	1.12E-14	4.14E-14	2.53E-04
vc59	9.15	22.11	2.96	7.47	8.24E-14	2.22E-13	6.29E-05
vc6	461.12	-1.04	2.53	-0.41	6.80E-01	8.22E-01	9.84E-04
vc60	44.13	-3.75	2.92	-1.28	1.99E-01	3.26E-01	1.68E-05
vc61	258.00	0.84	2.92	0.29	7.74E-01	8.77E-01	5.05E-03
vc62	14.98	22.79	2.96	7.70	1.38E-14	4.91E-14	2.91E-04

vc64	15.74	22.87	2.96	7.72	1.13E-14	4.14E-14	2.38E-04
vc65	1403.92	-6.89	2.92	-2.36	1.83E-02	4.44E-02	2.01E-02
vc66	45.03	2.36	2.92	0.81	4.19E-01	5.89E-01	2.79E-02
vc67	22.25	23.35	2.96	7.89	3.09E-15	1.44E-14	1.63E-03
vc68	7.09	6.02	2.96	2.03	4.20E-02	9.35E-02	1.97E-04
vc69	11.35	22.41	2.96	7.57	3.79E-14	1.17E-13	3.27E-04
vc7	15564.25	-0.41	2.21	-0.19	8.53E-01	8.98E-01	3.24E-02
vc70	7.44	0.12	2.92	0.04	9.66E-01	9.66E-01	5.58E-05
vc71	14.83	22.71	2.96	7.67	1.72E-14	5.93E-14	3.28E-04
vc72	59.64	24.27	2.96	8.20	2.41E-16	2.24E-15	4.21E-03
vc75	19.37	-0.43	2.92	-0.15	8.82E-01	9.12E-01	2.86E-04
vc78	4.46	-0.73	2.93	-0.25	8.03E-01	8.79E-01	2.66E-05
vc8	97.33	0.56	2.49	0.23	8.22E-01	8.79E-01	6.46E-04
vc80	3.13	4.84	2.96	1.63	1.02E-01	1.79E-01	7.79E-05
vc84	3.33	4.93	2.96	1.66	9.60E-02	1.76E-01	1.01E-04
vc87	8.72	-0.24	2.92	-0.08	9.35E-01	9.51E-01	2.31E-03
vc89	2.81	-5.20	2.95	-1.76	7.82E-02	1.49E-01	3.71E-06
vc9	77.08	25.09	2.96	8.47	2.36E-17	2.89E-16	1.30E-02
vc91	13.56	22.66	2.96	7.65	1.97E-14	6.63E-14	3.51E-04
vc93	23.88	23.44	2.96	7.92	2.39E-15	1.15E-14	1.74E-04
vc96	10.98	-2.39	2.92	-0.82	4.14E-01	5.89E-01	1.33E-02
vc99	4.03	5.21	2.96	1.76	7.88E-02	1.49E-01	1.07E-04
NG_14253_1 6_lib223966_ 5684_NODE _382_length_ 1481_cov_41. 2805	19.40	-24.88	2.95	-8.43	3.34E-17	3.67E-16	0
NG_14253_2 0_lib223970_ 5684_NODE _42_length_5	44.90	1.82	2.92	0.62	5.33E-01	6.82E-01	2.60E-04

833_cov_5.31 585							
NG_14253_2 6_lib223959_ 5684_NODE _300_length_ 1971_cov_2.2 6357	91.96	-2.52	2.92	-0.86	3.88E-01	5.72E-01	3.20E-04
NG_14253_4 7_lib223969_ 5684_NODE _36_length_3 850_cov_113. 131	8.90	-23.62	2.95	-8.01	1.19E-15	7.74E-15	0
NG_14253_8 _lib223960_5 684_NODE_ 65_length_11 69_cov_1.928 19	80.03	-26.81	2.95	-9.09	9.84E-20	2.38E-18	2.33E-04
NG_14571_1 04xxx_NOD E_95_length_ 3939_cov_97 2.235	18.37	23.08	2.96	7.80	6.35E-15	2.75E-14	8.11E-05
NG_14571_1 06xxx_NOD E_31_length_ 20289_cov_5. 6621	25.21	23.52	2.96	7.95	1.93E-15	1.03E-14	2.89E-04
NG_14571_1 08xxx_NOD E_53_length_ 4.26	4.26	5.29	2.96	1.78	7.43E-02	1.45E-01	7.54E-05

8858_cov_2.7 1146							
NG_14571_1 19xxx_NOD E_361_length _2175_cov_4 10.478	19.59	2.18	2.92	0.75	4.56E-01	6.23E-01	4.83E-04
NG_14571_5 8_NODE_50 _length_5461 _cov_3.79671	378.18	-0.10	0.38	-0.26	7.93E-01	8.79E-01	3.91E-04
NG_14571_6 9xxx_NODE _28_length_3 6772_cov_43. 1957	39.97	24.17	2.96	8.16	3.24E-16	2.35E-15	4.40E-04
NG_14571_9 2xxx_NODE _194_length_ 3135_cov_83. 3	4.31	5.30	2.96	1.79	7.34E-02	1.45E-01	3.98E-05
VC	UC Flare Median	UC Flare Present (n=23)	UC Remissio n Mean	UC Remissio n Median	UC Remission Present (n=17)	logfdr	Classification
vc1	4.69E-04	14	4.21E-02	1.65E-03	12	0.37	Podoviridae
vc10	8.10E-04	16	2.14E-01	6.28E-03	11	0.35	Unclassified
vc100	0	3	4.95E-05	0	2	0.06	Unclassified
vc103	0	3	3.56E-03	0	6	0.02	Unclassified
vc104	0	0	3.69E-03	0	4	1.03	Siphoviridae
vc106	0	2	5.50E-03	0	6	1.31	Unclassified
vc108	0	3	0	0	0	12.88	Unclassified
vc109	0	2	0	0	0	13.38	Siphoviridae

vc11	0	4	7.04E-03	0	2	0.06	Heterogeneous
vc111	0	2	0	0	0	15.54	Unclassified
vc112	0	3	7.89E-05	0	4	0.06	Genomoviridae
vc114	0	3	2.77E-05	0	1	13.94	Unclassified
vc115	0	4	0	0	0	13.38	Unclassified
vc119	0	1	3.63E-04	0	3	14.11	Unclassified
vc12	0	6	9.46E-03	0	7	0.14	Unclassified
vc122	0	2	0	0	0	0.95	Unclassified
vc126	0	4	4.64E-03	0	3	0.37	Unclassified
vc128	0	2	1.11E-05	0	1	14.63	Unclassified
vc13	0	4	1.60E-03	0	5	0.65	Unclassified
vc130	0	6	1.61E-03	0	5	0.02	Unclassified
vc138	0	2	0	0	0	0.95	Unclassified
vc14	0	5	5.46E-03	0	3	0.39	Siphoviridae
vc143	0	3	2.58E-03	0	1	17.15	Siphoviridae
vc145	0	1	4.71E-03	0	3	18.19	Microviridae
vc15	1.25E-04	13	8.84E-02	2.77E-03	13	0.57	Unclassified
vc159	0	2	0	0	0	14.63	Unclassified
vc16	0	1	4.75E-02	0	3	18.97	Unclassified
vc162	0	2	0	0	0	13.99	Unclassified
vc163	0	0	4.42E-04	0	2	15.10	Unclassified
vc168	0	2	0	0	0	1.08	Siphoviridae
vc17	0	10	1.77E-03	0	8	0.17	Microviridae
vc18	0	6	7.04E-03	0	8	0.17	Unclassified
vc19	0	2	5.34E-03	9.89E-05	9	2.84	Siphoviridae
vc193	0	0	1.03E-02	0	2	14.04	Unclassified
vc2	0	9	1.14E-03	1.43E-04	12	0.21	Unclassified
vc20	0	5	9.87E-05	0	2	0.07	Unclassified
vc207	0	2	0	0	0	0.75	Unclassified
vc21	0	10	1.01E-01	0	7	0.06	CrAss-like
vc215	0	2	0	0	0	14.63	Unclassified

vc22	0	4	4.04E-04	0	3	0.20	CrAss-like
vc220	0	2	1.26E-05	0	1	13.04	Unclassified
vc23	0	3	1.04E-02	0	1	13.13	Heterogeneous
vc231	0	2	0	0	0	0.80	Unclassified
vc24	0	6	1.37E-03	0	6	0.17	Unclassified
vc242	0	2	0	0	0	12.92	Unclassified
vc25	0	10	1.43E-02	0	6	0.30	Microviridae
vc26	0	4	0	0	0	0.75	Myoviridae
vc27	0	4	5.15E-03	0	3	0.06	Heterogeneous
vc28	0	4	4.31E-03	0	3	0.09	Myoviridae
vc29	1.84E-04	12	6.54E-02	3.97E-05	10	0.23	Unclassified
vc3	0	4	1.02E-03	0	4	0.04	Siphoviridae
vc30	0	9	1.30E-02	7.60E-05	9	0.28	Unclassified
vc31	0	4	2.03E-02	0	6	0.68	Microviridae
vc32	0	1	6.14E-03	0	5	18.93	Siphoviridae
vc33	0	3	2.65E-03	0	1	11.94	Siphoviridae
vc34	0	5	2.87E-04	0	3	0.23	Siphoviridae
vc340	0	4	9.23E-06	0	2	12.74	Unclassified
vc35	0	3	1.36E-04	0	1	14.09	Siphoviridae
vc359	0	2	0	0	0	0.84	Unclassified
vc36	0	2	4.44E-05	0	5	0.17	Heterogeneous
vc37	0	4	2.85E-02	0	6	0.06	Unclassified
vc374	0	3	0	0	0	12.28	Unclassified
vc38	0	6	0	0	0	15.72	Unclassified
vc39	0	5	7.14E-06	0	2	0.17	Unclassified
vc392	0	2	0	0	0	11.48	Unclassified
vc4	0	8	6.21E-03	0	7	0.06	Siphoviridae
vc40	0	11	3.60E-02	0	6	0.63	Unclassified
vc41	0	4	4.94E-03	0	4	0.06	Siphoviridae
vc416	0	3	9.25E-04	0	3	1.03	Unclassified

vc42	0	2	0	0	0	12.76	Siphoviridae
vc43	0	3	2.41E-03	0	1	13.45	Siphoviridae
vc45	0	2	0	0	0	0.95	Podoviridae
vc46	0	2	0	0	0	13.60	Unclassified
vc48	0	4	0	0	0	12.83	Unclassified
vc5	0	6	5.10E-03	0	3	0.08	Myoviridae
vc50	0	3	7.97E-05	0	2	0.09	Siphoviridae
vc51	0	2	2.20E-04	0	5	0.37	Siphoviridae
vc53	0	3	5.94E-04	0	1	1.00	Siphoviridae
vc54	0	4	3.23E-02	0	1	19.38	Unclassified
vc55	0	2	1.25E-03	0	4	0.21	Podoviridae
vc56	0	2	4.74E-04	0	2	16.62	Heterogeneous
vc57	0	3	6.05E-06	0	1	13.38	Unclassified
vc59	0	2	5.94E-06	0	1	12.65	Siphoviridae
vc6	0	7	4.30E-03	0	5	0.08	Myoviridae
vc60	0	2	2.78E-04	0	4	0.49	Unclassified
vc61	0	2	8.89E-04	0	3	0.06	Unclassified
vc62	0	4	0	0	0	13.31	Unclassified
vc64	0	3	8.55E-06	0	1	13.38	Unclassified
vc65	0	2	6.09E-02	0	4	1.35	Unclassified
vc66	0	3	2.62E-04	0	2	0.23	Podoviridae
vc67	0	4	0	0	0	13.84	Siphoviridae
vc68	0	3	0	0	0	1.03	Unclassified
vc69	0	4	0	0	0	12.93	Unclassified
vc7	0	8	5.42E-02	1.69E-04	10	0.05	CrAss-like
vc70	0	3	8.23E-04	0	2	0.01	Unclassified
vc71	0	3	2.02E-06	0	1	13.23	Unclassified
vc72	0	5	4.18E-04	0	1	14.65	Siphoviridae
vc75	0	2	1.04E-04	0	4	0.04	Unclassified
vc78	0	2	1.30E-04	0	3	0.06	Unclassified
vc8	0	5	2.72E-03	0	6	0.06	Heterogeneous

vc80	0	2	2.62E-05	0	1	0.75	Unclassified
vc84	0	2	0	0	0	0.75	Unclassified
vc87	0	2	1.46E-03	0	3	0.02	Unclassified
vc89	0	1	3.96E-05	0	2	0.83	Unclassified
vc9	0	5	5.82E-04	0	2	15.54	Siphoviridae
vc91	0	3	7.02E-05	0	1	13.18	Myoviridae
vc93	0	4	0	0	0	13.94	Anelloviridae
vc96	0	2	1.18E-03	0	3	0.23	Unclassified
vc99	0	3	2.51E-05	0	1	0.83	Unclassified
NG_14253_1 6_lib223966_ 5684_NODE _382_length_ 1481_cov_41. 2805	0	0	7.41E-04	0	2	15.44	CrAss-like
NG_14253_2 0_lib223970_ 5684_NODE _42_length_5 833_cov_5.31 585	0	4	7.54E-05	0	3	0.17	Unclassified
NG_14253_2 6_lib223959_ 5684_NODE _300_length_ 1971_cov_2.2 6357	0	2	1.13E-03	0	3	0.24	CrAss-like
NG_14253_4 7_lib223969_ 5684_NODE _36_length_3 850_cov_113. 131	0	0	1.18E-04	0	2	14.11	Unclassified

NG_14253_8 _lib223960_5 684_NODE_ 65_length_11 69_cov_1.928 19	0	1	1.29E-03	0	4	17.62	CrAss-like
NG_14571_1 04xxx_NOD E_95_length_ 3939_cov_97 2.235	0	3	0	0	0	13.56	Anelloviridae
NG_14571_1 06xxx_NOD E_31_length_ 20289_cov_5. 6621	0	3	1.69E-05	0	1	13.99	Unclassified
NG_14571_1 08xxx_NOD E_53_length_ 8858_cov_2.7 1146	0	2	0	0	0	0.84	Unclassified
NG_14571_1 19xxx_NOD E_361_length_ _2175_cov_4 10.478	0	3	1.01E-04	0	3	0.21	Unclassified
NG_14571_5 8_NODE_50 _length_5461 _cov_3.79671	2.94E-04	23	2.85E-04	1.96E-04	17	0.06	Microviridae
NG_14571_6 9xxx_NODE _28_length_3	0	3	0	0	0	14.63	Unclassified

6772_cov_43. 1957							
NG_14571_9 2xxx_NODE _194_length_ 3135_cov_83. 3	0	2	0	0	0	0.84	Unclassified

Table 10. DeSeq2 results of RSV counts comparing UC Flare to UC Remission

RSV	Base Mean	log2Fold Change	lfcSE	stat	pvalue	padj
Seq_000000 1	7586.48	-1.01	0.87	-1.16	2.47E-01	9.77E-01
Seq_000000 2	6657.27	-0.02	1.38	-0.01	9.91E-01	9.94E-01
Seq_000000 3	2087.52	1.70	1.23	1.38	1.66E-01	9.77E-01
Seq_000000 4	2906.82	-0.25	0.97	-0.26	7.97E-01	9.77E-01
Seq_000000 5	2021.44	-0.75	0.82	-0.92	3.60E-01	9.77E-01
Seq_000000 9	2505.52	-0.72	1.57	-0.46	6.44E-01	9.77E-01
Seq_000001 0	1176.61	0.04	2.15	0.02	9.84E-01	9.94E-01
Seq_000001 1	652.69	0.38	0.85	0.45	6.51E-01	9.77E-01
Seq_000001 2	2174.51	0.46	0.98	0.47	6.38E-01	9.77E-01
Seq_000001 3	927.47	1.83	1.12	1.64	1.02E-01	9.77E-01
Seq_000001 6	10.68	22.31	2.96	7.54	4.55E-14	5.06E-12

Seq_000001 7	147.98	4.66	1.72	2.70	6.83E-03	4.84E-01
Seq_000001 8	834.24	1.74	1.38	1.26	2.07E-01	9.77E-01
Seq_000001 9	108.45	2.73	2.91	0.94	3.49E-01	9.77E-01
Seq_000002 4	1275.24	1.26	1.30	0.96	3.35E-01	9.77E-01
Seq_000002 5	36.95	1.82	1.89	0.96	3.37E-01	9.77E-01
Seq_000002 6	962.91	-0.15	1.40	-0.11	9.14E-01	9.77E-01
Seq_000002 7	11.52	22.41	2.96	7.58	3.49E-14	4.53E-12
Seq_000002 8	53.47	1.89	1.84	1.03	3.03E-01	9.77E-01
Seq_000002 9	96.69	3.10	2.91	1.07	2.87E-01	9.77E-01
Seq_000003 0	575.41	0.53	1.11	0.48	6.31E-01	9.77E-01
Seq_000003 1	204.47	2.17	1.38	1.57	1.16E-01	9.77E-01
Seq_000003 3	836.17	-1.13	1.13	-1.00	3.15E-01	9.77E-01
Seq_000003 4	752.28	-0.12	1.26	-0.09	9.25E-01	9.78E-01
Seq_000003 5	954.50	0.01	1.66	0.01	9.93E-01	9.94E-01
Seq_000003 6	773.28	0.23	1.71	0.14	8.92E-01	9.77E-01
Seq_000003 8	80.64	-5.07	2.92	-1.74	8.19E-02	9.77E-01

Seq_000004 0	713.68	0.78	1.26	0.62	5.36E-01	9.77E-01
Seq_000004 3	715.94	-1.47	1.57	-0.94	3.49E-01	9.77E-01
Seq_000004 9	557.06	-0.75	1.44	-0.52	6.06E-01	9.77E-01
Seq_000005 1	4.71	-0.12	1.98	-0.06	9.52E-01	9.81E-01
Seq_000005 3	398.79	-0.96	1.05	-0.91	3.62E-01	9.77E-01
Seq_000005 5	6.56	5.98	2.96	2.02	4.31E-02	9.77E-01
Seq_000005 6	123.97	-1.34	2.34	-0.57	5.67E-01	9.77E-01
Seq_000005 9	25.74	22.02	2.96	7.45	9.62E-14	9.37E-12
Seq_000006 4	28.88	-5.61	2.89	-1.94	5.19E-02	9.77E-01
Seq_000006 8	74.71	6.35	2.39	2.65	8.00E-03	5.20E-01
Seq_000007 0	239.65	-0.45	1.36	-0.33	7.42E-01	9.77E-01
Seq_000007 4	42.54	-1.12	2.14	-0.52	6.00E-01	9.77E-01
Seq_000007 5	74.83	-0.08	1.88	-0.04	9.65E-01	9.84E-01
Seq_000008 3	44.98	-2.85	2.91	-0.98	3.28E-01	9.77E-01
Seq_000008 4	56.89	-4.00	2.52	-1.59	1.13E-01	9.77E-01
Seq_000008 6	26.96	9.59	2.44	3.92	8.70E-05	7.53E-03

Seq_000008 8	16.28	-24.41	2.95	-8.28	1.19E-16	4.64E-14
Seq_000009 2	44.14	2.37	2.91	0.81	4.17E-01	9.77E-01
Seq_000009 6	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000009 9	204.48	-2.49	1.75	-1.42	1.56E-01	9.77E-01
Seq_000010 2	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000010 9	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000011 4	0.80	2.94	2.97	0.99	3.22E-01	9.77E-01
Seq_000011 5	30.42	-1.91	2.27	-0.84	3.99E-01	9.77E-01
Seq_000011 7	132.17	0.67	1.59	0.42	6.71E-01	9.77E-01
Seq_000011 8	3.59	1.48	2.93	0.50	6.14E-01	9.77E-01
Seq_000012 0	227.58	-3.04	1.42	-2.13	3.30E-02	9.77E-01
Seq_000012 1	19.88	-3.47	2.18	-1.59	1.11E-01	9.77E-01
Seq_000012 3	21.13	2.94	2.33	1.26	2.07E-01	9.77E-01
Seq_000012 5	2.63	4.66	2.96	1.58	1.15E-01	9.77E-01
Seq_000012 6	19.73	2.19	2.07	1.06	2.88E-01	9.77E-01
Seq_000013 5	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01

Seq_000013 6	23.00	-3.21	2.18	-1.47	1.41E-01	9.77E-01
Seq_000013 9	0.50	-2.66	2.96	-0.90	3.70E-01	9.77E-01
Seq_000014 0	0.34	1.70	2.98	0.57	5.68E-01	9.77E-01
Seq_000014 1	45.93	1.89	2.45	0.77	4.40E-01	9.77E-01
Seq_000014 2	94.01	0.02	1.57	0.01	9.90E-01	9.94E-01
Seq_000014 6	15.39	-0.55	2.13	-0.26	7.96E-01	9.77E-01
Seq_000014 8	10.39	0.78	2.29	0.34	7.33E-01	9.77E-01
Seq_000014 9	31.98	7.35	2.92	2.52	1.18E-02	7.06E-01
Seq_000015 4	53.56	24.56	2.96	8.31	9.86E-17	4.64E-14
Seq_000015 5	113.70	-1.33	1.73	-0.77	4.40E-01	9.77E-01
Seq_000015 7	38.00	4.55	2.92	1.56	1.19E-01	9.77E-01
Seq_000015 9	45.97	-0.68	1.90	-0.36	7.21E-01	9.77E-01
Seq_000016 1	52.96	0.90	1.26	0.71	4.77E-01	9.77E-01
Seq_000016 8	2.34	-0.26	2.93	-0.09	9.29E-01	9.79E-01
Seq_000017 4	25.74	-2.46	2.49	-0.99	3.23E-01	9.77E-01
Seq_000017 5	24.66	2.47	2.51	0.98	3.25E-01	9.77E-01

Seq_000017 7	38.49	-2.65	2.19	-1.21	2.25E-01	9.77E-01
Seq_000018 0	73.68	2.82	1.90	1.48	1.38E-01	9.77E-01
Seq_000018 3	63.42	-0.75	2.04	-0.37	7.13E-01	9.77E-01
Seq_000018 6	17.41	-6.11	2.94	-2.08	3.78E-02	9.77E-01
Seq_000018 9	6.11	5.88	2.96	1.99	4.69E-02	9.77E-01
Seq_000019 4	17.49	22.99	2.96	7.77	7.62E-15	1.48E-12
Seq_000019 8	18.90	-1.12	1.78	-0.63	5.29E-01	9.77E-01
Seq_000020 4	27.77	0.34	1.61	0.21	8.31E-01	9.77E-01
Seq_000020 5	10.07	-4.65	2.25	-2.07	3.85E-02	9.77E-01
Seq_000020 7	15.15	-2.15	2.10	-1.03	3.05E-01	9.77E-01
Seq_000021 4	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000021 6	39.10	-0.49	1.54	-0.32	7.50E-01	9.77E-01
Seq_000021 8	22.40	-5.10	2.92	-1.74	8.10E-02	9.77E-01
Seq_000021 9	83.36	-5.94	1.85	-3.21	1.33E-03	1.04E-01
Seq_000022 0	2.86	4.78	2.96	1.62	1.06E-01	9.77E-01
Seq_000022 1	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01

Seq_000022 4	66.43	-1.83	1.72	-1.06	2.87E-01	9.77E-01
Seq_000022 8	87.91	-0.22	1.12	-0.20	8.45E-01	9.77E-01
Seq_000023 3	6.48	5.96	2.96	2.02	4.38E-02	9.77E-01
Seq_000024 0	3.53	5.09	2.96	1.72	8.55E-02	9.77E-01
Seq_000024 4	5.24	1.27	2.92	0.43	6.64E-01	9.77E-01
Seq_000024 5	0.98	-3.62	2.96	-1.23	2.20E-01	9.77E-01
Seq_000024 7	1.20	3.53	2.96	1.19	2.34E-01	9.77E-01
Seq_000024 9	21.47	-3.39	2.92	-1.16	2.45E-01	9.77E-01
Seq_000025 1	14.89	0.13	2.02	0.07	9.48E-01	9.81E-01
Seq_000025 2	34.11	-2.71	2.12	-1.28	2.01E-01	9.77E-01
Seq_000025 3	4.12	5.31	2.96	1.79	7.27E-02	9.77E-01
Seq_000026 0	2.05	4.30	2.96	1.45	1.46E-01	9.77E-01
Seq_000026 4	1.97	4.24	2.96	1.43	1.52E-01	9.77E-01
Seq_000026 6	0.50	2.28	2.98	0.77	4.43E-01	9.77E-01
Seq_000026 7	12.04	22.47	2.96	7.60	3.03E-14	4.53E-12
Seq_000027 6	21.11	-1.45	2.24	-0.65	5.18E-01	9.77E-01

Seq_000028	1.67	1.41	2.95	0.48	6.31E-01	9.77E-01
8						
Seq_000029	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
1						
Seq_000029	23.76	-3.22	1.54	-2.08	3.73E-02	9.77E-01
2						
Seq_000029	25.79	-0.89	1.74	-0.51	6.08E-01	9.77E-01
6						
Seq_000030	8.72	-1.38	2.11	-0.65	5.14E-01	9.77E-01
4						
Seq_000030	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
7						
Seq_000031	54.97	-2.32	1.55	-1.50	1.34E-01	9.77E-01
0						
Seq_000031	6.62	-3.69	2.93	-1.26	2.08E-01	9.77E-01
5						
Seq_000031	2.23	4.43	2.96	1.49	1.35E-01	9.77E-01
6						
Seq_000031	1.14	3.46	2.96	1.17	2.43E-01	9.77E-01
7						
Seq_000031	6.22	-2.76	2.73	-1.01	3.13E-01	9.77E-01
8						
Seq_000031	10.87	-3.05	1.83	-1.67	9.48E-02	9.77E-01
9						
Seq_000033	4.73	-0.90	2.58	-0.35	7.27E-01	9.77E-01
1						
Seq_000033	25.48	-5.87	2.93	-2.00	4.50E-02	9.77E-01
5						
Seq_000033	3.45	5.06	2.96	1.71	8.75E-02	9.77E-01
9						
Seq_000034	42.03	5.11	2.23	2.30	2.17E-02	9.77E-01
1						

Seq_000034 6	0.30	1.55	2.99	0.52	6.03E-01	9.77E-01
Seq_000034 8	0.15	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000035 0	1.91	4.20	2.96	1.42	1.56E-01	9.77E-01
Seq_000035 1	0.20	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000035 3	0.27	0.43	2.99	0.15	8.84E-01	9.77E-01
Seq_000035 6	24.10	4.47	2.73	1.64	1.01E-01	9.77E-01
Seq_000035 8	4.17	-1.05	2.92	-0.36	7.19E-01	9.77E-01
Seq_000036 1	12.93	4.99	2.34	2.13	3.32E-02	9.77E-01
Seq_000036 2	7.35	1.11	2.92	0.38	7.03E-01	9.77E-01
Seq_000036 8	2.37	0.79	2.92	0.27	7.87E-01	9.77E-01
Seq_000037 2	20.79	0.54	1.30	0.42	6.75E-01	9.77E-01
Seq_000037 7	0.45	2.12	2.98	0.71	4.76E-01	9.77E-01
Seq_000038 1	3.99	0.70	2.92	0.24	8.12E-01	9.77E-01
Seq_000039 0	8.14	2.21	2.64	0.84	4.02E-01	9.77E-01
Seq_000039 2	13.80	-0.88	2.47	-0.35	7.23E-01	9.77E-01
Seq_000039 6	4.69	-3.93	2.83	-1.39	1.65E-01	9.77E-01

Seq_000039 7	17.69	0.09	2.51	0.03	9.73E-01	9.87E-01
Seq_000040 1	10.50	0.50	2.92	0.17	8.64E-01	9.77E-01
Seq_000040 3	9.11	-2.49	2.92	-0.85	3.94E-01	9.77E-01
Seq_000040 5	7.63	6.20	2.96	2.10	3.61E-02	9.77E-01
Seq_000040 9	3.13	-5.29	2.66	-1.99	4.71E-02	9.77E-01
Seq_000041 0	23.96	-1.80	1.64	-1.10	2.72E-01	9.77E-01
Seq_000041 4	21.44	-24.00	2.95	-8.15	3.79E-16	9.83E-14
Seq_000042 8	0.69	-3.11	2.96	-1.05	2.93E-01	9.77E-01
Seq_000043 1	0.61	-2.94	2.96	-0.99	3.22E-01	9.77E-01
Seq_000043 3	37.63	-0.28	2.07	-0.13	8.94E-01	9.77E-01
Seq_000045 2	16.37	-0.76	2.32	-0.33	7.43E-01	9.77E-01
Seq_000045 6	0.94	3.17	2.97	1.07	2.85E-01	9.77E-01
Seq_000045 7	5.83	5.81	2.96	1.96	4.95E-02	9.77E-01
Seq_000045 8	10.82	0.81	2.02	0.40	6.88E-01	9.77E-01
Seq_000045 9	1.67	4.01	2.96	1.35	1.76E-01	9.77E-01
Seq_000046 2	1.37	-4.10	2.95	-1.39	1.65E-01	9.77E-01

Seq_000046 3	2.15	3.58	2.96	1.21	2.27E-01	9.77E-01
Seq_000046 4	4.20	5.34	2.78	1.92	5.52E-02	9.77E-01
Seq_000046 7	26.90	-0.30	2.15	-0.14	8.88E-01	9.77E-01
Seq_000047 2	5.88	5.82	2.96	1.97	4.90E-02	9.77E-01
Seq_000048 3	8.69	3.47	2.78	1.25	2.12E-01	9.77E-01
Seq_000049 3	5.18	0.85	2.79	0.30	7.61E-01	9.77E-01
Seq_000049 4	2.44	2.40	2.95	0.81	4.15E-01	9.77E-01
Seq_000050 2	3.03	0.44	2.93	0.15	8.80E-01	9.77E-01
Seq_000051 0	8.89	-0.11	2.56	-0.04	9.66E-01	9.84E-01
Seq_000051 7	1.94	4.22	2.96	1.43	1.54E-01	9.77E-01
Seq_000052 7	5.74	-1.03	1.92	-0.53	5.93E-01	9.77E-01
Seq_000053 2	12.40	1.04	2.09	0.50	6.17E-01	9.77E-01
Seq_000053 6	0.29	-1.87	2.98	-0.63	5.30E-01	9.77E-01
Seq_000053 7	7.27	0.26	2.67	0.10	9.23E-01	9.77E-01
Seq_000053 8	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000054 2	28.29	1.10	2.38	0.46	6.44E-01	9.77E-01

Seq_000054 4	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000054 8	1.01	-3.66	2.96	-1.24	2.16E-01	9.77E-01
Seq_000054 9	3.52	1.44	2.93	0.49	6.23E-01	9.77E-01
Seq_000055 7	2.43	-0.79	2.93	-0.27	7.88E-01	9.77E-01
Seq_000055 9	22.52	-0.96	2.12	-0.46	6.49E-01	9.77E-01
Seq_000056 1	20.10	-2.34	2.43	-0.96	3.35E-01	9.77E-01
Seq_000056 4	0.24	-1.59	2.99	-0.53	5.95E-01	9.77E-01
Seq_000057 2	4.51	5.44	2.96	1.84	6.58E-02	9.77E-01
Seq_000057 6	2.13	3.36	2.39	1.41	1.60E-01	9.77E-01
Seq_000058 1	7.16	-2.13	2.45	-0.87	3.84E-01	9.77E-01
Seq_000058 9	0.90	3.12	2.97	1.05	2.93E-01	9.77E-01
Seq_000060 4	5.30	1.05	2.78	0.38	7.07E-01	9.77E-01
Seq_000061 5	2.86	-3.02	2.81	-1.07	2.83E-01	9.77E-01
Seq_000061 9	6.37	-0.58	2.21	-0.26	7.93E-01	9.77E-01
Seq_000062 3	2.84	4.77	2.96	1.61	1.07E-01	9.77E-01
Seq_000062 6	0.73	2.82	2.97	0.95	3.42E-01	9.77E-01

Seq_000064 0	0.58	2.49	2.97	0.84	4.01E-01	9.77E-01
Seq_000064 5	9.29	-0.99	2.23	-0.44	6.57E-01	9.77E-01
Seq_000064 6	5.11	2.04	2.76	0.74	4.59E-01	9.77E-01
Seq_000065 1	5.30	-0.24	2.62	-0.09	9.28E-01	9.79E-01
Seq_000065 4	3.93	0.04	2.92	0.01	9.90E-01	9.94E-01
Seq_000065 7	2.76	-5.11	2.95	-1.73	8.30E-02	9.77E-01
Seq_000066 0	1.23	3.57	2.96	1.20	2.29E-01	9.77E-01
Seq_000066 1	1.17	-3.87	2.95	-1.31	1.90E-01	9.77E-01
Seq_000066 6	1.80	4.12	2.96	1.39	1.65E-01	9.77E-01
Seq_000066 8	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000067 1	4.80	5.53	2.96	1.87	6.15E-02	9.77E-01
Seq_000067 3	4.73	5.51	2.96	1.86	6.25E-02	9.77E-01
Seq_000067 6	1.67	0.40	2.94	0.14	8.92E-01	9.77E-01
Seq_000067 9	1.11	-2.45	2.96	-0.83	4.07E-01	9.77E-01
Seq_000068 3	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000069 1	7.13	-5.77	2.58	-2.24	2.52E-02	9.77E-01

Seq_000070 4	0.13	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000070 5	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000070 8	7.35	0.84	1.66	0.51	6.12E-01	9.77E-01
Seq_000071 0	1.78	4.10	2.96	1.38	1.66E-01	9.77E-01
Seq_000071 2	7.57	6.19	2.96	2.09	3.64E-02	9.77E-01
Seq_000072 0	5.82	-1.04	1.40	-0.74	4.57E-01	9.77E-01
Seq_000073 5	9.42	0.10	1.71	0.06	9.55E-01	9.81E-01
Seq_000074 0	0.66	2.68	2.97	0.90	3.67E-01	9.77E-01
Seq_000074 3	1.59	0.19	2.42	0.08	9.36E-01	9.81E-01
Seq_000075 3	1.65	-4.37	2.95	-1.48	1.39E-01	9.77E-01
Seq_000075 7	1.39	-4.12	2.95	-1.39	1.63E-01	9.77E-01
Seq_000076 0	0.40	1.94	2.98	0.65	5.15E-01	9.77E-01
Seq_000076 5	0.50	2.28	2.98	0.77	4.43E-01	9.77E-01
Seq_000077 1	12.26	-2.06	2.37	-0.87	3.84E-01	9.77E-01
Seq_000077 8	1.38	3.73	2.96	1.26	2.08E-01	9.77E-01
Seq_000078 0	3.46	-4.52	2.95	-1.53	1.25E-01	9.77E-01

Seq_000078 1	0.48	2.20	2.98	0.74	4.59E-01	9.77E-01
Seq_000078 5	9.68	-1.37	1.69	-0.81	4.17E-01	9.77E-01
Seq_000079 2	0.80	2.94	2.97	0.99	3.22E-01	9.77E-01
Seq_000079 4	2.20	-0.88	2.93	-0.30	7.63E-01	9.77E-01
Seq_000080 8	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000081 2	1.74	1.71	2.62	0.65	5.14E-01	9.77E-01
Seq_000081 4	0.95	-0.08	2.53	-0.03	9.76E-01	9.88E-01
Seq_000081 5	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000082 9	0.43	-2.41	2.97	-0.81	4.16E-01	9.77E-01
Seq_000083 1	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000084 3	1.99	4.26	2.96	1.44	1.50E-01	9.77E-01
Seq_000084 4	1.43	3.79	2.96	1.28	2.01E-01	9.77E-01
Seq_000084 9	1.12	-3.80	2.95	-1.29	1.98E-01	9.77E-01
Seq_000085 1	4.29	-1.69	2.92	-0.58	5.63E-01	9.77E-01
Seq_000086 5	0.74	2.84	2.97	0.96	3.39E-01	9.77E-01
Seq_000086 8	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01

Seq_000087 8	3.19	-5.32	2.95	-1.80	7.12E-02	9.77E-01
Seq_000087 9	2.50	4.59	2.96	1.55	1.21E-01	9.77E-01
Seq_000088 0	0.66	-3.06	2.96	-1.03	3.02E-01	9.77E-01
Seq_000088 5	0.82	-3.37	2.96	-1.14	2.55E-01	9.77E-01
Seq_000088 9	9.65	3.96	2.15	1.84	6.55E-02	9.77E-01
Seq_000089 4	0.48	2.20	2.98	0.74	4.59E-01	9.77E-01
Seq_000089 9	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000090 0	1.62	3.96	2.96	1.34	1.81E-01	9.77E-01
Seq_000090 9	1.78	4.10	2.96	1.38	1.66E-01	9.77E-01
Seq_000091 0	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000091 5	1.72	4.05	2.96	1.37	1.71E-01	9.77E-01
Seq_000092 8	0.40	1.94	2.98	0.65	5.15E-01	9.77E-01
Seq_000093 1	4.00	-0.37	2.74	-0.14	8.92E-01	9.77E-01
Seq_000093 4	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000093 6	2.59	-3.76	2.20	-1.71	8.77E-02	9.77E-01
Seq_000093 8	1.78	4.10	2.96	1.38	1.66E-01	9.77E-01

Seq_000094 8	2.43	-1.04	2.65	-0.39	6.96E-01	9.77E-01
Seq_000096 6	0.74	-3.22	2.96	-1.09	2.77E-01	9.77E-01
Seq_000097 3	1.88	1.66	2.80	0.59	5.54E-01	9.77E-01
Seq_000097 5	0.40	1.94	2.98	0.65	5.15E-01	9.77E-01
Seq_000097 9	0.17	1.11	2.99	0.37	7.11E-01	9.77E-01
Seq_000098 4	8.28	0.96	1.51	0.64	5.25E-01	9.77E-01
Seq_000099 1	2.88	1.96	2.49	0.79	4.31E-01	9.77E-01
Seq_000099 8	0.95	-0.76	2.95	-0.26	7.98E-01	9.77E-01
Seq_000101 2	1.99	4.26	2.73	1.56	1.18E-01	9.77E-01
Seq_000102 1	0.45	-2.50	2.97	-0.84	3.99E-01	9.77E-01
Seq_000102 3	0.69	2.73	2.97	0.92	3.57E-01	9.77E-01
Seq_000103 0	0.29	-1.87	2.98	-0.63	5.30E-01	9.77E-01
Seq_000104 0	0.13	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000104 2	0.61	-2.94	2.96	-0.99	3.22E-01	9.77E-01
Seq_000105 1	0.61	2.56	2.97	0.86	3.89E-01	9.77E-01
Seq_000105 2	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01

Seq_000105 5	0.54	2.36	2.97	0.79	4.27E-01	9.77E-01
Seq_000106 2	0.40	0.81	2.83	0.28	7.76E-01	9.77E-01
Seq_000108 4	6.69	-2.54	2.02	-1.26	2.08E-01	9.77E-01
Seq_000108 8	0.50	-2.66	2.96	-0.90	3.70E-01	9.77E-01
Seq_000109 2	5.84	3.82	2.72	1.41	1.60E-01	9.77E-01
Seq_000109 6	1.17	-3.87	2.95	-1.31	1.90E-01	9.77E-01
Seq_000111 2	1.22	3.55	2.96	1.20	2.31E-01	9.77E-01
Seq_000111 6	5.66	-2.25	2.12	-1.06	2.88E-01	9.77E-01
Seq_000111 8	0.98	-2.54	2.96	-0.86	3.90E-01	9.77E-01
Seq_000112 8	6.55	-0.40	2.19	-0.18	8.56E-01	9.77E-01
Seq_000112 9	1.53	3.88	2.96	1.31	1.90E-01	9.77E-01
Seq_000113 5	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000113 8	4.53	-2.76	2.34	-1.18	2.38E-01	9.77E-01
Seq_000114 4	2.44	-0.26	2.33	-0.11	9.10E-01	9.77E-01
Seq_000115 5	0.77	2.89	2.97	0.97	3.30E-01	9.77E-01
Seq_000116 0	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01

Seq_000116 3	1.43	3.79	2.96	1.28	2.01E-01	9.77E-01
Seq_000117 3	2.95	4.83	2.96	1.63	1.03E-01	9.77E-01
Seq_000118 0	0.56	2.43	2.97	0.82	4.14E-01	9.77E-01
Seq_000119 1	0.40	1.94	2.98	0.65	5.14E-01	9.77E-01
Seq_000119 4	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000121 2	3.87	0.91	2.24	0.40	6.86E-01	9.77E-01
Seq_000122 1	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000123 1	0.77	2.89	2.97	0.97	3.30E-01	9.77E-01
Seq_000123 5	5.53	-3.27	2.35	-1.39	1.64E-01	9.77E-01
Seq_000124 1	1.54	-4.27	2.95	-1.45	1.48E-01	9.77E-01
Seq_000125 2	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000126 5	0.24	-1.59	2.99	-0.53	5.95E-01	9.77E-01
Seq_000128 4	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000128 5	1.54	3.89	2.96	1.31	1.89E-01	9.77E-01
Seq_000128 9	1.38	-4.11	2.95	-1.39	1.64E-01	9.77E-01
Seq_000130 3	0.66	2.67	2.97	0.90	3.69E-01	9.77E-01

Seq_000131 0	1.06	3.36	2.97	1.13	2.58E-01	9.77E-01
Seq_000132 0	1.68	0.03	2.81	0.01	9.92E-01	9.94E-01
Seq_000133 0	0.98	3.24	2.97	1.09	2.74E-01	9.77E-01
Seq_000133 4	0.56	-2.80	2.96	-0.95	3.44E-01	9.77E-01
Seq_000133 8	3.37	-2.90	2.63	-1.10	2.71E-01	9.77E-01
Seq_000133 9	0.88	3.08	2.97	1.04	2.99E-01	9.77E-01
Seq_000134 5	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000134 6	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000134 7	0.40	-0.15	2.99	-0.05	9.59E-01	9.81E-01
Seq_000135 2	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000135 3	2.19	3.61	2.56	1.41	1.59E-01	9.77E-01
Seq_000135 8	1.38	3.73	2.96	1.26	2.08E-01	9.77E-01
Seq_000136 9	0.22	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000137 3	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000138 4	1.96	-4.61	2.95	-1.56	1.18E-01	9.77E-01
Seq_000141 1	0.10	0.43	2.99	0.14	8.87E-01	9.77E-01

Seq_000142 3	3.16	-3.44	2.59	-1.33	1.84E-01	9.77E-01
Seq_000142 7	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000143 3	0.51	-0.81	2.98	-0.27	7.85E-01	9.77E-01
Seq_000143 9	0.68	-1.59	2.96	-0.54	5.92E-01	9.77E-01
Seq_000144 4	1.75	2.27	2.96	0.77	4.44E-01	9.77E-01
Seq_000144 6	1.67	-4.39	2.95	-1.49	1.37E-01	9.77E-01
Seq_000144 8	1.28	2.98	2.96	1.01	3.14E-01	9.77E-01
Seq_000145 9	0.37	1.82	2.98	0.61	5.41E-01	9.77E-01
Seq_000146 4	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000147 1	0.43	-2.41	2.97	-0.81	4.16E-01	9.77E-01
Seq_000148 7	0.95	-3.39	2.43	-1.39	1.63E-01	9.77E-01
Seq_000148 8	0.66	2.68	2.97	0.90	3.67E-01	9.77E-01
Seq_000150 7	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000151 1	3.97	-1.70	2.22	-0.77	4.43E-01	9.77E-01
Seq_000153 4	3.14	-1.27	1.73	-0.73	4.63E-01	9.77E-01
Seq_000153 5	0.22	0.84	2.99	0.28	7.79E-01	9.77E-01

Seq_000156 0	0.93	3.16	2.97	1.07	2.86E-01	9.77E-01
Seq_000156 7	0.85	-3.41	2.96	-1.15	2.49E-01	9.77E-01
Seq_000157 6	1.65	-3.40	2.95	-1.15	2.50E-01	9.77E-01
Seq_000158 0	0.45	2.12	2.98	0.71	4.76E-01	9.77E-01
Seq_000158 2	0.70	2.75	2.97	0.92	3.55E-01	9.77E-01
Seq_000160 2	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000161 1	1.20	-3.91	2.95	-1.32	1.86E-01	9.77E-01
Seq_000165 0	0.40	-0.76	2.99	-0.26	7.98E-01	9.77E-01
Seq_000165 4	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000166 6	0.48	2.20	2.98	0.74	4.59E-01	9.77E-01
Seq_000166 7	1.17	-3.87	2.95	-1.31	1.90E-01	9.77E-01
Seq_000167 0	1.27	0.40	2.76	0.15	8.85E-01	9.77E-01
Seq_000167 3	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000168 2	2.28	-4.84	2.95	-1.64	1.01E-01	9.77E-01
Seq_000168 3	0.58	2.49	2.97	0.84	4.01E-01	9.77E-01
Seq_000168 8	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01

Seq_000169 5	0.66	-1.45	2.97	-0.49	6.25E-01	9.77E-01
Seq_000170 5	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000171 9	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000173 0	1.01	-3.66	2.96	-1.24	2.16E-01	9.77E-01
Seq_000173 6	0.72	2.79	2.97	0.94	3.48E-01	9.77E-01
Seq_000174 0	0.72	1.59	2.88	0.55	5.81E-01	9.77E-01
Seq_000174 4	0.35	1.74	2.98	0.58	5.59E-01	9.77E-01
Seq_000175 7	1.10	-2.00	2.96	-0.68	4.99E-01	9.77E-01
Seq_000176 3	0.32	1.64	2.99	0.55	5.83E-01	9.77E-01
Seq_000177 2	0.64	2.62	2.97	0.88	3.77E-01	9.77E-01
Seq_000177 4	0.53	2.35	2.97	0.79	4.30E-01	9.77E-01
Seq_000178 2	0.32	1.64	2.99	0.55	5.83E-01	9.77E-01
Seq_000178 8	1.67	4.01	2.96	1.35	1.76E-01	9.77E-01
Seq_000179 4	0.50	2.28	2.98	0.77	4.43E-01	9.77E-01
Seq_000180 6	0.40	-2.32	2.97	-0.78	4.35E-01	9.77E-01
Seq_000181 8	1.21	-3.43	2.64	-1.30	1.94E-01	9.77E-01

Seq_000183 4	1.89	-4.56	2.95	-1.55	1.22E-01	9.77E-01
Seq_000184 4	1.89	-2.49	2.39	-1.04	2.97E-01	9.77E-01
Seq_000186 2	0.29	1.51	2.99	0.50	6.14E-01	9.77E-01
Seq_000186 8	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000190 5	0.37	1.84	2.98	0.62	5.36E-01	9.77E-01
Seq_000190 9	0.16	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000193 7	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000194 0	0.80	2.94	2.97	0.99	3.22E-01	9.77E-01
Seq_000194 1	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000195 4	0.24	-1.57	2.99	-0.53	5.99E-01	9.77E-01
Seq_000195 8	1.17	-3.02	2.47	-1.22	2.21E-01	9.77E-01
Seq_000197 2	2.78	0.30	2.51	0.12	9.04E-01	9.77E-01
Seq_000197 3	0.31	0.57	2.99	0.19	8.48E-01	9.77E-01
Seq_000198 0	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000199 5	0.45	-2.50	2.97	-0.84	3.99E-01	9.77E-01
Seq_000202 1	0.93	3.16	2.97	1.07	2.86E-01	9.77E-01

Seq_000203 4	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000206 4	1.59	0.82	2.43	0.34	7.37E-01	9.77E-01
Seq_000206 6	1.12	3.44	2.96	1.16	2.46E-01	9.77E-01
Seq_000206 9	1.75	0.51	2.61	0.20	8.45E-01	9.77E-01
Seq_000207 5	1.17	-2.66	2.96	-0.90	3.68E-01	9.77E-01
Seq_000208 2	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000209 0	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000213 5	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000213 9	0.23	-1.53	2.99	-0.51	6.08E-01	9.77E-01
Seq_000214 3	1.14	2.38	2.97	0.80	4.22E-01	9.77E-01
Seq_000214 9	0.82	-3.35	2.96	-1.13	2.57E-01	9.77E-01
Seq_000215 3	0.80	2.95	2.97	0.99	3.21E-01	9.77E-01
Seq_000216 8	0.82	0.47	2.71	0.17	8.62E-01	9.77E-01
Seq_000217 2	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000218 1	0.35	1.74	2.98	0.58	5.59E-01	9.77E-01
Seq_000218 5	0.56	2.43	2.97	0.82	4.14E-01	9.77E-01

Seq_000219 3	1.54	-3.09	2.50	-1.24	2.15E-01	9.77E-01
Seq_000219 4	0.56	-2.80	2.96	-0.95	3.44E-01	9.77E-01
Seq_000221 2	0.37	1.84	2.98	0.62	5.37E-01	9.77E-01
Seq_000223 0	0.29	-1.87	2.98	-0.63	5.30E-01	9.77E-01
Seq_000223 3	0.97	1.21	2.96	0.41	6.82E-01	9.77E-01
Seq_000223 4	2.18	4.39	2.96	1.48	1.38E-01	9.77E-01
Seq_000224 1	0.53	-0.63	2.64	-0.24	8.12E-01	9.77E-01
Seq_000224 3	0.91	3.12	2.97	1.05	2.94E-01	9.77E-01
Seq_000225 4	1.71	-3.45	2.50	-1.38	1.66E-01	9.77E-01
Seq_000225 5	0.83	-2.24	2.64	-0.85	3.96E-01	9.77E-01
Seq_000228 6	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000228 8	1.62	3.96	2.96	1.34	1.81E-01	9.77E-01
Seq_000230 3	1.52	0.26	2.60	0.10	9.19E-01	9.77E-01
Seq_000232 2	0.90	-3.50	2.96	-1.18	2.37E-01	9.77E-01
Seq_000236 4	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000237 5	0.22	0.16	2.99	0.05	9.57E-01	9.81E-01

Seq_000237 7	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000238 9	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000240 0	0.72	-1.11	2.67	-0.42	6.77E-01	9.77E-01
Seq_000240 1	0.17	-0.11	2.99	-0.04	9.69E-01	9.86E-01
Seq_000241 0	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000241 3	0.59	-1.82	2.42	-0.75	4.52E-01	9.77E-01
Seq_000242 6	0.04	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000243 4	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000243 5	0.77	2.89	2.97	0.97	3.30E-01	9.77E-01
Seq_000243 8	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000244 3	0.58	-2.64	2.60	-1.02	3.09E-01	9.77E-01
Seq_000246 2	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000247 0	0.22	-1.49	2.99	-0.50	6.19E-01	9.77E-01
Seq_000248 0	0.44	2.07	2.98	0.70	4.86E-01	9.77E-01
Seq_000249 5	0.16	-1.22	2.99	-0.41	6.83E-01	9.77E-01
Seq_000251 2	0.86	3.04	2.97	1.03	3.05E-01	9.77E-01

Seq_000251 9	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000252 9	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000253 3	0.89	-3.48	2.96	-1.18	2.39E-01	9.77E-01
Seq_000254 4	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000256 5	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000257 2	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000258 7	0.53	-2.73	2.96	-0.92	3.56E-01	9.77E-01
Seq_000260 5	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000261 2	0.40	1.94	2.98	0.65	5.15E-01	9.77E-01
Seq_000261 3	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000267 7	0.56	0.86	2.98	0.29	7.73E-01	9.77E-01
Seq_000267 8	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000271 3	0.37	-2.22	2.97	-0.75	4.55E-01	9.77E-01
Seq_000271 4	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000271 6	0.23	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000273 6	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01

Seq_000274 3	0.06	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000274 5	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000275 9	0.16	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000276 0	0.45	2.12	2.98	0.71	4.76E-01	9.77E-01
Seq_000279 7	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000279 9	0.50	2.28	2.98	0.77	4.43E-01	9.77E-01
Seq_000280 5	0.58	2.49	2.97	0.84	4.01E-01	9.77E-01
Seq_000282 9	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000284 6	0.80	0.83	2.97	0.28	7.81E-01	9.77E-01
Seq_000285 6	0.90	-2.21	2.96	-0.75	4.56E-01	9.77E-01
Seq_000287 4	0.23	-1.27	2.99	-0.42	6.71E-01	9.77E-01
Seq_000287 6	0.48	2.21	2.98	0.74	4.58E-01	9.77E-01
Seq_000289 4	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000289 7	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000291 0	0.09	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000292 4	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01

Seq_000292 5	0.58	2.49	2.97	0.84	4.01E-01	9.77E-01
Seq_000293 6	0.20	-0.16	2.99	-0.05	9.58E-01	9.81E-01
Seq_000293 7	0.59	-2.88	2.80	-1.03	3.04E-01	9.77E-01
Seq_000293 8	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000293 9	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000294 6	0.45	0.14	2.99	0.05	9.63E-01	9.84E-01
Seq_000294 8	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000295 9	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000297 4	0.14	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000303 4	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000303 5	0.40	-1.84	2.97	-0.62	5.36E-01	9.77E-01
Seq_000303 6	0.48	-2.60	2.97	-0.88	3.82E-01	9.77E-01
Seq_000306 4	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000306 7	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000308 8	0.41	-0.43	2.99	-0.14	8.86E-01	9.77E-01
Seq_000309 7	0.69	2.73	2.97	0.92	3.57E-01	9.77E-01

Seq_000309	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000310	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000312	0.64	-3.00	2.80	-1.07	2.84E-01	9.77E-01
Seq_000312	0.16	-0.43	2.99	-0.14	8.85E-01	9.77E-01
Seq_000312	0.81	-3.34	2.82	-1.18	2.37E-01	9.77E-01
Seq_000312	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000312	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000314	0.50	-2.66	2.96	-0.90	3.70E-01	9.77E-01
Seq_000317	0.89	-3.48	2.96	-1.18	2.39E-01	9.77E-01
Seq_000317	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000318	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000319	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000321	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000323	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000325	0.37	-0.29	2.99	-0.10	9.23E-01	9.77E-01
Seq_000325	0.43	1.20	2.98	0.40	6.87E-01	9.77E-01

Seq_000325 6	0.37	1.84	2.98	0.62	5.36E-01	9.77E-01
Seq_000325 8	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000326 7	0.09	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000331 7	0.24	-0.34	2.99	-0.11	9.10E-01	9.77E-01
Seq_000333 6	0.24	-0.66	2.99	-0.22	8.26E-01	9.77E-01
Seq_000333 8	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000333 9	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000337 7	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000340 7	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000341 9	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000342 5	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000349 6	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000351 7	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000355 4	0.05	-0.03	2.99	-0.01	9.92E-01	9.94E-01
Seq_000355 6	0.15	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000355 9	0.21	1.26	2.99	0.42	6.74E-01	9.77E-01

Seq_000365 0	0.11	-0.39	2.99	-0.13	8.96E-01	9.77E-01
Seq_000365 4	0.18	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000365 5	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000365 6	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000368 1	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000370 8	0.12	-0.25	2.99	-0.08	9.33E-01	9.81E-01
Seq_000370 9	0.70	-0.85	2.96	-0.29	7.74E-01	9.77E-01
Seq_000371 0	0.06	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000371 6	0.35	-0.43	2.99	-0.14	8.86E-01	9.77E-01
Seq_000378 8	0.08	0.11	2.99	0.04	9.71E-01	9.86E-01
Seq_000379 3	0.54	2.39	2.97	0.80	4.22E-01	9.77E-01
Seq_000381 4	0.35	-2.11	2.97	-0.71	4.77E-01	9.77E-01
Seq_000381 8	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000382 1	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000382 3	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000388 7	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01

Seq_000388 8	0.21	0.80	2.99	0.27	7.90E-01	9.77E-01
Seq_000388 9	0.24	-0.02	2.99	-0.01	9.95E-01	9.95E-01
Seq_000389 2	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000391 7	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000392 0	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000392 8	0.56	2.43	2.84	0.86	3.92E-01	9.77E-01
Seq_000393 1	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000396 2	0.09	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000396 4	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000396 5	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000396 6	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000397 4	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000400 9	0.24	-1.59	2.99	-0.53	5.95E-01	9.77E-01
Seq_000401 2	0.49	-2.61	2.97	-0.88	3.79E-01	9.77E-01
Seq_000405 0	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000405 3	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01

Seq_000406 0	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000406 2	0.37	1.84	2.98	0.62	5.36E-01	9.77E-01
Seq_000411 7	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000412 6	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000412 8	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000418 0	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000418 1	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000418 2	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000418 5	0.05	-0.03	2.99	-0.01	9.92E-01	9.94E-01
Seq_000424 5	0.03	-0.17	2.99	-0.06	9.56E-01	9.81E-01
Seq_000424 6	0.21	-1.44	2.79	-0.52	6.06E-01	9.77E-01
Seq_000424 8	0.32	-1.18	2.99	-0.39	6.94E-01	9.77E-01
Seq_000425 2	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000426 6	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000426 8	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000431 7	0.20	0.48	2.99	0.16	8.73E-01	9.77E-01

Seq_000434 2	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000441 1	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000451 5	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000452 7	0.21	-1.11	2.99	-0.37	7.09E-01	9.77E-01
Seq_000458 9	0.09	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000459 5	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000460 8	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000461 4	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000461 5	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000461 6	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000462 3	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000462 4	0.29	1.53	2.99	0.51	6.09E-01	9.77E-01
Seq_000470 8	0.30	-1.91	2.98	-0.64	5.21E-01	9.77E-01
Seq_000471 0	0.23	-1.53	2.99	-0.51	6.08E-01	9.77E-01
Seq_000471 4	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000474 4	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01

Seq_000474 5	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000474 7	0.13	0.38	2.99	0.13	8.98E-01	9.77E-01
Seq_000475 4	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000475 5	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000475 7	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000475 8	0.27	-1.73	2.98	-0.58	5.61E-01	9.77E-01
Seq_000475 9	0.27	1.40	2.99	0.47	6.39E-01	9.77E-01
Seq_000482 8	0.24	-1.59	2.99	-0.53	5.95E-01	9.77E-01
Seq_000482 9	0.24	-1.59	2.99	-0.53	5.95E-01	9.77E-01
Seq_000483 0	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000484 9	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000485 0	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000485 1	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000485 8	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000485 9	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000486 0	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01

Seq_000486 1	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000486 3	0.23	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000486 5	0.24	-1.59	2.99	-0.53	5.95E-01	9.77E-01
Seq_000487 0	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000487 1	0.24	1.26	2.99	0.42	6.74E-01	9.77E-01
Seq_000498 9	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000499 0	0.09	-0.39	2.99	-0.13	8.96E-01	9.77E-01
Seq_000499 4	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000499 6	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000499 7	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000502 0	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000502 1	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000502 4	0.22	-1.49	2.99	-0.50	6.19E-01	9.77E-01
Seq_000502 5	0.22	-1.49	2.99	-0.50	6.19E-01	9.77E-01
Seq_000502 6	0.22	-1.49	2.99	-0.50	6.19E-01	9.77E-01
Seq_000502 7	0.22	-1.49	2.99	-0.50	6.19E-01	9.77E-01

Seq_000503 1	0.21	1.11	2.99	0.37	7.09E-01	9.77E-01
Seq_000503 6	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000504 2	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000504 9	0.21	-1.44	2.99	-0.48	6.31E-01	9.77E-01
Seq_000512 5	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000512 9	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000515 7	0.15	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000516 0	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000516 1	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000516 2	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000516 3	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000516 4	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000517 4	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000517 5	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000517 6	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000517 9	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01

Seq_000518 0	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000518 1	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000518 2	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000518 3	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000518 6	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000518 8	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000519 2	0.19	-1.25	2.99	-0.42	6.75E-01	9.77E-01
Seq_000519 3	0.19	0.98	2.99	0.33	7.44E-01	9.77E-01
Seq_000539 2	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000539 4	0.19	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000539 5	0.19	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000539 6	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000540 0	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000540 4	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000540 5	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000540 6	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01

Seq_000543 1	0.13	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000543 4	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000543 6	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000543 7	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000544 6	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000544 9	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000545 1	0.20	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000545 2	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000545 5	0.16	0.20	2.99	0.07	9.46E-01	9.81E-01
Seq_000545 6	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000545 7	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000546 4	0.16	-1.07	2.99	-0.36	7.21E-01	9.77E-01
Seq_000546 5	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000546 6	0.16	0.84	2.99	0.28	7.79E-01	9.77E-01
Seq_000561 5	0.16	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000561 6	0.16	0.70	2.99	0.23	8.15E-01	9.77E-01

Seq_000561 7	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000561 8	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000562 5	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000562 6	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000562 7	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000565 1	0.11	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000566 0	0.06	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000566 5	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000566 7	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000566 8	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000566 9	0.13	0.70	2.99	0.23	8.15E-01	9.77E-01
Seq_000567 0	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000567 2	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000567 3	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000568 2	0.13	-0.89	2.99	-0.30	7.67E-01	9.77E-01
Seq_000605 1	0.12	0.56	2.99	0.19	8.50E-01	9.77E-01

Seq_000605 3	0.09	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000605 4	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000605 6	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000605 7	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000606 6	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000606 7	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000606 9	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000607 0	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000608 9	0.08	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000609 0	0.08	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000609 1	0.08	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000609 5	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000609 6	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000609 7	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000610 8	0.11	-0.07	2.99	-0.02	9.81E-01	9.92E-01
Seq_000611 7	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01

Seq_000611 8	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000611 9	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000612 1	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000612 3	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000612 4	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000613 0	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000613 6	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000613 8	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000613 9	0.11	-0.71	2.99	-0.24	8.13E-01	9.77E-01
Seq_000614 0	0.15	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000614 1	0.15	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000616 0	0.11	0.56	2.99	0.19	8.50E-01	9.77E-01
Seq_000640 5	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000640 6	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000641 7	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000642 0	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01

Seq_000642 3	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000644 7	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000644 8	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000645 0	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000645 9	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000646 0	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000646 1	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000648 8	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000648 9	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000649 2	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000649 3	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000649 4	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000649 6	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000649 7	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000649 8	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000649 9	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01

Seq_000650 3	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000650 4	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000650 5	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000650 6	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000650 8	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000651 9	0.09	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000652 0	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000652 2	0.11	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000652 3	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000652 4	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000654 0	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000654 1	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000654 3	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000654 4	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000654 5	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01
Seq_000654 6	0.08	-0.53	2.99	-0.18	8.60E-01	9.77E-01

Seq_000654 8	0.08	0.43	2.99	0.14	8.87E-01	9.77E-01
Seq_000721 7	0.06	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000721 8	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000722 8	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 2	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 3	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 4	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 5	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 7	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 8	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000723 9	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000724 9	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000725 6	0.04	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000725 7	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000726 9	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000727 0	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01

Seq_000729 2	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000729 3	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000729 7	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000729 8	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000729 9	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000730 0	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000730 1	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000730 2	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000730 3	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000730 8	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000731 5	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000731 6	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000731 7	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000731 8	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000732 0	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000732 2	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01

Seq_000732 3	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000733 3	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000733 4	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000733 7	0.06	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000733 8	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000735 3	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000735 5	0.05	-0.35	2.99	-0.12	9.08E-01	9.77E-01
Seq_000735 6	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000735 7	0.05	0.29	2.99	0.10	9.23E-01	9.77E-01
Seq_000735 9	0.02	-0.17	2.99	-0.06	9.56E-01	9.81E-01
Seq_000736 0	0.03	-0.17	2.99	-0.06	9.56E-01	9.81E-01
Seq_000736 1	0.03	-0.17	2.99	-0.06	9.56E-01	9.81E-01
Seq_000736 2	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000736 9	0.02	0.15	2.99	0.05	9.60E-01	9.81E-01
Seq_000737 4	0.03	-0.17	2.99	-0.06	9.56E-01	9.81E-01
Seq_000737 9	0.03	0.15	2.99	0.05	9.60E-01	9.81E-01

RSV	UC Flare Mean	UC Flare Median	UC Flare Present (n=21)	UC Remission Mean	UC Remissio n Median	UC Remission Present (n=16)	logfdr
Seq_000000 1	6.54E-02	5.24E-02	19	1.14E-01	6.44E-02	16	1.01E-02
Seq_000000 2	7.36E-02	1.11E-02	15	9.77E-02	4.96E-02	13	2.53E-03
Seq_000000 3	3.88E-02	1.03E-02	16	2.07E-02	5.57E-03	14	1.01E-02
Seq_000000 4	4.47E-02	2.18E-02	18	4.63E-02	4.47E-02	15	1.01E-02
Seq_000000 5	2.30E-02	1.15E-02	20	3.49E-02	2.15E-02	16	1.01E-02
Seq_000000 9	2.20E-02	7.43E-05	12	5.24E-02	3.73E-02	12	1.01E-02
Seq_000001 0	3.43E-02	0	9	4.32E-02	0	7	2.53E-03
Seq_000001 1	1.55E-02	3.08E-03	19	3.68E-02	5.67E-03	16	1.01E-02
Seq_000001 2	3.84E-02	1.19E-02	18	3.47E-02	2.88E-02	15	1.01E-02
Seq_000001 3	3.51E-02	3.23E-03	20	1.89E-02	4.00E-04	14	1.01E-02
Seq_000001 6	1.53E-02	0	5	9.55E-04	0	1	1.13E+01
Seq_000001 7	2.04E-02	2.63E-04	12	5.23E-04	0	6	3.15E-01
Seq_000001 8	1.39E-02	1.38E-03	15	1.11E-02	5.89E-04	12	1.01E-02
Seq_000001 9	2.07E-02	0	5	3.20E-03	0	3	1.01E-02

Seq_000002 4	1.87E-02	1.53E-03	15	9.26E-03	3.60E-03	13	1.01E-02
Seq_000002 5	3.47E-03	0	8	1.45E-02	0	7	1.01E-02
Seq_000002 6	1.35E-02	1.49E-03	14	1.95E-02	9.87E-03	12	1.01E-02
Seq_000002 7	1.41E-03	0	5	1.82E-05	0	1	1.13E+01
Seq_000002 8	3.20E-02	0	8	1.99E-03	3.68E-05	8	1.01E-02
Seq_000002 9	2.41E-02	0	3	2.08E-03	0	2	1.01E-02
Seq_000003 0	9.26E-03	1.52E-03	15	9.12E-03	4.27E-03	15	1.01E-02
Seq_000003 1	8.25E-03	2.95E-04	14	3.69E-03	4.71E-04	11	1.01E-02
Seq_000003 3	1.60E-02	3.61E-03	15	1.76E-02	9.54E-03	15	1.01E-02
Seq_000003 4	1.12E-02	2.64E-04	13	8.75E-03	4.59E-03	15	9.58E-03
Seq_000003 5	1.32E-02	1.12E-03	13	1.46E-02	4.82E-04	9	2.53E-03
Seq_000003 6	1.01E-02	4.73E-03	11	1.18E-02	5.89E-03	9	1.01E-02
Seq_000003 8	4.46E-04	0	3	2.01E-02	0	4	1.01E-02
Seq_000004 0	1.39E-02	8.50E-04	14	8.62E-03	3.88E-03	14	1.01E-02
Seq_000004 3	6.07E-03	0	9	1.79E-02	6.15E-03	13	1.01E-02
Seq_000004 9	4.94E-03	1.40E-04	13	1.08E-02	8.45E-03	11	1.01E-02

Seq_000005 1	5.61E-04	0	7	2.26E-03	0	5	8.33E-03
Seq_000005 3	9.01E-03	4.85E-04	17	9.01E-03	2.44E-03	15	1.01E-02
Seq_000005 5	4.44E-03	0	3	0	0	0	1.01E-02
Seq_000005 6	4.03E-03	0	5	9.89E-03	0	7	1.01E-02
Seq_000005 9	1.53E-02	0	5	3.03E-03	0	1	1.10E+01
Seq_000006 4	3.68E-03	0	5	6.48E-03	0	4	1.01E-02
Seq_000006 8	9.22E-03	0	7	2.86E-03	0	3	2.84E-01
Seq_000007 0	3.16E-03	9.72E-04	12	5.75E-03	2.69E-03	12	1.01E-02
Seq_000007 4	2.64E-03	0	5	4.03E-03	1.05E-04	8	1.01E-02
Seq_000007 5	1.04E-03	0	6	1.32E-03	9.33E-04	10	7.04E-03
Seq_000008 3	1.83E-03	0	4	6.57E-03	0	4	1.01E-02
Seq_000008 4	5.02E-04	0	3	6.66E-03	0	6	1.01E-02
Seq_000008 6	2.33E-03	0	7	4.97E-03	0	1	2.12E+00
Seq_000008 8	9.55E-04	0	2	2.37E-03	0	4	1.33E+01
Seq_000009 2	3.37E-03	0	4	1.64E-03	0	2	1.01E-02
Seq_000009 6	1.00E-03	0	2	8.77E-04	0	2	1.01E-02

Seq_000009 9	1.10E-03	0	8	7.88E-03	1.51E-03	10	1.01E-02
Seq_000010 2	8.32E-04	0	1	6.27E-06	0	1	1.01E-02
Seq_000010 9	3.29E-06	0	1	0	0	0	1.01E-02
Seq_000011 4	3.81E-04	0	2	2.37E-05	0	1	1.01E-02
Seq_000011 5	3.17E-03	0	5	1.76E-03	0	6	1.01E-02
Seq_000011 7	2.06E-03	0	9	3.97E-03	1.61E-03	11	1.01E-02
Seq_000011 8	1.25E-03	0	2	6.57E-05	0	2	1.01E-02
Seq_000012 0	7.89E-04	0	9	6.77E-03	3.07E-03	13	1.01E-02
Seq_000012 1	2.89E-03	0	5	2.64E-03	0	6	1.01E-02
Seq_000012 3	3.54E-03	0	6	1.17E-03	0	4	1.01E-02
Seq_000012 5	1.50E-03	0	2	0	0	0	1.01E-02
Seq_000012 6	3.15E-03	0	8	9.93E-05	0	4	1.01E-02
Seq_000013 5	4.13E-03	0	2	0	0	0	1.01E-02
Seq_000013 6	2.40E-04	0	4	5.98E-03	0	7	1.01E-02
Seq_000013 9	0	0	0	2.70E-04	0	2	1.01E-02
Seq_000014 0	8.58E-06	0	2	0	0	0	1.01E-02

Seq_000014 1	3.01E-03	0	8	1.50E-03	0	2	1.01E-02
Seq_000014 2	1.45E-03	0	10	1.43E-03	5.40E-04	10	2.53E-03
Seq_000014 6	1.18E-03	0	6	4.89E-03	0	6	1.01E-02
Seq_000014 8	1.46E-03	0	5	1.08E-03	0	5	1.01E-02
Seq_000014 9	9.66E-03	0	6	1.99E-04	0	4	1.51E-01
Seq_000015 4	8.55E-03	0	3	0	0	0	1.33E+01
Seq_000015 5	2.03E-03	0	7	2.94E-03	1.20E-03	11	1.01E-02
Seq_000015 7	8.49E-03	0	5	8.13E-05	0	3	1.01E-02
Seq_000015 9	2.92E-03	0	5	1.68E-03	7.33E-04	10	1.01E-02
Seq_000016 1	1.40E-03	2.73E-04	12	1.91E-03	3.68E-04	12	1.01E-02
Seq_000016 8	3.20E-03	0	2	3.86E-03	0	3	9.07E-03
Seq_000017 4	1.78E-03	0	5	1.81E-03	0	4	1.01E-02
Seq_000017 5	2.47E-03	0	6	3.07E-04	0	3	1.01E-02
Seq_000017 7	5.80E-04	0	7	5.22E-03	0	5	1.01E-02
Seq_000018 0	1.67E-03	0	10	1.41E-03	0	5	1.01E-02
Seq_000018 3	7.46E-04	0	5	4.16E-03	3.30E-04	9	1.01E-02

Seq_000018 6	6.95E-05	0	2	7.72E-03	0	3	1.01E-02
Seq_000018 9	5.60E-04	0	5	2.68E-05	0	1	1.01E-02
Seq_000019 4	2.56E-03	0	5	0	0	0	1.18E+01
Seq_000019 8	2.16E-04	0	5	5.73E-04	1.53E-04	10	1.01E-02
Seq_000020 4	3.90E-04	1.93E-04	13	2.79E-04	0	5	1.01E-02
Seq_000020 5	1.38E-03	0	4	7.30E-04	0	7	1.01E-02
Seq_000020 7	1.58E-04	0	6	1.27E-03	0	6	1.01E-02
Seq_000021 4	1.93E-04	0	1	1.06E-03	0	3	1.01E-02
Seq_000021 6	2.13E-03	0	7	1.31E-03	6.07E-04	12	1.01E-02
Seq_000021 8	1.26E-03	0	2	4.76E-03	0	3	1.01E-02
Seq_000021 9	3.91E-05	0	5	4.21E-03	2.95E-04	9	9.85E-01
Seq_000022 0	3.25E-03	0	2	0	0	0	1.01E-02
Seq_000022 1	2.27E-03	0	2	0	0	0	1.01E-02
Seq_000022 4	1.63E-03	0	7	1.91E-03	4.28E-04	10	1.01E-02
Seq_000022 8	9.90E-04	4.88E-04	14	1.53E-03	1.29E-03	13	1.01E-02
Seq_000023 3	2.71E-03	0	4	0	0	0	1.01E-02

Seq_000024 0	5.94E-05	0	4	3.00E-05	0	1	1.01E-02
Seq_000024 4	5.69E-04	0	3	1.07E-03	0	2	1.01E-02
Seq_000024 5	1.24E-04	0	2	2.34E-03	0	2	1.01E-02
Seq_000024 7	2.11E-04	0	4	1.72E-03	0	1	1.01E-02
Seq_000024 9	3.74E-04	0	2	3.14E-03	0	4	1.01E-02
Seq_000025 1	1.33E-03	0	7	2.07E-03	0	6	8.33E-03
Seq_000025 2	2.47E-04	0	6	2.57E-03	0	6	1.01E-02
Seq_000025 3	9.65E-04	0	7	0	0	0	1.01E-02
Seq_000026 0	6.63E-03	0	3	2.05E-05	0	1	1.01E-02
Seq_000026 4	2.61E-03	0	2	0	0	0	1.01E-02
Seq_000026 6	1.11E-04	0	2	0	0	0	1.01E-02
Seq_000026 7	3.30E-03	0	4	8.87E-05	0	2	1.13E+01
Seq_000027 6	3.91E-04	0	7	2.23E-03	0	4	1.01E-02
Seq_000028 8	1.09E-04	0	2	4.44E-05	0	2	1.01E-02
Seq_000029 1	4.95E-06	0	1	3.00E-03	0	2	1.01E-02
Seq_000029 2	8.62E-04	0	5	2.18E-03	4.06E-04	12	1.01E-02

Seq_000029 6	3.11E-04	0	8	6.61E-04	2.83E-05	8	1.01E-02
Seq_000030 4	1.64E-04	0	5	2.24E-03	0	6	1.01E-02
Seq_000030 7	5.66E-06	0	1	2.85E-03	0	2	1.01E-02
Seq_000031 0	3.06E-04	0	7	1.46E-03	6.35E-04	12	1.01E-02
Seq_000031 5	1.05E-03	0	2	6.40E-04	0	4	1.01E-02
Seq_000031 6	4.79E-04	0	2	3.06E-03	0	1	1.01E-02
Seq_000031 7	1.89E-04	0	2	0	0	0	1.01E-02
Seq_000031 8	1.97E-04	0	2	2.73E-04	0	5	1.01E-02
Seq_000031 9	5.97E-04	0	3	6.60E-04	2.02E-04	10	1.01E-02
Seq_000033 1	5.56E-04	0	4	1.13E-04	0	5	1.01E-02
Seq_000033 5	2.56E-05	0	2	2.52E-03	0	5	1.01E-02
Seq_000033 9	1.50E-03	0	2	1.65E-04	0	1	1.01E-02
Seq_000034 1	1.79E-03	0	6	5.93E-04	0	5	1.01E-02
Seq_000034 6	1.37E-03	0	5	0	0	0	1.01E-02
Seq_000034 8	3.65E-04	0	1	3.10E-04	0	2	1.01E-02
Seq_000035 0	4.45E-04	0	2	0	0	0	1.01E-02

Seq_000035 1	4.42E-06	0	1	0	0	0	1.01E-02
Seq_000035 3	1.04E-05	0	2	1.10E-03	0	3	1.01E-02
Seq_000035 6	2.73E-03	0	5	6.29E-05	0	4	1.01E-02
Seq_000035 8	1.73E-04	0	2	1.38E-03	0	2	1.01E-02
Seq_000036 1	7.19E-04	0	7	5.51E-05	0	2	1.01E-02
Seq_000036 2	8.58E-04	0	4	2.95E-04	0	2	1.01E-02
Seq_000036 8	1.97E-03	0	4	4.98E-05	0	3	1.01E-02
Seq_000037 2	8.45E-04	0	10	2.12E-04	1.62E-04	12	1.01E-02
Seq_000037 7	1.98E-04	0	2	4.24E-05	0	1	1.01E-02
Seq_000038 1	1.14E-03	0	2	5.29E-04	0	2	1.01E-02
Seq_000039 0	3.16E-04	0	5	4.44E-05	0	3	1.01E-02
Seq_000039 2	9.23E-04	0	5	1.19E-03	0	4	1.01E-02
Seq_000039 6	1.96E-04	0	2	6.34E-04	0	5	1.01E-02
Seq_000039 7	1.33E-03	0	5	1.42E-03	0	4	5.80E-03
Seq_000040 1	3.62E-04	0	4	5.29E-04	0	4	1.01E-02
Seq_000040 3	4.14E-04	0	4	1.94E-03	0	4	1.01E-02

Seq_000040 5	1.37E-03	0	3	0	0	0	1.01E-02
Seq_000040 9	2.42E-05	0	1	9.80E-05	0	5	1.01E-02
Seq_000041 0	2.06E-04	0	6	8.67E-04	2.22E-04	11	1.01E-02
Seq_000041 4	0	0	0	2.79E-03	0	3	1.30E+01
Seq_000042 8	6.14E-05	0	1	2.31E-03	0	5	1.01E-02
Seq_000043 1	0	0	0	2.78E-03	0	2	1.01E-02
Seq_000043 3	4.95E-04	0	6	7.31E-04	0	7	1.01E-02
Seq_000045 2	1.96E-04	0	5	8.05E-04	0	5	1.01E-02
Seq_000045 6	3.44E-04	0	3	0	0	0	1.01E-02
Seq_000045 7	1.09E-03	0	2	6.04E-04	0	1	1.01E-02
Seq_000045 8	4.61E-04	0	6	9.86E-05	0	6	1.01E-02
Seq_000045 9	1.64E-04	0	3	0	0	0	1.01E-02
Seq_000046 2	6.68E-05	0	1	1.20E-03	0	3	1.01E-02
Seq_000046 3	4.40E-04	0	3	8.97E-05	0	2	1.01E-02
Seq_000046 4	3.09E-03	0	6	0	0	0	1.01E-02
Seq_000046 7	4.07E-04	0	5	5.50E-04	0	7	1.01E-02

Seq_000047 2	5.87E-04	0	5	0	0	0	1.01E-02
Seq_000048 3	5.29E-04	0	6	4.62E-05	0	2	1.01E-02
Seq_000049 3	1.65E-04	0	5	2.77E-04	0	3	1.01E-02
Seq_000049 4	1.16E-04	0	3	6.86E-05	0	3	1.01E-02
Seq_000050 2	3.88E-04	0	4	3.67E-04	0	2	1.01E-02
Seq_000051 0	3.48E-04	0	4	2.06E-04	0	4	7.04E-03
Seq_000051 7	9.06E-05	0	4	6.98E-05	0	1	1.01E-02
Seq_000052 7	6.42E-05	0	5	1.58E-04	0	7	1.01E-02
Seq_000053 2	7.22E-04	0	7	3.93E-04	0	5	1.01E-02
Seq_000053 6	1.06E-05	0	1	1.35E-04	0	2	1.01E-02
Seq_000053 7	1.65E-04	0	5	3.73E-04	0	3	1.01E-02
Seq_000053 8	2.00E-04	0	2	0	0	0	8.33E-03
Seq_000054 2	4.69E-04	0	6	2.63E-04	0	4	1.01E-02
Seq_000054 4	7.00E-05	0	2	5.71E-05	0	1	1.01E-02
Seq_000054 8	4.72E-05	0	1	4.15E-04	0	4	1.01E-02
Seq_000054 9	2.34E-04	0	4	7.19E-05	0	3	1.01E-02

Seq_000055 7	2.23E-04	0	3	1.03E-04	0	4	1.01E-02
Seq_000055 9	4.64E-04	0	5	6.41E-04	0	7	1.01E-02
Seq_000056 1	9.77E-05	0	3	6.77E-04	0	6	1.01E-02
Seq_000056 4	0	0	0	9.40E-06	0	1	1.01E-02
Seq_000057 2	5.31E-04	0	4	6.20E-05	0	1	1.01E-02
Seq_000057 6	4.70E-05	0	6	4.60E-06	0	1	1.01E-02
Seq_000058 1	1.18E-04	0	3	2.88E-04	0	6	1.01E-02
Seq_000058 9	1.64E-03	0	2	0	0	0	1.01E-02
Seq_000060 4	1.20E-04	0	5	1.29E-04	0	3	1.01E-02
Seq_000061 5	5.48E-05	0	4	1.99E-04	0	4	1.01E-02
Seq_000061 9	1.50E-04	0	4	4.20E-04	0	6	1.01E-02
Seq_000062 3	3.28E-04	0	3	0	0	0	1.01E-02
Seq_000062 6	2.95E-05	0	4	0	0	0	1.01E-02
Seq_000064 0	1.07E-04	0	2	1.72E-04	0	1	1.01E-02
Seq_000064 5	5.96E-05	0	3	2.18E-04	0	7	1.01E-02
Seq_000064 6	6.70E-04	0	7	6.21E-05	0	2	1.01E-02

Seq_000065 1	2.40E-04	0	4	2.00E-04	0	5	9.13E-03
Seq_000065 4	1.42E-04	0	4	1.83E-04	0	2	2.53E-03
Seq_000065 7	1.49E-05	0	1	1.51E-03	0	4	1.01E-02
Seq_000066 0	2.67E-04	0	5	0	0	0	1.01E-02
Seq_000066 1	0	0	0	9.94E-04	0	3	1.01E-02
Seq_000066 6	4.05E-04	0	3	0	0	0	1.01E-02
Seq_000066 8	3.27E-06	0	1	0	0	0	1.01E-02
Seq_000067 1	2.46E-04	0	5	7.28E-04	0	2	1.01E-02
Seq_000067 3	5.10E-04	0	5	0	0	0	1.01E-02
Seq_000067 6	3.89E-04	0	3	3.59E-04	0	2	1.01E-02
Seq_000067 9	4.23E-05	0	2	3.86E-05	0	3	1.01E-02
Seq_000068 3	1.44E-04	0	2	4.68E-04	0	2	1.01E-02
Seq_000069 1	4.13E-05	0	2	3.56E-04	0	5	1.01E-02
Seq_000070 4	3.11E-05	0	2	2.62E-04	0	1	1.01E-02
Seq_000070 5	7.53E-06	0	1	5.22E-06	0	1	1.01E-02
Seq_000070 8	4.61E-04	0	8	8.38E-05	7.68E-06	8	1.01E-02

Seq_000071 0	3.94E-04	0	2	0	0	0	1.01E-02
Seq_000071 2	4.03E-04	0	4	3.34E-05	0	1	1.01E-02
Seq_000072 0	6.57E-05	0	8	1.68E-04	6.41E-05	10	1.01E-02
Seq_000073 5	1.16E-04	0	9	1.49E-04	0	6	8.33E-03
Seq_000074 0	2.09E-04	0	2	1.76E-03	0	1	1.01E-02
Seq_000074 3	7.21E-05	0	5	1.31E-04	0	5	8.33E-03
Seq_000075 3	0	0	0	2.03E-04	0	3	1.01E-02
Seq_000075 7	0	0	0	6.27E-04	0	2	1.01E-02
Seq_000076 0	1.28E-04	0	2	3.65E-04	0	1	1.01E-02
Seq_000076 5	2.64E-05	0	2	0	0	0	1.01E-02
Seq_000077 1	1.13E-04	0	2	3.76E-04	0	7	1.01E-02
Seq_000077 8	1.38E-04	0	2	0	0	0	1.01E-02
Seq_000078 0	5.71E-05	0	2	5.08E-04	0	3	1.01E-02
Seq_000078 1	4.41E-04	0	2	0	0	0	1.01E-02
Seq_000078 5	8.99E-05	0	7	2.74E-04	1.19E-04	8	1.01E-02
Seq_000079 2	4.83E-04	0	3	0	0	0	1.01E-02

Seq_000079 4	4.77E-05	0	2	1.77E-04	0	3	1.01E-02
Seq_000080 8	2.12E-06	0	1	3.55E-04	0	1	1.01E-02
Seq_000081 2	6.57E-05	0	4	1.40E-04	0	4	1.01E-02
Seq_000081 4	1.69E-05	0	4	4.78E-05	0	3	5.05E-03
Seq_000081 5	3.61E-04	0	2	0	0	0	1.01E-02
Seq_000082 9	2.98E-05	0	1	3.80E-05	0	2	1.01E-02
Seq_000083 1	1.75E-04	0	3	0	0	0	1.01E-02
Seq_000084 3	3.08E-04	0	2	0	0	0	1.01E-02
Seq_000084 4	1.31E-04	0	3	0	0	0	1.01E-02
Seq_000084 9	2.26E-04	0	1	4.33E-04	0	2	1.01E-02
Seq_000085 1	1.15E-04	0	2	2.02E-04	0	3	1.01E-02
Seq_000086 5	1.36E-04	0	3	1.29E-05	0	1	1.01E-02
Seq_000086 8	0	0	0	1.26E-04	0	2	1.01E-02
Seq_000087 8	1.13E-05	0	1	5.71E-04	0	5	1.01E-02
Seq_000087 9	2.29E-04	0	2	6.13E-05	0	1	1.01E-02
Seq_000088 0	2.59E-04	0	2	2.36E-04	0	3	1.01E-02

Seq_000088 5	0	0	0	2.61E-05	0	2	1.01E-02
Seq_000088 9	2.15E-04	0	8	1.25E-05	0	2	1.01E-02
Seq_000089 4	6.13E-05	0	4	0	0	0	1.01E-02
Seq_000089 9	6.88E-04	0	1	6.30E-06	0	1	1.01E-02
Seq_000090 0	9.32E-05	0	2	0	0	0	1.01E-02
Seq_000090 9	2.34E-04	0	2	2.05E-05	0	1	1.01E-02
Seq_000091 0	4.68E-06	0	1	0	0	0	1.01E-02
Seq_000091 5	6.37E-05	0	4	0	0	0	1.01E-02
Seq_000092 8	1.45E-04	0	3	0	0	0	1.01E-02
Seq_000093 1	1.88E-04	0	4	1.38E-04	0	4	1.01E-02
Seq_000093 4	8.78E-06	0	1	6.02E-04	0	1	1.01E-02
Seq_000093 6	3.34E-05	0	2	1.15E-04	0	7	1.01E-02
Seq_000093 8	5.25E-04	0	3	1.46E-05	0	1	1.01E-02
Seq_000094 8	3.11E-04	0	4	1.56E-04	0	4	1.01E-02
Seq_000096 6	3.33E-05	0	2	6.21E-05	0	2	1.01E-02
Seq_000097 3	3.98E-05	0	4	4.18E-05	0	2	1.01E-02

Seq_000097 5	1.01E-04	0	3	3.97E-05	0	1	1.01E-02
Seq_000097 9	3.44E-05	0	2	3.91E-05	0	1	1.01E-02
Seq_000098 4	1.29E-04	0	9	6.68E-05	3.34E-05	8	1.01E-02
Seq_000099 1	2.52E-04	0	6	8.45E-06	0	2	1.01E-02
Seq_000099 8	9.33E-06	0	2	7.61E-05	0	2	1.01E-02
Seq_000101 2	4.44E-05	0	5	1.03E-05	0	1	1.01E-02
Seq_000102 1	1.63E-05	0	1	8.71E-05	0	2	1.01E-02
Seq_000102 3	4.33E-05	0	3	0	0	0	1.01E-02
Seq_000103 0	0	0	0	1.35E-03	0	2	1.01E-02
Seq_000104 0	4.93E-05	0	1	1.55E-04	0	2	1.01E-02
Seq_000104 2	0	0	0	1.35E-04	0	2	1.01E-02
Seq_000105 1	6.23E-05	0	2	0	0	0	1.01E-02
Seq_000105 2	2.31E-04	0	2	7.15E-05	0	1	1.01E-02
Seq_000105 5	2.80E-04	0	2	0	0	0	1.01E-02
Seq_000106 2	9.43E-05	0	3	4.82E-05	0	3	1.01E-02
Seq_000108 4	6.34E-05	0	3	2.16E-04	2.89E-05	8	1.01E-02

Seq_000108 8	6.70E-05	0	1	8.45E-05	0	3	1.01E-02
Seq_000109 2	2.57E-04	0	5	1.02E-05	0	2	1.01E-02
Seq_000109 6	0	0	0	1.33E-04	0	2	1.01E-02
Seq_000111 2	1.89E-04	0	3	0	0	0	1.01E-02
Seq_000111 6	2.55E-05	0	4	2.02E-04	0	6	1.01E-02
Seq_000111 8	4.24E-06	0	1	2.69E-05	0	2	1.01E-02
Seq_000112 8	6.26E-05	0	4	1.34E-04	0	6	1.01E-02
Seq_000112 9	2.26E-04	0	3	0	0	0	1.01E-02
Seq_000113 5	2.80E-05	0	2	0	0	0	1.01E-02
Seq_000113 8	1.49E-05	0	2	1.66E-04	0	6	1.01E-02
Seq_000114 4	1.47E-04	0	5	4.76E-05	0	4	1.01E-02
Seq_000115 5	2.32E-04	0	2	0	0	0	1.01E-02
Seq_000116 0	0	0	0	4.95E-06	0	1	1.01E-02
Seq_000116 3	1.45E-04	0	2	0	0	0	1.01E-02
Seq_000117 3	2.78E-04	0	3	0	0	0	1.01E-02
Seq_000118 0	3.47E-04	0	2	0	0	0	1.01E-02

Seq_000119 1	9.63E-06	0	2	0	0	0	1.01E-02
Seq_000119 4	2.61E-04	0	3	0	0	0	1.01E-02
Seq_000121 2	6.82E-05	0	5	4.07E-05	0	4	1.01E-02
Seq_000122 1	0	0	0	5.19E-05	0	2	1.01E-02
Seq_000123 1	2.30E-05	0	4	0	0	0	1.01E-02
Seq_000123 5	3.77E-05	0	2	2.35E-04	0	6	1.01E-02
Seq_000124 1	0	0	0	4.87E-04	0	4	1.01E-02
Seq_000125 2	7.69E-06	0	1	0	0	0	1.01E-02
Seq_000126 5	1.42E-04	0	1	1.08E-05	0	1	1.01E-02
Seq_000128 4	5.16E-05	0	2	0	0	0	1.01E-02
Seq_000128 5	7.00E-05	0	5	0	0	0	1.01E-02
Seq_000128 9	1.38E-05	0	1	1.68E-04	0	4	1.01E-02
Seq_000130 3	2.37E-05	0	3	0	0	0	1.01E-02
Seq_000131 0	1.81E-04	0	3	0	0	0	1.01E-02
Seq_000132 0	1.14E-04	0	4	3.21E-05	0	2	2.53E-03
Seq_000133 0	3.89E-05	0	3	5.39E-05	0	1	1.01E-02

Seq_000133 4	5.71E-05	0	1	6.62E-05	0	3	1.01E-02
Seq_000133 8	1.44E-05	0	2	1.24E-04	0	4	1.01E-02
Seq_000133 9	1.48E-04	0	4	2.40E-05	0	1	1.01E-02
Seq_000134 5	1.93E-05	0	2	0	0	0	1.01E-02
Seq_000134 6	0	0	0	2.03E-04	0	3	1.01E-02
Seq_000134 7	2.59E-05	0	2	8.42E-06	0	1	8.33E-03
Seq_000135 2	0	0	0	2.27E-05	0	2	1.01E-02
Seq_000135 3	8.19E-05	0	5	3.68E-06	0	1	1.01E-02
Seq_000135 8	6.23E-05	0	4	1.09E-05	0	1	1.01E-02
Seq_000136 9	1.49E-05	0	1	4.22E-04	0	1	1.01E-02
Seq_000137 3	3.65E-04	0	2	0	0	0	1.01E-02
Seq_000138 4	2.11E-05	0	1	1.53E-04	0	3	1.01E-02
Seq_000141 1	2.21E-06	0	1	6.79E-05	0	1	1.01E-02
Seq_000142 3	1.10E-05	0	1	1.03E-04	0	5	1.01E-02
Seq_000142 7	2.83E-06	0	1	0	0	0	1.01E-02
Seq_000143 3	5.38E-05	0	2	1.07E-05	0	1	1.01E-02

Seq_000143 9	2.29E-05	0	2	1.79E-05	0	2	1.01E-02
Seq_000144 4	6.12E-05	0	4	2.58E-05	0	2	1.01E-02
Seq_000144 6	0	0	0	2.06E-04	0	2	1.01E-02
Seq_000144 8	1.23E-04	0	2	7.79E-05	0	2	1.01E-02
Seq_000145 9	1.87E-04	0	2	0	0	0	1.01E-02
Seq_000146 4	1.93E-04	0	2	8.98E-06	0	1	1.01E-02
Seq_000147 1	1.00E-04	0	1	5.37E-05	0	2	1.01E-02
Seq_000148 7	6.02E-07	0	1	4.31E-05	0	6	1.01E-02
Seq_000148 8	3.46E-05	0	2	0	0	0	1.01E-02
Seq_000150 7	4.48E-05	0	1	2.76E-06	0	1	1.01E-02
Seq_000151 1	2.00E-05	0	3	1.29E-04	0	6	1.01E-02
Seq_000153 4	2.09E-05	0	6	9.39E-05	0	7	1.01E-02
Seq_000153 5	1.49E-05	0	1	0	0	0	1.01E-02
Seq_000156 0	1.90E-04	0	2	0	0	0	1.01E-02
Seq_000156 7	1.00E-04	0	1	1.01E-04	0	2	1.01E-02
Seq_000157 6	4.24E-06	0	1	1.47E-04	0	4	1.01E-02

Seq_000158 0	2.53E-04	0	2	0	0	0	1.01E-02
Seq_000158 2	1.72E-05	0	3	0	0	0	1.01E-02
Seq_000160 2	6.85E-05	0	3	0	0	0	1.01E-02
Seq_000161 1	0	0	0	2.26E-04	0	4	1.01E-02
Seq_000165 0	5.79E-05	0	2	6.36E-06	0	1	1.01E-02
Seq_000165 4	0	0	0	4.08E-06	0	1	1.01E-02
Seq_000166 6	1.07E-05	0	2	2.25E-05	0	1	1.01E-02
Seq_000166 7	5.42E-06	0	1	3.66E-05	0	3	1.01E-02
Seq_000167 0	2.10E-05	0	3	6.58E-05	0	3	1.01E-02
Seq_000167 3	4.23E-05	0	1	8.42E-06	0	1	1.01E-02
Seq_000168 2	2.85E-05	0	1	2.28E-04	0	3	1.01E-02
Seq_000168 3	1.02E-04	0	3	1.09E-05	0	1	1.01E-02
Seq_000168 8	1.72E-05	0	2	0	0	0	1.01E-02
Seq_000169 5	3.35E-05	0	2	5.42E-05	0	2	1.01E-02
Seq_000170 5	2.83E-06	0	1	0	0	0	1.01E-02
Seq_000171 9	5.41E-06	0	1	0	0	0	1.01E-02

Seq_000173 0	0	0	0	1.34E-04	0	2	1.01E-02
Seq_000173 6	3.78E-05	0	3	0	0	0	1.01E-02
Seq_000174 0	1.42E-05	0	3	4.08E-06	0	1	1.01E-02
Seq_000174 4	8.30E-06	0	2	2.34E-05	0	1	1.01E-02
Seq_000175 7	6.55E-06	0	1	8.08E-05	0	4	1.01E-02
Seq_000176 3	5.77E-05	0	2	0	0	0	1.01E-02
Seq_000177 2	8.99E-05	0	2	0	0	0	1.01E-02
Seq_000177 4	9.54E-05	0	3	0	0	0	1.01E-02
Seq_000178 2	5.00E-05	0	2	0	0	0	1.01E-02
Seq_000178 8	8.13E-05	0	4	0	0	0	1.01E-02
Seq_000179 4	5.32E-05	0	2	0	0	0	1.01E-02
Seq_000180 6	6.03E-05	0	2	1.79E-05	0	2	1.01E-02
Seq_000181 8	1.42E-06	0	1	4.51E-05	0	4	1.01E-02
Seq_000183 4	0	0	0	1.20E-04	0	4	1.01E-02
Seq_000184 4	5.40E-06	0	2	8.44E-05	0	5	1.01E-02
Seq_000186 2	7.03E-06	0	2	0	0	0	1.01E-02

Seq_000186 8	2.59E-05	0	2	0	0	0	1.01E-02
Seq_000190 5	7.49E-06	0	2	4.54E-06	0	1	1.01E-02
Seq_000190 9	4.98E-06	0	1	1.72E-05	0	1	1.01E-02
Seq_000193 7	0	0	0	1.52E-04	0	2	1.01E-02
Seq_000194 0	4.30E-05	0	2	0	0	0	1.01E-02
Seq_000194 1	4.23E-05	0	2	0	0	0	1.01E-02
Seq_000195 4	0	0	0	8.55E-06	0	1	1.01E-02
Seq_000195 8	1.15E-05	0	3	5.03E-05	0	4	1.01E-02
Seq_000197 2	4.05E-05	0	4	5.80E-05	0	3	1.01E-02
Seq_000197 3	2.48E-05	0	3	4.89E-05	0	2	1.01E-02
Seq_000198 0	0	0	0	1.06E-05	0	1	1.01E-02
Seq_000199 5	2.09E-05	0	1	2.27E-05	0	2	1.01E-02
Seq_000202 1	5.60E-05	0	2	0	0	0	1.01E-02
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Seq_000206 4	4.57E-05	0	4	1.62E-05	0	3	1.01E-02
Seq_000206 6	2.68E-05	0	4	0	0	0	1.01E-02

Seq_0002069	2.90E-05	0	4	1.59E-05	0	2	1.01E-02
Seq_0002075	2.53E-06	0	1	4.03E-05	0	3	1.01E-02
Seq_0002082	5.55E-05	0	1	4.95E-06	0	1	1.01E-02
Seq_0002090	7.64E-06	0	1	2.03E-05	0	3	1.01E-02
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Seq_0002139	0	0	0	4.80E-06	0	1	1.01E-02
Seq_0002143	2.15E-05	0	2	4.60E-06	0	1	1.01E-02
Seq_0002149	1.59E-05	0	1	3.82E-05	0	2	1.01E-02
Seq_0002153	5.06E-05	0	3	0	0	0	1.01E-02
Seq_0002168	9.28E-06	0	2	4.56E-05	0	4	1.01E-02
Seq_0002172	2.03E-06	0	1	1.34E-04	0	1	1.01E-02
Seq_0002181	3.92E-05	0	2	0	0	0	1.01E-02
Seq_0002185	3.36E-05	0	2	0	0	0	1.01E-02
Seq_0002193	8.89E-06	0	2	6.41E-05	0	4	1.01E-02
Seq_0002194	7.23E-05	0	1	5.56E-05	0	2	1.01E-02
Seq_0002212	3.74E-05	0	2	0	0	0	1.01E-02

Seq_000223 0	5.36E-06	0	1	5.02E-05	0	2	1.01E-02
Seq_000223 3	1.25E-05	0	2	9.40E-06	0	1	1.01E-02
Seq_000223 4	4.32E-05	0	3	0	0	0	1.01E-02
Seq_000224 1	7.44E-06	0	2	1.34E-05	0	3	1.01E-02
Seq_000224 3	8.07E-05	0	3	0	0	0	1.01E-02
Seq_000225 4	4.88E-06	0	1	8.30E-05	0	5	1.01E-02
Seq_000225 5	2.17E-06	0	1	3.33E-05	0	4	1.01E-02
Seq_000228 6	0	0	0	1.88E-05	0	2	1.01E-02
Seq_000228 8	6.61E-05	0	3	0	0	0	1.01E-02
Seq_000230 3	1.95E-05	0	3	2.46E-05	0	3	1.01E-02
Seq_000232 2	0	0	0	2.91E-05	0	2	1.01E-02
Seq_000236 4	7.07E-07	0	1	0	0	0	8.33E-03
Seq_000237 5	3.36E-06	0	2	1.61E-05	0	2	8.33E-03
Seq_000237 7	0	0	0	7.47E-05	0	2	1.01E-02
Seq_000238 9	0	0	0	6.35E-06	0	1	1.01E-02
Seq_000240 0	1.34E-05	0	3	1.96E-05	0	3	1.01E-02

Seq_000240 1	2.99E-06	0	1	4.18E-05	0	2	6.20E-03
Seq_000241 0	1.05E-04	0	2	0	0	0	1.01E-02
Seq_000241 3	3.54E-06	0	1	1.94E-05	0	5	1.01E-02
Seq_000242 6	1.08E-05	0	2	0	0	0	1.01E-02
Seq_000243 4	0	0	0	1.32E-05	0	1	1.01E-02
Seq_000243 5	3.62E-05	0	2	0	0	0	1.01E-02
Seq_000243 8	0	0	0	1.26E-05	0	1	1.01E-02
Seq_000244 3	8.13E-07	0	1	2.15E-05	0	4	1.01E-02
Seq_000246 2	2.10E-05	0	2	0	0	0	1.01E-02
Seq_000247 0	0	0	0	1.32E-05	0	1	1.01E-02
Seq_000248 0	7.38E-06	0	2	0	0	0	1.01E-02
Seq_000249 5	0	0	0	3.36E-06	0	1	1.01E-02
Seq_000251 2	2.75E-05	0	3	0	0	0	1.01E-02
Seq_000251 9	5.66E-06	0	1	2.64E-05	0	1	1.01E-02
Seq_000252 9	4.17E-05	0	2	0	0	0	1.01E-02
Seq_000253 3	6.63E-06	0	1	4.19E-05	0	3	1.01E-02

Seq_000254 4	0	0	0	9.01E-05	0	2	1.01E-02
Seq_000256 5	2.47E-06	0	1	0	0	0	1.01E-02
Seq_000257 2	0	0	0	9.01E-06	0	2	1.01E-02
Seq_000258 7	0	0	0	2.24E-05	0	2	1.01E-02
Seq_000260 5	6.50E-06	0	1	0	0	0	1.01E-02
Seq_000261 2	1.13E-05	0	2	0	0	0	1.01E-02
Seq_000261 3	0	0	0	1.11E-05	0	2	1.01E-02
Seq_000267 7	2.98E-05	0	3	7.93E-06	0	1	1.01E-02
Seq_000267 8	4.47E-06	0	1	0	0	0	1.01E-02
Seq_000271 3	4.48E-06	0	1	1.57E-05	0	2	1.01E-02
Seq_000271 4	6.69E-06	0	1	0	0	0	1.01E-02
Seq_000271 6	4.45E-06	0	1	2.69E-05	0	1	1.01E-02
Seq_000273 6	0	0	0	2.67E-05	0	2	1.01E-02
Seq_000274 3	1.42E-06	0	1	1.20E-05	0	1	1.01E-02
Seq_000274 5	4.47E-06	0	1	0	0	0	1.01E-02
Seq_000275 9	0	0	0	3.42E-05	0	2	1.01E-02

Seq_000276 0	3.35E-05	0	2	0	0	0	1.01E-02
Seq_000279 7	0	0	0	9.25E-06	0	1	1.01E-02
Seq_000279 9	1.45E-05	0	3	0	0	0	1.01E-02
Seq_000280 5	4.94E-05	0	2	0	0	0	1.01E-02
Seq_000282 9	0	0	0	1.84E-06	0	1	1.01E-02
Seq_000284 6	1.53E-05	0	2	2.87E-05	0	2	1.01E-02
Seq_000285 6	5.69E-06	0	1	2.84E-05	0	2	1.01E-02
Seq_000287 4	1.02E-05	0	2	4.32E-06	0	1	1.01E-02
Seq_000287 6	8.81E-06	0	2	0	0	0	1.01E-02
Seq_000289 4	0	0	0	1.80E-05	0	1	1.01E-02
Seq_000289 7	0	0	0	5.40E-06	0	1	1.01E-02
Seq_000291 0	2.99E-06	0	1	0	0	0	1.01E-02
Seq_000292 4	5.66E-06	0	1	0	0	0	1.01E-02
Seq_000292 5	1.22E-05	0	2	0	0	0	1.01E-02
Seq_000293 6	2.92E-06	0	2	1.92E-06	0	1	8.33E-03
Seq_000293 7	0	0	0	3.16E-05	0	4	1.01E-02

Seq_000293 8	0	0	0	1.80E-05	0	1	1.01E-02
Seq_000293 9	6.02E-06	0	1	0	0	0	1.01E-02
Seq_000294 6	6.69E-06	0	1	5.71E-06	0	1	7.20E-03
Seq_000294 8	4.52E-05	0	2	0	0	0	1.01E-02
Seq_000295 9	1.99E-05	0	2	0	0	0	1.01E-02
Seq_000297 4	0	0	0	8.24E-06	0	1	1.01E-02
Seq_000303 4	0	0	0	3.41E-05	0	2	1.01E-02
Seq_000303 5	7.23E-07	0	1	1.04E-05	0	2	1.01E-02
Seq_000303 6	0	0	0	8.25E-06	0	2	1.01E-02
Seq_000306 4	5.31E-06	0	1	0	0	0	1.01E-02
Seq_000306 7	3.95E-05	0	2	0	0	0	1.01E-02
Seq_000308 8	1.49E-05	0	1	3.87E-05	0	2	1.01E-02
Seq_000309 7	1.89E-05	0	2	0	0	0	1.01E-02
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Seq_000310 0	1.25E-05	0	1	0	0	0	1.01E-02
Seq_000312 2	0	0	0	2.99E-05	0	4	1.01E-02

Seq_0003123	7.23E-07	0	1	4.81E-06	0	1	1.01E-02
Seq_0003124	0	0	0	4.63E-05	0	4	1.01E-02
Seq_0003125	3.13E-06	0	1	0	0	0	1.01E-02
Seq_0003128	0	0	0	8.36E-06	0	1	1.01E-02
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Seq_0003177	0	0	0	3.33E-05	0	2	1.01E-02
Seq_0003179	3.17E-05	0	1	6.82E-06	0	1	1.01E-02
Seq_0003189	0	0	0	4.13E-06	0	1	1.01E-02
Seq_0003191	4.70E-06	0	1	0	0	0	1.01E-02
Seq_0003210	2.22E-05	0	2	0	0	0	1.01E-02
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Seq_0003251	5.31E-06	0	1	1.07E-05	0	2	1.01E-02
Seq_0003252	6.29E-06	0	2	5.39E-06	0	1	1.01E-02
Seq_0003256	7.14E-06	0	2	0	0	0	1.01E-02
Seq_0003258	2.60E-05	0	1	2.70E-06	0	1	1.01E-02
Seq_0003267	0	0	0	3.20E-06	0	1	1.01E-02

Seq_000331 7	3.25E-06	0	1	3.54E-06	0	1	1.01E-02
Seq_000333 6	8.96E-07	0	1	7.93E-06	0	1	1.01E-02
Seq_000333 8	6.50E-06	0	1	0	0	0	1.01E-02
Seq_000333 9	0	0	0	1.58E-05	0	1	1.01E-02
Seq_000337 7	7.23E-07	0	1	0	0	0	1.01E-02
Seq_000340 7	2.20E-05	0	2	0	0	0	1.01E-02
Seq_000341 9	0	0	0	2.48E-06	0	1	1.01E-02
Seq_000342 5	4.07E-07	0	1	0	0	0	8.33E-03
Seq_000349 6	2.39E-06	0	1	8.49E-06	0	1	1.01E-02
Seq_000351 7	3.61E-06	0	1	0	0	0	1.01E-02
Seq_000355 4	4.74E-07	0	1	1.20E-06	0	1	2.53E-03
Seq_000355 6	3.32E-06	0	1	0	0	0	1.01E-02
Seq_000355 9	2.03E-05	0	2	0	0	0	1.01E-02
Seq_000365 0	7.07E-07	0	1	3.56E-06	0	2	1.01E-02
Seq_000365 4	3.46E-06	0	1	0	0	0	1.01E-02
Seq_000365 5	0	0	0	6.44E-06	0	1	1.01E-02

Seq_000365 6	7.90E-06	0	1	0	0	0	1.01E-02
Seq_000368 1	7.31E-06	0	1	0	0	0	1.01E-02
Seq_000370 8	9.49E-07	0	1	3.61E-06	0	1	8.33E-03
Seq_000370 9	4.91E-06	0	1	1.11E-05	0	3	1.01E-02
Seq_000371 0	1.42E-06	0	1	0	0	0	1.01E-02
Seq_000371 6	4.24E-06	0	1	7.40E-06	0	1	1.01E-02
Seq_000378 8	7.23E-07	0	1	1.20E-06	0	1	6.02E-03
Seq_000379 3	1.23E-05	0	2	0	0	0	1.01E-02
Seq_000381 4	0	0	0	1.47E-05	0	2	1.01E-02
Seq_000381 8	3.96E-06	0	2	0	0	0	1.01E-02
Seq_000382 1	2.44E-06	0	1	0	0	0	1.01E-02
Seq_000382 3	5.41E-06	0	1	0	0	0	1.01E-02
Seq_000388 7	4.02E-06	0	1	0	0	0	1.01E-02
Seq_000388 8	4.38E-06	0	2	1.20E-06	0	1	1.01E-02
Seq_000388 9	4.06E-06	0	1	4.08E-06	0	2	2.36E-03
Seq_000389 2	6.02E-06	0	1	0	0	0	1.01E-02

Seq_000391 7	1.08E-06	0	1	0	0	0	1.01E-02
Seq_000392 0	0	0	0	6.61E-06	0	1	1.01E-02
Seq_000392 8	1.27E-05	0	4	0	0	0	1.01E-02
Seq_000393 1	2.03E-06	0	1	0	0	0	1.01E-02
Seq_000396 2	0	0	0	1.92E-06	0	1	1.01E-02
Seq_000396 4	0	0	0	6.61E-06	0	1	1.01E-02
Seq_000396 5	0	0	0	1.80E-05	0	1	1.01E-02
Seq_000396 6	0	0	0	8.98E-06	0	1	1.01E-02
Seq_000397 4	2.51E-06	0	1	0	0	0	1.01E-02
Seq_000400 9	0	0	0	9.41E-06	0	2	1.01E-02
Seq_000401 2	0	0	0	2.43E-05	0	3	1.01E-02
Seq_000405 0	3.61E-06	0	1	0	0	0	1.01E-02
Seq_000405 3	8.93E-07	0	1	0	0	0	1.01E-02
Seq_000406 0	2.07E-06	0	2	0	0	0	1.01E-02
Seq_000406 2	8.60E-06	0	2	0	0	0	1.01E-02
Seq_000411 7	0	0	0	7.93E-06	0	1	1.01E-02

Seq_0004126	8.13E-07	0	1	0	0	0	8.33E-03
Seq_0004128	4.88E-06	0	1	0	0	0	1.01E-02
Seq_0004180	0	0	0	9.25E-06	0	1	1.01E-02
Seq_0004181	0	0	0	2.89E-06	0	1	1.01E-02
Seq_0004182	0	0	0	1.32E-05	0	1	1.01E-02
Seq_0004185	4.47E-07	0	1	1.32E-06	0	1	2.53E-03
Seq_0004245	0	0	0	1.32E-06	0	1	8.33E-03
Seq_0004246	0	0	0	8.32E-06	0	4	1.01E-02
Seq_0004248	1.22E-06	0	1	1.19E-05	0	1	1.01E-02
Seq_0004252	0	0	0	2.70E-06	0	1	1.01E-02
Seq_0004266	0	0	0	7.07E-06	0	1	1.01E-02
Seq_0004268	5.27E-06	0	1	0	0	0	1.01E-02
Seq_0004317	3.52E-06	0	1	9.60E-07	0	1	1.01E-02
Seq_0004342	0	0	0	6.33E-06	0	2	1.01E-02
Seq_0004411	7.69E-06	0	1	0	0	0	1.01E-02
Seq_0004515	5.69E-06	0	1	0	0	0	1.01E-02

Seq_000452 7	4.47E-07	0	1	6.44E-06	0	1	1.01E-02
Seq_000458 9	0	0	0	3.20E-06	0	1	1.01E-02
Seq_000459 5	3.94E-06	0	1	0	0	0	1.01E-02
Seq_000460 8	2.44E-06	0	1	0	0	0	1.01E-02
Seq_000461 4	7.78E-06	0	1	0	0	0	1.01E-02
Seq_000461 5	5.70E-06	0	2	0	0	0	1.01E-02
Seq_000461 6	0	0	0	6.35E-06	0	1	1.01E-02
Seq_000462 3	4.91E-06	0	1	0	0	0	1.01E-02
Seq_000462 4	9.65E-06	0	1	0	0	0	1.01E-02
Seq_000470 8	0	0	0	1.07E-05	0	1	1.01E-02
Seq_000471 0	0	0	0	4.80E-06	0	1	1.01E-02
Seq_000471 4	6.69E-06	0	1	0	0	0	1.01E-02
Seq_000474 4	6.55E-06	0	1	0	0	0	1.01E-02
Seq_000474 5	1.09E-05	0	1	0	0	0	1.01E-02
Seq_000474 7	3.42E-06	0	1	1.58E-06	0	1	1.01E-02
Seq_000475 4	0	0	0	1.58E-05	0	1	1.01E-02

Seq_000475 5	0	0	0	1.58E-05	0	1	1.01E-02
Seq_000475 7	3.59E-06	0	1	0	0	0	1.01E-02
Seq_000475 8	0	0	0	8.15E-06	0	1	1.01E-02
Seq_000475 9	4.47E-06	0	1	0	0	0	1.01E-02
Seq_000482 8	0	0	0	1.08E-05	0	1	1.01E-02
Seq_000482 9	0	0	0	1.19E-05	0	1	1.01E-02
Seq_000483 0	3.25E-06	0	1	0	0	0	1.01E-02
Seq_000484 9	5.89E-06	0	1	0	0	0	1.01E-02
Seq_000485 0	7.31E-06	0	1	0	0	0	1.01E-02
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Seq_000485 9	6.37E-06	0	1	0	0	0	1.01E-02
Seq_000486 0	3.66E-06	0	1	0	0	0	1.01E-02
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Seq_000487 0	5.41E-06	0	1	0	0	0	1.01E-02
Seq_000487 1	4.02E-06	0	1	0	0	0	1.01E-02
Seq_000498 9	0	0	0	3.30E-06	0	1	1.01E-02
Seq_000499 0	7.07E-07	0	1	1.44E-06	0	1	1.01E-02
Seq_000499 4	5.35E-06	0	1	0	0	0	1.01E-02
Seq_000499 6	2.89E-06	0	1	0	0	0	1.01E-02
Seq_000499 7	2.89E-06	0	1	0	0	0	1.01E-02
Seq_000502 0	6.50E-06	0	1	0	0	0	1.01E-02
Seq_000502 1	6.50E-06	0	1	0	0	0	1.01E-02
Seq_000502 4	0	0	0	1.32E-05	0	1	1.01E-02
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Seq_000503 1	3.25E-06	0	1	0	0	0	1.01E-02
Seq_000503 6	0	0	0	1.26E-05	0	1	1.01E-02
Seq_000504 2	0	0	0	5.45E-06	0	1	1.01E-02

Seq_0005049	0	0	0	6.52E-06	0	1	1.01E-02
Seq_0005125	4.11E-06	0	1	0	0	0	1.01E-02
Seq_0005129	2.53E-06	0	1	0	0	0	1.01E-02
Seq_0005157	3.32E-06	0	1	0	0	0	1.01E-02
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Seq_0005163	5.69E-06	0	1	0	0	0	1.01E-02
Seq_0005164	0	0	0	7.31E-06	0	1	1.01E-02
Seq_0005174	4.95E-06	0	1	0	0	0	1.01E-02
Seq_0005175	4.95E-06	0	1	0	0	0	1.01E-02
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Seq_0005181	1.09E-05	0	1	0	0	0	1.01E-02
Seq_0005182	0	0	0	1.11E-05	0	1	1.01E-02

Seq_000518 3	0	0	0	1.11E-05	0	1	1.01E-02
Seq_000518 6	0	0	0	6.44E-06	0	1	1.01E-02
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Seq_000519 2	0	0	0	5.71E-06	0	1	1.01E-02
Seq_000519 3	3.13E-06	0	1	0	0	0	1.01E-02
Seq_000539 2	0	0	0	7.22E-06	0	1	1.01E-02
Seq_000539 4	5.98E-06	0	1	0	0	0	1.01E-02
Seq_000539 5	5.98E-06	0	1	0	0	0	1.01E-02
Seq_000539 6	0	0	0	1.08E-05	0	1	1.01E-02
Seq_000540 0	4.01E-06	0	1	0	0	0	1.01E-02
Seq_000540 4	2.17E-06	0	1	0	0	0	1.01E-02
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Seq_000545 5	1.79E-06	0	1	1.84E-06	0	1	8.33E-03
Seq_000545 6	0	0	0	4.09E-06	0	1	1.01E-02
Seq_000545 7	2.15E-06	0	1	0	0	0	1.01E-02
Seq_000546 4	0	0	0	4.89E-06	0	1	1.01E-02
Seq_000546 5	2.68E-06	0	1	0	0	0	1.01E-02
Seq_000546 6	5.27E-06	0	1	0	0	0	1.01E-02
Seq_000561 5	4.98E-06	0	1	0	0	0	1.01E-02
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Seq_000561 7	0	0	0	6.61E-06	0	1	1.01E-02
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Seq_000566 5	3.54E-06	0	1	0	0	0	1.01E-02
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Seq_000567 0	0	0	0	3.54E-06	0	1	1.01E-02
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Seq_000567 3	0	0	0	7.90E-06	0	1	1.01E-02
Seq_000568 2	0	0	0	4.60E-06	0	1	1.01E-02
Seq_000605 1	3.98E-06	0	1	0	0	0	1.01E-02
Seq_000605 3	0	0	0	1.92E-06	0	1	1.01E-02
Seq_000605 4	2.35E-06	0	1	0	0	0	1.01E-02
Seq_000605 6	0	0	0	5.29E-06	0	1	1.01E-02

Seq_000605 7	0	0	0	7.19E-06	0	1	1.01E-02
Seq_000606 6	2.67E-06	0	1	0	0	0	1.01E-02
Seq_000606 7	1.43E-06	0	1	0	0	0	1.01E-02
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Seq_000609 7	0	0	0	4.18E-06	0	1	1.01E-02
Seq_000610 8	8.13E-07	0	1	3.30E-06	0	1	3.36E-03
Seq_000611 7	1.63E-06	0	1	0	0	0	1.01E-02
Seq_000611 8	1.63E-06	0	1	0	0	0	1.01E-02
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Seq_000612 1	3.42E-06	0	1	0	0	0	1.01E-02

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Seq_000612 4	3.42E-06	0	1	0	0	0	1.01E-02
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Seq_000725 6	9.49E-07	0	1	0	0	0	1.01E-02
Seq_000725 7	0	0	0	1.80E-06	0	1	1.01E-02
Seq_000726 9	1.63E-06	0	1	0	0	0	1.01E-02
Seq_000727 0	0	0	0	2.09E-06	0	1	1.01E-02
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Seq_000730 3	3.12E-06	0	1	0	0	0	1.01E-02
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Seq_000731 5	0	0	0	1.41E-06	0	1	1.01E-02
Seq_000731 6	0	0	0	1.41E-06	0	1	1.01E-02
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Seq_000731 8	0	0	0	1.41E-06	0	1	1.01E-02
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Seq_000732 2	0	0	0	3.16E-06	0	1	1.01E-02
Seq_000732 3	0	0	0	3.16E-06	0	1	1.01E-02
Seq_000733 3	0	0	0	1.84E-06	0	1	1.01E-02
Seq_000733 4	0	0	0	1.84E-06	0	1	1.01E-02

Seq_0007337	0	0	0	2.30E-06	0	1	1.01E-02
Seq_0007338	0	0	0	1.36E-06	0	1	1.01E-02
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Seq_0007359	0	0	0	4.80E-07	0	1	8.33E-03
Seq_0007360	0	0	0	1.32E-06	0	1	8.33E-03
Seq_0007361	0	0	0	1.80E-06	0	1	8.33E-03
Seq_0007362	3.58E-07	0	1	0	0	0	8.33E-03
Seq_0007369	4.74E-07	0	1	0	0	0	8.33E-03
Seq_0007374	0	0	0	1.06E-06	0	1	8.33E-03
Seq_0007379	4.47E-07	0	1	0	0	0	8.33E-03
RSV	Domain	Phylum	Class	Order	Family	Genus	
Seq_0000001	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium	
Seq_0000002	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium	
Seq_0000003	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	

Seq_0000004	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000005	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000009	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0000010	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000011	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000012	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000013	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia/Shigella
Seq_0000016	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Pediococcus
Seq_0000017	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000018	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000019	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000024	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcaceae_unclassified
Seq_0000025	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000026	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000027	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000028	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter

Seq_0000029	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotellaceae_unclassified
Seq_0000030	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000031	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000033	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000034	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0000035	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0000036	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000038	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_0000040	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000043	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000049	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000051	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Pasteurellaceae_unclassified
Seq_0000053	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000055	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcaceae_unclassified
Seq_0000056	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000059	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella

Seq_0000064	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000068	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000070	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000074	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Parasutterella
Seq_0000075	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000083	Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobrevibacter
Seq_0000084	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Catenibacterium
Seq_0000086	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus
Seq_0000088	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000092	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000096	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0000099	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000102	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000109	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Sarcina
Seq_0000114	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000115	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Seq_0000117	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Anaerostipes
Seq_0000118	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000120	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000121	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0000123	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000125	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacteriaceae_unclassified
Seq_0000126	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000135	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000136	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000139	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0000140	Bacteria	Firmicutes	Bacilli	Lactobacillales	Leuconostocaceae	Weissella
Seq_0000141	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000142	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Clostridium_XI
Seq_0000146	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Phascolarctobacterium
Seq_0000148	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVIII
Seq_0000149	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcus

Seq_0000154	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000155	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coproccoccus
Seq_0000157	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Seq_0000159	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000161	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000168	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0000174	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000175	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Seq_0000177	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000180	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000183	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000186	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000189	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVa
Seq_0000194	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000198	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000204	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor

Seq_0000205	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000207	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Bilophila
Seq_0000214	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_0000216	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000218	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000219	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000220	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000221	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000224	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000228	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000233	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000240	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000244	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Acidaminococcaceae	Acidaminococcaceae_unclassified
Seq_0000245	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus
Seq_0000247	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000249	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus

Seq_0000251	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000252	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000253	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000260	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000264	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000266	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000267	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000276	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Clostridium_XI
Seq_0000288	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000291	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidiphilium
Seq_0000292	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000296	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000304	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000307	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000310	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000315	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes

Seq_0000316	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000317	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000318	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000319	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000331	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Eggerthella
Seq_0000335	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000339	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0000341	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000346	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Anaerococcus
Seq_0000348	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0000350	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000351	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000353	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000356	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0000358	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000361	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0000362	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XIII	Mogibacterium
Seq_0000368	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000372	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Seq_0000377	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	Lactobacillales_unclassified
Seq_0000381	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000390	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000392	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Enterorhabdus
Seq_0000396	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000397	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000401	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
Seq_0000403	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0000405	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000409	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000410	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000414	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0000428	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus

Seq_000043 1	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_000043 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000045 2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_000045 6	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000045 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000045 8	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVIII
Seq_000045 9	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_000046 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000046 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000046 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Subdoligranulum
Seq_000046 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000047 2	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XI	Gemella
Seq_000048 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000049 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000049 4	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_000050 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2

Seq_0000510	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000517	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000527	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000532	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Slackia
Seq_0000536	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0000537	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_0000538	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0000542	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000544	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0000548	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000549	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000557	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000559	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000561	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000564	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0000572	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000576	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000581	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000589	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000604	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000615	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000619	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000623	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Eggerthella
Seq_0000626	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000640	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0000645	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000646	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000651	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Odoribacter
Seq_0000654	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000657	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_0000660	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacteriaceae_unclassified
Seq_0000661	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus

Seq_0000666	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000668	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Moraxella
Seq_0000671	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0000673	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Peptoniphilus
Seq_0000676	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae_1	Peptococcus
Seq_0000679	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000683	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Ralstonia
Seq_0000691	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0000704	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0000705	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000708	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Seq_0000710	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000712	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Morganella
Seq_0000720	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0000735	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000740	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotellaceae_unclassified

Seq_0000743	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000753	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0000757	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000760	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Eggerthella
Seq_0000765	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000771	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000778	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_0000780	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000781	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000785	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000792	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Seq_0000794	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000808	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio
Seq_0000812	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000814	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0000815	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella

Seq_0000829	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Citrobacter
Seq_0000831	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000843	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000844	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVa
Seq_0000849	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000851	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000865	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0000868	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000878	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	Burkholderiales_unclassified
Seq_0000879	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000880	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000885	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0000889	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000894	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000899	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000900	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0000909	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0000910	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0000915	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0000928	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacteriaceae_unclassified
Seq_0000931	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_0000934	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0000936	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0000938	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000948	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000966	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0000973	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0000975	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0000979	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0000984	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0000991	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Seq_0000998	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa

Seq_0001012	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001021	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001023	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001030	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001040	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001042	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001051	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001052	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001055	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillaceae_unclassified
Seq_0001062	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001084	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001088	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001092	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001096	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001112	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Sutterellaceae	Sutterella
Seq_0001116	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0001118	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0001128	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001129	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0001135	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001138	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001144	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0001155	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0001160	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales_unclassified	Burkholderiales_unclassified
Seq_0001163	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0001173	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001180	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0001191	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Parvimonas
Seq_0001194	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Pediococcus
Seq_0001212	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001221	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0001231	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0001235	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0001241	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_0001252	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001265	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001284	Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Eubacterium
Seq_0001285	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001289	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001303	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001310	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_unclassified	Rhizobiales_unclassified
Seq_0001320	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0001330	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001334	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0001338	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001339	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001345	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001346	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus

Seq_0001347	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001352	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0001353	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001358	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0001369	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_0001373	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0001384	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001411	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0001423	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001427	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Phenylobacterium
Seq_0001433	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0001439	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001444	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001446	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001448	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001459	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera

Seq_0001464	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Peptoniphilus
Seq_0001471	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Allisonella
Seq_0001487	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001488	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Butyricimonas
Seq_0001507	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001511	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0001534	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001535	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricicoccus
Seq_0001560	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0001567	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001576	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001580	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0001582	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001602	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001611	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0001650	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified

Seq_0001654	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillales_unclassified	Lactobacillales_unclassified
Seq_0001666	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricoccus
Seq_0001667	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0001670	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Howardella
Seq_0001673	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Olsenella
Seq_0001682	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001683	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001688	Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus
Seq_0001695	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001705	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Chitinophagaceae_unclassified
Seq_0001719	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0001730	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0001736	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0001740	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Seq_0001744	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Finegoldia
Seq_0001757	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Gordonibacter

Seq_0001763	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0001772	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Peptoniphilus
Seq_0001774	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001782	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces
Seq_0001788	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001794	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001806	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0001818	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001834	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0001844	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001862	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001868	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0001905	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001909	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001937	Bacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	Actinobacteria_unclassified	Actinobacteria_unclassified
Seq_0001940	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Parvimonas

Seq_0001941	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001954	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001958	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0001972	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0001973	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0001980	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0001995	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002021	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0002034	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002064	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002066	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium
Seq_0002069	Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Anaerofustis
Seq_0002075	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002082	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia
Seq_0002090	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XV_III
Seq_0002135	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XI_Va

Seq_0002139	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Gordonibacter
Seq_0002143	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0002149	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002153	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0002168	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002172	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0002181	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002185	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0002193	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002194	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Olsenella
Seq_0002212	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002230	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002233	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0002234	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002241	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0002243	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella

Seq_000225 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000225 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000228 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000228 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000230 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000232 2	Bacteria	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Alicyclobacillus
Seq_000236 4	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_000237 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000237 7	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000238 9	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_000240 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000240 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000241 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_000241 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000242 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000243 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0002435	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002438	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002443	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002462	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002470	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0002480	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0002495	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002512	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XIII	Mogibacterium
Seq_0002519	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0002529	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0002533	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002544	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0002565	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0002572	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0002587	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Gordonibacter
Seq_0002605	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_000261 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_Xl Va
Seq_000261 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified
Seq_000267 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000267 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococ aceae	Clostridium_Xl
Seq_000271 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified
Seq_000271 4	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	Leptotrichia
Seq_000271 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_un classified
Seq_000273 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae _unclassified
Seq_000274 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000274 5	Bacteria	Firmicutes	Firmicutes_un classified	Firmicutes_uncla ssified	Firmicutes_uncl assified	Firmicutes_uncl assified
Seq_000275 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae _unclassified
Seq_000276 0	Bacteria	Firmicutes	Firmicutes_un classified	Firmicutes_uncla ssified	Firmicutes_uncl assified	Firmicutes_uncl assified
Seq_000279 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified
Seq_000279 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified
Seq_000280 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified
Seq_000282 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_Xl Va

Seq_0002846	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002856	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0002874	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0002876	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0002894	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Peptoniphilus
Seq_0002897	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_0002910	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0002924	Bacteria	Candidatus_Saccharibacteria	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified
Seq_0002925	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0002936	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0002937	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0002938	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Varibaculum
Seq_0002939	Bacteria	Candidatus_Saccharibacteria	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified
Seq_0002946	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Oribacterium
Seq_0002948	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_000295	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000297	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Sporobacter
Seq_000303	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000303	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000303	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_000306	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Holdemania
Seq_000306	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000308	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricicoccus
Seq_000309	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000309	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000310	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000312	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000312	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000312	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000312	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Pseudoflavonifractor
Seq_000312	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified

Seq_0003146	Archaea	Euryarchaeota	Thermoplasma	Thermoplasmatales	Ferroplasmaceae	Ferroplasma
Seq_0003177	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0003179	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0003189	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0003191	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyrivibrio
Seq_0003210	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003232	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Paraprevotella
Seq_0003251	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0003252	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003256	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003258	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0003267	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_0003317	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003336	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003338	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0003339	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_000337	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000340	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_000341	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVa
Seq_000342	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000349	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000351	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_000355	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_000355	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000355	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_000365	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000365	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000365	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Allisonella
Seq_000365	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVb
Seq_000368	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000370	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000370	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_0003710	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVb
Seq_0003716	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0003788	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003793	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003814	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Butyrivibrio
Seq_0003818	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Clostridium_XVIII
Seq_0003821	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0003823	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0003887	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0003888	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0003889	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0003892	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003917	Bacteria	Firmicutes	Clostridia	Clostridiales	Incertae_Sedis_XI	Murdochella
Seq_0003920	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0003928	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0003931	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_000396 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_000396 4	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_000396 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000396 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000397 4	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_000400 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000401 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000405 0	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000405 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_000406 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000406 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000411 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000412 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000412 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000418 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000418 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Robinsoniella

Seq_000418 2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000418 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae _unclassified
Seq_000424 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_un classified
Seq_000424 6	Bacteria	Firmicutes	Firmicutes_un classified	Firmicutes_uncla ssified	Firmicutes_uncl assified	Firmicutes_uncl assified
Seq_000424 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae _unclassified
Seq_000425 2	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_000426 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_000426 8	Bacteria	Bacteria_uncl assified	Bacteria_uncla ssified	Bacteria_unclassi fied	Bacteria_unclass ified	Bacteria_unclass ified
Seq_000431 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_un classified
Seq_000434 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_un classified	Clostridiales_un classified
Seq_000441 1	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonada ceae	Odoribacter
Seq_000451 5	Bacteria	Proteobacteria	Betaproteobact eria	Betaproteobacteri a_unclassified	Betaproteobacter ia_unclassified	Betaproteobacter ia_unclassified
Seq_000452 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000458 9	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_000459 5	Bacteria	Firmicutes	Erysipelotrichi a	Erysipelotrichales	Erysipelotrichac eae	Turicibacter
Seq_000460 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae _unclassified

Seq_0004614	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0004615	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0004616	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0004623	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Catenibacterium
Seq_0004624	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0004708	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0004710	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_0004714	Bacteria	Candidatus_Saccharibacteria	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified	Candidatus_Saccharibacteria_unclassified
Seq_0004744	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Seq_0004745	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0004747	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0004754	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0004755	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0004757	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus
Seq_0004758	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0004759	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified

Seq_0004828	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor
Seq_0004829	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0004830	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0004849	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
Seq_0004850	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0004851	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0004858	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Pediococcus
Seq_0004859	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0004860	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium
Seq_0004861	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0004863	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0004865	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0004870	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0004871	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0004989	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0004990	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified

Seq_0004994	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium
Seq_0004996	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotellaceae_unclassified
Seq_0004997	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0005020	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0005021	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0005024	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0005025	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella
Seq_0005026	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0005027	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0005031	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0005036	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005042	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacteriaceae_unclassified
Seq_0005049	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio
Seq_0005125	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005129	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus2
Seq_0005157	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_0005160	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005161	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus
Seq_0005162	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVa
Seq_0005163	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0005164	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005174	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0005175	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0005176	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0005179	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0005180	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_0005181	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0005182	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0005183	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0005186	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0005188	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacteriaceae_unclassified
Seq_0005192	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcaceae_unclassified

Seq_0005193	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0005392	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0005394	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_0005395	Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Haemophilus
Seq_0005396	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_0005400	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0005404	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0005405	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005406	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0005431	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_0005434	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Butyricoccus
Seq_0005436	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0005437	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Odoribacter
Seq_0005446	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_0005449	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0005451	Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Atopobium

Seq_000545 2	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000545 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000545 6	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillales_Incertae_Sedis_XI	Gemella
Seq_000545 7	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_000546 4	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_000546 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_000546 6	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_000561 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000561 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000561 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000561 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000562 5	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_000562 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Incertae_Sedis_XI	Anaerococcus
Seq_000562 7	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Seq_000565 1	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Pseudoflavonifractor
Seq_000566 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0005665	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005667	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacteraceae_unclassified
Seq_0005668	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0005669	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005670	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0005672	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_0005673	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0005682	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0006051	Bacteria	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_0006053	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0006054	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0006056	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006057	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVa
Seq_0006066	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0006067	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0006069	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella

Seq_0006070	Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	Leptotrichia
Seq_0006089	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0006090	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006091	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0006095	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0006096	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0006097	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_0006108	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006117	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter
Seq_0006118	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea
Seq_0006119	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0006121	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0006123	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006124	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium
Seq_0006130	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006136	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium

Seq_0006138	Archaea	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanosphaera
Seq_0006139	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0006140	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006141	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0006160	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006405	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia
Seq_0006406	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_0006417	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0006420	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Odoribacter
Seq_0006423	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0006447	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Caulobacteraceae	Phenyllobacterium
Seq_0006448	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0006450	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidocella
Seq_0006459	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0006460	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Butyricimonas
Seq_0006461	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides

Seq_000648 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000648 9	Bacteria	Acidobacteria	Acidobacteria_Gp1	Acidobacterium	Acidobacterium_unclassified	Acidobacterium_unclassified
Seq_000649 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000649 3	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonadaceae_unclassified
Seq_000649 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000649 6	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium
Seq_000649 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000649 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000649 9	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000650 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000650 4	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_000650 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000650 6	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000650 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000651 9	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_000652 0	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium

Seq_000652 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000652 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000652 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000654 0	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_000654 1	Bacteria	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio
Seq_000654 3	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Cloacibacterium
Seq_000654 4	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacteriaceae_unclassified
Seq_000654 5	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000654 6	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000654 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000721 7	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_000721 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000722 8	Bacteria	Verrucomicrobia	Verrucomicrobia_unclassified	Verrucomicrobia_unclassified	Verrucomicrobia_unclassified	Verrucomicrobia_unclassified
Seq_000723 2	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000723 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000723 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_0007235	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0007237	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0007238	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0007239	Bacteria	Bacteroidetes	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified	Bacteroidetes_unclassified
Seq_0007249	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0007256	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0007257	Archaea	Euryarchaeota	Thermoplasma	Thermoplasmatales	Thermoplasmatales_unclassified	Thermoplasmatales_unclassified
Seq_0007269	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_0007270	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0007292	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0007293	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0007297	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0007298	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacteriaceae_unclassified
Seq_0007299	Bacteria	Chlamydiae	Chlamydia	Chlamydiales	Chlamydiales_unclassified	Chlamydiales_unclassified
Seq_0007300	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0007301	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas

Seq_000730 2	Bacteria	Proteobacteria	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified	Proteobacteria_unclassified
Seq_000730 3	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000730 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000731 5	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000731 6	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium
Seq_000731 7	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000731 8	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000732 0	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000732 2	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000732 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000733 3	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000733 4	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000733 7	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella
Seq_000733 8	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000735 3	Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_000735 5	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonadaceae_unclassified

Seq_0007356	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0007357	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0007359	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_0007360	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0007361	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_0007362	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XlVa
Seq_0007369	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_0007374	Bacteria	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_0007379	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Table 11. Viral Clusters for which an Increase in Abundance is Associated with Crohn's Disease

VC	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
c13	421.1288	6.521004	2.291738	2.845441	0.004435	0.011899	9.3E-05
c77	62.03631	7.33111	3.133318	2.339727	0.019298	0.049367	2.83E-06
c15	324.4548	8.041608	3.130021	2.569186	0.010194	0.026384	7.98E-05
c28	258.0818	8.874406	3.131977	2.833484	0.004604	0.012204	0.00017
c14	696.7224	9.916292	2.7787	3.56868	0.000359	0.001012	1.12E-05
c113	4.257101	23.72319	3.139944	7.55529	4.18E-14	1.46E-13	0
c95	9.309923	23.77691	3.139524	7.573414	3.64E-14	1.31E-13	0
c69	4.605229	23.82878	3.139886	7.58906	3.22E-14	1.18E-13	5.51E-06

c117	4.654961	23.84744	3.139878	7.595023	3.08E-14	1.17E-13	7.94E-07
c218	4.654961	23.84744	3.139878	7.595023	3.08E-14	1.17E-13	0.000452
c232	4.863838	23.90769	3.139847	7.614284	2.65E-14	1.04E-13	5.05E-06
c97	4.963303	23.93744	3.139834	7.623793	2.46E-14	1E-13	8.86E-06
c298	5.003089	23.93984	3.139829	7.624569	2.45E-14	1E-13	0
c160	9.449174	23.97031	3.139518	7.635028	2.26E-14	9.55E-14	5.88E-06
c102	5.649611	24.11558	3.139753	7.680725	1.58E-14	6.82E-14	0
c264	7.042121	24.42466	3.139638	7.779452	7.28E-15	3.27E-14	0
c281	8.026824	24.60998	3.13958	7.838621	4.56E-15	2.14E-14	0
c178	9.45912	24.83944	3.139518	7.911864	2.54E-15	1.27E-14	0
c118	13.12938	25.22671	3.13942	8.035468	9.32E-16	5.26E-15	4.93E-05
c420	13.50735	25.33002	3.139413	8.068393	7.12E-16	4.12E-15	0
c48	22.75759	25.41073	3.139314	8.094359	5.76E-16	3.42E-15	1.87E-06
c132	18.64968	25.76722	3.139346	8.207831	2.25E-16	1.38E-15	0
c40	20.63898	25.83464	3.139329	8.229353	1.88E-16	1.18E-15	1.65E-05
ERR843 914 _NODE _16 _length_ 6283 _cov_8. 28276	25.04527	26.20219	3.139301	8.346507	7.03E-17	4.83E-16	0
c91	26.87544	26.29745	3.139292	8.376873	5.44E-17	3.86E-16	0
c68	34.59855	26.65662	3.139264	8.49136	2.04E-17	1.6E-16	0
c66	79.87038	27.59152	3.13921	8.789318	1.5E-18	1.38E-17	0
c80	117.1797	28.36354	3.139197	9.035287	1.64E-19	1.89E-18	7.73E-05
c142	139.2908	28.582	3.139192	9.104891	8.64E-20	1.06E-18	0
c36	180.8572	28.97249	3.139187	9.229298	2.72E-20	3.75E-19	5.79E-05
c94	352.4243	29.82685	3.139178	9.501483	2.07E-21	3.25E-20	7.72E-05
c71	372.2477	29.91142	3.139178	9.528426	1.6E-21	3.17E-20	0
c108	394.1002	30	3.139177	9.556645	1.22E-21	2.97E-20	0
c155	4298.962	30	3.139169	9.556668	1.22E-21	2.97E-20	1.2E-05

c73	716.138	30	3.139173	9.556656	1.22E-21	2.97E-20	0
c78	1992.781	30	3.13917	9.556665	1.22E-21	2.97E-20	0
c79	1677.477	30	3.139171	9.556664	1.22E-21	2.97E-20	2.2E-07
VC	Control Median	Control Present (n=61)	CD Mean	CD Median	CD Present (n=27)	logfdr	Classificatio n
c13	0	8	0.011734	0	10	1.924497	Siphoviridae
c77	0	2	0.001075	0	6	1.306567	Unclassified
c15	0	5	0.027067	0	7	1.578662	Siphoviridae
c28	0	3	0.00341	0	6	1.913486	Siphoviridae
c14	0	2	0.011406	0	10	2.994839	Siphoviridae
c113	0	0	8.83E-05	0	4	12.83582	Siphoviridae
c95	0	0	9.58E-05	0	5	12.88235	Unclassified
c69	0	2	5.81E-05	0	4	12.92756	Unclassified
c117	0	1	0.000695	0	3	12.93282	Unclassified
c218	0	1	0.000494	0	2	12.93282	Unclassified
c232	0	1	0.000288	0	2	12.98197	Unclassified
c97	0	1	4.5E-05	0	4	12.99846	Unclassified
c298	0	0	0.002098	0	2	12.99846	Unclassified
c160	0	2	0.001084	0	3	13.01991	Unclassified
c102	0	0	0.00029	0	2	13.16597	Heterogeneous
c264	0	0	0.000106	0	2	13.48541	Unclassified
c281	0	0	0.000241	0	2	13.66912	Unclassified
c178	0	0	0.000312	0	2	13.89694	Unclassified
c118	0	1	0.000646	0	2	14.27912	Unclassified
c420	0	0	6.45E-05	0	4	14.3847	Unclassified
c48	0	1	0.001132	0	6	14.46561	Siphoviridae
c132	0	0	0.006107	0	6	14.86127	Unclassified
c40	0	2	0.003882	0	6	14.92696	Siphoviridae
ERR843 914 _NODE	0	0	0.000452	0	3	15.3157	Unclassified

_16 _length_ 6283_co v_8.282 76							
c91	0	0	0.00181	0	5	15.41372	Siphoviridae
c68	0	0	0.002799	0	4	15.79461	Siphoviridae
c66	0	0	0.001926	0	4	16.86034	Myoviridae
c80	0	3	0.002874	0	2	17.72262	Unclassified
c142	0	0	0.000655	0	5	17.97657	Unclassified
c36	0	1	0.013451	0	5	18.42647	Heterogeneous
c94	0	1	0.007758	0	4	19.4879	Unclassified
c71	0	0	0.002849	0	6	19.49899	Heterogeneous
c108	0	0	0.04671	0	4	19.52676	Heterogeneous
c155	0	3	0.039058	0	2	19.52676	Unclassified
c73	0	0	0.016534	0	5	19.52676	Unclassified
c78	0	0	0.004963	0	5	19.52676	Heterogeneous
c79	0	1	0.040904	0	3	19.52676	Heterogeneous

Table 12. Viral Clusters for which an Increase in Abundance is Associated with Ulcerative Colitis

VC	Base Mean	log2Fold Change	lfcSE	stat	p-value	padj	Control Mean
c2	69904.251 87	4.1148677 95	0.8987599 46	4.578383 596	4.68583E -06	1.53266E-05	0.006243248
c13	194.29634 16	4.9953243 1	2.1254419 05	2.350252 105	0.018760 7	0.04992254	9.29665E-05

c21	1939.2942 53	5.2159316 3	1.9362155 03	2.693879 696	0.007062 565	0.019800406	0.000419858
c22	699.64117 43	6.2429537 99	2.4541712 98	2.543813 386	0.010964 965	0.030201745	0.000159805
c89	4380.9674 16	7.1114814 01	2.5218075 44	2.819993 706	0.004802 459	0.013954726	0.00061831
c14	152.69267 81	7.3495785 14	2.3995076 21	3.062952 77	0.002191 646	0.006746833	1.11758E-05
c17	2241.5898 52	9.5787195 15	1.8659447 81	5.133442 112	2.84491E -07	9.5032E-07	0.000131828
c152	5.4864232 05	23.350726 56	2.9480257 75	7.920801 357	2.35985E -15	8.23324E-15	0
c69	7.9986445 88	23.388688 09	2.9478104 49	7.934257 814	2.11758E -15	7.5559E-15	5.51471E-06
c102	6.1216932 6	23.891747 33	2.9479546 42	8.104516 6	5.29556E -16	1.9335E-15	0
c130	6.2124461 25	23.911365 54	2.9479456 81	8.111196 111	5.01239E -16	1.87368E-15	0
c95	6.5424565 44	23.980807 04	2.9479151 85	8.134836 161	4.12496E -16	1.57956E-15	0
c70	6.9962208 69	24.075615 02	2.9478779 72	8.167100 283	3.1589E- 16	1.23987E-15	4.09293E-05
c74	7.6408093 72	24.199887 42	2.9478327 24	8.209382 852	2.22328E -16	9.18567E-16	3.03988E-05
c263	8.4977682 72	24.349982 56	2.9477830 68	8.260439 114	1.45138E -16	6.32961E-16	0
c85	8.5307693 14	24.350213 23	2.9477813 58	8.260522 161	1.45037E -16	6.32961E-16	2.53256E-06
c122	14.809217 52	24.458397 88	2.9475946 28	8.297748 152	1.06103E -16	5.04795E-16	7.55579E-07
c88	9.7808739 73	24.546543 6	2.9477251 21	8.327283 787	8.27183E -17	4.05837E-16	2.81643E-06

c205	9.8095596 85	24.550906 15	2.9477239 41	8.328767 091	8.16886E -17	4.05837E-16	0.000657388
c115	10.906844 33	24.695652 56	2.9476854 02	8.377981 09	5.38433E -17	2.88154E-16	0
c413	11.220354 22	24.738421 88	2.9476757 76	8.392517 957	4.75839E -17	2.6681E-16	0
c123	11.335857 87	24.749258 43	2.9476723 63	8.396203 981	4.61144E -17	2.6681E-16	5.15078E-07
ERR 8440 74_N ODE _15_l ength _114 07_c ov_1 0.542 6	18.320697 17	25.145737 68	2.9475460 39	8.531075 46	1.44993E -17	9.10559E-17	0.000211977
c175	17.117101 91	25.329226 37	2.9475603 74	8.593285 005	8.45176E -18	5.76924E-17	1.81528E-05
c118	25.584057 68	25.891577 13	2.9474877	8.784286 744	1.5736E- 18	1.23527E-17	4.92807E-05
c181	29.115169 16	26.042557 02	2.9474698 66	8.835563 451	9.9595E- 19	8.6869E-18	1.82129E-05
c36	73.963585 01	26.054906 64	2.9473915 31	8.839988 296	9.57286E -19	8.6869E-18	5.78561E-05
c48	33.207298 35	26.252815 55	2.9474539 64	8.906946 766	5.24572E -19	5.14737E-18	1.87252E-06
c97	38.990730 93	26.480941 05	2.9474371 9	8.984395 372	2.60161E -19	3.14194E-18	8.86083E-06
c53	63.848765 69	27.172992 82	2.9473996 25	9.219310 675	2.99016E -20	4.26778E-19	0

c40	67.921469 81	27.224957 22	2.8066659 46	9.700106 014	3.01186E -22	1.18215E-20	1.64944E-05
c68	116.97219 28	27.375842 83	2.9473728 68	9.288218 374	1.56892E -20	2.46321E-19	0
c161	154.95639 19	28.064474 48	2.9473649 93	9.521886 346	1.70064E -21	3.81428E-20	0.000252667
c218	297.96022 22	29.330716 26	2.9473533 48	9.951543 91	2.48301E -23	1.94916E-21	0.000451703
VC	Control Median	Control Present (n=61)	UC Mean	UC Median	UC Present (n=42)	logfdr	Classificatio n
c2	0.0009042 78	47	0.0953629 07	0.000567 21	28	4.814555238	Podoviridae
c13	0	8	0.0067327 08	0	13	1.301703331	Siphoviridae
c21	0	12	0.0211632 31	0	12	1.703325907	Siphoviridae
c22	0	5	0.0113225 07	0	13	1.519967963	Myoviridae
c89	0	12	0.0288386 63	0	8	1.855278698	Unclassified
c14	0	2	0.0012414 2	0	13	2.170900022	Siphoviridae
c17	0	6	0.0165746 52	0	16	6.022130346	Siphoviridae
c152	0	0	4.55477E- 05	0	4	14.08442904	Unclassified
c69	0	2	0.0001383 94	0	7	14.1217136	Unclassified
c102	0	0	0.0001870 55	0	5	14.71365658	Heterogeneo us
c130	0	0	9.84302E- 05	0	4	14.72730494	Podoviridae

c95	0	0	0.0001875 65	0	3	14.80146464	Unclassified
c70	0	3	5.77256E- 05	0	4	14.90662405	Unclassified
c74	0	3	6.64757E- 05	0	4	15.03688927	Unclassified
c263	0	0	0.0004848 82	0	2	15.19862309	Unclassified
c85	0	1	0.0004741 17	0	5	15.19862309	Unclassified
c122	0	1	0.0084906 23	0	2	15.29688536	Unclassified
c88	0	3	0.0004803 43	0	4	15.39164878	Unclassified
c205	0	1	0.0008470 44	0	2	15.39164878	Unclassified
c115	0	0	9.22802E- 05	0	2	15.54037524	Siphoviridae
c413	0	0	0.0001538 53	0	2	15.57379807	Unclassified
c123	0	1	0.0004345	0	4	15.57379807	Unclassified
ERR 8440 74_N ODE _15_1 ength _114 07_c ov_1 0.542 6	0	1	0.0008897 26	0	3	16.04069207	Unclassified

c175	0	1	0.0001135 11	0	4	16.23888126	Unclassified
c118	0	1	0.0005454 43	0	4	16.90823652	Unclassified
c181	0	2	0.0003700 66	0	5	17.06113538	Unclassified
c36	0	1	0.0083977 59	0	5	17.06113538	Heterogeneous
c48	0	1	0.0004965 99	0	7	17.28841497	Siphoviridae
c97	0	1	0.0008295 92	0	5	17.50280189	Unclassified
c53	0	0	0.0016711 9	0	6	18.36979823	Myoviridae
c40	0	2	0.0005860 71	0	8	19.92732624	Siphoviridae
c68	0	0	0.0104267 04	0	6	18.60849836	Siphoviridae
c161	0	2	0.0030158 06	0	4	19.41858709	Unclassified
c218	0	1	0.0044627 01	0	6	20.71015236	Unclassified

Table 13. Viral Clusters for which a Decrease in Abundance is Associated with Crohn's Disease

VC	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
c82	976.7178	-30	2.446196	-12.2639	1.41E-34	3.11E-32	0.006513
c19	2317.614	-30	2.599391	-11.5412	8.18E-31	9E-29	0.013652
c62	6440.694	-30	2.678768	-11.1992	4.12E-29	3.02E-27	0.022597
c112	1678.849	-30	3.152829	-9.51526	1.81E-21	3.17E-20	0.01486
c24	364.0816	-29.9941	3.152839	-9.51336	1.85E-21	3.17E-20	0.003889

c55	335.4505	-29.9894	3.15284	-9.51185	1.87E-21	3.17E-20	0.000529
c136	236.3198	-29.8581	3.152846	-9.47021	2.79E-21	4.1E-20	0.019032
c29	38.21445	-28.3092	3.15295	-8.97865	2.74E-19	3.02E-18	0.000542
c104	256.0132	-28.1681	3.152845	-8.9342	4.1E-19	4.3E-18	0.000434
c284	199.9458	-27.8121	3.15285	-8.82124	1.13E-18	1.13E-17	0.002172
c209	188.2464	-27.7645	3.152851	-8.80617	1.29E-18	1.24E-17	0.00307
c75	174.6641	-27.6616	3.152853	-8.77351	1.73E-18	1.52E-17	0.001223
ERR843 946_NO DE_47_1 ength_13 56_cov_ 2.56341	192.1355	-27.3921	2.9901	-9.16093	5.15E-20	6.66E-19	0.000305
c86	142.9415	-27.2916	3.152859	-8.65615	4.88E-18	4.13E-17	0.001578
c92	98.58701	-26.878	3.152874	-8.52491	1.53E-17	1.25E-16	0.001031
c456	73.87546	-26.4844	3.15289	-8.40005	4.46E-17	3.27E-16	0.009278
c96	63.13121	-26.1718	3.152901	-8.30085	1.03E-16	6.89E-16	0.003812
c225	53.86907	-26.0486	2.372888	-10.9776	4.9E-28	2.69E-26	7.34E-05
c124	51.32553	-25.9768	3.152918	-8.23898	1.74E-16	1.12E-15	0.00047
c193	27.83038	-25.1481	3.152997	-7.97593	1.51E-15	8.12E-15	0.001044
c99	26.55657	-25.08	3.153005	-7.95433	1.8E-15	9.43E-15	0.000661
c84	57.86393	-25.0684	3.152908	-7.95089	1.85E-15	9.47E-15	0.000813
c154	23.05121	-24.8816	3.114884	-7.98795	1.37E-15	7.55E-15	0.000103
c89	87.97057	-24.7497	2.93041	-8.44581	3.02E-17	2.29E-16	0.000618
c58	30.65511	-24.739	3.152981	-7.84621	4.29E-15	2.1E-14	0.000147
c320	27.36292	-24.7133	3.152999	-7.83803	4.58E-15	2.14E-14	0.000244
c143	19.68412	-24.6662	3.153067	-7.82291	5.16E-15	2.37E-14	0.000311
c216	15.21763	-24.348	3.153137	-7.72184	1.15E-14	5.05E-14	0.000124
ERR844 022_NO DE_79_1 ength_17	12.085	-24.0092	3.153218	-7.6142	2.65E-14	1.04E-13	0.000163

66_cov_ 77.1251							
c467	11.44441	-23.9348	3.15324	-7.59054	3.19E-14	1.18E-13	5.11E-05
c138	31.87667	-23.8658	3.152975	-7.56929	3.75E-14	1.33E-13	0.004229
c109	10.39409	-23.8053	3.153282	-7.54937	4.37E-14	1.5E-13	0.000115
c190	27.11416	-23.7416	3.153001	-7.52985	5.08E-14	1.72E-13	0.004543
c411	9.309923	-23.6513	3.153335	-7.50039	6.36E-14	2.12E-13	5.95E-05
c56	3430.301	-16.8695	2.299969	-7.33466	2.22E-13	7.3E-13	0.010971
c42	1404.528	-15.9408	2.358171	-6.75983	1.38E-11	4.47E-11	0.016444
c37	3494.98	-12.9154	2.078145	-6.21486	5.14E-10	1.64E-09	0.008826
c76	15247.19	-11.9709	2.269396	-5.27492	1.33E-07	3.95E-07	0.03128
c45	17753.18	-11.3769	2.072861	-5.4885	4.05E-08	1.22E-07	0.024445
c61	2621.848	-10.439	1.75352	-5.95318	2.63E-09	8.27E-09	0.027828
c64	1352.903	-10.2523	2.234576	-4.58802	4.47E-06	1.3E-05	0.009362
c101	1999.088	-9.86549	2.238357	-4.40747	1.05E-05	2.99E-05	0.03432
c39	30825.66	-9.00743	1.580527	-5.699	1.21E-08	3.68E-08	0.032847
c60	3456.885	-8.7058	2.995543	-2.90625	0.003658	0.009935	0.02313
c23	28061.85	-8.45178	1.702269	-4.96501	6.87E-07	2.02E-06	0.031442
c25	7350.79	-8.2564	1.414778	-5.83583	5.35E-09	1.66E-08	0.02595
c38	71955.23	-5.60649	1.760404	-3.18477	0.001449	0.003984	0.075949
c6	935.5084	-4.40383	1.582926	-2.78208	0.005401	0.014146	0.002581
c7	26124.14	-3.62874	1.066999	-3.40088	0.000672	0.001871	0.026472
VC	Control Median	Control Present (n=61)	CD Mean	CD Median	CD Present (n=27)	logfdr	Classific ation
c82	0	16	3.294E-06	0	1	31.50695 8	Unclassif ied
c19	0	15	0	0	0	28.04579 5	CrAss- like
c62	0	15	0	0	0	26.52029 5	Unclassif ied
c112	0	12	9.552E-07	0	1	19.49899 2	Unclassif ied

c24	0	8	0	0	0	19.49899 2	Unclassif ied
c55	0	7	0.0033383	0	1	19.49899 2	Unclassif ied
c136	0	11	0	0	0	19.38762 4	Unclassif ied
c29	0	6	2.103E-05	0	2	17.52066 5	Siphoviri dae
c104	0	9	0	0	0	17.36686 8	Unclassif ied
c284	0	6	0	0	0	16.94616 5	Unclassif ied
c209	0	5	0	0	0	16.90705 3	Unclassif ied
c75	0	8	0.0021014	0	1	16.81700 1	Unclassif ied
ERR843 946_NO DE_47_1 ength_13 56_cov_ 2.56341	0	10	0.0001707	0	1	18.17662 6	Unclassif ied
c86	0	7	7.899E-05	0	2	16.38417 5	Unclassif ied
c92	0	6	0	0	0	15.90444 5	Unclassif ied
c456	0	3	0	0	0	15.48507 7	Unclassif ied
c96	0	7	2.391E-06	0	1	15.16169 7	Podoviri dae
c225	0	13	3.684E-06	0	1	25.56959 5	Unclassif ied

c124	0	5	0.0014179	0	1	14.949304	Unclassified
c193	0	4	0	0	0	14.090706	Unclassified
c99	0	7	6.69E-05	0	1	14.02529	Myoviridae
c84	0	6	0.0041938	0	1	14.023471	Unclassified
c154	0	9	2.08E-05	0	2	14.122292	Unclassified
c89	0	12	0.0248078	0	2	15.640046	Unclassified
c58	0	7	1.274E-05	0	1	13.678549	Unclassified
c320	0	6	0	0	0	13.669117	CrAss-like
c143	0	3	0	0	0	13.626041	Unclassified
c216	0	4	0	0	0	13.297123	Unclassified
ERR844022_NO DE_79_1 ength_17 66_cov_ 77.1251	0	3	0.0007924	0	1	12.98197	Unclassified
c467	0	2	0	0	0	12.927556	Unclassified
c138	0	7	0.000713	0	1	12.875638	Unclassified
c109	0	3	2.208E-05	0	1	12.822905	Unclassified

c190	0	5	0	0	0	12.76464 8	Unclassif ied
c411	0	2	0	0	0	12.67347 9	Unclassif ied
c56	0	17	2.475E-06	0	1	12.13673 2	Unclassif ied
c42	0	16	0.0044128	0	2	10.34972 1	Unclassif ied
c37	0	20	5.381E-06	0	2	8.785710 7	Unclassif ied
c76	0	19	2.952E-05	0	2	6.403554 2	Unclassif ied
c45	0	23	6.128E-05	0	1	6.913067 9	Unclassif ied
c61	0	26	4.479E-06	0	3	8.082747 2	Unclassif ied
c64	0	17	0.0036204	0	2	4.887622 5	Unclassif ied
c101	0	17	1.291E-05	0	3	4.524595 4	Microviri dae
c39	0.0001764	34	0.0182938	0	4	7.433887 8	Unclassif ied
c60	0	13	0.0343277	0	2	2.002832 8	Unclassif ied
c23	0.0001262	32	0.0072759	0	2	5.695689 4	Unclassif ied
c25	6.784E-05	36	0.0039722	0	4	7.780280 5	Unclassif ied
c38	4.889E-05	31	0.01076	0	5	2.399696 5	Unclassif ied
c6	0	28	0.011608	0	4	1.849369 7	Unclassif ied

c7	0.0025673	50	0.0174652	0	11	2.728036 9	Microviri dae
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Table 14. Viral Clusters for which a Decrease in Abundance is Associated with Ulcerative Colitis

VC	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
c24	301.99253	-28.800031	2.9525868	-9.7541691	1.77E-22	9.265E-21	0.0038885
c103	419.64125	-28.571172	2.952583	-9.6766704	3.789E-22	1.19E-20	0.0031482
c209	156.6797	-28.131918	2.9525994	-9.5278479	1.606E-21	3.814E-20	0.0030698
c75	152.28501	-27.77891	2.9526002	-9.4082872	5.043E-21	9.897E-20	0.001223
c55	94.39123	-27.461764	2.9526167	-9.3008226	1.394E-20	2.431E-19	0.0005286
c96	52.284114	-26.647812	2.9526517	-9.0250442	1.796E-19	2.35E-18	0.003812
c225	43.565508	-26.400168	2.164766	-12.195391	3.289E-34	5.164E-32	7.342E-05
c456	43.379546	-26.39463	2.9526679	-8.9392479	3.918E-19	4.394E-18	0.0092783
c84	40.514598	-26.304214	2.9526745	-8.908606	5.168E-19	5.147E-18	0.000813
c98	31.048086	-25.940155	2.9527054	-8.7852161	1.561E-18	1.235E-17	0.000572
c193	24.865293	-25.635715	2.9527384	-8.6820138	3.888E-18	2.907E-17	0.0010436
c320	22.72671	-25.498699	2.9527538	-8.6355654	5.844E-18	4.17E-17	0.0002441
c138	20.31591	-25.357423	2.9527753	-8.5876577	8.876E-18	5.806E-17	0.0042289
c143	16.327265	-25.054814	2.9528246	-8.485033	2.157E-17	1.302E-16	0.0003109
c216	12.820526	-24.731507	2.9528933	-8.3753472	5.506E-17	2.882E-16	0.000124
ERR8 44022 _NOD E_79_ length _1766 _cov_ 77.12 51	10.024066	-24.398351	2.9529826	-8.2622741	1.429E-16	6.33E-16	0.0001634

c467	9.5332559	-24.325189	2.9530036	-8.2374396	1.759E-16	7.465E-16	5.109E-05
c411	8.6127599	-24.185684	2.9530496	-8.1900705	2.611E-16	1.051E-15	5.953E-05
c62	4633.3093	-8.8287314	2.354701	-3.7494065	0.0001773	0.0005679	0.0225972
c112	1327.3607	-8.6613413	2.9374179	-2.9486242	0.0031919	0.0096371	0.0148598
c38	55886.731	-7.4710968	1.3687285	-5.4584213	4.804E-08	1.64E-07	0.0759486
c101	1671.1683	-6.2502416	1.9849873	-3.1487565	0.0016397	0.0051486	0.0343197
c23	25280.09	-4.7028261	1.5997984	-2.9396366	0.003286	0.0097339	0.0314418
c76	13263.323	-4.5677288	1.8023476	-2.5343217	0.0112665	0.0304973	0.0312797
c39	21658.16	-4.2805972	1.5210252	-2.8142842	0.0048886	0.0139547	0.0328473
VC	Control Median	Control Present (n=61)	UC Mean	UC Median	UC Present (n=42)	logfdr	Classifica tion
c24	0	8	0.0001716	0	2	20.033139	Unclassifi ed
c103	0	8	2.074E-06	0	1	19.924599	Siphovirid ae
c209	0	5	0	0	0	19.418587	Unclassifi ed
c75	0	8	1.558E-05	0	1	19.004512	Unclassifi ed
c55	0	7	0	0	0	18.614194	Unclassifi ed
c96	0	7	0.0001921	0	1	17.62892	Podovirid ae
c225	0	13	0	0	0	31.287011	Unclassifi ed
c456	0	3	0	0	0	17.357133	Unclassifi ed
c84	0	6	1.733E-05	0	1	17.288415	Unclassifi ed
c98	0	3	3.5E-06	0	2	16.908237	Siphovirid ae

c193	0	4	0	0	0	16.536568	Unclassified
c320	0	6	2.082E-06	0	1	16.379833	CrAss-like
c138	0	7	0.0001806	0	1	16.236093	Unclassified
c143	0	3	1.702E-06	0	1	15.885309	Unclassified
c216	0	4	0	0	0	15.540375	Unclassified
ERR8 44022 _NODE_79_ length _1766 _cov_ 77.12 51	0	3	0.0006415	0	2	15.198623	Unclassified
c467	0	2	0	0	0	15.12695	Unclassified
c411	0	2	0	0	0	14.978402	Unclassified
c62	0	15	0.0068752	0	4	3.2457015	Unclassified
c112	0	12	0.0001143	0	2	2.0160518	Unclassified
c38	4.889E-05	31	0.0031237	0	15	6.7852672	Unclassified
c101	0	17	0.0002311	0	6	2.2883145	Microviridae
c23	0.0001262	32	0.008828	0	5	2.0117121	Unclassified

c76	0	19	0.0302309	0	12	1.5157384	Unclassified
c39	0.0001764	34	0.0132151	0	6	1.8552787	Unclassified

Table 15. Bacterial taxa for which an Increase in Abundance is Associated with Crohn's Disease

RSV	Base Mean	log2Fold Change	lfcSE	stat	p-value	padj	Control Mean
Seq_0000236	20.28137	2.011272	0.740332	2.716717	0.006593	0.03267	0.001211
Seq_0000122	125.6541	2.590568	0.936966	2.764848	0.005695	0.029002	0.001573
Seq_0000153	22.39731	3.730738	1.440648	2.589626	0.009608	0.044037	8.74E-05
Seq_0000127	161.2392	4.604628	1.312875	3.507287	0.000453	0.003036	0.000895
Seq_0000196	29.93789	4.972102	1.786315	2.783441	0.005379	0.027908	5.23E-05
Seq_0000119	92.3124	5.157172	1.359764	3.792697	0.000149	0.001188	0.000147
Seq_0000229	6.485703	6.623851	2.045845	3.237709	0.001205	0.007283	3.36E-05
Seq_0000231	66.58209	6.661383	1.788413	3.724746	0.000196	0.001493	4.63E-05
Seq_0000132	44.71416	6.664723	2.180745	3.056168	0.002242	0.012712	5.49E-05
Seq_0000089	39.67258	7.48825	2.116666	3.537757	0.000404	0.002809	0.00728
Seq_0000101	15.76793	7.593127	2.997937	2.532784	0.011316	0.048624	1.8E-06
Seq_0000423	2.781729	22.31938	3.000098	7.43955	1.01E-13	1.68E-12	7.67E-06
Seq_0000309	21.42485	23.99216	2.402811	9.985041	1.77E-23	5.42E-22	4.27E-06
Seq_0000167	18.40277	24.06669	2.710259	8.879846	6.7E-19	1.47E-17	0
Seq_0000407	8.491631	24.08994	2.998334	8.034441	9.4E-16	1.85E-14	0.000154
Seq_0000697	9.072888	24.19048	2.657659	9.102176	8.85E-20	2.12E-18	2.92E-05
Seq_0000959	9.634949	24.27539	2.998232	8.096569	5.65E-16	1.15E-14	0
RSV	Control Median	Control Present (n=61)	CD Mean	CD Median	CD Present (n=27)	logfdr	Domain
Seq_0000236	0.0001137	28	0.001360 6	0.000456 8	21	1.4858571	Bacteria

Seq_0000122	0	23	0.009346 9	0.004772	22	1.5375723	Bacteria
Seq_0000153	0	14	0.001586 1	0	10	1.3561842	Bacteria
Seq_0000127	0	15	0.015557 3	0.001122 7	16	2.5176397	Bacteria
Seq_0000196	0	8	0.010636	0	10	1.5542765	Bacteria
Seq_0000119	0	14	0.010285 6	0.000392	15	2.9252425	Bacteria
Seq_0000229	0	1	0.000534 5	0	10	2.137714	Bacteria
Seq_0000231	0	4	0.005119 4	0	13	2.8257972	Bacteria
Seq_0000132	0	5	0.008571 4	0	9	1.8958019	Bacteria
Seq_0000089	0	5	0.017451 8	0	10	2.5513768	Bacteria
Seq_0000101	0	1	0.021922 9	0	3	1.313152	Bacteria
Seq_0000423	0	1	0.005500 3	0	4	11.773706	Bacteria
Seq_0000309	0	1	0.003030 3	0	9	21.266378	Bacteria
Seq_0000167	0	0	0.001606 8	0	6	16.831808	Bacteria
Seq_0000407	0	2	0.002066 5	0	4	13.733638	Bacteria
Seq_0000697	0	1	0.001163	0	6	17.674228	Bacteria
Seq_0000959	0	0	0.001007 6	0	4	13.938715	Bacteria
RSV	Phylum	Class	Order	Family	Genus		

Seq_0000236	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000122	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium_XIVa
Seq_0000153	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_0000127	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000196	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000119	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000229	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000231	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000132	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000089	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000101	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacteriaceae_unclassified
Seq_0000423	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Megasphaera
Seq_0000309	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella
Seq_0000167	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto
Seq_0000407	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Seq_0000697	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_0000959	Fusobacteriaria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium

Table 16. Bacterial taxa for which an Increase in Abundance is Associated with Ulcerative Colitis

RSV	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
Seq_0000100	141.09413	2.0990569	0.4957116	4.2344316	2.291E-05	0.0004571	0.0014535
Seq_0000037	306.26474	3.0006736	0.9617116	3.1201388	0.0018077	0.0248709	0.0022603
Seq_0000160	45.943379	3.0181245	0.7608213	3.9669297	7.28E-05	0.0013204	0.0002462
Seq_0000119	33.156032	3.2330051	1.0315239	3.1342029	0.0017232	0.0248709	0.0001467
Seq_0000132	23.907487	5.4133695	1.8193462	2.9754477	0.0029256	0.0376555	5.491E-05
Seq_0000607	5.7996844	23.208704	2.6471711	8.7673608	1.829E-18	4.865E-17	0
Seq_0000229	28.744397	25.451355	2.464175	10.32855	5.235E-25	1.899E-23	3.364E-05
RSV	Control Median	Control Present (n=47)	UC Mean	UC Median	UC Present (n=39)	logfdr	Domain
Seq_0000100	0.0007667	42	0.006977	0.002117	37	3.3399741	Bacteria
Seq_0000037	0	23	0.0141059	0.001647	27	1.6043087	Bacteria
Seq_0000160	3.877E-05	25	0.002094	0.000347	30	2.8792918	Bacteria

Seq_000011 9	0	14	0.0016457	0.000260 2	24	1.604308 7	Bacteria
Seq_000013 2	0	5	0.0045031	0	13	1.424172	Bacteria
Seq_000060 7	0	0	0.0008722	0	7	16.31289 8	Bacteria
Seq_000022 9	0	1	0.0036045	0	9	22.72153 8	Bacteria
RSV	Phylum	Class	Order	Family	Genus		
Seq_000010 0	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor		
Seq_000003 7	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides		
Seq_000016 0	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Pasteurellaceae_unclassified		
Seq_000011 9	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Veillonella		
Seq_000013 2	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto		
Seq_000060 7	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified		
Seq_000022 9	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_1	Clostridium_sensu_stricto		

Table 17. Bacterial taxa for which a Decrease in Abundance is Associated with Crohn's Disease

RSV	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
Seq_0000272	53.219635	-26.082279	2.5656564	-10.165928	2.814E-24	9.105E-23	0.0018236
Seq_0000299	81.885648	-25.878297	2.6031422	-9.9411769	2.756E-23	7.729E-22	0.0026192

Seq_000 0201	118.60798	-25.852613	2.3916551	-10.809507	3.103E-27	1.422E-25	0.0043023
Seq_000 0373	41.837099	-25.401626	2.29908	-11.048605	2.226E-28	1.749E-26	0.0014203
Seq_000 0528	30.69132	-25.323565	1.815756	-13.946568	3.301E-44	9.078E-42	0.0011655
Seq_000 0206	30.311998	-25.299615	2.3844273	-10.610353	2.667E-26	1.129E-24	0.0021875
Seq_000 0375	25.460569	-25.064958	1.5520319	-16.149769	1.14E-58	6.269E-56	0.0024483
Seq_000 0534	23.190963	-24.927629	2.1351487	-11.674892	1.713E-31	1.57E-29	0.0007857
Seq_000 0643	20.080908	-24.741846	1.9463304	-12.712048	5.069E-37	5.576E-35	0.0006498
Seq_000 0440	18.557977	-24.628144	2.7602166	-8.9225404	4.557E-19	1.044E-17	0.0013121
Seq_000 0466	17.273042	-24.521315	1.8334232	-13.374607	8.51E-41	1.56E-38	0.0005984
Seq_000 0421	16.216813	-24.458418	3.007753	-8.1317907	4.23E-16	8.948E-15	0.0014779
Seq_000 0756	16.124402	-24.439633	1.9175061	-12.745531	3.301E-37	4.539E-35	0.0004984
Seq_000 0360	27.341225	-24.401945	2.2559222	-10.816838	2.865E-27	1.422E-25	0.0011806
Seq_000 0835	14.277797	-24.279895	2.4428413	-9.939203	2.811E-23	7.729E-22	0.0004797
Seq_000 0863	14.088293	-24.255491	2.5791077	-9.4046057	5.223E-21	1.306E-19	0.0005303
Seq_000 0797	13.974818	-24.199775	2.1981478	-11.009166	3.452E-28	2.373E-26	0.0006175
Seq_000 0446	12.939315	-24.149211	3.0078232	-8.0288	9.843E-16	1.867E-14	0.001814

Seq_000 0284	12.346138	-24.03708	2.1970992	-10.940371	7.39E-28	4.516E-26	0.0025987
Seq_000 0243	10.97229	-23.914029	3.0078853	-7.9504456	1.858E-15	3.31E-14	0.0020654
Seq_000 0268	10.882425	-23.91258	3.0078886	-7.9499551	1.866E-15	3.31E-14	0.0022248
Seq_000 0395	10.831505	-23.903656	2.2841709	-10.464916	1.252E-25	4.918E-24	0.0007609
Seq_000 0937	10.857011	-23.894886	2.2980005	-10.39812	2.529E-25	8.692E-24	0.0003825
Seq_000 0551	10.296342	-23.827957	3.0079121	-7.9217597	2.342E-15	4.025E-14	0.0003617
Seq_000 0988	9.7685955	-23.747391	2.1812979	-10.886817	1.332E-27	7.327E-26	0.0003282
Seq_000 0827	8.5196893	-23.601406	2.2654158	-10.418134	2.049E-25	7.514E-24	0.0003846
Seq_000 0644	17.312567	-23.350181	2.4629702	-9.4804965	2.531E-21	6.628E-20	0.000706
Seq_000 0327	77.100425	-10.40391	2.2718207	-4.5795471	4.66E-06	5.339E-05	0.0023375
Seq_000 0063	273.13268	-10.239358	1.5070501	-6.7943049	1.088E-11	1.761E-10	0.0098973
Seq_000 0081	160.79438	-9.510953	1.7806337	-5.3413305	9.227E-08	1.208E-06	0.0056053
Seq_000 0166	164.80854	-9.4557291	1.8702437	-5.0558808	4.284E-07	5.355E-06	0.0057614
Seq_000 0501	13.332192	-8.3172468	2.2078868	-3.7670622	0.0001652	0.0012978	0.0004536
Seq_000 0131	210.62989	-8.0115669	1.8929315	-4.2323597	2.313E-05	0.0002193	0.0074563
Seq_000 0144	125.14371	-8.004541	1.3019056	-6.1483265	7.83E-10	1.196E-08	0.0047959

Seq_000 0364	27.667427	-7.798976	1.3234381	-5.8929663	3.793E-09	5.583E-08	0.0009794
Seq_000 0333	47.756166	-7.6797532	1.3692081	-5.6089014	2.036E-08	2.8E-07	0.0017735
Seq_000 0312	61.325817	-7.4998101	1.5637852	-4.7959338	1.619E-06	1.979E-05	0.0022974
Seq_000 0508	19.268057	-7.2768705	1.5657357	-4.6475728	3.359E-06	4.016E-05	0.0007407
Seq_000 0242	110.56838	-7.1969614	1.6991525	-4.2356183	2.279E-05	0.0002193	0.0040036
Seq_000 0192	99.342717	-6.9972788	1.9360994	-3.6141113	0.0003014	0.0021527	0.0039215
Seq_000 0152	58.810622	-6.9156137	1.1237047	-6.154298	7.541E-10	1.185E-08	0.003948
Seq_000 0758	14.907836	-6.9066636	1.2774654	-5.4065366	6.426E-08	8.62E-07	0.0005491
Seq_000 0573	14.644319	-6.8810039	1.5941777	-4.3163343	1.586E-05	0.0001593	0.0005309
Seq_000 0684	12.310606	-6.6307428	1.7332603	-3.8255897	0.0001305	0.0010759	0.0004663
Seq_000 0274	36.925011	-6.5751764	1.6433324	-4.0011239	6.304E-05	0.0005592	0.0020688
Seq_000 0852	11.350616	-6.5128971	1.1245147	-5.7917405	6.966E-09	9.824E-08	0.0003956
Seq_000 0786	9.8056343	-6.3024619	1.7871573	-3.5265288	0.000421	0.0028947	0.000359
Seq_000 0265	54.284571	-6.2679939	1.0641389	-5.8902027	3.857E-09	5.583E-08	0.0020329
Seq_000 0199	109.35494	-6.2282484	1.4432731	-4.3153638	1.593E-05	0.0001593	0.0046131
Seq_000 0833	9.1575904	-6.152675	2.4220132	-2.5403144	0.0110753	0.0479638	0.0003201

Seq_000 0519	10.841204	-6.0699899	2.3174898	-2.6192089	0.0088134	0.0417877	0.0003668
Seq_000 0383	34.044901	-6.0562844	1.5746401	-3.8461389	0.00012	0.0010153	0.001179
Seq_000 1143	8.1962113	-6.0437081	1.7664231	-3.4214386	0.0006229	0.0040786	0.0002784
Seq_000 0107	78.330906	-6.0142794	1.3659395	-4.4030349	1.067E-05	0.0001151	0.0041628
Seq_000 0867	7.8993904	-5.9903049	1.6795627	-3.566586	0.0003617	0.0025502	0.0003428
Seq_000 0151	141.57281	-5.9706553	1.6305412	-3.6617631	0.0002505	0.0018617	0.0049197
Seq_000 0628	7.7804869	-5.9689154	1.8458354	-3.2337203	0.0012219	0.0073048	0.0002999
Seq_000 0113	284.80846	-5.9327792	1.5526273	-3.8211226	0.0001328	0.0010759	0.0106946
Seq_000 0486	7.5125012	-5.9180763	2.2651671	-2.6126445	0.0089845	0.0422347	0.0010024
Seq_000 0983	7.2806979	-5.8730717	1.5371296	-3.8208045	0.000133	0.0010759	0.0002558
Seq_000 0609	12.966516	-5.8579405	1.3031405	-4.4952486	6.949E-06	7.644E-05	0.0004724
Seq_000 0271	48.964799	-5.8039167	1.3309401	-4.3607649	1.296E-05	0.0001371	0.0017191
Seq_000 0850	6.9108	-5.7978771	2.0139556	-2.8788505	0.0039913	0.0215942	0.0002602
Seq_000 0961	6.9063061	-5.796737	2.2454157	-2.5815875	0.0098347	0.0443368	0.0002786
Seq_000 0976	6.8742503	-5.7891065	1.422998	-4.0682464	4.737E-05	0.0004271	0.0002292
Seq_000 0237	67.824745	-5.7690417	1.4710105	-3.9218222	8.788E-05	0.0007552	0.0023295

Seq_000 0391	17.110253	-5.7491524	1.3862539	-4.147258	3.365E-05	0.0003137	0.0006702
Seq_000 0479	6.5051346	-5.7103297	2.1334151	-2.6766144	0.007437	0.0361979	0.0004304
Seq_000 1013	6.0163532	-5.5975254	2.1191763	-2.6413685	0.0082572	0.0398373	0.0001998
Seq_000 0275	61.958573	-5.5929779	1.8819207	-2.9719519	0.0029591	0.0162752	0.0023756
Seq_000 0338	32.389866	-5.5627529	1.0469919	-5.3130811	1.078E-07	1.379E-06	0.0012815
Seq_000 1029	5.7694088	-5.5365196	1.5853516	-3.4922975	0.0004789	0.0031733	0.0001963
Seq_000 0890	11.490768	-5.5353355	1.7860103	-3.0992741	0.00194	0.0111143	0.0004949
Seq_000 0418	37.655966	-5.5132396	2.0023733	-2.7533525	0.0058988	0.0297648	0.0014361
Seq_000 0701	5.6339436	-5.5027917	1.9121602	-2.877788	0.0040047	0.0215942	0.0001938
Seq_000 0193	73.773576	-5.4787039	1.373305	-3.9894297	6.623E-05	0.0005782	0.0026308
Seq_000 1313	5.4480857	-5.4546516	1.8187049	-2.9991956	0.0027069	0.015192	0.0002617
Seq_000 0326	42.473701	-5.2502538	1.4167642	-3.7058063	0.0002107	0.0015876	0.0014484
Seq_000 1395	4.6746521	-5.2338429	1.9865443	-2.6346469	0.0084225	0.0402814	0.0002472
Seq_000 0482	18.716434	-5.22653	1.2214701	-4.2788851	1.878E-05	0.0001845	0.0009508
Seq_000 0734	4.6497766	-5.2265205	1.439654	-3.6304006	0.000283	0.0020752	0.0001807
Seq_000 1169	4.3341529	-5.1243788	1.9748798	-2.5947801	0.0094651	0.0437465	0.0001665

Seq_000 1256	4.3050211	-5.1150217	1.7088342	-2.9932815	0.00276	0.0153331	0.0001604
Seq_000 1372	4.0971464	-5.043635	1.9709177	-2.5590287	0.0104965	0.0463123	0.0001311
Seq_000 0091	184.77238	-5.0242435	1.0824399	-4.6415914	3.457E-06	4.046E-05	0.0069056
Seq_000 0454	9.9315352	-4.9837209	1.4617206	-3.4094894	0.0006508	0.0042114	0.0012578
Seq_000 0571	11.68659	-4.7198881	1.437438	-3.283542	0.0010251	0.0064806	0.000478
Seq_000 0215	51.344753	-4.6991154	1.0864788	-4.3250869	1.525E-05	0.0001582	0.0018829
Seq_000 0158	136.18874	-4.603894	1.0229962	-4.5004017	6.783E-06	7.613E-05	0.005355
Seq_000 1748	2.5836491	-4.3788914	1.7344925	-2.5245952	0.0115832	0.0490057	9.558E-05
Seq_000 1253	5.4561222	-4.3653114	1.5720816	-2.7767715	0.0054902	0.0282205	0.0002057
Seq_000 1335	3.1087902	-4.1899351	1.6074257	-2.6066121	0.0091443	0.0426217	0.0001153
Seq_000 0869	10.695034	-4.0349154	1.2922963	-3.1222835	0.0017945	0.0103894	0.0003952
Seq_000 1057	5.5370759	-4.0304655	1.5934829	-2.5293434	0.0114276	0.0487224	0.0002243
Seq_000 0491	21.964573	-3.9833975	1.2271609	-3.2460271	0.0011703	0.007232	0.0007888
Seq_000 0439	36.146196	-3.9144762	1.3813248	-2.8338566	0.004599	0.0243216	0.0013565
Seq_000 0768	10.555403	-3.7837361	1.4791378	-2.5580688	0.0105255	0.0463123	0.0003915
Seq_000 0355	26.413194	-3.7482815	1.0647953	-3.5201898	0.0004312	0.0029282	0.0009187

Seq_000 0784	8.6881272	-3.6914706	1.1450583	-3.2238277	0.0012649	0.0074806	0.0003231
Seq_000 0664	14.827353	-3.6313729	1.426169	-2.5462431	0.0108889	0.0475311	0.000494
Seq_000 0599	21.087902	-3.5509988	1.3823831	-2.5687516	0.0102066	0.0456391	0.0007546
Seq_000 0731	8.6766401	-3.4735384	0.8457636	-4.1069849	4.009E-05	0.0003675	0.0003143
Seq_000 0078	156.61938	-3.4631068	1.0938055	-3.1661084	0.0015449	0.0090395	0.0050852
Seq_000 0032	662.52158	-3.1414794	0.8354555	-3.7601996	0.0001698	0.0013152	0.0213791
Seq_000 0020	1160.2848	-3.0910215	0.9533288	-3.2423457	0.0011855	0.0072447	0.0385559
Seq_000 0170	91.460041	-2.9878223	1.08943	-2.7425556	0.0060963	0.0304816	0.0033289
Seq_000 0425	25.151286	-2.9029201	0.8927114	-3.2518014	0.0011468	0.0071673	0.0008267
Seq_000 0489	17.236431	-2.8791195	0.7940747	-3.625754	0.0002881	0.0020851	0.0007202
Seq_000 0103	160.44044	-2.848016	1.0551709	-2.699104	0.0069526	0.0341425	0.0055631
Seq_000 0134	144.37276	-2.6697209	0.9317005	-2.8654282	0.0041645	0.0222374	0.0047267
Seq_000 0179	95.949883	-2.6058711	0.9259809	-2.8141736	0.0048903	0.0256158	0.0034828
Seq_000 0014	1389.0357	-2.5442077	0.7732058	-3.2904664	0.0010002	0.0063967	0.0457552
Seq_000 0287	44.456104	-2.2036409	0.8521562	-2.5859588	0.0097109	0.0441403	0.0015205
RSV	Control Median	Control Present (n=47)	CD Mean	CD Median	CD Present (n=28)	logfdr	Domain

Seq_000 0272	0	9	2.014E-05	0	1	22.040718	Bacteria
Seq_000 0299	0	9	0	0	0	21.111858	Bacteria
Seq_000 0201	0	11	0.000764	0	1	24.846991	Bacteria
Seq_000 0373	0	11	0	0	0	25.757116	Bacteria
Seq_000 0528	0	16	0	0	0	41.042004	Bacteria
Seq_000 0206	0	11	0	0	0	23.947491	Bacteria
Seq_000 0375	0	20	0	0	0	55.20278	Archaea
Seq_000 0534	0	12	0	0	0	28.804072	Bacteria
Seq_000 0643	0	14	0	0	0	34.253692	Bacteria
Seq_000 0440	0	8	0	0	0	16.981158	Bacteria
Seq_000 0466	0	15	0	0	0	37.806816	Bacteria
Seq_000 0421	0	6	0	0	0	14.048276	Bacteria
Seq_000 0756	0	14	0	0	0	34.343005	Bacteria
Seq_000 0360	0	11	0	0	0	24.846991	Bacteria
Seq_000 0835	0	9	0	0	0	21.111858	Bacteria
Seq_000 0863	0	8	0	0	0	18.884176	Bacteria

Seq_000 0797	0	11	0	0	0	25.624678	Bacteria
Seq_000 0446	0	7	0	0	0	13.728905	Bacteria
Seq_000 0284	0	13	0	0	0	25.345252	Bacteria
Seq_000 0243	0	7	0	0	0	13.480136	Bacteria
Seq_000 0268	0	5	0	0	0	13.480136	Bacteria
Seq_000 0395	0	11	0	0	0	23.308203	Bacteria
Seq_000 0937	0	10	0	0	0	23.060857	Bacteria
Seq_000 0551	0	6	0	0	0	13.395251	Bacteria
Seq_000 0988	0	11	0	0	0	25.135085	Bacteria
Seq_000 0827	0	10	6.486E-05	0	1	23.124116	Bacteria
Seq_000 0644	0	9	6.524E-05	0	1	19.178606	Bacteria
Seq_000 0327	0	11	2.225E-06	0	1	4.2725076	Bacteria
Seq_000 0063	0	23	1.437E-05	0	2	9.7543438	Bacteria
Seq_000 0081	0	18	0.0004002	0	1	5.9178408	Bacteria
Seq_000 0166	0	16	1.83E-05	0	2	5.2712316	Bacteria
Seq_000 0501	0	10	0.0009794	0	2	2.8867782	Bacteria

Seq_000 0131	0	17	3.19E-05	0	1	3.6589794	Bacteria
Seq_000 0144	0.0009321	27	0.0005665	0	1	7.9221519	Bacteria
Seq_000 0364	0.000112	24	0	0	0	7.2531463	Bacteria
Seq_000 0333	0.0001079	24	0.0005379	0	1	6.5528876	Bacteria
Seq_000 0312	0	20	6.86E-05	0	2	4.7035527	Bacteria
Seq_000 0508	0	19	0	0	0	4.3962322	Bacteria
Seq_000 0242	0	19	0.0004045	0	2	3.6589794	Bacteria
Seq_000 0192	0	15	0.0001621	0	2	2.6670142	Bacteria
Seq_000 0152	0.001063	29	4.137E-05	0	3	7.926272	Bacteria
Seq_000 0758	9.692E-05	24	0	0	0	6.0645135	Bacteria
Seq_000 0573	0	18	0	0	0	3.7976744	Bacteria
Seq_000 0684	0	16	0	0	0	2.9682389	Bacteria
Seq_000 0274	0	19	2.079E-05	0	1	3.2523966	Bacteria
Seq_000 0852	0.0002563	27	0	0	0	7.0077141	Bacteria
Seq_000 0786	0	15	2.552E-05	0	1	2.5383985	Bacteria
Seq_000 0265	0.0016061	31	0.0003028	0	2	7.2531463	Bacteria

Seq_000 0199	0	22	8.044E-05	0	4	3.7976744	Bacteria
Seq_000 0833	0	8	6.929E-06	0	1	1.3190861	Bacteria
Seq_000 0519	0	9	0.0002809	0	2	1.378952	Bacteria
Seq_000 0383	0	19	2.434E-05	0	2	2.993392	Bacteria
Seq_000 1143	0	15	0	0	0	2.3894928	Bacteria
Seq_000 0107	0.0003593	25	0.0053426	0	2	3.9388518	Bacteria
Seq_000 0867	0	16	0	0	0	2.5934288	Bacteria
Seq_000 0151	0	19	0.0063722	0	4	2.7300865	Bacteria
Seq_000 0628	0	14	0	0	0	2.1363928	Bacteria
Seq_000 0113	0	23	0.0001874	0	3	2.9682389	Bacteria
Seq_000 0486	0	11	0.0001597	0	2	1.3743307	Bacteria
Seq_000 0983	0	18	0	0	0	2.9682389	Bacteria
Seq_000 0609	0	23	7.248E-06	0	1	4.1166931	Bacteria
Seq_000 0271	0.0002036	24	0.0002168	0	3	3.8630069	Bacteria
Seq_000 0850	0	12	0	0	0	1.665663	Bacteria
Seq_000 0961	0	10	2.552E-05	0	1	1.3532357	Bacteria

Seq_000 0976	0	20	5.109E-05	0	1	3.3694796	Bacteria
Seq_000 0237	0	22	0.0006679	0	3	3.1219182	Bacteria
Seq_000 0391	0	22	1.384E-05	0	1	3.503529	Bacteria
Seq_000 0479	0	12	0	0	0	1.441317	Bacteria
Seq_000 1013	0	11	0	0	0	1.3997101	Bacteria
Seq_000 0275	0	15	4.813E-05	0	2	1.7884732	Bacteria
Seq_000 0338	0.0006906	31	4.247E-05	0	2	5.8605393	Bacteria
Seq_000 1029	0	17	0	0	0	2.4984846	Bacteria
Seq_000 0890	0	15	6.57E-06	0	1	1.954117	Bacteria
Seq_000 0418	0	13	2.562E-05	0	2	1.5262976	Bacteria
Seq_000 0701	0	13	0	0	0	1.665663	Bacteria
Seq_000 0193	0.0001796	25	5.716E-05	0	2	3.2379078	Bacteria
Seq_000 1313	0	14	0	0	0	1.8183856	Bacteria
Seq_000 0326	0	22	0.0002571	0	3	2.7992558	Bacteria
Seq_000 1395	0	12	0	0	0	1.3948949	Bacteria
Seq_000 0482	0.0002511	26	3.991E-05	0	1	3.7340562	Bacteria

Seq_000 0734	0	19	0	0	0	2.6829402	Bacteria
Seq_000 1169	0	12	0	0	0	1.359057	Bacteria
Seq_000 1256	0	15	0	0	0	1.8143712	Bacteria
Seq_000 1372	0	12	0	0	0	1.3343035	Bacteria
Seq_000 0091	0.0049558	32	0.0003153	0	6	4.3929905	Bacteria
Seq_000 0454	0	19	0.0001427	0	2	2.3755779	Bacteria
Seq_000 0571	0	21	4.721E-05	0	1	2.1883846	Bacteria
Seq_000 0215	0.0004976	32	0.0004857	0	3	3.8007238	Bacteria
Seq_000 0158	0.0014706	36	0.0002101	0	4	4.1184425	Bacteria
Seq_000 1748	0	14	0	0	0	1.3097535	Bacteria
Seq_000 1253	0	16	1.08E-05	0	2	1.5494348	Bacteria
Seq_000 1335	0	15	3.307E-06	0	1	1.3703694	Bacteria
Seq_000 0869	0	23	1.885E-05	0	2	1.9834077	Bacteria
Seq_000 1057	0	17	1.554E-05	0	1	1.3122714	Bacteria
Seq_000 0491	0.0003913	27	7.892E-05	0	1	2.1407386	Bacteria
Seq_000 0439	0.0002873	24	6.229E-05	0	2	1.6140075	Bacteria

Seq_000 0768	0	20	4.027E-05	0	1	1.3343035	Bacteria
Seq_000 0355	0.0005976	30	0.0001223	0	4	2.5334051	Bacteria
Seq_000 0784	0.000135	26	2.861E-05	0	2	2.1260658	Bacteria
Seq_000 0664	0	22	6.798E-05	0	1	1.3230225	Bacteria
Seq_000 0599	0.0001672	24	0.0001596	0	1	1.3406631	Bacteria
Seq_000 0731	0.0002518	36	3.436E-05	0	2	3.4347987	Bacteria
Seq_000 0078	0.0009548	31	0.0005871	0	9	2.0438558	Bacteria
Seq_000 0032	0.009373	41	0.0100398	8.85E-05	15	2.8810146	Bacteria
Seq_000 0020	0.0149118	39	0.0056335	0	12	2.1399778	Bacteria
Seq_000 0170	0.0016115	32	0.0006765	0	5	1.5159627	Bacteria
Seq_000 0425	0.0005985	35	0.0001767	0	6	2.144647	Bacteria
Seq_000 0489	0.0003943	39	0.0002006	0	5	2.6808782	Bacteria
Seq_000 0103	0.0027536	36	0.0010636	0	5	1.4667052	Bacteria
Seq_000 0134	0.0029961	38	0.0035154	0	7	1.6529161	Bacteria
Seq_000 0179	0.0016606	39	0.0008529	0	6	1.5914928	Bacteria
Seq_000 0014	0.025542	44	0.0102819	0.0003304	16	2.1940426	Bacteria

Seq_000 0287	0.0014266	37	0.0004641	0	8	1.3551652	Bacteria
RSV	Phylum	Class	Order	Family	Genus		
Seq_000 0272	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified		
Seq_000 0299	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Catenibacterium		
Seq_000 0201	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus		
Seq_000 0373	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus		
Seq_000 0528	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified		
Seq_000 0206	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified		
Seq_000 0375	Euryarchaeota	Methanobacteria	Methanobacteriales	Methanobacteriaceae	Methanobrevibacter		
Seq_000 0534	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified		
Seq_000 0643	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified		
Seq_000 0440	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV		
Seq_000 0466	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified		
Seq_000 0421	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium		

Seq_000 0756	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0360	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Barnesiella
Seq_000 0835	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0863	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0797	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0446	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000 0284	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0243	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dialister
Seq_000 0268	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_000 0395	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus 2
Seq_000 0937	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0551	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_000 0988	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0827	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_000 0644	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_000 0327	Firmicutes	Erysipelotricha	Erysipelotrichales	Erysipelotrichaceae	Erysipelotrichaceae_unclassified
Seq_000 0063	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0081	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000 0166	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0501	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0131	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_000 0144	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000 0364	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 0333	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0312	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0508	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Sporobacter
Seq_000 0242	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0192	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified

Seq_000 0152	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0758	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0573	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0684	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0274	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0852	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0786	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0265	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0199	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0833	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0519	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0383	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 1143	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Howardella
Seq_000 0107	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium

Seq_000 0867	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_000 0151	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_000 0628	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0113	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0486	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0983	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0609	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0271	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0850	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0961	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0976	Actinobacteria	Actinobacteria	Actinobacteria_unclassified	Actinobacteria_unclassified	Actinobacteria_unclassified
Seq_000 0237	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV
Seq_000 0391	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Clostridium_IV

Seq_000 0479	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 1013	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_000 0275	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0338	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 1029	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Flavonifractor
Seq_000 0890	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0418	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0701	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0193	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 1313	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 0326	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Ruminococcus 2
Seq_000 1395	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
Seq_000 0482	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 0734	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified

Seq_000 1169	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 1256	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 1372	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0091	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0454	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0571	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 0215	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillibacter
Seq_000 0158	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 1748	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Coriobacteriaceae_unclassified
Seq_000 1253	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 1335	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0869	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified

Seq_000 1057	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0491	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0439	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0768	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0355	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0784	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0664	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000 0599	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Dorea
Seq_000 0731	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0078	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus
Seq_000 0032	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0020	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0170	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia

Seq_000 0425	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0489	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Odoribacter
Seq_000 0103	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes
Seq_000 0134	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus
Seq_000 0179	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0014	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia
Seq_000 0287	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus

Table 18. Bacterial taxa for which a Decrease in Abundance is Associated with Ulcerative Colitis

RSV	Base Mean	log2FoldChange	lfcSE	stat	p-value	padj	Control Mean
Seq_000 0299	75.394273	-27.106863	2.4734585	-10.959093	6.01E-28	2.664E-26	0.002619 2
Seq_000 0242	103.6578	-27.098145	1.6276288	-16.648849	3.085E-62	1.231E-59	0.004003 6
Seq_000 0528	29.026273	-25.805116	1.7225062	-14.981145	9.752E-51	1.297E-48	0.001165 5
Seq_000 0446	24.834414	-25.615892	2.8356501	-9.0335163	1.662E-19	4.738E-18	0.001814
Seq_000 0421	15.523572	-24.981457	2.9165613	-8.5653803	1.077E-17	2.686E-16	0.001477 9
Seq_000 0756	15.143087	-24.927113	1.825086	-13.658048	1.808E-42	1.442E-40	0.000498 4

Seq_000 0383	31.313217	-24.74196	1.5376116	-16.091164	2.943E-58	5.87E-56	0.001179
Seq_000 0835	13.170012	-24.738616	2.3326007	-10.605594	2.807E-26	1.12E-24	0.000479 7
Seq_000 0284	11.500805	-24.558689	2.0961068	-11.716335	1.051E-31	5.992E-30	0.002598 7
Seq_000 0890	10.861799	-24.460365	1.7258632	-14.17283	1.35E-45	1.346E-43	0.000494 9
Seq_000 0496	9.3838114	-24.296018	2.5859736	-9.3953077	5.705E-21	1.751E-19	0.000567
Seq_000 0988	9.0310245	-24.243059	2.0814435	-11.647234	2.37E-31	1.182E-29	0.000328 2
Seq_000 0643	18.701219	-23.805797	1.8495797	-12.870922	6.561E-38	4.363E-36	0.000649 8
Seq_000 0863	12.90757	-23.25617	2.4641576	-9.4377771	3.808E-21	1.266E-19	0.000530 3
Seq_000 0131	189.37959	-11.223827	1.74257	-6.4409619	1.187E-10	2.493E-09	0.007456 3
Seq_000 0113	263.7258	-9.6179676	1.2946402	-7.4290658	1.094E-13	2.424E-12	0.010694 6
Seq_000 0041	269.40471	-8.5459554	1.0325205	-8.2767897	1.265E-16	2.97E-15	0.022152 4
Seq_000 0644	16.36076	-8.1993078	2.2506774	-3.64304	0.0002694	0.0044794	0.000706
Seq_000 0797	13.753236	-7.3611163	2.027835	-3.6300371	0.0002834	0.0045228	0.000617 5
Seq_000 0937	10.409892	-6.5401063	2.1214748	-3.0828112	0.0020506	0.0272723	0.000382 5
Seq_000 1143	7.4823259	-6.2479707	1.6817448	-3.7151718	0.0002031	0.0035227	0.000278 4
Seq_000 1013	5.5778757	-5.824007	2.0274206	-2.8726191	0.0040708	0.0495242	0.000199 8

Seq_000 0199	103.74554	-5.6702543	1.3948157	-4.0652355	4.798E-05	0.0009117	0.004613 1
Seq_000 0734	4.5899916	-4.2073933	1.3468459	-3.1238861	0.0017848	0.0248709	0.000180 7
Seq_000 0758	14.211789	-4.0415817	1.2666092	-3.1908671	0.0014185	0.021768	0.000549 1
Seq_000 0280	58.214405	-2.3270731	0.8106368	-2.870673	0.004096	0.0495242	0.002021 3
RSV	Control Median	Control Present (n=61)	CD Mean	CD Median	CD Present (n=27)	logfdr	Classific ation
Seq_000 0299	0	9	0.0002242	0	1	25.574406	Bacteria
Seq_000 0242	0	19	0	0	0	58.9098	Bacteria
Seq_000 0528	0	16	1.489E-05	0	1	47.887046	Bacteria
Seq_000 0446	0	7	0	0	0	17.324414	Bacteria
Seq_000 0421	0	6	9.854E-05	0	2	15.570852	Bacteria
Seq_000 0756	0	14	0	0	0	39.840886	Bacteria
Seq_000 0383	0	19	0	0	0	55.231338	Bacteria
Seq_000 0835	0	9	0	0	0	23.950824	Bacteria
Seq_000 0284	0	13	0.0001824	0	1	29.22243	Bacteria
Seq_000 0890	0	15	2.752E-05	0	1	42.870911	Bacteria
Seq_000 0496	0	8	0.0007268	0	1	18.756709	Bacteria

Seq_000 0988	0	11	1.274E-05	0	1	28.927318	Bacteria
Seq_000 0643	0	14	0	0	0	35.360182	Bacteria
Seq_000 0863	0	8	0	0	0	18.897544	Bacteria
Seq_000 0131	0	17	0.0008061	0	2	8.6032617	Bacteria
Seq_000 0113	0	23	0.000716	0	6	11.615412	Bacteria
Seq_000 0041	8.604E-05	28	0.0001724	0	14	14.527247	Bacteria
Seq_000 0644	0	9	2.039E-06	0	1	2.3487812	Bacteria
Seq_000 0797	0	11	1.65E-05	0	2	2.3445972	Bacteria
Seq_000 0937	0	10	4.078E-06	0	1	1.5642776	Bacteria
Seq_000 1143	0	15	0	0	0	2.4531184	Bacteria
Seq_000 1013	0	11	3.935E-05	0	1	1.3051822	Bacteria
Seq_000 0199	0	22	0.0009906	0	5	3.0401501	Bacteria
Seq_000 0734	0	19	0.0004573	0	3	1.6043087	Bacteria
Seq_000 0758	9.692E-05	24	3.816E-05	0	2	1.6621819	Bacteria
Seq_000 0280	0.0012941	36	0.000985	0	14	1.3051822	Bacteria
RSV	Phylum	Class	Order	Family	Genus		
Seq_000 0299	Firmicutes	Erysipelotrichi a	Erysipelotrichal es	Erysipelotrichace ae	Catenibacteriu m		

Seq_000 0242	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0528	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0446	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000 0421	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium
Seq_000 0756	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0383	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0835	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
Seq_000 0284	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0890	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0496	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Seq_000 0988	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0643	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0863	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 0131	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Coprococcus

Seq_000 0113	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae_unclassified
Seq_000 0041	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia
Seq_000 0644	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
Seq_000 0797	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0937	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
Seq_000 1143	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Howardella
Seq_000 1013	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Parabacteroides
Seq_000 0199	Firmicutes	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified	Firmicutes_unclassified
Seq_000 0734	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0758	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae_unclassified
Seq_000 0280	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia

Claims

1. A method for identifying a plurality of viral marker clusters for determining the presence of inflammatory bowel disease (IBD) using viral genome sequences, the method comprising:
 - obtaining a first dataset representing a first plurality of viral genome sequences derived from gastrointestinal (GI) microbiota samples of a healthy cohort;
 - obtaining a second dataset representing a second plurality of viral genome sequences derived from GI microbiota samples of a cohort diagnosed with IBD;
 - creating a first plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group viral genome sequences of the first dataset, each viral cluster in the first plurality of viral clusters comprising one or more viral genome sequences derived from the healthy cohort;
 - creating a second plurality of viral clusters by using protein clustering to group like proteins derived from the second dataset and by using protein homology to group viral genome sequences of the second dataset, each viral cluster in the second plurality of viral clusters comprising one or more viral genome sequences derived from the cohort diagnosed with IBD; and
 - identifying a plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters.
2. The method of claim 1,
 - wherein at least a portion of the first plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database, and
 - wherein at least a portion of the second plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database.
3. The method of claims 1 or 2, wherein a totality of the first plurality and second plurality of viral genome sequences are each unassociated with a viral taxonomic category derived from a viral genome database.
4. The method of any one of claims 1-3, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises using machine learning to identify the plurality of marker clusters.

5. The method of any one of claims 1-4, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises identifying the plurality of marker clusters unassociated with a known taxon.
6. The method of any one of claims 1-5, wherein each of the viral clusters in the plurality of marker clusters respectively represent an unidentified taxon of higher rank than a strain and of lower rank than a family.
7. The method of any one of claims 1-6, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises performing beta diversity analysis on the first plurality of viral clusters and the second plurality of viral clusters.
8. The method of claim 7, wherein performing the beta diversity analysis comprises performing a scaling and ordination technique selected from a group consisting of principal coordinates analysis (PCoA), principal components analysis (PCA), non-metric multidimensional scaling (NMDS), canonical correspondence analysis (CCA), and redundancy analysis (RDA).
9. The method of any one of claims 1-8, wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters comprises calculating differential abundance of viral clusters in the first plurality of viral clusters and the second plurality of viral clusters.
10. The method of any one of claims 1-9, wherein the healthy cohort and the cohort diagnosed with IBD are each human cohorts.
11. The method of any one of claims 1-10, further comprising:
associating a first data subset of the second dataset with a first sub-cohort diagnosed with IBD and Crohn's disease (CD);

associating a second data subset of the second dataset with a second sub-cohort diagnosed with IBD and ulcerative colitis (UC);

associating a first subset of viral clusters of the second plurality of viral clusters with the first sub-cohort;

associating a second subset of viral clusters of the second plurality of viral clusters with the second sub-cohort; and

identifying a first subset of marker clusters of the plurality of marker clusters and a second subset of marker clusters of the plurality of marker clusters by comparing the first subset of viral clusters to the second subset of viral clusters.

12. The method of any one of claims 1-11, further comprising:

representing the viral genome sequences in the first dataset each respectively as a first viral contig of a protein sequence; and

representing the viral genome sequences in the second dataset each respectively as a second viral contig of a protein sequence.

13. The method of any one of claims 1-12,

wherein the first dataset further represents a first plurality of identified viral genome sequences derived from the healthy cohort,

wherein the second dataset further represents a second plurality of identified viral genome sequences derived from the cohort diagnosed with IBD, and

wherein the method further comprises:

creating a first plurality of reference viral clusters using protein clustering to group like proteins and protein homology to group identified viral genome sequences of the first plurality of identified viral genome sequences;

creating a second plurality of reference viral clusters using protein clustering to group like proteins and protein homology to group identified viral genome sequences of the second plurality of identified viral genome sequences; and

wherein the step of identifying the plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters further comprises identifying the plurality of marker clusters by comparing a combination of the first plurality

of viral clusters and the first plurality of reference viral clusters to a combination of the second plurality of viral clusters and the second plurality of reference viral clusters.

14. The method of claim 13,
wherein the first plurality of identified viral genome sequences are associated with a viral taxonomic category present in a viral genome database, and
wherein the second plurality of identified viral genome sequences are associated with a viral taxonomic category present in a viral genome database.
15. A method for determining the presence of inflammatory bowel disease (IBD) in a subject, the method comprising:
obtaining an individual viral dataset representing a plurality of viral genome sequences derived from a GI microbiota sample obtained from the subject;
creating a plurality of subject viral clusters using protein clustering to group like proteins derived from the individual viral dataset and by using protein homology to group unidentified viral genome sequences of the individual viral dataset, each viral cluster in the plurality of subject viral clusters comprising one or more viral genome sequences derived from the subject;
obtaining a plurality of marker clusters indicative of the presence or absence of IBD; and
comparing the plurality of subject viral clusters to the plurality of marker clusters.
16. The method of claim 15, wherein at least a portion of the plurality of viral genome sequences are unassociated with a viral taxonomic category derived from a viral genome database.
17. The method of claims 15 or 16, wherein a totality of the plurality of viral genome sequences are each unassociated with a viral taxonomic category derived from a viral genome database.
18. The method of any one of claims 15-17, wherein at least a portion of the plurality of marker clusters are unassociated with a viral taxonomic category derived from a viral genome database.

19. The method of any one of claims 15-19, further comprising determining the presence of IBD in the subject based at least in part on the comparison of the plurality of subject viral clusters to the plurality of marker clusters.

20. The method of any one of claims 15-19, wherein the marker clusters comprise one or more viral clusters from taxa Siphoviridae, Myoviridae, Podoviridae, CrAss-like, or Microviridae.

21. The method of any one of claims 15-20, wherein the plurality of marker clusters comprises one or more viral clusters selected from vc2, vc6, vc7, vc13, vc14, vc15, vc17, vc19, vc21, vc22, vc23, vc24, vc25, vc28, vc29, vc36, vc37, vc38, vc39, vc40, vc42, vc45, vc48, vc53, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc75, vc76, vc77, vc78, vc79, vc80, vc82, vc84, vc85, vc86, vc88, vc89, vc91, vc92, vc94, vc95, vc96, vc97, vc98, vc99, vc101, vc102, vc103, vc104, vc108, vc109, vc112, vc113, vc115, vc117, vc118, vc122, vc123, vc124, vc130, vc132, vc136, vc138, vc142, vc143, vc152, vc154, vc155, vc160, vc161, vc175, vc178, vc181, vc190, vc193, vc205, vc209, vc216, vc218, vc225, vc232, vc263, vc264, vc281, vc284, vc298, vc320, vc411, vc413, vc420, vc456, and vc467.

22. The method of any one of claims 15-21, wherein an increased abundance of one or more viral clusters selected from vc2, vc13, vc14, vc15, vc17, vc21, vc22, vc36, vc40, vc48, vc53, vc66, vc68, vc69, vc70, vc71, vc73, vc74, vc77, vc78, vc79, vc80, vc85, vc88, vc89, vc91, vc94, vc95, vc97, vc102, vc108, vc113, vc115, vc117, vc118, vc122, vc123, vc130, vc132, vc142, vc152, vc155, vc160, vc161, vc175, vc178, vc181, vc205, vc218, vc232, vc263, vc264, vc281, vc298, vc413, and vc420 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of IBD in the subject.

23. The method of claim 22, wherein an increased abundance of one or more viral clusters selected from vc15, vc66, vc71, vc73, vc77, vc78, vc79, vc80, vc91, vc94, vc108, vc113, vc117, vc118, vc132, vc142, vc155, vc160, vc178, vc232, vc264, vc281, vc298, and vc420 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

24. The method of claim 22, wherein an increased abundance of one or more viral clusters selected from vc28 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

25. The method of claim 22, wherein an increased abundance of one or more viral clusters selected from vc2, vc17, vc21, vc22, vc53, vc70, vc74, vc85, vc88, vc89, vc115, vc122, vc123, vc130, vc152, vc161, vc175, vc181, vc205, vc218, vc263, and vc413 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

26. The method of claim 22, wherein an increased abundance of viral cluster vc2 in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

27. The method of any one of claims 15-21, wherein an increased abundance of one or more viral clusters selected from vc38, vc46, vc48, vc54, vc57, vc62, vc64, vc69, vc71, vc108, vc111, vc114, vc115, vc128, vc159, vc162, vc215, vc220, vc242, vc340, vc374, and vc392 in the subject sample as compared to a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject.

28. The method of any one of claims 15-21, wherein an increased abundance of one or more viral clusters selected from vc16, vc119, and vc163 in the subject sample as compared to a patient with a flare-up of ulcerative colitis (UC) is indicative of the presence of UC in remission in the subject.

29. The method of any one of claims 15-21, wherein a decreased abundance of one or more viral clusters selected from vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of IBD in the subject.

30. The method of claim 29, wherein a decreased abundance of one or more viral clusters selected from vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284 in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

31. The method of claim 29, wherein a decreased abundance of one or more viral clusters selected from vc7, vc25, vc47, and vc64 in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

32. The method of claim 29, wherein a decreased abundance of vc98 and/or vc103 viral cluster in the plurality of subject viral clusters as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

33. The method of any one of claims 15-32, wherein obtaining the dataset(s) is performed by sequencing VLP DNA isolated from GI microbiota sample(s).

34. The method of any one of claims 15-33, further comprising:
obtaining an individual bacteriome dataset representing bacterial sequences derived from the GI microbiota sample obtained from the subject; and
evaluating the individual bacteriome dataset for the presence of bacterial taxa associated with IBD.

35. The method of claim 34, further comprising determining the presence of IBD in the subject based at least in part on the comparison of the individual bacteriome dataset to at least one of a healthy control and a control diagnosed with IBD.

36. The method of claim 34 or claim 35, wherein the bacterial taxa associated with IBD comprise one or more bacterial genera selected from *Clostridium XIVa*, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, *Flavonifractor*, *Catenibacterium*,

Ruminococcus, *Coprococcus*, *Methanobrevibacter*, *Clostridium* IV, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus*2, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Dorea*, *Roseburia*, *Odoribacter*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

37. The method of claim 36, wherein an increased abundance of one or more bacterial genera selected from *Clostridium* XIVa, *Blautia*, *Veillonella*, *Clostridium sensu stricto*, *Megasphaera*, *Fusobacterium*, and *Flavonifractor* in the subject sample as compared to a healthy control is indicative of the presence of IBD in the subject.

38. The method of claim 37, wherein an increased abundance of one or more bacterial genera selected from *Clostridium* XIVa, *Blautia*, *Megasphaera*, and *Fusobacterium* in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.

39. The method of claim 34 or claim 35, wherein an increased abundance of one or more bacterial species selected from *Bacteroides fragilis* and *Ruminococcus gnavus* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.

40. The method of claim 34 or claim 35, wherein an increased abundance of *Ruminococcus gnavus* in the subject sample as compared to a control sample from a patient with ulcerative colitis (UC) in remission is indicative of the presence of a flare-up of UC in the subject.

41. The method of claim 34 or claim 35, wherein an increased abundance of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes* in the subject sample as compared to a control sample from a patient with a flare-up of ulcerative colitis (UC) in remission is indicative of the presence of UC in remission in the subject.

42. The method of claim 37, wherein an increased abundance of bacterial genus *Flavonifractor* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.
43. The method of claim 36, wherein a decreased abundance of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* in the subject sample as compared to a healthy control is indicative of the presence of IBD in the subject.
44. The method of claim 43, wherein a decreased abundance of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* in the subject sample as compared to a healthy control is indicative of the presence of Crohn's Disease (CD) in the subject.
45. The method of claim 43, wherein a decreased abundance of bacterial genus *Akkermansia* in the subject sample as compared to a healthy control is indicative of the presence of ulcerative colitis (UC) in the subject.
46. The method of any one of claims 34-45, wherein obtaining the individual bacteriome dataset is performed by sequencing 16S rDNA or a V region of 16S rDNA in the GI microbiota sample.
47. The method of claim 46, wherein the V region is V4 region.
48. The method of any one of claims 15-47, wherein the GI microbiota sample is a fecal sample.
49. The method of any one of claims 15-48, wherein the subject is a human.

50. The method of any one of claims 15-49, further comprising administering an IBD treatment to the subject.
51. The method of any one of claims 15-50, further comprising administering to the subject additional diagnostic tests for IBD, CD and/or UC.
52. The method of any one of claims 15-51, further comprising enrolling the subject in a clinical trial.
53. The method of any one of claims 15-52, wherein comparing the plurality of subject viral clusters to the plurality of marker clusters comprises:
- identifying common clusters present in the plurality of subject viral clusters and the plurality of marker clusters;
 - determining relative abundance of members within each common cluster in the plurality of subject viral clusters;
 - associating a correlation value with each common cluster in the plurality of marker clusters;
 - and
 - comparing the relative abundance of members within each common cluster in the plurality of subject viral clusters to the correlation value of each common cluster in the plurality of marker clusters.
54. A kit for determining the presence of inflammatory bowel disease (IBD) in a subject comprising:
- a device to:
 - receive a first dataset representing a plurality of unidentified viral genome sequences derived from a GI microbiota sample obtained from the subject;
 - receive a second dataset representing a plurality of viral genome IBD marker clusters;
 - create a plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group unidentified viral

genome sequences of the plurality of unidentified viral genome sequences, each viral cluster in the plurality of viral clusters comprising one or more unidentified viral genome sequences of the plurality of unidentified genome sequences; and

compare the first plurality of viral clusters to the second dataset; and

determine the presence of IBD based at least in part on the comparison of the plurality of viral clusters to the second dataset.

55. The kit of claim 54, wherein the device is further configured to:
receive a third dataset representing bacteria from the GI microbiota sample obtained from the subject;
evaluate the third dataset for the purpose of IBD diagnosis; and
determine the presence of IBD based at least in part on the evaluation of the third database.
56. The kit of claim 54 or 55, wherein the GI microbiota sample is one or more of group consisting a fecal sample, a cecal sample, an ileal sample, and a colonic microbiota sample.
57. The kit of any of claims 54-56, wherein the IBD is ulcerative colitis (UC).
58. The kit of any of claims 54-56, wherein the IBD is Crohn's disease (CD).
59. The kit of any one of claims 54-58, wherein the subject is human.
60. A system comprising:
one or more processors;
a memory in communication with the one or more processors and storing instructions thereon that, when executed by the one or more processors, are configured to cause the system to:
receive a first dataset representing a first plurality of viral genome sequences derived from a healthy cohort;
receive a second dataset representing a second plurality of viral genome sequences derived from a cohort diagnosed with IBD;

create a first plurality of viral clusters by using protein clustering to group like proteins derived from the first dataset and by using protein homology to group viral genome sequences of the first dataset, each viral cluster in the first plurality of viral clusters comprising one or more viral genome sequences derived from the healthy cohort;

create a second plurality of viral clusters by using protein clustering to group like proteins derived from the second dataset and by using protein homology to group viral genome sequences of the second dataset, each viral cluster in the second plurality of viral clusters comprising one or more viral genome sequences derived from the cohort diagnosed with IBD; and

identify a plurality of marker clusters by comparing the first plurality of viral clusters to the second plurality of viral clusters.

61. A method for preventing and/or treating inflammatory bowel disease (IBD) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc6, vc7, vc19, vc23, vc24, vc25, vc29, vc37, vc38, vc39, vc42, vc45, vc55, vc56, vc58, vc60, vc61, vc62, vc64, vc75, vc76, vc82, vc84, vc86, vc89, vc92, vc96, vc98, vc99, vc101, vc103, vc104, vc109, vc112, vc124, vc136, vc138, vc143, vc154, vc190, vc193, vc209, vc216, vc225, vc284, vc320, vc411, vc456, and vc467.

62. A method for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

63. A method for preventing and/or treating Crohn's disease (CD) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc6, vc7, vc19, vc25, vc29, vc37, vc42, vc45, vc56, vc58, vc60, vc61, vc64, vc82, vc86, vc89, vc92, vc99, vc104, vc109, vc124, vc136, vc154, vc190, and vc284.

64. A method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

65. A method for preventing and/or treating ulcerative colitis (UC) in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster vc98 and/or vc103.

66. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a virus from a viral cluster selected from vc10, vc23, and vc39.

67. The method of claim 1, further comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

68. The method of claim 63, further comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

69. The method of claim 65, further comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity in the GI microbiota of the subject of the bacterial

genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus.

70. A method for preventing and/or treating IBD in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of one or more bacterial genera selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

71. A method for preventing and/or treating CD in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of one or more bacterial genera selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said one or more bacterial genera.

72. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of the genus *Akkermansia* or a closely related OTU which has at least 90% sequence identity to 16S rRNA over its entire length or has at least 90% sequence identity to any single V region of 16S rRNA of said bacterial genus.

73. The method of claim 67 or claim 70, wherein said probiotic composition comprises one or more bacterial strains from the genus selected from *Catenibacterium*, *Ruminococcus*, *Coprococcus*, *Methanobrevibacter*, *Clostridium IV*, *Faecalibacterium*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Howardella*, *Bifidobacterium*, *Oscillibacter*, *Parabacteroides*, *Flavonifractor*, *Blautia*, *Dorea*, *Roseburia*, *Odoribacter*, *Catenibacterium*, and *Akkermansia*.

74. The method of claim 68 or claim 71, wherein said probiotic composition comprises one or more bacterial strains from the genus selected from *Ruminococcus*, *Methanobrevibacter*, *Clostridium IV*, *Barnesiella*, *Dialister*, *Ruminococcus2*, *Alistipes*, *Sporobacter*, *Bifidobacterium*, *Oscillibacter*, *Flavonifractor*, *Dorea*, *Roseburia*, and *Odoribacter*.

75. The method of claim 69 or claim 72, wherein said probiotic composition comprises one or more bacterial strains from the genus *Akkermansia*.

76. The method of any one of claims 67-75, wherein the V region is V4 region.

77. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic or a prebiotic composition or a combination thereof, wherein said composition(s) stimulates growth and/or activity of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes*.

78. A method for preventing and/or treating UC in a subject in need thereof, said method comprising administering to the subject an effective amount of a probiotic comprising one or more of *Faecalibacterium prausnitzii*, *Dorea longicatena* or *Coprococcus comes*.

79. The method of any one of claims 61-78, wherein the subject is human.

Figure 1A

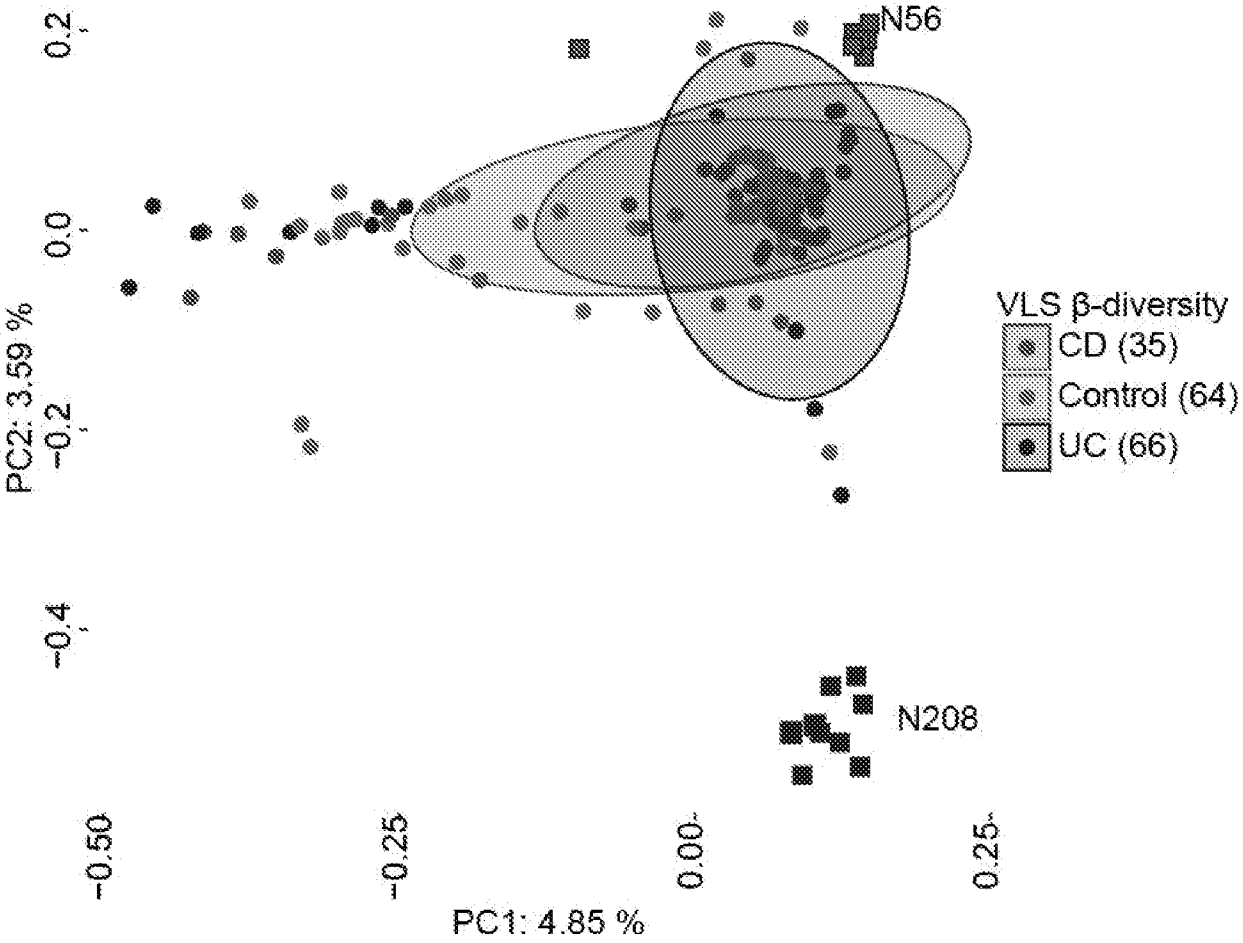


Figure 1B

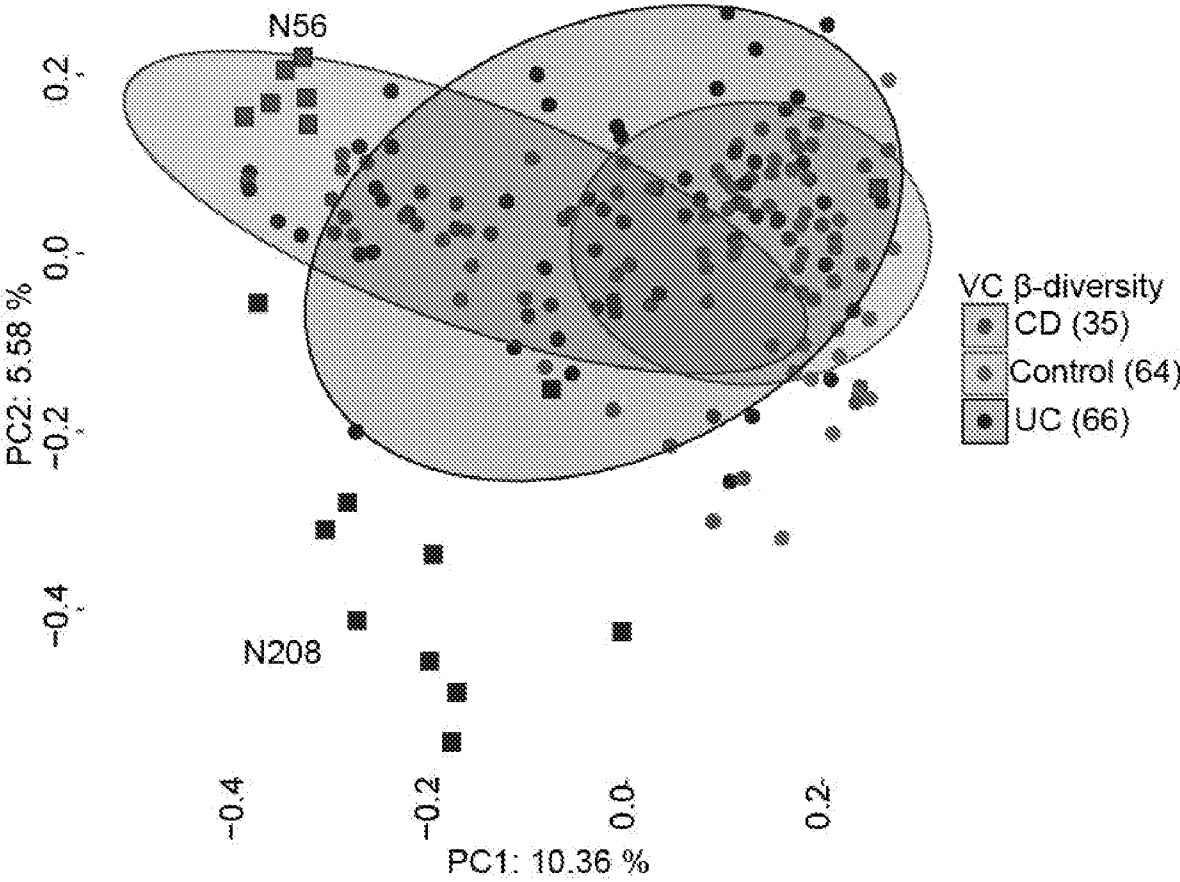


Figure 1C

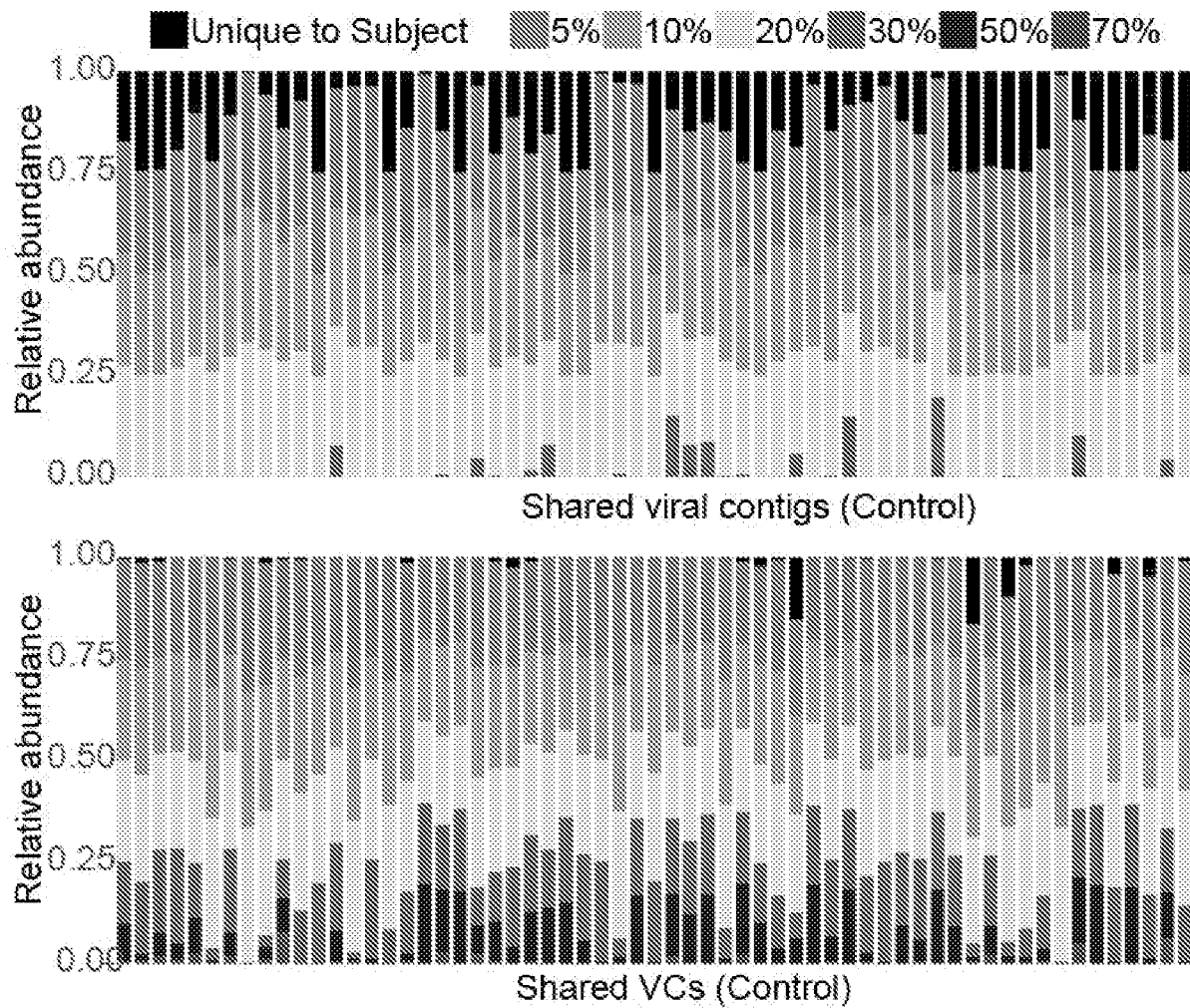


Figure 1D

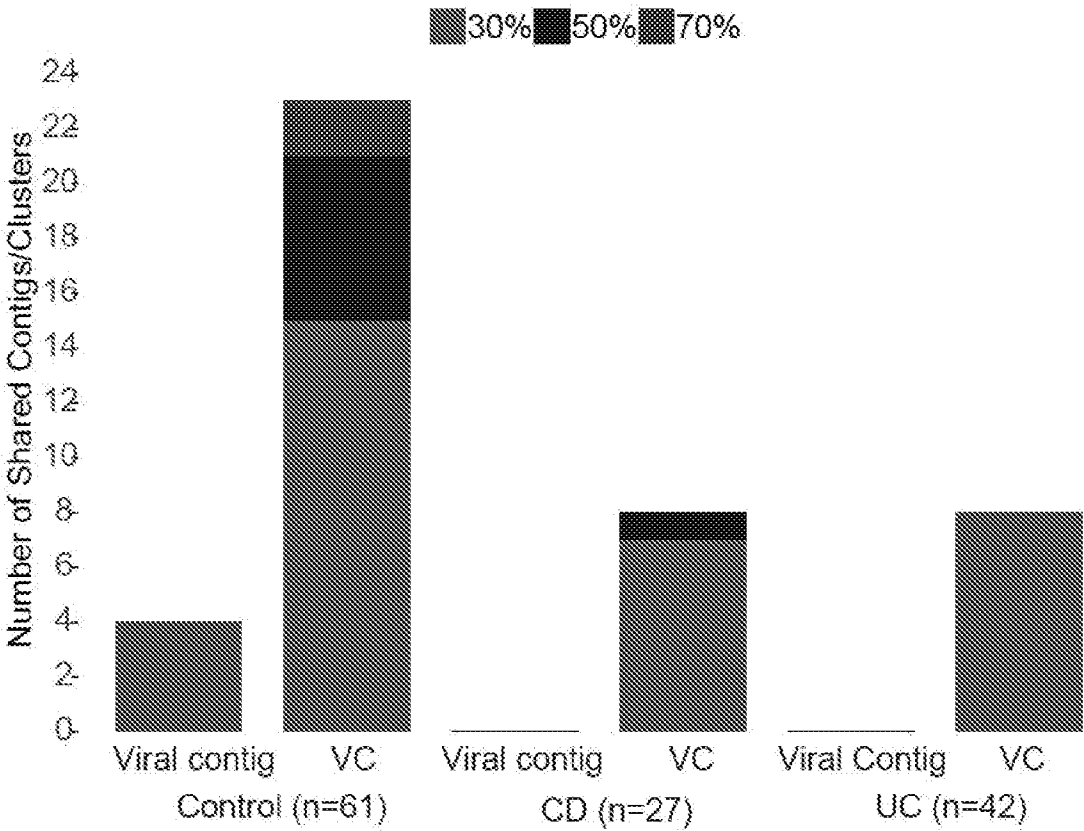


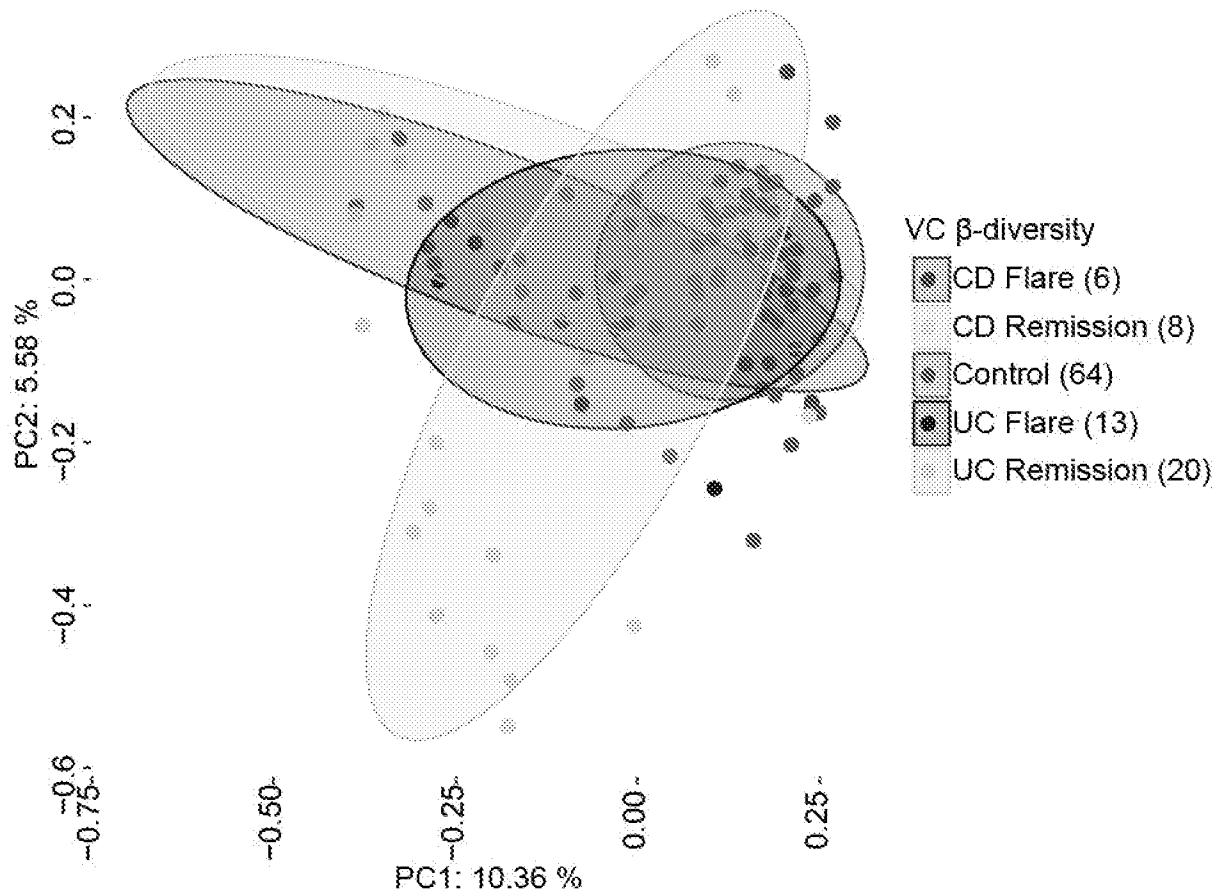
Figure 2A

Figure 2B

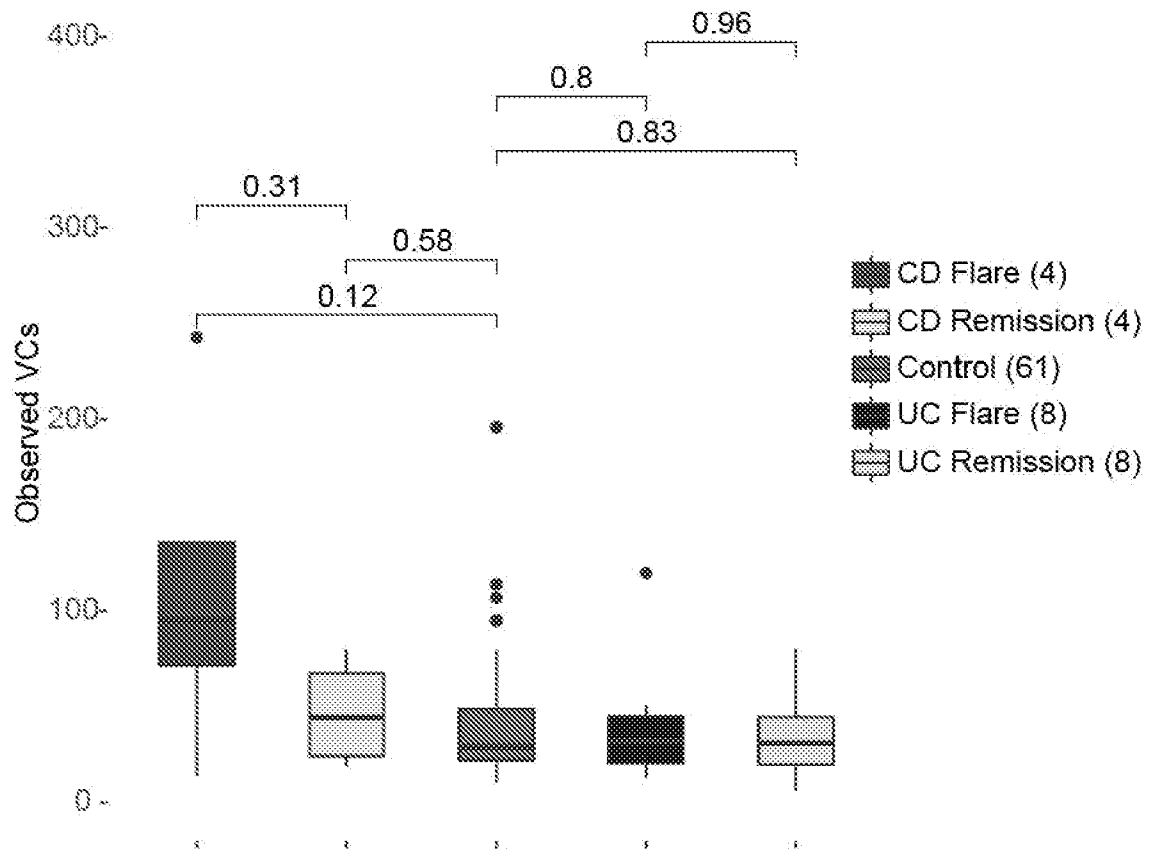


Figure 2C

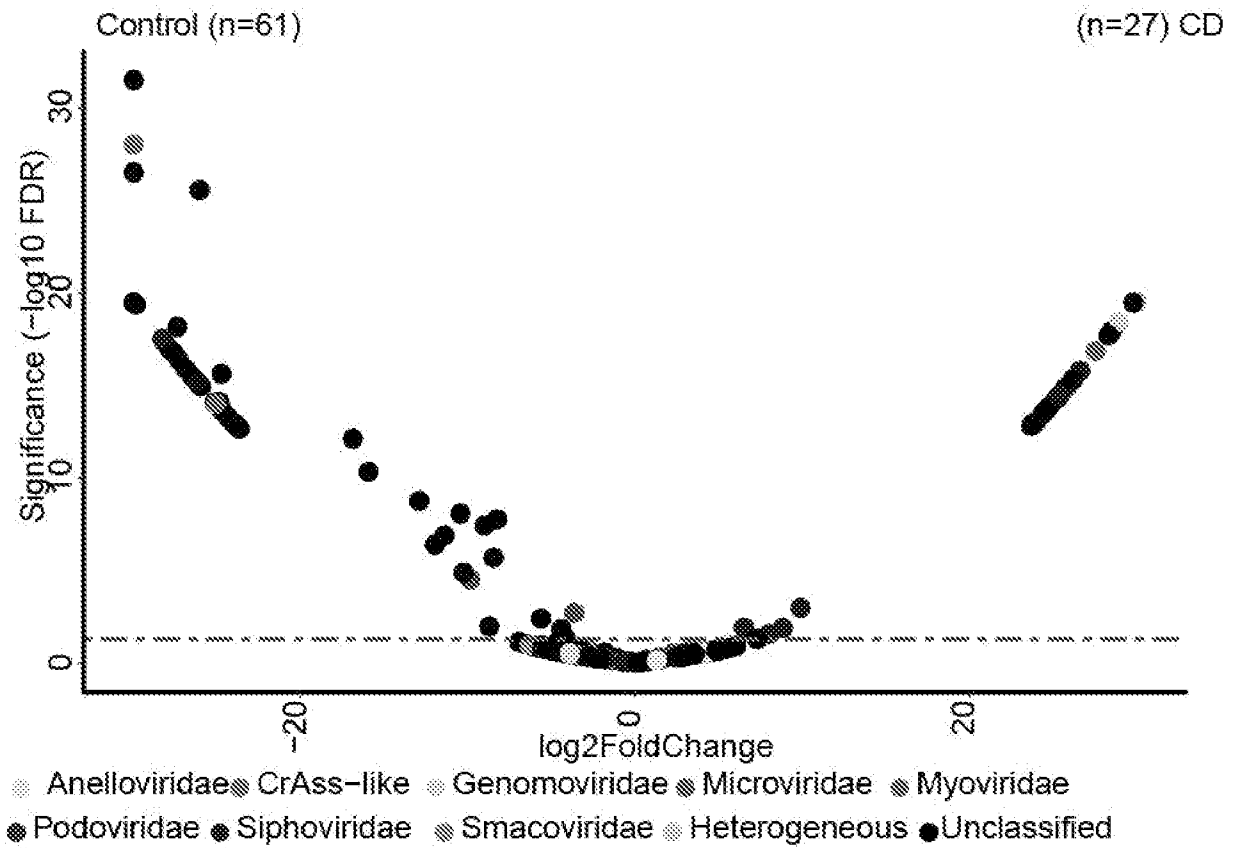


Figure 2D

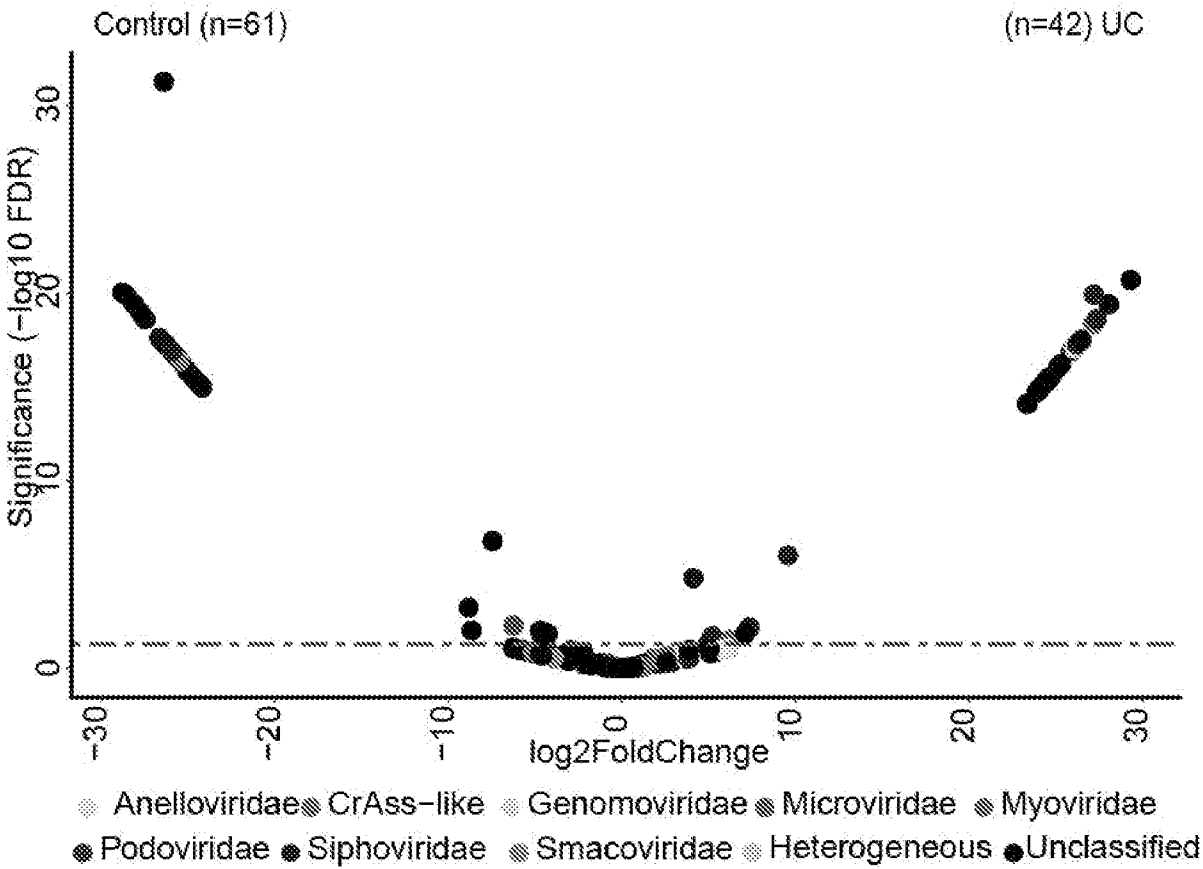


Figure 3A

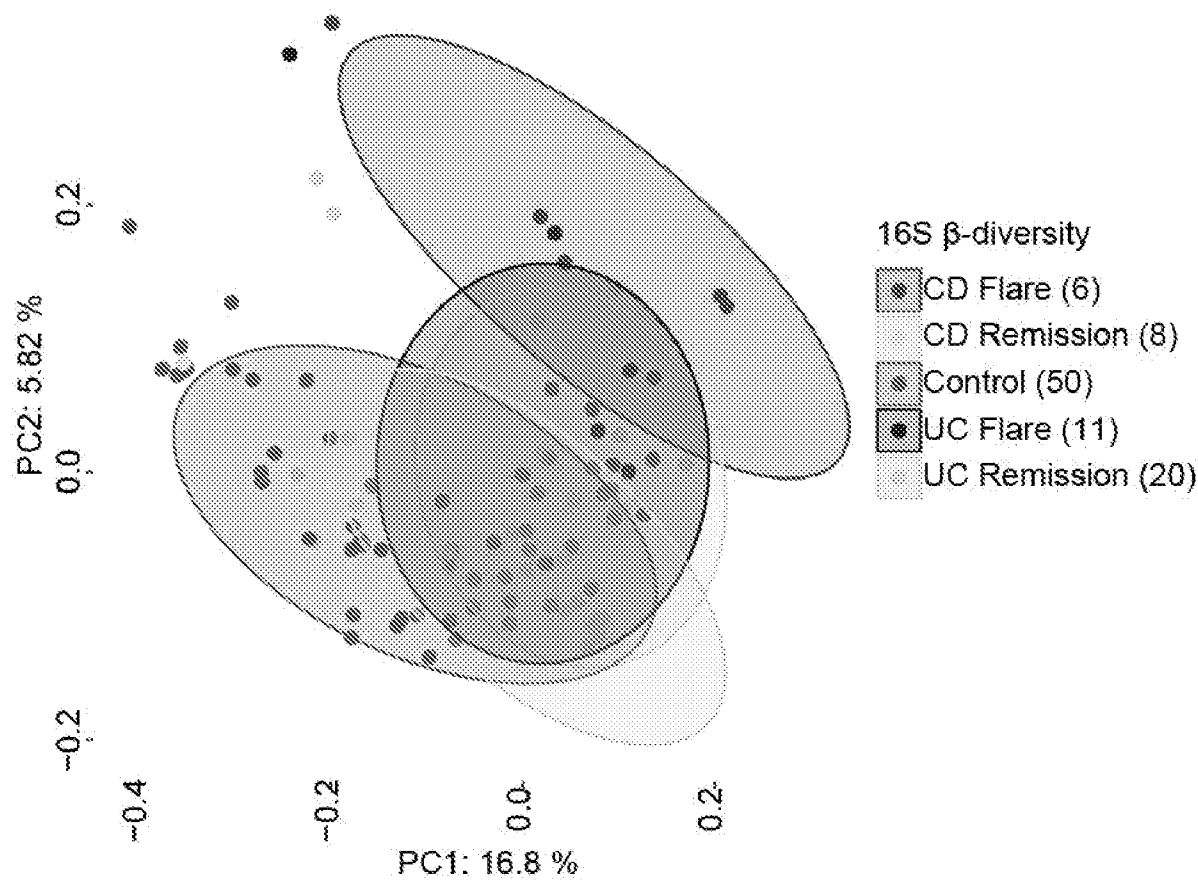


Figure 3B

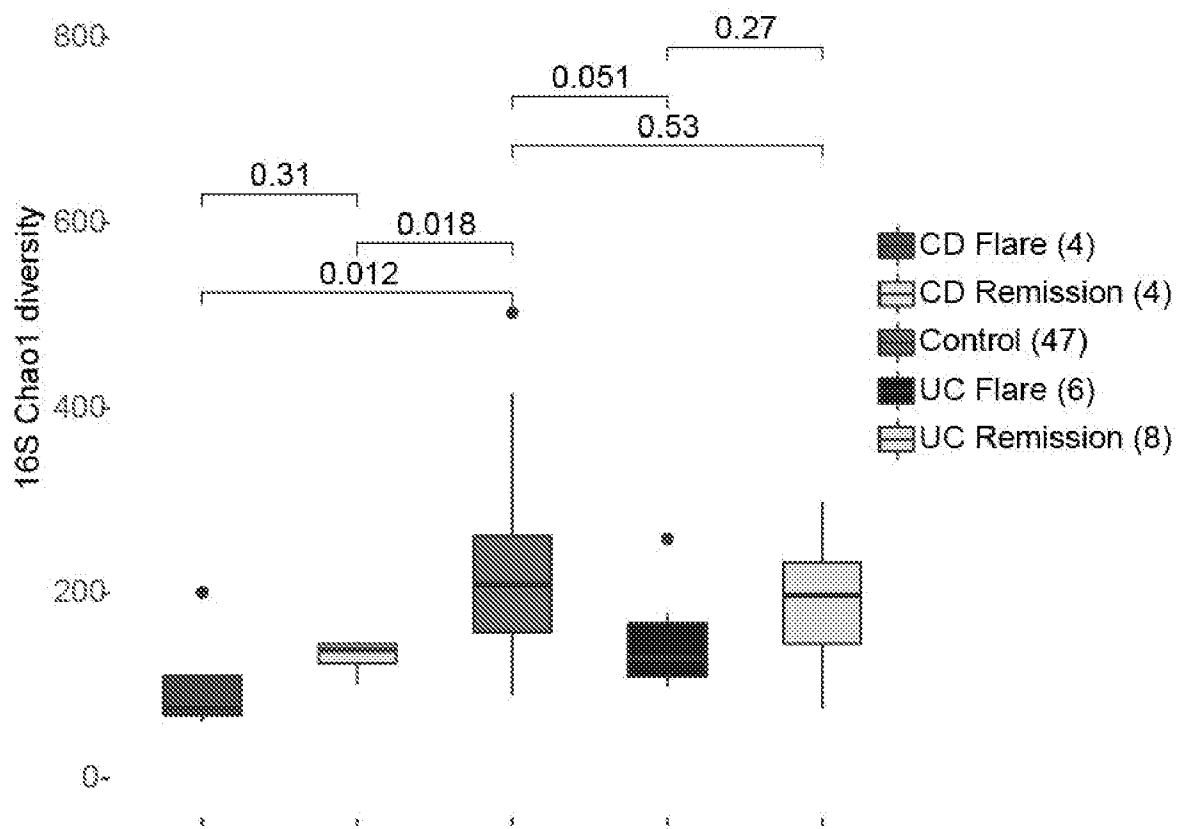


Figure 3C

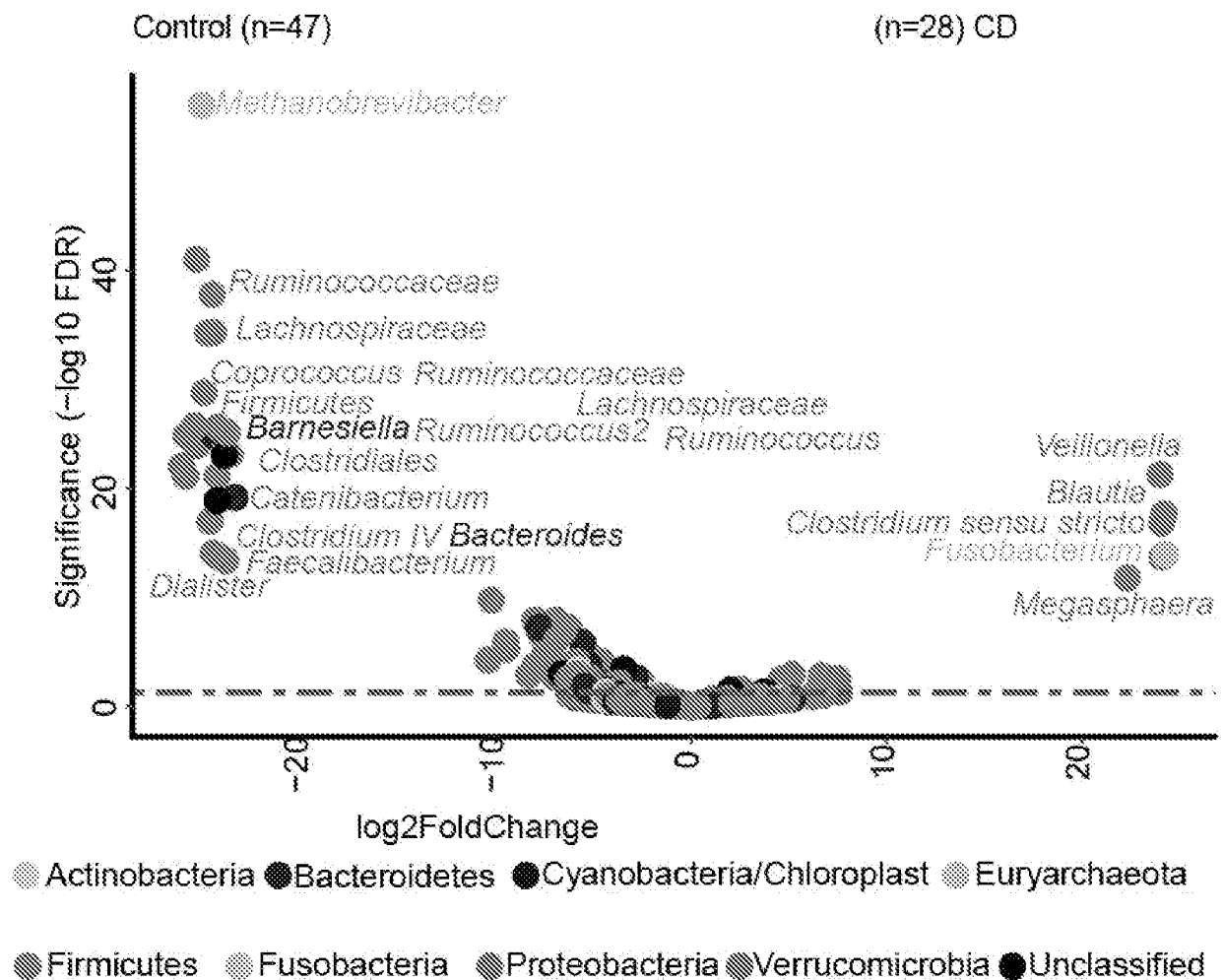


Figure 3D

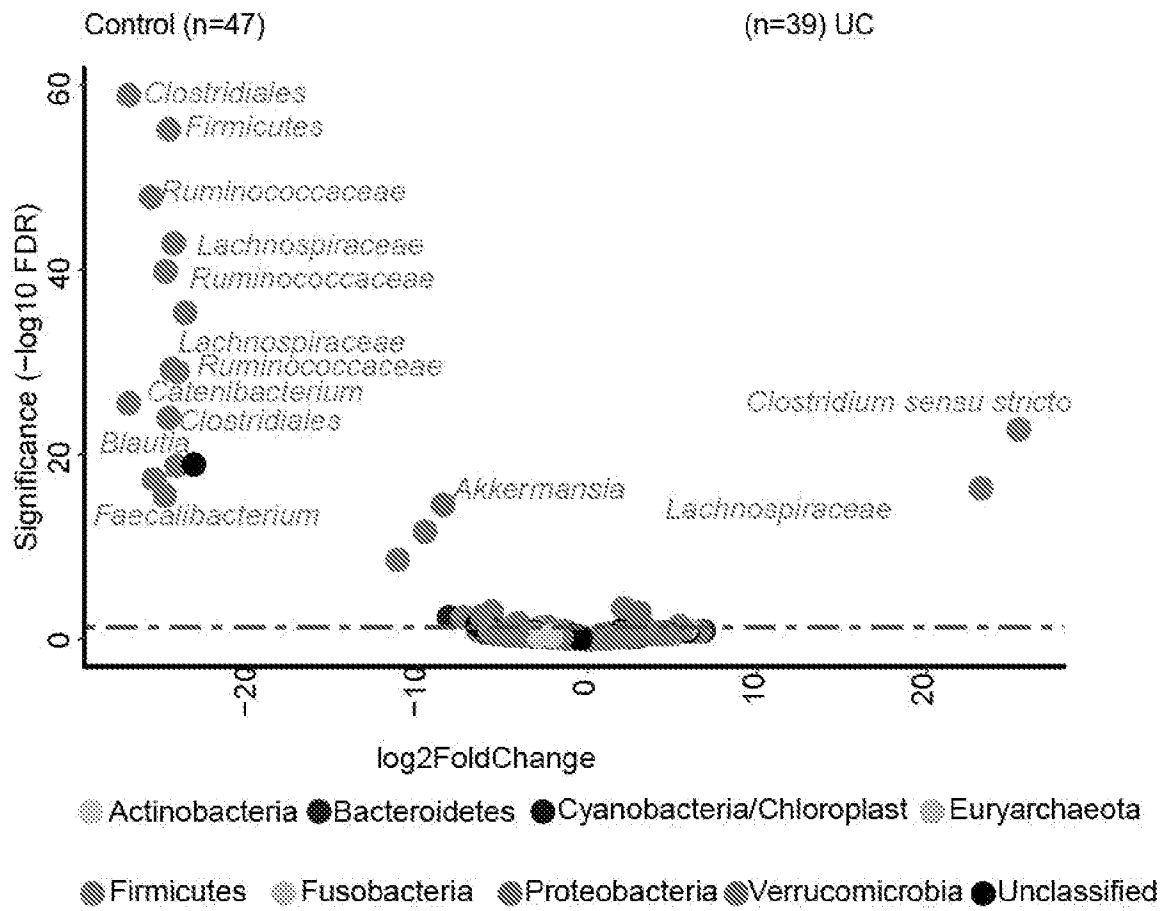


Figure 4A

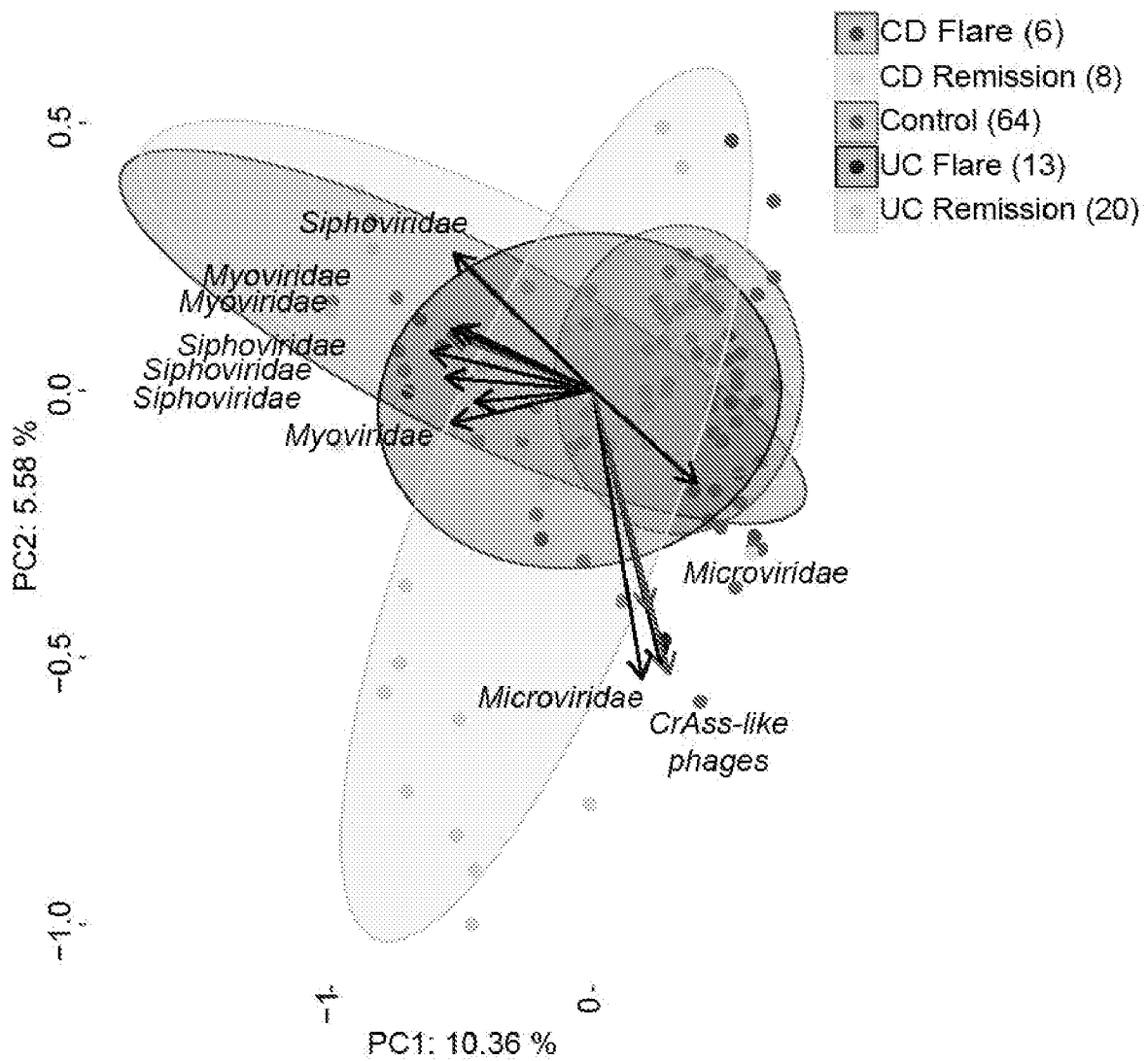


Figure 4B

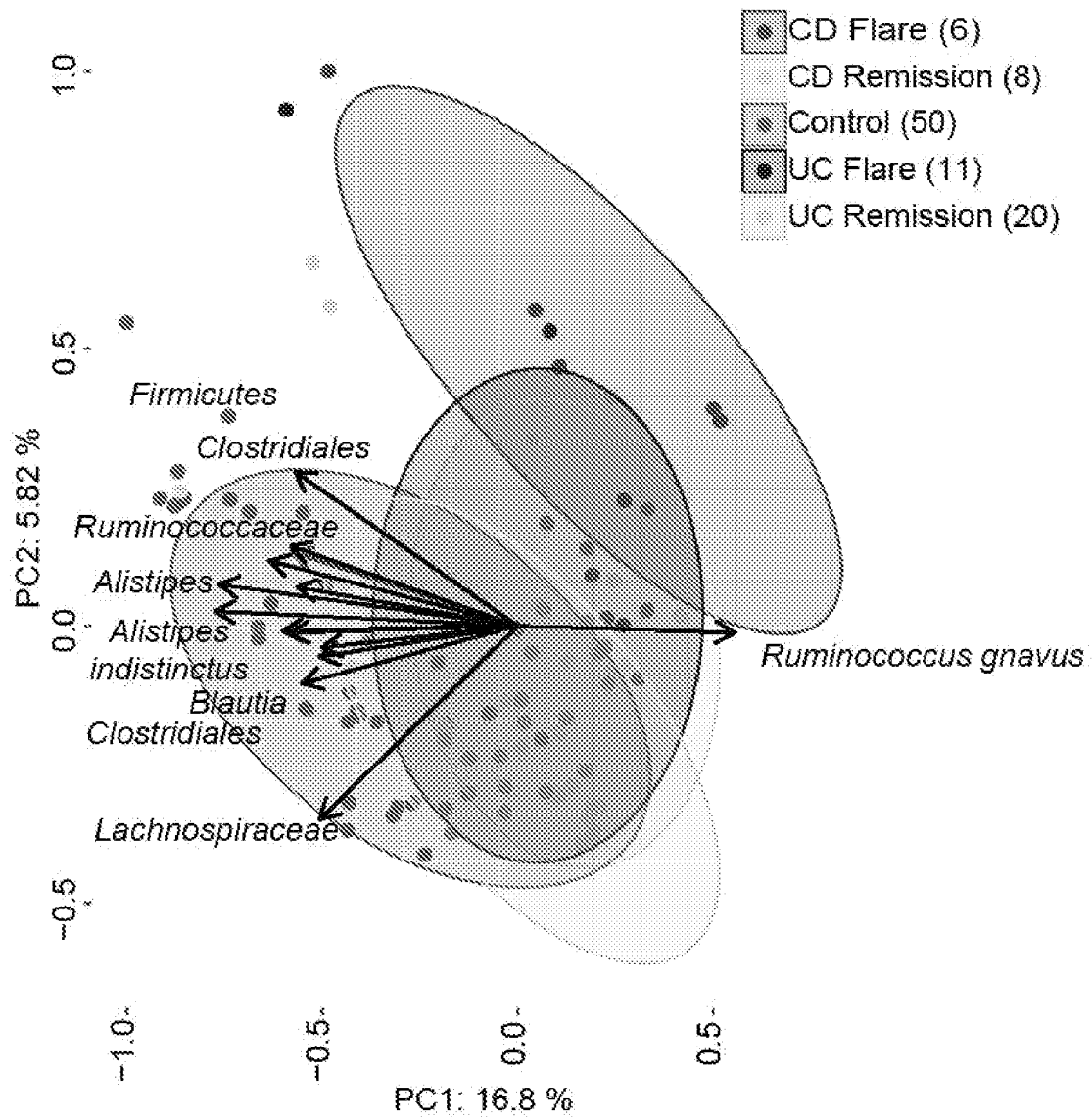


Figure 5A

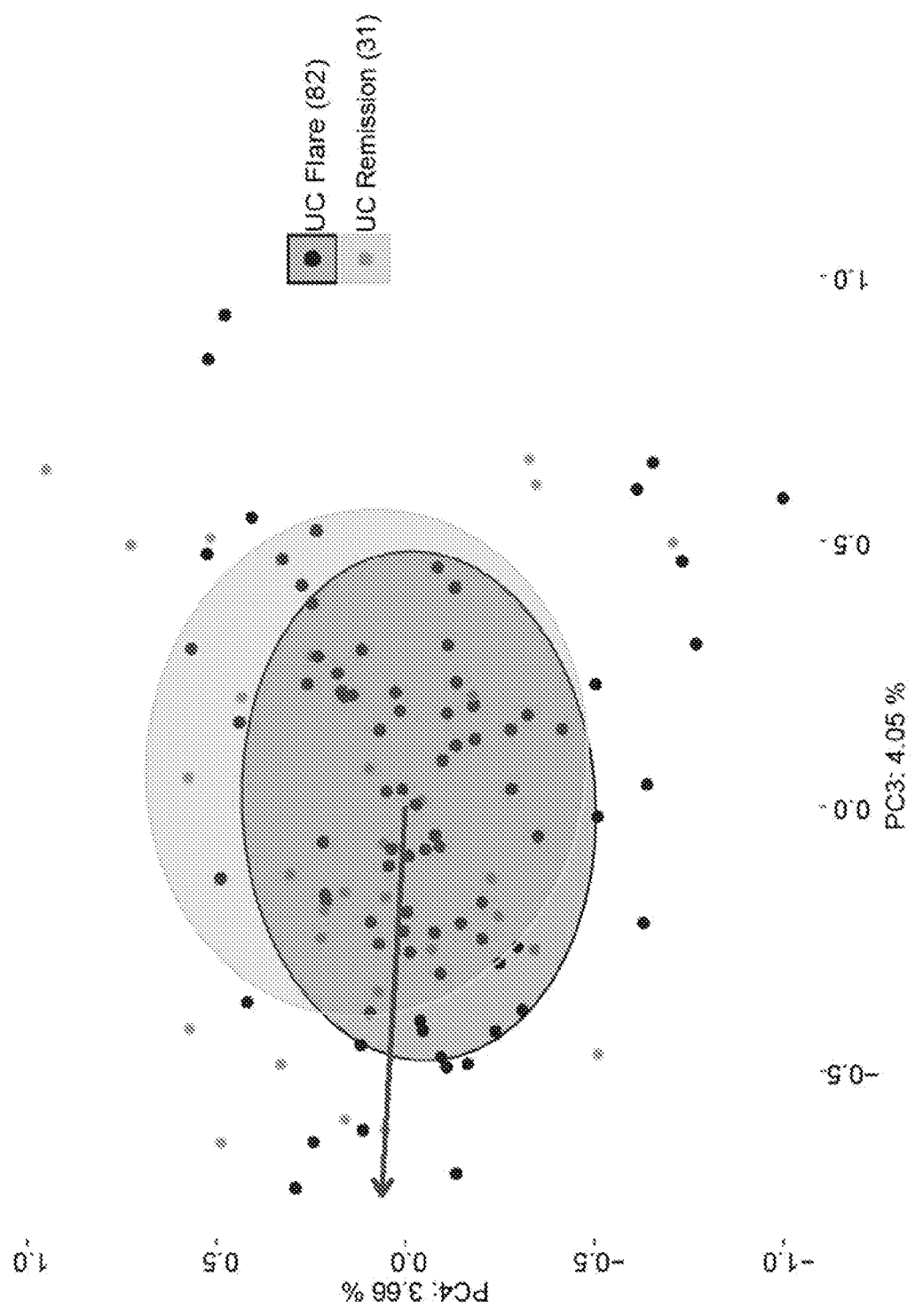


Figure 5B

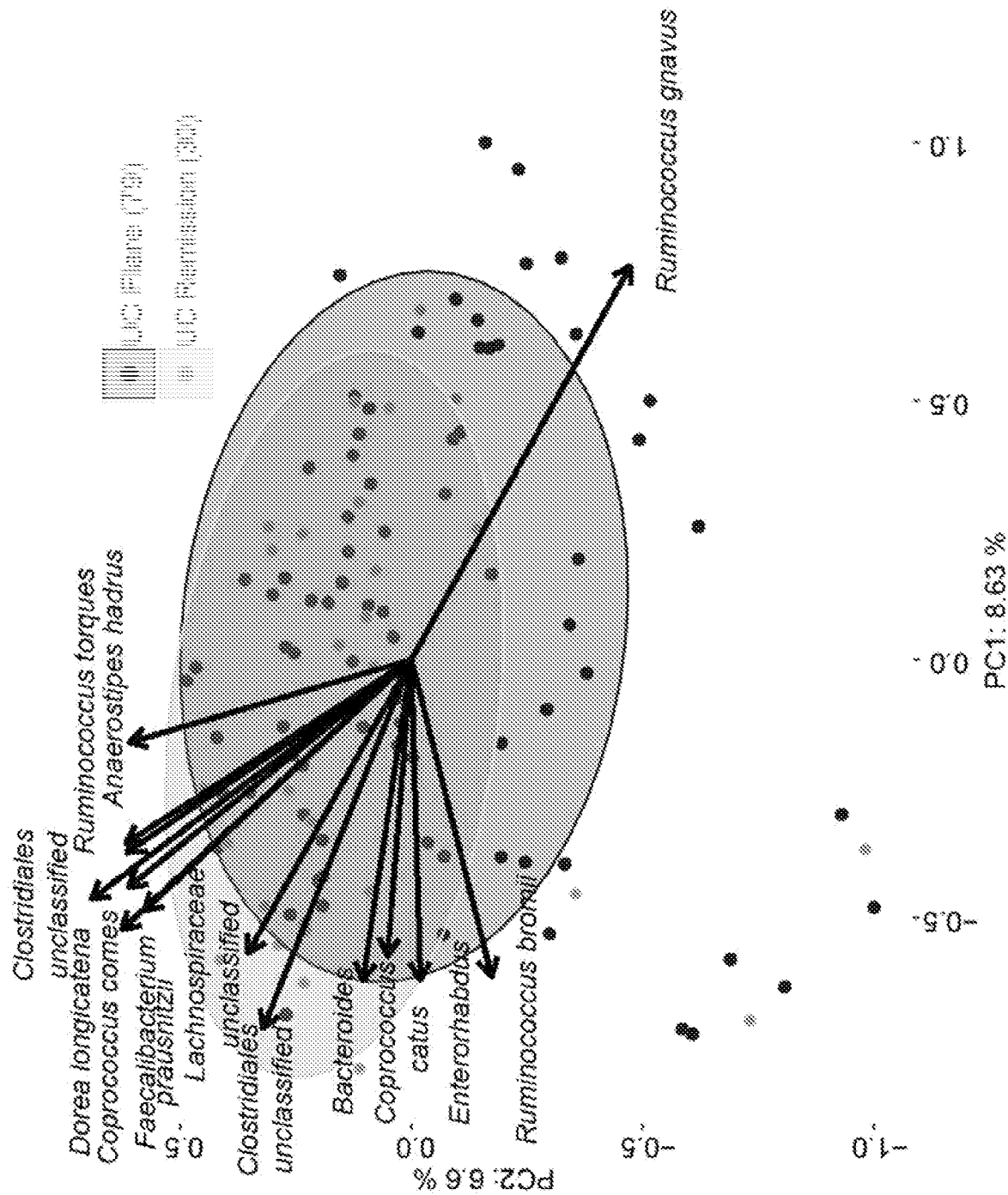


Figure 5C

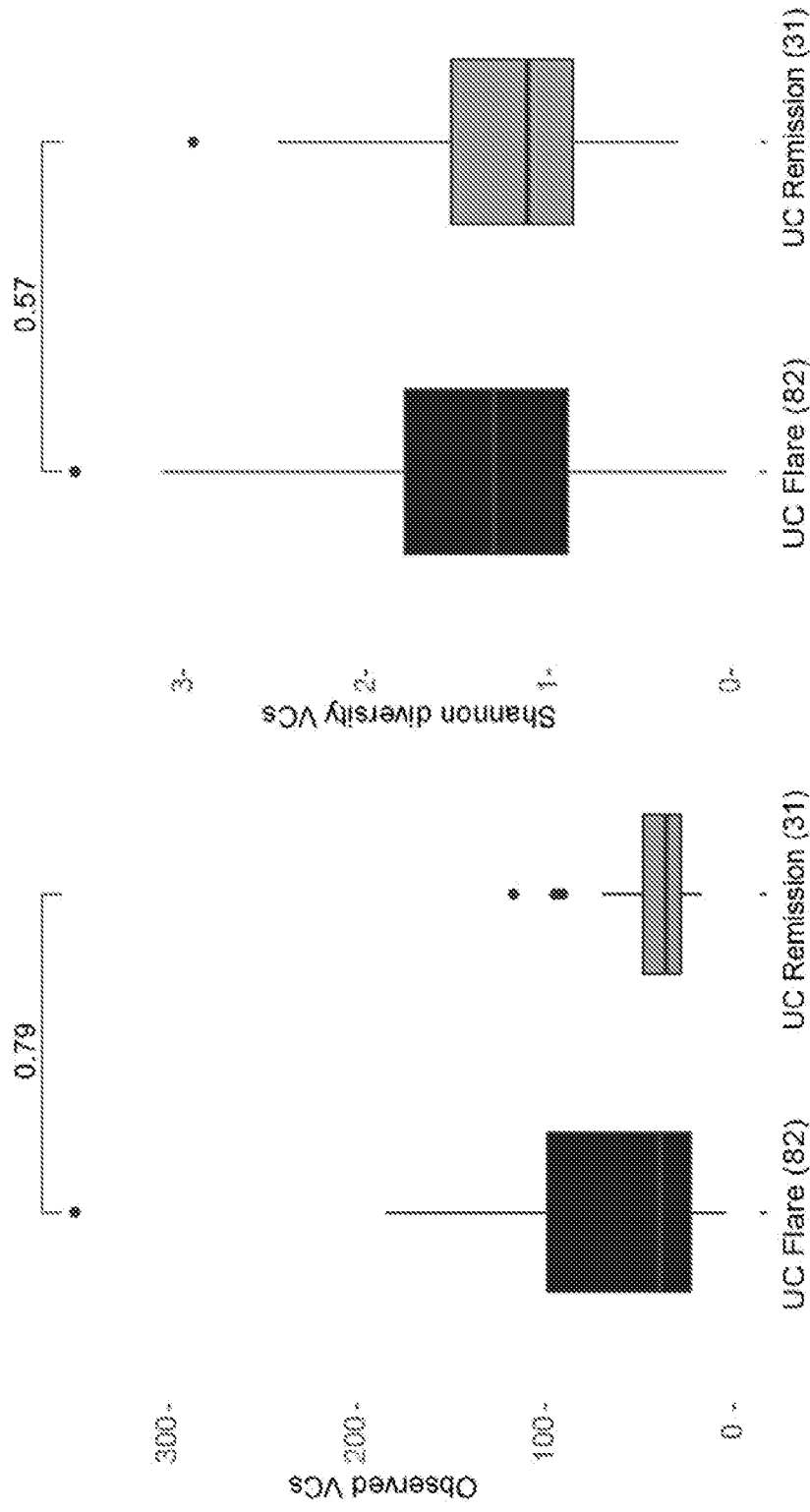


Figure 5D

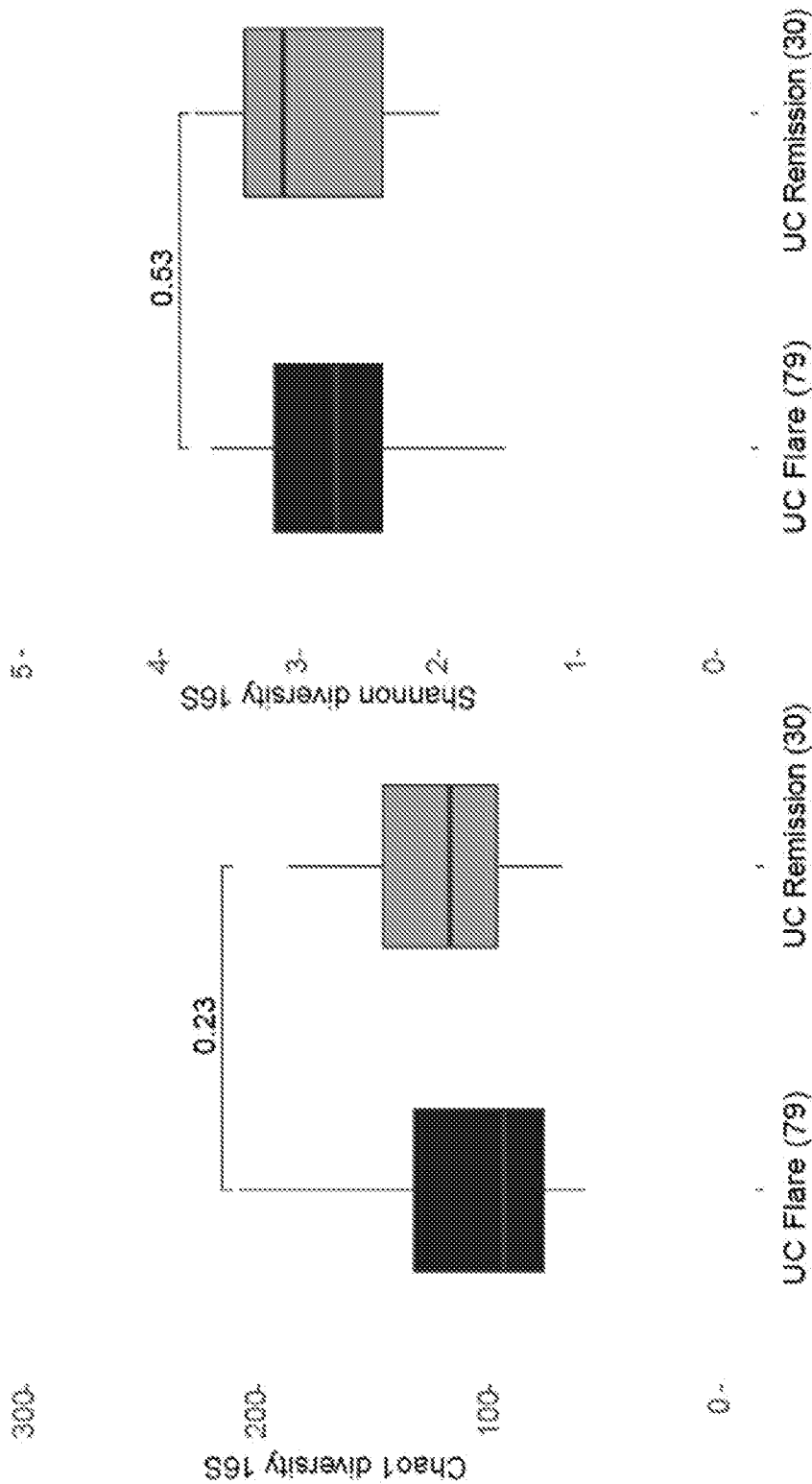


Figure 5E

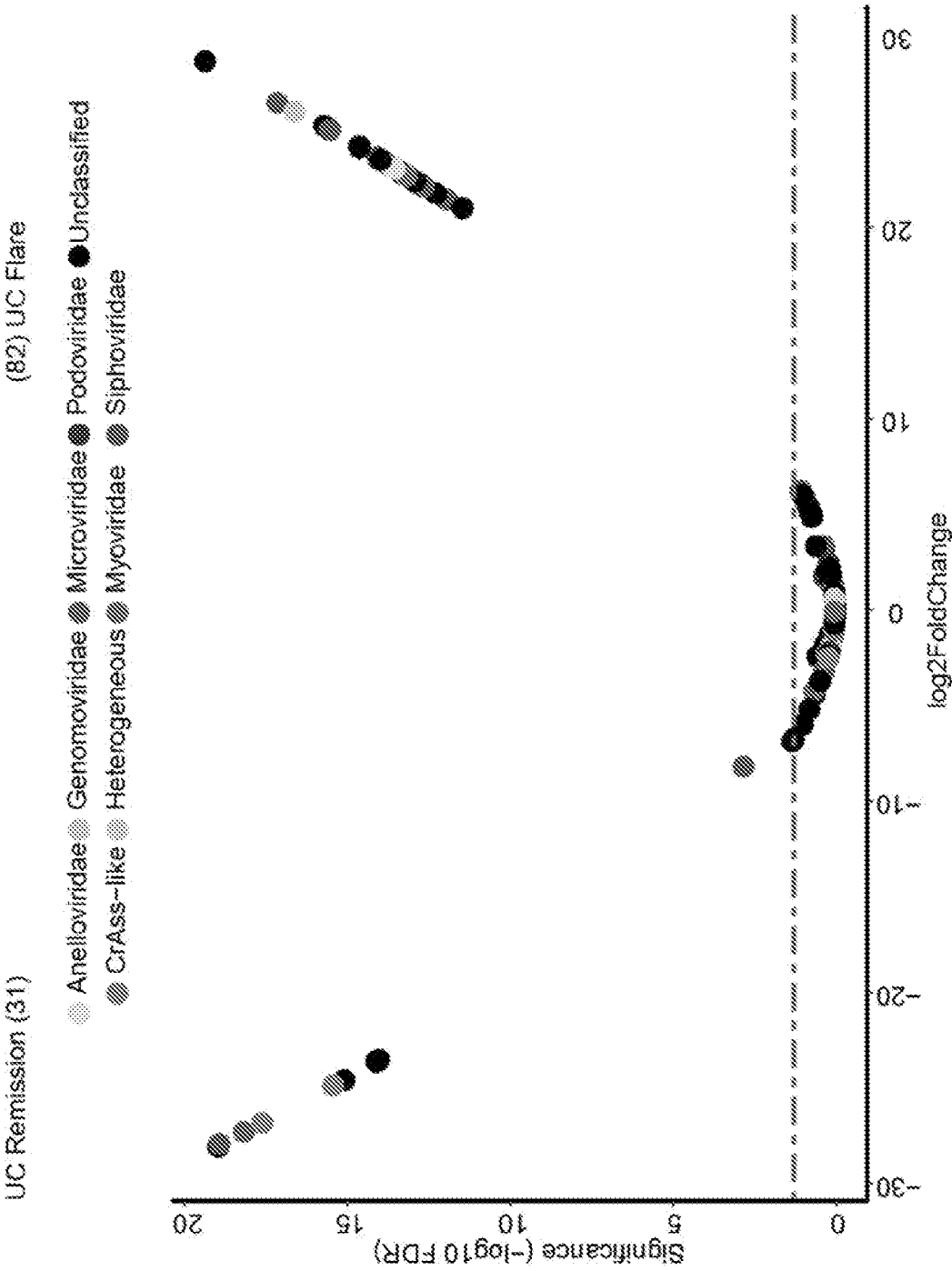


Figure 5F

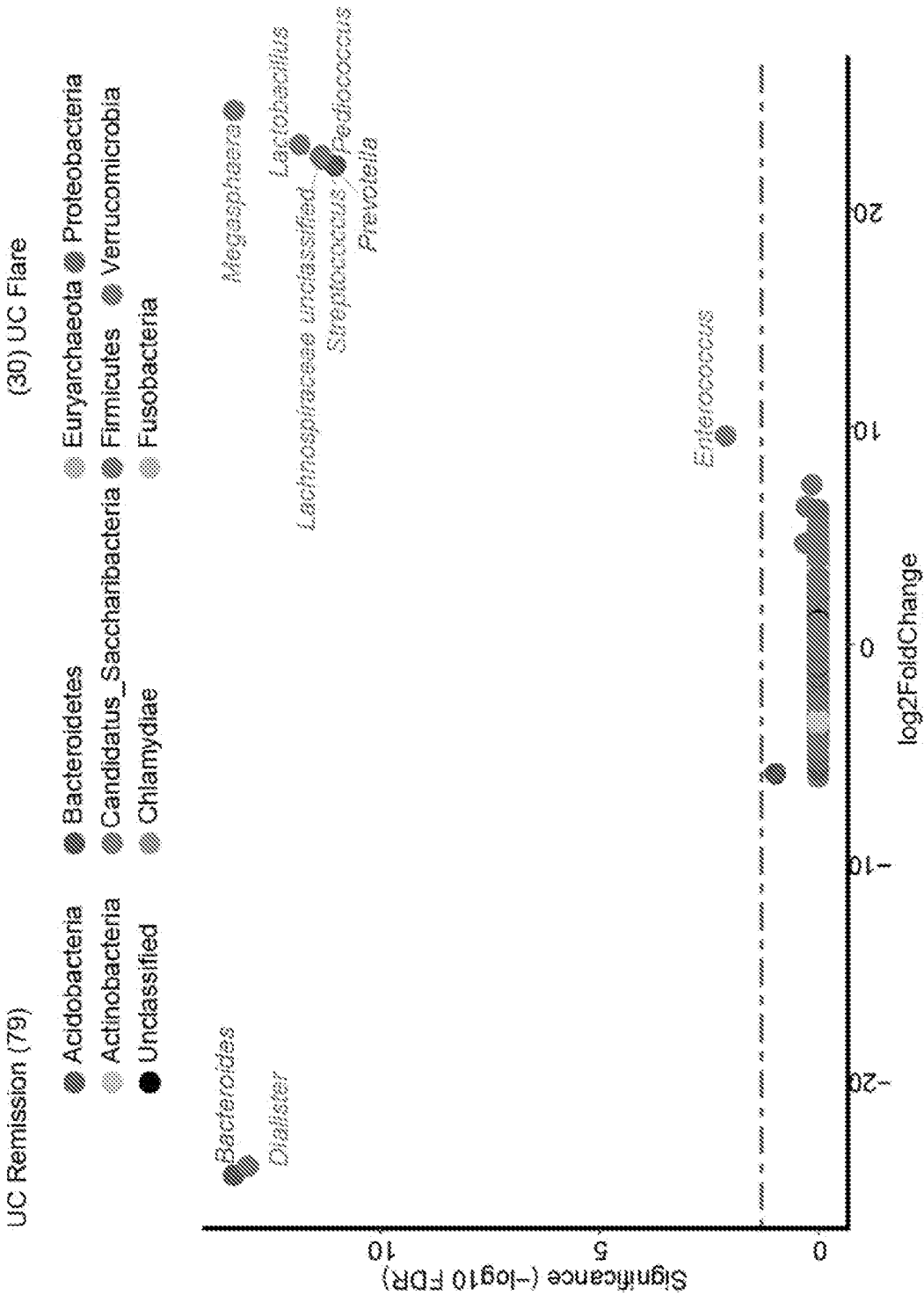


Figure 6A

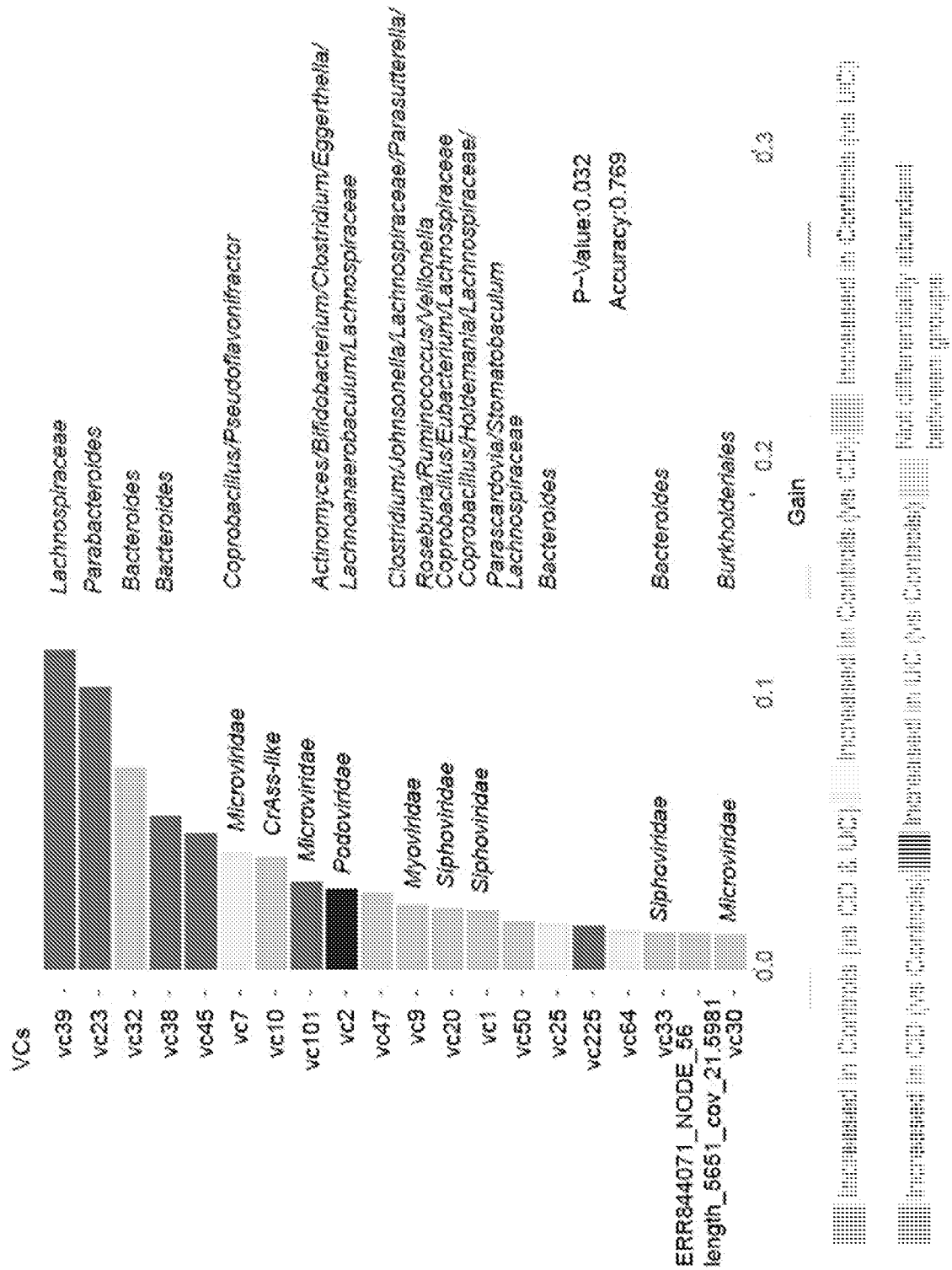


Figure 6B

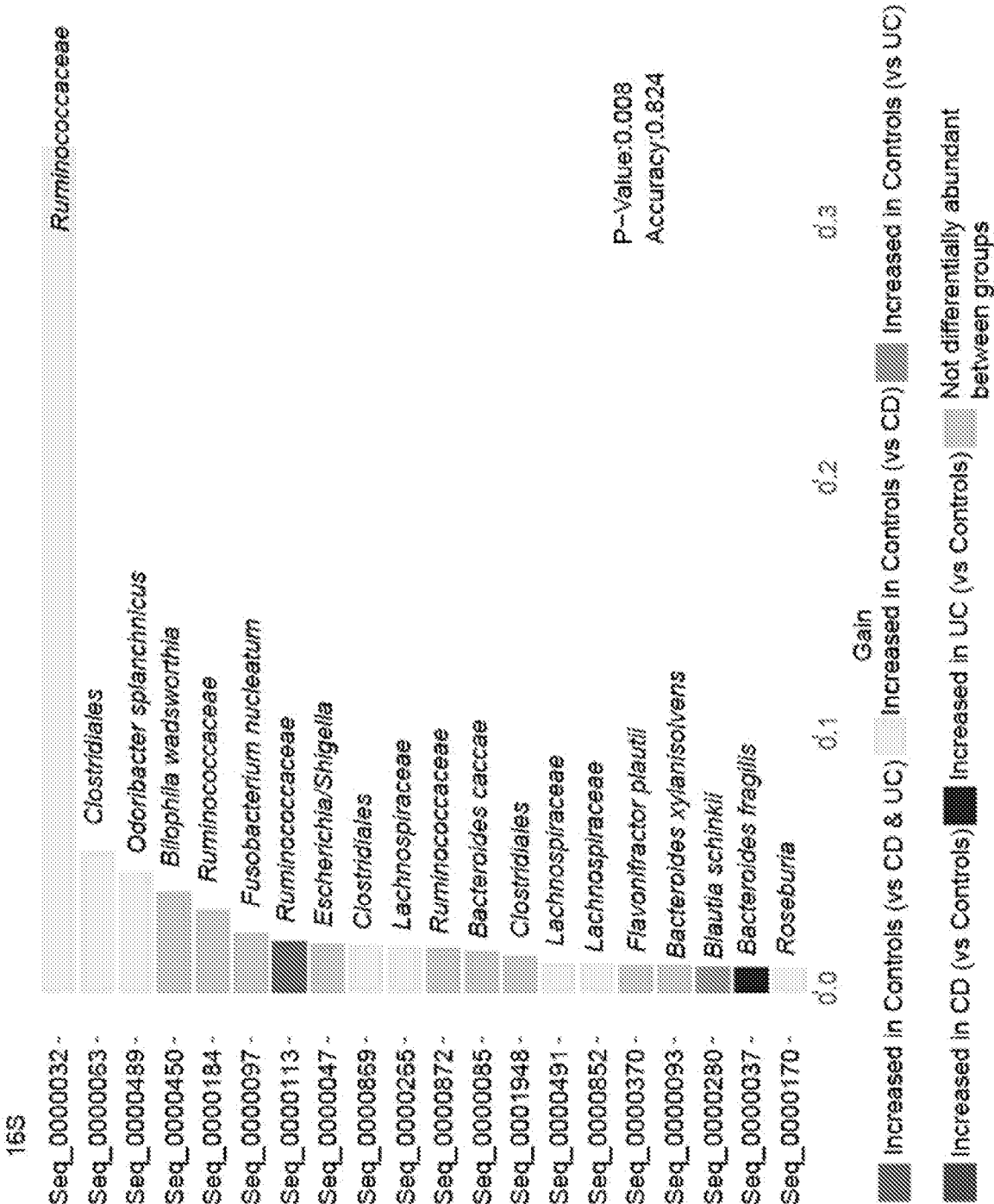


Figure 6C

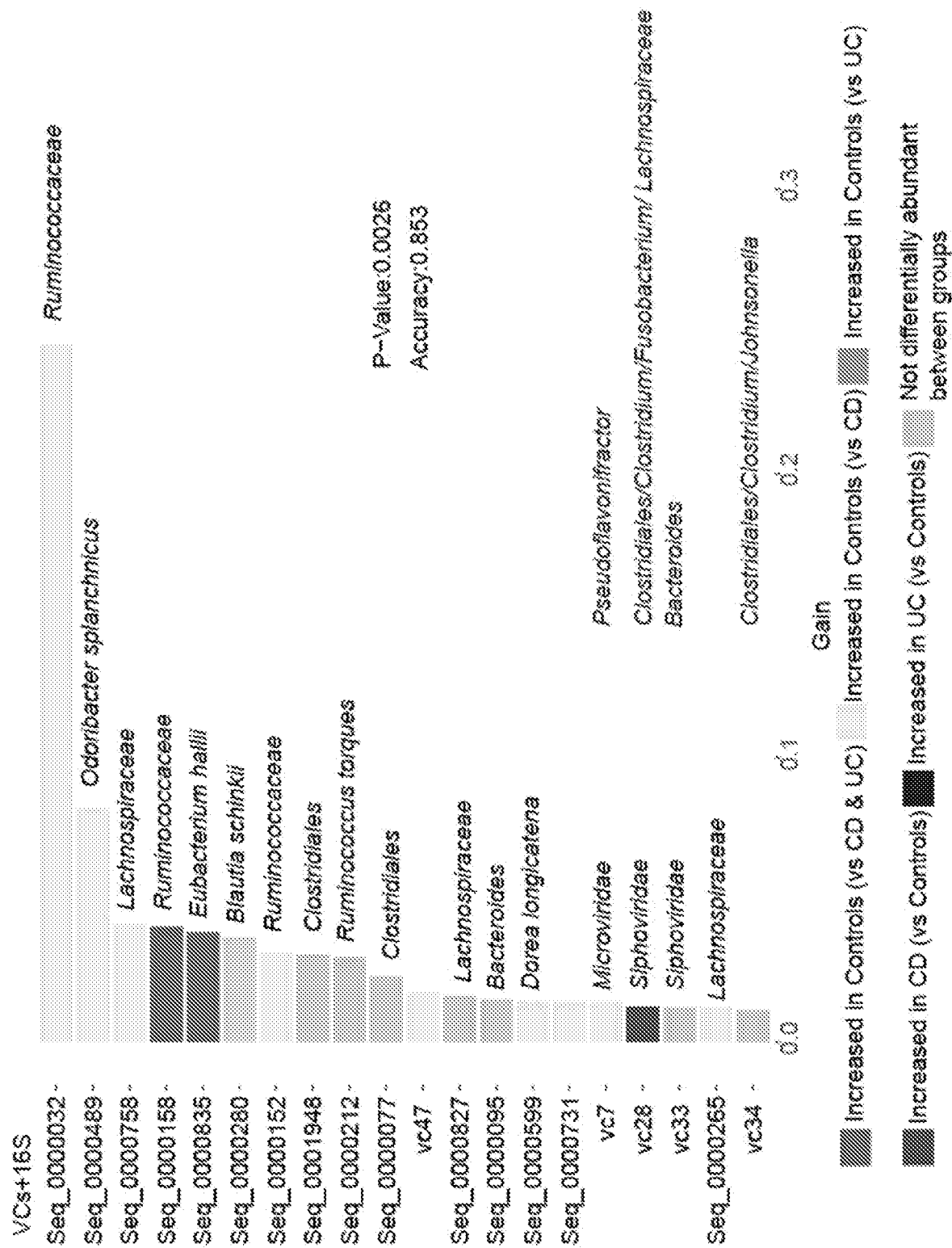


Figure 6D

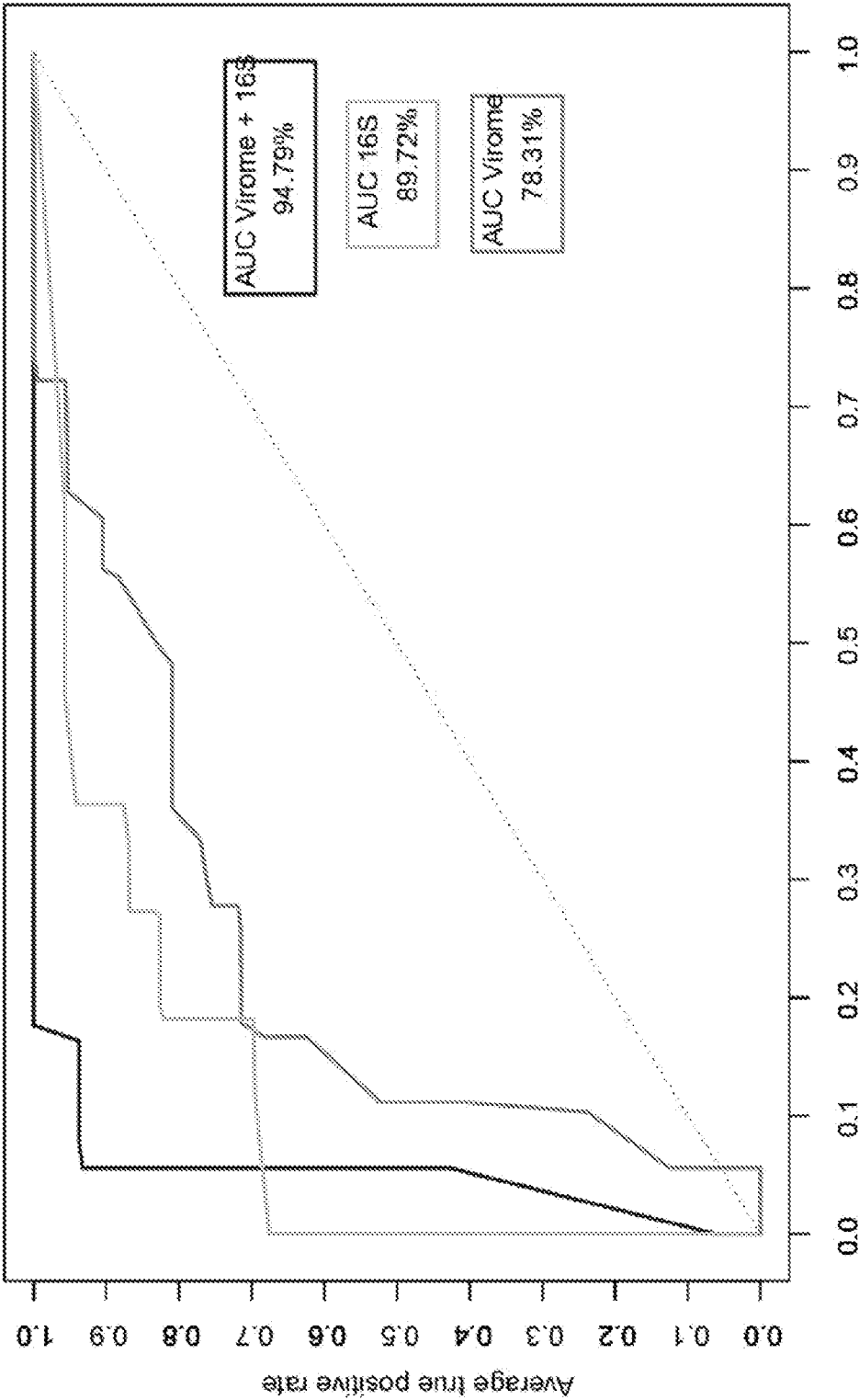


Figure 7A

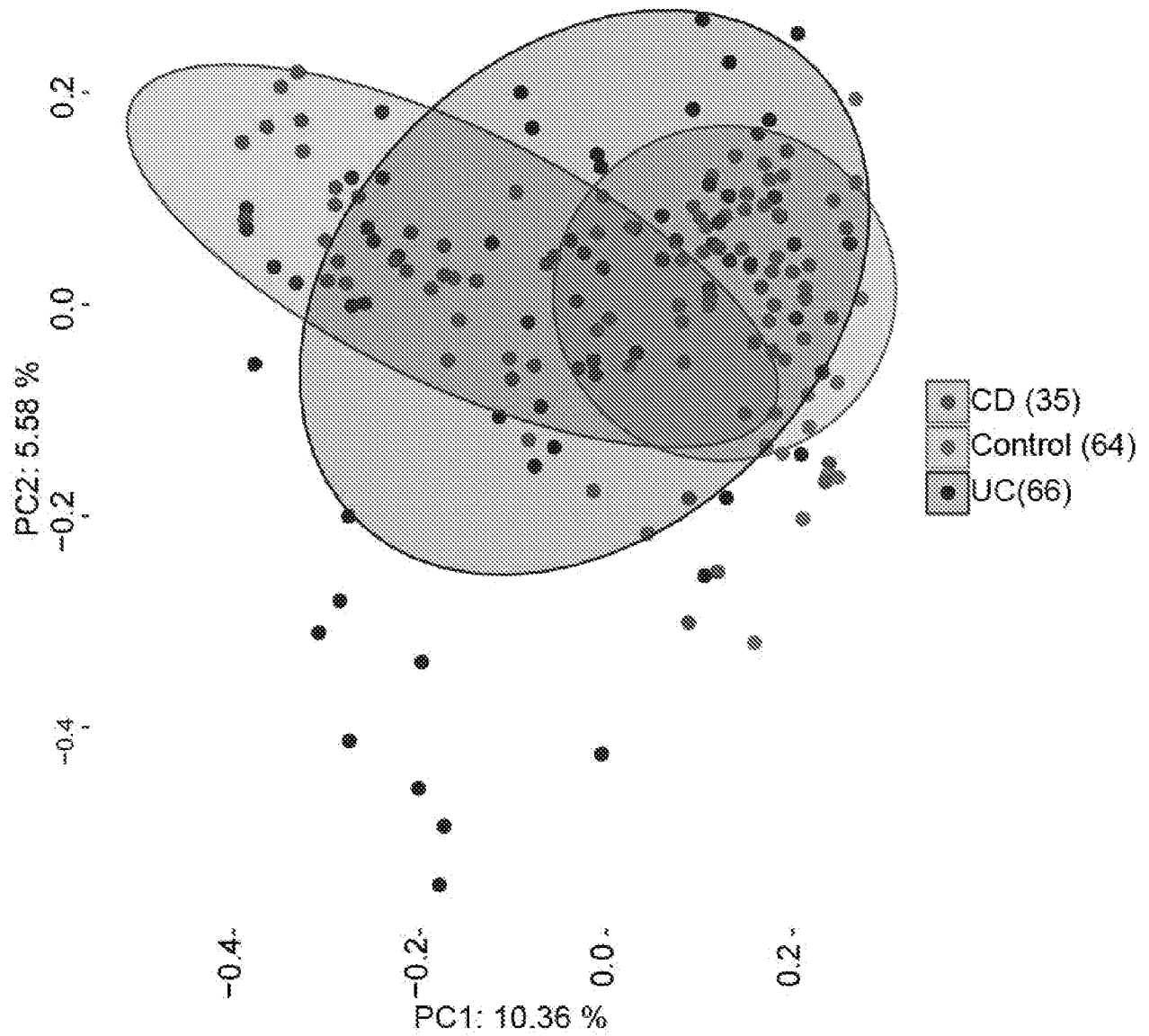


Figure 7B

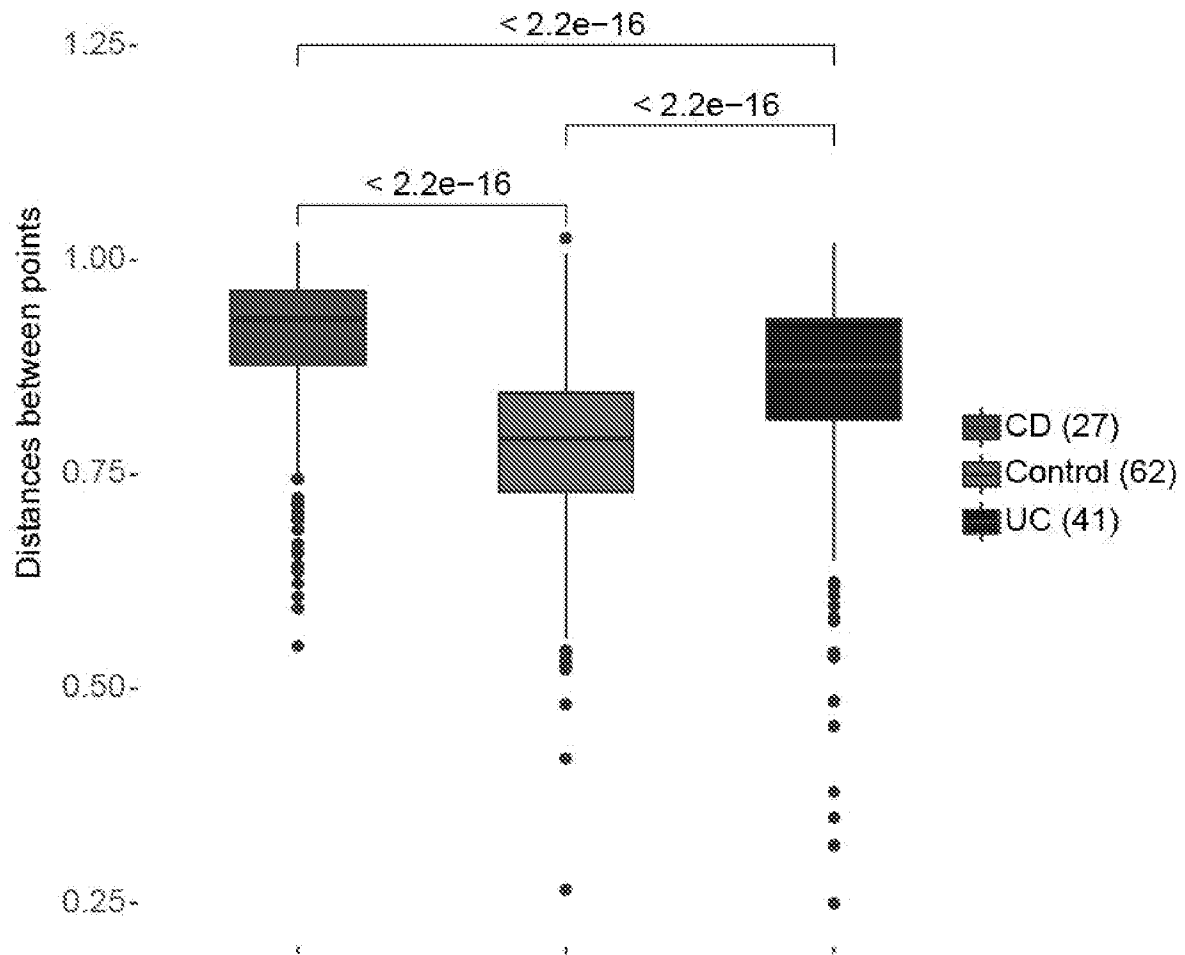


Figure 7C

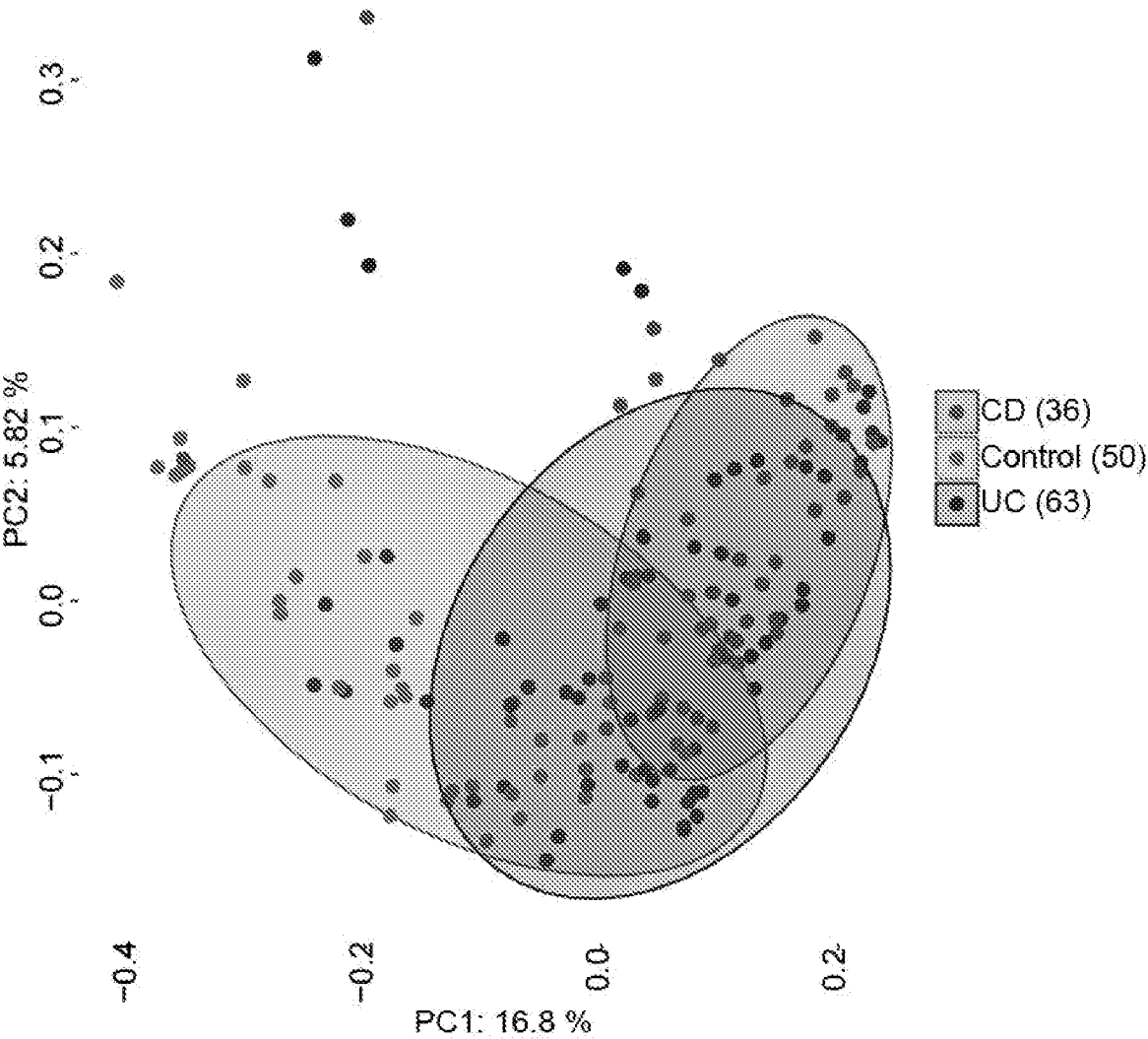


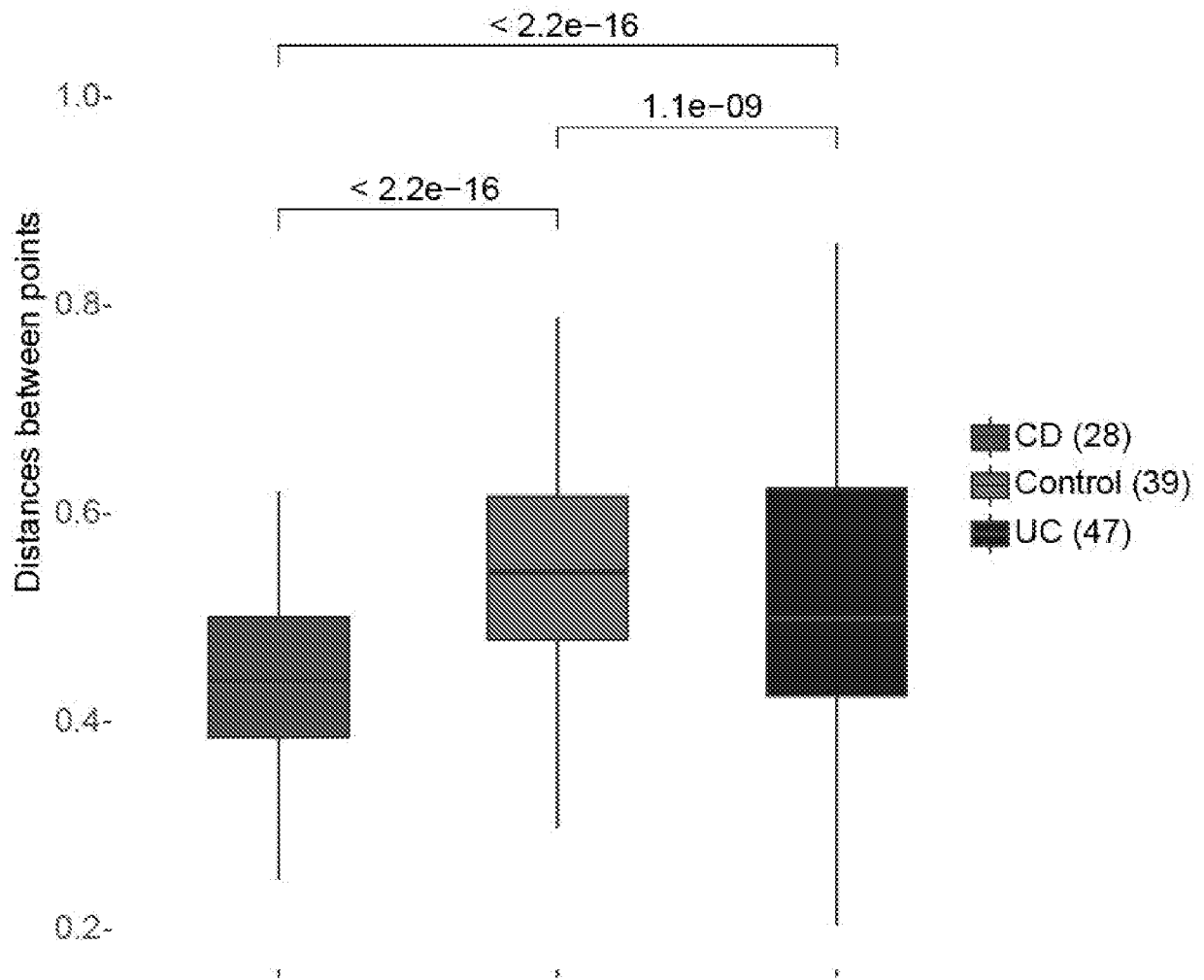
Figure 7D

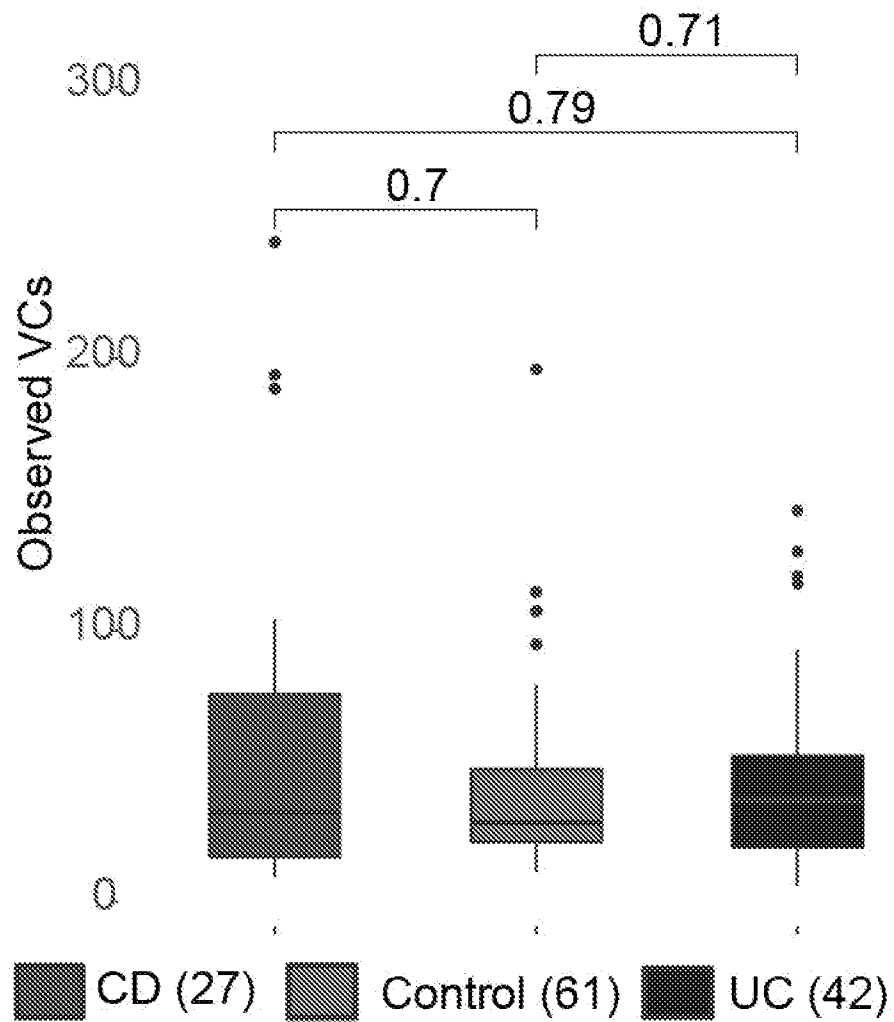
Figure 8A

Figure 8B

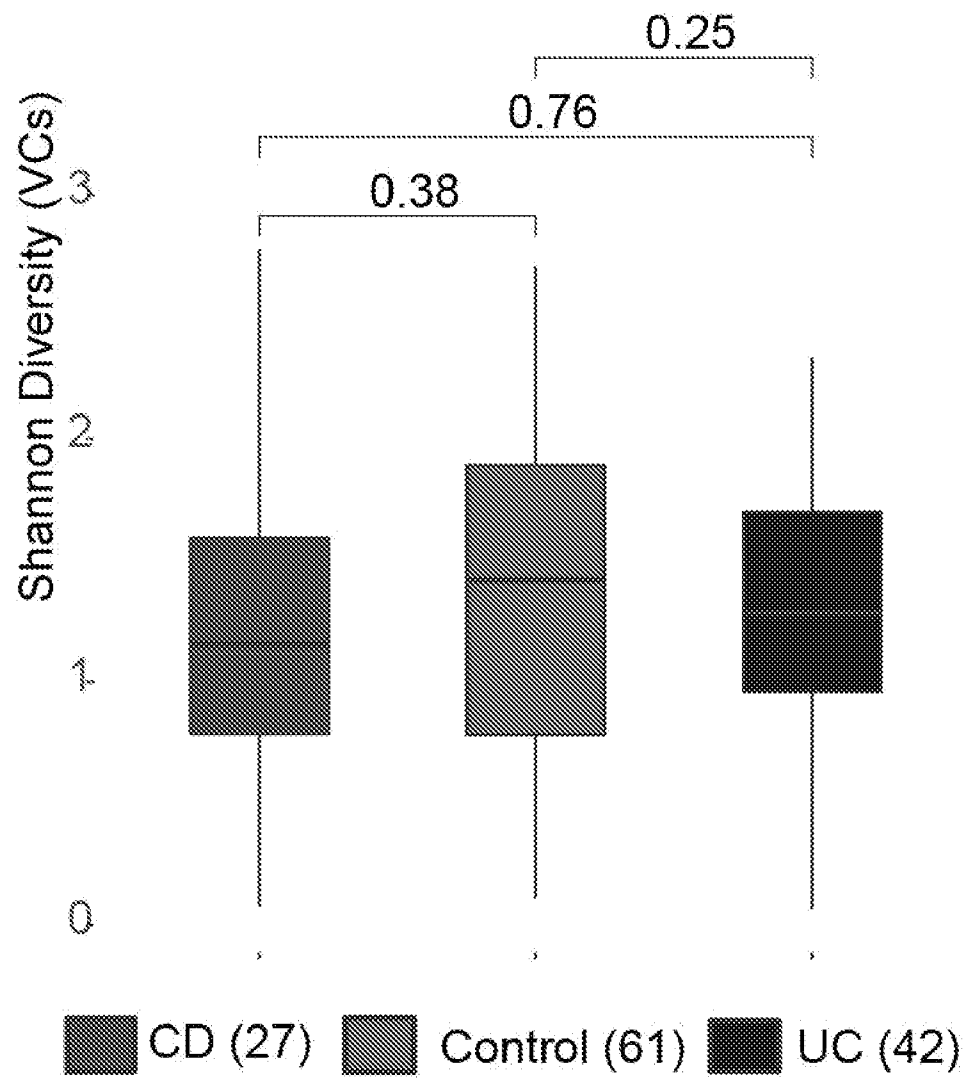


Figure 8C

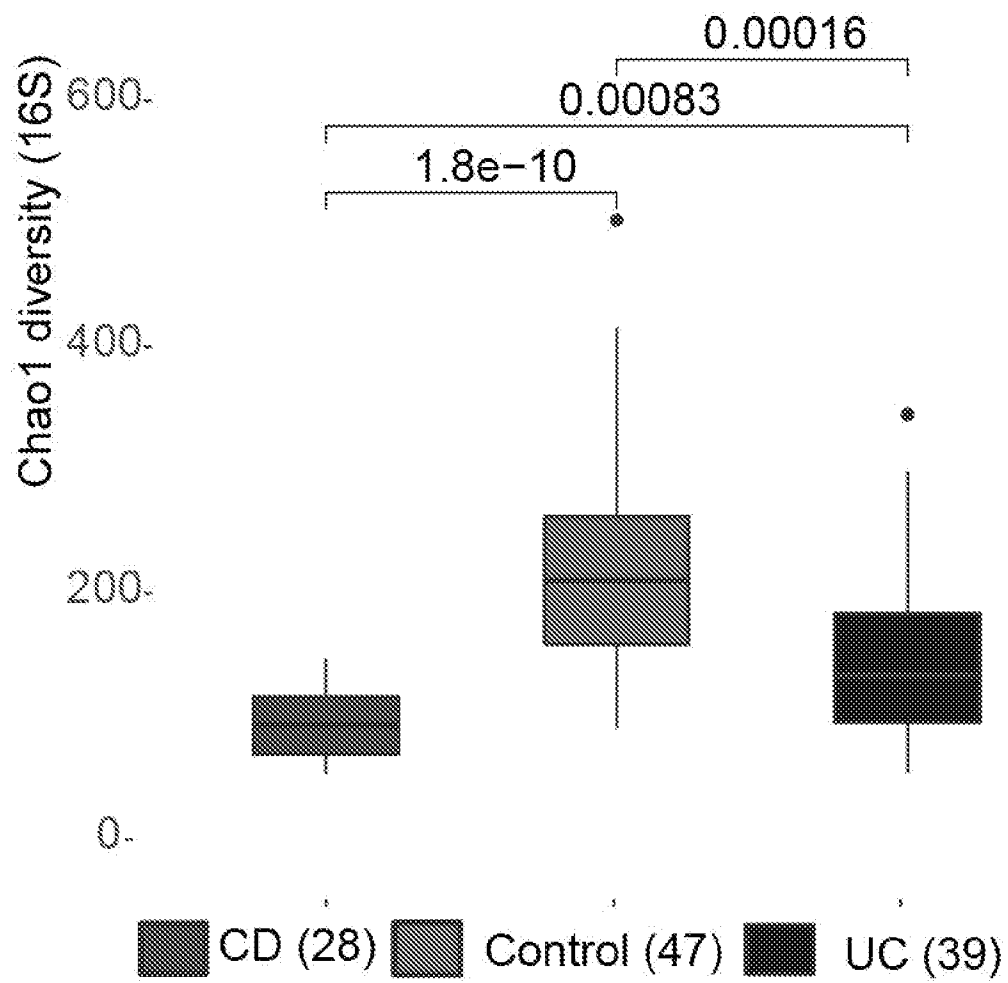


Figure 8D

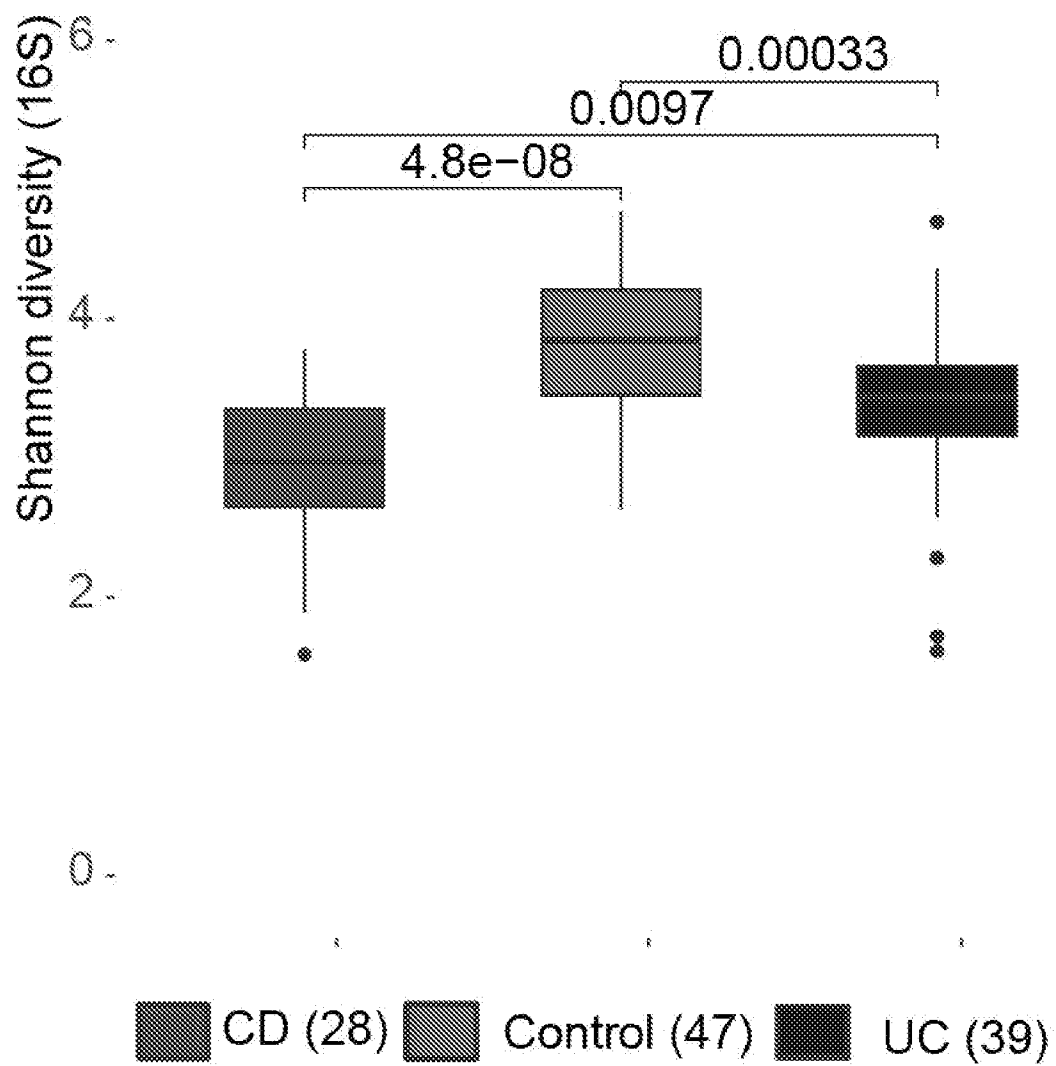


Figure 8E

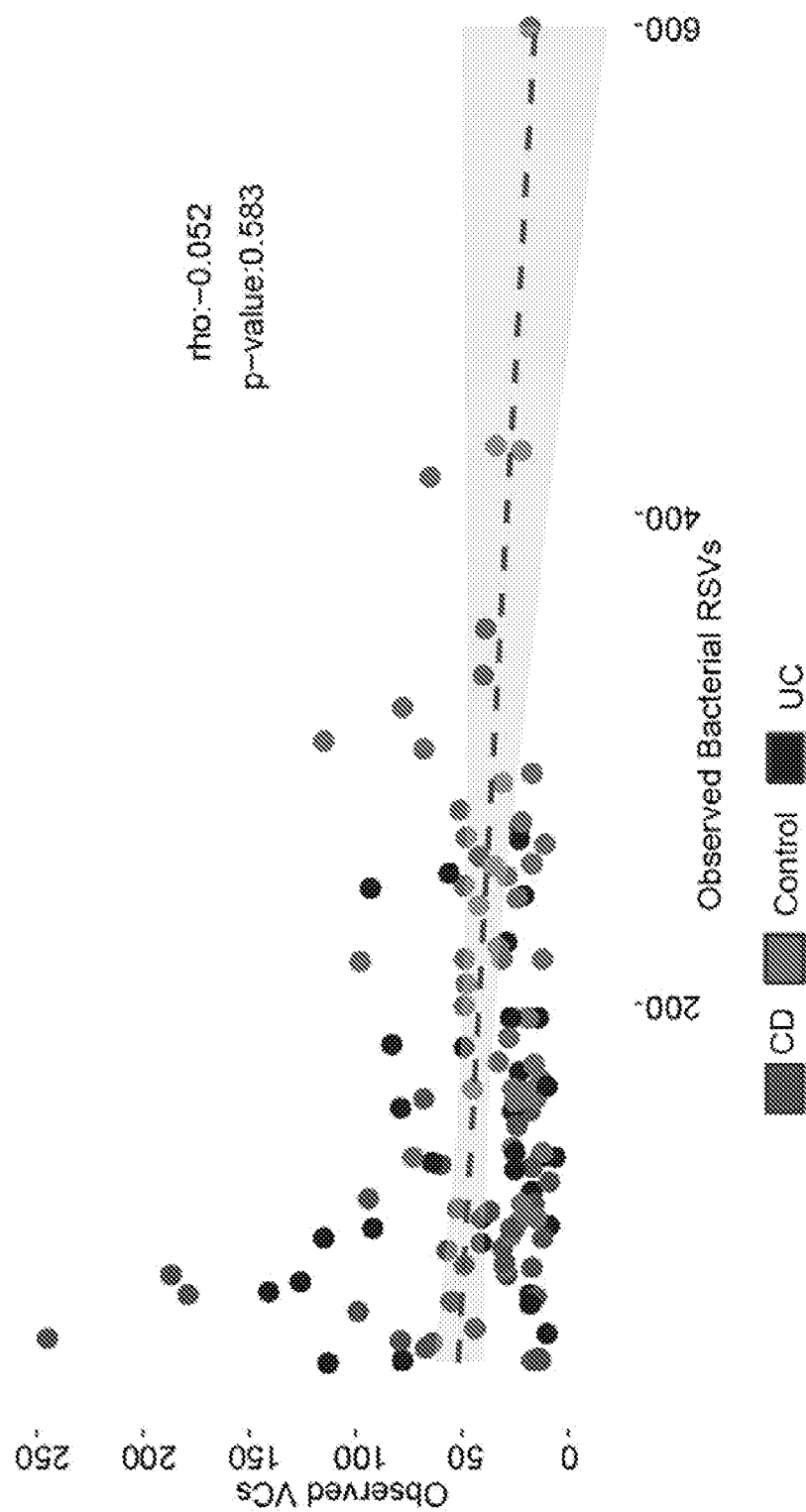


Figure 8F

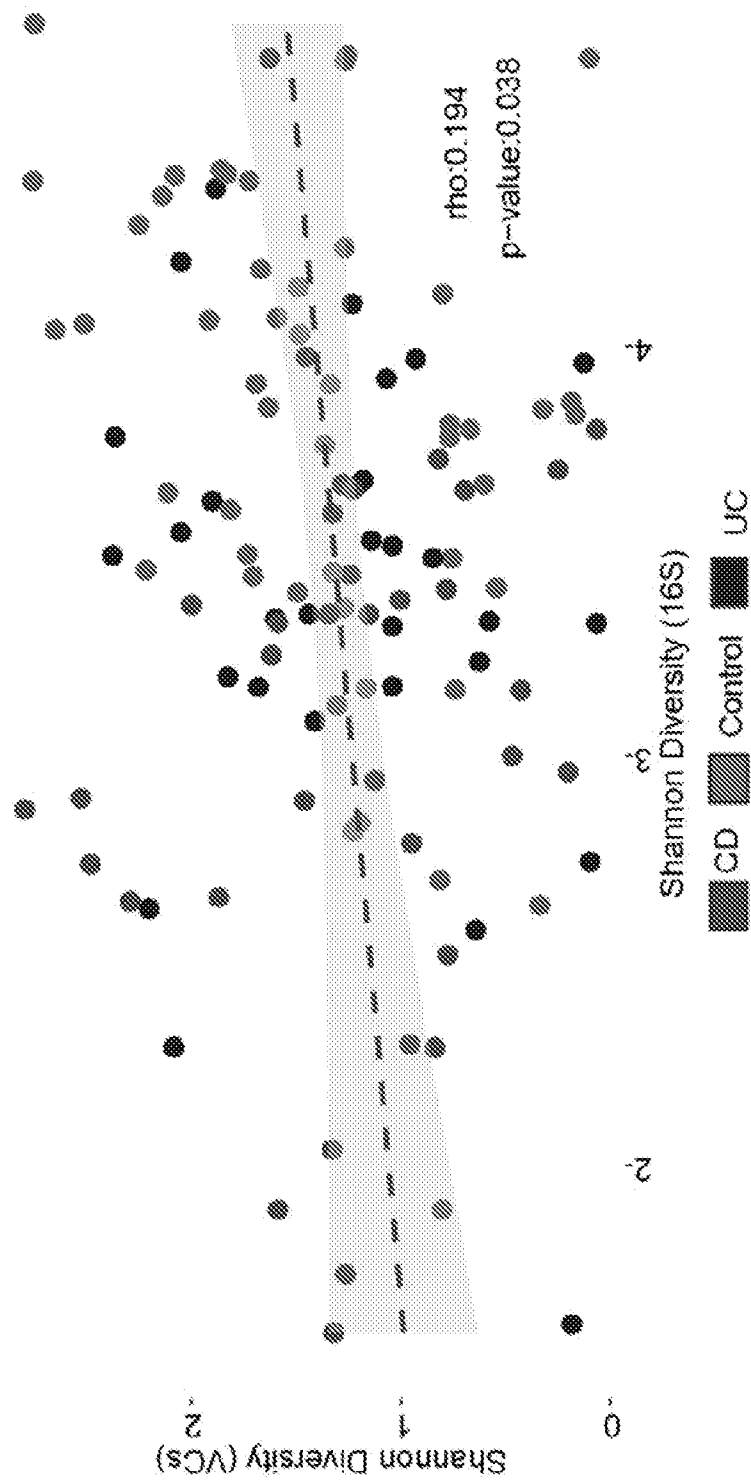


Figure 9A

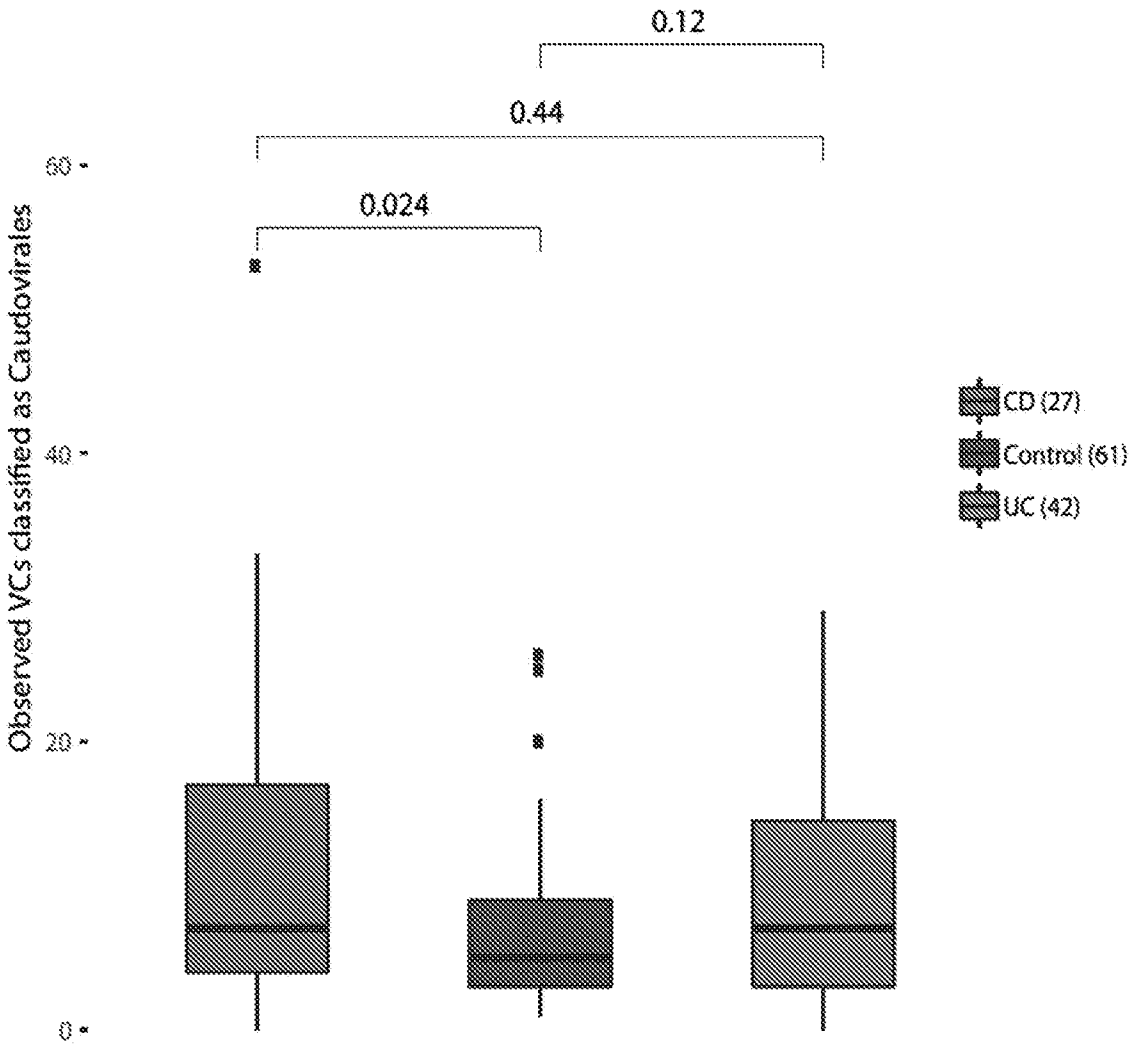


Figure 9B

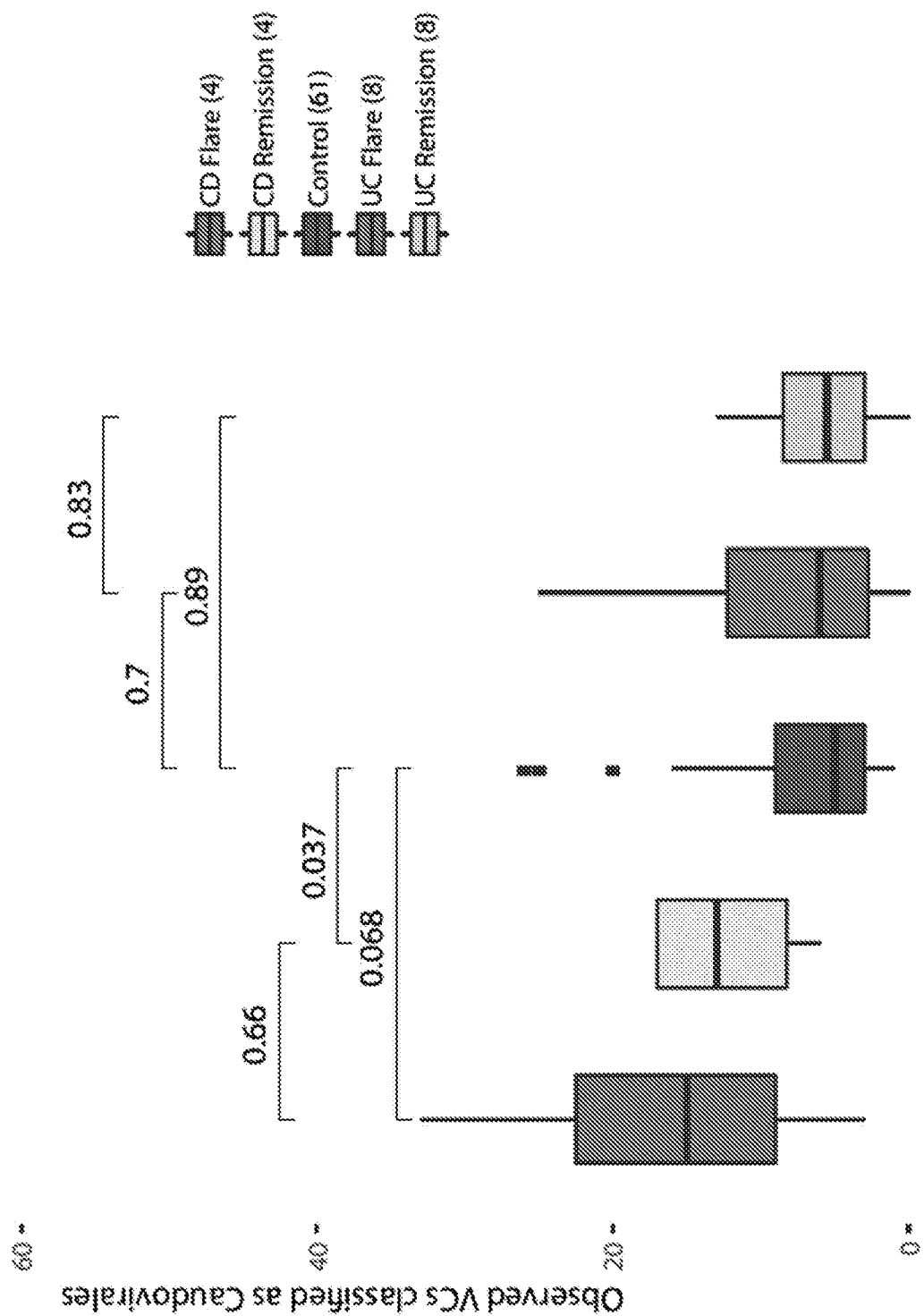


Figure 10A

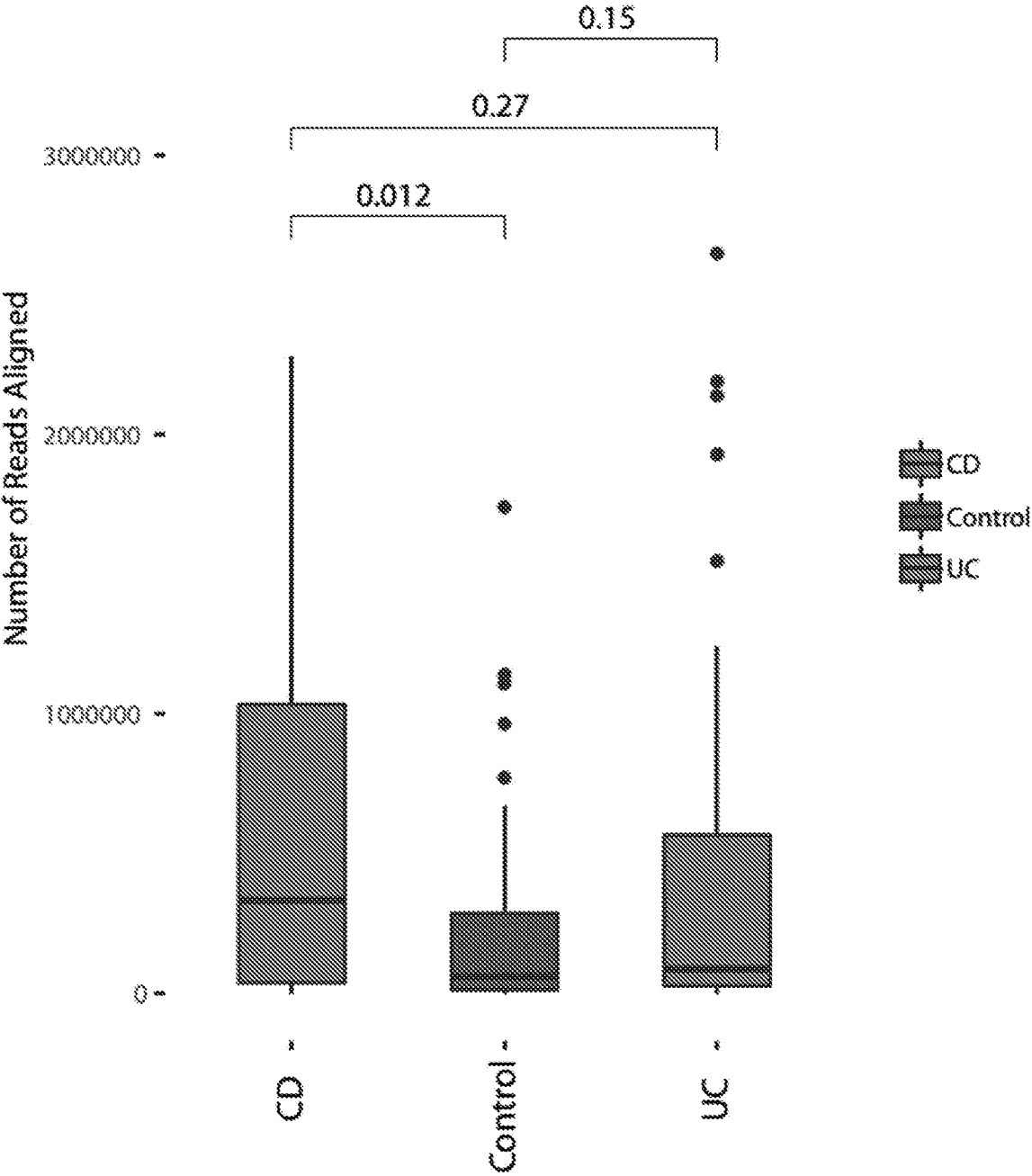


Figure 10B

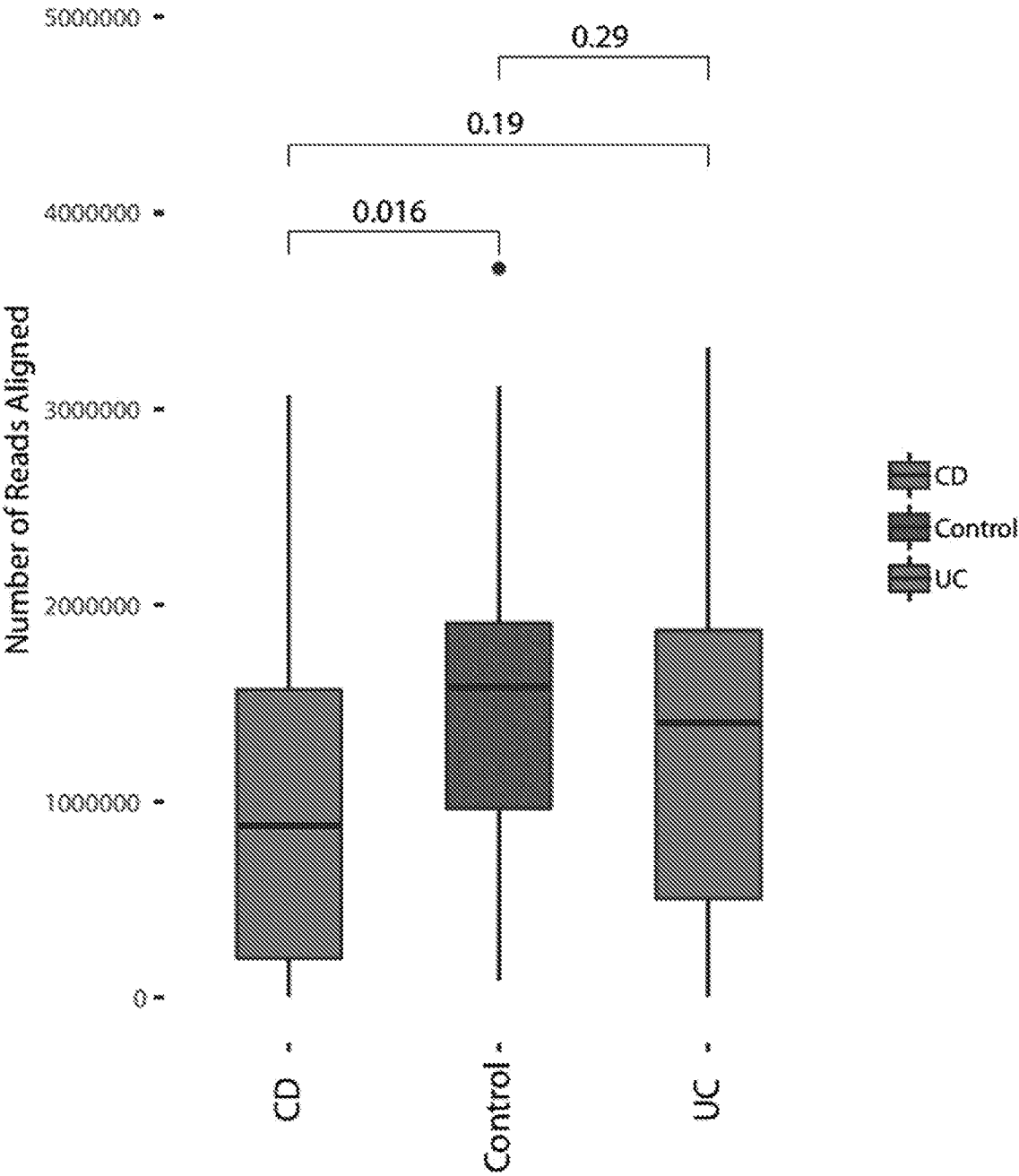


Figure 11

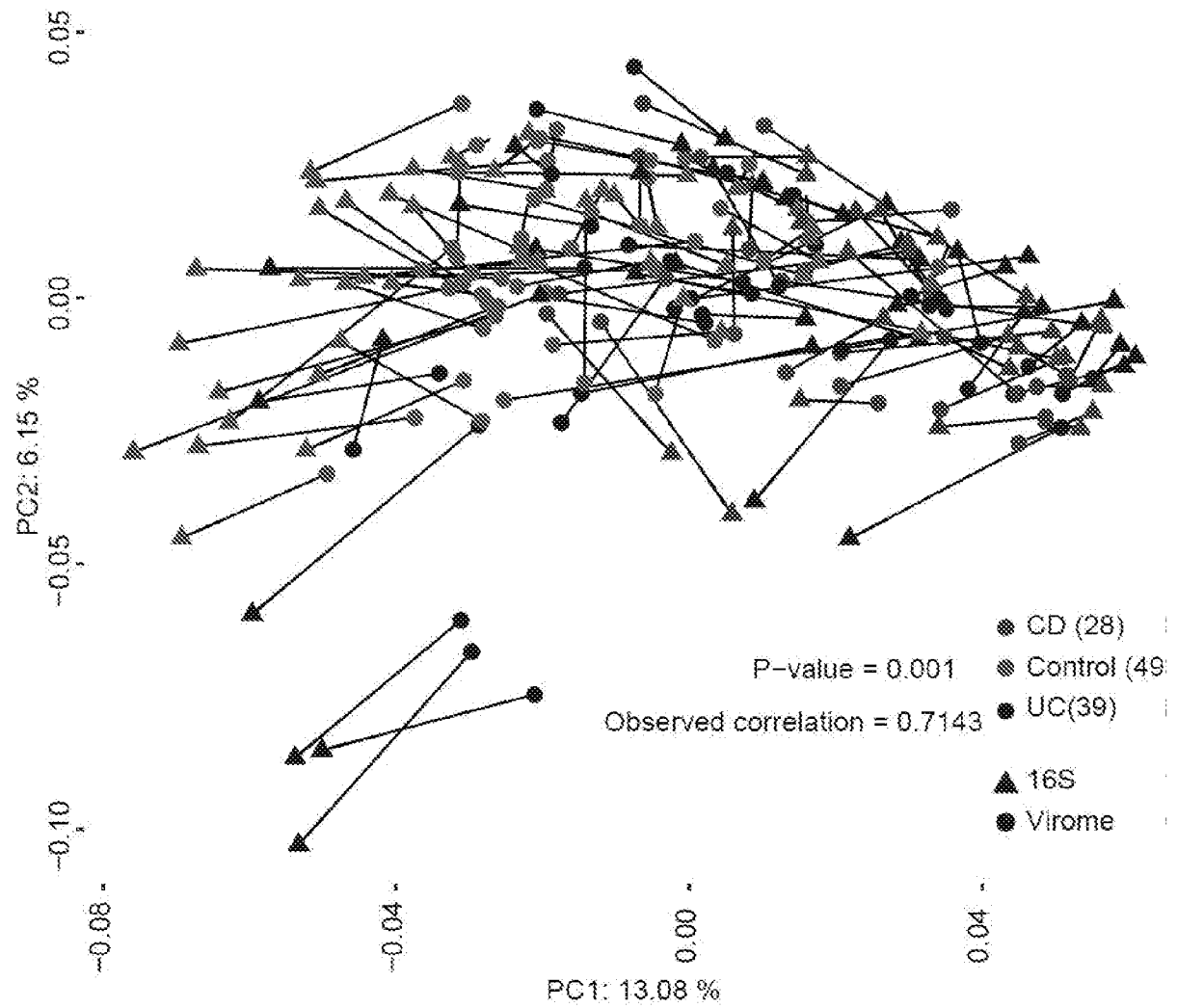


Figure 12

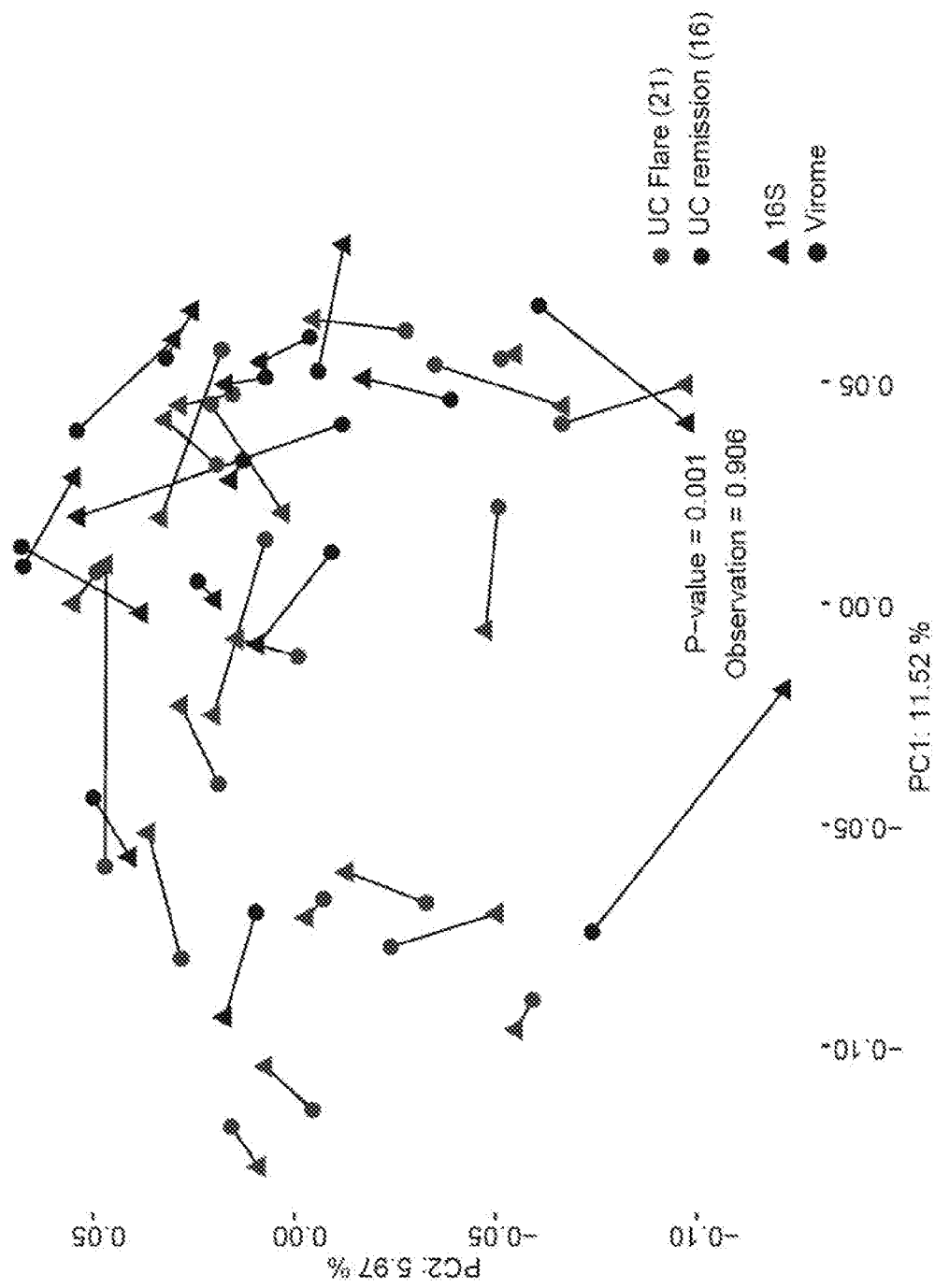


Figure 13A

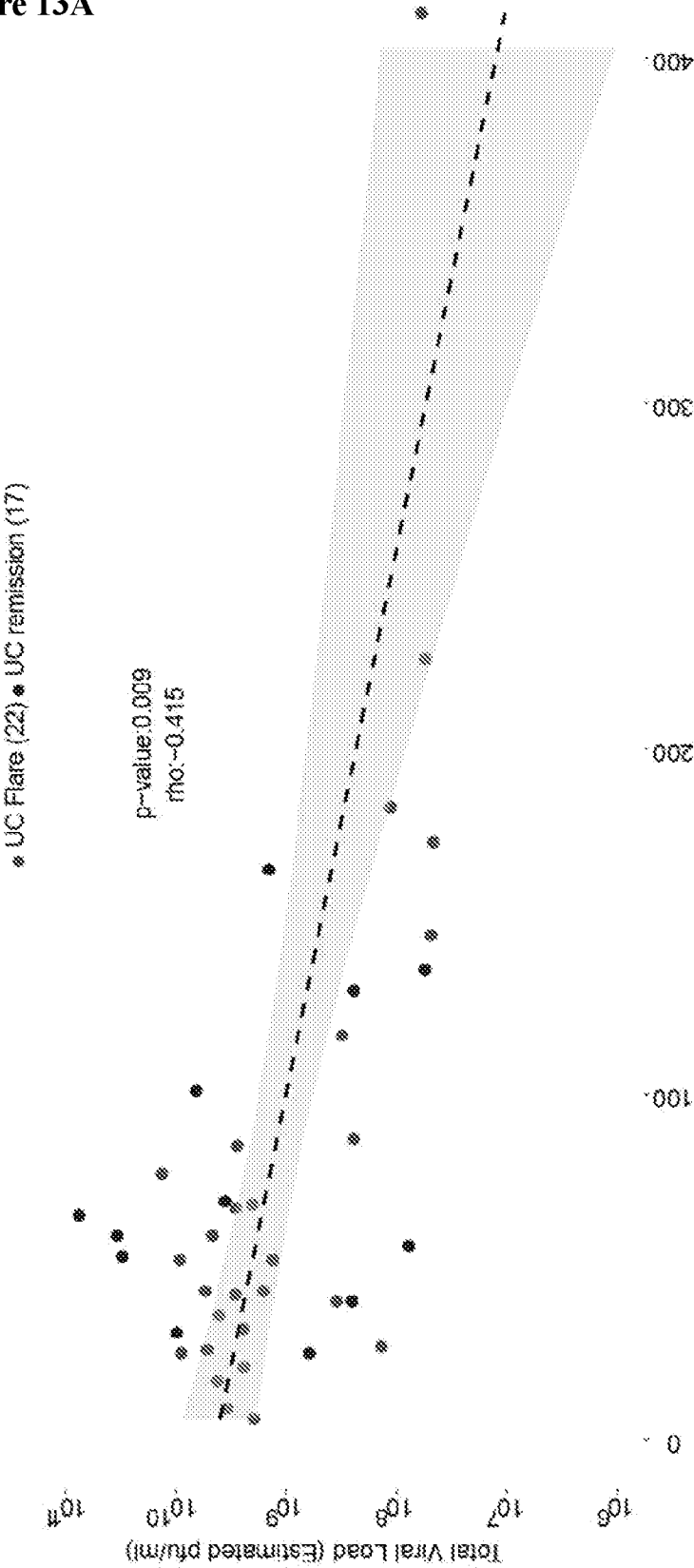


Figure 13B

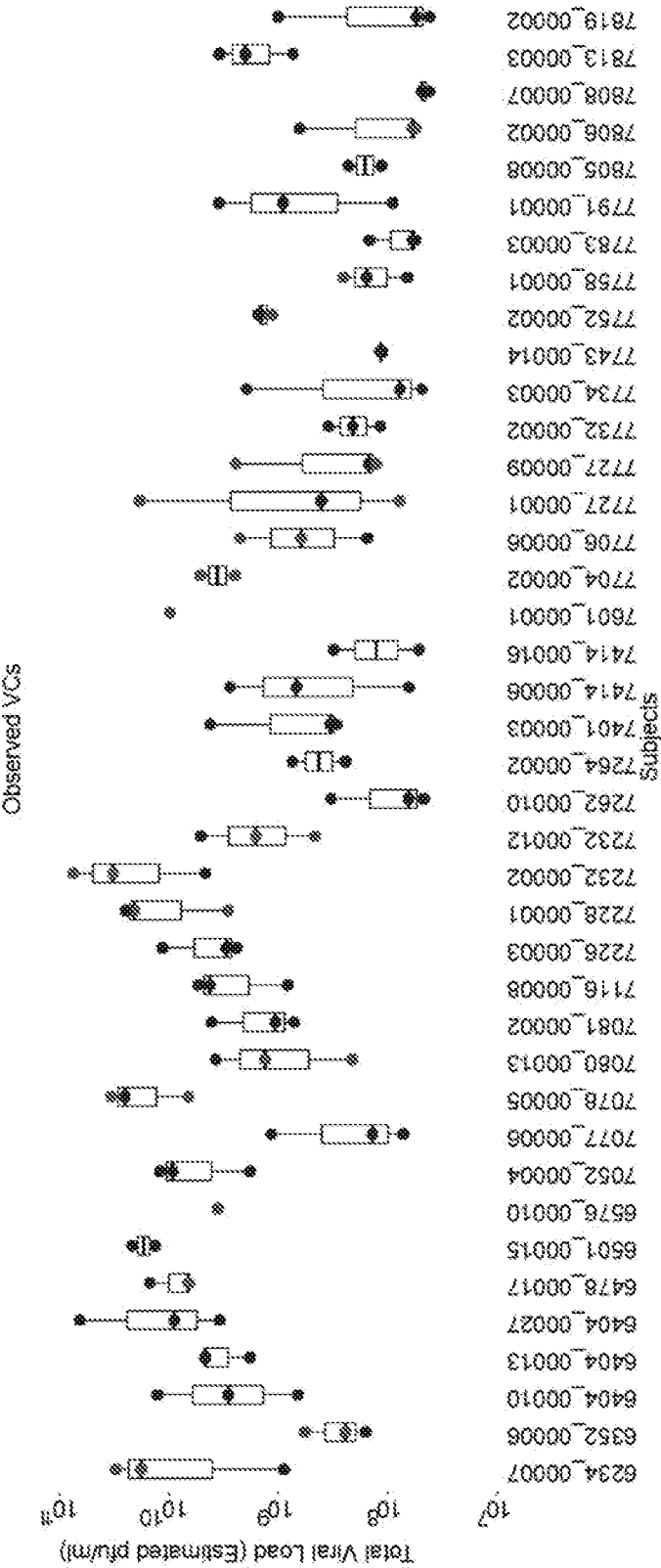


Figure 14

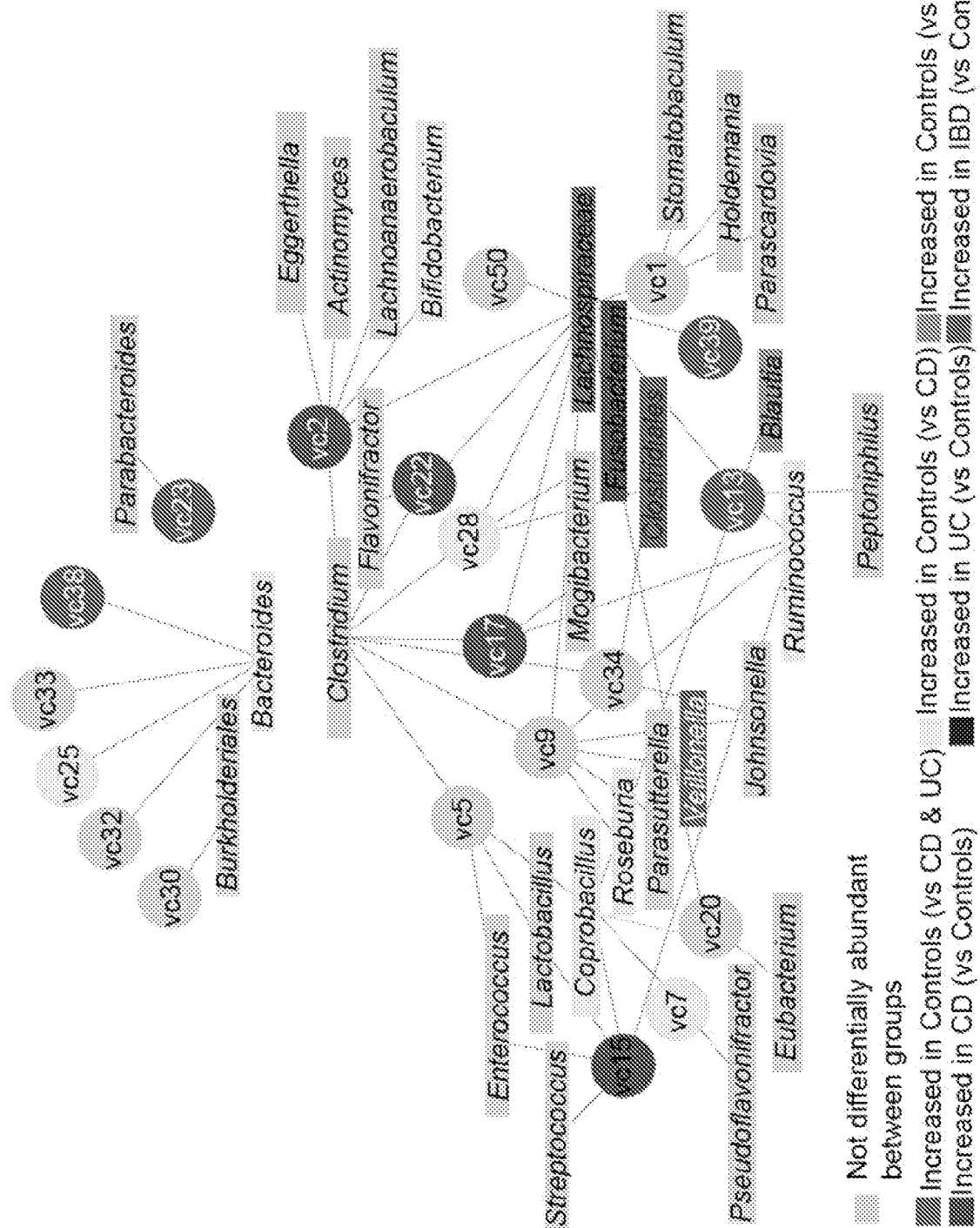


Figure 15A

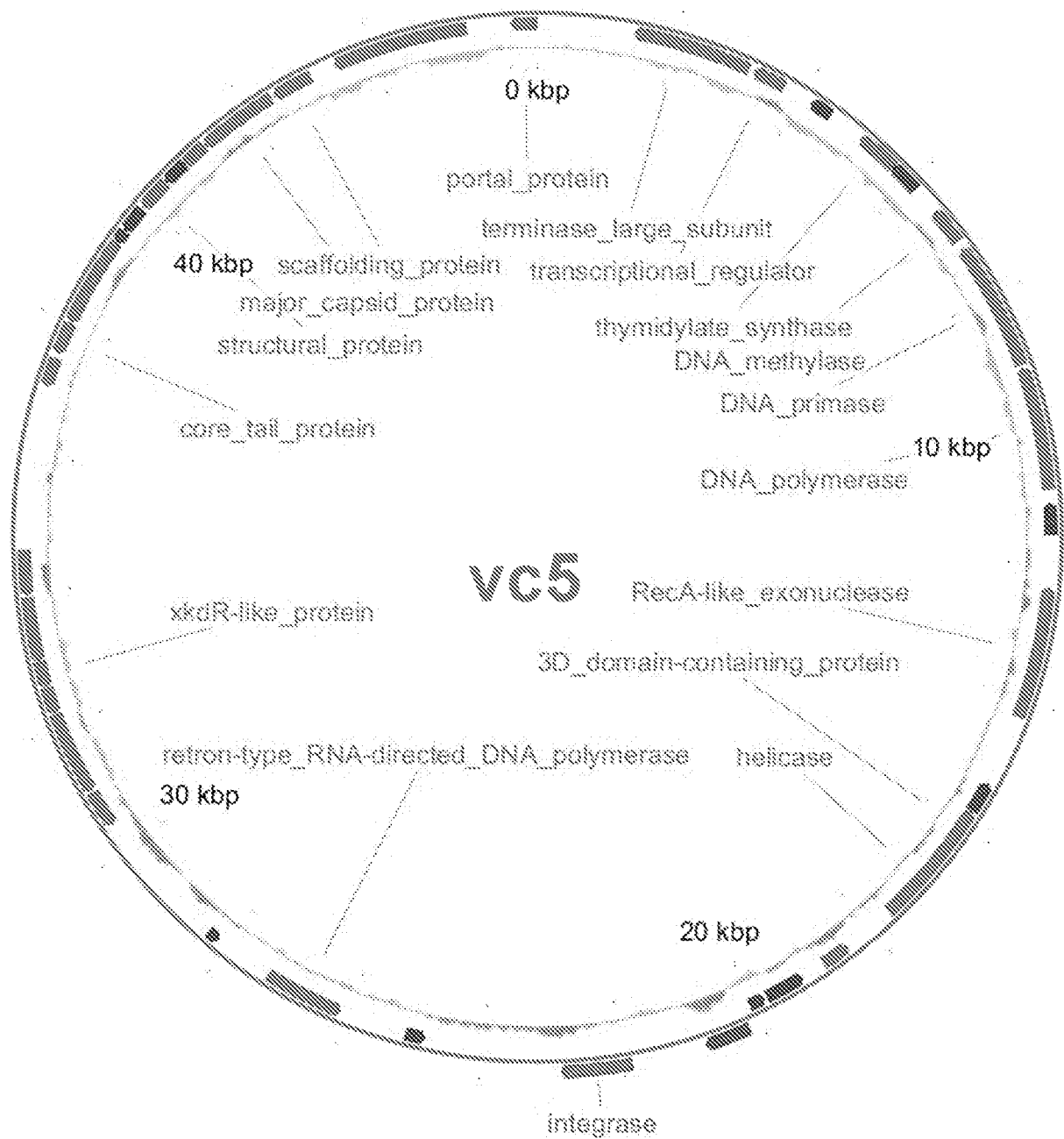


Figure 15B

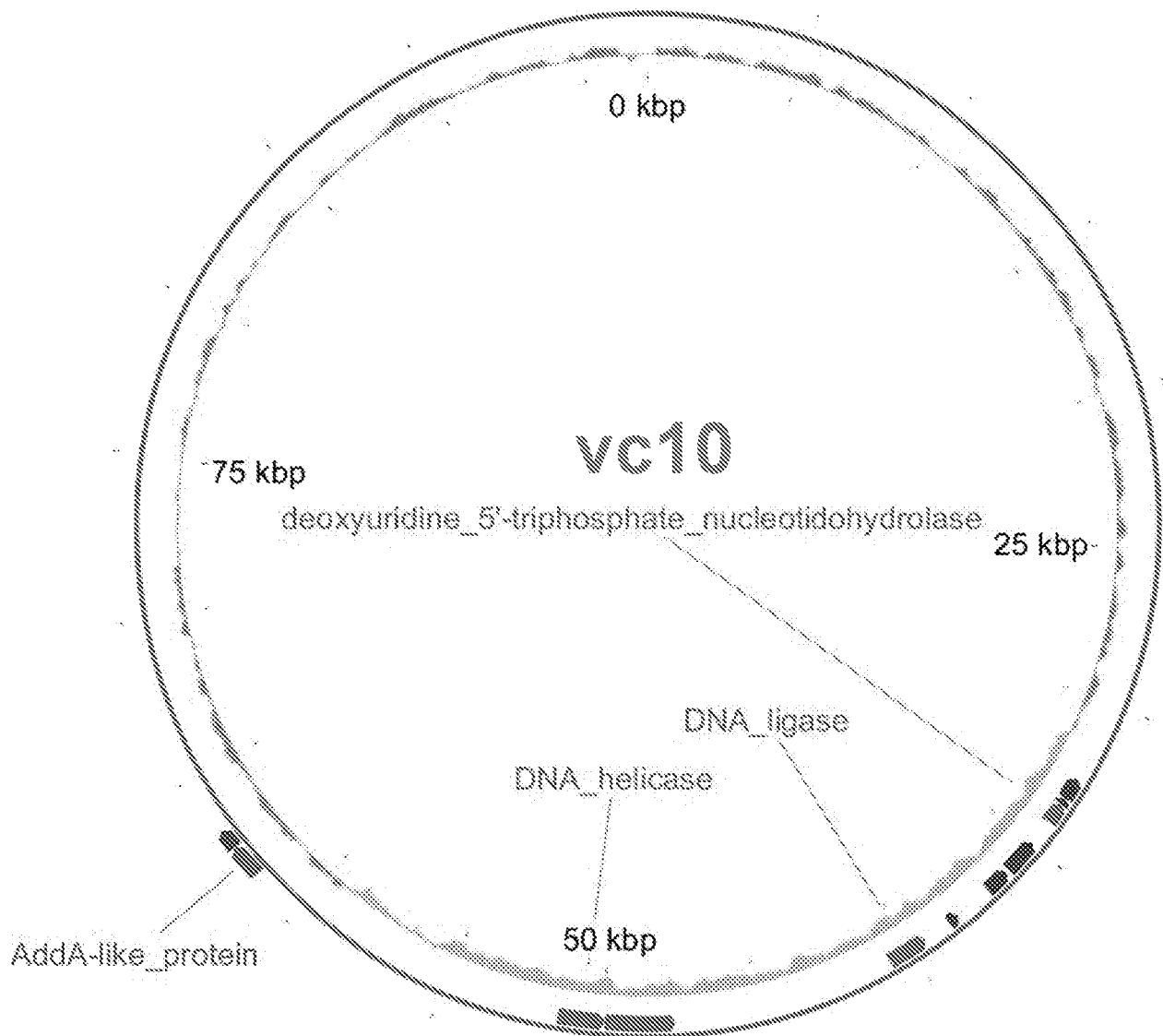


Figure 15C

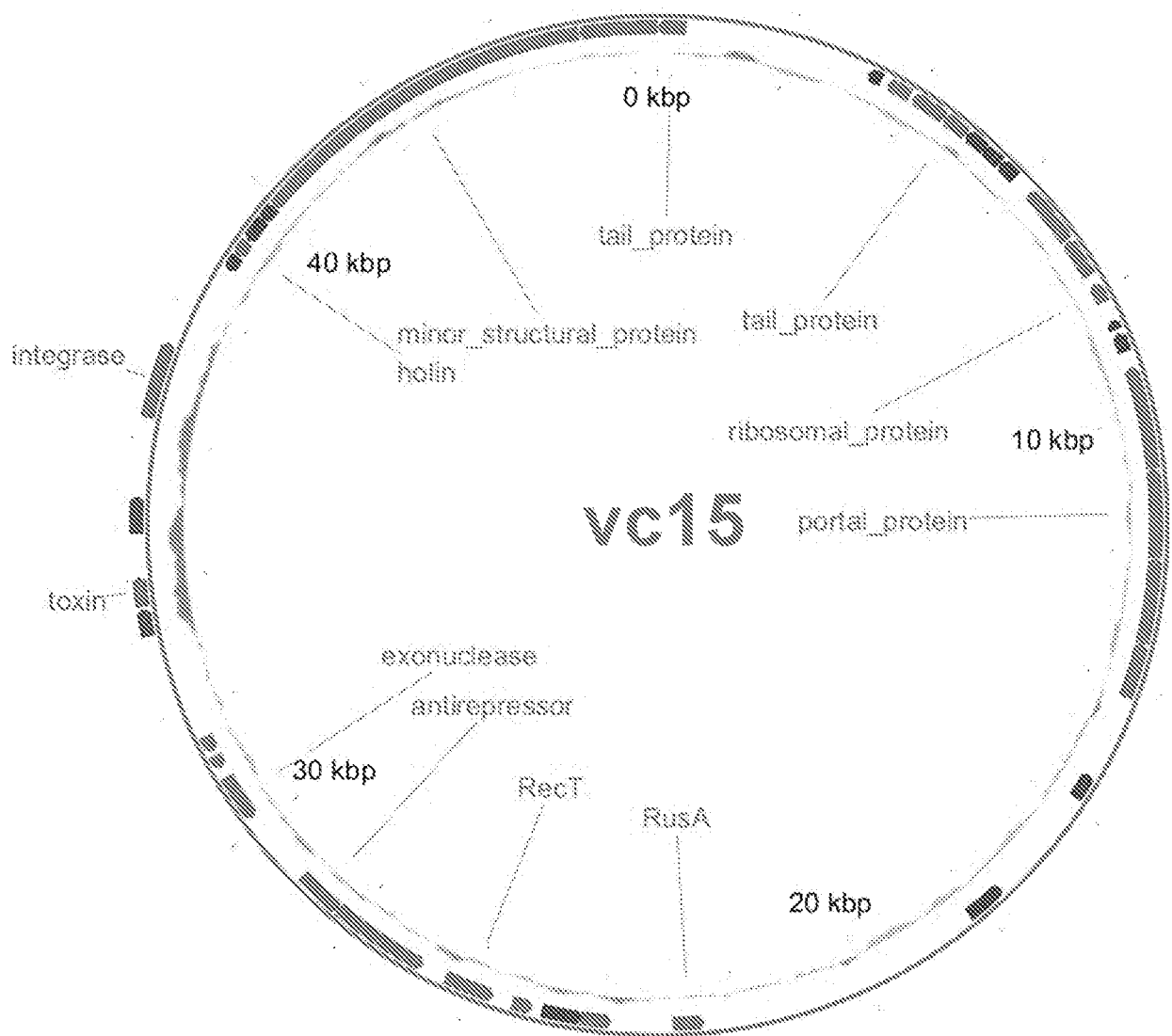


Figure 15D

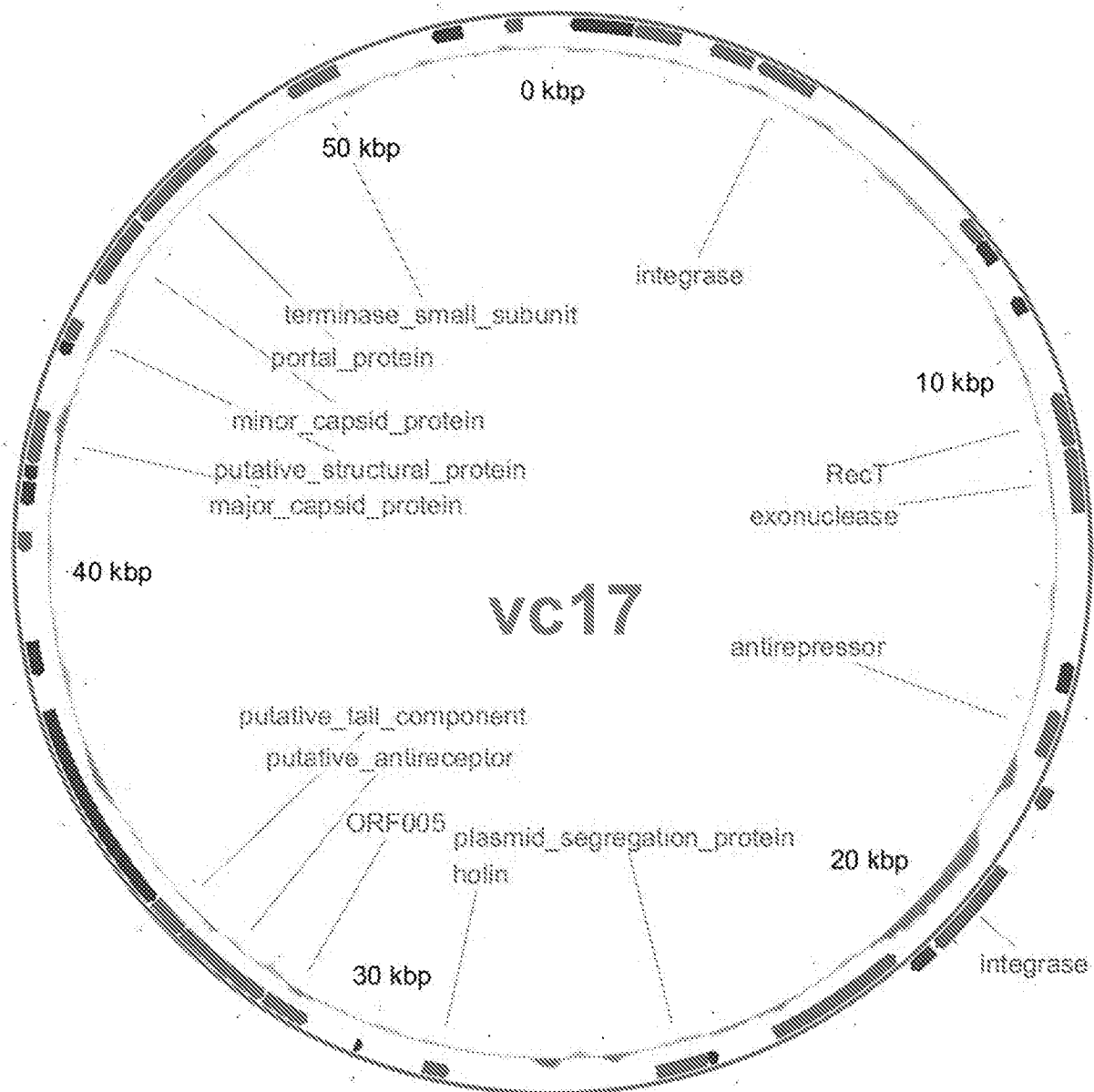


Figure 15E

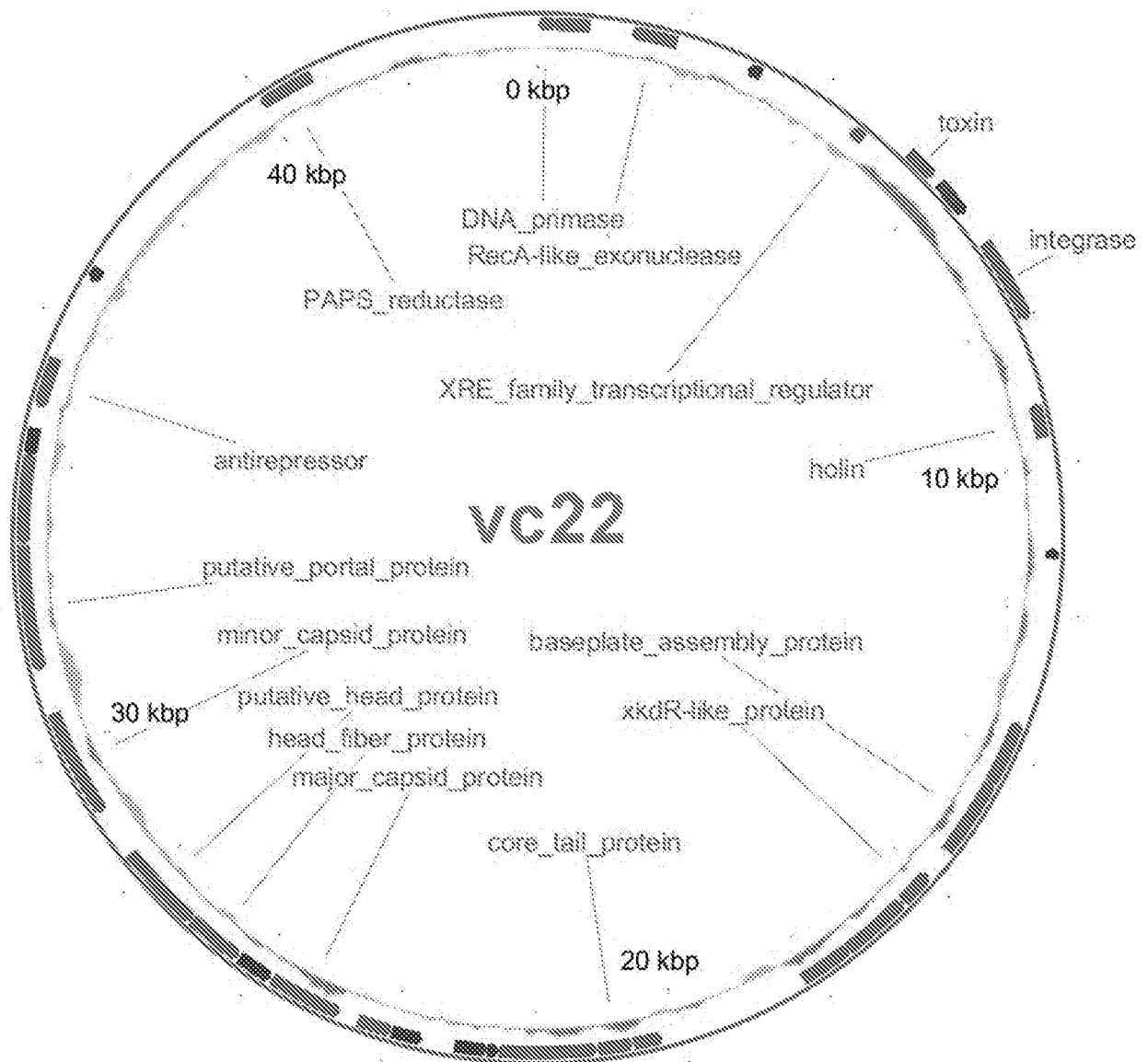


Figure 15F

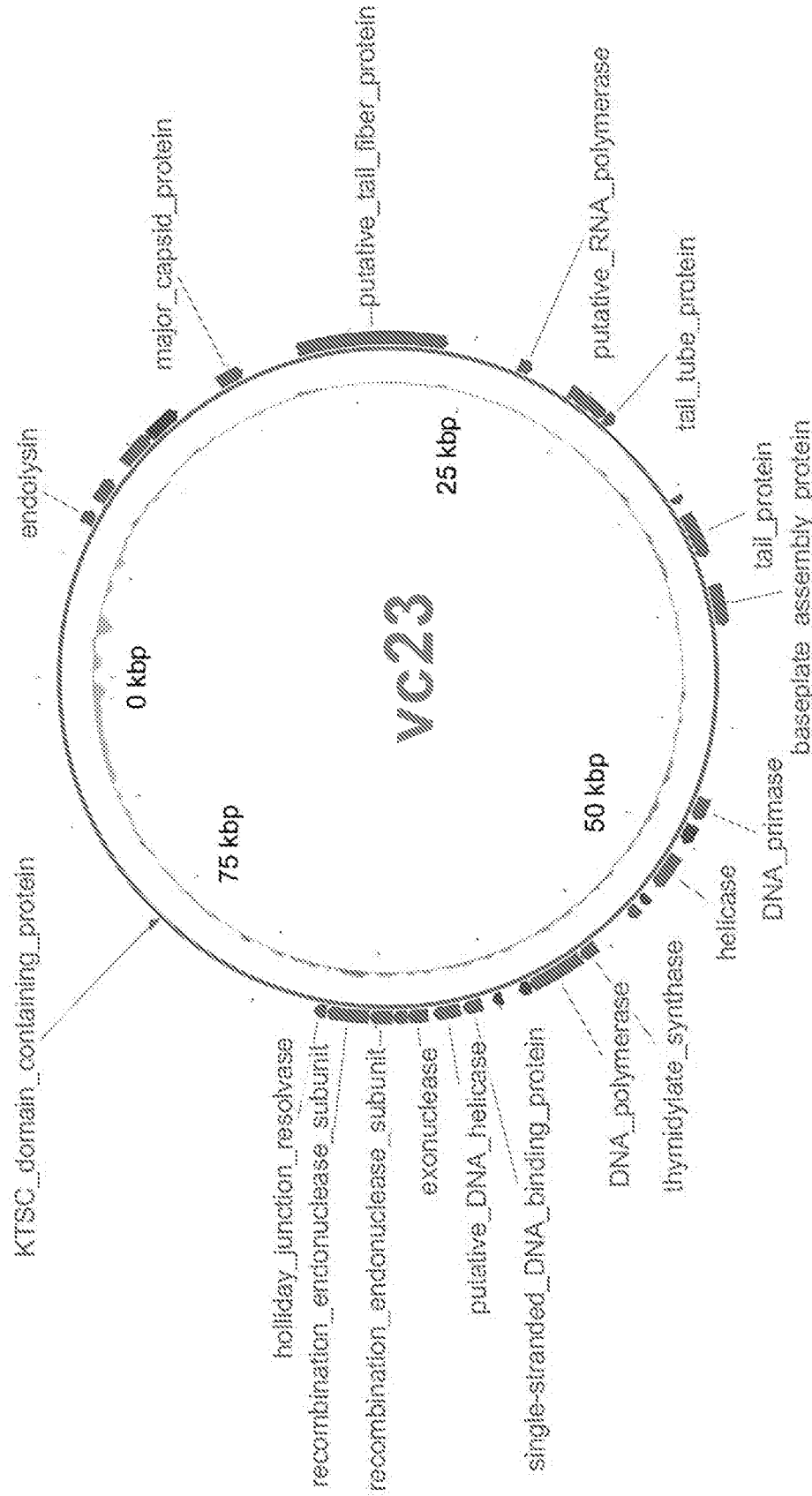


Figure 15G

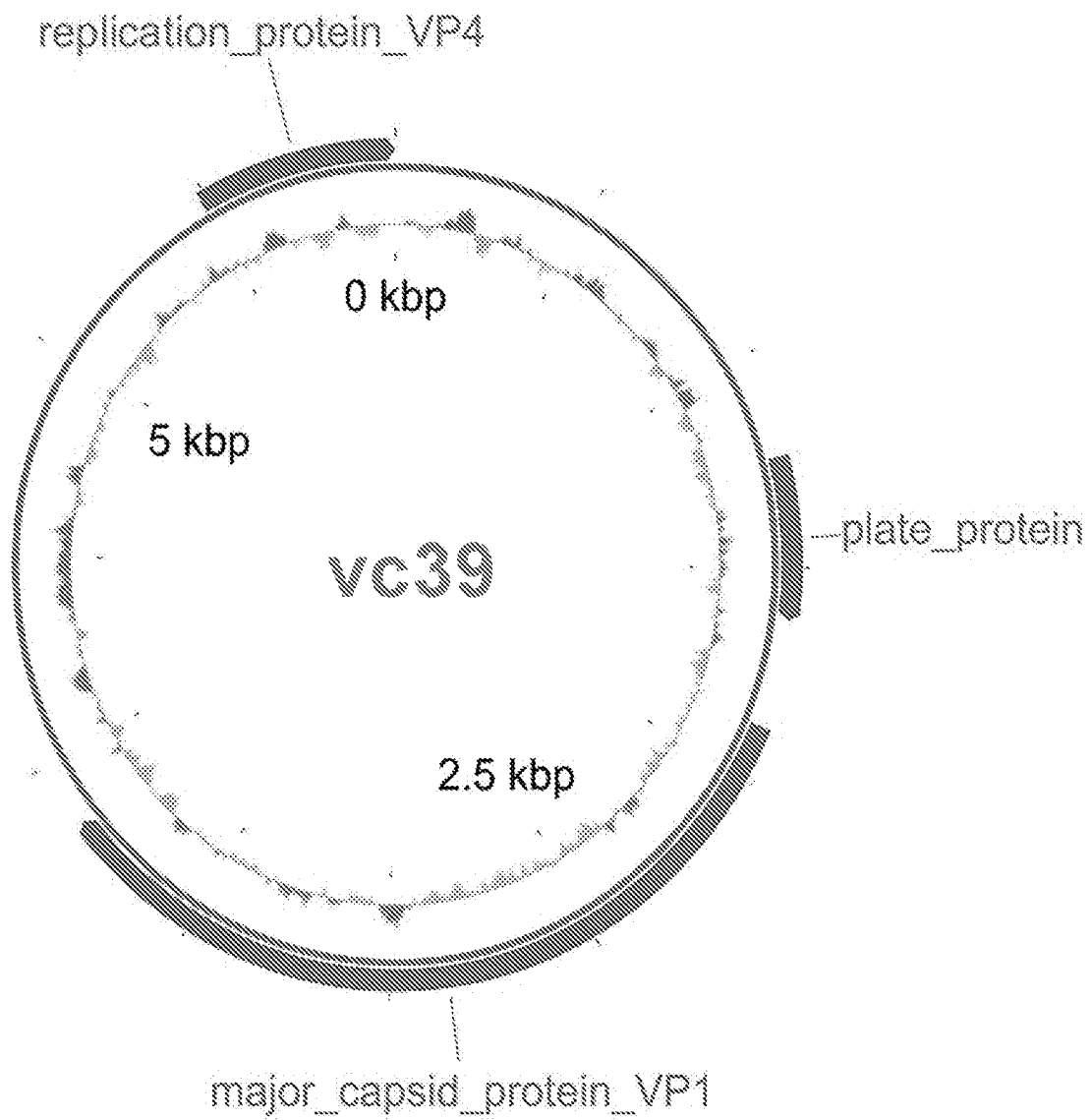


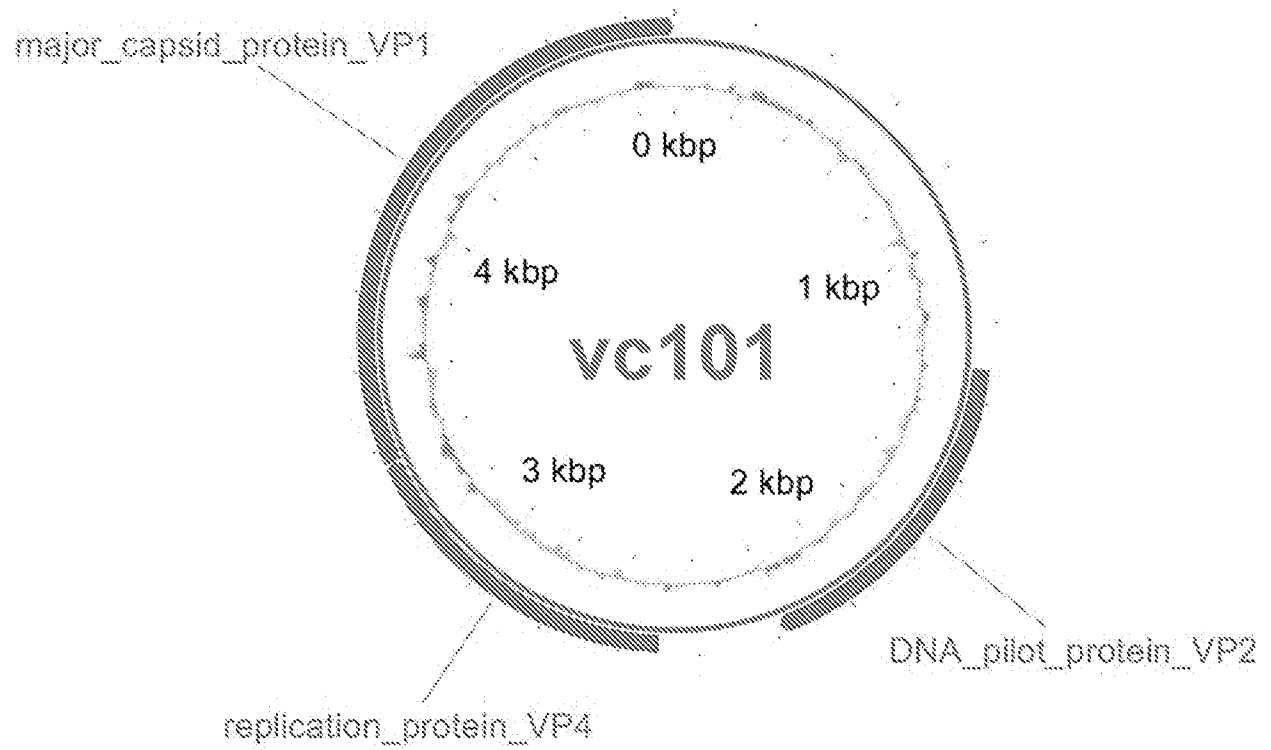
Figure 15H

Figure 15I

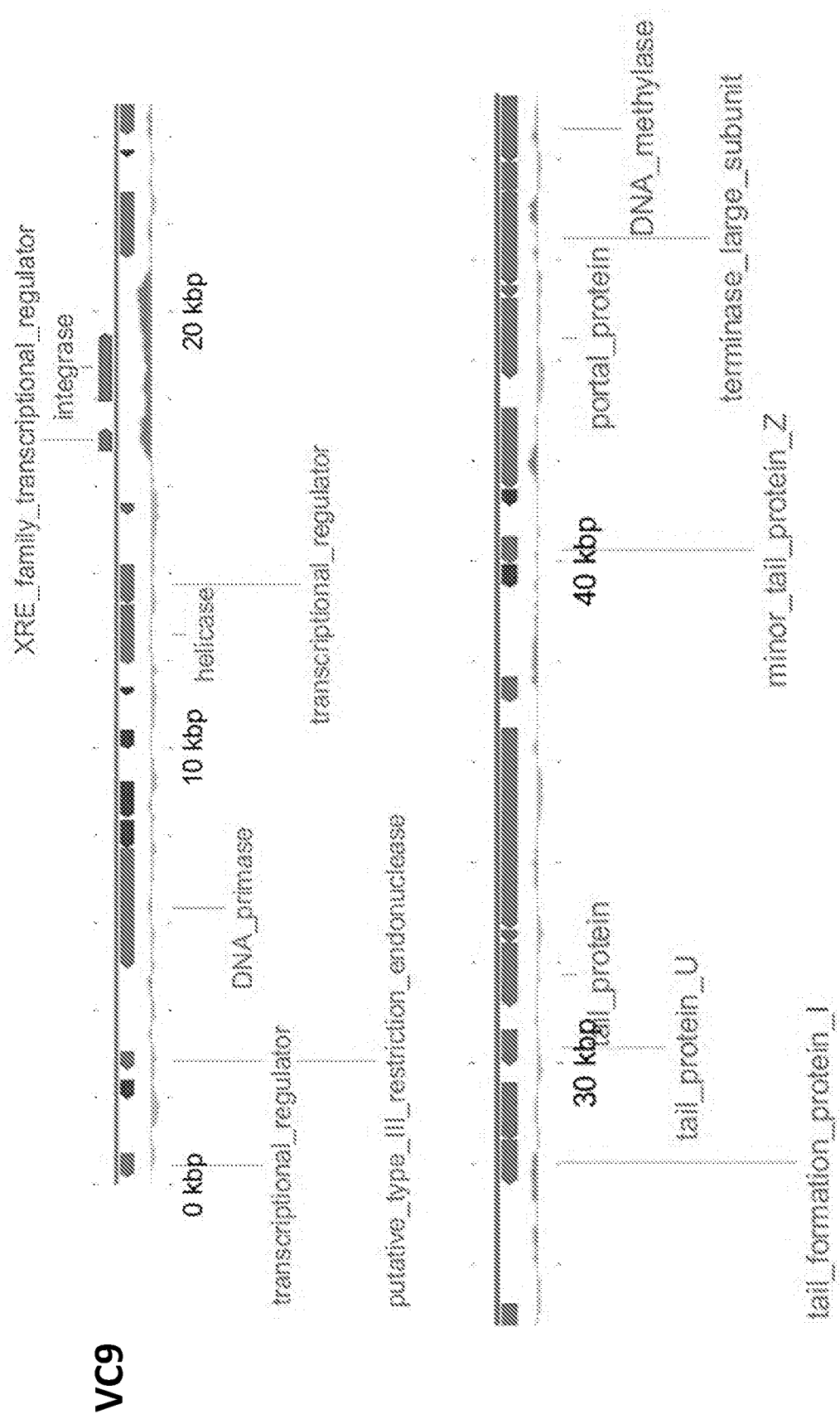


Figure 15J

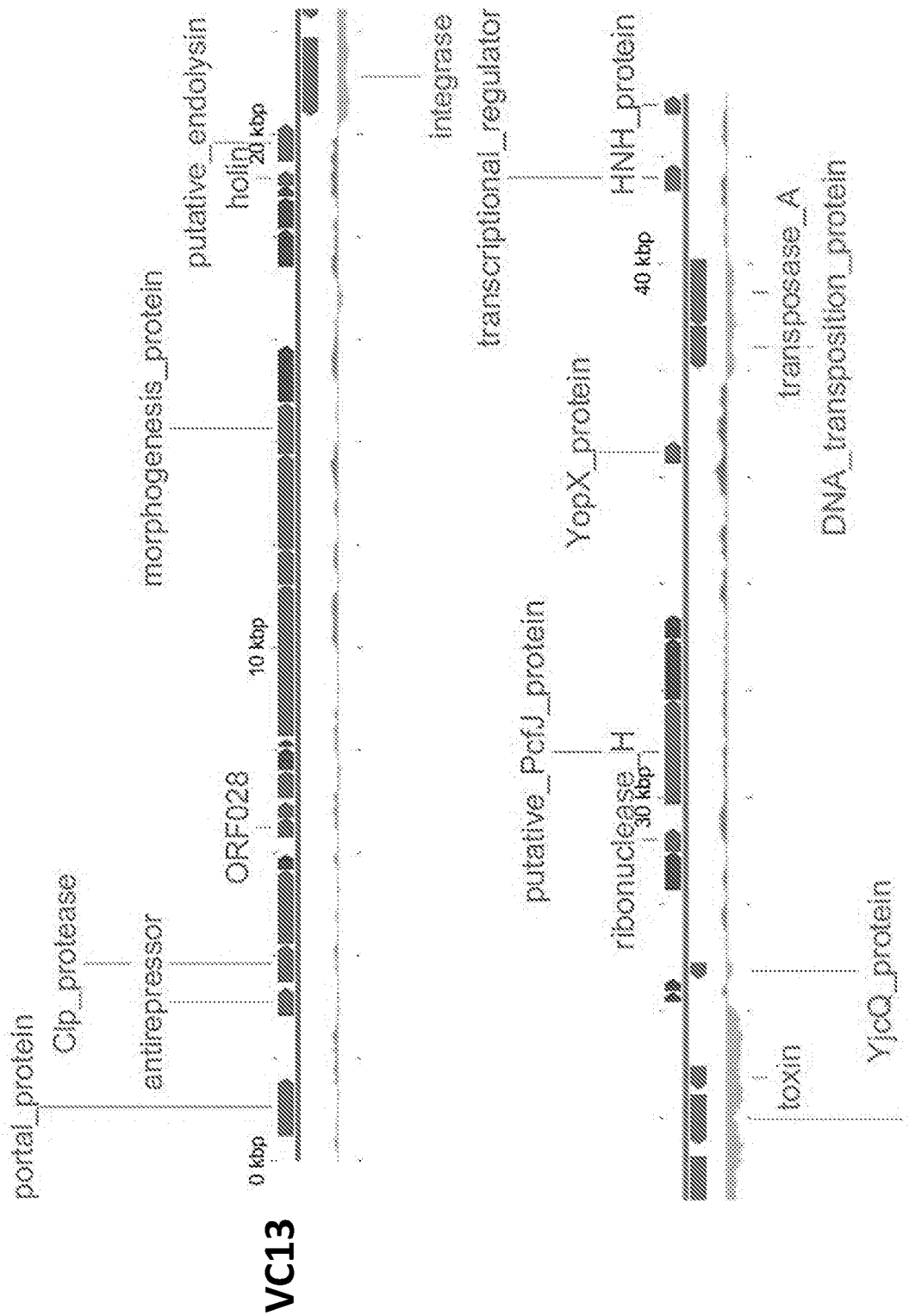


Figure 16

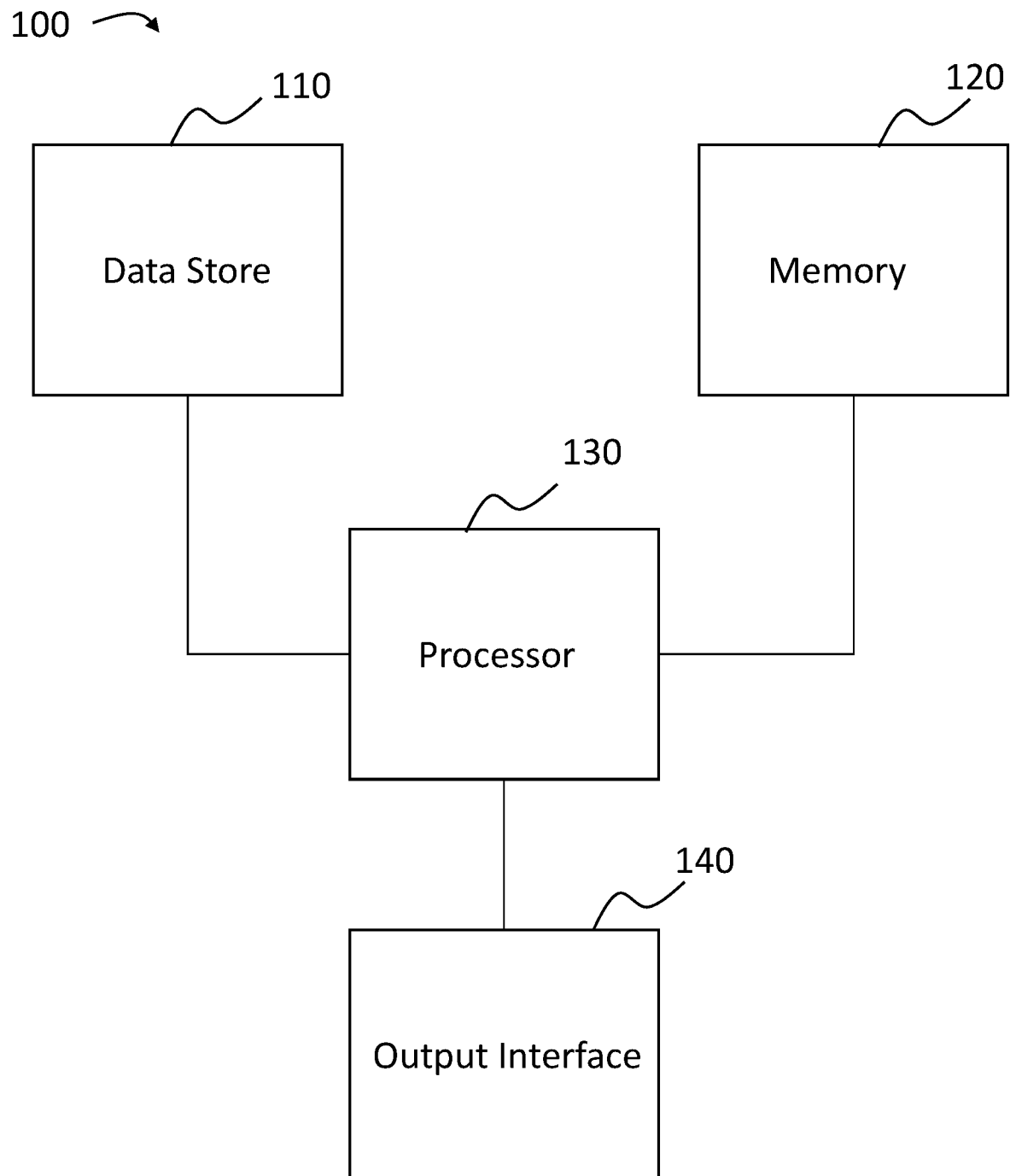
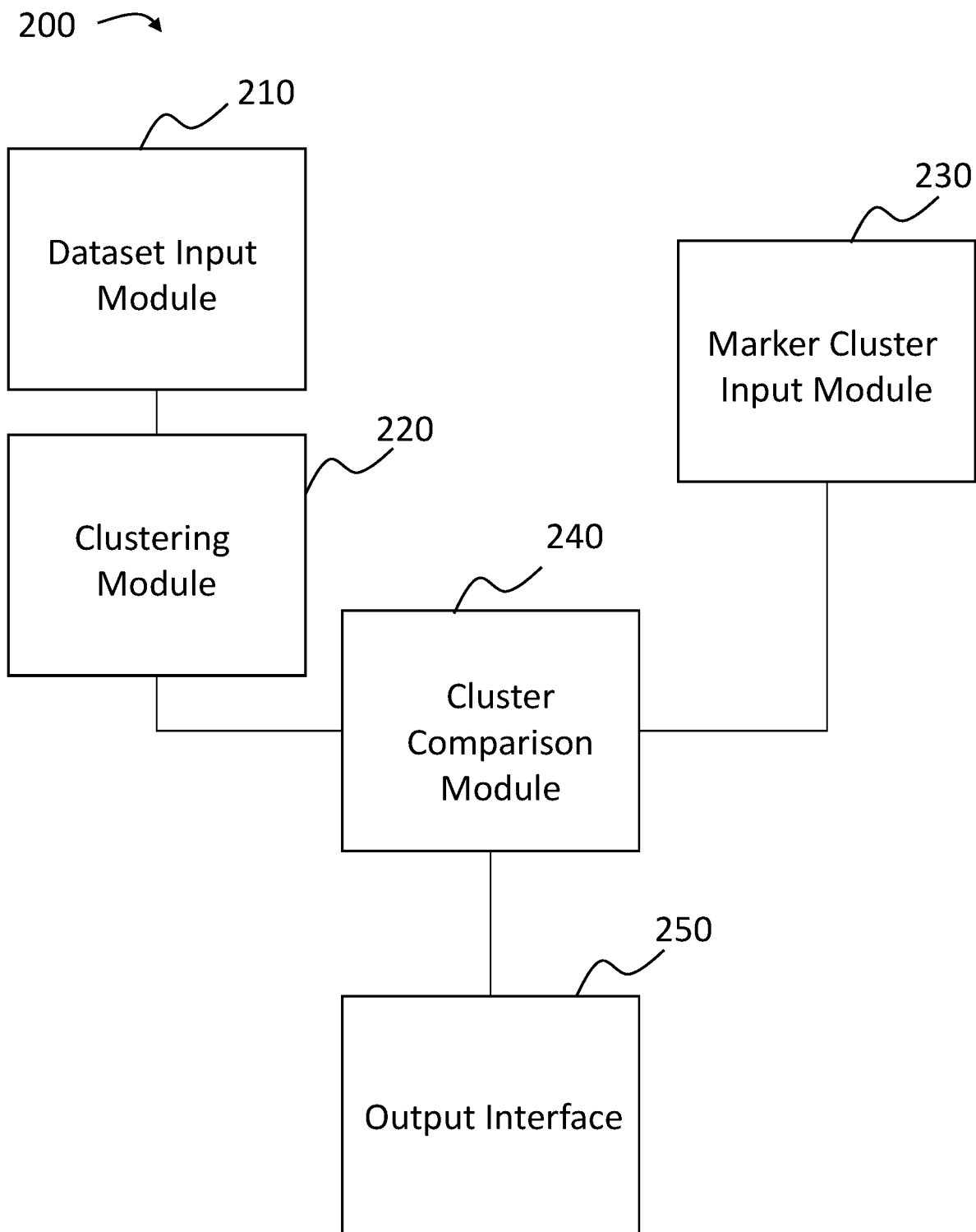


Figure 17



INTERNATIONAL SEARCH REPORT

International application No
PCT/IB2020/055047

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/70 A61K35/741
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12Q A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	TAO ZUO ET AL: "Gut mucosal virome alterations in ulcerative colitis", GUT MICROBIOTA, vol. 68, no. 7, 6 March 2019 (2019-03-06), pages 1169-1179, XP055720085, UK ISSN: 0017-5749, DOI: 10.1136/gutjnl-2018-318131 page 9; figures 1-3 page 6 abstract -/--	1-69, 73-76,79



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

7 August 2020

Date of mailing of the international search report

06/10/2020

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040,
Fax: (+31-70) 340-3016

Authorized officer

Tilkorn, A

INTERNATIONAL SEARCH REPORT

International application No

PCT/IB2020/055047

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	-& Tao Zuo: "Gut mucosal virome alterations in ulcerative colitis - Supplementary Appendix", Gut microbiota, 6 March 2019 (2019-03-06), XP055720350, Retrieved from the Internet: URL:https://gut.bmj.com/content/68/7/1169 [retrieved on 2020-08-05] page 1 - page 6 -----	
A	JASON M. NORMAN ET AL: "Disease-Specific Alterations in the Enteric Virome in Inflammatory Bowel Disease", CELL, vol. 160, no. 3, 1 January 2015 (2015-01-01), pages 447-460, XP055720670, AMSTERDAM, NL ISSN: 0092-8674, DOI: 10.1016/j.cell.2015.01.002 the whole document -----	1-69, 73-76,79
A	Andrey N. Shkoporov ET AL: "The human gut virome is highly diverse, stable and individual-specific", bioRxiv, 3 June 2019 (2019-06-03), XP055720288, DOI: 10.1101/657528 Retrieved from the Internet: URL:https://www.biorxiv.org/content/10.1101/657528v1 the whole document -----	1-69, 73-76,79
A	Ho Bin Jang ET AL: "Gene sharing networks to automate genome-based prokaryotic viral taxonomyABSTRACT", bioRxiv, 29 January 2019 (2019-01-29), XP055720424, DOI: 10.1101/533240 Retrieved from the Internet: URL:https://www.biorxiv.org/content/10.1101/533240v1 the whole document -----	1-69, 73-76,79
A	SHKOPOROV ANDREY N ET AL: "Bacteriophages of the Human Gut: The "Known Unknown" of the Microbiome", CELL HOST & MICROBE, vol. 25, no. 2, 13 February 2019 (2019-02-13), pages 195-209, XP085602333, ISSN: 1931-3128, DOI: 10.1016/J.CHOM.2019.01.017 the whole document -----	1-69, 73-76,79
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INTERNATIONAL SEARCH REPORT

International application No

PCT/IB2020/055047

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2018/125900 A1 (COX LAURA M [US] ET AL) 10 May 2018 (2018-05-10) the whole document -----	67-69, 73-76,79

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB2020/055047

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-69(completely); 73-76, 79(partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-69(completely); 73-76, 79(partially)

Method, kit or system based on the determination of viral marker clusters for determining the presence of inflammatory bowel disease (IBD), Crohn's disease (CD) or ulcerative colitis (UC) and use of the viral clusters for treatment

2. claims: 70-72, 77, 78(completely); 73-76, 79(partially)

Method for preventing or treating IBD, CD or UC comprising administering to the subject an effective amount of a prebiotic and/or probiotic composition

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/IB2020/055047

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2018125900	A1	10-05-2018	NONE
