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(54) **Title**: METHOD OF DIAGNOSTIC OF INFLAMMATORY BOWEL DISEASES

(57) **Abstract**: A new method for diagnosing an inflammatory bowel disease is herein described, based on the determination of the absence of at least one gene from the human' gut microbiome.

METHOD OF DIAGNOSTIC OF INFLAMMATORY BOWEL DISEASES

Inflammatory bowel diseases are chronic disorders of unknown aetiology characterized by persistent mucosal inflammation at different levels of the gastrointestinal tract. Ulcerative colitis and Crohn's disease are the two main types of inflammatory bowel diseases. Ulcerative colitis causes continuous mucosal inflammation that is restricted to the colon whereas Crohn's disease causes discontinuous transmural inflammation anywhere throughout the gastrointestinal tract, although it most frequently affects the terminal ileum. Most common intestinal lesions consist of mucosal ulcerations, bowel wall swelling and stricturing of the intestinal lumen. These chronic inflammatory lesions may cause symptoms such as diarrhoea, faecal urgency, abdominal pain and fever, as well as complications of variable severity including bleeding, intestinal obstruction, sepsis and malnutrition.

Epidemiological studies demonstrated a steady increase of the incidence of such diseases in Western Europe and North America during the last century since 1950. In Southern Europe and Japan the rise in incidence came two decades later, but today incidence rates are as important as in Northern Europe and North America. Recent data suggest increasing incidence in Eastern European countries as well as in South and East Asia. Changes in incidence seem to be related to the westernization of lifestyles, including changes in dietary habits and environmental changes such as improved sanitation and industrialization. Today, figures of combined prevalence (ulcerative colitis plus Crohn's disease) suggest that inflammatory bowel diseases affects up to 0.5 % of the population of developed societies.

The impact of inflammatory bowel diseases on society is disproportionately high, as presentation often occurs at a young age and has the potential to cause lifelong ill health. At present, there is no cure or eradication therapy for inflammatory bowel diseases. Typically, both ulcerative colitis and Crohn's disease exhibit undulating activity with bouts of uncontrolled, chronic mucosal inflammation, followed by remodelling processes that occur during periods of remission. The primary treatment approach is usually drug therapy to mitigate bouts of inflammatory activity and to prevent future relapses when in

remission. Patients can be treated with a variety of drugs, including 5-ASAs (e.g. mesalazine), steroids (e.g. prednisolone) and immunosuppressants (e.g. azathioprine). In addition, patients may also receive new biological drugs such as monoclonal antibodies (e.g. the anti-TNF-α antibody infliximab) when standard drug treatment fails. Despite their general efficacy, such drugs can carry a significant burden. They are not only expensive, but side effects are common, with an incidence of 28% for immunosuppressants, rising to 50% for steroids. Some patients may present severe side effects like systemic infections or neoplasia, and therefore current therapies require a close surveillance. In addition, approximately 30% of patients with ulcerative colitis and 50% of patients with Crohn's disease will require surgery at some point in their life.

Available medical therapies cannot achieve eradication or permanent cure of such diseases, and this is mainly due to that fact that the precise aetiologies of ulcerative colitis and Crohn's disease remain to be elucidated. However, the pathophysiological mechanisms that lead to the mucosal inflammatory lesions have been unveiled at least in part during the past few years. There is convincing evidence that the inflammation observed in inflammatory bowel diseases is caused by abnormal communication between the gut microbial communities and the mucosal immune system. The defensive response of T helper lymphocytes (Th) of the mucosal immune system against pathogens is associated with inflammatory processes aimed at the eliminations of the pathogen, but at the same time these processes also damage the host tissues. Under normal circumstances, some commensal gut microbes seem to play a major role for induction of regulatory T lymphocytes (Tregs) in gut lymphoid follicles. Regulatory T lymphocytes are key players of the phenomenon called 'immune tolerance', since these lymphocytes do not induce inflammation in response to the microbial antigens that are recognised as non-pathogenic. Immune tolerance mediated by regulatory T lymphocytes is the essential homeostatic mechanism by which the host can tolerate the massive burden of innocuous antigens within the gut or on other body surfaces without responding through inflammation. Several lines of evidence suggest that in individuals with genetic susceptibility, Th lymphocyte-mediated immunity against luminal bacteria is the key event in driving the inflammatory process that generates intestinal lesions and/or impairs resolution of the lesions. A defective interaction of the gut microbiota with the mucosal

immune compartments may result in the abnormalities leading to chronic intestinal inflammation.

Several studies have shown that the composition of the faecal microbiota differs between subjects with inflammatory bowel diseases and healthy controls. The reported differences are variable and not always consistent among the various studies. It is thus not possible to use the published differences to distinguish between patients with inflammatory bowel diseases and healthy people. However, as explained above, the indigenous gut microbes will be determinant under certain circumstances in the onset and maintenance of inflammatory bowel diseases, especially Crohn's disease. There is thus still a need for a new, reliable method allowing a consistent diagnostic of inflammatory bowel diseases.

Most intestinal commensals cannot be cultured. Genomic strategies have been developped to overcome this limitation (Hamady and Knight, *Genome Res*, **19**: 1141-1152, 2009). These strategies have allowed the definition of the microbiome as the collection of the genes comprised in the genomes of the microbiota (Turnbaugh *et al.*, *Nature*, **449**: 804-8010, 2007; Hamady and Knight, *Genome Res.*, **19**: 1141-1152, 2009). The existence of a small number of species shared by all individuals constituting the human intestinal microbiota phylogenetic core has been demonstrated (Tap *et al.*, *Environ Microbiol.*, **11**(10): 2574-2584, 2009). Recently, a metagenomic analysis has led to the identification of an extensive catalogue of 3.3 million non-redundant microbial genes of the human gut, corresponding to 576.7 gigabases of sequence (Qin *et al.*, *Nature*, 2010, doi:10.1038/nature08821).

The inventors have used a method based on the isolation and sequencing of DNA fragments from human faeces in different individuals. Since an extensive catalogue of microbial genes from the gut is now available (Qin *et al.*, *Nature*, 2010, doi:10.1038/nature08821), the number of copies and the frequency of a specific sequence in a specific population (e.g. patients suffering from inflammatory bowe diseases) can be calculated. It is thus possible to identify any correlation between the presence or absence of a specific gene and the presence or absence of a specific

pathology. In addition, the number of copies of a specific gene in an individual can be determined.

Crohn's disease and ulcerative colitis are chronic immune inflammatory conditions of the alimentary tract, referred to collectively as inflammatory bowel diseases. The inventors were able to identify genes which are significantly different between a group of patient suffering from Crohn's disease or ulcerative colitis, and a control group of healthy people. These genes are listed in Table 1 (Crohn's diseaese) and Table 2 (ulcerative colitis). The said genes are more numerous in healthy individuals than in the patients. This observation is statistically significant, since the total number of microbial genes is not different in both populations. There is thus a loss of specific human's gut microbial genes in individuals suffering from inflammatory bowel disease.

A first aspect of this invention is a method for diagnosing an inflammatory bowel disease, said method comprising a step of determining whether at least one gene is absent from an individual's gut microbiome. By "individual's gut microbiome", it is herein understood all the genes constituting the microbiota of the said individual. The term "individual's gut microbiome" thus corresponds to all the genes of all the bacteria present in the said individual's gut.

A gene is absent from the microbiome when its number of copies in the microbiome is under a certain threshold value. According to the present invention, a "threshold value" is intended to mean a value that permits to discriminate samples in which the number of copies of the gene of interest corresponds to a number of copies in the individual's microbiome that is low or high. In particular, if a number of copies is inferior or equal to the threshold value, then the number of copies of this gene in the microbiome is considered low, whereas if the number of copies is superior to the threshold value, then the number of copies of this gene in the microbiome is considered high. A low copy number means that the gene is absent from the microbiome, whereas a high number of copies means that the gene is present in the microbiome. For each gene, and depending on the method used for measuring the number of copies of the gene, the optimal

threshold value may vary. However, it may be easily determined by a skilled artisan based on the analysis of the microbiome of several individuals in which the number of copiesl (low or high) is known for this particular gene, and on the comparison thereof with the number of copies of a control gene.

The method of the invention thus allows the skilled person to diagnose a pathology solely on the basis of the presence or the absence of a gene from the individual's gut microbiome. There is a direct correlation between the number of copies of a specific gene and the number of bacterial cells carrying this gene. The method of the invention thus allows the skilled person to detect a dysbiosis, i.e. a microbial imbalance, by analysis of the microbiome. Not all the species in the gut have been identified, because most cannot be cultured, and identification is difficult. In addition, most species found in the gut of a given individual are rare, which makes them difficult to detect (Hamady and Knight, *Genome Res.*, **19**: 1141-1152, 2009). In this first aspect of the invention, no prior identification of the bacterial species the said gene belongs to is required. The method of diagnosis of the invention is thus not restricted to the determination of a change in the population of known gut's bacterial species, but encompasses also the bacteria which have not yet been characterized taxiconomically.

There are several ways to obtain samples of the said individual's gut microbial DNA (Sokol *et al.*, *Inflamm. Bowel Dis.*, **14**(6): 858-867, 2008). For example, it is possible to prepare mucosal specimens, or biopsies, obtained by coloscopy. However, coloscopy is an invasive procedure which is ill-defined in terms of collection procedure from study to sudy. Likewise, it is possible to obtain biopies through surgery. However, even more than coloscopy, surgery is an invasive procedure, which effects on the microbial population are not known. Preferred is the faecal analysis, a procedure which has been reliably been used in the art (Bullock *et al.*, *Curr Issues Intest Microbiol.*; **5**(2): 59-64, 2004; Manichanh *et al.*, *Gut*, **55**: 205-211, 2006; Bakir *et al.*, *Int J Syst Evol Microbiol*, **56**(5): 931-935, 2006; Manichanh *et al.*, *Nucl. Acids Res.*, **36**(16): 5180-5188, 2008; Sokol *et al.*, *Inflamm. Bowel Dis.*, **14**(6): 858-867, 2008). An example of this procedure is described in the Methods section of the Experimental Examples. Faeces contain about 10^{11} bacterial cells per gram (wet weight) and bacterial cells comprise about 50 % of

faecal mass. The microbiota of the faeces represent primarily the microbiology of the distal large bowel. It is thus possible to isolate and analyse large quantities of microbial DNA from the faeces of an individual. By "microbial DNA", it is herein understood the DNA from any of the resident bacterial communities of the human gut. The term "microbial DNA" encompasses both coding and non-coding sequences; it is in particular not restricted to complete genes, but also comprises fragments of coding sequences. Faecal analysis is thus a non-invasive procedure, which yields consistent and directly comparable results from patient to patient.

Therefore, in a preferred embodiment, the method of the invention comprises a step of obtaining microbial DNA from faeces of the said individual. In a further preferred embodiment, the faeces from said individual are collected, DNA is extracted, and the presence or absence from an individual's gut microbiome of at least one gene is determined. The presence or absence of a gene may be determined by all the methods known to the skilled person. For instance, the whole microbiome of the said individual may be sequenced, and the presence or absence of the said gene searched with the help of bioinformatics methods. One instance of such a strategy is described in the Methods section of the Experimental Examples. Alternatively, the gene of interest may be looked for in the microbiome by hybridization with a specific probe, e.g. by Southern hybridization. It will be immediately apparent to the person of skills in the art that, in this particular embodiment, although Southern hybridization is perfectly suitable, it is nevertheless more convenient and sensitive to use microarrays. In yet another embodiment, the presence of the gene of interest may be detected by amplification, in particular by quantitative PCR (qPCR). These technologies (Southern, microarrays, qPCR, etc) are now used routinely by those skilled in the art and thus do not need to be detailed here.

In another preferred embodiment, the inflammatory bowel disease is selected from the group of Crohn's disease and ulcerous colitis. In a further preferred embodiment, the said disease is Crohn's disease; in another further preferred embodiment, the said disease is ulcerous colitis.

In yet another preferred embodiment, the gene which absence or presence from the individual's gut microbiome is determined is selected from the group of genes listed in Tables 1 and 2. In a further preferred embodiment, the gene is selected from the group of genes listed in Table 1; in another further preferred embodiment, the gene is selected from the group of genes listed in Table 2. The skilled person will have no difficulty in realizing that the more genes are tested, the higher the degree of confidence of the result. According to another further preferred embodiment, the method of the invention comprises determining the presence or absence of at least 50% of the genes listed in Table 1, more preferably, at least 75 % of the genes of Table 1, even more preferably, at least 90 % of the genes of Table 1. According to another further preferred embodiment, the method of the invention comprises determining the presence or absence of at least 50% of the genes listed in Table 2, more preferably, at least 75 % of the genes of Table 2, even more preferably, at least 90 % of the genes of Table 2.

Even though a great number of the bacterial species found in the microbial flora have not been identified, it is known that most bacteria belong to the genera *Bacteroides*, *Clostridium*, *Fusobacterium*, *Eubacterium*, *Ruminococcus*, *Peptococcus*, *Peptostreptococcus*, and *Bifidobacterium*. Other genera such as *Escherichia* and *Lactobacillus* are present to a lesser extent. Some individual species belonging to these genera have been identified, and some of the genes of these species are known. The extensive metagenomic study which has led to the identification of 3.3 million non-redundant microbial genes has also permitted the assignment of most new sequences. A gene belonging to a given species is present in an individual at the same frequency as all the other genes of the said species. It is thus possible for each of the genes identified through the method of the invention to determine whether there is a correlation between the presence or absence of the said gene and the presence or absence of a set of genes known to belong to a specific bacterial species in various individuals. Such a correlation indicates that the unknown gene belongs to the said specific bacterial species. The inventors have thus shown that some bacterial species are associated with the inflammatory bowel disease phenotype whereas other bacterial species are associated with the healthy phenotype. The inflammatory bowel disease phenotype can be predicted by a linear combination of the said species, i.e. the more bacterial species associated with

the inflammatory bowel disease phenotype are present in an individual's gut, and the lesser species associated with the healthy phenotype in the said individual's gut, the higher the probability that the said individual suffers from an inflammatory disease. For example, the absence of *Faecalibacterium prausnitzii* and *Roseburia inulinivorans* and the presence of *Clostridium boltae*, *Clostridium ramosum* and *Ruminococcus gnavus* in the gut of a person indicates that this person suffers from Crohn's disease. Likewise, the absence of *Akkermansia muciniphila* and the presence of *Bacteroides capillosus* and *Clostridium leptum* in an individual's gut indicates that this person suffers from ulcerative colitis.

It will be clear for the person skilled in the art that the genes of the invention can be used as biomarkers, for example during the treatment of patients suffering from inflammatory bowel diseases. Therefore, in another embodiment, the invention includes a method for monitoring the efficacy of a treatment for an inflammatory bowel disease. When a treatment is efficacious against an inflammatory bowel disease, the dysbiosis initially observed gradually disappears. Whereas some specific genes are absent from the individual's guts when that said individual is sick (e.g. the genes of Table 1 when the disease is Crohn's disease, or the genes of Table 2, when the individual suffers from ulcerous colitis), these genes reappear during the treatment. In this embodiment, the method of the invention thus comprises the steps of first determining whether at least one gene is absent from the said patient's microbiome, administering the treatment, determining if the said at least one gene is present in the patient's microbiome. In a preferred embodiment, the method of the invention comprises the steps of obtaining microbial DNA from faeces of the said individual, before and after the treatment. In a further preferred embodiment, the faeces from said individual are collected before and after the treatment, DNA is extracted, and the presence or absence from an individual's gut microbiome of at least one gene is determined.

In another preferred embodiment, the inflammatory bowel disease is selected from the group of Crohn's disease and ulcerous colitis. In a further preferred embodiment, the said disease is Crohn's disease; in another further preferred embodiment, the said disease is ulcerous colitis.

In yet another preferred embodiment, the gene which absence or presence from the individual's gut microbiome is determined is selected from the group of genes listed in Tables 1 and 2. In a further preferred embodiment, the gene is selected from the group of genes listed in Table 1; in another further preferred embodiment, the gene is selected from the group of genes listed in Table 2. In a particular embodiment of the method of the invention, at least 50 %, 75 % or 90 % of the genes of Table 1 and/or Table 2 are absent from the said individual's gut microbiome before the treatment. Therefore, according to a preferred embodiment, the method of the invention comprises determining the presence or absence of at least 50% of the genes listed in Table 1, more preferably, at least 75 % of the genes of Table 1, even more preferably, at least 90 % of the genes of Table 1. According to another preferred embodiment, the method of the invention comprises determining the presence or absence of at least 50% of the genes listed in Table 2, more preferably, at least 75 % of the genes of Table 2, even more preferably, at least 90 % of the genes of Table 2.

The present invention also includes a kit dedicated to the implementation of the methods of the invention, comprising all the genes which are absent in a patient suffering from an inflammatory bowel disease and which are present in a healthy person. In particular, the present invention relates to a microarray dedicated to the implementation of the methods according to the invention, comprising probes binding to all the genes absent in a patient suffering from an inflammatory bowel disease and present in a healthy person. In a preferred embodiment, said microarray is a nucleic acid microarray. According to the invention, a "nucleic microarray" consists of different nucleic acid probes that are attached to a substrate, which can be a microchip, a glass slide or a microsphere-sized bead. A microchip may be constituted of polymers, plastics, resins, polysaccharides, silica or silica-based materials, carbon, metals, inorganic glasses, or nitrocellulose. Probes can be nucleic acids such as cDNAs ("cDNA microarray") or oligonucleotides ("oligonucleotide microarray", the oligonucleotides being about 25 to about 60 base pairs or less in length). Alternatively to nucleic acid technology, quantitative PCR may be used and amplification primers specific for the genes to be tested are thus also very useful for performing the methods according to the invention. The present invention thus

further relates to a kit for diagnosing an inflammatory bowel disease in a patient, comprising a dedicated microarray as described above or amplification primers specific for genes absent in a patient suffering from an inflammatory bowel disease and present in a healthy person. Whereas these kits may allow the skilled person to detect 10 %, 25 %, 50 % or 75 % of the said genes, they are most useful when they allow the detection of 90 %, 95 %, 97.5 % or even 99 % of the said genes. Thus a microarray according to the invention will comprise probes binding to at least 10 %, 25 %, 50 % or 75 %, and preferably 90 %, 95 %, 97.5 %, and even more preferably at least 99 % of the said genes. Likewise a kit for quantitative PCR will contain primers allowing the amplification of at least 10 %, 25 %, 50 % or 75 %, and preferably 90 %, 95 %, 97.5 %, and even more preferably at least 99 % of the said genes.

In a preferred embodiment, the inflammatory bowel disease is selected from the group of Crohn's disease and ulcerous colitis. In a further preferred embodiment, the said disease is Crohn's disease; in another further preferred embodiment, the said disease is ulcerous colitis. In another embodiment, the genes which are absent in a patient suffering from Cohn's disease and are present in healthy people are the genes listed in Table 1; in yet another embodiment, they are listed in Table 2.

FIGURE LEGENDS

Fig1: Overall analysis of the CD-related genes and of UC-related genes. **A)** More CD-related genes in healthy individuals. Plot of the number of genes per individual in function the CD-related genes indicates that the genes are more numerous in healthy individuals than the patients. **B)** More UC-related genes in healthy individuals. Plot of the number of genes per individual in function the UC-related genes indicates that the genes are more numerous in healthy individuals than the patients.

Fig. 2: A) A linear combination of the 5 species discriminates well the Crohn's disease phenotype for the part of the cohort that harbors them at the levels

defined (at least 50% of the genes); **B)** 3 species discriminate for ulcerative colitis.

METHODS

Human faecal sample collection. Spanish individuals were either healthy controls or patients with chronic inflammatory bowel diseases (Crohn's disease or ulcerative colitis) in clinical remission. Patients and healthy controls were asked to provide a frozen stool sample. Fresh stool samples were obtained at home, and samples were immediatelyfrozen by storing them in their home freezer. Frozen samples were delivered to the hospital using insulating polystyrene foam containers, and then they were stored at -80° C until analysis.

DNA extraction. A frozen aliquot (200 mg) of each faecal sample was suspended in 250 µl of guanidine thiocyanate, 0.1M Tris (pH 7.5) and 40 µl of 10 % N-lauroyl sarcosine. Then, DNA extraction was conducted as previously described (Manichanh *et al.*,. *Gut*, **55**: 205–211, 2006).. The DNA concentration and its molecular size were estimated by nanodrop (Thermo Scientific) and agarose gel electrophoresis.

DNA library construction and sequencing. DNA library preparation followed the manufacturer's instruction (Illumina). We used the same workflow as described elsewhere to perform cluster generation, template hybridization, isothermal amplification, linearization, blocking and denaturization and hybridization of the sequencing primers. The base-calling pipeline (version IlluminaPipeline-0.3) was used to process the raw fluorescent images and call sequences. We constructed one library (clone insert size 200 bp) for each of the first 15 samples, and two libraries with different clone insert sizes (135 bp and 400 bp) for each of the remaining 109 samples for validation of experimental reproducibility. To estimate the optimal return between the generation of novel sequence and sequencing depth, we aligned the Illumina GA reads from samples MH0006 and MH0012 onto 468,335 Sanger reads totalling to 311.7 Mb generated from the same two samples (156.9 and 154.7 Mb, respectively), using the Short Oligonucleotide Alignment Program (SOAP) (Li et al., *Bioinformatics*, **25:** 1966–1967, 2009). and a match

requirement of 95% sequence identity. With about 4 Gb of Illumina sequence, 94% and 89% of the Sanger reads (for MH0006 and MH0012, respectively) were covered. Further extensive sequencing, to 12.6 and 16.6 Gb for MH0006 and MH0012, respectively, brought only a moderate increase of coverage to about 95 %. More than 90 % of the Sanger reads were covered by the Illumina sequences to a very high and uniform level, indicating that there is little or no bias in the Illumina GA sequence. As expected, a large proportion of Illumina sequences (57% and 74% for M0006 and M0012, respectively) was novel and could not be mapped onto the Sanger reads. This fraction was similar at the 4 and 12–16 Gb sequencing levels, confirming that most of the novelty was captured already at 4 Gb.

We generated 35.4–97.6 million reads for the remaining 122 samples, with an average of 62.5 million reads. Sequencing read length of the first batch of 15 samples was 44 bp and the second batch was 75 bp.

Public data used The sequenced bacteria genomes (totally 806 genomes) deposited inGenBankwere downloaded from the NCBI database (http://www.ncbi.nlm.nih.gov/) on 10 January 2009. The known human gut bacteria genome sequences were downloaded from HMP database (http://www.hmpdacc-resources.org/cgi-bin/hmp_catalog/main.cgi), GenBank (67 genomes), Washington University in St Louis (85 genomes, version April 2009, http://genome.wustl.edu/pub/organism/Microbes/Human_Gut_Microbiome/), and sequenced by the MetaHIT project (17 genomes, version September 2009, http://www.sanger.ac.uk/pathogens/metahit/). The other gut metagenome data used in this project include: (1) human gut metagenomic data sequenced from US individuals (Zhang *et al.*, *Proc. Natl Acad. Sci. USA*, **106**: 2365–2370, 2009), which was downloaded from NCBI with the accession SRA002775; (2) human gut metagenomic data from Japanese individuals (Kurokawa *et al.*, *DNA Res.* **14**: 169–181, 2007), which was downloaded from P. Bork's group at EMBL (http://www.bork.embl.de). The integrated NR database we constructed in this study included NCBI-NR database (version April 2009) and all genes from the known human gut bacteria genomes.

Illumina GA short reads de novo assembly. High-quality short reads of each DNA sample were assembled by the SOAP de novo assembler (Li. & Zhu, *Genome Res.*,

20(2): 265-272, 2010). In brief, we first filtered the low abundant sequences from the assembly according to 17-mer frequencies The 17-mers with depth less than 5 were screened in front of assembly, for these low-frequency sequences were very unlikely to be assembled, whereas removing them would significantly reduce memory requirement and make assembly feasible in an ordinary supercomputer (512 GB memory in our institute). Then the sequences were processed one by one and the de Bruijn graph data format was used to store the overlap information among the sequences. The overlap paths supported by a single read were unreliable and removed. Short low-depth tips and bubbles that were caused by sequencing errors or genetic variations between microbial strains were trimmed and merged, respectively. Read paths were used to solve the tiny repeats. Finally, we broke the connections at repeat boundaries, and outputted the continuous sequences with unambiguous connections as contigs. The metagenomic special model was chosen, and parameters '-K 21' and '-K 23' were used for 44 bp and 75 bp reads, respectively, to indicate the minimal sequence overlap required. After de novo assembly for each sample independently, we merged all the unassembled reads together and performed assembly for them, as to maximize the usage of data and assemble the microbial genomes that have low frequency in each read set, but have sufficient sequence depth for assembly by putting the data of all samples together.

Validating Illumina contigs using Sanger reads. We used BLASTN (WUBLAST 2.0) to map Sanger reads from samples MH0006 and MH0012 (156.9 Mb and 154.7 Mb, respectively) to Illumina contigs (single best hit longer than 75 bp and over 95 % identity) from the same samples. Each alignment was scanned for breakage of collinearity where both sequences have at least 50 bases left unaligned at one end of the alignment. Each such breakage was considered an assembly error in the Illumina contig at the location where collinearity breaks. Errors within 30 bp from each other were merged. An error was discarded if there exists a Sanger read that agrees with the contig structure for 60 bp on both sides of the error. For comparison, we repeated this on a Newbler2 assembly of 454 Titanium reads from MH0006 (550 Mb reads). We estimate 14.12 errors per Mb of contigs for the Illumina assembly, which is comparable to that of the 454 assembly (20.73 per Mb). 98.7 % of Illumina contigs that map at least one Sanger

read were collinear over 99.55 % of the mapped regions, which is comparable to 97.86 % of such 454 contigs being collinear over 99.48 % of the mapped regions.

Evaluation of human gut microbiome coverage. The Illumina GA reads were aligned against the assembled contigs and known bacteria genomes using SOAP by allowing at most two mismatches in the first 35-bp region and 90 % identity over the read sequence. The Roche/454 and Sanger sequencing reads were aligned against the same reference using BLASTN with 1 x 10^{-8}, over 100 bp alignment length and minimal 90 % identity cutoff. Two mismatches were allowed and identity was set 95 % over the read sequence when aligned to the GA reads of MH0006 and MH0012 to Sanger reads from the same samples by SOAP.

Gene prediction and construction of the non-redundant gene set. We use MetaGene (Noguchi *et al.*, *Nucleic Acids Res*,. **34**, 5623–5630, 2006)—which uses di-codon frequencies estimated by the GC content of a given sequence, and predicts a whole range of ORFs based on the anonymous genomic sequences—to find ORFs from the contigs of each of the 124 samples as well as the contigs from the merged assembly. The predicted ORFs were then aligned to each other using BLAT (Kent *et al.*, *Genome Res.*, **12**: 656–664, 2002). A pair of genes with greater than 95 % identity and aligned length covered over 90 % of the shorter gene was grouped together. The groups sharing genes were then merged, and the longest ORF in each merged group was used to represent the group, and the other members of the group were taken as redundancy. Therefore, we organized the non-redundant gene set from all the predicted genes by excluding the redundancy. Finally, the ORFs with length less than 100 bp were filtered. We translated theORFs into protein sequences using the NCBI Genetic Codes (Ley et al., *Nature Rev. Microbiol*,. **6**: 776–788, 2008).

Identification of genes. To make a balance between identifying low-abundance genes and reducing the error-rate of identification, we explored the impact of the threshold set for read coverage required to identify a gene in individual microbiomes. The number of genes decreased about twice when the number of reads required for identification was

increased from 2 to 6, and changed slowly thereafter. Nevertheless, to include the rare genes into the analysis, we selected the threshold of 2 reads.

Gene taxonomic assignment. Taxonomic assignment of predicted genes was carried out using BLASTP alignment against the integrated NR database. BLASTP alignment hits with *e*-values larger than 1 x 10^{-5} were filtered, and for each gene the significant matcheswhich were defined by e-values $\leq$ 10 x *e*-value of the top hit were retained to distinguish taxonomic groups. Then we determined the taxonomical level of each gene by the lowest common ancestor (LCA)-based algorithm that was implemented in MEGAN (Huson *et al.*, *Genome Res.*, **17**: 377–386, 2007). The LCA-based algorithm assigns genes to taxa in the way that the taxonomical level of the assigned taxon reflects the level of conservation of the gene. For example, if a gene was conserved in many species, it was assigned to the LCA rather than to a species.

Gene functional classification. We used BLASTP to search the protein sequences of the predicted genes in the eggNOG database (Jensen *et al.*, *Nucleic Acids Res.*, **36**: D250–D254, 2008) and KEGG database (Kanehisa *et al.*, *Nucleic Acids Res.*, **32**: D277–D280, 2004) with *e*-value $\leq$ 1 x 10^{-5}. The genes were annotated as the function of the NOGs or KEGG homologues with lowest e-value. The eggNOG database is an integration of the COG and KOG databases. The genes annotated by COG were classified into the 25 COG categories, and genes that were annotated by KEGG were assigned into KEGG pathways.

Determination of minimal gut bacterial genome. The number of non-redundant genes assigned to the eggNOG clusters was normalized by gene length and cluster copy number.The clusters were ranked by normalized gene number and the range that included the clusters encoding essential *Bacillus subtilis* genes was determined, computing the proportion of these clusters among the successive groups of 100 clusters. Analysis of the range gene clusters involved, besides iPath projections, use of KEGG and manual verification of the completeness of the pathways and protein machineries they encode.

Determination of total functional complement and minimal metagenome. We computed the total and shared number of orthologous groups and/or gene families present in random combinations of *n* individuals (with *n* = 52 to 124, 100 replicates per bin). This analysis was performed on three groups of gene clusters: (1) known eggNOG orthologous groups (that is, those with functional annotation, excluding those in which the terms [Uu]ncharacteri[sz]ed, [Uu]nknown, [Pp]redicted or[Pp]utative occurred); (2) all eggNOG orthologous groups; (3) all orthologous groups plus gene families constructed from remaining genes not assigned to the two above categories. Families were clustered from all-against-all BLASTP results using MCL (van Dongen, Ph. D. Thesis, Univ.Utrecht, 2000) with an inflation factor of 1.1 and a bit-score cutoff of 60.

Rarefaction analysis. Estimation of total gene richness was done using EstimateS on 100 randomly picked samples due to memory limitations. Because the CV value was > 0.5, both chao2 (classic) and ICE richness estimators were calculated and the larger estimate of the two (ICE) was used. The estimate for this sample size was 3,621,646 genes (ICE) whereas S_{obs} (Mao Tau) was 3,090,575 genes, or 85.3 %. The ICE estimator curve did not completely saturate, indicating that additional samples will need to be added to achieve a final, conclusive estimate.

Common bacterial core. To eliminate the influence of very similar strains and assess the presence of known microbial species among the individuals of the cohort, we used 650 sequenced bacterial and archaeal genomes as a reference set. The set was composed from 932 publicly available genomes, which were grouped by similarity, using a 90 % identity cutoff and the similarity over at least 80 % of the length. From each group only the largest genome was used. Illumina reads from 124 individuals were mapped to the set, for species profiling analysis and the genomes originating from the same species (by differing in size > 20 %) curated by manual inspection and by using the 16S-based clustering when the sequences were available.

Relative abundance of microbial genomes among individuals. We computed the genome coverage by uniquely mapping Illumina reads and normalized it to 1 Gb of sequence, to correct for different sequencing levels in different individuals. The coverage

was summed over all species of the non-redundant bacterial genome set for each individual and the proportion of each species relative to the sum calculated.

Species co-existence network. For the 155 species that had genome coverage by the Illumina reads ≥ 1% in at least one individual we calculated the pair-wise inter-species Pearson correlations between sequencing depths (abundance) throughout the entire cohort of 124 individuals. From the resulting 11,175 inter-species correlations, correlations less than -0.4 or above 0.4 (n = 342) were visualized in a graph using Cytoscape (Shannon *et al.*,. *Genome Res.* **13**: 2498–2504, 2003). displaying the average genome coverage of each species as node size in the graph.

RESULTS

A summary description of the cohort & the method used. For Crohn's disease, the size of the cohorts was 8 patients and 13 healthy controls; for ulcerative colitis, it was 12 patients and 12 healthy controls. For each disease, the entire gene catalog of 3.3 million genes was searched by ranksum search for those that are significantly different between the two groups. Gene frequency was normalized by the gene size (larger genes are bigger targets and are seen more often) and the difference in the sequencing extent for different individuals. The number of significantly different genes is affected by the thresholds and the splits into groups. In brief, 3802 "CD (Crohn disease)-related genes" were found at $p < 3 \times 10^{-4}$ and 4841 "UC (ulcerative colitis)-related genes" were found at $p < 10^{-3}$.

Overall analysis of the BMI genes. The significantly different genes, i.e. either CD-related genes (Fig. 1A) or UC-related genes (Fig. 1B), were plotted by individual. The median number of CD-related genes in a healthy individual was 3038, and only 643 in a Crohn's disease patient. The median gene number is very significantly different among the 2 groups ($p < 2 \times 10^{-13}$, one-tailed t test). Likewise, the median number of UC-related genes was 3402 in a healthy individual and 1212 in a patient suffering from ulcerative colitis. The difference is statistically different ($p < 6.7 \times 10^{-5}$, one-tailed t test).

Comparison of the distribution of all genes and CD-related genes or UC-related genes. The distribution of all genes of the microbiome and of the CD-related genes or UC-related genes was compared. There is much less difference in all gene numbers and frequency between the two groups than the CD-related genes or UC-related genes. The CD-related gene distribution does not reflect simply the all gene distribution; similarly, the UC-related gene ditribution does not simply reflect a general trend in gene distribution. The loss of genes in the Crohn's disease patients and in the ulcerative disease patients is thus significant.

CD-related and UC-related species. The CD-related genes and the UC-related genes were allocated to species, using the taxonomic assignments attributed to the genes in the 3.3 million catalog (Qin *et al.* , *Nature*, 2010, *in press*, doi:10.1038/nature08821). It was found that 68 % of the CD-related genes, but only 32.8 % of all genes, were from firmicutes. On the other hand, the frequency of bacteroidetes was 22 % for CD-related genes and 18.4 % for all the genes of the microbiome. Likewise, 70 % of the UC-related genes were from firmicutes, and only 15 % were from bacteroidetes. Therefore, inflammatory-bowel diseases, such as Crohn's disease and ulcerative disease, are associated to changes in firmicutes. The species were first identified by the number of genes assigned to them amongst the CD-related genes and UC-related genes. Then other genes from the same species were pulled out of the catalog and the presence of 50 representative genes for each species assessed in different individuals (this compared very favorably with the use of a single 16S gene, which is currently done to identify a species). The species was considered present if at least half of the marker genes were found in an individual. The significance of the distribution between the healthy and the patients was estimated by the comparison with the all cohort distribution (13 to 8 for Crohn's disease; 12 to 12 for ulcerative colitis) using the Chi2 test. For Crohn disease, *Faecalibacterium prausnitzii* and *Roseburia inulinivorans* were associated with the healthy population ($p = 2.4 \times 10^{-2}$ and $p = 9.3 \times 10^{-3}$, respectively), i.e. they tended to be absent from the patients. On the other hand, *Clostridium boltae*, *Clostridium ramosum* and *Ruminococcus gnavus* were associated with the patient cohort ($p = 4 \times 10^{-3}$, $p = 1.8 \times 10^{-3}$ and $p = 6.4 \times 10^{-3}$). On the basis of the identification of species, it was demonstrated that the linear combination of these 5 species fully predicts the Crohn

disease phenotype (Fig. 2A). Healthy individuals and patients are shown as blue and red dots, respectively. The species presence (the ordinate) corresponds to the sum of the genes the of "good species" (anti-associated with Crohn's disease) minus the genes of the "bad species" (associated with Crohn's disease). The individuals are ranked by the species presence (the abscissa). If an individual has excess of the "good species" genes, he or she will be on the top of the rank and tend to be healthy, while if there is an excess of "bad species" genes, he or she will be at the right and tend to be sick. For ulcerative colitis, *Akkermansia muciniphila* was associated with a healthy phenotype, whereas *Bacteroides capillosus* and *Clostridium leptum* were associated with the patient population. As shown in Fig. 2B, a linear combination of the 3 species predicts the ulcerative colitis phenotype.

ID	GeneName	Name(NR)
3143	GL0008535_MH0001_[Lack_3'-end]_[mRNA]_locus=scaffold19876_1:2:421:-	Bacteroides pectinophilus
4616	GL0010202_MH0002_[Lack_5'-end]_[mRNA]_locus=scaffold1732_7:455:1216:-	Clostridium nexile
4618	GL0011110_MH0002_[Lack_5'-end]_[mRNA]_locus=scaffold1736_1:1:900:+	Faecalibacterium prausnitzii
6544	GL0102536_MH0002_[Lack_5'-end]_[mRNA]_locus=scaffold10330_1:1561:2916:-	Bacteroidales
8616	GL0009143_MH0002_[Complete]_[mRNA]_locus=scaffold21205_4:225:1004:-	Parabacteroides distasonis
8699	GL0129833_MH0002_[Complete]_[mRNA]_locus=scaffold21642_3:613:1413:-	Bacteroides
8953	GL0048861_MH0002_[Complete]_[mRNA]_locus=scaffold23139_1:379:939:+	-
8956	GL0112139_MH0002_[Lack_5'-end]_[mRNA]_locus=scaffold23153_3:405:2000:-	Bacteroides

10222	GL0040189_MH0002_[Lack_both_end]_[mRNA]_locus=scaffold31690_3:3:1676:-	Faecalibacterium prausnitzii
10816	GL0042567_MH0002_[Complete]_[mRNA]_locus=scaffold35656_2:1469:2728:-	Bacteroides
11510	GL0030242_MH0002_[Complete]_[mRNA]_locus=scaffold40203_1:29:505:+	Bacteroides vulgatus
12323	GL0113336_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold45493_1:652:1641:+	Parabacteroides merdae
14570	GL0069232_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold62021_3:820:2040:+	-
14573	GL0047082_MH0002_[Complete]_[mRNA]_locus=scaffold62057_4:99:1934:+	Streptococcus sanguinis
19042	GL0027549_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold88818_2:3:584:+	Bacteroides capillosus
20446	GL0010312_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold93833_1:175:3204:+	Bacteroides intestinalis
22045	GL0110975_MH0002_[Lack_both_end]_[mRNA]_locus=C3650934_1:2:535:+	Eubacterium hallii
26653	GL0004637_MH0003_[Complete]_[mRNA]_locus=scaffold2222_1:5671:7245:+	Firmicutes
26665	GL0137925_MH0003_[Complete]_[mRNA]_locus=scaffold2249_1:2258:3937:+	Firmicutes
27371	GL0111838_MH0003_[Complete]_[mRNA]_locus=scaffold3517_5:19:1371:+	Clostridium phytofermentans
28254	GL0028270_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold5485_1:3:680:-	Clostridium methylpentosum
29392	GL0001244_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold8040_1:1:426:+	Faecalibacterium prausnitzii

30779	GL0095400_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold12305_1:1:540:+	Clostridiales
32209	GL0093969_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold16247_1:1001:1810:-	Roseburia inulinivorans
34469	GL0081723_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold23367_1:2111:4600:+	Clostridium cellulolyticum
35828	GL0007094_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold28590_1:2192:2965:+	Eubacterium siraeum
36868	GL0135647_MH0003_[Complete]_[mRNA]_locus=scaffold32243_2:147:761:-	Faecalibacterium prausnitzii
37113	GL0003601_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold33263_1:1:642:+	Faecalibacterium prausnitzii
38433	GL0106465_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold39240_1:657:1406:-	Bacteria
39053	GL0022039_MH0003_[Complete]_[mRNA]_locus=scaffold42238_1:1645:2847:+	Desulfitobacterium hafniense
43261	GL0139780_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold64463_1:3:524:+	Clostridium methylpentosum
43439	GL0040705_MH0003_[Complete]_[mRNA]_locus=scaffold65445_1:774:2939:+	Bacteria
44721	GL0111948_MH0003_[Complete]_[mRNA]_locus=scaffold70726_1:149:670:+	Ruminococcus obeum
46561	GL0077007_MH0003_[Complete]_[mRNA]_locus=scaffold77216_4:2540:9154:+	Clostridium
50320	GL0053141_MH0003_[Complete]_[mRNA]_locus=C3904840_1:7:1404:+	Clostridiales
53699	GL0038264_MH0004_[Lack_5'-end]_[mRNA]_locus=C1489742_1:2:106:+	-

58703	GL0018039_MH0005_[Lack_5'-end]_[mRNA]_locus=scaffold3533_1:206:601:-	-
58873	GL0012779_MH0005_[Lack_5'-end]_[mRNA]_locus=scaffold5157_4:683:1303:-	Clostridium asparagiforme
60544	GL0020572_MH0005_[Lack_3'-end]_[mRNA]_locus=scaffold37821_1:1:528:-	-
63192	GL0170836_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold1994_3:348:920:-	Ruminococcus lactaris
63953	GL0034220_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold3625_2:1:720:+	Coprococcus comes
65345	GL0108117_MH0006_[Complete]_[mRNA]_locus=scaffold6995_1:126:1517:+	Clostridiales
69885	GL0014045_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold16159_4:3:1280:+	-
70887	GL0024686_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold18618_1:10196:10663:-	Roseburia inulinivorans
71389	GL0121312_MH0006_[Complete]_[mRNA]_locus=scaffold19961_1:273:1619:-	Clostridiales
72282	GL0048112_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold22187_1:291:992:-	Anaerotruncus colihominis
73201	GL0059178_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold25261_4:1:1467:-	Clostridiales
73374	GL0022415_MH0006_[Complete]_[mRNA]_locus=scaffold26025_2:254:1486:+	Bacteroides capillosus
75608	GL0245427_MH0006_[Complete]_[mRNA]_locus=scaffold31628_1:2647:3738:+	Ruminococcus gnavus

76991	GL0111542_MH0006_[Complete]_[mRNA]_locus=scaffold35614_1:1432:2934:-	Roseburia inulinivorans
76994	GL0241159_MH0006_[Complete]_[mRNA]_locus=scaffold35633_7:4457:5338:+	Roseburia inulinivorans
77183	GL0116585_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold36205_1:1:714:+	Ruminococcus obeum
77272	GL0109979_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold36416_3:2:4372:-	-
80341	GL0298792_MH0006_[Complete]_[mRNA]_locus=scaffold45426_1:634:1890:-	Roseburia inulinivorans
81446	GL0089446_MH0006_[Complete]_[mRNA]_locus=scaffold49881_1:114:950:-	Clostridium
89980	GL0195643_MH0006_[Complete]_[mRNA]_locus=scaffold80303_1:1068:2900:+	Roseburia inulinivorans
90761	GL0161233_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold82607_4:2:1024:-	-
93027	GL0184416_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold91842_2:2:718:+	Roseburia inulinivorans
94692	GL0270521_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold97853_1:1:648:+	Roseburia inulinivorans
95630	GL0018315_MH0006_[Complete]_[mRNA]_locus=scaffold101484_1:831:2285:+	Roseburia inulinivorans
95706	GL0092444_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold101851_3:3:515:-	-
98181	GL0181825_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold113896_1:1:1038:+	Clostridiales
98544	GL0200828_MH0006_[Complete]_[mRNA]_locus=scaffold116027_2:2897:4300:+	Ruminococcus torques

98684	GL0107159_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold116662_1:95:1108:+	Roseburia inulinivorans
98701	GL0211279_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold116739_1:2:760:-	Coprococcus comes
98871	GL0020959_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold117487_1:1103:1651:+	Clostridiales
100465	GL0125020_MH0006_[Complete]_[mRNA]_locus=scaffold124102_4:2:1015:+	Clostridiales
102150	GL0081464_MH0006_[Complete]_[mRNA]_locus=scaffold132504_1:824:1759:+	Clostridium thermocellum
103933	GL0259543_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold141019_1:3:1409:-	Anaerostipes caccae
104527	GL0252466_MH0006_[Complete]_[mRNA]_locus=scaffold144362_1:171:881:+	Clostridium butyricum
104759	GL0034617_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold146060_2:1:1119:+	-
104838	GL0162187_MH0006_[Complete]_[mRNA]_locus=scaffold146590_1:196:1404:-	Bacillus cereus
105824	GL0155537_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold151078_1:3:1484:-	Clostridiales
107213	GL0283965_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold158671_3:2:1252:-	Clostridium bartlettii
107439	GL0173315_MH0006_[Complete]_[mRNA]_locus=scaffold159924_3:78:1406:-	Clostridium nexile
107567	GL0234949_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold160621_2:1:783:+	Clostridium

108138	GL0128974_MH0006_[Complete]_[mRNA]_locus=scaffold163390_5:11:991:+	-
108570	GL0102243_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold165620_6:147:1394:+	Eubacterium hallii
112013	GL0064943_MH0006_[Complete]_[mRNA]_locus=scaffold182013_3:72:1247:+	Roseburia inulinivorans
112058	GL0273487_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold182338_1:1:1371:-	Dorea formicigenerans
113492	GL0283878_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold189690_2:1:990:-	Eubacterium ventriosum
116600	GL0238302_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold205449_2:2:1135:+	Eubacterium hallii
117635	GL0084418_MH0006_[Complete]_[mRNA]_locus=scaffold210785_1:193:672:-	Roseburia inulinivorans
119028	GL0035667_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold218366_1:139:519:+	Dorea formicigenerans
119567	GL0099412_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold220884_2:1:711:-	Clostridium hylemonae
120560	GL0204478_MH0006_[Complete]_[mRNA]_locus=scaffold226067_2:229:1497:+	Dorea formicigenerans
120668	GL0225432_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold226708_1:195:1133:-	-
121416	GL0048866_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold230118_3:2:724:+	Dorea formicigenerans
122087	GL0286042_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold233591_1:2:1705:+	Clostridiales
122419	GL0036540_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold235232_1:1:1080:+	-

123474	GL0230787_MH0006_[Complete]_[mRNA]_locus=scaffold240819_1:165:758:-	Bacteroides capillosus
124550	GL0112593_MH0006_[Complete]_[mRNA]_locus=scaffold245434_1:319:1839:-	Clostridiales
125013	GL0069094_MH0006_[Complete]_[mRNA]_locus=scaffold247418_2:118:1215:-	-
125126	GL0021817_MH0006_[Complete]_[mRNA]_locus=scaffold247995_1:158:1492:+	Ruminococcus obeum
129996	GL0170920_MH0006_[Complete]_[mRNA]_locus=scaffold268935_2:343:993:+	-
130932	GL0151955_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold272875_1:1:1149:+	Eubacterium hallii
131244	GL0066269_MH0006_[Complete]_[mRNA]_locus=scaffold274363_1:94:1290:+	Roseburia inulinivorans
131308	GL0273883_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold274605_2:2:1201:-	-
131309	GL0273884_MH0006_[Complete]_[mRNA]_locus=scaffold274605_2:1205:1681:-	Ruminococcus obeum
131549	GL0220544_MH0006_[Complete]_[mRNA]_locus=scaffold275771_2:120:1397:-	Clostridium hylemonae
132379	GL0064862_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold279240_1:3:746:+	-
133507	GL0270744_MH0006_[Complete]_[mRNA]_locus=scaffold283648_1:2465:3529:-	Roseburia inulinivorans
137126	GL0055584_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold298006_1:3:287:+	Clostridiales
138149	GL0085767_MH0006_[Complete]_[mRNA]_locus=scaffold301796_1:713:1210:+	Clostridium

139329	GL0024809_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold305583_1:286:1215:-	Clostridium hylemonae
139361	GL0247809_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold305682_1:2:652:-	Ruminococcus
140138	GL0150852_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold308477_2:1:1347:-	Clostridium
143170	GL0261750_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold316577_1:160:606:+	Clostridiales
143633	GL0127372_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold317229_1:3:707:+	-
145155	GL0003660_MH0006_[Complete]_[mRNA]_locus=scaffold318985_2:222:1625:+	-
149443	GL0070437_MH0006_[Lack_3'-end]_[mRNA]_locus=C14523153_1:29:796:+	Roseburia inulinivorans
149617	GL0247495_MH0006_[Lack_5'-end]_[mRNA]_locus=C14533697_1:564:833:-	Roseburia inulinivorans
150212	GL0280479_MH0006_[Lack_5'-end]_[mRNA]_locus=C14568264_1:103:1005:-	Roseburia inulinivorans
152637	GL0087233_MH0006_[Complete]_[mRNA]_locus=C14661642_1:5006:5737:+	Roseburia inulinivorans
152956	GL0015727_MH0007_[Complete]_[mRNA]_locus=scaffold8448_1:285:845:+	Roseburia inulinivorans
153403	GL0036324_MH0007_[Lack_5'-end]_[mRNA]_locus=scaffold25219_2:236:856:-	Roseburia inulinivorans
153657	GL0008742_MH0007_[Lack_5'-end]_[mRNA]_locus=scaffold36493_2:195:515:-	Roseburia inulinivorans
154150	GL0037723_MH0007_[Lack_3'-end]_[mRNA]_locus=scaffold56962_2:197:640:+	Clostridiales

154735	GL0018385_MH0007_[Lack_5'-end]_[mRNA]_locus=scaffold70496_1:2:718:+	Roseburia inulinivorans
156371	GL0050838_MH0008_[Complete]_[mRNA]_locus=scaffold61_4:1841:3103:-	Roseburia inulinivorans
156437	GL0048411_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold198_2:3126:4244:-	Roseburia inulinivorans
156767	GL0011045_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold2405_6:286:795:-	Roseburia inulinivorans
157133	GL0024584_MH0008_[Complete]_[mRNA]_locus=scaffold4520_6:281:1030:-	Roseburia inulinivorans
157551	GL0028833_MH0008_[Complete]_[mRNA]_locus=scaffold6565_7:1759:2844:-	Roseburia inulinivorans
158863	GL0042285_MH0008_[Complete]_[mRNA]_locus=scaffold12329_7:2664:3761:+	Roseburia inulinivorans
159728	GL0030127_MH0008_[Lack_both_end]_[mRNA]_locus=scaffold17757_1:2:721:+	Roseburia inulinivorans
160352	GL0048535_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold22732_5:3:866:+	Roseburia inulinivorans
160451	GL0034400_MH0008_[Complete]_[mRNA]_locus=scaffold23761_1:401:1261:+	Roseburia inulinivorans
160961	GL0044964_MH0008_[Complete]_[mRNA]_locus=scaffold28781_1:372:944:-	Roseburia inulinivorans
161335	GL0040040_MH0008_[Complete]_[mRNA]_locus=scaffold33064_3:482:1567:-	Roseburia inulinivorans
161511	GL0024960_MH0008_[Complete]_[mRNA]_locus=scaffold34303_5:3213:4478:+	Roseburia inulinivorans
161516	GL0033415_MH0008_[Complete]_[mRNA]_locus=scaffold34577_3:1852:3360:-	Roseburia inulinivorans

162160	GL0005286_MH0008_[Complete]_[mRNA]_locus=scaffold40850_2:4:417:-	Faecalibacterium prausnitzii
167766	GL0051111_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold2079_1:431:691:-	Faecalibacterium prausnitzii
169589	GL0062825_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold3784_1:1:318:+	Clostridiales
169606	GL0126427_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold3818_1:558:926:-	Faecalibacterium prausnitzii
170683	GL0119097_MH0009_[Complete]_[mRNA]_locus=scaffold5514_2:1893:2627:+	Faecalibacterium prausnitzii
170884	GL0083672_MH0009_[Complete]_[mRNA]_locus=scaffold5912_3:293:715:+	Faecalibacterium prausnitzii
172427	GL0071062_MH0009_[Lack_both_end]_[mRNA]_locus=scaffold7982_1:2:586:+	Faecalibacterium prausnitzii
174196	GL0057000_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold11242_2:861:1124:+	Faecalibacterium prausnitzii
176963	GL0032814_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold15584_3:605:937:+	Faecalibacterium prausnitzii
177765	GL0151999_MH0009_[Lack_both_end]_[mRNA]_locus=scaffold16879_1:2:841:-	Faecalibacterium prausnitzii
178307	GL0013803_MH0009_[Lack_both_end]_[mRNA]_locus=scaffold17951_4:2:1333:+	Faecalibacterium prausnitzii
179473	GL0057657_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold20635_1:1:285:+	Faecalibacterium prausnitzii
181590	GL0094581_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold25124_1:3:920:-	Faecalibacterium prausnitzii
183421	GL0145241_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold28930_1:1:441:+	Faecalibacterium prausnitzii

187236	GL0017293_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold40209_1:812:1078:-	Faecalibacterium prausnitzii
188040	GL0034759_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold43057_1:104:820:-	Faecalibacterium prausnitzii
191645	GL0001750_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold57295_1:1:381:+	Faecalibacterium prausnitzii
194698	GL0088712_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold69391_1:1:363:+	Faecalibacterium prausnitzii
194975	GL0133341_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold70750_1:3:215:-	Faecalibacterium prausnitzii
196344	GL0023443_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold76643_1:538:1320:+	Faecalibacterium prausnitzii
201001	GL0042351_MH0009_[Lack_both_end]_[mRNA]_locus=scaffold93476_1:1:708:-	Faecalibacterium prausnitzii
201628	GL0088977_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold95293_1:1:141:-	-
202031	GL0022667_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold96268_1:3:425:-	Faecalibacterium prausnitzii
211626	GL0042994_MH0010_[Lack_5'-end]_[mRNA]_locus=scaffold7855_1:2:598:+	Bacteroides pectinophilus
215502	GL0000554_MH0010_[Lack_5'-end]_[mRNA]_locus=scaffold27915_1:3:311:+	Faecalibacterium prausnitzii
215617	GL0011691_MH0010_[Complete]_[mRNA]_locus=scaffold28682_1:4563:5561:-	Faecalibacterium prausnitzii
216691	GL0043228_MH0010_[Complete]_[mRNA]_locus=scaffold36156_1:5099:6139:+	Blautia hydrogenotrophica
219373	GL0140051_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold833_1:2:148:+	Clostridiales

219979	GL0128305_MH0011_[Complete]_[mRNA]_locus=scaffold1423_3:1353:3341:+	Bacteria
220835	GL0101700_MH0011_[Complete]_[mRNA]_locus=scaffold2458_3:15053:16438:+	Bacteria
221459	GL0050617_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold3601_2:2:634:+	Clostridium asparagiforme
221600	GL0173957_MH0011_[Complete]_[mRNA]_locus=scaffold3932_4:597:1499:-	-
221631	GL0051315_MH0011_[Complete]_[mRNA]_locus=scaffold3968_4:2983:4371:+	Ruminococcus obeum
223337	GL0074417_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold6917_7:367:654:-	-
223471	GL0173713_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold7085_2:2:649:+	Roseburia inulinivorans
223552	GL0074036_MH0011_[Complete]_[mRNA]_locus=scaffold7275_1:52:2325:-	-
223754	GL0017696_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold7700_7:351:1295:-	Roseburia inulinivorans
225379	GL0109787_MH0011_[Complete]_[mRNA]_locus=scaffold10671_1:174:605:-	Faecalibacterium prausnitzii
227496	GL0066431_MH0011_[Complete]_[mRNA]_locus=scaffold14902_2:393:1082:-	Victivallis vadensis
228592	GL0121419_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold17222_1:2:505:-	Bacteria
229690	GL0088672_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold20227_1:3:1043:-	Clostridium
229925	GL0021403_MH0011_[Complete]_[mRNA]_locus=scaffold20922_3:2505:4184:-	Clostridiales

232533	GL0035598_MH0011_[Complete]_[mRNA]_locus=scaffold28305_2:681:1811:+	-
232584	GL0085534_MH0011_[Complete]_[mRNA]_locus=scaffold28473_12:417:1784:-	Holdemania filiformis
233264	GL0004112_MH0011_[Complete]_[mRNA]_locus=scaffold30754_1:1079:1828:-	-
234300	GL0080605_MH0011_[Complete]_[mRNA]_locus=scaffold34190_2:154:864:+	Eubacterium ventriosum
236319	GL0093985_MH0011_[Complete]_[mRNA]_locus=scaffold41732_3:575:3067:-	Serratia
237310	GL0124862_MH0011_[Complete]_[mRNA]_locus=scaffold45459_7:2016:3194:+	Clostridium
237577	GL0024202_MH0011_[Complete]_[mRNA]_locus=scaffold46656_3:217:957:-	Faecalibacterium prausnitzii
244157	GL0156202_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold75892_1:584:775:+	-
245517	GL0119062_MH0011_[Complete]_[mRNA]_locus=scaffold82648_3:141:554:-	Roseburia inulinivorans
245767	GL0082881_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold83753_4:482:3367:+	cellular organisms
250904	GL0063049_MH0011_[Complete]_[mRNA]_locus=scaffold105323_1:8:550:-	Roseburia inulinivorans
257172	GL0022565_MH0011_[Complete]_[mRNA]_locus=scaffold117049_1:594:1475:-	Firmicutes
260714	GL0036604_MH0011_[Complete]_[mRNA]_locus=C5352126_1:164:685:+	Roseburia inulinivorans
262019	GL0034902_MH0011_[Complete]_[mRNA]_locus=C5404370_1:158:1294:-	Parabacteroides johnsonii

263624	GL0284072_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold200_5:748:1845:+	Faecalibacterium prausnitzii
265464	GL0262883_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold771_1:3:305:-	Faecalibacterium prausnitzii
266331	GL0196210_MH0012_[Complete]_[mRNA]_locus=scaffold1217_1:870:1649:+	Coprococcus eutactus
267806	GL0159662_MH0012_[Complete]_[mRNA]_locus=scaffold1855_6:333:1241:-	Faecalibacterium prausnitzii
268335	GL0066819_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold2104_4:3:794:-	Faecalibacterium prausnitzii
269517	GL0284328_MH0012_[Complete]_[mRNA]_locus=scaffold2554_1:191:520:-	-
269518	GL0182464_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold2554_3:1540:1920:+	Faecalibacterium prausnitzii
270174	GL0094058_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold2788_4:710:2173:+	Bacteria
270820	GL0116861_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold3205_9:1:822:-	Faecalibacterium prausnitzii
271853	GL0219410_MH0012_[Complete]_[mRNA]_locus=scaffold3621_6:2369:4867:-	Bacteria
272237	GL0182607_MH0012_[Complete]_[mRNA]_locus=scaffold3702_1:363:566:+	Faecalibacterium prausnitzii
272240	GL0253689_MH0012_[Complete]_[mRNA]_locus=scaffold3710_3:267:857:-	Faecalibacterium prausnitzii
273377	GL0036640_MH0012_[Complete]_[mRNA]_locus=scaffold4221_2:411:1709:+	Faecalibacterium prausnitzii
275519	GL0161787_MH0012_[Complete]_[mRNA]_locus=scaffold5263_5:111:506:-	Faecalibacterium prausnitzii

275529	GL0033725_MH0012_[Complete]_[mRNA]_locus=scaffold5280_1:416:2803:-	-
276240	GL0066218_MH0012_[Complete]_[mRNA]_locus=scaffold5690_3:4395:4616:+	-
276286	GL0315354_MH0012_[Complete]_[mRNA]_locus=scaffold5712_1:1072:2109:+	Faecalibacterium prausnitzii
280427	GL0068599_MH0012_[Complete]_[mRNA]_locus=scaffold7852_3:394:750:+	Faecalibacterium prausnitzii
284262	GL0120527_MH0012_[Complete]_[mRNA]_locus=scaffold10095_5:94:447:-	Faecalibacterium prausnitzii
284344	GL0021691_MH0012_[Complete]_[mRNA]_locus=scaffold10197_7:544:1818:+	Faecalibacterium prausnitzii
284362	GL0011507_MH0012_[Complete]_[mRNA]_locus=scaffold10215_4:1692:2546:+	Faecalibacterium prausnitzii
284495	GL0261899_MH0012_[Complete]_[mRNA]_locus=scaffold10388_3:2147:2326:-	Faecalibacterium prausnitzii
287465	GL0088212_MH0012_[Complete]_[mRNA]_locus=scaffold12169_1:1062:1250:-	Clostridium bolteae
287916	GL0261317_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold12489_3:1:1758:-	Faecalibacterium prausnitzii
288543	GL0208903_MH0012_[Complete]_[mRNA]_locus=scaffold12825_1:1834:2883:-	Faecalibacterium prausnitzii
288544	GL0040333_MH0012_[Complete]_[mRNA]_locus=scaffold12825_2:477:1079:-	Faecalibacterium prausnitzii
293782	GL0261394_MH0012_[Complete]_[mRNA]_locus=scaffold16619_1:447:1160:-	Clostridium scindens
294008	GL0284147_MH0012_[Complete]_[mRNA]_locus=scaffold16743_2:91:1632:-	Faecalibacterium prausnitzii

294260	GL0146061_MH0012_[Complete]_[mRNA]_locus=scaffold16975_1:2900:3961:+	Clostridium bolteae
295204	GL0121206_MH0012_[Complete]_[mRNA]_locus=scaffold17607_3:81:401:-	Faecalibacterium prausnitzii
296454	GL0242635_MH0012_[Complete]_[mRNA]_locus=scaffold18596_2:430:1476:+	Ruminococcus obeum
296482	GL0120514_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold18616_4:697:855:+	Faecalibacterium prausnitzii
297331	GL0198635_MH0012_[Complete]_[mRNA]_locus=scaffold19339_7:2054:2758:+	Clostridium
300902	GL0153018_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold22528_1:1:999:-	Faecalibacterium prausnitzii
301389	GL0217724_MH0012_[Complete]_[mRNA]_locus=scaffold22954_2:115:636:-	Faecalibacterium prausnitzii
301392	GL0163994_MH0012_[Complete]_[mRNA]_locus=scaffold22962_5:3040:4752:+	-
303636	GL0264279_MH0012_[Complete]_[mRNA]_locus=scaffold25231_2:3600:4388:-	Clostridium beijerinckii
307311	GL0086447_MH0012_[Complete]_[mRNA]_locus=scaffold28633_1:1326:1583:+	Erysipelotrichaceae
311972	GL0256175_MH0012_[Complete]_[mRNA]_locus=scaffold33499_1:3653:4111:+	Faecalibacterium prausnitzii
312227	GL0210002_MH0012_[Complete]_[mRNA]_locus=scaffold33804_1:501:1262:-	Dorea longicatena
313580	GL0142448_MH0012_[Complete]_[mRNA]_locus=scaffold35270_1:843:2444:+	Firmicutes
315918	GL0303983_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold37966_4:2:1156:-	Faecalibacterium prausnitzii

319225	GL0247884_MH0012_[Complete]_[mRNA]_locus=scaffold41575_1:508:1212:+	Faecalibacterium prausnitzii
321330	GL0299989_MH0012_[Complete]_[mRNA]_locus=scaffold44191_6:1750:2388:+	Faecalibacterium prausnitzii
321671	GL0152611_MH0012_[Complete]_[mRNA]_locus=scaffold44741_3:1653:2963:+	-
321707	GL0091160_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold44805_5:213:2309:+	Clostridium phytofermentans
325834	GL0250872_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold50399_1:1196:4789:-	Bacteria
326836	GL0037290_MH0012_[Complete]_[mRNA]_locus=scaffold51875_4:948:1829:+	Clostridium hylemonae
327200	GL0085273_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold52287_6:1002:1496:-	Dorea longicatena
327612	GL0059024_MH0012_[Complete]_[mRNA]_locus=scaffold52956_4:581:2302:+	Clostridium asparagiforme
338908	GL0234638_MH0012_[Complete]_[mRNA]_locus=scaffold71822_2:1181:1753:-	Faecalibacterium prausnitzii
340577	GL0052851_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold74995_1:2:529:+	Faecalibacterium prausnitzii
352543	GL0252463_MH0012_[Complete]_[mRNA]_locus=scaffold98630_1:777:1109:+	Roseburia inulinivorans
354056	GL0312570_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold102484_1:3:629:+	Dorea longicatena
356148	GL0293951_MH0012_[Complete]_[mRNA]_locus=scaffold107307_1:342:971:+	Coprococcus eutactus
362137	GL0151845_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold121662_2:1:1335:-	-

370959	GL0152921_MH0012_[Complete]_[mRNA]_locus=scaffold143400_1:1269:1724:+	Roseburia inulinivorans
372737	GL0263029_MH0012_[Complete]_[mRNA]_locus=scaffold147610_5:228:1142:-	Ruminococcus torques
376563	GL0129141_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold155578_2:36:578:+	-
378531	GL0042048_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold159392_2:3:173:+	Clostridiales
387433	GL0010125_MH0012_[Complete]_[mRNA]_locus=scaffold173360_1:317:1228:-	Ruminococcus obeum
390066	GL0127145_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold175704_1:258:668:-	Catenibacterium mitsuokai
400930	GL0220481_MH0012_[Complete]_[mRNA]_locus=C18810086_1:58:492:-	Roseburia inulinivorans
407930	GL0044589_MH0013_[Complete]_[mRNA]_locus=scaffold29699_2:2208:3134:+	Clostridium difficile
408560	GL0027578_MH0013_[Complete]_[mRNA]_locus=scaffold34059_1:1:228:+	Clostridiales
408561	GL0027579_MH0013_[Lack_3'-end]_[mRNA]_locus=scaffold34059_1:161:559:+	Clostridiales
415942	GL0008004_MH0014_[Complete]_[mRNA]_locus=scaffold87_5:5770:6234:-	Ruminococcus gnavus
416200	GL0088532_MH0014_[Complete]_[mRNA]_locus=scaffold286_1:123:743:-	Ruminococcus gnavus
416201	GL0088533_MH0014_[Complete]_[mRNA]_locus=scaffold286_1:906:1673:+	Ruminococcus gnavus
416202	GL0088535_MH0014_[Complete]_[mRNA]_locus=scaffold286_1:2562:3935:-	Clostridiales

416208	GL0088541_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold286_1:10200:11315:-	Ruminococcus gnavus
416364	GL0129499_MH0014_[Complete]_[mRNA]_locus=scaffold440_3:290:1270:+	Ruminococcus gnavus
416613	GL0051658_MH0014_[Complete]_[mRNA]_locus=scaffold680_2:225:1166:-	-
416614	GL0051659_MH0014_[Complete]_[mRNA]_locus=scaffold680_2:1188:1679:-	-
417002	GL0038800_MH0014_[Complete]_[mRNA]_locus=scaffold948_2:1987:2178:-	-
417005	GL0038804_MH0014_[Complete]_[mRNA]_locus=scaffold948_2:6622:7896:-	Ruminococcus gnavus
417006	GL0038805_MH0014_[Complete]_[mRNA]_locus=scaffold948_2:7883:9340:-	Clostridiales
417010	GL0066978_MH0014_[Complete]_[mRNA]_locus=scaffold948_3:1637:2341:-	Ruminococcus gnavus
417077	GL0154007_MH0014_[Complete]_[mRNA]_locus=scaffold979_2:2331:2942:-	Ruminococcus gnavus
417561	GL0113960_MH0014_[Complete]_[mRNA]_locus=scaffold1462_3:1834:2454:-	Ruminococcus gnavus
417638	GL0043435_MH0014_[Complete]_[mRNA]_locus=scaffold1546_2:513:1787:+	Eubacterium biforme
417786	GL0105966_MH0014_[Complete]_[mRNA]_locus=scaffold1737_1:474:1709:+	Ruminococcus gnavus
417790	GL0059443_MH0014_[Complete]_[mRNA]_locus=scaffold1737_4:222:707:-	Ruminococcus gnavus
417794	GL0152733_MH0014_[Complete]_[mRNA]_locus=scaffold1737_6:216:1586:+	Ruminococcus gnavus

417798	GL0152737_MH0014_[Complete]_[mRNA]_locus=scaffold1737_6:5483:6796:-	Ruminococcus gnavus
417953	GL0112043_MH0014_[Complete]_[mRNA]_locus=scaffold1841_12:938:1699:-	Ruminococcus gnavus
417975	GL0125071_MH0014_[Complete]_[mRNA]_locus=scaffold1841_15:7194:7784:-	Ruminococcus gnavus
417997	GL0148371_MH0014_[Complete]_[mRNA]_locus=scaffold1841_16:14040:14957:-	Ruminococcus gnavus
418003	GL0097515_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold1841_17:1:354:-	Ruminococcus gnavus
418005	GL0097517_MH0014_[Complete]_[mRNA]_locus=scaffold1841_17:1002:1499:-	Ruminococcus gnavus
418290	GL0091345_MH0014_[Complete]_[mRNA]_locus=scaffold2077_1:4279:4722:+	Ruminococcus gnavus
418303	GL0025774_MH0014_[Complete]_[mRNA]_locus=scaffold2077_5:760:1581:-	Ruminococcus gnavus
418320	GL0046557_MH0014_[Complete]_[mRNA]_locus=scaffold2077_7:214:495:-	Ruminococcus gnavus
418330	GL0059763_MH0014_[Complete]_[mRNA]_locus=scaffold2077_9:2:2692:+	Clostridiales
418332	GL0059765_MH0014_[Complete]_[mRNA]_locus=scaffold2077_9:3678:4532:-	Ruminococcus gnavus
418333	GL0059766_MH0014_[Complete]_[mRNA]_locus=scaffold2077_9:4547:4990:-	Ruminococcus gnavus
418336	GL0059769_MH0014_[Complete]_[mRNA]_locus=scaffold2077_9:7602:8684:-	Clostridium botulinum
418358	GL0118593_MH0014_[Complete]_[mRNA]_locus=scaffold2077_10:10337:10510:-	Ruminococcus gnavus

418363	GL0118598_MH0014_[Complete]_[mRNA]_locus=scaffold2077_10:14584:15108:-	Ruminococcus gnavus
418416	GL0119635_MH0014_[Complete]_[mRNA]_locus=scaffold2112_9:705:1508:+	Roseburia inulinivorans
418487	GL0089670_MH0014_[Complete]_[mRNA]_locus=scaffold2179_1:856:1056:+	Firmicutes
418663	GL0048391_MH0014_[Complete]_[mRNA]_locus=scaffold2328_13:2581:3576:+	Roseburia inulinivorans
418676	GL0133471_MH0014_[Complete]_[mRNA]_locus=scaffold2329_2:607:891:-	Ruminococcus gnavus
418682	GL0133477_MH0014_[Complete]_[mRNA]_locus=scaffold2329_2:7332:7958:+	Ruminococcus gnavus
418859	GL0060269_MH0014_[Complete]_[mRNA]_locus=scaffold2529_1:2264:3979:+	Bacteria
419008	GL0001381_MH0014_[Complete]_[mRNA]_locus=scaffold2650_3:15520:16065:+	Ruminococcus gnavus
419011	GL0001384_MH0014_[Complete]_[mRNA]_locus=scaffold2650_3:19378:19731:-	Ruminococcus gnavus
419030	GL0049699_MH0014_[Complete]_[mRNA]_locus=scaffold2650_6:5998:7590:+	Clostridiales
419033	GL0049702_MH0014_[Complete]_[mRNA]_locus=scaffold2650_6:9503:10297:+	Ruminococcus gnavus
419034	GL0049703_MH0014_[Complete]_[mRNA]_locus=scaffold2650_6:10316:10849:+	Ruminococcus gnavus
419036	GL0154481_MH0014_[Complete]_[mRNA]_locus=scaffold2650_8:86:724:+	Ruminococcus gnavus
419039	GL0148601_MH0014_[Complete]_[mRNA]_locus=scaffold2650_9:1544:2581:+	Ruminococcus gnavus

419042	GL0148605_MH0014_[Complete]_[mRNA]_locus=scaffold2650_9:5156:5695:+	Ruminococcus gnavus
419044	GL0148607_MH0014_[Complete]_[mRNA]_locus=scaffold2650_9:7042:7971:+	Ruminococcus gnavus
419045	GL0148608_MH0014_[Complete]_[mRNA]_locus=scaffold2650_9:8093:8671:+	Ruminococcus gnavus
419062	GL0125414_MH0014_[Complete]_[mRNA]_locus=scaffold2650_11:2271:2750:-	Ruminococcus gnavus
419064	GL0125416_MH0014_[Complete]_[mRNA]_locus=scaffold2650_11:4030:4734:-	Ruminococcus gnavus
420021	GL0099174_MH0014_[Complete]_[mRNA]_locus=scaffold3354_2:1639:2367:+	Ruminococcus gnavus
420023	GL0134383_MH0014_[Complete]_[mRNA]_locus=scaffold3354_5:1371:2858:+	Ruminococcus gnavus
420093	GL0075499_MH0014_[Complete]_[mRNA]_locus=scaffold3405_1:102:971:+	Roseburia inulinivorans
420428	GL0028621_MH0014_[Complete]_[mRNA]_locus=scaffold3787_1:505:1035:+	Ruminococcus gnavus
420431	GL0028625_MH0014_[Complete]_[mRNA]_locus=scaffold3787_1:3047:3946:+	Ruminococcus gnavus
420437	GL0028632_MH0014_[Complete]_[mRNA]_locus=scaffold3787_1:10105:10992:+	Ruminococcus gnavus
420438	GL0028633_MH0014_[Complete]_[mRNA]_locus=scaffold3787_1:11534:11698:+	Ruminococcus gnavus
420625	GL0078327_MH0014_[Complete]_[mRNA]_locus=scaffold3957_3:1069:1608:-	Clostridiales
421128	GL0025929_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold4272_7:210:1238:+	-

421412	GL0091928_MH0014_[Complete]_[mRNA]_locus=scaffold4526_15:161:775:-	Clostridium
421524	GL0149460_MH0014_[Complete]_[mRNA]_locus=scaffold4612_1:1166:1900:-	-
421723	GL0021775_MH0014_[Complete]_[mRNA]_locus=scaffold4786_1:9520:9774:-	Ruminococcus gnavus
421724	GL0021777_MH0014_[Complete]_[mRNA]_locus=scaffold4786_1:10310:10594:-	Ruminococcus gnavus
421725	GL0021778_MH0014_[Complete]_[mRNA]_locus=scaffold4786_1:10675:10914:-	Ruminococcus gnavus
422092	GL0152334_MH0014_[Complete]_[mRNA]_locus=scaffold5234_26:480:1667:+	-
422476	GL0154184_MH0014_[Complete]_[mRNA]_locus=scaffold5627_2:20285:21190:+	Ruminococcus gnavus
422485	GL0154195_MH0014_[Complete]_[mRNA]_locus=scaffold5627_2:35198:35953:+	Ruminococcus gnavus
422989	GL0045473_MH0014_[Complete]_[mRNA]_locus=scaffold6248_12:57:386:-	Roseburia inulinivorans
423273	GL0150791_MH0014_[Complete]_[mRNA]_locus=scaffold6529_1:11945:12751:+	Ruminococcus gnavus
423274	GL0150792_MH0014_[Complete]_[mRNA]_locus=scaffold6529_1:12762:13601:+	Ruminococcus gnavus
423362	GL0080573_MH0014_[Complete]_[mRNA]_locus=scaffold6682_6:1001:2368:+	Bacteria
423884	GL0093147_MH0014_[Complete]_[mRNA]_locus=scaffold7306_10:818:1969:-	Clostridiales
424208	GL0122489_MH0014_[Complete]_[mRNA]_locus=scaffold7626_3:25:948:+	Clostridium bolteae

424462	GL0139292_MH0014_[Complete]_[mRNA]_locus=scaffold7780_3:8343:8798:-	Ruminococcus gnavus
424998	GL0097204_MH0014_[Complete]_[mRNA]_locus=scaffold8462_1:566:1048:-	Ruminococcus gnavus
424999	GL0097205_MH0014_[Complete]_[mRNA]_locus=scaffold8462_1:1084:1344:-	Ruminococcus gnavus
425000	GL0097206_MH0014_[Complete]_[mRNA]_locus=scaffold8462_1:1370:1816:-	Ruminococcus gnavus
425010	GL0097218_MH0014_[Complete]_[mRNA]_locus=scaffold8462_1:10028:10531:-	Ruminococcus gnavus
425013	GL0125263_MH0014_[Complete]_[mRNA]_locus=scaffold8462_2:1121:1609:-	Ruminococcus gnavus
425017	GL0087881_MH0014_[Complete]_[mRNA]_locus=scaffold8467_2:648:2132:+	Ruminococcus obeum
425452	GL0128661_MH0014_[Complete]_[mRNA]_locus=scaffold8957_1:7163:7738:-	Ruminococcus gnavus
425458	GL0078539_MH0014_[Complete]_[mRNA]_locus=scaffold8957_2:740:1396:-	Ruminococcus gnavus
425564	GL0044398_MH0014_[Complete]_[mRNA]_locus=scaffold9113_2:2212:2649:-	Ruminococcus gnavus
425669	GL0111454_MH0014_[Complete]_[mRNA]_locus=scaffold9178_5:11162:11506:+	Ruminococcus gnavus
425827	GL0094725_MH0014_[Complete]_[mRNA]_locus=scaffold9366_2:125:433:-	Roseburia inulinivorans
426111	GL0024773_MH0014_[Complete]_[mRNA]_locus=scaffold9675_10:3547:3993:-	Ruminococcus gnavus
426115	GL0024777_MH0014_[Complete]_[mRNA]_locus=scaffold9675_10:7405:7926:-	Ruminococcus gnavus

426124	GL0074685_MH0014_[Complete]_[mRNA]_locus=scaffold9675_11:12735:13685:-	Ruminococcus gnavus
426252	GL0076877_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold9799_3:3:1199:-	Bacteria
426950	GL0046305_MH0014_[Complete]_[mRNA]_locus=scaffold10778_13:6714:8639:-	Firmicutes
427231	GL0121974_MH0014_[Complete]_[mRNA]_locus=scaffold11239_2:1178:2149:-	Ruminococcus gnavus
427243	GL0010811_MH0014_[Complete]_[mRNA]_locus=scaffold11239_6:782:1375:-	Ruminococcus gnavus
427248	GL0010816_MH0014_[Complete]_[mRNA]_locus=scaffold11239_6:6046:6798:-	Ruminococcus gnavus
427249	GL0010817_MH0014_[Complete]_[mRNA]_locus=scaffold11239_6:6803:7780:-	Ruminococcus gnavus
427308	GL0097855_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold11312_1:2043:2399:+	Ruminococcus gnavus
427453	GL0124010_MH0014_[Complete]_[mRNA]_locus=scaffold11494_5:2205:2903:-	Ruminococcus gnavus
427459	GL0076092_MH0014_[Complete]_[mRNA]_locus=scaffold11494_6:147:1013:-	Ruminococcus gnavus
427468	GL0106691_MH0014_[Complete]_[mRNA]_locus=scaffold11494_9:149:505:-	Ruminococcus gnavus
427470	GL0106693_MH0014_[Complete]_[mRNA]_locus=scaffold11494_9:2559:3083:+	Ruminococcus gnavus
427475	GL0106698_MH0014_[Complete]_[mRNA]_locus=scaffold11494_9:5436:6284:-	Ruminococcus gnavus
427486	GL0014161_MH0014_[Complete]_[mRNA]_locus=scaffold11494_10:3742:4401:-	Ruminococcus gnavus

427603	GL0077774_MH0014_[Complete]_[mRNA]_locus=scaffold11722_1:3575:3931:+	Ruminococcus gnavus
428255	GL0051968_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold12771_1:1:528:+	Faecalibacterium prausnitzii
428351	GL0149888_MH0014_[Complete]_[mRNA]_locus=scaffold12998_1:900:1907:+	Bacteroides pectinophilus
428470	GL0143840_MH0014_[Complete]_[mRNA]_locus=scaffold13193_1:1627:1899:-	Ruminococcus gnavus
429137	GL0109951_MH0014_[Complete]_[mRNA]_locus=scaffold14024_4:169:630:+	Ruminococcus gnavus
429144	GL0001022_MH0014_[Complete]_[mRNA]_locus=scaffold14024_6:3620:4492:+	Ruminococcus gnavus
429237	GL0122428_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold14289_3:3:719:-	-
429406	GL0127468_MH0014_[Complete]_[mRNA]_locus=scaffold14664_3:1630:3438:+	Clostridium bolteae
429614	GL0095908_MH0014_[Complete]_[mRNA]_locus=scaffold15060_2:1193:2353:-	Clostridiales
429794	GL0048711_MH0014_[Complete]_[mRNA]_locus=scaffold15401_1:11829:12089:-	Ruminococcus gnavus
430128	GL0048641_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold15970_1:3:653:-	-
430133	GL0074500_MH0014_[Complete]_[mRNA]_locus=scaffold15973_3:3096:3665:-	Ruminococcus gnavus
430140	GL0102144_MH0014_[Complete]_[mRNA]_locus=scaffold15973_4:6575:7270:+	Ruminococcus gnavus
430152	GL0060714_MH0014_[Complete]_[mRNA]_locus=scaffold16002_1:1370:2206:-	Ruminococcus gnavus

430610	GL0129477_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold16704_4:596:721:+	-
430800	GL0136153_MH0014_[Complete]_[mRNA]_locus=scaffold16947_3:174:1049:+	Heliobacterium modesticaldum
430822	GL0016299_MH0014_[Complete]_[mRNA]_locus=scaffold16999_1:7785:8840:-	Ruminococcus gnavus
430835	GL0010149_MH0014_[Complete]_[mRNA]_locus=scaffold17017_1:4538:5182:-	Ruminococcus gnavus
430836	GL0153699_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold17036_2:2:589:+	Clostridiales
431020	GL0109054_MH0014_[Complete]_[mRNA]_locus=scaffold17180_11:449:1111:+	Ruminococcus gnavus
431038	GL0091931_MH0014_[Complete]_[mRNA]_locus=scaffold17180_13:343:1047:+	Ruminococcus gnavus
431040	GL0091933_MH0014_[Complete]_[mRNA]_locus=scaffold17180_13:2186:2818:+	Bacteroides coprophilus
431041	GL0091934_MH0014_[Complete]_[mRNA]_locus=scaffold17180_13:2916:3569:-	Ruminococcus gnavus
432080	GL0154380_MH0014_[Complete]_[mRNA]_locus=scaffold19253_2:3146:4261:-	Ruminococcus gnavus
432085	GL0154385_MH0014_[Complete]_[mRNA]_locus=scaffold19253_2:8374:9888:-	Bacteria
432121	GL0091275_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold19436_2:3:740:+	Clostridium
432447	GL0103275_MH0014_[Complete]_[mRNA]_locus=scaffold19905_1:2102:2332:-	Ruminococcus gnavus
432449	GL0103277_MH0014_[Complete]_[mRNA]_locus=scaffold19905_1:3968:5494:-	Ruminococcus gnavus

432450	GL0103278_MH0014_[Complete]_[mRNA]_locus=scaffold19905_1:5523:5723:-	-
432453	GL0103281_MH0014_[Complete]_[mRNA]_locus=scaffold19905_1:7935:9674:-	Ruminococcus gnavus
432631	GL0088883_MH0014_[Complete]_[mRNA]_locus=scaffold20153_1:1405:2517:+	Ruminococcus gnavus
432632	GL0088884_MH0014_[Complete]_[mRNA]_locus=scaffold20153_1:2561:2983:-	Ruminococcus gnavus
432634	GL0088886_MH0014_[Complete]_[mRNA]_locus=scaffold20153_1:4487:5569:+	Ruminococcus gnavus
432635	GL0088887_MH0014_[Complete]_[mRNA]_locus=scaffold20153_1:5566:6339:+	Ruminococcus gnavus
432637	GL0088890_MH0014_[Complete]_[mRNA]_locus=scaffold20153_1:8036:8350:+	Ruminococcus gnavus
432641	GL0088894_MH0014_[Complete]_[mRNA]_locus=scaffold20153_1:10737:11906:+	Ruminococcus gnavus
432647	GL0060753_MH0014_[Complete]_[mRNA]_locus=scaffold20153_2:2525:3787:+	Ruminococcus gnavus
432648	GL0060754_MH0014_[Complete]_[mRNA]_locus=scaffold20153_2:3784:4842:+	Ruminococcus gnavus
432649	GL0060755_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold20153_2:4839:5489:+	Ruminococcus gnavus
432656	GL0032263_MH0014_[Complete]_[mRNA]_locus=scaffold20153_3:6701:7630:+	Ruminococcus gnavus
432657	GL0032264_MH0014_[Complete]_[mRNA]_locus=scaffold20153_3:7652:8479:+	Ruminococcus gnavus
432663	GL0032270_MH0014_[Complete]_[mRNA]_locus=scaffold20153_3:13424:13942:+	Ruminococcus gnavus

432667	GL0032274_MH0014_[Complete]_[mRNA]_locus=scaffold20153_3:16743:17792:+	Ruminococcus gnavus
432806	GL0143896_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold20450_7:132:1142:-	Roseburia inulinivorans
432916	GL0028273_MH0014_[Complete]_[mRNA]_locus=scaffold20617_2:2346:2774:-	Ruminococcus gnavus
432991	GL0005552_MH0014_[Complete]_[mRNA]_locus=scaffold20692_3:601:1491:-	-
433533	GL0033835_MH0014_[Complete]_[mRNA]_locus=scaffold21849_2:987:1664:-	Ruminococcus gnavus
433539	GL0033841_MH0014_[Complete]_[mRNA]_locus=scaffold21849_2:6137:6403:-	Ruminococcus gnavus
434028	GL0131052_MH0014_[Complete]_[mRNA]_locus=scaffold22616_2:145:363:-	-
434029	GL0131053_MH0014_[Complete]_[mRNA]_locus=scaffold22616_2:382:648:-	-
434522	GL0121927_MH0014_[Complete]_[mRNA]_locus=scaffold23672_2:2793:3419:+	Ruminococcus gnavus
434724	GL0000806_MH0014_[Complete]_[mRNA]_locus=scaffold23993_1:5928:6590:+	Ruminococcus gnavus
434862	GL0113018_MH0014_[Complete]_[mRNA]_locus=scaffold24362_2:10010:11590:+	Firmicutes
434867	GL0146738_MH0014_[Complete]_[mRNA]_locus=scaffold24397_1:307:1242:+	Ruminococcus gnavus
435009	GL0018110_MH0014_[Complete]_[mRNA]_locus=scaffold24756_2:8844:9326:-	Ruminococcus gnavus
435240	GL0058960_MH0014_[Complete]_[mRNA]_locus=scaffold25324_2:4357:5160:-	Ruminococcus gnavus

435241	GL0058961_MH0014_[Complete]_[mRNA]_locus=scaffold25324_2:5200:6069:-	Ruminococcus gnavus
435244	GL0058964_MH0014_[Complete]_[mRNA]_locus=scaffold25324_2:8620:9969:-	Clostridiales
435257	GL0058978_MH0014_[Complete]_[mRNA]_locus=scaffold25324_2:20674:20877:-	Ruminococcus gnavus
435295	GL0002807_MH0014_[Complete]_[mRNA]_locus=scaffold25390_1:1304:2149:+	Roseburia inulinivorans
435317	GL0027279_MH0014_[Complete]_[mRNA]_locus=scaffold25493_3:1972:2745:+	Ruminococcus gnavus
435457	GL0007552_MH0014_[Complete]_[mRNA]_locus=scaffold25904_1:30510:31526:-	Ruminococcus gnavus
435518	GL0049942_MH0014_[Complete]_[mRNA]_locus=scaffold25960_1:6984:7985:+	Ruminococcus gnavus
435549	GL0141037_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold25987_11:3:842:+	-
435646	GL0124716_MH0014_[Complete]_[mRNA]_locus=scaffold26218_2:3138:3983:+	Ruminococcus gnavus
435650	GL0130189_MH0014_[Complete]_[mRNA]_locus=scaffold26218_3:453:1313:-	Ruminococcus gnavus
435694	GL0025701_MH0014_[Complete]_[mRNA]_locus=scaffold26245_1:607:897:+	Clostridium
436095	GL0125226_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold27262_1:3:848:-	Clostridium phytofermentans
436400	GL0137446_MH0014_[Complete]_[mRNA]_locus=scaffold27917_2:155:607:-	-
436611	GL0040355_MH0014_[Complete]_[mRNA]_locus=scaffold28650_4:774:1724:+	Ruminococcus gnavus

436671	GL0026623_MH0014_[Complete]_[mRNA]_locus=scaffold28876_1:10314:10931:+	Ruminococcus gnavus
436681	GL0026634_MH0014_[Complete]_[mRNA]_locus=scaffold28876_1:23676:24881:-	Clostridiales
436686	GL0026641_MH0014_[Complete]_[mRNA]_locus=scaffold28876_1:35072:35890:+	Ruminococcus gnavus
436710	GL0058835_MH0014_[Complete]_[mRNA]_locus=scaffold28946_2:549:1364:-	Roseburia inulinivorans
437083	GL0154966_MH0014_[Complete]_[mRNA]_locus=scaffold30137_7:1000:1863:+	Roseburia inulinivorans
437327	GL0127391_MH0014_[Complete]_[mRNA]_locus=scaffold31000_1:806:1327:-	Ruminococcus gnavus
437340	GL0127404_MH0014_[Complete]_[mRNA]_locus=scaffold31000_1:17367:18791:-	Ruminococcus
437392	GL0077655_MH0014_[Complete]_[mRNA]_locus=scaffold31160_3:2097:2573:+	Roseburia inulinivorans
437436	GL0124289_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold31228_4:2:865:-	-
437650	GL0101099_MH0014_[Complete]_[mRNA]_locus=scaffold31761_2:2882:3316:-	Ruminococcus gnavus
437653	GL0101102_MH0014_[Complete]_[mRNA]_locus=scaffold31761_2:5015:5593:+	Ruminococcus gnavus
438317	GL0052473_MH0014_[Complete]_[mRNA]_locus=scaffold34063_1:1662:2495:-	Ruminococcus gnavus
438446	GL0019859_MH0014_[Complete]_[mRNA]_locus=scaffold34423_3:198:1223:+	Roseburia inulinivorans
438504	GL0041587_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold34626_1:22315:23979	Ruminococcus gnavus

	:+	
438756	GL0079322_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold35556_1:503:1105:+	-
439085	GL0111710_MH0014_[Complete]_[mRNA]_locus=scaffold36620_2:163:2391:+	-
439225	GL0080735_MH0014_[Complete]_[mRNA]_locus=scaffold37334_1:426:917:+	-
439256	GL0075236_MH0014_[Complete]_[mRNA]_locus=scaffold37458_5:6730:7227:+	Ruminococcus gnavus
439322	GL0033940_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold37652_1:1:525:+	Roseburia inulinivorans
439571	GL0079532_MH0014_[Complete]_[mRNA]_locus=scaffold38673_1:3176:3958:+	Ruminococcus gnavus
439572	GL0079533_MH0014_[Complete]_[mRNA]_locus=scaffold38673_1:3955:4563:+	Ruminococcus gnavus
439573	GL0107614_MH0014_[Complete]_[mRNA]_locus=scaffold38673_2:1095:1865:+	Ruminococcus gnavus
439576	GL0107617_MH0014_[Complete]_[mRNA]_locus=scaffold38673_2:3615:4229:-	Ruminococcus gnavus
439775	GL0132472_MH0014_[Complete]_[mRNA]_locus=scaffold39332_1:2000:2875:+	Ruminococcus gnavus
439778	GL0132475_MH0014_[Complete]_[mRNA]_locus=scaffold39332_1:6179:6619:-	Ruminococcus gnavus
439790	GL0132488_MH0014_[Complete]_[mRNA]_locus=scaffold39332_1:21218:21565:+	Ruminococcus gnavus
440405	GL0142975_MH0014_[Complete]_[mRNA]_locus=scaffold41588_1:9632:10129:+	Ruminococcus gnavus

440439	GL0044168_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold41796_2:4155:4769:-	Ruminococcus gnavus
440442	GL0065201_MH0014_[Complete]_[mRNA]_locus=scaffold41800_2:251:1468:-	Clostridiales
440986	GL0084642_MH0014_[Complete]_[mRNA]_locus=scaffold43691_1:1578:2318:-	Ruminococcus torques
440987	GL0084643_MH0014_[Complete]_[mRNA]_locus=scaffold43691_1:2514:2903:-	Ruminococcus gnavus
440999	GL0041828_MH0014_[Complete]_[mRNA]_locus=scaffold43691_2:11923:12291:+	Ruminococcus gnavus
441359	GL0009479_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold44927_1:1:909:+	Roseburia inulinivorans
442066	GL0142402_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold47870_2:1:639:-	-
442232	GL0003281_MH0014_[Complete]_[mRNA]_locus=scaffold48584_4:1423:1938:+	Ruminococcus gnavus
442353	GL0062415_MH0014_[Complete]_[mRNA]_locus=scaffold49213_3:190:999:+	Roseburia inulinivorans
442410	GL0061090_MH0014_[Complete]_[mRNA]_locus=scaffold49700_1:55:702:+	Roseburia inulinivorans
442433	GL0112824_MH0014_[Complete]_[mRNA]_locus=scaffold49771_7:1332:3200:+	-
442586	GL0024460_MH0014_[Complete]_[mRNA]_locus=scaffold50503_1:4809:5852:-	Ruminococcus gnavus
442799	GL0042227_MH0014_[Complete]_[mRNA]_locus=scaffold51207_1:4194:4733:+	Ruminococcus gnavus
442800	GL0042230_MH0014_[Complete]_[mRNA]_locus=scaffold51207_1:6232:6915:+	Ruminococcus gnavus

442811	GL0063950_MH0014_[Complete]_[mRNA]_locus=scaffold51207_3:2190:2381:+	Ruminococcus gnavus
442815	GL0074359_MH0014_[Complete]_[mRNA]_locus=scaffold51207_5:599:1087:+	Ruminococcus gnavus
443268	GL0025401_MH0014_[Complete]_[mRNA]_locus=scaffold53176_3:13:651:-	Roseburia inulinivorans
443374	GL0090955_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold53544_1:1:564:+	-
443377	GL0001253_MH0014_[Complete]_[mRNA]_locus=scaffold53574_2:620:1639:-	Anaerostipes caccae
443488	GL0144719_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold54025_6:3:1271:-	Clostridium
443542	GL0067311_MH0014_[Complete]_[mRNA]_locus=scaffold54225_1:9813:11543:+	Clostridiales
443549	GL0067318_MH0014_[Complete]_[mRNA]_locus=scaffold54225_1:16738:17472:+	Ruminococcus gnavus
443550	GL0067319_MH0014_[Complete]_[mRNA]_locus=scaffold54225_1:17538:18290:+	Ruminococcus gnavus
443760	GL0079278_MH0014_[Complete]_[mRNA]_locus=scaffold55236_10:502:1368:-	Firmicutes
444093	GL0133319_MH0014_[Complete]_[mRNA]_locus=scaffold56515_2:514:1350:-	Clostridium hylemonae
444262	GL0024553_MH0014_[Complete]_[mRNA]_locus=scaffold57186_1:6440:6985:-	Ruminococcus gnavus
444665	GL0051085_MH0014_[Complete]_[mRNA]_locus=scaffold58912_1:1355:2761:-	Bacteria
444738	GL0042509_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold59369_5:1:1992:-	Clostridiales

445331	GL0122253_MH0014_[Complete]_[mRNA]_locus=scaffold62094_2:926:1744:+	Roseburia inulinivorans
445360	GL0129992_MH0014_[Complete]_[mRNA]_locus=scaffold62235_15:125:859:+	Firmicutes
445453	GL0038547_MH0014_[Complete]_[mRNA]_locus=scaffold62681_2:259:699:+	-
445480	GL0093339_MH0014_[Complete]_[mRNA]_locus=scaffold62801_1:3420:4481:-	Ruminococcus gnavus
445483	GL0093343_MH0014_[Complete]_[mRNA]_locus=scaffold62801_1:6575:7030:-	Ruminococcus gnavus
445629	GL0040108_MH0014_[Complete]_[mRNA]_locus=scaffold63510_1:85:855:-	-
446808	GL0085494_MH0014_[Complete]_[mRNA]_locus=scaffold69607_3:2628:3497:-	Ruminococcus gnavus
446896	GL0052423_MH0014_[Complete]_[mRNA]_locus=scaffold70287_1:1316:2014:+	Ruminococcus gnavus
447254	GL0100952_MH0014_[Complete]_[mRNA]_locus=scaffold71959_3:200:589:-	Ruminococcus gnavus
447256	GL0100954_MH0014_[Complete]_[mRNA]_locus=scaffold71959_3:2610:3008:-	Ruminococcus gnavus
448281	GL0036092_MH0014_[Lack_3'-end]_[mRNA]_locus=scaffold76369_2:2:826:-	-
449281	GL0136168_MH0014_[Complete]_[mRNA]_locus=scaffold80093_1:9021:9788:+	Ruminococcus gnavus
449282	GL0045008_MH0014_[Complete]_[mRNA]_locus=scaffold80093_2:86:1732:+	Bacteria
449284	GL0045010_MH0014_[Complete]_[mRNA]_locus=scaffold80093_2:2553:2720:+	Ruminococcus gnavus

449289	GL0033326_MH0014_[Complete]_[mRNA]_locus=scaffold80093_3:4987:6156:+	Ruminococcus gnavus
449525	GL0008557_MH0014_[Complete]_[mRNA]_locus=scaffold81143_2:1033:1347:-	Ruminococcus gnavus
449533	GL0008565_MH0014_[Complete]_[mRNA]_locus=scaffold81143_2:7172:7456:-	Ruminococcus gnavus
449716	GL0069681_MH0014_[Complete]_[mRNA]_locus=scaffold81724_2:5898:6218:-	Ruminococcus gnavus
449803	GL0044205_MH0014_[Complete]_[mRNA]_locus=scaffold82035_1:608:865:-	Ruminococcus gnavus
450561	GL0140689_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold84712_1:421:543:-	-
450935	GL0073736_MH0014_[Complete]_[mRNA]_locus=scaffold86270_1:7013:7753:-	Ruminococcus gnavus
450939	GL0073740_MH0014_[Complete]_[mRNA]_locus=scaffold86270_1:10929:12014:-	Ruminococcus gnavus
450940	GL0073741_MH0014_[Complete]_[mRNA]_locus=scaffold86270_1:12029:13387:-	Ruminococcus
450946	GL0073748_MH0014_[Complete]_[mRNA]_locus=scaffold86270_1:20452:20688:-	Ruminococcus gnavus
450948	GL0073750_MH0014_[Complete]_[mRNA]_locus=scaffold86270_1:21732:22967:-	Ruminococcus gnavus
451104	GL0069880_MH0014_[Complete]_[mRNA]_locus=scaffold86785_1:5035:6018:+	Ruminococcus gnavus
451302	GL0070815_MH0014_[Complete]_[mRNA]_locus=scaffold87281_2:5757:6314:-	Firmicutes
452445	GL0107472_MH0014_[Complete]_[mRNA]_locus=scaffold90521_1:1956:2456:+	Ruminococcus gnavus

452461	GL0035049_MH0014_[Complete]_[mRNA]_locus=scaffold90554_1:45:1445:-	Eubacterium ventriosum
452649	GL0118235_MH0014_[Complete]_[mRNA]_locus=scaffold90932_1:44:358:+	Roseburia inulinivorans
453139	GL0111826_MH0014_[Complete]_[mRNA]_locus=scaffold91805_3:406:1536:-	Firmicutes
453470	GL0034978_MH0014_[Complete]_[mRNA]_locus=scaffold92313_1:3478:4815:+	Listeria
453472	GL0034980_MH0014_[Complete]_[mRNA]_locus=scaffold92313_1:5985:7538:+	Clostridium asparagiforme
454132	GL0082228_MH0014_[Complete]_[mRNA]_locus=scaffold92917_1:4114:5229:-	Ruminococcus gnavus
454225	GL0031423_MH0014_[Complete]_[mRNA]_locus=scaffold93008_1:994:1989:-	Ruminococcus gnavus
454227	GL0031425_MH0014_[Complete]_[mRNA]_locus=scaffold93008_1:3311:4594:+	Ruminococcus gnavus
455737	GL0110134_MH0014_[Lack_5'-end]_[mRNA]_locus=C4742451_1:2:178:+	-
456160	GL0025111_MH0014_[Lack_5'-end]_[mRNA]_locus=C4773830_1:458:901:-	Ruminococcus gnavus
457873	GL0048946_MH0015_[Lack_both_end]_[mRNA]_locus=scaffold4972_1:3:2216:+	Bacteria
457967	GL0013318_MH0015_[Complete]_[mRNA]_locus=scaffold5662_3:1258:1992:+	Bacteroides capillosus
459205	GL0044551_MH0015_[Complete]_[mRNA]_locus=scaffold19794_1:32:1474:-	Clostridium thermocellum
460964	GL0009897_MH0015_[Lack_3'-end]_[mRNA]_locus=scaffold43262_3:864:1481:+	Bacteria

463217	GL0113676_MH0016_[Complete]_[mRNA]_locus=scaffold72_1:385:843:+	Clostridiales
463302	GL0051663_MH0016_[Complete]_[mRNA]_locus=scaffold163_3:642:1199:-	Roseburia inulinivorans
463446	GL0123170_MH0016_[Complete]_[mRNA]_locus=scaffold214_1:261:1553:+	Roseburia inulinivorans
463447	GL0123171_MH0016_[Complete]_[mRNA]_locus=scaffold214_1:1595:2752:-	Roseburia inulinivorans
463449	GL0066750_MH0016_[Complete]_[mRNA]_locus=scaffold214_4:324:1934:-	Roseburia inulinivorans
463922	GL0079390_MH0016_[Complete]_[mRNA]_locus=scaffold579_3:8268:8993:-	-
464558	GL0054191_MH0016_[Complete]_[mRNA]_locus=scaffold1075_4:569:1501:-	Roseburia inulinivorans
464705	GL0115113_MH0016_[Complete]_[mRNA]_locus=scaffold1204_6:3649:4251:+	Bacteria
464890	GL0114634_MH0016_[Complete]_[mRNA]_locus=scaffold1321_1:610:1248:+	Roseburia inulinivorans
464905	GL0135797_MH0016_[Complete]_[mRNA]_locus=scaffold1365_2:83:1957:-	Bacteria
464967	GL0019038_MH0016_[Complete]_[mRNA]_locus=scaffold1448_4:2637:3833:+	Roseburia inulinivorans
465140	GL0022693_MH0016_[Complete]_[mRNA]_locus=scaffold1559_7:46:789:-	Roseburia inulinivorans
465252	GL0106727_MH0016_[Complete]_[mRNA]_locus=scaffold1629_6:768:2267:+	Roseburia inulinivorans
465335	GL0015477_MH0016_[Complete]_[mRNA]_locus=scaffold1707_2:429:1286:-	Roseburia inulinivorans

465336	GL0140408_MH0016_[Complete]_[mRNA]_locus=scaffold1707_4:102:752:-	Roseburia inulinivorans
465337	GL0142745_MH0016_[Complete]_[mRNA]_locus=scaffold1707_8:6:1361:-	Roseburia inulinivorans
465442	GL0001144_MH0016_[Complete]_[mRNA]_locus=scaffold1805_4:296:1714:-	Roseburia inulinivorans
465794	GL0047334_MH0016_[Complete]_[mRNA]_locus=scaffold2013_8:611:1111:-	Roseburia inulinivorans
465795	GL0047335_MH0016_[Complete]_[mRNA]_locus=scaffold2013_8:1128:2414:-	Roseburia inulinivorans
465796	GL0136735_MH0016_[Complete]_[mRNA]_locus=scaffold2013_9:1019:1864:-	Roseburia inulinivorans
465797	GL0136736_MH0016_[Complete]_[mRNA]_locus=scaffold2013_9:1917:2600:-	Roseburia inulinivorans
465799	GL0145658_MH0016_[Complete]_[mRNA]_locus=scaffold2013_11:391:765:-	Roseburia inulinivorans
465800	GL0145659_MH0016_[Complete]_[mRNA]_locus=scaffold2013_11:770:1609:-	Roseburia inulinivorans
465807	GL0124150_MH0016_[Complete]_[mRNA]_locus=scaffold2017_4:795:4091:-	Roseburia inulinivorans
466236	GL0135703_MH0016_[Complete]_[mRNA]_locus=scaffold2329_5:354:1445:-	Roseburia inulinivorans
466437	GL0063167_MH0016_[Complete]_[mRNA]_locus=scaffold2490_6:980:1471:-	Roseburia inulinivorans
466539	GL0016029_MH0016_[Complete]_[mRNA]_locus=scaffold2541_4:2257:3576:+	-
466540	GL0113972_MH0016_[Complete]_[mRNA]_locus=scaffold2541_5:1611:2390:-	Roseburia inulinivorans

466689	GL0110436_MH0016_[Complete]_[mRNA]_locus=scaffold2601_2:1215:2531:+	Clostridiales
466727	GL0106742_MH0016_[Complete]_[mRNA]_locus=scaffold2636_1:2394:3224:+	-
466814	GL0019681_MH0016_[Complete]_[mRNA]_locus=scaffold2764_1:44:706:-	-
466815	GL0019682_MH0016_[Complete]_[mRNA]_locus=scaffold2764_1:722:1774:-	Roseburia inulinivorans
466907	GL0072344_MH0016_[Complete]_[mRNA]_locus=scaffold2856_6:1376:2161:-	Roseburia inulinivorans
467019	GL0005627_MH0016_[Complete]_[mRNA]_locus=scaffold2926_2:2473:3501:-	Roseburia inulinivorans
467343	GL0116684_MH0016_[Complete]_[mRNA]_locus=scaffold3236_2:604:1491:-	Roseburia inulinivorans
467344	GL0116685_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold3236_2:1495:1896:-	-
467497	GL0055545_MH0016_[Complete]_[mRNA]_locus=scaffold3493_2:415:1095:+	Dorea formicigenerans
467967	GL0125503_MH0016_[Complete]_[mRNA]_locus=scaffold4070_2:298:1188:-	Bacteroides capillosus
468207	GL0018719_MH0016_[Complete]_[mRNA]_locus=scaffold4193_7:892:1803:+	-
468616	GL0049739_MH0016_[Complete]_[mRNA]_locus=scaffold4665_3:426:1034:-	Roseburia inulinivorans
468617	GL0049740_MH0016_[Complete]_[mRNA]_locus=scaffold4665_3:1047:1532:-	Roseburia inulinivorans
469618	GL0108975_MH0016_[Complete]_[mRNA]_locus=scaffold5853_6:193:987:+	-

469631	GL0054311_MH0016_[Complete]_[mRNA]_locus=scaffold5889_11:475:1137:+	Dorea longicatena
469947	GL0067193_MH0016_[Complete]_[mRNA]_locus=scaffold6236_10:1992:2924:+	Roseburia inulinivorans
470033	GL0037034_MH0016_[Complete]_[mRNA]_locus=scaffold6324_8:245:1639:+	Clostridiales
470034	GL0037035_MH0016_[Complete]_[mRNA]_locus=scaffold6324_8:1836:3251:+	Roseburia inulinivorans
470035	GL0020139_MH0016_[Complete]_[mRNA]_locus=scaffold6324_9:1050:2108:+	Roseburia inulinivorans
470037	GL0013912_MH0016_[Complete]_[mRNA]_locus=scaffold6324_10:359:1018:+	Roseburia inulinivorans
470123	GL0079845_MH0016_[Complete]_[mRNA]_locus=scaffold6429_2:176:802:+	Roseburia inulinivorans
470188	GL0032884_MH0016_[Complete]_[mRNA]_locus=scaffold6463_6:117:1235:+	Roseburia inulinivorans
470462	GL0026685_MH0016_[Complete]_[mRNA]_locus=scaffold6735_8:2407:3441:-	Roseburia inulinivorans
470463	GL0064452_MH0016_[Complete]_[mRNA]_locus=scaffold6735_9:51:530:-	Roseburia inulinivorans
470520	GL0024662_MH0016_[Complete]_[mRNA]_locus=scaffold6758_7:1676:3496:-	Clostridiales
471124	GL0064433_MH0016_[Complete]_[mRNA]_locus=scaffold7178_4:627:1208:-	Roseburia inulinivorans
471345	GL0123638_MH0016_[Complete]_[mRNA]_locus=scaffold7463_1:141:1019:+	Roseburia inulinivorans
471751	GL0018301_MH0016_[Complete]_[mRNA]_locus=scaffold7925_13:517:1182:-	Roseburia inulinivorans

471926	GL0139147_MH0016_[Complete]_[mRNA]_locus=scaffold8178_2:2444:3082:-	Roseburia inulinivorans
472086	GL0059693_MH0016_[Complete]_[mRNA]_locus=scaffold8387_12:86:514:-	Bacteroides capillosus
472458	GL0064108_MH0016_[Complete]_[mRNA]_locus=scaffold8994_3:3440:5947:+	Bacteria
472766	GL0140695_MH0016_[Complete]_[mRNA]_locus=scaffold9371_3:247:945:-	Roseburia inulinivorans
472859	GL0053609_MH0016_[Complete]_[mRNA]_locus=scaffold9492_5:2057:2986:-	Roseburia inulinivorans
472905	GL0068776_MH0016_[Complete]_[mRNA]_locus=scaffold9565_5:322:2604:+	Clostridiales
473007	GL0076651_MH0016_[Complete]_[mRNA]_locus=scaffold9680_1:265:1515:+	Roseburia inulinivorans
473010	GL0129233_MH0016_[Complete]_[mRNA]_locus=scaffold9680_9:2705:4681:-	Clostridiales
473013	GL0045940_MH0016_[Complete]_[mRNA]_locus=scaffold9680_12:587:1537:-	Roseburia inulinivorans
473102	GL0128571_MH0016_[Complete]_[mRNA]_locus=scaffold9868_3:2741:3466:+	Roseburia inulinivorans
473600	GL0133015_MH0016_[Complete]_[mRNA]_locus=scaffold10377_10:203:1618:+	Roseburia inulinivorans
473602	GL0106154_MH0016_[Complete]_[mRNA]_locus=scaffold10377_12:640:1407:-	Roseburia inulinivorans
473666	GL0021955_MH0016_[Complete]_[mRNA]_locus=scaffold10443_5:45:419:+	Bacteroides capillosus
473668	GL0021957_MH0016_[Complete]_[mRNA]_locus=scaffold10443_5:1347:1775:+	Bacteroides capillosus

474003	GL0103619_MH0016_[Complete]_[mRNA]_locus=scaffold10776_2:931:2685:+	Clostridiales
474004	GL0103620_MH0016_[Complete]_[mRNA]_locus=scaffold10776_2:2679:3404:+	Roseburia inulinivorans
474006	GL0122933_MH0016_[Complete]_[mRNA]_locus=scaffold10776_10:750:1514:+	Roseburia inulinivorans
474252	GL0040832_MH0016_[Complete]_[mRNA]_locus=scaffold10943_5:717:2027:+	Roseburia inulinivorans
474256	GL0073636_MH0016_[Complete]_[mRNA]_locus=scaffold10943_7:3920:4876:+	Roseburia inulinivorans
474317	GL0064854_MH0016_[Complete]_[mRNA]_locus=scaffold10995_8:843:1448:-	Roseburia inulinivorans
474319	GL0002540_MH0016_[Complete]_[mRNA]_locus=scaffold10995_10:992:1594:+	Roseburia inulinivorans
474867	GL0138706_MH0016_[Complete]_[mRNA]_locus=scaffold11893_1:249:1346:+	Roseburia inulinivorans
474979	GL0127244_MH0016_[Complete]_[mRNA]_locus=scaffold12044_1:530:2233:+	Clostridiales
475311	GL0133825_MH0016_[Complete]_[mRNA]_locus=scaffold12600_2:416:763:+	Roseburia inulinivorans
475312	GL0133826_MH0016_[Complete]_[mRNA]_locus=scaffold12600_2:744:983:+	Roseburia inulinivorans
475749	GL0015864_MH0016_[Complete]_[mRNA]_locus=scaffold13366_3:662:1147:-	Roseburia inulinivorans
475750	GL0015865_MH0016_[Complete]_[mRNA]_locus=scaffold13366_3:1144:1500:-	Roseburia inulinivorans
475763	GL0077275_MH0016_[Complete]_[mRNA]_locus=scaffold13424_5:8585:9766:+	Clostridium leptum

475871	GL0089396_MH0016_[Complete]_[mRNA]_locus=scaffold13483_1:77:436:-	Roseburia inulinivorans
475939	GL0019586_MH0016_[Complete]_[mRNA]_locus=scaffold13622_1:1286:1834:+	Roseburia inulinivorans
476069	GL0102445_MH0016_[Complete]_[mRNA]_locus=scaffold13822_4:284:1483:-	Roseburia inulinivorans
476070	GL0053301_MH0016_[Complete]_[mRNA]_locus=scaffold13822_6:575:2056:-	Roseburia inulinivorans
476602	GL0092222_MH0016_[Complete]_[mRNA]_locus=scaffold14561_5:785:2428:-	Roseburia inulinivorans
476603	GL0146034_MH0016_[Complete]_[mRNA]_locus=scaffold14561_12:3418:5007:-	Roseburia inulinivorans
476638	GL0027075_MH0016_[Complete]_[mRNA]_locus=scaffold14615_2:1898:2971:+	Roseburia inulinivorans
476639	GL0027077_MH0016_[Complete]_[mRNA]_locus=scaffold14615_2:3604:4251:+	Roseburia inulinivorans
476640	GL0027079_MH0016_[Complete]_[mRNA]_locus=scaffold14615_2:5336:6409:-	Roseburia inulinivorans
476641	GL0116947_MH0016_[Complete]_[mRNA]_locus=scaffold14615_3:1055:1789:-	Roseburia inulinivorans
476715	GL0113060_MH0016_[Complete]_[mRNA]_locus=scaffold14860_2:1417:2508:-	Roseburia inulinivorans
476716	GL0113062_MH0016_[Complete]_[mRNA]_locus=scaffold14860_2:2734:3768:-	Roseburia inulinivorans
476867	GL0068768_MH0016_[Complete]_[mRNA]_locus=scaffold15098_2:278:835:+	Roseburia inulinivorans
476868	GL0068769_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold15098_2:935:1351:+	Roseburia inulinivorans

476976	GL0128423_MH0016_[Complete]_[mRNA]_locus=scaffold15448_4:562:1491:+	Roseburia inulinivorans
477063	GL0136303_MH0016_[Complete]_[mRNA]_locus=scaffold15637_3:1682:2332:+	Roseburia inulinivorans
477315	GL0036437_MH0016_[Complete]_[mRNA]_locus=scaffold16238_1:632:2332:+	Bacteria
477317	GL0126035_MH0016_[Complete]_[mRNA]_locus=scaffold16238_2:1350:4781:+	Clostridiales
477320	GL0112692_MH0016_[Complete]_[mRNA]_locus=scaffold16238_6:995:2395:+	Clostridiales
477321	GL0135539_MH0016_[Complete]_[mRNA]_locus=scaffold16238_7:711:1952:+	Roseburia inulinivorans
477435	GL0082744_MH0016_[Complete]_[mRNA]_locus=scaffold16664_2:1045:1842:-	Roseburia inulinivorans
477436	GL0065733_MH0016_[Complete]_[mRNA]_locus=scaffold16664_7:601:981:-	Roseburia inulinivorans
477515	GL0094640_MH0016_[Complete]_[mRNA]_locus=scaffold16724_1:379:1911:-	Roseburia inulinivorans
477786	GL0095864_MH0016_[Complete]_[mRNA]_locus=scaffold17229_2:86:778:-	Roseburia inulinivorans
478078	GL0120662_MH0016_[Complete]_[mRNA]_locus=scaffold17755_3:284:754:+	Roseburia inulinivorans
478127	GL0128266_MH0016_[Complete]_[mRNA]_locus=scaffold17855_2:180:2366:+	Roseburia inulinivorans
478128	GL0128267_MH0016_[Complete]_[mRNA]_locus=scaffold17855_2:2443:4014:+	Roseburia inulinivorans
478167	GL0068683_MH0016_[Complete]_[mRNA]_locus=scaffold17948_4:1873:2829:+	Roseburia inulinivorans

478351	GL0082892_MH0016_[Complete]_[mRNA]_locus=scaffold18370_5:178:951:+	Roseburia inulinivorans
478497	GL0055516_MH0016_[Complete]_[mRNA]_locus=scaffold18850_2:169:1065:-	Roseburia inulinivorans
478592	GL0089132_MH0016_[Complete]_[mRNA]_locus=scaffold19090_6:705:2060:-	Clostridiales
478615	GL0003709_MH0016_[Complete]_[mRNA]_locus=scaffold19201_7:139:750:+	Roseburia inulinivorans
478854	GL0059477_MH0016_[Complete]_[mRNA]_locus=scaffold19803_11:71:1417:+	Roseburia inulinivorans
479040	GL0019741_MH0016_[Complete]_[mRNA]_locus=scaffold20306_2:589:1833:+	Roseburia inulinivorans
479041	GL0109070_MH0016_[Complete]_[mRNA]_locus=scaffold20306_3:1700:2983:+	Roseburia inulinivorans
479042	GL0014815_MH0016_[Complete]_[mRNA]_locus=scaffold20306_4:1251:1832:+	Roseburia inulinivorans
479044	GL0013571_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold20306_8:572:943:-	Roseburia inulinivorans
479494	GL0020346_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold21151_4:228:587:-	Roseburia inulinivorans
479504	GL0073779_MH0016_[Complete]_[mRNA]_locus=scaffold21188_2:1277:2569:-	Roseburia inulinivorans
479590	GL0060311_MH0016_[Complete]_[mRNA]_locus=scaffold21413_3:1969:2952:-	Roseburia inulinivorans
479591	GL0136270_MH0016_[Complete]_[mRNA]_locus=scaffold21413_4:784:1761:-	Roseburia inulinivorans
479631	GL0104278_MH0016_[Complete]_[mRNA]_locus=scaffold21545_5:405:3329:-	Roseburia inulinivorans

479817	GL0072366_MH0016_[Complete]_[mRNA]_locus=scaffold21921_6:277:1119:-	Roseburia inulinivorans
480651	GL0123417_MH0016_[Complete]_[mRNA]_locus=scaffold23729_3:413:1114:-	Roseburia inulinivorans
480876	GL0014443_MH0016_[Complete]_[mRNA]_locus=scaffold24385_4:1396:2016:-	Roseburia inulinivorans
480877	GL0014444_MH0016_[Complete]_[mRNA]_locus=scaffold24385_4:2181:3518:-	Clostridiales
480878	GL0014445_MH0016_[Complete]_[mRNA]_locus=scaffold24385_4:3529:3975:-	Roseburia inulinivorans
480880	GL0121008_MH0016_[Complete]_[mRNA]_locus=scaffold24385_6:145:852:-	Roseburia inulinivorans
480998	GL0093967_MH0016_[Complete]_[mRNA]_locus=scaffold24733_1:3007:3954:-	Roseburia inulinivorans
481650	GL0098828_MH0016_[Complete]_[mRNA]_locus=scaffold26268_11:257:1522:-	Roseburia inulinivorans
481836	GL0081417_MH0016_[Complete]_[mRNA]_locus=scaffold26684_2:213:3389:+	Roseburia inulinivorans
481847	GL0145370_MH0016_[Complete]_[mRNA]_locus=scaffold26736_3:798:1628:-	-
481850	GL0061999_MH0016_[Complete]_[mRNA]_locus=scaffold26741_4:527:1399:-	Roseburia inulinivorans
482140	GL0036806_MH0016_[Complete]_[mRNA]_locus=scaffold27400_2:112:2463:+	Clostridia
482151	GL0031409_MH0016_[Complete]_[mRNA]_locus=scaffold27440_4:49:924:+	Roseburia inulinivorans
482249	GL0045320_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold27786_3:99:626:-	Clostridium bolteae

482251	GL0143726_MH0016_[Complete]_[mRNA]_locus=scaffold27800_1:473:1399:+	Roseburia inulinivorans
482327	GL0093175_MH0016_[Complete]_[mRNA]_locus=scaffold27941_1:93:605:-	Roseburia inulinivorans
482329	GL0135207_MH0016_[Complete]_[mRNA]_locus=scaffold27941_3:1773:2831:-	Roseburia inulinivorans
482330	GL0045590_MH0016_[Complete]_[mRNA]_locus=scaffold27941_4:361:3090:-	Clostridiales
482534	GL0066323_MH0016_[Complete]_[mRNA]_locus=scaffold28746_1:1596:2225:-	Roseburia inulinivorans
482535	GL0066324_MH0016_[Complete]_[mRNA]_locus=scaffold28746_1:2229:3539:-	Roseburia inulinivorans
482825	GL0109002_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold29621_1:3:512:-	-
482910	GL0127634_MH0016_[Complete]_[mRNA]_locus=scaffold29895_4:193:1131:+	Roseburia inulinivorans
482912	GL0127637_MH0016_[Complete]_[mRNA]_locus=scaffold29895_4:2639:3145:+	Roseburia inulinivorans
483000	GL0007023_MH0016_[Complete]_[mRNA]_locus=scaffold30257_1:941:2911:+	Roseburia inulinivorans
483475	GL0084208_MH0016_[Complete]_[mRNA]_locus=scaffold31981_3:4943:6514:-	Clostridiales
483870	GL0024524_MH0016_[Complete]_[mRNA]_locus=scaffold33058_2:198:941:-	Roseburia inulinivorans
483871	GL0024525_MH0016_[Complete]_[mRNA]_locus=scaffold33058_2:991:2271:-	Bacteria
484173	GL0118287_MH0016_[Complete]_[mRNA]_locus=scaffold33893_2:2205:2849:-	Roseburia inulinivorans

484174	GL0118288_MH0016_[Complete]_[mRNA]_locus=scaffold33893_2:2920:3801:-	Roseburia inulinivorans
484176	GL0003082_MH0016_[Complete]_[mRNA]_locus=scaffold33893_4:952:2340:-	Roseburia inulinivorans
484177	GL0003083_MH0016_[Complete]_[mRNA]_locus=scaffold33893_4:2719:3567:+	Roseburia inulinivorans
484307	GL0098388_MH0016_[Complete]_[mRNA]_locus=scaffold34142_1:25:888:+	Roseburia inulinivorans
484308	GL0098389_MH0016_[Complete]_[mRNA]_locus=scaffold34142_1:904:2559:+	-
484317	GL0020848_MH0016_[Complete]_[mRNA]_locus=scaffold34193_1:50:1408:+	Clostridiales
484551	GL0124596_MH0016_[Complete]_[mRNA]_locus=scaffold34755_4:210:707:+	Roseburia inulinivorans
484612	GL0125878_MH0016_[Complete]_[mRNA]_locus=scaffold34995_9:141:1514:-	Clostridiales
484614	GL0126821_MH0016_[Complete]_[mRNA]_locus=scaffold34995_12:1516:3348:-	Roseburia inulinivorans
484615	GL0126822_MH0016_[Complete]_[mRNA]_locus=scaffold34995_12:3421:5205:-	Roseburia inulinivorans
485103	GL0018814_MH0016_[Complete]_[mRNA]_locus=scaffold36804_2:13:1275:-	Clostridiales
485277	GL0117050_MH0016_[Complete]_[mRNA]_locus=scaffold37161_3:597:1913:+	-
485722	GL0048635_MH0016_[Complete]_[mRNA]_locus=scaffold38717_6:224:880:+	Roseburia inulinivorans
486008	GL0126913_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold39548_1:3:1055:-	Bacteria

486291	GL0146717_MH0016_[Complete]_[mRNA]_locus=scaffold40595_9:169:771:-	Roseburia inulinivorans
486589	GL0004750_MH0016_[Complete]_[mRNA]_locus=scaffold41630_2:362:1375:+	Roseburia inulinivorans
486653	GL0026725_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold41866_1:630:1286:-	Roseburia inulinivorans
486915	GL0119966_MH0016_[Complete]_[mRNA]_locus=scaffold42835_1:1102:2490:+	Roseburia inulinivorans
487105	GL0017535_MH0016_[Complete]_[mRNA]_locus=scaffold43641_2:807:1592:+	Roseburia inulinivorans
487148	GL0001289_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold43731_2:3:893:-	Dorea longicatena
487472	GL0014529_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold45095_10:1:162:-	Roseburia inulinivorans
488033	GL0040272_MH0016_[Complete]_[mRNA]_locus=scaffold47383_6:748:1569:+	Roseburia inulinivorans
488076	GL0013100_MH0016_[Complete]_[mRNA]_locus=scaffold47522_2:878:1165:-	-
488229	GL0058533_MH0016_[Complete]_[mRNA]_locus=scaffold48287_2:126:569:-	Roseburia inulinivorans
488283	GL0072968_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold48709_9:3:836:+	Roseburia inulinivorans
488284	GL0072969_MH0016_[Complete]_[mRNA]_locus=scaffold48709_9:812:1630:+	Roseburia inulinivorans
488783	GL0101649_MH0016_[Complete]_[mRNA]_locus=scaffold50753_3:1584:2642:-	Roseburia inulinivorans
489358	GL0090941_MH0016_[Complete]_[mRNA]_locus=scaffold53024_4:1645:2082:-	Roseburia inulinivorans

489472	GL0069489_MH0016_[Complete]_[mRNA]_locus=scaffold53372_6:815:1741:+	Roseburia inulinivorans
489473	GL0063230_MH0016_[Complete]_[mRNA]_locus=scaffold53372_7:734:2323:+	Roseburia inulinivorans
489538	GL0075872_MH0016_[Complete]_[mRNA]_locus=scaffold53725_3:27:737:-	Roseburia inulinivorans
489720	GL0074651_MH0016_[Complete]_[mRNA]_locus=scaffold54612_1:3644:4711:-	-
490115	GL0061358_MH0016_[Complete]_[mRNA]_locus=scaffold56519_4:3710:5317:-	-
490657	GL0137993_MH0016_[Complete]_[mRNA]_locus=scaffold58846_3:423:1904:-	Roseburia inulinivorans
490730	GL0046987_MH0016_[Complete]_[mRNA]_locus=scaffold59163_1:1186:1941:+	Roseburia inulinivorans
491412	GL0093219_MH0016_[Complete]_[mRNA]_locus=scaffold62133_2:11:805:-	Lachnospiraceae
491454	GL0074220_MH0016_[Complete]_[mRNA]_locus=scaffold62375_2:233:2164:-	Bacteria
491627	GL0022551_MH0016_[Complete]_[mRNA]_locus=scaffold63171_9:399:1037:+	Roseburia inulinivorans
491634	GL0139658_MH0016_[Complete]_[mRNA]_locus=scaffold63191_3:1264:2523:+	Roseburia inulinivorans
492255	GL0064832_MH0016_[Complete]_[mRNA]_locus=scaffold66329_1:517:1179:-	Roseburia inulinivorans
492592	GL0047210_MH0016_[Complete]_[mRNA]_locus=scaffold67790_2:192:1400:+	Bacteria
493837	GL0145478_MH0016_[Complete]_[mRNA]_locus=scaffold74142_1:767:1099:+	-

494055	GL0019556_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold75160_1:2:1732:+	Bacteroides capillosus
495793	GL0074257_MH0016_[Complete]_[mRNA]_locus=scaffold81267_3:118:825:-	Roseburia inulinivorans
495797	GL0090079_MH0016_[Complete]_[mRNA]_locus=scaffold81267_6:575:1051:+	Roseburia inulinivorans
495798	GL0090080_MH0016_[Complete]_[mRNA]_locus=scaffold81267_6:1084:1302:-	-
495800	GL0022825_MH0016_[Complete]_[mRNA]_locus=scaffold81267_7:2917:3654:+	Roseburia inulinivorans
495801	GL0022826_MH0016_[Complete]_[mRNA]_locus=scaffold81267_7:3766:4965:+	Roseburia inulinivorans
496032	GL0079349_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold81942_1:2:856:-	Clostridiales
496197	GL0096370_MH0016_[Complete]_[mRNA]_locus=scaffold82351_4:243:1082:-	Bacteroides capillosus
496987	GL0117903_MH0016_[Complete]_[mRNA]_locus=scaffold84229_1:335:1684:-	Roseburia inulinivorans
497283	GL0108658_MH0016_[Complete]_[mRNA]_locus=scaffold84831_1:211:1194:-	Roseburia inulinivorans
497287	GL0033429_MH0016_[Complete]_[mRNA]_locus=scaffold84834_3:239:2056:+	Clostridiales
497393	GL0071049_MH0016_[Complete]_[mRNA]_locus=scaffold85089_4:1066:1983:+	Roseburia inulinivorans
498046	GL0062231_MH0016_[Complete]_[mRNA]_locus=scaffold86285_1:2026:2814:-	Roseburia inulinivorans
498315	GL0136601_MH0016_[Complete]_[mRNA]_locus=scaffold86714_1:40:1638:+	Roseburia inulinivorans

498370	GL0069700_MH0016_[Complete]_[mRNA]_locus=scaffold86822_1:134:1165:+	Roseburia inulinivorans
499042	GL0139380_MH0016_[Complete]_[mRNA]_locus=scaffold87336_1:286:1245:-	Roseburia inulinivorans
499043	GL0091315_MH0016_[Complete]_[mRNA]_locus=scaffold87336_2:471:1457:-	Roseburia inulinivorans
499130	GL0040576_MH0016_[Complete]_[mRNA]_locus=scaffold87411_2:305:541:+	Eubacterium hallii
499243	GL0101164_MH0016_[Complete]_[mRNA]_locus=scaffold87486_2:776:1681:+	Roseburia inulinivorans
499320	GL0009416_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold87526_1:782:2290:+	Roseburia inulinivorans
499584	GL0032004_MH0016_[Complete]_[mRNA]_locus=scaffold87671_1:173:1417:+	Roseburia inulinivorans
499634	GL0138335_MH0016_[Complete]_[mRNA]_locus=scaffold87690_1:22:2229:-	Clostridiales
499635	GL0138336_MH0016_[Complete]_[mRNA]_locus=scaffold87690_1:2400:2762:-	Roseburia inulinivorans
499636	GL0138338_MH0016_[Complete]_[mRNA]_locus=scaffold87690_1:3639:4433:-	-
499696	GL0025712_MH0016_[Complete]_[mRNA]_locus=scaffold87716_2:418:1371:+	Roseburia inulinivorans
501195	GL0062160_MH0016_[Lack_3'-end]_[mRNA]_locus=C4050458_1:3:593:-	Clostridium
502187	GL0109330_MH0016_[Complete]_[mRNA]_locus=C4112025_1:497:1276:+	Roseburia inulinivorans
502626	GL0029137_MH0016_[Complete]_[mRNA]_locus=C4136699_1:2412:3047:+	Roseburia inulinivorans

503591	GL0007589_MH0017_[Lack_3'-end]_[mRNA]_locus=scaffold4039_1:1:540:-	Clostridium
504004	GL0042972_MH0017_[Complete]_[mRNA]_locus=scaffold6736_3:1101:2678:+	Clostridium hylemonae
504770	GL0012871_MH0017_[Lack_5'-end]_[mRNA]_locus=scaffold12217_2:805:1017:-	Faecalibacterium prausnitzii
505692	GL0018251_MH0017_[Complete]_[mRNA]_locus=scaffold19607_2:50:988:+	Faecalibacterium prausnitzii
508554	GL0021625_MH0017_[Complete]_[mRNA]_locus=scaffold41803_2:50:1621:-	-
511523	GL0005048_MH0018_[Lack_5'-end]_[mRNA]_locus=scaffold119_1:2:781:+	Bacteria
511524	GL0005049_MH0018_[Complete]_[mRNA]_locus=scaffold119_1:797:1048:+	Bacteria
511525	GL0006395_MH0018_[Lack_5'-end]_[mRNA]_locus=scaffold119_2:3:677:+	Roseburia inulinivorans
511887	GL0021215_MH0018_[Lack_both_end]_[mRNA]_locus=scaffold1963_2:2:979:-	-
512590	GL0002701_MH0018_[Lack_5'-end]_[mRNA]_locus=scaffold6183_1:3:812:+	-
512749	GL0009750_MH0018_[Complete]_[mRNA]_locus=scaffold7373_8:321:1040:-	Dorea formicigenerans
512750	GL0009751_MH0018_[Complete]_[mRNA]_locus=scaffold7373_8:1215:1607:+	Roseburia inulinivorans
513149	GL0000698_MH0018_[Lack_both_end]_[mRNA]_locus=scaffold10178_4:2:979:+	Bacteria
513653	GL0003732_MH0018_[Lack_both_end]_[mRNA]_locus=scaffold15057_4:1:561:-	-

513922	GL0018846_MH0018_[Lack_3'-end]_[mRNA]_locus=scaffold17833_3:401:1348:+	Clostridium
514321	GL0004511_MH0018_[Lack_3'-end]_[mRNA]_locus=scaffold20951_1:3:659:-	Roseburia inulinivorans
517161	GL0043476_MH0019_[Complete]_[mRNA]_locus=scaffold1020_3:184:660:-	Roseburia inulinivorans
517985	GL0019996_MH0019_[Lack_both_end]_[mRNA]_locus=scaffold6165_4:3:668:+	Roseburia inulinivorans
518546	GL0017079_MH0019_[Complete]_[mRNA]_locus=scaffold10380_6:562:972:+	Blautia hydrogenotrophica
518784	GL0016532_MH0019_[Lack_5'-end]_[mRNA]_locus=scaffold12053_2:3:347:+	Clostridium
519420	GL0019304_MH0019_[Complete]_[mRNA]_locus=scaffold16569_1:90:755:-	Clostridiales
521161	GL0044465_MH0019_[Lack_3'-end]_[mRNA]_locus=scaffold31675_2:1:297:-	Clostridium sporogenes
522194	GL0042736_MH0019_[Complete]_[mRNA]_locus=scaffold40509_6:1118:1513:-	Clostridium methylpentosum
522585	GL0003994_MH0019_[Complete]_[mRNA]_locus=scaffold43631_1:10:999:-	Bacteroides pectinophilus
527499	GL0032932_MH0020_[Lack_3'-end]_[mRNA]_locus=scaffold265_4:2:103:-	-
533337	GL0074950_MH0020_[Complete]_[mRNA]_locus=scaffold2109_3:1082:1384:+	Bacteroides capillosus
537857	GL0016497_MH0020_[Lack_3'-end]_[mRNA]_locus=scaffold4058_6:1:327:-	Faecalibacterium prausnitzii
537858	GL0016498_MH0020_[Complete]_[mRNA]_locus=scaffold4058_6:372:1031:-	Finegoldia magna

537859	GL0016499_MH0020_[Complete]_[mRNA]_locus=scaffold4058_6:1291:1896:-	Faecalibacterium prausnitzii
537860	GL0016500_MH0020_[Complete]_[mRNA]_locus=scaffold4058_6:1901:2461:-	Faecalibacterium prausnitzii
540152	GL0043123_MH0020_[Complete]_[mRNA]_locus=scaffold5119_2:3303:3485:+	Bacteroides pectinophilus
547388	GL0076663_MH0020_[Lack_3'-end]_[mRNA]_locus=scaffold9797_5:1905:3038:+	Clostridiales
547891	GL0015330_MH0020_[Complete]_[mRNA]_locus=scaffold10270_1:224:1696:-	Clostridium phytofermentans
552070	GL0091427_MH0020_[Complete]_[mRNA]_locus=scaffold15070_2:146:349:+	Clostridiales
552157	GL0046997_MH0020_[Complete]_[mRNA]_locus=scaffold15231_2:344:562:+	Clostridiales
552492	GL0027080_MH0020_[Complete]_[mRNA]_locus=scaffold15507_1:2383:2598:-	Clostridiales
555764	GL0066483_MH0020_[Complete]_[mRNA]_locus=scaffold20730_1:487:2235:-	Bacteria
556006	GL0044551_MH0020_[Complete]_[mRNA]_locus=scaffold21122_1:236:769:+	Clostridium leptum
560218	GL0051816_MH0020_[Complete]_[mRNA]_locus=scaffold30723_5:850:1419:+	Clostridium leptum
562524	GL0016907_MH0020_[Complete]_[mRNA]_locus=scaffold37438_2:161:844:-	Firmicutes
563136	GL0079430_MH0020_[Complete]_[mRNA]_locus=scaffold38902_11:639:1493:+	-
566687	GL0024968_MH0020_[Complete]_[mRNA]_locus=scaffold46875_2:32:586:+	Clostridium

569108	GL0022103_MH0020_[Complete]_[mRNA]_locus=C3124556_1:432:644:-	-
569586	GL0100041_MH0021_[Complete]_[mRNA]_locus=scaffold1800_2:305:904:-	Bacteroides capillosus
570047	GL0096087_MH0021_[Complete]_[mRNA]_locus=scaffold5118_2:157:645:+	Roseburia inulinivorans
571005	GL0091941_MH0021_[Complete]_[mRNA]_locus=scaffold12315_1:61:780:-	Roseburia inulinivorans
571087	GL0085788_MH0021_[Lack_3'-end]_[mRNA]_locus=scaffold13026_2:165:1316:+	Bifidobacterium breve
571790	GL0045699_MH0021_[Complete]_[mRNA]_locus=scaffold18174_4:217:513:+	Roseburia inulinivorans
572151	GL0015390_MH0021_[Complete]_[mRNA]_locus=scaffold20841_1:123:1031:+	Roseburia inulinivorans
572335	GL0090735_MH0021_[Complete]_[mRNA]_locus=scaffold22451_4:580:1098:+	Roseburia inulinivorans
572746	GL0066916_MH0021_[Complete]_[mRNA]_locus=scaffold26113_2:135:494:+	Roseburia inulinivorans
572946	GL0076017_MH0021_[Complete]_[mRNA]_locus=scaffold27404_1:393:1382:-	Roseburia inulinivorans
573549	GL0039886_MH0021_[Complete]_[mRNA]_locus=scaffold32225_6:68:412:+	Roseburia inulinivorans
574041	GL0010408_MH0021_[Complete]_[mRNA]_locus=scaffold35655_2:45:371:+	Clostridium
574100	GL0056947_MH0021_[Complete]_[mRNA]_locus=scaffold36168_3:25:681:+	Roseburia inulinivorans
574117	GL0065210_MH0021_[Complete]_[mRNA]_locus=scaffold36320_3:150:1199:+	Roseburia inulinivorans

574551	GL0041660_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold39714_1:112:567:-	Roseburia inulinivorans
574669	GL0042024_MH0021_[Complete]_[mRNA]_locus=scaffold40354_1:162:983:-	Clostridium
574676	GL0073236_MH0021_[Complete]_[mRNA]_locus=scaffold40425_3:889:1509:+	Roseburia inulinivorans
574796	GL0040825_MH0021_[Lack_both_end]_[mRNA]_locus=scaffold41475_1:3:773:+	Clostridiales
575135	GL0100154_MH0021_[Complete]_[mRNA]_locus=scaffold44058_3:49:933:-	Roseburia inulinivorans
575652	GL0015838_MH0021_[Complete]_[mRNA]_locus=scaffold47663_1:85:552:+	Roseburia inulinivorans
576140	GL0005704_MH0021_[Complete]_[mRNA]_locus=scaffold50885_1:191:757:-	Roseburia inulinivorans
576434	GL0074706_MH0021_[Complete]_[mRNA]_locus=scaffold52649_1:120:392:-	Roseburia inulinivorans
576781	GL0055312_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold54338_2:1:216:+	-
576922	GL0043615_MH0021_[Complete]_[mRNA]_locus=scaffold55089_1:1456:2058:-	Roseburia inulinivorans
577010	GL0065865_MH0021_[Complete]_[mRNA]_locus=scaffold55531_2:606:2354:+	Clostridiales
577841	GL0053192_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold60057_1:185:721:-	Roseburia inulinivorans
579423	GL0003183_MH0021_[Complete]_[mRNA]_locus=scaffold65428_2:155:808:-	Roseburia inulinivorans
579457	GL0063061_MH0021_[Complete]_[mRNA]_locus=scaffold65557_1:492:1286:-	Roseburia inulinivorans

579789	GL0082454_MH0021_[Complete]_[mRNA]_locus=scaffold66549_1:412:1167:+	Roseburia inulinivorans
579913	GL0003448_MH0021_[Complete]_[mRNA]_locus=scaffold66890_3:310:1215:+	Roseburia inulinivorans
580367	GL0032556_MH0021_[Complete]_[mRNA]_locus=scaffold68204_2:331:1623:+	Roseburia inulinivorans
580668	GL0086617_MH0021_[Complete]_[mRNA]_locus=scaffold68986_1:18:518:-	Bacteroides pectinophilus
580723	GL0058142_MH0021_[Complete]_[mRNA]_locus=scaffold69146_3:139:381:-	Roseburia inulinivorans
581407	GL0009451_MH0021_[Complete]_[mRNA]_locus=scaffold70243_1:180:827:-	Anaerostipes caccae
581659	GL0049094_MH0021_[Complete]_[mRNA]_locus=scaffold70635_1:272:1801:-	Bacteria
582303	GL0042721_MH0021_[Complete]_[mRNA]_locus=scaffold71410_1:272:727:+	Roseburia inulinivorans
583845	GL0003249_MH0021_[Complete]_[mRNA]_locus=scaffold72608_1:3114:3713:+	Eubacterium siraeum
585642	GL0001390_MH0021_[Lack_5'-end]_[mRNA]_locus=C2028683_1:1:261:+	Clostridium
585806	GL0058567_MH0021_[Complete]_[mRNA]_locus=C2032733_1:445:702:+	Roseburia inulinivorans
586115	GL0086012_MH0021_[Complete]_[mRNA]_locus=C2040879_1:52:405:-	Roseburia inulinivorans
586865	GL0092840_MH0021_[Complete]_[mRNA]_locus=C2056595_1:230:880:+	-
587272	GL0015198_MH0021_[Lack_5'-end]_[mRNA]_locus=C2063761_1:524:1147:-	-

587620	GL0069328_MH0021_[Complete]_[mRNA]_locus=C2068805_1:237:896:+	Roseburia inulinivorans
587621	GL0069329_MH0021_[Lack_3'-end]_[mRNA]_locus=C2068805_1:886:1287:+	Roseburia inulinivorans
591947	GL0017802_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold263_1:2:355:+	Anaerotruncus colihominis
592098	GL0023208_MH0022_[Complete]_[mRNA]_locus=scaffold1043_2:418:798:-	Roseburia inulinivorans
592417	GL0029148_MH0022_[Complete]_[mRNA]_locus=scaffold3297_2:370:2070:+	Clostridium
593205	GL0023957_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold8245_2:1:252:+	Clostridiales
594982	GL0010146_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold22035_2:9:923:-	-
595801	GL0032374_MH0022_[Lack_3'-end]_[mRNA]_locus=scaffold29383_2:2:682:-	Clostridium
597094	GL0037798_MH0022_[Complete]_[mRNA]_locus=scaffold41601_1:3891:5561:-	Clostridiales
597789	GL0004898_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold46772_2:2:676:+	Anaerotruncus colihominis
599049	GL0005677_MH0022_[Complete]_[mRNA]_locus=scaffold53056_2:950:1492:+	Bacteroides pectinophilus
603935	GL0010473_MH0023_[Complete]_[mRNA]_locus=scaffold2163_2:2556:3170:+	Bacteroides pectinophilus
604166	GL0000761_MH0023_[Lack_5'-end]_[mRNA]_locus=scaffold2898_1:675:797:-	-
604261	GL0006178_MH0023_[Complete]_[mRNA]_locus=scaffold3228_1:901:1398:-	-

604337	GL0011031_MH0023_[Lack_3'-end]_[mRNA]_locus=scaffold3566_5:726:1634:+	-
604339	GL0024491_MH0023_[Complete]_[mRNA]_locus=scaffold3566_7:996:2849:+	Clostridium beijerinckii
604461	GL0027688_MH0023_[Complete]_[mRNA]_locus=scaffold4022_2:766:951:-	Roseburia inulinivorans
605459	GL0027416_MH0023_[Lack_5'-end]_[mRNA]_locus=scaffold7335_2:3:524:+	Bacteroides stercoris
606842	GL0019955_MH0023_[Complete]_[mRNA]_locus=scaffold13359_3:164:1240:-	Eubacterium siraeum
606986	GL0008579_MH0023_[Lack_3'-end]_[mRNA]_locus=scaffold14158_1:47:4534:+	Bacteroides pectinophilus
607699	GL0016132_MH0023_[Lack_5'-end]_[mRNA]_locus=scaffold17931_2:2109:2465:-	Dorea longicatena
609012	GL0027694_MH0023_[Complete]_[mRNA]_locus=scaffold25765_2:225:554:+	Clostridium nexile
612772	GL0073728_MH0024_[Lack_5'-end]_[mRNA]_locus=scaffold28_3:115:900:-	Roseburia inulinivorans
612896	GL0050137_MH0024_[Complete]_[mRNA]_locus=scaffold217_4:344:757:+	-
613839	GL0031847_MH0024_[Complete]_[mRNA]_locus=scaffold2064_1:33:653:-	Clostridium bolteae
621109	GL0049178_MH0024_[Complete]_[mRNA]_locus=scaffold24888_2:281:1216:+	Ruminococcus obeum
626828	GL0049255_MH0024_[Complete]_[mRNA]_locus=scaffold58629_2:1539:2123:-	Eubacterium siraeum
628167	GL0000116_MH0024_[Complete]_[mRNA]_locus=scaffold67039_1:75:941:-	Dorea formicigenerans

629664	GL0009689_MH0024_[Lack_5'-end]_[mRNA]_locus=scaffold73002_1:2:106:+	-
632006	GL0052923_MH0025_[Complete]_[mRNA]_locus=scaffold635_11:4404:5060:-	Blautia hydrogenotrophica
632007	GL0052924_MH0025_[Complete]_[mRNA]_locus=scaffold635_11:5108:6493:-	Eubacterium ventriosum
632010	GL0148815_MH0025_[Complete]_[mRNA]_locus=scaffold635_12:465:1673:-	-
632398	GL0136493_MH0025_[Complete]_[mRNA]_locus=scaffold1043_1:8026:8616:-	Enterobacteriaceae
632802	GL0089868_MH0025_[Complete]_[mRNA]_locus=scaffold1513_4:1005:2189:-	Bacteroides pectinophilus
634192	GL0083923_MH0025_[Complete]_[mRNA]_locus=scaffold2646_1:404:1078:-	-
634194	GL0083925_MH0025_[Complete]_[mRNA]_locus=scaffold2646_1:1950:2975:-	-
634195	GL0083926_MH0025_[Complete]_[mRNA]_locus=scaffold2646_1:2979:3947:-	Clostridium asparagiforme
634576	GL0066439_MH0025_[Complete]_[mRNA]_locus=scaffold3043_4:41:541:-	Roseburia inulinivorans
635722	GL0063114_MH0025_[Complete]_[mRNA]_locus=scaffold4384_6:742:1983:-	Clostridiales
637011	GL0149559_MH0025_[Complete]_[mRNA]_locus=scaffold5732_2:4457:5572:+	-
637014	GL0077684_MH0025_[Complete]_[mRNA]_locus=scaffold5732_3:2727:3239:+	Ruminococcus lactaris
637016	GL0006211_MH0025_[Complete]_[mRNA]_locus=scaffold5732_8:280:2088:+	-

637017	GL0006212_MH0025_[Complete]_[mRNA]_locus=scaffold5732_8:2331:3185:+	-
637018	GL0006213_MH0025_[Complete]_[mRNA]_locus=scaffold5732_8:3201:4085:+	-
637934	GL0125028_MH0025_[Complete]_[mRNA]_locus=scaffold6583_5:347:601:+	Bacteroides capillosus
638775	GL0085294_MH0025_[Complete]_[mRNA]_locus=scaffold7547_3:830:3148:-	Bacteria
639039	GL0001432_MH0025_[Complete]_[mRNA]_locus=scaffold7831_3:2583:3311:-	-
639040	GL0001436_MH0025_[Complete]_[mRNA]_locus=scaffold7831_3:6420:7175:-	Catenibacterium mitsuokai
639041	GL0001437_MH0025_[Complete]_[mRNA]_locus=scaffold7831_3:7305:7742:+	Blautia hydrogenotrophica
639281	GL0032934_MH0025_[Complete]_[mRNA]_locus=scaffold8217_2:360:1913:-	Bacteroides capillosus
639282	GL0032936_MH0025_[Complete]_[mRNA]_locus=scaffold8217_2:2128:4062:-	Bacteroides capillosus
639283	GL0094229_MH0025_[Complete]_[mRNA]_locus=scaffold8217_4:590:997:-	Bacteroides capillosus
639959	GL0014368_MH0025_[Complete]_[mRNA]_locus=scaffold9224_4:2828:3373:-	Clostridium leptum
640725	GL0140824_MH0025_[Complete]_[mRNA]_locus=scaffold10104_2:3321:3932:-	Ruminococcus gnavus
642047	GL0041354_MH0025_[Complete]_[mRNA]_locus=scaffold11513_1:88:462:+	Roseburia inulinivorans
643470	GL0019050_MH0025_[Complete]_[mRNA]_locus=scaffold13358_1:50:796:-	Roseburia inulinivorans

644056	GL0027629_MH0025_[Complete]_[mRNA]_locus=scaffold14139_3:5949:6917:+	Clostridiales
644686	GL0081491_MH0025_[Complete]_[mRNA]_locus=scaffold14969_1:3771:4376:-	Bacteria
645338	GL0041769_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold15937_6:1:1104:+	Roseburia inulinivorans
647556	GL0053077_MH0025_[Complete]_[mRNA]_locus=scaffold19137_1:155:850:-	Roseburia inulinivorans
648534	GL0115866_MH0025_[Complete]_[mRNA]_locus=scaffold20911_1:119:1051:-	Firmicutes
648660	GL0126113_MH0025_[Complete]_[mRNA]_locus=scaffold21137_1:309:668:+	Clostridium leptum
648661	GL0126115_MH0025_[Complete]_[mRNA]_locus=scaffold21137_1:1127:1570:+	-
652138	GL0030434_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold26403_3:1:174:-	-
652844	GL0071300_MH0025_[Complete]_[mRNA]_locus=scaffold27520_1:5172:5963:+	Firmicutes
653494	GL0147518_MH0025_[Complete]_[mRNA]_locus=scaffold28908_1:12:707:+	Roseburia inulinivorans
654289	GL0153731_MH0025_[Complete]_[mRNA]_locus=scaffold30419_3:575:1000:-	Roseburia inulinivorans
655086	GL0104984_MH0025_[Complete]_[mRNA]_locus=scaffold32045_3:3856:4134:+	Clostridiales
655088	GL0076512_MH0025_[Complete]_[mRNA]_locus=scaffold32045_4:1408:3063:+	Clostridiales
655494	GL0001496_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold32776_5:1:471:+	Roseburia inulinivorans

655985	GL0143298_MH0025_[Complete]_[mRNA]_locus=scaffold33601_2:134:487:-	Roseburia inulinivorans
656072	GL0102978_MH0025_[Complete]_[mRNA]_locus=scaffold33846_2:1576:2226:+	-
656074	GL0102980_MH0025_[Complete]_[mRNA]_locus=scaffold33846_2:2983:3891:-	Clostridium
656075	GL0102981_MH0025_[Complete]_[mRNA]_locus=scaffold33846_2:4212:5504:-	Anaerotruncus colihominis
656076	GL0102982_MH0025_[Complete]_[mRNA]_locus=scaffold33846_2:5940:7469:+	Oenococcus oeni
657494	GL0090186_MH0025_[Complete]_[mRNA]_locus=scaffold36905_1:2616:3398:-	Clostridium nexile
658903	GL0047546_MH0025_[Complete]_[mRNA]_locus=scaffold39889_3:777:3392:-	Clostridium
659737	GL0146907_MH0025_[Complete]_[mRNA]_locus=scaffold41936_2:492:848:+	Ruminococcus obeum
660505	GL0121628_MH0025_[Complete]_[mRNA]_locus=scaffold43819_1:313:759:+	Roseburia inulinivorans
661562	GL0129617_MH0025_[Complete]_[mRNA]_locus=scaffold46285_2:134:757:+	Roseburia inulinivorans
661926	GL0139296_MH0025_[Complete]_[mRNA]_locus=scaffold47057_1:225:788:+	-
662206	GL0139079_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold47731_6:1983:3053:-	Listeria monocytogenes
662398	GL0118556_MH0025_[Complete]_[mRNA]_locus=scaffold48333_1:300:1082:-	Roseburia inulinivorans
662702	GL0075861_MH0025_[Complete]_[mRNA]_locus=scaffold49142_1:1385:2398:-	Ruminococcus gnavus

663582	GL0017517_MH0025_[Lack_both_end]_[mRNA]_locus=scaffold51743_3:2:577:+	Faecalibacterium prausnitzii
664476	GL0113608_MH0025_[Complete]_[mRNA]_locus=scaffold54169_3:301:1401:-	Roseburia inulinivorans
664896	GL0054256_MH0025_[Complete]_[mRNA]_locus=scaffold55488_2:1457:2632:+	Eubacterium hallii
665198	GL0063592_MH0025_[Complete]_[mRNA]_locus=scaffold56276_3:1288:1980:-	-
667189	GL0102271_MH0025_[Complete]_[mRNA]_locus=scaffold61093_1:56:484:+	Bacteroides pectinophilus
667585	GL0038780_MH0025_[Complete]_[mRNA]_locus=scaffold62094_1:586:1086:+	Clostridiales
667707	GL0132884_MH0025_[Complete]_[mRNA]_locus=scaffold62385_2:9255:10679:+	Cylindrospermopsis raciborskii
667797	GL0140199_MH0025_[Complete]_[mRNA]_locus=scaffold62592_2:173:631:+	Roseburia inulinivorans
668145	GL0123405_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold63414_2:2:424:+	Roseburia inulinivorans
668528	GL0022967_MH0025_[Complete]_[mRNA]_locus=scaffold63949_1:11119:12303:+	Clostridiales
668537	GL0047023_MH0025_[Complete]_[mRNA]_locus=scaffold63965_2:2484:3851:-	-
669568	GL0120673_MH0025_[Complete]_[mRNA]_locus=scaffold66618_4:53:556:-	Roseburia inulinivorans
669695	GL0138749_MH0025_[Complete]_[mRNA]_locus=scaffold66941_3:26:658:-	Roseburia inulinivorans
670908	GL0131393_MH0025_[Complete]_[mRNA]_locus=scaffold70299_2:10:321:-	Roseburia inulinivorans

670950	GL0053172_MH0025_[Complete]_[mRNA]_locus=scaffold70418_2:31:726:+	Roseburia inulinivorans
671274	GL0140979_MH0025_[Complete]_[mRNA]_locus=scaffold71331_2:2426:5227:+	Bacteria
671770	GL0035809_MH0025_[Complete]_[mRNA]_locus=scaffold72617_1:284:1798:+	Roseburia inulinivorans
673307	GL0003633_MH0025_[Complete]_[mRNA]_locus=scaffold76181_1:932:1882:-	Ruminococcus obeum
674499	GL0090238_MH0025_[Complete]_[mRNA]_locus=scaffold79400_2:461:1219:-	Roseburia inulinivorans
675410	GL0012632_MH0025_[Complete]_[mRNA]_locus=scaffold81920_2:172:771:-	Coprococcus eutactus
675632	GL0054465_MH0025_[Complete]_[mRNA]_locus=scaffold82626_2:137:478:-	-
676843	GL0140035_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold85651_1:3:1013:-	-
678123	GL0071520_MH0025_[Complete]_[mRNA]_locus=scaffold88829_5:1583:2797:-	Clostridium hylemonae
678905	GL0143589_MH0025_[Complete]_[mRNA]_locus=scaffold90462_1:265:417:-	Roseburia inulinivorans
680229	GL0120953_MH0025_[Complete]_[mRNA]_locus=scaffold93274_4:582:1094:-	Roseburia inulinivorans
682621	GL0112180_MH0025_[Complete]_[mRNA]_locus=scaffold97514_2:1189:1866:+	Clostridium methylpentosum
682650	GL0113556_MH0025_[Complete]_[mRNA]_locus=scaffold97543_7:367:984:+	-
684295	GL0104416_MH0025_[Complete]_[mRNA]_locus=scaffold100373_2:184:369:+	-

684717	GL0080881_MH0025_[Complete]_[mRNA]_locus=scaffold100969_4:110:391:-	Roseburia inulinivorans
684808	GL0139839_MH0025_[Complete]_[mRNA]_locus=scaffold101070_2:2611:3096:-	Clostridium
686172	GL0094207_MH0025_[Complete]_[mRNA]_locus=scaffold102659_2:13:342:-	Roseburia inulinivorans
686431	GL0014855_MH0025_[Complete]_[mRNA]_locus=scaffold102967_1:139:864:+	Roseburia inulinivorans
688140	GL0098837_MH0025_[Complete]_[mRNA]_locus=scaffold104175_1:134:1498:-	Roseburia inulinivorans
692100	GL0102286_MH0025_[Complete]_[mRNA]_locus=C3578712_1:101:406:-	-
692105	GL0151309_MH0025_[Complete]_[mRNA]_locus=C3579096_1:64:531:+	Roseburia inulinivorans
694340	GL0041318_MH0025_[Complete]_[mRNA]_locus=C3641408_1:216:971:+	Roseburia inulinivorans
694615	GL0072533_MH0025_[Complete]_[mRNA]_locus=C3649122_1:98:796:-	Roseburia inulinivorans
695039	GL0094684_MH0025_[Complete]_[mRNA]_locus=C3659080_1:256:1236:+	Roseburia inulinivorans
698466	GL0015364_MH0026_[Lack_3'-end]_[mRNA]_locus=scaffold88_2:521:1057:+	Bacteroides capillosus
698467	GL0018875_MH0026_[Complete]_[mRNA]_locus=scaffold88_6:106:606:+	Bacteroides capillosus
699152	GL0072087_MH0026_[Complete]_[mRNA]_locus=scaffold336_3:3172:4275:+	Roseburia inulinivorans
699405	GL0007718_MH0026_[Complete]_[mRNA]_locus=scaffold432_7:196:1611:-	Bacteria

699429	GL0041582_MH0026_[Lack_5'-end]_[mRNA]_locus=scaffold438_3:769:3135:-	Bacteria
699652	GL0009580_MH0026_[Complete]_[mRNA]_locus=scaffold544_1:6265:7269:-	Dorea formicigenerans
700127	GL0019399_MH0026_[Complete]_[mRNA]_locus=scaffold744_6:115:1599:-	Alkaliphilus oremlandii
700128	GL0019400_MH0026_[Complete]_[mRNA]_locus=scaffold744_6:1986:3209:-	Clostridia
701741	GL0013367_MH0026_[Complete]_[mRNA]_locus=scaffold1272_1:1093:1587:-	Clostridiales
702953	GL0034980_MH0026_[Complete]_[mRNA]_locus=scaffold1677_5:1317:3095:-	-
703062	GL0042499_MH0026_[Complete]_[mRNA]_locus=scaffold1700_6:65:2092:-	Bacteria
704294	GL0060180_MH0026_[Lack_3'-end]_[mRNA]_locus=scaffold2175_8:2930:3433:+	-
704305	GL0052668_MH0026_[Complete]_[mRNA]_locus=scaffold2183_5:649:2136:+	Bacteroides capillosus
705710	GL0082263_MH0026_[Complete]_[mRNA]_locus=scaffold2900_1:2013:3044:+	Clostridium phytofermentans
705768	GL0038587_MH0026_[Complete]_[mRNA]_locus=scaffold2948_3:2098:2592:+	Clostridiales
708304	GL0024119_MH0026_[Complete]_[mRNA]_locus=scaffold4228_8:423:1253:+	Catenibacterium mitsuokai
708448	GL0071730_MH0026_[Complete]_[mRNA]_locus=scaffold4266_9:1211:2812:+	Bacteria
709878	GL0000597_MH0026_[Complete]_[mRNA]_locus=scaffold5148_4:1513:3216:-	Bacteroides capillosus

710708	GL0040041_MH0026_[Complete]_[mRNA]_locus=scaffold5890_7:237:1124:-	Clostridium nexile
711632	GL0044334_MH0026_[Complete]_[mRNA]_locus=scaffold6805_3:1426:1611:-	-
711676	GL0003334_MH0026_[Complete]_[mRNA]_locus=scaffold6860_2:821:1195:-	Eubacterium siraeum
711755	GL0034287_MH0026_[Lack_3'-end]_[mRNA]_locus=scaffold6916_3:756:1229:+	-
713097	GL0009292_MH0026_[Complete]_[mRNA]_locus=scaffold7872_4:54:302:+	Roseburia inulinivorans
713231	GL0055644_MH0026_[Lack_3'-end]_[mRNA]_locus=scaffold8081_2:3:1409:-	Bacteria
713927	GL0007859_MH0026_[Complete]_[mRNA]_locus=scaffold8578_1:785:1177:+	Clostridium asparagiforme
713980	GL0037576_MH0026_[Complete]_[mRNA]_locus=scaffold8640_1:353:1189:-	Roseburia inulinivorans
714648	GL0085140_MH0026_[Complete]_[mRNA]_locus=scaffold9452_1:78:446:+	Roseburia inulinivorans
714649	GL0085141_MH0026_[Complete]_[mRNA]_locus=scaffold9452_1:564:881:-	Roseburia inulinivorans
715367	GL0011083_MH0026_[Lack_5'-end]_[mRNA]_locus=scaffold10253_2:2471:3235:-	Roseburia inulinivorans
716422	GL0051889_MH0026_[Complete]_[mRNA]_locus=scaffold11398_2:2516:3322:-	Acidaminococcus
716451	GL0056567_MH0026_[Complete]_[mRNA]_locus=scaffold11417_1:6303:7091:+	Lachnospiraceae
718063	GL0071819_MH0026_[Complete]_[mRNA]_locus=scaffold12896_5:674:2191:+	Clostridiales

718064	GL0071820_MH0026_[Complete]_[mRNA]_locus=scaffold12896_5:2269:3237:+	Clostridium
718065	GL0071824_MH0026_[Complete]_[mRNA]_locus=scaffold12896_5:7075:8580:+	-
720403	GL0016143_MH0026_[Complete]_[mRNA]_locus=scaffold16499_5:399:1361:+	Bacteroides capillosus
720435	GL0013046_MH0026_[Complete]_[mRNA]_locus=scaffold16573_1:235:486:+	Roseburia inulinivorans
721135	GL0031872_MH0026_[Complete]_[mRNA]_locus=scaffold17799_2:62:1282:-	Clostridium beijerinckii
725241	GL0045070_MH0026_[Lack_both_end]_[mRNA]_locus=scaffold27706_1:1:912:+	Bacteroides capillosus
726073	GL0006862_MH0026_[Complete]_[mRNA]_locus=scaffold30070_2:199:1203:-	-
728458	GL0085632_MH0026_[Complete]_[mRNA]_locus=scaffold41361_1:24:968:+	Faecalibacterium prausnitzii
728926	GL0015271_MH0026_[Lack_5'-end]_[mRNA]_locus=scaffold43391_3:296:604:-	Eubacterium biforme
731249	GL0027758_MH0026_[Complete]_[mRNA]_locus=C3273807_1:241:507:-	Roseburia inulinivorans
731413	GL0078591_MH0026_[Complete]_[mRNA]_locus=C3288769_1:54:410:-	-
732619	GL0008630_MH0027_[Lack_5'-end]_[mRNA]_locus=scaffold18502_2:380:730:-	Bacteroides capillosus
733723	GL0005041_MH0027_[Lack_3'-end]_[mRNA]_locus=C1897670_1:453:677:+	Bacteroides capillosus
734608	GL0071025_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold2197_2:945:1304:-	Clostridiales

735499	GL0116876_MH0028_[Complete]_[mRNA]_locus=scaffold5865_1:325:621:-	-
737494	GL0128400_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold15092_1:654:767:+	-
740478	GL0022549_MH0028_[Complete]_[mRNA]_locus=scaffold33827_3:3380:4945:+	Dorea formicigenerans
741245	GL0031503_MH0028_[Complete]_[mRNA]_locus=scaffold39321_3:267:2195:+	Syntrophomonas wolfei
743592	GL0116683_MH0028_[Lack_both_end]_[mRNA]_locus=scaffold54721_1:2:637:+	Faecalibacterium prausnitzii
748423	GL0095523_MH0028_[Lack_5'-end]_[mRNA]_locus=C2899085_1:40:828:-	Clostridium nexile
752369	GL0036381_MH0030_[Complete]_[mRNA]_locus=scaffold5639_3:7909:9240:+	Bacteria
753109	GL0055900_MH0030_[Complete]_[mRNA]_locus=scaffold7457_1:4057:4749:-	Eubacterium hallii
759811	GL0066073_MH0030_[Complete]_[mRNA]_locus=scaffold25037_3:230:448:-	Roseburia inulinivorans
760938	GL0021283_MH0030_[Lack_5'-end]_[mRNA]_locus=scaffold30219_2:1:1287:+	Roseburia inulinivorans
762126	GL0040777_MH0030_[Lack_both_end]_[mRNA]_locus=scaffold35033_1:3:815:-	Bacteria
762231	GL0041105_MH0030_[Lack_both_end]_[mRNA]_locus=scaffold35395_1:1:561:+	Roseburia inulinivorans
765256	GL0029233_MH0030_[Lack_5'-end]_[mRNA]_locus=scaffold50527_5:3:236:+	Roseburia inulinivorans
766904	GL0029316_MH0030_[Lack_5'-end]_[mRNA]_locus=scaffold58610_1:3:1265:+	Clostridiales

767885	GL0085541_MH0030_[Lack_5'-end]_[mRNA]_locus=scaffold63313_2:45:722:-	Roseburia inulinivorans
772094	GL0077579_MH0030_[Complete]_[mRNA]_locus=C3921301_1:12:476:+	Roseburia inulinivorans
790032	GL0054823_MH0031_[Lack_3'-end]_[mRNA]_locus=scaffold76035_1:1:588:+	-
790356	GL0019770_MH0031_[Complete]_[mRNA]_locus=scaffold77621_1:163:507:-	-
798412	GL0013692_MH0032_[Lack_5'-end]_[mRNA]_locus=scaffold5727_4:1:1014:+	Bacteroides pectinophilus
799110	GL0057629_MH0032_[Lack_5'-end]_[mRNA]_locus=scaffold10094_7:1:723:+	Roseburia inulinivorans
799325	GL0050251_MH0032_[Lack_5'-end]_[mRNA]_locus=scaffold11703_2:142:714:-	Roseburia inulinivorans
799611	GL0032201_MH0032_[Lack_5'-end]_[mRNA]_locus=scaffold13690_9:2:1192:+	Roseburia inulinivorans
799799	GL0073997_MH0032_[Lack_both_end]_[mRNA]_locus=scaffold15473_1:1:1047:+	Roseburia inulinivorans
799909	GL0022380_MH0032_[Lack_5'-end]_[mRNA]_locus=scaffold16430_3:3:899:+	-
800015	GL0051191_MH0032_[Complete]_[mRNA]_locus=scaffold17630_15:2146:2838:+	Eubacterium siraeum
802018	GL0067218_MH0032_[Lack_5'-end]_[mRNA]_locus=scaffold39058_1:2:652:+	Roseburia inulinivorans
804254	GL0066566_MH0032_[Lack_both_end]_[mRNA]_locus=scaffold56462_1:3:1193:-	Roseburia inulinivorans
806570	GL0023716_MH0033_[Lack_5'-end]_[mRNA]_locus=scaffold4518_2:1:165:+	Clostridiales

807499	GL0135202_MH0033_[Complete]_[mRNA]_locus=scaffold8416_1:1084:1959:-	Bacteroides pectinophilus
808066	GL0097976_MH0033_[Lack_3'-end]_[mRNA]_locus=scaffold10529_6:2:946:-	Eubacterium dolichum
808093	GL0108024_MH0033_[Complete]_[mRNA]_locus=scaffold10686_2:2826:3209:-	Lachnospiraceae
811080	GL0055705_MH0033_[Lack_3'-end]_[mRNA]_locus=scaffold25834_1:157:714:+	Roseburia inulinivorans
812094	GL0015226_MH0033_[Lack_3'-end]_[mRNA]_locus=scaffold32004_1:3:776:-	-
817450	GL0130845_MH0033_[Lack_5'-end]_[mRNA]_locus=scaffold72358_2:3:530:+	-
818499	GL0040982_MH0033_[Lack_3'-end]_[mRNA]_locus=scaffold81192_1:414:872:+	Clostridiales
818997	GL0136897_MH0033_[Complete]_[mRNA]_locus=scaffold85357_7:188:2083:+	Roseburia inulinivorans
828563	GL0038978_MH0034_[Lack_5'-end]_[mRNA]_locus=scaffold6769_1:1218:1646:-	Bacteroides capillosus
831425	GL0017409_MH0034_[Lack_5'-end]_[mRNA]_locus=scaffold30491_2:525:923:-	Clostridium
831875	GL0048506_MH0034_[Lack_5'-end]_[mRNA]_locus=scaffold36090_2:2:235:+	Clostridiales
832288	GL0015043_MH0034_[Lack_5'-end]_[mRNA]_locus=scaffold41887_2:3:218:+	Roseburia inulinivorans
838305	GL0017762_MH0035_[Lack_3'-end]_[mRNA]_locus=scaffold19013_2:2:679:+	Clostridium leptum
848354	GL0063171_MH0035_[Complete]_[mRNA]_locus=scaffold85564_1:13:879:-	Clostridiales

850048	GL0087750_MH0035_[Lack_both_end]_[mRNA]_locus=scaffold95450_1:3:644:+	Roseburia inulinivorans
854094	GL0118099_MH0035_[Lack_5'-end]_[mRNA]_locus=C4014319_1:2:523:+	-
855668	GL0106408_MH0035_[Lack_5'-end]_[mRNA]_locus=C4081875_1:1:726:+	-
858388	GL0062828_MH0036_[Lack_3'-end]_[mRNA]_locus=scaffold86_3:400:552:+	-
858494	GL0085446_MH0036_[Lack_3'-end]_[mRNA]_locus=scaffold464_3:148:585:+	Clostridium methylpentosum
861781	GL0112027_MH0036_[Complete]_[mRNA]_locus=scaffold13764_1:24:608:-	Clostridium
863186	GL0012244_MH0036_[Lack_5'-end]_[mRNA]_locus=scaffold22914_1:293:640:-	Bacteria
865213	GL0030556_MH0036_[Complete]_[mRNA]_locus=scaffold37128_3:273:614:+	Clostridium scindens
865401	GL0067982_MH0036_[Lack_3'-end]_[mRNA]_locus=scaffold38465_1:271:510:+	-
869011	GL0090994_MH0036_[Lack_both_end]_[mRNA]_locus=scaffold74849_1:2:823:+	Clostridium
872206	GL0045820_MH0036_[Lack_3'-end]_[mRNA]_locus=C3638607_1:1:690:+	-
873190	GL0056224_MH0037_[Complete]_[mRNA]_locus=scaffold257_5:575:2248:+	Bacteroidetes
873581	GL0031332_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold688_5:2:646:-	Alistipes putredinis
873934	GL0027472_MH0037_[Complete]_[mRNA]_locus=scaffold1265_5:669:1523:+	Clostridiales

874808	GL0069658_MH0037_[Complete]_[mRNA]_locus=scaffold2261_8:3108:4793:+	Clostridiales
874818	GL0043687_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold2279_2:365:682:+	Roseburia inulinivorans
874935	GL0041738_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold2387_11:740:1414:+	Alistipes putredinis
875339	GL0002675_MH0037_[Complete]_[mRNA]_locus=scaffold2921_2:2309:3709:-	Bacteroides
876041	GL0078676_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold3781_7:1:1437:+	Bacteroidales
876047	GL0094521_MH0037_[Complete]_[mRNA]_locus=scaffold3803_5:26:1567:-	Blautia hydrogenotrophica
876947	GL0083546_MH0037_[Complete]_[mRNA]_locus=scaffold5050_24:878:2755:-	Bacteria
877235	GL0003741_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold5669_1:3:776:+	Alistipes putredinis
877432	GL0098056_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold6189_7:3478:4188:+	Alistipes putredinis
878035	GL0056716_MH0037_[Lack_both_end]_[mRNA]_locus=scaffold7354_8:2:3724:-	Clostridiales
878087	GL0076060_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold7455_4:1:1044:+	Eubacterium ventriosum
878248	GL0103116_MH0037_[Complete]_[mRNA]_locus=scaffold7851_9:169:1545:-	Clostridium butyricum
878933	GL0101660_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold9302_1:1:1080:+	Alistipes putredinis
878987	GL0034018_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold9485_2:2:577:+	Clostridiales

879485	GL0051715_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold10994_1:1789:3411:-	Alistipes putredinis
880455	GL0016868_MH0037_[Complete]_[mRNA]_locus=scaffold13395_3:229:1353:+	Alistipes putredinis
881008	GL0070466_MH0037_[Complete]_[mRNA]_locus=scaffold15331_14:1343:3004:+	Alistipes putredinis
881229	GL0059714_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold15890_1:1:1434:+	Bacteroides capillosus
881506	GL0071346_MH0037_[Complete]_[mRNA]_locus=scaffold16566_3:428:1144:+	Alistipes putredinis
881901	GL0056404_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold17973_5:2:475:-	Faecalibacterium prausnitzii
881992	GL0082751_MH0037_[Complete]_[mRNA]_locus=scaffold18273_4:383:1066:-	Alistipes putredinis
883783	GL0002392_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold24606_5:2573:2953:-	Coprococcus eutactus
883784	GL0098514_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold24608_1:388:936:+	Alistipes putredinis
883983	GL0053964_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold25587_3:437:1414:+	Alistipes putredinis
884769	GL0042528_MH0037_[Complete]_[mRNA]_locus=scaffold28841_2:325:1572:+	Alistipes putredinis
885604	GL0039484_MH0037_[Complete]_[mRNA]_locus=scaffold32625_6:310:2505:+	Bacteroides ovatus
885655	GL0036390_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold32931_4:341:1084:+	Alistipes putredinis
885747	GL0081356_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold33335_1:1:636:-	Faecalibacterium prausnitzii

886016	GL0027313_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold34942_7:1:576:+	Roseburia inulinivorans
886388	GL0010560_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold36759_1:137:667:+	Ruminococcus torques
889402	GL0074369_MH0037_[Complete]_[mRNA]_locus=scaffold54267_1:162:1382:+	Bacteroidales
891099	GL0009502_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold65414_1:335:682:+	Faecalibacterium prausnitzii
891704	GL0084253_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold69195_3:1:1086:+	Clostridium
892652	GL0033020_MH0037_[Lack_both_end]_[mRNA]_locus=scaffold74893_1:2:505:-	Clostridiales
894082	GL0000401_MH0037_[Complete]_[mRNA]_locus=scaffold79924_1:69:440:+	Roseburia inulinivorans
895541	GL0041940_MH0038_[Lack_5'-end]_[mRNA]_locus=scaffold1179_6:1:678:+	Roseburia inulinivorans
895864	GL0038557_MH0038_[Complete]_[mRNA]_locus=scaffold2044_2:15:230:+	Clostridiales
898007	GL0094380_MH0038_[Lack_both_end]_[mRNA]_locus=scaffold8873_2:3:1916:-	Bacteria
898203	GL0112683_MH0038_[Lack_5'-end]_[mRNA]_locus=scaffold9522_2:611:1039:-	Eubacterium siraeum
898555	GL0056629_MH0038_[Lack_3'-end]_[mRNA]_locus=scaffold10722_2:1:450:-	Firmicutes
899208	GL0112960_MH0038_[Lack_both_end]_[mRNA]_locus=scaffold12914_1:1:1113:+	Clostridiales
899209	GL0077985_MH0038_[Lack_5'-end]_[mRNA]_locus=scaffold12914_3:3:839:+	Clostridiales

912713	GL0095438_MH0039_[Lack_5'-end]_[mRNA]_locus=scaffold8521_2:1:1095:+	Roseburia inulinivorans
912714	GL0027794_MH0039_[Lack_3'-end]_[mRNA]_locus=scaffold8521_3:2:112:-	-
913568	GL0139492_MH0039_[Complete]_[mRNA]_locus=scaffold13006_1:154:612:+	Bacteroides capillosus
913931	GL0065084_MH0039_[Lack_3'-end]_[mRNA]_locus=scaffold14830_4:1:1515:-	Roseburia inulinivorans
915103	GL0043519_MH0039_[Lack_3'-end]_[mRNA]_locus=scaffold23013_3:658:3126:+	Bacteria
917361	GL0069341_MH0039_[Complete]_[mRNA]_locus=scaffold40235_2:2:2368:+	Bacteria
918706	GL0015773_MH0039_[Lack_3'-end]_[mRNA]_locus=scaffold54520_2:1673:2917:+	Bacteroides capillosus
919042	GL0051877_MH0039_[Lack_5'-end]_[mRNA]_locus=scaffold57435_4:2:556:+	Roseburia inulinivorans
919662	GL0020140_MH0039_[Lack_3'-end]_[mRNA]_locus=scaffold63422_1:3:542:-	Roseburia inulinivorans
920808	GL0071912_MH0039_[Lack_5'-end]_[mRNA]_locus=scaffold75524_6:3:524:+	Roseburia inulinivorans
924683	GL0022290_MH0040_[Lack_3'-end]_[mRNA]_locus=scaffold2363_1:536:1564:+	Alistipes putredinis
925302	GL0113872_MH0040_[Complete]_[mRNA]_locus=scaffold3697_11:22:906:-	Bacteroides
926135	GL0147760_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold5852_1:2:721:-	Bacteroidetes
927782	GL0080356_MH0040_[Lack_5'-end]_[mRNA]_locus=scaffold9681_3:1033:1515:-	Clostridiales

929590	GL0140422_MH0040_[Lack_5'-end]_[mRNA]_locus=scaffold14812_4:776:1900:-	Bacteroides ovatus
931497	GL0137820_MH0040_[Complete]_[mRNA]_locus=scaffold20694_2:5522:8371:-	Bacteroides
934622	GL0029693_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold32681_1:1:1392:-	Alistipes putredinis
936570	GL0139417_MH0040_[Lack_5'-end]_[mRNA]_locus=scaffold39646_1:9:686:-	Clostridium butyricum
942015	GL0101773_MH0040_[Lack_5'-end]_[mRNA]_locus=scaffold66701_1:3:503:+	Roseburia inulinivorans
943696	GL0095781_MH0040_[Lack_3'-end]_[mRNA]_locus=scaffold74170_2:62:862:+	Alistipes putredinis
950376	GL0051806_MH0040_[Lack_3'-end]_[mRNA]_locus=scaffold103482_1:1125:1721:+	Alistipes putredinis
954027	GL0011057_MH0041_[Complete]_[mRNA]_locus=scaffold557_4:315:1040:-	Ruminococcus obeum
954560	GL0077379_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold2034_1:1:1113:+	Bacteroides capillosus
954686	GL0046563_MH0041_[Complete]_[mRNA]_locus=scaffold2269_1:2658:4061:-	Clostridiales
955691	GL0034675_MH0041_[Complete]_[mRNA]_locus=scaffold6284_6:3270:5219:-	Bacteroides capillosus
957019	GL0047058_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold13262_1:13:504:+	Roseburia inulinivorans
957164	GL0015775_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold14469_2:218:517:+	Ruminococcus lactaris

957546	GL0033350_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold16542_12:9173:10030:-	Clostridium leptum
957986	GL0022812_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold19722_2:3:851:+	Clostridium bolteae
958645	GL0017108_MH0041_[Complete]_[mRNA]_locus=scaffold24554_2:210:1184:-	Ruminococcus obeum
958734	GL0023698_MH0041_[Complete]_[mRNA]_locus=scaffold25429_1:538:1509:-	Bacteroides capillosus
958769	GL0002462_MH0041_[Complete]_[mRNA]_locus=scaffold25684_2:218:1411:-	Ruminococcus obeum
959297	GL0010001_MH0041_[Lack_both_end]_[mRNA]_locus=scaffold30746_1:3:1040:+	Bacteroides capillosus
959459	GL0101497_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold32020_6:1:795:-	Clostridium botulinum
959460	GL0110163_MH0041_[Complete]_[mRNA]_locus=scaffold32020_9:46:861:-	Blautia hydrogenotrophica
959691	GL0023971_MH0041_[Lack_both_end]_[mRNA]_locus=scaffold34676_7:1:657:-	Ruminococcus obeum
959731	GL0086728_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold35173_1:3:443:+	Ruminococcus obeum
961146	GL0034158_MH0041_[Complete]_[mRNA]_locus=scaffold50101_1:2080:2280:+	-
961286	GL0055219_MH0041_[Complete]_[mRNA]_locus=scaffold52017_11:33:962:+	Ruminococcus obeum
961426	GL0063143_MH0041_[Complete]_[mRNA]_locus=scaffold53692_2:120:1148:+	Ruminococcus obeum

961775	GL0046379_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold58294_2:2:148:+	-
962098	GL0085045_MH0041_[Complete]_[mRNA]_locus=scaffold61879_1:1421:3472:+	Clostridiales
962146	GL0023713_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold62300_1:120:671:-	Roseburia inulinivorans
962351	GL0027738_MH0041_[Complete]_[mRNA]_locus=scaffold65113_1:86:544:-	Ruminococcus obeum
962847	GL0122010_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold72053_1:3:791:-	Clostridiales
963526	GL0117250_MH0041_[Complete]_[mRNA]_locus=scaffold79130_1:588:1040:-	Clostridium thermocellum
964126	GL0110297_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold83655_1:1:672:+	Faecalibacterium prausnitzii
964505	GL0047029_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold85766_3:1:1332:-	Clostridiales
964506	GL0094997_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold85766_4:2:772:+	Clostridium nexile
968373	GL0043645_MH0042_[Lack_5'-end]_[mRNA]_locus=scaffold11718_3:2:847:+	Clostridiales
969032	GL0036684_MH0042_[Complete]_[mRNA]_locus=scaffold16496_1:774:995:-	Finegoldia magna
970602	GL0018387_MH0042_[Complete]_[mRNA]_locus=scaffold31762_1:1604:2182:-	Coprococcus eutactus
970729	GL0112658_MH0042_[Lack_3'-end]_[mRNA]_locus=scaffold33309_7:478:633:+	Catenibacterium mitsuokai
972911	GL0047578_MH0042_[Lack_both_end]_[mRNA]_locus=scaffold69953_1:1:549:-	Clostridium leptum

977138	GL0144488_MH0043_[Lack_5'-end]_[mRNA]_locus=scaffold1683_2:3:1496:+	Firmicutes
984746	GL0149270_MH0043_[Lack_5'-end]_[mRNA]_locus=scaffold43590_1:3:182:+	-
985997	GL0013104_MH0043_[Complete]_[mRNA]_locus=scaffold52772_2:400:798:-	Alistipes putredinis
986730	GL0048431_MH0043_[Lack_5'-end]_[mRNA]_locus=scaffold57787_1:286:603:-	-
989549	GL0151684_MH0043_[Complete]_[mRNA]_locus=scaffold76695_1:84:737:+	Bacteroides capillosus
1002420	GL0078992_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold74_12:562:2202:-	Clostridiales
1002642	GL0060144_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold607_2:1:507:+	Bacteroides pectinophilus
1002665	GL0097331_MH0044_[Complete]_[mRNA]_locus=scaffold704_1:222:971:-	Roseburia inulinivorans
1003078	GL0051970_MH0044_[Complete]_[mRNA]_locus=scaffold1968_1:923:2407:+	Clostridiales
1003164	GL0085954_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold2237_7:3:1001:+	Roseburia inulinivorans
1003183	GL0067464_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold2315_14:2444:3343:-	Roseburia inulinivorans
1003236	GL0116392_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold2458_1:438:1094:+	Faecalibacterium prausnitzii
1003430	GL0021025_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold3225_1:7993:8643:-	Roseburia inulinivorans
1004106	GL0018023_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold5323_2:2:535:+	Faecalibacterium prausnitzii

1004398	GL0085398_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold6764_7:82:1104:+	Roseburia inulinivorans
1004531	GL0022759_MH0044_[Complete]_[mRNA]_locus=scaffold7395_3:130:1326:+	Roseburia inulinivorans
1004532	GL0022760_MH0044_[Complete]_[mRNA]_locus=scaffold7395_3:1488:2717:+	Roseburia inulinivorans
1005421	GL0012788_MH0044_[Lack_both_end]_[mRNA]_locus=scaffold11272_3:3:917:+	Ruminococcus lactaris
1005529	GL0108744_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold11737_1:103:1572:+	Clostridiales
1005715	GL0063169_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold12343_20:1:360:-	Roseburia inulinivorans
1006600	GL0070412_MH0044_[Complete]_[mRNA]_locus=scaffold16571_2:2531:4180:-	Roseburia inulinivorans
1006601	GL0097135_MH0044_[Complete]_[mRNA]_locus=scaffold16571_4:1084:2511:-	Roseburia inulinivorans
1007464	GL0024052_MH0044_[Complete]_[mRNA]_locus=scaffold23211_1:579:728:-	Clostridiales
1007624	GL0111629_MH0044_[Complete]_[mRNA]_locus=scaffold24409_1:3222:5255:-	Roseburia inulinivorans
1008758	GL0023501_MH0044_[Complete]_[mRNA]_locus=scaffold34565_1:69:278:-	-
1014092	GL0001717_MH0044_[Lack_both_end]_[mRNA]_locus=scaffold76883_1:2:2008:+	Clostridium
1016053	GL0066458_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold1066_2:3302:4042:-	-
1016276	GL0130448_MH0045_[Complete]_[mRNA]_locus=scaffold2206_3:2435:4552:-	Bacteria

1019526	GL0114312_MH0045_[Complete]_[mRNA]_locus=scaffold16535_4:2300:3619:-	Roseburia inulinivorans
1019626	GL0053619_MH0045_[Complete]_[mRNA]_locus=scaffold17041_10:411:1751:-	Clostridiales
1019709	GL0015975_MH0045_[Complete]_[mRNA]_locus=scaffold17347_9:2588:3868:+	Roseburia inulinivorans
1019757	GL0080257_MH0045_[Complete]_[mRNA]_locus=scaffold17777_1:607:1017:-	-
1020458	GL0104916_MH0045_[Complete]_[mRNA]_locus=scaffold22380_1:93:1505:+	Roseburia inulinivorans
1020460	GL0018206_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold22380_3:4348:5880:-	Firmicutes
1020923	GL0103468_MH0045_[Lack_3'-end]_[mRNA]_locus=scaffold25332_3:1170:1808:+	Bacteroides capillosus
1021504	GL0086370_MH0045_[Complete]_[mRNA]_locus=scaffold28936_5:3:1751:+	Clostridium hylemonae
1021521	GL0104415_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold29283_1:1:909:+	Clostridium
1021902	GL0085870_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold32629_6:2:637:+	Anaerotruncus colihominis
1022160	GL0042762_MH0045_[Complete]_[mRNA]_locus=scaffold34466_1:3772:5091:+	Roseburia inulinivorans
1023330	GL0028277_MH0045_[Complete]_[mRNA]_locus=scaffold45345_2:7040:8425:-	Clostridium
1023791	GL0039792_MH0045_[Complete]_[mRNA]_locus=scaffold49946_1:639:965:+	Bacteroides capillosus
1027385	GL0011166_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold82361_1:1:1176:+	Bacteria

1037350	GL0100762_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold17343_4:1:651:-	-
1039358	GL0029210_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold25554_2:3:1064:-	Clostridium methylpentosum
1039452	GL0052109_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold26172_3:131:682:-	Bacteria
1041140	GL0100647_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold36451_1:21:1256:+	Clostridium thermocellum
1043216	GL0061229_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold51001_1:2:580:-	Bacteroides capillosus
1043285	GL0017420_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold51416_1:1:678:+	Coprococcus eutactus
1044556	GL0075417_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold60911_2:489:656:-	-
1045655	GL0043965_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold69464_1:2:889:-	-
1046276	GL0092163_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold74207_1:1:615:+	Bacteria
1046478	GL0099487_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold75557_1:161:535:+	Catenibacterium mitsuokai
1047083	GL0045521_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold79784_3:2:757:+	Bacteroides capillosus
1051998	GL0045610_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold899_1:13853:14155:-	Ruminococcus gnavus
1053356	GL0042206_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold6357_2:3182:4153:-	Ruminococcus gnavus
1053955	GL0058901_MH0047_[Complete]_[mRNA]_locus=scaffold8928_1:4740:5360:+	Ruminococcus gnavus

1056919	GL0014010_MH0047_[Lack_3'-end]_[mRNA]_locus=scaffold22069_1:3:698:-	Ruminococcus gnavus
1057176	GL0029714_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold23031_3:1:270:+	Ruminococcus gnavus
1057366	GL0025285_MH0047_[Complete]_[mRNA]_locus=scaffold23806_5:2286:3674:-	Clostridiales
1057500	GL0039566_MH0047_[Complete]_[mRNA]_locus=scaffold24326_3:1579:6843:-	Bacteria
1057569	GL0039012_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold24687_2:2:226:+	Ruminococcus gnavus
1057570	GL0039019_MH0047_[Complete]_[mRNA]_locus=scaffold24687_2:7146:8180:+	Ruminococcus gnavus
1057886	GL0024969_MH0047_[Lack_3'-end]_[mRNA]_locus=scaffold25953_2:3:410:-	Clostridium ramosum
1058053	GL0053126_MH0047_[Complete]_[mRNA]_locus=scaffold26710_2:5618:5914:-	Ruminococcus gnavus
1058302	GL0043114_MH0047_[Complete]_[mRNA]_locus=scaffold27675_1:159:668:-	-
1058391	GL0027820_MH0047_[Lack_both_end]_[mRNA]_locus=scaffold28002_1:2:595:+	Clostridium thermocellum
1060487	GL0037116_MH0047_[Lack_3'-end]_[mRNA]_locus=scaffold35317_1:3:524:-	Faecalibacterium prausnitzii
1060671	GL0020581_MH0047_[Complete]_[mRNA]_locus=scaffold35791_2:12558:13397:-	Ruminococcus gnavus
1062297	GL0050630_MH0047_[Complete]_[mRNA]_locus=scaffold40469_1:25:1032:-	Ruminococcus gnavus
1063811	GL0000329_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold43577_1:2:115:+	Ruminococcus gnavus

1064204	GL0062446_MH0047_[Lack_3'-end]_[mRNA]_locus=scaffold44212_1:1279:2019:+	Ruminococcus gnavus
1064568	GL0027408_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold44730_1:1904:2602:-	Ruminococcus gnavus
1064617	GL0048074_MH0047_[Complete]_[mRNA]_locus=scaffold44818_1:397:2505:-	Ruminococcus
1065327	GL0051998_MH0047_[Complete]_[mRNA]_locus=scaffold45533_1:4049:6094:-	Clostridiales
1065628	GL0034904_MH0047_[Lack_5'-end]_[mRNA]_locus=scaffold45767_1:7408:7686:-	Ruminococcus gnavus
1073539	GL0043230_MH0048_[Lack_5'-end]_[mRNA]_locus=scaffold3519_1:2:166:+	-
1075094	GL0053706_MH0048_[Lack_5'-end]_[mRNA]_locus=scaffold23467_1:147:533:-	Clostridiales
1075287	GL0065688_MH0048_[Lack_3'-end]_[mRNA]_locus=scaffold25459_1:96:572:+	Holdemania filiformis
1076737	GL0039425_MH0048_[Complete]_[mRNA]_locus=scaffold40794_1:3342:3929:-	Clostridium asparagiforme
1079274	GL0001145_MH0048_[Lack_both_end]_[mRNA]_locus=scaffold61849_1:3:551:-	-
1084600	GL0016538_MH0049_[Lack_3'-end]_[mRNA]_locus=scaffold607_1:164:754:+	Roseburia inulinivorans
1085452	GL0061501_MH0049_[Lack_3'-end]_[mRNA]_locus=scaffold5286_1:10:570:+	Candidatus Desulforudis audaxviator
1086639	GL0012917_MH0049_[Lack_5'-end]_[mRNA]_locus=scaffold15800_1:38:724:-	Roseburia inulinivorans

1087109	GL0056710_MH0049_[Lack_3'-end]_[mRNA]_locus=scaffold21249_1:212:1087:+	Roseburia inulinivorans
1087231	GL0049857_MH0049_[Lack_5'-end]_[mRNA]_locus=scaffold22848_3:353:838:-	Roseburia inulinivorans
1087665	GL0052176_MH0049_[Lack_5'-end]_[mRNA]_locus=scaffold27879_2:5:622:-	Roseburia inulinivorans
1090992	GL0115306_MH0050_[Lack_5'-end]_[mRNA]_locus=scaffold2842_2:2:187:+	-
1102933	GL0056513_MH0050_[Lack_5'-end]_[mRNA]_locus=scaffold66013_1:489:680:-	-
1106423	GL0056893_MH0050_[Lack_both_end]_[mRNA]_locus=scaffold88181_3:1:615:+	-
1117288	GL0054288_MH0051_[Lack_5'-end]_[mRNA]_locus=scaffold35293_1:38:559:-	Roseburia inulinivorans
1117846	GL0022802_MH0051_[Lack_both_end]_[mRNA]_locus=scaffold41194_1:3:515:+	Roseburia inulinivorans
1119473	GL0063414_MH0051_[Lack_3'-end]_[mRNA]_locus=scaffold53250_1:92:562:+	-
1120089	GL0057175_MH0051_[Complete]_[mRNA]_locus=scaffold56635_1:196:774:-	Bacteroides ovatus
1125582	GL0093615_MH0052_[Lack_5'-end]_[mRNA]_locus=scaffold4783_2:2:343:+	Clostridium nexile
1129281	GL0060555_MH0052_[Complete]_[mRNA]_locus=scaffold32807_3:2:1600:+	Bacteria
1138305	GL0094918_MH0052_[Lack_5'-end]_[mRNA]_locus=C2507727_1:3:467:+	Holdemania filiformis
1141534	GL0026910_MH0052_[Lack_3'-end]_[mRNA]_locus=C2575563_1:2:880:-	Roseburia inulinivorans

1151405	GL0090820_MH0053_[Lack_both_end]_[mRNA]_locus=scaffold15105_1:1:579:+	Roseburia inulinivorans
1154427	GL0115246_MH0053_[Lack_both_end]_[mRNA]_locus=scaffold23618_1:2:502:-	Faecalibacterium prausnitzii
1179023	GL0132509_MH0054_[Complete]_[mRNA]_locus=scaffold2158_1:1753:1920:+	Bacteria
1179369	GL0128132_MH0054_[Complete]_[mRNA]_locus=scaffold2982_1:568:1344:-	-
1179624	GL0021157_MH0054_[Lack_both_end]_[mRNA]_locus=scaffold3617_3:3:1235:+	Bacteria
1180329	GL0066104_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold5633_9:161:703:-	-
1182015	GL0072237_MH0054_[Lack_both_end]_[mRNA]_locus=scaffold10779_1:3:533:-	Coprococcus eutactus
1182402	GL0079693_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold12438_3:3:605:+	Bacteroides pectinophilus
1182757	GL0096613_MH0054_[Lack_both_end]_[mRNA]_locus=scaffold13947_3:2:1585:+	Bacteria
1183960	GL0054893_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold19145_2:801:3338:+	Bacteroides capillosus
1185547	GL0017063_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold26555_1:3:1022:-	-
1185568	GL0038960_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold26739_1:3:374:+	Clostridiales
1186214	GL0107115_MH0054_[Complete]_[mRNA]_locus=scaffold31362_1:879:1556:+	Clostridium spiroforme
1186707	GL0023496_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold34482_3:545:1435:+	Clostridiales

1187597	GL0021999_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold40018_5:287:703:-	Roseburia inulinivorans
1189138	GL0128654_MH0054_[Complete]_[mRNA]_locus=scaffold50874_1:12:947:-	-
1192021	GL0097318_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold71056_2:1:792:-	Ruminococcus obeum
1198525	GL0073676_MH0055_[Lack_3'-end]_[mRNA]_locus=scaffold660_4:143:922:+	Roseburia inulinivorans
1198526	GL0130848_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold661_4:1:729:+	Clostridium
1205589	GL0062981_MH0055_[Complete]_[mRNA]_locus=scaffold8888_7:254:1417:-	Clostridiales
1209518	GL0039489_MH0055_[Lack_3'-end]_[mRNA]_locus=scaffold16025_8:379:609:+	-
1213127	GL0053764_MH0055_[Lack_both_end]_[mRNA]_locus=scaffold24051_2:2:946:+	Ruminococcus obeum
1217705	GL0083559_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold39296_3:405:959:-	Roseburia inulinivorans
1217909	GL0083727_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold39954_1:3:389:+	Roseburia inulinivorans
1218372	GL0137675_MH0055_[Lack_both_end]_[mRNA]_locus=scaffold41784_1:2:697:+	Roseburia inulinivorans
1220231	GL0104557_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold49061_4:52:501:-	Roseburia inulinivorans
1220505	GL0022235_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold50515_2:2:121:+	-
1223066	GL0049954_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold61868_2:290:748:-	Roseburia inulinivorans

1224601	GL0095735_MH0055_[Lack_3'-end]_[mRNA]_locus=scaffold69045_3:319:651:+	-
1228766	GL0098020_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold82712_2:2:889:+	Roseburia inulinivorans
1233768	GL0098279_MH0056_[Lack_5'-end]_[mRNA]_locus=scaffold8505_1:365:1066:-	-
1246220	GL0065546_MH0056_[Complete]_[mRNA]_locus=scaffold112517_1:344:538:-	-
1252381	GL0057259_MH0057_[Lack_both_end]_[mRNA]_locus=scaffold1778_6:2:592:+	Faecalibacterium prausnitzii
1253341	GL0052586_MH0057_[Complete]_[mRNA]_locus=scaffold3284_1:244:1059:+	Collinsella aerofaciens
1254389	GL0031861_MH0057_[Complete]_[mRNA]_locus=scaffold4766_3:30:371:+	-
1254390	GL0031862_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold4766_3:373:735:+	Clostridiales
1254391	GL0088981_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold4766_4:2893:3507:+	-
1254534	GL0038166_MH0057_[Complete]_[mRNA]_locus=scaffold5123_5:362:535:-	Clostridium methylpentosum
1254535	GL0038167_MH0057_[Complete]_[mRNA]_locus=scaffold5123_5:546:1124:-	-
1254536	GL0038168_MH0057_[Complete]_[mRNA]_locus=scaffold5123_5:1134:2090:-	-
1254537	GL0025501_MH0057_[Complete]_[mRNA]_locus=scaffold5123_6:38:388:-	-
1254538	GL0025502_MH0057_[Complete]_[mRNA]_locus=scaffold5123_6:378:563:-	Bacteroides capillosus

1254540	GL0010404_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold5123_9:2:943:-	Clostridiales
1254619	GL0054000_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold5360_1:3:176:-	Faecalibacterium prausnitzii
1254767	GL0027518_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold5774_3:2:982:-	Bacteroides capillosus
1254768	GL0027520_MH0057_[Complete]_[mRNA]_locus=scaffold5774_3:1286:1798:-	Roseburia inulinivorans
1254770	GL0027522_MH0057_[Complete]_[mRNA]_locus=scaffold5774_3:2641:3507:-	Clostridium methylpentosum
1255182	GL0066219_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold6649_1:1:939:-	Atopobium rimae
1257515	GL0064897_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold15214_2:2787:2972:-	Roseburia inulinivorans
1258540	GL0000573_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold22435_1:3:449:-	-
1258909	GL0047278_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold26424_8:477:1430:+	Clostridium asparagiforme
1261254	GL0056352_MH0057_[Lack_both_end]_[mRNA]_locus=C3644200_1:3:551:-	Ruminococcus obeum
1262425	GL0035010_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold5529_2:1:762:-	Faecalibacterium prausnitzii
1264201	GL0136858_MH0058_[Complete]_[mRNA]_locus=scaffold18039_2:2024:3136:+	Roseburia inulinivorans
1267964	GL0132562_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold51741_1:671:1486:-	Roseburia inulinivorans
1274404	GL0043862_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold110467_1:109:513:-	-

1275691	GL0013031_MH0058_[Lack_5'-end]_[mRNA]_locus=C4099335_1:131:634:-	-
1286859	GL0161652_MH0059_[Lack_5'-end]_[mRNA]_locus=scaffold39868_1:1438:2091:-	Alkaliphilus oremlandii
1288224	GL0117452_MH0059_[Lack_5'-end]_[mRNA]_locus=scaffold49771_5:360:701:-	-
1290636	GL0108304_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold67017_1:286:948:+	Faecalibacterium prausnitzii
1291168	GL0105998_MH0059_[Lack_5'-end]_[mRNA]_locus=scaffold70977_2:160:567:-	-
1293440	GL0032369_MH0059_[Lack_both_end]_[mRNA]_locus=scaffold85616_1:3:587:-	Ruminococcus obeum
1294461	GL0018450_MH0059_[Lack_5'-end]_[mRNA]_locus=scaffold89840_1:183:617:-	Roseburia inulinivorans
1300077	GL0014922_MH0060_[Complete]_[mRNA]_locus=scaffold4327_3:398:1579:-	Eubacterium ventriosum
1306486	GL0074741_MH0060_[Complete]_[mRNA]_locus=scaffold28587_2:12:509:+	Eubacterium siraeum
1312056	GL0044962_MH0060_[Complete]_[mRNA]_locus=scaffold63462_1:56:208:-	Clostridium
1315295	GL0091119_MH0060_[Lack_3'-end]_[mRNA]_locus=scaffold88684_1:1:114:-	-
1315296	GL0091120_MH0060_[Complete]_[mRNA]_locus=scaffold88684_1:152:337:+	-
1318833	GL0120693_MH0060_[Lack_5'-end]_[mRNA]_locus=scaffold108845_2:409:531:-	-
1321749	GL0071835_MH0061_[Complete]_[mRNA]_locus=scaffold280_2:1419:3734:-	Bacteria

1321953	GL0033372_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold461_1:315:1424:-	Bacteria
1322947	GL0021403_MH0061_[Complete]_[mRNA]_locus=scaffold1938_2:3211:5673:-	Clostridiales
1322948	GL0057700_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold1938_5:969:1559:-	Roseburia inulinivorans
1322949	GL0020417_MH0061_[Lack_3'-end]_[mRNA]_locus=scaffold1938_6:1:963:-	Roseburia inulinivorans
1322950	GL0088070_MH0061_[Lack_3'-end]_[mRNA]_locus=scaffold1938_8:1:1035:-	Roseburia inulinivorans
1322951	GL0021073_MH0061_[Lack_3'-end]_[mRNA]_locus=scaffold1938_10:1:669:-	Roseburia inulinivorans
1323227	GL0021246_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold2446_2:544:2037:-	Bacteria
1323658	GL0057544_MH0061_[Complete]_[mRNA]_locus=scaffold3074_3:516:1505:-	Roseburia inulinivorans
1323877	GL0045544_MH0061_[Lack_both_end]_[mRNA]_locus=scaffold3456_5:3:533:-	Bacteroides capillosus
1324026	GL0058873_MH0061_[Complete]_[mRNA]_locus=scaffold3702_2:837:2789:-	Clostridiales
1324027	GL0058874_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold3702_2:2880:3095:-	-
1324162	GL0066579_MH0061_[Lack_3'-end]_[mRNA]_locus=scaffold3984_1:3:344:-	Faecalibacterium prausnitzii
1326231	GL0029958_MH0061_[Complete]_[mRNA]_locus=scaffold8417_7:7290:8645:+	Clostridiales
1326309	GL0088687_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold8680_1:57:857:-	Anaerotruncus colihominis

1326419	GL0080272_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold8974_2:1:555:+	Clostridium
1326502	GL0016655_MH0061_[Complete]_[mRNA]_locus=scaffold9201_3:109:2427:-	Bacteria
1327441	GL0091581_MH0061_[Lack_3'-end]_[mRNA]_locus=scaffold12183_4:1:798:-	Clostridium methylpentosum
1327849	GL0042873_MH0061_[Complete]_[mRNA]_locus=scaffold13469_1:122:388:-	Finegoldia magna
1330011	GL0033916_MH0061_[Complete]_[mRNA]_locus=scaffold22050_1:3181:4026:+	Roseburia inulinivorans
1330136	GL0009520_MH0061_[Lack_both_end]_[mRNA]_locus=scaffold22695_1:3:563:-	-
1330544	GL0003647_MH0061_[Lack_3'-end]_[mRNA]_locus=scaffold24406_1:280:957:+	Eubacterium siraeum
1336282	GL0024805_MH0061_[Complete]_[mRNA]_locus=scaffold48178_1:406:663:-	Roseburia inulinivorans
1337744	GL0096310_MH0062_[Lack_3'-end]_[mRNA]_locus=scaffold190_1:1492:2169:+	Bacteroidales
1337897	GL0009294_MH0062_[Complete]_[mRNA]_locus=scaffold777_1:737:1882:-	Thermosinus carboxydivorans
1337898	GL0009296_MH0062_[Complete]_[mRNA]_locus=scaffold777_1:2500:4335:-	Alistipes putredinis
1338088	GL0011017_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold1304_7:261:2507:-	Bacteroides
1338511	GL0032252_MH0062_[Complete]_[mRNA]_locus=scaffold2265_2:1702:3111:+	Alistipes putredinis
1338562	GL0123209_MH0062_[Lack_both_end]_[mRNA]_locus=scaffold2332_1:3:1982:-	Bacteroidales

1338742	GL0054374_MH0062_[Complete]_[mRNA]_locus=scaffold2800_2:233:763:+	Alistipes putredinis
1338874	GL0012326_MH0062_[Lack_3'-end]_[mRNA]_locus=scaffold3221_2:3:2054:-	Methanosarcina acetivorans
1338971	GL0080855_MH0062_[Complete]_[mRNA]_locus=scaffold3592_1:52:1464:-	Bacteroides ovatus
1339011	GL0021101_MH0062_[Complete]_[mRNA]_locus=scaffold3722_7:2947:3615:+	Alistipes putredinis
1339056	GL0108331_MH0062_[Complete]_[mRNA]_locus=scaffold3799_13:916:3705:+	Bacteroides cellulosilyticus
1339200	GL0025151_MH0062_[Complete]_[mRNA]_locus=scaffold4255_1:769:2748:-	Bacteroides ovatus
1339293	GL0119228_MH0062_[Complete]_[mRNA]_locus=scaffold4509_3:587:2497:+	Alistipes putredinis
1339575	GL0121267_MH0062_[Complete]_[mRNA]_locus=scaffold5388_3:606:1403:-	Bacteroidales
1339789	GL0079493_MH0062_[Complete]_[mRNA]_locus=scaffold6133_2:1660:2082:+	-
1339828	GL0044156_MH0062_[Lack_3'-end]_[mRNA]_locus=scaffold6209_2:2491:5211:+	Ornithorhynchus
1340590	GL0063053_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold8835_5:2:1942:+	Bacteroides coprocola
1340647	GL0012112_MH0062_[Complete]_[mRNA]_locus=scaffold9033_1:2735:3748:+	Alistipes putredinis
1340709	GL0114944_MH0062_[Complete]_[mRNA]_locus=scaffold9282_6:772:1767:-	Alistipes putredinis
1340736	GL0032129_MH0062_[Complete]_[mRNA]_locus=scaffold9402_7:1754:2494:+	Parabacteroides johnsonii

1340808	GL0005602_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold9668_1:1410:3785:-	Bacteria
1340891	GL0111358_MH0062_[Lack_both_end]_[mRNA]_locus=scaffold9935_3:3:2081:-	Bacteroidales
1341195	GL0068555_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold10968_4:1260:2315:-	Parabacteroides merdae
1341570	GL0107100_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold12290_2:1:399:+	Roseburia inulinivorans
1341703	GL0075711_MH0062_[Complete]_[mRNA]_locus=scaffold12752_4:1613:3271:-	Alistipes putredinis
1341704	GL0071055_MH0062_[Complete]_[mRNA]_locus=scaffold12752_8:982:2022:-	Alistipes putredinis
1341774	GL0109030_MH0062_[Lack_3'-end]_[mRNA]_locus=scaffold13045_2:2:1369:-	Alistipes putredinis
1341783	GL0075122_MH0062_[Complete]_[mRNA]_locus=scaffold13098_1:104:874:-	Alistipes putredinis
1341954	GL0072165_MH0062_[Lack_both_end]_[mRNA]_locus=scaffold13790_3:3:3248:-	Clostridiales
1342216	GL0012586_MH0062_[Complete]_[mRNA]_locus=scaffold14851_3:77:994:-	Alistipes putredinis
1342236	GL0094213_MH0062_[Complete]_[mRNA]_locus=scaffold14927_6:4770:7847:+	Bacteroides cellulosilyticus
1342280	GL0055292_MH0062_[Complete]_[mRNA]_locus=scaffold15207_1:340:843:+	-
1342532	GL0064892_MH0062_[Complete]_[mRNA]_locus=scaffold16281_1:314:1003:+	Alistipes putredinis
1342732	GL0037762_MH0062_[Complete]_[mRNA]_locus=scaffold16839_10:3450:4022:-	Alistipes putredinis

1342861	GL0090504_MH0062_[Complete]_[mRNA]_locus=scaffold17538_1:64:996:-	Alistipes putredinis
1343013	GL0107485_MH0062_[Complete]_[mRNA]_locus=scaffold18346_2:170:1156:-	Alistipes putredinis
1343084	GL0055846_MH0062_[Complete]_[mRNA]_locus=scaffold18851_13:20:2221:-	Bacteroidales
1343921	GL0102215_MH0062_[Complete]_[mRNA]_locus=scaffold22937_3:1483:2541:+	Alistipes putredinis
1344563	GL0026836_MH0062_[Complete]_[mRNA]_locus=scaffold26107_1:383:1981:-	Bacteroides capillosus
1344622	GL0013626_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold26497_1:554:718:-	Clostridiales
1345774	GL0083230_MH0062_[Lack_both_end]_[mRNA]_locus=scaffold33817_4:2:2044:-	-
1345782	GL0083017_MH0062_[Complete]_[mRNA]_locus=scaffold33881_2:1891:2895:-	Alistipes putredinis
1346963	GL0087229_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold41206_2:3:992:+	Alistipes putredinis
1347859	GL0097437_MH0062_[Complete]_[mRNA]_locus=scaffold47512_3:3232:4254:+	Firmicutes
1348329	GL0023120_MH0062_[Lack_3'-end]_[mRNA]_locus=scaffold50103_2:189:986:+	Parabacteroides distasonis
1350342	GL0077644_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold63777_2:2:946:+	Anaerostipes caccae
1350479	GL0093333_MH0062_[Complete]_[mRNA]_locus=scaffold64689_2:598:2658:-	Bacteroidales
1350998	GL0005962_MH0062_[Complete]_[mRNA]_locus=scaffold67660_3:1380:4571:+	Bacteroidetes

1351451	GL0091787_MH0062_[Lack_both_end]_[mRNA]_locus=scaffold70634_2:2:568:+	Faecalibacterium prausnitzii
1355950	GL0093806_MH0062_[Lack_both_end]_[mRNA]_locus=scaffold92338_2:2:517:-	-
1360881	GL0086076_MH0063_[Lack_3'-end]_[mRNA]_locus=scaffold2667_3:1:420:-	Clostridium leptum
1360995	GL0050032_MH0063_[Complete]_[mRNA]_locus=scaffold2804_7:554:3943:-	-
1361103	GL0089912_MH0063_[Complete]_[mRNA]_locus=scaffold3010_2:59:256:+	Campylobacter coli
1365204	GL0046576_MH0063_[Lack_5'-end]_[mRNA]_locus=scaffold10763_1:1:615:+	Roseburia inulinivorans
1367107	GL0078638_MH0063_[Lack_3'-end]_[mRNA]_locus=scaffold17334_6:48:716:+	Roseburia inulinivorans
1368086	GL0015910_MH0063_[Complete]_[mRNA]_locus=scaffold21147_1:663:1256:+	Roseburia inulinivorans
1371452	GL0012605_MH0063_[Lack_both_end]_[mRNA]_locus=scaffold36331_1:3:572:-	Faecalibacterium prausnitzii
1373752	GL0099187_MH0063_[Complete]_[mRNA]_locus=scaffold50155_2:1054:2367:-	Clostridium
1376425	GL0054972_MH0063_[Lack_both_end]_[mRNA]_locus=scaffold67042_2:1:705:+	Eubacterium hallii
1380300	GL0076491_MH0063_[Lack_3'-end]_[mRNA]_locus=scaffold89715_1:1:132:-	-
1384282	GL0046193_MH0063_[Lack_5'-end]_[mRNA]_locus=C4862499_1:2:133:+	-
1389373	GL0078563_MH0064_[Complete]_[mRNA]_locus=scaffold7904_1:109:468:-	Clostridium leptum

1392030	GL0029062_MH0064_[Lack_5'-end]_[mRNA]_locus=scaffold17700_2:2:1594:+	Bacteria
1396018	GL0036436_MH0064_[Lack_5'-end]_[mRNA]_locus=scaffold44164_1:1:459:+	Clostridiales
1405901	GL0102824_MH0065_[Lack_both_end]_[mRNA]_locus=scaffold7363_2:3:1232:-	Faecalibacterium prausnitzii
1428303	GL0010359_MH0065_[Lack_both_end]_[mRNA]_locus=scaffold73475_1:3:530:-	Faecalibacterium prausnitzii
1428562	GL0144974_MH0065_[Complete]_[mRNA]_locus=scaffold74880_2:362:622:-	-
1429341	GL0054431_MH0065_[Complete]_[mRNA]_locus=scaffold78427_1:183:887:+	Clostridiales
1432535	GL0027184_MH0065_[Lack_5'-end]_[mRNA]_locus=scaffold92188_1:2509:2616:-	Clostridiales
1445209	GL0000571_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold690_5:271:2937:-	Bacteroidales
1445724	GL0053917_MH0066_[Complete]_[mRNA]_locus=scaffold1185_2:676:1548:-	-
1446629	GL0102374_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold2373_3:3:2738:+	Bacteroides
1446638	GL0044210_MH0066_[Complete]_[mRNA]_locus=scaffold2405_12:2735:4345:+	Alistipes putredinis
1447422	GL0049120_MH0066_[Complete]_[mRNA]_locus=scaffold3599_2:4677:7457:-	Bacteroidales
1447423	GL0049121_MH0066_[Complete]_[mRNA]_locus=scaffold3599_2:7469:8509:-	Alistipes putredinis
1448580	GL0039959_MH0066_[Complete]_[mRNA]_locus=scaffold6037_3:2250:3131:-	Alistipes putredinis

1449245	GL0001460_MH0066_[Complete]_[mRNA]_locus=scaffold7485_3:52:1344:-	Alistipes putredinis
1449478	GL0104468_MH0066_[Complete]_[mRNA]_locus=scaffold8013_1:449:2224:+	Parabacteroides merdae
1449518	GL0048888_MH0066_[Complete]_[mRNA]_locus=scaffold8051_2:2097:2657:+	Bacteroides eggerthii
1449755	GL0011658_MH0066_[Complete]_[mRNA]_locus=scaffold8560_1:145:873:+	Clostridium methylpentosum
1451197	GL0118484_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold11929_2:1:843:+	Alistipes putredinis
1451256	GL0055150_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold12071_1:769:1248:-	Bacteroides capillosus
1452767	GL0121047_MH0066_[Lack_3'-end]_[mRNA]_locus=scaffold17418_1:492:1190:+	Bacteroidetes
1452887	GL0083446_MH0066_[Complete]_[mRNA]_locus=scaffold17973_4:4328:5098:-	Bacteroides
1452894	GL0087903_MH0066_[Complete]_[mRNA]_locus=scaffold18010_2:624:1394:+	Alistipes putredinis
1454179	GL0113381_MH0066_[Lack_3'-end]_[mRNA]_locus=scaffold22482_1:3:605:-	Bacteroidetes
1454555	GL0024838_MH0066_[Complete]_[mRNA]_locus=scaffold23387_3:5929:9282:-	Bacteroides
1454814	GL0001352_MH0066_[Complete]_[mRNA]_locus=scaffold24773_4:813:1655:-	Parabacteroides merdae
1454940	GL0001399_MH0066_[Complete]_[mRNA]_locus=scaffold25089_2:79:1002:+	Parabacteroides johnsonii
1455404	GL0059466_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold26974_1:2:1219:+	Alistipes putredinis

1456308	GL0109362_MH0066_[Complete]_[mRNA]_locus=scaffold31567_2:78:890:-	Alistipes putredinis
1457740	GL0083664_MH0066_[Complete]_[mRNA]_locus=scaffold38483_3:247:2583:-	Bacteroidales
1459723	GL0072076_MH0066_[Complete]_[mRNA]_locus=scaffold49614_1:620:1714:-	Alistipes putredinis
1466096	GL0076363_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold341_2:1:750:-	Clostridium phytofermentans
1466498	GL0054579_MH0067_[Complete]_[mRNA]_locus=scaffold922_2:2211:5585:+	Clostridiales
1466528	GL0019809_MH0067_[Lack_both_end]_[mRNA]_locus=scaffold1062_1:1:876:+	Roseburia inulinivorans
1466608	GL0068872_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold1225_1:215:535:-	Faecalibacterium prausnitzii
1466613	GL0050661_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold1229_1:1:267:-	Faecalibacterium prausnitzii
1466688	GL0042081_MH0067_[Complete]_[mRNA]_locus=scaffold1340_1:258:1337:+	Faecalibacterium prausnitzii
1467045	GL0017055_MH0067_[Complete]_[mRNA]_locus=scaffold1431_3:311:1828:-	Bacteria
1467534	GL0050520_MH0067_[Lack_both_end]_[mRNA]_locus=scaffold1962_3:3:716:-	Clostridium
1467813	GL0018597_MH0067_[Lack_both_end]_[mRNA]_locus=scaffold2351_4:2:1183:+	Clostridiales
1468020	GL0063311_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold2805_3:1472:2071:+	Faecalibacterium prausnitzii
1468285	GL0083074_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold3503_5:10476:11387:	Roseburia inulinivorans

	+	
1468546	GL0064174_MH0067_[Complete]_[mRNA]_locus=scaffold3911_3:12311:13132:+	Roseburia inulinivorans
1468598	GL0053244_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold4030_1:2:667:-	Bacteroides capillosus
1468988	GL0073587_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold4600_1:3:401:-	Faecalibacterium prausnitzii
1469823	GL0064515_MH0067_[Complete]_[mRNA]_locus=scaffold6614_1:29:2146:-	Bacteria
1469891	GL0058544_MH0067_[Complete]_[mRNA]_locus=scaffold6743_1:140:2593:+	Roseburia inulinivorans
1469934	GL0096538_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold6886_1:912:1313:-	Faecalibacterium prausnitzii
1470077	GL0082334_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold7228_3:65:694:-	Clostridium asparagiforme
1470078	GL0022634_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold7233_1:1:1800:+	Firmicutes
1470276	GL0055012_MH0067_[Complete]_[mRNA]_locus=scaffold7499_2:12560:14308:-	Roseburia inulinivorans
1470297	GL0002339_MH0067_[Complete]_[mRNA]_locus=scaffold7570_3:5796:6845:+	Roseburia inulinivorans
1470985	GL0066474_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold9521_1:26:1297:-	Roseburia inulinivorans
1470986	GL0057157_MH0067_[Complete]_[mRNA]_locus=scaffold9527_3:9668:10234:+	Roseburia inulinivorans
1471601	GL0003624_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold10997_4:2:190:+	Faecalibacterium prausnitzii

1471604	GL0102445_MH0067_[Complete]_[mRNA]_locus=scaffold11019_1:8045:9013:-	Roseburia inulinivorans
1471605	GL0102472_MH0067_[Complete]_[mRNA]_locus=scaffold11019_1:35193:36848:-	Roseburia inulinivorans
1471637	GL0008001_MH0067_[Complete]_[mRNA]_locus=scaffold11134_5:2060:3853:+	cellular organisms
1471922	GL0083884_MH0067_[Complete]_[mRNA]_locus=scaffold11771_3:4879:6972:-	Bacteria
1472031	GL0090533_MH0067_[Complete]_[mRNA]_locus=scaffold12095_6:2189:2878:-	Faecalibacterium prausnitzii
1472153	GL0045236_MH0067_[Complete]_[mRNA]_locus=scaffold12343_1:184:1617:-	Bacteria
1472445	GL0096277_MH0067_[Complete]_[mRNA]_locus=scaffold12861_2:6662:8629:-	Bacteria
1472577	GL0020123_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold13370_2:818:1939:+	Faecalibacterium prausnitzii
1472792	GL0107525_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold13610_1:30:563:+	Finegoldia magna
1472804	GL0000340_MH0067_[Lack_both_end]_[mRNA]_locus=scaffold13688_1:3:593:-	Faecalibacterium prausnitzii
1472859	GL0049760_MH0067_[Complete]_[mRNA]_locus=scaffold13866_3:293:1141:-	Roseburia inulinivorans
1473393	GL0007299_MH0067_[Complete]_[mRNA]_locus=scaffold15650_1:47:1861:-	Clostridium
1473866	GL0094277_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold18034_1:451:1683:-	Faecalibacterium prausnitzii
1474383	GL0039537_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold20988_3:1:495:-	Ruminococcus torques

1474886	GL0088233_MH0067_[Complete]_[mRNA]_locus=scaffold23309_1:2176:3144:+	Roseburia inulinivorans
1475340	GL0001314_MH0067_[Complete]_[mRNA]_locus=scaffold25766_1:3:221:+	Faecalibacterium prausnitzii
1475401	GL0028650_MH0067_[Lack_both_end]_[mRNA]_locus=scaffold25873_2:1:3387:+	Firmicutes
1475534	GL0093395_MH0067_[Complete]_[mRNA]_locus=scaffold26585_4:1281:2819:+	Clostridiales
1475863	GL0001124_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold28293_1:1:405:+	Clostridium asparagiforme
1476420	GL0007463_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold31736_1:2:460:+	Bacteroides capillosus
1476614	GL0075125_MH0067_[Complete]_[mRNA]_locus=scaffold33515_1:757:3288:+	Clostridiales
1477418	GL0091706_MH0067_[Complete]_[mRNA]_locus=scaffold39366_1:274:1215:+	-
1478293	GL0053864_MH0067_[Complete]_[mRNA]_locus=scaffold44720_2:5368:6339:+	Roseburia inulinivorans
1478502	GL0087404_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold45840_1:382:636:+	Bacteria
1478848	GL0016096_MH0067_[Complete]_[mRNA]_locus=scaffold48214_1:417:1298:-	Clostridium
1479438	GL0002157_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold50428_1:5634:5840:-	Bacteria
1480272	GL0037322_MH0067_[Lack_5'-end]_[mRNA]_locus=C2951230_1:2:838:+	Blautia hydrogenotrophica
1481865	GL0006783_MH0068_[Lack_5'-end]_[mRNA]_locus=scaffold1887_3:4005:5681:-	-

1482585	GL0090219_MH0068_[Lack_5'-end]_[mRNA]_locus=scaffold3080_6:296:1057:-	Coprococcus comes
1483271	GL0061100_MH0068_[Lack_both_end]_[mRNA]_locus=scaffold4657_2:2:1234:-	Bacteria
1483501	GL0022659_MH0068_[Complete]_[mRNA]_locus=scaffold5296_7:7556:8527:+	Clostridium nexile
1484296	GL0022115_MH0068_[Lack_5'-end]_[mRNA]_locus=scaffold7549_2:1:540:+	Faecalibacterium prausnitzii
1484700	GL0032343_MH0068_[Lack_3'-end]_[mRNA]_locus=scaffold8427_2:123:1583:+	Clostridiales
1485026	GL0084031_MH0068_[Complete]_[mRNA]_locus=scaffold9724_1:3163:4698:+	Roseburia inulinivorans
1489853	GL0008997_MH0068_[Lack_5'-end]_[mRNA]_locus=scaffold35937_1:3:323:+	Bacteroides pectinophilus
1491236	GL0030504_MH0068_[Lack_3'-end]_[mRNA]_locus=scaffold47606_1:921:1103:+	Faecalibacterium prausnitzii
1491622	GL0059636_MH0068_[Lack_5'-end]_[mRNA]_locus=scaffold51189_4:262:2109:-	Clostridium asparagiforme
1503702	GL0007751_MH0069_[Complete]_[mRNA]_locus=scaffold25130_5:1224:2594:+	Bacteria
1506821	GL0040610_MH0069_[Lack_5'-end]_[mRNA]_locus=scaffold37939_1:878:1006:-	-
1518892	GL0110536_MH0069_[Lack_both_end]_[mRNA]_locus=scaffold108578_1:3:854:-	Ruminococcus gnavus
1518969	GL0108632_MH0069_[Lack_both_end]_[mRNA]_locus=scaffold108846_3:1:669:-	-
1523731	GL0116410_MH0069_[Lack_3'-end]_[mRNA]_locus=C6803741_1:117:581:+	-

1524332	GL0004928_MH0069_[Lack_3'-end]_[mRNA]_locus=C6836397_1:181:684:+	-
1524845	GL0131999_MH0069_[Lack_both_end]_[mRNA]_locus=C6870811_1:1:861:+	-
1525944	GL0039165_MH0070_[Complete]_[mRNA]_locus=scaffold1240_7:1798:2394:+	Coprococcus eutactus
1525962	GL0111182_MH0070_[Complete]_[mRNA]_locus=scaffold1379_2:27:1925:-	Bacteria
1526320	GL0065284_MH0070_[Complete]_[mRNA]_locus=scaffold2367_3:7554:8918:-	Roseburia inulinivorans
1526616	GL0080536_MH0070_[Lack_5'-end]_[mRNA]_locus=scaffold3376_3:4467:5291:-	Roseburia inulinivorans
1526717	GL0102694_MH0070_[Complete]_[mRNA]_locus=scaffold3733_3:2181:4175:-	Bacteria
1527645	GL0082087_MH0070_[Lack_5'-end]_[mRNA]_locus=scaffold7797_1:1:735:+	Roseburia inulinivorans
1527646	GL0082091_MH0070_[Complete]_[mRNA]_locus=scaffold7797_1:3392:5113:-	Roseburia inulinivorans
1527679	GL0144568_MH0070_[Complete]_[mRNA]_locus=scaffold8013_1:17105:18406:+	Roseburia inulinivorans
1527764	GL0010446_MH0070_[Complete]_[mRNA]_locus=scaffold8362_2:1764:2897:+	Bacteria
1528098	GL0071767_MH0070_[Complete]_[mRNA]_locus=scaffold9863_2:1889:3700:-	Clostridiales
1528452	GL0034042_MH0070_[Complete]_[mRNA]_locus=scaffold11350_3:3321:4523:+	Roseburia inulinivorans
1529128	GL0105196_MH0070_[Complete]_[mRNA]_locus=scaffold14254_1:5666:7309:-	Roseburia inulinivorans

1529370	GL0066691_MH0070_[Lack_3'-end]_[mRNA]_locus=scaffold15410_1:3:1337:-	Bacteria
1529558	GL0038851_MH0070_[Complete]_[mRNA]_locus=scaffold16207_1:1271:2530:+	Clostridiales
1531695	GL0130529_MH0070_[Complete]_[mRNA]_locus=scaffold26103_5:13956:16757:-	Bacteria
1532646	GL0117364_MH0070_[Complete]_[mRNA]_locus=scaffold30906_2:3255:5963:+	Firmicutes
1532815	GL0144902_MH0070_[Lack_5'-end]_[mRNA]_locus=scaffold31571_2:2:1393:+	Clostridiales
1533743	GL0030357_MH0070_[Complete]_[mRNA]_locus=scaffold37235_1:3487:4677:+	Roseburia inulinivorans
1533878	GL0140835_MH0070_[Complete]_[mRNA]_locus=scaffold38165_1:917:1552:+	Eubacterium siraeum
1536761	GL0026412_MH0070_[Complete]_[mRNA]_locus=scaffold55832_1:1687:3735:-	Roseburia inulinivorans
1536762	GL0094550_MH0070_[Lack_both_end]_[mRNA]_locus=scaffold55832_2:1:1155:-	Roseburia inulinivorans
1536763	GL0008532_MH0070_[Complete]_[mRNA]_locus=scaffold55832_3:4610:6145:-	Clostridiales
1539608	GL0107706_MH0070_[Complete]_[mRNA]_locus=scaffold75059_1:1:1701:-	Clostridiales
1539652	GL0118536_MH0070_[Complete]_[mRNA]_locus=scaffold75649_1:1516:2010:-	Roseburia inulinivorans
1546760	GL0148562_MH0070_[Complete]_[mRNA]_locus=scaffold113160_3:292:1353:-	Roseburia inulinivorans
1547492	GL0041673_MH0070_[Complete]_[mRNA]_locus=scaffold114769_1:3043:4689:+	Roseburia inulinivorans

1548064	GL0133730_MH0070_[Complete]_[mRNA]_locus=scaffold115516_1:3339:4622:+	Roseburia inulinivorans
1553430	GL0113644_MH0071_[Complete]_[mRNA]_locus=scaffold2221_2:1292:3385:-	Bacteroides pectinophilus
1554019	GL0023610_MH0071_[Lack_both_end]_[mRNA]_locus=scaffold3152_1:3:536:-	Faecalibacterium prausnitzii
1557846	GL0059596_MH0071_[Complete]_[mRNA]_locus=scaffold10614_12:252:1835:+	Holdemania filiformis
1562806	GL0093044_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold25523_1:3605:4255:-	Leeuwenhoekiella blandensis
1567120	GL0055741_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold43947_4:927:1598:+	Anaerotruncus colihominis
1567125	GL0022421_MH0071_[Complete]_[mRNA]_locus=scaffold43947_7:246:1175:+	Clostridium methylpentosum
1577852	GL0105410_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold2125_8:3:1877:+	Bacteria
1578082	GL0032552_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold2676_1:3:656:-	Anaerotruncus colihominis
1578618	GL0058868_MH0072_[Complete]_[mRNA]_locus=scaffold4403_3:561:1676:-	Coprococcus comes
1579186	GL0077405_MH0072_[Lack_both_end]_[mRNA]_locus=scaffold5936_2:2:751:+	Bacteroides capillosus
1580404	GL0036727_MH0072_[Complete]_[mRNA]_locus=scaffold8933_1:383:1366:-	-
1581889	GL0013387_MH0072_[Complete]_[mRNA]_locus=scaffold14256_1:353:1192:-	Clostridium
1582220	GL0026009_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold15770_3:538:1374:+	Eubacterium hallii

1582736	GL0078700_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold17286_1:3:989:-	Bacteroides capillosus
1583380	GL0089447_MH0072_[Complete]_[mRNA]_locus=scaffold20612_3:413:1420:+	Faecalibacterium prausnitzii
1584181	GL0019976_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold24906_2:1:315:+	Bacteria
1585228	GL0100913_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold31190_1:110:655:+	Faecalibacterium prausnitzii
1585918	GL0076152_MH0072_[Complete]_[mRNA]_locus=scaffold35445_3:1250:1486:-	Faecalibacterium prausnitzii
1586227	GL0044416_MH0072_[Complete]_[mRNA]_locus=scaffold37930_7:1408:2088:+	Bacteroides capillosus
1586365	GL0093688_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold39318_1:1:264:+	Faecalibacterium prausnitzii
1588450	GL0084607_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold55614_3:1:390:+	Clostridium kluyveri
1588766	GL0003317_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold58683_1:76:612:+	Clostridiales
1589306	GL0063181_MH0072_[Lack_both_end]_[mRNA]_locus=scaffold62729_3:3:869:+	-
1589564	GL0084676_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold64998_2:1:960:-	Clostridium bolteae
1590065	GL0067007_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold68849_3:435:911:+	Eubacterium hallii
1592487	GL0066354_MH0073_[Complete]_[mRNA]_locus=scaffold1480_2:1285:2502:+	Roseburia inulinivorans
1592896	GL0035521_MH0073_[Complete]_[mRNA]_locus=scaffold2712_3:330:1799:+	Clostridiales

1592910	GL0097272_MH0073_[Complete]_[mRNA]_locus=scaffold2759_1:2367:3407:+	Roseburia inulinivorans
1593012	GL0060767_MH0073_[Lack_5'-end]_[mRNA]_locus=scaffold3024_1:11084:12157:-	Roseburia inulinivorans
1593106	GL0046358_MH0073_[Lack_5'-end]_[mRNA]_locus=scaffold3466_2:2:493:+	Bacteria
1593326	GL0086350_MH0073_[Complete]_[mRNA]_locus=scaffold4146_1:936:1550:+	Faecalibacterium prausnitzii
1594276	GL0095989_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold7406_1:3:209:-	Clostridium
1594543	GL0007849_MH0073_[Complete]_[mRNA]_locus=scaffold8324_1:7059:8051:+	Roseburia inulinivorans
1594586	GL0022815_MH0073_[Complete]_[mRNA]_locus=scaffold8571_1:255:2312:-	Clostridiales
1596894	GL0055050_MH0073_[Complete]_[mRNA]_locus=scaffold18666_1:208:1494:+	Roseburia inulinivorans
1597533	GL0092679_MH0073_[Lack_both_end]_[mRNA]_locus=scaffold22251_1:3:641:-	Clostridium
1597594	GL0078565_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold22494_1:11539:12048:+	Bacteroides pectinophilus
1597877	GL0020244_MH0073_[Lack_both_end]_[mRNA]_locus=scaffold23633_1:1:513:-	-
1598682	GL0006159_MH0073_[Lack_5'-end]_[mRNA]_locus=scaffold28652_2:3:2795:+	Clostridiales
1599527	GL0010897_MH0073_[Complete]_[mRNA]_locus=scaffold33803_1:1650:2210:-	Roseburia inulinivorans

1599543	GL0040799_MH0073_[Complete]_[mRNA]_locus=scaffold33890_1:5559:6482:-	Roseburia inulinivorans
1601365	GL0019280_MH0073_[Lack_5'-end]_[mRNA]_locus=scaffold46042_2:561:713:-	-
1602664	GL0023860_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold55223_2:1:126:-	-
1603204	GL0074575_MH0073_[Complete]_[mRNA]_locus=scaffold59089_1:11403:12587:+	Roseburia inulinivorans
1603788	GL0007333_MH0073_[Complete]_[mRNA]_locus=scaffold64519_1:299:844:-	Holdemania filiformis
1606828	GL0005976_MH0073_[Lack_5'-end]_[mRNA]_locus=scaffold84884_4:2:1366:+	Roseburia inulinivorans
1607115	GL0003866_MH0073_[Complete]_[mRNA]_locus=scaffold85885_1:1595:2686:-	Roseburia inulinivorans
1609211	GL0094258_MH0074_[Lack_both_end]_[mRNA]_locus=scaffold116_7:3:3662:-	Bacteria
1609275	GL0063375_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold139_2:2:319:-	-
1609276	GL0063376_MH0074_[Complete]_[mRNA]_locus=scaffold139_2:379:699:-	Bacteria
1609277	GL0073846_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold139_3:1:255:-	Roseburia inulinivorans
1609734	GL0107062_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold370_10:1:696:-	Clostridium perfringens
1610675	GL0089043_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold1030_2:23:2644:-	Bacteria
1610676	GL0006352_MH0074_[Complete]_[mRNA]_locus=scaffold1030_4:197:1882:-	Coprococcus eutactus

1610752	GL0050875_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold1086_14:1:282:-	Clostridium bolteae
1614236	GL0016652_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold3830_1:386:823:-	Faecalibacterium prausnitzii
1614390	GL0038107_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold3981_2:2:187:+	Roseburia inulinivorans
1615533	GL0111123_MH0074_[Complete]_[mRNA]_locus=scaffold4927_2:109:861:-	Roseburia inulinivorans
1615991	GL0075644_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold5424_3:830:1501:+	Eubacterium hallii
1616022	GL0001776_MH0074_[Complete]_[mRNA]_locus=scaffold5461_12:1096:1302:+	-
1617017	GL0015964_MH0074_[Complete]_[mRNA]_locus=scaffold6623_6:247:1482:-	Roseburia inulinivorans
1617203	GL0033291_MH0074_[Lack_both_end]_[mRNA]_locus=scaffold6923_2:2:865:+	Faecalibacterium prausnitzii
1618045	GL0029243_MH0074_[Complete]_[mRNA]_locus=scaffold7831_4:240:2042:+	Firmicutes
1619129	GL0115869_MH0074_[Complete]_[mRNA]_locus=scaffold9230_4:803:2482:-	Enterococcus
1619640	GL0085473_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold10001_14:366:614:+	Clostridium bolteae
1620108	GL0093625_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold10843_1:1:276:-	Clostridium bolteae
1620792	GL0084849_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold12058_10:2:1801:-	-
1620968	GL0058482_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold12231_5:2:181:+	Clostridium bolteae

1622954	GL0050181_MH0074_[Lack_both_end]_[mRNA]_locus=scaffold15609_3:2:595:+	Clostridium bolteae
1623434	GL0007257_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold16571_7:507:761:+	Clostridium bolteae
1625469	GL0116519_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold20772_4:203:517:+	Clostridium bolteae
1626331	GL0011581_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold22857_7:1605:1853:-	Clostridium bolteae
1626410	GL0012839_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold23079_2:84:785:-	Roseburia inulinivorans
1626976	GL0037833_MH0074_[Complete]_[mRNA]_locus=scaffold24527_4:1144:2511:+	-
1627223	GL0039710_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold25218_2:109:684:+	Clostridium bolteae
1628232	GL0044054_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold27865_4:1:447:+	Roseburia inulinivorans
1630560	GL0056100_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold33988_2:1:129:+	-
1630709	GL0001950_MH0074_[Complete]_[mRNA]_locus=scaffold34449_2:469:2139:-	Roseburia inulinivorans
1631554	GL0050421_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold37050_2:257:1063:-	Roseburia inulinivorans
1632110	GL0055196_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold38756_3:664:822:+	Clostridium bolteae
1633933	GL0103871_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold43694_4:1463:2353:-	Roseburia inulinivorans
1634778	GL0112885_MH0074_[Lack_3'-end]_[mRNA]_locus=scaffold46100_2:172:678:+	Roseburia inulinivorans

1635485	GL0033222_MH0074_[Complete]_[mRNA]_locus=scaffold47480_2:105:1076:-	Roseburia inulinivorans
1637693	GL0025252_MH0074_[Lack_5'-end]_[mRNA]_locus=C4262037_1:141:695:-	Roseburia inulinivorans
1638441	GL0017898_MH0075_[Complete]_[mRNA]_locus=scaffold456_3:80:667:+	Faecalibacterium prausnitzii
1639196	GL0051077_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold2692_3:3:629:+	Faecalibacterium prausnitzii
1639515	GL0034539_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold3860_1:1:729:+	Faecalibacterium prausnitzii
1639528	GL0029953_MH0075_[Complete]_[mRNA]_locus=scaffold3903_1:20:397:-	Faecalibacterium prausnitzii
1639629	GL0136108_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold4247_1:745:855:+	-
1639856	GL0016206_MH0075_[Complete]_[mRNA]_locus=scaffold5543_1:149:769:-	-
1640195	GL0008691_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold6707_2:1323:2987:-	Faecalibacterium prausnitzii
1641233	GL0063844_MH0075_[Complete]_[mRNA]_locus=scaffold11803_1:1763:2863:+	Roseburia inulinivorans
1641858	GL0060862_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold15225_2:169:873:+	Ruminococcus obeum
1643003	GL0042085_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold23148_1:1180:1317:-	-
1644087	GL0045731_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold30304_5:1:504:-	Faecalibacterium prausnitzii
1644603	GL0027111_MH0075_[Complete]_[mRNA]_locus=scaffold33821_2:322:2046:+	-

1645140	GL0099744_MH0075_[Complete]_[mRNA]_locus=scaffold37485_3:256:1536:-	Roseburia inulinivorans
1645901	GL0005786_MH0075_[Complete]_[mRNA]_locus=scaffold42898_3:428:1201:-	-
1645955	GL0036374_MH0075_[Lack_both_end]_[mRNA]_locus=scaffold43480_1:1:837:+	-
1646060	GL0065834_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold44102_5:440:1012:+	-
1646555	GL0082869_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold48068_2:1:1071:+	Clostridium phytofermentans
1648439	GL0003873_MH0075_[Complete]_[mRNA]_locus=scaffold63358_1:249:1262:+	Roseburia inulinivorans
1648704	GL0011760_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold65657_2:1:966:-	Eubacterium siraeum
1650432	GL0093766_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold78439_1:519:1556:+	Roseburia inulinivorans
1650685	GL0018977_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold80177_1:251:919:+	Faecalibacterium prausnitzii
1650890	GL0104124_MH0075_[Lack_both_end]_[mRNA]_locus=scaffold81563_1:3:584:-	Ruminococcus obeum
1652348	GL0139112_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold89539_1:3:848:-	-
1652365	GL0041402_MH0075_[Complete]_[mRNA]_locus=scaffold89599_2:1053:2171:-	-
1653946	GL0042911_MH0075_[Complete]_[mRNA]_locus=scaffold94486_1:721:1872:+	Anaerofustis stercorihominis
1655195	GL0126202_MH0075_[Lack_3'-end]_[mRNA]_locus=scaffold96471_1:1:1077:-	-

1656725	GL0022131_MH0075_[Complete]_[mRNA]_locus=C4268225_1:213:860:-	Clostridium scindens
1657109	GL0062931_MH0075_[Lack_3'-end]_[mRNA]_locus=C4300841_1:220:1464:+	Roseburia inulinivorans
1657678	GL0047171_MH0076_[Lack_5'-end]_[mRNA]_locus=scaffold2083_1:1:255:+	Roseburia inulinivorans
1659701	GL0002216_MH0076_[Lack_both_end]_[mRNA]_locus=scaffold23421_2:2:619:+	Roseburia inulinivorans
1662137	GL0110476_MH0076_[Lack_5'-end]_[mRNA]_locus=scaffold46680_3:3:665:+	Roseburia inulinivorans
1662636	GL0045978_MH0076_[Lack_both_end]_[mRNA]_locus=scaffold50855_2:1:729:+	Roseburia inulinivorans
1665868	GL0052686_MH0076_[Lack_both_end]_[mRNA]_locus=scaffold69976_2:2:1033:+	Clostridium asparagiforme
1669076	GL0106750_MH0076_[Lack_5'-end]_[mRNA]_locus=C2806864_1:48:665:-	Roseburia inulinivorans
1669466	GL0051771_MH0076_[Complete]_[mRNA]_locus=C2826708_1:503:808:+	Roseburia inulinivorans
1674051	GL0160130_MH0077_[Lack_5'-end]_[mRNA]_locus=scaffold4122_2:3:302:+	Bacteria
1676369	GL0124544_MH0077_[Complete]_[mRNA]_locus=scaffold8021_7:271:693:-	Roseburia inulinivorans
1680835	GL0152883_MH0077_[Lack_5'-end]_[mRNA]_locus=scaffold18632_3:295:549:-	-
1682275	GL0094030_MH0077_[Complete]_[mRNA]_locus=scaffold22453_6:231:884:-	Roseburia inulinivorans
1686960	GL0120095_MH0077_[Lack_3'-end]_[mRNA]_locus=scaffold37528_3:1:1257:-	Clostridium

1687287	GL0125360_MH0077_[Complete]_[mRNA]_locus=scaffold38351_7:787:1545:-	-
1695446	GL0001953_MH0077_[Lack_5'-end]_[mRNA]_locus=scaffold74609_1:725:1405:-	Faecalibacterium prausnitzii
1702913	GL0055470_MH0077_[Lack_3'-end]_[mRNA]_locus=scaffold110010_2:355:705:+	Roseburia inulinivorans
1719620	GL0079974_MH0079_[Lack_both_end]_[mRNA]_locus=scaffold15941_1:3:599:-	Clostridium ramosum
1721785	GL0085587_MH0079_[Lack_both_end]_[mRNA]_locus=scaffold28548_1:1:699:+	Clostridiales
1723341	GL0041242_MH0079_[Complete]_[mRNA]_locus=scaffold36541_2:1980:2141:-	-
1746002	GL0116039_MH0080_[Complete]_[mRNA]_locus=scaffold5866_4:306:818:+	Roseburia inulinivorans
1746333	GL0051099_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold7156_1:2:1783:+	Bacteria
1747905	GL0152809_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold14290_2:3:977:+	Roseburia inulinivorans
1750344	GL0035213_MH0080_[Lack_both_end]_[mRNA]_locus=scaffold26639_7:1:801:+	Clostridium asparagiforme
1751679	GL0083146_MH0080_[Complete]_[mRNA]_locus=scaffold33351_1:497:1039:+	Roseburia inulinivorans
1752195	GL0119420_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold36441_3:219:665:-	Roseburia inulinivorans
1752426	GL0143933_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold38165_1:1:195:+	Bacteria
1752731	GL0148743_MH0080_[Lack_both_end]_[mRNA]_locus=scaffold39788_3:2:832:+	Clostridium asparagiforme

1752732	GL0136564_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold39788_4:1:702:-	Clostridia
1753098	GL0041050_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold41953_2:1:840:+	Clostridium hylemonae
1753730	GL0123615_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold45717_3:3:965:+	Roseburia inulinivorans
1753857	GL0131589_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold46270_4:73:696:+	Clostridium scindens
1754196	GL0121662_MH0080_[Lack_both_end]_[mRNA]_locus=scaffold48525_1:3:521:+	Bacteroides capillosus
1755273	GL0148485_MH0080_[Complete]_[mRNA]_locus=scaffold54149_1:269:1642:-	-
1758507	GL0096352_MH0080_[Complete]_[mRNA]_locus=scaffold74059_1:316:879:+	Roseburia inulinivorans
1758891	GL0053839_MH0080_[Complete]_[mRNA]_locus=scaffold76292_2:967:1962:+	-
1760419	GL0100900_MH0080_[Lack_both_end]_[mRNA]_locus=scaffold83581_2:2:733:+	Ruminococcus lactaris
1760979	GL0141469_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold85981_1:3:515:+	Roseburia inulinivorans
1760980	GL0046361_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold85983_4:1:1521:+	Roseburia inulinivorans
1762913	GL0073911_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold93189_2:777:1241:+	Coprococcus eutactus
1768494	GL0100647_MH0080_[Lack_3'-end]_[mRNA]_locus=C3234942_1:1:486:-	-
1768691	GL0085729_MH0080_[Lack_both_end]_[mRNA]_locus=C3244434_1:1:768:+	Clostridiales

1772934	GL0123607_MH0081_[Complete]_[mRNA]_locus=scaffold5850_2:86:1333:-	Alistipes putredinis
1774465	GL0131324_MH0081_[Lack_5'-end]_[mRNA]_locus=scaffold9427_2:2:559:+	-
1774681	GL0124355_MH0081_[Complete]_[mRNA]_locus=scaffold10060_1:618:1508:+	Alistipes putredinis
1778069	GL0023069_MH0081_[Complete]_[mRNA]_locus=scaffold21921_1:202:1011:+	Eubacterium biforme
1779093	GL0062513_MH0081_[Complete]_[mRNA]_locus=scaffold25250_1:1206:2072:-	Bacteroides
1784583	GL0093607_MH0081_[Lack_both_end]_[mRNA]_locus=scaffold51507_3:1:1032:-	Alistipes putredinis
1786221	GL0152519_MH0081_[Complete]_[mRNA]_locus=scaffold58720_1:310:1017:-	Alistipes putredinis
1794442	GL0060600_MH0081_[Lack_3'-end]_[mRNA]_locus=scaffold97251_1:233:1657:+	Pedobacter
1795949	GL0114318_MH0081_[Complete]_[mRNA]_locus=scaffold99611_1:1338:1856:+	Alistipes putredinis
1796507	GL0127420_MH0081_[Lack_3'-end]_[mRNA]_locus=C3623596_1:1:543:-	Ruminococcus gnavus
1797654	GL0126325_MH0081_[Complete]_[mRNA]_locus=C3694391_1:27:755:-	Clostridium methylpentosum
1801168	GL0063006_MH0082_[Lack_5'-end]_[mRNA]_locus=scaffold1489_2:3:605:+	Roseburia inulinivorans
1804305	GL0005903_MH0082_[Complete]_[mRNA]_locus=scaffold6528_2:75:569:-	Eubacterium siraeum
1808154	GL0145873_MH0082_[Lack_5'-end]_[mRNA]_locus=scaffold13269_4:1706:1975:-	-

1809611	GL0050033_MH0082_[Complete]_[mRNA]_locus=scaffold17403_2:860:1747:-	Clostridium nexile
1816568	GL0119844_MH0082_[Lack_both_end]_[mRNA]_locus=scaffold38388_2:1:540:-	Bacteroides pectinophilus
1823474	GL0042396_MH0082_[Lack_5'-end]_[mRNA]_locus=scaffold67140_3:154:942:-	Thermosinus carboxydivorans
1827790	GL0002313_MH0082_[Lack_both_end]_[mRNA]_locus=scaffold87816_2:2:658:+	Roseburia inulinivorans
1828436	GL0086669_MH0082_[Complete]_[mRNA]_locus=scaffold90677_3:1221:3431:+	Clostridiales
1831882	GL0118162_MH0082_[Lack_5'-end]_[mRNA]_locus=scaffold102666_1:3:791:+	Clostridium asparagiforme
1842962	GL0058760_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold15504_2:2:469:+	Clostridium hylemonae
1843371	GL0009162_MH0083_[Complete]_[mRNA]_locus=scaffold16846_2:1885:3354:+	Clostridiales
1843720	GL0136462_MH0083_[Complete]_[mRNA]_locus=scaffold18310_3:1652:2410:+	Clostridiales
1844265	GL0093507_MH0083_[Complete]_[mRNA]_locus=scaffold21060_7:4856:6160:+	Bacteroides plebeius
1845435	GL0060351_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold26814_1:276:584:-	Roseburia inulinivorans
1845749	GL0040887_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold28792_1:1110:1835:-	Bacteroides capillosus
1845854	GL0102385_MH0083_[Lack_both_end]_[mRNA]_locus=scaffold29535_3:3:1658:-	Clostridiales
1847779	GL0140689_MH0083_[Complete]_[mRNA]_locus=scaffold41109_3:860:1792:-	Dorea formicigenerans

1848760	GL0135433_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold47893_2:13055:13225:-	-
1853635	GL0093852_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold81185_1:119:766:-	Roseburia inulinivorans
1860557	GL0034513_MH0084_[Complete]_[mRNA]_locus=scaffold547_2:620:2878:-	Bacteria
1860671	GL0044663_MH0084_[Complete]_[mRNA]_locus=scaffold806_1:3190:4791:-	Roseburia inulinivorans
1860674	GL0032787_MH0084_[Complete]_[mRNA]_locus=scaffold806_4:7273:9015:-	Roseburia inulinivorans
1860766	GL0036525_MH0084_[Complete]_[mRNA]_locus=scaffold1022_4:317:1141:+	-
1861009	GL0067909_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold1425_2:1:3177:+	Clostridiales
1861099	GL0044338_MH0084_[Complete]_[mRNA]_locus=scaffold1633_4:1128:2480:-	Roseburia inulinivorans
1861101	GL0067099_MH0084_[Complete]_[mRNA]_locus=scaffold1633_8:5345:7996:-	Bacteria
1861118	GL0001328_MH0084_[Complete]_[mRNA]_locus=scaffold1693_3:834:1619:-	Roseburia inulinivorans
1861119	GL0001331_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold1693_3:3910:5073:-	Clostridiales
1861182	GL0052183_MH0084_[Complete]_[mRNA]_locus=scaffold1807_2:1385:3856:+	Clostridiales
1861331	GL0038886_MH0084_[Complete]_[mRNA]_locus=scaffold2350_2:2359:3537:-	Roseburia inulinivorans

1861524	GL0004405_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold2987_2:808:996:+	Faecalibacterium prausnitzii
1861553	GL0024287_MH0084_[Complete]_[mRNA]_locus=scaffold3065_2:2185:3087:+	Roseburia inulinivorans
1861667	GL0023169_MH0084_[Complete]_[mRNA]_locus=scaffold3587_1:6055:8580:+	Roseburia inulinivorans
1862059	GL0004885_MH0084_[Complete]_[mRNA]_locus=scaffold4973_4:1953:3401:+	Roseburia inulinivorans
1862823	GL0067789_MH0084_[Complete]_[mRNA]_locus=scaffold7431_4:520:1665:-	Roseburia inulinivorans
1863125	GL0015767_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold8894_1:3:1397:-	Clostridiales
1863273	GL0061957_MH0084_[Complete]_[mRNA]_locus=scaffold9619_8:167:976:+	Roseburia inulinivorans
1863584	GL0062735_MH0084_[Complete]_[mRNA]_locus=scaffold11288_2:5105:6562:-	Roseburia inulinivorans
1864649	GL0025808_MH0084_[Lack_both_end]_[mRNA]_locus=scaffold17344_3:2:1129:+	Clostridiales
1864657	GL0060663_MH0084_[Complete]_[mRNA]_locus=scaffold17480_1:1835:4162:+	Clostridiales
1864953	GL0061705_MH0084_[Complete]_[mRNA]_locus=scaffold19143_1:6365:8137:+	Clostridiales
1865311	GL0057825_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold22211_1:3:200:+	Roseburia inulinivorans
1865331	GL0050601_MH0084_[Complete]_[mRNA]_locus=scaffold22400_1:215:652:+	Roseburia inulinivorans
1865335	GL0029842_MH0084_[Complete]_[mRNA]_locus=scaffold22477_1:1662:2678:+	Roseburia inulinivorans

1865747	GL0060840_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold26372_5:1156:1500:-	Parabacteroides
1865876	GL0044966_MH0084_[Complete]_[mRNA]_locus=scaffold27163_8:2076:3818:-	Clostridiales
1865971	GL0033077_MH0084_[Complete]_[mRNA]_locus=scaffold27538_2:685:1377:-	Roseburia inulinivorans
1865997	GL0059132_MH0084_[Complete]_[mRNA]_locus=scaffold27825_1:1463:2371:-	Clostridiales
1865998	GL0059133_MH0084_[Complete]_[mRNA]_locus=scaffold27825_1:2428:3360:-	Clostridium
1866091	GL0052411_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold28785_1:732:1370:+	Clostridiales
1867094	GL0015269_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold39140_1:3:563:+	Roseburia inulinivorans
1867653	GL0018539_MH0084_[Complete]_[mRNA]_locus=scaffold44599_5:892:2526:+	Roseburia inulinivorans
1868026	GL0041761_MH0084_[Complete]_[mRNA]_locus=scaffold48423_1:2137:2931:+	Clostridium
1870530	GL0022518_MH0085_[Lack_both_end]_[mRNA]_locus=scaffold502_2:1:498:+	Clostridiales
1870531	GL0064863_MH0085_[Complete]_[mRNA]_locus=scaffold502_5:232:663:+	Bacteroides capillosus
1871083	GL0007521_MH0085_[Lack_both_end]_[mRNA]_locus=scaffold1619_2:1:939:-	Clostridium
1872081	GL0053799_MH0085_[Complete]_[mRNA]_locus=scaffold3373_1:1524:1763:-	-
1873392	GL0075998_MH0085_[Complete]_[mRNA]_locus=scaffold6840_4:5328:7166:+	Clostridiales

1873393	GL0106424_MH0085_[Complete]_[mRNA]_locus=scaffold6840_6:504:1520:-	Bacteroides capillosus
1873471	GL0083204_MH0085_[Lack_3'-end]_[mRNA]_locus=scaffold7143_8:900:2195:+	Bacteroides capillosus
1873473	GL0086679_MH0085_[Lack_both_end]_[mRNA]_locus=scaffold7148_6:3:827:+	Eubacterium hallii
1874399	GL0072452_MH0085_[Complete]_[mRNA]_locus=scaffold10532_4:815:2026:+	Clostridium leptum
1874421	GL0048145_MH0085_[Complete]_[mRNA]_locus=scaffold10593_9:6235:8022:-	Clostridiales
1874463	GL0100833_MH0085_[Lack_3'-end]_[mRNA]_locus=scaffold10729_1:1634:2863:+	Roseburia inulinivorans
1875876	GL0081336_MH0085_[Lack_both_end]_[mRNA]_locus=scaffold19036_4:2:790:-	Roseburia inulinivorans
1876534	GL0064765_MH0085_[Complete]_[mRNA]_locus=scaffold23735_2:485:709:+	Firmicutes
1876813	GL0087086_MH0085_[Lack_both_end]_[mRNA]_locus=scaffold26306_1:3:944:-	Clostridium methylpentosum
1877164	GL0006393_MH0085_[Lack_3'-end]_[mRNA]_locus=scaffold29550_2:3:1487:-	Roseburia inulinivorans
1877982	GL0016141_MH0085_[Lack_5'-end]_[mRNA]_locus=scaffold37814_5:2784:3095:-	Clostridiales
1880075	GL0065388_MH0085_[Lack_5'-end]_[mRNA]_locus=scaffold57005_1:1:543:+	Bacteroides capillosus
1880264	GL0034511_MH0085_[Lack_both_end]_[mRNA]_locus=scaffold58572_1:1:531:+	Bacteroides capillosus
1882555	GL0022102_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold299_1:3:305:+	-

1882815	GL0120743_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold594_4:1812:2246:+	Roseburia inulinivorans
1883024	GL0003955_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold768_6:450:2132:-	Roseburia inulinivorans
1883030	GL0030210_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold771_3:1455:2171:-	Roseburia inulinivorans
1883119	GL0113193_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold830_6:205:3750:+	Ruminococcus obeum
1883137	GL0129215_MH0086_[Complete]_[mRNA]_locus=scaffold839_4:3336:4799:+	Coprococcus eutactus
1883975	GL0006357_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold1606_13:1:2232:-	Ruminococcus gnavus
1884226	GL0071603_MH0086_[Complete]_[mRNA]_locus=scaffold1774_1:256:2049:-	Bacteria
1885109	GL0013024_MH0086_[Complete]_[mRNA]_locus=scaffold2459_1:99:947:+	Clostridiales
1885408	GL0087360_MH0086_[Complete]_[mRNA]_locus=scaffold2696_4:2472:2879:-	Roseburia inulinivorans
1885480	GL0081066_MH0086_[Complete]_[mRNA]_locus=scaffold2743_6:192:2474:-	Bacteria
1885688	GL0069186_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold2893_6:699:1958:+	Roseburia inulinivorans
1885781	GL0003609_MH0086_[Complete]_[mRNA]_locus=scaffold3010_4:1476:2486:+	-
1885782	GL0132473_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold3010_9:1:1020:+	-
1886131	GL0113435_MH0086_[Complete]_[mRNA]_locus=scaffold3326_35:247:1596:-	-

1886384	GL0098388_MH0086_[Complete]_[mRNA]_locus=scaffold3576_6:381:842:+	Roseburia inulinivorans
1886400	GL0139712_MH0086_[Complete]_[mRNA]_locus=scaffold3602_8:381:3950:-	Bacteria
1887195	GL0129905_MH0086_[Complete]_[mRNA]_locus=scaffold4137_4:539:1309:-	-
1887203	GL0150535_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold4137_16:154:804:-	-
1887328	GL0087127_MH0086_[Complete]_[mRNA]_locus=scaffold4230_7:716:1639:-	Roseburia inulinivorans
1887718	GL0075291_MH0086_[Complete]_[mRNA]_locus=scaffold4570_2:1925:3304:+	Roseburia intestinalis
1887752	GL0069886_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold4616_2:3:617:-	Roseburia inulinivorans
1887764	GL0144861_MH0086_[Complete]_[mRNA]_locus=scaffold4622_12:39:1841:-	Firmicutes
1887856	GL0013068_MH0086_[Complete]_[mRNA]_locus=scaffold4726_4:166:774:+	Roseburia inulinivorans
1887914	GL0109745_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold4756_7:3:428:-	Clostridium asparagiforme
1887915	GL0109746_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold4756_7:484:1224:-	Roseburia
1888207	GL0166864_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold4953_3:283:990:-	Eubacterium rectale
1888674	GL0156028_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold5261_6:807:2549:+	Clostridiales
1889430	GL0043137_MH0086_[Complete]_[mRNA]_locus=scaffold6101_11:1641:2258:-	Roseburia intestinalis

1889663	GL0084464_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold6393_1:1:843:+	Roseburia inulinivorans
1890265	GL0138499_MH0086_[Complete]_[mRNA]_locus=scaffold7236_3:1212:2573:-	Roseburia inulinivorans
1890268	GL0072727_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold7236_11:64:1800:+	Roseburia
1890269	GL0198035_MH0086_[Complete]_[mRNA]_locus=scaffold7236_13:505:3864:-	Clostridiales
1891689	GL0063320_MH0086_[Complete]_[mRNA]_locus=scaffold9200_18:2192:3058:+	Roseburia inulinivorans
1891691	GL0035232_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold9200_22:2740:4188:+	Roseburia inulinivorans
1891714	GL0094187_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold9235_2:1:1224:-	Bacteroides pectinophilus
1891834	GL0159661_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold9350_1:1:675:+	Roseburia
1892177	GL0108228_MH0086_[Complete]_[mRNA]_locus=scaffold9747_1:943:2220:+	Clostridium scindens
1892186	GL0028146_MH0086_[Complete]_[mRNA]_locus=scaffold9774_1:550:2085:+	Lachnospiraceae
1892520	GL0187022_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold10114_5:1:1593:-	Roseburia inulinivorans
1892522	GL0011103_MH0086_[Complete]_[mRNA]_locus=scaffold10114_15:101:532:-	-
1892539	GL0060946_MH0086_[Complete]_[mRNA]_locus=scaffold10142_6:11:1012:-	-
1892588	GL0115618_MH0086_[Complete]_[mRNA]_locus=scaffold10177_2:240:956:-	Roseburia inulinivorans

1892597	GL0023366_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold10177_16:3:1190:-	-
1894706	GL0074002_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold12668_7:2:874:-	Clostridiales
1896277	GL0013150_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold15151_2:1570:2157:-	Roseburia inulinivorans
1896366	GL0196712_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold15352_1:1:1272:+	-
1896368	GL0193838_MH0086_[Complete]_[mRNA]_locus=scaffold15352_4:390:1109:+	Roseburia inulinivorans
1896562	GL0126756_MH0086_[Complete]_[mRNA]_locus=scaffold15705_1:492:1466:-	Roseburia inulinivorans
1897339	GL0090202_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold16708_13:3:857:+	Ruminococcus obeum
1897404	GL0090734_MH0086_[Complete]_[mRNA]_locus=scaffold16841_3:865:1590:-	-
1898011	GL0196788_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold17933_7:3:1118:+	Roseburia inulinivorans
1898198	GL0021654_MH0086_[Complete]_[mRNA]_locus=scaffold18174_7:1177:1977:-	-
1898245	GL0088024_MH0086_[Complete]_[mRNA]_locus=scaffold18284_7:3179:3868:-	Bacteroides pectinophilus
1898247	GL0030855_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold18289_2:3:1031:-	-
1898250	GL0191620_MH0086_[Complete]_[mRNA]_locus=scaffold18289_5:590:1462:-	-
1898595	GL0137074_MH0086_[Complete]_[mRNA]_locus=scaffold18908_8:866:1456:+	-

1898812	GL0153540_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold19294_1:3:1124:-	Clostridiales
1899023	GL0051387_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold19743_11:803:1822:+	Clostridium asparagiforme
1899326	GL0117557_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold20222_3:2:442:+	Roseburia inulinivorans
1899356	GL0008886_MH0086_[Complete]_[mRNA]_locus=scaffold20259_1:467:1624:-	Clostridiales
1899854	GL0026800_MH0086_[Complete]_[mRNA]_locus=scaffold21169_10:289:1881:-	-
1900260	GL0169858_MH0086_[Complete]_[mRNA]_locus=scaffold21861_2:255:2558:+	-
1900496	GL0052635_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold22393_6:3:674:+	-
1901059	GL0058235_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold23467_1:3:506:-	-
1901062	GL0063485_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold23467_4:2:1186:-	-
1901238	GL0119399_MH0086_[Complete]_[mRNA]_locus=scaffold23930_7:58:663:-	-
1901465	GL0167777_MH0086_[Complete]_[mRNA]_locus=scaffold24359_1:1115:2332:+	Bacteria
1901972	GL0084363_MH0086_[Complete]_[mRNA]_locus=scaffold25612_1:125:1612:-	-
1901976	GL0102889_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold25625_3:2:331:+	-
1902169	GL0046221_MH0086_[Complete]_[mRNA]_locus=scaffold25952_2:441:1559:-	Roseburia inulinivorans

1903630	GL0181512_MH0086_[Complete]_[mRNA]_locus=scaffold29056_19:167:2641:-	Bacteroides capillosus
1904230	GL0042809_MH0086_[Complete]_[mRNA]_locus=scaffold30439_2:531:1403:-	Roseburia inulinivorans
1904306	GL0152605_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold30586_1:3:137:+	-
1904347	GL0040543_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold30641_3:47:517:+	Clostridiales
1904876	GL0165099_MH0086_[Complete]_[mRNA]_locus=scaffold31748_1:28:1038:+	Enterobacteriaceae
1904958	GL0040808_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold31932_2:2:664:+	-
1904988	GL0059429_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold32017_8:1:831:-	Ruminococcus obeum
1905506	GL0064515_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold33188_5:2:1471:+	Clostridium cellulolyticum
1905510	GL0027690_MH0086_[Complete]_[mRNA]_locus=scaffold33188_8:110:529:+	Roseburia inulinivorans
1906401	GL0129250_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold35606_2:1:1500:-	Bacteria
1906986	GL0005056_MH0086_[Complete]_[mRNA]_locus=scaffold37313_2:21:1118:-	Roseburia inulinivorans
1907219	GL0003727_MH0086_[Complete]_[mRNA]_locus=scaffold37908_6:1894:3780:-	Bacteria
1907238	GL0088428_MH0086_[Complete]_[mRNA]_locus=scaffold37973_3:291:1241:-	Clostridium hylemonae
1907460	GL0077670_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold38863_2:1:183:+	Roseburia inulinivorans

1907590	GL0107588_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold39171_6:1:1128:-	-
1907650	GL0090684_MH0086_[Complete]_[mRNA]_locus=scaffold39383_6:493:1071:-	Clostridium bolteae
1908669	GL0049265_MH0086_[Complete]_[mRNA]_locus=scaffold41523_4:401:805:+	-
1909876	GL0036317_MH0086_[Complete]_[mRNA]_locus=scaffold44709_1:43:228:+	Bacteroides capillosus
1909964	GL0108481_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold45003_1:3:1208:-	Bacteroidales
1910379	GL0177496_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold46510_9:229:1842:-	Firmicutes
1910452	GL0105183_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold46822_5:1:762:-	Dorea longicatena
1911452	GL0125918_MH0086_[Complete]_[mRNA]_locus=scaffold50239_1:2293:4053:+	Clostridiales
1911627	GL0123059_MH0086_[Complete]_[mRNA]_locus=scaffold50826_4:97:984:+	-
1911854	GL0012155_MH0086_[Complete]_[mRNA]_locus=scaffold51509_5:1049:2434:-	Roseburia inulinivorans
1912296	GL0191694_MH0086_[Complete]_[mRNA]_locus=scaffold53198_3:1061:2158:+	Clostridium thermocellum
1913265	GL0046714_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold56809_3:1:1167:+	Roseburia inulinivorans
1913286	GL0147182_MH0086_[Complete]_[mRNA]_locus=scaffold56936_2:1301:2080:-	Roseburia inulinivorans
1913570	GL0057338_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold57747_4:158:943:-	Clostridium asparagiforme

1913650	GL0178621_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold57961_13:806:2518:-	-
1915608	GL0025553_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold65864_7:3:731:-	-
1916294	GL0129969_MH0086_[Complete]_[mRNA]_locus=scaffold68812_7:2:2317:+	Clostridiales
1916889	GL0143428_MH0086_[Complete]_[mRNA]_locus=scaffold71446_1:251:580:-	Faecalibacterium prausnitzii
1916942	GL0091664_MH0086_[Complete]_[mRNA]_locus=scaffold71631_2:140:979:+	-
1918004	GL0059408_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold76403_5:268:1359:-	-
1918153	GL0196655_MH0086_[Complete]_[mRNA]_locus=scaffold77014_7:2746:3897:+	-
1918894	GL0178720_MH0086_[Complete]_[mRNA]_locus=scaffold80521_3:254:1546:-	Roseburia inulinivorans
1919229	GL0016760_MH0086_[Complete]_[mRNA]_locus=scaffold82233_1:470:1867:+	Clostridiales
1919306	GL0073640_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold82532_5:2:2356:-	Roseburia inulinivorans
1920865	GL0036780_MH0086_[Complete]_[mRNA]_locus=scaffold89837_4:143:1501:+	Clostridiales
1922023	GL0014856_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold95239_3:844:1680:+	-
1923385	GL0191384_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold101647_2:3:863:-	Clostridium difficile
1923875	GL0040231_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold103542_1:1:1290:+	Clostridiales

1924867	GL0150550_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold106362_2:827:1390:-	Alistipes putredinis
1926590	GL0191880_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold110386_2:3:1040:-	Clostridium hylemonae
1929455	GL0063518_O2_[Complete]_[mRNA]_locus=scaffold562_5:380:3172:-	Roseburia inulinivorans
1929780	GL0038612_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1127_8:1054:2145:-	Roseburia inulinivorans
1929791	GL0022978_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1150_1:1:690:+	Roseburia inulinivorans
1929843	GL0059718_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1251_4:2125:2361:-	Roseburia inulinivorans
1930163	GL0010261_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1895_2:2:1039:+	Faecalibacterium prausnitzii
1930186	GL0037496_O2_[Complete]_[mRNA]_locus=scaffold1967_7:753:2483:+	Clostridiales
1930187	GL0037500_O2_[Complete]_[mRNA]_locus=scaffold1967_7:6690:7766:+	Roseburia inulinivorans
1930593	GL0053607_O2_[Complete]_[mRNA]_locus=scaffold2905_5:627:1238:-	Roseburia inulinivorans
1930890	GL0048735_O2_[Complete]_[mRNA]_locus=scaffold3711_1:211:2250:-	Bacteria
1931355	GL0034358_O2_[Lack_5'-end]_[mRNA]_locus=scaffold4933_1:406:576:-	Faecalibacterium prausnitzii
1931402	GL0051722_O2_[Lack_both_end]_[mRNA]_locus=scaffold5022_2:1:885:+	-
1931796	GL0059668_O2_[Complete]_[mRNA]_locus=scaffold5971_4:402:914:+	Roseburia inulinivorans

1931947	GL0015757_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6361_1:281:517:+	-
1931963	GL0048010_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6401_4:1783:2349:-	Erysipelotrichaceae
1932068	GL0050533_O2_[Complete]_[mRNA]_locus=scaffold6713_2:4470:5249:-	Roseburia inulinivorans
1932147	GL0049197_O2_[Complete]_[mRNA]_locus=scaffold7004_2:2306:3568:-	Roseburia inulinivorans
1932149	GL0049199_O2_[Complete]_[mRNA]_locus=scaffold7004_2:4929:5783:-	Roseburia inulinivorans
1933326	GL0060746_O2_[Complete]_[mRNA]_locus=scaffold10074_1:22:1704:-	Firmicutes
1933621	GL0007672_O2_[Lack_3'-end]_[mRNA]_locus=scaffold10931_1:239:715:+	Proteobacteria
1934866	GL0024311_O2_[Lack_3'-end]_[mRNA]_locus=scaffold14201_1:107:511:+	Faecalibacterium prausnitzii
1935610	GL0021303_O2_[Lack_5'-end]_[mRNA]_locus=scaffold16423_4:2:1009:+	Roseburia inulinivorans
1935688	GL0075567_O2_[Complete]_[mRNA]_locus=scaffold16726_1:2254:4347:+	Roseburia inulinivorans
1935824	GL0006378_O2_[Lack_5'-end]_[mRNA]_locus=scaffold17139_5:194:991:-	Roseburia inulinivorans
1936107	GL0070333_O2_[Lack_3'-end]_[mRNA]_locus=scaffold17949_1:584:694:+	-
1936305	GL0060765_O2_[Complete]_[mRNA]_locus=scaffold18668_1:297:737:-	Faecalibacterium prausnitzii
1936520	GL0049950_O2_[Lack_5'-end]_[mRNA]_locus=scaffold19274_1:504:917:-	Faecalibacterium prausnitzii

1936538	GL0019647_O2_[Complete]_[mRNA]_locus=scaffold19331_12:3548:6112:+	Bacteria
1936635	GL0069166_O2_[Complete]_[mRNA]_locus=scaffold19653_3:386:1402:+	Roseburia inulinivorans
1937410	GL0043859_O2_[Lack_5'-end]_[mRNA]_locus=scaffold22019_1:1:579:+	Clostridium methylpentosum
1938545	GL0071469_O2_[Lack_5'-end]_[mRNA]_locus=scaffold25722_2:71:535:-	Bacteroides capillosus
1938576	GL0009993_O2_[Complete]_[mRNA]_locus=scaffold25874_3:2908:3600:-	Roseburia inulinivorans
1944834	GL0006151_O2_[Lack_3'-end]_[mRNA]_locus=scaffold44080_1:1:468:-	Roseburia inulinivorans
1945807	GL0071951_O2_[Lack_5'-end]_[mRNA]_locus=scaffold46155_1:30:1547:-	Roseburia inulinivorans
1950188	GL0053055_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1306_1:1:138:-	-
1952247	GL0029368_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3698_4:2:1537:+	Bacteroides pectinophilus
1954322	GL0100532_O2_[Complete]_[mRNA]_locus=scaffold7151_5:3:1766:+	Bacteria
1954686	GL0088831_O2_[Complete]_[mRNA]_locus=scaffold7907_1:789:2618:+	Bacteria
1957755	GL0036296_O2_[Complete]_[mRNA]_locus=scaffold15634_1:1282:2292:+	Ruminococcus obeum
1960572	GL0038672_O2_[Lack_3'-end]_[mRNA]_locus=scaffold26398_1:54:884:+	Ruminococcus obeum
1963938	GL0008446_O2_[Lack_both_end]_[mRNA]_locus=scaffold43973_1:1:510:+	Ruminococcus obeum

1966807	GL0091856_O2_[Lack_3'-end]_[mRNA]_locus=scaffold57422_1:3:623:-	Clostridiales
1967141	GL0086174_O2_[Lack_both_end]_[mRNA]_locus=scaffold58487_1:3:944:+	Ruminococcus obeum
1967183	GL0048645_O2_[Lack_3'-end]_[mRNA]_locus=scaffold58603_1:3:581:-	Ruminococcus obeum
1967229	GL0061477_O2_[Lack_3'-end]_[mRNA]_locus=scaffold58730_1:1:672:-	Ruminococcus obeum
1967901	GL0057842_O2_[Lack_3'-end]_[mRNA]_locus=scaffold60354_1:2:451:-	-
1971431	GL0080269_O2_[Complete]_[mRNA]_locus=scaffold2609_4:23385:24746:-	Bacteria
1973227	GL0009559_O2_[Lack_3'-end]_[mRNA]_locus=scaffold7319_1:3:1223:-	Bacteroides capillosus
1973957	GL0002897_O2_[Complete]_[mRNA]_locus=scaffold9291_2:497:1453:+	Clostridium phytofermentans
1976012	GL0112056_O2_[Complete]_[mRNA]_locus=scaffold15651_1:95:1219:+	Roseburia inulinivorans
1985805	GL0021091_O2_[Lack_3'-end]_[mRNA]_locus=scaffold58315_1:99:821:+	-
1991535	GL0023300_O2_[Complete]_[mRNA]_locus=scaffold3815_4:60:476:-	Bacteroides capillosus
1991709	GL0042277_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4873_1:529:864:+	Clostridium asparagiforme
1997457	GL0013232_O2_[Complete]_[mRNA]_locus=scaffold48_1:18588:19157:+	-
1998261	GL0028973_O2_[Lack_3'-end]_[mRNA]_locus=scaffold2118_1:153:803:+	Faecalibacterium prausnitzii

2000547	GL0046973_O2_[Complete]_[mRNA]_locus=scaffold12303_1:351:791:+	Roseburia inulinivorans
2001457	GL0006010_O2_[Complete]_[mRNA]_locus=scaffold19202_1:64:543:+	Bacteria
2001931	GL0015466_O2_[Lack_3'-end]_[mRNA]_locus=scaffold22965_1:39:608:+	Roseburia inulinivorans
2007172	GL0017695_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6538_2:214:798:+	Bacillales
2007517	GL0005911_O2_[Lack_5'-end]_[mRNA]_locus=scaffold9448_1:415:585:-	Bacteria
2007608	GL0029530_O2_[Lack_both_end]_[mRNA]_locus=scaffold10356_1:1:2451:+	Bacteria
2008265	GL0000555_O2_[Complete]_[mRNA]_locus=scaffold17934_1:720:2246:+	-
2011951	GL0073015_O2_[Complete]_[mRNA]_locus=scaffold103_2:787:2076:+	Clostridium bolteae
2011978	GL0079476_O2_[Lack_5'-end]_[mRNA]_locus=scaffold112_18:2:262:+	Ruminococcus gnavus
2011979	GL0018694_O2_[Lack_3'-end]_[mRNA]_locus=scaffold112_23:2:1060:-	Ruminococcus gnavus
2012100	GL0071224_O2_[Complete]_[mRNA]_locus=scaffold141_5:893:1636:-	Clostridium bolteae
2012457	GL0056674_O2_[Lack_both_end]_[mRNA]_locus=scaffold199_8:2:598:-	Clostridium bolteae
2012926	GL0049100_O2_[Complete]_[mRNA]_locus=scaffold292_8:740:1399:-	Ruminococcus torques
2013196	GL0079163_O2_[Lack_5'-end]_[mRNA]_locus=scaffold350_1:3:587:+	Clostridium bolteae

2014768	GL0060146_O2_[Lack_5'-end]_[mRNA]_locus=scaffold634_1:1:285:+	Clostridium bolteae
2015685	GL0053610_O2_[Lack_5'-end]_[mRNA]_locus=scaffold833_6:2097:2930:-	Clostridium bolteae
2017296	GL0013515_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1156_8:1:594:-	Clostridium bolteae
2017314	GL0041855_O2_[Complete]_[mRNA]_locus=scaffold1164_3:1503:2204:+	Clostridium bolteae
2017667	GL0069680_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1255_6:3058:4146:+	Clostridium bolteae
2017872	GL0053632_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1298_2:2:514:+	Clostridium bolteae
2018070	GL0043430_O2_[Complete]_[mRNA]_locus=scaffold1340_2:1056:1316:-	Ruminococcus gnavus
2018392	GL0010859_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1406_13:2:1033:+	Clostridium bolteae
2018899	GL0082894_O2_[Lack_both_end]_[mRNA]_locus=scaffold1556_2:2:658:+	Clostridium bolteae
2019521	GL0086906_O2_[Complete]_[mRNA]_locus=scaffold1728_12:5263:6243:-	Clostridium bolteae
2019845	GL0015776_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1828_1:3:665:-	Clostridium bolteae
2019882	GL0079810_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1844_4:124:834:+	Clostridium bolteae
2020051	GL0004505_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1892_6:1507:2445:-	Clostridium bolteae
2020609	GL0093493_O2_[Complete]_[mRNA]_locus=scaffold1992_5:106:723:-	Clostridium bolteae

2021067	GL0068290_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2133_1:3420:3521:-	Ruminococcus gnavus
2021068	GL0051857_O2_[Complete]_[mRNA]_locus=scaffold2133_6:1639:2550:-	Ruminococcus gnavus
2021122	GL0044220_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2170_2:2:1057:+	Clostridium bolteae
2021908	GL0079885_O2_[Complete]_[mRNA]_locus=scaffold2327_5:639:1967:+	Bacteria
2022648	GL0047592_O2_[Lack_3'-end]_[mRNA]_locus=scaffold2510_2:1:630:-	Clostridium bolteae
2022860	GL0048694_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2556_2:2:436:+	Clostridium bolteae
2023714	GL0029203_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2933_1:1:168:+	Clostridium bolteae
2024053	GL0025094_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3061_3:3907:4278:-	-
2024148	GL0040331_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3110_2:2:1207:+	Clostridium bolteae
2024538	GL0074654_O2_[Complete]_[mRNA]_locus=scaffold3231_2:886:2337:-	Clostridium bolteae
2025038	GL0027712_O2_[Complete]_[mRNA]_locus=scaffold3429_2:211:1563:-	Clostridium bolteae
2025494	GL0009369_O2_[Complete]_[mRNA]_locus=scaffold3657_2:14:385:-	Clostridium ramosum
2025709	GL0078135_O2_[Complete]_[mRNA]_locus=scaffold3714_15:9436:10089:-	Clostridium
2026643	GL0034222_O2_[Lack_both_end]_[mRNA]_locus=scaffold4089_2:1:1089:-	Clostridium bolteae

2026778	GL0090066_O2_[Complete]_[mRNA]_locus=scaffold4139_3:355:1014:-	Clostridium bolteae
2027013	GL0003988_O2_[Lack_5'-end]_[mRNA]_locus=scaffold4197_6:69:674:-	Clostridium ramosum
2027016	GL0015315_O2_[Lack_5'-end]_[mRNA]_locus=scaffold4197_10:2:1279:+	Clostridium ramosum
2027647	GL0038676_O2_[Lack_both_end]_[mRNA]_locus=scaffold4411_1:1:552:-	-
2027754	GL0003997_O2_[Lack_both_end]_[mRNA]_locus=scaffold4455_4:2:1306:+	Clostridium bolteae
2027898	GL0006585_O2_[Lack_both_end]_[mRNA]_locus=scaffold4529_1:2:739:+	Clostridium ramosum
2027901	GL0013655_O2_[Complete]_[mRNA]_locus=scaffold4529_2:960:1709:-	Clostridium ramosum
2028225	GL0010108_O2_[Complete]_[mRNA]_locus=scaffold4700_3:1005:2024:-	Clostridium bolteae
2028583	GL0018476_O2_[Lack_5'-end]_[mRNA]_locus=scaffold4792_11:3:296:+	Ruminococcus gnavus
2028663	GL0008988_O2_[Lack_5'-end]_[mRNA]_locus=scaffold4827_11:288:959:-	Clostridium
2029240	GL0078624_O2_[Complete]_[mRNA]_locus=scaffold5044_4:1045:1872:-	Clostridium ramosum
2029245	GL0089384_O2_[Lack_3'-end]_[mRNA]_locus=scaffold5044_9:3:1100:-	Clostridium ramosum
2029279	GL0064027_O2_[Complete]_[mRNA]_locus=scaffold5048_25:2378:2878:+	Ruminococcus gnavus
2029298	GL0085275_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5053_14:3:314:+	Ruminococcus gnavus

2029727	GL0086265_O2_[Lack_3'-end]_[mRNA]_locus=scaffold5244_2:2:169:-	Clostridium bolteae
2029819	GL0008349_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5288_5:2:1087:+	Clostridium
2030739	GL0074188_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5634_4:2443:2748:-	Clostridium ramosum
2031270	GL0025812_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5872_8:186:800:-	Clostridium hylemonae
2032414	GL0014501_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6327_20:1898:2206:-	Clostridium ramosum
2032422	GL0011478_O2_[Complete]_[mRNA]_locus=scaffold6327_26:970:2910:+	Clostridium ramosum
2032430	GL0014503_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6328_10:653:1264:-	Clostridium bolteae
2032677	GL0069702_O2_[Lack_both_end]_[mRNA]_locus=scaffold6472_4:2:856:+	Clostridium bolteae
2032888	GL0061516_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6521_12:2155:2715:+	Clostridium bolteae
2033168	GL0048745_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6693_2:50:508:-	Clostridium bolteae
2033860	GL0070161_O2_[Complete]_[mRNA]_locus=scaffold7141_5:1577:2920:-	Clostridiales
2034149	GL0007848_O2_[Complete]_[mRNA]_locus=scaffold7335_1:1070:1600:+	Ruminococcus gnavus
2034829	GL0038149_O2_[Lack_5'-end]_[mRNA]_locus=scaffold7953_4:2:340:+	Ruminococcus gnavus
2035749	GL0051573_O2_[Lack_3'-end]_[mRNA]_locus=scaffold8481_1:3:1067:-	Clostridium bolteae

2035927	GL0022530_O2_[Complete]_[mRNA]_locus=scaffold8591_4:631:993:+	Clostridium bolteae
2037031	GL0034427_O2_[Complete]_[mRNA]_locus=scaffold9199_9:535:1299:-	Ruminococcus gnavus
2037586	GL0004332_O2_[Complete]_[mRNA]_locus=scaffold9678_1:148:1233:-	Clostridium bolteae
2037886	GL0056866_O2_[Lack_3'-end]_[mRNA]_locus=scaffold9891_5:3:308:-	Ruminococcus gnavus
2038054	GL0018911_O2_[Lack_3'-end]_[mRNA]_locus=scaffold10025_1:418:1884:+	Clostridium bolteae
2038265	GL0092902_O2_[Lack_5'-end]_[mRNA]_locus=scaffold10183_2:472:1500:-	Clostridium bolteae
2038468	GL0018349_O2_[Lack_3'-end]_[mRNA]_locus=scaffold10376_2:204:1298:+	Ruminococcus gnavus
2038697	GL0084228_O2_[Lack_3'-end]_[mRNA]_locus=scaffold10516_5:1:228:-	Clostridium ramosum
2038839	GL0026607_O2_[Complete]_[mRNA]_locus=scaffold10665_2:79:495:+	Clostridium bolteae
2039668	GL0059754_O2_[Lack_3'-end]_[mRNA]_locus=scaffold11326_9:1:378:-	Finegoldia magna
2039789	GL0012366_O2_[Complete]_[mRNA]_locus=scaffold11421_5:301:774:-	Clostridium ramosum
2040208	GL0083107_O2_[Complete]_[mRNA]_locus=scaffold11724_12:4430:4663:+	Ruminococcus gnavus
2040215	GL0035862_O2_[Lack_5'-end]_[mRNA]_locus=scaffold11726_20:4464:4970:-	Ruminococcus gnavus
2040789	GL0039314_O2_[Lack_3'-end]_[mRNA]_locus=scaffold12163_2:1:675:-	Clostridium bolteae

2040815	GL0016245_O2_[Lack_3'-end]_[mRNA]_locus=scaffold12180_3:359:1045:+	Clostridium ramosum
2041050	GL0062302_O2_[Complete]_[mRNA]_locus=scaffold12290_7:1121:1375:+	-
2041156	GL0051946_O2_[Complete]_[mRNA]_locus=scaffold12375_1:319:699:-	Clostridium bolteae
2041160	GL0042908_O2_[Lack_both_end]_[mRNA]_locus=scaffold12385_2:3:1211:+	Erysipelotrichaceae
2041230	GL0038932_O2_[Complete]_[mRNA]_locus=scaffold12422_7:145:978:+	Clostridium ramosum
2041414	GL0049348_O2_[Complete]_[mRNA]_locus=scaffold12595_12:238:807:-	Clostridium ramosum
2041417	GL0036341_O2_[Complete]_[mRNA]_locus=scaffold12595_13:522:2150:+	Erysipelotrichaceae
2041644	GL0024758_O2_[Lack_3'-end]_[mRNA]_locus=scaffold12873_7:3:797:-	Clostridium ramosum
2041727	GL0059699_O2_[Lack_5'-end]_[mRNA]_locus=scaffold12942_8:1:408:+	Clostridium bolteae
2041729	GL0061374_O2_[Lack_both_end]_[mRNA]_locus=scaffold12942_13:1:687:+	Clostridium bolteae
2041882	GL0002952_O2_[Lack_5'-end]_[mRNA]_locus=scaffold13041_1:1:234:+	Clostridium bolteae
2042002	GL0034597_O2_[Lack_5'-end]_[mRNA]_locus=scaffold13205_1:300:599:-	-
2042967	GL0004591_O2_[Lack_5'-end]_[mRNA]_locus=scaffold14014_5:581:1057:-	Clostridium methylpentosum
2043397	GL0055744_O2_[Complete]_[mRNA]_locus=scaffold14484_8:114:1085:+	Clostridium ramosum

2043774	GL0028288_O2_[Lack_3'-end]_[mRNA]_locus=scaffold14704_1:3:257:-	Clostridium bolteae
2045113	GL0084927_O2_[Lack_5'-end]_[mRNA]_locus=scaffold16213_2:2:253:+	Clostridium ramosum
2045474	GL0031550_O2_[Lack_3'-end]_[mRNA]_locus=scaffold16612_1:435:665:+	Clostridium bolteae
2045842	GL0050146_O2_[Complete]_[mRNA]_locus=scaffold17013_3:674:928:-	Ruminococcus gnavus
2045873	GL0086759_O2_[Complete]_[mRNA]_locus=scaffold17097_2:826:1506:+	Clostridium ramosum
2046521	GL0029586_O2_[Lack_5'-end]_[mRNA]_locus=scaffold17747_14:2:1864:+	Clostridium ramosum
2046573	GL0040993_O2_[Complete]_[mRNA]_locus=scaffold17862_3:24:611:+	Clostridium ramosum
2046715	GL0061820_O2_[Lack_3'-end]_[mRNA]_locus=scaffold18032_2:2:1186:-	Erysipelotrichaceae
2046768	GL0036908_O2_[Complete]_[mRNA]_locus=scaffold18094_2:191:457:+	Clostridium bolteae
2047230	GL0018082_O2_[Complete]_[mRNA]_locus=scaffold18755_8:863:1615:+	Clostridium ramosum
2047340	GL0067256_O2_[Lack_both_end]_[mRNA]_locus=scaffold18907_5:3:899:+	Clostridium ramosum
2047480	GL0069173_O2_[Complete]_[mRNA]_locus=scaffold19109_16:2560:2811:+	Clostridium ramosum
2047604	GL0063309_O2_[Lack_both_end]_[mRNA]_locus=scaffold19270_2:1:747:+	Clostridium ramosum
2047626	GL0012153_O2_[Lack_3'-end]_[mRNA]_locus=scaffold19298_2:3:1001:-	Clostridium ramosum

2048063	GL0073919_O2_[Lack_5'-end]_[mRNA]_locus=scaffold19796_8:3:512:+	Clostridium ramosum
2048076	GL0009209_O2_[Complete]_[mRNA]_locus=scaffold19796_14:3551:4624:+	Clostridium ramosum
2048549	GL0060215_O2_[Lack_3'-end]_[mRNA]_locus=scaffold20288_1:2:649:-	Clostridium bolteae
2049146	GL0089614_O2_[Complete]_[mRNA]_locus=scaffold21113_2:1465:2397:+	Clostridium ramosum
2049349	GL0071448_O2_[Lack_5'-end]_[mRNA]_locus=scaffold21305_12:2:784:+	Clostridium ramosum
2049361	GL0008800_O2_[Lack_3'-end]_[mRNA]_locus=scaffold21339_4:839:2608:+	Vibrio parahaemolyticus
2049424	GL0045226_O2_[Complete]_[mRNA]_locus=scaffold21483_4:1054:1674:-	Clostridium ramosum
2049429	GL0077218_O2_[Complete]_[mRNA]_locus=scaffold21483_7:961:1833:-	Clostridium ramosum
2050101	GL0085185_O2_[Lack_3'-end]_[mRNA]_locus=scaffold22240_7:3:710:-	Clostridium ramosum
2050572	GL0009941_O2_[Complete]_[mRNA]_locus=scaffold23076_5:236:1300:+	Clostridium bolteae
2050765	GL0027269_O2_[Lack_5'-end]_[mRNA]_locus=scaffold23388_2:1:534:+	Ruminococcus gnavus
2051147	GL0083267_O2_[Lack_both_end]_[mRNA]_locus=scaffold24157_1:3:974:-	Roseburia inulinivorans
2051336	GL0062796_O2_[Lack_both_end]_[mRNA]_locus=scaffold24509_1:3:1109:-	Clostridium ramosum
2051395	GL0031413_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24600_2:2:694:-	Clostridium ramosum

2051409	GL0088648_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24600_11:435:938:+	Clostridium ramosum
2051415	GL0082022_O2_[Complete]_[mRNA]_locus=scaffold24600_18:790:1524:-	Clostridium ramosum
2051416	GL0082023_O2_[Lack_5'-end]_[mRNA]_locus=scaffold24600_18:1540:2145:-	Clostridium ramosum
2051487	GL0070638_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24657_5:2:529:-	Clostridium ramosum
2051551	GL0078181_O2_[Complete]_[mRNA]_locus=scaffold24752_8:2321:2638:-	Clostridium ramosum
2051573	GL0032049_O2_[Complete]_[mRNA]_locus=scaffold24802_4:1263:1805:+	Clostridium ramosum
2051627	GL0032993_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24902_2:3:758:-	Clostridium ramosum
2051738	GL0006133_O2_[Lack_5'-end]_[mRNA]_locus=scaffold25187_8:3:632:+	Clostridium ramosum
2051741	GL0050890_O2_[Lack_5'-end]_[mRNA]_locus=scaffold25187_9:2:568:+	Clostridium ramosum
2051975	GL0006820_O2_[Complete]_[mRNA]_locus=scaffold25654_2:567:1472:-	Clostridium bolteae
2051999	GL0038968_O2_[Lack_3'-end]_[mRNA]_locus=scaffold25725_1:2:1345:-	Bacteroides cellulosilyticus
2052011	GL0000878_O2_[Lack_3'-end]_[mRNA]_locus=scaffold25766_1:3:380:-	Bacteria
2052312	GL0092340_O2_[Lack_both_end]_[mRNA]_locus=scaffold26229_10:2:1309:-	Clostridium ramosum

2052586	GL0086645_O2_[Lack_5'-end]_[mRNA]_locus=scaffold26821_5:1286:1960:-	Clostridium ramosum
2052619	GL0041503_O2_[Lack_3'-end]_[mRNA]_locus=scaffold26894_1:2198:4033:+	Clostridium hylemonae
2052732	GL0054010_O2_[Lack_3'-end]_[mRNA]_locus=scaffold27185_2:207:650:+	Roseburia inulinivorans
2053338	GL0011375_O2_[Lack_5'-end]_[mRNA]_locus=scaffold28400_3:1:762:+	Clostridium ramosum
2053549	GL0039293_O2_[Lack_5'-end]_[mRNA]_locus=scaffold28847_2:703:1302:-	Clostridium ramosum
2053708	GL0024787_O2_[Complete]_[mRNA]_locus=scaffold29092_12:187:531:+	Clostridium ramosum
2053922	GL0007991_O2_[Lack_both_end]_[mRNA]_locus=scaffold29395_3:3:683:+	Clostridium ramosum
2054727	GL0085323_O2_[Lack_3'-end]_[mRNA]_locus=scaffold31115_3:1:225:-	Bacteria
2055127	GL0092898_O2_[Lack_both_end]_[mRNA]_locus=scaffold31866_10:2:1744:-	Clostridium ramosum
2055250	GL0088120_O2_[Lack_3'-end]_[mRNA]_locus=scaffold32121_2:203:562:+	Clostridium bolteae
2055349	GL0057529_O2_[Lack_both_end]_[mRNA]_locus=scaffold32359_5:1:1044:-	Clostridium ramosum
2055351	GL0071686_O2_[Complete]_[mRNA]_locus=scaffold32359_6:1563:2573:+	Clostridium ramosum
2055408	GL0040959_O2_[Complete]_[mRNA]_locus=scaffold32473_3:88:873:-	Clostridium ramosum
2055419	GL0051305_O2_[Complete]_[mRNA]_locus=scaffold32484_2:2177:3001:+	Eubacterium ventriosum

2055589	GL0050261_O2_[Lack_5'-end]_[mRNA]_locus=scaffold32740_6:227:1831:-	Clostridium ramosum
2055706	GL0004603_O2_[Complete]_[mRNA]_locus=scaffold32898_3:105:980:+	Clostridium ramosum
2055707	GL0004604_O2_[Complete]_[mRNA]_locus=scaffold32898_3:1062:1934:-	Clostridium ramosum
2055810	GL0065207_O2_[Lack_3'-end]_[mRNA]_locus=scaffold33125_6:616:1509:+	Clostridium ramosum
2055919	GL0014607_O2_[Lack_5'-end]_[mRNA]_locus=scaffold33398_6:267:587:-	Clostridium ramosum
2055944	GL0093332_O2_[Lack_3'-end]_[mRNA]_locus=scaffold33441_3:2614:3024:+	Clostridium ramosum
2055966	GL0066228_O2_[Complete]_[mRNA]_locus=scaffold33501_4:50:880:-	Clostridium ramosum
2056129	GL0008496_O2_[Lack_5'-end]_[mRNA]_locus=scaffold33895_5:32:946:-	Clostridium ramosum
2056179	GL0081516_O2_[Lack_3'-end]_[mRNA]_locus=scaffold33932_6:3869:4291:+	Clostridium ramosum
2056184	GL0008308_O2_[Complete]_[mRNA]_locus=scaffold33932_8:1918:2685:-	Clostridium ramosum
2056205	GL0037899_O2_[Complete]_[mRNA]_locus=scaffold33948_5:183:665:+	Clostridium ramosum
2056240	GL0085265_O2_[Lack_3'-end]_[mRNA]_locus=scaffold34022_1:289:1110:+	Clostridium ramosum
2056241	GL0019582_O2_[Lack_5'-end]_[mRNA]_locus=scaffold34022_2:3:440:+	Clostridium ramosum
2056759	GL0026145_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35193_1:2:706:+	Clostridium ramosum

2056914	GL0042221_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35508_4:3:479:+	Clostridium ramosum
2057147	GL0028447_O2_[Complete]_[mRNA]_locus=scaffold35893_5:156:1307:+	Erysipelotrichaceae
2057157	GL0038895_O2_[Complete]_[mRNA]_locus=scaffold35911_1:2134:3069:+	Clostridium ramosum
2057161	GL0064896_O2_[Lack_3'-end]_[mRNA]_locus=scaffold35911_2:1143:2357:+	Erysipelotrichaceae
2057229	GL0051619_O2_[Complete]_[mRNA]_locus=scaffold36097_2:838:2190:-	Erysipelotrichaceae
2057349	GL0045898_O2_[Lack_3'-end]_[mRNA]_locus=scaffold36296_7:1:2814:-	Erysipelotrichaceae
2057356	GL0054437_O2_[Lack_both_end]_[mRNA]_locus=scaffold36297_4:1:570:-	Clostridium ramosum
2057379	GL0073936_O2_[Lack_5'-end]_[mRNA]_locus=scaffold36335_1:384:1565:-	Clostridium ramosum
2057490	GL0059348_O2_[Lack_3'-end]_[mRNA]_locus=scaffold36519_2:2014:2586:+	Clostridium ramosum
2057948	GL0021064_O2_[Lack_both_end]_[mRNA]_locus=scaffold37031_4:3:1448:-	Clostridium ramosum
2058009	GL0066989_O2_[Lack_3'-end]_[mRNA]_locus=scaffold37108_6:2:661:-	Clostridium ramosum
2058091	GL0000875_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37245_6:117:896:-	Clostridium ramosum
2058191	GL0003321_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37369_1:923:1852:-	Clostridium ramosum
2058250	GL0061449_O2_[Complete]_[mRNA]_locus=scaffold37467_3:93:971:-	Clostridium ramosum

2058587	GL0008705_O2_[Complete]_[mRNA]_locus=scaffold37962_2:321:1067:-	Clostridium ramosum
2058657	GL0052584_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38035_4:2550:3122:+	Clostridium ramosum
2058938	GL0079054_O2_[Complete]_[mRNA]_locus=scaffold38187_2:981:1442:-	Clostridium ramosum
2058941	GL0020471_O2_[Complete]_[mRNA]_locus=scaffold38190_1:1092:2015:+	Clostridium ramosum
2059835	GL0081153_O2_[Lack_3'-end]_[mRNA]_locus=scaffold30_2:1:1086:-	Bacteroides capillosus
2060424	GL0083739_O2_[Complete]_[mRNA]_locus=scaffold1352_1:161:1258:+	Alistipes putredinis
2060771	GL0013372_O2_[Complete]_[mRNA]_locus=scaffold2399_2:382:1275:+	Alistipes putredinis
2061520	GL0121607_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4222_12:1708:2892:+	Alistipes putredinis
2061948	GL0112213_O2_[Complete]_[mRNA]_locus=scaffold5733_3:157:2364:+	Bacteroidetes
2063426	GL0048845_O2_[Complete]_[mRNA]_locus=scaffold11024_10:212:1507:+	Alistipes putredinis
2063610	GL0051974_O2_[Lack_5'-end]_[mRNA]_locus=scaffold11814_6:721:1395:-	Alistipes putredinis
2064197	GL0095870_O2_[Lack_5'-end]_[mRNA]_locus=scaffold13550_9:1796:3373:-	Bacteria
2064430	GL0091427_O2_[Complete]_[mRNA]_locus=scaffold14824_1:956:2032:-	Bacteroides uniformis
2064619	GL0096606_O2_[Complete]_[mRNA]_locus=scaffold15973_9:320:1756:-	Bacteroides uniformis

2065555	GL0034571_O2_[Complete]_[mRNA]_locus=scaffold19287_2:1359:2261:-	Alistipes putredinis
2065569	GL0111944_O2_[Lack_3'-end]_[mRNA]_locus=scaffold19406_2:3:779:-	Alistipes putredinis
2066020	GL0092412_O2_[Lack_3'-end]_[mRNA]_locus=scaffold22195_6:1:1434:-	Bacteroidales
2066444	GL0095102_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24510_1:215:1507:+	Alistipes putredinis
2066573	GL0057809_O2_[Complete]_[mRNA]_locus=scaffold25292_1:1440:2981:-	Bacteria
2066803	GL0064906_O2_[Complete]_[mRNA]_locus=scaffold26918_3:369:1352:-	Alistipes putredinis
2066980	GL0118911_O2_[Lack_both_end]_[mRNA]_locus=scaffold27786_4:1:906:-	Alistipes putredinis
2067379	GL0039101_O2_[Complete]_[mRNA]_locus=scaffold30552_4:789:4355:+	Bacteroidetes
2067726	GL0006721_O2_[Lack_3'-end]_[mRNA]_locus=scaffold32607_3:129:692:+	Clostridiales
2068729	GL0005685_O2_[Complete]_[mRNA]_locus=scaffold39227_1:53:1195:-	Bacteroides thetaiotaomicron
2070504	GL0092289_O2_[Complete]_[mRNA]_locus=scaffold55080_3:598:1704:+	Alistipes putredinis
2070606	GL0066793_O2_[Complete]_[mRNA]_locus=scaffold56067_5:84:989:-	Alistipes putredinis
2070757	GL0003627_O2_[Lack_both_end]_[mRNA]_locus=scaffold57635_3:3:782:-	Clostridium
2070849	GL0085031_O2_[Complete]_[mRNA]_locus=scaffold58869_2:1636:3216:-	Bacteroidetes

2071016	GL0002687_O2_[Complete]_[mRNA]_locus=scaffold60870_1:174:572:-	Clostridium asparagiforme
2071429	GL0113401_O2_[Lack_3'-end]_[mRNA]_locus=scaffold64030_1:542:1363:+	Alistipes putredinis
2073194	GL0058990_O2_[Lack_3'-end]_[mRNA]_locus=scaffold78808_3:905:1528:+	Alistipes putredinis
2073258	GL0122747_O2_[Complete]_[mRNA]_locus=scaffold79273_2:141:1040:-	Anaerostipes caccae
2073765	GL0026207_O2_[Complete]_[mRNA]_locus=scaffold84777_5:267:1529:+	Bacteroides uniformis
2074241	GL0045350_O2_[Complete]_[mRNA]_locus=scaffold89210_2:1437:2501:-	Alistipes putredinis
2074401	GL0060928_O2_[Complete]_[mRNA]_locus=scaffold90533_4:257:1087:-	Alistipes putredinis
2075712	GL0062384_O2_[Complete]_[mRNA]_locus=scaffold99010_2:47:874:-	Ruminococcus obeum
2079191	GL0056542_O2_[Complete]_[mRNA]_locus=scaffold1018_1:201:527:-	Roseburia inulinivorans
2079517	GL0065609_O2_[Complete]_[mRNA]_locus=scaffold1569_2:2700:4340:+	Clostridium methylpentosum
2087805	GL0069650_O2_[Complete]_[mRNA]_locus=scaffold23892_1:216:848:+	Roseburia inulinivorans
2088593	GL0041545_O2_[Complete]_[mRNA]_locus=scaffold27057_1:367:1170:-	Clostridium asparagiforme
2091064	GL0006377_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38289_3:3:467:-	Clostridium
2097542	GL0077525_O2_[Lack_3'-end]_[mRNA]_locus=scaffold76710_1:113:598:+	Clostridiales

2102209	GL0069799_O2_[Lack_5'-end]_[mRNA]_locus=scaffold700_3:596:1117:-	Faecalibacterium prausnitzii
2102363	GL0058269_O2_[Complete]_[mRNA]_locus=scaffold1234_8:5794:6927:+	Bacteroides capillosus
2102376	GL0100251_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1308_1:2:1339:+	Ruminococcus lactaris
2102800	GL0088522_O2_[Complete]_[mRNA]_locus=scaffold2596_1:1990:4404:-	Bacteria
2102952	GL0006289_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3061_1:91:1170:-	Bacteroides capillosus
2102968	GL0030832_O2_[Complete]_[mRNA]_locus=scaffold3095_1:868:2556:+	Firmicutes
2103048	GL0060587_O2_[Lack_3'-end]_[mRNA]_locus=scaffold3390_2:1:528:-	Faecalibacterium prausnitzii
2103081	GL0025164_O2_[Lack_both_end]_[mRNA]_locus=scaffold3489_1:1:900:+	Faecalibacterium prausnitzii
2103105	GL0043563_O2_[Complete]_[mRNA]_locus=scaffold3580_3:133:1323:+	-
2103423	GL0106068_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4613_2:3:782:-	Ruminococcus obeum
2103868	GL0035510_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6168_3:135:749:-	-
2103983	GL0021890_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6523_2:3:941:-	-
2103984	GL0021891_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6523_2:1115:1456:-	-
2105538	GL0100708_O2_[Complete]_[mRNA]_locus=scaffold12636_6:2948:5197:+	Syntrophomonas wolfei

2105589	GL0057066_O2_[Complete]_[mRNA]_locus=scaffold12840_6:845:2506:+	Bacteria
2106156	GL0114824_O2_[Lack_3'-end]_[mRNA]_locus=scaffold14745_3:23:1033:+	Ruminococcus obeum
2106157	GL0080421_O2_[Complete]_[mRNA]_locus=scaffold14745_4:194:2311:+	Ruminococcus obeum
2106863	GL0096694_O2_[Lack_5'-end]_[mRNA]_locus=scaffold18394_1:1:630:+	Bacteroides capillosus
2107224	GL0040902_O2_[Lack_3'-end]_[mRNA]_locus=scaffold20294_4:2772:3686:+	Bacteroides capillosus
2107642	GL0103372_O2_[Lack_both_end]_[mRNA]_locus=scaffold22869_1:3:770:-	Clostridium methylpentosum
2108513	GL0017551_O2_[Lack_3'-end]_[mRNA]_locus=scaffold28235_2:537:1547:+	Roseburia inulinivorans
2108607	GL0083515_O2_[Lack_5'-end]_[mRNA]_locus=scaffold28759_3:923:1084:-	Clostridiales
2109731	GL0055173_O2_[Complete]_[mRNA]_locus=scaffold37032_2:122:484:-	Bacteroides pectinophilus
2109845	GL0096116_O2_[Complete]_[mRNA]_locus=scaffold37967_2:945:1823:-	Clostridiales
2110926	GL0064074_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46122_2:371:2077:+	Clostridiales
2111043	GL0031269_O2_[Complete]_[mRNA]_locus=scaffold47314_1:92:487:-	Firmicutes
2111240	GL0105284_O2_[Lack_3'-end]_[mRNA]_locus=scaffold48987_3:47:1012:+	Ruminococcus obeum
2111336	GL0033517_O2_[Lack_3'-end]_[mRNA]_locus=scaffold49288_1:532:924:+	Clostridiales

2112248	GL0083769_O2_[Lack_3'-end]_[mRNA]_locus=scaffold57140_2:1:684:-	Ruminococcus obeum
2112849	GL0036143_O2_[Lack_both_end]_[mRNA]_locus=scaffold62834_1:3:1490:-	Bacteria
2113844	GL0061344_O2_[Lack_3'-end]_[mRNA]_locus=scaffold70847_2:1:432:-	Ruminococcus obeum
2115885	GL0004825_O2_[Lack_both_end]_[mRNA]_locus=scaffold84513_2:2:910:-	-
2117694	GL0038644_O2_[Lack_both_end]_[mRNA]_locus=scaffold43_8:2:1201:+	Roseburia inulinivorans
2117781	GL0002053_O2_[Lack_5'-end]_[mRNA]_locus=scaffold506_1:3:659:+	Clostridiales
2118109	GL0019336_O2_[Lack_both_end]_[mRNA]_locus=scaffold2129_1:2:1483:+	Clostridiales
2118302	GL0035210_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3273_1:110:544:-	Clostridiales
2118492	GL0036434_O2_[Complete]_[mRNA]_locus=scaffold4523_3:5563:5862:+	Bacteria
2119025	GL0011144_O2_[Lack_5'-end]_[mRNA]_locus=scaffold8681_3:143:787:-	Roseburia inulinivorans
2120364	GL0060152_O2_[Lack_5'-end]_[mRNA]_locus=scaffold20577_4:415:543:-	-
2120687	GL0000654_O2_[Complete]_[mRNA]_locus=scaffold23977_2:643:2409:+	Clostridium bolteae
2121657	GL0046341_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37283_1:3:1148:+	Clostridiales
2123049	GL0054059_O2_[Complete]_[mRNA]_locus=scaffold64417_1:253:648:+	Bacteroides capillosus

2124240	GL0025431_O2_[Complete]_[mRNA]_locus=scaffold2437_1:990:2549:+	Ruminococcus gnavus
2124280	GL0031535_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2579_1:1:450:+	Clostridium
2124575	GL0107289_O2_[Complete]_[mRNA]_locus=scaffold3501_7:2204:3952:-	Bacteria
2124786	GL0004189_O2_[Complete]_[mRNA]_locus=scaffold4001_2:4616:5878:-	-
2124787	GL0004190_O2_[Complete]_[mRNA]_locus=scaffold4001_2:6937:8325:+	Catenibacterium mitsuokai
2124894	GL0030171_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4398_1:859:1191:+	Ruminococcus lactaris
2125251	GL0018115_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5875_4:1:2367:+	Bacteria
2125275	GL0101115_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5950_2:3:305:+	Bacteroides capillosus
2125630	GL0060254_O2_[Lack_5'-end]_[mRNA]_locus=scaffold7427_2:3:1439:+	Bacteroides intestinalis
2126038	GL0090842_O2_[Lack_5'-end]_[mRNA]_locus=scaffold9129_1:441:836:-	Finegoldia magna
2126125	GL0019146_O2_[Complete]_[mRNA]_locus=scaffold9395_1:906:1910:-	-
2126431	GL0089921_O2_[Lack_3'-end]_[mRNA]_locus=scaffold11121_1:4541:5710:+	Ruminococcus lactaris
2126491	GL0051538_O2_[Lack_5'-end]_[mRNA]_locus=scaffold11395_1:2076:2492:-	Roseburia inulinivorans
2126703	GL0063981_O2_[Complete]_[mRNA]_locus=scaffold12510_3:594:1460:-	Alistipes putredinis

2128083	GL0087966_O2_[Complete]_[mRNA]_locus=scaffold20268_7:991:1833:-	Alistipes putredinis
2128597	GL0103937_O2_[Complete]_[mRNA]_locus=scaffold23511_2:110:523:+	Pseudoalteromonas atlantica
2129131	GL0020414_O2_[Complete]_[mRNA]_locus=scaffold27468_2:28:1179:-	Clostridium leptum
2129132	GL0020415_O2_[Complete]_[mRNA]_locus=scaffold27468_2:1248:3431:-	Bacteria
2129347	GL0034689_O2_[Lack_3'-end]_[mRNA]_locus=scaffold28678_4:636:767:+	-
2129789	GL0079616_O2_[Complete]_[mRNA]_locus=scaffold31803_2:404:1228:-	Dorea longicatena
2132412	GL0116574_O2_[Complete]_[mRNA]_locus=scaffold52367_5:3004:4704:-	Clostridiales
2132418	GL0082054_O2_[Lack_5'-end]_[mRNA]_locus=scaffold52409_4:2:358:+	Eubacterium ventriosum
2133126	GL0071571_O2_[Lack_5'-end]_[mRNA]_locus=scaffold59293_2:3:506:+	Alistipes putredinis
2133314	GL0097986_O2_[Complete]_[mRNA]_locus=scaffold60983_1:556:2139:+	Bacteroides caccae
2133617	GL0090722_O2_[Complete]_[mRNA]_locus=scaffold64203_1:369:1676:-	Alistipes putredinis
2138780	GL0031955_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1972_1:1737:2264:+	Bacteroides capillosus
2139325	GL0048571_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3518_1:2139:2765:-	Clostridiales
2140849	GL0012065_O2_[Lack_both_end]_[mRNA]_locus=scaffold8972_1:1:552:+	Roseburia inulinivorans

2141606	GL0073017_O2_[Lack_both_end]_[mRNA]_locus=scaffold11767_1:3:641:+	Bacteroides capillosus
2143825	GL0086696_O2_[Lack_5'-end]_[mRNA]_locus=scaffold22016_1:1:483:+	Bacteroides coprocola
2144193	GL0029190_O2_[Complete]_[mRNA]_locus=scaffold24110_1:1111:2562:+	Clostridium phytofermentans
2144609	GL0050046_O2_[Complete]_[mRNA]_locus=scaffold26519_1:190:558:-	Bacteroides capillosus
2147470	GL0017199_O2_[Complete]_[mRNA]_locus=scaffold44910_2:1212:2861:+	Eubacterium hallii
2150730	GL0082448_O2_[Lack_3'-end]_[mRNA]_locus=scaffold67820_1:209:772:+	Parabacteroides
2151169	GL0063460_O2_[Complete]_[mRNA]_locus=scaffold70115_1:56:955:-	Alistipes putredinis
2155354	GL0086925_O2_[Lack_both_end]_[mRNA]_locus=scaffold1121_2:2:1021:+	Firmicutes
2162627	GL0026504_O2_[Complete]_[mRNA]_locus=scaffold11939_4:1844:2107:-	Clostridiales
2166514	GL0103668_O2_[Lack_3'-end]_[mRNA]_locus=scaffold22836_2:521:700:+	-
2172205	GL0011762_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45590_1:3:113:-	-
2173578	GL0100309_O2_[Lack_both_end]_[mRNA]_locus=scaffold51684_1:1:540:-	Roseburia inulinivorans
2180837	GL0080112_O2_[Lack_5'-end]_[mRNA]_locus=C5350098_1:2:712:+	Petrotoga mobilis
2184589	GL0084091_O2_[Complete]_[mRNA]_locus=scaffold4602_2:410:667:+	Faecalibacterium prausnitzii

2187659	GL0043785_O2_[Complete]_[mRNA]_locus=scaffold12943_1:18:194:-	Roseburia inulinivorans
2190417	GL0023926_O2_[Lack_5'-end]_[mRNA]_locus=scaffold23925_1:612:1433:-	Faecalibacterium prausnitzii
2199061	GL0016048_O2_[Lack_both_end]_[mRNA]_locus=C3545736_1:1:531:+	Clostridium
2202399	GL0013006_V1_[Complete]_[mRNA]_locus=scaffold933_2:1289:2332:-	Bacteroides pectinophilus
2203204	GL0044028_V1_[Lack_both_end]_[mRNA]_locus=scaffold1712_2:1:957:-	Bacteroides pectinophilus
2203706	GL0010715_V1_[Complete]_[mRNA]_locus=scaffold2186_2:3502:5148:+	Firmicutes
2203709	GL0010721_V1_[Complete]_[mRNA]_locus=scaffold2186_2:8135:10087:+	Clostridium
2204333	GL0074274_V1_[Complete]_[mRNA]_locus=scaffold2670_1:2572:3801:+	Roseburia inulinivorans
2204514	GL0097834_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2908_5:142:921:+	-
2204515	GL0087195_V1_[Lack_both_end]_[mRNA]_locus=scaffold2908_6:2:1138:+	Clostridium
2204516	GL0102106_V1_[Complete]_[mRNA]_locus=scaffold2908_8:2280:3473:+	Bacteria
2204631	GL0062933_V1_[Lack_both_end]_[mRNA]_locus=scaffold2975_2:1:843:-	Roseburia inulinivorans
2206258	GL0012901_V1_[Complete]_[mRNA]_locus=scaffold4742_7:1091:2443:+	Bacteria
2206460	GL0002991_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4996_4:16116:16874:-	Coprococcus comes

2206684	GL0088245_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5215_2:2:385:-	-
2207144	GL0090605_V1_[Complete]_[mRNA]_locus=scaffold5887_2:93:344:-	Clostridiales
2209222	GL0029049_V1_[Lack_both_end]_[mRNA]_locus=scaffold8681_2:1:876:+	Faecalibacterium prausnitzii
2210510	GL0045731_V1_[Complete]_[mRNA]_locus=scaffold10665_3:607:1089:+	Clostridium bolteae
2211845	GL0083054_V1_[Complete]_[mRNA]_locus=scaffold13455_8:3280:4593:+	Firmicutes
2211965	GL0052036_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13624_1:3:896:-	Bacteroides pectinophilus
2212455	GL0057255_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14412_1:362:523:-	-
2212932	GL0022333_V1_[Complete]_[mRNA]_locus=scaffold15286_1:153:323:+	Clostridium methylpentosum
2212933	GL0022334_V1_[Complete]_[mRNA]_locus=scaffold15286_1:417:629:+	Clostridium
2213893	GL0077757_V1_[Lack_both_end]_[mRNA]_locus=scaffold17313_1:1:1092:+	Bacteroides pectinophilus
2214052	GL0028386_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17693_1:76:801:+	Eubacterium hallii
2219225	GL0046407_V1_[Lack_both_end]_[mRNA]_locus=scaffold31947_3:1:537:-	Clostridium bolteae
2220629	GL0059216_V1_[Complete]_[mRNA]_locus=scaffold37020_1:27:665:-	Bacteria
2221290	GL0078037_V1_[Lack_5'-end]_[mRNA]_locus=scaffold39255_3:578:1294:-	Roseburia inulinivorans

2224962	GL0091369_V1_[Lack_3'-end]_[mRNA]_locus=scaffold54740_6:1:714:-	-
2228028	GL0091058_V1_[Lack_3'-end]_[mRNA]_locus=scaffold68347_2:749:1000:+	Clostridium bolteae
2228427	GL0040348_V1_[Complete]_[mRNA]_locus=scaffold69504_1:4659:6125:+	Firmicutes
2229691	GL0020445_V1_[Lack_5'-end]_[mRNA]_locus=C4641145_1:1:798:+	Roseburia inulinivorans
2229818	GL0053699_V1_[Complete]_[mRNA]_locus=C4656437_1:30:917:+	Dorea formicigenerans
2230604	GL0069447_V1_[Lack_5'-end]_[mRNA]_locus=scaffold941_1:3:350:+	Clostridium bolteae
2230605	GL0069448_V1_[Lack_3'-end]_[mRNA]_locus=scaffold941_1:343:753:+	Clostridium bolteae
2230640	GL0062293_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1008_1:3:611:-	Clostridium bolteae
2230737	GL0080161_V1_[Lack_both_end]_[mRNA]_locus=scaffold1193_1:1:684:+	Clostridium bolteae
2231373	GL0078958_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2043_1:3:836:-	Clostridium bolteae
2231427	GL0000496_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2137_2:1:285:-	Clostridium bolteae
2231640	GL0017361_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2528_1:1:312:-	Clostridium
2231705	GL0031287_V1_[Complete]_[mRNA]_locus=scaffold2608_4:163:2568:-	Clostridium asparagiforme
2232029	GL0074892_V1_[Complete]_[mRNA]_locus=scaffold3123_3:757:2127:+	Clostridiales

2232260	GL0070083_V1_[Complete]_[mRNA]_locus=scaffold3695_2:1219:1932:-	Ruminococcus gnavus
2232596	GL0027524_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4264_1:100:882:-	Clostridium bolteae
2232695	GL0050894_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4495_1:1:252:+	Clostridium bolteae
2232891	GL0046532_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4962_1:122:511:-	Ruminococcus gnavus
2233217	GL0074864_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5524_1:1:375:-	Clostridium bolteae
2233475	GL0038148_V1_[Lack_both_end]_[mRNA]_locus=scaffold6104_1:2:2389:+	Clostridium
2234311	GL0010803_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7652_1:512:1126:-	Anaerotruncus colihominis
2234876	GL0008442_V1_[Complete]_[mRNA]_locus=scaffold8849_2:283:1179:-	Candidatus Cloacamonas
2235225	GL0051935_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9423_2:1:846:-	Clostridium hylemonae
2235226	GL0038975_V1_[Complete]_[mRNA]_locus=scaffold9423_3:96:719:-	Clostridium hylemonae
2235242	GL0022566_V1_[Complete]_[mRNA]_locus=scaffold9423_6:1800:2342:-	Clostridium hylemonae
2235462	GL0062486_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9799_1:494:796:-	Clostridium bolteae
2235557	GL0034188_V1_[Complete]_[mRNA]_locus=scaffold9991_1:550:735:-	-
2235589	GL0019528_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10040_1:2474:2989:-	Ruminococcus gnavus

2235720	GL0061916_V1_[Complete]_[mRNA]_locus=scaffold10330_1:298:1020:+	Clostridium bolteae
2235766	GL0016936_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10461_2:1:549:-	-
2235783	GL0051878_V1_[Lack_both_end]_[mRNA]_locus=scaffold10488_1:1:570:+	Clostridium bolteae
2235834	GL0077793_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10595_1:3:203:+	Clostridium bolteae
2235884	GL0062198_V1_[Complete]_[mRNA]_locus=scaffold10703_1:182:445:-	Clostridium bolteae
2236247	GL0048942_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11404_1:470:622:-	Clostridium bolteae
2237054	GL0020938_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13212_1:3:221:-	Clostridium bolteae
2237740	GL0058038_V1_[Complete]_[mRNA]_locus=scaffold14931_6:31:1056:+	Ruminococcus gnavus
2238171	GL0010115_V1_[Lack_both_end]_[mRNA]_locus=scaffold15923_3:1:927:-	Clostridiales
2238420	GL0027601_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16516_1:3:347:+	Clostridium bolteae
2238655	GL0037038_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17041_1:338:526:+	Clostridium bolteae
2238995	GL0064241_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17747_1:1:642:+	Clostridium bolteae
2240076	GL0074128_V1_[Lack_3'-end]_[mRNA]_locus=scaffold20405_1:1481:1960:+	Ruminococcus gnavus
2240175	GL0009188_V1_[Lack_3'-end]_[mRNA]_locus=scaffold20594_2:3:287:-	Clostridium

2240470	GL0010725_V1_[Lack_3'-end]_[mRNA]_locus=scaffold21304_1:237:572:+	Clostridium bolteae
2240545	GL0076107_V1_[Lack_3'-end]_[mRNA]_locus=scaffold21471_1:2:484:-	Roseburia inulinivorans
2240774	GL0016885_V1_[Lack_both_end]_[mRNA]_locus=scaffold22161_2:1:621:-	Clostridium phytofermentans
2241164	GL0063051_V1_[Lack_both_end]_[mRNA]_locus=scaffold23117_1:3:650:-	Clostridium bolteae
2241313	GL0039051_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23464_1:563:895:+	Clostridium bolteae
2241469	GL0049730_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23831_1:2:457:-	Clostridium bolteae
2241685	GL0078931_V1_[Lack_3'-end]_[mRNA]_locus=scaffold24291_1:3:128:-	Ruminococcus gnavus
2241793	GL0016970_V1_[Complete]_[mRNA]_locus=scaffold24602_7:294:986:-	Ruminococcus gnavus
2242184	GL0046432_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25916_1:926:1570:+	Ruminococcus gnavus
2242378	GL0056291_V1_[Lack_5'-end]_[mRNA]_locus=scaffold26375_1:1:315:+	Clostridium bolteae
2242504	GL0029921_V1_[Complete]_[mRNA]_locus=scaffold26659_1:2070:2648:+	Clostridiales
2242740	GL0007679_V1_[Lack_3'-end]_[mRNA]_locus=scaffold27175_1:60:500:+	Clostridium bolteae
2242941	GL0037589_V1_[Lack_5'-end]_[mRNA]_locus=scaffold27659_1:1:225:+	Clostridium bolteae
2243048	GL0049687_V1_[Lack_both_end]_[mRNA]_locus=scaffold28053_1:3:557:-	Clostridium bolteae

2243168	GL0044523_V1_[Lack_3'-end]_[mRNA]_locus=scaffold28415_1:3:602:-	Clostridium bolteae
2243359	GL0013870_V1_[Lack_5'-end]_[mRNA]_locus=scaffold28960_2:129:755:-	-
2243393	GL0057415_V1_[Lack_both_end]_[mRNA]_locus=scaffold29002_1:3:539:-	-
2243572	GL0079651_V1_[Complete]_[mRNA]_locus=scaffold29511_1:191:976:-	Carboxydothermus hydrogenoformans
2243691	GL0060563_V1_[Lack_5'-end]_[mRNA]_locus=scaffold29837_2:2:205:+	Ruminococcus gnavus
2244265	GL0066203_V1_[Lack_3'-end]_[mRNA]_locus=scaffold31526_1:3:290:-	Clostridium bolteae
2244655	GL0040882_V1_[Lack_5'-end]_[mRNA]_locus=scaffold32487_1:1:525:+	Clostridium bolteae
2244819	GL0046436_V1_[Lack_5'-end]_[mRNA]_locus=scaffold32967_1:3:305:+	-
2244835	GL0076928_V1_[Lack_both_end]_[mRNA]_locus=scaffold32986_2:2:949:+	Clostridium bolteae
2245053	GL0009147_V1_[Lack_3'-end]_[mRNA]_locus=scaffold33404_1:1471:2262:+	Bacillus halodurans
2245404	GL0000722_V1_[Lack_both_end]_[mRNA]_locus=scaffold34356_1:2:583:+	Clostridium bolteae
2245789	GL0054201_V1_[Complete]_[mRNA]_locus=scaffold35342_1:60:908:-	Carnobacterium
2245834	GL0032869_V1_[Lack_3'-end]_[mRNA]_locus=scaffold35475_1:2:166:-	Clostridium bolteae
2245996	GL0011702_V1_[Lack_3'-end]_[mRNA]_locus=scaffold35830_1:131:556:+	Clostridium bolteae

2246257	GL0016388_V1_[Lack_3'-end]_[mRNA]_locus=scaffold36543_2:3:677:-	-
2246301	GL0010145_V1_[Complete]_[mRNA]_locus=scaffold36630_1:647:1423:+	Streptococcus suis
2246449	GL0055850_V1_[Complete]_[mRNA]_locus=scaffold36958_2:94:846:+	Firmicutes
2246492	GL0039344_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37048_1:293:631:-	Clostridium bolteae
2246781	GL0011495_V1_[Lack_both_end]_[mRNA]_locus=scaffold37667_1:1:501:-	Clostridium bolteae
2247710	GL0027243_V1_[Lack_5'-end]_[mRNA]_locus=scaffold39667_1:2:538:+	Clostridium bolteae
2247809	GL0053263_V1_[Lack_3'-end]_[mRNA]_locus=scaffold39913_1:715:819:+	Clostridium bolteae
2248783	GL0055500_V1_[Lack_5'-end]_[mRNA]_locus=scaffold42031_1:491:745:-	Clostridium bolteae
2248942	GL0008493_V1_[Lack_3'-end]_[mRNA]_locus=scaffold42317_1:504:803:+	Clostridium bolteae
2249485	GL0001487_V1_[Lack_5'-end]_[mRNA]_locus=scaffold43230_2:154:714:-	Escherichia coli
2250301	GL0045702_V1_[Lack_3'-end]_[mRNA]_locus=scaffold44574_1:2:802:+	Clostridium bolteae
2250756	GL0036104_V1_[Lack_5'-end]_[mRNA]_locus=scaffold45247_2:1:1353:+	Ruminococcus gnavus
2250848	GL0031816_V1_[Complete]_[mRNA]_locus=scaffold45367_2:2106:2588:+	Clostridium bolteae
2250849	GL0031817_V1_[Complete]_[mRNA]_locus=scaffold45367_2:2692:3426:+	Clostridium bolteae

2251940	GL0034812_V1_[Lack_5'-end]_[mRNA]_locus=C2646221_1:1:162:+	Clostridium bolteae
2251941	GL0034813_V1_[Lack_3'-end]_[mRNA]_locus=C2646221_1:173:508:+	Clostridium bolteae
2252358	GL0018588_V1_[Lack_3'-end]_[mRNA]_locus=C2657849_1:3:437:-	Clostridium bolteae
2252420	GL0063885_V1_[Lack_5'-end]_[mRNA]_locus=C2659497_1:64:570:-	Clostridium bolteae
2253010	GL0001103_V1_[Lack_both_end]_[mRNA]_locus=C2675321_1:3:668:-	Clostridium bolteae
2253076	GL0009711_V1_[Lack_5'-end]_[mRNA]_locus=C2677097_1:489:683:-	Clostridium bolteae
2253809	GL0032330_V1_[Complete]_[mRNA]_locus=C2696749_1:290:463:+	-
2254618	GL0000808_V1_[Lack_3'-end]_[mRNA]_locus=C2717939_1:3:1007:-	-
2255563	GL0108520_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1321_1:395:1063:-	Roseburia inulinivorans
2257123	GL0012679_V1_[Complete]_[mRNA]_locus=scaffold5617_2:116:1060:-	Roseburia inulinivorans
2257285	GL0013482_V1_[Complete]_[mRNA]_locus=scaffold6446_3:521:1654:-	Roseburia inulinivorans
2257628	GL0089718_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7866_1:3:1298:-	Bacteria
2258308	GL0018377_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10109_5:415:543:+	-
2260062	GL0083122_V1_[Complete]_[mRNA]_locus=scaffold17523_2:408:1232:+	Roseburia inulinivorans

2260174	GL0126897_V1_[Complete]_[mRNA]_locus=scaffold17821_8:727:1806:+	-
2262165	GL0047343_V1_[Lack_both_end]_[mRNA]_locus=scaffold27395_3:2:736:-	Bacteroides capillosus
2267036	GL0041956_V1_[Complete]_[mRNA]_locus=scaffold61067_1:248:709:+	Roseburia inulinivorans
2268146	GL0106463_V1_[Lack_5'-end]_[mRNA]_locus=scaffold69891_2:605:1741:-	Eubacterium
2268794	GL0063036_V1_[Lack_5'-end]_[mRNA]_locus=scaffold75666_1:1:246:+	Bacteroides capillosus
2269727	GL0125840_V1_[Complete]_[mRNA]_locus=scaffold83003_1:754:1539:+	Roseburia inulinivorans
2270099	GL0089822_V1_[Lack_5'-end]_[mRNA]_locus=scaffold85825_1:95:1255:-	Roseburia inulinivorans
2270652	GL0004230_V1_[Lack_both_end]_[mRNA]_locus=scaffold89212_1:1:921:+	Clostridium perfringens
2272004	GL0117691_V1_[Lack_5'-end]_[mRNA]_locus=scaffold96565_1:1:222:+	-
2272514	GL0116654_V1_[Lack_5'-end]_[mRNA]_locus=scaffold98523_3:426:650:-	Roseburia inulinivorans
2272762	GL0079193_V1_[Lack_3'-end]_[mRNA]_locus=scaffold99369_1:3:347:-	Roseburia inulinivorans
2274006	GL0005708_V1_[Lack_5'-end]_[mRNA]_locus=C4350381_1:32:541:-	Desulfurococcus kamchatkensis
2275696	GL0155840_V1_[Complete]_[mRNA]_locus=scaffold110_10:1290:3575:-	-
2276553	GL0089224_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2188_4:2:2206:-	Clostridiales

2277085	GL0011810_V1_[Complete]_[mRNA]_locus=scaffold3286_3:7390:10479:-	Bacteria
2277086	GL0011812_V1_[Complete]_[mRNA]_locus=scaffold3286_3:11541:13658:-	Clostridium
2277679	GL0085959_V1_[Complete]_[mRNA]_locus=scaffold4756_21:1669:2763:+	Bacteroides pectinophilus
2278648	GL0038551_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7326_2:2:457:+	-
2280673	GL0133620_V1_[Complete]_[mRNA]_locus=scaffold13352_9:9808:12330:-	Syntrophomonas wolfei
2282122	GL0115801_V1_[Complete]_[mRNA]_locus=scaffold18520_2:5216:7456:-	Clostridiales
2283803	GL0071551_V1_[Lack_5'-end]_[mRNA]_locus=scaffold25304_2:3:1136:+	Clostridium leptum
2285004	GL0015252_V1_[Complete]_[mRNA]_locus=scaffold31160_4:364:1773:-	Clostridiales
2286676	GL0023234_V1_[Lack_5'-end]_[mRNA]_locus=scaffold40263_1:1:240:+	Clostridiales
2287765	GL0139577_V1_[Lack_5'-end]_[mRNA]_locus=scaffold47039_2:434:802:-	Eubacterium biforme
2290315	GL0053333_V1_[Complete]_[mRNA]_locus=scaffold64676_1:464:1357:-	Roseburia inulinivorans
2292050	GL0073133_V1_[Complete]_[mRNA]_locus=scaffold76197_1:628:2355:+	-
2292733	GL0101081_V1_[Lack_3'-end]_[mRNA]_locus=scaffold81004_1:3:680:-	-
2293058	GL0077446_V1_[Lack_3'-end]_[mRNA]_locus=scaffold83460_1:2:685:-	Blautia hydrogenotrophica

2294356	GL0049132_V1_[Lack_5'-end]_[mRNA]_locus=scaffold91820_3:2:1066:+	-
2295220	GL0025804_V1_[Lack_3'-end]_[mRNA]_locus=scaffold96522_2:211:732:+	-
2295784	GL0133511_V1_[Lack_3'-end]_[mRNA]_locus=scaffold99337_2:2:1429:-	-
2296037	GL0015999_V1_[Lack_5'-end]_[mRNA]_locus=scaffold100337_2:3:551:+	Clostridium
2296859	GL0115955_V1_[Complete]_[mRNA]_locus=scaffold103039_1:240:719:-	Bacteroides pectinophilus
2297686	GL0024688_V1_[Lack_3'-end]_[mRNA]_locus=scaffold105288_2:172:1233:+	Coprococcus eutactus
2299727	GL0030535_V1_[Lack_5'-end]_[mRNA]_locus=C4119344_1:555:1208:-	-
2300667	GL0032897_V1_[Lack_5'-end]_[mRNA]_locus=scaffold934_1:1:513:+	Clostridium bolteae
2301592	GL0030454_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2525_2:2:184:-	Clostridium bolteae
2301794	GL0021703_V1_[Lack_both_end]_[mRNA]_locus=scaffold3009_4:2:526:+	Clostridium
2301859	GL0035938_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3193_2:399:638:+	-
2301991	GL0066204_V1_[Complete]_[mRNA]_locus=scaffold3519_1:167:589:-	Clostridium bolteae
2302872	GL0060963_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5454_1:444:695:+	Clostridium bolteae
2302873	GL0026784_V1_[Complete]_[mRNA]_locus=scaffold5455_3:156:380:-	Ruminococcus gnavus

2304818	GL0012143_V1_[Complete]_[mRNA]_locus=scaffold11929_3:7:612:-	Ruminococcus gnavus
2305558	GL0040889_V1_[Lack_3'-end]_[mRNA]_locus=scaffold15251_1:1:597:-	Ruminococcus gnavus
2305626	GL0023258_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15473_3:64:567:-	Ruminococcus gnavus
2306071	GL0002022_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17311_2:2:250:+	Ruminococcus gnavus
2306768	GL0007891_V1_[Lack_3'-end]_[mRNA]_locus=scaffold20231_1:3:764:-	Clostridium bolteae
2306899	GL0035399_V1_[Lack_3'-end]_[mRNA]_locus=scaffold20806_1:3:644:+	Clostridium bolteae
2307240	GL0038482_V1_[Lack_3'-end]_[mRNA]_locus=scaffold22460_3:48:617:+	Clostridium bolteae
2307381	GL0004980_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23088_4:295:702:+	Clostridium bolteae
2307511	GL0070186_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23629_2:1:300:-	Clostridium bolteae
2307816	GL0051612_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25303_2:372:767:+	Clostridium bolteae
2308792	GL0044696_V1_[Lack_both_end]_[mRNA]_locus=scaffold30816_4:2:550:-	Clostridium bolteae
2308933	GL0059743_V1_[Complete]_[mRNA]_locus=scaffold31647_2:64:615:+	Clostridium bolteae
2308974	GL0029311_V1_[Complete]_[mRNA]_locus=scaffold31842_1:185:481:+	Clostridium bolteae
2309072	GL0042311_V1_[Lack_3'-end]_[mRNA]_locus=scaffold32370_3:3:509:-	Clostridium bolteae

2309717	GL0069077_V1_[Lack_both_end]_[mRNA]_locus=scaffold35423_2:2:634:-	Ruminococcus gnavus
2310070	GL0063071_V1_[Lack_3'-end]_[mRNA]_locus=scaffold36988_3:46:552:+	Clostridium bolteae
2310234	GL0054326_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37809_2:3:614:+	Ruminococcus gnavus
2310431	GL0028809_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38546_2:1:231:+	Clostridium bolteae
2310432	GL0052936_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38552_1:1:744:+	Clostridium bolteae
2310578	GL0008950_V1_[Lack_both_end]_[mRNA]_locus=scaffold39109_3:1:504:+	Clostridium bolteae
2310590	GL0049957_V1_[Lack_both_end]_[mRNA]_locus=scaffold39158_1:1:507:+	Clostridium bolteae
2311519	GL0054418_V1_[Lack_5'-end]_[mRNA]_locus=scaffold43070_1:1:138:+	Clostridium bolteae
2311555	GL0036053_V1_[Lack_5'-end]_[mRNA]_locus=scaffold43167_3:2:415:+	Ruminococcus gnavus
2311560	GL0000553_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43190_1:47:547:+	Clostridium bolteae
2311870	GL0021541_V1_[Complete]_[mRNA]_locus=scaffold44118_1:68:3106:+	Bacteroidales
2311879	GL0045561_V1_[Lack_3'-end]_[mRNA]_locus=scaffold44152_1:1:468:-	Clostridium bolteae
2312102	GL0011771_V1_[Lack_3'-end]_[mRNA]_locus=scaffold44675_1:3:674:-	Clostridium bolteae
2312110	GL0034827_V1_[Lack_both_end]_[mRNA]_locus=scaffold44696_1:1:822:-	Clostridium bolteae

2312922	GL0032830_V1_[Lack_both_end]_[mRNA]_locus=scaffold46261_1:3:737:+	Coprococcus comes
2313202	GL0058850_V1_[Lack_both_end]_[mRNA]_locus=C3311842_1:3:527:+	Clostridium bolteae
2313211	GL0004223_V1_[Lack_3'-end]_[mRNA]_locus=C3312514_1:144:530:+	Clostridium bolteae
2313227	GL0069993_V1_[Lack_3'-end]_[mRNA]_locus=C3313142_1:2:136:-	Ruminococcus gnavus
2313349	GL0048452_V1_[Lack_5'-end]_[mRNA]_locus=C3317960_1:139:564:-	Clostridium bolteae
2313353	GL0024504_V1_[Lack_both_end]_[mRNA]_locus=C3318196_1:2:565:-	Ruminococcus gnavus
2313409	GL0030639_V1_[Lack_5'-end]_[mRNA]_locus=C3320644_1:391:582:-	Clostridium bolteae
2313526	GL0047202_V1_[Lack_3'-end]_[mRNA]_locus=C3326309_1:3:422:-	Clostridium bolteae
2317198	GL0030493_V1_[Lack_both_end]_[mRNA]_locus=scaffold5383_3:1:1029:-	Bacteria
2318076	GL0014161_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7727_9:511:675:-	Ruminococcus gnavus
2318848	GL0052020_V1_[Complete]_[mRNA]_locus=scaffold10402_1:311:808:-	Ruminococcus gnavus
2319306	GL0055872_V1_[Complete]_[mRNA]_locus=scaffold12231_6:424:924:+	Ruminococcus gnavus
2319736	GL0045852_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13574_3:1:141:-	-
2323014	GL0050534_V1_[Complete]_[mRNA]_locus=scaffold32377_3:204:515:+	Ruminococcus gnavus

2323156	GL0047244_V1_[Lack_5'-end]_[mRNA]_locus=scaffold33567_2:333:521:-	Ruminococcus gnavus
2323257	GL0061294_V1_[Complete]_[mRNA]_locus=scaffold34319_3:671:1657:-	Ruminococcus gnavus
2324094	GL0062202_V1_[Complete]_[mRNA]_locus=scaffold40434_2:134:664:+	Ruminococcus gnavus
2326307	GL0002661_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1642_4:610:1242:+	Coprococcus eutactus
2326873	GL0024513_V1_[Lack_3'-end]_[mRNA]_locus=scaffold4744_1:3:371:-	Roseburia inulinivorans
2330107	GL0006388_V1_[Complete]_[mRNA]_locus=scaffold26891_3:366:779:-	Roseburia inulinivorans
2330929	GL0003989_V1_[Lack_5'-end]_[mRNA]_locus=scaffold34382_2:3:275:+	Clostridiales
2334739	GL0000547_V1_[Lack_3'-end]_[mRNA]_locus=C12298330_1:315:779:+	Blautia hydrogenotrophica
2336764	GL0102986_V1_[Complete]_[mRNA]_locus=scaffold6358_1:1438:3201:-	Bacteria
2337493	GL0100454_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9353_2:2:472:+	Alistipes putredinis
2337877	GL0048618_V1_[Complete]_[mRNA]_locus=scaffold11862_1:90:752:+	Ruminococcus obeum
2338223	GL0034443_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14298_2:1:444:+	Clostridium
2338479	GL0091798_V1_[Lack_both_end]_[mRNA]_locus=scaffold16607_1:1:1098:+	Firmicutes
2339423	GL0052771_V1_[Lack_3'-end]_[mRNA]_locus=scaffold24348_1:3:401:-	Ruminococcus obeum

2341129	GL0012267_V1_[Lack_5'-end]_[mRNA]_locus=scaffold41419_10:1024:1134:-	-
2342672	GL0010052_V1_[Lack_5'-end]_[mRNA]_locus=scaffold61836_8:61:540:-	Alistipes putredinis
2346684	GL0000005_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5526_2:1:294:-	Clostridiales
2347397	GL0052701_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7414_2:1097:2275:-	Clostridium nexile
2348319	GL0136430_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10748_2:1:468:-	Clostridium asparagiforme
2348493	GL0063756_V1_[Complete]_[mRNA]_locus=scaffold11301_1:109:957:+	Faecalibacterium prausnitzii
2348935	GL0114235_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12932_11:436:801:-	Clostridium
2349751	GL0056735_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16533_1:215:1009:+	Eubacterium ventriosum
2350556	GL0001802_V1_[Complete]_[mRNA]_locus=scaffold19776_6:4132:5001:-	-
2353322	GL0054075_V1_[Lack_5'-end]_[mRNA]_locus=scaffold33142_8:50:607:-	Clostridiales
2353323	GL0101760_V1_[Complete]_[mRNA]_locus=scaffold33142_11:174:1628:-	-
2353568	GL0130246_V1_[Lack_3'-end]_[mRNA]_locus=scaffold34645_1:3:1859:-	Firmicutes
2354027	GL0037376_V1_[Complete]_[mRNA]_locus=scaffold37567_1:970:3009:+	Clostridium

2354217	GL0088335_V1_[Lack_3'-end]_[mRNA]_locus=scaffold38672_1:3:287:-	Firmicutes
2357873	GL0057257_V1_[Complete]_[mRNA]_locus=scaffold62500_1:2648:2953:+	Blautia hydrogenotrophica
2358181	GL0101236_V1_[Complete]_[mRNA]_locus=scaffold64842_1:1069:1623:-	-
2359537	GL0042175_V1_[Lack_both_end]_[mRNA]_locus=scaffold73358_1:3:569:-	Clostridium thermocellum
2373217	GL0013071_V1_[Complete]_[mRNA]_locus=scaffold26563_3:215:460:+	Eubacterium hallii
2384708	GL0114004_V1_[Complete]_[mRNA]_locus=scaffold7165_3:39:800:+	Holdemania filiformis
2388463	GL0083240_V1_[Complete]_[mRNA]_locus=scaffold18833_2:1158:2795:-	-
2388561	GL0083338_V1_[Lack_5'-end]_[mRNA]_locus=scaffold19261_6:1:534:+	Holdemania filiformis
2389430	GL0054036_V1_[Lack_5'-end]_[mRNA]_locus=scaffold22933_2:519:1241:-	Roseburia inulinivorans
2391491	GL0047683_V1_[Complete]_[mRNA]_locus=scaffold32221_2:530:1741:-	Roseburia inulinivorans
2391729	GL0123783_V1_[Lack_3'-end]_[mRNA]_locus=scaffold33151_5:132:902:+	Roseburia inulinivorans
2391917	GL0043453_V1_[Lack_5'-end]_[mRNA]_locus=scaffold34057_1:176:754:-	Clostridium bolteae
2392396	GL0110364_V1_[Lack_5'-end]_[mRNA]_locus=scaffold36223_2:3:230:+	Bacteroides cellulosilyticus
2392957	GL0090715_V1_[Complete]_[mRNA]_locus=scaffold39066_1:528:983:-	Clostridium butyricum

2393750	GL0090845_V1_[Complete]_[mRNA]_locus=scaffold43741_3:1107:2792:+	Bacteroides capillosus
2393941	GL0141229_V1_[Lack_both_end]_[mRNA]_locus=scaffold44986_4:1:717:+	-
2396040	GL0040781_V1_[Lack_5'-end]_[mRNA]_locus=scaffold57277_2:2:418:+	Roseburia inulinivorans
2396921	GL0129761_V1_[Lack_3'-end]_[mRNA]_locus=scaffold62990_1:52:771:+	Roseburia inulinivorans
2397065	GL0077567_V1_[Complete]_[mRNA]_locus=scaffold63900_2:130:1470:-	Opitutaceae
2398415	GL0026797_V1_[Complete]_[mRNA]_locus=scaffold72488_3:283:1590:-	Clostridiales
2399466	GL0013537_V1_[Complete]_[mRNA]_locus=scaffold78991_1:39:1154:+	Alistipes putredinis
2400011	GL0125127_V1_[Lack_5'-end]_[mRNA]_locus=scaffold82252_2:1183:1728:-	Roseburia inulinivorans
2402329	GL0159166_V1_[Lack_both_end]_[mRNA]_locus=scaffold97076_3:3:632:-	-
2404357	GL0091011_V1_[Lack_5'-end]_[mRNA]_locus=scaffold107755_2:25:2148:-	Clostridia
2405674	GL0101145_V1_[Lack_5'-end]_[mRNA]_locus=scaffold113259_1:3:164:+	-
2413088	GL0002478_V1_[Complete]_[mRNA]_locus=scaffold191_1:655:1728:+	Bacteroides fragilis
2413129	GL0009934_V1_[Complete]_[mRNA]_locus=scaffold262_3:1631:4945:-	Bacteroides ovatus
2413130	GL0009935_V1_[Complete]_[mRNA]_locus=scaffold262_3:4977:6731:-	Bacteroides cellulosilyticus

2419953	GL0078271_V1_[Complete]_[mRNA]_locus=scaffold5529_1:520:1479:-	-
2420069	GL0105986_V1_[Complete]_[mRNA]_locus=scaffold5709_5:486:1928:+	Parabacteroides distasonis
2420174	GL0061913_V1_[Complete]_[mRNA]_locus=scaffold5904_2:6288:6536:-	-
2420279	GL0073996_V1_[Complete]_[mRNA]_locus=scaffold6046_1:933:2030:-	Bacteroides thetaiotaomicron
2421568	GL0037248_V1_[Complete]_[mRNA]_locus=scaffold7073_2:906:1634:+	Alistipes putredinis
2422373	GL0015136_V1_[Complete]_[mRNA]_locus=scaffold8355_1:479:1678:+	Alistipes putredinis
2426128	GL0008789_V1_[Complete]_[mRNA]_locus=scaffold12462_4:457:1683:+	Alistipes putredinis
2426165	GL0120645_V1_[Complete]_[mRNA]_locus=scaffold12503_1:215:1351:-	Alistipes putredinis
2426581	GL0059925_V1_[Lack_5'-end]_[mRNA]_locus=scaffold13066_1:21:1037:-	Clostridium nexile
2427003	GL0001462_V1_[Complete]_[mRNA]_locus=scaffold13586_1:523:1353:+	Bacteroides fragilis
2427305	GL0119145_V1_[Complete]_[mRNA]_locus=scaffold14025_3:1625:3301:-	Bacteroides
2427750	GL0037239_V1_[Complete]_[mRNA]_locus=scaffold14642_1:3293:3475:+	Flavobacteriales
2427937	GL0091377_V1_[Lack_both_end]_[mRNA]_locus=scaffold14940_1:3:587:-	Bacteria
2428414	GL0117827_V1_[Complete]_[mRNA]_locus=scaffold15785_3:187:492:-	Alistipes putredinis

2428910	GL0038687_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16503_2:2:622:+	Finegoldia magna
2428911	GL0038688_V1_[Complete]_[mRNA]_locus=scaffold16503_2:667:1041:+	Clostridium asparagiforme
2429656	GL0010554_V1_[Complete]_[mRNA]_locus=scaffold17584_7:1426:2337:-	Clostridium leptum
2431103	GL0014921_V1_[Lack_5'-end]_[mRNA]_locus=scaffold20446_1:423:1040:-	Bacteroides uniformis
2431119	GL0065284_V1_[Complete]_[mRNA]_locus=scaffold20537_8:1465:2505:-	Clostridium
2431223	GL0008904_V1_[Complete]_[mRNA]_locus=scaffold20763_1:296:1474:-	Alistipes putredinis
2431332	GL0111070_V1_[Lack_3'-end]_[mRNA]_locus=scaffold21019_1:660:1367:+	Coprococcus eutactus
2431358	GL0125810_V1_[Complete]_[mRNA]_locus=scaffold21051_2:2524:4311:-	Bacteroides intestinalis
2431477	GL0027688_V1_[Complete]_[mRNA]_locus=scaffold21269_2:1120:2283:+	Alistipes putredinis
2432429	GL0050754_V1_[Complete]_[mRNA]_locus=scaffold22863_1:316:1563:+	Alistipes putredinis
2433358	GL0013004_V1_[Complete]_[mRNA]_locus=scaffold24749_1:906:2885:+	Bacteroidales
2433379	GL0003544_V1_[Complete]_[mRNA]_locus=scaffold24794_1:396:1442:-	Alistipes putredinis
2433460	GL0056510_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25042_7:1:672:-	Clostridium phytofermentans
2433599	GL0059650_V1_[Complete]_[mRNA]_locus=scaffold25307_1:3304:4596:-	Alistipes putredinis

2434212	GL0118918_V1_[Complete]_[mRNA]_locus=scaffold26812_2:1501:2961:-	Alistipes putredinis
2436857	GL0068110_V1_[Complete]_[mRNA]_locus=scaffold34626_1:1054:1644:+	Alistipes putredinis
2436859	GL0116427_V1_[Complete]_[mRNA]_locus=scaffold34626_2:767:2104:-	Parabacteroides
2436913	GL0057532_V1_[Complete]_[mRNA]_locus=scaffold34738_2:377:958:+	Alistipes putredinis
2437058	GL0087384_V1_[Complete]_[mRNA]_locus=scaffold34935_1:534:1241:-	Alistipes putredinis
2437156	GL0056496_V1_[Complete]_[mRNA]_locus=scaffold35190_1:809:2560:-	Alistipes putredinis
2438648	GL0044978_V1_[Complete]_[mRNA]_locus=scaffold39579_1:852:3059:-	Parabacteroides distasonis
2438649	GL0044979_V1_[Complete]_[mRNA]_locus=scaffold39579_1:3291:4277:-	Alistipes putredinis
2438958	GL0013911_V1_[Lack_3'-end]_[mRNA]_locus=scaffold40363_1:242:2545:+	Ruminococcus lactaris
2439548	GL0030411_V1_[Complete]_[mRNA]_locus=scaffold42263_3:42:1466:-	Bacteroides ovatus
2439549	GL0030412_V1_[Complete]_[mRNA]_locus=scaffold42263_3:1477:2937:-	Bacteroides ovatus
2439668	GL0091760_V1_[Complete]_[mRNA]_locus=scaffold42634_2:2372:5299:+	Pedobacter
2439978	GL0076041_V1_[Lack_5'-end]_[mRNA]_locus=scaffold43450_2:909:1400:-	Ruminococcus obeum
2440158	GL0069699_V1_[Complete]_[mRNA]_locus=scaffold44200_1:419:1126:+	Chloroherpeton thalassium

2440253	GL0053267_V1_[Complete]_[mRNA]_locus=scaffold44740_1:578:2629:-	Alistipes putredinis
2441062	GL0115991_V1_[Lack_3'-end]_[mRNA]_locus=scaffold47710_1:3:578:-	Clostridiales
2441248	GL0017781_V1_[Complete]_[mRNA]_locus=scaffold48234_1:372:998:-	Bacteroides caccae
2441261	GL0092469_V1_[Complete]_[mRNA]_locus=scaffold48321_1:621:1427:+	-
2442197	GL0094211_V1_[Complete]_[mRNA]_locus=scaffold51996_4:1348:4671:+	Bacteroidetes
2442445	GL0009714_V1_[Complete]_[mRNA]_locus=scaffold52978_3:968:1786:+	Bacteroides capillosus
2442715	GL0071626_V1_[Lack_5'-end]_[mRNA]_locus=scaffold54141_1:446:1903:-	Alistipes putredinis
2442885	GL0042878_V1_[Complete]_[mRNA]_locus=scaffold54961_3:1362:2354:-	Bacteroides
2443447	GL0032014_V1_[Complete]_[mRNA]_locus=scaffold57359_3:2279:3754:+	Bacteroides
2443691	GL0107422_V1_[Complete]_[mRNA]_locus=scaffold58087_2:36:878:-	Alistipes putredinis
2443728	GL0047471_V1_[Complete]_[mRNA]_locus=scaffold58338_1:529:738:-	Clostridium methylpentosum
2444401	GL0112926_V1_[Complete]_[mRNA]_locus=scaffold61101_1:306:2009:-	Bacteroides ovatus
2445129	GL0110625_V1_[Complete]_[mRNA]_locus=scaffold64270_2:1767:3512:+	Bacteroides coprophilus
2445378	GL0082806_V1_[Complete]_[mRNA]_locus=scaffold65394_1:1000:2118:+	Alistipes putredinis

2445988	GL0113931_V1_[Complete]_[mRNA]_locus=scaffold67913_1:809:1492:+	Alistipes putredinis
2446456	GL0113697_V1_[Complete]_[mRNA]_locus=scaffold70075_1:1061:3340:+	Bacteroides
2446712	GL0083239_V1_[Lack_3'-end]_[mRNA]_locus=scaffold71144_1:101:1327:+	Polaribacter irgensii
2447129	GL0011994_V1_[Complete]_[mRNA]_locus=scaffold72768_1:359:2680:+	Alistipes putredinis
2447447	GL0058065_V1_[Complete]_[mRNA]_locus=scaffold74089_1:633:1190:-	Methanosarcina barkeri
2447557	GL0095266_V1_[Lack_3'-end]_[mRNA]_locus=scaffold74524_1:19:864:+	Alistipes putredinis
2448202	GL0096035_V1_[Lack_5'-end]_[mRNA]_locus=scaffold76402_1:3:779:+	Parabacteroides merdae
2448236	GL0108747_V1_[Complete]_[mRNA]_locus=scaffold76484_1:504:1163:-	-
2448581	GL0032110_V1_[Complete]_[mRNA]_locus=scaffold77292_2:162:3029:+	Parabacteroides merdae
2448877	GL0091352_V1_[Complete]_[mRNA]_locus=scaffold77963_1:1582:2550:-	Alistipes putredinis
2449111	GL0091973_V1_[Complete]_[mRNA]_locus=scaffold78459_1:1092:2225:-	Ruminococcus lactaris
2449114	GL0013790_V1_[Complete]_[mRNA]_locus=scaffold78467_1:597:1571:-	Bacteroides ovatus
2449996	GL0082769_V1_[Complete]_[mRNA]_locus=scaffold79826_1:36:1763:-	-
2451519	GL0095295_V1_[Complete]_[mRNA]_locus=C3432582_1:65:976:+	Eukaryota

2451947	GL0034817_V1_[Lack_3'-end]_[mRNA]_locus=scaffold627_16:366:965:+	Bacteroides capillosus
2453723	GL0146985_V1_[Complete]_[mRNA]_locus=scaffold5039_4:704:1738:+	Roseburia inulinivorans
2453782	GL0142133_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5226_3:1:1689:+	Bacteria
2454187	GL0150840_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6225_4:3:1055:-	Clostridiales
2454324	GL0020214_V1_[Complete]_[mRNA]_locus=scaffold6560_3:500:1042:+	Clostridium hylemonae
2454774	GL0016389_V1_[Complete]_[mRNA]_locus=scaffold7927_2:3478:4803:-	Holdemania filiformis
2455411	GL0021846_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9761_1:3:758:-	Blautia hydrogenotrophica
2456127	GL0108676_V1_[Complete]_[mRNA]_locus=scaffold12163_2:264:1142:+	-
2457439	GL0119090_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17068_1:1277:2701:-	Bacteria
2461721	GL0037561_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37939_1:26:814:-	Eubacterium hallii
2462932	GL0079329_V1_[Lack_5'-end]_[mRNA]_locus=scaffold44588_2:2351:2584:-	Bacteroides pectinophilus
2469886	GL0133983_V1_[Lack_5'-end]_[mRNA]_locus=scaffold86981_1:368:547:-	-
2478301	GL0022869_V1_[Complete]_[mRNA]_locus=scaffold65_3:17066:18517:+	Bacteria
2479238	GL0083052_V1_[Lack_3'-end]_[mRNA]_locus=scaffold727_3:389:574:+	Clostridiales

2479239	GL0093672_V1_[Lack_5'-end]_[mRNA]_locus=scaffold727_4:3:254:+	Bacteria
2479240	GL0093674_V1_[Lack_3'-end]_[mRNA]_locus=scaffold727_4:669:1670:+	Bacteroides capillosus
2479324	GL0086035_V1_[Complete]_[mRNA]_locus=scaffold804_5:1714:2505:-	Clostridiales
2479881	GL0044330_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1157_3:1:240:-	Faecalibacterium prausnitzii
2480755	GL0069672_V1_[Complete]_[mRNA]_locus=scaffold1826_3:2320:2853:+	Roseburia inulinivorans
2481181	GL0046601_V1_[Complete]_[mRNA]_locus=scaffold2164_1:49:513:+	Roseburia inulinivorans
2481182	GL0046603_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2164_1:878:2728:+	Firmicutes
2481183	GL0054554_V1_[Complete]_[mRNA]_locus=scaffold2164_4:2549:2911:+	Roseburia inulinivorans
2481184	GL0054556_V1_[Complete]_[mRNA]_locus=scaffold2164_4:3159:4187:+	Roseburia inulinivorans
2481185	GL0054557_V1_[Complete]_[mRNA]_locus=scaffold2164_4:4360:6402:+	Bacteria
2481344	GL0002914_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2309_3:389:10774:+	Clostridium asparagiforme
2481681	GL0097194_V1_[Complete]_[mRNA]_locus=scaffold2482_1:945:2354:-	Bacteria
2481682	GL0097199_V1_[Complete]_[mRNA]_locus=scaffold2482_1:4116:4466:-	Clostridium methylpentosum
2481683	GL0097200_V1_[Complete]_[mRNA]_locus=scaffold2482_1:4456:4641:-	Bacteroides capillosus

2484652	GL0046695_V1_[Complete]_[mRNA]_locus=scaffold5199_1:2189:3694:-	Bacteria
2485076	GL0048250_V1_[Complete]_[mRNA]_locus=scaffold5563_3:3405:4787:-	Bacteria
2487734	GL0019922_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8277_1:2990:3340:+	Faecalibacterium prausnitzii
2488982	GL0057565_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9928_4:3633:5732:-	Bacteria
2489563	GL0021355_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10619_2:1:3420:-	Clostridiales
2489564	GL0034725_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10619_3:1171:2748:-	Roseburia inulinivorans
2490998	GL0112981_V1_[Complete]_[mRNA]_locus=scaffold12484_1:336:2438:-	Clostridiales
2491657	GL0090647_V1_[Lack_5'-end]_[mRNA]_locus=scaffold13329_1:2:277:+	Clostridium leptum
2492763	GL0082655_V1_[Complete]_[mRNA]_locus=scaffold14983_5:10008:12830:-	Clostridiales
2494412	GL0028612_V1_[Complete]_[mRNA]_locus=scaffold17447_2:3117:3950:+	Clostridium
2494629	GL0092778_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17736_1:1:507:-	-
2496376	GL0037668_V1_[Lack_both_end]_[mRNA]_locus=scaffold20952_1:1:1941:-	Clostridia
2496652	GL0082445_V1_[Lack_both_end]_[mRNA]_locus=scaffold21308_1:1:1236:+	Moorella thermoacetica
2497507	GL0096666_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23223_2:2:760:-	Bacteroides capillosus

2497637	GL0084707_V1_[Complete]_[mRNA]_locus=scaffold23511_7:2816:3919:+	-
2498307	GL0080403_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25282_1:3:521:-	Faecalibacterium prausnitzii
2501168	GL0078439_V1_[Complete]_[mRNA]_locus=scaffold32761_1:2157:4853:+	Thermoanaerobacter pseudethanolicus
2501514	GL0101670_V1_[Lack_5'-end]_[mRNA]_locus=scaffold33584_1:1416:2036:-	Thermoanaerobacter tengcongensis
2503299	GL0029028_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38511_1:944:2038:-	Firmicutes
2505683	GL0045724_V1_[Complete]_[mRNA]_locus=scaffold45726_4:797:1297:+	Roseburia inulinivorans
2505688	GL0107225_V1_[Complete]_[mRNA]_locus=scaffold45726_7:4124:5782:+	Roseburia inulinivorans
2505689	GL0107226_V1_[Complete]_[mRNA]_locus=scaffold45726_7:5767:7293:+	-
2506032	GL0006679_V1_[Complete]_[mRNA]_locus=scaffold46717_1:675:1226:-	-
2506346	GL0098304_V1_[Complete]_[mRNA]_locus=scaffold47612_2:46:435:+	Alistipes putredinis
2507303	GL0001078_V1_[Complete]_[mRNA]_locus=scaffold50573_2:43:849:-	Anaerotruncus colihominis
2508107	GL0031756_V1_[Complete]_[mRNA]_locus=scaffold53172_1:1970:3412:+	Clostridium
2510763	GL0051332_V1_[Complete]_[mRNA]_locus=scaffold61469_2:188:652:-	Alistipes putredinis
2513716	GL0105417_V1_[Complete]_[mRNA]_locus=scaffold67810_1:113:790:-	Alistipes putredinis

2519312	GL0050207_V1_[Complete]_[mRNA]_locus=scaffold542_4:7799:8599:+	Faecalibacterium prausnitzii
2519747	GL0081565_V1_[Complete]_[mRNA]_locus=scaffold1256_1:3228:4628:-	Ruminococcus gnavus
2520303	GL0128632_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2307_1:1192:2325:-	Clostridiales
2520324	GL0118250_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2355_5:596:760:+	-
2520737	GL0014563_V1_[Complete]_[mRNA]_locus=scaffold2737_1:642:1967:+	Clostridiales
2521932	GL0061954_V1_[Complete]_[mRNA]_locus=scaffold5932_3:4041:5540:-	Ruminococcus obeum
2522412	GL0032080_V1_[Complete]_[mRNA]_locus=scaffold6943_1:15:1244:-	Clostridiales
2522648	GL0081054_V1_[Complete]_[mRNA]_locus=scaffold7396_3:1738:3558:+	Clostridiales
2522706	GL0082661_V1_[Complete]_[mRNA]_locus=scaffold7489_10:3908:7243:-	-
2522786	GL0080189_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7721_1:122:904:+	Clostridium methylpentosum
2523741	GL0094778_V1_[Complete]_[mRNA]_locus=scaffold10490_1:147:404:-	-
2524096	GL0002845_V1_[Complete]_[mRNA]_locus=scaffold11300_2:797:3064:+	Clostridiales
2524141	GL0133874_V1_[Complete]_[mRNA]_locus=scaffold11473_1:75:566:-	Bacteroides capillosus
2525056	GL0009058_V1_[Lack_both_end]_[mRNA]_locus=scaffold13999_1:2:1375:-	Faecalibacterium prausnitzii

2526585	GL0014190_V1_[Complete]_[mRNA]_locus=scaffold18667_3:794:3013:+	Firmicutes
2528637	GL0089686_V1_[Complete]_[mRNA]_locus=scaffold26226_4:462:1409:+	-
2529910	GL0134700_V1_[Complete]_[mRNA]_locus=scaffold32294_1:385:2076:-	-
2532045	GL0125860_V1_[Complete]_[mRNA]_locus=scaffold42670_1:1514:3775:+	Clostridiales
2536323	GL0051464_V1_[Lack_3'-end]_[mRNA]_locus=scaffold68343_1:3:305:-	Atopobium rimae
2536398	GL0114956_V1_[Lack_5'-end]_[mRNA]_locus=scaffold68778_1:1:2703:+	Clostridiales
2538306	GL0098275_V1_[Lack_5'-end]_[mRNA]_locus=scaffold79320_1:324:542:-	-
2540181	GL0030726_V1_[Lack_5'-end]_[mRNA]_locus=scaffold85965_1:3:260:+	Roseburia inulinivorans
2541645	GL0073945_V1_[Complete]_[mRNA]_locus=scaffold88903_1:8289:10034:-	-
2547015	GL0086014_V1_[Complete]_[mRNA]_locus=scaffold455_3:4967:5953:-	Faecalibacterium prausnitzii
2547058	GL0135421_V1_[Complete]_[mRNA]_locus=scaffold484_1:7986:8474:+	Faecalibacterium prausnitzii
2547092	GL0081499_V1_[Complete]_[mRNA]_locus=scaffold502_5:110:1996:+	Clostridiales
2547551	GL0099093_V1_[Lack_3'-end]_[mRNA]_locus=scaffold887_1:163:750:+	Faecalibacterium prausnitzii
2548575	GL0027944_V1_[Complete]_[mRNA]_locus=scaffold1406_4:1178:2578:-	Clostridiales

2549062	GL0031026_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1753_2:2:1417:+	Clostridiales
2549205	GL0016961_V1_[Complete]_[mRNA]_locus=scaffold1824_9:703:1377:+	Ruminococcus obeum
2549564	GL0059762_V1_[Complete]_[mRNA]_locus=scaffold2086_2:1105:1536:-	Coprococcus eutactus
2549727	GL0101997_V1_[Complete]_[mRNA]_locus=scaffold2173_2:585:1445:+	Faecalibacterium prausnitzii
2550130	GL0119155_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2343_1:3:956:-	Faecalibacterium prausnitzii
2550285	GL0119669_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2474_5:1:1818:+	Faecalibacterium prausnitzii
2550286	GL0119672_V1_[Complete]_[mRNA]_locus=scaffold2474_5:4749:6059:-	Faecalibacterium prausnitzii
2550339	GL0073017_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2505_1:3:248:+	Faecalibacterium prausnitzii
2550340	GL0073018_V1_[Complete]_[mRNA]_locus=scaffold2505_1:300:581:+	Faecalibacterium prausnitzii
2551129	GL0036580_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3096_1:10:558:+	Faecalibacterium prausnitzii
2551279	GL0090696_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3218_2:3:1184:-	Clostridiales
2551280	GL0090697_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3218_2:1204:2256:-	Blautia hydrogenotrophica
2551812	GL0023314_V1_[Lack_both_end]_[mRNA]_locus=scaffold3507_1:3:767:-	Faecalibacterium prausnitzii
2552489	GL0068527_V1_[Complete]_[mRNA]_locus=scaffold4095_10:310:1905:-	-

2553004	GL0049160_V1_[Lack_3'-end]_[mRNA]_locus=scaffold4517_3:1402:2622:+	-
2553235	GL0046034_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4625_5:926:1561:-	Bacteroides pectinophilus
2554247	GL0029096_V1_[Complete]_[mRNA]_locus=scaffold5737_1:1632:2318:-	Faecalibacterium prausnitzii
2554674	GL0080344_V1_[Complete]_[mRNA]_locus=scaffold6053_3:1472:2584:+	Ruminococcus obeum
2554904	GL0117320_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6257_1:3:866:-	Ruminococcus obeum
2555198	GL0068509_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6546_3:2:919:-	Ruminococcus obeum
2555328	GL0070139_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6693_2:529:825:+	Ruminococcus obeum
2556030	GL0081754_V1_[Complete]_[mRNA]_locus=scaffold7395_1:417:2018:-	Faecalibacterium prausnitzii
2556468	GL0072880_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7877_1:3:800:-	Ruminococcus obeum
2556657	GL0076684_V1_[Complete]_[mRNA]_locus=scaffold8160_8:235:1089:+	Ruminococcus obeum
2556729	GL0004195_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8243_3:2546:3358:+	Ruminococcus obeum
2557397	GL0014805_V1_[Complete]_[mRNA]_locus=scaffold8979_6:29:841:-	Clostridium
2557600	GL0068922_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9127_5:1:831:-	Ruminococcus obeum
2557601	GL0068923_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9127_5:1431:2603:-	Clostridiales

2557938	GL0131462_V1_[Lack_both_end]_[mRNA]_locus=scaffold9338_2:3:1622:+	Clostridiales
2558107	GL0038510_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9505_4:239:1201:-	Ruminococcus obeum
2558222	GL0030017_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9605_4:45:1160:-	Faecalibacterium prausnitzii
2558410	GL0092961_V1_[Complete]_[mRNA]_locus=scaffold9773_6:1874:3214:+	Ruminococcus obeum
2558411	GL0102367_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9788_2:235:1017:+	Faecalibacterium prausnitzii
2558697	GL0041787_V1_[Complete]_[mRNA]_locus=scaffold10084_2:175:744:+	Clostridiales
2558734	GL0132689_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10130_2:426:1067:+	Ruminococcus obeum
2558820	GL0121689_V1_[Lack_both_end]_[mRNA]_locus=scaffold10333_4:2:1075:+	Clostridiales
2559835	GL0079815_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11750_2:1514:2209:+	Bacteroides capillosus
2560231	GL0048514_V1_[Complete]_[mRNA]_locus=scaffold12154_1:341:1468:-	Ruminococcus obeum
2560407	GL0058274_V1_[Complete]_[mRNA]_locus=scaffold12374_3:7224:7874:+	Blautia hydrogenotrophica
2560532	GL0007581_V1_[Lack_3'-end]_[mRNA]_locus=scaffold12496_1:429:1772:+	Faecalibacterium prausnitzii
2560619	GL0042533_V1_[Lack_both_end]_[mRNA]_locus=scaffold12650_1:1:591:+	Faecalibacterium prausnitzii
2560949	GL0039145_V1_[Complete]_[mRNA]_locus=scaffold13033_8:1844:2743:+	Clostridium nexile

2561189	GL0031085_V1_[Complete]_[mRNA]_locus=scaffold13357_7:1854:3119:-	Bacteroides pectinophilus
2561206	GL0121348_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13381_10:9388:10809:+	Blautia hydrogenotrophica
2562088	GL0037235_V1_[Complete]_[mRNA]_locus=scaffold14770_5:806:2179:+	Clostridiales
2562383	GL0016926_V1_[Complete]_[mRNA]_locus=scaffold15286_2:442:1737:+	Ruminococcus obeum
2562533	GL0124012_V1_[Complete]_[mRNA]_locus=scaffold15502_14:3163:4602:+	Ruminococcus obeum
2563079	GL0125985_V1_[Complete]_[mRNA]_locus=scaffold16227_2:329:1819:-	-
2563458	GL0118161_V1_[Complete]_[mRNA]_locus=scaffold17056_1:1394:4123:+	Faecalibacterium prausnitzii
2564542	GL0030241_V1_[Lack_both_end]_[mRNA]_locus=scaffold18927_2:1:1158:-	Ruminococcus torques
2565446	GL0067753_V1_[Lack_5'-end]_[mRNA]_locus=scaffold20399_1:2371:3045:-	Coprococcus eutactus
2565543	GL0017109_V1_[Complete]_[mRNA]_locus=scaffold20626_6:621:878:-	-
2565919	GL0102217_V1_[Complete]_[mRNA]_locus=scaffold21206_1:276:1241:-	Ruminococcus obeum
2566067	GL0023400_V1_[Lack_3'-end]_[mRNA]_locus=scaffold21394_1:970:1719:+	Bacteroides capillosus
2566236	GL0000314_V1_[Lack_3'-end]_[mRNA]_locus=scaffold21781_7:288:755:+	-

2566596	GL0051315_V1_[Lack_5'-end]_[mRNA]_locus=scaffold22423_10:3:1262:+	Clostridiales
2566661	GL0113175_V1_[Complete]_[mRNA]_locus=scaffold22589_1:3692:4735:+	Clostridiales
2567461	GL0031892_V1_[Complete]_[mRNA]_locus=scaffold24289_2:326:2029:+	Clostridiales
2567660	GL0092990_V1_[Complete]_[mRNA]_locus=scaffold24788_4:460:1161:-	Coprococcus eutactus
2568556	GL0063042_V1_[Complete]_[mRNA]_locus=scaffold26416_2:10814:11161:-	Clostridium leptum
2569205	GL0128076_V1_[Lack_3'-end]_[mRNA]_locus=scaffold27890_4:3:659:-	Clostridia
2569378	GL0071067_V1_[Complete]_[mRNA]_locus=scaffold28268_1:382:1299:+	Ruminococcus obeum
2569388	GL0115602_V1_[Complete]_[mRNA]_locus=scaffold28289_2:215:1561:+	-
2570193	GL0087814_V1_[Complete]_[mRNA]_locus=scaffold30242_1:1:354:+	Clostridiales
2570551	GL0124461_V1_[Complete]_[mRNA]_locus=scaffold31307_3:16:504:-	-
2570558	GL0014407_V1_[Lack_3'-end]_[mRNA]_locus=scaffold31321_4:1:696:-	-
2571016	GL0062442_V1_[Lack_3'-end]_[mRNA]_locus=scaffold32490_1:1:1152:-	-
2571189	GL0114047_V1_[Complete]_[mRNA]_locus=scaffold32966_5:1128:2291:-	Anaerotruncus colihominis
2571235	GL0050631_V1_[Complete]_[mRNA]_locus=scaffold33088_2:8:1486:-	Bacteroides pectinophilus

2571511	GL0083116_V1_[Complete]_[mRNA]_locus=scaffold33854_2:1190:2443:+	Holdemania filiformis
2571515	GL0105143_V1_[Lack_3'-end]_[mRNA]_locus=scaffold33854_5:3:710:-	Clostridium
2572198	GL0125570_V1_[Complete]_[mRNA]_locus=scaffold35465_1:2129:3088:-	Ruminococcus obeum
2572478	GL0080804_V1_[Complete]_[mRNA]_locus=scaffold36291_7:131:1360:+	Clostridiales
2572719	GL0094410_V1_[Complete]_[mRNA]_locus=scaffold37106_2:1828:2883:+	Ruminococcus obeum
2572795	GL0013437_V1_[Lack_both_end]_[mRNA]_locus=scaffold37300_2:3:662:+	Thermomicrobium roseum
2572805	GL0093263_V1_[Complete]_[mRNA]_locus=scaffold37320_1:1778:3001:-	Faecalibacterium prausnitzii
2572819	GL0004668_V1_[Complete]_[mRNA]_locus=scaffold37369_1:638:1162:-	Ruminococcus obeum
2572918	GL0099350_V1_[Complete]_[mRNA]_locus=scaffold37579_1:1994:2860:-	Faecalibacterium prausnitzii
2573321	GL0026423_V1_[Complete]_[mRNA]_locus=scaffold38641_4:2317:2865:-	-
2573322	GL0026424_V1_[Lack_3'-end]_[mRNA]_locus=scaffold38641_4:3236:3685:+	Bacteroides pectinophilus
2573354	GL0048229_V1_[Complete]_[mRNA]_locus=scaffold38802_6:246:863:-	Alistipes putredinis
2574975	GL0089287_V1_[Complete]_[mRNA]_locus=scaffold43077_1:680:2236:-	Clostridium
2575767	GL0108463_V1_[Complete]_[mRNA]_locus=scaffold45479_3:173:916:+	Firmicutes

2575772	GL0036623_V1_[Complete]_[mRNA]_locus=scaffold45479_9:2001:3152:+	Dorea longicatena
2576107	GL0047883_V1_[Complete]_[mRNA]_locus=scaffold46294_3:8359:9876:+	Anaerotruncus colihominis
2576319	GL0128874_V1_[Complete]_[mRNA]_locus=scaffold46811_1:649:1374:+	Ruminococcus obeum
2576542	GL0024341_V1_[Complete]_[mRNA]_locus=scaffold47452_2:3611:4864:-	Clostridium phytofermentans
2577199	GL0021765_V1_[Lack_5'-end]_[mRNA]_locus=scaffold49706_6:1:1005:+	Clostridium asparagiforme
2577687	GL0031074_V1_[Complete]_[mRNA]_locus=scaffold51169_6:704:1384:-	Clostridium
2577751	GL0069093_V1_[Complete]_[mRNA]_locus=scaffold51402_7:164:934:+	Alistipes putredinis
2577856	GL0109861_V1_[Complete]_[mRNA]_locus=scaffold51744_5:1676:2326:+	-
2578133	GL0103890_V1_[Lack_5'-end]_[mRNA]_locus=scaffold52423_1:1:489:+	Clostridiales
2578152	GL0010837_V1_[Lack_3'-end]_[mRNA]_locus=scaffold52453_1:1:777:-	Bacteroides pectinophilus
2578806	GL0068604_V1_[Lack_both_end]_[mRNA]_locus=scaffold54534_4:3:752:+	-
2578899	GL0128351_V1_[Lack_3'-end]_[mRNA]_locus=scaffold54802_10:1389:1856:+	Firmicutes
2579469	GL0079503_V1_[Complete]_[mRNA]_locus=scaffold56544_3:45:293:+	Clostridium asparagiforme

2579910	GL0000726_V1_[Lack_both_end]_[mRNA]_locus=scaffold58083_1:1:1464:+	Eubacterium ventriosum
2580083	GL0098130_V1_[Complete]_[mRNA]_locus=scaffold58769_2:151:705:+	Clostridiales
2580142	GL0120480_V1_[Lack_both_end]_[mRNA]_locus=scaffold58926_7:2:1372:+	Clostridiales
2581286	GL0074275_V1_[Lack_3'-end]_[mRNA]_locus=scaffold62368_1:2:976:-	Alkaliphilus oremlandii
2582623	GL0024741_V1_[Complete]_[mRNA]_locus=scaffold66311_1:63:860:-	Blautia hydrogenotrophica
2583048	GL0079161_V1_[Complete]_[mRNA]_locus=scaffold67493_4:463:897:-	Dorea formicigenerans
2583150	GL0118911_V1_[Lack_5'-end]_[mRNA]_locus=scaffold67720_2:1:621:+	Holdemania filiformis
2583230	GL0045467_V1_[Lack_both_end]_[mRNA]_locus=scaffold67970_3:1:864:+	Clostridium phytofermentans
2583382	GL0081747_V1_[Lack_3'-end]_[mRNA]_locus=scaffold68316_1:2:1039:-	-
2583615	GL0010338_V1_[Lack_both_end]_[mRNA]_locus=scaffold68757_2:2:943:-	Clostridium thermocellum
2583882	GL0013189_V1_[Lack_both_end]_[mRNA]_locus=scaffold69306_2:1:1077:-	Roseburia inulinivorans
2584220	GL0077356_V1_[Lack_both_end]_[mRNA]_locus=scaffold70018_2:3:986:-	Caldicellulosiruptor saccharolyticus
2584342	GL0109749_V1_[Lack_3'-end]_[mRNA]_locus=scaffold70242_2:2:835:-	Ruminococcus gnavus
2584637	GL0099344_V1_[Lack_3'-end]_[mRNA]_locus=scaffold70874_2:3:1229:-	Clostridium scindens

2584683	GL0088524_V1_[Lack_both_end]_[mRNA]_locus=scaffold70950_2:2:613:+	-
2584987	GL0086297_V1_[Complete]_[mRNA]_locus=scaffold71509_2:1:633:+	Ruminococcus obeum
2586649	GL0086630_V1_[Lack_5'-end]_[mRNA]_locus=C4849449_1:138:677:-	Clostridium scindens
2586833	GL0064808_V1_[Lack_5'-end]_[mRNA]_locus=C4868861_1:59:781:-	Clostridiales
2587133	GL0119886_V1_[Lack_5'-end]_[mRNA]_locus=C4910770_1:1:1002:+	Ruminococcus lactaris
2587748	GL0041275_V1_[Lack_both_end]_[mRNA]_locus=scaffold730_1:2:1033:-	Bacteroides capillosus
2587764	GL0075083_V1_[Lack_both_end]_[mRNA]_locus=scaffold780_1:2:532:-	Bacteria
2588524	GL0024869_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2305_1:928:1587:+	Faecalibacterium prausnitzii
2588692	GL0107399_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2590_1:43:1020:+	Clostridium methylpentosum
2588834	GL0093841_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2848_1:762:1322:-	Roseburia inulinivorans
2589338	GL0055628_V1_[Complete]_[mRNA]_locus=scaffold4059_2:1339:1677:+	Roseburia inulinivorans
2589802	GL0107141_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5433_4:1282:1926:-	Bacteroides capillosus
2589855	GL0048819_V1_[Complete]_[mRNA]_locus=scaffold5619_1:113:1084:+	Faecalibacterium prausnitzii
2590017	GL0079963_V1_[Complete]_[mRNA]_locus=scaffold6267_1:314:1687:-	Clostridium methylpentosum

2590943	GL0019774_V1_[Lack_5'-end]_[mRNA]_locus=scaffold8338_2:1977:3146:-	Bacteroides capillosus
2590967	GL0023304_V1_[Complete]_[mRNA]_locus=scaffold8460_2:600:2234:+	Clostridiales
2591328	GL0067766_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9771_1:768:1499:-	Bacteroides capillosus
2591444	GL0091775_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10194_2:1:915:+	Faecalibacterium prausnitzii
2591658	GL0001953_V1_[Complete]_[mRNA]_locus=scaffold10803_6:906:1466:-	Faecalibacterium prausnitzii
2591838	GL0039429_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11370_3:2:922:+	Bacteroides capillosus
2592064	GL0033249_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11919_3:604:1239:-	Clostridiales
2592558	GL0046361_V1_[Complete]_[mRNA]_locus=scaffold13330_9:2955:3866:+	Streptococcus pyogenes
2593883	GL0065952_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17239_1:1:480:+	Roseburia inulinivorans
2593884	GL0069190_V1_[Complete]_[mRNA]_locus=scaffold17239_2:162:755:+	Roseburia inulinivorans
2594038	GL0103914_V1_[Lack_both_end]_[mRNA]_locus=scaffold17769_1:3:896:+	Roseburia inulinivorans
2594571	GL0101205_V1_[Complete]_[mRNA]_locus=scaffold19705_2:313:1227:+	Roseburia inulinivorans
2598003	GL0052892_V1_[Lack_5'-end]_[mRNA]_locus=scaffold33212_1:1:285:+	Firmicutes
2598383	GL0088111_V1_[Complete]_[mRNA]_locus=scaffold35072_1:1588:3159:-	Clostridium

2598616	GL0088583_V1_[Complete]_[mRNA]_locus=scaffold36384_1:146:424:+	Clostridiales
2599247	GL0101221_V1_[Lack_5'-end]_[mRNA]_locus=scaffold39539_1:1:2397:+	Bacteria
2599288	GL0088498_V1_[Complete]_[mRNA]_locus=scaffold39963_1:80:2458:-	Bacteria
2599752	GL0063438_V1_[Lack_3'-end]_[mRNA]_locus=scaffold41821_1:3:338:-	Holdemania filiformis
2605263	GL0048419_V1_[Lack_5'-end]_[mRNA]_locus=scaffold70929_2:670:1431:-	Bacteroides pectinophilus
2608831	GL0072755_V1_[Complete]_[mRNA]_locus=scaffold79483_1:4895:6616:-	-
2609281	GL0065711_V1_[Complete]_[mRNA]_locus=scaffold79930_1:109:1080:+	Bacteroides capillosus
2610399	GL0089732_V1_[Lack_5'-end]_[mRNA]_locus=scaffold80595_1:2:1411:+	Clostridium phytofermentans
2610759	GL0063019_V1_[Lack_3'-end]_[mRNA]_locus=C9417573_1:427:573:+	-
2612112	GL0011020_V1_[Complete]_[mRNA]_locus=scaffold39_15:3377:4768:-	Clostridiales
2612171	GL0047045_V1_[Complete]_[mRNA]_locus=scaffold109_1:1122:1970:-	Roseburia inulinivorans
2612551	GL0045690_V1_[Complete]_[mRNA]_locus=scaffold526_4:5333:5842:+	-
2612552	GL0002096_V1_[Complete]_[mRNA]_locus=scaffold526_5:536:1903:+	-
2612556	GL0018347_V1_[Lack_5'-end]_[mRNA]_locus=scaffold528_1:15:1904:-	Faecalibacterium prausnitzii

2612887	GL0093372_V1_[Complete]_[mRNA]_locus=scaffold880_5:2151:2798:+	Firmicutes
2612890	GL0078318_V1_[Complete]_[mRNA]_locus=scaffold880_10:2988:4136:+	Clostridiales
2613067	GL0087726_V1_[Complete]_[mRNA]_locus=scaffold1033_2:316:852:+	Roseburia inulinivorans
2613068	GL0004881_V1_[Complete]_[mRNA]_locus=scaffold1035_1:5900:7141:-	Roseburia inulinivorans
2613103	GL0051522_V1_[Complete]_[mRNA]_locus=scaffold1108_4:1874:4576:-	Clostridiales
2613106	GL0016036_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1108_7:1195:1986:-	Blautia hydrogenotrophica
2613118	GL0007393_V1_[Complete]_[mRNA]_locus=scaffold1129_6:2025:3749:+	Firmicutes
2613202	GL0032691_V1_[Lack_both_end]_[mRNA]_locus=scaffold1218_1:2:1114:-	Clostridium methylpentosum
2613206	GL0004197_V1_[Complete]_[mRNA]_locus=scaffold1219_8:2192:4534:+	Clostridiales
2613266	GL0113810_V1_[Complete]_[mRNA]_locus=scaffold1224_4:369:2111:+	-
2613373	GL0081977_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1336_5:2:1093:+	Roseburia inulinivorans
2613452	GL0094025_V1_[Complete]_[mRNA]_locus=scaffold1453_1:738:1661:-	Roseburia inulinivorans
2613605	GL0034506_V1_[Complete]_[mRNA]_locus=scaffold1631_4:747:1940:-	Clostridiales
2613615	GL0087946_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1660_3:5841:6365:-	Roseburia inulinivorans

2613653	GL0098673_V1_[Complete]_[mRNA]_locus=scaffold1689_5:2913:4004:+	Clostridiales
2613654	GL0120953_V1_[Complete]_[mRNA]_locus=scaffold1692_2:242:2284:-	Bacteria
2613789	GL0004502_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1890_1:1:597:+	Roseburia inulinivorans
2613999	GL0039577_V1_[Complete]_[mRNA]_locus=scaffold2069_3:1900:2664:-	Roseburia inulinivorans
2614131	GL0109557_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2234_2:5804:7621:+	Roseburia inulinivorans
2614132	GL0031428_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2234_5:1357:2391:+	Roseburia inulinivorans
2614170	GL0017309_V1_[Complete]_[mRNA]_locus=scaffold2290_3:1375:3468:-	Bacteria
2614171	GL0121019_V1_[Complete]_[mRNA]_locus=scaffold2290_17:9256:10716:-	Roseburia inulinivorans
2614539	GL0072851_V1_[Complete]_[mRNA]_locus=scaffold2725_4:590:2047:+	Clostridiales
2614814	GL0089328_V1_[Complete]_[mRNA]_locus=scaffold2986_12:12236:12592:-	Ruminococcus obeum
2614861	GL0023506_V1_[Complete]_[mRNA]_locus=scaffold3030_5:383:1405:+	Roseburia inulinivorans
2614883	GL0039299_V1_[Complete]_[mRNA]_locus=scaffold3069_2:6036:6983:-	Roseburia inulinivorans
2615083	GL0083042_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3261_1:853:1980:-	Roseburia inulinivorans
2615084	GL0030956_V1_[Complete]_[mRNA]_locus=scaffold3261_2:1240:2052:-	Roseburia inulinivorans

2615178	GL0018128_V1_[Complete]_[mRNA]_locus=scaffold3361_6:1739:3076:+	Ruminococcus obeum
2615268	GL0066005_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3527_5:3754:4536:-	Roseburia inulinivorans
2615311	GL0115334_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3595_1:1210:2064:+	Clostridium leptum
2615438	GL0011709_V1_[Lack_both_end]_[mRNA]_locus=scaffold3712_4:3:746:+	Bacteria
2615471	GL0019828_V1_[Complete]_[mRNA]_locus=scaffold3805_4:3142:3669:+	Roseburia inulinivorans
2615852	GL0045529_V1_[Complete]_[mRNA]_locus=scaffold4416_3:1278:2159:+	Clostridiales
2616161	GL0067939_V1_[Complete]_[mRNA]_locus=scaffold4988_2:809:1159:-	-
2616332	GL0070184_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5271_1:482:760:-	Faecalibacterium prausnitzii
2616667	GL0081404_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5645_3:528:1454:+	Roseburia inulinivorans
2616791	GL0100137_V1_[Complete]_[mRNA]_locus=scaffold5972_1:1982:4594:-	Roseburia inulinivorans
2616792	GL0010435_V1_[Complete]_[mRNA]_locus=scaffold5972_2:2769:4862:-	Roseburia inulinivorans
2616819	GL0046518_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6026_2:1:1422:-	Clostridiales
2616821	GL0100501_V1_[Complete]_[mRNA]_locus=scaffold6026_8:1241:2230:-	Roseburia inulinivorans
2616822	GL0100502_V1_[Complete]_[mRNA]_locus=scaffold6026_8:2248:3756:-	Firmicutes

2616973	GL0062443_V1_[Complete]_[mRNA]_locus=scaffold6258_3:12301:15411:+	Clostridia
2616974	GL0062444_V1_[Complete]_[mRNA]_locus=scaffold6258_3:15544:16566:-	-
2616975	GL0062445_V1_[Complete]_[mRNA]_locus=scaffold6258_3:16618:17685:-	-
2616976	GL0062446_V1_[Complete]_[mRNA]_locus=scaffold6258_3:17903:20143:+	-
2617186	GL0071787_V1_[Complete]_[mRNA]_locus=scaffold6664_1:1885:2934:+	Roseburia inulinivorans
2617200	GL0105961_V1_[Complete]_[mRNA]_locus=scaffold6694_3:3978:6668:+	Clostridiales
2617292	GL0080776_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6838_1:146:916:+	Roseburia inulinivorans
2617832	GL0120047_V1_[Lack_both_end]_[mRNA]_locus=scaffold7570_1:3:521:+	Bacteroides pectinophilus
2617893	GL0066060_V1_[Complete]_[mRNA]_locus=scaffold7688_8:806:2416:-	Bacteria
2619144	GL0068252_V1_[Complete]_[mRNA]_locus=scaffold10283_1:5033:5872:+	Clostridium phytofermentans
2619288	GL0002736_V1_[Complete]_[mRNA]_locus=scaffold10540_6:2615:7153:-	Clostridiales
2619289	GL0077756_V1_[Complete]_[mRNA]_locus=scaffold10540_7:7044:8735:-	Roseburia inulinivorans
2619513	GL0105573_V1_[Complete]_[mRNA]_locus=scaffold10885_1:3215:3829:-	Roseburia inulinivorans
2619514	GL0115397_V1_[Complete]_[mRNA]_locus=scaffold10885_2:243:1586:-	Roseburia inulinivorans

2619555	GL0014659_V1_[Complete]_[mRNA]_locus=scaffold10940_2:1900:3729:+	Clostridiales
2619682	GL0093317_V1_[Complete]_[mRNA]_locus=scaffold11170_2:1066:1983:-	Roseburia inulinivorans
2619711	GL0012362_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11208_1:6130:7371:+	Roseburia inulinivorans
2619798	GL0047997_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11334_2:1:930:-	Roseburia inulinivorans
2620123	GL0085152_V1_[Complete]_[mRNA]_locus=scaffold11936_1:4238:4858:+	Roseburia inulinivorans
2620431	GL0034216_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12568_4:2:601:+	Roseburia inulinivorans
2620456	GL0099989_V1_[Complete]_[mRNA]_locus=scaffold12669_2:1365:2219:-	Roseburia inulinivorans
2620582	GL0122949_V1_[Complete]_[mRNA]_locus=scaffold12937_5:6016:6747:-	Eubacterium biforme
2621032	GL0104789_V1_[Complete]_[mRNA]_locus=scaffold14106_1:1820:4222:-	Lachnospiraceae
2621255	GL0065944_V1_[Complete]_[mRNA]_locus=scaffold14598_1:1483:2820:-	Ruminococcus gnavus
2621697	GL0083402_V1_[Complete]_[mRNA]_locus=scaffold16145_1:581:1525:+	Roseburia inulinivorans
2621915	GL0053743_V1_[Complete]_[mRNA]_locus=scaffold16512_2:2846:4012:-	Roseburia inulinivorans
2622034	GL0009726_V1_[Complete]_[mRNA]_locus=scaffold16952_6:188:1630:-	Roseburia inulinivorans
2622073	GL0002655_V1_[Lack_both_end]_[mRNA]_locus=scaffold17037_2:2:565:+	-

2622552	GL0110148_V1_[Complete]_[mRNA]_locus=scaffold18408_18:738:2324:+	Bacteroides pectinophilus
2622803	GL0010675_V1_[Lack_5'-end]_[mRNA]_locus=scaffold19253_1:3:281:+	Faecalibacterium prausnitzii
2623662	GL0012726_V1_[Complete]_[mRNA]_locus=scaffold22244_5:1110:2135:+	Clostridium
2624605	GL0084093_V1_[Complete]_[mRNA]_locus=scaffold25360_1:1553:2476:+	Bacteroides pectinophilus
2624606	GL0084094_V1_[Complete]_[mRNA]_locus=scaffold25360_1:2496:3875:-	Clostridiales
2625484	GL0057774_V1_[Complete]_[mRNA]_locus=scaffold29011_1:230:1876:-	Anaerotruncus colihominis
2626406	GL0074136_V1_[Complete]_[mRNA]_locus=scaffold33544_2:1055:1735:-	Roseburia inulinivorans
2626407	GL0074138_V1_[Complete]_[mRNA]_locus=scaffold33544_2:2645:4282:-	Roseburia inulinivorans
2626408	GL0074139_V1_[Complete]_[mRNA]_locus=scaffold33544_2:4631:5824:-	Roseburia inulinivorans
2626425	GL0088096_V1_[Lack_5'-end]_[mRNA]_locus=scaffold33569_1:3:611:+	Roseburia inulinivorans
2626490	GL0053310_V1_[Complete]_[mRNA]_locus=scaffold33918_1:3302:4588:-	Roseburia inulinivorans
2626859	GL0006540_V1_[Lack_5'-end]_[mRNA]_locus=scaffold35586_1:3:425:+	Bacteria
2628040	GL0017899_V1_[Complete]_[mRNA]_locus=scaffold42767_1:231:1931:-	Clostridiales
2628783	GL0122583_V1_[Complete]_[mRNA]_locus=scaffold48205_1:152:991:+	Roseburia inulinivorans

2629138	GL0069801_V1_[Complete]_[mRNA]_locus=scaffold50407_3:268:1395:-	Anaerotruncus colihominis
2629247	GL0049095_V1_[Lack_3'-end]_[mRNA]_locus=scaffold51252_1:100:756:+	-
2629326	GL0002063_V1_[Lack_3'-end]_[mRNA]_locus=scaffold51844_1:1:441:-	Bacteroides capillosus
2629581	GL0059705_V1_[Complete]_[mRNA]_locus=scaffold53787_1:61:474:-	Clostridium
2631321	GL0079249_V1_[Lack_5'-end]_[mRNA]_locus=scaffold66245_4:1:786:+	Clostridium leptum
2631380	GL0079941_V1_[Complete]_[mRNA]_locus=scaffold66604_5:529:2271:-	Clostridiales
2633407	GL0068760_V1_[Lack_5'-end]_[mRNA]_locus=C3938183_1:145:789:-	Roseburia inulinivorans
2635224	GL0025219_V1_[Complete]_[mRNA]_locus=scaffold1619_4:2012:3280:+	Roseburia inulinivorans
2635388	GL0120465_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1819_1:455:943:-	-
2635436	GL0009265_V1_[Lack_both_end]_[mRNA]_locus=scaffold1894_1:1:639:+	Faecalibacterium prausnitzii
2635637	GL0062466_V1_[Complete]_[mRNA]_locus=scaffold2119_2:721:1686:+	Roseburia inulinivorans
2635863	GL0084526_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2409_1:3:1232:-	Bacteroides capillosus
2636114	GL0011542_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2631_2:1070:1759:-	Roseburia inulinivorans
2636349	GL0024602_V1_[Complete]_[mRNA]_locus=scaffold2897_2:56:2296:-	Clostridiales

2636810	GL0092807_V1_[Complete]_[mRNA]_locus=scaffold3764_2:2130:2990:+	Roseburia inulinivorans
2637372	GL0001830_V1_[Complete]_[mRNA]_locus=scaffold4421_4:4719:5513:-	Roseburia inulinivorans
2638946	GL0066668_V1_[Complete]_[mRNA]_locus=scaffold7548_2:2229:3599:-	Clostridiales
2639643	GL0130120_V1_[Complete]_[mRNA]_locus=scaffold8722_1:457:1482:-	Roseburia inulinivorans
2640272	GL0047937_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10210_1:3:467:-	Roseburia inulinivorans
2641137	GL0020229_V1_[Complete]_[mRNA]_locus=scaffold12236_3:5771:7258:-	Roseburia inulinivorans
2641244	GL0081820_V1_[Complete]_[mRNA]_locus=scaffold12434_1:317:1183:-	Roseburia inulinivorans
2641262	GL0079089_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12471_6:3:452:+	-
2641457	GL0096425_V1_[Complete]_[mRNA]_locus=scaffold12988_2:869:1504:-	Roseburia inulinivorans
2641946	GL0065230_V1_[Complete]_[mRNA]_locus=scaffold14400_6:1471:2586:-	Roseburia inulinivorans
2642464	GL0039881_V1_[Complete]_[mRNA]_locus=scaffold15816_2:810:1643:-	Roseburia inulinivorans
2642968	GL0001382_V1_[Complete]_[mRNA]_locus=scaffold17186_2:2162:3247:-	Ruminococcus obeum
2643252	GL0001242_V1_[Complete]_[mRNA]_locus=scaffold18144_6:7989:9020:+	Roseburia inulinivorans
2643564	GL0134387_V1_[Complete]_[mRNA]_locus=scaffold19592_3:2718:4403:-	Roseburia inulinivorans

2643716	GL0032780_V1_[Complete]_[mRNA]_locus=scaffold19962_6:369:1310:-	Clostridium
2643845	GL0017088_V1_[Complete]_[mRNA]_locus=scaffold20436_1:428:1369:-	Roseburia inulinivorans
2644503	GL0123110_V1_[Complete]_[mRNA]_locus=scaffold22767_2:1582:3132:-	Roseburia inulinivorans
2644592	GL0026962_V1_[Complete]_[mRNA]_locus=scaffold23033_4:156:1226:+	Roseburia inulinivorans
2644696	GL0096112_V1_[Complete]_[mRNA]_locus=scaffold23248_3:13:672:-	Roseburia inulinivorans
2644816	GL0080002_V1_[Complete]_[mRNA]_locus=scaffold23470_12:778:1308:-	Ruminococcus gnavus
2645847	GL0088126_V1_[Lack_5'-end]_[mRNA]_locus=scaffold28377_2:2:211:+	-
2646262	GL0069057_V1_[Complete]_[mRNA]_locus=scaffold30357_4:48:5936:+	Bacillus thuringiensis
2646685	GL0006004_V1_[Complete]_[mRNA]_locus=scaffold32914_2:1788:3194:-	Collinsella stercoris
2647607	GL0027710_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38081_1:2299:2481:-	Coprococcus eutactus
2647619	GL0065742_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38152_1:1:1953:+	Bacteria
2648918	GL0100347_V1_[Complete]_[mRNA]_locus=scaffold48261_1:792:1028:+	Clostridiales
2649772	GL0082716_V1_[Complete]_[mRNA]_locus=scaffold53481_2:482:2563:-	Clostridiales
2651181	GL0068379_V1_[Lack_both_end]_[mRNA]_locus=scaffold64098_1:1:1071:+	Faecalibacterium prausnitzii

2652205	GL0025213_V1_[Complete]_[mRNA]_locus=scaffold71813_4:2343:3605:+	Clostridium perfringens
2652662	GL0023827_V1_[Complete]_[mRNA]_locus=scaffold74632_4:1037:2365:-	Firmicutes
2652732	GL0123078_V1_[Lack_5'-end]_[mRNA]_locus=scaffold75459_3:2:955:+	Roseburia inulinivorans
2653472	GL0120138_V1_[Complete]_[mRNA]_locus=scaffold80951_1:145:798:+	Roseburia inulinivorans
2653982	GL0118417_V1_[Complete]_[mRNA]_locus=scaffold84211_2:132:614:-	-
2654461	GL0045794_V1_[Complete]_[mRNA]_locus=scaffold86757_1:986:1912:+	Roseburia inulinivorans
2654968	GL0139358_V1_[Complete]_[mRNA]_locus=scaffold88999_1:2010:3791:-	Roseburia inulinivorans
2655259	GL0077462_V1_[Complete]_[mRNA]_locus=scaffold90147_1:470:772:+	Roseburia inulinivorans
2655622	GL0069664_V1_[Lack_5'-end]_[mRNA]_locus=scaffold91431_1:89:1159:-	Roseburia inulinivorans
2658787	GL0107568_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1_3:2:766:+	Roseburia inulinivorans
2658936	GL0019245_V1_[Lack_both_end]_[mRNA]_locus=scaffold142_1:3:1157:+	Bacteroides capillosus
2659286	GL0072550_V1_[Complete]_[mRNA]_locus=scaffold406_1:5290:6492:+	Roseburia inulinivorans
2659994	GL0010873_V1_[Lack_3'-end]_[mRNA]_locus=scaffold793_2:172:555:+	Bacteroides
2660034	GL0039159_V1_[Complete]_[mRNA]_locus=scaffold842_16:7434:8465:+	-

2660111	GL0038842_V1_[Complete]_[mRNA]_locus=scaffold989_1:732:1241:+	Faecalibacterium prausnitzii
2660753	GL0070832_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1469_2:1:552:+	Blautia hydrogenotrophica
2662580	GL0084023_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3473_12:3:656:+	Roseburia inulinivorans
2662582	GL0092726_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3474_6:2:1282:+	Roseburia inulinivorans
2662697	GL0095420_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3657_8:174:536:+	Faecalibacterium prausnitzii
2663068	GL0002419_V1_[Complete]_[mRNA]_locus=scaffold3985_4:2208:2795:+	Faecalibacterium prausnitzii
2664116	GL0050740_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5520_1:35:676:-	Alistipes putredinis
2665050	GL0004783_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7046_2:720:947:-	Bacteria
2665086	GL0012494_V1_[Complete]_[mRNA]_locus=scaffold7108_1:11434:12783:-	Roseburia inulinivorans
2665364	GL0117070_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7507_3:1311:3215:+	Clostridiales
2665405	GL0110643_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7616_1:3:383:+	Bacteroides capillosus
2666775	GL0065329_V1_[Complete]_[mRNA]_locus=scaffold9943_3:531:1469:-	Faecalibacterium prausnitzii
2666908	GL0107178_V1_[Lack_both_end]_[mRNA]_locus=scaffold10344_2:1:1371:+	Clostridiales
2667612	GL0034407_V1_[Complete]_[mRNA]_locus=scaffold11566_1:2589:3350:+	Roseburia inulinivorans

2668016	GL0072825_V1_[Complete]_[mRNA]_locus=scaffold12176_4:40:1203:-	Roseburia inulinivorans
2668035	GL0035328_V1_[Complete]_[mRNA]_locus=scaffold12231_3:2649:3176:+	Roseburia inulinivorans
2668080	GL0079833_V1_[Complete]_[mRNA]_locus=scaffold12301_2:119:1045:+	Faecalibacterium prausnitzii
2668086	GL0107420_V1_[Complete]_[mRNA]_locus=scaffold12347_2:1202:1474:-	Roseburia inulinivorans
2668530	GL0105374_V1_[Complete]_[mRNA]_locus=scaffold13069_1:2074:4299:+	Bacteria
2669089	GL0082392_V1_[Complete]_[mRNA]_locus=scaffold14187_1:623:1276:-	Faecalibacterium prausnitzii
2669849	GL0111893_V1_[Complete]_[mRNA]_locus=scaffold16089_1:163:1095:-	Faecalibacterium prausnitzii
2670083	GL0076973_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16518_1:2:118:-	-
2670303	GL0029154_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16707_2:1:693:-	Bacteroides capillosus
2670467	GL0057423_V1_[Complete]_[mRNA]_locus=scaffold17084_2:14:1471:-	Roseburia inulinivorans
2670672	GL0066782_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17541_1:280:774:+	Bacteroides capillosus
2671140	GL0062286_V1_[Complete]_[mRNA]_locus=scaffold18664_1:1512:2192:-	Holdemania filiformis
2673937	GL0031258_V1_[Complete]_[mRNA]_locus=scaffold25864_3:18271:19635:-	Clostridiales
2673958	GL0082257_V1_[Complete]_[mRNA]_locus=scaffold25864_4:7366:8457:-	Coprococcus eutactus

2673965	GL0039871_V1_[Complete]_[mRNA]_locus=scaffold25864_6:2397:5723:-	Clostridiales
2674471	GL0007644_V1_[Lack_5'-end]_[mRNA]_locus=scaffold27466_4:1605:2579:-	Eubacterium hallii
2674800	GL0070568_V1_[Lack_3'-end]_[mRNA]_locus=scaffold28059_1:482:892:+	Anaerotruncus colihominis
2674933	GL0026064_V1_[Complete]_[mRNA]_locus=scaffold28563_1:80:3052:-	cellular organisms
2676125	GL0080601_V1_[Complete]_[mRNA]_locus=scaffold32951_1:301:1614:+	Bacteria
2677012	GL0048993_V1_[Lack_5'-end]_[mRNA]_locus=scaffold35838_3:605:1579:-	Roseburia inulinivorans
2677748	GL0103611_V1_[Complete]_[mRNA]_locus=scaffold38797_9:1254:2600:-	Roseburia inulinivorans
2678301	GL0100110_V1_[Complete]_[mRNA]_locus=scaffold41536_1:1430:2041:-	Clostridium asparagiforme
2680539	GL0009120_V1_[Complete]_[mRNA]_locus=scaffold50303_3:697:2244:-	Roseburia inulinivorans
2680698	GL0038194_V1_[Complete]_[mRNA]_locus=scaffold51118_3:33:1694:+	cellular organisms
2685272	GL0109130_V1_[Complete]_[mRNA]_locus=scaffold70390_1:29:826:-	Clostridiales
2685762	GL0103421_V1_[Lack_both_end]_[mRNA]_locus=scaffold71698_2:1:690:-	Roseburia inulinivorans
2687862	GL0078680_V1_[Complete]_[mRNA]_locus=scaffold282_2:455:1585:-	-
2687865	GL0090947_V1_[Lack_5'-end]_[mRNA]_locus=scaffold282_3:867:1097:-	Roseburia inulinivorans

2687982	GL0138133_V1_[Complete]_[mRNA]_locus=scaffold362_8:164:1405:-	Roseburia inulinivorans
2688088	GL0167253_V1_[Complete]_[mRNA]_locus=scaffold564_10:1208:1810:+	Ruminococcus obeum
2688191	GL0154473_V1_[Lack_3'-end]_[mRNA]_locus=scaffold814_4:2:2392:-	Clostridiales
2688222	GL0071856_V1_[Lack_both_end]_[mRNA]_locus=scaffold899_6:1:954:+	Roseburia inulinivorans
2688487	GL0138616_V1_[Complete]_[mRNA]_locus=scaffold1480_2:384:782:-	-
2688489	GL0020981_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1480_4:202:1074:-	-
2688504	GL0001605_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1511_13:1:642:-	-
2688743	GL0012285_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2085_2:2275:2859:-	Clostridium cellulolyticum
2689006	GL0128451_V1_[Complete]_[mRNA]_locus=scaffold2745_3:3328:3750:+	Clostridium
2689126	GL0055356_V1_[Complete]_[mRNA]_locus=scaffold2995_9:586:1503:+	-
2689233	GL0117973_V1_[Complete]_[mRNA]_locus=scaffold3179_9:618:1655:-	-
2689259	GL0151752_V1_[Complete]_[mRNA]_locus=scaffold3242_7:966:2024:+	Clostridiales
2689369	GL0052308_V1_[Complete]_[mRNA]_locus=scaffold3577_3:892:1680:+	Clostridium
2689636	GL0056417_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4334_6:97:1059:-	-

2689942	GL0104671_V1_[Complete]_[mRNA]_locus=scaffold5226_2:1770:3035:+	Clostridium
2690352	GL0005926_V1_[Complete]_[mRNA]_locus=scaffold6331_1:362:1111:+	-
2690544	GL0090035_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6871_4:631:1113:+	-
2690889	GL0076992_V1_[Lack_both_end]_[mRNA]_locus=scaffold7737_2:2:832:-	Clostridium methylpentosum
2690913	GL0173831_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7808_2:740:1168:-	Roseburia inulinivorans
2691043	GL0060702_V1_[Complete]_[mRNA]_locus=scaffold8062_2:322:1179:-	-
2691054	GL0012293_V1_[Complete]_[mRNA]_locus=scaffold8062_15:186:1478:+	Clostridiales
2691101	GL0131332_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8162_5:1448:4168:+	Clostridiales
2691131	GL0107759_V1_[Complete]_[mRNA]_locus=scaffold8207_3:614:1597:-	-
2691519	GL0136902_V1_[Complete]_[mRNA]_locus=scaffold9063_4:78:1232:-	Clostridiales
2691529	GL0089529_V1_[Complete]_[mRNA]_locus=scaffold9087_1:183:1205:+	Roseburia inulinivorans
2691996	GL0164391_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10075_5:39:551:-	Roseburia inulinivorans
2692002	GL0099512_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10075_13:922:1737:-	-
2692100	GL0125021_V1_[Complete]_[mRNA]_locus=scaffold10317_2:955:2466:+	Clostridiales

2692232	GL0099214_V1_[Lack_both_end]_[mRNA]_locus=scaffold10740_3:1:594:-	Roseburia inulinivorans
2692682	GL0160020_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11487_8:1961:2566:-	Roseburia inulinivorans
2692702	GL0020394_V1_[Complete]_[mRNA]_locus=scaffold11567_4:2542:3825:+	Bacteria
2693130	GL0171385_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12840_2:635:1267:-	Roseburia inulinivorans
2693139	GL0130474_V1_[Complete]_[mRNA]_locus=scaffold12870_2:746:1249:-	Roseburia inulinivorans
2693197	GL0038857_V1_[Lack_both_end]_[mRNA]_locus=scaffold12967_2:3:728:+	-
2693309	GL0086033_V1_[Complete]_[mRNA]_locus=scaffold13191_15:324:1103:-	-
2693347	GL0103803_V1_[Complete]_[mRNA]_locus=scaffold13242_4:1776:2621:+	-
2693545	GL0023411_V1_[Complete]_[mRNA]_locus=scaffold13800_1:1029:2369:-	Roseburia inulinivorans
2693611	GL0086513_V1_[Complete]_[mRNA]_locus=scaffold13929_8:16:1194:+	Clostridium asparagiforme
2693616	GL0034195_V1_[Complete]_[mRNA]_locus=scaffold13929_11:883:1533:+	Clostridium asparagiforme
2693798	GL0163800_V1_[Complete]_[mRNA]_locus=scaffold14413_2:2154:3263:+	Coprococcus comes
2693935	GL0142700_V1_[Complete]_[mRNA]_locus=scaffold14813_2:933:1601:+	Clostridiales
2694022	GL0156632_V1_[Complete]_[mRNA]_locus=scaffold15061_1:1648:2391:+	Roseburia inulinivorans

2694204	GL0123872_V1_[Lack_both_end]_[mRNA]_locus=scaffold15591_4:1:1371:-	-
2694281	GL0124911_V1_[Complete]_[mRNA]_locus=scaffold15891_2:1631:2605:+	-
2694423	GL0152070_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16387_3:153:515:-	-
2694471	GL0060683_V1_[Complete]_[mRNA]_locus=scaffold16511_2:533:1279:-	Roseburia inulinivorans
2694472	GL0060684_V1_[Complete]_[mRNA]_locus=scaffold16511_2:1575:2078:+	Roseburia inulinivorans
2694567	GL0105893_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16820_2:7186:8709:+	Clostridiales
2694896	GL0102674_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17843_1:644:1552:+	-
2695283	GL0125009_V1_[Complete]_[mRNA]_locus=scaffold18842_2:1077:3047:+	Clostridiales
2695360	GL0089729_V1_[Complete]_[mRNA]_locus=scaffold19058_5:3064:3720:+	Coprococcus eutactus
2695506	GL0084179_V1_[Complete]_[mRNA]_locus=scaffold19526_8:170:658:-	Bacteroides pectinophilus
2695611	GL0022621_V1_[Complete]_[mRNA]_locus=scaffold19751_1:704:1207:-	Roseburia inulinivorans
2695625	GL0128287_V1_[Lack_3'-end]_[mRNA]_locus=scaffold19805_6:297:1301:+	Roseburia inulinivorans
2695814	GL0167247_V1_[Lack_5'-end]_[mRNA]_locus=scaffold20508_7:100:1293:-	Lachnospiraceae
2695997	GL0029023_V1_[Complete]_[mRNA]_locus=scaffold21133_4:1042:1629:-	-

2696210	GL0045636_V1_[Complete]_[mRNA]_locus=scaffold21916_8:1263:3662:+	Bacteria
2696269	GL0141542_V1_[Complete]_[mRNA]_locus=scaffold22099_2:263:1582:-	Clostridiales
2696309	GL0169411_V1_[Complete]_[mRNA]_locus=scaffold22271_14:1999:4026:+	-
2696421	GL0110391_V1_[Complete]_[mRNA]_locus=scaffold22678_1:1496:2467:+	Roseburia inulinivorans
2696493	GL0063808_V1_[Lack_5'-end]_[mRNA]_locus=scaffold22899_5:1:1011:+	-
2696495	GL0085650_V1_[Complete]_[mRNA]_locus=scaffold22899_11:1717:2331:+	Roseburia inulinivorans
2696629	GL0168057_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23534_4:1:1227:-	Eubacterium hallii
2696952	GL0118384_V1_[Complete]_[mRNA]_locus=scaffold24658_3:4302:5105:-	-
2697000	GL0019035_V1_[Complete]_[mRNA]_locus=scaffold24849_12:1089:1877:+	Roseburia inulinivorans
2697088	GL0098090_V1_[Complete]_[mRNA]_locus=scaffold25045_3:809:2017:+	-
2697452	GL0052859_V1_[Complete]_[mRNA]_locus=scaffold26211_1:2790:4781:+	Holdemania filiformis
2697651	GL0098922_V1_[Complete]_[mRNA]_locus=scaffold26957_3:256:450:+	Faecalibacterium prausnitzii
2697670	GL0084919_V1_[Complete]_[mRNA]_locus=scaffold27123_1:1529:2140:-	Roseburia inulinivorans
2697696	GL0119574_V1_[Complete]_[mRNA]_locus=scaffold27232_3:397:921:+	Roseburia inulinivorans

2697813	GL0144371_V1_[Lack_5'-end]_[mRNA]_locus=scaffold27786_1:2:796:+	-
2697814	GL0173006_V1_[Lack_5'-end]_[mRNA]_locus=scaffold27786_4:1:1215:+	Bacteria
2697969	GL0170380_V1_[Lack_5'-end]_[mRNA]_locus=scaffold28569_1:2:1186:+	Roseburia inulinivorans
2698359	GL0006144_V1_[Complete]_[mRNA]_locus=scaffold30061_2:210:1394:-	Roseburia inulinivorans
2698408	GL0164191_V1_[Complete]_[mRNA]_locus=scaffold30210_6:707:1549:-	-
2698657	GL0172979_V1_[Complete]_[mRNA]_locus=scaffold31161_2:1129:2073:+	Clostridium
2698661	GL0071177_V1_[Complete]_[mRNA]_locus=scaffold31161_4:1621:2556:+	Roseburia inulinivorans
2698699	GL0095008_V1_[Lack_3'-end]_[mRNA]_locus=scaffold31331_1:394:1197:+	Clostridium ramosum
2698792	GL0114799_V1_[Complete]_[mRNA]_locus=scaffold31579_1:983:1984:+	-
2698875	GL0107913_V1_[Complete]_[mRNA]_locus=scaffold31969_9:1222:2721:-	-
2699109	GL0064860_V1_[Complete]_[mRNA]_locus=scaffold32982_2:1283:2989:+	Roseburia inulinivorans
2699163	GL0103914_V1_[Complete]_[mRNA]_locus=scaffold33232_5:1877:2773:+	Roseburia inulinivorans
2699210	GL0035299_V1_[Lack_3'-end]_[mRNA]_locus=scaffold33449_4:3:1175:-	Roseburia inulinivorans
2699535	GL0081621_V1_[Lack_3'-end]_[mRNA]_locus=scaffold34883_4:1142:1864:+	-

2699564	GL0029117_V1_[Complete]_[mRNA]_locus=scaffold35055_5:6449:7645:-	Bacteria
2699569	GL0114223_V1_[Complete]_[mRNA]_locus=scaffold35120_2:503:1435:+	-
2699570	GL0114224_V1_[Complete]_[mRNA]_locus=scaffold35120_2:1428:2657:+	Roseburia inulinivorans
2699571	GL0114225_V1_[Complete]_[mRNA]_locus=scaffold35120_2:2676:3338:+	Roseburia inulinivorans
2699781	GL0113155_V1_[Complete]_[mRNA]_locus=scaffold36127_4:177:1649:+	Roseburia inulinivorans
2699962	GL0145146_V1_[Lack_5'-end]_[mRNA]_locus=scaffold36818_7:2:718:+	Clostridium scindens
2700016	GL0072259_V1_[Complete]_[mRNA]_locus=scaffold36990_4:2686:3696:+	-
2700391	GL0019471_V1_[Complete]_[mRNA]_locus=scaffold37772_1:52:462:+	Faecalibacterium prausnitzii
2700393	GL0104283_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37790_1:1:1197:+	-
2700503	GL0170738_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38259_3:619:1317:-	Roseburia inulinivorans
2700781	GL0035981_V1_[Complete]_[mRNA]_locus=scaffold39495_2:449:1489:+	Roseburia inulinivorans
2700843	GL0141443_V1_[Complete]_[mRNA]_locus=scaffold39810_2:1513:2151:-	Roseburia inulinivorans
2700879	GL0118935_V1_[Complete]_[mRNA]_locus=scaffold39974_1:801:1715:+	Roseburia inulinivorans
2700892	GL0060148_V1_[Lack_both_end]_[mRNA]_locus=scaffold40057_1:1:930:+	Clostridiales

2700982	GL0057244_V1_[Complete]_[mRNA]_locus=scaffold40566_1:721:1293:-	Roseburia inulinivorans
2701091	GL0018511_V1_[Complete]_[mRNA]_locus=scaffold41112_1:143:622:-	Coprococcus eutactus
2701331	GL0147854_V1_[Lack_5'-end]_[mRNA]_locus=scaffold41964_11:3:1403:+	Roseburia inulinivorans
2701427	GL0097609_V1_[Complete]_[mRNA]_locus=scaffold42660_3:242:895:-	Roseburia inulinivorans
2701750	GL0092535_V1_[Lack_3'-end]_[mRNA]_locus=scaffold44238_3:1:663:-	Clostridium
2701822	GL0157229_V1_[Complete]_[mRNA]_locus=scaffold44559_3:339:1310:-	Roseburia inulinivorans
2701838	GL0144382_V1_[Complete]_[mRNA]_locus=scaffold44706_4:81:2234:-	Bacteria
2701963	GL0094362_V1_[Complete]_[mRNA]_locus=scaffold45498_2:929:1753:+	Bacteroides pectinophilus
2702101	GL0171245_V1_[Complete]_[mRNA]_locus=scaffold46118_1:120:1517:-	Firmicutes
2702102	GL0171246_V1_[Complete]_[mRNA]_locus=scaffold46118_1:1565:2509:-	-
2702264	GL0029608_V1_[Complete]_[mRNA]_locus=scaffold46947_3:1274:1810:+	Roseburia inulinivorans
2702400	GL0075990_V1_[Complete]_[mRNA]_locus=scaffold47564_1:1947:3311:+	Clostridium leptum
2702438	GL0142520_V1_[Complete]_[mRNA]_locus=scaffold47739_2:2066:2923:-	Clostridium bolteae
2702441	GL0036460_V1_[Lack_5'-end]_[mRNA]_locus=scaffold47739_6:541:1842:-	Coprococcus eutactus

2702655	GL0128956_V1_[Lack_3'-end]_[mRNA]_locus=scaffold48951_1:3:500:-	Faecalibacterium prausnitzii
2702712	GL0141836_V1_[Complete]_[mRNA]_locus=scaffold49213_1:350:1273:-	Clostridiales
2702716	GL0014422_V1_[Complete]_[mRNA]_locus=scaffold49213_2:1103:1933:-	Eubacterium ventriosum
2702717	GL0014424_V1_[Complete]_[mRNA]_locus=scaffold49213_2:2824:4086:-	Clostridium scindens
2702741	GL0017799_V1_[Complete]_[mRNA]_locus=scaffold49361_4:174:743:-	Roseburia inulinivorans
2702965	GL0057929_V1_[Complete]_[mRNA]_locus=scaffold50934_4:108:1163:-	Roseburia inulinivorans
2703023	GL0163491_V1_[Lack_5'-end]_[mRNA]_locus=scaffold51227_5:3:806:+	Dorea longicatena
2703054	GL0148454_V1_[Complete]_[mRNA]_locus=scaffold51320_1:46:1020:-	Roseburia inulinivorans
2703055	GL0148455_V1_[Complete]_[mRNA]_locus=scaffold51320_1:1017:1535:-	Roseburia inulinivorans
2703470	GL0135607_V1_[Lack_both_end]_[mRNA]_locus=scaffold53417_2:3:530:+	-
2703607	GL0121537_V1_[Complete]_[mRNA]_locus=scaffold54122_4:619:3453:+	Bacteria
2703642	GL0120282_V1_[Complete]_[mRNA]_locus=scaffold54337_1:896:1711:+	Clostridiales
2703992	GL0164666_V1_[Lack_5'-end]_[mRNA]_locus=scaffold56087_1:238:1068:-	Roseburia inulinivorans
2704721	GL0050501_V1_[Complete]_[mRNA]_locus=scaffold59977_11:369:1775:-	-

2704811	GL0131114_V1_[Complete]_[mRNA]_locus=scaffold60375_1:3265:4404:-	Firmicutes
2704860	GL0048943_V1_[Complete]_[mRNA]_locus=scaffold60535_1:224:775:+	Roseburia inulinivorans
2704870	GL0116240_V1_[Complete]_[mRNA]_locus=scaffold60646_2:235:996:-	Roseburia inulinivorans
2705048	GL0163030_V1_[Complete]_[mRNA]_locus=scaffold61820_3:297:683:-	-
2705224	GL0126916_V1_[Complete]_[mRNA]_locus=scaffold62944_9:92:745:-	Roseburia inulinivorans
2705385	GL0128516_V1_[Complete]_[mRNA]_locus=scaffold64017_2:4181:5584:-	Roseburia inulinivorans
2705387	GL0128519_V1_[Lack_5'-end]_[mRNA]_locus=scaffold64017_2:6600:7589:-	-
2705434	GL0013768_V1_[Complete]_[mRNA]_locus=scaffold64244_1:122:1735:-	Clostridiales
2705502	GL0116187_V1_[Complete]_[mRNA]_locus=scaffold64620_1:188:1249:+	Bacteria
2705503	GL0116188_V1_[Complete]_[mRNA]_locus=scaffold64620_1:1328:2104:+	Firmicutes
2705678	GL0035594_V1_[Complete]_[mRNA]_locus=scaffold65602_1:496:1620:+	Roseburia inulinivorans
2706072	GL0147703_V1_[Complete]_[mRNA]_locus=scaffold68029_3:136:1020:+	Bacteroides pectinophilus
2706228	GL0136072_V1_[Complete]_[mRNA]_locus=scaffold69137_1:298:1530:-	Clostridiales
2706333	GL0128493_V1_[Lack_both_end]_[mRNA]_locus=scaffold69643_6:1:942:+	Lachnospiraceae

2706541	GL0072084_V1_[Complete]_[mRNA]_locus=scaffold70826_1:504:2825:+	Coprococcus eutactus
2706610	GL0059218_V1_[Complete]_[mRNA]_locus=scaffold71419_1:13:846:-	Roseburia inulinivorans
2706671	GL0103112_V1_[Complete]_[mRNA]_locus=scaffold71804_1:5167:6168:+	Roseburia inulinivorans
2706969	GL0041201_V1_[Complete]_[mRNA]_locus=scaffold73542_2:809:1960:-	Roseburia inulinivorans
2707122	GL0135849_V1_[Lack_5'-end]_[mRNA]_locus=scaffold74371_7:2172:5627:-	-
2707128	GL0134507_V1_[Complete]_[mRNA]_locus=scaffold74371_12:4425:4961:-	Clostridium scindens
2707199	GL0163916_V1_[Complete]_[mRNA]_locus=scaffold74834_1:2252:3178:+	Roseburia inulinivorans
2707505	GL0105475_V1_[Lack_5'-end]_[mRNA]_locus=scaffold76218_2:2:832:+	Clostridiales
2707576	GL0023651_V1_[Lack_3'-end]_[mRNA]_locus=scaffold76631_2:1:696:-	Clostridium thermocellum
2707965	GL0099388_V1_[Lack_5'-end]_[mRNA]_locus=scaffold78912_4:1034:2032:-	Clostridiales
2708451	GL0143564_V1_[Lack_5'-end]_[mRNA]_locus=scaffold82575_3:2:961:+	Bacteroides pectinophilus
2708517	GL0156692_V1_[Complete]_[mRNA]_locus=scaffold83124_4:48:632:+	Roseburia inulinivorans
2708592	GL0050446_V1_[Complete]_[mRNA]_locus=scaffold83585_4:274:891:-	Roseburia inulinivorans
2708616	GL0029140_V1_[Complete]_[mRNA]_locus=scaffold83665_3:1494:2654:+	Roseburia inulinivorans

2708698	GL0006497_V1_[Complete]_[mRNA]_locus=scaffold84201_1:3402:4472:-	-
2708803	GL0096060_V1_[Complete]_[mRNA]_locus=scaffold84825_2:247:1488:+	Roseburia inulinivorans
2708816	GL0145026_V1_[Complete]_[mRNA]_locus=scaffold84895_3:371:1663:-	Bacteroides pectinophilus
2708848	GL0080377_V1_[Complete]_[mRNA]_locus=scaffold85098_1:176:2887:-	Clostridia
2709683	GL0107672_V1_[Lack_both_end]_[mRNA]_locus=scaffold89613_1:3:782:-	Roseburia inulinivorans
2710340	GL0018556_V1_[Lack_5'-end]_[mRNA]_locus=scaffold93111_1:189:1205:-	-
2710358	GL0009466_V1_[Complete]_[mRNA]_locus=scaffold93141_1:803:1606:-	Roseburia inulinivorans
2710359	GL0175003_V1_[Complete]_[mRNA]_locus=scaffold93141_2:75:2015:-	Roseburia inulinivorans
2711115	GL0168088_V1_[Complete]_[mRNA]_locus=scaffold96990_2:593:1207:-	Coprococcus comes
2711311	GL0177228_V1_[Complete]_[mRNA]_locus=scaffold97709_3:79:945:+	-
2711312	GL0177229_V1_[Lack_5'-end]_[mRNA]_locus=scaffold97709_3:1112:1834:-	Roseburia inulinivorans
2711659	GL0099279_V1_[Complete]_[mRNA]_locus=scaffold99302_5:568:1146:-	Roseburia inulinivorans
2711725	GL0028811_V1_[Complete]_[mRNA]_locus=scaffold99484_3:17:1213:+	Treponema denticola
2711726	GL0028812_V1_[Complete]_[mRNA]_locus=scaffold99484_3:1338:1835:+	Clostridium asparagiforme

2712015	GL0098675_V1_[Complete]_[mRNA]_locus=scaffold100800_1:301:1407:-	Roseburia inulinivorans
2712155	GL0041364_V1_[Complete]_[mRNA]_locus=scaffold101314_1:737:2047:+	Clostridiales
2712344	GL0012241_V1_[Lack_3'-end]_[mRNA]_locus=scaffold101910_1:3:140:-	Clostridiales
2712642	GL0152047_V1_[Lack_3'-end]_[mRNA]_locus=scaffold103108_2:1:231:-	-
2712782	GL0001421_V1_[Lack_5'-end]_[mRNA]_locus=scaffold103574_2:3:746:+	Clostridiales
2713115	GL0157000_V1_[Complete]_[mRNA]_locus=scaffold104420_3:102:884:-	Roseburia inulinivorans
2713539	GL0023437_V1_[Complete]_[mRNA]_locus=scaffold105498_1:132:1619:-	Clostridiales
2713776	GL0136019_V1_[Lack_3'-end]_[mRNA]_locus=scaffold106086_1:2:733:-	Roseburia inulinivorans
2713847	GL0042871_V1_[Complete]_[mRNA]_locus=scaffold106265_1:3715:3996:-	Roseburia inulinivorans
2713962	GL0127799_V1_[Lack_3'-end]_[mRNA]_locus=scaffold106546_2:349:951:+	-
2714799	GL0080881_V1_[Complete]_[mRNA]_locus=scaffold108010_1:26:1468:-	Roseburia inulinivorans
2714981	GL0082805_V1_[Complete]_[mRNA]_locus=scaffold108276_1:36:1238:-	Roseburia inulinivorans
2715046	GL0106577_V1_[Lack_5'-end]_[mRNA]_locus=scaffold108338_3:3:887:+	-
2715047	GL0106578_V1_[Complete]_[mRNA]_locus=scaffold108338_3:1006:1890:+	-

2715194	GL0138331_V1_[Lack_both_end]_[mRNA]_locus=scaffold108532_2:2:1111:+	Clostridium phytofermentans
2717512	GL0054465_V1_[Complete]_[mRNA]_locus=C4263366_1:65:535:+	Eubacterium biforme
2717635	GL0083456_V1_[Complete]_[mRNA]_locus=C4270598_1:156:839:+	Roseburia inulinivorans
2718451	GL0062408_V1_[Complete]_[mRNA]_locus=C4310926_1:32:1270:-	Roseburia inulinivorans
2719706	GL0044462_V1_[Complete]_[mRNA]_locus=scaffold10_1:665:1762:-	Clostridiales
2719707	GL0044463_V1_[Complete]_[mRNA]_locus=scaffold10_1:1998:3530:-	Clostridiales
2719713	GL0034555_V1_[Complete]_[mRNA]_locus=scaffold10_2:15158:16273:-	Roseburia inulinivorans
2719714	GL0034556_V1_[Complete]_[mRNA]_locus=scaffold10_2:16276:17556:-	Roseburia inulinivorans
2719715	GL0034561_V1_[Complete]_[mRNA]_locus=scaffold10_2:21555:22769:-	Roseburia inulinivorans
2719719	GL0069054_V1_[Complete]_[mRNA]_locus=scaffold10_3:6741:7391:-	Roseburia inulinivorans
2719728	GL0029771_V1_[Complete]_[mRNA]_locus=scaffold10_11:3288:4169:-	Roseburia inulinivorans
2719730	GL0037027_V1_[Complete]_[mRNA]_locus=scaffold10_12:2653:4524:-	Clostridiales
2719731	GL0065580_V1_[Complete]_[mRNA]_locus=scaffold10_13:1203:2807:+	Bacteria
2719744	GL0036435_V1_[Complete]_[mRNA]_locus=scaffold49_2:1716:3038:-	Roseburia inulinivorans
2719745	GL0036437_V1_[Complete]_[mRNA]_locus=scaffold49_2:4856:6037:+	Firmicutes

2720152	GL0010971_V1_[Complete]_[mRNA]_locus=scaffold610_1:7569:9005:+	Clostridiales
2720156	GL0052681_V1_[Complete]_[mRNA]_locus=scaffold610_4:809:1663:+	Roseburia inulinivorans
2720158	GL0052683_V1_[Complete]_[mRNA]_locus=scaffold610_4:2743:3519:+	Roseburia inulinivorans
2720159	GL0052686_V1_[Complete]_[mRNA]_locus=scaffold610_4:6403:7284:+	Roseburia inulinivorans
2720160	GL0052689_V1_[Complete]_[mRNA]_locus=scaffold610_4:8630:9226:+	Roseburia inulinivorans
2720164	GL0052699_V1_[Complete]_[mRNA]_locus=scaffold610_4:17189:19387:+	Roseburia inulinivorans
2720166	GL0052702_V1_[Complete]_[mRNA]_locus=scaffold610_4:22278:22730:+	Roseburia inulinivorans
2720178	GL0050869_V1_[Complete]_[mRNA]_locus=scaffold659_1:6196:6633:-	Roseburia inulinivorans
2720179	GL0050871_V1_[Complete]_[mRNA]_locus=scaffold659_1:7100:8416:-	Roseburia inulinivorans
2720181	GL0050876_V1_[Complete]_[mRNA]_locus=scaffold659_1:12057:13040:-	Roseburia inulinivorans
2720182	GL0050877_V1_[Complete]_[mRNA]_locus=scaffold659_1:13138:16002:-	Roseburia inulinivorans
2720184	GL0050881_V1_[Complete]_[mRNA]_locus=scaffold659_1:19277:20461:-	Roseburia inulinivorans
2720190	GL0032194_V1_[Complete]_[mRNA]_locus=scaffold661_1:4628:5986:-	Roseburia inulinivorans
2720191	GL0032196_V1_[Complete]_[mRNA]_locus=scaffold661_1:6686:7897:-	Bacteria

2720194	GL0032200_V1_[Complete]_[mRNA]_locus=scaffold661_1:13365:13598:-	Roseburia inulinivorans
2720196	GL0009055_V1_[Complete]_[mRNA]_locus=scaffold661_3:353:1642:+	Roseburia inulinivorans
2720197	GL0068398_V1_[Complete]_[mRNA]_locus=scaffold661_4:643:1821:-	Clostridiales
2720198	GL0068399_V1_[Complete]_[mRNA]_locus=scaffold661_4:1872:2621:-	Roseburia inulinivorans
2720199	GL0068400_V1_[Complete]_[mRNA]_locus=scaffold661_4:2833:4197:-	Clostridiales
2720200	GL0068403_V1_[Complete]_[mRNA]_locus=scaffold661_4:5453:7726:-	Clostridiales
2720202	GL0068406_V1_[Complete]_[mRNA]_locus=scaffold661_4:11186:12976:-	Firmicutes
2720203	GL0068409_V1_[Complete]_[mRNA]_locus=scaffold661_4:14267:16822:-	Roseburia inulinivorans
2720204	GL0068410_V1_[Complete]_[mRNA]_locus=scaffold661_4:16854:18650:-	Roseburia inulinivorans
2720264	GL0027043_V1_[Lack_3'-end]_[mRNA]_locus=scaffold755_3:556:657:+	-
2720286	GL0018122_V1_[Complete]_[mRNA]_locus=scaffold769_3:9041:11458:+	Clostridiales
2720287	GL0018123_V1_[Complete]_[mRNA]_locus=scaffold769_3:11537:12574:+	Roseburia inulinivorans
2720289	GL0052545_V1_[Complete]_[mRNA]_locus=scaffold769_5:5138:6247:-	Roseburia inulinivorans
2720290	GL0047059_V1_[Complete]_[mRNA]_locus=scaffold769_6:305:2410:+	Clostridiales

2720291	GL0047060_V1_[Complete]_[mRNA]_locus=scaffold769_6:2429:3742:+	Roseburia inulinivorans
2720292	GL0047064_V1_[Complete]_[mRNA]_locus=scaffold769_6:5209:6267:+	Roseburia inulinivorans
2720296	GL0003499_V1_[Complete]_[mRNA]_locus=scaffold769_7:6904:7896:+	Roseburia inulinivorans
2720300	GL0003505_V1_[Complete]_[mRNA]_locus=scaffold769_7:14924:16594:+	Clostridiales
2720303	GL0019736_V1_[Complete]_[mRNA]_locus=scaffold769_9:60:2333:+	Clostridiales
2720305	GL0019740_V1_[Complete]_[mRNA]_locus=scaffold769_9:4477:5478:+	-
2720306	GL0019742_V1_[Complete]_[mRNA]_locus=scaffold769_9:6660:7157:+	Roseburia inulinivorans
2720309	GL0019747_V1_[Complete]_[mRNA]_locus=scaffold769_9:12403:15045:+	Clostridiales
2720310	GL0019748_V1_[Complete]_[mRNA]_locus=scaffold769_9:15085:17028:+	Bacteria
2720311	GL0019749_V1_[Complete]_[mRNA]_locus=scaffold769_9:17034:17987:+	Roseburia inulinivorans
2720313	GL0019752_V1_[Complete]_[mRNA]_locus=scaffold769_9:20116:21213:+	Roseburia inulinivorans
2720315	GL0019756_V1_[Complete]_[mRNA]_locus=scaffold769_9:25501:26307:+	Roseburia inulinivorans
2720316	GL0019763_V1_[Complete]_[mRNA]_locus=scaffold769_9:30015:31367:+	Roseburia inulinivorans
2720317	GL0019767_V1_[Complete]_[mRNA]_locus=scaffold769_9:33444:34544:+	Roseburia inulinivorans

2720322	GL0047980_V1_[Complete]_[mRNA]_locus=scaffold770_3:90:2921:+	Clostridiales
2720419	GL0029922_V1_[Lack_5'-end]_[mRNA]_locus=scaffold908_2:2094:2867:-	Roseburia inulinivorans
2720420	GL0051349_V1_[Complete]_[mRNA]_locus=scaffold908_4:3154:3897:-	Roseburia inulinivorans
2720421	GL0051350_V1_[Complete]_[mRNA]_locus=scaffold908_4:4620:5486:-	Roseburia inulinivorans
2720424	GL0051354_V1_[Complete]_[mRNA]_locus=scaffold908_4:8426:11674:-	Clostridiales
2720501	GL0014635_V1_[Complete]_[mRNA]_locus=scaffold963_2:5076:7073:-	Clostridiales
2720513	GL0016668_V1_[Complete]_[mRNA]_locus=scaffold989_2:68:568:+	Roseburia inulinivorans
2720521	GL0016677_V1_[Complete]_[mRNA]_locus=scaffold989_2:5837:7399:+	Roseburia inulinivorans
2720541	GL0054041_V1_[Complete]_[mRNA]_locus=scaffold1038_1:1586:3625:-	Clostridiales
2720548	GL0008121_V1_[Complete]_[mRNA]_locus=scaffold1038_3:980:1771:-	Roseburia inulinivorans
2720550	GL0023329_V1_[Complete]_[mRNA]_locus=scaffold1038_5:957:1817:-	Roseburia inulinivorans
2720551	GL0023331_V1_[Complete]_[mRNA]_locus=scaffold1038_5:2938:4305:-	Clostridiales
2720553	GL0037561_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1038_6:2:1564:+	Bacteria
2720617	GL0049547_V1_[Complete]_[mRNA]_locus=scaffold1154_1:4746:5774:-	Roseburia inulinivorans

2720624	GL0008914_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1166_7:12093:13172:+	Roseburia inulinivorans
2720674	GL0028262_V1_[Complete]_[mRNA]_locus=scaffold1182_1:329:1339:-	Roseburia inulinivorans
2720676	GL0028266_V1_[Complete]_[mRNA]_locus=scaffold1182_1:3467:3913:+	Roseburia inulinivorans
2720677	GL0028268_V1_[Complete]_[mRNA]_locus=scaffold1182_1:4938:6269:+	Clostridiales
2720678	GL0028270_V1_[Complete]_[mRNA]_locus=scaffold1182_1:6636:8102:+	Clostridiales
2720679	GL0028271_V1_[Complete]_[mRNA]_locus=scaffold1182_1:8119:9549:+	Bacteria
2720682	GL0053294_V1_[Complete]_[mRNA]_locus=scaffold1182_3:2333:3004:+	Roseburia inulinivorans
2720683	GL0053298_V1_[Complete]_[mRNA]_locus=scaffold1182_3:6969:8513:+	Roseburia inulinivorans
2720756	GL0040624_V1_[Complete]_[mRNA]_locus=scaffold1235_4:2002:2163:+	-
2720791	GL0014980_V1_[Complete]_[mRNA]_locus=scaffold1316_2:2056:2949:-	-
2720792	GL0014982_V1_[Complete]_[mRNA]_locus=scaffold1316_2:4827:5807:-	Roseburia inulinivorans
2720793	GL0014984_V1_[Complete]_[mRNA]_locus=scaffold1316_2:6908:8521:-	Bacteria
2720795	GL0033878_V1_[Complete]_[mRNA]_locus=scaffold1316_4:1199:2527:-	Roseburia inulinivorans

2720848	GL0065015_V1_[Complete]_[mRNA]_locus=scaffold1383_1:3538:5292:-	Clostridiales
2720851	GL0065021_V1_[Complete]_[mRNA]_locus=scaffold1383_1:11790:13028:-	Clostridiales
2720852	GL0065023_V1_[Complete]_[mRNA]_locus=scaffold1383_1:15681:17057:-	Bacteria
2720863	GL0013745_V1_[Complete]_[mRNA]_locus=scaffold1397_1:424:1656:-	Clostridiales
2720910	GL0054626_V1_[Complete]_[mRNA]_locus=scaffold1565_3:4946:6697:+	Roseburia inulinivorans
2721052	GL0019360_V1_[Complete]_[mRNA]_locus=scaffold1813_3:4119:6722:+	Roseburia inulinivorans
2721053	GL0019361_V1_[Complete]_[mRNA]_locus=scaffold1813_3:6722:7450:+	Roseburia inulinivorans
2721178	GL0020319_V1_[Complete]_[mRNA]_locus=scaffold2232_2:3438:4532:-	Roseburia inulinivorans
2721179	GL0020320_V1_[Complete]_[mRNA]_locus=scaffold2232_2:4618:8145:+	Roseburia inulinivorans
2721181	GL0009528_V1_[Complete]_[mRNA]_locus=scaffold2232_3:146:2152:+	Bacteria
2721182	GL0009529_V1_[Complete]_[mRNA]_locus=scaffold2232_3:2522:3931:+	Clostridiales
2721183	GL0009530_V1_[Complete]_[mRNA]_locus=scaffold2232_3:3942:5777:+	Bacteria
2721185	GL0009535_V1_[Complete]_[mRNA]_locus=scaffold2232_3:9930:10838:-	Roseburia inulinivorans
2721189	GL0009544_V1_[Complete]_[mRNA]_locus=scaffold2232_3:18818:20428:+	Roseburia inulinivorans

2721197	GL0008360_V1_[Complete]_[mRNA]_locus=scaffold2232_4:6704:7483:+	Roseburia inulinivorans
2721200	GL0008366_V1_[Complete]_[mRNA]_locus=scaffold2232_4:13581:14654:+	Roseburia inulinivorans
2721201	GL0008367_V1_[Complete]_[mRNA]_locus=scaffold2232_4:14656:16755:+	Bacteria
2721202	GL0008369_V1_[Complete]_[mRNA]_locus=scaffold2232_4:17302:17931:+	Roseburia inulinivorans
2721204	GL0008372_V1_[Complete]_[mRNA]_locus=scaffold2232_4:18750:19520:+	Roseburia inulinivorans
2721297	GL0008144_V1_[Complete]_[mRNA]_locus=scaffold2426_1:4285:5214:+	Roseburia inulinivorans
2721300	GL0005752_V1_[Complete]_[mRNA]_locus=scaffold2426_8:930:2951:-	Roseburia inulinivorans
2721306	GL0005763_V1_[Complete]_[mRNA]_locus=scaffold2426_8:10658:11236:-	Roseburia inulinivorans
2721326	GL0022205_V1_[Complete]_[mRNA]_locus=scaffold2485_1:7072:7680:-	Roseburia inulinivorans
2721327	GL0022206_V1_[Complete]_[mRNA]_locus=scaffold2485_1:8031:9608:+	Roseburia inulinivorans
2721328	GL0022207_V1_[Complete]_[mRNA]_locus=scaffold2485_1:9619:10608:+	Roseburia inulinivorans
2721329	GL0022209_V1_[Complete]_[mRNA]_locus=scaffold2485_1:11159:12334:+	Clostridiales
2721377	GL0054919_V1_[Complete]_[mRNA]_locus=scaffold2695_1:229:1518:+	Bacteria
2721379	GL0054922_V1_[Complete]_[mRNA]_locus=scaffold2695_1:2830:4053:-	Roseburia inulinivorans

2721380	GL0054923_V1_[Complete]_[mRNA]_locus=scaffold2695_1:4481:5965:+	Clostridiales
2721384	GL0052184_V1_[Complete]_[mRNA]_locus=scaffold2695_3:5698:7500:+	Clostridiales
2721385	GL0052185_V1_[Complete]_[mRNA]_locus=scaffold2695_3:7538:8818:+	Roseburia inulinivorans
2721399	GL0066030_V1_[Complete]_[mRNA]_locus=scaffold2753_6:2999:3895:-	Roseburia inulinivorans
2721400	GL0066031_V1_[Complete]_[mRNA]_locus=scaffold2753_6:4016:5200:+	Roseburia inulinivorans
2721401	GL0066032_V1_[Complete]_[mRNA]_locus=scaffold2753_6:5310:5822:-	Roseburia inulinivorans
2721499	GL0017944_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2965_3:1:342:-	Roseburia inulinivorans
2721578	GL0027548_V1_[Complete]_[mRNA]_locus=scaffold3133_1:551:1828:+	Roseburia inulinivorans
2721580	GL0062644_V1_[Complete]_[mRNA]_locus=scaffold3133_2:1713:3545:+	Clostridia
2721587	GL0030268_V1_[Complete]_[mRNA]_locus=scaffold3163_2:1446:2324:+	Roseburia inulinivorans
2721591	GL0051491_V1_[Complete]_[mRNA]_locus=scaffold3163_4:1766:3757:+	Clostridiales
2721596	GL0005354_V1_[Complete]_[mRNA]_locus=scaffold3163_5:741:2036:+	Roseburia inulinivorans
2721597	GL0005357_V1_[Complete]_[mRNA]_locus=scaffold3163_5:3451:5319:+	Clostridiales
2721682	GL0039406_V1_[Complete]_[mRNA]_locus=scaffold3307_2:15188:16072:-	Roseburia inulinivorans

2721685	GL0039411_V1_[Complete]_[mRNA]_locus=scaffold3307_2:22905:23672:+	Roseburia inulinivorans
2721687	GL0039416_V1_[Complete]_[mRNA]_locus=scaffold3307_2:26249:28276:+	Clostridiales
2721704	GL0005066_V1_[Complete]_[mRNA]_locus=scaffold3368_5:3227:4084:+	Roseburia inulinivorans
2721728	GL0033512_V1_[Complete]_[mRNA]_locus=scaffold3436_2:1265:1798:-	Roseburia inulinivorans
2721730	GL0033514_V1_[Complete]_[mRNA]_locus=scaffold3436_2:3154:4338:-	Roseburia inulinivorans
2721743	GL0040648_V1_[Complete]_[mRNA]_locus=scaffold3452_1:1467:2600:+	Roseburia inulinivorans
2721746	GL0040652_V1_[Complete]_[mRNA]_locus=scaffold3452_1:5672:6343:+	-
2721747	GL0040654_V1_[Complete]_[mRNA]_locus=scaffold3452_1:7470:7982:+	Roseburia inulinivorans
2721748	GL0040656_V1_[Complete]_[mRNA]_locus=scaffold3452_1:9170:10033:+	Roseburia inulinivorans
2721795	GL0013571_V1_[Complete]_[mRNA]_locus=scaffold3536_1:1641:2684:-	Roseburia inulinivorans
2721796	GL0013575_V1_[Complete]_[mRNA]_locus=scaffold3536_1:5694:9095:-	Clostridiales
2721797	GL0013579_V1_[Complete]_[mRNA]_locus=scaffold3536_1:12982:14016:-	Roseburia inulinivorans
2721801	GL0038755_V1_[Complete]_[mRNA]_locus=scaffold3536_2:10505:11317:-	Roseburia inulinivorans
2721836	GL0015173_V1_[Complete]_[mRNA]_locus=scaffold3636_1:93:827:+	Roseburia inulinivorans

2721837	GL0056829_V1_[Complete]_[mRNA]_locus=scaffold3636_2:2372:4600:-	Bacteria
2721848	GL0044912_V1_[Complete]_[mRNA]_locus=scaffold3647_2:350:661:-	Roseburia inulinivorans
2721857	GL0064022_V1_[Complete]_[mRNA]_locus=scaffold3672_2:1921:3837:+	Clostridiales
2721861	GL0013377_V1_[Complete]_[mRNA]_locus=scaffold3672_4:989:5587:+	Bacteria
2721862	GL0013378_V1_[Complete]_[mRNA]_locus=scaffold3672_4:5628:7121:+	Bacteria
2721913	GL0031971_V1_[Complete]_[mRNA]_locus=scaffold3802_1:12274:13953:-	Bacteria
2722085	GL0021234_V1_[Complete]_[mRNA]_locus=scaffold4293_2:2864:3367:+	Roseburia inulinivorans
2722086	GL0021235_V1_[Complete]_[mRNA]_locus=scaffold4293_2:3875:5137:-	Roseburia inulinivorans
2722088	GL0053424_V1_[Complete]_[mRNA]_locus=scaffold4293_4:1888:4191:-	Roseburia inulinivorans
2722089	GL0053425_V1_[Complete]_[mRNA]_locus=scaffold4293_4:4309:6027:-	Bacteria
2722093	GL0053433_V1_[Complete]_[mRNA]_locus=scaffold4293_4:13105:14010:-	Roseburia inulinivorans
2722094	GL0053435_V1_[Complete]_[mRNA]_locus=scaffold4293_4:14712:16433:-	Clostridiales
2722095	GL0053436_V1_[Complete]_[mRNA]_locus=scaffold4293_4:16527:17480:-	Roseburia inulinivorans
2722096	GL0053437_V1_[Complete]_[mRNA]_locus=scaffold4293_4:17615:18106:-	Roseburia inulinivorans

2722192	GL0021814_V1_[Complete]_[mRNA]_locus=scaffold4602_4:3405:5024:+	Roseburia inulinivorans
2722197	GL0029177_V1_[Complete]_[mRNA]_locus=scaffold4602_5:5957:7189:+	Clostridiales
2722314	GL0053526_V1_[Complete]_[mRNA]_locus=scaffold4843_1:900:2594:+	Firmicutes
2722315	GL0053527_V1_[Complete]_[mRNA]_locus=scaffold4843_1:2621:3967:+	Roseburia inulinivorans
2722317	GL0055822_V1_[Complete]_[mRNA]_locus=scaffold4843_2:1784:2089:+	Roseburia inulinivorans
2722422	GL0000455_V1_[Complete]_[mRNA]_locus=scaffold5130_1:674:1666:-	Roseburia inulinivorans
2722511	GL0016819_V1_[Complete]_[mRNA]_locus=scaffold5250_1:24:1802:-	Roseburia inulinivorans
2722590	GL0072075_V1_[Complete]_[mRNA]_locus=scaffold5371_1:3310:4191:-	Roseburia inulinivorans
2722593	GL0066905_V1_[Complete]_[mRNA]_locus=scaffold5371_2:10944:12623:-	Clostridiales
2722597	GL0000252_V1_[Complete]_[mRNA]_locus=scaffold5380_2:3429:5834:+	Clostridiales
2722598	GL0064070_V1_[Complete]_[mRNA]_locus=scaffold5380_3:650:2062:+	Roseburia inulinivorans
2722614	GL0010574_V1_[Complete]_[mRNA]_locus=scaffold5413_2:1636:2430:+	Roseburia inulinivorans
2722633	GL0040191_V1_[Complete]_[mRNA]_locus=scaffold5502_2:265:3105:-	Bacteria
2722703	GL0041286_V1_[Complete]_[mRNA]_locus=scaffold5684_1:2628:4400:+	Bacteria

2722704	GL0041287_V1_[Complete]_[mRNA]_locus=scaffold5684_1:4485:6170:+	Bacteria
2722707	GL0041294_V1_[Complete]_[mRNA]_locus=scaffold5684_1:15689:16543:+	Roseburia inulinivorans
2722708	GL0037857_V1_[Complete]_[mRNA]_locus=scaffold5684_2:1170:1799:+	Roseburia inulinivorans
2722947	GL0055410_V1_[Complete]_[mRNA]_locus=scaffold6412_3:8357:10153:+	Firmicutes
2722948	GL0027941_V1_[Complete]_[mRNA]_locus=scaffold6412_4:123:3980:+	Clostridiales
2722949	GL0027942_V1_[Complete]_[mRNA]_locus=scaffold6412_4:4079:5797:+	Clostridiales
2722952	GL0027948_V1_[Complete]_[mRNA]_locus=scaffold6412_4:10886:12442:+	Clostridiales
2723037	GL0003282_V1_[Complete]_[mRNA]_locus=scaffold6536_3:4087:5460:-	Clostridiales
2723039	GL0057430_V1_[Lack_5'-end]_[mRNA]_locus=scaffold6536_4:2:580:+	Roseburia inulinivorans
2723040	GL0057431_V1_[Complete]_[mRNA]_locus=scaffold6536_4:730:3345:+	Clostridiales
2723042	GL0069206_V1_[Complete]_[mRNA]_locus=scaffold6536_6:158:2146:+	Roseburia inulinivorans
2723043	GL0069210_V1_[Complete]_[mRNA]_locus=scaffold6536_6:4068:5552:+	Bacteria
2723083	GL0028392_V1_[Complete]_[mRNA]_locus=scaffold6798_1:403:1155:+	Roseburia inulinivorans
2723100	GL0047097_V1_[Complete]_[mRNA]_locus=scaffold6838_1:1524:3551:+	Clostridiales

2723129	GL0040534_V1_[Complete]_[mRNA]_locus=scaffold6989_1:1910:2977:+	Roseburia inulinivorans
2723132	GL0040541_V1_[Complete]_[mRNA]_locus=scaffold6989_1:9901:11220:+	Bacteria
2723160	GL0012961_V1_[Complete]_[mRNA]_locus=scaffold7075_4:1029:2237:+	Roseburia inulinivorans
2723350	GL0069750_V1_[Complete]_[mRNA]_locus=scaffold7438_1:4790:5227:-	Roseburia inulinivorans
2723351	GL0069753_V1_[Complete]_[mRNA]_locus=scaffold7438_1:6933:9074:-	Clostridiales
2723352	GL0069754_V1_[Complete]_[mRNA]_locus=scaffold7438_1:9319:10725:+	Bacteria
2723353	GL0060890_V1_[Complete]_[mRNA]_locus=scaffold7438_2:2009:3262:-	Roseburia inulinivorans
2723362	GL0003436_V1_[Complete]_[mRNA]_locus=scaffold7486_1:4212:6050:-	Bacteria
2723363	GL0028449_V1_[Complete]_[mRNA]_locus=scaffold7486_2:2722:4677:+	Clostridiales
2723364	GL0054450_V1_[Complete]_[mRNA]_locus=scaffold7486_3:254:1336:+	Roseburia inulinivorans
2723365	GL0054453_V1_[Complete]_[mRNA]_locus=scaffold7486_3:2743:3399:+	Roseburia inulinivorans
2723366	GL0054455_V1_[Complete]_[mRNA]_locus=scaffold7486_3:4001:4987:-	Roseburia inulinivorans
2723369	GL0054462_V1_[Complete]_[mRNA]_locus=scaffold7486_3:12141:13463:+	Roseburia inulinivorans
2723372	GL0054467_V1_[Complete]_[mRNA]_locus=scaffold7486_3:18467:19165:+	Roseburia inulinivorans

2723401	GL0041048_V1_[Complete]_[mRNA]_locus=scaffold7508_2:4964:5488:-	Roseburia inulinivorans
2723402	GL0041049_V1_[Complete]_[mRNA]_locus=scaffold7508_2:5481:6533:-	Roseburia inulinivorans
2723404	GL0041056_V1_[Complete]_[mRNA]_locus=scaffold7508_2:13773:15146:-	Roseburia inulinivorans
2723407	GL0031505_V1_[Complete]_[mRNA]_locus=scaffold7508_3:4749:5402:-	Roseburia inulinivorans
2723409	GL0031507_V1_[Complete]_[mRNA]_locus=scaffold7508_3:8295:10043:+	Roseburia inulinivorans
2723468	GL0008671_V1_[Complete]_[mRNA]_locus=scaffold7698_1:3479:5284:-	Roseburia inulinivorans
2723522	GL0049155_V1_[Complete]_[mRNA]_locus=scaffold7843_4:402:1082:+	Roseburia inulinivorans
2723523	GL0049157_V1_[Complete]_[mRNA]_locus=scaffold7843_4:2147:3475:+	Roseburia inulinivorans
2723601	GL0058623_V1_[Complete]_[mRNA]_locus=scaffold8103_6:165:1487:+	Roseburia inulinivorans
2723610	GL0000424_V1_[Lack_5'-end]_[mRNA]_locus=scaffold8142_3:294:509:-	Roseburia inulinivorans
2723815	GL0030127_V1_[Complete]_[mRNA]_locus=scaffold8793_1:6272:6964:-	Roseburia inulinivorans
2723854	GL0000381_V1_[Complete]_[mRNA]_locus=scaffold8955_1:1279:5082:+	Bacteria
2723856	GL0000386_V1_[Complete]_[mRNA]_locus=scaffold8955_1:8297:10201:-	Roseburia inulinivorans
2723875	GL0004822_V1_[Complete]_[mRNA]_locus=scaffold9005_5:2126:2788:+	Faecalibacterium prausnitzii

2723947	GL0007993_V1_[Complete]_[mRNA]_locus=scaffold9218_1:5109:6314:+	Ruminococcus obeum
2723968	GL0038048_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9284_5:780:905:+	-
2724158	GL0063580_V1_[Complete]_[mRNA]_locus=scaffold9977_2:3348:5516:+	Bacteria
2724159	GL0063581_V1_[Complete]_[mRNA]_locus=scaffold9977_2:5509:7362:+	Bacteria
2724161	GL0063583_V1_[Complete]_[mRNA]_locus=scaffold9977_2:9044:10003:+	Roseburia inulinivorans
2724162	GL0063584_V1_[Complete]_[mRNA]_locus=scaffold9977_2:10049:11164:+	Roseburia inulinivorans
2724164	GL0063587_V1_[Complete]_[mRNA]_locus=scaffold9977_2:13708:15714:+	Firmicutes
2724367	GL0064098_V1_[Complete]_[mRNA]_locus=scaffold10688_2:662:1402:-	-
2724668	GL0038797_V1_[Complete]_[mRNA]_locus=scaffold11520_1:1254:2702:+	Clostridiales
2724741	GL0055076_V1_[Complete]_[mRNA]_locus=scaffold11912_2:2668:4938:+	Firmicutes
2724743	GL0055081_V1_[Complete]_[mRNA]_locus=scaffold11912_2:9266:10444:-	Roseburia inulinivorans
2724744	GL0055084_V1_[Complete]_[mRNA]_locus=scaffold11912_2:12962:14341:-	Roseburia inulinivorans
2724746	GL0055090_V1_[Complete]_[mRNA]_locus=scaffold11912_2:19030:22581:+	Clostridiales
2724747	GL0055094_V1_[Complete]_[mRNA]_locus=scaffold11912_2:26254:27546:+	Clostridiales

2724763	GL0017208_V1_[Complete]_[mRNA]_locus=scaffold12025_1:562:1191:+	Roseburia inulinivorans
2724767	GL0017214_V1_[Complete]_[mRNA]_locus=scaffold12025_1:6085:7734:+	Clostridiales
2724768	GL0017215_V1_[Complete]_[mRNA]_locus=scaffold12025_1:7799:8767:+	-
2724769	GL0017216_V1_[Complete]_[mRNA]_locus=scaffold12025_1:8831:10192:+	Roseburia inulinivorans
2724772	GL0017219_V1_[Complete]_[mRNA]_locus=scaffold12025_1:12484:13671:+	Roseburia inulinivorans
2724774	GL0017224_V1_[Complete]_[mRNA]_locus=scaffold12025_1:17978:18460:+	Roseburia inulinivorans
2724775	GL0017227_V1_[Complete]_[mRNA]_locus=scaffold12025_1:20286:22073:+	Clostridiales
2724778	GL0017232_V1_[Complete]_[mRNA]_locus=scaffold12025_1:24330:25481:+	Roseburia inulinivorans
2724780	GL0007924_V1_[Complete]_[mRNA]_locus=scaffold12025_3:645:1697:+	Roseburia inulinivorans
2724781	GL0007926_V1_[Complete]_[mRNA]_locus=scaffold12025_3:2548:4083:+	Clostridiales
2724784	GL0007931_V1_[Complete]_[mRNA]_locus=scaffold12025_3:8691:11123:+	Bacteria
2724785	GL0007932_V1_[Complete]_[mRNA]_locus=scaffold12025_3:11147:12655:+	Lachnospiraceae
2724786	GL0007934_V1_[Complete]_[mRNA]_locus=scaffold12025_3:14116:16527:+	Lachnospiraceae
2724969	GL0029467_V1_[Complete]_[mRNA]_locus=scaffold12532_1:1960:2907:-	Roseburia inulinivorans

2724970	GL0046455_V1_[Complete]_[mRNA]_locus=scaffold12532_4:2087:3259:-	Roseburia inulinivorans
2725027	GL0062758_V1_[Complete]_[mRNA]_locus=scaffold12694_2:2441:2911:+	Coprococcus eutactus
2725029	GL0062762_V1_[Complete]_[mRNA]_locus=scaffold12694_2:5452:6711:-	Roseburia inulinivorans
2725031	GL0037546_V1_[Complete]_[mRNA]_locus=scaffold12694_4:261:1271:+	Roseburia inulinivorans
2725032	GL0068021_V1_[Complete]_[mRNA]_locus=scaffold12694_6:853:2697:+	Clostridiales
2725033	GL0068022_V1_[Complete]_[mRNA]_locus=scaffold12694_6:2854:3936:+	Roseburia inulinivorans
2725034	GL0068023_V1_[Complete]_[mRNA]_locus=scaffold12694_6:4070:5560:+	Roseburia inulinivorans
2725035	GL0068025_V1_[Complete]_[mRNA]_locus=scaffold12694_6:6542:7846:+	Roseburia inulinivorans
2725036	GL0068026_V1_[Complete]_[mRNA]_locus=scaffold12694_6:8005:9597:+	Clostridiales
2725037	GL0068027_V1_[Complete]_[mRNA]_locus=scaffold12694_6:9756:11120:+	Roseburia inulinivorans
2725039	GL0068031_V1_[Complete]_[mRNA]_locus=scaffold12694_6:14962:16470:+	Roseburia inulinivorans
2725046	GL0010166_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12718_2:2:166:+	Roseburia inulinivorans
2725071	GL0051436_V1_[Complete]_[mRNA]_locus=scaffold12790_1:435:1784:-	Roseburia inulinivorans
2725072	GL0051437_V1_[Complete]_[mRNA]_locus=scaffold12790_1:2081:3244:-	Roseburia inulinivorans

2725074	GL0015986_V1_[Complete]_[mRNA]_locus=scaffold12790_2:2793:4979:-	Bacteria
2725077	GL0007729_V1_[Complete]_[mRNA]_locus=scaffold12790_3:6037:7107:+	Roseburia inulinivorans
2725199	GL0002967_V1_[Complete]_[mRNA]_locus=scaffold13358_2:293:2803:-	Bacteria
2725201	GL0002969_V1_[Complete]_[mRNA]_locus=scaffold13358_2:3840:4766:-	Roseburia inulinivorans
2725208	GL0044398_V1_[Complete]_[mRNA]_locus=scaffold13372_2:5610:7487:+	Roseburia inulinivorans
2725211	GL0030344_V1_[Complete]_[mRNA]_locus=scaffold13372_3:6521:8626:+	Clostridiales
2725212	GL0018283_V1_[Complete]_[mRNA]_locus=scaffold13372_4:117:1196:-	Roseburia inulinivorans
2725215	GL0018289_V1_[Complete]_[mRNA]_locus=scaffold13372_4:8762:10402:+	Roseburia inulinivorans
2725216	GL0015188_V1_[Complete]_[mRNA]_locus=scaffold13372_5:62:2083:-	Roseburia inulinivorans
2725217	GL0065632_V1_[Complete]_[mRNA]_locus=scaffold13372_6:2899:3771:+	Roseburia inulinivorans
2725234	GL0045713_V1_[Complete]_[mRNA]_locus=scaffold13571_1:41:1186:-	Clostridiales
2725300	GL0035720_V1_[Complete]_[mRNA]_locus=scaffold13961_1:6957:8861:+	Bacteria
2725322	GL0031285_V1_[Complete]_[mRNA]_locus=scaffold14008_2:2602:3909:+	Roseburia inulinivorans
2725342	GL0045496_V1_[Complete]_[mRNA]_locus=scaffold14069_2:668:1789:-	Roseburia inulinivorans

2725393	GL0002765_V1_[Complete]_[mRNA]_locus=scaffold14305_1:4803:6335:-	Roseburia inulinivorans
2725394	GL0002766_V1_[Complete]_[mRNA]_locus=scaffold14305_1:6386:7693:-	Roseburia inulinivorans
2725395	GL0002767_V1_[Complete]_[mRNA]_locus=scaffold14305_1:7686:8858:-	Roseburia inulinivorans
2725402	GL0017889_V1_[Complete]_[mRNA]_locus=scaffold14305_4:347:2038:-	Roseburia inulinivorans
2725440	GL0068312_V1_[Complete]_[mRNA]_locus=scaffold14409_1:23:373:-	Roseburia inulinivorans
2725441	GL0068313_V1_[Complete]_[mRNA]_locus=scaffold14409_1:500:2071:-	Clostridiales
2725442	GL0068315_V1_[Complete]_[mRNA]_locus=scaffold14409_1:3548:6202:-	Bacteria
2725466	GL0025248_V1_[Complete]_[mRNA]_locus=scaffold14463_5:1746:3644:+	Clostridiales
2725496	GL0004861_V1_[Complete]_[mRNA]_locus=scaffold14523_1:1426:2928:-	Clostridiales
2725716	GL0003740_V1_[Complete]_[mRNA]_locus=scaffold15299_3:1317:2006:-	-
2725730	GL0058165_V1_[Complete]_[mRNA]_locus=scaffold15329_1:7984:9312:-	Roseburia inulinivorans
2725906	GL0000010_V1_[Lack_3'-end]_[mRNA]_locus=scaffold15859_1:6642:7031:+	Roseburia inulinivorans
2725917	GL0024447_V1_[Complete]_[mRNA]_locus=scaffold15920_1:1486:3567:+	Bacteria
2725920	GL0024451_V1_[Complete]_[mRNA]_locus=scaffold15920_1:11768:12946:-	Roseburia inulinivorans

2725922	GL0024453_V1_[Complete]_[mRNA]_locus=scaffold15920_1:14873:15742:-	Roseburia inulinivorans
2726157	GL0020536_V1_[Complete]_[mRNA]_locus=scaffold17097_1:1205:2914:-	Roseburia inulinivorans
2726158	GL0010904_V1_[Complete]_[mRNA]_locus=scaffold17097_4:744:2147:-	Clostridiales
2726159	GL0010911_V1_[Complete]_[mRNA]_locus=scaffold17097_4:7504:8577:+	Roseburia inulinivorans
2726160	GL0010914_V1_[Complete]_[mRNA]_locus=scaffold17097_4:10186:11262:+	Roseburia inulinivorans
2726161	GL0010918_V1_[Complete]_[mRNA]_locus=scaffold17097_4:14869:16080:-	Roseburia inulinivorans
2726163	GL0010920_V1_[Complete]_[mRNA]_locus=scaffold17097_4:17927:18379:-	Roseburia inulinivorans
2726164	GL0010923_V1_[Complete]_[mRNA]_locus=scaffold17097_4:20119:21990:-	Clostridiales
2726166	GL0010926_V1_[Complete]_[mRNA]_locus=scaffold17097_4:23218:24423:-	Roseburia inulinivorans
2726167	GL0010931_V1_[Complete]_[mRNA]_locus=scaffold17097_4:26933:27976:-	Roseburia inulinivorans
2726538	GL0050811_V1_[Lack_3'-end]_[mRNA]_locus=scaffold18752_2:1812:2090:+	Roseburia inulinivorans
2726539	GL0045940_V1_[Lack_5'-end]_[mRNA]_locus=scaffold18752_3:2:1678:+	Clostridiales
2726541	GL0050934_V1_[Complete]_[mRNA]_locus=scaffold18756_2:11595:12902:+	Roseburia inulinivorans
2726543	GL0050936_V1_[Lack_5'-end]_[mRNA]_locus=scaffold18756_2:13452:14114	Roseburia inulinivorans

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2726602	GL0017017_V1_[Complete]_[mRNA]_locus=scaffold19022_1:1:462:+	-
2727304	GL0047914_V1_[Complete]_[mRNA]_locus=scaffold22361_1:38:868:-	Roseburia inulinivorans
2727324	GL0047936_V1_[Complete]_[mRNA]_locus=scaffold22361_1:28420:29604:+	Roseburia inulinivorans
2727367	GL0065169_V1_[Complete]_[mRNA]_locus=scaffold22511_3:1082:2575:-	Roseburia inulinivorans
2727368	GL0065171_V1_[Complete]_[mRNA]_locus=scaffold22511_3:3398:4273:-	Roseburia inulinivorans
2727480	GL0013330_V1_[Lack_both_end]_[mRNA]_locus=scaffold23162_3:3:947:-	Roseburia inulinivorans
2727547	GL0029422_V1_[Complete]_[mRNA]_locus=scaffold23512_3:2914:4251:+	Lachnospiraceae
2727548	GL0050325_V1_[Complete]_[mRNA]_locus=scaffold23512_6:818:1780:+	Roseburia inulinivorans
2727550	GL0008953_V1_[Complete]_[mRNA]_locus=scaffold23512_7:2939:5305:+	Clostridiales
2727552	GL0008955_V1_[Complete]_[mRNA]_locus=scaffold23512_7:6892:7779:+	Roseburia inulinivorans
2727556	GL0021404_V1_[Complete]_[mRNA]_locus=scaffold23532_1:378:1340:+	Roseburia inulinivorans
2727733	GL0013351_V1_[Complete]_[mRNA]_locus=scaffold24419_1:8776:9477:-	Roseburia inulinivorans
2728019	GL0033576_V1_[Complete]_[mRNA]_locus=scaffold26041_1:100:2058:-	Clostridiales

2728021	GL0033578_V1_[Complete]_[mRNA]_locus=scaffold26041_1:3106:4752:+	Bacteria
2728150	GL0032617_V1_[Complete]_[mRNA]_locus=scaffold26831_3:1892:2095:+	-
2728151	GL0032618_V1_[Complete]_[mRNA]_locus=scaffold26831_3:2267:5188:+	Clostridiales
2728178	GL0027867_V1_[Complete]_[mRNA]_locus=scaffold26934_1:23056:24816:+	Clostridiales
2728179	GL0027869_V1_[Complete]_[mRNA]_locus=scaffold26934_1:25670:26989:+	Roseburia inulinivorans
2728180	GL0027870_V1_[Complete]_[mRNA]_locus=scaffold26934_1:27224:30520:+	Bacteria
2728218	GL0007786_V1_[Complete]_[mRNA]_locus=scaffold27126_2:1802:2365:+	Roseburia inulinivorans
2728396	GL0029118_V1_[Complete]_[mRNA]_locus=scaffold28264_1:5353:7908:+	Bacteria
2728503	GL0018436_V1_[Complete]_[mRNA]_locus=scaffold29061_2:1471:4476:-	Bacteria
2728504	GL0018437_V1_[Complete]_[mRNA]_locus=scaffold29061_2:4610:6166:-	Bacteria
2728505	GL0018439_V1_[Complete]_[mRNA]_locus=scaffold29061_2:8346:9611:-	Roseburia inulinivorans
2728506	GL0018440_V1_[Complete]_[mRNA]_locus=scaffold29061_2:9614:10318:-	Roseburia inulinivorans
2728508	GL0018442_V1_[Complete]_[mRNA]_locus=scaffold29061_2:12701:13546:-	Roseburia inulinivorans
2728509	GL0018443_V1_[Complete]_[mRNA]_locus=scaffold29061_2:13598:16348:-	Roseburia inulinivorans

2728627	GL0054427_V1_[Complete]_[mRNA]_locus=scaffold29837_2:54:1352:+	Clostridiales
2728628	GL0054430_V1_[Complete]_[mRNA]_locus=scaffold29837_2:3218:5341:+	Roseburia inulinivorans
2728748	GL0054250_V1_[Complete]_[mRNA]_locus=scaffold30616_2:5632:7794:-	Bacteria
2728749	GL0054252_V1_[Complete]_[mRNA]_locus=scaffold30616_2:8690:10438:+	Bacteria
2728750	GL0054253_V1_[Complete]_[mRNA]_locus=scaffold30616_2:10438:12351:+	Bacteria
2728758	GL0067225_V1_[Complete]_[mRNA]_locus=scaffold30769_1:217:1419:+	Roseburia inulinivorans
2728759	GL0067226_V1_[Complete]_[mRNA]_locus=scaffold30769_1:1892:2827:+	Roseburia inulinivorans
2728860	GL0017204_V1_[Complete]_[mRNA]_locus=scaffold31414_1:586:1509:+	Roseburia inulinivorans
2729173	GL0027017_V1_[Complete]_[mRNA]_locus=scaffold32945_2:3644:4213:+	Roseburia inulinivorans
2729174	GL0027018_V1_[Complete]_[mRNA]_locus=scaffold32945_2:4270:5292:-	Roseburia inulinivorans
2729228	GL0000719_V1_[Complete]_[mRNA]_locus=scaffold33150_1:1499:3598:-	Roseburia inulinivorans
2729555	GL0057744_V1_[Complete]_[mRNA]_locus=scaffold35088_1:6029:6934:+	Roseburia inulinivorans
2729556	GL0057746_V1_[Complete]_[mRNA]_locus=scaffold35088_1:7888:9039:+	Roseburia inulinivorans
2729774	GL0066941_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37081_2:77:1219:-	Roseburia inulinivorans

2729775	GL0039935_V1_[Complete]_[mRNA]_locus=scaffold37081_3:39:1046:-	Roseburia inulinivorans
2729776	GL0039938_V1_[Complete]_[mRNA]_locus=scaffold37081_3:3188:4084:+	Roseburia inulinivorans
2729778	GL0051548_V1_[Complete]_[mRNA]_locus=scaffold37081_4:99:1214:+	Roseburia inulinivorans
2729779	GL0051549_V1_[Complete]_[mRNA]_locus=scaffold37081_4:1680:2831:+	Roseburia inulinivorans
2729835	GL0016838_V1_[Complete]_[mRNA]_locus=scaffold37273_1:1034:2818:+	Bacteria
2729957	GL0032945_V1_[Complete]_[mRNA]_locus=scaffold37968_1:2093:4009:-	Bacteria
2730036	GL0070701_V1_[Complete]_[mRNA]_locus=scaffold38616_1:343:1158:-	Roseburia inulinivorans
2730037	GL0070703_V1_[Complete]_[mRNA]_locus=scaffold38616_1:2175:3449:-	Clostridiales
2730038	GL0070705_V1_[Complete]_[mRNA]_locus=scaffold38616_1:4130:5155:-	Roseburia inulinivorans
2730063	GL0047317_V1_[Complete]_[mRNA]_locus=scaffold38724_3:926:1930:-	Roseburia inulinivorans
2730064	GL0047318_V1_[Complete]_[mRNA]_locus=scaffold38724_3:1947:2657:-	Roseburia inulinivorans
2730194	GL0063557_V1_[Complete]_[mRNA]_locus=scaffold39541_1:15448:16677:-	Roseburia inulinivorans
2730352	GL0021247_V1_[Complete]_[mRNA]_locus=scaffold40247_1:8687:10153:-	Roseburia inulinivorans
2730353	GL0021251_V1_[Complete]_[mRNA]_locus=scaffold40247_1:13658:14341:-	Roseburia inulinivorans

2730358	GL0019089_V1_[Complete]_[mRNA]_locus=scaffold40249_1:4324:6210:+	Roseburia inulinivorans
2730455	GL0057575_V1_[Complete]_[mRNA]_locus=scaffold41006_3:6687:7694:-	Roseburia inulinivorans
2730457	GL0069532_V1_[Complete]_[mRNA]_locus=scaffold41006_4:9704:10846:-	Roseburia inulinivorans
2730460	GL0069536_V1_[Complete]_[mRNA]_locus=scaffold41006_4:13369:15204:-	Roseburia inulinivorans
2730461	GL0069538_V1_[Complete]_[mRNA]_locus=scaffold41006_4:17134:17796:-	Roseburia inulinivorans
2730794	GL0065973_V1_[Complete]_[mRNA]_locus=scaffold43491_1:1432:2598:-	Roseburia inulinivorans
2730922	GL0021885_V1_[Complete]_[mRNA]_locus=scaffold43778_1:12261:13790:+	Holdemania filiformis
2731007	GL0055699_V1_[Complete]_[mRNA]_locus=scaffold44312_1:2393:4219:+	Bacteria
2731471	GL0005144_V1_[Complete]_[mRNA]_locus=scaffold46941_1:5425:7215:+	Clostridia
2732008	GL0062104_V1_[Complete]_[mRNA]_locus=scaffold49351_1:7470:8399:-	Roseburia inulinivorans
2732107	GL0053045_V1_[Complete]_[mRNA]_locus=scaffold49673_1:8018:9880:-	Bacteria
2732648	GL0062990_V1_[Complete]_[mRNA]_locus=scaffold51369_1:304:1701:-	Roseburia inulinivorans
2733009	GL0005055_V1_[Complete]_[mRNA]_locus=scaffold52061_1:1679:2515:-	Roseburia inulinivorans
2733095	GL0038109_V1_[Complete]_[mRNA]_locus=scaffold52137_1:3122:4402:+	Roseburia inulinivorans

2733096	GL0038110_V1_[Complete]_[mRNA]_locus=scaffold52137_1:4399:5148:+	Roseburia inulinivorans
2733165	GL0010409_V1_[Complete]_[mRNA]_locus=scaffold52196_1:5497:6621:-	Roseburia inulinivorans
2733166	GL0010410_V1_[Complete]_[mRNA]_locus=scaffold52196_1:6635:8053:-	Clostridiales
2733260	GL0043614_V1_[Complete]_[mRNA]_locus=scaffold52243_1:43:2331:-	Roseburia inulinivorans
2733261	GL0043615_V1_[Complete]_[mRNA]_locus=scaffold52243_1:2543:3565:-	Roseburia inulinivorans
2733266	GL0045527_V1_[Complete]_[mRNA]_locus=scaffold52246_1:6436:7533:+	Roseburia inulinivorans
2733663	GL0068737_V1_[Complete]_[mRNA]_locus=C6253293_1:161:766:-	Holdemania filiformis
2733761	GL0053220_V1_[Complete]_[mRNA]_locus=C6269009_1:19:1233:-	Eubacterium dolichum
2734715	GL0007252_V1_[Complete]_[mRNA]_locus=scaffold998_6:5083:5691:-	Clostridiales
2734779	GL0061081_V1_[Complete]_[mRNA]_locus=scaffold1092_2:1470:2240:+	Blautia hydrogenotrophica
2735029	GL0145780_V1_[Complete]_[mRNA]_locus=scaffold1607_4:3364:4551:-	Ruminococcus lactaris
2735703	GL0157819_V1_[Complete]_[mRNA]_locus=scaffold2434_9:388:1188:+	Clostridium ramosum
2736809	GL0028160_V1_[Complete]_[mRNA]_locus=scaffold3893_1:38:1351:-	Clostridium nexile
2736815	GL0128686_V1_[Complete]_[mRNA]_locus=scaffold3904_1:2156:4207:+	Firmicutes

2738366	GL0062586_V1_[Complete]_[mRNA]_locus=scaffold7217_2:1644:3053:-	Clostridium
2738616	GL0033294_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7668_3:213:746:-	Clostridium bolteae
2738687	GL0162231_V1_[Complete]_[mRNA]_locus=scaffold7745_2:12804:13439:-	Ruminococcus obeum
2738997	GL0030654_V1_[Complete]_[mRNA]_locus=scaffold8285_3:1603:2292:+	Bacteroides capillosus
2740005	GL0041059_V1_[Complete]_[mRNA]_locus=scaffold10818_6:263:2854:-	Bacteria
2740314	GL0099689_V1_[Complete]_[mRNA]_locus=scaffold11709_1:910:1437:-	Clostridiales
2740389	GL0095014_V1_[Complete]_[mRNA]_locus=scaffold11875_2:965:1852:-	-
2741056	GL0048647_V1_[Complete]_[mRNA]_locus=scaffold13408_1:287:436:+	-
2741748	GL0147277_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14938_1:108:917:-	Eubacterium siraeum
2741753	GL0082758_V1_[Complete]_[mRNA]_locus=scaffold14965_1:3:257:+	Faecalibacterium prausnitzii
2742536	GL0052965_V1_[Complete]_[mRNA]_locus=scaffold16847_1:6032:6568:+	Coprococcus comes
2742863	GL0057112_V1_[Complete]_[mRNA]_locus=scaffold17545_1:1849:3117:+	Bacteroides capillosus
2743218	GL0136987_V1_[Complete]_[mRNA]_locus=scaffold18716_6:29:1027:-	-
2743666	GL0085884_V1_[Complete]_[mRNA]_locus=scaffold19848_2:2432:3685:-	Bacteria

2743746	GL0146450_V1_[Complete]_[mRNA]_locus=scaffold20145_1:1669:3738:-	Firmicutes
2745199	GL0159585_V1_[Lack_5'-end]_[mRNA]_locus=scaffold24634_3:1786:1905:-	-
2745337	GL0110715_V1_[Complete]_[mRNA]_locus=scaffold25044_2:35:412:-	Faecalibacterium prausnitzii
2746517	GL0158798_V1_[Lack_5'-end]_[mRNA]_locus=scaffold29142_2:730:1182:-	Anaerofustis stercorihominis
2747094	GL0142480_V1_[Complete]_[mRNA]_locus=scaffold31245_3:1095:1856:+	Clostridium butyricum
2747636	GL0135588_V1_[Lack_3'-end]_[mRNA]_locus=scaffold32875_1:377:625:+	Epulopiscium
2749471	GL0054808_V1_[Lack_3'-end]_[mRNA]_locus=scaffold40098_3:839:2161:+	Clostridium ramosum
2751061	GL0046393_V1_[Lack_3'-end]_[mRNA]_locus=scaffold46272_1:3:197:-	Faecalibacterium prausnitzii
2751192	GL0008406_V1_[Complete]_[mRNA]_locus=scaffold46725_2:120:362:+	Faecalibacterium prausnitzii
2751243	GL0007821_V1_[Complete]_[mRNA]_locus=scaffold46949_1:2669:4684:+	Ruminococcus obeum
2752906	GL0071522_V1_[Lack_both_end]_[mRNA]_locus=scaffold53994_2:1:762:-	Blautia hydrogenotrophica
2754837	GL0065630_V1_[Lack_both_end]_[mRNA]_locus=scaffold60760_1:3:506:-	Faecalibacterium prausnitzii
2754880	GL0165446_V1_[Complete]_[mRNA]_locus=scaffold60987_1:9951:10655:+	-
2757960	GL0100774_V1_[Complete]_[mRNA]_locus=scaffold73003_4:4803:5657:+	Anaerostipes caccae

2759442	GL0084534_V1_[Complete]_[mRNA]_locus=scaffold79407_2:1669:2112:+	Clostridium ramosum
2760723	GL0098606_V1_[Complete]_[mRNA]_locus=scaffold84257_3:1149:2330:-	Ruminococcus torques
2761572	GL0105661_V1_[Complete]_[mRNA]_locus=scaffold87366_1:210:1082:-	Blautia hydrogenotrophica
2761856	GL0039788_V1_[Complete]_[mRNA]_locus=scaffold88079_2:9719:10324:-	Clostridium
2762919	GL0162907_V1_[Complete]_[mRNA]_locus=scaffold91185_1:795:1349:+	Clostridium bolteae
2764145	GL0141809_V1_[Complete]_[mRNA]_locus=scaffold94240_7:340:1239:+	-
2764881	GL0053314_V1_[Complete]_[mRNA]_locus=scaffold95588_1:795:1040:+	-
2767223	GL0072807_V1_[Complete]_[mRNA]_locus=scaffold98596_1:1347:2153:+	Clostridium thermocellum
2767483	GL0167062_V1_[Complete]_[mRNA]_locus=scaffold98800_1:3310:4143:-	Clostridium ramosum
2768180	GL0038800_V1_[Complete]_[mRNA]_locus=scaffold99209_1:433:1353:-	Clostridium ramosum
2772738	GL0080904_V1_[Lack_5'-end]_[mRNA]_locus=scaffold122_48:1857:3116:-	Dorea longicatena
2774989	GL0110026_V1_[Lack_both_end]_[mRNA]_locus=scaffold2036_4:3:1460:-	Bacteria
2775212	GL0079280_V1_[Lack_both_end]_[mRNA]_locus=scaffold2188_4:2:778:+	Faecalibacterium prausnitzii
2777929	GL0103944_V1_[Complete]_[mRNA]_locus=scaffold4684_4:1877:3562:-	Thermoanaerobacter

2777948	GL0130812_V1_[Complete]_[mRNA]_locus=scaffold4715_5:675:2051:-	Eubacterium siraeum
2778425	GL0023315_V1_[Complete]_[mRNA]_locus=scaffold5235_1:2439:3140:+	Coprococcus eutactus
2781390	GL0113884_V1_[Complete]_[mRNA]_locus=scaffold7939_2:7354:8403:+	Anaerostipes caccae
2782296	GL0024299_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8914_3:2:616:-	Thermoanaerobacter
2783766	GL0119205_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10824_1:3:800:+	Clostridium thermocellum
2785573	GL0053276_V1_[Lack_5'-end]_[mRNA]_locus=scaffold13226_4:2:1192:+	Faecalibacterium prausnitzii
2787747	GL0024410_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16570_1:1:504:+	Anaerotruncus colihominis
2790228	GL0005934_V1_[Complete]_[mRNA]_locus=scaffold20573_2:62:2458:-	Epulopiscium
2796754	GL0064545_V1_[Lack_5'-end]_[mRNA]_locus=scaffold34992_1:3:578:+	Faecalibacterium prausnitzii
2800152	GL0064183_V1_[Lack_both_end]_[mRNA]_locus=scaffold45950_4:1:3654:-	Clostridiales
2800154	GL0037427_V1_[Complete]_[mRNA]_locus=scaffold45950_5:2978:5161:-	Clostridium bolteae
2800981	GL0116520_V1_[Lack_both_end]_[mRNA]_locus=scaffold48772_3:3:767:+	Clostridium kluyveri
2802708	GL0060787_V1_[Lack_both_end]_[mRNA]_locus=scaffold54769_2:2:625:-	Clostridium
2804326	GL0025002_V1_[Complete]_[mRNA]_locus=scaffold61207_2:295:690:+	Clostridiales

2807212	GL0050060_V1_[Lack_5'-end]_[mRNA]_locus=scaffold72965_1:1:468:+	Firmicutes
2807966	GL0121179_V1_[Complete]_[mRNA]_locus=scaffold76251_1:1028:1636:-	Clostridium
2808311	GL0038566_V1_[Lack_3'-end]_[mRNA]_locus=scaffold77714_6:1061:1537:+	Clostridiales
2810793	GL0001548_V1_[Lack_3'-end]_[mRNA]_locus=scaffold86931_2:3:464:-	Firmicutes
2814970	GL0081991_V1_[Lack_3'-end]_[mRNA]_locus=C4439716_1:1:582:+	-
2815008	GL0080075_V1_[Lack_5'-end]_[mRNA]_locus=C4441588_1:2:190:+	-
2815965	GL0083668_V1_[Lack_5'-end]_[mRNA]_locus=C4485406_1:1:525:+	Dorea formicigenerans
2817841	GL0254950_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold1326_1:107:832:+	Roseburia inulinivorans
2820969	GL0264501_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold7425_2:1:399:+	Bacteroides capillosus
2821092	GL0208596_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold7660_2:1:1518:+	Clostridium phytofermentans
2821093	GL0208597_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold7660_2:1617:2876:+	Ruminococcus obeum
2821590	GL0390289_unmapped_[Complete]_[mRNA]_locus=scaffold8928_1:390:941:-	Bacteroides
2824783	GL0311807_unmapped_[Complete]_[mRNA]_locus=scaffold15113_4:269:1252:-	Bacteroides ovatus
2825907	GL0601456_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold17551_1:38:1264:+	Clostridium methylpentosum

2827055	GL0146220_unmapped_[Complete]_[mRNA]_locus =scaffold19901_2:425:949:-	Roseburia inulinivorans
2827083	GL0007250_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold19921_1:1:654:-	Clostridium asparagiforme
2827365	GL0309323_unmapped_[Complete]_[mRNA]_locus =scaffold20479_1:500:1399:+	Roseburia inulinivorans
2828436	GL0096575_unmapped_[Complete]_[mRNA]_locus =scaffold22392_1:571:2466:-	Clostridium methylpentosum
2829505	GL0287293_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold24488_1:648:1892:+	Heliobacterium modesticaldum
2829804	GL0120714_unmapped_[Complete]_[mRNA]_locus =scaffold24963_1:282:1205:-	Clostridium
2830946	GL0155383_unmapped_[Complete]_[mRNA]_locus =scaffold27465_1:238:1284:+	Clostridium bartlettii
2831332	GL0127497_unmapped_[Complete]_[mRNA]_locus =scaffold28248_1:116:874:+	-
2831385	GL0234148_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold28368_2:2:532:-	Clostridium bolteae
2833251	GL0444235_unmapped_[Complete]_[mRNA]_locus =scaffold32208_2:176:1030:-	Clostridium bartlettii
2833273	GL0449574_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold32267_4:2:799:+	-
2834003	GL0147929_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold33571_1:3:734:-	Clostridium scindens
2835505	GL0244174_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold36576_1:1:2205:+	-
2837304	GL0025424_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold40300_1:170:913:+	Clostridium ramosum

2840714	GL0298439_unmapped_[Complete]_[mRNA]_locus =scaffold47549_4:1327:2208:+	Eubacterium dolichum
2841563	GL0015552_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold49268_2:496:1293:-	-
2842134	GL0410537_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold50520_1:80:1390:-	Clostridium asparagiforme
2842520	GL0333208_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold51429_2:406:732:+	Clostridium bolteae
2845176	GL0017569_unmapped_[Complete]_[mRNA]_locus =scaffold57380_2:964:2148:+	-
2848458	GL0224274_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold64665_1:3:629:-	Saccharophagus degradans
2852268	GL0454774_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold72828_4:2:1273:+	Clostridium bolteae
2854650	GL0593743_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold78119_1:1:267:+	Clostridium bolteae
2855844	GL0516250_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold80865_1:518:1780:+	Roseburia inulinivorans
2855979	GL0418787_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold81181_7:3:1148:-	-
2856235	GL0561512_unmapped_[Complete]_[mRNA]_locus =scaffold81739_4:193:1728:+	Bacteria
2857337	GL0277352_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold84202_2:104:583:-	Bacteroides capillosus
2858446	GL0636883_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold86741_1:3:689:-	Clostridium bolteae
2858492	GL0365261_unmapped_[Complete]_[mRNA]_locus =scaffold86828_3:12:1328:-	Bacteroides fragilis

2858515	GL0082040_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold86888_1:1:549:+	Clostridium bolteae
2863563	GL0098507_unmapped_[Complete]_[mRNA]_locus=scaffold98011_2:540:1469:+	Holdemania filiformis
2867697	GL0540375_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold107132_2:3:668:-	Bacteroides capillosus
2868993	GL0058436_unmapped_[Complete]_[mRNA]_locus=scaffold110613_2:121:513:-	-
2869502	GL0451721_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold111746_4:1:507:-	Clostridium asparagiforme
2869652	GL0631949_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold112112_3:1:255:-	Clostridium phytofermentans
2873800	GL0609190_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold121318_4:1:834:-	-
2875105	GL0160412_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold124362_1:1:330:-	Clostridium nexile
2875797	GL0572400_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold126144_1:3:434:+	Clostridium asparagiforme
2875865	GL0008373_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold126292_3:3:1724:-	Clostridiales
2876407	GL0000874_unmapped_[Complete]_[mRNA]_locus=scaffold127744_1:519:1619:+	Roseburia inulinivorans
2876552	GL0600564_unmapped_[Complete]_[mRNA]_locus=scaffold128126_1:358:1494:+	-
2878126	GL0427820_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold131638_1:1:858:-	Anaerostipes caccae
2881233	GL0226217_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold138799_4:526:1035:+	-

2888147	GL0194191_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold155414_1:29:1009:+	Roseburia inulinivorans
2890721	GL0195481_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold162497_1:3:284:-	Clostridium bolteae
2893226	GL0558152_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold168829_2:273:710:-	Clostridium bolteae
2895078	GL0386927_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold173227_2:1:696:+	Roseburia inulinivorans
2896585	GL0478071_unmapped_[Complete]_[mRNA]_locus=scaffold176875_1:203:1435:-	Roseburia inulinivorans
2896983	GL0355672_unmapped_[Complete]_[mRNA]_locus=scaffold177928_1:249:1379:-	-
2897766	GL0380706_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold179797_2:2:436:+	Clostridium
2898355	GL0450114_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold181307_3:460:1014:-	Clostridium
2899554	GL0505336_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold184404_1:3:395:-	Clostridium bolteae
2902456	GL0480223_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold191235_1:79:1056:+	Clostridium nexile
2902653	GL0274209_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold191772_1:170:2047:-	Roseburia inulinivorans
2902977	GL0253212_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold192555_4:2:730:-	Eubacterium hallii
2903971	GL0210635_unmapped_[Complete]_[mRNA]_locus=scaffold194857_1:490:1602:+	Clostridium
2903975	GL0348812_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold194857_2:842:2626:+	Clostridium nexile

2904824	GL0019370_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold196977_3:3:584:+	-
2906044	GL0132160_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold200146_1:2:790:-	Roseburia inulinivorans
2907480	GL0012866_unmapped_[Complete]_[mRNA]_locus=scaffold204093_1:5:223:-	-
2910724	GL0471455_unmapped_[Complete]_[mRNA]_locus=scaffold212272_5:91:507:-	-
2911136	GL0046641_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold213398_2:2:700:+	Clostridium bolteae
2912069	GL0221231_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold215894_1:3:626:-	-
2912574	GL0401941_unmapped_[Complete]_[mRNA]_locus=scaffold217281_11:129:323:-	Clostridium bolteae
2912652	GL0229890_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold217424_5:1:561:-	Ruminococcus gnavus
2913324	GL0273593_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold219059_1:266:802:-	Roseburia inulinivorans
2915343	GL0389912_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold224308_2:2:1915:+	Clostridiales
2917768	GL0325941_unmapped_[Complete]_[mRNA]_locus=scaffold230695_1:2315:2848:-	Alistipes putredinis
2918366	GL0290905_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold232462_2:91:861:+	Clostridium
2919952	GL0410192_unmapped_[Complete]_[mRNA]_locus=scaffold236818_1:344:925:-	Alistipes putredinis
2923419	GL0016098_unmapped_[Complete]_[mRNA]_locus=scaffold246001_2:578:1327:+	Roseburia inulinivorans

2923762	GL0487020_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold246882_1:2:775:+	Clostridium bolteae
2927092	GL0464110_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold255878_2:1:699:+	Clostridiales
2927137	GL0319576_unmapped_[Complete]_[mRNA]_locus=scaffold256001_1:65:1090:-	-
2927410	GL0296987_unmapped_[Complete]_[mRNA]_locus=scaffold256739_1:1397:1993:+	Streptococcus
2932841	GL0335127_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold271096_1:3:191:+	-
2934144	GL0429359_unmapped_[Complete]_[mRNA]_locus=scaffold274556_2:853:1683:+	Roseburia inulinivorans
2935259	GL0489575_unmapped_[Complete]_[mRNA]_locus=scaffold277387_2:206:1093:+	Clostridium
2936286	GL0548693_unmapped_[Complete]_[mRNA]_locus=scaffold280265_1:549:1079:-	Catenibacterium mitsuokai
2937957	GL0582520_unmapped_[Complete]_[mRNA]_locus=scaffold284784_2:474:1250:-	Clostridium
2942618	GL0531504_unmapped_[Complete]_[mRNA]_locus=scaffold296770_1:733:1017:+	-
2948963	GL0457097_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold314379_1:1:843:+	Clostridiales
2948964	GL0457098_unmapped_[Complete]_[mRNA]_locus=scaffold314379_1:919:2046:+	Epulopiscium
2949205	GL0599773_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold315145_1:1:549:-	Holdemania filiformis
2950065	GL0197481_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold317845_2:223:810:-	Bacteroides capillosus

2951703	GL0050043_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold322469_2:3:971:-	Alkaliphilus oremlandii
2951778	GL0016711_unmapped_[Complete]_[mRNA]_locus=scaffold322636_1:134:1171:+	Roseburia inulinivorans
2951783	GL0260080_unmapped_[Complete]_[mRNA]_locus=scaffold322650_1:299:655:+	Ruminococcus obeum
2951784	GL0260081_unmapped_[Complete]_[mRNA]_locus=scaffold322650_1:680:1306:+	Blautia hydrogenotrophica
2957650	GL0399152_unmapped_[Complete]_[mRNA]_locus=scaffold339262_2:1106:1564:-	-
2958012	GL0194836_unmapped_[Complete]_[mRNA]_locus=scaffold340236_1:911:1942:+	Bacteroides plebeius
2958901	GL0239710_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold342912_1:1:654:-	Bacteroides capillosus
2959303	GL0146698_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold344024_1:1:1566:-	Dorea
2959840	GL0188925_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold345635_1:2:883:-	Roseburia inulinivorans
2959995	GL0409497_unmapped_[Complete]_[mRNA]_locus=scaffold346126_3:56:724:+	Bacteroides capillosus
2961711	GL0061315_unmapped_[Complete]_[mRNA]_locus=scaffold350877_1:103:1605:+	Desulfitobacterium hafniense
2961807	GL0241088_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold351163_1:3:1880:-	Clostridium bolteae
2964464	GL0463410_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold358665_1:1:1221:+	Roseburia inulinivorans
2964518	GL0062523_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold358767_1:1:1260:+	Chloroherpeton thalassium

2965757	GL0264344_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold362253_1:1:1395:+	Clostridiales
2968871	GL0382104_unmapped_[Complete]_[mRNA]_locus=scaffold371308_1:760:1731:-	Ruminococcus lactaris
2968872	GL0382105_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold371308_1:1732:2934:-	-
2968896	GL0156664_unmapped_[Complete]_[mRNA]_locus=scaffold371362_1:1464:2021:+	-
2971989	GL0247255_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold380456_3:1:441:-	-
2973513	GL0200505_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold384759_1:3:677:-	-
2974458	GL0137989_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold387278_2:3:518:-	Roseburia inulinivorans
2974459	GL0137990_unmapped_[Complete]_[mRNA]_locus=scaffold387278_2:580:1098:-	-
2976350	GL0566443_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold392856_2:632:1396:-	Ruminococcus lactaris
2976952	GL0042589_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold394611_2:3:710:+	Clostridium asparagiforme
2977681	GL0222327_unmapped_[Complete]_[mRNA]_locus=scaffold396750_1:1271:2047:+	Methylibium petroleiphilum
2977682	GL0222328_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold396750_1:2060:2473:+	Methylibium petroleiphilum
2979927	GL0196908_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold403534_2:921:1784:-	Blautia hydrogenotrophica

2982919	GL0323079_unmapped_[Complete]_[mRNA]_locus =scaffold412265_2:3203:4459:-	Eubacterium siraeum
2985858	GL0169575_unmapped_[Complete]_[mRNA]_locus =scaffold420857_1:46:816:-	Faecalibacterium prausnitzii
2988007	GL0607802_unmapped_[Complete]_[mRNA]_locus =scaffold427451_1:890:1477:+	Bacteroides capillosus
2989793	GL0221912_unmapped_[Complete]_[mRNA]_locus =scaffold433008_1:1516:2487:+	-
2990059	GL0191843_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold433881_1:3:620:-	-
2990894	GL0551756_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold436478_1:2:2305:-	Clostridiales
2991868	GL0256413_unmapped_[Complete]_[mRNA]_locus =scaffold439391_1:116:1594:-	-
2992911	GL0105476_unmapped_[Complete]_[mRNA]_locus =scaffold442665_1:165:902:-	Roseburia inulinivorans
2993587	GL0189696_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold444819_1:3:845:-	-
2995620	GL0085215_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold451457_2:1:429:-	Clostridium bolteae
2995860	GL0055468_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold452119_2:278:736:-	Clostridium ramosum
2999292	GL0302404_unmapped_[Complete]_[mRNA]_locus =scaffold462452_1:93:701:-	Eubacterium hallii
2999546	GL0249611_unmapped_[Complete]_[mRNA]_locus =scaffold463308_2:934:2436:-	Firmicutes
3005368	GL0067112_unmapped_[Complete]_[mRNA]_locus =scaffold480894_1:673:1080:+	Bacteria

3008463	GL0323978_unmapped_[Complete]_[mRNA]_locus =scaffold490445_1:209:871:+	Roseburia inulinivorans
3009964	GL0200216_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold495388_2:3:1052:+	Clostridium hylemonae
3010142	GL0405979_unmapped_[Complete]_[mRNA]_locus =scaffold495961_3:462:797:+	-
3012167	GL0190513_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold502283_2:552:1232:-	Clostridium bolteae
3016507	GL0372106_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold515128_2:1:645:-	Atopobium rimae
3018526	GL0572960_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold521416_2:3:317:-	cellular organisms
3021740	GL0378071_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold531457_2:2:748:+	Roseburia inulinivorans
3024535	GL0310812_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold539725_1:540:1175:+	Clostridium bolteae
3025362	GL0160103_unmapped_[Complete]_[mRNA]_locus =scaffold542258_1:470:1015:-	Ruminococcus obeum
3025794	GL0329453_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold543574_1:2:538:-	Clostridium
3026796	GL0399219_unmapped_[Complete]_[mRNA]_locus =scaffold546691_2:71:832:+	Clostridium
3027018	GL0174130_unmapped_[Complete]_[mRNA]_locus =scaffold547403_2:17:514:-	Bacteria
3028515	GL0181737_unmapped_[Complete]_[mRNA]_locus =scaffold551703_1:290:1405:+	Clostridium
3028857	GL0386377_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold552782_1:1:168:-	Clostridium bolteae

3028858	GL0386378_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold552782_1:186:500:-	Clostridiales
3033538	GL0318303_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold567391_1:3:1481:+	Bacteroides capillosus
3033730	GL0591873_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold568023_1:489:917:-	-
3036231	GL0444860_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold575304_1:3:572:-	Clostridium bolteae
3036875	GL0006011_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold577343_6:103:1020:-	Clostridium difficile
3039302	GL0172231_unmapped_[Complete]_[mRNA]_locus=scaffold584425_1:188:757:+	Dorea longicatena
3048014	GL0414874_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold610533_1:448:732:+	Clostridium bolteae
3049929	GL0307341_unmapped_[Complete]_[mRNA]_locus=scaffold616321_1:27:761:-	-
3053668	GL0533011_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold627603_1:3:1295:-	Clostridium bartlettii
3054856	GL0008711_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold631152_1:1:519:-	Clostridium bolteae
3059295	GL0291636_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold644262_2:273:1070:-	Roseburia inulinivorans
3063349	GL0185802_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold656595_1:2:532:+	Syntrophomonas wolfei
3074622	GL0414622_unmapped_[Complete]_[mRNA]_locus=scaffold689048_2:144:782:+	Clostridium bartlettii
3075638	GL0066217_unmapped_[Complete]_[mRNA]_locus=scaffold691985_2:1438:2619:-	Clostridium kluyveri

3083814	GL0226370_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold715569_1:2:1198:-	Roseburia inulinivorans
3086031	GL0142990_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold721618_1:231:1322:+	-
3086548	GL0393225_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold722982_1:760:1314:-	Roseburia inulinivorans
3087204	GL0397601_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold724730_1:3:368:-	Clostridium asparagiforme
3088629	GL0229293_unmapped_[Complete]_[mRNA]_locus=scaffold728463_2:165:1586:+	Coprococcus eutactus
3092290	GL0353496_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold737618_1:274:516:-	Clostridium bolteae
3092461	GL0005317_unmapped_[Complete]_[mRNA]_locus=scaffold738117_1:440:1858:-	Firmicutes
3096023	GL0049857_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold747448_2:3:602:-	Desulfitobacterium hafniense
3097663	GL0147289_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold751590_2:2:181:+	-
3100471	GL0598690_unmapped_[Complete]_[mRNA]_locus=scaffold758345_1:14:823:-	Sorangium cellulosum
3110176	GL0142411_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold780321_1:351:1283:-	Bacteria
3113013	GL0487389_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold786086_2:2:829:+	Ruminococcus lactaris
3115565	GL0050532_unmapped_[Complete]_[mRNA]_locus=scaffold791075_1:130:1332:+	Bacillus pumilus
3118152	GL0223587_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold796254_1:1:1203:-	-

3125774	GL0595811_unmapped_[Complete]_[mRNA]_locus=scaffold810761_1:172:489:-	-
3126947	GL0455586_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold812917_1:100:1050:-	Clostridiales
3126948	GL0015747_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold812917_2:1:1221:-	Clostridiales
3136917	GL0528559_unmapped_[Complete]_[mRNA]_locus=scaffold829590_1:941:1444:-	-
3138413	GL0540213_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold831740_1:2:2125:-	Clostridium methylpentosum
3138414	GL0540214_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold831740_1:2181:3413:-	Dorea formicigenerans
3138877	GL0469351_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold832405_1:3:1022:+	-
3144131	GL0432694_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold838490_1:1:654:+	Blautia hydrogenotrophica
3159597	GL0572051_unmapped_[Lack_3'-end]_[mRNA]_locus=C219827617_1:138:566:+	Roseburia inulinivorans
3164154	GL0547154_unmapped_[Lack_both_end]_[mRNA]_locus=C219878981_1:2:601:+	Polaribacter
3164839	GL0266119_unmapped_[Lack_5'-end]_[mRNA]_locus=C219886937_1:105:608:-	Bacteria
3166691	GL0319696_unmapped_[Lack_3'-end]_[mRNA]_locus=C219906577_1:1:615:-	Clostridium botulinum
3175620	GL0267845_unmapped_[Lack_5'-end]_[mRNA]_locus=C219999762_1:37:732:-	Clostridium bolteae

3179749	GL0196070_unmapped_[Lack_5'-end]_[mRNA]_locus=C220041315_1:70:807:-	Roseburia inulinivorans
3184736	GL0501874_unmapped_[Lack_both_end]_[mRNA]_locus=C220089093_1:1:945:-	Clostridium bolteae

Table 1: CD-related genes

ID	GeneName	Name(NR)
4317	GL0092655_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold133_1:42341:42583:+	Akkermansia muciniphila
5216	GL0099159_MH0002_[Complete]_[mRNA]_locus=scaffold3917_1:4059:4847:+	Akkermansia muciniphila
6810	GL0048749_MH0002_[Lack_5'-end]_[mRNA]_locus=scaffold11195_1:19:564:-	-
7333	GL0105937_MH0002_[Complete]_[mRNA]_locus=scaffold13909_3:13600:14277:+	Akkermansia muciniphila
8130	GL0085187_MH0002_[Complete]_[mRNA]_locus=scaffold18066_2:9754:10797:-	Akkermansia muciniphila
8131	GL0085192_MH0002_[Complete]_[mRNA]_locus=scaffold18066_2:16773:17561:-	Akkermansia muciniphila
8588	GL0042542_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold21050_3:270:1364:+	Akkermansia muciniphila
8590	GL0000012_MH0002_[Complete]_[mRNA]_locus=scaffold21050_7:4219:4791:+	Akkermansia muciniphila
12300	GL0037795_MH0002_[Lack_5'-end]_[mRNA]_locus=scaffold45331_2:11:619:-	-
12447	GL0033927_MH0002_[Lack_3'-end]_[mRNA]_locus=scaffold46619_1:3:302:-	Bacteria

12470	GL0010013_MH0002_[Complete]_[mRNA]_locus=scaffold46792_2:6:677:-	-
17994	GL0013046_MH0002_[Complete]_[mRNA]_locus=scaffold83677_1:6797:7603:-	Akkermansia muciniphila
21545	GL0106621_MH0002_[Lack_both_end]_[mRNA]_locus=scaffold95488_1:2:7978:-	Akkermansia muciniphila
21727	GL0012309_MH0002_[Lack_5'-end]_[mRNA]_locus=C3640695_1:260:508:-	-
21986	GL0093242_MH0002_[Lack_3'-end]_[mRNA]_locus=C3648634_1:3:104:-	-
23112	GL0128131_MH0002_[Complete]_[mRNA]_locus=C3684302_1:116:361:+	Bacteroides capillosus
25699	GL0050928_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold1144_2:302:937:-	Holdemania filiformis
26562	GL0019287_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold1966_2:1:1140:-	Bacteroides capillosus
27396	GL0146997_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold3559_5:59:1231:+	Streptococcus thermophilus
27504	GL0068012_MH0003_[Complete]_[mRNA]_locus=scaffold3774_2:606:2705:+	Bacteroides capillosus
27605	GL0056015_MH0003_[Complete]_[mRNA]_locus=scaffold4000_3:16:1143:-	-
28176	GL0129068_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold5338_2:952:1512:+	Bacteroides capillosus
28192	GL0115280_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold5366_3:3:563:+	Bacteroides capillosus

28515	GL0128952_MH0003_[Complete]_[mRNA]_locus=scaffold6047_1:764:1096:-	Bacteroides capillosus
28537	GL0013941_MH0003_[Complete]_[mRNA]_locus=scaffold6125_1:713:2653:-	Clostridium
28588	GL0028971_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold6336_2:1:564:-	Bacteroides capillosus
29009	GL0039256_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold7154_1:3:254:-	Bacteria
29087	GL0076884_MH0003_[Complete]_[mRNA]_locus=scaffold7337_1:4215:5390:+	Clostridium
29611	GL0051802_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold8639_3:361:1287:-	Desulfotomaculum reducens
29846	GL0098360_MH0003_[Complete]_[mRNA]_locus=scaffold9176_2:127:615:-	Bacteria
29912	GL0027901_MH0003_[Complete]_[mRNA]_locus=scaffold9358_1:51:1088:-	Klebsiella pneumoniae
30016	GL0021770_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold9520_2:2394:2894:-	Clostridiales
31165	GL0141629_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold13210_5:1:468:-	Clostridiales
31394	GL0144264_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold13664_3:1292:1567:-	Bacteria
31446	GL0022599_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold13826_3:379:768:+	-
31999	GL0104218_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold15503_3:2:499:+	-
32001	GL0104220_MH0003_[Complete]_[mRNA]_locus=scaffold15503_3:1025:1744:+	Faecalibacterium prausnitzii

32091	GL0001662_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold15750_3:371:1186:+	Bacteroides capillosus
32359	GL0099275_MH0003_[Complete]_[mRNA]_locus=scaffold16804_1:2355:3530:+	Eubacterium biforme
32516	GL0129778_MH0003_[Complete]_[mRNA]_locus=scaffold17263_2:732:2480:-	Eubacterium siraeum
32751	GL0016794_MH0003_[Complete]_[mRNA]_locus=scaffold17989_5:138:572:-	Eubacterium hallii
32755	GL0037249_MH0003_[Complete]_[mRNA]_locus=scaffold17992_5:1295:2719:-	Geobacillus
33018	GL0150058_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold19215_1:3:1070:-	Bacteroides capillosus
33071	GL0145922_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold19337_1:3:1073:-	Bacteroides capillosus
33422	GL0097915_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold20643_2:2:751:-	Clostridium leptum
33586	GL0048165_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold21194_4:1067:2365:-	Anaerotruncus colihominis
33663	GL0094867_MH0003_[Complete]_[mRNA]_locus=scaffold21446_1:276:827:-	Bacteroides capillosus
34225	GL0076390_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold23106_5:524:646:+	Bacteria
35102	GL0007436_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold25683_2:3:1001:-	Ruminococcus obeum
35936	GL0092609_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold29021_2:2419:3435:+	Roseburia inulinivorans
36125	GL0124759_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold29945_1:3:356:+	Clostridiales

36229	GL0038146_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold30287_2:2:697:-	Clostridium leptum
38065	GL0008578_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold37299_1:3:476:+	Clostridiales
38244	GL0057049_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold38323_5:1:744:+	Pedobacter
38437	GL0139552_MH0003_[Complete]_[mRNA]_locus=scaffold39290_1:745:1494:-	Capnocytophaga sputigena
38663	GL0119852_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold40613_1:2:829:-	Clostridiales
39077	GL0145418_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold42341_1:802:1023:-	Bacteroides capillosus
39370	GL0056867_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold44190_5:2:655:-	Clostridium methylpentosum
40316	GL0080368_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold49382_3:164:1300:-	Holdemania filiformis
40862	GL0146946_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold52321_2:3:554:+	Bacteroides capillosus
41358	GL0033020_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold54741_1:430:1167:-	Ruminococcaceae
41526	GL0049149_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold55781_2:2:796:+	Faecalibacterium prausnitzii
41556	GL0084218_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold55950_1:1:867:+	Bacteroides capillosus
42576	GL0046533_MH0003_[Lack_3'-end]_[mRNA]_locus=scaffold61778_1:1:2028:-	Bacteroides capillosus
42718	GL0133550_MH0003_[Complete]_[mRNA]_locus=scaffold62568_4:463:876:-	-

43576	GL0007335_MH0003_[Lack_both_end]_[mRNA]_locus=scaffold65929_1:3:524:+	Eubacterium hallii
46027	GL0112352_MH0003_[Complete]_[mRNA]_locus=scaffold75456_2:121:1029:+	-
46965	GL0071408_MH0003_[Lack_5'-end]_[mRNA]_locus=scaffold78213_3:405:605:-	-
63191	GL0122092_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold1994_1:3:647:-	Coprococcus comes
63784	GL0186656_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold3166_4:1:696:-	Ruminococcus obeum
63953	GL0034220_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold3625_2:1:720:+	Coprococcus comes
65345	GL0108117_MH0006_[Complete]_[mRNA]_locus=scaffold6995_1:126:1517:+	Clostridiales
65484	GL0099686_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold7229_2:2:892:+	-
65852	GL0189130_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold8342_3:350:706:+	Blautia hydrogenotrophica
66548	GL0002424_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold9557_3:1:585:-	Clostridiales
67400	GL0149448_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold11087_1:1:495:+	Roseburia inulinivorans
68844	GL0144329_MH0006_[Complete]_[mRNA]_locus=scaffold13691_1:2799:4046:+	Ruminococcus obeum
69313	GL0203128_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold14535_5:2:559:+	Ruminococcus obeum
70738	GL0160918_MH0006_[Complete]_[mRNA]_locus=scaffold18288_3:3902:4690:+	Clostridium

71052	GL0017380_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold18881_6:1:579:-	Bacteroides coprophilus
71259	GL0088404_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold19436_2:638:934:+	Clostridiales
71339	GL0117867_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold19740_1:1:684:+	Clostridium
72447	GL0251265_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold22739_2:1:693:-	Clostridiales
72715	GL0011973_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold23719_1:822:1655:-	Roseburia inulinivorans
72949	GL0103248_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold24386_6:2:1090:-	Clostridium
72950	GL0074028_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold24386_7:353:712:-	Bacteria
74966	GL0090190_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold30381_1:370:987:-	Clostridium acetobutylicum
74971	GL0101837_MH0006_[Complete]_[mRNA]_locus=scaffold30404_2:292:1092:-	Lachnospiraceae
76921	GL0035034_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold35372_1:2:559:-	-
77149	GL0090483_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold36118_2:2:739:-	Anaerotruncus colihominis
77183	GL0116585_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold36205_1:1:714:+	Ruminococcus obeum
77580	GL0077651_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold37303_3:2:598:-	Ruminococcus lactaris
78120	GL0058890_MH0006_[Complete]_[mRNA]_locus=scaffold38624_1:208:489:+	-

79087	GL0175226_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold41289_2:255:1799:-	Clostridiales
79746	GL0292806_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold43270_3:240:515:+	Clostridium bolteae
80638	GL0020421_MH0006_[Complete]_[mRNA]_locus=scaffold46593_3:181:1557:-	Coprococcus comes
81577	GL0176205_MH0006_[Complete]_[mRNA]_locus=scaffold50261_2:763:1716:-	Janibacter
84157	GL0135336_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold58735_1:288:1046:+	Dorea formicigenerans
84173	GL0268145_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold58767_4:282:782:-	Ruminococcus lactaris
86017	GL0273286_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold64668_2:1:297:+	Clostridiales
86018	GL0273287_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold64668_2:294:986:+	Ruminococcus obeum
86704	GL0222039_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold67392_1:1:696:-	Bacteroides fragilis
87208	GL0150442_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold69639_1:352:666:+	-
89833	GL0131504_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold79721_5:2089:2202:+	-
90312	GL0029026_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold81206_2:3848:4180:+	Bacteria
90519	GL0212573_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold82033_1:1324:2124:-	Blautia hydrogenotrophica
90520	GL0244120_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold82033_2:3:620:-	Clostridium

90760	GL0205851_MH0006_[Complete]_[mRNA]_locus=scaffold82607_3:107:646:-	-
90761	GL0161233_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold82607_4:2:1024:-	-
91964	GL0116328_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold87107_1:3:653:-	Clostridiales
92838	GL0269155_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold91065_5:871:1206:+	Dorea longicatena
92986	GL0047988_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold91731_1:533:1657:-	Bacteroides pectinophilus
93582	GL0162781_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold94177_2:1:813:+	-
94717	GL0144208_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold97878_2:1:588:-	Clostridium
94968	GL0255296_MH0006_[Complete]_[mRNA]_locus=scaffold98993_1:108:1319:+	-
95591	GL0245642_MH0006_[Complete]_[mRNA]_locus=scaffold101385_5:126:1052:-	Clostridium bolteae
95856	GL0099252_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold102455_1:1:744:+	-
96599	GL0021346_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold106232_1:3:584:+	Blautia hydrogenotrophica
98345	GL0244753_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold114586_1:3:569:+	Anaerotruncus colihominis
99073	GL0031183_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold118350_8:1:699:-	Parabacteroides distasonis
99171	GL0241500_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold118738_12:214:1029:	Clostridium methylpentosum

	-	
99173	GL0231348_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold118738_23:1:423:-	-
99291	GL0203369_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold119174_8:2:808:+	Dorea longicatena
99330	GL0029163_MH0006_[Complete]_[mRNA]_locus=scaffold119389_2:42:686:+	Faecalibacterium prausnitzii
99751	GL0264948_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold120982_1:146:760:-	-
99855	GL0212048_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold121226_1:1:399:-	-
101690	GL0203433_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold130121_1:182:508:-	Clostridiales
102657	GL0250191_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold134384_1:3:509:-	-
103933	GL0259543_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold141019_1:3:1409:-	Anaerostipes caccae
103934	GL0044562_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold141019_2:1:465:-	Clostridiales
104043	GL0265207_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold141807_3:1:303:-	-
104095	GL0002430_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold142057_1:3:770:+	Clostridium
104177	GL0064406_MH0006_[Complete]_[mRNA]_locus=scaffold142467_1:130:786:-	Ruminococcus
104759	GL0034617_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold146060_2:1:1119:+	-

104838	GL0162187_MH0006_[Complete]_[mRNA]_locus=scaffold146590_1:196:1404:-	Bacillus cereus
105064	GL0041476_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold147634_2:207:506:+	-
105254	GL0209107_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold148211_1:1:687:+	Faecalibacterium prausnitzii
106779	GL0018896_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold156168_2:3:791:+	Clostridium hiranonis
107439	GL0173315_MH0006_[Complete]_[mRNA]_locus=scaffold159924_3:78:1406:-	Clostridium nexile
107562	GL0159872_MH0006_[Complete]_[mRNA]_locus=scaffold160597_1:817:1464:-	-
107756	GL0144679_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold161515_1:1:1107:+	Clostridium thermocellum
108026	GL0161405_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold162775_2:2:331:+	Clostridiales
108138	GL0128974_MH0006_[Complete]_[mRNA]_locus=scaffold163390_5:11:991:+	-
108327	GL0252296_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold164408_1:3:674:+	Clostridium scindens
108329	GL0074464_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold164408_2:2:595:+	Coprococcus comes
108399	GL0041566_MH0006_[Complete]_[mRNA]_locus=scaffold164757_3:613:804:-	-
108556	GL0016200_MH0006_[Complete]_[mRNA]_locus=scaffold165555_1:26:1405:-	Bacteroides plebeius
109751	GL0162330_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold171519_2:3:1175:+	Clostridium hylemonae

111686	GL0272095_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold180410_2:1:708:+	Bacteroides capillosus
111892	GL0246825_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold181405_3:3:641:+	-
112012	GL0262906_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold182013_2:1:573:+	Faecalibacterium prausnitzii
112013	GL0064943_MH0006_[Complete]_[mRNA]_locus=scaffold182013_3:72:1247:+	Roseburia inulinivorans
114120	GL0291891_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold192697_2:131:583:-	Ruminococcus obeum
114274	GL0014620_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold193715_2:2:574:-	Epulopiscium
114536	GL0294413_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold195211_1:220:621:-	Anaerostipes caccae
114992	GL0046185_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold197425_1:3:521:-	Bacteria
115965	GL0029791_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold202170_3:513:1451:+	Bacteroides capillosus
117565	GL0292516_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold210367_1:106:747:-	Bacteroides capillosus
118101	GL0193240_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold213495_2:1:507:-	Clostridiales
118682	GL0236605_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold216639_3:765:1220:+	Eubacterium ventriosum
119843	GL0266333_MH0006_[Complete]_[mRNA]_locus=scaffold222142_1:309:518:+	Clostridiales
119885	GL0082902_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold222423_1:3:665:+	Clostridium scindens

120298	GL0043279_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold224704_1:1:660:+	Ruminococcus obeum
122087	GL0286042_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold233591_1:2:1705:+	Clostridiales
122088	GL0286043_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold233591_1:1709:2233:+	Dorea longicatena
122545	GL0224235_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold236012_2:1:690:-	Anaerostipes caccae
122556	GL0229633_MH0006_[Complete]_[mRNA]_locus=scaffold236114_2:12:2102:+	-
122723	GL0000724_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold237226_1:1:276:-	Clostridia
122724	GL0000725_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold237226_1:287:664:-	-
123246	GL0192013_MH0006_[Complete]_[mRNA]_locus=scaffold239799_2:246:485:+	Clostridiales
123628	GL0102858_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold241492_2:2:382:+	-
123792	GL0102910_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold242246_1:3:395:+	Bacteria
123861	GL0156491_MH0006_[Complete]_[mRNA]_locus=scaffold242696_2:2:418:+	Clostridium methylpentosum
124034	GL0283109_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold243477_1:2:415:+	-
124861	GL0047148_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold246601_2:2:775:+	Dorea formicigenerans

125789	GL0121661_MH0006_[Complete]_[mRNA]_locus=scaffold250617_1:3:668:+	-
126066	GL0150272_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold251786_3:2:514:+	Corynebacterium glutamicum
126177	GL0000815_MH0006_[Complete]_[mRNA]_locus=scaffold252334_1:237:800:-	Clostridium
126352	GL0278208_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold252836_2:3:1265:+	-
126721	GL0181458_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold254702_1:661:1215:-	Clostridium
126962	GL0050303_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold255758_4:2:742:+	Clostridiales
127166	GL0294038_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold256518_3:2:790:+	Clostridium cellulolyticum
127856	GL0205304_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold259807_3:2:739:-	Blautia hydrogenotrophica
128296	GL0039499_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold261551_3:2:958:+	Clostridium scindens
128875	GL0055185_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold264297_2:3:1421:+	-
129743	GL0040057_MH0006_[Complete]_[mRNA]_locus=scaffold267870_2:120:842:+	Bacteroides ovatus
129813	GL0041130_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold268096_1:2:667:-	Clostridium asparagiforme
130406	GL0200983_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold270422_1:171:656:+	-
131553	GL0077314_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold275794_1:2:976:-	-

133221	GL0090666_MH0006_[Complete]_[mRNA]_locus=scaffold282289_2:3491:4996:-	Ruminococcus gnavus
133505	GL0071003_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold283637_1:2:769:+	Methanosarcina barkeri
134774	GL0052587_MH0006_[Complete]_[mRNA]_locus=scaffold288638_1:39:1214:-	Bacteroidales
134928	GL0046910_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold288994_1:3:617:-	-
135040	GL0230798_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold289496_1:127:576:+	Clostridium
135146	GL0088590_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold289989_1:62:517:+	-
135326	GL0264224_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold290708_1:3:503:+	Dorea formicigenerans
135677	GL0010338_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold292061_3:1:444:-	Clostridiales
136516	GL0029253_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold295342_1:288:2951:-	Salinibacter ruber
136704	GL0145674_MH0006_[Complete]_[mRNA]_locus=scaffold296205_1:43:495:+	Dorea longicatena
136966	GL0275711_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold297316_2:2:505:+	Clostridium
137101	GL0110170_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold297838_1:169:642:+	Clostridiales
137192	GL0131970_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold298264_1:607:1554:+	Bacteroides capillosus
137686	GL0042792_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold300035_1:476:1009:+	-

137781	GL0167365_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold300332_2:1:663:+	Clostridium bolteae
138460	GL0048614_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold302781_2:744:1451:-	-
138915	GL0188986_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold304245_3:3:221:-	Clostridia
139464	GL0120422_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold306103_1:3:899:+	-
140337	GL0165598_MH0006_[Complete]_[mRNA]_locus=scaffold309197_1:62:730:+	Ruminococcus obeum
140394	GL0036977_MH0006_[Lack_both_end]_[mRNA]_locus=scaffold309443_1:2:772:+	Clostridium ramosum
140592	GL0182452_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold310206_3:2:664:+	Clostridiales
141116	GL0205069_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold311839_2:3:431:-	Clostridiales
141237	GL0032304_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold312225_1:2:1009:-	Coprococcus eutactus
141492	GL0273663_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold312902_1:903:1247:-	-
142842	GL0010305_MH0006_[Complete]_[mRNA]_locus=scaffold316181_1:92:574:+	Clostridium asparagiforme
143284	GL0000758_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold316775_1:299:1351:+	Ruminococcus torques
143505	GL0052779_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold317049_1:1:255:+	Eubacterium hallii
143506	GL0052780_MH0006_[Complete]_[mRNA]_locus=scaffold317049_1:281:1012:+	-

144794	GL0281444_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold318608_1:137:715:+	Clostridium bolteae
145156	GL0003661_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold318985_2:1704:2342:+	Clostridium
145251	GL0131019_MH0006_[Lack_3'-end]_[mRNA]_locus=scaffold319095_1:326:832:+	-
145299	GL0205040_MH0006_[Complete]_[mRNA]_locus=scaffold319146_1:290:655:+	Clostridium
145951	GL0008655_MH0006_[Lack_5'-end]_[mRNA]_locus=scaffold319764_1:72:1217:-	Enterococcus faecalis
147258	GL0263768_MH0006_[Lack_both_end]_[mRNA]_locus=C14407031_1:1:540:+	Coprococcus comes
148447	GL0099982_MH0006_[Lack_3'-end]_[mRNA]_locus=C14467301_1:319:645:+	Clostridiales
148734	GL0078146_MH0006_[Complete]_[mRNA]_locus=C14483650_1:155:472:+	Ruminococcus gnavus
149497	GL0105517_MH0006_[Lack_3'-end]_[mRNA]_locus=C14526715_1:378:809:+	Ruminococcus gnavus
150464	GL0004783_MH0006_[Lack_5'-end]_[mRNA]_locus=C14581067_1:423:1094:-	Clostridium difficile
150973	GL0216502_MH0006_[Complete]_[mRNA]_locus=C14608712_1:725:1324:-	-
156519	GL0039693_MH0008_[Lack_both_end]_[mRNA]_locus=scaffold448_1:3:596:-	-
157839	GL0032936_MH0008_[Complete]_[mRNA]_locus=scaffold7411_1:741:1100:+	-

160140	GL0002643_MH0008_[Lack_3'-end]_[mRNA]_locus=scaffold20537_5:1:144:-	-
160141	GL0003797_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold20538_4:1:708:+	-
160208	GL0014033_MH0008_[Lack_3'-end]_[mRNA]_locus=scaffold21200_1:3:185:-	-
161074	GL0002881_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold30779_1:441:695:-	-
161484	GL0042694_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold33552_1:2:496:+	-
161969	GL0030584_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold37998_1:3:182:+	-
162499	GL0023431_MH0008_[Lack_3'-end]_[mRNA]_locus=scaffold44818_1:1:717:-	-
162867	GL0026310_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold48262_2:272:601:-	-
163015	GL0035150_MH0008_[Lack_5'-end]_[mRNA]_locus=scaffold49223_3:480:692:-	-
167994	GL0051241_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold2293_2:1:129:+	-
178470	GL0142440_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold18394_1:3:518:-	-
178621	GL0030481_MH0009_[Complete]_[mRNA]_locus=scaffold18679_2:411:1496:-	Akkermansia muciniphila
187412	GL0046210_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold40753_1:1:156:+	-
188255	GL0037446_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold44479_6:247:858:-	Akkermansia muciniphila

188957	GL0136217_MH0009_[Lack_both_end]_[mRNA]_locus=scaffold47450_1:3:1097:+	Enterobacteriaceae
194855	GL0074613_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold70183_3:114:818:-	Akkermansia muciniphila
195177	GL0129815_MH0009_[Complete]_[mRNA]_locus=scaffold71576_1:76:1470:+	Bacteria
195920	GL0053982_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold74838_3:1:747:+	Akkermansia muciniphila
196238	GL0119494_MH0009_[Lack_5'-end]_[mRNA]_locus=scaffold76078_3:3:863:+	-
196853	GL0100533_MH0009_[Lack_3'-end]_[mRNA]_locus=scaffold78634_1:3:497:-	Faecalibacterium prausnitzii
202594	GL0059774_MH0009_[Complete]_[mRNA]_locus=scaffold97518_1:84:644:-	-
204667	GL0118988_MH0009_[Lack_both_end]_[mRNA]_locus=scaffold101114_2:2:757:+	Akkermansia muciniphila
205689	GL0016852_MH0009_[Complete]_[mRNA]_locus=C5204897_1:1:465:+	Akkermansia muciniphila
206265	GL0138025_MH0009_[Lack_3'-end]_[mRNA]_locus=C5223628_1:2:550:-	-
207386	GL0071599_MH0009_[Lack_5'-end]_[mRNA]_locus=C5269665_1:248:718:-	Akkermansia muciniphila
208104	GL0056284_MH0009_[Complete]_[mRNA]_locus=C5306345_1:65:916:-	Akkermansia muciniphila
210956	GL0035200_MH0010_[Complete]_[mRNA]_locus=scaffold5479_3:3833:4600:+	Faecalibacterium prausnitzii
218744	GL0113781_MH0011_[Complete]_[mRNA]_locus=scaffold14_6:39:1601:+	Bacteria

218819	GL0076794_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold55_2:2531:3586:-	-
218820	GL0106601_MH0011_[Complete]_[mRNA]_locus=scaffold55_3:512:1279:-	-
218829	GL0058563_MH0011_[Complete]_[mRNA]_locus=scaffold61_2:643:1278:-	-
219057	GL0026331_MH0011_[Complete]_[mRNA]_locus=scaffold323_3:4118:4381:+	-
219327	GL0053609_MH0011_[Complete]_[mRNA]_locus=scaffold799_1:343:1476:+	-
219522	GL0143284_MH0011_[Complete]_[mRNA]_locus=scaffold1034_1:2748:3098:+	-
219526	GL0156721_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold1065_4:578:1960:-	-
219760	GL0018640_MH0011_[Complete]_[mRNA]_locus=scaffold1136_19:103:852:+	Akkermansia muciniphila
219791	GL0141746_MH0011_[Complete]_[mRNA]_locus=scaffold1202_1:3:695:+	-
219808	GL0126145_MH0011_[Complete]_[mRNA]_locus=scaffold1251_8:664:2385:-	-
219809	GL0173738_MH0011_[Complete]_[mRNA]_locus=scaffold1251_11:13:1830:-	Faecalibacterium prausnitzii
219810	GL0173740_MH0011_[Complete]_[mRNA]_locus=scaffold1251_11:2443:3675:-	-
219811	GL0173741_MH0011_[Complete]_[mRNA]_locus=scaffold1251_11:3680:4210:-	-
219993	GL0135826_MH0011_[Complete]_[mRNA]_locus=scaffold1450_4:1676:2905:+	-

219994	GL0040420_MH0011_[Complete]_[mRNA]_locus=scaffold1450_13:5603:6496:+	-
220112	GL0050341_MH0011_[Complete]_[mRNA]_locus=scaffold1580_8:6860:8608:-	Akkermansia muciniphila
220228	GL0105761_MH0011_[Complete]_[mRNA]_locus=scaffold1710_6:204:704:+	-
220230	GL0032717_MH0011_[Complete]_[mRNA]_locus=scaffold1710_8:184:927:+	-
220603	GL0131901_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold2091_2:317:2137:-	Bacteria
220922	GL0075895_MH0011_[Complete]_[mRNA]_locus=scaffold2589_1:3276:4085:-	Akkermansia muciniphila
220946	GL0133537_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold2590_5:3:1799:+	Faecalibacterium prausnitzii
221101	GL0079847_MH0011_[Complete]_[mRNA]_locus=scaffold2901_8:1153:1827:+	-
221112	GL0121624_MH0011_[Complete]_[mRNA]_locus=scaffold2933_1:971:2194:-	-
221138	GL0135254_MH0011_[Complete]_[mRNA]_locus=scaffold2953_1:96:1055:+	Faecalibacterium prausnitzii
221471	GL0021466_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold3626_13:2:4018:-	Firmicutes
221561	GL0135880_MH0011_[Complete]_[mRNA]_locus=scaffold3842_1:1539:2447:-	-
221562	GL0135881_MH0011_[Complete]_[mRNA]_locus=scaffold3842_1:2515:3888:+	-
221571	GL0122153_MH0011_[Complete]_[mRNA]_locus=scaffold3875_6:61:879:-	-

221572	GL0122154_MH0011_[Complete]_[mRNA]_locus=scaffold3875_6:1111:1788:-	-
221908	GL0059224_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold4346_3:1:903:+	-
222430	GL0114645_MH0011_[Complete]_[mRNA]_locus=scaffold4947_2:1901:3466:+	Bacteria
222431	GL0055164_MH0011_[Complete]_[mRNA]_locus=scaffold4947_3:226:891:+	Clostridium
222496	GL0077040_MH0011_[Complete]_[mRNA]_locus=scaffold5087_2:694:870:+	Faecalibacterium prausnitzii
222560	GL0005969_MH0011_[Complete]_[mRNA]_locus=scaffold5218_1:100:555:-	-
222561	GL0123788_MH0011_[Complete]_[mRNA]_locus=scaffold5218_3:1:978:-	-
222674	GL0134371_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold5445_2:83:589:+	Bacillus clausii
222684	GL0000384_MH0011_[Complete]_[mRNA]_locus=scaffold5462_5:564:1151:-	-
222953	GL0022026_MH0011_[Complete]_[mRNA]_locus=scaffold6031_3:2216:2974:-	Clostridium beijerinckii
223125	GL0168224_MH0011_[Complete]_[mRNA]_locus=scaffold6362_10:32:703:-	Akkermansia muciniphila
223178	GL0101466_MH0011_[Complete]_[mRNA]_locus=scaffold6530_11:1402:2385:-	Akkermansia muciniphila
223181	GL0171011_MH0011_[Complete]_[mRNA]_locus=scaffold6530_20:3490:4056:+	Akkermansia muciniphila
223211	GL0031167_MH0011_[Complete]_[mRNA]_locus=scaffold6530_67:5921:6736:-	Akkermansia muciniphila

223257	GL0018035_MH0011_[Complete]_[mRNA]_locus=scaffold6673_2:13:462:-	Roseburia inulinivorans
223476	GL0085437_MH0011_[Complete]_[mRNA]_locus=scaffold7114_5:1:465:-	-
223531	GL0048391_MH0011_[Complete]_[mRNA]_locus=scaffold7206_2:2425:4470:-	Clostridium hylemonae
223700	GL0110661_MH0011_[Complete]_[mRNA]_locus=scaffold7619_2:660:2177:-	-
223870	GL0020012_MH0011_[Complete]_[mRNA]_locus=scaffold7899_5:1785:3095:-	-
224622	GL0011239_MH0011_[Complete]_[mRNA]_locus=scaffold9199_21:1843:2394:+	Akkermansia muciniphila
225287	GL0002448_MH0011_[Complete]_[mRNA]_locus=scaffold10499_2:42:2213:+	Bacteria
225321	GL0106157_MH0011_[Complete]_[mRNA]_locus=scaffold10613_6:1186:1851:+	-
225471	GL0179350_MH0011_[Complete]_[mRNA]_locus=scaffold10892_3:60:1829:-	Clostridiales
225585	GL0146445_MH0011_[Complete]_[mRNA]_locus=scaffold11141_3:1784:3007:-	-
225771	GL0099438_MH0011_[Complete]_[mRNA]_locus=scaffold11482_1:3129:4883:+	Clostridium asparagiforme
225772	GL0178902_MH0011_[Complete]_[mRNA]_locus=scaffold11482_2:1237:3669:+	-
225778	GL0083241_MH0011_[Complete]_[mRNA]_locus=scaffold11503_6:351:1637:-	Clostridium thermocellum
225872	GL0129925_MH0011_[Complete]_[mRNA]_locus=scaffold11675_1:2929:3996:+	Clostridium

225891	GL0111286_MH0011_[Complete]_[mRNA]_locus=scaffold11741_11:122:1120:+	Catenibacterium mitsuokai
225908	GL0096580_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold11816_1:4:906:-	-
225909	GL0063280_MH0011_[Complete]_[mRNA]_locus=scaffold11816_2:1229:2596:+	Roseburia inulinivorans
225994	GL0037879_MH0011_[Complete]_[mRNA]_locus=scaffold11985_5:182:2410:-	Enterococcus faecalis
226216	GL0110190_MH0011_[Complete]_[mRNA]_locus=scaffold12419_3:1987:3153:-	-
226291	GL0142752_MH0011_[Complete]_[mRNA]_locus=scaffold12554_3:651:2129:-	Dehalococcoides ethenogenes
226327	GL0177011_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold12688_1:2:979:-	-
226328	GL0097167_MH0011_[Complete]_[mRNA]_locus=scaffold12688_2:14:820:+	-
226335	GL0106547_MH0011_[Complete]_[mRNA]_locus=scaffold12699_3:1350:2243:-	-
226383	GL0158649_MH0011_[Complete]_[mRNA]_locus=scaffold12802_1:419:1342:+	-
226840	GL0106954_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold13655_2:1048:1770:+	Anaerotruncus colihominis
226980	GL0151603_MH0011_[Complete]_[mRNA]_locus=scaffold14170_3:1468:2442:-	Clostridiales
226981	GL0017614_MH0011_[Complete]_[mRNA]_locus=scaffold14170_7:2132:2773:-	-

227491	GL0134374_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold14884_2:2:793:+	Dorea formicigenerans
227492	GL0134375_MH0011_[Complete]_[mRNA]_locus=scaffold14884_2:790:3699:+	Clostridiales
228867	GL0002176_MH0011_[Complete]_[mRNA]_locus=scaffold17880_8:2196:4631:+	Akkermansia muciniphila
229325	GL0081596_MH0011_[Complete]_[mRNA]_locus=scaffold19267_1:738:1724:+	-
229406	GL0019928_MH0011_[Complete]_[mRNA]_locus=scaffold19515_2:6:1844:-	Faecalibacterium prausnitzii
229520	GL0125563_MH0011_[Complete]_[mRNA]_locus=scaffold19860_3:605:1090:-	-
229792	GL0038247_MH0011_[Complete]_[mRNA]_locus=scaffold20582_11:136:1128:+	-
229913	GL0093991_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold20862_1:11:913:-	Clostridium nexile
230245	GL0159305_MH0011_[Complete]_[mRNA]_locus=scaffold21629_5:9:1160:-	-
230246	GL0172603_MH0011_[Complete]_[mRNA]_locus=scaffold21629_6:1244:2050:-	-
230376	GL0012971_MH0011_[Complete]_[mRNA]_locus=scaffold21880_2:617:1789:-	Faecalibacterium prausnitzii
230705	GL0094300_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold22986_9:2:652:+	-
230706	GL0042121_MH0011_[Complete]_[mRNA]_locus=scaffold22986_10:653:1228:+	-
230884	GL0038339_MH0011_[Complete]_[mRNA]_locus=scaffold23644_1:3195:4181:+	Roseburia inulinivorans

230885	GL0038341_MH0011_[Complete]_[mRNA]_locus=scaffold23644_1:5147:6145:-	-
230886	GL0038342_MH0011_[Complete]_[mRNA]_locus=scaffold23644_1:6272:6925:-	-
230887	GL0038343_MH0011_[Complete]_[mRNA]_locus=scaffold23644_1:6922:8889:-	-
230888	GL0111509_MH0011_[Complete]_[mRNA]_locus=scaffold23644_3:4821:6713:-	-
230892	GL0149477_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold23646_3:1072:1299:-	-
231131	GL0095014_MH0011_[Complete]_[mRNA]_locus=scaffold24260_5:94:690:+	Faecalibacterium prausnitzii
231208	GL0135162_MH0011_[Complete]_[mRNA]_locus=scaffold24528_2:165:1577:-	-
231477	GL0148534_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold25037_6:820:1824:-	Clostridium
231560	GL0015415_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold25294_1:3:968:+	Bacteroides capillosus
232072	GL0182312_MH0011_[Complete]_[mRNA]_locus=scaffold26556_4:814:2013:-	Akkermansia muciniphila
232073	GL0182325_MH0011_[Complete]_[mRNA]_locus=scaffold26556_4:10162:11316:+	Akkermansia muciniphila
232174	GL0134902_MH0011_[Complete]_[mRNA]_locus=scaffold26869_2:208:990:+	-
232251	GL0118412_MH0011_[Complete]_[mRNA]_locus=scaffold27353_2:77:982:-	-
232287	GL0063882_MH0011_[Complete]_[mRNA]_locus=scaffold27540_4:182:1036:-	-

232288	GL0025968_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold27540_6:2:148:-	-
232531	GL0080186_MH0011_[Complete]_[mRNA]_locus=scaffold28281_1:2632:3600:-	-
232759	GL0147950_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold29136_5:31:1110:-	-
232867	GL0047494_MH0011_[Complete]_[mRNA]_locus=scaffold29464_1:33:410:-	-
232918	GL0168883_MH0011_[Complete]_[mRNA]_locus=scaffold29554_2:295:897:-	Streptococcus mutans
233237	GL0105291_MH0011_[Complete]_[mRNA]_locus=scaffold30723_3:19:1794:+	-
234262	GL0176892_MH0011_[Complete]_[mRNA]_locus=scaffold34022_1:4800:6302:-	-
234419	GL0121805_MH0011_[Complete]_[mRNA]_locus=scaffold34605_4:1979:2560:-	Akkermansia muciniphila
234422	GL0067448_MH0011_[Complete]_[mRNA]_locus=scaffold34605_16:4647:5387:-	Akkermansia muciniphila
234427	GL0034235_MH0011_[Complete]_[mRNA]_locus=scaffold34605_34:1860:2768:-	Akkermansia muciniphila
234683	GL0175451_MH0011_[Complete]_[mRNA]_locus=scaffold35764_1:421:972:+	Alphaproteobacteria
235164	GL0080389_MH0011_[Complete]_[mRNA]_locus=scaffold37430_16:3912:4748:-	Akkermansia muciniphila
235352	GL0101912_MH0011_[Complete]_[mRNA]_locus=scaffold38061_6:541:1605:+	-
235382	GL0160261_MH0011_[Complete]_[mRNA]_locus=scaffold38183_2:3781:4356:-	-

235383	GL0160265_MH0011_[Complete]_[mRNA]_locus=scaffold38183_2:6158:6394:+	-
235391	GL0117430_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold38228_4:3:7478:+	Anaerostipes caccae
235981	GL0098557_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold40158_2:1:858:-	Bacteria
236484	GL0138226_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold42377_2:1436:1981:-	Faecalibacterium prausnitzii
236701	GL0079896_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold43318_2:2:511:+	Clostridium leptum
237403	GL0112801_MH0011_[Complete]_[mRNA]_locus=scaffold45816_13:1520:2455:+	Akkermansia muciniphila
237441	GL0026942_MH0011_[Complete]_[mRNA]_locus=scaffold46023_1:21:1580:-	-
237564	GL0002675_MH0011_[Complete]_[mRNA]_locus=scaffold46560_1:808:1293:-	-
237884	GL0129877_MH0011_[Complete]_[mRNA]_locus=scaffold47823_6:1539:3548:-	Clostridium botulinum
238640	GL0047947_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold50925_1:3:152:+	-
238840	GL0176723_MH0011_[Complete]_[mRNA]_locus=scaffold51784_4:265:960:+	-
239857	GL0102073_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold56625_2:2:505:+	Bacteria
240284	GL0084350_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold58612_8:31:1143:-	-
241204	GL0181277_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold62712_1:60:506:+	Clostridium nexile

241380	GL0030667_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold63297_2:1:411:+	Clostridium
241416	GL0044243_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold63542_2:1:402:+	Bacteroides capillosus
243992	GL0156917_MH0011_[Complete]_[mRNA]_locus=scaffold75291_1:512:1201:+	-
244242	GL0095453_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold76332_3:2:508:-	Clostridiales
244405	GL0178250_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold77093_1:1:366:+	-
244936	GL0085277_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold79932_2:2:913:-	Enterocytozoon bieneusi
245225	GL0072842_MH0011_[Complete]_[mRNA]_locus=scaffold81049_3:2:358:+	-
245433	GL0170434_MH0011_[Complete]_[mRNA]_locus=scaffold82248_1:1:501:+	Clostridium
246221	GL0176865_MH0011_[Complete]_[mRNA]_locus=scaffold85845_3:529:1344:+	Ruminococcus torques
247647	GL0083441_MH0011_[Lack_3'-end]_[mRNA]_locus=scaffold91895_2:223:786:+	Clostridium asparagiforme
248333	GL0109323_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold94736_1:3:506:+	Bacteria
249608	GL0082609_MH0011_[Lack_both_end]_[mRNA]_locus=scaffold100609_1:3:656:+	Clostridium methylpentosum
250293	GL0135215_MH0011_[Complete]_[mRNA]_locus=scaffold103191_1:1:411:+	Bacteroides capillosus
252786	GL0134219_MH0011_[Complete]_[mRNA]_locus=scaffold110397_1:270:1595:+	-

253391	GL0148550_MH0011_[Complete]_[mRNA]_locus=scaffold111611_1:1691:2176:+	Clostridium
253991	GL0136358_MH0011_[Complete]_[mRNA]_locus=scaffold113119_1:415:1269:+	-
256607	GL0048803_MH0011_[Lack_5'-end]_[mRNA]_locus=scaffold116666_2:3:464:+	-
256832	GL0087131_MH0011_[Complete]_[mRNA]_locus=scaffold116886_1:479:928:+	-
258252	GL0024671_MH0011_[Complete]_[mRNA]_locus=C5271820_1:182:520:+	Bacteroides capillosus
258275	GL0024337_MH0011_[Lack_3'-end]_[mRNA]_locus=C5272662_1:2:394:-	Clostridiales
258582	GL0004684_MH0011_[Lack_5'-end]_[mRNA]_locus=C5281988_1:2:433:+	Clostridium
259256	GL0086249_MH0011_[Lack_3'-end]_[mRNA]_locus=C5302282_1:458:616:+	Clostridium leptum
259547	GL0060043_MH0011_[Complete]_[mRNA]_locus=C5311590_1:20:580:-	-
260783	GL0184768_MH0011_[Lack_5'-end]_[mRNA]_locus=C5354128_1:460:840:-	Bacteroides capillosus
263245	GL0050135_MH0012_[Complete]_[mRNA]_locus=scaffold10_1:1226:3808:+	Bacteria
263565	GL0009214_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold147_4:3:875:+	Rhizobium leguminosarum
264543	GL0005721_MH0012_[Complete]_[mRNA]_locus=scaffold539_6:524:2785:-	Bacteria
266474	GL0275841_MH0012_[Complete]_[mRNA]_locus=scaffold1325_5:5768:7507:+	Akkermansia muciniphila

269035	GL0044243_MH0012_[Complete]_[mRNA]_locus=scaffold2352_2:18401:18850:-	Akkermansia muciniphila
269065	GL0153843_MH0012_[Complete]_[mRNA]_locus=scaffold2366_7:7112:7753:+	Akkermansia muciniphila
269066	GL0067038_MH0012_[Complete]_[mRNA]_locus=scaffold2366_8:3352:4044:+	Akkermansia muciniphila
269466	GL0043416_MH0012_[Complete]_[mRNA]_locus=scaffold2505_1:403:1209:-	Akkermansia muciniphila
269467	GL0220512_MH0012_[Complete]_[mRNA]_locus=scaffold2505_3:3392:4348:+	Faecalibacterium prausnitzii
269469	GL0220529_MH0012_[Complete]_[mRNA]_locus=scaffold2505_3:20338:20646:-	Akkermansia muciniphila
269538	GL0158336_MH0012_[Complete]_[mRNA]_locus=scaffold2559_2:8637:9185:-	Akkermansia muciniphila
269540	GL0213704_MH0012_[Complete]_[mRNA]_locus=scaffold2559_5:6669:7922:-	Akkermansia muciniphila
269543	GL0231595_MH0012_[Complete]_[mRNA]_locus=scaffold2559_7:7907:8926:-	Akkermansia muciniphila
269544	GL0231601_MH0012_[Complete]_[mRNA]_locus=scaffold2559_7:15719:16861:-	Akkermansia muciniphila
269547	GL0158662_MH0012_[Complete]_[mRNA]_locus=scaffold2559_9:17396:18727:+	Akkermansia muciniphila
269550	GL0158676_MH0012_[Complete]_[mRNA]_locus=scaffold2559_9:38476:39225:+	Akkermansia muciniphila
269555	GL0184793_MH0012_[Complete]_[mRNA]_locus=scaffold2559_12:4919:5560:-	Akkermansia muciniphila
269707	GL0233259_MH0012_[Complete]_[mRNA]_locus=scaffold2610_1:2569:3405:+	Akkermansia muciniphila

269708	GL0091210_MH0012_[Complete]_[mRNA]_locus=scaffold2610_3:497:1339:-	Akkermansia muciniphila
269727	GL0181880_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold2610_5:26758:27867:-	Akkermansia muciniphila
269728	GL0082094_MH0012_[Complete]_[mRNA]_locus=scaffold2610_7:6765:8522:+	Verrucomicrobia
269731	GL0311168_MH0012_[Complete]_[mRNA]_locus=scaffold2610_12:1138:3369:+	Akkermansia muciniphila
269733	GL0269183_MH0012_[Complete]_[mRNA]_locus=scaffold2610_17:7951:10338:+	Akkermansia muciniphila
269734	GL0182945_MH0012_[Complete]_[mRNA]_locus=scaffold2610_18:28525:29475:-	Akkermansia muciniphila
269735	GL0182947_MH0012_[Complete]_[mRNA]_locus=scaffold2610_18:30599:31618:-	Akkermansia muciniphila
269738	GL0053344_MH0012_[Complete]_[mRNA]_locus=scaffold2610_25:104:2371:-	Bacteria
269740	GL0053348_MH0012_[Complete]_[mRNA]_locus=scaffold2610_25:5735:7087:-	Akkermansia muciniphila
273301	GL0066693_MH0012_[Complete]_[mRNA]_locus=scaffold4193_2:50:280:+	-
277302	GL0075477_MH0012_[Complete]_[mRNA]_locus=scaffold6345_2:8625:9425:+	Akkermansia muciniphila
277806	GL0019494_MH0012_[Complete]_[mRNA]_locus=scaffold6676_1:10294:13836:+	Akkermansia muciniphila
280508	GL0031149_MH0012_[Complete]_[mRNA]_locus=scaffold7942_2:3160:3822:-	Akkermansia muciniphila

280510	GL0031156_MH0012_[Complete]_[mRNA]_locus=scaffold7942_2:11721:13238:+	Akkermansia muciniphila
280514	GL0092996_MH0012_[Complete]_[mRNA]_locus=scaffold7942_3:16201:17049:-	Akkermansia muciniphila
280694	GL0198536_MH0012_[Complete]_[mRNA]_locus=scaffold8052_4:10427:12226:+	Akkermansia muciniphila
280697	GL0003868_MH0012_[Complete]_[mRNA]_locus=scaffold8052_8:18783:22652:+	Bacteria
280698	GL0003872_MH0012_[Complete]_[mRNA]_locus=scaffold8052_8:28399:29469:-	Akkermansia muciniphila
280699	GL0003873_MH0012_[Complete]_[mRNA]_locus=scaffold8052_8:29906:31150:-	Akkermansia muciniphila
283773	GL0015893_MH0012_[Complete]_[mRNA]_locus=scaffold9686_4:13326:14057:-	Akkermansia muciniphila
283777	GL0136176_MH0012_[Complete]_[mRNA]_locus=scaffold9686_9:3183:5294:-	Bacteria
283781	GL0136188_MH0012_[Complete]_[mRNA]_locus=scaffold9686_9:17271:18224:-	Akkermansia muciniphila
285531	GL0283754_MH0012_[Complete]_[mRNA]_locus=scaffold10924_3:757:975:-	Firmicutes
286523	GL0022597_MH0012_[Complete]_[mRNA]_locus=scaffold11521_1:9426:10715:-	Verrucomicrobiaceae
287429	GL0146622_MH0012_[Complete]_[mRNA]_locus=scaffold12135_2:5226:6890:-	Akkermansia muciniphila
289443	GL0191940_MH0012_[Complete]_[mRNA]_locus=scaffold13449_4:11509:13167:+	Verrucomicrobia
289444	GL0191941_MH0012_[Complete]_[mRNA]_locus=scaffold13449_4:13239:14507:+	Akkermansia muciniphila

289445	GL0191944_MH0012_[Complete]_[mRNA]_locus=scaffold13449_4:16282:17139:+	Akkermansia muciniphila
290005	GL0086248_MH0012_[Complete]_[mRNA]_locus=scaffold13974_1:1718:3325:-	Bacteria
290110	GL0029313_MH0012_[Complete]_[mRNA]_locus=scaffold14050_1:8830:10992:+	Bacteroides coprocola
291633	GL0186139_MH0012_[Complete]_[mRNA]_locus=scaffold15176_7:13773:15779:-	Verrucomicrobiaceae
292023	GL0038011_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold15534_4:777:2084:+	Clostridium
294270	GL0146995_MH0012_[Complete]_[mRNA]_locus=scaffold16979_3:7669:9033:-	Akkermansia muciniphila
294388	GL0147304_MH0012_[Complete]_[mRNA]_locus=scaffold17013_4:1785:3512:-	Akkermansia muciniphila
297083	GL0002058_MH0012_[Complete]_[mRNA]_locus=scaffold19101_3:13811:14989:-	Akkermansia muciniphila
297086	GL0086529_MH0012_[Complete]_[mRNA]_locus=scaffold19101_4:12849:13721:+	Akkermansia muciniphila
297087	GL0159633_MH0012_[Complete]_[mRNA]_locus=scaffold19101_6:1531:2466:-	Akkermansia muciniphila
297091	GL0287498_MH0012_[Complete]_[mRNA]_locus=scaffold19101_7:9729:11015:+	Akkermansia muciniphila
297092	GL0287502_MH0012_[Complete]_[mRNA]_locus=scaffold19101_7:13969:15171:+	Akkermansia muciniphila
297093	GL0287510_MH0012_[Complete]_[mRNA]_locus=scaffold19101_7:24374:25417:-	Akkermansia muciniphila
300628	GL0061701_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold22160_3:3:950:+	Clostridia

304045	GL0208193_MH0012_[Complete]_[mRNA]_locus=scaffold25621_4:10208:12262:+	Akkermansia muciniphila
304052	GL0283744_MH0012_[Complete]_[mRNA]_locus=scaffold25621_7:907:2097:-	Akkermansia muciniphila
304720	GL0158155_MH0012_[Complete]_[mRNA]_locus=scaffold26061_4:5999:7039:-	Akkermansia muciniphila
304721	GL0106642_MH0012_[Complete]_[mRNA]_locus=scaffold26061_5:8032:9552:+	Akkermansia muciniphila
305014	GL0293977_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold26425_5:1:1824:-	-
306583	GL0093908_MH0012_[Complete]_[mRNA]_locus=scaffold27921_2:10557:11159:+	Akkermansia muciniphila
306584	GL0093911_MH0012_[Complete]_[mRNA]_locus=scaffold27921_2:12649:13635:+	Akkermansia muciniphila
306585	GL0093919_MH0012_[Complete]_[mRNA]_locus=scaffold27921_2:19146:20159:-	Akkermansia muciniphila
307539	GL0076300_MH0012_[Complete]_[mRNA]_locus=scaffold28794_1:11411:12835:-	Akkermansia muciniphila
307543	GL0128813_MH0012_[Complete]_[mRNA]_locus=scaffold28794_3:6017:7315:-	Akkermansia muciniphila
307544	GL0154576_MH0012_[Complete]_[mRNA]_locus=scaffold28794_6:11347:12183:+	Akkermansia muciniphila
307546	GL0154579_MH0012_[Complete]_[mRNA]_locus=scaffold28794_6:16817:18094:+	Akkermansia muciniphila
308832	GL0124663_MH0012_[Complete]_[mRNA]_locus=scaffold30256_5:202:4140:-	Bacteria
310632	GL0184772_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold32106_4:1479:1853:-	Akkermansia muciniphila

313193	GL0031716_MH0012_[Complete]_[mRNA]_locus=scaffold34825_4:4551:5051:+	Akkermansia muciniphila
315194	GL0252722_MH0012_[Complete]_[mRNA]_locus=scaffold37275_2:234:1622:-	Akkermansia muciniphila
315628	GL0306389_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold37692_2:1155:2072:-	Bacteria
321709	GL0273098_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold44806_2:13:1560:+	Clostridiaceae
322568	GL0268501_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold45904_3:373:1140:-	Coprococcus comes
323416	GL0138676_MH0012_[Complete]_[mRNA]_locus=scaffold47130_1:1531:2031:-	Parabacteroides merdae
323563	GL0138932_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold47267_2:43:672:+	-
323944	GL0055152_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold47700_2:2:1891:+	Clostridiales
325409	GL0234750_MH0012_[Complete]_[mRNA]_locus=scaffold49778_8:527:709:-	-
326922	GL0289331_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold52024_2:670:897:-	Clostridiales
327513	GL0185748_MH0012_[Complete]_[mRNA]_locus=scaffold52769_2:901:1314:+	-
333796	GL0176561_MH0012_[Complete]_[mRNA]_locus=scaffold62541_2:5942:7264:-	Akkermansia muciniphila
334181	GL0216893_MH0012_[Complete]_[mRNA]_locus=scaffold63215_1:237:2309:+	-
334936	GL0183022_MH0012_[Complete]_[mRNA]_locus=scaffold64366_5:13:519:-	Clostridia

335584	GL0261791_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold65699_2:2:2656:-	Heliobacterium modesticaldum
335587	GL0050256_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold65699_3:495:1157:-	-
338312	GL0048679_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold70652_3:3:908:+	Holdemania filiformis
338744	GL0115260_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold71506_2:2:2191:-	Alkaliphilus
339150	GL0227246_MH0012_[Complete]_[mRNA]_locus=scaffold72261_1:521:1606:+	Eubacterium siraeum
339288	GL0135715_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold72467_2:158:655:+	Bacteroides
339291	GL0284561_MH0012_[Complete]_[mRNA]_locus=scaffold72467_4:296:910:+	Clostridium leptum
339818	GL0203696_MH0012_[Complete]_[mRNA]_locus=scaffold73602_1:200:889:+	Bacteria
342157	GL0135257_MH0012_[Complete]_[mRNA]_locus=scaffold77934_1:3243:4016:-	Akkermansia muciniphila
342159	GL0135261_MH0012_[Complete]_[mRNA]_locus=scaffold77934_1:8418:9440:+	Akkermansia muciniphila
346251	GL0284317_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold85857_4:215:1243:-	Clostridia
351771	GL0118856_MH0012_[Complete]_[mRNA]_locus=scaffold97141_4:7269:8423:+	Akkermansia muciniphila
352100	GL0284304_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold97881_1:333:1013:-	-

353019	GL0079491_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold99889_2:1:477:-	Clostridium bartlettii
353924	GL0116233_MH0012_[Complete]_[mRNA]_locus=scaffold102038_2:1621:1992:+	Akkermansia muciniphila
353925	GL0116236_MH0012_[Complete]_[mRNA]_locus=scaffold102038_2:3313:4443:+	Akkermansia muciniphila
360843	GL0016890_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold118680_5:3:764:+	Clostridium bartlettii
361168	GL0242859_MH0012_[Complete]_[mRNA]_locus=scaffold119507_1:58:2760:-	Bacteria
363265	GL0045664_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold124176_2:641:1495:+	Clostridium hiranonis
364931	GL0084924_MH0012_[Complete]_[mRNA]_locus=scaffold128252_1:252:1298:-	Akkermansia muciniphila
364932	GL0084925_MH0012_[Complete]_[mRNA]_locus=scaffold128252_1:1319:3004:-	Akkermansia muciniphila
374150	GL0262880_MH0012_[Complete]_[mRNA]_locus=scaffold150785_1:158:988:+	Alkaliphilus oremlandii
375160	GL0155844_MH0012_[Lack_5'-end]_[mRNA]_locus=scaffold152822_2:64:831:-	Clostridiales
377289	GL0034733_MH0012_[Complete]_[mRNA]_locus=scaffold156831_1:1983:3260:-	Akkermansia muciniphila
382810	GL0101950_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold167032_1:1270:1992:+	Alkaliphilus oremlandii
383963	GL0170196_MH0012_[Lack_3'-end]_[mRNA]_locus=scaffold168602_5:215:1414:+	Eubacterium ventriosum

384134	GL0144615_MH0012_[Lack_both_end]_[mRNA]_locus=scaffold168818_4:2:577:+	Anaerofustis stercorihominis
388033	GL0186539_MH0012_[Complete]_[mRNA]_locus=scaffold174033_2:78:1103:-	Candidatus Solibacter usitatus
399741	GL0172296_MH0012_[Complete]_[mRNA]_locus=C18759098_1:609:875:-	-
402852	GL0037195_MH0013_[Complete]_[mRNA]_locus=scaffold8_2:2659:3153:+	Akkermansia muciniphila
402856	GL0012462_MH0013_[Complete]_[mRNA]_locus=scaffold25_1:5093:6484:+	Akkermansia muciniphila
402858	GL0012469_MH0013_[Complete]_[mRNA]_locus=scaffold25_1:13103:14524:+	Akkermansia muciniphila
402859	GL0012470_MH0013_[Complete]_[mRNA]_locus=scaffold25_1:14543:15511:+	Akkermansia muciniphila
402861	GL0012477_MH0013_[Complete]_[mRNA]_locus=scaffold25_1:24339:27005:+	Akkermansia muciniphila
402862	GL0012478_MH0013_[Complete]_[mRNA]_locus=scaffold25_1:26995:27462:+	Akkermansia muciniphila
402920	GL0002711_MH0013_[Complete]_[mRNA]_locus=scaffold335_4:6353:6940:+	Akkermansia muciniphila
402921	GL0016440_MH0013_[Complete]_[mRNA]_locus=scaffold335_6:677:1567:+	Akkermansia muciniphila
402922	GL0016441_MH0013_[Complete]_[mRNA]_locus=scaffold335_6:1586:2200:+	Akkermansia muciniphila
403033	GL0044975_MH0013_[Complete]_[mRNA]_locus=scaffold612_1:3735:4991:+	Akkermansia muciniphila

403034	GL0013548_MH0013_[Complete]_[mRNA]_locus=scaffold612_3:973:2631:-	Akkermansia muciniphila
403036	GL0013557_MH0013_[Complete]_[mRNA]_locus=scaffold612_3:8482:9456:-	Akkermansia muciniphila
403037	GL0013558_MH0013_[Complete]_[mRNA]_locus=scaffold612_3:9478:10479:-	Akkermansia muciniphila
403969	GL0031567_MH0013_[Complete]_[mRNA]_locus=scaffold4483_4:3098:4513:+	Akkermansia muciniphila
403971	GL0031570_MH0013_[Complete]_[mRNA]_locus=scaffold4483_4:6360:7577:-	Akkermansia muciniphila
404228	GL0041038_MH0013_[Complete]_[mRNA]_locus=scaffold5549_4:27902:28879:-	Akkermansia muciniphila
404233	GL0034363_MH0013_[Complete]_[mRNA]_locus=scaffold5549_7:5152:6384:+	Akkermansia muciniphila
404335	GL0006087_MH0013_[Complete]_[mRNA]_locus=scaffold6105_1:1502:2665:-	Akkermansia muciniphila
404461	GL0021152_MH0013_[Complete]_[mRNA]_locus=scaffold6726_2:4604:5968:-	Akkermansia muciniphila
404462	GL0021153_MH0013_[Complete]_[mRNA]_locus=scaffold6726_2:5965:6669:-	Akkermansia muciniphila
404465	GL0011030_MH0013_[Complete]_[mRNA]_locus=scaffold6726_3:13375:15276:-	Akkermansia muciniphila
404554	GL0029198_MH0013_[Complete]_[mRNA]_locus=scaffold7370_2:34:3033:-	Akkermansia muciniphila
404560	GL0026019_MH0013_[Complete]_[mRNA]_locus=scaffold7370_5:3855:6962:-	Bacteria
404561	GL0000011_MH0013_[Complete]_[mRNA]_locus=scaffold7370_7:256:759:+	Akkermansia muciniphila

404613	GL0044993_MH0013_[Complete]_[mRNA]_locus=scaffold7589_3:2069:3064:+	Akkermansia muciniphila
405409	GL0037928_MH0013_[Complete]_[mRNA]_locus=scaffold12616_1:2041:3246:+	Akkermansia muciniphila
405411	GL0037932_MH0013_[Complete]_[mRNA]_locus=scaffold12616_1:5656:7056:-	Verrucomicrobia
405412	GL0037933_MH0013_[Complete]_[mRNA]_locus=scaffold12616_1:7132:8412:-	Akkermansia muciniphila
405437	GL0023916_MH0013_[Complete]_[mRNA]_locus=scaffold12734_2:9598:10986:-	Akkermansia muciniphila
405443	GL0023924_MH0013_[Complete]_[mRNA]_locus=scaffold12734_2:21778:22578:+	Akkermansia muciniphila
405444	GL0023926_MH0013_[Complete]_[mRNA]_locus=scaffold12734_2:23431:24435:+	Akkermansia muciniphila
405446	GL0023932_MH0013_[Complete]_[mRNA]_locus=scaffold12734_2:28369:29442:+	Akkermansia muciniphila
405691	GL0019828_MH0013_[Complete]_[mRNA]_locus=scaffold14125_1:1642:2748:+	Akkermansia muciniphila
405867	GL0013907_MH0013_[Complete]_[mRNA]_locus=scaffold15134_2:2379:3578:+	Akkermansia muciniphila
405868	GL0013908_MH0013_[Complete]_[mRNA]_locus=scaffold15134_2:3644:5440:-	Akkermansia muciniphila
405922	GL0023484_MH0013_[Complete]_[mRNA]_locus=scaffold15697_3:168:1046:-	Akkermansia muciniphila
405923	GL0026751_MH0013_[Complete]_[mRNA]_locus=scaffold15697_9:3264:4034:+	Akkermansia muciniphila
406070	GL0029868_MH0013_[Complete]_[mRNA]_locus=scaffold16760_2:7236:7769:-	Geobacillus kaustophilus

406071	GL0029870_MH0013_[Complete]_[mRNA]_locus=scaffold16760_2:8697:9548:-	Akkermansia muciniphila
406072	GL0029881_MH0013_[Complete]_[mRNA]_locus=scaffold16760_2:16537:17301:-	Akkermansia muciniphila
406073	GL0029883_MH0013_[Complete]_[mRNA]_locus=scaffold16760_2:17777:18427:-	Akkermansia muciniphila
406080	GL0000002_MH0013_[Complete]_[mRNA]_locus=scaffold16859_5:884:1096:-	-
406084	GL0022009_MH0013_[Complete]_[mRNA]_locus=scaffold16859_11:635:2278:+	Akkermansia muciniphila
406089	GL0024380_MH0013_[Complete]_[mRNA]_locus=scaffold16859_13:7381:8709:-	Akkermansia muciniphila
406090	GL0031418_MH0013_[Complete]_[mRNA]_locus=scaffold16859_14:6804:9380:+	Bacteria
406092	GL0005928_MH0013_[Complete]_[mRNA]_locus=scaffold16859_16:1438:2538:+	Akkermansia muciniphila
406260	GL0031675_MH0013_[Complete]_[mRNA]_locus=scaffold18144_2:1407:2282:-	Akkermansia muciniphila
406265	GL0043730_MH0013_[Complete]_[mRNA]_locus=scaffold18144_3:10845:12878:+	root
406268	GL0043737_MH0013_[Complete]_[mRNA]_locus=scaffold18144_3:20809:21915:+	Akkermansia muciniphila
406606	GL0022063_MH0013_[Complete]_[mRNA]_locus=scaffold20324_2:8122:9267:-	Akkermansia muciniphila
406608	GL0022071_MH0013_[Complete]_[mRNA]_locus=scaffold20324_2:18529:19428:-	Akkermansia muciniphila
406609	GL0022072_MH0013_[Complete]_[mRNA]_locus=scaffold20324_2:19425:20918:-	Bacteria

406610	GL0022075_MH0013_[Complete]_[mRNA]_locus=scaffold20324_2:24122:26119:+	Akkermansia muciniphila
407198	GL0028185_MH0013_[Complete]_[mRNA]_locus=scaffold24129_1:6017:7162:+	Akkermansia muciniphila
407200	GL0028187_MH0013_[Complete]_[mRNA]_locus=scaffold24129_1:8375:10894:+	Verrucomicrobiaceae
407203	GL0028193_MH0013_[Complete]_[mRNA]_locus=scaffold24129_1:16482:17408:+	Akkermansia muciniphila
407204	GL0028201_MH0013_[Complete]_[mRNA]_locus=scaffold24129_1:26439:28493:+	Akkermansia muciniphila
407444	GL0025939_MH0013_[Complete]_[mRNA]_locus=scaffold26202_1:2348:3913:-	Bacteria
407446	GL0012895_MH0013_[Complete]_[mRNA]_locus=scaffold26202_2:3650:4075:-	Akkermansia muciniphila
407596	GL0044084_MH0013_[Complete]_[mRNA]_locus=scaffold27516_2:6356:7147:+	Akkermansia muciniphila
407598	GL0036884_MH0013_[Complete]_[mRNA]_locus=scaffold27516_3:2653:4458:+	Akkermansia muciniphila
407847	GL0023313_MH0013_[Complete]_[mRNA]_locus=scaffold28964_2:32:1150:-	Akkermansia muciniphila
407848	GL0040083_MH0013_[Complete]_[mRNA]_locus=scaffold28964_3:689:1537:-	Akkermansia muciniphila
407849	GL0016494_MH0013_[Complete]_[mRNA]_locus=scaffold28964_5:827:2008:+	Akkermansia muciniphila
408378	GL0009163_MH0013_[Complete]_[mRNA]_locus=scaffold32560_2:692:3283:-	Akkermansia muciniphila
408379	GL0009164_MH0013_[Complete]_[mRNA]_locus=scaffold32560_2:3291:4130:-	Akkermansia muciniphila

408509	GL0030620_MH0013_[Complete]_[mRNA]_locus=scaffold33760_1:15412:16152:+	Akkermansia muciniphila
408515	GL0034537_MH0013_[Complete]_[mRNA]_locus=scaffold33760_4:677:1801:+	Akkermansia muciniphila
408516	GL0034540_MH0013_[Complete]_[mRNA]_locus=scaffold33760_4:5148:6047:+	Akkermansia muciniphila
408582	GL0023489_MH0013_[Complete]_[mRNA]_locus=scaffold34236_7:1995:2510:+	Akkermansia muciniphila
408584	GL0023494_MH0013_[Complete]_[mRNA]_locus=scaffold34236_7:11017:13257:+	Akkermansia muciniphila
408765	GL0030845_MH0013_[Complete]_[mRNA]_locus=scaffold35402_2:307:1455:-	Akkermansia muciniphila
408766	GL0040507_MH0013_[Complete]_[mRNA]_locus=scaffold35402_3:389:1732:-	Akkermansia muciniphila
408770	GL0018538_MH0013_[Complete]_[mRNA]_locus=scaffold35402_5:162:1919:+	Akkermansia muciniphila
408884	GL0007889_MH0013_[Complete]_[mRNA]_locus=scaffold36352_1:812:5251:+	Bacteria
409210	GL0003762_MH0013_[Complete]_[mRNA]_locus=scaffold38341_1:6398:7408:-	Akkermansia muciniphila
409211	GL0003764_MH0013_[Complete]_[mRNA]_locus=scaffold38341_1:8409:9986:+	Akkermansia muciniphila
409212	GL0003765_MH0013_[Complete]_[mRNA]_locus=scaffold38341_1:10135:11397:-	Akkermansia muciniphila
409215	GL0003773_MH0013_[Complete]_[mRNA]_locus=scaffold38341_1:20825:21235:-	Akkermansia muciniphila
409218	GL0003785_MH0013_[Complete]_[mRNA]_locus=scaffold38341_1:35076:36002:+	Akkermansia muciniphila

409222	GL0041512_MH0013_[Complete]_[mRNA]_locus=scaffold38341_3:6067:6936:+	Akkermansia muciniphila
409223	GL0041519_MH0013_[Complete]_[mRNA]_locus=scaffold38341_3:11665:12678:-	Akkermansia muciniphila
409225	GL0041524_MH0013_[Complete]_[mRNA]_locus=scaffold38341_3:17134:18429:+	Akkermansia muciniphila
409227	GL0008672_MH0013_[Complete]_[mRNA]_locus=scaffold38341_4:137:1294:-	Akkermansia muciniphila
409228	GL0008679_MH0013_[Complete]_[mRNA]_locus=scaffold38341_4:6234:8735:+	Akkermansia muciniphila
409230	GL0008683_MH0013_[Complete]_[mRNA]_locus=scaffold38341_4:11846:13123:-	Akkermansia muciniphila
409267	GL0035532_MH0013_[Complete]_[mRNA]_locus=scaffold38541_1:360:2774:+	Akkermansia muciniphila
409272	GL0005931_MH0013_[Complete]_[mRNA]_locus=scaffold38541_5:833:1528:+	Akkermansia muciniphila
409279	GL0010284_MH0013_[Complete]_[mRNA]_locus=scaffold38541_8:1154:2539:+	Akkermansia muciniphila
409284	GL0017771_MH0013_[Complete]_[mRNA]_locus=scaffold38541_10:6667:7113:+	Akkermansia muciniphila
409312	GL0014730_MH0013_[Complete]_[mRNA]_locus=scaffold38693_1:3663:5264:+	Akkermansia muciniphila
409313	GL0014733_MH0013_[Complete]_[mRNA]_locus=scaffold38693_1:6745:7746:+	Akkermansia muciniphila
409315	GL0014737_MH0013_[Complete]_[mRNA]_locus=scaffold38693_1:10189:12030:-	Bacteria
409317	GL0014740_MH0013_[Complete]_[mRNA]_locus=scaffold38693_1:13653:15638:+	Verrucomicrobiaceae

409320	GL0027331_MH0013_[Complete]_[mRNA]_locus= scaffold38693_2:1319:2212:-	Akkermansia muciniphila
409324	GL0027342_MH0013_[Complete]_[mRNA]_locus= scaffold38693_2:13811:16705:-	Akkermansia muciniphila
409454	GL0015421_MH0013_[Complete]_[mRNA]_locus= scaffold39835_3:3299:5506:+	Akkermansia muciniphila
409456	GL0015425_MH0013_[Complete]_[mRNA]_locus= scaffold39835_3:8129:9154:+	Akkermansia muciniphila
409457	GL0015426_MH0013_[Complete]_[mRNA]_locus= scaffold39835_3:9322:10533:+	Akkermansia muciniphila
409519	GL0023517_MH0013_[Complete]_[mRNA]_locus= scaffold40401_1:561:1661:-	Akkermansia muciniphila
409631	GL0031072_MH0013_[Complete]_[mRNA]_locus= scaffold41315_1:2809:4590:-	Akkermansia muciniphila
409635	GL0014310_MH0013_[Complete]_[mRNA]_locus= scaffold41315_3:1502:2518:+	Akkermansia muciniphila
409745	GL0003347_MH0013_[Complete]_[mRNA]_locus= scaffold42186_3:2233:5403:-	Bacteria
409748	GL0003351_MH0013_[Complete]_[mRNA]_locus= scaffold42186_3:10359:12896:-	Akkermansia muciniphila
409749	GL0003353_MH0013_[Complete]_[mRNA]_locus= scaffold42186_3:14226:15992:+	Akkermansia muciniphila
409879	GL0042389_MH0013_[Complete]_[mRNA]_locus= scaffold42803_2:489:1391:+	Akkermansia muciniphila
409880	GL0042390_MH0013_[Complete]_[mRNA]_locus= scaffold42803_2:1527:2081:+	Akkermansia muciniphila
409881	GL0019775_MH0013_[Complete]_[mRNA]_locus= scaffold42803_5:569:1246:-	Akkermansia muciniphila

409883	GL0029280_MH0013_[Complete]_[mRNA]_locus=scaffold42803_6:1682:2629:+	Akkermansia muciniphila
409895	GL0037906_MH0013_[Complete]_[mRNA]_locus=scaffold42882_2:2137:3417:-	Akkermansia muciniphila
410000	GL0009576_MH0013_[Complete]_[mRNA]_locus=scaffold43936_1:8473:10335:-	Akkermansia muciniphila
410001	GL0009577_MH0013_[Complete]_[mRNA]_locus=scaffold43936_1:10350:13832:-	Bacteria
410084	GL0026803_MH0013_[Complete]_[mRNA]_locus=scaffold44536_2:5656:6468:-	Akkermansia muciniphila
410187	GL0042759_MH0013_[Complete]_[mRNA]_locus=scaffold45386_2:4003:4584:+	Akkermansia muciniphila
410258	GL0027733_MH0013_[Complete]_[mRNA]_locus=scaffold45909_1:4381:8103:+	Bacteria
410261	GL0027750_MH0013_[Complete]_[mRNA]_locus=scaffold45909_1:26050:27297:+	Akkermansia muciniphila
410349	GL0020988_MH0013_[Complete]_[mRNA]_locus=scaffold46469_3:1251:3338:-	Bacteria
410352	GL0040496_MH0013_[Complete]_[mRNA]_locus=scaffold46469_6:5222:6475:-	Akkermansia muciniphila
410442	GL0006392_MH0013_[Complete]_[mRNA]_locus=scaffold46941_1:2001:2705:+	Akkermansia muciniphila
410447	GL0043979_MH0013_[Complete]_[mRNA]_locus=scaffold46941_7:1817:3196:+	Akkermansia muciniphila
410470	GL0011088_MH0013_[Complete]_[mRNA]_locus=scaffold47139_3:3948:4130:+	-
410471	GL0001508_MH0013_[Complete]_[mRNA]_locus=scaffold47139_6:596:1375:-	Akkermansia muciniphila

410472	GL0001509_MH0013_[Complete]_[mRNA]_locus=scaffold47139_6:1389:3443:-	Akkermansia muciniphila
410473	GL0001512_MH0013_[Complete]_[mRNA]_locus=scaffold47139_6:5915:6850:-	Akkermansia muciniphila
410623	GL0035403_MH0013_[Complete]_[mRNA]_locus=scaffold48073_1:2971:3840:+	Akkermansia muciniphila
410624	GL0014854_MH0013_[Complete]_[mRNA]_locus=scaffold48073_4:1109:3703:+	Verrucomicrobiaceae
410625	GL0014855_MH0013_[Complete]_[mRNA]_locus=scaffold48073_4:3677:4942:-	Akkermansia muciniphila
410626	GL0014859_MH0013_[Complete]_[mRNA]_locus=scaffold48073_4:7168:9471:-	Bacteria
410708	GL0010323_MH0013_[Complete]_[mRNA]_locus=scaffold48402_2:5028:6509:-	Akkermansia muciniphila
410778	GL0044945_MH0013_[Complete]_[mRNA]_locus=scaffold48682_2:467:1882:+	Akkermansia muciniphila
410846	GL0021386_MH0013_[Complete]_[mRNA]_locus=scaffold48869_3:6403:7338:-	Akkermansia muciniphila
410911	GL0020347_MH0013_[Complete]_[mRNA]_locus=scaffold49082_2:5687:7207:+	Akkermansia muciniphila
410923	GL0004836_MH0013_[Complete]_[mRNA]_locus=scaffold49094_1:2172:2927:-	Akkermansia muciniphila
410924	GL0039489_MH0013_[Complete]_[mRNA]_locus=scaffold49094_2:1802:2812:+	Akkermansia muciniphila
410926	GL0041472_MH0013_[Complete]_[mRNA]_locus=scaffold49094_4:614:931:-	Akkermansia muciniphila
410927	GL0041475_MH0013_[Complete]_[mRNA]_locus=scaffold49094_4:2293:3561:-	Akkermansia muciniphila

411076	GL0024403_MH0013_[Complete]_[mRNA]_locus=scaffold49525_2:818:1345:+	Akkermansia muciniphila
411117	GL0029358_MH0013_[Complete]_[mRNA]_locus=scaffold49627_2:7711:8595:-	Akkermansia muciniphila
411120	GL0012636_MH0013_[Complete]_[mRNA]_locus=scaffold49637_1:5047:6081:-	Akkermansia muciniphila
411121	GL0034056_MH0013_[Complete]_[mRNA]_locus=scaffold49637_2:173:2500:-	Bacteria
411154	GL0035792_MH0013_[Complete]_[mRNA]_locus=scaffold49793_1:4923:5117:-	-
411155	GL0035795_MH0013_[Complete]_[mRNA]_locus=scaffold49793_1:7556:8332:+	Akkermansia muciniphila
411174	GL0019265_MH0013_[Complete]_[mRNA]_locus=scaffold49839_4:1469:5230:+	Bacteria
411189	GL0004371_MH0013_[Complete]_[mRNA]_locus=scaffold49877_1:2069:3382:-	Akkermansia muciniphila
411191	GL0001457_MH0013_[Complete]_[mRNA]_locus=scaffold49877_2:2464:3159:+	Akkermansia muciniphila
411193	GL0001468_MH0013_[Complete]_[mRNA]_locus=scaffold49877_2:11558:14752:+	cellular organisms
411228	GL0039201_MH0013_[Complete]_[mRNA]_locus=scaffold50020_2:1314:2234:-	Akkermansia muciniphila
411229	GL0023717_MH0013_[Complete]_[mRNA]_locus=scaffold50020_3:1060:2313:+	Akkermansia muciniphila
411466	GL0014382_MH0013_[Complete]_[mRNA]_locus=scaffold50591_3:3462:4742:-	Akkermansia muciniphila
411482	GL0042801_MH0013_[Complete]_[mRNA]_locus=scaffold50623_1:5172:5954:+	Akkermansia muciniphila

411483	GL0042802_MH0013_[Complete]_[mRNA]_locus=scaffold50623_1:5996:7300:-	Akkermansia muciniphila
411484	GL0042812_MH0013_[Complete]_[mRNA]_locus=scaffold50623_1:18592:19662:+	Akkermansia muciniphila
411564	GL0018165_MH0013_[Complete]_[mRNA]_locus=scaffold50828_1:992:2152:+	Akkermansia muciniphila
411581	GL0001241_MH0013_[Complete]_[mRNA]_locus=scaffold50836_1:7649:9205:-	Akkermansia muciniphila
411582	GL0001242_MH0013_[Complete]_[mRNA]_locus=scaffold50836_1:9417:9578:+	-
411583	GL0026624_MH0013_[Complete]_[mRNA]_locus=scaffold50839_1:127:972:-	Akkermansia muciniphila
411625	GL0001400_MH0013_[Complete]_[mRNA]_locus=scaffold50925_1:2127:3131:+	Akkermansia muciniphila
411627	GL0001402_MH0013_[Complete]_[mRNA]_locus=scaffold50925_1:4297:5130:+	Akkermansia muciniphila
411628	GL0001403_MH0013_[Complete]_[mRNA]_locus=scaffold50925_1:5279:6112:-	Akkermansia muciniphila
411629	GL0008830_MH0013_[Complete]_[mRNA]_locus=scaffold50925_4:2470:5646:+	Bacteria
411654	GL0029288_MH0013_[Complete]_[mRNA]_locus=scaffold50952_1:1020:2114:+	Akkermansia muciniphila
411662	GL0035498_MH0013_[Complete]_[mRNA]_locus=scaffold50952_5:825:1622:-	Akkermansia muciniphila
411669	GL0012150_MH0013_[Complete]_[mRNA]_locus=scaffold50954_1:10547:12127:-	Akkermansia muciniphila
411670	GL0012151_MH0013_[Complete]_[mRNA]_locus=scaffold50954_1:12187:13497:-	Akkermansia muciniphila

411672	GL0012160_MH0013_[Complete]_[mRNA]_locus=scaffold50954_1:21189:22469:+	Akkermansia muciniphila
411810	GL0038893_MH0013_[Complete]_[mRNA]_locus=scaffold51091_1:4902:6308:-	Akkermansia muciniphila
411845	GL0044375_MH0013_[Complete]_[mRNA]_locus=scaffold51123_1:20362:21564:-	Akkermansia muciniphila
411861	GL0026691_MH0013_[Complete]_[mRNA]_locus=scaffold51123_5:8291:9073:-	Akkermansia muciniphila
411894	GL0016858_MH0013_[Complete]_[mRNA]_locus=scaffold51148_2:2582:3952:+	Akkermansia muciniphila
411899	GL0017373_MH0013_[Complete]_[mRNA]_locus=scaffold51149_2:6048:8516:+	Akkermansia muciniphila
411904	GL0016386_MH0013_[Complete]_[mRNA]_locus=scaffold51153_3:734:2113:+	Akkermansia muciniphila
411942	GL0010182_MH0013_[Complete]_[mRNA]_locus=scaffold51166_1:695:1423:-	Akkermansia muciniphila
411943	GL0010183_MH0013_[Complete]_[mRNA]_locus=scaffold51166_1:1428:1997:-	Akkermansia muciniphila
411944	GL0010187_MH0013_[Complete]_[mRNA]_locus=scaffold51166_1:4444:5454:+	Akkermansia muciniphila
411956	GL0009709_MH0013_[Complete]_[mRNA]_locus=scaffold51179_1:1034:2647:-	Akkermansia muciniphila
411994	GL0009935_MH0013_[Complete]_[mRNA]_locus=scaffold51204_1:908:1642:+	Akkermansia muciniphila
411998	GL0019260_MH0013_[Complete]_[mRNA]_locus=scaffold51204_2:7205:7738:-	Akkermansia muciniphila
411999	GL0038552_MH0013_[Complete]_[mRNA]_locus=scaffold51204_5:3510:4121:-	Akkermansia muciniphila

412000	GL0038555_MH0013_[Complete]_[mRNA]_locus=scaffold51204_5:5900:7000:-	Akkermansia muciniphila
412018	GL0024496_MH0013_[Complete]_[mRNA]_locus=scaffold51218_1:550:1239:-	Akkermansia muciniphila
412045	GL0008799_MH0013_[Complete]_[mRNA]_locus=scaffold51244_1:5396:5611:+	-
412140	GL0044278_MH0013_[Complete]_[mRNA]_locus=scaffold51291_1:1752:2963:-	Akkermansia muciniphila
412141	GL0044279_MH0013_[Complete]_[mRNA]_locus=scaffold51291_1:3184:3870:+	Akkermansia muciniphila
412184	GL0019569_MH0013_[Complete]_[mRNA]_locus=scaffold51302_1:1960:2157:+	Akkermansia muciniphila
412185	GL0019570_MH0013_[Complete]_[mRNA]_locus=scaffold51302_1:2159:3157:+	Akkermansia muciniphila
413248	GL0007213_MH0013_[Lack_both_end]_[mRNA]_locus=C1631067_1:1:1179:-	Desulfitobacterium hafniense
413573	GL0034804_MH0013_[Lack_both_end]_[mRNA]_locus=C1635149_1:1:1548:-	Akkermansia muciniphila
413905	GL0041118_MH0013_[Complete]_[mRNA]_locus=C1637987_1:111:1601:+	Bacteria
414891	GL0039252_MH0013_[Complete]_[mRNA]_locus=C1642565_1:1935:2720:+	Akkermansia muciniphila
415211	GL0003628_MH0013_[Complete]_[mRNA]_locus=C1643323_1:404:3583:-	Akkermansia muciniphila
415214	GL0003631_MH0013_[Complete]_[mRNA]_locus=C1643323_1:5253:5981:+	Akkermansia muciniphila
415442	GL0012846_MH0013_[Complete]_[mRNA]_locus=C1643619_1:5048:5791:+	Akkermansia muciniphila

415443	GL0012847_MH0013_[Complete]_[mRNA]_locus=C1643619_1:5895:7127:+	Akkermansia muciniphila
421350	GL0028279_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold4438_1:1:336:+	-
422727	GL0149521_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold5896_1:1:1410:-	Bacteria
425609	GL0063945_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold9145_2:318:509:-	-
430791	GL0115301_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold16905_2:2:112:+	-
435373	GL0047418_MH0014_[Lack_both_end]_[mRNA]_locus=scaffold25707_2:3:1166:-	Ruminococcus obeum
438622	GL0013900_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold34966_1:445:555:-	-
444173	GL0023544_MH0014_[Complete]_[mRNA]_locus=scaffold56873_3:335:706:-	Clostridiales
445287	GL0063979_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold61864_1:215:1135:-	-
447159	GL0010321_MH0014_[Complete]_[mRNA]_locus=scaffold71559_4:169:948:-	Bacteria
448720	GL0008335_MH0014_[Lack_5'-end]_[mRNA]_locus=scaffold78177_1:2:136:+	-
455111	GL0083074_MH0014_[Lack_3'-end]_[mRNA]_locus=C4700793_1:269:538:+	Roseburia inulinivorans
463192	GL0039803_MH0016_[Complete]_[mRNA]_locus=scaffold40_3:2261:2731:+	-
463230	GL0095083_MH0016_[Complete]_[mRNA]_locus=scaffold86_1:3478:4512:+	Anaerotruncus colihominis

463238	GL0085137_MH0016_[Complete]_[mRNA]_locus=scaffold86_2:2816:3640:+	Desulfitobacterium hafniense
463299	GL0023255_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold161_1:1:2103:+	Bacteria
463300	GL0023256_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold161_1:2167:3006:+	-
463301	GL0016585_MH0016_[Complete]_[mRNA]_locus=scaffold161_2:543:1460:-	Anaerococcus hydrogenalis
463309	GL0117699_MH0016_[Complete]_[mRNA]_locus=scaffold168_3:1178:2086:+	-
463311	GL0138384_MH0016_[Complete]_[mRNA]_locus=scaffold168_4:2115:3323:-	-
463312	GL0138385_MH0016_[Complete]_[mRNA]_locus=scaffold168_4:3482:4204:+	-
463314	GL0100774_MH0016_[Complete]_[mRNA]_locus=scaffold168_11:514:2856:-	-
463315	GL0100775_MH0016_[Complete]_[mRNA]_locus=scaffold168_11:2878:4629:-	-
463606	GL0120290_MH0016_[Complete]_[mRNA]_locus=scaffold351_2:985:2340:+	Faecalibacterium prausnitzii
463607	GL0120291_MH0016_[Complete]_[mRNA]_locus=scaffold351_2:2401:4527:-	Faecalibacterium prausnitzii
463614	GL0120776_MH0016_[Complete]_[mRNA]_locus=scaffold358_1:1254:4277:-	-
463615	GL0115876_MH0016_[Complete]_[mRNA]_locus=scaffold358_2:485:2380:-	-
463616	GL0074991_MH0016_[Complete]_[mRNA]_locus=	-

	scaffold358_4:6:623:-	
463706	GL0040409_MH0016_[Complete]_[mRNA]_locus=scaffold393_2:12:1436:-	-
463732	GL0109837_MH0016_[Complete]_[mRNA]_locus=scaffold409_1:60:1427:+	Coprococcus comes
463733	GL0014809_MH0016_[Complete]_[mRNA]_locus=scaffold410_1:284:1204:+	-
463734	GL0014810_MH0016_[Complete]_[mRNA]_locus=scaffold410_1:1232:2446:+	-
463735	GL0014811_MH0016_[Complete]_[mRNA]_locus=scaffold410_1:2606:3823:+	-
463736	GL0132202_MH0016_[Complete]_[mRNA]_locus=scaffold410_2:58:1071:-	-
463737	GL0038295_MH0016_[Complete]_[mRNA]_locus=scaffold410_3:1018:2745:-	Clostridiales
463738	GL0014888_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold410_5:1325:1984:-	-
463740	GL0028150_MH0016_[Complete]_[mRNA]_locus=scaffold410_7:435:1700:+	Faecalibacterium prausnitzii
463743	GL0028153_MH0016_[Complete]_[mRNA]_locus=scaffold410_7:3153:3851:+	-
463746	GL0110086_MH0016_[Complete]_[mRNA]_locus=scaffold410_11:452:1273:+	-
463747	GL0110088_MH0016_[Complete]_[mRNA]_locus=scaffold410_11:2129:3370:+	-
463752	GL0077909_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:535:1398:+	-

463753	GL0077910_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:1398:2063:+	-
463754	GL0077911_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:2078:4483:+	Bacteria
463755	GL0077912_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:4593:5954:+	Clostridium
463756	GL0077913_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:6024:7550:+	Clostridium botulinum
463757	GL0077915_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:9088:10257:+	Bacteroides pectinophilus
463758	GL0077917_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:10787:12508:+	-
463759	GL0077919_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:12882:13481:+	-
463761	GL0077922_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:16159:17352:-	-
463763	GL0077926_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:18712:19437:+	-
463765	GL0077929_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:20892:21281:+	-
463766	GL0077930_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:21297:22106:+	-
463767	GL0077931_MH0016_[Complete]_[mRNA]_locus=scaffold410_13:22245:23567:+	-
463768	GL0068120_MH0016_[Complete]_[mRNA]_locus=scaffold417_1:156:1628:+	Bacteria
463769	GL0001249_MH0016_[Complete]_[mRNA]_locus=scaffold417_2:52:1374:-	-

463846	GL0146248_MH0016_[Complete]_[mRNA]_locus=scaffold561_1:1270:1788:-	-
463847	GL0146249_MH0016_[Complete]_[mRNA]_locus=scaffold561_1:2180:2677:+	-
463848	GL0031867_MH0016_[Complete]_[mRNA]_locus=scaffold561_3:592:1185:+	-
463849	GL0031868_MH0016_[Complete]_[mRNA]_locus=scaffold561_3:1363:2094:+	-
463913	GL0002036_MH0016_[Complete]_[mRNA]_locus=scaffold578_8:1552:2613:-	-
463948	GL0009104_MH0016_[Complete]_[mRNA]_locus=scaffold608_1:959:2845:-	-
464063	GL0142726_MH0016_[Complete]_[mRNA]_locus=scaffold687_4:383:1267:-	-
464066	GL0049634_MH0016_[Complete]_[mRNA]_locus=scaffold687_5:213:1967:-	Faecalibacterium prausnitzii
464067	GL0049635_MH0016_[Complete]_[mRNA]_locus=scaffold687_5:1983:2738:-	-
464068	GL0101955_MH0016_[Complete]_[mRNA]_locus=scaffold687_6:23:697:-	-
464069	GL0101956_MH0016_[Complete]_[mRNA]_locus=scaffold687_6:684:890:-	-
464071	GL0101958_MH0016_[Complete]_[mRNA]_locus=scaffold687_6:3250:4686:-	Lactobacillus sakei
464073	GL0101960_MH0016_[Complete]_[mRNA]_locus=scaffold687_6:5201:5761:-	-
464075	GL0062609_MH0016_[Complete]_[mRNA]_locus=scaffold687_9:30:2105:-	Faecalibacterium prausnitzii

464076	GL0062610_MH0016_[Complete]_[mRNA]_locus=scaffold687_9:2102:2485:-	-
464078	GL0082653_MH0016_[Complete]_[mRNA]_locus=scaffold689_1:113:1240:+	-
464079	GL0135755_MH0016_[Complete]_[mRNA]_locus=scaffold689_2:2302:2829:-	-
464080	GL0111349_MH0016_[Complete]_[mRNA]_locus=scaffold689_3:12:746:-	-
464096	GL0015083_MH0016_[Complete]_[mRNA]_locus=scaffold708_3:30:1007:+	-
464133	GL0006399_MH0016_[Complete]_[mRNA]_locus=scaffold735_3:373:3288:+	Bacteria
464134	GL0006400_MH0016_[Complete]_[mRNA]_locus=scaffold735_3:3288:4091:+	-
464401	GL0096640_MH0016_[Complete]_[mRNA]_locus=scaffold874_1:2513:3169:-	-
464443	GL0049133_MH0016_[Complete]_[mRNA]_locus=scaffold908_1:2444:3607:-	-
464444	GL0049134_MH0016_[Complete]_[mRNA]_locus=scaffold908_1:3831:4637:+	-
464445	GL0049135_MH0016_[Complete]_[mRNA]_locus=scaffold908_1:4795:5562:+	-
464446	GL0049136_MH0016_[Complete]_[mRNA]_locus=scaffold908_1:5578:6873:+	-
464447	GL0049137_MH0016_[Complete]_[mRNA]_locus=scaffold908_1:7077:8954:-	-
464448	GL0061267_MH0016_[Complete]_[mRNA]_locus=scaffold908_2:600:1613:+	-

464449	GL0072805_MH0016_[Complete]_[mRNA]_locus=scaffold908_6:478:1671:+	-
464469	GL0046161_MH0016_[Complete]_[mRNA]_locus=scaffold947_3:729:1853:-	-
464470	GL0116068_MH0016_[Complete]_[mRNA]_locus=scaffold947_4:253:2328:-	Bacteria
464471	GL0116069_MH0016_[Complete]_[mRNA]_locus=scaffold947_4:2588:3598:-	-
464473	GL0049817_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold947_8:134:616:-	-
464517	GL0081764_MH0016_[Complete]_[mRNA]_locus=scaffold1018_1:40:2553:-	Bacteria
464557	GL0089295_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold1073_2:1:1155:-	-
464746	GL0049705_MH0016_[Complete]_[mRNA]_locus=scaffold1236_1:58:768:+	-
464747	GL0049706_MH0016_[Complete]_[mRNA]_locus=scaffold1236_1:758:1210:+	-
464884	GL0069096_MH0016_[Complete]_[mRNA]_locus=scaffold1295_2:412:1356:-	-
464885	GL0069097_MH0016_[Complete]_[mRNA]_locus=scaffold1295_2:1545:3041:-	-
464912	GL0128459_MH0016_[Complete]_[mRNA]_locus=scaffold1378_9:50:1372:-	Faecalibacterium prausnitzii
464913	GL0128460_MH0016_[Complete]_[mRNA]_locus=scaffold1378_9:1439:2431:-	-
464914	GL0128461_MH0016_[Complete]_[mRNA]_locus=scaffold1378_9:2428:3543:-	-

464917	GL0074847_MH0016_[Complete]_[mRNA]_locus=scaffold1378_12:248:1162:+	Faecalibacterium prausnitzii
464918	GL0074848_MH0016_[Complete]_[mRNA]_locus=scaffold1378_12:1305:3179:+	-
464919	GL0074849_MH0016_[Complete]_[mRNA]_locus=scaffold1378_12:3241:3516:+	-
464921	GL0074851_MH0016_[Complete]_[mRNA]_locus=scaffold1378_12:4032:4667:+	-
464922	GL0074852_MH0016_[Complete]_[mRNA]_locus=scaffold1378_12:4803:5999:-	Faecalibacterium prausnitzii
465035	GL0049482_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold1540_2:10:639:-	-
465163	GL0083283_MH0016_[Complete]_[mRNA]_locus=scaffold1578_1:801:2084:+	Faecalibacterium prausnitzii
465166	GL0137268_MH0016_[Complete]_[mRNA]_locus=scaffold1578_6:214:933:+	-
465167	GL0131615_MH0016_[Complete]_[mRNA]_locus=scaffold1578_7:225:1085:+	-
465168	GL0033464_MH0016_[Complete]_[mRNA]_locus=scaffold1578_9:1146:2198:+	-
465169	GL0021595_MH0016_[Complete]_[mRNA]_locus=scaffold1578_10:42:4349:+	Clostridiales
465172	GL0014336_MH0016_[Complete]_[mRNA]_locus=scaffold1578_11:2160:3440:+	-
465173	GL0014337_MH0016_[Complete]_[mRNA]_locus=scaffold1578_11:3613:5532:+	Bacteria
465174	GL0014338_MH0016_[Complete]_[mRNA]_locus=scaffold1578_11:5715:8714:+	Bacteria

465175	GL0113953_MH0016_[Complete]_[mRNA]_locus=scaffold1578_12:2261:2713:-	-
465176	GL0035281_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold1578_14:1:1077:-	-
465177	GL0035282_MH0016_[Complete]_[mRNA]_locus=scaffold1578_14:1080:1457:-	-
465188	GL0022504_MH0016_[Complete]_[mRNA]_locus=scaffold1588_5:2863:3861:+	-
465189	GL0145898_MH0016_[Complete]_[mRNA]_locus=scaffold1588_7:1901:2761:+	Faecalibacterium prausnitzii
465190	GL0145899_MH0016_[Complete]_[mRNA]_locus=scaffold1588_7:2793:3518:-	-
465191	GL0104311_MH0016_[Complete]_[mRNA]_locus=scaffold1588_9:1058:3259:-	Bacteria
465192	GL0104312_MH0016_[Complete]_[mRNA]_locus=scaffold1588_9:3243:3749:-	Faecalibacterium prausnitzii
465193	GL0104313_MH0016_[Complete]_[mRNA]_locus=scaffold1588_9:3884:5377:-	-
465195	GL0104315_MH0016_[Complete]_[mRNA]_locus=scaffold1588_9:5753:7960:+	Bacteroides capillosus
465261	GL0074543_MH0016_[Complete]_[mRNA]_locus=scaffold1636_1:4231:5094:+	-
465262	GL0109414_MH0016_[Complete]_[mRNA]_locus=scaffold1636_3:1131:2183:+	-
465268	GL0023518_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:2636:3502:+	-
465269	GL0023519_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:3516:3773:+	-

465270	GL0023520_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:3902:5680:+	Eubacterium siraeum
465271	GL0023521_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:5696:6808:+	-
465272	GL0023522_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:6824:8188:+	-
465274	GL0023524_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:9306:10211:-	-
465275	GL0023525_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:10396:11034:+	-
465276	GL0023526_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:11117:12247:+	Clostridium bartlettii
465277	GL0023528_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:13154:13627:+	-
465278	GL0023530_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:14475:15398:+	-
465279	GL0023531_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:15411:15890:+	-
465280	GL0023532_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:15980:18553:+	-
465281	GL0023533_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:18618:19982:+	-
465282	GL0023534_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:20016:21026:+	-
465283	GL0023535_MH0016_[Complete]_[mRNA]_locus=scaffold1636_7:21088:22380:+	-
465317	GL0039248_MH0016_[Complete]_[mRNA]_locus=scaffold1687_1:316:1671:+	-

465318	GL0039249_MH0016_[Complete]_[mRNA]_locus=scaffold1687_1:1692:3413:+	-
465369	GL0105941_MH0016_[Complete]_[mRNA]_locus=scaffold1741_2:1601:3034:+	-
465370	GL0105942_MH0016_[Complete]_[mRNA]_locus=scaffold1741_2:3042:3830:+	-
465444	GL0119317_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold1808_3:3:1016:+	Lachnospiraceae
465448	GL0098735_MH0016_[Complete]_[mRNA]_locus=scaffold1808_4:961:2061:+	-
465449	GL0132652_MH0016_[Complete]_[mRNA]_locus=scaffold1808_6:1845:3158:+	Faecalibacterium prausnitzii
465505	GL0142217_MH0016_[Complete]_[mRNA]_locus=scaffold1849_1:66:2108:+	Clostridiales
465506	GL0047510_MH0016_[Complete]_[mRNA]_locus=scaffold1849_2:682:2127:+	Clostridiales
465509	GL0108549_MH0016_[Complete]_[mRNA]_locus=scaffold1849_3:1551:2204:+	-
465510	GL0108550_MH0016_[Complete]_[mRNA]_locus=scaffold1849_3:2241:3125:-	-
465512	GL0016004_MH0016_[Complete]_[mRNA]_locus=scaffold1849_4:937:1311:+	-
465513	GL0058231_MH0016_[Complete]_[mRNA]_locus=scaffold1849_5:19:1107:+	-
465516	GL0024399_MH0016_[Complete]_[mRNA]_locus=scaffold1849_7:1990:3573:+	Faecalibacterium prausnitzii
465517	GL0024400_MH0016_[Complete]_[mRNA]_locus=scaffold1849_7:3570:4856:+	Faecalibacterium prausnitzii

465518	GL0024401_MH0016_[Complete]_[mRNA]_locus=scaffold1849_7:4928:5383:+	Bacteria
465519	GL0024402_MH0016_[Complete]_[mRNA]_locus=scaffold1849_7:5380:6444:+	-
465521	GL0024404_MH0016_[Complete]_[mRNA]_locus=scaffold1849_7:7192:7911:+	-
465865	GL0008938_MH0016_[Complete]_[mRNA]_locus=scaffold2062_2:548:1024:+	-
465866	GL0008940_MH0016_[Complete]_[mRNA]_locus=scaffold2062_2:1540:3183:-	-
465867	GL0061047_MH0016_[Complete]_[mRNA]_locus=scaffold2062_3:36:773:-	-
465868	GL0061048_MH0016_[Complete]_[mRNA]_locus=scaffold2062_3:884:2257:-	-
465895	GL0106615_MH0016_[Complete]_[mRNA]_locus=scaffold2096_1:1886:2407:+	-
465896	GL0062813_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold2096_3:222:1859:+	Bacteria
465900	GL0042409_MH0016_[Complete]_[mRNA]_locus=scaffold2096_11:3080:4378:+	-
465901	GL0042411_MH0016_[Complete]_[mRNA]_locus=scaffold2096_11:4892:5326:+	-
465902	GL0042412_MH0016_[Complete]_[mRNA]_locus=scaffold2096_11:5358:6041:+	-
465917	GL0102521_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold2111_1:1:1185:+	Faecalibacterium prausnitzii
465918	GL0102522_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:1488:2120:+	-

465920	GL0102525_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:2928:3869:-	-
465921	GL0102526_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:3892:5391:-	-
465922	GL0102527_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:5405:5941:-	-
465923	GL0102528_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:6130:7620:-	-
465924	GL0102529_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:7610:8740:-	-
465925	GL0102531_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:9729:10895:+	-
465926	GL0102533_MH0016_[Complete]_[mRNA]_locus=scaffold2111_1:11974:12696:-	Faecalibacterium prausnitzii
465928	GL0049724_MH0016_[Complete]_[mRNA]_locus=scaffold2111_2:233:667:+	-
465929	GL0079252_MH0016_[Complete]_[mRNA]_locus=scaffold2111_3:37:1026:+	-
466026	GL0009680_MH0016_[Complete]_[mRNA]_locus=scaffold2179_4:725:1498:+	Faecalibacterium prausnitzii
466027	GL0117491_MH0016_[Complete]_[mRNA]_locus=scaffold2179_5:22:1701:+	Bacteria
466028	GL0025233_MH0016_[Complete]_[mRNA]_locus=scaffold2179_6:1582:3015:-	-
466033	GL0037837_MH0016_[Complete]_[mRNA]_locus=scaffold2185_2:583:2493:-	Eubacterium hallii
466034	GL0037838_MH0016_[Complete]_[mRNA]_locus=scaffold2185_2:2493:3176:-	-

466035	GL0037839_MH0016_[Complete]_[mRNA]_locus=scaffold2185_2:3204:4652:-	Faecalibacterium prausnitzii
466036	GL0086536_MH0016_[Complete]_[mRNA]_locus=scaffold2185_3:278:925:-	-
466038	GL0075443_MH0016_[Complete]_[mRNA]_locus=scaffold2185_4:396:1046:-	-
466039	GL0075444_MH0016_[Complete]_[mRNA]_locus=scaffold2185_4:1021:2886:-	Bacteria
466041	GL0075446_MH0016_[Complete]_[mRNA]_locus=scaffold2185_4:3369:4172:-	-
466042	GL0019290_MH0016_[Complete]_[mRNA]_locus=scaffold2185_5:5:385:-	-
466043	GL0019292_MH0016_[Complete]_[mRNA]_locus=scaffold2185_5:2629:3090:-	-
466044	GL0019294_MH0016_[Complete]_[mRNA]_locus=scaffold2185_5:3470:4081:+	-
466045	GL0118328_MH0016_[Complete]_[mRNA]_locus=scaffold2185_6:21:800:-	-
466046	GL0118330_MH0016_[Complete]_[mRNA]_locus=scaffold2185_6:1555:2250:-	-
466048	GL0118332_MH0016_[Complete]_[mRNA]_locus=scaffold2185_6:3318:4742:-	Dorea formicigenerans
466049	GL0118334_MH0016_[Complete]_[mRNA]_locus=scaffold2185_6:5882:6817:-	Ruminococcus obeum
466050	GL0118335_MH0016_[Complete]_[mRNA]_locus=scaffold2185_6:6938:9310:-	Clostridiales
466051	GL0059936_MH0016_[Complete]_[mRNA]_locus=scaffold2185_7:525:1436:-	-

466052	GL0103236_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:820:1968:-	-
466053	GL0103237_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:1965:2276:-	-
466054	GL0103238_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:2335:3519:+	-
466055	GL0103240_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:3785:4636:+	-
466056	GL0103241_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:4978:6369:-	-
466058	GL0103244_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:7574:8593:-	-
466059	GL0103245_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:8598:9686:-	-
466060	GL0103247_MH0016_[Complete]_[mRNA]_locus= scaffold2185_9:10137:11045:+	-
466063	GL0055226_MH0016_[Complete]_[mRNA]_locus= scaffold2185_10:414:1175:-	-
466064	GL0055227_MH0016_[Complete]_[mRNA]_locus= scaffold2185_10:1176:2261:-	-
466065	GL0008809_MH0016_[Complete]_[mRNA]_locus= scaffold2185_12:898:1473:+	-
466303	GL0104883_MH0016_[Complete]_[mRNA]_locus= scaffold2361_3:1089:2033:+	-
466345	GL0028654_MH0016_[Complete]_[mRNA]_locus= scaffold2431_1:925:1704:-	-
466346	GL0049091_MH0016_[Complete]_[mRNA]_locus= scaffold2431_2:910:1800:-	Clostridium

466660	GL0089550_MH0016_[Complete]_[mRNA]_locus=scaffold2593_1:60:1349:-	-
466663	GL0089553_MH0016_[Complete]_[mRNA]_locus=scaffold2593_1:3357:4376:-	-
466664	GL0089554_MH0016_[Complete]_[mRNA]_locus=scaffold2593_1:4392:5045:-	-
466665	GL0142791_MH0016_[Complete]_[mRNA]_locus=scaffold2593_2:36:971:-	-
466666	GL0094593_MH0016_[Complete]_[mRNA]_locus=scaffold2593_4:910:1962:-	-
466667	GL0094594_MH0016_[Complete]_[mRNA]_locus=scaffold2593_4:1959:3113:-	-
466668	GL0094595_MH0016_[Complete]_[mRNA]_locus=scaffold2593_4:3147:4559:-	-
466669	GL0005384_MH0016_[Complete]_[mRNA]_locus=scaffold2593_5:68:1063:-	-
466670	GL0005385_MH0016_[Complete]_[mRNA]_locus=scaffold2593_5:1184:2071:-	-
466671	GL0005387_MH0016_[Complete]_[mRNA]_locus=scaffold2593_5:3003:3845:+	-
466673	GL0005389_MH0016_[Complete]_[mRNA]_locus=scaffold2593_5:5186:6235:+	-
466674	GL0005390_MH0016_[Complete]_[mRNA]_locus=scaffold2593_5:6367:7479:+	-
466675	GL0005391_MH0016_[Complete]_[mRNA]_locus=scaffold2593_5:7499:8758:+	-
466676	GL0062828_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:330:1646:+	-

466677	GL0062829_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:1653:2507:+	-
466678	GL0062830_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:2572:3258:-	-
466679	GL0062831_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:3255:4508:-	-
466680	GL0062832_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:4584:5561:-	-
466681	GL0062833_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:5571:6503:-	-
466682	GL0062834_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:6725:8134:+	-
466683	GL0062835_MH0016_[Complete]_[mRNA]_locus=scaffold2593_6:8150:9211:+	-
466867	GL0000536_MH0016_[Complete]_[mRNA]_locus=scaffold2807_1:539:2014:-	Faecalibacterium prausnitzii
466868	GL0000537_MH0016_[Complete]_[mRNA]_locus=scaffold2807_1:2030:3577:-	-
466869	GL0000538_MH0016_[Complete]_[mRNA]_locus=scaffold2807_1:3803:4435:-	-
466871	GL0000541_MH0016_[Complete]_[mRNA]_locus=scaffold2807_1:7218:7967:-	-
466873	GL0000544_MH0016_[Complete]_[mRNA]_locus=scaffold2807_1:10387:11307:-	-
466874	GL0000545_MH0016_[Complete]_[mRNA]_locus=scaffold2807_1:11313:11828:-	-
466875	GL0058866_MH0016_[Complete]_[mRNA]_locus=scaffold2807_2:1179:1757:-	-

466876	GL0058868_MH0016_[Complete]_[mRNA]_locus=scaffold2807_2:2027:2905:-	-
466888	GL0089121_MH0016_[Complete]_[mRNA]_locus=scaffold2825_2:2114:2434:-	-
466890	GL0104285_MH0016_[Complete]_[mRNA]_locus=scaffold2825_3:1394:2788:+	Faecalibacterium prausnitzii
466891	GL0104286_MH0016_[Complete]_[mRNA]_locus=scaffold2825_3:2847:3821:+	Faecalibacterium prausnitzii
466893	GL0104288_MH0016_[Complete]_[mRNA]_locus=scaffold2825_3:5021:5884:-	-
466894	GL0104289_MH0016_[Complete]_[mRNA]_locus=scaffold2825_3:6039:7568:+	Faecalibacterium prausnitzii
466895	GL0037686_MH0016_[Complete]_[mRNA]_locus=scaffold2825_4:565:1395:+	Ruminococcus gnavus
467080	GL0078984_MH0016_[Complete]_[mRNA]_locus=scaffold2951_1:1382:2140:-	Coprococcus eutactus
467099	GL0091509_MH0016_[Complete]_[mRNA]_locus=scaffold2999_2:78:1019:-	Faecalibacterium prausnitzii
467192	GL0145400_MH0016_[Complete]_[mRNA]_locus=scaffold3094_6:205:1242:-	Clostridium bolteae
467193	GL0145401_MH0016_[Complete]_[mRNA]_locus=scaffold3094_6:1336:3948:-	Bacteria
467194	GL0092616_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold3094_7:3:914:+	Faecalibacterium prausnitzii
467235	GL0101967_MH0016_[Complete]_[mRNA]_locus=scaffold3155_1:1089:1577:-	-
467337	GL0118394_MH0016_[Complete]_[mRNA]_locus=scaffold3230_3:813:1988:-	Collinsella aerofaciens

467339	GL0118397_MH0016_[Complete]_[mRNA]_locus=scaffold3230_3:4491:6026:+	Butyrivibrio
467340	GL0118399_MH0016_[Complete]_[mRNA]_locus=scaffold3230_3:7161:8423:+	Clostridium
467399	GL0104503_MH0016_[Complete]_[mRNA]_locus=scaffold3320_2:9:1625:-	Clostridiaceae
467484	GL0051590_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold3436_1:1448:6619:-	Clostridium methylpentosum
467549	GL0006363_MH0016_[Complete]_[mRNA]_locus=scaffold3524_1:81:1664:-	-
467550	GL0006364_MH0016_[Complete]_[mRNA]_locus=scaffold3524_1:1843:2772:-	-
467551	GL0006365_MH0016_[Complete]_[mRNA]_locus=scaffold3524_1:2903:3928:-	-
467624	GL0043885_MH0016_[Complete]_[mRNA]_locus=scaffold3577_1:123:1808:-	Faecalibacterium prausnitzii
467625	GL0043887_MH0016_[Complete]_[mRNA]_locus=scaffold3577_1:2421:2867:+	-
467626	GL0043888_MH0016_[Complete]_[mRNA]_locus=scaffold3577_1:3240:6434:-	Clostridium kluyveri
467641	GL0006475_MH0016_[Complete]_[mRNA]_locus=scaffold3594_2:2:556:-	-
467643	GL0006477_MH0016_[Complete]_[mRNA]_locus=scaffold3594_2:977:1732:-	-
467644	GL0006478_MH0016_[Complete]_[mRNA]_locus=scaffold3594_2:1868:2920:+	Faecalibacterium prausnitzii
467645	GL0006479_MH0016_[Complete]_[mRNA]_locus=scaffold3594_2:3073:3504:-	-

467646	GL0006480_MH0016_[Complete]_[mRNA]_locus=scaffold3594_2:3575:4366:-	-
467647	GL0006481_MH0016_[Complete]_[mRNA]_locus=scaffold3594_2:4519:6036:-	-
468145	GL0102429_MH0016_[Complete]_[mRNA]_locus=scaffold4165_1:122:1915:+	Clostridiales
468146	GL0117425_MH0016_[Complete]_[mRNA]_locus=scaffold4165_2:648:2093:+	-
468147	GL0060705_MH0016_[Complete]_[mRNA]_locus=scaffold4165_3:65:964:-	-
468148	GL0060706_MH0016_[Complete]_[mRNA]_locus=scaffold4165_3:1095:1751:+	-
468149	GL0065490_MH0016_[Complete]_[mRNA]_locus=scaffold4166_2:1641:2576:-	-
468150	GL0065491_MH0016_[Complete]_[mRNA]_locus=scaffold4166_2:2584:3477:-	-
468193	GL0078993_MH0016_[Complete]_[mRNA]_locus=scaffold4188_2:119:1123:+	-
468194	GL0078994_MH0016_[Complete]_[mRNA]_locus=scaffold4188_2:1173:2654:+	Eubacterium hallii
468214	GL0040294_MH0016_[Complete]_[mRNA]_locus=scaffold4203_1:61:1812:+	Bacteria
468215	GL0020090_MH0016_[Complete]_[mRNA]_locus=scaffold4203_2:1792:2709:+	-
468245	GL0104968_MH0016_[Complete]_[mRNA]_locus=scaffold4240_1:100:948:+	Faecalibacterium prausnitzii
468248	GL0093737_MH0016_[Complete]_[mRNA]_locus=scaffold4240_2:491:3262:-	Bacteria

468659	GL0118741_MH0016_[Complete]_[mRNA]_locus=scaffold4753_1:260:1225:+	-
468746	GL0139785_MH0016_[Complete]_[mRNA]_locus=scaffold4864_2:628:1524:-	-
468747	GL0018198_MH0016_[Complete]_[mRNA]_locus=scaffold4864_3:1432:2325:-	-
468765	GL0113171_MH0016_[Complete]_[mRNA]_locus=scaffold4902_1:559:1734:+	-
468937	GL0060765_MH0016_[Complete]_[mRNA]_locus=scaffold5068_1:1509:2879:-	-
468938	GL0040243_MH0016_[Complete]_[mRNA]_locus=scaffold5068_2:1:819:-	-
468940	GL0040245_MH0016_[Complete]_[mRNA]_locus=scaffold5068_2:1724:2497:-	-
468941	GL0040246_MH0016_[Complete]_[mRNA]_locus=scaffold5068_2:2499:5105:-	Bacteria
468942	GL0028974_MH0016_[Complete]_[mRNA]_locus=scaffold5068_3:37:1095:-	-
468943	GL0028975_MH0016_[Complete]_[mRNA]_locus=scaffold5068_3:1485:3734:-	Faecalibacterium prausnitzii
469055	GL0046557_MH0016_[Complete]_[mRNA]_locus=scaffold5236_1:769:1335:-	-
469056	GL0104334_MH0016_[Complete]_[mRNA]_locus=scaffold5236_2:537:1712:-	-
469057	GL0104335_MH0016_[Complete]_[mRNA]_locus=scaffold5236_2:1859:3148:-	-
469058	GL0104336_MH0016_[Complete]_[mRNA]_locus=scaffold5236_2:3158:4450:-	Faecalibacterium prausnitzii

469060	GL0104339_MH0016_[Complete]_[mRNA]_locus=scaffold5236_2:6270:7199:+	-
469066	GL0099676_MH0016_[Complete]_[mRNA]_locus=scaffold5243_4:9:986:-	-
469067	GL0099677_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold5243_4:990:2045:-	-
469068	GL0042369_MH0016_[Complete]_[mRNA]_locus=scaffold5243_5:981:2246:-	-
469069	GL0042370_MH0016_[Complete]_[mRNA]_locus=scaffold5243_5:2289:3509:-	-
469071	GL0042372_MH0016_[Complete]_[mRNA]_locus=scaffold5243_5:4495:5610:-	-
469072	GL0019737_MH0016_[Complete]_[mRNA]_locus=scaffold5243_7:615:2123:-	-
469073	GL0019738_MH0016_[Complete]_[mRNA]_locus=scaffold5243_7:2120:2803:-	-
469075	GL0072834_MH0016_[Complete]_[mRNA]_locus=scaffold5243_8:4134:4754:-	-
469109	GL0145480_MH0016_[Complete]_[mRNA]_locus=scaffold5267_2:3:1295:-	-
469111	GL0145482_MH0016_[Complete]_[mRNA]_locus=scaffold5267_2:2128:2532:+	-
469120	GL0019554_MH0016_[Complete]_[mRNA]_locus=scaffold5267_3:719:1300:-	Clostridium perfringens
469139	GL0116611_MH0016_[Complete]_[mRNA]_locus=scaffold5337_1:966:1613:-	-
469140	GL0137633_MH0016_[Complete]_[mRNA]_locus=scaffold5337_2:85:1002:-	-

469141	GL0137634_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold5337_2:993:2261:-	-
469142	GL0034743_MH0016_[Complete]_[mRNA]_locus=scaffold5337_4:533:1759:-	-
469179	GL0045404_MH0016_[Complete]_[mRNA]_locus=scaffold5374_1:7856:8875:-	Anoxybacillus flavithermus
469267	GL0138186_MH0016_[Complete]_[mRNA]_locus=scaffold5448_2:431:1426:-	-
469268	GL0138187_MH0016_[Complete]_[mRNA]_locus=scaffold5448_2:1419:2162:-	-
469269	GL0024313_MH0016_[Complete]_[mRNA]_locus=scaffold5448_3:35:382:-	-
469270	GL0024314_MH0016_[Complete]_[mRNA]_locus=scaffold5448_3:651:3083:+	-
469271	GL0082447_MH0016_[Complete]_[mRNA]_locus=scaffold5448_4:1217:2107:+	-
469272	GL0056924_MH0016_[Complete]_[mRNA]_locus=scaffold5448_6:1559:2884:+	-
469273	GL0056925_MH0016_[Complete]_[mRNA]_locus=scaffold5448_6:2874:4172:+	-
469274	GL0056926_MH0016_[Complete]_[mRNA]_locus=scaffold5448_6:4189:5226:+	-
469318	GL0134247_MH0016_[Complete]_[mRNA]_locus=scaffold5531_1:748:1551:-	-
469319	GL0043806_MH0016_[Complete]_[mRNA]_locus=scaffold5531_2:437:1345:-	Faecalibacterium prausnitzii
469320	GL0043807_MH0016_[Complete]_[mRNA]_locus=scaffold5531_2:1342:2097:-	Faecalibacterium prausnitzii

469321	GL0018574_MH0016_[Complete]_[mRNA]_locus=scaffold5531_3:3623:4957:+	-
469322	GL0018575_MH0016_[Complete]_[mRNA]_locus=scaffold5531_3:5030:6217:+	-
469358	GL0058581_MH0016_[Complete]_[mRNA]_locus=scaffold5565_2:82:1377:-	Faecalibacterium prausnitzii
469359	GL0058583_MH0016_[Complete]_[mRNA]_locus=scaffold5565_2:2523:3722:+	Bacteria
469360	GL0009495_MH0016_[Complete]_[mRNA]_locus=scaffold5565_3:1232:2449:+	-
469434	GL0033106_MH0016_[Complete]_[mRNA]_locus=scaffold5649_3:4288:5226:-	Faecalibacterium prausnitzii
469435	GL0066600_MH0016_[Complete]_[mRNA]_locus=scaffold5649_5:438:1592:-	-
469436	GL0066601_MH0016_[Complete]_[mRNA]_locus=scaffold5649_5:1971:2828:-	-
469438	GL0066603_MH0016_[Complete]_[mRNA]_locus=scaffold5649_5:3476:4168:-	-
469439	GL0066604_MH0016_[Complete]_[mRNA]_locus=scaffold5649_5:4171:4746:-	-
469440	GL0066605_MH0016_[Complete]_[mRNA]_locus=scaffold5649_5:4746:5702:-	-
469441	GL0066606_MH0016_[Complete]_[mRNA]_locus=scaffold5649_5:5706:7043:-	-
469442	GL0043558_MH0016_[Complete]_[mRNA]_locus=scaffold5649_6:2047:2937:-	Faecalibacterium prausnitzii
469443	GL0043559_MH0016_[Complete]_[mRNA]_locus=scaffold5649_6:2952:3608:-	Faecalibacterium prausnitzii

469499	GL0036418_MH0016_[Complete]_[mRNA]_locus=scaffold5725_3:335:937:+	Faecalibacterium prausnitzii
469513	GL0007423_MH0016_[Complete]_[mRNA]_locus=scaffold5771_2:552:2924:+	Firmicutes
469514	GL0091852_MH0016_[Complete]_[mRNA]_locus=scaffold5771_4:84:1346:+	Bacteria
469515	GL0091853_MH0016_[Complete]_[mRNA]_locus=scaffold5771_4:1365:1697:+	Faecalibacterium prausnitzii
469517	GL0039439_MH0016_[Complete]_[mRNA]_locus=scaffold5771_6:1267:1713:+	-
469518	GL0130632_MH0016_[Complete]_[mRNA]_locus=scaffold5771_7:1252:2643:+	-
469520	GL0030332_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold5771_10:123:797:+	-
469532	GL0141215_MH0016_[Complete]_[mRNA]_locus=scaffold5784_3:453:1625:-	-
469533	GL0024501_MH0016_[Complete]_[mRNA]_locus=scaffold5784_4:789:2435:-	Clostridium hylemonae
469534	GL0024502_MH0016_[Complete]_[mRNA]_locus=scaffold5784_4:2432:3388:-	Roseburia inulinivorans
469537	GL0024508_MH0016_[Complete]_[mRNA]_locus=scaffold5784_4:10815:12155:-	Bacteria
469539	GL0024510_MH0016_[Complete]_[mRNA]_locus=scaffold5784_4:14156:15238:-	Bacteria
469540	GL0024511_MH0016_[Complete]_[mRNA]_locus=scaffold5784_4:15238:16020:-	Roseburia inulinivorans
469551	GL0031627_MH0016_[Complete]_[mRNA]_locus=scaffold5810_4:902:2224:+	-

469552	GL0048135_MH0016_[Complete]_[mRNA]_locus=scaffold5810_5:23:238:+	-
469553	GL0048136_MH0016_[Complete]_[mRNA]_locus=scaffold5810_5:238:1332:+	-
469555	GL0044032_MH0016_[Complete]_[mRNA]_locus=scaffold5814_1:197:1876:+	-
469556	GL0044034_MH0016_[Complete]_[mRNA]_locus=scaffold5814_1:2720:4609:+	Faecalibacterium prausnitzii
469557	GL0044035_MH0016_[Complete]_[mRNA]_locus=scaffold5814_1:4721:5491:+	-
469558	GL0019124_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:572:2293:+	-
469559	GL0019125_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:2293:3339:+	-
469561	GL0019127_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:4206:6149:+	-
469562	GL0019128_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:6156:7562:+	-
469563	GL0019129_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:7638:8582:+	-
469564	GL0019130_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:8688:9647:+	-
469565	GL0019131_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:9666:10415:+	-
469566	GL0019132_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:10412:11368:+	-
469568	GL0019134_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:12339:13202:+	-

469569	GL0019135_MH0016_[Complete]_[mRNA]_locus=scaffold5814_2:13286:14158:+	-
469570	GL0077138_MH0016_[Complete]_[mRNA]_locus=scaffold5814_3:2965:3939:+	-
469572	GL0093536_MH0016_[Complete]_[mRNA]_locus=scaffold5814_5:1958:2302:+	-
469573	GL0093537_MH0016_[Complete]_[mRNA]_locus=scaffold5814_5:2355:2894:+	-
469574	GL0085623_MH0016_[Complete]_[mRNA]_locus=scaffold5814_6:1632:2660:+	-
469577	GL0144409_MH0016_[Complete]_[mRNA]_locus=scaffold5814_7:3634:4089:-	-
469578	GL0144410_MH0016_[Complete]_[mRNA]_locus=scaffold5814_7:4107:5333:-	-
469579	GL0144411_MH0016_[Complete]_[mRNA]_locus=scaffold5814_7:5330:6097:-	-
469580	GL0144412_MH0016_[Complete]_[mRNA]_locus=scaffold5814_7:6177:7067:-	-
469583	GL0118344_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:753:1781:+	-
469584	GL0118347_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:3556:4689:+	Faecalibacterium prausnitzii
469585	GL0118348_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:4771:5121:+	-
469586	GL0118351_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:6178:7254:-	-
469587	GL0118352_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:7741:7950:+	-

469588	GL0118354_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:8288:9217:-	-
469589	GL0118355_MH0016_[Complete]_[mRNA]_locus=scaffold5814_8:9214:10098:-	-
469599	GL0036126_MH0016_[Complete]_[mRNA]_locus=scaffold5834_5:238:1377:+	Faecalibacterium prausnitzii
469600	GL0010837_MH0016_[Complete]_[mRNA]_locus=scaffold5834_6:1255:1563:+	-
469601	GL0010838_MH0016_[Complete]_[mRNA]_locus=scaffold5834_6:1577:2626:+	-
469602	GL0139928_MH0016_[Complete]_[mRNA]_locus=scaffold5834_7:8:814:-	-
469604	GL0117052_MH0016_[Complete]_[mRNA]_locus=scaffold5834_8:1383:3698:-	-
469605	GL0062721_MH0016_[Complete]_[mRNA]_locus=scaffold5834_9:9:1325:-	-
469606	GL0062722_MH0016_[Complete]_[mRNA]_locus=scaffold5834_9:1466:2605:-	-
469678	GL0109204_MH0016_[Complete]_[mRNA]_locus=scaffold5906_5:941:1909:-	-
469681	GL0109213_MH0016_[Complete]_[mRNA]_locus=scaffold5906_5:9469:10584:-	-
469738	GL0031623_MH0016_[Complete]_[mRNA]_locus=scaffold5993_1:3533:4915:+	Firmicutes
469739	GL0072316_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold5993_3:3:1118:+	-
469849	GL0117469_MH0016_[Complete]_[mRNA]_locus=scaffold6109_2:188:1537:-	-

469850	GL0060368_MH0016_[Complete]_[mRNA]_locus=scaffold6109_3:1278:2060:-	-
469851	GL0075767_MH0016_[Complete]_[mRNA]_locus=scaffold6109_4:1416:2408:-	Ruminococcus obeum
469852	GL0075768_MH0016_[Complete]_[mRNA]_locus=scaffold6109_4:2410:3513:-	Clostridium bolteae
470208	GL0096434_MH0016_[Complete]_[mRNA]_locus=scaffold6482_1:425:1369:+	-
470209	GL0096435_MH0016_[Complete]_[mRNA]_locus=scaffold6482_1:1381:2697:+	Enterococcus faecium
470210	GL0145549_MH0016_[Complete]_[mRNA]_locus=scaffold6482_3:60:2483:+	Clostridiales
470211	GL0145551_MH0016_[Complete]_[mRNA]_locus=scaffold6482_3:3926:5767:+	Clostridiales
470212	GL0145552_MH0016_[Complete]_[mRNA]_locus=scaffold6482_3:5939:7933:+	Faecalibacterium prausnitzii
470213	GL0145554_MH0016_[Complete]_[mRNA]_locus=scaffold6482_3:8812:9897:+	-
470377	GL0023025_MH0016_[Complete]_[mRNA]_locus=scaffold6645_2:975:2321:-	Faecalibacterium prausnitzii
470380	GL0100312_MH0016_[Complete]_[mRNA]_locus=scaffold6645_3:312:1070:-	Faecalibacterium prausnitzii
470381	GL0100313_MH0016_[Complete]_[mRNA]_locus=scaffold6645_3:1072:2979:-	Faecalibacterium prausnitzii
470382	GL0100314_MH0016_[Complete]_[mRNA]_locus=scaffold6645_3:2976:3995:-	Faecalibacterium prausnitzii
470383	GL0100315_MH0016_[Complete]_[mRNA]_locus=scaffold6645_3:4124:5245:-	Faecalibacterium prausnitzii

470661	GL0140182_MH0016_[Complete]_[mRNA]_locus=scaffold6810_2:32:2011:-	Bacteria
470662	GL0140183_MH0016_[Complete]_[mRNA]_locus=scaffold6810_2:2197:3081:-	-
470663	GL0005979_MH0016_[Complete]_[mRNA]_locus=scaffold6810_3:459:1370:-	-
470664	GL0034390_MH0016_[Complete]_[mRNA]_locus=scaffold6810_4:221:1108:+	-
470987	GL0144119_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold7076_1:1:273:-	-
470988	GL0054097_MH0016_[Complete]_[mRNA]_locus=scaffold7076_4:43:1098:+	-
470989	GL0133564_MH0016_[Complete]_[mRNA]_locus=scaffold7076_7:77:1309:-	-
470990	GL0133565_MH0016_[Complete]_[mRNA]_locus=scaffold7076_7:1466:2428:-	-
470992	GL0060881_MH0016_[Complete]_[mRNA]_locus=scaffold7076_10:1950:3143:-	-
470994	GL0143834_MH0016_[Complete]_[mRNA]_locus=scaffold7076_14:1537:2391:+	-
470995	GL0143836_MH0016_[Complete]_[mRNA]_locus=scaffold7076_14:3371:4051:-	-
470996	GL0143837_MH0016_[Complete]_[mRNA]_locus=scaffold7076_14:4051:5037:-	-
470997	GL0078154_MH0016_[Complete]_[mRNA]_locus=scaffold7076_18:565:1395:-	Ruminococcus obeum
470998	GL0078155_MH0016_[Complete]_[mRNA]_locus=scaffold7076_18:1385:3109:-	Firmicutes

470999	GL0078156_MH0016_[Complete]_[mRNA]_locus=scaffold7076_18:3193:3741:-	Ruminococcus obeum
471005	GL0111654_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:290:2167:-	Faecalibacterium prausnitzii
471006	GL0111656_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:2663:3556:-	-
471008	GL0111658_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:3774:4991:-	-
471010	GL0111660_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:5911:6324:-	-
471012	GL0111663_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:7483:8013:-	-
471013	GL0111664_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:8010:8441:-	-
471014	GL0111665_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:8438:9478:-	-
471016	GL0111667_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:9865:10059:-	-
471018	GL0111669_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:10542:11429:-	-
471019	GL0111670_MH0016_[Complete]_[mRNA]_locus=scaffold7092_1:11616:13607:-	Clostridia
471020	GL0022251_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:1070:1663:+	-
471021	GL0022252_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:1927:3321:+	-
471022	GL0022253_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:3338:4522:+	-

471023	GL0022254_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:4570:5484:-	-
471024	GL0022255_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:5454:6452:-	-
471025	GL0022256_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:6442:7887:-	-
471027	GL0022259_MH0016_[Complete]_[mRNA]_locus=scaffold7092_2:8964:9437:-	-
471201	GL0098620_MH0016_[Complete]_[mRNA]_locus=scaffold7272_2:2661:3095:-	-
471202	GL0098621_MH0016_[Complete]_[mRNA]_locus=scaffold7272_2:3112:3384:-	-
471203	GL0098622_MH0016_[Complete]_[mRNA]_locus=scaffold7272_2:3489:3827:-	Dorea formicigenerans
471205	GL0098624_MH0016_[Complete]_[mRNA]_locus=scaffold7272_2:4605:5948:-	Ruminococcaceae
471226	GL0144668_MH0016_[Complete]_[mRNA]_locus=scaffold7303_2:820:2094:+	-
471227	GL0133427_MH0016_[Complete]_[mRNA]_locus=scaffold7303_3:3090:5387:+	-
471229	GL0133429_MH0016_[Complete]_[mRNA]_locus=scaffold7303_3:6715:8256:+	-
471501	GL0024983_MH0016_[Complete]_[mRNA]_locus=scaffold7627_3:348:1226:+	-
471502	GL0001630_MH0016_[Complete]_[mRNA]_locus=scaffold7627_4:1000:1968:+	-
471504	GL0132218_MH0016_[Complete]_[mRNA]_locus=scaffold7627_5:377:1111:+	-

471505	GL0132219_MH0016_[Complete]_[mRNA]_locus=scaffold7627_5:1104:2663:+	-
471506	GL0132221_MH0016_[Complete]_[mRNA]_locus=scaffold7627_5:3181:5805:+	-
471508	GL0132223_MH0016_[Complete]_[mRNA]_locus=scaffold7627_5:7095:7814:+	-
471509	GL0038930_MH0016_[Complete]_[mRNA]_locus=scaffold7627_6:85:372:+	-
471599	GL0120841_MH0016_[Complete]_[mRNA]_locus=scaffold7754_4:1330:2409:-	Eubacterium biforme
471600	GL0120842_MH0016_[Complete]_[mRNA]_locus=scaffold7754_4:2441:3307:-	Faecalibacterium prausnitzii
471601	GL0120844_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold7754_4:4345:6378:+	Firmicutes
471645	GL0144954_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:1167:2072:+	-
471646	GL0144955_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:2286:3284:+	-
471647	GL0144956_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:3284:3982:+	-
471648	GL0144957_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:4311:5363:-	-
471649	GL0144958_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:5608:6975:+	-
471651	GL0144961_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:7766:8539:-	-
471652	GL0144963_MH0016_[Complete]_[mRNA]_locus=scaffold7818_1:9369:9902:+	-

471654	GL0092199_MH0016_[Complete]_[mRNA]_locus=scaffold7818_2:380:955:+	-
471656	GL0104799_MH0016_[Complete]_[mRNA]_locus=scaffold7818_3:74:484:-	-
471657	GL0104800_MH0016_[Complete]_[mRNA]_locus=scaffold7818_3:506:1690:-	-
471658	GL0104801_MH0016_[Complete]_[mRNA]_locus=scaffold7818_3:1879:2259:-	Faecalibacterium prausnitzii
471659	GL0104802_MH0016_[Complete]_[mRNA]_locus=scaffold7818_3:2338:2547:-	Faecalibacterium prausnitzii
471661	GL0074729_MH0016_[Complete]_[mRNA]_locus=scaffold7826_1:227:2299:+	Bacteria
471761	GL0091867_MH0016_[Complete]_[mRNA]_locus=scaffold7945_1:1966:2937:+	Collinsella aerofaciens
471762	GL0091868_MH0016_[Complete]_[mRNA]_locus=scaffold7945_1:2934:3743:+	Collinsella aerofaciens
471763	GL0091869_MH0016_[Complete]_[mRNA]_locus=scaffold7945_1:3752:4831:+	-
471765	GL0091873_MH0016_[Complete]_[mRNA]_locus=scaffold7945_1:7598:8296:+	-
471766	GL0091874_MH0016_[Complete]_[mRNA]_locus=scaffold7945_1:8315:9301:+	-
471768	GL0080940_MH0016_[Complete]_[mRNA]_locus=scaffold7945_4:2734:3705:-	-
471769	GL0055974_MH0016_[Complete]_[mRNA]_locus=scaffold7945_5:1094:2347:-	-
471772	GL0114169_MH0016_[Complete]_[mRNA]_locus=scaffold7945_11:1819:2712:+	-

471774	GL0091946_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:274:1413:-	-
471777	GL0091950_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:2955:3272:-	-
471778	GL0091951_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:3356:3601:-	-
471779	GL0091952_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:3674:3946:-	-
471780	GL0091953_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:4018:4710:-	-
471781	GL0091956_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:6295:7755:-	-
471782	GL0091957_MH0016_[Complete]_[mRNA]_locus=scaffold7945_13:7755:8360:-	-
471783	GL0055182_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold7945_14:2:2116:-	Bacteria
471784	GL0055183_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:2183:4216:-	Faecalibacterium prausnitzii
471785	GL0055185_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:5465:7066:-	Faecalibacterium prausnitzii
471786	GL0055186_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:7202:8515:-	-
471787	GL0055187_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:8499:9395:-	-
471788	GL0055188_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:9544:10680:-	-
471789	GL0055189_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:10877:12238:-	Faecalibacterium prausnitzii

471791	GL0055191_MH0016_[Complete]_[mRNA]_locus=scaffold7945_14:12964:13875:+	Faecalibacterium prausnitzii
471792	GL0046514_MH0016_[Complete]_[mRNA]_locus=scaffold7965_4:4:1314:+	-
471793	GL0046515_MH0016_[Complete]_[mRNA]_locus=scaffold7965_4:1385:1957:+	-
471794	GL0140149_MH0016_[Complete]_[mRNA]_locus=scaffold7965_5:1550:2014:-	Bacteria
471795	GL0140150_MH0016_[Complete]_[mRNA]_locus=scaffold7965_5:2173:3162:+	-
471799	GL0095781_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold7971_3:487:1080:+	-
471800	GL0116692_MH0016_[Complete]_[mRNA]_locus=scaffold7971_4:1821:2621:+	-
471801	GL0116693_MH0016_[Complete]_[mRNA]_locus=scaffold7971_4:2647:3765:+	-
471802	GL0084116_MH0016_[Complete]_[mRNA]_locus=scaffold7971_6:45:707:+	-
471891	GL0038488_MH0016_[Complete]_[mRNA]_locus=scaffold8137_1:191:1330:-	-
471892	GL0038489_MH0016_[Complete]_[mRNA]_locus=scaffold8137_1:1809:3530:+	Clostridiales
471893	GL0038490_MH0016_[Complete]_[mRNA]_locus=scaffold8137_1:3807:5066:+	Faecalibacterium prausnitzii
471895	GL0126949_MH0016_[Complete]_[mRNA]_locus=scaffold8137_6:40:735:-	-
471896	GL0126951_MH0016_[Complete]_[mRNA]_locus=scaffold8137_6:1224:2237:-	-

471897	GL0126952_MH0016_[Complete]_[mRNA]_locus=scaffold8137_6:2237:2776:-	-
471898	GL0126953_MH0016_[Complete]_[mRNA]_locus=scaffold8137_6:2779:4167:-	-
471929	GL0046090_MH0016_[Complete]_[mRNA]_locus=scaffold8190_1:1758:3704:+	-
471930	GL0046091_MH0016_[Complete]_[mRNA]_locus=scaffold8190_1:3701:4609:+	-
471940	GL0059521_MH0016_[Complete]_[mRNA]_locus=scaffold8221_4:27:878:-	Faecalibacterium prausnitzii
471941	GL0059522_MH0016_[Complete]_[mRNA]_locus=scaffold8221_4:883:1980:-	Collinsella aerofaciens
471944	GL0059525_MH0016_[Complete]_[mRNA]_locus=scaffold8221_4:4172:5188:-	-
471945	GL0059526_MH0016_[Complete]_[mRNA]_locus=scaffold8221_4:5192:5605:-	-
471947	GL0059529_MH0016_[Complete]_[mRNA]_locus=scaffold8221_4:7423:8151:+	-
471948	GL0064086_MH0016_[Complete]_[mRNA]_locus=scaffold8221_5:75:1103:-	-
471960	GL0078408_MH0016_[Complete]_[mRNA]_locus=scaffold8254_1:30:848:-	-
471961	GL0078409_MH0016_[Complete]_[mRNA]_locus=scaffold8254_1:841:1719:-	-
471962	GL0078410_MH0016_[Complete]_[mRNA]_locus=scaffold8254_1:1865:2707:-	-
472019	GL0146729_MH0016_[Complete]_[mRNA]_locus=scaffold8311_4:1085:2086:+	-

472020	GL0102472_MH0016_[Complete]_[mRNA]_locus=scaffold8311_6:125:679:-	-
472080	GL0000527_MH0016_[Complete]_[mRNA]_locus=scaffold8371_2:907:1800:-	-
472081	GL0000529_MH0016_[Complete]_[mRNA]_locus=scaffold8371_2:2391:3155:-	-
472193	GL0102482_MH0016_[Complete]_[mRNA]_locus=scaffold8599_1:935:2395:-	-
472194	GL0102484_MH0016_[Complete]_[mRNA]_locus=scaffold8599_1:3516:3899:+	-
472200	GL0062654_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold8599_11:1:768:+	-
472201	GL0062655_MH0016_[Complete]_[mRNA]_locus=scaffold8599_11:779:2401:+	-
472202	GL0062656_MH0016_[Complete]_[mRNA]_locus=scaffold8599_11:2401:4347:+	-
472203	GL0062657_MH0016_[Complete]_[mRNA]_locus=scaffold8599_11:4341:4898:+	-
472204	GL0062659_MH0016_[Complete]_[mRNA]_locus=scaffold8599_11:6074:6943:-	-
472205	GL0000219_MH0016_[Complete]_[mRNA]_locus=scaffold8599_12:243:1775:+	-
472206	GL0000220_MH0016_[Complete]_[mRNA]_locus=scaffold8599_12:2289:2711:+	-
472207	GL0000222_MH0016_[Complete]_[mRNA]_locus=scaffold8599_12:3043:4314:+	-
472208	GL0000223_MH0016_[Complete]_[mRNA]_locus=scaffold8599_12:4342:5772:+	-

472209	GL0010046_MH0016_[Complete]_[mRNA]_locus=scaffold8599_13:845:1222:+	-
472215	GL0010053_MH0016_[Complete]_[mRNA]_locus=scaffold8599_13:5383:5730:+	Clostridium ramosum
472219	GL0021997_MH0016_[Complete]_[mRNA]_locus=scaffold8599_18:1370:1933:-	-
472220	GL0021998_MH0016_[Complete]_[mRNA]_locus=scaffold8599_18:1978:2871:-	Anaerostipes caccae
472221	GL0043472_MH0016_[Complete]_[mRNA]_locus=scaffold8599_19:1265:2056:-	Clostridium scindens
472354	GL0018768_MH0016_[Complete]_[mRNA]_locus=scaffold8847_2:229:1239:-	-
472507	GL0135596_MH0016_[Complete]_[mRNA]_locus=scaffold9084_1:391:2250:+	-
472508	GL0135597_MH0016_[Complete]_[mRNA]_locus=scaffold9084_1:2422:3186:+	-
472509	GL0135598_MH0016_[Complete]_[mRNA]_locus=scaffold9084_1:3226:3630:+	-
472510	GL0135599_MH0016_[Complete]_[mRNA]_locus=scaffold9084_1:3700:4716:-	-
472701	GL0024280_MH0016_[Complete]_[mRNA]_locus=scaffold9266_3:334:1539:-	-
472704	GL0144659_MH0016_[Complete]_[mRNA]_locus=scaffold9271_1:132:1295:+	Faecalibacterium prausnitzii
472710	GL0117031_MH0016_[Complete]_[mRNA]_locus=scaffold9290_7:1506:2825:+	Faecalibacterium prausnitzii
472711	GL0117032_MH0016_[Complete]_[mRNA]_locus=scaffold9290_7:3013:3666:-	-

472719	GL0015808_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold9325_1:2:790:+	-
472720	GL0015809_MH0016_[Complete]_[mRNA]_locus=scaffold9325_1:802:1854:+	Faecalibacterium prausnitzii
472721	GL0110511_MH0016_[Complete]_[mRNA]_locus=scaffold9325_4:313:1455:-	Faecalibacterium prausnitzii
472722	GL0110514_MH0016_[Complete]_[mRNA]_locus=scaffold9325_4:2627:3511:+	Faecalibacterium prausnitzii
472724	GL0004597_MH0016_[Complete]_[mRNA]_locus=scaffold9325_6:630:1568:+	-
472725	GL0004598_MH0016_[Complete]_[mRNA]_locus=scaffold9325_6:1571:2323:+	-
472726	GL0004599_MH0016_[Complete]_[mRNA]_locus=scaffold9325_6:2332:3582:+	-
472802	GL0075280_MH0016_[Complete]_[mRNA]_locus=scaffold9434_1:205:846:-	-
472803	GL0075281_MH0016_[Complete]_[mRNA]_locus=scaffold9434_1:843:2939:-	-
472804	GL0137022_MH0016_[Complete]_[mRNA]_locus=scaffold9434_4:26:1708:-	-
472805	GL0137023_MH0016_[Complete]_[mRNA]_locus=scaffold9434_4:1836:2855:-	-
472808	GL0103543_MH0016_[Complete]_[mRNA]_locus=scaffold9434_6:67:996:+	-
472809	GL0103544_MH0016_[Complete]_[mRNA]_locus=scaffold9434_6:993:1463:+	-
473089	GL0085863_MH0016_[Complete]_[mRNA]_locus=scaffold9851_2:1535:2167:+	-

473090	GL0085864_MH0016_[Complete]_[mRNA]_locus=scaffold9851_2:2174:2947:+	-
473092	GL0093430_MH0016_[Complete]_[mRNA]_locus=scaffold9851_5:500:1459:+	-
473160	GL0124009_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold9958_1:3:1025:-	-
473367	GL0039216_MH0016_[Complete]_[mRNA]_locus=scaffold10238_9:841:2238:-	Roseburia inulinivorans
473432	GL0093941_MH0016_[Complete]_[mRNA]_locus=scaffold10267_1:25:1647:+	Ruminococcus obeum
473433	GL0093943_MH0016_[Complete]_[mRNA]_locus=scaffold10267_1:2962:3501:+	-
473537	GL0119998_MH0016_[Complete]_[mRNA]_locus=scaffold10316_1:409:1584:-	-
473539	GL0078902_MH0016_[Complete]_[mRNA]_locus=scaffold10316_3:2406:3689:-	-
473541	GL0078905_MH0016_[Complete]_[mRNA]_locus=scaffold10316_3:5743:6657:-	-
473640	GL0117914_MH0016_[Complete]_[mRNA]_locus=scaffold10406_1:416:1348:-	-
473641	GL0060474_MH0016_[Complete]_[mRNA]_locus=scaffold10406_2:63:1070:-	-
474122	GL0012248_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold10905_1:1071:1988:+	Streptococcus
474123	GL0078342_MH0016_[Complete]_[mRNA]_locus=scaffold10905_5:529:1935:+	Coprococcus
474124	GL0078343_MH0016_[Complete]_[mRNA]_locus=scaffold10905_5:2137:2706:+	Faecalibacterium prausnitzii

474125	GL0078344_MH0016_[Complete]_[mRNA]_locus=scaffold10905_5:2703:5075:+	Bacteria
474126	GL0078345_MH0016_[Complete]_[mRNA]_locus=scaffold10905_5:5066:6451:+	Faecalibacterium prausnitzii
474127	GL0078346_MH0016_[Complete]_[mRNA]_locus=scaffold10905_5:6444:8123:+	Faecalibacterium prausnitzii
474270	GL0082687_MH0016_[Complete]_[mRNA]_locus=scaffold10965_2:1174:2076:-	-
474271	GL0082688_MH0016_[Complete]_[mRNA]_locus=scaffold10965_2:2073:2582:-	-
474272	GL0082690_MH0016_[Complete]_[mRNA]_locus=scaffold10965_2:3083:3934:-	-
474273	GL0082693_MH0016_[Complete]_[mRNA]_locus=scaffold10965_2:5442:6536:-	-
474275	GL0094226_MH0016_[Complete]_[mRNA]_locus=scaffold10965_3:3988:4734:+	-
474276	GL0094227_MH0016_[Complete]_[mRNA]_locus=scaffold10965_3:4822:5583:-	-
474277	GL0094228_MH0016_[Complete]_[mRNA]_locus=scaffold10965_3:5871:6197:-	-
474278	GL0094229_MH0016_[Complete]_[mRNA]_locus=scaffold10965_3:6329:7105:+	-
474343	GL0000464_MH0016_[Complete]_[mRNA]_locus=scaffold11037_2:232:729:+	-
474344	GL0051678_MH0016_[Complete]_[mRNA]_locus=scaffold11037_3:89:1162:+	-
474627	GL0105833_MH0016_[Complete]_[mRNA]_locus=scaffold11512_1:17:1144:-	-

474660	GL0070349_MH0016_[Complete]_[mRNA]_locus=scaffold11575_1:539:1762:+	-
474770	GL0094239_MH0016_[Complete]_[mRNA]_locus=scaffold11703_2:397:984:-	-
474771	GL0094240_MH0016_[Complete]_[mRNA]_locus=scaffold11703_2:1199:2977:+	Bacteria
474774	GL0131565_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold11703_6:2:1678:+	Clostridiales
474775	GL0131566_MH0016_[Complete]_[mRNA]_locus=scaffold11703_6:2216:2797:+	-
474843	GL0132394_MH0016_[Complete]_[mRNA]_locus=scaffold11795_1:501:1079:-	-
474844	GL0132395_MH0016_[Complete]_[mRNA]_locus=scaffold11795_1:1089:2543:-	-
474860	GL0011139_MH0016_[Complete]_[mRNA]_locus=scaffold11859_2:972:2225:-	Ruminococcus obeum
474861	GL0068655_MH0016_[Complete]_[mRNA]_locus=scaffold11859_3:745:1512:-	-
474983	GL0005210_MH0016_[Complete]_[mRNA]_locus=scaffold12062_1:93:956:-	Faecalibacterium prausnitzii
474984	GL0005211_MH0016_[Complete]_[mRNA]_locus=scaffold12062_1:975:1892:-	Faecalibacterium prausnitzii
474985	GL0131335_MH0016_[Complete]_[mRNA]_locus=scaffold12062_2:150:1955:+	Faecalibacterium prausnitzii
474986	GL0036838_MH0016_[Complete]_[mRNA]_locus=scaffold12062_3:689:2512:+	Faecalibacterium prausnitzii
474987	GL0036839_MH0016_[Complete]_[mRNA]_locus=scaffold12062_3:2529:3320:+	Faecalibacterium prausnitzii

475177	GL0123743_MH0016_[Complete]_[mRNA]_locus=scaffold12300_1:4897:6747:-	Bacteria
475178	GL0123745_MH0016_[Complete]_[mRNA]_locus=scaffold12300_1:7409:8623:-	Clostridium acetobutylicum
475179	GL0123746_MH0016_[Complete]_[mRNA]_locus=scaffold12300_1:8604:9674:-	Clostridium acetobutylicum
475318	GL0092536_MH0016_[Complete]_[mRNA]_locus=scaffold12617_2:171:791:-	-
475319	GL0092537_MH0016_[Complete]_[mRNA]_locus=scaffold12617_2:843:1730:+	Ruminococcus gnavus
475320	GL0002418_MH0016_[Complete]_[mRNA]_locus=scaffold12617_3:1052:1879:+	-
475321	GL0102734_MH0016_[Complete]_[mRNA]_locus=scaffold12617_5:1042:1437:+	-
475322	GL0012824_MH0016_[Complete]_[mRNA]_locus=scaffold12617_6:639:1520:+	-
475323	GL0012825_MH0016_[Complete]_[mRNA]_locus=scaffold12617_6:1528:3594:+	-
475438	GL0058761_MH0016_[Complete]_[mRNA]_locus=scaffold12719_3:881:1525:-	-
475590	GL0131332_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold13058_1:1302:2912:-	-
475591	GL0110308_MH0016_[Complete]_[mRNA]_locus=scaffold13058_3:124:1044:-	-
475592	GL0110309_MH0016_[Complete]_[mRNA]_locus=scaffold13058_3:1041:2339:-	-
475594	GL0110311_MH0016_[Complete]_[mRNA]_locus=scaffold13058_3:2969:3481:+	-

475595	GL0121230_MH0016_[Complete]_[mRNA]_locus=scaffold13058_4:15:1505:-	-
475596	GL0121232_MH0016_[Complete]_[mRNA]_locus=scaffold13058_4:2713:3468:-	Faecalibacterium prausnitzii
475662	GL0032792_MH0016_[Complete]_[mRNA]_locus=scaffold13127_2:8994:9464:+	-
475708	GL0000305_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold13251_2:1:387:+	-
475709	GL0000307_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold13251_2:759:2408:+	Bacteria
475880	GL0064718_MH0016_[Complete]_[mRNA]_locus=scaffold13492_2:980:1864:+	-
475881	GL0064719_MH0016_[Complete]_[mRNA]_locus=scaffold13492_2:1883:2788:+	-
475896	GL0056106_MH0016_[Complete]_[mRNA]_locus=scaffold13544_1:71:838:+	-
475897	GL0013441_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold13544_4:2:520:+	-
475898	GL0013443_MH0016_[Complete]_[mRNA]_locus=scaffold13544_4:1453:2562:-	-
475899	GL0013444_MH0016_[Complete]_[mRNA]_locus=scaffold13544_4:2663:3838:-	-
475901	GL0013446_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold13544_4:4910:5272:-	-
475937	GL0104105_MH0016_[Complete]_[mRNA]_locus=scaffold13613_1:342:2030:-	-
476122	GL0090761_MH0016_[Complete]_[mRNA]_locus=scaffold13861_1:13:711:+	-

476217	GL0141723_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold13984_1:347:1708:+	Faecalibacterium prausnitzii
476218	GL0023130_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold13984_8:393:1355:+	-
476241	GL0122345_MH0016_[Complete]_[mRNA]_locus=scaffold14000_1:1424:2329:-	-
476242	GL0122346_MH0016_[Complete]_[mRNA]_locus=scaffold14000_1:2329:3099:-	-
476243	GL0133864_MH0016_[Complete]_[mRNA]_locus=scaffold14000_2:2436:3086:+	-
476245	GL0108491_MH0016_[Complete]_[mRNA]_locus=scaffold14000_4:1192:3060:-	-
476246	GL0108492_MH0016_[Complete]_[mRNA]_locus=scaffold14000_4:3064:3840:-	-
476320	GL0119549_MH0016_[Complete]_[mRNA]_locus=scaffold14143_4:1117:1875:-	-
476375	GL0108535_MH0016_[Complete]_[mRNA]_locus=scaffold14194_3:384:1382:+	-
476376	GL0108536_MH0016_[Complete]_[mRNA]_locus=scaffold14194_3:1379:2008:+	-
476760	GL0082526_MH0016_[Complete]_[mRNA]_locus=scaffold14936_1:1174:2955:-	Bacteria
476848	GL0004117_MH0016_[Complete]_[mRNA]_locus=scaffold15040_3:8643:9575:+	Faecalibacterium prausnitzii
476849	GL0004118_MH0016_[Complete]_[mRNA]_locus=scaffold15040_3:9763:10617:+	Bacteroides capillosus
476850	GL0004119_MH0016_[Complete]_[mRNA]_locus=scaffold15040_3:10683:13715:+	-

476851	GL0004120_MH0016_[Complete]_[mRNA]_locus=scaffold15040_3:13867:15204:-	Eubacterium hallii
477066	GL0056568_MH0016_[Complete]_[mRNA]_locus=scaffold15688_2:40:2658:+	Clostridiales
477067	GL0056569_MH0016_[Complete]_[mRNA]_locus=scaffold15688_2:2674:4794:+	Faecalibacterium prausnitzii
477068	GL0003525_MH0016_[Complete]_[mRNA]_locus=scaffold15688_3:1042:1845:+	-
477069	GL0003526_MH0016_[Complete]_[mRNA]_locus=scaffold15688_3:1920:2888:+	-
477070	GL0025138_MH0016_[Complete]_[mRNA]_locus=scaffold15688_4:2233:2730:+	-
477071	GL0025140_MH0016_[Complete]_[mRNA]_locus=scaffold15688_4:3646:4482:+	-
477072	GL0025141_MH0016_[Complete]_[mRNA]_locus=scaffold15688_4:4485:4958:+	-
477185	GL0000024_MH0016_[Complete]_[mRNA]_locus=scaffold16019_1:1064:1645:-	-
477283	GL0062497_MH0016_[Complete]_[mRNA]_locus=scaffold16150_4:3384:4298:-	Faecalibacterium prausnitzii
477284	GL0062498_MH0016_[Complete]_[mRNA]_locus=scaffold16150_4:4295:5980:-	Faecalibacterium prausnitzii
477285	GL0028344_MH0016_[Complete]_[mRNA]_locus=scaffold16150_5:325:2310:+	Clostridiales
477286	GL0028345_MH0016_[Complete]_[mRNA]_locus=scaffold16150_5:2408:3859:+	-
477401	GL0110861_MH0016_[Complete]_[mRNA]_locus=scaffold16451_2:592:894:-	-

478233	GL0121497_MH0016_[Complete]_[mRNA]_locus=scaffold18176_1:55:2421:+	Clostridiales
478234	GL0121501_MH0016_[Complete]_[mRNA]_locus=scaffold18176_1:4656:5711:+	Clostridium
478235	GL0085280_MH0016_[Complete]_[mRNA]_locus=scaffold18176_3:153:458:+	Bacteria
478236	GL0085281_MH0016_[Complete]_[mRNA]_locus=scaffold18176_3:470:1060:+	Clostridium leptum
478237	GL0145214_MH0016_[Complete]_[mRNA]_locus=scaffold18176_5:603:1226:+	Clostridium methylpentosum
478362	GL0002715_MH0016_[Complete]_[mRNA]_locus=scaffold18409_2:402:1328:-	-
478363	GL0076740_MH0016_[Complete]_[mRNA]_locus=scaffold18409_3:1:705:-	-
478364	GL0076741_MH0016_[Complete]_[mRNA]_locus=scaffold18409_3:728:2077:-	-
478384	GL0110317_MH0016_[Complete]_[mRNA]_locus=scaffold18437_2:38:1798:-	-
478437	GL0020099_MH0016_[Complete]_[mRNA]_locus=scaffold18634_3:722:2467:-	Clostridia
478438	GL0020100_MH0016_[Complete]_[mRNA]_locus=scaffold18634_3:2815:3990:+	-
478439	GL0020101_MH0016_[Complete]_[mRNA]_locus=scaffold18634_3:3974:4807:+	-
478440	GL0020102_MH0016_[Complete]_[mRNA]_locus=scaffold18634_3:4820:5581:+	-
478441	GL0020103_MH0016_[Complete]_[mRNA]_locus=scaffold18634_3:5607:7115:+	-

478442	GL0020104_MH0016_[Complete]_[mRNA]_locus=scaffold18634_3:7218:8348:+	Faecalibacterium prausnitzii
479121	GL0079944_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold20487_2:20:937:-	-
479181	GL0055077_MH0016_[Complete]_[mRNA]_locus=scaffold20616_1:758:1945:-	-
479381	GL0083186_MH0016_[Complete]_[mRNA]_locus=scaffold21000_3:70:1014:-	-
479632	GL0134425_MH0016_[Complete]_[mRNA]_locus=scaffold21546_1:776:1333:-	-
479839	GL0036484_MH0016_[Complete]_[mRNA]_locus=scaffold21986_1:1309:1566:+	Clostridium cellulolyticum
480428	GL0074574_MH0016_[Complete]_[mRNA]_locus=scaffold23290_4:541:2877:+	Lachnospiraceae
480682	GL0101667_MH0016_[Complete]_[mRNA]_locus=scaffold23836_2:353:1177:-	-
480768	GL0009660_MH0016_[Complete]_[mRNA]_locus=scaffold24019_1:1022:1798:-	-
480769	GL0096901_MH0016_[Complete]_[mRNA]_locus=scaffold24019_2:589:1560:-	-
480770	GL0117701_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold24019_3:2:1600:-	-
480771	GL0117702_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold24019_3:1683:2159:-	Desulfotomaculum reducens
480825	GL0042686_MH0016_[Complete]_[mRNA]_locus=scaffold24137_2:655:1050:+	-
481154	GL0112857_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold25033_1:2:3295:-	Eubacterium hallii

481156	GL0112859_MH0016_[Complete]_[mRNA]_locus=scaffold25033_1:5498:6217:-	Clostridium
481187	GL0038245_MH0016_[Complete]_[mRNA]_locus=scaffold25072_1:104:1057:+	-
481188	GL0038246_MH0016_[Complete]_[mRNA]_locus=scaffold25072_1:1054:1815:+	-
481189	GL0038247_MH0016_[Complete]_[mRNA]_locus=scaffold25072_1:1808:2581:+	-
481769	GL0014695_MH0016_[Complete]_[mRNA]_locus=scaffold26504_2:890:1756:+	-
481943	GL0055612_MH0016_[Complete]_[mRNA]_locus=scaffold26925_1:217:981:+	-
481944	GL0055613_MH0016_[Complete]_[mRNA]_locus=scaffold26925_1:994:1878:+	-
482378	GL0071980_MH0016_[Complete]_[mRNA]_locus=scaffold28083_1:835:2151:+	-
482379	GL0104880_MH0016_[Complete]_[mRNA]_locus=scaffold28083_3:87:923:+	-
482380	GL0104881_MH0016_[Complete]_[mRNA]_locus=scaffold28083_3:920:1816:+	-
482395	GL0033733_MH0016_[Complete]_[mRNA]_locus=scaffold28125_2:1900:2166:+	Bacteria
482396	GL0138657_MH0016_[Complete]_[mRNA]_locus=scaffold28125_4:145:624:+	-
482397	GL0138659_MH0016_[Complete]_[mRNA]_locus=scaffold28125_4:1738:3396:-	Bacteria
482438	GL0105384_MH0016_[Complete]_[mRNA]_locus=scaffold28372_2:703:1932:+	Faecalibacterium prausnitzii

482470	GL0143663_MH0016_[Complete]_[mRNA]_locus=scaffold28463_1:772:2007:-	-
482471	GL0051345_MH0016_[Complete]_[mRNA]_locus=scaffold28463_2:48:1406:-	-
482771	GL0079673_MH0016_[Complete]_[mRNA]_locus=scaffold29547_1:8024:9331:-	-
482772	GL0095474_MH0016_[Complete]_[mRNA]_locus=scaffold29547_2:1303:2148:-	Clostridiales
482773	GL0095477_MH0016_[Complete]_[mRNA]_locus=scaffold29547_2:7070:7657:+	-
482774	GL0095478_MH0016_[Complete]_[mRNA]_locus=scaffold29547_2:7824:8342:+	-
483224	GL0013118_MH0016_[Complete]_[mRNA]_locus=scaffold31095_1:260:1075:+	-
483225	GL0013120_MH0016_[Complete]_[mRNA]_locus=scaffold31095_1:1508:2383:+	-
483226	GL0070677_MH0016_[Complete]_[mRNA]_locus=scaffold31095_2:308:847:+	-
483386	GL0095536_MH0016_[Complete]_[mRNA]_locus=scaffold31639_6:510:1253:-	-
483586	GL0008288_MH0016_[Complete]_[mRNA]_locus=scaffold32252_1:212:1558:-	-
483887	GL0131065_MH0016_[Complete]_[mRNA]_locus=scaffold33184_4:11:637:-	-
483888	GL0131066_MH0016_[Complete]_[mRNA]_locus=scaffold33184_4:634:2118:-	Clostridiales
484014	GL0050281_MH0016_[Complete]_[mRNA]_locus=scaffold33512_4:910:1491:+	-

484404	GL0015333_MH0016_[Complete]_[mRNA]_locus=scaffold34417_3:3:1004:-	-
484405	GL0015334_MH0016_[Complete]_[mRNA]_locus=scaffold34417_3:1101:1718:-	-
484573	GL0135856_MH0016_[Complete]_[mRNA]_locus=scaffold34838_1:1657:2991:+	Atopobium rimae
484589	GL0085170_MH0016_[Complete]_[mRNA]_locus=scaffold34886_1:591:1484:+	-
484590	GL0085171_MH0016_[Complete]_[mRNA]_locus=scaffold34886_1:1694:2302:+	-
484591	GL0085172_MH0016_[Complete]_[mRNA]_locus=scaffold34886_1:2319:3002:+	-
484592	GL0098815_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold34886_2:12:827:+	-
485275	GL0109969_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold37161_1:2:1798:-	Clostridiales
485284	GL0134899_MH0016_[Complete]_[mRNA]_locus=scaffold37220_1:1236:2369:+	-
485285	GL0134900_MH0016_[Complete]_[mRNA]_locus=scaffold37220_1:2366:4861:+	-
485321	GL0084860_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold37344_1:3:476:-	-
485511	GL0142338_MH0016_[Complete]_[mRNA]_locus=scaffold38057_1:213:1124:+	Desulfitobacterium hafniense
485513	GL0016515_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold38057_2:3:1250:+	Anaerotruncus colihominis
485519	GL0045729_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold38068_1:1:1422:+	-

485853	GL0021458_MH0016_[Complete]_[mRNA]_locus=scaffold39165_1:848:2200:-	-
485868	GL0062057_MH0016_[Complete]_[mRNA]_locus=scaffold39196_1:1430:3232:-	Catenibacterium mitsuokai
485869	GL0062058_MH0016_[Complete]_[mRNA]_locus=scaffold39196_1:3355:3780:-	-
486100	GL0086948_MH0016_[Complete]_[mRNA]_locus=scaffold39793_1:40:477:+	-
486556	GL0007124_MH0016_[Complete]_[mRNA]_locus=scaffold41558_1:177:1385:+	-
486623	GL0028090_MH0016_[Complete]_[mRNA]_locus=scaffold41703_3:549:1073:+	-
486624	GL0097607_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold41703_4:1100:1870:+	-
486921	GL0016380_MH0016_[Complete]_[mRNA]_locus=scaffold42898_1:976:2412:+	-
487256	GL0040225_MH0016_[Complete]_[mRNA]_locus=scaffold44238_1:95:1069:-	-
487257	GL0040226_MH0016_[Complete]_[mRNA]_locus=scaffold44238_1:1079:2278:-	-
487311	GL0077477_MH0016_[Complete]_[mRNA]_locus=scaffold44413_1:126:905:-	-
487418	GL0108770_MH0016_[Complete]_[mRNA]_locus=scaffold44831_2:1721:2905:-	-
487419	GL0108771_MH0016_[Complete]_[mRNA]_locus=scaffold44831_2:3269:4198:+	-
487421	GL0108773_MH0016_[Complete]_[mRNA]_locus=scaffold44831_2:4996:6228:+	-

487965	GL0134731_MH0016_[Complete]_[mRNA]_locus=scaffold46978_1:192:680:+	-
488044	GL0141149_MH0016_[Complete]_[mRNA]_locus=scaffold47424_4:1:1185:-	-
488046	GL0141151_MH0016_[Complete]_[mRNA]_locus=scaffold47424_4:3132:4589:+	-
488349	GL0094847_MH0016_[Complete]_[mRNA]_locus=scaffold48770_1:119:772:-	-
488653	GL0127386_MH0016_[Complete]_[mRNA]_locus=scaffold50115_2:546:1409:+	-
489016	GL0011562_MH0016_[Complete]_[mRNA]_locus=scaffold51647_1:55:732:-	-
489017	GL0011565_MH0016_[Complete]_[mRNA]_locus=scaffold51647_1:3275:4699:+	-
489019	GL0105310_MH0016_[Complete]_[mRNA]_locus=scaffold51652_1:906:1250:+	Eubacterium hallii
489020	GL0105311_MH0016_[Complete]_[mRNA]_locus=scaffold51652_1:1384:4308:+	Eubacterium hallii
489908	GL0053506_MH0016_[Complete]_[mRNA]_locus=scaffold55489_1:68:1177:+	-
490611	GL0138139_MH0016_[Complete]_[mRNA]_locus=scaffold58613_1:216:1550:+	Bacteroides capillosus
490612	GL0138140_MH0016_[Complete]_[mRNA]_locus=scaffold58613_1:1826:4369:+	Bacteria
490613	GL0138141_MH0016_[Complete]_[mRNA]_locus=scaffold58613_1:4422:5882:+	Bacteria
490615	GL0138146_MH0016_[Complete]_[mRNA]_locus=scaffold58613_1:11538:12899:+	Bacteroides capillosus

490651	GL0024423_MH0016_[Complete]_[mRNA]_locus=scaffold58817_2:214:1881:-	Faecalibacterium prausnitzii
490652	GL0024424_MH0016_[Complete]_[mRNA]_locus=scaffold58817_2:1908:2378:-	-
490653	GL0024425_MH0016_[Complete]_[mRNA]_locus=scaffold58817_2:2375:3229:-	-
490661	GL0123964_MH0016_[Complete]_[mRNA]_locus=scaffold58852_1:763:1680:-	Ruminococcus obeum
490662	GL0123965_MH0016_[Complete]_[mRNA]_locus=scaffold58852_1:1702:2235:-	Ruminococcus obeum
490663	GL0123966_MH0016_[Complete]_[mRNA]_locus=scaffold58852_1:2237:3103:-	Clostridiales
490664	GL0123967_MH0016_[Complete]_[mRNA]_locus=scaffold58852_1:3096:4388:-	Ruminococcus obeum
491687	GL0141815_MH0016_[Complete]_[mRNA]_locus=scaffold63488_2:56:1231:+	-
491688	GL0141816_MH0016_[Complete]_[mRNA]_locus=scaffold63488_2:1228:2244:+	-
491689	GL0141817_MH0016_[Complete]_[mRNA]_locus=scaffold63488_2:2396:3508:+	-
491690	GL0141818_MH0016_[Complete]_[mRNA]_locus=scaffold63488_2:3501:4409:+	-
491691	GL0141819_MH0016_[Complete]_[mRNA]_locus=scaffold63488_2:4629:5735:+	-
491692	GL0014863_MH0016_[Complete]_[mRNA]_locus=scaffold63488_4:108:1628:+	-
491693	GL0014864_MH0016_[Complete]_[mRNA]_locus=scaffold63488_4:1762:2610:+	-

491694	GL0014865_MH0016_[Complete]_[mRNA]_locus=scaffold63488_4:2607:4343:+	-
491695	GL0014866_MH0016_[Complete]_[mRNA]_locus=scaffold63488_4:4439:4957:+	-
491951	GL0021976_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold65033_1:2:1462:+	-
493681	GL0061077_MH0016_[Lack_5'-end]_[mRNA]_locus=scaffold73115_1:1:375:+	Faecalibacterium prausnitzii
493683	GL0061079_MH0016_[Complete]_[mRNA]_locus=scaffold73115_1:1561:2385:+	-
493684	GL0061080_MH0016_[Complete]_[mRNA]_locus=scaffold73115_1:2378:3118:+	-
493800	GL0015856_MH0016_[Complete]_[mRNA]_locus=scaffold73927_1:183:1205:+	-
494060	GL0141778_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold75172_1:194:841:+	-
494758	GL0098481_MH0016_[Lack_both_end]_[mRNA]_locus=scaffold77843_3:3:1316:+	-
497104	GL0145570_MH0016_[Complete]_[mRNA]_locus=scaffold84454_1:355:1449:+	Porphyromonas gingivalis
498147	GL0100446_MH0016_[Lack_3'-end]_[mRNA]_locus=scaffold86524_1:138:989:+	-
498839	GL0092093_MH0016_[Complete]_[mRNA]_locus=scaffold87148_1:149:1090:+	-
502528	GL0035875_MH0016_[Complete]_[mRNA]_locus=C4132825_1:1249:2475:+	-
506686	GL0006187_MH0017_[Complete]_[mRNA]_locus=scaffold28088_1:2059:2841:+	Bacteroides vulgatus

508564	GL0022330_MH0017_[Complete]_[mRNA]_locus=scaffold41868_2:1339:2328:+	Heliobacterium modesticaldum
515353	GL0011167_MH0018_[Complete]_[mRNA]_locus=scaffold29365_1:2362:4608:+	Bacteroides
517499	GL0023829_MH0019_[Complete]_[mRNA]_locus=scaffold2856_3:83:568:-	Clostridiales
518009	GL0034534_MH0019_[Complete]_[mRNA]_locus=scaffold6282_1:381:1154:+	Anaerostipes caccae
518139	GL0053949_MH0019_[Lack_3'-end]_[mRNA]_locus=scaffold7312_1:1:528:-	-
518332	GL0046098_MH0019_[Complete]_[mRNA]_locus=scaffold9158_2:336:950:+	Ruminococcus obeum
518739	GL0013364_MH0019_[Complete]_[mRNA]_locus=scaffold11682_1:415:630:-	-
519102	GL0007521_MH0019_[Complete]_[mRNA]_locus=scaffold14369_4:2503:3504:-	Anaerotruncus colihominis
520308	GL0015101_MH0019_[Complete]_[mRNA]_locus=scaffold23451_3:313:534:+	-
521069	GL0039963_MH0019_[Lack_3'-end]_[mRNA]_locus=scaffold30997_2:105:581:+	-
521538	GL0011506_MH0019_[Complete]_[mRNA]_locus=scaffold35170_1:122:475:+	Clostridiales
521665	GL0027864_MH0019_[Complete]_[mRNA]_locus=scaffold36306_1:108:1181:+	Clostridium hiranonis
522342	GL0052535_MH0019_[Lack_3'-end]_[mRNA]_locus=scaffold42105_1:1:480:-	-

522826	GL0031049_MH0019_[Lack_5'-end]_[mRNA]_locus=scaffold45515_2:392:808:-	Clostridium acetobutylicum
523241	GL0010725_MH0019_[Complete]_[mRNA]_locus=scaffold47713_2:3234:3806:-	Alistipes putredinis
523770	GL0007756_MH0019_[Complete]_[mRNA]_locus=scaffold49387_1:340:681:-	-
524668	GL0056485_MH0019_[Complete]_[mRNA]_locus=C1431983_1:189:680:-	-
528631	GL0041412_MH0020_[Complete]_[mRNA]_locus=scaffold605_8:2936:4321:-	Clostridium botulinum
544400	GL0104762_MH0020_[Complete]_[mRNA]_locus=scaffold7588_10:302:991:+	Clostridiales
544406	GL0102825_MH0020_[Lack_5'-end]_[mRNA]_locus=scaffold7588_17:1:792:+	Clostridium leptum
568354	GL0017307_MH0020_[Complete]_[mRNA]_locus=scaffold48150_1:416:1588:+	Cyanobacteria
569361	GL0094582_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold273_1:2:112:+	-
569395	GL0017548_MH0021_[Complete]_[mRNA]_locus=scaffold437_2:343:1392:+	Faecalibacterium prausnitzii
569408	GL0014975_MH0021_[Complete]_[mRNA]_locus=scaffold581_1:1980:3551:+	Butyrivibrio
569959	GL0060203_MH0021_[Complete]_[mRNA]_locus=scaffold4311_1:185:550:+	-
570198	GL0008028_MH0021_[Complete]_[mRNA]_locus=scaffold6112_1:424:1050:+	-
570283	GL0087206_MH0021_[Complete]_[mRNA]_locus=scaffold6804_1:515:799:-	-

570290	GL0096854_MH0021_[Complete]_[mRNA]_locus=scaffold6860_1:153:1193:-	-
570665	GL0103324_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold9589_1:4:984:-	-
570674	GL0020982_MH0021_[Lack_3'-end]_[mRNA]_locus=scaffold9748_1:1:501:-	-
570861	GL0020316_MH0021_[Complete]_[mRNA]_locus=scaffold11179_1:249:638:-	-
570892	GL0050598_MH0021_[Lack_3'-end]_[mRNA]_locus=scaffold11413_2:61:921:+	-
571170	GL0094159_MH0021_[Complete]_[mRNA]_locus=scaffold13432_1:3:458:-	-
571784	GL0071839_MH0021_[Complete]_[mRNA]_locus=scaffold18128_1:258:596:+	Blautia hydrogenotrophica
571814	GL0088297_MH0021_[Complete]_[mRNA]_locus=scaffold18361_1:25:690:-	-
572012	GL0019024_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold20060_2:2:871:+	-
572541	GL0100023_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold24534_3:432:707:-	Clostridium methylpentosum
572623	GL0004733_MH0021_[Complete]_[mRNA]_locus=scaffold25089_1:306:722:-	-
572646	GL0072261_MH0021_[Complete]_[mRNA]_locus=scaffold25384_1:711:1499:-	-
572909	GL0018629_MH0021_[Complete]_[mRNA]_locus=scaffold27180_1:335:1294:+	-
573177	GL0099827_MH0021_[Complete]_[mRNA]_locus=scaffold29146_1:163:999:+	Firmicutes

573564	GL0032913_MH0021_[Complete]_[mRNA]_locus=scaffold32312_1:334:600:+	-
573818	GL0078603_MH0021_[Complete]_[mRNA]_locus=scaffold34119_1:182:826:+	Clostridiales
573867	GL0050742_MH0021_[Complete]_[mRNA]_locus=scaffold34532_1:243:1031:+	-
574059	GL0061467_MH0021_[Complete]_[mRNA]_locus=scaffold35864_1:28:726:-	-
574529	GL0046257_MH0021_[Complete]_[mRNA]_locus=scaffold39434_1:310:768:-	-
575273	GL0002671_MH0021_[Complete]_[mRNA]_locus=scaffold45245_1:113:769:+	-
575507	GL0073509_MH0021_[Lack_3'-end]_[mRNA]_locus=scaffold46810_1:2:607:-	-
575718	GL0028567_MH0021_[Complete]_[mRNA]_locus=scaffold47919_1:389:1297:+	-
576079	GL0014016_MH0021_[Complete]_[mRNA]_locus=scaffold50520_1:164:673:-	Clostridium bolteae
576275	GL0088936_MH0021_[Complete]_[mRNA]_locus=scaffold51809_1:211:1044:-	-
576353	GL0004823_MH0021_[Complete]_[mRNA]_locus=scaffold52133_1:26:571:-	-
577334	GL0033780_MH0021_[Lack_3'-end]_[mRNA]_locus=scaffold57464_1:2:466:-	Bacteroidales
577444	GL0091758_MH0021_[Complete]_[mRNA]_locus=scaffold58011_1:3121:3609:+	-
577558	GL0037903_MH0021_[Complete]_[mRNA]_locus=scaffold58620_1:343:1338:+	-

577647	GL0032806_MH0021_[Complete]_[mRNA]_locus=scaffold59142_1:133:852:-	-
577682	GL0049350_MH0021_[Complete]_[mRNA]_locus=scaffold59339_1:382:1239:+	-
577685	GL0025592_MH0021_[Complete]_[mRNA]_locus=scaffold59349_1:151:420:+	-
578029	GL0101879_MH0021_[Lack_both_end]_[mRNA]_locus=scaffold60788_2:2:1486:-	Bacteria
578537	GL0013918_MH0021_[Complete]_[mRNA]_locus=scaffold62563_1:53:1399:+	Dorea formicigenerans
578896	GL0050148_MH0021_[Complete]_[mRNA]_locus=scaffold63882_1:322:1191:-	Clostridia
579082	GL0077671_MH0021_[Complete]_[mRNA]_locus=scaffold64486_1:240:668:+	-
579195	GL0029978_MH0021_[Complete]_[mRNA]_locus=scaffold64908_1:1411:2484:-	Faecalibacterium prausnitzii
579430	GL0032030_MH0021_[Complete]_[mRNA]_locus=scaffold65456_1:270:1025:-	-
579477	GL0075555_MH0021_[Complete]_[mRNA]_locus=scaffold65611_1:46:456:+	-
579551	GL0082541_MH0021_[Complete]_[mRNA]_locus=scaffold65851_1:80:613:+	Coprococcus comes
579643	GL0070848_MH0021_[Complete]_[mRNA]_locus=scaffold66156_2:22:228:-	-
579669	GL0041816_MH0021_[Complete]_[mRNA]_locus=scaffold66248_1:519:989:+	-
580306	GL0052028_MH0021_[Complete]_[mRNA]_locus=scaffold68071_1:1076:1771:+	Faecalibacterium prausnitzii

580326	GL0099472_MH0021_[Complete]_[mRNA]_locus=scaffold68113_1:111:950:-	-
580504	GL0060012_MH0021_[Complete]_[mRNA]_locus=scaffold68613_1:362:1153:+	-
580762	GL0083779_MH0021_[Complete]_[mRNA]_locus=scaffold69207_1:635:1156:+	-
580776	GL0006132_MH0021_[Complete]_[mRNA]_locus=scaffold69268_1:230:523:+	-
580812	GL0078698_MH0021_[Complete]_[mRNA]_locus=scaffold69313_1:902:1570:+	Roseburia inulinivorans
581154	GL0018329_MH0021_[Complete]_[mRNA]_locus=scaffold69762_1:1084:2208:-	-
581629	GL0027267_MH0021_[Complete]_[mRNA]_locus=scaffold70596_1:153:1016:-	-
581679	GL0037815_MH0021_[Complete]_[mRNA]_locus=scaffold70655_1:365:844:-	-
582072	GL0003955_MH0021_[Lack_5'-end]_[mRNA]_locus=scaffold71115_1:80:694:-	-
582824	GL0047323_MH0021_[Complete]_[mRNA]_locus=scaffold71928_1:25:942:-	-
582825	GL0047324_MH0021_[Complete]_[mRNA]_locus=scaffold71928_1:942:1265:-	-
582826	GL0047325_MH0021_[Complete]_[mRNA]_locus=scaffold71928_1:1301:1945:-	-
585028	GL0067430_MH0021_[Complete]_[mRNA]_locus=C2011993_1:116:499:-	Bifidobacterium catenulatum
585071	GL0024837_MH0021_[Lack_5'-end]_[mRNA]_locus=C2013451_1:236:610:-	Bacteria

585142	GL0070764_MH0021_[Complete]_[mRNA]_locus=C2015189_1:314:568:+	-
585250	GL0005321_MH0021_[Complete]_[mRNA]_locus=C2018032_1:128:634:+	-
585553	GL0056371_MH0021_[Complete]_[mRNA]_locus=C2026475_1:178:657:-	-
585799	GL0103281_MH0021_[Complete]_[mRNA]_locus=C2032567_1:144:518:-	Clostridiales
586456	GL0004551_MH0021_[Complete]_[mRNA]_locus=C2048491_1:398:883:-	-
586709	GL0092755_MH0021_[Complete]_[mRNA]_locus=C2053401_1:522:869:+	-
586710	GL0087566_MH0021_[Complete]_[mRNA]_locus=C2053411_1:282:857:+	-
586833	GL0045925_MH0021_[Complete]_[mRNA]_locus=C2055969_1:180:908:-	-
587307	GL0048364_MH0021_[Complete]_[mRNA]_locus=C2064403_1:52:993:-	-
587319	GL0048958_MH0021_[Complete]_[mRNA]_locus=C2064537_1:435:1106:-	-
587338	GL0086228_MH0021_[Complete]_[mRNA]_locus=C2064791_1:127:984:-	-
587342	GL0085731_MH0021_[Complete]_[mRNA]_locus=C2064829_1:351:890:+	-
587401	GL0074121_MH0021_[Complete]_[mRNA]_locus=C2065709_1:129:719:-	-
587977	GL0094736_MH0021_[Lack_5'-end]_[mRNA]_locus=C2074067_1:2:1330:+	-

588132	GL0005047_MH0021_[Complete]_[mRNA]_locus=C2075681_1:276:776:+	-
588415	GL0012900_MH0021_[Complete]_[mRNA]_locus=C2078487_1:428:1405:-	Epulopiscium
588514	GL0018258_MH0021_[Complete]_[mRNA]_locus=C2079277_1:96:830:-	Faecalibacterium prausnitzii
588515	GL0018259_MH0021_[Complete]_[mRNA]_locus=C2079277_1:834:1586:-	Faecalibacterium prausnitzii
591932	GL0010961_MH0022_[Complete]_[mRNA]_locus=scaffold229_6:1697:2515:+	Akkermansia muciniphila
591934	GL0010965_MH0022_[Complete]_[mRNA]_locus=scaffold229_6:3823:4263:+	Akkermansia muciniphila
591935	GL0000009_MH0022_[Complete]_[mRNA]_locus=scaffold229_7:444:1880:+	Verrucomicrobia
592478	GL0025758_MH0022_[Complete]_[mRNA]_locus=scaffold3612_1:32:652:+	Akkermansia muciniphila
592479	GL0007562_MH0022_[Complete]_[mRNA]_locus=scaffold3612_3:61:1419:-	Akkermansia muciniphila
592481	GL0024571_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold3612_6:1156:2502:-	Akkermansia muciniphila
592482	GL0019454_MH0022_[Complete]_[mRNA]_locus=scaffold3612_8:1670:2755:+	Akkermansia muciniphila
592483	GL0019455_MH0022_[Complete]_[mRNA]_locus=scaffold3612_8:2788:3681:+	Akkermansia muciniphila
592484	GL0019456_MH0022_[Complete]_[mRNA]_locus=scaffold3612_8:3887:4321:-	Akkermansia muciniphila
592489	GL0039010_MH0022_[Complete]_[mRNA]_locus=scaffold3684_10:240:557:-	Alkaliphilus oremlandii

592497	GL0030750_MH0022_[Complete]_[mRNA]_locus=scaffold3696_1:2564:3883:+	Akkermansia muciniphila
592733	GL0027716_MH0022_[Complete]_[mRNA]_locus=scaffold4966_1:814:1902:+	Akkermansia muciniphila
592734	GL0030873_MH0022_[Complete]_[mRNA]_locus=scaffold4966_7:904:1929:-	Akkermansia muciniphila
592735	GL0012983_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold4966_15:715:876:-	-
592763	GL0003582_MH0022_[Complete]_[mRNA]_locus=scaffold5198_5:2455:3726:-	Akkermansia muciniphila
592784	GL0039117_MH0022_[Complete]_[mRNA]_locus=scaffold5351_1:1811:2686:+	Akkermansia muciniphila
592785	GL0039118_MH0022_[Complete]_[mRNA]_locus=scaffold5351_1:2742:3548:+	Akkermansia muciniphila
592786	GL0039119_MH0022_[Complete]_[mRNA]_locus=scaffold5351_1:3718:5106:+	Akkermansia muciniphila
592787	GL0005853_MH0022_[Complete]_[mRNA]_locus=scaffold5351_8:275:1294:-	Akkermansia muciniphila
592795	GL0000936_MH0022_[Complete]_[mRNA]_locus=scaffold5351_11:569:2392:-	Bacteria
592797	GL0029471_MH0022_[Complete]_[mRNA]_locus=scaffold5351_13:931:1581:+	Akkermansia muciniphila
592798	GL0020836_MH0022_[Complete]_[mRNA]_locus=scaffold5351_14:161:2209:-	Akkermansia muciniphila
592799	GL0002987_MH0022_[Complete]_[mRNA]_locus=scaffold5351_18:747:1562:+	Akkermansia muciniphila
592863	GL0000643_MH0022_[Complete]_[mRNA]_locus=scaffold5753_10:1266:2225:+	Akkermansia muciniphila

592864	GL0000644_MH0022_[Complete]_[mRNA]_locus= scaffold5753_10:2222:3577:+	Akkermansia muciniphila
592866	GL0024868_MH0022_[Complete]_[mRNA]_locus= scaffold5753_12:553:933:-	Akkermansia muciniphila
592867	GL0024869_MH0022_[Complete]_[mRNA]_locus= scaffold5753_12:948:1367:-	Akkermansia muciniphila
592869	GL0038197_MH0022_[Complete]_[mRNA]_locus= scaffold5753_15:2274:3671:+	Akkermansia muciniphila
592870	GL0029691_MH0022_[Complete]_[mRNA]_locus= scaffold5753_16:668:1258:+	Akkermansia muciniphila
592871	GL0029692_MH0022_[Complete]_[mRNA]_locus= scaffold5753_16:1283:2950:-	Akkermansia muciniphila
592873	GL0020017_MH0022_[Complete]_[mRNA]_locus= scaffold5753_17:1157:2014:-	Akkermansia muciniphila
592902	GL0011297_MH0022_[Complete]_[mRNA]_locus= scaffold5864_2:1343:2404:-	Akkermansia muciniphila
592905	GL0011301_MH0022_[Complete]_[mRNA]_locus= scaffold5864_2:6567:7997:-	Akkermansia muciniphila
592907	GL0025878_MH0022_[Complete]_[mRNA]_locus= scaffold5864_5:814:2385:-	Akkermansia muciniphila
592911	GL0025882_MH0022_[Complete]_[mRNA]_locus= scaffold5864_5:6584:7507:-	Akkermansia muciniphila
592912	GL0025883_MH0022_[Complete]_[mRNA]_locus= scaffold5864_5:7658:8077:+	Akkermansia muciniphila
593204	GL0018180_MH0022_[Complete]_[mRNA]_locus= scaffold8242_7:814:1263:-	Verrucomicrobium spinosum
593464	GL0021935_MH0022_[Complete]_[mRNA]_locus= scaffold10639_1:2378:3049:-	Akkermansia muciniphila

593466	GL0026536_MH0022_[Complete]_[mRNA]_locus=scaffold10639_5:1788:3038:-	Akkermansia muciniphila
593467	GL0017675_MH0022_[Complete]_[mRNA]_locus=scaffold10639_6:1663:3111:+	Akkermansia muciniphila
593530	GL0032074_MH0022_[Complete]_[mRNA]_locus=scaffold11171_1:527:910:-	Akkermansia muciniphila
593531	GL0032076_MH0022_[Complete]_[mRNA]_locus=scaffold11171_1:1695:2579:+	Akkermansia muciniphila
593533	GL0001604_MH0022_[Complete]_[mRNA]_locus=scaffold11171_2:2253:3623:-	Akkermansia muciniphila
593535	GL0001606_MH0022_[Complete]_[mRNA]_locus=scaffold11171_2:4032:5012:-	Akkermansia muciniphila
593536	GL0001607_MH0022_[Complete]_[mRNA]_locus=scaffold11171_2:5048:6229:-	Akkermansia muciniphila
593538	GL0015462_MH0022_[Complete]_[mRNA]_locus=scaffold11171_7:1406:2635:+	Akkermansia muciniphila
593544	GL0012283_MH0022_[Complete]_[mRNA]_locus=scaffold11171_13:60:1910:-	Akkermansia muciniphila
593545	GL0026686_MH0022_[Complete]_[mRNA]_locus=scaffold11171_16:543:989:+	Akkermansia muciniphila
593631	GL0032015_MH0022_[Complete]_[mRNA]_locus=scaffold11651_4:2935:4311:+	Akkermansia muciniphila
593667	GL0036020_MH0022_[Complete]_[mRNA]_locus=scaffold12112_2:190:1797:+	Bacteria
593694	GL0034109_MH0022_[Complete]_[mRNA]_locus=scaffold12377_2:2858:4750:+	-
593695	GL0034111_MH0022_[Complete]_[mRNA]_locus=scaffold12377_2:4983:5789:+	-

593749	GL0022064_MH0022_[Complete]_[mRNA]_locus=scaffold12734_2:4:2643:-	Akkermansia muciniphila
593788	GL0004988_MH0022_[Complete]_[mRNA]_locus=scaffold12927_7:395:1357:+	Akkermansia muciniphila
593790	GL0004990_MH0022_[Complete]_[mRNA]_locus=scaffold12927_7:1538:2854:-	Akkermansia muciniphila
593794	GL0006040_MH0022_[Complete]_[mRNA]_locus=scaffold12927_13:867:1877:-	Akkermansia muciniphila
593795	GL0006041_MH0022_[Complete]_[mRNA]_locus=scaffold12927_13:1870:2835:-	Akkermansia muciniphila
593798	GL0004490_MH0022_[Complete]_[mRNA]_locus=scaffold12927_19:1275:2699:-	Verrucomicrobiaceae
593799	GL0021464_MH0022_[Complete]_[mRNA]_locus=scaffold12927_25:278:1144:+	Akkermansia muciniphila
593802	GL0021468_MH0022_[Complete]_[mRNA]_locus=scaffold12927_25:5359:5973:-	Akkermansia muciniphila
593806	GL0022709_MH0022_[Complete]_[mRNA]_locus=scaffold12927_27:444:650:-	-
593864	GL0013723_MH0022_[Complete]_[mRNA]_locus=scaffold13352_2:1560:2213:+	Akkermansia muciniphila
593866	GL0009927_MH0022_[Complete]_[mRNA]_locus=scaffold13352_4:1104:2570:-	Akkermansia muciniphila
593869	GL0031734_MH0022_[Complete]_[mRNA]_locus=scaffold13352_5:274:1326:+	Akkermansia muciniphila
593871	GL0031736_MH0022_[Complete]_[mRNA]_locus=scaffold13352_5:2418:3119:-	Akkermansia muciniphila
593922	GL0009457_MH0022_[Complete]_[mRNA]_locus=scaffold14006_1:683:1777:+	Akkermansia muciniphila

594064	GL0011955_MH0022_[Complete]_[mRNA]_locus=scaffold15498_1:291:1211:-	Akkermansia muciniphila
594065	GL0011957_MH0022_[Complete]_[mRNA]_locus=scaffold15498_1:1976:2620:-	Akkermansia muciniphila
594066	GL0023527_MH0022_[Complete]_[mRNA]_locus=scaffold15498_2:313:1608:+	Akkermansia muciniphila
594094	GL0014163_MH0022_[Complete]_[mRNA]_locus=scaffold15784_3:211:1251:-	Akkermansia muciniphila
594095	GL0014164_MH0022_[Complete]_[mRNA]_locus=scaffold15784_3:1248:2240:-	Akkermansia muciniphila
594097	GL0017488_MH0022_[Complete]_[mRNA]_locus=scaffold15785_1:155:808:+	Akkermansia muciniphila
594099	GL0036292_MH0022_[Complete]_[mRNA]_locus=scaffold15785_3:4084:5499:-	Akkermansia muciniphila
594122	GL0018432_MH0022_[Complete]_[mRNA]_locus=scaffold15901_4:351:2876:-	Akkermansia muciniphila
594208	GL0019692_MH0022_[Complete]_[mRNA]_locus=scaffold16624_5:1786:2589:+	Akkermansia muciniphila
594379	GL0009307_MH0022_[Complete]_[mRNA]_locus=scaffold18034_8:62:1153:-	Akkermansia muciniphila
594380	GL0018909_MH0022_[Complete]_[mRNA]_locus=scaffold18034_9:2370:3407:-	Akkermansia muciniphila
594458	GL0011184_MH0022_[Complete]_[mRNA]_locus=scaffold18589_3:161:1318:-	Akkermansia muciniphila
594480	GL0003498_MH0022_[Complete]_[mRNA]_locus=scaffold18786_8:661:1797:+	Akkermansia muciniphila
594481	GL0016178_MH0022_[Complete]_[mRNA]_locus=scaffold18786_9:937:1752:-	Akkermansia muciniphila

594516	GL0022352_MH0022_[Complete]_[mRNA]_locus=scaffold19108_1:733:1482:+	Akkermansia muciniphila
594517	GL0022353_MH0022_[Complete]_[mRNA]_locus=scaffold19108_1:1612:2127:-	Akkermansia muciniphila
594518	GL0022354_MH0022_[Complete]_[mRNA]_locus=scaffold19108_1:2531:3913:-	Akkermansia muciniphila
594519	GL0022355_MH0022_[Complete]_[mRNA]_locus=scaffold19108_1:4170:4742:+	Akkermansia muciniphila
594520	GL0010886_MH0022_[Complete]_[mRNA]_locus=scaffold19108_2:112:759:-	Akkermansia muciniphila
594521	GL0017464_MH0022_[Complete]_[mRNA]_locus=scaffold19108_4:1498:3648:-	Akkermansia muciniphila
594582	GL0012113_MH0022_[Complete]_[mRNA]_locus=scaffold19533_1:2667:3263:+	Akkermansia muciniphila
594583	GL0012115_MH0022_[Complete]_[mRNA]_locus=scaffold19533_1:3986:4507:-	Akkermansia muciniphila
594586	GL0012118_MH0022_[Complete]_[mRNA]_locus=scaffold19533_1:6362:7504:+	Akkermansia muciniphila
594587	GL0012119_MH0022_[Complete]_[mRNA]_locus=scaffold19533_1:7932:8396:-	Akkermansia muciniphila
594588	GL0012120_MH0022_[Complete]_[mRNA]_locus=scaffold19533_1:8477:9040:+	Akkermansia muciniphila
594589	GL0012121_MH0022_[Complete]_[mRNA]_locus=scaffold19533_1:9227:9685:-	Akkermansia muciniphila
594590	GL0011965_MH0022_[Complete]_[mRNA]_locus=scaffold19533_8:204:1148:-	Akkermansia muciniphila
594591	GL0029902_MH0022_[Complete]_[mRNA]_locus=scaffold19533_11:2286:2795:-	Akkermansia muciniphila

594592	GL0005168_MH0022_[Complete]_[mRNA]_locus=scaffold19533_13:1499:2590:-	Akkermansia muciniphila
594595	GL0000604_MH0022_[Complete]_[mRNA]_locus=scaffold19533_17:168:1523:-	Akkermansia muciniphila
594599	GL0009860_MH0022_[Complete]_[mRNA]_locus=scaffold19533_27:542:2278:-	Akkermansia muciniphila
594600	GL0009861_MH0022_[Complete]_[mRNA]_locus=scaffold19533_27:2331:3731:-	Akkermansia muciniphila
594601	GL0026624_MH0022_[Complete]_[mRNA]_locus=scaffold19533_30:753:2366:+	Akkermansia muciniphila
594602	GL0026626_MH0022_[Complete]_[mRNA]_locus=scaffold19533_30:3188:4048:-	Akkermansia muciniphila
594604	GL0034166_MH0022_[Complete]_[mRNA]_locus=scaffold19533_34:2709:4409:-	Verrucomicrobiales
594605	GL0034167_MH0022_[Complete]_[mRNA]_locus=scaffold19533_34:4573:6819:-	Akkermansia muciniphila
594607	GL0037654_MH0022_[Complete]_[mRNA]_locus=scaffold19533_37:2134:3360:+	Akkermansia muciniphila
594608	GL0037655_MH0022_[Complete]_[mRNA]_locus=scaffold19533_37:3357:4751:+	Akkermansia muciniphila
594609	GL0017328_MH0022_[Complete]_[mRNA]_locus=scaffold19533_38:3570:4298:+	Akkermansia muciniphila
594610	GL0017329_MH0022_[Complete]_[mRNA]_locus=scaffold19533_38:4271:5146:+	Akkermansia muciniphila
594612	GL0009857_MH0022_[Complete]_[mRNA]_locus=scaffold19533_39:164:1303:-	Akkermansia muciniphila
594653	GL0006826_MH0022_[Complete]_[mRNA]_locus=scaffold19883_3:831:2216:+	Akkermansia muciniphila

594654	GL0006827_MH0022_[Complete]_[mRNA]_locus=scaffold19883_3:2547:4010:+	Bacteria
594655	GL0006829_MH0022_[Complete]_[mRNA]_locus=scaffold19883_3:4766:5251:+	Akkermansia muciniphila
594659	GL0023905_MH0022_[Complete]_[mRNA]_locus=scaffold19883_4:2122:3129:-	Akkermansia muciniphila
594661	GL0037478_MH0022_[Complete]_[mRNA]_locus=scaffold19883_6:553:879:-	Akkermansia muciniphila
594663	GL0037829_MH0022_[Complete]_[mRNA]_locus=scaffold19883_12:1405:2928:-	Akkermansia muciniphila
594664	GL0037830_MH0022_[Complete]_[mRNA]_locus=scaffold19883_12:2944:4155:-	Akkermansia muciniphila
594665	GL0014863_MH0022_[Complete]_[mRNA]_locus=scaffold19883_14:576:908:+	Akkermansia muciniphila
594666	GL0014865_MH0022_[Complete]_[mRNA]_locus=scaffold19883_14:1299:2711:+	Akkermansia muciniphila
594683	GL0004566_MH0022_[Complete]_[mRNA]_locus=scaffold19995_1:640:1032:+	Akkermansia muciniphila
594688	GL0026442_MH0022_[Complete]_[mRNA]_locus=scaffold19995_10:1219:2082:+	Akkermansia muciniphila
594689	GL0026446_MH0022_[Complete]_[mRNA]_locus=scaffold19995_10:3236:3985:-	Akkermansia muciniphila
594691	GL0026448_MH0022_[Complete]_[mRNA]_locus=scaffold19995_10:4909:5583:-	Akkermansia muciniphila
594779	GL0022631_MH0022_[Complete]_[mRNA]_locus=scaffold20694_8:411:1073:+	Akkermansia muciniphila
594780	GL0022632_MH0022_[Complete]_[mRNA]_locus=scaffold20694_8:1239:2249:+	Akkermansia muciniphila

594781	GL0022633_MH0022_[Complete]_[mRNA]_locus=scaffold20694_8:2288:3181:+	Akkermansia muciniphila
594783	GL0032184_MH0022_[Complete]_[mRNA]_locus=scaffold20694_9:429:1955:-	Akkermansia muciniphila
594922	GL0027130_MH0022_[Complete]_[mRNA]_locus=scaffold21691_6:1003:1740:+	Akkermansia muciniphila
594926	GL0012933_MH0022_[Complete]_[mRNA]_locus=scaffold21691_8:488:1072:-	Akkermansia muciniphila
594927	GL0012934_MH0022_[Complete]_[mRNA]_locus=scaffold21691_8:1153:1818:+	Akkermansia muciniphila
594928	GL0012936_MH0022_[Complete]_[mRNA]_locus=scaffold21691_8:2571:3521:-	Akkermansia muciniphila
594935	GL0022797_MH0022_[Complete]_[mRNA]_locus=scaffold21691_11:968:1780:-	Akkermansia muciniphila
594936	GL0032506_MH0022_[Complete]_[mRNA]_locus=scaffold21691_12:179:1183:-	Akkermansia muciniphila
594937	GL0032508_MH0022_[Complete]_[mRNA]_locus=scaffold21691_12:1774:3048:+	Akkermansia muciniphila
594939	GL0031911_MH0022_[Complete]_[mRNA]_locus=scaffold21691_17:848:1555:-	Akkermansia muciniphila
594943	GL0012876_MH0022_[Complete]_[mRNA]_locus=scaffold21691_19:346:1308:+	Akkermansia muciniphila
594980	GL0028208_MH0022_[Complete]_[mRNA]_locus=scaffold21979_4:615:1787:+	Akkermansia muciniphila
595026	GL0040635_MH0022_[Complete]_[mRNA]_locus=scaffold22389_2:2671:3600:+	Akkermansia muciniphila
595083	GL0005000_MH0022_[Complete]_[mRNA]_locus=scaffold22682_2:260:1351:+	Akkermansia muciniphila

595086	GL0011872_MH0022_[Complete]_[mRNA]_locus=scaffold22682_3:3956:4357:+	Akkermansia muciniphila
595089	GL0009338_MH0022_[Complete]_[mRNA]_locus=scaffold22682_6:21:1778:-	Bacteria
595095	GL0016932_MH0022_[Complete]_[mRNA]_locus=scaffold22682_15:1441:2298:+	Akkermansia muciniphila
595096	GL0016934_MH0022_[Complete]_[mRNA]_locus=scaffold22682_15:2929:4035:-	Akkermansia muciniphila
595097	GL0016935_MH0022_[Complete]_[mRNA]_locus=scaffold22682_15:4396:5676:+	Akkermansia muciniphila
595098	GL0016936_MH0022_[Complete]_[mRNA]_locus=scaffold22682_15:5713:6492:+	Akkermansia muciniphila
595231	GL0016950_MH0022_[Complete]_[mRNA]_locus=scaffold23740_1:2199:3371:-	Akkermansia muciniphila
595375	GL0000095_MH0022_[Complete]_[mRNA]_locus=scaffold25210_2:2736:3551:+	Akkermansia muciniphila
595474	GL0032065_MH0022_[Complete]_[mRNA]_locus=scaffold25940_2:2416:4749:+	Akkermansia muciniphila
595475	GL0032066_MH0022_[Complete]_[mRNA]_locus=scaffold25940_2:5000:7201:+	Akkermansia muciniphila
595478	GL0032071_MH0022_[Complete]_[mRNA]_locus=scaffold25940_2:9769:11301:+	Verrucomicrobia
595563	GL0035065_MH0022_[Complete]_[mRNA]_locus=scaffold26931_2:276:1733:-	Akkermansia muciniphila
595564	GL0035067_MH0022_[Complete]_[mRNA]_locus=scaffold26931_2:2399:3283:+	Akkermansia muciniphila
595565	GL0007208_MH0022_[Complete]_[mRNA]_locus=scaffold26931_3:378:959:+	Akkermansia muciniphila

595566	GL0031429_MH0022_[Complete]_[mRNA]_locus=scaffold26931_5:1590:3068:+	Akkermansia muciniphila
595567	GL0031430_MH0022_[Complete]_[mRNA]_locus=scaffold26931_5:3098:3748:+	Akkermansia muciniphila
595568	GL0031431_MH0022_[Complete]_[mRNA]_locus=scaffold26931_5:3762:4559:+	Akkermansia muciniphila
595606	GL0041150_MH0022_[Complete]_[mRNA]_locus=scaffold27388_3:2486:3661:+	Akkermansia muciniphila
595875	GL0011425_MH0022_[Complete]_[mRNA]_locus=scaffold30011_2:1600:2463:-	Akkermansia muciniphila
596012	GL0007950_MH0022_[Complete]_[mRNA]_locus=scaffold31219_6:106:930:+	Akkermansia muciniphila
596015	GL0017793_MH0022_[Complete]_[mRNA]_locus=scaffold31219_13:3945:5108:+	Akkermansia muciniphila
596052	GL0016172_MH0022_[Complete]_[mRNA]_locus=scaffold31484_3:1927:2334:-	Akkermansia muciniphila
596056	GL0035540_MH0022_[Complete]_[mRNA]_locus=scaffold31484_4:3903:4925:+	Akkermansia muciniphila
596059	GL0035543_MH0022_[Complete]_[mRNA]_locus=scaffold31484_4:6982:8934:-	Akkermansia muciniphila
596103	GL0038835_MH0022_[Complete]_[mRNA]_locus=scaffold31924_2:468:1076:-	Akkermansia muciniphila
596104	GL0038836_MH0022_[Complete]_[mRNA]_locus=scaffold31924_2:1118:1753:-	Akkermansia muciniphila
596188	GL0011832_MH0022_[Complete]_[mRNA]_locus=scaffold32865_3:396:1124:-	Akkermansia muciniphila
596189	GL0011833_MH0022_[Complete]_[mRNA]_locus=scaffold32865_3:1130:2257:-	Akkermansia muciniphila

596203	GL0023469_MH0022_[Complete]_[mRNA]_locus=scaffold33047_1:431:1210:+	Akkermansia muciniphila
596205	GL0037576_MH0022_[Complete]_[mRNA]_locus=scaffold33047_3:1079:1489:+	Akkermansia muciniphila
596206	GL0022283_MH0022_[Complete]_[mRNA]_locus=scaffold33047_8:642:1814:-	Akkermansia muciniphila
596208	GL0022286_MH0022_[Complete]_[mRNA]_locus=scaffold33047_8:3230:4822:-	Bacteria
596210	GL0037779_MH0022_[Complete]_[mRNA]_locus=scaffold33047_12:1464:2204:-	Akkermansia muciniphila
596211	GL0037780_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold33047_12:2296:3372:-	Akkermansia muciniphila
596212	GL0025709_MH0022_[Complete]_[mRNA]_locus=scaffold33047_13:788:1471:-	Akkermansia muciniphila
596213	GL0023323_MH0022_[Complete]_[mRNA]_locus=scaffold33047_18:1345:3336:-	Akkermansia muciniphila
596215	GL0023325_MH0022_[Complete]_[mRNA]_locus=scaffold33047_18:4299:5735:-	Akkermansia muciniphila
596216	GL0013985_MH0022_[Complete]_[mRNA]_locus=scaffold33047_19:572:1966:+	Akkermansia muciniphila
596217	GL0025373_MH0022_[Complete]_[mRNA]_locus=scaffold33047_20:629:1555:-	Akkermansia muciniphila
596325	GL0018726_MH0022_[Complete]_[mRNA]_locus=scaffold33828_2:314:1372:+	Akkermansia muciniphila
596327	GL0009408_MH0022_[Complete]_[mRNA]_locus=scaffold33828_3:1084:1788:+	Akkermansia muciniphila

596329	GL0009411_MH0022_[Complete]_[mRNA]_locus=scaffold33828_3:2491:2721:-	Akkermansia muciniphila
596408	GL0007177_MH0022_[Complete]_[mRNA]_locus=scaffold34450_1:955:1656:-	Akkermansia muciniphila
596412	GL0039721_MH0022_[Complete]_[mRNA]_locus=scaffold34450_5:1460:3742:+	Akkermansia muciniphila
596415	GL0039726_MH0022_[Complete]_[mRNA]_locus=scaffold34450_5:9499:10161:+	Akkermansia muciniphila
596416	GL0039728_MH0022_[Complete]_[mRNA]_locus=scaffold34450_5:10664:11890:+	Akkermansia muciniphila
596445	GL0025916_MH0022_[Complete]_[mRNA]_locus=scaffold34825_5:182:823:-	Akkermansia muciniphila
596519	GL0000756_MH0022_[Complete]_[mRNA]_locus=scaffold35550_3:799:1461:-	Akkermansia muciniphila
596522	GL0005223_MH0022_[Complete]_[mRNA]_locus=scaffold35550_7:1223:1675:-	Akkermansia muciniphila
596551	GL0041692_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold36045_3:390:533:-	-
596666	GL0021386_MH0022_[Complete]_[mRNA]_locus=scaffold37536_2:744:1283:-	Akkermansia muciniphila
596668	GL0034937_MH0022_[Complete]_[mRNA]_locus=scaffold37536_8:741:1415:+	Akkermansia muciniphila
596757	GL0026664_MH0022_[Complete]_[mRNA]_locus=scaffold38240_1:3713:5371:-	Akkermansia muciniphila
596758	GL0026665_MH0022_[Complete]_[mRNA]_locus=scaffold38240_1:5459:7357:+	Akkermansia muciniphila
596760	GL0026667_MH0022_[Complete]_[mRNA]_locus=scaffold38240_1:8556:9764:-	Akkermansia muciniphila

596762	GL0026669_MH0022_[Complete]_[mRNA]_locus= scaffold38240_1:10804:12408:-	Verrucomicrobia
596763	GL0026671_MH0022_[Complete]_[mRNA]_locus= scaffold38240_1:13130:13951:+	Akkermansia muciniphila
596868	GL0034795_MH0022_[Complete]_[mRNA]_locus= scaffold39184_3:1468:2313:-	Akkermansia muciniphila
596948	GL0000659_MH0022_[Complete]_[mRNA]_locus= scaffold39980_1:4760:5656:+	Akkermansia muciniphila
597145	GL0035052_MH0022_[Complete]_[mRNA]_locus= scaffold42044_3:296:1201:-	Akkermansia muciniphila
597146	GL0035053_MH0022_[Complete]_[mRNA]_locus= scaffold42044_3:1218:2294:-	Akkermansia muciniphila
597148	GL0024222_MH0022_[Complete]_[mRNA]_locus= scaffold42044_4:146:1087:-	Akkermansia muciniphila
597156	GL0025165_MH0022_[Complete]_[mRNA]_locus= scaffold42108_1:98:553:-	Akkermansia muciniphila
597160	GL0022619_MH0022_[Complete]_[mRNA]_locus= scaffold42108_4:1332:2681:-	Akkermansia muciniphila
597161	GL0022620_MH0022_[Complete]_[mRNA]_locus= scaffold42108_4:2678:3844:-	Akkermansia muciniphila
597167	GL0009786_MH0022_[Complete]_[mRNA]_locus= scaffold42108_5:13046:14065:-	Akkermansia muciniphila
597168	GL0009787_MH0022_[Complete]_[mRNA]_locus= scaffold42108_5:14187:15359:-	Akkermansia muciniphila
597233	GL0001059_MH0022_[Complete]_[mRNA]_locus= scaffold42780_5:466:1653:+	Akkermansia muciniphila
597234	GL0001060_MH0022_[Complete]_[mRNA]_locus= scaffold42780_5:1812:2360:-	Akkermansia muciniphila

597236	GL0001064_MH0022_[Complete]_[mRNA]_locus=scaffold42780_5:4909:5409:+	Akkermansia muciniphila
597274	GL0008867_MH0022_[Complete]_[mRNA]_locus=scaffold42971_2:6357:7688:-	Akkermansia muciniphila
597275	GL0017988_MH0022_[Complete]_[mRNA]_locus=scaffold42971_3:1132:2187:-	Akkermansia muciniphila
597292	GL0008770_MH0022_[Complete]_[mRNA]_locus=scaffold43107_4:865:1290:-	Akkermansia muciniphila
597293	GL0008771_MH0022_[Complete]_[mRNA]_locus=scaffold43107_4:1287:2345:-	Akkermansia muciniphila
597295	GL0019880_MH0022_[Complete]_[mRNA]_locus=scaffold43107_7:1634:2200:+	Akkermansia muciniphila
597296	GL0006442_MH0022_[Complete]_[mRNA]_locus=scaffold43107_11:2224:3036:-	Akkermansia muciniphila
597299	GL0025951_MH0022_[Complete]_[mRNA]_locus=scaffold43107_13:2653:4200:+	Verrucomicrobiaceae
597302	GL0025955_MH0022_[Complete]_[mRNA]_locus=scaffold43107_13:6490:8400:-	Bacteria
597303	GL0025956_MH0022_[Complete]_[mRNA]_locus=scaffold43107_13:8570:9241:+	Akkermansia muciniphila
597419	GL0015956_MH0022_[Complete]_[mRNA]_locus=scaffold43979_1:2287:3171:+	Akkermansia muciniphila
597420	GL0009179_MH0022_[Complete]_[mRNA]_locus=scaffold43979_2:1178:2632:+	Akkermansia muciniphila
597422	GL0038683_MH0022_[Complete]_[mRNA]_locus=scaffold43979_3:2404:3753:+	Akkermansia muciniphila
597473	GL0014130_MH0022_[Lack_5'-end]_[mRNA]_locus=scaffold44425_4:2:616:+	Akkermansia muciniphila

597485	GL0015494_MH0022_[Complete]_[mRNA]_locus=scaffold44550_2:1531:3684:+	Akkermansia muciniphila
597707	GL0008070_MH0022_[Complete]_[mRNA]_locus=scaffold46145_5:940:1839:+	Akkermansia muciniphila
597708	GL0008071_MH0022_[Complete]_[mRNA]_locus=scaffold46145_5:1829:3271:+	Akkermansia muciniphila
597709	GL0008072_MH0022_[Complete]_[mRNA]_locus=scaffold46145_5:3283:4710:+	Akkermansia muciniphila
597767	GL0008556_MH0022_[Complete]_[mRNA]_locus=scaffold46656_1:829:1914:+	Akkermansia muciniphila
597768	GL0008558_MH0022_[Complete]_[mRNA]_locus=scaffold46656_1:2461:5307:+	Bacteria
597769	GL0008560_MH0022_[Complete]_[mRNA]_locus=scaffold46656_1:6660:7292:-	Akkermansia muciniphila
597776	GL0002898_MH0022_[Complete]_[mRNA]_locus=scaffold46656_5:416:3076:+	Akkermansia muciniphila
597848	GL0034441_MH0022_[Complete]_[mRNA]_locus=scaffold47325_1:4353:5012:+	Akkermansia muciniphila
597849	GL0034442_MH0022_[Complete]_[mRNA]_locus=scaffold47325_1:5009:6067:-	Akkermansia muciniphila
597850	GL0034444_MH0022_[Complete]_[mRNA]_locus=scaffold47325_1:7353:8069:+	Akkermansia muciniphila
597851	GL0034445_MH0022_[Complete]_[mRNA]_locus=scaffold47325_1:8170:9954:+	Akkermansia muciniphila
597852	GL0034446_MH0022_[Complete]_[mRNA]_locus=scaffold47325_1:9984:10937:+	Akkermansia muciniphila
597853	GL0034447_MH0022_[Complete]_[mRNA]_locus=scaffold47325_1:10973:11986:+	Akkermansia muciniphila

597865	GL0007763_MH0022_[Complete]_[mRNA]_locus=scaffold47409_2:255:1052:+	Akkermansia muciniphila
597896	GL0036547_MH0022_[Complete]_[mRNA]_locus=scaffold47582_6:1809:2312:-	Akkermansia muciniphila
597898	GL0036550_MH0022_[Complete]_[mRNA]_locus=scaffold47582_6:3958:4476:-	Akkermansia muciniphila
597953	GL0039042_MH0022_[Complete]_[mRNA]_locus=scaffold47997_2:823:1917:+	Akkermansia muciniphila
597955	GL0028241_MH0022_[Complete]_[mRNA]_locus=scaffold47997_3:143:538:+	Akkermansia muciniphila
597956	GL0028242_MH0022_[Complete]_[mRNA]_locus=scaffold47997_3:646:2025:+	Akkermansia muciniphila
597957	GL0028243_MH0022_[Complete]_[mRNA]_locus=scaffold47997_3:2256:3473:-	Akkermansia muciniphila
597959	GL0023607_MH0022_[Lack_3'-end]_[mRNA]_locus=scaffold47997_9:3:1481:-	Akkermansia muciniphila
598019	GL0030051_MH0022_[Complete]_[mRNA]_locus=scaffold48460_4:469:1512:-	Akkermansia muciniphila
598024	GL0024986_MH0022_[Complete]_[mRNA]_locus=scaffold48511_2:2066:3352:-	Bacteria
598113	GL0017357_MH0022_[Complete]_[mRNA]_locus=scaffold48932_8:884:1783:+	Akkermansia muciniphila
598114	GL0017358_MH0022_[Complete]_[mRNA]_locus=scaffold48932_8:2401:2781:+	Akkermansia muciniphila
598115	GL0017359_MH0022_[Complete]_[mRNA]_locus=scaffold48932_8:3002:4162:+	Akkermansia muciniphila
598118	GL0029072_MH0022_[Complete]_[mRNA]_locus=scaffold48932_9:2049:3434:+	Akkermansia muciniphila

598121	GL0023205_MH0022_[Complete]_[mRNA]_locus=scaffold48937_1:174:1838:+	Akkermansia muciniphila
598276	GL0041980_MH0022_[Complete]_[mRNA]_locus=scaffold50127_4:5560:5742:+	Akkermansia muciniphila
598298	GL0020747_MH0022_[Complete]_[mRNA]_locus=scaffold50305_2:4236:5123:-	Akkermansia muciniphila
598299	GL0014820_MH0022_[Complete]_[mRNA]_locus=scaffold50305_6:311:2644:+	Akkermansia muciniphila
598301	GL0014822_MH0022_[Complete]_[mRNA]_locus=scaffold50305_6:3502:4095:-	Akkermansia muciniphila
598357	GL0001464_MH0022_[Complete]_[mRNA]_locus=scaffold50498_6:187:1830:-	Akkermansia muciniphila
598358	GL0015206_MH0022_[Complete]_[mRNA]_locus=scaffold50498_7:581:3157:-	Bacteria
598374	GL0037682_MH0022_[Complete]_[mRNA]_locus=scaffold50610_1:1869:3536:-	Akkermansia muciniphila
598375	GL0037683_MH0022_[Complete]_[mRNA]_locus=scaffold50610_1:3756:4652:-	Akkermansia muciniphila
598454	GL0038531_MH0022_[Complete]_[mRNA]_locus=scaffold50979_4:370:1449:+	Akkermansia muciniphila
598455	GL0019722_MH0022_[Complete]_[mRNA]_locus=scaffold50979_6:285:1532:+	Akkermansia muciniphila
598457	GL0025568_MH0022_[Complete]_[mRNA]_locus=scaffold50979_8:678:899:+	-
598458	GL0010725_MH0022_[Complete]_[mRNA]_locus=scaffold50979_9:2266:3168:+	Akkermansia muciniphila
598461	GL0027907_MH0022_[Complete]_[mRNA]_locus=scaffold50979_10:5147:7669:-	Akkermansia muciniphila

598462	GL0037143_MH0022_[Complete]_[mRNA]_locus=scaffold50979_11:465:1424:+	Akkermansia muciniphila
598463	GL0037145_MH0022_[Complete]_[mRNA]_locus=scaffold50979_11:2343:3125:-	Akkermansia muciniphila
598467	GL0034145_MH0022_[Complete]_[mRNA]_locus=scaffold50990_2:336:1607:+	Akkermansia muciniphila
598468	GL0022513_MH0022_[Complete]_[mRNA]_locus=scaffold50990_3:3585:5216:+	Akkermansia muciniphila
598469	GL0022514_MH0022_[Complete]_[mRNA]_locus=scaffold50990_3:5456:6196:+	Akkermansia muciniphila
598471	GL0034575_MH0022_[Complete]_[mRNA]_locus=scaffold50990_6:3247:4581:+	Akkermansia muciniphila
598472	GL0017924_MH0022_[Complete]_[mRNA]_locus=scaffold50990_7:5556:6557:+	Akkermansia muciniphila
598493	GL0028537_MH0022_[Complete]_[mRNA]_locus=scaffold51082_3:1478:2098:+	Akkermansia muciniphila
598506	GL0040105_MH0022_[Complete]_[mRNA]_locus=scaffold51184_2:3144:4904:-	Akkermansia muciniphila
598507	GL0040106_MH0022_[Complete]_[mRNA]_locus=scaffold51184_2:4910:5959:-	Akkermansia muciniphila
598508	GL0040108_MH0022_[Complete]_[mRNA]_locus=scaffold51184_2:6925:7269:-	Akkermansia muciniphila
598509	GL0040109_MH0022_[Complete]_[mRNA]_locus=scaffold51184_2:7325:8371:-	Akkermansia muciniphila
598582	GL0013059_MH0022_[Complete]_[mRNA]_locus=scaffold51416_1:981:1673:+	Akkermansia muciniphila
598584	GL0023668_MH0022_[Complete]_[mRNA]_locus=scaffold51416_6:637:1299:-	Akkermansia muciniphila

598644	GL0023288_MH0022_[Complete]_[mRNA]_locus=scaffold51649_3:381:2015:-	Bacteria
598654	GL0016575_MH0022_[Complete]_[mRNA]_locus=scaffold51668_1:3179:3967:+	Akkermansia muciniphila
598655	GL0016576_MH0022_[Complete]_[mRNA]_locus=scaffold51668_1:4036:4917:+	Akkermansia muciniphila
598656	GL0016578_MH0022_[Complete]_[mRNA]_locus=scaffold51668_1:5850:6704:-	Akkermansia muciniphila
598768	GL0034753_MH0022_[Complete]_[mRNA]_locus=scaffold52123_2:1907:3349:-	Akkermansia muciniphila
598769	GL0027380_MH0022_[Complete]_[mRNA]_locus=scaffold52123_3:1075:1827:-	Akkermansia muciniphila
598773	GL0014151_MH0022_[Complete]_[mRNA]_locus=scaffold52123_5:151:1299:-	Akkermansia muciniphila
598775	GL0014154_MH0022_[Complete]_[mRNA]_locus=scaffold52123_5:4368:5513:-	Akkermansia muciniphila
598847	GL0021946_MH0022_[Complete]_[mRNA]_locus=scaffold52474_1:2844:3224:-	Akkermansia muciniphila
598848	GL0021947_MH0022_[Complete]_[mRNA]_locus=scaffold52474_1:3596:5905:+	Akkermansia muciniphila
598889	GL0019591_MH0022_[Complete]_[mRNA]_locus=scaffold52602_3:630:2033:-	Akkermansia muciniphila
598890	GL0019592_MH0022_[Complete]_[mRNA]_locus=scaffold52602_3:2408:3073:+	Akkermansia muciniphila
598891	GL0019593_MH0022_[Complete]_[mRNA]_locus=scaffold52602_3:3280:3987:-	Akkermansia muciniphila
598907	GL0020583_MH0022_[Complete]_[mRNA]_locus=scaffold52662_3:538:1509:+	Akkermansia muciniphila

598911	GL0031870_MH0022_[Complete]_[mRNA]_locus=scaffold52704_1:2258:3280:+	Akkermansia muciniphila
598913	GL0009021_MH0022_[Complete]_[mRNA]_locus=scaffold52704_3:148:1197:-	Akkermansia muciniphila
598929	GL0006503_MH0022_[Complete]_[mRNA]_locus=scaffold52754_4:1197:3056:-	Akkermansia muciniphila
598933	GL0006511_MH0022_[Complete]_[mRNA]_locus=scaffold52754_4:10518:13313:-	Bacteria
598934	GL0015652_MH0022_[Complete]_[mRNA]_locus=scaffold52754_5:24:1055:+	Akkermansia muciniphila
598935	GL0015653_MH0022_[Complete]_[mRNA]_locus=scaffold52754_5:1252:2847:+	Verrucomicrobia
598936	GL0015654_MH0022_[Complete]_[mRNA]_locus=scaffold52754_5:2912:4033:+	Akkermansia muciniphila
598937	GL0032894_MH0022_[Complete]_[mRNA]_locus=scaffold52754_6:556:3789:-	Akkermansia muciniphila
598940	GL0032897_MH0022_[Complete]_[mRNA]_locus=scaffold52754_6:6005:6796:-	Akkermansia muciniphila
598944	GL0032901_MH0022_[Complete]_[mRNA]_locus=scaffold52754_6:10166:10951:+	Akkermansia muciniphila
598946	GL0032903_MH0022_[Complete]_[mRNA]_locus=scaffold52754_6:11483:12127:-	Akkermansia muciniphila
598947	GL0032904_MH0022_[Complete]_[mRNA]_locus=scaffold52754_6:12132:13544:-	Akkermansia muciniphila
598948	GL0032907_MH0022_[Complete]_[mRNA]_locus=scaffold52754_6:15141:16433:+	Akkermansia muciniphila
598949	GL0014475_MH0022_[Complete]_[mRNA]_locus=scaffold52754_8:345:1109:+	Akkermansia muciniphila

598950	GL0028061_MH0022_[Complete]_[mRNA]_locus= scaffold52754_10:562:1362:-	Akkermansia muciniphila
598953	GL0028065_MH0022_[Complete]_[mRNA]_locus= scaffold52754_10:3007:4065:+	Akkermansia muciniphila
598954	GL0028067_MH0022_[Complete]_[mRNA]_locus= scaffold52754_10:5363:6568:+	Akkermansia muciniphila
598983	GL0030221_MH0022_[Complete]_[mRNA]_locus= scaffold52850_1:982:1551:+	Akkermansia muciniphila
598984	GL0030222_MH0022_[Complete]_[mRNA]_locus= scaffold52850_1:1618:2046:+	Akkermansia muciniphila
598986	GL0039435_MH0022_[Complete]_[mRNA]_locus= scaffold52850_2:925:1350:+	Akkermansia muciniphila
598995	GL0004876_MH0022_[Complete]_[mRNA]_locus= scaffold52903_2:1435:2088:-	Akkermansia muciniphila
599057	GL0005127_MH0022_[Complete]_[mRNA]_locus= scaffold53068_3:1575:2216:+	Akkermansia muciniphila
599099	GL0034486_MH0022_[Complete]_[mRNA]_locus= scaffold53196_2:1489:2673:-	Akkermansia muciniphila
599101	GL0034488_MH0022_[Complete]_[mRNA]_locus= scaffold53196_2:3735:4319:-	Akkermansia muciniphila
599102	GL0034489_MH0022_[Complete]_[mRNA]_locus= scaffold53196_2:4649:5293:+	Akkermansia muciniphila
599201	GL0029538_MH0022_[Complete]_[mRNA]_locus= scaffold53386_1:502:1155:+	Akkermansia muciniphila
599231	GL0021644_MH0022_[Complete]_[mRNA]_locus= scaffold53488_1:1142:2080:-	Akkermansia muciniphila
599232	GL0021645_MH0022_[Complete]_[mRNA]_locus= scaffold53488_1:2179:3402:-	Bacteria

599245	GL0033043_MH0022_[Complete]_[mRNA]_locus=scaffold53516_2:1291:2400:-	Akkermansia muciniphila
599247	GL0033045_MH0022_[Complete]_[mRNA]_locus=scaffold53516_2:3208:4041:+	Akkermansia muciniphila
599296	GL0039140_MH0022_[Complete]_[mRNA]_locus=scaffold53591_1:882:1994:+	Akkermansia muciniphila
599297	GL0039142_MH0022_[Complete]_[mRNA]_locus=scaffold53591_1:2925:4202:+	Akkermansia muciniphila
599313	GL0005272_MH0022_[Complete]_[mRNA]_locus=scaffold53625_2:702:1256:+	Akkermansia muciniphila
599314	GL0005273_MH0022_[Complete]_[mRNA]_locus=scaffold53625_2:1343:4336:-	Akkermansia muciniphila
599315	GL0025197_MH0022_[Complete]_[mRNA]_locus=scaffold53625_3:180:1670:-	Akkermansia muciniphila
599318	GL0028738_MH0022_[Complete]_[mRNA]_locus=scaffold53625_4:2232:4193:-	Akkermansia muciniphila
599369	GL0024758_MH0022_[Complete]_[mRNA]_locus=scaffold53700_2:1929:3344:+	Akkermansia muciniphila
599370	GL0024759_MH0022_[Complete]_[mRNA]_locus=scaffold53700_2:3307:5241:-	Akkermansia muciniphila
599371	GL0024760_MH0022_[Complete]_[mRNA]_locus=scaffold53700_2:5431:6495:-	Akkermansia muciniphila
599372	GL0001918_MH0022_[Complete]_[mRNA]_locus=scaffold53705_1:341:1381:+	Akkermansia muciniphila
599385	GL0036631_MH0022_[Complete]_[mRNA]_locus=scaffold53719_1:4905:6977:+	Akkermansia muciniphila
599386	GL0036633_MH0022_[Complete]_[mRNA]_locus=scaffold53719_1:8335:8646:-	-

599387	GL0036639_MH0022_[Complete]_[mRNA]_locus=scaffold53719_1:15746:17677:-	Akkermansia muciniphila
599389	GL0036642_MH0022_[Complete]_[mRNA]_locus=scaffold53719_1:19817:20965:+	Akkermansia muciniphila
599390	GL0036644_MH0022_[Complete]_[mRNA]_locus=scaffold53719_1:22460:22927:-	Akkermansia muciniphila
599392	GL0036647_MH0022_[Complete]_[mRNA]_locus=scaffold53719_1:25108:26073:+	Akkermansia muciniphila
599415	GL0016388_MH0022_[Complete]_[mRNA]_locus=scaffold53744_2:4293:5450:-	Akkermansia muciniphila
599416	GL0016392_MH0022_[Complete]_[mRNA]_locus=scaffold53744_2:8780:9652:+	Akkermansia muciniphila
599417	GL0016393_MH0022_[Complete]_[mRNA]_locus=scaffold53744_2:9942:10808:-	Akkermansia muciniphila
599418	GL0016394_MH0022_[Complete]_[mRNA]_locus=scaffold53744_2:11016:12851:+	Bacteria
599440	GL0008712_MH0022_[Complete]_[mRNA]_locus=scaffold53778_1:770:1402:-	Akkermansia muciniphila
599452	GL0005913_MH0022_[Complete]_[mRNA]_locus=scaffold53794_3:2406:5564:+	Bacteria
599453	GL0005914_MH0022_[Complete]_[mRNA]_locus=scaffold53794_3:5745:6323:+	Akkermansia muciniphila
599454	GL0020926_MH0022_[Complete]_[mRNA]_locus=scaffold53794_4:414:1151:-	Akkermansia muciniphila
599455	GL0020927_MH0022_[Complete]_[mRNA]_locus=scaffold53794_4:1204:2121:-	Akkermansia muciniphila
599457	GL0020931_MH0022_[Complete]_[mRNA]_locus=scaffold53794_4:7078:7734:+	Akkermansia muciniphila

599495	GL0027665_MH0022_[Complete]_[mRNA]_locus=scaffold53821_1:6343:8919:+	Akkermansia muciniphila
599503	GL0002910_MH0022_[Complete]_[mRNA]_locus=scaffold53826_1:4614:6065:+	Verrucomicrobiaceae
599504	GL0002911_MH0022_[Complete]_[mRNA]_locus=scaffold53826_1:6078:7601:+	Verrucomicrobiaceae
599526	GL0003912_MH0022_[Complete]_[mRNA]_locus=scaffold53840_1:2134:3072:+	Akkermansia muciniphila
599529	GL0003917_MH0022_[Complete]_[mRNA]_locus=scaffold53840_1:7901:9250:-	Bacteria
599542	GL0011326_MH0022_[Complete]_[mRNA]_locus=scaffold53856_2:93:908:+	Akkermansia muciniphila
599546	GL0025826_MH0022_[Complete]_[mRNA]_locus=scaffold53856_5:1013:2581:-	Akkermansia muciniphila
599547	GL0027603_MH0022_[Complete]_[mRNA]_locus=scaffold53857_1:1700:2482:-	Akkermansia muciniphila
599549	GL0032476_MH0022_[Complete]_[mRNA]_locus=scaffold53859_2:2638:4461:-	Akkermansia muciniphila
599550	GL0032479_MH0022_[Complete]_[mRNA]_locus=scaffold53859_2:6331:8022:+	Akkermansia muciniphila
599551	GL0015030_MH0022_[Complete]_[mRNA]_locus=scaffold53861_4:1523:2386:+	Akkermansia muciniphila
599552	GL0015031_MH0022_[Complete]_[mRNA]_locus=scaffold53861_4:2376:3272:+	Akkermansia muciniphila
599555	GL0040047_MH0022_[Complete]_[mRNA]_locus=scaffold53864_1:319:1509:-	Akkermansia muciniphila
599556	GL0040050_MH0022_[Complete]_[mRNA]_locus=scaffold53864_1:3223:3810:+	Akkermansia muciniphila

599582	GL0006266_MH0022_[Complete]_[mRNA]_locus=scaffold53880_2:173:1555:+	Akkermansia muciniphila
599583	GL0006267_MH0022_[Complete]_[mRNA]_locus=scaffold53880_2:1580:2899:+	Akkermansia muciniphila
599584	GL0006268_MH0022_[Complete]_[mRNA]_locus=scaffold53880_2:2982:4991:+	Verrucomicrobia
599593	GL0017390_MH0022_[Complete]_[mRNA]_locus=scaffold53884_1:4915:5976:+	Akkermansia muciniphila
599605	GL0031533_MH0022_[Complete]_[mRNA]_locus=scaffold53888_2:331:1035:+	Akkermansia muciniphila
599607	GL0020391_MH0022_[Complete]_[mRNA]_locus=scaffold53890_1:3232:4548:-	Akkermansia muciniphila
599615	GL0002756_MH0022_[Complete]_[mRNA]_locus=scaffold53895_1:925:1362:-	Akkermansia muciniphila
599616	GL0002758_MH0022_[Complete]_[mRNA]_locus=scaffold53895_1:1890:4058:-	Akkermansia muciniphila
599617	GL0002759_MH0022_[Complete]_[mRNA]_locus=scaffold53895_1:4076:4843:-	Akkermansia muciniphila
599626	GL0002822_MH0022_[Complete]_[mRNA]_locus=scaffold53901_1:2001:3545:-	Verrucomicrobia
599629	GL0027031_MH0022_[Complete]_[mRNA]_locus=scaffold53901_3:663:1199:+	Akkermansia muciniphila
599630	GL0027032_MH0022_[Complete]_[mRNA]_locus=scaffold53901_3:1351:2442:+	Akkermansia muciniphila
599649	GL0021453_MH0022_[Complete]_[mRNA]_locus=scaffold53917_1:709:1878:+	Akkermansia muciniphila
599650	GL0021454_MH0022_[Complete]_[mRNA]_locus=scaffold53917_1:1882:3171:+	Akkermansia muciniphila

599651	GL0001475_MH0022_[Complete]_[mRNA]_locus=scaffold53918_2:397:1098:+	Akkermansia muciniphila
599667	GL0030656_MH0022_[Complete]_[mRNA]_locus=scaffold53926_1:8986:9765:+	Akkermansia muciniphila
599668	GL0030657_MH0022_[Complete]_[mRNA]_locus=scaffold53926_1:9893:11578:+	Akkermansia muciniphila
599669	GL0030658_MH0022_[Complete]_[mRNA]_locus=scaffold53926_1:11601:13721:+	Bacteria
599671	GL0029130_MH0022_[Complete]_[mRNA]_locus=scaffold53927_1:356:994:+	Akkermansia muciniphila
599674	GL0023378_MH0022_[Complete]_[mRNA]_locus=scaffold53927_2:1520:3094:+	Akkermansia muciniphila
599677	GL0027792_MH0022_[Complete]_[mRNA]_locus=scaffold53928_1:3640:4650:+	Akkermansia muciniphila
600204	GL0032312_MH0022_[Complete]_[mRNA]_locus=C1732778_1:353:775:+	Akkermansia muciniphila
600265	GL0001534_MH0022_[Complete]_[mRNA]_locus=C1734138_1:727:1149:+	Akkermansia muciniphila
600620	GL0011291_MH0022_[Complete]_[mRNA]_locus=C1739046_1:1030:1776:-	Akkermansia muciniphila
600772	GL0001468_MH0022_[Complete]_[mRNA]_locus=C1740092_1:599:1291:-	Akkermansia muciniphila
601002	GL0018493_MH0022_[Complete]_[mRNA]_locus=C1741190_1:233:1315:-	Akkermansia muciniphila
601012	GL0033931_MH0022_[Complete]_[mRNA]_locus=C1741232_1:1663:2160:-	Akkermansia muciniphila
601254	GL0029661_MH0022_[Complete]_[mRNA]_locus=C1742214_1:89:1591:+	Akkermansia muciniphila

601261	GL0010104_MH0022_[Complete]_[mRNA]_locus=C1742228_1:892:1488:+	Akkermansia muciniphila
601262	GL0010105_MH0022_[Complete]_[mRNA]_locus=C1742228_1:1528:2565:+	Akkermansia muciniphila
601913	GL0025036_MH0022_[Complete]_[mRNA]_locus=C1743842_1:699:1814:-	Akkermansia muciniphila
601914	GL0025037_MH0022_[Complete]_[mRNA]_locus=C1743842_1:1807:2931:-	Akkermansia muciniphila
601938	GL0032435_MH0022_[Lack_5'-end]_[mRNA]_locus=C1743892_1:1:141:+	-
602313	GL0017521_MH0022_[Complete]_[mRNA]_locus=C1744470_1:955:1785:+	Akkermansia muciniphila
602314	GL0017522_MH0022_[Complete]_[mRNA]_locus=C1744470_1:1856:2884:-	Akkermansia muciniphila
602315	GL0017523_MH0022_[Complete]_[mRNA]_locus=C1744470_1:2896:4059:-	Akkermansia muciniphila
607807	GL0006590_MH0023_[Complete]_[mRNA]_locus=scaffold18564_4:6884:7270:+	Bacteroides pectinophilus
607809	GL0006592_MH0023_[Complete]_[mRNA]_locus=scaffold18564_4:8299:9072:+	Bacteroides pectinophilus
608477	GL0004990_MH0023_[Complete]_[mRNA]_locus=scaffold22394_1:672:1163:+	-
608783	GL0011522_MH0023_[Lack_3'-end]_[mRNA]_locus=scaffold24575_1:1049:1726:+	Faecalibacterium prausnitzii
617897	GL0003273_MH0024_[Complete]_[mRNA]_locus=scaffold11910_1:836:2113:+	Clostridiales
620621	GL0077728_MH0024_[Complete]_[mRNA]_locus=scaffold22744_3:3693:4544:+	Parabacteroides distasonis

621346	GL0005130_MH0024_[Complete]_[mRNA]_locus=scaffold25914_1:682:1071:-	-
625016	GL0065022_MH0024_[Complete]_[mRNA]_locus=scaffold45998_1:91:1056:-	Bacteria
631936	GL0045379_MH0025_[Complete]_[mRNA]_locus=scaffold602_2:115:591:-	Akkermansia muciniphila
631937	GL0045380_MH0025_[Complete]_[mRNA]_locus=scaffold602_2:951:2414:+	Akkermansia muciniphila
631938	GL0045381_MH0025_[Complete]_[mRNA]_locus=scaffold602_2:2651:3172:+	Akkermansia muciniphila
632809	GL0008794_MH0025_[Complete]_[mRNA]_locus=scaffold1533_4:735:1337:-	Akkermansia muciniphila
633791	GL0091555_MH0025_[Complete]_[mRNA]_locus=scaffold2277_2:690:1322:+	Akkermansia muciniphila
634600	GL0139956_MH0025_[Complete]_[mRNA]_locus=scaffold3085_1:1411:1923:+	Akkermansia muciniphila
636072	GL0148674_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold4725_1:365:1465:-	Akkermansia muciniphila
636145	GL0084576_MH0025_[Complete]_[mRNA]_locus=scaffold4795_3:1087:1395:-	Clostridium difficile
636346	GL0091094_MH0025_[Complete]_[mRNA]_locus=scaffold4850_2:120:479:-	Holdemania filiformis
637040	GL0125617_MH0025_[Complete]_[mRNA]_locus=scaffold5768_2:238:729:+	Akkermansia muciniphila
637041	GL0033411_MH0025_[Complete]_[mRNA]_locus=scaffold5768_4:356:853:+	Akkermansia muciniphila
637569	GL0003696_MH0025_[Complete]_[mRNA]_locus=scaffold6269_1:1064:1783:-	Akkermansia muciniphila

637570	GL0028356_MH0025_[Complete]_[mRNA]_locus=scaffold6269_6:247:828:+	Akkermansia muciniphila
638705	GL0112491_MH0025_[Complete]_[mRNA]_locus=scaffold7391_2:183:509:-	Akkermansia muciniphila
639034	GL0089923_MH0025_[Complete]_[mRNA]_locus=scaffold7825_3:2858:4129:+	Akkermansia muciniphila
639073	GL0094387_MH0025_[Complete]_[mRNA]_locus=scaffold7863_3:129:638:-	-
639570	GL0064312_MH0025_[Complete]_[mRNA]_locus=scaffold8628_3:766:1575:-	Akkermansia muciniphila
639695	GL0054795_MH0025_[Complete]_[mRNA]_locus=scaffold8764_6:1182:2132:-	Akkermansia muciniphila
639696	GL0054796_MH0025_[Complete]_[mRNA]_locus=scaffold8764_6:2196:2687:-	Akkermansia muciniphila
639743	GL0106689_MH0025_[Complete]_[mRNA]_locus=scaffold8906_1:2670:3509:-	Akkermansia muciniphila
639744	GL0106690_MH0025_[Complete]_[mRNA]_locus=scaffold8906_1:3674:3886:-	Akkermansia muciniphila
639746	GL0029732_MH0025_[Complete]_[mRNA]_locus=scaffold8906_3:1734:2318:-	Akkermansia muciniphila
639788	GL0151170_MH0025_[Complete]_[mRNA]_locus=scaffold8972_3:388:1971:-	Akkermansia muciniphila
639880	GL0018520_MH0025_[Complete]_[mRNA]_locus=scaffold9130_3:45:1256:-	Catenibacterium mitsuokai
640039	GL0130219_MH0025_[Complete]_[mRNA]_locus=scaffold9316_1:945:1235:+	Anaerotruncus colihominis
640516	GL0064657_MH0025_[Lack_both_end]_[mRNA]_locus=scaffold9831_6:3:662:-	Akkermansia muciniphila

640517	GL0060228_MH0025_[Complete]_[mRNA]_locus=scaffold9831_7:181:333:+	-
640752	GL0087105_MH0025_[Complete]_[mRNA]_locus=scaffold10142_3:374:1000:+	Gammaproteobacteria
640753	GL0087106_MH0025_[Complete]_[mRNA]_locus=scaffold10142_3:1166:1408:+	Akkermansia muciniphila
642168	GL0131003_MH0025_[Complete]_[mRNA]_locus=scaffold11677_3:1500:1799:-	Akkermansia muciniphila
643872	GL0069761_MH0025_[Complete]_[mRNA]_locus=scaffold13930_1:113:709:-	Akkermansia muciniphila
645645	GL0033985_MH0025_[Complete]_[mRNA]_locus=scaffold16201_4:1191:1364:+	Akkermansia muciniphila
645646	GL0033986_MH0025_[Complete]_[mRNA]_locus=scaffold16201_4:1351:1641:+	Akkermansia muciniphila
645816	GL0060542_MH0025_[Complete]_[mRNA]_locus=scaffold16444_3:337:885:+	Akkermansia muciniphila
645860	GL0149639_MH0025_[Complete]_[mRNA]_locus=scaffold16559_3:861:1430:-	Akkermansia muciniphila
645861	GL0149640_MH0025_[Complete]_[mRNA]_locus=scaffold16559_3:1548:2321:-	Akkermansia muciniphila
647558	GL0015879_MH0025_[Complete]_[mRNA]_locus=scaffold19139_11:552:815:-	Akkermansia muciniphila
647559	GL0015880_MH0025_[Complete]_[mRNA]_locus=scaffold19139_11:1007:1468:-	Akkermansia muciniphila
647741	GL0085736_MH0025_[Complete]_[mRNA]_locus=scaffold19427_1:10:441:-	Akkermansia muciniphila
648533	GL0014583_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold20910_6:232:633:-	Akkermansia muciniphila

650252	GL0147636_MH0025_[Complete]_[mRNA]_locus=scaffold23237_3:63:446:-	Akkermansia muciniphila
650386	GL0039454_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold23496_13:672:797:+	-
651264	GL0151960_MH0025_[Complete]_[mRNA]_locus=scaffold24891_7:443:976:+	Akkermansia muciniphila
651328	GL0150437_MH0025_[Complete]_[mRNA]_locus=scaffold25113_3:712:1635:+	Akkermansia muciniphila
652576	GL0054454_MH0025_[Complete]_[mRNA]_locus=scaffold27012_4:737:1066:-	Akkermansia muciniphila
652577	GL0054455_MH0025_[Complete]_[mRNA]_locus=scaffold27012_4:1145:1528:-	Akkermansia muciniphila
652683	GL0054989_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold27189_5:543:677:+	-
652720	GL0031825_MH0025_[Complete]_[mRNA]_locus=scaffold27295_2:424:1275:-	Akkermansia muciniphila
652972	GL0131813_MH0025_[Complete]_[mRNA]_locus=scaffold27786_2:639:1787:-	Akkermansia muciniphila
653559	GL0022335_MH0025_[Complete]_[mRNA]_locus=scaffold28988_4:931:1821:+	Akkermansia muciniphila
654669	GL0018058_MH0025_[Complete]_[mRNA]_locus=scaffold31151_1:370:1176:+	Roseburia inulinivorans
654778	GL0053242_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold31373_3:1:969:+	Akkermansia muciniphila
656063	GL0091797_MH0025_[Complete]_[mRNA]_locus=scaffold33823_4:539:1018:+	Akkermansia muciniphila
656399	GL0150891_MH0025_[Complete]_[mRNA]_locus=scaffold34677_1:621:1763:+	Akkermansia muciniphila

657786	GL0047721_MH0025_[Complete]_[mRNA]_locus=scaffold37540_1:302:877:-	Akkermansia muciniphila
659754	GL0102415_MH0025_[Complete]_[mRNA]_locus=scaffold41962_9:179:652:-	Akkermansia muciniphila
660357	GL0031790_MH0025_[Complete]_[mRNA]_locus=scaffold43311_1:181:696:-	Akkermansia muciniphila
661136	GL0100540_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold45180_9:3:176:-	Akkermansia muciniphila
661776	GL0063308_MH0025_[Complete]_[mRNA]_locus=scaffold46729_2:356:844:+	Akkermansia muciniphila
661918	GL0051283_MH0025_[Complete]_[mRNA]_locus=scaffold47036_5:848:1309:+	Akkermansia muciniphila
661990	GL0138643_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold47203_3:2:403:-	Dorea longicatena
662607	GL0152430_MH0025_[Complete]_[mRNA]_locus=scaffold48865_2:672:1430:+	Akkermansia muciniphila
662771	GL0052479_MH0025_[Complete]_[mRNA]_locus=scaffold49320_4:894:1376:-	Akkermansia muciniphila
662772	GL0052480_MH0025_[Complete]_[mRNA]_locus=scaffold49320_4:1498:2961:-	Akkermansia muciniphila
662773	GL0052481_MH0025_[Complete]_[mRNA]_locus=scaffold49320_4:3155:4318:+	Akkermansia muciniphila
662976	GL0070753_MH0025_[Complete]_[mRNA]_locus=scaffold49916_4:121:1869:+	Akkermansia muciniphila
663302	GL0008168_MH0025_[Complete]_[mRNA]_locus=scaffold50764_2:213:575:-	Akkermansia muciniphila
663345	GL0050969_MH0025_[Complete]_[mRNA]_locus=scaffold50934_4:974:1534:-	Akkermansia muciniphila

663748	GL0096249_MH0025_[Complete]_[mRNA]_locus=scaffold51958_5:36:521:-	Akkermansia muciniphila
663807	GL0079214_MH0025_[Complete]_[mRNA]_locus=scaffold52158_1:3625:4497:-	Akkermansia muciniphila
663934	GL0135099_MH0025_[Complete]_[mRNA]_locus=scaffold52556_4:452:1231:-	Akkermansia muciniphila
663935	GL0081279_MH0025_[Complete]_[mRNA]_locus=scaffold52556_8:156:641:-	Akkermansia muciniphila
664131	GL0077892_MH0025_[Complete]_[mRNA]_locus=scaffold53120_3:315:845:+	Akkermansia muciniphila
665090	GL0001303_MH0025_[Complete]_[mRNA]_locus=scaffold55973_2:438:1448:+	Akkermansia muciniphila
665091	GL0001304_MH0025_[Complete]_[mRNA]_locus=scaffold55973_2:1455:2138:+	Akkermansia muciniphila
665092	GL0128727_MH0025_[Complete]_[mRNA]_locus=scaffold55973_3:313:1353:-	Akkermansia muciniphila
665093	GL0128728_MH0025_[Complete]_[mRNA]_locus=scaffold55973_3:1499:2314:+	Akkermansia muciniphila
665133	GL0071836_MH0025_[Complete]_[mRNA]_locus=scaffold56080_4:437:910:-	Akkermansia muciniphila
666219	GL0083278_MH0025_[Complete]_[mRNA]_locus=scaffold58256_4:251:730:+	Akkermansia muciniphila
666568	GL0085263_MH0025_[Complete]_[mRNA]_locus=scaffold59212_4:846:2168:+	Akkermansia muciniphila
666772	GL0089858_MH0025_[Complete]_[mRNA]_locus=scaffold59876_4:323:856:-	Akkermansia muciniphila
667014	GL0068366_MH0025_[Complete]_[mRNA]_locus=scaffold60564_3:198:545:+	Akkermansia muciniphila

667083	GL0106609_MH0025_[Complete]_[mRNA]_locus=scaffold60814_1:1043:1981:-	-
667372	GL0003180_MH0025_[Complete]_[mRNA]_locus=scaffold61648_2:870:1379:+	Akkermansia muciniphila
667386	GL0096151_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold61685_6:2:523:+	Akkermansia muciniphila
668157	GL0043494_MH0025_[Complete]_[mRNA]_locus=scaffold63441_2:557:973:+	Akkermansia muciniphila
668158	GL0065844_MH0025_[Complete]_[mRNA]_locus=scaffold63441_4:341:904:-	Akkermansia muciniphila
668644	GL0036357_MH0025_[Complete]_[mRNA]_locus=scaffold64237_1:46:477:-	Akkermansia muciniphila
668831	GL0014473_MH0025_[Complete]_[mRNA]_locus=scaffold64839_9:1505:2179:+	Akkermansia muciniphila
668844	GL0004950_MH0025_[Complete]_[mRNA]_locus=scaffold64877_2:862:1401:-	Akkermansia muciniphila
668846	GL0004953_MH0025_[Complete]_[mRNA]_locus=scaffold64877_2:2777:3298:-	Akkermansia muciniphila
668848	GL0093524_MH0025_[Complete]_[mRNA]_locus=scaffold64877_3:1163:2164:-	Akkermansia muciniphila
669196	GL0126292_MH0025_[Complete]_[mRNA]_locus=scaffold65715_2:586:993:-	Akkermansia muciniphila
669554	GL0080444_MH0025_[Complete]_[mRNA]_locus=scaffold66571_3:1274:1657:-	Akkermansia muciniphila
670872	GL0094958_MH0025_[Complete]_[mRNA]_locus=scaffold70204_5:138:482:-	Akkermansia muciniphila
671687	GL0066934_MH0025_[Complete]_[mRNA]_locus=scaffold72423_1:636:1835:+	Akkermansia muciniphila

671688	GL0066935_MH0025_[Complete]_[mRNA]_locus=scaffold72423_1:1972:2193:-	Methylacidiphilum infernorum
672125	GL0153068_MH0025_[Complete]_[mRNA]_locus=scaffold73511_1:495:1217:+	Akkermansia muciniphila
672307	GL0099398_MH0025_[Complete]_[mRNA]_locus=scaffold73972_12:329:1195:-	Akkermansia muciniphila
672572	GL0080400_MH0025_[Complete]_[mRNA]_locus=scaffold74671_2:57:929:+	Akkermansia muciniphila
673271	GL0060112_MH0025_[Complete]_[mRNA]_locus=scaffold76084_6:589:1185:+	Akkermansia muciniphila
673292	GL0118038_MH0025_[Lack_3'-end]_[mRNA]_locus=scaffold76129_1:173:697:+	Bacteroides capillosus
674320	GL0142260_MH0025_[Complete]_[mRNA]_locus=scaffold78978_4:413:1168:-	Akkermansia muciniphila
674707	GL0150507_MH0025_[Complete]_[mRNA]_locus=scaffold80051_1:72:554:-	Akkermansia muciniphila
674759	GL0057761_MH0025_[Complete]_[mRNA]_locus=scaffold80219_6:300:1196:-	Akkermansia muciniphila
674877	GL0096188_MH0025_[Complete]_[mRNA]_locus=scaffold80531_2:296:904:+	Akkermansia muciniphila
674933	GL0109884_MH0025_[Complete]_[mRNA]_locus=scaffold80763_3:1363:1989:+	Akkermansia muciniphila
675208	GL0101147_MH0025_[Complete]_[mRNA]_locus=scaffold81386_3:188:646:+	Akkermansia muciniphila
675511	GL0125014_MH0025_[Complete]_[mRNA]_locus=scaffold82238_8:764:1237:-	Akkermansia muciniphila
675512	GL0125015_MH0025_[Complete]_[mRNA]_locus=scaffold82238_8:1358:1576:+	Akkermansia muciniphila

675513	GL0125016_MH0025_[Complete]_[mRNA]_locus=scaffold82238_8:1648:1842:-	Akkermansia muciniphila
675514	GL0125017_MH0025_[Complete]_[mRNA]_locus=scaffold82238_8:1859:2374:-	Akkermansia muciniphila
675812	GL0009628_MH0025_[Complete]_[mRNA]_locus=scaffold82962_7:281:1402:-	Akkermansia muciniphila
676321	GL0006562_MH0025_[Complete]_[mRNA]_locus=scaffold84277_2:1968:2663:+	Akkermansia muciniphila
676379	GL0007528_MH0025_[Complete]_[mRNA]_locus=scaffold84442_3:1125:2549:+	Akkermansia muciniphila
677272	GL0007055_MH0025_[Complete]_[mRNA]_locus=scaffold86787_1:525:1532:+	Akkermansia muciniphila
677312	GL0051773_MH0025_[Complete]_[mRNA]_locus=scaffold86859_2:180:464:-	Akkermansia muciniphila
677910	GL0102958_MH0025_[Complete]_[mRNA]_locus=scaffold88369_5:306:1319:+	Akkermansia muciniphila
678623	GL0094261_MH0025_[Complete]_[mRNA]_locus=scaffold89906_1:1998:2693:-	Akkermansia muciniphila
678626	GL0094264_MH0025_[Complete]_[mRNA]_locus=scaffold89906_1:4945:5454:-	Akkermansia muciniphila
678627	GL0097308_MH0025_[Complete]_[mRNA]_locus=scaffold89906_3:174:1226:+	Akkermansia muciniphila
679021	GL0154062_MH0025_[Complete]_[mRNA]_locus=scaffold90719_6:533:1324:+	Akkermansia muciniphila
679129	GL0112883_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold90995_2:294:875:-	Akkermansia muciniphila
679478	GL0118495_MH0025_[Complete]_[mRNA]_locus=scaffold91717_2:401:973:+	Akkermansia muciniphila

679533	GL0142612_MH0025_[Complete]_[mRNA]_locus=scaffold91807_2:58:543:-	Clostridium asparagiforme
679661	GL0128785_MH0025_[Complete]_[mRNA]_locus=scaffold92077_1:370:1728:+	Akkermansia muciniphila
679662	GL0117470_MH0025_[Complete]_[mRNA]_locus=scaffold92077_2:4:612:-	Akkermansia muciniphila
679967	GL0143791_MH0025_[Complete]_[mRNA]_locus=scaffold92691_3:651:866:+	Akkermansia muciniphila
680015	GL0024030_MH0025_[Complete]_[mRNA]_locus=scaffold92839_3:697:1704:-	Akkermansia muciniphila
680257	GL0053862_MH0025_[Complete]_[mRNA]_locus=scaffold93330_1:1071:1739:+	Akkermansia muciniphila
680726	GL0024557_MH0025_[Complete]_[mRNA]_locus=scaffold94247_3:1271:1636:-	Akkermansia muciniphila
680728	GL0024559_MH0025_[Complete]_[mRNA]_locus=scaffold94247_3:1995:2198:-	Akkermansia muciniphila
681133	GL0022902_MH0025_[Complete]_[mRNA]_locus=scaffold95000_2:229:501:-	Akkermansia muciniphila
681704	GL0148766_MH0025_[Complete]_[mRNA]_locus=scaffold95955_4:599:976:+	Akkermansia muciniphila
681782	GL0000833_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold96135_1:339:737:-	Akkermansia muciniphila
681870	GL0087201_MH0025_[Complete]_[mRNA]_locus=scaffold96239_2:104:589:-	Akkermansia muciniphila
682659	GL0123579_MH0025_[Complete]_[mRNA]_locus=scaffold97560_7:846:1562:-	Akkermansia muciniphila
683242	GL0119480_MH0025_[Complete]_[mRNA]_locus=scaffold98545_6:1197:2822:+	Akkermansia muciniphila

683570	GL0137015_MH0025_[Lack_5'-end]_[mRNA]_locus=scaffold99028_2:1:381:+	Akkermansia muciniphila
684283	GL0068796_MH0025_[Complete]_[mRNA]_locus=scaffold100355_2:327:1028:+	Akkermansia muciniphila
684412	GL0036987_MH0025_[Complete]_[mRNA]_locus=scaffold100561_4:19:834:-	Akkermansia muciniphila
684834	GL0138307_MH0025_[Complete]_[mRNA]_locus=scaffold101111_1:46:1083:-	Akkermansia muciniphila
685267	GL0056212_MH0025_[Complete]_[mRNA]_locus=scaffold101708_1:14:1585:+	Akkermansia muciniphila
685580	GL0057372_MH0025_[Complete]_[mRNA]_locus=scaffold102040_1:811:1419:+	Akkermansia muciniphila
685607	GL0124610_MH0025_[Complete]_[mRNA]_locus=scaffold102067_2:1065:2384:-	Akkermansia muciniphila
685686	GL0006849_MH0025_[Complete]_[mRNA]_locus=scaffold102165_3:598:1302:-	Akkermansia muciniphila
686353	GL0065022_MH0025_[Complete]_[mRNA]_locus=scaffold102881_1:474:794:-	Akkermansia muciniphila
686440	GL0023384_MH0025_[Complete]_[mRNA]_locus=scaffold102977_2:615:968:+	Akkermansia muciniphila
686930	GL0053806_MH0025_[Complete]_[mRNA]_locus=scaffold103398_1:70:297:-	Akkermansia muciniphila
687376	GL0068558_MH0025_[Complete]_[mRNA]_locus=scaffold103720_1:917:1420:+	Akkermansia muciniphila
687399	GL0145576_MH0025_[Complete]_[mRNA]_locus=scaffold103740_1:1545:1979:+	-
687675	GL0113741_MH0025_[Complete]_[mRNA]_locus=scaffold103891_2:473:694:+	Akkermansia muciniphila

687708	GL0002891_MH0025_[Complete]_[mRNA]_locus=scaffold103914_3:67:648:-	Akkermansia muciniphila
689362	GL0145185_MH0025_[Complete]_[mRNA]_locus=scaffold104814_1:3640:4755:-	Akkermansia muciniphila
689928	GL0077502_MH0025_[Complete]_[mRNA]_locus=scaffold104988_2:140:619:+	Akkermansia muciniphila
689929	GL0077503_MH0025_[Complete]_[mRNA]_locus=scaffold104988_2:632:1591:+	Akkermansia muciniphila
693714	GL0050646_MH0025_[Complete]_[mRNA]_locus=C3623102_1:531:764:+	Akkermansia muciniphila
693901	GL0091345_MH0025_[Complete]_[mRNA]_locus=C3628304_1:53:265:-	Akkermansia muciniphila
696451	GL0106527_MH0025_[Complete]_[mRNA]_locus=C3684948_1:654:1901:-	Akkermansia muciniphila
696624	GL0113186_MH0025_[Complete]_[mRNA]_locus=C3687044_1:1021:1635:-	-
696625	GL0113187_MH0025_[Complete]_[mRNA]_locus=C3687044_1:1632:2339:-	Clostridium
696734	GL0087909_MH0025_[Complete]_[mRNA]_locus=C3688316_1:981:2081:-	Akkermansia muciniphila
699282	GL0013353_MH0026_[Complete]_[mRNA]_locus=scaffold357_8:2500:5736:+	Bacteroides
699283	GL0013354_MH0026_[Complete]_[mRNA]_locus=scaffold357_8:5740:7473:+	Bacteroides
699438	GL0032747_MH0026_[Complete]_[mRNA]_locus=scaffold445_3:280:537:+	Clostridiales
700566	GL0046584_MH0026_[Complete]_[mRNA]_locus=scaffold921_2:9440:10159:-	Bacteroides ovatus

702092	GL0067197_MH0026_[Complete]_[mRNA]_locus=scaffold1415_2:536:1225:-	Faecalibacterium prausnitzii
709995	GL0061512_MH0026_[Complete]_[mRNA]_locus=scaffold5269_1:12410:12727:-	Bacteria
709996	GL0061513_MH0026_[Complete]_[mRNA]_locus=scaffold5269_1:12724:13500:-	Desulfitobacterium hafniense
710610	GL0057962_MH0026_[Complete]_[mRNA]_locus=scaffold5793_2:288:1196:-	Bacteroides ovatus
710857	GL0056834_MH0026_[Complete]_[mRNA]_locus=scaffold6047_1:490:1506:+	Roseburia inulinivorans
710858	GL0056835_MH0026_[Complete]_[mRNA]_locus=scaffold6047_1:1620:2444:+	Roseburia inulinivorans
711216	GL0071668_MH0026_[Complete]_[mRNA]_locus=scaffold6371_1:199:435:-	-
711418	GL0040692_MH0026_[Complete]_[mRNA]_locus=scaffold6600_3:405:1097:-	Bacteria
711909	GL0011984_MH0026_[Complete]_[mRNA]_locus=scaffold7079_1:9:1280:-	Clostridium perfringens
711910	GL0051871_MH0026_[Complete]_[mRNA]_locus=scaffold7085_1:106:651:+	Bacteroides
711919	GL0051880_MH0026_[Complete]_[mRNA]_locus=scaffold7085_1:16121:17620:+	Bacteroidales
711920	GL0051881_MH0026_[Complete]_[mRNA]_locus=scaffold7085_1:17671:19944:+	Bacteroidetes
712858	GL0037559_MH0026_[Complete]_[mRNA]_locus=scaffold7608_6:2350:3429:+	-
713354	GL0028303_MH0026_[Lack_3'-end]_[mRNA]_locus=scaffold8177_2:1:108:-	-

713355	GL0028304_MH0026_[Complete]_[mRNA]_locus=scaffold8177_2:205:777:+	-
714430	GL0057945_MH0026_[Complete]_[mRNA]_locus=scaffold9168_3:54:1601:-	Bacteroides
715841	GL0084441_MH0026_[Lack_5'-end]_[mRNA]_locus=scaffold10711_5:1:486:+	-
716190	GL0001517_MH0026_[Complete]_[mRNA]_locus=scaffold11178_1:354:1097:-	-
719755	GL0066606_MH0026_[Complete]_[mRNA]_locus=scaffold15523_2:760:1794:-	Arthrobacter chlorophenolicus
719756	GL0007255_MH0026_[Complete]_[mRNA]_locus=scaffold15523_10:208:987:-	Roseiflexus
719757	GL0047521_MH0026_[Complete]_[mRNA]_locus=scaffold15523_13:139:1314:-	Thermotoga
719758	GL0056062_MH0026_[Complete]_[mRNA]_locus=scaffold15523_14:363:830:-	-
719773	GL0009679_MH0026_[Complete]_[mRNA]_locus=scaffold15589_1:200:667:-	-
721145	GL0060285_MH0026_[Complete]_[mRNA]_locus=scaffold17885_2:171:545:+	-
721205	GL0072793_MH0026_[Lack_both_end]_[mRNA]_locus=scaffold17942_1:3:533:-	-
721876	GL0001313_MH0026_[Complete]_[mRNA]_locus=scaffold18890_1:221:571:+	-
721980	GL0002072_MH0026_[Complete]_[mRNA]_locus=scaffold19146_1:69:707:+	-

723249	GL0012333_MH0026_[Complete]_[mRNA]_locus=scaffold21762_2:529:1440:+	Eubacterium hallii
724221	GL0011232_MH0026_[Complete]_[mRNA]_locus=scaffold24521_3:258:935:-	-
724636	GL0001805_MH0026_[Complete]_[mRNA]_locus=scaffold25595_2:35:886:-	-
724657	GL0050822_MH0026_[Complete]_[mRNA]_locus=scaffold25621_4:3918:4751:-	Bacteroides thetaiotaomicron
725723	GL0045770_MH0026_[Complete]_[mRNA]_locus=scaffold28932_1:635:1738:+	Roseburia inulinivorans
726363	GL0012597_MH0026_[Complete]_[mRNA]_locus=scaffold31323_1:494:1123:-	-
726617	GL0013191_MH0026_[Lack_3'-end]_[mRNA]_locus=scaffold32633_3:4260:4487:+	-
726935	GL0004177_MH0026_[Complete]_[mRNA]_locus=scaffold34174_2:13:1380:-	-
727023	GL0001610_MH0026_[Complete]_[mRNA]_locus=scaffold34692_3:94:357:-	-
728261	GL0066370_MH0026_[Complete]_[mRNA]_locus=scaffold40591_2:58:453:-	-
728262	GL0066371_MH0026_[Complete]_[mRNA]_locus=scaffold40591_2:475:936:-	-
728402	GL0004727_MH0026_[Complete]_[mRNA]_locus=scaffold41203_1:244:711:+	-
728501	GL0042316_MH0026_[Complete]_[mRNA]_locus=scaffold41528_3:803:1531:+	-
729022	GL0014064_MH0026_[Complete]_[mRNA]_locus=scaffold44022_1:139:459:+	Eubacterium siraeum

729254	GL0040197_MH0026_[Complete]_[mRNA]_locus=scaffold44940_2:134:1033:+	Clostridium perfringens
729698	GL0009164_MH0026_[Complete]_[mRNA]_locus=scaffold46470_1:50:916:-	Faecalibacterium prausnitzii
729699	GL0009165_MH0026_[Complete]_[mRNA]_locus=scaffold46470_1:919:1860:-	Faecalibacterium prausnitzii
729700	GL0009166_MH0026_[Complete]_[mRNA]_locus=scaffold46470_1:2083:2760:+	Faecalibacterium prausnitzii
729701	GL0009167_MH0026_[Complete]_[mRNA]_locus=scaffold46470_1:2757:3893:+	Faecalibacterium prausnitzii
731007	GL0059595_MH0026_[Complete]_[mRNA]_locus=scaffold48832_1:84:1262:-	-
731363	GL0050064_MH0026_[Complete]_[mRNA]_locus=C3283863_1:175:504:-	-
731407	GL0019392_MH0026_[Lack_3'-end]_[mRNA]_locus=C3287547_1:91:654:+	-
731988	GL0023266_MH0027_[Lack_5'-end]_[mRNA]_locus=scaffold1771_3:3:152:+	-
731989	GL0023267_MH0027_[Complete]_[mRNA]_locus=scaffold1771_3:196:756:+	Anaerotruncus colihominis
732024	GL0019493_MH0027_[Complete]_[mRNA]_locus=scaffold2235_2:5:619:-	Faecalibacterium prausnitzii
732062	GL0022482_MH0027_[Complete]_[mRNA]_locus=scaffold2993_7:263:481:+	Listeria
732097	GL0030307_MH0027_[Complete]_[mRNA]_locus=scaffold3508_2:76:1002:+	Faecalibacterium prausnitzii
732138	GL0004737_MH0027_[Complete]_[mRNA]_locus=scaffold4277_2:199:774:+	-

732192	GL0019701_MH0027_[Complete]_[mRNA]_locus=scaffold5419_1:62:892:+	-
732399	GL0024909_MH0027_[Complete]_[mRNA]_locus=scaffold9604_2:2:313:-	Eubacterium biforme
733052	GL0028459_MH0027_[Lack_5'-end]_[mRNA]_locus=scaffold37940_3:263:970:-	Clostridium bolteae
733073	GL0014742_MH0027_[Lack_both_end]_[mRNA]_locus=scaffold39155_2:1:804:+	-
733093	GL0001063_MH0027_[Lack_5'-end]_[mRNA]_locus=scaffold40081_1:1:126:+	-
733455	GL0025671_MH0027_[Lack_5'-end]_[mRNA]_locus=scaffold56961_1:302:655:-	-
733910	GL0075443_MH0028_[Complete]_[mRNA]_locus=scaffold124_4:5098:5529:-	-
733972	GL0083629_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold325_3:8702:11896:-	Bacteria
734073	GL0093564_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold527_1:1:477:+	-
734099	GL0087713_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold605_2:1215:1337:-	-
734122	GL0121626_MH0028_[Complete]_[mRNA]_locus=scaffold724_2:1180:2916:-	-
734227	GL0040081_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold1094_1:107:904:-	Anaerotruncus colihominis
734677	GL0063292_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold2480_2:1945:2487:+	-
734689	GL0074469_MH0028_[Complete]_[mRNA]_locus=scaffold2505_1:4:1305:+	Faecalibacterium prausnitzii

734749	GL0078483_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold2816_5:1:1218:-	Faecalibacterium prausnitzii
735231	GL0109244_MH0028_[Complete]_[mRNA]_locus=scaffold4821_2:10173:11171:-	Bacteroides capillosus
735263	GL0110164_MH0028_[Complete]_[mRNA]_locus=scaffold4987_2:16:1221:-	-
735267	GL0132667_MH0028_[Complete]_[mRNA]_locus=scaffold5038_3:1631:2620:+	-
735481	GL0013719_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold5798_1:3:545:-	-
735696	GL0023512_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold6503_1:3789:3914:+	-
735765	GL0034094_MH0028_[Complete]_[mRNA]_locus=scaffold6874_1:155:1801:+	-
735796	GL0087083_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold7036_1:700:2124:-	-
736291	GL0086775_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold9010_1:2044:2433:+	-
736429	GL0030200_MH0028_[Complete]_[mRNA]_locus=scaffold9696_1:428:1276:-	Faecalibacterium prausnitzii
737211	GL0047656_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold13658_1:3:1130:+	-
737801	GL0012978_MH0028_[Complete]_[mRNA]_locus=scaffold16405_2:49:2052:-	Bacteria
738199	GL0102773_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold18636_1:823:3156:+	Faecalibacterium prausnitzii
738583	GL0071041_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold21073_1:2:532:-	-

739088	GL0012366_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold24243_1:2:604:-	-
739212	GL0064196_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold24901_1:1716:2321:-	Bacillus
739252	GL0136614_MH0028_[Lack_3'-end]_[mRNA]_locus=scaffold25195_2:421:717:+	Faecalibacterium prausnitzii
739445	GL0035783_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold26617_4:1:540:+	-
739600	GL0055068_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold27658_2:3:917:+	-
739772	GL0001013_MH0028_[Complete]_[mRNA]_locus=scaffold29078_2:68:787:-	Roseburia inulinivorans
740048	GL0092216_MH0028_[Complete]_[mRNA]_locus=scaffold30961_2:38:820:-	-
740985	GL0101897_MH0028_[Lack_both_end]_[mRNA]_locus=scaffold37385_1:3:647:-	-
742373	GL0107239_MH0028_[Complete]_[mRNA]_locus=scaffold47079_2:621:1523:+	Roseburia inulinivorans
743349	GL0060320_MH0028_[Lack_both_end]_[mRNA]_locus=scaffold52843_1:2:1516:+	Coprococcus eutactus
744599	GL0048470_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold61441_1:24:1283:-	-
744666	GL0119141_MH0028_[Lack_5'-end]_[mRNA]_locus=scaffold61812_1:75:1109:-	-
745335	GL0010715_MH0028_[Lack_both_end]_[mRNA]_locus=scaffold65343_1:1:594:+	Clostridiales
750122	GL0078272_MH0030_[Lack_5'-end]_[mRNA]_locus=scaffold1763_2:3:308:+	Clostridiales

767871	GL0074976_MH0030_[Complete]_[mRNA]_locus=scaffold63220_1:471:842:+	-
788168	GL0100289_MH0031_[Complete]_[mRNA]_locus=scaffold66494_1:47:994:+	Ruminococcus torques
806868	GL0086019_MH0033_[Lack_3'-end]_[mRNA]_locus=scaffold5539_1:3:755:-	-
807405	GL0012651_MH0033_[Lack_5'-end]_[mRNA]_locus=scaffold7954_3:676:816:-	-
808769	GL0093287_MH0033_[Lack_5'-end]_[mRNA]_locus=scaffold13785_1:604:849:-	-
811178	GL0090623_MH0033_[Lack_both_end]_[mRNA]_locus=scaffold26372_1:3:503:-	-
813365	GL0060137_MH0033_[Lack_5'-end]_[mRNA]_locus=scaffold41161_2:294:695:-	-
815466	GL0103787_MH0033_[Lack_5'-end]_[mRNA]_locus=scaffold56984_2:1:405:+	-
831253	GL0039057_MH0034_[Lack_5'-end]_[mRNA]_locus=scaffold28000_2:1327:1953:-	Roseburia inulinivorans
834155	GL0133719_MH0035_[Complete]_[mRNA]_locus=scaffold1764_19:1286:2077:-	Akkermansia muciniphila
835232	GL0074821_MH0035_[Complete]_[mRNA]_locus=scaffold5644_15:329:994:+	Akkermansia muciniphila
835584	GL0130036_MH0035_[Complete]_[mRNA]_locus=scaffold6960_8:5177:6082:+	Akkermansia muciniphila
835721	GL0111210_MH0035_[Complete]_[mRNA]_locus=scaffold7493_9:285:1847:-	Akkermansia muciniphila
836166	GL0085717_MH0035_[Lack_3'-end]_[mRNA]_locus=scaffold9449_2:4228:8712:+	Akkermansia muciniphila

836242	GL0041207_MH0035_[Complete]_[mRNA]_locus=scaffold9735_1:614:1060:+	Akkermansia muciniphila
837019	GL0028961_MH0035_[Complete]_[mRNA]_locus=scaffold13002_13:1518:2345:+	Akkermansia muciniphila
837021	GL0123624_MH0035_[Complete]_[mRNA]_locus=scaffold13002_19:2859:3716:-	Akkermansia muciniphila
841081	GL0023541_MH0035_[Complete]_[mRNA]_locus=scaffold34874_9:1596:2663:+	Akkermansia muciniphila
845420	GL0105319_MH0035_[Lack_3'-end]_[mRNA]_locus=scaffold65709_1:40:555:+	Ruminococcus gnavus
848592	GL0068967_MH0035_[Lack_5'-end]_[mRNA]_locus=scaffold86966_4:3:533:+	Akkermansia muciniphila
848593	GL0110095_MH0035_[Lack_5'-end]_[mRNA]_locus=scaffold86966_5:801:2441:-	Akkermansia muciniphila
874521	GL0060436_MH0037_[Complete]_[mRNA]_locus=scaffold1946_9:4348:5184:-	Ruminococcaceae
875087	GL0107093_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold2543_3:2055:2753:-	Bacteroides capillosus
876870	GL0083555_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold4923_13:1:1353:+	Akkermansia muciniphila
877218	GL0108437_MH0037_[Complete]_[mRNA]_locus=scaffold5592_4:414:890:-	Bacteroides pectinophilus
877477	GL0097110_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold6282_4:794:1963:-	-
877577	GL0107391_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold6411_3:441:572:-	Betaproteobacteria
877883	GL0102787_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold7216_2:1:1140:-	Clostridium leptum

878335	GL0005830_MH0037_[Complete]_[mRNA]_locus=scaffold8043_28:5723:6178:+	Akkermansia muciniphila
879282	GL0068902_MH0037_[Lack_both_end]_[mRNA]_locus=scaffold10473_3:1:507:+	Clostridium
879356	GL0042923_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold10558_10:477:818:+	Akkermansia muciniphila
880079	GL0042573_MH0037_[Complete]_[mRNA]_locus=scaffold12389_1:1105:2607:+	Akkermansia muciniphila
880402	GL0103277_MH0037_[Complete]_[mRNA]_locus=scaffold13298_3:1772:3031:+	Bacteroides ovatus
881845	GL0074230_MH0037_[Complete]_[mRNA]_locus=scaffold17719_3:1912:2904:+	Akkermansia muciniphila
883400	GL0045099_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold23212_1:1:375:+	-
884577	GL0083552_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold27935_2:6056:6829:-	-
885348	GL0018784_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold31504_3:3:182:-	-
887678	GL0010096_MH0037_[Complete]_[mRNA]_locus=scaffold43606_10:5103:6215:+	Akkermansia muciniphila
889593	GL0102553_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold55579_2:3:116:-	-
889872	GL0016884_MH0037_[Complete]_[mRNA]_locus=scaffold57522_3:34:621:+	Faecalibacterium prausnitzii
890593	GL0058926_MH0037_[Lack_5'-end]_[mRNA]_locus=scaffold61964_2:752:919:-	-
891294	GL0025599_MH0037_[Lack_3'-end]_[mRNA]_locus=scaffold66453_1:34:4359:+	Akkermansia muciniphila

894502	GL0006604_MH0037_[Lack_both_end]_[mRNA]_locus=C3813966_1:2:592:+	Blautia hydrogenotrophica
894557	GL0005650_MH0037_[Lack_3'-end]_[mRNA]_locus=C3821146_1:1:210:-	-
896935	GL0061429_MH0038_[Complete]_[mRNA]_locus=scaffold5114_2:1820:3274:-	Clostridiaceae
898310	GL0080875_MH0038_[Lack_5'-end]_[mRNA]_locus=scaffold9844_2:1:198:+	-
899795	GL0096215_MH0038_[Lack_3'-end]_[mRNA]_locus=scaffold15797_2:440:826:+	Firmicutes
929374	GL0117253_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold14317_2:1:795:-	Eubacterium ventriosum
932166	GL0060284_MH0040_[Lack_3'-end]_[mRNA]_locus=scaffold23194_2:489:905:+	Clostridium leptum
934075	GL0002741_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold30363_3:1:1026:-	Clostridium cellulolyticum
937254	GL0030643_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold42845_1:1:588:+	Ruminococcus gnavus
943572	GL0111524_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold73582_2:1:606:-	Bifidobacterium
944854	GL0150397_MH0040_[Complete]_[mRNA]_locus=scaffold80801_1:190:387:+	Clostridium cellulolyticum
946515	GL0066655_MH0040_[Lack_both_end]_[mRNA]_locus=scaffold89485_2:2:499:+	Fusobacterium nucleatum
954342	GL0045324_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold1591_2:1:288:-	-
954394	GL0091057_MH0041_[Lack_both_end]_[mRNA]_locus=scaffold1731_1:3:1004:-	Ruminococcus lactaris

956609	GL0020936_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold10354_3:1:402:-	-
957095	GL0081269_MH0041_[Complete]_[mRNA]_locus=scaffold13990_4:1694:2446:+	Bacteroides pectinophilus
958656	GL0024781_MH0041_[Lack_5'-end]_[mRNA]_locus=scaffold24648_3:1531:1755:-	-
960350	GL0111797_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold41393_5:3:638:-	Clostridiales
960573	GL0039191_MH0041_[Complete]_[mRNA]_locus=scaffold43463_4:370:675:-	Faecalibacterium prausnitzii
960732	GL0085858_MH0041_[Complete]_[mRNA]_locus=scaffold45442_5:50:1006:+	-
962152	GL0112497_MH0041_[Complete]_[mRNA]_locus=scaffold62461_1:97:1104:-	Ruminococcus obeum
962483	GL0008241_MH0041_[Lack_3'-end]_[mRNA]_locus=scaffold67155_2:1:567:-	Pedobacter
962508	GL0038246_MH0041_[Complete]_[mRNA]_locus=scaffold67448_1:315:1031:-	Streptococcus suis
962760	GL0013053_MH0041_[Complete]_[mRNA]_locus=scaffold70774_2:355:789:+	Eubacterium hallii
963953	GL0100735_MH0041_[Complete]_[mRNA]_locus=scaffold82459_2:591:902:+	Bacteroides pectinophilus
965667	GL0079446_MH0041_[Lack_5'-end]_[mRNA]_locus=C3273208_1:83:616:-	Bacteria
966431	GL0002436_MH0042_[Lack_3'-end]_[mRNA]_locus=scaffold91_2:787:2691:+	Clostridiales
973658	GL0082734_MH0042_[Lack_5'-end]_[mRNA]_locus=scaffold84292_3:517:657:-	-

979508	GL0150505_MH0043_[Lack_3'-end]_[mRNA]_locus=scaffold12796_3:830:1723:+	Bacteroides ovatus
979884	GL0034179_MH0043_[Lack_3'-end]_[mRNA]_locus=scaffold14777_2:327:1394:+	Bacteria
980104	GL0129726_MH0043_[Lack_3'-end]_[mRNA]_locus=scaffold16047_12:728:1102:+	-
985695	GL0025017_MH0043_[Lack_both_end]_[mRNA]_locus=scaffold50431_1:1:984:+	Clostridium
988415	GL0051944_MH0043_[Lack_both_end]_[mRNA]_locus=scaffold69498_2:1:513:+	Clostridium botulinum
989433	GL0130503_MH0043_[Lack_5'-end]_[mRNA]_locus=scaffold76052_2:2:196:+	Akkermansia muciniphila
992483	GL0024993_MH0043_[Lack_3'-end]_[mRNA]_locus=scaffold93162_1:472:774:+	Akkermansia muciniphila
993469	GL0103732_MH0043_[Lack_3'-end]_[mRNA]_locus=scaffold97966_2:101:502:+	Bacteria
994791	GL0107318_MH0043_[Lack_5'-end]_[mRNA]_locus=scaffold104232_2:270:851:-	Akkermansia muciniphila
995992	GL0156563_MH0043_[Lack_5'-end]_[mRNA]_locus=scaffold108582_3:1:366:+	Akkermansia muciniphila
1002408	GL0097821_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold31_3:10282:10629:+	-
1002599	GL0043552_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold480_2:2097:4274:+	-
1002600	GL0089808_MH0044_[Complete]_[mRNA]_locus=scaffold480_3:1345:4833:+	Faecalibacterium prausnitzii
1002639	GL0013902_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold576_8:2643:3443:-	-

1002747	GL0056198_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold790_2:1:354:+	-
1002792	GL0049552_MH0044_[Lack_both_end]_[mRNA]_locus=scaffold1020_10:1:903:-	-
1002812	GL0032763_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold1118_1:6092:7282:-	-
1003083	GL0023862_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold2018_2:319:1557:-	Roseburia inulinivorans
1003084	GL0071784_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold2018_3:451:1677:+	-
1003408	GL0112190_MH0044_[Complete]_[mRNA]_locus=scaffold3119_1:2379:3320:-	Roseburia inulinivorans
1003595	GL0077086_MH0044_[Complete]_[mRNA]_locus=scaffold3493_9:223:570:-	-
1003987	GL0121124_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold4845_1:5:757:-	-
1004020	GL0088091_MH0044_[Complete]_[mRNA]_locus=scaffold5102_4:3347:4576:-	-
1004287	GL0049150_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold6155_1:520:681:-	-
1004322	GL0085711_MH0044_[Complete]_[mRNA]_locus=scaffold6378_8:2116:3321:+	-
1004537	GL0050745_MH0044_[Complete]_[mRNA]_locus=scaffold7407_5:1623:2624:+	-
1004616	GL0023426_MH0044_[Complete]_[mRNA]_locus=scaffold7619_2:1932:2648:-	-
1004690	GL0017021_MH0044_[Complete]_[mRNA]_locus=scaffold7841_12:32:2836:+	Faecalibacterium prausnitzii

1005078	GL0096665_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold9568_2:2:1807:+	-
1005136	GL0118935_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold9756_2:2807:3136:-	-
1005191	GL0090135_MH0044_[Complete]_[mRNA]_locus=scaffold10142_2:28:1839:+	Faecalibacterium prausnitzii
1005763	GL0026109_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold12470_3:2:2218:-	Bacteria
1005764	GL0026110_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold12470_3:2215:3732:-	Clostridiales
1005975	GL0080612_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold13598_1:1:798:-	-
1006745	GL0021575_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold17581_2:1:132:+	-
1006848	GL0095528_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold18098_2:2:1465:+	-
1007005	GL0054179_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold19244_1:1:357:+	-
1007413	GL0040611_MH0044_[Lack_3'-end]_[mRNA]_locus=scaffold22779_2:2:1564:-	Bacteroides capillosus
1007455	GL0015111_MH0044_[Lack_both_end]_[mRNA]_locus=scaffold23112_3:1:690:+	-
1008071	GL0112301_MH0044_[Complete]_[mRNA]_locus=scaffold28096_2:6690:11357:+	Firmicutes
1010004	GL0084034_MH0044_[Lack_5'-end]_[mRNA]_locus=scaffold46391_1:1:387:+	Firmicutes
1011451	GL0091894_MH0044_[Lack_both_end]_[mRNA]_locus=scaffold59693_1:1:597:+	-

1015946	GL0029183_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold459_1:1296:1469:-	-
1017031	GL0057095_MH0045_[Complete]_[mRNA]_locus=scaffold5326_2:865:1497:-	-
1017065	GL0018228_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold5390_5:2:346:+	-
1017421	GL0077369_MH0045_[Lack_3'-end]_[mRNA]_locus=scaffold6735_1:3:347:-	-
1017443	GL0054086_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold6922_1:42:698:-	-
1017505	GL0096079_MH0045_[Complete]_[mRNA]_locus=scaffold7259_2:94:1389:+	Bacteroides capillosus
1017537	GL0085341_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold7434_2:163:642:-	-
1017768	GL0060181_MH0045_[Lack_both_end]_[mRNA]_locus=scaffold8763_4:1:1110:+	-
1018010	GL0126413_MH0045_[Lack_3'-end]_[mRNA]_locus=scaffold9767_5:515:1474:+	-
1018578	GL0069777_MH0045_[Lack_3'-end]_[mRNA]_locus=scaffold12078_1:1:591:-	-
1019465	GL0065130_MH0045_[Complete]_[mRNA]_locus=scaffold16102_1:654:1862:-	-
1020999	GL0126605_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold25655_2:2:724:+	-
1021289	GL0055385_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold27759_3:279:1157:-	-
1021351	GL0064074_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold27903_1:1:285:+	Acholeplasma laidlawii

1021644	GL0044167_MH0045_[Lack_3'-end]_[mRNA]_locus=scaffold30625_2:3:482:-	Bacteroides
1021701	GL0088080_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold31063_2:123:980:-	-
1021860	GL0058702_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold32244_1:1:2031:+	Clostridiales
1024022	GL0071279_MH0045_[Lack_both_end]_[mRNA]_locus=scaffold51996_1:1:663:+	-
1024256	GL0073246_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold54075_1:1:588:+	Clostridium leptum
1025149	GL0093851_MH0045_[Lack_5'-end]_[mRNA]_locus=scaffold63103_4:107:580:-	Collinsella aerofaciens
1025616	GL0128731_MH0045_[Complete]_[mRNA]_locus=scaffold67499_1:509:1033:+	Bacteria
1028998	GL0028943_MH0045_[Complete]_[mRNA]_locus=scaffold92403_1:290:2434:+	Staphylococcus aureus
1031862	GL0072816_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold501_2:1:864:+	Clostridium leptum
1034658	GL0070619_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold7549_6:1959:2240:-	Bacteria
1035119	GL0067774_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold8690_4:70:918:-	Clostridium bolteae
1037350	GL0100762_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold17343_4:1:651:-	-
1038544	GL0107772_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold22192_1:3:584:+	Clostridiales
1039044	GL0069912_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold24657_1:3:395:+	Bacteroides pectinophilus

1040303	GL0059592_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold30642_9:146:592:+	Bacteroides capillosus
1040459	GL0055178_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold31978_3:108:932:+	Coprococcus eutactus
1040605	GL0099106_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold32754_4:2:304:-	Roseburia inulinivorans
1041581	GL0003140_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold39834_7:1:513:-	Bacillus licheniformis
1042345	GL0035649_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold45795_1:3:500:-	Coprococcus comes
1042897	GL0081594_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold48811_2:1:618:-	Anaerostipes caccae
1043285	GL0017420_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold51416_1:1:678:+	Coprococcus eutactus
1044711	GL0065810_MH0046_[Complete]_[mRNA]_locus=scaffold62004_3:47:739:-	Ruminococcus obeum
1044744	GL0026896_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold62257_2:2:631:+	Bacteria
1044920	GL0027512_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold63835_2:2:892:-	-
1045039	GL0052717_MH0046_[Complete]_[mRNA]_locus=scaffold64670_1:2:514:+	Ruminococcus obeum
1045137	GL0003432_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold65863_2:2:280:+	-
1045310	GL0031628_MH0046_[Lack_3'-end]_[mRNA]_locus=scaffold67109_4:1:570:-	Eubacterium hallii
1045354	GL0057507_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold67385_1:2:928:-	-

1047477	GL0078939_MH0046_[Lack_both_end]_[mRNA]_locus=scaffold81869_1:3:680:+	Blautia hydrogenotrophica
1047953	GL0099084_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold84150_1:3:572:+	Clostridium nexile
1049154	GL0064362_MH0046_[Lack_5'-end]_[mRNA]_locus=scaffold86926_1:206:598:-	Blautia hydrogenotrophica
1050030	GL0005162_MH0046_[Lack_3'-end]_[mRNA]_locus=C3025137_1:1:477:-	Blautia hydrogenotrophica
1066366	GL0009567_MH0047_[Lack_both_end]_[mRNA]_locus=C1863293_1:1:522:-	Coprococcus comes
1067574	GL0050054_MH0047_[Lack_5'-end]_[mRNA]_locus=C1878209_1:3:551:+	-
1068144	GL0017486_MH0047_[Lack_3'-end]_[mRNA]_locus=C1884753_1:1:483:-	Bacteroides capillosus
1068344	GL0008644_MH0047_[Lack_3'-end]_[mRNA]_locus=C1887101_1:171:671:+	-
1068360	GL0064881_MH0047_[Lack_5'-end]_[mRNA]_locus=C1887369_1:2:640:+	Clostridium leptum
1074209	GL0003571_MH0048_[Complete]_[mRNA]_locus=scaffold12042_1:81:608:+	-
1078493	GL0090760_MH0048_[Lack_3'-end]_[mRNA]_locus=scaffold56453_2:2:112:-	-
1083179	GL0017794_MH0048_[Complete]_[mRNA]_locus=C2529371_1:153:668:+	Clostridium thermocellum
1083723	GL0088115_MH0048_[Lack_5'-end]_[mRNA]_locus=C2549317_1:3:500:+	-

1092256	GL0064299_MH0050_[Lack_both_end]_[mRNA]_locus=scaffold6968_1:1:510:+	Anaerocellum thermophilum
1094550	GL0018446_MH0050_[Lack_5'-end]_[mRNA]_locus=scaffold15043_1:1:444:+	Akkermansia muciniphila
1094868	GL0105123_MH0050_[Lack_3'-end]_[mRNA]_locus=scaffold16127_4:2:1447:-	Bacteroides thetaiotaomicron
1094869	GL0105124_MH0050_[Complete]_[mRNA]_locus=scaffold16127_4:1452:4691:-	Bacteroidetes
1095489	GL0011086_MH0050_[Lack_3'-end]_[mRNA]_locus=scaffold19061_4:573:3179:+	Pedobacter
1096712	GL0008871_MH0050_[Lack_3'-end]_[mRNA]_locus=scaffold24688_2:2:463:-	-
1098726	GL0107809_MH0050_[Lack_both_end]_[mRNA]_locus=scaffold36869_3:3:2288:+	Bacteroides
1099705	GL0071286_MH0050_[Complete]_[mRNA]_locus=scaffold44243_2:73:684:+	Clostridiales
1100018	GL0036922_MH0050_[Lack_3'-end]_[mRNA]_locus=scaffold46686_3:104:2611:+	-
1100202	GL0098695_MH0050_[Complete]_[mRNA]_locus=scaffold47862_1:103:522:+	Akkermansia muciniphila
1103517	GL0132224_MH0050_[Lack_5'-end]_[mRNA]_locus=scaffold70740_3:2:460:+	Akkermansia muciniphila
1103687	GL0070557_MH0050_[Complete]_[mRNA]_locus=scaffold72372_2:504:2792:-	Pedobacter
1103688	GL0150197_MH0050_[Lack_5'-end]_[mRNA]_locus=scaffold72372_5:58:693:-	Bacteroides

1104785	GL0085914_MH0050_[Complete]_[mRNA]_locus=scaffold79565_5:214:1713:-	Bacteroides ovatus
1104786	GL0084658_MH0050_[Lack_3'-end]_[mRNA]_locus=scaffold79565_6:3:1742:-	-
1104787	GL0084660_MH0050_[Lack_5'-end]_[mRNA]_locus=scaffold79565_6:3196:5772:-	Bacteroides ovatus
1105195	GL0078554_MH0050_[Lack_3'-end]_[mRNA]_locus=scaffold82110_1:3:464:-	Akkermansia muciniphila
1111320	GL0076372_MH0050_[Lack_3'-end]_[mRNA]_locus=C3895191_1:465:602:+	-
1115996	GL0064698_MH0051_[Complete]_[mRNA]_locus=scaffold19703_1:254:919:+	Clostridium nexile
1120062	GL0081728_MH0051_[Lack_5'-end]_[mRNA]_locus=scaffold56479_1:1:675:+	-
1129623	GL0023262_MH0052_[Lack_5'-end]_[mRNA]_locus=scaffold35487_1:250:1656:-	-
1144564	GL0018397_MH0053_[Lack_5'-end]_[mRNA]_locus=scaffold1275_1:3:359:+	Bacteria
1178635	GL0028304_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold1298_1:3:734:-	Bacteria
1179204	GL0079009_MH0054_[Complete]_[mRNA]_locus=scaffold2543_2:783:1661:-	Akkermansia muciniphila
1181446	GL0101983_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold8884_1:3:401:+	Clostridium
1181823	GL0073381_MH0054_[Lack_both_end]_[mRNA]_locus=scaffold10073_1:2:529:-	-
1182565	GL0095075_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold13083_2:1:144:-	-

1188515	GL0060126_MH0054_[Complete]_[mRNA]_locus=scaffold46359_2:23743:24597:+	Akkermansia muciniphila
1188516	GL0112232_MH0054_[Complete]_[mRNA]_locus=scaffold46359_3:73:543:-	Akkermansia muciniphila
1190301	GL0102747_MH0054_[Lack_3'-end]_[mRNA]_locus=scaffold58976_2:3:461:-	Eubacterium siraeum
1190567	GL0108412_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold61005_2:1:129:+	-
1190591	GL0123827_MH0054_[Complete]_[mRNA]_locus=scaffold61092_1:15879:17507:+	Akkermansia muciniphila
1192719	GL0100734_MH0054_[Complete]_[mRNA]_locus=scaffold75066_2:8250:8855:+	Akkermansia muciniphila
1192760	GL0033846_MH0054_[Lack_5'-end]_[mRNA]_locus=scaffold75391_1:1:1512:+	Akkermansia muciniphila
1193485	GL0118805_MH0054_[Complete]_[mRNA]_locus=scaffold78663_2:1298:2023:+	Marinobacter algicola
1196349	GL0026954_MH0054_[Lack_5'-end]_[mRNA]_locus=C3252926_1:493:660:-	-
1196721	GL0046612_MH0054_[Lack_3'-end]_[mRNA]_locus=C3287704_1:1:576:-	Clostridiales
1198538	GL0070276_MH0055_[Lack_both_end]_[mRNA]_locus=scaffold677_16:3:530:+	Ruminococcus obeum
1204994	GL0025256_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold8044_2:2:454:+	Dorea longicatena
1205784	GL0014554_MH0055_[Lack_3'-end]_[mRNA]_locus=scaffold9342_10:1:2148:-	Bacteria
1206398	GL0091829_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold10564_3:2:709:+	Bacteroides capillosus

1206705	GL0095457_MH0055_[Lack_5'-end]_[mRNA]_locus=scaffold10903_2:1:558:+	Clostridium asparagiforme
1222202	GL0028257_MH0055_[Lack_both_end]_[mRNA]_locus=scaffold58046_3:1:942:-	Bacteria
1228377	GL0013822_MH0055_[Lack_3'-end]_[mRNA]_locus=scaffold82302_2:3:590:-	Eubacterium hallii
1234426	GL0105825_MH0056_[Lack_5'-end]_[mRNA]_locus=scaffold11058_2:3:341:+	-
1240242	GL0046128_MH0056_[Lack_both_end]_[mRNA]_locus=scaffold48193_2:3:638:-	Ruminococcus torques
1250918	GL0071321_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold196_1:1211:2035:-	-
1250977	GL0073701_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold293_6:1589:2020:+	Faecalibacterium prausnitzii
1251173	GL0014651_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold423_2:3:953:+	-
1251189	GL0036350_MH0057_[Complete]_[mRNA]_locus=scaffold433_1:1904:3688:-	Acholeplasma laidlawii
1251190	GL0055307_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold433_4:1435:3009:-	Clostridiales
1251329	GL0045434_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold499_2:1:2244:-	Clostridiales
1251378	GL0050692_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold644_4:1:894:-	-
1252072	GL0024644_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold1410_3:8371:9498:-	Bacteria
1252382	GL0033853_MH0057_[Complete]_[mRNA]_locus=scaffold1779_2:119:1135:+	-

1252592	GL0037970_MH0057_[Complete]_[mRNA]_locus=scaffold2073_2:293:1498:-	Faecalibacterium prausnitzii
1252593	GL0072394_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold2080_10:1:732:+	-
1252626	GL0071394_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold2178_21:3:587:+	-
1252687	GL0034014_MH0057_[Complete]_[mRNA]_locus=scaffold2290_1:4201:5184:-	-
1253142	GL0068064_MH0057_[Lack_both_end]_[mRNA]_locus=scaffold3022_9:1:639:-	-
1253210	GL0032530_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold3144_1:370:1032:+	-
1253683	GL0085832_MH0057_[Complete]_[mRNA]_locus=scaffold3698_3:116:1135:+	-
1253908	GL0082343_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold3976_1:210:1541:-	-
1253971	GL0060716_MH0057_[Complete]_[mRNA]_locus=scaffold4167_3:945:2450:-	-
1254450	GL0082607_MH0057_[Complete]_[mRNA]_locus=scaffold4930_12:92:523:-	-
1255469	GL0036411_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold7459_2:2:136:+	-
1255517	GL0078120_MH0057_[Lack_both_end]_[mRNA]_locus=scaffold7639_2:3:1088:-	-
1255523	GL0068625_MH0057_[Complete]_[mRNA]_locus=scaffold7668_2:3496:5187:+	Clostridium scindens
1255643	GL0068760_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold8128_2:1:1176:+	Faecalibacterium prausnitzii

1255653	GL0038449_MH0057_[Complete]_[mRNA]_locus=scaffold8197_19:504:1409:+	-
1255998	GL0071929_MH0057_[Complete]_[mRNA]_locus=scaffold8982_2:522:1937:+	Faecalibacterium prausnitzii
1255999	GL0072029_MH0057_[Complete]_[mRNA]_locus=scaffold8982_9:2698:3609:+	-
1256505	GL0051237_MH0057_[Complete]_[mRNA]_locus=scaffold10842_4:1419:2549:+	-
1256980	GL0050896_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold12927_12:656:1030:-	-
1257299	GL0025041_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold14259_1:7:585:-	-
1257408	GL0054915_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold14931_3:1730:3226:+	Clostridiales
1257548	GL0088410_MH0057_[Complete]_[mRNA]_locus=scaffold15480_3:493:2322:+	Clostridium hylemonae
1257697	GL0063129_MH0057_[Lack_3'-end]_[mRNA]_locus=scaffold16774_2:52:963:+	-
1258344	GL0013800_MH0057_[Complete]_[mRNA]_locus=scaffold20875_9:433:1566:-	-
1258376	GL0030800_MH0057_[Complete]_[mRNA]_locus=scaffold21139_1:188:2632:-	-
1258820	GL0009793_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold25134_3:2:646:+	Faecalibacterium prausnitzii
1259228	GL0035311_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold30432_3:3:1583:+	Firmicutes
1259377	GL0047881_MH0057_[Lack_5'-end]_[mRNA]_locus=scaffold32481_1:3:317:+	-

1260311	GL0085222_MH0057_[Complete]_[mRNA]_locus=scaffold45030_2:144:1079:+	-
1261277	GL0057139_MH0057_[Lack_both_end]_[mRNA]_locus=C3652518_1:1:591:+	-
1261524	GL0034907_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold385_5:601:1101:-	-
1261529	GL0112769_MH0058_[Complete]_[mRNA]_locus=scaffold427_7:454:1437:+	-
1261531	GL0125561_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold427_8:3439:3852:+	-
1261605	GL0075000_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold829_5:9980:13609:+	Firmicutes
1261665	GL0094290_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold1072_9:1:1623:-	Faecalibacterium prausnitzii
1261666	GL0094291_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold1072_9:1845:2468:-	-
1261826	GL0040666_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold2136_1:3:200:-	Faecalibacterium prausnitzii
1261910	GL0083054_MH0058_[Complete]_[mRNA]_locus=scaffold2590_3:135:1511:+	Faecalibacterium prausnitzii
1262211	GL0128618_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold4211_8:440:643:+	-
1262214	GL0137990_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold4268_2:3:1043:+	-
1262338	GL0099583_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold5114_4:1:522:+	-
1262645	GL0115906_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold6841_4:3:788:+	Faecalibacterium prausnitzii

1262692	GL0117566_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold7016_7:2615:3577:-	-
1262804	GL0146718_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold7948_4:3:1067:+	Akkermansia muciniphila
1263028	GL0072116_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold9535_2:429:1370:+	-
1263043	GL0053970_MH0058_[Complete]_[mRNA]_locus=scaffold9616_7:1970:3310:-	Faecalibacterium prausnitzii
1263087	GL0075949_MH0058_[Complete]_[mRNA]_locus=scaffold9942_4:313:1131:-	-
1263239	GL0156353_MH0058_[Complete]_[mRNA]_locus=scaffold10455_5:2952:3833:-	-
1263927	GL0151572_MH0058_[Lack_both_end]_[mRNA]_locus=scaffold16043_1:1:543:+	-
1264511	GL0058424_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold20371_2:1:768:+	-
1264600	GL0049687_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold20734_4:2:907:+	Faecalibacterium prausnitzii
1265435	GL0066881_MH0058_[Complete]_[mRNA]_locus=scaffold27376_2:573:1529:+	Akkermansia muciniphila
1265447	GL0064488_MH0058_[Complete]_[mRNA]_locus=scaffold27645_1:159:1637:-	Faecalibacterium prausnitzii
1265829	GL0088645_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold30974_4:103:771:-	Plasmodium yoelii
1265945	GL0064914_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold31995_5:1:162:+	-
1266122	GL0153993_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold33467_1:3:800:-	-

1266872	GL0115054_MH0058_[Complete]_[mRNA]_locus=scaffold41452_1:461:1042:+	-
1268125	GL0003298_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold53186_4:6:548:-	Akkermansia muciniphila
1268363	GL0034725_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold55775_4:589:789:-	-
1270663	GL0147231_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold81490_2:1:354:+	Akkermansia muciniphila
1270799	GL0119291_MH0058_[Lack_5'-end]_[mRNA]_locus=scaffold82767_4:2:547:+	Eubacterium ventriosum
1271398	GL0005952_MH0058_[Lack_both_end]_[mRNA]_locus=scaffold88961_10:1:2343:+	Bacteroides intestinalis
1271476	GL0131590_MH0058_[Complete]_[mRNA]_locus=scaffold89723_1:1047:2099:+	-
1272087	GL0038009_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold95623_2:383:574:+	-
1272339	GL0029845_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold98209_2:2:271:-	Bacteroides fragilis
1272397	GL0067726_MH0058_[Lack_3'-end]_[mRNA]_locus=scaffold98769_2:1:927:-	Akkermansia muciniphila
1277101	GL0039150_MH0059_[Complete]_[mRNA]_locus=scaffold353_8:610:1662:-	Akkermansia muciniphila
1278595	GL0065462_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold3902_3:2:193:-	-
1281565	GL0031966_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold13552_9:1290:1403:+	-
1281826	GL0108885_MH0059_[Lack_5'-end]_[mRNA]_locus=scaffold14787_10:1:615:+	Akkermansia muciniphila

1283462	GL0130510_MH0059_[Lack_both_end]_[mRNA]_locus=scaffold21174_27:3:542:+	Akkermansia muciniphila
1283742	GL0159832_MH0059_[Lack_5'-end]_[mRNA]_locus=scaffold22831_4:2:568:+	Akkermansia muciniphila
1285024	GL0117892_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold28832_4:3:1943:-	Akkermansia muciniphila
1285096	GL0081582_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold29327_6:1:129:-	-
1286228	GL0108900_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold35658_8:456:578:+	-
1287938	GL0012324_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold47351_4:1:132:-	-
1293429	GL0159500_MH0059_[Lack_3'-end]_[mRNA]_locus=scaffold85566_2:2:151:-	-
1298860	GL0026615_MH0060_[Complete]_[mRNA]_locus=scaffold779_3:157:813:+	-
1301049	GL0105653_MH0060_[Lack_3'-end]_[mRNA]_locus=scaffold7204_3:247:765:+	Alkaliphilus oremlandii
1301391	GL0066886_MH0060_[Complete]_[mRNA]_locus=scaffold8188_3:5582:7606:+	Akkermansia muciniphila
1303038	GL0106793_MH0060_[Complete]_[mRNA]_locus=scaffold13597_2:21399:22787:+	Akkermansia muciniphila
1304227	GL0000617_MH0060_[Lack_5'-end]_[mRNA]_locus=scaffold18325_2:12175:13209:-	Akkermansia muciniphila
1304254	GL0129755_MH0060_[Complete]_[mRNA]_locus=scaffold18420_3:88:771:+	Eubacterium siraeum

1304405	GL0121769_MH0060_[Lack_5'-end]_[mRNA]_locus=scaffold18767_3:3:1256:+	Akkermansia muciniphila
1307103	GL0019232_MH0060_[Complete]_[mRNA]_locus=scaffold32130_3:464:1837:-	-
1307461	GL0085311_MH0060_[Complete]_[mRNA]_locus=scaffold34430_3:9526:10908:+	Akkermansia muciniphila
1307583	GL0053931_MH0060_[Lack_3'-end]_[mRNA]_locus=scaffold35392_2:2:103:-	-
1307767	GL0038340_MH0060_[Complete]_[mRNA]_locus=scaffold36303_4:7741:10083:-	Akkermansia muciniphila
1309631	GL0044512_MH0060_[Lack_5'-end]_[mRNA]_locus=scaffold46567_2:2:586:+	Bacteria
1310064	GL0019473_MH0060_[Lack_3'-end]_[mRNA]_locus=scaffold49285_1:3:593:-	Clostridiales
1312871	GL0121830_MH0060_[Complete]_[mRNA]_locus=scaffold69677_1:6494:7927:+	Akkermansia muciniphila
1313656	GL0041410_MH0060_[Complete]_[mRNA]_locus=scaffold76065_3:3229:3939:+	Akkermansia muciniphila
1313994	GL0078056_MH0060_[Lack_5'-end]_[mRNA]_locus=scaffold78541_1:2213:3865:-	Akkermansia muciniphila
1318894	GL0044134_MH0060_[Complete]_[mRNA]_locus=scaffold109052_1:6012:7568:-	Akkermansia muciniphila
1318926	GL0049404_MH0060_[Complete]_[mRNA]_locus=scaffold109113_1:6548:8518:-	Akkermansia muciniphila
1321237	GL0129557_MH0060_[Lack_5'-end]_[mRNA]_locus=C3878473_1:1:579:+	Bacteria
1321809	GL0009126_MH0061_[Lack_both_end]_[mRNA]_locus=scaffold316_2:1:2451:+	Clostridiales

1324365	GL0077562_MH0061_[Lack_both_end]_[mRNA]_locus=scaffold4295_11:1:585:+	Clostridiales
1324944	GL0085213_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold5486_2:2:652:+	-
1325208	GL0014920_MH0061_[Complete]_[mRNA]_locus=scaffold5964_1:5930:6490:+	Janthinobacterium
1325699	GL0006832_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold7169_1:1:1176:+	Bacteroides eggerthii
1326418	GL0048481_MH0061_[Complete]_[mRNA]_locus=scaffold8974_1:4878:5276:+	Clostridiales
1336444	GL0030077_MH0061_[Lack_5'-end]_[mRNA]_locus=scaffold48435_1:410:517:-	-
1341716	GL0044764_MH0062_[Lack_3'-end]_[mRNA]_locus=scaffold12834_11:993:3107:+	Clostridium scindens
1343373	GL0072947_MH0062_[Lack_5'-end]_[mRNA]_locus=scaffold20445_1:3967:4164:-	-
1346719	GL0007423_MH0062_[Complete]_[mRNA]_locus=scaffold39537_1:1401:3032:+	Heliobacterium modesticaldum
1358128	GL0010075_MH0062_[Lack_5'-end]_[mRNA]_locus=C5383420_1:392:850:-	Bacteroides capillosus
1372173	GL0083388_MH0063_[Lack_both_end]_[mRNA]_locus=scaffold40468_1:2:649:-	Desulfitobacterium hafniense
1386738	GL0010699_MH0064_[Lack_5'-end]_[mRNA]_locus=scaffold1710_1:1210:2172:-	-
1388787	GL0017560_MH0064_[Lack_both_end]_[mRNA]_locus=scaffold6420_1:3:1031:-	-

1397235	GL0060244_MH0064_[Lack_5'-end]_[mRNA]_locus=scaffold55180_2:97:798:-	-
1400482	GL0022360_MH0064_[Lack_5'-end]_[mRNA]_locus=C6278931_1:2:199:+	-
1425387	GL0011573_MH0065_[Lack_3'-end]_[mRNA]_locus=scaffold59945_1:329:517:+	Ruminococcus gnavus
1444711	GL0053550_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold59_7:3179:3355:-	Alistipes putredinis
1445277	GL0116330_MH0066_[Complete]_[mRNA]_locus=scaffold766_5:6064:6918:-	Akkermansia muciniphila
1446086	GL0117402_MH0066_[Lack_3'-end]_[mRNA]_locus=scaffold1674_1:1:723:-	Akkermansia muciniphila
1447023	GL0050202_MH0066_[Complete]_[mRNA]_locus=scaffold2986_1:2519:2854:-	Akkermansia muciniphila
1447235	GL0117470_MH0066_[Lack_5'-end]_[mRNA]_locus=scaffold3338_8:2:1381:+	Akkermansia muciniphila
1447656	GL0052182_MH0066_[Complete]_[mRNA]_locus=scaffold4136_3:12023:12730:+	Akkermansia muciniphila
1449272	GL0019628_MH0066_[Complete]_[mRNA]_locus=scaffold7573_7:1666:2880:-	Clostridium
1453475	GL0070954_MH0066_[Lack_3'-end]_[mRNA]_locus=scaffold19594_2:1347:2333:+	Bacteroides capillosus
1454749	GL0036451_MH0066_[Complete]_[mRNA]_locus=scaffold24362_5:123:632:+	-
1455545	GL0105639_MH0066_[Complete]_[mRNA]_locus=scaffold27608_6:965:2212:-	Akkermansia muciniphila
1457088	GL0000259_MH0066_[Lack_3'-end]_[mRNA]_locus=scaffold35113_1:1:411:-	Akkermansia muciniphila

1470533	GL0084302_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold8100_7:1:375:-	Clostridiales
1470868	GL0065626_MH0067_[Lack_3'-end]_[mRNA]_locus=scaffold9207_1:3:1013:-	Clostridium
1476765	GL0090432_MH0067_[Lack_5'-end]_[mRNA]_locus=scaffold34744_2:2:1099:+	Streptococcus equi
1477954	GL0029576_MH0067_[Complete]_[mRNA]_locus=scaffold42179_1:80:1063:+	Bacteroides capillosus
1482944	GL0045157_MH0068_[Complete]_[mRNA]_locus=scaffold4041_1:2228:7099:+	Clostridium methylpentosum
1482945	GL0045158_MH0068_[Complete]_[mRNA]_locus=scaffold4041_1:7103:8224:+	Firmicutes
1484199	GL0092552_MH0068_[Lack_5'-end]_[mRNA]_locus=scaffold7172_2:2:757:+	-
1490173	GL0009065_MH0068_[Lack_both_end]_[mRNA]_locus=scaffold39133_1:1:501:+	Clostridiales
1500932	GL0044329_MH0069_[Lack_3'-end]_[mRNA]_locus=scaffold16659_4:85:873:+	Clostridiales
1523307	GL0126228_MH0069_[Lack_both_end]_[mRNA]_locus=C6783995_1:1:537:+	Bacteroides capillosus
1523885	GL0066107_MH0069_[Lack_3'-end]_[mRNA]_locus=C6810744_1:202:600:+	Holdemania filiformis
1524931	GL0025997_MH0069_[Lack_5'-end]_[mRNA]_locus=C6876275_1:101:901:-	-
1526715	GL0114146_MH0070_[Complete]_[mRNA]_locus=scaffold3733_1:89:262:-	Firmicutes
1529468	GL0149602_MH0070_[Lack_5'-end]_[mRNA]_locus=scaffold15789_3:3:980:+	-

1532861	GL0091161_MH0070_[Lack_5'-end]_[mRNA]_locus=scaffold31983_1:1:1422:+	Clostridium asparagiforme
1538618	GL0108281_MH0070_[Lack_5'-end]_[mRNA]_locus=scaffold68237_2:432:533:-	-
1545712	GL0052950_MH0070_[Lack_3'-end]_[mRNA]_locus=scaffold110121_2:2:298:-	-
1554962	GL0072306_MH0071_[Lack_both_end]_[mRNA]_locus=scaffold4732_3:2:1303:-	Clostridiales
1555441	GL0073778_MH0071_[Complete]_[mRNA]_locus=scaffold5478_3:1082:1327:+	-
1556130	GL0077483_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold6661_22:983:3799:-	Alkaliphilus oremlandii
1556393	GL0070662_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold7259_1:510:1148:-	Akkermansia muciniphila
1557006	GL0043280_MH0071_[Complete]_[mRNA]_locus=scaffold8897_5:371:1471:+	Ruminococcus gnavus
1557007	GL0003525_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold8897_6:3:542:+	Ruminococcus gnavus
1557010	GL0018889_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold8897_15:1:846:+	Eubacterium hallii
1558984	GL0027333_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold13307_4:32:688:-	Akkermansia muciniphila
1560183	GL0115716_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold16504_5:1:951:+	Akkermansia muciniphila
1561950	GL0065194_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold22252_8:2:241:-	-
1562126	GL0022522_MH0071_[Lack_both_end]_[mRNA]_locus=scaffold22974_1:1:606:+	Clostridium thermocellum

1562205	GL0058691_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold23142_5:3:155:+	-
1564285	GL0069461_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold30877_1:1:213:-	-
1568141	GL0003330_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold49543_11:3:134:+	-
1570044	GL0025786_MH0071_[Complete]_[mRNA]_locus=scaffold58406_2:77:1036:+	Ruminococcus lactaris
1570237	GL0083081_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold59498_1:673:969:-	Akkermansia muciniphila
1570671	GL0025567_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold62092_6:3:380:-	Akkermansia muciniphila
1570853	GL0020517_MH0071_[Lack_both_end]_[mRNA]_locus=scaffold63268_1:3:587:-	Clostridium methylpentosum
1571203	GL0003311_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold65374_1:3:290:+	Clostridium thermocellum
1571641	GL0100377_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold67838_3:2:643:+	Akkermansia muciniphila
1571950	GL0091486_MH0071_[Complete]_[mRNA]_locus=scaffold69204_1:1723:2256:+	Clostridium
1572143	GL0051916_MH0071_[Complete]_[mRNA]_locus=scaffold70061_2:725:1534:-	Akkermansia muciniphila
1572380	GL0053658_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold71291_1:217:564:+	-
1572429	GL0038828_MH0071_[Lack_both_end]_[mRNA]_locus=scaffold71585_1:3:587:-	Clostridiales
1572550	GL0072017_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold72156_1:3:791:-	Clostridium

1572946	GL0046023_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold74113_2:3:317:+	Clostridia
1573070	GL0052258_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold74824_1:1603:1770:+	-
1573125	GL0006642_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold75088_1:59:541:-	Carnobacterium
1573467	GL0041026_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold76415_2:400:534:+	-
1573551	GL0069597_MH0071_[Lack_3'-end]_[mRNA]_locus=scaffold76760_1:3:269:-	Akkermansia muciniphila
1573686	GL0066793_MH0071_[Lack_5'-end]_[mRNA]_locus=scaffold77270_3:2:466:+	Akkermansia muciniphila
1577879	GL0053331_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold2192_1:3:968:-	Clostridium leptum
1581009	GL0023947_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold11033_2:1:219:-	Parabacteroides johnsonii
1581115	GL0062834_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold11405_2:32:556:-	-
1584778	GL0007457_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold28185_2:1873:2616:+	Physcomitrella patens
1584835	GL0095215_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold28733_1:2515:3429:-	-
1586056	GL0062522_MH0072_[Lack_both_end]_[mRNA]_locus=scaffold36600_1:3:566:-	Clostridium leptum
1587755	GL0000370_MH0072_[Lack_3'-end]_[mRNA]_locus=scaffold50321_1:456:593:+	-
1588412	GL0036975_MH0072_[Lack_5'-end]_[mRNA]_locus=scaffold55204_2:2:280:+	-

1592437	GL0026575_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold1241_2:1:1299:-	Lactobacillales
1593129	GL0054820_MH0073_[Lack_both_end]_[mRNA]_locus=scaffold3543_6:3:572:+	Ruminococcus lactaris
1593329	GL0114728_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold4164_1:824:1072:+	Ruminococcus lactaris
1594353	GL0089602_MH0073_[Complete]_[mRNA]_locus=scaffold7731_1:372:1133:-	Ruminococcus lactaris
1597037	GL0008733_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold19400_1:1370:1588:+	-
1598308	GL0069264_MH0073_[Complete]_[mRNA]_locus=scaffold26194_5:105:1115:-	Dorea longicatena
1598934	GL0025231_MH0073_[Lack_both_end]_[mRNA]_locus=scaffold30434_3:2:562:+	Ruminococcus
1602519	GL0028952_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold54430_2:135:1178:+	Coprococcus comes
1603154	GL0001078_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold58636_3:3:470:-	Clostridium nexile
1603158	GL0097210_MH0073_[Lack_3'-end]_[mRNA]_locus=scaffold58652_1:2:103:-	-
1604044	GL0076928_MH0073_[Lack_5'-end]_[mRNA]_locus=scaffold66609_1:2:664:+	Dorea formicigenerans
1606776	GL0074623_MH0073_[Lack_both_end]_[mRNA]_locus=scaffold84562_1:1:831:+	Bacteroides capillosus
1607962	GL0022157_MH0073_[Lack_5'-end]_[mRNA]_locus=C3667040_1:1:387:+	-
1617460	GL0025758_MH0074_[Lack_5'-end]_[mRNA]_locus=scaffold7060_1:1:162:+	Bacteroides capillosus

1621344	GL0065048_MH0074_[Lack_both_end]_[mRNA]_locus=scaffold12800_2:2:565:+	-
1626250	GL0063823_MH0074_[Lack_both_end]_[mRNA]_locus=scaffold22747_2:2:541:+	Clostridium
1627542	GL0096062_MH0074_[Complete]_[mRNA]_locus=scaffold26117_2:1678:3216:+	Pedobacter
1630180	GL0064129_MH0074_[Complete]_[mRNA]_locus=scaffold32977_2:557:1165:-	-
1638286	GL0087408_MH0074_[Complete]_[mRNA]_locus=C4345175_1:2902:3393:-	Burkholderia
1643529	GL0104127_MH0075_[Complete]_[mRNA]_locus=scaffold26560_2:595:933:-	-
1644077	GL0103010_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold30170_4:264:779:-	Anaerotruncus colihominis
1651005	GL0045847_MH0075_[Lack_5'-end]_[mRNA]_locus=scaffold82173_3:571:909:-	-
1658561	GL0039282_MH0076_[Complete]_[mRNA]_locus=scaffold10939_1:3066:3500:+	Coprococcus eutactus
1659405	GL0088058_MH0076_[Complete]_[mRNA]_locus=scaffold20017_1:79:384:+	Clostridiales
1661518	GL0025351_MH0076_[Complete]_[mRNA]_locus=scaffold40916_1:38:952:+	Firmicutes
1663357	GL0067558_MH0076_[Lack_5'-end]_[mRNA]_locus=scaffold56222_1:199:711:-	-
1681360	GL0147399_MH0077_[Lack_3'-end]_[mRNA]_locus=scaffold19570_7:1:1137:-	Firmicutes
1694835	GL0000803_MH0077_[Lack_3'-end]_[mRNA]_locus=scaffold71434_4:84:1073:+	Clostridium leptum

1695951	GL0012402_MH0077_[Lack_5'-end]_[mRNA]_locus=scaffold77157_2:561:1145:-	-
1699212	GL0098762_MH0077_[Lack_5'-end]_[mRNA]_locus=scaffold93816_1:2:211:+	-
1703513	GL0100750_MH0077_[Lack_5'-end]_[mRNA]_locus=scaffold111751_1:3:344:+	Firmicutes
1706572	GL0136407_MH0077_[Lack_both_end]_[mRNA]_locus=C4465976_1:3:647:+	Eubacterium siraeum
1716965	GL0030185_MH0078_[Complete]_[mRNA]_locus=C3056122_1:510:1097:+	Anaerotruncus colihominis
1718175	GL0018296_MH0079_[Lack_5'-end]_[mRNA]_locus=scaffold6925_3:227:538:-	Bacteria
1726402	GL0014672_MH0079_[Complete]_[mRNA]_locus=scaffold48030_4:63:512:-	Firmicutes
1734878	GL0077349_MH0079_[Lack_3'-end]_[mRNA]_locus=C2003495_1:3:149:-	-
1737755	GL0035987_MH0079_[Lack_5'-end]_[mRNA]_locus=C2039722_1:2:583:+	Porphyromonas gingivalis
1748013	GL0021479_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold14910_2:1:327:-	Clostridium bolteae
1748776	GL0110476_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold18653_2:217:669:+	Clostridiales
1751712	GL0052442_MH0080_[Complete]_[mRNA]_locus=scaffold33558_1:92:325:-	Clostridium asparagiforme
1752313	GL0006387_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold37270_5:31:993:+	Anaerostipes caccae
1753352	GL0103690_MH0080_[Complete]_[mRNA]_locus=scaffold43671_1:1549:2313:-	Bacteroides capillosus

1753940	GL0103208_MH0080_[Lack_both_end]_[mRNA]_locus=scaffold46871_1:2:817:-	Ruminococcus obeum
1753941	GL0012853_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold46882_1:27:533:+	-
1754917	GL0012793_MH0080_[Complete]_[mRNA]_locus=scaffold52213_6:2211:2510:-	Ruminococcus torques
1758405	GL0005516_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold73310_1:162:596:-	Clostridiales
1758761	GL0135889_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold75371_1:3:557:-	Clostridiales
1760419	GL0100900_MH0080_[Lack_both_end]_[mRNA]_locus=scaffold83581_2:2:733:+	Ruminococcus lactaris
1760612	GL0137507_MH0080_[Lack_5'-end]_[mRNA]_locus=scaffold84374_1:2:169:+	-
1760643	GL0125447_MH0080_[Lack_3'-end]_[mRNA]_locus=scaffold84564_1:234:1319:+	Eubacterium hallii
1770083	GL0018867_MH0080_[Lack_3'-end]_[mRNA]_locus=C3313250_1:139:1767:+	Ruminococcus gnavus
1772019	GL0153712_MH0081_[Complete]_[mRNA]_locus=scaffold3143_3:8384:10714:+	Bacteroides ovatus
1774996	GL0037628_MH0081_[Lack_5'-end]_[mRNA]_locus=scaffold10971_1:1:195:+	-
1779112	GL0026410_MH0081_[Complete]_[mRNA]_locus=scaffold25317_2:891:1208:+	-
1782373	GL0091054_MH0081_[Complete]_[mRNA]_locus=scaffold39825_6:470:2035:-	-
1783230	GL0146278_MH0081_[Complete]_[mRNA]_locus=scaffold44743_2:348:1262:+	Pedobacter

1785168	GL0061082_MH0081_[Complete]_[mRNA]_locus=scaffold53982_13:206:1177:-	-
1789431	GL0030457_MH0081_[Lack_both_end]_[mRNA]_locus=scaffold76409_2:1:609:+	Bacteroides fragilis
1789463	GL0021954_MH0081_[Complete]_[mRNA]_locus=scaffold76600_5:281:1201:+	Pedobacter
1789826	GL0019225_MH0081_[Lack_3'-end]_[mRNA]_locus=scaffold78561_3:111:2117:+	-
1791993	GL0115557_MH0081_[Complete]_[mRNA]_locus=scaffold89331_4:1081:1731:-	-
1794059	GL0135238_MH0081_[Lack_5'-end]_[mRNA]_locus=scaffold96243_1:110:1390:-	-
1804736	GL0022436_MH0082_[Complete]_[mRNA]_locus=scaffold7065_3:475:1671:-	Bacteroides capillosus
1806580	GL0054708_MH0082_[Complete]_[mRNA]_locus=scaffold10565_7:111:674:+	-
1826451	GL0078110_MH0082_[Lack_5'-end]_[mRNA]_locus=scaffold81710_1:57:707:-	-
1840286	GL0036565_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold5134_1:3:767:+	Bacteroides capillosus
1843863	GL0117361_MH0083_[Complete]_[mRNA]_locus=scaffold19009_1:7633:8841:+	Desulfitobacterium hafniense
1846270	GL0117178_MH0083_[Lack_5'-end]_[mRNA]_locus=scaffold32077_2:775:1167:-	-
1860583	GL0068004_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold639_2:3662:4144:-	-
1861643	GL0022876_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold3470_1:3:374:-	-

1861865	GL0041795_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold4165_2:1:540:+	-
1862434	GL0055386_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold6118_8:1379:1549:+	-
1863603	GL0055401_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold11314_4:3:1142:-	-
1863685	GL0063033_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold11581_1:3:512:-	Clostridium
1864174	GL0013352_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold14546_2:753:1037:-	Ruminococcus obeum
1864228	GL0003931_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold14984_3:379:645:+	-
1864418	GL0012593_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold15792_1:3:758:+	Faecalibacterium prausnitzii
1864654	GL0045403_MH0084_[Complete]_[mRNA]_locus=scaffold17449_1:334:900:-	-
1864947	GL0031832_MH0084_[Complete]_[mRNA]_locus=scaffold19110_1:605:1087:+	Eubacterium siraeum
1865216	GL0067242_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold21494_1:1:333:-	-
1865411	GL0008305_MH0084_[Lack_3'-end]_[mRNA]_locus=scaffold23135_1:3:527:-	-
1866458	GL0050005_MH0084_[Complete]_[mRNA]_locus=scaffold33290_1:460:927:+	Anaerotruncus colihominis
1866956	GL0057236_MH0084_[Lack_both_end]_[mRNA]_locus=scaffold38135_1:2:676:-	-
1867510	GL0047930_MH0084_[Lack_5'-end]_[mRNA]_locus=scaffold42651_1:506:643:-	-

1879213	GL0065856_MH0085_[Lack_3'-end]_[mRNA]_locus=scaffold49506_1:131:517:+	-
1879338	GL0050270_MH0085_[Lack_5'-end]_[mRNA]_locus=scaffold50639_1:3:461:+	-
1885253	GL0168865_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold2581_1:1:594:+	Faecalibacterium prausnitzii
1890918	GL0109270_MH0086_[Complete]_[mRNA]_locus=scaffold8199_4:58:237:+	-
1894242	GL0032381_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold11887_3:1:1020:+	Ruminococcus gnavus
1895056	GL0166789_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold13192_1:666:1010:-	-
1895347	GL0079298_MH0086_[Complete]_[mRNA]_locus=scaffold13458_3:94:546:+	-
1895489	GL0107927_MH0086_[Complete]_[mRNA]_locus=scaffold13576_6:3743:4165:+	Clostridiales
1897345	GL0102386_MH0086_[Complete]_[mRNA]_locus=scaffold16727_2:19:1344:-	-
1898583	GL0050612_MH0086_[Complete]_[mRNA]_locus=scaffold18865_4:2189:3238:-	-
1898826	GL0107990_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold19316_1:3:851:+	-
1900351	GL0137442_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold22102_12:236:829:-	Roseburia inulinivorans
1900884	GL0195380_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold23305_2:2:790:+	-
1901094	GL0089634_MH0086_[Complete]_[mRNA]_locus=scaffold23536_4:105:1532:+	Faecalibacterium prausnitzii

1902168	GL0070451_MH0086_[Complete]_[mRNA]_locus=scaffold25945_9:2272:4104:-	cellular organisms
1902312	GL0121339_MH0086_[Complete]_[mRNA]_locus=scaffold26328_1:190:1305:-	-
1902434	GL0027900_MH0086_[Complete]_[mRNA]_locus=scaffold26558_1:4190:5128:-	Collinsella aerofaciens
1904351	GL0044204_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold30657_4:812:1363:+	Ruminococcus lactaris
1904500	GL0067854_MH0086_[Complete]_[mRNA]_locus=scaffold31026_2:31:1407:+	Faecalibacterium prausnitzii
1907309	GL0195948_MH0086_[Lack_both_end]_[mRNA]_locus=scaffold38310_2:3:764:-	-
1909609	GL0068346_MH0086_[Complete]_[mRNA]_locus=scaffold43950_3:114:1076:+	Faecalibacterium prausnitzii
1910032	GL0001270_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold45261_5:3:1073:+	-
1910314	GL0120134_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold46314_1:2:613:+	Faecalibacterium prausnitzii
1913098	GL0161750_MH0086_[Complete]_[mRNA]_locus=scaffold56234_1:356:820:+	Holdemania filiformis
1913191	GL0074873_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold56418_1:3:599:+	-
1918684	GL0024641_MH0086_[Complete]_[mRNA]_locus=scaffold79455_3:49:504:-	Ruminococcus lactaris
1921324	GL0073049_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold92034_4:1:948:+	-
1921466	GL0102656_MH0086_[Lack_3'-end]_[mRNA]_locus=scaffold92694_1:3:410:-	-

1921758	GL0100121_MH0086_[Complete]_[mRNA]_locus=scaffold94074_1:366:1061:-	-
1925795	GL0100616_MH0086_[Lack_5'-end]_[mRNA]_locus=scaffold108883_1:503:1330:-	-
1929278	GL0062591_O2_[Lack_5'-end]_[mRNA]_locus=scaffold84_1:346:972:-	-
1929403	GL0016766_O2_[Lack_5'-end]_[mRNA]_locus=scaffold375_1:3:1085:+	Clostridium phytofermentans
1929744	GL0068857_O2_[Lack_both_end]_[mRNA]_locus=scaffold1037_2:1:579:+	-
1929799	GL0051968_O2_[Complete]_[mRNA]_locus=scaffold1165_1:567:1823:+	Clostridiales
1929804	GL0061954_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1165_3:91:672:+	-
1929848	GL0034348_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1269_1:3:482:-	Clostridium leptum
1929969	GL0044639_O2_[Complete]_[mRNA]_locus=scaffold1549_4:557:1927:-	Clostridiales
1929970	GL0044640_O2_[Complete]_[mRNA]_locus=scaffold1549_4:2081:3346:-	Dorea longicatena
1929979	GL0056900_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1549_9:3:3008:-	-
1930051	GL0041893_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1695_2:630:1112:-	Clostridium leptum
1930171	GL0059290_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1917_1:1:864:-	Clostridium leptum
1930416	GL0050179_O2_[Lack_3'-end]_[mRNA]_locus=scaffold2540_1:278:766:+	Clostridium leptum

1930556	GL0012148_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2781_1:1:438:+	Ruminococcus obeum
1930633	GL0033610_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2994_1:196:588:-	Bacteroides capillosus
1930676	GL0070067_O2_[Lack_both_end]_[mRNA]_locus=scaffold3119_1:3:503:-	Clostridium leptum
1930711	GL0041789_O2_[Lack_3'-end]_[mRNA]_locus=scaffold3243_1:266:622:+	Alistipes putredinis
1930762	GL0018300_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3385_1:3:716:+	Clostridium methylpentosum
1930902	GL0026022_O2_[Lack_3'-end]_[mRNA]_locus=scaffold3738_1:3:365:-	Anaerotruncus colihominis
1930934	GL0046390_O2_[Lack_3'-end]_[mRNA]_locus=scaffold3854_1:3:1025:-	Bacteroides capillosus
1931011	GL0048898_O2_[Complete]_[mRNA]_locus=scaffold3964_1:79:333:+	Clostridium leptum
1931022	GL0054490_O2_[Lack_3'-end]_[mRNA]_locus=scaffold3988_1:3:230:-	Clostridium asparagiforme
1931023	GL0054491_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3988_1:308:823:-	Firmicutes
1931109	GL0012327_O2_[Lack_both_end]_[mRNA]_locus=scaffold4227_3:1:834:+	Clostridium leptum
1931199	GL0043573_O2_[Lack_both_end]_[mRNA]_locus=scaffold4541_1:3:509:-	Clostridium leptum
1931225	GL0038378_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4592_1:586:900:+	-
1931232	GL0068886_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4618_1:2:757:+	Clostridiales

1931422	GL0005249_O2_[Lack_3'-end]_[mRNA]_locus=scaffold5072_1:389:808:+	Clostridium leptum
1931443	GL0065165_O2_[Lack_3'-end]_[mRNA]_locus=scaffold5135_1:2:508:-	Lactobacillus acidophilus
1931530	GL0048019_O2_[Complete]_[mRNA]_locus=scaffold5301_6:2643:3875:+	Ruminococcus lactaris
1931550	GL0064315_O2_[Lack_3'-end]_[mRNA]_locus=scaffold5351_2:1013:1483:+	-
1931601	GL0046398_O2_[Complete]_[mRNA]_locus=scaffold5445_1:557:832:-	-
1931715	GL0043862_O2_[Lack_3'-end]_[mRNA]_locus=scaffold5694_1:3:155:-	Bacteria
1931748	GL0058860_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5809_1:1:654:+	Clostridium leptum
1931749	GL0058861_O2_[Complete]_[mRNA]_locus=scaffold5809_1:651:914:+	Clostridium leptum
1931768	GL0058382_O2_[Lack_both_end]_[mRNA]_locus=scaffold5924_1:2:520:-	Clostridium methylpentosum
1931790	GL0040192_O2_[Lack_both_end]_[mRNA]_locus=scaffold5959_1:1:633:-	Bacteroides capillosus
1931887	GL0061694_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6173_2:355:612:+	Clostridiales
1931946	GL0049599_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6352_3:1:294:-	Clostridium asparagiforme
1932039	GL0019902_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6636_1:193:714:-	Clostridium leptum
1932110	GL0072510_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6884_1:2:505:+	Clostridium cellulolyticum

1932364	GL0059966_O2_[Lack_5'-end]_[mRNA]_locus=scaffold7480_2:3:305:+	Clostridium leptum
1932497	GL0050231_O2_[Lack_3'-end]_[mRNA]_locus=scaffold7812_1:763:1104:+	Clostridium asparagiforme
1932542	GL0069199_O2_[Lack_both_end]_[mRNA]_locus=scaffold7982_1:3:503:-	Clostridiales
1932628	GL0013494_O2_[Lack_3'-end]_[mRNA]_locus=scaffold8243_1:2080:4332:+	Bacteria
1932711	GL0064970_O2_[Lack_3'-end]_[mRNA]_locus=scaffold8449_1:343:855:+	Clostridium leptum
1932810	GL0013666_O2_[Complete]_[mRNA]_locus=scaffold8776_2:2057:3184:-	Coprococcus comes
1932960	GL0001568_O2_[Lack_both_end]_[mRNA]_locus=scaffold9108_1:1:513:+	Clostridium leptum
1932996	GL0069938_O2_[Lack_both_end]_[mRNA]_locus=scaffold9134_1:3:509:+	Clostridium hylemonae
1933037	GL0031871_O2_[Lack_both_end]_[mRNA]_locus=scaffold9301_1:3:980:+	Clostridium leptum
1933110	GL0067454_O2_[Lack_5'-end]_[mRNA]_locus=scaffold9598_1:3:491:+	Clostridium leptum
1933139	GL0074740_O2_[Lack_both_end]_[mRNA]_locus=scaffold9660_1:1:603:+	Eubacterium siraeum
1933184	GL0043258_O2_[Complete]_[mRNA]_locus=scaffold9817_1:139:411:+	Bacteroides capillosus
1933185	GL0043259_O2_[Lack_3'-end]_[mRNA]_locus=scaffold9817_1:404:817:+	Clostridium leptum
1933218	GL0073209_O2_[Complete]_[mRNA]_locus=scaffold9880_2:292:711:+	Clostridiales

1933254	GL0069214_O2_[Complete]_[mRNA]_locus=scaffold9963_2:2:778:+	Eubacterium siraeum
1933403	GL0043771_O2_[Lack_3'-end]_[mRNA]_locus=scaffold10297_2:538:768:+	Bacteria
1933507	GL0003294_O2_[Complete]_[mRNA]_locus=scaffold10614_1:40:867:-	Clostridium acetobutylicum
1933688	GL0027946_O2_[Lack_both_end]_[mRNA]_locus=scaffold11145_1:3:614:+	Clostridium leptum
1933729	GL0074578_O2_[Lack_3'-end]_[mRNA]_locus=scaffold11287_1:410:847:+	Dorea longicatena
1933754	GL0050605_O2_[Complete]_[mRNA]_locus=scaffold11419_1:163:720:+	Blautia hydrogenotrophica
1933845	GL0073983_O2_[Complete]_[mRNA]_locus=scaffold11582_1:471:998:+	Clostridium leptum
1933846	GL0073984_O2_[Lack_3'-end]_[mRNA]_locus=scaffold11582_1:1198:1494:+	Clostridium leptum
1933876	GL0073494_O2_[Lack_both_end]_[mRNA]_locus=scaffold11744_1:3:779:-	Clostridium
1933880	GL0004362_O2_[Lack_3'-end]_[mRNA]_locus=scaffold11763_1:3:467:-	Anaerotruncus colihominis
1934154	GL0021650_O2_[Lack_3'-end]_[mRNA]_locus=scaffold12440_1:1:141:-	Clostridium
1934253	GL0072306_O2_[Complete]_[mRNA]_locus=scaffold12708_10:234:1685:+	Clostridiales
1934277	GL0006022_O2_[Complete]_[mRNA]_locus=scaffold12752_1:164:340:-	Clostridium leptum
1934291	GL0063744_O2_[Lack_both_end]_[mRNA]_locus=scaffold12828_2:2:1246:+	Bacteroides capillosus

1934551	GL0009641_O2_[Lack_5'-end]_[mRNA]_locus=scaffold13430_1:3:248:+	Symbiobacterium thermophilum
1934561	GL0045786_O2_[Lack_5'-end]_[mRNA]_locus=scaffold13439_1:343:642:-	Eubacterium siraeum
1934609	GL0071343_O2_[Lack_both_end]_[mRNA]_locus=scaffold13509_1:3:977:-	Eubacterium siraeum
1934660	GL0040130_O2_[Lack_both_end]_[mRNA]_locus=scaffold13683_1:3:632:-	Clostridium
1934707	GL0034345_O2_[Lack_both_end]_[mRNA]_locus=scaffold13844_6:2:892:+	Dorea
1934773	GL0058520_O2_[Complete]_[mRNA]_locus=scaffold13887_1:929:1576:+	Enterococcus
1934933	GL0016203_O2_[Lack_5'-end]_[mRNA]_locus=scaffold14377_1:3:656:+	Clostridium leptum
1934978	GL0061268_O2_[Lack_both_end]_[mRNA]_locus=scaffold14486_1:3:521:-	Clostridium
1935004	GL0006083_O2_[Lack_both_end]_[mRNA]_locus=scaffold14603_1:1:618:+	Anaerotruncus colihominis
1935132	GL0049299_O2_[Lack_3'-end]_[mRNA]_locus=scaffold14907_1:927:1640:+	Clostridium leptum
1935138	GL0014861_O2_[Lack_3'-end]_[mRNA]_locus=scaffold14932_2:238:1017:+	Clostridium cellulolyticum
1935143	GL0023440_O2_[Lack_5'-end]_[mRNA]_locus=scaffold14945_2:693:1055:-	Thermoanaerobacter tengcongensis
1935159	GL0016927_O2_[Lack_3'-end]_[mRNA]_locus=scaffold14996_1:3:743:-	Clostridium leptum

1935282	GL0013680_O2_[Lack_3'-end]_[mRNA]_locus=scaffold15392_1:3:464:-	Clostridiales
1935284	GL0012517_O2_[Lack_5'-end]_[mRNA]_locus=scaffold15401_5:243:2549:-	Firmicutes
1935405	GL0054613_O2_[Lack_3'-end]_[mRNA]_locus=scaffold15774_3:830:1219:+	Eubacterium siraeum
1935406	GL0061280_O2_[Lack_both_end]_[mRNA]_locus=scaffold15782_1:3:527:-	-
1935409	GL0074124_O2_[Lack_both_end]_[mRNA]_locus=scaffold15798_3:1:582:+	-
1935447	GL0075237_O2_[Lack_3'-end]_[mRNA]_locus=scaffold15948_1:4:699:+	Clostridium leptum
1935492	GL0006776_O2_[Lack_5'-end]_[mRNA]_locus=scaffold16089_2:1:243:+	Clostridium leptum
1935493	GL0006777_O2_[Complete]_[mRNA]_locus=scaffold16089_2:283:807:+	Clostridium leptum
1935546	GL0023710_O2_[Complete]_[mRNA]_locus=scaffold16301_1:187:567:+	Clostridium leptum
1935625	GL0037884_O2_[Lack_3'-end]_[mRNA]_locus=scaffold16486_1:153:809:+	Clostridium perfringens
1935708	GL0003495_O2_[Lack_5'-end]_[mRNA]_locus=scaffold16753_10:531:1877:-	Firmicutes
1935826	GL0001195_O2_[Lack_5'-end]_[mRNA]_locus=scaffold17151_1:3:803:+	-
1935987	GL0051330_O2_[Lack_5'-end]_[mRNA]_locus=scaffold17536_1:2:469:+	Bacteroides capillosus
1935994	GL0022816_O2_[Lack_5'-end]_[mRNA]_locus=scaffold17575_1:1:405:+	Ruminococcus lactaris

1936005	GL0005313_O2_[Lack_both_end]_[mRNA]_locus=scaffold17595_2:1:693:-	Clostridium leptum
1936064	GL0053528_O2_[Complete]_[mRNA]_locus=scaffold17780_1:112:1464:-	Firmicutes
1936110	GL0018427_O2_[Complete]_[mRNA]_locus=scaffold17960_2:716:1378:-	-
1936111	GL0018428_O2_[Complete]_[mRNA]_locus=scaffold17960_2:1460:2059:-	Ruminococcus gnavus
1936195	GL0063060_O2_[Lack_both_end]_[mRNA]_locus=scaffold18172_1:1:537:+	Clostridium leptum
1936314	GL0004077_O2_[Complete]_[mRNA]_locus=scaffold18709_1:767:1078:-	Ruminococcus obeum
1936327	GL0028880_O2_[Complete]_[mRNA]_locus=scaffold18713_14:319:1326:+	Holdemania filiformis
1936392	GL0008174_O2_[Lack_both_end]_[mRNA]_locus=scaffold18845_1:1:543:+	Clostridium leptum
1936589	GL0042353_O2_[Lack_3'-end]_[mRNA]_locus=scaffold19504_1:2:685:-	Clostridium leptum
1936633	GL0057089_O2_[Complete]_[mRNA]_locus=scaffold19647_1:44:580:+	Firmicutes
1936639	GL0028290_O2_[Lack_5'-end]_[mRNA]_locus=scaffold19669_1:2:370:+	Clostridiales
1936640	GL0028291_O2_[Complete]_[mRNA]_locus=scaffold19669_1:451:753:+	Clostridiales
1936762	GL0071450_O2_[Lack_both_end]_[mRNA]_locus=scaffold19982_1:2:562:-	Clostridium leptum
1936837	GL0071511_O2_[Lack_3'-end]_[mRNA]_locus=scaffold20229_1:1:252:-	Clostridium leptum

1936884	GL0071375_O2_[Lack_3'-end]_[mRNA]_locus=scaffold20357_2:3:434:-	Clostridium ramosum
1936898	GL0055361_O2_[Complete]_[mRNA]_locus=scaffold20379_2:494:958:+	Clostridium thermocellum
1936901	GL0037459_O2_[Complete]_[mRNA]_locus=scaffold20386_1:68:1240:+	Eubacterium siraeum
1936903	GL0059069_O2_[Complete]_[mRNA]_locus=scaffold20387_2:372:899:-	Clostridium leptum
1936907	GL0028889_O2_[Lack_5'-end]_[mRNA]_locus=scaffold20400_1:1:435:+	Clostridiales
1936971	GL0025233_O2_[Lack_both_end]_[mRNA]_locus=scaffold20551_2:3:680:-	Eubacterium siraeum
1937041	GL0072128_O2_[Lack_5'-end]_[mRNA]_locus=scaffold20787_2:254:1060:-	Anaerostipes caccae
1937100	GL0054246_O2_[Lack_3'-end]_[mRNA]_locus=scaffold20997_1:372:683:+	Roseburia inulinivorans
1937282	GL0016865_O2_[Lack_5'-end]_[mRNA]_locus=scaffold21612_4:1392:2054:-	-
1937299	GL0023916_O2_[Complete]_[mRNA]_locus=scaffold21684_4:1256:3901:+	Bacteria
1937325	GL0047810_O2_[Lack_3'-end]_[mRNA]_locus=scaffold21777_4:279:665:+	Clostridium cellulolyticum
1937380	GL0071895_O2_[Complete]_[mRNA]_locus=scaffold21944_1:1011:1400:+	Firmicutes
1937393	GL0054691_O2_[Lack_both_end]_[mRNA]_locus=scaffold21969_2:1:669:-	Trichomonas vaginalis
1937518	GL0054716_O2_[Lack_5'-end]_[mRNA]_locus=scaffold22366_1:2:355:+	Bacteria

1937520	GL0068999_O2_[Complete]_[mRNA]_locus=scaffold22371_1:359:619:-	Clostridium leptum
1937558	GL0065990_O2_[Lack_5'-end]_[mRNA]_locus=scaffold22550_1:1:1818:+	Enterocytozoon bieneusi
1937559	GL0065991_O2_[Complete]_[mRNA]_locus=scaffold22550_1:2048:3145:+	Ruminococcus gnavus
1937607	GL0009005_O2_[Lack_3'-end]_[mRNA]_locus=scaffold22693_5:1:576:-	Ruminococcus lactaris
1937626	GL0041507_O2_[Lack_5'-end]_[mRNA]_locus=scaffold22773_1:3:245:+	Clostridium methylpentosum
1937951	GL0014207_O2_[Complete]_[mRNA]_locus=scaffold23784_1:7:771:-	Clostridiales
1937952	GL0014208_O2_[Complete]_[mRNA]_locus=scaffold23784_1:1065:1841:-	-
1937953	GL0014209_O2_[Lack_5'-end]_[mRNA]_locus=scaffold23784_1:2220:2669:-	-
1938038	GL0029523_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24029_1:339:872:+	Firmicutes
1938129	GL0017691_O2_[Lack_3'-end]_[mRNA]_locus=scaffold24323_1:2:586:-	Clostridium leptum
1938249	GL0045616_O2_[Complete]_[mRNA]_locus=scaffold24705_1:731:1189:+	-
1938364	GL0042672_O2_[Lack_3'-end]_[mRNA]_locus=scaffold25116_1:3:398:-	Acholeplasma laidlawii
1938386	GL0036021_O2_[Lack_both_end]_[mRNA]_locus=scaffold25163_1:1:657:+	Clostridium
1938519	GL0075310_O2_[Complete]_[mRNA]_locus=scaffold25589_1:409:894:+	Clostridium

1938553	GL0064071_O2_[Complete]_[mRNA]_locus=scaffold25770_1:150:476:+	Epulopiscium
1938592	GL0029105_O2_[Lack_both_end]_[mRNA]_locus=scaffold25943_1:1:687:+	Clostridium leptum
1938855	GL0009995_O2_[Complete]_[mRNA]_locus=scaffold26718_1:109:408:-	Clostridium leptum
1938876	GL0069749_O2_[Lack_5'-end]_[mRNA]_locus=scaffold26756_1:205:609:-	Elusimicrobium minutum
1938972	GL0003109_O2_[Lack_5'-end]_[mRNA]_locus=scaffold27086_1:3:668:+	Coprococcus comes
1938973	GL0003110_O2_[Lack_3'-end]_[mRNA]_locus=scaffold27086_1:665:1393:+	Clostridium
1939032	GL0073160_O2_[Lack_5'-end]_[mRNA]_locus=scaffold27256_1:611:1642:-	Bacteria
1939035	GL0055637_O2_[Lack_both_end]_[mRNA]_locus=scaffold27269_1:3:581:-	Clostridium
1939066	GL0011323_O2_[Lack_3'-end]_[mRNA]_locus=scaffold27422_1:597:794:+	Bacteria
1939152	GL0007331_O2_[Lack_both_end]_[mRNA]_locus=scaffold27700_1:1:747:-	Dorea formicigenerans
1939228	GL0016777_O2_[Lack_3'-end]_[mRNA]_locus=scaffold27923_2:20:937:+	Clostridium leptum
1939239	GL0000505_O2_[Complete]_[mRNA]_locus=scaffold27975_1:239:628:-	Clostridium bolteae
1939274	GL0017456_O2_[Lack_5'-end]_[mRNA]_locus=scaffold28102_2:3:452:+	Faecalibacterium prausnitzii
1939438	GL0070619_O2_[Lack_both_end]_[mRNA]_locus=scaffold28635_1:3:731:+	Clostridium leptum

1939526	GL0046998_O2_[Lack_5'-end]_[mRNA]_locus=scaffold28878_5:846:1529:-	Ruminococcus obeum
1939551	GL0035940_O2_[Lack_5'-end]_[mRNA]_locus=scaffold28982_1:3:395:+	Bacteria
1939681	GL0040440_O2_[Lack_5'-end]_[mRNA]_locus=scaffold29445_3:3:476:+	-
1939697	GL0025257_O2_[Lack_3'-end]_[mRNA]_locus=scaffold29510_1:3:581:-	Anaerotruncus colihominis
1939746	GL0030821_O2_[Lack_3'-end]_[mRNA]_locus=scaffold29679_1:523:756:+	Clostridiales
1939830	GL0072134_O2_[Lack_3'-end]_[mRNA]_locus=scaffold29939_1:366:755:+	Clostridiales
1939844	GL0004407_O2_[Lack_both_end]_[mRNA]_locus=scaffold29947_2:2:1219:+	Clostridium leptum
1939889	GL0026109_O2_[Complete]_[mRNA]_locus=scaffold30071_2:494:760:-	-
1939986	GL0031750_O2_[Lack_3'-end]_[mRNA]_locus=scaffold30365_1:216:548:+	Clostridium leptum
1940063	GL0020667_O2_[Lack_both_end]_[mRNA]_locus=scaffold30543_1:1:981:+	Bacteroides capillosus
1940082	GL0052388_O2_[Lack_3'-end]_[mRNA]_locus=scaffold30606_1:259:1503:+	Clostridium phytofermentans
1940093	GL0006795_O2_[Complete]_[mRNA]_locus=scaffold30639_3:33:473:-	-
1940110	GL0011428_O2_[Lack_5'-end]_[mRNA]_locus=scaffold30671_1:376:603:-	Clostridium
1940157	GL0004332_O2_[Lack_both_end]_[mRNA]_locus=scaffold30843_2:1:573:+	Ruminococcus obeum

1940267	GL0009776_O2_[Lack_3'-end]_[mRNA]_locus=scaffold31265_1:1:456:-	Clostridium leptum
1940268	GL0009777_O2_[Complete]_[mRNA]_locus=scaffold31265_1:453:1379:-	Clostridium leptum
1940330	GL0029975_O2_[Lack_3'-end]_[mRNA]_locus=scaffold31493_1:3:362:-	Clostridium leptum
1940421	GL0069255_O2_[Lack_5'-end]_[mRNA]_locus=scaffold31866_4:163:1281:-	Ruminococcus gnavus
1940431	GL0033571_O2_[Lack_5'-end]_[mRNA]_locus=scaffold31903_2:2:583:+	Clostridiales
1940478	GL0006525_O2_[Complete]_[mRNA]_locus=scaffold32048_1:653:916:-	Clostridiales
1940535	GL0010037_O2_[Lack_both_end]_[mRNA]_locus=scaffold32280_3:2:550:+	Clostridium leptum
1940642	GL0059950_O2_[Complete]_[mRNA]_locus=scaffold32510_1:1529:2188:-	-
1940666	GL0039555_O2_[Lack_5'-end]_[mRNA]_locus=scaffold32551_3:290:724:-	-
1940749	GL0070320_O2_[Complete]_[mRNA]_locus=scaffold32756_1:154:501:-	Clostridium leptum
1940795	GL0022451_O2_[Lack_3'-end]_[mRNA]_locus=scaffold32841_2:277:597:+	Clostridium leptum
1940921	GL0042387_O2_[Lack_3'-end]_[mRNA]_locus=scaffold33362_3:1:711:-	Eubacterium siraeum
1940950	GL0070637_O2_[Lack_both_end]_[mRNA]_locus=scaffold33482_1:2:523:-	Clostridium thermocellum
1940953	GL0013452_O2_[Lack_3'-end]_[mRNA]_locus=scaffold33486_1:1:438:-	Clostridium leptum

1940964	GL0047721_O2_[Lack_both_end]_[mRNA]_locus=scaffold33501_1:2:655:-	Clostridium methylpentosum
1941025	GL0048810_O2_[Complete]_[mRNA]_locus=scaffold33714_1:394:972:-	Clostridium ramosum
1941044	GL0030665_O2_[Lack_3'-end]_[mRNA]_locus=scaffold33733_1:3:422:-	Clostridiales
1941046	GL0030667_O2_[Lack_5'-end]_[mRNA]_locus=scaffold33733_1:1192:2073:-	Roseburia inulinivorans
1941203	GL0050828_O2_[Lack_3'-end]_[mRNA]_locus=scaffold34233_1:480:902:+	Bacteria
1941354	GL0042008_O2_[Complete]_[mRNA]_locus=scaffold34835_1:145:498:+	Clostridium leptum
1941408	GL0024923_O2_[Lack_3'-end]_[mRNA]_locus=scaffold35010_1:3:317:-	-
1941409	GL0024924_O2_[Lack_3'-end]_[mRNA]_locus=scaffold35010_1:562:1377:+	Clostridium leptum
1941413	GL0037960_O2_[Lack_3'-end]_[mRNA]_locus=scaffold35015_1:3:572:-	Coprothermobacter proteolyticus
1941449	GL0028990_O2_[Lack_3'-end]_[mRNA]_locus=scaffold35122_1:10:537:+	Clostridium
1941462	GL0033141_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35169_2:3:338:+	Clostridium bolteae
1941481	GL0006269_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35212_1:1288:1593:-	Desulfitobacterium hafniense
1941484	GL0024845_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35240_1:3:347:+	-

1941500	GL0014265_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35307_2:819:1883:-	-
1941741	GL0036853_O2_[Complete]_[mRNA]_locus=scaffold36032_1:119:682:-	-
1941791	GL0006873_O2_[Complete]_[mRNA]_locus=scaffold36121_1:472:966:+	Clostridium leptum
1941801	GL0060385_O2_[Lack_3'-end]_[mRNA]_locus=scaffold36162_1:3:431:-	Coprococcus comes
1941835	GL0064778_O2_[Lack_3'-end]_[mRNA]_locus=scaffold36267_1:329:823:+	Clostridiales
1941890	GL0059682_O2_[Lack_3'-end]_[mRNA]_locus=scaffold36462_1:3:248:-	Clostridiales
1942093	GL0057357_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37091_1:339:1274:-	Holdemania filiformis
1942099	GL0046768_O2_[Complete]_[mRNA]_locus=scaffold37135_1:66:650:-	Clostridium leptum
1942141	GL0001130_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37279_1:315:539:-	Clostridiales
1942150	GL0046549_O2_[Lack_3'-end]_[mRNA]_locus=scaffold37302_1:24:650:+	Clostridium
1942174	GL0002089_O2_[Lack_3'-end]_[mRNA]_locus=scaffold37351_4:1:1425:+	Clostridium asparagiforme
1942180	GL0073796_O2_[Lack_both_end]_[mRNA]_locus=scaffold37386_1:2:553:+	Blautia hydrogenotrophica
1942201	GL0068361_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37442_1:3:602:+	Clostridium leptum
1942204	GL0073125_O2_[Lack_both_end]_[mRNA]_locus=scaffold37457_2:2:1105:-	-

1942205	GL0006689_O2_[Complete]_[mRNA]_locus=scaffold37461_1:2:475:+	-
1942239	GL0034668_O2_[Complete]_[mRNA]_locus=scaffold37542_1:264:1199:+	-
1942240	GL0063903_O2_[Complete]_[mRNA]_locus=scaffold37542_2:1130:1777:+	-
1942255	GL0031008_O2_[Complete]_[mRNA]_locus=scaffold37578_2:316:504:-	Clostridium
1942269	GL0042561_O2_[Complete]_[mRNA]_locus=scaffold37606_2:292:843:-	Clostridium leptum
1942270	GL0042562_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37606_2:873:1226:-	Clostridium leptum
1942309	GL0040065_O2_[Lack_5'-end]_[mRNA]_locus=scaffold37707_1:361:1605:-	Actinobacillus succinogenes
1942373	GL0035691_O2_[Lack_3'-end]_[mRNA]_locus=scaffold37926_2:310:891:+	Clostridium phytofermentans
1942414	GL0044917_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38069_2:2:541:-	Clostridium
1942480	GL0004940_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38208_1:3:500:-	Clostridium
1942514	GL0002150_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38310_1:95:532:+	Eubacterium biforme
1942546	GL0059522_O2_[Lack_5'-end]_[mRNA]_locus=scaffold38422_2:162:572:-	Bacillales
1942581	GL0028614_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38561_3:1:1005:-	-
1942587	GL0007935_O2_[Lack_5'-end]_[mRNA]_locus=scaffold38578_1:1:480:+	Faecalibacterium prausnitzii

1942640	GL0032007_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38737_2:169:900:+	Bacteroides capillosus
1942708	GL0005468_O2_[Lack_3'-end]_[mRNA]_locus=scaffold38899_4:3:593:-	-
1942768	GL0036254_O2_[Lack_3'-end]_[mRNA]_locus=scaffold39036_1:54:626:+	Clostridium leptum
1942783	GL0028586_O2_[Complete]_[mRNA]_locus=scaffold39086_2:6:296:+	Clostridiales
1942800	GL0029082_O2_[Lack_3'-end]_[mRNA]_locus=scaffold39143_1:3:401:-	-
1942859	GL0009545_O2_[Lack_3'-end]_[mRNA]_locus=scaffold39290_4:1:525:-	Clostridium methylpentosum
1942880	GL0025511_O2_[Lack_5'-end]_[mRNA]_locus=scaffold39353_1:3:854:+	Clostridium leptum
1942963	GL0065324_O2_[Lack_both_end]_[mRNA]_locus=scaffold39580_1:3:503:+	Clostridium cellulolyticum
1943013	GL0045897_O2_[Lack_5'-end]_[mRNA]_locus=scaffold39673_1:1:276:+	Clostridium leptum
1943028	GL0050141_O2_[Lack_both_end]_[mRNA]_locus=scaffold39713_1:2:595:-	Clostridium leptum
1943057	GL0043594_O2_[Lack_3'-end]_[mRNA]_locus=scaffold39758_2:99:863:+	Halothermothrix orenii
1943140	GL0058331_O2_[Lack_both_end]_[mRNA]_locus=scaffold40074_2:1:531:+	Eubacterium dolichum
1943203	GL0019263_O2_[Lack_3'-end]_[mRNA]_locus=scaffold40246_1:519:998:+	Clostridium beijerinckii
1943254	GL0056445_O2_[Lack_3'-end]_[mRNA]_locus=scaffold40364_2:2:481:-	-

1943275	GL0022767_O2_[Lack_both_end]_[mRNA]_locus=scaffold40460_1:3:824:-	Clostridium leptum
1943291	GL0045535_O2_[Lack_5'-end]_[mRNA]_locus=scaffold40505_1:1256:1630:-	Clostridium leptum
1943294	GL0035316_O2_[Lack_3'-end]_[mRNA]_locus=scaffold40509_1:143:826:+	-
1943300	GL0016436_O2_[Lack_3'-end]_[mRNA]_locus=scaffold40535_1:1:1575:+	Bacteroides capillosus
1943310	GL0063893_O2_[Lack_3'-end]_[mRNA]_locus=scaffold40561_1:2:418:-	Clostridium leptum
1943311	GL0041971_O2_[Lack_both_end]_[mRNA]_locus=scaffold40561_3:1:576:-	Clostridium phytofermentans
1943409	GL0051953_O2_[Complete]_[mRNA]_locus=scaffold40859_1:232:801:+	Desulfitobacterium hafniense
1943422	GL0061097_O2_[Lack_3'-end]_[mRNA]_locus=scaffold40879_1:120:824:+	-
1943426	GL0045384_O2_[Lack_both_end]_[mRNA]_locus=scaffold40891_2:3:539:+	Coprococcus comes
1943427	GL0047856_O2_[Lack_both_end]_[mRNA]_locus=scaffold40895_1:3:647:+	Clostridium thermocellum
1943440	GL0008409_O2_[Complete]_[mRNA]_locus=scaffold40920_1:234:731:+	Clostridium
1943540	GL0075461_O2_[Lack_5'-end]_[mRNA]_locus=scaffold41218_1:286:723:-	Streptococcus
1943557	GL0014685_O2_[Lack_both_end]_[mRNA]_locus=scaffold41261_1:2:520:+	Clostridium scindens
1943562	GL0009510_O2_[Lack_5'-end]_[mRNA]_locus=scaffold41276_1:241:780:-	Ruminococcus lactaris

1943720	GL0069769_O2_[Lack_both_end]_[mRNA]_locus=scaffold41689_1:1:651:+	Clostridium leptum
1943768	GL0055264_O2_[Lack_3'-end]_[mRNA]_locus=scaffold41813_1:3:173:-	Atopobium rimae
1943777	GL0023647_O2_[Lack_5'-end]_[mRNA]_locus=scaffold41849_1:3:422:+	Clostridium leptum
1943783	GL0058500_O2_[Complete]_[mRNA]_locus=scaffold41851_1:628:2157:+	-
1943812	GL0033567_O2_[Lack_5'-end]_[mRNA]_locus=scaffold41888_1:97:1092:-	-
1943876	GL0069020_O2_[Lack_5'-end]_[mRNA]_locus=scaffold42001_1:1:540:+	Bacteroides capillosus
1943901	GL0029100_O2_[Lack_both_end]_[mRNA]_locus=scaffold42059_1:2:607:+	Parabacteroides
1943906	GL0056484_O2_[Complete]_[mRNA]_locus=scaffold42064_1:217:684:+	Clostridium leptum
1943935	GL0060614_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42108_1:3:416:-	Clostridium
1943951	GL0048118_O2_[Lack_5'-end]_[mRNA]_locus=scaffold42144_1:217:600:-	Alkaliphilus oremlandii
1944029	GL0024594_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42309_1:2:625:-	Bacteroides capillosus
1944054	GL0008803_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42352_2:450:650:+	Clostridiales
1944110	GL0072286_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42480_1:1:534:-	Bacteroides capillosus
1944173	GL0062061_O2_[Lack_both_end]_[mRNA]_locus=scaffold42625_1:1:642:+	-

1944185	GL0040721_O2_[Lack_5'-end]_[mRNA]_locus=scaffold42656_2:1552:2157:-	Clostridium scindens
1944248	GL0019375_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42750_1:191:730:+	Eubacterium siraeum
1944276	GL0027884_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42803_1:1:768:-	Clostridium thermocellum
1944277	GL0073718_O2_[Lack_both_end]_[mRNA]_locus=scaffold42806_1:2:568:-	Clostridium
1944343	GL0041132_O2_[Lack_5'-end]_[mRNA]_locus=scaffold42930_3:2:607:+	Bacteroides capillosus
1944344	GL0041133_O2_[Lack_3'-end]_[mRNA]_locus=scaffold42930_3:623:904:+	Bacteroides capillosus
1944457	GL0070471_O2_[Lack_5'-end]_[mRNA]_locus=scaffold43163_2:3:629:+	Clostridium
1944466	GL0074180_O2_[Lack_3'-end]_[mRNA]_locus=scaffold43177_2:1:1053:-	Bacteroides capillosus
1944470	GL0006631_O2_[Lack_5'-end]_[mRNA]_locus=scaffold43209_1:206:571:-	Geobacillus
1944471	GL0066428_O2_[Lack_5'-end]_[mRNA]_locus=scaffold43212_1:2:601:+	Clostridium leptum
1944497	GL0009126_O2_[Lack_5'-end]_[mRNA]_locus=scaffold43275_1:2:481:+	Roseburia inulinivorans
1944498	GL0009127_O2_[Lack_3'-end]_[mRNA]_locus=scaffold43275_1:493:939:+	Roseburia inulinivorans
1944499	GL0017652_O2_[Lack_both_end]_[mRNA]_locus=scaffold43275_2:1:582:+	Bacteria
1944523	GL0073199_O2_[Lack_3'-end]_[mRNA]_locus=scaffold43331_2:29:1414:+	Clostridium methylpentosum

1944591	GL0007325_O2_[Lack_3'-end]_[mRNA]_locus=scaffold43510_2:447:737:+	Clostridium cellulolyticum
1944621	GL0051165_O2_[Lack_3'-end]_[mRNA]_locus=scaffold43614_1:406:900:+	Clostridium kluyveri
1944734	GL0051562_O2_[Lack_both_end]_[mRNA]_locus=scaffold43832_1:2:1102:-	Clostridium scindens
1944801	GL0006358_O2_[Lack_5'-end]_[mRNA]_locus=scaffold43982_1:3:386:+	Clostridium methylpentosum
1944875	GL0034024_O2_[Complete]_[mRNA]_locus=scaffold44149_1:371:979:-	Bacteria
1944886	GL0010648_O2_[Lack_3'-end]_[mRNA]_locus=scaffold44170_1:3:569:-	Clostridium difficile
1944915	GL0052650_O2_[Complete]_[mRNA]_locus=scaffold44223_1:283:780:-	Bacteria
1944954	GL0023244_O2_[Complete]_[mRNA]_locus=scaffold44302_1:838:1161:-	Clostridium hylemonae
1945031	GL0071229_O2_[Complete]_[mRNA]_locus=scaffold44510_1:699:1094:+	Eubacterium hallii
1945032	GL0071230_O2_[Lack_5'-end]_[mRNA]_locus=scaffold44510_1:1246:1650:-	Clostridium leptum
1945055	GL0037347_O2_[Complete]_[mRNA]_locus=scaffold44537_2:397:1020:-	Clostridium
1945089	GL0025052_O2_[Lack_5'-end]_[mRNA]_locus=scaffold44625_1:223:690:-	-
1945184	GL0022941_O2_[Complete]_[mRNA]_locus=scaffold44810_1:27:614:-	Clostridium scindens
1945198	GL0034837_O2_[Complete]_[mRNA]_locus=scaffold44844_1:3:851:+	Clostridium leptum

1945216	GL0064617_O2_[Lack_5'-end]_[mRNA]_locus=scaffold44893_1:120:995:-	-
1945245	GL0058799_O2_[Complete]_[mRNA]_locus=scaffold44990_1:5:622:+	Clostridiales
1945274	GL0023658_O2_[Lack_both_end]_[mRNA]_locus=scaffold45030_1:3:671:-	-
1945303	GL0029443_O2_[Lack_both_end]_[mRNA]_locus=scaffold45081_1:2:622:-	-
1945319	GL0056428_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45114_1:3:440:-	Clostridiales
1945356	GL0026377_O2_[Lack_both_end]_[mRNA]_locus=scaffold45175_1:3:809:-	Clostridium hylemonae
1945432	GL0025476_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45343_1:3:230:-	-
1945443	GL0034439_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45381_1:1:516:-	Clostridium leptum
1945456	GL0001604_O2_[Complete]_[mRNA]_locus=scaffold45388_2:180:986:-	Firmicutes
1945470	GL0011785_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45418_1:3:611:-	Anaerofustis stercorihominis
1945471	GL0035291_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45418_3:119:1228:+	Bacillaceae
1945496	GL0049536_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45495_1:878:1246:+	Clostridium leptum
1945516	GL0016261_O2_[Complete]_[mRNA]_locus=scaffold45548_1:571:987:+	Clostridium

1945517	GL0032226_O2_[Lack_both_end]_[mRNA]_locus=scaffold45548_3:3:569:+	Eubacterium siraeum
1945518	GL0059435_O2_[Complete]_[mRNA]_locus=scaffold45548_4:230:1561:+	-
1945704	GL0027566_O2_[Complete]_[mRNA]_locus=scaffold45925_1:783:1058:-	Clostridiales
1945717	GL0048155_O2_[Complete]_[mRNA]_locus=scaffold45964_2:935:1606:-	Desulfitobacterium hafniense
1945718	GL0048156_O2_[Complete]_[mRNA]_locus=scaffold45964_2:1781:2155:+	Dorea formicigenerans
1945719	GL0048157_O2_[Complete]_[mRNA]_locus=scaffold45964_2:2207:3664:+	-
1945720	GL0048158_O2_[Lack_3'-end]_[mRNA]_locus=scaffold45964_2:3709:4926:+	Clostridium asparagiforme
1945728	GL0069569_O2_[Lack_5'-end]_[mRNA]_locus=scaffold45983_2:31:696:-	Clostridiales
1945774	GL0005206_O2_[Lack_5'-end]_[mRNA]_locus=scaffold46085_2:3:878:+	Eubacterium ventriosum
1945776	GL0075232_O2_[Lack_5'-end]_[mRNA]_locus=scaffold46086_1:351:842:-	Clostridium leptum
1945811	GL0045600_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46173_1:3:596:-	-
1945821	GL0016457_O2_[Complete]_[mRNA]_locus=scaffold46191_1:286:771:+	Clostridium leptum
1945848	GL0071083_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46247_2:934:1527:+	Bacteroides capillosus
1945993	GL0030716_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46504_1:1:693:-	-

1945999	GL0029185_O2_[Lack_5'-end]_[mRNA]_locus=scaffold46511_1:247:864:-	Clostridium leptum
1946121	GL0055652_O2_[Lack_both_end]_[mRNA]_locus=scaffold46704_1:1:510:+	Ruminococcus gnavus
1946161	GL0021631_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46781_1:3:467:-	Bacteroides capillosus
1946181	GL0028426_O2_[Lack_5'-end]_[mRNA]_locus=scaffold46797_1:831:1085:-	Clostridium leptum
1946240	GL0047160_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46919_1:406:1182:+	Anoxybacillus flavithermus
1946252	GL0008066_O2_[Lack_both_end]_[mRNA]_locus=scaffold46938_2:3:524:+	Bacteroidales
1946334	GL0068028_O2_[Lack_both_end]_[mRNA]_locus=scaffold47071_1:2:592:-	Clostridium
1946462	GL0009709_O2_[Lack_3'-end]_[mRNA]_locus=scaffold47209_2:55:594:+	Anaerotruncus colihominis
1946464	GL0046306_O2_[Lack_both_end]_[mRNA]_locus=scaffold47212_2:3:671:-	Clostridium phytofermentans
1946580	GL0001986_O2_[Lack_3'-end]_[mRNA]_locus=scaffold47343_1:3:761:-	Clostridium leptum
1946588	GL0030340_O2_[Lack_3'-end]_[mRNA]_locus=scaffold47354_2:3:749:-	Bacteroides capillosus
1946613	GL0055639_O2_[Complete]_[mRNA]_locus=scaffold47378_2:179:532:+	Clostridium methylpentosum
1946615	GL0003607_O2_[Lack_both_end]_[mRNA]_locus=scaffold47379_1:2:619:-	Bacteroides capillosus
1946894	GL0000133_O2_[Complete]_[mRNA]_locus=scaffold47673_1:520:1200:-	Bacteria

1946895	GL0000134_O2_[Lack_5'-end]_[mRNA]_locus=scaffold47673_1:1197:1457:-	-
1946938	GL0042742_O2_[Lack_both_end]_[mRNA]_locus=C4401206_1:3:503:-	Clostridium leptum
1946969	GL0072681_O2_[Lack_3'-end]_[mRNA]_locus=C4402086_1:3:497:-	Clostridium leptum
1946982	GL0063426_O2_[Lack_both_end]_[mRNA]_locus=C4402244_1:2:505:+	-
1947111	GL0025745_O2_[Lack_both_end]_[mRNA]_locus=C4405474_1:3:518:-	Clostridium nexile
1947346	GL0072944_O2_[Lack_both_end]_[mRNA]_locus=C4411428_1:2:547:+	Faecalibacterium prausnitzii
1947359	GL0020212_O2_[Complete]_[mRNA]_locus=C4411656_1:340:537:-	Bacteria
1947372	GL0010609_O2_[Lack_both_end]_[mRNA]_locus=C4412016_1:1:549:+	Clostridium leptum
1947385	GL0034296_O2_[Lack_3'-end]_[mRNA]_locus=C4412362_1:1:141:-	-
1947406	GL0058217_O2_[Lack_both_end]_[mRNA]_locus=C4412700_1:3:554:-	Clostridiales
1947481	GL0045966_O2_[Lack_both_end]_[mRNA]_locus=C4414590_1:2:562:-	Anaerotruncus colihominis
1947503	GL0051396_O2_[Lack_both_end]_[mRNA]_locus=C4415278_1:2:565:-	Victivallis vadensis
1947552	GL0048341_O2_[Lack_3'-end]_[mRNA]_locus=C4416408_1:357:572:+	Bacteroides capillosus
1947564	GL0073693_O2_[Complete]_[mRNA]_locus=C4416692_1:2:340:+	-

1947599	GL0061444_O2_[Lack_5'-end]_[mRNA]_locus=C4417828_1:26:580:-	-
1947657	GL0013006_O2_[Lack_both_end]_[mRNA]_locus=C4419344_1:2:589:+	Clostridium leptum
1947665	GL0067010_O2_[Lack_3'-end]_[mRNA]_locus=C4419626_1:2:520:-	-
1947667	GL0044409_O2_[Lack_3'-end]_[mRNA]_locus=C4419696_1:1:213:-	Anaerotruncus colihominis
1947734	GL0040261_O2_[Lack_3'-end]_[mRNA]_locus=C4421658_1:3:527:-	Clostridium leptum
1947740	GL0019073_O2_[Lack_both_end]_[mRNA]_locus=C4421882_1:1:603:+	Clostridium leptum
1947837	GL0017927_O2_[Lack_5'-end]_[mRNA]_locus=C4424292_1:114:620:-	Clostridium acetobutylicum
1947847	GL0010423_O2_[Lack_both_end]_[mRNA]_locus=C4424596_1:2:622:-	-
1947884	GL0044836_O2_[Lack_5'-end]_[mRNA]_locus=C4425968_1:1:234:+	Clostridium leptum
1947916	GL0033809_O2_[Lack_5'-end]_[mRNA]_locus=C4426864_1:3:593:+	Clostridium phytofermentans
1947934	GL0015691_O2_[Lack_5'-end]_[mRNA]_locus=C4427506_1:1:528:+	Bacteria
1947953	GL0021780_O2_[Lack_both_end]_[mRNA]_locus=C4428058_1:3:647:+	Anaerotruncus colihominis
1947982	GL0058077_O2_[Lack_3'-end]_[mRNA]_locus=C4429060_1:3:644:-	Clostridium asparagiforme
1948005	GL0022226_O2_[Complete]_[mRNA]_locus=C4429394_1:244:615:-	Bacteroides capillosus

1948037	GL0039869_O2_[Lack_both_end]_[mRNA]_locus=C4430210_1:1:663:+	Heliobacterium modesticaldum
1948155	GL0012236_O2_[Lack_3'-end]_[mRNA]_locus=C4433794_1:1:495:-	Thermotoga
1948168	GL0044448_O2_[Lack_both_end]_[mRNA]_locus=C4434156_1:3:695:+	-
1948180	GL0029838_O2_[Lack_5'-end]_[mRNA]_locus=C4434600_1:174:698:-	Clostridium scindens
1948192	GL0066807_O2_[Lack_5'-end]_[mRNA]_locus=C4434888_1:3:218:+	Bacteroides capillosus
1948201	GL0010154_O2_[Lack_both_end]_[mRNA]_locus=C4435094_1:3:704:-	Bacteroides capillosus
1948236	GL0062524_O2_[Lack_3'-end]_[mRNA]_locus=C4436264_1:306:713:+	Firmicutes
1948239	GL0062773_O2_[Complete]_[mRNA]_locus=C4436298_1:99:458:-	Bacteroides capillosus
1948284	GL0018925_O2_[Lack_3'-end]_[mRNA]_locus=C4437372_1:374:724:+	Clostridium bolteae
1948382	GL0015321_O2_[Lack_3'-end]_[mRNA]_locus=C4440076_1:2:517:-	cellular organisms
1948384	GL0048200_O2_[Lack_5'-end]_[mRNA]_locus=C4440122_1:459:752:-	Eubacterium dolichum
1948403	GL0074535_O2_[Lack_5'-end]_[mRNA]_locus=C4440566_1:3:635:+	Clostridium hylemonae
1948405	GL0066829_O2_[Lack_both_end]_[mRNA]_locus=C4440614_1:3:758:-	Clostridium cellulolyticum
1948424	GL0053796_O2_[Complete]_[mRNA]_locus=C4441046_1:177:383:+	-

1948481	GL0020728_O2_[Lack_both_end]_[mRNA]_locus=C4442716_1:2:781:-	Bacteroides fragilis
1948531	GL0074450_O2_[Lack_5'-end]_[mRNA]_locus=C4444180_1:237:800:-	Chthoniobacter flavus
1948581	GL0016244_O2_[Complete]_[mRNA]_locus=C4445606_1:218:628:-	Eubacterium hallii
1948597	GL0014453_O2_[Lack_3'-end]_[mRNA]_locus=C4446226_1:1:711:-	Clostridium scindens
1948609	GL0007158_O2_[Lack_both_end]_[mRNA]_locus=C4446716_1:3:836:-	-
1948670	GL0024521_O2_[Lack_3'-end]_[mRNA]_locus=C4448736_1:19:864:+	Clostridium leptum
1948691	GL0028428_O2_[Lack_3'-end]_[mRNA]_locus=C4450016_1:478:885:+	Clostridium leptum
1948700	GL0065375_O2_[Lack_3'-end]_[mRNA]_locus=C4450230_1:3:368:-	Bacteria
1948724	GL0001362_O2_[Lack_3'-end]_[mRNA]_locus=C4451070_1:3:881:-	Clostridium leptum
1948812	GL0043426_O2_[Lack_both_end]_[mRNA]_locus=C4454002_1:2:958:+	Coprococcus comes
1948820	GL0053691_O2_[Complete]_[mRNA]_locus=C4454252_1:443:703:+	-
1948836	GL0050110_O2_[Lack_3'-end]_[mRNA]_locus=C4454728_1:3:902:-	Clostridium leptum
1948839	GL0051759_O2_[Lack_3'-end]_[mRNA]_locus=C4455166_1:2:589:-	Clostridium leptum
1948877	GL0033691_O2_[Lack_5'-end]_[mRNA]_locus=C4456740_1:358:1020:-	Bacteroides capillosus

1948962	GL0023108_O2_[Complete]_[mRNA]_locus=C4460342_1:502:681:-	Clostridium difficile
1948978	GL0061863_O2_[Lack_3'-end]_[mRNA]_locus=C4460826_1:521:1132:+	Coprococcus comes
1949001	GL0001939_O2_[Complete]_[mRNA]_locus=C4461436_1:21:272:-	Eubacterium siraeum
1949049	GL0013379_O2_[Complete]_[mRNA]_locus=C4463312_1:512:1216:-	Clostridium leptum
1949074	GL0056851_O2_[Lack_both_end]_[mRNA]_locus=C4464308_1:3:1259:-	Clostridium cellulolyticum
1949080	GL0073850_O2_[Complete]_[mRNA]_locus=C4464460_1:194:727:+	Clostridium leptum
1949089	GL0050335_O2_[Lack_3'-end]_[mRNA]_locus=C4464830_1:941:1279:+	-
1949090	GL0074835_O2_[Lack_3'-end]_[mRNA]_locus=C4464954_1:1:540:-	Holdemania filiformis
1949110	GL0070447_O2_[Lack_3'-end]_[mRNA]_locus=C4466246_1:2:769:-	-
1949116	GL0065254_O2_[Lack_both_end]_[mRNA]_locus=C4466380_1:2:1351:-	-
1949119	GL0019003_O2_[Lack_5'-end]_[mRNA]_locus=C4466592_1:2:346:+	Clostridium hylemonae
1949204	GL0023026_O2_[Lack_5'-end]_[mRNA]_locus=C4471820_1:1272:1766:-	Clostridium leptum
1949216	GL0035147_O2_[Lack_5'-end]_[mRNA]_locus=C4472906_1:1:657:+	Anaerostipes caccae
1949217	GL0035148_O2_[Complete]_[mRNA]_locus=C4472906_1:652:876:-	-

1949224	GL0027395_O2_[Lack_3'-end]_[mRNA]_locus=C4473190_1:813:1952:+	-
1949225	GL0033050_O2_[Lack_3'-end]_[mRNA]_locus=C4473342_1:2:706:-	Victivallis vadensis
1954685	GL0002718_O2_[Complete]_[mRNA]_locus=scaffold7900_1:315:1211:-	Clostridium asparagiforme
1961315	GL0084731_O2_[Lack_5'-end]_[mRNA]_locus=scaffold30000_2:427:543:-	-
1962728	GL0047200_O2_[Lack_5'-end]_[mRNA]_locus=scaffold36739_1:27:2369:-	Ruminococcus torques
1978367	GL0081257_O2_[Complete]_[mRNA]_locus=scaffold24691_1:138:782:+	Oenococcus oeni
2012176	GL0055685_O2_[Complete]_[mRNA]_locus=scaffold149_7:7343:8512:+	Rhodoferax ferrireducens
2015196	GL0076064_O2_[Lack_3'-end]_[mRNA]_locus=scaffold693_14:1:1770:-	Clostridiales
2015225	GL0000125_O2_[Complete]_[mRNA]_locus=scaffold693_35:713:1627:+	Desulfitobacterium hafniense
2020446	GL0065888_O2_[Complete]_[mRNA]_locus=scaffold1974_6:166:1290:-	unclassified phages
2022495	GL0005052_O2_[Lack_3'-end]_[mRNA]_locus=scaffold2480_8:3761:4852:+	Roseburia inulinivorans
2022571	GL0009767_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2480_30:1:1731:+	Bacteria
2022726	GL0010212_O2_[Complete]_[mRNA]_locus=scaffold2535_10:71:1453:-	-
2023138	GL0046588_O2_[Lack_3'-end]_[mRNA]_locus=scaffold2660_21:1:1425:-	-

2030582	GL0027628_O2_[Lack_both_end]_[mRNA]_locus=scaffold5585_20:3:965:-	Clostridium
2033260	GL0006561_O2_[Lack_5'-end]_[mRNA]_locus=scaffold6720_21:1634:2650:-	Lactobacillus delbrueckii
2036849	GL0024187_O2_[Lack_5'-end]_[mRNA]_locus=scaffold9121_25:2358:2855:-	Clostridiales
2038535	GL0065548_O2_[Complete]_[mRNA]_locus=scaffold10418_10:4047:4442:+	-
2039451	GL0072177_O2_[Lack_both_end]_[mRNA]_locus=scaffold11155_3:1:1467:-	Holdemania filiformis
2041447	GL0084997_O2_[Lack_5'-end]_[mRNA]_locus=scaffold12611_5:135:1397:-	Ruminococcus obeum
2060490	GL0086591_O2_[Lack_5'-end]_[mRNA]_locus=scaffold1654_2:1020:1481:-	Clostridium asparagiforme
2060573	GL0003557_O2_[Lack_3'-end]_[mRNA]_locus=scaffold1866_1:3:275:-	Roseburia inulinivorans
2060988	GL0011455_O2_[Lack_both_end]_[mRNA]_locus=scaffold2872_1:1:543:-	Sulfolobus solfataricus
2062995	GL0096554_O2_[Complete]_[mRNA]_locus=scaffold8837_1:1822:2256:-	Bacteroides capillosus
2063154	GL0082811_O2_[Lack_both_end]_[mRNA]_locus=scaffold9422_1:2:550:+	Bacteroides capillosus
2063249	GL0071955_O2_[Lack_3'-end]_[mRNA]_locus=scaffold9770_1:142:843:+	Ruminococcaceae
2063250	GL0120925_O2_[Lack_5'-end]_[mRNA]_locus=scaffold9770_2:2:1084:+	-
2063401	GL0012099_O2_[Complete]_[mRNA]_locus=scaffold10815_2:1467:1724:+	-

2065911	GL0119084_O2_[Lack_3'-end]_[mRNA]_locus=scaffold21600_3:1:738:-	Firmicutes
2066125	GL0118719_O2_[Lack_both_end]_[mRNA]_locus=scaffold22799_3:2:505:-	Bacteroides capillosus
2070503	GL0017729_O2_[Lack_3'-end]_[mRNA]_locus=scaffold55071_1:101:526:+	Bacteroides capillosus
2070791	GL0015405_O2_[Lack_5'-end]_[mRNA]_locus=scaffold58021_4:88:753:-	Clostridiales
2071244	GL0017090_O2_[Lack_3'-end]_[mRNA]_locus=scaffold62728_2:2:514:-	Desulfitobacterium hafniense
2071245	GL0017091_O2_[Lack_5'-end]_[mRNA]_locus=scaffold62728_2:511:975:-	Anaerotruncus colihominis
2072434	GL0030115_O2_[Lack_3'-end]_[mRNA]_locus=scaffold72858_1:3:359:-	Clostridium methylpentosum
2074740	GL0105254_O2_[Lack_3'-end]_[mRNA]_locus=scaffold93362_2:371:958:+	Bacteria
2078819	GL0024123_O2_[Complete]_[mRNA]_locus=scaffold566_1:499:1815:+	Bacteroides capillosus
2079253	GL0024400_O2_[Lack_both_end]_[mRNA]_locus=scaffold1257_1:3:1727:-	Firmicutes
2079856	GL0044951_O2_[Complete]_[mRNA]_locus=scaffold1948_4:1340:3328:+	Clostridium phytofermentans
2079954	GL0054037_O2_[Lack_5'-end]_[mRNA]_locus=scaffold2141_1:541:903:-	-
2094654	GL0071731_O2_[Lack_3'-end]_[mRNA]_locus=scaffold59666_2:254:877:+	Clostridium leptum
2095807	GL0001504_O2_[Lack_5'-end]_[mRNA]_locus=scaffold66754_1:391:621:-	-

2098480	GL0101630_O2_[Complete]_[mRNA]_locus=scaffold80748_1:53:1669:-	Clostridium bolteae
2098613	GL0065463_O2_[Lack_3'-end]_[mRNA]_locus=scaffold81298_1:299:1705:+	Clostridium bolteae
2098788	GL0091836_O2_[Complete]_[mRNA]_locus=scaffold81787_2:1565:2422:+	Clostridium bolteae
2099188	GL0021814_O2_[Lack_5'-end]_[mRNA]_locus=scaffold83095_1:3:806:+	Clostridium bolteae
2104864	GL0021554_O2_[Complete]_[mRNA]_locus=scaffold9691_6:940:1332:-	Coprococcus comes
2105031	GL0059579_O2_[Complete]_[mRNA]_locus=scaffold10338_2:7938:8810:-	-
2107776	GL0114939_O2_[Lack_5'-end]_[mRNA]_locus=scaffold23680_3:2:688:+	Collinsella aerofaciens
2107857	GL0085457_O2_[Complete]_[mRNA]_locus=scaffold24078_2:7120:7884:-	Bacteroides capillosus
2109410	GL0049470_O2_[Lack_5'-end]_[mRNA]_locus=scaffold34514_3:449:640:-	Blautia hydrogenotrophica
2110992	GL0076441_O2_[Lack_3'-end]_[mRNA]_locus=scaffold46822_2:1:687:-	Firmicutes
2115033	GL0114819_O2_[Lack_3'-end]_[mRNA]_locus=scaffold79979_1:190:534:+	Clostridium leptum
2118056	GL0057165_O2_[Complete]_[mRNA]_locus=scaffold1712_1:304:1047:+	Roseburia inulinivorans
2120990	GL0052457_O2_[Lack_5'-end]_[mRNA]_locus=scaffold26744_2:838:972:-	-
2121435	GL0007602_O2_[Complete]_[mRNA]_locus=scaffold33430_4:33:326:-	-

2121451	GL0058872_O2_[Lack_5'-end]_[mRNA]_locus=scaffold33671_3:1:354:+	-
2122688	GL0015337_O2_[Lack_5'-end]_[mRNA]_locus=scaffold57935_1:1328:1855:-	-
2122701	GL0006007_O2_[Lack_5'-end]_[mRNA]_locus=scaffold58113_1:145:507:-	-
2123131	GL0032272_O2_[Lack_3'-end]_[mRNA]_locus=scaffold65685_2:2:259:-	Roseburia inulinivorans
2123434	GL0068279_O2_[Lack_5'-end]_[mRNA]_locus=C5604183_1:3:188:+	-
2123778	GL0064225_O2_[Complete]_[mRNA]_locus=scaffold957_3:1729:2859:-	Firmicutes
2123793	GL0071257_O2_[Lack_5'-end]_[mRNA]_locus=scaffold991_1:3:899:+	-
2123844	GL0132365_O2_[Complete]_[mRNA]_locus=scaffold1153_1:2615:3514:+	-
2124067	GL0005499_O2_[Complete]_[mRNA]_locus=scaffold1848_6:1138:1719:+	Erysipelotrichaceae
2124294	GL0131910_O2_[Complete]_[mRNA]_locus=scaffold2592_3:802:2148:-	-
2124504	GL0085828_O2_[Complete]_[mRNA]_locus=scaffold3227_2:293:670:-	-
2124543	GL0128784_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3354_3:1:186:+	-
2124839	GL0065900_O2_[Complete]_[mRNA]_locus=scaffold4164_1:2165:4432:+	Faecalibacterium prausnitzii
2124840	GL0122288_O2_[Complete]_[mRNA]_locus=scaffold4164_2:936:2282:+	-

2124879	GL0134849_O2_[Complete]_[mRNA]_locus=scaffold4293_15:3109:4179:-	-
2124882	GL0067120_O2_[Lack_3'-end]_[mRNA]_locus=scaffold4335_2:327:3176:+	Clostridiales
2125040	GL0086254_O2_[Complete]_[mRNA]_locus=scaffold4969_4:101:1543:-	-
2125166	GL0084148_O2_[Lack_5'-end]_[mRNA]_locus=scaffold5511_1:1127:1795:-	-
2125362	GL0075395_O2_[Complete]_[mRNA]_locus=scaffold6411_2:412:3186:-	Bacteria
2125454	GL0061271_O2_[Complete]_[mRNA]_locus=scaffold6792_4:1492:2046:-	-
2125487	GL0045831_O2_[Lack_3'-end]_[mRNA]_locus=scaffold6889_17:2137:3543:+	Clostridiales
2125498	GL0119535_O2_[Complete]_[mRNA]_locus=scaffold6927_1:871:2259:+	Bacteria
2125859	GL0125375_O2_[Complete]_[mRNA]_locus=scaffold8445_9:1176:3512:+	Faecalibacterium prausnitzii
2125880	GL0126801_O2_[Complete]_[mRNA]_locus=scaffold8500_1:37:1455:-	Bacteria
2126000	GL0016033_O2_[Complete]_[mRNA]_locus=scaffold8976_1:4025:5296:+	-
2126082	GL0124764_O2_[Complete]_[mRNA]_locus=scaffold9233_2:11041:14688:+	Firmicutes
2126265	GL0063691_O2_[Complete]_[mRNA]_locus=scaffold10219_6:680:1219:-	Bacteria
2126511	GL0068930_O2_[Complete]_[mRNA]_locus=scaffold11538_2:165:1541:-	Faecalibacterium prausnitzii

2126634	GL0131485_O2_[Complete]_[mRNA]_locus=scaffold12202_3:2485:3525:+	-
2126702	GL0032068_O2_[Lack_3'-end]_[mRNA]_locus=scaffold12486_10:42:974:+	-
2126970	GL0055893_O2_[Complete]_[mRNA]_locus=scaffold13616_2:2934:3794:-	Physcomitrella patens
2127495	GL0063449_O2_[Complete]_[mRNA]_locus=scaffold16709_4:95:1417:-	Roseburia inulinivorans
2127496	GL0083514_O2_[Complete]_[mRNA]_locus=scaffold16709_6:1808:3043:+	Faecalibacterium prausnitzii
2127581	GL0060582_O2_[Lack_5'-end]_[mRNA]_locus=scaffold17318_7:2:2236:+	Bacteria
2128132	GL0047465_O2_[Lack_3'-end]_[mRNA]_locus=scaffold20699_1:1431:1934:+	-
2128362	GL0093085_O2_[Complete]_[mRNA]_locus=scaffold22217_6:616:1110:-	-
2128794	GL0079669_O2_[Complete]_[mRNA]_locus=scaffold24840_1:1285:2859:+	Faecalibacterium prausnitzii
2128872	GL0129559_O2_[Lack_5'-end]_[mRNA]_locus=scaffold25309_1:3:152:+	-
2129861	GL0034662_O2_[Lack_5'-end]_[mRNA]_locus=scaffold32250_3:2557:3369:-	-
2130311	GL0028477_O2_[Lack_5'-end]_[mRNA]_locus=scaffold35216_2:2373:3128:-	-
2130880	GL0119881_O2_[Complete]_[mRNA]_locus=scaffold39008_1:839:1639:+	-
2132482	GL0021842_O2_[Lack_5'-end]_[mRNA]_locus=scaffold52962_1:1:216:+	-

2133397	GL0113696_O2_[Lack_5'-end]_[mRNA]_locus=scaffold61800_3:57:1340:-	-
2134926	GL0105468_O2_[Lack_5'-end]_[mRNA]_locus=scaffold75656_2:95:2503:-	-
2135166	GL0094908_O2_[Complete]_[mRNA]_locus=scaffold77433_4:60:1148:+	-
2138246	GL0035525_O2_[Complete]_[mRNA]_locus=scaffold144_21:1748:3352:-	Akkermansia muciniphila
2139015	GL0058257_O2_[Complete]_[mRNA]_locus=scaffold2622_16:1387:2523:+	Akkermansia muciniphila
2139441	GL0056136_O2_[Lack_5'-end]_[mRNA]_locus=scaffold3818_2:1:1362:+	Bacteria
2140562	GL0051361_O2_[Lack_5'-end]_[mRNA]_locus=scaffold7910_6:556:5004:-	Bacteria
2141162	GL0017133_O2_[Complete]_[mRNA]_locus=scaffold10103_2:3265:3435:-	-
2141234	GL0005403_O2_[Complete]_[mRNA]_locus=scaffold10559_2:3981:8411:-	Akkermansia muciniphila
2144508	GL0004433_O2_[Complete]_[mRNA]_locus=scaffold25930_10:3507:4439:+	Akkermansia muciniphila
2167836	GL0037364_O2_[Lack_both_end]_[mRNA]_locus=scaffold27039_1:2:586:+	Clostridiales
2169744	GL0041979_O2_[Complete]_[mRNA]_locus=scaffold34944_2:341:919:+	-
2173894	GL0069978_O2_[Lack_3'-end]_[mRNA]_locus=scaffold52897_1:3:575:-	Bacteroides capillosus
2181350	GL0038871_O2_[Complete]_[mRNA]_locus=C5374981_1:55:825:+	Clostridium scindens

2182958	GL0006977_O2_[Lack_both_end]_[mRNA]_locus=scaffold1495_1:3:1157:-	Clostridiales
2189975	GL0102544_O2_[Complete]_[mRNA]_locus=scaffold22110_2:441:7976:-	Bacteria
2205466	GL0073334_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4038_7:8640:8759:-	-
2209061	GL0029984_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8441_2:2:355:-	Ruminococcus torques
2209121	GL0033980_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8549_1:4784:4966:+	-
2218638	GL0025462_V1_[Lack_5'-end]_[mRNA]_locus=scaffold29948_3:3:104:+	-
2223042	GL0051877_V1_[Lack_both_end]_[mRNA]_locus=scaffold46243_1:3:755:-	Holdemania filiformis
2223606	GL0089289_V1_[Lack_3'-end]_[mRNA]_locus=scaffold48506_1:116:751:+	Haemophilus influenzae
2237053	GL0041131_V1_[Lack_5'-end]_[mRNA]_locus=scaffold13209_4:1:1338:+	Clostridium bolteae
2251390	GL0049491_V1_[Complete]_[mRNA]_locus=scaffold45889_1:3264:4079:-	Clostridium asparagiforme
2255253	GL0107694_V1_[Lack_5'-end]_[mRNA]_locus=scaffold277_2:1:1197:+	-
2255498	GL0050453_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1104_6:4132:6321:-	Bacteria
2256439	GL0072479_V1_[Complete]_[mRNA]_locus=scaffold3906_1:25:651:+	-
2256687	GL0112044_V1_[Lack_3'-end]_[mRNA]_locus=scaffold4478_1:514:978:+	Clostridiales

2257314	GL0138370_V1_[Lack_5'-end]_[mRNA]_locus=scaffold6627_2:1:546:+	-
2258700	GL0074389_V1_[Complete]_[mRNA]_locus=scaffold11915_1:246:989:-	Faecalibacterium prausnitzii
2258941	GL0111374_V1_[Complete]_[mRNA]_locus=scaffold12703_2:8:778:+	-
2259435	GL0068910_V1_[Complete]_[mRNA]_locus=scaffold14430_2:1917:2432:+	-
2259519	GL0062870_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14866_1:1:408:+	-
2260096	GL0049030_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17550_2:1:1752:+	Faecalibacterium prausnitzii
2260548	GL0024294_V1_[Lack_3'-end]_[mRNA]_locus=scaffold19302_5:592:1077:+	Ruminococcus obeum
2265964	GL0085501_V1_[Lack_both_end]_[mRNA]_locus=scaffold51705_1:3:1760:-	-
2266532	GL0115705_V1_[Complete]_[mRNA]_locus=scaffold56410_1:35:793:+	-
2268122	GL0061216_V1_[Complete]_[mRNA]_locus=scaffold69599_2:350:1462:-	-
2269655	GL0097809_V1_[Lack_3'-end]_[mRNA]_locus=scaffold82306_1:248:1528:+	-
2276578	GL0107212_V1_[Complete]_[mRNA]_locus=scaffold2230_2:313:846:+	Akkermansia muciniphila
2276662	GL0148391_V1_[Lack_both_end]_[mRNA]_locus=scaffold2426_2:2:1624:+	Bacteroides capillosus
2278727	GL0130794_V1_[Lack_both_end]_[mRNA]_locus=scaffold7457_1:3:779:-	Bacteroides capillosus

2279933	GL0144653_V1_[Complete]_[mRNA]_locus=scaffold11073_16:2959:3924:-	Akkermansia muciniphila
2279983	GL0014371_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11310_6:883:1629:-	Akkermansia muciniphila
2279984	GL0066732_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11310_22:304:924:-	Akkermansia muciniphila
2280418	GL0061364_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12645_2:741:1520:-	Akkermansia muciniphila
2280870	GL0047981_V1_[Complete]_[mRNA]_locus=scaffold14180_6:342:1652:+	Akkermansia muciniphila
2284987	GL0084254_V1_[Lack_5'-end]_[mRNA]_locus=scaffold31067_1:1:705:+	-
2285144	GL0093089_V1_[Lack_5'-end]_[mRNA]_locus=scaffold31983_1:3:344:+	Bacteria
2285764	GL0104672_V1_[Lack_3'-end]_[mRNA]_locus=scaffold35018_3:3554:3670:+	-
2287590	GL0071200_V1_[Lack_5'-end]_[mRNA]_locus=scaffold45763_2:2:139:+	-
2287926	GL0136165_V1_[Complete]_[mRNA]_locus=scaffold47987_2:65:370:-	-
2288214	GL0121432_V1_[Complete]_[mRNA]_locus=scaffold49994_3:5076:6530:-	Akkermansia muciniphila
2290405	GL0112759_V1_[Complete]_[mRNA]_locus=scaffold65268_9:1866:2726:+	Akkermansia muciniphila
2290728	GL0004192_V1_[Lack_5'-end]_[mRNA]_locus=scaffold67421_1:2:1414:+	Akkermansia muciniphila
2294992	GL0127017_V1_[Lack_5'-end]_[mRNA]_locus=scaffold95491_1:2:1489:+	Bacteria

2296694	GL0074265_V1_[Complete]_[mRNA]_locus=scaffold102479_1:378:959:-	Anaerotruncus colihominis
2301500	GL0035296_V1_[Complete]_[mRNA]_locus=scaffold2288_2:71:487:-	Bacteroides capillosus
2301833	GL0035811_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3063_1:1:594:+	Bacteroides capillosus
2301835	GL0003336_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3063_3:1:1194:+	Clostridium ramosum
2302773	GL0057860_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5206_1:323:931:-	-
2303521	GL0036354_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7300_1:218:652:+	Bacteroides capillosus
2303925	GL0057204_V1_[Complete]_[mRNA]_locus=scaffold8763_1:186:398:+	Anaerofustis stercorihominis
2304424	GL0006015_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10440_2:405:677:+	Bacteroides capillosus
2304457	GL0009121_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10567_1:3:665:-	Bacteroides capillosus
2304458	GL0064424_V1_[Lack_both_end]_[mRNA]_locus=scaffold10571_2:1:564:-	Bacteroides capillosus
2304823	GL0016008_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11946_3:2:391:+	Clostridium
2304836	GL0059567_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11988_7:168:836:-	Bacteria
2304949	GL0055234_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12389_1:2:625:+	Halothermothrix orenii

2305052	GL0034006_V1_[Complete]_[mRNA]_locus=scaffold12844_2:118:597:+	Clostridium
2305292	GL0067041_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13905_2:1:1056:-	Clostridiales
2305407	GL0028039_V1_[Lack_3'-end]_[mRNA]_locus=scaffold14340_2:113:517:+	Bacteroides capillosus
2305421	GL0003489_V1_[Lack_both_end]_[mRNA]_locus=scaffold14437_2:1:756:-	Firmicutes
2305542	GL0053302_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15205_1:583:1137:-	Blautia hydrogenotrophica
2305728	GL0059255_V1_[Lack_both_end]_[mRNA]_locus=scaffold15897_2:1:573:-	Bacteroides capillosus
2305959	GL0007933_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16843_1:1:447:+	Clostridium
2306378	GL0013004_V1_[Lack_both_end]_[mRNA]_locus=scaffold18382_3:3:524:-	Bacteroides capillosus
2306568	GL0011810_V1_[Lack_3'-end]_[mRNA]_locus=scaffold19316_1:3:473:-	Faecalibacterium prausnitzii
2307138	GL0052134_V1_[Lack_3'-end]_[mRNA]_locus=scaffold22011_2:300:572:+	-
2307146	GL0048327_V1_[Lack_both_end]_[mRNA]_locus=scaffold22061_3:2:586:+	Firmicutes
2307370	GL0070302_V1_[Lack_both_end]_[mRNA]_locus=scaffold23051_1:3:569:-	Bacteroides capillosus
2307408	GL0070108_V1_[Lack_both_end]_[mRNA]_locus=scaffold23271_1:3:548:-	Clostridium phytofermentans
2307409	GL0060385_V1_[Lack_both_end]_[mRNA]_locus=scaffold23271_3:1:879:-	Clostridiales

2307472	GL0039505_V1_[Lack_3'-end]_[mRNA]_locus=scaffold23507_1:223:1035:+	-
2307824	GL0013165_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25345_3:44:661:+	Bacteroides capillosus
2307987	GL0053126_V1_[Lack_5'-end]_[mRNA]_locus=scaffold26304_2:181:804:-	Campylobacterales
2308211	GL0007706_V1_[Lack_both_end]_[mRNA]_locus=scaffold27566_3:1:534:-	Anaerotruncus colihominis
2308369	GL0039169_V1_[Lack_5'-end]_[mRNA]_locus=scaffold28328_1:278:619:-	Bacteria
2308399	GL0008640_V1_[Lack_both_end]_[mRNA]_locus=scaffold28483_2:2:607:-	Clostridiales
2308585	GL0006981_V1_[Lack_3'-end]_[mRNA]_locus=scaffold29608_2:1:933:-	Bacteroides capillosus
2308608	GL0040899_V1_[Complete]_[mRNA]_locus=scaffold29736_3:276:662:-	Bacteroides capillosus
2308705	GL0048796_V1_[Lack_3'-end]_[mRNA]_locus=scaffold30247_4:2:964:-	Alkaliphilus metalliredigens
2308793	GL0022755_V1_[Lack_3'-end]_[mRNA]_locus=scaffold30817_1:3:614:-	Bacteroides capillosus
2308796	GL0042238_V1_[Lack_3'-end]_[mRNA]_locus=scaffold30832_3:2:541:-	Firmicutes
2308823	GL0067744_V1_[Lack_both_end]_[mRNA]_locus=scaffold31016_1:3:815:-	Bacteroides capillosus
2308853	GL0034132_V1_[Lack_5'-end]_[mRNA]_locus=scaffold31206_2:1:678:+	Clostridium phytofermentans
2309029	GL0016776_V1_[Lack_3'-end]_[mRNA]_locus=scaffold32084_2:3:350:-	Clostridium botulinum

2309680	GL0051593_V1_[Lack_5'-end]_[mRNA]_locus=scaffold35214_4:429:623:-	-
2309765	GL0063364_V1_[Lack_3'-end]_[mRNA]_locus=scaffold35682_1:3:1898:-	Bacteria
2309845	GL0068422_V1_[Lack_5'-end]_[mRNA]_locus=scaffold36032_1:204:515:-	Bacteroides capillosus
2310032	GL0064482_V1_[Lack_3'-end]_[mRNA]_locus=scaffold36849_2:501:1064:+	Bacteroides capillosus
2310142	GL0022232_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37398_1:235:513:-	-
2310188	GL0015585_V1_[Lack_both_end]_[mRNA]_locus=scaffold37585_1:2:586:+	Clostridiales
2310648	GL0045105_V1_[Lack_both_end]_[mRNA]_locus=scaffold39419_1:1:663:-	Dorea longicatena
2310865	GL0015155_V1_[Complete]_[mRNA]_locus=scaffold40425_2:3:278:-	Clostridium
2311076	GL0042630_V1_[Lack_5'-end]_[mRNA]_locus=scaffold41328_2:514:1005:-	Bacteroides capillosus
2311434	GL0013244_V1_[Lack_5'-end]_[mRNA]_locus=scaffold42770_1:115:834:-	Bacteroides capillosus
2311583	GL0010787_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43280_1:3:359:-	cellular organisms
2311584	GL0010788_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43280_1:664:900:+	Bacteria
2311766	GL0007290_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43850_1:82:606:+	Ruminococcus obeum
2311791	GL0054883_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43905_1:70:558:+	Bacteroides capillosus

2311872	GL0053120_V1_[Lack_5'-end]_[mRNA]_locus=scaffold44127_3:111:506:-	Clostridiales
2311998	GL0024582_V1_[Lack_3'-end]_[mRNA]_locus=scaffold44428_1:2:625:-	Faecalibacterium prausnitzii
2312366	GL0047825_V1_[Lack_3'-end]_[mRNA]_locus=scaffold45244_1:422:772:+	-
2312523	GL0021183_V1_[Lack_5'-end]_[mRNA]_locus=scaffold45663_2:3:611:+	-
2312743	GL0028377_V1_[Complete]_[mRNA]_locus=scaffold46024_1:652:1548:-	Bacteroides capillosus
2312746	GL0047322_V1_[Lack_5'-end]_[mRNA]_locus=scaffold46024_2:582:1001:-	Bacteroides capillosus
2312805	GL0006698_V1_[Complete]_[mRNA]_locus=scaffold46089_2:61:825:-	Bacteria
2312806	GL0006699_V1_[Lack_3'-end]_[mRNA]_locus=scaffold46089_2:761:862:+	-
2312809	GL0029290_V1_[Lack_5'-end]_[mRNA]_locus=scaffold46097_1:1:252:+	Bacteria
2312810	GL0029291_V1_[Lack_3'-end]_[mRNA]_locus=scaffold46097_1:463:1167:+	Clostridiaceae
2313190	GL0064712_V1_[Lack_both_end]_[mRNA]_locus=C3311462_1:3:524:+	Clostridium asparagiforme
2313473	GL0065866_V1_[Lack_5'-end]_[mRNA]_locus=C3323630_1:3:581:+	Roseburia inulinivorans
2313507	GL0049112_V1_[Lack_5'-end]_[mRNA]_locus=C3325704_1:298:621:-	Bacteroides capillosus
2313565	GL0032377_V1_[Lack_5'-end]_[mRNA]_locus=C3328623_1:1:615:+	Clostridium leptum

2313773	GL0038822_V1_[Lack_both_end]_[mRNA]_locus=C3342909_1:1:807:-	Bacteroides capillosus
2313979	GL0053122_V1_[Complete]_[mRNA]_locus=C3363015_1:30:809:-	Blautia hydrogenotrophica
2313995	GL0054784_V1_[Lack_3'-end]_[mRNA]_locus=C3364883_1:2:1189:-	Clostridiales
2319585	GL0067393_V1_[Complete]_[mRNA]_locus=scaffold13296_5:1033:1449:-	-
2322898	GL0045210_V1_[Lack_both_end]_[mRNA]_locus=scaffold31302_1:2:538:-	Bacteroides capillosus
2343162	GL0045045_V1_[Lack_both_end]_[mRNA]_locus=scaffold67928_1:3:896:-	Clostridiales
2348409	GL0094034_V1_[Lack_both_end]_[mRNA]_locus=scaffold10997_3:1:618:-	-
2348735	GL0046313_V1_[Complete]_[mRNA]_locus=scaffold12282_2:1433:2047:+	-
2349127	GL0091238_V1_[Lack_5'-end]_[mRNA]_locus=scaffold13772_4:364:2604:-	Bacteria
2349744	GL0136939_V1_[Complete]_[mRNA]_locus=scaffold16470_1:672:1037:-	Clostridium
2350067	GL0025002_V1_[Lack_both_end]_[mRNA]_locus=scaffold17675_2:2:613:+	Faecalibacterium prausnitzii
2351421	GL0018416_V1_[Complete]_[mRNA]_locus=scaffold23573_1:341:1057:+	-
2352400	GL0034899_V1_[Lack_3'-end]_[mRNA]_locus=scaffold28085_6:3:158:-	-
2353081	GL0120624_V1_[Complete]_[mRNA]_locus=scaffold31652_1:41:3754:-	Eubacterium biforme

2354421	GL0136064_V1_[Lack_3'-end]_[mRNA]_locus=scaffold40237_3:2:181:-	-
2355131	GL0034619_V1_[Complete]_[mRNA]_locus=scaffold44696_1:460:1194:+	-
2355545	GL0081764_V1_[Lack_3'-end]_[mRNA]_locus=scaffold47482_3:1:147:-	-
2356732	GL0082822_V1_[Lack_3'-end]_[mRNA]_locus=scaffold54873_1:198:740:+	-
2356752	GL0013136_V1_[Lack_3'-end]_[mRNA]_locus=scaffold55003_3:267:983:+	-
2357459	GL0092138_V1_[Lack_both_end]_[mRNA]_locus=scaffold59650_5:1:996:+	-
2358090	GL0080445_V1_[Lack_5'-end]_[mRNA]_locus=scaffold64171_1:64:1050:-	-
2358186	GL0100025_V1_[Lack_5'-end]_[mRNA]_locus=scaffold64919_1:401:802:-	-
2358344	GL0025819_V1_[Lack_5'-end]_[mRNA]_locus=scaffold65930_3:20:859:-	-
2359618	GL0123389_V1_[Complete]_[mRNA]_locus=scaffold73993_2:183:446:-	Bacteria
2359656	GL0081077_V1_[Lack_5'-end]_[mRNA]_locus=scaffold74293_1:67:1296:-	-
2360937	GL0005160_V1_[Lack_both_end]_[mRNA]_locus=scaffold81814_4:3:641:-	-
2361038	GL0073190_V1_[Complete]_[mRNA]_locus=scaffold82494_1:167:2164:-	-
2366193	GL0067602_V1_[Complete]_[mRNA]_locus=scaffold51_5:1067:2824:-	Bacteria

2366194	GL0092246_V1_[Complete]_[mRNA]_locus=scaffold51_6:2525:4660:-	Faecalibacterium prausnitzii
2366196	GL0009099_V1_[Complete]_[mRNA]_locus=scaffold51_9:2406:4352:-	Firmicutes
2366197	GL0009102_V1_[Complete]_[mRNA]_locus=scaffold51_9:6467:8941:-	Bacteria
2366198	GL0060614_V1_[Lack_both_end]_[mRNA]_locus=scaffold51_10:2:1261:+	Faecalibacterium prausnitzii
2366204	GL0069610_V1_[Complete]_[mRNA]_locus=scaffold68_4:212:2584:-	Bacteria
2366221	GL0067845_V1_[Complete]_[mRNA]_locus=scaffold95_4:123:812:-	-
2366368	GL0074531_V1_[Complete]_[mRNA]_locus=scaffold362_1:1398:2243:-	-
2366369	GL0089230_V1_[Complete]_[mRNA]_locus=scaffold362_2:3596:5068:+	Faecalibacterium prausnitzii
2366373	GL0079370_V1_[Lack_3'-end]_[mRNA]_locus=scaffold377_1:2:253:-	-
2366386	GL0025003_V1_[Complete]_[mRNA]_locus=scaffold415_4:1501:2589:-	Faecalibacterium prausnitzii
2366475	GL0075425_V1_[Complete]_[mRNA]_locus=scaffold633_8:3194:4180:+	-
2366555	GL0023443_V1_[Complete]_[mRNA]_locus=scaffold785_1:378:3038:-	Bacteria
2366656	GL0025012_V1_[Complete]_[mRNA]_locus=scaffold1075_3:2794:3636:-	-
2366658	GL0096238_V1_[Complete]_[mRNA]_locus=scaffold1075_8:2773:3228:-	Roseburia inulinivorans

2366685	GL0037460_V1_[Complete]_[mRNA]_locus=scaffold1188_5:535:1362:+	-
2366708	GL0080662_V1_[Complete]_[mRNA]_locus=scaffold1204_2:5968:6870:+	-
2366727	GL0066858_V1_[Complete]_[mRNA]_locus=scaffold1290_3:1764:3653:-	Clostridiales
2366728	GL0066861_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1290_3:5314:6660:-	-
2366729	GL0097622_V1_[Complete]_[mRNA]_locus=scaffold1290_5:5704:6534:+	-
2366736	GL0070772_V1_[Complete]_[mRNA]_locus=scaffold1300_1:6930:9425:-	Holdemania filiformis
2366739	GL0083863_V1_[Complete]_[mRNA]_locus=scaffold1300_2:678:1400:-	-
2366740	GL0083865_V1_[Complete]_[mRNA]_locus=scaffold1300_2:1792:8070:-	Firmicutes
2366901	GL0104475_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1736_7:2:1132:-	-
2366902	GL0062604_V1_[Complete]_[mRNA]_locus=scaffold1736_8:5212:5847:-	-
2366903	GL0020610_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1736_9:578:1969:-	-
2367053	GL0053432_V1_[Complete]_[mRNA]_locus=scaffold2094_1:6602:8350:-	Ruminococcus obeum
2367086	GL0041527_V1_[Complete]_[mRNA]_locus=scaffold2190_2:5:562:-	-
2367122	GL0069590_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2256_5:1:270:-	-

2367256	GL0089486_V1_[Complete]_[mRNA]_locus=scaffold2462_3:841:2505:-	Bacteria
2367318	GL0028869_V1_[Complete]_[mRNA]_locus=scaffold2530_3:975:2198:+	Faecalibacterium prausnitzii
2367320	GL0059275_V1_[Complete]_[mRNA]_locus=scaffold2530_12:91:1860:-	Bacteroides capillosus
2367352	GL0000967_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2654_4:2:3229:-	Bacteria
2367359	GL0067236_V1_[Complete]_[mRNA]_locus=scaffold2686_1:841:1551:-	-
2367360	GL0042430_V1_[Complete]_[mRNA]_locus=scaffold2686_3:274:1497:-	Clostridiales
2367406	GL0001803_V1_[Lack_both_end]_[mRNA]_locus=scaffold2816_1:2:532:-	Ruminococcus
2367408	GL0085049_V1_[Complete]_[mRNA]_locus=scaffold2827_2:3189:5156:+	-
2367411	GL0054803_V1_[Complete]_[mRNA]_locus=scaffold2827_7:5019:6305:+	-
2367412	GL0054804_V1_[Complete]_[mRNA]_locus=scaffold2827_7:6403:7926:-	Bacteria
2367419	GL0075587_V1_[Complete]_[mRNA]_locus=scaffold2851_2:3666:4004:+	-
2367420	GL0075589_V1_[Complete]_[mRNA]_locus=scaffold2851_2:5905:7959:-	Faecalibacterium prausnitzii
2367421	GL0034514_V1_[Lack_both_end]_[mRNA]_locus=scaffold2851_4:1:606:-	-
2367426	GL0017791_V1_[Complete]_[mRNA]_locus=scaffold2875_1:977:3970:-	-
2367637	GL0002777_V1_[Complete]_[mRNA]_locus=scaffo	-

	ld3323_5:10:1236:+	
2367639	GL0094100_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3323_6:3798:6086:+	Bacteria
2367657	GL0092310_V1_[Complete]_[mRNA]_locus=scaffold3375_9:1704:3989:+	Faecalibacterium prausnitzii
2367691	GL0028206_V1_[Complete]_[mRNA]_locus=scaffold3448_3:1210:2721:+	-
2367750	GL0048034_V1_[Complete]_[mRNA]_locus=scaffold3660_1:706:3108:+	Eubacterium siraeum
2367819	GL0014239_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3889_2:2:754:+	-
2367841	GL0052689_V1_[Lack_both_end]_[mRNA]_locus=scaffold3926_2:2:1135:-	Akkermansia muciniphila
2367887	GL0062552_V1_[Complete]_[mRNA]_locus=scaffold4077_2:2441:3010:-	Bacteroides capillosus
2367946	GL0103441_V1_[Complete]_[mRNA]_locus=scaffold4260_5:1109:1777:-	-
2368053	GL0080000_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4569_3:473:1252:-	Faecalibacterium prausnitzii
2368054	GL0088697_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4569_7:2894:4252:-	Eubacterium ventriosum
2368081	GL0071762_V1_[Complete]_[mRNA]_locus=scaffold4679_6:4759:5748:-	Roseburia inulinivorans
2368114	GL0096704_V1_[Complete]_[mRNA]_locus=scaffold4787_2:138:1994:+	Bacteria
2368138	GL0081709_V1_[Complete]_[mRNA]_locus=scaffold4787_6:2:346:+	-

2368261	GL0034010_V1_[Complete]_[mRNA]_locus=scaffold5165_2:588:2342:-	Firmicutes
2368262	GL0030197_V1_[Complete]_[mRNA]_locus=scaffold5165_4:6168:7289:-	-
2368268	GL0036556_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5187_1:4632:8240:-	Bacteria
2368415	GL0022623_V1_[Complete]_[mRNA]_locus=scaffold5417_3:1210:2637:-	-
2368430	GL0047225_V1_[Complete]_[mRNA]_locus=scaffold5472_2:5870:6889:-	-
2368450	GL0076023_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5583_1:76:1755:-	Bacteria
2368453	GL0003232_V1_[Complete]_[mRNA]_locus=scaffold5583_8:42:896:+	-
2368501	GL0082237_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5747_2:1061:2647:+	Clostridiales
2368502	GL0064518_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5747_10:1:1125:+	-
2368652	GL0057510_V1_[Complete]_[mRNA]_locus=scaffold6253_4:4250:5638:+	-
2368653	GL0057511_V1_[Complete]_[mRNA]_locus=scaffold6253_4:5762:6352:+	-
2368693	GL0003219_V1_[Complete]_[mRNA]_locus=scaffold6302_1:30:2801:-	-
2368730	GL0055738_V1_[Complete]_[mRNA]_locus=scaffold6410_9:2616:4859:-	Clostridiales
2368731	GL0037607_V1_[Lack_5'-end]_[mRNA]_locus=scaffold6410_11:1631:2878:-	Bacteria

2368734	GL0054091_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6427_1:1221:2534:+	-
2368801	GL0071008_V1_[Complete]_[mRNA]_locus=scaffold6636_3:1587:2333:+	Faecalibacterium prausnitzii
2368802	GL0082669_V1_[Complete]_[mRNA]_locus=scaffold6636_4:62:643:-	-
2368905	GL0106056_V1_[Complete]_[mRNA]_locus=scaffold7023_4:1821:2789:+	-
2368906	GL0035046_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7023_7:1188:2183:+	-
2368907	GL0040304_V1_[Complete]_[mRNA]_locus=scaffold7023_8:835:3189:+	Faecalibacterium prausnitzii
2369015	GL0006687_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7311_1:58:1212:-	Faecalibacterium prausnitzii
2369016	GL0031339_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7311_3:1:330:-	-
2369049	GL0011000_V1_[Complete]_[mRNA]_locus=scaffold7443_3:13:810:-	-
2369091	GL0069135_V1_[Complete]_[mRNA]_locus=scaffold7568_2:30:1925:-	Bacteria
2369132	GL0009231_V1_[Complete]_[mRNA]_locus=scaffold7834_2:10089:11636:+	Bacteria
2369250	GL0015947_V1_[Complete]_[mRNA]_locus=scaffold8232_2:1945:3261:-	-
2369251	GL0015949_V1_[Complete]_[mRNA]_locus=scaffold8232_2:4310:4729:+	Bacteria
2369352	GL0058653_V1_[Complete]_[mRNA]_locus=scaffold8630_1:47:781:+	-

2369424	GL0094880_V1_[Lack_5'-end]_[mRNA]_locus=scaffold8911_1:1686:4076:-	Faecalibacterium prausnitzii
2369574	GL0004465_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9613_3:2:571:+	-
2369575	GL0004466_V1_[Complete]_[mRNA]_locus=scaffold9613_3:617:1597:+	-
2369704	GL0070186_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9965_2:2:1084:+	-
2369717	GL0039751_V1_[Complete]_[mRNA]_locus=scaffold9994_1:514:810:-	-
2369921	GL0043724_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10497_1:3:812:-	-
2369922	GL0057420_V1_[Complete]_[mRNA]_locus=scaffold10497_2:2282:4252:-	Bacteria
2369993	GL0081009_V1_[Complete]_[mRNA]_locus=scaffold10740_1:2809:3960:+	Faecalibacterium prausnitzii
2369994	GL0081014_V1_[Complete]_[mRNA]_locus=scaffold10740_1:7674:8348:-	Dorea formicigenerans
2370066	GL0079018_V1_[Complete]_[mRNA]_locus=scaffold11018_2:1858:2799:+	-
2370098	GL0045296_V1_[Complete]_[mRNA]_locus=scaffold11098_2:159:1670:+	-
2370300	GL0072275_V1_[Complete]_[mRNA]_locus=scaffold12106_1:225:1940:+	Bacteria
2370423	GL0007684_V1_[Lack_both_end]_[mRNA]_locus=scaffold12579_2:3:794:-	-
2370491	GL0026602_V1_[Complete]_[mRNA]_locus=scaffold12900_1:2649:4151:+	Clostridiales

2370492	GL0026603_V1_[Complete]_[mRNA]_locus=scaffold12900_1:4243:5844:+	Clostridiales
2370496	GL0091154_V1_[Complete]_[mRNA]_locus=scaffold12918_6:149:1405:+	Faecalibacterium prausnitzii
2370796	GL0021478_V1_[Complete]_[mRNA]_locus=scaffold14030_4:267:485:+	-
2371163	GL0049414_V1_[Lack_3'-end]_[mRNA]_locus=scaffold15812_5:2:1222:-	-
2371164	GL0060916_V1_[Complete]_[mRNA]_locus=scaffold15812_11:566:1822:+	Faecalibacterium prausnitzii
2371205	GL0083410_V1_[Complete]_[mRNA]_locus=scaffold16042_2:3327:5264:-	Bacteria
2371206	GL0010012_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16042_4:1:900:-	-
2371234	GL0089196_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16129_2:79:2739:-	-
2371399	GL0027581_V1_[Lack_5'-end]_[mRNA]_locus=scaffold16873_2:2:865:+	-
2371489	GL0071577_V1_[Complete]_[mRNA]_locus=scaffold17171_2:249:929:+	Ruminococcus torques
2371918	GL0039081_V1_[Complete]_[mRNA]_locus=scaffold19499_3:16:873:-	-
2371919	GL0047922_V1_[Lack_both_end]_[mRNA]_locus=scaffold19499_4:1:582:-	-
2372066	GL0059033_V1_[Complete]_[mRNA]_locus=scaffold20134_1:8326:9237:+	Clostridium phytofermentans
2372068	GL0051178_V1_[Complete]_[mRNA]_locus=scaffold20134_11:1094:1741:-	-

2372071	GL0062928_V1_[Complete]_[mRNA]_locus=scaffold20134_14:956:4432:+	Ruminococcaceae
2372688	GL0096762_V1_[Lack_5'-end]_[mRNA]_locus=scaffold23550_1:2520:3344:-	Streptococcus
2372932	GL0047135_V1_[Complete]_[mRNA]_locus=scaffold24719_1:2631:4478:+	Clostridiales
2373130	GL0059812_V1_[Complete]_[mRNA]_locus=scaffold25909_4:950:3352:-	-
2373169	GL0073643_V1_[Lack_5'-end]_[mRNA]_locus=scaffold26313_3:514:942:-	-
2373862	GL0072057_V1_[Lack_5'-end]_[mRNA]_locus=scaffold31166_1:3:773:+	-
2374124	GL0103957_V1_[Lack_5'-end]_[mRNA]_locus=scaffold32916_2:2:922:+	-
2374325	GL0043949_V1_[Complete]_[mRNA]_locus=scaffold33975_1:272:535:-	Akkermansia muciniphila
2374523	GL0034377_V1_[Lack_3'-end]_[mRNA]_locus=scaffold35277_2:240:554:+	-
2374691	GL0068669_V1_[Complete]_[mRNA]_locus=scaffold36235_1:231:950:+	-
2375798	GL0016661_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43401_1:3:728:-	-
2378038	GL0017033_V1_[Lack_5'-end]_[mRNA]_locus=scaffold60866_2:203:685:-	Roseburia inulinivorans
2378121	GL0042569_V1_[Lack_5'-end]_[mRNA]_locus=scaffold61515_1:3:617:+	-
2378565	GL0088459_V1_[Complete]_[mRNA]_locus=scaffold64695_2:101:1042:+	Ruminococcus torques

2379238	GL0061578_V1_[Complete]_[mRNA]_locus=scaffold69979_1:53:892:-	-
2380286	GL0031433_V1_[Lack_5'-end]_[mRNA]_locus=scaffold76226_1:1:2037:+	-
2380287	GL0031434_V1_[Complete]_[mRNA]_locus=scaffold76226_1:2038:2676:+	-
2383072	GL0150471_V1_[Complete]_[mRNA]_locus=scaffold3148_17:3542:4354:-	Clostridium leptum
2384768	GL0103581_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7339_4:2:796:+	-
2385696	GL0141962_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9955_1:161:817:+	Akkermansia muciniphila
2386382	GL0113808_V1_[Complete]_[mRNA]_locus=scaffold11667_1:893:1942:+	Akkermansia muciniphila
2386823	GL0046257_V1_[Complete]_[mRNA]_locus=scaffold13276_66:3571:4569:-	Akkermansia muciniphila
2387121	GL0085544_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14200_1:3:218:+	-
2390613	GL0115235_V1_[Complete]_[mRNA]_locus=scaffold28041_2:7244:7681:+	Holdemania filiformis
2393283	GL0028271_V1_[Lack_5'-end]_[mRNA]_locus=scaffold40766_1:1:246:+	-
2399498	GL0054728_V1_[Complete]_[mRNA]_locus=scaffold79215_1:2375:3913:+	Akkermansia muciniphila
2400102	GL0007511_V1_[Complete]_[mRNA]_locus=scaffold82869_15:88:468:-	-
2402382	GL0152529_V1_[Complete]_[mRNA]_locus=scaffold97381_3:881:2524:-	Akkermansia muciniphila

2419677	GL0089614_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5166_4:239:1177:+	-
2421375	GL0088633_V1_[Complete]_[mRNA]_locus=scaffold6840_1:804:2306:-	-
2422187	GL0075469_V1_[Complete]_[mRNA]_locus=scaffold7988_1:276:1298:-	Bacteroides capillosus
2422984	GL0030812_V1_[Lack_both_end]_[mRNA]_locus=scaffold8884_3:3:635:-	Clostridium methylpentosum
2424213	GL0072273_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10073_3:268:576:+	Bacteria
2424761	GL0010211_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10757_1:1:531:+	Holdemania filiformis
2425800	GL0121400_V1_[Complete]_[mRNA]_locus=scaffold12086_1:874:1236:+	Roseburia inulinivorans
2425816	GL0060178_V1_[Complete]_[mRNA]_locus=scaffold12098_2:1086:2033:-	Candidatus Desulforudis audaxviator
2425890	GL0090765_V1_[Complete]_[mRNA]_locus=scaffold12218_1:218:1030:+	Bacteroides capillosus
2429208	GL0079944_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16777_2:1:219:-	-
2429357	GL0047217_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16917_1:705:914:+	Clostridiales
2430181	GL0121375_V1_[Lack_both_end]_[mRNA]_locus=scaffold18507_1:2:667:-	Clostridiales
2430241	GL0030108_V1_[Lack_3'-end]_[mRNA]_locus=scaffold18654_1:3:473:-	Coprococcus comes

2430814	GL0015608_V1_[Lack_both_end]_[mRNA]_locus=scaffold19829_3:2:1255:+	Bacteria
2433787	GL0108261_V1_[Lack_5'-end]_[mRNA]_locus=scaffold25776_1:3:104:+	-
2438207	GL0118836_V1_[Lack_5'-end]_[mRNA]_locus=scaffold38137_3:111:569:-	Bacteroides pectinophilus
2439655	GL0039801_V1_[Lack_5'-end]_[mRNA]_locus=scaffold42595_1:430:642:-	-
2452436	GL0045654_V1_[Lack_both_end]_[mRNA]_locus=scaffold1531_1:2:1342:+	Akkermansia muciniphila
2458867	GL0056673_V1_[Lack_5'-end]_[mRNA]_locus=scaffold23666_1:748:3102:-	Bacteroides pectinophilus
2465756	GL0072078_V1_[Lack_3'-end]_[mRNA]_locus=scaffold61823_11:1:561:-	Akkermansia muciniphila
2466550	GL0085308_V1_[Lack_3'-end]_[mRNA]_locus=scaffold65853_1:1:393:-	Akkermansia muciniphila
2467445	GL0007054_V1_[Lack_5'-end]_[mRNA]_locus=scaffold72011_1:778:948:-	-
2468872	GL0038841_V1_[Complete]_[mRNA]_locus=scaffold81389_2:182:757:+	Bacteroides fragilis
2472238	GL0079816_V1_[Lack_5'-end]_[mRNA]_locus=scaffold95357_1:1401:1511:-	-
2478480	GL0091644_V1_[Lack_5'-end]_[mRNA]_locus=scaffold196_1:3:218:+	Clostridiales
2478885	GL0063936_V1_[Complete]_[mRNA]_locus=scaffold470_1:11924:12478:-	Eubacterium siraeum
2478890	GL0063941_V1_[Complete]_[mRNA]_locus=scaffold470_1:13728:15020:-	Eubacterium siraeum

2478891	GL0063944_V1_[Complete]_[mRNA]_locus=scaffold470_1:15481:16041:-	-
2478892	GL0063945_V1_[Complete]_[mRNA]_locus=scaffold470_1:16777:17106:-	Eubacterium siraeum
2478894	GL0109110_V1_[Lack_3'-end]_[mRNA]_locus=scaffold470_2:2:859:-	Eubacterium siraeum
2478895	GL0109111_V1_[Complete]_[mRNA]_locus=scaffold470_2:1704:4739:+	Bacteroides capillosus
2478896	GL0109112_V1_[Complete]_[mRNA]_locus=scaffold470_2:4732:5634:+	Bacteroides capillosus
2478899	GL0089627_V1_[Lack_3'-end]_[mRNA]_locus=scaffold470_3:434:1009:+	Eubacterium biforme
2479046	GL0035734_V1_[Complete]_[mRNA]_locus=scaffold548_1:419:760:+	Clostridium bolteae
2479119	GL0053225_V1_[Lack_5'-end]_[mRNA]_locus=scaffold606_1:776:1837:-	Heliobacterium modesticaldum
2480746	GL0117446_V1_[Complete]_[mRNA]_locus=scaffold1818_1:1:330:+	Clostridium leptum
2481258	GL0038056_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2245_3:669:1943:-	Roseburia inulinivorans
2482254	GL0113062_V1_[Complete]_[mRNA]_locus=scaffold2928_1:327:809:-	Clostridiales
2482256	GL0040259_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2928_2:1:645:-	Clostridium
2482317	GL0065861_V1_[Lack_both_end]_[mRNA]_locus=scaffold2981_1:3:722:-	Clostridium leptum
2482735	GL0004181_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3369_8:5747:7045:+	Clostridium cellulolyticum

2482810	GL0037533_V1_[Complete]_[mRNA]_locus=scaffold3388_11:1378:2310:+	-
2482813	GL0037536_V1_[Complete]_[mRNA]_locus=scaffold3388_11:3022:3978:+	Clostridium kluyveri
2482826	GL0065591_V1_[Complete]_[mRNA]_locus=scaffold3388_12:7363:7698:+	Firmicutes
2482828	GL0065593_V1_[Complete]_[mRNA]_locus=scaffold3388_12:7946:8656:-	Eubacterium dolichum
2483365	GL0112267_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3832_2:257:769:+	Clostridiales
2483406	GL0110296_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3866_2:5200:7896:+	-
2484179	GL0004752_V1_[Lack_both_end]_[mRNA]_locus=scaffold4674_2:2:559:-	Blautia hydrogenotrophica
2484563	GL0007923_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5078_1:2:229:+	Firmicutes
2485910	GL0081256_V1_[Complete]_[mRNA]_locus=scaffold6349_3:1051:2880:+	Bacteria
2486998	GL0110450_V1_[Complete]_[mRNA]_locus=scaffold7562_2:1136:3118:+	Bacteria
2487671	GL0106600_V1_[Complete]_[mRNA]_locus=scaffold8206_2:3406:5103:+	Clostridiales
2488546	GL0031311_V1_[Complete]_[mRNA]_locus=scaffold9378_1:1498:2589:+	Clostridium
2489054	GL0011822_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10000_3:1:819:-	Clostridium cellulolyticum
2489461	GL0048872_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10483_3:1:321:-	-

2490351	GL0013303_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11592_2:1482:1760:+	Faecalibacterium prausnitzii
2491478	GL0083505_V1_[Lack_5'-end]_[mRNA]_locus=scaffold13174_4:181:777:-	Clostridium leptum
2491855	GL0116987_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13774_3:1:1107:-	Clostridiales
2492400	GL0103491_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14666_1:90:1028:-	Clostridium
2492404	GL0010857_V1_[Lack_both_end]_[mRNA]_locus=scaffold14666_3:2:682:-	Clostridium leptum
2494316	GL0053221_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17358_5:2:484:-	Clostridium
2494612	GL0066257_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17684_1:1:1404:+	Anaerotruncus colihominis
2494618	GL0066263_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17684_1:4513:4701:+	-
2494686	GL0017673_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17843_1:3:1373:-	Clostridium thermocellum
2495700	GL0034119_V1_[Lack_5'-end]_[mRNA]_locus=scaffold19785_2:2607:3068:-	Desulfitobacterium hafniense
2495750	GL0080957_V1_[Lack_5'-end]_[mRNA]_locus=scaffold19941_3:2:715:+	Clostridium kluyveri
2495810	GL0066579_V1_[Complete]_[mRNA]_locus=scaffold20077_3:145:624:+	Bacteria
2496223	GL0065690_V1_[Lack_3'-end]_[mRNA]_locus=scaffold20772_1:321:893:+	-
2499871	GL0052996_V1_[Lack_3'-end]_[mRNA]_locus=scaffold29023_2:445:726:+	Clostridium leptum

2500641	GL0021196_V1_[Lack_3'-end]_[mRNA]_locus=scaffold31302_2:63:578:+	Holdemania filiformis
2500920	GL0021768_V1_[Lack_3'-end]_[mRNA]_locus=scaffold31990_1:1:231:-	-
2500948	GL0060329_V1_[Lack_5'-end]_[mRNA]_locus=scaffold32153_1:1:405:+	Clostridiales
2502084	GL0029501_V1_[Lack_3'-end]_[mRNA]_locus=scaffold35014_1:3:560:-	Lachnospiraceae
2506838	GL0013552_V1_[Lack_5'-end]_[mRNA]_locus=scaffold49174_1:1:822:+	Dorea formicigenerans
2507977	GL0069332_V1_[Lack_5'-end]_[mRNA]_locus=scaffold52595_1:323:940:-	Ruminococcus obeum
2509279	GL0085841_V1_[Lack_both_end]_[mRNA]_locus=scaffold56948_2:1:597:-	-
2512239	GL0065238_V1_[Lack_both_end]_[mRNA]_locus=scaffold64948_1:3:851:+	Coprococcus comes
2512316	GL0118167_V1_[Lack_3'-end]_[mRNA]_locus=scaffold65167_1:1:747:+	Ruminococcus gnavus
2516230	GL0024004_V1_[Complete]_[mRNA]_locus=C5314710_1:240:479:-	-
2516456	GL0117992_V1_[Lack_5'-end]_[mRNA]_locus=C5321898_1:1:471:+	Clostridium leptum
2516884	GL0002475_V1_[Lack_both_end]_[mRNA]_locus=C5335674_1:1:597:+	Clostridium leptum
2517508	GL0037022_V1_[Complete]_[mRNA]_locus=C5358214_1:222:707:-	Clostridium kluyveri
2519620	GL0009510_V1_[Complete]_[mRNA]_locus=scaffold1067_4:545:1420:+	-

2519721	GL0000445_V1_[Complete]_[mRNA]_locus=scaffold1176_2:1426:2331:+	Ruminococcus obeum
2521021	GL0115166_V1_[Complete]_[mRNA]_locus=scaffold3500_1:903:1733:-	-
2521325	GL0079513_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4259_6:1:645:+	Clostridiales
2521692	GL0093450_V1_[Complete]_[mRNA]_locus=scaffold5186_1:355:975:+	-
2522398	GL0018407_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6913_1:359:538:+	-
2522967	GL0114731_V1_[Complete]_[mRNA]_locus=scaffold8153_2:408:1274:+	Enterococcus faecium
2523318	GL0081797_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9141_8:2:556:+	-
2523427	GL0026013_V1_[Complete]_[mRNA]_locus=scaffold9447_3:223:1815:+	Bacteria
2523955	GL0068582_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11032_3:1:120:-	-
2523956	GL0096160_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11032_6:396:1358:+	-
2524303	GL0044971_V1_[Complete]_[mRNA]_locus=scaffold11966_2:227:1396:+	Clostridiales
2524404	GL0054742_V1_[Complete]_[mRNA]_locus=scaffold12296_3:3:920:-	-
2528900	GL0050133_V1_[Lack_3'-end]_[mRNA]_locus=scaffold27599_1:3:533:-	Faecalibacterium prausnitzii
2546709	GL0048976_V1_[Complete]_[mRNA]_locus=scaffold305_2:6167:8179:-	Bacteroides thetaiotaomicron

2546977	GL0100787_V1_[Lack_5'-end]_[mRNA]_locus=scaffold444_10:3448:3879:-	Bacteria
2549941	GL0056718_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2229_9:3:938:-	Clostridium leptum
2549943	GL0119459_V1_[Complete]_[mRNA]_locus=scaffold2229_10:447:872:-	Clostridium leptum
2550051	GL0049750_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2290_1:303:755:+	-
2553773	GL0125360_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5244_2:3:311:-	-
2555333	GL0037274_V1_[Lack_both_end]_[mRNA]_locus=scaffold6711_1:2:1222:-	Roseburia inulinivorans
2563388	GL0038951_V1_[Complete]_[mRNA]_locus=scaffold16866_2:145:384:+	Clostridium bolteae
2564115	GL0021465_V1_[Complete]_[mRNA]_locus=scaffold18178_2:520:732:+	Ruminococcus gnavus
2567651	GL0061068_V1_[Lack_3'-end]_[mRNA]_locus=scaffold24753_2:320:877:+	Heliobacterium modesticaldum
2568136	GL0082454_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25707_2:137:691:+	Clostridium bolteae
2569334	GL0081444_V1_[Lack_both_end]_[mRNA]_locus=scaffold28140_1:3:503:-	Clostridiales
2569661	GL0135241_V1_[Complete]_[mRNA]_locus=scaffold29218_2:116:526:+	Thermoanaerobacterales
2569918	GL0084356_V1_[Lack_both_end]_[mRNA]_locus=scaffold29636_6:3:644:-	Clostridium methylpentosum

2570948	GL0081313_V1_[Lack_3'-end]_[mRNA]_locus=scaffold32273_2:225:905:+	Clostridium leptum
2570959	GL0135907_V1_[Lack_both_end]_[mRNA]_locus=scaffold32294_1:3:620:-	Firmicutes
2572356	GL0067995_V1_[Lack_both_end]_[mRNA]_locus=scaffold36062_2:1:522:+	Clostridium leptum
2572969	GL0081224_V1_[Lack_both_end]_[mRNA]_locus=scaffold37753_2:3:587:+	Clostridium difficile
2573180	GL0086681_V1_[Lack_both_end]_[mRNA]_locus=scaffold38102_1:1:879:+	Clostridium leptum
2573691	GL0014005_V1_[Lack_5'-end]_[mRNA]_locus=scaffold39741_2:2:253:+	Clostridiales
2574974	GL0091774_V1_[Lack_both_end]_[mRNA]_locus=scaffold43074_2:2:808:+	Clostridium leptum
2575314	GL0101469_V1_[Lack_both_end]_[mRNA]_locus=scaffold44048_2:1:654:-	Clostridium leptum
2575733	GL0063115_V1_[Lack_3'-end]_[mRNA]_locus=scaffold45337_3:1:369:-	Firmicutes
2576832	GL0045332_V1_[Complete]_[mRNA]_locus=scaffold48413_1:531:803:-	Clostridium
2576977	GL0024538_V1_[Lack_5'-end]_[mRNA]_locus=scaffold48929_1:28:543:-	Bacteroides capillosus
2577426	GL0029435_V1_[Lack_both_end]_[mRNA]_locus=scaffold50525_4:1:570:-	-
2580127	GL0102069_V1_[Lack_3'-end]_[mRNA]_locus=scaffold58904_1:5:766:+	-
2580193	GL0041900_V1_[Lack_5'-end]_[mRNA]_locus=scaffold59038_2:416:1042:-	Clostridium

2583074	GL0060282_V1_[Lack_5'-end]_[mRNA]_locus=scaffold67523_2:2:373:+	Anaerotruncus colihominis
2583508	GL0127085_V1_[Lack_3'-end]_[mRNA]_locus=scaffold68543_1:49:1062:+	Desulfitobacterium hafniense
2583509	GL0069735_V1_[Lack_5'-end]_[mRNA]_locus=scaffold68543_2:1:798:+	Streptococcus equi
2583749	GL0116282_V1_[Lack_both_end]_[mRNA]_locus=scaffold68990_2:2:502:-	Clostridiales
2583788	GL0125410_V1_[Lack_3'-end]_[mRNA]_locus=scaffold69074_2:81:731:+	Dethiobacter alkaliphilus
2584799	GL0021834_V1_[Lack_5'-end]_[mRNA]_locus=scaffold71155_2:2:427:+	Clostridium leptum
2586095	GL0063581_V1_[Lack_both_end]_[mRNA]_locus=C4804934_1:2:523:-	Clostridium leptum
2586104	GL0050263_V1_[Lack_both_end]_[mRNA]_locus=C4805762_1:2:523:-	-
2586148	GL0086333_V1_[Lack_both_end]_[mRNA]_locus=C4809030_1:1:534:+	Ruminococcus gnavus
2586542	GL0008743_V1_[Lack_5'-end]_[mRNA]_locus=C4840779_1:3:617:+	Bacteria
2586647	GL0098889_V1_[Lack_3'-end]_[mRNA]_locus=C4849357_1:92:676:+	Clostridium hylemonae
2589904	GL0032841_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5802_2:614:766:+	Anaerotruncus colihominis
2612188	GL0016938_V1_[Lack_3'-end]_[mRNA]_locus=scaffold114_5:447:1277:+	Faecalibacterium prausnitzii
2612329	GL0080666_V1_[Lack_3'-end]_[mRNA]_locus=scaffold345_2:371:1174:+	-

2612541	GL0114045_V1_[Lack_5'-end]_[mRNA]_locus=scaffold509_4:1965:2789:-	-
2612544	GL0037348_V1_[Complete]_[mRNA]_locus=scaffold509_13:2046:2894:-	-
2615087	GL0096365_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3264_5:1:135:-	-
2615576	GL0098322_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3886_3:179:568:-	-
2615577	GL0054437_V1_[Lack_both_end]_[mRNA]_locus=scaffold3886_5:3:1184:-	-
2615645	GL0113475_V1_[Complete]_[mRNA]_locus=scaffold4017_6:199:1353:-	-
2616220	GL0053885_V1_[Complete]_[mRNA]_locus=scaffold5110_2:881:1969:+	Bacteroidales
2616769	GL0067306_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5920_2:2:478:+	-
2616790	GL0024855_V1_[Complete]_[mRNA]_locus=scaffold5971_2:8:1105:-	-
2617025	GL0102437_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6325_2:1510:1983:+	-
2617172	GL0066147_V1_[Complete]_[mRNA]_locus=scaffold6613_5:1042:1284:+	-
2617236	GL0014533_V1_[Complete]_[mRNA]_locus=scaffold6767_2:316:1260:+	-
2617696	GL0107173_V1_[Complete]_[mRNA]_locus=scaffold7318_2:1568:2542:+	Enterococcus faecalis
2617697	GL0107174_V1_[Lack_3'-end]_[mRNA]_locus=scaffold7318_2:2539:3825:+	-

2617701	GL0076539_V1_[Complete]_[mRNA]_locus=scaffold7318_11:2982:3509:+	Faecalibacterium prausnitzii
2617812	GL0014857_V1_[Complete]_[mRNA]_locus=scaffold7517_1:7321:9591:+	Firmicutes
2617992	GL0037859_V1_[Complete]_[mRNA]_locus=scaffold7806_1:4041:5342:-	-
2618710	GL0051611_V1_[Complete]_[mRNA]_locus=scaffold9367_2:1247:2524:+	-
2618773	GL0056982_V1_[Complete]_[mRNA]_locus=scaffold9417_3:270:932:+	Anaerotruncus colihominis
2619002	GL0065589_V1_[Complete]_[mRNA]_locus=scaffold9939_10:441:1187:-	-
2619429	GL0113893_V1_[Lack_3'-end]_[mRNA]_locus=scaffold10729_1:3:599:-	-
2619436	GL0072118_V1_[Complete]_[mRNA]_locus=scaffold10755_5:93:914:-	-
2619438	GL0085447_V1_[Complete]_[mRNA]_locus=scaffold10760_4:11:1171:-	-
2619450	GL0104754_V1_[Lack_5'-end]_[mRNA]_locus=scaffold10789_2:2:487:+	-
2619709	GL0053385_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11205_1:3:338:-	-
2620784	GL0069767_V1_[Complete]_[mRNA]_locus=scaffold13513_1:30:1451:-	Ruminococcus obeum
2620792	GL0092161_V1_[Lack_both_end]_[mRNA]_locus=scaffold13564_2:2:778:-	-
2620906	GL0112840_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13818_2:44:2353:+	Bacteroidales

2620907	GL0037735_V1_[Complete]_[mRNA]_locus=scaffold13818_3:1948:3246:+	Bacteroidales
2620908	GL0108544_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13818_9:290:2956:+	Bacteroides
2620909	GL0049184_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13818_10:704:2251:+	Bacteroides thetaiotaomicron
2621433	GL0074134_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15193_4:39:653:-	Clostridiales
2621602	GL0015192_V1_[Lack_3'-end]_[mRNA]_locus=scaffold15763_1:2:1276:-	-
2621603	GL0015193_V1_[Complete]_[mRNA]_locus=scaffold15763_1:1618:2604:+	-
2621642	GL0075809_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15918_8:398:628:-	Bacteria
2622397	GL0042014_V1_[Lack_3'-end]_[mRNA]_locus=scaffold18007_1:3:617:-	Faecalibacterium prausnitzii
2622783	GL0049083_V1_[Lack_5'-end]_[mRNA]_locus=scaffold19165_1:3:545:+	Faecalibacterium prausnitzii
2623224	GL0016453_V1_[Lack_3'-end]_[mRNA]_locus=scaffold20736_1:1429:1797:+	Coprococcus eutactus
2623283	GL0098200_V1_[Lack_5'-end]_[mRNA]_locus=scaffold20891_2:603:2339:-	Clostridiales
2623477	GL0031144_V1_[Complete]_[mRNA]_locus=scaffold21571_4:1328:2311:-	Bacteroides dorei
2623478	GL0087709_V1_[Lack_3'-end]_[mRNA]_locus=scaffold21571_6:1:789:-	Bacteroides dorei
2623479	GL0113252_V1_[Complete]_[mRNA]_locus=scaffold21571_7:572:1987:-	Bacteroides ovatus

2623509	GL0043376_V1_[Complete]_[mRNA]_locus=scaffold21653_2:284:799:-	-
2623589	GL0066528_V1_[Complete]_[mRNA]_locus=scaffold21968_4:3:1187:+	Bacteroidetes
2623590	GL0066529_V1_[Complete]_[mRNA]_locus=scaffold21968_4:1331:2659:+	Parabacteroides distasonis
2623777	GL0047306_V1_[Complete]_[mRNA]_locus=scaffold22642_1:3266:3853:-	-
2623778	GL0080542_V1_[Complete]_[mRNA]_locus=scaffold22642_3:132:329:+	-
2623779	GL0007973_V1_[Complete]_[mRNA]_locus=scaffold22642_4:1948:2883:-	Bacteroides pectinophilus
2623780	GL0054677_V1_[Complete]_[mRNA]_locus=scaffold22642_5:731:1309:+	Faecalibacterium prausnitzii
2624292	GL0120520_V1_[Complete]_[mRNA]_locus=scaffold24148_2:335:619:+	-
2624418	GL0044050_V1_[Lack_5'-end]_[mRNA]_locus=scaffold24782_5:429:551:-	-
2624467	GL0109427_V1_[Complete]_[mRNA]_locus=scaffold24968_3:2:1045:+	Ruminococcus obeum
2624546	GL0098141_V1_[Complete]_[mRNA]_locus=scaffold25191_6:78:1442:-	-
2624737	GL0021640_V1_[Complete]_[mRNA]_locus=scaffold25797_5:4:1494:-	Ruminococcus gnavus
2624814	GL0038016_V1_[Lack_5'-end]_[mRNA]_locus=scaffold26253_4:820:1404:-	-
2624832	GL0101861_V1_[Complete]_[mRNA]_locus=scaffold26438_2:2333:3727:+	Bacteroides capillosus
2624835	GL0104592_V1_[Complete]_[mRNA]_locus=scaffo	Bacteroides

	ld26463_1:111:500:-	capillosus
2624889	GL0024183_V1_[Complete]_[mRNA]_locus=scaffold26639_6:3770:4585:+	-
2624890	GL0024184_V1_[Lack_3'-end]_[mRNA]_locus=scaffold26639_6:4589:5413:+	-
2624967	GL0014653_V1_[Lack_3'-end]_[mRNA]_locus=scaffold27046_2:289:1791:+	Faecalibacterium prausnitzii
2625377	GL0004553_V1_[Complete]_[mRNA]_locus=scaffold28361_1:1229:1909:-	Anaerostipes caccae
2625379	GL0029531_V1_[Lack_5'-end]_[mRNA]_locus=scaffold28382_2:1:1293:+	-
2625454	GL0065037_V1_[Lack_5'-end]_[mRNA]_locus=scaffold28808_1:1:237:+	Clostridium leptum
2625462	GL0028218_V1_[Lack_both_end]_[mRNA]_locus=scaffold28910_7:2:607:+	-
2625732	GL0052951_V1_[Lack_3'-end]_[mRNA]_locus=scaffold30077_5:1:1353:-	Dorea formicigenerans
2625808	GL0107901_V1_[Complete]_[mRNA]_locus=scaffold30510_9:432:1826:+	Bacteroides capillosus
2625849	GL0008815_V1_[Lack_both_end]_[mRNA]_locus=scaffold30764_2:1:594:+	-
2626182	GL0093265_V1_[Complete]_[mRNA]_locus=scaffold32548_5:349:1149:-	-
2626384	GL0048646_V1_[Complete]_[mRNA]_locus=scaffold33442_2:1062:2669:+	-
2626569	GL0078292_V1_[Complete]_[mRNA]_locus=scaffold34414_5:51:698:-	Bacteria

2626774	GL0059656_V1_[Complete]_[mRNA]_locus=scaffold35339_6:2012:3337:+	Pedobacter
2626775	GL0059657_V1_[Complete]_[mRNA]_locus=scaffold35339_6:3334:4677:+	Pedobacter
2627162	GL0054408_V1_[Complete]_[mRNA]_locus=scaffold37244_1:151:1731:-	Chlorobium phaeobacteroides
2627317	GL0094636_V1_[Lack_5'-end]_[mRNA]_locus=scaffold37861_2:1:507:+	-
2627400	GL0115123_V1_[Complete]_[mRNA]_locus=scaffold38329_6:4750:5823:+	Bacteroides
2627402	GL0009821_V1_[Complete]_[mRNA]_locus=scaffold38329_9:19:981:+	Bacteroides ovatus
2627462	GL0085194_V1_[Lack_both_end]_[mRNA]_locus=scaffold38872_2:3:1172:+	-
2627635	GL0029571_V1_[Complete]_[mRNA]_locus=scaffold40556_11:3987:4991:+	Bacteroides dorei
2628162	GL0034372_V1_[Lack_3'-end]_[mRNA]_locus=scaffold43660_2:383:535:+	-
2628486	GL0088079_V1_[Complete]_[mRNA]_locus=scaffold46182_1:1432:2616:-	-
2628934	GL0097224_V1_[Lack_3'-end]_[mRNA]_locus=scaffold49079_16:2:346:-	Bacteroidales
2629138	GL0069801_V1_[Complete]_[mRNA]_locus=scaffold50407_3:268:1395:-	Anaerotruncus colihominis
2629140	GL0082012_V1_[Complete]_[mRNA]_locus=scaffold50407_5:6811:8031:-	-
2629388	GL0118324_V1_[Lack_both_end]_[mRNA]_locus=scaffold52233_4:3:500:+	-

2629405	GL0056135_V1_[Lack_3'-end]_[mRNA]_locus=scaffold52342_1:308:706:+	-
2629746	GL0046234_V1_[Complete]_[mRNA]_locus=scaffold54980_1:2977:4104:-	Bacteroidetes
2629748	GL0013623_V1_[Lack_5'-end]_[mRNA]_locus=scaffold54980_9:114:1817:-	-
2629767	GL0114631_V1_[Complete]_[mRNA]_locus=scaffold55154_2:723:2303:-	Pedobacter
2629996	GL0064751_V1_[Lack_5'-end]_[mRNA]_locus=scaffold57025_1:778:1026:-	Bacteria
2631130	GL0093350_V1_[Complete]_[mRNA]_locus=scaffold65062_10:1153:2223:+	-
2631269	GL0081843_V1_[Complete]_[mRNA]_locus=scaffold65876_1:64:804:-	-
2632080	GL0099698_V1_[Lack_5'-end]_[mRNA]_locus=scaffold69718_1:47:826:-	-
2633615	GL0027575_V1_[Lack_5'-end]_[mRNA]_locus=C3971229_1:2:199:+	Bacteroides thetaiotaomicron
2633883	GL0000946_V1_[Complete]_[mRNA]_locus=scaffold163_4:54080:57700:-	Akkermansia muciniphila
2634285	GL0011792_V1_[Complete]_[mRNA]_locus=scaffold497_5:4282:4773:+	Akkermansia muciniphila
2635641	GL0118025_V1_[Lack_both_end]_[mRNA]_locus=scaffold2125_1:2:2377:-	-
2635801	GL0139224_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2275_23:5573:6118:-	Akkermansia muciniphila
2636297	GL0109818_V1_[Complete]_[mRNA]_locus=scaffold2822_4:19685:21445:+	Akkermansia muciniphila

2636302	GL0090131_V1_[Lack_3'-end]_[mRNA]_locus=scaffold2822_7:28854:32954:+	Bacteria
2636475	GL0083695_V1_[Complete]_[mRNA]_locus=scaffold3183_6:15565:15876:-	-
2636652	GL0087588_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3424_2:2:457:-	Clostridium leptum
2636654	GL0029115_V1_[Complete]_[mRNA]_locus=scaffold3424_3:17:844:-	Bacteroides capillosus
2638113	GL0098679_V1_[Complete]_[mRNA]_locus=scaffold5918_1:49:2607:+	Akkermansia muciniphila
2640703	GL0112220_V1_[Complete]_[mRNA]_locus=scaffold11227_4:6196:7236:-	Akkermansia muciniphila
2642842	GL0068514_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16941_1:2:697:-	-
2643374	GL0044906_V1_[Lack_5'-end]_[mRNA]_locus=scaffold18832_1:80:1096:-	Clostridium scindens
2645928	GL0010294_V1_[Complete]_[mRNA]_locus=scaffold28604_1:2305:3294:-	Akkermansia muciniphila
2645929	GL0010296_V1_[Complete]_[mRNA]_locus=scaffold28604_1:4309:5997:-	Verrucomicrobia
2647995	GL0143182_V1_[Complete]_[mRNA]_locus=scaffold40692_2:618:1727:+	Bifidobacterium adolescentis
2648894	GL0141288_V1_[Lack_3'-end]_[mRNA]_locus=scaffold48084_1:315:1208:+	Bacteroides caccae
2651248	GL0045325_V1_[Complete]_[mRNA]_locus=scaffold64356_1:2199:3470:+	Bacteroides dorei

2654036	GL0039887_V1_[Complete]_[mRNA]_locus=scaffold84584_1:126:2063:-	Streptococcus equi
2655015	GL0098500_V1_[Lack_both_end]_[mRNA]_locus=scaffold89135_2:3:584:+	-
2655889	GL0001297_V1_[Complete]_[mRNA]_locus=scaffold92201_1:2165:2422:+	Clostridium
2673054	GL0077463_V1_[Complete]_[mRNA]_locus=scaffold23448_1:155:487:+	Streptococcus thermophilus
2683695	GL0049319_V1_[Lack_3'-end]_[mRNA]_locus=scaffold64361_3:327:950:+	Blautia hydrogenotrophica
2688033	GL0022765_V1_[Lack_5'-end]_[mRNA]_locus=scaffold475_3:1225:2595:-	Ruminococcus lactaris
2688255	GL0118929_V1_[Complete]_[mRNA]_locus=scaffold966_1:159:1073:+	Bacteroides capillosus
2688397	GL0122183_V1_[Complete]_[mRNA]_locus=scaffold1282_16:1074:2360:+	Bacteroides capillosus
2688408	GL0170888_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1343_2:2:1510:+	-
2688726	GL0089274_V1_[Complete]_[mRNA]_locus=scaffold2045_2:475:1596:+	Clostridiales
2688818	GL0031393_V1_[Complete]_[mRNA]_locus=scaffold2364_3:7564:8145:+	Akkermansia muciniphila
2688820	GL0018469_V1_[Complete]_[mRNA]_locus=scaffold2364_4:4006:5217:-	Akkermansia muciniphila
2688862	GL0151342_V1_[Complete]_[mRNA]_locus=scaffold2535_5:9984:11342:+	Akkermansia muciniphila

2688924	GL0054249_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2601_5:1838:3070:-	Bacillales
2689090	GL0166974_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2915_15:238:1065:-	Clostridium
2689325	GL0143770_V1_[Lack_3'-end]_[mRNA]_locus=scaffold3483_2:1821:3122:+	-
2689351	GL0141808_V1_[Complete]_[mRNA]_locus=scaffold3515_1:232:963:+	-
2689795	GL0003677_V1_[Complete]_[mRNA]_locus=scaffold4823_3:6236:8008:-	Akkermansia muciniphila
2689811	GL0157527_V1_[Lack_5'-end]_[mRNA]_locus=scaffold4853_23:1:1569:+	Akkermansia muciniphila
2689857	GL0061600_V1_[Complete]_[mRNA]_locus=scaffold4989_1:2905:3123:+	Bacteria
2690333	GL0108042_V1_[Complete]_[mRNA]_locus=scaffold6314_3:754:1773:-	-
2690655	GL0065264_V1_[Complete]_[mRNA]_locus=scaffold7124_1:137:358:-	-
2690690	GL0022331_V1_[Complete]_[mRNA]_locus=scaffold7235_2:261:2042:+	-
2691195	GL0049724_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8273_7:2:1063:-	Bacteroides capillosus
2691321	GL0027421_V1_[Complete]_[mRNA]_locus=scaffold8662_3:23:916:+	-
2691557	GL0152325_V1_[Lack_both_end]_[mRNA]_locus=scaffold9122_1:3:1094:-	-
2692170	GL0099885_V1_[Complete]_[mRNA]_locus=scaffold10581_1:503:1453:-	Faecalibacterium prausnitzii

2692589	GL0012661_V1_[Lack_3'-end]_[mRNA]_locus=scaffold11332_2:1133:2092:+	Bacteroides capillosus
2692653	GL0089636_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11410_2:2:628:+	-
2692679	GL0049972_V1_[Complete]_[mRNA]_locus=scaffold11479_5:60:869:+	-
2692680	GL0062828_V1_[Complete]_[mRNA]_locus=scaffold11479_7:165:1013:-	-
2692691	GL0120478_V1_[Complete]_[mRNA]_locus=scaffold11543_1:690:2945:+	-
2692798	GL0120297_V1_[Complete]_[mRNA]_locus=scaffold11771_4:804:1598:-	Bacteroides capillosus
2692889	GL0156702_V1_[Complete]_[mRNA]_locus=scaffold12049_1:41:1657:-	Clostridia
2692992	GL0012788_V1_[Complete]_[mRNA]_locus=scaffold12362_9:597:881:+	Clostridium
2693037	GL0099739_V1_[Complete]_[mRNA]_locus=scaffold12424_1:4771:5529:-	-
2693394	GL0146419_V1_[Complete]_[mRNA]_locus=scaffold13338_1:1057:2829:-	Faecalibacterium prausnitzii
2693644	GL0126458_V1_[Complete]_[mRNA]_locus=scaffold13966_3:584:1657:+	-
2693697	GL0132310_V1_[Complete]_[mRNA]_locus=scaffold14165_1:1521:2864:+	Psychromonas ingrahamii
2693699	GL0154870_V1_[Complete]_[mRNA]_locus=scaffold14174_3:51:1226:+	-
2693755	GL0135119_V1_[Complete]_[mRNA]_locus=scaffold14252_1:778:1521:+	-

2693756	GL0072577_V1_[Complete]_[mRNA]_locus=scaffold14252_3:294:1658:+	Blautia hydrogenotrophica
2693841	GL0146107_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14574_2:3:584:+	-
2694670	GL0027425_V1_[Lack_5'-end]_[mRNA]_locus=scaffold17070_2:499:708:-	-
2694759	GL0097776_V1_[Complete]_[mRNA]_locus=scaffold17438_1:123:1334:+	Faecalibacterium prausnitzii
2694823	GL0111082_V1_[Complete]_[mRNA]_locus=scaffold17585_1:922:2703:-	Clostridium phytofermentans
2694824	GL0111083_V1_[Complete]_[mRNA]_locus=scaffold17585_1:2855:4105:-	Roseobacter
2694825	GL0111084_V1_[Complete]_[mRNA]_locus=scaffold17585_1:4122:4904:-	Opitutaceae
2694826	GL0111085_V1_[Complete]_[mRNA]_locus=scaffold17585_1:4911:5909:-	Clostridium phytofermentans
2694827	GL0111086_V1_[Complete]_[mRNA]_locus=scaffold17585_1:5936:6874:-	-
2694828	GL0111089_V1_[Complete]_[mRNA]_locus=scaffold17585_1:8850:11168:-	-
2694829	GL0111092_V1_[Complete]_[mRNA]_locus=scaffold17585_1:13162:15177:-	Candidatus Solibacter usitatus
2694830	GL0111093_V1_[Complete]_[mRNA]_locus=scaffold17585_1:15284:16936:-	-
2694923	GL0137452_V1_[Complete]_[mRNA]_locus=scaffold17948_3:287:1600:-	-
2694986	GL0141454_V1_[Complete]_[mRNA]_locus=scaffold18148_1:336:1340:+	-

2694987	GL0141455_V1_[Complete]_[mRNA]_locus=scaffold18148_1:1459:2823:+	-
2695151	GL0046900_V1_[Complete]_[mRNA]_locus=scaffold18531_1:1714:2913:-	Thermoanaerobacter
2695590	GL0126746_V1_[Lack_3'-end]_[mRNA]_locus=scaffold19690_1:6679:7632:+	Bacteroides capillosus
2696238	GL0051637_V1_[Complete]_[mRNA]_locus=scaffold22019_1:495:884:-	-
2696266	GL0106430_V1_[Complete]_[mRNA]_locus=scaffold22092_1:1198:1662:+	Eubacterium ventriosum
2696891	GL0059390_V1_[Lack_3'-end]_[mRNA]_locus=scaffold24428_6:3:1463:-	Akkermansia muciniphila
2697321	GL0014140_V1_[Complete]_[mRNA]_locus=scaffold25835_3:1057:3291:+	Akkermansia muciniphila
2697322	GL0014152_V1_[Complete]_[mRNA]_locus=scaffold25835_3:20511:22331:+	Akkermansia muciniphila
2698502	GL0004408_V1_[Lack_3'-end]_[mRNA]_locus=scaffold30624_1:279:929:+	-
2699373	GL0164065_V1_[Complete]_[mRNA]_locus=scaffold34155_1:38:1435:-	Coprococcus eutactus
2699469	GL0085759_V1_[Lack_5'-end]_[mRNA]_locus=scaffold34644_1:1:2607:+	-
2700896	GL0103582_V1_[Lack_5'-end]_[mRNA]_locus=scaffold40081_2:1886:2449:-	Anaerotruncus colihominis
2700962	GL0080512_V1_[Complete]_[mRNA]_locus=scaffold40413_1:482:895:-	Faecalibacterium prausnitzii
2701200	GL0154298_V1_[Complete]_[mRNA]_locus=scaffold41472_1:89:1126:+	Clostridium thermocellum

2701219	GL0139011_V1_[Lack_both_end]_[mRNA]_locus=scaffold41572_5:1:900:+	-
2702691	GL0051252_V1_[Complete]_[mRNA]_locus=scaffold49144_1:6954:7973:-	Akkermansia muciniphila
2703411	GL0093800_V1_[Complete]_[mRNA]_locus=scaffold53147_1:44:601:+	-
2706103	GL0005558_V1_[Complete]_[mRNA]_locus=scaffold68157_1:162:1106:+	-
2706394	GL0085698_V1_[Complete]_[mRNA]_locus=scaffold70058_7:11271:12470:+	Akkermansia muciniphila
2706813	GL0032242_V1_[Complete]_[mRNA]_locus=scaffold72527_2:267:992:+	-
2708172	GL0108319_V1_[Lack_3'-end]_[mRNA]_locus=scaffold80531_2:423:776:+	-
2708209	GL0171751_V1_[Lack_both_end]_[mRNA]_locus=scaffold80801_1:2:1411:+	Bacteria
2708865	GL0131548_V1_[Lack_3'-end]_[mRNA]_locus=scaffold85177_3:1:144:-	-
2710724	GL0002422_V1_[Complete]_[mRNA]_locus=scaffold95277_1:7091:9007:-	Akkermansia muciniphila
2710912	GL0002049_V1_[Complete]_[mRNA]_locus=scaffold96099_1:2772:5939:+	Bacteria
2713813	GL0176903_V1_[Lack_3'-end]_[mRNA]_locus=scaffold106191_2:197:508:+	-
2715274	GL0082500_V1_[Complete]_[mRNA]_locus=scaffold108650_1:781:2556:+	Akkermansia muciniphila
2715494	GL0085591_V1_[Complete]_[mRNA]_locus=scaffold108890_1:835:1644:+	Bacteroides capillosus

2718072	GL0041279_V1_[Complete]_[mRNA]_locus=C4293466_1:13:645:+	Akkermansia muciniphila
2722460	GL0047822_V1_[Complete]_[mRNA]_locus=scaffold5174_2:2914:3387:-	Clostridium
2723920	GL0001102_V1_[Lack_3'-end]_[mRNA]_locus=scaffold9152_2:557:676:+	-
2725694	GL0042973_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15065_2:1:204:+	-
2727201	GL0051695_V1_[Complete]_[mRNA]_locus=scaffold21834_6:1651:2643:+	Clostridium bolteae
2727762	GL0016370_V1_[Lack_5'-end]_[mRNA]_locus=scaffold24586_1:2:526:+	Ruminococcus gnavus
2728798	GL0063825_V1_[Lack_5'-end]_[mRNA]_locus=scaffold30894_7:1:540:+	Akkermansia muciniphila
2728962	GL0047355_V1_[Lack_3'-end]_[mRNA]_locus=scaffold31931_2:676:783:+	-
2729462	GL0004667_V1_[Complete]_[mRNA]_locus=scaffold34327_2:230:910:-	Akkermansia muciniphila
2730625	GL0030184_V1_[Lack_3'-end]_[mRNA]_locus=scaffold42089_2:4:975:+	Bacteroides thetaiotaomicron
2732308	GL0020679_V1_[Lack_3'-end]_[mRNA]_locus=scaffold50473_1:2523:3188:+	Dorea longicatena
2732593	GL0049980_V1_[Complete]_[mRNA]_locus=scaffold51236_1:2163:3749:+	Clostridium cellulolyticum
2732821	GL0036648_V1_[Complete]_[mRNA]_locus=scaffold51800_1:126:509:+	Akkermansia muciniphila
2733735	GL0063540_V1_[Lack_3'-end]_[mRNA]_locus=C6264593_1:346:1239:+	Giardia intestinalis

2734065	GL0077847_V1_[Lack_both_end]_[mRNA]_locus=scaffold160_4:2:847:-	-
2734311	GL0160772_V1_[Complete]_[mRNA]_locus=scaffold432_4:993:2954:-	-
2734527	GL0004975_V1_[Complete]_[mRNA]_locus=scaffold762_1:2799:3662:-	-
2734528	GL0004977_V1_[Complete]_[mRNA]_locus=scaffold762_1:4969:5730:-	-
2734529	GL0074434_V1_[Complete]_[mRNA]_locus=scaffold762_2:16:1899:-	Acholeplasma laidlawii
2734593	GL0105405_V1_[Complete]_[mRNA]_locus=scaffold844_1:739:2730:+	Coprothermobacter proteolyticus
2734594	GL0152655_V1_[Lack_5'-end]_[mRNA]_locus=scaffold844_4:14118:14594:-	-
2734610	GL0067340_V1_[Complete]_[mRNA]_locus=scaffold895_2:2407:3105:-	Ruminococcus lactaris
2734717	GL0037694_V1_[Complete]_[mRNA]_locus=scaffold1003_1:36:2108:-	Bacteria
2734719	GL0037697_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1003_1:4218:5153:+	Clostridium
2734721	GL0097415_V1_[Complete]_[mRNA]_locus=scaffold1008_3:1154:2173:-	Clostridium asparagiforme
2734722	GL0144716_V1_[Complete]_[mRNA]_locus=scaffold1008_4:127:1530:+	Bacilli
2734723	GL0144717_V1_[Lack_3'-end]_[mRNA]_locus=scaffold1008_4:1540:3039:+	-
2734724	GL0156191_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1008_5:2:1033:+	-

2734731	GL0022428_V1_[Complete]_[mRNA]_locus=scaffold1008_8:5758:6810:+	Eubacterium biforme
2734802	GL0097634_V1_[Complete]_[mRNA]_locus=scaffold1105_2:111:2282:-	Faecalibacterium prausnitzii
2734867	GL0038743_V1_[Complete]_[mRNA]_locus=scaffold1211_6:240:1427:-	Clostridiales
2734981	GL0151474_V1_[Complete]_[mRNA]_locus=scaffold1440_1:51:1304:-	-
2734982	GL0025032_V1_[Complete]_[mRNA]_locus=scaffold1440_2:649:1452:-	-
2735002	GL0120926_V1_[Lack_5'-end]_[mRNA]_locus=scaffold1506_5:2:811:+	Faecalibacterium prausnitzii
2735004	GL0053307_V1_[Complete]_[mRNA]_locus=scaffold1506_11:12:1187:-	-
2735325	GL0129583_V1_[Complete]_[mRNA]_locus=scaffold2016_1:570:1364:-	-
2735333	GL0053036_V1_[Complete]_[mRNA]_locus=scaffold2034_1:78:941:+	-
2735364	GL0135590_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2089_4:1280:4087:-	Bacteria
2735365	GL0055804_V1_[Complete]_[mRNA]_locus=scaffold2089_7:428:1375:-	-
2735366	GL0113820_V1_[Complete]_[mRNA]_locus=scaffold2089_9:797:3571:-	Bacteria
2735417	GL0145833_V1_[Complete]_[mRNA]_locus=scaffold2164_2:250:1470:+	-
2735723	GL0021376_V1_[Complete]_[mRNA]_locus=scaffold2454_6:2563:3870:+	Anaerostipes caccae
2735724	GL0021380_V1_[Complete]_[mRNA]_locus=scaffold2454_6:6176:7864:+	Anaerostipes caccae

2735725	GL0021381_V1_[Complete]_[mRNA]_locus=scaffold2454_6:8038:9087:+	Anaerostipes caccae
2735833	GL0086996_V1_[Lack_both_end]_[mRNA]_locus=scaffold2544_1:3:1118:+	-
2735942	GL0067955_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2703_2:3:1043:+	-
2735943	GL0117927_V1_[Lack_5'-end]_[mRNA]_locus=scaffold2703_4:2106:4709:-	Bacteria
2735984	GL0125918_V1_[Complete]_[mRNA]_locus=scaffold2721_6:3828:5744:-	-
2736113	GL0090697_V1_[Complete]_[mRNA]_locus=scaffold2885_6:51:950:+	Faecalibacterium prausnitzii
2736314	GL0006044_V1_[Complete]_[mRNA]_locus=scaffold3110_1:580:2022:+	-
2736358	GL0050400_V1_[Complete]_[mRNA]_locus=scaffold3156_7:1161:1652:-	Dorea longicatena
2736400	GL0061051_V1_[Complete]_[mRNA]_locus=scaffold3186_6:3453:5039:-	-
2736813	GL0056043_V1_[Complete]_[mRNA]_locus=scaffold3898_3:2354:3736:+	-
2736965	GL0072775_V1_[Complete]_[mRNA]_locus=scaffold4143_2:370:2934:+	Bacteria
2737009	GL0007173_V1_[Complete]_[mRNA]_locus=scaffold4247_5:1691:2869:+	-
2737075	GL0071958_V1_[Complete]_[mRNA]_locus=scaffold4365_1:36:1406:+	-
2737076	GL0007737_V1_[Complete]_[mRNA]_locus=scaffold4365_12:602:1375:+	Clostridium scindens

2737175	GL0148691_V1_[Complete]_[mRNA]_locus=scaffold4568_4:79:1245:+	-
2737176	GL0031962_V1_[Complete]_[mRNA]_locus=scaffold4568_5:29:1222:+	-
2737437	GL0121103_V1_[Complete]_[mRNA]_locus=scaffold5098_5:80:898:-	-
2737471	GL0097435_V1_[Complete]_[mRNA]_locus=scaffold5162_1:1644:2198:+	-
2737495	GL0025324_V1_[Complete]_[mRNA]_locus=scaffold5255_3:452:685:-	-
2737769	GL0076862_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5892_2:1776:3104:+	Clostridiales
2737909	GL0155016_V1_[Complete]_[mRNA]_locus=scaffold6206_4:4:1221:-	-
2737976	GL0018822_V1_[Complete]_[mRNA]_locus=scaffold6414_2:2323:3807:+	Bacteria
2737977	GL0018823_V1_[Complete]_[mRNA]_locus=scaffold6414_2:3808:5007:+	Clostridiales
2738020	GL0036146_V1_[Complete]_[mRNA]_locus=scaffold6546_5:2442:3839:+	Faecalibacterium prausnitzii
2738059	GL0119708_V1_[Complete]_[mRNA]_locus=scaffold6642_1:1465:2136:-	Faecalibacterium prausnitzii
2738060	GL0139624_V1_[Complete]_[mRNA]_locus=scaffold6642_2:678:902:-	-
2738062	GL0060896_V1_[Complete]_[mRNA]_locus=scaffold6642_5:2650:4407:+	Bacteria
2738099	GL0023537_V1_[Complete]_[mRNA]_locus=scaffold6714_1:44:487:+	Faecalibacterium prausnitzii
2738166	GL0042791_V1_[Complete]_[mRNA]_locus=scaffo	-

	ld6877_4:15:1313:-	
2738262	GL0166676_V1_[Complete]_[mRNA]_locus=scaffold7081_4:12041:12469:-	Akkermansia muciniphila
2738381	GL0016740_V1_[Complete]_[mRNA]_locus=scaffold7254_6:1895:2716:-	-
2738402	GL0142036_V1_[Lack_5'-end]_[mRNA]_locus=scaffold7287_5:3:1310:+	-
2738703	GL0064568_V1_[Complete]_[mRNA]_locus=scaffold7799_4:781:2010:+	-
2738711	GL0147802_V1_[Complete]_[mRNA]_locus=scaffold7814_1:1713:1946:-	-
2739065	GL0098885_V1_[Complete]_[mRNA]_locus=scaffold8475_2:3033:4079:+	Ruminococcus lactaris
2739305	GL0024507_V1_[Complete]_[mRNA]_locus=scaffold9060_2:2:913:-	-
2739346	GL0072941_V1_[Complete]_[mRNA]_locus=scaffold9178_4:1163:2518:-	-
2739421	GL0031264_V1_[Complete]_[mRNA]_locus=scaffold9371_1:3099:4688:+	-
2739431	GL0086044_V1_[Complete]_[mRNA]_locus=scaffold9471_5:4106:5323:+	Bacteria
2739440	GL0134603_V1_[Complete]_[mRNA]_locus=scaffold9512_3:327:1268:+	-
2739736	GL0040169_V1_[Complete]_[mRNA]_locus=scaffold10183_11:2877:3596:-	-
2739737	GL0040173_V1_[Complete]_[mRNA]_locus=scaffold10183_11:6582:7805:-	-

2740090	GL0142640_V1_[Lack_5'-end]_[mRNA]_locus=scaffold11112_3:810:1820:-	-
2740672	GL0135030_V1_[Complete]_[mRNA]_locus=scaffold12516_1:2529:3077:-	Bacteroides capillosus
2740909	GL0024835_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13007_4:5018:6127:+	-
2740935	GL0097165_V1_[Lack_both_end]_[mRNA]_locus=scaffold13107_5:3:803:-	-
2741600	GL0085457_V1_[Complete]_[mRNA]_locus=scaffold14597_5:1186:3762:-	Ruminococcus obeum
2741894	GL0158975_V1_[Lack_3'-end]_[mRNA]_locus=scaffold15325_1:1:2817:-	Roseburia inulinivorans
2741897	GL0041850_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15325_2:2448:3431:-	-
2741951	GL0040820_V1_[Complete]_[mRNA]_locus=scaffold15537_3:1864:3003:-	-
2741952	GL0119903_V1_[Complete]_[mRNA]_locus=scaffold15537_6:443:1846:-	-
2741953	GL0152038_V1_[Complete]_[mRNA]_locus=scaffold15537_7:100:2100:-	Clostridia
2741964	GL0063022_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15555_6:38:586:-	Faecalibacterium prausnitzii
2742018	GL0074936_V1_[Complete]_[mRNA]_locus=scaffold15639_1:23:1048:-	-
2742020	GL0052620_V1_[Lack_5'-end]_[mRNA]_locus=scaffold15639_5:1895:2002:-	-
2742051	GL0090212_V1_[Complete]_[mRNA]_locus=scaffold15691_3:3770:4243:+	Ruminococcus gnavus

2742082	GL0070310_V1_[Complete]_[mRNA]_locus=scaffold15741_1:50:1591:+	Bacteria
2742179	GL0012815_V1_[Complete]_[mRNA]_locus=scaffold16058_1:1399:2628:+	Anaerotruncus colihominis
2742180	GL0066356_V1_[Complete]_[mRNA]_locus=scaffold16058_2:2183:5860:+	-
2742776	GL0110496_V1_[Complete]_[mRNA]_locus=scaffold17235_2:660:1718:-	Clostridium scindens
2742777	GL0110498_V1_[Complete]_[mRNA]_locus=scaffold17235_2:3254:5857:+	Bacteria
2742958	GL0053649_V1_[Complete]_[mRNA]_locus=scaffold17815_1:1429:3354:-	-
2742973	GL0068359_V1_[Lack_3'-end]_[mRNA]_locus=scaffold17962_2:1589:2497:+	-
2743215	GL0052743_V1_[Complete]_[mRNA]_locus=scaffold18701_5:348:788:-	-
2743674	GL0033735_V1_[Complete]_[mRNA]_locus=scaffold19882_1:1764:4706:+	Clostridiales
2743769	GL0081261_V1_[Complete]_[mRNA]_locus=scaffold20191_3:65860:66177:+	Akkermansia muciniphila
2744024	GL0162538_V1_[Complete]_[mRNA]_locus=scaffold20910_2:22:1497:-	-
2744473	GL0090807_V1_[Lack_3'-end]_[mRNA]_locus=scaffold22510_2:1:711:-	Butyrivibrio
2744474	GL0090808_V1_[Complete]_[mRNA]_locus=scaffold22510_2:783:1229:-	Roseburia inulinivorans
2744563	GL0078695_V1_[Complete]_[mRNA]_locus=scaffold22740_10:2299:3048:-	Akkermansia muciniphila

2744582	GL0085562_V1_[Lack_5'-end]_[mRNA]_locus=scaffold22842_2:2:1546:+	-
2744664	GL0006152_V1_[Complete]_[mRNA]_locus=scaffold23131_2:11727:12947:+	Akkermansia muciniphila
2745154	GL0119876_V1_[Complete]_[mRNA]_locus=scaffold24484_5:591:2312:+	Akkermansia muciniphila
2745618	GL0151501_V1_[Complete]_[mRNA]_locus=scaffold25974_1:391:2256:+	Bacteria
2745696	GL0131091_V1_[Complete]_[mRNA]_locus=scaffold26063_1:1118:1720:-	-
2745915	GL0103389_V1_[Complete]_[mRNA]_locus=scaffold26835_2:249:794:+	Bacteroides capillosus
2745967	GL0022454_V1_[Lack_3'-end]_[mRNA]_locus=scaffold27037_1:686:1378:+	-
2746037	GL0044187_V1_[Complete]_[mRNA]_locus=scaffold27380_2:172:2244:+	-
2746194	GL0165512_V1_[Lack_5'-end]_[mRNA]_locus=scaffold27819_3:1:1473:+	Firmicutes
2746523	GL0029913_V1_[Complete]_[mRNA]_locus=scaffold29168_1:1784:2725:+	Roseburia inulinivorans
2746524	GL0053700_V1_[Complete]_[mRNA]_locus=scaffold29168_2:723:1643:-	-
2746815	GL0027073_V1_[Complete]_[mRNA]_locus=scaffold30244_2:1300:3465:-	Eubacterium biforme
2747670	GL0007855_V1_[Complete]_[mRNA]_locus=scaffold33031_2:1336:2007:+	Faecalibacterium prausnitzii
2747861	GL0110075_V1_[Complete]_[mRNA]_locus=scaffold33746_1:818:1663:-	Ruminococcus lactaris

2748209	GL0028819_V1_[Complete]_[mRNA]_locus=scaffold34986_1:1781:3544:+	Clostridium leptum
2748405	GL0002448_V1_[Complete]_[mRNA]_locus=scaffold35664_2:120:869:+	Dorea formicigenerans
2749050	GL0055067_V1_[Complete]_[mRNA]_locus=scaffold38446_5:2202:4400:+	Akkermansia muciniphila
2749257	GL0064312_V1_[Complete]_[mRNA]_locus=scaffold39358_2:2132:2929:-	Bacteria
2749258	GL0064313_V1_[Complete]_[mRNA]_locus=scaffold39358_2:2934:3128:-	Bacteria
2749600	GL0119730_V1_[Lack_3'-end]_[mRNA]_locus=scaffold40328_1:3:1517:-	-
2749615	GL0143756_V1_[Lack_3'-end]_[mRNA]_locus=scaffold40396_2:28:738:+	-
2749958	GL0098361_V1_[Complete]_[mRNA]_locus=scaffold41867_2:2945:3223:-	Dorea formicigenerans
2750284	GL0056500_V1_[Complete]_[mRNA]_locus=scaffold43282_1:10871:11818:-	Akkermansia muciniphila
2750498	GL0077592_V1_[Lack_3'-end]_[mRNA]_locus=scaffold44326_1:3:587:-	Alkaliphilus metalliredigens
2750540	GL0061236_V1_[Complete]_[mRNA]_locus=scaffold44436_3:14:1258:+	-
2750800	GL0078538_V1_[Complete]_[mRNA]_locus=scaffold45498_1:96:383:+	-
2750900	GL0135931_V1_[Complete]_[mRNA]_locus=scaffold45784_2:36:1940:+	Clostridium leptum

2751209	GL0150716_V1_[Complete]_[mRNA]_locus=scaffold46783_1:2570:4156:-	Dehalococcoides ethenogenes
2751933	GL0049509_V1_[Lack_3'-end]_[mRNA]_locus=scaffold49759_2:361:570:+	Parabacteroides distasonis
2752327	GL0031896_V1_[Complete]_[mRNA]_locus=scaffold51115_2:3542:5023:+	Akkermansia muciniphila
2752343	GL0157875_V1_[Complete]_[mRNA]_locus=scaffold51230_4:13394:15478:+	Bacteroides vulgatus
2752411	GL0163227_V1_[Complete]_[mRNA]_locus=scaffold51646_1:418:2349:-	-
2752412	GL0163228_V1_[Complete]_[mRNA]_locus=scaffold51646_1:2499:3161:+	-
2752532	GL0049433_V1_[Complete]_[mRNA]_locus=scaffold52245_2:12946:15774:+	Bacteria
2752866	GL0045965_V1_[Lack_5'-end]_[mRNA]_locus=scaffold53754_1:3:290:+	-
2752867	GL0045966_V1_[Complete]_[mRNA]_locus=scaffold53754_1:284:676:+	Clostridium spiroforme
2753600	GL0009307_V1_[Lack_5'-end]_[mRNA]_locus=scaffold56447_2:2:553:+	Anaerostipes caccae
2754607	GL0113108_V1_[Complete]_[mRNA]_locus=scaffold59910_1:3817:4767:-	Listeria
2755685	GL0054756_V1_[Lack_both_end]_[mRNA]_locus=scaffold64177_2:3:635:-	Ruminococcus
2756530	GL0029164_V1_[Complete]_[mRNA]_locus=scaffold67587_1:6449:9424:-	Bacteria

2756579	GL0098866_V1_[Complete]_[mRNA]_locus=scaffold67795_2:5934:6143:+	-
2756580	GL0098867_V1_[Complete]_[mRNA]_locus=scaffold67795_2:6186:7427:+	Bacteroides pectinophilus
2756970	GL0137349_V1_[Lack_5'-end]_[mRNA]_locus=scaffold69514_1:1:2328:+	-
2756972	GL0137351_V1_[Complete]_[mRNA]_locus=scaffold69514_1:3822:4772:+	-
2758869	GL0062454_V1_[Complete]_[mRNA]_locus=scaffold76965_1:846:1340:-	-
2760011	GL0033396_V1_[Complete]_[mRNA]_locus=scaffold81661_1:6043:6753:+	Akkermansia muciniphila
2760693	GL0098063_V1_[Complete]_[mRNA]_locus=scaffold84198_1:4104:5006:-	Roseburia inulinivorans
2760694	GL0098065_V1_[Lack_5'-end]_[mRNA]_locus=scaffold84198_1:5841:6707:-	-
2760837	GL0117496_V1_[Lack_3'-end]_[mRNA]_locus=scaffold84513_3:269:802:+	Clostridium
2760851	GL0095839_V1_[Complete]_[mRNA]_locus=scaffold84565_3:2621:3577:+	Akkermansia muciniphila
2762871	GL0035858_V1_[Lack_3'-end]_[mRNA]_locus=scaffold91103_2:2030:5290:+	Akkermansia muciniphila
2763742	GL0047943_V1_[Lack_5'-end]_[mRNA]_locus=scaffold93349_1:2:505:+	Bacilli
2764503	GL0067976_V1_[Complete]_[mRNA]_locus=scaffold94925_1:2688:3890:-	Coprococcus comes
2764504	GL0067977_V1_[Complete]_[mRNA]_locus=scaffold94925_1:4056:6488:+	Lachnospiraceae

2764506	GL0067980_V1_[Complete]_[mRNA]_locus=scaffold94925_1:10555:13296:+	Bacteria
2764509	GL0067983_V1_[Complete]_[mRNA]_locus=scaffold94925_1:18528:20066:+	Coprococcus comes
2765248	GL0079280_V1_[Complete]_[mRNA]_locus=scaffold96185_1:351:950:+	-
2765528	GL0029237_V1_[Lack_5'-end]_[mRNA]_locus=scaffold96654_1:2:217:+	-
2767734	GL0050640_V1_[Complete]_[mRNA]_locus=scaffold98990_1:226:927:+	Bacteria
2767735	GL0050642_V1_[Complete]_[mRNA]_locus=scaffold98990_1:1960:2847:-	Dorea longicatena
2767835	GL0098538_V1_[Complete]_[mRNA]_locus=scaffold99048_1:184:1308:-	-
2768364	GL0162659_V1_[Complete]_[mRNA]_locus=scaffold99290_1:7220:7834:-	Akkermansia muciniphila
2768865	GL0026038_V1_[Lack_both_end]_[mRNA]_locus=C3837736_1:3:542:+	-
2770298	GL0112778_V1_[Lack_3'-end]_[mRNA]_locus=C3905991_1:2:220:-	Clostridiales
2771892	GL0058860_V1_[Complete]_[mRNA]_locus=C3976066_1:365:1783:-	Anaerocellum thermophilum
2772574	GL0009584_V1_[Complete]_[mRNA]_locus=scaffold48_1:32:334:-	-
2773096	GL0109549_V1_[Complete]_[mRNA]_locus=scaffold428_2:881:1261:+	Clostridiales
2773543	GL0117861_V1_[Complete]_[mRNA]_locus=scaffold720_1:1129:2772:+	-

2773544	GL0128185_V1_[Complete]_[mRNA]_locus=scaffold720_6:633:1388:+	-
2773678	GL0036250_V1_[Complete]_[mRNA]_locus=scaffold793_6:5241:6017:+	Akkermansia muciniphila
2773679	GL0106049_V1_[Lack_5'-end]_[mRNA]_locus=scaffold793_7:1121:2689:-	Bacteria
2773680	GL0050403_V1_[Complete]_[mRNA]_locus=scaffold793_9:1140:2687:-	Akkermansia muciniphila
2773681	GL0050405_V1_[Complete]_[mRNA]_locus=scaffold793_9:3888:4757:-	Akkermansia muciniphila
2774699	GL0136510_V1_[Complete]_[mRNA]_locus=scaffold1762_1:2794:3660:-	Akkermansia muciniphila
2774985	GL0117361_V1_[Complete]_[mRNA]_locus=scaffold2035_1:2168:3232:+	-
2775251	GL0018930_V1_[Complete]_[mRNA]_locus=scaffold2249_6:96:890:-	-
2775284	GL0091610_V1_[Complete]_[mRNA]_locus=scaffold2282_1:15372:15779:+	Akkermansia muciniphila
2775639	GL0022973_V1_[Complete]_[mRNA]_locus=scaffold2566_3:7801:10029:-	Bacteria
2775640	GL0008603_V1_[Complete]_[mRNA]_locus=scaffold2566_4:33836:34627:-	Akkermansia muciniphila
2776635	GL0086231_V1_[Lack_both_end]_[mRNA]_locus=scaffold3294_2:2:1495:-	Faecalibacterium prausnitzii
2776882	GL0109839_V1_[Complete]_[mRNA]_locus=scaffold3609_6:61:702:+	-
2776931	GL0104020_V1_[Lack_5'-end]_[mRNA]_locus=scaffold3660_1:2:694:+	-

2776936	GL0135252_V1_[Complete]_[mRNA]_locus=scaffold3664_1:808:957:-	-
2777233	GL0103794_V1_[Complete]_[mRNA]_locus=scaffold3891_1:49:561:-	-
2777921	GL0049930_V1_[Lack_3'-end]_[mRNA]_locus=scaffold4675_1:724:1899:+	Ruminococcus obeum
2778085	GL0053173_V1_[Complete]_[mRNA]_locus=scaffold4942_1:156:737:+	-
2778662	GL0025453_V1_[Lack_3'-end]_[mRNA]_locus=scaffold5422_5:838:1590:+	-
2778834	GL0040776_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5517_1:2:214:+	-
2778835	GL0040778_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5517_1:1298:2365:-	-
2778837	GL0135204_V1_[Complete]_[mRNA]_locus=scaffold5521_2:374:1966:+	-
2778840	GL0135207_V1_[Complete]_[mRNA]_locus=scaffold5521_2:4306:5235:+	-
2778842	GL0135211_V1_[Complete]_[mRNA]_locus=scaffold5521_2:8952:9818:+	-
2778997	GL0063429_V1_[Lack_5'-end]_[mRNA]_locus=scaffold5660_2:168:1205:-	Faecalibacterium prausnitzii
2779179	GL0079637_V1_[Complete]_[mRNA]_locus=scaffold5776_5:5151:5852:-	Akkermansia muciniphila
2779296	GL0141208_V1_[Complete]_[mRNA]_locus=scaffold5946_3:19:942:-	Clostridium bolteae
2779316	GL0058910_V1_[Complete]_[mRNA]_locus=scaffold5972_1:875:1441:+	-

2779412	GL0078250_V1_[Lack_3'-end]_[mRNA]_locus=scaffold6041_4:2:955:-	-
2779419	GL0100571_V1_[Complete]_[mRNA]_locus=scaffold6055_1:1083:2642:-	Clostridiales
2779755	GL0004875_V1_[Complete]_[mRNA]_locus=scaffold6331_1:7783:9138:-	Akkermansia muciniphila
2779991	GL0029667_V1_[Lack_5'-end]_[mRNA]_locus=scaffold6580_2:396:980:-	Bacteroides capillosus
2780210	GL0059377_V1_[Complete]_[mRNA]_locus=scaffold6788_17:26:250:-	-
2780786	GL0046680_V1_[Complete]_[mRNA]_locus=scaffold7383_4:569:1333:-	-
2781230	GL0064787_V1_[Complete]_[mRNA]_locus=scaffold7747_1:82:1602:+	Ruminococcus gnavus
2781437	GL0060598_V1_[Complete]_[mRNA]_locus=scaffold7998_2:537:1901:+	-
2781547	GL0032529_V1_[Complete]_[mRNA]_locus=scaffold8101_3:21174:23570:-	Bacteria
2782025	GL0130228_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8585_6:1:753:-	-
2782342	GL0044328_V1_[Lack_3'-end]_[mRNA]_locus=scaffold8987_4:1:477:-	-
2782344	GL0042645_V1_[Lack_5'-end]_[mRNA]_locus=scaffold8987_10:232:699:-	-
2782378	GL0061304_V1_[Complete]_[mRNA]_locus=scaffold9049_1:227:763:-	-
2782379	GL0074691_V1_[Complete]_[mRNA]_locus=scaffold9051_3:24:1415:+	-

2782452	GL0032857_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9182_1:828:1478:-	-
2782497	GL0025770_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9259_1:1250:2155:-	-
2782521	GL0005260_V1_[Complete]_[mRNA]_locus=scaffold9297_12:474:908:+	-
2782575	GL0026238_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9412_1:1:726:+	Faecalibacterium prausnitzii
2782896	GL0077182_V1_[Lack_5'-end]_[mRNA]_locus=scaffold9947_1:1:747:+	-
2783433	GL0125792_V1_[Complete]_[mRNA]_locus=scaffold10373_3:4136:4903:-	Bacteroides capillosus
2784091	GL0087270_V1_[Complete]_[mRNA]_locus=scaffold11115_2:1087:2106:-	Firmicutes
2784744	GL0124574_V1_[Complete]_[mRNA]_locus=scaffold11903_9:1510:2781:+	Faecalibacterium prausnitzii
2784823	GL0089618_V1_[Lack_3'-end]_[mRNA]_locus=scaffold12006_1:385:939:+	Firmicutes
2784879	GL0064723_V1_[Complete]_[mRNA]_locus=scaffold12121_4:21:869:-	-
2785051	GL0010781_V1_[Lack_5'-end]_[mRNA]_locus=scaffold12401_1:2:1024:+	Ruminococcus lactaris
2785270	GL0104886_V1_[Complete]_[mRNA]_locus=scaffold12724_3:11019:11897:+	Akkermansia muciniphila
2785377	GL0025491_V1_[Complete]_[mRNA]_locus=scaffold12937_4:2:559:+	-
2785935	GL0085561_V1_[Lack_3'-end]_[mRNA]_locus=scaffold13547_2:170:1087:+	Streptococcus

2786094	GL0084182_V1_[Complete]_[mRNA]_locus=scaffold13764_4:724:1530:+	Akkermansia muciniphila
2786234	GL0000113_V1_[Lack_5'-end]_[mRNA]_locus=scaffold14022_1:2:1360:+	-
2787459	GL0136963_V1_[Lack_3'-end]_[mRNA]_locus=scaffold16079_2:161:802:+	-
2787766	GL0142734_V1_[Complete]_[mRNA]_locus=scaffold16627_2:5584:6561:+	-
2788390	GL0136018_V1_[Complete]_[mRNA]_locus=scaffold17346_3:383:1264:+	-
2788853	GL0078066_V1_[Lack_3'-end]_[mRNA]_locus=scaffold18306_1:1:597:+	-
2789561	GL0006398_V1_[Lack_both_end]_[mRNA]_locus=scaffold19652_3:1:2697:+	Clostridium kluyveri
2789843	GL0068877_V1_[Complete]_[mRNA]_locus=scaffold20111_2:28:939:+	-
2789934	GL0008528_V1_[Complete]_[mRNA]_locus=scaffold20196_5:5683:6522:+	Akkermansia muciniphila
2789935	GL0008531_V1_[Complete]_[mRNA]_locus=scaffold20196_5:8369:9238:+	Akkermansia muciniphila
2790240	GL0097095_V1_[Lack_both_end]_[mRNA]_locus=scaffold20594_1:3:3881:+	Akkermansia muciniphila
2791497	GL0079987_V1_[Lack_5'-end]_[mRNA]_locus=scaffold23122_5:1:210:+	-
2791498	GL0079988_V1_[Complete]_[mRNA]_locus=scaffold23122_5:350:1504:-	-
2792796	GL0109560_V1_[Lack_both_end]_[mRNA]_locus=scaffold25551_1:2:556:+	-

2792907	GL0113010_V1_[Lack_3'-end]_[mRNA]_locus=scaffold25799_2:2:412:-	-
2792915	GL0042760_V1_[Complete]_[mRNA]_locus=scaffold25819_3:484:1311:+	-
2793024	GL0135851_V1_[Complete]_[mRNA]_locus=scaffold26063_2:762:1646:+	-
2793169	GL0101458_V1_[Lack_5'-end]_[mRNA]_locus=scaffold26402_3:40:1545:-	-
2793317	GL0023445_V1_[Complete]_[mRNA]_locus=scaffold26641_2:44:1375:-	-
2794206	GL0085501_V1_[Complete]_[mRNA]_locus=scaffold28418_2:18501:19568:+	Bacteria
2794209	GL0085511_V1_[Complete]_[mRNA]_locus=scaffold28418_2:31090:31536:-	Akkermansia muciniphila
2795185	GL0117681_V1_[Complete]_[mRNA]_locus=scaffold30485_5:52748:53284:-	Akkermansia muciniphila
2795832	GL0132794_V1_[Complete]_[mRNA]_locus=scaffold32409_4:12276:14510:-	Akkermansia muciniphila
2795834	GL0018405_V1_[Complete]_[mRNA]_locus=scaffold32409_5:10258:11727:+	Akkermansia muciniphila
2796417	GL0035962_V1_[Complete]_[mRNA]_locus=scaffold33931_1:465:1592:-	-
2797285	GL0012251_V1_[Complete]_[mRNA]_locus=scaffold36735_1:344:2902:+	Bacteria
2797965	GL0042070_V1_[Complete]_[mRNA]_locus=scaffold39065_2:4767:6659:-	cellular organisms
2797966	GL0134012_V1_[Complete]_[mRNA]_locus=scaffold39065_4:7134:10649:-	Verrucomicrobiales

2798058	GL0038112_V1_[Complete]_[mRNA]_locus=scaffold39438_6:2974:3774:+	Akkermansia muciniphila
2800384	GL0131390_V1_[Complete]_[mRNA]_locus=scaffold46529_1:54494:55582:+	Akkermansia muciniphila
2800560	GL0051019_V1_[Complete]_[mRNA]_locus=scaffold47247_2:476:2734:+	Bacteria
2800823	GL0020802_V1_[Complete]_[mRNA]_locus=scaffold48227_1:5716:8913:+	Akkermansia muciniphila
2803964	GL0122964_V1_[Complete]_[mRNA]_locus=scaffold59651_1:842:2377:-	Akkermansia muciniphila
2803967	GL0003209_V1_[Complete]_[mRNA]_locus=scaffold59651_2:4559:10438:+	Akkermansia muciniphila
2803973	GL0106172_V1_[Complete]_[mRNA]_locus=scaffold59687_2:1840:3492:-	root
2804204	GL0100793_V1_[Lack_5'-end]_[mRNA]_locus=scaffold60668_1:622:1086:-	-
2806331	GL0110731_V1_[Complete]_[mRNA]_locus=scaffold69580_4:24:593:-	Coprococcus comes
2811106	GL0100596_V1_[Complete]_[mRNA]_locus=scaffold87737_2:125:679:-	Bacteroides stercoris
2817386	GL0104232_unmapped_[Complete]_[mRNA]_locus=scaffold413_1:83:934:+	Anaerostipes caccae
2817952	GL0402307_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold1530_1:2264:3112:+	Clostridium methylpentosum
2818424	GL0302751_unmapped_[Complete]_[mRNA]_locus=scaffold2427_1:1:237:+	Desulfitobacterium hafniense
2818425	GL0302753_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold2427_1:581:1180:+	Clostridiales

2818630	GL0363913_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold2779_2:3:281:-	Clostridium
2819671	GL0538118_unmapped_[Complete]_[mRNA]_locus=scaffold4855_1:471:665:-	Clostridium
2820028	GL0197155_unmapped_[Complete]_[mRNA]_locus=scaffold5396_4:2197:3381:+	Ruminococcus obeum
2820475	GL0147630_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold6296_1:947:1129:+	-
2820686	GL0277059_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold6839_1:746:1147:+	-
2820910	GL0587580_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold7314_2:334:1878:+	Bacteroides capillosus
2821372	GL0104460_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold8427_2:1043:3532:+	Roseburia inulinivorans
2821571	GL0632470_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold8885_2:118:999:-	Dorea longicatena
2822733	GL0615990_unmapped_[Complete]_[mRNA]_locus=scaffold10903_2:31:1068:-	Dorea longicatena
2822734	GL0615991_unmapped_[Complete]_[mRNA]_locus=scaffold10903_2:1072:1308:-	Dorea longicatena
2825548	GL0092702_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold16768_1:3:581:+	Clostridium leptum
2825587	GL0336501_unmapped_[Complete]_[mRNA]_locus=scaffold16880_2:116:1066:+	Clostridium asparagiforme
2826861	GL0478466_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold19497_2:2:1135:+	Dorea formicigenerans
2827483	GL0343762_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold20687_4:2:940:+	Catenibacterium mitsuokai

2827728	GL0129816_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold21083_1:1:351:+	Anaerotruncus colihominis
2827729	GL0129817_unmapped_[Complete]_[mRNA]_locus=scaffold21083_1:508:876:+	Clostridium
2828032	GL0428891_unmapped_[Complete]_[mRNA]_locus=scaffold21639_1:96:392:-	Clostridiales
2828243	GL0484659_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold22061_1:1:546:+	-
2828437	GL0125428_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold22392_2:2:1687:-	Clostridium methylpentosum
2828484	GL0232460_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold22517_1:3:584:+	Clostridium
2828775	GL0427886_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold22972_2:2:793:+	Clostridium hylemonae
2828806	GL0539934_unmapped_[Complete]_[mRNA]_locus=scaffold23015_3:214:1104:-	Clostridium leptum
2828905	GL0499490_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold23212_3:2:406:-	Clostridium leptum
2832821	GL0465491_unmapped_[Complete]_[mRNA]_locus=scaffold31219_1:158:688:+	Clostridium leptum
2833000	GL0353132_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold31604_1:488:1351:+	Anaerotruncus colihominis
2833133	GL0334711_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold31883_3:2:517:+	Clostridium asparagiforme
2833280	GL0406581_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold32281_1:2:793:-	-
2833281	GL0304814_unmapped_[Complete]_[mRNA]_locus=scaffold32281_3:9:1256:-	Clostridium cellulovorans

2833282	GL0304815_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold32281_3:1249:1737:-	-
2833283	GL0036354_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold32281_4:1:702:-	Clostridiales
2833892	GL0270745_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold33344_3:3:713:+	Akkermansia muciniphila
2834211	GL0141781_unmapped_[Complete]_[mRNA]_locus=scaffold33970_2:169:450:+	Clostridiales
2834915	GL0261921_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold35374_3:296:1201:+	Clostridium scindens
2835714	GL0322795_unmapped_[Complete]_[mRNA]_locus=scaffold36971_3:286:615:+	Clostridiales
2835799	GL0053607_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold37141_2:2:529:-	-
2836205	GL0305940_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold37936_1:1:324:+	Clostridiales
2838335	GL0431021_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold42382_2:2:523:-	Clostridium methylpentosum
2838336	GL0538287_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold42382_3:3:689:-	Ruminococcus torques
2838481	GL0079075_unmapped_[Complete]_[mRNA]_locus=scaffold42655_2:497:931:-	Bacteroides capillosus
2838652	GL0627126_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold42987_1:3:1289:-	Eubacterium hallii
2838673	GL0588447_unmapped_[Complete]_[mRNA]_locus=scaffold43005_1:1383:1889:+	Ruminococcus gnavus
2838675	GL0588449_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold43005_1:2493:3224:-	Clostridium leptum

2839275	GL0523304_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold44341_2:202:741:-	Clostridium thermocellum
2839586	GL0352871_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold45079_2:103:1425:-	Clostridium cellulolyticum
2839636	GL0632595_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold45176_3:1:774:+	Clostridium
2839746	GL0246270_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold45386_3:1:573:+	Ruminococcus gnavus
2840608	GL0261968_unmapped_[Complete]_[mRNA]_locus=scaffold47339_3:718:1317:+	Firmicutes
2840790	GL0596995_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold47606_3:2:727:+	Clostridium leptum
2841549	GL0065199_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold49214_1:3:1742:-	Bacteria
2841550	GL0518421_unmapped_[Complete]_[mRNA]_locus=scaffold49215_1:34:348:+	-
2842585	GL0236313_unmapped_[Complete]_[mRNA]_locus=scaffold51529_3:553:1011:-	Faecalibacterium prausnitzii
2842586	GL0236314_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold51529_3:1171:1449:+	Clostridium methylpentosum
2843369	GL0625936_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold53262_1:330:989:-	Clostridium
2843778	GL0509871_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold54227_1:2:808:-	Ruminococcus obeum
2844619	GL0183285_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold56164_3:1180:1602:-	-
2845111	GL0392473_unmapped_[Complete]_[mRNA]_locus=scaffold57247_1:338:1075:-	Blautia hydrogenotrophica

2845175	GL0017568_unmapped_[Complete]_[mRNA]_locus=scaffold57380_2:122:967:+	Clostridiales
2846166	GL0129654_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold59792_2:117:797:+	Clostridiales
2846170	GL0052336_unmapped_[Complete]_[mRNA]_locus=scaffold59792_4:337:1620:+	Thermoanaerobacter tengcongensis
2846174	GL0205230_unmapped_[Complete]_[mRNA]_locus=scaffold59792_7:387:1256:+	Clostridiales
2846518	GL0514990_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold60518_3:1:513:-	Bacteroides capillosus
2846663	GL0115066_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold60801_1:459:677:+	Clostridium leptum
2846664	GL0302699_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold60801_2:2:742:+	Clostridium leptum
2846695	GL0326280_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold60861_5:305:790:-	Akkermansia muciniphila
2846750	GL0406476_unmapped_[Complete]_[mRNA]_locus=scaffold60925_1:114:1019:-	Clostridium leptum
2847183	GL0188132_unmapped_[Complete]_[mRNA]_locus=scaffold61966_3:162:881:-	Anaerostipes caccae
2847313	GL0588089_unmapped_[Complete]_[mRNA]_locus=scaffold62235_2:33:1118:+	Clostridium
2847532	GL0386935_unmapped_[Complete]_[mRNA]_locus=scaffold62744_2:698:1462:-	-
2848905	GL0329924_unmapped_[Complete]_[mRNA]_locus=scaffold65451_1:190:360:+	-

2848907	GL0309160_unmapped_[Complete]_[mRNA]_locus =scaffold65451_2:196:399:+	Clostridiales
2848911	GL0438669_unmapped_[Complete]_[mRNA]_locus =scaffold65451_3:2444:3118:+	Clostridium asparagiforme
2849050	GL0066064_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold65759_2:935:1429:-	Clostridium leptum
2849053	GL0413313_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold65759_4:141:533:-	Clostridium leptum
2849704	GL0070731_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold67163_3:2:979:+	-
2851451	GL0473474_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold70827_3:539:1108:+	-
2851685	GL0099455_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold71452_1:20:652:+	Clostridium leptum
2852078	GL0583324_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold72367_1:268:591:-	Anaerostipes caccae
2852142	GL0482324_unmapped_[Complete]_[mRNA]_locus =scaffold72489_2:1529:1963:-	-
2853629	GL0355686_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold75985_1:1:558:-	-
2854366	GL0197671_unmapped_[Complete]_[mRNA]_locus =scaffold77471_1:129:899:-	Clostridium botulinum
2855394	GL0418353_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold79847_1:88:522:+	Bacteria
2855977	GL0224942_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold81181_4:3:1037:-	-
2856022	GL0290534_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold81301_3:74:607:-	Clostridium leptum

2856644	GL0531443_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold82619_1:3:956:-	Bacteria
2857155	GL0344365_unmapped_[Complete]_[mRNA]_locus=scaffold83770_8:55:1038:+	Ruminococcus obeum
2857452	GL0031959_unmapped_[Complete]_[mRNA]_locus=scaffold84431_1:1872:2408:-	Blautia hydrogenotrophica
2857550	GL0284119_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold84623_1:3:275:-	Clostridiales
2857604	GL0478844_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold84765_1:3:611:-	Clostridium methylpentosum
2857740	GL0131270_unmapped_[Complete]_[mRNA]_locus=scaffold85053_1:414:1157:+	Akkermansia muciniphila
2857851	GL0514855_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold85285_1:3:668:-	Clostridium methylpentosum
2858335	GL0208361_unmapped_[Complete]_[mRNA]_locus=scaffold86491_3:230:1435:+	Ruminococcus gnavus
2858507	GL0166532_unmapped_[Complete]_[mRNA]_locus=scaffold86879_2:721:1221:+	-
2860943	GL0611449_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold92245_1:3:875:-	Clostridium scindens
2860944	GL0611450_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold92245_1:1002:1220:+	Bacteroides capillosus
2861064	GL0457016_unmapped_[Complete]_[mRNA]_locus=scaffold92566_1:66:479:-	Clostridiales
2861166	GL0236461_unmapped_[Complete]_[mRNA]_locus=scaffold92765_3:236:727:-	Clostridium leptum
2861640	GL0327982_unmapped_[Complete]_[mRNA]_locus=scaffold93697_1:97:444:+	Clostridium leptum

2861641	GL0199552_unmapped_[Complete]_[mRNA]_locus =scaffold93697_2:147:686:+	Clostridium leptum
2861643	GL0425526_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold93697_3:3:962:+	Clostridium leptum
2861927	GL0621195_unmapped_[Lack_5'- end]_[mRNA]_locus=scaffold94265_1:3:323:+	Thermotoga
2861928	GL0621196_unmapped_[Lack_5'- end]_[mRNA]_locus=scaffold94265_1:328:975:-	Clostridium leptum
2862785	GL0274487_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold96184_1:124:600:+	Clostridium leptum
2862845	GL0268856_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold96367_1:3:137:-	Clostridium bolteae
2863411	GL0561814_unmapped_[Complete]_[mRNA]_locus =scaffold97631_3:393:632:-	Clostridiales
2863632	GL0151618_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold98137_2:421:1056:+	Bacteria
2864155	GL0264197_unmapped_[Complete]_[mRNA]_locus =scaffold99241_2:261:512:+	Clostridiales
2864460	GL0587545_unmapped_[Complete]_[mRNA]_locus =scaffold99942_1:550:1293:+	Clostridium leptum
2864468	GL0625137_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold99949_1:279:644:+	Clostridiales
2864496	GL0453788_unmapped_[Complete]_[mRNA]_locus =scaffold100001_2:4174:5598:+	Clostridiales
2864714	GL0265534_unmapped_[Complete]_[mRNA]_locus =scaffold100464_1:192:1052:+	Clostridium bolteae
2864715	GL0265535_unmapped_[Complete]_[mRNA]_locus =scaffold100464_1:1068:1934:+	-

2865598	GL0281093_unmapped_[Complete]_[mRNA]_locus =scaffold102288_2:959:1522:-	Coprococcus comes
2865627	GL0129021_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold102344_1:1:555:+	Clostridium leptum
2865648	GL0464466_unmapped_[Complete]_[mRNA]_locus =scaffold102415_1:46:489:-	Clostridium leptum
2866222	GL0146001_unmapped_[Complete]_[mRNA]_locus =scaffold103575_3:740:1120:+	-
2866234	GL0090044_unmapped_[Complete]_[mRNA]_locus =scaffold103598_4:1156:1944:+	Akkermansia muciniphila
2866254	GL0593532_unmapped_[Complete]_[mRNA]_locus =scaffold103640_1:516:992:-	-
2866330	GL0298315_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold103783_2:2:1336:-	Ruminococcus obeum
2866332	GL0638198_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold103788_2:3:932:+	Eubacterium biforme
2866622	GL0090305_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold104406_2:137:640:+	Clostridium spiroforme
2867125	GL0546090_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold105654_1:2:544:+	Clostridium leptum
2867350	GL0396680_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold106305_1:333:605:+	Alkaliphilus oremlandii
2867800	GL0019873_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold107404_1:2294:3217:-	Clostridium hylemonae
2868371	GL0077545_unmapped_[Complete]_[mRNA]_locus =scaffold108878_2:309:1244:+	Clostridium methylpentosum

2868640	GL0161323_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold109693_1:3:428:+	-
2868716	GL0513489_unmapped_[Complete]_[mRNA]_locus=scaffold109913_1:541:1113:+	Faecalibacterium prausnitzii
2868832	GL0283687_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold110188_1:3:704:-	Firmicutes
2868835	GL0397697_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold110188_2:1:363:+	Clostridiales
2868991	GL0191546_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold110613_1:1:303:-	Ruminococcus gnavus
2868993	GL0058436_unmapped_[Complete]_[mRNA]_locus=scaffold110613_2:121:513:-	-
2869573	GL0108197_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold111898_1:2:577:+	Clostridium leptum
2869593	GL0065722_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold111955_1:2:502:-	Clostridium scindens
2869691	GL0601356_unmapped_[Complete]_[mRNA]_locus=scaffold112186_2:22:462:+	Clostridiales
2870217	GL0166035_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold113487_2:1:447:+	Clostridium leptum
2870526	GL0603265_unmapped_[Complete]_[mRNA]_locus=scaffold114227_1:3:332:+	-
2870613	GL0485805_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold114406_4:3:971:+	Blautia hydrogenotrophica
2870772	GL0454553_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold114725_1:817:1029:-	cellular organisms
2871710	GL0515338_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold116927_1:400:894:-	Clostridium leptum

2871918	GL0093270_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold117324_2:2:346:+	-
2872450	GL0615036_unmapped_[Complete]_[mRNA]_locus=scaffold118598_2:115:1110:+	Dorea formicigenerans
2872483	GL0310188_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold118678_2:2:1141:+	Bacteroides capillosus
2872558	GL0636540_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold118873_1:3:323:-	Clostridium methylpentosum
2873171	GL0159742_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold120046_1:77:805:+	Ruminococcus obeum
2873545	GL0328159_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold120863_1:3:452:+	Thermoanaerobacter
2873616	GL0003333_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold121011_2:3:431:-	Clostridium
2874499	GL0394006_unmapped_[Complete]_[mRNA]_locus=scaffold122999_4:172:771:-	Clostridium beijerinckii
2874707	GL0263430_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold123496_1:2:1762:-	Clostridium hylemonae
2874720	GL0018756_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold123525_2:1:465:+	Clostridium leptum
2874734	GL0168163_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold123554_2:201:719:+	Clostridium
2875296	GL0449475_unmapped_[Complete]_[mRNA]_locus=scaffold124821_1:120:353:-	-
2875440	GL0183546_unmapped_[Complete]_[mRNA]_locus=scaffold125233_1:13:666:-	Clostridium nexile
2875830	GL0577167_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold126247_3:2:475:+	Dorea

2875864	GL0234782_unmapped_[Complete]_[mRNA]_locus =scaffold126292_2:336:1136:-	-
2875949	GL0083699_unmapped_[Complete]_[mRNA]_locus =scaffold126510_1:220:1260:+	Clostridium asparagiforme
2876004	GL0596240_unmapped_[Complete]_[mRNA]_locus =scaffold126614_2:342:767:-	Thermoanaerobacter pseudethanolicus
2876246	GL0311110_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold127360_3:1:450:+	-
2876272	GL0000930_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold127421_1:1:645:-	Clostridiales
2876552	GL0600564_unmapped_[Complete]_[mRNA]_locus =scaffold128126_1:358:1494:+	-
2877438	GL0180479_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold130122_1:1:648:+	Ruminococcus
2877833	GL0626934_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold130841_2:2:559:+	-
2878129	GL0284778_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold131651_2:1:1368:+	Clostridium leptum
2878133	GL0392399_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold131683_2:1:606:+	Clostridiales
2878373	GL0040281_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold132217_1:3:581:-	Clostridium difficile
2878730	GL0342228_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold132958_1:1:309:+	Clostridium leptum
2878732	GL0342230_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold132958_1:635:1141:-	Eubacterium siraeum

2878746	GL0573507_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold132993_2:2:751:+	-
2879615	GL0270578_unmapped_[Complete]_[mRNA]_locus=scaffold134925_1:57:269:-	Clostridium bartlettii
2879652	GL0545802_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold135003_1:1266:1622:-	Clostridium
2881179	GL0099276_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold138694_1:1:645:+	Roseburia inulinivorans
2881265	GL0610620_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold138862_1:2:532:+	Clostridium cellulolyticum
2881812	GL0417702_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold140145_1:3:839:-	Actinobacillus
2881963	GL0566163_unmapped_[Complete]_[mRNA]_locus=scaffold140410_3:2098:3213:-	-
2882125	GL0094703_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold140883_1:3:392:+	Clostridium leptum
2882729	GL0012175_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold142223_2:1:825:-	Ruminococcus obeum
2882897	GL0055711_unmapped_[Complete]_[mRNA]_locus=scaffold142580_1:800:1144:+	Firmicutes
2884183	GL0361172_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold145442_1:1:558:+	Ruminococcus torques
2884192	GL0446221_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold145457_3:3:1409:+	Akkermansia muciniphila
2884756	GL0462317_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold146843_1:28:840:-	Clostridium leptum

2885064	GL0121551_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold147555_3:1:381:-	Clostridiales
2885801	GL0617942_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold149353_2:1:549:+	Firmicutes
2885903	GL0414334_unmapped_[Complete]_[mRNA]_locus=scaffold149541_2:2154:3011:-	Ruminococcus obeum
2885993	GL0022937_unmapped_[Complete]_[mRNA]_locus=scaffold149832_1:215:1129:+	Bacteroides capillosus
2886318	GL0424691_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold150625_1:355:837:-	Dorea formicigenerans
2886518	GL0347273_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold151038_1:156:515:-	Clostridium scindens
2887292	GL0197352_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold153038_2:2:652:+	Clostridium leptum
2887359	GL0557144_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold153248_1:1:408:+	Clostridium nexile
2888647	GL0092620_unmapped_[Complete]_[mRNA]_locus=scaffold156738_3:38:478:+	Clostridium leptum
2888874	GL0092997_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold157396_2:820:1341:+	Clostridium asparagiforme
2889088	GL0495719_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold157954_1:2:664:+	Clostridium leptum
2890259	GL0228673_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold161236_2:2:571:+	-
2890314	GL0380789_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold161387_2:41:622:-	-
2890357	GL0633200_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold161504_2:144:1016:-	-

2890533	GL0125526_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold162036_2:1:468:+	Anaerotruncus colihominis
2890992	GL0354285_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold163203_1:201:566:+	-
2891806	GL0552045_unmapped_[Complete]_[mRNA]_locus=scaffold165398_1:170:691:+	Clostridium hylemonae
2893252	GL0291013_unmapped_[Complete]_[mRNA]_locus=scaffold168914_1:123:395:+	Bacteroides pectinophilus
2893254	GL0098756_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold168914_2:2:220:+	Roseburia inulinivorans
2893256	GL0098758_unmapped_[Complete]_[mRNA]_locus=scaffold168914_2:1263:1673:+	Clostridium
2893527	GL0351785_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold169510_2:1:894:-	Clostridium nexile
2893697	GL0023005_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold169939_3:2:649:+	Clostridium leptum
2893698	GL0023006_unmapped_[Complete]_[mRNA]_locus=scaffold169939_3:662:985:+	Bacteria
2893741	GL0335083_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold170081_1:333:680:-	Clostridium
2894426	GL0478519_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold171692_2:2:592:+	Eubacterium hallii
2895107	GL0450691_unmapped_[Complete]_[mRNA]_locus=scaffold173301_1:1219:2052:-	Clostridium asparagiforme
2896861	GL0299191_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold177542_2:834:1034:+	Clostridiales
2897521	GL0132775_unmapped_[Complete]_[mRNA]_locus=scaffold179176_1:833:1402:-	-

2897758	GL0406610_unmapped_[Complete]_[mRNA]_locus=scaffold179785_1:66:1058:+	Bacteroides capillosus
2897759	GL0406611_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold179785_1:1216:1503:+	Dorea formicigenerans
2898377	GL0457838_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold181355_1:2:559:-	Clostridium leptum
2898886	GL0032355_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold182640_1:2:550:+	Clostridiales
2899225	GL0154574_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold183494_1:1:927:+	Ruminococcus obeum
2901930	GL0207034_unmapped_[Complete]_[mRNA]_locus=scaffold189876_2:317:754:-	-
2902358	GL0382686_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold190953_1:3:344:+	Clostridium leptum
2902456	GL0480223_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold191235_1:79:1056:+	Clostridium nexile
2902500	GL0036993_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold191334_1:101:883:+	Victivallis vadensis
2902917	GL0280365_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold192385_1:3:854:+	Clostridium leptum
2903503	GL0205316_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold193684_2:127:519:+	Bacteria
2903766	GL0519579_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold194383_1:2:247:-	Clostridium leptum
2903881	GL0316877_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold194679_2:1:573:-	Clostridium leptum

2903973	GL0210637_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold194857_1:2116:2316:+	Ruminococcus gnavus
2904417	GL0027000_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold195990_1:3:725:+	Bacillus amyloliquefaciens
2905480	GL0331118_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold198611_1:174:1169:+	Firmicutes
2905555	GL0376101_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold198807_3:1:342:-	Firmicutes
2905556	GL0376102_unmapped_[Complete]_[mRNA]_locus=scaffold198807_3:317:1375:-	Clostridium bartlettii
2905887	GL0485451_unmapped_[Complete]_[mRNA]_locus=scaffold199771_1:1310:2506:+	Ruminococcus obeum
2906174	GL0408875_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold200521_3:3:491:+	Roseburia inulinivorans
2906297	GL0427294_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold200855_1:234:572:+	Clostridium leptum
2907710	GL0428291_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold204655_2:760:1233:-	Clostridium leptum
2907940	GL0638352_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold205345_1:2:490:+	-
2908290	GL0295345_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold206131_1:861:1403:+	-
2909039	GL0636352_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold208123_1:352:681:-	Clostridium leptum
2909127	GL0417772_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold208311_2:301:1119:-	Clostridium leptum

2909336	GL0047211_unmapped_[Complete]_[mRNA]_locus =scaffold208752_1:1:549:+	Coprococcus comes
2909705	GL0235539_unmapped_[Complete]_[mRNA]_locus =scaffold209810_2:256:981:-	Blautia hydrogenotrophica
2910073	GL0259151_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold210771_1:383:733:+	Bacteria
2910398	GL0020340_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold211552_2:2:433:+	Clostridium leptum
2911032	GL0415693_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold213114_1:2:925:-	Eubacterium hallii
2911071	GL0554994_unmapped_[Complete]_[mRNA]_locus =scaffold213224_1:178:882:+	Clostridium asparagiforme
2911297	GL0143719_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold213863_1:2:556:+	Holdemania filiformis
2911964	GL0614181_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold215564_1:3:755:+	Anaerotruncus colihominis
2912180	GL0464742_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold216238_2:2:421:+	Desulfitobacterium hafniense
2912207	GL0345630_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold216310_1:719:1462:+	-
2912323	GL0391791_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold216540_4:742:954:-	Clostridiales
2913325	GL0374087_unmapped_[Complete]_[mRNA]_locus =scaffold219063_3:248:799:-	-
2914564	GL0318435_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold222475_1:1:399:+	-
2914873	GL0487645_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold223316_2:1:792:-	Eubacterium hallii

2915023	GL0623010_unmapped_[Complete]_[mRNA]_locus =scaffold223622_2:979:1719:-	-
2915037	GL0328492_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold223645_1:1:594:+	-
2915135	GL0348016_unmapped_[Complete]_[mRNA]_locus =scaffold223900_5:2584:3504:+	Clostridium
2915709	GL0565552_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold225143_2:2:598:-	Clostridiales
2915814	GL0183913_unmapped_[Complete]_[mRNA]_locus =scaffold225382_1:288:1100:-	-
2916554	GL0258467_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold227496_2:284:868:+	Enterococcus faecium
2916755	GL0030145_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold228036_1:3:1142:-	Blautia hydrogenotrophica
2916813	GL0197423_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold228203_1:1:804:+	Brevibacillus brevis
2918624	GL0284663_unmapped_[Complete]_[mRNA]_locus =scaffold233117_1:1267:2028:-	Clostridium
2918667	GL0372559_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold233209_3:3:809:-	Anaerotruncus colihominis
2918951	GL0034577_unmapped_[Complete]_[mRNA]_locus =scaffold234031_1:1:264:+	Bacteroides uniformis
2919049	GL0230076_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold234266_1:3:500:-	Clostridiales
2919135	GL0453165_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold234563_2:56:598:+	Clostridium bartlettii
2920261	GL0120824_unmapped_[Complete]_[mRNA]_locus =scaffold237642_1:101:1477:+	-

2921326	GL0344577_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold240420_3:2:1150:+	-
2921853	GL0361944_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold241836_1:3:842:+	Clostridium hylemonae
2922056	GL0432716_unmapped_[Complete]_[mRNA]_locus=scaffold242332_2:10:408:-	Coprococcus comes
2922241	GL0344944_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold242886_1:1:441:+	Coprococcus comes
2922652	GL0601386_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold243863_1:325:870:+	Dorea longicatena
2924264	GL0391757_unmapped_[Complete]_[mRNA]_locus=scaffold248226_1:88:1284:-	Firmicutes
2924266	GL0298054_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold248226_2:2:634:-	-
2925171	GL0545946_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold250717_2:3:467:+	Ruminococcus obeum
2925727	GL0038591_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold252118_1:238:1434:+	Clostridium
2925754	GL0220414_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold252158_1:436:930:+	-
2926252	GL0607342_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold253606_4:2:595:-	Anaerotruncus colihominis
2926580	GL0422077_unmapped_[Complete]_[mRNA]_locus=scaffold254522_1:3:317:+	Clostridium spiroforme
2926581	GL0422078_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold254522_1:335:1000:+	Clostridium leptum
2927022	GL0126485_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold255673_1:1251:1925:	Clostridium leptum

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2927528	GL0265557_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold257105_1:3:545:+	Clostridium leptum
2928153	GL0337306_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold258675_1:1:630:-	Clostridium leptum
2928154	GL0337307_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold258675_1:791:1141:+	Clostridium ramosum
2928313	GL0417431_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold259025_1:2:934:+	Blautia hydrogenotrophica
2928581	GL0053044_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold259700_1:147:875:+	Blautia hydrogenotrophica
2928583	GL0184314_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold259700_2:182:832:+	-
2928960	GL0600336_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold260678_1:3:797:-	Ruminococcus obeum
2930085	GL0201340_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold263702_1:3:503:-	Clostridium leptum
2930087	GL0201342_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold263702_1:1238:1789:-	Clostridium leptum
2930843	GL0531939_unmapped_[Complete]_[mRNA]_locus=scaffold265722_2:51:395:-	Ruminococcus obeum
2930936	GL0446037_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold265963_2:1:321:+	Clostridium
2931027	GL0537119_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold266174_1:3:692:-	-

2931235	GL0627146_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold266758_2:3:572:-	Ruminococcus obeum
2931536	GL0561927_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold267695_3:1:741:-	Bacteroides capillosus
2932614	GL0554076_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold270347_3:1:585:-	Bacteroides capillosus
2933113	GL0354953_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold271816_1:1:1662:-	-
2933822	GL0377967_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold273663_1:1:570:+	Clostridium leptum
2934335	GL0135537_unmapped_[Complete]_[mRNA]_locus=scaffold275067_1:78:863:+	Clostridium nexile
2934612	GL0020383_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold275751_4:1:276:+	Firmicutes
2935283	GL0342495_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold277439_2:1:177:-	-
2935710	GL0021329_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold278545_2:2:802:+	-
2936251	GL0341141_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold280171_1:3:341:-	Clostridium spiroforme
2936874	GL0435352_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold281751_1:2:712:+	Clostridium leptum
2937052	GL0381744_unmapped_[Complete]_[mRNA]_locus=scaffold282179_1:554:1027:-	Coprococcus comes
2937056	GL0111980_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold282179_4:1:570:-	-
2937632	GL0115601_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold283804_1:1:456:-	Clostridium bolteae

2937878	GL0265424_unmapped_[Complete]_[mRNA]_locus=scaffold284564_1:1:357:+	Clostridiales
2937882	GL0365892_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold284574_1:1056:1340:-	Bacteria
2937958	GL0582521_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold284784_2:1237:1635:-	Eubacterium ventriosum
2938082	GL0248017_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold285051_1:44:508:-	Thermoanaerobacteraceae
2938411	GL0092064_unmapped_[Complete]_[mRNA]_locus=scaffold285998_1:132:1028:-	Clostridium leptum
2939389	GL0280202_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold288631_2:1:588:-	-
2940010	GL0614734_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold290194_3:2:775:-	Clostridium leptum
2940612	GL0569556_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold291725_2:3:587:+	Clostridium leptum
2940932	GL0145154_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold292571_1:1:966:+	Bacteroides coprocola
2941253	GL0148542_unmapped_[Complete]_[mRNA]_locus=scaffold293239_1:2825:3577:-	Anaerotruncus colihominis
2941349	GL0249520_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold293508_1:1:951:+	Blautia hydrogenotrophica
2941383	GL0034949_unmapped_[Complete]_[mRNA]_locus=scaffold293606_2:2:436:+	Clostridium leptum
2941384	GL0034950_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold293606_2:436:1362:+	Clostridium leptum

2942117	GL0390217_unmapped_[Complete]_[mRNA]_locus =scaffold295353_1:450:1280:-	Clostridium
2942543	GL0040318_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold296490_2:2:952:-	-
2942981	GL0329687_unmapped_[Lack_5'- end]_[mRNA]_locus=scaffold297567_1:1:594:+	Clostridium leptum
2943128	GL0009404_unmapped_[Complete]_[mRNA]_locus =scaffold297918_1:181:939:+	Ruminococcus obeum
2943136	GL0521684_unmapped_[Lack_5'- end]_[mRNA]_locus=scaffold297924_1:225:1310:-	Atopobium rimae
2943358	GL0063615_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold298615_2:1:726:-	Clostridium leptum
2943440	GL0089310_unmapped_[Complete]_[mRNA]_locus =scaffold298804_1:1107:1859:+	-
2944280	GL0089551_unmapped_[Complete]_[mRNA]_locus =scaffold301130_2:233:1207:-	Clostridium leptum
2945265	GL0096120_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold303781_1:249:743:+	Blautia hydrogenotrophica
2945347	GL0376235_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold304034_1:3:827:-	Alkaliphilus oremlandii
2945850	GL0357283_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold305446_4:1:291:-	Dorea longicatena
2946485	GL0203647_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold307282_2:2:982:+	Bacteroidales
2946550	GL0052374_unmapped_[Lack_3'- end]_[mRNA]_locus=scaffold307440_1:39:905:+	Lysinibacillus sphaericus
2947056	GL0065134_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold308988_1:2:571:+	-

2947153	GL0127403_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold309302_2:1:1302:+	Clostridium
2947639	GL0461761_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold310839_2:1:294:-	Clostridium hylemonae
2948909	GL0573292_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold314196_2:2:745:+	Clostridium
2949497	GL0558010_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold316058_1:3:800:+	Clostridium leptum
2951408	GL0102029_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold321698_2:3:575:-	Eubacterium ventriosum
2951409	GL0102030_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold321698_2:597:1583:-	Clostridium leptum
2951498	GL0439614_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold321909_2:1:789:+	Clostridiales
2952093	GL0372016_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold323548_2:3:902:-	Bacteroides capillosus
2952094	GL0524171_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold323548_3:1:513:-	Clostridium leptum
2952265	GL0123616_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold324099_1:784:1020:+	Clostridiales
2952411	GL0269145_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold324522_3:505:1176:+	Anaerostipes caccae
2953450	GL0532175_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold327332_1:1747:2034:+	Clostridium nexile
2954512	GL0239215_unmapped_[Complete]_[mRNA]_locus=scaffold330509_2:35:1618:-	Eubacterium siraeum

2954885	GL0364539_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold331380_1:3:647:-	Clostridium bolteae
2955989	GL0062438_unmapped_[Complete]_[mRNA]_locus=scaffold334609_2:537:1286:-	Clostridium butyricum
2958581	GL0035646_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold342028_1:3:1028:-	Clostridium leptum
2958932	GL0477010_unmapped_[Complete]_[mRNA]_locus=scaffold342989_2:333:884:-	Clostridium leptum
2959310	GL0373468_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold344039_1:1:285:+	Bacilli
2959853	GL0306367_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold345686_2:1:627:+	Clostridium asparagiforme
2960249	GL0601903_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold346876_1:2:664:+	Clostridium methylpentosum
2960529	GL0010011_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold347685_2:145:912:-	Bacteroides capillosus
2960797	GL0034094_unmapped_[Complete]_[mRNA]_locus=scaffold348326_1:293:1195:+	Clostridium hylemonae
2960824	GL0584743_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold348397_1:3:416:+	Clostridium leptum
2960968	GL0350868_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold348776_1:3:296:+	Bacteria
2961327	GL0205376_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold349874_1:3:236:-	Clostridiales
2961328	GL0205377_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold349874_1:273:530:-	Anaerotruncus colihominis
2961495	GL0419798_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold350339_1:640:1134:+	Ruminococcus obeum

2962444	GL0052758_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold353174_1:2:274:-	Ruminococcus torques
2963825	GL0440046_unmapped_[Complete]_[mRNA]_locus=scaffold356889_2:2255:2590:-	-
2963939	GL0255686_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold357176_1:1:429:-	Clostridium asparagiforme
2964246	GL0124326_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold358052_2:579:1013:+	-
2965473	GL0127765_unmapped_[Complete]_[mRNA]_locus=scaffold361382_1:1954:2493:+	Clostridiales
2967215	GL0233735_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold366243_1:184:786:+	Bacteria
2967821	GL0586371_unmapped_[Complete]_[mRNA]_locus=scaffold368213_2:1596:2459:+	Bacteria
2967978	GL0402775_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold368627_1:1:861:+	-
2969876	GL0463661_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold373989_1:194:982:+	Clostridium leptum
2972008	GL0422437_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold380533_1:30:530:+	Clostridium leptum
2972396	GL0557734_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold381523_3:2:871:+	Bacteria
2973650	GL0030950_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold385194_1:1:126:-	-
2974534	GL0107417_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold387503_1:48:953:-	Streptococcus pneumoniae
2975060	GL0538711_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold389091_1:1:576:+	Clostridium leptum

2975366	GL0470659_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold389954_3:3:965:+	-
2975455	GL0522535_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold390170_2:2:535:+	Clostridium leptum
2975808	GL0337791_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold391175_1:1:930:-	Clostridium leptum
2976181	GL0136225_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold392336_2:1:234:-	-
2976576	GL0448155_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold393489_1:1:741:-	Ruminococcus gnavus
2976868	GL0306815_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold394364_1:286:1674:+	-
2978137	GL0093144_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold398270_1:2:781:-	-
2978398	GL0637982_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold398905_2:1:789:-	Clostridium methylpentosum
2978720	GL0347677_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold399890_1:1:306:-	Clostridium
2981727	GL0381253_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold408451_1:1:261:-	Clostridium
2981875	GL0392909_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold409022_2:1:555:+	-
2982680	GL0024922_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold411417_2:1:591:-	-
2983526	GL0124116_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold413951_1:2:640:-	-
2983529	GL0099674_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold413951_2:76:588:+	Clostridium

2984814	GL0026883_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold417789_1:1403:1639:+	Clostridiales
2985125	GL0594419_unmapped_[Complete]_[mRNA]_locus=scaffold418663_1:344:1012:+	Bacteroides pectinophilus
2986582	GL0262333_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold423145_1:3:476:-	Clostridium leptum
2987488	GL0166022_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold425879_5:30:1223:+	Eubacterium ventriosum
2987534	GL0312490_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold426008_1:1:1272:+	-
2987841	GL0620975_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold426857_1:2:457:+	Akkermansia muciniphila
2987850	GL0168000_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold426894_3:616:768:+	-
2988815	GL0528825_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold429835_1:3:599:+	Clostridium cellulolyticum
2988880	GL0084329_unmapped_[Complete]_[mRNA]_locus=scaffold430032_1:129:695:-	cellular organisms
2989345	GL0249183_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold431556_1:295:669:+	-
2989508	GL0099373_unmapped_[Complete]_[mRNA]_locus=scaffold432159_2:1:1251:+	Clostridium leptum
2989565	GL0333622_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold432337_2:1:951:-	Clostridium methylpentosum
2989821	GL0360188_unmapped_[Complete]_[mRNA]_locus=scaffold433109_1:494:1081:+	Clostridium phytofermentans

2991371	GL0416303_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold437948_5:1:555:+	Clostridium phytofermentans
2992266	GL0324031_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold440641_1:441:893:+	Desulfitobacterium hafniense
2992570	GL0382003_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold441545_1:2:574:-	Eubacterium siraeum
2994055	GL0016788_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold446308_1:3:974:+	-
2994835	GL0605203_unmapped_[Complete]_[mRNA]_locus=scaffold448857_1:56:379:-	Bacillus
2994961	GL0245802_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold449200_1:3:1664:+	Clostridium leptum
2995392	GL0329855_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold450562_4:2:1222:+	Bacteria
2995763	GL0125140_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold451858_3:10344:10601:-	Clostridium
2997120	GL0039901_unmapped_[Complete]_[mRNA]_locus=scaffold455953_1:586:1452:-	-
2998447	GL0014115_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold459913_1:2:1195:+	Clostridium leptum
2998761	GL0305303_unmapped_[Complete]_[mRNA]_locus=scaffold460851_1:332:592:+	-
2999204	GL0022055_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold462141_1:449:928:-	Bacteroides capillosus
2999292	GL0302404_unmapped_[Complete]_[mRNA]_locus=scaffold462452_1:93:701:-	Eubacterium hallii

2999342	GL0550667_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold462575_3:2:592:+	Ruminococcaceae
3000008	GL0200740_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold464672_1:1:597:+	Bacteria
3000134	GL0001034_unmapped_[Complete]_[mRNA]_locus=scaffold465098_1:386:829:+	Clostridium leptum
3001012	GL0558501_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold467732_1:4281:4550:-	Firmicutes
3002306	GL0458483_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold471781_1:3:584:+	Clostridium leptum
3002947	GL0482500_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold473719_2:270:962:+	Clostridium methylpentosum
3003420	GL0281388_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold475134_1:3:731:-	Holdemania filiformis
3003457	GL0171682_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold475231_3:2:316:-	Bacteria
3003487	GL0504064_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold475276_1:1:417:+	Eubacterium siraeum
3003567	GL0422931_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold475578_1:2:346:+	Faecalibacterium prausnitzii
3004099	GL0603411_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold477378_1:2:673:+	Anaerofustis stercorihominis
3004100	GL0428256_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold477378_2:3:566:+	Anaerofustis stercorihominis
3006898	GL0275026_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold485594_1:2:757:+	Holdemania filiformis

3007088	GL0194043_unmapped_[Complete]_[mRNA]_locus=scaffold486160_1:272:592:+	Eubacterium biforme
3007090	GL0001148_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold486160_2:2:691:+	Clostridium leptum
3007429	GL0461575_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold487122_1:41:1084:-	Clostridiales
3007827	GL0284543_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold488348_1:1:651:+	Ruminococcus obeum
3008291	GL0534174_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold489789_1:2:787:-	Blautia hydrogenotrophica
3008731	GL0413090_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold491243_1:3:398:+	Akkermansia muciniphila
3008876	GL0082633_unmapped_[Complete]_[mRNA]_locus=scaffold491737_1:129:848:+	Clostridium leptum
3009219	GL0273396_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold492890_1:114:917:+	Clostridium scindens
3009759	GL0256271_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold494796_1:22:771:-	Clostridium
3009868	GL0023724_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold495166_2:1015:1473:+	-
3010459	GL0604775_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold497018_1:1:399:-	Lachnospiraceae
3010864	GL0501858_unmapped_[Complete]_[mRNA]_locus=scaffold498343_1:30:278:+	Faecalibacterium prausnitzii
3011736	GL0528381_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold500997_1:763:1113:+	-

3011740	GL0137651_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold500997_2:1951:2664:+	Thermotoga
3012669	GL0603343_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold503601_1:2:472:+	-
3014963	GL0501773_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold510595_2:1:531:-	Clostridiales
3015401	GL0208393_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold511820_1:3:542:-	Clostridium leptum
3016243	GL0184428_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold514394_2:164:601:-	Bacillus
3017051	GL0116267_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold516877_2:1:561:-	-
3017085	GL0022187_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold517027_1:3:638:-	Clostridium leptum
3019802	GL0302155_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold525189_1:3:530:-	Eubacterium hallii
3020085	GL0030202_unmapped_[Complete]_[mRNA]_locus=scaffold526106_2:70:1674:+	Clostridium
3021724	GL0607952_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold531397_1:1213:2487:-	Clostridium nexile
3021824	GL0420412_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold531780_1:30:509:+	Clostridium leptum
3022936	GL0633609_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold535043_2:74:1114:+	Clostridium leptum
3023031	GL0299220_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold535331_1:2:766:+	Clostridium phytofermentans

3023067	GL0421362_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold535438_1:2:892:-	Brevibacillus brevis
3023201	GL0154981_unmapped_[Complete]_[mRNA]_locus=scaffold535815_1:189:644:-	Clostridium leptum
3023695	GL0094985_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold537216_2:163:804:+	Bacteroides vulgatus
3024387	GL0372206_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold539389_2:3:1847:-	Clostridium cellulolyticum
3025362	GL0160103_unmapped_[Complete]_[mRNA]_locus=scaffold542258_1:470:1015:-	Ruminococcus obeum
3025703	GL0435112_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold543262_1:1:735:+	Roseburia inulinivorans
3026481	GL0448254_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold545657_1:4:507:-	-
3026793	GL0524226_unmapped_[Complete]_[mRNA]_locus=scaffold546680_2:35:1543:+	Blautia hydrogenotrophica
3026794	GL0524227_unmapped_[Complete]_[mRNA]_locus=scaffold546680_2:1621:2358:+	Clostridium nexile
3027166	GL0403126_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold547733_1:1:735:-	Clostridium leptum
3027530	GL0067445_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold548982_3:1:822:-	Clostridium perfringens
3028169	GL0036243_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold550742_2:1:228:-	Clostridium leptum
3028170	GL0036244_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold550742_2:225:779:-	Clostridium leptum
3028597	GL0022002_unmapped_[Complete]_[mRNA]_locus=scaffold551971_3:295:882:-	Clostridium leptum

3029163	GL0348107_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold553767_1:545:829:-	Bacteroides capillosus
3029236	GL0401737_unmapped_[Complete]_[mRNA]_locus=scaffold554014_2:21:479:-	Roseburia inulinivorans
3031329	GL0282741_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold560628_3:3:596:+	Alkaliphilus metalliredigens
3031572	GL0444449_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold561335_2:3:509:+	Lactococcus phage 936 sensu lato
3032540	GL0081735_unmapped_[Complete]_[mRNA]_locus=scaffold564321_2:3:1052:+	Coprothermobacter proteolyticus
3032603	GL0487930_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold564592_2:252:698:-	Desulfitobacterium hafniense
3032739	GL0050197_unmapped_[Complete]_[mRNA]_locus=scaffold564979_1:186:623:+	-
3033075	GL0281163_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold565997_1:1000:1653:-	-
3033384	GL0137374_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold566975_1:3:365:-	Clostridiales
3034130	GL0056115_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold569277_1:3:479:+	Bacteroides fragilis
3034398	GL0342526_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold569970_1:3:1484:-	Vibrio
3034502	GL0041607_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold570234_1:3:512:-	-
3035778	GL0252552_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold574088_1:3:620:+	Akkermansia muciniphila

3036317	GL0490328_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold575555_1:313:588:+	-
3036625	GL0617866_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold576605_1:3:587:+	-
3037196	GL0433476_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold578330_1:2:619:-	-
3037357	GL0442851_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold578863_2:3:944:-	Clostridium leptum
3037712	GL0639858_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold579946_1:3:536:-	Clostridium leptum
3038375	GL0167574_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold581806_3:140:631:+	Clostridium leptum
3038459	GL0342434_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold582062_1:63:722:+	Clostridium
3038570	GL0562873_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold582406_1:1:696:+	Bacteria
3038704	GL0312035_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold582771_1:3:581:+	Clostridium leptum
3038997	GL0466833_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold583543_1:1:264:+	Bacteria
3038998	GL0466834_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold583543_1:353:778:+	Clostridium leptum
3039551	GL0351534_unmapped_[Complete]_[mRNA]_locus=scaffold585251_1:697:1518:+	Clostridium cellulolyticum
3040256	GL0383805_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold587335_1:543:887:+	Clostridium leptum
3041614	GL0014246_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold591330_2:691:1236:-	-

3041866	GL0453131_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold592144_1:1:510:+	-
3043111	GL0174573_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold595842_3:565:978:+	Bacteroides capillosus
3044229	GL0585112_unmapped_[Complete]_[mRNA]_locus=scaffold599368_1:453:1430:+	Clostridium beijerinckii
3044673	GL0508893_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold600590_1:3:401:-	Ruminococcus
3044868	GL0312741_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold601173_2:1:348:-	Firmicutes
3045411	GL0441238_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold602893_2:31:1131:+	-
3045580	GL0253864_unmapped_[Complete]_[mRNA]_locus=scaffold603346_2:48:335:+	Ruminococcus torques
3046127	GL0468444_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold604920_1:3:860:-	Bacteria
3046570	GL0124274_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold606312_1:402:761:+	Clostridium methylpentosum
3046970	GL0370868_unmapped_[Complete]_[mRNA]_locus=scaffold607388_1:3954:5627:+	Clostridia
3046971	GL0370869_unmapped_[Complete]_[mRNA]_locus=scaffold607388_1:5648:6769:+	Clostridium botulinum
3046972	GL0370870_unmapped_[Complete]_[mRNA]_locus=scaffold607388_1:6774:7535:-	Carnobacterium
3046978	GL0096947_unmapped_[Complete]_[mRNA]_locus=scaffold607388_5:187:1218:+	Clostridium
3046979	GL0096948_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold607388_5:1234:2514:	Clostridium scindens

	+	
3046981	GL0307343_unmapped_[Complete]_[mRNA]_locus=scaffold607388_6:235:1107:+	Clostridium scindens
3046982	GL0307344_unmapped_[Complete]_[mRNA]_locus=scaffold607388_6:1137:2189:+	Clostridium perfringens
3048135	GL0215136_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold610940_4:1:465:-	Desulfitobacterium hafniense
3048656	GL0504957_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold612375_1:3:761:-	-
3048809	GL0206116_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold612902_1:3:1088:-	Coprococcus comes
3049228	GL0304703_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold614150_2:1216:1650:-	Flavobacteriales
3050076	GL0273765_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold616739_2:2:802:+	-
3050453	GL0095816_unmapped_[Complete]_[mRNA]_locus=scaffold617947_1:324:1052:-	-
3050889	GL0311413_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold619316_1:3:422:+	Ruminococcus obeum
3051367	GL0243186_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold620698_2:3:1124:+	Clostridium thermocellum
3051404	GL0503072_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold620856_2:2:817:-	Clostridium
3051710	GL0621607_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold621854_2:2:610:-	Blautia hydrogenotrophica

3052764	GL0434061_unmapped_[Complete]_[mRNA]_locus =scaffold624851_1:38:853:-	Reinekea blandensis
3053412	GL0277447_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold626800_2:567:935:-	Clostridium methylpentosum
3053532	GL0620378_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold627187_1:1:486:+	Ruminococcus torques
3053888	GL0414331_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold628302_1:56:562:+	Roseburia inulinivorans
3054551	GL0091047_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold630288_1:1:813:+	Eubacterium hallii
3055289	GL0460477_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold632381_2:3:557:+	Clostridium leptum
3056711	GL0139961_unmapped_[Complete]_[mRNA]_locus =scaffold636451_1:133:555:-	Parabacteroides
3057072	GL0142211_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold637603_1:541:1302:-	Clostridium leptum
3058859	GL0023215_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold642858_2:106:570:+	Clostridium phytofermentans
3059723	GL0452532_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold645505_1:1:1308:+	Blautia hydrogenotrophica
3059724	GL0061871_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold645505_2:1:651:+	-
3059730	GL0585407_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold645520_1:187:900:-	Roseburia inulinivorans
3059766	GL0126799_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold645613_2:739:1569:-	Bacteroides capillosus
3060120	GL0412616_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold646677_3:1:1488:+	-

3060653	GL0594527_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold648337_2:3:1634:+	Clostridium spiroforme
3063285	GL0402070_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold656406_2:1:318:-	-
3063382	GL0255164_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold656652_1:1:1230:-	-
3063383	GL0255165_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold656652_1:1272:1673:-	cellular organisms
3063554	GL0254756_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold657150_1:1:348:+	-
3064446	GL0043498_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold659828_2:2:670:+	Clostridium ramosum
3065322	GL0545149_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold662564_1:459:857:-	Clostridium
3065854	GL0053385_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold664037_1:1:1494:+	-
3066475	GL0014344_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold665785_2:2:955:+	Clostridium leptum
3066486	GL0457255_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold665802_2:1:621:-	-
3068713	GL0630690_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold672029_1:2:700:+	Faecalibacterium prausnitzii
3068714	GL0404308_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold672029_2:2:919:+	Clostridium leptum
3069490	GL0499952_unmapped_[Complete]_[mRNA]_locus=scaffold674405_2:22:807:-	Clostridium

3069491	GL0499953_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold674405_2:807:1610:-	Clostridium hylemonae
3070145	GL0221508_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold676230_1:2:301:-	Anaerotruncus colihominis
3070820	GL0490461_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold678213_3:1:306:-	Bacteria
3071729	GL0628748_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold680810_1:442:675:+	-
3071730	GL0496811_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold680810_2:2:496:+	-
3071877	GL0265081_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold681257_1:41:673:+	Fusobacterium nucleatum
3072208	GL0507068_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold682188_1:3:806:-	Epulopiscium
3072249	GL0639295_unmapped_[Complete]_[mRNA]_locus=scaffold682268_3:110:1165:-	Clostridium leptum
3073464	GL0435616_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold685564_1:3:506:-	-
3073759	GL0278348_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold686376_2:3:599:+	Clostridiales
3074374	GL0576410_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold688308_1:68:514:-	Clostridiales
3074983	GL0068955_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold690097_1:1:600:+	Bacteria
3076481	GL0252866_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold694577_1:2:886:+	Eubacterium hallii
3077448	GL0278315_unmapped_[Complete]_[mRNA]_locus=scaffold697497_1:168:578:-	Clostridium leptum

3077634	GL0166447_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold698048_1:48:1157:+	Clostridium methylpentosum
3077734	GL0234031_unmapped_[Complete]_[mRNA]_locus=scaffold698351_1:531:1121:+	Brevibacillus brevis
3078944	GL0588995_unmapped_[Complete]_[mRNA]_locus=scaffold701929_1:711:1298:-	Firmicutes
3079562	GL0108460_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold703715_1:3:656:+	Anaerotruncus colihominis
3080203	GL0606551_unmapped_[Complete]_[mRNA]_locus=scaffold705598_1:2:523:+	Clostridium
3080400	GL0423291_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold705993_1:1:720:+	Bacteroides capillosus
3080595	GL0247276_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold706520_1:1:672:-	Clostridium bolteae
3080596	GL0247277_unmapped_[Complete]_[mRNA]_locus=scaffold706520_1:784:1662:-	-
3080597	GL0247278_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold706520_1:1766:2428:-	-
3080599	GL0506985_unmapped_[Complete]_[mRNA]_locus=scaffold706520_3:572:1108:-	Ruminococcus obeum
3080986	GL0211959_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold707672_1:1:483:-	Clostridium scindens
3082052	GL0251995_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold710718_1:740:1090:+	Victivallis vadensis
3083624	GL0230504_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold715080_1:1:1071:+	Parabacteroides distasonis

3083643	GL0326013_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold715123_1:1:810:+	Clostridium ramosum
3083644	GL0326014_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold715123_1:829:1371:+	Bacteroides capillosus
3087245	GL0272307_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold724854_3:2:970:+	Blautia hydrogenotrophica
3087251	GL0302436_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold724862_1:2:697:-	Akkermansia muciniphila
3088182	GL0107420_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold727365_1:1:504:+	Clostridiales
3089157	GL0089427_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold729802_3:3:527:-	-
3090788	GL0057209_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold733947_1:3:446:-	Desulfitobacterium hafniense
3091140	GL0609053_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold734738_1:3:554:+	Clostridia
3092906	GL0369229_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold739447_1:3:287:-	Clostridiales
3092907	GL0369230_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold739447_1:275:523:-	-
3093887	GL0563124_unmapped_[Complete]_[mRNA]_locus=scaffold742164_1:42:317:-	-
3094050	GL0268552_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold742530_1:3:848:+	Clostridium leptum
3094965	GL0165343_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold744758_1:2:367:-	Bacteria
3094966	GL0165344_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold744758_1:485:799:+	-

3095858	GL0370794_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold746985_1:1:591:+	Clostridium phytofermentans
3096994	GL0502852_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold749972_1:330:692:-	-
3097411	GL0313735_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold751032_1:3:560:-	Roseburia inulinivorans
3097654	GL0011678_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold751557_2:3:677:+	-
3098307	GL0494407_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold753069_1:1:351:+	Clostridiales
3098605	GL0248851_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold753866_1:3:617:-	Akkermansia muciniphila
3099848	GL0524568_unmapped_[Complete]_[mRNA]_locus=scaffold756785_1:7:486:+	Clostridium leptum
3101577	GL0429374_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold760974_1:1212:1829:+	Clostridium botulinum
3102797	GL0206977_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold763921_1:276:644:-	Eubacterium siraeum
3102955	GL0193301_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold764295_1:2:655:+	-
3103619	GL0452902_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold765730_1:390:947:+	Bacteroides capillosus
3104025	GL0113661_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold766657_2:456:677:+	Epulopiscium
3104687	GL0126329_unmapped_[Complete]_[mRNA]_locus=scaffold768253_1:91:405:-	Eubacterium biforme

3105413	GL0370132_unmapped_[Complete]_[mRNA]_locus =scaffold769929_1:176:631:-	-
3106050	GL0447114_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold771419_1:1:888:+	Clostridium phytofermentans
3106554	GL0189220_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold772547_1:46:645:+	Clostridiales
3106983	GL0343196_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold773534_1:31:921:-	Clostridium phytofermentans
3107932	GL0472941_unmapped_[Complete]_[mRNA]_locus =scaffold775517_1:183:374:+	-
3112022	GL0338881_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold784064_1:25:576:+	Eubacterium siraeum
3112574	GL0075806_unmapped_[Complete]_[mRNA]_locus =scaffold785133_1:144:1694:+	-
3113013	GL0487389_unmapped_[Lack_both_end]_[mRNA] _locus=scaffold786086_2:2:829:+	Ruminococcus lactaris
3113433	GL0127399_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold786872_1:298:780:+	Roseburia inulinivorans
3114223	GL0355863_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold788389_2:119:694:+	Clostridium
3114349	GL0031896_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold788614_1:166:1044:+	Clostridium leptum
3116005	GL0457941_unmapped_[Complete]_[mRNA]_locus =scaffold791892_1:1482:2210:-	Geobacter sulfurreducens
3117765	GL0586374_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold795486_1:291:635:-	Faecalibacterium prausnitzii
3118218	GL0596500_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold796371_1:2:487:+	Paenibacillus larvae

3119308	GL0625778_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold798597_1:2:712:+	-
3120218	GL0627882_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold800389_1:2:358:+	Clostridiales
3120264	GL0159821_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold800482_1:3:254:-	Clostridiales
3121176	GL0036433_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold802297_1:397:759:-	Clostridium leptum
3121370	GL0438449_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold802697_2:3:623:-	Bifidobacterium adolescentis
3121626	GL0374158_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold803172_2:2:1900:-	Clostridiales
3124354	GL0577527_unmapped_[Complete]_[mRNA]_locus=scaffold808160_1:95:526:+	Clostridium asparagiforme
3125274	GL0217286_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold809778_1:1:468:+	Clostridium leptum
3125997	GL0464352_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold811197_1:3:857:+	Clostridium leptum
3126658	GL0126964_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold812418_1:24:587:-	Parabacteroides distasonis
3126659	GL0169167_unmapped_[Complete]_[mRNA]_locus=scaffold812420_1:47:1036:+	Thermoanaerobacter
3127383	GL0286121_unmapped_[Complete]_[mRNA]_locus=scaffold813669_1:35:466:-	Clostridium
3128101	GL0073929_unmapped_[Complete]_[mRNA]_locus=scaffold814955_2:625:1098:+	-
3128424	GL0045265_unmapped_[Complete]_[mRNA]_locus=scaffold815529_1:60:431:-	Clostridium leptum

3129812	GL0591548_unmapped_[Complete]_[mRNA]_locus=scaffold817908_1:358:879:-	Clostridium methylpentosum
3130539	GL0261617_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold819207_2:3:524:+	Clostridium perfringens
3132480	GL0300002_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold822250_1:3:1502:-	Serratia proteamaculans
3132701	GL0051778_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold822599_1:163:768:-	-
3134610	GL0024404_unmapped_[Complete]_[mRNA]_locus=scaffold825849_1:407:1087:+	-
3136100	GL0202502_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold828361_2:3:1019:-	-
3136521	GL0595512_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold828959_2:3:1268:+	-
3136984	GL0615064_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold829710_1:2:823:-	Clostridium leptum
3137125	GL0526467_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold829905_1:3:626:-	Anaerotruncus colihominis
3137166	GL0552949_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold829970_1:1:837:-	Dorea longicatena
3137760	GL0633501_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold830764_1:2:811:+	Firmicutes
3138622	GL0256046_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold832064_1:910:1098:+	-
3138877	GL0469351_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold832405_1:3:1022:+	-
3139217	GL0338818_unmapped_[Complete]_[mRNA]_locus=scaffold832943_1:570:1232:-	Clostridium scindens

3139884	GL0029923_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold833809_1:2:943:+	Natranaerobius thermophilus
3140020	GL0265172_unmapped_[Lack_5'-end]_[mRNA]_locus=scaffold833990_2:3:545:+	Bacteroides capillosus
3141870	GL0422967_unmapped_[Complete]_[mRNA]_locus=scaffold836324_1:94:372:+	-
3142237	GL0287811_unmapped_[Complete]_[mRNA]_locus=scaffold836729_1:88:903:-	Bacteroides capillosus
3143066	GL0101559_unmapped_[Complete]_[mRNA]_locus=scaffold837593_1:221:502:+	-
3143093	GL0009437_unmapped_[Complete]_[mRNA]_locus=scaffold837629_1:40:1113:+	Parabacteroides johnsonii
3144175	GL0204542_unmapped_[Lack_both_end]_[mRNA]_locus=scaffold838521_1:3:740:+	Clostridiales
3146857	GL0604931_unmapped_[Complete]_[mRNA]_locus=scaffold840657_1:148:438:+	Bacteria
3146858	GL0604932_unmapped_[Complete]_[mRNA]_locus=scaffold840657_1:503:1828:+	Clostridium asparagiforme
3147973	GL0125081_unmapped_[Lack_3'-end]_[mRNA]_locus=scaffold841441_1:1:1026:-	Parabacteroides
3153025	GL0176746_unmapped_[Lack_both_end]_[mRNA]_locus=C219751543_1:3:524:+	-
3161050	GL0312096_unmapped_[Lack_3'-end]_[mRNA]_locus=C219844394_1:1:318:-	Clostridiales
3164839	GL0266119_unmapped_[Lack_5'-end]_[mRNA]_locus=C219886937_1:105:608:-	Bacteria

3168584	GL0524879_unmapped_[Lack_both_end]_[mRNA]_locus=C219927828_1:3:644:+	Coprococcus comes
3173389	GL0026670_unmapped_[Lack_3'-end]_[mRNA]_locus=C219977132_1:1:501:-	Clostridium
3173902	GL0379377_unmapped_[Lack_5'-end]_[mRNA]_locus=C219982246_1:112:705:-	Ruminococcus gnavus
3177824	GL0256008_unmapped_[Lack_5'-end]_[mRNA]_locus=C220021985_1:1:381:+	Blautia hydrogenotrophica
3179119	GL0600216_unmapped_[Lack_both_end]_[mRNA]_locus=C220034931_1:2:793:+	Trichomonas vaginalis
3179868	GL0303732_unmapped_[Complete]_[mRNA]_locus=C220042671_1:186:677:+	-
3188868	GL0151918_unmapped_[Lack_5'-end]_[mRNA]_locus=C220126887_1:1:1185:+	Clostridium ramosum

Table 2: UC-related genes

CLAIMS

1. A method for diagnosing an inflammatory bowel disease, said method comprising a step of determining whether at least one gene from Table 1 and/or Table 2 is absent from an individual's gut microbiome.

2. The method of claim 1 wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

3. The method of claim 1, wherein at least 50 %, 75 % or 90 % of the genes of Table 1 and/or Table 2 are absent from the said individual's gut microbiome.

4. The method of claim 1, said method comprising a step of obtaining microbial DNA from faeces of the said individual.

5. A method for monitoring the efficacy of a treatment for an inflammatory bowel disease, said method comprising the steps of first determining whether at least one gene is absent from the said patient's microbiome, administering the treatment, determining if the said at least one gene is present in the patient's microbiome.

6. The method of claim 5 wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

7. The method of claim 5, wherein at least 50 %, 75 % or 90 % of the genes of Table 1 and/or Table 2 are absent from the said individual's gut microbiome before the treatment.

8. The method of claim 5, said method comprising at least one step of obtaining microbial DNA from faeces of the said individual.

9. A microarray comprising probes hybridizing to at least 10 %, 25 %, 50 %, 75 %, 90 %, 95 %, 97.5 %, or 99 % of the genes of Table 1 and/or Table 2.

10. A kit for diagnosing an inflammatory bowel disease, comprising the microarray of claim 9 or amplification primers specific for at least 10 %, 25 %, 50 %, 75 %, 90 %, 95 %, 97.5 %, or 99 % of the genes of Table 1 and/or Table 2.

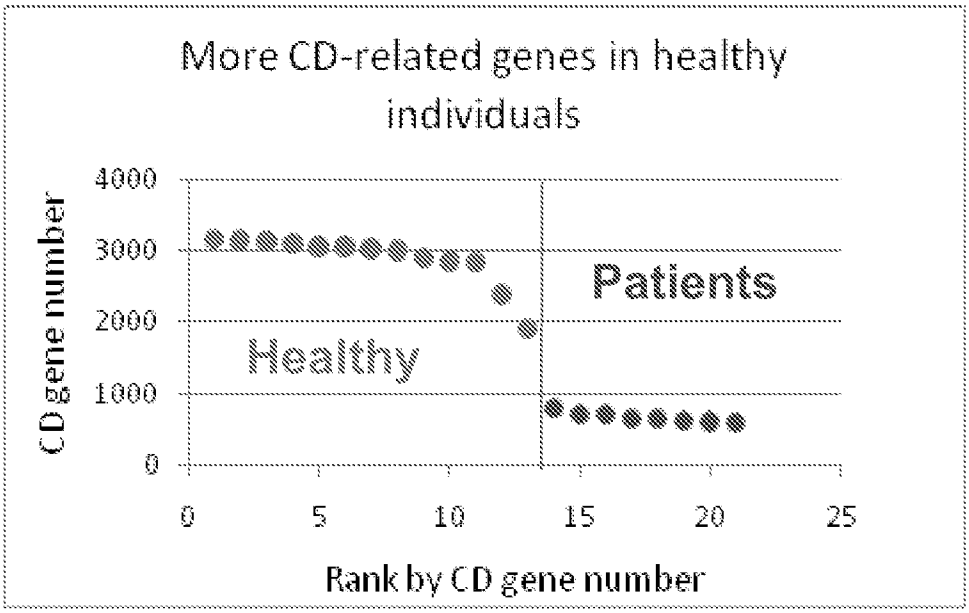

More CD-related genes in healthy individuals
CD gene number
4000
3000
2000
1000
0
Healthy
Patients
0
5
10
15
20
25
Rank by CD gene number

Fig. 1A

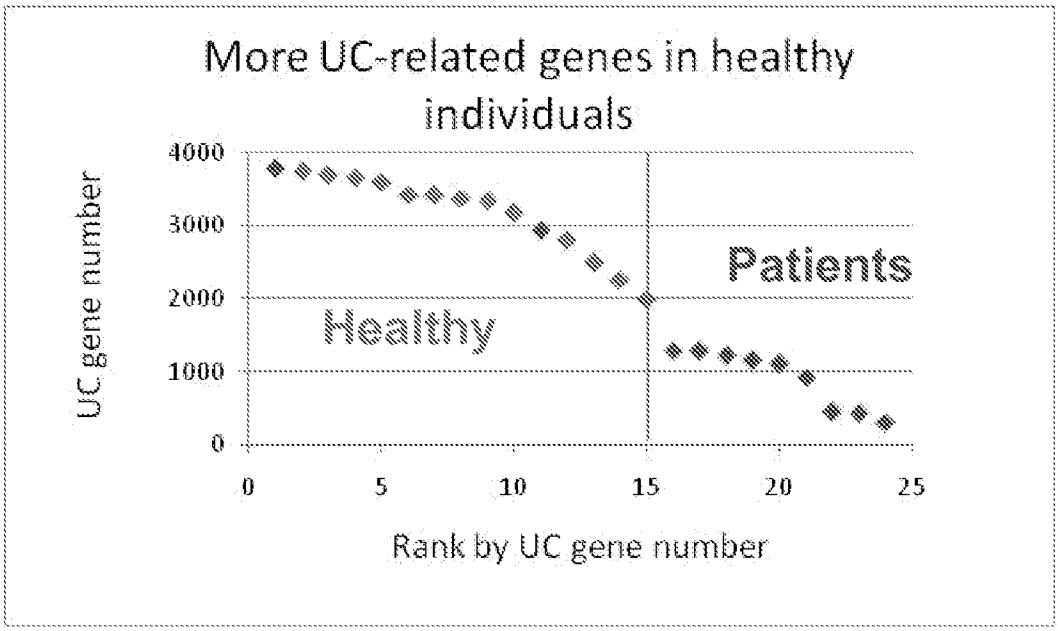

More UC-related genes in healthy individuals
UC gene number
4000
3000
2000
1000
0
Healthy
Patients
0
5
10
15
20
25
Rank by UC gene number

Fig1B

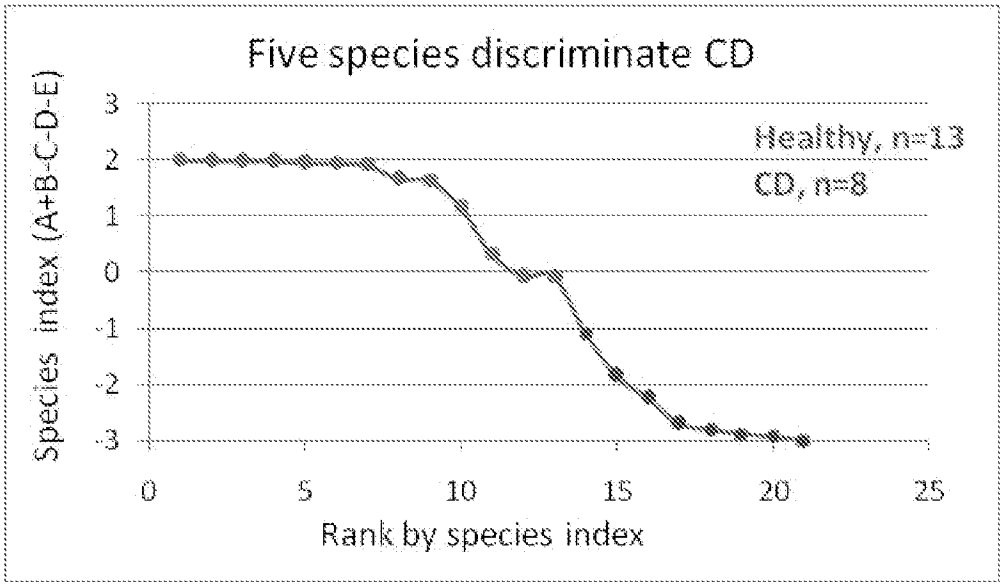

Five species discriminate CD
Species index (A+B-C-D-E)
3
2
1
0
-1
-2
-3
0
5
10
15
20
25
Rank by species index
Healthy, n=13
CD, n=8

Fig. 2A

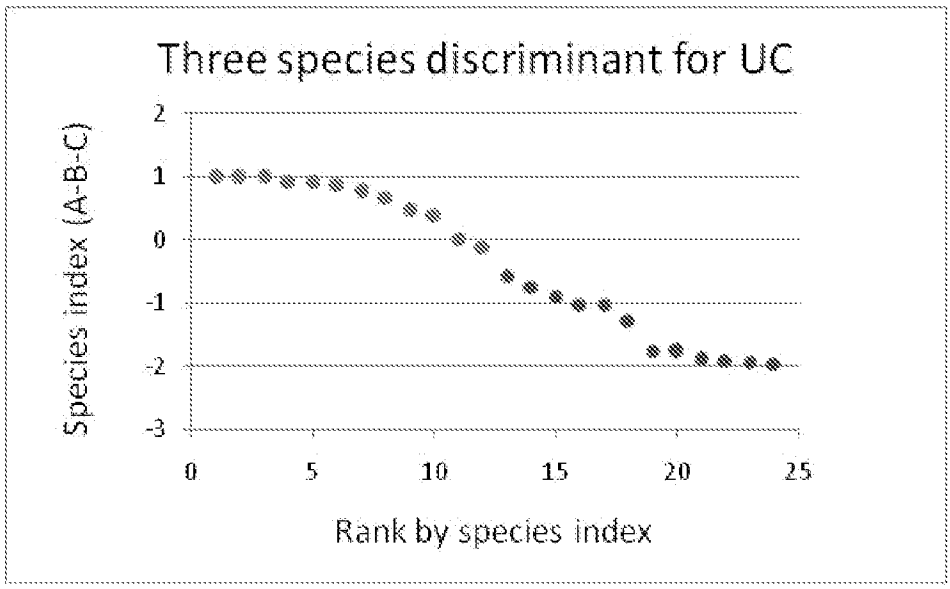

Three species discriminant for UC
Species index (A-B-C)
2
1
0
-1
-2
-3
0
5
10
15
20
25
Rank by species index

Fig. 2B