Comprehensive longitudinal microbiome analysis of the chicken cecum reveals a shift from competitive to environmental drivers and a window of opportunity for *Campylobacter*

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Abstract

Chickens are a key food source for humans yet their microbiome contains bacteria that can be pathogenic to humans, and indeed potentially to chickens themselves. *Campylobacter* is present within the chicken gut and is the leading cause of bacterial foodborne gastroenteritis within humans worldwide. Infection can lead to secondary sequelae such as Guillain-Barré syndrome and stunted growth in children from low-resource areas. Despite the global health impact and economic burden of *Campylobacter*, how and when *Campylobacter* appears within chickens remains unclear. As such, there has been a motivation to decrease the number of *Campylobacter* within chickens and thus reduce the risk of infection to humans. The lack of day-to-day microbiome data with replicates, relevant metadata, and a lack of natural infection studies have delayed our understanding of the chicken gut microbiome and *Campylobacter*. Here, we performed a comprehensive day-to-day microbiome analysis of the chicken cecum from day 3 to 35 (12 replicates each day; n=396) combining metadata such as chicken weight and feed conversion rates to investigate what the driving forces are for the microbial changes within the chicken gut over time, and how this relates to *Campylobacter* appearance within a natural habitat setting. We found a rapidly increasing microbial diversity up to day 12 with variation observed both in terms of genera and abundance, before a stabilisation of the microbial diversity after day 20. In particular, we identified a shift from competitive to environmental drivers of microbial community from days 12 to 20 creating a window of opportunity whereby *Campylobacter* appears. *Campylobacter* was identified at day 16 which was one day after the most substantial changes in metabolic profiles observed. In addition, microbial variation over time is most likely influenced by the diet of the chickens whereby significant shifts in OTU abundances and beta dispersion of samples often corresponded with changes in feed. This study is unique in comparison to the most recent studies as neither sampling was sporadic nor *Campylobacter* was artificially introduced, thus the experiments were performed in a natural setting. We believe that our findings can be useful for future intervention strategies and can help elucidate the mechanism through which *Campylobacter* within chickens can be reduced.

Introduction

Chickens (*Gallus gallus domesticus*) are an important food source for humans with over 50 billion reared annually for meat and eggs (Part et al., 2016). Feed conversion and the health of chickens is heavily dependent on the largely unexplored complex gut microbial community which plays a role in nutrient assimilation, vitamin and amino acid production and prevention of pathogen colonization (Sergeant et al., 2014, Apajalahti, 2005, McNab, 2007, Józefiak et al., 2004). In chickens, the organ with the highest number and variety of bacteria is the cecum (10^{10}-10^{11} cells/g) which plays an essential role in the digestion of non-starch polysaccharides (NSPs) found in chicken feed (Jozefiak et al., 2004, Barnes et al., 1972, Bjerrum et al., 2006). The importance of this organ is demonstrated when up to 10% of energy needs can be recovered from a well-functioning cecum (Jozefiak et al., 2004, Hegde et al., 1982), and also that the cecum remains a source of bacterial human infection and a reservoir of antibiotic resistance determinants.

The chicken cecum contracts several times a day releasing contents towards the ileum and the cloaca (Pauwels et al., 2015). Notably the cecal drop contains *Campylobacter*, a Gram-negative spiral shaped bacterium which causes an estimated 400 million human infections each year (Friedman et al., 2000, Walker, 2005). *Campylobacter* causes bloody diarrhoea, fever and abdominal pains in humans and can also cause post infectious sequelae such as Guillain-Barré syndrome which is a potentially fatal paralytic autoimmune illness. In low-resource areas, asymptomatic and occasionally persistent *Campylobacter* infections are common in children younger than one year and correlate with stunted growth and therefore life-long physical and cognitive deficits (Amour et al., 2016). Approximately 80-90% of these infections are attributed to *Campylobacter jejuni*, with poultry as the most important source of human campylobacteriosis within industrialized countries (Humphrey et al., 2007, Mullner et al., 2009, Sheppard et al., 2009). *C. jejuni* colonizes the chicken cecum with relatively high numbers (10^9 CFU per gram) and whereas traditionally was considered a commensal of the chicken gut, more recently has been demonstrated to be pathogenic to the chicken, with this dependent on the genetics of the host and the strain of infection (Van Deun et al., 2008, Hermans et al., 2012, Wigley, 2015, Humphrey et al., 2014, Humphrey et al., 2015). Natural colonisation of chickens is reported to be typically at approximately day 14 of the chicken life cycle, although we do not know how and why this occurs, and what the impact of *Campylobacter* is on the microbiome (Kalupahana et al., 2013, Neill et al., 1984, Thibodeau et al., 2015).

The microbiome of chickens develop rapidly from days 1-3 where *Enterobacteriaceae* dominate, with *Firmicutes* increasing in abundance and taxonomic diversity from approximately day 7 onwards (Ballou et al., 2016, Mancabelli et al., 2016, Danzeisen et al., 2011). Bacterial populations within the chicken gut are subsequently driven by the rearing environment and from the bacteria present in food and water (Connerton et al., 2018). How and when *Campylobacter* appears and the impact on the chicken gut microbiome remains unanswered. The presence of *Campylobacter* has been noted to prompt an increase in *Bifidobacterium* and modify abundances of *Clostridia* and *Mollicutes* (Thibodeau et al., 2015). The identification of a number of hydrogenases within the ceca may lead to a potential hydrogen sink and provide an explanation as to the high abundance of genera such as *Campylobacter* (Sergeant et al., 2014). Comparison of broilers not exposed and exposed to *C. jejuni* at day 6 or day 20 revealed reductions in the relative abundance of operational taxonomic units (OTUs) within the taxonomic family *Lactobacillaceae* and the *Clostridium* cluster XIVa, with specific members of the *Lachnospiraceae* and *Ruminococcaceae* families exhibiting transient shifts in microbial community populations dependent upon the age at which the birds become colonized by *C. jejuni* (Connerton et al., 2018). These studies have enhanced our understanding of the chicken cecal microbiome, however the lack of day-to-day microbiome data, suitable replicate numbers, relevant metadata, and lack of natural infectivity studies have not allowed us to fully appreciate what is occurring in a natural habitat in relation to how and when *Campylobacter* appears within the chicken gut. To answer these questions, in this study we have performed a comprehensive analysis of the chicken cecal microbiome from days 3 to 35, with 12 replicates per day (n=396), correlating additional metadata such as chicken weight and feed conversion rates with *Campylobacter* detection in a natural environmental setting.

Experimental procedures

Experimental design, broilers and sample collection

This study was performed using a total of 396 Ross-308 male broiler chickens provided by Moy Park (39 Seagoe Industrial Estate, Portadown, Craigavon, Co. Armagh, BT63 5QE, UK). The birds were divided into 12 pens; each pen contained 33 chickens (Supplementary Figure 1). Birds were raised on three phase diets from day 0 to day 35. Starter diets were offered to the birds from days 0-10, grower diets from days 11-25 and finisher diets from days 26-35. Every 24 hours, a single chicken from each of the 12 pens was removed at random, euthanized by cervical dislocation or anaesthesia combined with cervical dislocation, followed by genomic DNA (gDNA) extracted from the chicken cecum. A total of 16 samples were removed from the final analysis due to poor gDNA quality.

Poultry growth and performance measurements

The performance parameters investigated were mean body weight (BW_mean), body weight gain (Gain), feed intake (FI) and feed conversion ratio (FCR). Measurements were taken at time points 3-7 days, 8-14 days, 15-24 days and 25-35 days. These variables were then correlated with the microbial community's composition in various statistical analyses.

DNA extraction, 16S rRNA amplification and sequencing

Cecal gDNA was extracted using the QIAamp DNA Stool Mini Kit according to the manufacturer's instructions and stored at -20°C. 16S metagenomic sequencing library construction was performed using Illumina guidelines (Illumina, U.S.A). The 16S ribosomal primers used were V3 (tcgtcggcagcgtcagatgtgtataagagacagcctacgggnggcwgcag) and V4 (gtctcgtgggctcggagatgtgtataagagacaggactachvgggtatctaatcc) (Klindworth et al., 2013, D'Amore et al., 2016). A second PCR step was performed to attach dual indices and Illumina sequencing adapters using the Nextera XT Index kit. Sequencing was performed on the Illumina MiSeq at LSHTM using a v3 300 bp paired-end kit.

Bioinformatics

Abundance tables were obtained by constructing OTUs (a proxy for species) as follows. Paired-end reads were trimmed and filtered using Sickle v1.200 (Joshi and Fass, 2011) by applying a sliding window approach and trimming regions where the average base quality drops below 20. Following this we applied a 10 bp length threshold to discard reads that fall below this length. We then used BayesHammer (Nikolenko et al., 2013) from the Spades v2.5.0 assembler to error correct the paired-end reads followed by pandaseq (v2.4) with a minimum overlap of 20 bp to assemble the forward and reverse reads into a single sequence spanning the entire V3-V4 region. The above choice of software was as a result of author's recent work (Schirmer et al., 2015, D'Amore et al., 2016) where it was shown that the above strategy reduces the substitution rates (main form of error) significantly. After having obtained the consensus sequences from each sample, we used the VSEARCH (v2.3.4) pipeline (all these steps are documented in https://github.com/torognes/vsearch/wiki/VSEARCH-pipeline) for OTU construction. The approach is as follows: we pool the reads from different samples together and add barcodes to keep an account of the samples these reads originate from. We then dereplicate the reads and sort them by decreasing abundance and discard singletons. In the next step, the reads are clustered based on 97% similarity, followed by removing clusters that have chimeric models built from more abundant reads (--uchime_denovo option in vsearch). A few chimeras may be missed, especially if they have parents that are absent from the reads or are present with very low abundance. Therefore, in the next step, we use a reference-based chimera filtering step (--uchime_ref option in vsearch) using a gold database (https://www.mothur.org/w/images/f/f1/Silva.gold.bacteria.zip). The original barcoded reads were matched against clean OTUs with 97% similarity (a proxy for species level separation) to generate OTU table (a total of 18,588 unique sequences) for n=382 samples.

The representative OTUs were then taxonomically classified against the SILVA SSU Ref NR database release v123 database with assign_taxonomy.py script from the Qiime (Caporaso et al., 2010) workflow. To find the phylogenetic distances between OTUs, we first multisequence aligned the OTUs against each other using Kalign v2.0.4 (Lassmann and Sonnhammer, 2005) (using the options -gpo 11 -gpe 0.85) and then used FastTree v2.1.7 (Price et al., 2010) to generate the phylogenetic tree in NEWICK format. Finally make_otu_table.py from Qiime workflow was employed to combine abundance table with taxonomy information to generate biome file for OTUs. Tax4Fun (Asshauer et al., 2015) was used to predict the functional capabilities of microbial communities based on 16S rRNA datasets (all prokaryotic KEGG organisms are available in Tax4Fun for SILVA v123 and KEGG database release 64.0) and then utilising ultrafast protein classification (UProC) tool (Meinicke, 2015) to generate metabolic functional profiles after normalising the data for 16S rRNA gene copy numbers. In Tax4Fun, we used MoP-Pro approach (Asshauer and Meinicke, 2013) to give pre-computed 274 KEGG Pathway reference profiles. Although Tax4Fun based metabolic prediction is constrained by the taxa available in the reference database, it gives a statistic called fraction-of-taxonomic-units-unexplained (FTU) which reflects the amount of sequences assigned to a taxonomic unit and not transferable to KEGG reference organisms. This can be used as a measure of confidence in trusting the predictions. Summary statistics of FTUs returned in this study are as follows: 1st Quantile:0.09129; Median:0.13995; Mean:0.14902; and 3rd Quantile:0.19800 (Figure 1h). Thus, on average metabolic profiles of ~86% of the taxa were present and therefore with this high representation, we used the pathways in the statistical analysis.

Statistical analysis

Statistical analyses were performed in R using the tables and data generated as above as well as the meta data associated with the study. For community analysis (including alpha and beta diversity analyses) we used the vegan package (Oksanen et al., 2015). For alpha diversity measures, we calculated: *Richness*, estimated number of species/features per sample; and *Shannon* entropy: a commonly used index to characterise species diversity. To calculate Unifrac distances (that account for phylogenetic closeness), we used the phyloseq (McMurdie and Holmes, 2013) package. Nonmetric Distance Scaling (NMDS) plot of community data (OTUs) used different distance measures (Vegan's metamds() function): *Bray-Curtis*, considers the species abundance count; *Unweighted Unifrac,* considers the phylogenetic distance between the branch lengths of OTUs observed in different samples without taking into account the abundances; and *Weighted Unifrac,* unweighted unifrac distance weighted by the abundances of OTUs. The samples are grouped for different treatments as well as the mean ordination value and spread of points (ellipses were drawn using Vegan's ordiellipse() function that represent the 95% confidence interval of the standard errors of the groups).

To understand multivariate homogeneity of groups dispersion (variances) between multiple conditions, we used Vegan's betadisper() function in which the distances between objects and group centroids are handled by reducing the original distances (BrayCurtis, Unweighted Unifrac, or Weighted Unifrac) to principal coordinates and then performing ANOVA on them. We used Vegan's adonis() for analysis of variance using distance matrices (BrayCurtis/Unweighted Unifrac/Weighted Unifrac) i.e., partitioning distance matrices among sources of variation (Grouping type i.e., weeks, body weight, feed intake, feed conversion ratio etc.). This function, henceforth referred to as PERMANOVA, fits linear models to distance matrices and uses a permutation test with pseudo-F ratios.

To find OTUs that are significantly different between multiple conditions (days/weeks), we used DESeqDataSetFromMatrix() function from DESeq2 (Love et al., 2014) package with the adjusted p-value significance cut-off of 0.05 and log2 fold change cut-off of 2. This function uses negative binomial GLM to obtain maximum likelihood estimates for OTUs log fold change between two conditions. Then Bayesian shrinkage is applied to obtain shrunken log fold changes subsequently employing the Wald test for obtaining significances. To find KEGG pathways significantly up/down-regulated between multiple conditions (days/weeks), the Kruskal-Wallis test was used with p-values adjusted for multiple comparisons using the fdrtool package (Klaus and Strimmer, 2013, Klaus and Strimmer, 2015).

We performed Local Contribution to Beta Diversity (LCBD) analysis (Legendre and De Caceres, 2013) by using LCBD.comp() from adespatial package (Dray et al., 2018). We used the Hellinger distance (abundances), unweighted (phylogenetic distance) and weighted Unifrac (phylogenetic distance weighted by abundance) dissimilarities. LCBD gives the sample-wise local contributions to beta diversity that could be derived as a proportion of the total beta diversity. In the context of this longitudinal study, it provides a mean to show how markedly different the microbial community structure of a single sample is from the average (with higher LCBD values representing outliers), and also provides a mean to show when the community structure has stabilised in a temporal setting.

To characterise the phylogenetic community composition within each sample whether the microbial community structure is stochastic (driven by competition among taxa) or deterministic (driven by strong environmental pressure i.e. host environment), we quantified: mean-nearest-taxon-distance (MNTD) and the nearest-taxon-index (NTI) using mntd(), and ses.mntd(); and mean-phylogenetic-diversity (MPD) and nearest-relative-index (NRI) using mpd() and ses.mpd() function from the picante (Kembel et al., 2010) package. NTI and NRI represent the negative of the output from ses.mntd() and ses.mpd(), respectively. They also quantify the number of standard deviations that the observed MNTD/MPD is from the mean of the null distribution (999 randomization by using null.model='richness' in the ses.mntd() and ses.mpd() functions and only considering the taxa as present/absent without taking their abundances). We used the top 1000 most abundant OTUs for calculation of these measures based on the recommendations given in (Stegen et al., 2012).

We used the "BVSTEP" routine (Clarke and Ainsworth, 1993), an algorithm that searches for highest correlation (Mantel test) between dissimilarities of a fixed and variable multivariate datasets using bvStep() from sinkr package (Taylor, 2014) by permuting through 2^n-1 possible combinations of features in the variable dataset. Testing all feature combinations is unrealistic and computationally intractable when the feature space is high (18,588 OTUs in our case). Thus, we used the abundance table with 1000 most abundant OTUs (with the premise that the most abundant species that may have a significant role to play) to best correlate with the overall similarities given all the OTUs (18,588 in our case). This analysis is complimentary to the differential analysis and identified the OTUs that were causing the major shifts in beta diversity.

The phylogenetic tree and annotations summarizing the findings of this study were drawn using Evolview (http://www.evolgenius.info/evolview/).

We considered analyses on two different groupings of the sample data, comparison of microbial profiles on a daily basis to reveal temporal patterns, and on a weekly basis (4 weeks), primarily because the poultry growth and performance parameters were recorded on a weekly basis. The statistical scripts and workflows for all above can be found at http://userweb.eng.gla.ac.uk/umer.ijaz#bioinformatics

Results

Daily diversity patterns converge to a stable community as we go forward in time

Although alpha diversity (Shannon) on microbial counts (Figure 1a) shows a rapid increase over the first ten days, it follows a plateauing effect where the microbiome normalises at approximately day 12. This is in line with previous reports whereby the gastrointestinal (GI) tract of poultry comes into contact with exogenous microorganisms immediately after hatch and as the host grows, this microbiome becomes highly diverse until it reaches a relatively stable yet dynamic state (Pan and Yu, 2014). The same temporal phenomenon can be observed when considering local contributions to beta diversity based on abundance count (Hellinger distance; Figure 1b). When considering phylogenetic distances only (Unweighted Unifrac; Figure 1c), although the decrease in beta diversity contributions is marginally slower than the abundance counts counterpart, there is a sudden increase around day 20. Using both abundances and phylogenetic distances this seems to disappear (Weighted Unifrac; Figure 1d). It should be noted that a higher LCBD value suggests the diversity patterns of a sample is markedly different from the rest of the samples in an average sense. In contrast, the level of microbial diversity between the different pens was relatively stable (results not significant and thus not shown) suggesting less or no variability amongst pens. *Campylobacter* was detected in three chickens from the 12 pens at day 16 (Figure 1a). This is in line with previous reports where natural colonisation of chickens has been reported at approximately day 14 of the chicken life cycle (Kalupahana et al., 2013, Neill et al., 1984, Thibodeau et al., 2015, Hermans et al., 2011). *Campylobacter* was also identified in one of the chickens at day 3 and previously it has also been reported that chickens between 0 and 3 days of age can become infected with *Campylobacter* (Cawthraw et al., 1996).

Window of opportunity for Campylobacter between day 12 and day 20

Next, we explored ecological drivers of microbial community to determine whether there is any environmental pressure (host environment) responsible for assemblage of microbial community or if it is driven purely by competition. Using NTI and NRI (Figure 1e, f), one can observe a step function response around day 12. For a single community, NTI/NRI greater than +2 indicates strong phylogenetic clustering (driven by environmental filtering) and less than -2 indicates phylogenetic overdispersion (environment has little or no role to play). Since chicken ceca are already a constrained environment to begin with (as opposed to real environmental datasets), the lower bound of -2 may not be feasible and hence the values should be taken relatively with an increasing value implying increasing host environmental pressure. It should be noted that whilst NRI reflects the phylogenetic clustering in a broad sense (whole phylogenetic tree) with the negative values representing evenly spread community, NTI focuses more on the tips of the tree with positive values of NTI indicating that species co-occur with more closely related species than expected, and negative values indicate that closely related species do not co-occur. We have chosen presence/absence of species while calculating these measures without taking into account the abundances as they mask the phenomenon similar to LCBD profiles (Figure 1c, d). When we consider differential analysis of OTUs (Supplementary Table 1), we can notice that between days 9 and 11 there is a high proportion of OTUs that were log2 fold different. After day 20, we also observe the same between days 26 and 28 with the changes in phylogenetic structure responsible for peaks in NTI/NRI. Interestingly, chickens were raised on three phase diets; starter diets (days 0-10), grower diets (days 11-25) and finisher diets (days 26-35). The high proportion of OTUs that were log2 fold different between days 26 and 28 may be attributed to the change in feed from grower to finisher feed. Since the NTI/NRI are already significantly higher than 2, we do not consider this as an upper bound and revert back to day 20 as an upper bound for the window. Based on beta dispersion analysis (Table 1), we observe days 11 to 13 and days 19 to 21 when the dispersions of the microbial communities are changing significantly. The alteration in the chicken feed from starter diet (days 0-10) to grower diets (days 11-25) may also play a role in the significant beta dispersion between days 11 to 13, although the feed change does not seem a likely explanation for days 19 to 21. For completeness we also generated differential analysis of genus level where *Campylobacter* was identified as being significantly down-regulated between day 16 to day 17 (Supplementary Table 2).

If we consider the richness of metabolic pathways (Figure 1g), we notice that they achieve stability before the microbial community at around day 6 with no obvious patterns to suggest anything apparent between day 12 and day 20 other than a marginal decrease to day 16 and increasing again onwards. However, if we consider the differential expression analysis of pathways (Supplementary Table 3), we can notice a large proportion of these pathways changing between day 14 and 15, a day before *Campylobacter* was first observed. We identified a reduction in lysine degradation (ko00310) from day 14 to day 15, and an increase in D-Alanine metabolism (ko00473) from day 14 to day 15. *C. jejuni* typically cannot utilize sugars as a carbon source as it lacks the glycolytic enzyme phosphofructokinase and so depends on the availability of free amino and keto acids scavenged from the host or from the intestinal microbiome (Parkhill et al., 2000, Velayudhan and Kelly, 2002, Lee and Newell, 2006). *C. jejuni* utilizes serine, aspartate, glutamate and proline preferentially as nutritional substrates *in vitro* with serine catabolism required for colonization of the intestinal tract (Leach et al., 1997, Elharrif and Mégraud, 1986, Velayudhan et al., 2004, Hendrixson and DiRita, 2004). Amino acids can also potentially be deaminated to a small number of intermediates that can directly feed into the central metabolism, including pyruvate (from serine and alanine), oxaloacetate (from aspartate), and 2-oxoglutarate (from glutamate) (Velayudhan et al., 2004). The variation of such metabolic pathways may give an indication as to the appearance of *Campylobacter* at this time point. We also identified a reduction from days 14 to day 15 of a number of pathways relating to specific bacteria; *Vibrio cholerae* pathogenic cycle (ko05111; Biofilm formation - *Vibrio cholerae*), *Escherichia coli* (ko05130; Pathogenic *Escherichia coli* infection), *Salmonella* species (ko05132; *Salmonella* infection). In addition, we identified a reduction from day 14 to 15 of Bacterial secretion systems (ko03070). Future studies are needed to elucidate and confirm the predicted pathways. In view of these findings, *Camplyobacter* appears in day 16 within this window of opportunity (Figure 1) where there exists a shift from competitive to environmental drivers of microbial community, with day 16 lying immediately after the most substantial changes in metabolic profiles observed over the whole period.

Analysis of dominant bacterial group over time

Analysis of the 50 most abundant genera (Supplementary Figure 2) identified trends that have been reported previously in that the chicken microbiome contains *Enterobacteriaceae* at early days of development, and that *Firmicutes* increase in abundance and taxonomic diversity over time (Ballou et al., 2016, Mancabelli et al., 2016, Danzeisen et al., 2011). *Escherichia.Shigella* (Phylum *Proteobacteria*; Family *Enterobacteriaceae*) was identified as being highly abundant at day 3 and showed a general reduction up to approximately day 7. *Escherichia.Shigella* was also noted to be present after day 28. This pattern was observed for *Eisenbergiella* (Phylum *Firmicutes*; Family *Lachnospiraceae*) which displayed a decrease from early time points, but remained present throughout. This pattern was also observed for *Ruminiclostridium* (Phylum *Firmicutes*; Family *Ruminococcaceae*) which however was not in the abundant genera after day 23. *Flavonifractor* (Phylum *Firmicutes*; Family -) was identified consistently at early time points but was rarely abundant after day 19. *Enterobacter* (Phylum *Proteobacteria*; Family *Enterobacteriaceae)* was only observed at days 3 and 4 and was not abundant at any other time points. Here we identified that *Ruminiclostridium.5* and *Ruminiclostridium.9* (Phylum *Firmicutes*; Family *Ruminococcaceae*) were consistently present throughout at a relatively significant level of abundance. This was also the case for *Anaerotruncus* (Phylum *Firmicutes*; Family *Clostridiaceae*), but at a lower level of abundance, especially before day 7. *Faecalibacterium* (Phylum *Firmicutes*; Family *Clostridiaceae*) was rarely abudant at early time points, however was observed consistently at a relative high abundance after day 14. *Lachnoclostridium* (Phylum *Firmicutes*; Family *Lachnospiraceae*) was found to be present throughout with a relatively high level of fluctuation. Certain genera such as *Ruminococcaceae.UCG.005* and *Ruminococcaceae.UCG.014* (Phylum *Firmicutes*; Family *Ruminococcaceae*) were not abundant at high levels at early time points however increased significantly at approximately days 16-19. Finally, *Megamonas* (Phylum *Firmicutes*; Family *Veillonellaceae*) and *Intestinimonas* (Phylum *Firmicutes*; Family -) were not abundant throughout most time points, before appearing post day 22-25 onwards.

Weekly microbial profiles and analysis of poultry performance metadata

The metadata collected here included Bird Weight (BW_Mean; grams), Body Weight Gain (Gain; g/bird), Feed Intake (FI), Feed Conversion Ratio (FCR), and was recorded on a weekly basis where we have considered grouping the microbiome samples accordingly; days 03-07 (week 1), days 08-14 (week 2), days 15-24 (week 3), and days 25-35 (week 4). As is the case with the daily microbiome profile, alpha diversity (rarefied richness and Shannon; Figure 2a) increases over time, however, due to the nature of this grouping, we lose the plateauing effect over time. In accordance with daily analysis, we can see a major shift in the parameters as we transition from days 08-14 to days 15-24 (Figure 2b). FCR in particular increases substantially in this period remaining stable for week 4 (days 25-35). Gain is also significantly elevated in this transition period (days 08-14 to days 15-24) when compared to other periods. In terms of beta diversity (Figure 2c), we observe the samples more sparsely spread in the first week (days 03-07) as compared to other weeks on abundance (Bray-Curtis) alone. The phylogenetic dispersion (Unweighted Unifrac) on the other hand is more preserved. We can also notice a gradient forming with later weeks more or less close to suggest convergence as we established in the case of daily profiles. Based on beta dispersion analysis (Table 2), we can notice that the dispersion in week 1 is significantly different to other weeks with 16%, 6%, and 17% variability in microbial community explained by PERMANOVA using counts alone (Bray-Curtis), phylogenetic distance alone (Unweighted Unifrac), and combination of two (Weighted Unifrac), respectively. With this grouping, main sources of variation are then the distribution of species rather than their phylogenetic relatedness. The metadata explains 10-12% variability (all significant) in terms of counts alone (Bray-Curtis) with 3-6% in terms of phylogeny (Unweighted Unifrac). For the sake of completeness, we also performed differential analysis of OTUs and pathways on a consecutive weekly basis (lower halves of Supplementary Tables 1, 2 and 3); however, these should be interpreted with great care as main source of variability are the daily changes and grouping samples on weekly basis will always return more significant OTUs and pathways.

Key species representing majority of the shift in community dynamics

In addition to differential analysis on OTUs (Supplementary Table 1) which returned OTUs that were log2 fold different between consecutive days, we also considered the subset analysis where we imploded the abundance table to the minimum set of OTUs, the resulting reduced-order abundance table correlated highly with the full table by preserving the beta diversity between the samples (Table 3). To see how much variability is lost, the PERMANOVA with full OTU table (18,588 OTUs) is provided as a reference. The 17 OTUs listed represent only ~2% (subset S1) loss in variability and thus represent the main OTUs that are driving the community dynamics. In terms of metadata, the loss in variability is ~ 1% (subset S1). The subset of the phylogenetic tree of these OTUs in addition to those selected in the differential analysis (daily comparisons), a total of 110 OTUs, was then extracted and annotated with these analysis in Figure 3 along with taxonomy information. It can be seen that majority of these (>50%) belong to *Firmicutes* (*Bacillaceae*, *Ruminococcaceae*, *Lachnospiracaeae*, *Lactobacillaceae*, *Peptostreptococcaceae*, and *Clostridiales vadin BB60 group*), with a small proportion belonging to *Actinobacteria* (*Coriobacteriacaea*), *Tenericutes* (*Mollicutes RF9*), and *Proteobacteria* (*Enterobacteriaceae* including *Escherichia.Shigella* as mentioned before).

Discussion

Comprehensive investigation of the chicken cecal microbiome at a day-to-day level revealed a rapid increase in diversity up to day 12, with microbial variation observed both in terms of genera and abundance. We suspect this early variation is due to competitive factors determined by space and available food resources. Post day 20 there exists a considerable stabilisation of the chicken cecal microbiome where the relative microbial diversity and abundances are standardised, with environmental factors (in this case the host chicken) exerting a greater influence on any change in the microbial diversity. Between days 12 and 20 we observe a shift from competitive to environmental drivers of microbial community creating a window of opportunity whereby *Campylobacter* appears. We identified *Campylobacter* at day 16 with this day lying immediately after the most substantial changes in metabolic profiles observed over the whole period. Whilst we identified *Campylobacter* within 25% of the pens on day 16, we would naturally expect *Campylobacter* to spread to other chickens and pens and also be identified on subsequent days. We suspect that the experimental set-up here was such that following random selection of birds from each pen on each day, sacrificing the bird (to perform gDNA extraction from the ceca) did not allow for an opportunity for *Campylobacter* to spread to other chickens or pens. Clearly in a typical farm set-up this would not be the case and *Campylobacter* would spread naturally.

Microbial variation over time is most likely influenced by diet of the chickens whereby significant shifts in OTU abundances and beta dispersion of the samples often corresponded with changes in feed. Notably, the relatively high proportion of OTUs that were log2 fold different between days 9 and 11, and days 26 and 28, and beta dispersion for days 11-13 corresponded with changes in feed from grower to finisher. Further studies investigating different feed content is required to ascertain the complete impact on chicken cecal microbiome.

Previous microbiome studies of chicken ceca have often lacked the day-to-day sampling points, replicate numbers, relevant metadata and have often provided external *Campylobacter* infection that may potentially perturb the natural habitat. These have not allowed us to fully appreciate what is occurring in a natural environment in relation to how and when *Campylobacter* appears within the chicken gut. Thus, we believe the major strength of this study is that we achieve these missing points as we have performed the most comprehensive analysis of the chicken cecal microbiome to date, sampling from days 3 to 35, with 12 replicates per day (n=396), correlating additional metadata such as chicken weight and feed conversion rates and with *Campylobacter* detection in a natural environmental setting giving the most comparable experimental design to a farm set-up. As we were not able to sample the same chicken for all time points, future studies should investigate this further with added dietary information than what we have considered here, with experimental designs also to investigate and confirm the predicted pathways.

Conclusions

Industry has endeavoured to reduce the burden of *Campylobacter* within chicken production lines with supplements often administered with the aim of performance enhancing and/or reducing bacteria such as *Campylobacter*, typically post day 25. The relative stability of the chicken cecal microbiota at this time point may explain the efficacy of such products, however the identification of a window of opportunity for bacteria such as *Campylobacter* may call for intervention strategies between days 12 to 20, or even earlier. This study can act as a baseline for future intervention strategies and help reduce the burden of *Campylobacter* within chickens.

Availability of supporting data

The raw sequence files supporting the results of this article are available in the European Nucleotide Archive under the project accession number PRJEB25776.

Author contributions

AM, AR, UL, BW, ND, NC and OG contributed to the study design. ND, NC and OG managed the study. CK, AM. AS and ML performed the sample collection and DNA extraction. LS, AM, AE and OG performed the library preparation and Illumina MiSeq sequencing at the LSHTM. UZI wrote the analysis scripts to generate the figures and tables in this paper. UZI and OG performed the bioinformatics and statistical analysis. UZI, ND, NC and OG drafted the initial version of the manuscript with all authors contributed to redrafting.

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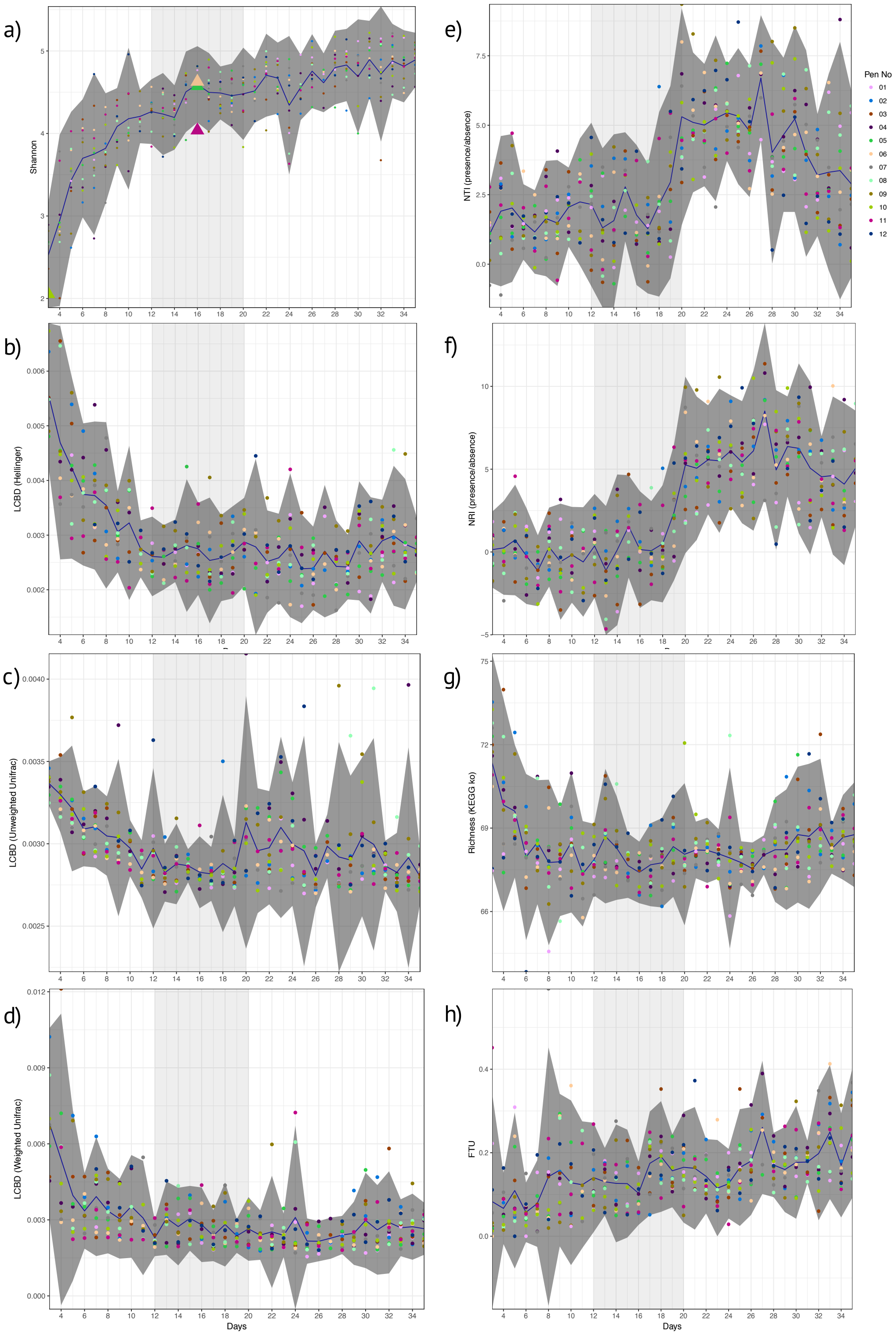

Figure 1: Day-wise statistical measures calculated on the microbiome data. a) Shannon entropy with first appearance of *Campylobacter* (>=5 sequences) highlighted as triangles. b), c), and d) Local contribution to beta diversity (LCBD) calculated by using Hellinger transform on the microbial counts, Unweighted Unifrac dissimilarity (phylogenetic distances only), and Weighted Unifrac dissimilarity (phylogenetic distances weighted with abundance counts) respectively e) and f) Nearest-Taxon-Index (NTI) and nearest-relative-

index (NRI) considering presence/absence of OTUs in samples g) Richness calculated as exponentiation of Shannon entropy on the proportional representation of KEGG pathways on samples, and h) fraction-of-taxonomic-units-unexplained (FTU) calculated on each sample. In all subfigures, the mean value is represented by solid blue line with 95% confidence interval of standard deviation given as dark shaded region around the mean. The samples are coloured with respect to the pens they originate from. Based on the analysis given in this study, we have identified days 12 to 20 of importance and are thus highlighted as lighter shaded regions.

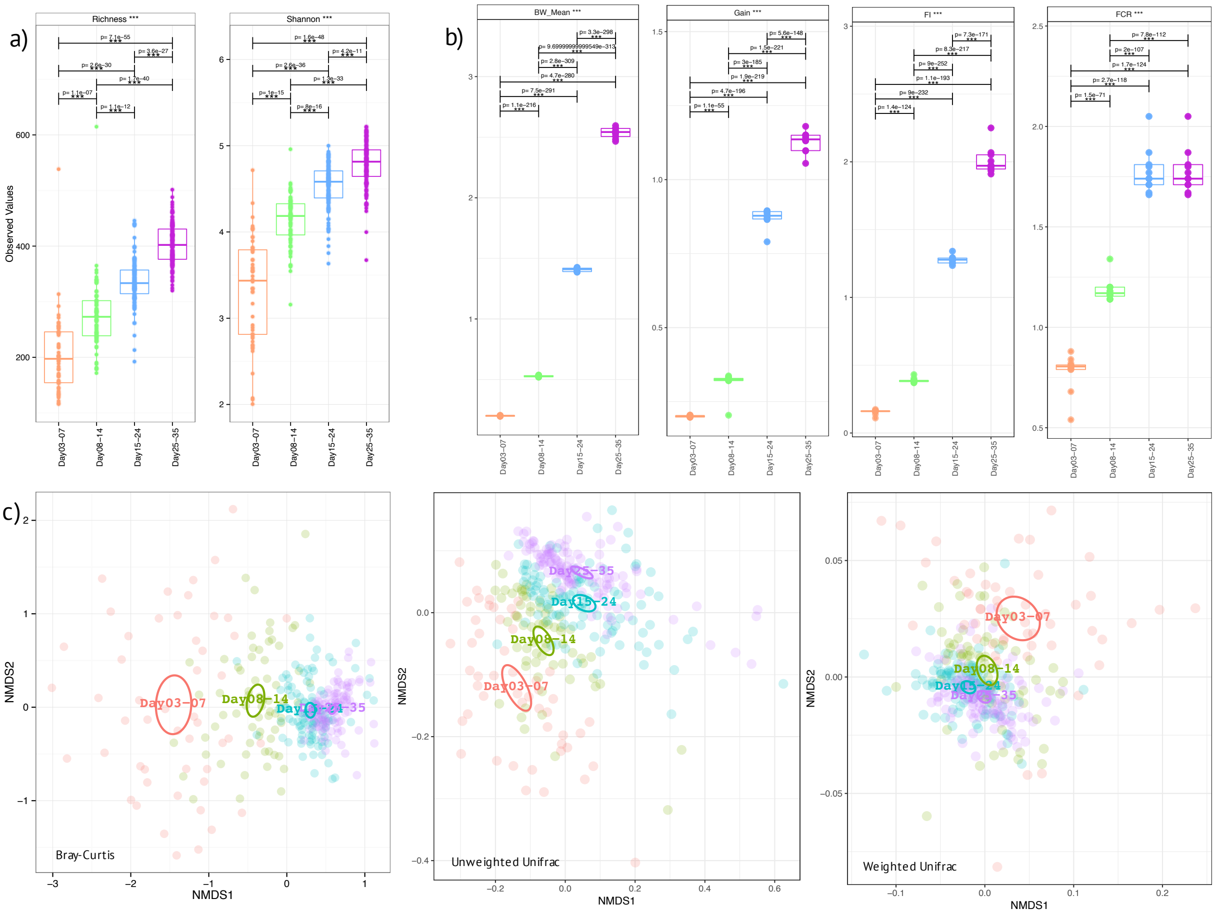

Figure 2: Week-wise measures calculated on the microbiome data a) Alpha diversity measures: Richness (after rarefying the samples to minimum library size) and Shannon entropy b) Extrinsic parameters calculated on weekly basis were mean body weight (BW_mean), body weight gain (Gain), feed intake (FI), feed conversion ratio (FCR), and c) Beta diversity measures using Bray-Curtis (counts), Unweighted Unifrac (phylogenetic distance), and Weighted Unifrac (phylogenetic distance weighted by abundance counts). In a) and b) we have performed pair-wise ANOVA and where significant the pairs were connected with p-values drawn on top. In c) the ellipses represent the 95% confidence interval of the standard error of the ordination points of a given grouping with labels drawn at the centre (mean) of the ordination points.

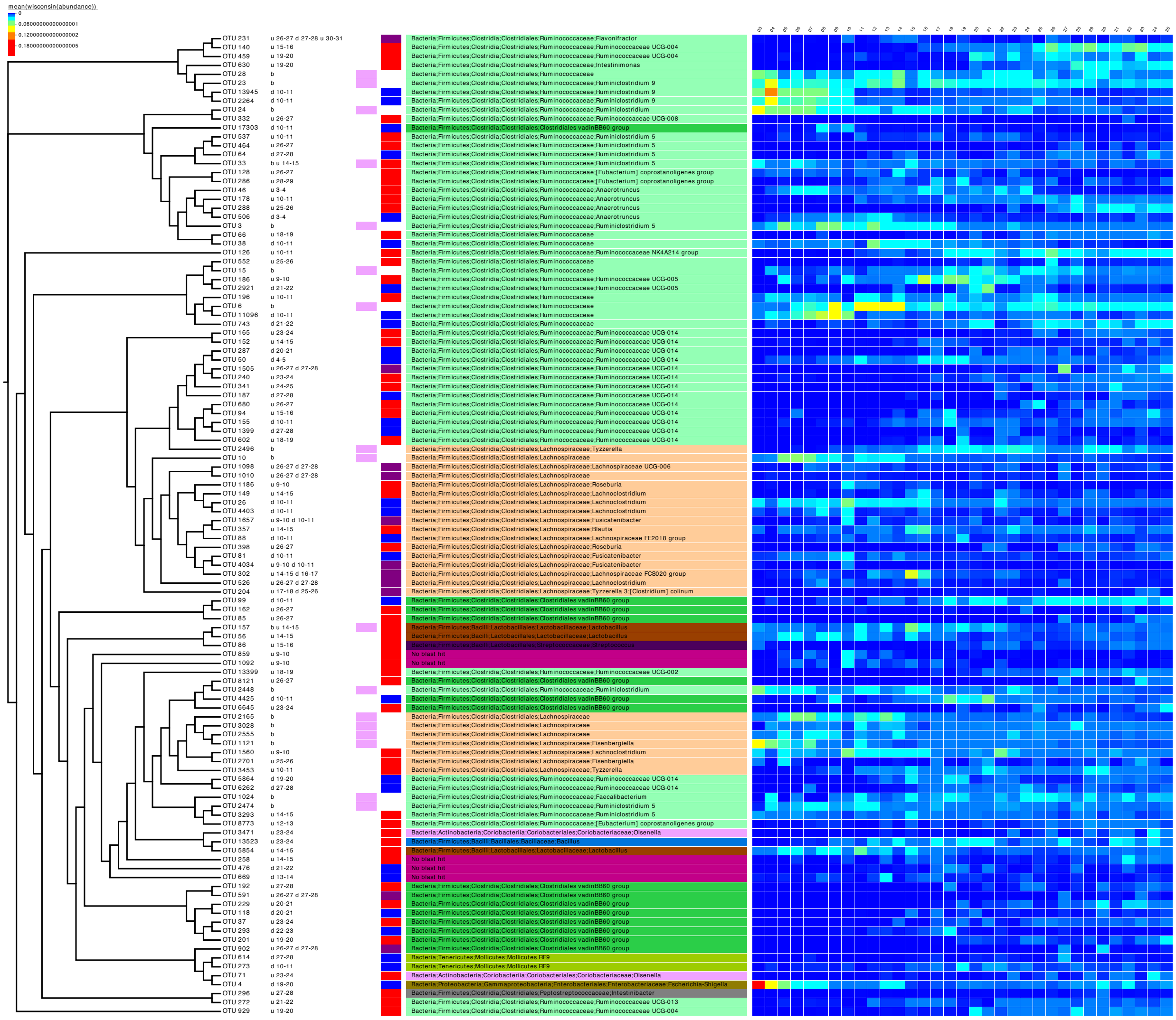

Figure 3: Phylogenetic tree of the subset of OTUs selected as significant on differential analysis (based on Table 3 and Supplementary Table 1). Next to the OTU labels are descriptive text representing where the OTUs were found to be significant, for example, the first entry for OTU 231, "u 26-27 d 27-28 u 30-31", can be read as upregulated going from day 26 to 27 and then from day 30 to 31 and downregulated going from day 27 to 28. "b" represents the OTUs selected in the subset analysis. The next two columns are a pictorial representation of the above-mentioned descriptive text with pink colour representing OTUs selected in subset analysis, red colour for upregulated OTUs, blue for downregulated OTUs, and purple for OTUs which show the both trends (up/down regulation). The next column shows the taxonomy of the OTUs according to SILVA v123 with colouring at unique family level. The heatmap was drawn by collating the

mean values of OTUs for samples from the same day after performing proportional standardization on the full OTU table using wisconsin() function.

622 Table 1: Statistics for beta dispersion comparison on daily microbiome data.

Day Comparisons	Bray-Curtis	Unweighted Unifrac	Weighted Unifrac
3 - 4	p = 0.018071 (*)	p = 0.18436	p = 0.085112
4 - 5	p = 0.85255	p = 0.18547	p = 0.25546
5 - 6	p = 0.60961	p = 0.1225	p = 0.73468
6 - 7	p = 0.82972	p = 0.94104	p = 0.21369
7 - 8	p = 0.71257	p = 0.88392	p = 0.47401
8 - 9	p = 0.060007	p = 0.94453	p = 0.36231
9 - 10	p = 0.9966	p = 0.11357	p = 0.53314
10 - 11	p = 0.20247	p = 0.20845	p = 0.13289
11 - 12	p = 0.38794	p = 0.014818 (*)	p = 0.62198
12 - 13	p = 0.88847	p = 0.064143	p = 0.013623 (*)
13 - 14	p = 0.63766	p = 0.16696	p = 0.41304
14 - 15	p = 0.9467	p = 0.64383	p = 0.46855
15 - 16	p = 0.89972	p = 0.055618	p = 0.79989
16 - 17	p = 0.59807	p = 0.37379	p = 0.41167
17 - 18	p = 0.70773	p = 0.66013	p = 0.30413
18 - 19	p = 0.40112	p = 0.92525	p = 0.5994
19 - 20	p = 0.020548 (*)	p = 0.087076	p = 0.56858
20 - 21	p = 0.033097 (*)	p = 0.12251	p = 0.52086
21 - 22	p = 0.29506	p = 0.055585	p = 0.90226
22 - 23	p = 0.24688	p = 0.90221	p = 0.99695
23 - 24	p = 0.79886	p = 0.71275	p = 0.34913
24 - 25	p = 0.21019	p = 0.67687	p = 0.11096
25 - 26	p = 0.14334	p = 0.20716	p = 0.97116
26 - 27	p = 0.96286	p = 0.044866 (*)	p = 0.80425
27 - 28	p = 0.50377	p = 0.096107	p = 0.1382
28 - 29	p = 0.91052	p = 0.87339	p = 0.69398
29 - 30	p = 0.34265	p = 0.60245	p = 0.11773
30 - 31	p = 0.61843	p = 0.55324	p = 0.20403
31 - 32	p = 0.24674	p = 0.082761	p = 0.50328
32 - 33	p = 0.73392	p = 0.53114	p = 0.62586
33 - 34	p = 0.7431	p = 0.36694	p = 0.57642
34 - 35	p = 0.16111	p = 0.20181	p = 0.77382

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Table 2: Statistics for pairwise beta dispersion and PERMANOVA when using different dissimilarity measures on weekly microbiome data. In beta dispersion analysis, the pair-wise differences in distances from group centre/mean were subjected to ANOVA after performing Principle Coordinate Analysis, and if significant ($p \leq 0.05$) the values are shown. In PERMANOVA analysis, R^2 represents the proportion of variability explained, for example, using "Groups" and "Bray-Curtis" dissimilarity, the weeks explain 16.8% variability in microbial community structure.

Beta dispersion		Bray-Curtis	Unweighted Unifrac	Weighted Unifrac
Day03-07	Day08-14	p = 0.0061142 (**)	p = 0.00014712 (***)	p = 9.6914e−05 (***)
	Day15-24	n.s.	p = 0.010418 (*)	p = 2.5203e−09 (***)
	Day25-35	p = 0.042066 (*)	p = 0.00015112 (***)	p = 3.5789e−12 (***)
Day08-14	Day15-24	p = 0.00077017 (***)	n.s.	p = 0.019953 (*)
	Day25-35	n.s.	n.s.	p = 0.0011717 (**)
Day15-24	Day25-35	p = 0.0075651 (**)	p = 0.020128 *	n.s.
PERMANOVA				
Groups		R^2 = 0.16763 (p = 0.001) (***)	R^2 = 0.06048 (p = 0.001) (***)	R^2 = 0.17577 (p = 0.001) (***)
BW_Mean		R^2 = 0.11721 (p = 0.001) (***)	R^2 = 0.03964 (p = 0.001) (***)	R^2 = 0.08723 (p = 0.001) (***)
FI		R^2 = 0.11856 (p = 0.001) (***)	R^2 = 0.04069 (p = 0.001) (***)	R^2 = 0.09301 (p = 0.001) (***)
FCR		R^2 = 0.1086 (p = 0.001) (***)	R^2 = 0.03842 (p = 0.001) (***)	R^2 = 0.11787 (p = 0.001) (***)
Gain		R^2 = 0.11886 (p = 0.001) (***)	R^2 = 0.04146 (p = 0.001) (***)	R^2 = 0.0998 (p = 0.001) (***)

Table 3: Subset analysis from BVSTEP routine listing top 18 subsets with highest correlation with the full OTU table considering Bray-Curtis distance done on weekly basis. For each subset, PERMANOVA was performed against different sources of variations.

Subsets of top 1000 most abundant OTUs		Correlation with full OTU table (R)	PERMANOVA (full OTU table)				
			Groups	BW_Mean	FI	FCR	Gain
			R^2 = 0.16763 (p = 0.001) (***)	R^2 = 0.11721 (p = 0.001) (***)	R^2 = 0.11856 (p = 0.001) (***)	R^2 = 0.1086 (p = 0.001) (***)	R^2 = 0.11886 (p = 0.001) (***)
			PERMANOVA (subsets)				
			Groups	BW_Mean	FI	FCR	Gain
S1	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_23 + OTU_2474 + OTU_6 + OTU_28 + OTU_157 + OTU_15 + OTU_24 + OTU_3028 + OTU_2496 + OTU_1024 + OTU_10 + OTU_3 + OTU_2555	0.833	R^2 = 0.14768 (p = 0.001) (***)	R^2 = 0.10732 (p = 0.001) (***)	R^2 = 0.10784 (p = 0.001) (***)	R^2 = 0.10117 (p = 0.001) (***)	R^2 = 0.11143 (p = 0.001) (***)
S2	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_23 + OTU_2474 + OTU_6 + OTU_28 + OTU_157 + OTU_15 + OTU_24 + OTU_3028 + OTU_2496 + OTU_1024 + OTU_3 + OTU_2555	0.83	R^2 = 0.13977 (p = 0.001) (***)	R^2 = 0.10028 (p = 0.001) (***)	R^2 = 0.09987 (p = 0.001) (***)	R^2 = 0.09203 (p = 0.001) (***)	R^2 = 0.1025 (p = 0.001) (***)
S3	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_23 + OTU_2474 + OTU_6 + OTU_28 + OTU_157 + OTU_15 + OTU_24 + OTU_3028 + OTU_2496 + OTU_1024 + OTU_3	0.827	R^2 = 0.14186 (p = 0.001) (***)	R^2 = 0.10205 (p = 0.001) (***)	R^2 = 0.10165 (p = 0.001) (***)	R^2 = 0.09344 (p = 0.001) (***)	R^2 = 0.10435 (p = 0.001) (***)

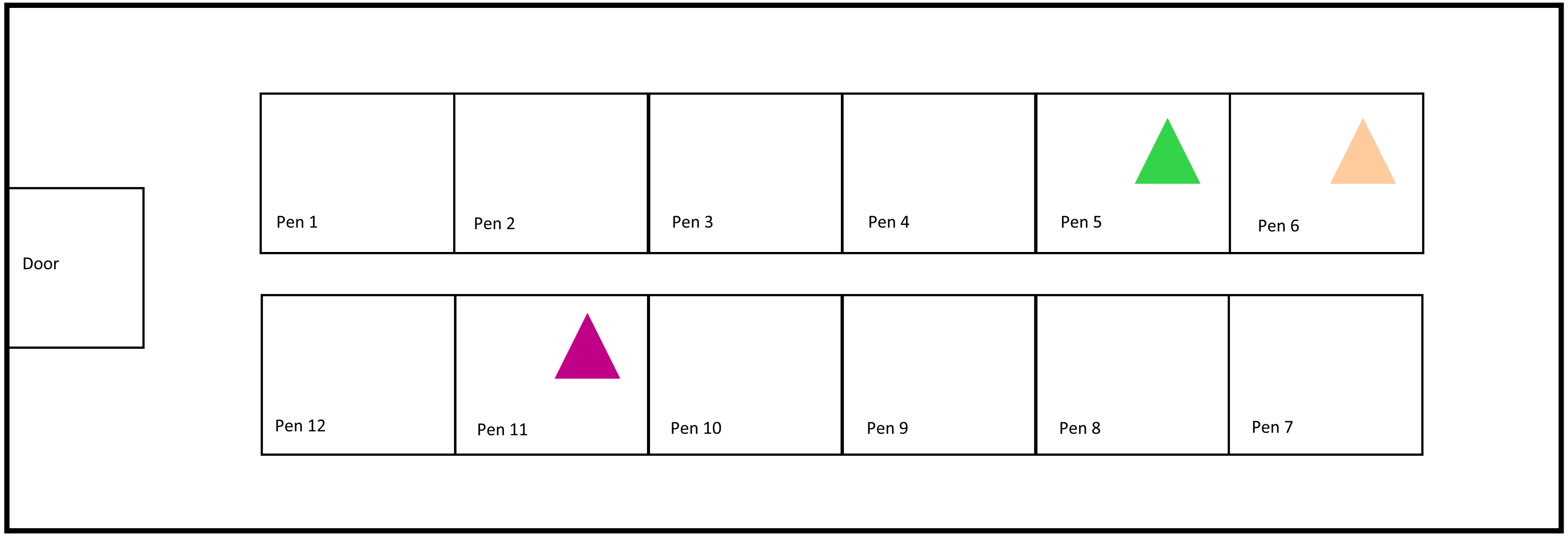
S4	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_23 + OTU_2474 + OTU_6 + OTU_28 + OTU_157 + OTU_15 + OTU_24 + OTU_2496 + OTU_1024 + OTU_3	0.823	R^2 = 0.14241 (p = 0.001) (***)	R^2 = 0.10262 (p = 0.001) (***)	R^2 = 0.10228 (p = 0.001) (***)	R^2 = 0.0939 (p = 0.001) (***)	R^2 = 0.10509 (p = 0.001) (***)
S5	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_23 + OTU_2474 + OTU_6 + OTU_28 + OTU_15 + OTU_24 + OTU_2496 + OTU_1024 + OTU_3	0.816	R^2 = 0.14289 (p = 0.001) (***)	R^2 = 0.10313 (p = 0.001) (***)	R^2 = 0.10279 (p = 0.001) (***)	R^2 = 0.09436 (p = 0.001) (***)	R^2 = 0.1056 (p = 0.001) (***)
S6	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_23 + OTU_2474 + OTU_6 + OTU_28 + OTU_15 + OTU_24 + OTU_2496 + OTU_1024	0.809	R^2 = 0.14742 (p = 0.001) (***)	R^2 = 0.10587 (p = 0.001) (***)	R^2 = 0.10556 (p = 0.001) (***)	R^2 = 0.098 (p = 0.001) (***)	R^2 = 0.1084 (p = 0.001) (***)
S7	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474 + OTU_6 + OTU_28 + OTU_15 + OTU_24 + OTU_2496 + OTU_1024	0.799	R^2 = 0.17779 (p = 0.001) (***)	R^2 = 0.12583 (p = 0.001) (***)	R^2 = 0.12598 (p = 0.001) (***)	R^2 = 0.11968 (p = 0.001) (***)	R^2 = 0.12936 (p = 0.001) (***)
S8	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474 + OTU_6 + OTU_28 + OTU_15 + OTU_24 + OTU_2496	0.789	R^2 = 0.14605 (p = 0.001) (***)	R^2 = 0.0875 (p = 0.001) (***)	R^2 = 0.08646 (p = 0.001) (***)	R^2 = 0.08927 (p = 0.001) (***)	R^2 = 0.08866 (p = 0.001) (***)
S9	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474 + OTU_28 + OTU_15 + OTU_24 + OTU_2496	0.777	R^2 = 0.14132 (p = 0.001) (***)	R^2 = 0.10216 (p = 0.001) (***)	R^2 = 0.10313 (p = 0.001) (***)	R^2 = 0.0989 (p = 0.001) (***)	R^2 = 0.10736 (p = 0.001) (***)

S10	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474 + OTU_28 + OTU_15 + OTU_24	0.763	R^2 = 0.13922 (p = 0.001) (***)	R^2 = 0.10051 (p = 0.001) (***)	R^2 = 0.10121 (p = 0.001) (***)	R^2 = 0.09676 (p = 0.001) (***)	R^2 = 0.10532 (p = 0.001) (***)
S11	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474 + OTU_28 + OTU_15	0.746	R^2 = 0.13173 (p = 0.001) (***)	R^2 = 0.09081 (p = 0.001) (***)	R^2 = 0.09291 (p = 0.001) (***)	R^2 = 0.09023 (p = 0.001) (***)	R^2 = 0.09828 (p = 0.001) (***)
S12	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474 + OTU_28	0.723	R^2 = 0.09574 (p = 0.001) (***)	R^2 = 0.04819 (p = 0.001) (***)	R^2 = 0.04936 (p = 0.001) (***)	R^2 = 0.05663 (p = 0.001) (***)	R^2 = 0.05163 (p = 0.001) (***)
S13	OTU_2165 + OTU_2448 + OTU_33 + OTU_1121 + OTU_2474	0.696	R^2 = 0.0952 (p = 0.001) (***)	R^2 = 0.04875 (p = 0.001) (***)	R^2 = 0.05019 (p = 0.001) (***)	R^2 = 0.05606 (p = 0.001) (***)	R^2 = 0.05246 (p = 0.001) (***)
S14	OTU_2165 + OTU_2448 + OTU_1121 + OTU_2474	0.661	R^2 = 0.10232 (p = 0.001) (***)	R^2 = 0.05483 (p = 0.001) (***)	R^2 = 0.05623 (p = 0.001) (***)	R^2 = 0.06108 (p = 0.001) (***)	R^2 = 0.05869 (p = 0.001) (***)
S15	OTU_2448 + OTU_33 + OTU_1121 + OTU_2474	0.655	R^2 = 0.06994 (p = 0.001) (***)	R^2 = 0.02489 (p = 0.001) (***)	R^2 = 0.02416 (p = 0.001) (***)	R^2 = 0.03155 (p = 0.001) (***)	R^2 = 0.02375 (p = 0.001) (***)
S16	OTU_2448 + OTU_33 + OTU_2474	0.604	R^2 = 0.03489 (p = 0.001) (***)	R^2 = 0.01348 (p = 0.003) (**)	R^2 = 0.01238 (p = 0.005) (**)	R^2 = 0.01154 (p = 0.006) (**)	R^2 = 0.01053 (p = 0.012) (*)
S17	OTU_33 + OTU_1121 + OTU_2474	0.599	R^2 = 0.06662 (p = 0.001) (***)	R^2 = 0.01995 (p = 0.001) (***)	R^2 = 0.02047 (p = 0.001) (***)	R^2 = 0.03201 (p = 0.001) (***)	R^2 = 0.02183 (p = 0.001) (***)
S18	OTU_1121 + OTU_2474	0.538	R^2 = 0.07 (p = 0.001) (***)	R^2 = 0.02571 (p = 0.001) (***)	R^2 = 0.02628 (p = 0.001) (***)	R^2 = 0.03796 (p = 0.001) (***)	R^2 = 0.02793 (p = 0.001) (***)

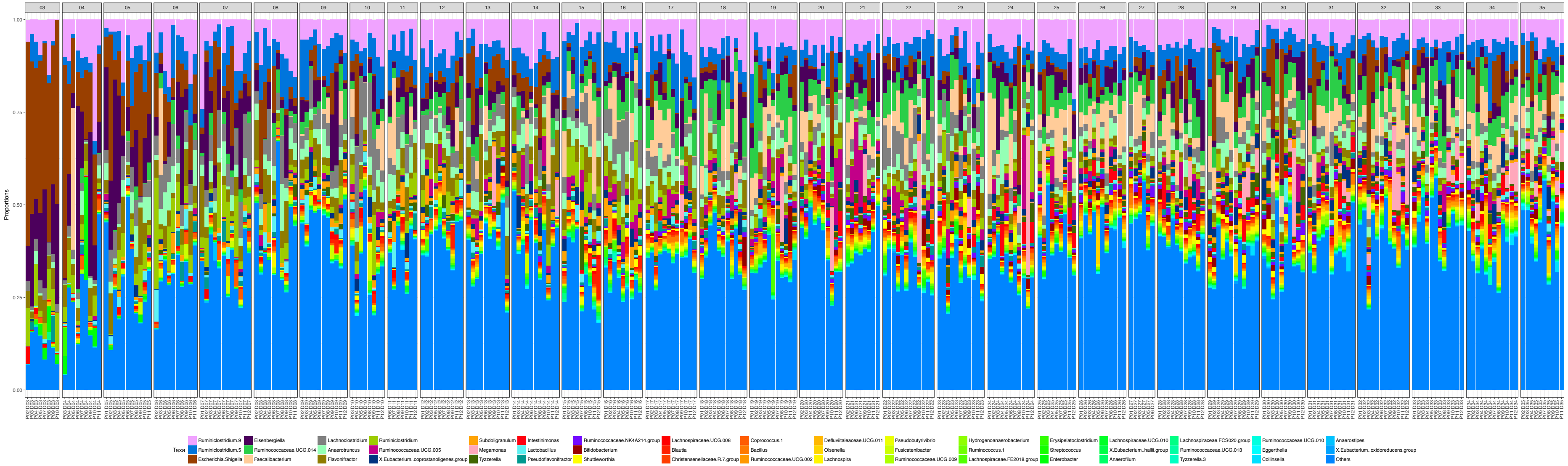
OTU_2165:Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae
OTU_2448:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium
OTU_33:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5
OTU_1121:Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella
OTU_23:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9
OTU_2474:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5
OTU_6:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae
OTU_28:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae
OTU_157:Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus
OTU_15:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae
OTU_24:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium
OTU_3028:Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae

OTU_2496:Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella
OTU_1024:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium
OTU_10:Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae
OTU_3:Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5
OTU_2555:Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae

Supplementary Figure 1: Spatial arrangement of pens. Triangles indicate pens with *Campylobacter*.



Supplementary Figure 2: Relative abundance of 50 most abundant genera in this study.



Supplementary Table 1: Differential analysis of OTUs that are up/down-regulated between different groups (Adjusted P values ≤ 0.05) where positive log2 fold change represent OTUs becoming abundant as we go forward in time. Here only the significant OTUs are shown for both daily and weekly comparisons.

OTUs	Base Mean Abundance	Log2 Fold Change	Group Comparison
OTU_46 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	85.84	2.11	03-04
OTU_504 No blast hit	10.63	-2.01	03-04
OTU_50 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	20.53	-2.24	04-05
OTU_1186 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	9.07	2.40	09-10
OTU_1560 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	1405.48	2.11	09-10
OTU_859 No blast hit	5.11	2.22	09-10
OTU_1657 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Fusicatenibacter	4.98	2.12	09-10
OTU_186 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	28.35	2.19	09-10
OTU_1092 No blast hit	4.39	2.05	09-10
OTU_4034 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Fusicatenibacter	5.71	2.10	09-10
OTU_537 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	4.95	2.05	10-11
OTU_196 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	21.31	2.29	10-11
OTU_3453 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	145.35	2.32	10-11
OTU_126 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	7.97	2.34	10-11
OTU_178 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	19.30	3.14	10-11
OTU_13945 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	18.09	-2.92	10-11
OTU_11096 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	7.83	-2.30	10-11
OTU_16519 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	7.75	-2.29	10-11
OTU_155 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	27.48	-2.25	10-11
OTU_99 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	46.84	-2.24	10-11
OTU_4425 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	53.73	-2.24	10-11
OTU_2264 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	12.43	-2.23	10-11
OTU_4403 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	7.48	-2.21	10-11
OTU_273 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	9.76	-2.20	10-11
OTU_81 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Fusicatenibacter	650.85	-2.17	10-11
OTU_17303 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	23.24	-2.17	10-11
OTU_38 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	678.29	-2.14	10-11
OTU_88 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae FE2018 group	496.93	-2.11	10-11

OTU_26 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	5197.77	-2.06	10-11
OTU_1657 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Fusicatenibacter	6.10	-2.06	10-11
OTU_4034 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Fusicatenibacter	7.03	-2.04	10-11
OTU_8773 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	27.71	2.03	12-13
OTU_669 No blast hit	8.63	-2.03	13-14
OTU_5854 Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	277.21	2.44	14-15
OTU_56 Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	446.98	2.41	14-15
OTU_157 Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	225.97	2.43	14-15
OTU_302 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae FCS020 group	86.06	2.37	14-15
OTU_152 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	29.02	2.38	14-15
OTU_149 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	182.29	2.34	14-15
OTU_258 No blast hit	11.99	2.28	14-15
OTU_3293 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	318.03	2.20	14-15
OTU_33 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	815.02	2.14	14-15
OTU_357 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia	21.50	2.10	14-15
OTU_86 Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	11.32	2.19	15-16
OTU_140 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	12.64	2.17	15-16
OTU_94 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	277.06	2.06	15-16
OTU_302 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae FCS020 group	62.39	-2.00	16-17
OTU_204 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella 3;[Clostridium] colinum	29.20	2.49	17-18
OTU_602 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	94.56	2.40	18-19
OTU_13399 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	10.76	2.07	18-19
OTU_66 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	25.13	2.02	18-19
OTU_201 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	17.76	2.11	19-20
OTU_459 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	7.79	2.16	19-20
OTU_929 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	10.94	2.40	19-20
OTU_630 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	22.84	2.42	19-20
OTU_4 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella	1987.33	-2.25	19-20
OTU_5864 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	302.73	-2.21	19-20
OTU_229 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	13.95	2.13	20-21
OTU_287 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	65.90	-2.13	20-21
OTU_118 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	195.16	-2.07	20-21
OTU_272 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-013	26.90	2.31	21-22

OTU_2921 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	6.80	-2.17	21-22
OTU_743 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	5.46	-2.03	21-22
OTU_476 No blast hit	8.71	-2.01	21-22
OTU_293 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	24.80	-2.17	22-23
OTU_71 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Olsenella	28.83	2.26	23-24
OTU_3471 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Olsenella	17.11	2.30	23-24
OTU_165 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	18.76	2.16	23-24
OTU_6645 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	16.81	2.14	23-24
OTU_240 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	66.78	2.13	23-24
OTU_13523 Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	137.89	2.01	23-24
OTU_37 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	310.22	2.12	23-24
OTU_341 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	12.91	2.25	24-25
OTU_288 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	29.58	2.07	25-26
OTU_552 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	326.78	2.10	25-26
OTU_2701 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	19.60	2.12	25-26
OTU_204 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella 3;[Clostridium] colinum	14.58	-2.14	25-26
OTU_128 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	71.82	2.91	26-27
OTU_398 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	13.92	2.79	26-27
OTU_85 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	782.32	2.68	26-27
OTU_591 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	10.78	2.63	26-27
OTU_680 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	13.73	2.63	26-27
OTU_1505 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.09	2.48	26-27
OTU_8121 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	299.08	2.53	26-27
OTU_902 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	9.22	2.55	26-27
OTU_526 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	34.07	2.42	26-27
OTU_231 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	30.02	2.46	26-27
OTU_1010 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	9.02	2.33	26-27
OTU_464 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	5.89	2.28	26-27
OTU_332 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-008	7.27	2.21	26-27
OTU_162 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	8.07	2.07	26-27
OTU_1098 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-006	6.95	2.04	26-27
OTU_192 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	35.57	2.16	27-28
OTU_296 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Intestinibacter	24.92	2.19	27-28
OTU_187 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	30.56	-3.16	27-28
OTU_64 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	710.20	-3.01	27-28

OTU_591 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	10.79	-2.72	27-28
OTU_231 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	29.68	-2.71	27-28
OTU_902 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	9.22	-2.63	27-28
OTU_1505 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.36	-2.34	27-28
OTU_614 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	14.55	-2.34	27-28
OTU_1010 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	9.09	-2.33	27-28
OTU_1098 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-006	6.77	-2.23	27-28
OTU_6262 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	431.75	-2.13	27-28
OTU_526 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	35.09	-2.12	27-28
OTU_1399 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	4.77	-2.03	27-28
OTU_286 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	29.74	2.15	28-29
OTU_231 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	41.42	2.04	30-31
OTU_95 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Subdoligranulum	81.73	5.92	Day03-07-Day08-14
OTU_248 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	43.97	5.71	Day03-07-Day08-14
OTU_155 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	24.39	5.05	Day03-07-Day08-14
OTU_172 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	25.21	4.76	Day03-07-Day08-14
OTU_136 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Enterobacter	217.12	-5.40	Day03-07-Day08-14
OTU_195 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Pseudobutyrivibrio	72.67	4.13	Day03-07-Day08-14
OTU_1016 Bacteria;Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus;unidentified marine bacterioplankton	7.52	-3.91	Day03-07-Day08-14
OTU_343 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	13.41	4.16	Day03-07-Day08-14
OTU_6332 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	92.80	-4.83	Day03-07-Day08-14
OTU_293 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	16.96	4.83	Day03-07-Day08-14
OTU_336 Bacteria;Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus;Enterococcus faecium DO	21.88	-3.91	Day03-07-Day08-14
OTU_113 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	299.35	-5.09	Day03-07-Day08-14

OTU_4065 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Subdoligranulum	39.33	3.86	Day03-07-Day08-14
OTU_170 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	24.40	3.96	Day03-07-Day08-14
OTU_34 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Subdoligranulum	158.74	4.41	Day03-07-Day08-14
OTU_275 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Acetitomaculum	6.90	3.30	Day03-07-Day08-14
OTU_12052 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella	21.11	-2.74	Day03-07-Day08-14
OTU_11502 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella;Shigella flexneri K-671	7.52	-2.24	Day03-07-Day08-14
OTU_123 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Eggerthella	104.91	3.16	Day03-07-Day08-14
OTU_3738 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella	47.68	-2.83	Day03-07-Day08-14
OTU_298 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	11.11	2.82	Day03-07-Day08-14
OTU_31 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	19.39	4.19	Day03-07-Day08-14
OTU_2587 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella	64.83	-2.78	Day03-07-Day08-14
OTU_109 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	35.09	4.06	Day03-07-Day08-14
OTU_13523 Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	71.97	4.09	Day03-07-Day08-14
OTU_86 Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	8.28	-3.17	Day03-07-Day08-14
OTU_466 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	4.88	2.56	Day03-07-Day08-14
OTU_5864 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.47	3.61	Day03-07-Day08-14
OTU_418 Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus;Lactobacillus coleohominis	4.54	2.79	Day03-07-Day08-14

OTU_179 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Acetanaerobacterium;Acetanaerobacterium elongatum	5.73	3.19	Day03-07-Day08-14
OTU_266 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	8.23	3.20	Day03-07-Day08-14
OTU_11103 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	7.31	-2.19	Day03-07-Day08-14
OTU_374 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	8.76	3.61	Day03-07-Day08-14
OTU_12293 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	8.47	3.29	Day03-07-Day08-14
OTU_2701 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	39.36	-4.00	Day03-07-Day08-14
OTU_327 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	7.65	2.37	Day03-07-Day08-14
OTU_290 Bacteria;Firmicutes;Clostridia;Clostridiales;Family XIII;[Eubacterium] nodatum group	7.78	2.67	Day03-07-Day08-14
OTU_99 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	39.47	3.76	Day03-07-Day08-14
OTU_16 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	48.58	3.80	Day03-07-Day08-14
OTU_92 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	17.26	3.67	Day03-07-Day08-14
OTU_198 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	8.28	3.38	Day03-07-Day08-14
OTU_477 NA;NA;NA;NA;NA;NA;NA	3.91	-2.94	Day03-07-Day08-14
OTU_507 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Cronobacter;Enterobacter sp. enrichment culture clone HSL2	3.97	-2.64	Day03-07-Day08-14
OTU_1369 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	11.53	-2.10	Day03-07-Day08-14
OTU_230 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	22.45	2.78	Day03-07-Day08-14
OTU_279 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	7.50	2.16	Day03-07-Day08-14

OTU_610 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	4.11	2.31	Day03-07-Day08-14
OTU_382 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	3.78	2.43	Day03-07-Day08-14
OTU_54 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	373.84	4.15	Day03-07-Day08-14
OTU_3453 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	122.69	3.52	Day03-07-Day08-14
OTU_286 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	6.63	3.10	Day03-07-Day08-14
OTU_12120 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	6.75	3.08	Day03-07-Day08-14
OTU_6707 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	21.36	3.60	Day03-07-Day08-14
OTU_305 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	11.30	3.12	Day03-07-Day08-14
OTU_417 No blast hit	5.16	2.84	Day03-07-Day08-14
OTU_138 Bacteria;Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus;Lactobacillus salivarius GJ-24	32.04	2.92	Day03-07-Day08-14
OTU_2496 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	8.43	3.02	Day03-07-Day08-14
OTU_80 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia	251.36	3.23	Day03-07-Day08-14
OTU_119 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia	138.97	2.84	Day03-07-Day08-14
OTU_180 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcus 1	8.05	2.89	Day03-07-Day08-14
OTU_105 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	5.21	2.95	Day03-07-Day08-14
OTU_686 No blast hit	2.82	-2.16	Day03-07-Day08-14
OTU_117 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	83.04	2.93	Day03-07-Day08-14
OTU_178 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	11.14	3.04	Day03-07-Day08-14

OTU_217 Bacteria;Firmicutes;Clostridia;Clostridiales;Family XIII;Family XIII UCG-001	3.71	2.37	Day03-07-Day08-14
OTU_235 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	7.07	2.80	Day03-07-Day08-14
OTU_67 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	32.67	3.20	Day03-07-Day08-14
OTU_83 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcus 1	5.08	3.00	Day03-07-Day08-14
OTU_454 No blast hit	7.13	2.29	Day03-07-Day08-14
OTU_285 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	3.57	2.43	Day03-07-Day08-14
OTU_15571 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	5.12	2.62	Day03-07-Day08-14
OTU_1047 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	3.80	2.53	Day03-07-Day08-14
OTU_73 Bacteria;Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	108.30	3.58	Day03-07-Day08-14
OTU_59 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	394.86	3.73	Day03-07-Day08-14
OTU_3700 Bacteria;Firmicutes;Clostridia;Clostridiales;Defluviitaleaceae;Defluviitaleaceae UCG-011	41.17	2.79	Day03-07-Day08-14
OTU_126 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	10.01	2.81	Day03-07-Day08-14
OTU_132 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	16.50	2.80	Day03-07-Day08-14
OTU_35 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	529.57	3.05	Day03-07-Day08-14
OTU_370 No blast hit	10.54	2.16	Day03-07-Day08-14
OTU_1 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	526.62	3.93	Day03-07-Day08-14
OTU_3296 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	7.38	2.07	Day03-07-Day08-14
OTU_13602 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	4.85	2.72	Day03-07-Day08-14

OTU_13 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	338.74	3.23	Day03-07-Day08-14
OTU_360 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcus 2	3.97	2.31	Day03-07-Day08-14
OTU_414 No blast hit	8.64	2.14	Day03-07-Day08-14
OTU_48 Bacteria;Firmicutes;Clostridia;Clostridiales;Defluviitaleaceae;Defluviitaleaceae UCG-011	101.45	2.81	Day03-07-Day08-14
OTU_218 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Butyricicoccus;Butyricicoccus pullicaecorum 1.2	6.60	2.63	Day03-07-Day08-14
OTU_242 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	2.88	2.07	Day03-07-Day08-14
OTU_127 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	41.18	2.37	Day03-07-Day08-14
OTU_267 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae	3.16	2.23	Day03-07-Day08-14
OTU_234 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae	10.21	2.00	Day03-07-Day08-14
OTU_319 No blast hit	9.23	2.24	Day03-07-Day08-14
OTU_3390 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	212.08	3.05	Day03-07-Day08-14
OTU_37 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	3.76	2.51	Day03-07-Day08-14
OTU_64 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	7.52	2.70	Day03-07-Day08-14
OTU_3027 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	16.05	2.80	Day03-07-Day08-14
OTU_149 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	10.91	2.39	Day03-07-Day08-14
OTU_9 Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Megamonas	3.26	2.28	Day03-07-Day08-14
OTU_314 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	2.92	2.06	Day03-07-Day08-14
OTU_68 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	3.48	2.39	Day03-07-Day08-14

OTU_148 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	48.86	2.87	Day03-07-Day08-14
OTU_301 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	16.18	2.15	Day03-07-Day08-14
OTU_5053 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	21.53	2.42	Day03-07-Day08-14
OTU_541 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-013	21.29	2.06	Day03-07-Day08-14
OTU_6463 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	11.11	2.29	Day03-07-Day08-14
OTU_358 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	8.39	2.09	Day03-07-Day08-14
OTU_243 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	38.69	2.85	Day03-07-Day08-14
OTU_220 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	34.91	2.23	Day03-07-Day08-14
OTU_778 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	4.12	2.18	Day03-07-Day08-14
OTU_21 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	10.68	2.49	Day03-07-Day08-14
OTU_526 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	7.88	2.17	Day03-07-Day08-14
OTU_167 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Shuttleworthia	30.99	2.31	Day03-07-Day08-14
OTU_185 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	5.43	2.08	Day03-07-Day08-14
OTU_42 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	5.73	2.42	Day03-07-Day08-14
OTU_36 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	378.13	2.82	Day03-07-Day08-14
OTU_101 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	2.98	2.13	Day03-07-Day08-14
OTU_130 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	9.26	2.24	Day03-07-Day08-14
OTU_14105 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-009	250.90	2.23	Day03-07-Day08-14

OTU_43 Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium;Bifidobacterium saeculare	4.58	2.15	Day03-07-Day08-14
OTU_6238 Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium;Bifidobacterium saeculare	3.20	2.00	Day03-07-Day08-14
OTU_79 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	2.87	2.07	Day03-07-Day08-14
OTU_108 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerofilum	48.59	2.53	Day03-07-Day08-14
OTU_1190 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium;Clostridiales bacterium DJF_B152	4.01	2.06	Day03-07-Day08-14
OTU_88 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae FE2018 group	174.59	2.33	Day03-07-Day08-14
OTU_605 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	14.53	2.06	Day03-07-Day08-14
OTU_4425 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	93.57	2.53	Day03-07-Day08-14
OTU_3463 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	7.95	2.06	Day03-07-Day08-14
OTU_380 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	35.61	2.06	Day03-07-Day08-14
OTU_315 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	38.25	-2.20	Day03-07-Day08-14
OTU_53 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	75.08	2.03	Day03-07-Day08-14
OTU_1729 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	539.18	2.68	Day03-07-Day08-14
OTU_14 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	1344.43	2.73	Day03-07-Day08-14
OTU_90 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	310.12	2.09	Day03-07-Day08-14
OTU_1024 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	637.20	2.02	Day03-07-Day08-14
OTU_86 Bacteria;Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	146.99	6.84	Day08-14-Day15-24

OTU_70 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	131.80	7.61	Day08-14-Day15-24
OTU_82 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	204.30	8.37	Day08-14-Day15-24
OTU_75 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	213.10	8.11	Day08-14-Day15-24
OTU_3674 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	96.35	7.18	Day08-14-Day15-24
OTU_94 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	65.43	6.19	Day08-14-Day15-24
OTU_97 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	67.16	6.27	Day08-14-Day15-24
OTU_7 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	132.53	7.44	Day08-14-Day15-24
OTU_199 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	41.01	5.24	Day08-14-Day15-24
OTU_102 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	74.23	6.48	Day08-14-Day15-24
OTU_207 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	41.70	5.76	Day08-14-Day15-24
OTU_116 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	140.11	5.88	Day08-14-Day15-24
OTU_137 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	47.10	6.14	Day08-14-Day15-24
OTU_6238 Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium;Bifidobacterium saeculare	160.11	5.64	Day08-14-Day15-24
OTU_101 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	159.98	5.74	Day08-14-Day15-24
OTU_114 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	53.67	6.44	Day08-14-Day15-24
OTU_63 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	115.45	5.83	Day08-14-Day15-24
OTU_142 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-010	42.68	5.53	Day08-14-Day15-24

OTU_214 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	116.69	6.62	Day08-14-Day15-24
OTU_140 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	20.32	4.52	Day08-14-Day15-24
OTU_1938 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	78.43	6.48	Day08-14-Day15-24
OTU_154 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	95.76	5.25	Day08-14-Day15-24
OTU_43 Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium;Bifidobacterium saeculare	410.24	5.72	Day08-14-Day15-24
OTU_111 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	37.58	5.92	Day08-14-Day15-24
OTU_6396 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	64.58	5.88	Day08-14-Day15-24
OTU_55 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	438.98	6.96	Day08-14-Day15-24
OTU_173 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	47.69	4.95	Day08-14-Day15-24
OTU_151 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	32.42	5.66	Day08-14-Day15-24
OTU_84 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	142.18	5.44	Day08-14-Day15-24
OTU_156 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillospira	31.57	5.18	Day08-14-Day15-24
OTU_66 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	43.21	5.76	Day08-14-Day15-24
OTU_6262 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	268.68	5.27	Day08-14-Day15-24
OTU_87 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	128.64	5.16	Day08-14-Day15-24
OTU_118 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	54.77	5.99	Day08-14-Day15-24
OTU_7674 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	26.95	5.43	Day08-14-Day15-24

OTU_191 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	25.65	4.22	Day08-14-Day15-24
OTU_228 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	20.31	5.02	Day08-14-Day15-24
OTU_233 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 1	16.34	4.43	Day08-14-Day15-24
OTU_15527 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	20.71	5.04	Day08-14-Day15-24
OTU_124 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	79.40	4.90	Day08-14-Day15-24
OTU_105 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	101.24	4.19	Day08-14-Day15-24
OTU_159 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	100.19	4.93	Day08-14-Day15-24
OTU_5826 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	22.74	5.04	Day08-14-Day15-24
OTU_8131 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	58.18	4.54	Day08-14-Day15-24
OTU_213 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	19.70	4.97	Day08-14-Day15-24
OTU_6791 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	8.57	3.54	Day08-14-Day15-24
OTU_169 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	22.49	5.08	Day08-14-Day15-24
OTU_179 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Acetanaerobacterium;Acetanaerobacterium elongatum	52.84	3.14	Day08-14-Day15-24
OTU_254 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	19.07	3.45	Day08-14-Day15-24
OTU_438 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium	27.85	4.88	Day08-14-Day15-24
OTU_184 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	16.28	4.20	Day08-14-Day15-24
OTU_263 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	14.70	4.52	Day08-14-Day15-24

OTU_249 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerofilum	9.72	3.88	Day08-14-Day15-24
OTU_7826 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	90.77	4.58	Day08-14-Day15-24
OTU_130 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	96.14	3.42	Day08-14-Day15-24
OTU_14407 Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Megamonas;unidentified	132.33	5.81	Day08-14-Day15-24
OTU_162 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	22.40	5.05	Day08-14-Day15-24
OTU_369 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	10.35	3.69	Day08-14-Day15-24
OTU_201 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	14.31	4.48	Day08-14-Day15-24
OTU_74 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	106.89	3.98	Day08-14-Day15-24
OTU_602 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	35.39	4.55	Day08-14-Day15-24
OTU_13399 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	18.11	3.79	Day08-14-Day15-24
OTU_292 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	10.58	3.41	Day08-14-Day15-24
OTU_229 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	13.21	4.38	Day08-14-Day15-24
OTU_283 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	9.75	3.86	Day08-14-Day15-24
OTU_100 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	76.00	4.46	Day08-14-Day15-24
OTU_9 Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Megamonas	142.36	5.55	Day08-14-Day15-24
OTU_37 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	124.49	5.12	Day08-14-Day15-24
OTU_312 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	11.39	4.16	Day08-14-Day15-24
OTU_15345 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	10.57	4.05	Day08-14-Day15-24

OTU_250 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	8.07	3.47	Day08-14-Day15-24
OTU_399 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	12.76	3.95	Day08-14-Day15-24
OTU_552 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	21.66	3.88	Day08-14-Day15-24
OTU_209 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	13.63	3.77	Day08-14-Day15-24
OTU_630 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	12.89	3.64	Day08-14-Day15-24
OTU_242 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	24.98	3.17	Day08-14-Day15-24
OTU_6645 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	11.08	4.12	Day08-14-Day15-24
OTU_241 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae V9D2013 group	12.69	3.40	Day08-14-Day15-24
OTU_368 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae 1;Candidatus Arthromitus	9.66	-2.54	Day08-14-Day15-24
OTU_135 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	9.60	3.86	Day08-14-Day15-24
OTU_208 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	18.06	3.22	Day08-14-Day15-24
OTU_389 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	8.64	2.93	Day08-14-Day15-24
OTU_240 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	15.05	3.26	Day08-14-Day15-24
OTU_329 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	6.40	3.11	Day08-14-Day15-24
OTU_373 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-010	6.91	3.11	Day08-14-Day15-24
OTU_328 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia	20.30	-2.76	Day08-14-Day15-24
OTU_149 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	137.68	3.67	Day08-14-Day15-24
OTU_346 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-010	6.55	2.35	Day08-14-Day15-24

OTU_126 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	81.97	2.99	Day08-14-Day15-24
OTU_359 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Marvinbryantia	7.61	3.01	Day08-14-Day15-24
OTU_113 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	8.98	-3.23	Day08-14-Day15-24
OTU_237 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	17.34	2.81	Day08-14-Day15-24
OTU_225 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	43.80	3.44	Day08-14-Day15-24
OTU_152 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	65.87	3.73	Day08-14-Day15-24
OTU_83 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcus 1	198.87	3.72	Day08-14-Day15-24
OTU_287 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.93	3.36	Day08-14-Day15-24
OTU_197 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelatoclostridium;bacterium ic1391	63.37	2.83	Day08-14-Day15-24
OTU_622 Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;Corynebacterium 1;Corynebacterium glutamicum	3.64	-2.20	Day08-14-Day15-24
OTU_371 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae NK4A136 group	5.52	2.36	Day08-14-Day15-24
OTU_76 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	7.77	3.58	Day08-14-Day15-24
OTU_386 Bacteria;Firmicutes;Clostridia;Clostridiales;Caldicoprobacteraceae;Caldicoprobacter	5.64	3.09	Day08-14-Day15-24
OTU_193 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	7.05	3.39	Day08-14-Day15-24
OTU_16519 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	3.22	-2.17	Day08-14-Day15-24
OTU_153 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;[Eubacterium] oxidoreducens group	9.27	3.58	Day08-14-Day15-24
OTU_222 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	11.37	2.94	Day08-14-Day15-24

OTU_284 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	10.44	2.70	Day08-14-Day15-24
OTU_270 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	5.73	2.82	Day08-14-Day15-24
OTU_12120 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	54.10	2.92	Day08-14-Day15-24
OTU_6463 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	66.64	2.56	Day08-14-Day15-24
OTU_180 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcus 1	57.87	2.77	Day08-14-Day15-24
OTU_2511 Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium;Bifidobacterium saeculare	6.48	2.90	Day08-14-Day15-24
OTU_2496 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	53.00	2.55	Day08-14-Day15-24
OTU_295 No blast hit	9.62	-2.60	Day08-14-Day15-24
OTU_388 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	4.74	2.82	Day08-14-Day15-24
OTU_204 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella 3;[Clostridium] colinum	9.45	3.33	Day08-14-Day15-24
OTU_510 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	12.38	2.87	Day08-14-Day15-24
OTU_364 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Candidatus Soleaferrea	8.15	2.80	Day08-14-Day15-24
OTU_309 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	6.77	2.57	Day08-14-Day15-24
OTU_343 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	90.41	2.58	Day08-14-Day15-24
OTU_16 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	683.60	3.70	Day08-14-Day15-24
OTU_500 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-010	4.57	2.71	Day08-14-Day15-24
OTU_79 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	180.56	4.01	Day08-14-Day15-24

OTU_880 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	7.07	2.97	Day08-14-Day15-24
OTU_174 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelatoclostridium	46.11	2.87	Day08-14-Day15-24
OTU_6638 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	5.68	2.93	Day08-14-Day15-24
OTU_264 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	8.25	2.88	Day08-14-Day15-24
OTU_2701 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Eisenbergiella	45.88	3.77	Day08-14-Day15-24
OTU_746 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-010	6.32	2.88	Day08-14-Day15-24
OTU_202 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	35.96	2.28	Day08-14-Day15-24
OTU_646 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	8.52	2.51	Day08-14-Day15-24
OTU_767 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.86	2.54	Day08-14-Day15-24
OTU_172 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	222.20	2.98	Day08-14-Day15-24
OTU_424 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	12.02	2.38	Day08-14-Day15-24
OTU_92 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	137.86	2.88	Day08-14-Day15-24
OTU_564 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	4.01	2.39	Day08-14-Day15-24
OTU_185 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	33.33	2.63	Day08-14-Day15-24
OTU_1277 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	7.89	-2.46	Day08-14-Day15-24
OTU_12336 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	4.75	2.39	Day08-14-Day15-24
OTU_3027 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	479.66	3.46	Day08-14-Day15-24
OTU_219 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	15.89	3.21	Day08-14-Day15-24

OTU_67 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	209.10	2.56	Day08-14-Day15-24
OTU_5864 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	189.15	3.27	Day08-14-Day15-24
OTU_217 Bacteria;Firmicutes;Clostridia;Clostridiales;Family XIII;Family XIII UCG-001	17.87	2.19	Day08-14-Day15-24
OTU_9820 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium	57.03	3.14	Day08-14-Day15-24
OTU_421 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	7.36	2.58	Day08-14-Day15-24
OTU_305 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	72.72	2.58	Day08-14-Day15-24
OTU_17 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	165.76	3.90	Day08-14-Day15-24
OTU_194 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	20.71	3.12	Day08-14-Day15-24
OTU_255 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	9.58	2.65	Day08-14-Day15-24
OTU_13320 Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium;Bifidobacterium saeculare	4.16	2.39	Day08-14-Day15-24
OTU_763 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	10.16	2.37	Day08-14-Day15-24
OTU_146 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	4.25	2.65	Day08-14-Day15-24
OTU_31 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	1100.28	4.04	Day08-14-Day15-24
OTU_378 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	4.19	2.51	Day08-14-Day15-24
OTU_7809 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;[Eubacterium] oxidoreducens group	6.94	2.84	Day08-14-Day15-24
OTU_316 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-013	4.43	2.64	Day08-14-Day15-24
OTU_15166 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	5.87	2.41	Day08-14-Day15-24

OTU_317 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	4.68	2.58	Day08-14-Day15-24
OTU_273 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	30.80	2.69	Day08-14-Day15-24
OTU_750 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	8.33	2.45	Day08-14-Day15-24
OTU_6846 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	7.33	2.43	Day08-14-Day15-24
OTU_356 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Faecalitalea	6.25	2.43	Day08-14-Day15-24
OTU_479 No blast hit	3.23	-2.01	Day08-14-Day15-24
OTU_182 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	20.17	2.98	Day08-14-Day15-24
OTU_836 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	5.15	2.14	Day08-14-Day15-24
OTU_107 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium	148.00	3.17	Day08-14-Day15-24
OTU_577 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	3.81	2.38	Day08-14-Day15-24
OTU_166 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelatoclostridium	65.59	2.06	Day08-14-Day15-24
OTU_6332 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor	3.83	-2.15	Day08-14-Day15-24
OTU_161 Bacteria;Firmicutes;Clostridia;Clostridiales;Family XII;Fusibacter	3.99	2.55	Day08-14-Day15-24
OTU_177 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-009	24.17	2.97	Day08-14-Day15-24
OTU_165 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	4.10	2.56	Day08-14-Day15-24
OTU_315 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	7.89	-2.18	Day08-14-Day15-24
OTU_210 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	23.28	2.21	Day08-14-Day15-24
OTU_497 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	4.96	2.09	Day08-14-Day15-24

OTU_106 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	104.58	2.08	Day08-14-Day15-24
OTU_423 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae UCG-008	7.32	2.08	Day08-14-Day15-24
OTU_13602 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	41.62	3.06	Day08-14-Day15-24
OTU_6277 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Pseudobutyrivibrio	87.04	2.87	Day08-14-Day15-24
OTU_62 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Pseudobutyrivibrio	131.08	2.89	Day08-14-Day15-24
OTU_1549 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	3.94	2.10	Day08-14-Day15-24
OTU_192 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	3.99	2.55	Day08-14-Day15-24
OTU_508 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	49.63	2.70	Day08-14-Day15-24
OTU_203 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	11.94	2.47	Day08-14-Day15-24
OTU_353 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	3.95	2.35	Day08-14-Day15-24
OTU_71 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Olsenella	12.89	2.88	Day08-14-Day15-24
OTU_422 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	5.90	2.05	Day08-14-Day15-24
OTU_367 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	3.25	2.21	Day08-14-Day15-24
OTU_291 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae NK4A136 group	3.47	2.32	Day08-14-Day15-24
OTU_68 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	99.81	3.08	Day08-14-Day15-24
OTU_1194 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	14.01	2.35	Day08-14-Day15-24
OTU_132 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	90.58	2.35	Day08-14-Day15-24
OTU_282 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	3.15	2.16	Day08-14-Day15-24

OTU_311 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	3.33	2.25	Day08-14-Day15-24
OTU_285 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	15.67	2.03	Day08-14-Day15-24
OTU_322 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	3.16	2.19	Day08-14-Day15-24
OTU_390 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.20	2.18	Day08-14-Day15-24
OTU_605 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	63.31	2.07	Day08-14-Day15-24
OTU_3471 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Olsenella	7.95	2.54	Day08-14-Day15-24
OTU_47 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	53.47	2.70	Day08-14-Day15-24
OTU_2618 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	49.41	2.38	Day08-14-Day15-24
OTU_168 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	226.03	2.17	Day08-14-Day15-24
OTU_296 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;Intestinibacter	5.42	2.08	Day08-14-Day15-24
OTU_198 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium	43.74	2.23	Day08-14-Day15-24
OTU_4604 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	12.66	2.43	Day08-14-Day15-24
OTU_89 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	119.98	2.03	Day08-14-Day15-24
OTU_2398 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	3.54	2.00	Day08-14-Day15-24
OTU_6012 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	55.27	2.67	Day08-14-Day15-24
OTU_64 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	57.47	2.89	Day08-14-Day15-24
OTU_261 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	2.93	2.04	Day08-14-Day15-24
OTU_271 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	5.35	2.09	Day08-14-Day15-24

OTU_12293 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	44.09	2.22	Day08-14-Day15-24
OTU_178 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	53.06	2.09	Day08-14-Day15-24
OTU_109 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	171.14	2.06	Day08-14-Day15-24
OTU_6707 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	196.56	2.59	Day08-14-Day15-24
OTU_3463 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	232.87	2.24	Day08-14-Day15-24
OTU_21 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	511.16	2.44	Day08-14-Day15-24
OTU_218 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Butyricicoccus;Butyricicoccus pullicaecorum 1.2	50.48	2.03	Day08-14-Day15-24
OTU_293 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	102.58	2.38	Day08-14-Day15-24
OTU_145 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	139.30	7.98	Day15-24-Day25-35
OTU_58 Bacteria;Cyanobacteria;Melainabacteria;Gastranaerophilales	900.13	9.81	Day15-24-Day25-35
OTU_160 Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Gelria	82.01	6.61	Day15-24-Day25-35
OTU_143 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	120.12	7.06	Day15-24-Day25-35
OTU_221 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnoclostridium	48.19	6.25	Day15-24-Day25-35
OTU_85 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	73.47	7.07	Day15-24-Day25-35
OTU_288 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	28.95	4.91	Day15-24-Day25-35
OTU_120 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	97.46	6.93	Day15-24-Day25-35
OTU_211 Bacteria;Tenericutes;Mollicutes;NB1-n	55.87	6.57	Day15-24-Day25-35
OTU_308 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	21.44	5.28	Day15-24-Day25-35

OTU_343 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	620.73	2.98	Day15-24-Day25-35
OTU_341 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	17.13	4.53	Day15-24-Day25-35
OTU_625 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	29.50	4.00	Day15-24-Day25-35
OTU_13431 Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;Thermoanaerobacteraceae;Gelria	34.18	5.11	Day15-24-Day25-35
OTU_8121 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	31.11	5.85	Day15-24-Day25-35
OTU_430 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	9.34	3.40	Day15-24-Day25-35
OTU_347 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-010	18.21	5.03	Day15-24-Day25-35
OTU_146 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	109.29	4.96	Day15-24-Day25-35
OTU_293 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	98.26	-5.68	Day15-24-Day25-35
OTU_339 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	17.88	2.86	Day15-24-Day25-35
OTU_350 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	17.76	3.21	Day15-24-Day25-35
OTU_496 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	8.16	2.89	Day15-24-Day25-35
OTU_671 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	13.18	4.04	Day15-24-Day25-35
OTU_144 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	51.35	-4.37	Day15-24-Day25-35
OTU_338 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	18.09	3.71	Day15-24-Day25-35
OTU_298 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	116.07	2.55	Day15-24-Day25-35
OTU_244 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	29.45	5.01	Day15-24-Day25-35
OTU_404 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	10.09	3.86	Day15-24-Day25-35

OTU_640 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	12.65	4.39	Day15-24-Day25-35
OTU_1020 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	23.11	4.15	Day15-24-Day25-35
OTU_277 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	24.63	4.62	Day15-24-Day25-35
OTU_697 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	11.56	4.11	Day15-24-Day25-35
OTU_216 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	46.16	4.37	Day15-24-Day25-35
OTU_282 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	31.78	3.32	Day15-24-Day25-35
OTU_161 Bacteria;Firmicutes;Clostridia;Clostridiales;Family XII;Fusibacter	132.46	4.35	Day15-24-Day25-35
OTU_355 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	12.62	4.27	Day15-24-Day25-35
OTU_410 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Subdoligranulum	23.11	4.51	Day15-24-Day25-35
OTU_379 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	7.50	3.68	Day15-24-Day25-35
OTU_530 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Gordonibacter	4.96	2.88	Day15-24-Day25-35
OTU_141 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	194.57	4.91	Day15-24-Day25-35
OTU_542 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae 1	6.06	2.87	Day15-24-Day25-35
OTU_572 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	5.30	3.18	Day15-24-Day25-35
OTU_577 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	28.51	3.14	Day15-24-Day25-35
OTU_280 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	21.26	3.22	Day15-24-Day25-35
OTU_6791 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	42.99	2.38	Day15-24-Day25-35
OTU_2200 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	7.14	3.14	Day15-24-Day25-35

OTU_278 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	16.49	-3.13	Day15-24-Day25-35
OTU_115 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Collinsella;Enorma massiliensis phI	184.33	4.87	Day15-24-Day25-35
OTU_557 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	5.43	2.82	Day15-24-Day25-35
OTU_270 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	31.95	2.62	Day15-24-Day25-35
OTU_165 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	149.80	4.40	Day15-24-Day25-35
OTU_549 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	5.28	3.17	Day15-24-Day25-35
OTU_481 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	6.78	2.29	Day15-24-Day25-35
OTU_398 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	6.82	3.54	Day15-24-Day25-35
OTU_392 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	14.64	2.21	Day15-24-Day25-35
OTU_3813 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	10.60	-2.95	Day15-24-Day25-35
OTU_400 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	10.69	2.81	Day15-24-Day25-35
OTU_322 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Tyzzerella	21.49	3.01	Day15-24-Day25-35
OTU_140 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-004	107.30	2.43	Day15-24-Day25-35
OTU_365 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	9.73	3.25	Day15-24-Day25-35
OTU_763 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	47.88	2.38	Day15-24-Day25-35
OTU_520 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	6.91	2.85	Day15-24-Day25-35
OTU_276 Bacteria;Proteobacteria;Gammaproteobacteria;Pasteurellales;Pasteurellaceae;Gallibacterium;Gallibacterium anatis	14.63	3.35	Day15-24-Day25-35

OTU_47 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	531.12	3.55	Day15-24-Day25-35
OTU_585 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-010	3.94	2.29	Day15-24-Day25-35
OTU_311 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	55.18	3.47	Day15-24-Day25-35
OTU_580 Bacteria;Tenericutes;Mollicutes;Mollicutes RF9	3.86	2.55	Day15-24-Day25-35
OTU_3471 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Olsenella	197.09	4.30	Day15-24-Day25-35
OTU_548 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	6.75	2.33	Day15-24-Day25-35
OTU_2760 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	189.84	-2.95	Day15-24-Day25-35
OTU_46 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Anaerotruncus	359.69	-2.94	Day15-24-Day25-35
OTU_200 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	6.22	3.34	Day15-24-Day25-35
OTU_302 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae FCS020 group	21.20	-2.37	Day15-24-Day25-35
OTU_304 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-010	25.57	2.90	Day15-24-Day25-35
OTU_294 Bacteria;Cyanobacteria;Melainabacteria;Gastranaerophilales	5.32	3.14	Day15-24-Day25-35
OTU_71 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Olsenella	321.67	4.29	Day15-24-Day25-35
OTU_203 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	56.27	2.37	Day15-24-Day25-35
OTU_187 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	32.88	3.78	Day15-24-Day25-35
OTU_547 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	6.03	2.32	Day15-24-Day25-35
OTU_15166 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	33.90	2.72	Day15-24-Day25-35
OTU_425 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	4.72	2.80	Day15-24-Day25-35

OTU_442 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-013	9.14	2.42	Day15-24-Day25-35
OTU_281 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	27.93	2.94	Day15-24-Day25-35
OTU_158 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-008	37.33	3.20	Day15-24-Day25-35
OTU_579 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	5.14	2.28	Day15-24-Day25-35
OTU_13511 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-005	5.65	2.37	Day15-24-Day25-35
OTU_372 Bacteria;Actinobacteria;Coriobacteriia;Coriobacteriales;Coriobacteriaceae;Coriobacteriaceae UCG-002	8.28	2.73	Day15-24-Day25-35
OTU_250 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	37.27	2.25	Day15-24-Day25-35
OTU_76 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	415.79	3.79	Day15-24-Day25-35
OTU_630 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Intestinimonas	106.71	2.89	Day15-24-Day25-35
OTU_853 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	2.85	2.14	Day15-24-Day25-35
OTU_128 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	80.82	-3.70	Day15-24-Day25-35
OTU_332 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-008	5.84	2.83	Day15-24-Day25-35
OTU_153 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;[Eubacterium] oxidoreducens group	101.01	2.81	Day15-24-Day25-35
OTU_13399 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-002	97.82	2.49	Day15-24-Day25-35
OTU_680 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	9.12	2.91	Day15-24-Day25-35
OTU_7809 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;[Eubacterium] oxidoreducens group	54.13	2.64	Day15-24-Day25-35
OTU_1505 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	3.65	2.21	Day15-24-Day25-35
OTU_317 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	22.02	2.36	Day15-24-Day25-35

OTU_436 No blast hit	3.45	2.48	Day15-24-Day25-35
OTU_464 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	3.98	2.52	Day15-24-Day25-35
OTU_291 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae NK4A136 group	18.43	2.58	Day15-24-Day25-35
OTU_6396 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	512.09	3.06	Day15-24-Day25-35
OTU_775 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae	2.85	2.16	Day15-24-Day25-35
OTU_381 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	46.10	2.15	Day15-24-Day25-35
OTU_503 No blast hit	3.74	2.03	Day15-24-Day25-35
OTU_135 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae NK4A214 group	260.87	3.08	Day15-24-Day25-35
OTU_3901 Bacteria;Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia-Shigella;Shigella flexneri K-671	14.27	2.32	Day15-24-Day25-35
OTU_655 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium	2.77	2.10	Day15-24-Day25-35
OTU_380 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	422.96	2.15	Day15-24-Day25-35
OTU_100 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	402.31	2.43	Day15-24-Day25-35
OTU_2893 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	4.84	2.08	Day15-24-Day25-35
OTU_761 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Hydrogenoanaerobacterium	2.67	2.04	Day15-24-Day25-35
OTU_6645 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	179.75	3.40	Day15-24-Day25-35
OTU_534 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 5	8.06	2.02	Day15-24-Day25-35
OTU_555 No blast hit	3.26	2.05	Day15-24-Day25-35
OTU_491 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	10.10	2.32	Day15-24-Day25-35

OTU_439 Bacteria;Lentisphaerae;Lentisphaeria;Victivallales;Victivallaceae;Victivallis;Victivallis vadensis	2.98	2.18	Day15-24-Day25-35
OTU_177 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-009	114.43	2.33	Day15-24-Day25-35
OTU_169 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	158.72	2.51	Day15-24-Day25-35
OTU_252 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Coprococcus 1	29.25	2.37	Day15-24-Day25-35
OTU_271 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	48.59	2.32	Day15-24-Day25-35
OTU_245 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	33.84	2.44	Day15-24-Day25-35
OTU_38 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	529.38	-2.14	Day15-24-Day25-35
OTU_97 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	287.01	2.03	Day15-24-Day25-35
OTU_1938 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	956.00	2.61	Day15-24-Day25-35
OTU_156 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillospira	133.49	2.03	Day15-24-Day25-35
OTU_261 Bacteria;Firmicutes;Clostridia;Clostridiales;Christensenellaceae;Christensenellaceae R-7 group	37.88	2.33	Day15-24-Day25-35
OTU_316 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-013	17.58	2.05	Day15-24-Day25-35
OTU_627 Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;[Eubacterium] hallii group	9.47	2.01	Day15-24-Day25-35
OTU_209 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	63.75	2.22	Day15-24-Day25-35
OTU_4604 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	297.46	2.37	Day15-24-Day25-35
OTU_5826 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	191.24	2.25	Day15-24-Day25-35
OTU_8773 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	264.42	2.38	Day15-24-Day25-35
OTU_7 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	1138.83	2.43	Day15-24-Day25-35

OTU_201 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	93.80	2.33	Day15-24-Day25-35
OTU_102 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminiclostridium 9	327.51	2.08	Day15-24-Day25-35
OTU_42 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	503.33	2.42	Day15-24-Day25-35
OTU_17 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	1202.77	2.37	Day15-24-Day25-35
OTU_66 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	367.68	2.23	Day15-24-Day25-35
OTU_15345 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	46.80	2.14	Day15-24-Day25-35
OTU_29 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;[Eubacterium] coprostanoligenes group	694.79	2.37	Day15-24-Day25-35
OTU_15527 Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Ruminococcaceae UCG-014	114.74	2.02	Day15-24-Day25-35
OTU_192 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales vadinBB60 group	48.17	2.23	Day15-24-Day25-35

Supplementary Table 2: Differential analysis of genera that are up/down regulated between different groups (Adjusted P values ≤ 0.05) where positive log2 fold change represent genera becoming abundant as we go forward in time. Here only the significant genera are shown for daily comparisons.

Genus	Base Mean	Log2 Fold	Group
Ruminococcaceae UCG-002	27.48	4.73	03-04
Ruminococcaceae UCG-014	84.78	4.17	03-04
Ruminococcaceae UCG-005	10.12	3.50	03-04
Lachnospiraceae;Lachnospira	19.72	2.71	04-05
[Eubacterium] hallii group	83.69	2.48	04-05
Enterobacter	1975.82	-2.55	04-05
Candidatus Arthromitus	5.21	2.54	05-06
Prevotellaceae;Prevotella 7	3.27	2.13	05-06
Tyzzerella	7.12	2.56	05-06
Anaerofilum	4.03	2.25	05-06
Enterococcus	65.50	-3.33	05-06
Defluviitaleaceae UCG-011	24.57	-3.43	05-06
Lachnospiraceae UCG-010	160.54	2.97	06-07
Coprococcus 1	1124.60	2.09	06-07
Shuttleworthia	145.95	2.13	06-07
Brevibacillus	4.21	-2.27	06-07
Prevotella 7	3.12	-2.06	06-07
Tyzzerella	73.83	2.90	07-08
Faecalibacterium	405.59	4.04	08-09
Enterobacter	35.00	-3.30	08-09
Family XIII UCG-001	4.18	2.19	09-10
Roseburia	10.30	2.26	09-10
Tyzzerella	488.55	-2.38	09-10
Corynebacterium 1	5.29	2.10	10-11
Ruminococcaceae UCG-008	4.46	2.17	10-11
Tyzzerella	492.04	2.76	10-11
Fusicatenibacter	694.62	-3.07	10-11
Lachnospiraceae FE2018 group	507.70	-2.97	10-11

Ruminococcus 1	19.47	-2.54	10-11
Defluviitaleaceae UCG-011	212.59	-2.44	10-11
Ruminococcaceae UCG-005	783.84	-2.24	10-11
Comamonadaceae; Delftia	5.50	2.03	12-13
Ruminococcus 1	50.97	3.13	12-13
Butyricicoccus	26.20	3.16	12-13
Megamonas	13.32	-2.73	12-13
Faecalitalea	37.63	3.47	13-14
Enterorhabdus	6.48	-2.03	13-14
Ruminococcus 1	64.03	2.17	14-15
Acetitomaculum	38.98	2.17	14-15
Family XIII UCG-001	20.64	2.39	14-15
Bifidobacterium	83.86	2.54	14-15
Lachnospiraceae FCS020 group	303.03	2.57	14-15
Lactobacillus	1058.97	2.80	14-15
Butyricicoccus	118.45	3.01	14-15
Faecalitalea	35.59	-4.53	14-15
Escherichia-Shigella	3107.38	-2.08	14-15
Enterobacteriaceae;Enterobacter	3.81	-2.05	14-15
Streptococcus	8.08	2.91	15-16
Ruminococcaceae UCG-009	334.48	2.44	16-17
Ruminococcaceae V9D2013 group	10.84	3.39	16-17
Erysipelatoclostridium	423.97	-2.09	16-17
Marvinbryantia	22.84	-2.70	16-17
Intestinimonas	538.49	2.23	16-17
Tyzzerella 3	171.81	-2.19	16-17
Campylobacter	3.74	-2.35	16-17
Hydrogenoanaerobacterium	21.04	2.82	17-18
Ruminococcaceae UCG-008	10.47	2.52	18-19
Ruminococcaceae UCG-004	40.26	2.15	18-19
Oscillospira	12.08	2.56	18-19
Intestinimonas	1028.88	2.10	19-20
Escherichia-Shigella	1946.88	-2.68	19-20
Proteus	4.49	2.02	20-21
Bacillus	329.21	2.52	23-24

Holdemania	11.81	2.29	23-24
Faecalibacterium	8727.64	2.15	23-24
Oscillibacter	11.58	2.00	25-26
Collinsella	11.63	-2.31	25-26
Lachnospiraceae UCG-006	6.87	2.46	26-27
Erysipelotrichaceae;Dielma	3.46	2.17	26-27
Intestinibacter	22.43	2.78	27-28
Dielma	3.57	-2.30	27-28
Lachnospiraceae UCG-006	7.16	-2.41	27-28
Faecalitalea	21.99	-2.02	27-28
Coriobacteriaceae UCG-002	25.30	3.37	28-29
Bacillus	562.14	3.18	30-31

Supplementary Table 3: Differential analysis of pathways becoming significant based on Kruskal-Wallis test (Adjusted P values ≤ 0.05). Here results are shown for both daily and weekly comparisons.

KEGG KOs	P Values	Adjusted P Values	Upregulated	Group Comparison
ko00061; Fatty acid biosynthesis	0.007911789	0.037310224	03	03 - 04
ko00240; Pyrimidine metabolism	0.009374768	0.037310224	04	03 - 04
ko00250; Alanine, aspartate and glutamate metabolism	0.006656727	0.037310224	04	03 - 04
ko00290; Valine, leucine and isoleucine biosynthesis	0.009374768	0.037310224	04	03 - 04
ko00330; Arginine and proline metabolism	0.009374768	0.037310224	04	03 - 04
ko00350; Tyrosine metabolism	0.011074438	0.037310224	04	03 - 04
ko00460; Cyanoamino acid metabolism	0.002213692	0.037310224	03	03 - 04
ko00524; Butirosin and neomycin biosynthesis	0.009374768	0.037310224	03	03 - 04
ko00562; Inositol phosphate metabolism	0.006656727	0.037310224	03	03 - 04
ko00624; Polycyclic aromatic hydrocarbon degradation	0.01304252	0.037310224	04	03 - 04
ko00730; Thiamine metabolism	0.011074438	0.037310224	04	03 - 04
ko00740; Riboflavin metabolism	0.01304252	0.037310224	03	03 - 04
ko00750; Vitamin B6 metabolism	0.007911789	0.037310224	04	03 - 04
ko00770; Pantothenate and CoA biosynthesis	0.009374768	0.037310224	04	03 - 04
ko00780; Biotin metabolism	0.01304252	0.037310224	04	03 - 04
ko00906; Carotenoid biosynthesis	0.01304252	0.037310224	04	03 - 04
ko00960; Tropane, piperidine and pyridine alkaloid biosynthesis	0.007911789	0.037310224	03	03 - 04
ko01051; Biosynthesis of ansamycins	0.009374768	0.037310224	03	03 - 04
ko02010; ABC transporters	0.009374768	0.037310224	03	03 - 04
ko03008; Ribosome biogenesis in eukaryotes	0.011074438	0.037310224	03	03 - 04
ko03018; RNA degradation	0.006656727	0.037310224	03	03 - 04
ko03410; Base excision repair	0.011074438	0.037310224	03	03 - 04
ko04020; Calcium signaling pathway	0.009374768	0.037310224	04	03 - 04
ko04122; Sulfur relay system	0.009374768	0.037310224	04	03 - 04
ko04141; Protein processing in endoplasmic reticulum	0.007911789	0.037310224	04	03 - 04
ko04146; Peroxisome	0.007911789	0.037310224	03	03 - 04
ko04260; Cardiac muscle contraction	0.011074438	0.037310224	03	03 - 04
ko04370; VEGF signaling pathway	0.011074438	0.037310224	04	03 - 04
ko04626; Plant-pathogen interaction	0.007911789	0.037310224	03	03 - 04
ko04666; Fc gamma R-mediated phagocytosis	0.009374768	0.037310224	04	03 - 04
ko04728; Dopaminergic synapse	0.01304252	0.037310224	03	03 - 04

ko04930; Type II diabetes mellitus	0.011074438	0.037310224	03	03 - 04
ko04974; Protein digestion and absorption	0.007911789	0.037310224	03	03 - 04
ko05030; Cocaine addiction	0.005583617	0.037310224	03	03 - 04
ko05031; Amphetamine addiction	0.005583617	0.037310224	03	03 - 04
ko05034; Alcoholism	0.01304252	0.037310224	03	03 - 04
ko00190; Oxidative phosphorylation	0.015313822	0.03909974	04	03 - 04
ko00561; Glycerolipid metabolism	0.015313822	0.03909974	03	03 - 04
ko04070; Phosphatidylinositol signaling system	0.015313822	0.03909974	03	03 - 04
ko04112; Cell cycle - Caulobacter	0.015313822	0.03909974	04	03 - 04
ko04726; Serotonergic synapse	0.015313822	0.03909974	03	03 - 04
ko05032; Morphine addiction	0.015313822	0.03909974	03	03 - 04
ko05203; Viral carcinogenesis	0.015313822	0.03909974	03	03 - 04
ko04144; Endocytosis	0.000219851	0.007285107	05	05-06
ko04912; GnRH signaling pathway	0.000219851	0.007285107	05	05-06
ko05012; Parkinsons disease	0.000219851	0.007285107	05	05-06
ko00030; Pentose phosphate pathway	0.001822735	0.013247142	05	05-06
ko00053; Ascorbate and aldarate metabolism	0.002213692	0.013247142	05	05-06
ko00100; Steroid biosynthesis	0.001822735	0.013247142	05	05-06
ko00196; Photosynthesis - antenna proteins	0.002208779	0.013247142	05	05-06
ko00540; Lipopolysaccharide biosynthesis	0.000998686	0.013247142	05	05-06
ko00592; alpha-Linolenic acid metabolism	0.000275504	0.013247142	05	05-06
ko00623; Toluene degradation	0.000275504	0.013247142	05	05-06
ko00965; Betalain biosynthesis	0.000532006	0.013247142	05	05-06
ko00984; Steroid degradation	0.001496164	0.013247142	05	05-06
ko01057; Biosynthesis of type II polyketide products	0.000998686	0.013247142	05	05-06
ko02060; Phosphotransferase system (PTS)	0.001224283	0.013247142	05	05-06
ko04610; Complement and coagulation cascades	0.001221273	0.013247142	05	05-06
ko05014; Amyotrophic lateral sclerosis (ALS)	0.000998686	0.013247142	05	05-06
ko05020; Prion diseases	0.000658337	0.013247142	05	05-06
ko05131; Shigellosis	0.001221273	0.013247142	05	05-06
ko05142; Chagas disease (American trypanosomiasis)	0.001822735	0.013247142	05	05-06
ko05204; Chemical carcinogenesis	0.001224283	0.013247142	05	05-06
ko00363; Bisphenol degradation	0.002680172	0.036672283	05	05-06
ko00630; Glyoxylate and dicarboxylate metabolism	0.002680172	0.036672283	05	05-06
ko00901; Indole alkaloid biosynthesis	0.002680172	0.036672283	05	05-06

ko00920; Sulfur metabolism	0.002680172	0.036672283	05	05-06
ko00945; Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.002680172	0.036672283	05	05-06
ko00980; Metabolism of xenobiotics by cytochrome P450	0.002680172	0.036672283	05	05-06
ko00982; Drug metabolism - cytochrome P450	0.002680172	0.036672283	05	05-06
ko05111; Vibrio cholerae pathogenic cycle	0.002680172	0.036672283	05	05-06
ko05132; Salmonella infection	0.002680172	0.036672283	05	05-06
ko04115; p53 signaling pathway	0.00128048	0.028496707	10	10 -11
ko00909; Sesquiterpenoid and triterpenoid biosynthesis	0.001702519	0.045759699	10	10 -11
ko05168; Herpes simplex infection	0.001702519	0.045759699	10	10 -11
ko05210; Colorectal cancer	0.001702519	0.045759699	10	10 -11
ko05416; Viral myocarditis	0.001702519	0.045759699	10	10 -11
ko02040; Flagellar assembly	0.000165522	0.012327241	14	14 - 15
ko05111; Vibrio cholerae pathogenic cycle	0.000219473	0.012327241	14	14 - 15
ko05130; Pathogenic Escherichia coli infection	0.000380365	0.012327241	14	14 - 15
ko00364; Fluorobenzoate degradation	0.001078987	0.0146559	14	14 - 15
ko00592; alpha-Linolenic acid metabolism	0.001078987	0.0146559	14	14 - 15
ko00633; Nitrotoluene degradation	0.000646749	0.0146559	14	14 - 15
ko00710; Carbon fixation in photosynthetic organisms	0.000497167	0.0146559	15	14 - 15
ko03070; Bacterial secretion system	0.000497167	0.0146559	14	14 - 15
ko05132; Salmonella infection	0.000497167	0.0146559	14	14 - 15
ko00240; Pyrimidine metabolism	0.001766337	0.01897042	15	14 - 15
ko00760; Nicotinate and nicotinamide metabolism	0.001383791	0.01897042	15	14 - 15
ko00920; Sulfur metabolism	0.001383791	0.01897042	14	14 - 15
ko00960; Tropane, piperidine and pyridine alkaloid biosynthesis	0.001383791	0.01897042	14	14 - 15
ko02020; Two-component system	0.001383791	0.01897042	14	14 - 15
ko03440; Homologous recombination	0.001766337	0.01897042	15	14 - 15
ko05032; Morphine addiction	0.001383791	0.01897042	14	14 - 15
ko05133; Pertussis	0.001383791	0.01897042	14	14 - 15
ko00020; Citrate cycle (TCA cycle)	0.002837545	0.022375931	14	14 - 15
ko00232; Caffeine metabolism	0.003571236	0.022375931	14	14 - 15
ko00281; Geraniol degradation	0.003571236	0.022375931	14	14 - 15
ko00310; Lysine degradation	0.001766337	0.022375931	14	14 - 15
ko00473; D-Alanine metabolism	0.002837545	0.022375931	15	14 - 15
ko00511; Other glycan degradation	0.003571236	0.022375931	15	14 - 15
ko00603; Glycosphingolipid biosynthesis - globo series	0.003571236	0.022375931	15	14 - 15

ko00624; Polycyclic aromatic hydrocarbon degradation	0.002837545	0.022375931	15	14 - 15
ko00630; Glyoxylate and dicarboxylate metabolism	0.002837545	0.022375931	14	14 - 15
ko00640; Propanoate metabolism	0.002244033	0.022375931	14	14 - 15
ko00740; Riboflavin metabolism	0.003571236	0.022375931	14	14 - 15
ko03030; DNA replication	0.003571236	0.022375931	15	14 - 15
ko04113; Meiosis - yeast	0.002244033	0.022375931	14	14 - 15
ko00791; Atrazine degradation	0.004473649	0.041073328	14	14 - 15
ko00906; Carotenoid biosynthesis	0.004473649	0.041073328	15	14 - 15
ko00910; Nitrogen metabolism	0.004473649	0.041073328	14	14 - 15
ko01040; Biosynthesis of unsaturated fatty acids	0.004473649	0.041073328	14	14 - 15
ko03010; Ribosome	0.004473649	0.041073328	15	14 - 15
ko05150; Staphylococcus aureus infection	0.004473649	0.041073328	15	14 - 15
ko00331; Clavulanic acid biosynthesis	1.16E-09	4.38E-09	Day03-07	Day03-07 - Day08-14
ko00592; alpha-Linolenic acid metabolism	1.05E-09	4.38E-09	Day03-07	Day03-07 - Day08-14
ko00920; Sulfur metabolism	1.07E-09	4.38E-09	Day03-07	Day03-07 - Day08-14
ko04011; MAPK signaling pathway - yeast	1.13E-09	4.38E-09	Day08-14	Day03-07 - Day08-14
ko04723; Retrograde endocannabinoid signaling	8.68E-10	4.38E-09	Day03-07	Day03-07 - Day08-14
ko04726; Serotonergic synapse	8.91E-10	4.38E-09	Day03-07	Day03-07 - Day08-14
ko05020; Prion diseases	4.30E-10	4.38E-09	Day03-07	Day03-07 - Day08-14
ko05132; Salmonella infection	2.56E-10	4.38E-09	Day03-07	Day03-07 - Day08-14
ko05133; Pertussis	8.01E-10	4.38E-09	Day03-07	Day03-07 - Day08-14
ko05014; Amyotrophic lateral sclerosis (ALS)	1.19E-09	6.19E-09	Day03-07	Day03-07 - Day08-14
ko00380; Tryptophan metabolism	6.45E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko01053; Biosynthesis of siderophore group nonribosomal peptides	5.26E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko04144; Endocytosis	5.98E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko04610; Complement and coagulation cascades	5.13E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko04912; GnRH signaling pathway	5.98E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko05034; Alcoholism	3.15E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko05110; Vibrio cholerae infection	1.36E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko05111; Vibrio cholerae pathogenic cycle	4.63E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko05131; Shigellosis	4.40E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko05219; Bladder cancer	3.32E-09	1.99E-08	Day03-07	Day03-07 - Day08-14
ko00030; Pentose phosphate pathway	2.42E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko00480; Glutathione metabolism	1.67E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko00540; Lipopolysaccharide biosynthesis	1.63E-08	8.26E-08	Day03-07	Day03-07 - Day08-14

ko00562; Inositol phosphate metabolism	2.73E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko00901; Indole alkaloid biosynthesis	6.79E-09	8.26E-08	Day03-07	Day03-07 - Day08-14
ko00965; Betalain biosynthesis	2.04E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko00982; Drug metabolism - cytochrome P450	3.01E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko01040; Biosynthesis of unsaturated fatty acids	1.15E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko05100; Bacterial invasion of epithelial cells	2.94E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko05204; Chemical carcinogenesis	1.21E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko05340; Primary immunodeficiency	1.84E-08	8.26E-08	Day03-07	Day03-07 - Day08-14
ko00564; Glycerophospholipid metabolism	3.16E-08	1.95E-07	Day03-07	Day03-07 - Day08-14
ko00980; Metabolism of xenobiotics by cytochrome P450	4.43E-08	1.95E-07	Day03-07	Day03-07 - Day08-14
ko03010; Ribosome	4.02E-08	1.95E-07	Day08-14	Day03-07 - Day08-14
ko00196; Photosynthesis - antenna proteins	6.04E-08	3.54E-07	Day03-07	Day03-07 - Day08-14
ko05142; Chagas disease (American trypanosomiasis)	4.76E-08	3.54E-07	Day03-07	Day03-07 - Day08-14
ko05030; Cocaine addiction	7.66E-08	6.61E-07	Day03-07	Day03-07 - Day08-14
ko05031; Amphetamine addiction	7.66E-08	6.61E-07	Day03-07	Day03-07 - Day08-14
ko00310; Lysine degradation	1.85E-07	1.40E-06	Day03-07	Day03-07 - Day08-14
ko00660; C5-Branched dibasic acid metabolism	2.73E-07	1.40E-06	Day03-07	Day03-07 - Day08-14
ko00945; Stilbenoid, diarylheptanoid and gingerol biosynthesis	9.46E-08	1.40E-06	Day03-07	Day03-07 - Day08-14
ko04728; Dopaminergic synapse	2.03E-07	1.40E-06	Day03-07	Day03-07 - Day08-14
ko05012; Parkinsons disease	2.79E-07	1.40E-06	Day03-07	Day03-07 - Day08-14
ko00071; Fatty acid metabolism	1.15E-06	4.07E-06	Day03-07	Day03-07 - Day08-14
ko00232; Caffeine metabolism	7.11E-07	4.07E-06	Day03-07	Day03-07 - Day08-14
ko00363; Bisphenol degradation	1.68E-06	4.07E-06	Day03-07	Day03-07 - Day08-14
ko00471; D-Glutamine and D-glutamate metabolism	1.51E-06	4.07E-06	Day08-14	Day03-07 - Day08-14
ko00601; Glycosphingolipid biosynthesis - lacto and neolacto series	9.04E-07	4.07E-06	Day08-14	Day03-07 - Day08-14
ko00642; Ethylbenzene degradation	2.86E-07	4.07E-06	Day08-14	Day03-07 - Day08-14
ko00680; Methane metabolism	1.42E-06	4.07E-06	Day08-14	Day03-07 - Day08-14
ko00830; Retinol metabolism	1.68E-06	4.07E-06	Day03-07	Day03-07 - Day08-14
ko04727; GABAergic synapse	1.15E-06	4.07E-06	Day08-14	Day03-07 - Day08-14
ko04940; Type I diabetes mellitus	4.09E-07	4.07E-06	Day08-14	Day03-07 - Day08-14
ko05032; Morphine addiction	1.05E-06	4.07E-06	Day03-07	Day03-07 - Day08-14
ko05130; Pathogenic Escherichia coli infection	9.64E-07	4.07E-06	Day03-07	Day03-07 - Day08-14
ko05164; Influenza A	1.76E-06	4.07E-06	Day08-14	Day03-07 - Day08-14
ko05203; Viral carcinogenesis	1.83E-06	4.07E-06	Day03-07	Day03-07 - Day08-14
ko00740; Riboflavin metabolism	1.95E-06	4.65E-06	Day03-07	Day03-07 - Day08-14

ko04724; Glutamatergic synapse	1.95E-06	4.65E-06	Day08-14	Day03-07 - Day08-14
ko00630; Glyoxylate and dicarboxylate metabolism	2.08E-06	6.01E-06	Day03-07	Day03-07 - Day08-14
ko00640; Propanoate metabolism	2.26E-06	6.01E-06	Day03-07	Day03-07 - Day08-14
ko04930; Type II diabetes mellitus	2.41E-06	1.82E-05	Day03-07	Day03-07 - Day08-14
ko00603; Glycosphingolipid biosynthesis - globo series	4.56E-06	2.31E-05	Day08-14	Day03-07 - Day08-14
ko00860; Porphyrin and chlorophyll metabolism	5.93E-06	2.31E-05	Day03-07	Day03-07 - Day08-14
ko04146; Peroxisome	4.65E-06	2.31E-05	Day03-07	Day03-07 - Day08-14
ko04910; Insulin signaling pathway	2.90E-06	2.31E-05	Day03-07	Day03-07 - Day08-14
ko05168; Herpes simplex infection	5.58E-06	2.31E-05	Day08-14	Day03-07 - Day08-14
ko00130; Ubiquinone and other terpenoid-quinone biosynthesis	6.05E-06	2.46E-05	Day03-07	Day03-07 - Day08-14
ko04070; Phosphatidylinositol signaling system	6.96E-06	2.46E-05	Day03-07	Day03-07 - Day08-14
ko00312; beta-Lactam resistance	1.14E-05	2.59E-05	Day08-14	Day03-07 - Day08-14
ko00350; Tyrosine metabolism	9.76E-06	2.59E-05	Day08-14	Day03-07 - Day08-14
ko00400; Phenylalanine, tyrosine and tryptophan biosynthesis	1.39E-05	2.59E-05	Day08-14	Day03-07 - Day08-14
ko00623; Toluene degradation	1.56E-05	2.59E-05	Day03-07	Day03-07 - Day08-14
ko00710; Carbon fixation in photosynthetic organisms	1.44E-05	2.59E-05	Day08-14	Day03-07 - Day08-14
ko01057; Biosynthesis of type II polyketide products	1.33E-05	2.59E-05	Day03-07	Day03-07 - Day08-14
ko02060; Phosphotransferase system (PTS)	7.39E-06	2.59E-05	Day03-07	Day03-07 - Day08-14
ko03008; Ribosome biogenesis in eukaryotes	1.47E-05	2.59E-05	Day03-07	Day03-07 - Day08-14
ko03018; RNA degradation	1.50E-05	2.59E-05	Day03-07	Day03-07 - Day08-14
ko03060; Protein export	1.44E-05	2.59E-05	Day08-14	Day03-07 - Day08-14
ko05210; Colorectal cancer	1.16E-05	2.59E-05	Day08-14	Day03-07 - Day08-14
ko05416; Viral myocarditis	1.16E-05	2.59E-05	Day08-14	Day03-07 - Day08-14
ko00061; Fatty acid biosynthesis	1.59E-05	3.45E-05	Day03-07	Day03-07 - Day08-14
ko00100; Steroid biosynthesis	1.68E-05	8.68E-05	Day03-07	Day03-07 - Day08-14
ko00340; Histidine metabolism	1.96E-05	8.68E-05	Day08-14	Day03-07 - Day08-14
ko00401; Novobiocin biosynthesis	2.16E-05	0.000109709	Day08-14	Day03-07 - Day08-14
ko00621; Dioxin degradation	2.51E-05	0.000109709	Day08-14	Day03-07 - Day08-14
ko00010; Glycolysis / Gluconeogenesis	6.52E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko00053; Ascorbate and aldarate metabolism	0.000110879	0.000145793	Day03-07	Day03-07 - Day08-14
ko00140; Steroid hormone biosynthesis	2.75E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko00361; Chlorocyclohexane and chlorobenzene degradation	7.13E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko00430; Taurine and hypotaurine metabolism	0.000120947	0.000145793	Day03-07	Day03-07 - Day08-14
ko00524; Butirosin and neomycin biosynthesis	9.31E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko00565; Ether lipid metabolism	8.52E-05	0.000145793	Day03-07	Day03-07 - Day08-14

ko00970; Aminoacyl-tRNA biosynthesis	0.000114808	0.000145793	Day08-14	Day03-07 - Day08-14
ko02040; Flagellar assembly	3.26E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko03030; DNA replication	0.000107078	0.000145793	Day08-14	Day03-07 - Day08-14
ko03450; Non-homologous end-joining	7.53E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko04310; Wnt signaling pathway	8.98E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko04330; Notch signaling pathway	8.98E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko04514; Cell adhesion molecules (CAMs)	6.25E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko04640; Hematopoietic cell lineage	6.76E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko04721; Synaptic vesicle cycle	0.000108963	0.000145793	Day08-14	Day03-07 - Day08-14
ko04725; Cholinergic synapse	6.41E-05	0.000145793	Day03-07	Day03-07 - Day08-14
ko04810; Regulation of actin cytoskeleton	0.000118694	0.000145793	Day08-14	Day03-07 - Day08-14
ko04962; Vasopressin-regulated water reabsorption	0.000108963	0.000145793	Day08-14	Day03-07 - Day08-14
ko04975; Fat digestion and absorption	8.22E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko05202; Transcriptional misregulation in cancer	9.32E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko05220; Chronic myeloid leukemia	8.98E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko05412; Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6.25E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko05414; Dilated cardiomyopathy	6.25E-05	0.000145793	Day08-14	Day03-07 - Day08-14
ko00450; Selenocompound metabolism	0.000131872	0.000236604	Day03-07	Day03-07 - Day08-14
ko00604; Glycosphingolipid biosynthesis - ganglio series	0.000123061	0.000236604	Day08-14	Day03-07 - Day08-14
ko00240; Pyrimidine metabolism	0.000215926	0.000470296	Day08-14	Day03-07 - Day08-14
ko01055; Biosynthesis of vancomycin group antibiotics	0.000219572	0.000470296	Day08-14	Day03-07 - Day08-14
ko02010; ABC transporters	0.00017638	0.000470296	Day03-07	Day03-07 - Day08-14
ko04064; NF-kappa B signaling pathway	0.000233992	0.000470296	Day08-14	Day03-07 - Day08-14
ko04112; Cell cycle - Caulobacter	0.000191949	0.000470296	Day08-14	Day03-07 - Day08-14
ko04626; Plant-pathogen interaction	0.000167617	0.000470296	Day03-07	Day03-07 - Day08-14
ko04916; Melanogenesis	0.000135979	0.000470296	Day08-14	Day03-07 - Day08-14
ko05140; Leishmaniasis	0.000233992	0.000470296	Day08-14	Day03-07 - Day08-14
ko00253; Tetracycline biosynthesis	0.000277087	0.000568971	Day03-07	Day03-07 - Day08-14
ko00785; Lipoic acid metabolism	0.000300849	0.000568971	Day03-07	Day03-07 - Day08-14
ko03070; Bacterial secretion system	0.000268084	0.000568971	Day03-07	Day03-07 - Day08-14
ko03440; Homologous recombination	0.000238688	0.000568971	Day08-14	Day03-07 - Day08-14
ko04080; Neuroactive ligand-receptor interaction	0.000292503	0.000568971	Day08-14	Day03-07 - Day08-14
ko04622; RIG-I-like receptor signaling pathway	0.000321219	0.000568971	Day03-07	Day03-07 - Day08-14
ko00300; Lysine biosynthesis	0.000331881	0.000834975	Day08-14	Day03-07 - Day08-14
ko00364; Fluorobenzoate degradation	0.00038409	0.000834975	Day03-07	Day03-07 - Day08-14

ko00720; Carbon fixation pathways in prokaryotes	0.000360004	0.000834975	Day08-14	Day03-07 - Day08-14
ko05169; Epstein-Barr virus infection	0.000419343	0.000834975	Day03-07	Day03-07 - Day08-14
ko04141; Protein processing in endoplasmic reticulum	0.000423057	0.002396589	Day08-14	Day03-07 - Day08-14
ko00460; Cyanoamino acid metabolism	0.000590446	0.002834065	Day03-07	Day03-07 - Day08-14
ko00523; Polyketide sugar unit biosynthesis	0.000700997	0.002834065	Day08-14	Day03-07 - Day08-14
ko04122; Sulfur relay system	0.00074576	0.002834065	Day08-14	Day03-07 - Day08-14
ko05016; Huntingtons disease	0.000856352	0.002834065	Day03-07	Day03-07 - Day08-14
ko05134; Legionellosis	0.000488481	0.002834065	Day08-14	Day03-07 - Day08-14
ko05200; Pathways in cancer	0.000896474	0.002834065	Day08-14	Day03-07 - Day08-14
ko00250; Alanine, aspartate and glutamate metabolism	0.001324644	0.005498727	Day08-14	Day03-07 - Day08-14
ko00730; Thiamine metabolism	0.001364383	0.005498727	Day08-14	Day03-07 - Day08-14
ko00940; Phenylpropanoid biosynthesis	0.001826811	0.005498727	Day03-07	Day03-07 - Day08-14
ko05120; Epithelial cell signaling in Helicobacter pylori infection	0.001468591	0.005498727	Day03-07	Day03-07 - Day08-14
ko05211; Renal cell carcinoma	0.001774802	0.005498727	Day08-14	Day03-07 - Day08-14
ko05222; Small cell lung cancer	0.000952682	0.005498727	Day08-14	Day03-07 - Day08-14
ko00020; Citrate cycle (TCA cycle)	0.001853337	0.005535155	Day03-07	Day03-07 - Day08-14
ko00195; Photosynthesis	0.006251038	0.005535155	Day08-14	Day03-07 - Day08-14
ko00330; Arginine and proline metabolism	0.002463965	0.005535155	Day08-14	Day03-07 - Day08-14
ko00351; DDT degradation	0.00279471	0.005535155	Day08-14	Day03-07 - Day08-14
ko00472; D-Arginine and D-ornithine metabolism	0.003344319	0.005535155	Day03-07	Day03-07 - Day08-14
ko00561; Glycerolipid metabolism	0.002913663	0.005535155	Day03-07	Day03-07 - Day08-14
ko00591; Linoleic acid metabolism	0.00481191	0.005535155	Day03-07	Day03-07 - Day08-14
ko00600; Sphingolipid metabolism	0.003390427	0.005535155	Day08-14	Day03-07 - Day08-14
ko00620; Pyruvate metabolism	0.00415511	0.005535155	Day03-07	Day03-07 - Day08-14
ko00622; Xylene degradation	0.00514041	0.005535155	Day08-14	Day03-07 - Day08-14
ko00624; Polycyclic aromatic hydrocarbon degradation	0.003209399	0.005535155	Day08-14	Day03-07 - Day08-14
ko00633; Nitrotoluene degradation	0.006581604	0.005535155	Day03-07	Day03-07 - Day08-14
ko00750; Vitamin B6 metabolism	0.004268115	0.005535155	Day08-14	Day03-07 - Day08-14
ko00770; Pantothenate and CoA biosynthesis	0.002395511	0.005535155	Day08-14	Day03-07 - Day08-14
ko00906; Carotenoid biosynthesis	0.004211269	0.005535155	Day08-14	Day03-07 - Day08-14
ko01051; Biosynthesis of ansamycins	0.002498859	0.005535155	Day03-07	Day03-07 - Day08-14
ko03015; mRNA surveillance pathway	0.006251038	0.005535155	Day03-07	Day03-07 - Day08-14
ko03050; Proteasome	0.003580706	0.005535155	Day08-14	Day03-07 - Day08-14
ko04020; Calcium signaling pathway	0.004502523	0.005535155	Day08-14	Day03-07 - Day08-14
ko04114; Oocyte meiosis	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14

ko04270; Vascular smooth muscle contraction	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko04370; VEGF signaling pathway	0.002913663	0.005535155	Day08-14	Day03-07 - Day08-14
ko04666; Fc gamma R-mediated phagocytosis	0.004099632	0.005535155	Day08-14	Day03-07 - Day08-14
ko04720; Long-term potentiation	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko04722; Neurotrophin signaling pathway	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko04740; Olfactory transduction	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko04744; Phototransduction	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko04745; Phototransduction - fly	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko05150; Staphylococcus aureus infection	0.002078632	0.005535155	Day08-14	Day03-07 - Day08-14
ko05152; Tuberculosis	0.006332247	0.005535155	Day08-14	Day03-07 - Day08-14
ko05160; Hepatitis C	0.005480406	0.005535155	Day08-14	Day03-07 - Day08-14
ko05162; Measles	0.005480406	0.005535155	Day08-14	Day03-07 - Day08-14
ko05214; Glioma	0.006799255	0.005535155	Day08-14	Day03-07 - Day08-14
ko00040; Pentose and glucuronate interconversions	0.007965754	0.009152701	Day03-07	Day03-07 - Day08-14
ko00473; D-Alanine metabolism	0.007865947	0.009152701	Day08-14	Day03-07 - Day08-14
ko00960; Tropane, piperidine and pyridine alkaloid biosynthesis	0.006839757	0.009152701	Day03-07	Day03-07 - Day08-14
ko04961; Endocrine and other factor-regulated calcium reabsorption	0.007965754	0.009152701	Day08-14	Day03-07 - Day08-14
ko04972; Pancreatic secretion	0.007290285	0.009152701	Day08-14	Day03-07 - Day08-14
ko00052; Galactose metabolism	0.014999488	0.030178743	Day03-07	Day03-07 - Day08-14
ko00190; Oxidative phosphorylation	0.012553962	0.030178743	Day08-14	Day03-07 - Day08-14
ko00670; One carbon pool by folate	0.016468133	0.030178743	Day08-14	Day03-07 - Day08-14
ko00780; Biotin metabolism	0.016660318	0.030178743	Day08-14	Day03-07 - Day08-14
ko02030; Bacterial chemotaxis	0.017448893	0.030178743	Day08-14	Day03-07 - Day08-14
ko03410; Base excision repair	0.016089595	0.030178743	Day03-07	Day03-07 - Day08-14
ko04210; Apoptosis	0.013486272	0.030178743	Day08-14	Day03-07 - Day08-14
ko04612; Antigen processing and presentation	0.014309398	0.030178743	Day03-07	Day03-07 - Day08-14
ko04914; Progesterone-mediated oocyte maturation	0.014309398	0.030178743	Day03-07	Day03-07 - Day08-14
ko04960; Aldosterone-regulated sodium reabsorption	0.008588768	0.030178743	Day08-14	Day03-07 - Day08-14
ko04970; Salivary secretion	0.008588768	0.030178743	Day08-14	Day03-07 - Day08-14
ko04971; Gastric acid secretion	0.008588768	0.030178743	Day08-14	Day03-07 - Day08-14
ko05215; Prostate cancer	0.014309398	0.030178743	Day03-07	Day03-07 - Day08-14
ko05014; Amyotrophic lateral sclerosis (ALS)	3.10E-09	2.80E-07	Day08-14	Day08-14 - Day15-24
ko03050; Proteasome	4.41E-09	3.83E-07	Day15-24	Day08-14 - Day15-24
ko00331; Clavulanic acid biosynthesis	7.43E-09	4.28E-07	Day08-14	Day08-14 - Day15-24
ko00592; alpha-Linolenic acid metabolism	1.77E-08	4.28E-07	Day08-14	Day08-14 - Day15-24

ko04723; Retrograde endocannabinoid signaling	1.34E-08	4.28E-07	Day08-14	Day08-14 - Day15-24
ko05020; Prion diseases	1.56E-08	4.28E-07	Day08-14	Day08-14 - Day15-24
ko04974; Protein digestion and absorption	2.09E-08	3.33E-06	Day15-24	Day08-14 - Day15-24
ko00380; Tryptophan metabolism	4.72E-08	4.96E-06	Day08-14	Day08-14 - Day15-24
ko00400; Phenylalanine, tyrosine and tryptophan biosynthesis	5.90E-07	1.25E-05	Day15-24	Day08-14 - Day15-24
ko03040; Spliceosome	7.74E-07	1.25E-05	Day08-14	Day08-14 - Day15-24
ko04514; Cell adhesion molecules (CAMs)	7.77E-07	1.25E-05	Day15-24	Day08-14 - Day15-24
ko04610; Complement and coagulation cascades	2.49E-07	1.25E-05	Day08-14	Day08-14 - Day15-24
ko04724; Glutamatergic synapse	9.61E-07	1.25E-05	Day15-24	Day08-14 - Day15-24
ko04810; Regulation of actin cytoskeleton	6.82E-07	1.25E-05	Day15-24	Day08-14 - Day15-24
ko05131; Shigellosis	8.63E-08	1.25E-05	Day08-14	Day08-14 - Day15-24
ko05412; Arrhythmogenic right ventricular cardiomyopathy (ARVC)	7.77E-07	1.25E-05	Day15-24	Day08-14 - Day15-24
ko05414; Dilated cardiomyopathy	7.77E-07	1.25E-05	Day15-24	Day08-14 - Day15-24
ko00520; Amino sugar and nucleotide sugar metabolism	9.74E-07	7.45E-05	Day15-24	Day08-14 - Day15-24
ko00471; D-Glutamine and D-glutamate metabolism	4.59E-06	0.000191679	Day15-24	Day08-14 - Day15-24
ko04916; Melanogenesis	1.56E-06	0.000191679	Day15-24	Day08-14 - Day15-24
ko05202; Transcriptional misregulation in cancer	4.37E-06	0.000191679	Day15-24	Day08-14 - Day15-24
ko04080; Neuroactive ligand-receptor interaction	1.26E-05	0.000351318	Day15-24	Day08-14 - Day15-24
ko04975; Fat digestion and absorption	1.26E-05	0.000351318	Day15-24	Day08-14 - Day15-24
ko05169; Epstein-Barr virus infection	6.10E-06	0.000351318	Day15-24	Day08-14 - Day15-24
ko00232; Caffeine metabolism	7.33E-05	0.000771811	Day08-14	Day08-14 - Day15-24
ko00253; Tetracycline biosynthesis	4.09E-05	0.000771811	Day08-14	Day08-14 - Day15-24
ko00401; Novobiocin biosynthesis	7.75E-05	0.000771811	Day15-24	Day08-14 - Day15-24
ko00500; Starch and sucrose metabolism	6.78E-05	0.000771811	Day15-24	Day08-14 - Day15-24
ko00513; Various types of N-glycan biosynthesis	1.44E-05	0.000771811	Day15-24	Day08-14 - Day15-24
ko00623; Toluene degradation	7.75E-05	0.000771811	Day08-14	Day08-14 - Day15-24
ko01053; Biosynthesis of siderophore group nonribosomal peptides	6.49E-05	0.000771811	Day08-14	Day08-14 - Day15-24
ko01057; Biosynthesis of type II polyketide products	5.80E-05	0.000771811	Day08-14	Day08-14 - Day15-24
ko03010; Ribosome	5.13E-05	0.000771811	Day15-24	Day08-14 - Day15-24
ko04640; Hematopoietic cell lineage	2.40E-05	0.000771811	Day15-24	Day08-14 - Day15-24
ko05100; Bacterial invasion of epithelial cells	2.93E-05	0.000771811	Day08-14	Day08-14 - Day15-24
ko00310; Lysine degradation	0.000145273	0.001828317	Day08-14	Day08-14 - Day15-24
ko00603; Glycosphingolipid biosynthesis - globo series	8.74E-05	0.001828317	Day15-24	Day08-14 - Day15-24
ko00984; Steroid degradation	0.000156489	0.001828317	Day08-14	Day08-14 - Day15-24
ko01055; Biosynthesis of vancomycin group antibiotics	8.74E-05	0.001828317	Day15-24	Day08-14 - Day15-24

ko05130; Pathogenic Escherichia coli infection	0.000136266	0.001828317	Day08-14	Day08-14 - Day15-24
ko05164; Influenza A	0.000161541	0.001828317	Day15-24	Day08-14 - Day15-24
ko05204; Chemical carcinogenesis	0.000163258	0.001828317	Day08-14	Day08-14 - Day15-24
ko00363; Bisphenol degradation	0.000173932	0.002295258	Day08-14	Day08-14 - Day15-24
ko00473; D-Alanine metabolism	0.000221233	0.002295258	Day15-24	Day08-14 - Day15-24
ko00901; Indole alkaloid biosynthesis	0.000203556	0.002295258	Day08-14	Day08-14 - Day15-24
ko00051; Fructose and mannose metabolism	0.000564731	0.009251318	Day15-24	Day08-14 - Day15-24
ko00531; Glycosaminoglycan degradation	0.000228226	0.009251318	Day15-24	Day08-14 - Day15-24
ko03015; mRNA surveillance pathway	0.00050698	0.009251318	Day08-14	Day08-14 - Day15-24
ko04727; GABAergic synapse	0.000323394	0.009251318	Day15-24	Day08-14 - Day15-24
ko05111; Vibrio cholerae pathogenic cycle	0.000383863	0.009251318	Day08-14	Day08-14 - Day15-24
ko04064; NF-kappa B signaling pathway	0.001256247	0.017059387	Day15-24	Day08-14 - Day15-24
ko04940; Type I diabetes mellitus	0.000887451	0.017059387	Day15-24	Day08-14 - Day15-24
ko05110; Vibrio cholerae infection	0.001041361	0.017059387	Day08-14	Day08-14 - Day15-24
ko05140; Leishmaniasis	0.001256247	0.017059387	Day15-24	Day08-14 - Day15-24
ko05145; Toxoplasmosis	0.000592958	0.017059387	Day15-24	Day08-14 - Day15-24
ko00982; Drug metabolism - cytochrome P450	0.001465349	0.017880782	Day08-14	Day08-14 - Day15-24
ko05133; Pertussis	0.001265523	0.017880782	Day08-14	Day08-14 - Day15-24
ko00590; Arachidonic acid metabolism	0.001547502	0.018567059	Day08-14	Day08-14 - Day15-24
ko00071; Fatty acid metabolism	0.001954847	0.020888313	Day08-14	Day08-14 - Day15-24
ko00600; Sphingolipid metabolism	0.0025238	0.020888313	Day15-24	Day08-14 - Day15-24
ko00627; Aminobenzoate degradation	0.002501893	0.020888313	Day08-14	Day08-14 - Day15-24
ko00790; Folate biosynthesis	0.00248016	0.020888313	Day15-24	Day08-14 - Day15-24
ko00980; Metabolism of xenobiotics by cytochrome P450	0.001693903	0.020888313	Day08-14	Day08-14 - Day15-24
ko05012; Parkinsons disease	0.002545882	0.020888313	Day08-14	Day08-14 - Day15-24
ko00965; Betalain biosynthesis	0.002682127	0.024353449	Day08-14	Day08-14 - Day15-24
ko00960; Tropane, piperidine and pyridine alkaloid biosynthesis	0.003468705	0.045274535	Day08-14	Day08-14 - Day15-24
ko05132; Salmonella infection	0.002874153	0.045274535	Day08-14	Day08-14 - Day15-24
ko00340; Histidine metabolism	1.31E-09	1.21E-07	Day15-24	Day15-24 - Day25-35
ko00030; Pentose phosphate pathway	2.08E-08	1.16E-06	Day25-35	Day15-24 - Day25-35
ko04622; RIG-I-like receptor signaling pathway	2.16E-09	1.16E-06	Day25-35	Day15-24 - Day25-35
ko05168; Herpes simplex infection	2.35E-08	1.16E-06	Day15-24	Day15-24 - Day25-35
ko00710; Carbon fixation in photosynthetic organisms	3.31E-08	1.46E-06	Day25-35	Day15-24 - Day25-35
ko00790; Folate biosynthesis	6.64E-08	1.46E-06	Day25-35	Day15-24 - Day25-35
ko00010; Glycolysis / Gluconeogenesis	1.08E-07	3.74E-06	Day25-35	Day15-24 - Day25-35

ko00521; Streptomycin biosynthesis	2.34E-07	3.74E-06	Day25-35	Day15-24 - Day25-35
ko04112; Cell cycle - Caulobacter	1.82E-07	3.74E-06	Day15-24	Day15-24 - Day25-35
ko04115; p53 signaling pathway	1.82E-07	3.74E-06	Day15-24	Day15-24 - Day25-35
ko05164; Influenza A	2.56E-07	3.74E-06	Day25-35	Day15-24 - Day25-35
ko05210; Colorectal cancer	7.21E-08	3.74E-06	Day15-24	Day15-24 - Day25-35
ko05416; Viral myocarditis	7.21E-08	3.74E-06	Day15-24	Day15-24 - Day25-35
ko02030; Bacterial chemotaxis	2.72E-07	1.40E-05	Day15-24	Day15-24 - Day25-35
ko04210; Apoptosis	5.01E-07	1.40E-05	Day15-24	Day15-24 - Day25-35
ko00472; D-Arginine and D-ornithine metabolism	5.21E-07	3.11E-05	Day25-35	Day15-24 - Day25-35
ko00941; Flavonoid biosynthesis	7.97E-07	3.20E-05	Day15-24	Day15-24 - Day25-35
ko00312; beta-Lactam resistance	5.76E-06	0.000163818	Day15-24	Day15-24 - Day25-35
ko00523; Polyketide sugar unit biosynthesis	2.65E-06	0.000163818	Day25-35	Day15-24 - Day25-35
ko02020; Two-component system	1.25E-05	0.000163818	Day15-24	Day15-24 - Day25-35
ko02060; Phosphotransferase system (PTS)	1.08E-06	0.000163818	Day25-35	Day15-24 - Day25-35
ko03010; Ribosome	1.17E-05	0.000163818	Day25-35	Day15-24 - Day25-35
ko04940; Type I diabetes mellitus	6.13E-06	0.000163818	Day25-35	Day15-24 - Day25-35
ko05219; Bladder cancer	1.06E-05	0.000163818	Day25-35	Day15-24 - Day25-35
ko05222; Small cell lung cancer	7.00E-06	0.000163818	Day15-24	Day15-24 - Day25-35
ko00052; Galactose metabolism	2.38E-05	0.000392037	Day25-35	Day15-24 - Day25-35
ko00130; Ubiquinone and other terpenoid-quinone biosynthesis	1.27E-05	0.000392037	Day25-35	Day15-24 - Day25-35
ko00290; Valine, leucine and isoleucine biosynthesis	3.03E-05	0.000392037	Day15-24	Day15-24 - Day25-35
ko03450; Non-homologous end-joining	2.70E-05	0.000392037	Day25-35	Day15-24 - Day25-35
ko04070; Phosphatidylinositol signaling system	1.69E-05	0.000392037	Day25-35	Day15-24 - Day25-35
ko05146; Amoebiasis	2.79E-05	0.000392037	Day15-24	Day15-24 - Day25-35
ko00604; Glycosphingolipid biosynthesis - ganglio series	5.21E-05	0.001884939	Day15-24	Day15-24 - Day25-35
ko04930; Type II diabetes mellitus	3.37E-05	0.001884939	Day25-35	Day15-24 - Day25-35
ko00053; Ascorbate and aldarate metabolism	0.000196433	0.00197874	Day25-35	Day15-24 - Day25-35
ko00072; Synthesis and degradation of ketone bodies	0.000154622	0.00197874	Day15-24	Day15-24 - Day25-35
ko00196; Photosynthesis - antenna proteins	0.000150028	0.00197874	Day25-35	Day15-24 - Day25-35
ko00350; Tyrosine metabolism	0.000159347	0.00197874	Day15-24	Day15-24 - Day25-35
ko00450; Selenocompound metabolism	0.000179642	0.00197874	Day25-35	Day15-24 - Day25-35
ko00471; D-Glutamine and D-glutamate metabolism	8.71E-05	0.00197874	Day25-35	Day15-24 - Day25-35
ko00909; Sesquiterpenoid and triterpenoid biosynthesis	0.00021469	0.00197874	Day15-24	Day15-24 - Day25-35
ko03430; Mismatch repair	0.000109797	0.00197874	Day15-24	Day15-24 - Day25-35
ko04974; Protein digestion and absorption	6.72E-05	0.00197874	Day25-35	Day15-24 - Day25-35

ko05142; Chagas disease (American trypanosomiasis)	0.000241519	0.00197874	Day25-35	Day15-24 - Day25-35
ko00524; Butirosin and neomycin biosynthesis	0.000243296	0.002969885	Day25-35	Day15-24 - Day25-35
ko04310; Wnt signaling pathway	0.000347041	0.002969885	Day15-24	Day15-24 - Day25-35
ko04330; Notch signaling pathway	0.000347041	0.002969885	Day15-24	Day15-24 - Day25-35
ko05203; Viral carcinogenesis	0.000367481	0.002969885	Day25-35	Day15-24 - Day25-35
ko05220; Chronic myeloid leukemia	0.000347041	0.002969885	Day15-24	Day15-24 - Day25-35
ko00061; Fatty acid biosynthesis	0.000605033	0.004279392	Day15-24	Day15-24 - Day25-35
ko00195; Photosynthesis	0.000661672	0.004279392	Day25-35	Day15-24 - Day25-35
ko00253; Tetracycline biosynthesis	0.000375432	0.004279392	Day15-24	Day15-24 - Day25-35
ko00540; Lipopolysaccharide biosynthesis	0.00052298	0.004279392	Day25-35	Day15-24 - Day25-35
ko00630; Glyoxylate and dicarboxylate metabolism	0.000661672	0.004279392	Day25-35	Day15-24 - Day25-35
ko01051; Biosynthesis of ansamycins	0.000657146	0.004279392	Day25-35	Day15-24 - Day25-35
ko03060; Protein export	0.000605033	0.004279392	Day25-35	Day15-24 - Day25-35
ko05322; Systemic lupus erythematosus	0.000541518	0.004279392	Day15-24	Day15-24 - Day25-35
ko00051; Fructose and mannose metabolism	0.001580412	0.011322937	Day25-35	Day15-24 - Day25-35
ko00230; Purine metabolism	0.001388759	0.011322937	Day25-35	Day15-24 - Day25-35
ko00281; Geraniol degradation	0.000934912	0.011322937	Day15-24	Day15-24 - Day25-35
ko00331; Clavulanic acid biosynthesis	0.001663673	0.011322937	Day25-35	Day15-24 - Day25-35
ko00351; DDT degradation	0.001251127	0.011322937	Day15-24	Day15-24 - Day25-35
ko00362; Benzoate degradation	0.001962938	0.011322937	Day15-24	Day15-24 - Day25-35
ko00562; Inositol phosphate metabolism	0.001026433	0.011322937	Day25-35	Day15-24 - Day25-35
ko00623; Toluene degradation	0.002000478	0.011322937	Day25-35	Day15-24 - Day25-35
ko01055; Biosynthesis of vancomycin group antibiotics	0.000680068	0.011322937	Day25-35	Day15-24 - Day25-35
ko01056; Biosynthesis of type II polyketide backbone	0.002064511	0.011322937	Day15-24	Day15-24 - Day25-35
ko02010; ABC transporters	0.001111408	0.011322937	Day25-35	Day15-24 - Day25-35
ko03008; Ribosome biogenesis in eukaryotes	0.001762155	0.011322937	Day25-35	Day15-24 - Day25-35
ko03020; RNA polymerase	0.001621551	0.011322937	Day25-35	Day15-24 - Day25-35
ko04975; Fat digestion and absorption	0.001226767	0.011322937	Day15-24	Day15-24 - Day25-35
ko00300; Lysine biosynthesis	0.002383987	0.019852813	Day15-24	Day15-24 - Day25-35
ko00643; Styrene degradation	0.002090647	0.019852813	Day15-24	Day15-24 - Day25-35
ko00270; Cysteine and methionine metabolism	0.002443962	0.021979557	Day15-24	Day15-24 - Day25-35
ko02040; Flagellar assembly	0.002697924	0.021979557	Day15-24	Day15-24 - Day25-35
ko05010; Alzheimers disease	0.002903976	0.021979557	Day15-24	Day15-24 - Day25-35
ko00280; Valine, leucine and isoleucine degradation	0.003030708	0.030943195	Day15-24	Day15-24 - Day25-35
ko00360; Phenylalanine metabolism	0.003833813	0.030943195	Day15-24	Day15-24 - Day25-35

ko00473; D-Alanine metabolism	0.003743341	0.030943195	Day25-35	Day15-24 - Day25-35