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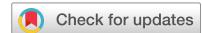
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scientific data



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DATA DESCRIPTOR

A multi-omics dataset of the response to early plant polysaccharide ingestion in rabbits

Charlotte Paës^{1,2,3}✉, Martin Beaumont¹, Thierry Gidenne¹, Karine Bébin², Joël Duperray⁴, Charly Gohier⁵, Emeline Guéné-Grand⁶, Gwénaël Rebours⁷, Adrien Castinel⁸, Céline Barilly¹, Béatrice Gabinaud¹, Carole Bannelier¹, Laure Gress¹, François Laperruque¹, Patrick Aymard¹, Anne-Marie Debrusse¹, Laurent Cauquil¹, Géraldine Pascal¹ & Sylvie Combes¹✉

The transition from a milk-based diet to exclusive solid feeding deeply modifies microbiota-host crosstalk. Specifically, early ingestion of plant polysaccharides would be one of the main nutritional components to drive host-microbiota-interaction. To capture the effects of polysaccharides early-life nutrition (starch vs rapidly fermentable fiber) on the holobiont development, we investigated on the one hand the gut bacteriome and metabolome and on the other hand the transcriptome of two host gut tissues. Rabbit model was used to study post-natal co-development of the gut microbiota and its host around weaning transition. The assessment of the microbial composition of the gut appendix together with the caecum was provided for the first time. Gene expression signatures were analyzed along the gut (ileum and caecum) through high-throughput qPCR. The data collected were completed by the analysis of animal growth changes and time-series assessment of blood biomarkers. Those accessible and reusable data could help highlight the gut development dynamics as well as biological adaptation processes at the onset of solid feeding.

Background & Summary

The digestive microbiota of mammals represents an ecological community of microorganisms that resides in the gastrointestinal tract and acts as a symbiotic partner through a dynamic crosstalk with the host, affecting its digestive and immune functions^{1–3}. While the holobiont is still in construction, the introduction of solid food in the diet reshapes the gut microbiome through the provision of new nutritional substrates resistant to host digestion^{4–6}. The influx of such new nutrients directly modulates the host physiology as well⁷. If this diet transition is recognized as a major step in the young's development, the mechanistic understanding of the changes occurring in the gut and the long-term consequences of pre-weaning experiences remain unknown. A multi-level approach, from the molecular to the animal levels, with a dynamic follow-up appears necessary to capture the process occurring at the suckling-weaning transition.

In this study, three conditions at the onset of solid food ingestion were tested to investigate the effects of 1/ the timing of solid food introduction and 2/ dietary polysaccharides content on the co-maturation of rabbits and their microbiota. In classical breeding systems, solid food is reachable for suckling rabbits as of 16–18 days of age⁸. Following the feeding behaviour of wild rabbits in the nest, we investigated the effects of an earlier access to solid substrates, available from 3 days of age. Two polysaccharide contents differing by their levels of rapidly fermentable fibers and starch were tested to assess the effects of these two major components of solid-based diets on the gut bacteriome. Rabbit model was used since it is a monogastric species that strongly relies on gut homeostasis for its health and has been successfully used for modeling infections with enteric pathogens^{9,10}. Besides, rabbits present a specific behaviour pattern allowing mother-offspring separation most of the time. Easy control of early-life ingestion (milk and food) can therefore be performed to investigate post-natal food ingestion apart

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Effects of different post-natal feeding strategies on gut ecosystems and host development

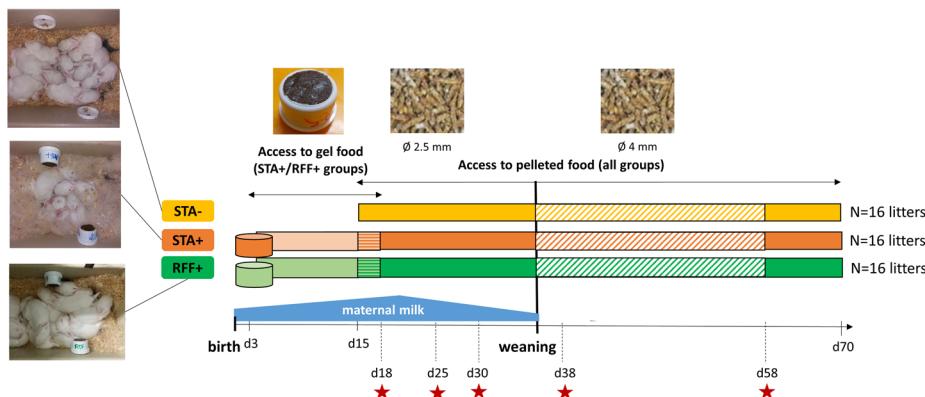
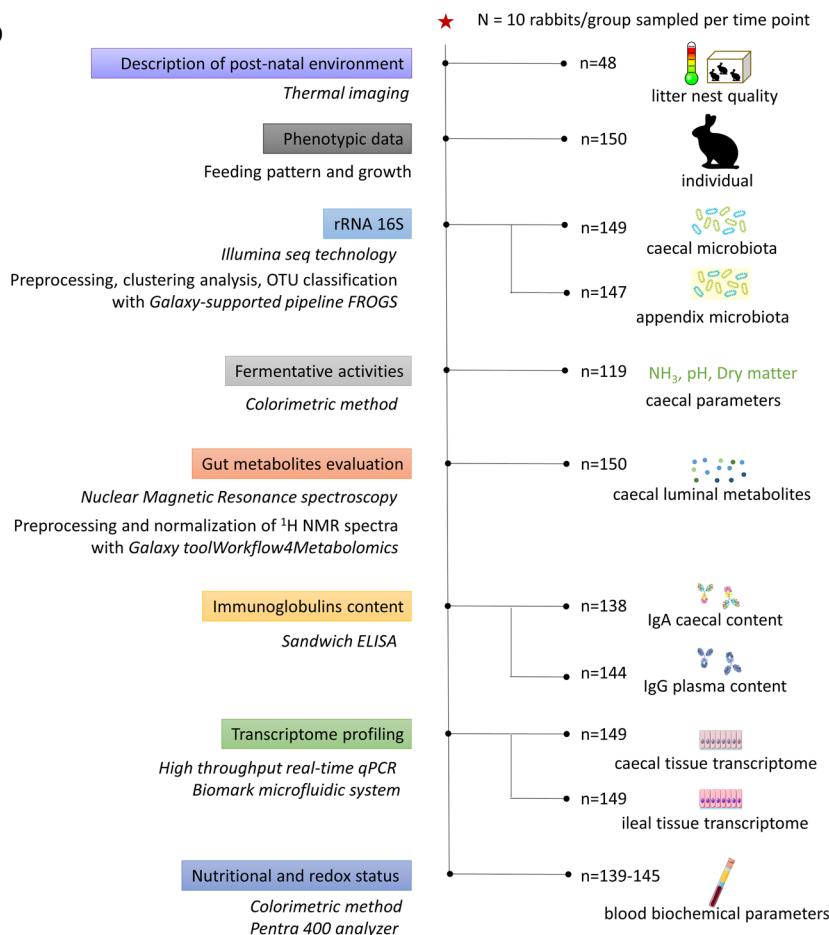
a**b**

Fig. 1 Experimental design (a) and data collection (b). This study aimed to provide insights into host and gut microbiota responses to changes in the timing of solid food introduction (groups STA-/STA+) when two different diets were provided throughout the life (diets STA and RFF). STA-: access to starch-enriched food in a pellet form from 15 to 70 days-old. STA+: access to starch-enriched food from 3 to 18 days-old in a gel form and from 15 to 70 days-old in a pellet form. RFF+: access to food rich in rapidly fermentable fibers from 3 to 18 days-old in a gel form and from 15 to 70 days-old in a pellet form.

from nursing influence. Last but not least, a better understanding of the multidimensional aspects of gut health in rabbits appears essential to improve rabbit breeding practices.

In this data descriptor, we present time-series data collected at the weaning transition (Fig. 1). Information regarding the growth of rabbits and their feeding behavior were included. At an individual-based level, we

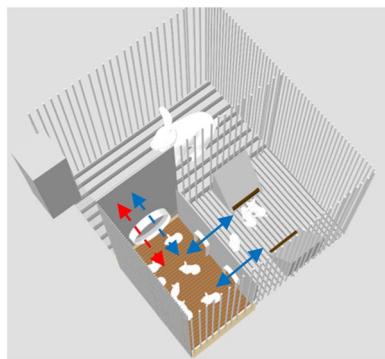


Fig. 2 3D model of the experimental housing system used before weaning. View from the top of a nursing cage where the doe and its kits are raised together for 35 days. Blue arrows represent possible movements of the kits while red arrow represents possible path for the doe. Until day 21, the nest was only opened once a day for suckling (dotted arrows).

provide information relative to gut communities (16S ADNr) and their activities (luminal metabolome) together with rabbit gene expression (high-throughput qPCR) to uncover some aspects of host/microbiota co-maturation that cannot be fully understood with a unique data-type. We report data on 150 rabbits sampled from 30 litters, giving access to information regarding the proportions of 1 197 taxa in the appendix (lymphoid organ) and caecal microbiota, the levels of 29 luminal metabolites and the expression of 48 transcripts of two rabbit gut tissues. Quantification of caecal IgA, plasma IgG and serum redox parameters complement those data. We aimed to generate a comprehensive and combined multi-omics dataset with samplings distributed at 5 different dates, corresponding to the critical phases of food transition¹¹. We intended to follow FAIR principles by providing machine-readable and detailed metadata. Data collection, analysis strategies and corresponding repositories are detailed in this data descriptor to enable a human-friendly data mining.

A part of these datasets were previously disclosed in our associated results paper¹², with this work intended to provide further methods descriptions and validation to facilitate re-use. New data are presented compared to our previous publication, e.g., biochemical measurements of blood content, technical replicates for 16S rDNA sequencing, control strains characterization, rabbit nest quality evaluation and ileal gene expression.

In our companion paper¹², we demonstrated that the ingestion of small quantity of solid food in early life while maintaining milking could effectively accelerate gut microbiota maturation, with spatial-specific effects in the gut. Increasing the ingestion of rapidly fermentable fibers contributed to a specialization of the microbiota towards fibers-degradation activities. Effects of those strategies on the gut transcriptome and the host phenotype were limited in a context of good sanitation facilities. In our results paper, data analysis was restricted to single-omics approach.

Time-monitoring of gut bacterial communities with associated host responses can allow researchers to extract a better picture of early-life developmental process. This comprehensive and reusable collection of data can be further explored by integrating the different types of datasets provided (multi-omics approaches). This could help reveal some interplay mechanisms. To our knowledge, some data were generated for the first time with this experiment, thus providing new information to scientific community (e.g. investigation of caecal and appendix microbiomes in the same individuals or evaluation of plasmatic fatty acids and protein contents in rabbits at different stages). Controls for technical and biological reproducibility of the data were generated, thus leading to valuable data resources for microbiologists and physiologists. We provided herein the description of the methods used together with raw and processed data to ensure easy sharing and re-processing thanks to analysis script provided on the Github platform.

Methods

Rabbits breeding and feeding, sampling conditions, biological acquisition and bioinformatics pipelines (including amplicon sequencing and sequence-based microbiota analysis) were previously disclosed in our associated results paper¹². Detailed procedures or additional information such as complete lab steps for performing NMR measurements and RNA extraction are provided here to ensure that our datasets are understandable and reusable.

Animal management and housing. The animal husbandry procedure is described in our previous article¹². In this data descriptor, the cages used for the experiment are described in more detail, as the housing system was specifically designed for this study. Additional data collection on nest quality is also presented.

Forty-eight crossbred litters (Hyplus PS19 × Hyplus PS59) were raised with their doe in wire cages (width: 62 × length: 69 × height: 62 cm) equipped with nests for the pups (width: 25 cm; length: 38 cm; height: 20 cm). Starter food gels were produced daily and were provided to suckling rabbits directly in the nest inside plastic cups (30 mL; height: 32 mm; diameter: 40 mm; GOSSELIN®, Le Mans, France). Cages were designed to allow the mother and its litter to be fed separately (Fig. 2). In that respect, a wire mesh partition separated the doe from the area containing the kits' feeders. The doe's feeder in the cage was elevated so that the kits could not access to the doe's feed. The day following parturition, the thermal quality of the nests was evaluated using a thermal infrared camera (Fluke Ti450, Everett, Wash, USA). After nest quality assessment, litter size was standardized

to 10 kits. At 3 days, litters were allocated to the three experimental groups according to their body weight (kit weight: 99 ± 9 g) and the doe's parity (5 ± 2 parturitions) (Fig. 1a).

Experimental design. Two diets were formulated for the experiment. They differed only in the ratio of rapidly fermentable fibers (RFF)/starch (STA) (0.6 for STA diet and 2.0 for RFF diet). Detailed diet formulations are provided in our companion paper, together with the procedure for feed distribution¹².

In-farm measurements. We provide herein more detailed information on the collection of performance data (feed ingestion and animal weight). The ingestion of starter food gel was measured daily from 7 days (start of significant ingestion) by the difference in weight between gel offered and gel left. Individual gel ingestion was obtained after correction for gel water loss and final division by the number of kits in the nest. Water loss was estimated inside breeding rooms in empty nests (n=3 measurements/day for each gel type) and averaged to 8% of the initial gel weight. The dry matter content of the starter feed gels was 26% and 89% in the pellets. Milk consumption was measured by weighing the rabbit doe before and after nursing on 3, 7, 10, 14, 17 and 21 days¹³. Pellet ingestion before weaning was assessed at 18, 21, 25, 28, 32 and 36 days of age. Mortality was registered daily and growth was assessed before weaning by weighing the litters at 3, 14, 21 and 28 days of age. After weaning, individual rabbit weights were recorded at 36, 50, 64 and 71 days of age. Live body weights were recorded automatically using a scale (SWR08-10S Plateforme 310 × 275 Trolley, Balea, Saint Mathieu de Tréviers, France) connected to an automatic recording system (Teo or AGPA, Balea, Saint Mathieu de Tréviers, France) with a Bluetooth connection^{14,15}.

Killings and sampling. Ten healthy pups per group (one pup per litter) were selected the days of sampling (n=150 pups euthanized in total). Description of the criteria and procedure for euthanasia are detailed below to supplement the methods provided before¹².

The sampling dates were chosen based on the feed transition process¹¹:

- 18 days of age (solid food consumption remains minor)
- 25 days (dietary switch with marked increase of solid food ingestion proportion compared to milk)
- 30 days (solid-based diet with low amounts of milk consumed)
- 38 days (beginning of exclusive solid diet related with high susceptibility to digestive diseases)
- 58 days (settled exclusive solid feeding with more stable sanitary status)

At days 18, pups that exhibited interest for gel food were preferably selected while at days 25, 30, 38 and 58, the pups were randomly chosen. Before weaning, the killing procedure was performed 1 to 2 hours after suckling, while after weaning the rabbits were sampled 2 to 3 hours after feed distribution to obtain similar postprandial state. After the determination of sex and body weight of the animals chosen, they were killed by electronarcosis and exsanguination.

Blood was collected at exsanguination in EDTA and dry tubes for plasma and serum preparation respectively. EDTA tubes were immediately put on ice until centrifugation (800g for 10 min at 4 °C). After collection of 2.5 mL of blood, dry tubes were let undisturbed at room temperature for 20 minutes. The clot was then removed by centrifugation (1 800 g for 10 min in a regular centrifuge). Resulting supernatants were collected and stored at –20 °C. After isolation of the caecum and the appendix vermiciformis, they were weighted (OHAUS scale, Parsippany, NJ, USA) and up to 500 mg of luminal contents were collected in sterile tubes stored at –80 °C until the extraction step. Between samples, protective gloves were replaced and the material was sterilized to prevent crossed contamination. 0.5 cm of tissues from proximal caecum and distal ileon were quickly extracted at 3 cm up and down the *Sacculus Rototondus*. After washing in ice-cold PBS, they were immediately snap-frozen in liquid nitrogen and stored at –80 °C prior to further processing. 1 g of caecal content was collected and diluted in H₂SO₄ (at 2% w/v) to quantify ammoniac (NH₃) concentrations at days 25, 30, 38 and 58 (insufficient quantities at day 18). Caecal pH was measured after previous samplings by introducing a glass electrode at the ileocecal junction (VWR Collection SP225, Radnor, Pennsylvania, USA). Finally, around 2 g of caecal contents were collected to determine dry matter level after heating at 103 °C for 24 h.

Metabolomics. Caecal contents (100 mg) were homogenized in 500 μL phosphate buffer (sodium phosphate 0.2 M, pH 7.4, trimethylsilylpropanoic acid 1 mmol/L, 80% deuterated water, and 20% water) in 2 mL FastPrep tubes (Lysing D matrix) by using a FastPrep Instrument (MP biomedicals, Irvine, CA). After centrifugation (12 000g, 4 °C, 10 min), the supernatant was transferred to a new tube. The pellet was resuspended in 500 μL phosphate buffer and the homogenization and centrifugation steps were repeated. Supernatants from both extraction steps were pooled and centrifuged twice to remove particles (18 000g, 30 min, 4 °C). The resulting supernatants (600 μL) were transferred to 5 mm NMR tubes. NMR spectra were obtained with an Avance III HD NMR spectrometer operating at 600.13 MHz for 1H resonance frequency using a 5 mm inverse detection CryoProbe (Bruker Biospin, Rheinstetten, Germany) in the MetaboHUB-MetaToul-AXIOM metabolomics platform (Toulouse, France). The 1H NMR spectra were acquired at 300 K using the Carr-Purcell-Meiboom-Gill (CPMG) spin-echo pulse sequence with presaturation. A total of 128 scans (16 dummy scans) were collected in 32 K data points using a spectral width of 20 ppm and an acquisition time of 1.36 s.

Pre-processing of the spectra (group delay correction, solvent suppression, apodization with a line broadening of 0.3 Hz, Fourier transform, zero order phase correction, shift referencing on TSP, baseline correction, setting of negative values to zero) was performed in the Galaxy tool Workflow4Metabolomics following guidelines¹⁶. After water region (4.5–5.1 ppm) exclusion, spectra (0.5–9 ppm) were bucketed (0.01 ppm bucket width) and normalized

| Data set | Database | Accession |
|--|---|---|
| Thermal images used to assess nest quality at day 1 | Data INRAE, "J1_1802_cagenumber.jpg" | https://doi.org/10.15454/QSTXWF |
| Feeding pattern before weaning of all the rabbits raised during the experiment | Data INRAE, "Milk_consumption.csv", "Gel_consumption.csv", "Pellet_consumption.csv", "Gel_consumption.mp4" and "Gel_consumption_access.mp4" | https://doi.org/10.15454/QSTXWF |
| Growth data before and after weaning of all the rabbits raised during the experiment | Data INRAE, "Rabbits_weight.xlsx" | https://doi.org/10.15454/QSTXWF |
| Phenotypic characterization of the rabbits sampled | Data INRAE, "Host_data.csv" | https://doi.org/10.15454/QSTXWF |
| Transcript profiling | Data INRAE, "RNA_caecum.csv" and "RNA ileon.csv" | https://doi.org/10.15454/QSTXWF |
| 16S rDNA sequences | NCBI SRA | PRJNA615661 |
| OTU table and taxonomic affiliations | Data INRAE, "caecal_appendix_microbiome_rabbit_newSILVAdatabase.rdata" and "OTU_abundances.xlsx" | https://doi.org/10.15454/QSTXWF |
| Unstratified pathway abundance per sample (from PICRUSt2) | Data INRAE, "Path_abun_unstrat_transpo.csv" | https://doi.org/10.15454/QSTXWF |
| Microbiota analysis | Data INRAE, "Within_distance_wunifrac.csv" | https://doi.org/10.15454/QSTXWF |
| Metabolites quantification | Data INRAE, "Metabolites_caecum.csv" | https://doi.org/10.15454/QSTXWF |
| Nest quality assessment using infrared camera | DATA INRAE, Files from "J1_1802_101" to "J1_1802_329" | https://doi.org/10.15454/QSTXWF |

Table 1. Accessibility of the public data sets provided.

by sample weight in Workflow4Metabolomics. Representative samples were characterized by 2D NMR experiments (1H-1H COSY and 13C-1H HSQC). For metabolite identification, 1D and 2D NMR spectra of pure compounds prepared in the same buffer and acquired with the same spectrometer were overlayed with samples spectra. For each metabolite identified ($n = 29$), one bucket non-overlapping with other metabolites was selected and its value (area under the curve of the 0.01 ppm segment, normalized to the sample weight) was used for quantification. The chemical shift of buckets selected for quantification of each metabolite is indicated in supplemental table S1.

Gene expression profiling. To improve the reproducibility of our work, we provide below new information on our RT-qPCR protocol.

Caecal ($n = 149$) and ileal ($n = 149$) tissues were homogenized in 800 μL TRI reagent (ZymoResearch) with one sterile stainless steel 5 mm diameter bead (Qiagen, Hilden, Germany) by using a TissueLyzer (Qiagen) with two 3 min cycles at 30 Hz. After centrifugation (12 000 g, 4 °C, 10 min), 300 μL of supernatant was used for RNA extraction by using Direct-zol kit (ZymoResearch) following the manufacturer instruction, including a DNase I treatment with DNA digestion buffer. RNA concentration and quality (260:280 and 260:230 ratios) were analyzed with NanoDrop 8000 (Thermo Fisher Scientific). cDNA were prepared from 1 μg RNA, 1 μL Oligo(dT) (100 μM) and 1 μL dNTP Mix (10 mM each) (Promega, Madison, WISC, USA). After heating the mixture to 65 °C for 5 min and quick chill on ice, the contents of the tube was mixed with 4 μL 5X First-Strand Buffer (Invitrogen, ThermoFisher Scientific), 2 μL 0.1 M DTT, 1 μL Superscript II Reverse Transcriptase (ThermoFisher Scientific) and 1 μL RNasin® Ribonuclease Inhibitor (Promega). After incubation (42 °C for 60 min), the reaction was inactivated by heating at 70 °C for 15 min. cDNA synthesis was checked with the house keeping gene GAPDH by using real-time quantitative PCR performed in QuantStudio 6 (Thermo Fisher Scientific, Waltham, MA, USA) with a reaction solution containing 2.5 μl of SybrGreen fluorescent DNA-binding dye (ThermoFisher Scientific), 0.2 μl of each primer at 10 μM , 0.9 μM of sterile water and 1 μL of DNA diluted at 1:10. We performed 40 PCR amplification cycles with an annealing temperature of 60 °C. After this control, high throughput real-time qPCR was performed for each tissue using the Biomark microfluidics system using a 96.96 Dynamic Array™ IFC for gene expression (Fluidigm, San Francisco, CA, USA). 1.3 μL of cDNA (5 ng. μl^{-1}) was added to the array and processed on the fluidics system according to the guidelines of the GENOTOUL platform. Briefly, an initial high temperature activation step of 10 minutes was performed into the PCR reaction with 35 amplification cycles at 60 °C later on. The sequences of the primers used are presented in our companion paper. Genes with suitable melt curve aspect, good efficiency (>90% and < 110%) and linearity were kept for statistical analysis. GAPDH and TOP1 gene were selected as housekeeping genes for caecal and ileal tissue respectively, based on their stability over time and between groups, in order to calculate gene expression using the $2^{-\Delta\Delta\text{Ct}}$ method.

Enzyme-linked immunosorbent assay (ELISA) measurements. The ELISA laboratory procedure has been shortly described in our companion document¹². Further details, such as the construction of the calibration curve, are given below for better reproducibility.

In order to extract the immunoglobulins A (IgA) from the caecal content, 200–500 mg of digesta was diluted at 50 mg/mL in cold TBS. After shaking the solution thoroughly, and centrifugation at 3000 g for 10 min at 4 °C, the supernatant was collected for measurement. Total plasma IgG or caecal content IgA levels were determined in duplicates by sandwich ELISA in 96-well plates coated with specific polyclonal goat anti-rabbit IgG or IgA antibody (Bethyl Laboratories, Montgomery, Texas, USA) with further plate reading at 450 nm after fixation of the reaction between HRP conjugated antibodies (Bethyl Laboratories) and TMB. IgG were quantified using a reference IgG serum (Bethyl Laboratories). Regarding IgA, 12 samples were pooled to build a reference sample for the standard curve construction. For both measurements, seven calibrator points and water blank were added in duplicate to the microwell plates along with the samples. While linear standard curves were sufficient to fit the seven calibrators used for IgG quantification in plasma, a 4-parametric logistic model (4-PL) was used to improve the fit of caecal IgA calibration curve (average R^2 with the 7 calibrators points = 0.98).

| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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Continued

| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430091 | SRP254184 | PRJNA615661 | SAMN14464050 | 312 | caecum | CP1802-cc312_TGTCTA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc312_TGTCTA-C43D4_L001_R1.fastq.gz | CP1802-cc312_TGTCTA-C43D4_L001_R2.fastq.gz |
| SRR11430080 | SRP254184 | PRJNA615661 | SAMN14464051 | 313 | caecum | CP1802-cc313_CGCATT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc313_CGCATT-C43D4_L001_R1.fastq.gz | CP1802-cc313_CGCATT-C43D4_L001_R2.fastq.gz |
| SRR11430069 | SRP254184 | PRJNA615661 | SAMN14464052 | 314 | caecum | CP1802-cc314_CCCACG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc314_CCCACG-C43D4_L001_R1.fastq.gz | CP1802-cc314_CCCACG-C43D4_L001_R2.fastq.gz |
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| SRR11430027 | SRP254184 | PRJNA615661 | SAMN14464056 | 321 | caecum | CP1802-cc321_TC GGCC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc321_TC GGCC-C43D4_L001_R1.fastq.gz | CP1802-cc321_TC GGCC-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430016 | SRP254184 | PRJNA615661 | SAMN14464057 | 322 | caecum | CP1802-cc322_GTCAGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc322_GTCAGG-C43D4_L001_R1.fastq.gz | CP1802-cc322_GTCAGG-C43D4_L001_R2.fastq.gz |
| SRR11430005 | SRP254184 | PRJNA615661 | SAMN14464058 | 324 | caecum | CP1802-cc324_TAACCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc324_TAACCG-C43D4_L001_R1.fastq.gz | CP1802-cc324_TAACCG-C43D4_L001_R2.fastq.gz |
| SRR11429894 | SRP254184 | PRJNA615661 | SAMN14464059 | 326 | caecum | CP1802-cc326_CAAATTA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc326_CAAATTA-C43D4_L001_R1.fastq.gz | CP1802-cc326_CAAATTA-C43D4_L001_R2.fastq.gz |
| SRR11429883 | SRP254184 | PRJNA615661 | SAMN14464060 | 327 | caecum | CP1802-cc327_ATGTGTC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc327_ATGTGTC-C43D4_L001_R1.fastq.gz | CP1802-cc327_ATGTGTC-C43D4_L001_R2.fastq.gz |
| SRR11429872 | SRP254184 | PRJNA615661 | SAMN14464061 | 328 | caecum | CP1802-cc328_ATTGAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc328_ATTGAG-C43D4_L001_R1.fastq.gz | CP1802-cc328_ATTGAG-C43D4_L001_R2.fastq.gz |
| SRR11429861 | SRP254184 | PRJNA615661 | SAMN14464062 | 329 | caecum | CP1802-cc329_TATTGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc329_TATTGG-C43D4_L001_R1.fastq.gz | CP1802-cc329_TATTGG-C43D4_L001_R2.fastq.gz |
| SRR11429849 | SRP254184 | PRJNA615661 | SAMN14464063 | 330 | caecum | CP1802-cc330_AACGCA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc330_AACGCA-C43D4_L001_R1.fastq.gz | CP1802-cc330_AACGCA-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429838 | SRP254184 | PRJNA615661 | SAMN14464064 | 331 | caecum | CP1802-cc331_ACGTCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc331_ACGTCG-C43D4_L001_R1.fastq.gz | CP1802-cc331_ACGTCG-C43D4_L001_R2.fastq.gz |
| SRR11429991 | SRP254184 | PRJNA615661 | SAMN14464065 | 332 | caecum | CP1802-cc332_GTACAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc332_GTACAG-C43D4_L001_R1.fastq.gz | CP1802-cc332_GTACAG-C43D4_L001_R2.fastq.gz |
| SRR11429980 | SRP254184 | PRJNA615661 | SAMN14464066 | 333 | caecum | CP1802-cc332_GTGCTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc332_GTGCTG-C43D4_L001_R1.fastq.gz | CP1802-cc332_GTGCTG-C43D4_L001_R2.fastq.gz |
| SRR11429969 | SRP254184 | PRJNA615661 | SAMN14464067 | 334 | caecum | CP1802-cc334_CAAATGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc334_CAAATGC-C43D4_L001_R1.fastq.gz | CP1802-cc334_CAAATGC-C43D4_L001_R2.fastq.gz |
| SRR11429958 | SRP254184 | PRJNA615661 | SAMN14464068 | 335 | caecum | CP1802-cc335_CCGTAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc335_CCGTAG-C43D4_L001_R1.fastq.gz | CP1802-cc335_CCGTAG-C43D4_L001_R2.fastq.gz |
| SRR11429947 | SRP254184 | PRJNA615661 | SAMN14464069 | 337 | caecum | CP1802-cc337_CTCGCC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc337_CTCGCC-C43D4_L001_R1.fastq.gz | CP1802-cc337_CTCGCC-C43D4_L001_R2.fastq.gz |
| SRR11429936 | SRP254184 | PRJNA615661 | SAMN14464070 | 338 | caecum | CP1802-cc338_GACTAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc338_GACTAC-C43D4_L001_R1.fastq.gz | CP1802-cc338_GACTAC-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429825 | SRP254184 | PRJNA615661 | SAMN14464071 | 340 | caecum | CP1802-cc340_CATAAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc340_CATAAC-C43D4_L001_R1.fastq.gz | CP1802-cc340_CATAAC-C43D4_L001_R2.fastq.gz |
| SRR11429814 | SRP254184 | PRJNA615661 | SAMN14464072 | 341 | caecum | CP1802-cc341_CCCTCC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc341_CCCTCC-C43D4_L001_R1.fastq.gz | CP1802-cc341_CCCTCC-C43D4_L001_R2.fastq.gz |
| SRR11429806 | SRP254184 | PRJNA615661 | SAMN14464073 | 342 | caecum | CP1802-cc342_TGTTTCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc342_TGTTTCG-C43D4_L001_R1.fastq.gz | CP1802-cc342_TGTTTCG-C43D4_L001_R2.fastq.gz |
| SRR11429805 | SRP254184 | PRJNA615661 | SAMN14464074 | 343 | caecum | CP1802-cc343_CATGAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc343_CATGAG-C43D4_L001_R1.fastq.gz | CP1802-cc343_CATGAG-C43D4_L001_R2.fastq.gz |
| SRR11429804 | SRP254184 | PRJNA615661 | SAMN14464075 | 344 | caecum | CP1802-cc344_AAGTGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc344_AAGTGG-C43D4_L001_R1.fastq.gz | CP1802-cc344_AAGTGG-C43D4_L001_R2.fastq.gz |
| SRR11429803 | SRP254184 | PRJNA615661 | SAMN14464076 | 347 | caecum | CP1802-cc347_CTTTAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc347_CTTTAG-C43D4_L001_R1.fastq.gz | CP1802-cc347_CTTTAG-C43D4_L001_R2.fastq.gz |
| SRR11429802 | SRP254184 | PRJNA615661 | SAMN14464077 | 349 | caecum | CP1802-cc349_GAGAAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc349_GAGAAC-C43D4_L001_R1.fastq.gz | CP1802-cc349_GAGAAC-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429801 | SRP254184 | PRJNA615661 | SAMN14464078 | 350 | caecum | CP1802-cc350_CCAACAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc350_CCAACAA-C43D4_L001_R1.fastq.gz | CP1802-cc350_CCAACAA-C43D4_L001_R2.fastq.gz |
| SRR11429800 | SRP254184 | PRJNA615661 | SAMN14464079 | 352 | caecum | CP1802-cc352_GTCAAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc352_GTCAAA-C43D4_L001_R1.fastq.gz | CP1802-cc352_GTCAAA-C43D4_L001_R2.fastq.gz |
| SRR11429799 | SRP254184 | PRJNA615661 | SAMN14464080 | 353 | caecum | CP1802-cc352_CCCTGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc352_CCCTGG-C43D4_L001_R1.fastq.gz | CP1802-cc352_CCCTGG-C43D4_L001_R2.fastq.gz |
| SRR11429930 | SRP254184 | PRJNA615661 | SAMN14464081 | 354 | caecum | CP1802-cc354_CGCCAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc354_CGCCAC-C43D4_L001_R1.fastq.gz | CP1802-cc354_CGCCAC-C43D4_L001_R2.fastq.gz |
| SRR11429929 | SRP254184 | PRJNA615661 | SAMN14464082 | 356 | caecum | CP1802-cc356_TAAATAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc356_TAAATAT-C43D4_L001_R1.fastq.gz | CP1802-cc356_TAAATAT-C43D4_L001_R2.fastq.gz |
| SRR11429927 | SRP254184 | PRJNA615661 | SAMN14464083 | 357 | caecum | CP1802-cc357_TGGTGT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc357_TGGTGT-C43D4_L001_R1.fastq.gz | CP1802-cc357_TGGTGT-C43D4_L001_R2.fastq.gz |
| SRR11429926 | SRP254184 | PRJNA615661 | SAMN14464084 | 358 | caecum | CP1802-cc358_CIACCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc358_CIACCG-C43D4_L001_R1.fastq.gz | CP1802-cc358_CIACCG-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429925 | SRP254184 | PRJNA615661 | SAMN14464085 | 359 | caecum | CP1802-cc359_CGTGCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc359_CGTGCG-C43D4_L001_R1.fastq.gz | CP1802-cc359_CGTGCG-C43D4_L001_R2.fastq.gz |
| SRR11429924 | SRP254184 | PRJNA615661 | SAMN14464086 | 360 | caecum | CP1802-cc360_GA1TC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc360_GA1TC-C43D4_L001_R1.fastq.gz | CP1802-cc360_GA1TC-C43D4_L001_R2.fastq.gz |
| SRR11429923 | SRP254184 | PRJNA615661 | SAMN14464087 | 362 | caecum | CP1802-cc362_TACCAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc362_TACCAA-C43D4_L001_R1.fastq.gz | CP1802-cc362_TACCAA-C43D4_L001_R2.fastq.gz |
| SRR11429922 | SRP254184 | PRJNA615661 | SAMN14464088 | 364 | caecum | CP1802-cc364_CGTACT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc364_CGTACT-C43D4_L001_R1.fastq.gz | CP1802-cc364_CGTACT-C43D4_L001_R2.fastq.gz |
| SRR11429921 | SRP254184 | PRJNA615661 | SAMN14464089 | 366 | caecum | CP1802-cc366_CACACT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc366_CACACT-C43D4_L001_R1.fastq.gz | CP1802-cc366_CACACT-C43D4_L001_R2.fastq.gz |
| SRR11429920 | SRP254184 | PRJNA615661 | SAMN14464090 | 367 | caecum | CP1802-cc367_GAGCAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc367_GAGCAA-C9F6L_L001_R1.fastq.gz | CP1802-cc367_GAGCAA-C9F6L_L001_R2.fastq.gz |
| SRR11429919 | SRP254184 | PRJNA615661 | SAMN14464091 | 368 | caecum | CP1802-cc368_ACTTTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc368_ACTTTT-C9F6L_L001_R1.fastq.gz | CP1802-cc368_ACTTTT-C9F6L_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429918 | SRP254184 | PRJNA615661 | SAMN14464092 | 369 | caecum | CP1802-cc369_ACTCGA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc369_ACTCGA-C43D4_L001_R1.fastq.gz | CP1802-cc369_ACTCGA-C43D4_L001_R2.fastq.gz |
| SRR11429916 | SRP254184 | PRJNA615661 | SAMN14464093 | 370 | caecum | CP1802-cc370_TACICA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc370_TACICA-C9F6J_L001_R1.fastq.gz | CP1802-cc370_TACICA-C9F6J_L001_R2.fastq.gz |
| SRR11429915 | SRP254184 | PRJNA615661 | SAMN14464094 | 371 | caecum | CP1802-cc371_CAGAGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc371_CAGAGC-C43D4_L001_R1.fastq.gz | CP1802-cc371_CAGAGC-C43D4_L001_R2.fastq.gz |
| SRR11429914 | SRP254184 | PRJNA615661 | SAMN14464095 | 372 | caecum | CP1802-cc372_GGCCCTC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc372_GGCCCTC-C9F6J_L001_R1.fastq.gz | CP1802-cc372_GGCCCTC-C9F6J_L001_R2.fastq.gz |
| SRR11429913 | SRP254184 | PRJNA615661 | SAMN14464096 | 373 | caecum | CP1802-cc373_AATCAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc373_AATCAC-C43D4_L001_R1.fastq.gz | CP1802-cc373_AATCAC-C43D4_L001_R2.fastq.gz |
| SRR11429912 | SRP254184 | PRJNA615661 | SAMN14464097 | 374 | caecum | CP1802-cc374_CCCGGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc374_CCCGGC-C9F6J_L001_R1.fastq.gz | CP1802-cc374_CCCGGC-C9F6J_L001_R2.fastq.gz |
| SRR11429911 | SRP254184 | PRJNA615661 | SAMN14464098 | 375 | caecum | CP1802-cc375_TCCCCA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc375_TCCCCA-C43D4_L001_R1.fastq.gz | CP1802-cc375_TCCCCA-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429910 | SRP254184 | PRJNA615661 | SAMN14464099 | 377 | caecum | CP1802-cc377_CTCICG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc377_CTCICG-C43D4_L001_R1.fastq.gz | CP1802-cc377_CTCICG-C43D4_L001_R2.fastq.gz |
| SRR11429909 | SRP254184 | PRJNA615661 | SAMN14464100 | 378 | caecum | CP1802-cc378_CAGATG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc378_CAGATG-C43D4_L001_R1.fastq.gz | CP1802-cc378_CAGATG-C43D4_L001_R2.fastq.gz |
| SRR11429908 | SRP254184 | PRJNA615661 | SAMN14464101 | 380 | caecum | CP1802-cc380_GCCGGT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc380_GCCGGT-C9F6J_L001_R1.fastq.gz | CP1802-cc380_GCCGGT-C9F6J_L001_R2.fastq.gz |
| SRR11429907 | SRP254184 | PRJNA615661 | SAMN14464102 | 381 | caecum | CP1802-cc381_CAGCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc381_CAGCT-C43D4_L001_R1.fastq.gz | CP1802-cc381_CAGCT-C43D4_L001_R2.fastq.gz |
| SRR11429905 | SRP254184 | PRJNA615661 | SAMN14464103 | 382 | caecum | CP1802-cc382_AAATTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc382_AAATTG-C43D4_L001_R1.fastq.gz | CP1802-cc382_AAATTG-C43D4_L001_R2.fastq.gz |
| SRR11429904 | SRP254184 | PRJNA615661 | SAMN14464104 | 383 | caecum | CP1802-cc383_AGTITG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc383_AGTITG-C43D4_L001_R1.fastq.gz | CP1802-cc383_AGTITG-C43D4_L001_R2.fastq.gz |
| SRR11429903 | SRP254184 | PRJNA615661 | SAMN14464105 | 384 | caecum | CP1802-cc384_TCTCGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc384_TCTCGG-C43D4_L001_R1.fastq.gz | CP1802-cc384_TCTCGG-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429902 | SRP254184 | PRJNA615661 | SAMN14464106 | 387 | caecum | CP1802-cc387-ACTGCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc387-ACTGCG-C9F6J_L001_R1.fastq.gz | CP1802-cc387-ACTGCG-C9F6J_L001_R2.fastq.gz |
| SRR11429901 | SRP254184 | PRJNA615661 | SAMN14464107 | 389 | caecum | CP1802-cc389-ATTAGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc389-ATTAGG-C9F6J_L001_R1.fastq.gz | CP1802-cc389-ATTAGG-C9F6J_L001_R2.fastq.gz |
| SRR11429900 | SRP254184 | PRJNA615661 | SAMN14464108 | 390 | caecum | CP1802-cc390_ACAGTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc390_ACAGTT-C43D4_L001_R1.fastq.gz | CP1802-cc390_ACAGTT-C43D4_L001_R2.fastq.gz |
| SRR11429899 | SRP254184 | PRJNA615661 | SAMN14464109 | 392 | caecum | CP1802-cc392_GCTATC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc392_GCTATC-C43D4_L001_R1.fastq.gz | CP1802-cc392_GCTATC-C43D4_L001_R2.fastq.gz |
| SRR11430094 | SRP254184 | PRJNA615661 | SAMN14464110 | 393 | caecum | CP1802-cc393_TTAAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc393_TTAAT-C43D4_L001_R1.fastq.gz | CP1802-cc393_TTAAT-C43D4_L001_R2.fastq.gz |
| SRR11430093 | SRP254184 | PRJNA615661 | SAMN14464111 | 394 | caecum | CP1802-cc394_TTTGTAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc394_TTTGTAA-C43D4_L001_R1.fastq.gz | CP1802-cc394_TTTGTAA-C43D4_L001_R2.fastq.gz |
| SRR11430092 | SRP254184 | PRJNA615661 | SAMN14464112 | 396 | caecum | CP1802-cc396_GTTACC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc396_GTTACC-C43D4_L001_R1.fastq.gz | CP1802-cc396_GTTACC-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430090 | SRP254184 | PRJNA615661 | SAMN14464113 | 397 | caecum | CP1802-cc397_CCATTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc397_CCATTG-C43D4_L001_R1.fastq.gz | CP1802-cc397_CCATTG-C43D4_L001_R2.fastq.gz |
| SRR11430089 | SRP254184 | PRJNA615661 | SAMN14464114 | 398 | caecum | CP1802-cc398_TCGCGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc398_TCGCGC-C43D4_L001_R1.fastq.gz | CP1802-cc398_TCGCGC-C43D4_L001_R2.fastq.gz |
| SRR11430088 | SRP254184 | PRJNA615661 | SAMN14464115 | 399 | caecum | CP1802-cc399_TAACTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc399_TAACTT-C43D4_L001_R1.fastq.gz | CP1802-cc399_TAACTT-C43D4_L001_R2.fastq.gz |
| SRR11430087 | SRP254184 | PRJNA615661 | SAMN14464116 | 400 | caecum | CP1802-cc400_GGACTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc400_GGACTT-C43D4_L001_R1.fastq.gz | CP1802-cc400_GGACTT-C43D4_L001_R2.fastq.gz |
| SRR11430086 | SRP254184 | PRJNA615661 | SAMN14464117 | 402 | caecum | CP1802-cc402_TCGAAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc402_TCGAAC-C43D4_L001_R1.fastq.gz | CP1802-cc402_TCGAAC-C43D4_L001_R2.fastq.gz |
| SRR11430085 | SRP254184 | PRJNA615661 | SAMN14464118 | 404 | caecum | CP1802-cc404_CCGACC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc404_CCGACC-C43D4_L001_R1.fastq.gz | CP1802-cc404_CCGACC-C43D4_L001_R2.fastq.gz |
| SRR11430084 | SRP254184 | PRJNA615661 | SAMN14464119 | 406 | caecum | CP1802-cc406_CAGTCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc406_CAGTCT-C43D4_L001_R1.fastq.gz | CP1802-cc406_CAGTCT-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430083 | SRP254184 | PRJNA615661 | SAMN14464120 | 407 | caecum | CP1802-cc407_GACAGT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc407_GACAGT-C9F6J_L001_R1.fastq.gz | CP1802-cc407_GACAGT-C9F6J_L001_R2.fastq.gz |
| SRR11430082 | SRP254184 | PRJNA615661 | SAMN14464121 | 408 | caecum | CP1802-cc408_TTTTC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc408_TTTTC-C9F6J_L001_R1.fastq.gz | CP1802-cc408_TTTTC-C9F6J_L001_R2.fastq.gz |
| SRR11430081 | SRP254184 | PRJNA615661 | SAMN14464122 | 409 | caecum | CP1802-cc409_TGCCCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc409_TGCCCT-C9F6J_L001_R1.fastq.gz | CP1802-cc409_TGCCCT-C9F6J_L001_R2.fastq.gz |
| SRR11430079 | SRP254184 | PRJNA615661 | SAMN14464123 | 410 | caecum | CP1802-cc410_GGTAGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc410_GGTAGC-C43D4_L001_R1.fastq.gz | CP1802-cc410_GGTAGC-C43D4_L001_R2.fastq.gz |
| SRR11430078 | SRP254184 | PRJNA615661 | SAMN14464124 | 411 | caecum | CP1802-cc411_GCTATC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc411_GCTATC-C9F6J_L001_R1.fastq.gz | CP1802-cc411_GCTATC-C9F6J_L001_R2.fastq.gz |
| SRR11430077 | SRP254184 | PRJNA615661 | SAMN14464125 | 412 | caecum | CP1802-cc412_TTAGCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc412_TTAGCT-C9F6J_L001_R1.fastq.gz | CP1802-cc412_TTAGCT-C9F6J_L001_R2.fastq.gz |
| SRR11430076 | SRP254184 | PRJNA615661 | SAMN14464126 | 413 | caecum | CP1802-cc413_GCAAAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc413_GCAAAT-C43D4_L001_R1.fastq.gz | CP1802-cc413_GCAAAT-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430075 | SRP254184 | PRJNA615661 | SAMN14464127 | 414 | caecum | CP1802-cc414_TCGCGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc414_TCGCGC-C9F6J_L001_R1.fastq.gz | CP1802-cc414_TCGCGC-C9F6J_L001_R2.fastq.gz |
| SRR11430074 | SRP254184 | PRJNA615661 | SAMN14464128 | 415 | caecum | CP1802-cc415_ACATAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc415_ACATAT-C43D4_L001_R1.fastq.gz | CP1802-cc415_ACATAT-C43D4_L001_R2.fastq.gz |
| SRR11430073 | SRP254184 | PRJNA615661 | SAMN14464129 | 417 | caecum | CP1802-cc417_GAGCTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc417_GAGCTT-C43D4_L001_R1.fastq.gz | CP1802-cc417_GAGCTT-C43D4_L001_R2.fastq.gz |
| SRR11430072 | SRP254184 | PRJNA615661 | SAMN14464130 | 418 | caecum | CP1802-cc418_CTAGGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc418_CTAGGC-C9F6J_L001_R1.fastq.gz | CP1802-cc418_CTAGGC-C9F6J_L001_R2.fastq.gz |
| SRR11430071 | SRP254184 | PRJNA615661 | SAMN14464131 | 420 | caecum | CP1802-cc420_GCCAAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc420_GCCAAG-C43D4_L001_R1.fastq.gz | CP1802-cc420_GCCAAG-C43D4_L001_R2.fastq.gz |
| SRR11430070 | SRP254184 | PRJNA615661 | SAMN14464132 | 421 | caecum | CP1802-cc421_TGCTGCA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc421_TGCTGCA-C9F6J_L001_R1.fastq.gz | CP1802-cc421_TGCTGCA-C9F6J_L001_R2.fastq.gz |
| SRR11430068 | SRP254184 | PRJNA615661 | SAMN14464133 | 422 | caecum | CP1802-cc422_TTTTC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc422_TTTTC-C43D4_L001_R1.fastq.gz | CP1802-cc422_TTTTC-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430067 | SRP254184 | PRJNA615661 | SAMN14464134 | 423 | caecum | CP1802-cc423_GTCGTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc423_GTCGTG-C43D4_L001_R1.fastq.gz | CP1802-cc423_GTCGTG-C43D4_L001_R2.fastq.gz |
| SRR11430066 | SRP254184 | PRJNA615661 | SAMN14464135 | 424 | caecum | CP1802-cc424_GAGCTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc424_GAGCTT-C9F6J_L001_R1.fastq.gz | CP1802-cc424_GAGCTT-C9F6J_L001_R2.fastq.gz |
| SRR11430065 | SRP254184 | PRJNA615661 | SAMN14464136 | 427 | caecum | CP1802-cc427_GCCTAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc427_GCCTAA-C9F6J_L001_R1.fastq.gz | CP1802-cc427_GCCTAA-C9F6J_L001_R2.fastq.gz |
| SRR11430064 | SRP254184 | PRJNA615661 | SAMN14464137 | 429 | caecum | CP1802-cc429_TTGCTA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc429_TTGCTA-C9F6J_L001_R1.fastq.gz | CP1802-cc429_TTGCTA-C9F6J_L001_R2.fastq.gz |
| SRR11430063 | SRP254184 | PRJNA615661 | SAMN14464138 | 430 | caecum | CP1802-cc430_GCAAAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc430_GCAAAT-C9F6J_L001_R1.fastq.gz | CP1802-cc430_GCAAAT-C9F6J_L001_R2.fastq.gz |
| SRR11429898 | SRP254184 | PRJNA615661 | SAMN14464139 | 432 | caecum | CP1802-cc432_TACCTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc432_TACCTG-C9F6J_L001_R1.fastq.gz | CP1802-cc432_TACCTG-C9F6J_L001_R2.fastq.gz |
| SRR11429897 | SRP254184 | PRJNA615661 | SAMN14464140 | 433 | caecum | CP1802-cc433_GTAACA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc433_GTAACA-C43D4_L001_R1.fastq.gz | CP1802-cc433_GTAACA-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429896 | SRP254184 | PRJNA615661 | SAMN14464141 | 434 | caecum | CP1802-cc434_GTGGGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc434_GTGGGG-C9F6J_L001_R1.fastq.gz | CP1802-cc434_GTGGGG-C9F6J_L001_R2.fastq.gz |
| SRR11429895 | SRP254184 | PRJNA615661 | SAMN14464142 | 436 | caecum | CP1802-cc436_TGCTCC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc436_TGCTCC-C9F6J_L001_R1.fastq.gz | CP1802-cc436_TGCTCC-C9F6J_L001_R2.fastq.gz |
| SRR11430059 | SRP254184 | PRJNA615661 | SAMN14464143 | 437 | caecum | CP1802-cc437_TCACAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc437_TCACAC-C9F6J_L001_R1.fastq.gz | CP1802-cc437_TCACAC-C9F6J_L001_R2.fastq.gz |
| SRR11430058 | SRP254184 | PRJNA615661 | SAMN14464144 | 438 | caecum | CP1802-cc438_CIACAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc438_CIACAT-C9F6J_L001_R1.fastq.gz | CP1802-cc438_CIACAT-C9F6J_L001_R2.fastq.gz |
| SRR11430057 | SRP254184 | PRJNA615661 | SAMN14464145 | 439 | caecum | CP1802-cc439_GCAGCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc439_GCAGCT-C43D4_L001_R1.fastq.gz | CP1802-cc439_GCAGCT-C43D4_L001_R2.fastq.gz |
| SRR11430056 | SRP254184 | PRJNA615661 | SAMN14464146 | 440 | caecum | CP1802-cc440_AACGCA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc440_AACGCA-C9F6J_L001_R1.fastq.gz | CP1802-cc440_AACGCA-C9F6J_L001_R2.fastq.gz |
| SRR11430055 | SRP254184 | PRJNA615661 | SAMN14464147 | 442 | caecum | CP1802-cc442_GGAGGT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc442_GGAGGT-C43D4_L001_R1.fastq.gz | CP1802-cc442_GGAGGT-C43D4_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection | library layout | instrument model | design descriptor | file type | filename | filename2 |
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| SRR11430054 | SRP254184 | PRJNA615661 | SAMN14464148 | 444 | caecum | CP1802-cc444_TGCCGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc444_TGCCGG-C9F6J_L001_R1.fastq.gz | CP1802-cc444_TGCCGG-C9F6J_L001_R2.fastq.gz |
| SRR11430053 | SRP254184 | PRJNA615661 | SAMN14464149 | 446 | caecum | CP1802-cc446_GGACGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc446_GGACGG-C9F6J_L001_R1.fastq.gz | CP1802-cc446_GGACGG-C9F6J_L001_R2.fastq.gz |
| SRR11430052 | SRP254184 | PRJNA615661 | SAMN14464150 | 447 | caecum | CP1802-cc447_GTTTCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc447_GTTTCT-C9F6J_L001_R1.fastq.gz | CP1802-cc447_GTTTCT-C9F6J_L001_R2.fastq.gz |
| SRR11430051 | SRP254184 | PRJNA615661 | SAMN14464151 | 448 | caecum | CP1802-cc448_ATGAAAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc448_ATGAAAC-C9F6J_L001_R1.fastq.gz | CP1802-cc448_ATGAAAC-C9F6J_L001_R2.fastq.gz |
| SRR11430050 | SRP254184 | PRJNA615661 | SAMN14464152 | 449 | caecum | CP1802-cc449_TCCTATG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc449_TCCTATG-C9F6J_L001_R1.fastq.gz | CP1802-cc449_TCCTATG-C9F6J_L001_R2.fastq.gz |
| SRR11430048 | SRP254184 | PRJNA615661 | SAMN14464153 | 450 | caecum | CP1802-cc450_CTAGAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc450_CTAGAG-C9F6J_L001_R1.fastq.gz | CP1802-cc450_CTAGAG-C9F6J_L001_R2.fastq.gz |
| SRR11430047 | SRP254184 | PRJNA615661 | SAMN14464154 | 451 | caecum | CP1802-cc451_AAITGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc451_AAITGC-C9F6J_L001_R1.fastq.gz | CP1802-cc451_AAITGC-C9F6J_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430046 | SRP254184 | PRJNA615661 | SAMN14464155 | 452 | caecum | CP1802-cc452_ATGCTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc452_ATGCTT-C9F6J_L001_R1.fastq.gz | CP1802-cc452_ATGCTT-C9F6J_L001_R2.fastq.gz |
| SRR11430045 | SRP254184 | PRJNA615661 | SAMN14464156 | 453 | caecum | CP1802-cc453_AGAGGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc453_AGAGGG-C9F6J_L001_R1.fastq.gz | CP1802-cc453_AGAGGG-C9F6J_L001_R2.fastq.gz |
| SRR11430044 | SRP254184 | PRJNA615661 | SAMN14464157 | 454 | caecum | CP1802-cc454_CCCAAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc454_CCCAAA-C9F6J_L001_R1.fastq.gz | CP1802-cc454_CCCAAA-C9F6J_L001_R2.fastq.gz |
| SRR11430043 | SRP254184 | PRJNA615661 | SAMN14464158 | 455 | caecum | CP1802-cc455_GATGCT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc455_GATGCT-C9F6J_L001_R1.fastq.gz | CP1802-cc455_GATGCT-C9F6J_L001_R2.fastq.gz |
| SRR11430042 | SRP254184 | PRJNA615661 | SAMN14464159 | 457 | caecum | CP1802-cc455_CTCCTAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc455_CTCCTAC-C9F6J_L001_R1.fastq.gz | CP1802-cc455_CTCCTAC-C9F6J_L001_R2.fastq.gz |
| SRR11430041 | SRP254184 | PRJNA615661 | SAMN14464160 | 458 | caecum | CP1802-cc458_CAGGAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc458_CAGGAC-C43D4_L001_R1.fastq.gz | CP1802-cc458_CAGGAC-C43D4_L001_R2.fastq.gz |
| SRR11430040 | SRP254184 | PRJNA615661 | SAMN14464161 | 460 | caecum | CP1802-cc460_CCITGA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc460_CCITGA-C9F6J_L001_R1.fastq.gz | CP1802-cc460_CCITGA-C9F6J_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection | library layout | platform | instrument model | design description | file type | filename | filename2 |
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| SRR1143039 | SRP254184 | PRJNA615661 | SAMN14464162 | 461 | caecum | CPI1802-cc461_GTAGAA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc461_GTAGAA-C9f6j_L001_R1.fastq.gz | CP1802-cc461_GTAGAA-C9f6j_L001_R2.fastq.gz |
| SRR1143037 | SRP254184 | PRJNA615661 | SAMN14464163 | 463 | caecum | CPI1802-cc463_CAA \bar{C} AG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc463_CAA \bar{C} AG-C9f6j_L001_R1.fastq.gz | CP1802-cc463_CAA \bar{C} AG-C9f6j_L001_R2.fastq.gz |
| SRR1143036 | SRP254184 | PRJNA615661 | SAMN14464164 | 465 | caecum | CPI1802-cc465_CTTGCA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc465_CTTGCA-C9f6j_L001_R1.fastq.gz | CP1802-cc465_CTTGCA-C9f6j_L001_R2.fastq.gz |
| SRR1143035 | SRP254184 | PRJNA615661 | SAMN14464165 | 466 | caecum | CPI1802-cc466_GGTAGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc466_GGTAGC-C9f6j_L001_R1.fastq.gz | CP1802-cc466_GGTAGC-C9f6j_L001_R2.fastq.gz |
| SRR1143034 | SRP254184 | PRJNA615661 | SAMN14464166 | 467 | caecum | CPI1802-cc467_TGGATT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc467_TGGATT-C9f6j_L001_R1.fastq.gz | CP1802-cc467_TGGATT-C9f6j_L001_R2.fastq.gz |
| SRR1143033 | SRP254184 | PRJNA615661 | SAMN14464167 | 468 | caecum | CPI1802-cc468_ AGGATA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc468_ AGGATA-C43D4_L001_R1.fastq.gz | CP1802-cc468_ AGGATA-C43D4_L001_R2.fastq.gz |
| SRR1143032 | SRP254184 | PRJNA615661 | SAMN14464168 | 469 | caecum | CPI1802-cc469_TTCGGAG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802-cc469_TTCGGAG-C9f6j_L001_R1.fastq.gz | CP1802-cc469_TTCGGAG-C9f6j_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430031 | SRP254184 | PRJNA615661 | SAMN14464169 | 471 | caecum | CP1802-cc471_CTGTAAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc471_CTGTAAC-C9F6J_L001_R1.fastq.gz | CP1802-cc471_CTGTAAC-C9F6J_L001_R2.fastq.gz |
| SRR11430030 | SRP254184 | PRJNA615661 | SAMN14464170 | 472 | caecum | CP1802-cc472_TCCCCA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc472_TCCTCCA-C9F6J_L001_R1.fastq.gz | CP1802-cc472_TCCTCCA-C9F6J_L001_R2.fastq.gz |
| SRR11430029 | SRP254184 | PRJNA615661 | SAMN14464171 | 474 | caecum | CP1802-cc474_GTTTCGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc474_GTTTCGG-C9F6J_L001_R1.fastq.gz | CP1802-cc474_GTTTCGG-C9F6J_L001_R2.fastq.gz |
| SRR11430028 | SRP254184 | PRJNA615661 | SAMN14464172 | 475 | caecum | CP1802-cc475_TCTTCGG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc475_TCTTCGG-C9F6J_L001_R1.fastq.gz | CP1802-cc475_TCTTCGG-C9F6J_L001_R2.fastq.gz |
| SRR11430026 | SRP254184 | PRJNA615661 | SAMN14464173 | 476 | caecum | CP1802-cc476_ATAAAGA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc476_ATAAAGA-C9F6J_L001_R1.fastq.gz | CP1802-cc476_ATAAAGA-C9F6J_L001_R2.fastq.gz |
| SRR11430025 | SRP254184 | PRJNA615661 | SAMN14464174 | 478 | caecum | CP1802-cc478_ACAGTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc478_ACAGTT-C9F6J_L001_R1.fastq.gz | CP1802-cc478_ACAGTT-C9F6J_L001_R2.fastq.gz |
| SRR11430024 | SRP254184 | PRJNA615661 | SAMN14464175 | 479 | caecum | CP1802-cc479_TTGCCC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc479_TTGCCC-C9F6J_L001_R1.fastq.gz | CP1802-cc479_TTGCCC-C9F6J_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430023 | SRP254184 | PRJNA615661 | SAMN14464176 | 480 | caecum | CP1802-cc480-AAATTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc480-AAATTG-C9F6J_L001_R1.fastq.gz | CP1802-cc480-AAATTG-C9F6J_L001_R2.fastq.gz |
| SRR11430022 | SRP254184 | PRJNA615661 | SAMN14464177 | 481 | caecum | CP1802-cc481-TTAAAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc481-TTAAAT-C9F6J_L001_R1.fastq.gz | CP1802-cc481-TTAAAT-C9F6J_L001_R2.fastq.gz |
| SRR11430021 | SRP254184 | PRJNA615661 | SAMN14464178 | 482 | caecum | CP1802-cc482-AGGTTC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc482-AGGTTC-C9F6J_L001_R1.fastq.gz | CP1802-cc482-AGGTTC-C9F6J_L001_R2.fastq.gz |
| SRR11430020 | SRP254184 | PRJNA615661 | SAMN14464179 | 483 | caecum | CP1802-cc483-ACTCGA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc483-ACTCGA-C9F6J_L001_R1.fastq.gz | CP1802-cc483-ACTCGA-C9F6J_L001_R2.fastq.gz |
| SRR11430019 | SRP254184 | PRJNA615661 | SAMN14464180 | 484 | caecum | CP1802-cc484_TTTGTA | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc484_TTTGTA-C9F6J_L001_R1.fastq.gz | CP1802-cc484_TTTGTA-C9F6J_L001_R2.fastq.gz |
| SRR11430018 | SRP254184 | PRJNA615661 | SAMN14464181 | 485 | caecum | CP1802-cc485-CAGATG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc485-CAGATG-C9F6J_L001_R1.fastq.gz | CP1802-cc485-CAGATG-C9F6J_L001_R2.fastq.gz |
| SRR11430017 | SRP254184 | PRJNA615661 | SAMN14464182 | 486 | caecum | CP1802-cc486-AGCCTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc486-AGCCTG-C9F6J_L001_R1.fastq.gz | CP1802-cc486-AGCCTG-C9F6J_L001_R2.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | library strategy | library source | library selection layout | library platform | instrument model | design description | file type | filename | filename2 |
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| SRR11430015 | SRP254184 | PRJNA615661 | SAMN14464183 | 488 | caecum | CP1802-cc488-CATGTT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc488-CATGTT-C9F6J_L001_R1.fastq.gz | CP1802-cc488-CATGTT-C9F6J_L001_R2.fastq.gz |
| SRR11430014 | SRP254184 | PRJNA615661 | SAMN14464184 | 489 | caecum | CP1802-cc489-CCATTG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc489-CCATTG-C9F6J_L001_R1.fastq.gz | CP1802-cc489-CCATTG-C9F6J_L001_R2.fastq.gz |
| SRR11430013 | SRP254184 | PRJNA615661 | SAMN14464185 | 491 | caecum | CP1802-cc491_L-TATGCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc491_TATGCG-C9F6J_L001_R1.fastq.gz | CP1802-cc491_TATGCG-C9F6J_L001_R2.fastq.gz |
| SRR11430012 | SRP254184 | PRJNA615661 | SAMN14464186 | 493 | caecum | CP1802-cc493_ACATAT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc493_ACATAT-C9F6J_L001_R1.fastq.gz | CP1802-cc493_ACATAT-C9F6J_L001_R2.fastq.gz |
| SRR11430011 | SRP254184 | PRJNA615661 | SAMN14464187 | 494 | caecum | CP1802-cc494_CAGAGC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc494_CAGAGC-C9F6J_L001_R1.fastq.gz | CP1802-cc494_CAGAGC-C9F6J_L001_R2.fastq.gz |
| SRR11430010 | SRP254184 | PRJNA615661 | SAMN14464188 | 495 | caecum | CP1802-cc495_AATATG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc495_AATATG-C9F6J_L001_R1.fastq.gz | CP1802-cc495_AATATG-C9F6J_L001_R2.fastq.gz |
| SRR11430009 | SRP254184 | PRJNA615661 | SAMN14464189 | 497 | caecum | CP1802-cc497_AATCAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc497_AATCAC-C9F6J_L001_R1.fastq.gz | CP1802-cc497_AATCAC-C9F6J_L001_R2.fastq.gz |

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| SRR11430008 | SRP254184 | PRJNA615661 | SAMN14464190 | 499 | caecum | CP1802-cc499-CTCTCG | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc499-CTCTCG-C9f6j_L001_R1.fastq.gz | CP1802-cc499-CTCTCG-C9f6j_L001_R2.fastq.gz |
| SRR11430007 | SRP254184 | PRJNA615661 | SAMN14464191 | 500 | caecum | CP1802-cc500_CACACT | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802-cc500_CACACT-C9f6j_L001_R1.fastq.gz | CP1802-cc500_CACACT-C9f6j_L001_R2.fastq.gz |
| SRR11430006 | SRP254184 | PRJNA615661 | SAMN14464192 | 301 | appendix_vermiformis | CP1802v301_CTAGGG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v301_CTAGGG-CCCBN_L001_R1.fastq.gz | CP1802v301_CTAGGG-CCCBN_L001_R2.fastq.gz |
| SRR11430004 | SRP254184 | PRJNA615661 | SAMN14464193 | 302 | appendix_vermiformis | CP1802v302_TCATCA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v302_TCATCA-CCCBN_L001_R1.fastq.gz | CP1802v302_TCATCA-CCCBN_L001_R2.fastq.gz |
| SRR11430003 | SRP254184 | PRJNA615661 | SAMN14464194 | 303 | appendix_vermiformis | CP1802v303_CTTGCA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v303_CTTGCA-CCCBN_L001_R1.fastq.gz | CP1802v303_CTTGCA-CCCBN_L001_R2.fastq.gz |
| SRR11430002 | SRP254184 | PRJNA615661 | SAMN14464195 | 304 | appendix_vermiformis | CP1802v304_CATGTT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v304_CATGTT-CCCBN_L001_R1.fastq.gz | CP1802v304_CATGTT-CCCBN_L001_R2.fastq.gz |
| SRR11430001 | SRP254184 | PRJNA615661 | SAMN14464196 | 309 | appendix_vermiformis | CP1802v309_TTCGAG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v309_TTCGAG-CCCBN_L001_R1.fastq.gz | CP1802v309_TTCGAG-CCCBN_L001_R2.fastq.gz |
| SRR11430000 | SRP254184 | PRJNA615661 | SAMN14464197 | 310 | appendix_vermiformis | CP1802v310_AAGCTA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v310_AAGCTA-CCCBN_L001_R1.fastq.gz | CP1802v310_AAGCTA-CCCBN_L001_R2.fastq.gz |

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| accession | study | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_description | file_type | filename | filename2 |
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| SRR11429999 | SRP254184 | PRJNA615661 | SAMN14464198 | 312 | appendix_vermiformis | CPI1802v312_TCCCCA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v312_TCCCCA-CCCBN_L001_R2.fastq.gz | CP1802v312_TCCCCA-CCCBN_L001_R2.fastq.gz |
| SRR11429998 | SRP254184 | PRJNA615661 | SAMN14464199 | 313 | appendix_vermiformis | CPI1802v313_AACTAG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v313_AACTAG-CCCBN_L001_R2.fastq.gz | CP1802v313_AACTAG-CCCBN_L001_R2.fastq.gz |
| SRR11429997 | SRP254184 | PRJNA615661 | SAMN14464200 | 314 | appendix_vermiformis | CPI1802v314_GTTTCGC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v314_GTTTCGC-CCCBN_L001_R2.fastq.gz | CP1802v314_GTTTCGC-CCCBN_L001_R2.fastq.gz |
| SRR11429996 | SRP254184 | PRJNA615661 | SAMN14464201 | 316 | appendix_vermiformis | CPI1802v316_ATAAAGA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v316_ATAAAGA-CCCBN_L001_R2.fastq.gz | CP1802v316_ATAAAGA-CCCBN_L001_R2.fastq.gz |
| SRR11429995 | SRP254184 | PRJNA615661 | SAMN14464202 | 319 | appendix_vermiformis | CPI1802v319_ACAGTT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v319_ACAGTT-CCCBN_L001_R2.fastq.gz | CP1802v319_ACAGTT-CCCBN_L001_R2.fastq.gz |
| SRR11429893 | SRP254184 | PRJNA615661 | SAMN14464203 | 320 | appendix_vermiformis | CPI1802v320_TTGCCC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v320_TTGCCC-CCCBN_L001_R2.fastq.gz | CP1802v320_TTGCCC-CCCBN_L001_R2.fastq.gz |
| SRR11429892 | SRP254184 | PRJNA615661 | SAMN14464204 | 321 | appendix_vermiformis | CP1802v321_CAGTCT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v321_CAGTCT-CCCBN_L001_R1.fastq.gz | CP1802v321_CAGTCT-CCCBN_L001_R1.fastq.gz |
| SRR11429891 | SRP254184 | PRJNA615661 | SAMN14464205 | 322 | appendix_vermiformis | CP1802v322_TTAAT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v322_TTAAT-CCCBN_L001_R1.fastq.gz | CP1802v322_TTAAT-CCCBN_L001_R1.fastq.gz |

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| accession | study | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection | library_layout | platform | instrument_model | design_description | file-type | filename | filename2 |
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| SRR11429890 | SRP254184 | PRJNA615661 | SAMN14464206 | 324 | appendix_vermiformis | CPI1802v324_ACTCGA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v324_ACTCGA-CCCBN_L001_R1.fastq.gz | CP1802v324_ACTCGA-CCCBN_L001_R2.fastq.gz |
| SRR11429889 | SRP254184 | PRJNA615661 | SAMN14464207 | 326 | appendix_vermiformis | CPI1802v326_CAGATG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v326_CAGATG-CCCBN_L001_R1.fastq.gz | CP1802v326_CAGATG-CCCBN_L001_R2.fastq.gz |
| SRR11429888 | SRP254184 | PRJNA615661 | SAMN14464208 | 327 | appendix_vermiformis | CPI1802v327_TC GCGC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v327_TC GCGC-CCCBN_L001_R1.fastq.gz | CP1802v327_TC GCGC-CCCBN_L001_R2.fastq.gz |
| SRR11429887 | SRP254184 | PRJNA615661 | SAMN14464209 | 328 | appendix_vermiformis | CPI1802v328_TA ACTT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v328_TA ACTT-CCCBN_L001_R1.fastq.gz | CP1802v328_TA ACTT-CCCBN_L001_R2.fastq.gz |
| SRR11429886 | SRP254184 | PRJNA615661 | SAMN14464210 | 329 | appendix_vermiformis | CPI1802v329_C TGTAA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v329_C TGTAA-CCCBN_L001_R1.fastq.gz | CP1802v329_C TGTAA-CCCBN_L001_R2.fastq.gz |
| SRR11429885 | SRP254184 | PRJNA615661 | SAMN14464211 | 330 | appendix_vermiformis | CPI1802v330_CCATTG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v330_CCATTG-CCCBN_L001_R1.fastq.gz | CP1802v330_CCATTG-CCCBN_L001_R2.fastq.gz |
| SRR11429884 | SRP254184 | PRJNA615661 | SAMN14464212 | 331 | appendix_vermiformis | CPI1802v331_TAGGCT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v331_TAGGCT-CCCBN_L001_R1.fastq.gz | CP1802v331_TAGGCT-CCCBN_L001_R2.fastq.gz |
| SRR11429882 | SRP254184 | PRJNA615661 | SAMN14464213 | 332 | appendix_vermiformis | CPI1802v332_TTC TTG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v332_TTC TTG-CCCBN_L001_R1.fastq.gz | CP1802v332_TTC TTG-CCCBN_L001_R2.fastq.gz |

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| accession | study | bioproject_accession | biosample_accession | sample_ID | luminal_content | library_ID | library_strategy | library_source | library_selection | library_layout | platform | instrument_model | design_description | file-type | filename | filename2 |
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| SRR11429881 | SRP254184 | PRJNA615661 | SAMN14464214 | 333 | appendix_vermiformis | CP1802n333_CCGACC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n333_CCGACC-CCCBN_L001_R2.fastq.gz | CP1802n333_CCGACC-CCCBN_L001_R1.fastq.gz |
| SRR11429880 | SRP254184 | PRJNA615661 | SAMN14464215 | 334 | appendix_vermiformis | CP1802n334_TTAGCT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n334_TTAGCT-CCCBN_L001_R2.fastq.gz | CP1802n334_TTAGCT-CCCBN_L001_R1.fastq.gz |
| SRR11429879 | SRP254184 | PRJNA615661 | SAMN14464216 | 335 | appendix_vermiformis | CP1802n335_CAGAGC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n335_CAGAGC-CCCBN_L001_R2.fastq.gz | CP1802n335_CAGAGC-CCCBN_L001_R1.fastq.gz |
| SRR11429878 | SRP254184 | PRJNA615661 | SAMN14464217 | 337 | appendix_vermiformis | CP1802n337_ATTCTC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n337_ATTCTC-CCCBN_L001_R2.fastq.gz | CP1802n337_ATTCTC-CCCBN_L001_R1.fastq.gz |
| SRR11429877 | SRP254184 | PRJNA615661 | SAMN14464218 | 338 | appendix_vermiformis | CP1802n338_CGAAGG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n338_CGAAGG-CCCBN_L001_R2.fastq.gz | CP1802n338_CGAAGG-CCCBN_L001_R1.fastq.gz |
| SRR11429876 | SRP254184 | PRJNA615661 | SAMN14464219 | 340 | appendix_vermiformis | CP1802n340_AAAGTA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n340_AAAGTA-CCCBN_L001_R2.fastq.gz | CP1802n340_AAAGTA-CCCBN_L001_R1.fastq.gz |
| SRR11429875 | SRP254184 | PRJNA615661 | SAMN14464220 | 341 | appendix_vermiformis | CP1802n341_TCAGCG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n341_TCAGCG-CCCBN_L001_R2.fastq.gz | CP1802n341_TCAGCG-CCCBN_L001_R1.fastq.gz |
| SRR11429874 | SRP254184 | PRJNA615661 | SAMN14464221 | 342 | appendix_vermiformis | CP1802n342_AGGCAC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802n342_AGGCAC-CCCBN_L001_R2.fastq.gz | CP1802n342_AGGCAC-CCCBN_L001_R1.fastq.gz |

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| accession | study | bioproject accession | biosample accession | sample ID | luminal content | library ID | title | library strategy | library source | library selection | library layout | platform | instrument model | design description | file type | filename | filename2 |
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| SRR11429873 | SRP254184 | PRJNA615661 | SAMN14464222 | 343 | appendix_vermiformis | CPI1802v343_AATCCG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v343_AATCCG-CCCBN_L001_R1.fastq.gz | CP1802v343_AATCCG-CCCBN_L001_R2.fastq.gz |
| SRR11429871 | SRP254184 | PRJNA615661 | SAMN14464223 | 344 | appendix_vermiformis | CPI1802v344_TGATGC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v344_TGATGC-CCCBN_L001_R1.fastq.gz | CP1802v344_TGATGC-CCCBN_L001_R2.fastq.gz |
| SRR11429870 | SRP254184 | PRJNA615661 | SAMN14464224 | 347 | appendix_vermiformis | CPI1802v347_GTGAAAT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v347_GTGAAAT-CCCBN_L001_R1.fastq.gz | CP1802v347_GTGAAAT-CCCBN_L001_R2.fastq.gz |
| SRR11429869 | SRP254184 | PRJNA615661 | SAMN14464225 | 349 | appendix_vermiformis | CPI1802v349_TGTCCGT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v349_TGTCCGT-CCCBN_L001_R1.fastq.gz | CP1802v349_TGTCCGT-CCCBN_L001_R2.fastq.gz |
| SRR11429868 | SRP254184 | PRJNA615661 | SAMN14464226 | 350 | appendix_vermiformis | CPI1802v350_CACTAA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v350_CACTAA-CCCBN_L001_R1.fastq.gz | CP1802v350_CACTAA-CCCBN_L001_R2.fastq.gz |
| SRR11429867 | SRP254184 | PRJNA615661 | SAMN14464227 | 352 | appendix_vermiformis | CPI1802v352_ACATTAA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v352_ACATTAA-CCCBN_L001_R1.fastq.gz | CP1802v352_ACATTAA-CCCBN_L001_R2.fastq.gz |
| SRR11429866 | SRP254184 | PRJNA615661 | SAMN14464228 | 353 | appendix_vermiformis | CPI1802v353_GGGTCT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v353_GGGTCT-CCCBN_L001_R1.fastq.gz | CP1802v353_GGGTCT-CCCBN_L001_R2.fastq.gz |
| SRR11429865 | SRP254184 | PRJNA615661 | SAMN14464229 | 354 | appendix_vermiformis | CPI1802v354_CCAAGC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v354_CCAAGC-CCCBN_L001_R1.fastq.gz | CP1802v354_CCAAGC-CCCBN_L001_R2.fastq.gz |

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| SRR11429864 | SRP254184 | PRJNA615661 | SAMN14464230 | 356 | appendix_vermiformis | CPI1802v356_CGTTAA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v356_CGTTAA-CCCBN_L001_R2.fastq.gz | CP1802v356_CGTTAA-CCCBN_L001_R2.fastq.gz |
| SRR11429863 | SRP254184 | PRJNA615661 | SAMN14464231 | 357 | appendix_vermiformis | CPI1802v357_GTAGTAG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v357_GTAGTAG-CCCBN_L001_R2.fastq.gz | CP1802v357_GTAGTAG-CCCBN_L001_R2.fastq.gz |
| SRR11429862 | SRP254184 | PRJNA615661 | SAMN14464232 | 358 | appendix_vermiformis | CPI1802v358_CACCTC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v358_CACCTC-CCCBN_L001_R2.fastq.gz | CP1802v358_CACCTC-CCCBN_L001_R2.fastq.gz |
| SRR11429860 | SRP254184 | PRJNA615661 | SAMN14464233 | 359 | appendix_vermiformis | CPI1802v359_TAAATG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v359_TAAATG-CCCBN_L001_R2.fastq.gz | CP1802v359_TAAATG-CCCBN_L001_R2.fastq.gz |
| SRR11429859 | SRP254184 | PRJNA615661 | SAMN14464234 | 360 | appendix_vermiformis | CPI1802v360_CTTGAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v360_CTTGAC-CCCBN_L001_R2.fastq.gz | CP1802v360_CTTGAC-CCCBN_L001_R2.fastq.gz |
| SRR11429858 | SRP254184 | PRJNA615661 | SAMN14464235 | 362 | appendix_vermiformis | CPI1802v362_AAGTAA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v362_AAGTAA-CCCBN_L001_R2.fastq.gz | CP1802v362_AAGTAA-CCCBN_L001_R2.fastq.gz |
| SRR11429857 | SRP254184 | PRJNA615661 | SAMN14464236 | 364 | appendix_vermiformis | CPI1802v364_AGAATC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v364_AGAATC-CCCBN_L001_R1.fastq.gz | CP1802v364_AGAATC-CCCBN_L001_R1.fastq.gz |
| SRR11429856 | SRP254184 | PRJNA615661 | SAMN14464237 | 366 | appendix_vermiformis | CPI1802v366_CGGAAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v366_CGGAAC-CCCBN_L001_R1.fastq.gz | CP1802v366_CGGAAC-CCCBN_L001_R1.fastq.gz |

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| SRR11429855 | SRP254184 | PRJNA615661 | SAMN14464238 | 367 | appendix_vermiformis | CPI1802v367_ATTTGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v367_ATTTGT-CCCBN_L001_R1.fastq.gz | CP1802v367_ATTTGT-CCCBN_L001_R2.fastq.gz |
| SRR11429854 | SRP254184 | PRJNA615661 | SAMN14464239 | 368 | appendix_vermiformis | CPI1802v368_GCCCAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v368_GCCCAC-CCCBN_L001_R1.fastq.gz | CP1802v368_GCCCAC-CCCBN_L001_R2.fastq.gz |
| SRR11429853 | SRP254184 | PRJNA615661 | SAMN14464240 | 369 | appendix_vermiformis | CPI1802v369_AACCAT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v369_AACCAT-CCCBN_L001_R1.fastq.gz | CP1802v369_AACCAT-CCCBN_L001_R2.fastq.gz |
| SRR11429852 | SRP254184 | PRJNA615661 | SAMN14464241 | 370 | appendix_vermiformis | CPI1802v370_GGGGA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v370_GGGGA-CCCBN_L001_R1.fastq.gz | CP1802v370_GGGGA-CCCBN_L001_R2.fastq.gz |
| SRR11429851 | SRP254184 | PRJNA615661 | SAMN14464242 | 371 | appendix_vermiformis | CPI1802v371_TAGTAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v371_TAGTAC-CCCBN_L001_R1.fastq.gz | CP1802v371_TAGTAC-CCCBN_L001_R2.fastq.gz |
| SRR11429848 | SRP254184 | PRJNA615661 | SAMN14464243 | 372 | appendix_vermiformis | CPI1802v372_GTTCTT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v372_GTTCTT-CCCBN_L001_R1.fastq.gz | CP1802v372_GTTCTT-CCCBN_L001_R2.fastq.gz |
| SRR11429847 | SRP254184 | PRJNA615661 | SAMN14464244 | 373 | appendix_vermiformis | CPI1802v373_ACAGAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v373_ACAGAC-CCCBN_L001_R1.fastq.gz | CP1802v373_ACAGAC-CCCBN_L001_R2.fastq.gz |
| SRR11429846 | SRP254184 | PRJNA615661 | SAMN14464245 | 374 | appendix_vermiformis | CPI1802v374_GTTGCG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v374_GTTGCG-CCCBN_L001_R1.fastq.gz | CP1802v374_GTTGCG-CCCBN_L001_R2.fastq.gz |

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| SRR11429845 | SRP254184 | PRJNA615661 | SAMN14464246 | 375 | appendix_vermiformis | CPI1802v375_-AAACTC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v375_-AAACTC-CCCBN_-L001_R2.fastq.gz | CP1802v375_-AAACTC-CCCBN_-L001_R2.fastq.gz |
| SRR11429844 | SRP254184 | PRJNA615661 | SAMN14464247 | 377 | appendix_vermiformis | CPI1802v377_-TCCTAA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v377_-TCCTAA-CCCBN_-L001_R2.fastq.gz | CP1802v377_-TCCTAA-CCCBN_-L001_R2.fastq.gz |
| SRR11429843 | SRP254184 | PRJNA615661 | SAMN14464248 | 378 | appendix_vermiformis | CPI1802v378_-CGCGTG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v378_-CGCGTG-CCCBN_-L001_R2.fastq.gz | CP1802v378_-CGCGTG-CCCBN_-L001_R2.fastq.gz |
| SRR11429842 | SRP254184 | PRJNA615661 | SAMN14464249 | 380 | appendix_vermiformis | CPI1802v380_-AAGGCC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v380_-AAGGCC-CCCBN_-L001_R2.fastq.gz | CP1802v380_-AAGGCC-CCCBN_-L001_R2.fastq.gz |
| SRR11429841 | SRP254184 | PRJNA615661 | SAMN14464250 | 381 | appendix_vermiformis | CPI1802v381_-TGCACG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v381_-TGCACG-CCCBN_-L001_R2.fastq.gz | CP1802v381_-TGCACG-CCCBN_-L001_R2.fastq.gz |
| SRR11429840 | SRP254184 | PRJNA615661 | SAMN14464251 | 382 | appendix_vermiformis | CPI1802v382_-CAGTGA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v382_-CAGTGA-CCCBN_-L001_R2.fastq.gz | CP1802v382_-CAGTGA-CCCBN_-L001_R2.fastq.gz |
| SRR11429839 | SRP254184 | PRJNA615661 | SAMN14464252 | 383 | appendix_vermiformis | CPI1802v383_-GCCGGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v383_-GCCGGT-CCCBN_-L001_R2.fastq.gz | CP1802v383_-GCCGGT-CCCBN_-L001_R2.fastq.gz |
| SRR11429837 | SRP254184 | PRJNA615661 | SAMN14464253 | 384 | appendix_vermiformis | CPI1802v384_-CTTAAA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v384_-CTTAAA-CCCBN_-L001_R2.fastq.gz | CP1802v384_-CTTAAA-CCCBN_-L001_R2.fastq.gz |

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| SRR11429836 | SRP254184 | PRJNA615661 | SAMN14464254 | 387 | appendix_vermiformis | CP1802v387_GAGCAA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v387_GAGCAA-CCCBN_L001_R1.fastq.gz | CP1802v387_GAGCAA-CCCBN_L001_R2.fastq.gz |
| SRR11429835 | SRP254184 | PRJNA615661 | SAMN14464255 | 389 | appendix_vermiformis | CP1802v389_GGCCTC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v389_GGCCTC-CCCBN_L001_R1.fastq.gz | CP1802v389_GGCCTC-CCCBN_L001_R2.fastq.gz |
| SRR11429834 | SRP254184 | PRJNA615661 | SAMN14464256 | 390 | appendix_vermiformis | CP1802v390_ATCGGG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v390_ATCGGG-CCCBN_L001_R1.fastq.gz | CP1802v390_ATCGGG-CCCBN_L001_R2.fastq.gz |
| SRR11429833 | SRP254184 | PRJNA615661 | SAMN14464257 | 392 | appendix_vermiformis | CP1802v392_TACTCA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v392_TACTCA-CCCBN_L001_R1.fastq.gz | CP1802v392_TACTCA-CCCBN_L001_R2.fastq.gz |
| SRR11429832 | SRP254184 | PRJNA615661 | SAMN14464258 | 393 | appendix_vermiformis | CP1802v393_ATAAACG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v393_ATAAACG-CCCBN_L001_R1.fastq.gz | CP1802v393_ATAAACG-CCCBN_L001_R2.fastq.gz |
| SRR11429831 | SRP254184 | PRJNA615661 | SAMN14464259 | 394 | appendix_vermiformis | CP1802v394_GAGGGC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v394_GAGGGC-CCCBN_L001_R1.fastq.gz | CP1802v394_GAGGGC-CCCBN_L001_R2.fastq.gz |
| SRR11429994 | SRP254184 | PRJNA615661 | SAMN14464260 | 396 | appendix_vermiformis | CP1802v396_CGTTTC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v396_CGTTTC-CCCBN_L001_R1.fastq.gz | CP1802v396_CGTTTC-CCCBN_L001_R2.fastq.gz |
| SRR11429993 | SRP254184 | PRJNA615661 | SAMN14464261 | 397 | appendix_vermiformis | CP1802v397_CCCGTT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v397_CCCGTT-CCCBN_L001_R1.fastq.gz | CP1802v397_CCCGTT-CCCBN_L001_R2.fastq.gz |

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| SRR11429992 | SRP254184 | PRJNA615661 | SAMN14464262 | 398 | appendix_vermiformis | CPI1802v398_GGTCAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v398_GGTCAC-CCCBN_L001_R2.fastq.gz | CP1802v398_GGTCAC-CCCBN_L001_R2.fastq.gz |
| SRR11429990 | SRP254184 | PRJNA615661 | SAMN14464263 | 399 | appendix_vermiformis | CPI1802v399_AGTGCT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v399_AGTGCT-CCCBN_L001_R2.fastq.gz | CP1802v399_AGTGCT-CCCBN_L001_R2.fastq.gz |
| SRR11429989 | SRP254184 | PRJNA615661 | SAMN14464264 | 400 | appendix_vermiformis | CPI1802v400_GACATC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v400_GACATC-CCCBN_L001_R2.fastq.gz | CP1802v400_GACATC-CCCBN_L001_R2.fastq.gz |
| SRR11429988 | SRP254184 | PRJNA615661 | SAMN14464265 | 402 | appendix_vermiformis | CPI1802v402_CTCGGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v402_CTCGGT-CCCBN_L001_R2.fastq.gz | CP1802v402_CTCGGT-CCCBN_L001_R2.fastq.gz |
| SRR11429987 | SRP254184 | PRJNA615661 | SAMN14464266 | 404 | appendix_vermiformis | CPI1802v404_GTTT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v404_GTTT-CCCBN_L001_R2.fastq.gz | CP1802v404_GTTT-CCCBN_L001_R2.fastq.gz |
| SRR11429986 | SRP254184 | PRJNA615661 | SAMN14464267 | 406 | appendix_vermiformis | CPI1802v406_ACTTT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v406_ACTTT-CCCBN_L001_R2.fastq.gz | CP1802v406_ACTTT-CCCBN_L001_R2.fastq.gz |
| SRR11429985 | SRP254184 | PRJNA615661 | SAMN14464268 | 407 | appendix_vermiformis | CPI1802v407_GGCCAA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v407_GGCCAA-CCCBN_L001_R2.fastq.gz | CP1802v407_GGCCAA-CCCBN_L001_R2.fastq.gz |
| SRR11429984 | SRP254184 | PRJNA615661 | SAMN14464269 | 408 | appendix_vermiformis | CP1802v408_GACAGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v408_GACAGT-CCCBN_L001_R2.fastq.gz | CP1802v408_GACAGT-CCCBN_L001_R2.fastq.gz |

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|-------------|-----------|-----------------------|----------------------|------------|-----------------------|-----------------------|-------------------|-----------------|--------------------|-----------------|----------|-------------------|---------------------|----------------------------|----------|--|
| SRR11429983 | SRP254184 | PRJNA615661 | SAMN14464270 | 409 | appendix_vermiformis | CP1802v409_ATGTCAC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v409_ATGTCAC-CCCBN_L001_R1.fastq.gz |
| SRR11429982 | SRP254184 | PRJNA615661 | SAMN14464271 | 410 | appendix_vermiformis | CP1802v410_GCAGCTC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v410_GCAGCT-CCCBN_L001_R1.fastq.gz |
| SRR11429981 | SRP254184 | PRJNA615661 | SAMN14464272 | 411 | appendix_vermiformis | CP1802v411_CGTCGC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v411_CGTCGC-CCCBN_L001_R1.fastq.gz |
| SRR11429979 | SRP254184 | PRJNA615661 | SAMN14464273 | 412 | appendix_vermiformis | CP1802v412_CGTTGGC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v412_CGTTGG-CCCBN_L001_R1.fastq.gz |
| SRR11429978 | SRP254184 | PRJNA615661 | SAMN14464274 | 413 | appendix_vermiformis | CP1802v413_ACCAGGC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v413_ACCAGG-CCCBN_L001_R1.fastq.gz |
| SRR11429977 | SRP254184 | PRJNA615661 | SAMN14464275 | 414 | appendix_vermiformis | CP1802v414_TGTGCC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v414_TGTGCC-CCCBN_L001_R1.fastq.gz |
| SRR11429976 | SRP254184 | PRJNA615661 | SAMN14464276 | 415 | appendix_vermiformis | CP1802v415_GGACTTC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v415_GGACTT-CCCBN_L001_R1.fastq.gz |
| SRR11429975 | SRP254184 | PRJNA615661 | SAMN14464277 | 417 | appendix_vermiformis | CP1802v417_CATCCCTC- | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | fastq | CP1802v417_CATCCCT-CCCBN_L001_R1.fastq.gz |

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| accession | study | biosample_accession | library_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_description | file_type | filename | filename2 |
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| SRR11429974 | SRP254184 | PRJNA615661 | SAMN14464278 | 418 | appendix_vermiformis | CPI1802v418_GTCGGC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v418_GTCGGC-CCCBN_L001_R2.fastq.gz | CP1802v418_GTCGGC-CCCBN_L001_R2.fastq.gz |
| SRR11429973 | SRP254184 | PRJNA615661 | SAMN14464279 | 420 | appendix_vermiformis | CPI1802v420_CAGCGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v420_CAGCGT-CCCBN_L001_R2.fastq.gz | CP1802v420_CAGCGT-CCCBN_L001_R2.fastq.gz |
| SRR11429972 | SRP254184 | PRJNA615661 | SAMN14464280 | 421 | appendix_vermiformis | CPI1802v421_GGATCA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v421_GGATCA-CCCBN_L001_R2.fastq.gz | CP1802v421_GGATCA-CCCBN_L001_R2.fastq.gz |
| SRR11429971 | SRP254184 | PRJNA615661 | SAMN14464281 | 422 | appendix_vermiformis | CPI1802v422_CCCCCAT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v422_CCCCCAT-CCCBN_L001_R2.fastq.gz | CP1802v422_CCCCCAT-CCCBN_L001_R2.fastq.gz |
| SRR11429970 | SRP254184 | PRJNA615661 | SAMN14464282 | 423 | appendix_vermiformis | CPI1802v423_TTGTTGA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v423_TTGTTGA-CCCBN_L001_R2.fastq.gz | CP1802v423_TTGTTGA-CCCBN_L001_R2.fastq.gz |
| SRR11429968 | SRP254184 | PRJNA615661 | SAMN14464283 | 424 | appendix_vermiformis | CPI1802v424_AGATAG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v424_AGATAG-CCCBN_L001_R2.fastq.gz | CP1802v424_AGATAG-CCCBN_L001_R2.fastq.gz |
| SRR11429967 | SRP254184 | PRJNA615661 | SAMN14464284 | 427 | appendix_vermiformis | CPI1802v427_ATTAGG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v427_ATTAGG-CCCBN_L001_R2.fastq.gz | CP1802v427_ATTAGG-CCCBN_L001_R2.fastq.gz |
| SRR11429966 | SRP254184 | PRJNA615661 | SAMN14464285 | 429 | appendix_vermiformis | CP1802v429_AAAGCG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v429_AAAGCG-CCCBN_L001_R2.fastq.gz | CP1802v429_AAAGCG-CCCBN_L001_R2.fastq.gz |

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| SRR11429965 | SRP254184 | PRJNA615661 | SAMN14464286 | 430 | appendix_vermiformis | CPI1802v430_TTGCTA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v430_TTGCTA-CCCBN_L001_R1.fastq.gz | CP1802v430_TTGCTA-CCCBN_L001_R2.fastq.gz |
| SRR11429964 | SRP254184 | PRJNA615661 | SAMN14464287 | 432 | appendix_vermiformis | CPI1802v432_CTACTA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v432_CTACTA-CCCBN_L001_R1.fastq.gz | CP1802v432_CTACTA-CCCBN_L001_R2.fastq.gz |
| SRR11429963 | SRP254184 | PRJNA615661 | SAMN14464288 | 433 | appendix_vermiformis | CPI1802v433_TGGCT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v433_TGGCT-CCCBN_L001_R1.fastq.gz | CP1802v433_TGGCT-CCCBN_L001_R2.fastq.gz |
| SRR11429962 | SRP254184 | PRJNA615661 | SAMN14464289 | 434 | appendix_vermiformis | CPI1802v434_ACGATC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v434_ACGATC-CCCBN_L001_R1.fastq.gz | CP1802v434_ACGATC-CCCBN_L001_R2.fastq.gz |
| SRR11429961 | SRP254184 | PRJNA615661 | SAMN14464290 | 436 | appendix_vermiformis | CPI1802v436_GATACA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v436_GATACA-CCCBN_L001_R1.fastq.gz | CP1802v436_GATACA-CCCBN_L001_R2.fastq.gz |
| SRR11429960 | SRP254184 | PRJNA615661 | SAMN14464291 | 437 | appendix_vermiformis | CPI1802v437_TATCAT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v437_TATCAT-CCCBN_L001_R1.fastq.gz | CP1802v437_TATCAT-CCCBN_L001_R2.fastq.gz |
| SRR11429959 | SRP254184 | PRJNA615661 | SAMN14464292 | 438 | appendix_vermiformis | CPI1802v438_CTAGTC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v438_CTAGTC-CCCBN_L001_R1.fastq.gz | CP1802v438_CTAGTC-CCCBN_L001_R2.fastq.gz |
| SRR11429957 | SRP254184 | PRJNA615661 | SAMN14464293 | 439 | appendix_vermiformis | CPI1802v439_GGCCTTG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v439_GGCCTTG-CCCBN_L001_R1.fastq.gz | CP1802v439_GGCCTTG-CCCBN_L001_R2.fastq.gz |

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| accession | study | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_description | file_type | filename | filename2 |
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| SRR11429956 | SRP254184 | PRJNA615661 | SAMN14464294 | 440 | appendix_vermiformis | CPI1802v440_CCTCCC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v440_CCTCCC-CCCBN_L001_R2.fastq.gz | CP1802v440_CCTCCC-CCCBN_L001_R2.fastq.gz |
| SRR11429955 | SRP254184 | PRJNA615661 | SAMN14464295 | 442 | appendix_vermiformis | CPI1802v442_AGGGCA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v442_AGGGCA-CCCBN_L001_R2.fastq.gz | CP1802v442_AGGGCA-CCCBN_L001_R2.fastq.gz |
| SRR11429954 | SRP254184 | PRJNA615661 | SAMN14464296 | 444 | appendix_vermiformis | CPI1802v444_GATCTG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v444_GATCTG-CCCBN_L001_R2.fastq.gz | CP1802v444_GATCTG-CCCBN_L001_R2.fastq.gz |
| SRR11429953 | SRP254184 | PRJNA615661 | SAMN14464297 | 446 | appendix_vermiformis | CPI1802v446_GCCGCG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v446_GCCGCG-CCCBN_L001_R2.fastq.gz | CP1802v446_GCCGCG-CCCBN_L001_R2.fastq.gz |
| SRR11429952 | SRP254184 | PRJNA615661 | SAMN14464298 | 447 | appendix_vermiformis | CPI1802v447_TAGGAA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v447_TAGGAA-CCCBN_L001_R2.fastq.gz | CP1802v447_TAGGAA-CCCBN_L001_R2.fastq.gz |
| SRR11429951 | SRP254184 | PRJNA615661 | SAMN14464299 | 448 | appendix_vermiformis | CPI1802v448_TATCGA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v448_TATCGA-CCCBN_L001_R2.fastq.gz | CP1802v448_TATCGA-CCCBN_L001_R2.fastq.gz |
| SRR11429950 | SRP254184 | PRJNA615661 | SAMN14464300 | 449 | appendix_vermiformis | CP1802v449_TCAGGC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v449_TCAGGC-CCCBN_L001_R1.fastq.gz | CP1802v449_TCAGGC-CCCBN_L001_R1.fastq.gz |
| SRR11429949 | SRP254184 | PRJNA615661 | SAMN14464301 | 450 | appendix_vermiformis | CP1802v450_CGATAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v450_CGATAC-CCCBN_L001_R1.fastq.gz | CP1802v450_CGATAC-CCCBN_L001_R1.fastq.gz |

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| accession | study | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_description | file_type | filename | filename2 |
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| SRR11429948 | SRP254184 | PRJNA615661 | SAMN1446302 | 451 | appendix_vermiformis | CPI1802v451_-TGGTCA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v451_-TGGTCA-C | CP1802v451_-TGGTCA-C |
| SRR11429946 | SRP254184 | PRJNA615661 | SAMN1446303 | 452 | appendix_vermiformis | CPI1802v452_-CACCGG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v452_-CACCGG-C | CP1802v452_-CACCGG-C |
| SRR11429945 | SRP254184 | PRJNA615661 | SAMN1446304 | 453 | appendix_vermiformis | CPI1802v453_-TCATGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v453_-TCATGT-C | CP1802v453_-TCATGT-C |
| SRR11429944 | SRP254184 | PRJNA615661 | SAMN1446305 | 454 | appendix_vermiformis | CPI1802v454_-TCTCTC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v454_-TCTCTC-C | CP1802v454_-TCTCTC-C |
| SRR11429943 | SRP254184 | PRJNA615661 | SAMN1446306 | 455 | appendix_vermiformis | CPI1802v455_-GTAGTT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v455_-GTAGTT-C | CP1802v455_-GTAGTT-C |
| SRR11429942 | SRP254184 | PRJNA615661 | SAMN1446307 | 457 | appendix_vermiformis | CPI1802v457_-AACCGA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v457_-AACCGA-C | CP1802v457_-AACCGA-C |
| SRR11429941 | SRP254184 | PRJNA615661 | SAMN1446308 | 458 | appendix_vermiformis | CP1802v458_-GGCAAAT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v458_-GGCAAAT-C | CP1802v458_-GGCAAAT-C |
| SRR11429940 | SRP254184 | PRJNA615661 | SAMN1446309 | 460 | appendix_vermiformis | CP1802v460_-CTCATAC | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v460_-CTCATAC | CP1802v460_-CTCATAC |

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| accession | study | bioproject_accession | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_description | file_type | filename | filename2 |
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| SRR1429939 | SRP254184 | PRJNA615661 | SAMN14464310 | 461 | appendix_vermiformis | CP1802v461_GAGTTG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v461_GAGTTG-CCCBN_L001_R1.fastq.gz | CP1802v461_GAGTTG-CCCBN_L001_R2.fastq.gz |
| SRR1429938 | SRP254184 | PRJNA615661 | SAMN14464311 | 463 | appendix_vermiformis | CP1802v463_AATTCCT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v463_AATTCCT-CCCBN_L001_R1.fastq.gz | CP1802v463_AATTCCT-CCCBN_L001_R2.fastq.gz |
| SRR1429937 | SRP254184 | PRJNA615661 | SAMN14464312 | 465 | appendix_vermiformis | CP1802v465_CTAGGA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v465_CTAGGA-CCCBN_L001_R1.fastq.gz | CP1802v465_CTAGGA-CCCBN_L001_R2.fastq.gz |
| SRR1429935 | SRP254184 | PRJNA615661 | SAMN14464313 | 466 | appendix_vermiformis | CP1802v466_TGACCT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v466_TGACCT-CCCBN_L001_R1.fastq.gz | CP1802v466_TGACCT-CCCBN_L001_R2.fastq.gz |
| SRR1429934 | SRP254184 | PRJNA615661 | SAMN14464314 | 467 | appendix_vermiformis | CP1802v467_CAGTTT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v467_CAGTTT-CCCBN_L001_R1.fastq.gz | CP1802v467_CAGTTT-CCCBN_L001_R2.fastq.gz |
| SRR1429933 | SRP254184 | PRJNA615661 | SAMN14464315 | 468 | appendix_vermiformis | CP1802v468_TGCAGTC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v468_TGCAGTC-CCCBN_L001_R1.fastq.gz | CP1802v468_TGCAGTC-CCCBN_L001_R2.fastq.gz |
| SRR1429932 | SRP254184 | PRJNA615661 | SAMN14464316 | 469 | appendix_vermiformis | CP1802v469_AATGAA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v469_AATGAA-CCCBN_L001_R1.fastq.gz | CP1802v469_AATGAA-CCCBN_L001_R2.fastq.gz |
| SRR1429931 | SRP254184 | PRJNA615661 | SAMN14464317 | 471 | appendix_vermiformis | CP1802v471_CACTGT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v471_CACTGT-CCCBN_L001_R1.fastq.gz | CP1802v471_CACTGT-CCCBN_L001_R2.fastq.gz |

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| accession | study | bioproject_accession | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_description | file_type | filename | filename2 |
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| SRR11429830 | SRP254184 | PRJNA615661 | SAMN14464318 | 472 | appendix_vermiformis | CP1802v472_GTGCCA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v472_GTGCCA-CCCBN_L001_R2.fastq.gz | CP1802v472_GTGCCA-CCCBN_L001_R2.fastq.gz |
| SRR11429829 | SRP254184 | PRJNA615661 | SAMN14464319 | 474 | appendix_vermiformis | CP1802v474_GTGACG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v474_GTGACG-CCCBN_L001_R2.fastq.gz | CP1802v474_GTGACG-CCCBN_L001_R2.fastq.gz |
| SRR11429828 | SRP254184 | PRJNA615661 | SAMN14464320 | 475 | appendix_vermiformis | CP1802v475_GGTCCG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v475_GGTCCG-CCCBN_L001_R2.fastq.gz | CP1802v475_GGTCCG-CCCBN_L001_R2.fastq.gz |
| SRR11429827 | SRP254184 | PRJNA615661 | SAMN14464321 | 476 | appendix_vermiformis | CP1802v476_AACTTA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v476_AACTTA-CCCBN_L001_R2.fastq.gz | CP1802v476_AACTTA-CCCBN_L001_R2.fastq.gz |
| SRR11429826 | SRP254184 | PRJNA615661 | SAMN14464322 | 478 | appendix_vermiformis | CP1802v478_CAACGA-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v478_CAACGA-CCCBN_L001_R2.fastq.gz | CP1802v478_CAACGA-CCCBN_L001_R2.fastq.gz |
| SRR11429824 | SRP254184 | PRJNA615661 | SAMN14464323 | 479 | appendix_vermiformis | CP1802v479_AAGGTG-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v479_AAGGTG-CCCBN_L001_R2.fastq.gz | CP1802v479_AAGGTG-CCCBN_L001_R2.fastq.gz |
| SRR11429823 | SRP254184 | PRJNA615661 | SAMN14464324 | 480 | appendix_vermiformis | CP1802v480_TTCAAC-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v480_TTCAAC-CCCBN_L001_R2.fastq.gz | CP1802v480_TTCAAC-CCCBN_L001_R2.fastq.gz |
| SRR11429822 | SRP254184 | PRJNA615661 | SAMN14464325 | 481 | appendix_vermiformis | CP1802v481_ACGAAT-C | 16S rDNA caecum | AMPLICON | METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | PCR of V3-V4 DNA16S region | CP1802v481_ACGAAT-CCCBN_L001_R2.fastq.gz | CP1802v481_ACGAAT-CCCBN_L001_R2.fastq.gz |

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|-------------|-----------|---------------------|-------------|-----------------|----------------------|----------------------|------------------|----------------------|--------------------------|------------------|------------------|--------------------|-----------|--|--|
| SRR11429821 | SRP254184 | PRJNA615661 | SAMN1446326 | 482 | appendix_vermiformis | CPI1802v482_GGATTC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v482_GGATTC-CCCBN_L001_R2.fastq.gz | CP1802v482_GGATTC-CCCBN_L001_R2.fastq.gz |
| SRR11429820 | SRP254184 | PRJNA615661 | SAMN1446327 | 483 | appendix_vermiformis | CPI1802v483_CAGGAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v483_CAGGAC-CCCBN_L001_R2.fastq.gz | CP1802v483_CAGGAC-CCCBN_L001_R2.fastq.gz |
| SRR11429819 | SRP254184 | PRJNA615661 | SAMN1446328 | 484 | appendix_vermiformis | CPI1802v484_GCATGG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v484_GCATGG-CCCBN_L001_R2.fastq.gz | CP1802v484_GCATGG-CCCBN_L001_R2.fastq.gz |
| SRR11429818 | SRP254184 | PRJNA615661 | SAMN1446329 | 485 | appendix_vermiformis | CPI1802v485_CTGCAC-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v485_CTGCAC-CCCBN_L001_R2.fastq.gz | CP1802v485_CTGCAC-CCCBN_L001_R2.fastq.gz |
| SRR11429817 | SRP254184 | PRJNA615661 | SAMN1446330 | 486 | appendix_vermiformis | CPI1802v486_TTTCGG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v486_TTTCGG-CCCBN_L001_R2.fastq.gz | CP1802v486_TTTCGG-CCCBN_L001_R2.fastq.gz |
| SRR11429816 | SRP254184 | PRJNA615661 | SAMN1446331 | 488 | appendix_vermiformis | CPI1802v488_AATGGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v488_AATGGT-CCCBN_L001_R1.fastq.gz | CP1802v488_AATGGT-CCCBN_L001_R2.fastq.gz |
| SRR11429815 | SRP254184 | PRJNA615661 | SAMN1446332 | 489 | appendix_vermiformis | CPI1802v489_GTAACA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v489_GTAACA-CCCBN_L001_R1.fastq.gz | CP1802v489_GTAACA-CCCBN_L001_R2.fastq.gz |
| SRR11429813 | SRP254184 | PRJNA615661 | SAMN1446333 | 491 | appendix_vermiformis | CP1802v491_CAGGCG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v491_CAGGCG-CCCBN_L001_R1.fastq.gz | CP1802v491_CAGGCG-CCCBN_L001_R2.fastq.gz |

Continued

| accession | study | biosample_accession | sample_ID | luminal_content | library_ID | title | library_strategy | library_source | library_selection_layout | library_platform | instrument_model | design_descrpition | file_type | filename | filename2 |
|-------------|-----------|---------------------|--------------|-----------------|----------------------|----------------------|------------------|----------------------|--------------------------|------------------|------------------|--------------------|-----------|--|--|
| SRR11429812 | SRP254184 | PRJNA615661 | SAMN14464334 | 493 | appendix_vermiformis | CPI1802v493_ACGGTA-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v493_ACGGTA-CCCBN_L001_R2.fastq.gz | CP1802v493_ACGGTA-CCCBN_L001_R2.fastq.gz |
| SRR11429811 | SRP254184 | PRJNA615661 | SAMN14464335 | 494 | appendix_vermiformis | CPI1802v494_ACACCG-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v494_ACACCG-CCCBN_L001_R2.fastq.gz | CP1802v494_ACACCG-CCCBN_L001_R2.fastq.gz |
| SRR11429810 | SRP254184 | PRJNA615661 | SAMN14464336 | 495 | appendix_vermiformis | CPI1802v495_AGTATT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v495_AGTATT-CCCBN_L001_R2.fastq.gz | CP1802v495_AGTATT-CCCBN_L001_R2.fastq.gz |
| SRR11429809 | SRP254184 | PRJNA615661 | SAMN14464337 | 499 | appendix_vermiformis | CPI1802v499_CGGGT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v499_CGGGT-CCCBN_L001_R2.fastq.gz | CP1802v499_CGGGT-CCCBN_L001_R2.fastq.gz |
| SRR11429808 | SRP254184 | PRJNA615661 | SAMN14464338 | 500 | appendix_vermiformis | CPI1802v500_GTCATT-C | 16S rDNA caecum | AMPLICON METAGENOMIC | PCR | paired | ILLUMINA | Illumina MiSeq | fastq | CP1802v500_GTCATT-CCCBN_L001_R2.fastq.gz | CP1802v500_GTCATT-CCCBN_L001_R2.fastq.gz |

Table 2. Metadata for 16S rRNA gene amplicons sequencing.

| Genus | Relative abundance (%) |
|---|------------------------|
| Enterobacterales Pseudoalteromonadaceae Pseudoalteromonas | 46.39 ± 1.27 |
| Bacillales Planococcaceae Bhargavaea | 44.19 ± 0.96 |
| Sphingomonadales Sphingomonadaceae Erythrobacter | 4.87 ± 0.67 |
| Sphingomonadales Sphingomonadaceae Porphyrobacter | 4.47 ± 0.85 |

Table 3. Proportions of four standard bacterial strains within control samples. Those control samples aimed to validate the metagenomics assembly procedure across the three runs performed ($n=3$ with one control sample per run, mean \pm sd). The results obtained from 16S rRNA sequencing (Illumina MiSeq) after computational steps showed expected relative abundances.

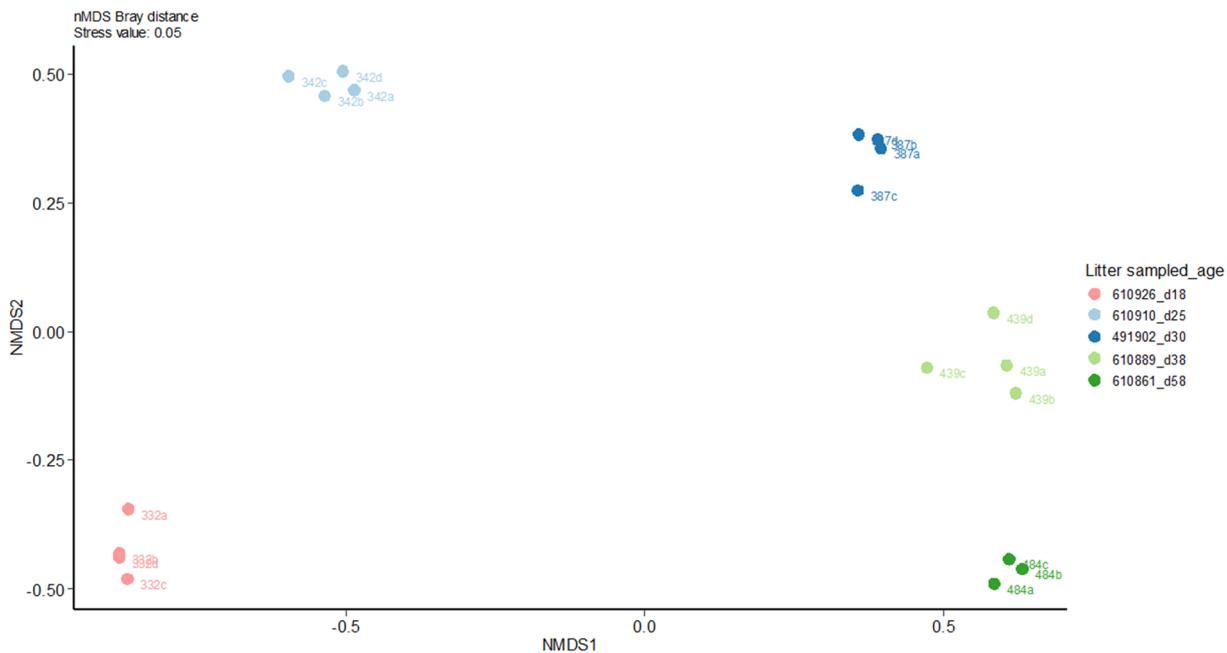


Fig. 3 Assessment of microbiota variability due to the DNA extraction step. Bray Curtis dissimilarities were computed using 16S rDNA from caecal contents extracted several time with the same procedure and similar follow-up processing (sequencing and bioinformatics analysis). The numbers refer to the individuals sampled (rabbits of different litters aged from 18 to 58 days) and the letters a, b, c, d refer to the replicates.

Biochemical evaluation of blood nutritional and redox status. 26 µL of plasma per sample were collected for the dosage of free fatty acids, triglycerides and total protein. After storage at -20°C , the dosages were performed with Pentra 400 device (HORIBA Medical, Grabels, France) at the Anexplo Phenotypage GENOTOUL platform (Toulouse, France). One sample (ID: 334) was diluted at 1:30 to fit the absorbance linearity range.

Data analysis. One analytical workflow using R version 4.0.0 is shared publicly in the repository https://github.com/paescharlotte/early_life_nutrition_rabbit¹⁷.

Data Records

A summary of all the data collected during this experiment and their repository access are given in Table 1 and Fig. 1b.

Raw 16S rRNA gene reads files (fastq format) were deposited in the National Center for Biotechnology Information Sequence Read Archive (NCBI accession PRJNA615661¹⁸, see Table 2). All other raw and processed data used for analysis are provided in Data INRAE repository¹⁹ [<https://doi.org/10.15454/QSTXWF>].

Technical Validation

Amplicon generation and sequencing. The quality of the Miseq runs was checked internally using PhiX control as recommended by manufacturer. The quality of the stitching procedure was controlled using four bacterial samples (marine strains) that are run routinely in the sequencing facility in parallel to the current samples. Expected proportions of the latter strains were observed in the corresponding samples (Table 3). Further processing of the amplicon reads (pre-cleaning, chimera removal, filtering following quality-filtering strategies guidelines²⁰) led to high-quality sequences for further statistical analysis.

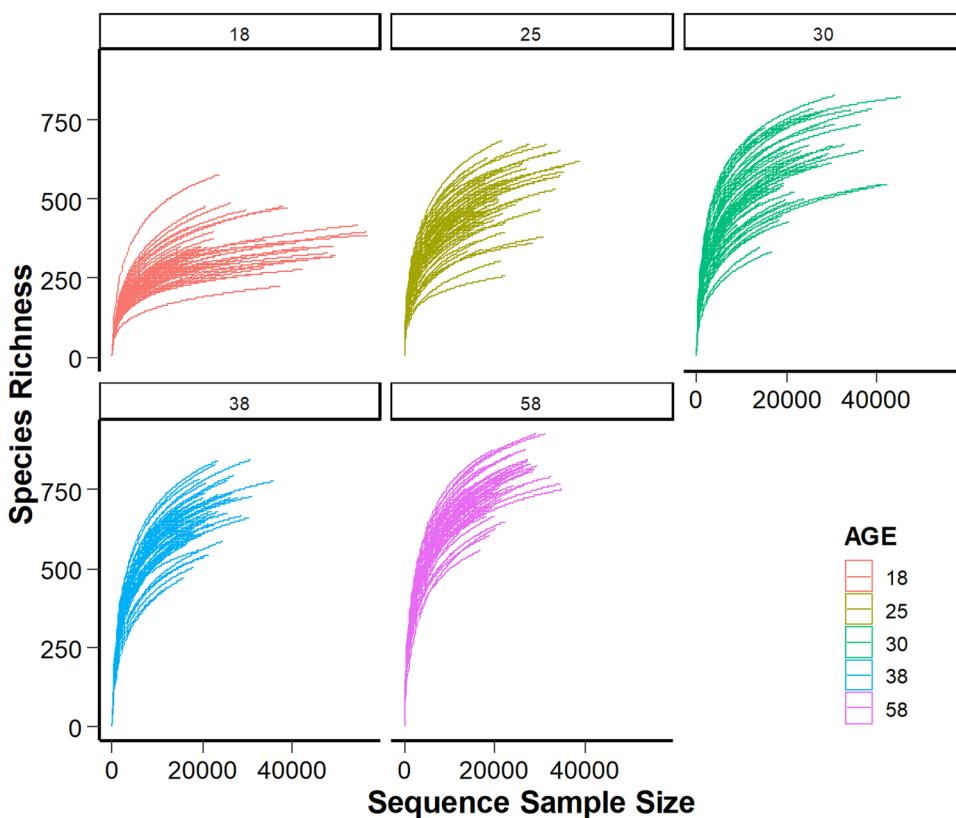


Fig. 4 Rarefaction curves for caecal and appendix sites of each individuals ($n=30$ individuals per sampling time with two gut sections investigated, i.e. 60 samples on average per age).

Controls for technical reproducibility were performed by assessing the variability due to DNA extraction. Five samples were extracted three or four times in one plate, following similar protocol, and were then sequenced in one MiSeq Illumina Sequencing runs (Supplementary Table S2). Non-metric Multidimensional Scaling (nMDS) projections of Bray-Curtis dissimilarities confirmed limited effect of the extraction protocol on the microbiota structure (Fig. 3).

Rarefaction curves, constructed for each individual sample, generally approached saturation which indicated sufficient read depth (Fig. 4). Furthermore, rarefaction curves showed different asymptotes according to rabbit physiological development, which was expected given the limited amount of plant polysaccharides in the diets of young suckling rabbits.

Gene expression profiling. Regarding the high throughput real-time qPCR performed, blank and water controls present in each sample plate allowed us verifying the amplification process per gene. Seven samples were also replicated in each 96-well plate to assess plate-to-plate consistency for caecal and ileal tissue. Based on the Ct values of those samples, we respectively obtained inter-assay coefficients of variation (CV) of 3.0% and 4.0% in the caecum and ileon. The CV of each replicates are specified in Supplemental Fig. 1 for GAPDH housekeeping gene and the two genes whose expression was significantly modulated by one of the experimental treatments¹².

Blood nutritional status. Biochemical measurements of blood content were performed on two batches with a repeated control of known concentration (human serum) and a repeated pool of samples (two repetitions per batch). The control measurements fell within appropriate confidence limits and the CV values for the pool repetitions were between 2 and 4% thus ensuring comparable results between batches for the three analytes measured.

Code availability

The workflow for data analysis using R version 4.0.0 is proposed at this address: https://github.com/paescharlotte/early_life_nutrition_rabbit/¹⁷.

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Author contributions

C.P. summarized the data results and drafted the manuscript. S.C. coordinated the project. C.P., M.B., T.G., K.B., J.D., C.G., E.G.-G., G.R. and S.C. conceived and designed the experiments. P.A. and A.-M.D. carried out the *in vivo* experiments and measured the phenotypes with the data recording system built by F.L. A.C. and B.G. contributed to the sequencing of 16S rDNA amplicons. G.P. helped to perform the Galaxy-supported pipeline FROGS. CBar analyzed diet fiber content. M.B. performed NMR analysis. CBar and L.G. contributed to transcript profiling. S.C. and M.B. revised the manuscript. C.P., M.B., S.C. and L.C. wrote the R codes proposed.

Competing interests

The research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41597-024-03471-1>.

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