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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 Guené-Grand⁶, Gwénaél 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 functions¹⁻³. 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 digestion⁴⁻⁶. 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

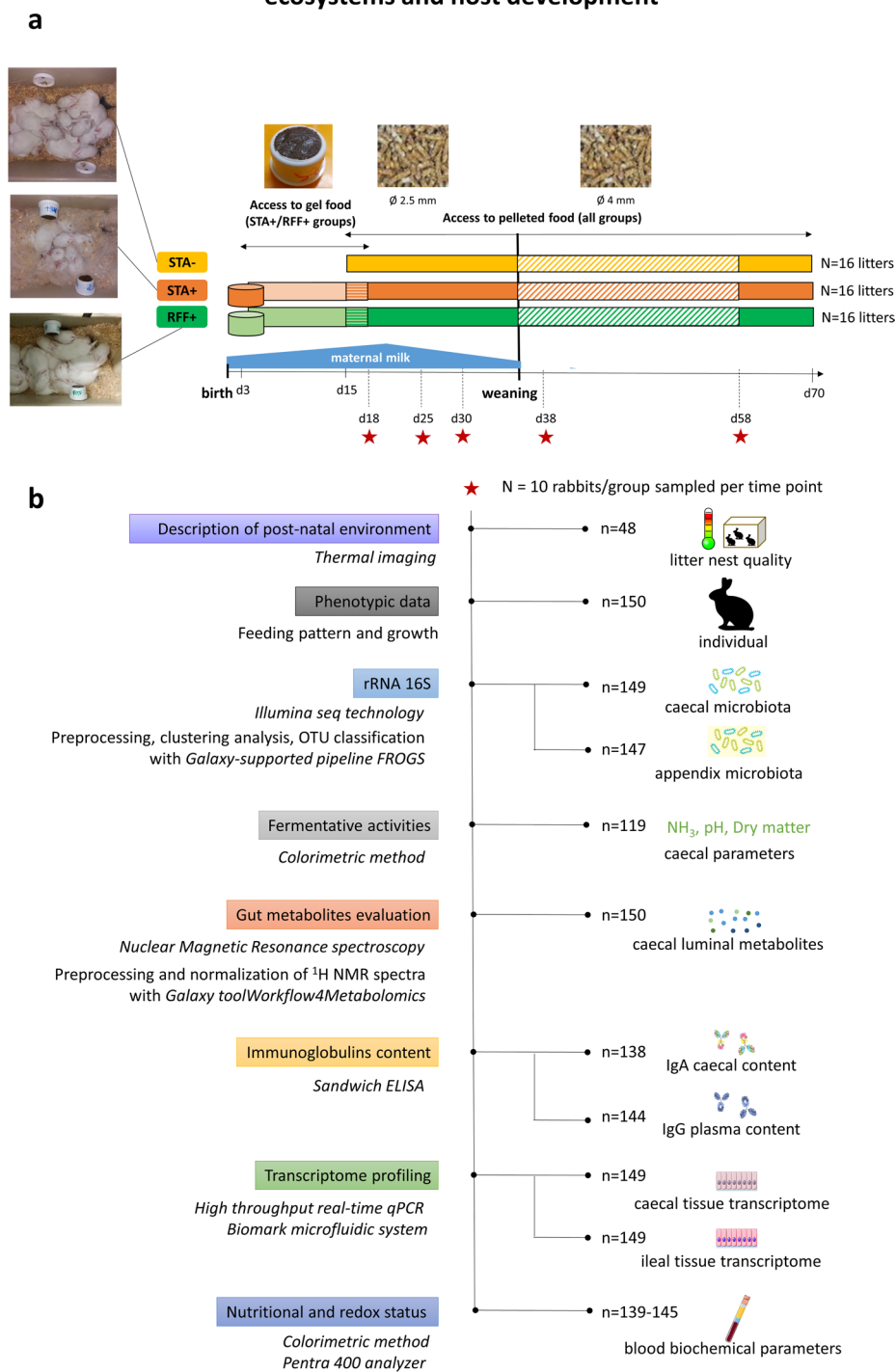


Fig. 1 Experimental design (a) and data collection (b). This study aimed to provide insights into host and gut microbiota responses to changes in the timing of solid food introduction (groups STA-/STA+) when two different diets were provided throughout the life (diets STA and RFF). STA-: access to starch-enriched 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

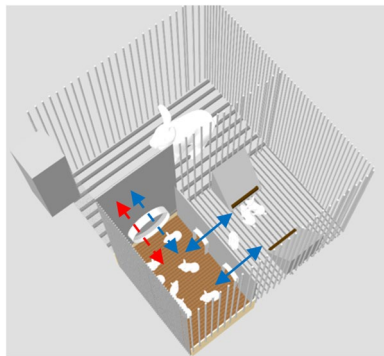


Fig. 2 3D model of the experimental housing system used before weaning. View from the top of a nursing cage where the doe and its kits are raised together for 35 days. Blue arrows represent possible movements of the kits while red arrow represents possible path for the doe. Until day 21, the nest was 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 \times 275 Trolley, Balea, Saint Mathieu de Trévières, France) connected to an automatic recording system (Teo or AGPA, Balea, Saint Mathieu de Trévières, 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 (800 g 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 vermiformis, 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 H_2SO_4 (at 2% w/v) to quantify ammoniac (NH_3) 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 μ L 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 biomedical, Irvine, CA). After centrifugation (12 000 g, 4 °C, 10 min), the supernatant was transferred to a new tube. The pellet was resuspended in 500 μ L phosphate buffer and the homogenization and centrifugation steps were repeated. Supernatants from both extraction steps were pooled and centrifuged twice to remove particles (18 000 g, 30 min, 4 °C). The resulting supernatants (600 μ L) 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_cagnumber.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 overlaid 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 μL 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 *TOPI* 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	title	library_strategy	library_source	library_selection	library_layout	platform	instrument_model	design_description	file_type	filename	filename2
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SRR11430061	SRP254184	PRJNA615661	SAMN14464044	302	caecum	CP1802-cc302_AAACAA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc302_AAACAA-C43D4_L001_R1.fastq.gz	CP1802-cc302_AAACAA-C43D4_L001_R2.fastq.gz
SRR11429850	SRP254184	PRJNA615661	SAMN14464045	303	caecum	CP1802-cc303_AATAAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc303_AATAAT-C43D4_L001_R1.fastq.gz	CP1802-cc303_AATAAT-C43D4_L001_R2.fastq.gz
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SRR11429928	SRP254184	PRJNA615661	SAMN14464047	307	caecum	CP1802-cc307_ACCGAA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc307_ACCGAA-C43D4_L001_R1.fastq.gz	CP1802-cc307_ACCGAA-C43D4_L001_R2.fastq.gz
SRR11429917	SRP254184	PRJNA615661	SAMN14464048	309	caecum	CP1802-cc309_ACCTCA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc309_ACCTCA-C43D4_L001_R1.fastq.gz	CP1802-cc309_ACCTCA-C43D4_L001_R2.fastq.gz
SRR11429906	SRP254184	PRJNA615661	SAMN14464049	310	caecum	CP1802-cc310_AGGGAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc310_AGGGAT-C43D4_L001_R1.fastq.gz	CP1802-cc310_AGGGAT-C43D4_L001_R2.fastq.gz

Continued

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
SRR11430091	SRP254184	PRJNA615661	SAMN14464050	312	caecum	CP1802-cc312-TGTCTA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc314_CCCACG-C43D4_L001_R1.fastq.gz	CP1802-cc314_CCCACG-C43D4_L001_R2.fastq.gz
SRR11430060	SRP254184	PRJNA615661	SAMN14464053	317	caecum	CP1802-cc317_CCCGAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc317_CCCGAG-C43D4_L001_R1.fastq.gz	CP1802-cc317_CCCGAG-C43D4_L001_R2.fastq.gz
SRR11430049	SRP254184	PRJNA615661	SAMN14464054	319	caecum	CP1802-cc319_TTCCGT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc319_TTCCGT-C43D4_L001_R1.fastq.gz	CP1802-cc319_TTCCGT-C43D4_L001_R2.fastq.gz
SRR11430038	SRP254184	PRJNA615661	SAMN14464055	320	caecum	CP1802-cc320_ATATCC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc320_ATATCC-C43D4_L001_R1.fastq.gz	CP1802-cc320_ATATCC-C43D4_L001_R2.fastq.gz
SRR11430027	SRP254184	PRJNA615661	SAMN14464056	321	caecum	CP1802-cc321_TCGGCC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc321_TCGGCC-C43D4_L001_R1.fastq.gz	CP1802-cc321_TCGGCC-C43D4_L001_R2.fastq.gz

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SRR11430016	SRP254184	PRJNA615661	SAMN14464057	322	caecum	CP1802-cc322-GTCAGG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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-CAATTA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc326-CAATTA-C43D4_L001_R1.fastq.gz	CP1802-cc326-CAATTA-C43D4_L001_R2.fastq.gz
SRR11429883	SRP254184	PRJNA615661	SAMN14464060	327	caecum	CP1802-cc327-AGTGTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc327-AGTGTG-C43D4_L001_R1.fastq.gz	CP1802-cc327-AGTGTG-C43D4_L001_R2.fastq.gz
SRR11429872	SRP254184	PRJNA615661	SAMN14464061	328	caecum	CP1802-cc328-ATTGAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc330-AACGCA-C43D4_L001_R1.fastq.gz	CP1802-cc330-AACGCA-C43D4_L001_R2.fastq.gz

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SRR11429838	SRP254184	PRJNA615661	SAMN14464064	331	caecum	CP1802-cc331-ACGTGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc331-ACGTGC-C43D4_L001_R1.fastq.gz	CP1802-cc331-ACGTGC-C43D4_L001_R2.fastq.gz
SRR11429991	SRP254184	PRJNA615661	SAMN14464065	332	caecum	CP1802-cc332-GTACAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc332-GTACAG-C43D4_L001_R1.fastq.gz	CP1802-cc332-GTACAG-C43D4_L001_R2.fastq.gz
SRR11429980	SRP254184	PRJNA615661	SAMN14464066	333	caecum	CP1802-cc333-GTGCTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc333-GTGCTG-C43D4_L001_R1.fastq.gz	CP1802-cc333-GTGCTG-C43D4_L001_R2.fastq.gz
SRR11429969	SRP254184	PRJNA615661	SAMN14464067	334	caecum	CP1802-cc334-CAATGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc334-CAATGC-C43D4_L001_R1.fastq.gz	CP1802-cc334-CAATGC-C43D4_L001_R2.fastq.gz
SRR11429958	SRP254184	PRJNA615661	SAMN14464068	335	caecum	CP1802-cc335-CCGTAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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-CTCCC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc337-CTCCC-C43D4_L001_R1.fastq.gz	CP1802-cc337-CTCCC-C43D4_L001_R2.fastq.gz
SRR11429936	SRP254184	PRJNA615661	SAMN14464070	338	caecum	CP1802-cc338-GACTAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc338-GACTAC-C43D4_L001_R1.fastq.gz	CP1802-cc338-GACTAC-C43D4_L001_R2.fastq.gz

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SRR11429825	SRP254184	PRJNA615661	SAMN14464071	340	caecum	CP1802-cc340-CATAAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc349-GAGAAC-C43D4_L001_R1.fastq.gz	CP1802-cc349-GAGAAC-C43D4_L001_R2.fastq.gz

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SRR11429801	SRP254184	PRJNA615661	SAMN14464078	350	caecum	CP1802-cc350-CCAAACA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc350-CCAAACA-C43D4_L001_R1.fastq.gz	CP1802-cc350-CCAAACA-C43D4_L001_R2.fastq.gz
SRR11429800	SRP254184	PRJNA615661	SAMN14464079	352	caecum	CP1802-cc352-GTCAA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc352-GTCAA-C43D4_L001_R1.fastq.gz	CP1802-cc352-GTCAA-C43D4_L001_R2.fastq.gz
SRR11429799	SRP254184	PRJNA615661	SAMN14464080	353	caecum	CP1802-cc353-CCCTGG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc353-CCCTGG-C43D4_L001_R1.fastq.gz	CP1802-cc353-CCCTGG-C43D4_L001_R2.fastq.gz
SRR11429930	SRP254184	PRJNA615661	SAMN14464081	354	caecum	CP1802-cc354-CGCCAC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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-TAATAT	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc356-TAATAT-C43D4_L001_R1.fastq.gz	CP1802-cc356-TAATAT-C43D4_L001_R2.fastq.gz
SRR11429927	SRP254184	PRJNA615661	SAMN14464083	357	caecum	CP1802-cc357-TGGTGT	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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-CTACCG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc358-CTACCG-C43D4_L001_R1.fastq.gz	CP1802-cc358-CTACCG-C43D4_L001_R2.fastq.gz

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SRR11429925	SRP254184	PRJNA615661	SAMN14464085	359	caecum	CP1802-cc359_CGTGGC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc359_CGTGGC-C43D4_L001_R1.fastq.gz	CP1802-cc359_CGTGGC-C43D4_L001_R2.fastq.gz
SRR11429924	SRP254184	PRJNA615661	SAMN14464086	360	caecum	CP1802-cc360_GATTCA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc360_GATTCA-C43D4_L001_R1.fastq.gz	CP1802-cc360_GATTCA-C43D4_L001_R2.fastq.gz
SRR11429923	SRP254184	PRJNA615661	SAMN14464087	362	caecum	CP1802-cc362_TACCAA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc367_GAGCAA-C9F6_L001_R1.fastq.gz	CP1802-cc367_GAGCAA-C9F6_L001_R2.fastq.gz
SRR11429919	SRP254184	PRJNA615661	SAMN14464091	368	caecum	CP1802-cc368_ACTTTT	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc368_ACTTTT-C9F6_L001_R1.fastq.gz	CP1802-cc368_ACTTTT-C9F6_L001_R2.fastq.gz

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SRR11429918	SRP254184	PRJNA615661	SAMN14464092	369	caecum	CP1802-cc369-CTCGA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc369-CTCGA-C43D4_L001_R1.fastq.gz	CP1802-cc369-CTCGA-C43D4_L001_R2.fastq.gz
SRR11429916	SRP254184	PRJNA615661	SAMN14464093	370	caecum	CP1802-cc370-TACTCA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc370-TACTCA-C9F6_L001_R1.fastq.gz	CP1802-cc370-TACTCA-C9F6_L001_R2.fastq.gz
SRR11429915	SRP254184	PRJNA615661	SAMN14464094	371	caecum	CP1802-cc371-CAGAGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc371-CAGAGC-C43D4_L001_R1.fastq.gz	CP1802-cc371-CAGAGC-C43D4_L001_R2.fastq.gz
SRR11429913	SRP254184	PRJNA615661	SAMN14464095	372	caecum	CP1802-cc372-GGCCCTC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc372-GGCCCTC-C9F6_L001_R1.fastq.gz	CP1802-cc372-GGCCCTC-C9F6_L001_R2.fastq.gz
SRR11429913	SRP254184	PRJNA615661	SAMN14464096	373	caecum	CP1802-cc373-AATCAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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-CCCCGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc374-CCCCGC-C9F6_L001_R1.fastq.gz	CP1802-cc374-CCCCGC-C9F6_L001_R2.fastq.gz
SRR11429911	SRP254184	PRJNA615661	SAMN14464098	375	caecum	CP1802-cc375-TCCCCA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc375-TCCCCA-C43D4_L001_R1.fastq.gz	CP1802-cc375-TCCCCA-C43D4_L001_R2.fastq.gz

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SRR11429910	SRP254184	PRJNA615661	SAMN14464099	377	caecum	CP1802-cc377_CTCTCG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc377_CTCTCG-C43D4_L001_R1.fastq.gz	CP1802-cc377_CTCTCG-C43D4_L001_R2.fastq.gz
SRR11429909	SRP254184	PRJNA615661	SAMN14464100	378	caecum	CP1802-cc378_CAGATG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc380_GCCGGT-C9f6_L001_R1.fastq.gz	CP1802-cc380_GCCGGT-C9f6_L001_R2.fastq.gz
SRR11429907	SRP254184	PRJNA615661	SAMN14464102	381	caecum	CP1802-cc381_CAGTCT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc381_CAGTCT-C43D4_L001_R1.fastq.gz	CP1802-cc381_CAGTCT-C43D4_L001_R2.fastq.gz
SRR11429905	SRP254184	PRJNA615661	SAMN14464103	382	caecum	CP1802-cc382_AAATTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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_AGTTTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc383_AGTTTG-C43D4_L001_R1.fastq.gz	CP1802-cc383_AGTTTG-C43D4_L001_R2.fastq.gz
SRR11429903	SRP254184	PRJNA615661	SAMN14464105	384	caecum	CP1802-cc384_TCTCGG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc384_TCTCGG-C43D4_L001_R1.fastq.gz	CP1802-cc384_TCTCGG-C43D4_L001_R2.fastq.gz

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SRR11429902	SRP254184	PRJNA615661	SAMN14464106	387	caecum	CP1802-cc387-CTGCG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc387-CTGCG-C9F6_L001_R1.fastq.gz	CP1802-cc387-CTGCG-C9F6_L001_R2.fastq.gz
SRR11429901	SRP254184	PRJNA615661	SAMN14464107	389	caecum	CP1802-cc389-ATTAGG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc389-ATTAGG-C9F6_L001_R1.fastq.gz	CP1802-cc389-ATTAGG-C9F6_L001_R2.fastq.gz
SRR11429900	SRP254184	PRJNA615661	SAMN14464108	390	caecum	CP1802-cc390-ACAGTT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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-TTAAAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc393-TTAAAT-C43D4_L001_R1.fastq.gz	CP1802-cc393-TTAAAT-C43D4_L001_R2.fastq.gz
SRR11430093	SRP254184	PRJNA615661	SAMN14464111	394	caecum	CP1802-cc394-TTTGTA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc394-TTTGTA-C43D4_L001_R1.fastq.gz	CP1802-cc394-TTTGTA-C43D4_L001_R2.fastq.gz
SRR11430092	SRP254184	PRJNA615661	SAMN14464112	396	caecum	CP1802-cc396-GTTACC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc396-GTTACC-C43D4_L001_R1.fastq.gz	CP1802-cc396-GTTACC-C43D4_L001_R2.fastq.gz

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SRR11430090	SRP254184	PRJNA615661	SAMN14464113	397	caecum	CP1802-cc397-CCATTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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-TCGGCG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc398-TCGGCG-C43D4_L001_R1.fastq.gz	CP1802-cc398-TCGGCG-C43D4_L001_R2.fastq.gz
SRR11430088	SRP254184	PRJNA615661	SAMN14464115	399	caecum	CP1802-cc399-TAACTT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc400-GGACTT-C9F6_L001_R1.fastq.gz	CP1802-cc400-GGACTT-C9F6_L001_R2.fastq.gz
SRR11430086	SRP254184	PRJNA615661	SAMN14464117	402	caecum	CP1802-cc402-TCGAAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc402-TCGAAC-C9F6_L001_R1.fastq.gz	CP1802-cc402-TCGAAC-C9F6_L001_R2.fastq.gz
SRR11430085	SRP254184	PRJNA615661	SAMN14464118	404	caecum	CP1802-cc404-CCGACC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc406-CAGTCT-C9F6_L001_R1.fastq.gz	CP1802-cc406-CAGTCT-C9F6_L001_R2.fastq.gz

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SRR11430083	SRP254184	PRJNA615661	SAMN14464120	407	caecum	CP1802-cc407_GACAGT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc407_GACAGT-C9F6_L001_R1.fastq.gz	CP1802-cc407_GACAGT-C9F6_L001_R2.fastq.gz
SRR11430082	SRP254184	PRJNA615661	SAMN14464121	408	caecum	CP1802-cc408_TTTTTC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc408_TTTTTC-C9F6_L001_R1.fastq.gz	CP1802-cc408_TTTTTC-C9F6_L001_R2.fastq.gz
SRR11430081	SRP254184	PRJNA615661	SAMN14464122	409	caecum	CP1802-cc409_TGCCCT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc409_TGCCCT-C9F6_L001_R1.fastq.gz	CP1802-cc409_TGCCCT-C9F6_L001_R2.fastq.gz
SRR11430079	SRP254184	PRJNA615661	SAMN14464123	410	caecum	CP1802-cc410_GGTAGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc411_GCTATC-C9F6_L001_R1.fastq.gz	CP1802-cc411_GCTATC-C9F6_L001_R2.fastq.gz
SRR11430077	SRP254184	PRJNA615661	SAMN14464125	412	caecum	CP1802-cc412_TTAGCT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc412_TTAGCT-C9F6_L001_R1.fastq.gz	CP1802-cc412_TTAGCT-C9F6_L001_R2.fastq.gz
SRR11430076	SRP254184	PRJNA615661	SAMN14464126	413	caecum	CP1802-cc413_GCAAAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc413_GCAAAT-C43D4_L001_R1.fastq.gz	CP1802-cc413_GCAAAT-C43D4_L001_R2.fastq.gz

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SRR11430075	SRP254184	PRJNA615661	SAMN14464127	414	caecum	CP1802-cc414_TCGCGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc414_TCGCGC-C9F6_L001_R1.fastq.gz	CP1802-cc414_TCGCGC-C9F6_L001_R2.fastq.gz
SRR11430074	SRP254184	PRJNA615661	SAMN14464128	415	caecum	CP1802-cc415_ACATAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	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_CTACGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc418_CTACGC-C9F6_L001_R1.fastq.gz	CP1802-cc418_CTACGC-C9F6_L001_R2.fastq.gz
SRR11430071	SRP254184	PRJNA615661	SAMN14464131	420	caecum	CP1802-cc420_GCCAAAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc420_GCCAAAG-C43D4_L001_R1.fastq.gz	CP1802-cc420_GCCAAAG-C43D4_L001_R2.fastq.gz
SRR11430070	SRP254184	PRJNA615661	SAMN14464132	421	caecum	CP1802-cc421_TGCTGA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc421_TGCTGA-C9F6_L001_R1.fastq.gz	CP1802-cc421_TGCTGA-C9F6_L001_R2.fastq.gz
SRR11430068	SRP254184	PRJNA615661	SAMN14464133	422	caecum	CP1802-cc422_TTTTTC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc422_TTTTTC-C43D4_L001_R1.fastq.gz	CP1802-cc422_TTTTTC-C43D4_L001_R2.fastq.gz

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SRR11430067	SRP254184	PRJNA615661	SAMN14464134	423	caecum	CP1802-cc423_GTCGTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc424_GAGCTT-C9F6_L001_R1.fastq.gz	CP1802-cc424_GAGCTT-C9F6_L001_R2.fastq.gz
SRR11430065	SRP254184	PRJNA615661	SAMN14464136	427	caecum	CP1802-cc427_GCCTAA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc427_GCCTAA-C9F6_L001_R1.fastq.gz	CP1802-cc427_GCCTAA-C9F6_L001_R2.fastq.gz
SRR11430064	SRP254184	PRJNA615661	SAMN14464137	429	caecum	CP1802-cc429_TTGCTA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc429_TTGCTA-C9F6_L001_R1.fastq.gz	CP1802-cc429_TTGCTA-C9F6_L001_R2.fastq.gz
SRR11430063	SRP254184	PRJNA615661	SAMN14464138	430	caecum	CP1802-cc430_GCAAAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc430_GCAAAT-C9F6_L001_R1.fastq.gz	CP1802-cc430_GCAAAT-C9F6_L001_R2.fastq.gz
SRR11429898	SRP254184	PRJNA615661	SAMN14464139	432	caecum	CP1802-cc432_TACCTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc432_TACCTG-C9F6_L001_R1.fastq.gz	CP1802-cc432_TACCTG-C9F6_L001_R2.fastq.gz
SRR11429897	SRP254184	PRJNA615661	SAMN14464140	433	caecum	CP1802-cc433_GTAACA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc433_GTAACA-C43D4_L001_R1.fastq.gz	CP1802-cc433_GTAACA-C43D4_L001_R2.fastq.gz

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SRR11429896	SRP254184	PRJNA615661	SAMN14464141	434	caecum	CP1802-cc434-GTGGGG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc434-GTGGGG-C9F6_L001_R1.fastq.gz	CP1802-cc434-GTGGGG-C9F6_L001_R2.fastq.gz
SRR11429895	SRP254184	PRJNA615661	SAMN14464142	436	caecum	CP1802-cc436-TGCTCC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc436-TGCTCC-C9F6_L001_R1.fastq.gz	CP1802-cc436-TGCTCC-C9F6_L001_R2.fastq.gz
SRR11430059	SRP254184	PRJNA615661	SAMN14464143	437	caecum	CP1802-cc437-TCACAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc437-TCACAC-C9F6_L001_R1.fastq.gz	CP1802-cc437-TCACAC-C9F6_L001_R2.fastq.gz
SRR11430058	SRP254184	PRJNA615661	SAMN14464144	438	caecum	CP1802-cc438-CTACAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc438-CTACAT-C9F6_L001_R1.fastq.gz	CP1802-cc438-CTACAT-C9F6_L001_R2.fastq.gz
SRR11430057	SRP254184	PRJNA615661	SAMN14464145	439	caecum	CP1802-cc439-GCAGCT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	PCR of V3-V4 DNA16S region	fastq	CP1802-cc440-AACGCA-C9F6_L001_R1.fastq.gz	CP1802-cc440-AACGCA-C9F6_L001_R2.fastq.gz
SRR11430055	SRP254184	PRJNA615661	SAMN14464147	442	caecum	CP1802-cc442-GGAGGT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc442-GGAGGT-C43D4_L001_R1.fastq.gz	CP1802-cc442-GGAGGT-C43D4_L001_R2.fastq.gz

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SRR11430053	SRP254184	PRJNA615661	SAMN14464149	446	caecum	CP1802-cc446-GGACGG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc446-GGACGG-C9F6_L001_R1.fastq.gz	CP1802-cc446-GGACGG-C9F6_L001_R2.fastq.gz
SRR11430052	SRP254184	PRJNA615661	SAMN14464150	447	caecum	CP1802-cc447-GTTTCT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc447-GTTTCT-C9F6_L001_R1.fastq.gz	CP1802-cc447-GTTTCT-C9F6_L001_R2.fastq.gz
SRR11430051	SRP254184	PRJNA615661	SAMN14464151	448	caecum	CP1802-cc448-ATGAAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc448-ATGAAC-C9F6_L001_R1.fastq.gz	CP1802-cc448-ATGAAC-C9F6_L001_R2.fastq.gz
SRR11430050	SRP254184	PRJNA615661	SAMN14464152	449	caecum	CP1802-cc449-TCTATG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc449-TCTATG-C9F6_L001_R1.fastq.gz	CP1802-cc449-TCTATG-C9F6_L001_R2.fastq.gz
SRR11430048	SRP254184	PRJNA615661	SAMN14464153	450	caecum	CP1802-cc450-CTAGAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc450-CTAGAG-C9F6_L001_R1.fastq.gz	CP1802-cc450-CTAGAG-C9F6_L001_R2.fastq.gz
SRR11430047	SRP254184	PRJNA615661	SAMN14464154	451	caecum	CP1802-cc451-AAATTGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc451-AAATTGC-C9F6_L001_R1.fastq.gz	CP1802-cc451-AAATTGC-C9F6_L001_R2.fastq.gz

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SRR11430046	SRP254184	PRJNA615661	SAMN14464155	452	caecum	CP1802-cc452-ATGCTT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc452-ATGCTT-C9F6_L001_R1.fastq.gz	CP1802-cc452-ATGCTT-C9F6_L001_R2.fastq.gz
SRR11430045	SRP254184	PRJNA615661	SAMN14464156	453	caecum	CP1802-cc453-AGAGGG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc453-AGAGGG-C9F6_L001_R1.fastq.gz	CP1802-cc453-AGAGGG-C9F6_L001_R2.fastq.gz
SRR11430044	SRP254184	PRJNA615661	SAMN14464157	454	caecum	CP1802-cc454-CCCAA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc454-CCCAA-C9F6_L001_R1.fastq.gz	CP1802-cc454-CCCAA-C9F6_L001_R2.fastq.gz
SRR11430043	SRP254184	PRJNA615661	SAMN14464158	455	caecum	CP1802-cc455-GATGCT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc455-GATGCT-C9F6_L001_R1.fastq.gz	CP1802-cc455-GATGCT-C9F6_L001_R2.fastq.gz
SRR11430042	SRP254184	PRJNA615661	SAMN14464159	457	caecum	CP1802-cc457-CTCTAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc457-CTCTAC-C9F6_L001_R1.fastq.gz	CP1802-cc457-CTCTAC-C9F6_L001_R2.fastq.gz
SRR11430041	SRP254184	PRJNA615661	SAMN14464160	458	caecum	CP1802-cc458-CAGGAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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-CCTTGA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc460-CCTTGA-C9F6_L001_R1.fastq.gz	CP1802-cc460-CCTTGA-C9F6_L001_R2.fastq.gz

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SRR11430039	SRP254184	PRJNA615661	SAMN14464162	461	caecum	CP1802-cc461-GTAGAA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc461-GTAGAA-C9F6_L001_R1.fastq.gz	CP1802-cc461-GTAGAA-C9F6_L001_R2.fastq.gz
SRR11430037	SRP254184	PRJNA615661	SAMN14464163	463	caecum	CP1802-cc463-CAACAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc463-CAACAG-C9F6_L001_R1.fastq.gz	CP1802-cc463-CAACAG-C9F6_L001_R2.fastq.gz
SRR11430036	SRP254184	PRJNA615661	SAMN14464164	465	caecum	CP1802-cc465-CTTGCA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc465-CTTGCA-C9F6_L001_R1.fastq.gz	CP1802-cc465-CTTGCA-C9F6_L001_R2.fastq.gz
SRR11430035	SRP254184	PRJNA615661	SAMN14464165	466	caecum	CP1802-cc466-GGTAGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc466-GGTAGC-C9F6_L001_R1.fastq.gz	CP1802-cc466-GGTAGC-C9F6_L001_R2.fastq.gz
SRR11430034	SRP254184	PRJNA615661	SAMN14464166	467	caecum	CP1802-cc467-TGGATT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc467-TGGATT-C9F6_L001_R1.fastq.gz	CP1802-cc467-TGGATT-C9F6_L001_R2.fastq.gz
SRR11430033	SRP254184	PRJNA615661	SAMN14464167	468	caecum	CP1802-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
SRR11430032	SRP254184	PRJNA615661	SAMN14464168	469	caecum	CP1802-cc469-TTCGAG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc469-TTCGAG-C9F6_L001_R1.fastq.gz	CP1802-cc469-TTCGAG-C9F6_L001_R2.fastq.gz

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SRR11430031	SRP254184	PRJNA615661	SAMN14464169	471	caecum	CP1802-cc471-CTGTAA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc471-CTGTAA-C9F6_L001_R1.fastq.gz	CP1802-cc471-CTGTAA-C9F6_L001_R2.fastq.gz
SRR11430030	SRP254184	PRJNA615661	SAMN14464170	472	caecum	CP1802-cc472-TCCCA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc472-TCCCA-C9F6_L001_R1.fastq.gz	CP1802-cc472-TCCCA-C9F6_L001_R2.fastq.gz
SRR11430029	SRP254184	PRJNA615661	SAMN14464171	474	caecum	CP1802-cc474-GTTCCG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc474-GTTCCG-C9F6_L001_R1.fastq.gz	CP1802-cc474-GTTCCG-C9F6_L001_R2.fastq.gz
SRR11430028	SRP254184	PRJNA615661	SAMN14464172	475	caecum	CP1802-cc475-TCTCCG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc475-TCTCCG-C9F6_L001_R1.fastq.gz	CP1802-cc475-TCTCCG-C9F6_L001_R2.fastq.gz
SRR11430026	SRP254184	PRJNA615661	SAMN14464173	476	caecum	CP1802-cc476-ATAAGA	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc476-ATAAGA-C9F6_L001_R1.fastq.gz	CP1802-cc476-ATAAGA-C9F6_L001_R2.fastq.gz
SRR11430025	SRP254184	PRJNA615661	SAMN14464174	478	caecum	CP1802-cc478-ACAGTT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc478-ACAGTT-C9F6_L001_R1.fastq.gz	CP1802-cc478-ACAGTT-C9F6_L001_R2.fastq.gz
SRR11430024	SRP254184	PRJNA615661	SAMN14464175	479	caecum	CP1802-cc479-TTGCC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc479-TTGCC-C9F6_L001_R1.fastq.gz	CP1802-cc479-TTGCC-C9F6_L001_R2.fastq.gz

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SRR11430023	SRP254184	PRJNA615661	SAMN14464176	480	caecum	CP1802-cc480-AAATTG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc480-AAATTG-C9F6_L001_R1.fastq.gz	CP1802-cc480-AAATTG-C9F6_L001_R2.fastq.gz
SRR11430022	SRP254184	PRJNA615661	SAMN14464177	481	caecum	CP1802-cc481-TTAAAT	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc481-TTAAAT-C9F6_L001_R1.fastq.gz	CP1802-cc481-TTAAAT-C9F6_L001_R2.fastq.gz
SRR11430021	SRP254184	PRJNA615661	SAMN14464178	482	caecum	CP1802-cc482-AGGTTC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc482-AGGTTC-C9F6_L001_R1.fastq.gz	CP1802-cc482-AGGTTC-C9F6_L001_R2.fastq.gz
SRR11430020	SRP254184	PRJNA615661	SAMN14464179	483	caecum	CP1802-cc483-ACTCGA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc483-ACTCGA-C9F6_L001_R1.fastq.gz	CP1802-cc483-ACTCGA-C9F6_L001_R2.fastq.gz
SRR11430019	SRP254184	PRJNA615661	SAMN14464180	484	caecum	CP1802-cc484-TTTGTA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc484-TTTGTA-C9F6_L001_R1.fastq.gz	CP1802-cc484-TTTGTA-C9F6_L001_R2.fastq.gz
SRR11430018	SRP254184	PRJNA615661	SAMN14464181	485	caecum	CP1802-cc485-CAGATG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc485-CAGATG-C9F6_L001_R1.fastq.gz	CP1802-cc485-CAGATG-C9F6_L001_R2.fastq.gz
SRR11430017	SRP254184	PRJNA615661	SAMN14464182	486	caecum	CP1802-cc486-AGCCTG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc486-AGCCTG-C9F6_L001_R1.fastq.gz	CP1802-cc486-AGCCTG-C9F6_L001_R2.fastq.gz

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SRR11430015	SRP254184	PRJNA615661	SAMN14464183	488	caecum	CP1802-cc488-CATGTT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc488-CATGTT-C9F6_L001_R1.fastq.gz	CP1802-cc488-CATGTT-C9F6_L001_R2.fastq.gz
SRR11430014	SRP254184	PRJNA615661	SAMN14464184	489	caecum	CP1802-cc489-CCATTG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc489-CCATTG-C9F6_L001_R1.fastq.gz	CP1802-cc489-CCATTG-C9F6_L001_R2.fastq.gz
SRR11430013	SRP254184	PRJNA615661	SAMN14464185	491	caecum	CP1802-cc491-TATGCG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc491-TATGCG-C9F6_L001_R1.fastq.gz	CP1802-cc491-TATGCG-C9F6_L001_R2.fastq.gz
SRR11430012	SRP254184	PRJNA615661	SAMN14464186	493	caecum	CP1802-cc493-ACATAT	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc493-ACATAT-C9F6_L001_R1.fastq.gz	CP1802-cc493-ACATAT-C9F6_L001_R2.fastq.gz
SRR11430011	SRP254184	PRJNA615661	SAMN14464187	494	caecum	CP1802-cc494-CAGAGC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc494-CAGAGC-C9F6_L001_R1.fastq.gz	CP1802-cc494-CAGAGC-C9F6_L001_R2.fastq.gz
SRR11430010	SRP254184	PRJNA615661	SAMN14464188	495	caecum	CP1802-cc495-AAATATG	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc495-AAATATG-C9F6_L001_R1.fastq.gz	CP1802-cc495-AAATATG-C9F6_L001_R2.fastq.gz
SRR11430009	SRP254184	PRJNA615661	SAMN14464189	497	caecum	CP1802-cc497-AAATCAC	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802-cc497-AAATCAC-C9F6_L001_R1.fastq.gz	CP1802-cc497-AAATCAC-C9F6_L001_R2.fastq.gz

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SRR11430008	SRP254184	PRJNA615661	SAMN14464190	499	caecum	CP1802-cc499-CTCTCG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc499-CTCTCG-C9F6_L001_R1.fastq.gz	CP1802-cc499-CTCTCG-C9F6_L001_R2.fastq.gz
SRR11430007	SRP254184	PRJNA615661	SAMN14464191	500	caecum	CP1802-cc500-CACACT	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802-cc500-CACACT-C9F6_L001_R1.fastq.gz	CP1802-cc500-CACACT-C9F6_L001_R2.fastq.gz
SRR11430006	SRP254184	PRJNA615661	SAMN14464192	301	appendix_vermiformis	CP1802v301-CTGAGG-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v301-CTGAGG-CCCBN_L001_R1.fastq.gz	CP1802v301-CTGAGG-CCCBN_L001_R2.fastq.gz
SRR11430004	SRP254184	PRJNA615661	SAMN14464193	302	appendix_vermiformis	CP1802v302-TCATCA-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	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	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v310-AAGCTA-CCCBN_L001_R1.fastq.gz	CP1802v310-AAGCTA-CCCBN_L001_R2.fastq.gz

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SRR11429999	SRP254184	PRJNA615661	SAMN14464198	312	appendix_vermiformis	CP1802x312_TCCCA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x312_TCCCA_CCCBN_L001_R1.fastq.gz	CP1802x312_TCCCA_CCCBN_L001_R2.fastq.gz
SRR11429998	SRP254184	PRJNA615661	SAMN14464199	313	appendix_vermiformis	CP1802x313_AACTAG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x313_AACTAG_CCCBN_L001_R1.fastq.gz	CP1802x313_AACTAG_CCCBN_L001_R2.fastq.gz
SRR11429997	SRP254184	PRJNA615661	SAMN14464200	314	appendix_vermiformis	CP1802x314_GTTCCG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x314_GTTCCG_CCCBN_L001_R1.fastq.gz	CP1802x314_GTTCCG_CCCBN_L001_R2.fastq.gz
SRR11429996	SRP254184	PRJNA615661	SAMN14464201	316	appendix_vermiformis	CP1802x316_ATAAGA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x316_ATAAGA_CCCBN_L001_R1.fastq.gz	CP1802x316_ATAAGA_CCCBN_L001_R2.fastq.gz
SRR11429995	SRP254184	PRJNA615661	SAMN14464202	319	appendix_vermiformis	CP1802x319_ACAGTT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x319_ACAGTT_CCCBN_L001_R1.fastq.gz	CP1802x319_ACAGTT_CCCBN_L001_R2.fastq.gz
SRR11429893	SRP254184	PRJNA615661	SAMN14464203	320	appendix_vermiformis	CP1802x320_TTGCC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x320_TTGCC_CCCBN_L001_R1.fastq.gz	CP1802x320_TTGCC_CCCBN_L001_R2.fastq.gz
SRR11429892	SRP254184	PRJNA615661	SAMN14464204	321	appendix_vermiformis	CP1802x321_CAGTCT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x321_CAGTCT_CCCBN_L001_R1.fastq.gz	CP1802x321_CAGTCT_CCCBN_L001_R2.fastq.gz
SRR11429891	SRP254184	PRJNA615661	SAMN14464205	322	appendix_vermiformis	CP1802x322_TTAAAT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x322_TTAAAT_CCCBN_L001_R1.fastq.gz	CP1802x322_TTAAAT_CCCBN_L001_R2.fastq.gz

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SRR11429890	SRP254184	PRJNA615661	SAMN14464206	324	appendix_vermiformis	CP1802v324_ACTCGA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v324_ACTCGA_CCCBN_L001_R1.fastq.gz	CP1802v324_ACTCGA_CCCBN_L001_R2.fastq.gz
SRR11429889	SRP254184	PRJNA615661	SAMN14464207	326	appendix_vermiformis	CP1802v326_CAGATG_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v326_CAGATG_CCCBN_L001_R1.fastq.gz	CP1802v326_CAGATG_CCCBN_L001_R2.fastq.gz
SRR11429888	SRP254184	PRJNA615661	SAMN14464208	327	appendix_vermiformis	CP1802v327_TCGCGC_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v327_TCGCGC_CCCBN_L001_R1.fastq.gz	CP1802v327_TCGCGC_CCCBN_L001_R2.fastq.gz
SRR11429887	SRP254184	PRJNA615661	SAMN14464209	328	appendix_vermiformis	CP1802v328_TAACTT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v328_TAACTT_CCCBN_L001_R1.fastq.gz	CP1802v328_TAACTT_CCCBN_L001_R2.fastq.gz
SRR11429886	SRP254184	PRJNA615661	SAMN14464210	329	appendix_vermiformis	CP1802v329_CTGTAA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v329_CTGTAA_CCCBN_L001_R1.fastq.gz	CP1802v329_CTGTAA_CCCBN_L001_R2.fastq.gz
SRR11429885	SRP254184	PRJNA615661	SAMN14464211	330	appendix_vermiformis	CP1802v330_CCATTT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v330_CCATTT_CCCBN_L001_R1.fastq.gz	CP1802v330_CCATTT_CCCBN_L001_R2.fastq.gz
SRR11429884	SRP254184	PRJNA615661	SAMN14464212	331	appendix_vermiformis	CP1802v331_TAGGCT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v331_TAGGCT_CCCBN_L001_R1.fastq.gz	CP1802v331_TAGGCT_CCCBN_L001_R2.fastq.gz
SRR11429882	SRP254184	PRJNA615661	SAMN14464213	332	appendix_vermiformis	CP1802v332_TTCTTG_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v332_TTCTTG_CCCBN_L001_R1.fastq.gz	CP1802v332_TTCTTG_CCCBN_L001_R2.fastq.gz

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SRR11429881	SRP254184	PRJNA615661	SAMN14464214	333	appendix_vermiiformis	CP1802v333_CCGACC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v333_CCGACC_CCCBN_L001_R1.fastq.gz	CP1802v333_CCGACC_CCCBN_L001_R2.fastq.gz
SRR11429880	SRP254184	PRJNA615661	SAMN14464215	334	appendix_vermiiformis	CP1802v334_TTAGCT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v334_TTAGCT_CCCBN_L001_R1.fastq.gz	CP1802v334_TTAGCT_CCCBN_L001_R2.fastq.gz
SRR11429879	SRP254184	PRJNA615661	SAMN14464216	335	appendix_vermiiformis	CP1802v335_CAGACC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v335_CAGACC_CCCBN_L001_R1.fastq.gz	CP1802v335_CAGACC_CCCBN_L001_R2.fastq.gz
SRR11429878	SRP254184	PRJNA615661	SAMN14464217	337	appendix_vermiiformis	CP1802v337_ATTCTC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v337_ATTCTC_CCCBN_L001_R1.fastq.gz	CP1802v337_ATTCTC_CCCBN_L001_R2.fastq.gz
SRR11429877	SRP254184	PRJNA615661	SAMN14464218	338	appendix_vermiiformis	CP1802v338_CGAAAGG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v338_CGAAAGG_CCCBN_L001_R1.fastq.gz	CP1802v338_CGAAAGG_CCCBN_L001_R2.fastq.gz
SRR11429876	SRP254184	PRJNA615661	SAMN14464219	340	appendix_vermiiformis	CP1802v340_AAAGTA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v340_AAAGTA_CCCBN_L001_R1.fastq.gz	CP1802v340_AAAGTA_CCCBN_L001_R2.fastq.gz
SRR11429875	SRP254184	PRJNA615661	SAMN14464220	341	appendix_vermiiformis	CP1802v341_TCAGCG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v341_TCAGCG_CCCBN_L001_R1.fastq.gz	CP1802v341_TCAGCG_CCCBN_L001_R2.fastq.gz
SRR11429874	SRP254184	PRJNA615661	SAMN14464221	342	appendix_vermiiformis	CP1802v342_AGGCCG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v342_AGGCCG_CCCBN_L001_R1.fastq.gz	CP1802v342_AGGCCG_CCCBN_L001_R2.fastq.gz

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SRR11429873	SRP254184	PRJNA615661	SAMN14464222	343	appendix-vermiformis	CP1802v343_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	CP1802v344_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	CP1802v347_GTGAAT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v347_GTGAAT_CCCBN_L001_R1.fastq.gz	CP1802v347_GTGAAT_CCCBN_L001_R2.fastq.gz
SRR11429869	SRP254184	PRJNA615661	SAMN14464225	349	appendix-vermiformis	CP1802v349_TGTCGT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v349_TGTCGT_CCCBN_L001_R1.fastq.gz	CP1802v349_TGTCGT_CCCBN_L001_R2.fastq.gz
SRR11429868	SRP254184	PRJNA615661	SAMN14464226	350	appendix-vermiformis	CP1802v350_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	CP1802v352_ACATTA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v352_ACATTA_CCCBN_L001_R1.fastq.gz	CP1802v352_ACATTA_CCCBN_L001_R2.fastq.gz
SRR11429866	SRP254184	PRJNA615661	SAMN14464228	353	appendix-vermiformis	CP1802v353_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	CP1802v354_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	CP1802x356_CGTTAA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x356_CGTTAA_CCCBN_L001_R1.fastq.gz	CP1802x356_CGTTAA_CCCBN_L001_R2.fastq.gz
SRR11429863	SRP254184	PRJNA615661	SAMN14464231	357	appendix_vermiformis	CP1802x357_GTGTAG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x357_GTGTAG_CCCBN_L001_R1.fastq.gz	CP1802x357_GTGTAG_CCCBN_L001_R2.fastq.gz
SRR11429862	SRP254184	PRJNA615661	SAMN14464232	358	appendix_vermiformis	CP1802x358_CACCTC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x358_CACCTC_CCCBN_L001_R1.fastq.gz	CP1802x358_CACCTC_CCCBN_L001_R2.fastq.gz
SRR11429860	SRP254184	PRJNA615661	SAMN14464233	359	appendix_vermiformis	CP1802x359_TAAATG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x359_TAAATG_CCCBN_L001_R1.fastq.gz	CP1802x359_TAAATG_CCCBN_L001_R2.fastq.gz
SRR11429859	SRP254184	PRJNA615661	SAMN14464234	360	appendix_vermiformis	CP1802x360_CTTGAC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x360_CTTGAC_CCCBN_L001_R1.fastq.gz	CP1802x360_CTTGAC_CCCBN_L001_R2.fastq.gz
SRR11429858	SRP254184	PRJNA615661	SAMN14464235	362	appendix_vermiformis	CP1802x362_AAGTAA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x362_AAGTAA_CCCBN_L001_R1.fastq.gz	CP1802x362_AAGTAA_CCCBN_L001_R2.fastq.gz
SRR11429857	SRP254184	PRJNA615661	SAMN14464236	364	appendix_vermiformis	CP1802x364_AGAATC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x364_AGAATC_CCCBN_L001_R1.fastq.gz	CP1802x364_AGAATC_CCCBN_L001_R2.fastq.gz
SRR11429856	SRP254184	PRJNA615661	SAMN14464237	366	appendix_vermiformis	CP1802x366_CGGAAC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x366_CGGAAC_CCCBN_L001_R1.fastq.gz	CP1802x366_CGGAAC_CCCBN_L001_R2.fastq.gz

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SRR11429855	SRP254184	PRJNA615661	SAMN14464238	367	appendix_vermiformis	CP1802x367_ATTGTGTC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x367_ATTGTGTC_CCBN_L001_R1.fastq.gz	CP1802x367_ATTGTGTC_CCBN_L001_R2.fastq.gz
SRR11429854	SRP254184	PRJNA615661	SAMN14464239	368	appendix_vermiformis	CP1802x368_GCCAC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x368_GCCAC_CCBN_L001_R1.fastq.gz	CP1802x368_GCCAC_CCBN_L001_R2.fastq.gz
SRR11429853	SRP254184	PRJNA615661	SAMN14464240	369	appendix_vermiformis	CP1802x369_AACCATC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x369_AACCATC_CCBN_L001_R1.fastq.gz	CP1802x369_AACCATC_CCBN_L001_R2.fastq.gz
SRR11429852	SRP254184	PRJNA615661	SAMN14464241	370	appendix_vermiformis	CP1802x370_GGGGGA	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x370_GGGGGA_CCBN_L001_R1.fastq.gz	CP1802x370_GGGGGA_CCBN_L001_R2.fastq.gz
SRR11429851	SRP254184	PRJNA615661	SAMN14464242	371	appendix_vermiformis	CP1802x371_TAGTAC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x371_TAGTAC_CCBN_L001_R1.fastq.gz	CP1802x371_TAGTAC_CCBN_L001_R2.fastq.gz
SRR11429848	SRP254184	PRJNA615661	SAMN14464243	372	appendix_vermiformis	CP1802x372_GTTCTT	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x372_GTTCTT_CCBN_L001_R1.fastq.gz	CP1802x372_GTTCTT_CCBN_L001_R2.fastq.gz
SRR11429847	SRP254184	PRJNA615661	SAMN14464244	373	appendix_vermiformis	CP1802x373_ACAGAC	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x373_ACAGAC_CCBN_L001_R1.fastq.gz	CP1802x373_ACAGAC_CCBN_L001_R2.fastq.gz
SRR11429846	SRP254184	PRJNA615661	SAMN14464245	374	appendix_vermiformis	CP1802x374_GTTGCG	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x374_GTTGCG_CCBN_L001_R1.fastq.gz	CP1802x374_GTTGCG_CCBN_L001_R2.fastq.gz

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SRR11429845	SRP254184	PRJNA615661	SAMN14464246	375	appendix_vermiformis	CP1802x375_AAACCTC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x375_AAACCTC_CCCBN_L001_R1.fastq.gz	CP1802x375_AAACCTC_CCCBN_L001_R2.fastq.gz
SRR11429844	SRP254184	PRJNA615661	SAMN14464247	377	appendix_vermiformis	CP1802x377_TCTTAA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x377_TCTTAA_CCCBN_L001_R1.fastq.gz	CP1802x377_TCTTAA_CCCBN_L001_R2.fastq.gz
SRR11429843	SRP254184	PRJNA615661	SAMN14464248	378	appendix_vermiformis	CP1802x378_GCGGTG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x378_GCGGTG_CCCBN_L001_R1.fastq.gz	CP1802x378_GCGGTG_CCCBN_L001_R2.fastq.gz
SRR11429842	SRP254184	PRJNA615661	SAMN14464249	380	appendix_vermiformis	CP1802x380_AAGGCC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x380_AAGGCC_CCCBN_L001_R1.fastq.gz	CP1802x380_AAGGCC_CCCBN_L001_R2.fastq.gz
SRR11429841	SRP254184	PRJNA615661	SAMN14464250	381	appendix_vermiformis	CP1802x381_TGCACG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x381_TGCACG_CCCBN_L001_R1.fastq.gz	CP1802x381_TGCACG_CCCBN_L001_R2.fastq.gz
SRR11429840	SRP254184	PRJNA615661	SAMN14464251	382	appendix_vermiformis	CP1802x382_CAGTGA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x382_CAGTGA_CCCBN_L001_R1.fastq.gz	CP1802x382_CAGTGA_CCCBN_L001_R2.fastq.gz
SRR11429839	SRP254184	PRJNA615661	SAMN14464252	383	appendix_vermiformis	CP1802x383_GCCGGT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x383_GCCGGT_CCCBN_L001_R1.fastq.gz	CP1802x383_GCCGGT_CCCBN_L001_R2.fastq.gz
SRR11429837	SRP254184	PRJNA615661	SAMN14464253	384	appendix_vermiformis	CP1802x384_CTTAAA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802x384_CTTAAA_CCCBN_L001_R1.fastq.gz	CP1802x384_CTTAAA_CCCBN_L001_R2.fastq.gz

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SRR11429836	SRP254184	PRJNA615661	SAMN14464254	387	appendix_vermiiformis	CP1802v387_GAGCAA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v387_GAGCAA_CCCBN_L001_R1.fastq.gz	CP1802v387_GAGCAA_CCCBN_L001_R2.fastq.gz
SRR11429835	SRP254184	PRJNA615661	SAMN14464255	389	appendix_vermiiformis	CP1802v389_GGCCCTC_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v389_GGCCCTC_CCCBN_L001_R1.fastq.gz	CP1802v389_GGCCCTC_CCCBN_L001_R2.fastq.gz
SRR11429834	SRP254184	PRJNA615661	SAMN14464256	390	appendix_vermiiformis	CP1802v390_ATCGGG_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v390_ATCGGG_CCCBN_L001_R1.fastq.gz	CP1802v390_ATCGGG_CCCBN_L001_R2.fastq.gz
SRR11429833	SRP254184	PRJNA615661	SAMN14464257	392	appendix_vermiiformis	CP1802v392_TACTCA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v392_TACTCA_CCCBN_L001_R1.fastq.gz	CP1802v392_TACTCA_CCCBN_L001_R2.fastq.gz
SRR11429832	SRP254184	PRJNA615661	SAMN14464258	393	appendix_vermiiformis	CP1802v393_ATAACG_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v393_ATAACG_CCCBN_L001_R1.fastq.gz	CP1802v393_ATAACG_CCCBN_L001_R2.fastq.gz
SRR11429831	SRP254184	PRJNA615661	SAMN14464259	394	appendix_vermiiformis	CP1802v394_GAGGGC_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v394_GAGGGC_CCCBN_L001_R1.fastq.gz	CP1802v394_GAGGGC_CCCBN_L001_R2.fastq.gz
SRR11429994	SRP254184	PRJNA615661	SAMN14464260	396	appendix_vermiiformis	CP1802v396_CGTTTC_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v396_CGTTTC_CCCBN_L001_R1.fastq.gz	CP1802v396_CGTTTC_CCCBN_L001_R2.fastq.gz
SRR11429993	SRP254184	PRJNA615661	SAMN14464261	397	appendix_vermiiformis	CP1802v397_CCCGTT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v397_CCCGTT_CCCBN_L001_R1.fastq.gz	CP1802v397_CCCGTT_CCCBN_L001_R2.fastq.gz

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SRR1142992	SRP254184	PRJNA615661	SAMN14464262	398	appendix_vermiformis	CP1802v398_GGTCAC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v398_GGTCAC_CCCBN_L001_R1.fastq.gz	CP1802v398_GGTCAC_CCCBN_L001_R2.fastq.gz
SRR1142990	SRP254184	PRJNA615661	SAMN14464263	399	appendix_vermiformis	CP1802v399_AGTGCT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v399_AGTGCT_CCCBN_L001_R1.fastq.gz	CP1802v399_AGTGCT_CCCBN_L001_R2.fastq.gz
SRR1142989	SRP254184	PRJNA615661	SAMN14464264	400	appendix_vermiformis	CP1802v400_GACATC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v400_GACATC_CCCBN_L001_R1.fastq.gz	CP1802v400_GACATC_CCCBN_L001_R2.fastq.gz
SRR1142988	SRP254184	PRJNA615661	SAMN14464265	402	appendix_vermiformis	CP1802v402_CTCCGT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v402_CTCCGT_CCCBN_L001_R1.fastq.gz	CP1802v402_CTCCGT_CCCBN_L001_R2.fastq.gz
SRR1142987	SRP254184	PRJNA615661	SAMN14464266	404	appendix_vermiformis	CP1802v404_GTGTTT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v404_GTGTTT_CCCBN_L001_R1.fastq.gz	CP1802v404_GTGTTT_CCCBN_L001_R2.fastq.gz
SRR1142986	SRP254184	PRJNA615661	SAMN14464267	406	appendix_vermiformis	CP1802v406_ACTTTT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v406_ACTTTT_CCCBN_L001_R1.fastq.gz	CP1802v406_ACTTTT_CCCBN_L001_R2.fastq.gz
SRR1142985	SRP254184	PRJNA615661	SAMN14464268	407	appendix_vermiformis	CP1802v407_GGCCAA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v407_GGCCAA_CCCBN_L001_R1.fastq.gz	CP1802v407_GGCCAA_CCCBN_L001_R2.fastq.gz
SRR1142984	SRP254184	PRJNA615661	SAMN14464269	408	appendix_vermiformis	CP1802v408_GACAGT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v408_GACAGT_CCCBN_L001_R1.fastq.gz	CP1802v408_GACAGT_CCCBN_L001_R2.fastq.gz

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SRR11429983	SRP254184	PRJNA615661	SAMN14464270	409	appendix_vermiiformis	CP1802v409_ATGTCA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v409_ATGTCA_CCCBN_L001_R1.fastq.gz	CP1802v409_ATGTCA_CCCBN_L001_R2.fastq.gz
SRR11429982	SRP254184	PRJNA615661	SAMN14464271	410	appendix_vermiiformis	CP1802v410_GCAGCT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v410_GCAGCT_CCCBN_L001_R1.fastq.gz	CP1802v410_GCAGCT_CCCBN_L001_R2.fastq.gz
SRR11429981	SRP254184	PRJNA615661	SAMN14464272	411	appendix_vermiiformis	CP1802v411_CGTCGC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v411_CGTCGC_CCCBN_L001_R1.fastq.gz	CP1802v411_CGTCGC_CCCBN_L001_R2.fastq.gz
SRR11429979	SRP254184	PRJNA615661	SAMN14464273	412	appendix_vermiiformis	CP1802v412_CGTTGG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v412_CGTTGG_CCCBN_L001_R1.fastq.gz	CP1802v412_CGTTGG_CCCBN_L001_R2.fastq.gz
SRR11429978	SRP254184	PRJNA615661	SAMN14464274	413	appendix_vermiiformis	CP1802v413_ACCAGG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v413_ACCAGG_CCCBN_L001_R1.fastq.gz	CP1802v413_ACCAGG_CCCBN_L001_R2.fastq.gz
SRR11429977	SRP254184	PRJNA615661	SAMN14464275	414	appendix_vermiiformis	CP1802v414_TGTGCC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v414_TGTGCC_CCCBN_L001_R1.fastq.gz	CP1802v414_TGTGCC_CCCBN_L001_R2.fastq.gz
SRR11429976	SRP254184	PRJNA615661	SAMN14464276	415	appendix_vermiiformis	CP1802v415_GGACTT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v415_GGACTT_CCCBN_L001_R1.fastq.gz	CP1802v415_GGACTT_CCCBN_L001_R2.fastq.gz
SRR11429975	SRP254184	PRJNA615661	SAMN14464277	417	appendix_vermiiformis	CP1802v417_CATCCT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v417_CATCCT_CCCBN_L001_R1.fastq.gz	CP1802v417_CATCCT_CCCBN_L001_R2.fastq.gz

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SRR11429974	SRP254184	PRJNA615661	SAMN14464278	418	appendix_vermiformis	CP1802v418_GTCGGC-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v418_GTCGGC-C CCCBN_L001_R1.fastq.gz	CP1802v418_GTCGGC-C CCCBN_L001_R2.fastq.gz
SRR11429973	SRP254184	PRJNA615661	SAMN14464279	420	appendix_vermiformis	CP1802v420_CAGCGT-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v420_CAGCGT-C CCCBN_L001_R1.fastq.gz	CP1802v420_CAGCGT-C CCCBN_L001_R2.fastq.gz
SRR11429972	SRP254184	PRJNA615661	SAMN14464280	421	appendix_vermiformis	CP1802v421_GGATCA-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v421_GGATCA-C CCCBN_L001_R1.fastq.gz	CP1802v421_GGATCA-C CCCBN_L001_R2.fastq.gz
SRR11429971	SRP254184	PRJNA615661	SAMN14464281	422	appendix_vermiformis	CP1802v422_CCCCAT-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v422_CCCCAT-C CCCBN_L001_R1.fastq.gz	CP1802v422_CCCCAT-C CCCBN_L001_R2.fastq.gz
SRR11429970	SRP254184	PRJNA615661	SAMN14464282	423	appendix_vermiformis	CP1802v423_TTGTGA-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v423_TTGTGA-C CCCBN_L001_R1.fastq.gz	CP1802v423_TTGTGA-C CCCBN_L001_R2.fastq.gz
SRR11429968	SRP254184	PRJNA615661	SAMN14464283	424	appendix_vermiformis	CP1802v424_AGATAG-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v424_AGATAG-C CCCBN_L001_R1.fastq.gz	CP1802v424_AGATAG-C CCCBN_L001_R2.fastq.gz
SRR11429967	SRP254184	PRJNA615661	SAMN14464284	427	appendix_vermiformis	CP1802v427_ATTAGG-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v427_ATTAGG-C CCCBN_L001_R1.fastq.gz	CP1802v427_ATTAGG-C CCCBN_L001_R2.fastq.gz
SRR11429966	SRP254184	PRJNA615661	SAMN14464285	429	appendix_vermiformis	CP1802v429_AAAGCC-C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v429_AAAGCC-C CCCBN_L001_R1.fastq.gz	CP1802v429_AAAGCC-C CCCBN_L001_R2.fastq.gz

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SRR11429965	SRP254184	PRJNA615661	SAMN14464286	430	appendix_vermiformis	CP1802v430_TTGCTA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v430_TTGCTA_CCCBN_L001_R1.fastq.gz	CP1802v430_TTGCTA_CCCBN_L001_R2.fastq.gz
SRR11429964	SRP254184	PRJNA615661	SAMN14464287	432	appendix_vermiformis	CP1802v432_CTACTA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v432_CTACTA_CCCBN_L001_R1.fastq.gz	CP1802v432_CTACTA_CCCBN_L001_R2.fastq.gz
SRR11429963	SRP254184	PRJNA615661	SAMN14464288	433	appendix_vermiformis	CP1802v433_TGCGCT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v433_TGCGCT_CCCBN_L001_R1.fastq.gz	CP1802v433_TGCGCT_CCCBN_L001_R2.fastq.gz
SRR11429962	SRP254184	PRJNA615661	SAMN14464289	434	appendix_vermiformis	CP1802v434_ACGATC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v434_ACGATC_CCCBN_L001_R1.fastq.gz	CP1802v434_ACGATC_CCCBN_L001_R2.fastq.gz
SRR11429961	SRP254184	PRJNA615661	SAMN14464290	436	appendix_vermiformis	CP1802v436_GATAGA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v436_GATAGA_CCCBN_L001_R1.fastq.gz	CP1802v436_GATAGA_CCCBN_L001_R2.fastq.gz
SRR11429960	SRP254184	PRJNA615661	SAMN14464291	437	appendix_vermiformis	CP1802v437_TATCAT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v437_TATCAT_CCCBN_L001_R1.fastq.gz	CP1802v437_TATCAT_CCCBN_L001_R2.fastq.gz
SRR11429959	SRP254184	PRJNA615661	SAMN14464292	438	appendix_vermiformis	CP1802v438_CTAGTC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v438_CTAGTC_CCCBN_L001_R1.fastq.gz	CP1802v438_CTAGTC_CCCBN_L001_R2.fastq.gz
SRR11429957	SRP254184	PRJNA615661	SAMN14464293	439	appendix_vermiformis	CP1802v439_GGCTTG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v439_GGCTTG_CCCBN_L001_R1.fastq.gz	CP1802v439_GGCTTG_CCCBN_L001_R2.fastq.gz

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SRR11429956	SRP254184	PRJNA615661	SAMN14464294	440	appendix_vermiformis	CP1802v440_CCTCCC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v440_CCTCCC_CCCBN_L001_R1.fastq.gz	CP1802v440_CCTCCC_CCCBN_L001_R2.fastq.gz
SRR11429955	SRP254184	PRJNA615661	SAMN14464295	442	appendix_vermiformis	CP1802v442_AGGGCA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v442_AGGGCA_CCCBN_L001_R1.fastq.gz	CP1802v442_AGGGCA_CCCBN_L001_R2.fastq.gz
SRR11429954	SRP254184	PRJNA615661	SAMN14464296	444	appendix_vermiformis	CP1802v444_GATCTG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v444_GATCTG_CCCBN_L001_R1.fastq.gz	CP1802v444_GATCTG_CCCBN_L001_R2.fastq.gz
SRR11429953	SRP254184	PRJNA615661	SAMN14464297	446	appendix_vermiformis	CP1802v446_GCCGCG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v446_GCCGCG_CCCBN_L001_R1.fastq.gz	CP1802v446_GCCGCG_CCCBN_L001_R2.fastq.gz
SRR11429952	SRP254184	PRJNA615661	SAMN14464298	447	appendix_vermiformis	CP1802v447_TAGGAA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v447_TAGGAA_CCCBN_L001_R1.fastq.gz	CP1802v447_TAGGAA_CCCBN_L001_R2.fastq.gz
SRR11429951	SRP254184	PRJNA615661	SAMN14464299	448	appendix_vermiformis	CP1802v448_TATCGA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v448_TATCGA_CCCBN_L001_R1.fastq.gz	CP1802v448_TATCGA_CCCBN_L001_R2.fastq.gz
SRR11429950	SRP254184	PRJNA615661	SAMN14464300	449	appendix_vermiformis	CP1802v449_TCGAGG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v449_TCGAGG_CCCBN_L001_R1.fastq.gz	CP1802v449_TCGAGG_CCCBN_L001_R2.fastq.gz
SRR11429949	SRP254184	PRJNA615661	SAMN14464301	450	appendix_vermiformis	CP1802v450_CGATAC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI16S region	fastq	CP1802v450_CGATAC_CCCBN_L001_R1.fastq.gz	CP1802v450_CGATAC_CCCBN_L001_R2.fastq.gz

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SRR11429948	SRP254184	PRJNA615661	SAMN14464302	451	appendix_vermiformis	CP1802v451_TGGTCA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v451_TGGTCA_CCCBN_L001_R1.fastq.gz	CP1802v451_TGGTCA_CCCBN_L001_R2.fastq.gz
SRR11429946	SRP254184	PRJNA615661	SAMN14464303	452	appendix_vermiformis	CP1802v452_CACCGG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v452_CACCGG_CCCBN_L001_R1.fastq.gz	CP1802v452_CACCGG_CCCBN_L001_R2.fastq.gz
SRR11429945	SRP254184	PRJNA615661	SAMN14464304	453	appendix_vermiformis	CP1802v453_TCATGT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v453_TCATGT_CCCBN_L001_R1.fastq.gz	CP1802v453_TCATGT_CCCBN_L001_R2.fastq.gz
SRR11429944	SRP254184	PRJNA615661	SAMN14464305	454	appendix_vermiformis	CP1802v454_TCTCTC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v454_TCTCTC_CCCBN_L001_R1.fastq.gz	CP1802v454_TCTCTC_CCCBN_L001_R2.fastq.gz
SRR11429943	SRP254184	PRJNA615661	SAMN14464306	455	appendix_vermiformis	CP1802v455_GTAGTT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v455_GTAGTT_CCCBN_L001_R1.fastq.gz	CP1802v455_GTAGTT_CCCBN_L001_R2.fastq.gz
SRR11429942	SRP254184	PRJNA615661	SAMN14464307	457	appendix_vermiformis	CP1802v457_AACCGA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v457_AACCGA_CCCBN_L001_R1.fastq.gz	CP1802v457_AACCGA_CCCBN_L001_R2.fastq.gz
SRR11429941	SRP254184	PRJNA615661	SAMN14464308	458	appendix_vermiformis	CP1802v458_GGCAAT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v458_GGCAAT_CCCBN_L001_R1.fastq.gz	CP1802v458_GGCAAT_CCCBN_L001_R2.fastq.gz
SRR11429940	SRP254184	PRJNA615661	SAMN14464309	460	appendix_vermiformis	CP1802v460_CTCATA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v460_CTCATA_CCCBN_L001_R1.fastq.gz	CP1802v460_CTCATA_CCCBN_L001_R2.fastq.gz

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SRR11429939	SRP254184	PRJNA615661	SAMN14464310	461	appendix_vermiformis	CP1802v461_GAGTTG_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v461_GAGTTG_CCCBN_L001_R1.fastq.gz	CP1802v461_GAGTTG_CCCBN_L001_R2.fastq.gz
SRR11429938	SRP254184	PRJNA615661	SAMN14464311	463	appendix_vermiformis	CP1802v463_AATTCT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v463_AATTCT_CCCBN_L001_R1.fastq.gz	CP1802v463_AATTCT_CCCBN_L001_R2.fastq.gz
SRR11429937	SRP254184	PRJNA615661	SAMN14464312	465	appendix_vermiformis	CP1802v465_CTAGGA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v465_CTAGGA_CCCBN_L001_R1.fastq.gz	CP1802v465_CTAGGA_CCCBN_L001_R2.fastq.gz
SRR11429935	SRP254184	PRJNA615661	SAMN14464313	466	appendix_vermiformis	CP1802v466_TGACCT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v466_TGACCT_CCCBN_L001_R1.fastq.gz	CP1802v466_TGACCT_CCCBN_L001_R2.fastq.gz
SRR11429934	SRP254184	PRJNA615661	SAMN14464314	467	appendix_vermiformis	CP1802v467_CAGTTC_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v467_CAGTTC_CCCBN_L001_R1.fastq.gz	CP1802v467_CAGTTC_CCCBN_L001_R2.fastq.gz
SRR11429933	SRP254184	PRJNA615661	SAMN14464315	468	appendix_vermiformis	CP1802v468_TGCAGT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v468_TGCAGT_CCCBN_L001_R1.fastq.gz	CP1802v468_TGCAGT_CCCBN_L001_R2.fastq.gz
SRR11429932	SRP254184	PRJNA615661	SAMN14464316	469	appendix_vermiformis	CP1802v469_AATGAA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v469_AATGAA_CCCBN_L001_R1.fastq.gz	CP1802v469_AATGAA_CCCBN_L001_R2.fastq.gz
SRR11429931	SRP254184	PRJNA615661	SAMN14464317	471	appendix_vermiformis	CP1802v471_CACTGT_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	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	library_layout	platform	instrument_model	design_description	file_type	filename	filename2
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	fastq	CP1802v472_GTGCCA_CCCBN_L001_R1.fastq.gz	CP1802v472_GTGCCA_CCCBN_L001_R2.fastq.gz
SRR11429829	SRP254184	PRJNA615661	SAMN14464319	474	appendix_vermiformis	CP1802v474_GTGACC_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	illumina_MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v474_GTGACC_CCCBN_L001_R1.fastq.gz	CP1802v474_GTGACC_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	fastq	CP1802v475_GGTCCG_CCCBN_L001_R1.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	fastq	CP1802v476_AACTTA_CCCBN_L001_R1.fastq.gz	CP1802v476_AACTTA_CCCBN_L001_R2.fastq.gz
SRR11429826	SRP254184	PRJNA615661	SAMN14464322	478	appendix_vermiformis	CP1802v478_CAAACA_C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	illumina_MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v478_CAAACA_CCCBN_L001_R1.fastq.gz	CP1802v478_CAAACA_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	fastq	CP1802v479_AAGGTG_CCCBN_L001_R1.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	fastq	CP1802v480_TTCAAC_CCCBN_L001_R1.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	fastq	CP1802v481_ACGAAT_CCCBN_L001_R1.fastq.gz	CP1802v481_ACGAAT_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	library_layout	platform	instrument_model	design_description	file_type	filename	filename2
SRR11429821	SRP254184	PRJNA615661	SAMN14464326	482	appendix_vermiformis	CP1802v482_GGATTC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v482_GGATTC_CCCBN_L001_R1.fastq.gz	CP1802v482_GGATTC_CCCBN_L001_R2.fastq.gz
SRR11429820	SRP254184	PRJNA615661	SAMN14464327	483	appendix_vermiformis	CP1802v483_CAGGAC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v483_CAGGAC_CCCBN_L001_R1.fastq.gz	CP1802v483_CAGGAC_CCCBN_L001_R2.fastq.gz
SRR11429819	SRP254184	PRJNA615661	SAMN14464328	484	appendix_vermiformis	CP1802v484_GCATTG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v484_GCATTG_CCCBN_L001_R1.fastq.gz	CP1802v484_GCATTG_CCCBN_L001_R2.fastq.gz
SRR11429818	SRP254184	PRJNA615661	SAMN14464329	485	appendix_vermiformis	CP1802v485_CTGCAC_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v485_CTGCAC_CCCBN_L001_R1.fastq.gz	CP1802v485_CTGCAC_CCCBN_L001_R2.fastq.gz
SRR11429817	SRP254184	PRJNA615661	SAMN14464330	486	appendix_vermiformis	CP1802v486_TTTCCG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v486_TTTCCG_CCCBN_L001_R1.fastq.gz	CP1802v486_TTTCCG_CCCBN_L001_R2.fastq.gz
SRR11429816	SRP254184	PRJNA615661	SAMN14464331	488	appendix_vermiformis	CP1802v488_AATGGT_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v488_AATGGT_CCCBN_L001_R1.fastq.gz	CP1802v488_AATGGT_CCCBN_L001_R2.fastq.gz
SRR11429815	SRP254184	PRJNA615661	SAMN14464332	489	appendix_vermiformis	CP1802v489_GTAACA_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v489_GTAACA_CCCBN_L001_R1.fastq.gz	CP1802v489_GTAACA_CCCBN_L001_R2.fastq.gz
SRR11429813	SRP254184	PRJNA615661	SAMN14464333	491	appendix_vermiformis	CP1802v491_CAGGCG_C	I6S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNAI6S region	fastq	CP1802v491_CAGGCG_CCCBN_L001_R1.fastq.gz	CP1802v491_CAGGCG_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	library_layout	platform	instrument_model	design_description	file_type	filename	filename2
SRR11429812	SRP254184	PRJNA615661	SAMN14464334	493	appendix_vermiformis	CP1802v493_ ACGGTA- C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v493_ ACGGTA- CCCBN_ L001_ R1.fastq.gz	CP1802v493_ ACGGTA- CCCBN_ L001_ R2.fastq.gz
SRR11429811	SRP254184	PRJNA615661	SAMN14464335	494	appendix_vermiformis	CP1802v494_ ACACCG- C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v494_ ACACCG- CCCBN_ L001_ R1.fastq.gz	CP1802v494_ ACACCG- CCCBN_ L001_ R2.fastq.gz
SRR11429810	SRP254184	PRJNA615661	SAMN14464336	495	appendix_vermiformis	CP1802v495_ AGTATT- C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v495_ AGTATT- CCCBN_ L001_ R1.fastq.gz	CP1802v495_ AGTATT- CCCBN_ L001_ R2.fastq.gz
SRR11429809	SRP254184	PRJNA615661	SAMN14464337	499	appendix_vermiformis	CP1802v499_ CCGGGT- C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v499_ CCGGGT- CCCBN_ L001_ R1.fastq.gz	CP1802v499_ CCGGGT- CCCBN_ L001_ R2.fastq.gz
SRR11429808	SRP254184	PRJNA615661	SAMN14464338	500	appendix_vermiformis	CP1802v500_ GTCATT- C	16S rDNA caecum	AMPLICON	METAGENOMIC	PCR	paired	ILLUMINA	Illumina MiSeq	PCR of V3-V4 DNA16S region	fastq	CP1802v500_ GTCATT- CCCBN_ L001_ R1.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 ± sd). The results obtained from 16S rRNA sequencing (Illumina MiSeq) after computational steps showed expected relative abundances.

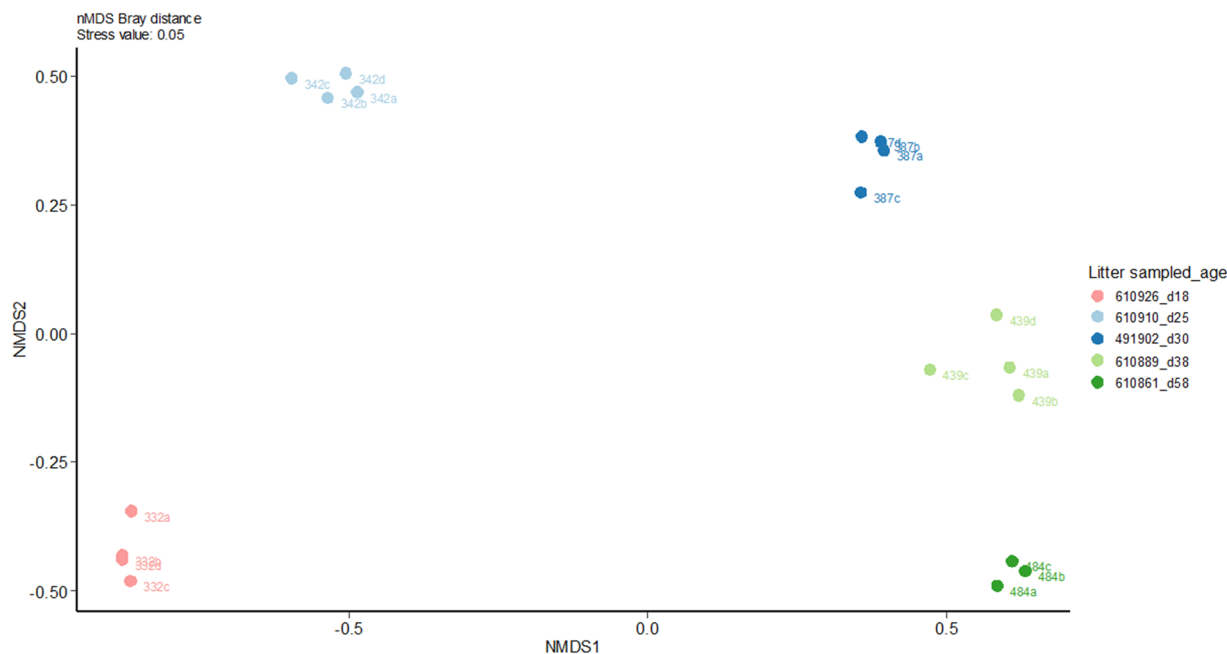


Fig. 3 Assessment of microbiota variability due to the DNA extraction step. Bray-Curtis dissimilarities were computed using 16S rDNA from caecal contents extracted several times with the same procedure and similar follow-up processing (sequencing and bioinformatics analysis). The numbers refer to the 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 μ L 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 Phenotype GENOTOU 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.

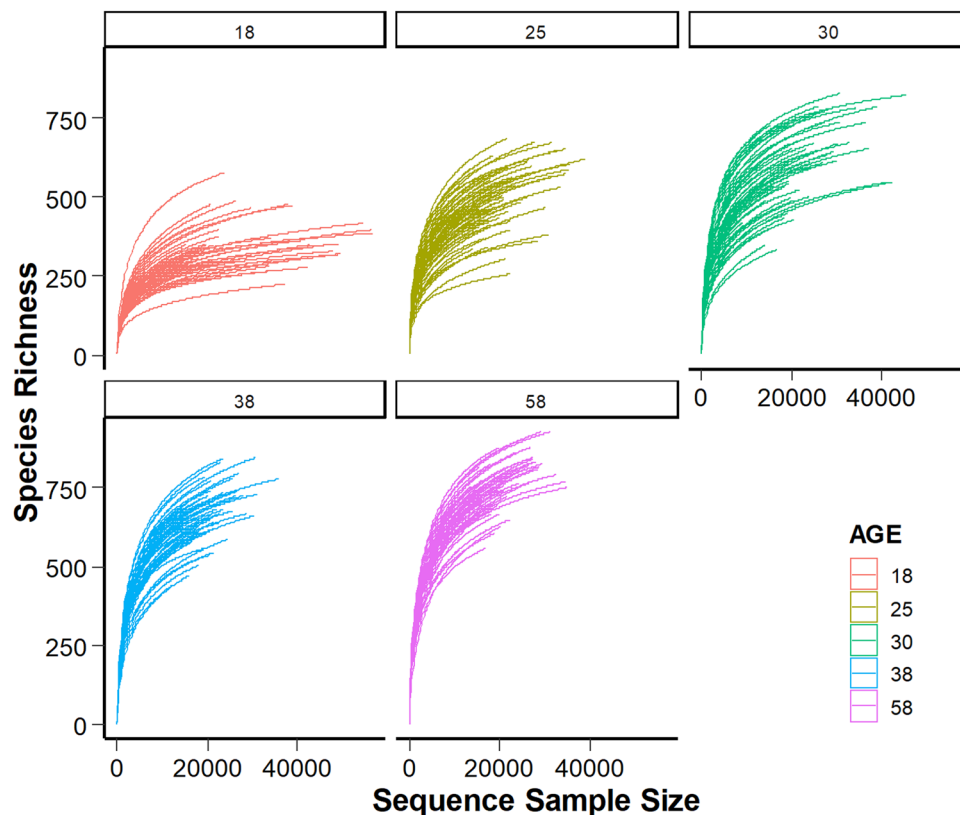


Fig. 4 Rarefaction curves for caecal and appendix sites of each individuals ($n = 30$ individuals per sampling time with two gut sections investigated, i.e. 60 samples on average per age).

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_rabbit¹⁷.

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References

- Mackie, R. I. Mutualistic fermentative digestion in the gastrointestinal tract: diversity and evolution. *Integr. Comp. Biol.* **42**, 319–326 (2002).
- Kamada, N., Seo, S.-U., Chen, G. Y. & Núñez, G. Role of the gut microbiota in immunity and inflammatory disease. *Nat. Rev. Immunol.* **13**, 321–335 (2013).
- Thaiss, C. A., Zmora, N., Levy, M. & Elinav, E. The microbiome and innate immunity. *Nature* **535**, 65–74 (2016).
- Koenig, J. E. *et al.* Succession of microbial consortia in the developing infant gut microbiome. *Proc. Natl. Acad. Sci. USA* **108**(Suppl 1), 4578–4585 (2011).
- Bian, G. *et al.* Age, introduction of solid feed and weaning are more important determinants of gut bacterial succession in piglets than breed and nursing mother as revealed by a reciprocal cross-fostering model. *Environ. Microbiol.* **18**, 1566–1577 (2016).
- Meale, S. J., Chaucheyras-Durand, F., Berends, H., Guan, L. L. & Steele, M. A. From pre- to postweaning: Transformation of the young calf's gastrointestinal tract. *Journal of Dairy Science* **100**, 5984–5995 (2017).
- Suzuki, T. Regulation of intestinal epithelial permeability by tight junctions. *Cell. Mol. Life Sci.* **70**, 631–659 (2013).
- Gidenne, T. & Fortun-Lamothe, L. Feeding strategy for young rabbit around weaning: a review of digestive capacity and nutritional needs. *Animal Science* **75**, 169–184 (2002).
- Ritchie, J. M. & Waldor, M. K. The Locus of Enterocyte Effacement-Encoded Effector Proteins All Promote Enterohemorrhagic *Escherichia coli* Pathogenicity in Infant Rabbits. *Infection and Immunity* **73**, 1466–1474 (2005).
- Yum, L. K. & Agaisse, H. Mechanisms of bacillary dysentery: lessons learnt from infant rabbits. *Gut Microbes* 1–6 <https://doi.org/10.1080/19490976.2019.1667726> (2019).
- Read, T. *et al.* Diversity and Co-occurrence Pattern Analysis of Cecal Microbiota Establishment at the Onset of Solid Feeding in Young Rabbits. *Front. Microbiol.* **10** (2019).
- Paës, C. *et al.* Early Introduction of Plant Polysaccharides Drives the Establishment of Rabbit Gut Bacterial Ecosystems and the Acquisition of Microbial Functions. *mSystems* <https://doi.org/10.1128/msystems.00243-22> (2022).
- Lebas, F. Mesure quantitative de la production laitière chez la lapine. *Annales de Zootechnie* **17**, 169–182 (1968).
- Laperruque, F. & Staub, C. Le système d'information Sicpa Experimentations. 78–81 (2018).
- Lagant, H. *et al.* Les systèmes d'Informations de phénotypage des animaux à l'Inra. 53–67 (2018).
- Giacomoni, F. *et al.* Workflow4Metabolomics: a collaborative research infrastructure for computational metabolomics. *Bioinformatics* **31**, 1493–1495 (2015).
- Paës, C. *et al.* Source code for present data analysis. *GitHub*. https://github.com/charlottepaes/early_life_nutrition_rabbit (2020).
- NCBI Sequence Read. <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA615661> ID 615661 - BioProject.
- Paës, C. & Combes, S. Impact of feeding strategies on young rabbit and its gut microbiota. *Data INRAE*. <https://doi.org/10.15454/QSTXWF> (2021).
- Bokulich, N. A. *et al.* Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. *Nat Methods* **10**, 57–59 (2013).

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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. C.B. analyzed diet fiber content. M.B. performed NMR analysis. C.B. 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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