Table S1 Analysis of species diversity in cecal digestives of different groups

Postnatal day(day)	Group	observed_species	shannon	simpson	chao1	ACE	PD_whole_tree	goods_coverage
28	NG	307.167	4.542	0.873	334.235	324.820	22.775	0.999
	CG	269.397	3.836	0.831	296.204	289.944	21.824	0.999
	WG	282.809	4.127	0.845	308.240	301.774	21.981	0.999
	CWG	263.655	3.842	0.844	298.137	291.794	21.900	0.999
56	NG	521.667	6.761	0.978	535.665	536.206	36.383	0.999
	CG	461.667	6.206	0.964	477.126	477.467	35.213	0.999
	WG	520.833	6.809	0.979	537.375	537.733	35.438	0.999
	CWG	527.667	6.588	0.979	544.729	545.422	37.629	0.999

Note: The diversity index reflects the richness and evenness of species in microbial community. The increase in observed_species, chao1, ACE and PD_whole_tree showed an increase in the number of species, and the increase in shannon and simpson indicated an increase in species evenness. goods_coverage is an index of sequencing depth in this method.

Table S2 The difference of each group gut microbiota (α-diversity) based on Shannon index

Postnatal day(day)	Group-Pair	Tukey-test				Wilcoxon-test				
		difference	lwr	upr	p-adjust	difference	p-value	sig.	LCL	UCL
28	CWG-CG	-0.150	-1.322	1.022	0.983	0	1		-4.193	4.193
	NG-CG	1.531	0.358	2.703	0.008	-10.167	0.000	***	-14.360	-5.974
	WG-CG	2.133	0.822	3.443	0.001	-12.250	0.000	***	-16.938	-7.562
	NG-CWG	1.681	0.509	2.853	0.003	-10.167	0.000	***	-14.360	-5.974
	WG-CWG	2.283	0.972	3.593	0.001	-12.250	0.000	***	-16.938	-7.562
	WG-NG	0.602	-0.708	1.913	0.575	-2.083	0.363		-6.771	2.604
56	CWG-CG	0.535	0.133	0.937	0.007	-11.000	0.002	**	-17.558	-4.442
	NG-CG	0.555	0.153	0.957	0.005	-10.833	0.003	**	-17.391	-4.276
	WG-CG	0.604	0.202	1.006	0.002	-11.500	0.002	**	-18.058	-4.942
	NG-CWG	0.019	-0.383	0.421	0.999	0.167	0.958		-6.391	6.724
	WG-CWG	0.068	-0.334	0.470	0.964	-0.500	0.875		-7.058	6.058
	WG-NG	0.049	-0.353	0.451	0.986	-0.667	0.834		-7.224	5.891

Note: *** means highly significant difference (*P*<0.001). LCL and lwr, lower confidence limits for difference; UCL and upr, upper confidence limits for differenc

TableS3 (1) The Operational Taxonomic Units (OTUs) relative abundances for groups at postnatal day 28 at phylum level

Taxonomy	NG	CG	WG	CWG	Tax_detail
Firmicutes	74.92%	85.82%	44.59%	41.18%	k__Bacteria;p__Firmicutes;
Bacteroidetes	19.93%	1.79%	50.72%	33.58%	k__Bacteria;p__Bacteroidetes;
Tenericutes	0.51%	11.56%	0.23%	9.68%	k__Bacteria;p__Tenericutes;
Proteobacteria	1.57%	0.38%	1.71%	8.81%	k__Bacteria;p__Proteobacteria;
Actinobacteria	2.77%	0.34%	0.42%	4.57%	k__Bacteria;p__Actinobacteria;
Verrucomicrobia	0.24%	0.01%	0.05%	1.93%	k__Bacteria;p__Verrucomicrobia;
unidentified_Bacteria	1.05%	0.04%	0.96%	0.03%	k__Bacteria;p__unidentified_Bacteria;
Deferribacteres	0.51%	0.01%	1.35%	0.02%	k__Bacteria;p__Deferribacteres;
Fusobacteria	0.01%	0.02%	0.04%	0.02%	k__Bacteria;p__Fusobacteria;
Acidobacteria	0.00%	0.00%	0.00%	0.02%	k__Bacteria;p__Acidobacteria;
Cyanobacteria	0.02%	0.00%	0.03%	0.00%	k__Bacteria;p__Cyanobacteria;
Melainabacteria	0.02%	0.00%	0.00%	0.00%	k__Bacteria;p__Melainabacteria;
Chloroflexi	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Chloroflexi;
Synergistetes	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Synergistetes;
Nitrospirae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Nitrospirae;
Gemmatimonadetes	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Gemmatimonadetes;
Elusimicrobia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Elusimicrobia;
Others	0.01%	0.01%	0.00%	0.07%	Others

Table S3(2) The Operational Taxonomic Units (OTUs) relative abundances for groups at postnatal day 56 at phylum level

Taxonomy	N.G	C.W.G	W.G	C.G	Tax_detail
Firmicutes	53.06%	36.56%	48.98%	44.65%	k__Bacteria;p__Firmicutes;
Bacteroidetes	32.47%	48.58%	39.34%	42.55%	k__Bacteria;p__Bacteroidetes;
Proteobacteria	8.38%	11.16%	9.40%	9.04%	k__Bacteria;p__Proteobacteria;
unidentified_Bacteria	4.82%	0.86%	1.23%	2.09%	k__Bacteria;p__unidentified_Bacteria;
Verrucomicrobia	0.17%	1.93%	0.24%	0.35%	k__Bacteria;p__Verrucomicrobia;
Actinobacteria	0.52%	0.42%	0.38%	0.49%	k__Bacteria;p__Actinobacteria;
Deferribacteres	0.25%	0.23%	0.14%	0.27%	k__Bacteria;p__Deferribacteres;
Melainabacteria	0.14%	0.01%	0.04%	0.05%	k__Bacteria;p__Melainabacteria;
Cyanobacteria	0.00%	0.10%	0.10%	0.21%	k__Bacteria;p__Cyanobacteria;
Tenericutes	0.15%	0.05%	0.07%	0.15%	k__Bacteria;p__Tenericutes;
Acidobacteria	0.00%	0.00%	0.03%	0.03%	k__Bacteria;p__Acidobacteria;
Chloroflexi	0.00%	0.01%	0.00%	0.02%	k__Bacteria;p__Chloroflexi;
Fusobacteria	0.01%	0.04%	0.02%	0.02%	k__Bacteria;p__Fusobacteria;
Synergistetes	0.00%	0.01%	0.00%	0.02%	k__Bacteria;p__Synergistetes;
Euryarchaeota	0.00%	0.00%	0.00%	0.00%	k__Archaea;p__Euryarchaeota;
Atribacteria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Atribacteria;
Deinococcus-Thermus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Deinococcus-Thermus;
Gemmatimonadetes	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Gemmatimonadetes;
Elusimicrobia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Elusimicrobia;
Nitrospirae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Nitrospirae;
Armatimonadetes	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Armatimonadetes;
Others	0.01%	0.02%	0.02%	0.06%	Others

Table S4 (1) The Operational Taxonomic Units (OTUs) relative abundances for groups at postnatal day 28 at genus level

Taxonomy	NG	CG	WG	CWG	Tax_detail
Lactobacillus	38.90%	12.06%	41.51%	18.87%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;
Anaeroplasma	0.51%	11.56%	0.12%	1.68%	k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales;f__Anaeroplasmataceae;g__Anaeroplasma;
Parasutterella	0.60%	0.16%	0.75%	8.64%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Parasutterella;
Enterococcus	0.47%	20.32%	0.45%	8.11%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;
Dubosiella	7.09%	0.24%	1.23%	0.36%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Dubosiella;
Bifidobacterium	2.57%	0.26%	0.13%	2.85%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;
Alistipes	2.90%	0.08%	1.14%	0.15%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;
Ileibacterium	4.62%	0.14%	0.59%	2.67%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Ileibacterium;
unidentified_Clostridiales	0.56%	6.68%	0.29%	1.44%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__unidentified_Clostridiales;
unidentified_Lachnospiraceae	0.69%	0.09%	3.00%	0.31%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__unidentified_Lachnospiraceae;
Bacteroides	0.44%	0.07%	2.59%	0.11%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;
Akkermansia	0.24%	0.01%	0.05%	1.61%	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia;

Clostridioides	0.06%	0.09%	0.05%	1.29%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Clostridioides;
Muribaculum	0.26%	0.08%	1.22%	1.95%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculum;
Helicobacter	0.83%	0.03%	0.82%	0.02%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter;
Lachnoclostridium	0.43%	0.04%	1.28%	0.05%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium;
Mucispirillum	0.51%	0.01%	1.35%	0.02%	k__Bacteria;p__Deferribacteres;c__unidentified_Deferribacteres;o__Deferribacterales;f__Deferribacteraceae;g__Mucispirillum;
Odoribacter	0.25%	0.02%	1.03%	0.01%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Odoribacter;
Faecalibaculum	0.88%	0.70%	0.27%	0.63%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Faecalibaculum;
Paraprevotella	0.32%	0.01%	0.01%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Paraprevotella;
Turicibacter	0.60%	0.50%	0.57%	0.56%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;
Parabacteroides	0.47%	0.03%	1.04%	0.02%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides;
unidentified_Ruminococcaceae	0.29%	0.06%	0.93%	0.05%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__unidentified_Ruminococcaceae;
Alloprevotella	0.26%	0.02%	0.49%	0.02%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Alloprevotella;
Roseburia	0.19%	0.04%	0.33%	0.03%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Roseburia;
Ruminiclostridium	0.10%	0.02%	0.81%	0.04%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__

					Ruminococcaceae;g__Ruminiclostridium;
Anaerotruncus	0.05%	0.01%	0.50%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Anaerotruncus;
Desulfovibrio	0.23%	0.02%	0.57%	0.01%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio;
Intestinimonas	0.17%	0.03%	0.41%	0.03%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Intestinimonas;
unidentified_Erysipelotrichaceae	0.01%	0.01%	0.01%	0.21%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__unidentified_Erysipelotrichaceae;
Angelakisella	0.01%	0.00%	0.24%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Angelakisella;
Streptococcus	0.08%	0.12%	0.13%	0.10%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;
Anaerostipes	0.10%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Anaerostipes;
Candidatus_Saccharimonas	0.22%	0.00%	0.13%	0.00%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__unidentified_Bacteria;f__unidentified_Bacteria;g__Candidatus_Saccharimonas;
Candidatus_Arthromitus	0.00%	0.09%	0.00%	0.06%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Candidatus_Arthromitus;
Blautia	0.02%	0.08%	0.05%	0.07%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;
Enterorhabdus	0.11%	0.04%	0.06%	0.05%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Enterorhabdus;
Gordonibacter	0.05%	0.01%	0.18%	0.02%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Gordonibacter;
Rikenella	0.07%	0.01%	0.10%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Rikenella;

Bilophila	0.01%	0.00%	0.18%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Bilophila;
Enhydrobacter	0.00%	0.05%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter;
Faecalibacterium	0.00%	0.06%	0.00%	0.05%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Faecalibacterium;
Oscillibacter	0.03%	0.01%	0.12%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Oscillibacter;
unidentified_Prevotellaceae	0.01%	0.04%	0.03%	0.04%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__unidentified_Prevotellaceae;
Neisseria	0.02%	0.01%	0.05%	0.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Neisseriaceae;g__Neisseria;
Marvinbryantia	0.04%	0.00%	0.02%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Marvinbryantia;
Gemella	0.02%	0.03%	0.01%	0.02%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__unidentified_Bacillales;g__Gemella;
Granulicatella	0.02%	0.01%	0.04%	0.01%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella;
Haemophilus	0.02%	0.02%	0.03%	0.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;
Subdoligranulum	0.00%	0.03%	0.00%	0.02%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Subdoligranulum;
Holdemanella	0.00%	0.02%	0.00%	0.02%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Holdemanella;
Dorea	0.02%	0.03%	0.02%	0.02%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea;
Hydrogenoanaerobacterium	0.02%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Hydrogenoanaerobacterium;

Peptoniphilus	0.00%	0.02%	0.00%	0.02%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Peptoniphilus;
Serratia	0.00%	0.02%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia;
Veillonella	0.01%	0.02%	0.03%	0.01%	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;
Erysipelatoclostridium	0.03%	0.00%	0.04%	0.01%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Erysipelatoclostridium;
Leptotrichia	0.01%	0.02%	0.03%	0.01%	k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Leptotrichia;
unidentified_Cyanobacteria	0.02%	0.00%	0.03%	0.00%	k__Bacteria;p__Cyanobacteria;c__unidentified_Cyanobacteria;o__unidentified_Cyanobacteria;f__unidentified_Cyanobacteria;g__unidentified_Cyanobacteria;
Megasphaera	0.01%	0.01%	0.02%	0.00%	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera;
Actinomyces	0.01%	0.00%	0.02%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;
Negativibacillus	0.00%	0.00%	0.04%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Negativibacillus;
Rothia	0.01%	0.01%	0.02%	0.01%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Rothia;
Lachnoanaerobaculum	0.01%	0.01%	0.01%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoanaerobaculum;
Klebsiella	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella;
Ralstonia	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Ralstonia;
Lautropia	0.01%	0.00%	0.02%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__u

					nidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Lautropia;
Stomatobaculum	0.01%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Stomatobaculum;
Ezakiella	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Ezakiella;
Harryflintia	0.01%	0.00%	0.03%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Harryflintia;
Campylobacter	0.01%	0.01%	0.01%	0.00%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__Campylobacterales;f__Campylobacteraceae;g__Campylobacter;
unidentified_Enterobacteriaceae	0.00%	0.01%	0.00%	0.02%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__unidentified_Enterobacteriaceae;
Methylobacterium	0.00%	0.01%	0.00%	0.02%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylobacterium;
Parvibacter	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Parvibacter;
Anaerovorax	0.00%	0.00%	0.03%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Anaerovorax;
Collinsella	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella;
Dialister	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Dialister;
Peptostreptococcus	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus;
Romboutsia	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Romboutsia;
Tyzzerella	0.01%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__

					Lachnospiraceae;g__Tyzzerella;
Butyricicoccus	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Butyricicoccus;
Allobaculum	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Allobaculum;
Candidatus_Stoquefichus	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Candidatus_Stoquefichus;
Candidatus_Solibacter	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Solibacterales;f__unidentified_Solibacterales;g__Candidatus_Solibacter;
Sphingomonas	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;
Porphyromonas	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;
Fusobacterium	0.00%	0.00%	0.01%	0.00%	k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;
Fusibacter	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Fusibacter;
Prevotella	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;
Atopobium	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Atopobium;
Oribacterium	0.01%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Oribacterium;
Staphylococcus	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;
Peptococcus	0.00%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Peptococcus;
unidentified_Christensenellaceae	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__unidentified_Christensenellaceae;

Candidatus_Soleaferrea	0.00%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Candidatus_Soleaferrea;
Catabacter	0.00%	0.00%	0.01%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__Catabacter;
Others	33.41%	45.70%	34.66%	47.53%	Others

Table S4 (2) The Operational Taxonomic Units (OTUs) relative abundances for groups at postnatal day 56 at genus level

Taxonomy	N.G	C.W.G	W.G	C.G	Tax_detail
Alloprevotella	3.25%	4.31%	5.31%	6.07%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Alloprevotella;
Ileibacterium	5.55%	4.30%	1.25%	1.08%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Ileibacterium;
Bacteroides	1.28%	1.97%	1.96%	1.83%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;
Helicobacter	4.14%	0.73%	0.58%	1.85%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter;
unidentified_Lachnospiraceae	8.35%	3.25%	6.44%	5.57%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__unidentified_Lachnospiraceae;
Akkermansia	0.17%	1.93%	0.24%	0.35%	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia;
Blautia	1.02%	3.98%	1.47%	3.35%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Blautia;
unidentified_Ruminococcaceae	3.04%	0.93%	2.28%	2.16%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__unidentified_Ruminococcaceae;
Dubosiella	1.35%	1.98%	1.54%	1.46%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Dubosiella;
Ruminiclostridium	1.54%	1.56%	2.07%	2.15%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium;
Alistipes	1.65%	1.13%	1.40%	1.27%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes;
Oscillibacter	1.58%	1.13%	2.14%	1.86%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Oscillibacter;
Muribaculum	0.73%	1.28%	1.08%	1.07%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculum;
Parabacteroides	0.85%	0.98%	1.17%	0.97%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f

					__Tannerellaceae;g__Parabacteroides;
Gemella	0.04%	0.45%	0.02%	0.04%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__unidentified_Bacillales;g__Gemella;
Lachnoclostridium	1.05%	1.05%	1.14%	1.10%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium;
Candidatus_Saccharimonas	0.68%	0.12%	0.65%	0.23%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__unidentified_Bacteria;f__unidentified_Bacteria;g__Candidatus_Saccharimonas;
Acinetobacter	0.07%	0.40%	0.03%	0.07%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;
Parasutterella	1.06%	1.13%	0.49%	1.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Parasutterella;
Lactobacillus	0.79%	0.60%	0.61%	0.87%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;
Intestinimonas	0.69%	0.53%	0.78%	0.75%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Intestinimonas;
Odoribacter	0.51%	0.59%	0.31%	0.56%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Odoribacter;
Desulfovibrio	0.79%	0.55%	0.71%	0.37%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio;
unidentified_Enterobacteriaceae	0.07%	0.36%	0.18%	0.13%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__unidentified_Enterobacteriaceae;
Anaerostipes	0.13%	0.12%	0.54%	0.17%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Anaerostipes;
Roseburia	0.48%	0.57%	0.68%	0.55%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Roseburia;
Mucispirillum	0.25%	0.23%	0.14%	0.27%	k__Bacteria;p__Deferribacteres;c__unidentified_Deferribacteres;

					o__Deferribacterales;f__Deferribacteraceae;g__Mucispirillum;
Pseudomonas	0.10%	0.09%	0.20%	0.27%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;
Acetatifactor	0.05%	0.02%	0.16%	0.04%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Acetatifactor;
Achromobacter	0.01%	0.10%	0.00%	0.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Achromobacter;
Erysipelatoclostridium	0.06%	0.13%	0.04%	0.06%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Erysipelatoclostridium;
Brevundimonas	0.05%	0.19%	0.10%	0.31%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas;
Lachnospira	0.01%	0.17%	0.09%	0.09%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospira;
Tyzzerella	0.20%	0.19%	0.18%	0.32%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella;
Geobacter	0.00%	0.06%	0.00%	0.07%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Geobacteraceae;g__Geobacter;
Limnobacter	0.01%	0.12%	0.06%	0.21%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Limnobacter;
Anaerotruncus	0.21%	0.22%	0.31%	0.23%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Anaerotruncus;
Butyricicoccus	0.13%	0.15%	0.18%	0.18%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Butyricicoccus;
Angelakisella	0.15%	0.14%	0.18%	0.18%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Angelakisella;
Marvinbryantia	0.03%	0.03%	0.03%	0.12%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Marvinbryantia;

unidentified_Cyanobacteria	0.00%	0.10%	0.10%	0.21%	k__Bacteria;p__Cyanobacteria;c__unidentified_Cyanobacteria;o__unidentified_Cyanobacteria;f__unidentified_Cyanobacteria;g__unidentified_Cyanobacteria;
Enterorhabdus	0.18%	0.13%	0.15%	0.17%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Enterorhabdus;
Anaeroplasma	0.06%	0.01%	0.01%	0.11%	k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales;f__Anaeroplasmataceae;g__Anaeroplasma;
unidentified_Clostridiales	0.16%	0.14%	0.14%	0.14%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__unidentified_Clostridiales;
Rikenella	0.01%	0.10%	0.10%	0.08%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Rikenella;
Negativibacillus	0.07%	0.07%	0.09%	0.10%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Negativibacillus;
Psychrobacter	0.05%	0.04%	0.01%	0.03%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter;
Bilophila	0.06%	0.10%	0.11%	0.05%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Bilophila;
Romboutsia	0.01%	0.07%	0.04%	0.04%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Romboutsia;
Bifidobacterium	0.04%	0.07%	0.04%	0.07%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium;
unidentified_Beijerinckiaceae	0.00%	0.02%	0.03%	0.04%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__unidentified_Beijerinckiaceae;
Faecalibaculum	0.05%	0.03%	0.05%	0.02%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Faecalibaculum;
Flavonifractor	0.03%	0.05%	0.03%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Flavonifractor;
Candidatus_Arthromitus	0.06%	0.03%	0.05%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Candidatus_Arthromitus;

Turicibacter	0.01%	0.02%	0.04%	0.01%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;
Terriglobus	0.00%	0.00%	0.03%	0.02%	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__unidentified_Acidobacteriales;g__Terriglobus;
Enhydrobacter	0.03%	0.03%	0.00%	0.02%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter;
Harryflintia	0.05%	0.05%	0.09%	0.06%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Harryflintia;
Peptococcus	0.08%	0.07%	0.06%	0.10%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Peptococcus;
Cupriavidus	0.01%	0.00%	0.02%	0.03%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Cupriavidus;
Acidiphilium	0.00%	0.00%	0.02%	0.03%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__unidentified_Alphaproteobacteria;f__Acetobacteraceae;g__Acidiphilium;
Gordonibacter	0.06%	0.04%	0.06%	0.05%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Gordonibacter;
Anaerovorax	0.04%	0.02%	0.05%	0.03%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Anaerovorax;
unidentified_Christensenellaceae	0.02%	0.02%	0.03%	0.03%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__unidentified_Christensenellaceae;
Methylobacterium	0.01%	0.01%	0.02%	0.03%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylobacterium;
unidentified_Rhizobiaceae	0.00%	0.02%	0.00%	0.01%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__unidentified_Rhizobiaceae;
Devosia	0.01%	0.02%	0.00%	0.02%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unidentified_Rhizobiales;g__Devosia;
Allobaculum	0.03%	0.00%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotric

					hales;f__Erysipelotrichaceae;g__Allobaculum;
Fusobacterium	0.01%	0.04%	0.02%	0.02%	k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium;
Sphingomonas	0.00%	0.01%	0.02%	0.03%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;
Phascolarctobacterium	0.01%	0.04%	0.02%	0.01%	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Acidaminococcaceae;g__Phascolarctobacterium;
Pygmaiobacter	0.03%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Pygmaiobacter;
Staphylococcus	0.00%	0.01%	0.01%	0.02%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus;
Halomonas	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas;
Streptococcus	0.01%	0.02%	0.01%	0.01%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;
unidentified_Anaerolineaceae	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__unidentified_Anaerolineaceae;
Fusicatenibacter	0.00%	0.03%	0.01%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Fusicatenibacter;
Dietzia	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Corynebacteriales;f__Dietziaceae;g__Dietzia;
Rhodococcus	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Rhodococcus;
Caldicoprobacter	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Caldicoprobacteraceae;g__Caldicoprobacter;
Papillibacter	0.02%	0.02%	0.02%	0.02%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Papillibacter;
Ralstonia	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Ralsto

					nia;
Halocella	0.00%	0.00%	0.01%	0.01%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__Halanaerobiales;f__Halanaerobiaceae;g__Halocella;
Parvibacter	0.01%	0.01%	0.00%	0.02%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Parvibacter;
Lentimicrobium	0.00%	0.01%	0.00%	0.01%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Lentimicrobiaceae;g__Lentimicrobium;
Alcaligenes	0.01%	0.01%	0.00%	0.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Alcaligenes;
Arcobacter	0.01%	0.01%	0.00%	0.00%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__Campylobacterales;f__unidentified_Campylobacterales;g__Arcobacter;
Thermovirga	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Synergistaceae;g__Thermovirga;
Clostridioides	0.00%	0.00%	0.01%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Clostridioides;
Haemophilus	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus;
Hirschia	0.00%	0.01%	0.00%	0.02%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Hyphomonadaceae;g__Hirschia;
Soonwooa	0.01%	0.01%	0.01%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__unidentified_Flavobacteriales;g__Soonwooa;
Caproiciproducens	0.02%	0.01%	0.01%	0.02%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Caproiciproducens;
unidentified_Erysipelotrichaceae	0.01%	0.01%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__unidentified_Erysipelotrichaceae;
Serratia	0.00%	0.01%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Ent

					erobacteriales;f__Enterobacteriaceae;g__Serratia;
Stenotrophomonas	0.01%	0.01%	0.00%	0.01%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas;
Hymenobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Hymenobacteraceae;g__Hymenobacter;
Candidatus_Soleaferrea	0.01%	0.01%	0.01%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Candidatus_Soleaferrea;
Chryseobacterium	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__unidentified_Flavobacteriales;g__Chryseobacterium;
Paraprevotella	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Paraprevotella;
Syntrophaceticus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Thermoanaerobacterales;f__Thermoanaerobacteraceae;g__Syntrophaceticus;
Anaerofustis	0.01%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Eubacteriaceae;g__Anaerofustis;
Faecalibacterium	0.01%	0.00%	0.01%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Faecalibacterium;
Desulfobulbus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae;g__Desulfobulbus;
Tepidimicrobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Tepidimicrobium;
Methanosaeta	0.00%	0.00%	0.00%	0.00%	k__Archaea;p__Euryarchaeota;c__Methanomicrobia;o__Methanosarcinales;f__Methanosaetaceae;g__Methanosaeta;
Fastidiosipila	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Fastidiosipila;
Cutibacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium;
Blastococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o

					__Frankiales;f__Geodermatophilaceae;g__Blastococcus;
Amycolatopsis	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae;g__Amycolatopsis;
Proteiniphilum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__unidentified_Bacteroidales;g__Proteiniphilum;
Microbacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Microbacterium;
Acidothermus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Frankiales;f__Acidothermaceae;g__Acidothermus;
Massilia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Massilia;
Bryocella	0.00%	0.00%	0.00%	0.01%	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__unidentified_Acidobacteriales;g__Bryocella;
Sedimentibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Sedimentibacter;
Sphingobacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium;
Rothia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Rothia;
Desulfuromonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Desulfuromonadaceae;g__Desulfuromonas;
Nitriliruptor	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__Nitriliruptoria;o__Nitriliruptorales;f__Nitriliruptoraceae;g__Nitriliruptor;
Alkaliphilus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Alkaliphilus;
Subdoligranulum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Subdoligranulum;
Petrimonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f

					__unidentified_Bacteroidales;g__Petrimonas;
unidentified_Corynebacteriaceae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__unidentified_Corynebacteriaceae;
Desulfomicrobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfomicrobiaceae;g__Desulfomicrobium;
Kocuria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Kocuria;
Macrococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Macrococcus;
Proteocatella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Proteocatella;
Phaselicystis	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Phaselicystidaceae;g__Phaselicystis;
Paracoccus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus;
Isoptericola	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Promicromonosporaceae;g__Isoptericola;
Peptostreptococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus;
Georgenia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Bogoriellaceae;g__Georgenia;
Gallicola	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Gallicola;
Geodermatophilus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Frankiales;f__Geodermatophilaceae;g__Geodermatophilus;
Kineococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Kineosporiales;f__Kineosporiaceae;g__Kineococcus;
Cetobacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacterial

					es;f__Fusobacteriaceae;g__Cetobacterium;
Pasteurella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Pasteurella;
Pseudochrobactrum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Pseudochrobactrum;
Actinomadura	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Streptosporangiales;f__Thermomonosporaceae;g__Actinomadura;
Listeria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Listeriaceae;g__Listeria;
Mariniphaga	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prolixibacteraceae;g__Mariniphaga;
Macellibacteroides	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Macellibacteroides;
Friedmanniella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Friedmanniella;
Comamonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Comamonas;
Asticcacaulis	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Asticcacaulis;
Alkalicoccus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Sporolactobacillaceae;g__Alkalicoccus;
Sporacetigenium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Sporacetigenium;
Actinomyces	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces;
Lawsonella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o

					__Corynebacteriales;f__Corynebacteriaceae;g__Lawsonella;
Rubrivivax	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Rubrivivax;
Zoogloea	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Rhodocyclaceae;g__Zoogloea;
Holdemania	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Holdemania;
Gelria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Thermoanaerobacterales;f__Thermoanaerobacteraceae;g__Gelria;
Truepera	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Deinococcales;f__Trueperaceae;g__Truepera;
Lactococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;
Catabacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__Catabacter;
Pelotomaculum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Pelotomaculum;
Aerococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerococcus;
Marmoricola	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Marmoricola;
Veillonella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella;
Methyloversatilis	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Rhodocyclaceae;g__Methyloversatilis;

Paenarthrobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Paenarthrobacter;
Aeribacillus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Aeribacillus;
Planococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planococcus;
Limnohabitans	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Limnohabitans;
Acidipila	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__unidentified_Acidobacteriales;g__Acidipila;
Gracilibacillus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Gracilibacillus;
Thermomonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Thermomonas;
Sediminibacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Sediminibacterium;
Nordella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unidentified_Rhizobiales;g__Nordella;
Piscibacillus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Piscibacillus;
Lutispora	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Gracilibacteraceae;g__Lutispora;
Mycobacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Corynebacteriales;f__Mycobacteriaceae;g__Mycobacterium;
Hydrogenispora	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Heliobacteriaceae;g__Hydrogenispora;
Eggerthella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Eggerthella;

Actinomycetospora	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae;g__Actinomycetospora;
Actinophytocola	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae;g__Actinophytocola;
unidentified_Prevotellaceae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__unidentified_Prevotellaceae;
Butyricimonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Butyricimonas;
Ornithinimicrobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Intrasporangiaceae;g__Ornithinimicrobium;
Marinospirillum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Marinospirillum;
Pseudogracilibacillus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Pseudogracilibacillus;
Alkanindiges	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Alkanindiges;
Corynebacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium;
Quadrisphaera	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Kineosporiales;f__Kineosporiaceae;g__Quadrisphaera;
Tissierella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Tissierella;
Ilumatobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__unidentified_Acidimicrobiia;f__unidentified_Acidimicrobiia;g__Ilumatobacter;
Gemmobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhod

					obacterales;f__Rhodobacteraceae;g__Gemmobacter;
unidentified_Melainabacteria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Melainabacteria;c__unidentified_Melainabacteria;o__unidentified_Melainabacteria;f__unidentified_Melainabacteria;g__unidentified_Melainabacteria;
Desulfatitalea	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobacteraceae;g__Desulfatitalea;
Enterococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;
Macromonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Macromonas;
Nakamurella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Frankiales;f__Nakamurellaceae;g__Nakamurella;
Tepidanaerobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Thermoanaerobacterales;f__unidentified_Thermoanaerobacterales;g__Tepidanaerobacter;
Aureimonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Aureimonas;
Salinicola	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Salinicola;
Altererythrobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;
Gottschalkia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Gottschalkia;
Aeromonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Aeromonas;
Syntrophococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Syntrophococcus;
Atopostipes	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Car

					nobacteriaceae;g__Atopostipes;
Parvimonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__unidentified_Clostridiales;g__Parvimonas;
Sphingopyxis	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingopyxis;
Neisseria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Neisseriaceae;g__Neisseria;
Pullulanibacillus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Sporolactobacillaceae;g__Pullulanibacillus;
Fermentimonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__unidentified_Bacteroidales;g__Fermentimonas;
Hydrogenoanaerobacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Hydrogenoanaerobacterium;
Leucobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Leucobacter;
Erythrobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Erythrobacter;
Olivibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Olivibacter;
Bacillus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;
Candidatus_Endomicrobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Elusimicrobia;c__Endomicrobia;o__Endomicrobiales;f__Endomicrobiaceae;g__Candidatus_Endomicrobium;
Kineosporia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Kineosporiales;f__Kineosporiaceae;g__Kineosporia;
Mucilaginibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Mucilaginibacter;
Gardnerella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Gardnerella;

Azospirillum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__unidentified_Alphaproteobacteria;f__unidentified_Alphaproteobacteria;g__Azospirillum;
Holdemanella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Holdemanella;
Streptomyces	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Streptomycetales;f__Streptomycetaceae;g__Streptomyces;
Granulicatella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella;
Candidatus_Entotheonella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__unidentified_Bacteria;f__unidentified_Bacteria;g__Candidatus_Entotheonella;
Rhodomicrobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unidentified_Rhizobiales;g__Rhodomicrobium;
Porphyromonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas;
Candidatus_Blochmannia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Candidatus_Blochmannia;
Megamonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megamonas;
Desulfitobacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__Desulfitobacterium;
Flavobacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;
Bradyrhizobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Bradyrhizobium;
Anaeromyxobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Archangiaceae;g__Anaeromyxobacter;

Nocardia	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Nocardia;
Syntrophorhabdus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__unidentified_Deltaproteobacteria;f__Syntrophorhabdaceae;g__Syntrophorhabdus;
Proteus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Proteus;
Sphingosinicella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingosinicella;
unidentified_Rikenellaceae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__unidentified_Rikenellaceae;
Candidatus_Planktoluna	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Candidatus_Planktoluna;
Nocardioides	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Actinobacteria;c__unidentified_Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides;
Skermanella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__unidentified_Alphaproteobacteria;f__unidentified_Alphaproteobacteria;g__Skermanella;
Legionella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Legionella;
Sulfurospirillum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__unidentified_Bacteria;c__unidentified_Bacteria;o__Campylobacterales;f__unidentified_Campylobacterales;g__Sulfurospirillum;
Peredibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bacteriovoracaceae;g__Peredibacter;
unidentified_Ignavibacteria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Ignavibacteria;o__unidentified_Ignavibacteria;f__unidentified_Ignavibacteria;g__unidentified_Ignavibacteria;

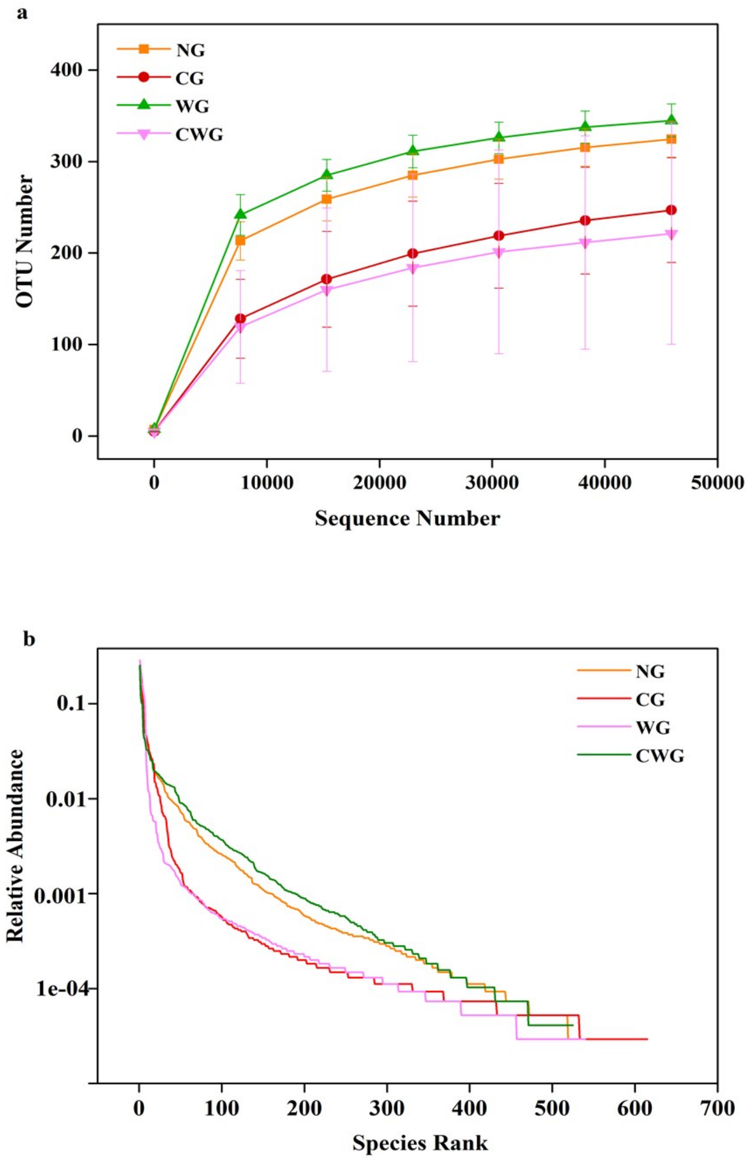
Prevotella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;
Amaricoccus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Amaricoccus;
Oribacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Oribacterium;
Vibrio	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Vibrio;
unidentified_Burkholderiaceae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__unidentified_Burkholderiaceae;
Phreatobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unidentified_Rhizobiales;g__Phreatobacter;
Methanobacterium	0.00%	0.00%	0.00%	0.00%	k__Archaea;p__Euryarchaeota;c__Methanobacteria;o__Methanobacteriales;f__Methanobacteriaceae;g__Methanobacterium;
Trichococcus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Trichococcus;
Ercella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ercella;
Aquabacterium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Aquabacterium;
Alcanivorax	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Alcanivoracaceae;g__Alcanivorax;
Barnesiella	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Barnesiellaceae;g__Barnesiella;
Sphingobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium;
Anaerosalibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__uni

					dentified_Clostridiales;g__Anaerosalibacter;
Propionivibrio	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Rhodocyclaceae;g__Propionivibrio;
Ammoniphilus	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Ammoniphilus;
unidentified_Alphaproteobacteria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__unidentified_Alphaproteobacteria;f__unidentified_Alphaproteobacteria;g__unidentified_Alphaproteobacteria;
Noviherbaspirillum	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Noviherbaspirillum;
Capnocytophaga	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga;
Spirosoma	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Spirosomaceae;g__Spirosoma;
Hyphomicrobium	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium;
Paludibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Paludibacter;
Caulobacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Caulobacter;
unidentified_Acidobacteria	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Acidobacteria;c__unidentified_Acidobacteria;o__unidentified_Acidobacteria;f__unidentified_Acidobacteria;g__unidentified_Acidobacteria;
Roseomonas	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__unidentified_Alphaproteobacteria;f__Acetobacteraceae;g__Roseomonas;
unidentified_Rhizobiales	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhiz

					obiales;f__unidentified_Rhizobiales;g__unidentified_Rhizobiales;
Ramlibacter	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__unidentified_Gammaproteobacteria;f__Burkholderiaceae;g__Ramlibacter;
unidentified_Anaerolineae	0.00%	0.00%	0.00%	0.00%	k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__unidentified_Anaerolineae;f__unidentified_Anaerolineae;g__unidentified_Anaerolineae;
Others	56.54%	60.63%	61.72%	58.92%	Others

Supplementary Figure

Figure S1



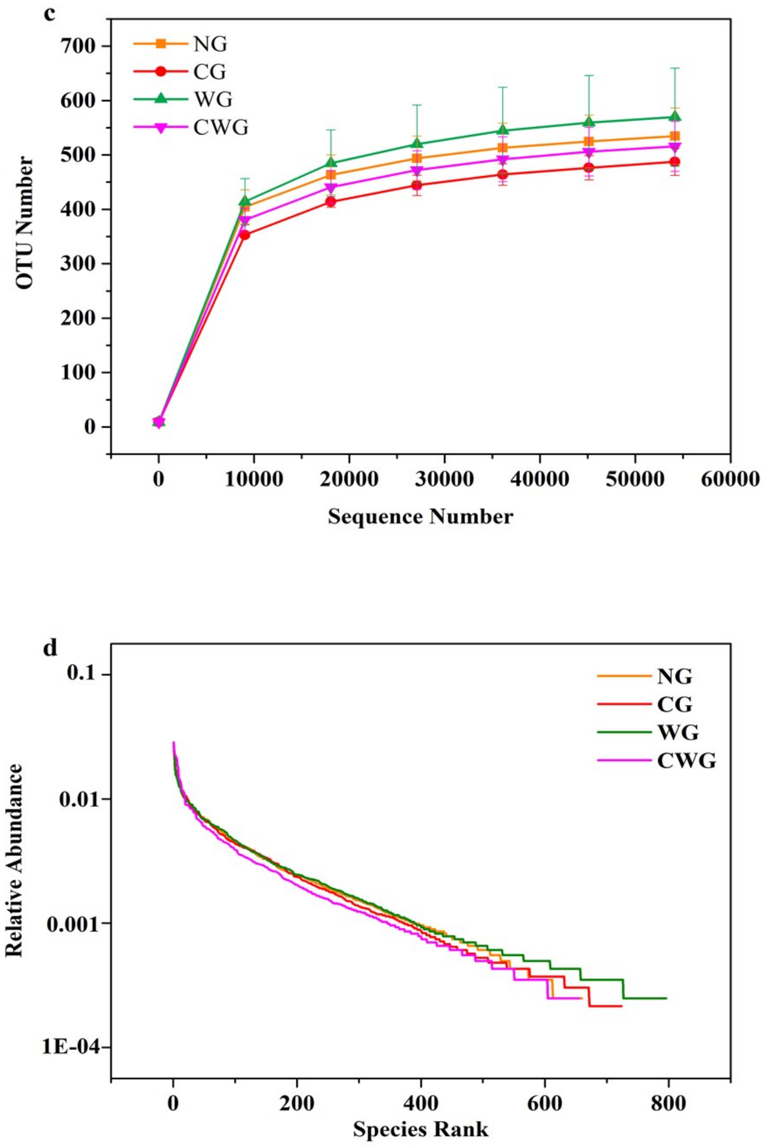
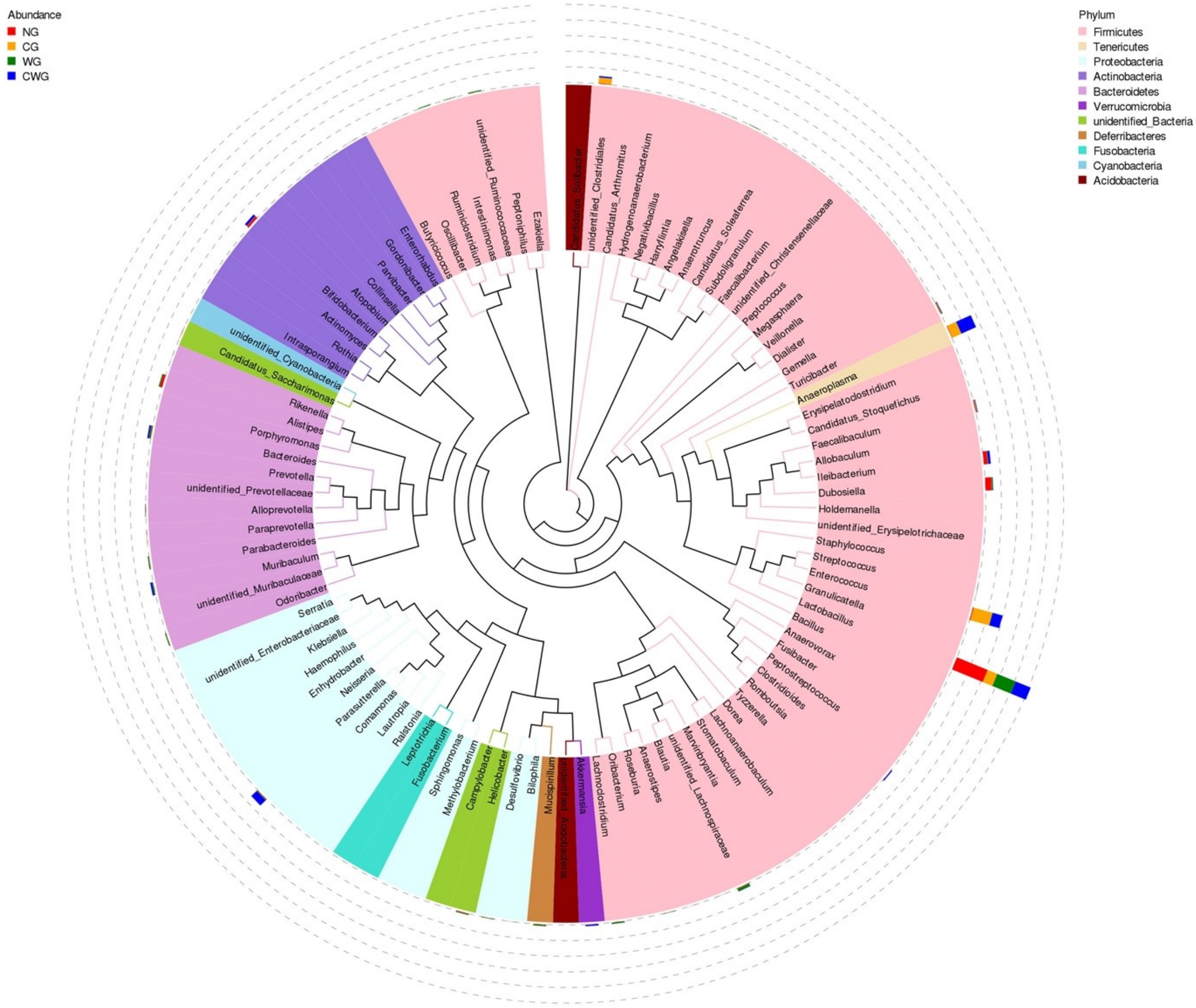


Figure S1. Gut microbiota diversity curve of different groups. a: The rarefaction curve of gut microbiota based on random extraction of sequencing data from cecal digestives at postnatal day 28. b: Rank abundance based on the relative abundance of OTUs at postnatal day 28. c: The rarefaction curve of gut microbiota based on random extraction of sequencing data from cecal digestives at postnatal day 56. d: Rank abundance based on the relative abundance of OTUs at postnatal day 56.

Figure S2

A


Abundance
NG
CG
WG
CWG
Phylum
Firmicutes
Tenericutes
Proteobacteria
Actinobacteria
Bacteroidetes
Verrucomicrobia
unidentified_Bacteria
Deferribacteres
Fusobacteria
Cyanobacteria
Acidobacteria
Candidatus_Solibacter
unidentified_Clostridiales
Candidatus_Arthromitus
Hydrogenoanaerobacterium
Negativibacillus
Harryflintia
Angelakisella
Anaerotruncus
Candidatus_Soleaferrea
Subdoligranulum
Faecalibacterium
unidentified_Christensenellaceae
Peptococcus
Megasphaera
Veillonella
Dialister
Gemella
Turicibacter
Anaeroplasma
Erysipelatoclostridium
Candidatus_Stoquefichus
Faecalibaculum
Allobaculum
Ileibacterium
Dubosiella
Holdemanella
unidentified_Erysipelotrichaceae
Staphylococcus
Streptococcus
Enterococcus
Granulicatella
Lactobacillus
Bacillus
Anaerovorax
Fusibacter
Peptostreptococcus
Clostridioides
Romboutsia
Tyzzerella
Dorea
Lachnoanaerobaculum
Stomatobaculum
Marvinbryantia
unidentified_Lachnospiraceae
Blautia
Anaerostipes
Roseburia
Oribacterium
Lachnoclostridium
Akkermansia
unidentified_Acidobacteria
Mucispirillum
Bilophila
Desulfovibrio
Helicobacter
Campylobacter
Methylobacterium
Sphingomonas
Fusobacterium
Leptotrichia
Ralstonia
Lautropia
Comamonas
Parasutterella
Neisseria
Enhydrobacter
Haemophilus
Klebsiella
unidentified_Enterobacteriaceae
Serratia
Odoribacter
unidentified_Muribaculaceae
Muribaculum
Parabacteroides
Paraprevotella
Alloprevotella
unidentified_Prevotellaceae
Prevotella
Bacteroides
Porphyromonas
Alistipes
Rikenella
Candidatus_Saccharimonas
unidentified_Cyanobacteria
Intrasporangium
Rothia
Actinomyces
Bifidobacterium
Atopobium
Collinsella
Parvibacter
Gordonibacter
Enterorhabdus
Butyricicoccus
Oscillibacter
Ruminiclostridium
Intestinimonas
unidentified_Ruminococcaceae
Peptoniphilus
Ezakiella

B

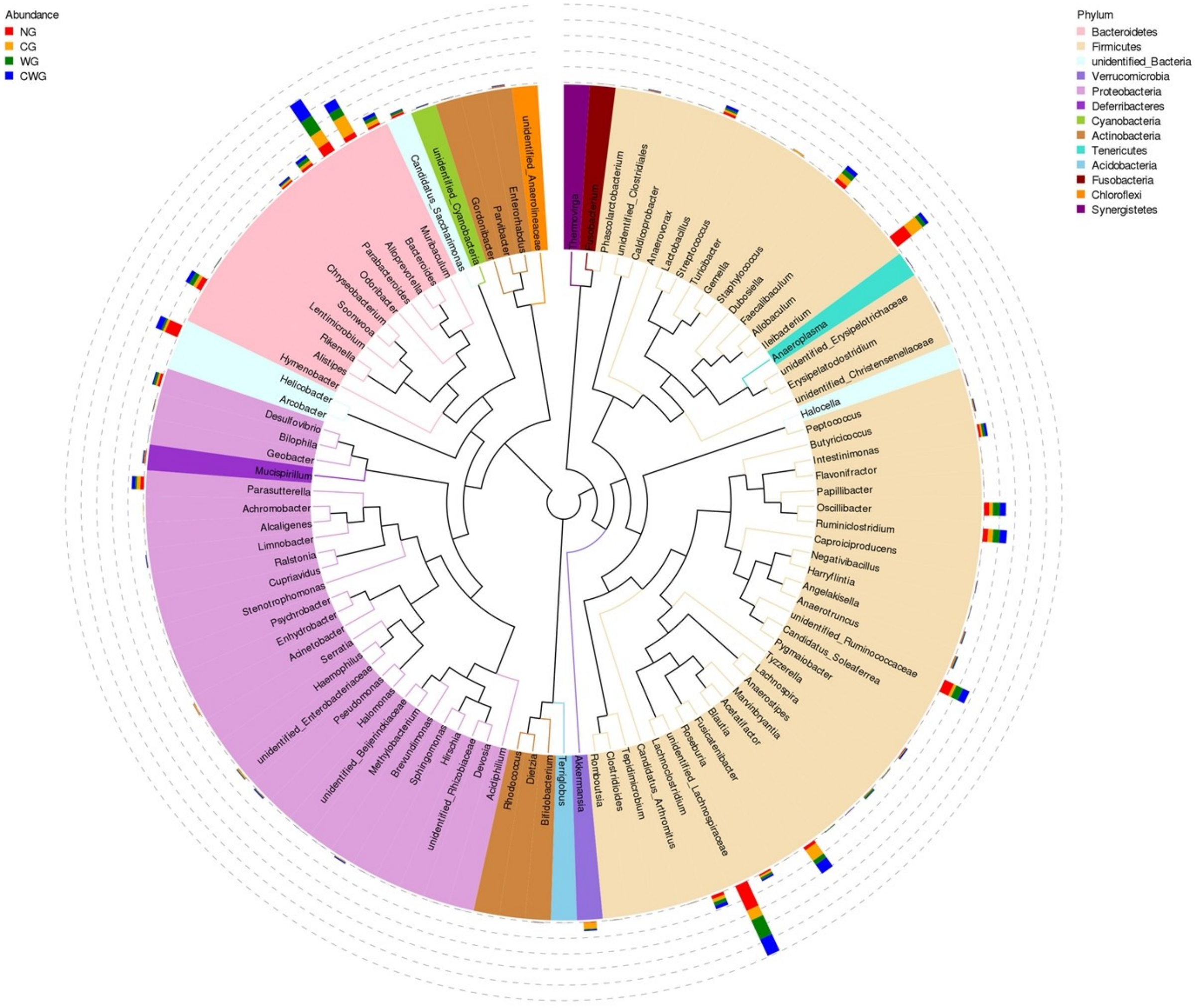


Figure S2 Representation of the changes in the top 100 genus taxa of cecal digest in mice of different groups at postnatal day 28(A) and postnatal day 56(B)