**Supplementary Figure 1. Aggregate daily growth rate distributions of human and mouse gut microbiota**. Daily growth rates of gut microbiota were defined as the logarithm of successive abundance ratios, $\mu = \log(X(t+1)/X(t))$, where $X(t)$ is relative abundance of an OTU on day t. Growth rates aggregated over the community closely follow a Laplace distribution of the form: $p(\mu) = (1/2b)\exp(-|\mu|/b)$ in all **(a)** humans ($b = 0.83 \pm 0.1, 0.67 \pm 0.1, 0.71 \pm 0.07, 0.73 \pm 0.05$, A, B, M3, F4 respectively; mean $\pm$ .s.d, see Methods) and **(b)** mice ($b = 0.82 \pm 0.1, 0.67 \pm 0.03$, LFPP and HFHS diets respectively mean $\pm$ s.d. across individual mice). **(c)** Daily growth rates of gut microbiota defined at different taxonomic resolutions were calculated as the logarithm of successive abundance ratios, $\mu = \log(X(t+1)/X(t))$, where $X(t)$ corresponds to the sum of all OTU abundances falling within the same assigned taxonomy on day t. Distributions of daily growth rates at different taxonomic resolutions are described well by the Laplace distribution. Species were defined at the level of 97% sequence similarity in 16S rRNA. Solid lines indicate MLE fits to the data.
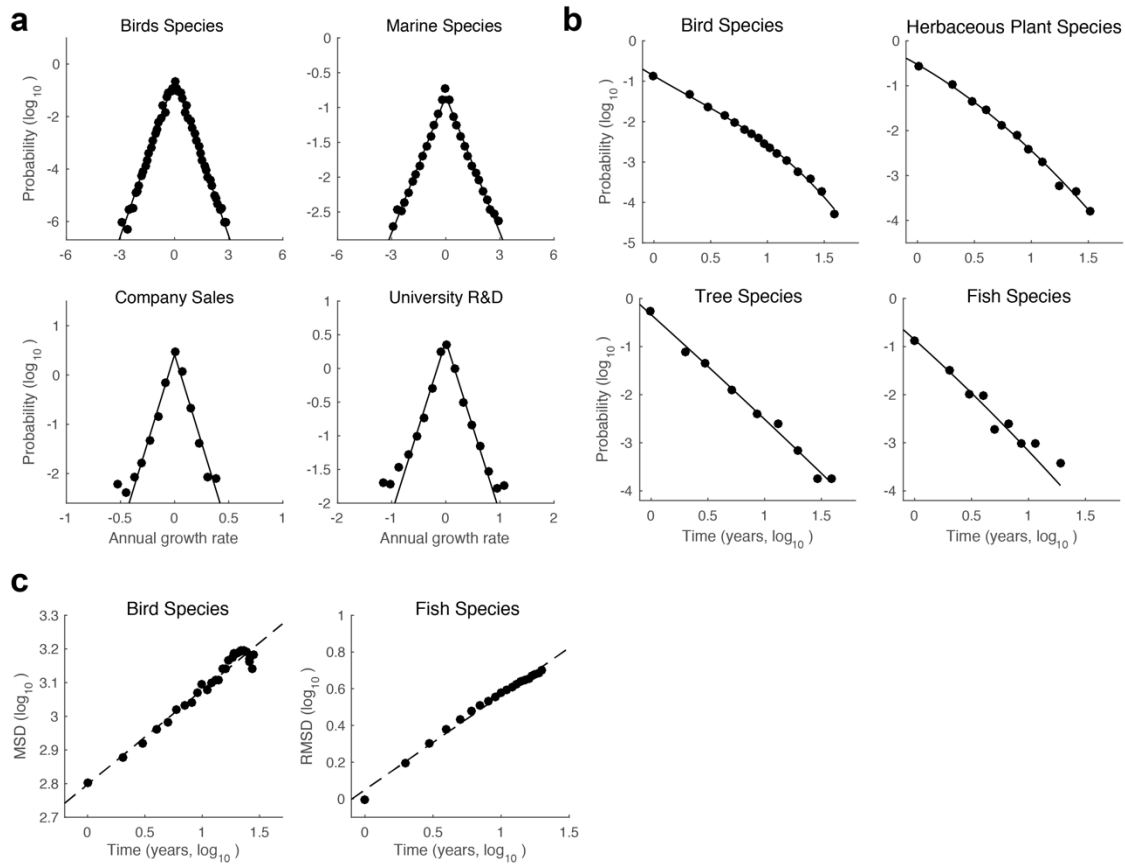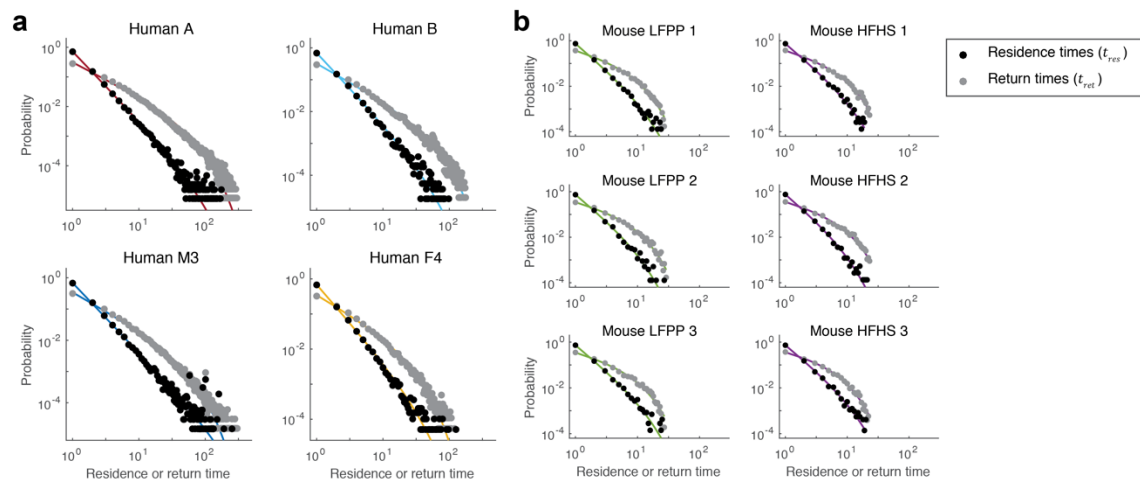
Supplementary Figure 2. Growth rate distributions in diverse ecological communities and economic systems. **(a)** Annual growth rate distributions of North American bird populations[9], marine species abundances[11], publicly-traded company sales[13] and university R&D expenditures[22] follow a Laplace form. Figures were adapted from their original text. Distributions of company sales and R&D expenditures were re-plotted for companies with initial dollar sales of 4^{15} and universities with large R&D expenditures (see refs. 13 and 22 for details). Lines are provided for visual purposes only. **(b)** Residence time distributions of species belonging to diverse ecosystems follow a power law with exponential cutoff. Figures were adapted from ref. 5, with original data comprising North American breeding bird species, estuarine fish species, and plant species collected from both prairie and forest ecosystems. Lines are provided for visual purposes only. **(c)** Long-term behavior of bird species abundances[9] and North Atlantic fish stock abundances[23] follow a diffusion process. Figures were adapted from their original text.
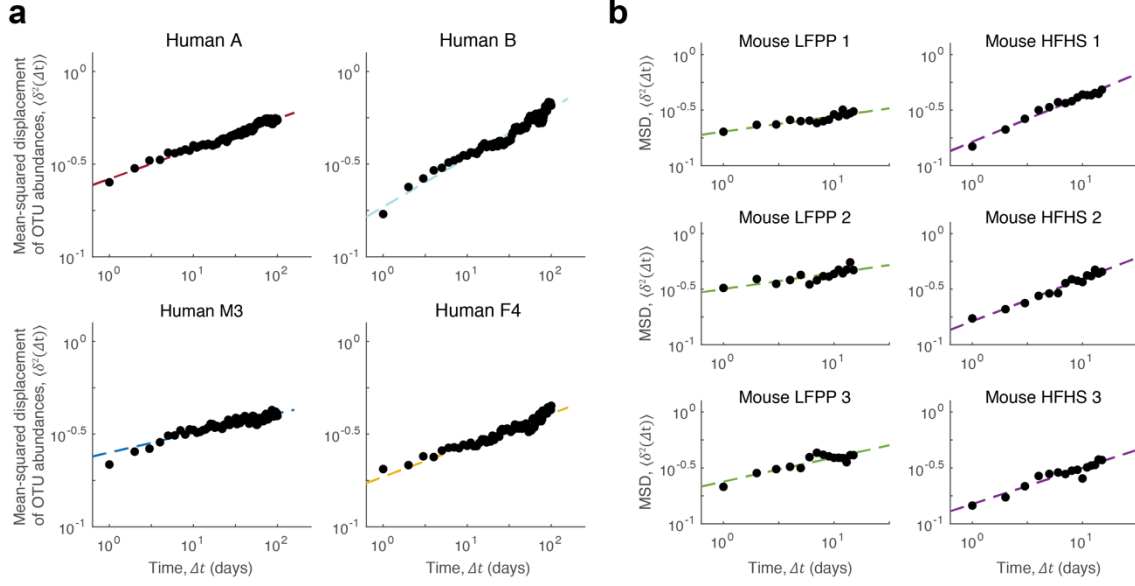
Supplementary Figure 3. Long-term dynamics of gut microbiota abundances in humans and mice. (a,b) The mean-squared displacement of log OTU abundances $\langle \delta^2(\Delta t) \rangle$ scales with time as a power law of the form $\langle \delta^2(\Delta t) \rangle \propto \Delta t^{2H}$, where H is the Hurst exponent characterizing the diffusion process. Hurst exponents are $H = 0.07 \pm 0.03$, 0.10 ± 0.04, 0.08 ± 0.02, 0.1 ± 0.07 for humans A, B, M3, and F4 respectively, and $H = 0.08 \pm 0.02$, 0.19 ± 0.02 for LFPP and HFHS mice (mean $\pm$ s.d., see Methods).
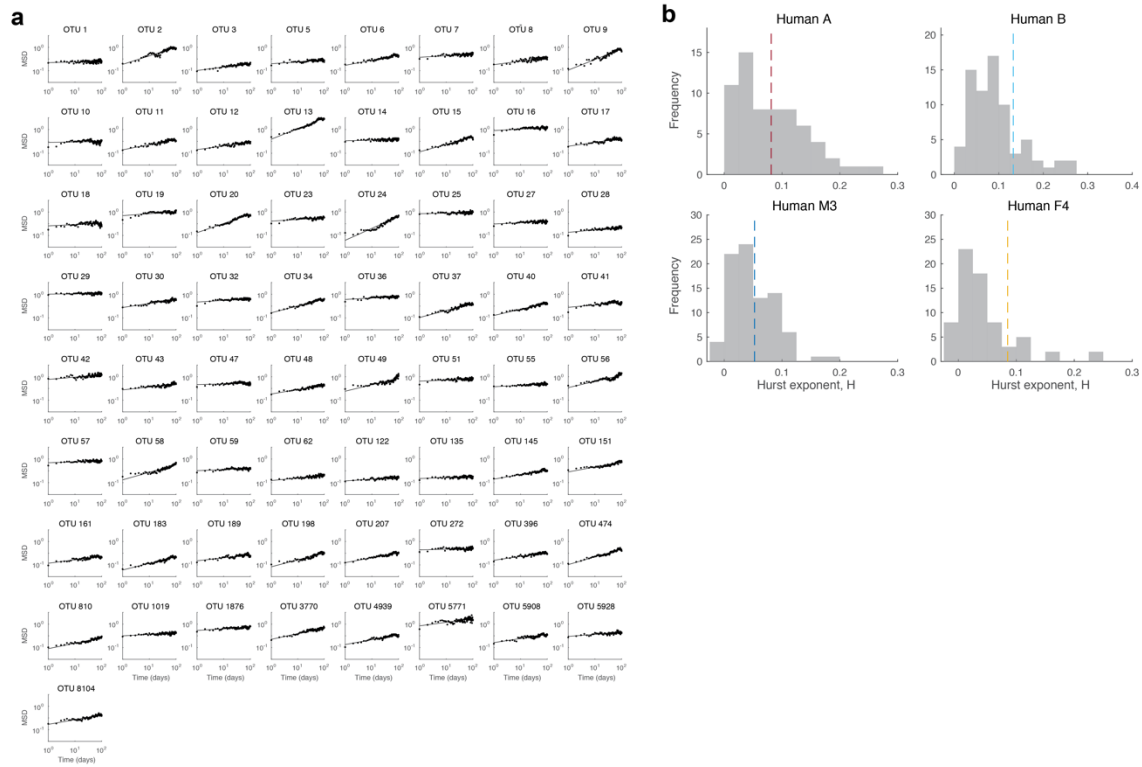
Supplementary Figure 4. Long-term behavior of individual OTU abundances. **(a)** The mean-squared-displacements of individual OTU abundances $\langle \delta^2(\Delta t) \rangle_k$ can be described with the equation of anomalous diffusion, $\langle \delta^2(\Delta t) \rangle_k \propto \Delta t^{2H}$. Panels correspond to OTUs analyzed from human A. **(b)** Distributions of Hurst exponents for individual OTUs in humans display variability around the community average (see Methods), which is indicated by a dashed line.

Supplementary Figure 5. Residence and return times of gut microbiota in humans and mice. Residence times (t_{res}) and return times (t_{ret}) of OTUs follow power law distributions with exponential tails of the form $p(t) \propto t^{-\alpha}e^{-\lambda t}$. **(a)** In humans, power law exponents are $\alpha_{res} = 2.3 \pm 0.04, 2.2 \pm 0.05, 2.2 \pm 0.07, 2.14 \pm 0.08$ for residence times and $\alpha_{ret} = 1.1 \pm 0.02, 1.15 \pm 0.03, 1.2 \pm 0.05, 1.09 \pm 0.07, 1$ for return times (A, B, M3, F4 respectively; mean $\pm$ s.d., see Methods). **(b)** In mice, $\alpha_{res} = 2.2 \pm 0.04, 2.2 \pm 0.03$ and $\alpha_{ret} = 0.72 \pm 0.03, 0.67 \pm 0.06$ for the LFPP and HFHS groups respectively (mean $\pm$ s.d. across individual mice). Solid lines are fits to the data using MLE.
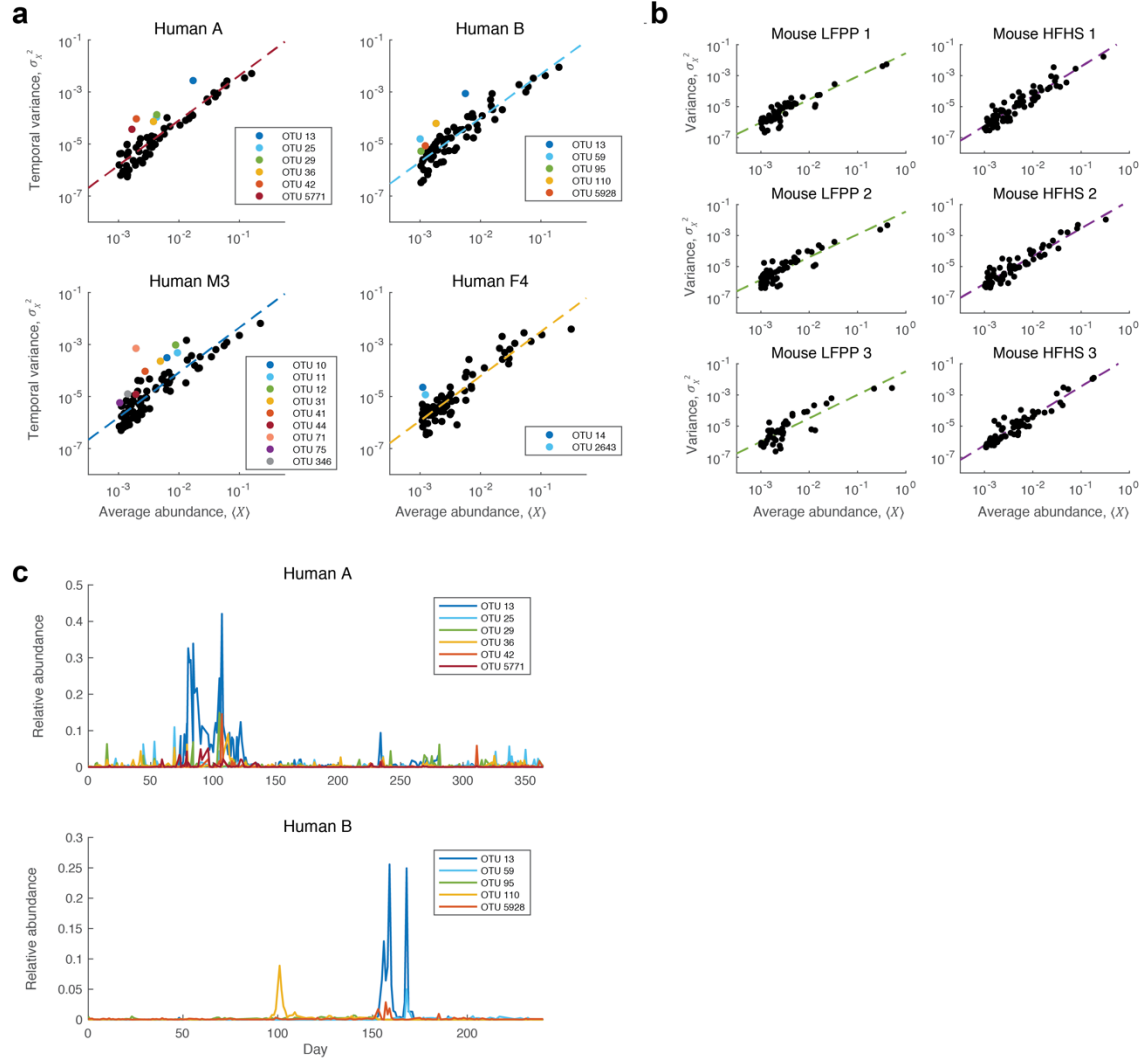
Supplementary Figure 6. Taylor's power law in the human and mouse gut microbiome. In humans and mice, average species abundances $\langle X \rangle$ scale with temporal variances σ_X^2 following Taylor's power law of the form $\sigma_X^2 \propto \langle X \rangle^\beta$. Each dot represents the mean and temporal variance of a single OTU. **(a)** Power law exponents in human individuals are β =1.66 $\pm$ 0.09, 1.60 $\pm$ 0.08, 1.71 $\pm$ 0.07, 1.71 $\pm$ 0.07 for A, B, M3, and F4 respectively (mean $\pm$ s.d., see Methods). Colored dots denote OTUs described in the main text whose abundances on any day exceeded the average abundance over all other days by over 25-fold (see Supplementary Table 1). **(b)** Power law exponents in mice are $\beta = 1.49 \pm 0.02$ and 1.86 ± 0.07 for LFPP and HFHS diets respectively (mean $\pm$ s.d. across individual mice). Dashed lines indicate least-squares regression fits to the data. **(c)** Relative abundances of spiking OTUs identified in **(a)** for two human subjects (A and B) whose lifestyles were closely documented over the time series reveal major events affecting the gut microbiota of both individuals. These include the travel of individual A to a developing country near day 100 and an enteric infection in individual B near day 150.

Supplementary Table 1. OTUs in humans with a single day abundance exceeding the average abundance over all others days by over 25-fold.

Human	OTU	Phylum	Class	Order	Family	Genus
A	13	Proteobacteria (100%)	Gammaproteobacteria (97%)	Enterobacteriales (85%)	Enterobacteriaceae (85%)	Escherichia/Shigella (37%)
A	25	Firmicutes (98%)	Clostridia (98%)	Clostridiales (98%)	Peptostreptococcaceae (93%)	Clostridium XI (71%)
A	29	Proteobacteria (100%)	Gammaproteobacteria (100%)	Pasteurellales (100%)	Pasteurellaceae (100%)	Haemophilus (76%)
A	36	Firmicutes (100%)	Negativicutes (100%)	Selenomonadales (100%)	Veillonellaceae (100%)	Veillonella (100%)
A	42	Firmicutes (100%)	Clostridia (99%)	Clostridiales (99%)	Clostridiaceae 1 (99%)	Clostridium sensu stricto (99%)
A	5771	Proteobacteria (100%)	Gammaproteobacteria (100%)	Enterobacteriales (95%)	Enterobacteriaceae (95%)	Salmonella (91%)
B	13	Proteobacteria (100%)	Gammaproteobacteria (97%)	Enterobacteriales (85%)	Enterobacteriaceae (85%)	Escherichia/Shigella (37%)
B	59	Actinobacteria (100%)	Actinobacteria (100%)	Coriobacteriales (100%)	Coriobacteriaceae (100%)	Eggerthella (100%)
B	95	Firmicutes (71%)	Clostridia (59%)	Clostridiales (55%)	Ruminococcaceae (23%)	Gemmiger (12%)
B	110	Firmicutes (67%)	Clostridia (60%)	Clostridiales (53%)	Ruminococcaceae (20%)	Butyricicoccus (11%)
B	5928	Firmicutes (99%)	Clostridia (99%)	Clostridiales (99%)	Lachnospiraceae (99%)	Oribacterium (60%)
M3	10	Verrucomicrobia (100%)	Verrucomicrobiae (100%)	Verrucomicrobiales (100%)	Verrucomicrobiaceae (100%)	Akkermansia (100%)
M3	11	Bacteroidetes (100%)	Bacteroidia (100%)	Bacteroidales (100%)	Bacteroidaceae (100%)	Bacteroides (100%)
M3	12	Proteobacteria (100%)	Gammaproteobacteria (98%)	Enterobacteriales (85%)	Enterobacteriaceae (85%)	Cronobacter (30%)
M3	31	Bacteroidetes (100%)	Bacteroidia (100%)	Bacteroidales (100%)	Porphyromonadaceae (100%)	Porphyromonas (99%)
M3	41	Firmicutes (53%)	Clostridia (45%)	Clostridiales (41%)	Clostridiales_Incertae Sedis XIII (7%)	Anaerovorax (7%)
M3	44	Firmicutes (86%)	Clostridia (86%)	Clostridiales (86%)	Ruminococcaceae (85%)	Oscillibacter (77%)
M3	71	Firmicutes (100%)	Bacilli (100%)	Lactobacillales (100%)	Streptococcaceae (100%)	Streptococcus (100%)
M3	75	Firmicutes (94%)	Clostridia (94%)	Clostridiales (94%)	Ruminococcaceae (93%)	Subdoligranulum (78%)
M3	346	Firmicutes (100%)	Clostridia (93%)	Clostridiales (93%)	Lachnospiraceae (92%)	Roseburia (86%)
F4	14	Bacteroidetes (100%)	Bacteroidia (99%)	Bacteroidales (99%)	Prevotellaceae (99%)	Prevotella (99%)
F4	2643	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Lachnospiraceae (100%)	Ruminococcus2 (94%)

Supplementary Table 2. OTUs in LFPP and HFHS mice with significantly higher or lower variability than expected from Taylor's power law

Mouse	OTU	Direction	Phylum	Class	Order	Family	Genus
HFHS1	4	High	Firmicutes (51%)	Clostridia (49%)	Clostridiales (45%)	Ruminococcaceae (16%)	Butyricicoccus (9%)
HFHS1	33	High	Firmicutes (61%)	Clostridia (58%)	Clostridiales (51%)	Ruminococcaceae (19%)	Butyricicoccus (8%)
HFHS1	36	High	Firmicutes (28%)	Erysipelotrichia (8%)	Erysipelotrichales (8%)	Erysipelotrichaceae (8%)	Allobaculum (3%)
HFHS1	55	High	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Lachnospiraceae (100%)	Robinsoniella (32%)
HFHS2	67	High	Firmicutes (38%)	Clostridia (27%)	Clostridiales (26%)	Clostridiaceae 3 (7%)	Brassicibacter (6%)
HFHS2	264	High	Firmicutes (53%)	Clostridia (49%)	Clostridiales (43%)	Lachnospiraceae (28%)	Robinsoniella (2%)
HFHS2	183	Low	Bacteroidetes (67%)	Sphingobacteriia (16%)	Sphingobacteriales (16%)	Cyclobacteriaceae (15%)	Indibacter (4%)
HFHS3	5	High	Firmicutes (95%)	Clostridia (92%)	Clostridiales (92%)	Lachnospiraceae (91%)	Clostridium XlVa (59%)
HFHS3	21	High	Firmicutes (98%)	Clostridia (98%)	Clostridiales (98%)	Lachnospiraceae (96%)	Ruminococcus2 (15%)
HFHS3	33	High	Firmicutes (61%)	Clostridia (58%)	Clostridiales (51%)	Ruminococcaceae (19%)	Butyricicoccus (8%)
HFHS3	2431	High	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Ruminococcaceae (98%)	Pseudoflavonifractor (71%)
LFPP1	237	Low	Bacteroidetes (84%)	Bacteroidia (61%)	Bacteroidales (61%)	Porphyromonadaceae (38%)	Barnesiella (2%)
LFPP1	364	Low	Bacteroidetes (86%)	Bacteroidia (77%)	Bacteroidales (77%)	Porphyromonadaceae (63%)	Barnesiella (5%)
LFPP2	93	High	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Clostridiaceae 1 (23%)	Anaerosporobacter (23%)
LFPP2	99	High	Firmicutes (83%)	Clostridia (73%)	Clostridiales (73%)	Ruminococcaceae (50%)	Clostridium IV (26%)
LFPP2	276	High	Firmicutes (99%)	Clostridia (98%)	Clostridiales (98%)	Lachnospiraceae (97%)	Dorea (30%)
LFPP2	237	Low	Bacteroidetes (84%)	Bacteroidia (61%)	Bacteroidales (61%)	Porphyromonadaceae (38%)	Barnesiella (2%)
LFPP3	16	High	Firmicutes (90%)	Clostridia (90%)	Clostridiales (90%)	Lachnospiraceae (86%)	Butyrivibrio (16%)
LFPP3	22	Low	Firmicutes (82%)	Clostridia (82%)	Clostridiales (82%)	Ruminococcaceae (55%)	Saccharofermentans (20%)
LFPP3	118	Low	Bacteroidetes (83%)	Bacteroidia (73%)	Bacteroidales (73%)	Porphyromonadaceae (46%)	Butyricimonas (19%)
LFPP3	237	Low	Bacteroidetes (84%)	Bacteroidia (61%)	Bacteroidales (61%)	Porphyromonadaceae (38%)	Barnesiella (2%)
LFPP3	364	Low	Bacteroidetes (86%)	Bacteroidia (77%)	Bacteroidales (77%)	Porphyromonadaceae (63%)	Barnesiella (5%)