

Supplementary Figure

Fig. S1. Body weight, and food intake of dams, and body weight of offspring. (A) Maternal body weight at baseline and prepregnancy. (B) Maternal energy intake. (C) Body weight of offspring from 1 week of age to 3 weeks of age. n=11 litters/group, one male offspring per litter. *P < 0.05 , HF vs. NC group.

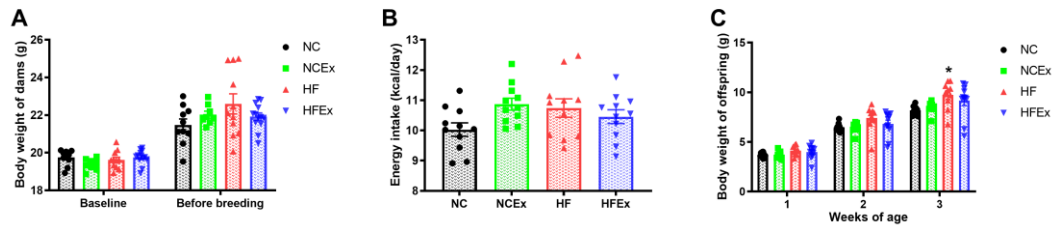
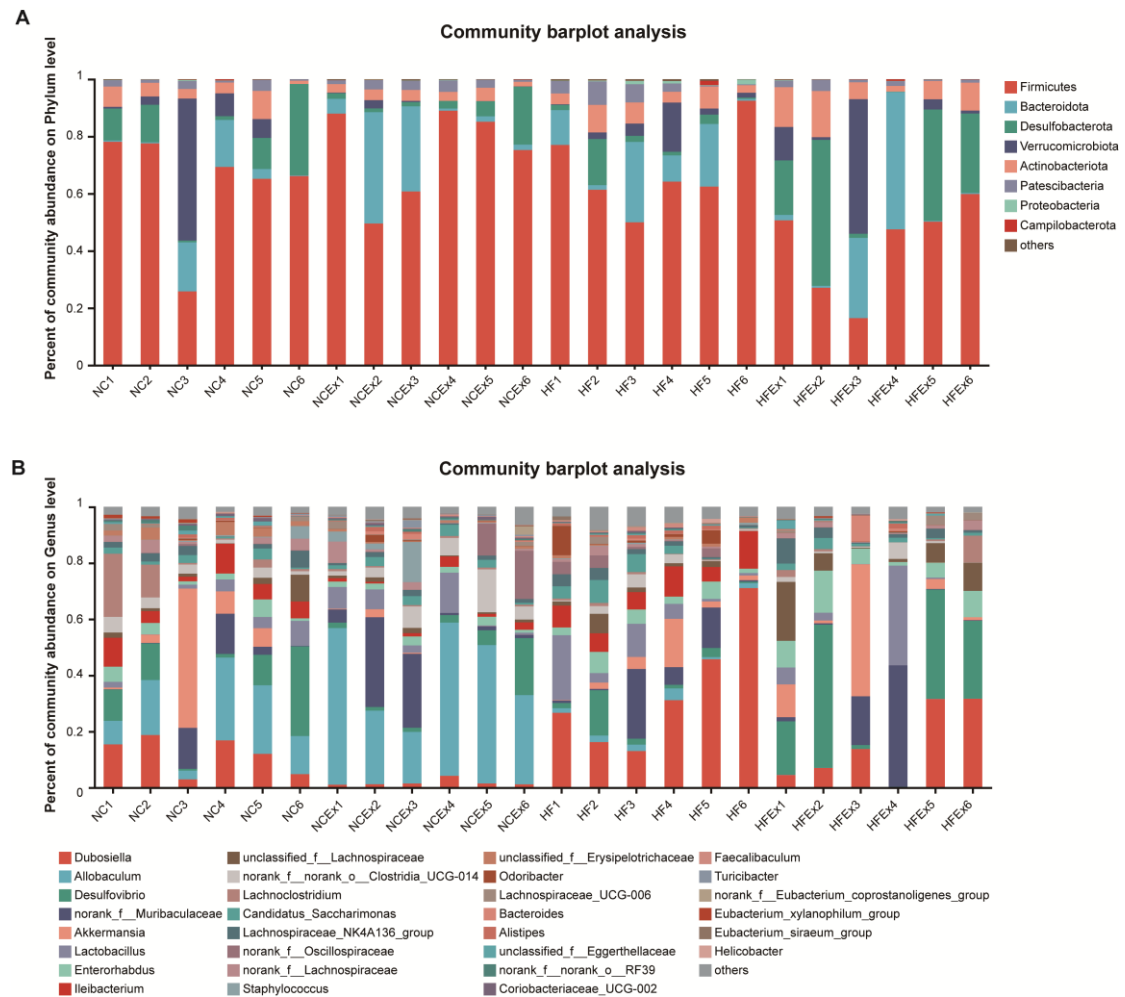


Fig. S2. Maternal exercise altered structures and composition of gut microbiota in offspring. (A) Relative abundance of the bacterial population at the phylum level of each mouse. (B) Relative abundance of the bacterial population at the genus level of each mouse.



Supplementary Tables

Table S1. Primer sequences of genes.

Genes	Forward	Reverse
G6Pc	CGACTCGCTATCTCCAAGTGA	GTTGAACCAGTCTCCGACCA
FBP1	CACCGCGATCAAAGCCATCT	AGGTAGCGTAGGACGACTTCA
FBP2	ACCCTGACCCGTTACGTTATG	ACATTCACGCTCCCCGAAATC
PCx	CTGAAGTTCCAAACAGTTTCGAGG	CGCACGAAACACTCGGATG
PCK1	CTGCATAACGGTCTGGACTTC	CAGCAACTGCCCCGTACTION
Mut	TTTTTGCTATCGCCCCATTACC	CCTCTGGGTTTTTGCCTTTCAG
β-actin	TATTGGCAACGAGCGGTTCC	GGCATAGAGGTCTTTACGGATGTC

G6P, glucose 6-phosphate; FBP1, fructose-1,6-bisphosphatase 1; FBP2, fructose-1,6-bisphosphatase 2; Pcx, pyruvate carboxylase; PCK1, phosphoenolpyruvate carboxykinase 1; Mut, methylmalonyl-coA mutase.

Table S2. Alpha diversity of gut microbiota community in offspring.

Index	NC	NCEx	HF	HFEx	P value (HF vs. NC)	P value (HFEx vs. HF)
Shannon	3.04±0.14	2.88±0.78	3.00±0.87	2.70±0.60	0.99	0.86
Simpson	0.13±0.06	0.20±0.12	0.18±0.18	0.19±0.09	0.89	0.99
Ace	348.60±31.27	344.40±28.60	365.90±49.89	320.80±33.69	0.85	0.18
Chao	340.60±33.22	341.60±28.03	362.40±51.92	327.10±36.70	0.76	0.41

Table S3. Differential species at the genus level among the four groups.

Species name	NC-Mean (%)	NCEx-Mean (%)	HF-Mean (%)	HFEx-Mean (%)	P value
g__Flavobacterium	0.000	0.000	0.014	0.000	0.000
g__Allorhizobium-Neorhizobium-Pararhizobium- Rhizobium	0.000	0.000	0.197	0.000	0.000
g__Roseomonas	0.000	0.000	0.015	0.000	0.000
g__Allobaculum	16.430	39.360	2.172	0.061	0.000
g__Turicibacter	0.230	0.807	0.000	0.001	0.000
g__Ileibacterium	6.374	1.733	8.314	0.012	0.000
g__Cyanobium_PCC-6307	0.000	0.000	0.007	0.000	0.000
g__Bifidobacterium	0.001	0.012	0.245	0.031	0.001
g__Faecalibaculum	0.113	0.391	0.667	0.031	0.001
g__unclassified_f__Erysipelotrichaceae	2.665	0.598	0.887	0.010	0.001
g__norank_f__T34	0.000	0.000	0.012	0.001	0.001
g__Limnohabitans	0.000	0.000	0.005	0.001	0.002
g__norank_f__Candidatus_Hepaticicola	0.000	0.000	0.018	0.000	0.003
g__Dubosiella	11.750	1.716	33.940	14.720	0.005
g__Prevotellaceae_NK3B31_group	0.018	0.001	0.009	0.001	0.010

g__Eubacterium_ventriosum_group	0.017	0.101	0.000	0.002	0.012
g__Coriobacteriaceae_UCG-002	0.541	0.539	0.247	0.084	0.013
g__unclassified_p__Firmicutes	0.007	0.039	0.001	0.000	0.013
g__Pluralibacter	0.000	0.001	0.007	0.000	0.013
g__Herbaspirillum	0.000	0.001	0.004	0.000	0.013
g__Anaerofustis	0.107	0.017	0.009	0.020	0.018
g__NK4A214_group	0.023	0.016	0.087	0.003	0.019
g__Anaerovorax	0.003	0.000	0.020	0.000	0.019
g__Aeromonas	0.000	0.000	0.207	0.000	0.020
g__Fournierella	0.000	0.000	0.012	0.000	0.020
g__Staphylococcus	0.925	3.385	0.305	0.047	0.028
g__Burkholderia-Caballeronia-Paraburkholderia	0.002	0.007	0.033	0.008	0.028
g__Clostridium_sensu_stricto_1	0.117	0.372	0.006	0.001	0.032
g__Eubacterium_xylanophilum_group	0.636	0.033	0.009	0.156	0.032
g__unclassified_c__Bacilli	0.102	0.087	0.076	0.003	0.035
g__norank_f__norank_o__Clostridia_UCG-014	3.150	6.486	1.992	1.572	0.038
g__Christensenellaceae_R-7_group	0.320	0.031	0.168	0.060	0.038
g__norank_f__norank_o__norank_c__Clostridia	0.002	0.003	0.045	0.003	0.049

Table S4. Functional predictions of bacterial communities by KEGG pathway database in offspring.

	Name	P value	NC- Mean (%)	NCEx- Mean (%)	HF- Mean (%)	HFEx- Mean (%)
KEGG-level 1	Metabolism	0.964	76.590	76.710	76.520	76.850
	Genetic Information Processing	0.132	8.502	8.509	8.774	8.224
	Environmental Information Processing	0.867	6.267	6.261	6.202	6.293
	Cellular Processes	0.774	3.870	3.810	3.648	3.942
	Human Diseases	0.337	3.125	3.089	3.204	3.067
	Organismal Systems	0.704	1.643	1.621	1.649	1.625
KEGG-level 2	Carbohydrate metabolism	0.044	10.620	11.080	10.780	10.170
	Amino acid metabolism	0.963	6.997	7.009	7.017	6.937
	Energy metabolism	0.138	4.205	4.147	4.185	4.423
	Metabolism of cofactors and vitamins	0.012	3.726	3.557	3.475	4.003
	Lipid metabolism	0.650	1.731	1.810	1.728	1.775
	Biosynthesis of other secondary metabolites	0.082	1.551	1.480	1.557	1.568
	Glycan biosynthesis and metabolism	0.609	1.557	1.362	1.533	1.641

	Metabolism of other amino acids	0.311	1.182	1.250	1.242	1.248
	Metabolism of terpenoids and polyketides	0.005	1.043	1.069	1.089	0.987
	Endocrine system	0.682	0.605	0.630	0.625	0.575
	Transport and catabolism	0.726	0.241	0.193	0.216	0.286
	Endocrine and metabolic disease	0.051	0.232	0.242	0.256	0.204
	Cancer: specific types	0.021	0.055	0.058	0.070	0.046
	Infectious disease: viral	0.005	0.054	0.056	0.069	0.044
	Circulatory system	0.024	0.000	0.000	0.003	0.000
	Signaling molecules and interaction	0.637	0.000	0.000	0.000	0.000
KEGG-level 3	Fatty acid degradation	0.001	0.002	0.016	0.012	0.001
	Synthesis and degradation of ketone bodies	0.001	0.034	0.072	0.056	0.025
	Photosynthesis - antenna proteins	0.002	0.001	0.010	0.005	0.000
	Tetracycline biosynthesis	0.002	0.001	0.001	0.006	0.001
	Valine, leucine and isoleucine degradation	0.002	0.020	0.030	0.030	0.011
	Geraniol degradation	0.003	0.000	0.000	0.000	0.000
	Lysine degradation	0.003	0.000	0.000	0.000	0.000

Chlorocyclohexane and chlorobenzene degradation	0.003	0.000	0.000	0.000	0.000
Furfural degradation	0.004	0.000	0.000	0.001	0.000
Tryptophan metabolism	0.005	0.016	0.022	0.023	0.011
Phenylalanine, tyrosine and tryptophan biosynthesis	0.006	0.000	0.000	0.002	0.000
Staurosporine biosynthesis	0.007	0.144	0.199	0.167	0.155
Starch and sucrose metabolism	0.007	0.001	0.000	0.002	0.002
Lipoarabinomannan (LAM) biosynthesis	0.008	0.125	0.206	0.162	0.118
Arachidonic acid metabolism	0.008	0.296	0.277	0.264	0.351
Chloroalkane and chloroalkene degradation	0.008	0.000	0.000	0.001	0.000
C5-Branched dibasic acid metabolism	0.009	0.015	0.021	0.024	0.008
Carbon fixation in photosynthetic organisms	0.009	0.015	0.021	0.024	0.008
Biotin metabolism	0.009	0.000	0.001	0.006	0.000
Retinol metabolism	0.010	0.000	0.000	0.000	0.000
Terpenoid backbone biosynthesis	0.011	0.053	0.055	0.059	0.043
Indole alkaloid biosynthesis	0.011	0.053	0.055	0.059	0.043

Sesquiterpenoid and triterpenoid biosynthesis	0.012	0.025	0.033	0.026	0.016
Sulfur metabolism	0.014	0.025	0.034	0.029	0.016
Isoflavonoid biosynthesis	0.014	0.000	0.000	0.001	0.000
Flavone and flavonol biosynthesis	0.014	0.112	0.149	0.121	0.106
Isoquinoline alkaloid biosynthesis	0.015	0.000	0.000	0.000	0.000
Betalain biosynthesis	0.015	0.000	0.000	0.004	0.000
Drug metabolism - cytochrome P450	0.015	0.000	0.000	0.004	0.000
Steroid degradation	0.016	0.000	0.000	0.001	0.000
Biosynthesis of vancomycin group antibiotics	0.016	0.000	0.000	0.001	0.000
Biosynthesis of type II polyketide products	0.016	0.000	0.000	0.001	0.000
Basal transcription factors	0.016	0.000	0.000	0.001	0.000
Spliceosome	0.016	0.000	0.000	0.001	0.000
Bacterial secretion system	0.016	0.000	0.000	0.001	0.000
Homologous recombination	0.016	0.000	0.000	0.001	0.000
Calcium signaling pathway	0.016	0.000	0.000	0.001	0.000
p53 signaling pathway	0.016	0.000	0.000	0.001	0.000
Peroxisome	0.016	0.000	0.000	0.001	0.000

Apoptosis - multiple species	0.016	0.000	0.000	0.001	0.000
Cardiac muscle contraction	0.016	0.000	0.000	0.001	0.000
Dorso-ventral axis formation	0.016	0.000	0.000	0.001	0.000
Platelet activation	0.016	0.000	0.000	0.001	0.000
NOD-like receptor signaling pathway	0.018	0.000	0.000	0.000	0.000
RIG-I-like receptor signaling pathway	0.018	0.000	0.000	0.000	0.000
Retrograde endocannabinoid signaling	0.019	0.003	0.002	0.008	0.004
Type II diabetes mellitus	0.021	0.493	0.526	0.516	0.465
Cushing syndrome	0.022	0.000	0.000	0.000	0.000
Type I diabetes mellitus	0.022	0.272	0.246	0.246	0.273
Parkinson disease	0.023	0.055	0.058	0.068	0.046
Huntington disease	0.024	0.003	0.013	0.009	0.003
Bacterial invasion of epithelial cells	0.024	0.000	0.000	0.003	0.000
Pertussis	0.024	0.026	0.016	0.017	0.049
Yersinia infection	0.025	0.000	0.000	0.000	0.000
Chagas disease (American trypanosomiasis)	0.025	0.000	0.000	0.000	0.000
African trypanosomiasis	0.026	0.714	0.850	0.871	0.400

Hepatitis C	0.026	0.588	0.596	0.607	0.541
Hepatitis B	0.027	0.000	0.000	0.000	0.000
Measles	0.030	0.555	0.512	0.527	0.643
Human cytomegalovirus infection	0.030	0.108	0.113	0.111	0.092
Influenza A	0.032	0.214	0.273	0.236	0.208
Kaposi sarcoma-associated herpesvirus infection	0.032	1.288	1.350	1.368	1.027
Herpes simplex virus 1 infection	0.033	0.950	0.961	1.010	0.881
Epstein-Barr virus infection	0.034	0.000	0.000	0.001	0.000
Human immunodeficiency virus 1 infection	0.034	0.000	0.000	0.000	0.000
Chemical carcinogenesis	0.035	0.000	0.000	0.001	0.000
Colorectal cancer	0.035	0.000	0.000	0.000	0.000
Renal cell carcinoma	0.037	0.053	0.055	0.059	0.045
Bladder cancer	0.039	0.394	0.323	0.342	0.512
Small cell lung cancer	0.039	0.000	0.000	0.000	0.000
Hepatocellular carcinoma	0.047	0.088	0.111	0.089	0.101
Viral myocarditis	0.049	0.153	0.132	0.127	0.156