

Figure S1. The effect of HFD and OFS supplementation on postprandial gut microbiota diversity and bacterial profile. (A) Alpha diversity measured as an ASV species richness of the gut microbiota from the cecum of chow, HFD, and HFD+OFS rats (n=4-6 per group at each timepoint) 0-8h following a meal. *p<0.05 compared to HFD. (B) Bray-Curtis dissimilarity based NMDS of chow, HFD, and HFD+OFS rats (n=4-6 per group at each timepoint) PERMANOVA (ADONIS, permutations = 999) for diet p<0.001, for time p=0.925, for diet:time p<0.001. (C) Average relative abundance of bacterial families from chow, HFD, and HFD+OFS rats (n=4-6 per group at each timepoint) 0-8h postprandially. (D) Average relative abundance of bacterial genera from chow, HFD, and HFD+OFS rats (n=4-6 per group at each timepoint) 0-8h postprandially.

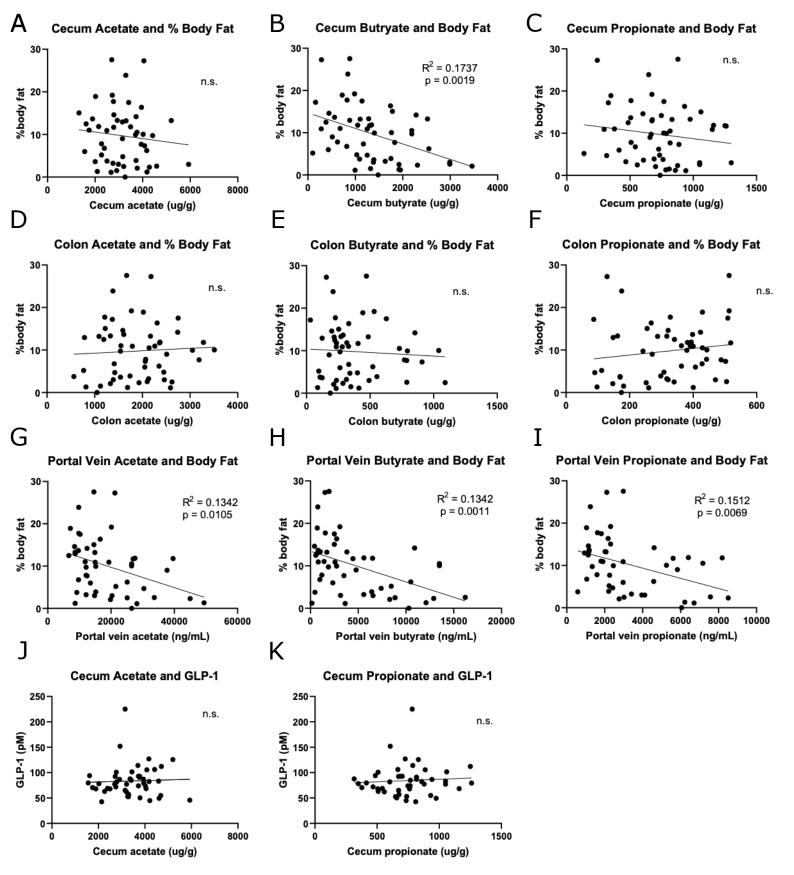


Figure S2. Correlation of short chain fatty acids with body fat and glucagon-like peptide 1. Association (simple linear regression) between percent body fat and cecum acetate (A), butyrate (B), and propionate (C) 4-8h postprandially, colon acetate (D), butyrate (E), and propionate (F) 4-8h postprandially, and portal vein acetate (G), butyrate (H), and propionate (I) 4-8h postprandially. Association between portal vein glucagon-like peptide 1 (GLP-1) and cecum acetate (J) and propionate (K) 4-8h postprandially. Significance and coefficient of determination (R²) values presented on graphs with p<0.05.

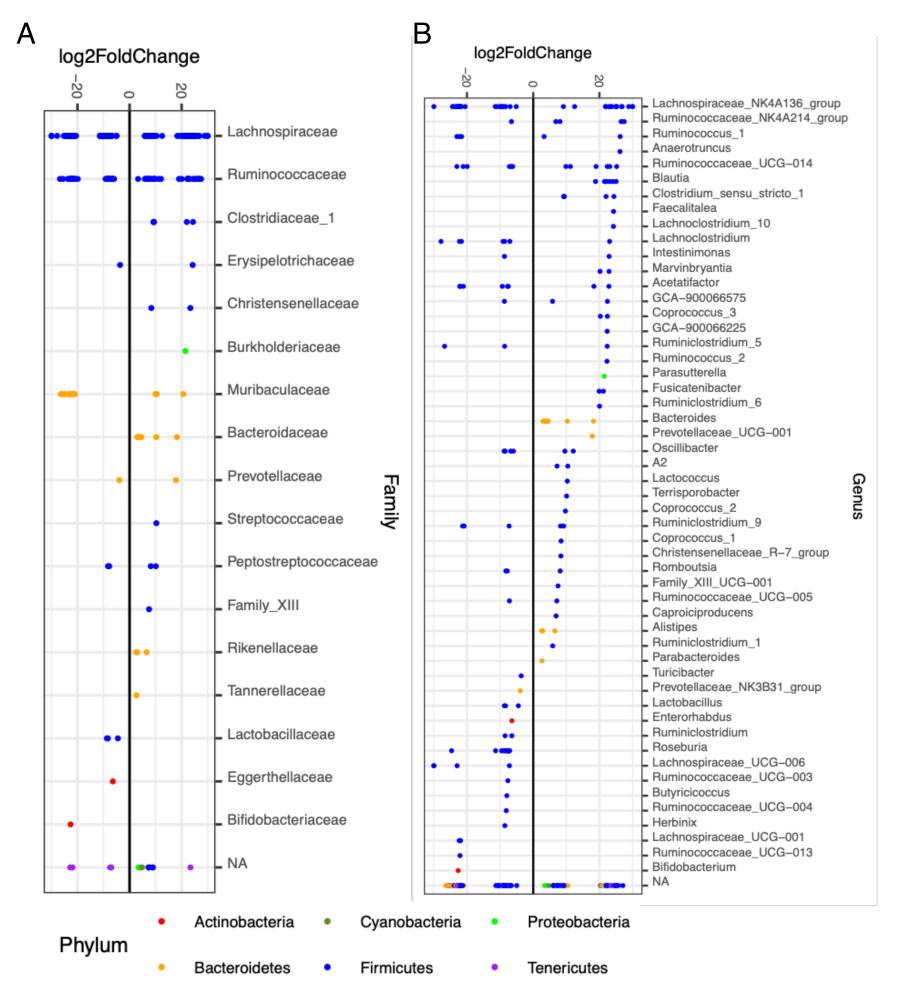


Figure S3. Comparison of the cecal microbiota between healthy chow and obese HFD-fed rats. Significant (corrected p<0.05, Wald test) microbiota differences at the family (A) and genus (B) level in HFD-fed rats compared to chow determined by DESeq2 analysis.

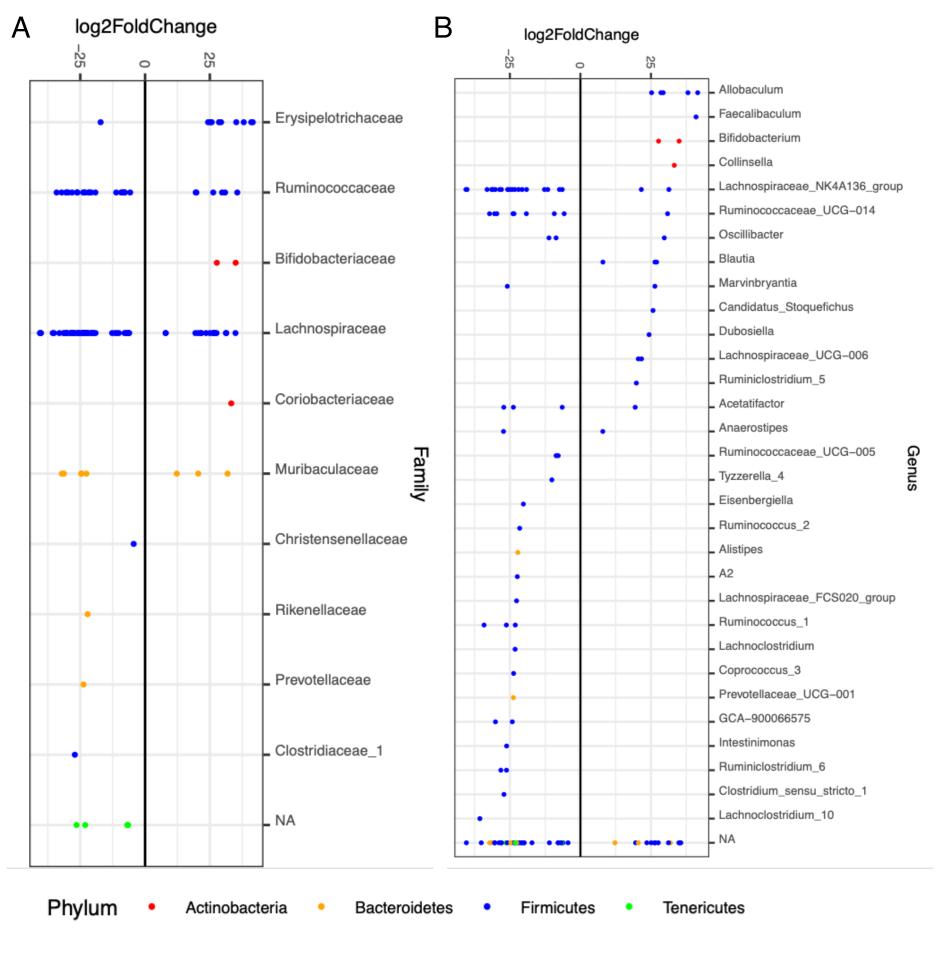


Figure S4. Comparison of the cecal microbiota between obese HFD-fed and OFS supplemented rats. Significant (corrected p<0.05, Wald test) microbiota differences at the family (A) and genus (B) level in HFD-fed rats supplemented with OFS compared to HFD determined by DESeq2 analysis.