Figure S1

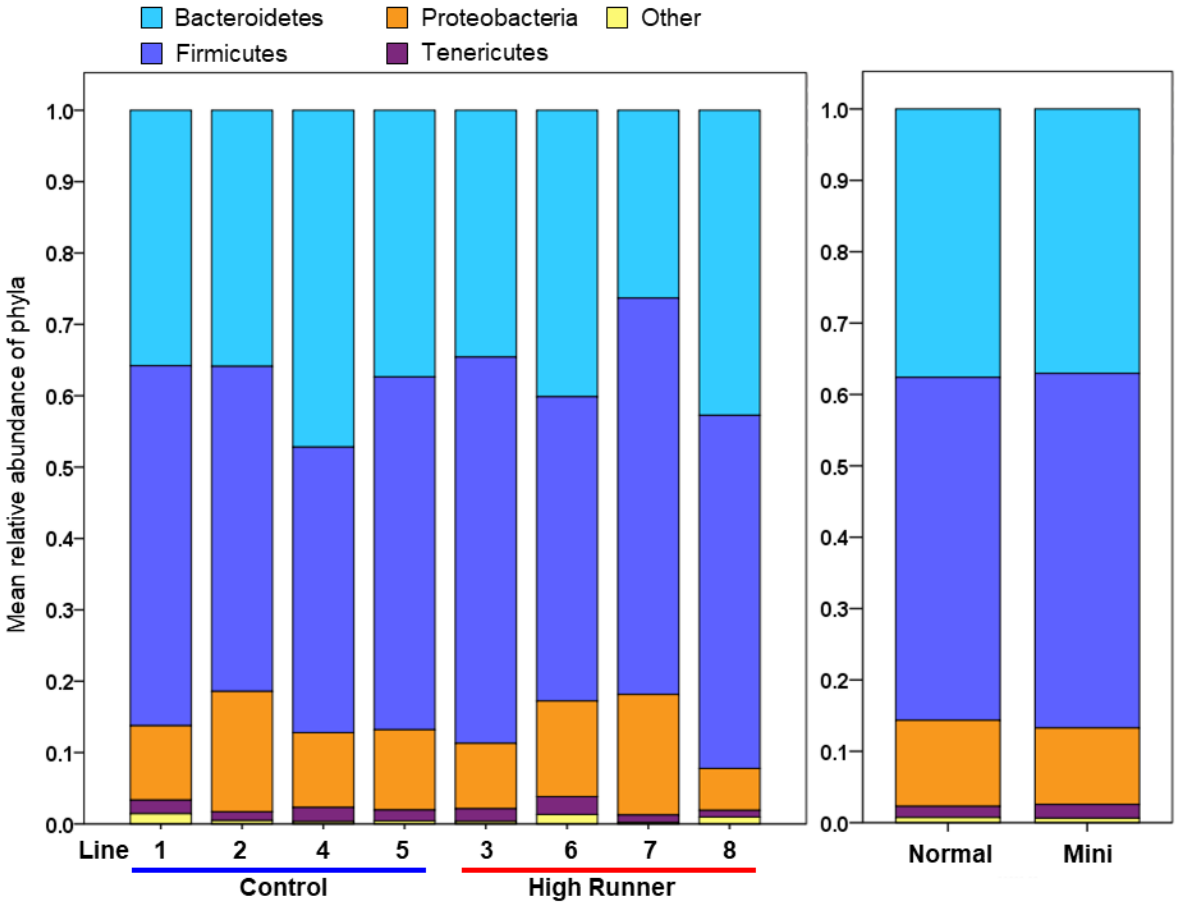

Fig. S1. Community composition of the weanling gut microbiome for all experimental mice (N=95) was dominated by Firmicutes (48.4 ± 14%) (mean ± S.D.) and Bacteroidetes (37.5 ± 17.1%), with additional phyla being much less abundant: Proteobacteria (11.8 ± 8.7%), Tenericutes (1.6 ± 2%), Cyanobacteria (0.28 ± 0.53%), Verrucomicrobia (0.24 ± 1.1%), Actinobacteria (0.09 ± 0.16%), Deferribacteres (0.08 ± 0.24%), Fusobacteria (0.0002 ± 0006%), and TM7 (0.0001 ± 0.0004%).

Figure S2

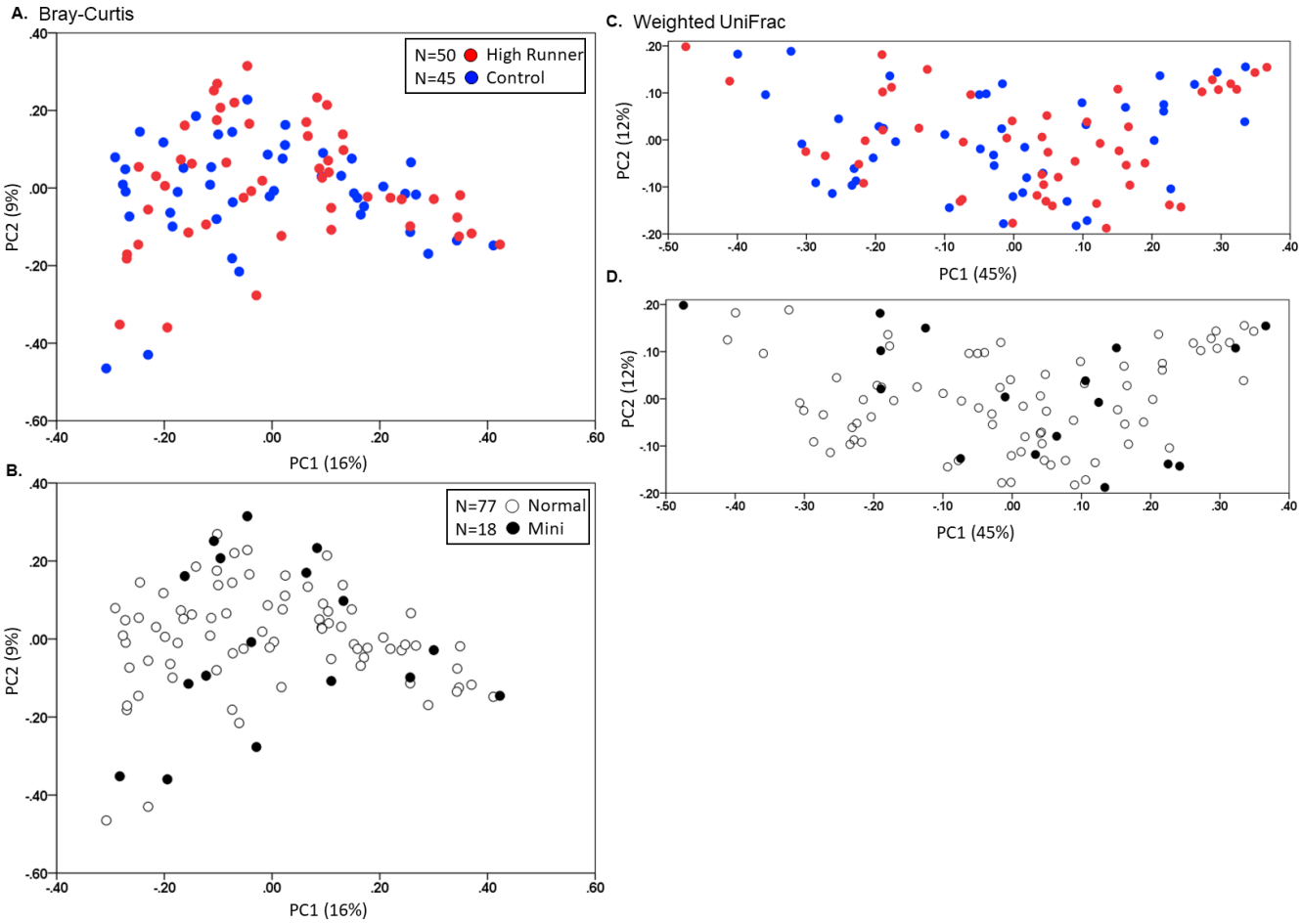

Fig. S2. Beta diversity (among experimental groups) of the weanling fecal microbiome based on 16S rRNA sequence data. A and B are PCoA plots based on Bray-Curtis distances, which consider bacterial OTU sequence relative abundances. C and D are PCoA plots based on weighted UniFrac distances, which consider both bacterial OTU sequence relative abundances and phylogenetic distances. PERMANOVAs based on Bray-Curtis or weighted UniFrac distance matrices indicated no statistically significant separation based on either linetype (Bray-Curtis: R^2=0.0147, P=0.108, weighted UniFrac: R^2=0.0116, P=0.307) or mini-muscle status (Bray-Curtis: R^2=0.009, P=0.638, weighted UniFrac: R^2=0.005, P=0.773).

Figure S3

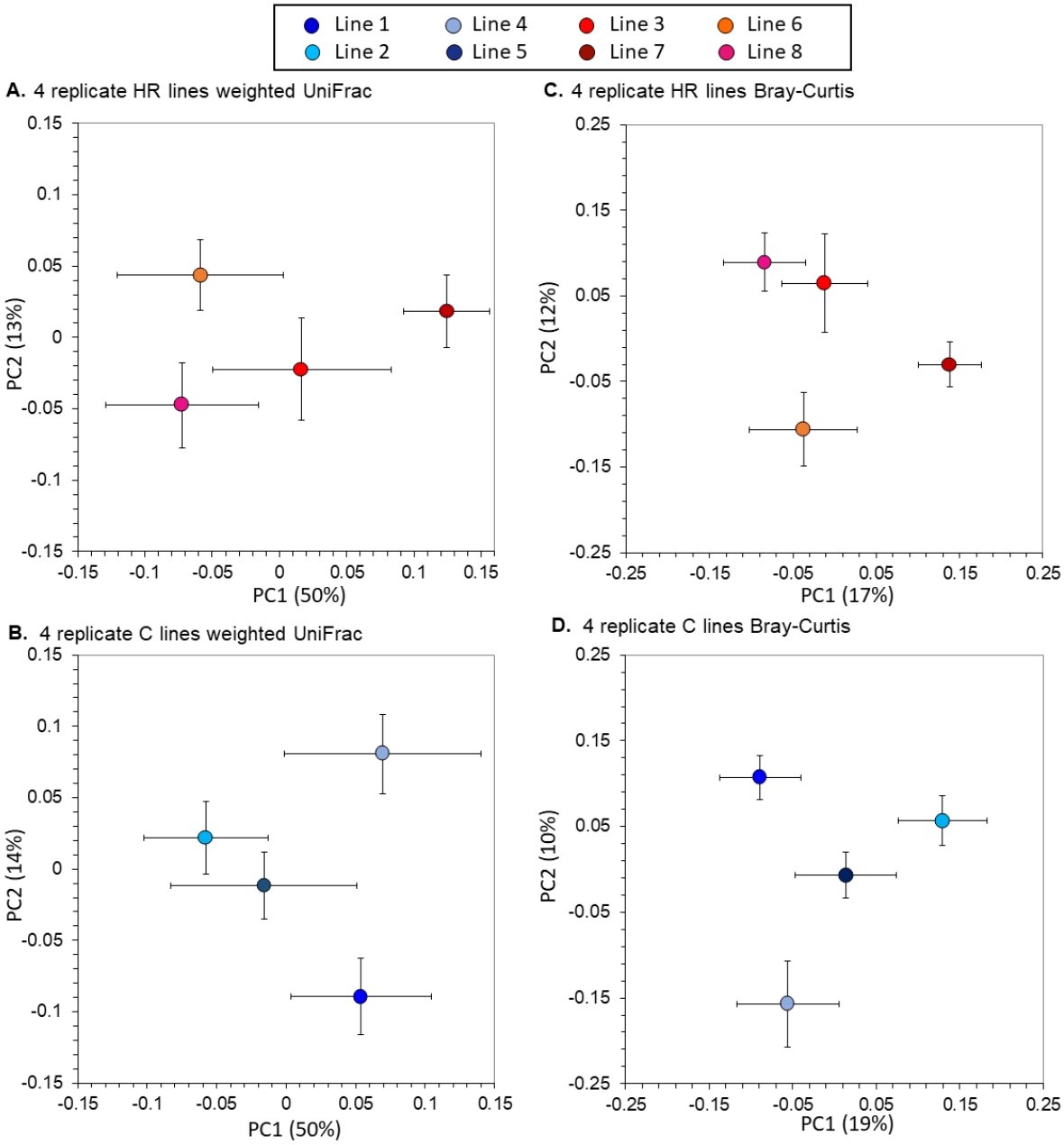

Fig. S3. PCoA plots from separate weighted UniFrac and Bray-Curtis analyses of the 4 HR lines (lab designations 3,6,7,8: A and C) and of the 4 C lines (lab designations 1,2,4,5: B and D). Values are means and standard errors for scores on PCoA axes. Separately, we used PERMANOVAs to test for significant separation among the 4 replicate HR lines and among the 4 non-selected C lines. Differences among the 4 replicate C lines were statistically significant based on Bray-Curtis (R^2=0.051, P=0.005), but not among the 4 replicate HR lines (R^2=0.014, P=0.839). Weighted UniFrac indicated no significant separation among replicate lines for either linetype (HR lines: R^2=0.005, P=0.957; C lines: R^2=0.030, P=0.228).