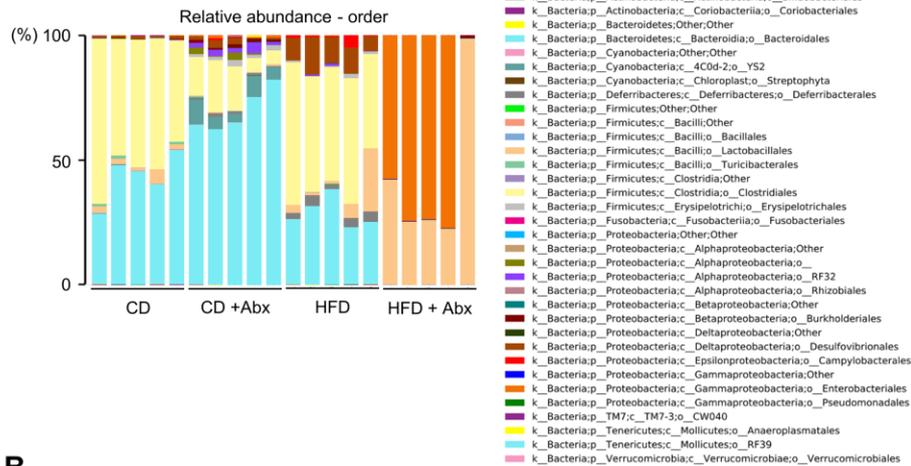
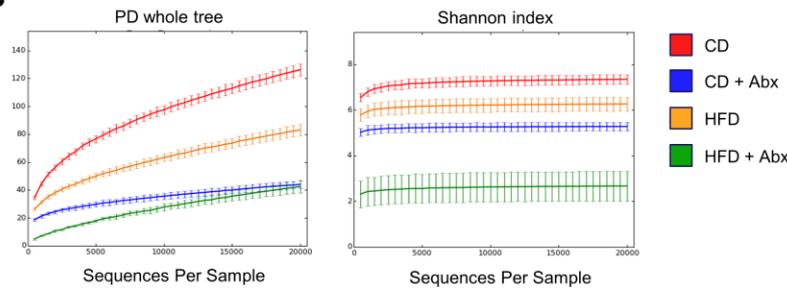


# Supplementary Figure S2.

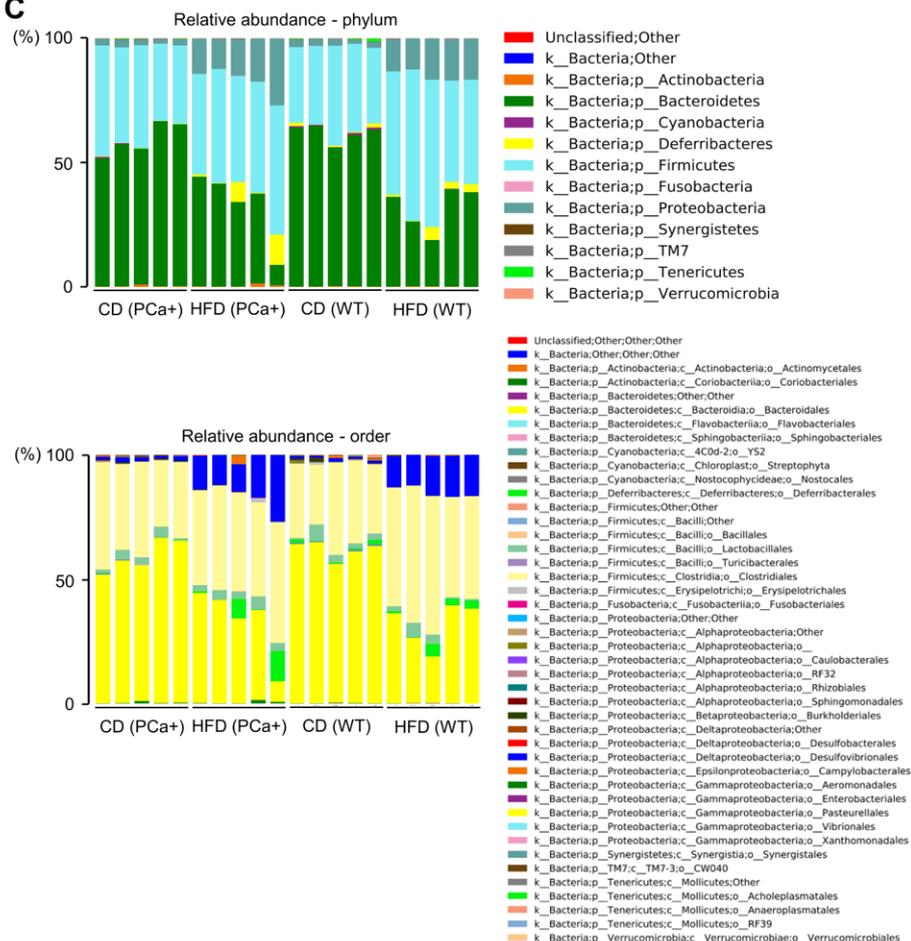
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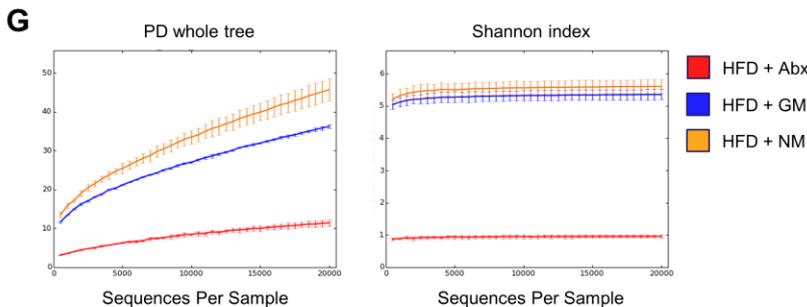
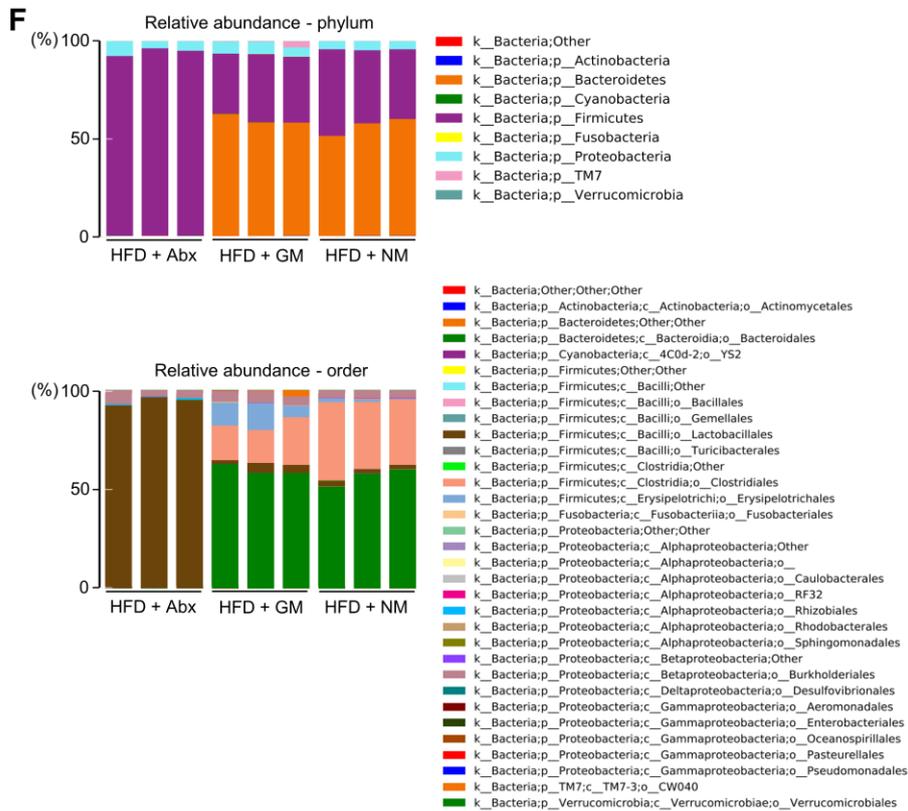
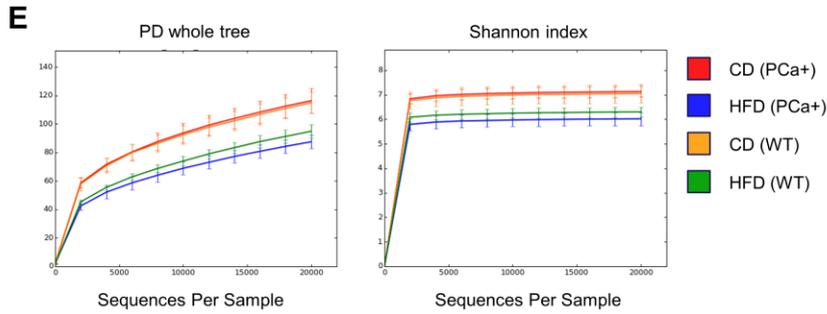
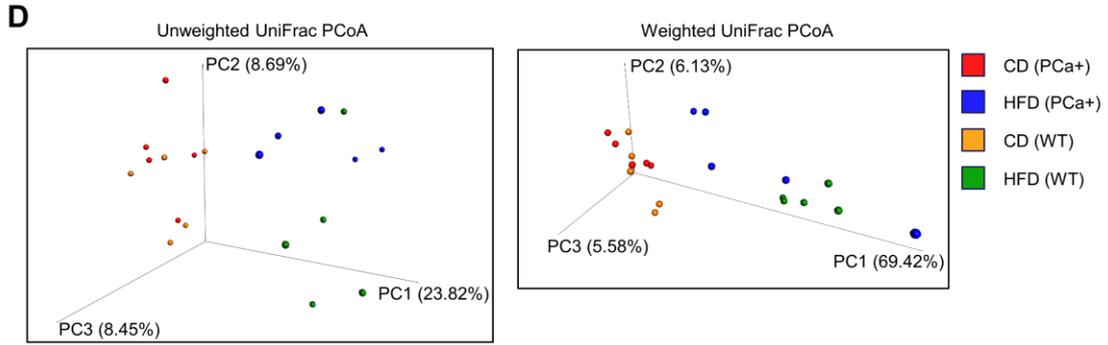


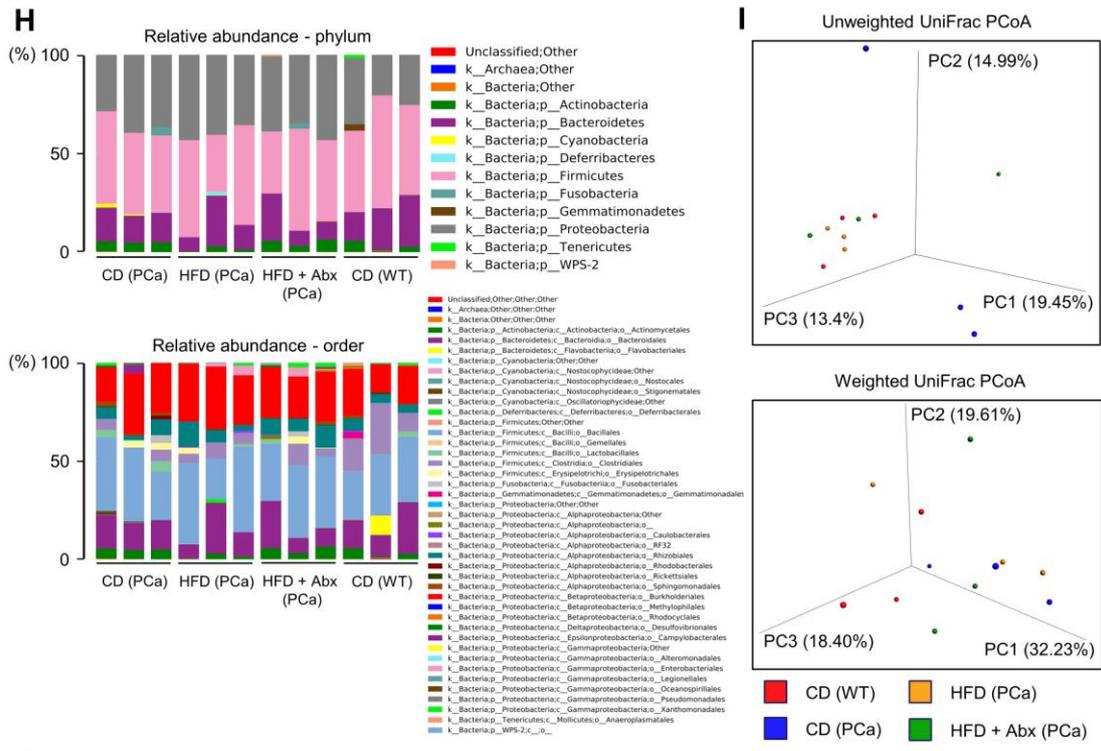
**B**



**C**







**Supplementary Fig. S2**

Variation in the composition of gut and prostate tissue microbiota. **(A)** Relative abundance of taxonomic classifications at the order level in fecal samples from CD, CD + Abx, HFD, and HFD + Abx PCa mice. **(B)** Rarefaction analysis of the profiling data sets from the gut microbiota of CD, CD + Abx, HFD, and HFD + Abx PCa mice (n = 5). **(C)** Relative abundance of taxonomic classifications at the phylum (upper) and order (lower) levels in fecal samples from CD and HFD PCa mice, and CD and HFD WT mice. **(D)** PCoA of the profiling data from the gut microbiota of CD and HFD PCa mice, and CD and HFD WT mice (based on UniFrac distance). **(E)** Rarefaction analysis of the profiling data sets from the gut microbiota of CD and HFD PCa mice, and CD and HFD WT mice (n = 5). **(F)** Relative abundance of taxonomic classifications at the phylum (upper) and order (lower) levels in fecal samples from Abx, GM, and NM-administered HFD PCa mice. **(G)** Rarefaction analysis of the profiling data sets from the gut microbiota of Abx, GM, and NM-administered HFD PCa mice (n = 3). **(H)** Relative abundance of taxonomic classifications at the phylum (upper) and order (lower) levels in prostate tissue from CD, HFD, and HFD + Abx PCa mice and CD WT mice. **(I)** PCoA of the profiling data from the prostate tissue microbiota of CD, HFD, and HFD + Abx PCa mice, and CD WT mice (based on UniFrac distance). **(J)** Rarefaction analysis of the profiling data sets from the prostate tissue microbiota of CD, HFD, and HFD + Abx PCa mice, and CD WT mice (n = 3). The rarefaction curves represent PD and Shannon index vs. sequences per sample. PD: phylogenetic diversity.