



Supplement 9: Complex proteins did not reduce the influence of fiber source on gut microbiome composition. Samples were rarefied a constant depth of 12274 sequences for alpha and beta diversity calculations, while relative abundance was used to visualize phylum-level composition. (A) depicts phyla relative abundance. NMDS ordinations were generated for (B) weighted and (C) unweighted Bray-Curtis dissimilarity and assessed for significance with PERMANOVA. Alpha diversity measures (D) observed ASVs, (E) Shannon index, and (F) Pielou's evenness are plotted with boxplots and statistics were calculated using Kruskal test. MCC: microcrystalline cellulose; S: standard diet; KT: Kruskal test