



**Supplementary Figure 1. F4 intake on CUS-exposed animals changes in caecum bacterial community.**

(A-B) The richness (Chao 1, A) and diversity (Simpson's index, B) of caecum bacterial community in each group. (C-E) Principal coordinate analysis (PCoA) plots of caecal bacterial community in each group. (F) Average relative abundance of the genus level of taxonomy in each group. (G-H) LEfSe (Linear discriminant analysis Effect Size) LEfSe analysis of caecum microbiota in each group. Cladogram generated by LEfSe indicating differences at phylum, class, and family levels. Regions in blue indicate taxa enriched control group, green indicate taxa enriched CUS group and red indicate taxa enriched F4 treated group. Differing taxa are listed under the cladogram. Bar graph showing LDA scores. Significance is determined using default parameters (Kruskal Wallis test  $p < 0.05$  and LDA score  $> 2$ ).