



Supplemental Figure 1. Beta-diversity clustering of all four mouse groups stratified by sex | PCA plot comparing beta-diversity of HLA-DR3, HLA-DQ8, HLA-DR3.DQ8 transgenic mice and AE-KO control mice at the genus level demonstrated similar microbiota compositions in both sexes within each group. Axis 1 and 2 are the first and second principal components, respectively, and represent the most and second-most amount of variation in the bacterial abundance data between all the samples.