**A**

B

Supplemental Figure 1. Oral bacterial species diversity was similar between wild type and AD mice. Oral swabs were taken from male and female WT, App^{NL-G-F}, APP/PS1, and APP$^{-/-}$ mice for 16S rRNA sequencing. The overall species diversity (Shannon Diversity), determined by both richness and evenness, and the Chao1 Richness Estimate (number of distinct organisms) were used to examine male and female WT, App^{NL-G-F}, APP/PS1, and APP$^{-/-}$ relative bacterial abundance. Data are graphed as mean values +/- SEM, n=3-7. Statistical differences were calculated by one-way ANOVA with Tukey post-hoc analysis.
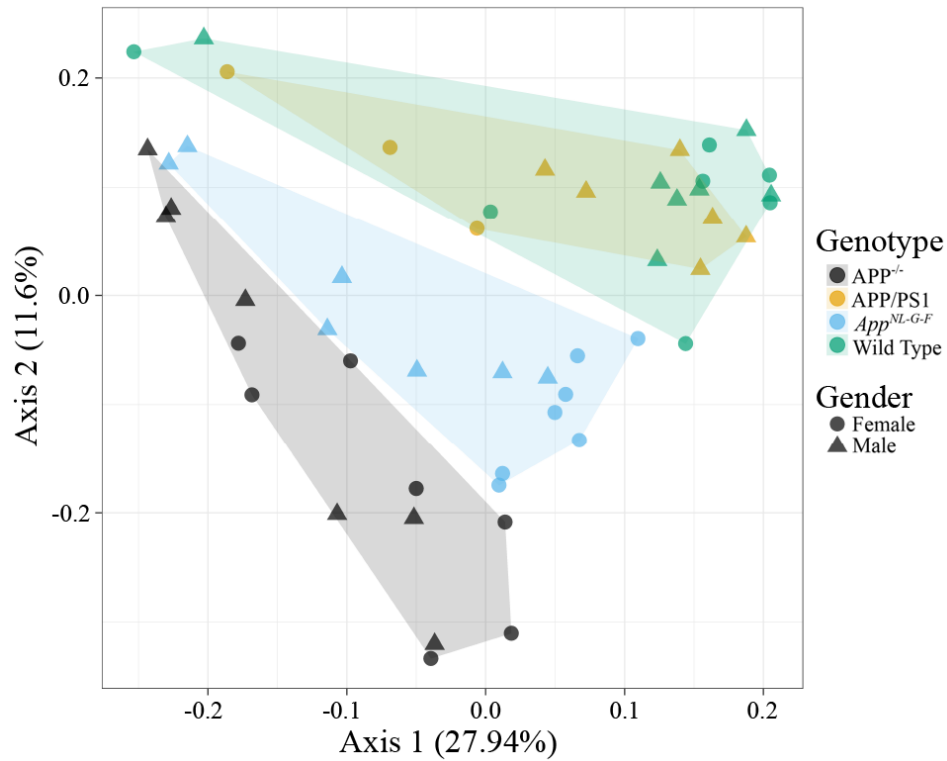
Supplemental Figure 2. APP$^{-/-}$ and App^{NL-G-F} mouse oral microbiome composition was distinct from WT and APP/PS1 mice. Oral swabs were taken from male and female WT, App^{NL-G-F}, APP/PS1, and APP$^{-/-}$ mice for 16S rRNA sequencing. Principal Coordinate Analysis based on unweighted Unifrac distances was graphed to demonstrate how different oral microbial compositions were between each group (n=3-7).