



**S4 Fig. Only subtle microbiota population changes in *Cd4<sup>cre</sup>Ahr<sup>fl/fl</sup>* mice (A) PCA plot and (B) microbiome composition at the genus level obtained from 16S sequencing performed on feces collected from cohoused animals. (Males; n=6/group) (C) PCA plot and (D) microbiome composition at the genus level obtained from 16S sequencing performed on feces collected from separately housed animals. (Males and Females; n= 10/group) (E) PCA plot and (F) microbiome composition at the genus level obtained from 16S sequencing performed on cecum collected from separately housed animals. (Males and Females; n=12/group)**