

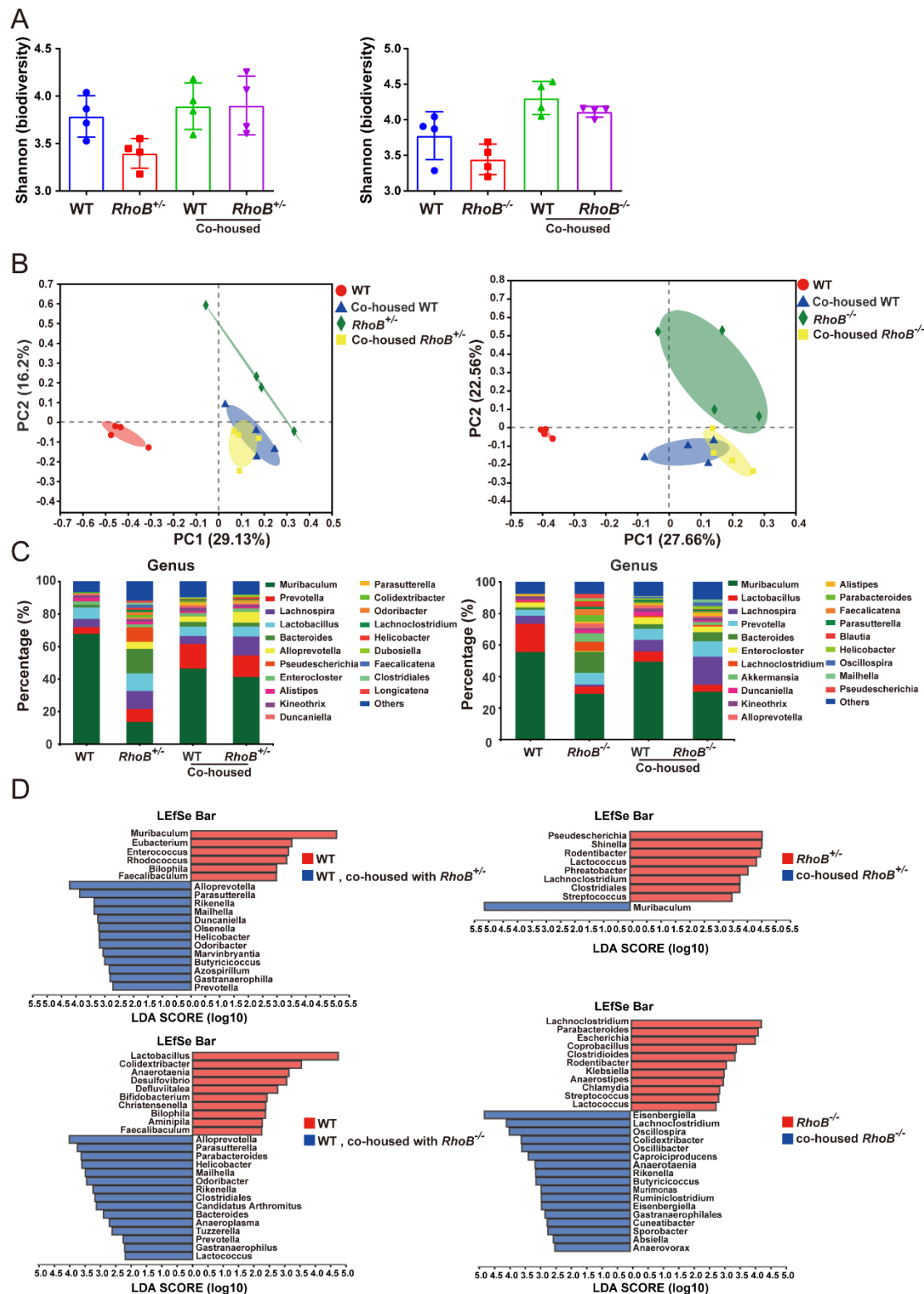


Figure S7. The microbiota composition in the feces from WT mice shifts toward that of $RhoB$ -deficient mice after cohousing. Stool samples from WT and $RhoB$ -deficient mice before and after cohousing were collected and analyzed by 16S rRNA gene sequencing ($n = 4$). **(A)** Analysis of the Shannon diversity index of microbiota in the indicated genotypes. **(B)** PCoA analysis of microbiota. **(C)** Relative abundance of fecal microbiota at the genus level. **(D)** LefSe analysis of distinctive microbiota composition as indicated.