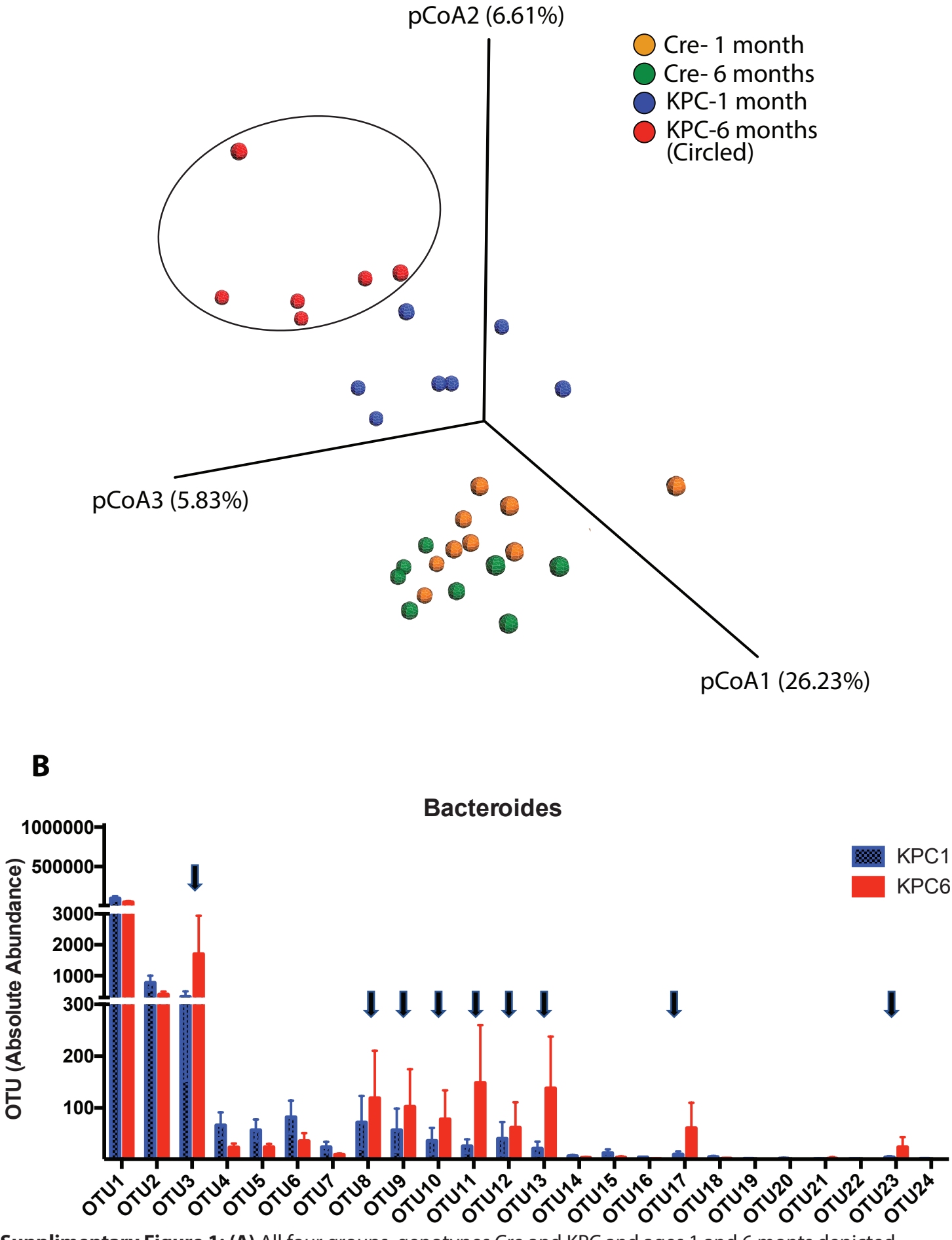
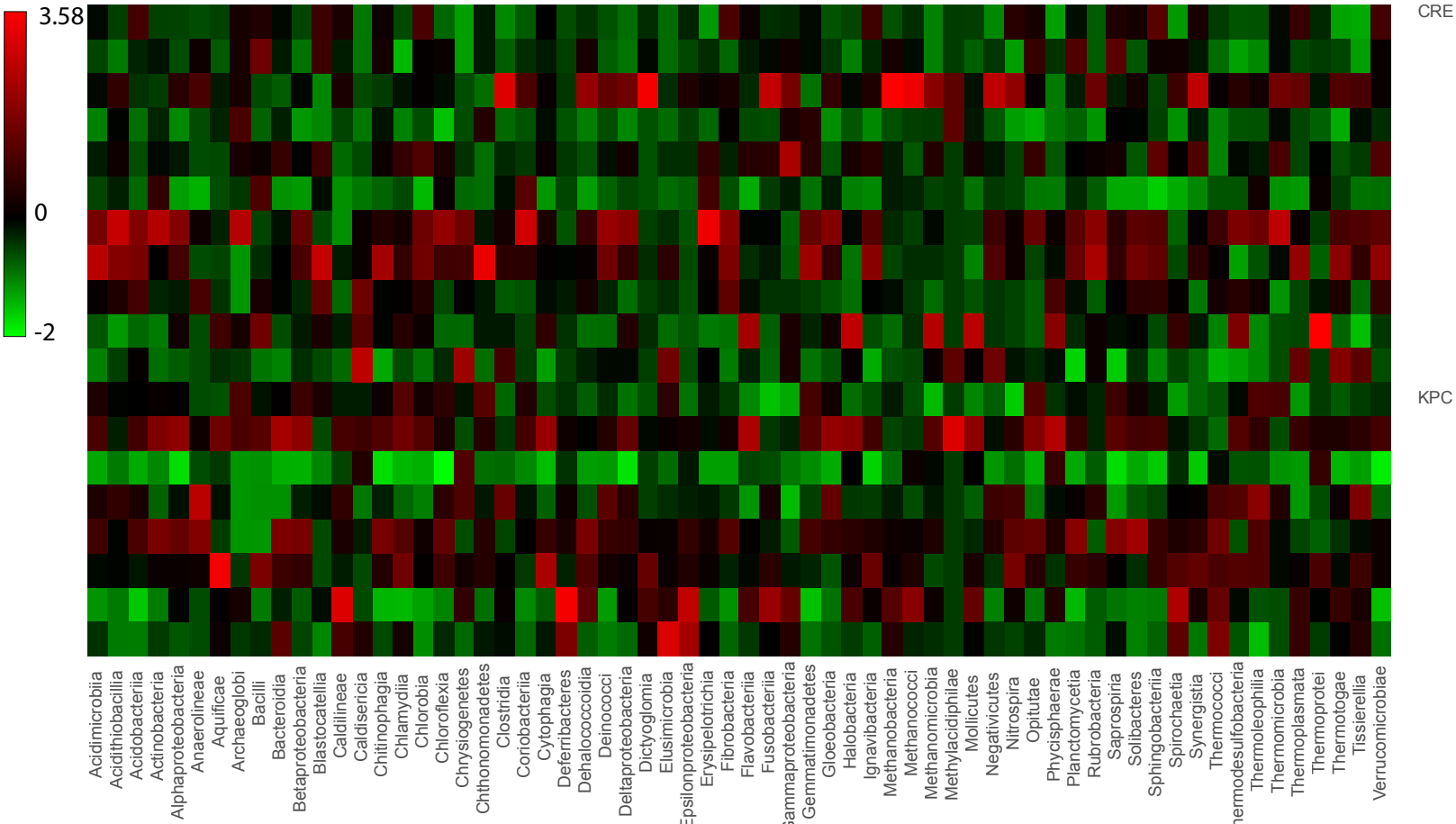
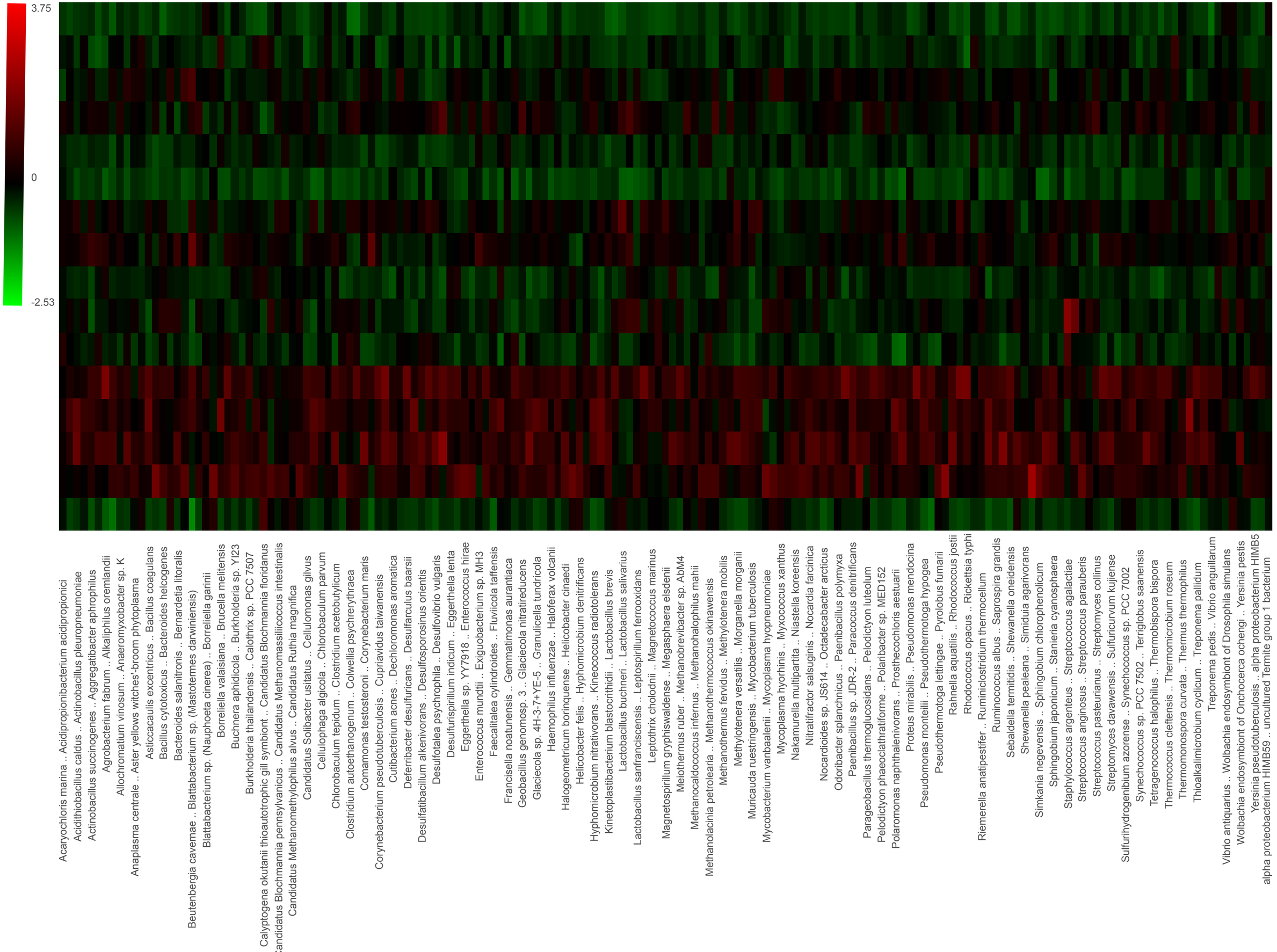



**Supplimentary Figure 1: (A)** All four groups, genotypes Cre and KPC and ages 1 and 6 monts depicted together in a Bray-Curtis pCoA plot. As shown in Figure 1 E-F, there is no perceptible change in Cre microbiome 1 and 6 months, KPC microbiome clusters separately for the age-groups. **(B)** Several OTUs mapping to the genus *Bacteroides* showing increased or decreased relative abundance between 1 and 6 months old KPC microbiome. Overall output shows "no change". Hence, deeper analysis of microbial species, with higher species-level identification is the only way to decipher the actual role of microbiota in host health and disease.

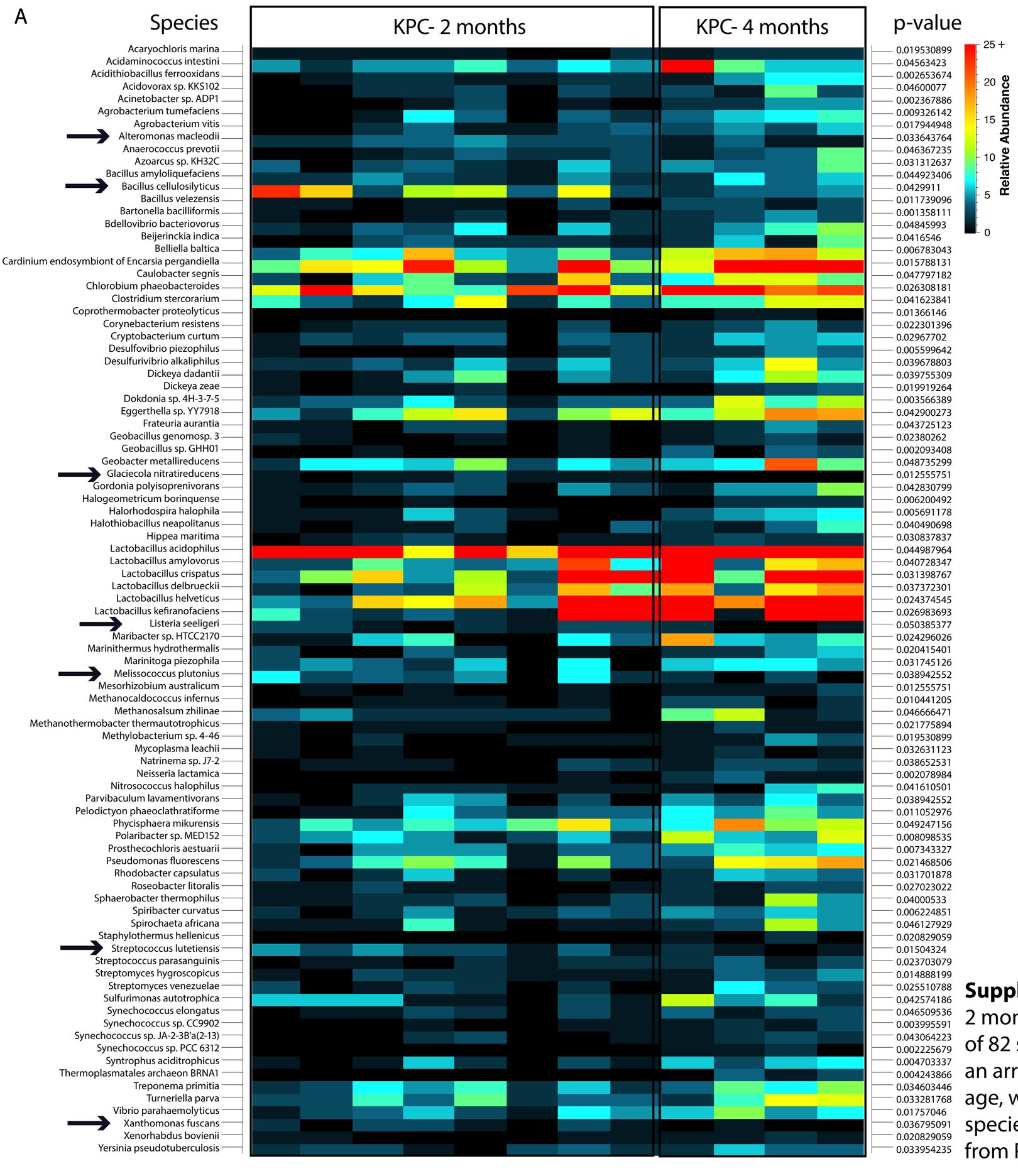



**Supplementary Figure 2:** Heatmap of bacterial classes at two months age in 'Cre' and 'KPC' gut microbiome. There is an even spread of the classes within the two genotypes.

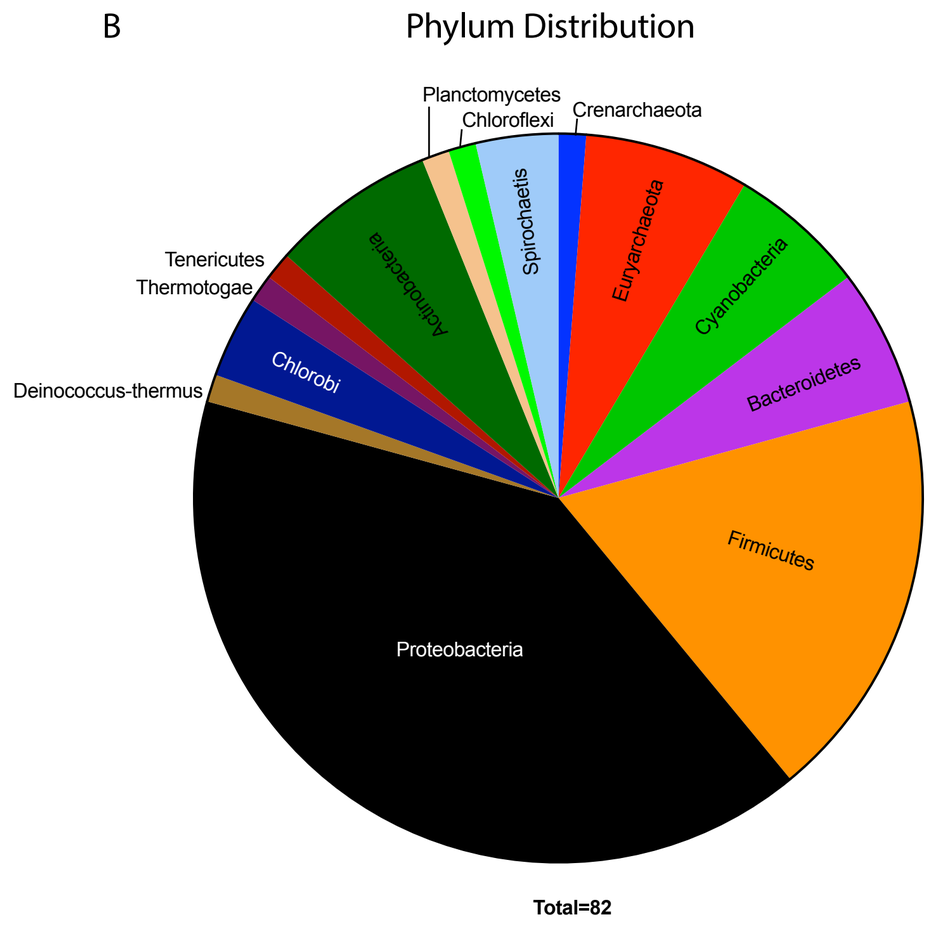



**Supplementary Figure 3:** Heatmap of bacterial species in 4 months old 'Cre' and 'KPC' mice with major changes (both up and down) in many species. The differences have been further elaborated in other figures and the manuscript text.

A




B




**Supplementary Figure 4:** Significantly changed species between 2 months old and 4 months old KPC mice microbiome. (**A**) A heatmap of 82 species found to be significantly changed. Species marked with an arrow had significantly diminished relative abundance at 4 months age, while the others had expanded relative abundance. (**B**) All 82 species represented 14 different phyla, with dominant representation from Proteobacteria, followed by Firmicutes.