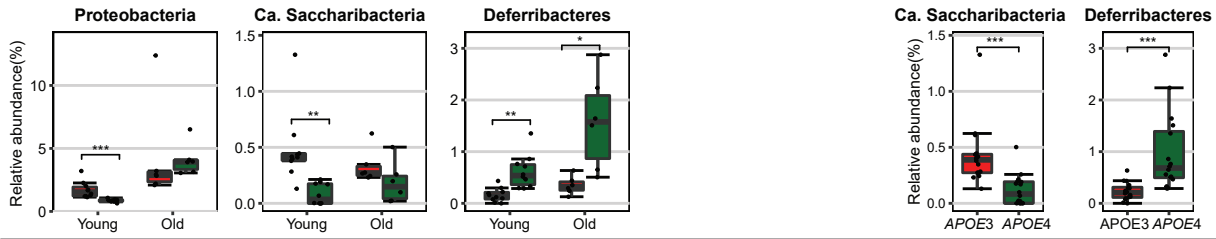


Genotype  *APOE3*  *APOE4*

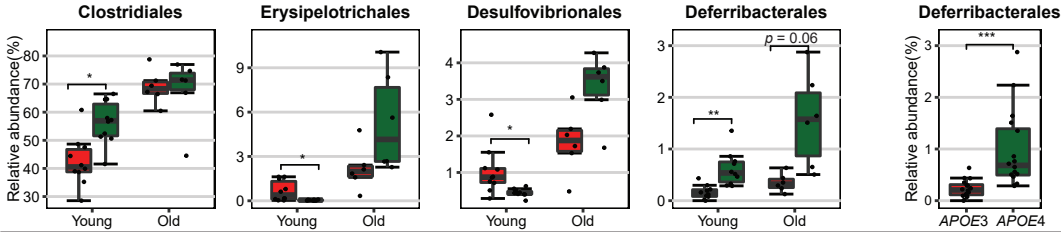
Young or old mice

Young & Old

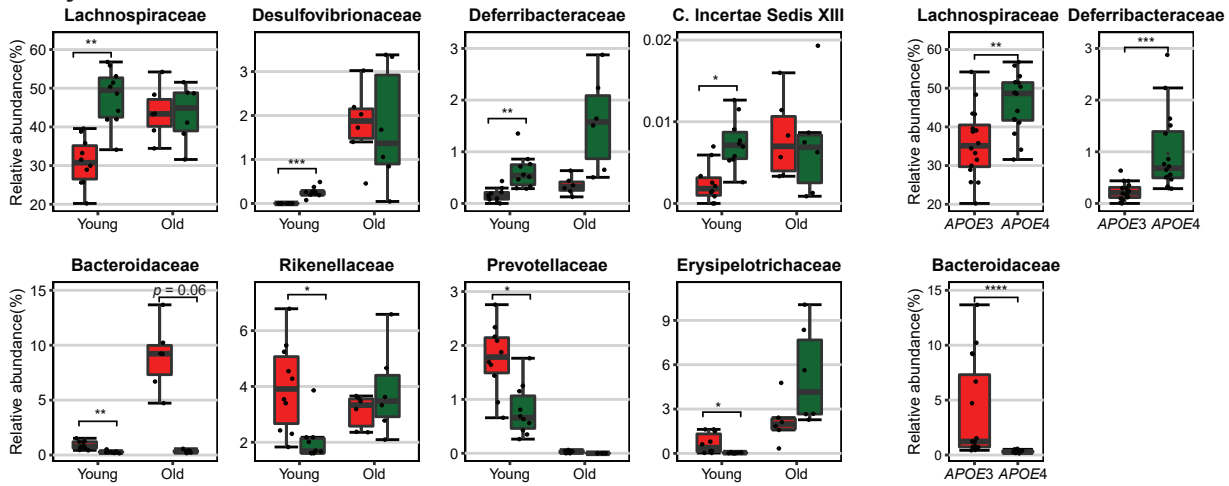
**Phylum**



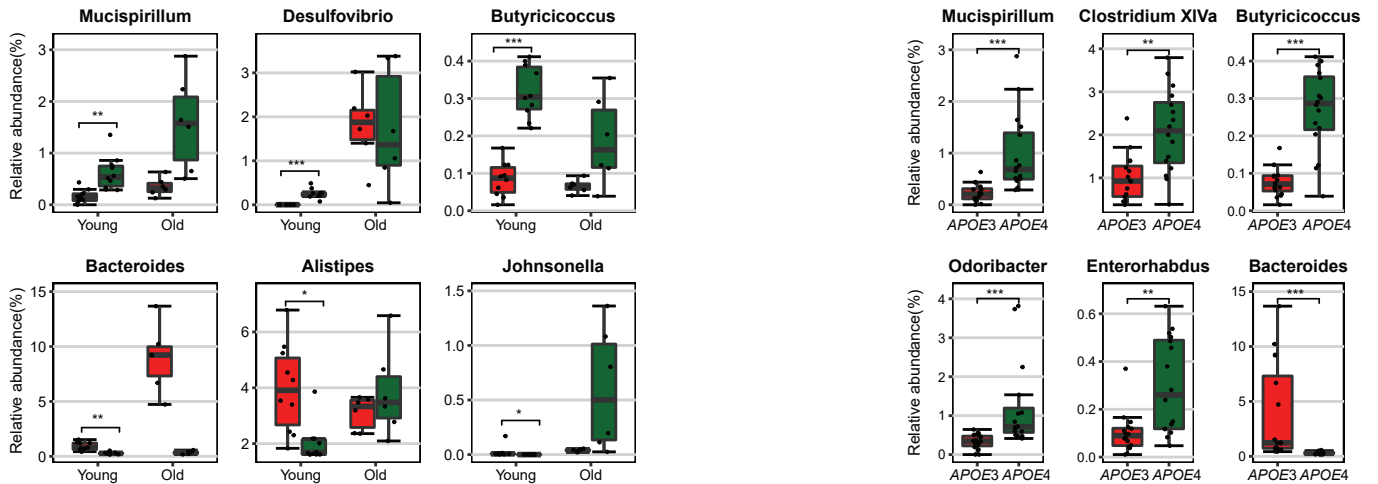
**Order**



**Family**



**Genus**



**Figure S7.** Box plot of the relative abundance of significantly differentially abundant faecal microbiota taxa from phylum to genus associated with murine *APOE* genotypes in young mice samples, old mice samples and both age groups combined. Statistical significances between *APOE3* and *APOE4* were determined by the Mann–Whitney U test and were corrected for the multiple comparison using the Benjamini–Hochberg adjustment, \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .