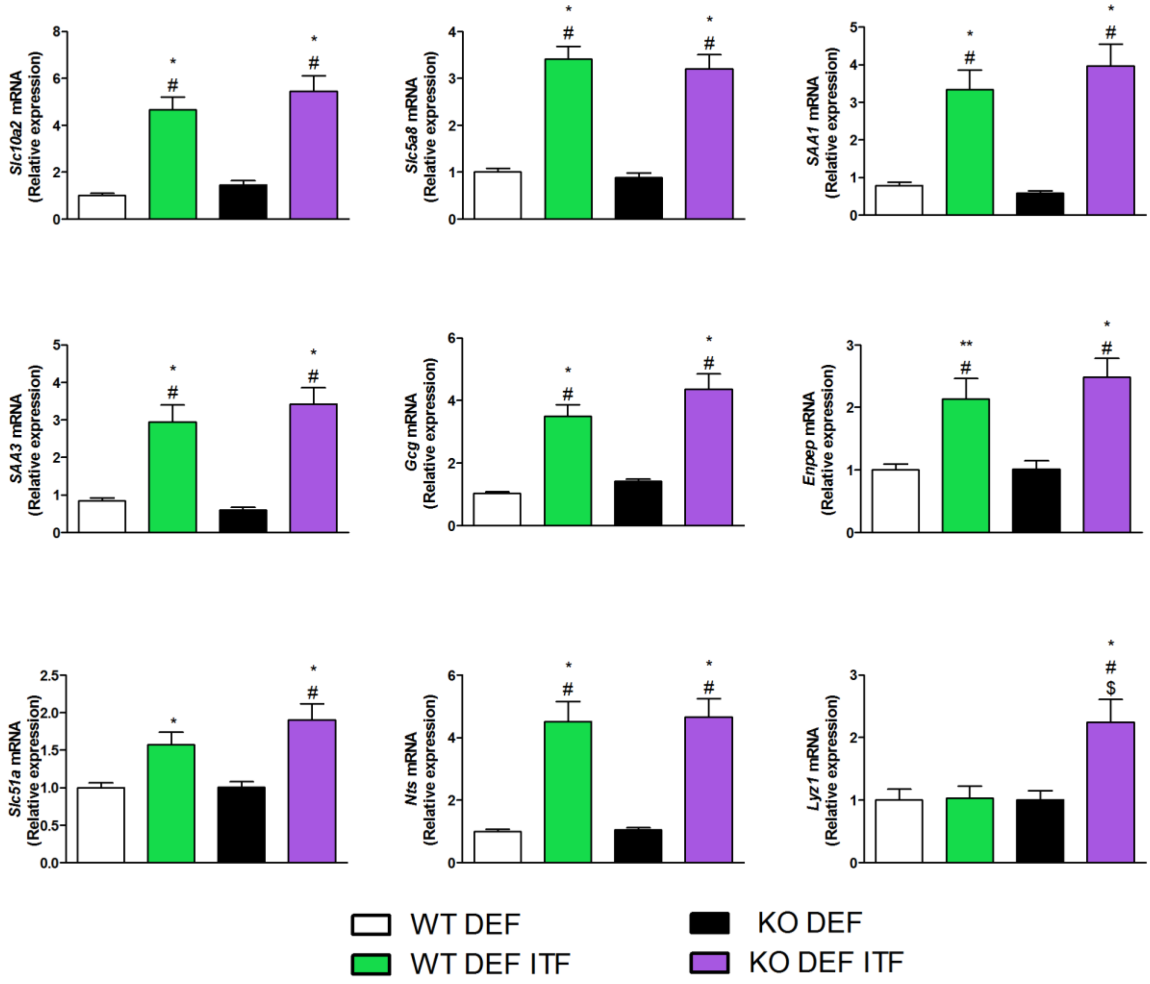
Figure S1. Related to Figure 3: *Slc10a2*, *Slc5a8*, *SAA1*, *SAA3*, *Gcg*, *Enpep*, *OSTα*, *Nts* and *Lyz1* mRNA levels in the caecal tissue.



qPCR results in the caecal tissue of n-3 PUFA depleted wild-type mice (WT DEF), of n-3 PUFA depleted wild-type mice supplemented in ITF for the last fifteen days (WT DEF ITF), of n-3 PUFA depleted Apoe$^{-/-}$ mice (KO DEF) and of n-3 PUFA depleted Apoe$^{-/-}$ mice supplemented in ITF for the last fifteen days (KO DEF ITF). Data (N=11-15) are expressed as mean ± SEM. Data were analysed by one-way ANOVA followed by Tukey's post-tests: * vs WT DEF, $ vs WT DEF ITF, # vs KO DEF.

Figure S2. Related to Figure 5: LDA scores in green for the taxa enriched in prebiotics treated mice and in red for the taxa enriched in untreated mice, generated using LEfSe.

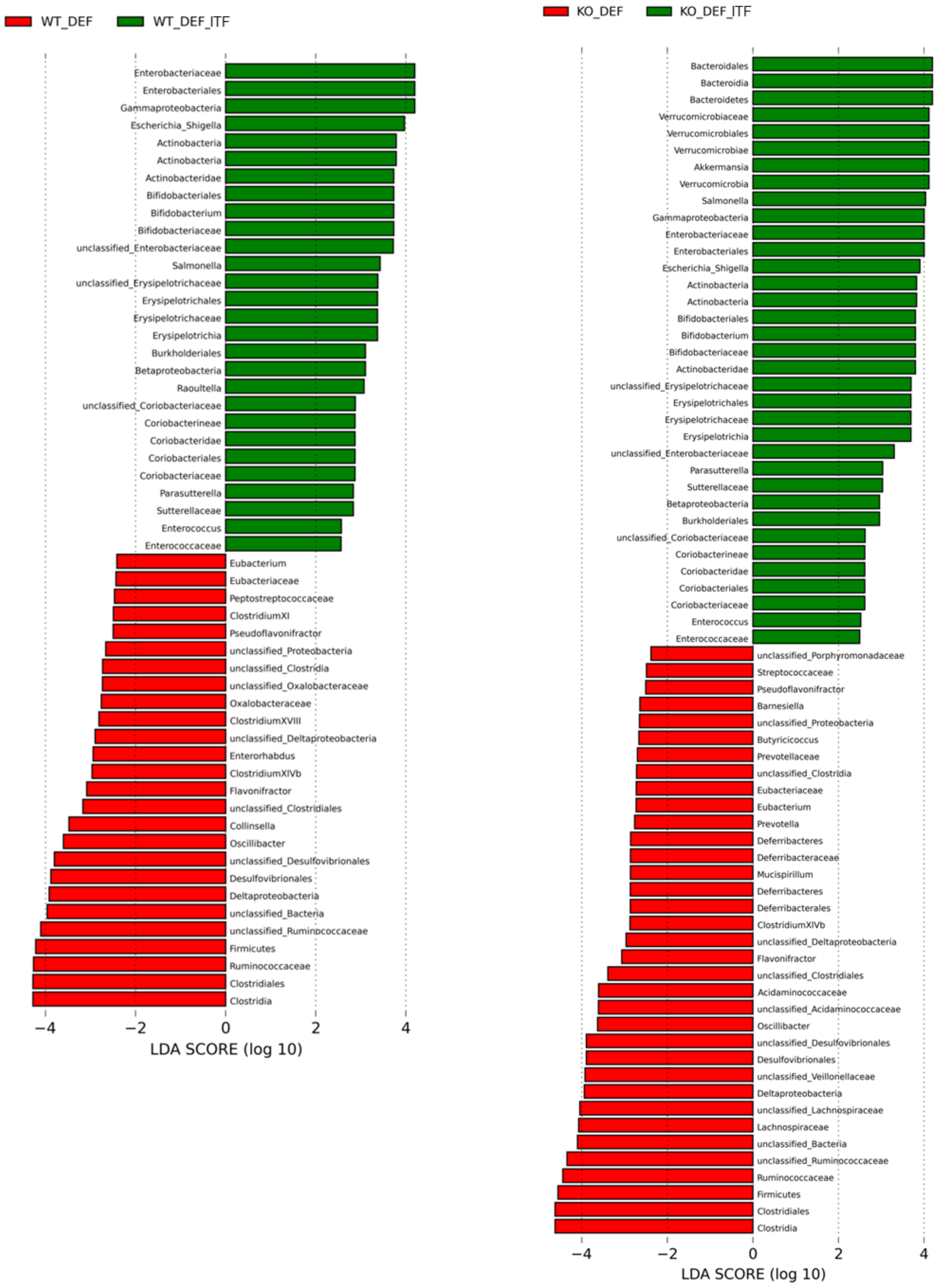


Figure S3. Related to Figure 7: Heatmap representation of the Spearman r correlation coefficient between systemic or portal bile acid profiles and bacterial taxa. Only the bacteria for which at least one significant correlation to bile acid levels was found, are displayed.

(c, class; o, order; f, family; g, genus; s, species). *Adjusted pvalue<0.05.