Figure S4. Principle Coordinates Analysis based on unweighted and weighted UniFrac distances of bacterial 16S rRNA amplicon sequences from human faecal samples showing gut microbiota beta diversity grouped according to (**a**) *APOE* genotypes, (**b**) sex or (**c**) BMI categories. Beta diversity analysis reveals revealed significant separation of microbial communities according to gender and BMI categories, but not *APOE* genotypes. The significant differences between groups were determined by PERMANOVA tests.