



Figure S3. MDS plot of intestinal microbiota compositions in the individuals with FUT2 non-secretor genotype AA (white), secretor genotype AG (grey) and GG (black) based on band intensities of the DGGE analysis (A), on abundances of genera by pyrosequencing (B), on abundances of level 2 taxa by HITchip (C), on abundances of OTUs by pyrosequencing (D) and on abundances of genera in subsampled pyrosequencing data.