



Fig. S4. Comparison of the functional gene category compositions of (A) the *E. faecium* recombination-free versus the recombinant core genome and of (B-D) the recombinant core genome originating from a specific source versus that of all sources, except the corresponding specific source. The specific sources that were analysed were: clade A, clade B and outside *E. faecium* (panels B-D, respectively). Left panels show bar charts of COG category relative abundances (% of total category counts); right panels show scatterplots of COG category counts. Outliers of the regression lines were identified using Grubb's test (99% confidence level) and are indicated with red arrows and letters.