

Legends for supplementary figures

Supplementary figure 1: Flowchart showing donor screening

Supplementary figure 2: Demonstration of anti-microbial resistance gene testing in donors

Supplementary figure 3: Robust Aitchison PCA for analysis of beta-diversity in donor samples. Compositional biplot link specific taxonomic features with the beta diversity ordination of the donor samples. The method uses Aitchison distance as the compositional distance metric. Pseudo-F statistic ratio and PERMANOVA test on these distances reveal that the donor effect seems to explain the clustering of donors on the PCA. Performed using Qiime2 plugin DEICODE version 0.2.3 (<https://github.com/biocore/DEICODE>)

Supplementary figure 4: Differentially abundant bacterial taxa between donors associated with significantly better response vs other donors. Analysis was performed using the R package DeSeq2, with FDR < 0.01 and with adjustment for confounders (Age, Gender, and BMI), at the Genera level, where each circle represents a Species. Analysis revealed significant enhancement of beneficial bacterial members like *Catenibacterium*, *Eubacterium rectale*, *Dorea*, *Clostridium*, *Ruminococcus faecis*, *Roseburia*, *Fusicatenibacter saccharivorans*, *Intestinimonas butyriciproducens*, *Gemmiger formicilis*, *Coprococcus catus*, *Megasphaera*, *Eubacterium eligens*, *Anaerobutyricum*, *Faecalibacterium prausnitzii*, *Blautia*, *Bifidobacterium* and *Agathobaculum*, in donors implicated with positive FMT outcome and while other donors had an enhanced abundance of pathobionts like *Enterococcus*, *Rothia*, *Weissella*, *Haemophilus parainfluenzae*, *Acinetobacter*, *Pseudomonas*, *Turicibacter*, and *Veillonella*

Supplementary figure 5: Principal Component Analysis (PCA) biplot of abundances of bacterial taxa and peak intensities of butyrate in donor stool samples. The ellipses show the clustering of effective (1) and in-effective (2) donors, and the arrows show the contribution of individual bacterial taxa in the sample clustering. It highlights that the donors harbouring the gut microbiota enriched in beneficial microbes involved in SCFA production seem to drive a positive response to FMT.