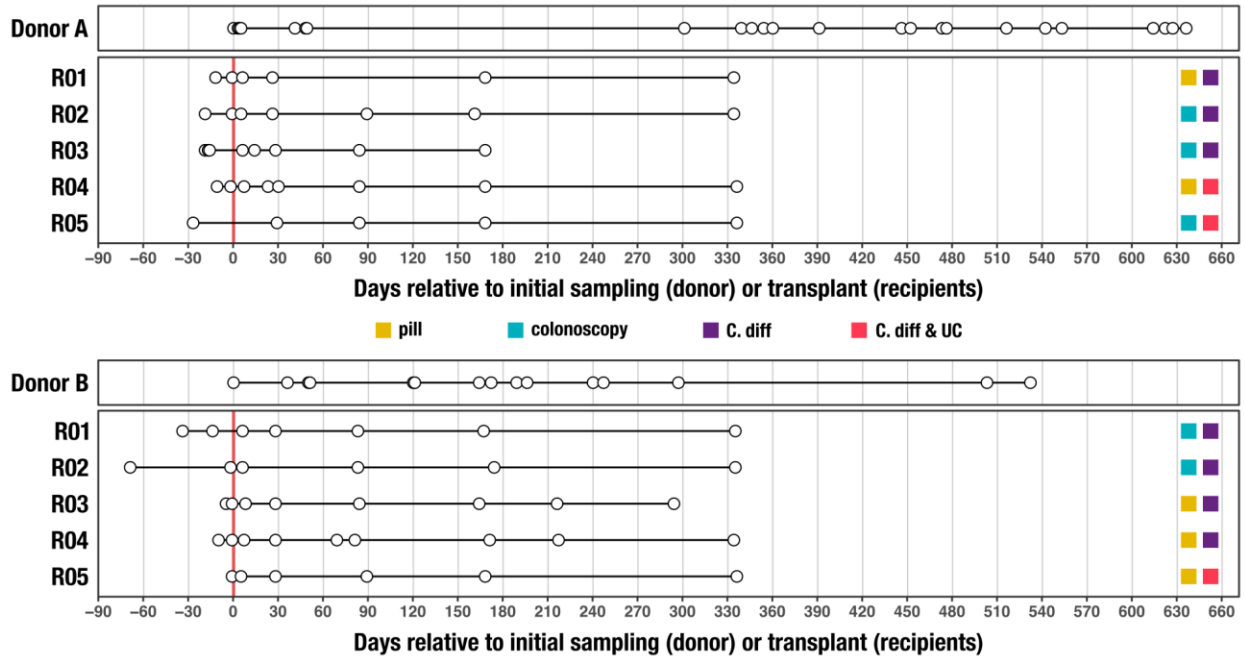# Supplementary Figures

Fig. S1. Timeline of stool samples collected from FMT study. Each circle represents a stool sample collected from either an FMT donor or FMT recipient. The thicker, red vertical line at day 0 represents the FMT event for each recipient. FMT method (pill or colonoscopy) and FMT recipient health and disease state (C. diff - chronic recurrent *Clostridium difficile* infection, UC - ulcerative colitis) are indicated on the right.

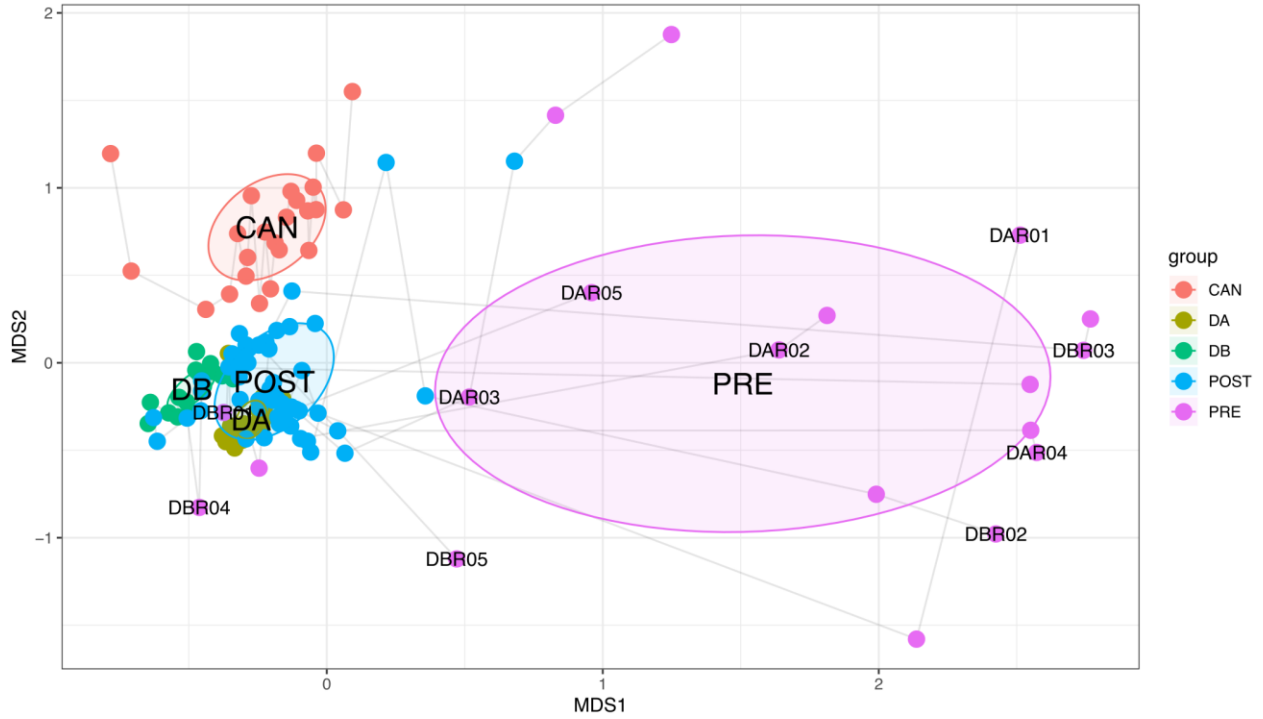**Fig. S2. Nonmetric multidimensional scaling (NMDS) ordination of the taxonomic composition of donor, recipient, and Canadian gut metagenomes at the genus level based on Morisita-Horn dissimilarity.** Samples from the same participant are joined by lines with the earliest time point labeled. CAN: Canadian gut metagenomes, DA: donor A, DB: donor B, POST: recipients post-FMT, PRE: recipients pre-FMT.
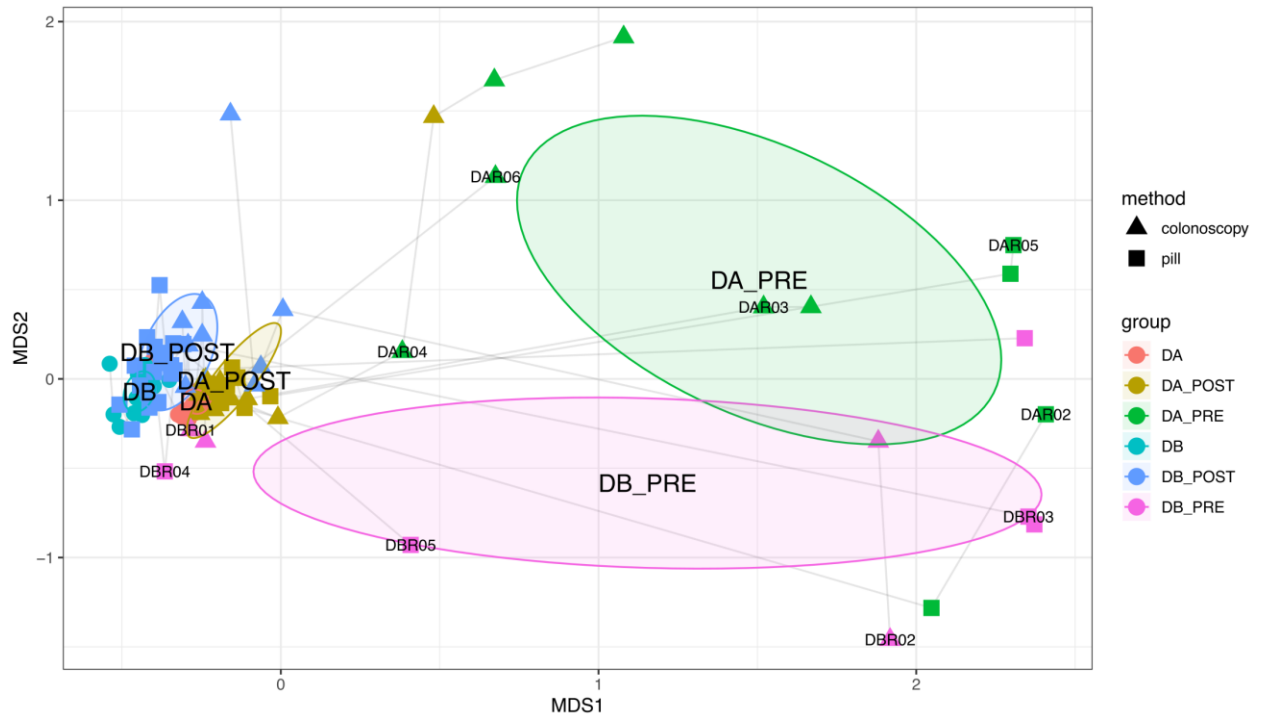
Fig. S3. Nonmetric multidimensional scaling (NMDS) ordination of the taxonomic composition of the donor and recipient metagenomes at genus level based on Morisita-Horn dissimilarity. Samples from the same participant are joined by lines with the earliest time point labeled. DA_POST: donor A recipients post-FMT, DA_PRE: donor A recipients pre-FMT, DA: donor A, DB_POST: donor B recipients post-FMT, DB_PRE: donor B recipients pre-FMT, DB: donor B.
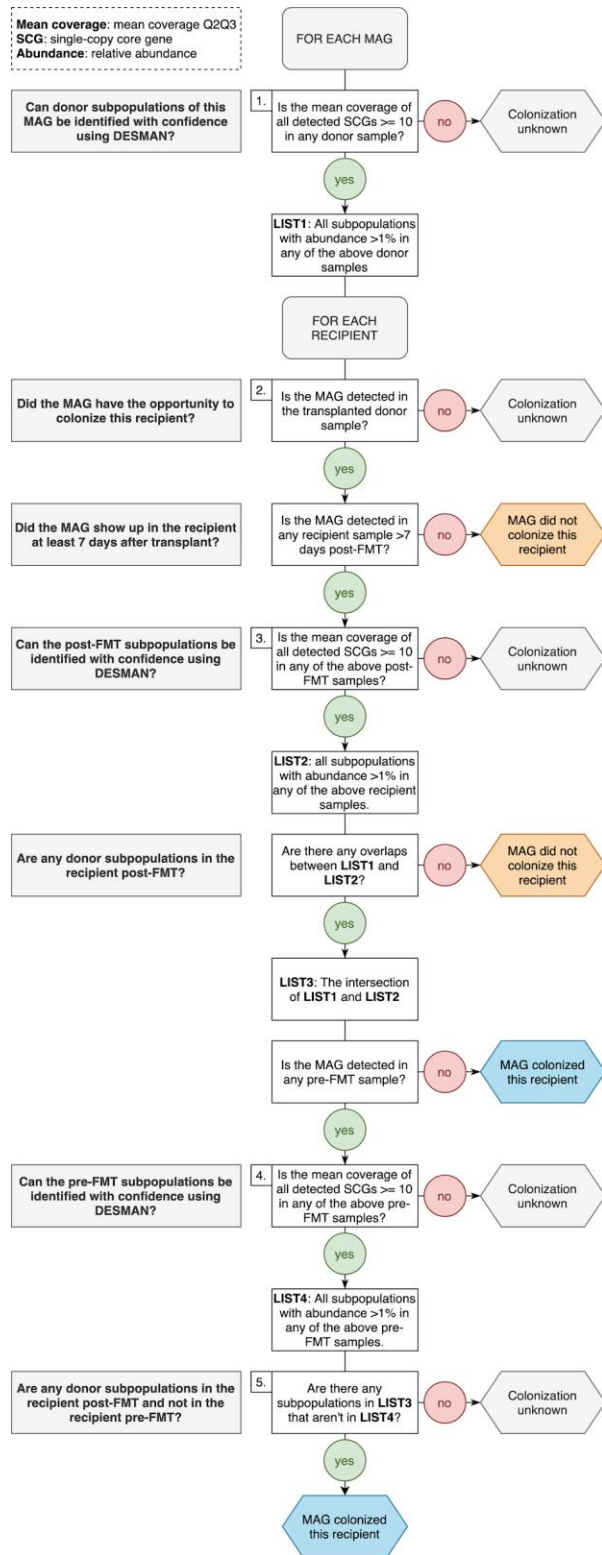
Mean coverage: mean coverage Q2Q3
SCG: single-copy core gene
Abundance: relative abundance

FOR EACH MAG

Can donor subpopulations of this MAG be identified with confidence using DESMAN?

1. Is the mean coverage of all detected SCGs >= 10 in any donor sample?
— no → Colonization unknown
— yes ↓

LIST1: All subpopulations with abundance >1% in any of the above donor samples

FOR EACH RECIPIENT

Did the MAG have the opportunity to colonize this recipient?

2. Is the MAG detected in the transplanted donor sample?
— no → Colonization unknown
— yes ↓

Did the MAG show up in the recipient at least 7 days after transplant?

Is the MAG detected in any recipient sample >7 days post-FMT?
— no → MAG did not colonize this recipient
— yes ↓

Can the post-FMT subpopulations be identified with confidence using DESMAN?

3. Is the mean coverage of all detected SCGs >= 10 in any of the above post-FMT samples?
— no → Colonization unknown
— yes ↓

LIST2: all subpopulations with abundance >1% in any of the above recipient samples.

Are any donor subpopulations in the recipient post-FMT?

Are there any overlaps between **LIST1** and **LIST2**?
— no → MAG did not colonize this recipient
— yes ↓

LIST3: The intersection of **LIST1** and **LIST2**

Is the MAG detected in any pre-FMT sample?
— no → MAG colonized this recipient
— yes ↓

Can the pre-FMT subpopulations be identified with confidence using DESMAN?

4. Is the mean coverage of all detected SCGs >= 10 in any of the above pre-FMT samples?
— no → Colonization unknown
— yes ↓

LIST4: All subpopulations with abundance >1% in any of the above pre-FMT samples.

Are any donor subpopulations in the recipient post-FMT and not in the recipient pre-FMT?

5. Are there any subpopulations in **LIST3** that aren't in **LIST4**?
— no → Colonization unknown
— yes ↓

MAG colonized this recipient

Fig. S4. A flowchart outlining our method to assign successful colonization, failed colonization, or undetermined colonization phenotypes to donor-derived populations in the recipients of that donor's stool.