SUPPLEMENTARY MATERIAL

Figures overview:

Figure 1*, 4*: Linear Discriminant Analysis Effect Size (Lefse) in some specific group combinations, representing the bacteria significantly enriched for each cohort, separated in green and red colour, depending on if they are enriched or reduced compared to the other.

Figure 2*: Stacked Bars Charts represent the average relative abundance of the most frequent 25 organisms in each cohort.

Figure 3*: Heatmap representing the abundance of species. Different colors show differences for lower-abundant organisms.

Figure 5*: Bray-Curtis Coordinate Analysis (PCoA) showing the difference in beta diversity between 2 groups.

Table 1*. Overview of all p values for microbial diversity

Comparison	Alpha diversity			Beta diversity	
	Chao, p	Shannon, p	Simpson, p	Bray-Curtis, p	Jaccard, p
G(HC) vs G(MS), S1	0.14	0.81	0.62	0.12	0.09
G(DMT) vs G(DMT+Y), S1	**0.01***	0.63	0.86	0.46	0.54
G(IFN) vs G(IFN+Y), S1	**0.00097***	0.6	1	0.26	0.27
G(TER) vs G(TER+Y), S1	0.91	0.97	0.97	0.9	0.86
G(HC) vs G(MS), S2	0.67	0.71	0.81	0.23	0.25
G(DMT) vs G(DMT+Y), S2	0.18	0.53	0.75	0.39	0.4
G(IFN) vs G(IFN+Y), S2	**0.01***	0.6	0.66	0.22	0.2
G(TER) vs G(TER+Y), S2	0.55	0.17	0.44	0.51	0.6
S1 vs S2, G(MS)	0.55	0.46	0.77	0.12	0.09
S1 vs S2, G(HC)	0.83	0.64	0.62	0.99	0.99
S1 vs S2, G(DMT)	0.81	0.66	0.84	0.98	0.99
S1 vs S2, G(IFN)	0.85	0.91	0.85	0.98	0.99
S1 vs S2, G(TER)	0.73	0.63	0.91	0.91	0.96
S1 vs S2, G(DMT+Y)	0.34	0.73	0.84	0.99	0.99
S1 vs S2, G(IFN+Y)	0.63	0.3	0.16	0.96	0.98
S1 vs S2, G(TER+Y)	0.45	0.63	0.44	0.98	0.99

Values in bold are statistically significant. This table presents specific comparisons between our cohorts and diversity indexes applied, along with the p value of each test. Abbreviations: S1=sample 1; S2=sample 2.

Fig.1*. Lefse analysis at species level between sample 1 and sample 2, for MS cohort, G(MS).
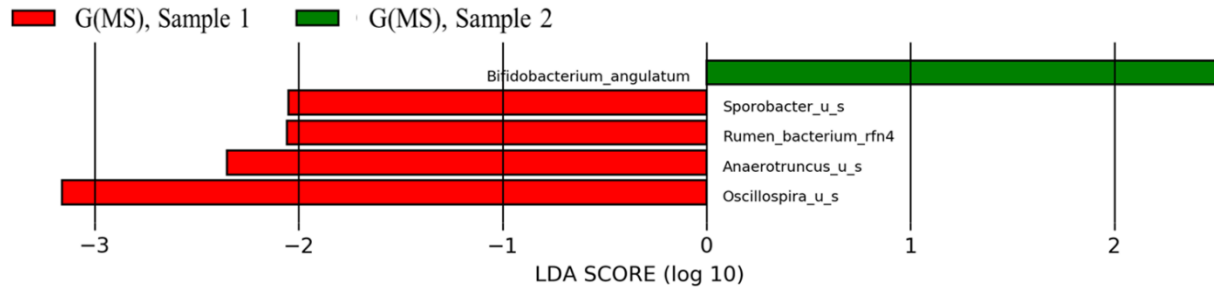

Fig.2*. Stacked Bars Charts: comparison between sample 1 and sample 2 for MS cohort, G(MS), top 25 species.
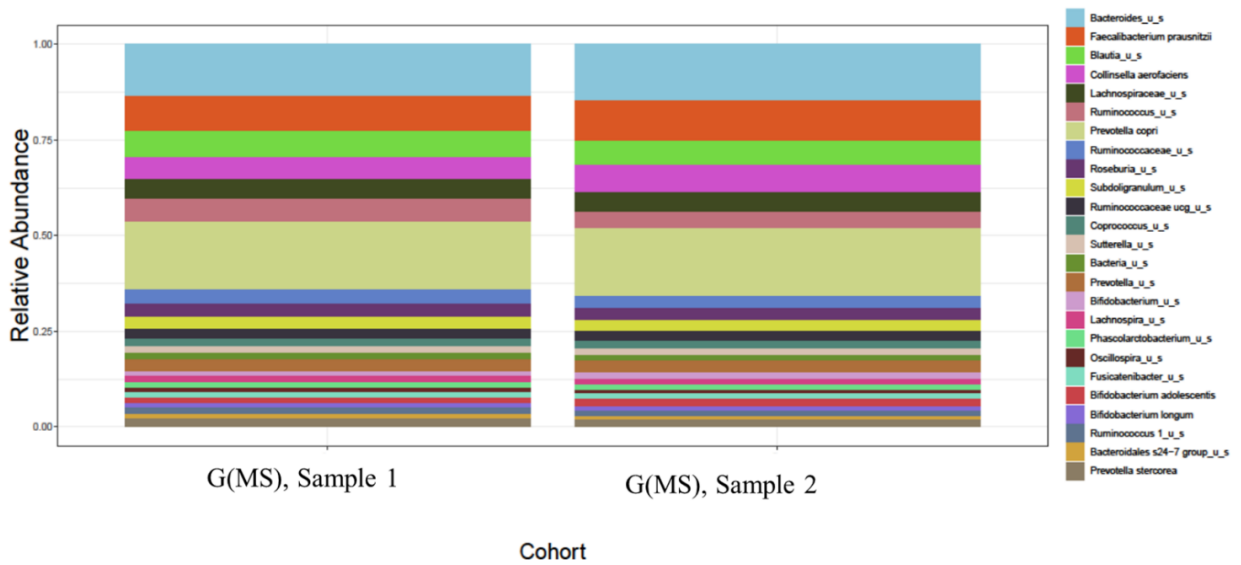
Fig.3*. Relative abundance heatmap (species level)- sample 1 vs sample 2 for G(MS), unclustered
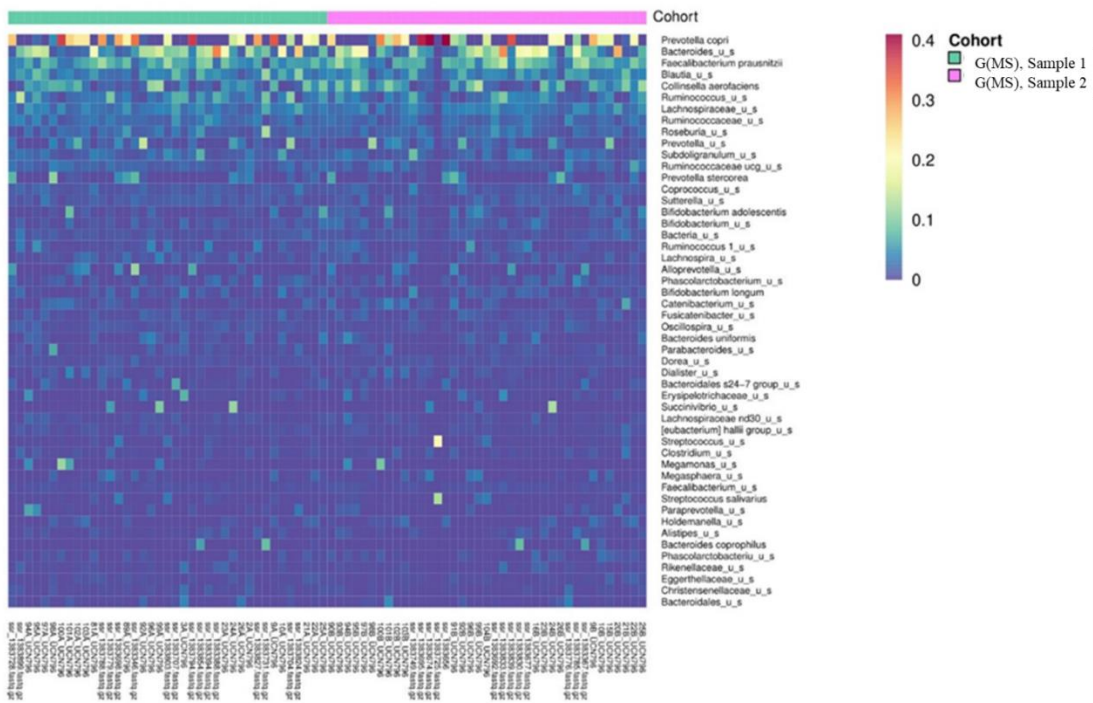

Fig.4*. Lefse analysis at species level between sample 1 and sample 2 for G(DMT) group
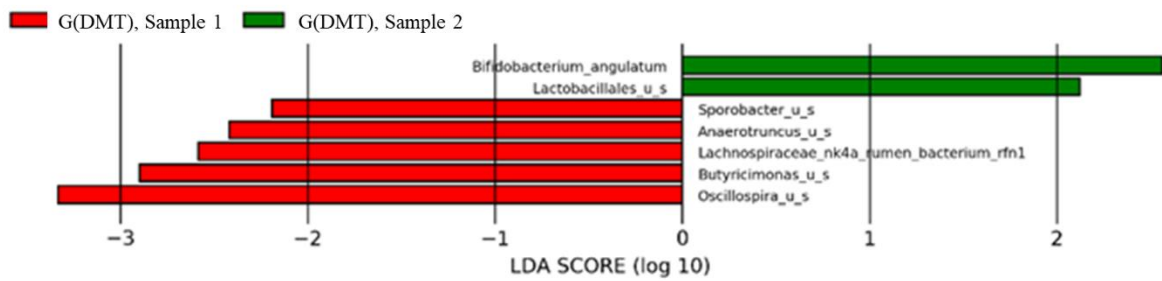
Fig.5*. Bray-Curtis Principal Coordinate Analysis (PCoA) beta diversity sample 1 vs sample 2, G(TER), species level

Bray−Curtis PCoA − Species − Sample 1 vs Sample 2, G (TER)

PERMANOVA

	Df	SumOfSqs	R2	F	p-value	SIG
Cohort	1	0.09386069	0.02983172	0.5534823	0.912	NS
Residual	18	3.05247773	0.97016828	NA	NA	NA
Total	19	3.14633842	1.00000000	NA	NA	NA

Cohort
- G(TER), Sample 1
- G(TER), Sample 2

***: p <= 0.001.   **: p <= 0.01.   *: p <= 0.05.   NS: p > 0.05