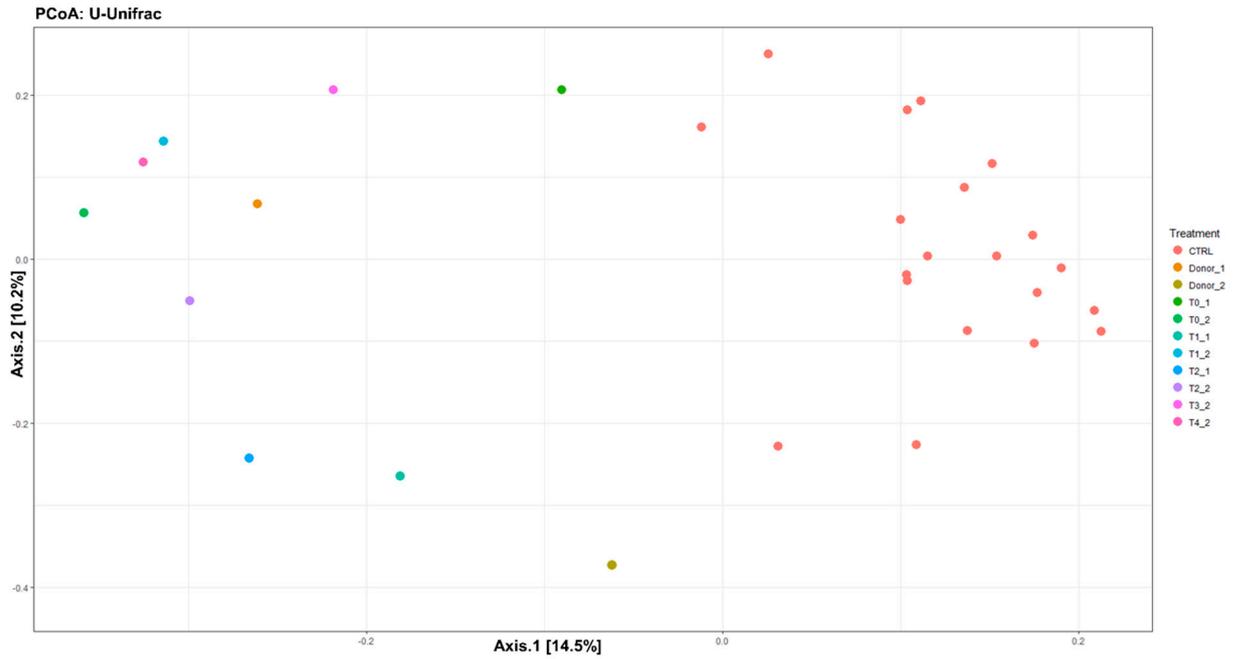
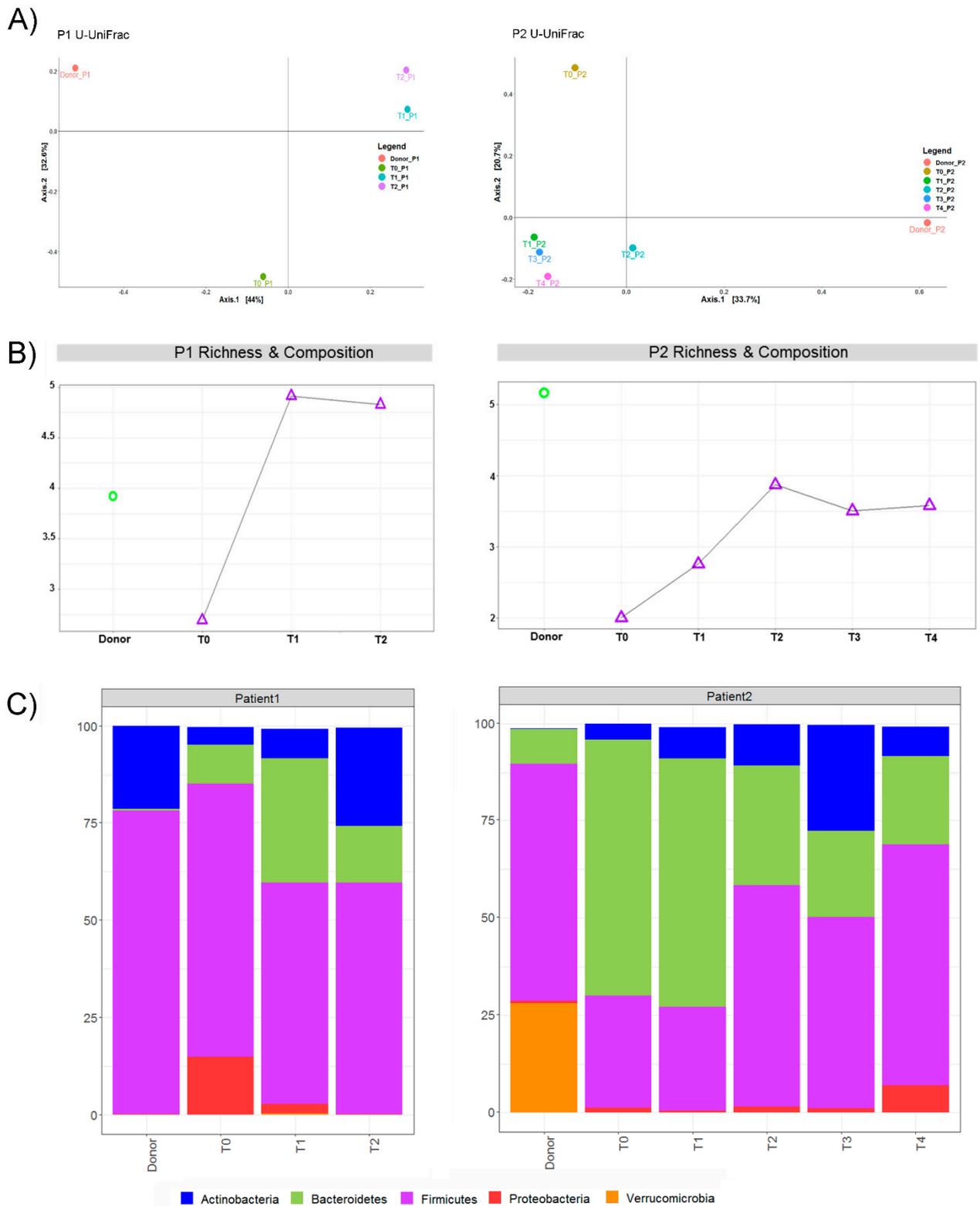


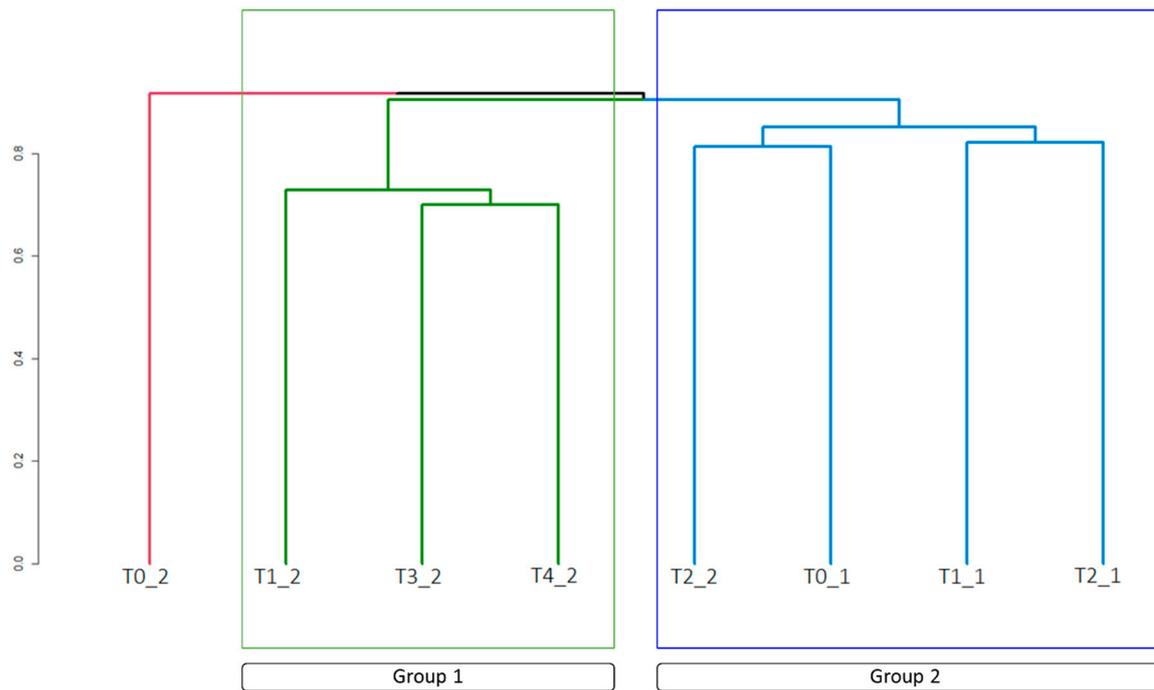
## Supplementary information.



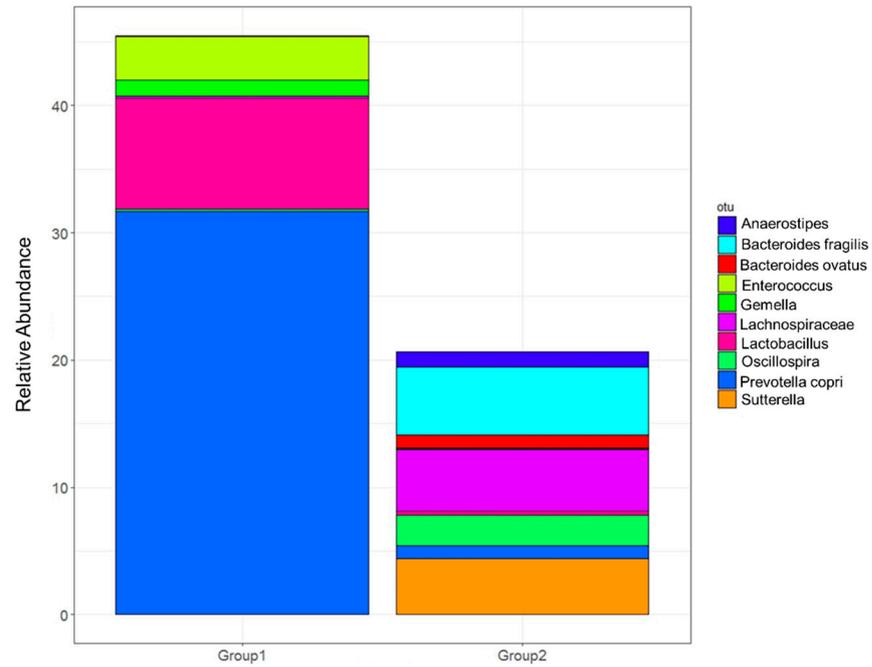
**Supplementary figure S1: Unweighted UniFrac analyses on the whole dataset.** Samples from recipients, donors and controls were analyzed through Unweighted UniFrac analysis. Two main clusters are evident: one composed by all recipients' samples and one by donors and control samples.



**Supplementary figure S2: Microbiota profile variations during time.** A) Unweighted UniFrac analyses for P1 and P2 with their respective donor (red dot) samples. In Panel B, Shannon index from  $\alpha$ -diversity analysis is reported for both patients (violet triangles) and donors (green circles). Finally, in Panel C, bar plots show microbiota variation at phylum level for each sample.



**Supplementary figure S3: Hierarchical cluster analysis based on Jaccard Distance among patients' samples.** This analysis depicts two main clusters based on bacterial ecology: group 1 (green box) composed by almost all samples of P2 and group 2 (blue box) by all P1 samples and T<sub>2</sub> sample from P2.



**Supplementary figure S4: Mean relative abundance of significant species (DESeq2 FDR-p<0.05) in groups 1 and 2 as detected by hierarchical cluster analysis. Only bacterial genera with a relative abundance greater than 1% are displayed.**