

Supplementary Material

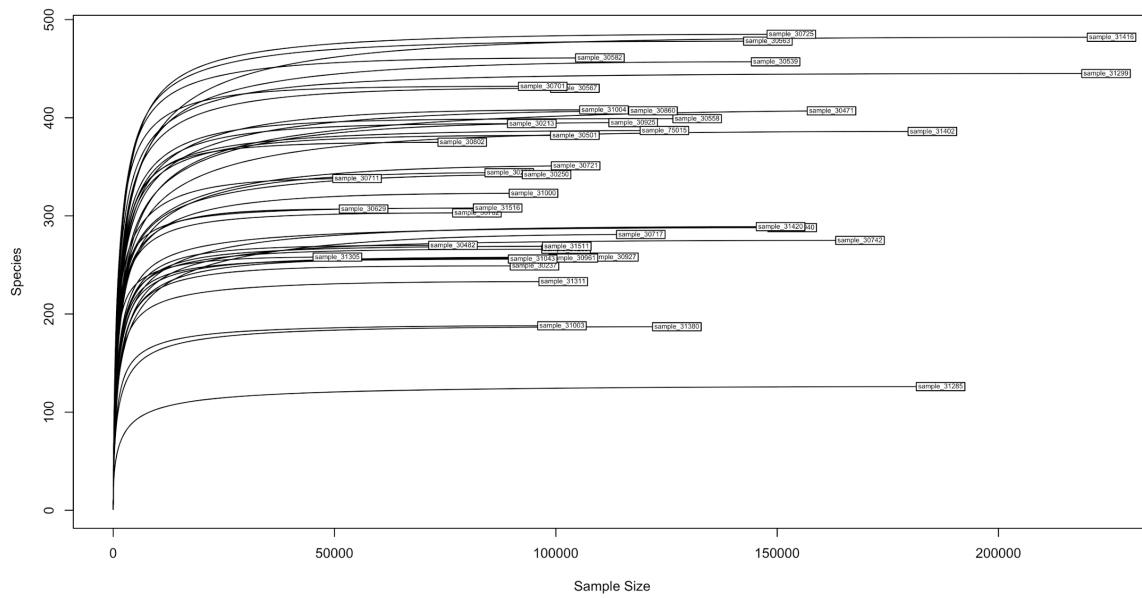


Figure S1-C. Rarefaction curve for IGT patients

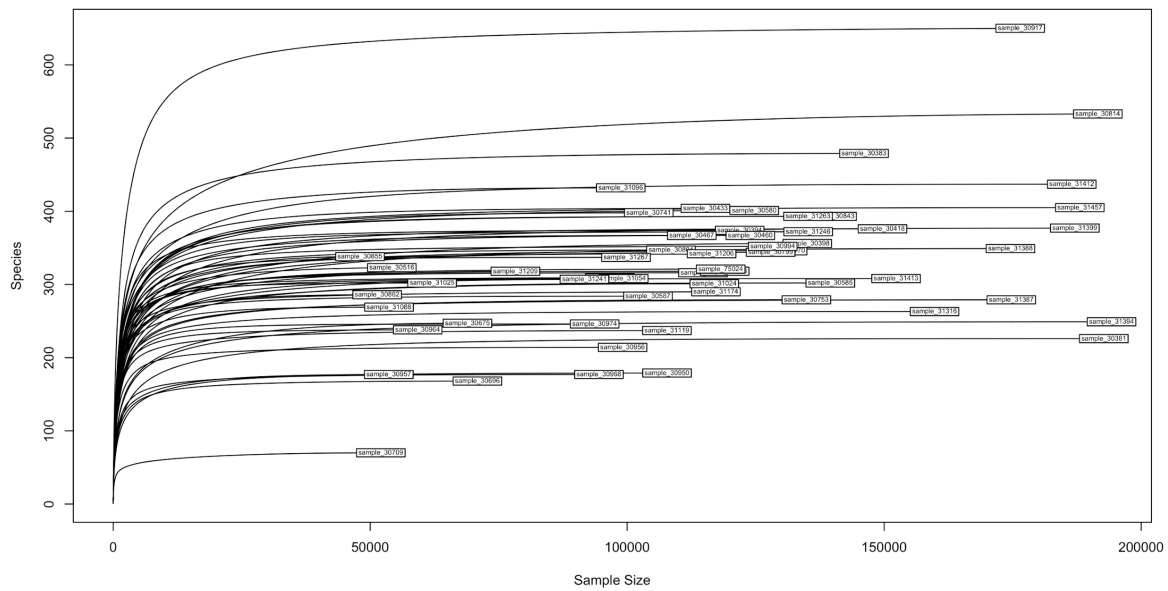


Figure S1-D. Rarefaction curve for IFG+IGT patients

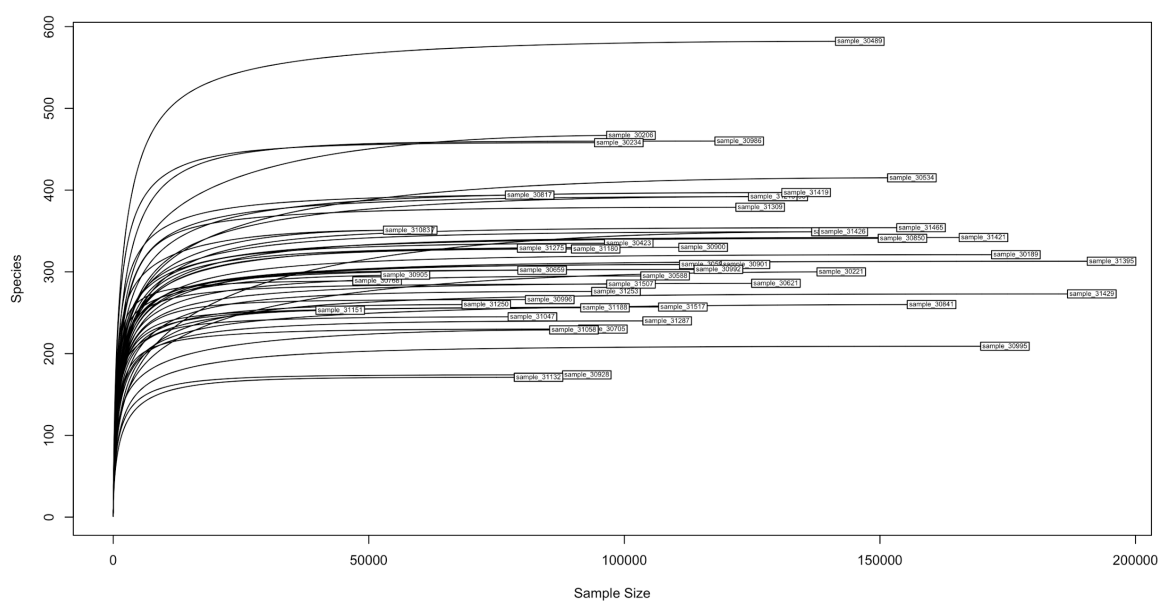


Figure S1-E. Rarefaction curve for T2D patients

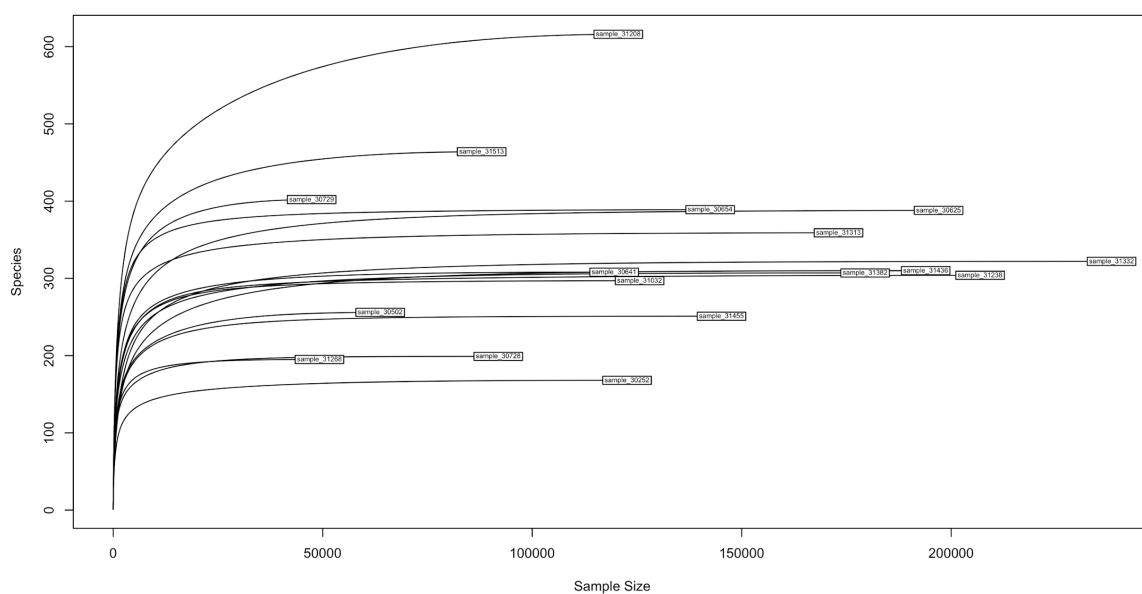


Figure S1-F. Rarefaction curve for T2D_treated patients

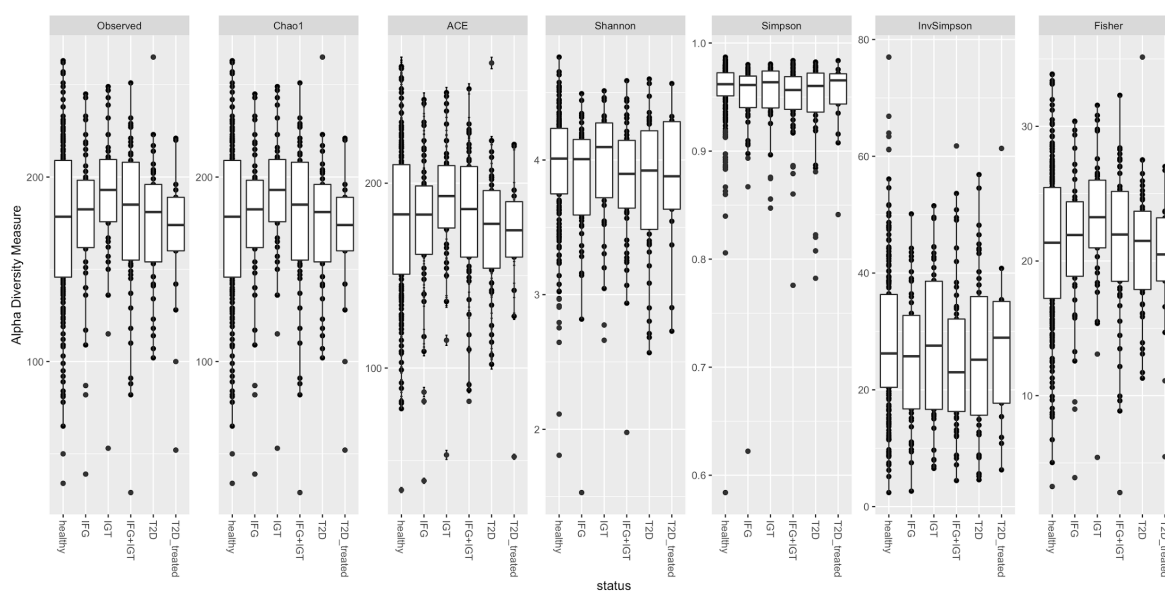


Figure S2. Alpha diversity index for all groups: Healthy, IFG, IGT, IFG+IGT, T2D, and T2D_treated

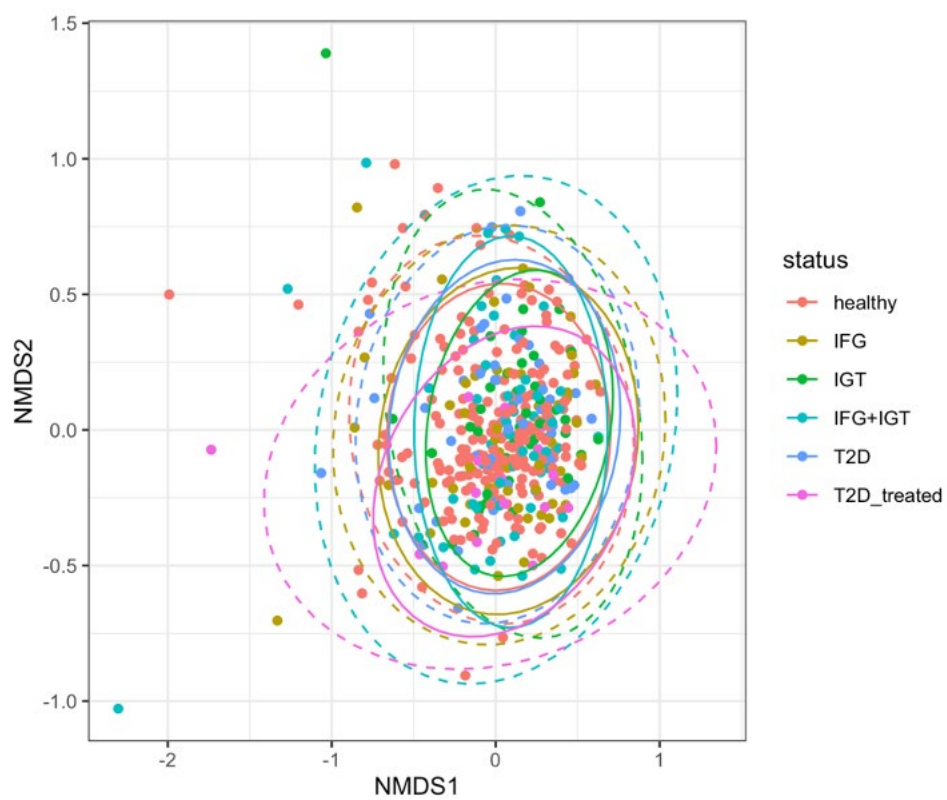


Figure S3-A NMDS analysis colored by groups: Healthy, IFG, IGT, IFG+IGT, T2D, and T2D_treated.

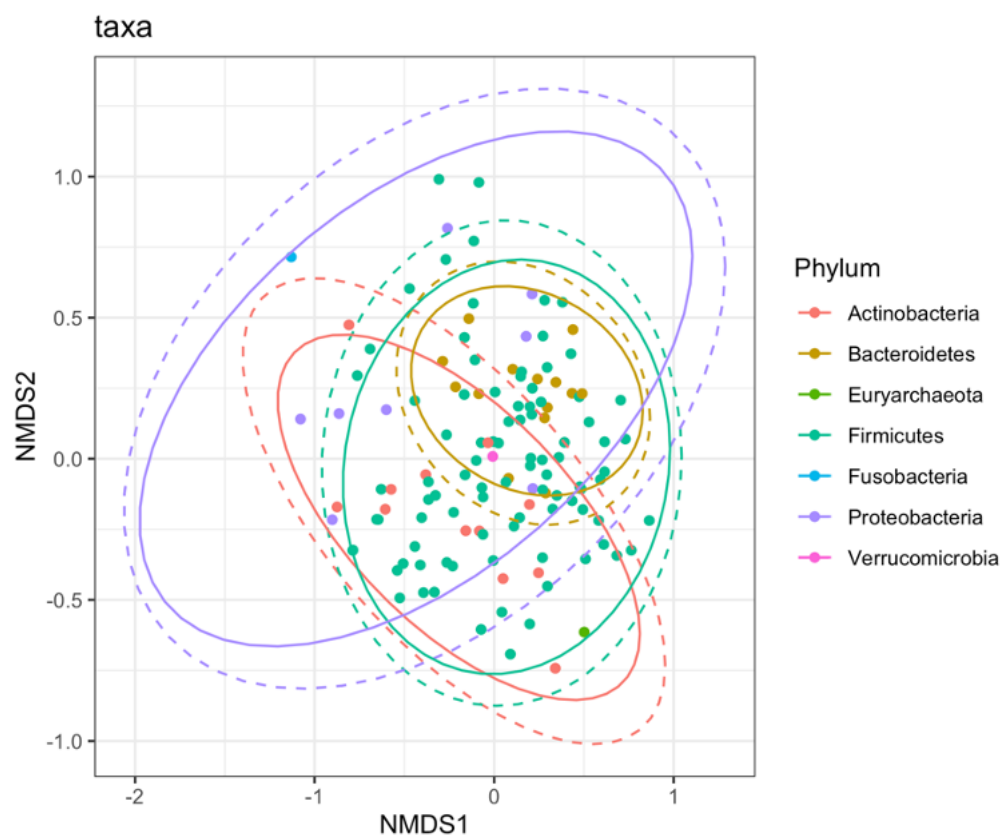


Figure S3-B NMDS analysis colored by phyla: *Actinobacteria*, *Bacteroidetes*, *Euryarchaeota*, *Firmicutes*, *Fusobacteria*, *Proteobacteria*, *Verrucomicrobia*.

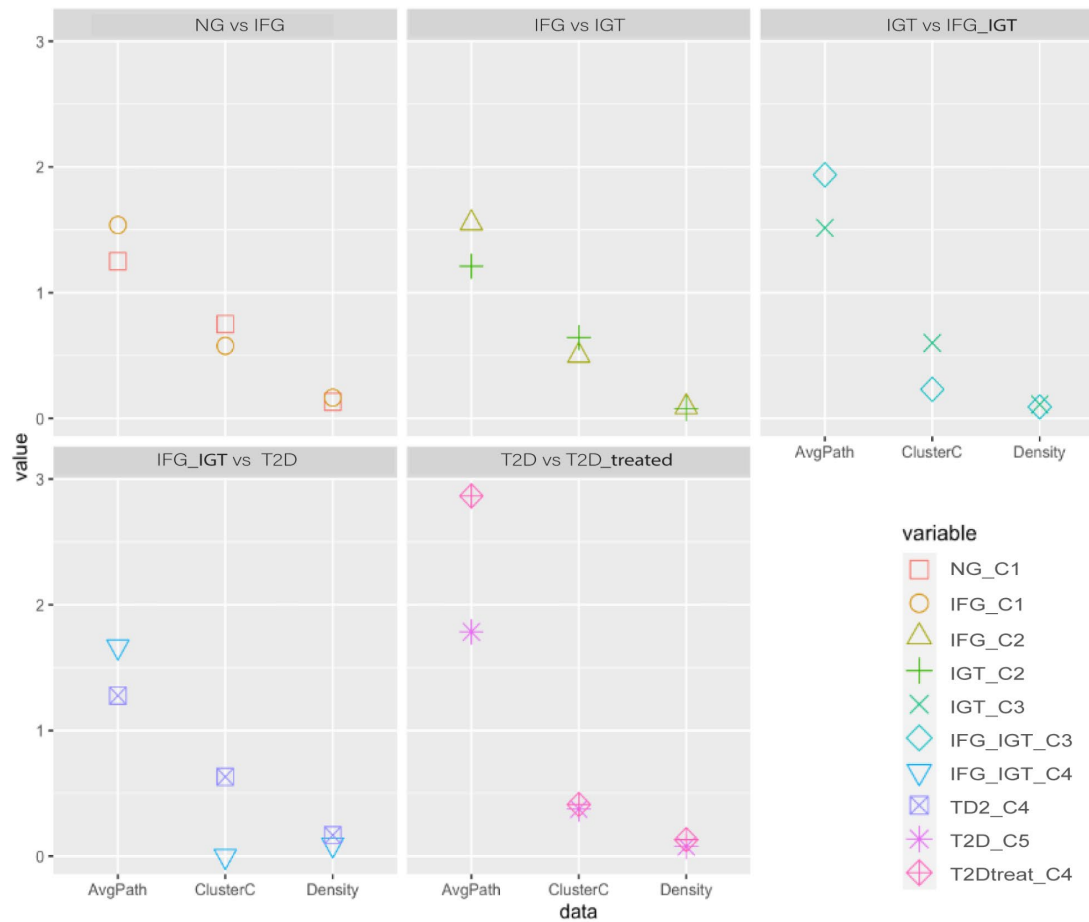


Figure S4-A Network statistics for all pairwise comparisons between groups (NG, IFG, IGT, IFG+IGT, T2D, and T2D treated). The X-axis indicates network statistics (AvgPath: Average Path, ClusterC: Cluster coefficient, and Density) while Y-axis indicates their corresponding values.

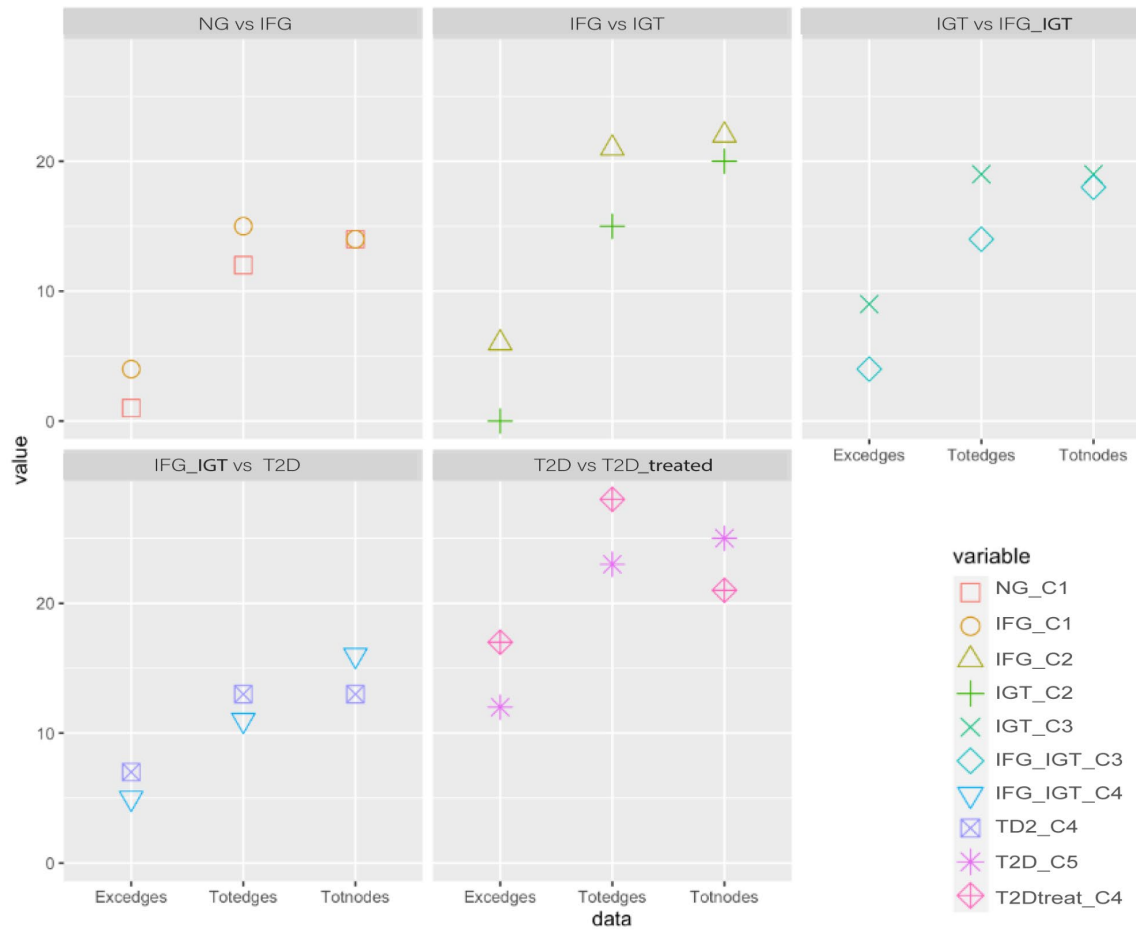


Figure S4-B Network statistics for all pairwise comparisons between groups (NG, IFG, IGT, IFG+IGT, T2D, and T2D treated). The X-axis indicates network statistics (Excedges: Exclusive edges, Totedges: Total edges, Totnodes: Total nodes) all of these are for each network while Y-axis indicates their corresponding values.

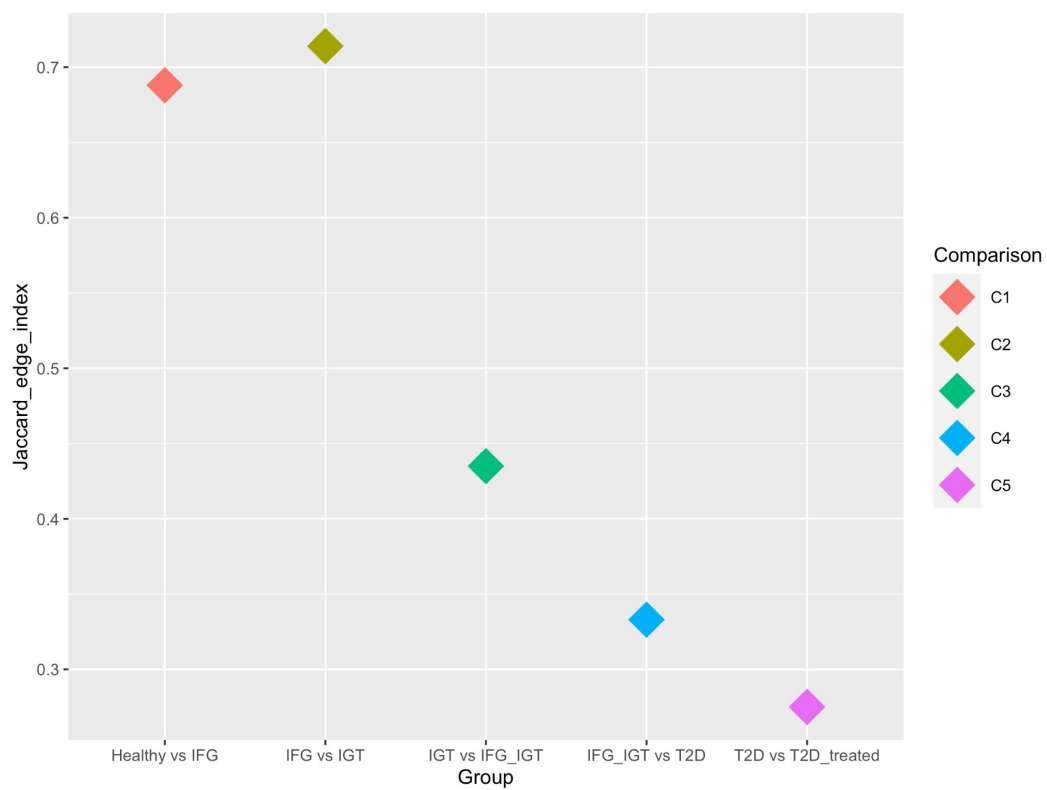


Figure S4-C. Jaccard Edge Index (JEI) for all pairwise comparisons in the T2D Mexican cohort.

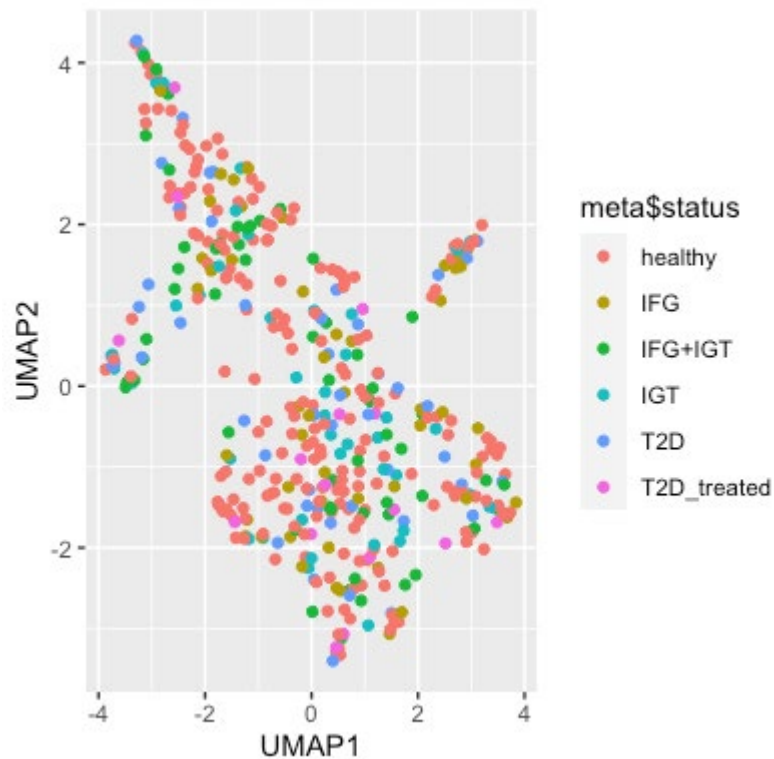


Figure S5-A UMAP analysis colored by groups: Healthy, IFG, IGT, IFG+IGT, T2D, and T2D_treated.

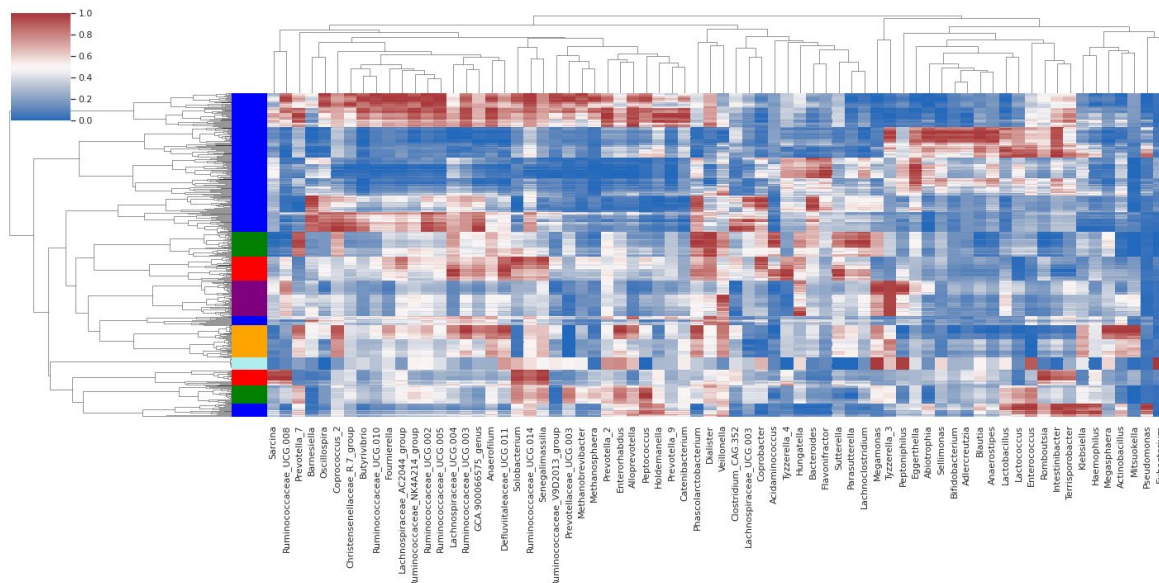


Figure S5-B Hierarchical analysis of the data imputed by mb-PHENIX imputed data.

We observed the top variable taxa (percentile=60) relevant abundance taxa data.

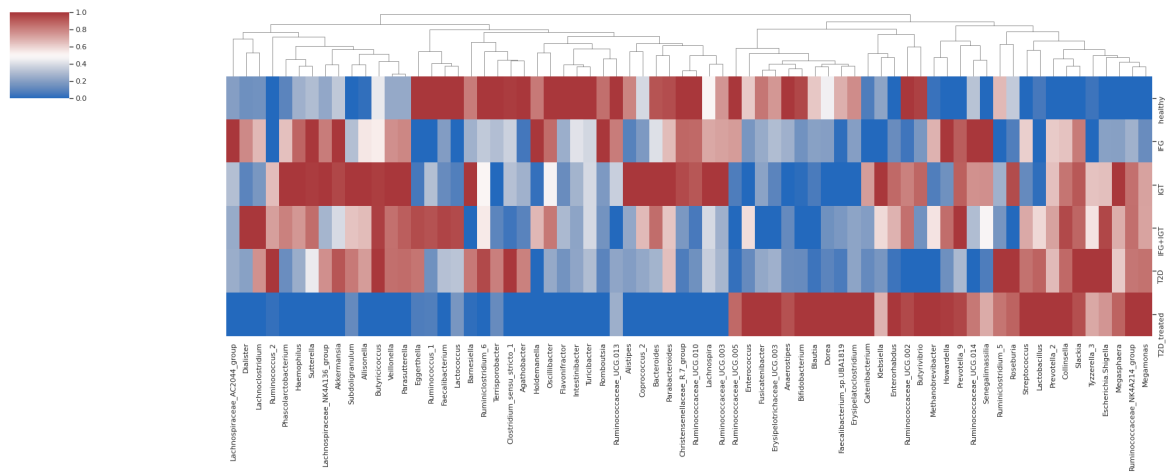


Figure S5-C Hierarchical analysis of the top 70 most relevant taxa before mb-PHENIX imputation among T2D states.