

## Differential microbial pattern description in subjects with autoimmune-based thyroid diseases

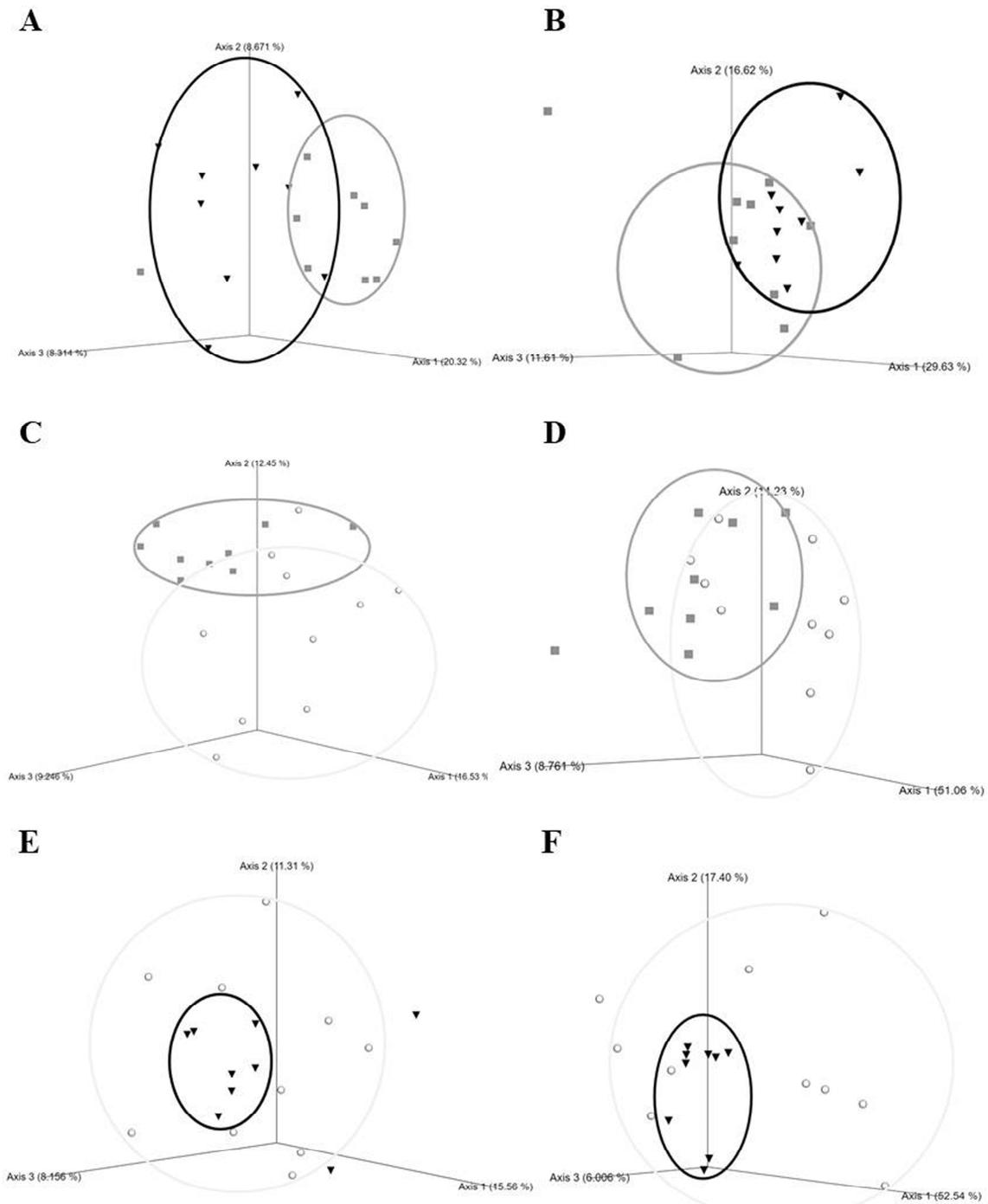
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### Supplementary Materials

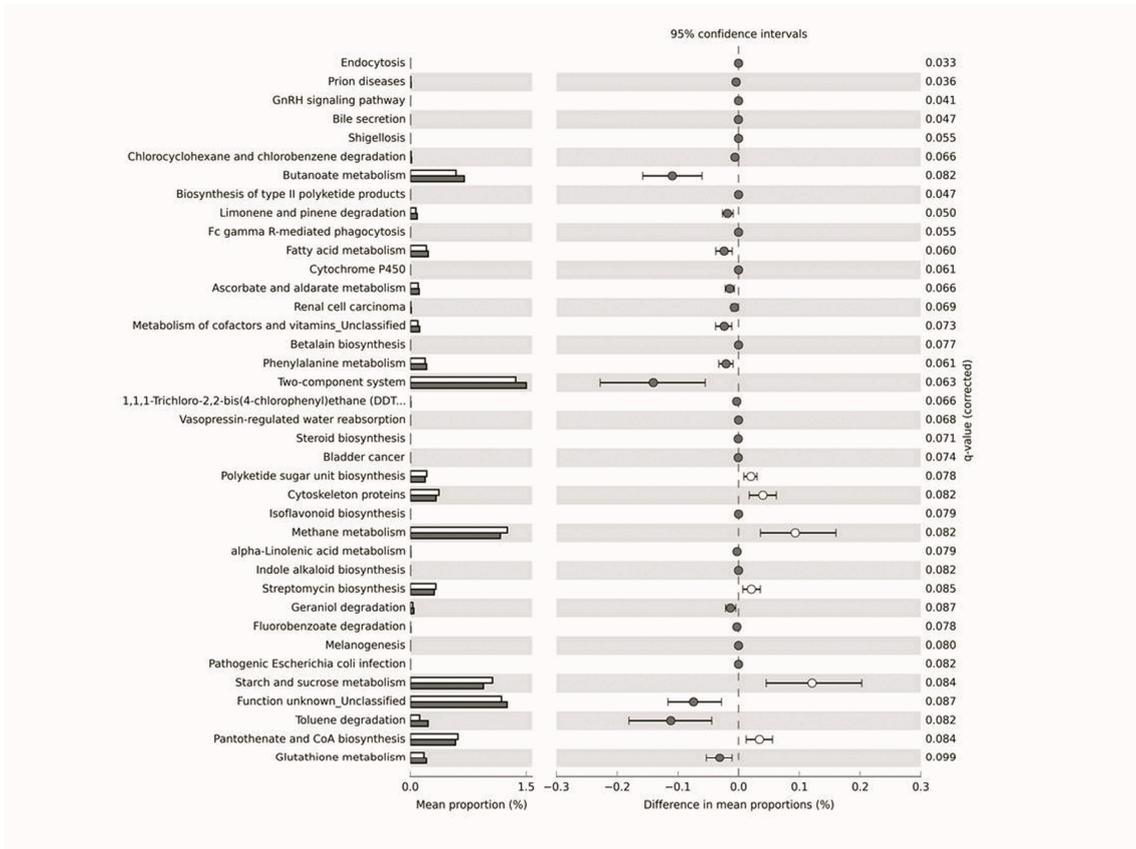
**Table S1.** Shared families and genera from each core microbiomes of the study group.

<b>15 common families in HT patients, GD patients and HDs</b>
<i>Bacteroidaceae</i>
<i>Lachnospiraceae</i>
<i>Ruminococcaceae</i>
<i>Alcaligenaceae</i>
<i>Desulfovibrionaceae</i>
<i>Rikenellaceae</i>
<i>Porphyomonadaceae</i>
<i>Odoribacteriaceae</i>
<i>Erysipelotrichaceae</i>
<i>Barnesiellaceae</i>
<i>Coriobacteriaceae</i>
<i>Veillonellaceae</i>
<i>Enterobacteriaceae</i>
<i>Bifidobacteriaceae</i>
<i>Clostridiaceae</i>
<b>12 common genera in HT patients, GD patients and HDs</b>
<i>Bacteroides</i>
<i>Sutterella</i>
<i>Parabacteroides</i>
<i>Bilophila</i>
<i>Ruminococcus</i>
<i>Odoribacter</i>
<i>Oscillospira</i>
<i>Faecalibacterium</i>
<i>Blautia</i>
<i>Lachnospira</i>
<i>Bifidobacterium</i>
<i>Coprococcus</i>

GD, Graves-Basedow's disease; HDs, healthy donors; HT, Hashimoto's thyroiditis.



**Figure S1.** Clustering of fecal bacterial communities according to the different study groups by PCoA using unweighted and weighted UniFrac distances. **(A)** Unweighted UniFrac distances between both AITDs patients,  $p=0.115$  and **(B)** Weighted UniFrac distances between AITD patients,  $p=0.169$ . **(C)** Unweighted UniFrac distances between GD patients and HDs,  $p=0.005$  and **(D)** Weighted UniFrac distances between GD patients and HDs,  $p=0.007$ . **(E)** Unweighted UniFrac distances between HT patients and HDs,  $p=0.05$  and **(F)** Weighted UniFrac distances between HT patients and HDs,  $p=0.021$ . Circles belong to the HDs; squares to GD patients and triangles to HT patients.



**Figure S2.** Significant differences in predicted functional composition at the level 3 of KEGG Pathways of the gut microbiota among HDs (white) and GD patients (dark grey). Only functional capacities with  $p < 0.1$  are shown;  $q = p$ -value FDR corrected.