

## Supplementary Material

### Title

Functional host-specific adaptation of the intestinal microbiome in Hominids

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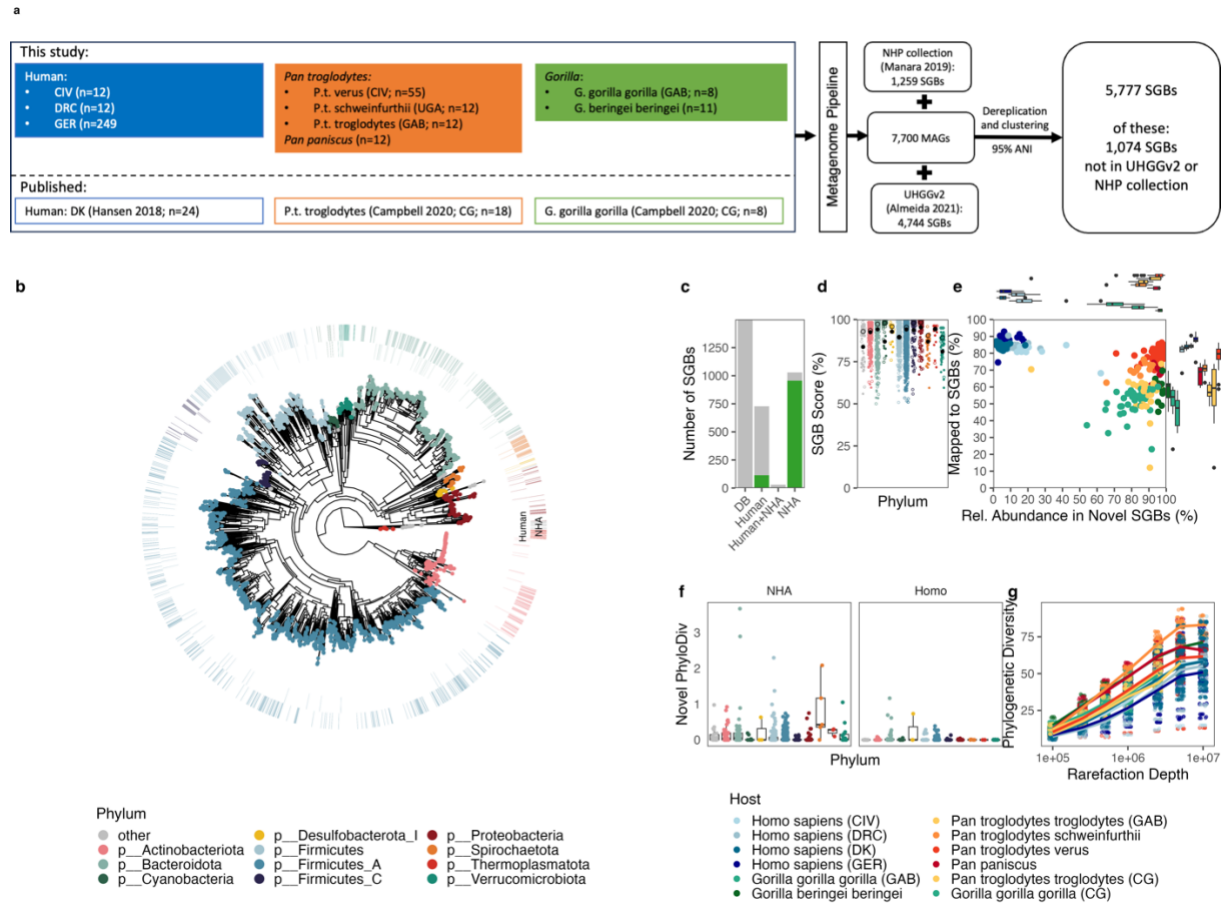
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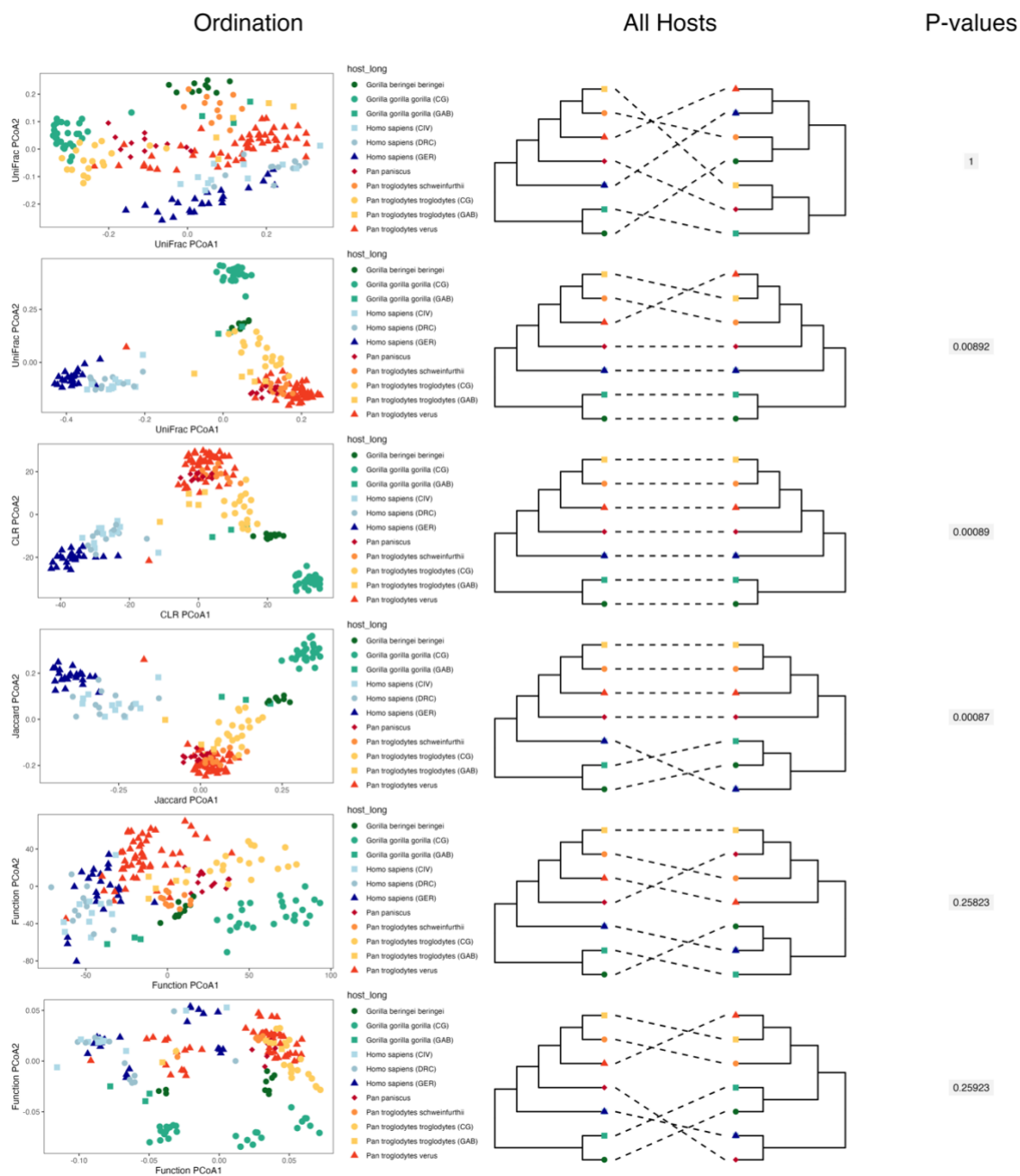
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## Supplementary Figures



**Supplementary Figure S1:** Genome statistics of newly reconstructed MAGs and representative MAGs from UHGGv2 and Manara et al. (2019). (a) overview on included datasets and data processing (b) Phylogeny of all 2,943 SGB representative MAGs based on 120 bacterial and 53 archaeal universal single-copy marker genes. (c) SGB origin and novelty (green) based on reconstructed MAG sequences from human and NHP hosts, as well as reference databases (UHGGv2 and Manara et al. 2019). (d) MAGScoT scores of all SGB representative genome sequences. Filled shapes represent previously recovered SGBs, unfilled shapes represent novel SGBs. (e) Mapping success and relative abundance in novel SGBs for the different host groups (n=211). (f) overall novelty by NHP and Human host groups measured by Faith's phylogenetic diversity. (g) per-sample and per-group phylogenetic diversity in relation to metagenomic rarefaction depth based on n=211 independent samples (n<sub>Human</sub>=71, n<sub>Chimpanzee</sub>=91, n<sub>Bonobo</sub>=12, n<sub>Gorilla</sub>=40)



**Supplementary Figure S2:** Ordination, hierarchical clustering and results from the phyllosymbiosis analysis for six distance measures: weighted UniFrac, unweighted UniFrac, genus-level Aitchison distance (CLR-transformed genus abundances), genus-level Jaccard distance, as well as distances based on KEGG ontology functional abundances and presence/absence patterns of KEGG ontology functions.