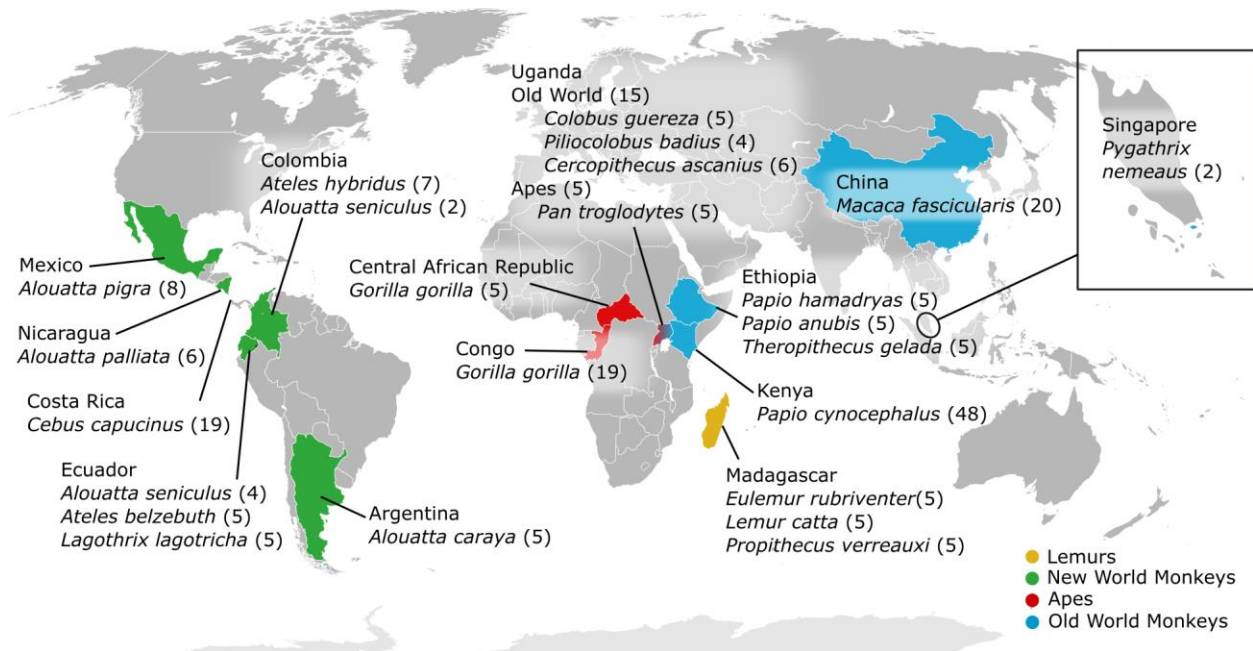
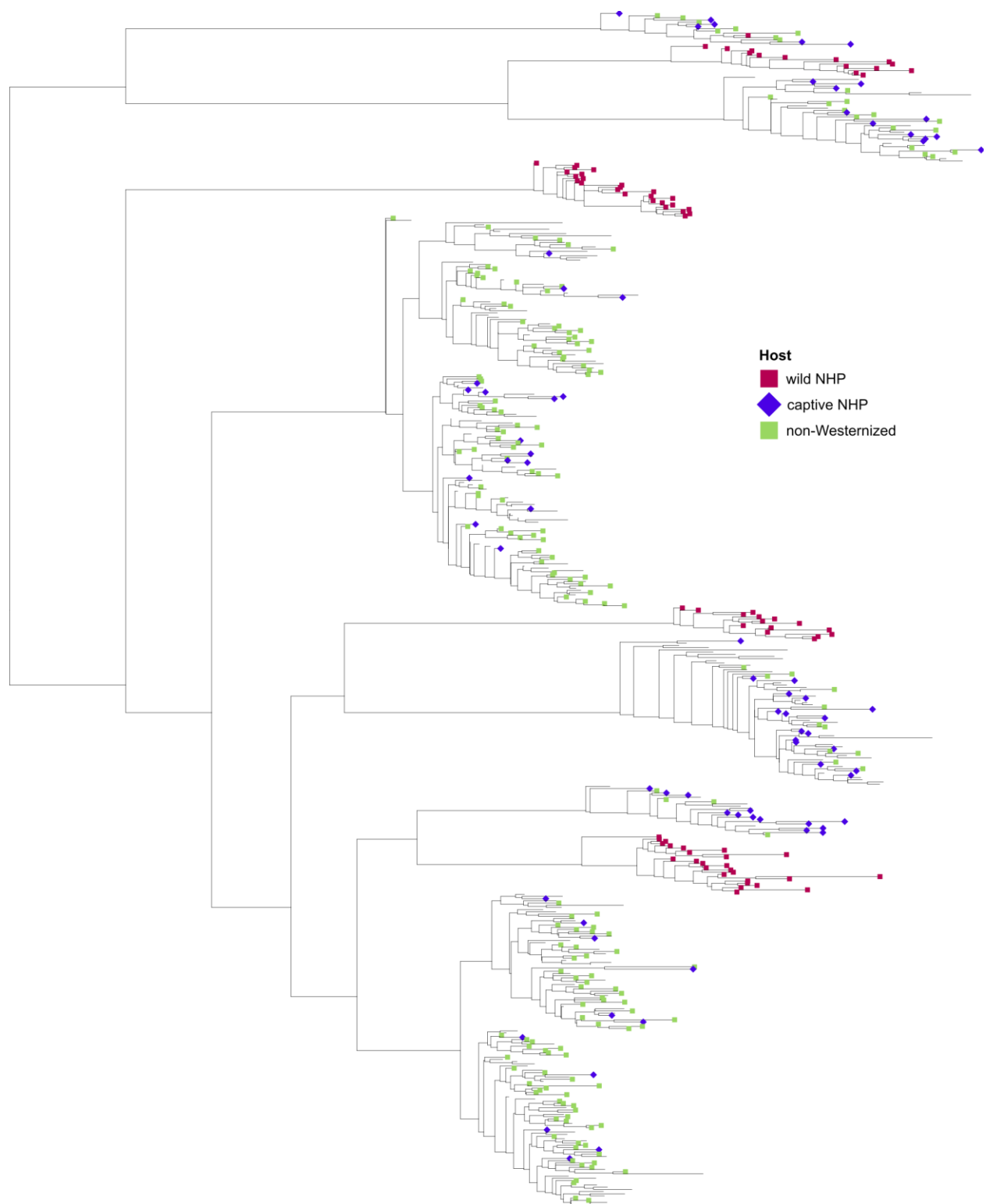


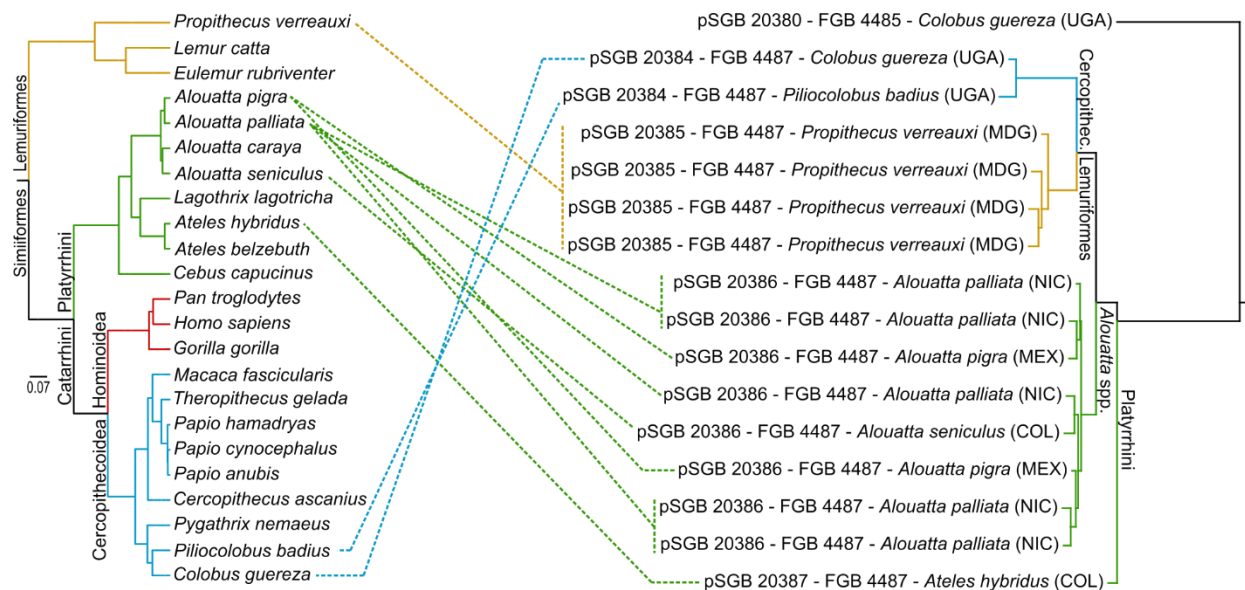
Supplementary Figures



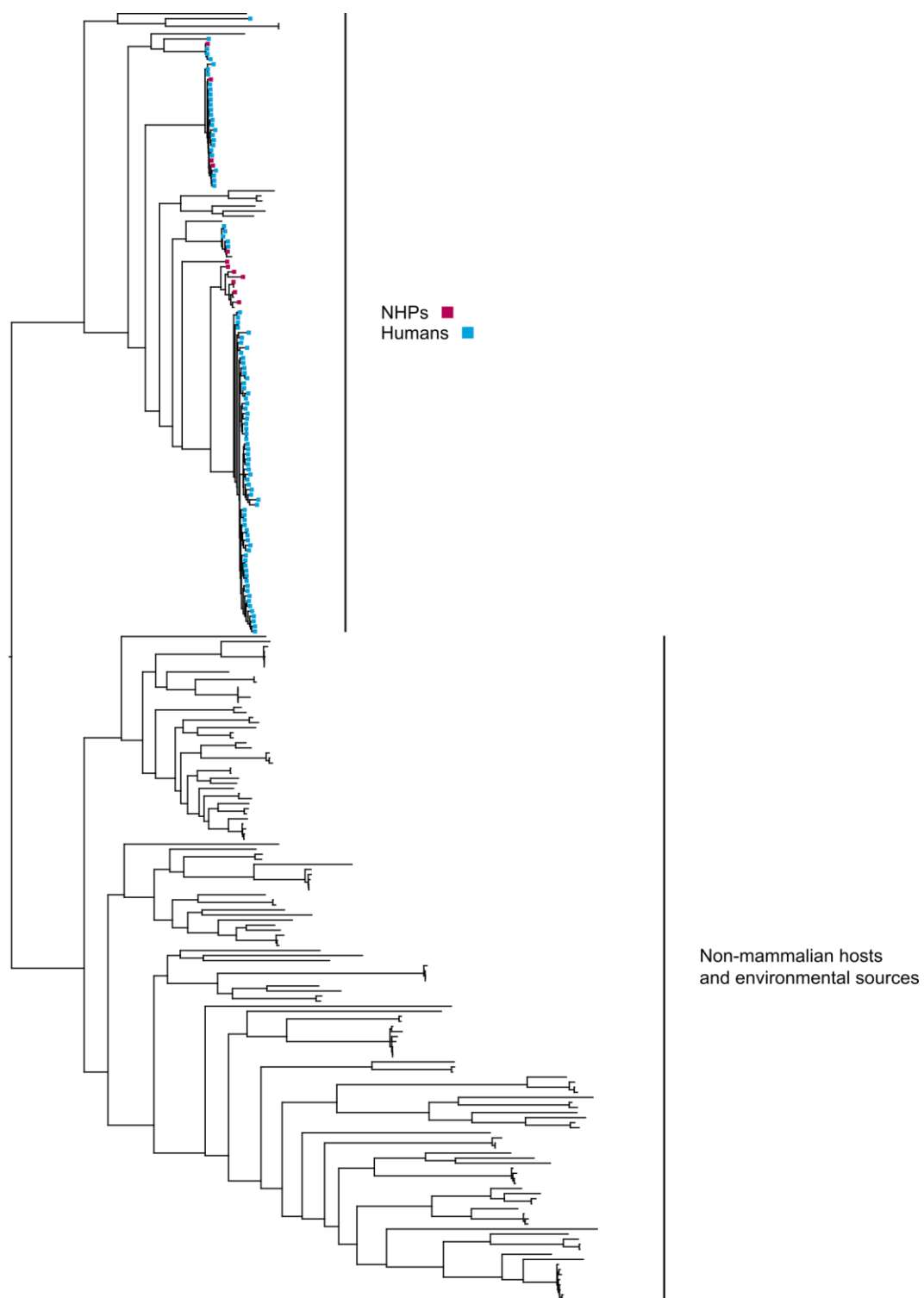
Additional file 2: Figure S1. World map reporting NHP metagenomic samples considered in this study together with host and country information.



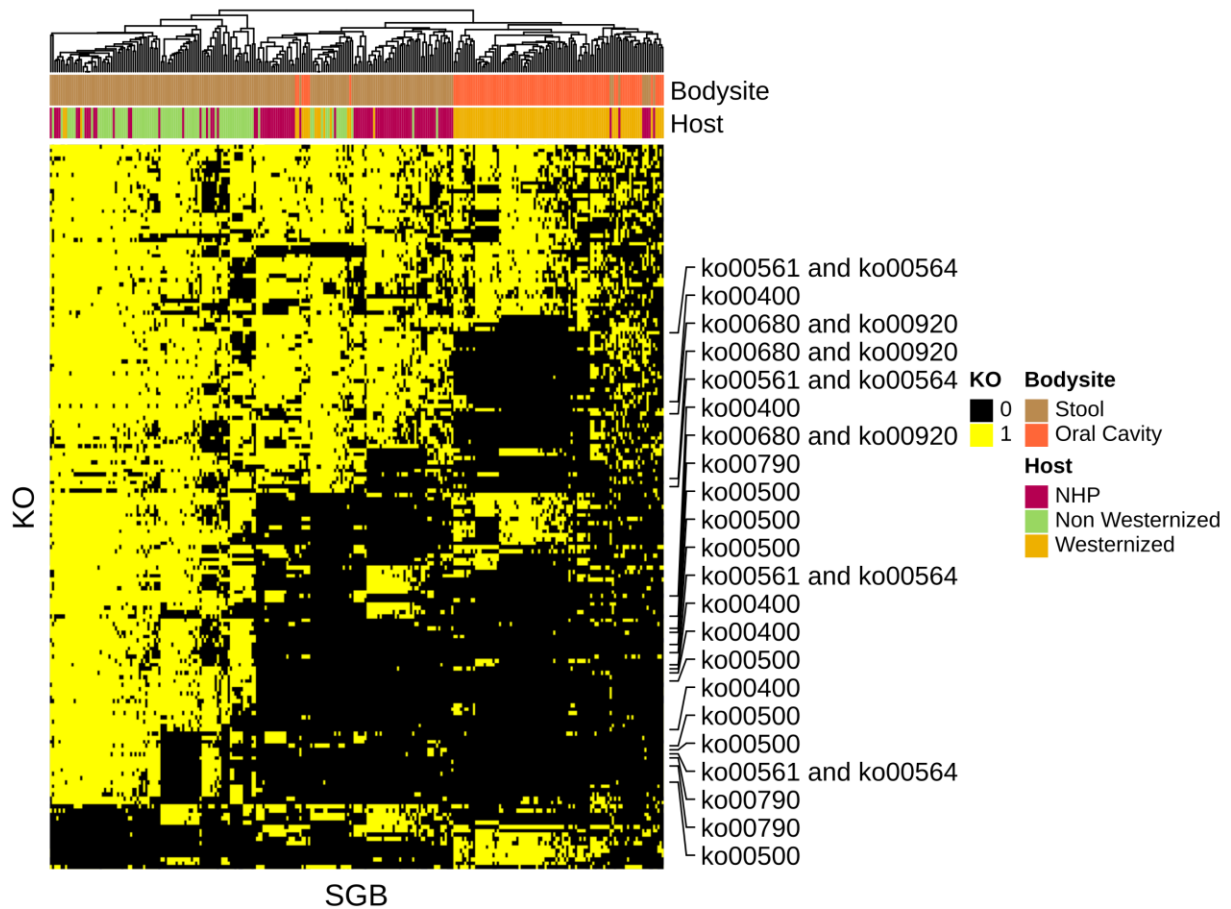
Additional file 2: Figure S2. Phylogenetic tree of the Bacteroidetes phylum (uncollapsed version of the tree in **Figure 4B**).



Additional file 2: Figure S3. Comparison between the phylogeny of the host species surveyed in this study and the one of FGB 4487, the only FGB spanning three out of the four host clades. Dashed lines link each MAG of the FGB 4487 tree with the host it was retrieved from, thus showing that genetically close hosts tend to harbor genetically similar bacterial strains.



Additional file 2: Figure S4. Phylogenetic tree of the Elusimicrobia phylum (uncollapsed version of the tree in **Figure 4C**).



Additional file 2: Figure S5. KO presence/absence profile in *Treponema* MAGs recovered from both stool and oral cavity samples. Only KOs related to metabolism and present in at least 20% and less than 80% of samples are reported.