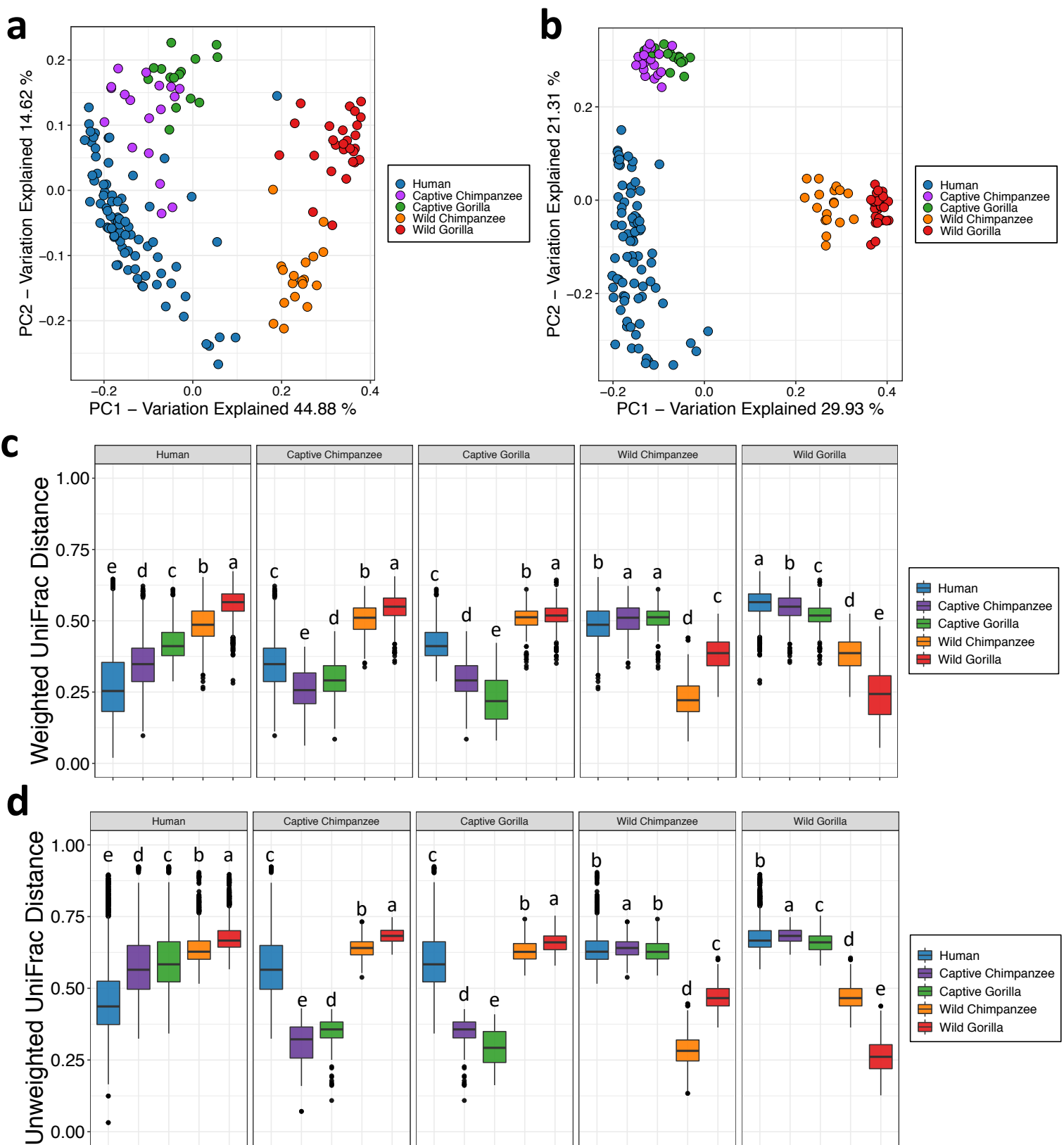
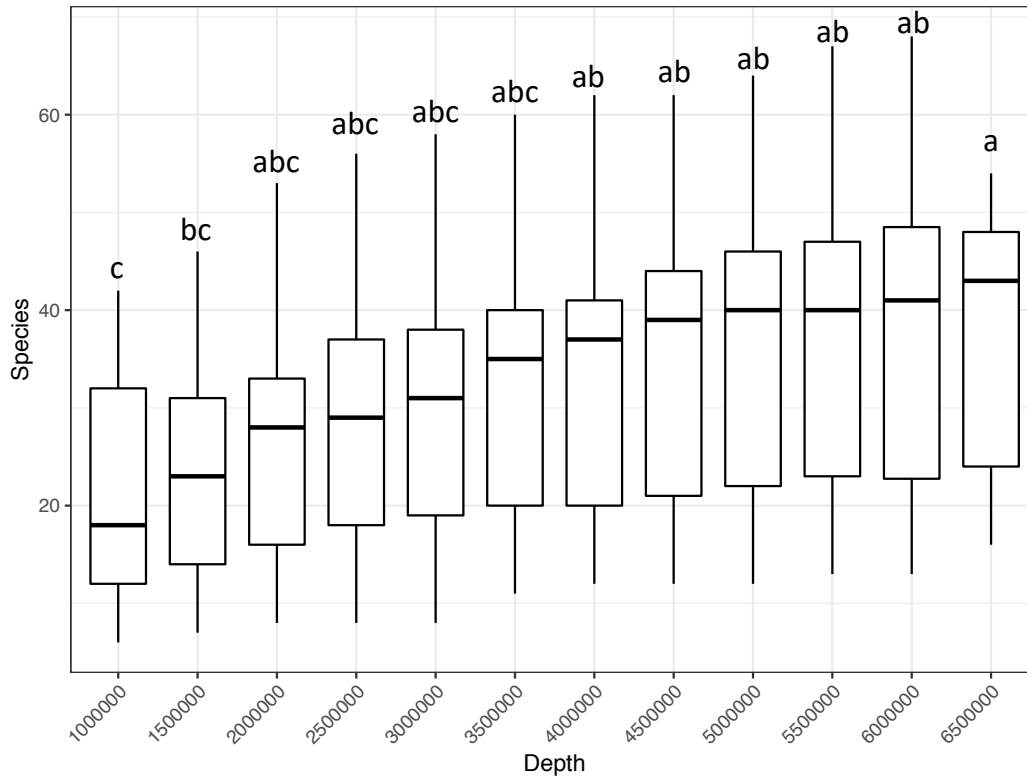


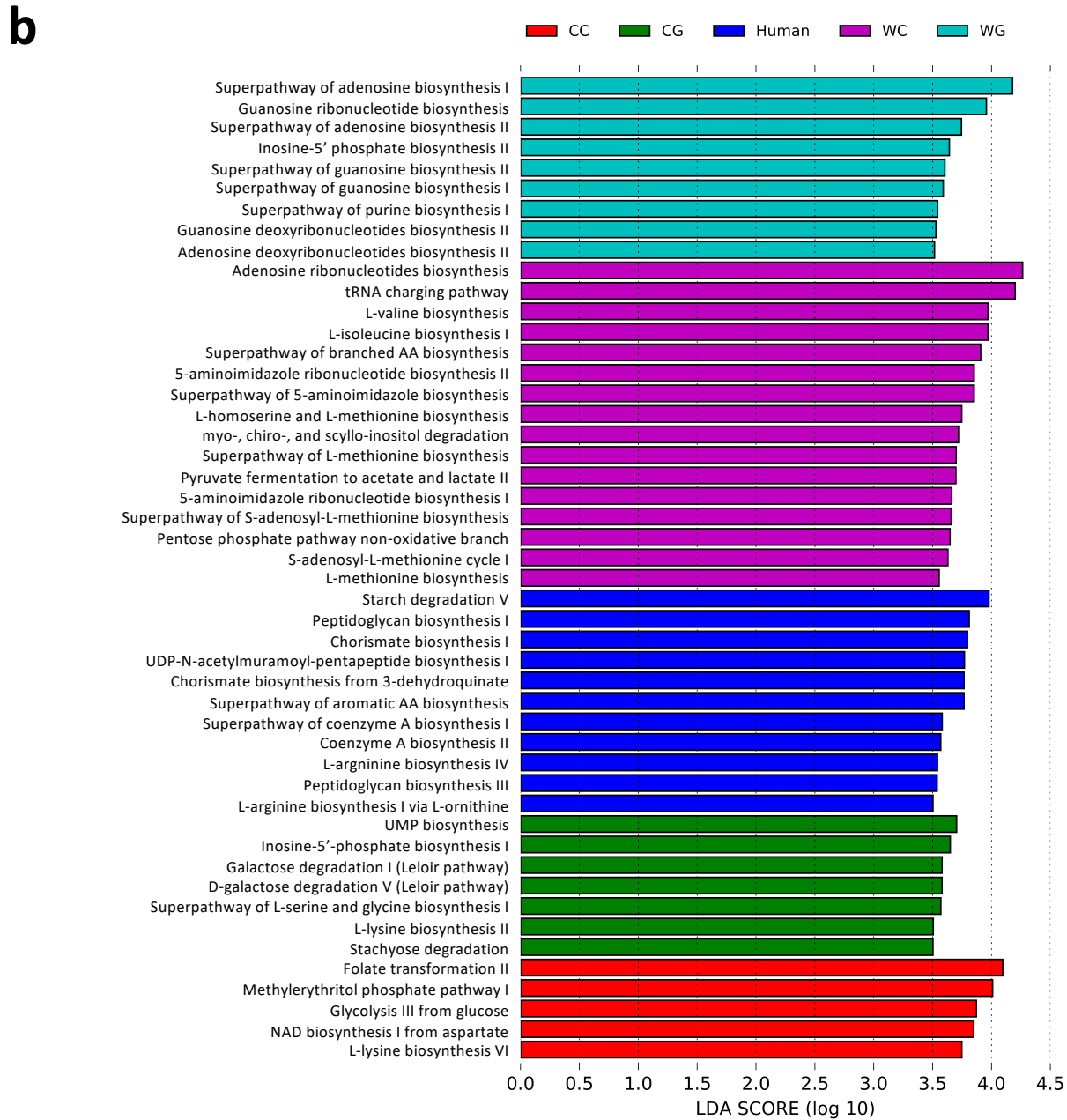
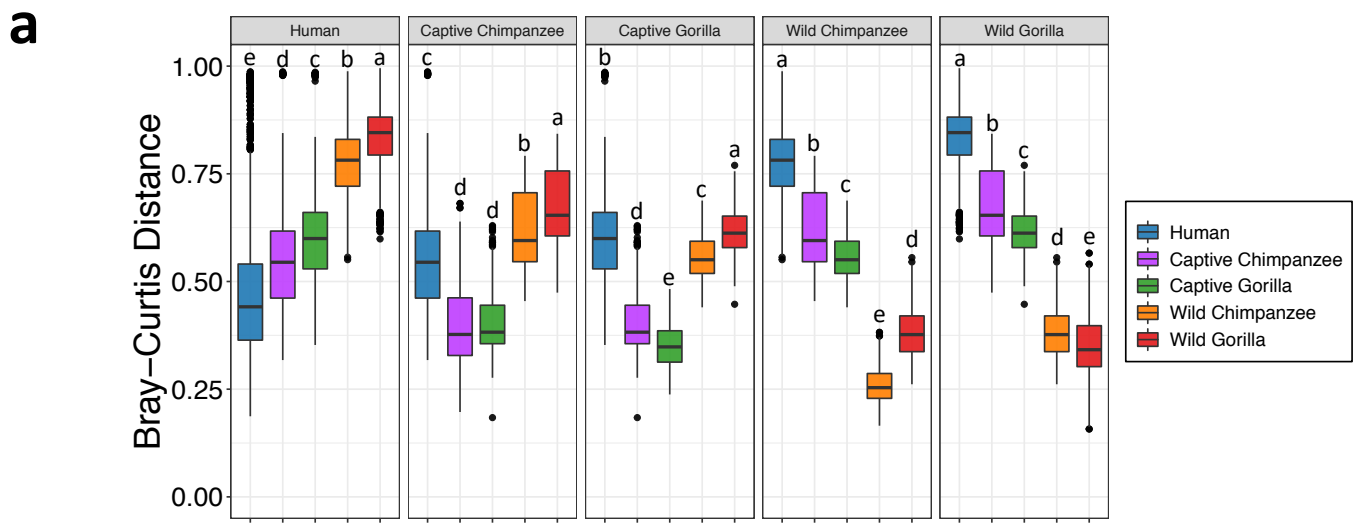
Supplementary Fig. 1: Taxonomic differences in host cohorts. **a**, Boxplot of Bray-Curtis distances between host cohorts (Kruskal-Wallis sum-rank test $P < 2.2e-16$; Wilcoxon sum rank test with BH correction, all significant differences $P \leq 0.044$). Significant differences across facets are not indicated. **b**, Shannon diversity index (Kruskal-Wallis $P = 8.9e-6$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.0076$). **c**, Faith's Phylogenetic Diversity (PD) (Kruskal-Wallis $P = 5.31e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.0005$). **d**, Boxplot of log transformed 16S sequencing depth (Kruskal-Wallis $P = 0.18$). **e**, Cladogram of discriminatory taxa identified in captive and wild chimpanzees (LEfSe LDA log score >4.5 , $P = 0.05$). **f**, Cladogram of discriminatory taxa identified in captive and wild gorillas (LEfSe LDA log score >4.5 , $P = 0.05$).



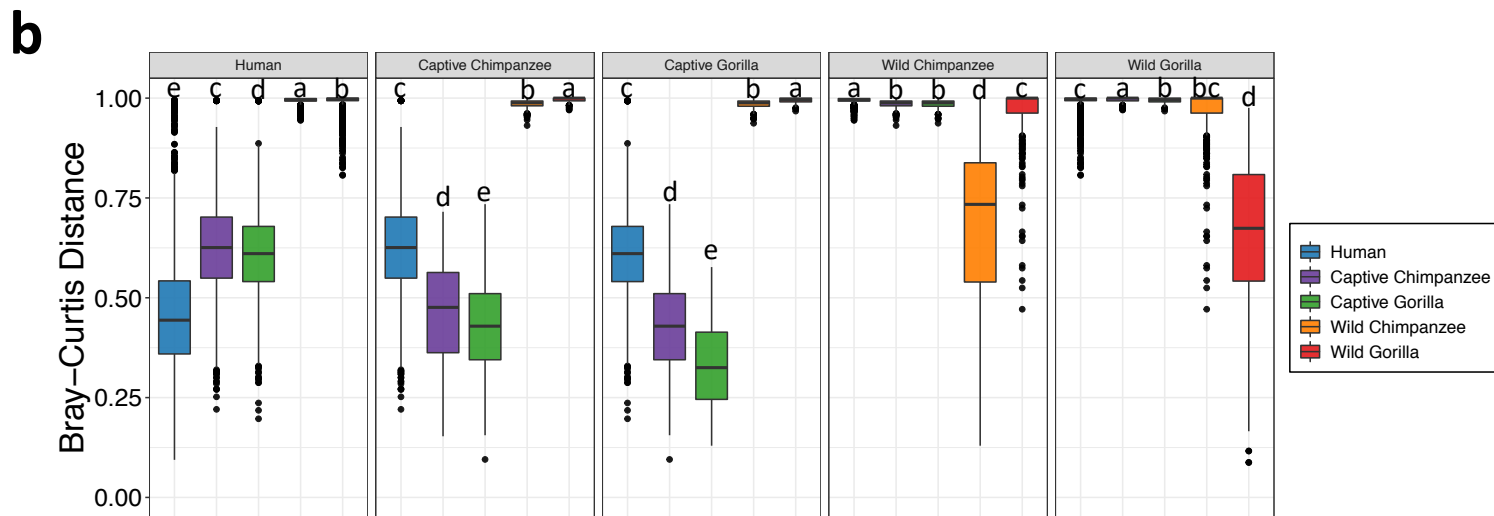
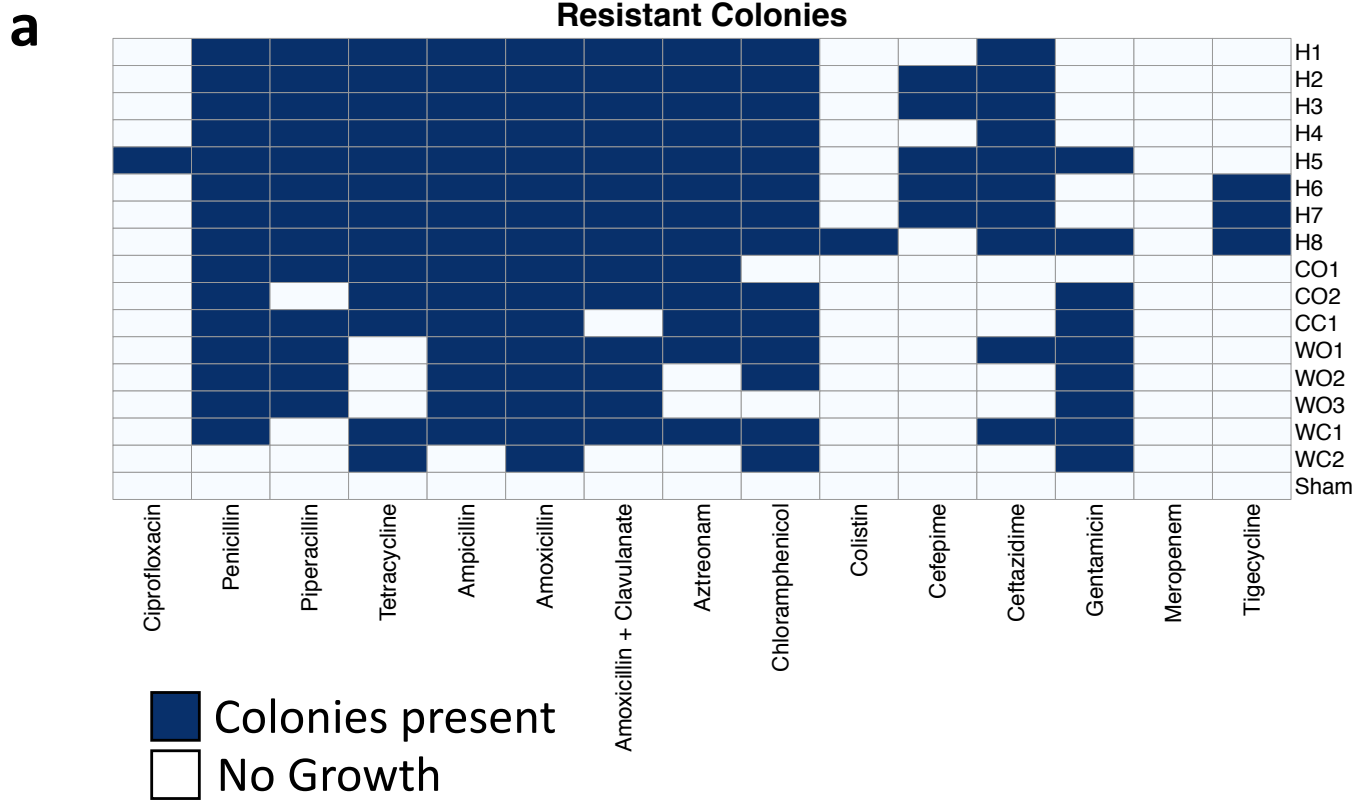
Supplementary Fig. 2: UniFrac distance analysis of 16S taxonomic data. **a**, PCoA plot of weighted UniFrac distances from individual human, chimpanzee, and gorilla fecal samples (adonis, $R^2 = 0.58$, $P = 0.001$). **b**, PCoA plot of unweighted UniFrac distances (adonis, $R^2 = 0.53$, $P = 0.001$). **c**, Boxplot of weighted UniFrac distances (Kruskal-Wallis sum-rank test $P < 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.024$). Significant differences across facets are not indicated. **d**, Boxplot of unweighted UniFrac distances (Kruskal-Wallis sum-rank test $P < 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.002$). Significant differences across facets are not indicated.



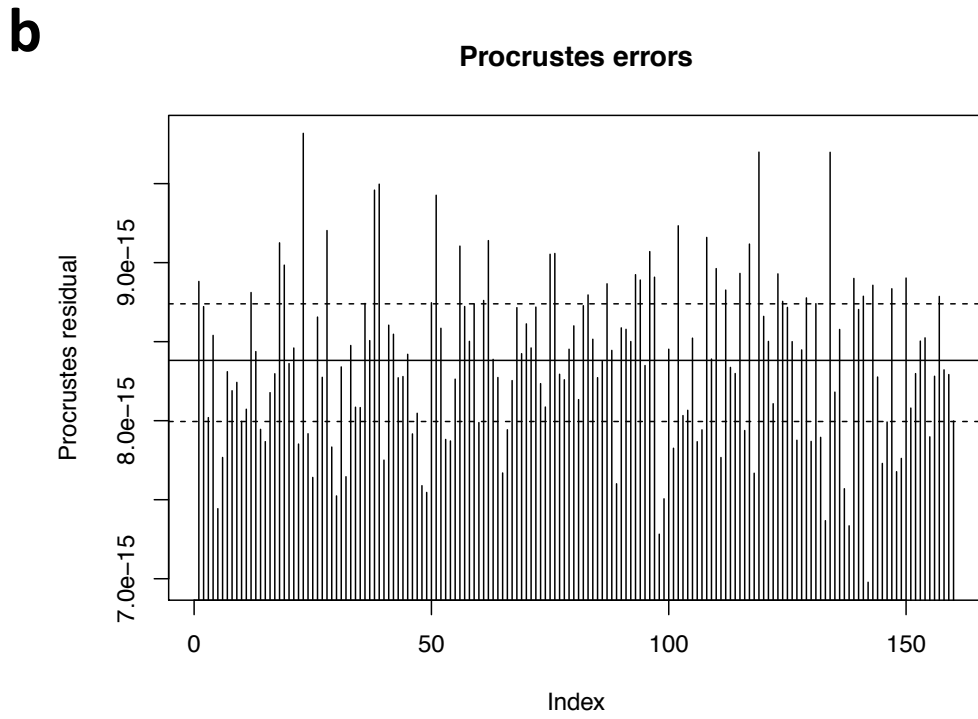
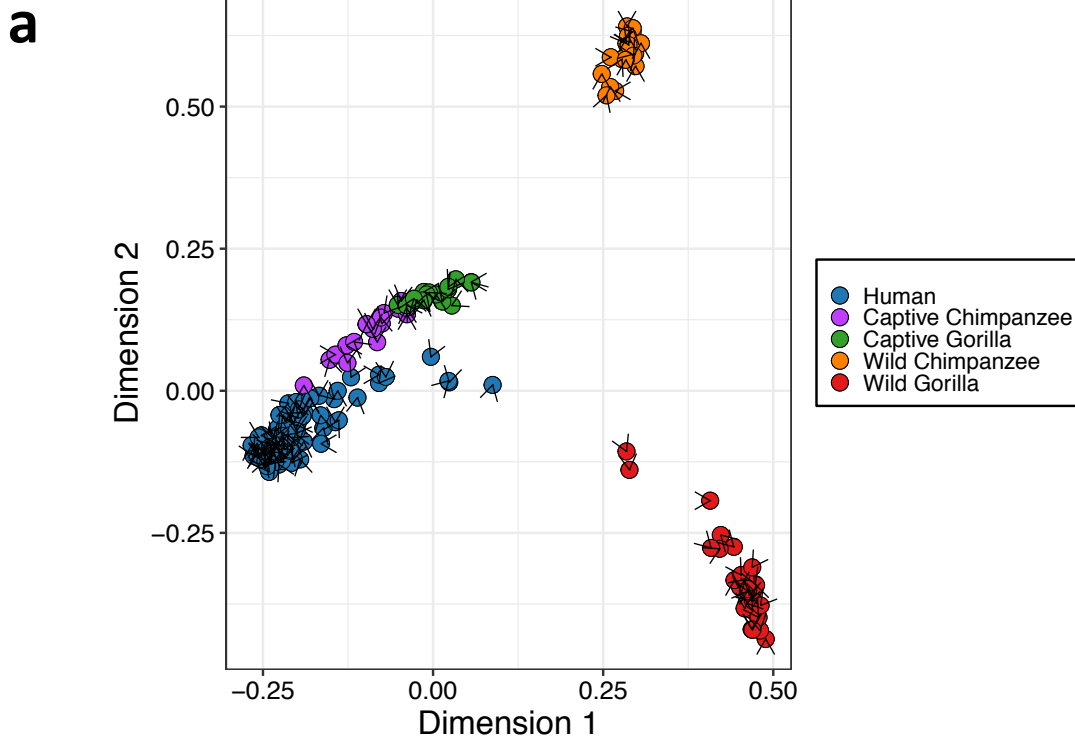
Supplementary Fig. 3: Shotgun metagenomic rarefaction analysis. a, Rarefaction analysis on shotgun reads performed using a subset of 25 samples including all 5 cohorts (Kruskal-Wallis sum-rank test $P < 2.3e-4$; Wilcoxon rank sum test with BH correction, for significant differences $P \leq 0.042$). Species were identified from metagenomic reads using MetaPhlan2.



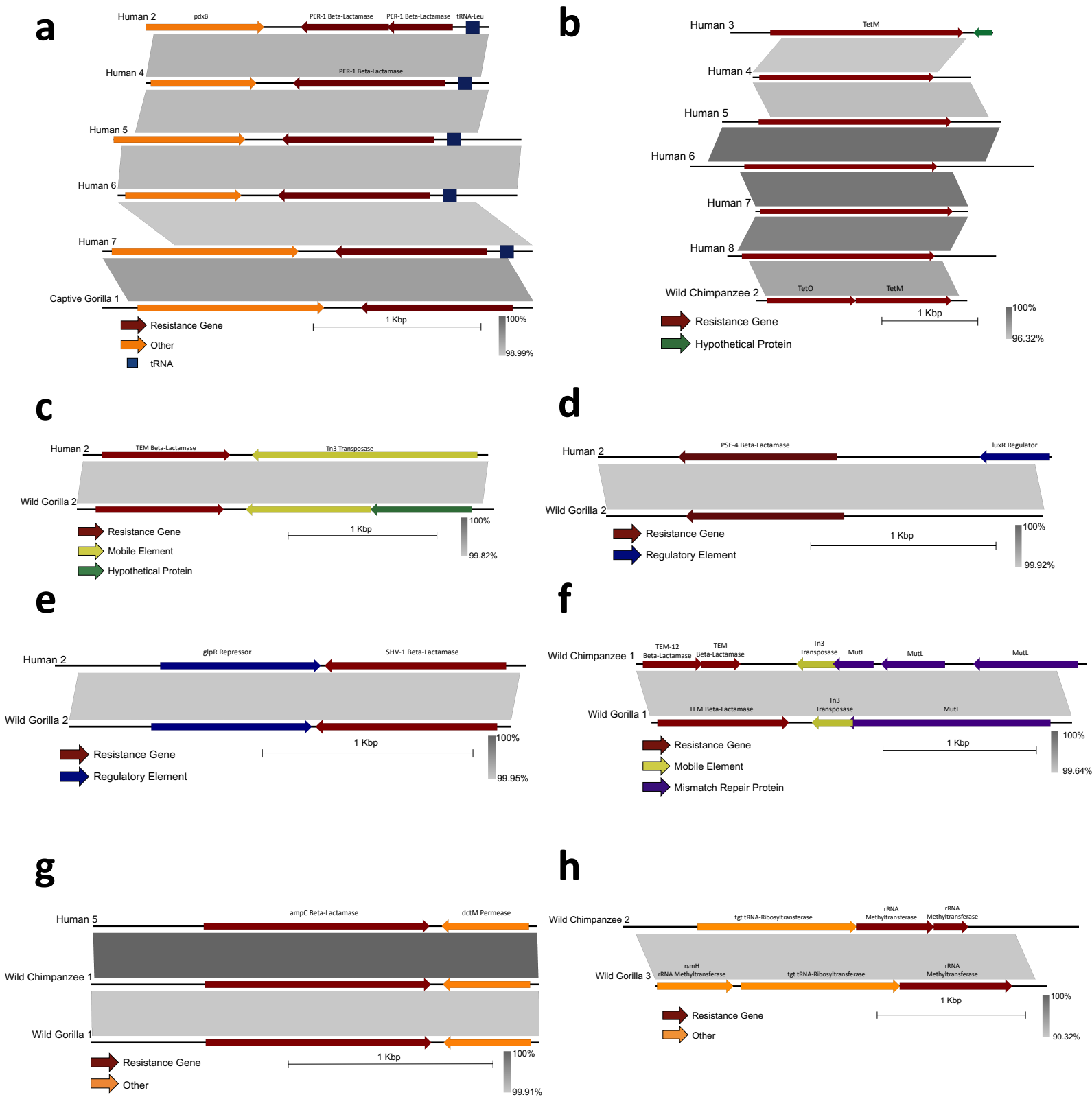
Supplementary Fig. 4: Gene family and functional pathway analysis of host microbiota. a, Boxplot of Bray-Curtis distances of gene families (Kruskal-Wallis sum-rank test $P < 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.034$). Significant differences across facets are not indicated. **b**, Discriminatory functional pathways identified in captive chimpanzees (CC), captive gorillas (CG), humans, wild chimpanzees (WC), and wild gorillas (WG) (LefSe log score > 3.5 , $P = 0.05$).



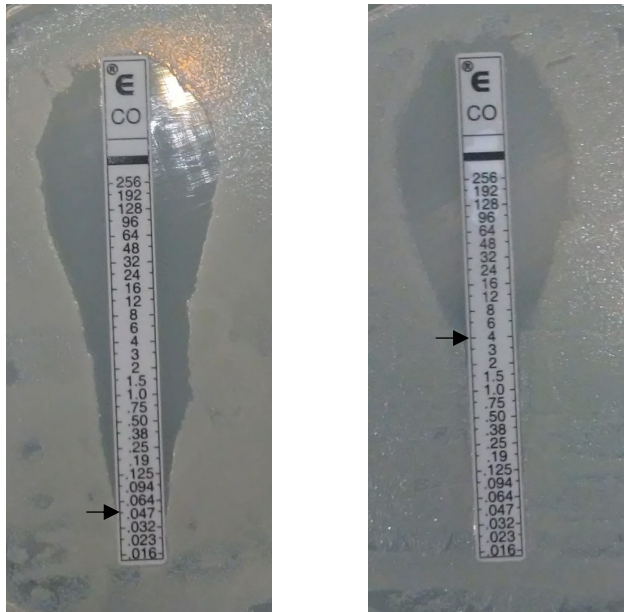
Supplementary Fig. 5: Resistome analysis of humans, chimpanzees, and gorillas. a, Heatmap showing functional metagenome growth results on selective media. Blue squares indicate that colonies were present and white squares indicate no growth was present. Functional libraries are named as described in Supplementary Table 1. **b,** Boxplot of Bray-Curtis distances of ARG RPKM abundance (Kruskal-Wallis sum-rank test $P < 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.008$). Significant differences across facets are not indicated.



Supplementary Fig. 6: Procrustes analysis comparing taxonomic and ARG results. **a**, Procrustes analysis of the correlation between taxonomic communities and ARGs (PROTEST: sum of squares = 0.13; Correlation = 0.93; $P = 0.001$). **b**, Procrustes residual errors for each individual sample.



Supplementary Fig. 7: Alignments of ARG containing DNA fragments with high similarity across host cohorts. a-h, The library from which the contig originated is indicated.

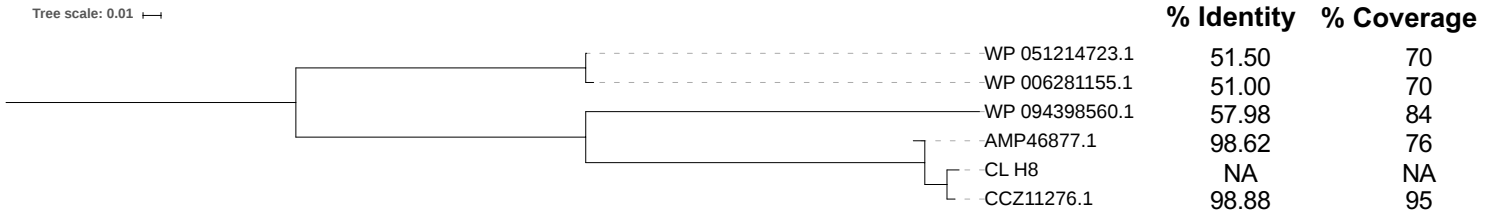
a

EV Control

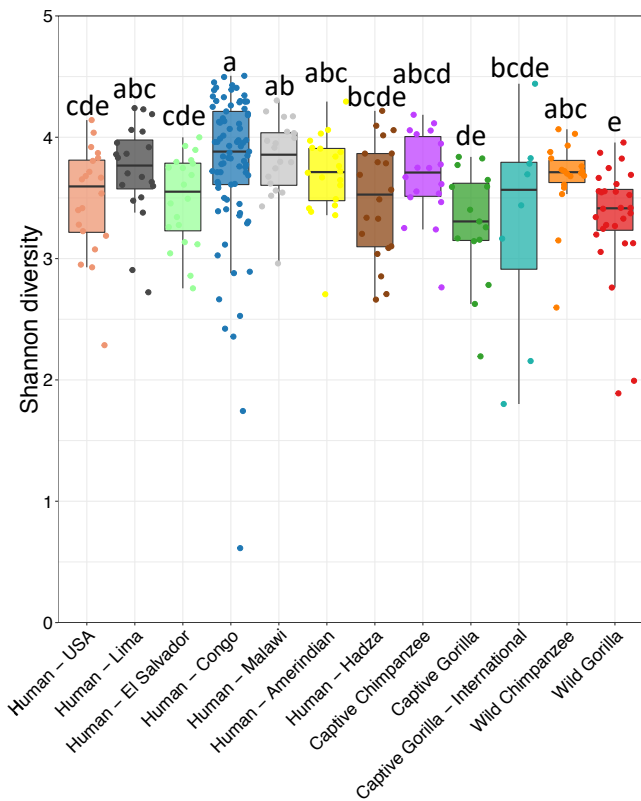
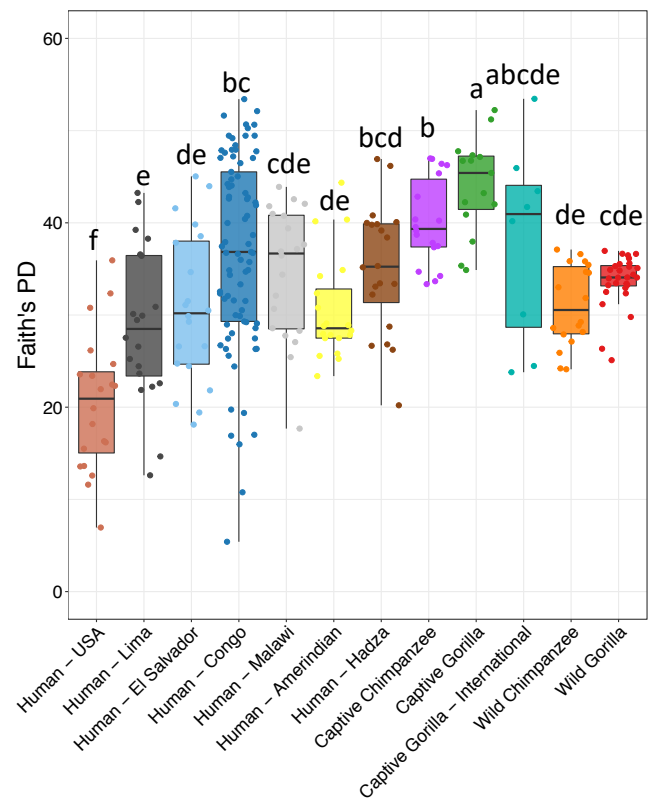
CL H8 Protein

b

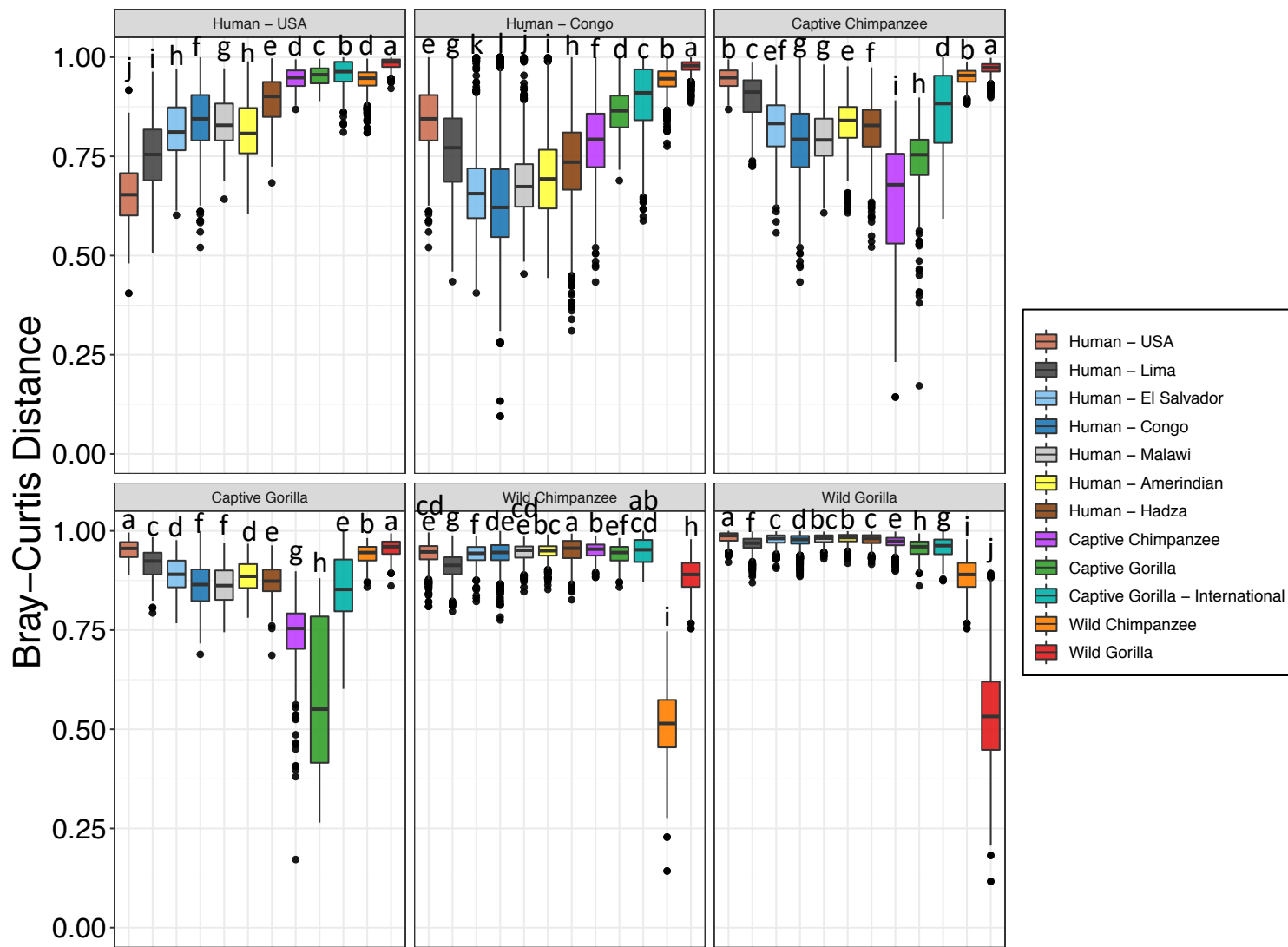
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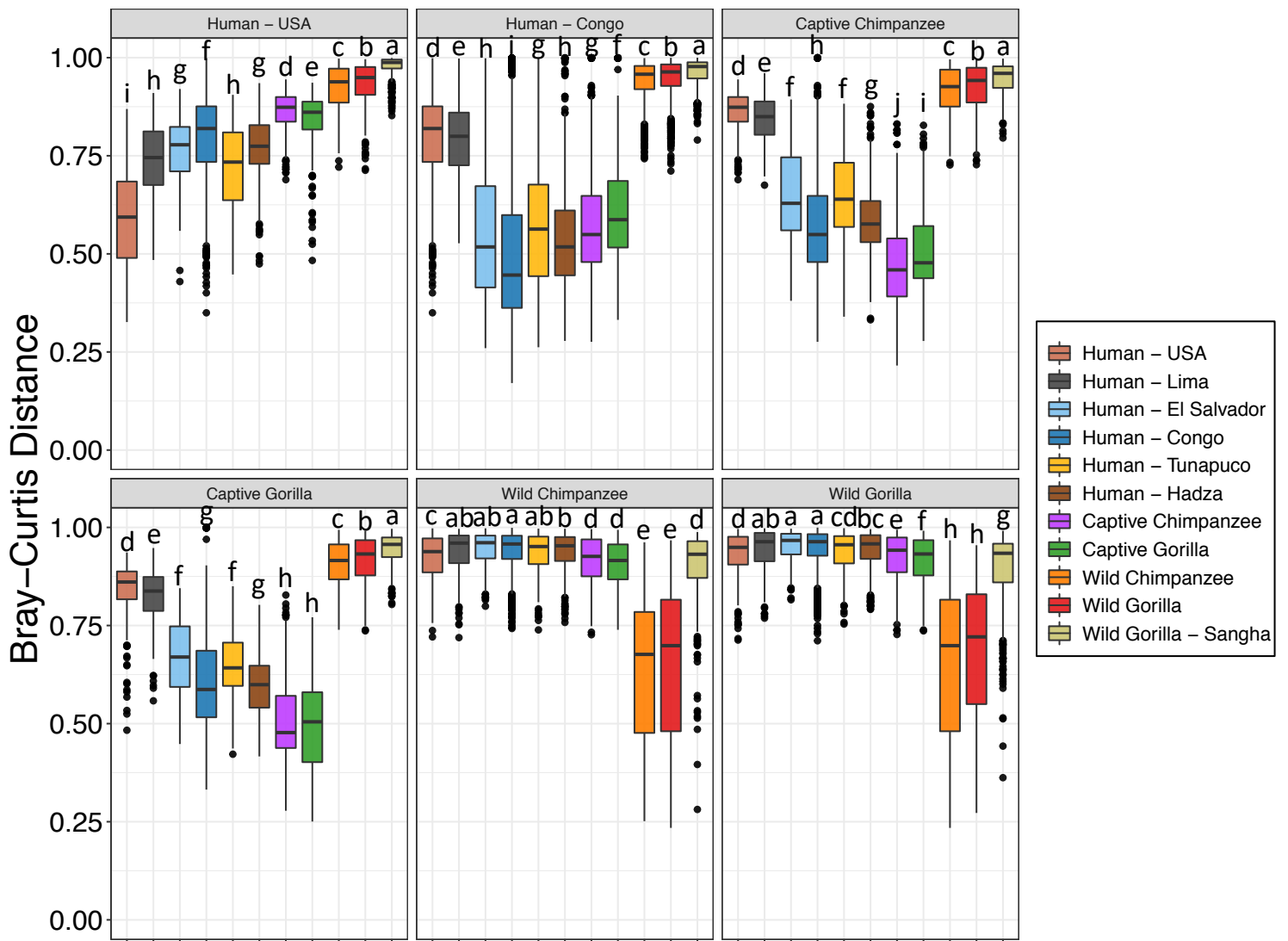
Supplementary Fig. 8: Endogenous expression of colistin ARG is highly resistant to colistin. a, MIC of colistin against empty vector (EV) control and the novel colistin resistance protein (CL H8). **b**, Phylogenetic tree of the colistin resistance protein to the closest BLAST hits from the NCBI non-redundant protein database accessed May 18, 2019. Percent identity and percent coverage are given for each protein in comparison to CL H8.

a**b**

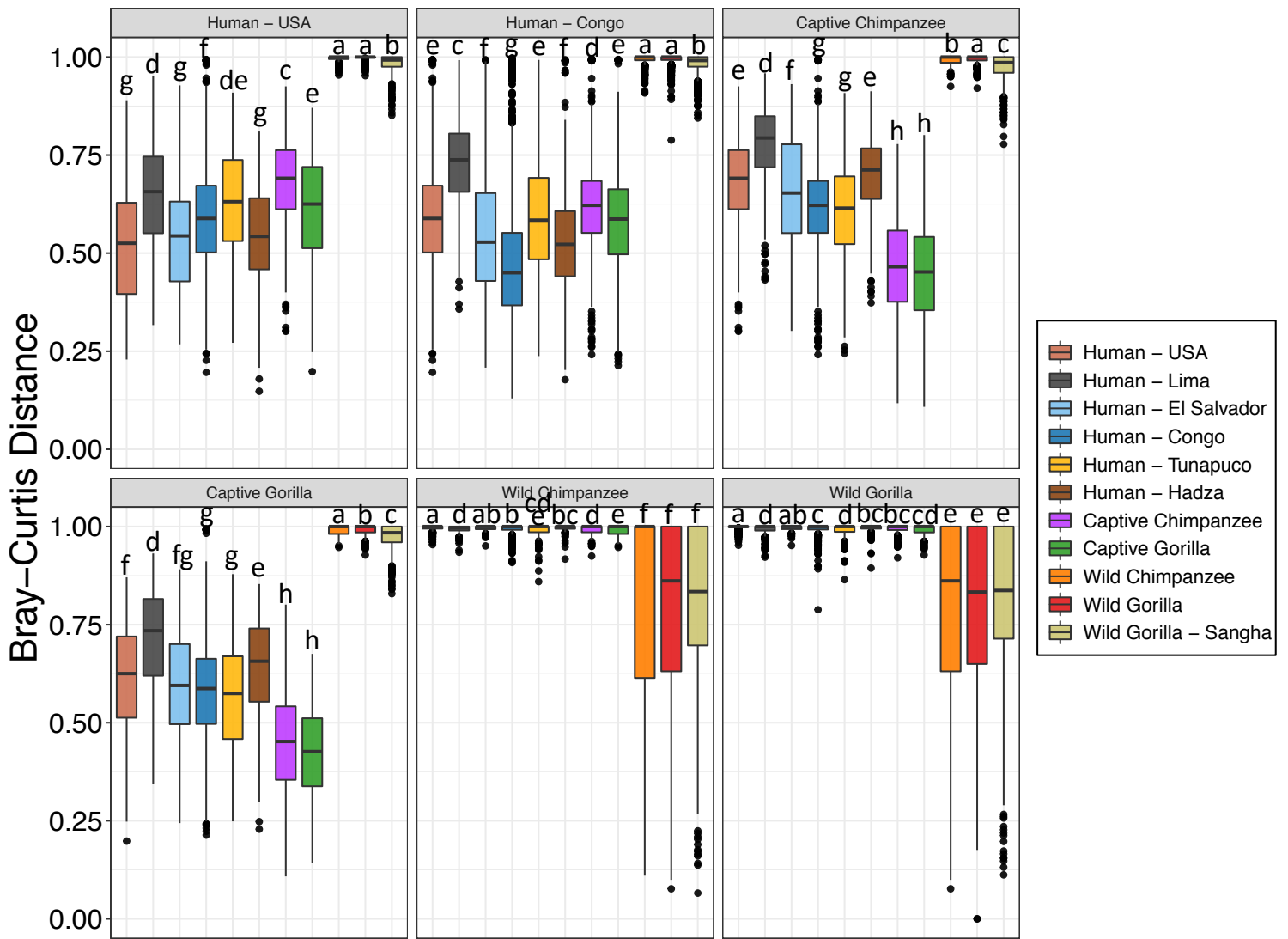
Supplementary Fig. 9: Alpha diversity of human and ape microbiomes across a gradient of Westernization. **a**, Shannon diversity of apes and humans (Kruskal-Wallis sum-rank test $P = 1.5e-6$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.049$). **b**, Faith's Phylogenetic Diversity (PD) (Kruskal-Wallis sum-rank test $P = 4.05e-14$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.05$).



Supplementary Fig. 10: Bray-Curtis distances of microbiome taxa across a gradient of Westernization. Bray-Curtis distance of apes and humans (Kruskal-Wallis sum-rank test $P = 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.045$). Significant differences across facets are not indicated.



Supplementary Fig. 11: Bray-Curtis distances of microbiome gene families across a gradient of Westernization. Bray-Curtis distance of apes and humans (Kruskal-Wallis sum-rank test $P = 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.044$). Significant differences across facets are not indicated.



Supplementary Fig. 12: Bray-Curtis distances of resistomes across a gradient of Westernization. Bray-Curtis distance of apes and humans (Kruskal-Wallis sum-rank test $P = 2.2e-16$; Wilcoxon rank sum test with BH correction, all significant differences $P \leq 0.039$). Significant differences across facets are not indicated.

Host Species	Samples	Library Name	# of samples included in library	Library Size (GB)
Human	81	H1	11	1.04-2.61
		H2	10	1.26-3.02
		H3	9	2.06-3.13
		H4	10	1.81-5.61
		H5	10	12.37-30.96
		H6	10	5.23-12.68
		H7	9	2.01-5.14
		H8	10	4.18-10.8
Captive Gorilla	15	CO1	7	3.87-5.46
		CO2	8	4.37-6.61
Captive Chimpanzee	17	CC1	17	1.46-4.29
Wild Gorilla	28	WO1	8	2.73-10.73
		WO2	10	0.41-2.51
		WO3	9	2.42-6.23
Wild Chimpanzee	18	WC1	9	3.58-7.05
		WC2	9	1.09-6.53

Supplementary Table 1: Pooling scheme for functional metagenomic library preparation. Extracted fecal DNA was pooled to create 5 μg expression libraries for functional metagenomic library preparation. Extractions with low concentrations required pooling of more samples to achieve a final DNA yield of 5 μg .

Data sets

Data set 1: Statistical test output file

Data set 2: Metadata for all external samples included

Data set 3: 16S counts file

Data set 4: 16S taxonomy file

Data set 5: Metagenome gene families counts file

Data set 6: Metagenome functional pathways counts file

Data set 7: Resistome RPKM counts file

Data set 8: 16S counts file with published data

Data set 9: 16S taxonomy file with published data

Data set 10: Metagenome gene families counts file with published data

Data set 11: Resistome RPKM counts file with published data

Data set 12: LEfSe 16S all samples output file

Data set 13: LEfSe 16S chimpanzee only output file

Data set 14: LEfSe 16S gorilla only output file

Data set 15: LEfSe functional pathway output file