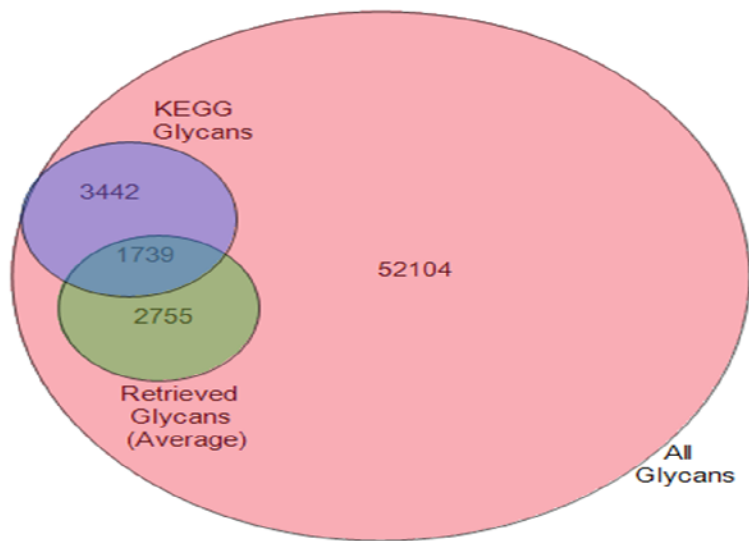
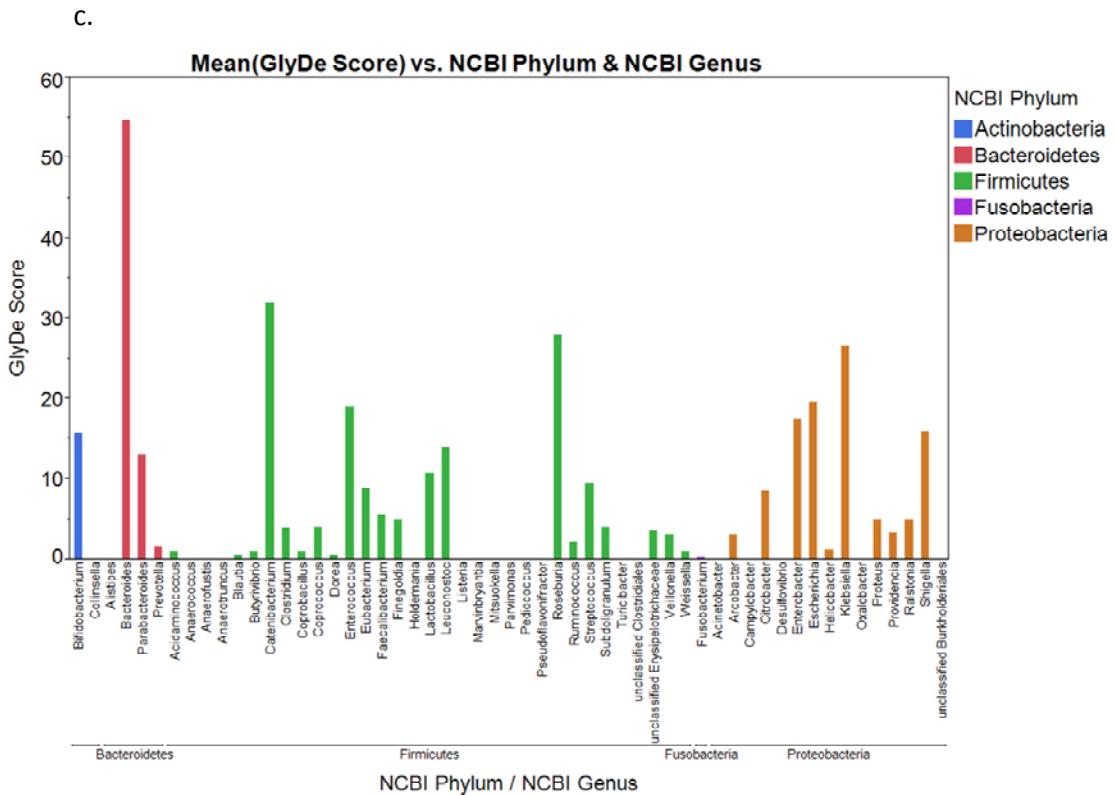
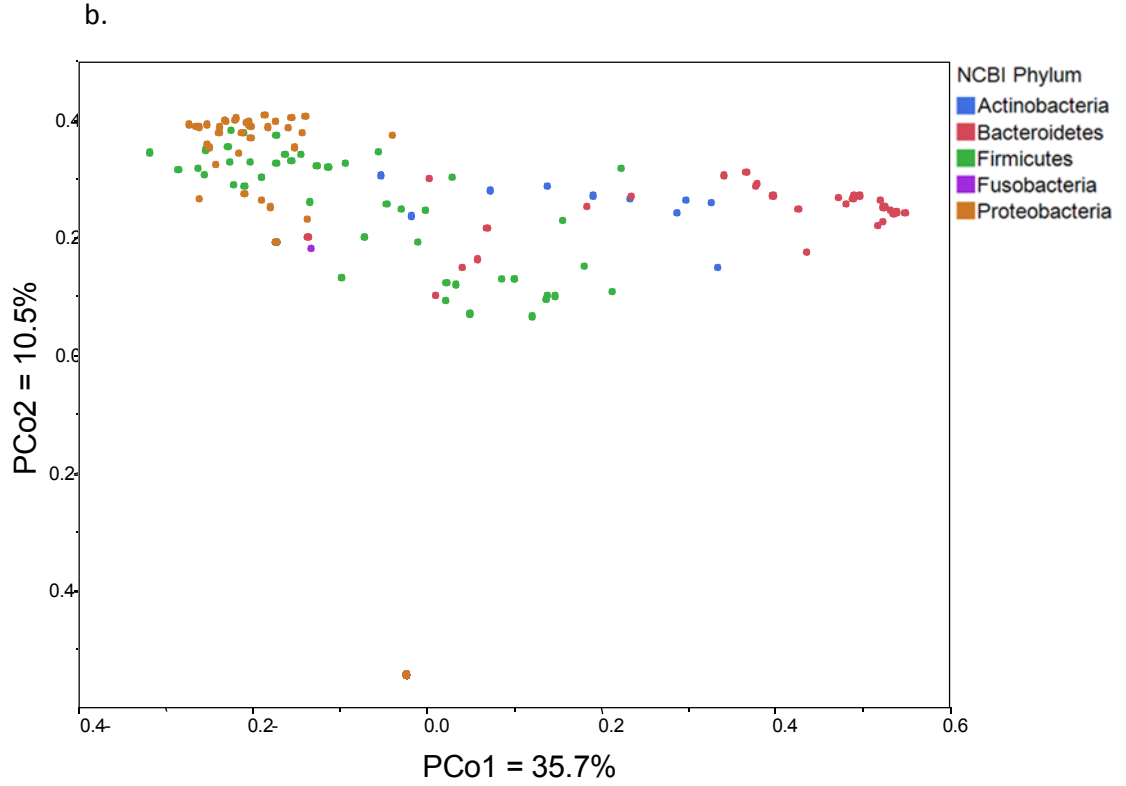


a.

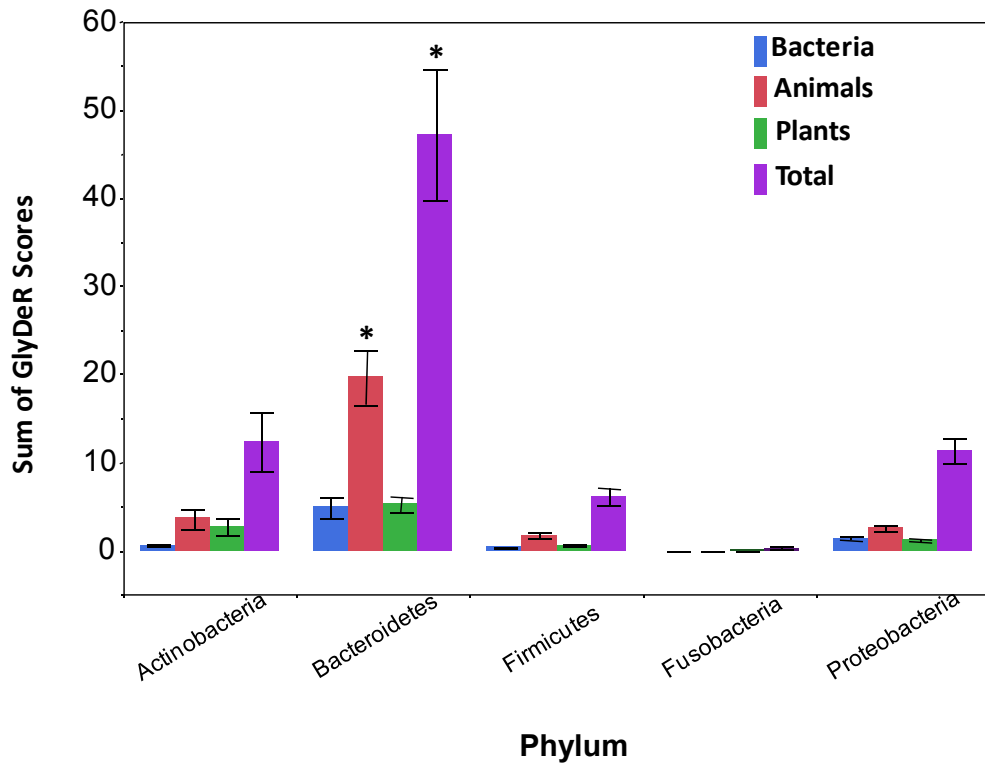


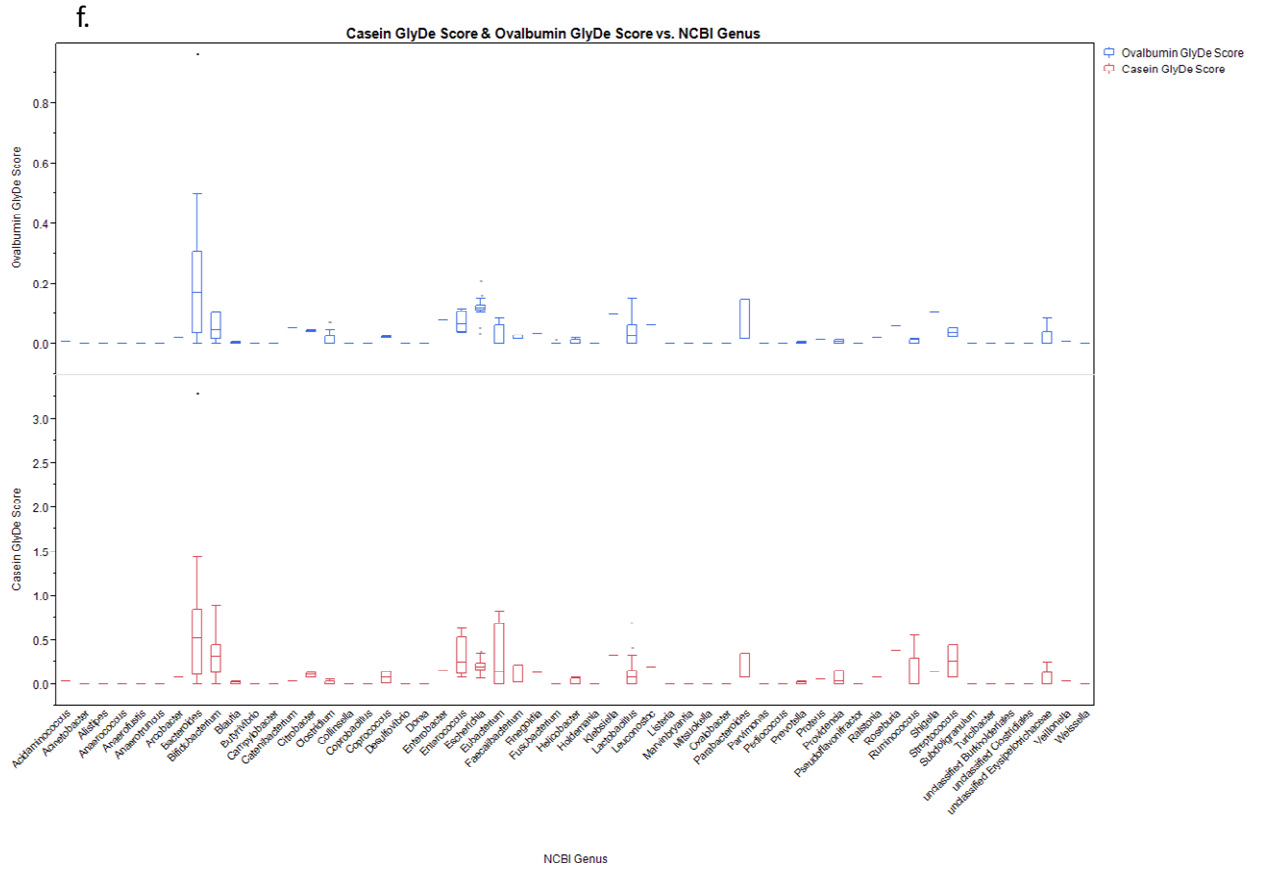


d.

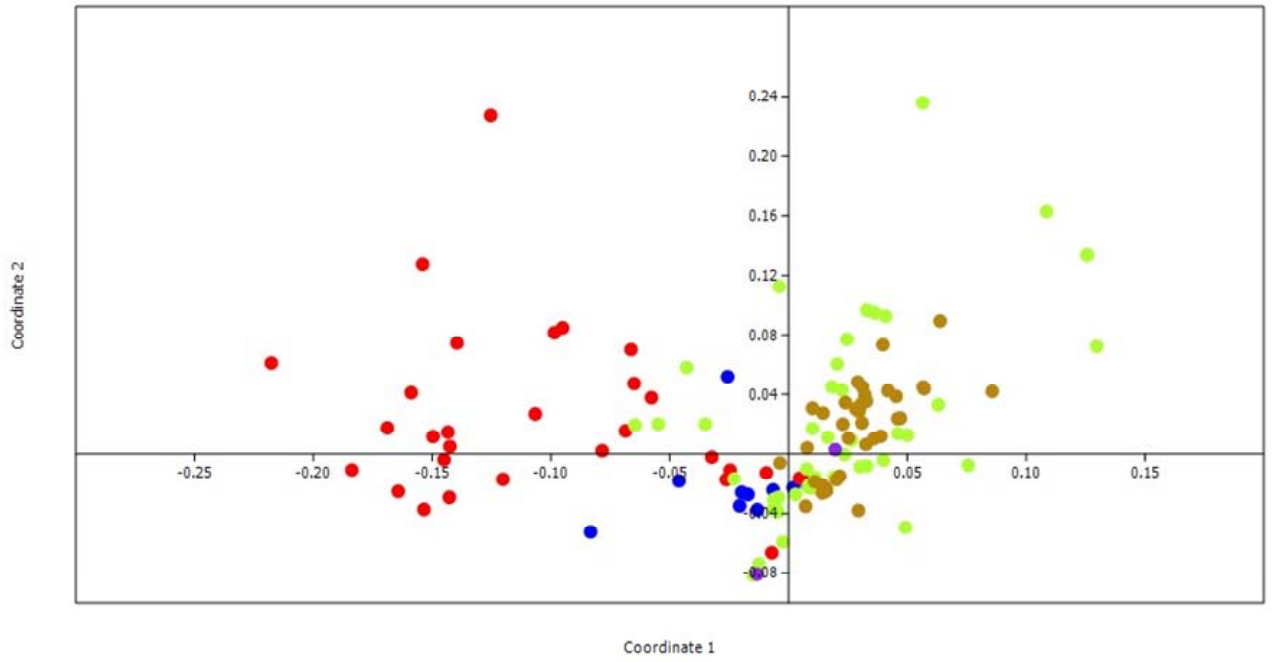
Phylum	Genus\Glycan Type	Disaccharides	Oligosaccharides	Short Polysaccharides	Long Polysaccharides
<b>Actinobacteria</b>	<i>Bifidobacterium</i>	4.4%	5.1%	2.2%	3.6%
<b>Bacteroidetes</b>	<i>Prevotella</i>	0.0%	0.3%	0.7%	0.7%
	<i>Parabacteroides</i>	8.8%	3.3%	3.0%	5.4%
	<i>Bacteroides</i>	26.3%	15.5%	6.7%	19.8%
<b>Firmicutes</b>	<i>Dorea</i>	0.0%	0.2%	0.0%	0.0%
	<i>Blautia</i>	0.0%	0.0%	0.7%	0.0%
	<i>Coprobacillus</i>	0.0%	0.2%	0.0%	0.9%
	<i>Acidaminococcus</i>	0.0%	0.1%	1.5%	0.0%
	<i>Butyrivibrio</i>	1.3%	0.2%	0.0%	0.5%
	<i>Weissella</i>	1.3%	0.2%	0.0%	0.5%
	<i>Ruminococcus</i>	0.4%	0.4%	1.1%	1.1%
	<i>Coprococcus</i>	0.0%	1.3%	0.0%	1.8%
	<i>Clostridium</i>	0.4%	1.4%	0.6%	0.7%
	<i>unclassified Erysipelotrichaceae</i>	3.1%	1.0%	0.7%	0.4%
	<i>Veillonella</i>	3.1%	0.7%	1.5%	0.0%
	<i>Fingoldia</i>	0.0%	0.8%	5.9%	0.0%
	<i>Subdoligranulum</i>	4.4%	0.6%	0.0%	1.8%
	<i>Faecalibacterium</i>	2.6%	1.4%	0.4%	3.6%
	<i>Streptococcus</i>	0.4%	3.2%	4.1%	0.5%
	<i>Lactobacillus</i>	3.1%	3.0%	4.3%	1.8%
	<i>Eubacterium</i>	2.2%	1.4%	5.0%	3.6%
	<i>Enterococcus</i>	1.8%	6.2%	7.0%	1.8%
	<i>Leuconostoc</i>	2.2%	3.5%	7.9%	3.6%
	<i>Catenibacterium</i>	8.8%	12.1%	1.7%	5.4%
<i>Roseburia</i>	8.8%	6.8%	4.1%	18.0%	
<b>Fusobacteria</b>	<i>Fusobacterium</i>	0.0%	0.1%	0.0%	0.4%
<b>Proteobacteria</b>	<i>Helicobacter</i>	0.0%	0.2%	1.3%	0.0%
	<i>Providencia</i>	0.4%	0.8%	1.7%	1.3%
	<i>Arcobacter</i>	0.0%	0.3%	4.4%	0.0%
	<i>Ralstonia</i>	0.0%	1.2%	4.4%	0.0%
	<i>Proteus</i>	0.0%	1.1%	3.7%	1.1%
	<i>Citrobacter</i>	0.9%	2.6%	3.1%	1.8%
	<i>Enterobacter</i>	2.2%	5.6%	6.1%	3.6%
	<i>Shigella</i>	4.4%	5.1%	4.4%	3.6%
	<i>Escherichia</i>	4.4%	5.3%	7.6%	5.4%
	<i>Klebsiella</i>	4.4%	8.8%	4.3%	7.2%

e.

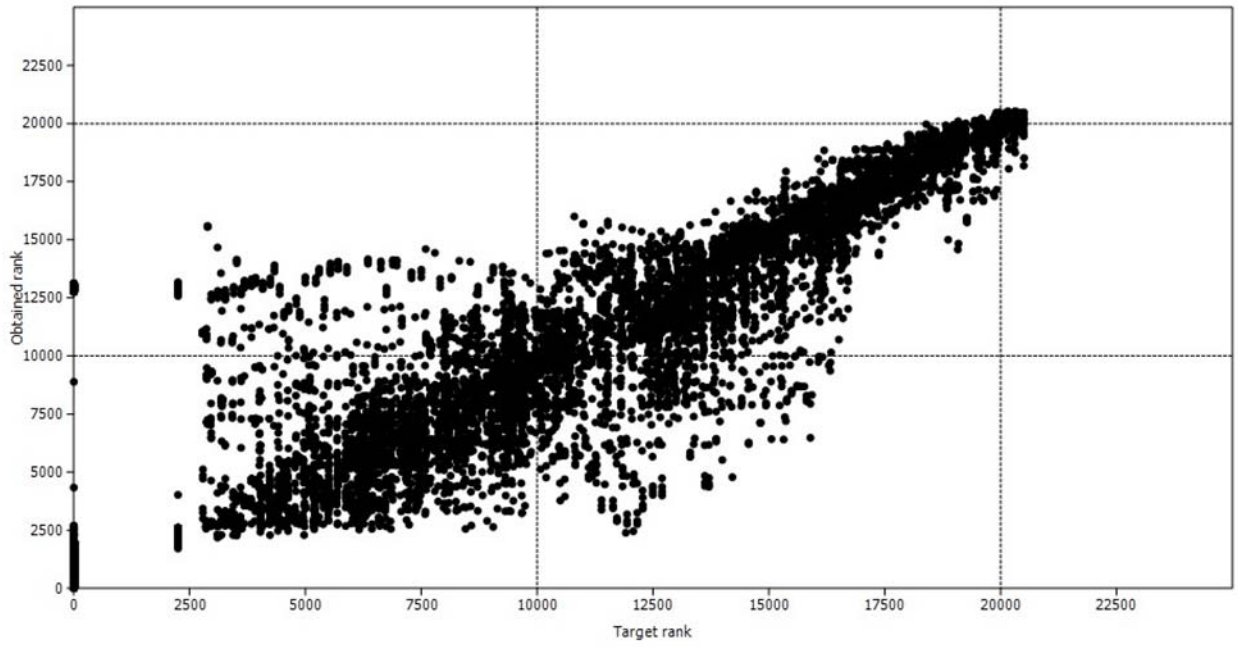




g.



h.



**Supplementary Figure 2: Glycan Degradation of the gut microbiota reference genomes.** (a) A cross-validation process was performed to see that GlyDeR reaction products are enriched with existing glycans rather than hypothetical ones. The Venn diagram depicts a significant overlap between the products created by GlyDeR (green) and the original glycans in the KEGG Glycan database (purple). (b) Principle Coordinates Analysis (PCoA) of the glycan degradation profiles of the species colored according to their respected phyla. (c) The bar chart depicts the median GlyDeR score of the species belonging to each genus and colored according to their respected phyla. (d) A heatmap denoting the average relative glycan degradation potency of the different bacterial genera in the study. Each entry was calculated based on the average sum of GlyDeR scores per genus for a specific degree of polymerization (DP) category (e.g. Disaccharides) and normalized by the overall sum of GlyDeR scores of all the genera for the same DP category. (e) A bar plot depicting the Total GlyDe scores (and error bars) of strains belonging to each phylum. Purple indicates all glycans, red indicates glycans derived from animals, blue indicates glycans derived from bacteria and green indicates glycans derived from plants. (f) The bar plot compares the glycan degradation potential of the different bacterial genera for ovalbumin (blue) and casein (red). Each bar depicts the median of the GlyDe scores of organisms belonging to their respected genus. (g) Non-metric multidimensional scaling (NMDS) of the glycan degradation profiles of the species colored according to their respected phyla. (h) A Shepard plot of obtained versus observed (target) ranks indicates the quality of the NMDS result.