



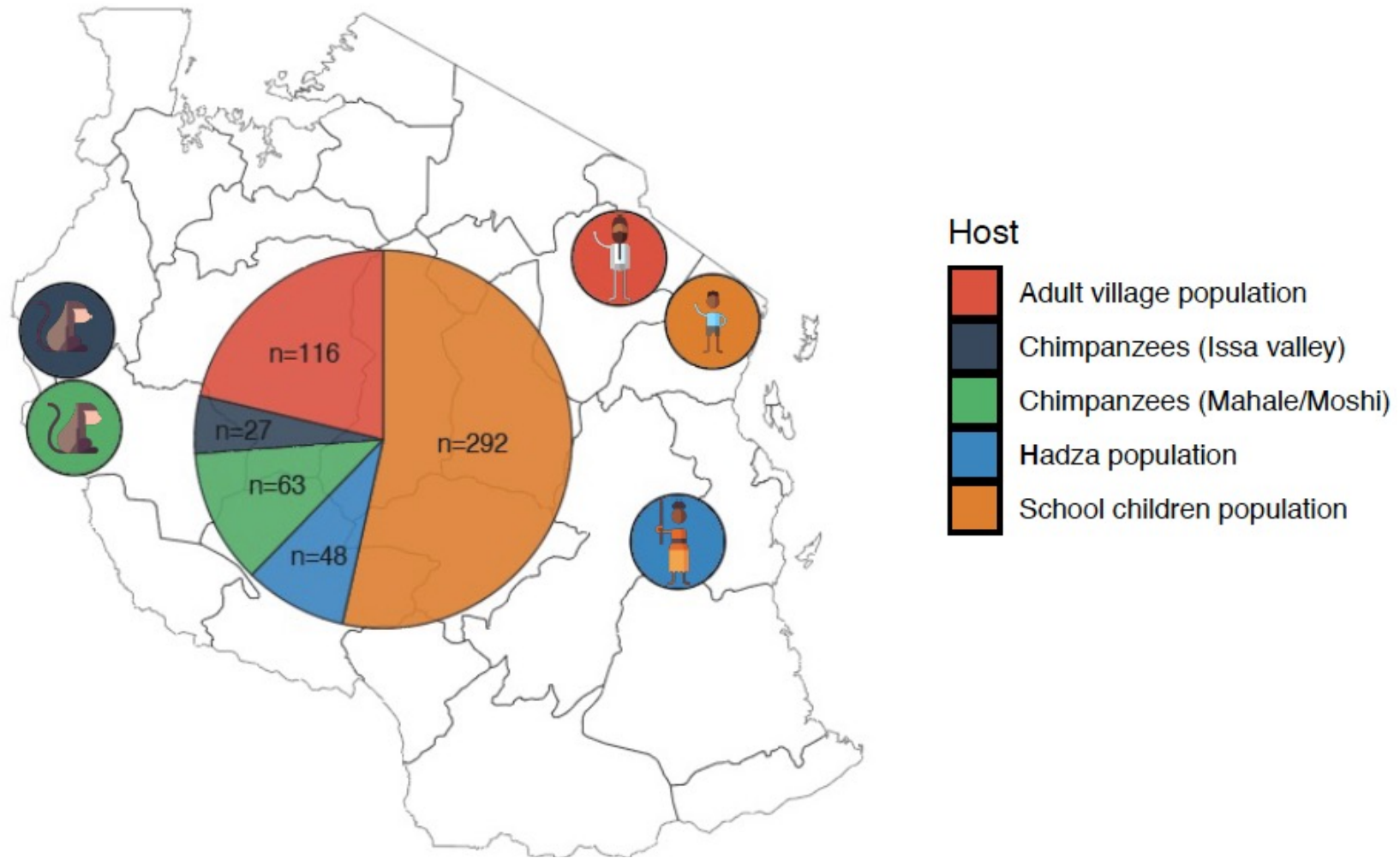
# Gene adaptations in Tanzanian hominid gut microbiomes

Marie Louise Jespersen

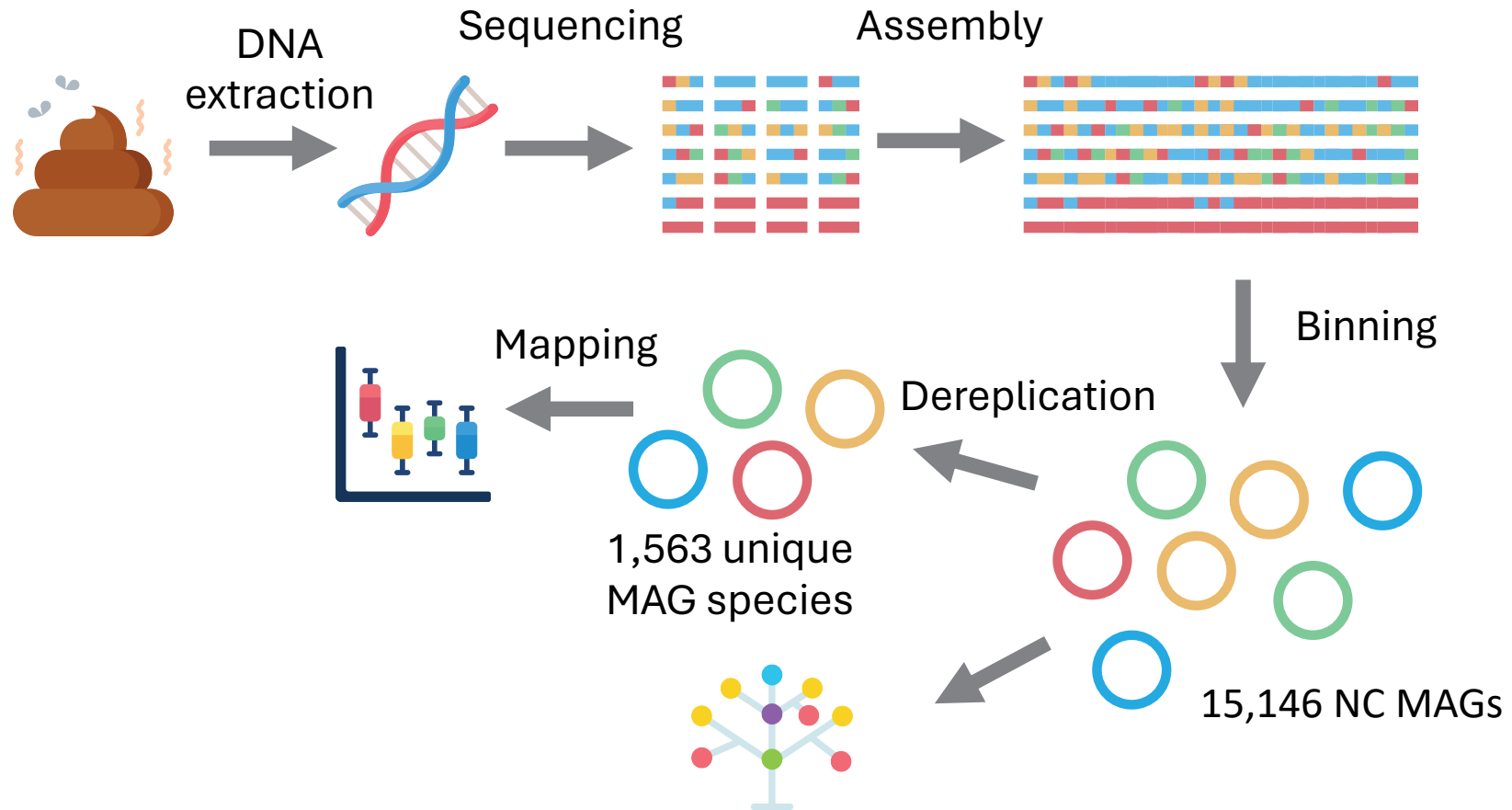
2024.04.08



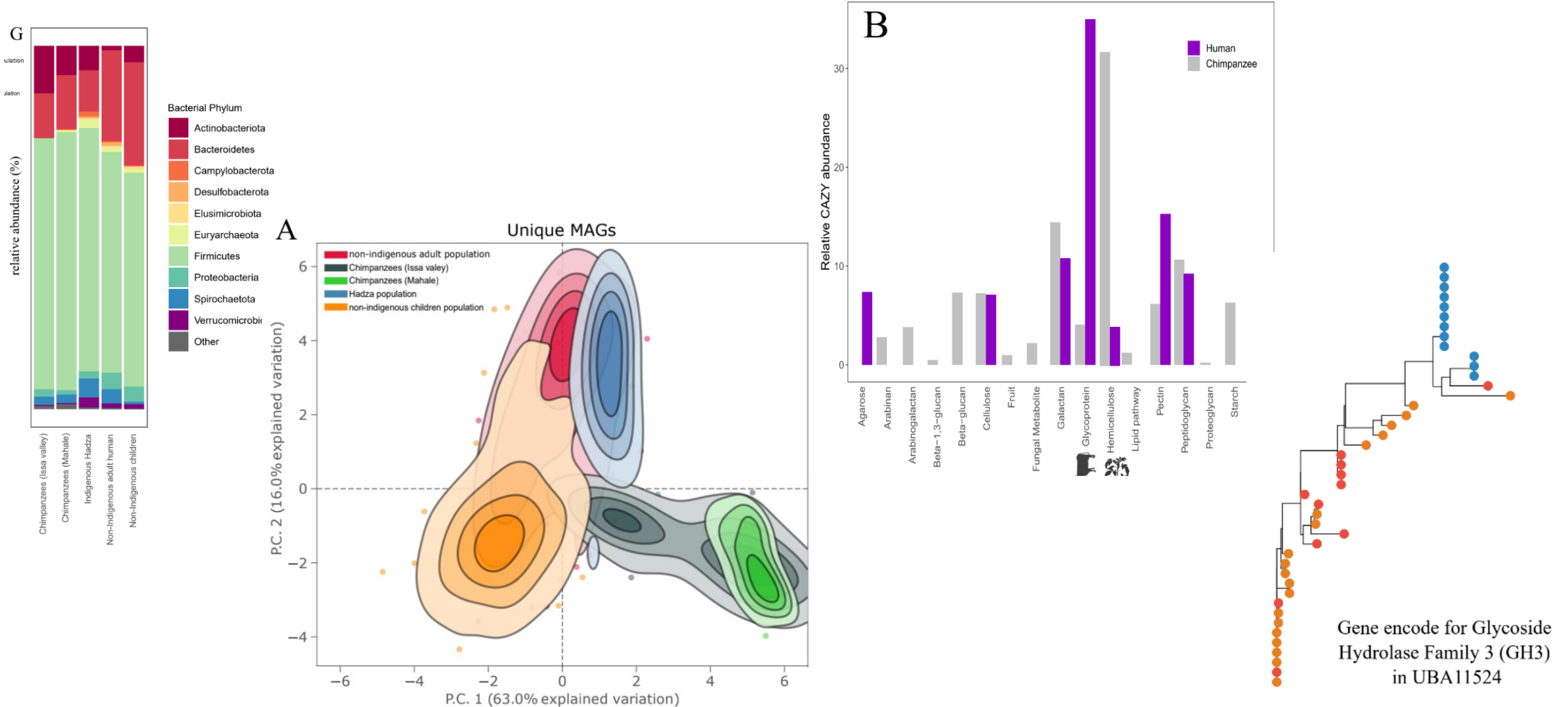
# 546 fecal samples from different lifestyles and hominid species



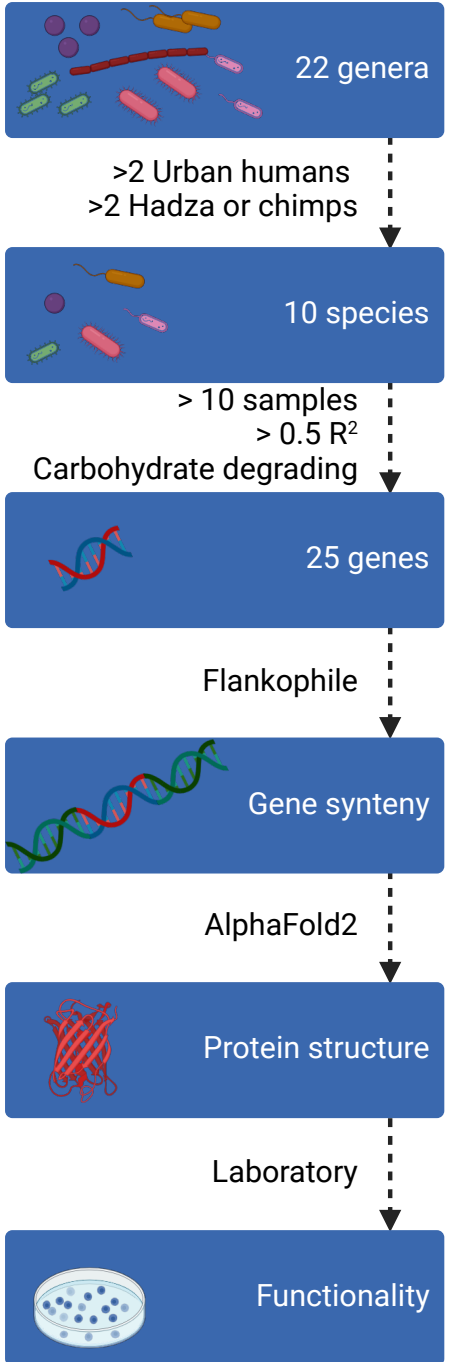
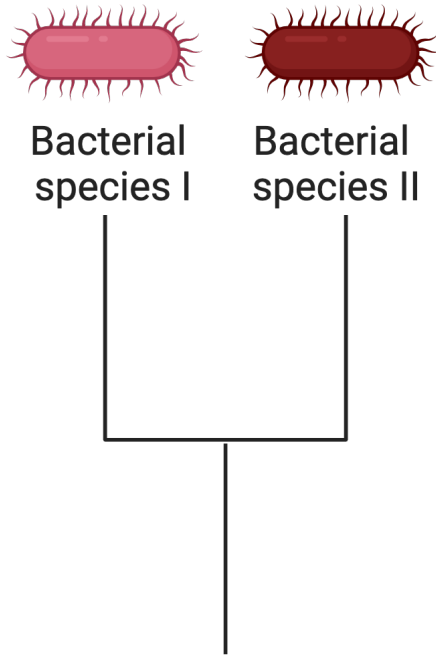
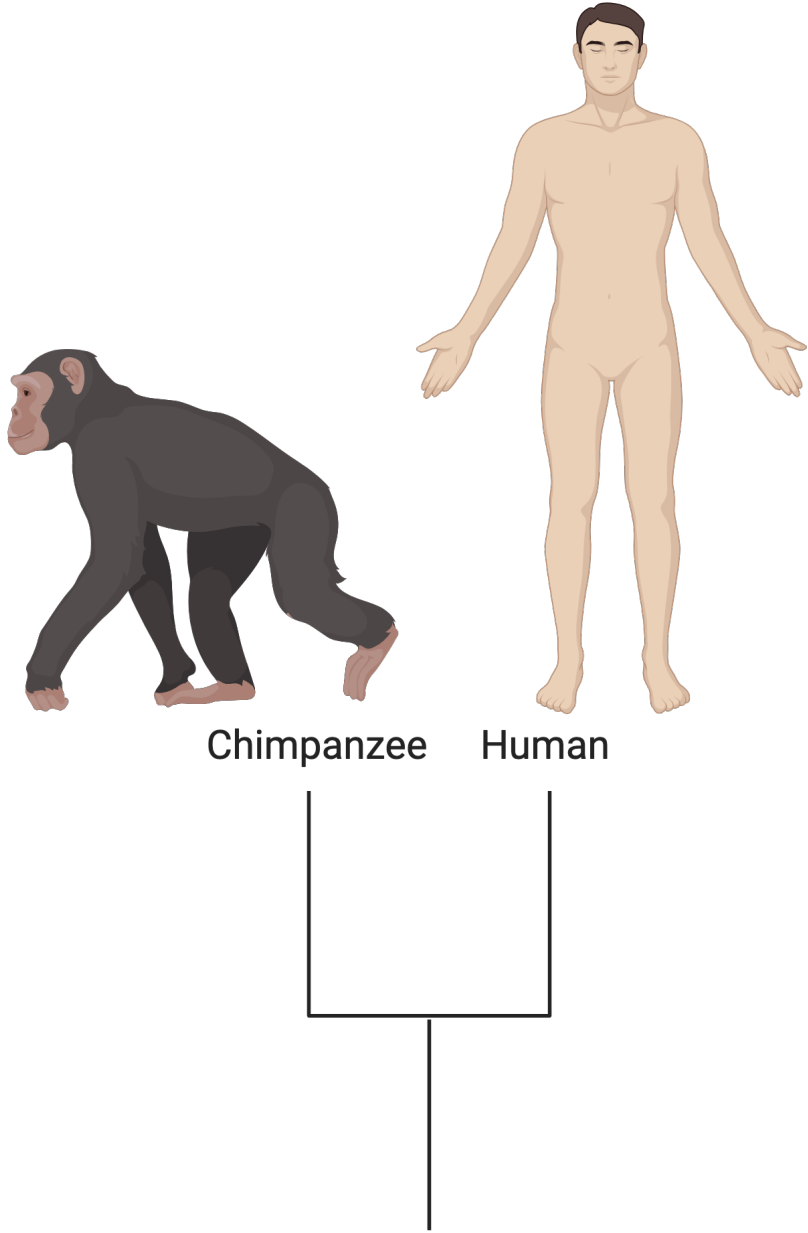
# High resolution investigation with metagenomic binning

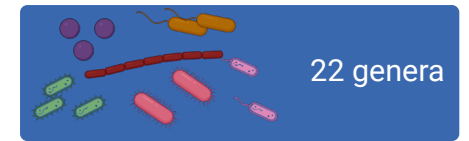


# The gut microbiomes of chimps and humans vary at multiple taxonomic levels, in gene content and gene sequences

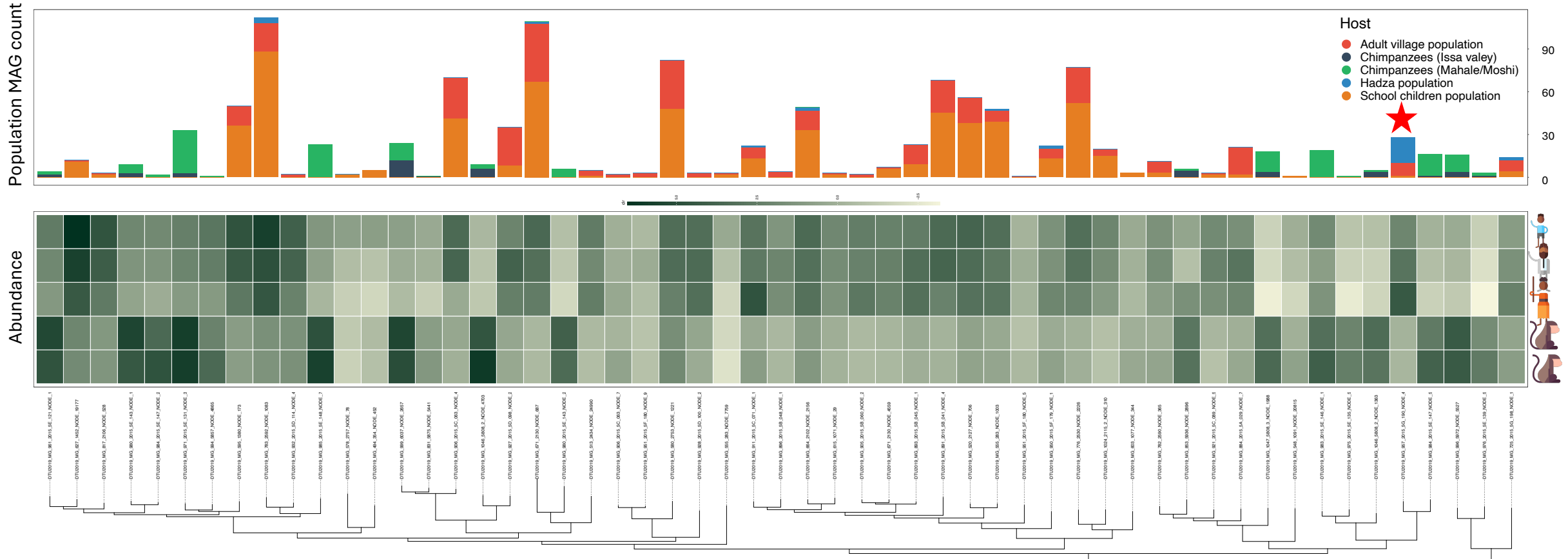
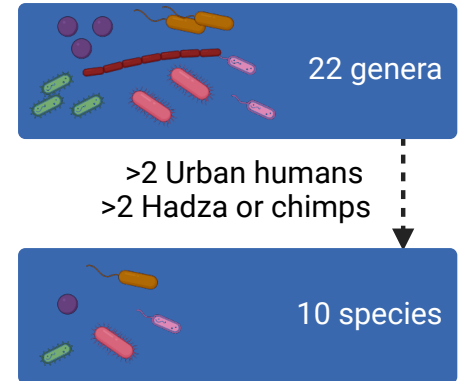


# Co-evolution?



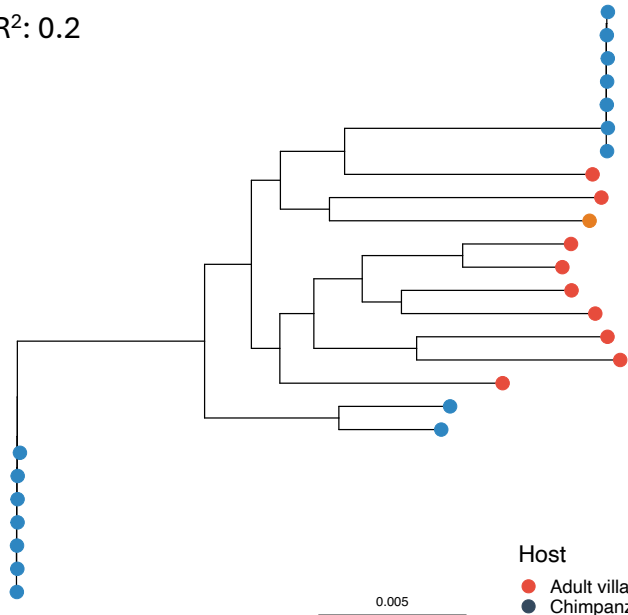


# Host segregation signals across taxonomic levels

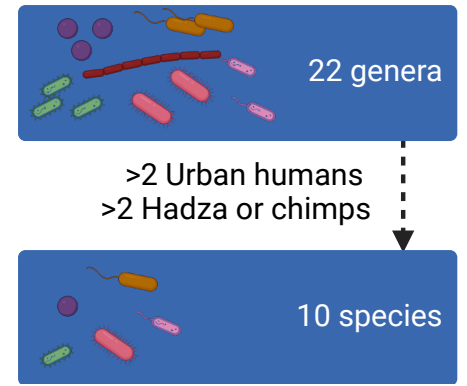


C26, *Prevotella* sp002251295

R<sup>2</sup>: 0.2

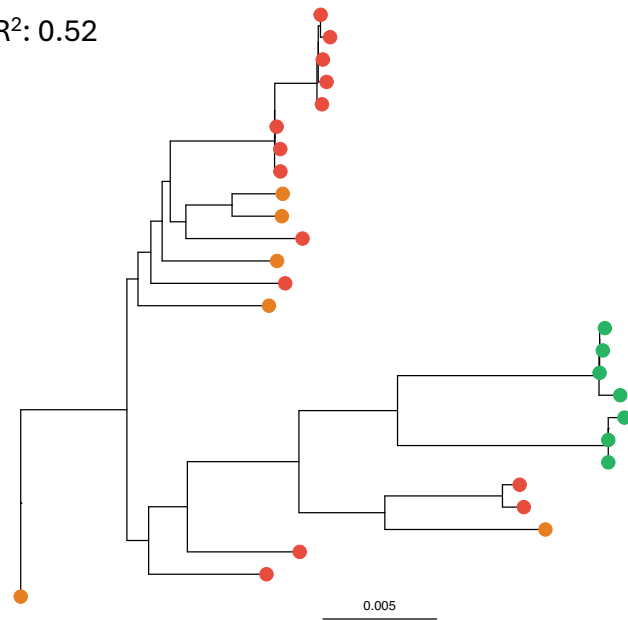


# Highest variation found between humans and chimpanzees



C27, *Ruminococcus* sp900540005

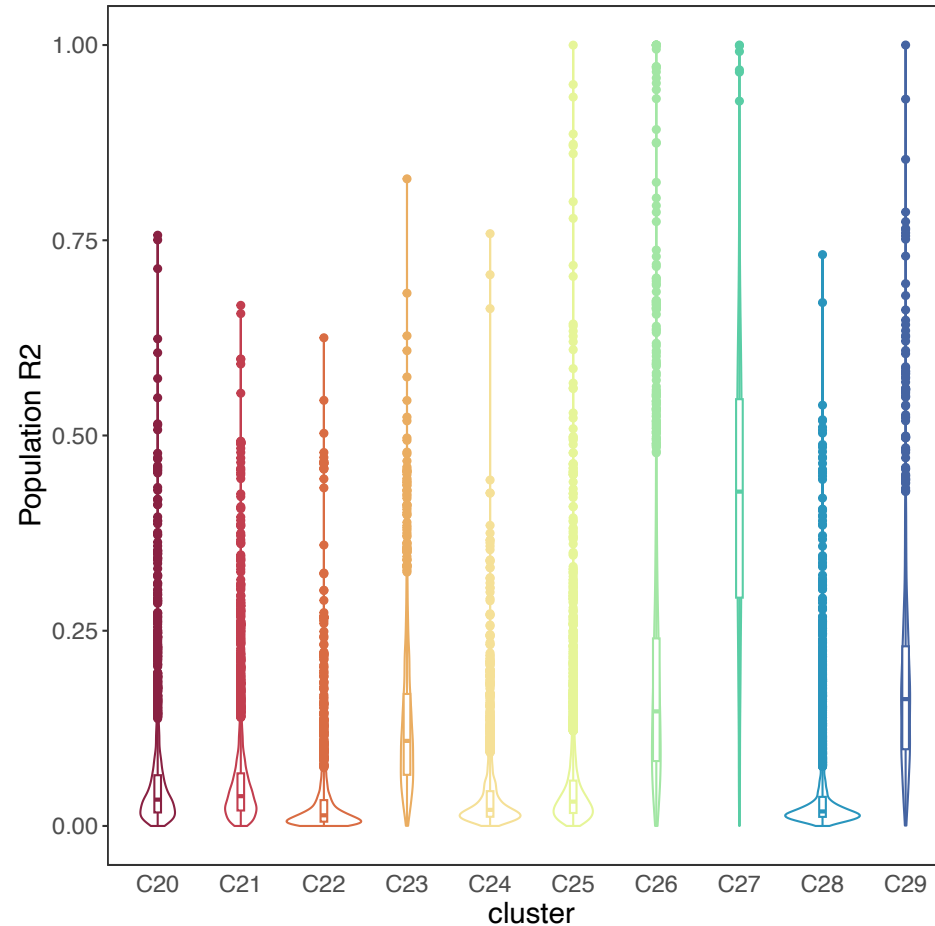
R<sup>2</sup>: 0.52



Host

- Adult village population
- Chimpanzees (Issa valey)
- Chimpanzees (Mahale/Moshi)
- Hadza population
- School children population

R<sup>2</sup> per species

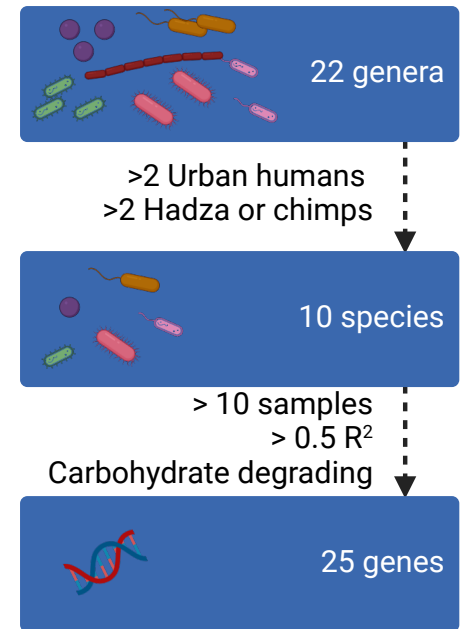
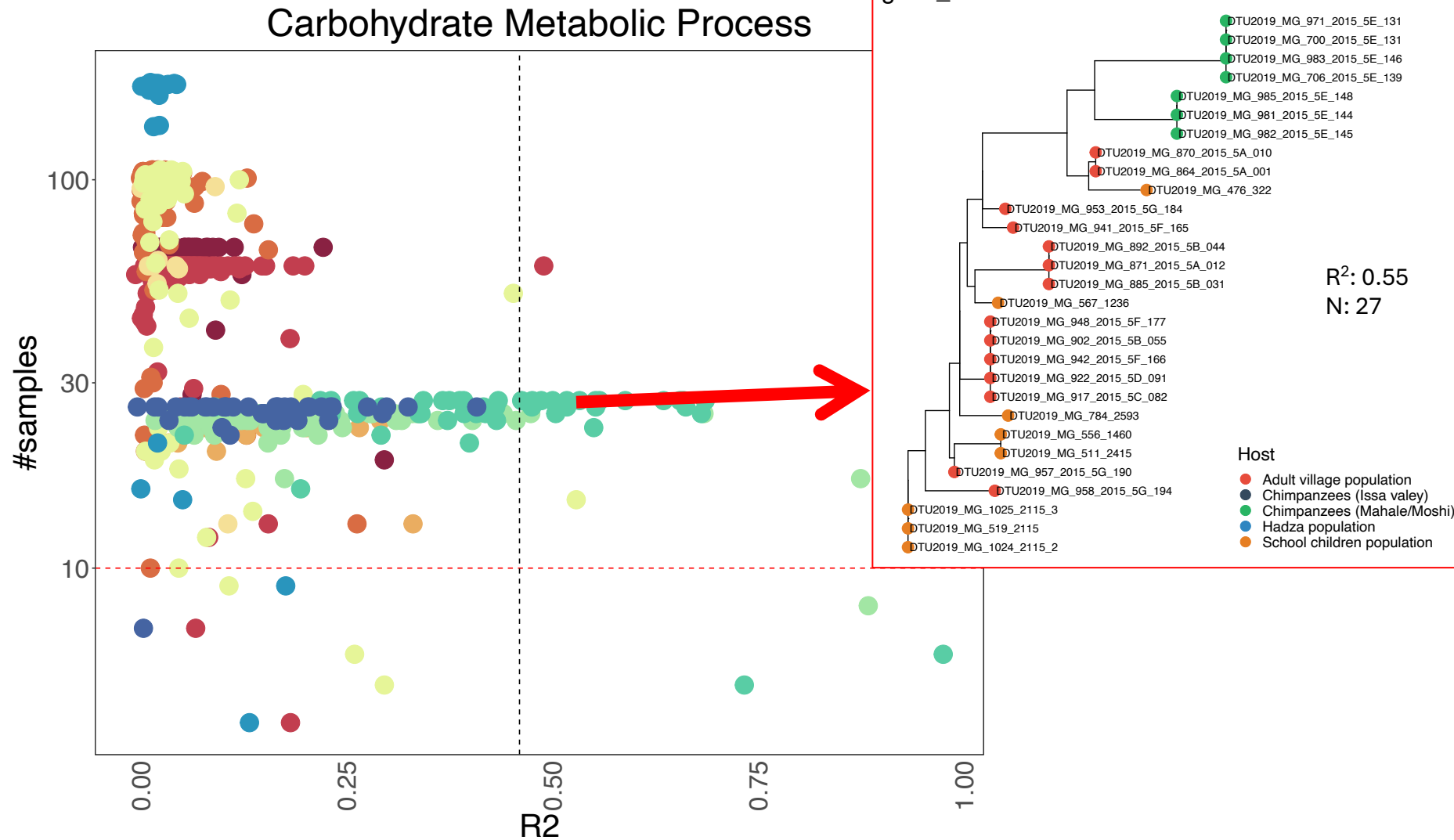


species

- █ Akkermansia muciniphila
- █ Bacteroides fragilis
- █ Bifidobacterium adolescentis
- █ Desulfovibrio sp900556755
- █ Dialister sp000434475
- █ Prevotella sp900313215
- █ Prevotella sp002251295
- █ Ruminococcus sp900540005
- █ Ruminococcus\_E bromii\_B
- █ Ruminococcus\_F champanellensis

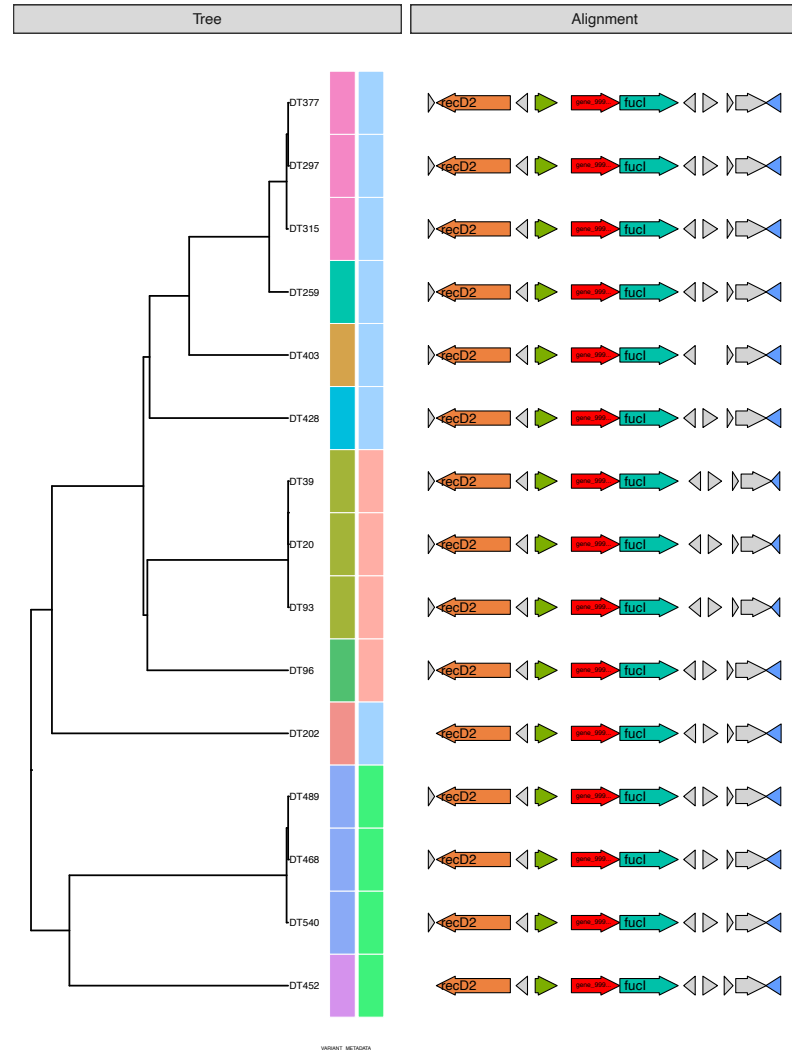


# Important genes for diet degradation

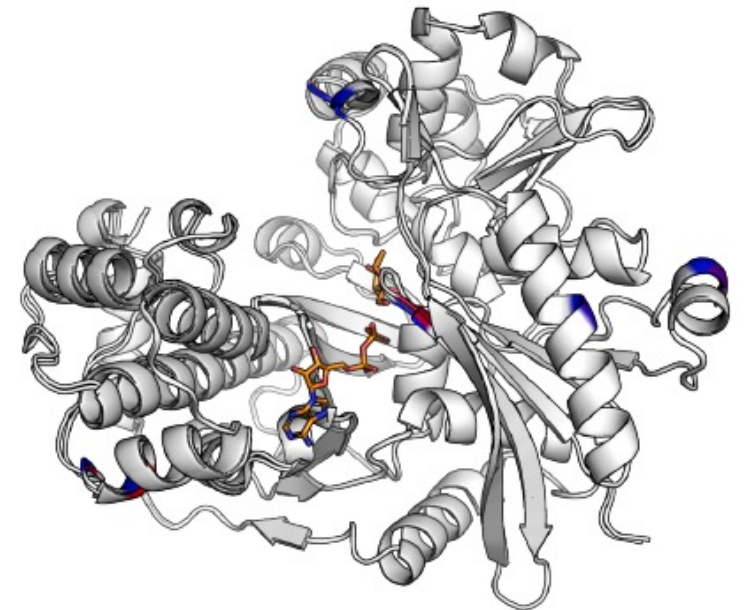
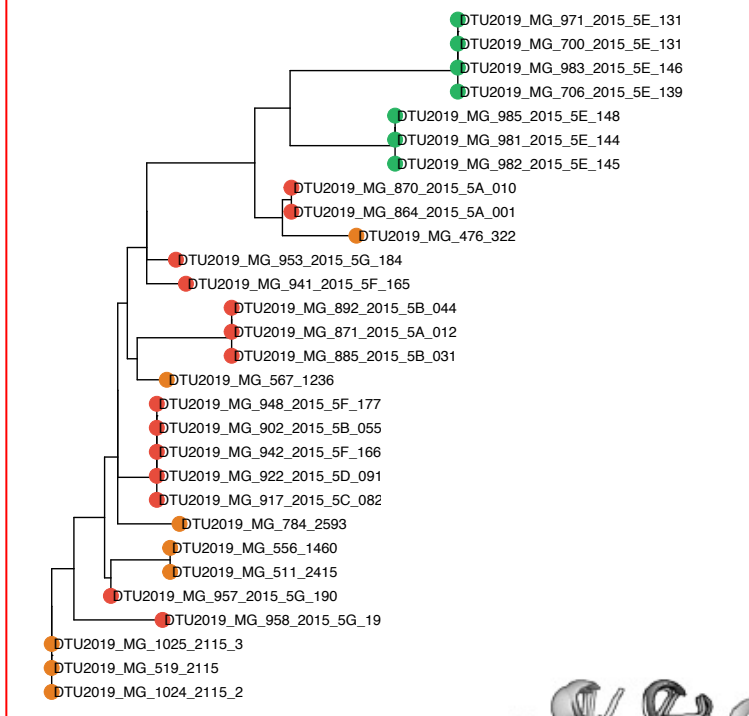


# L-Rhamnulose Kinase: Breaking Down L-Rhamnose in Plants

Cluster 2\_gene\_999 – distance tree based on flanking region sequences only

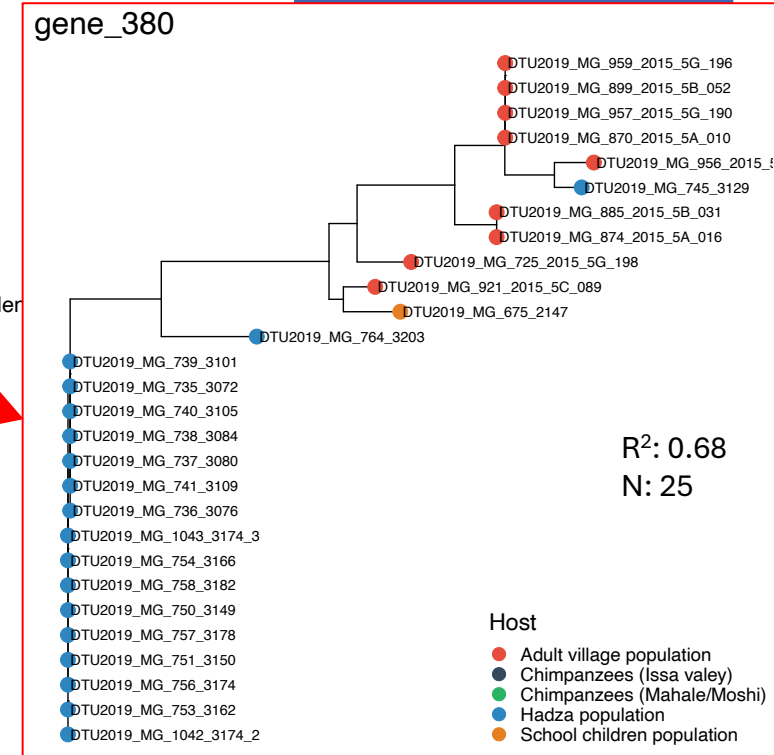
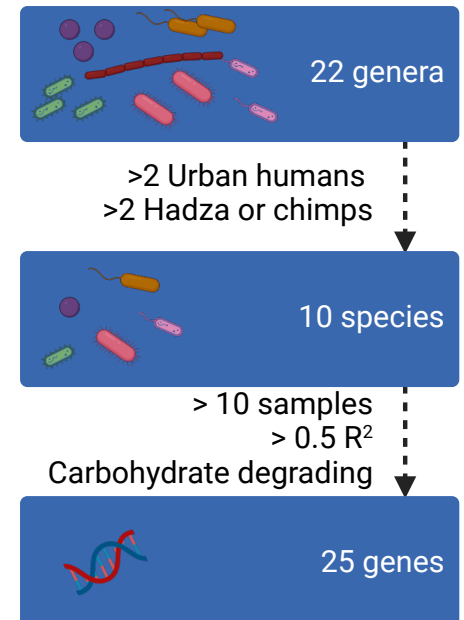
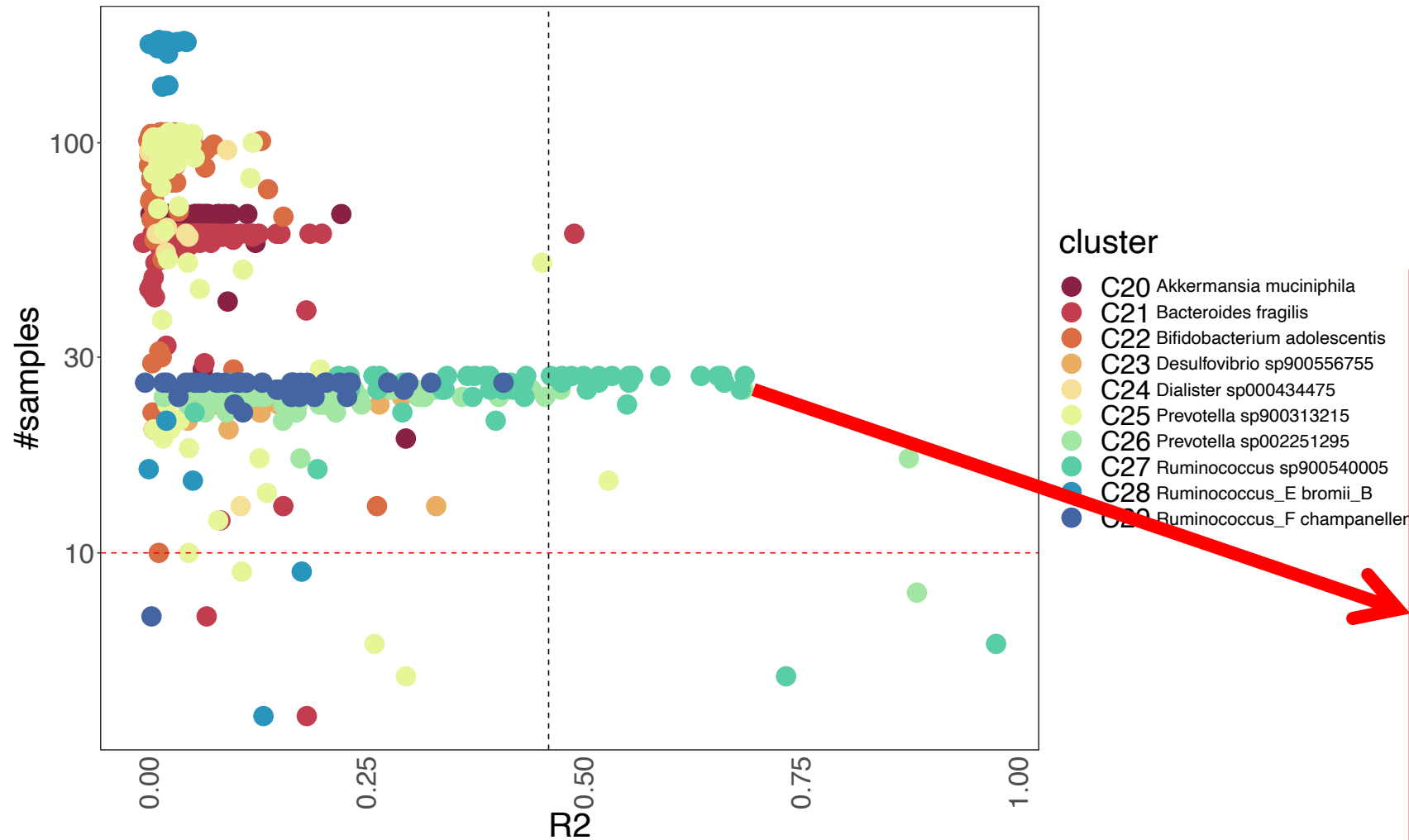


gene\_999



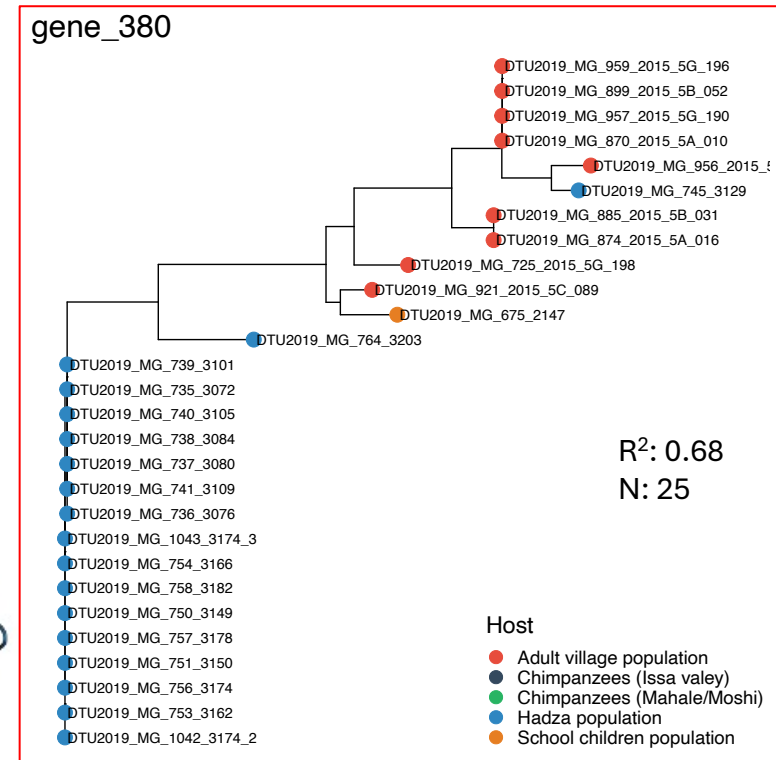
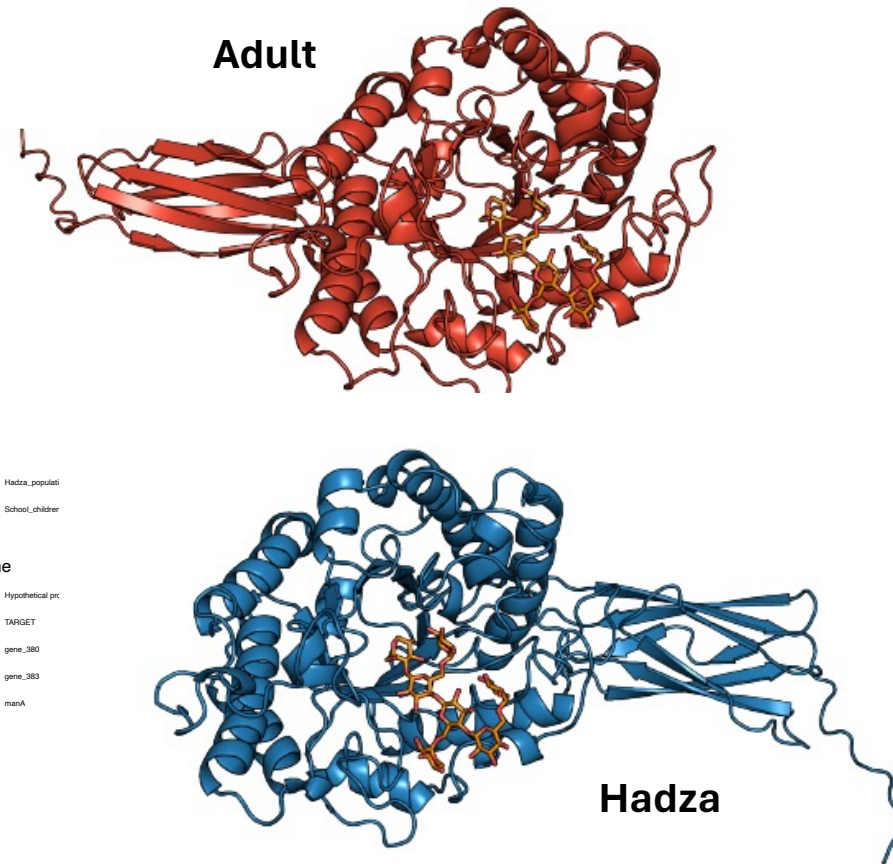
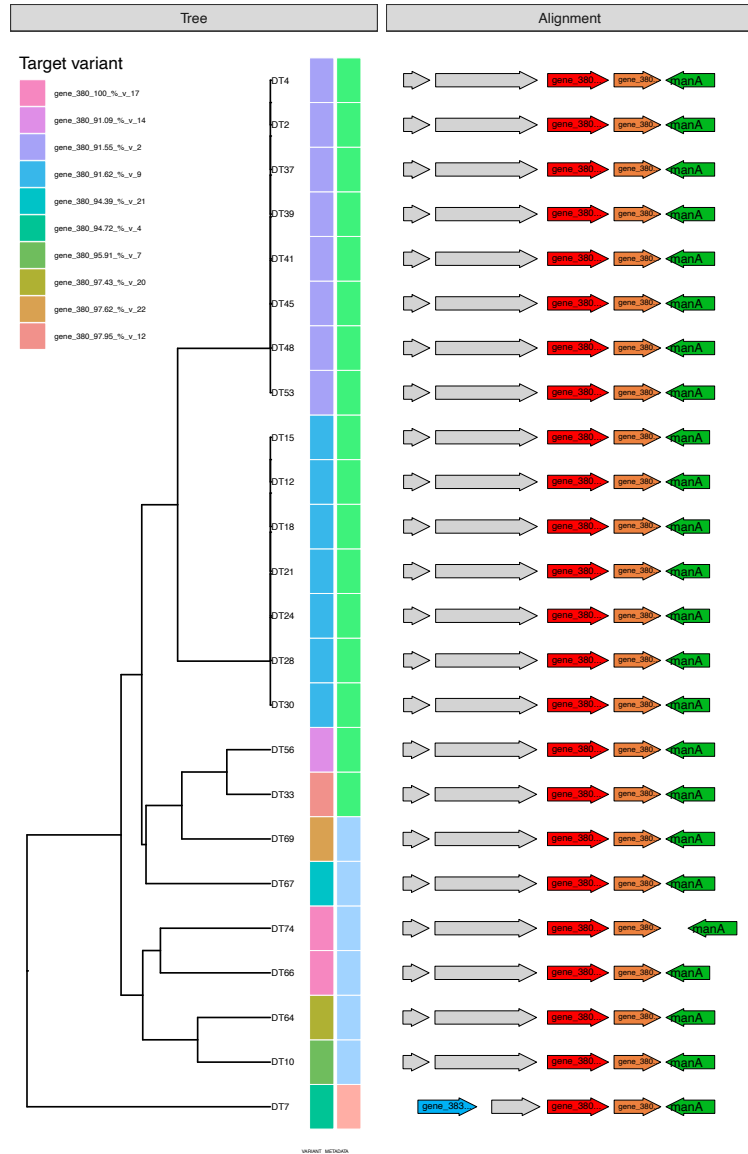
# Important genes for diet degradation

Carbohydrate Metabolic Process



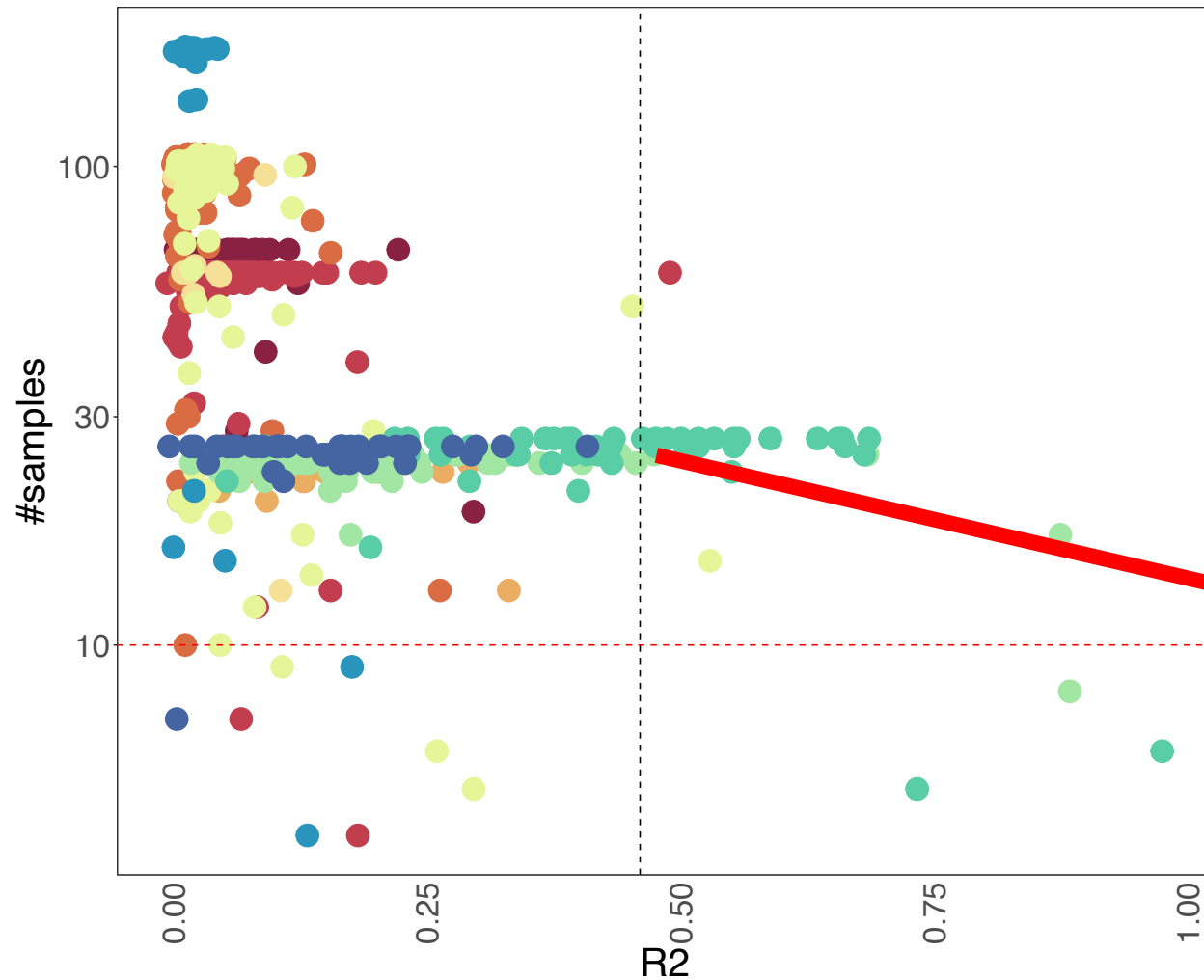
# Xyloglucanase: degrading hemicellulose from plant cell walls

Cluster 1\_gene\_380 – distance tree based on flanking region sequences only



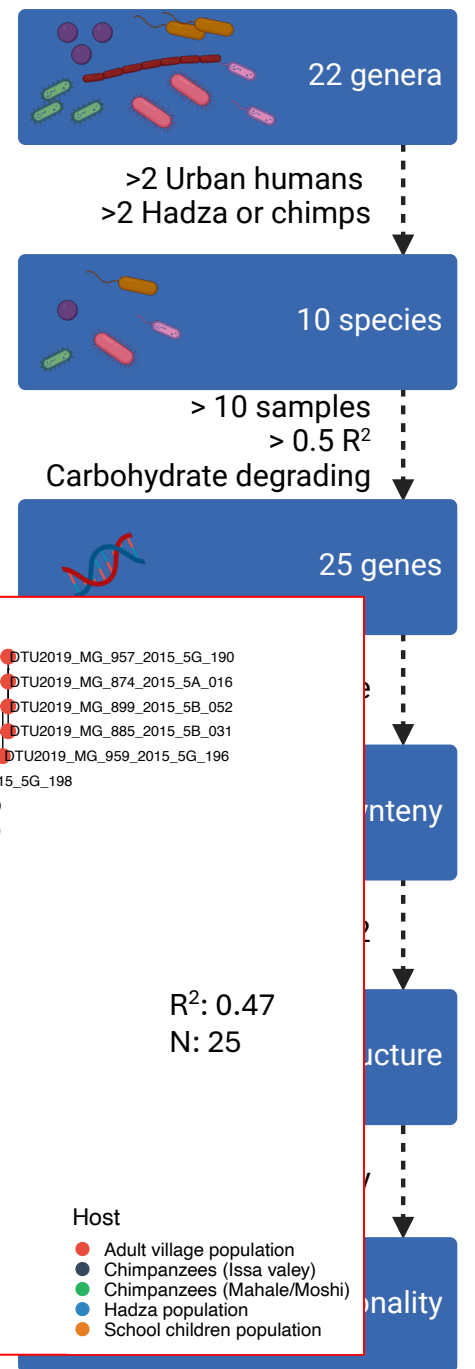
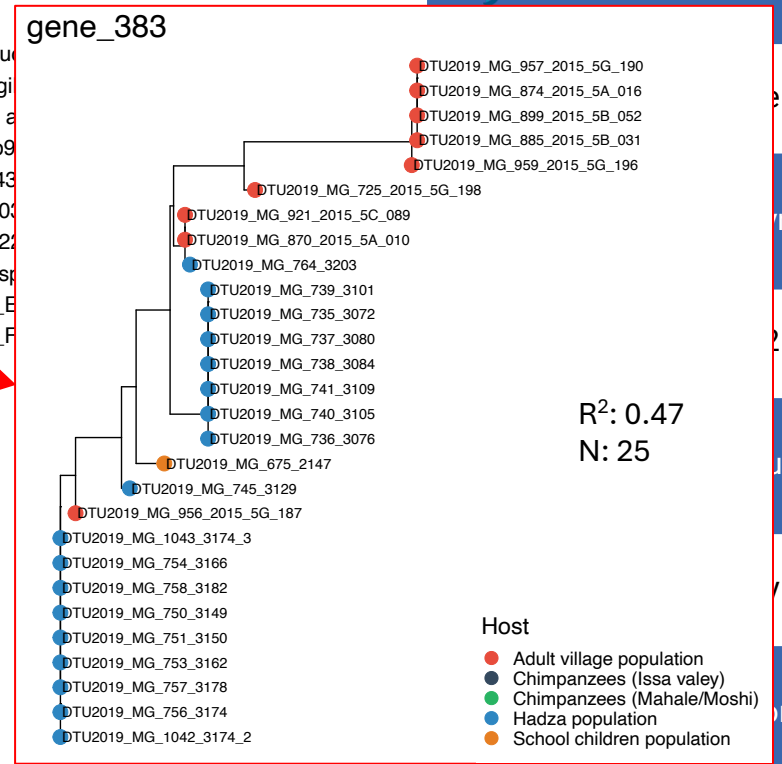
# Important genes for diet degradation

Carbohydrate Metabolic Process

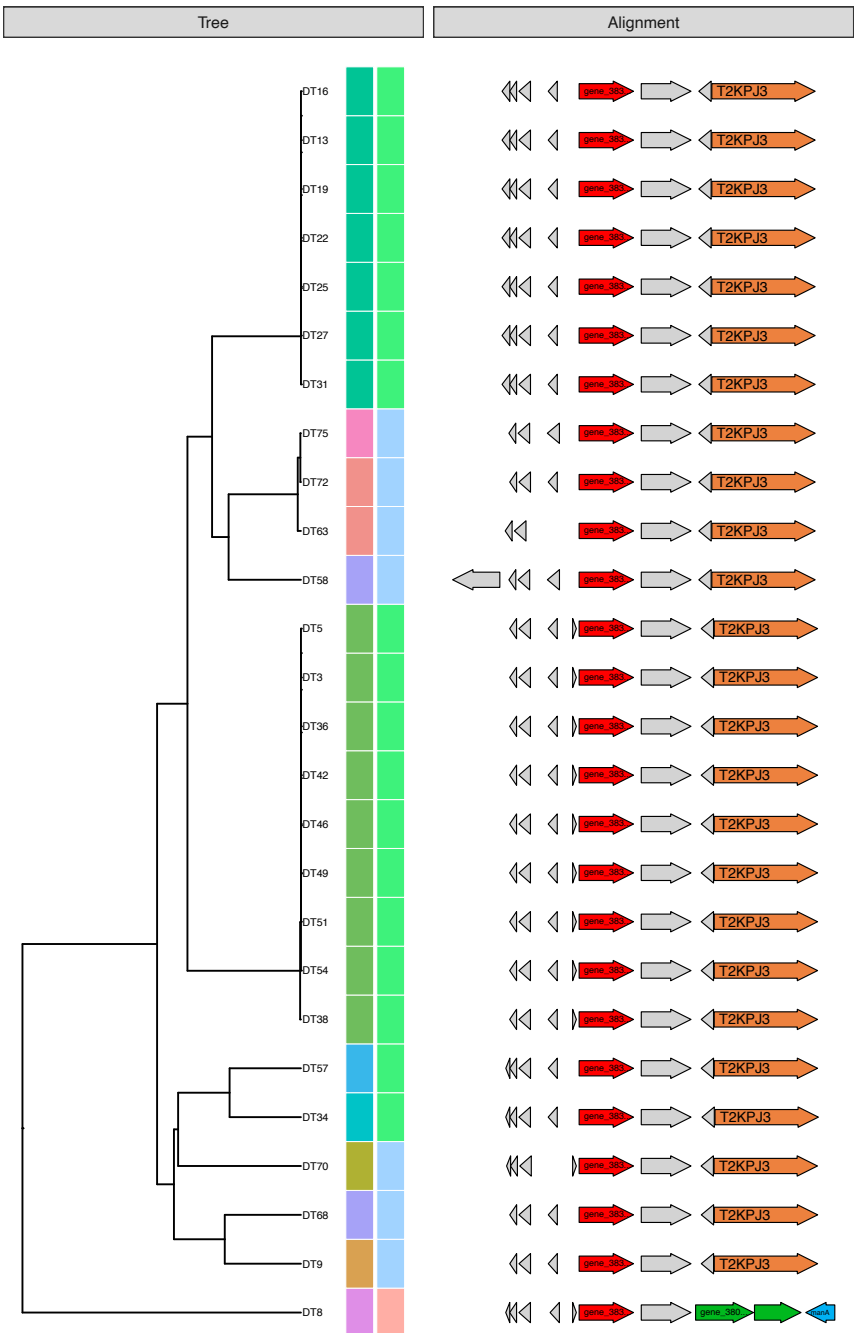


cluster

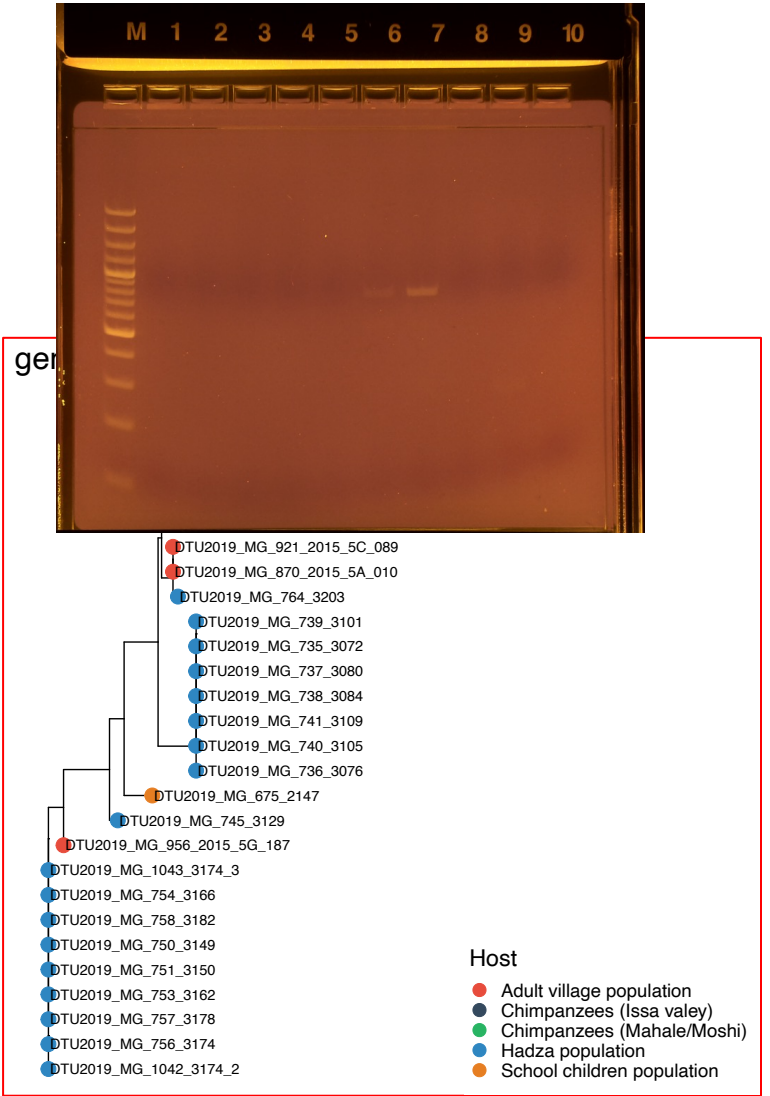
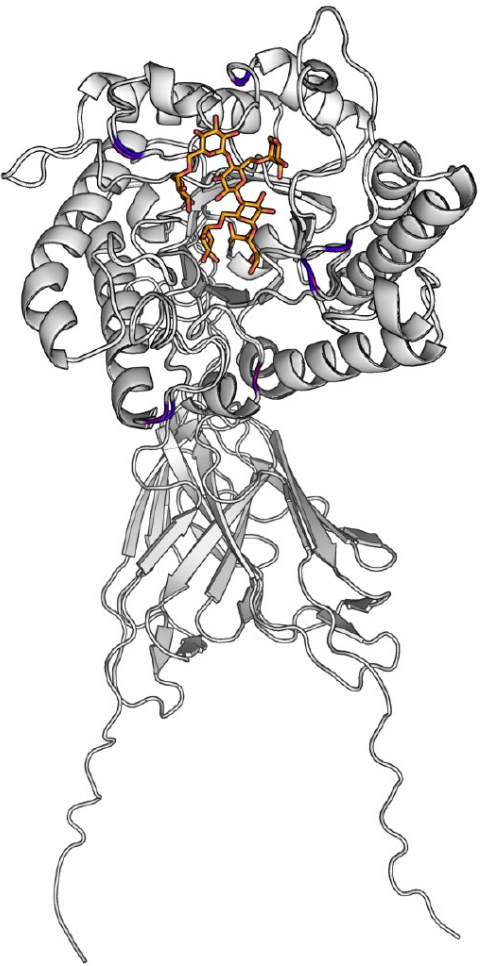
- C20 Akkermansia mu
- C21 Bacteroides fragi
- C22 Bifidobacterium a
- C23 Desulfovibrio sp9
- C24 Dialister sp00043
- C25 Prevotella sp900
- C26 Prevotella sp002
- C27 Ruminococcus sp
- C28 Ruminococcus\_E
- C29 Ruminococcus\_F



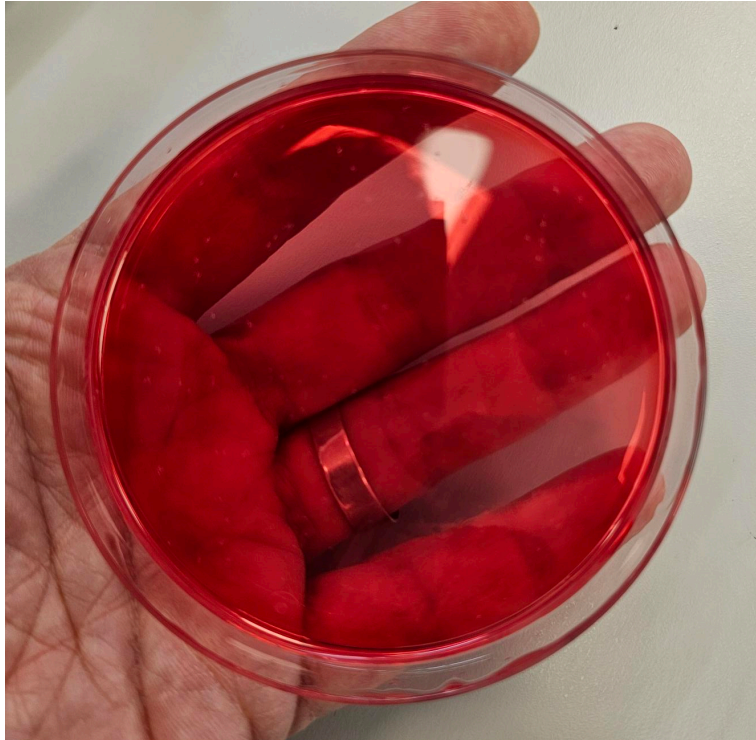
Cluster 0\_gene\_383 – distance tree based on flanking region sequences only



# More hemicellulose degradation



# Future: testing functions



**Control**  
no growth



**Gene clone**  
growth +  
Arabinose degradation (color change)