

CMG Lab Report

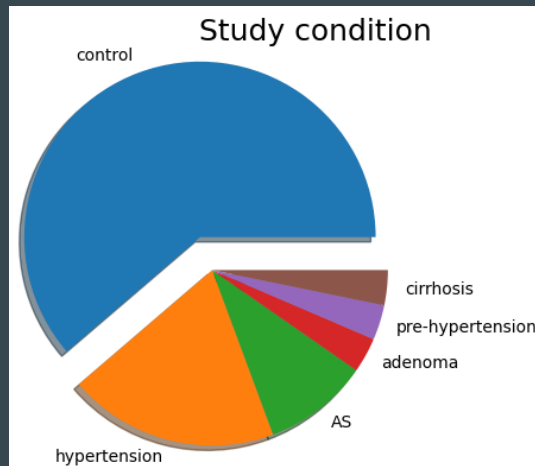
Group 5



SGB15132

Our Data

Completeness			Redundancy		
Min (%)	Average (%)	Max (%)	Min (%)	Average (%)	Max (%)
97.32	98.2	99.33	0.0	0.57	2.25



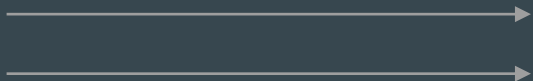
Methods

Gene Annotation



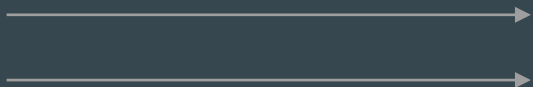
Prokka

Pangenome Building



Roary
(Core Gene Alignment)

Tree Building



FastTreeMP
Web Visualiser (*iTOL*)

Additional Tools



PhyloPhlAn

Prokka results

Hypothetical proteins

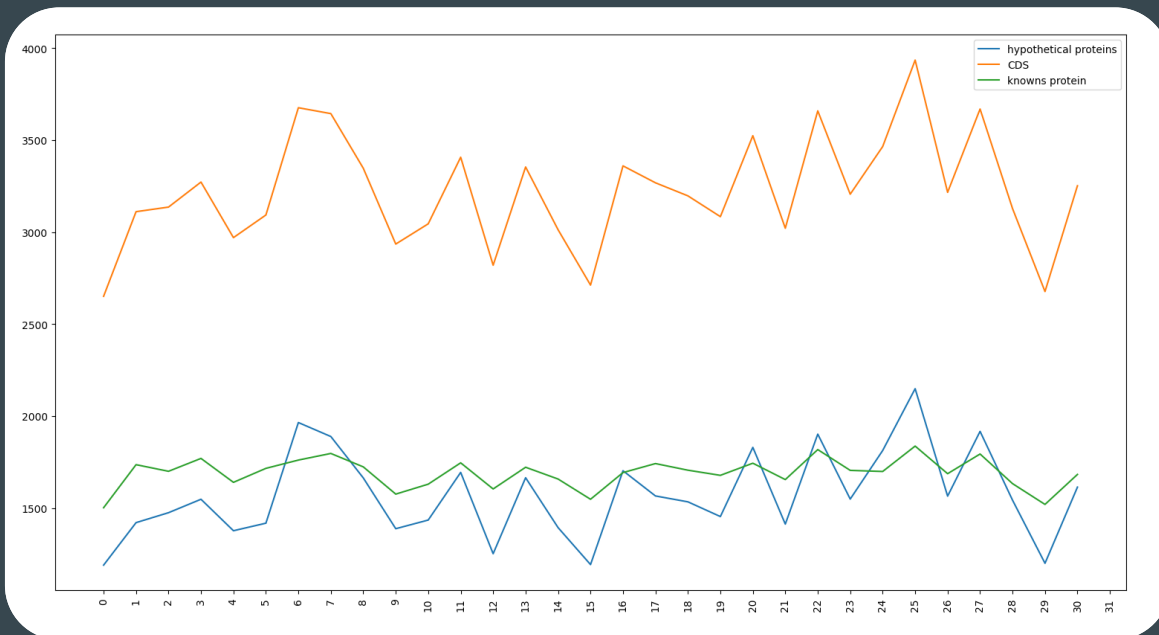
Min	Avarage	Max
1190	1517.6	2149

Coding sequences

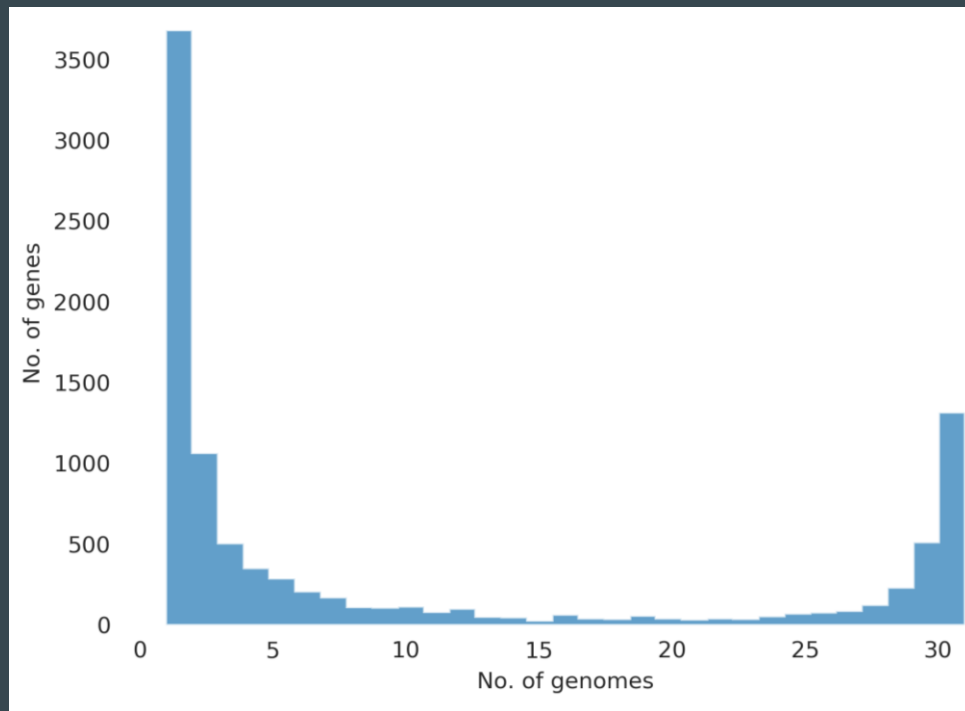
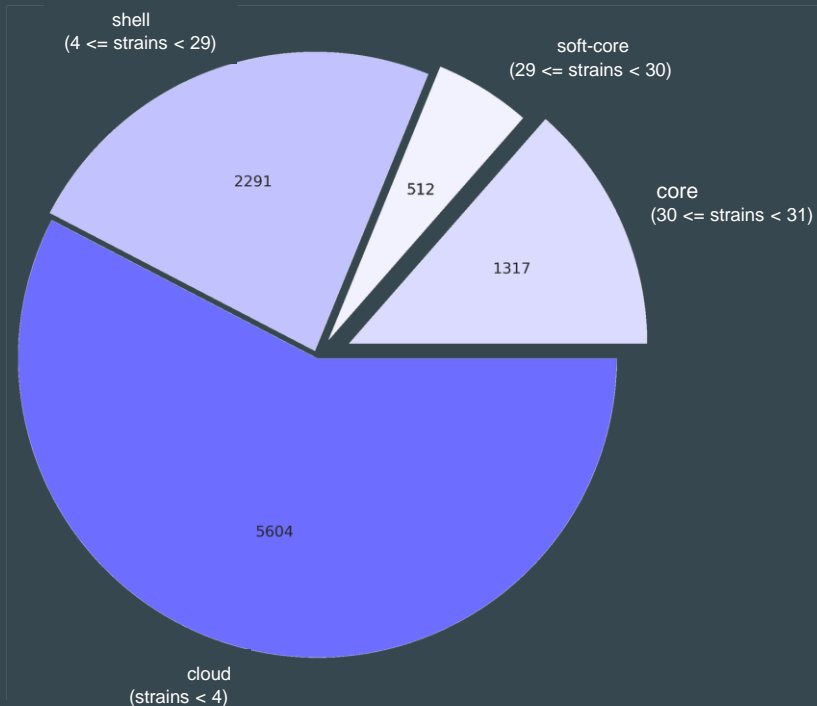
Min	Avarage	Max
2651	3220.9	3935

Known proteins

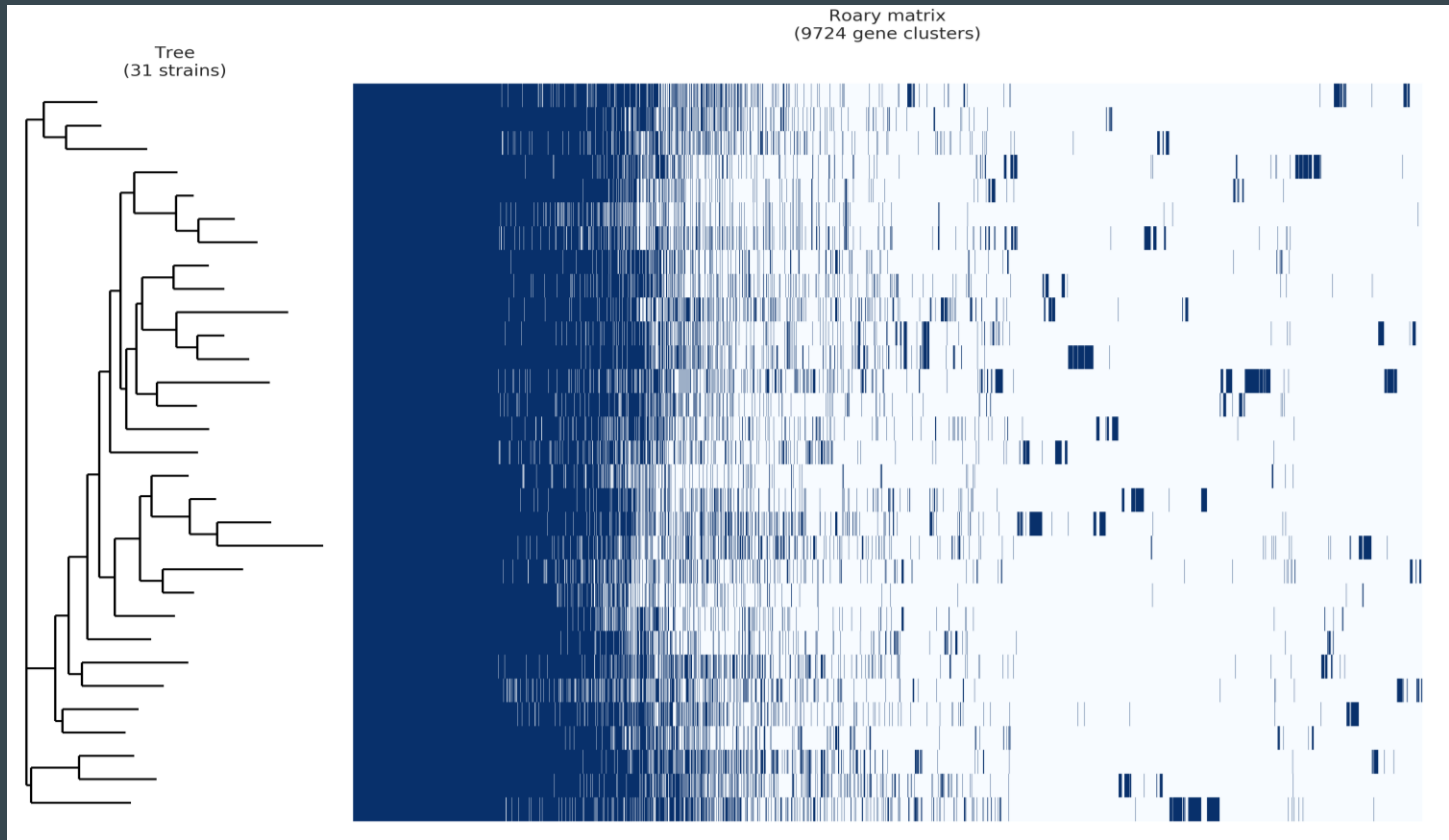
Min	Avarage	Max
1502	1691.1	1837



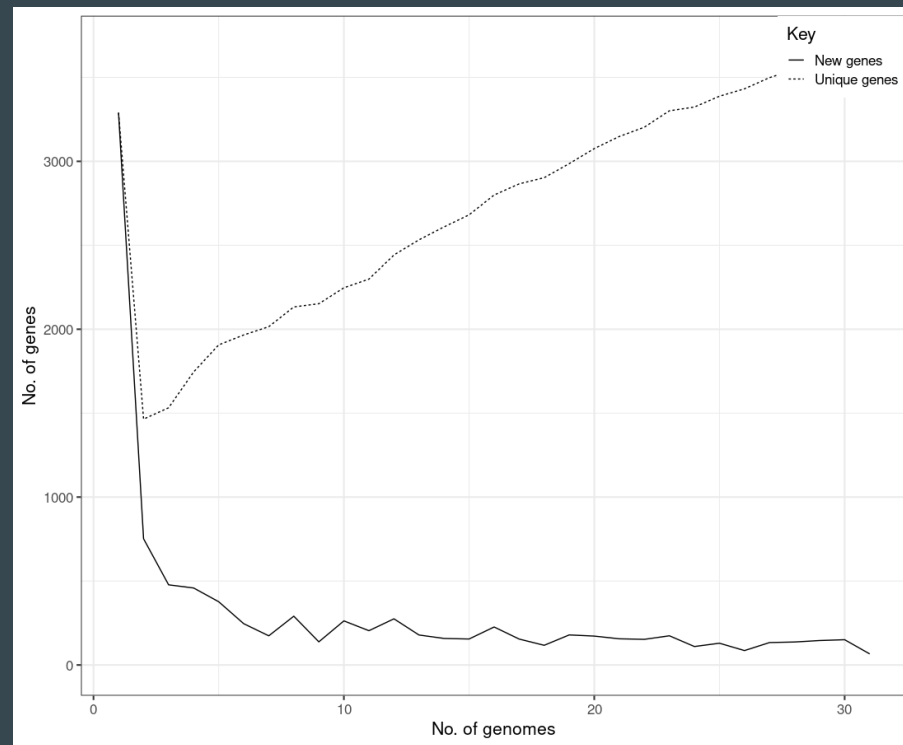
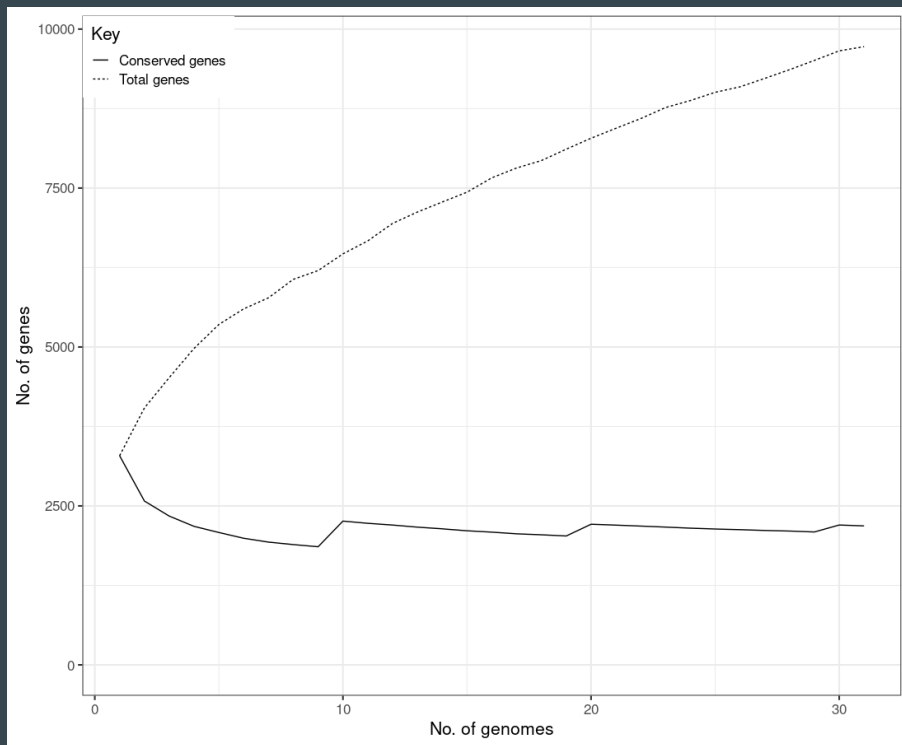
Pangenome analysis



Presence-absence pangenome matrix

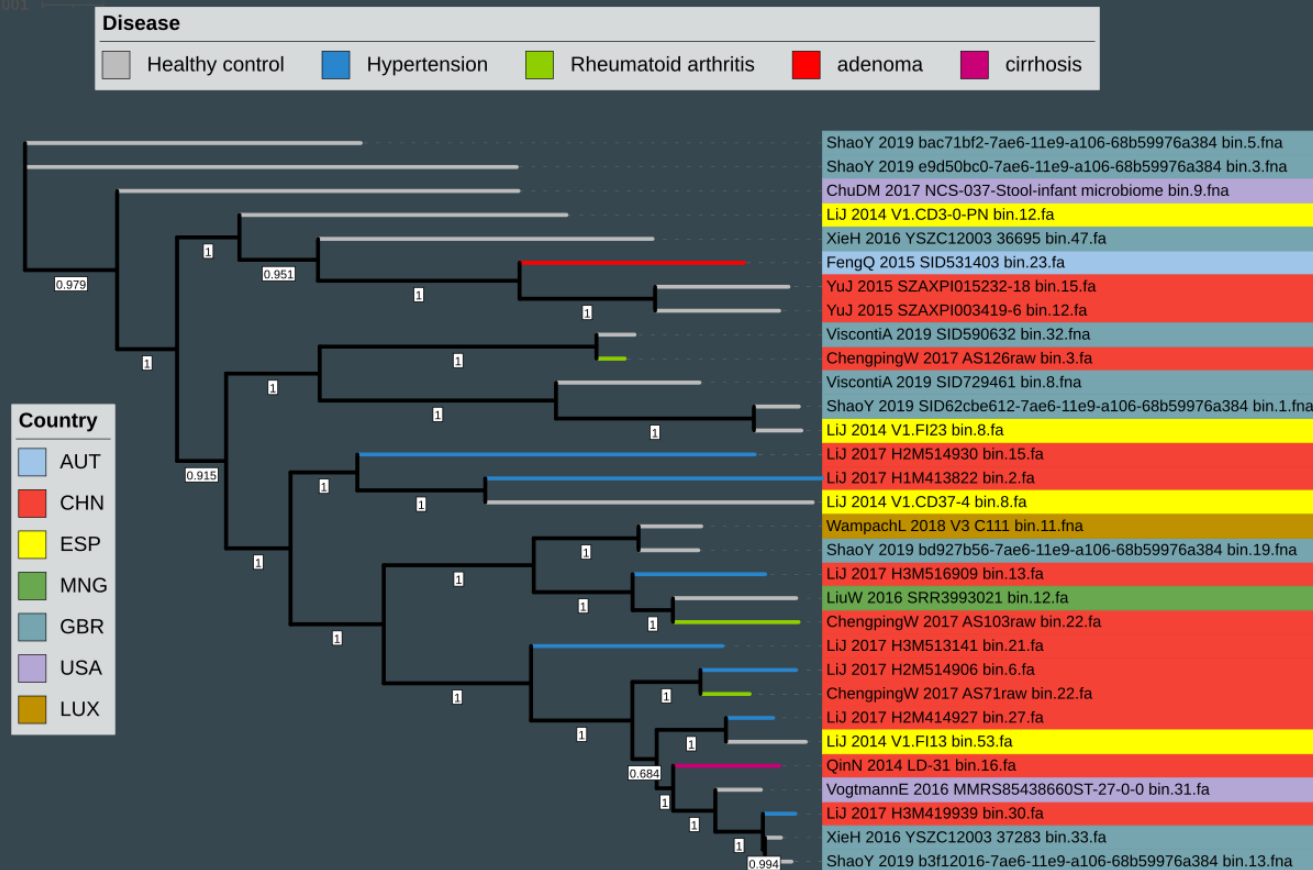


Pangenome Genes Comparison



Core gene alignment phylogenetic tree

Tree scale: 0.001



Conclusion

- Taxonomic assignment:

```
k__Bacteria|p__Firmicutes|c__Clostridia|o__Eubacteriales|f__Oscillospira  
ceae|g__Flavonifractor|s__Flavonifractor_plautii|t__SGB15132
```

- no notable differences between the genomes
- future work: run again the pipeline with more genomes and different parameters

Thank you for your kind attention!