The effect of pipelines and databases on the analysis of the fecal microbiota of dairy cattle

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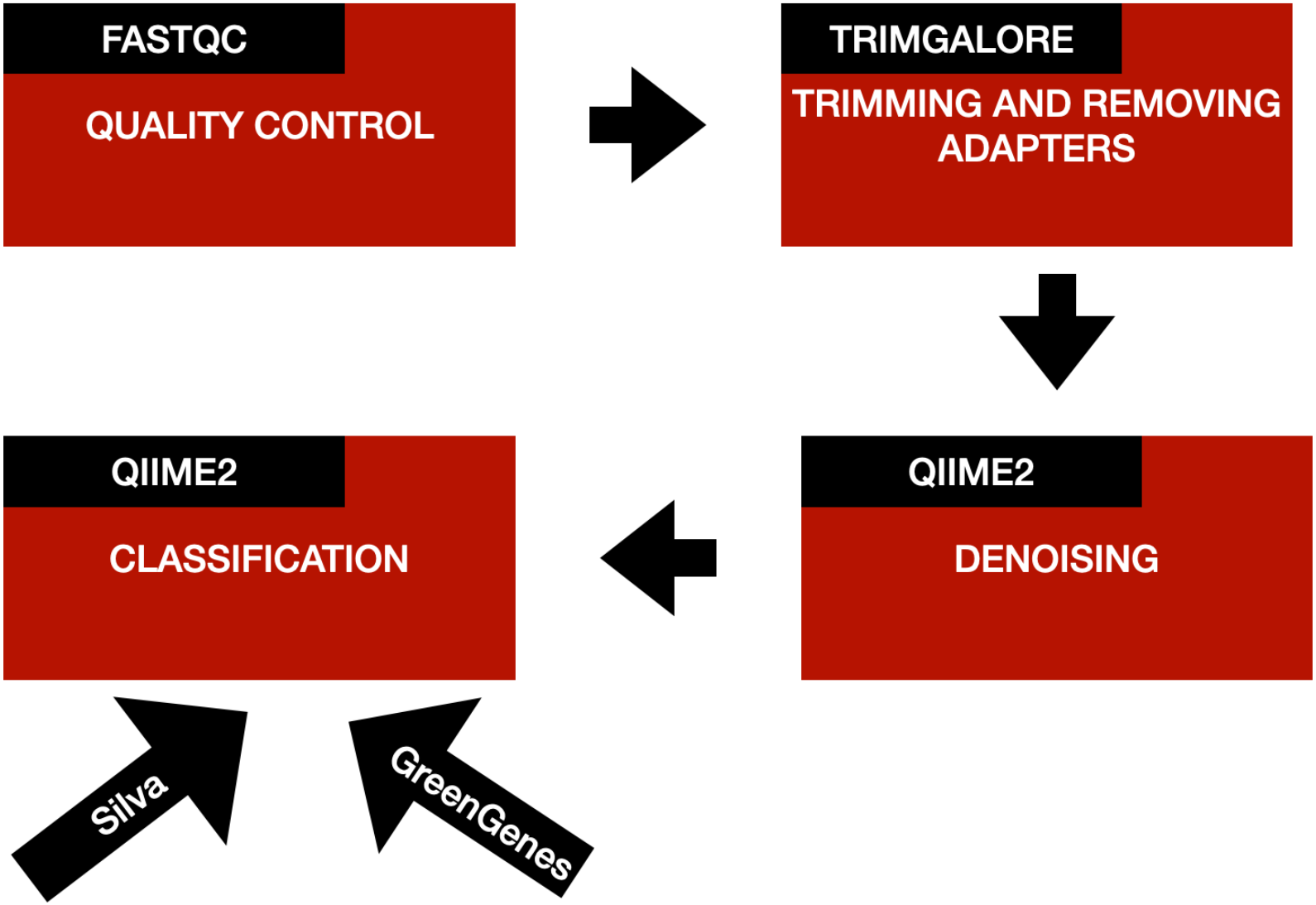
Objective

Identification of the effect of 16S rRNA databases on the results of the classification of OTU in fecal microbiota of dairy cattle

Material

- 138 fecal samples of dairy cattle
- amplicons of the V3-V4 region of bacterial 16S rRNA
- Illumina MiSeq
- Silva and GreenGenes databases of bacterial 16S rRNA

Methods


FASTQC
QUALITY CONTROL
TRIMGALORE
TRIMMING AND REMOVING ADAPTERS
QIIME2
DENOISING
QIIME2
CLASSIFICATION
Silva
GreenGenes

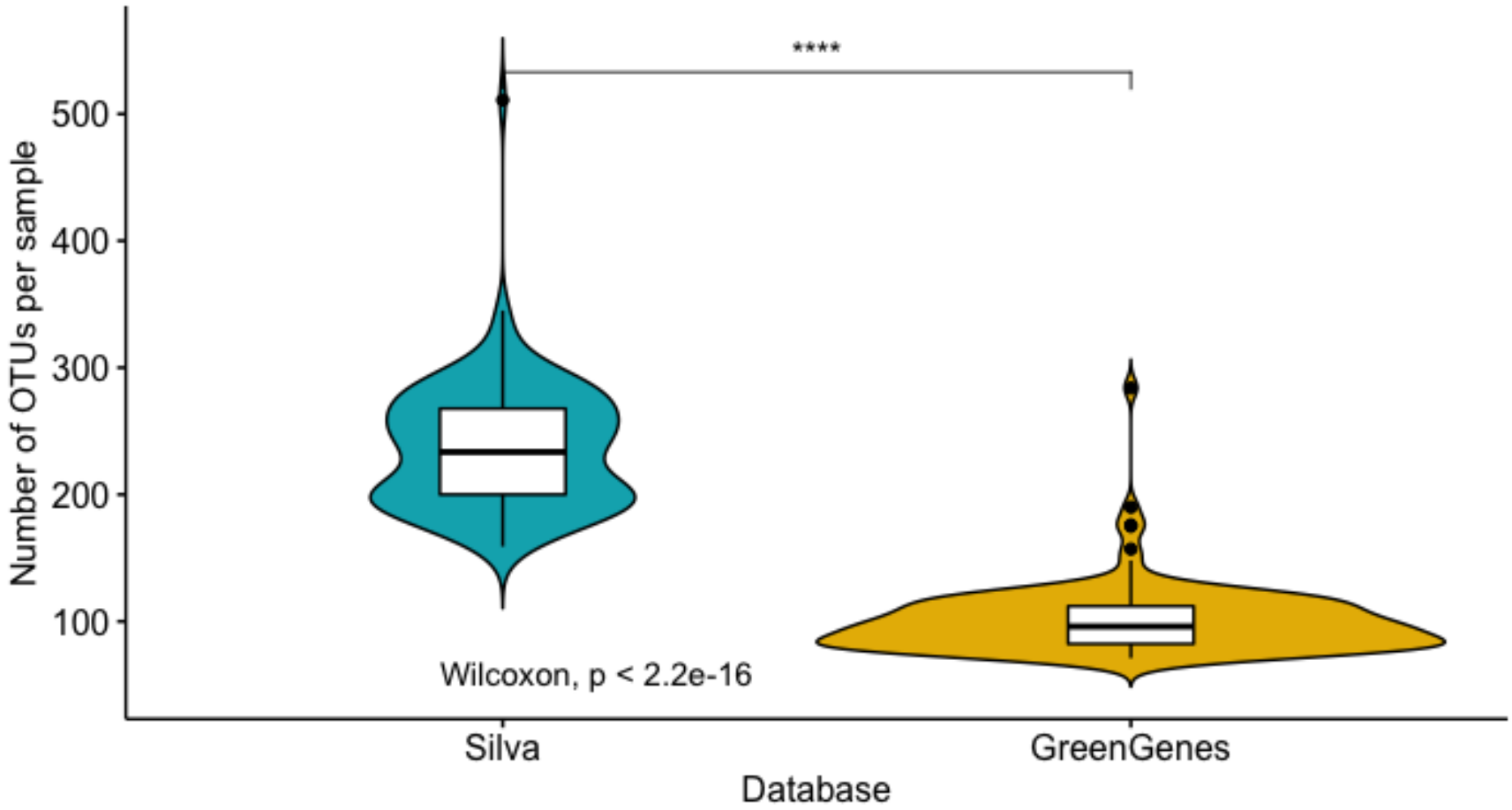
Results

Silva:

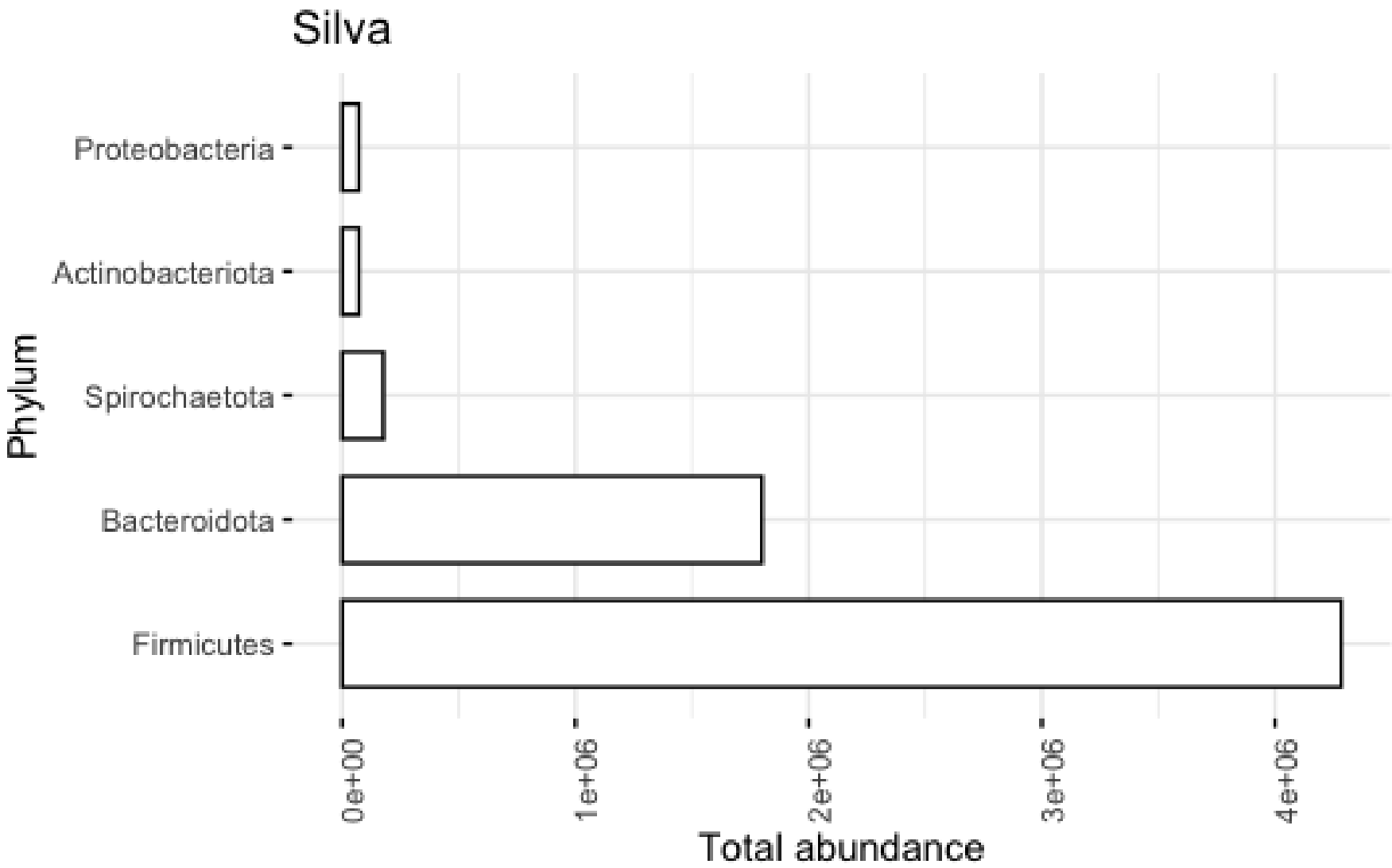
- 1405 OTUs

GreenGenes:

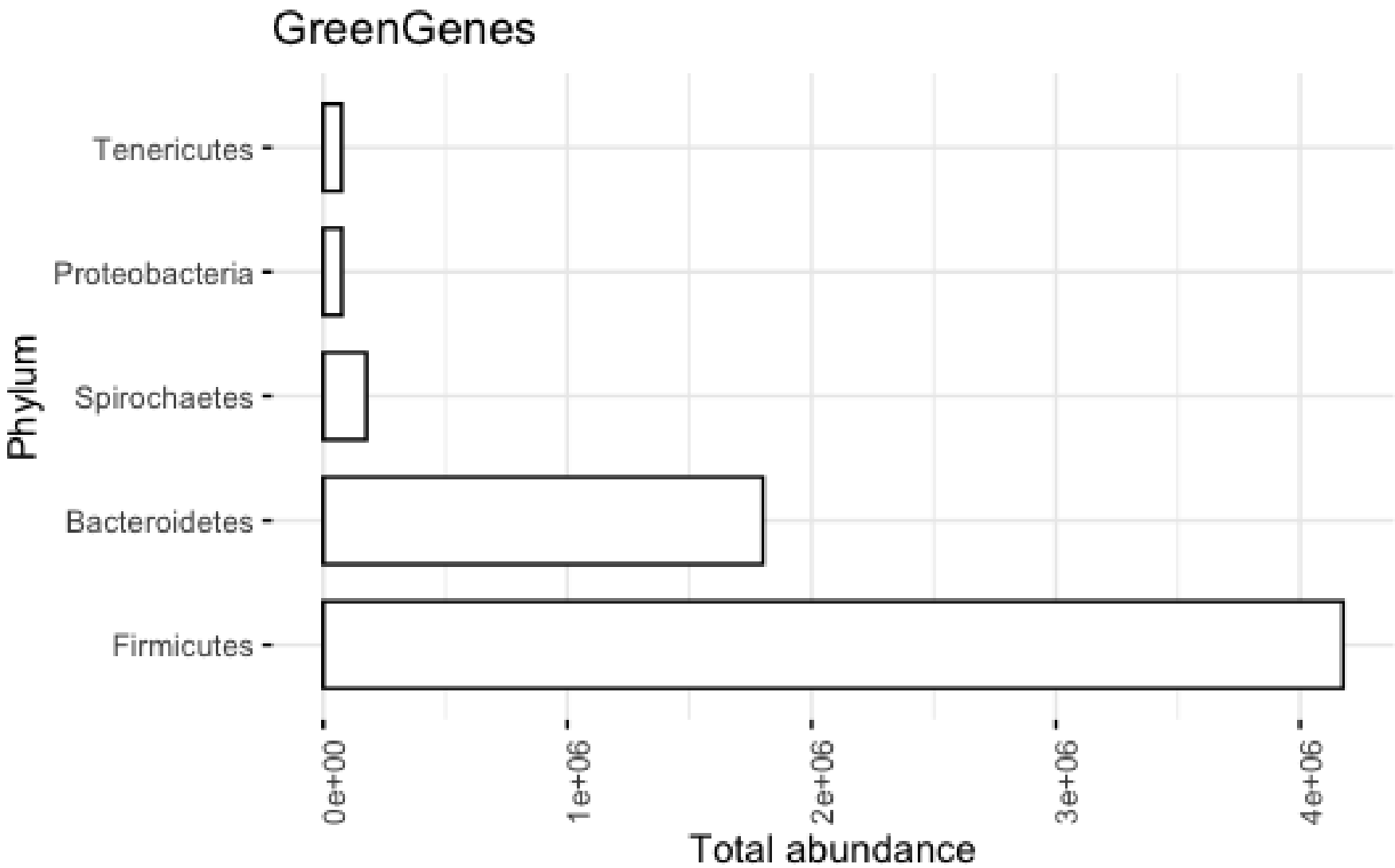
- 624 OTUs



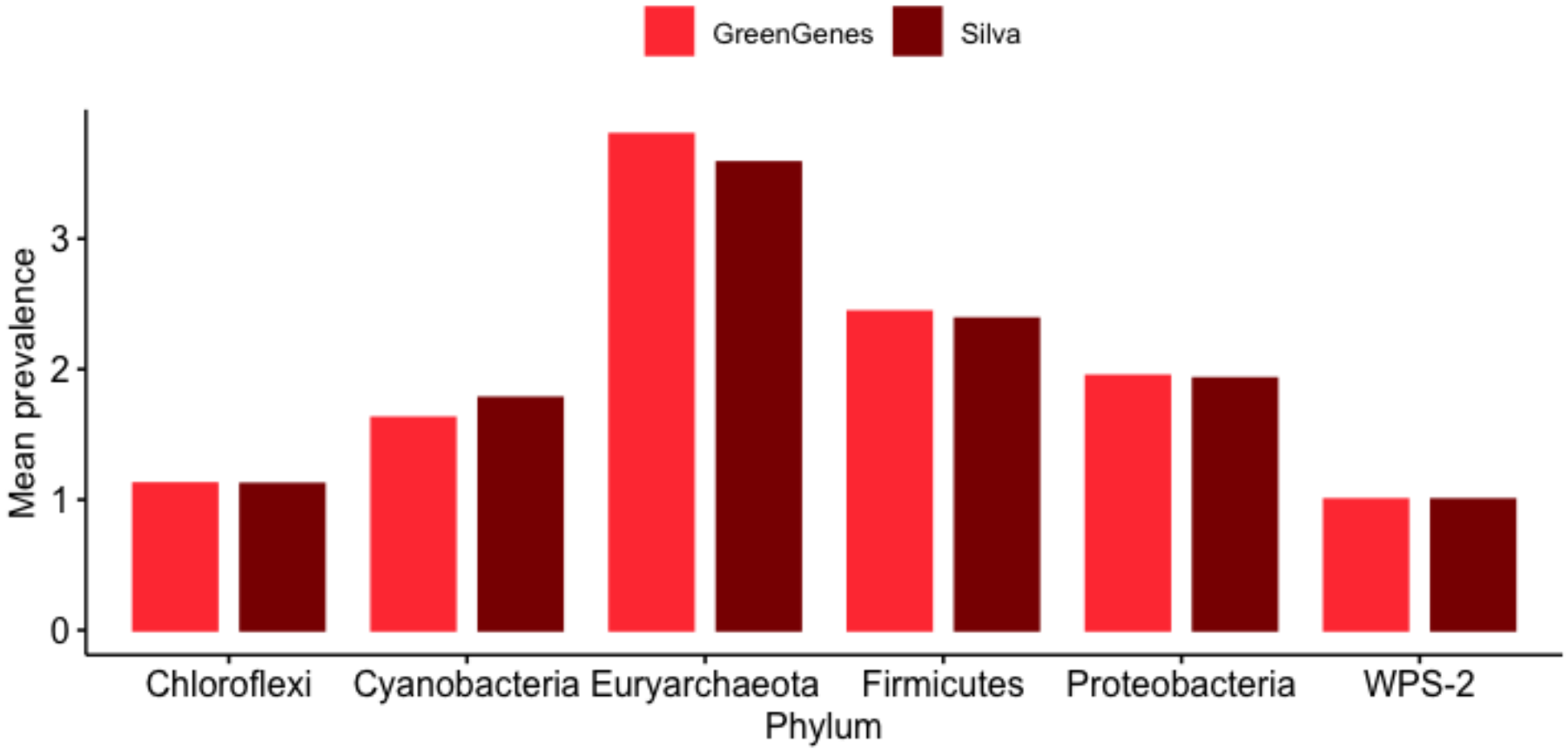
Results – top 5 phyla



Results – top 5 phyla



Results – common phyla



Conclusions

- Silva database shows more detailed classification of OTUs, while GreenGenes can create bigger clusters.
- Two databases classified large OTUs into different phyla. Common phyla in both databases shows similar results.

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Thanks for your attention!