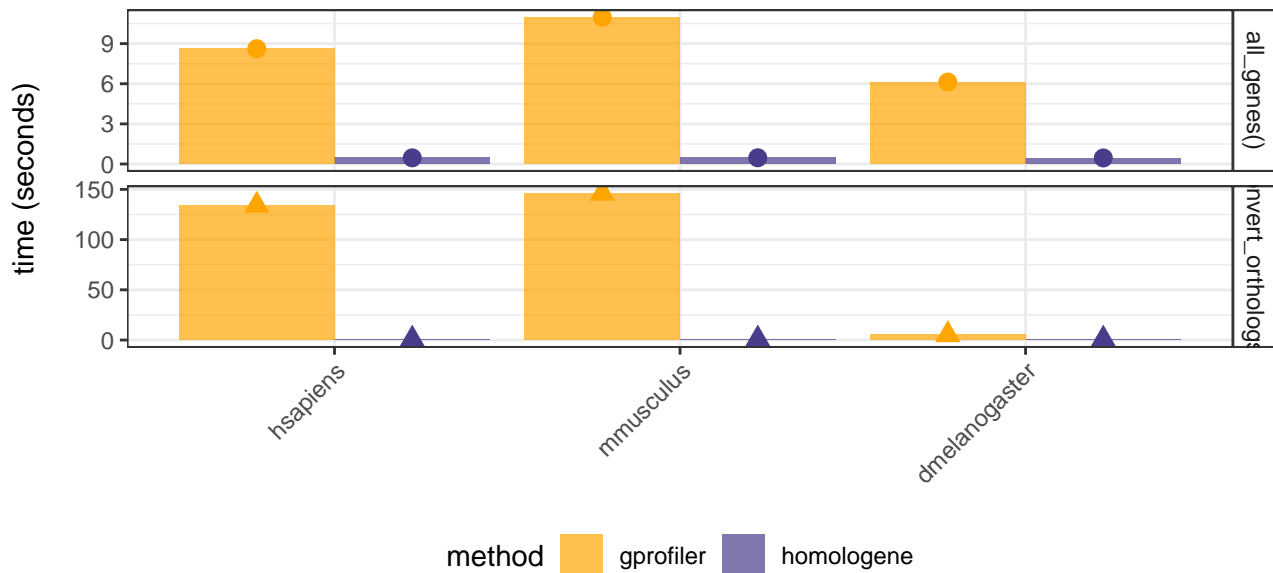


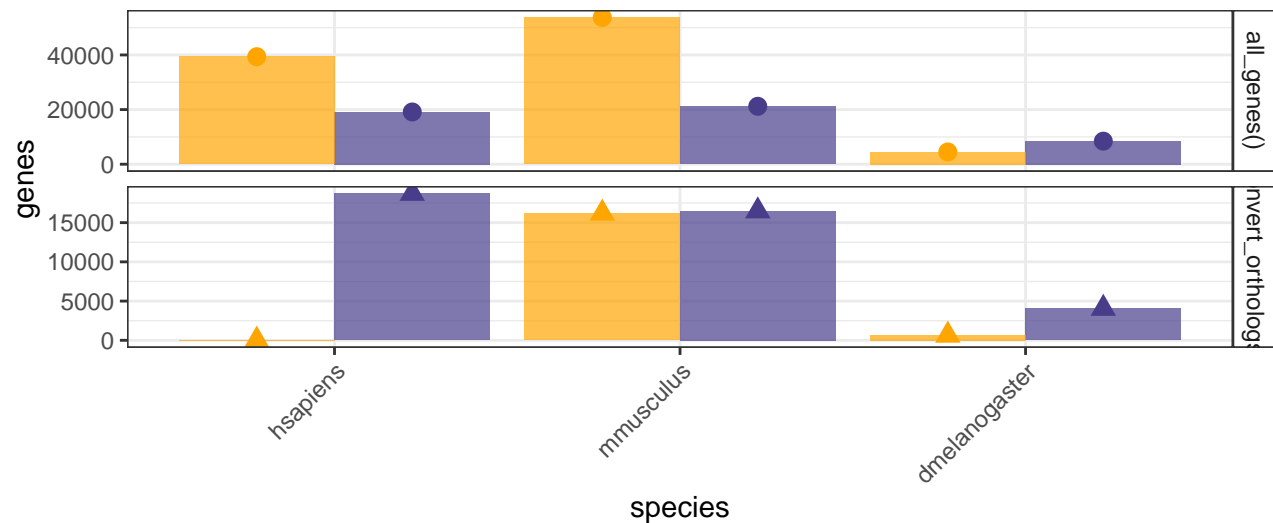
a

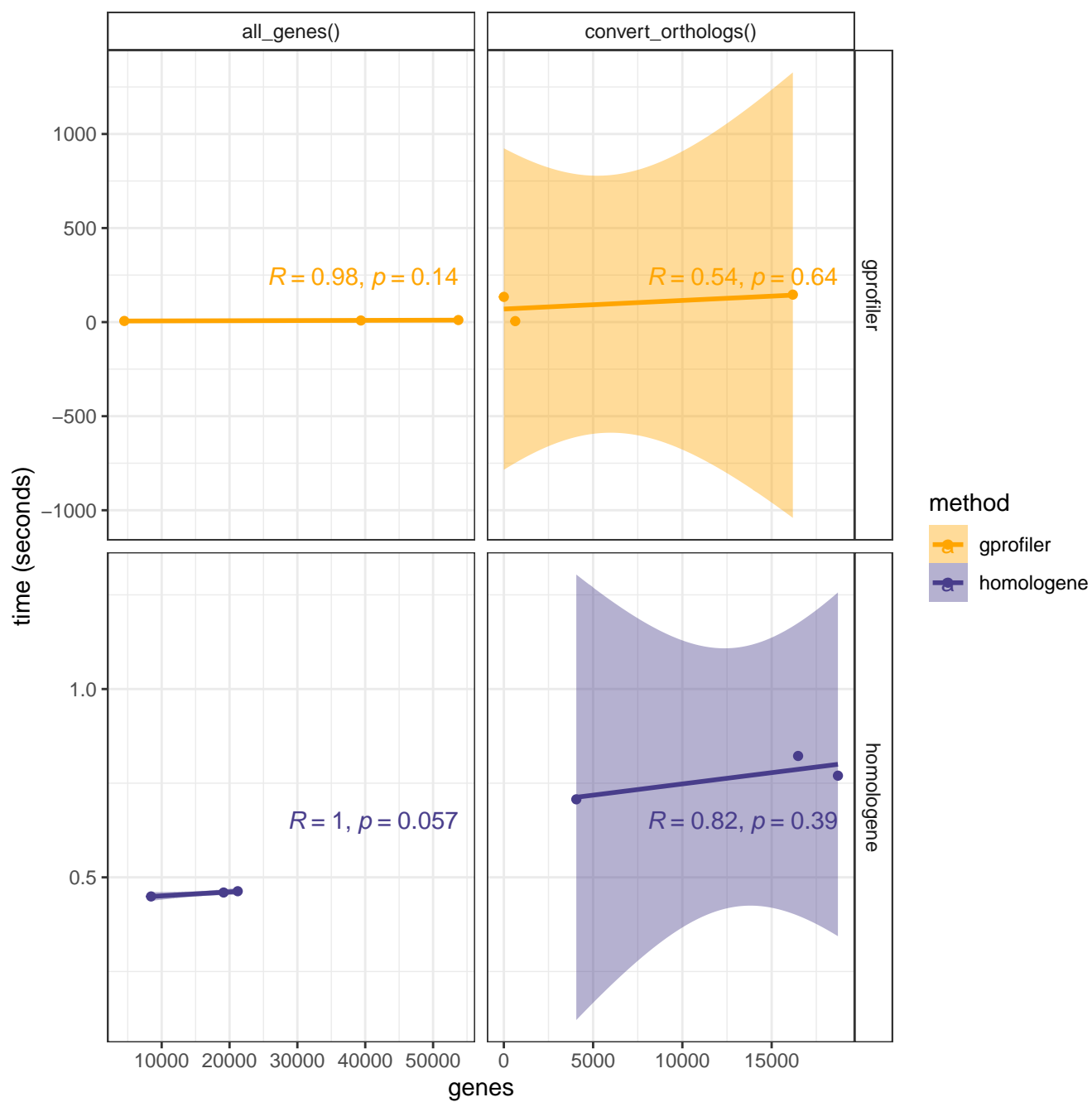
## Run time by method

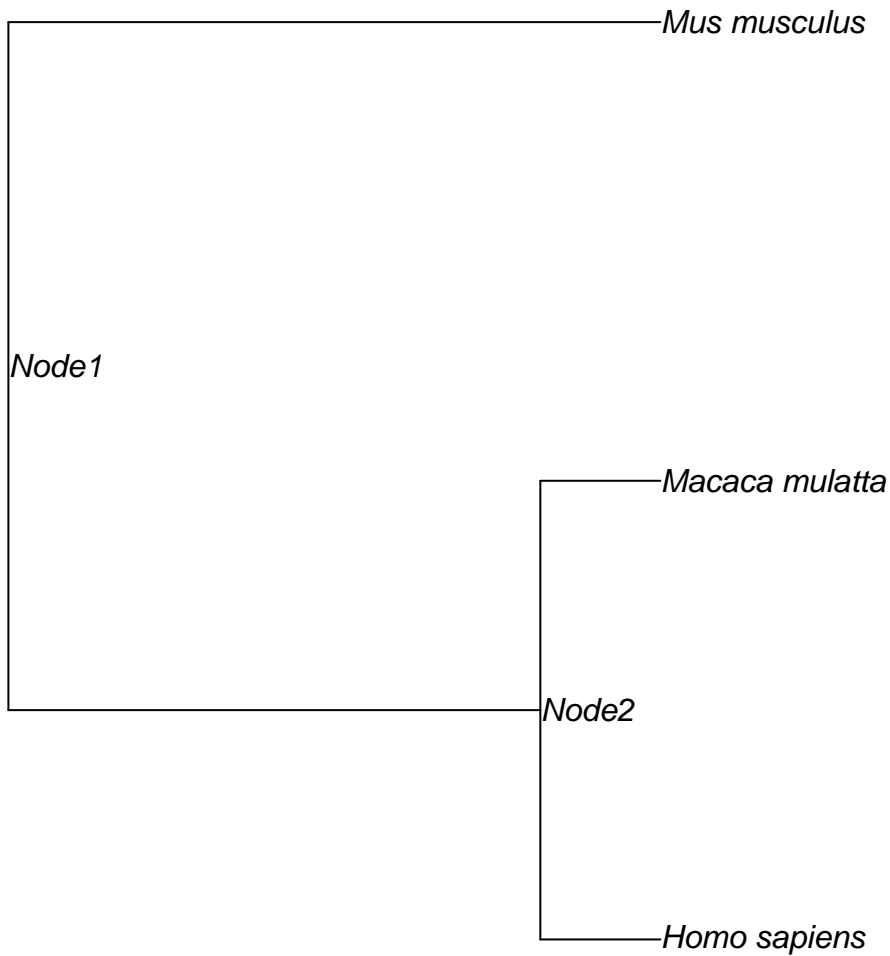


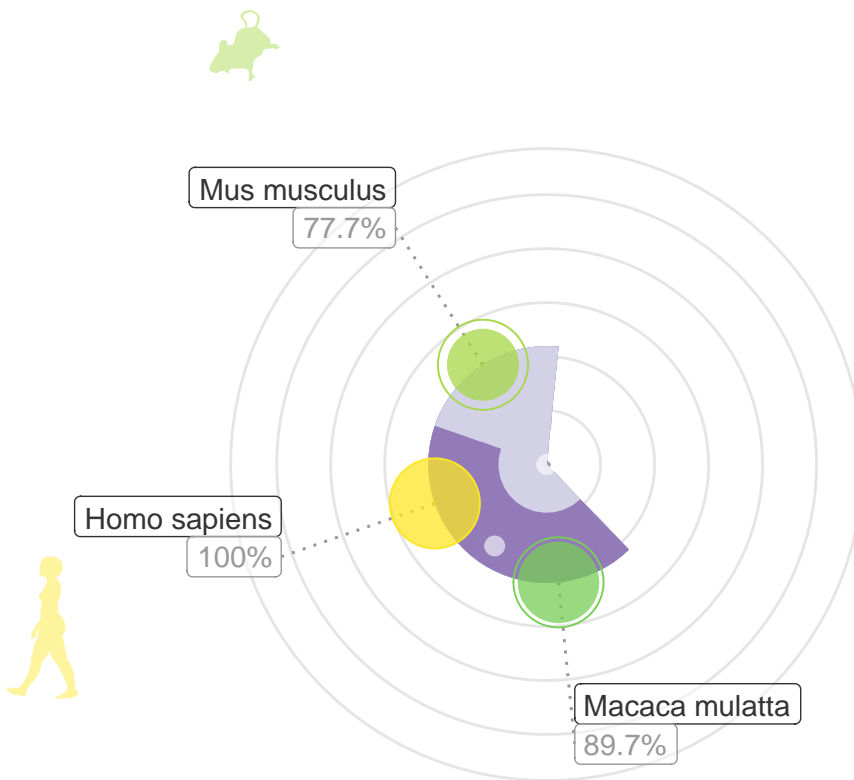
b

## Genes retrieved by method





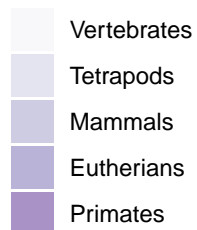




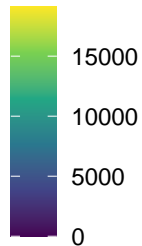
1:1 human orthologs (%)

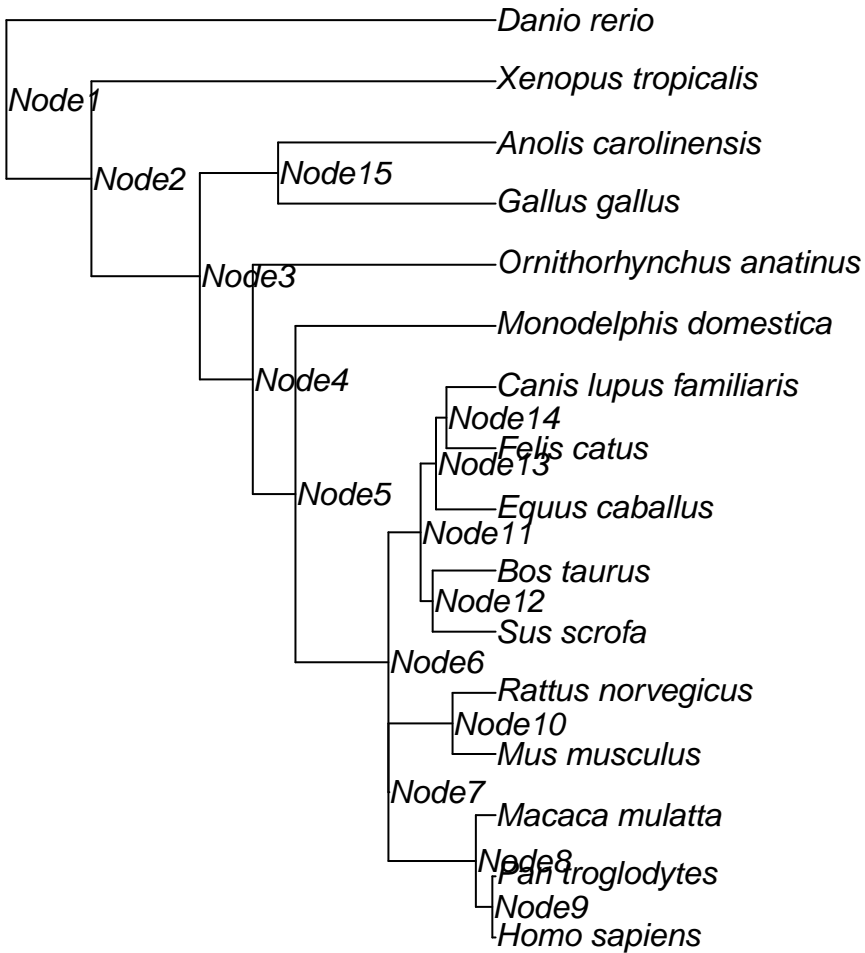
- 25
- 50
- 75
- 100

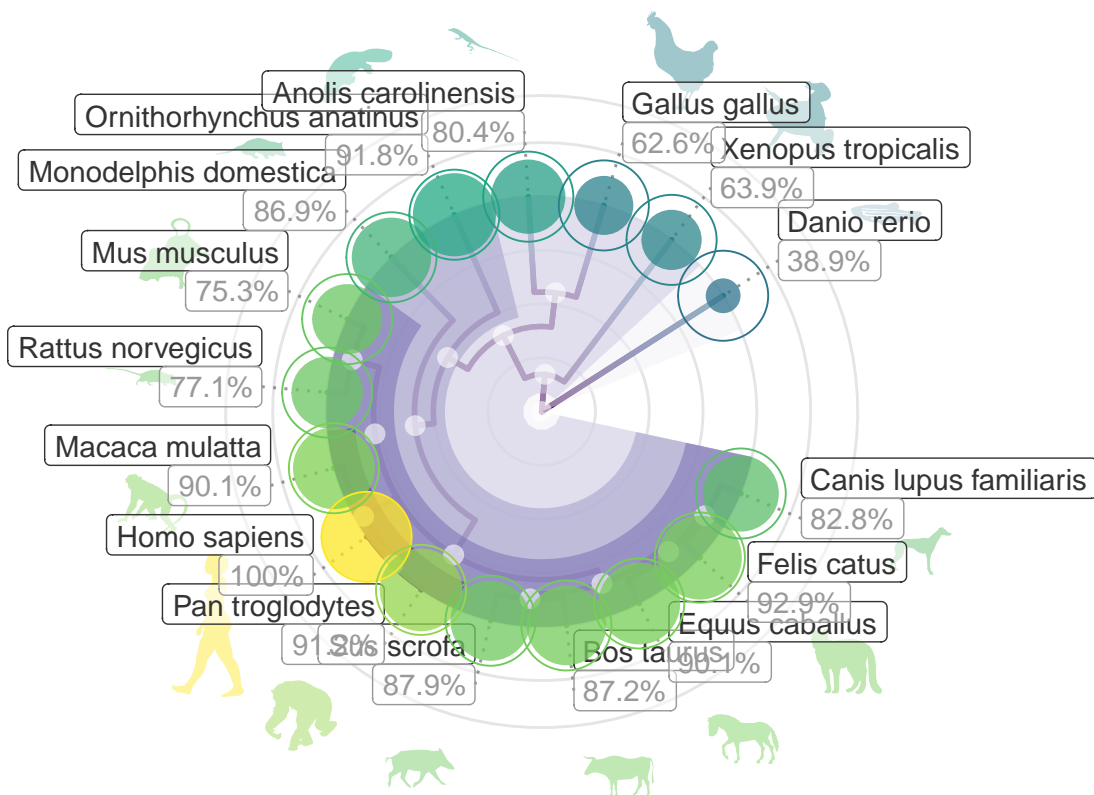
Clade



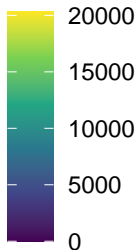
1:1 human orthologs (count)







1:1 human orthologs (count)



1:1 human orthologs (%)

- 25
- 50
- 75
- 100

Clade

