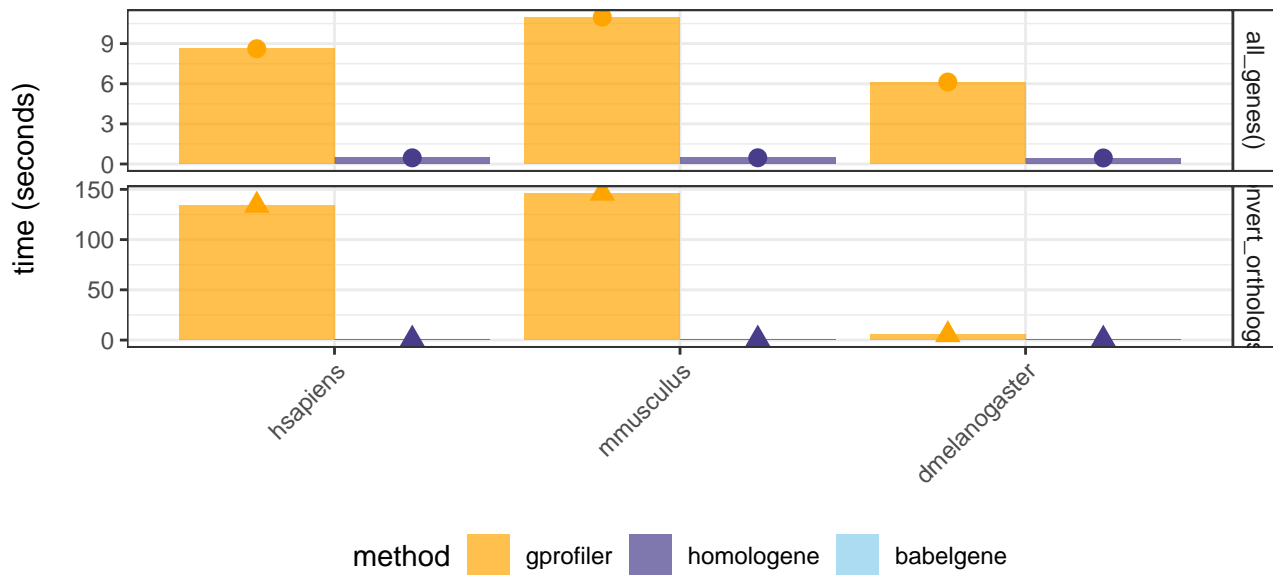


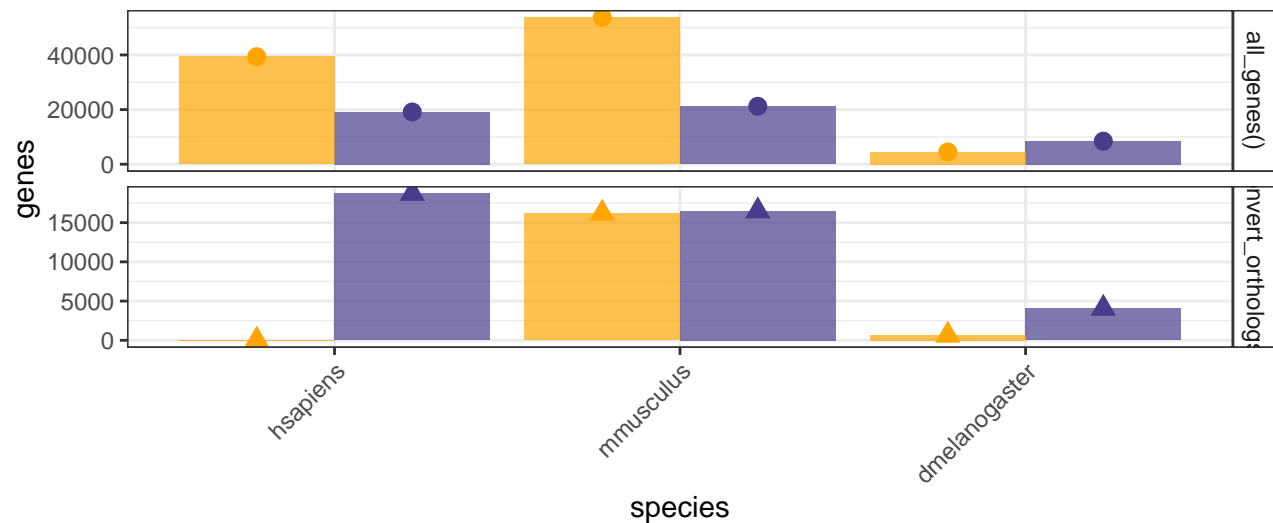
a

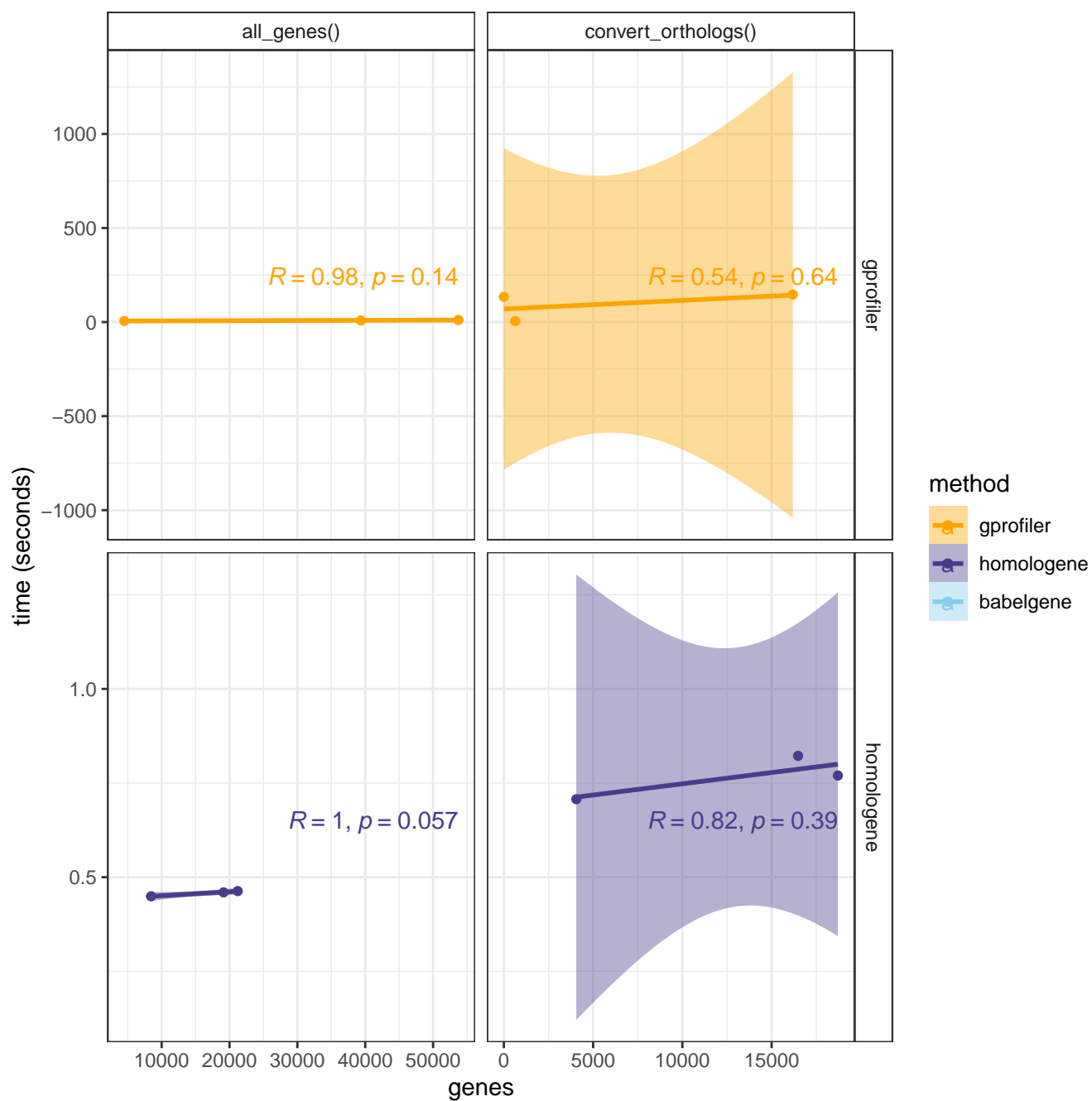
Run time by method

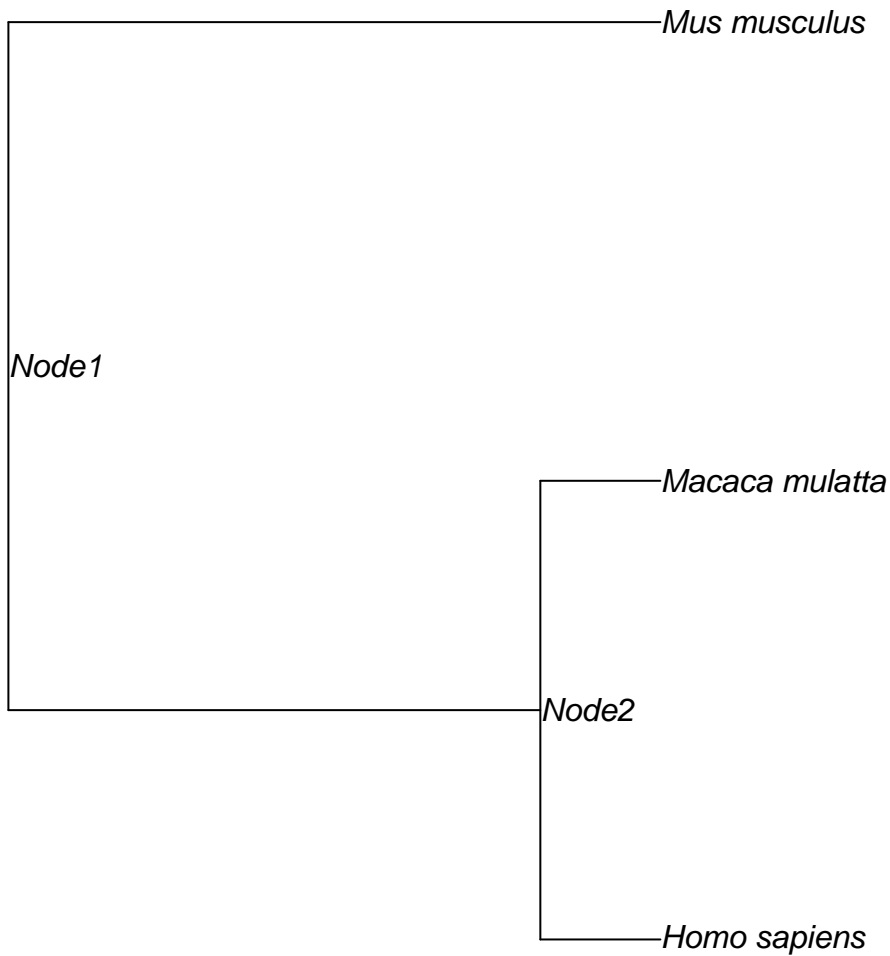


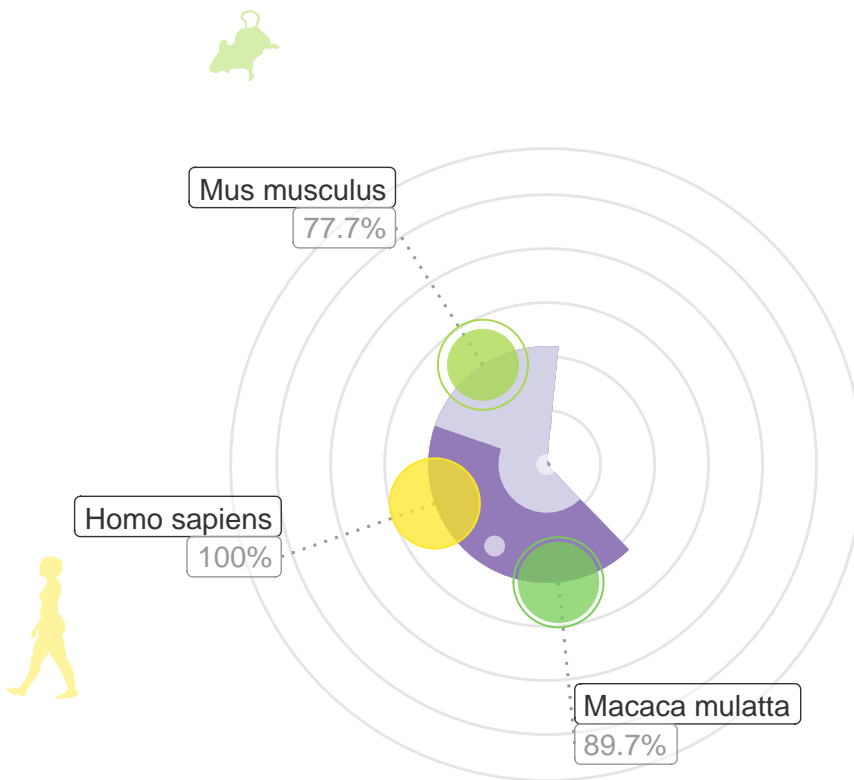
b

Genes retrieved by method





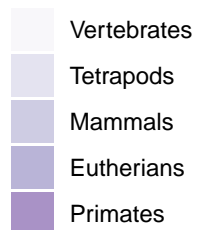




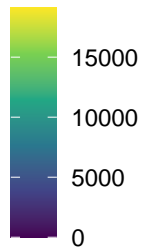
1:1 human orthologs (%)

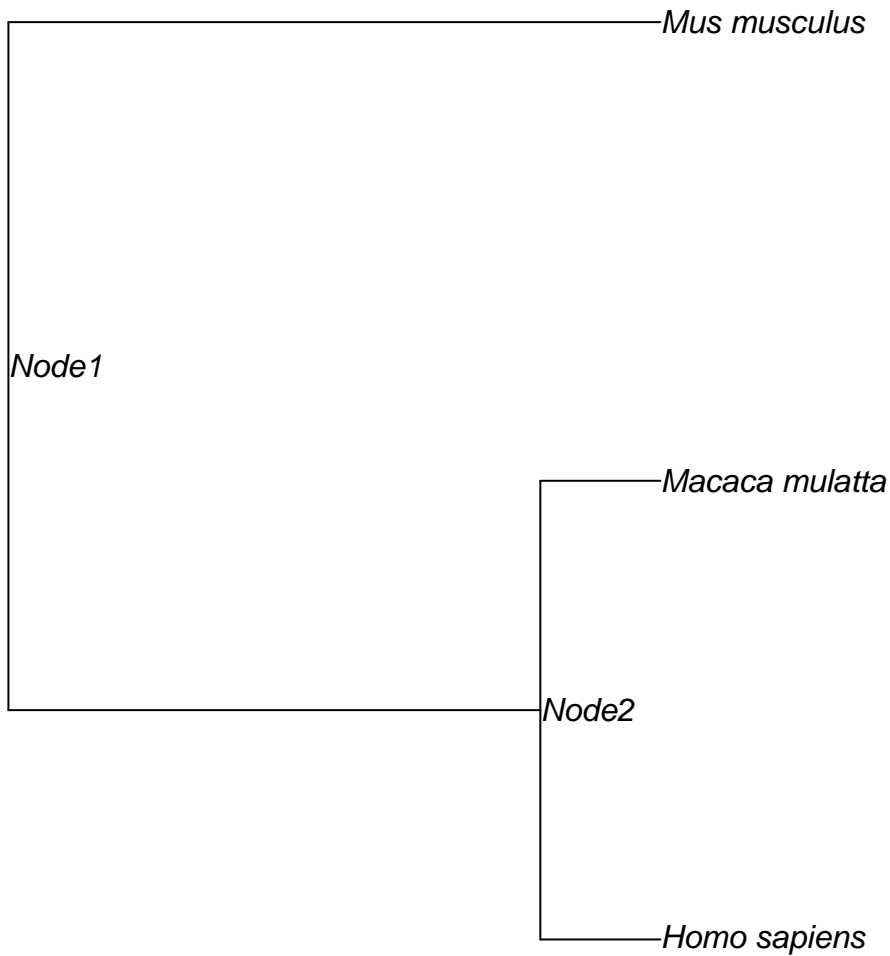
- 25
- 50
- 75
- 100

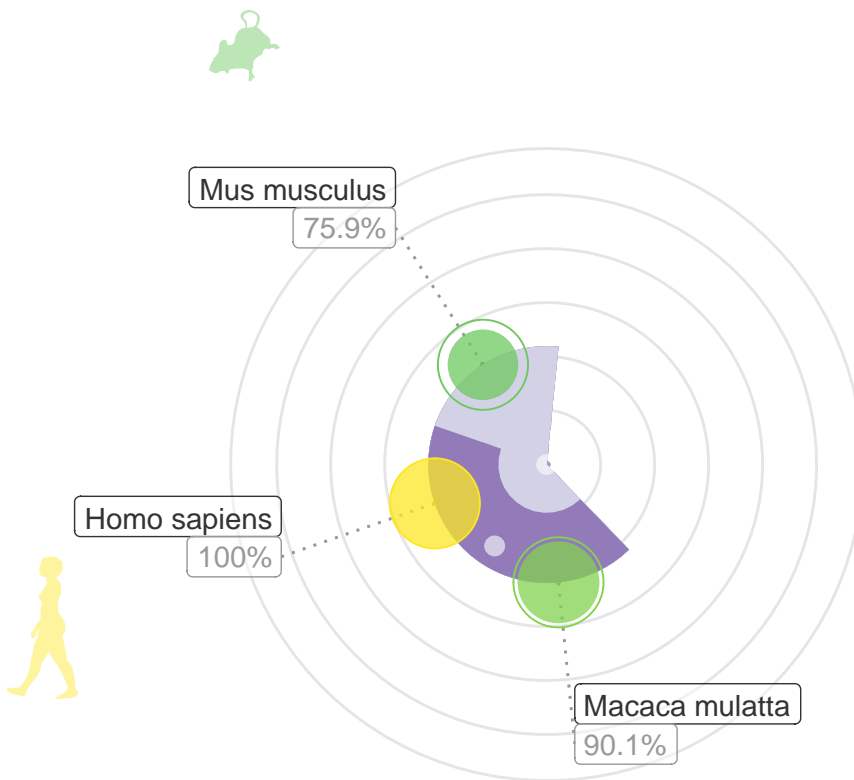
Clade



1:1 human orthologs (count)



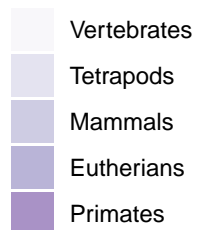




1:1 human orthologs (%)

- 25
- 50
- 75
- 100

Clade



1:1 human orthologs (count)

