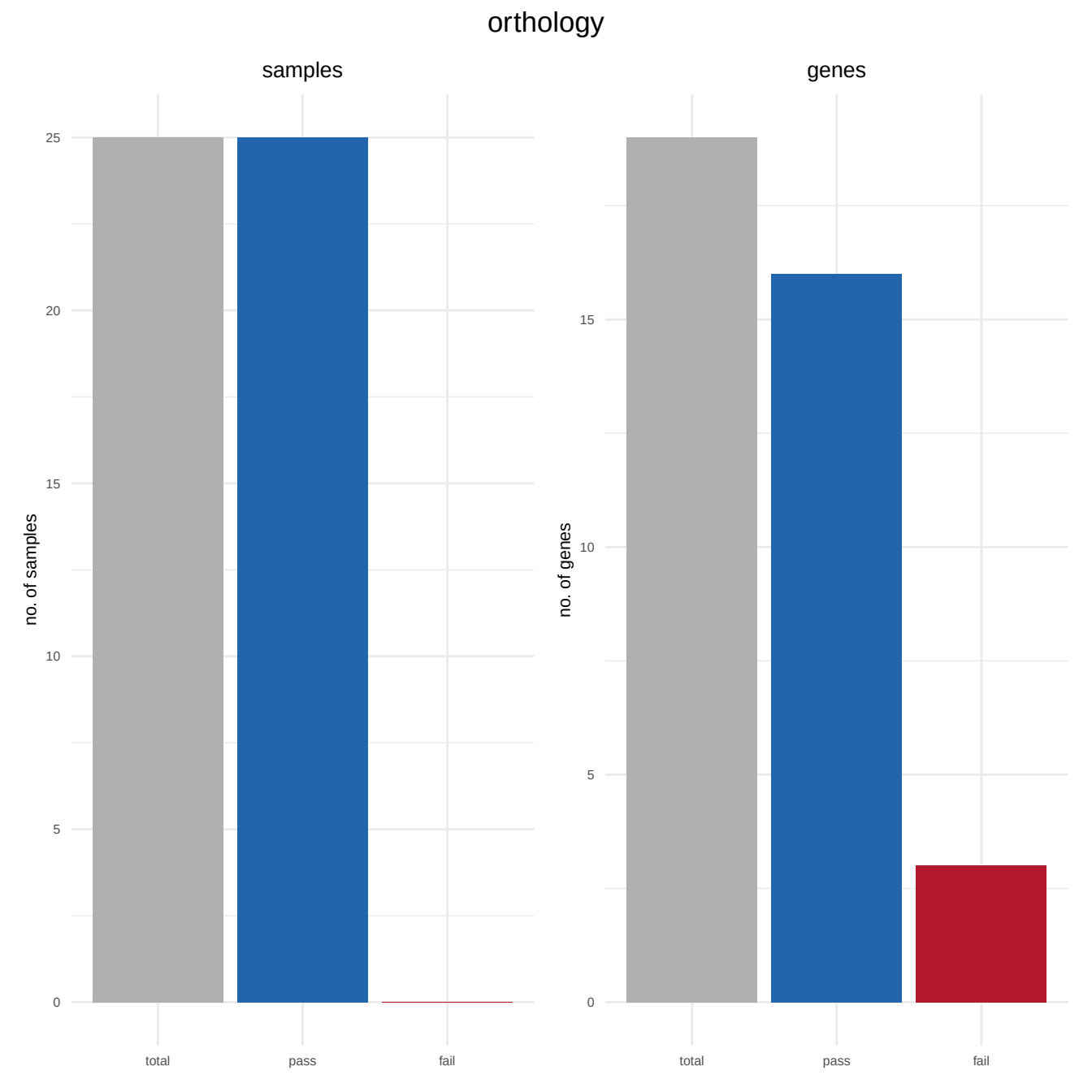
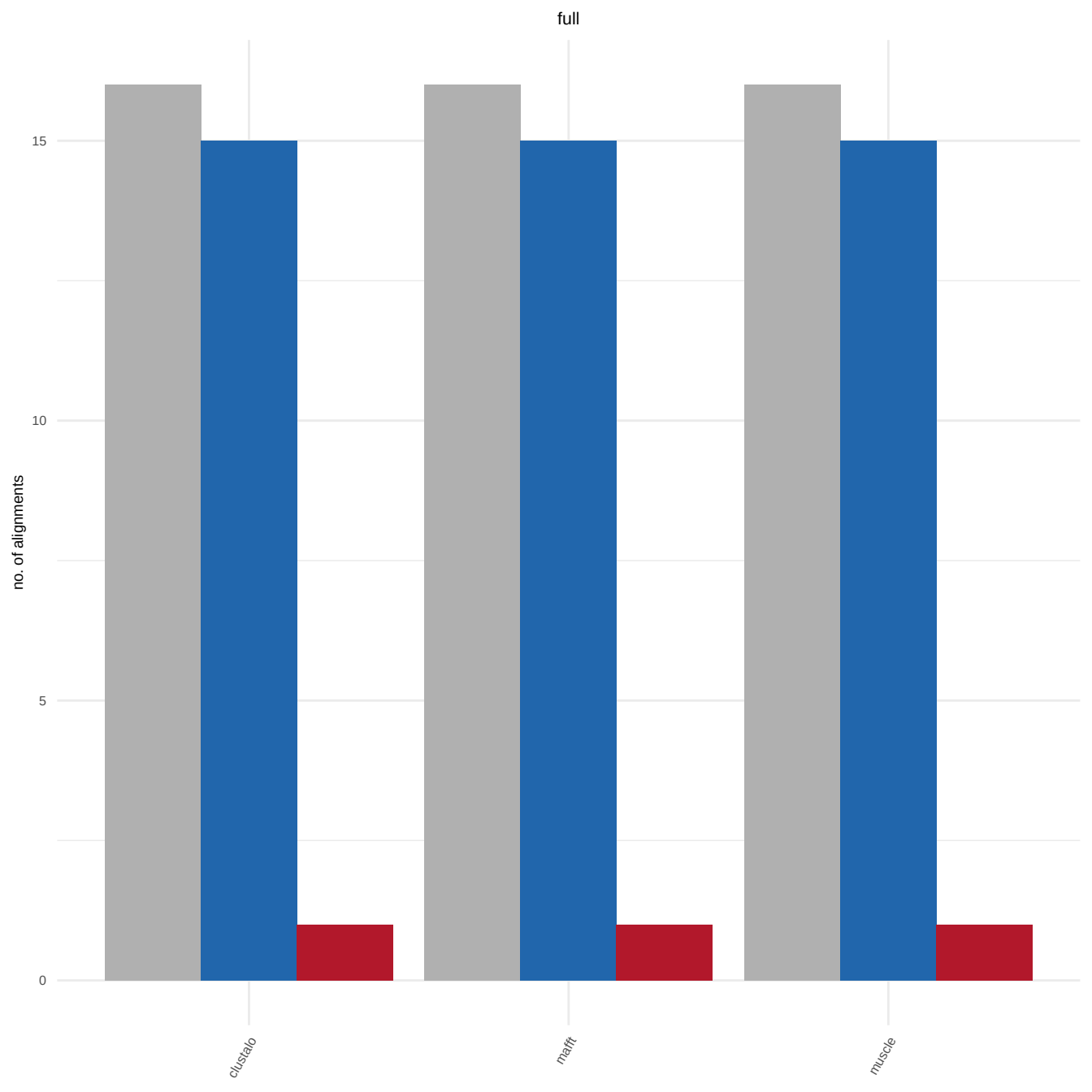
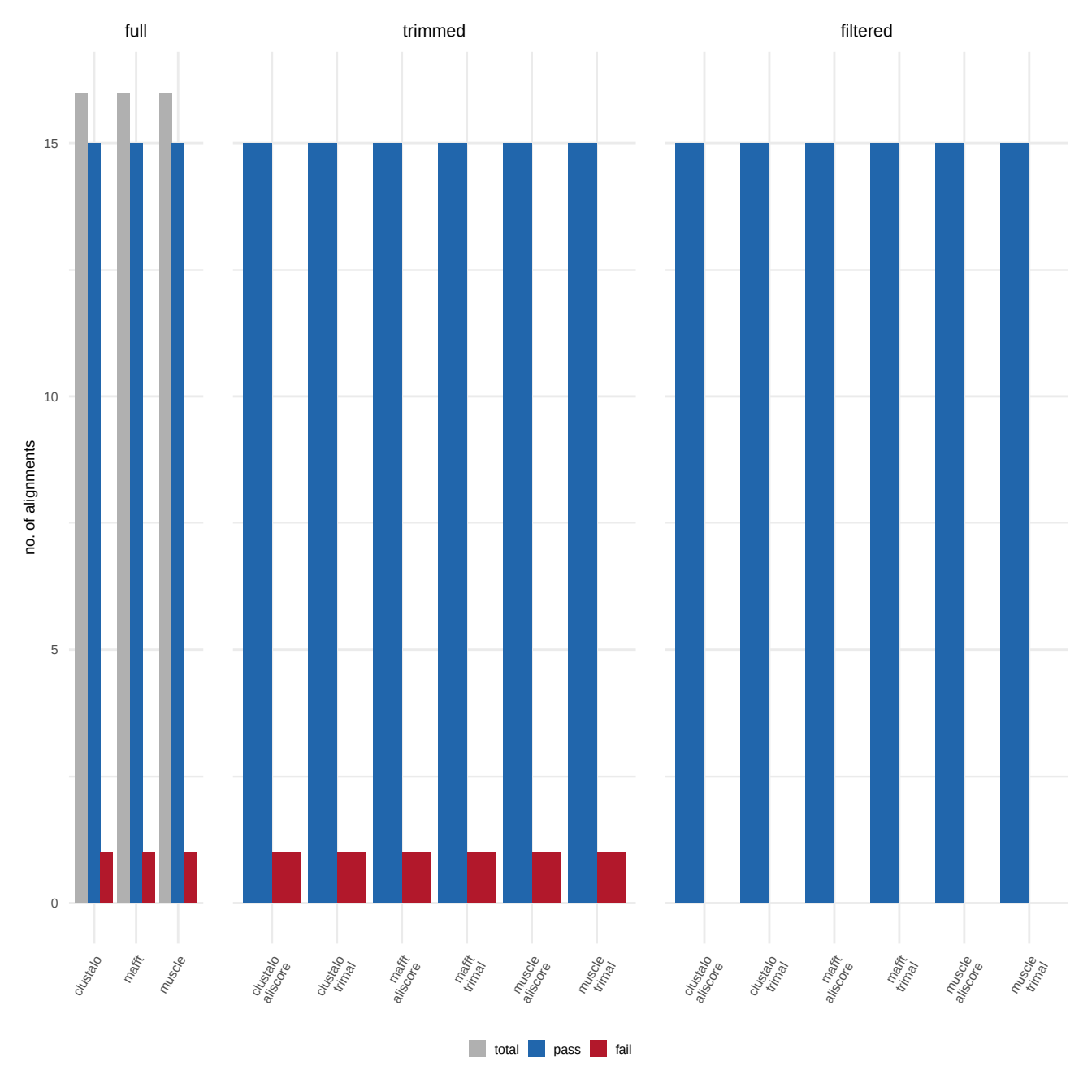

orthology
samples
genes
no. of samples
no. of genes
25
20
15
10
5
0
total
pass
fail


full
no. of alignments
15
10
5
0
clustalo
mafft
muscle


full
trimmed
filtered
no. of alignments
0
5
10
15
clustalo
mafft
muscle
clustalo aliscore
clustalo trimal
mafft aliscore
mafft trimal
muscle aliscore
muscle trimal
total
pass
fail

modeltest
clustalo−aliscore
clustalo−trimal
mafft−aliscore
mafft−trimal
muscle−aliscore
muscle−trimal
model
LG+G4
JTT+R3
LG+I+G4
JTT+I+G4
JTT+G4
VT+R2
JTTDCMut+G4
JTT+R2
JTTDCMut+F+R3
VT+G4

overview

setup:

Total samples: 25
Successfully downloaded: 24
Failed to download: 0
Locally provided: 1

orthology:

Method: BUSCO 5.2.1
BUSCO set: vertebrata_odb10
No. of BUSCO genes: 20
Minimum BUSCO completeness: 0.5

alignments:

Aligners and settings:
  clustalo
Sequence type: aa
Parsimony informative sites cut−off: 50
Alignment trimmers:
  aliscore, trimal
Filtering duplicated sequences: persample
Minimum number of sequences per alignment: 20

Analysis seed: 42