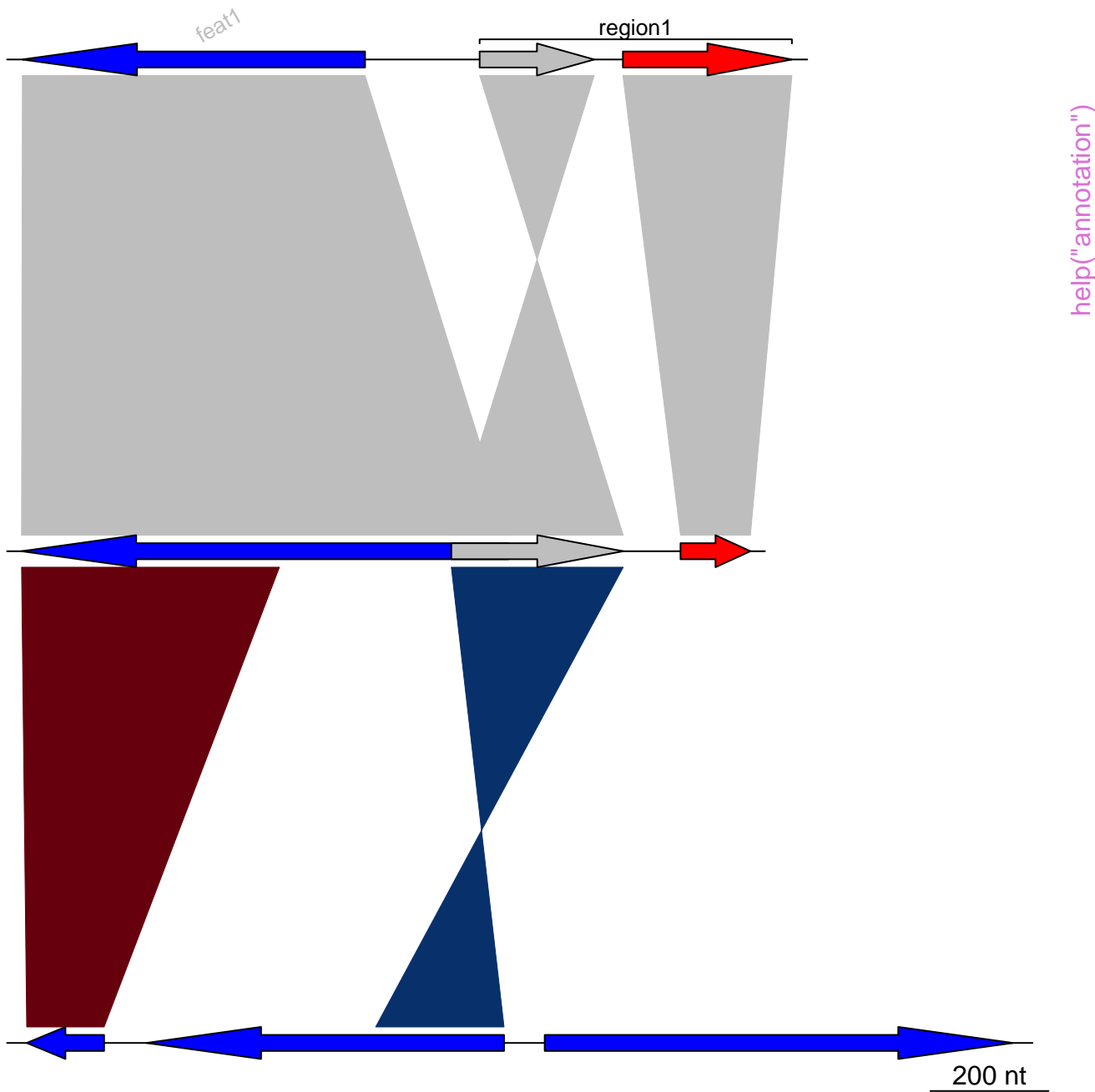
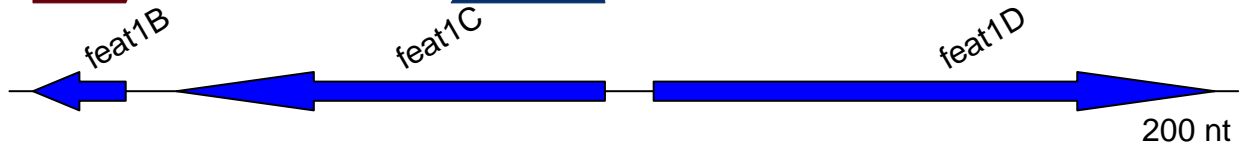
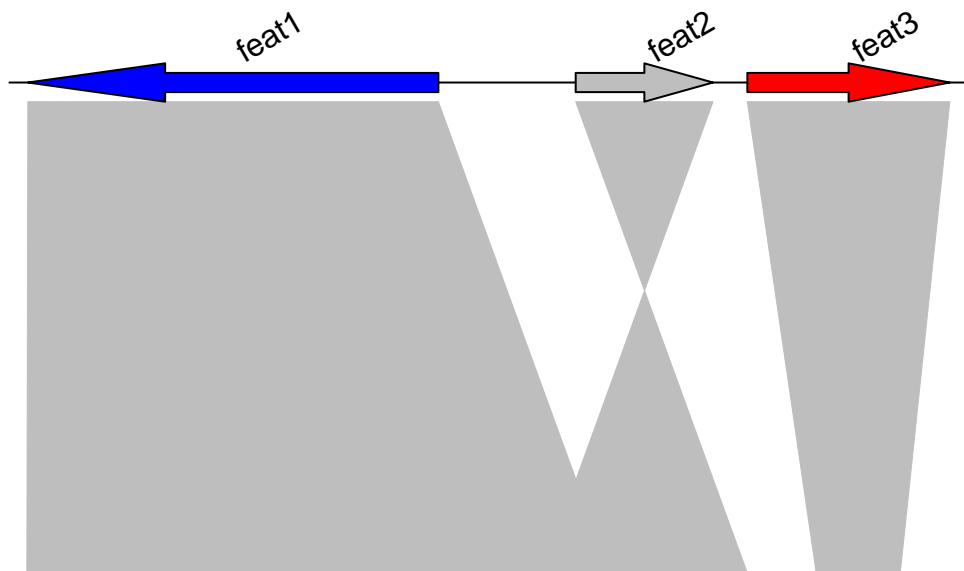
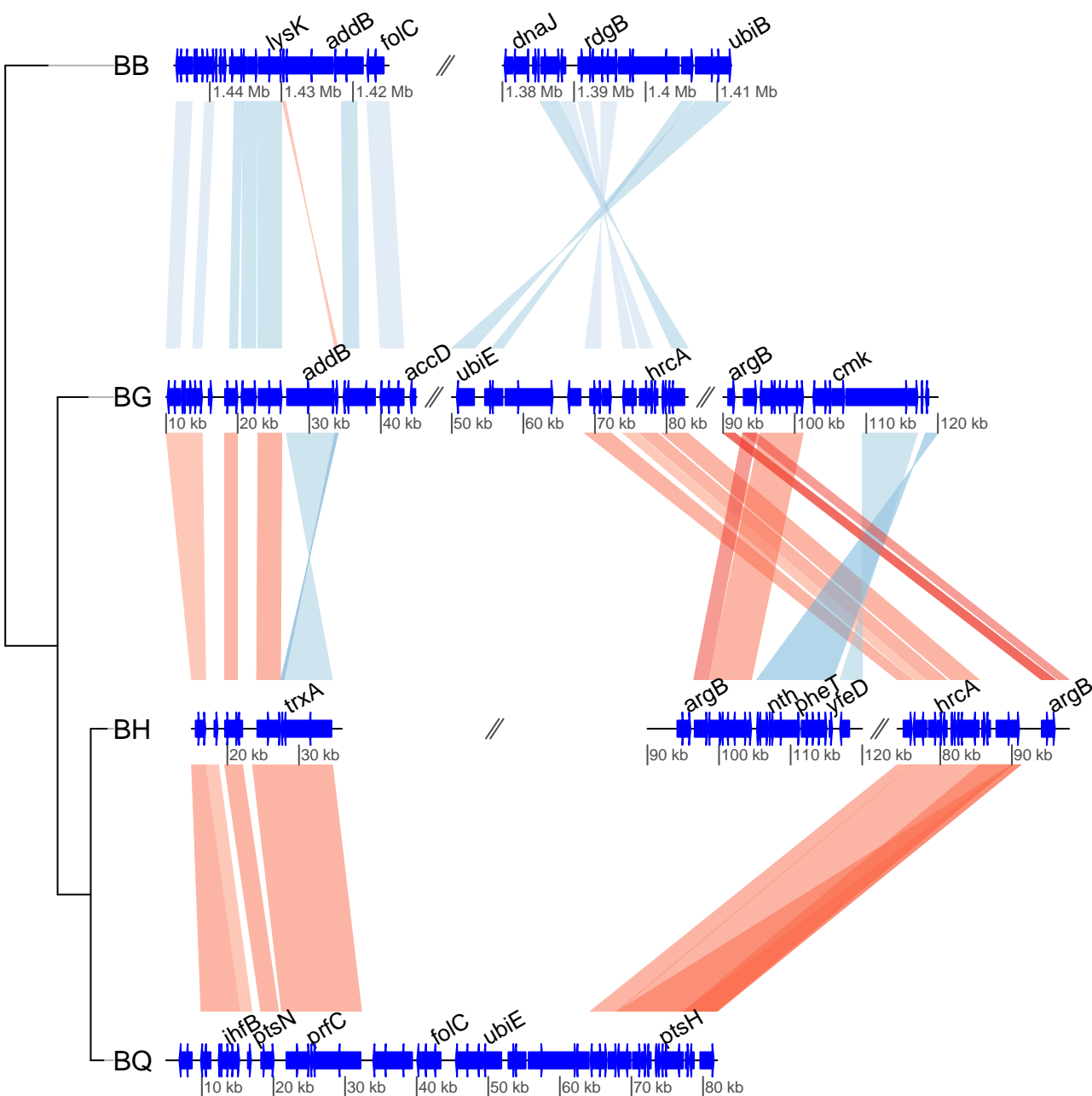


```
help("annotation")
```

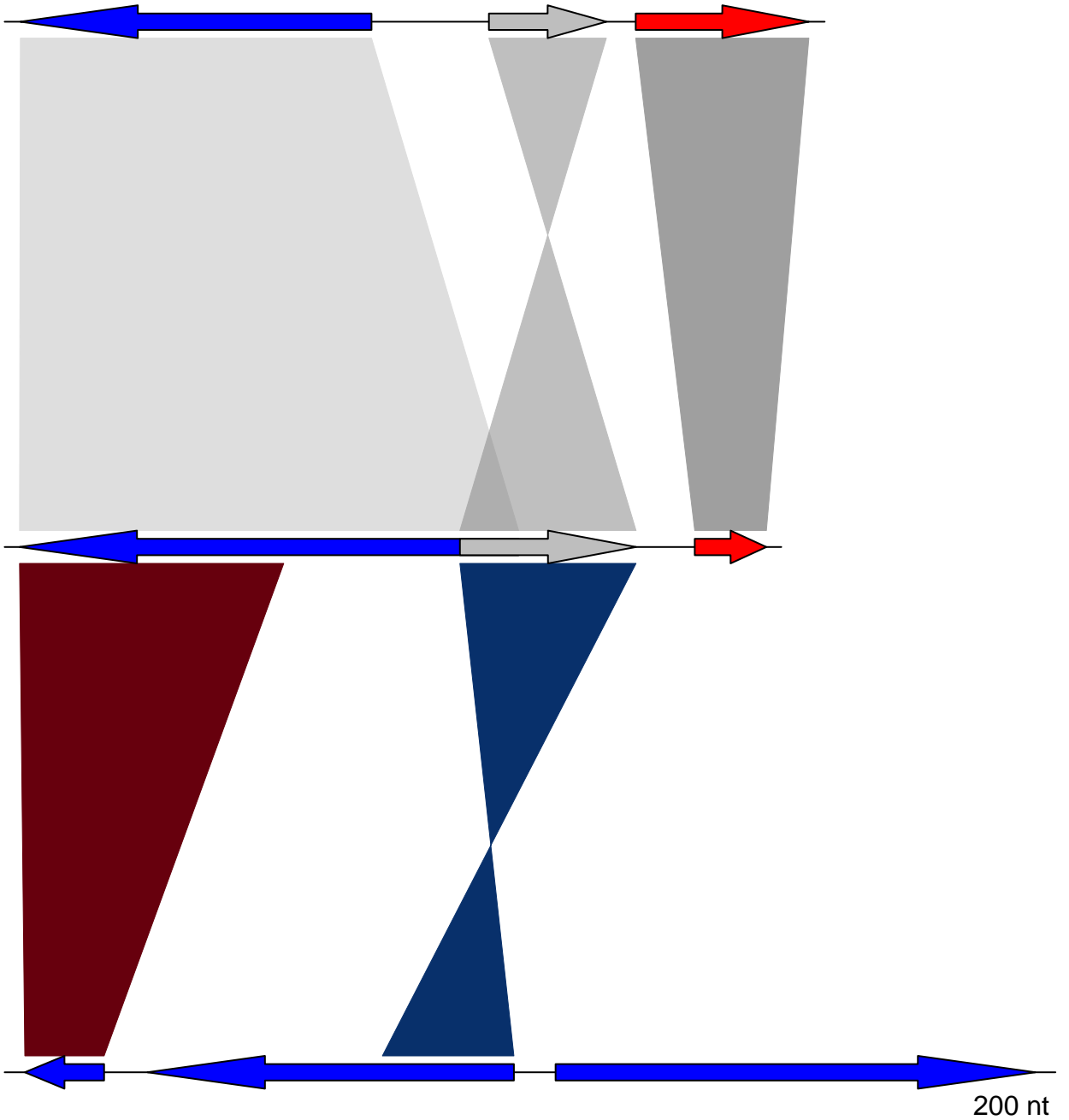




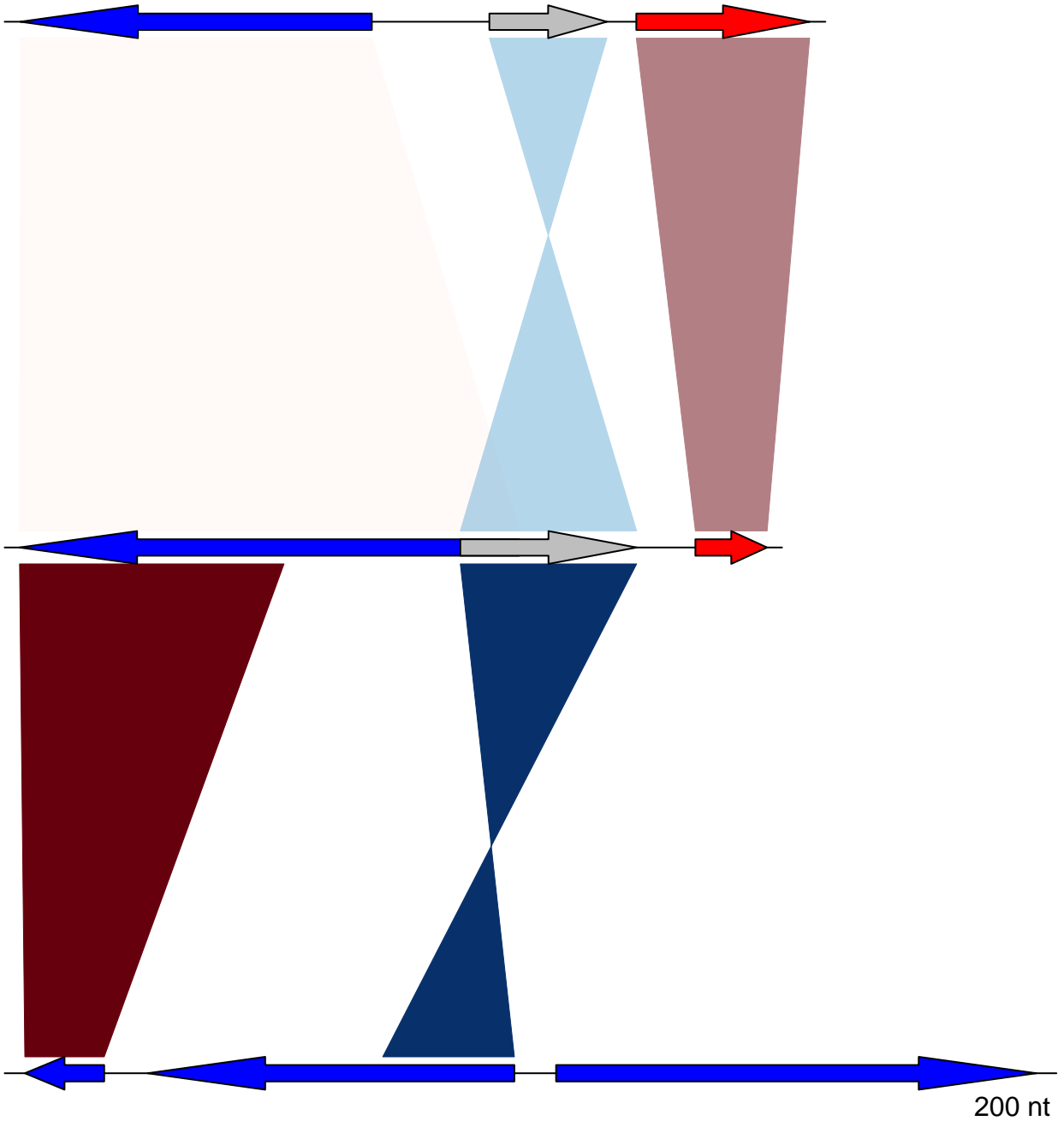
help("annotation")



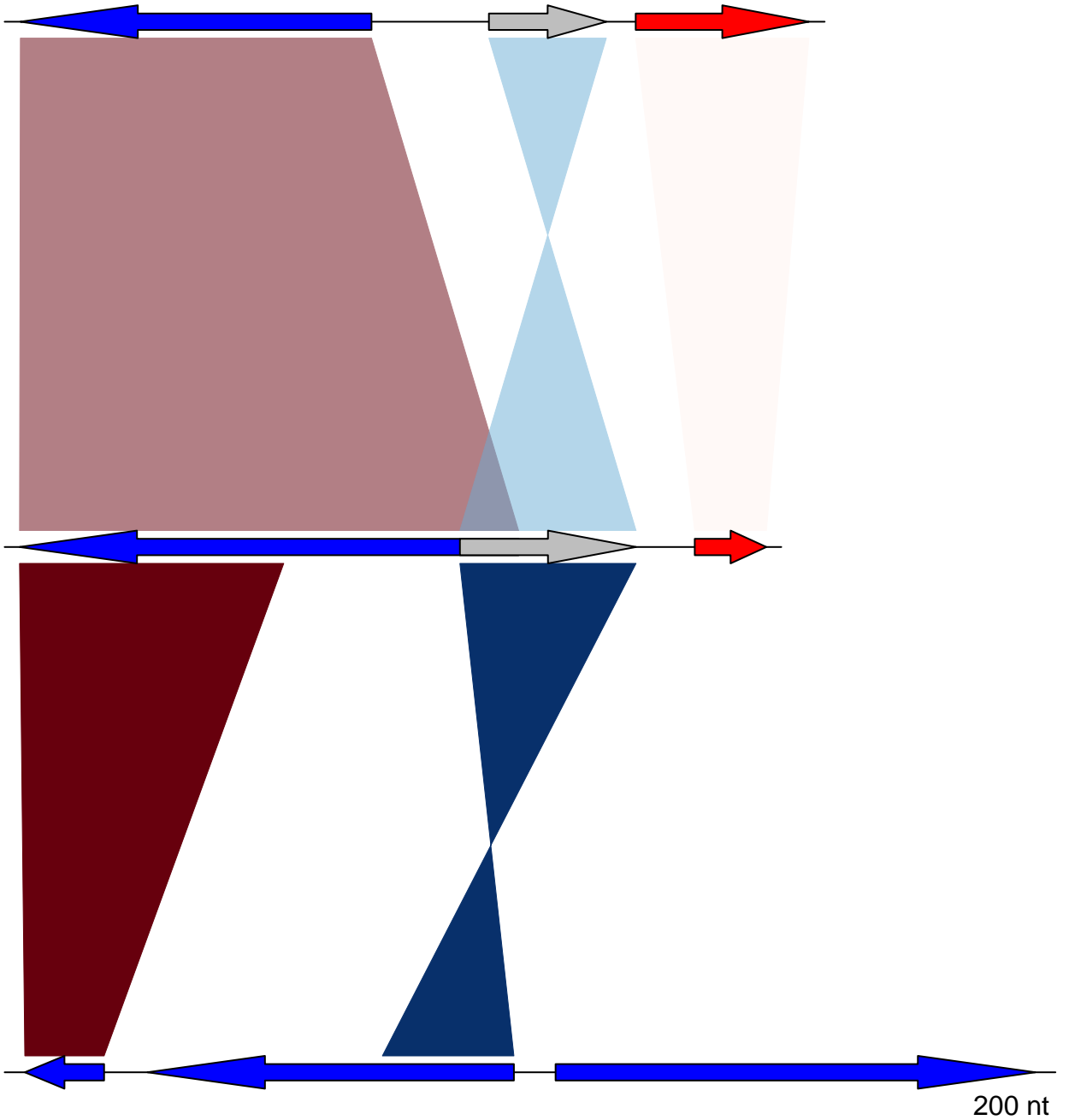
20 kb



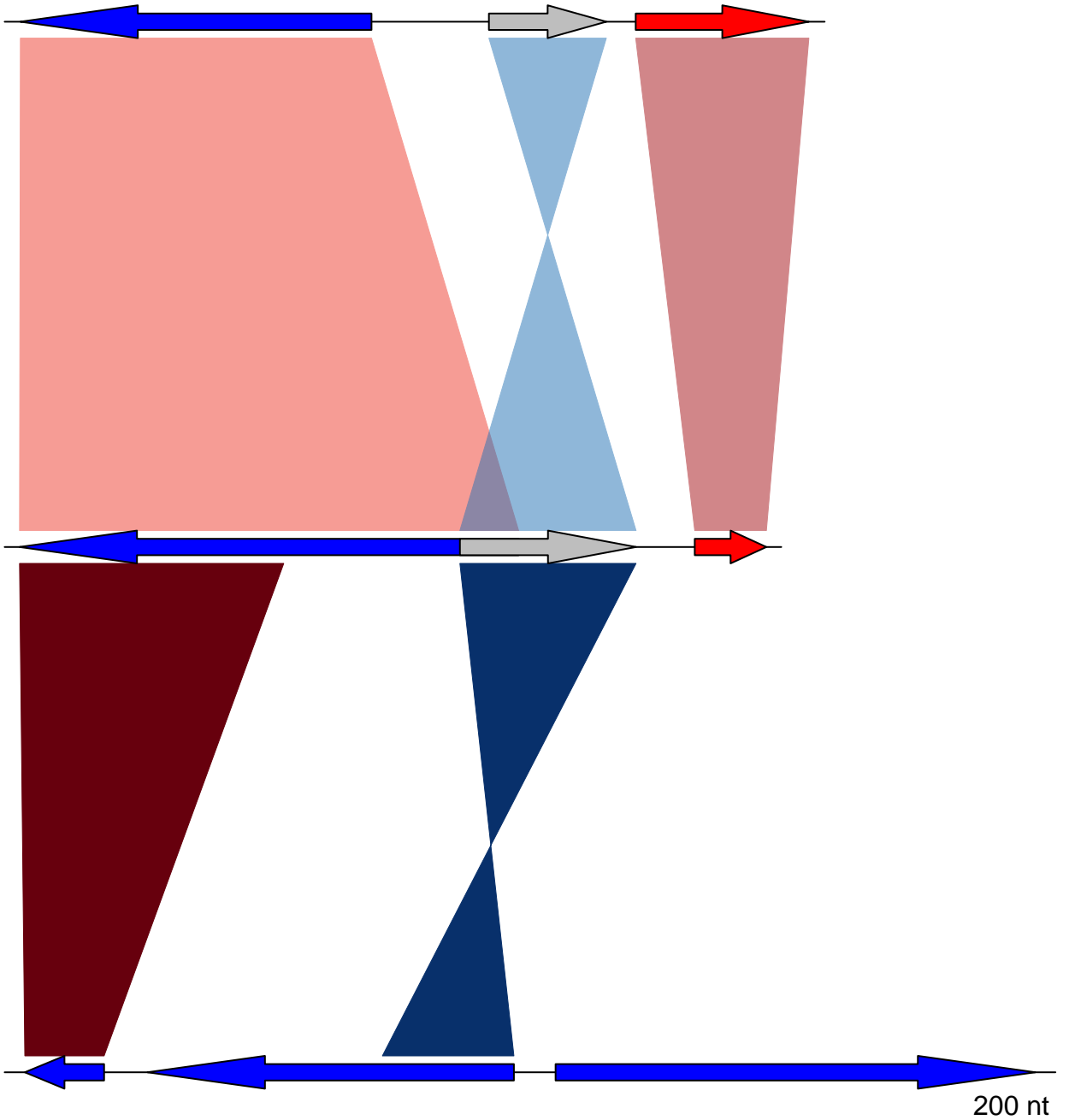
help("apply\_color\_scheme")



help("apply\_color\_scheme")

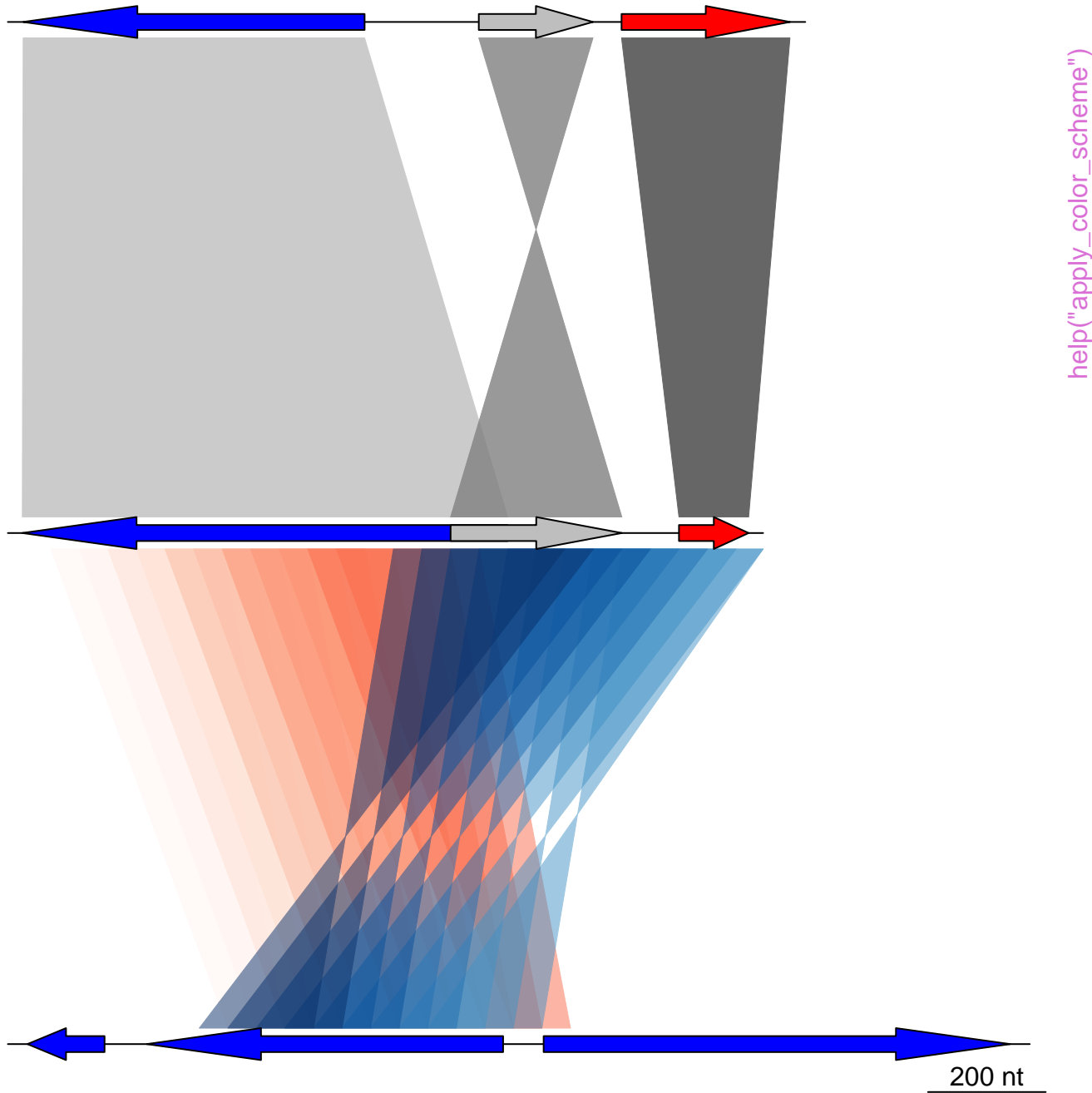


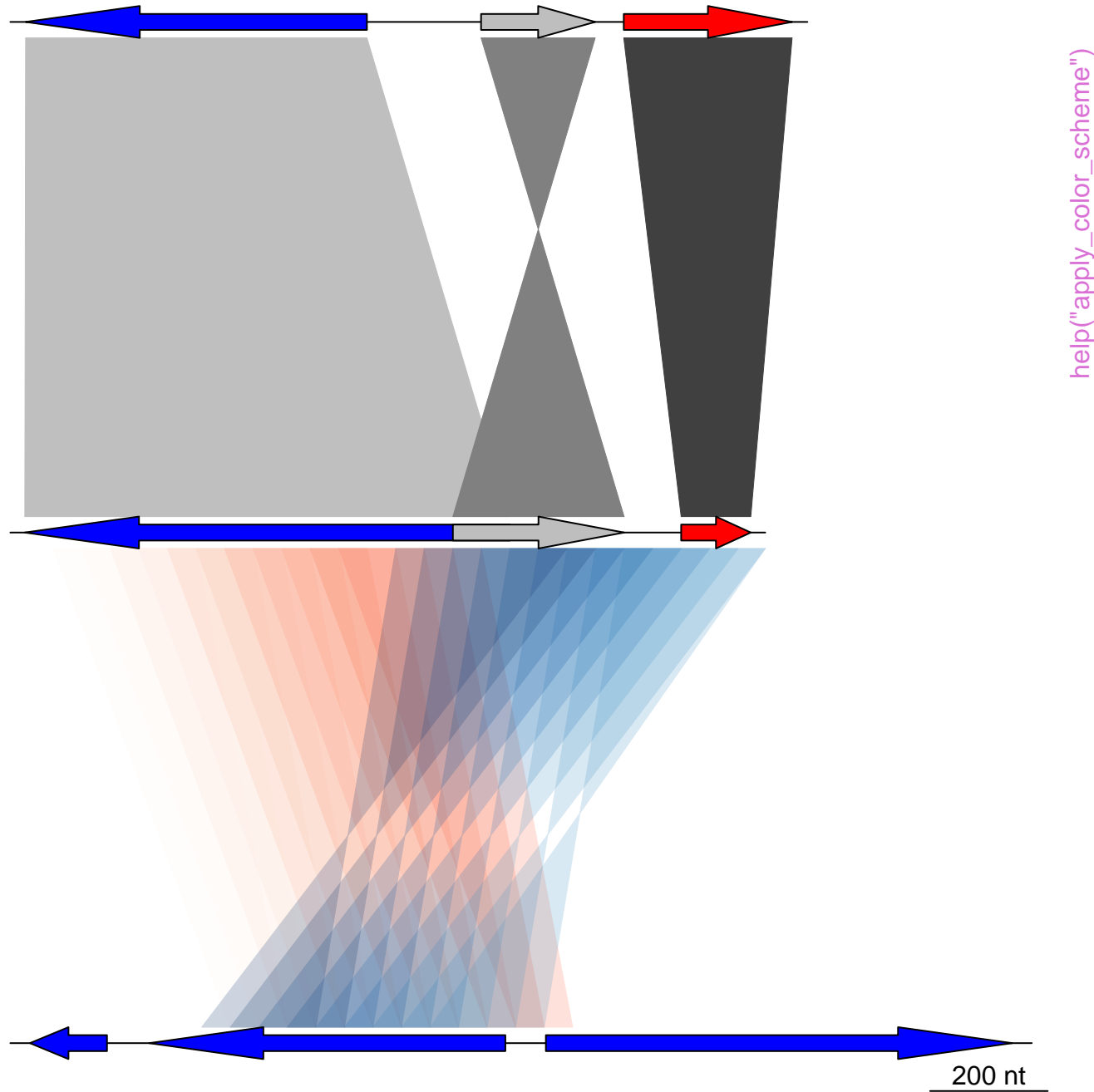
help("apply\_color\_scheme")

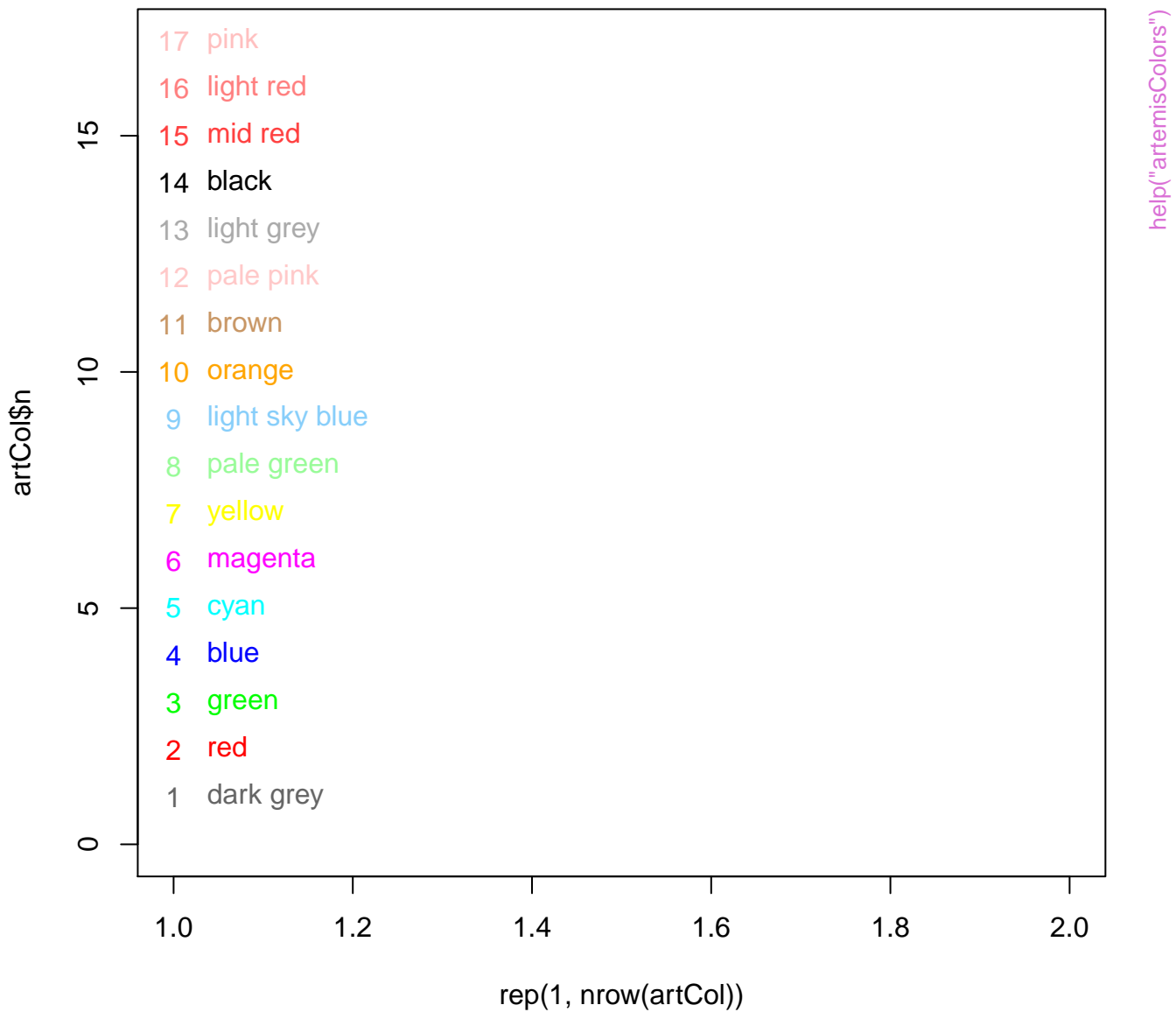


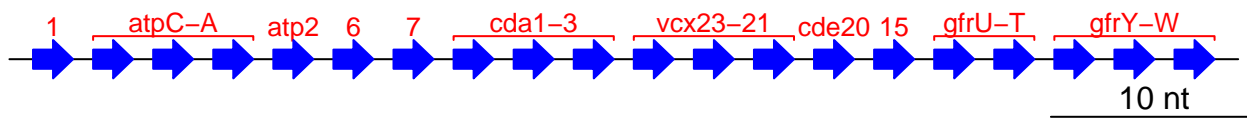
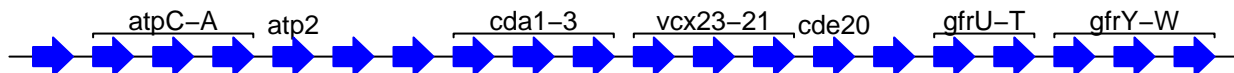
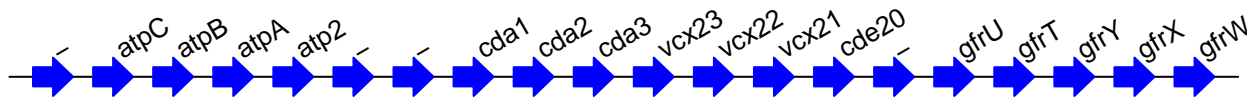
help("apply\_color\_scheme")











help("auto\_annotate")

BB

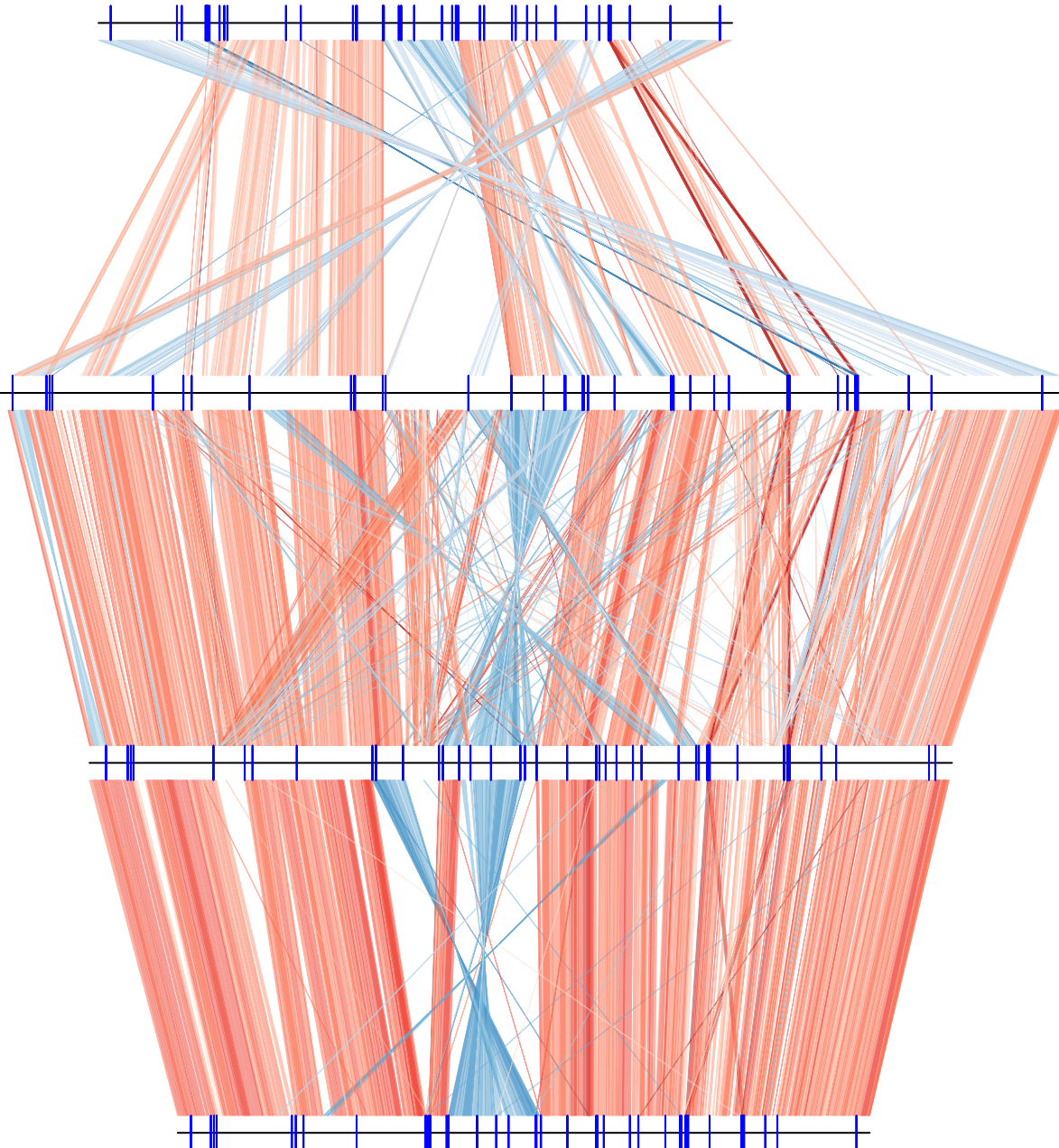
BG

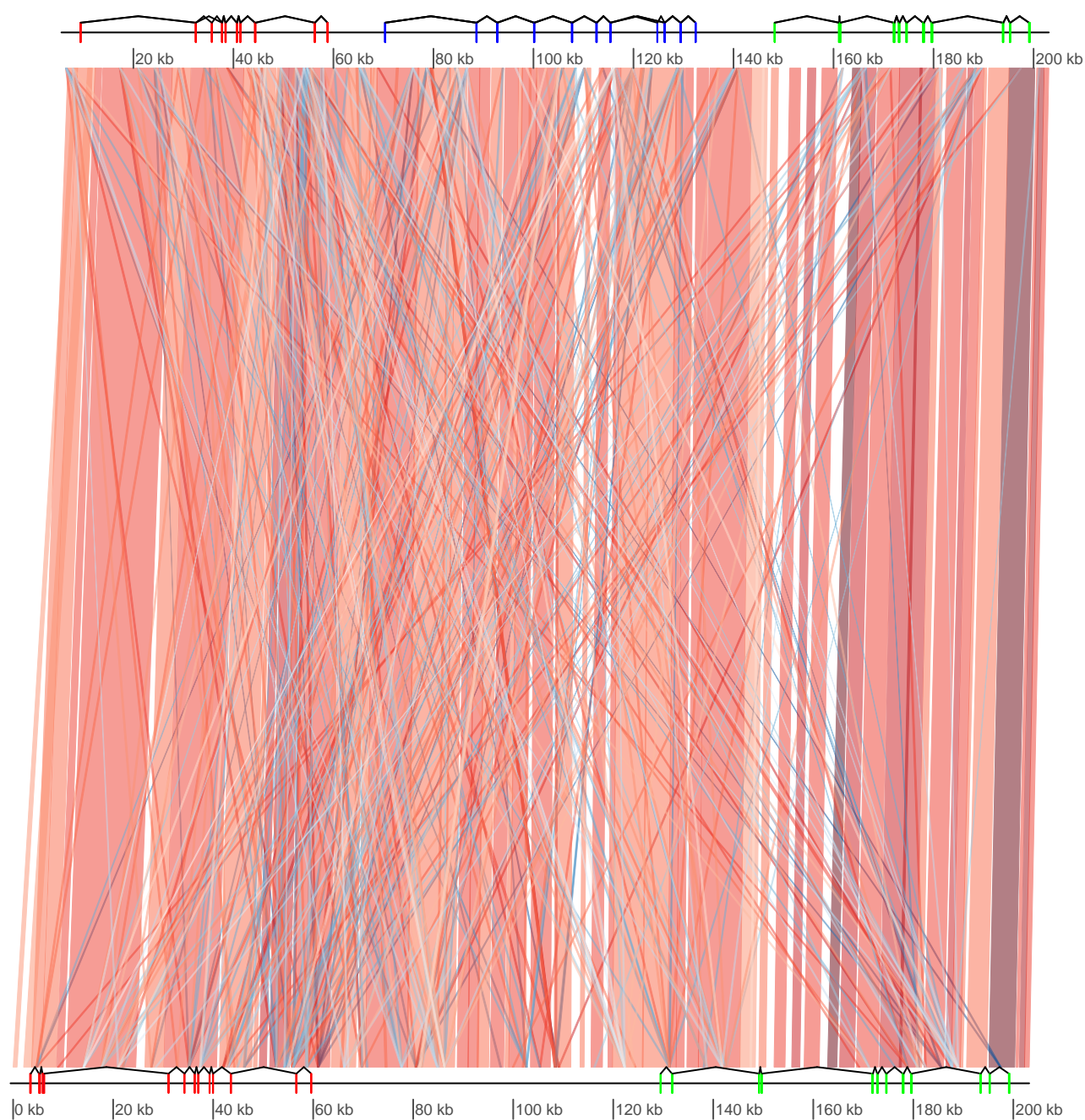
BH

BQ

help("barto")

500 kb



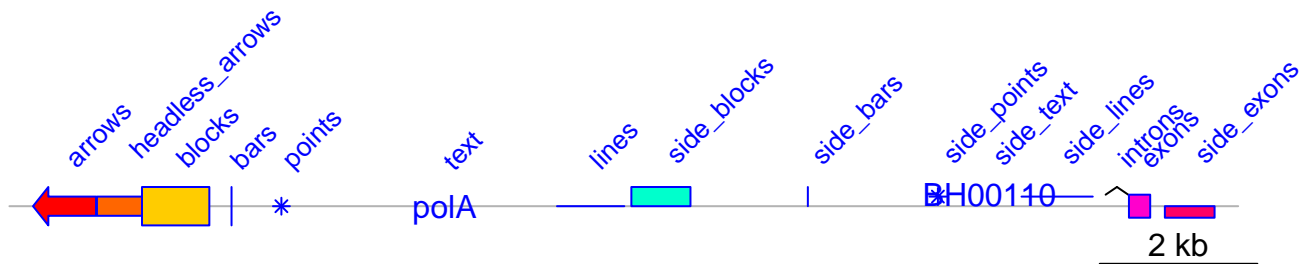
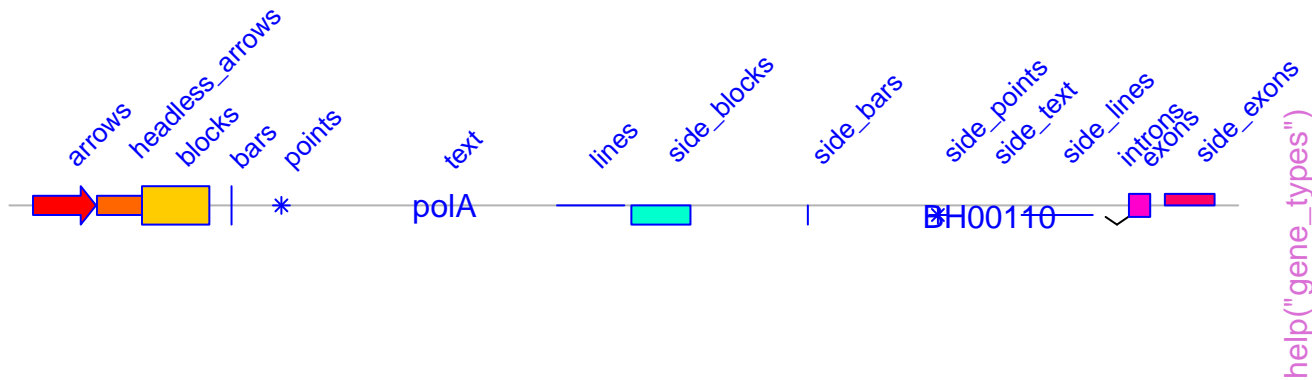


help("chrY\_subseg")

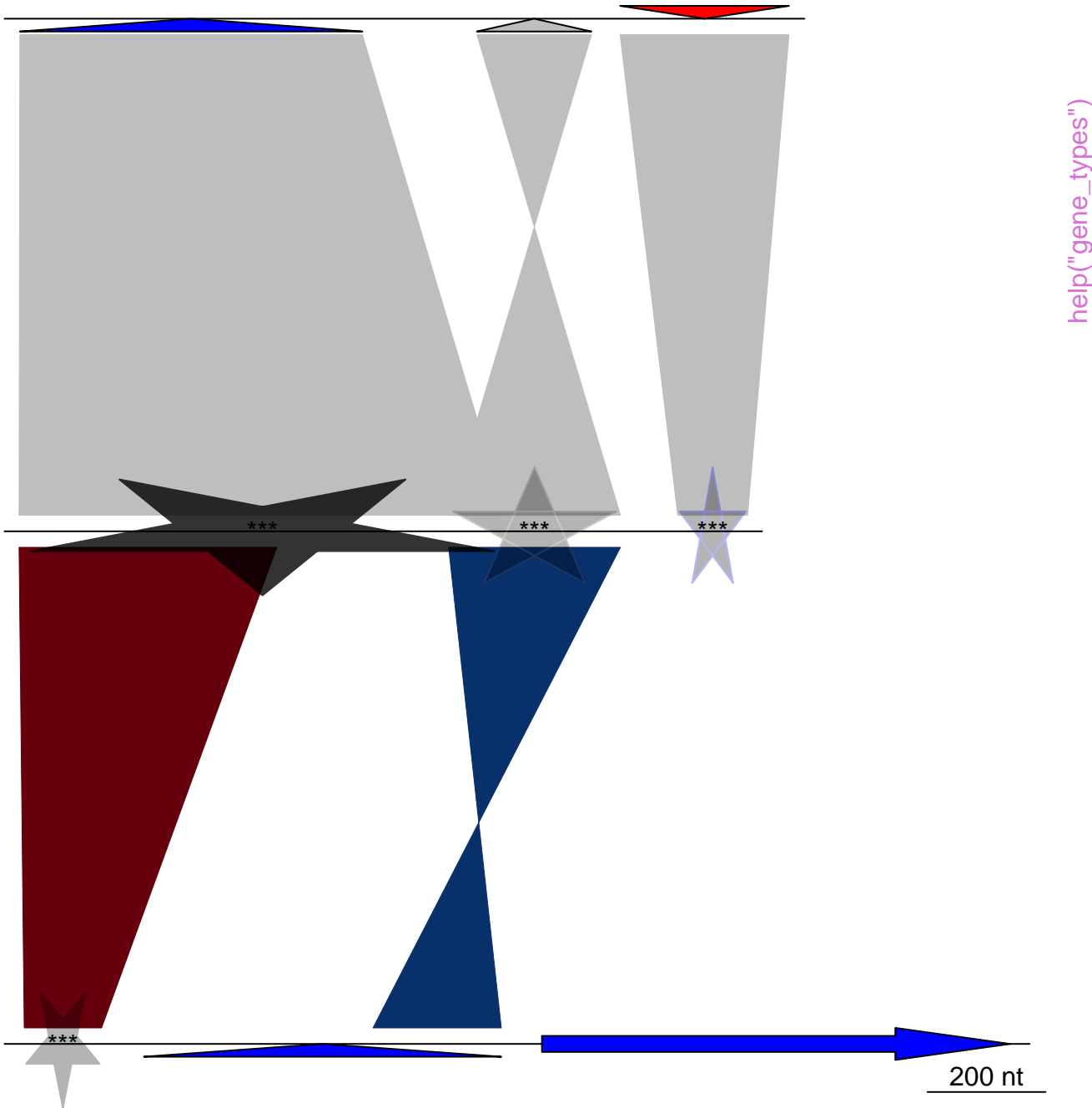


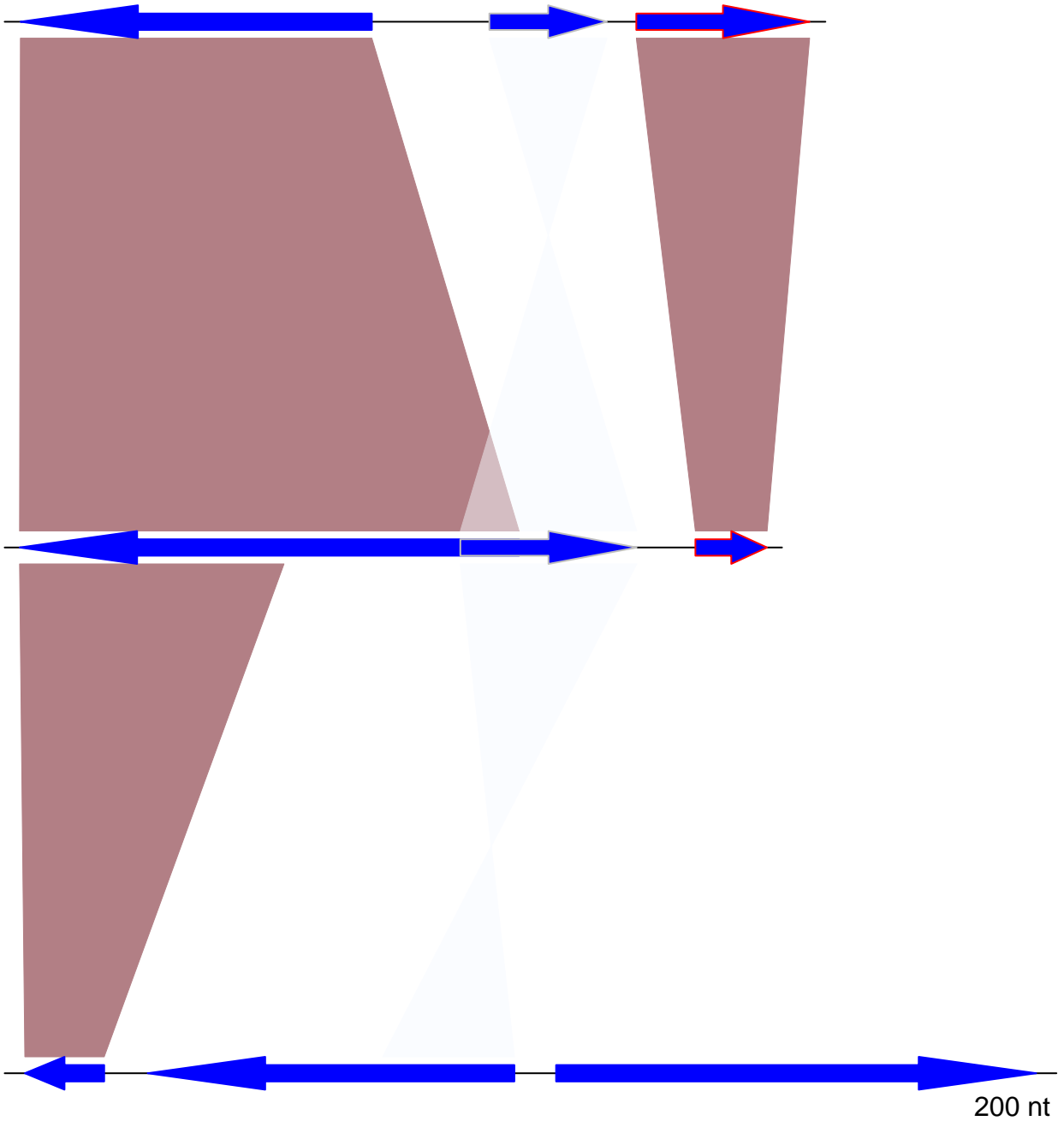
2 kb

help("gene\_types")









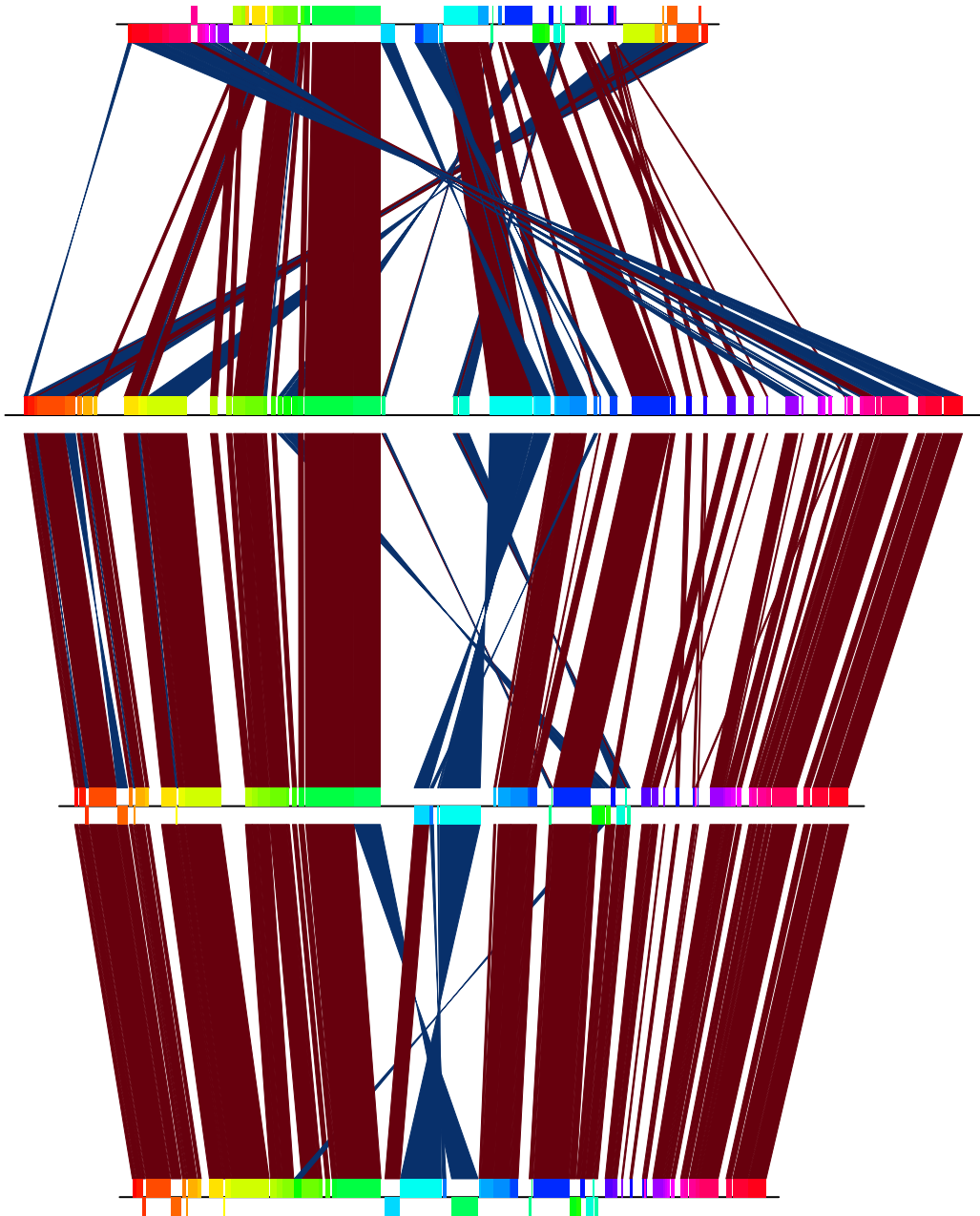
help("genoPlotR-package")

B\_bacilliformis

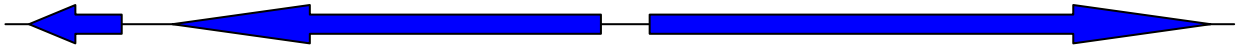
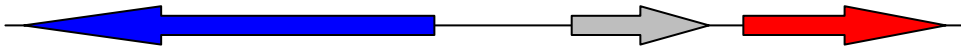
B\_grahamii

B\_henselae

B\_quintana

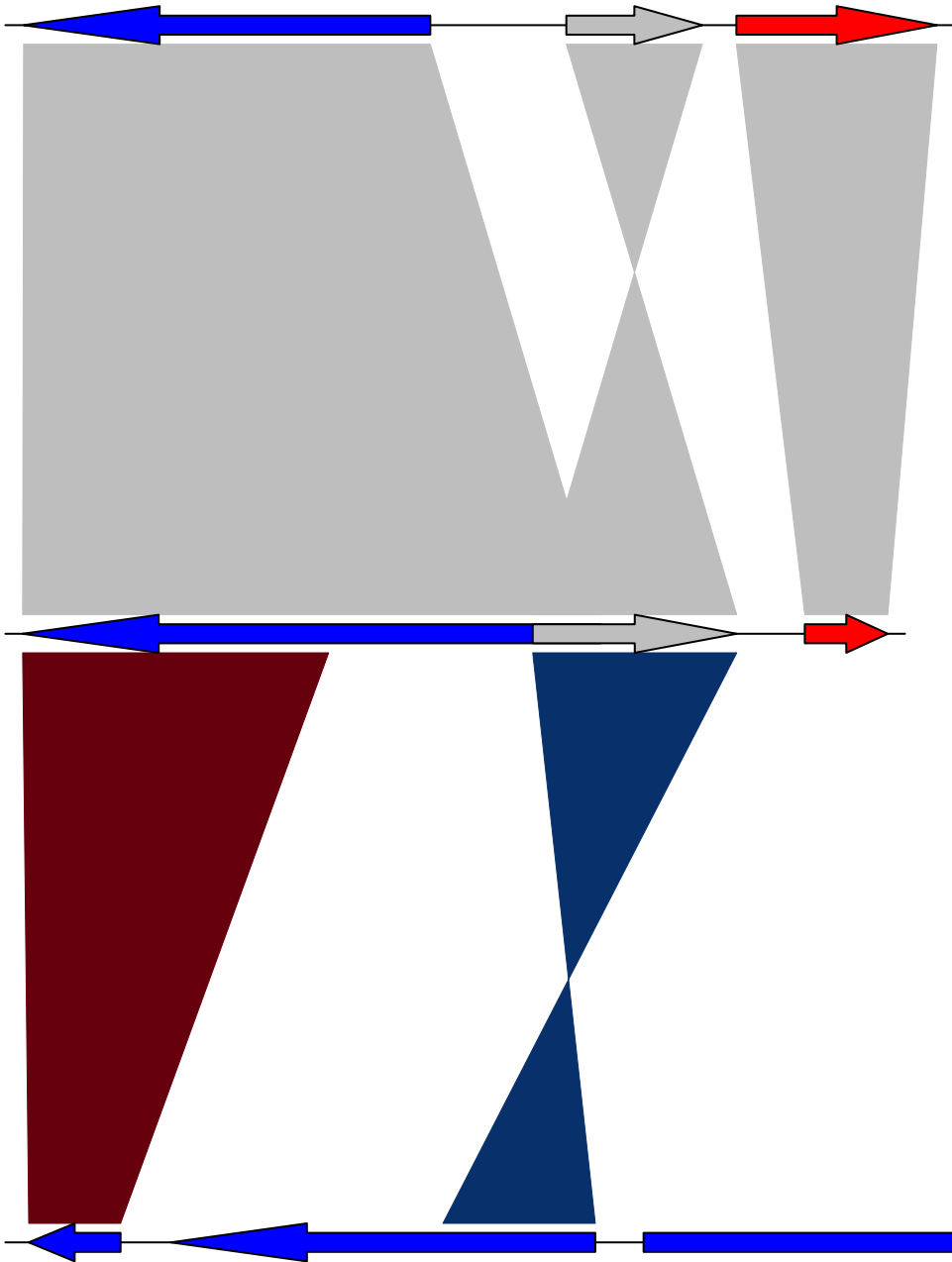


help("mauve.bbone")



200 nt

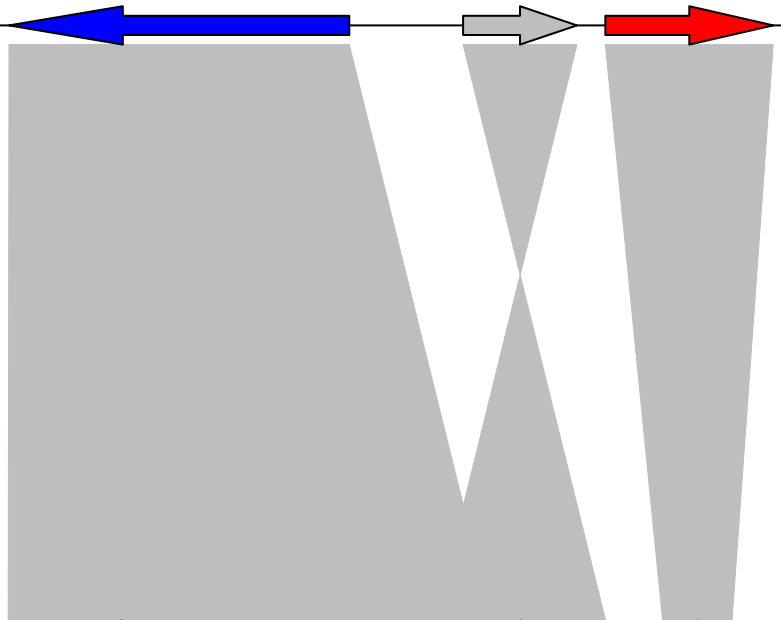
help("plot\_gene\_map")



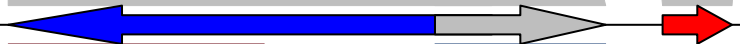
help("plot\_gene\_map")

200 nt

A aaa



B bbb

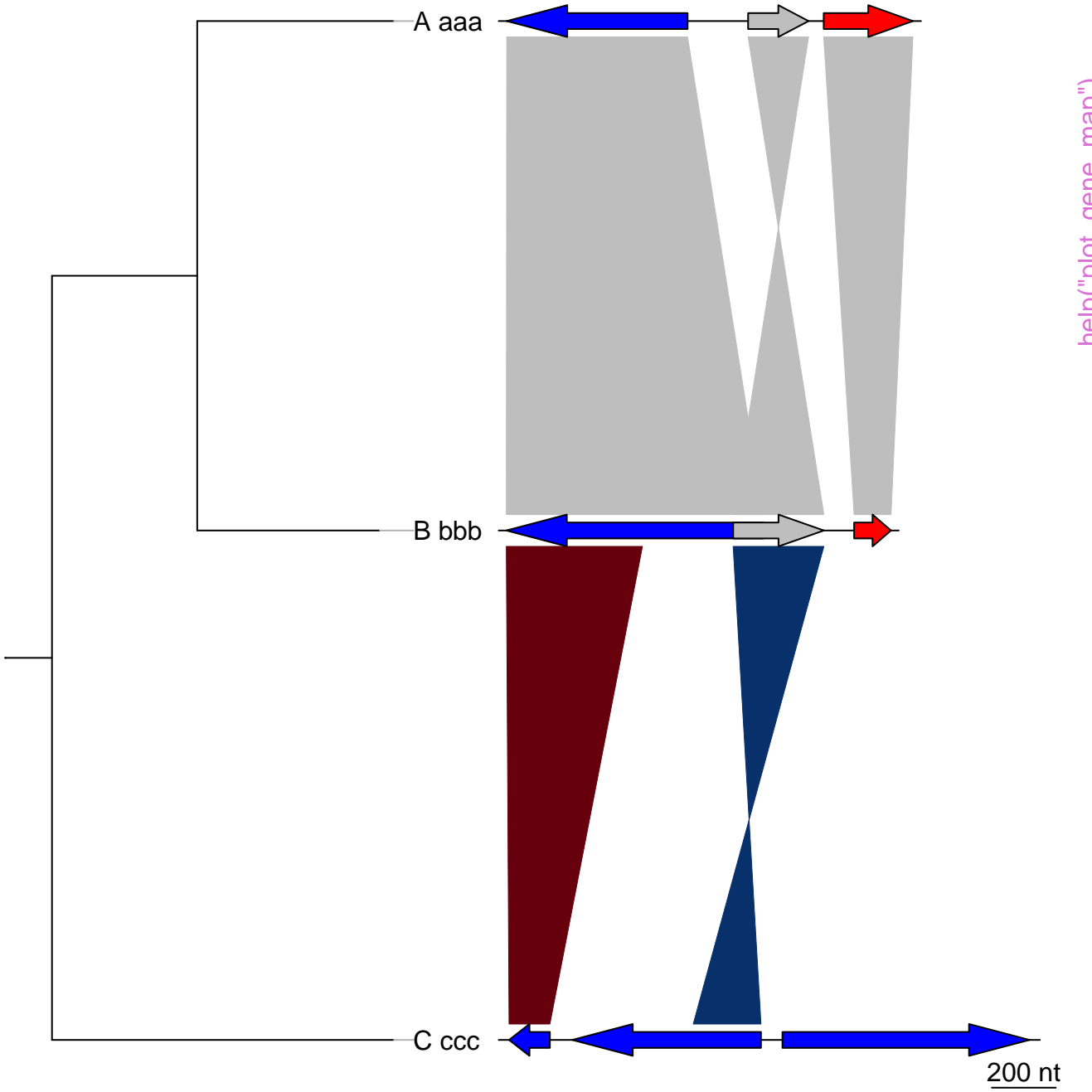


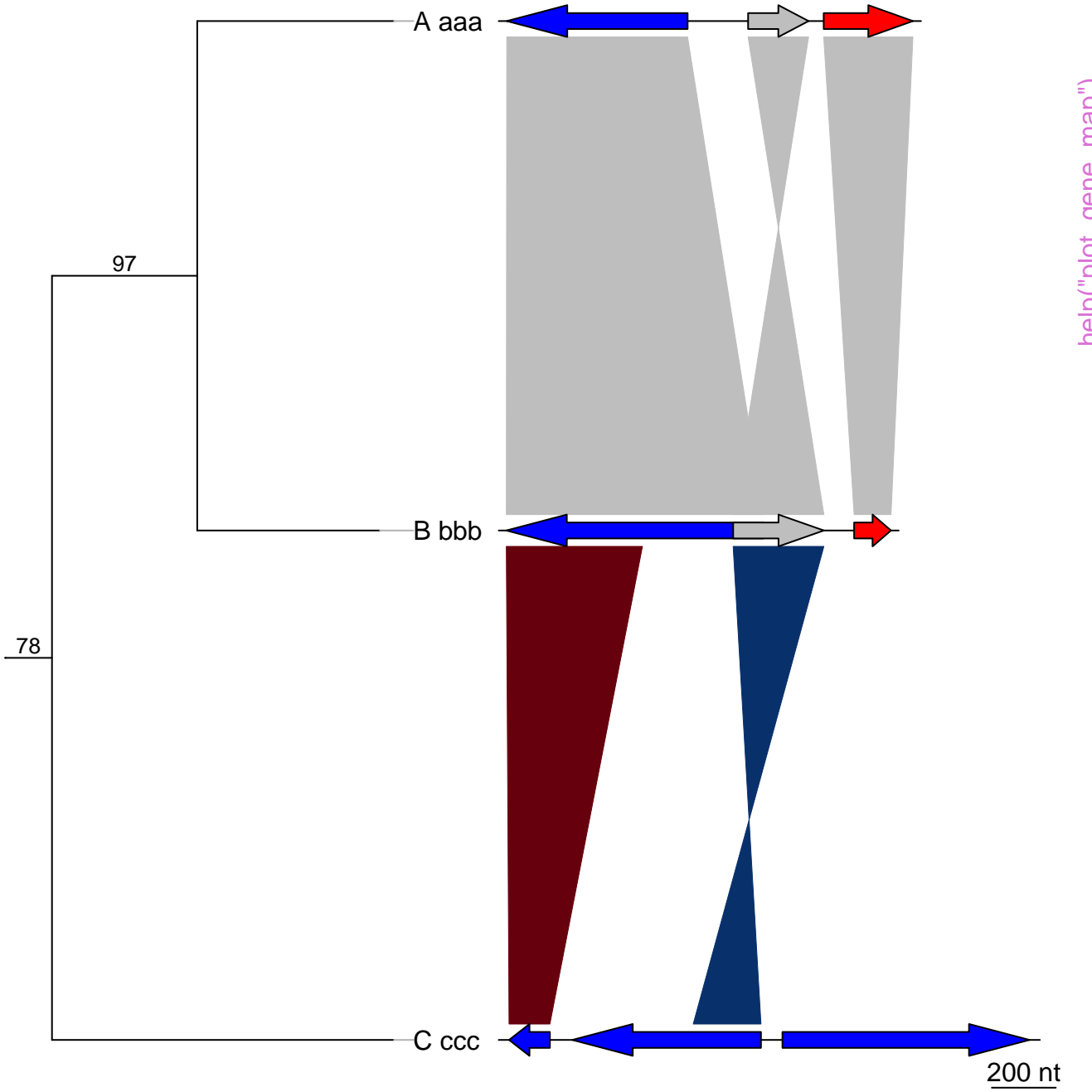
C ccc



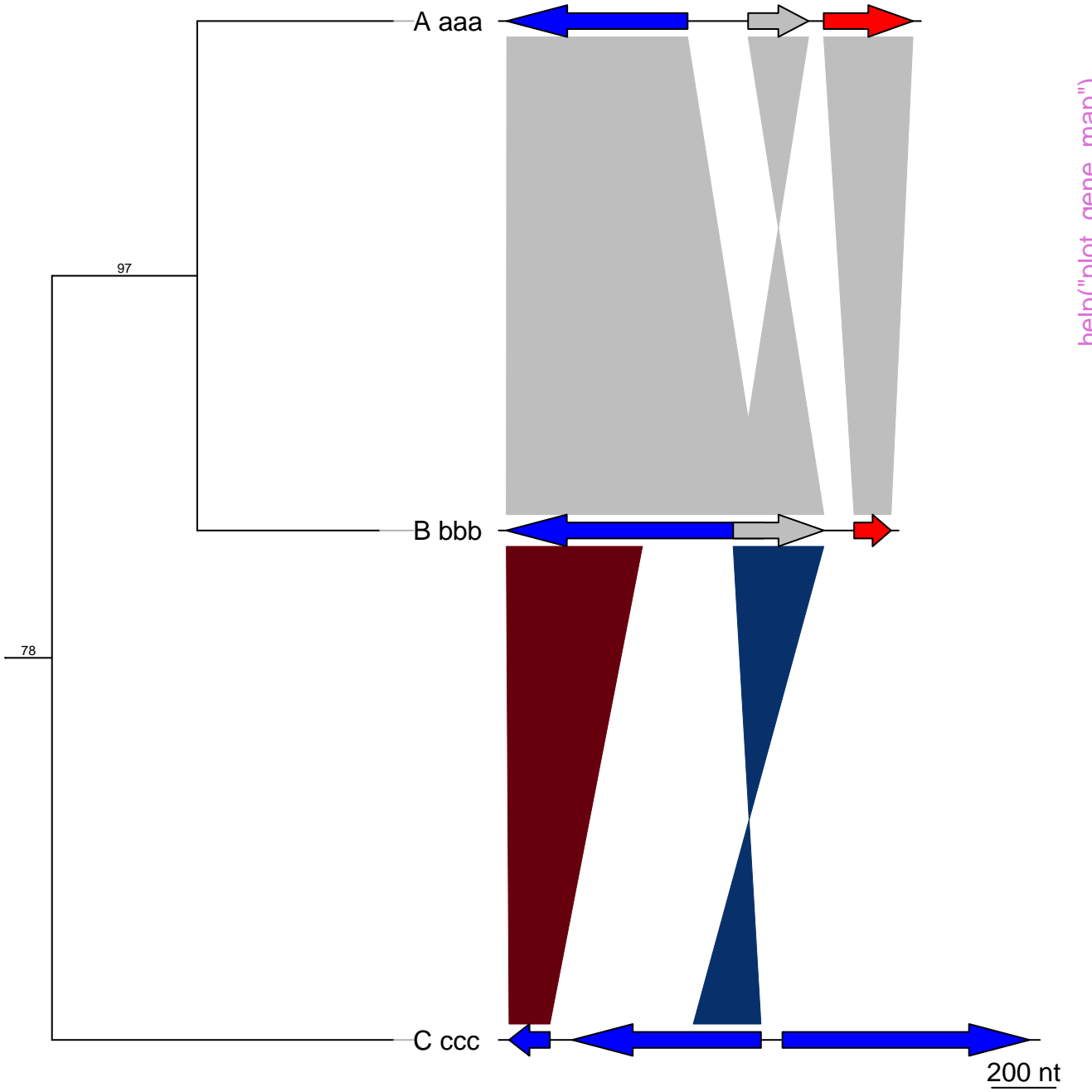
200 nt

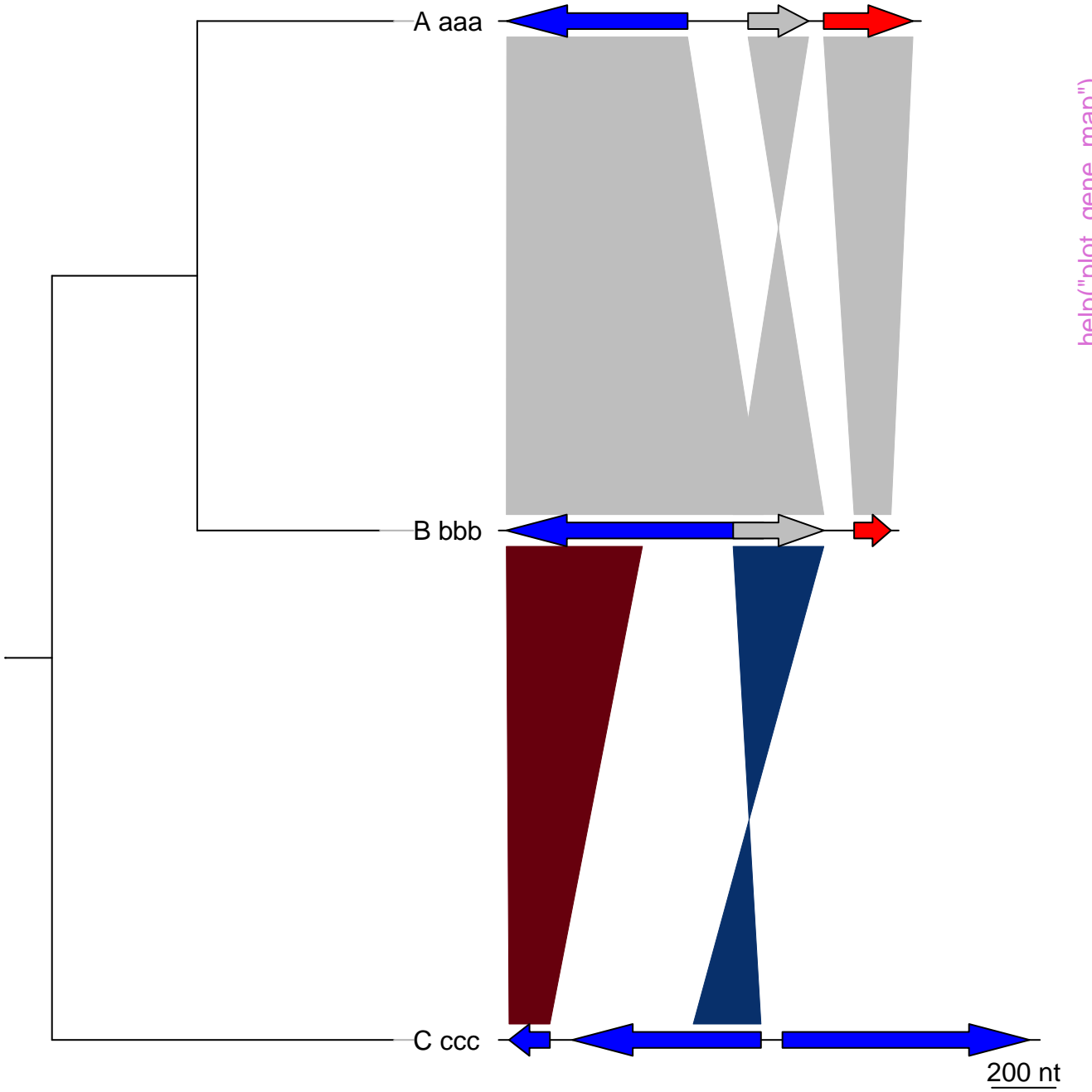
help("plot\_gene\_map")

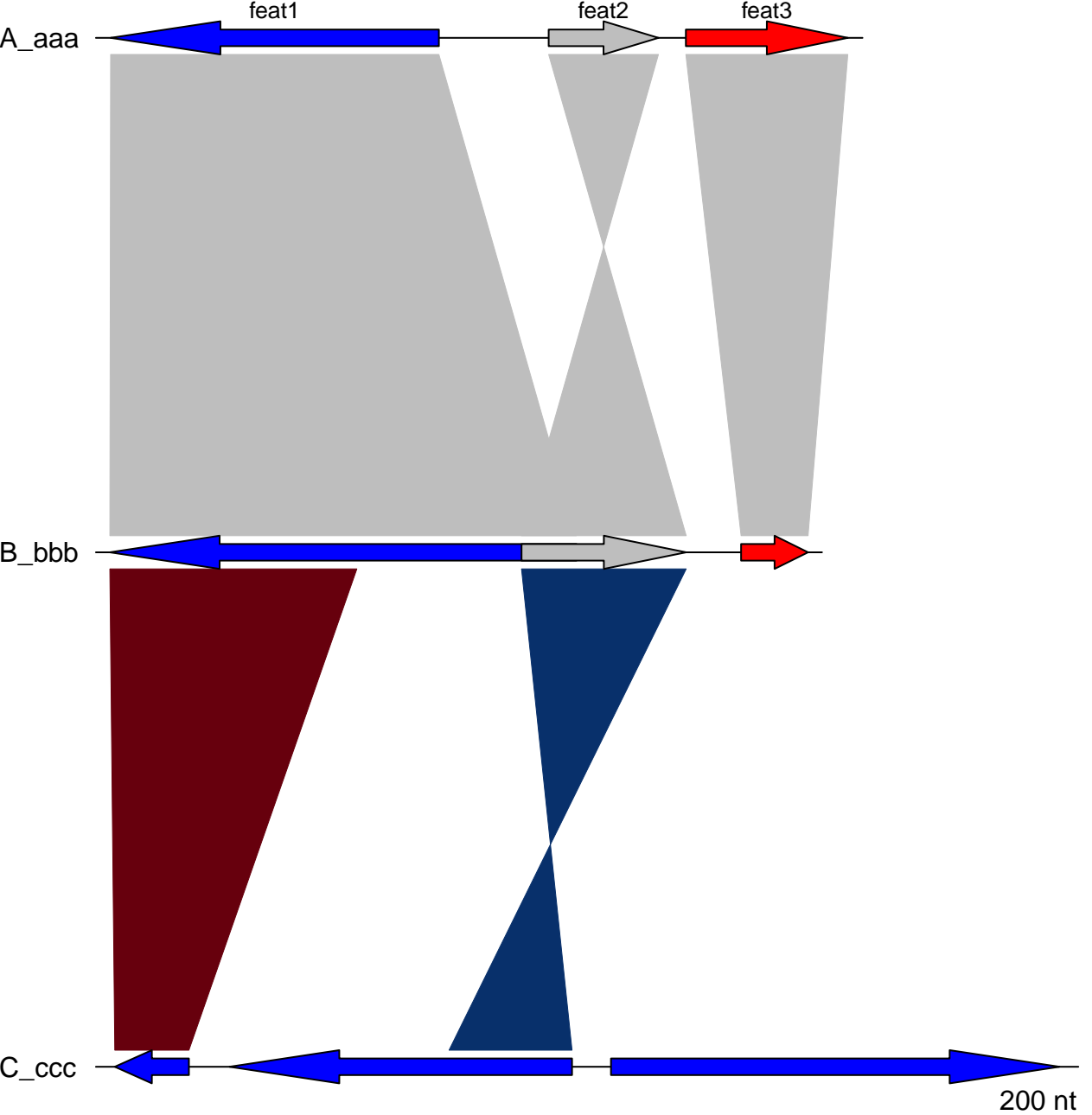




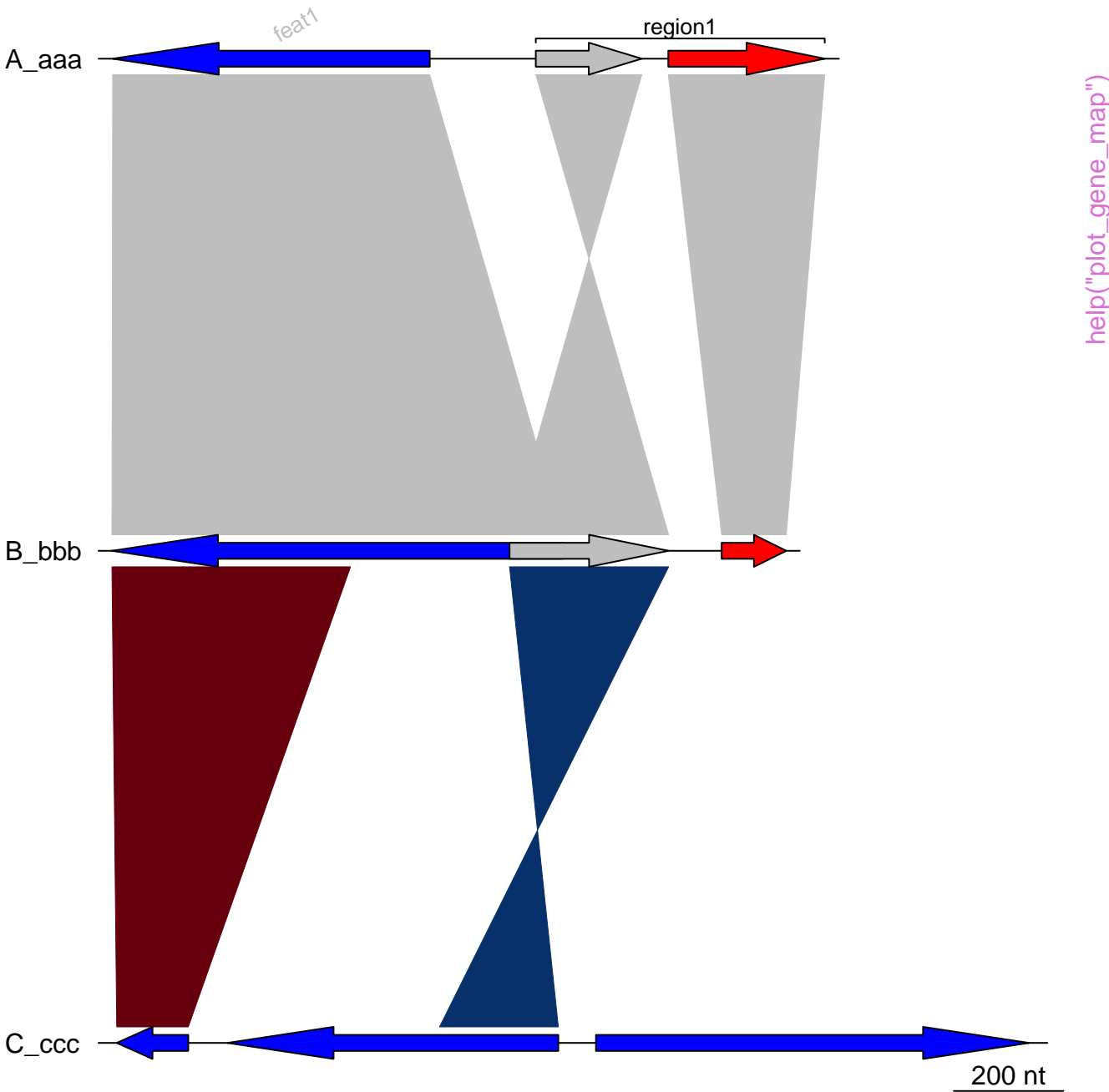


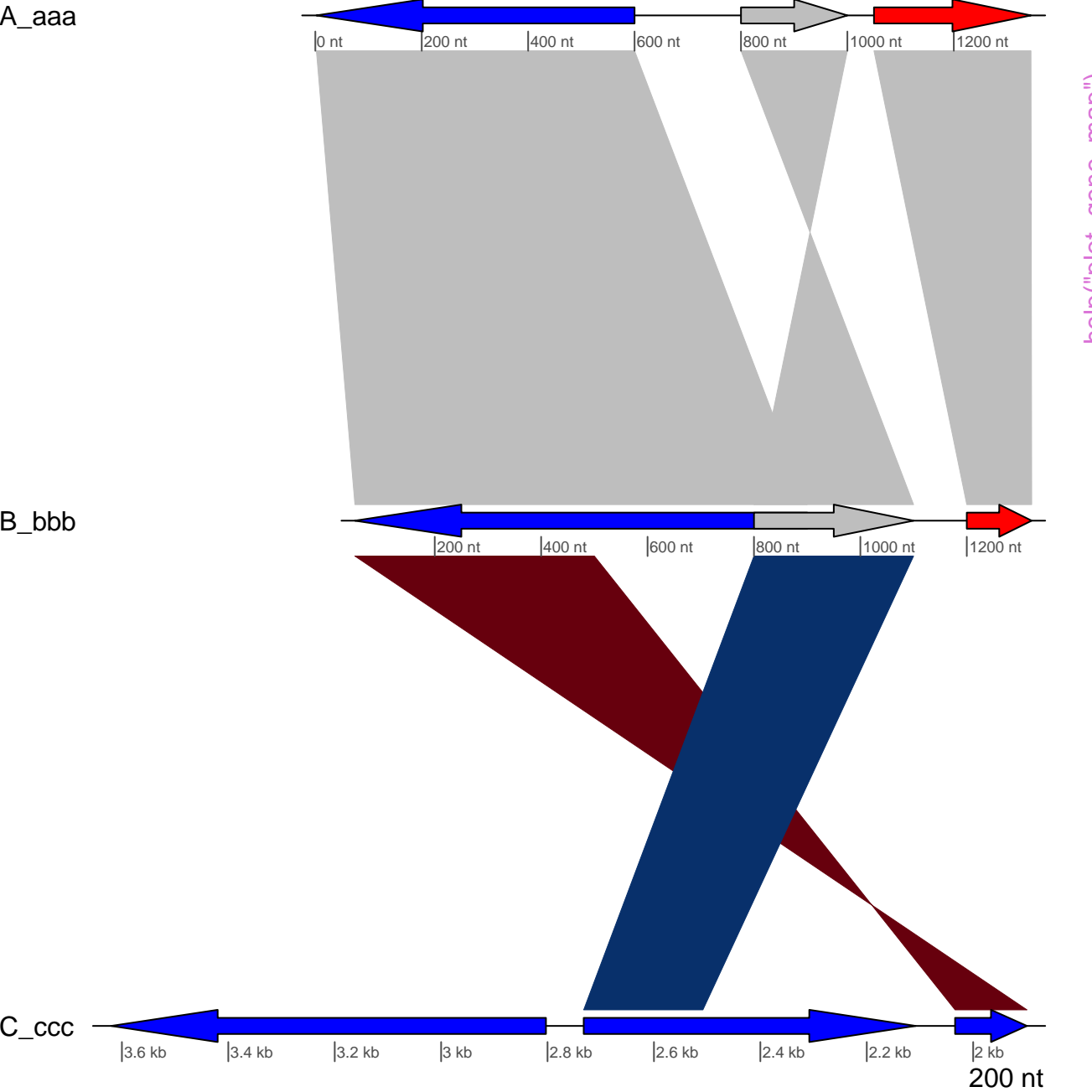


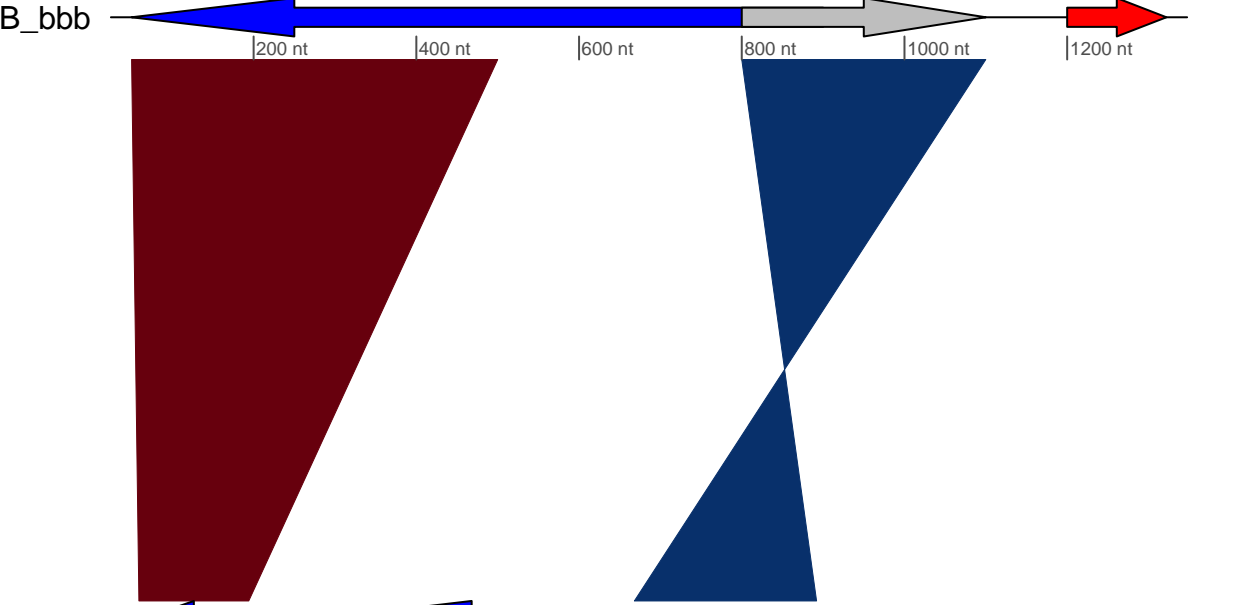
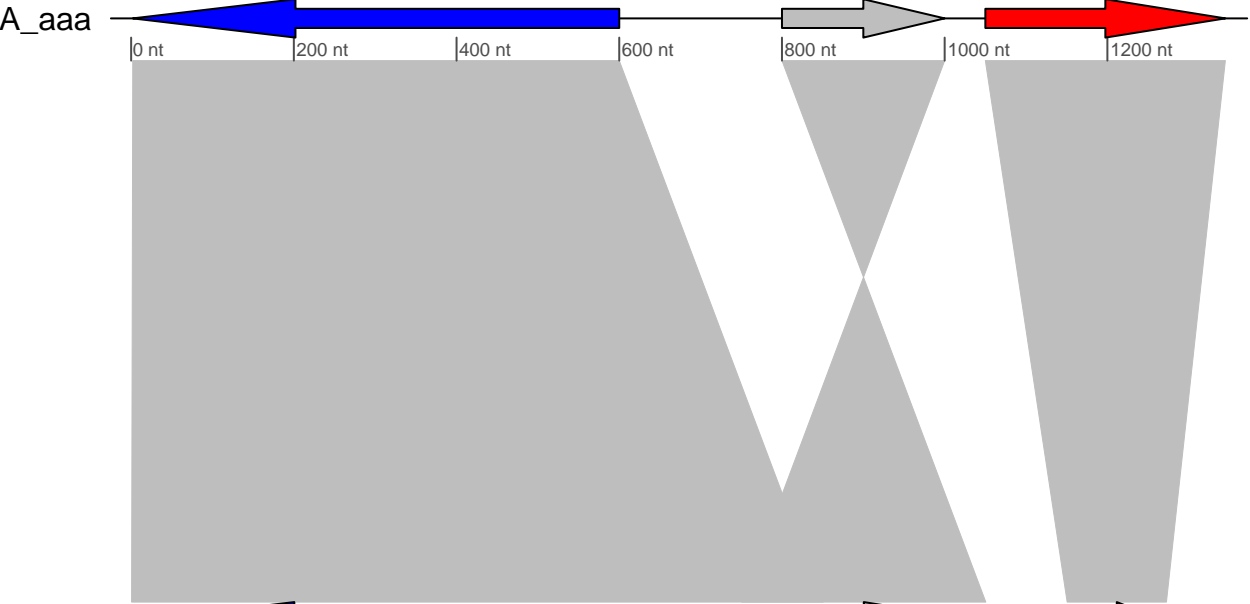




help("plot\_gene\_map")



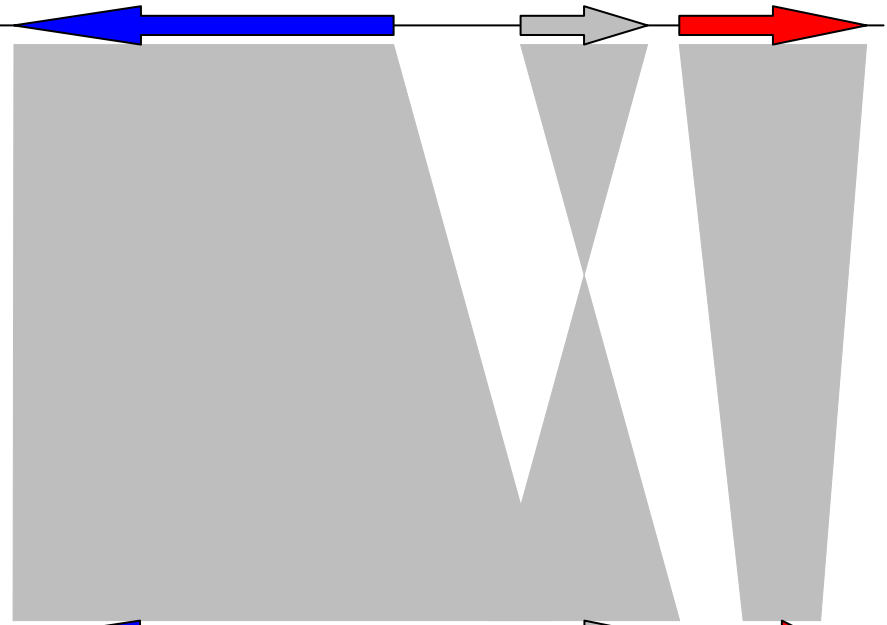




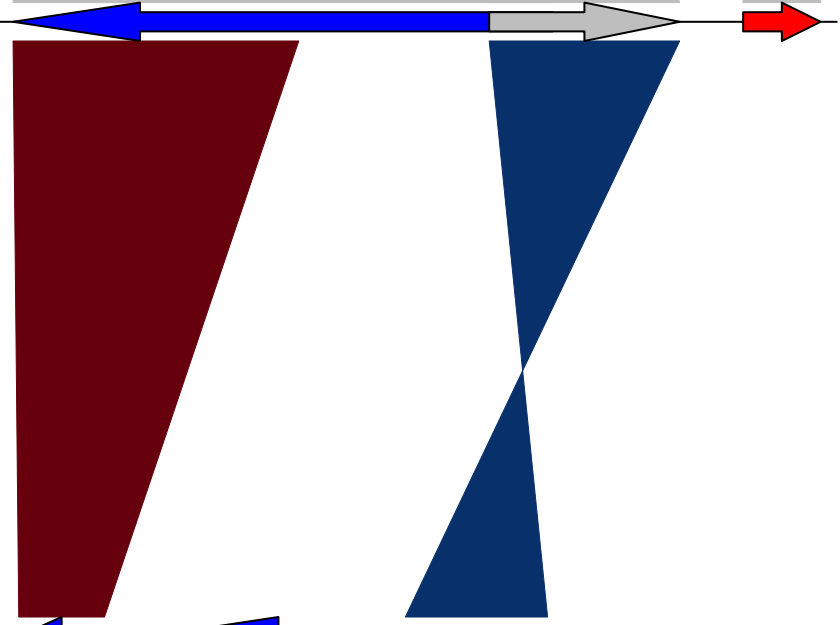
200 nt

help("plot\_gene\_map")

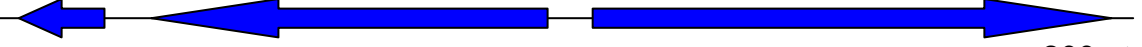
A\_aaa



B\_bbb



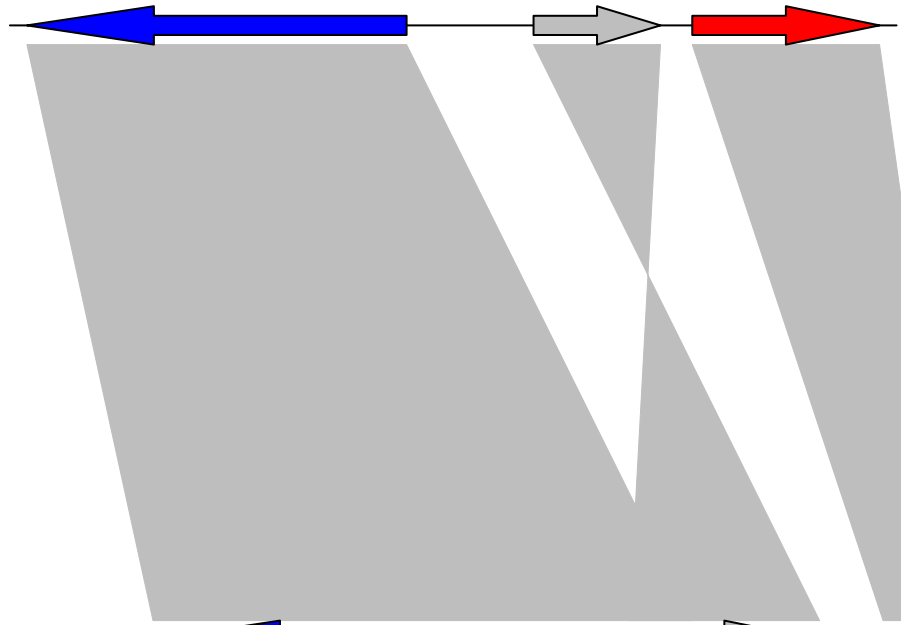
C\_ccc



200 nt

help("plot\_gene\_map")

A\_aaa



B\_bbb



C\_ccc

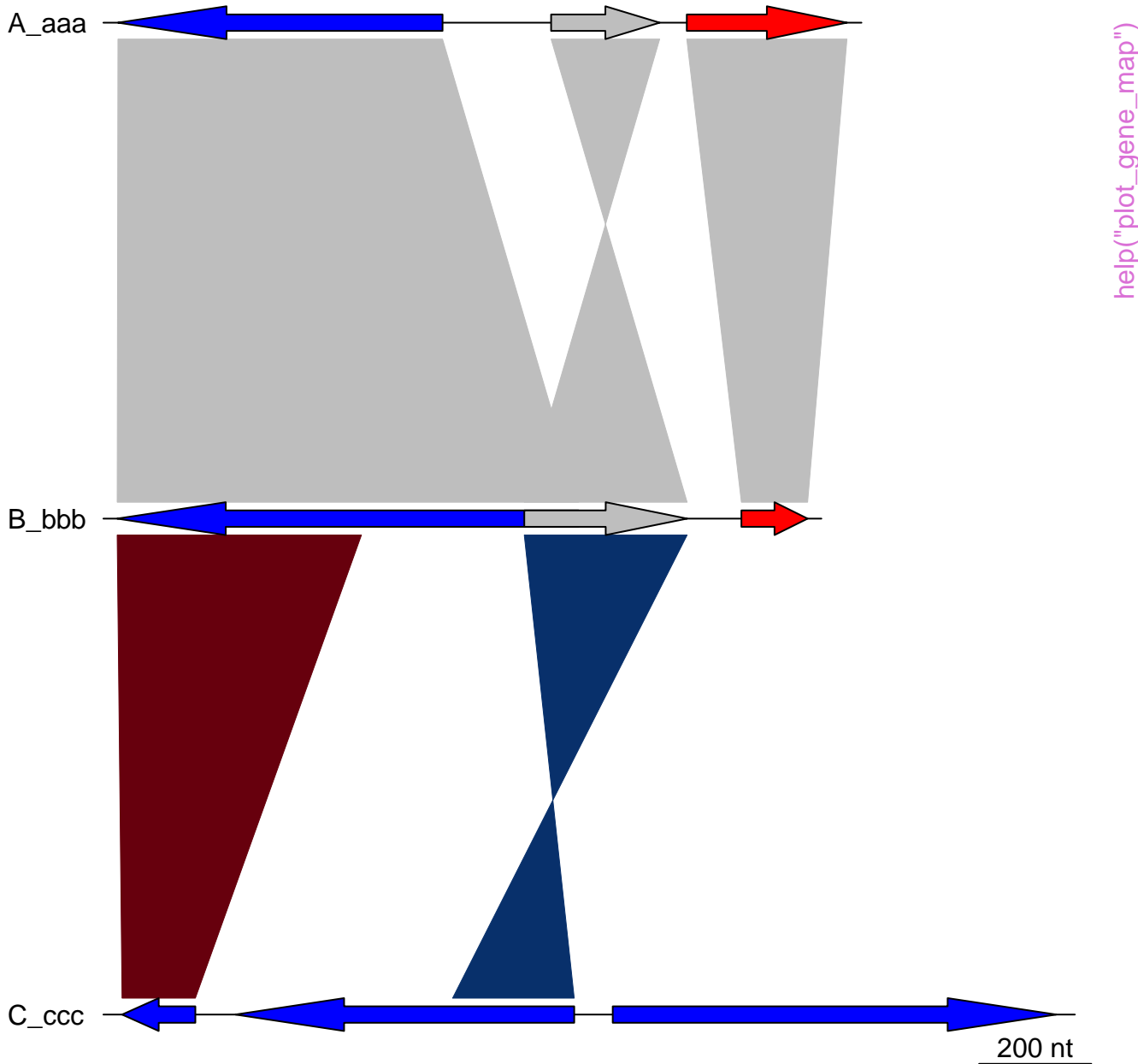


200 nt

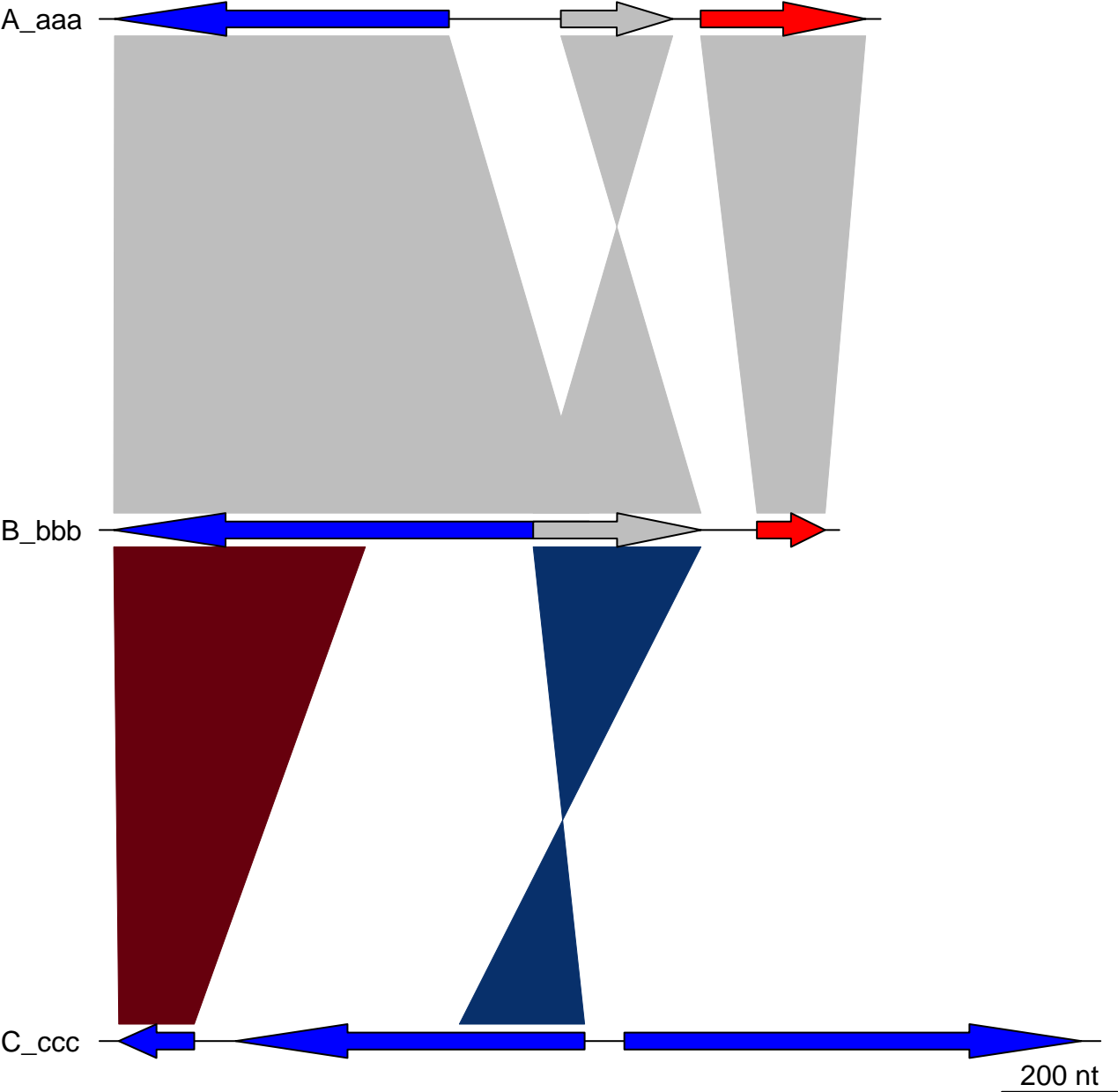
help("plot\_gene\_map")



# Comparison of A, B and C

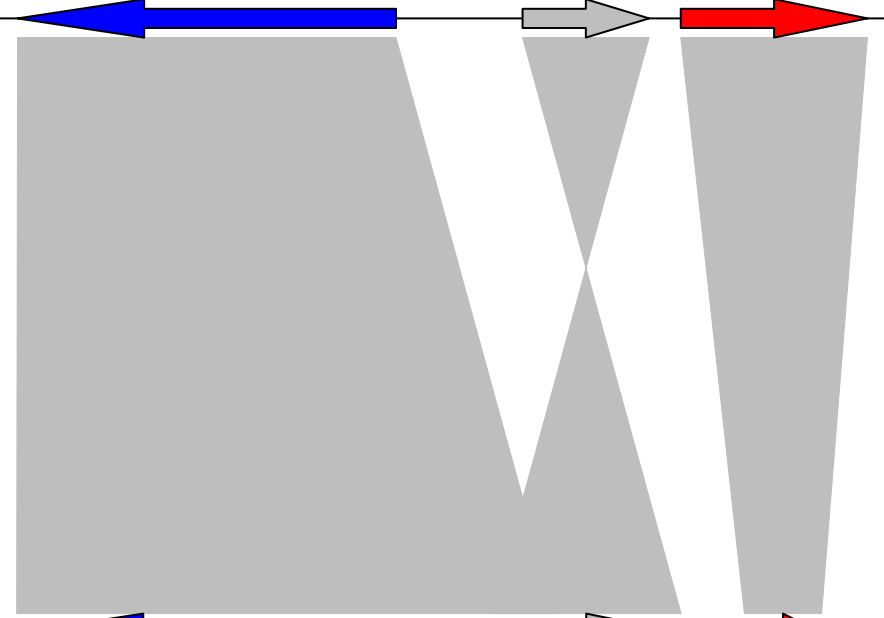


Comparison of A, B and C

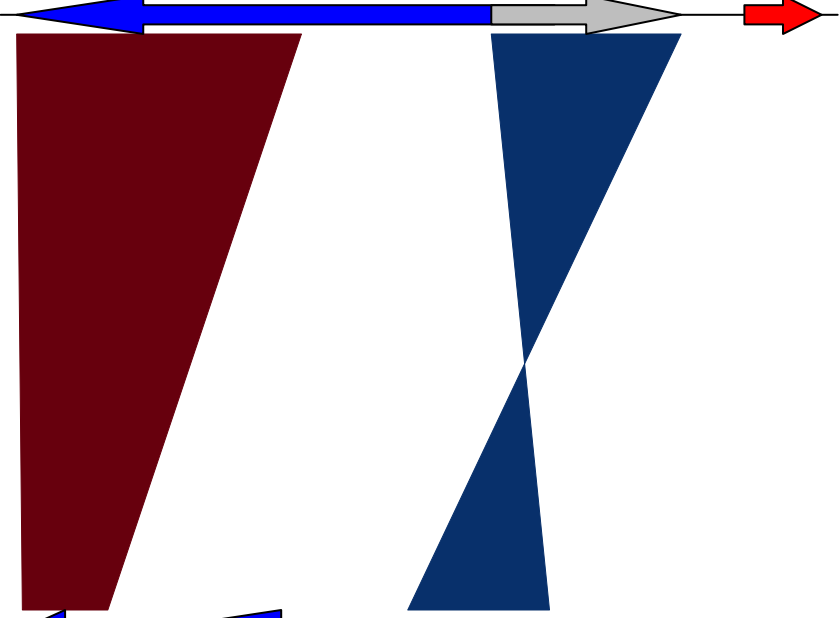


help("plot\_gene\_map")

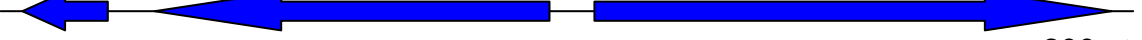
Huey



Dewey



Louie



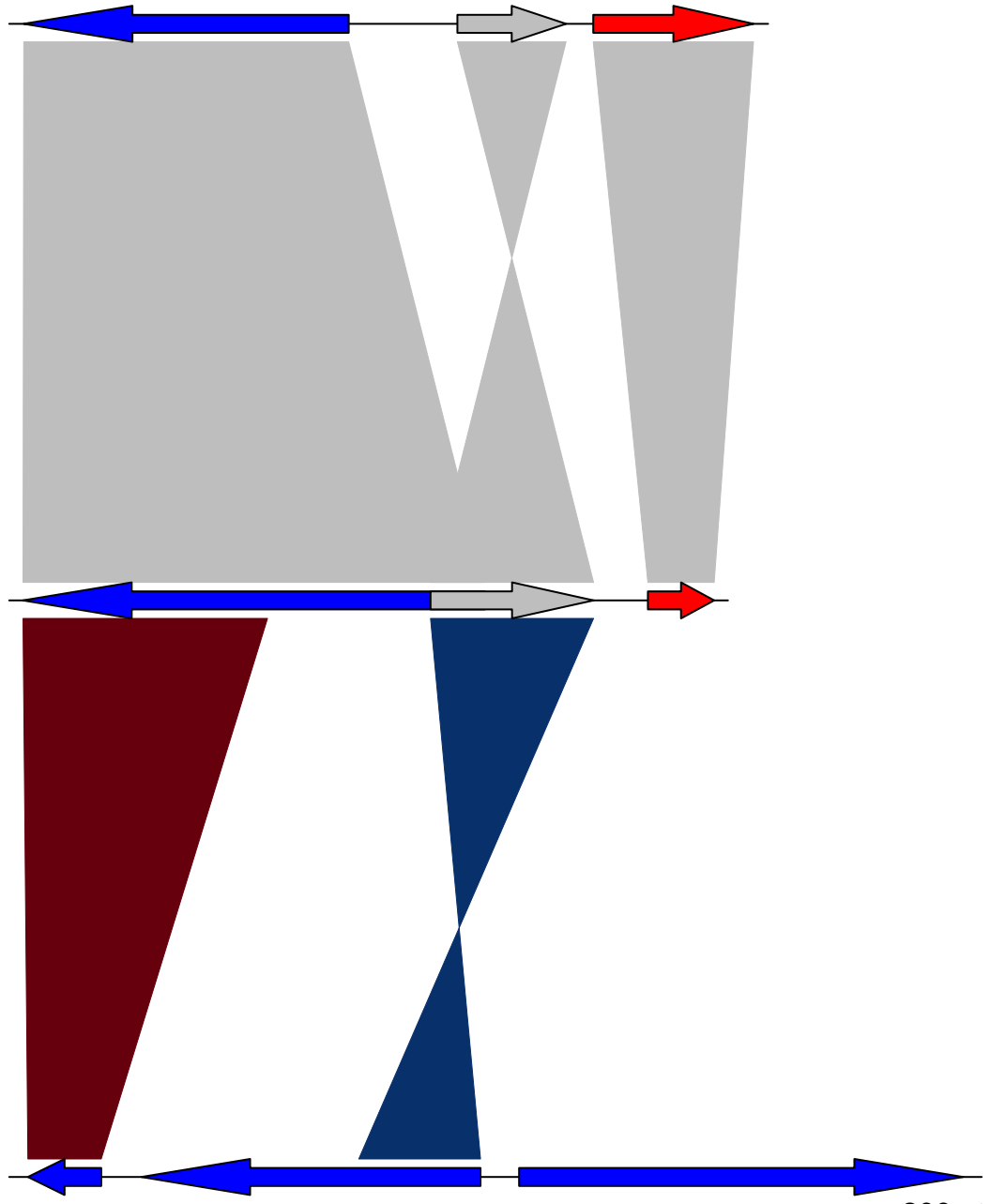
200 nt

help("plot\_gene\_map")

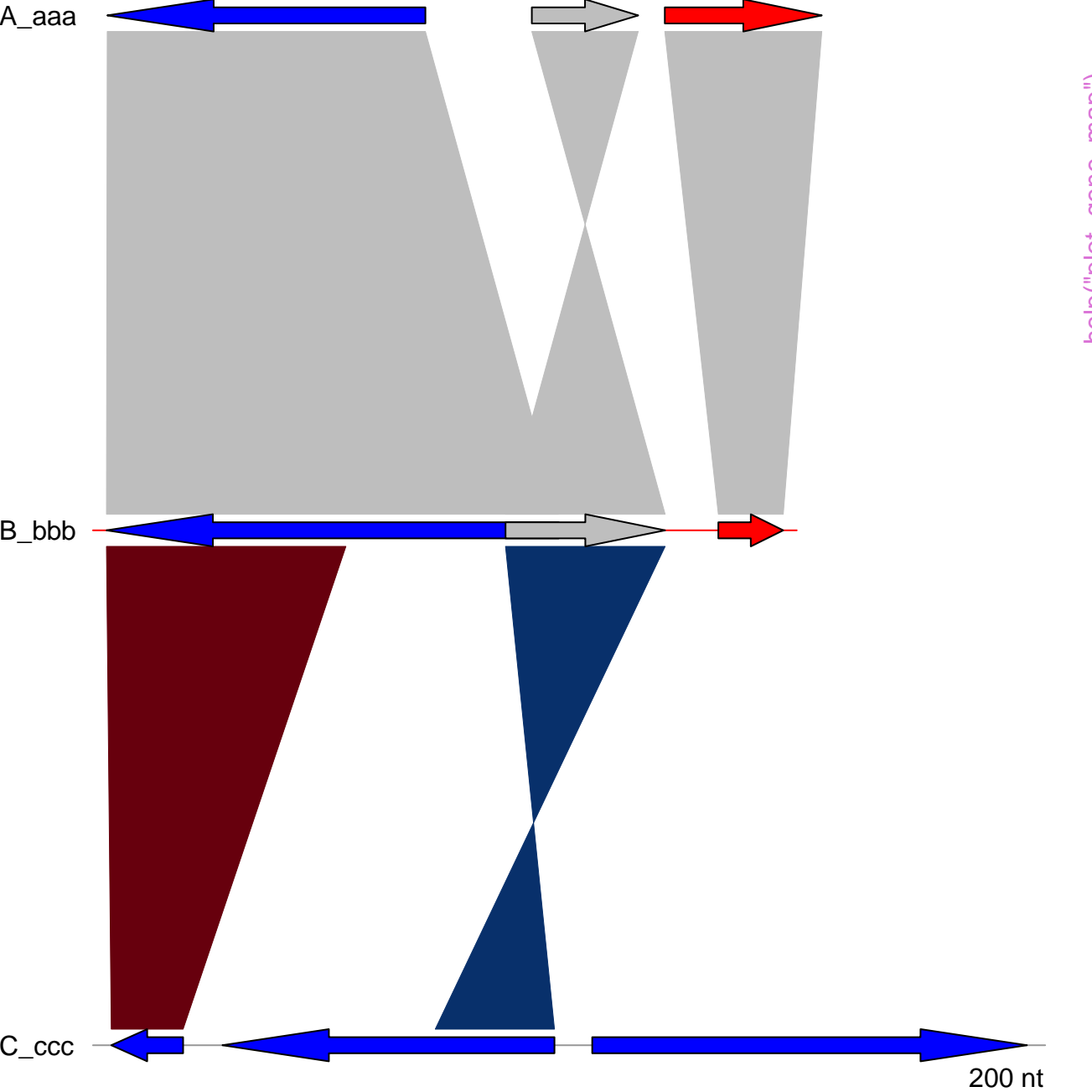
Huey

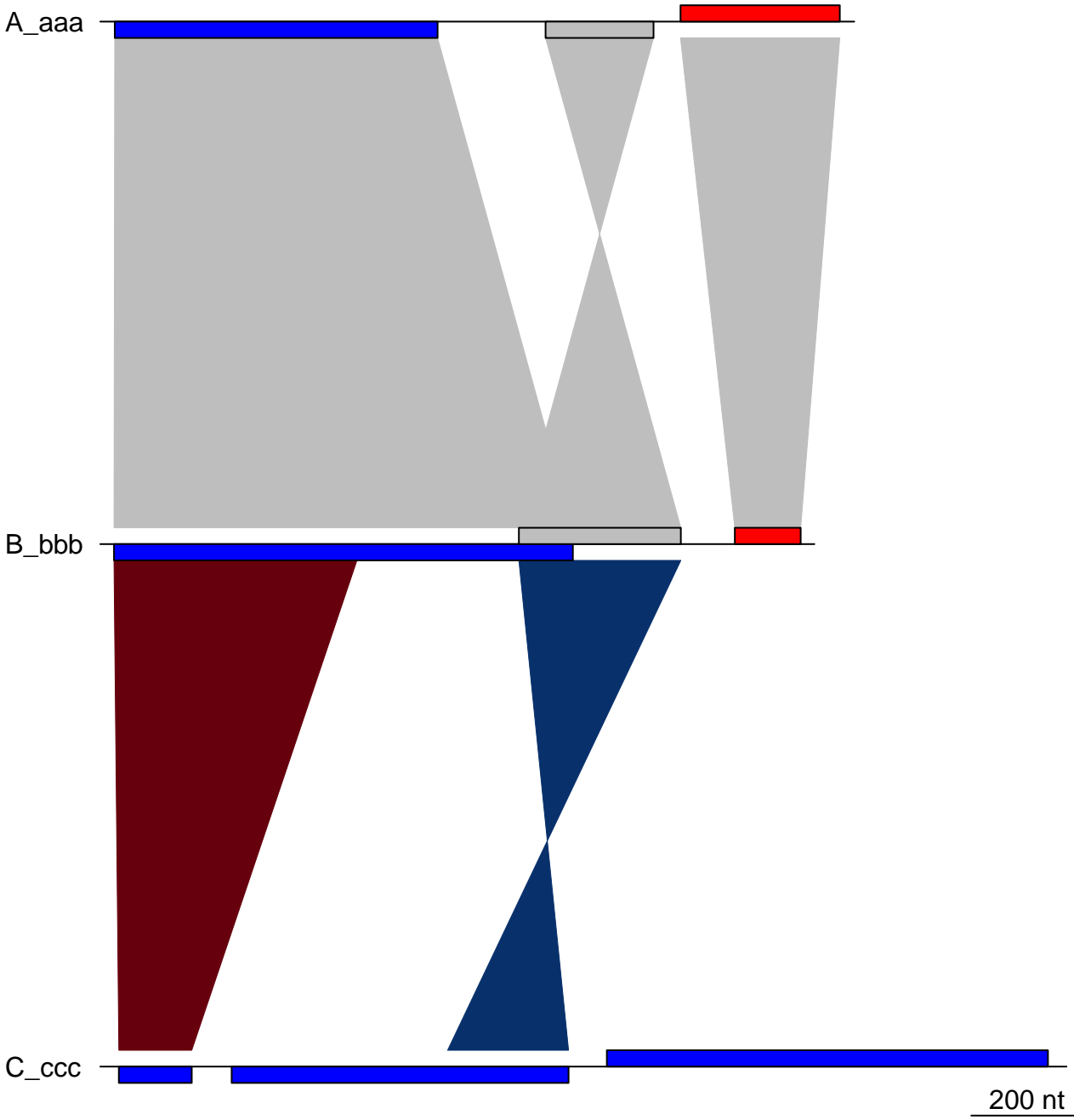
Dewey

Louie



help("plot\_gene\_map")





help("plot\_gene\_map")

BB |1.38 Mb |1.39 Mb |1.4 Mb |1.41 Mb |1.42 Mb |1.43 Mb |1.44 Mb

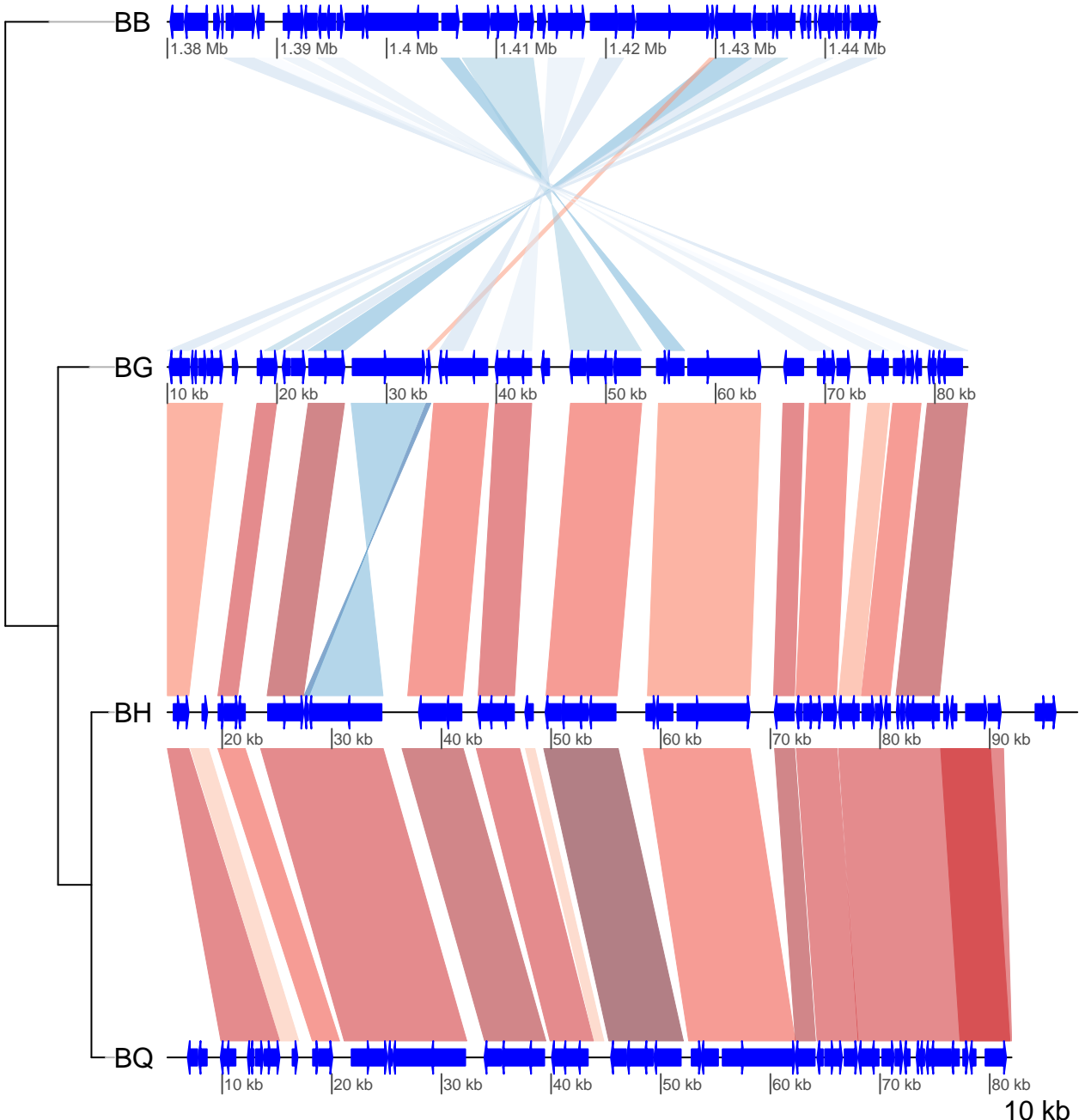
BG |10 kb |20 kb |30 kb |40 kb |50 kb |60 kb |70 kb |80 kb

BH |20 kb |30 kb |40 kb |50 kb |60 kb |70 kb |80 kb |90 kb

BQ |10 kb |20 kb |30 kb |40 kb |50 kb |60 kb |70 kb |80 kb

10 kb

help("plot\_gene\_map")



BB

1.44 Mb

1.42 Mb

1.38 Mb

1.4 Mb

BG

BH

BQ

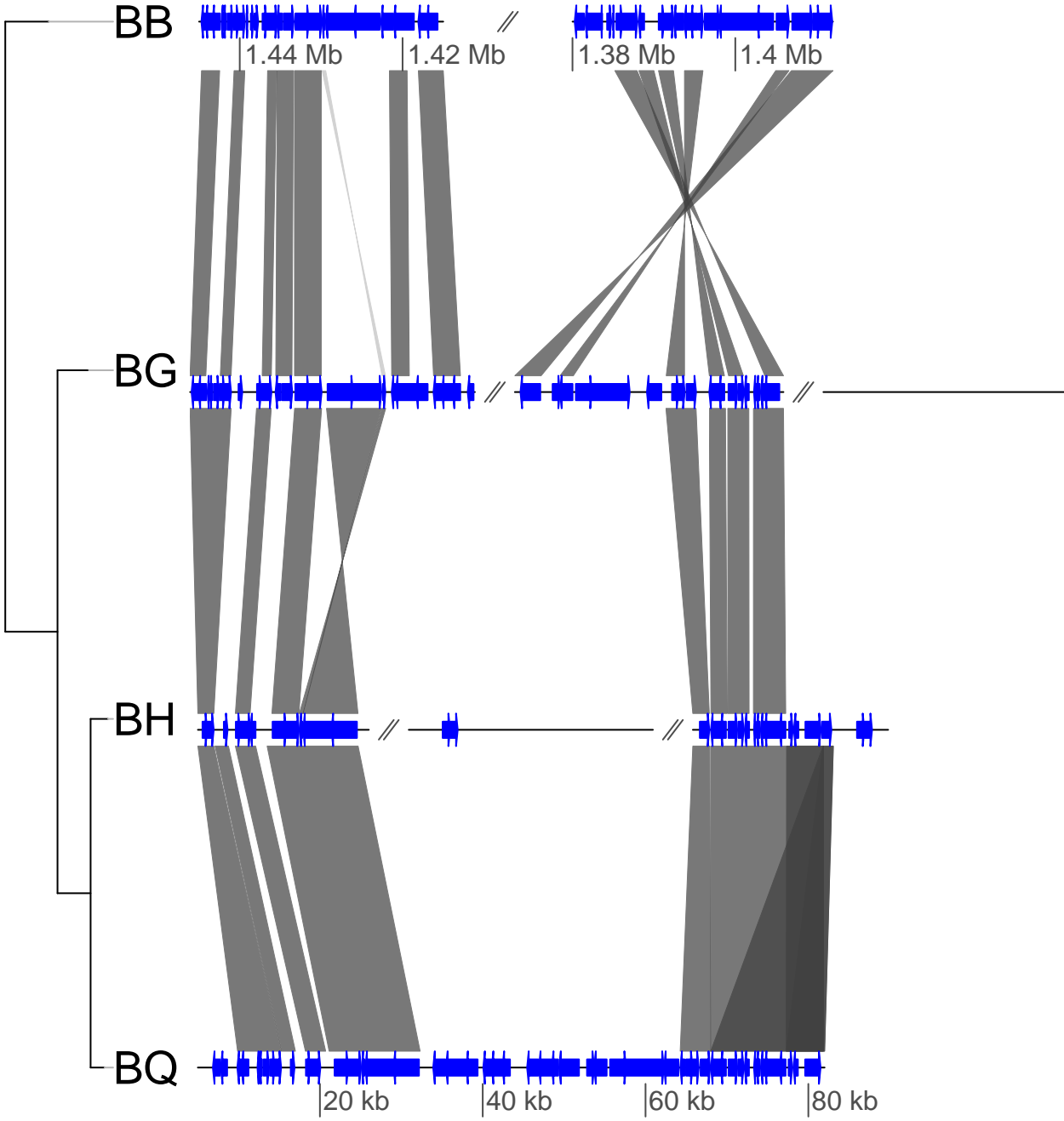
20 kb

40 kb

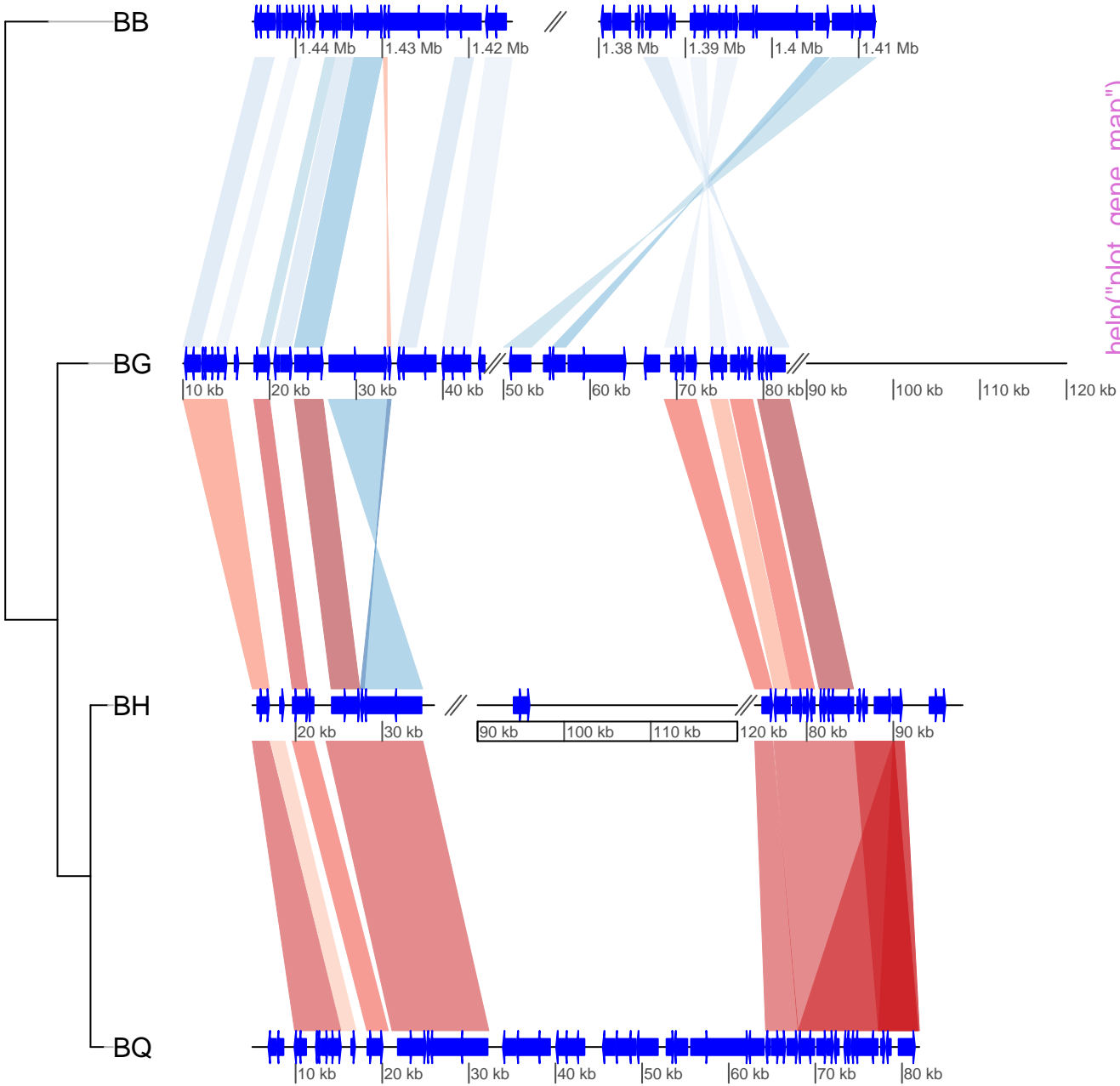
60 kb

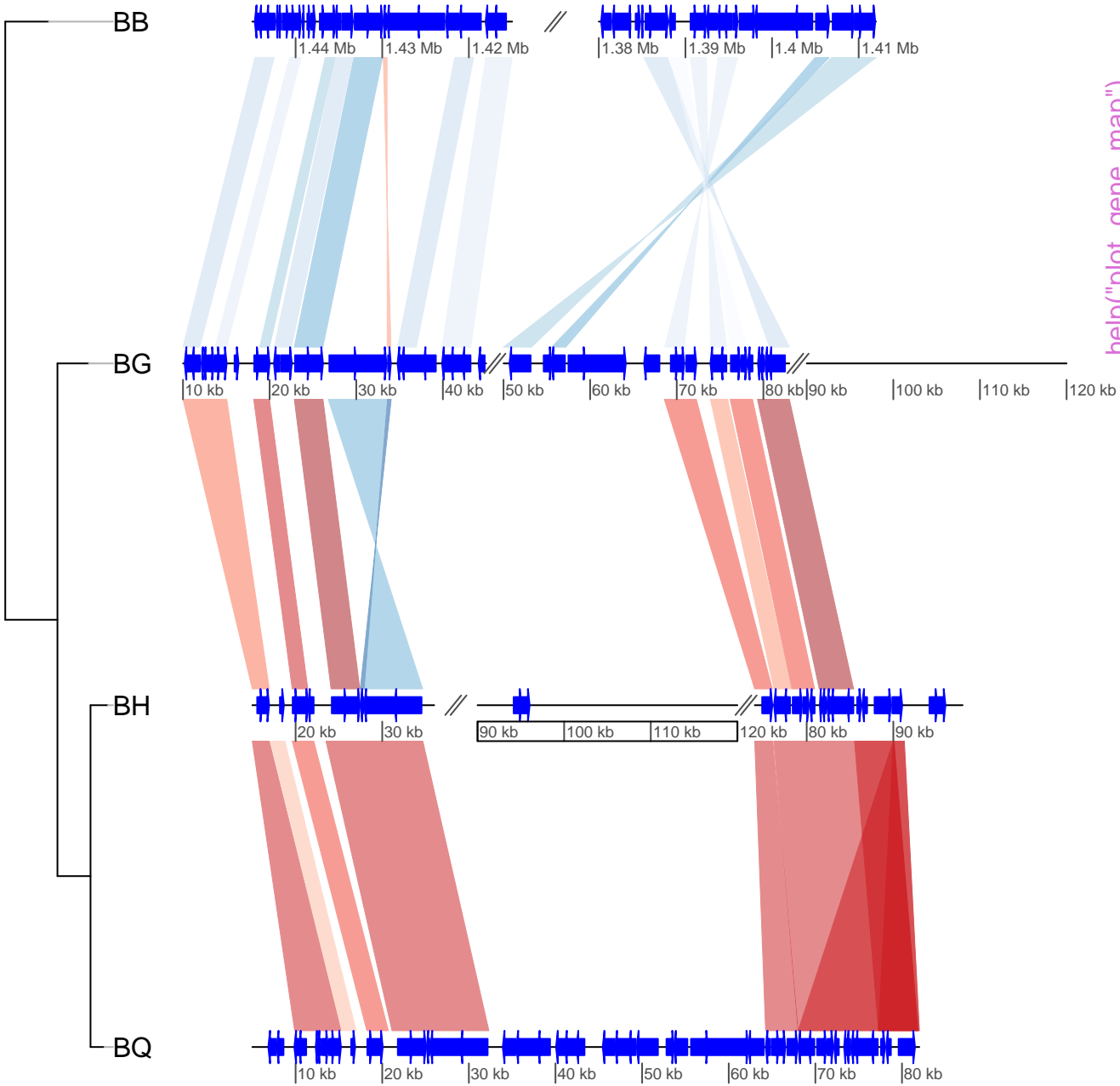
80 kb

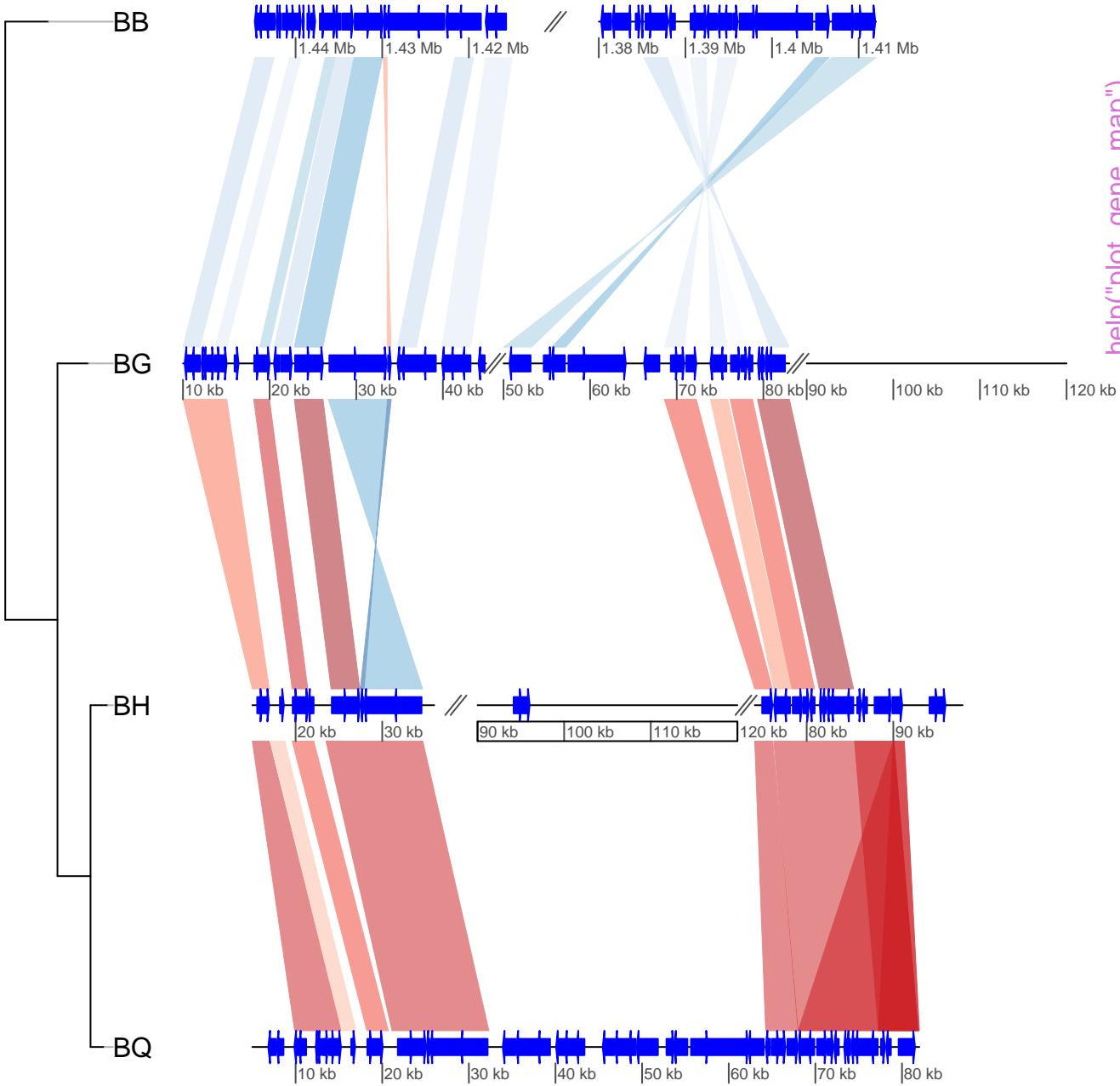
help("plot\_gene\_map")



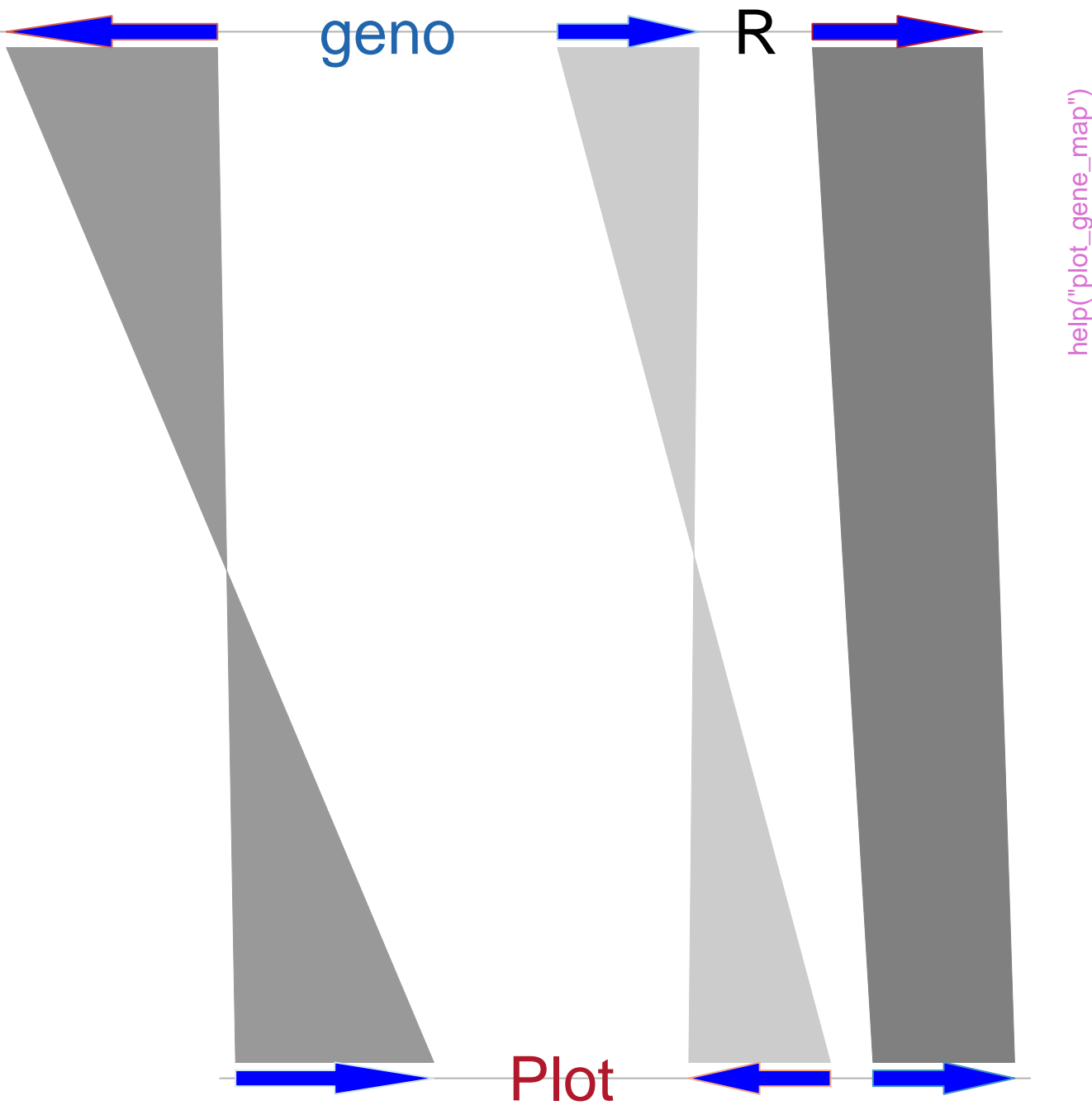








10 kb

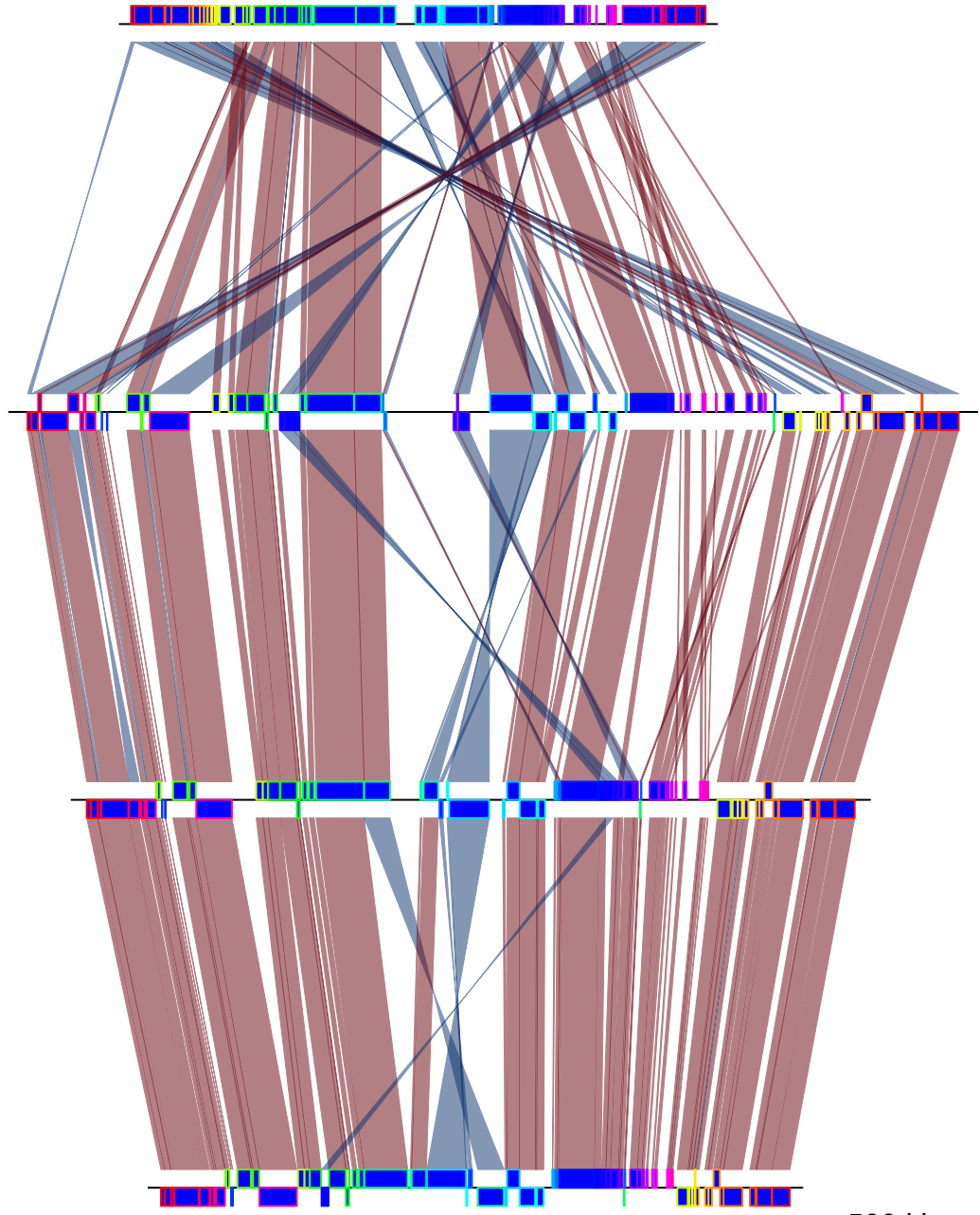


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



500 kb

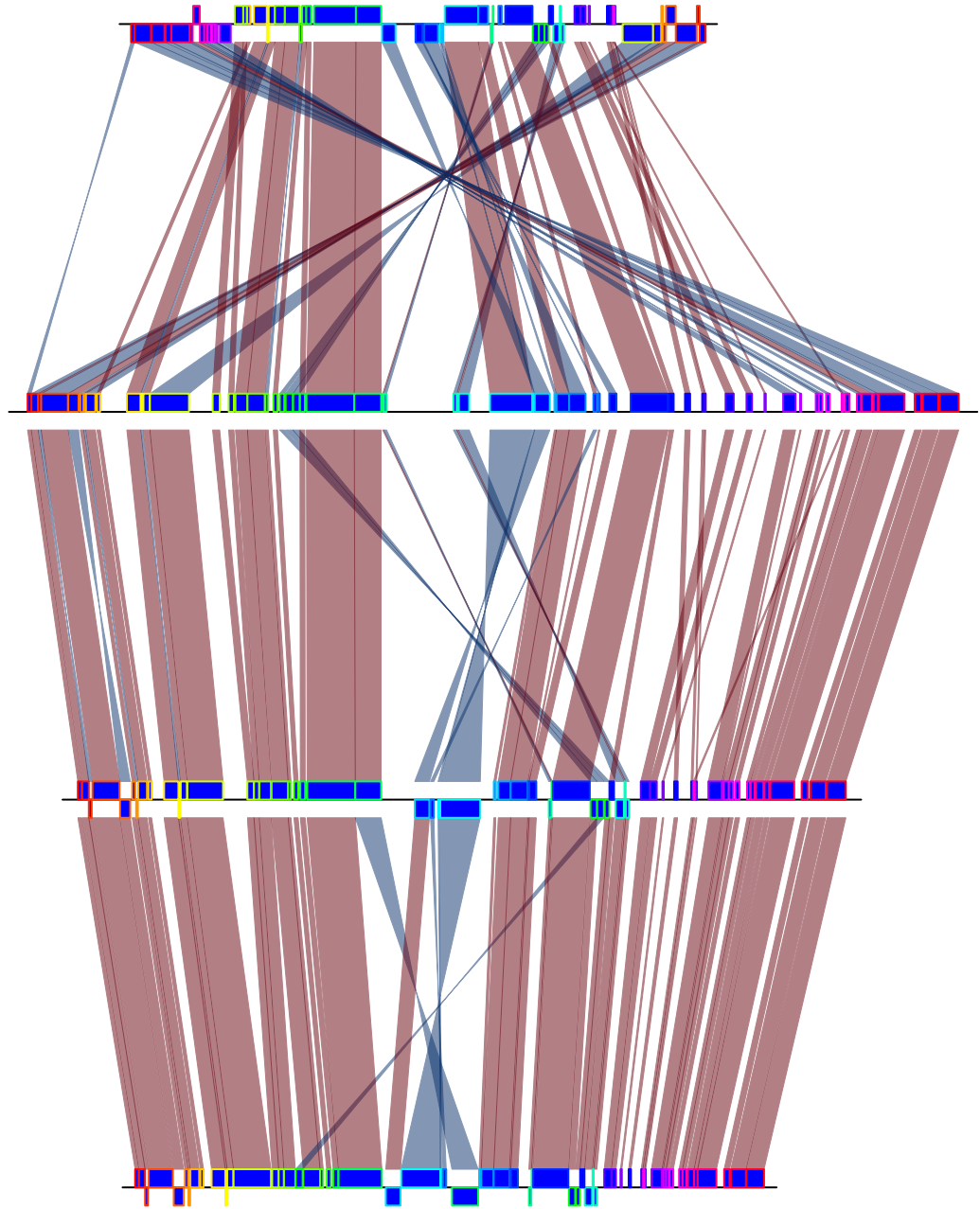
help("read\_functions")

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

B bacilliformis

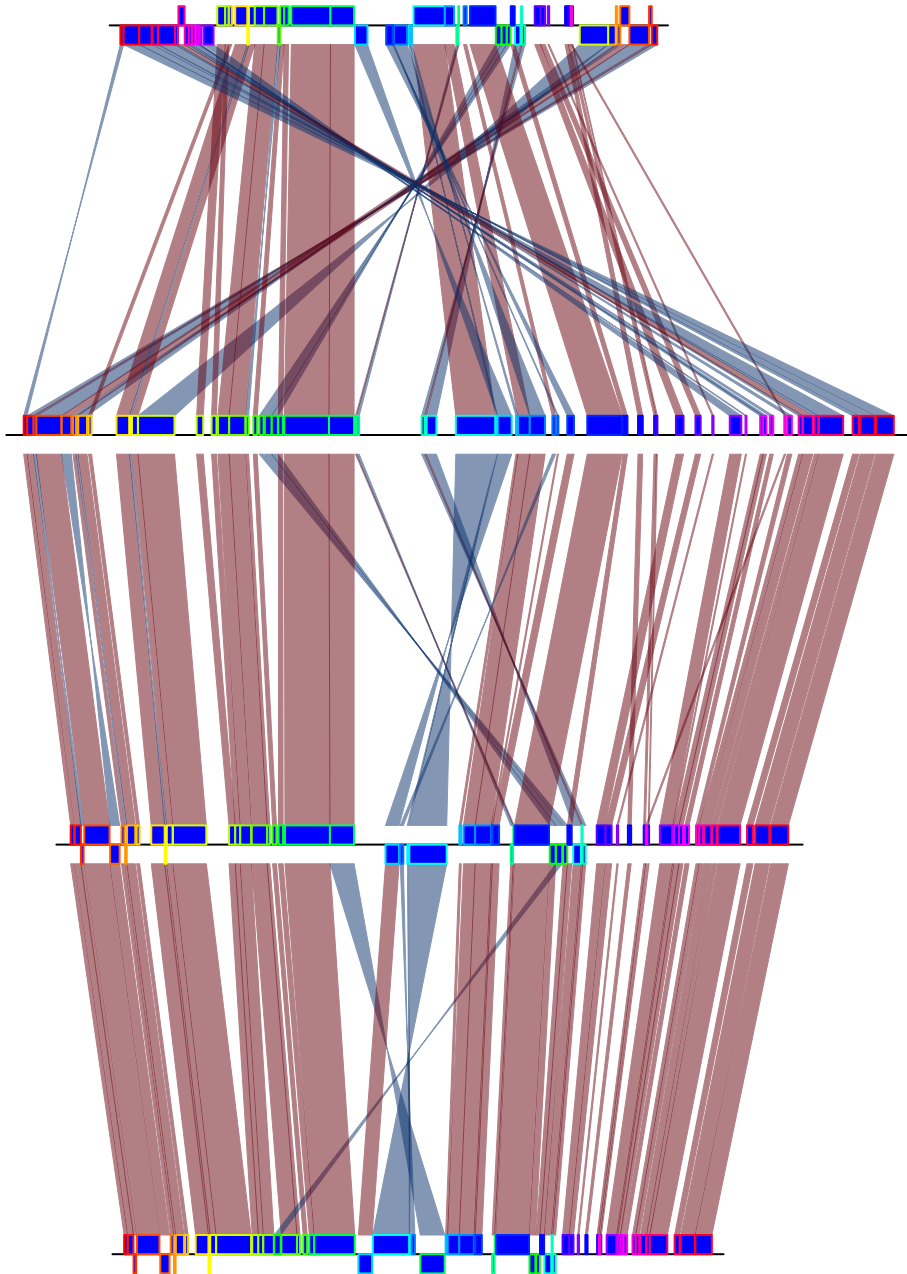
B grahamii

B henselae

B quintana

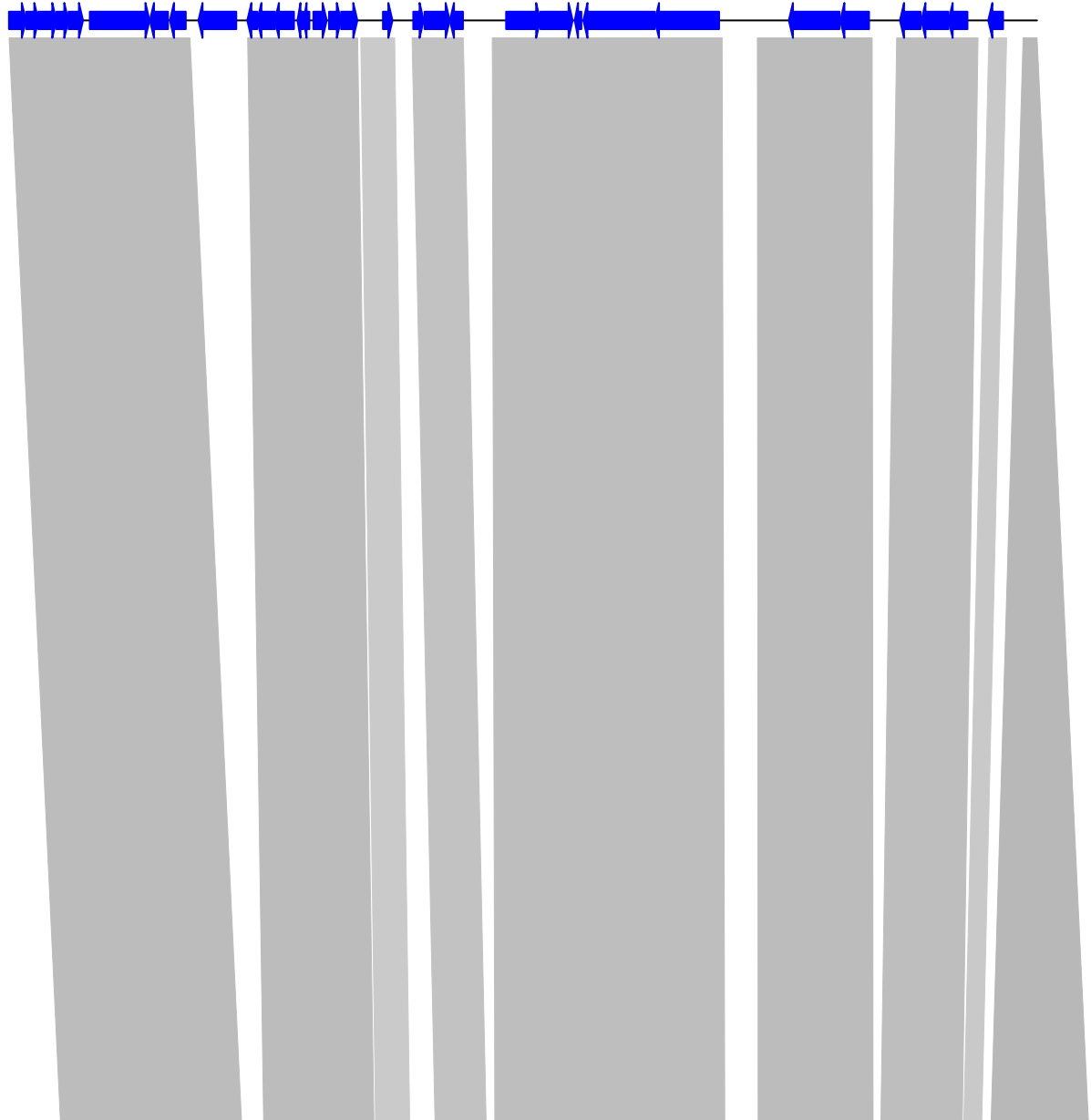
help("read\_functions")

500 kb



BH

BQ



help("read\_functions")

5 kb

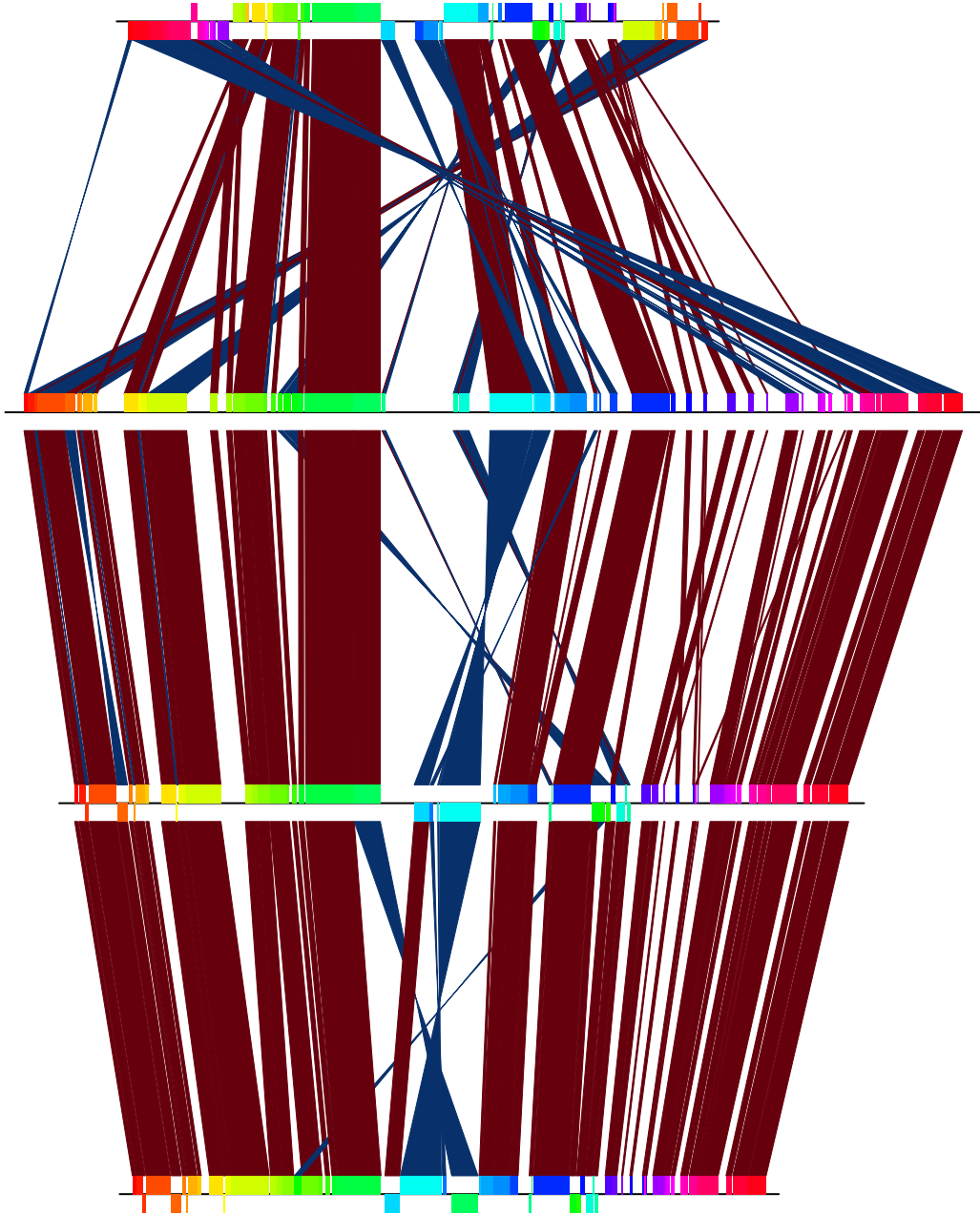


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



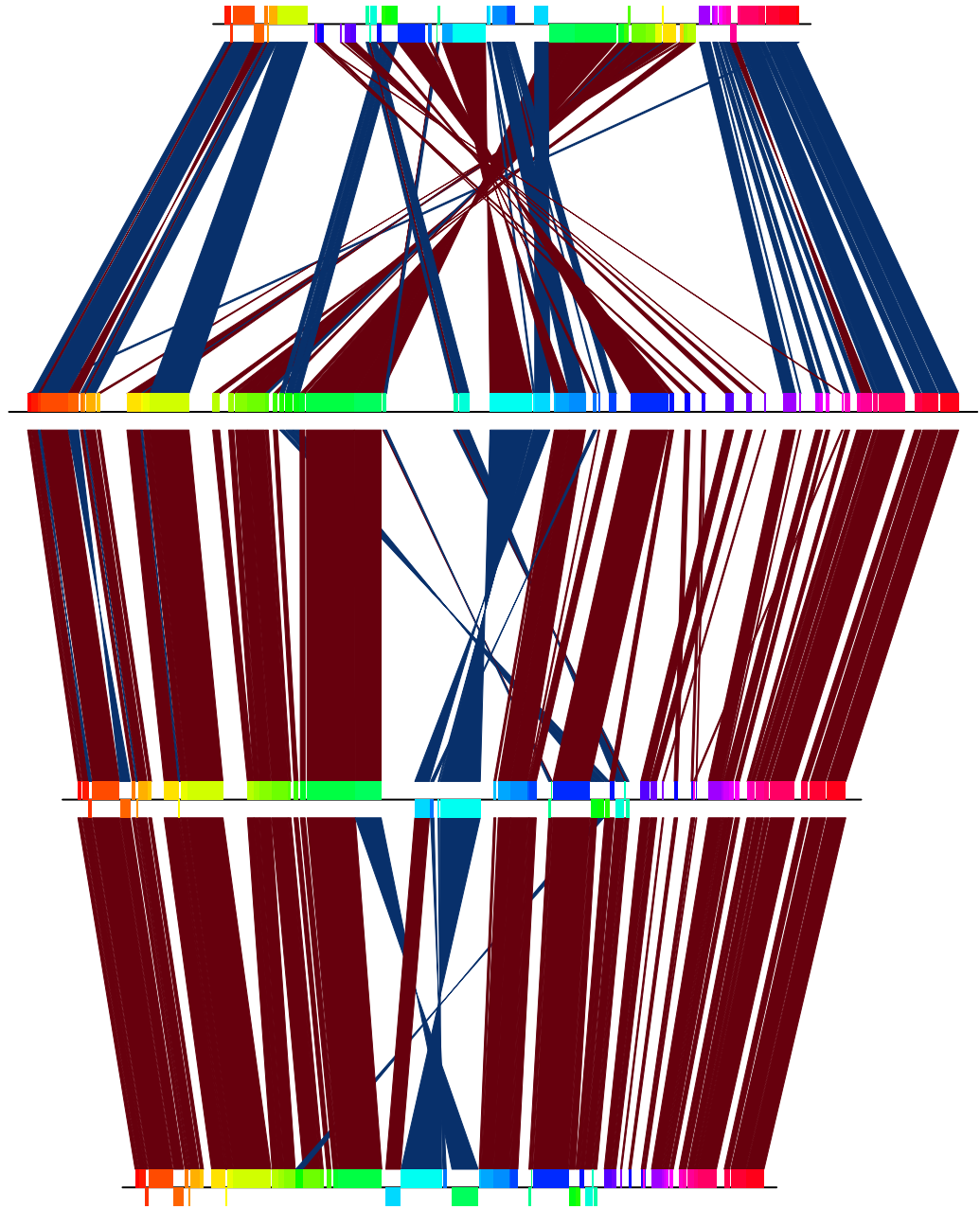
help("reverse")

B\_bacilliformis

B\_grahamii

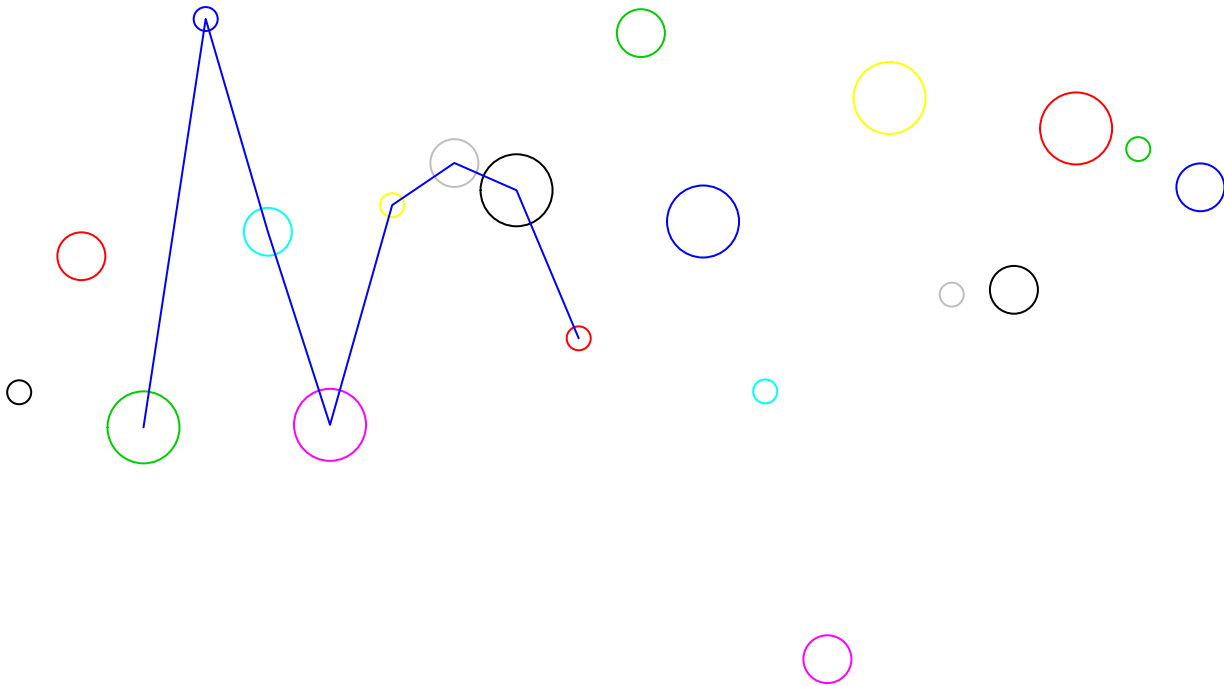
B\_henselae

B\_quintana

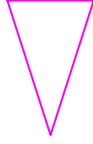
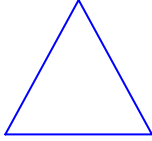


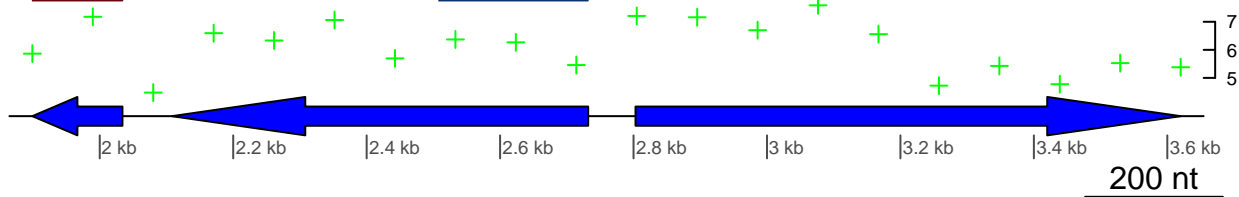
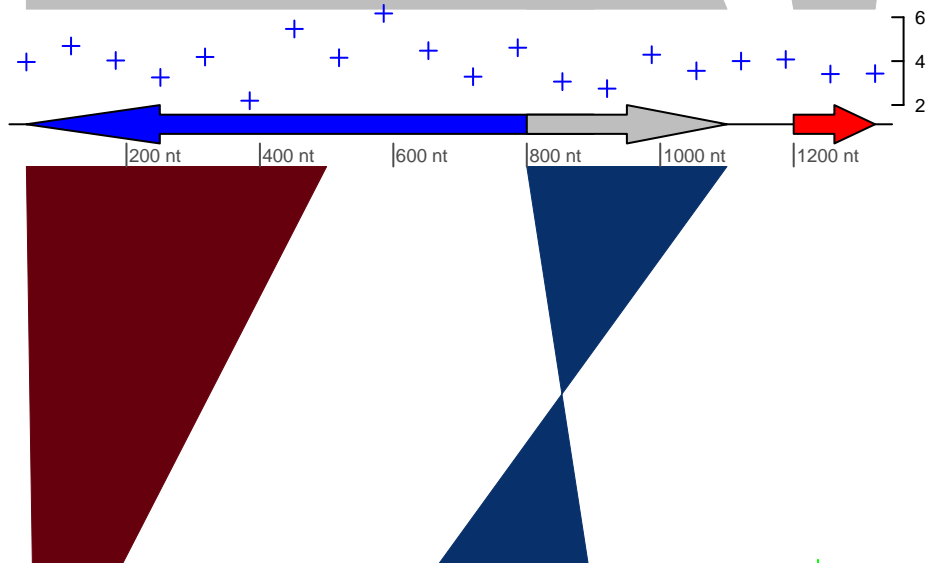
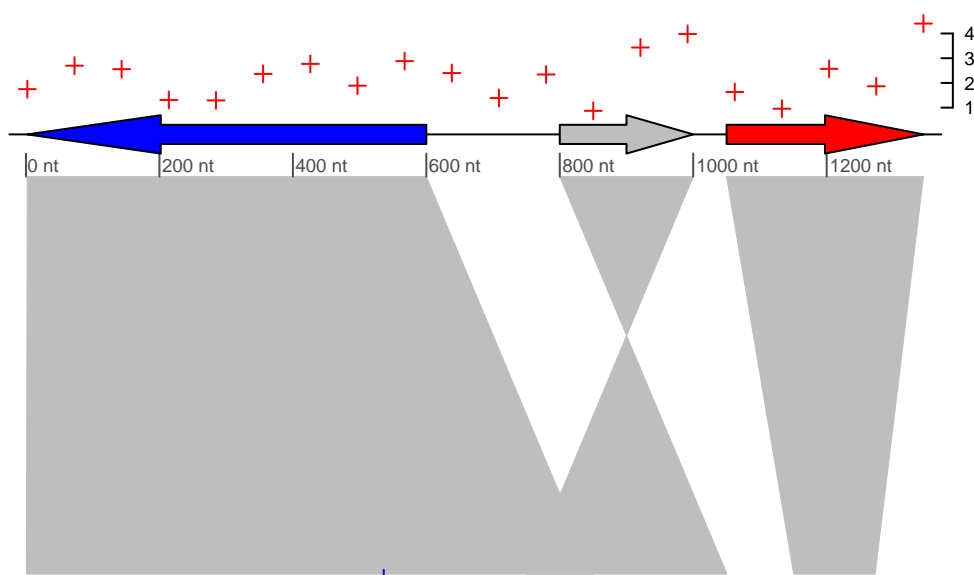
help("reverse")

500 kb



help("seg\_plot")

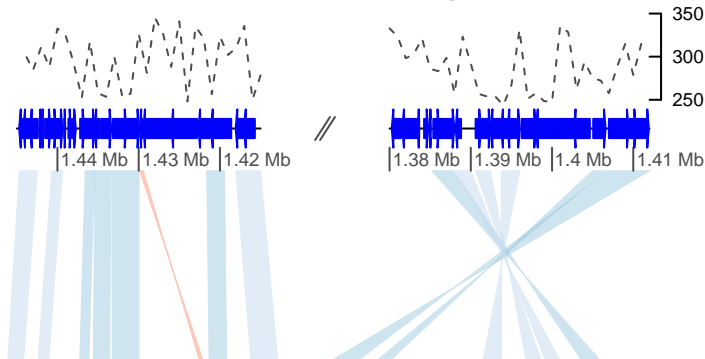




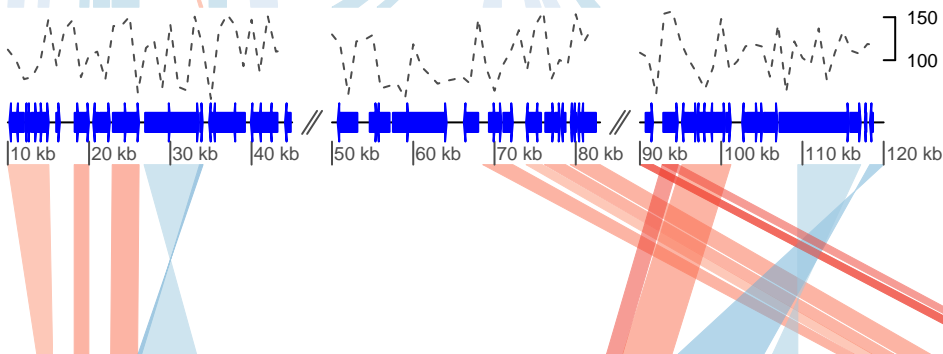
help("seg\_plot")

# Random plots for the same segment in 4 *Bartonella* genomes

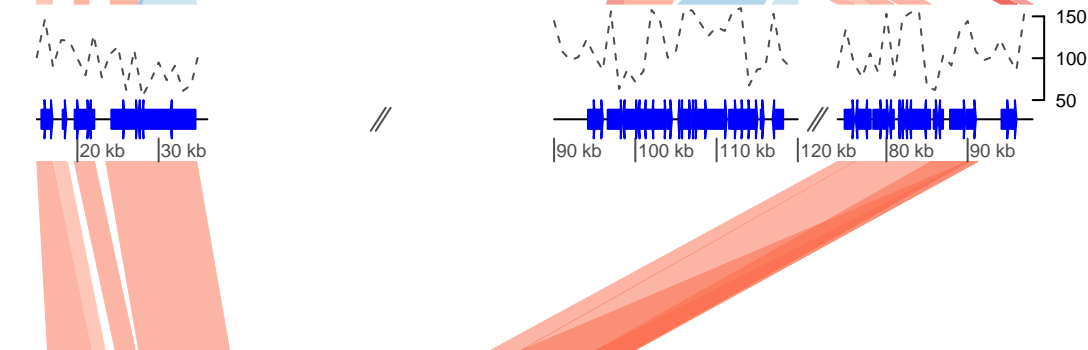
BB



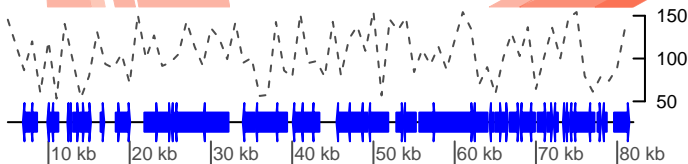
BG



BH

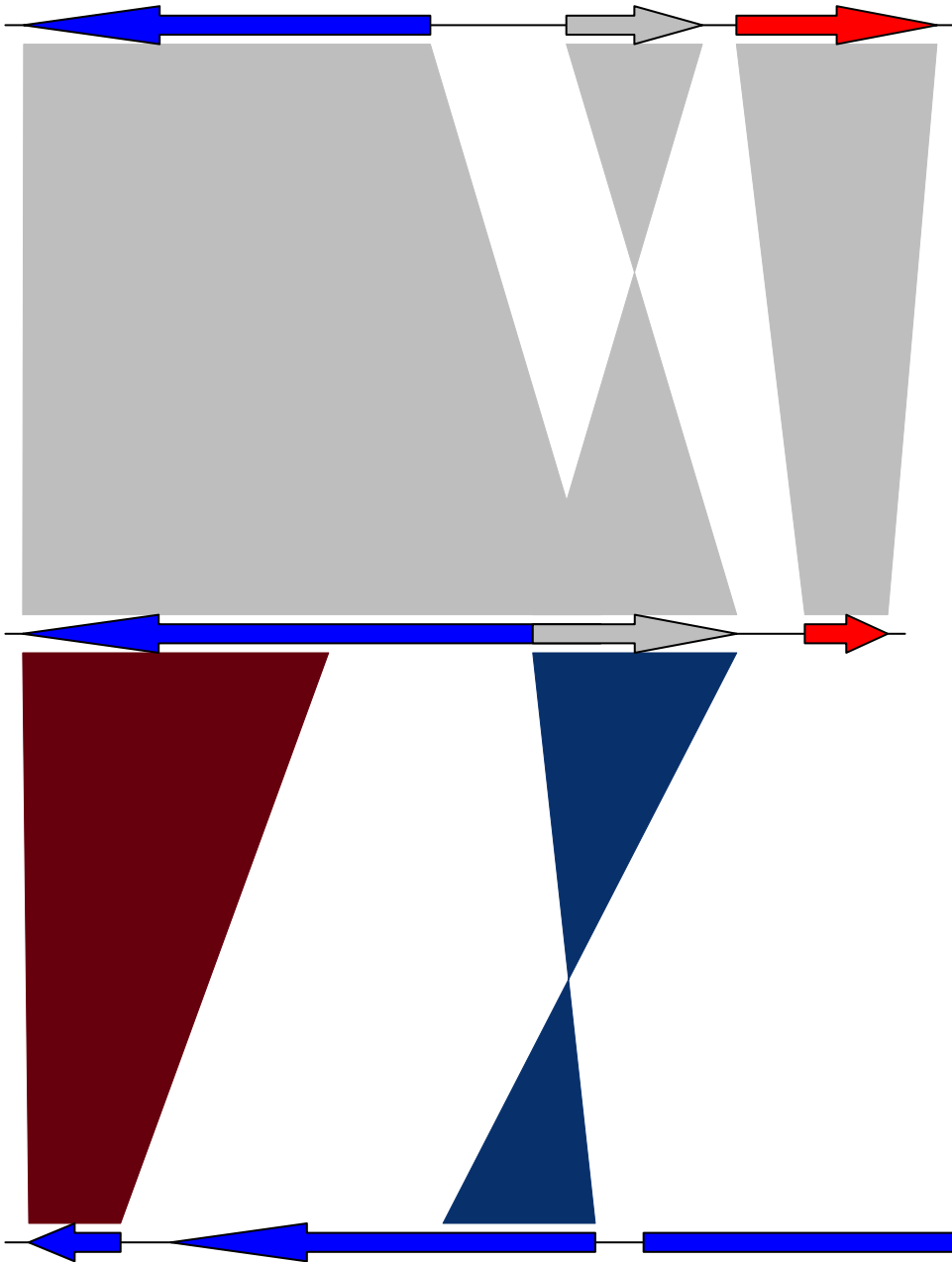


BQ



20 kb

help("seg\_plot")



help("three\_genes")

200 nt

