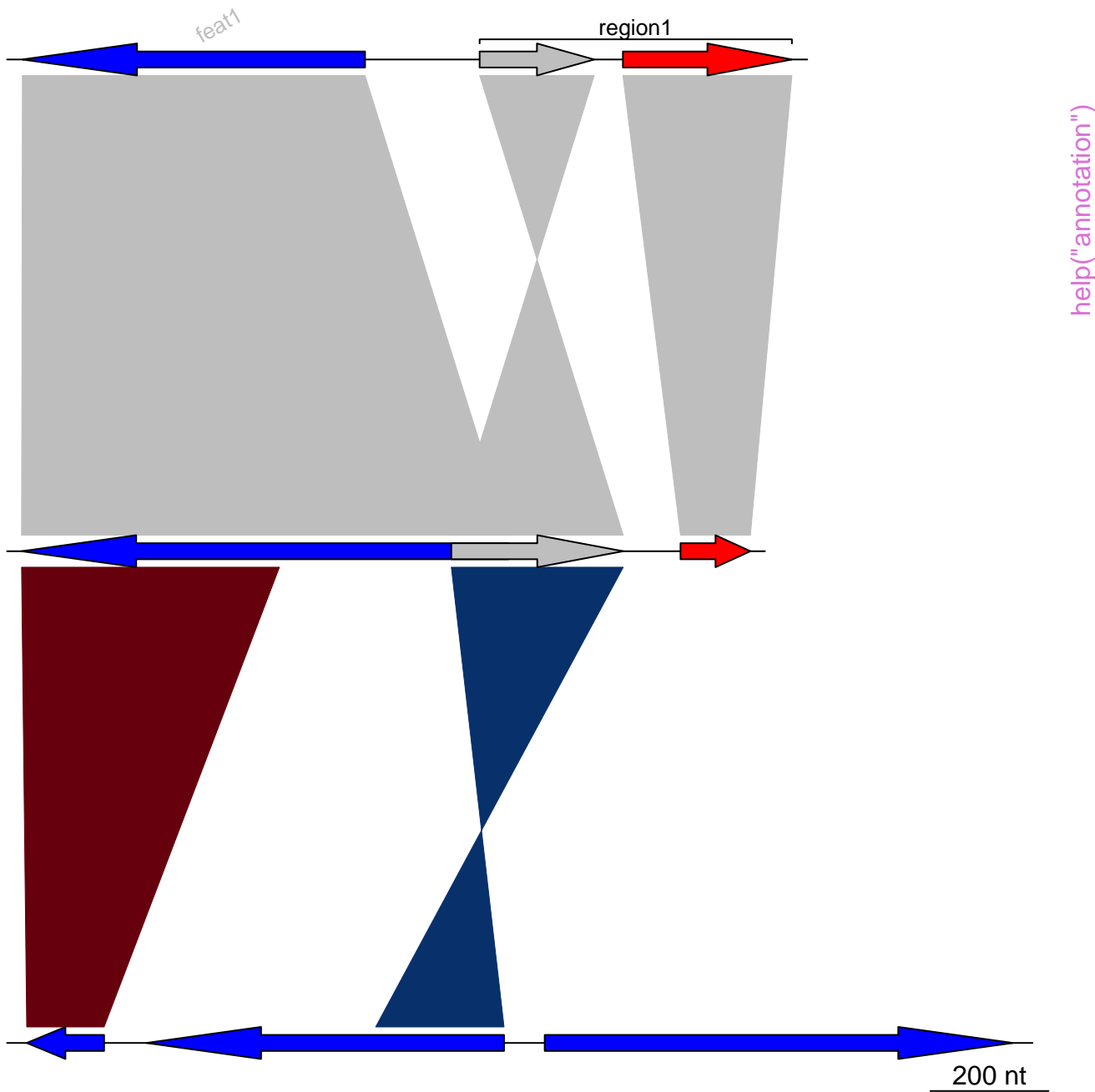
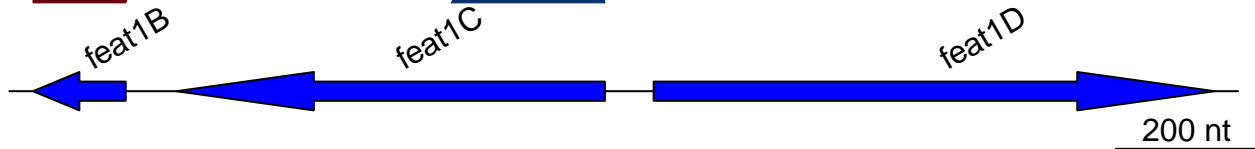
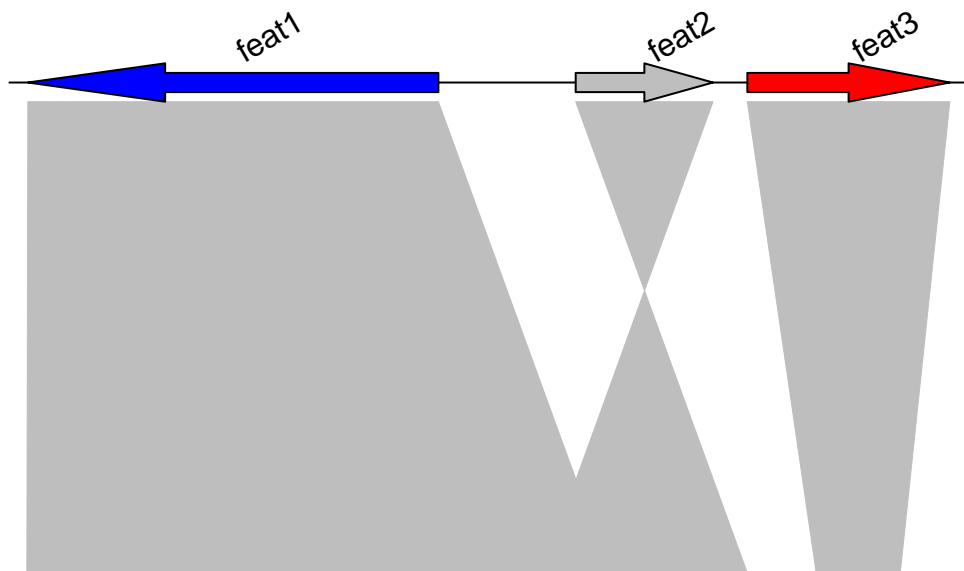


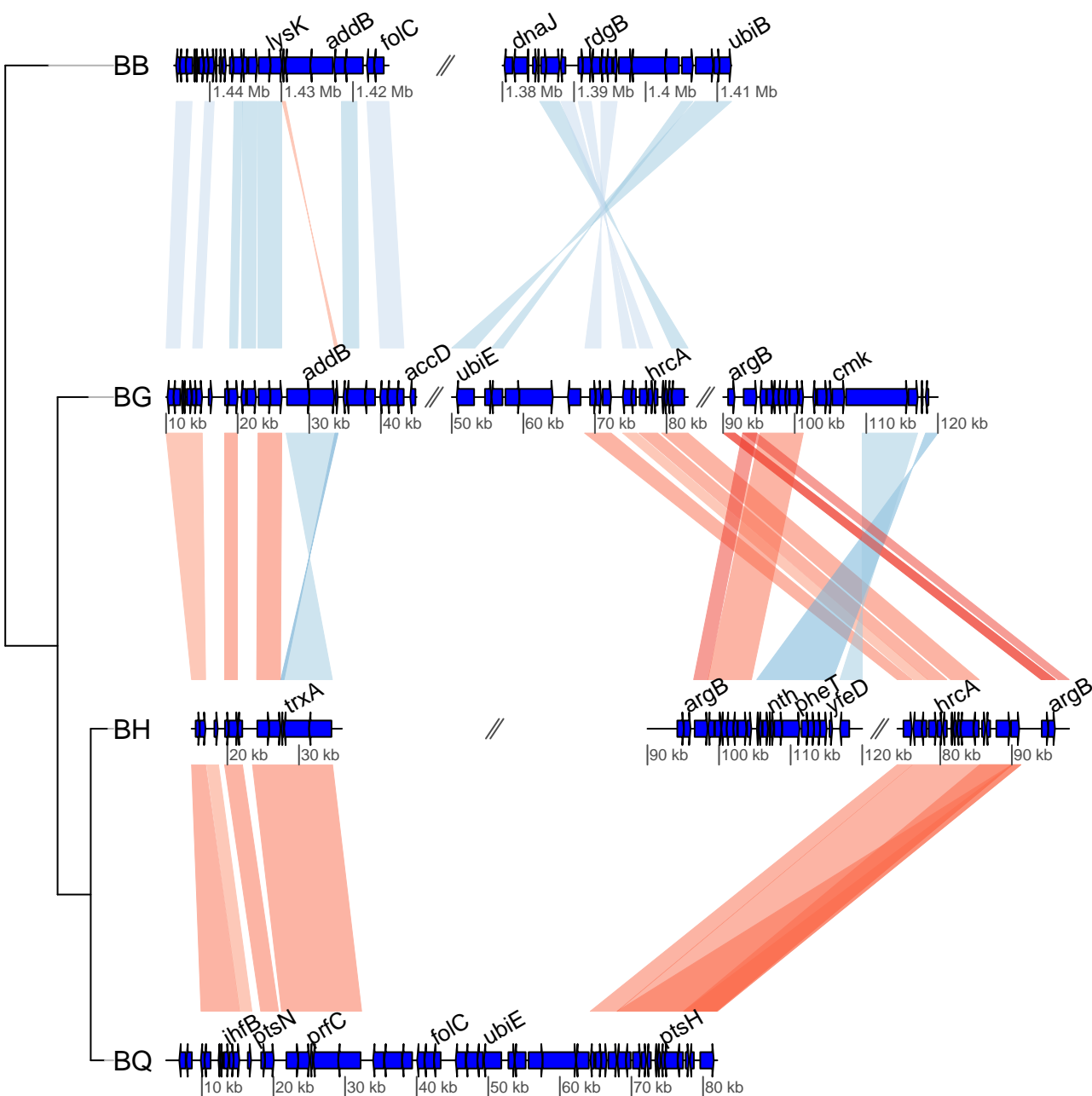
help("annotation")

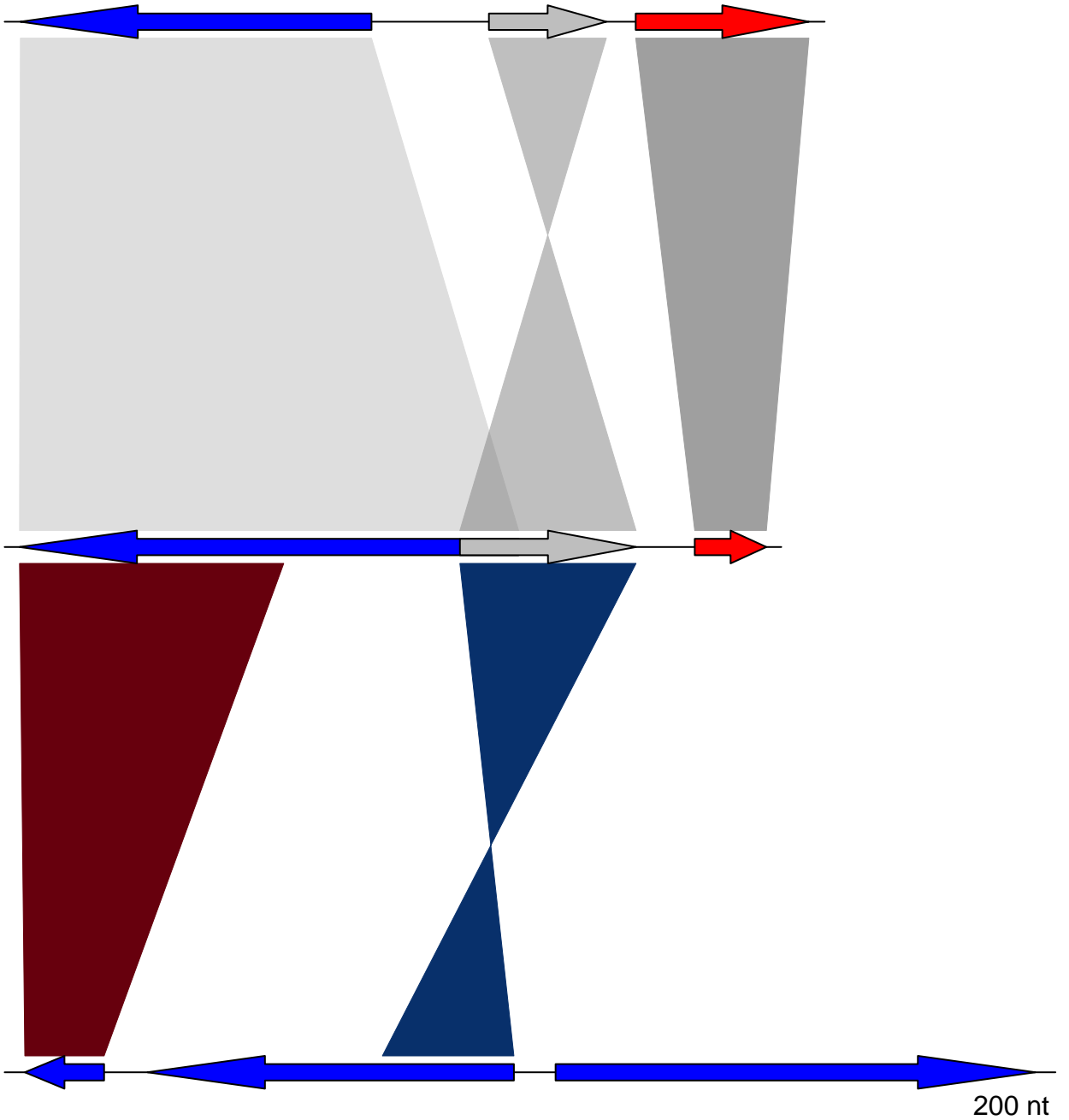
200 nt



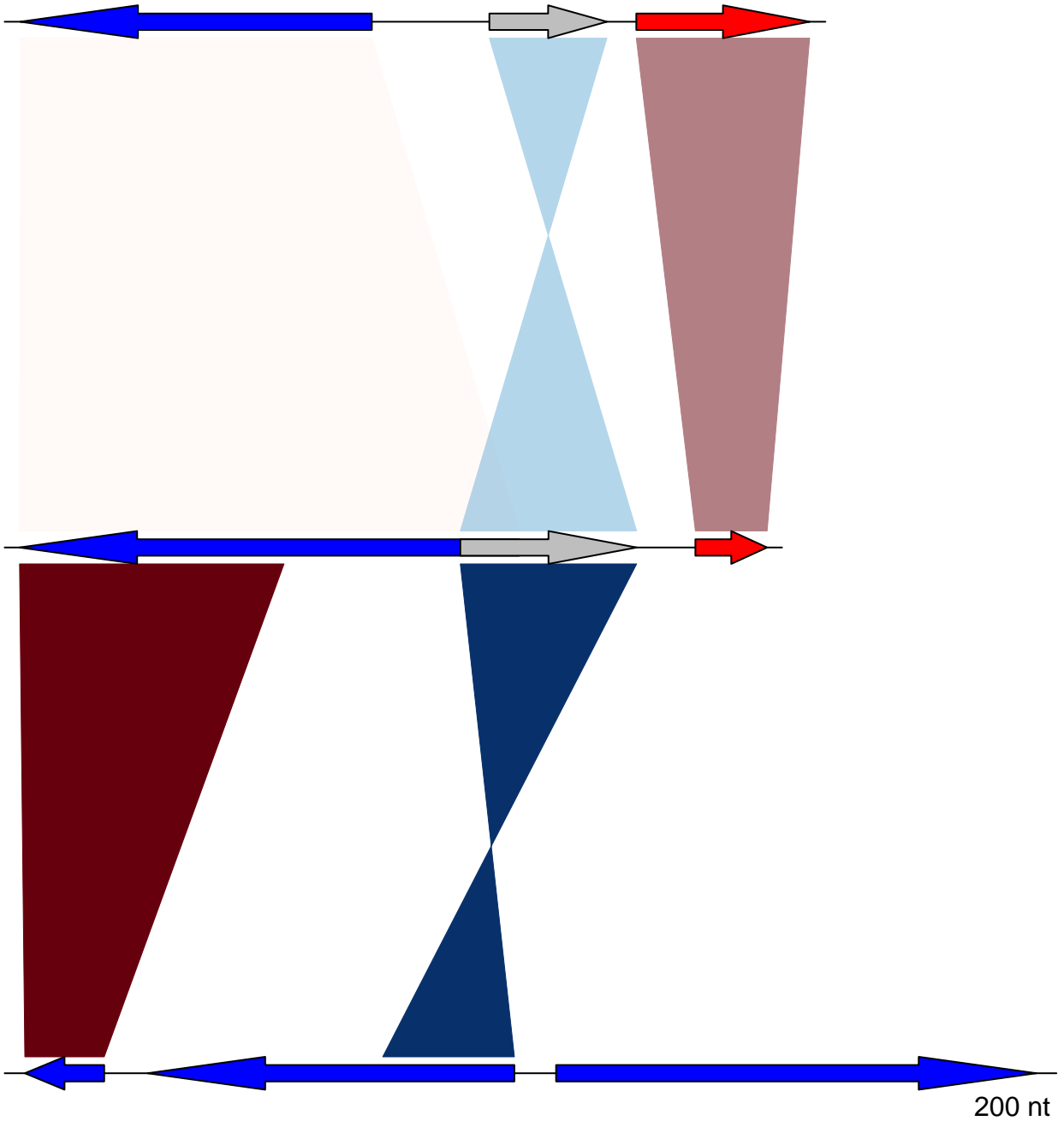


help("annotation")

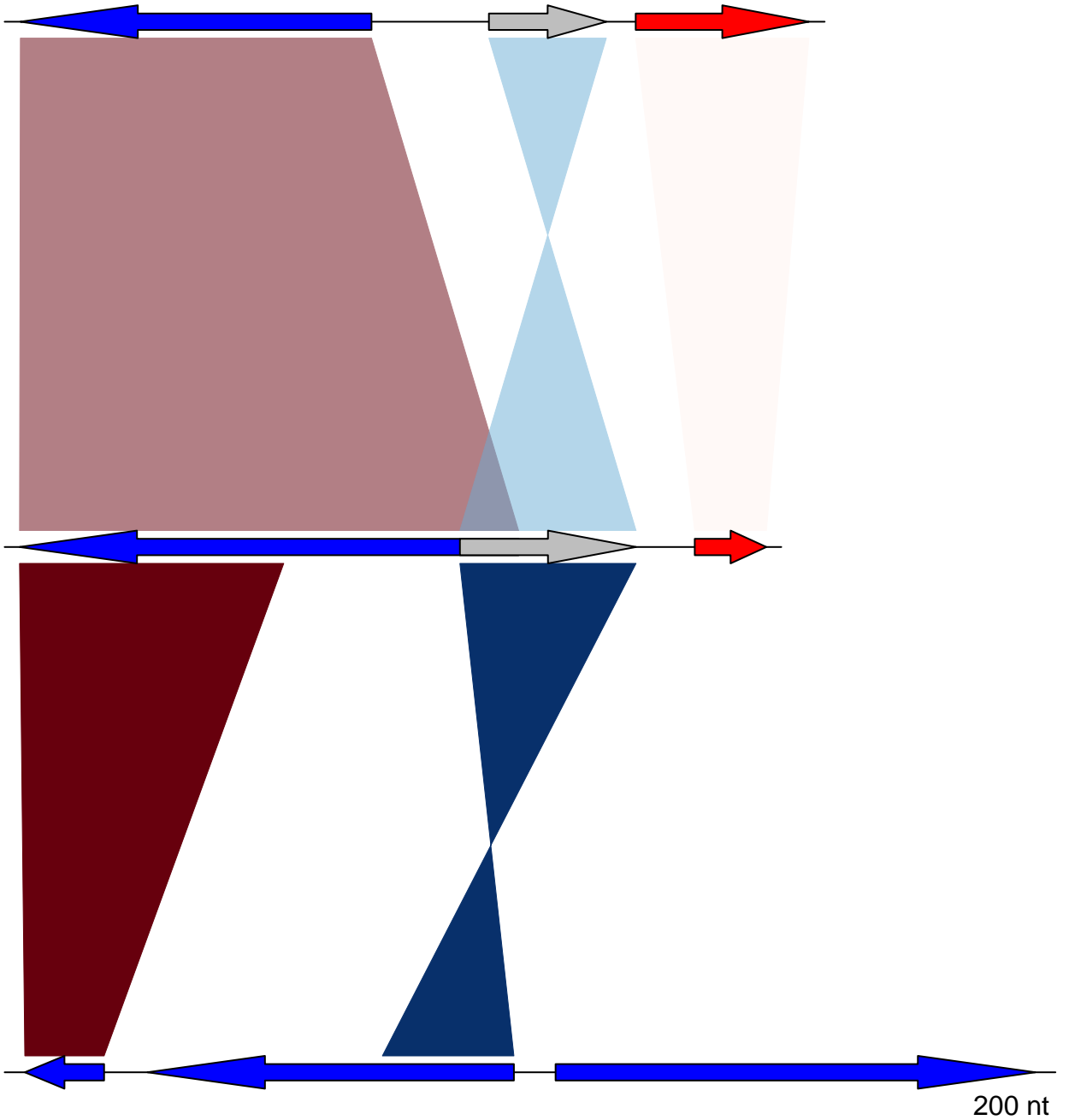




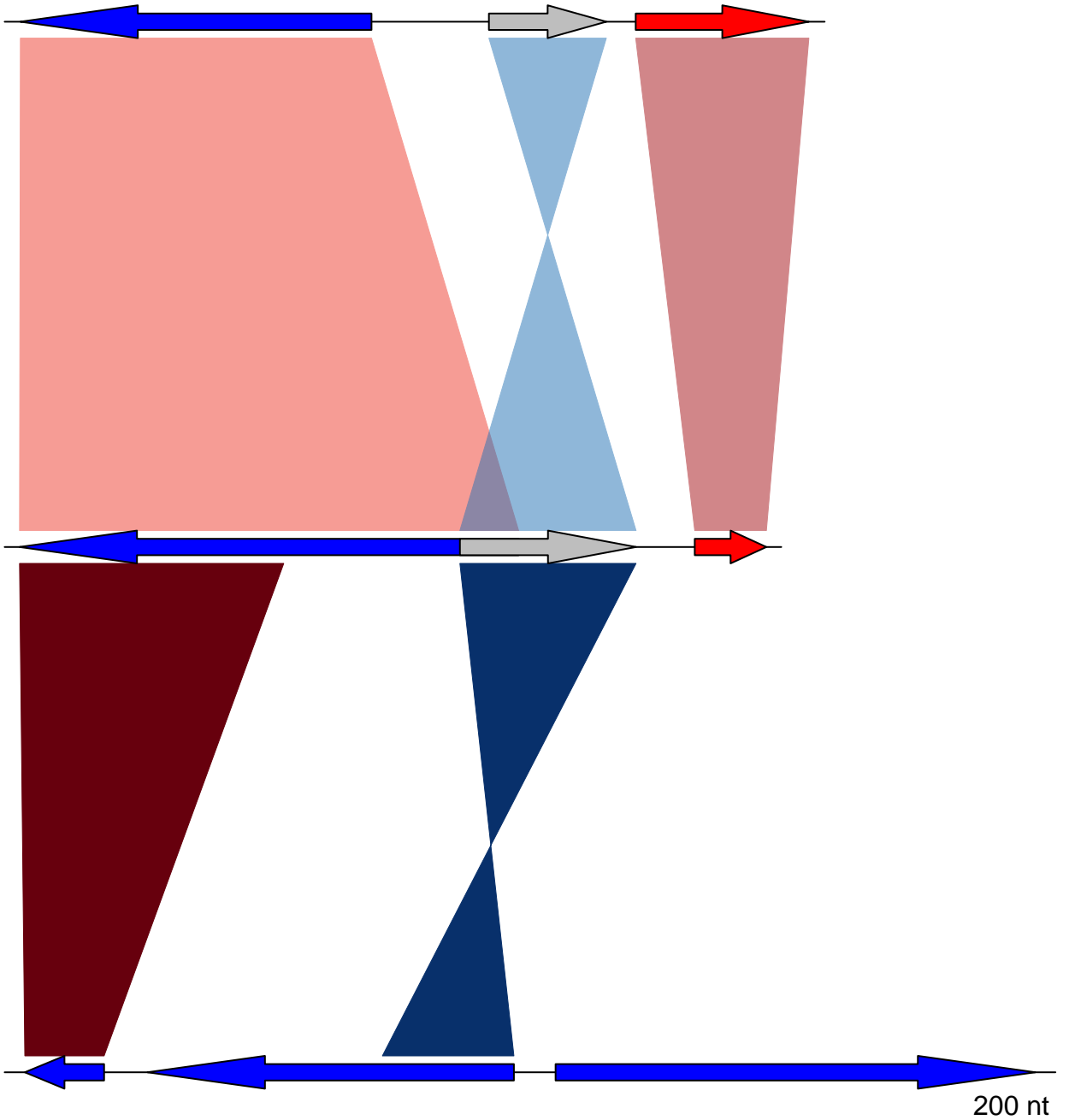
help("apply\_color\_scheme")



help("apply\_color\_scheme")

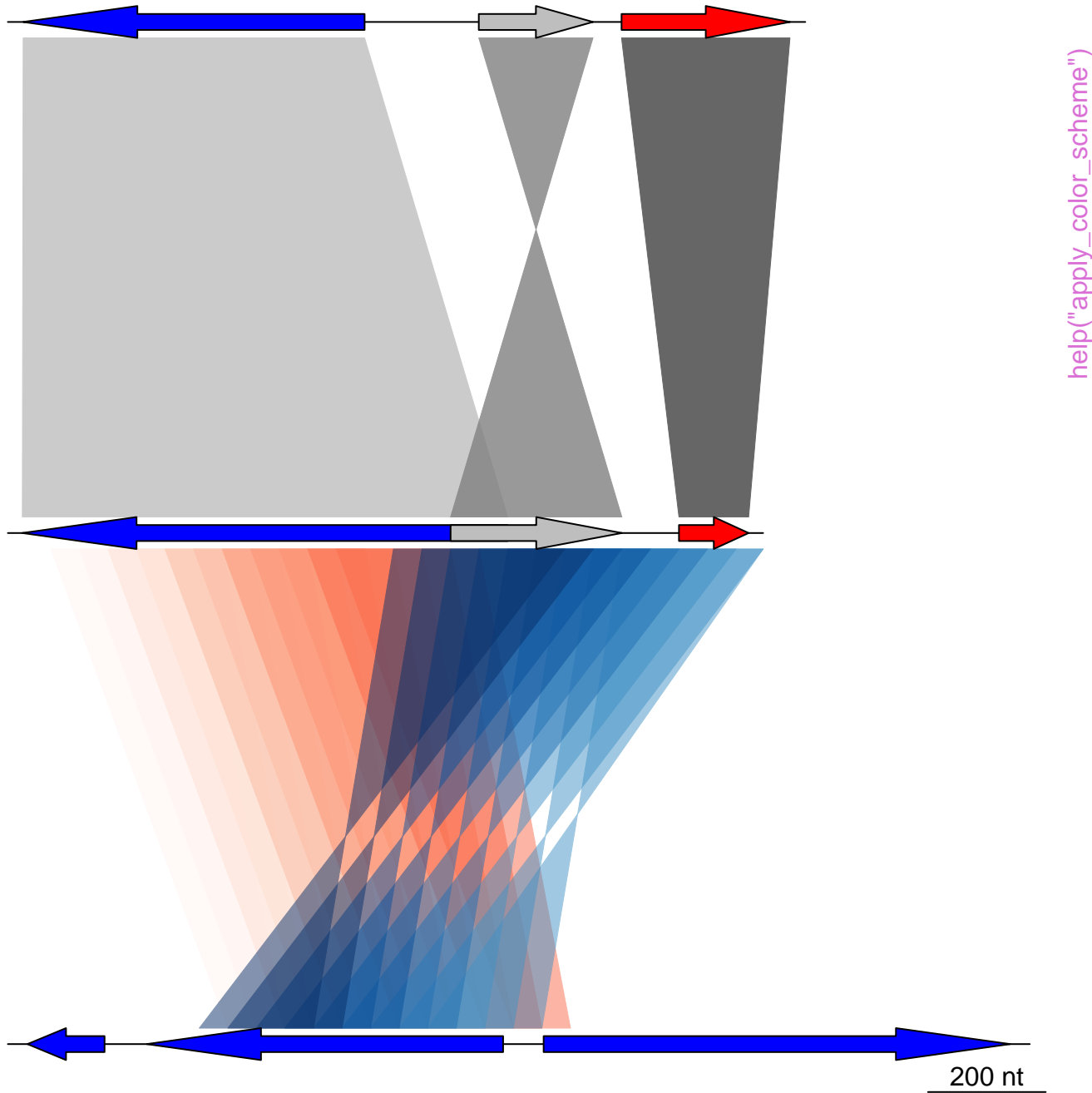


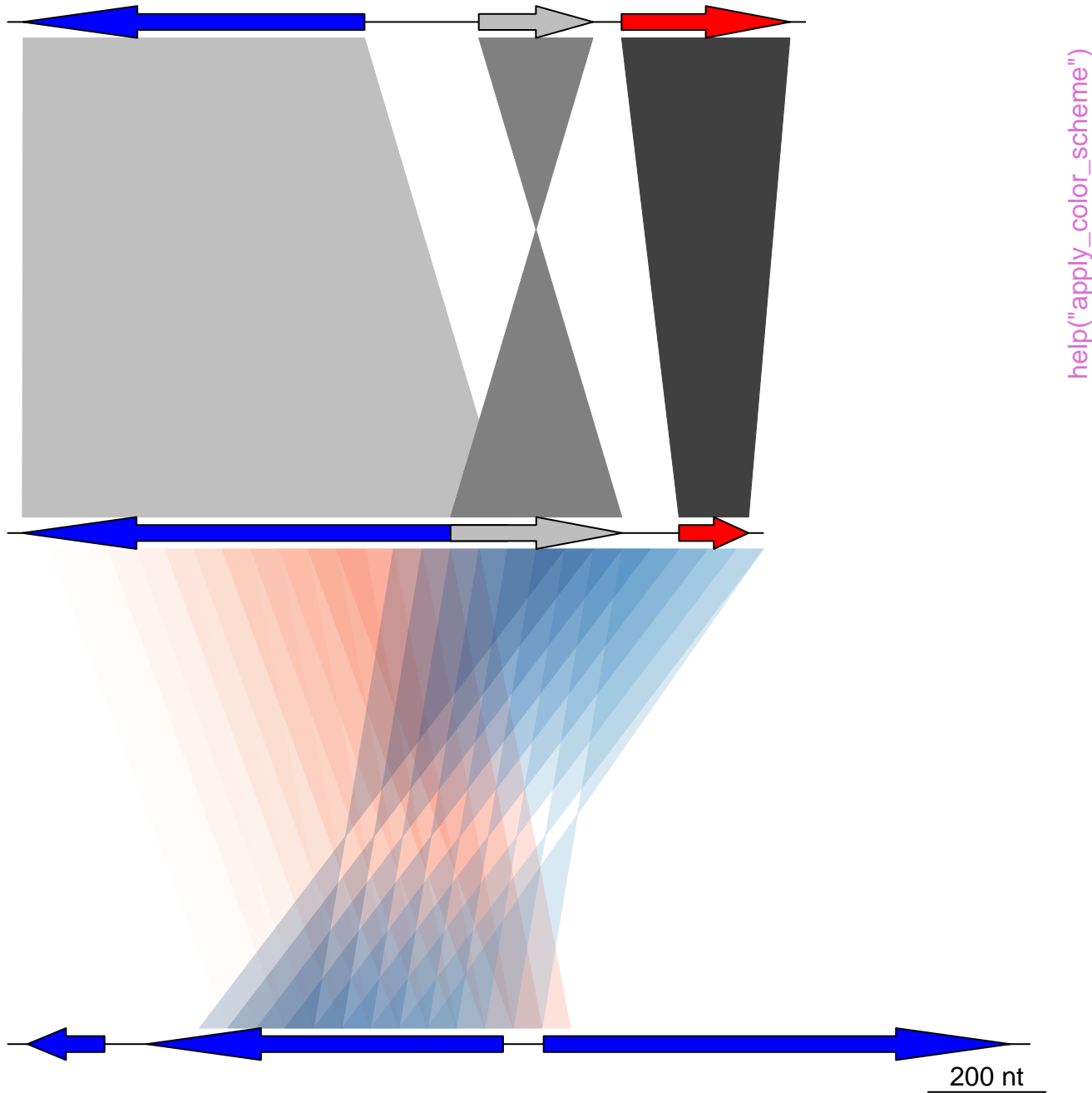
help("apply\_color\_scheme")

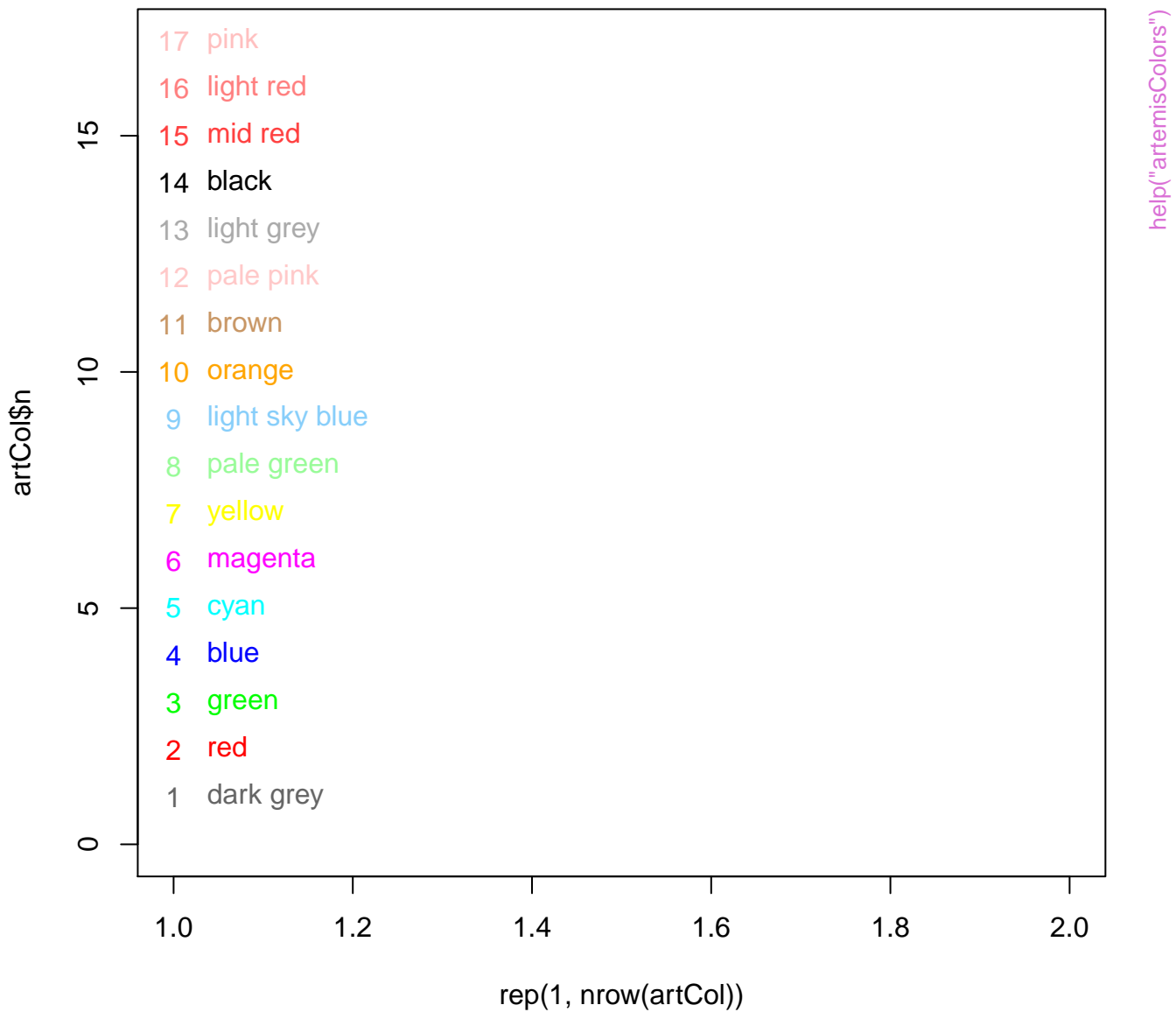


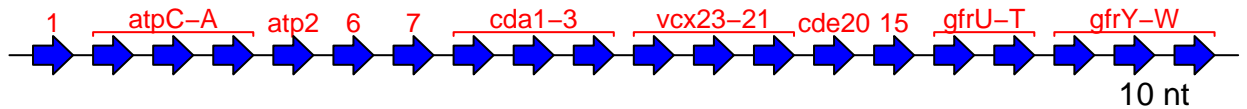
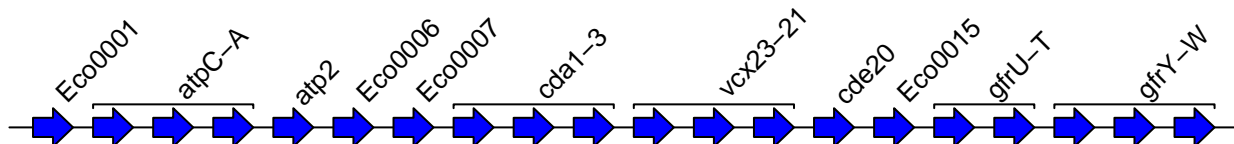
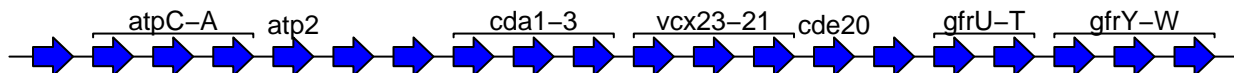
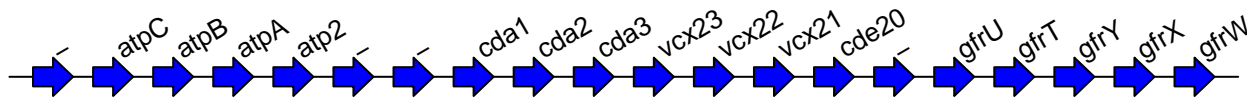
help("apply\_color\_scheme")











help("auto\_annotate")

BB

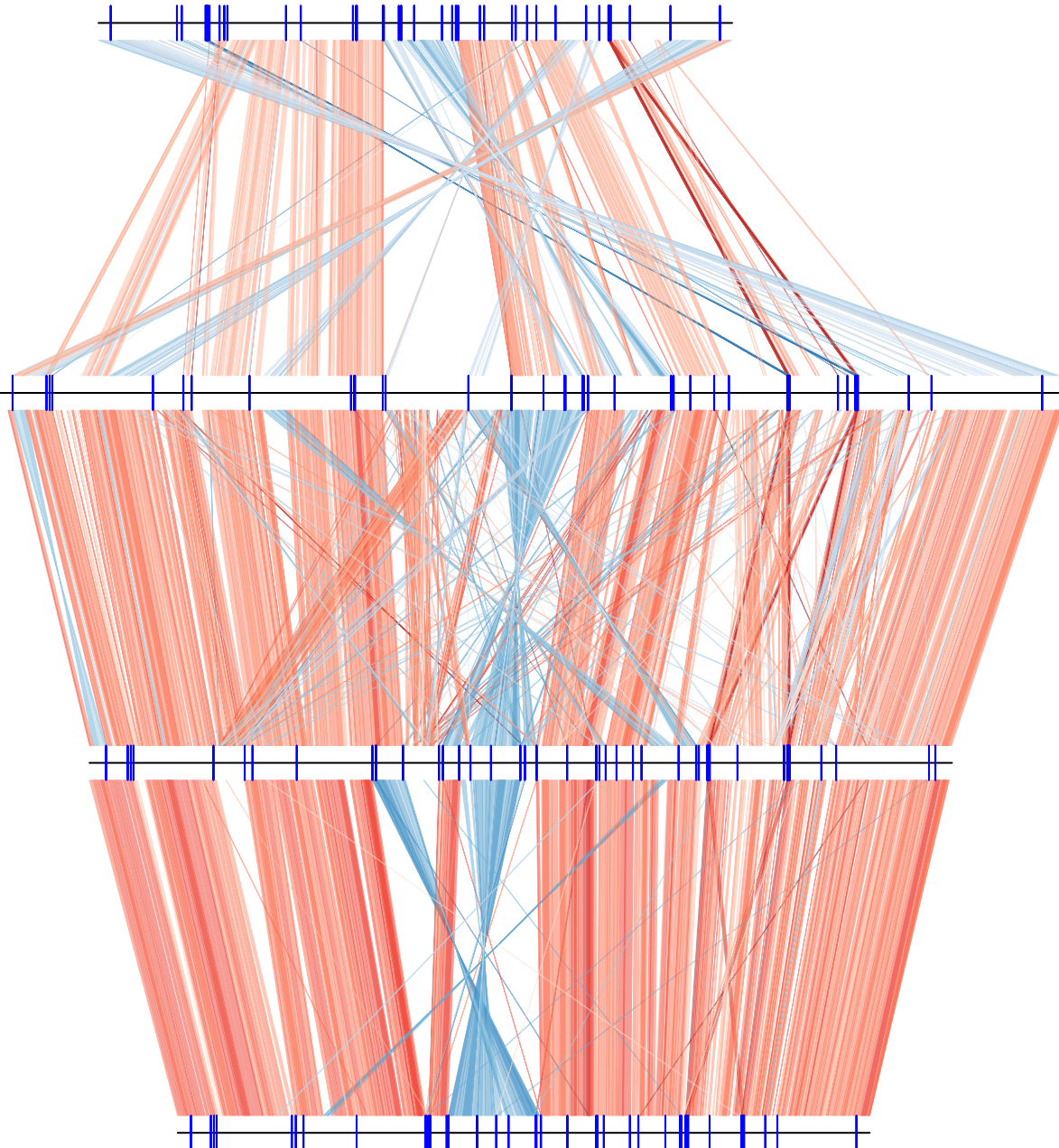
BG

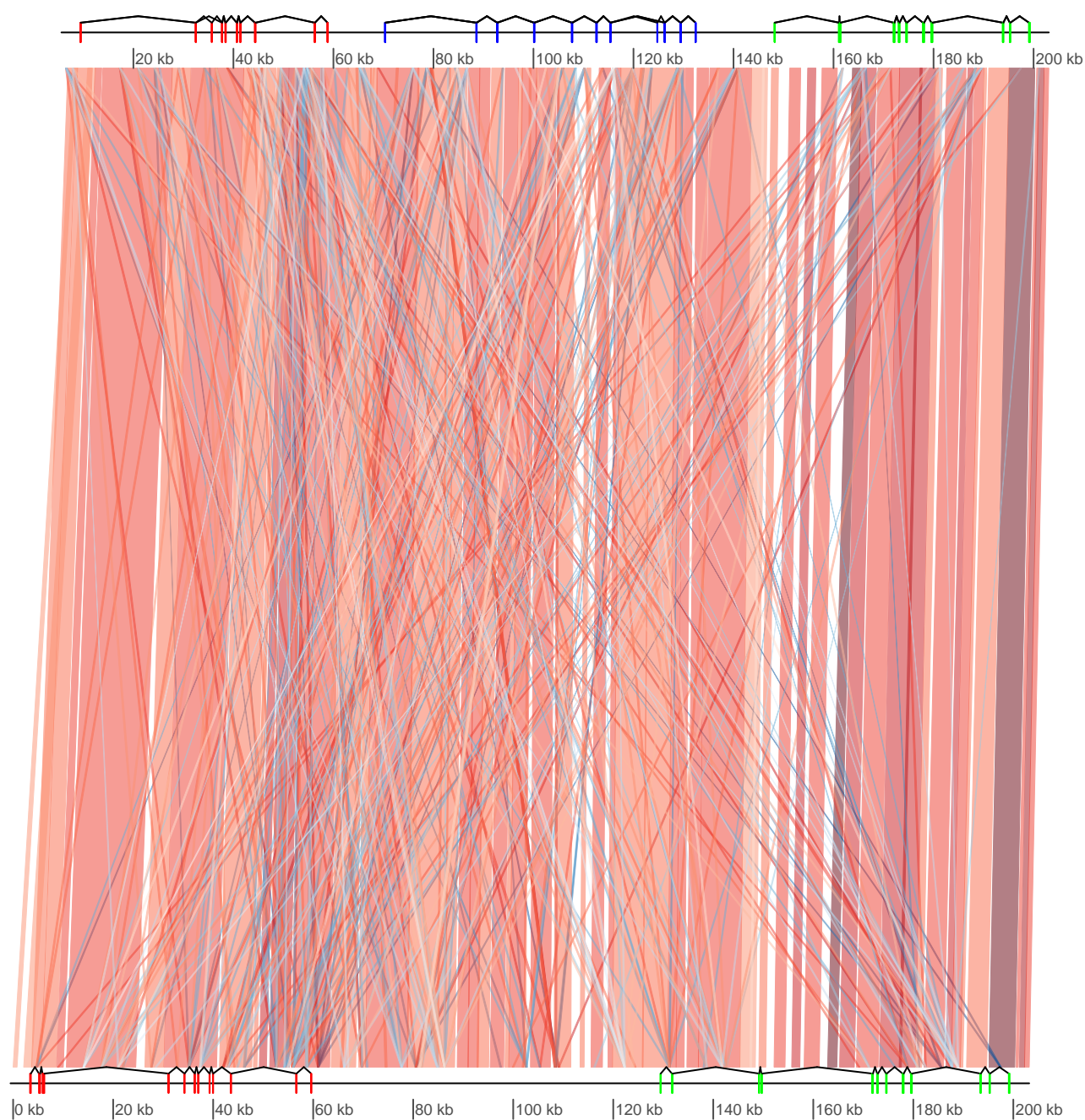
BH

BQ

help("barto")

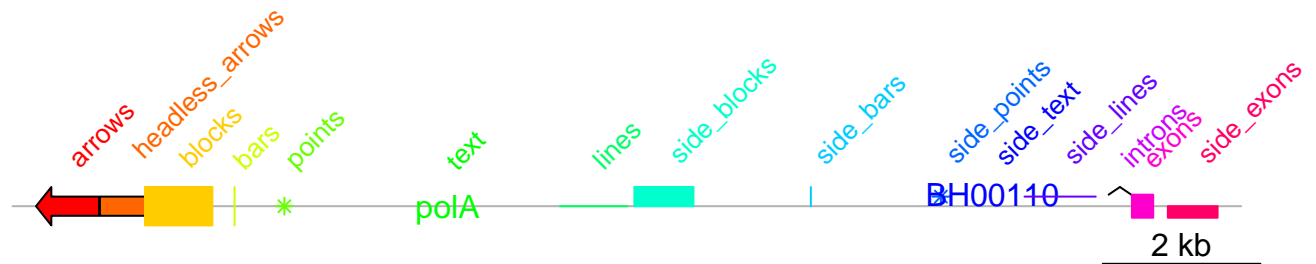
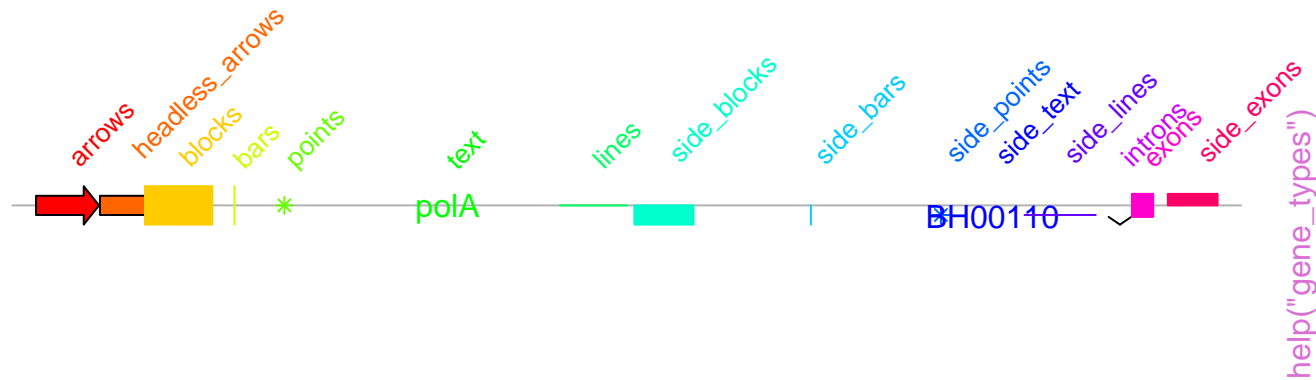
500 kb



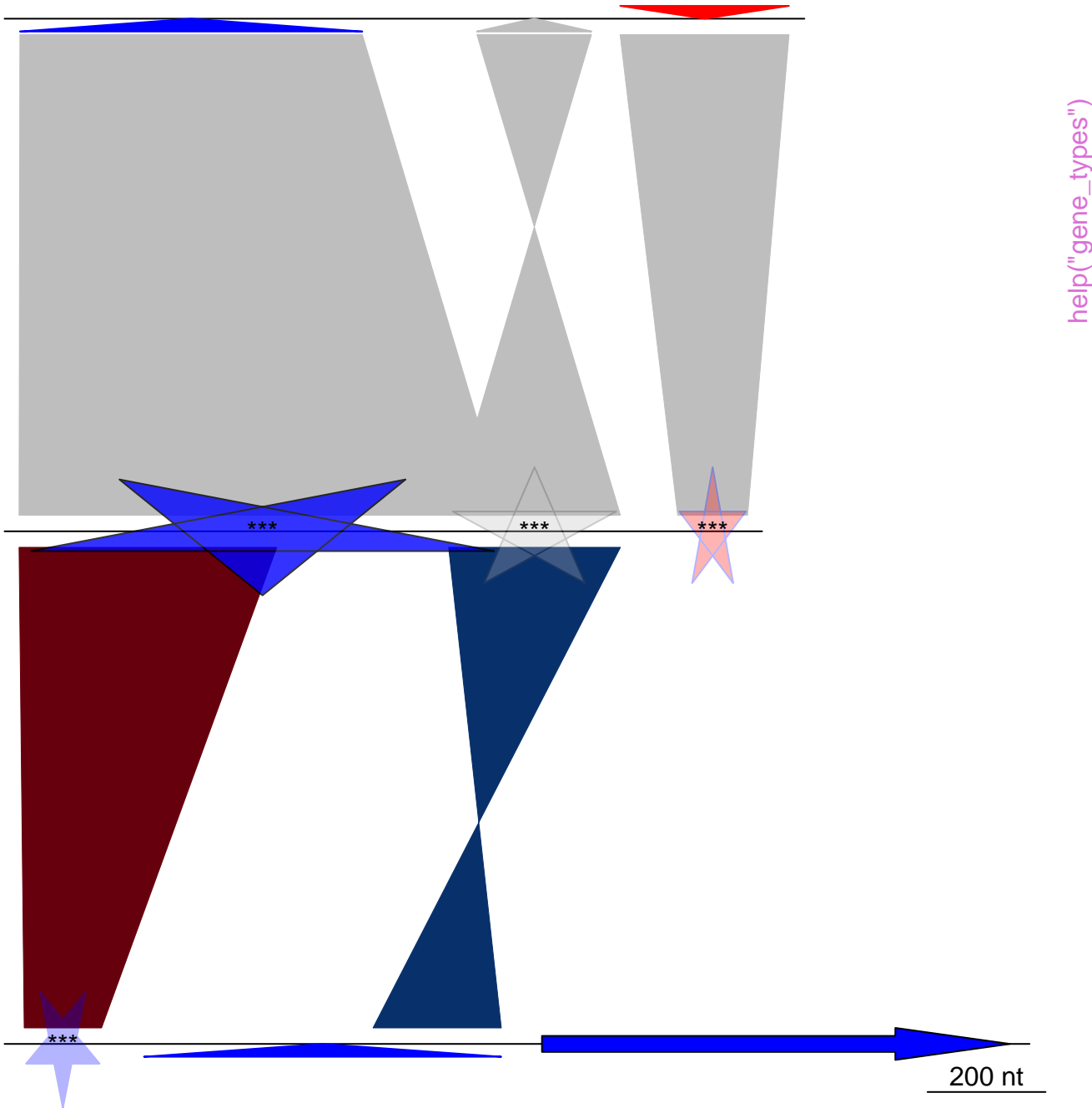


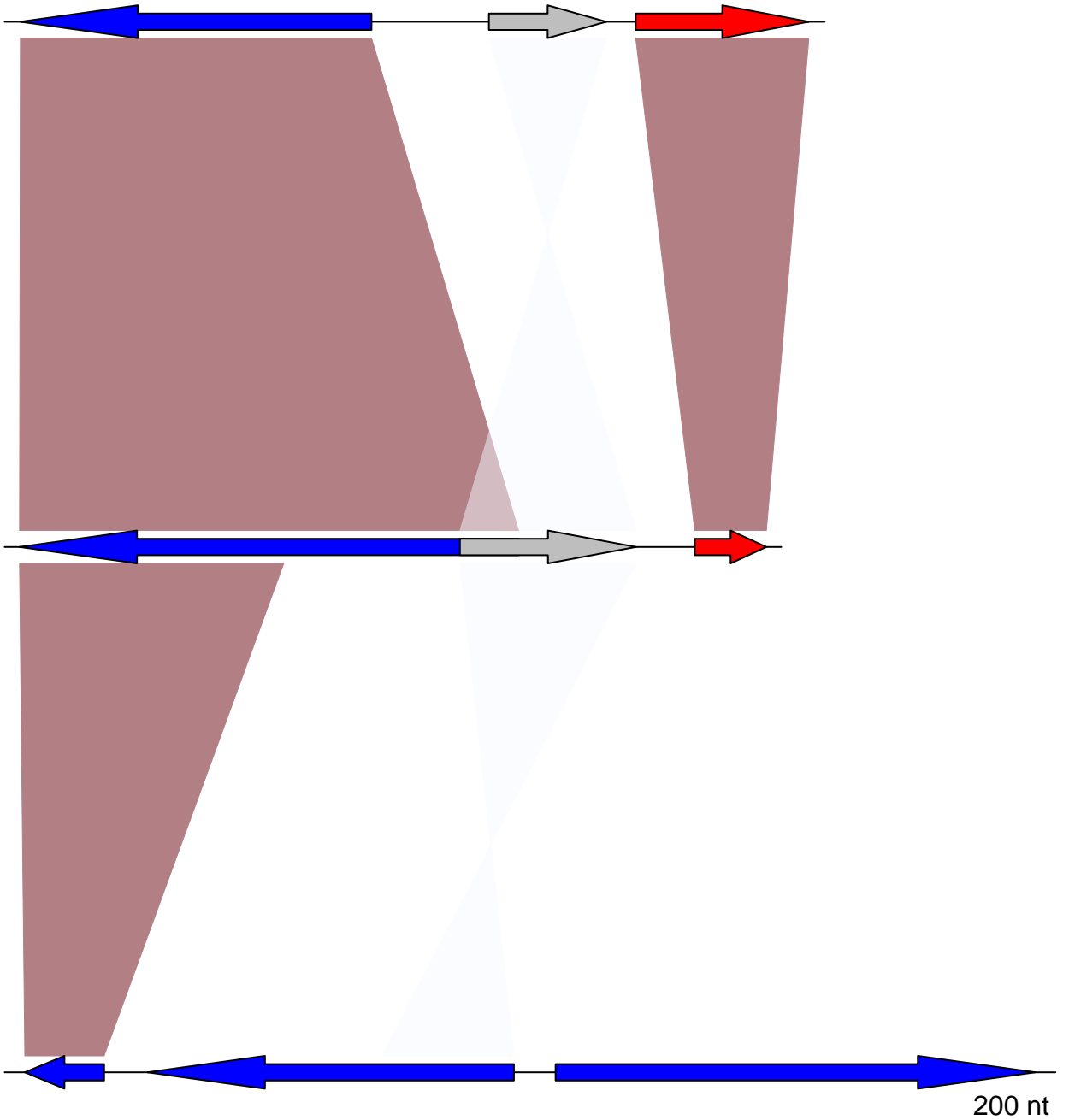
help("chrY\_subseg")











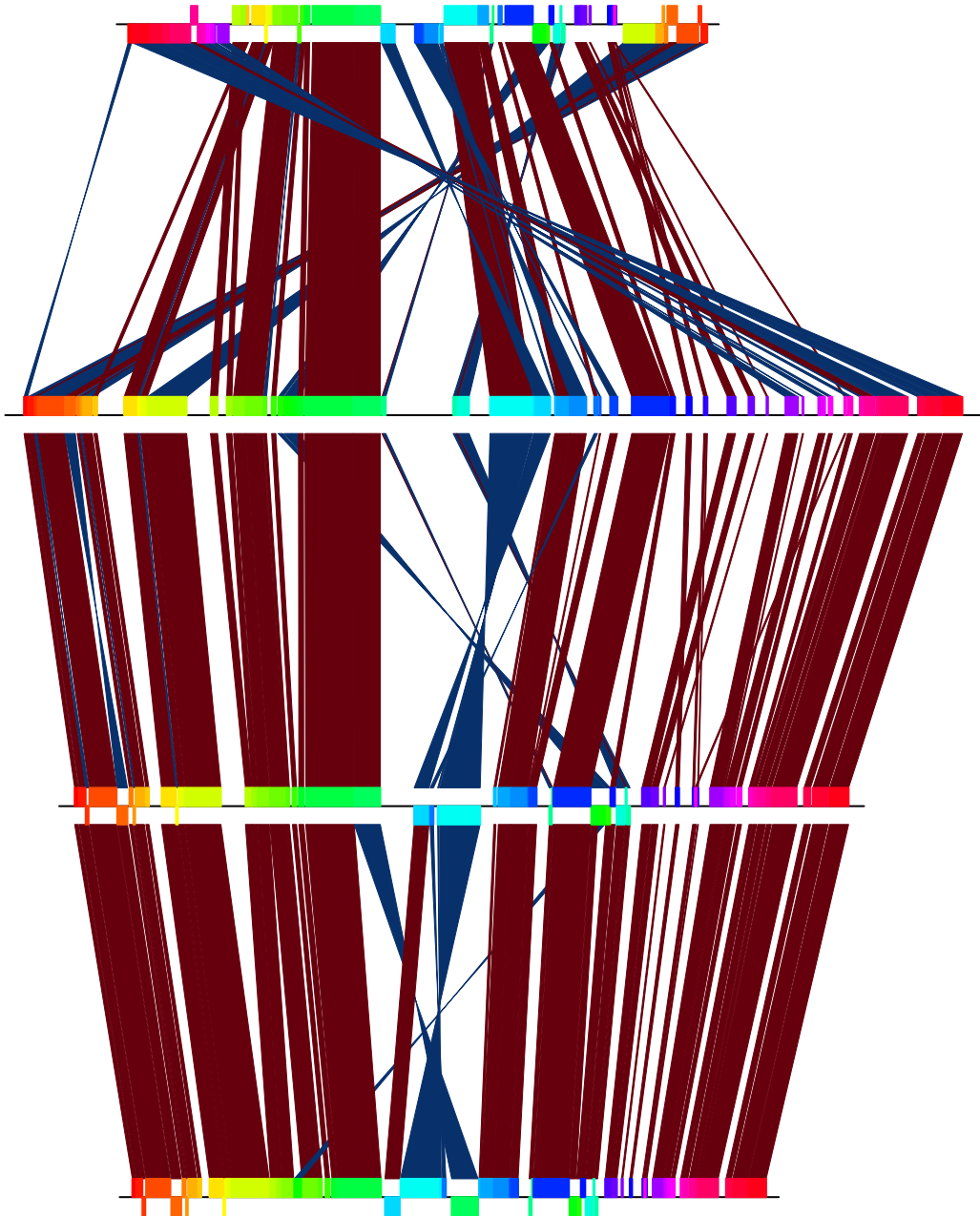
help("genoPlotR-package")

B\_bacilliformis

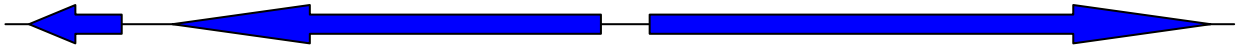
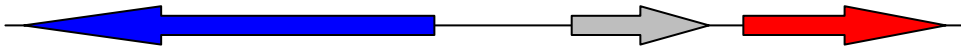
B\_grahamii

B\_henselae

B\_quintana

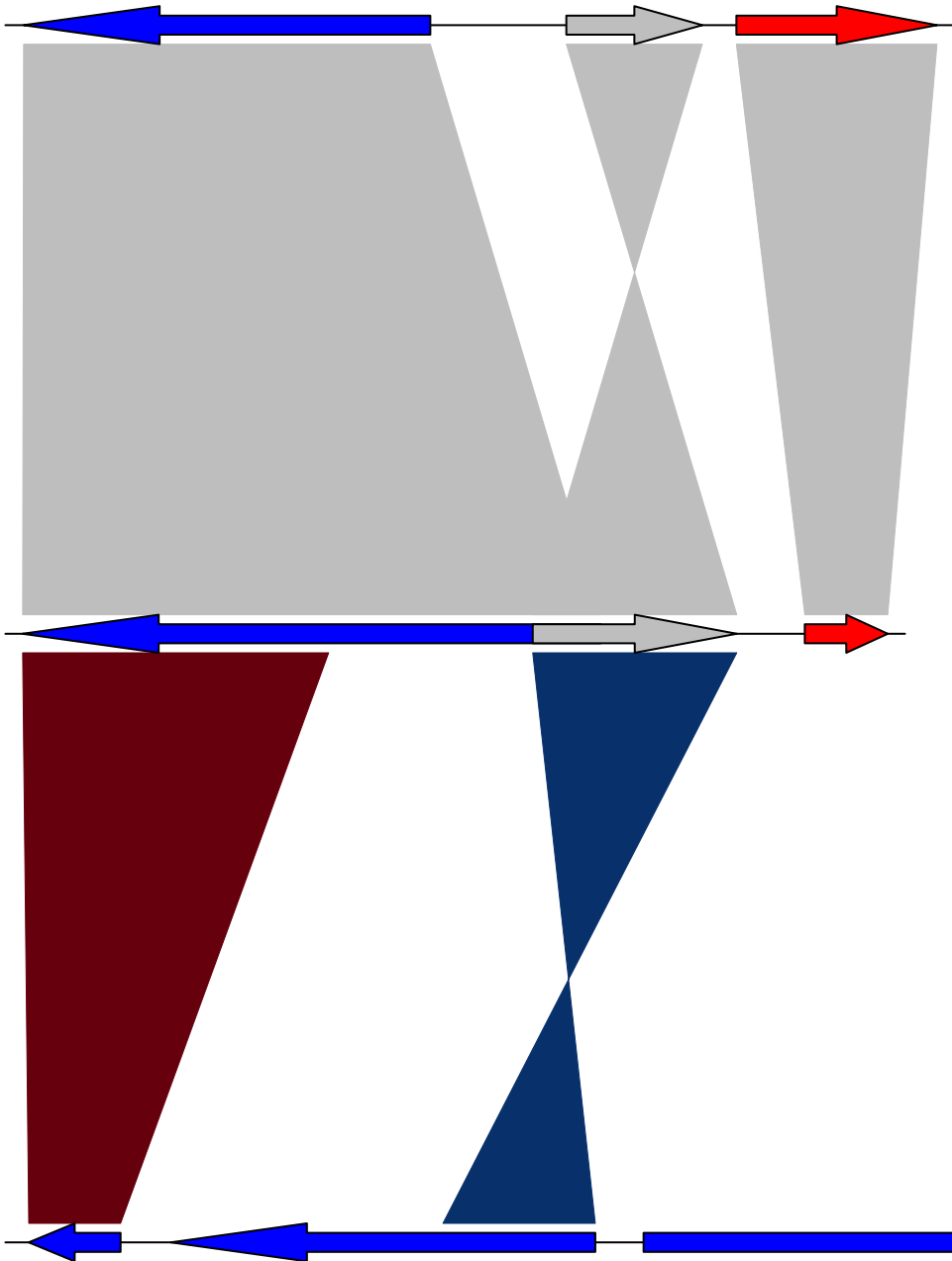


help("mauve.bbone")



200 nt

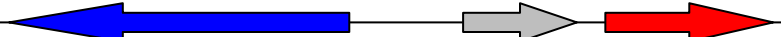
help("plot\_gene\_map")



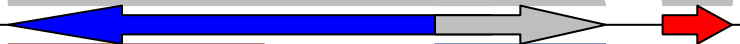
help("plot\_gene\_map")

200 nt

A aaa



B bbb

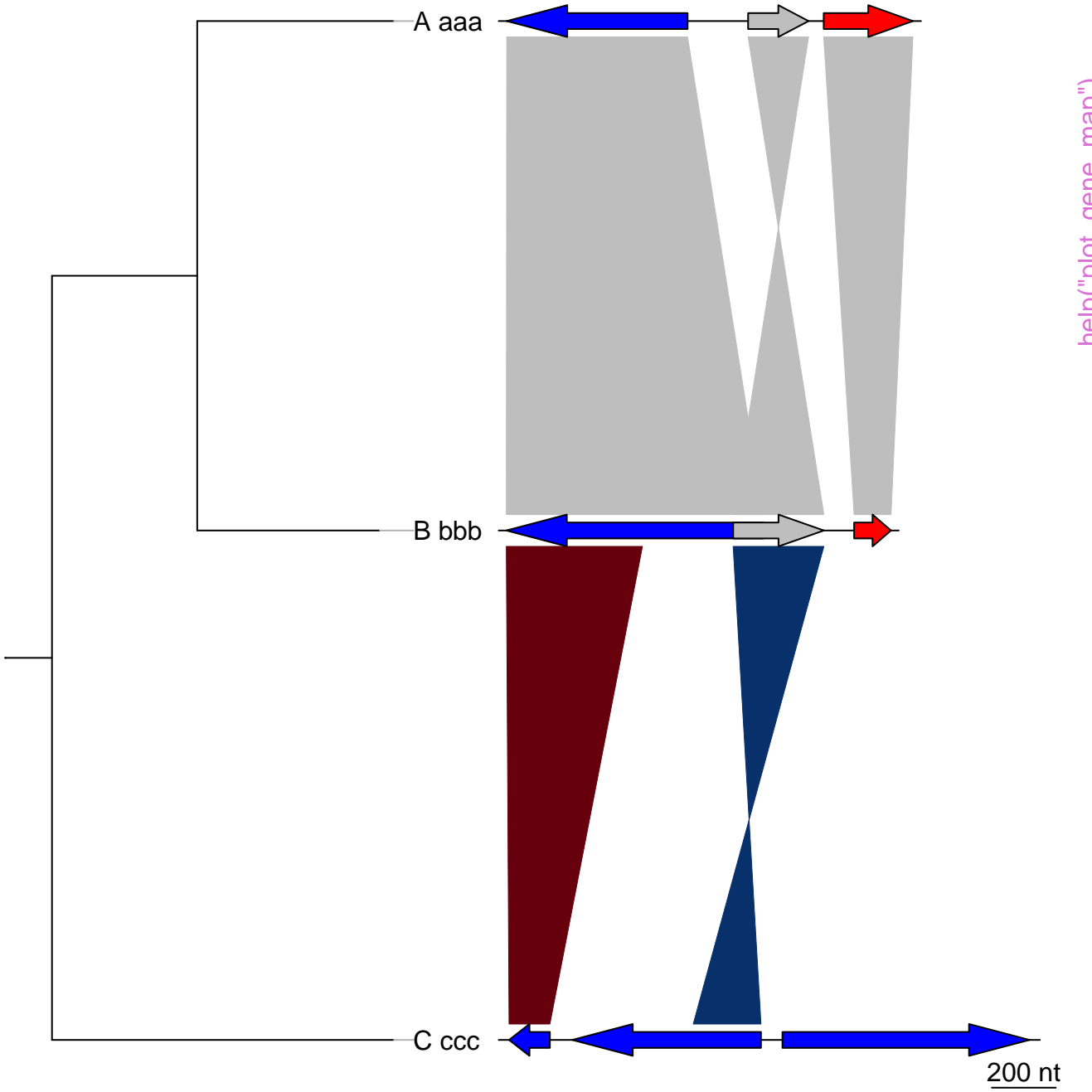


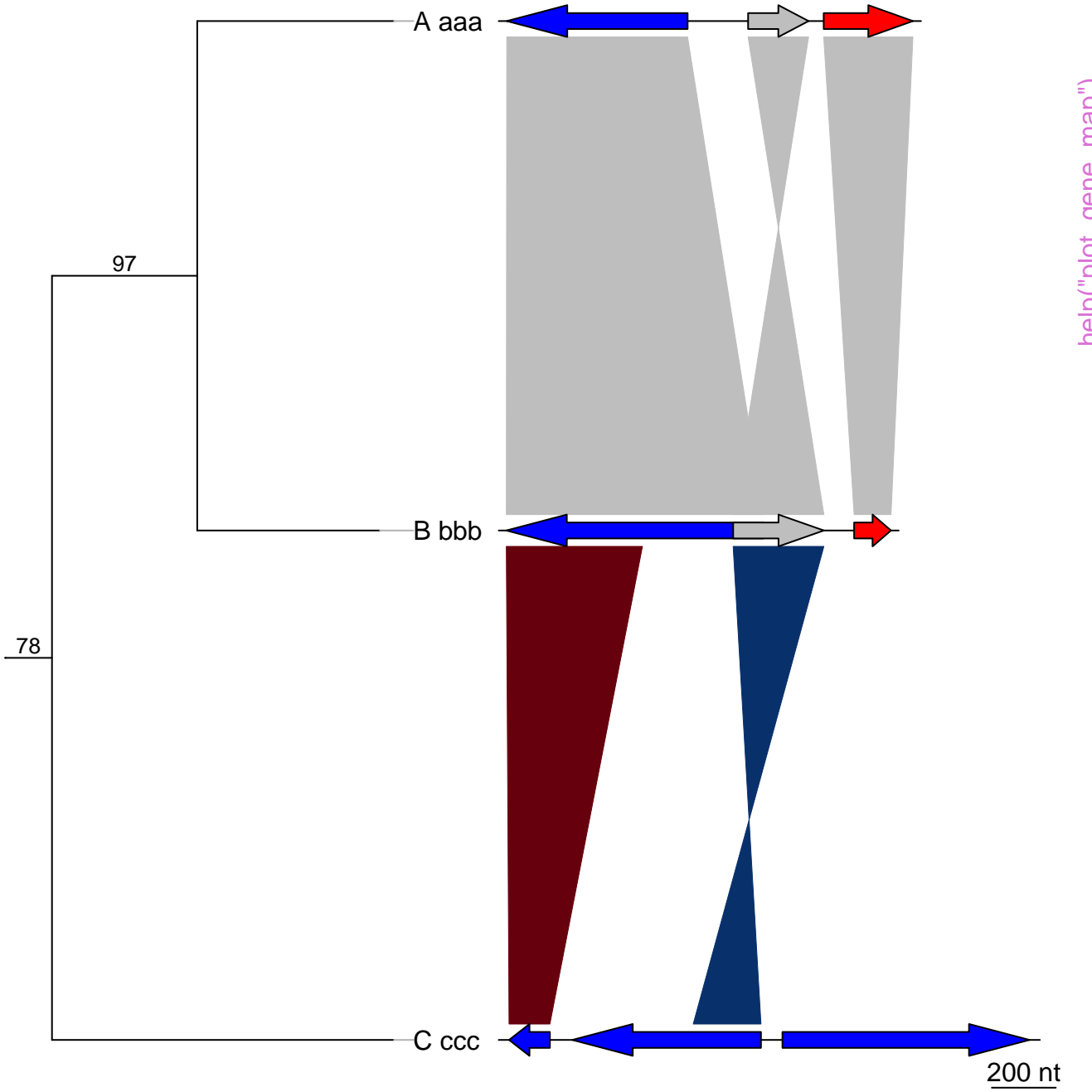
C ccc



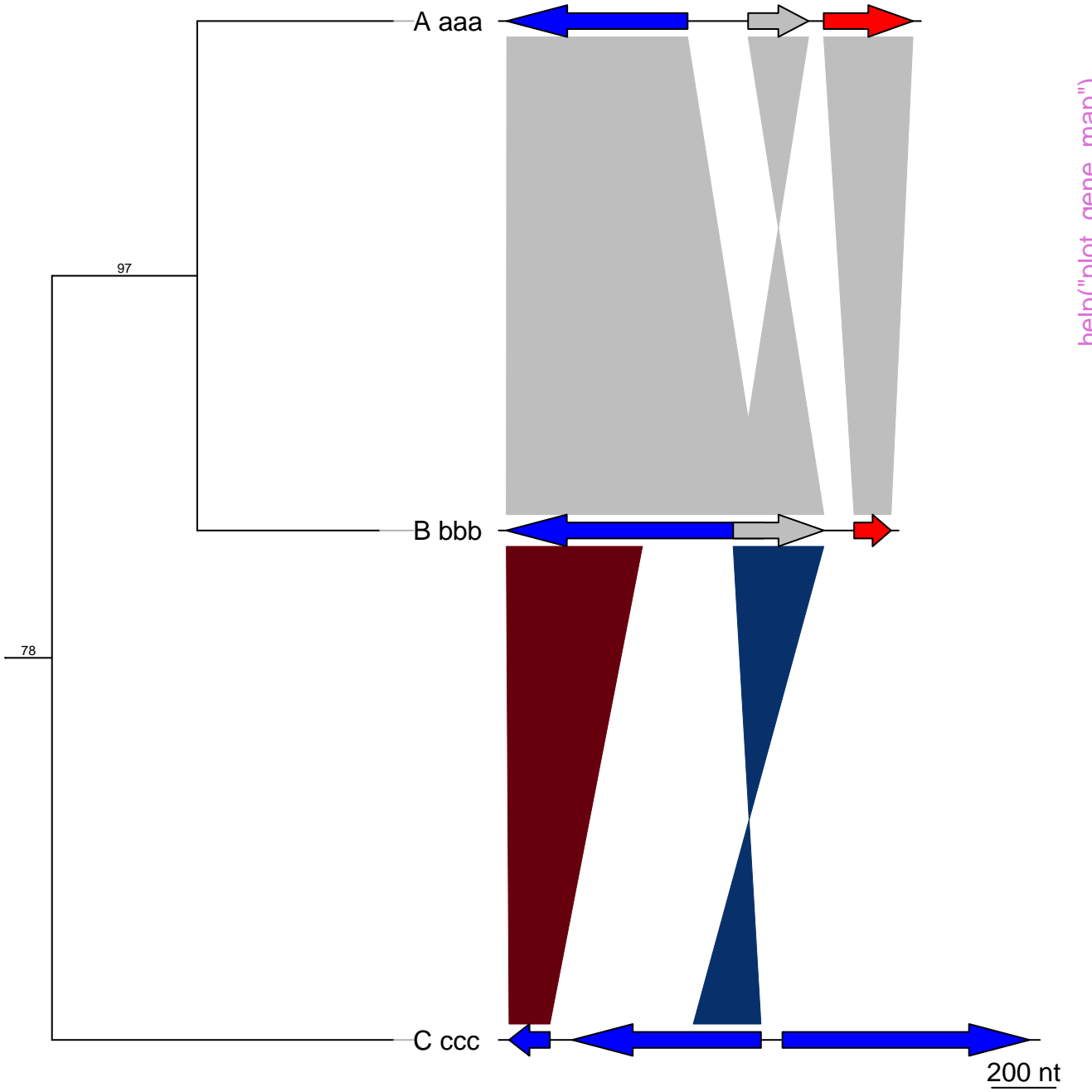
200 nt

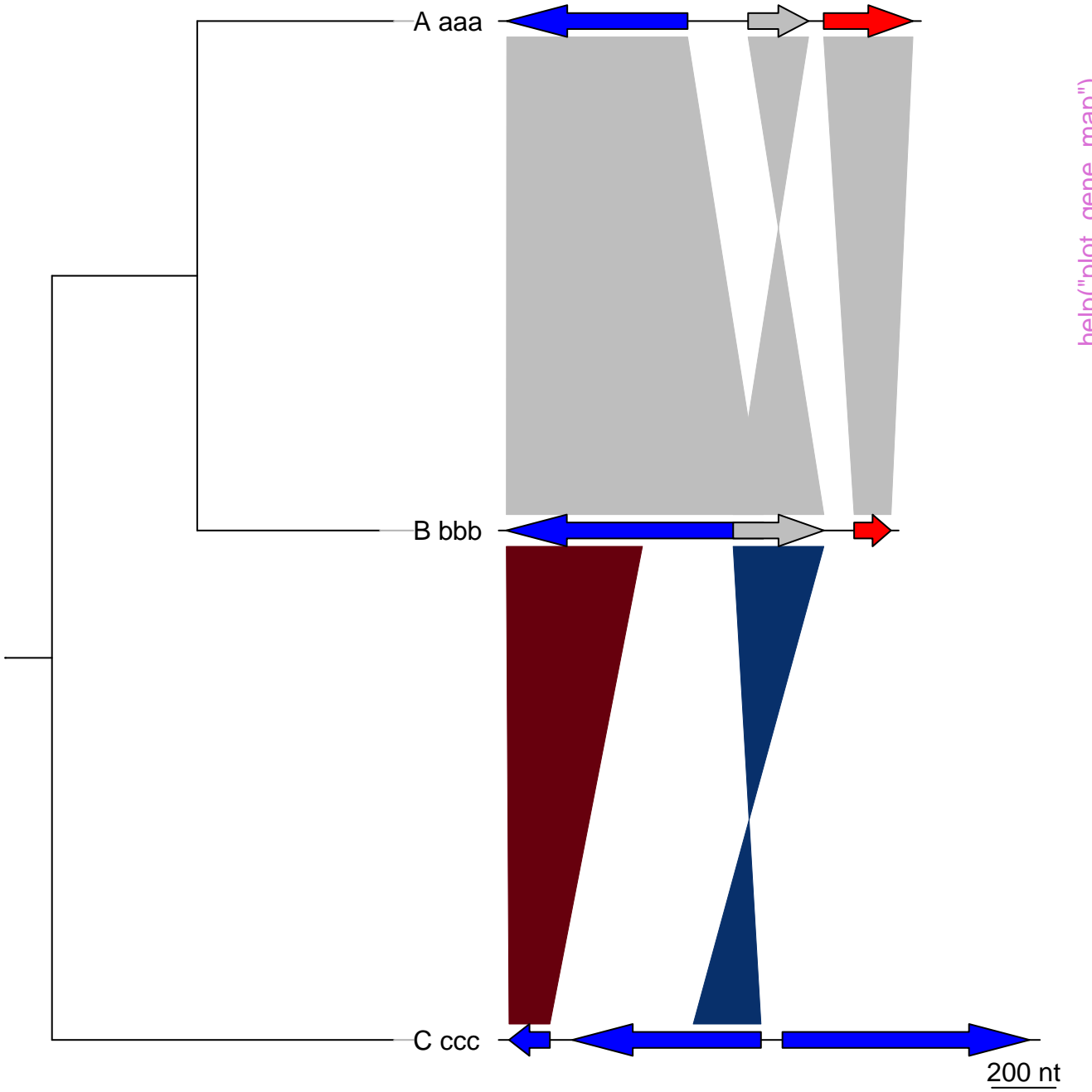
help("plot\_gene\_map")

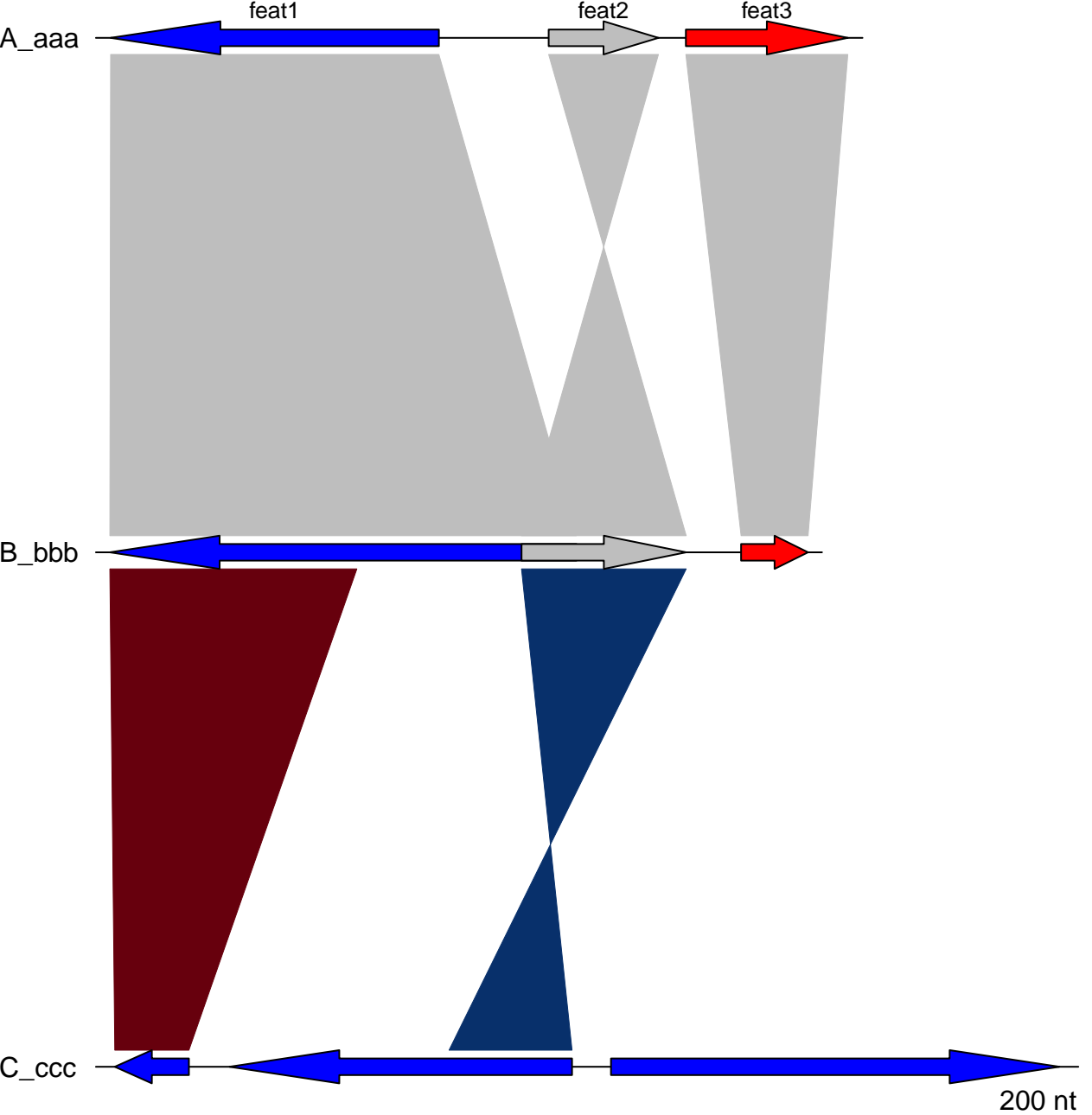




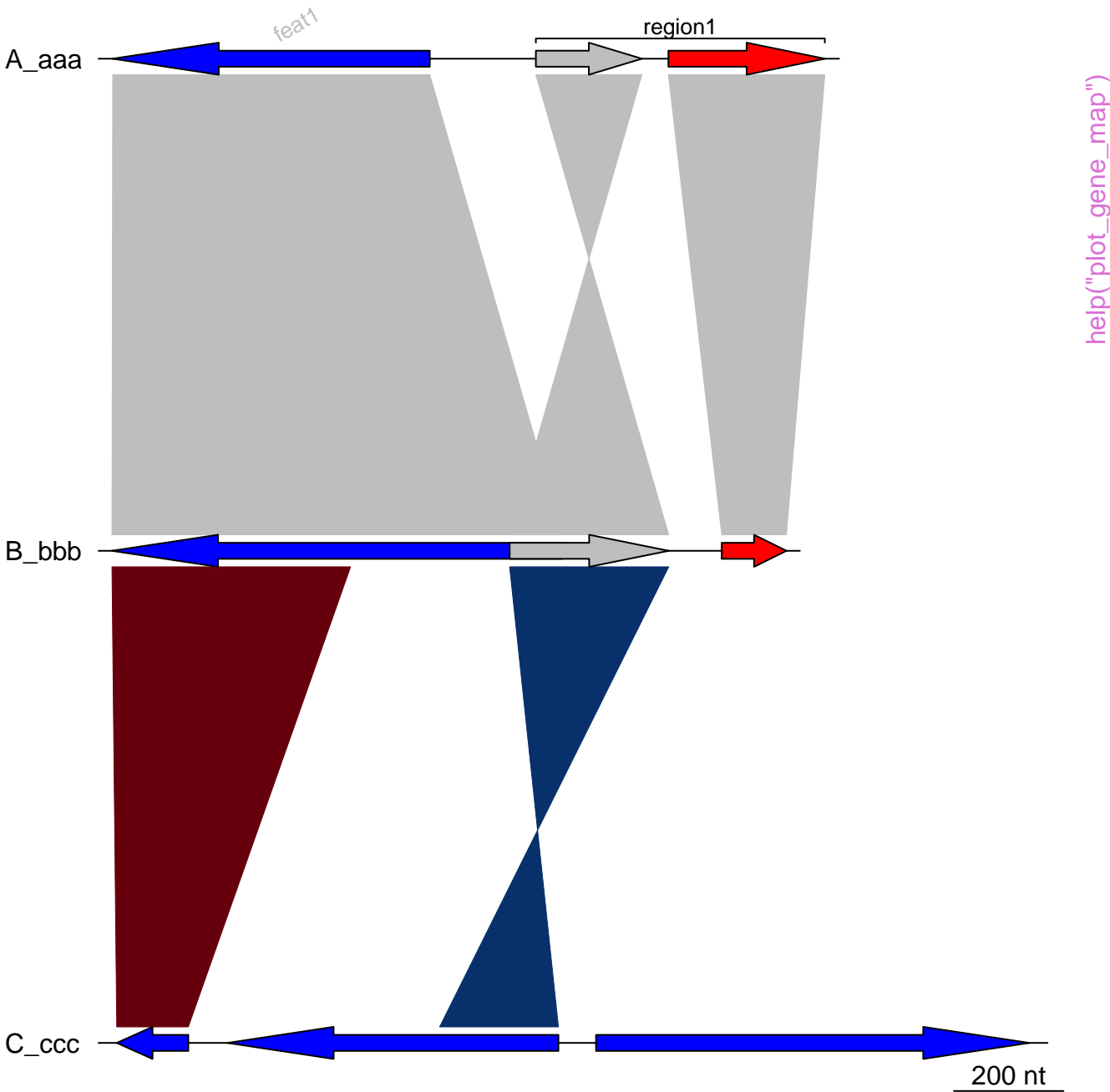


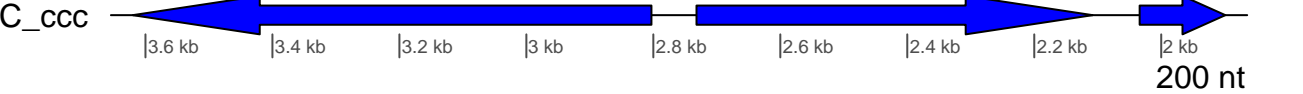
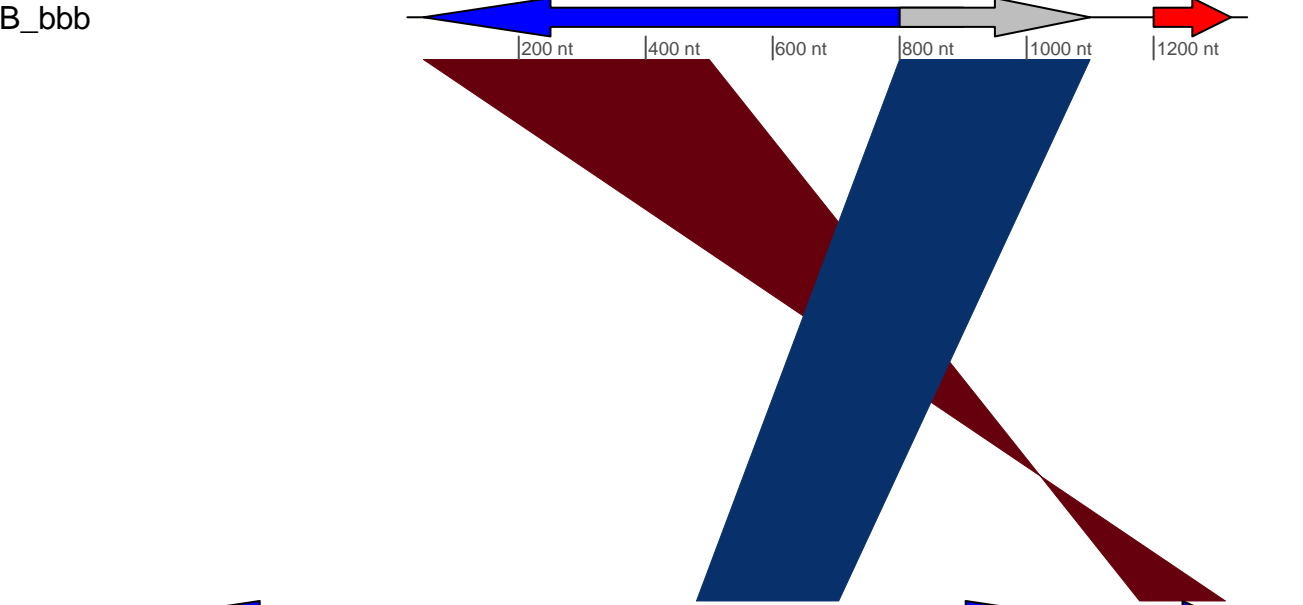
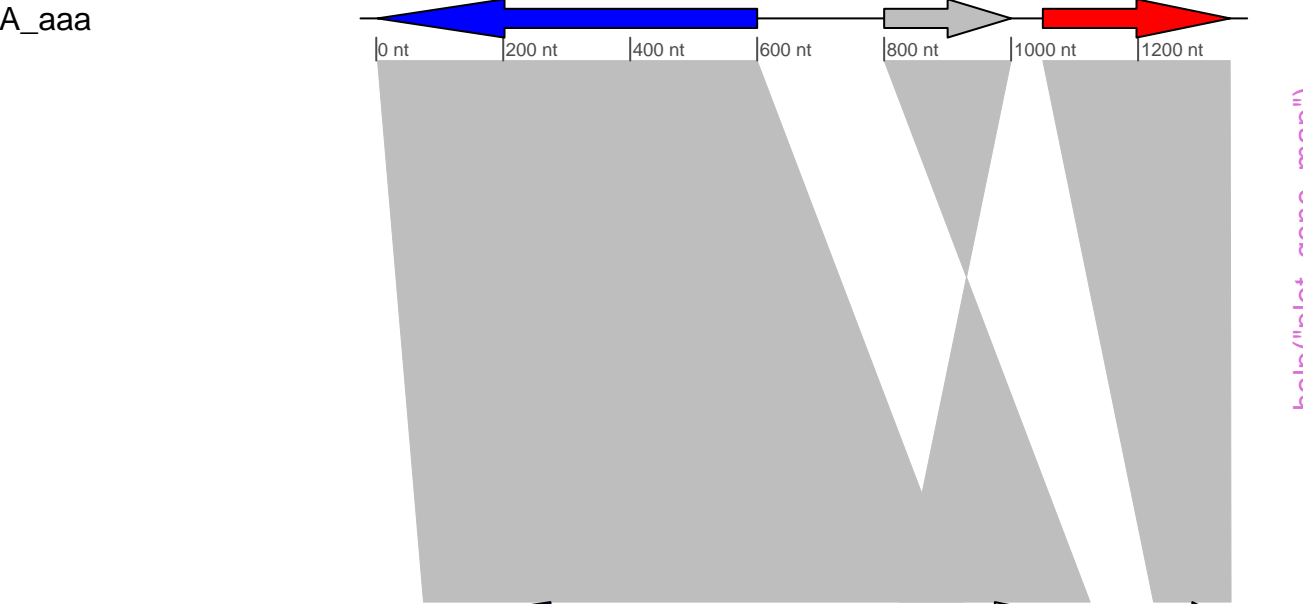


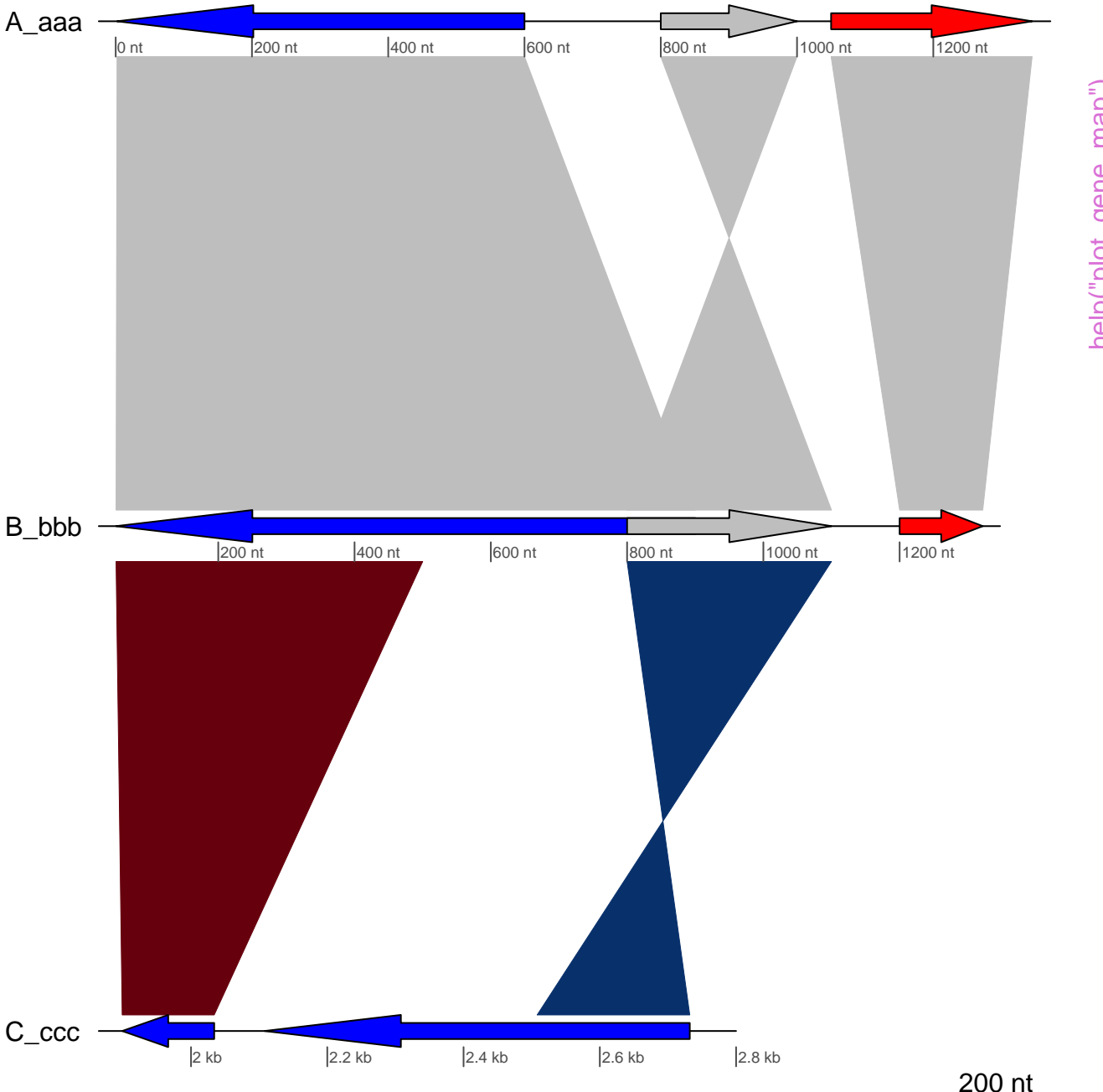




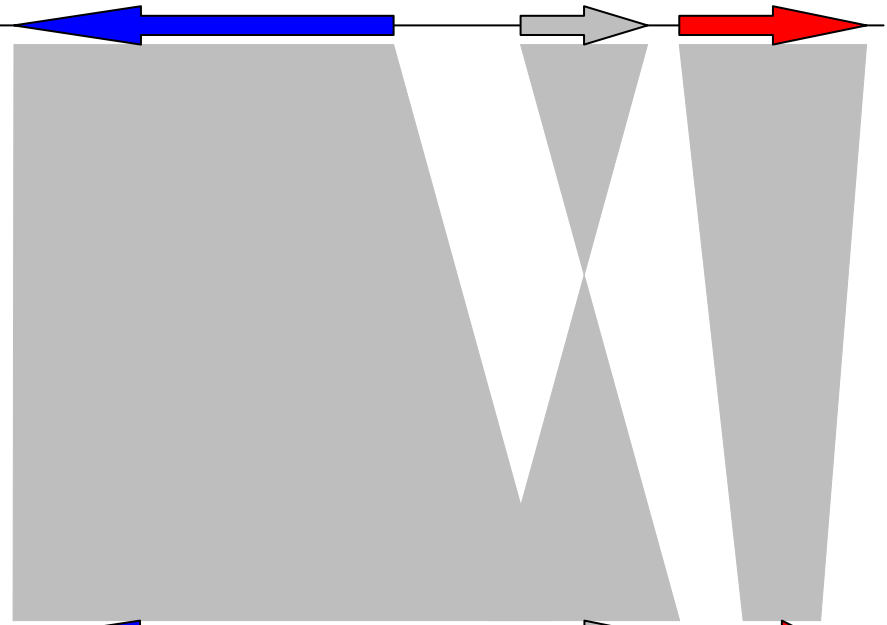
help("plot\_gene\_map")



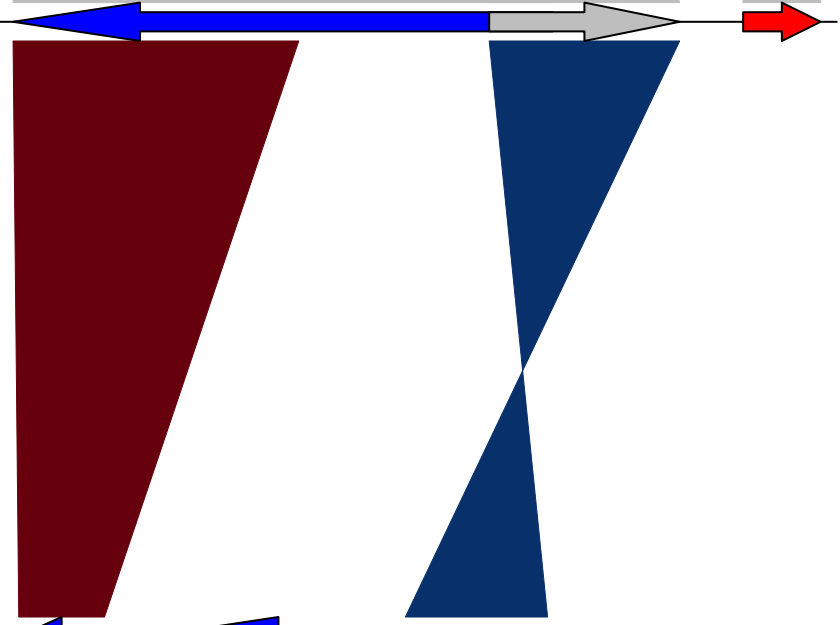




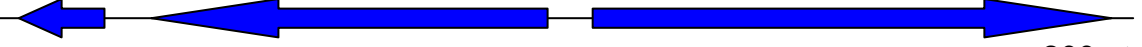
A\_aaa



B\_bbb

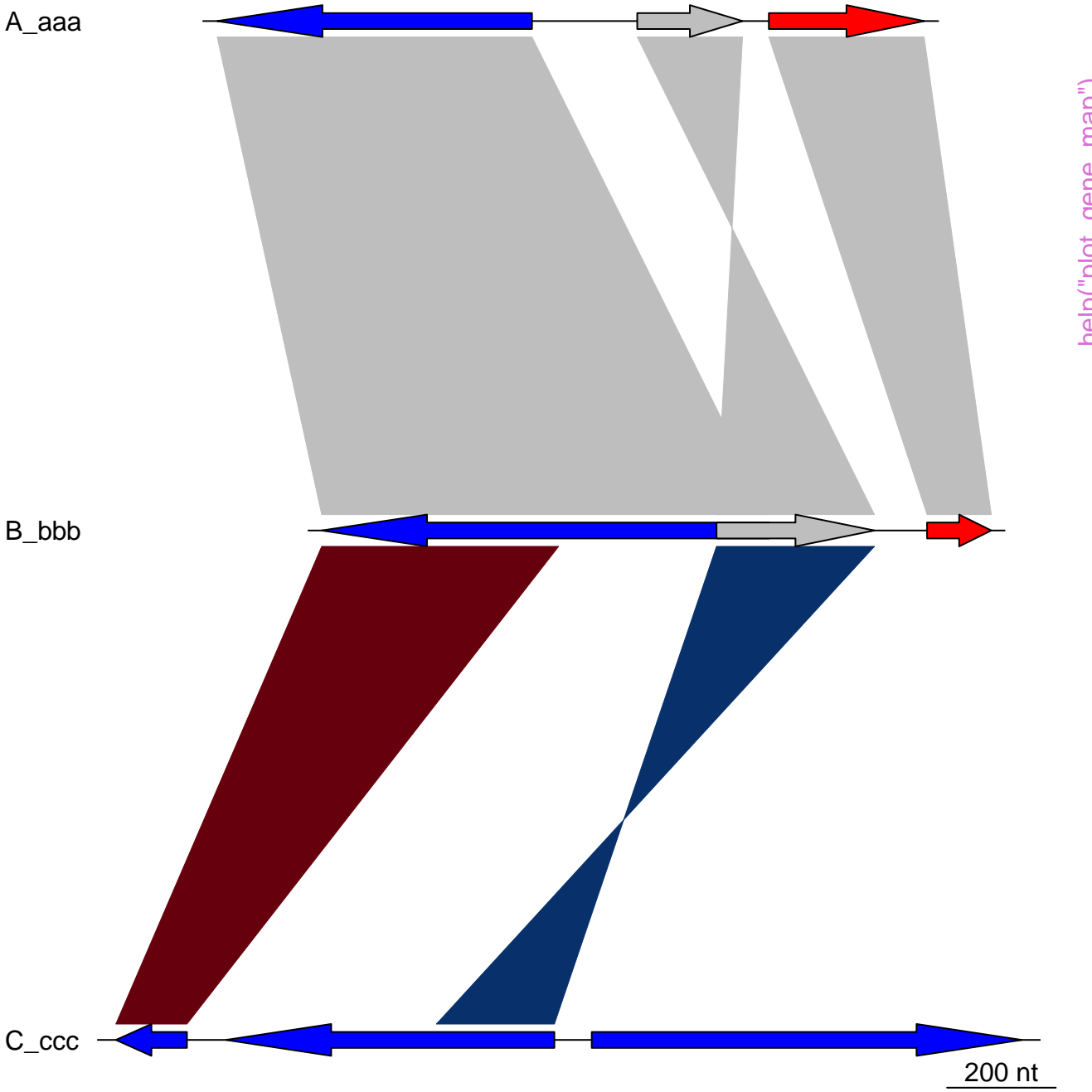


C\_ccc



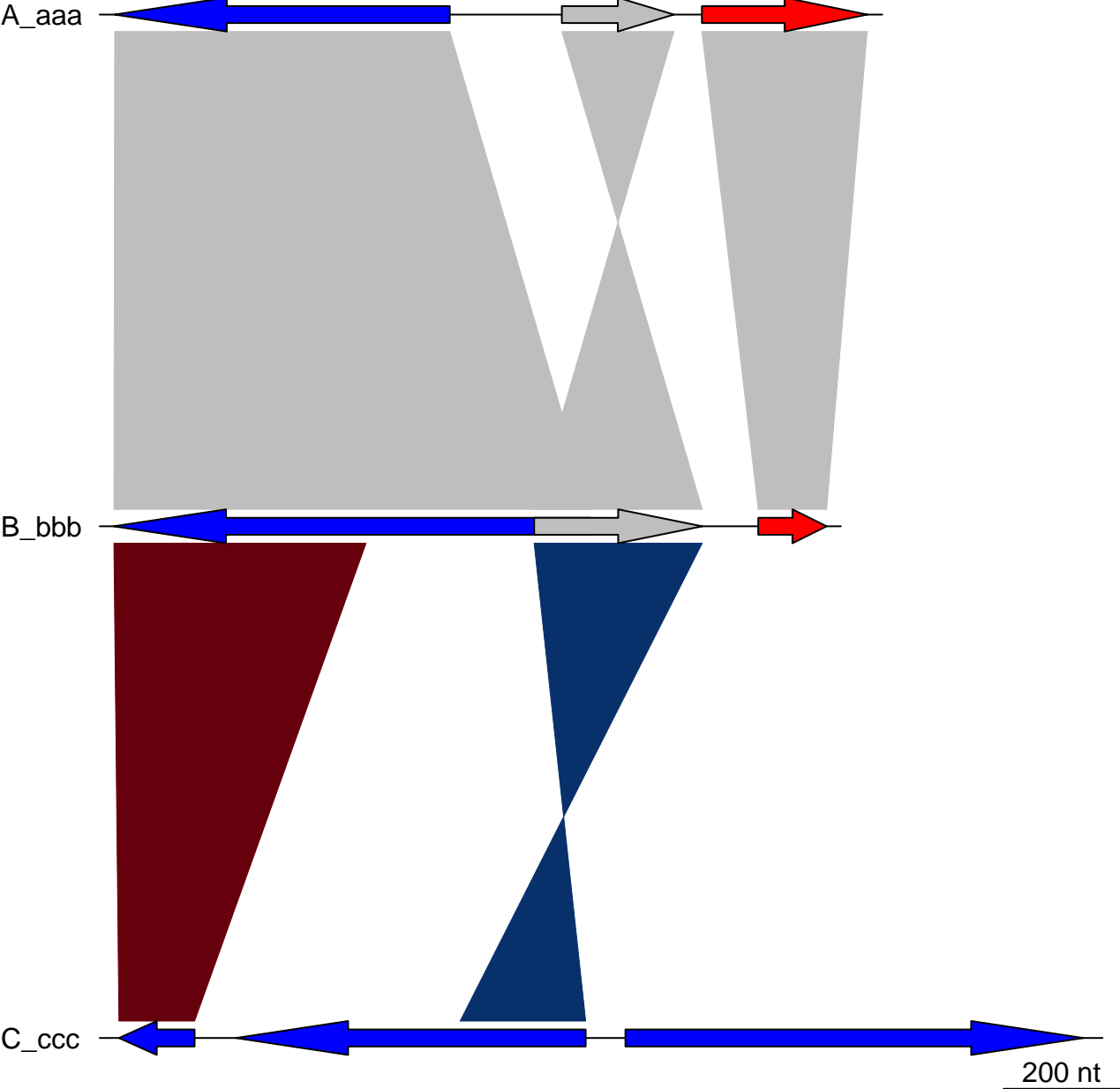
200 nt

help("plot\_gene\_map")

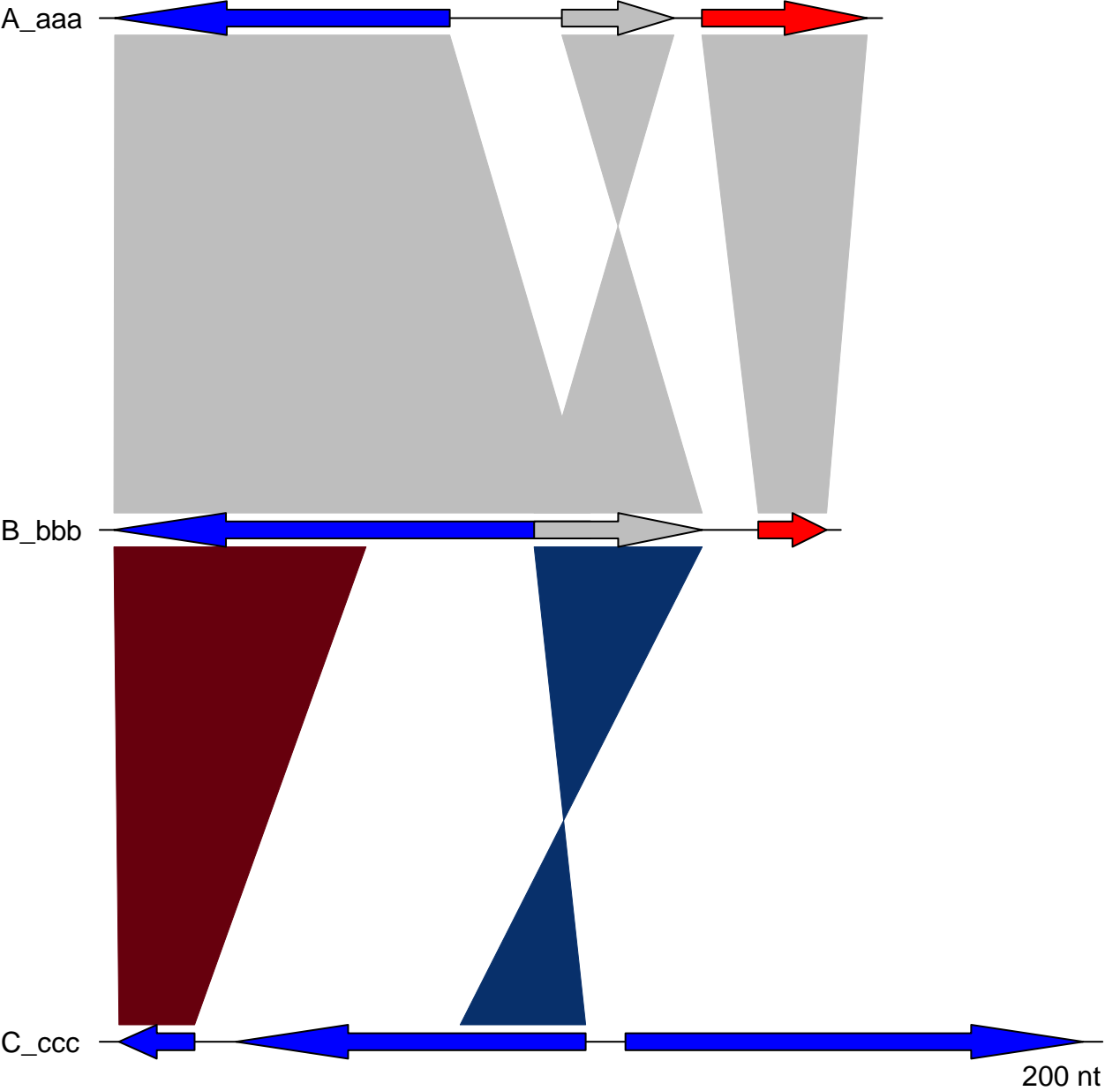




Comparison of A, B and C

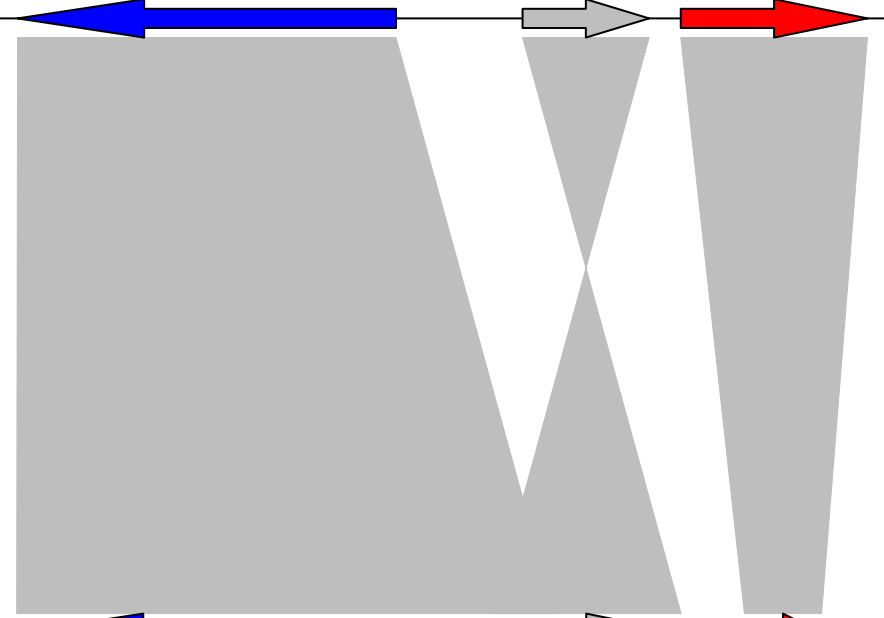


Comparison of A, B and C

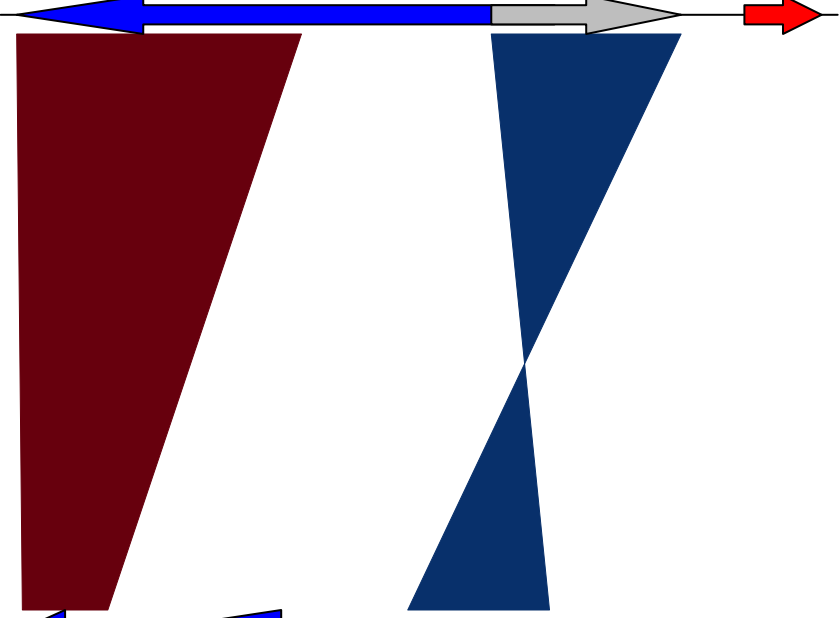


help("plot\_gene\_map")

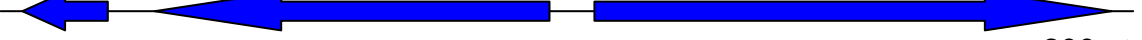
Huey



Dewey



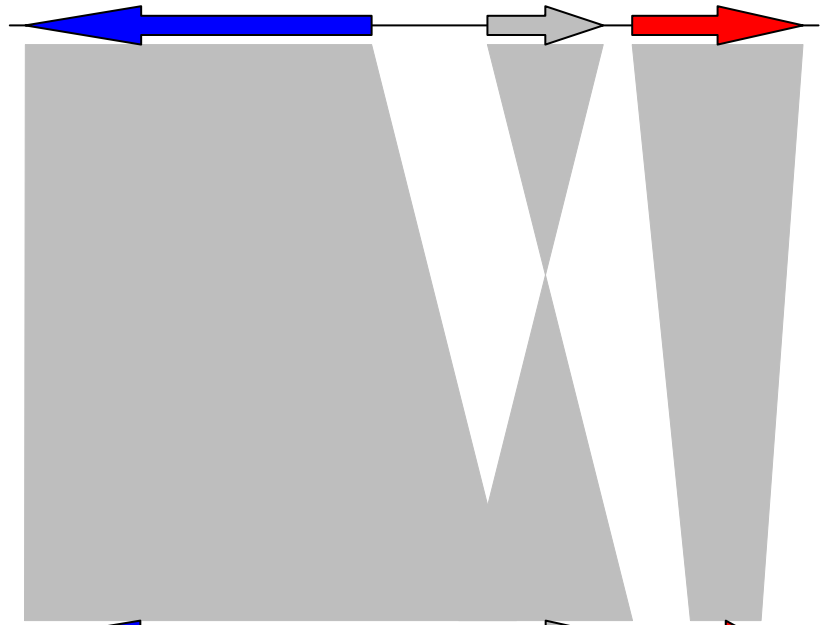
Louie



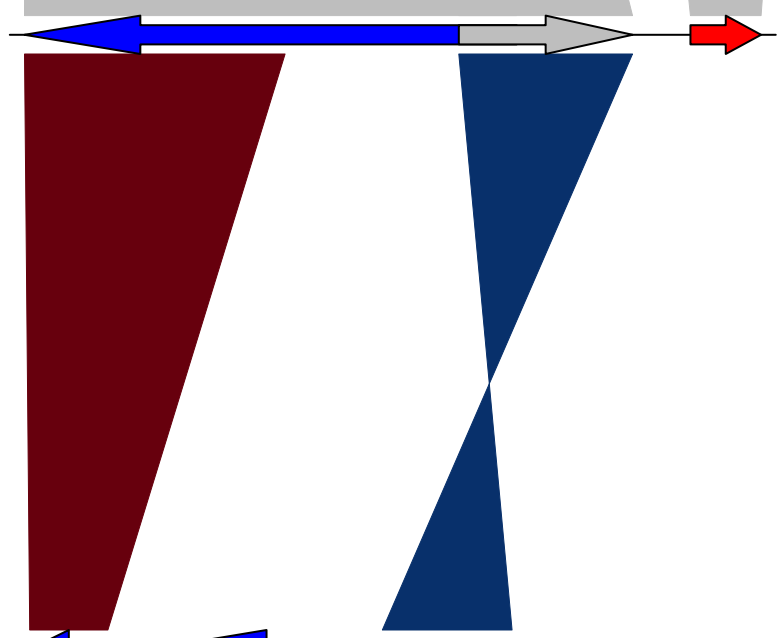
200 nt

help("plot\_gene\_map")

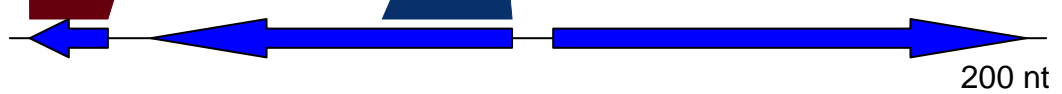
Huey



Dewey

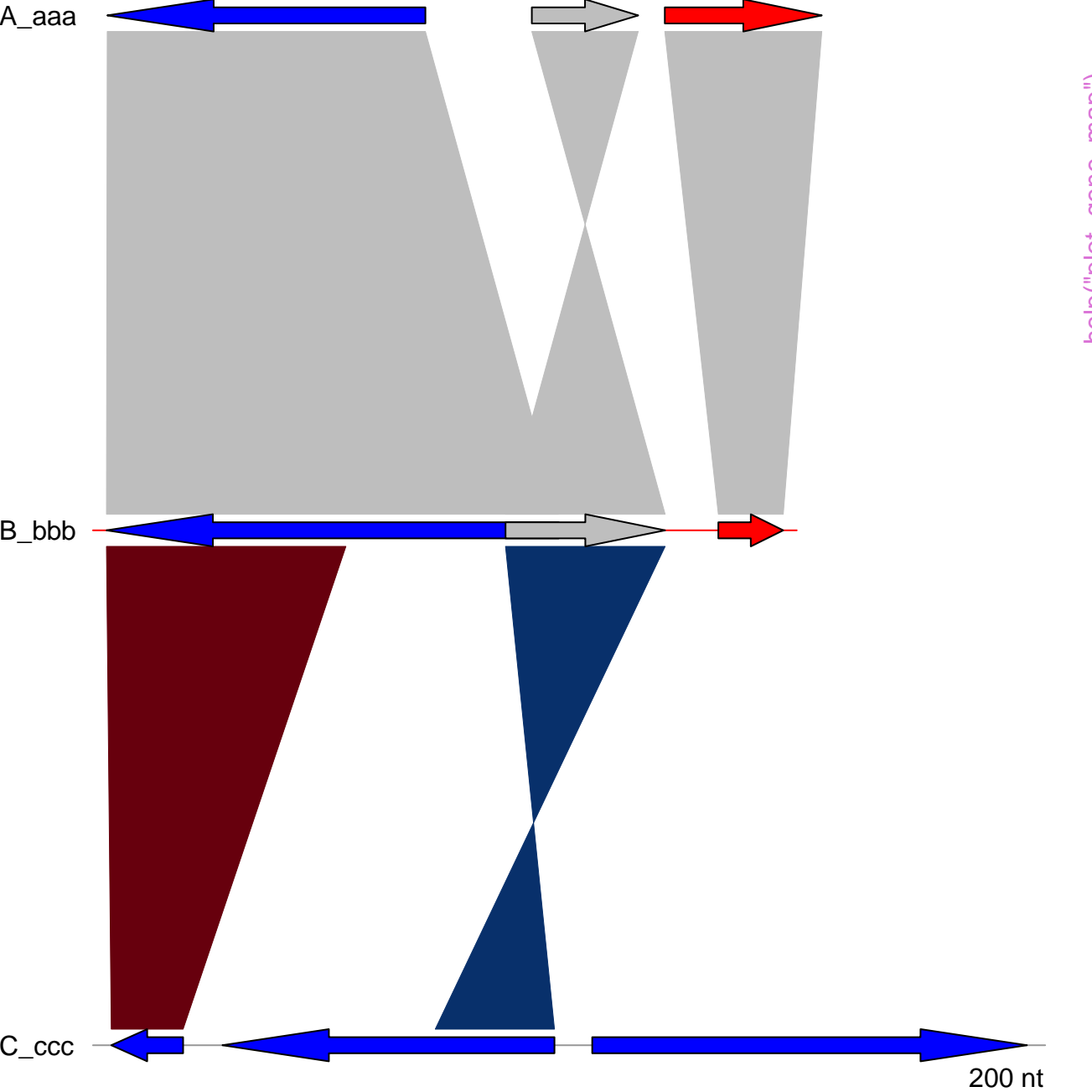


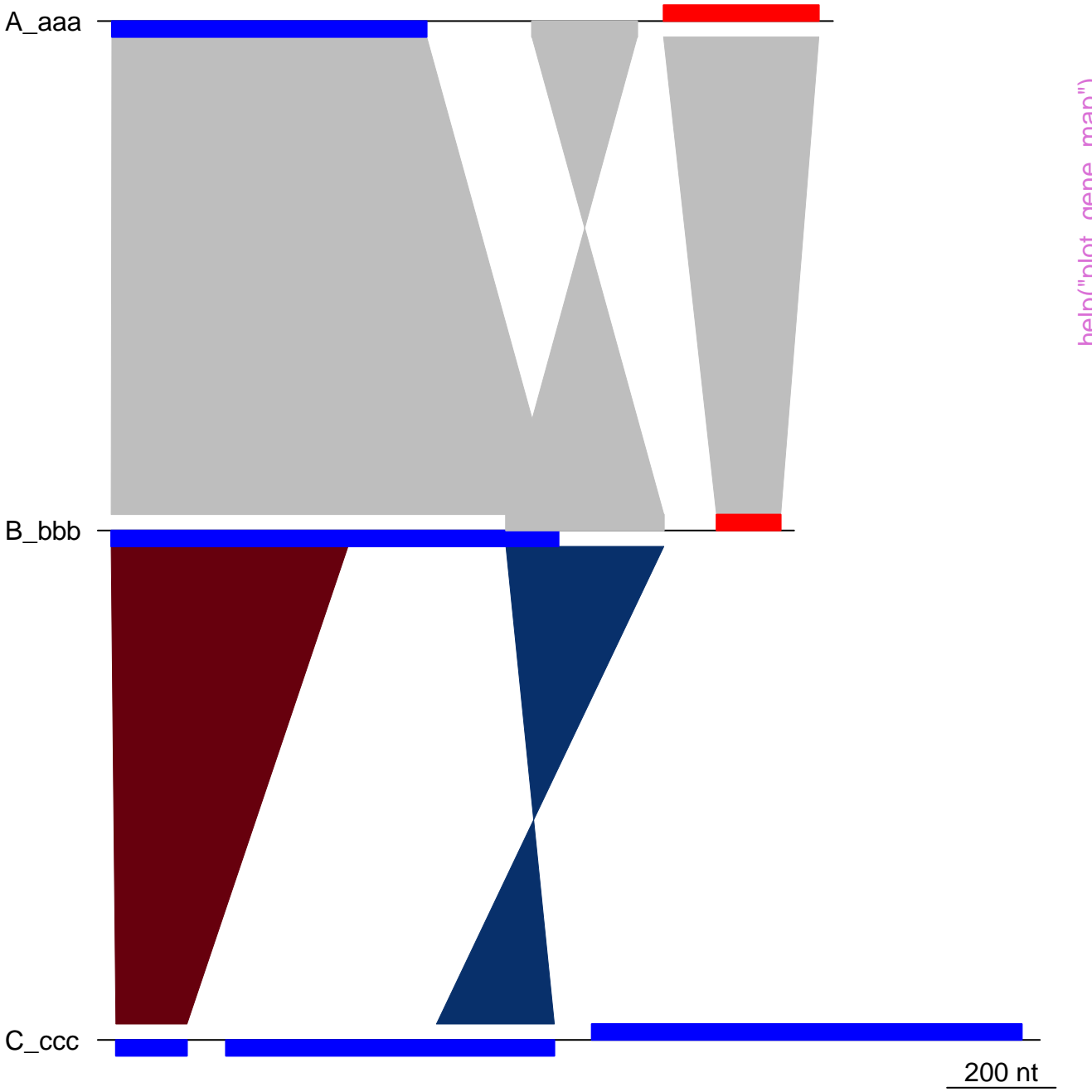
Louie



200 nt

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

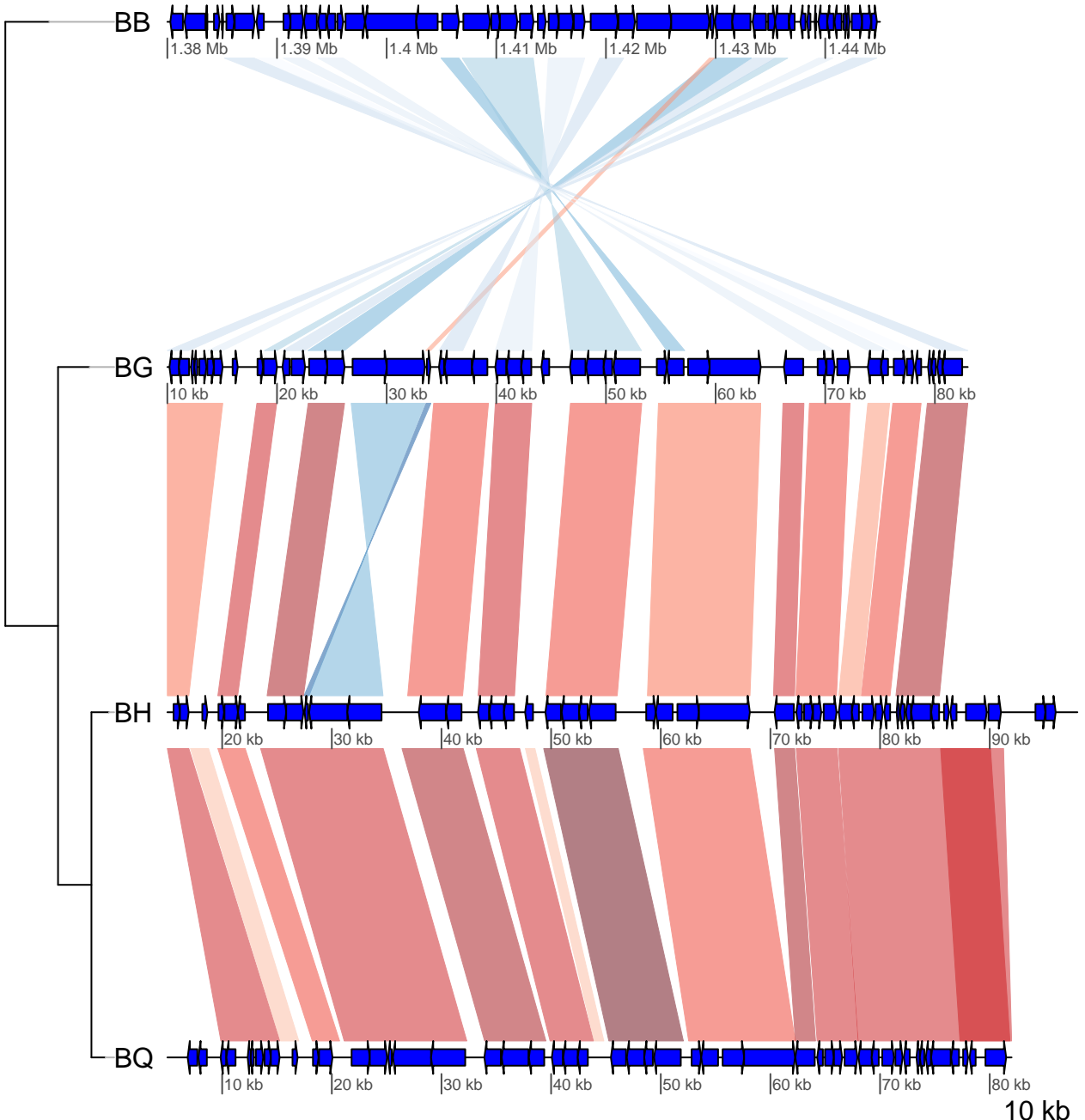
BG 10 kb 20 kb 30 kb 40 kb 50 kb 60 kb 70 kb 80 kb

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

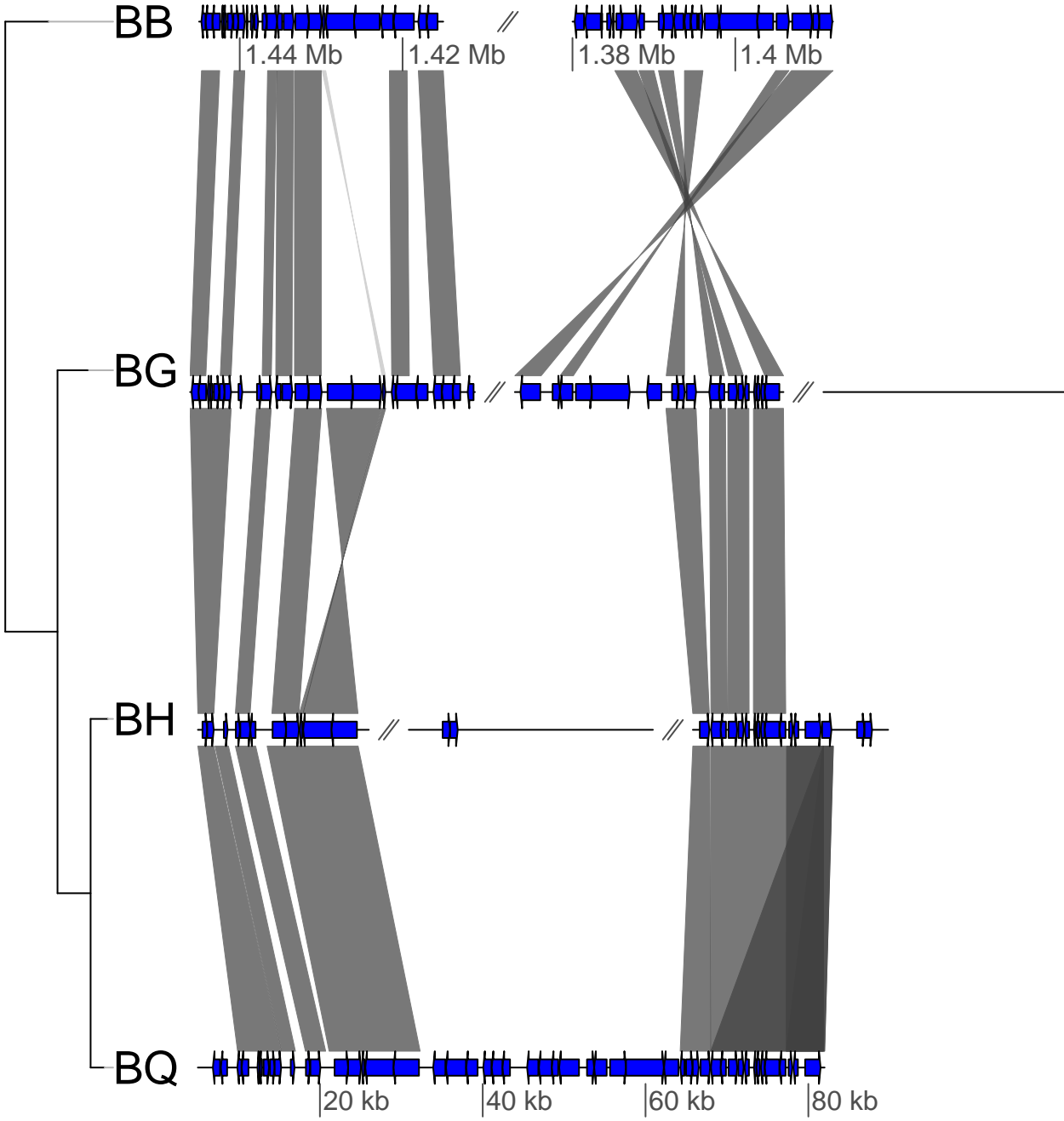
20 kb

40 kb

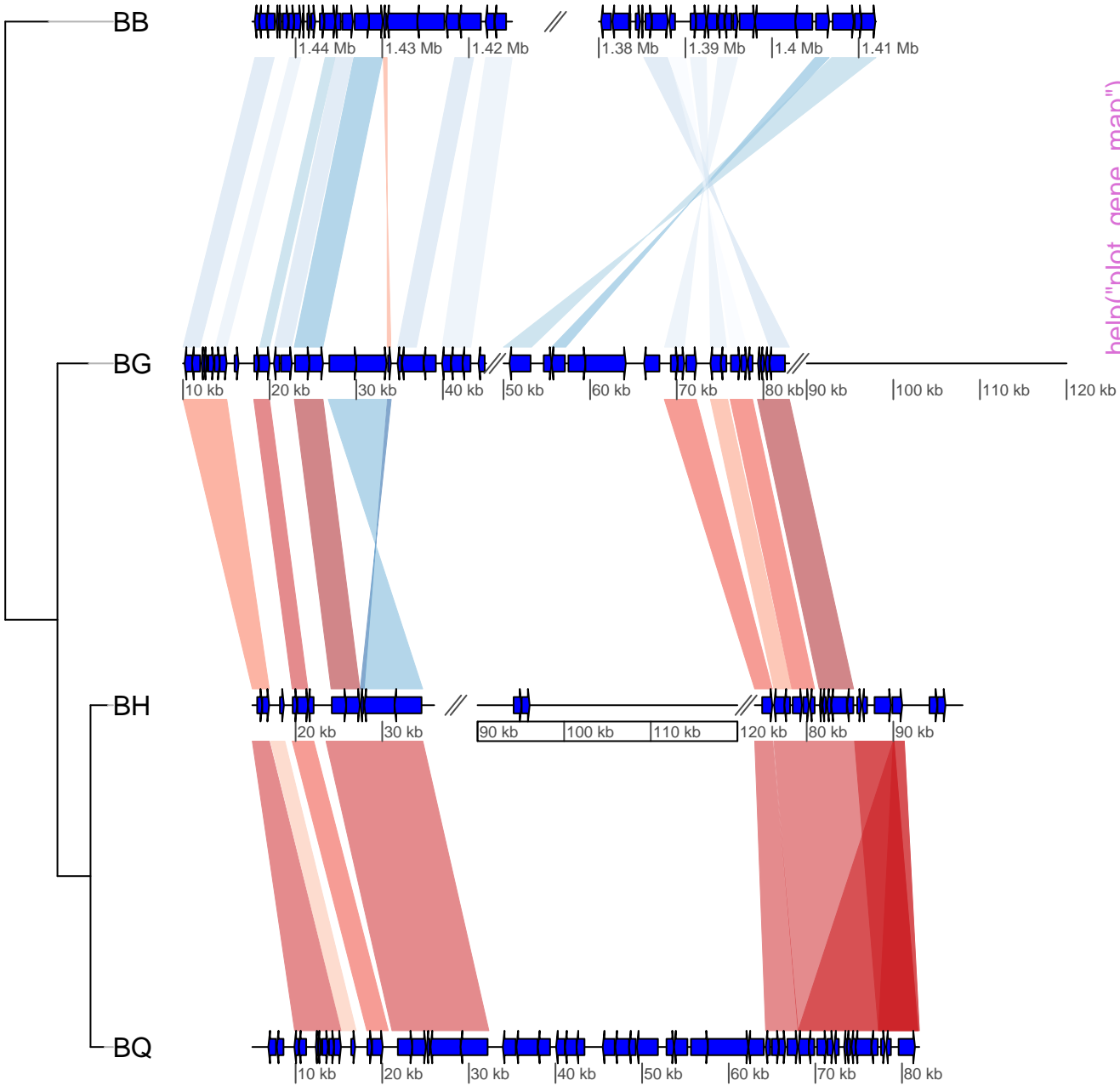
60 kb

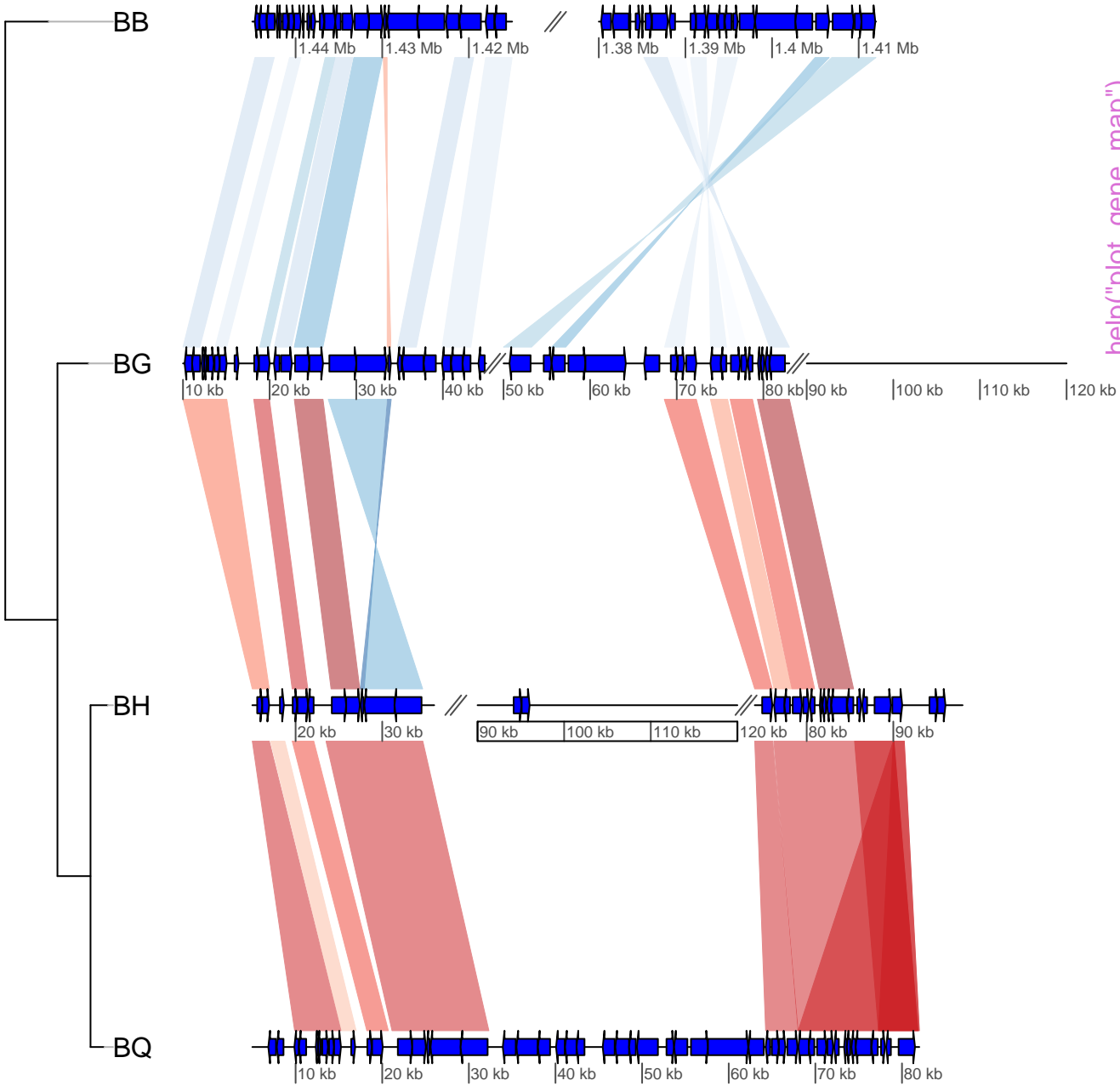
80 kb

help("plot\_gene\_map")

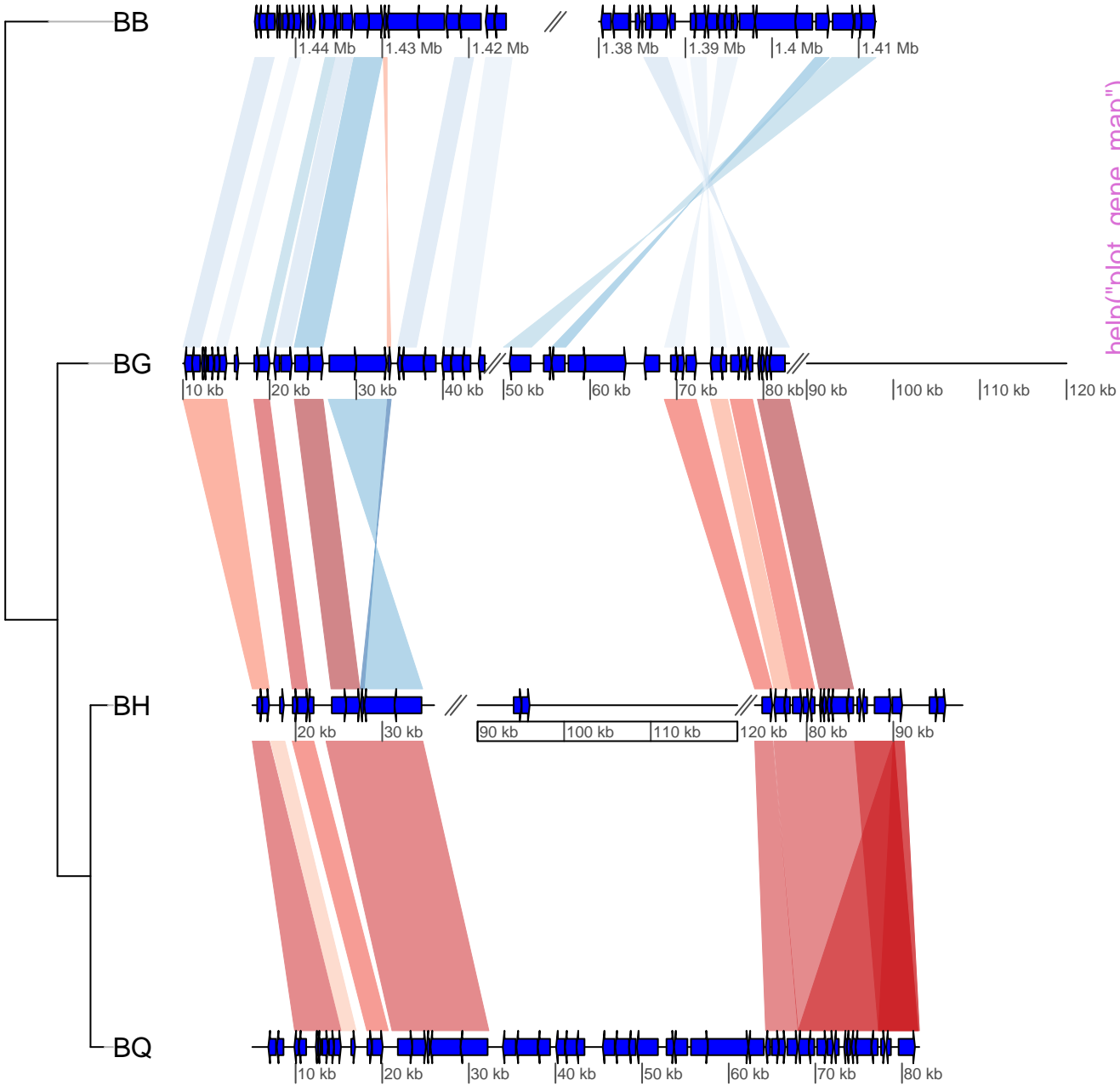




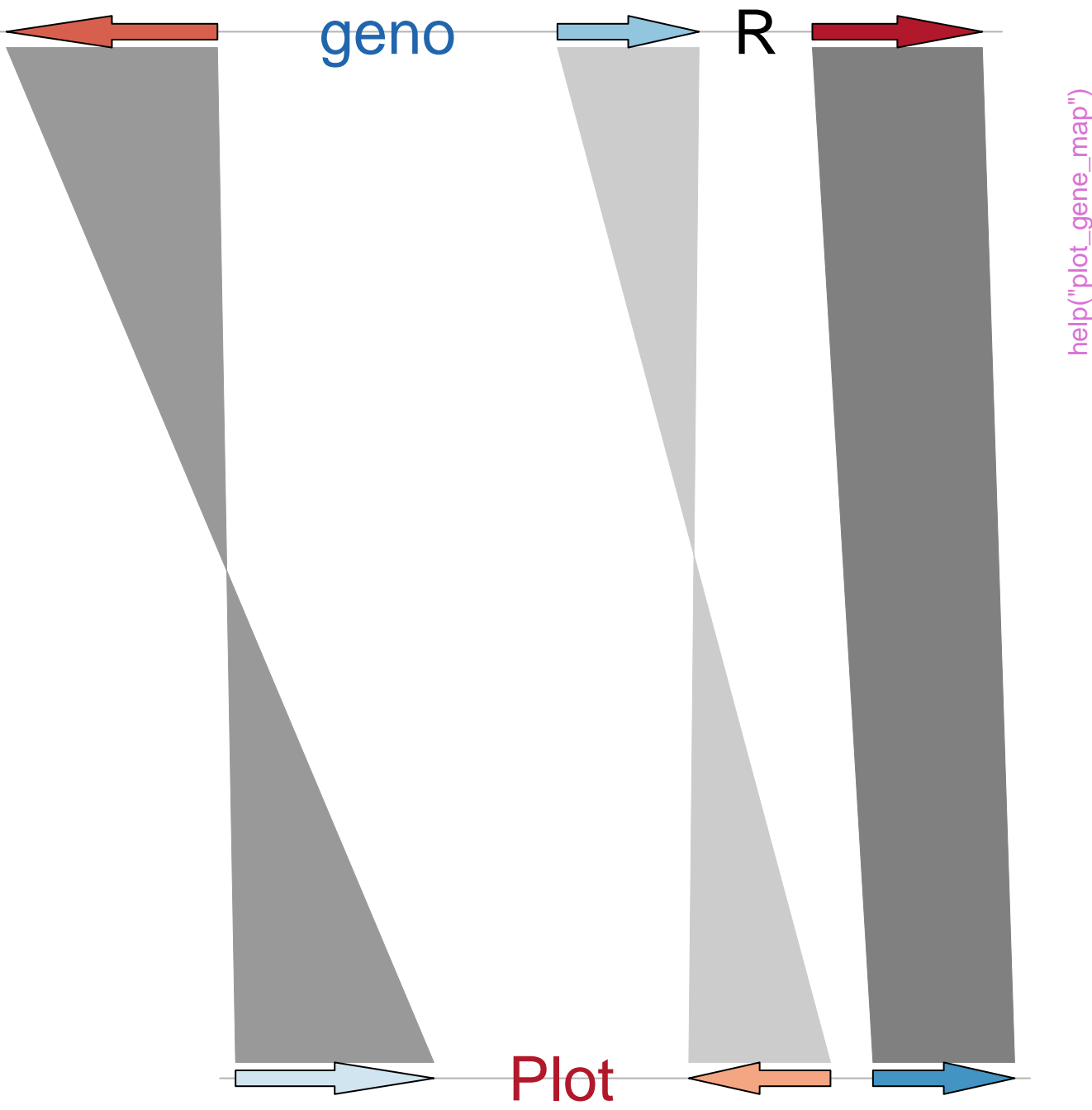




10 kb



10 kb

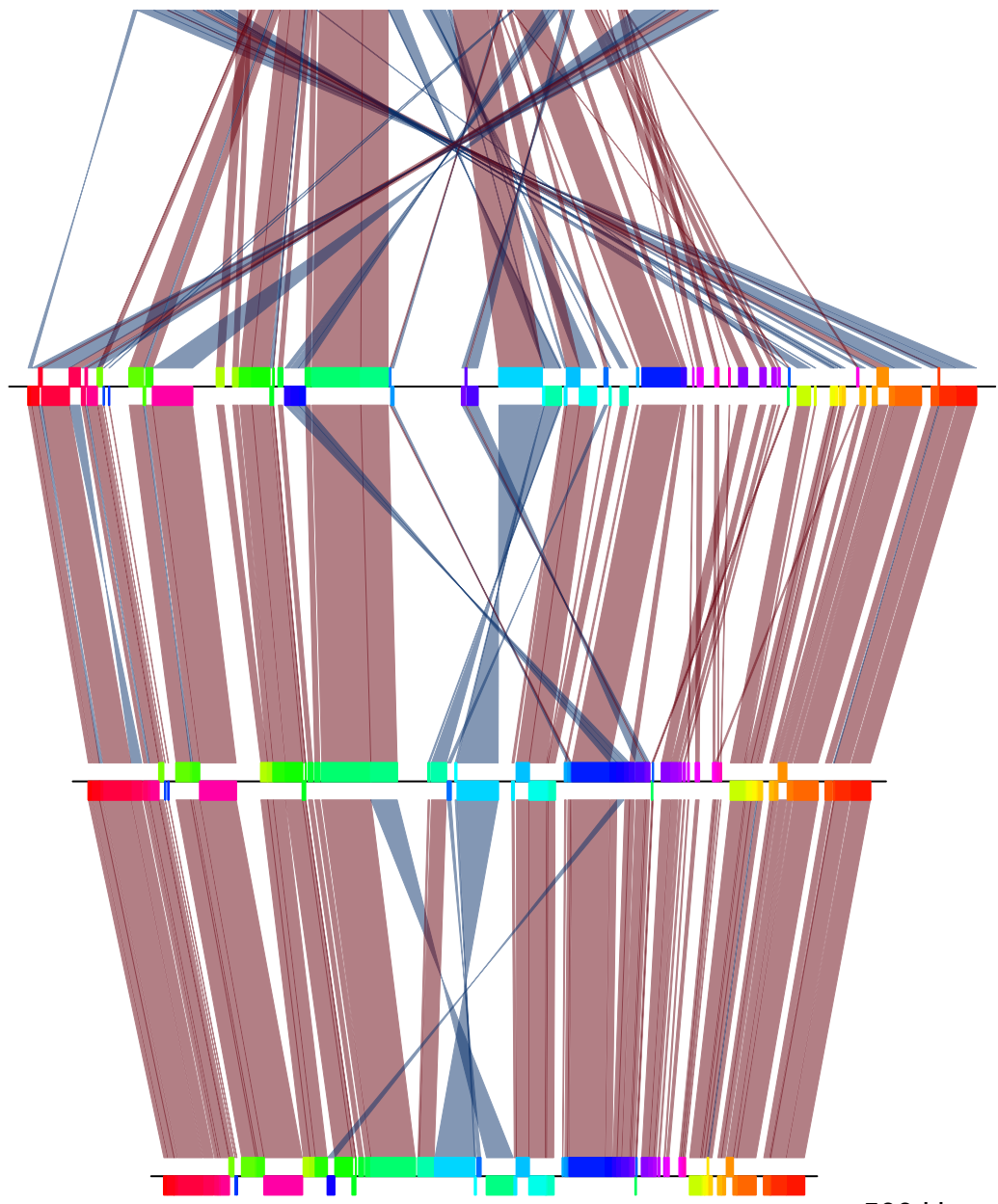
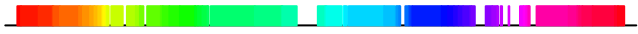


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

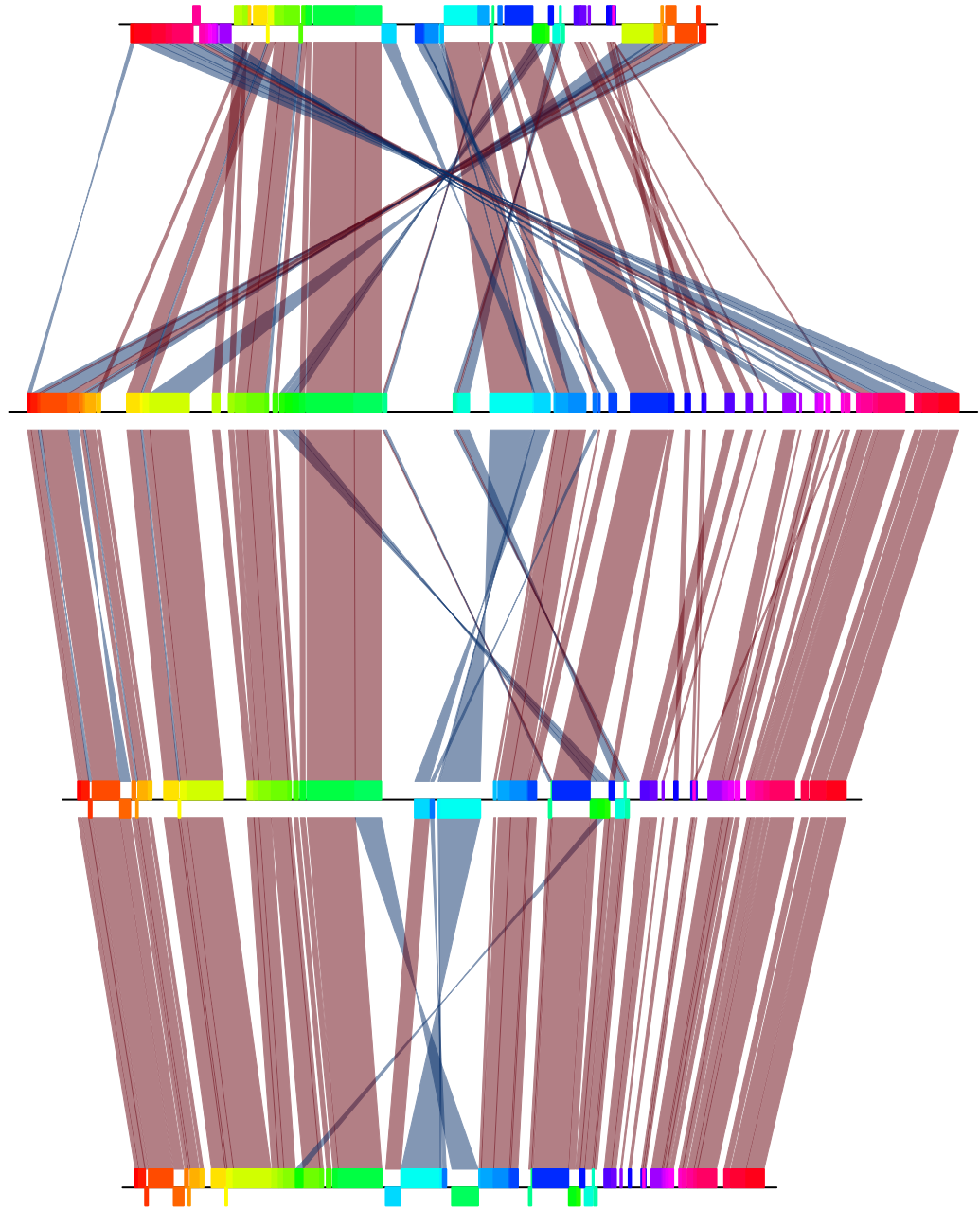
500 kb

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



B bacilliformis

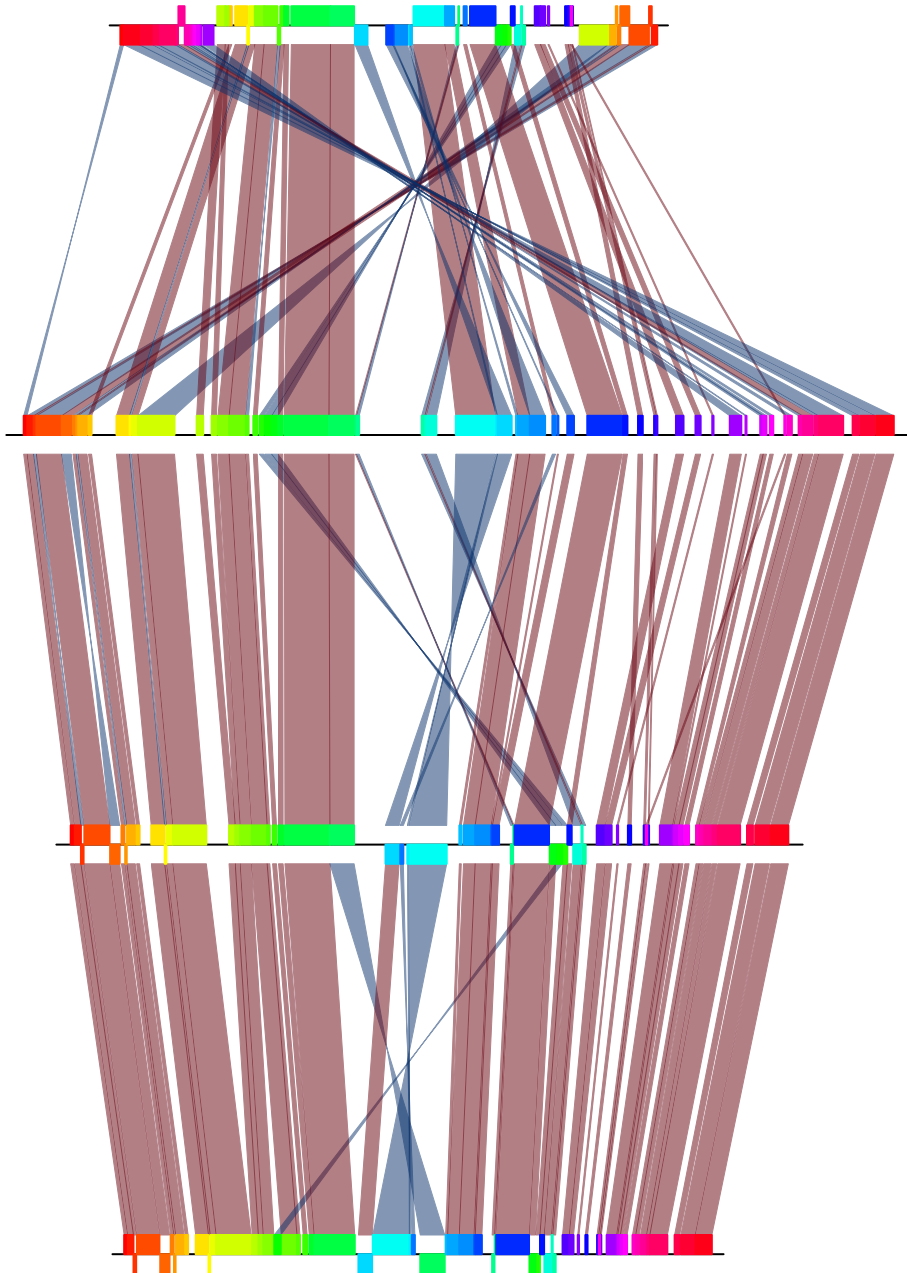
B grahamii

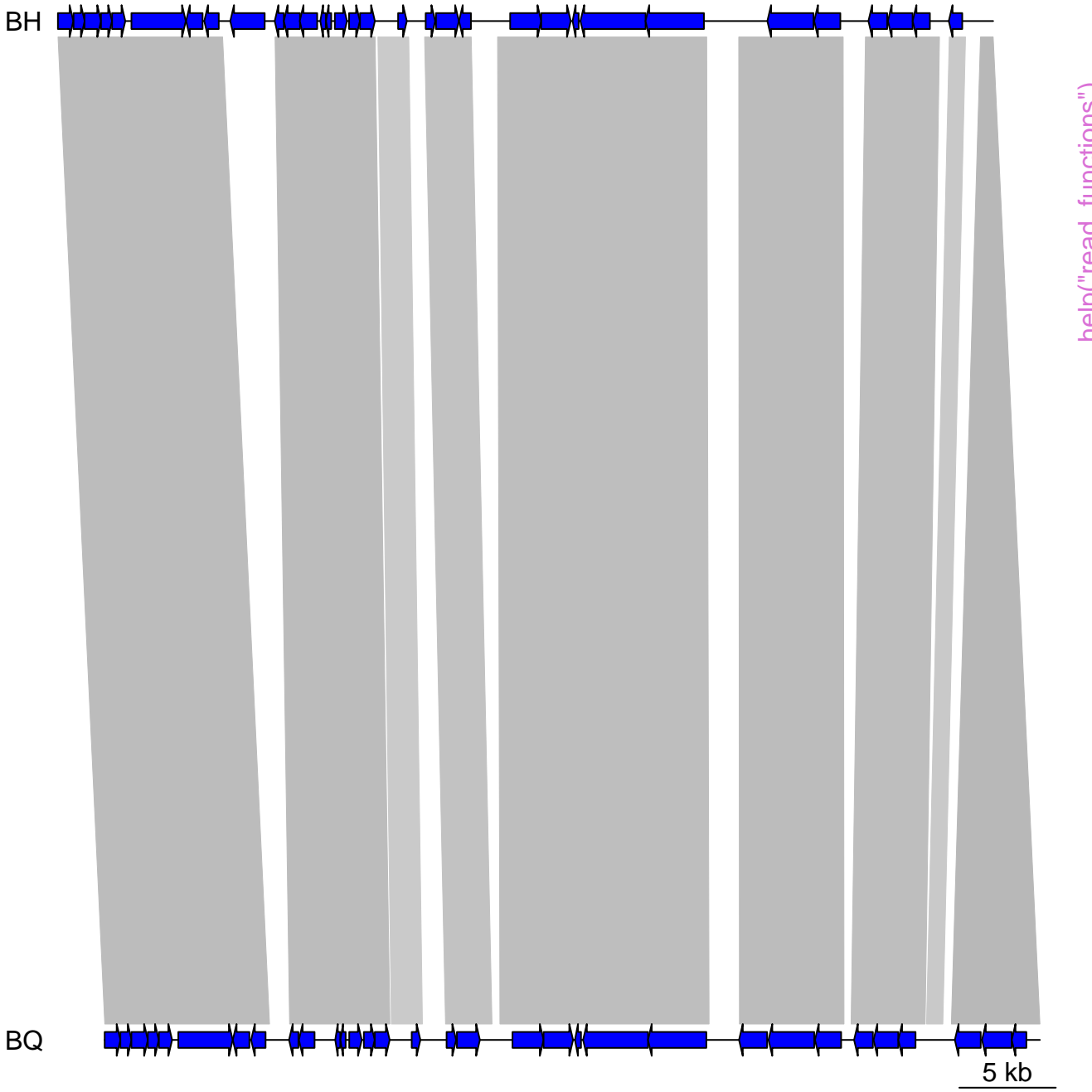
B henselae

B quintana

help("read\_functions")

500 kb





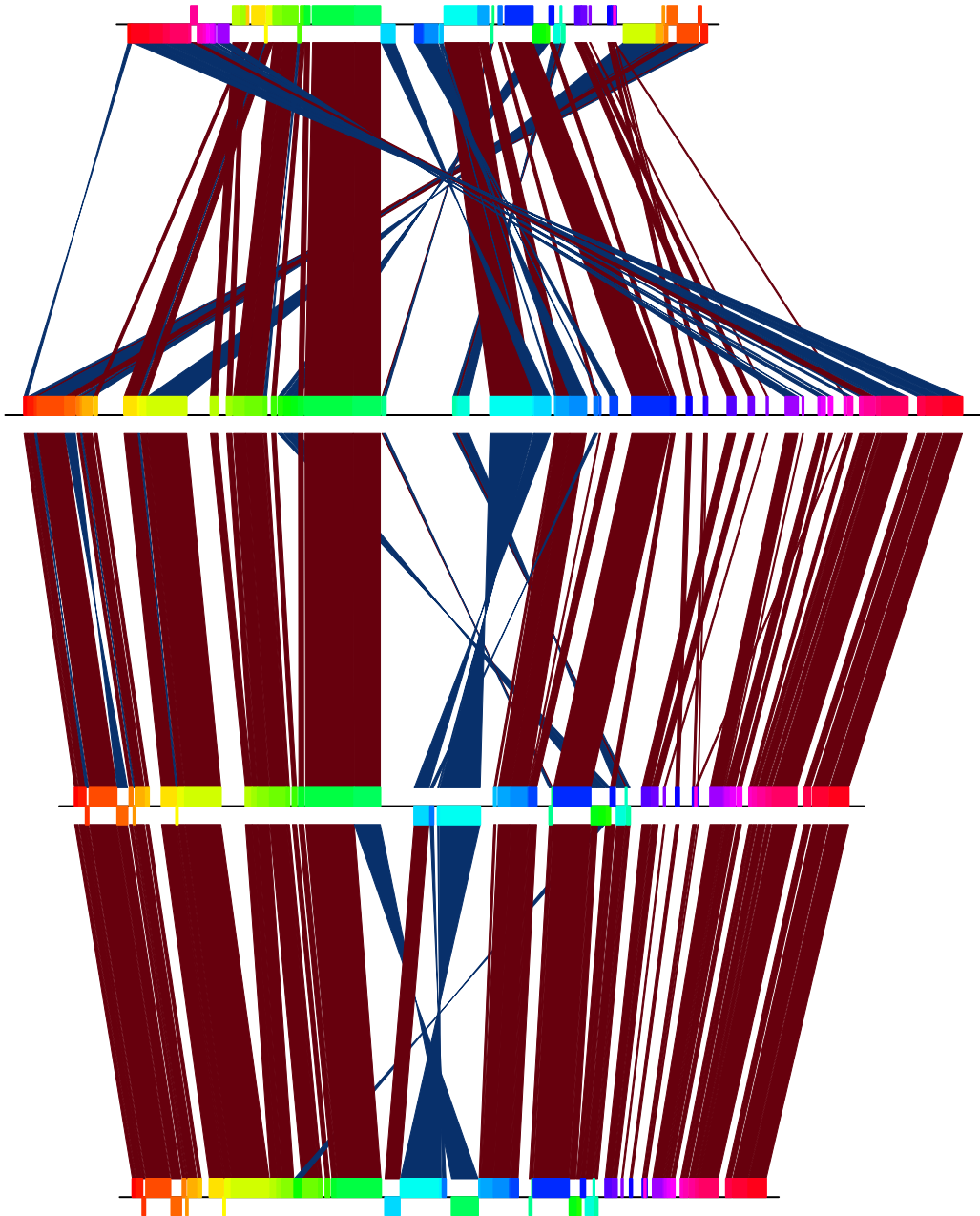


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("reverse")

B\_bacilliformis

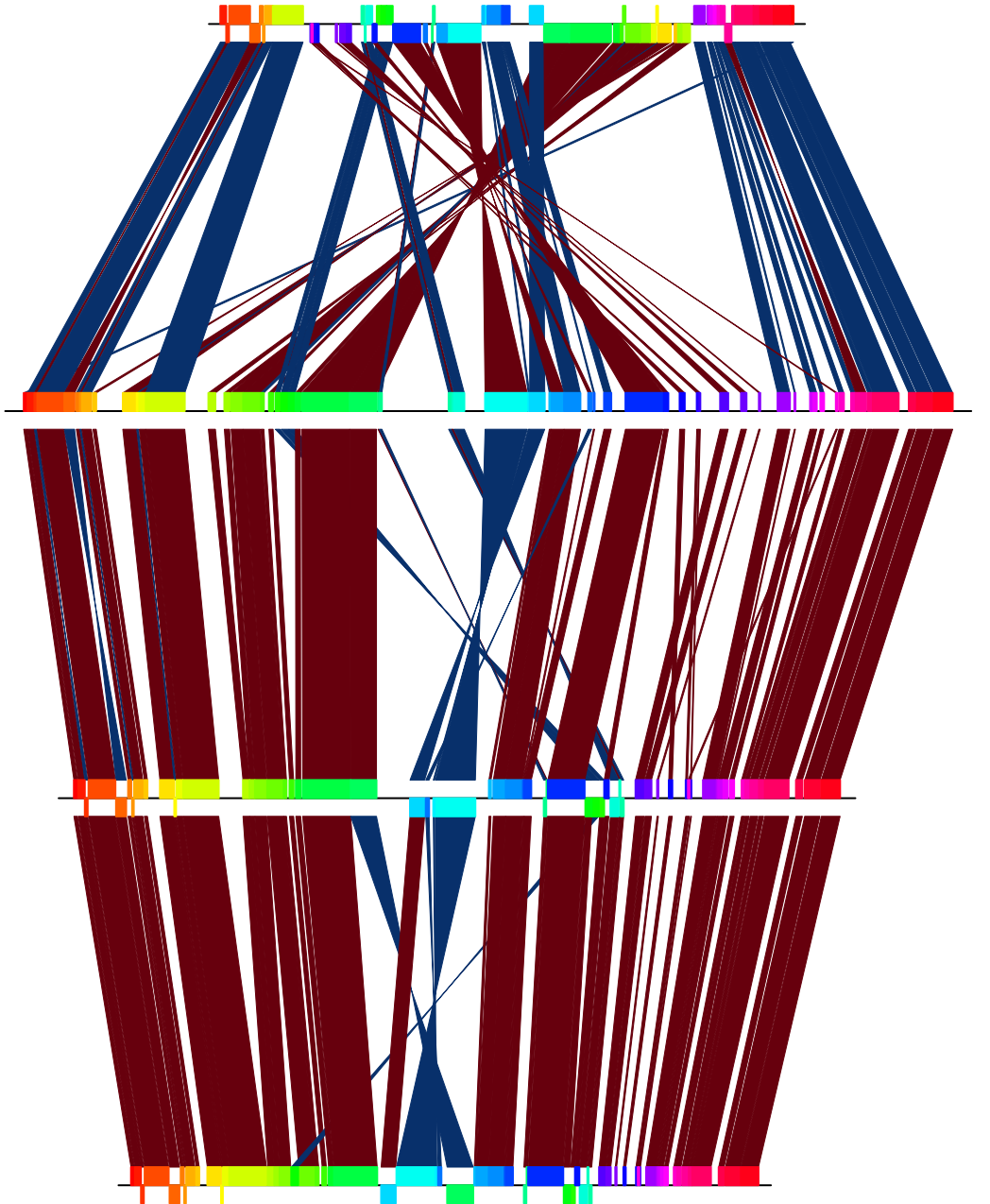
B\_grahamii

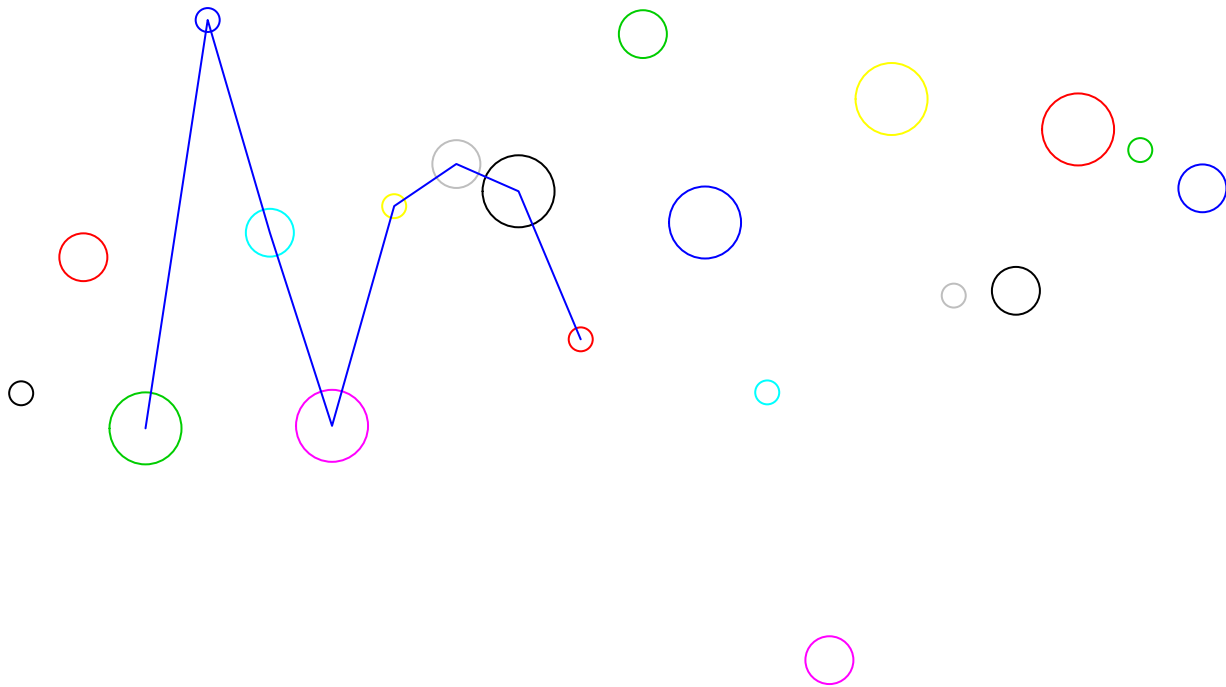
B\_henselae

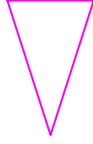
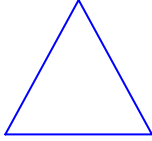
B\_quintana

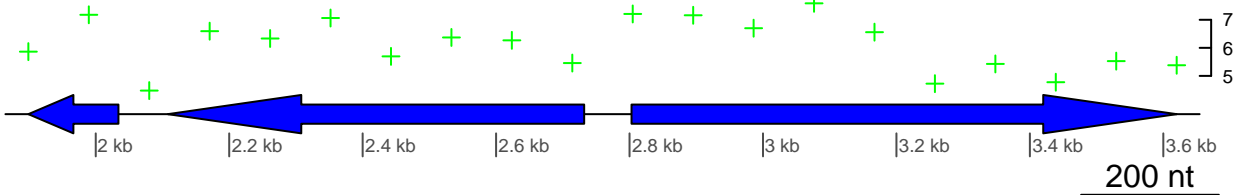
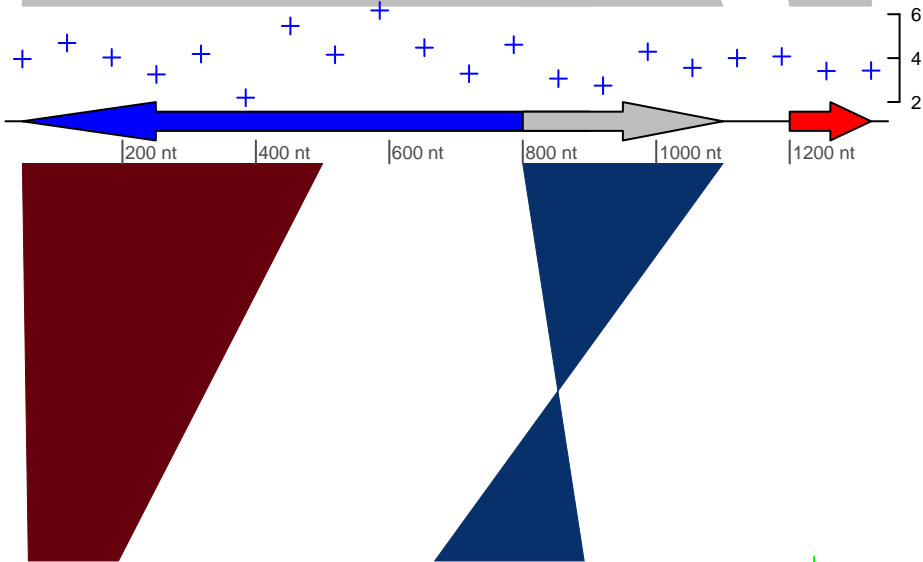
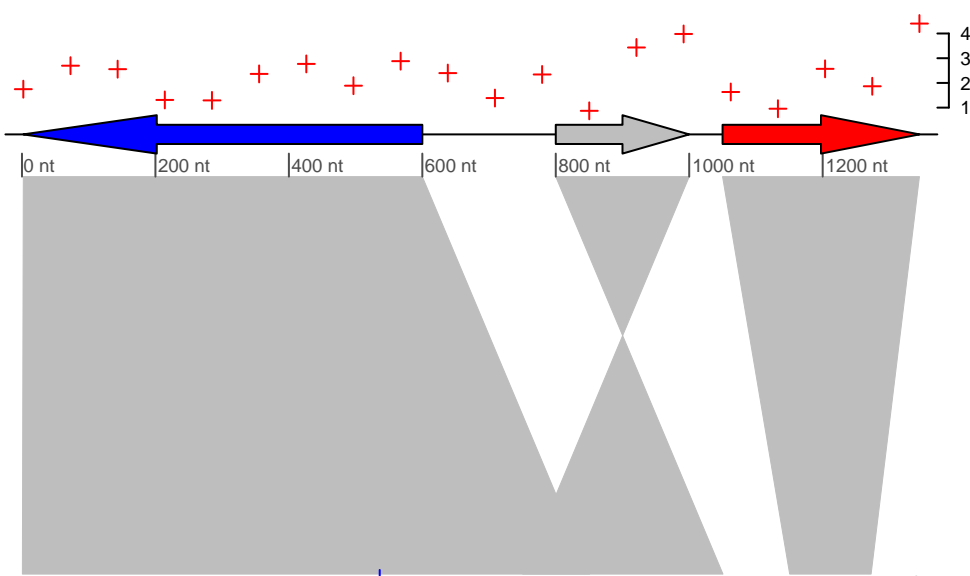
help("reverse")

500 kb



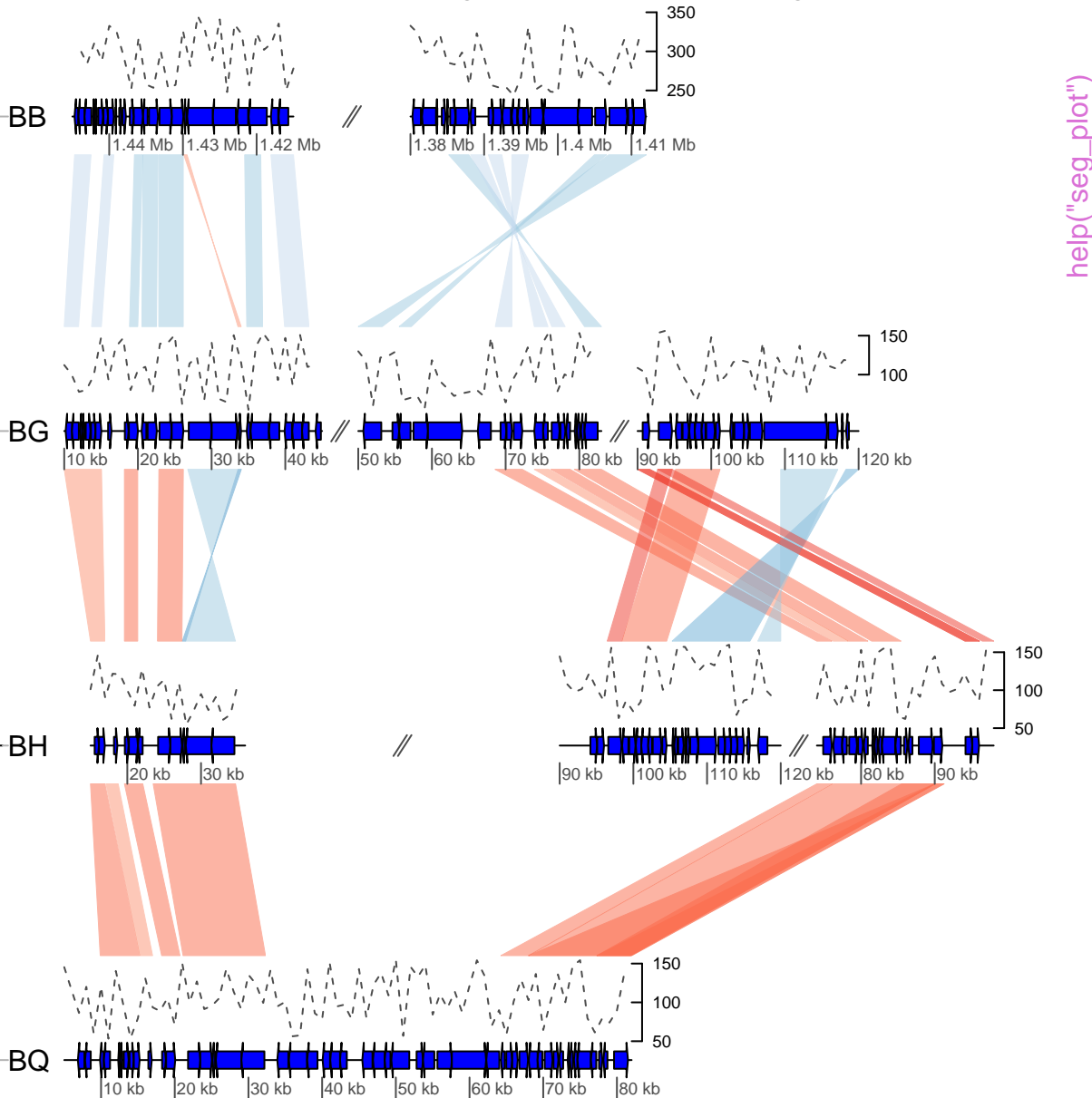


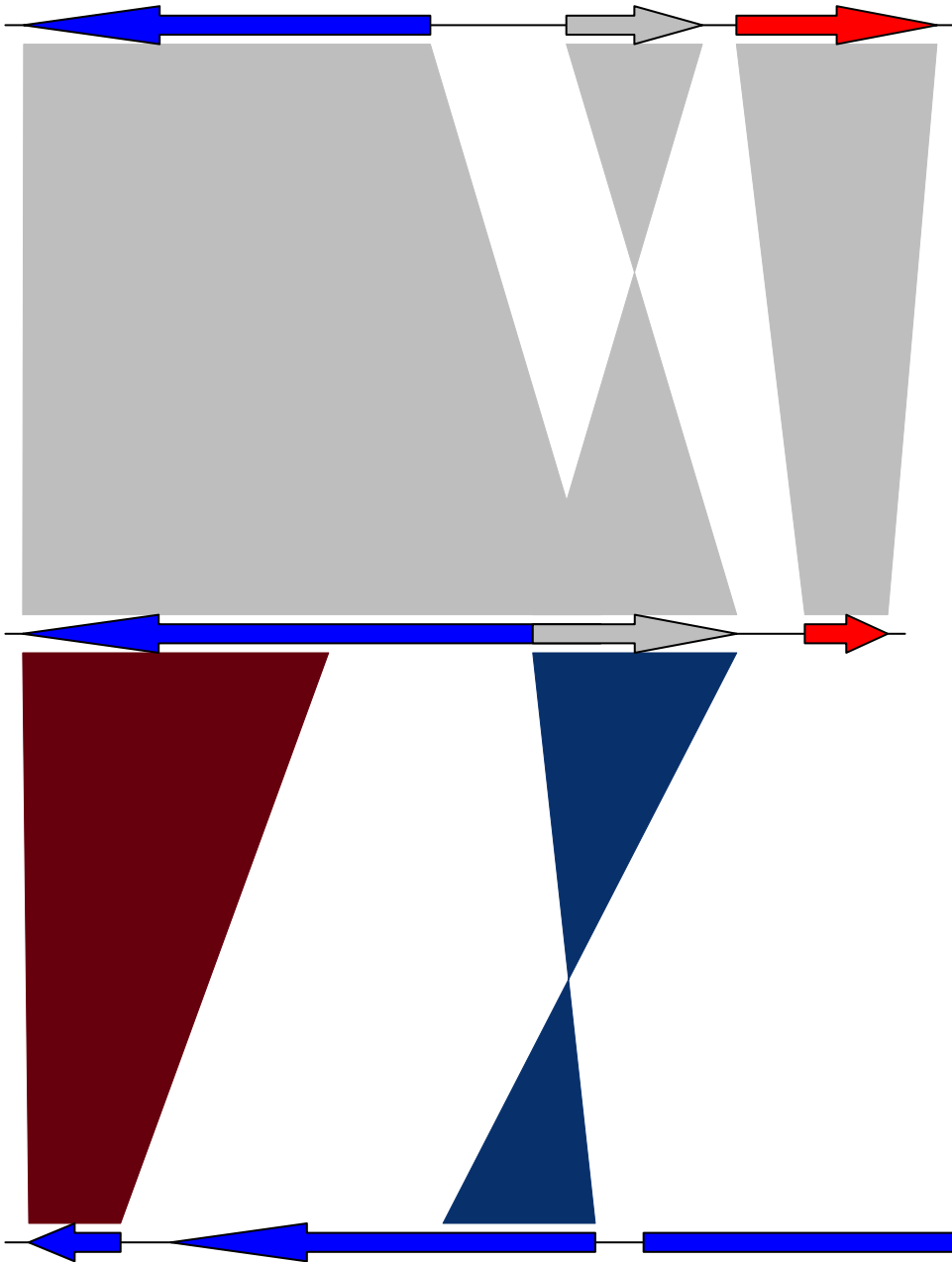




help("seg\_plot")

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





help("three\_genes")

