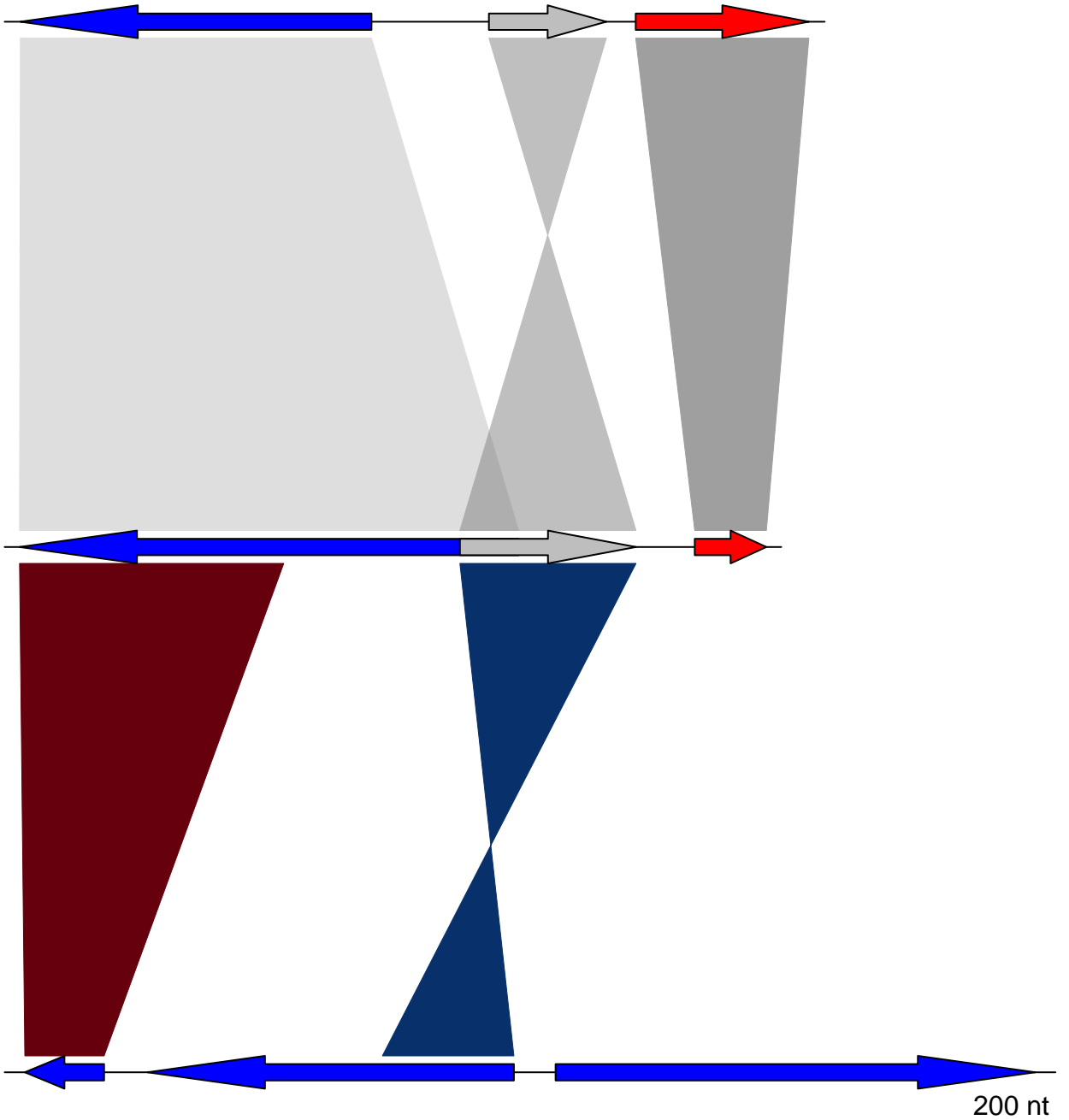
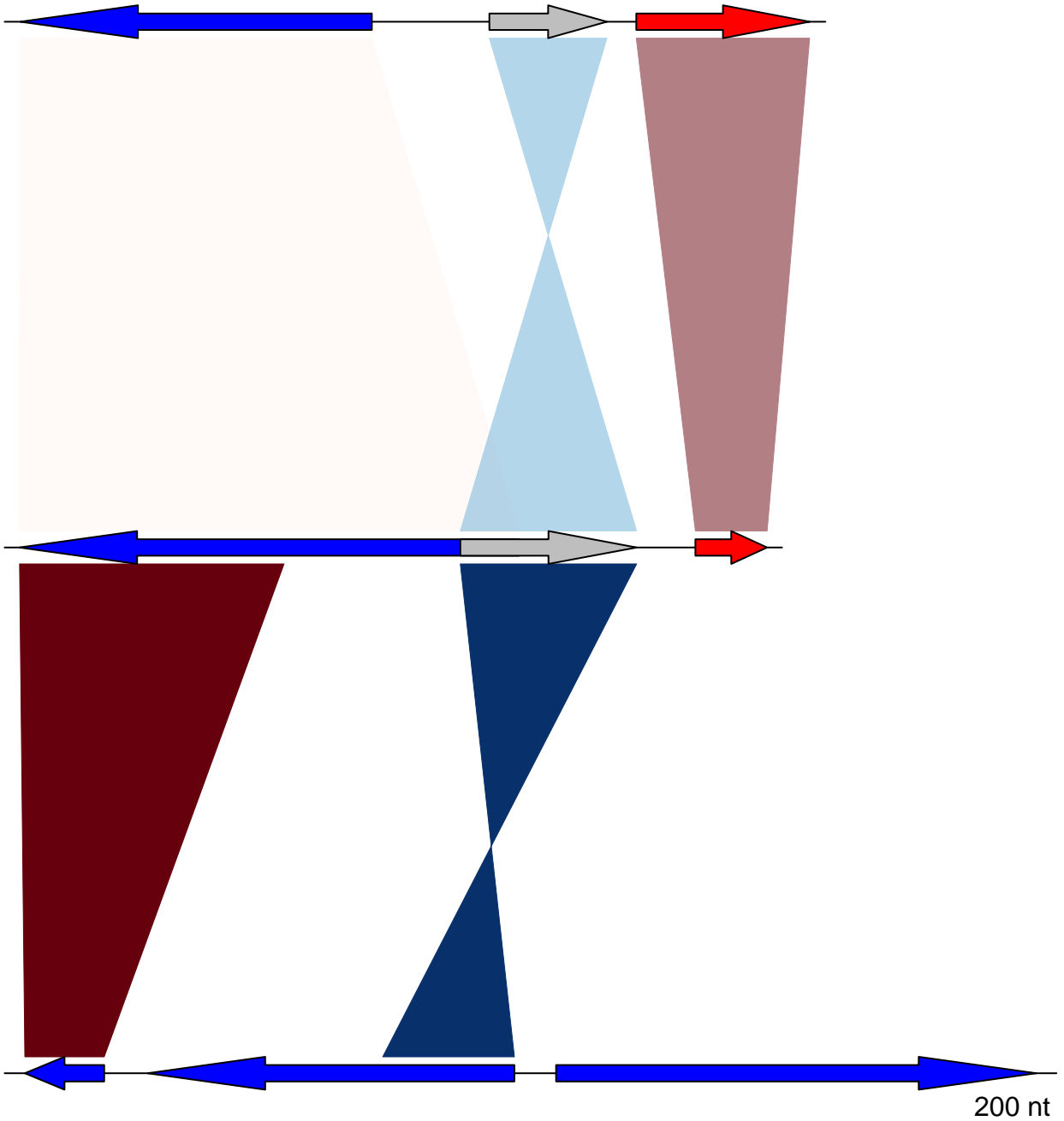


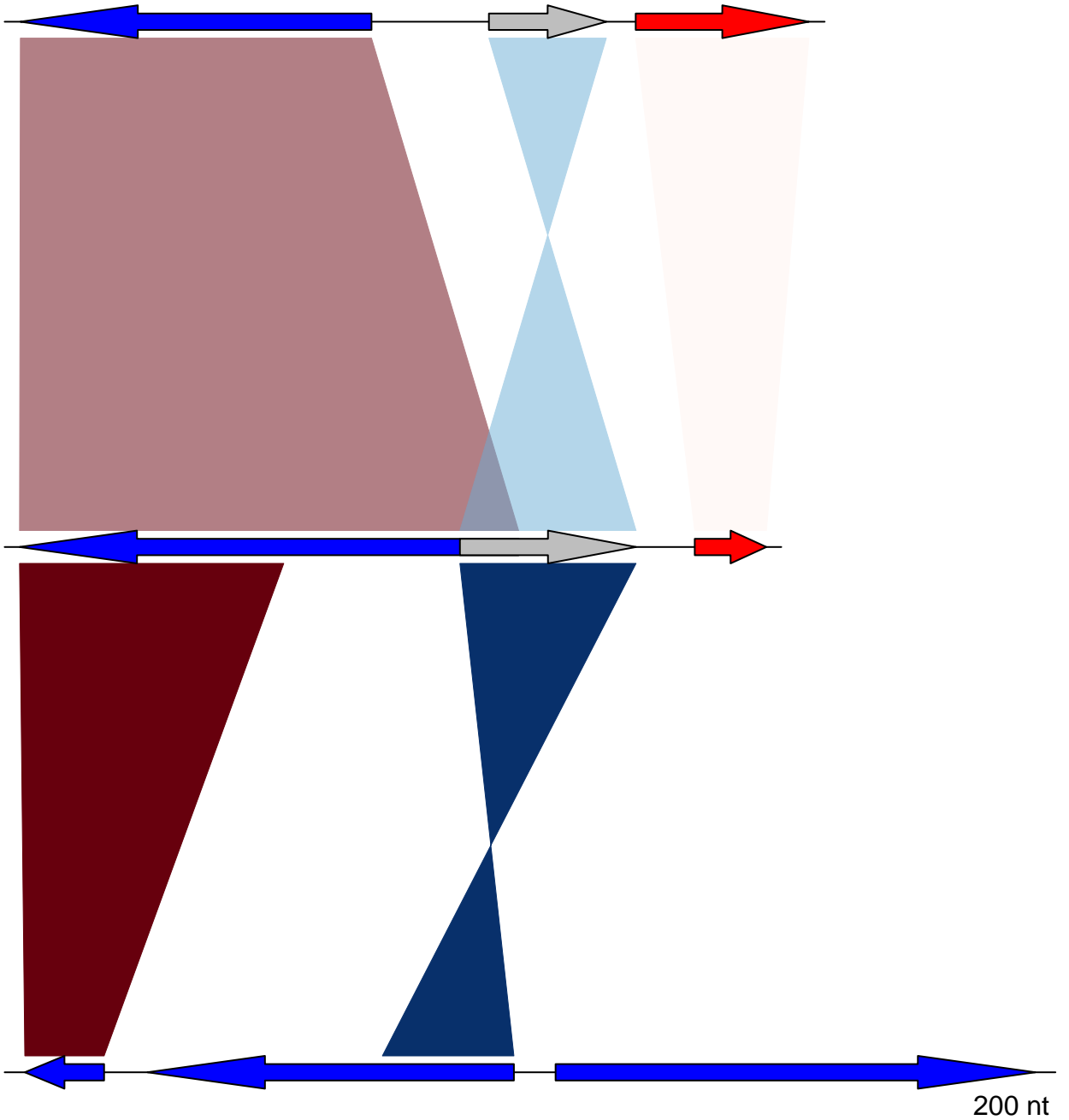
help("annotation")



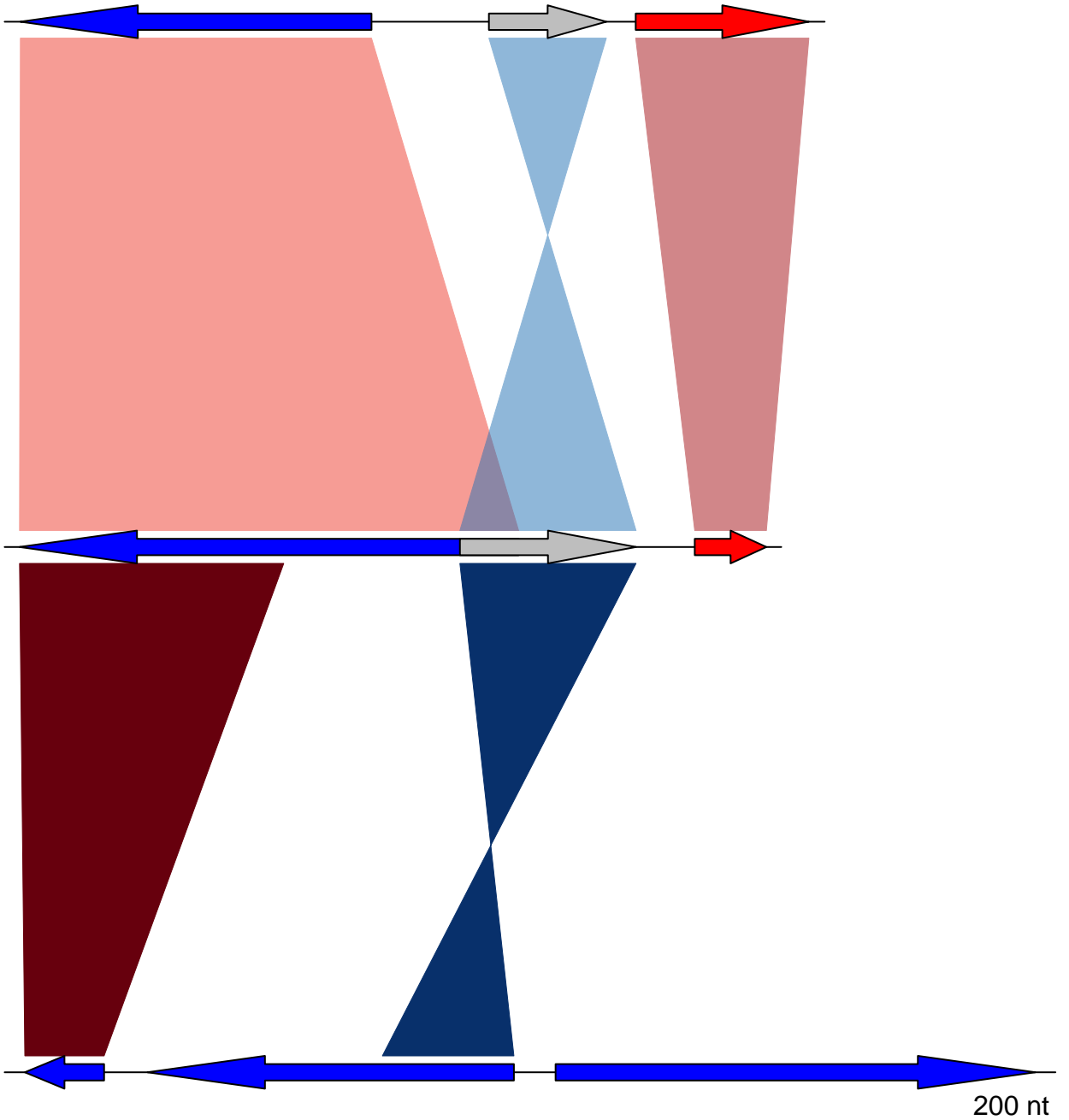
help("apply\_color\_scheme")



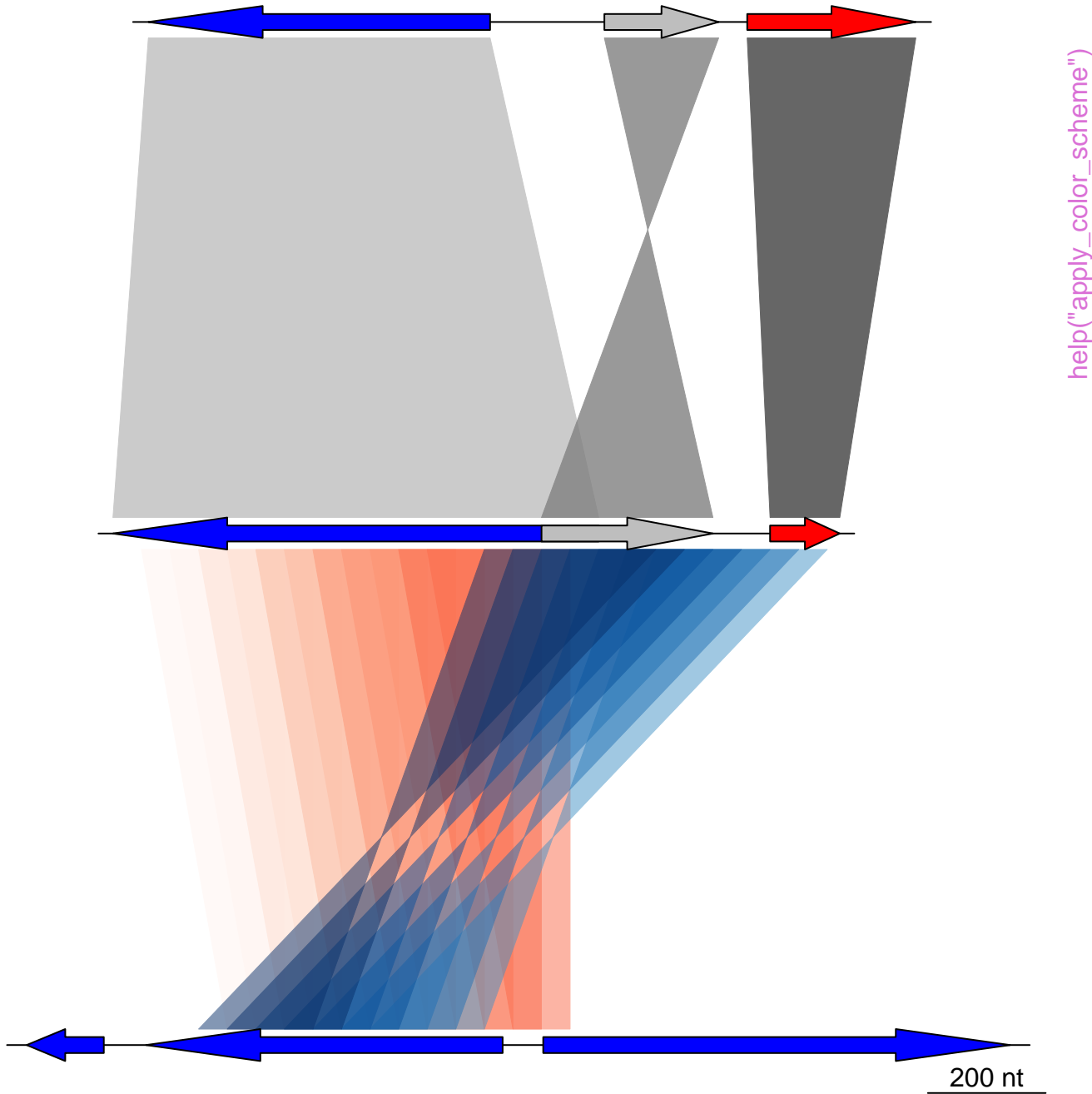
help("apply\_color\_scheme")



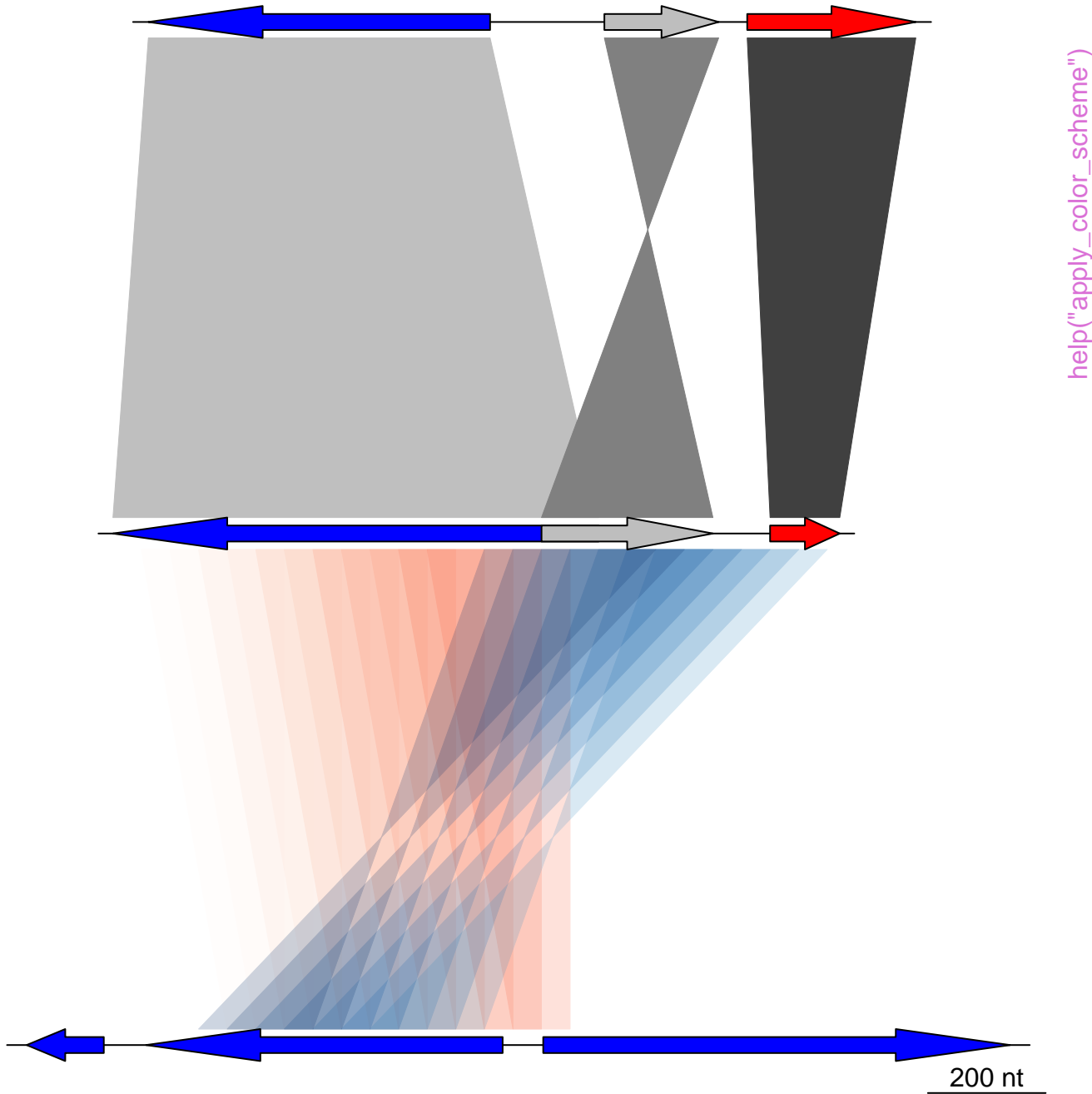
help("apply\_color\_scheme")

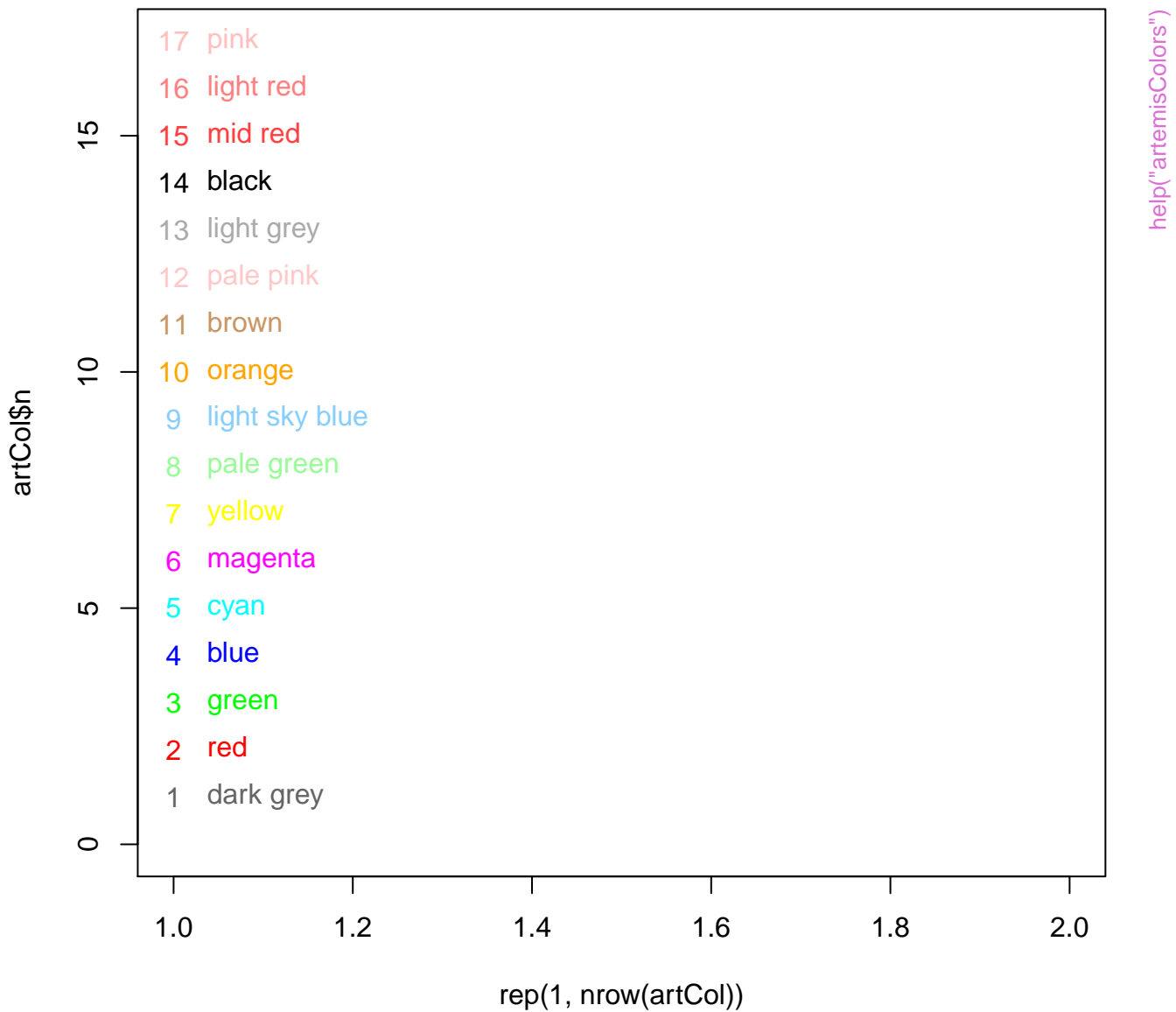


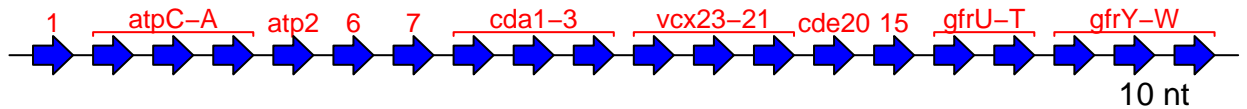
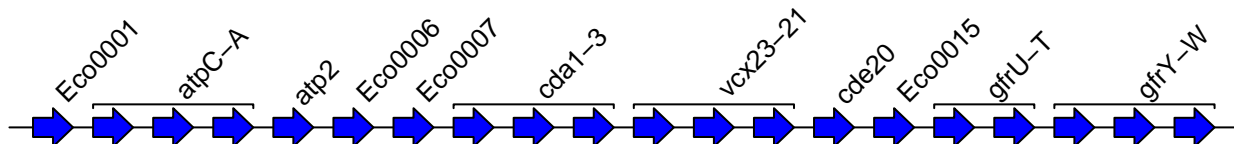
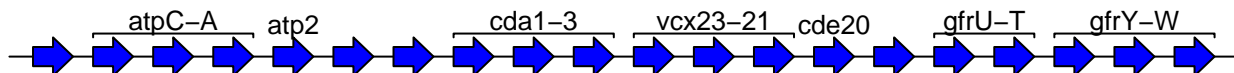
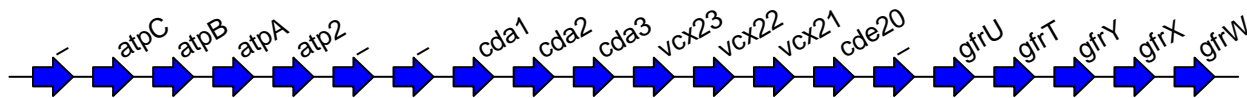
help("apply\_color\_scheme")











help("auto\_annotate")

BB

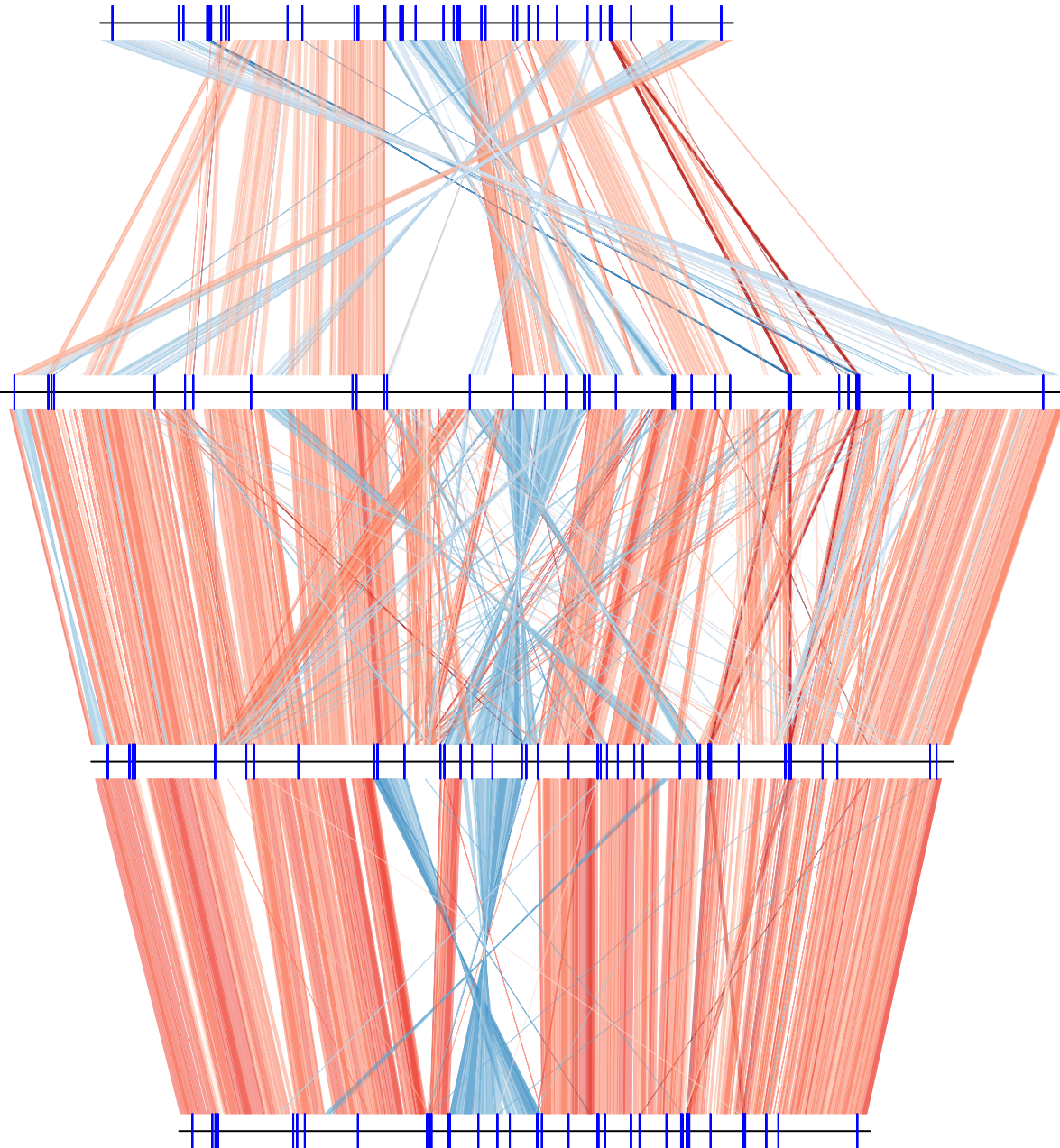
BG

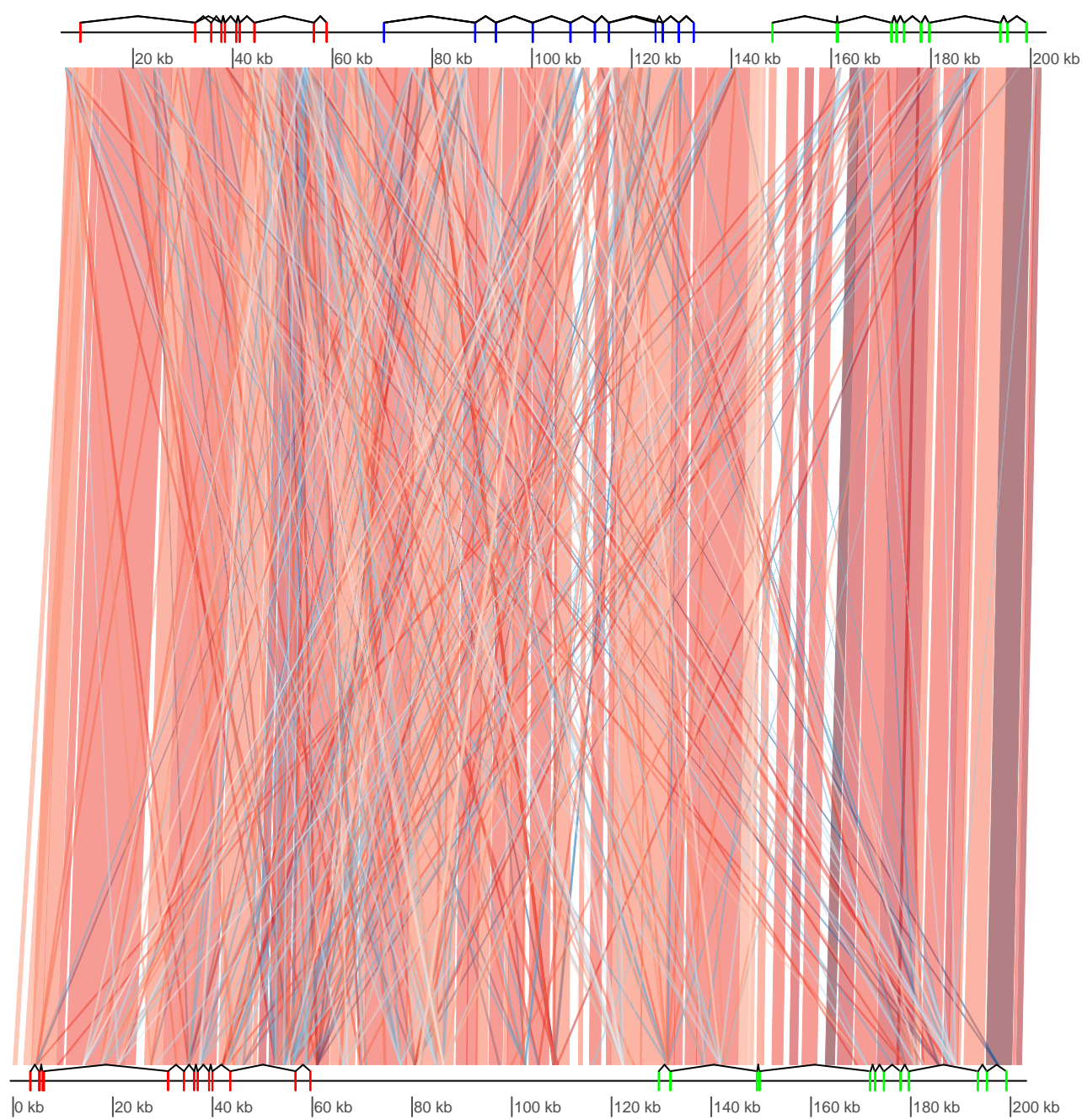
BH

BQ

500 kb

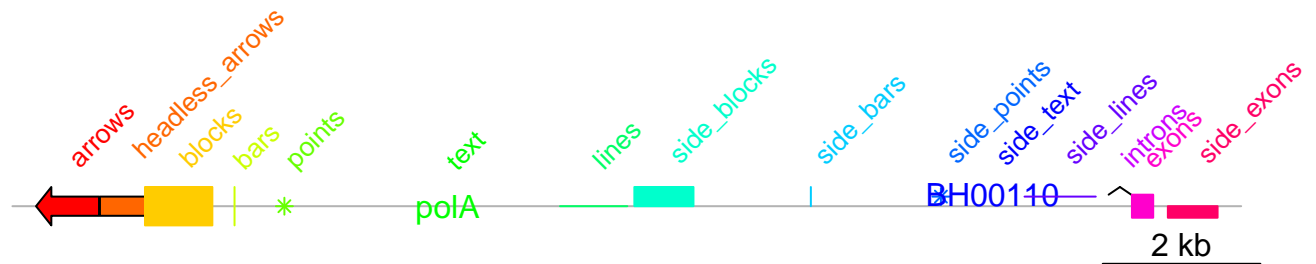
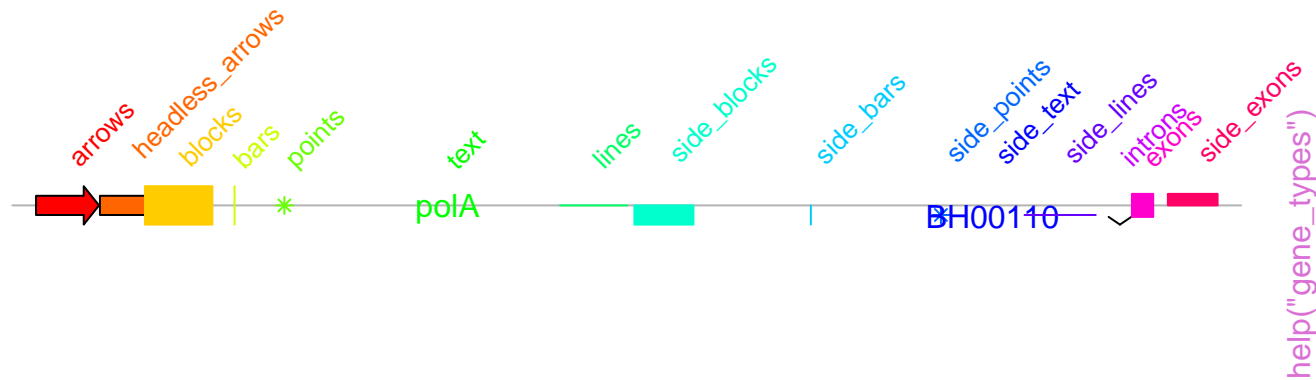
help("barto")

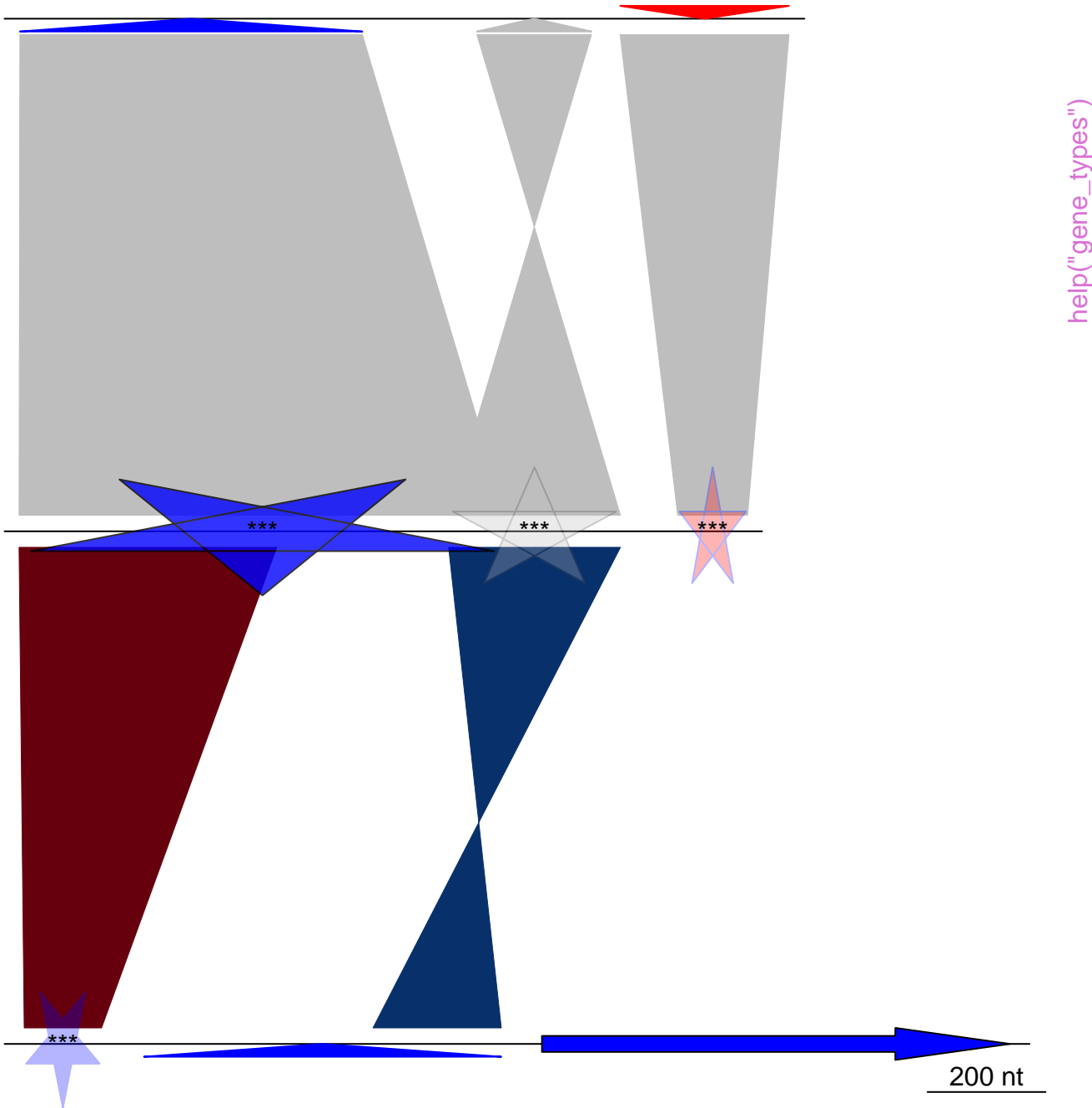




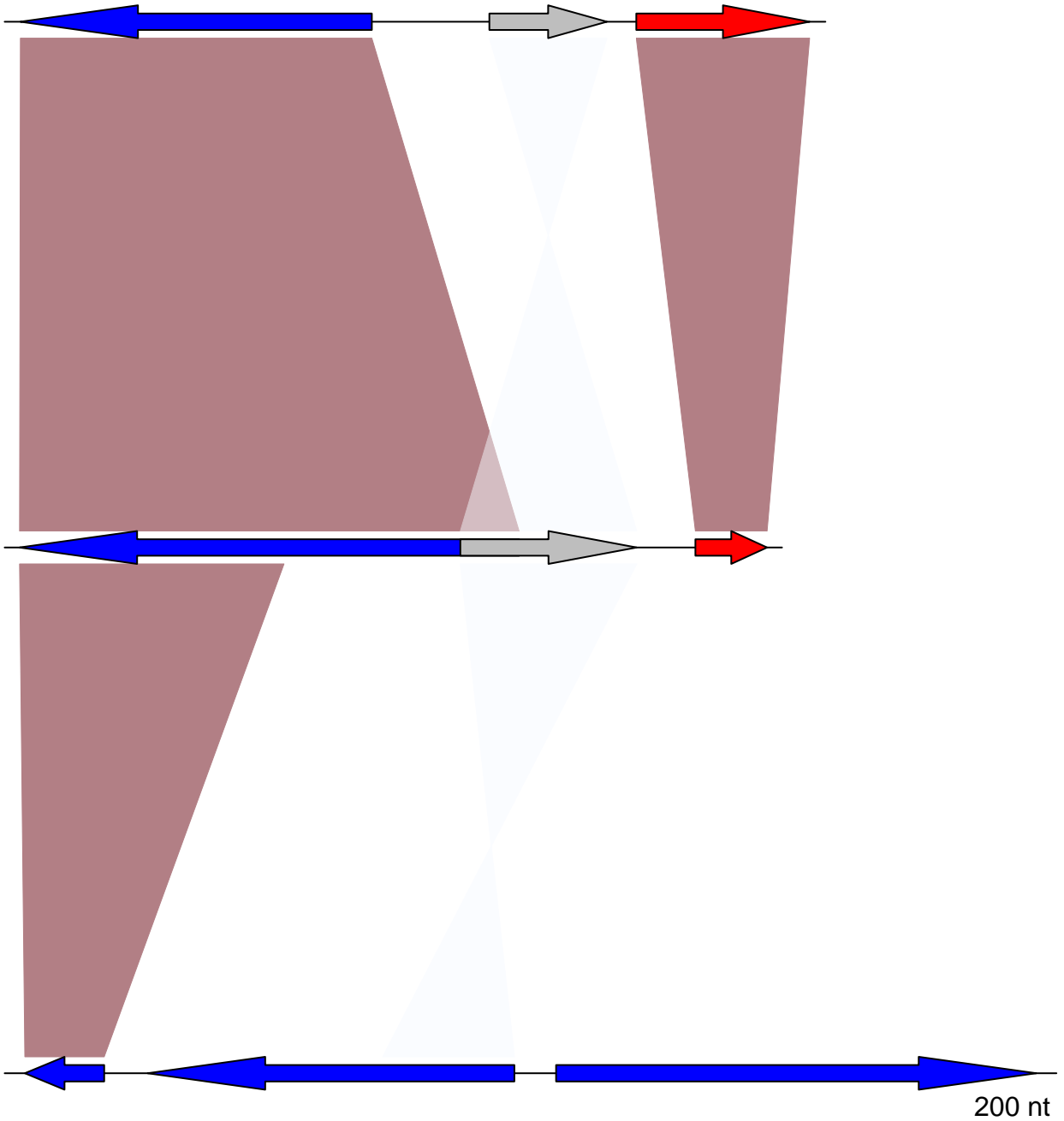
help("chrY\_subseg")











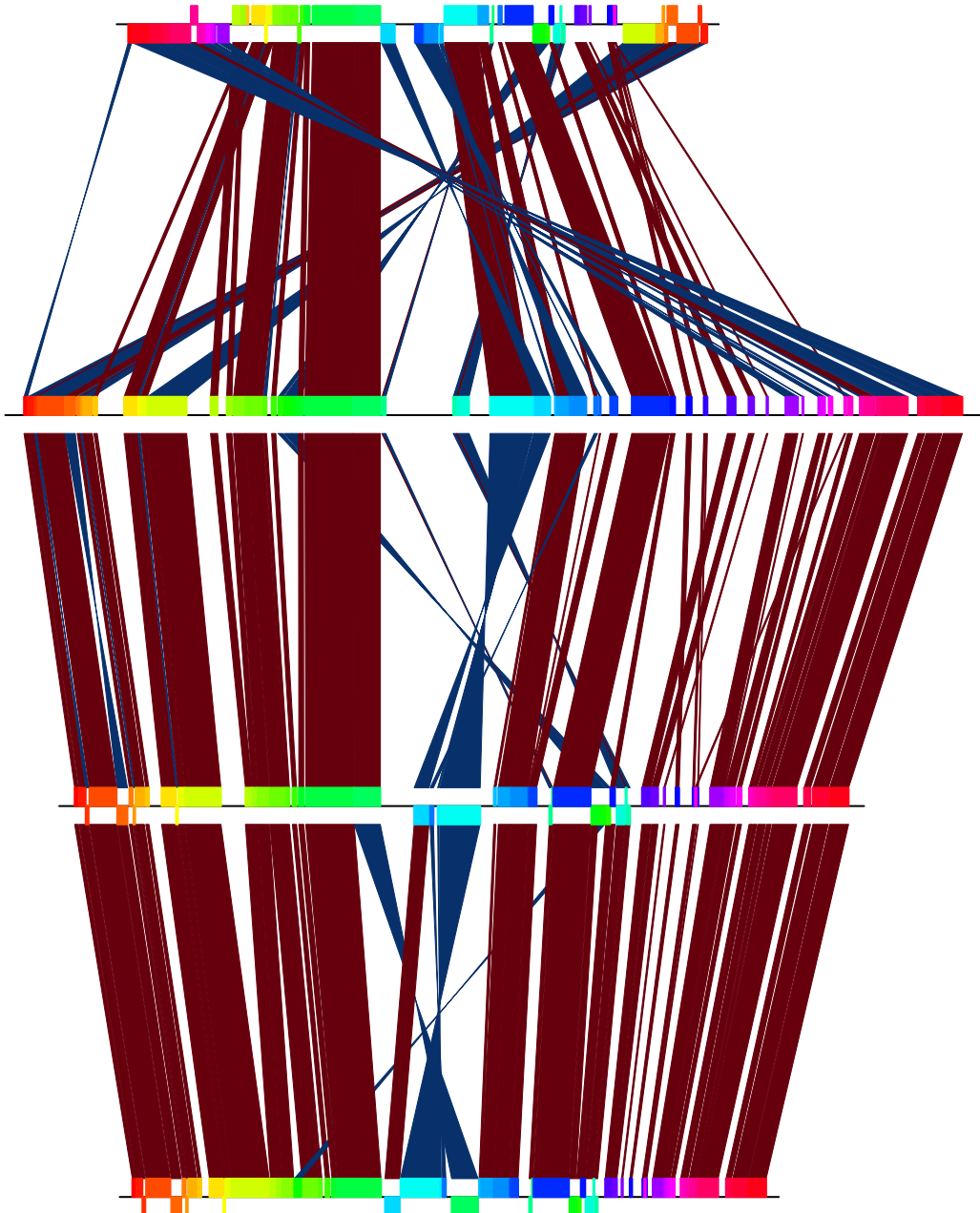
help("genoPlotR-package")

B\_bacilliformis

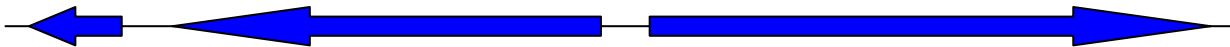
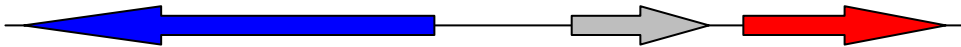
B\_grahamii

B\_henselae

B\_quintana

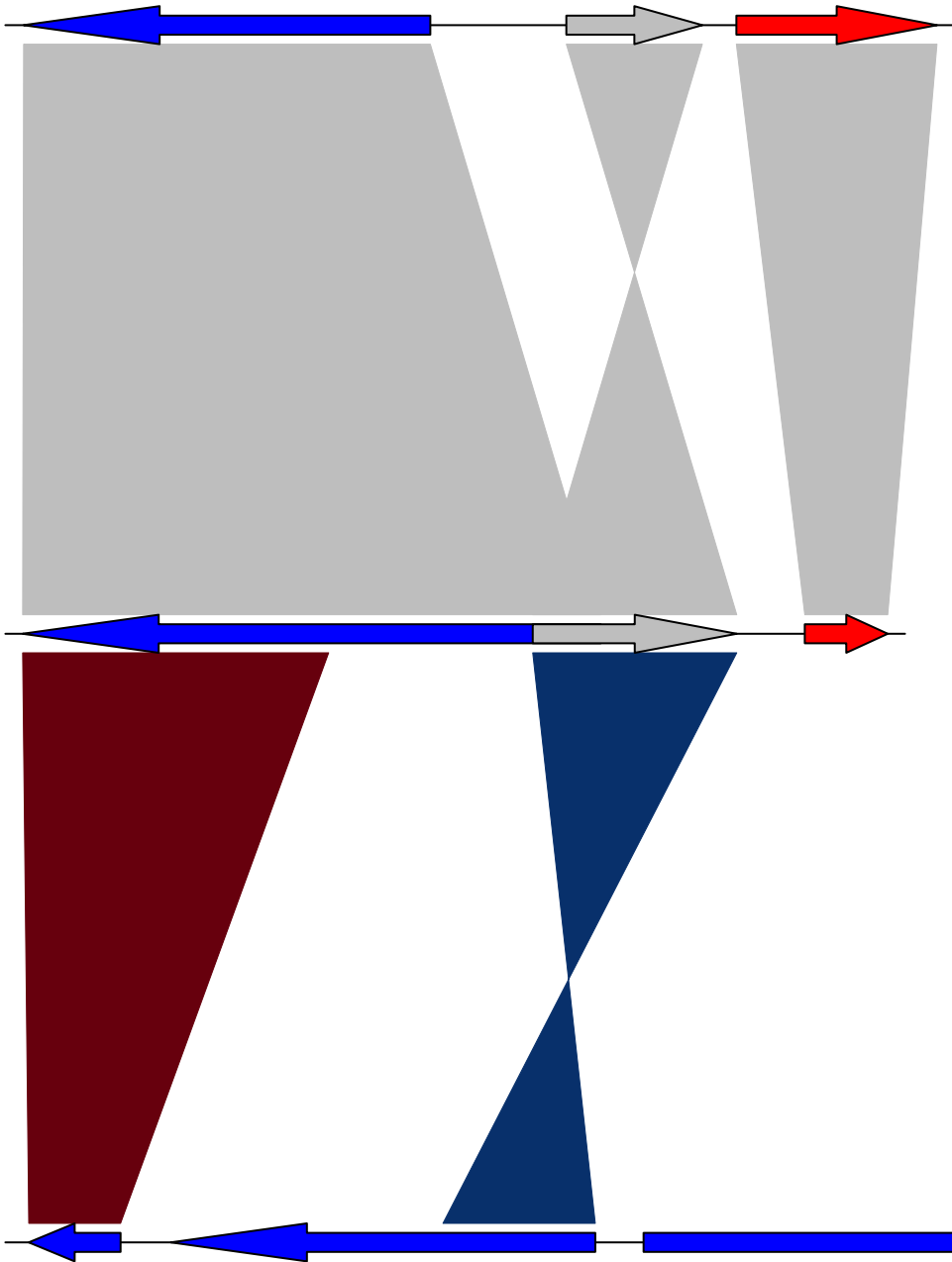


help("mauve.bbone")



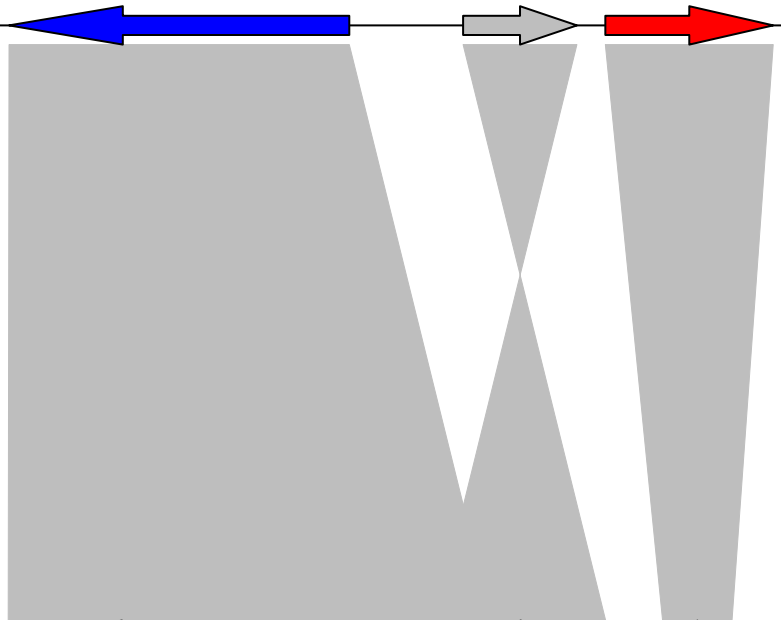
200 nt

help("plot\_gene\_map")

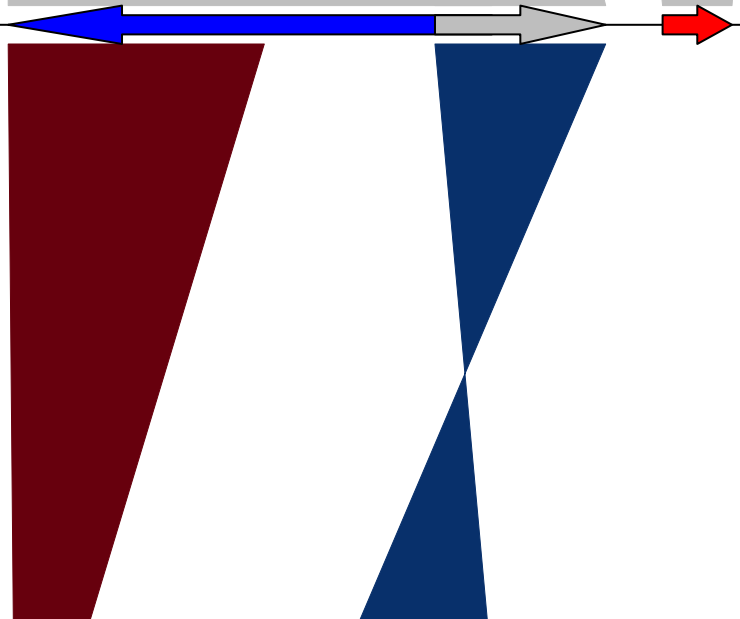


help("plot\_gene\_map")

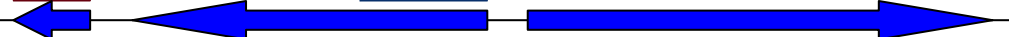
A aaa



B bbb

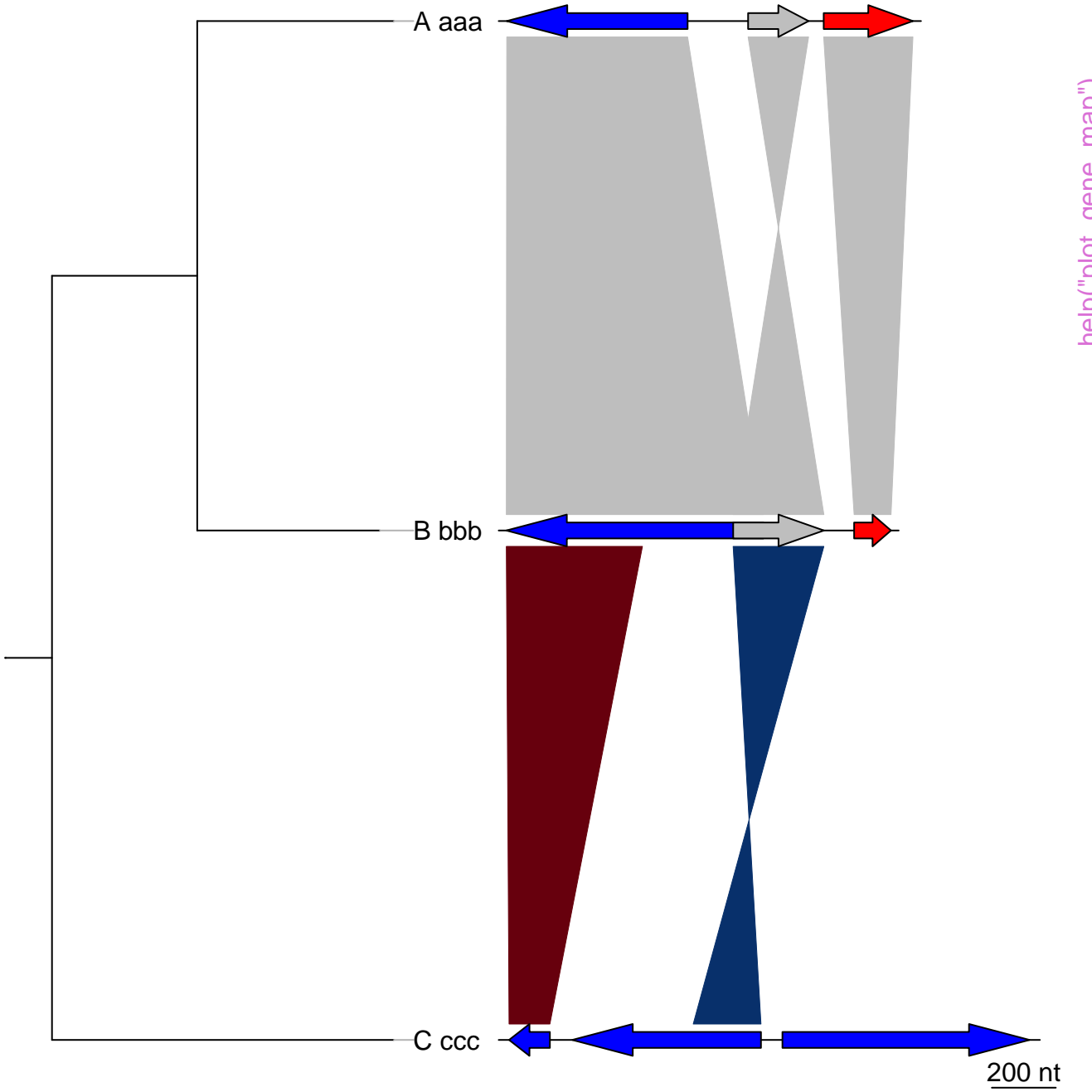


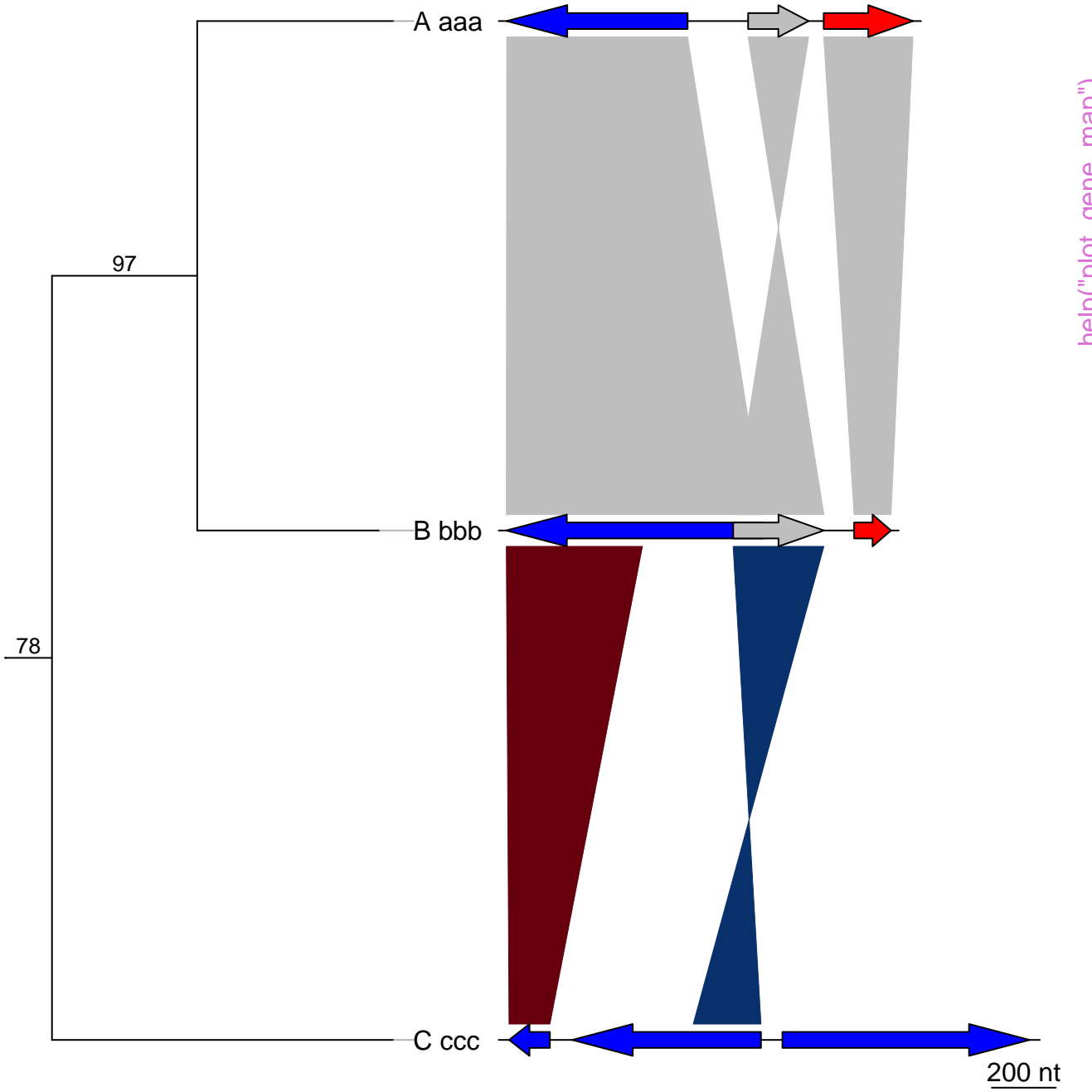
C ccc

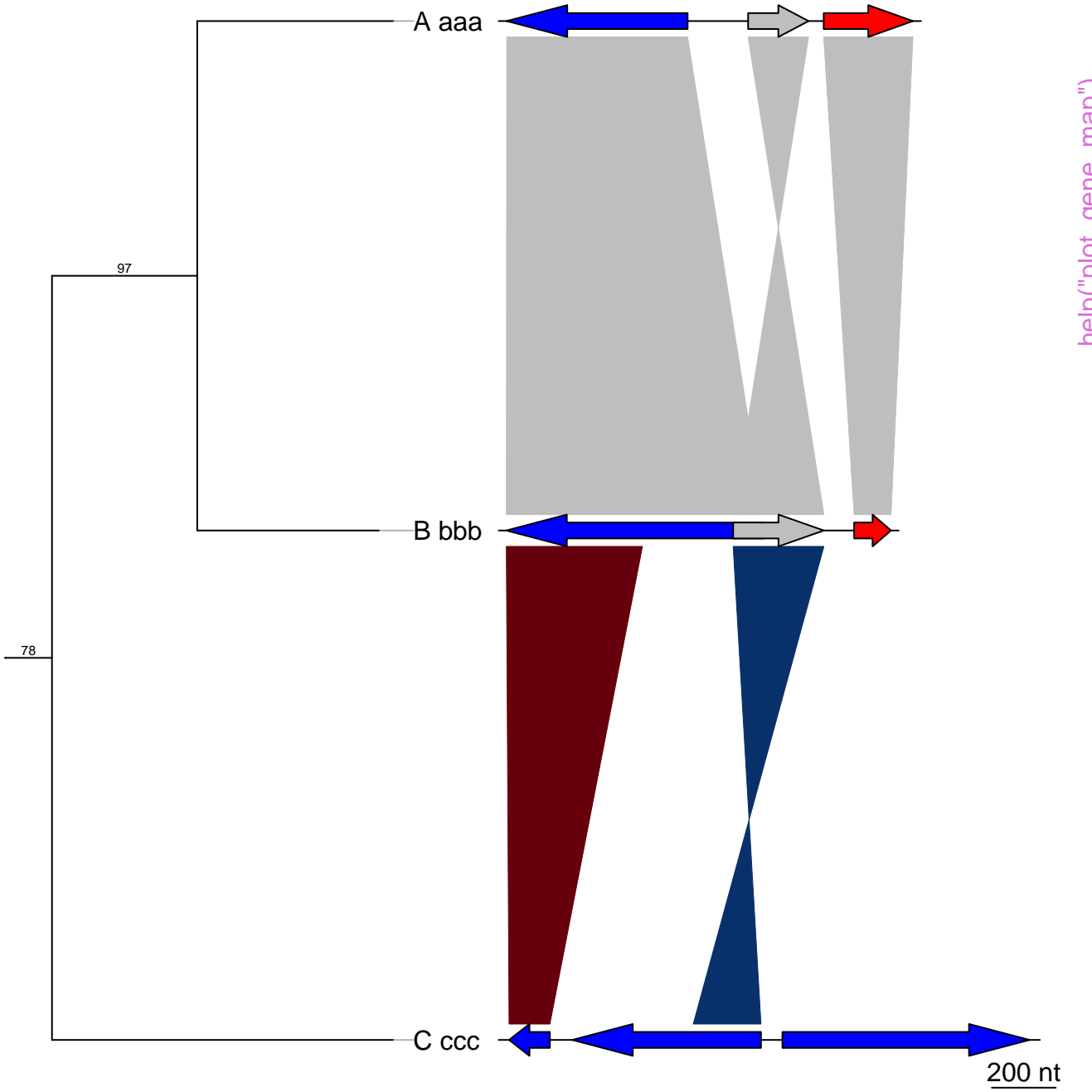


200 nt

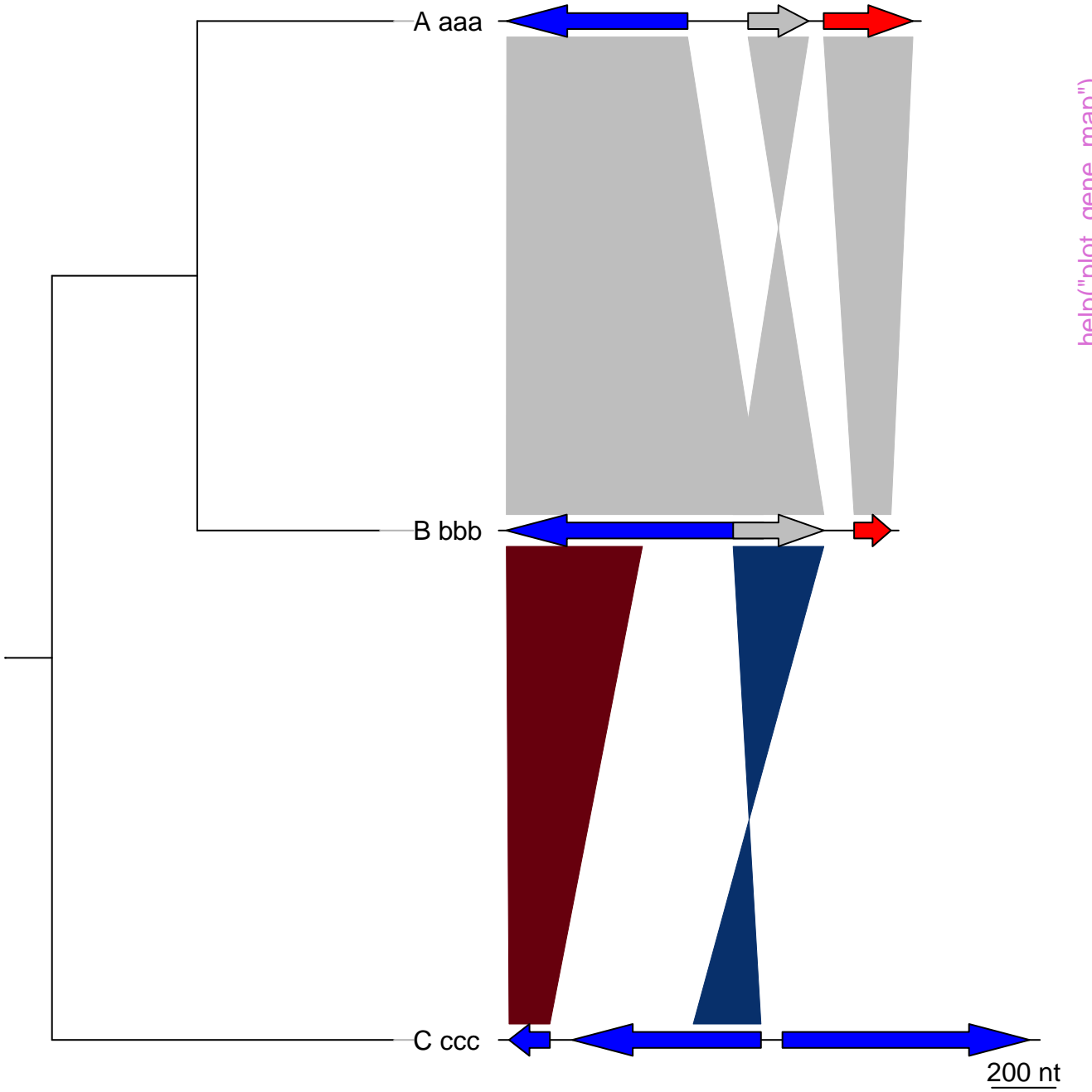
help("plot\_gene\_map")

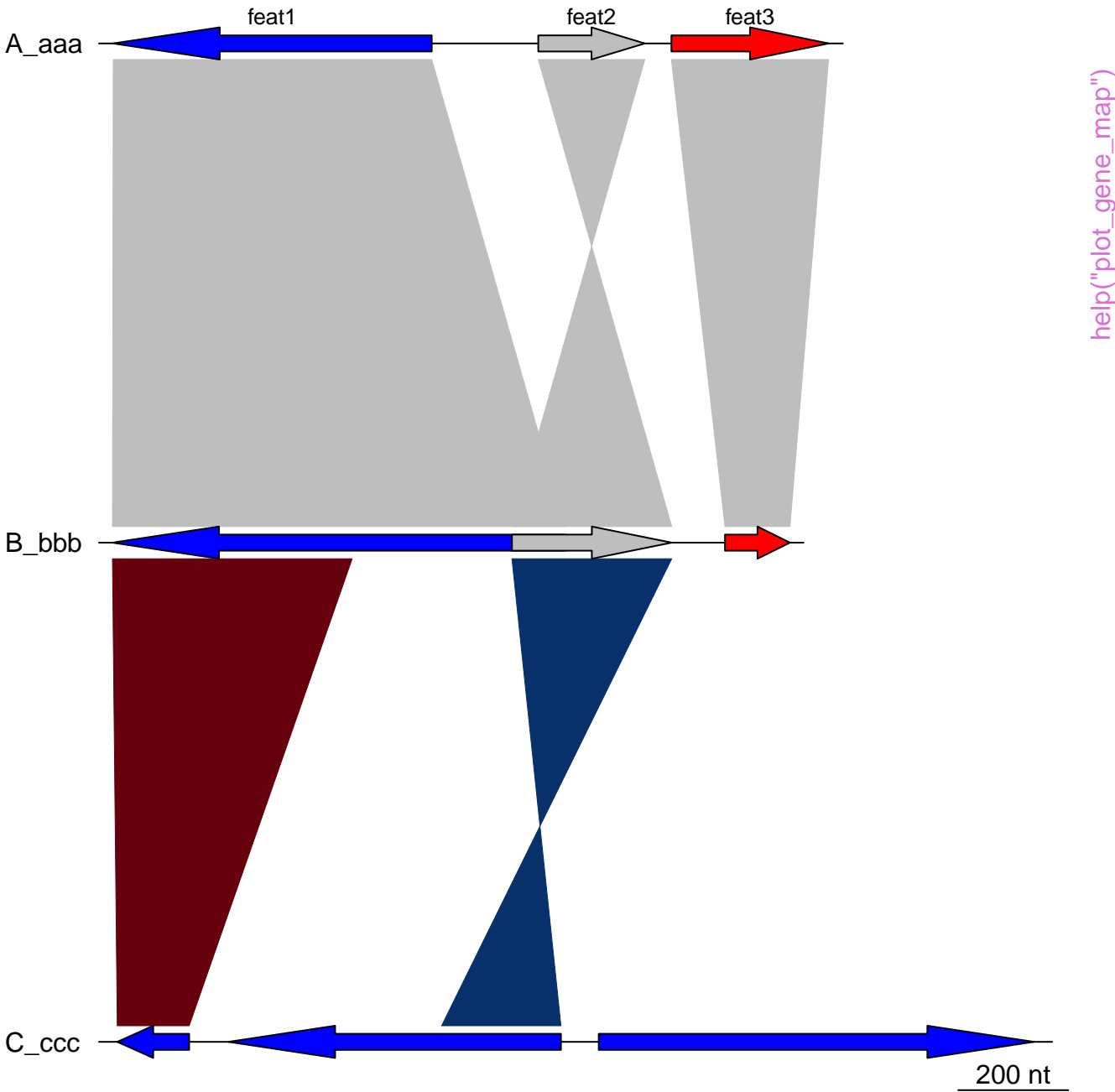


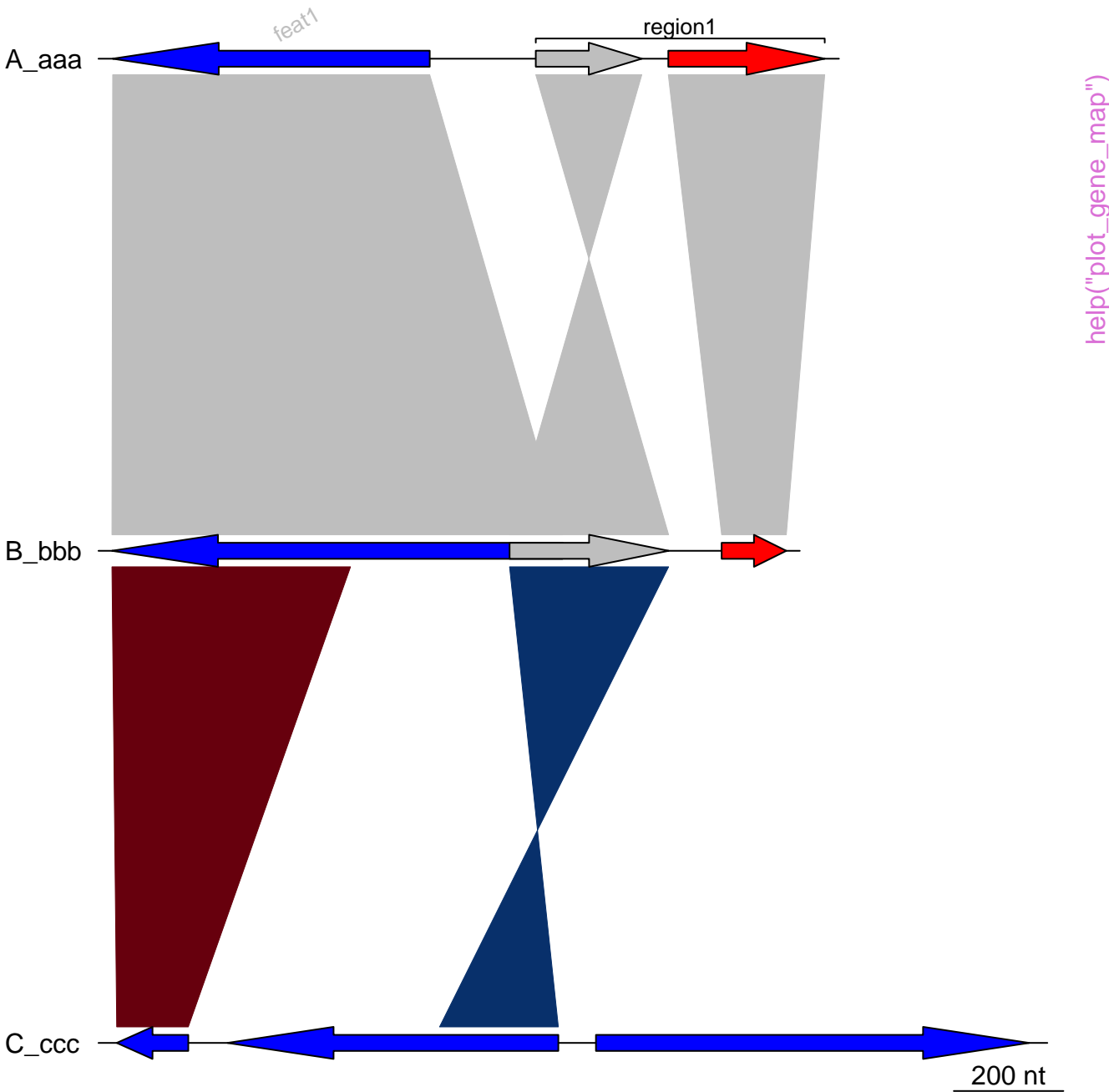


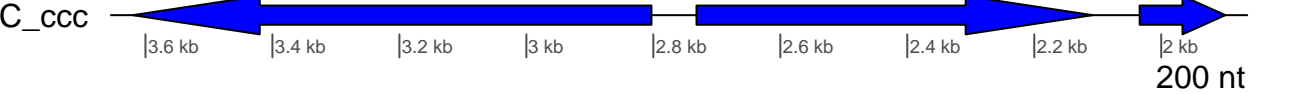
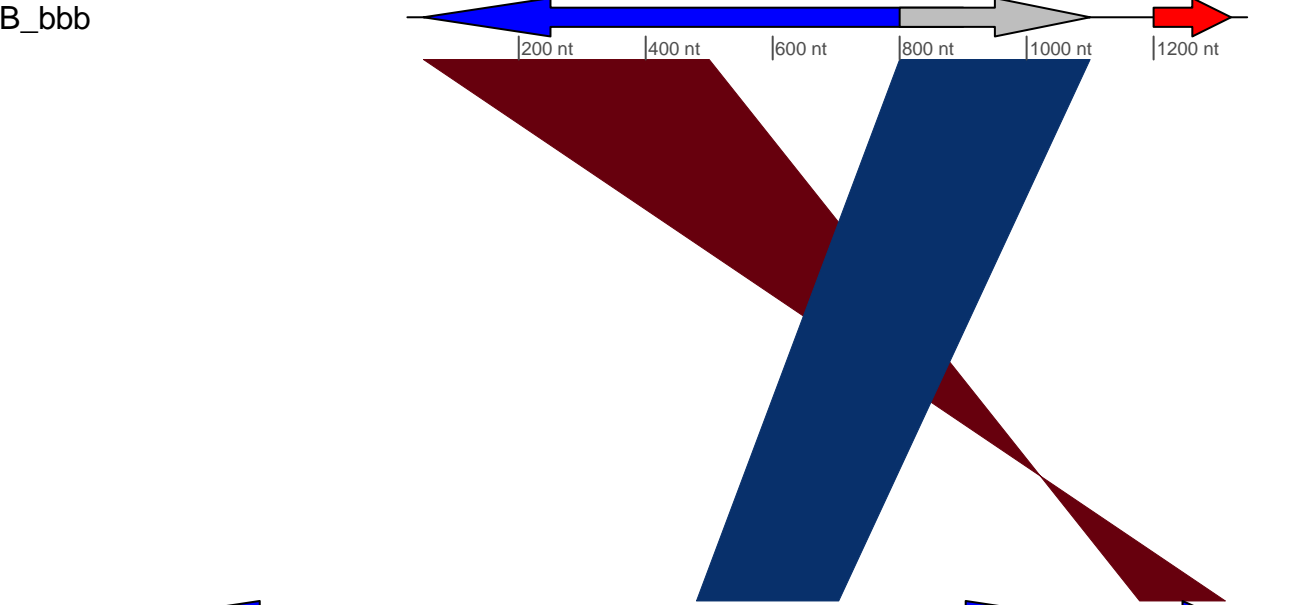
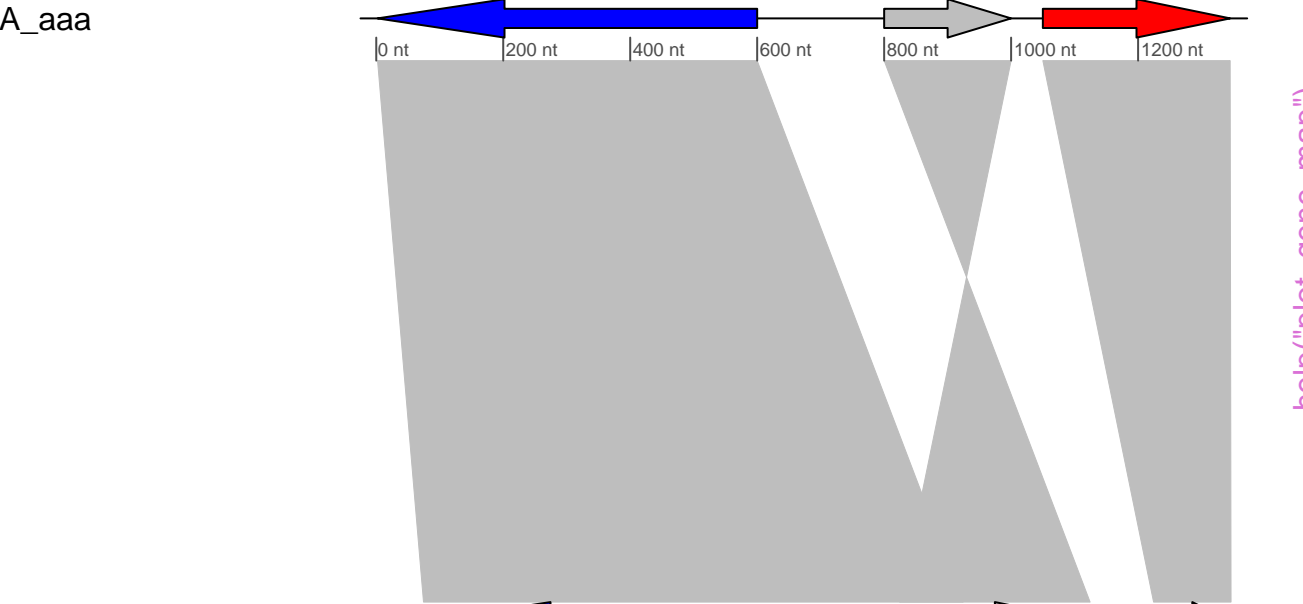


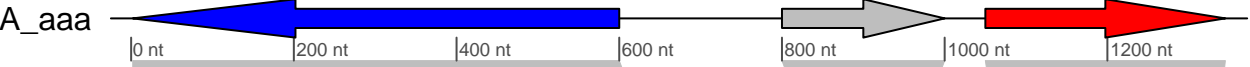






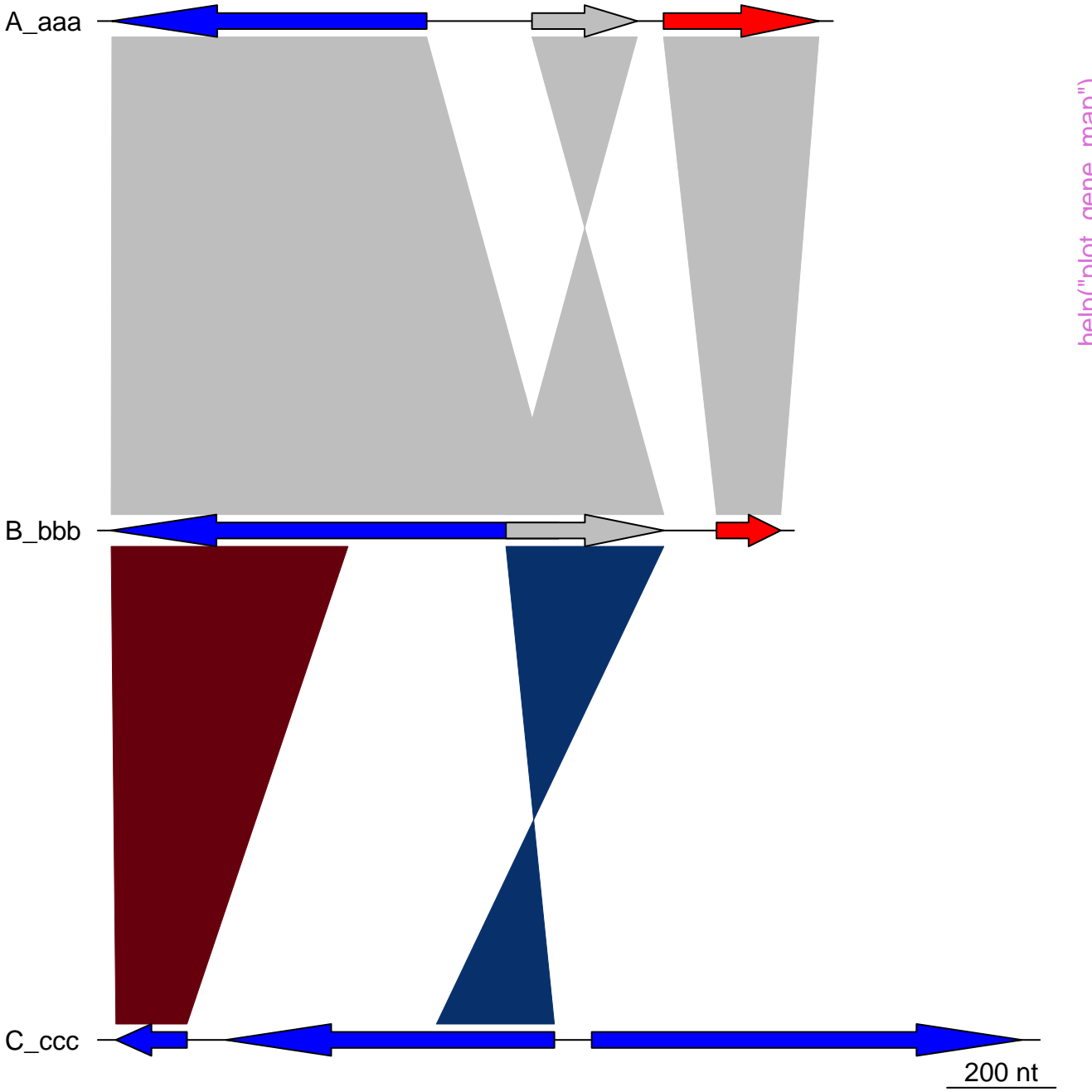




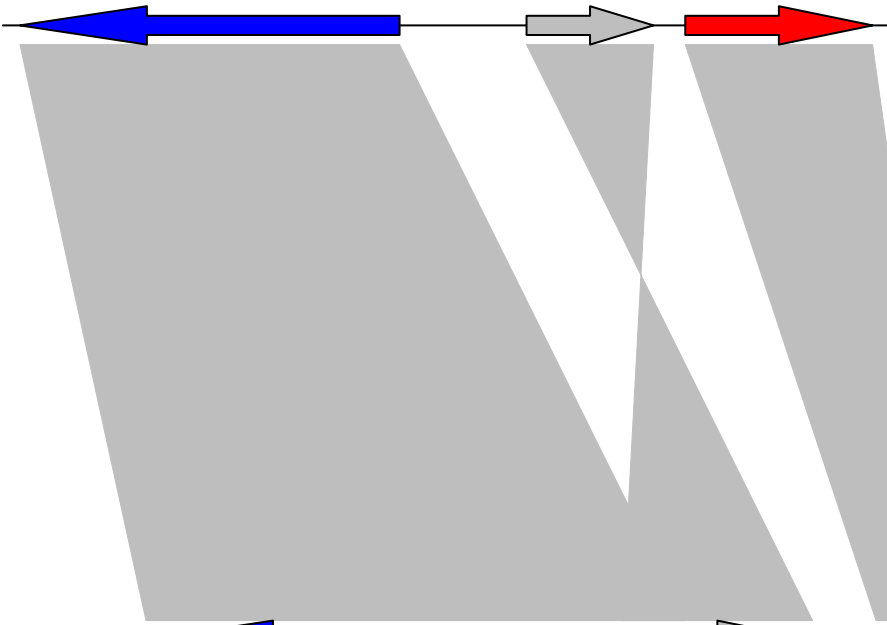


200 nt

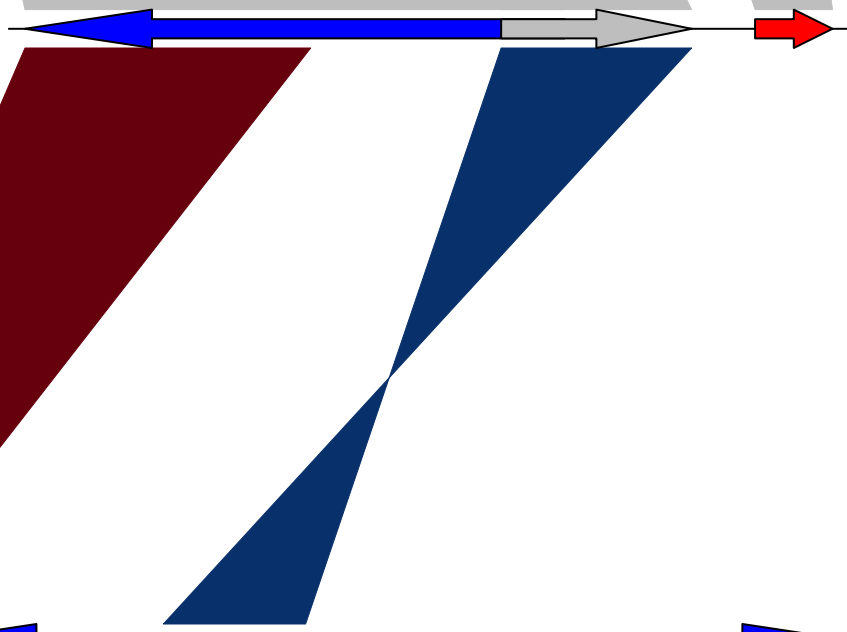
help("plot\_gene\_map")



A\_aaa



B\_bbb



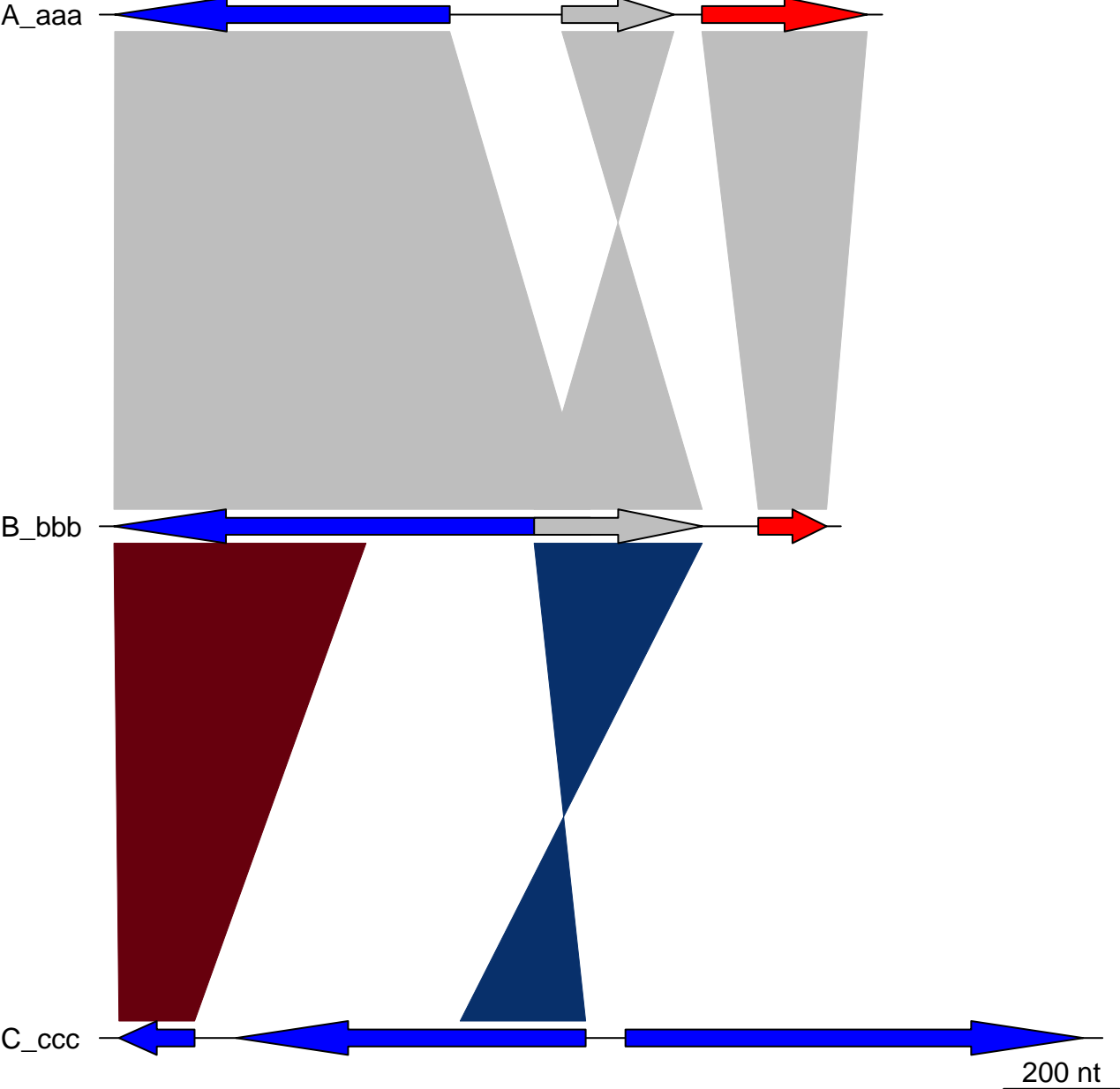
C\_ccc



200 nt

help("plot\_gene\_map")

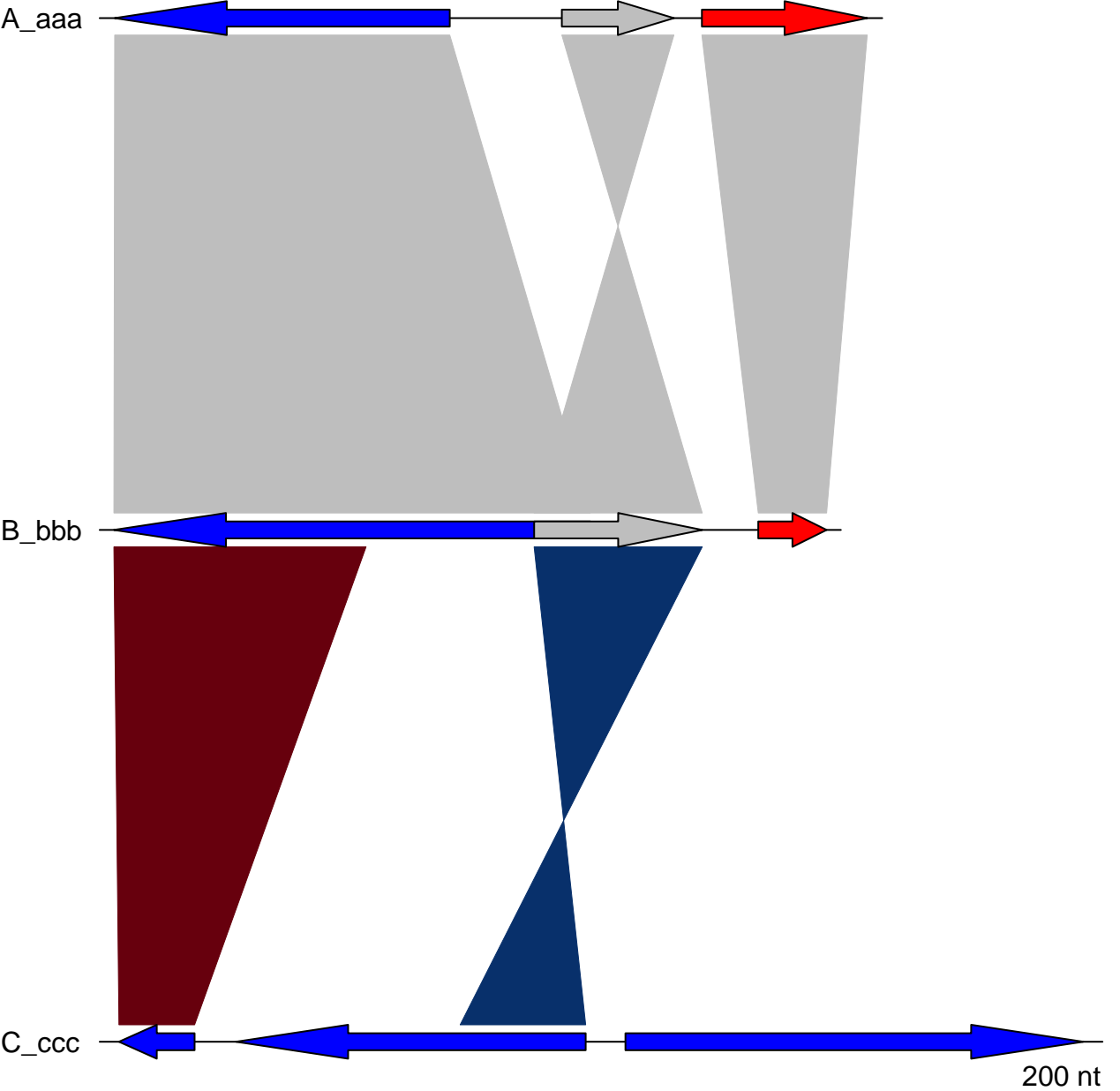
Comparison of A, B and C



help("plot\_gene\_map")

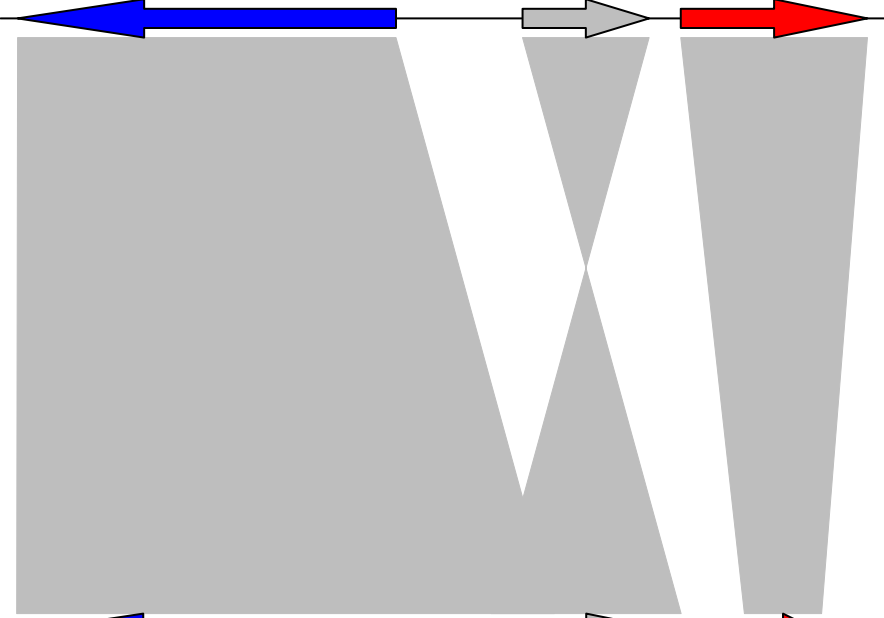


Comparison of A, B and C

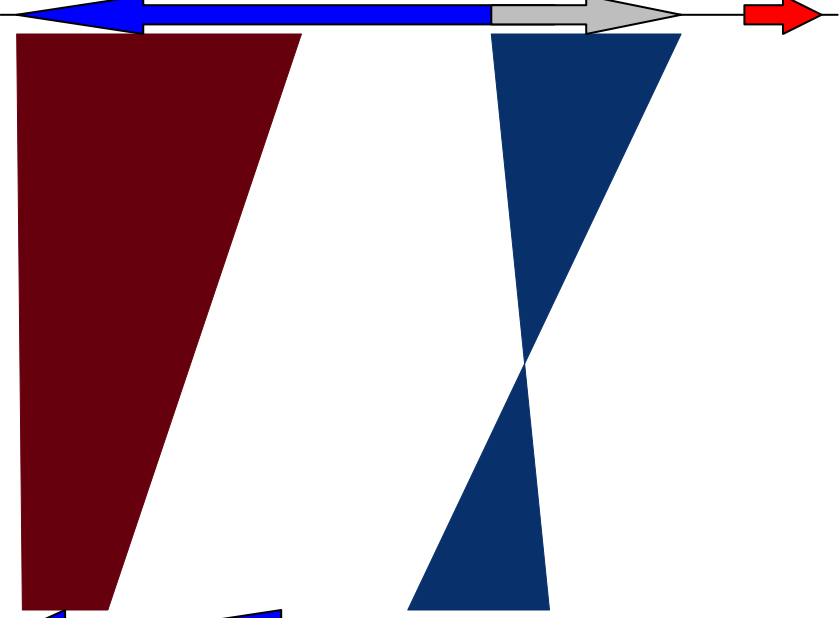


help("plot\_gene\_map")

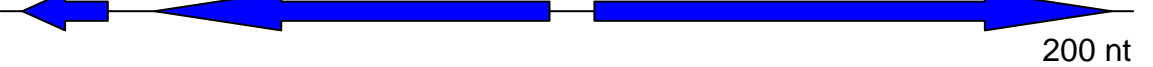
Huey



Dewey



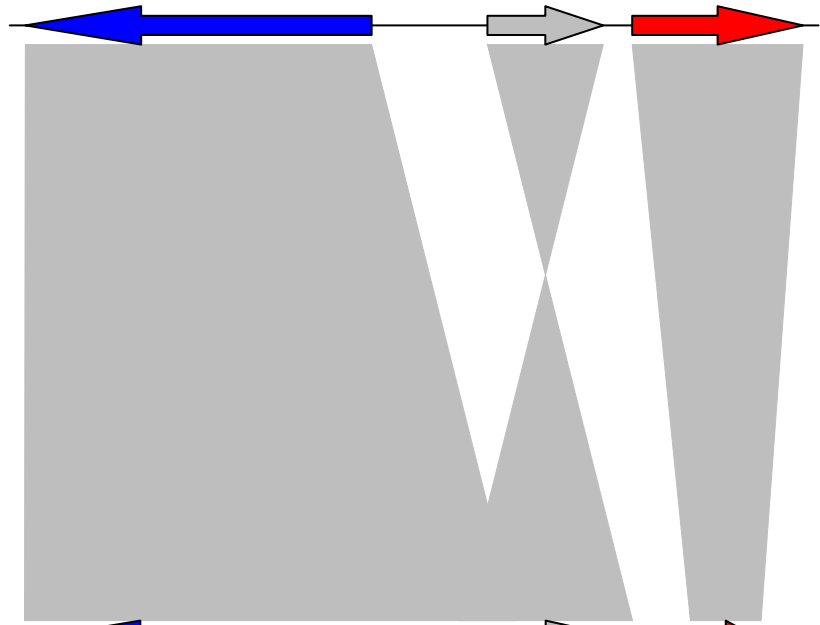
Louie



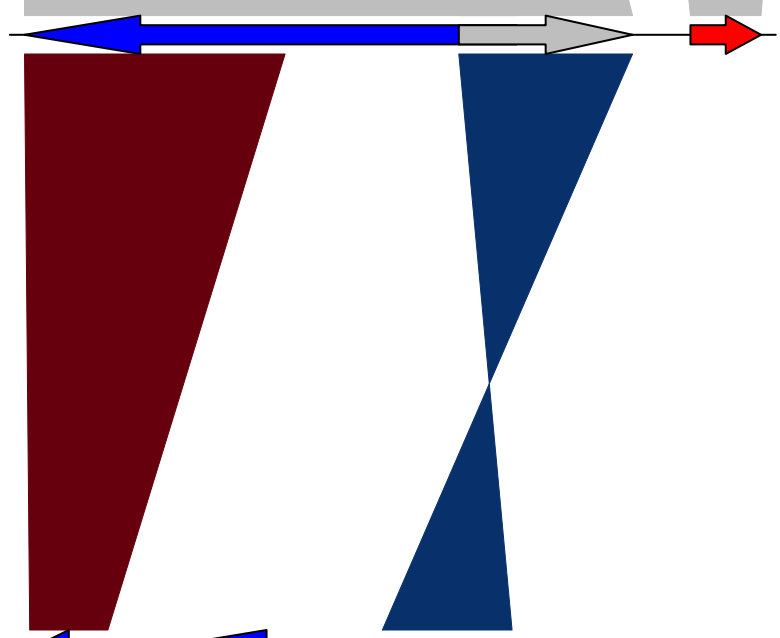
200 nt

help("plot\_gene\_map")

Huey



Dewey

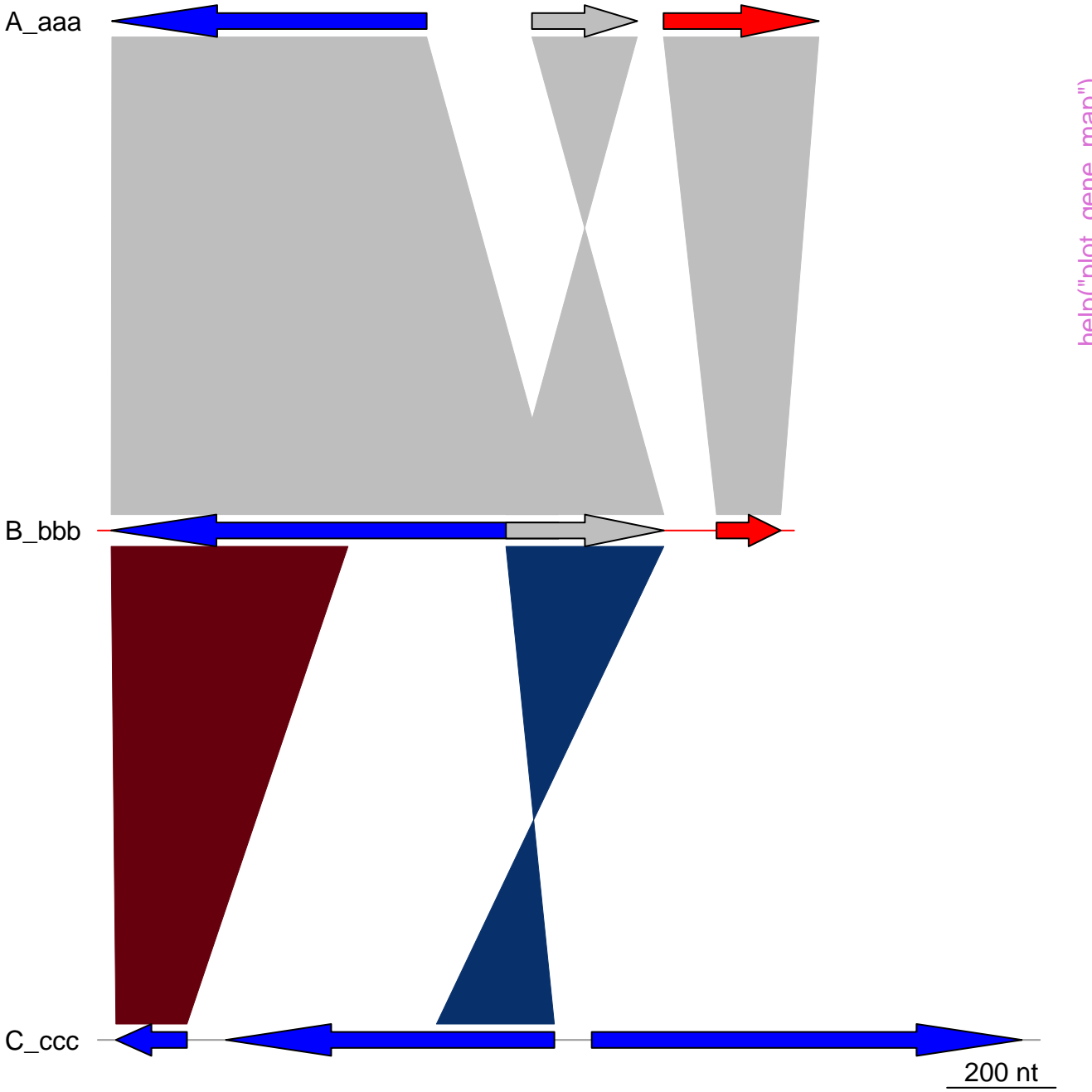


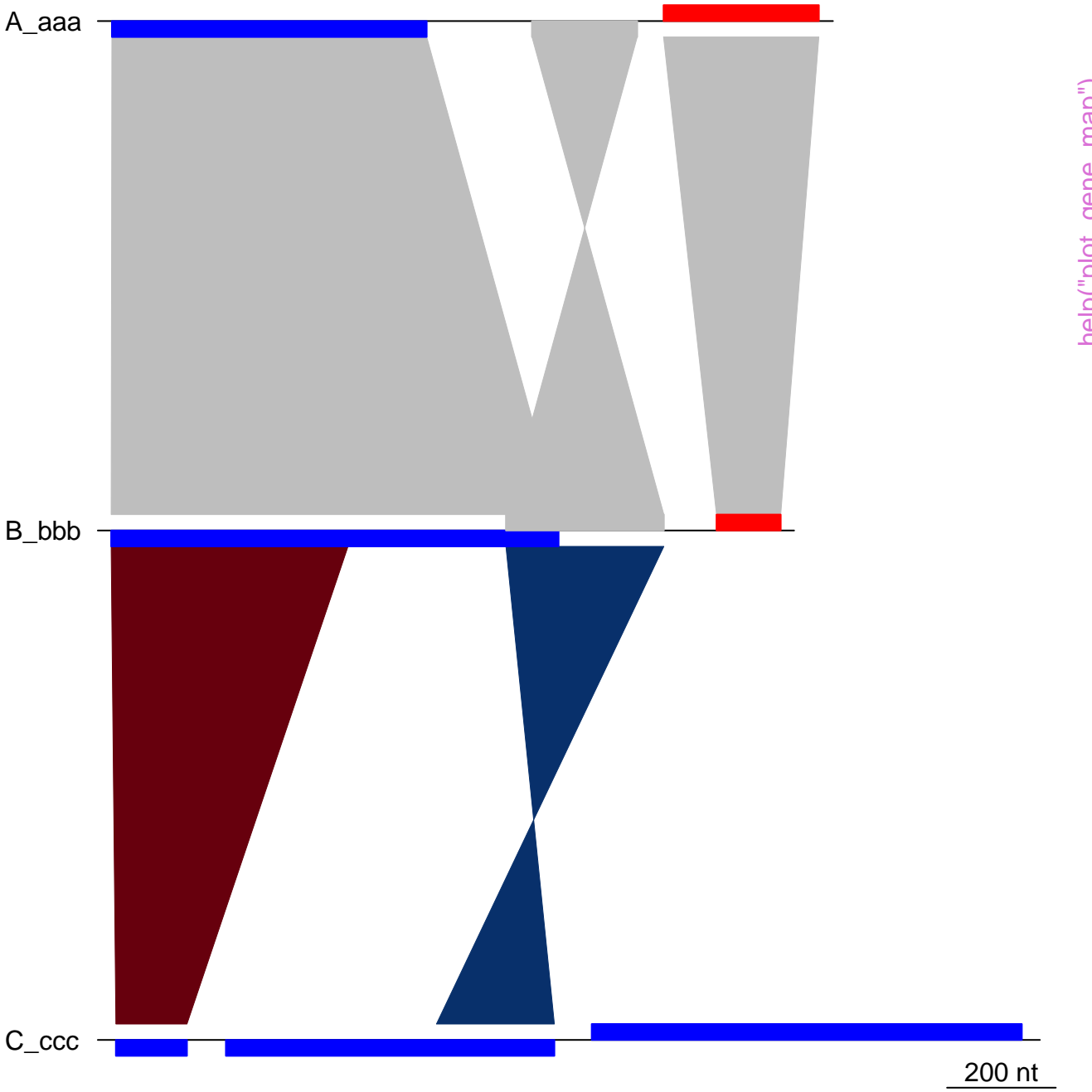
Louie

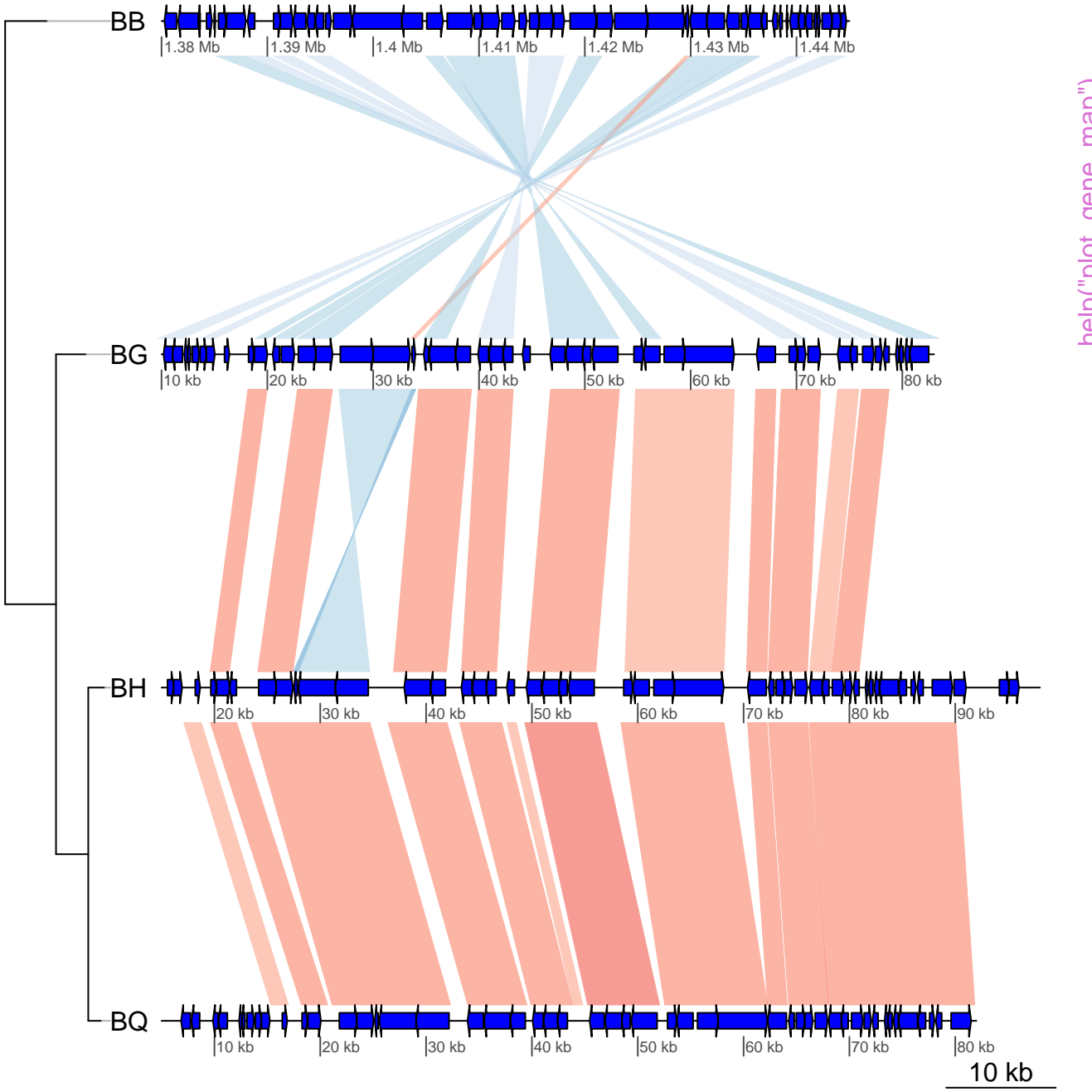


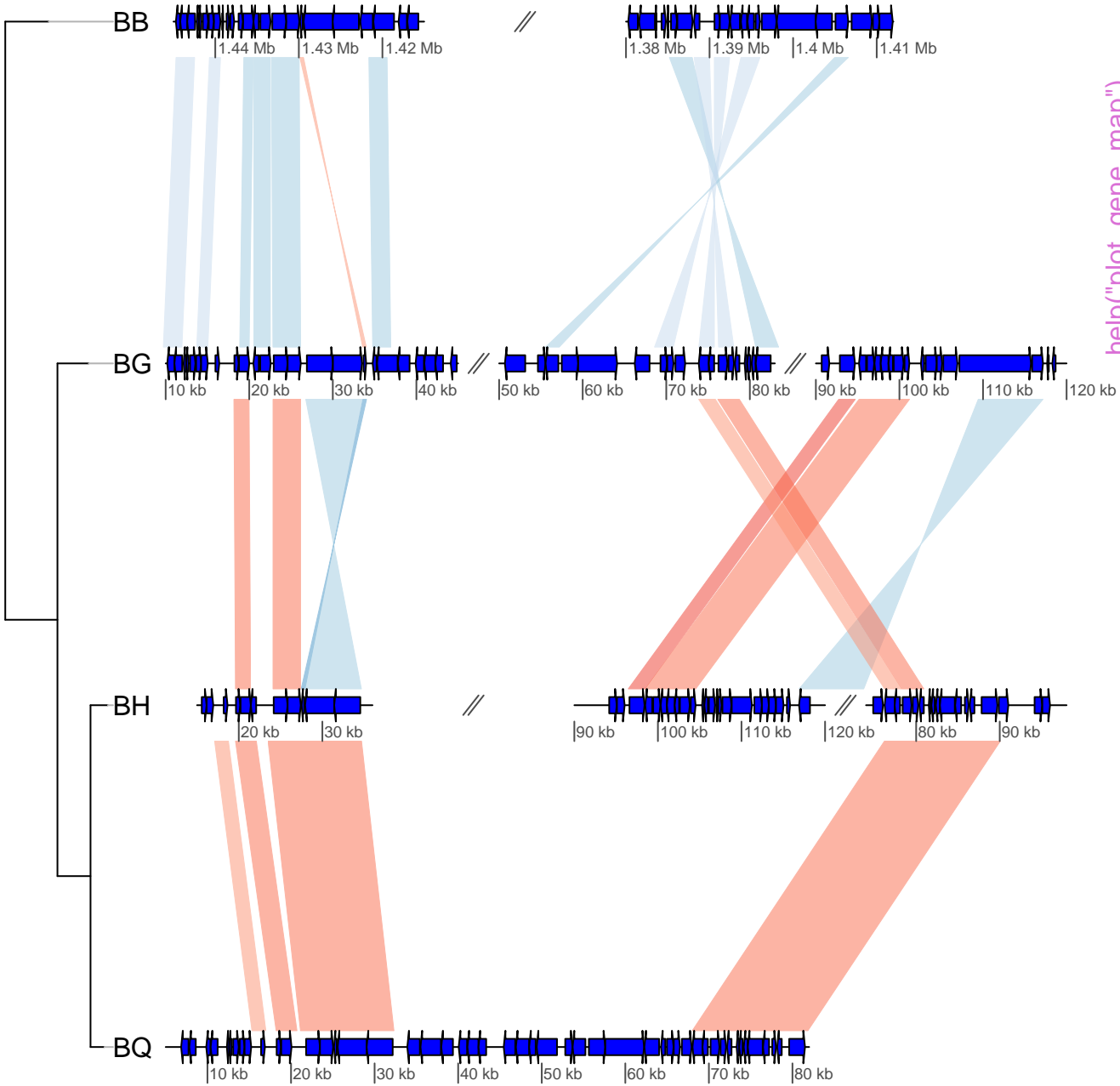
200 nt

help("plot\_gene\_map")









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

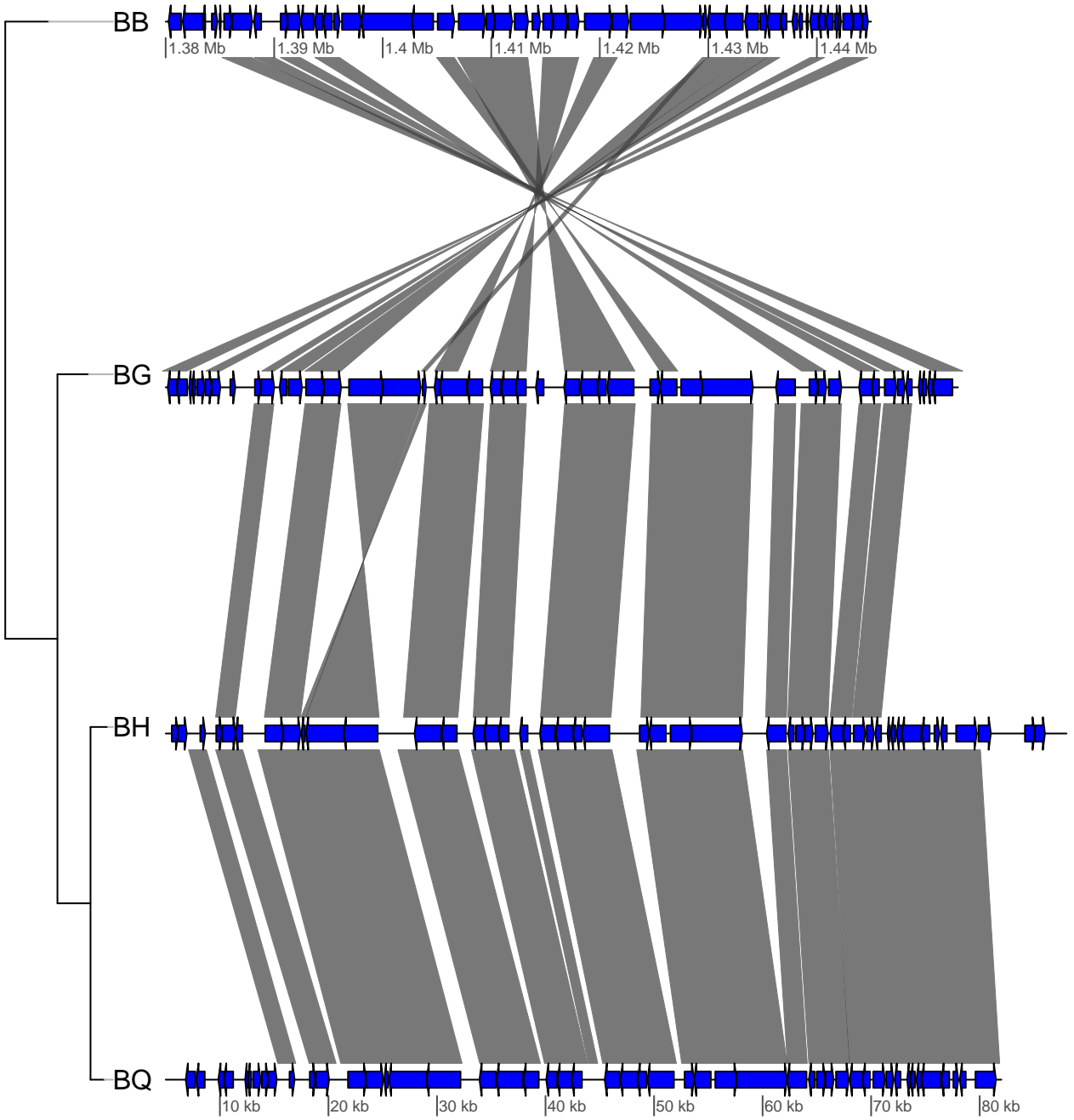
BG

BH

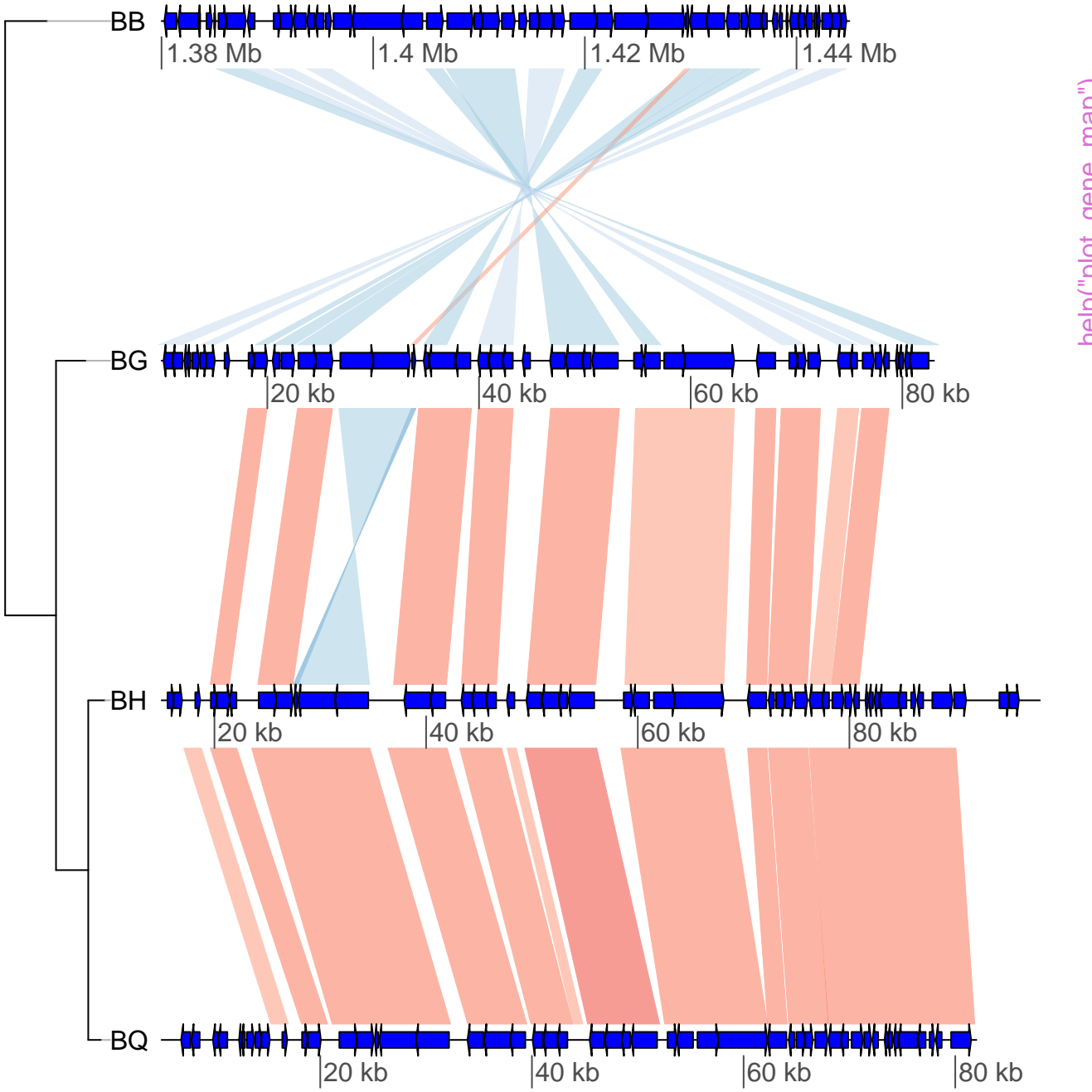
BQ

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

help("plot\_gene\_map")



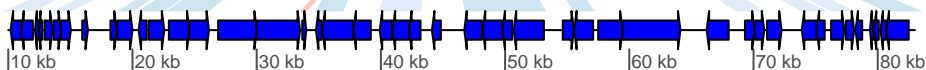




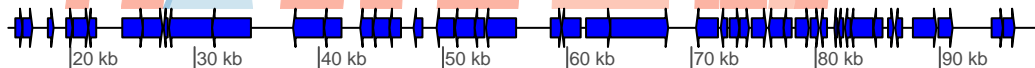
BB



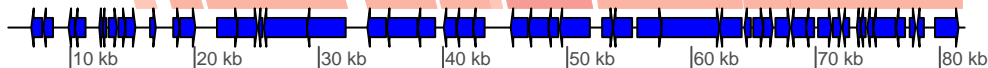
BG



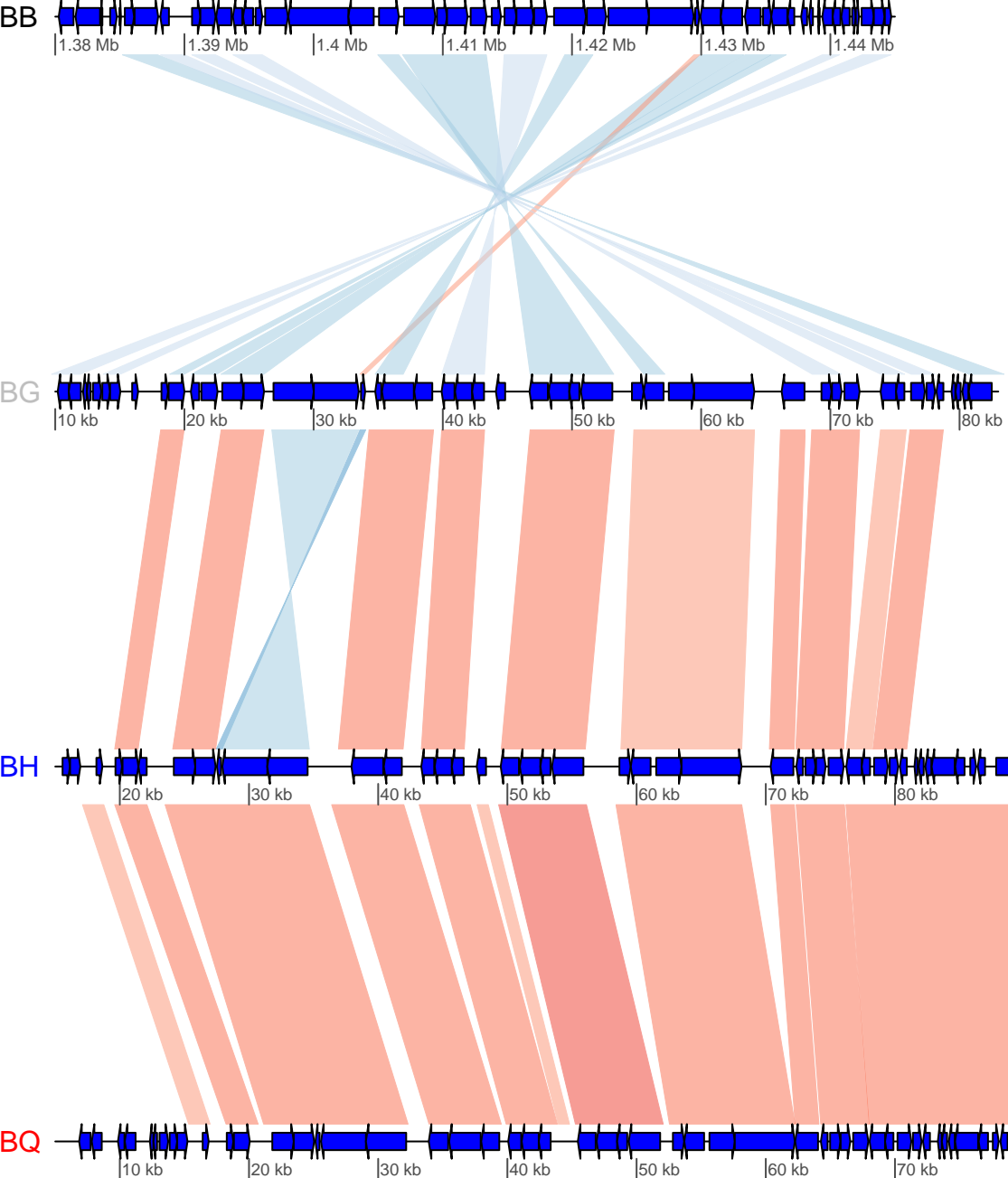
BH



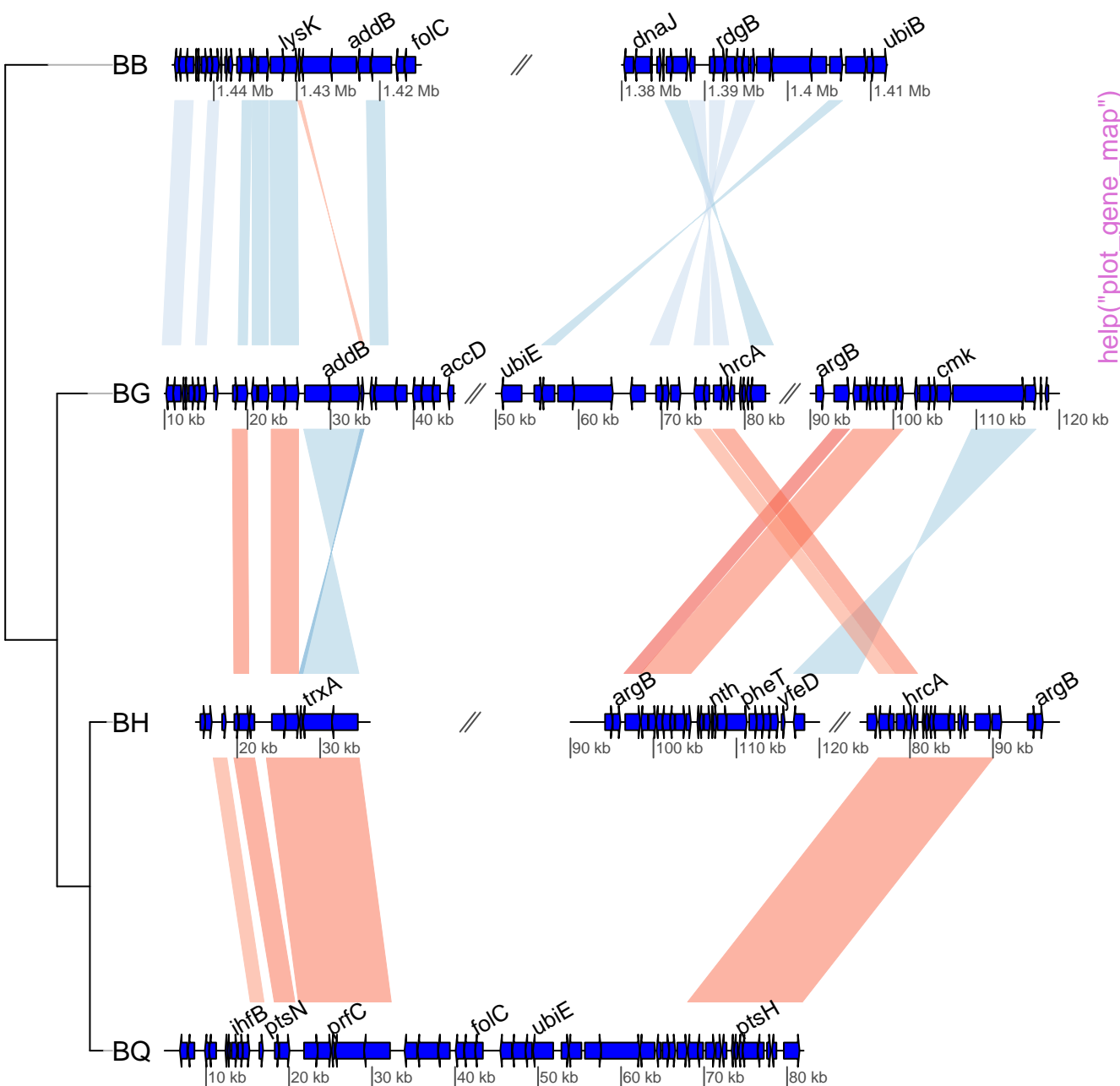
BQ



help("plot\_gene\_map")



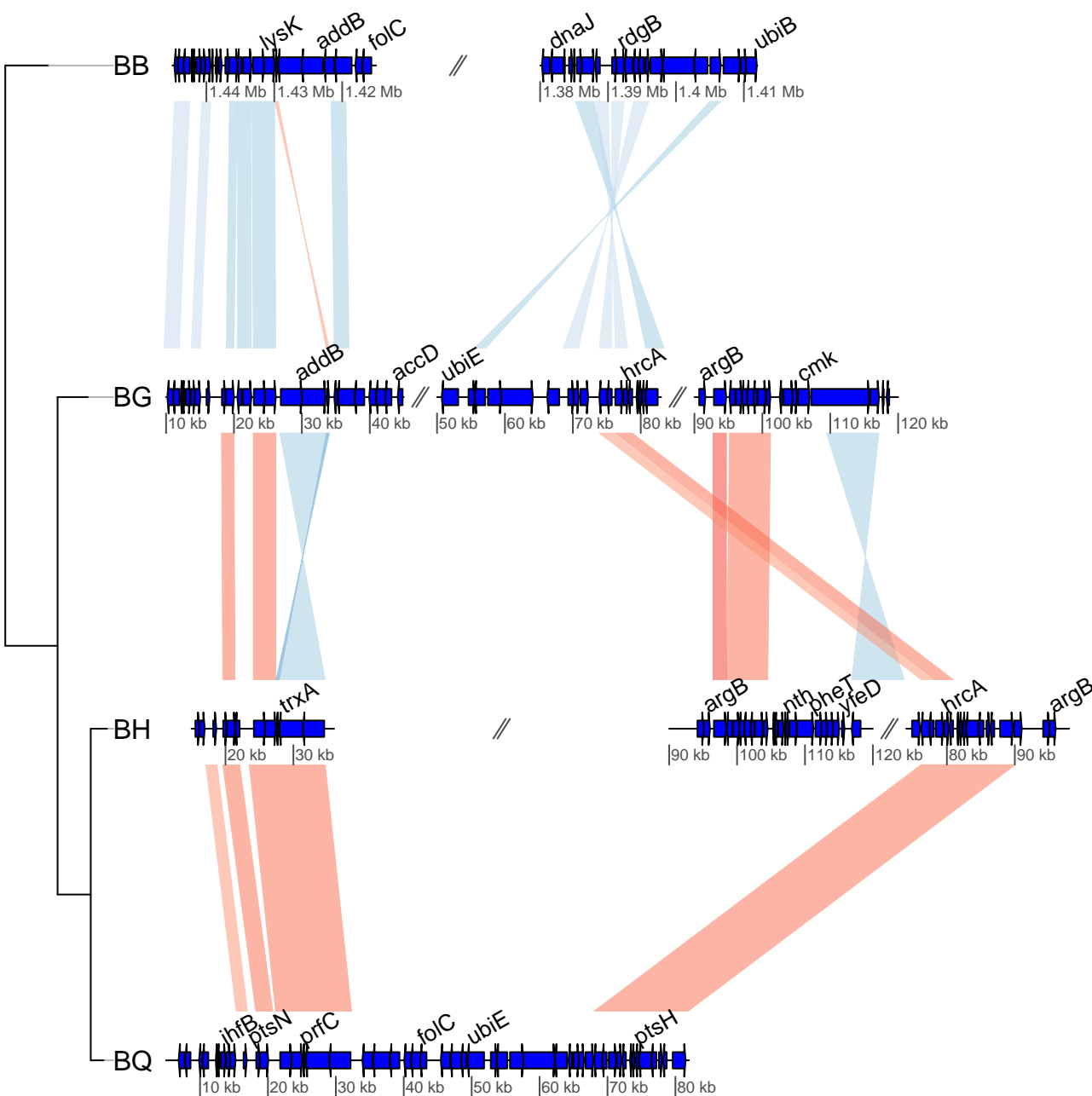
help("plot\_gene\_map")



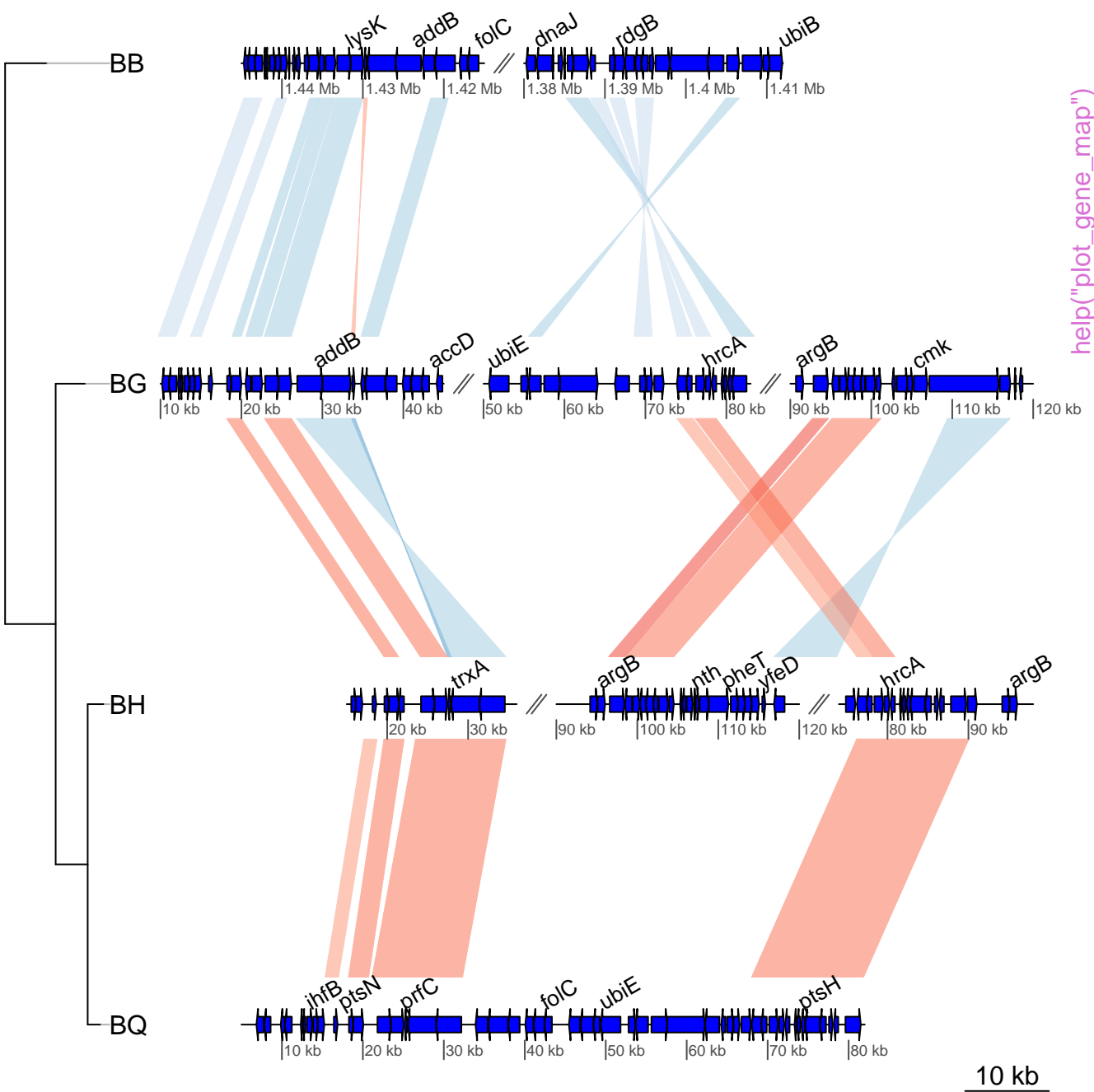
help("plot\_gene\_map")

10 kb

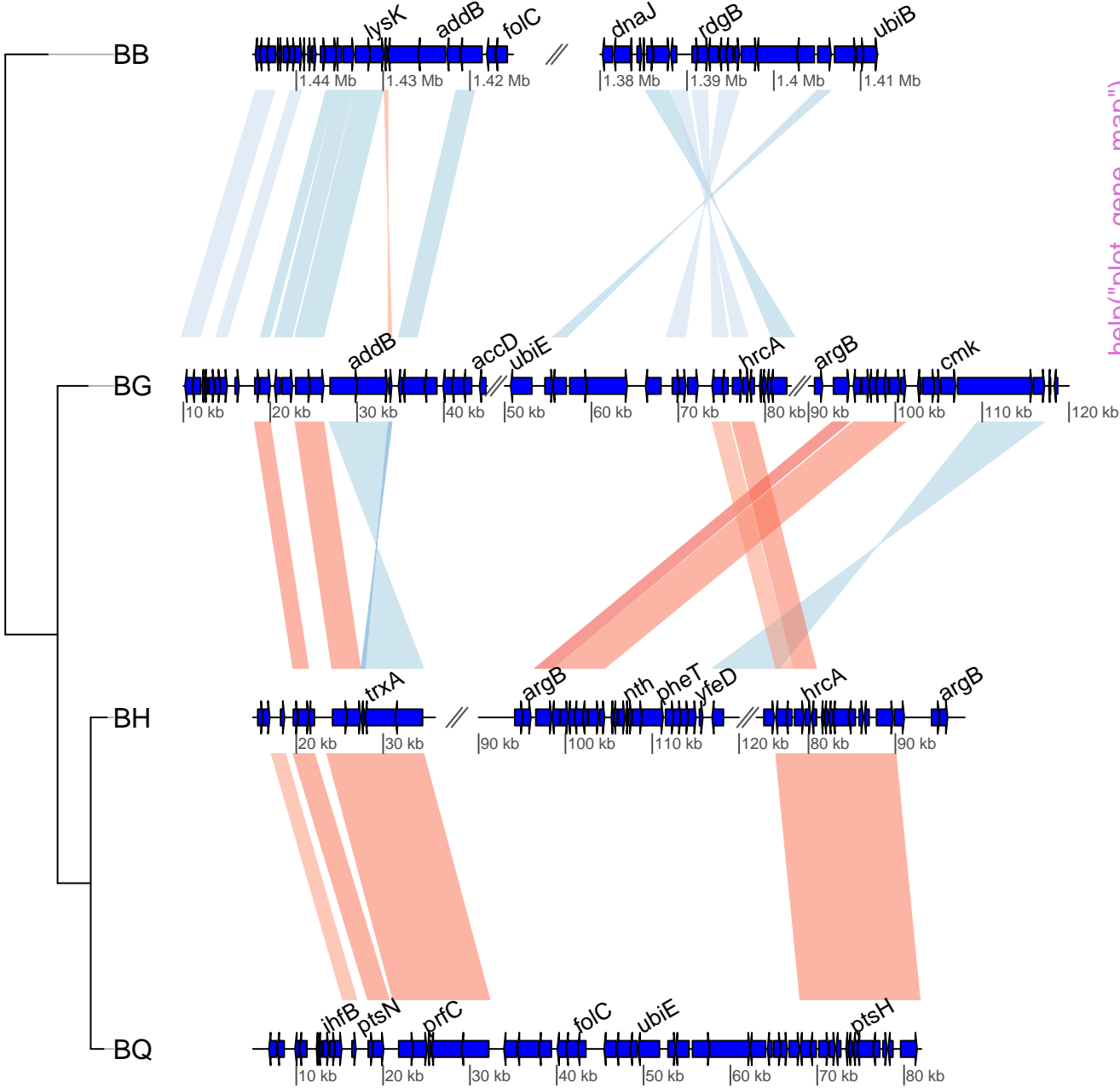
help("plot\_gene\_map")



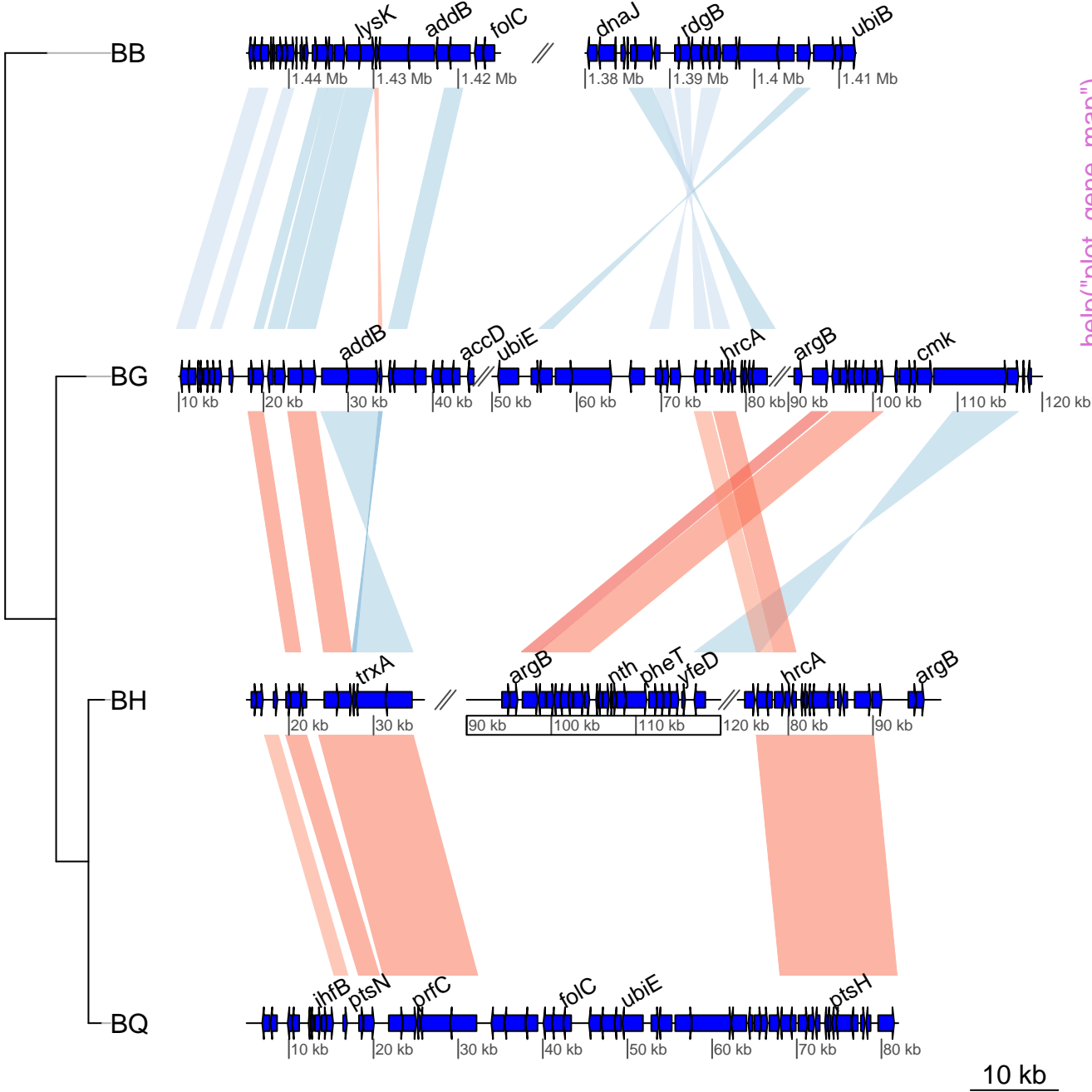
20 kb



help("plot\_gene\_map")

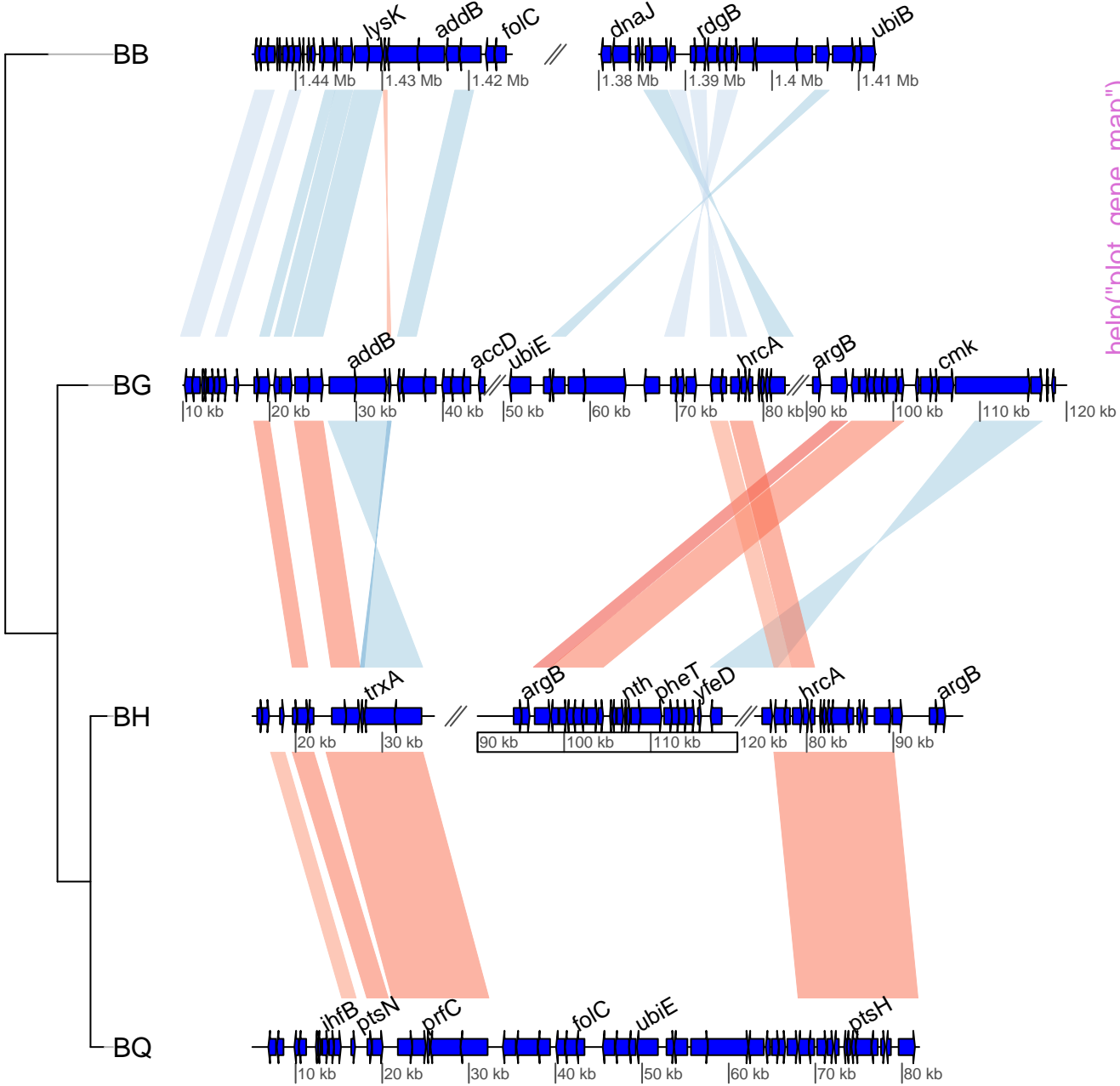


help("plot\_gene\_map")



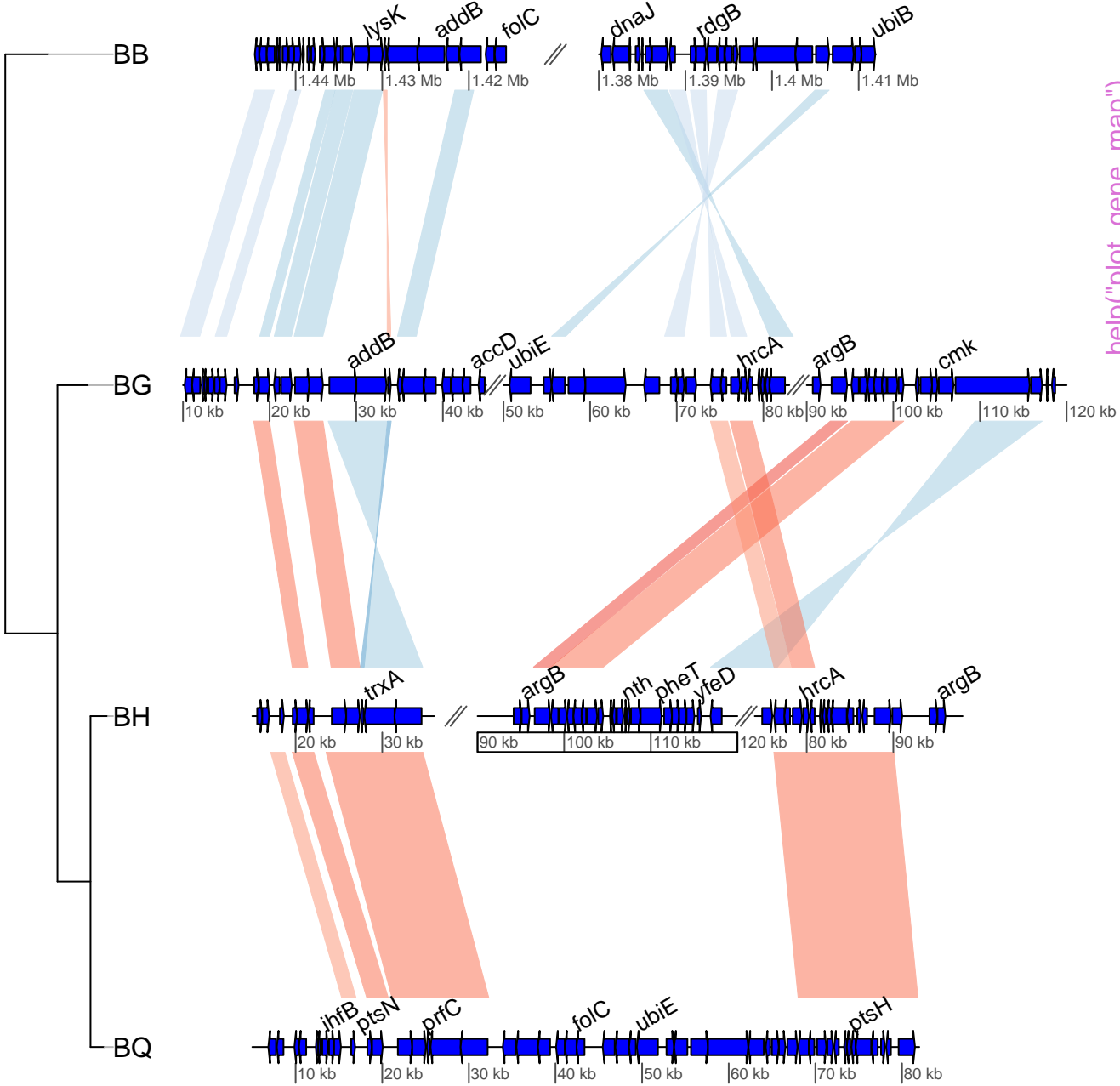


help("plot\_gene\_map")

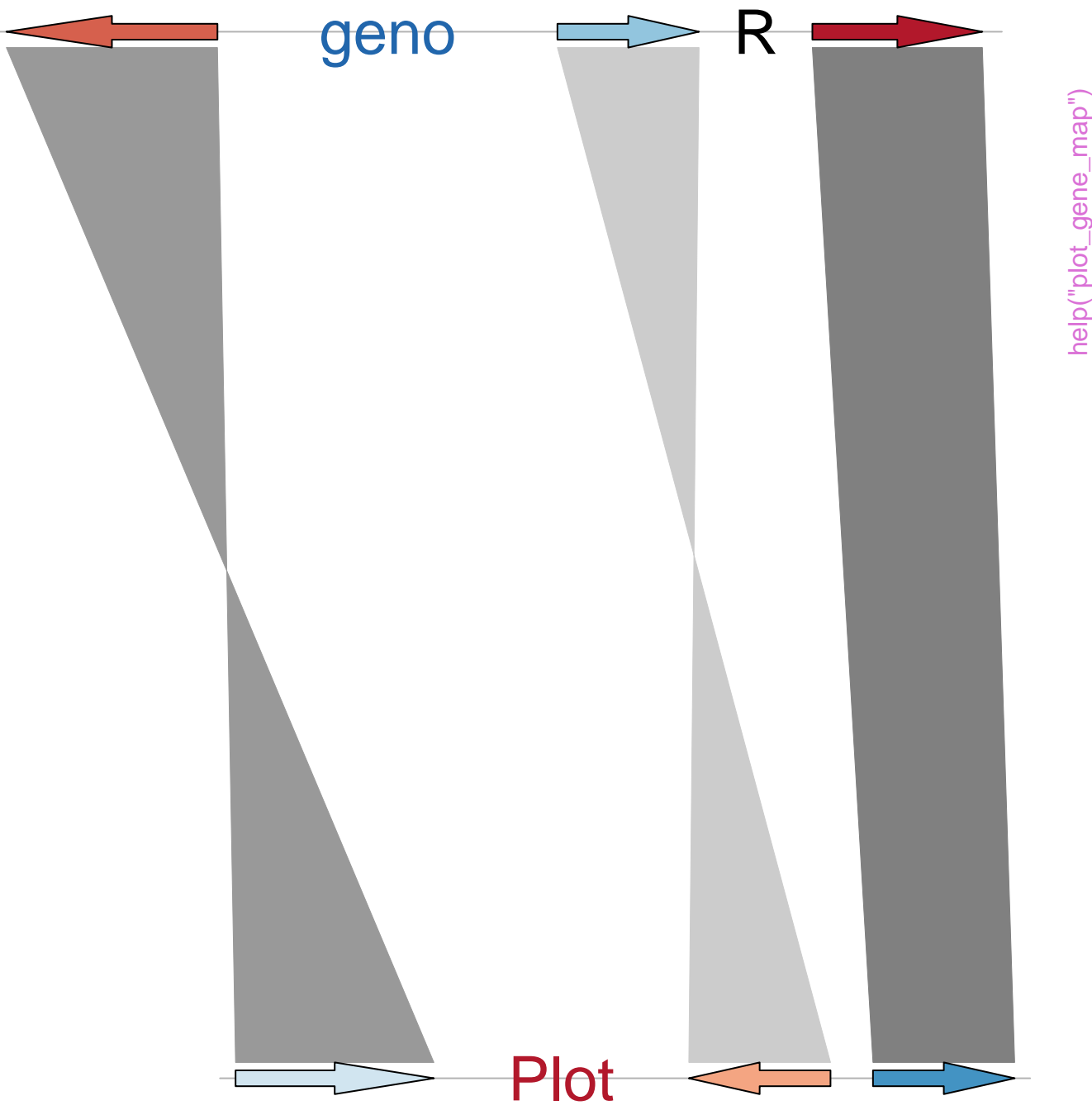


10 kb

help("plot\_gene\_map")



10 kb

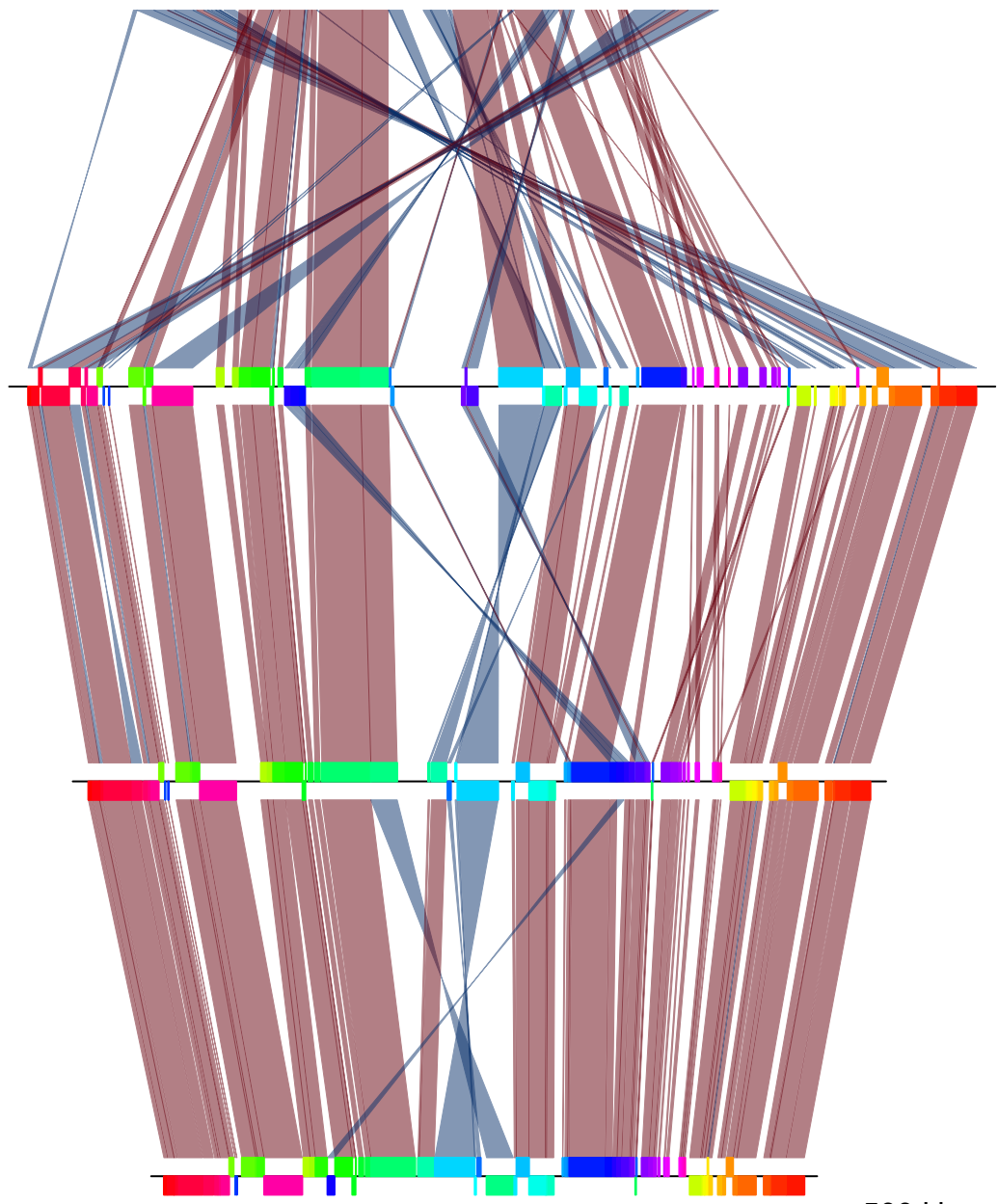
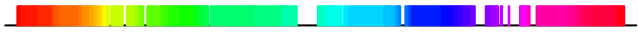


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

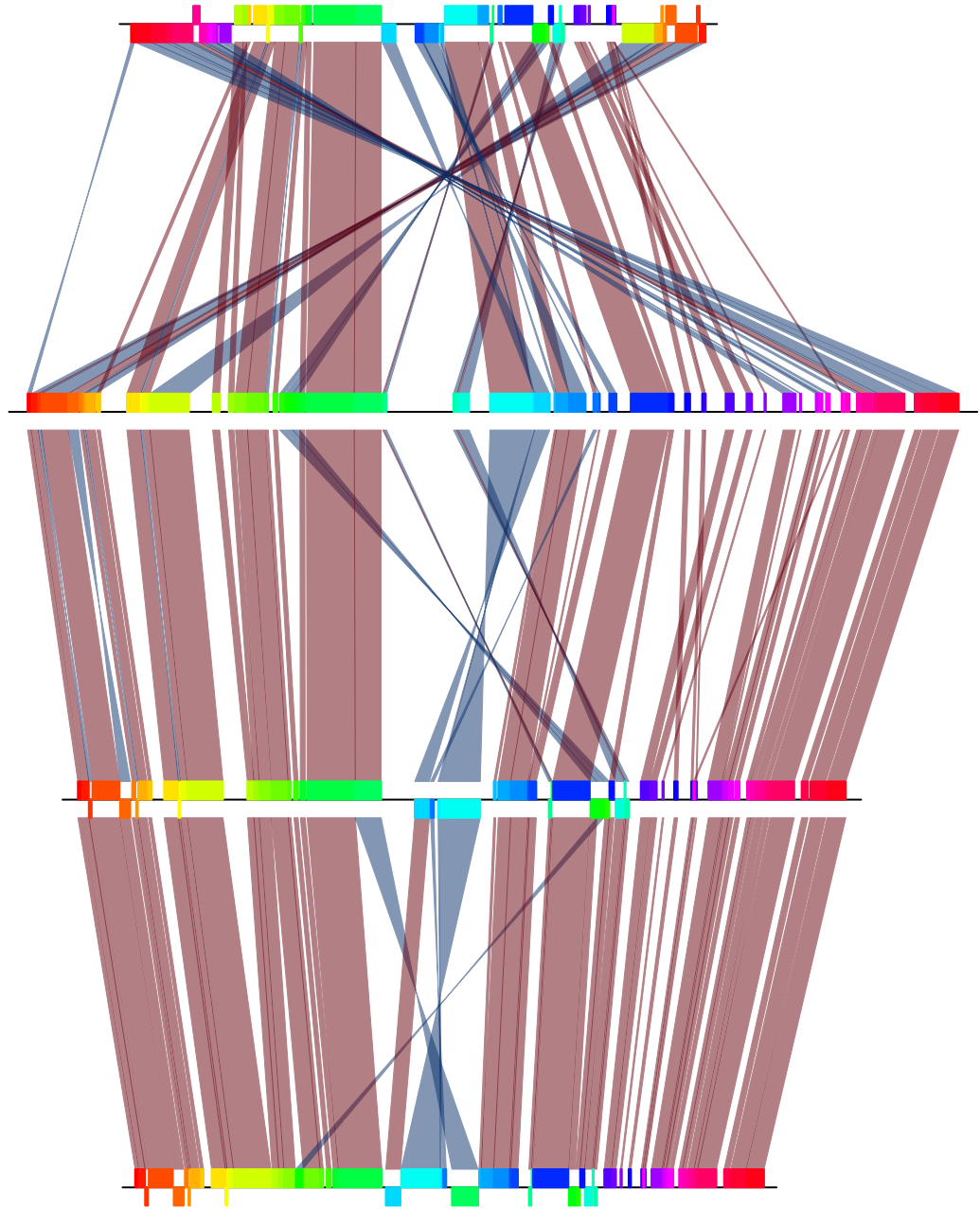
500 kb

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



B bacilliformis

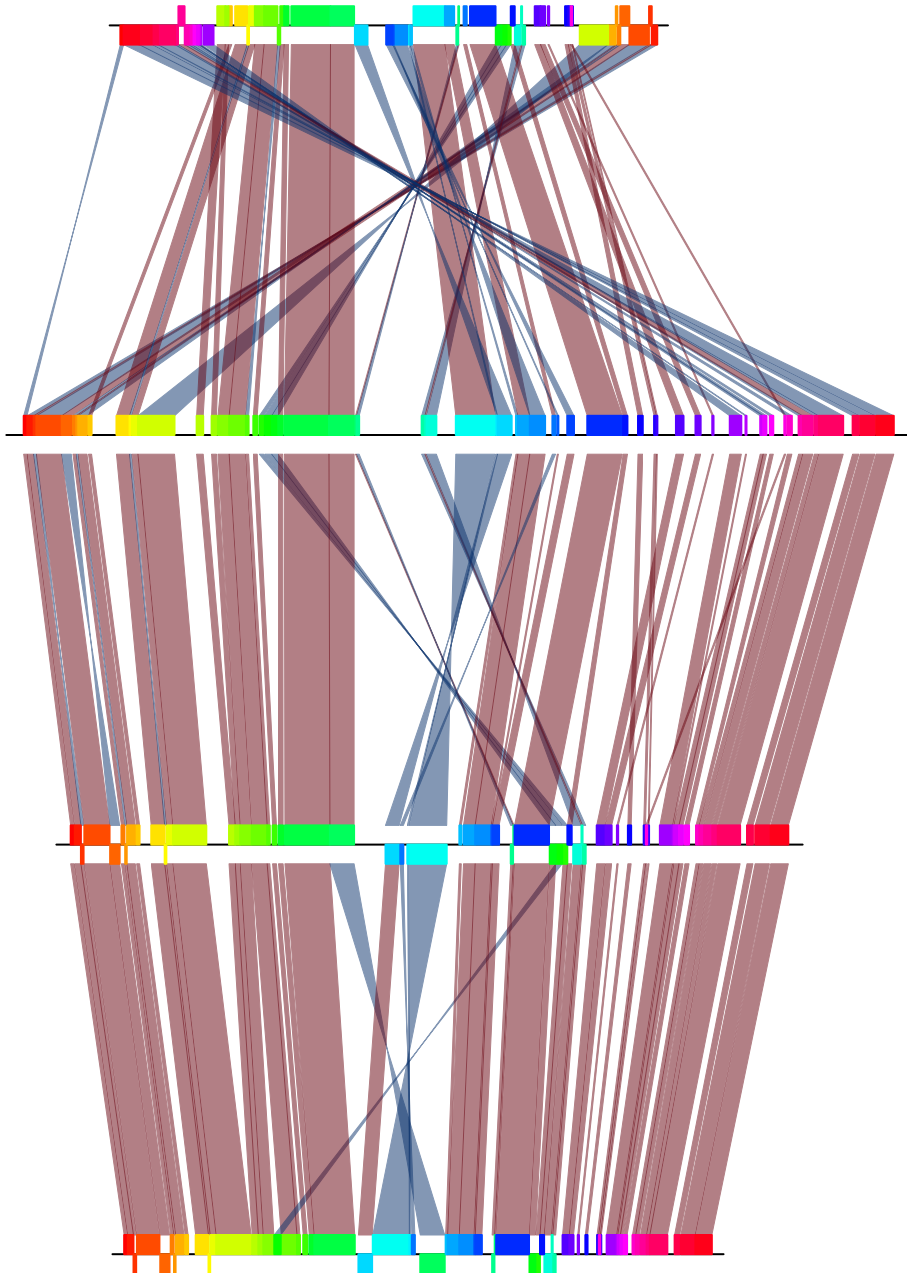
B grahamii

B henselae

B quintana

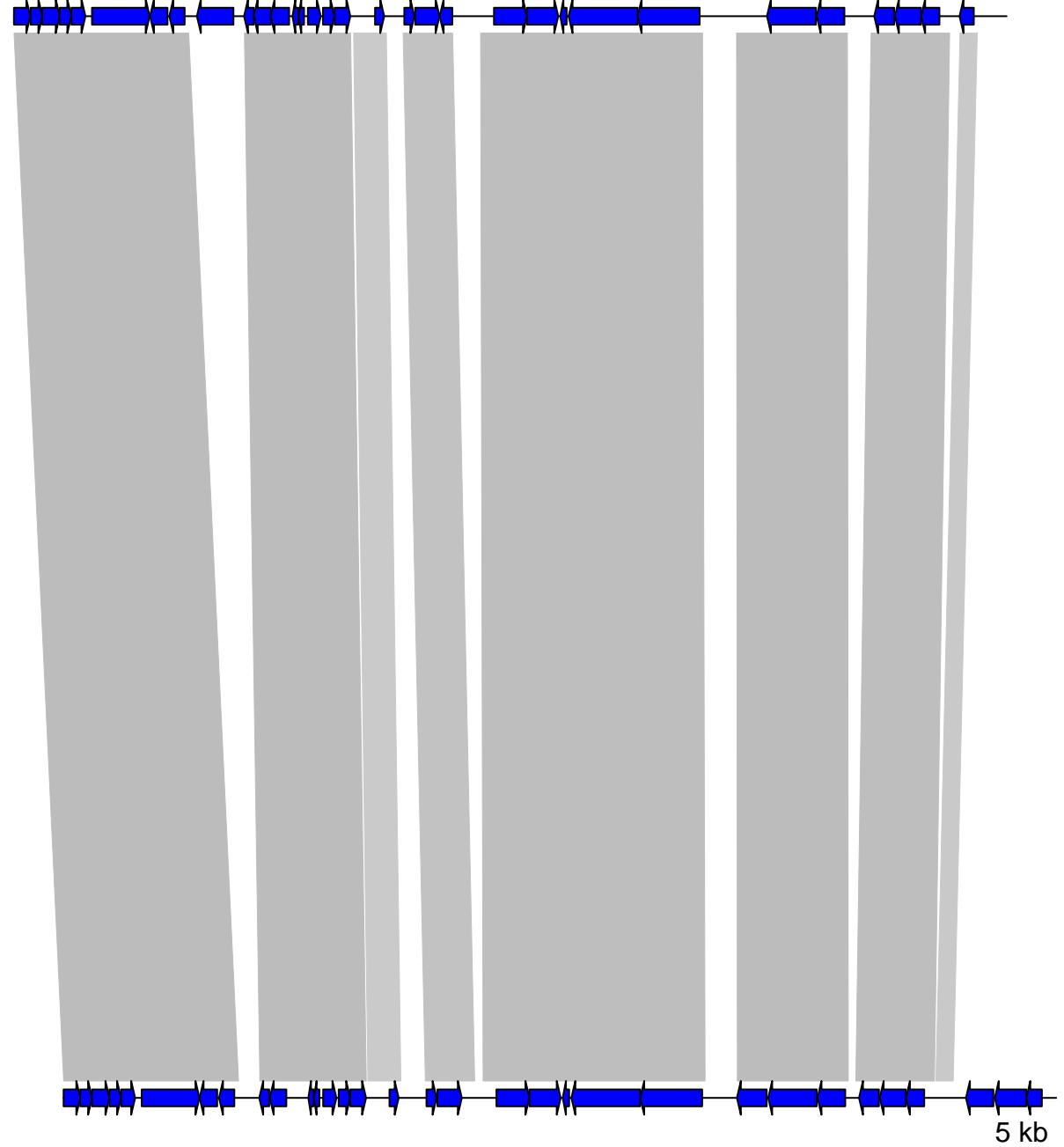
help("read\_functions")

500 kb



BH

BQ



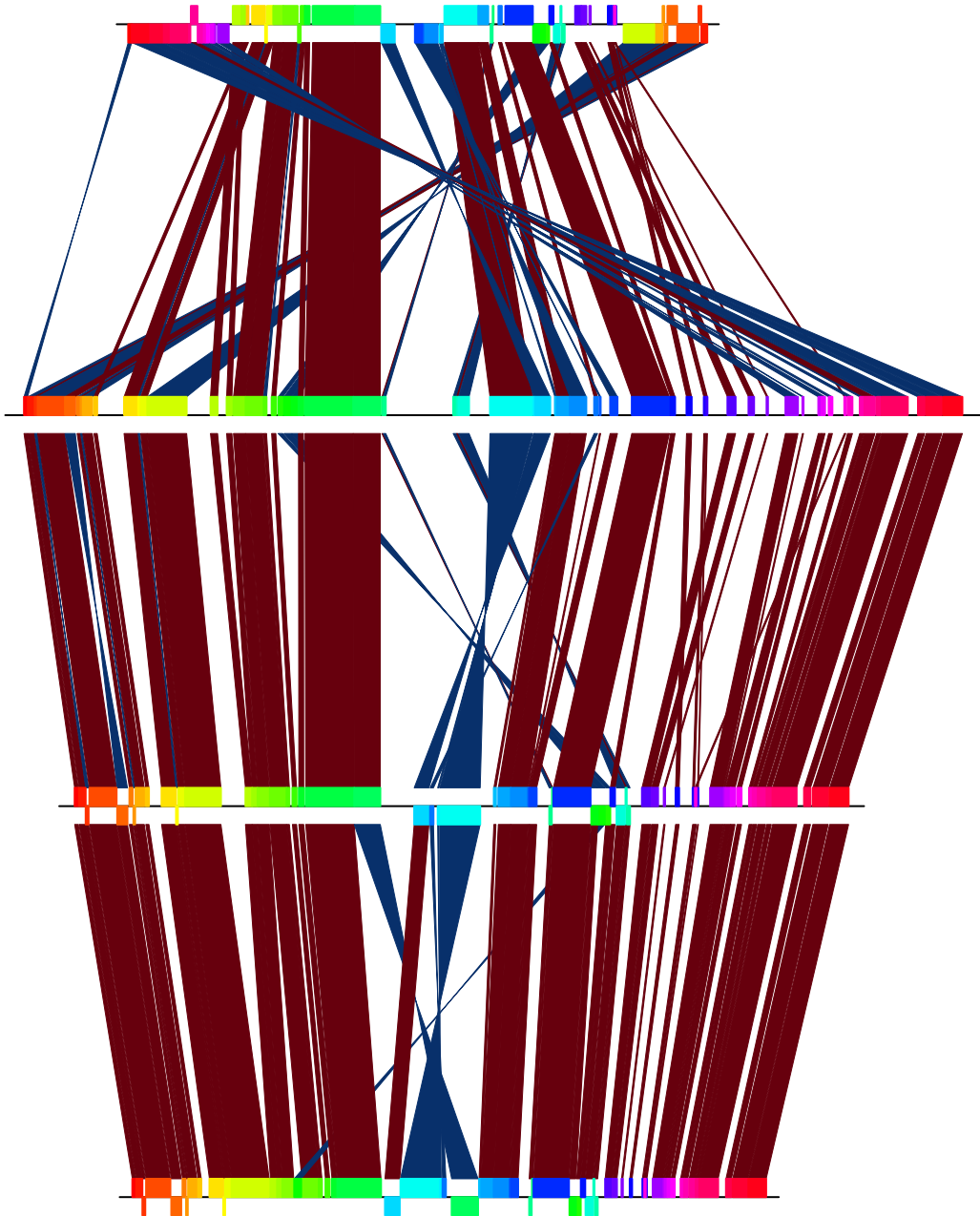
help("read\_functions")

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("reverse")

500 kb



B\_bacilliformis

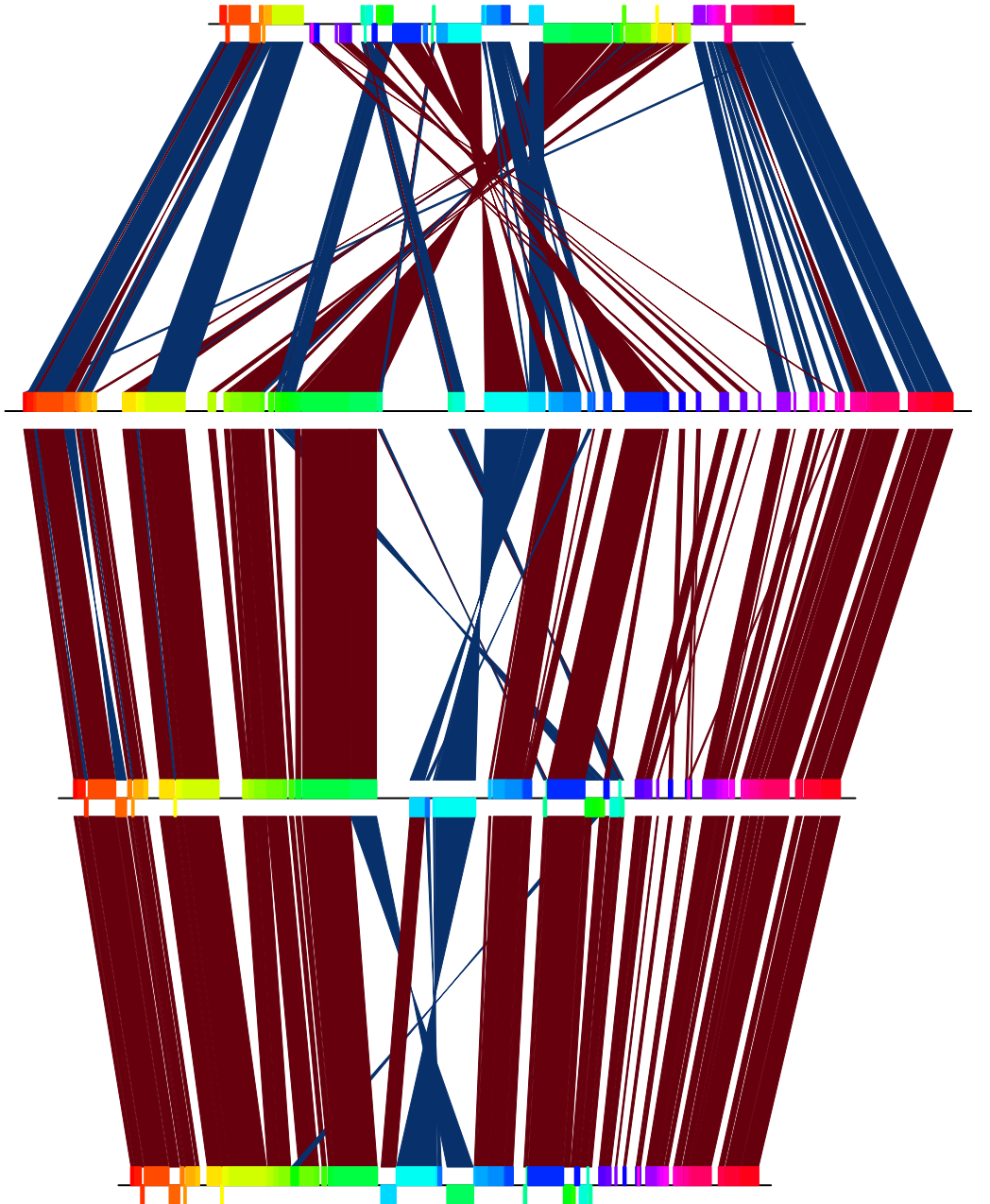
B\_grahamii

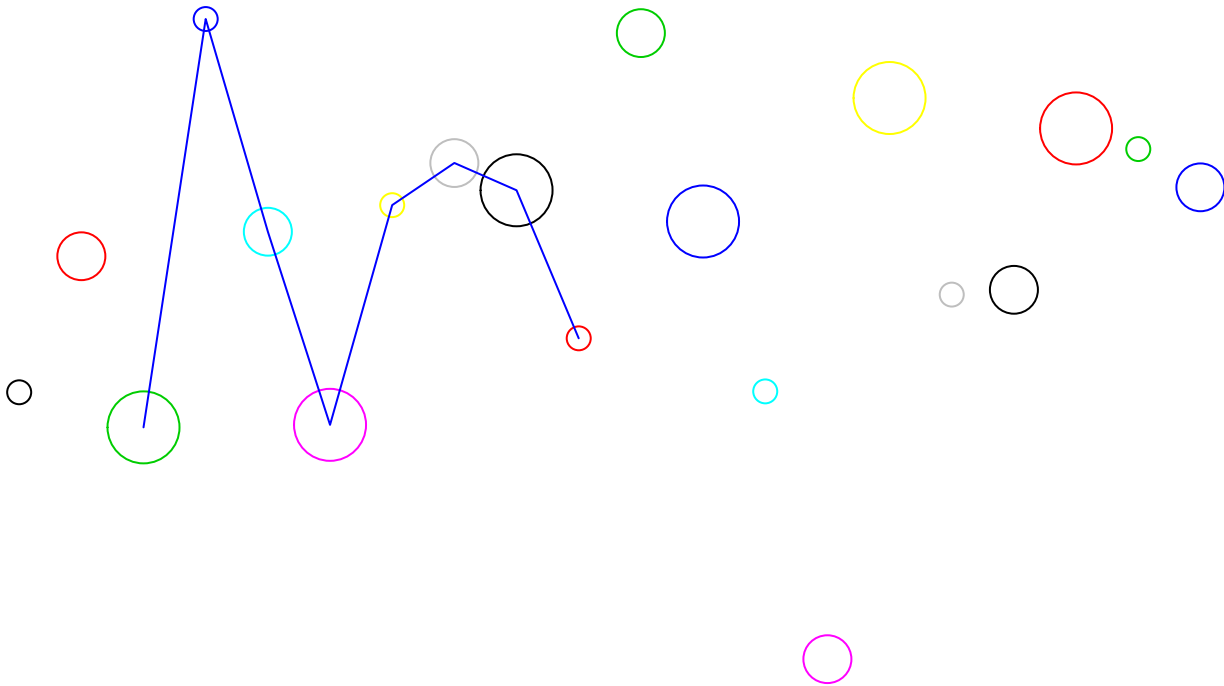
B\_henselae

B\_quintana

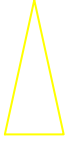
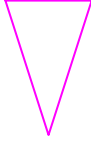
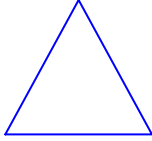
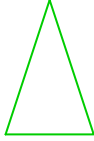
help("reverse")

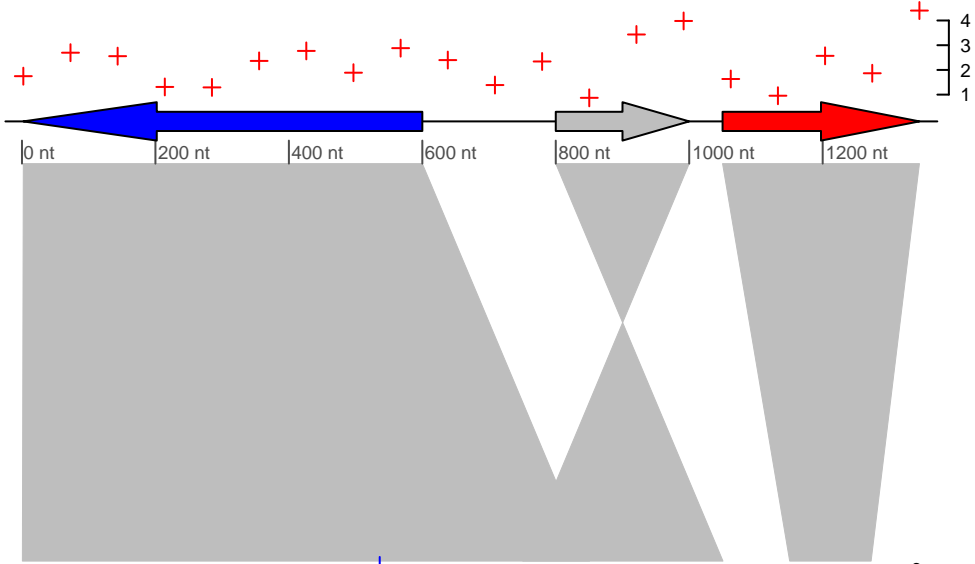
500 kb



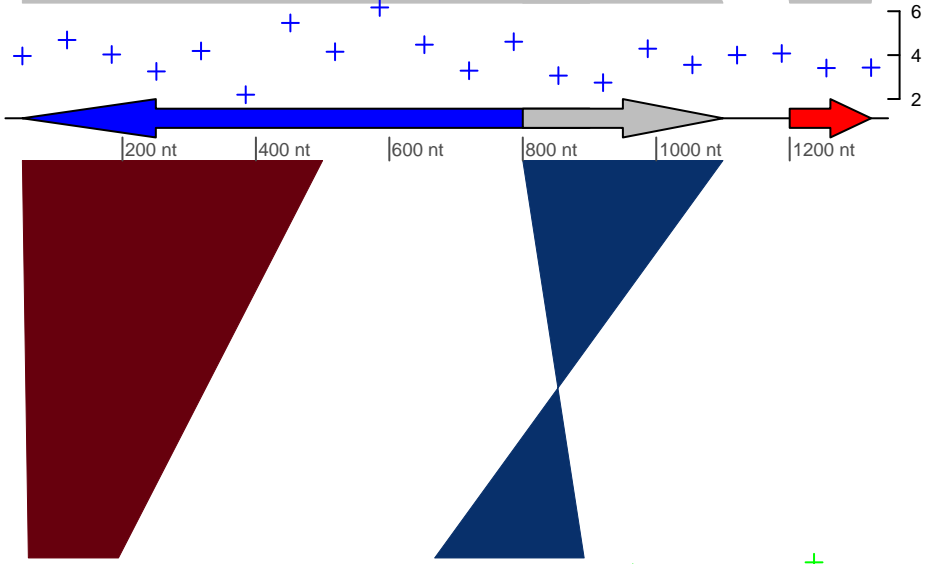


help("seg\_plot")

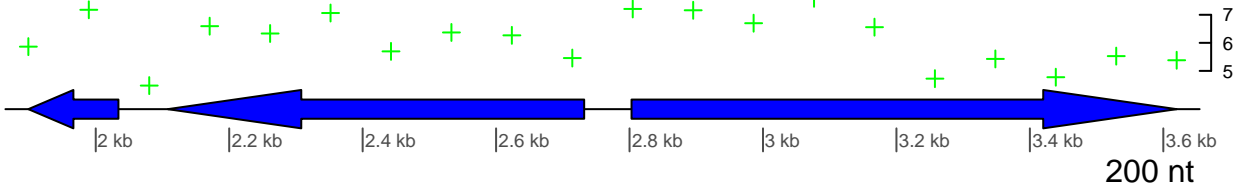




4  
3  
2  
1



6  
4  
2



7  
6  
5

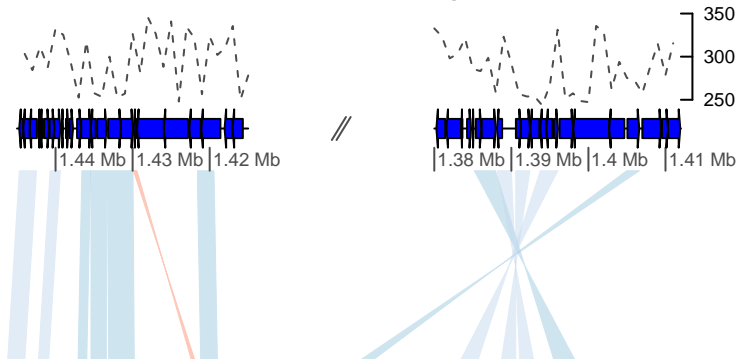
200 nt

help("seg\_plot")

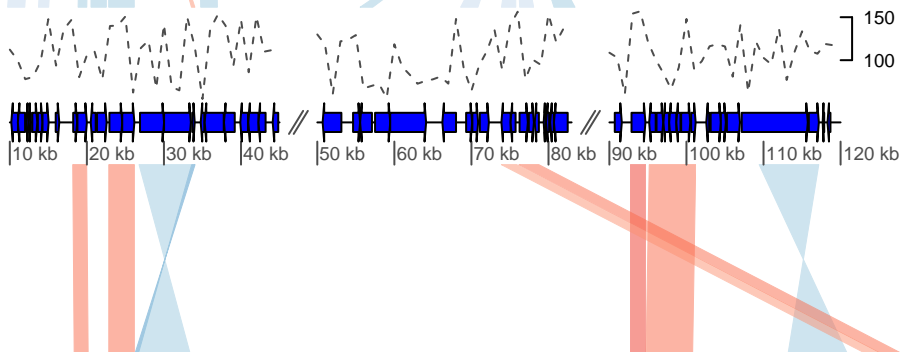
# Random plots for the same segment in 4 *Bartonella* genomes

help("seg\_plot")

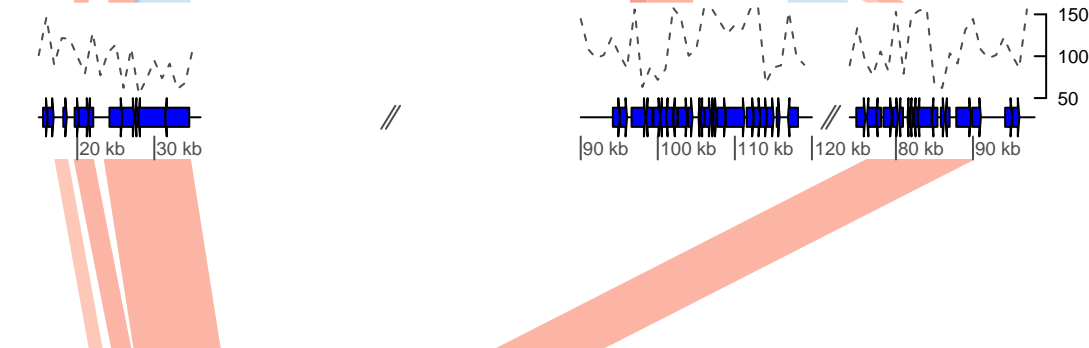
BB



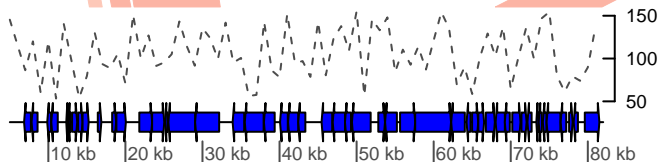
BG



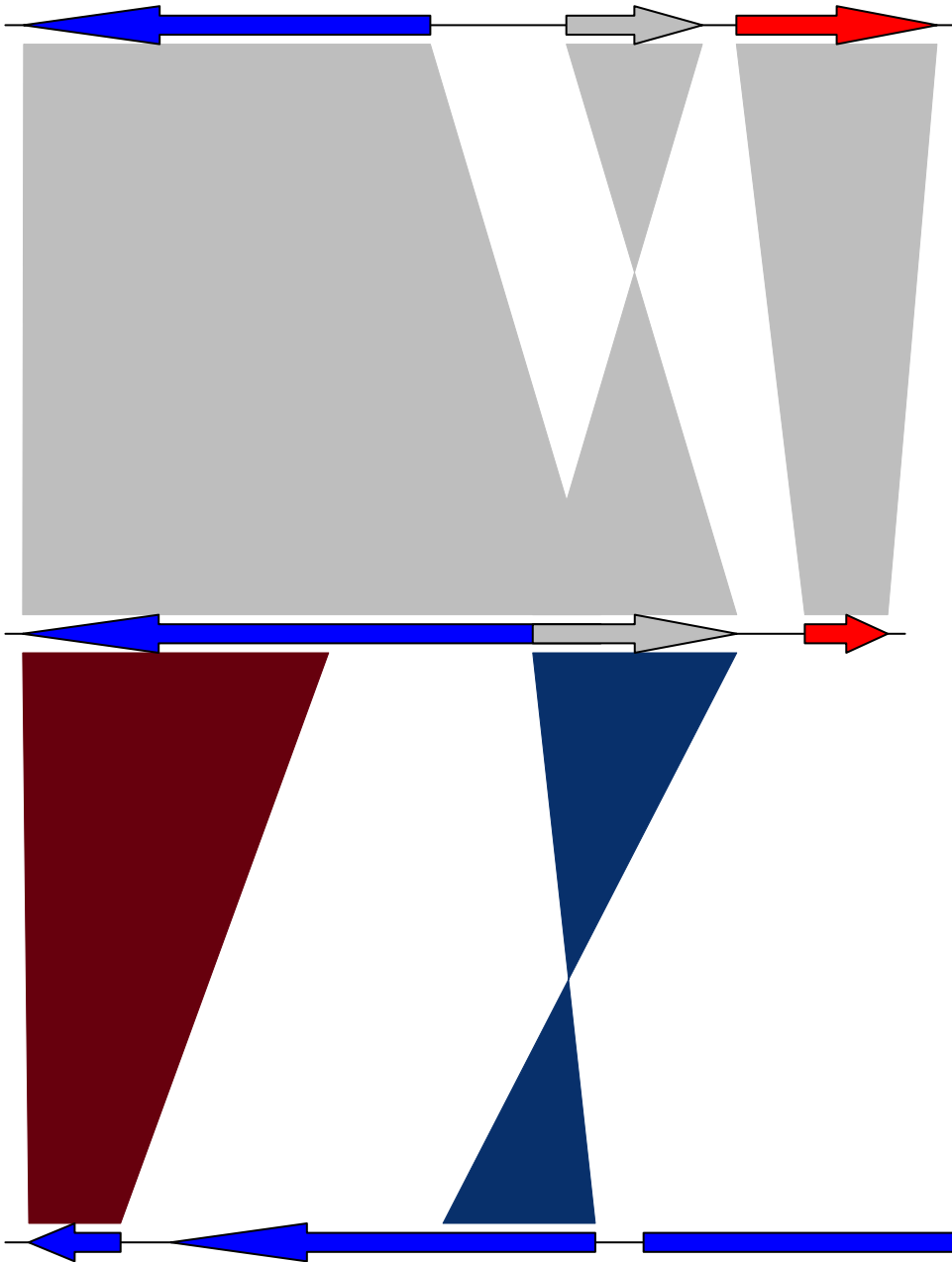
BH



BQ



20 kb



help("three\_genes")

