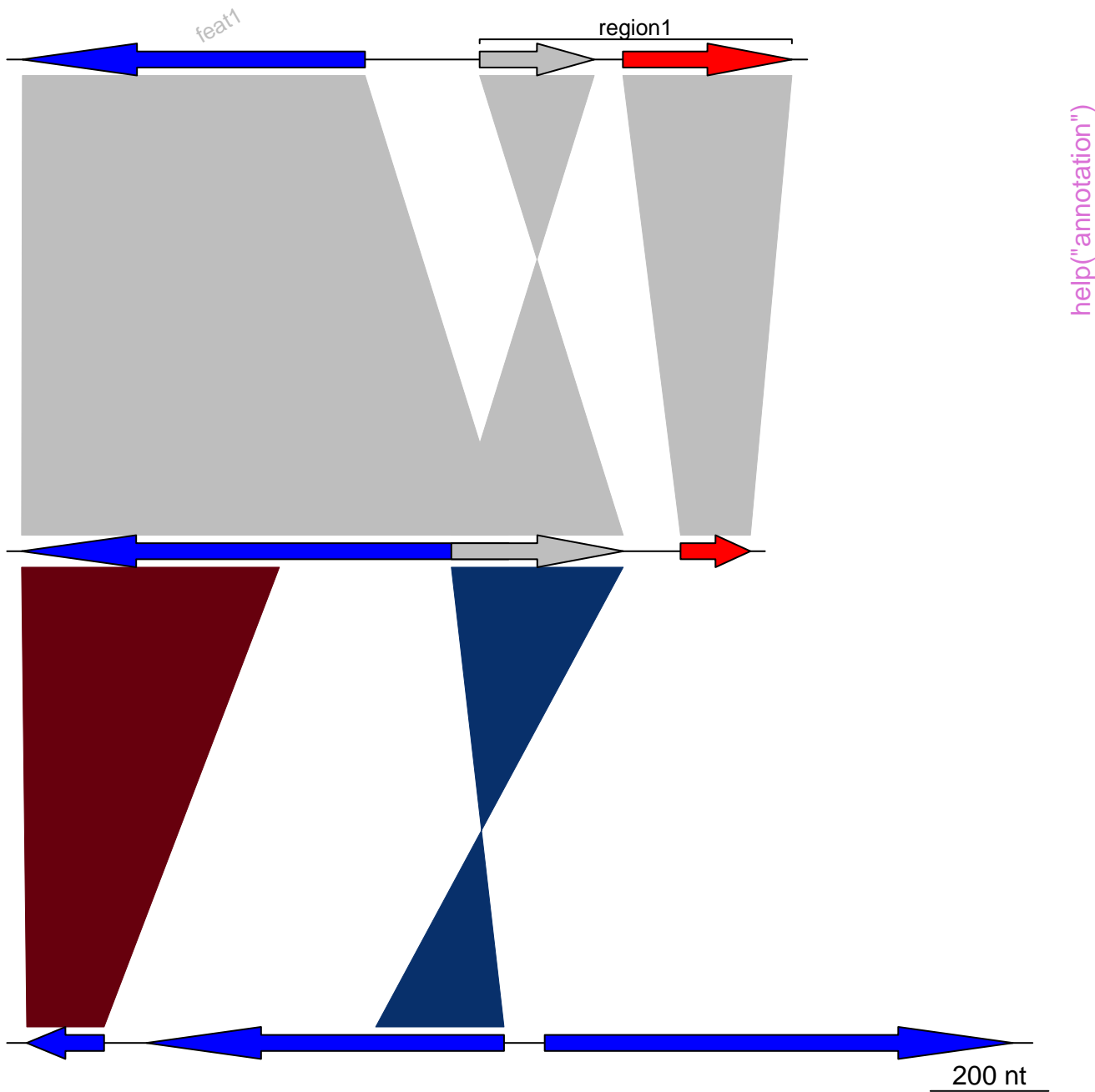
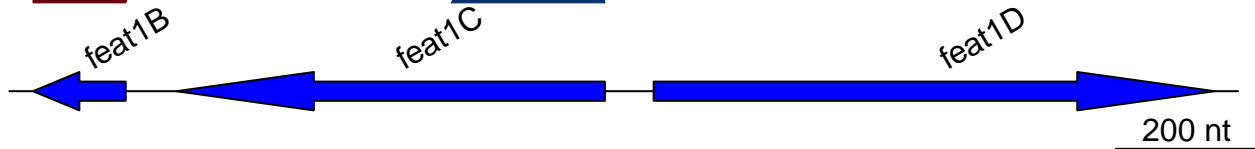
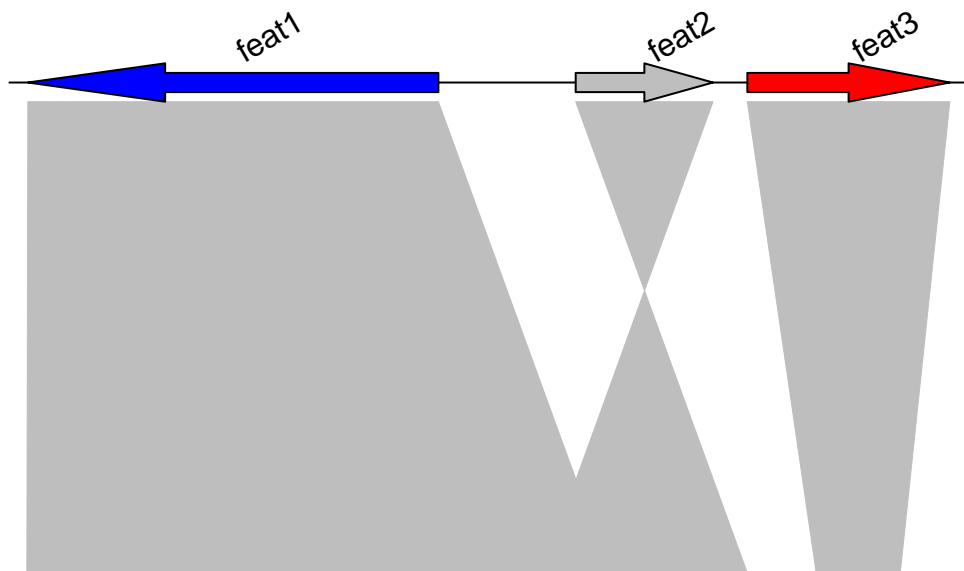


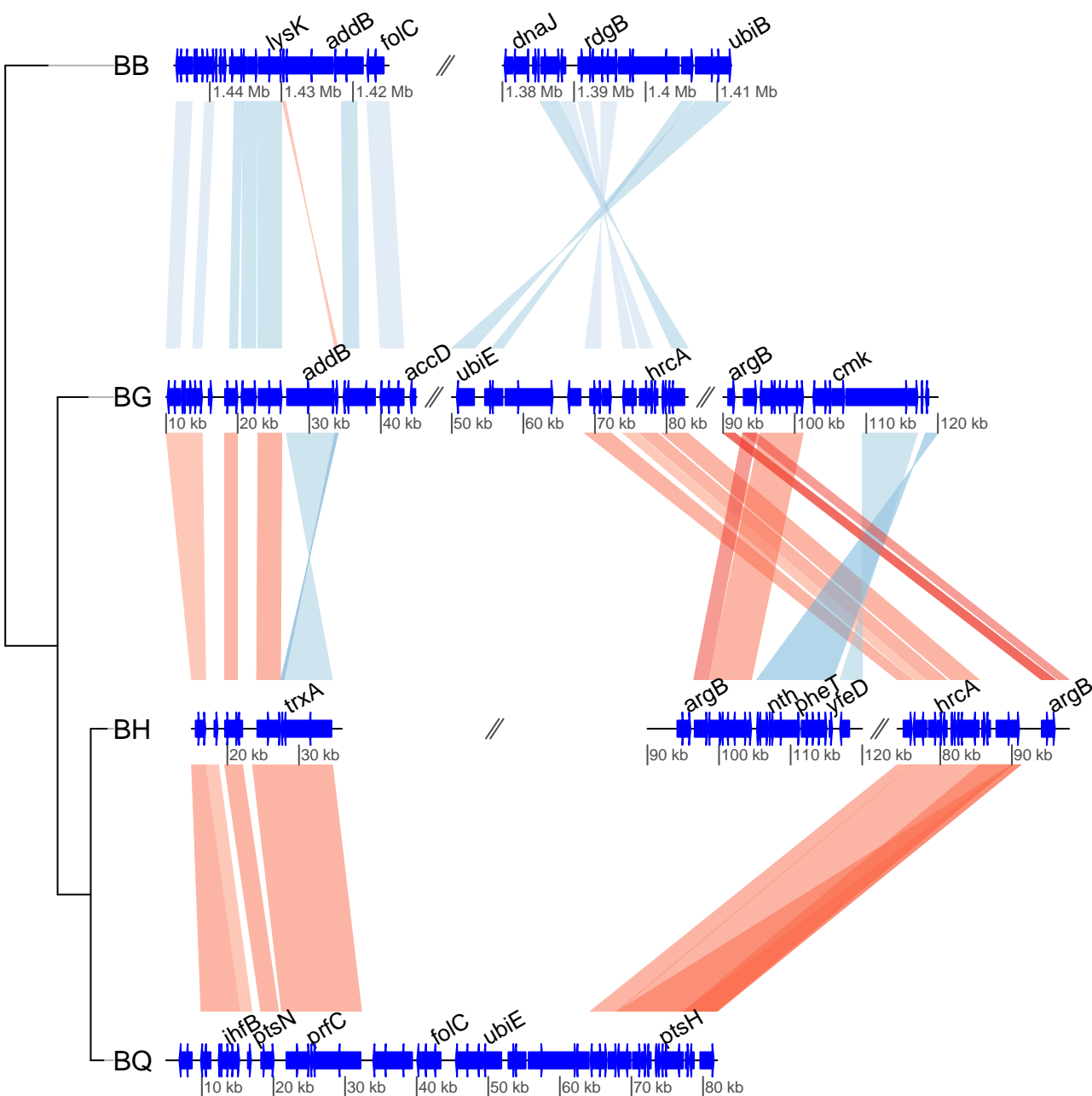
help("annotation")

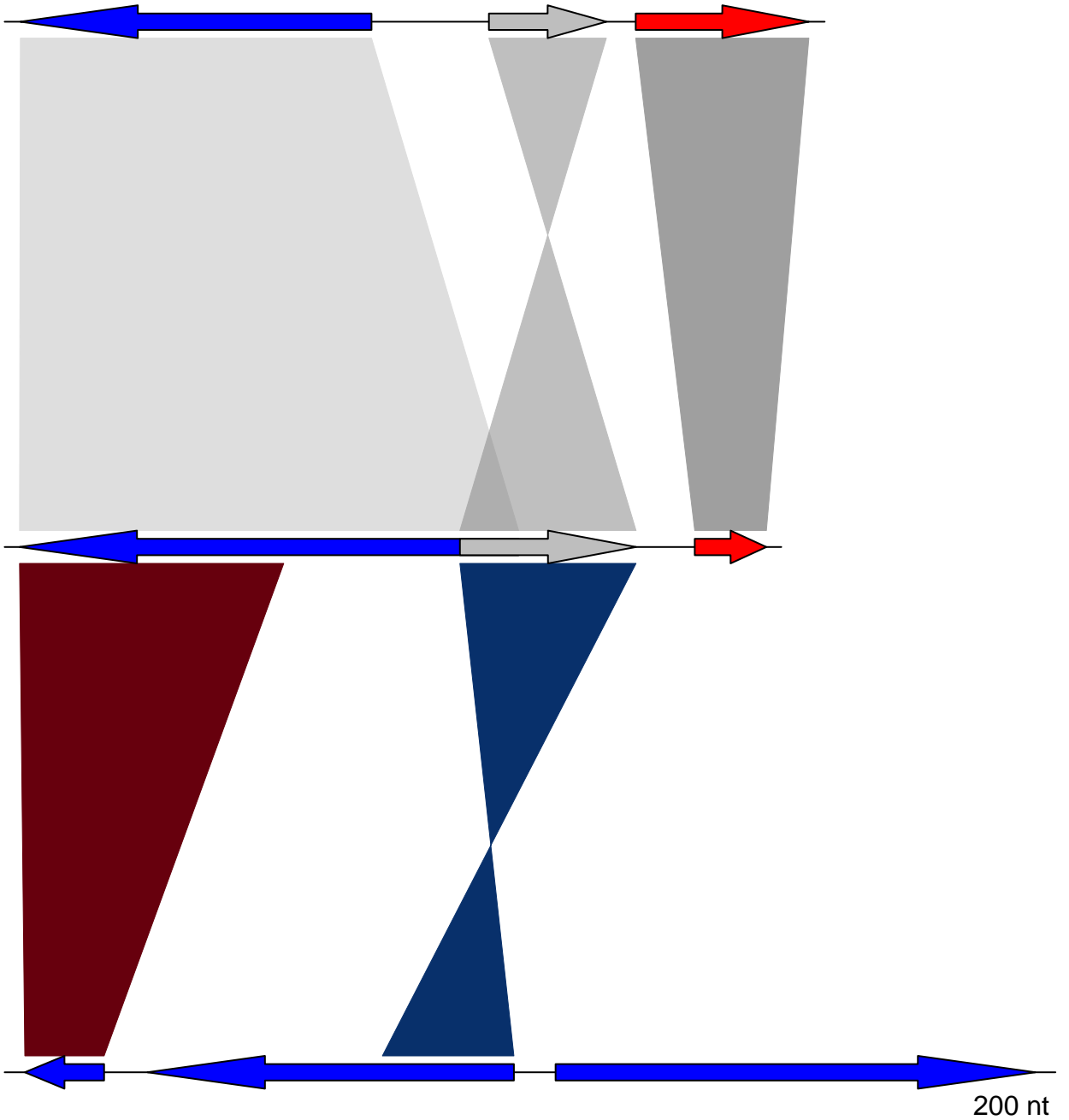
200 nt



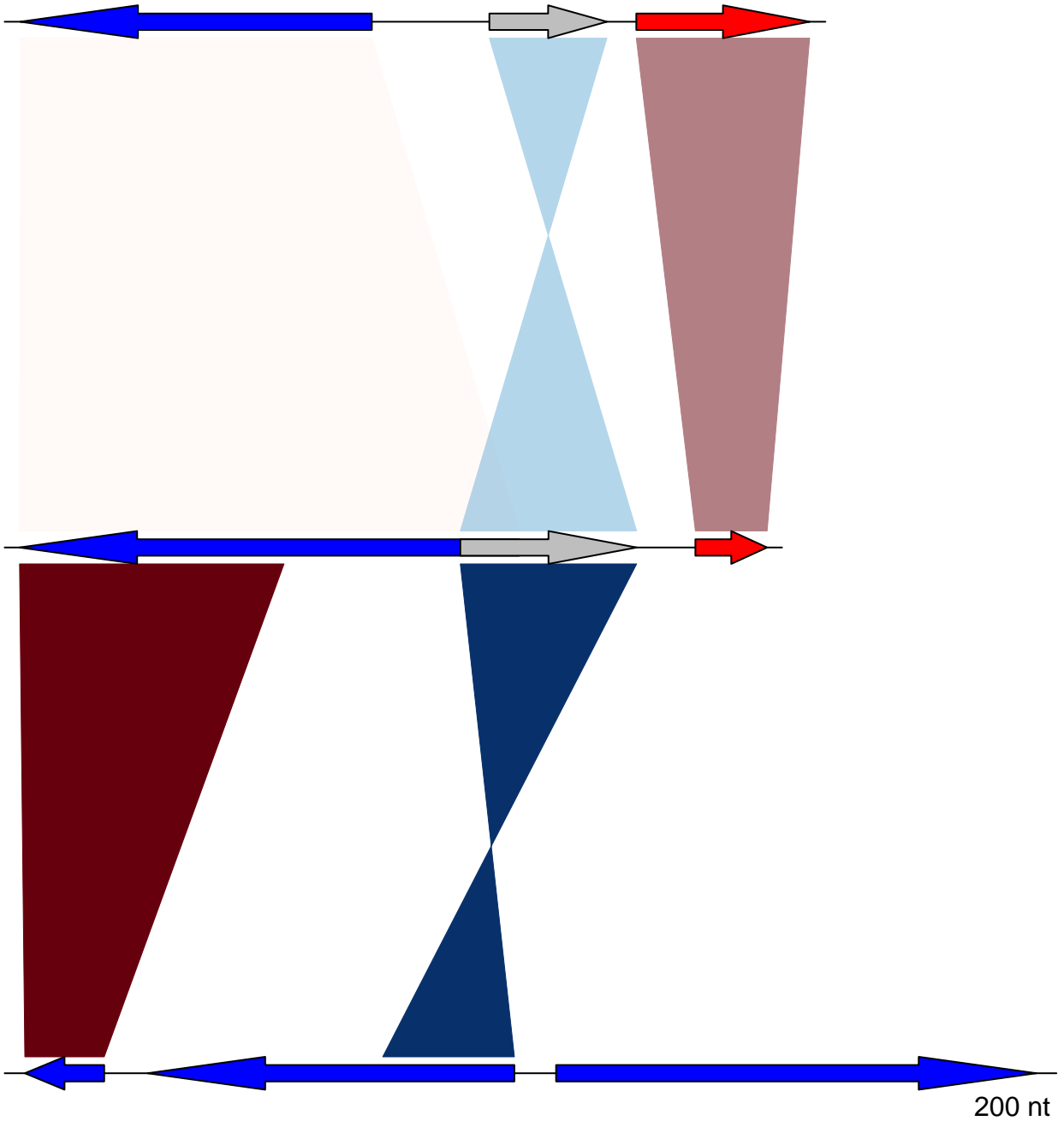


help("annotation")

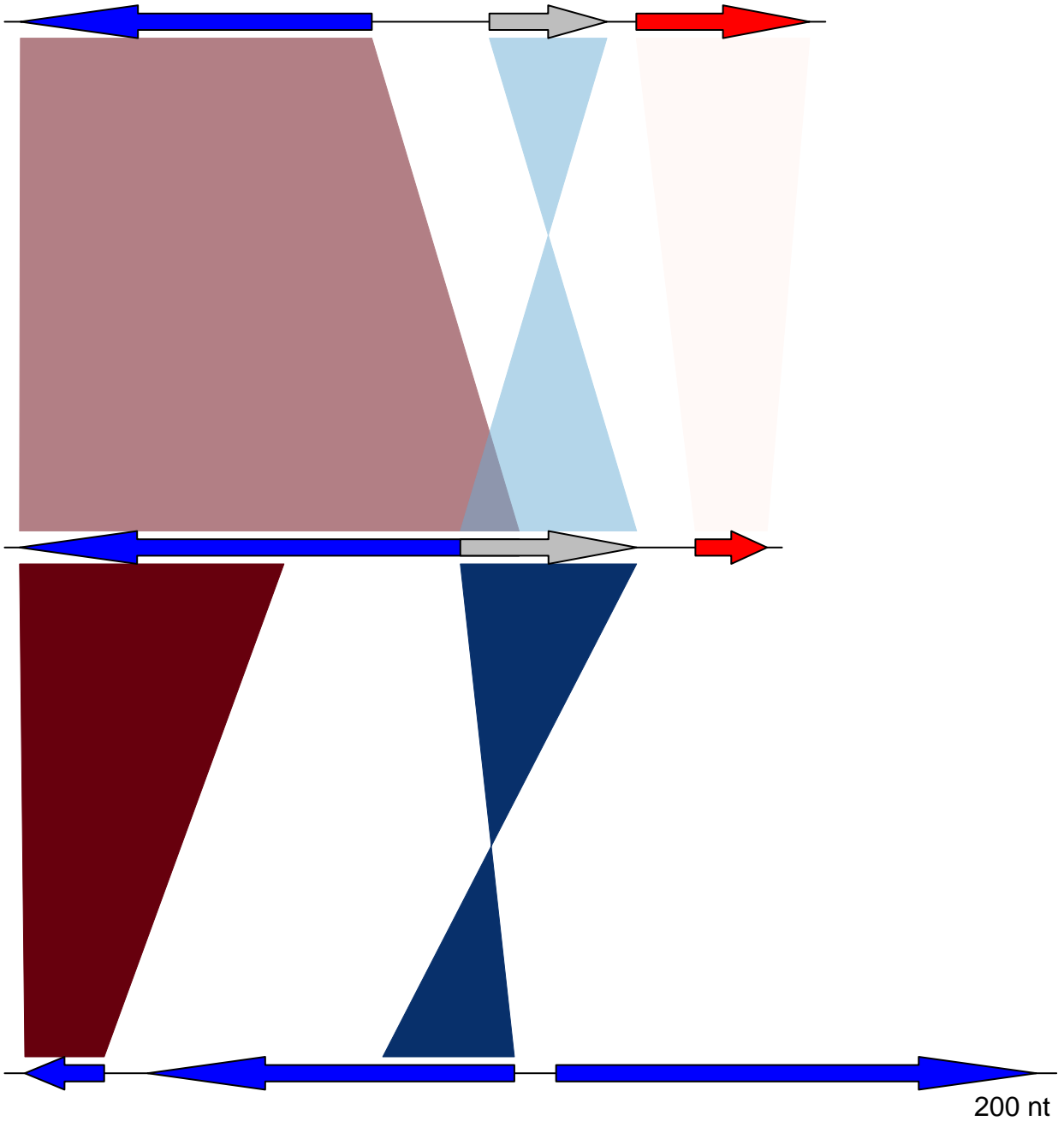




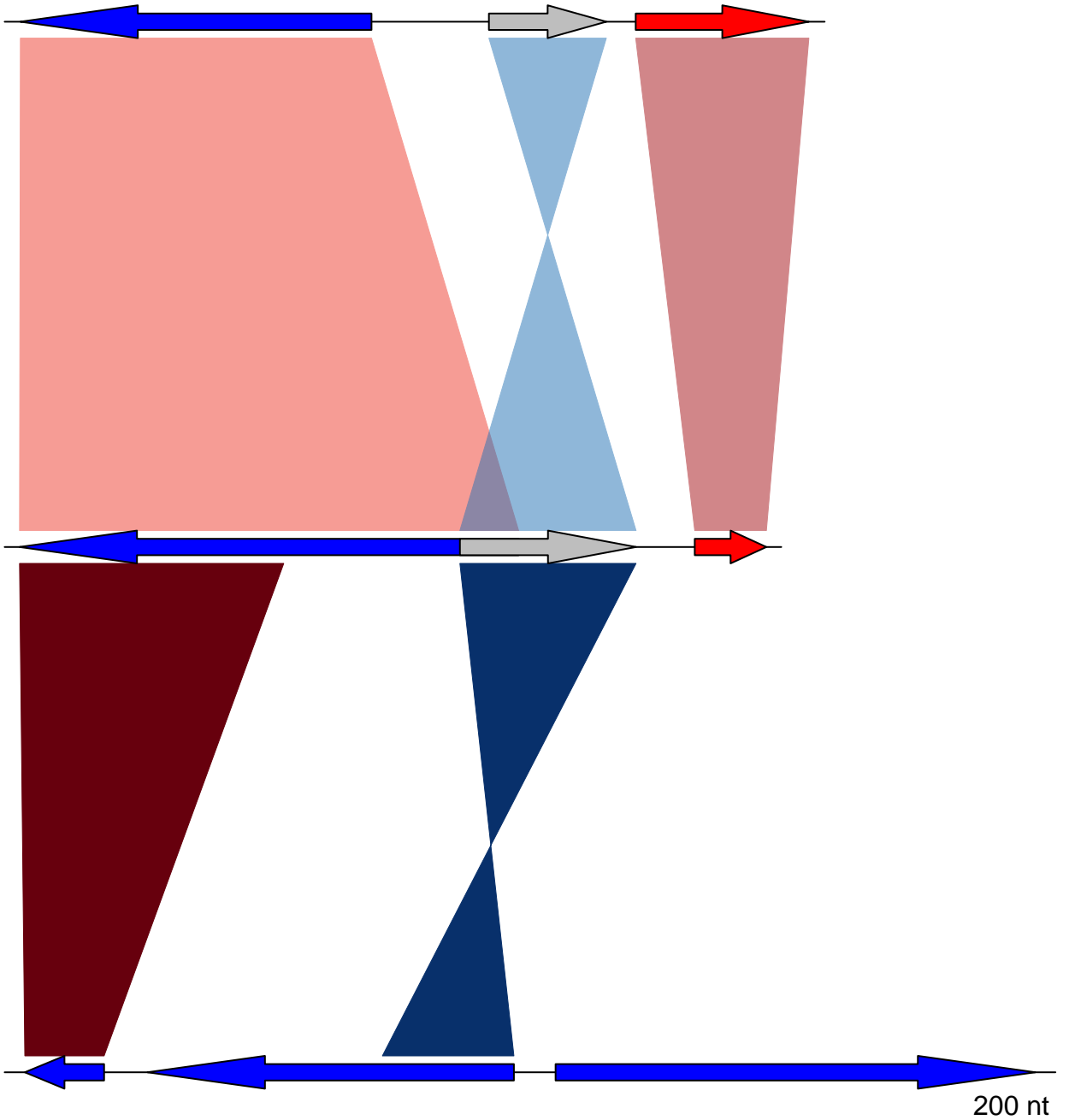
help("apply\_color\_scheme")



help("apply\_color\_scheme")

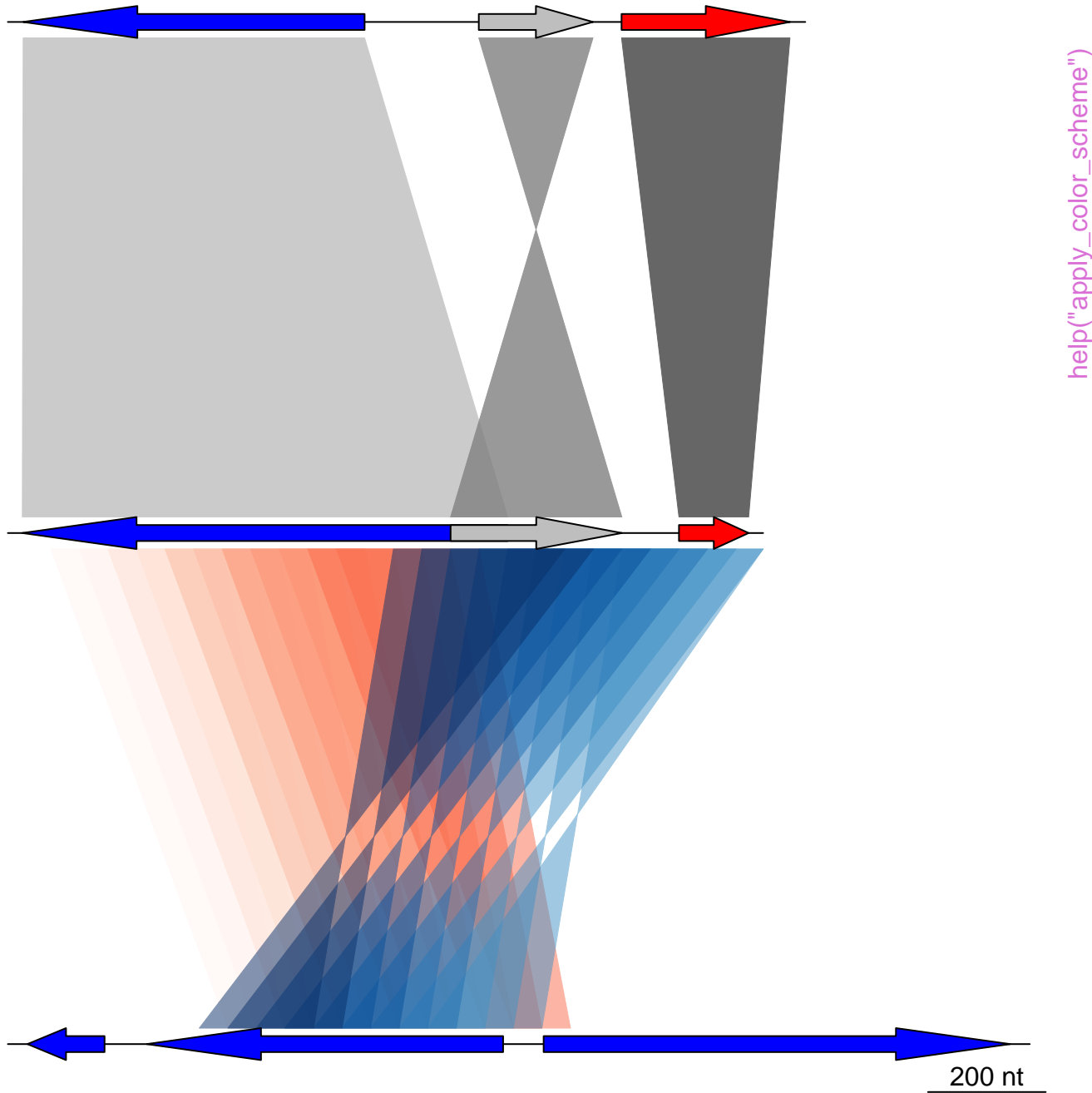


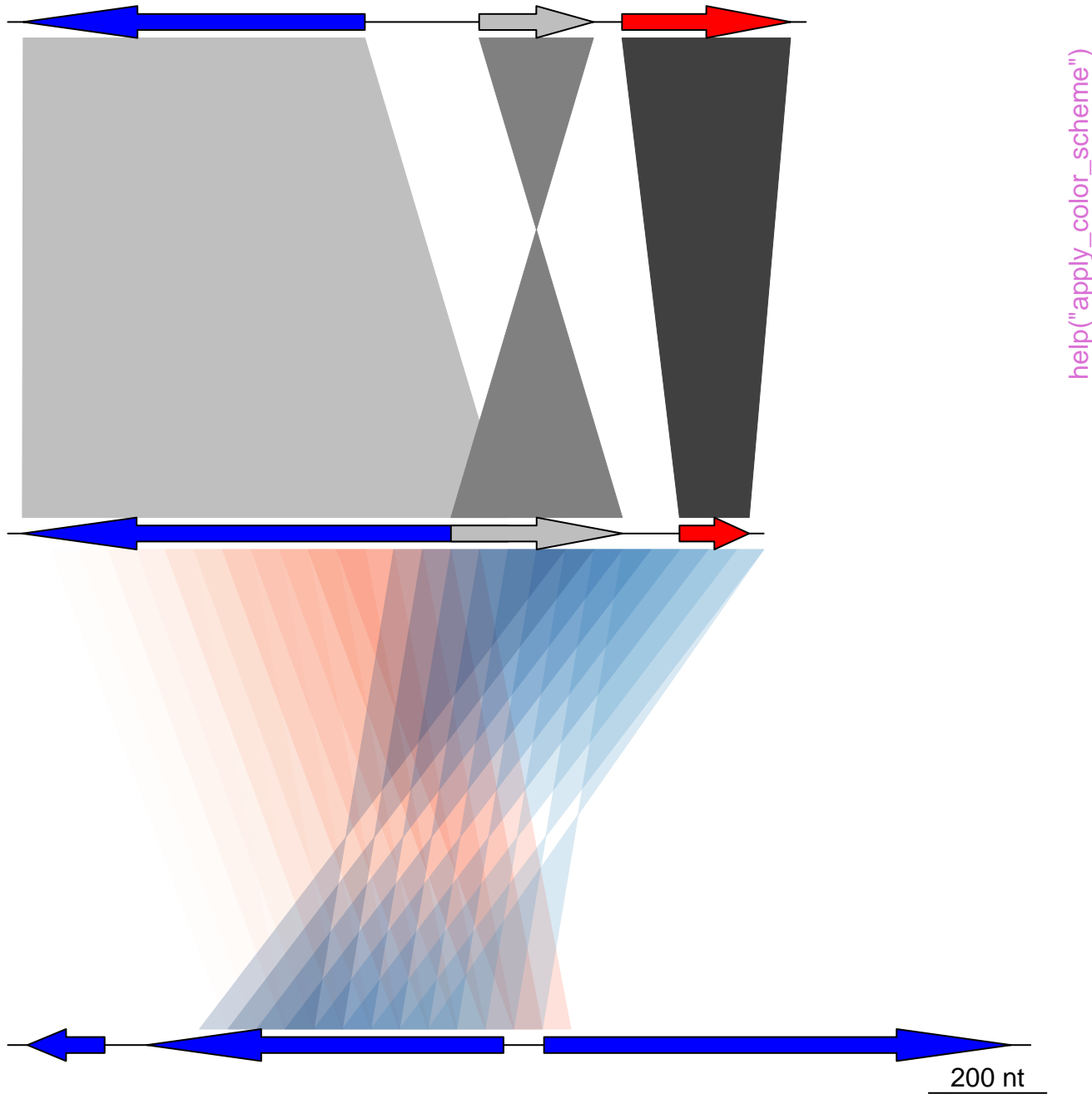
help("apply\_color\_scheme")

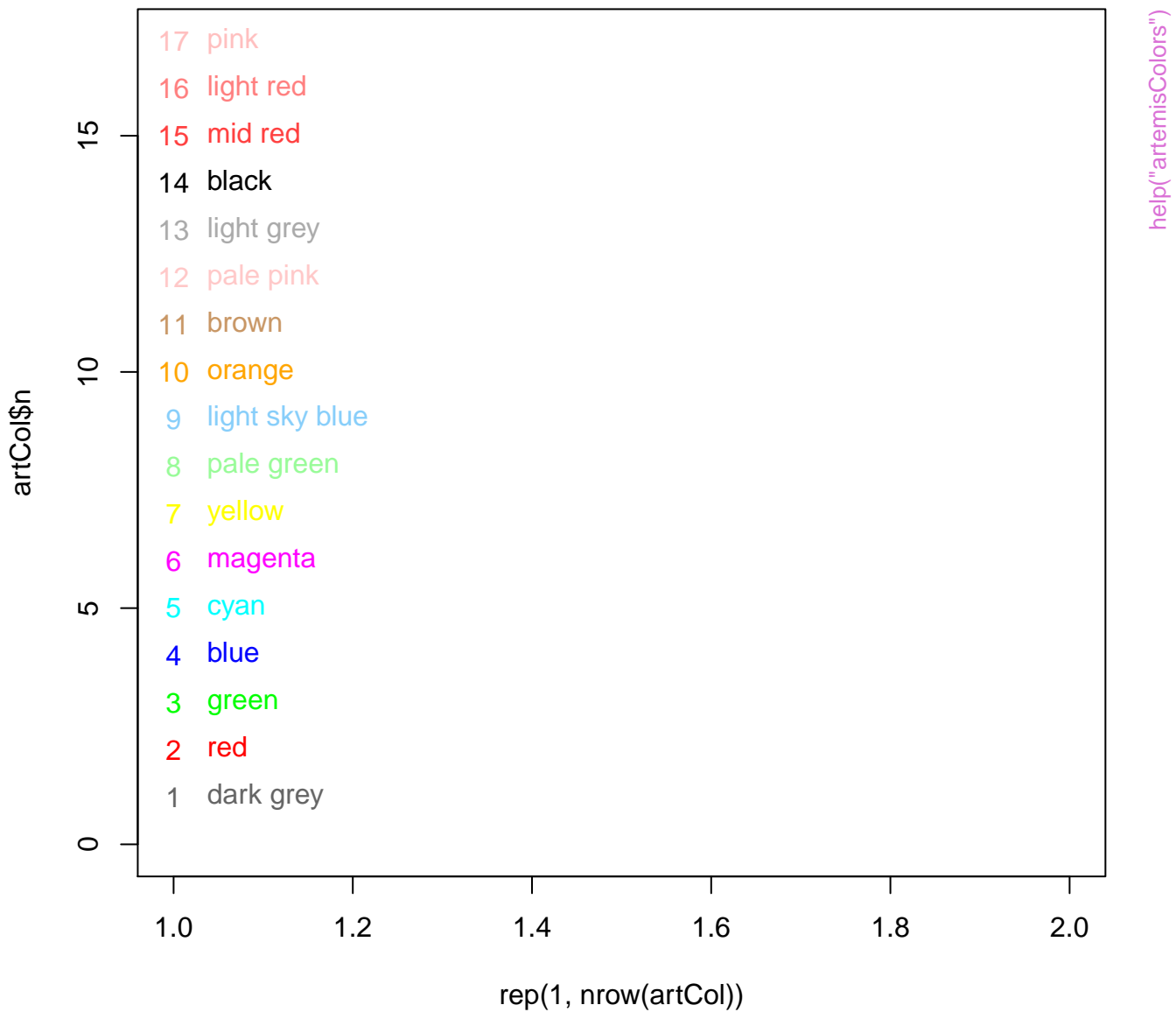


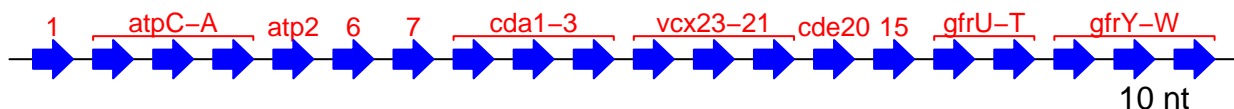
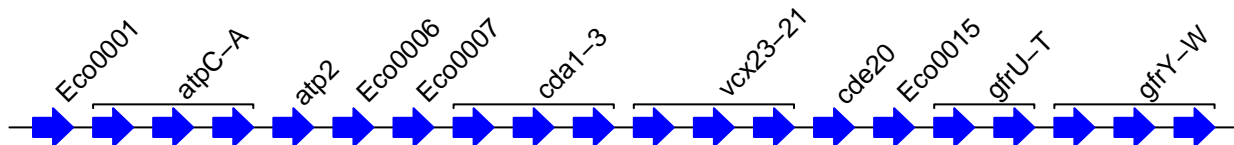
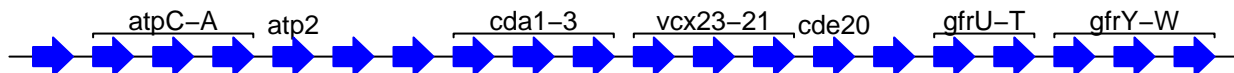
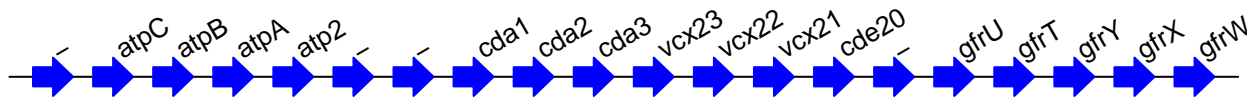
help("apply\_color\_scheme")











help("auto\_annotate")

BB

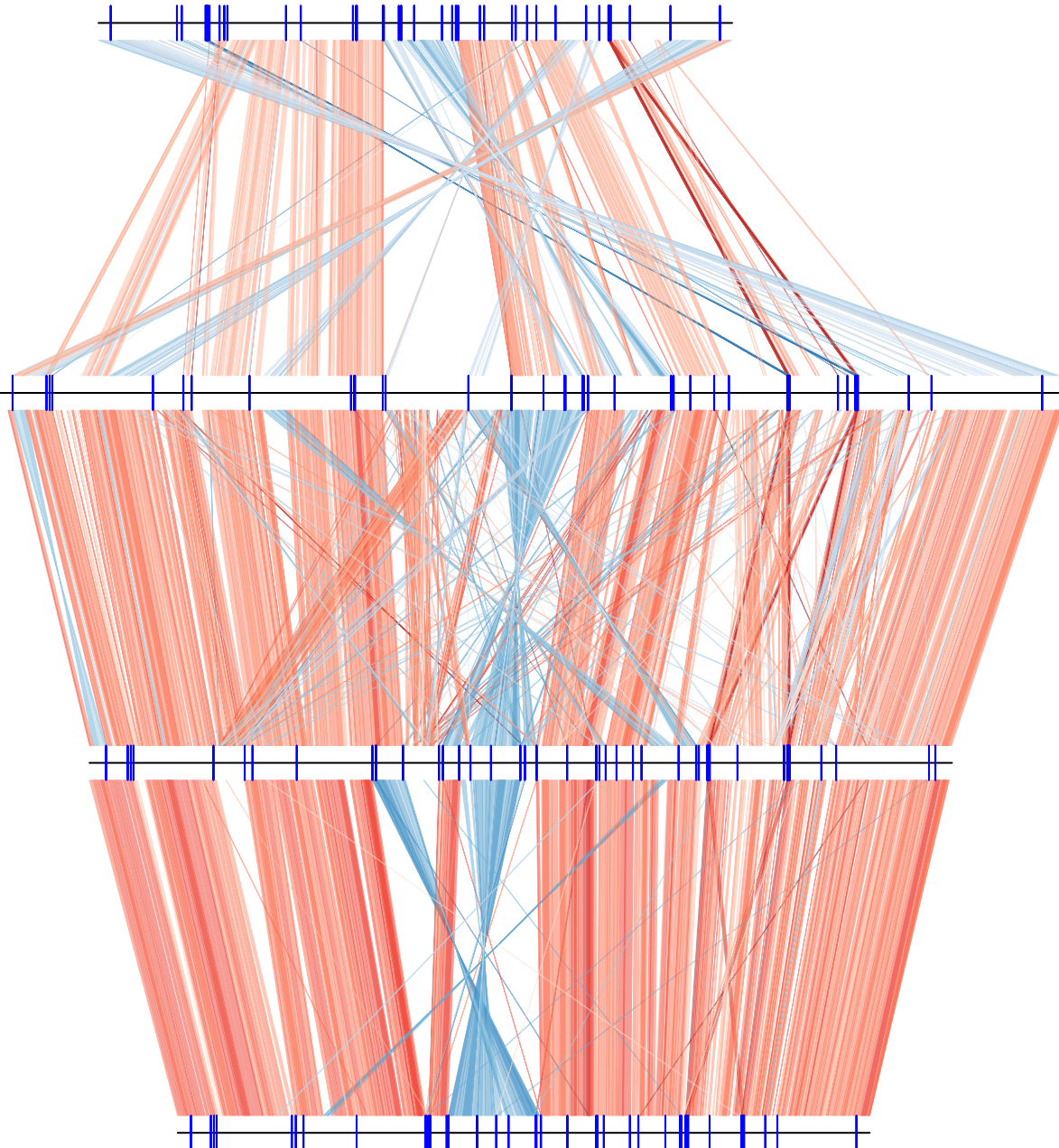
BG

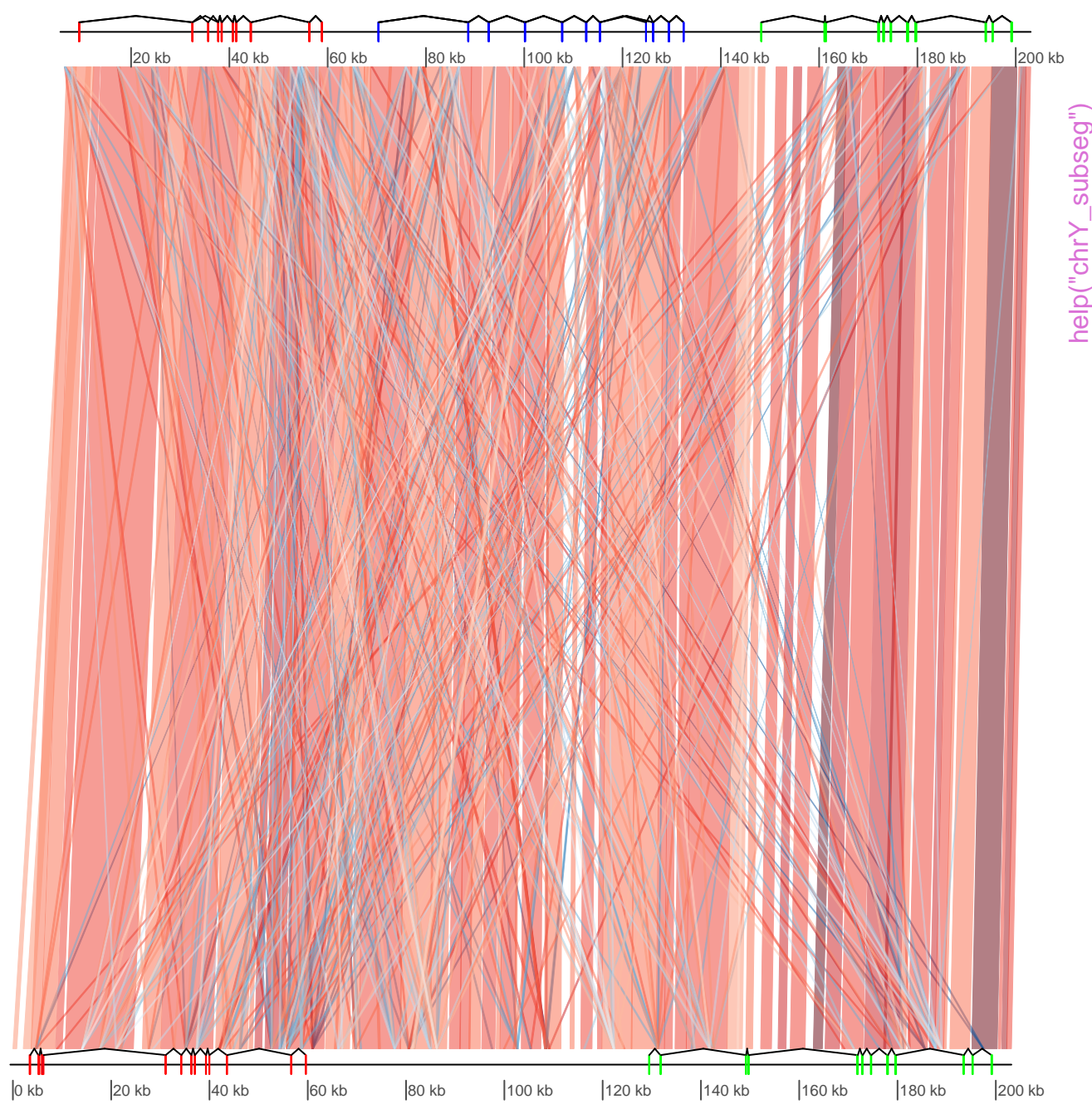
BH

BQ

help("barto")

500 kb





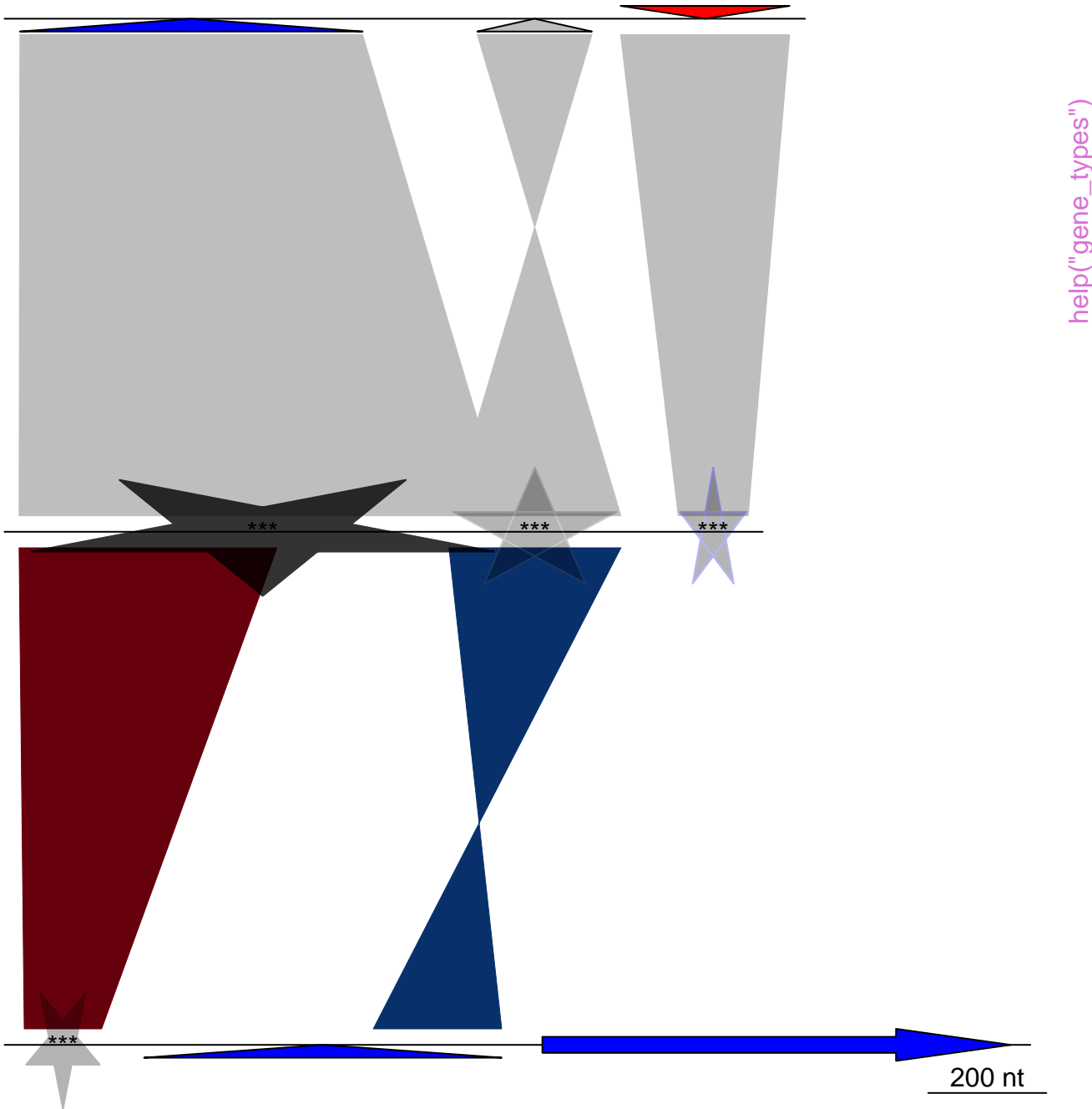


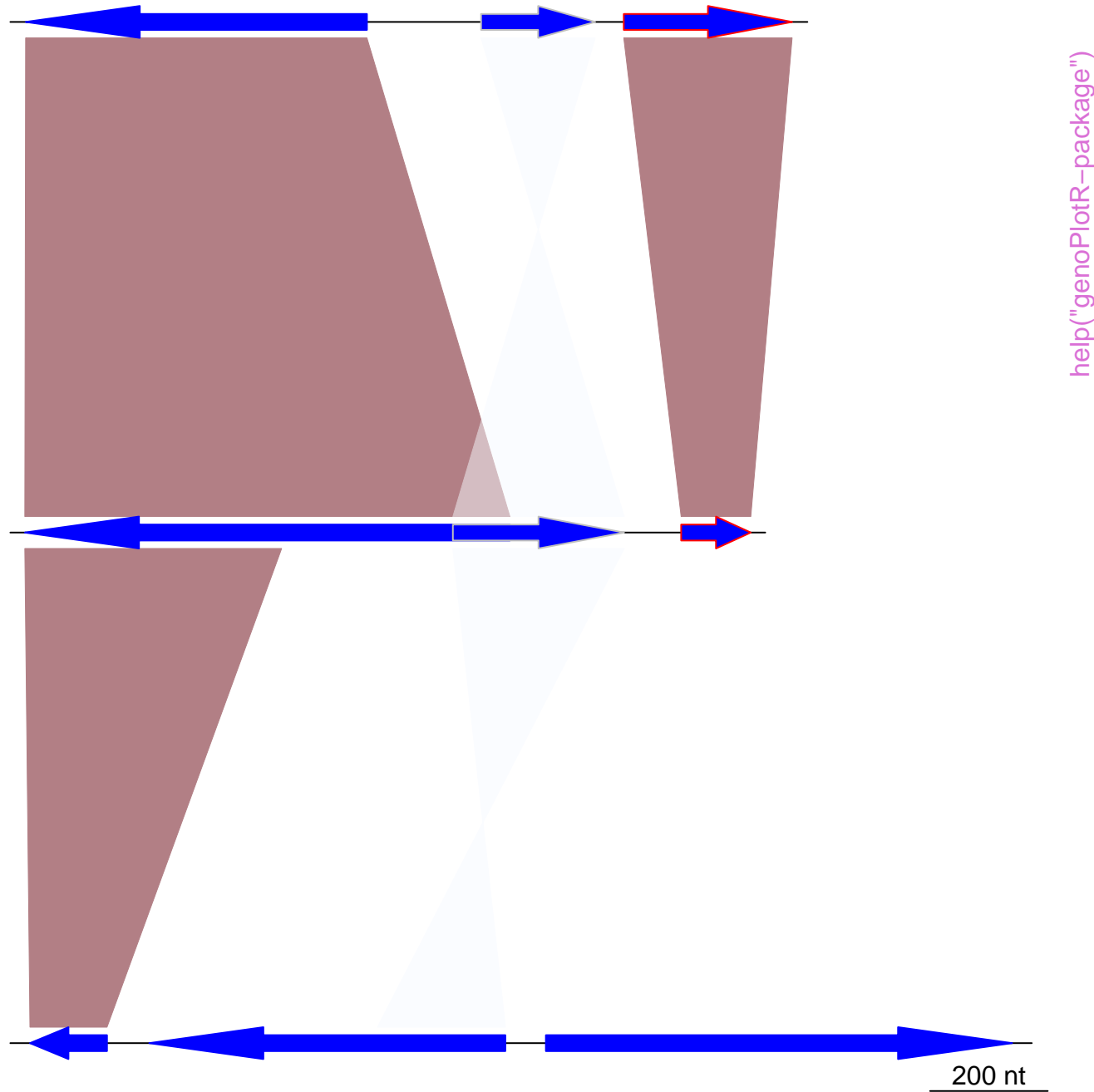
2 kb

help("gene\_types")







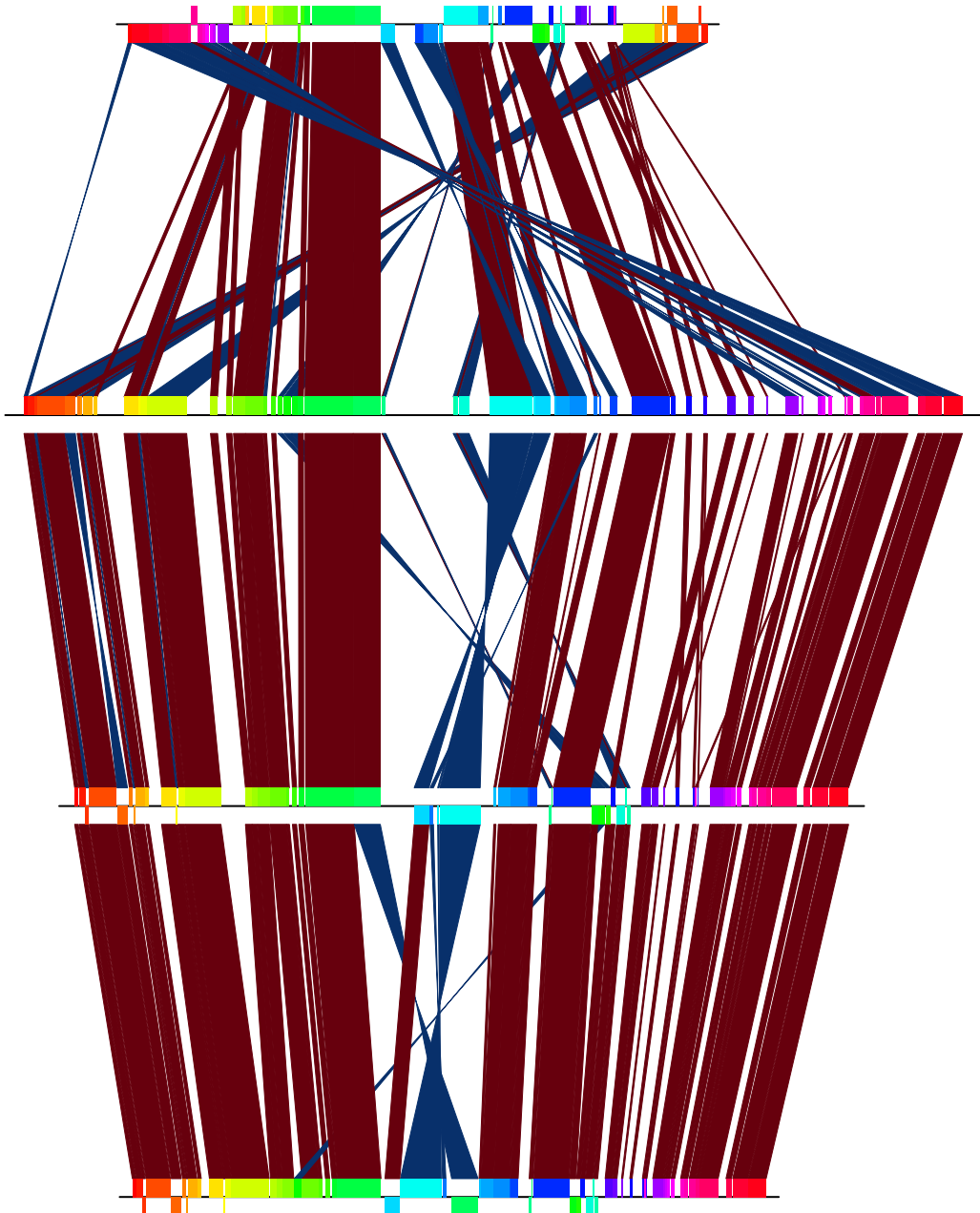


B\_bacilliformis

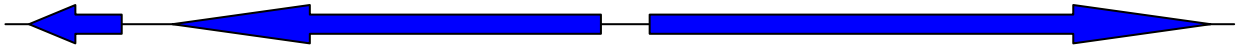
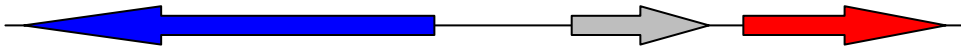
B\_grahamii

B\_henselae

B\_quintana

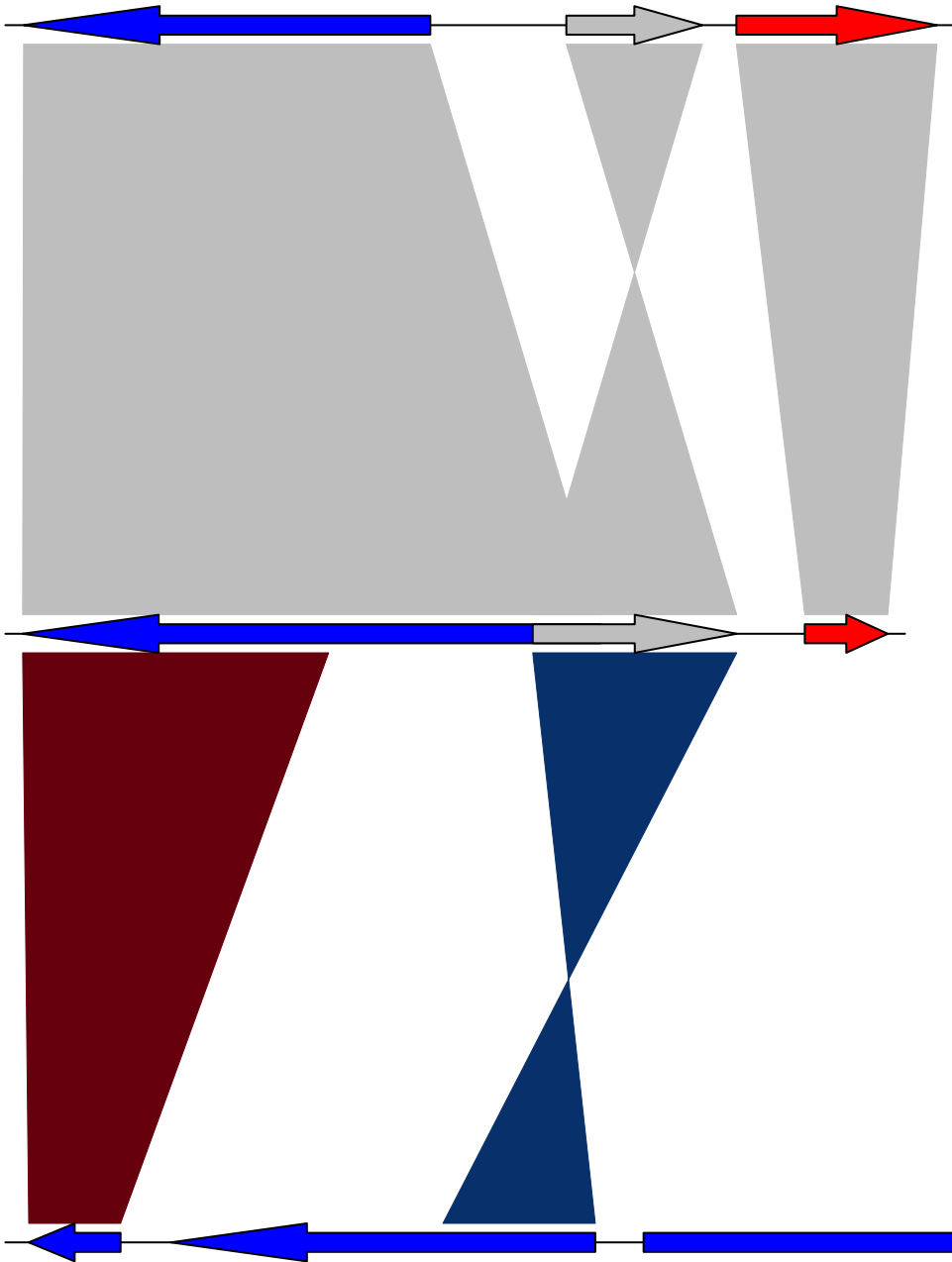


help("mauve.bbone")



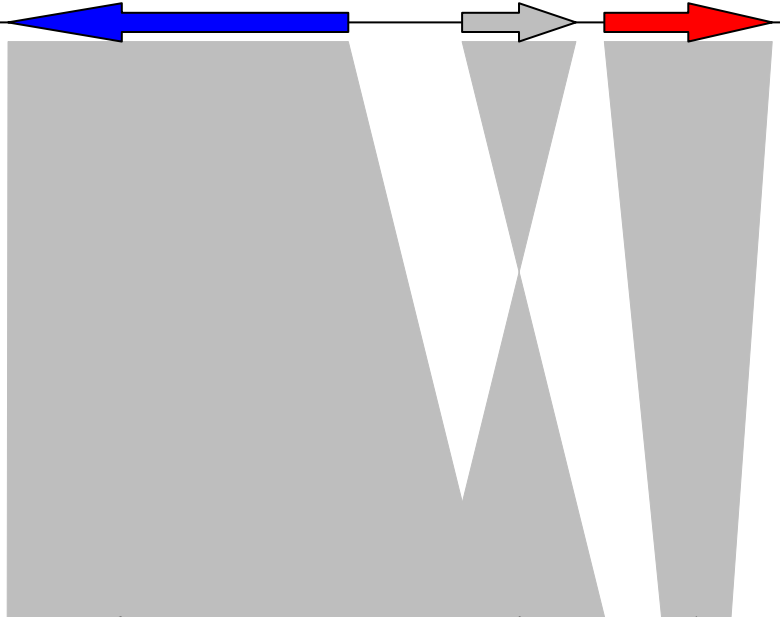
200 nt

help("plot\_gene\_map")

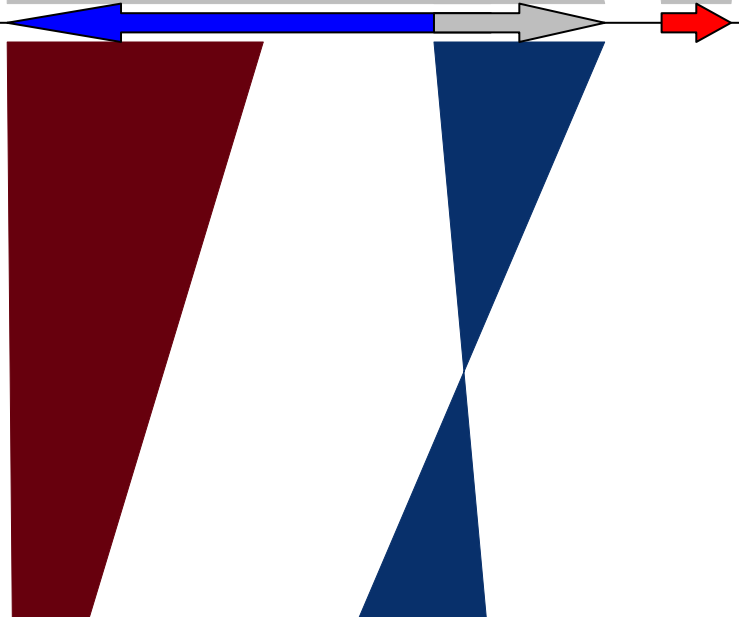


help("plot\_gene\_map")

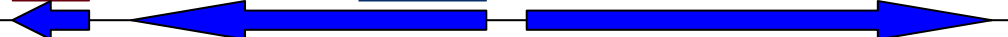
A aaa



B bbb

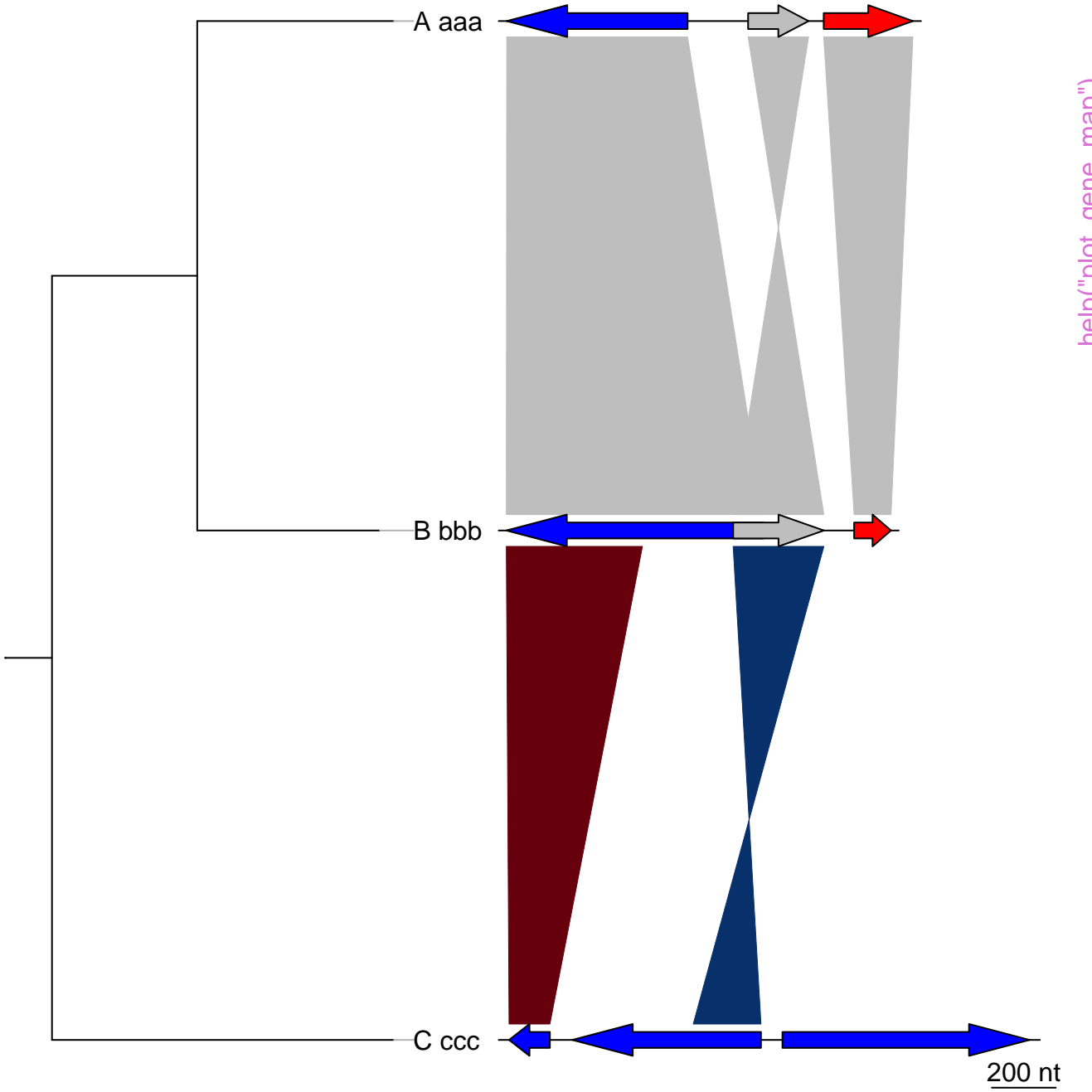


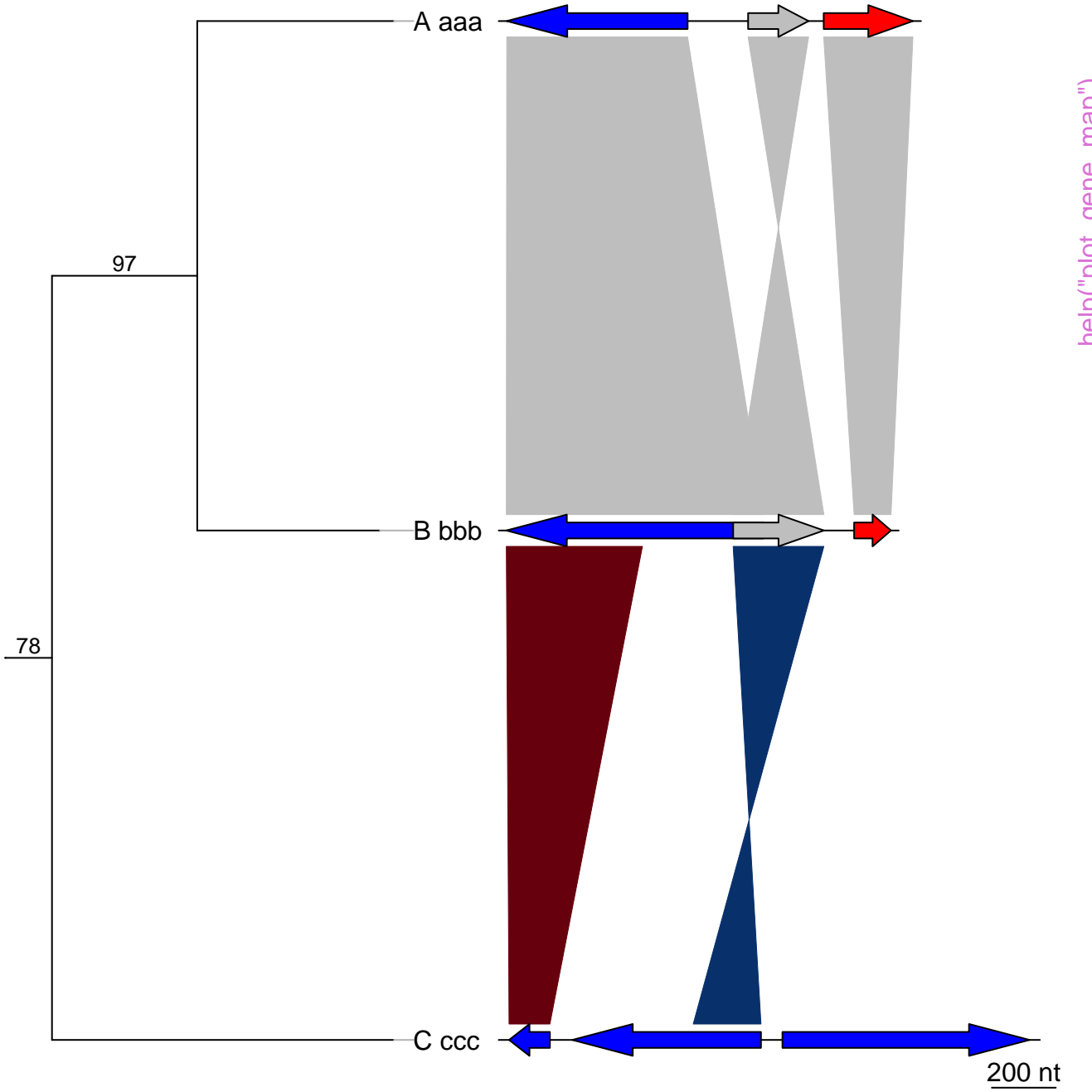
C ccc



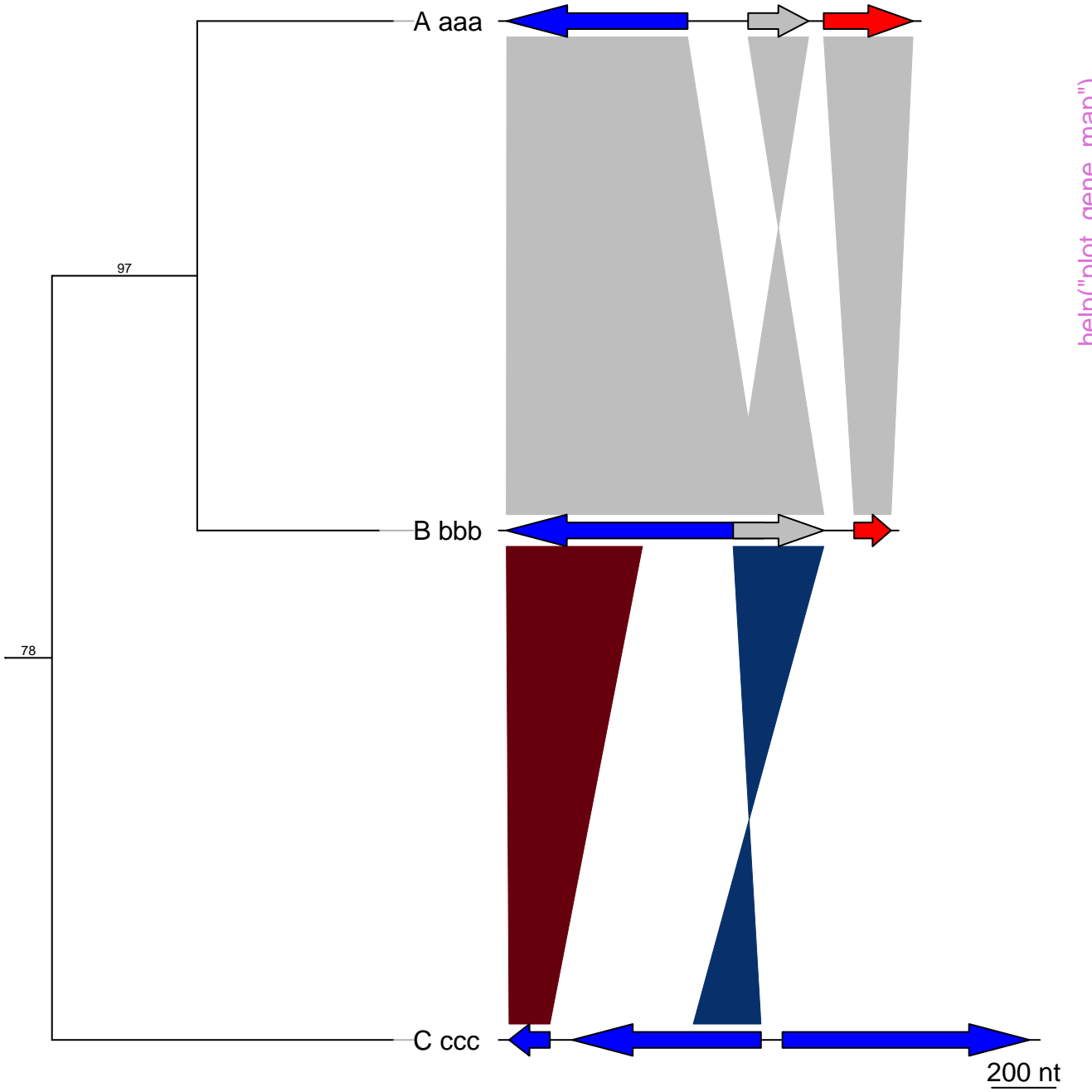
200 nt

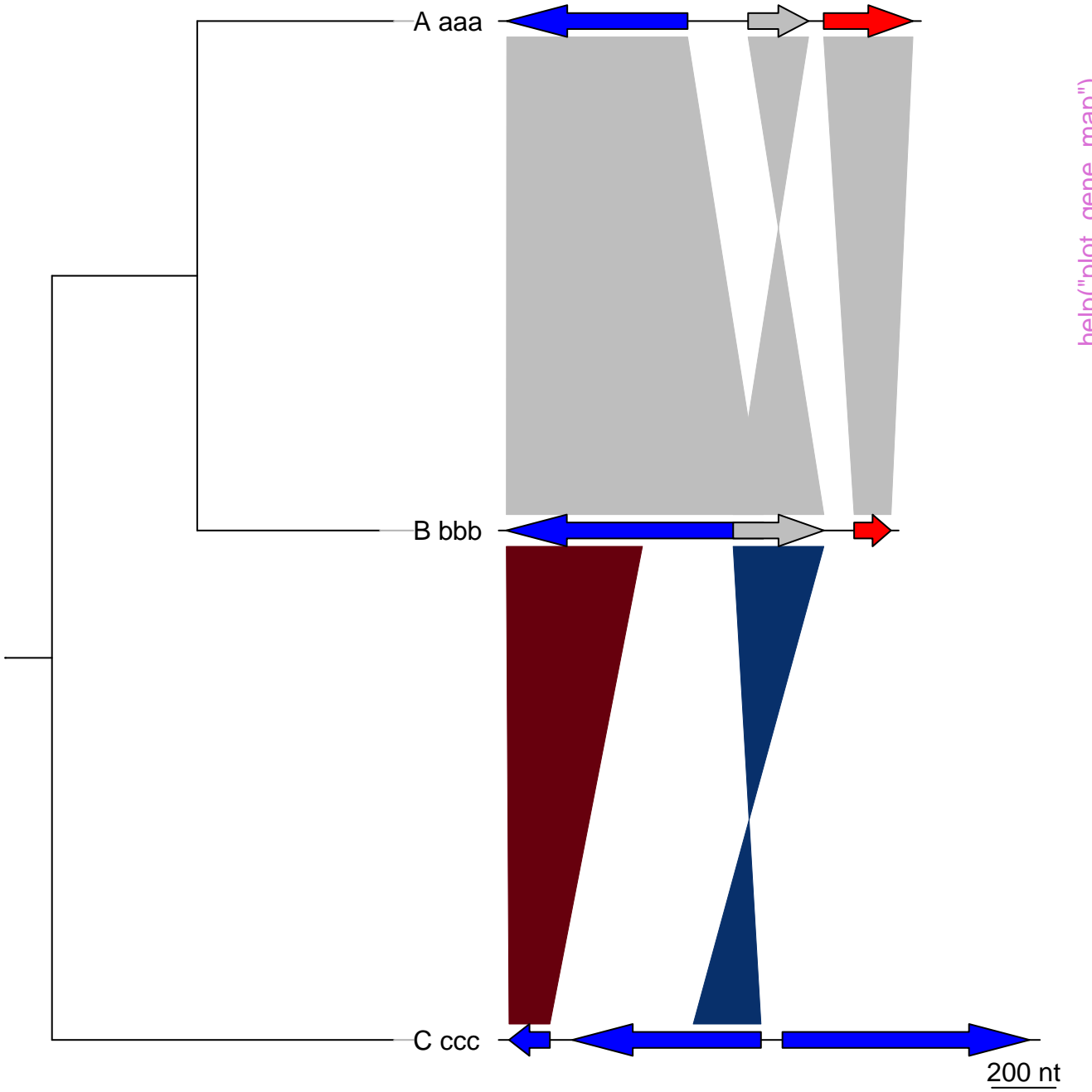
help("plot\_gene\_map")

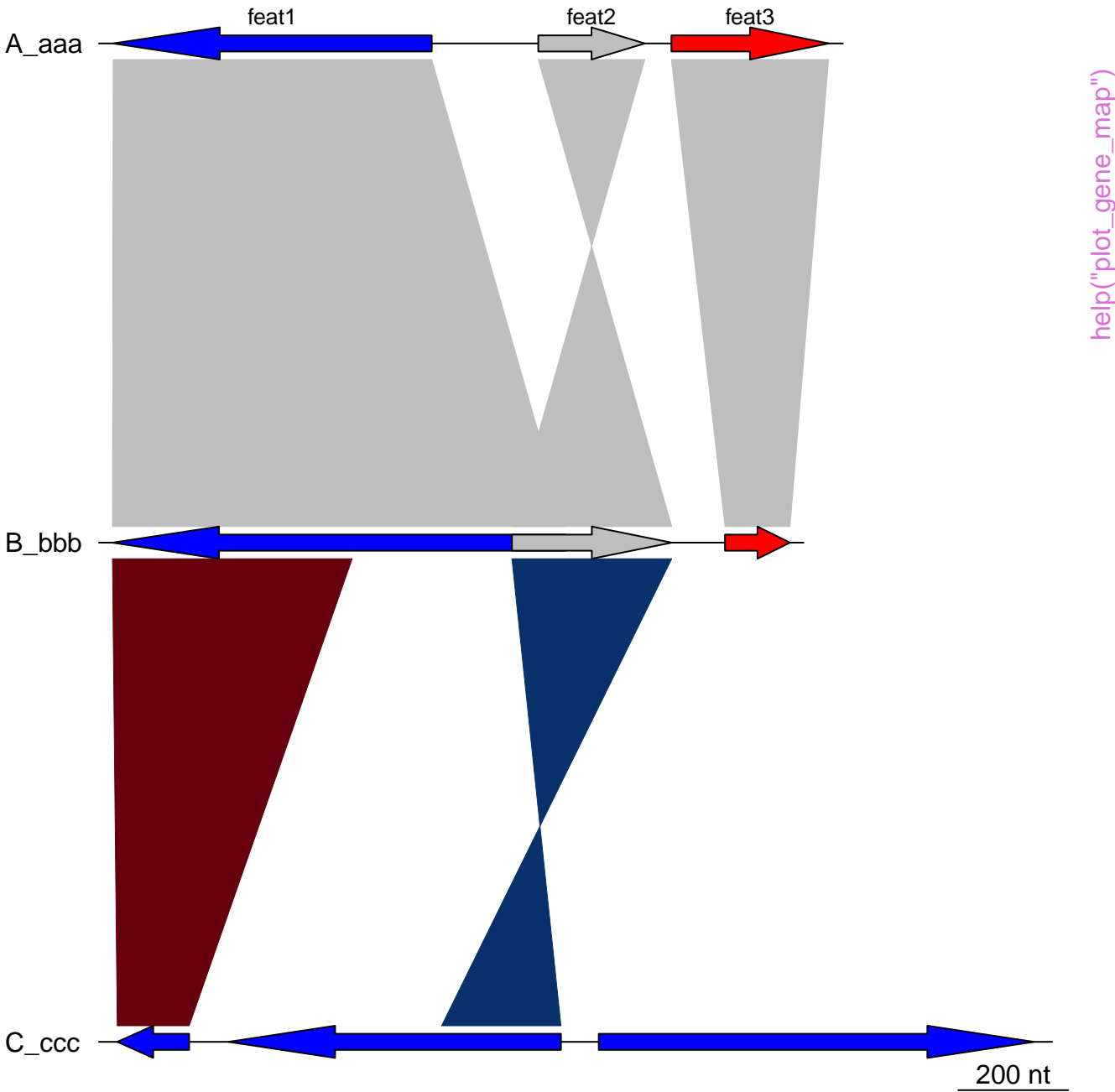


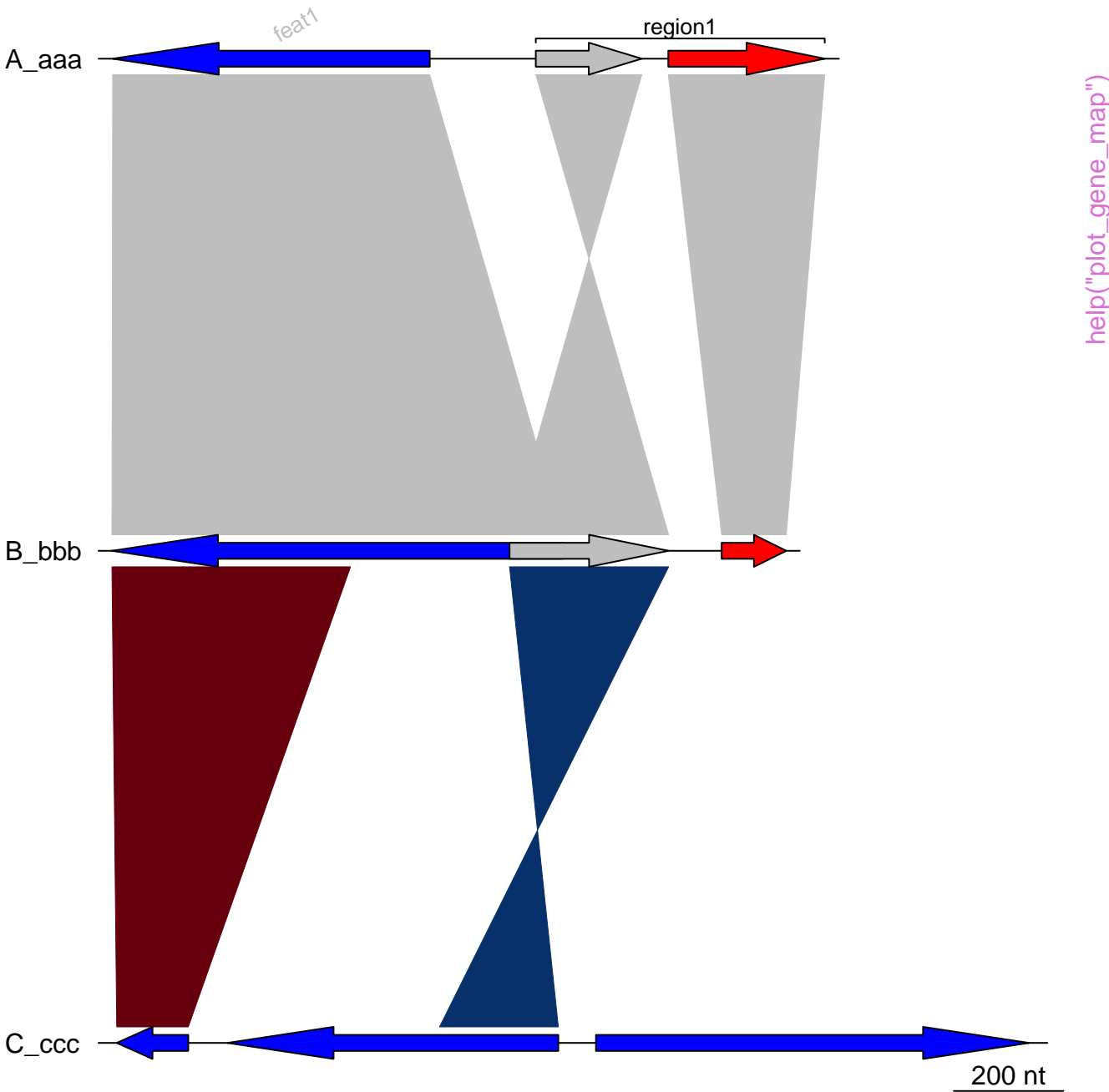




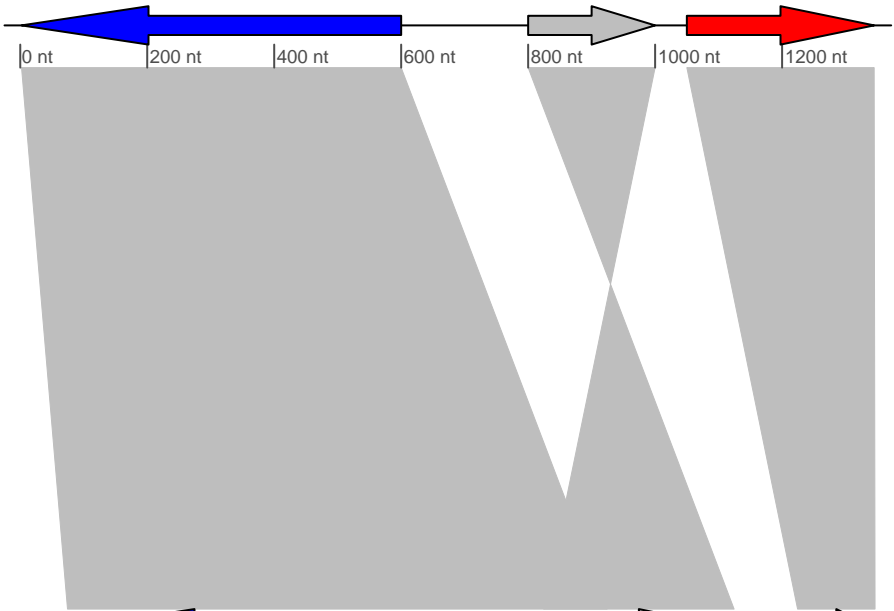




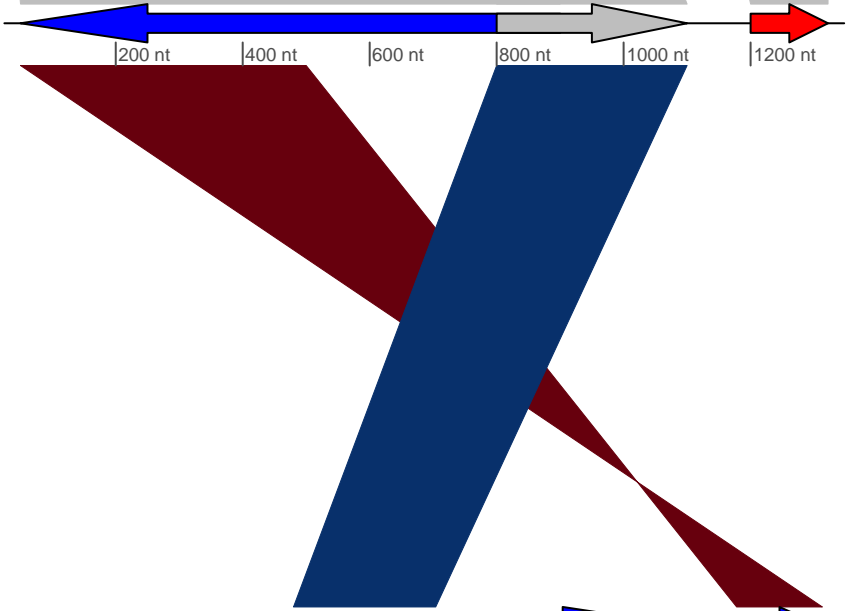




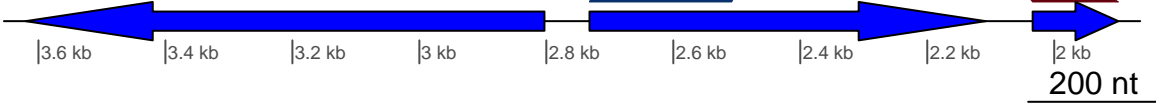
A\_aaa

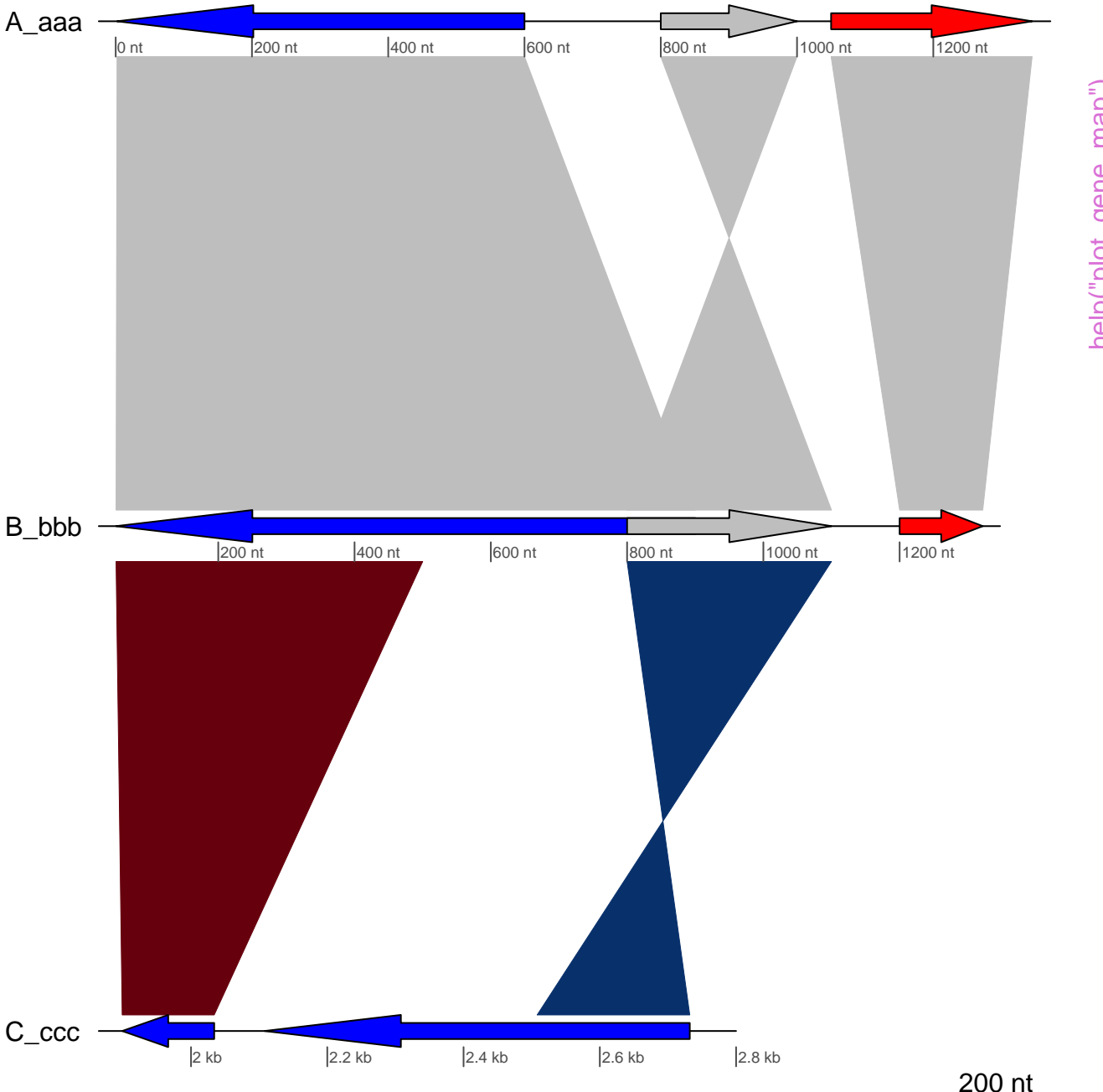


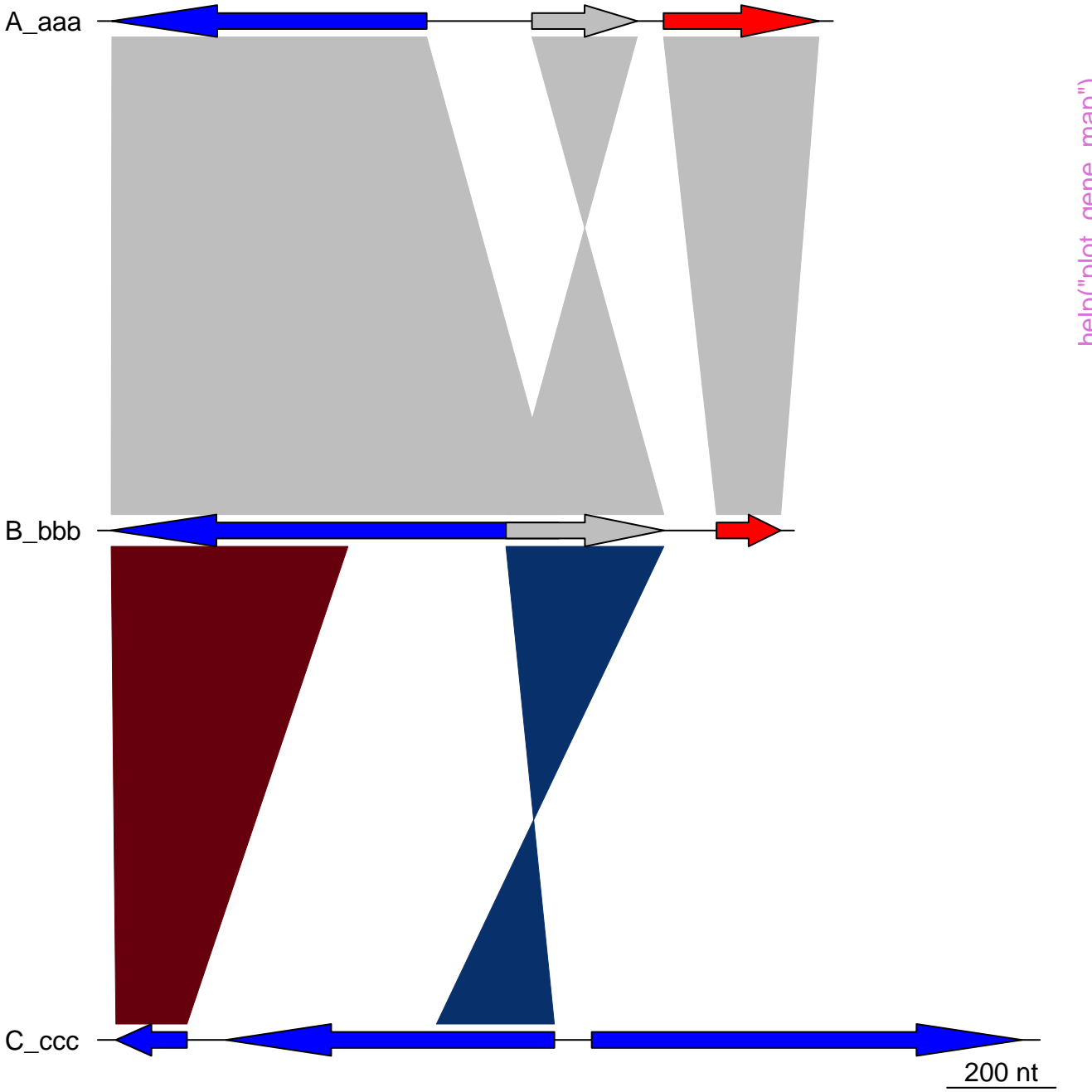
B\_bbb



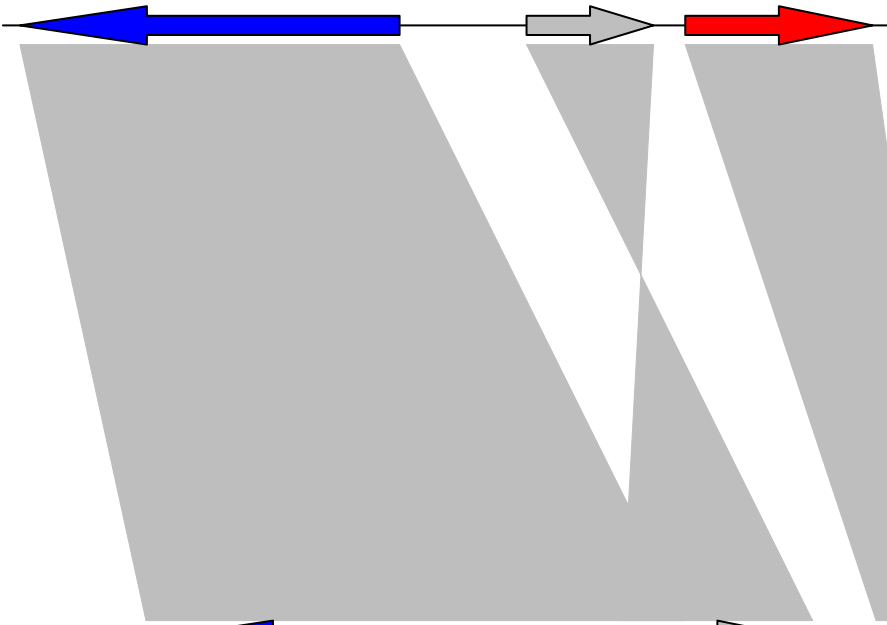
C\_ccc



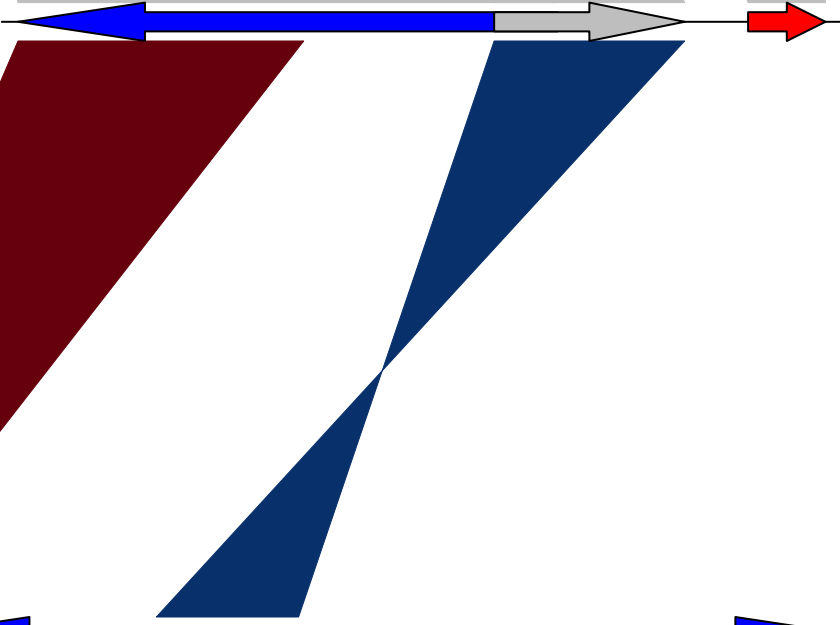




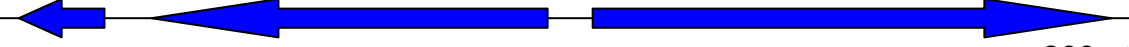
A\_aaa



B\_bbb



C\_ccc

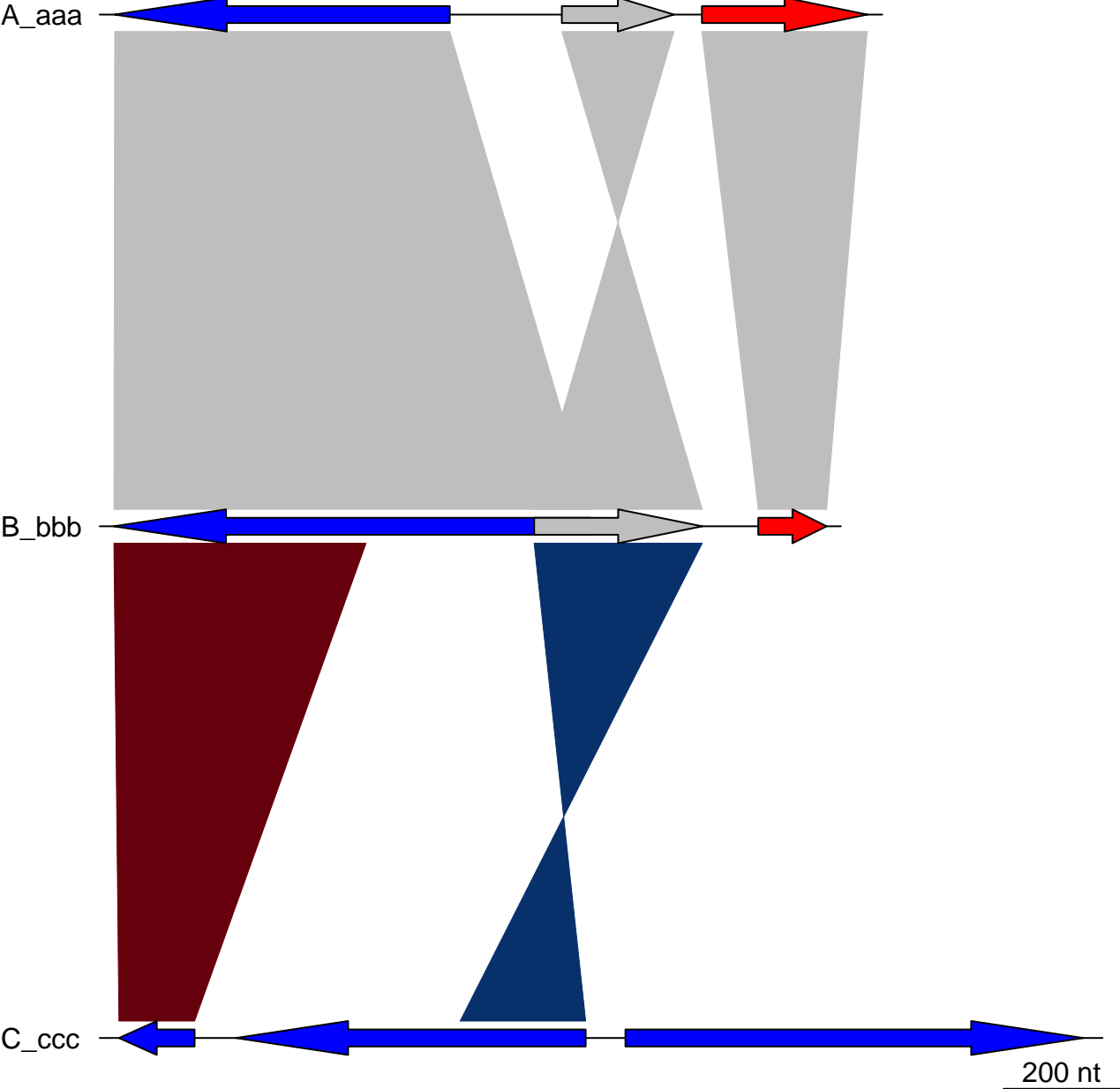


200 nt

help("plot\_gene\_map")

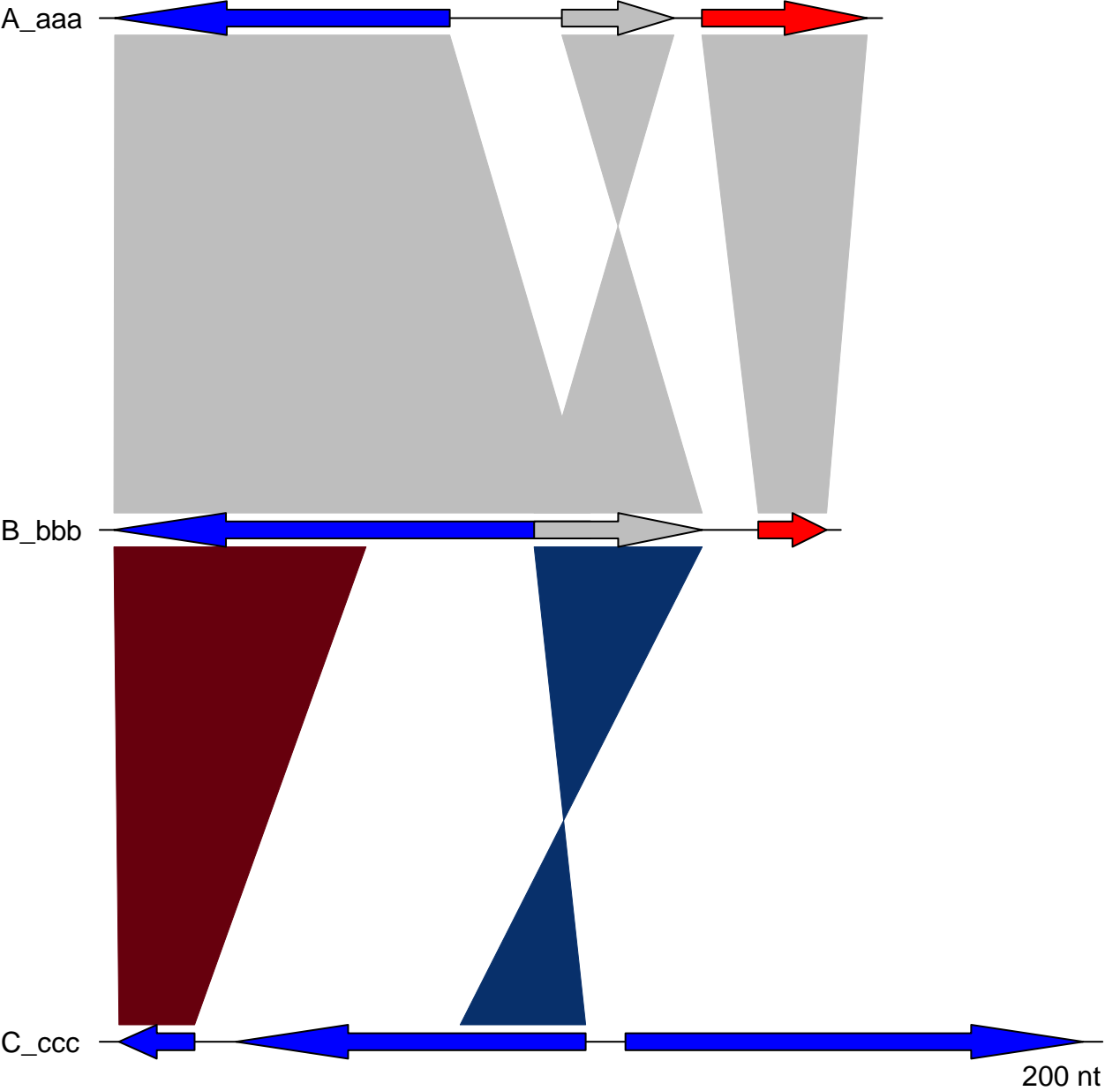


Comparison of A, B and C



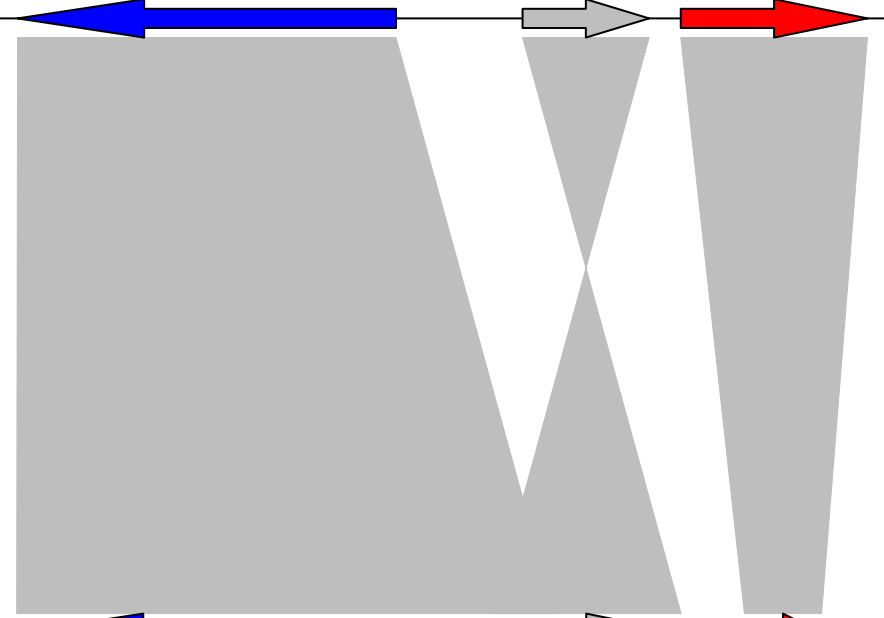
help("plot\_gene\_map")

Comparison of A, B and C

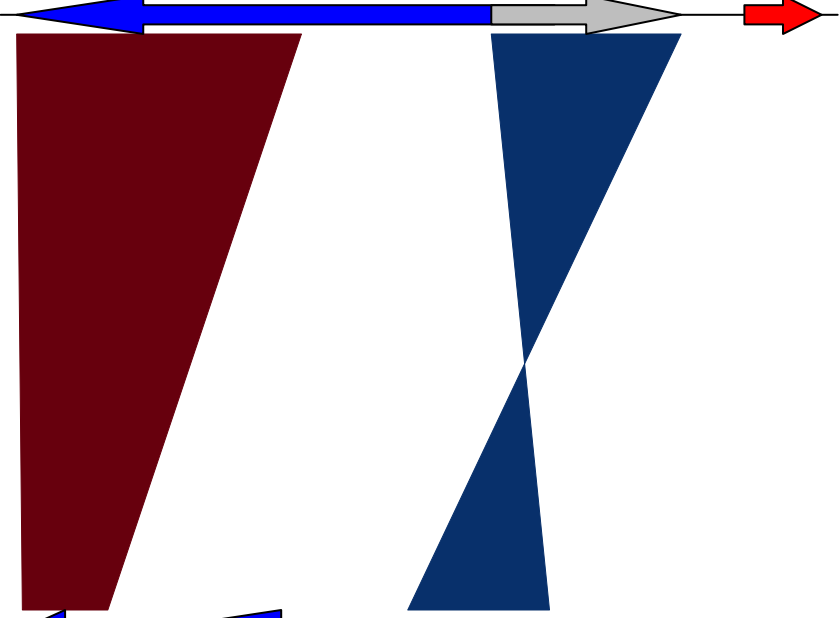


help("plot\_gene\_map")

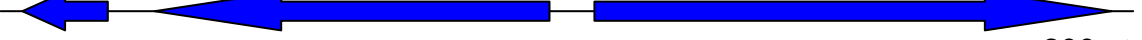
Huey



Dewey



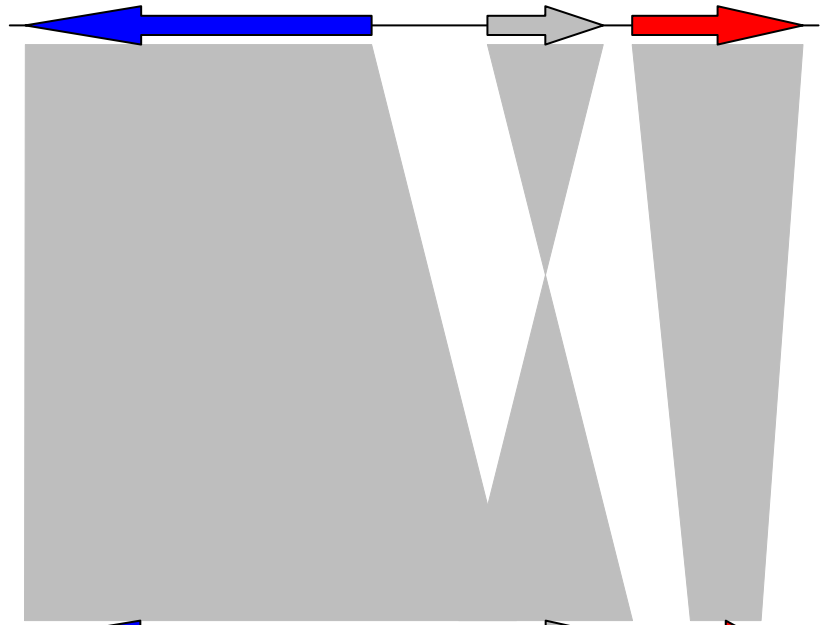
Louie



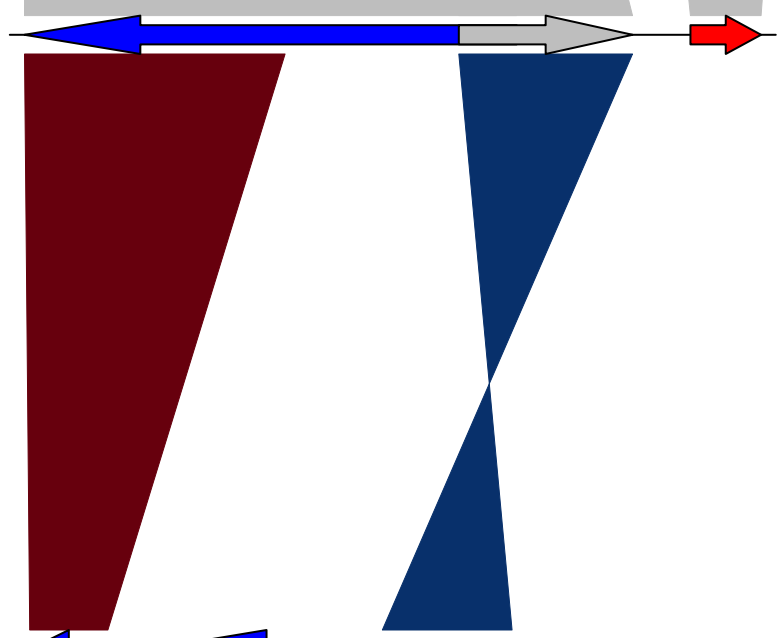
200 nt

help("plot\_gene\_map")

Huey



Dewey

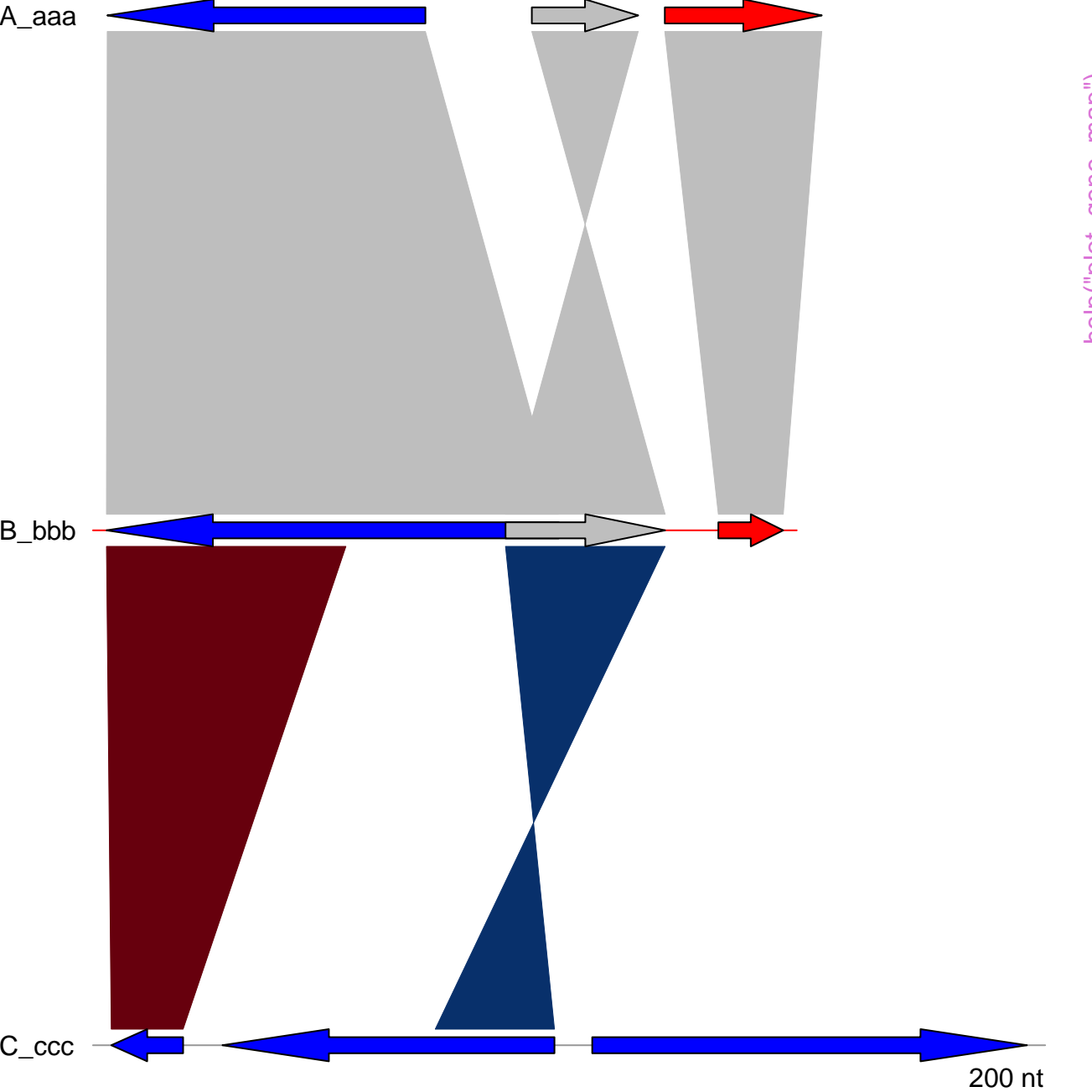


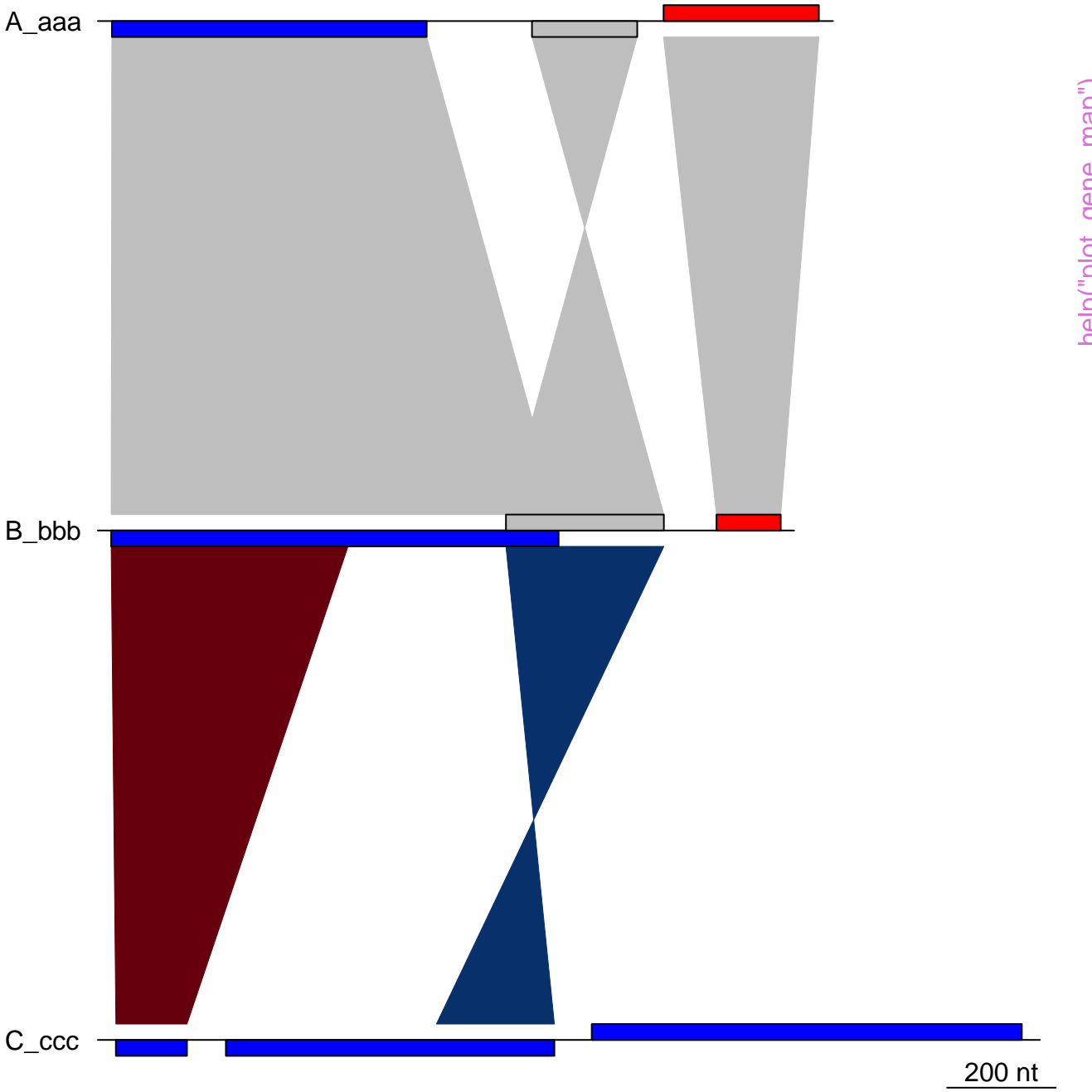
Louie



200 nt

help("plot\_gene\_map")





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

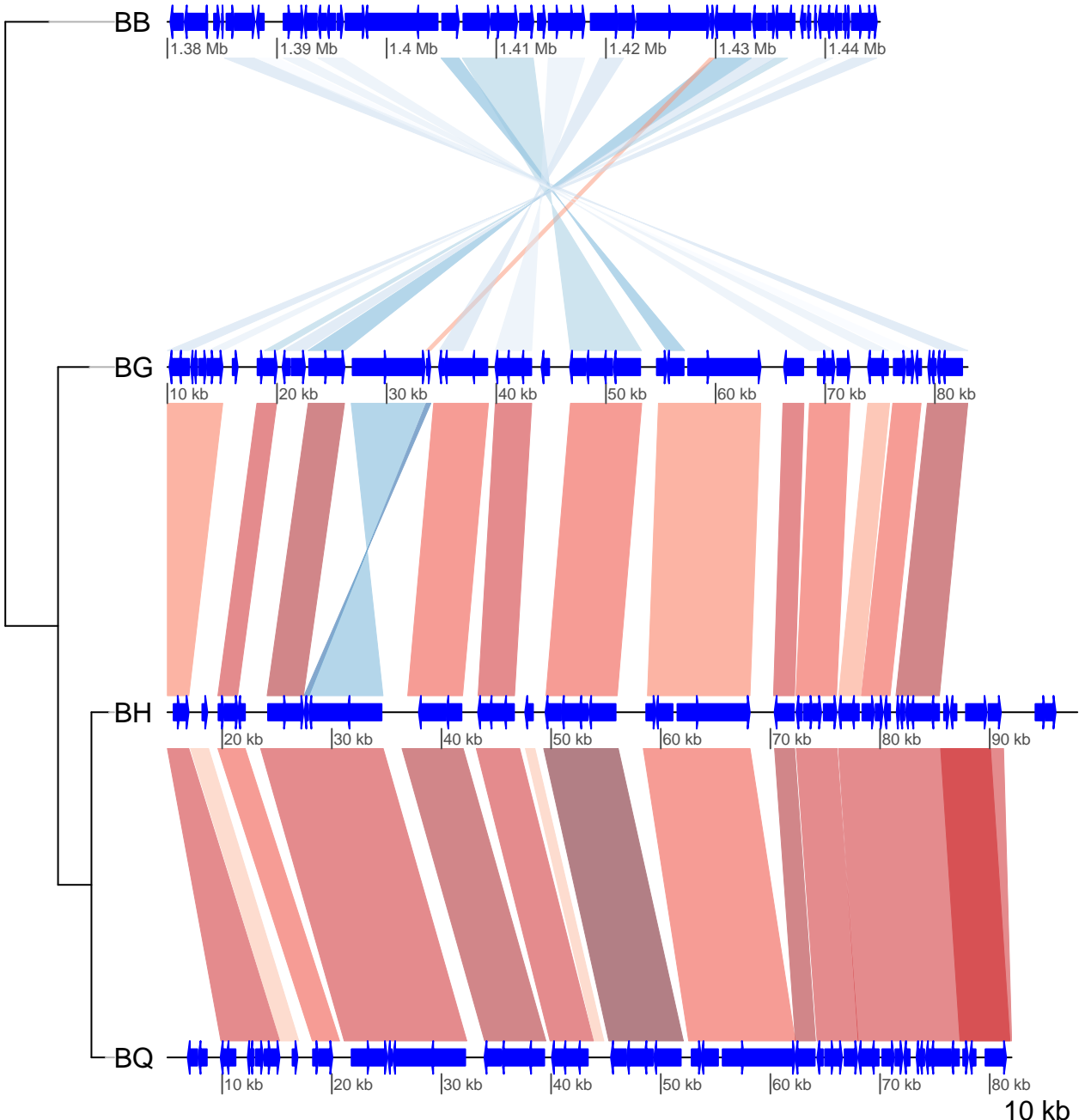
BG | 10 kb | 20 kb | 30 kb | 40 kb | 50 kb | 60 kb | 70 kb | 80 kb

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

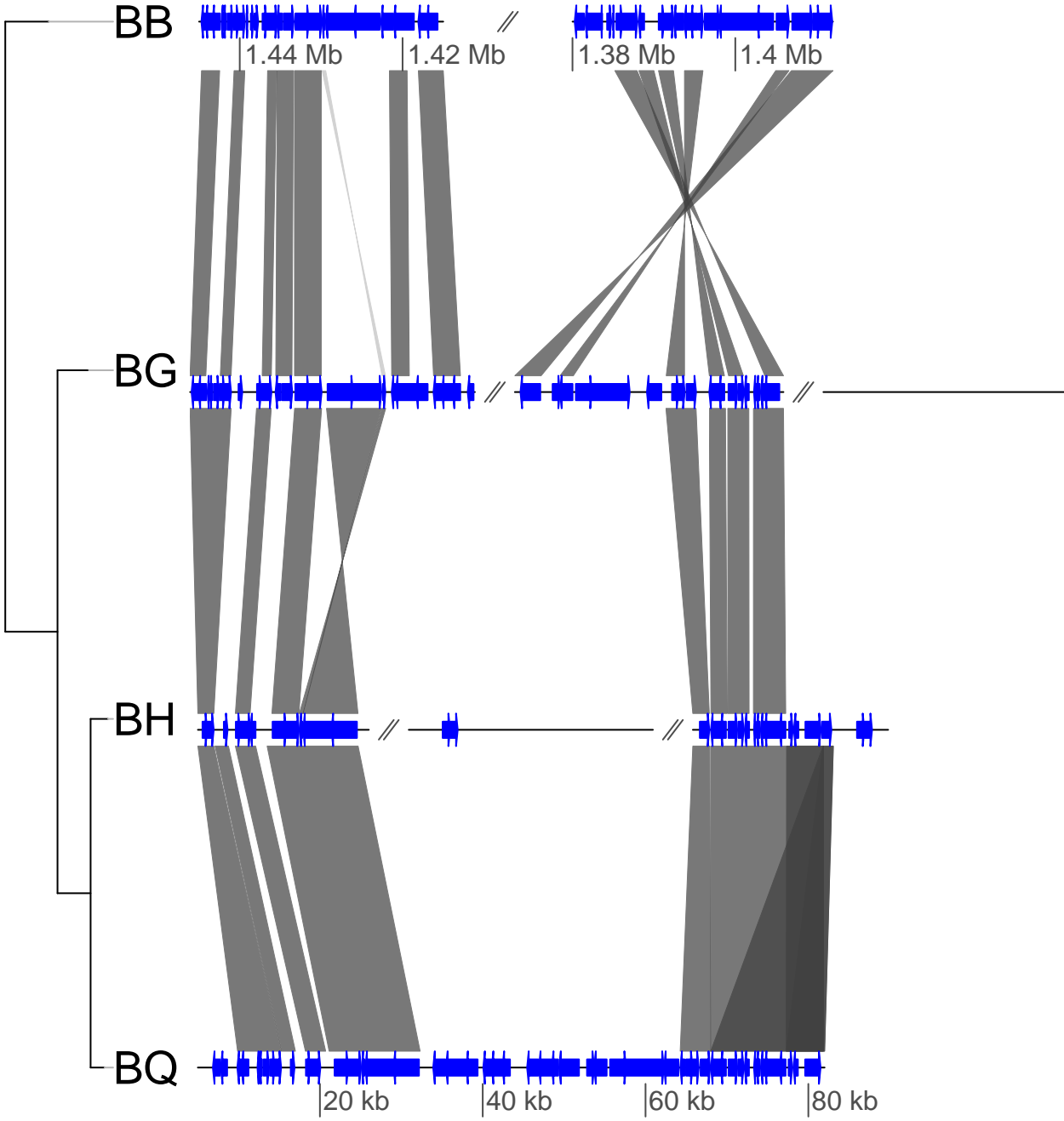
20 kb

40 kb

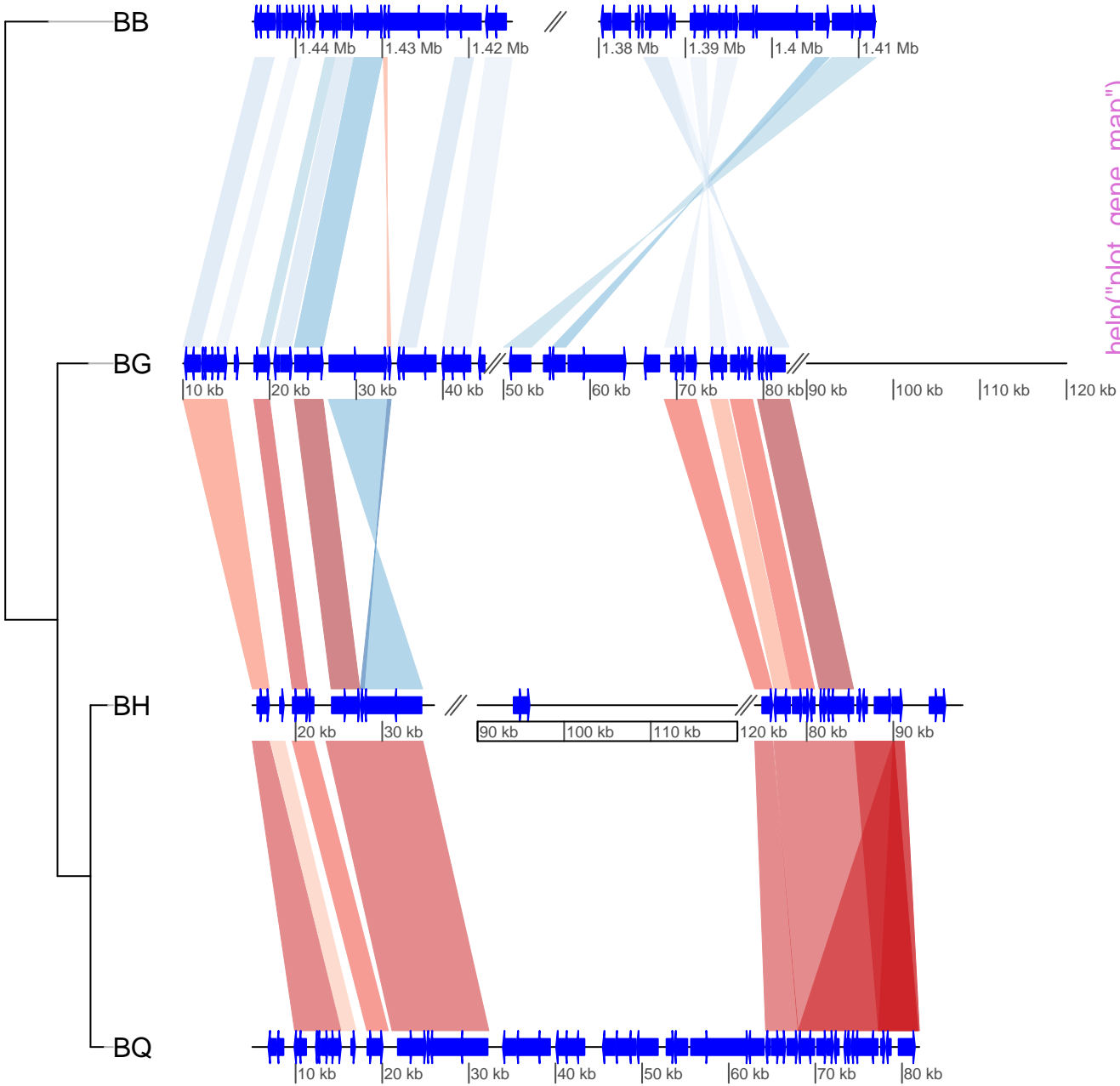
60 kb

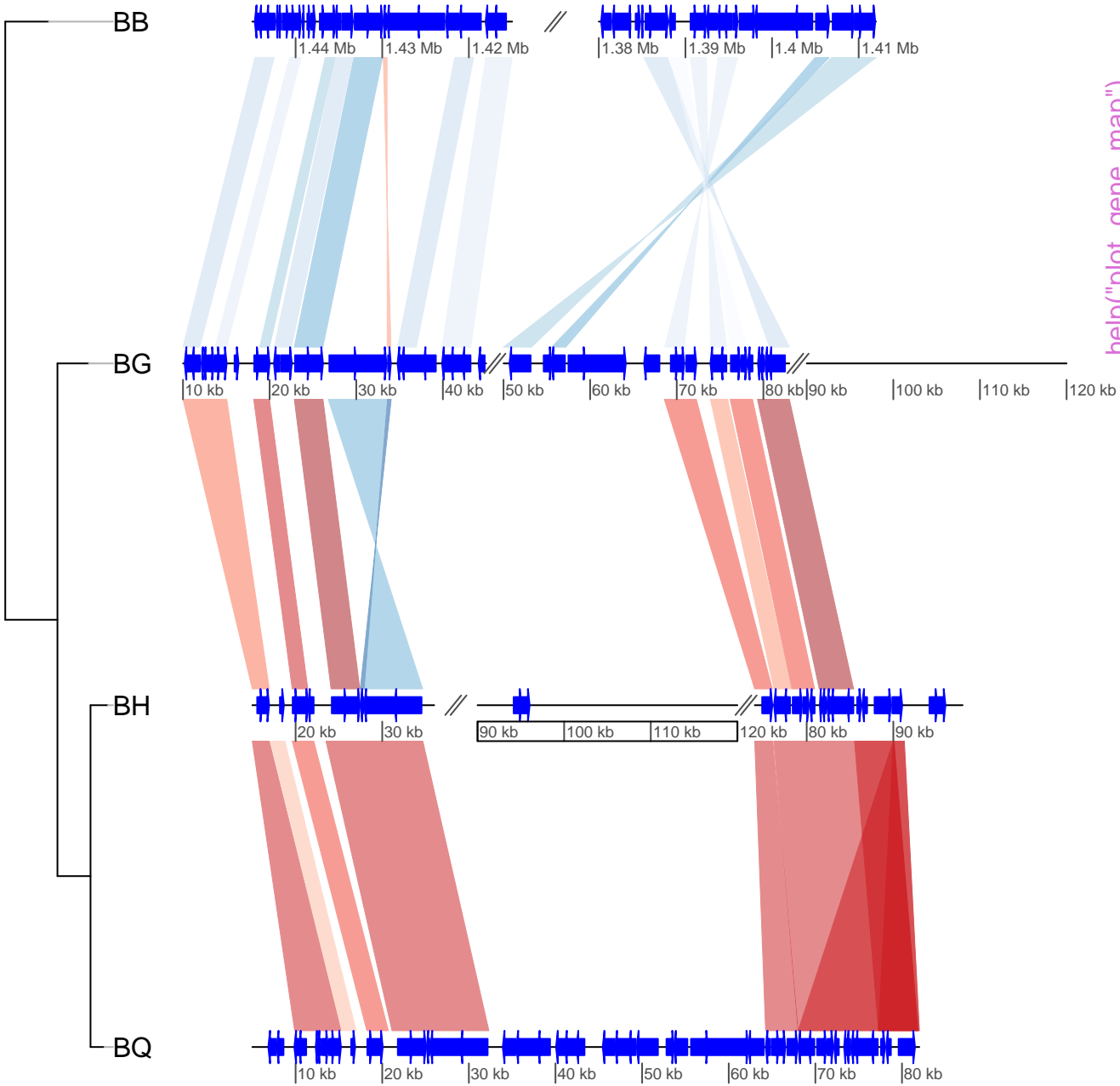
80 kb

help("plot\_gene\_map")

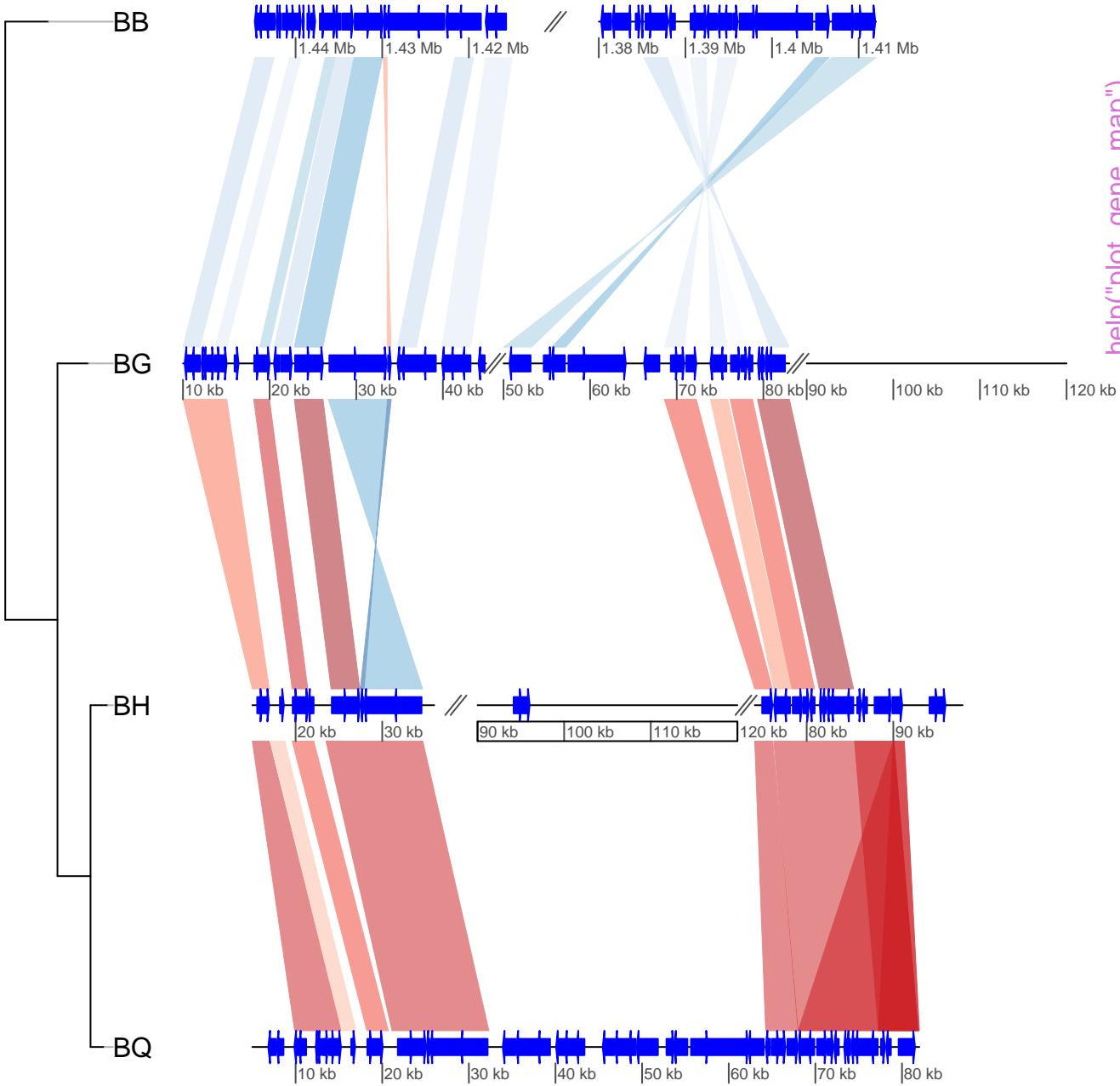




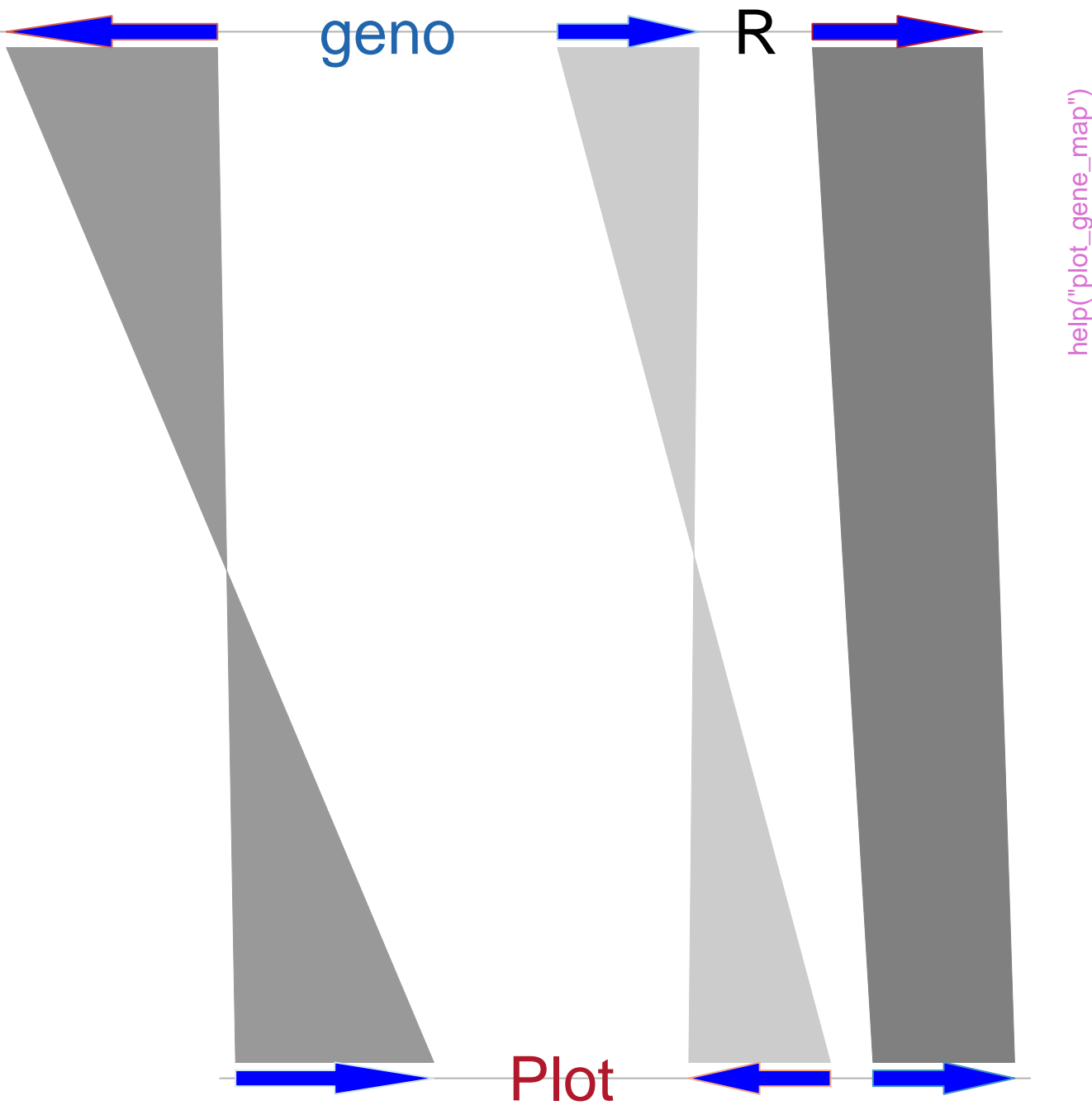




10 kb



help("plot\_gene\_map")

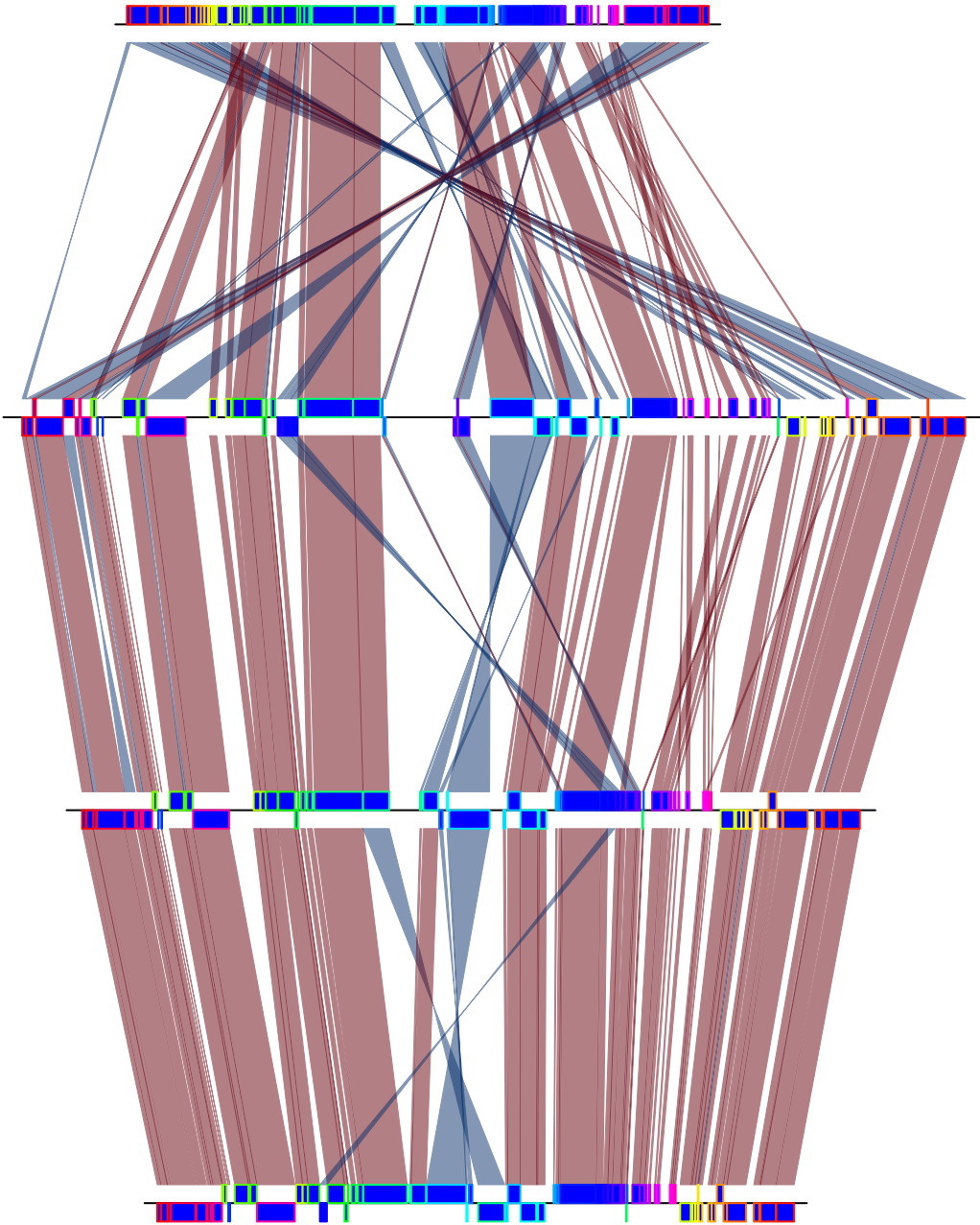


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

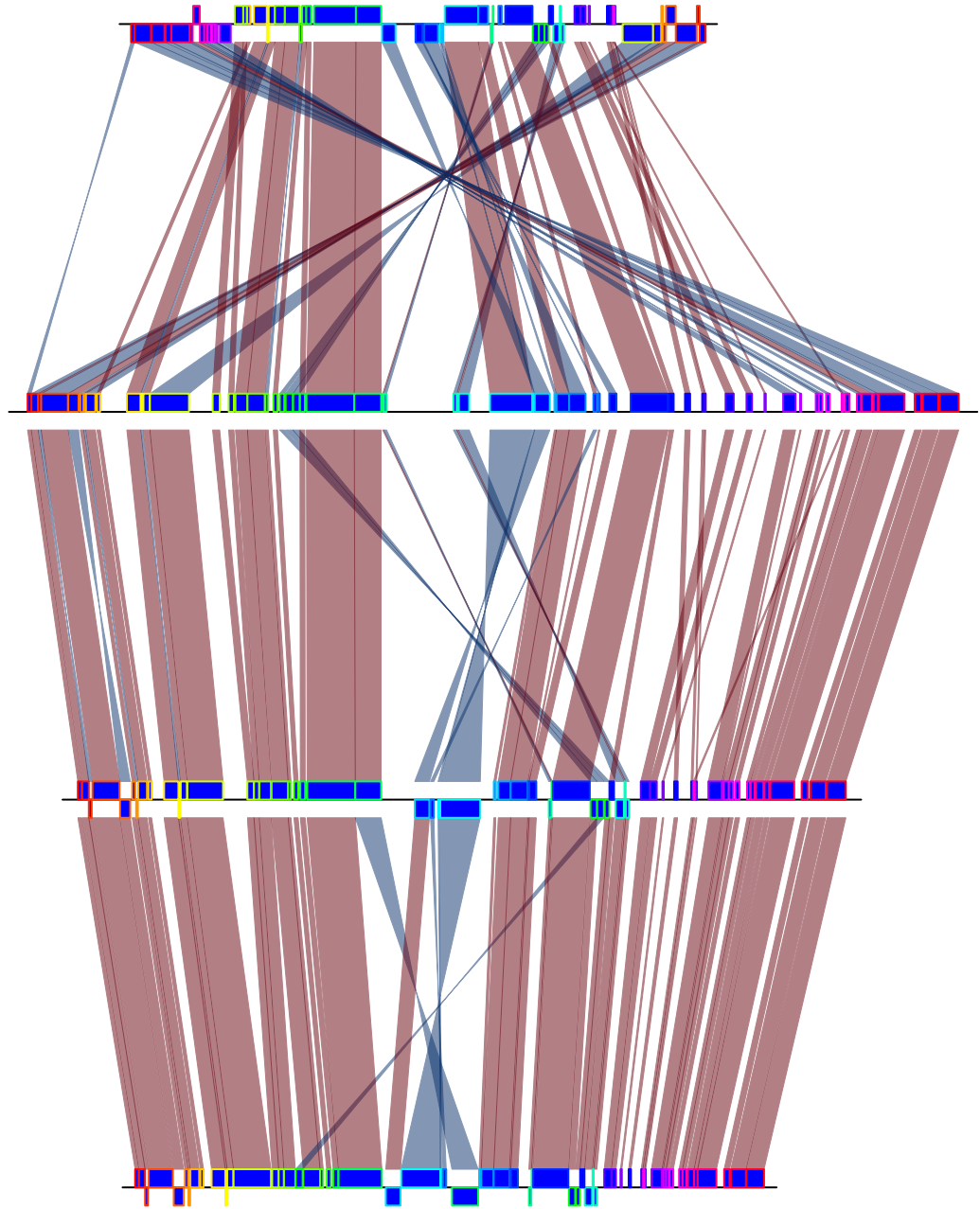
500 kb

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

500 kb

B bacilliformis

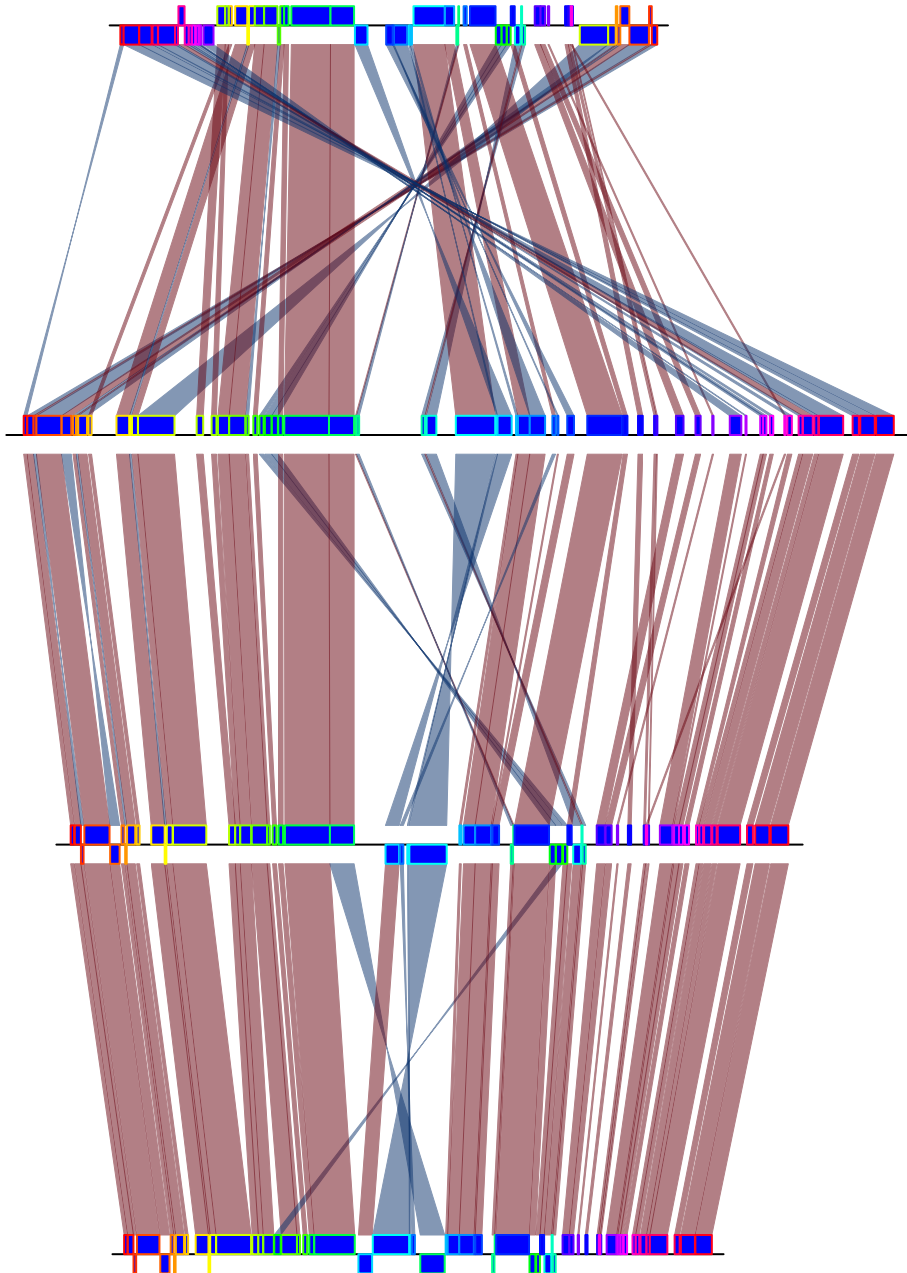
B grahamii

B henselae

B quintana

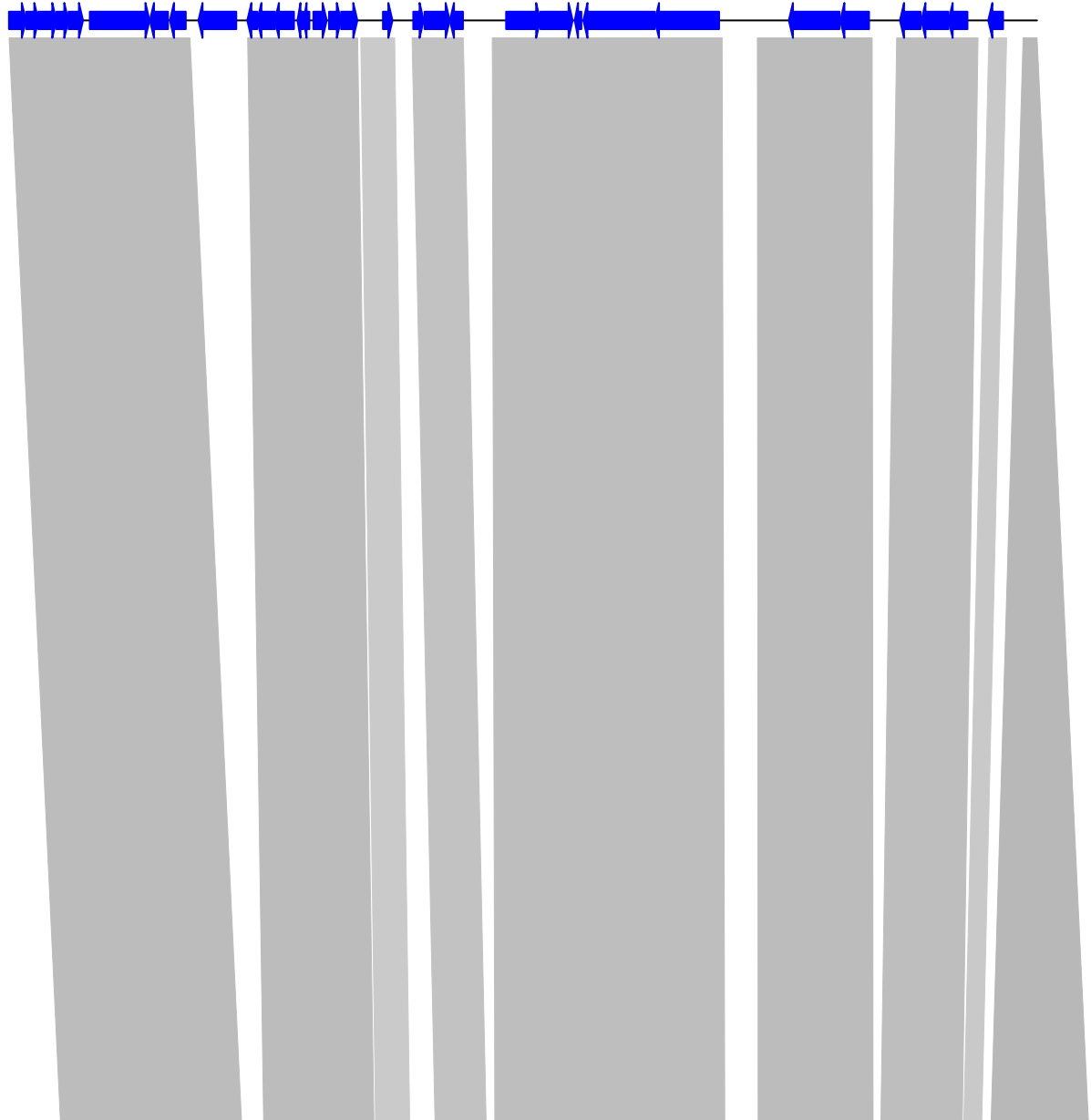
help("read\_functions")

500 kb



BH

BQ



help("read\_functions")

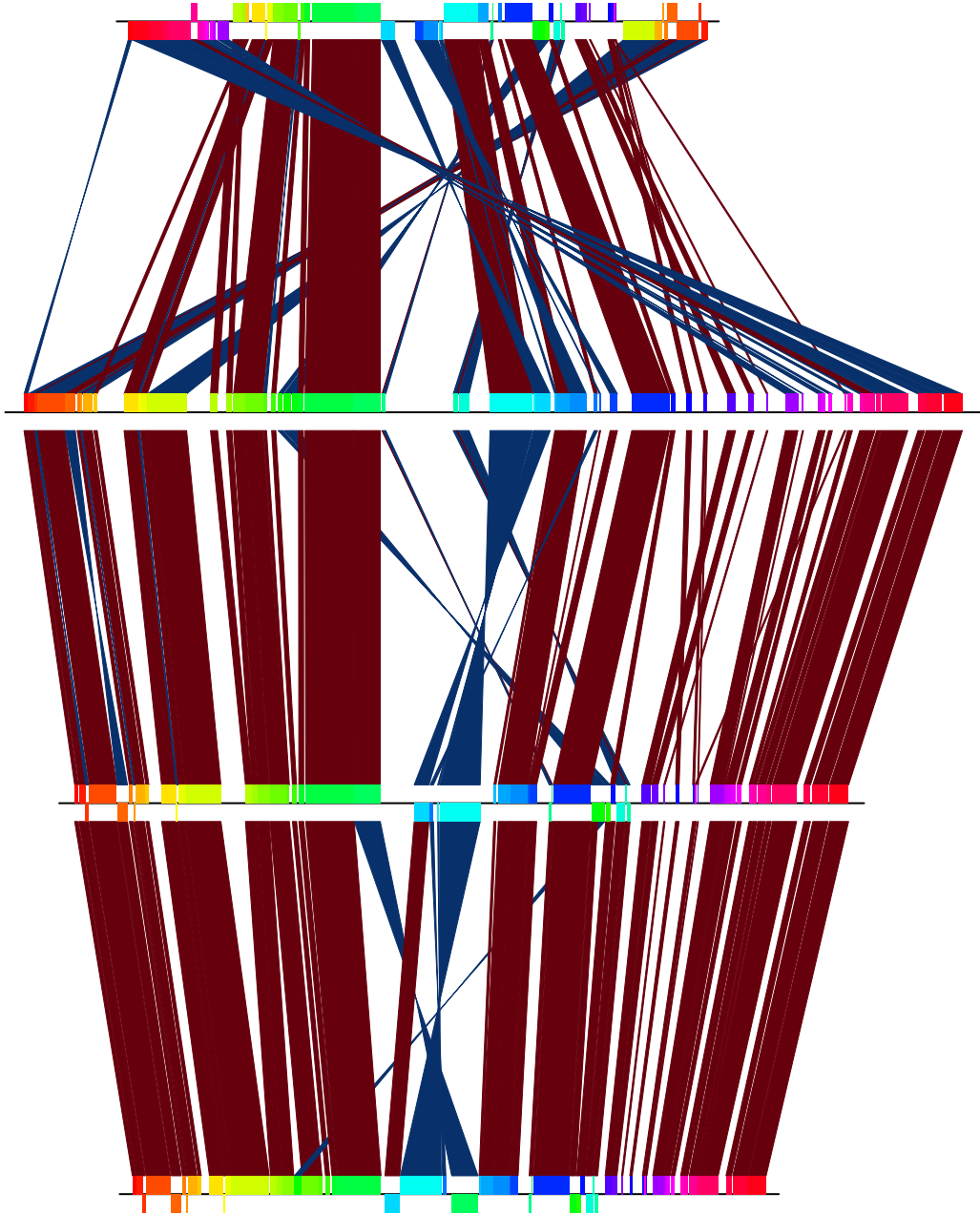


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



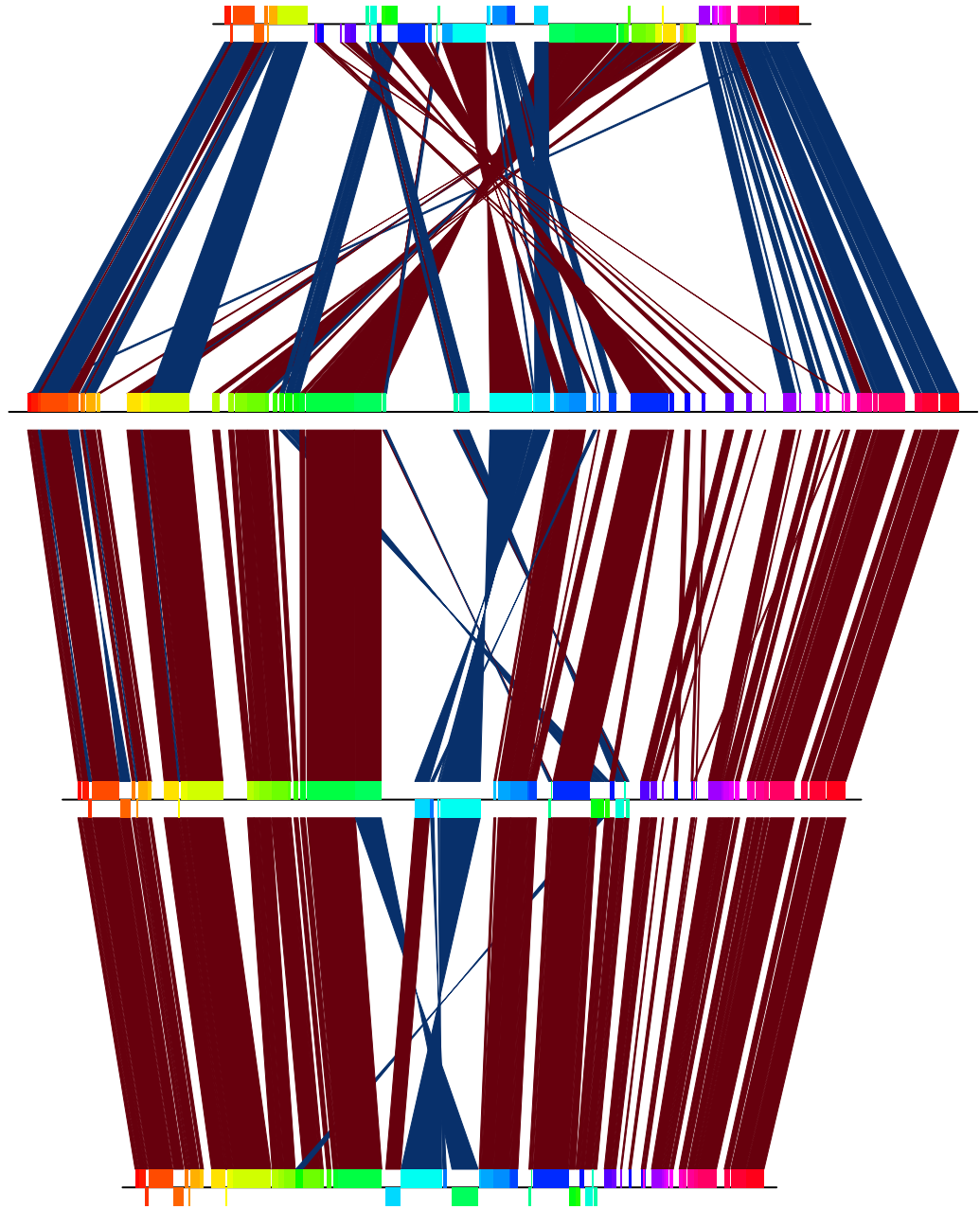
help("reverse")

B\_bacilliformis

B\_grahamii

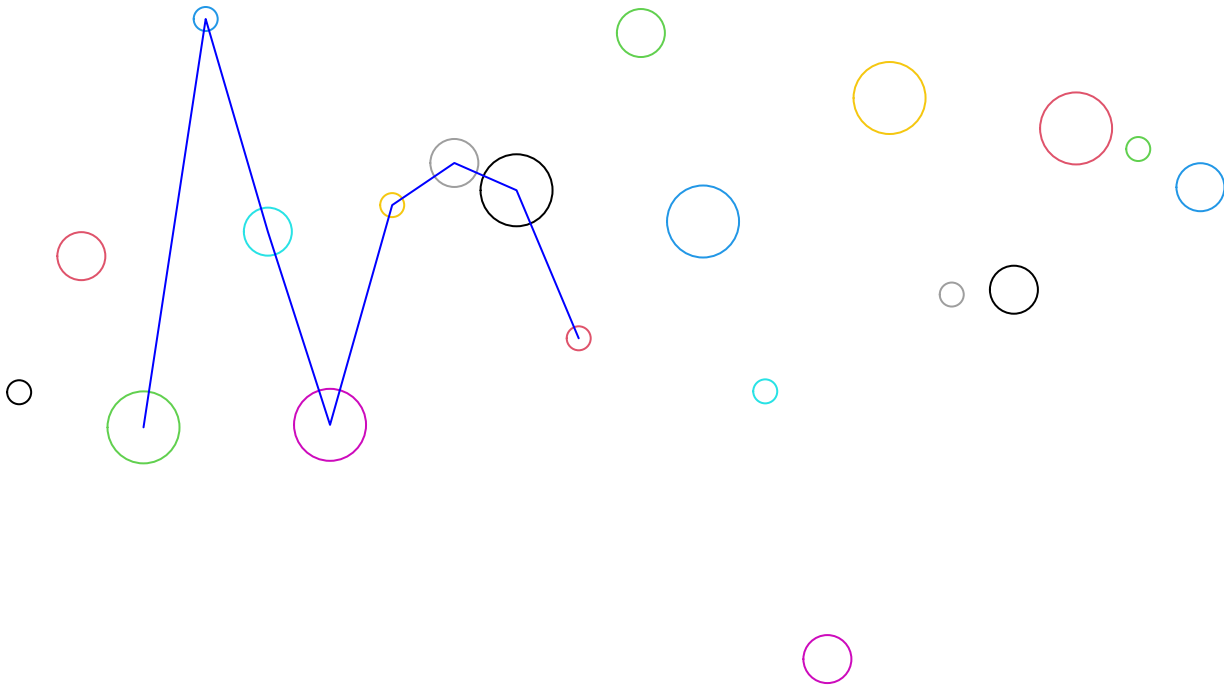
B\_henselae

B\_quintana

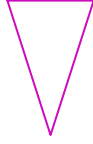
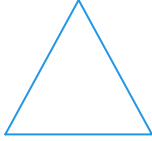


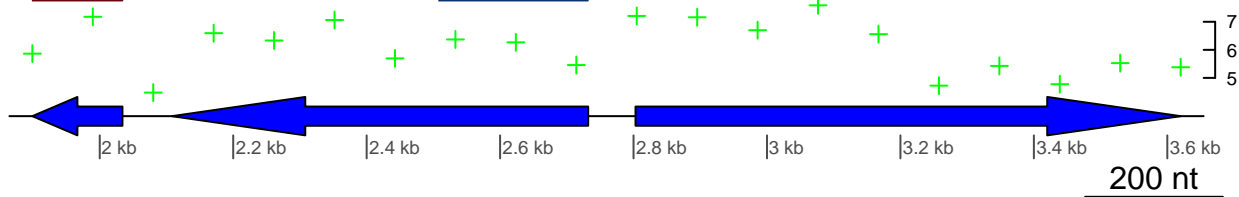
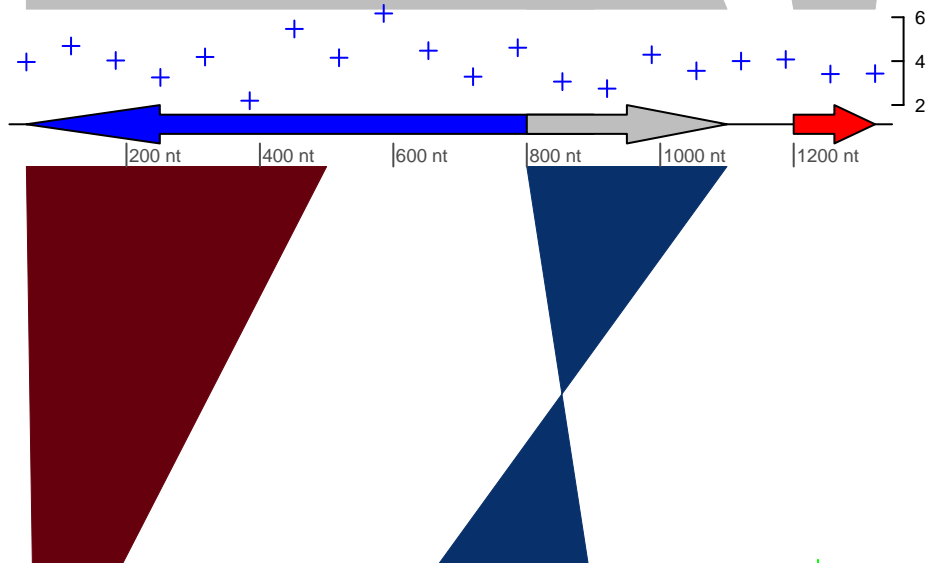
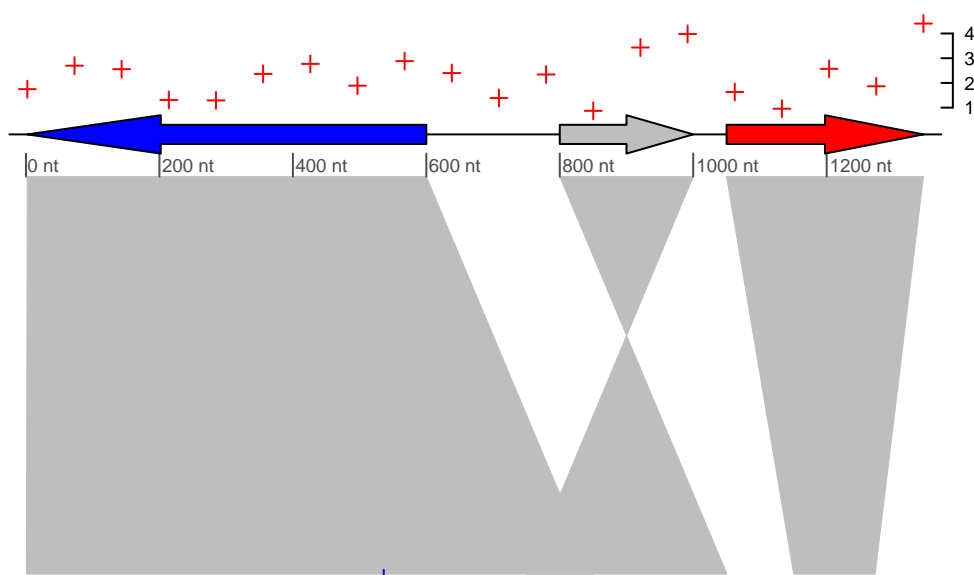
help("reverse")

500 kb



help("seg\_plot")

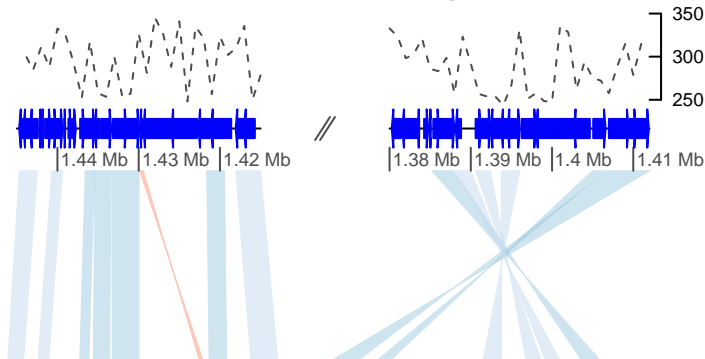




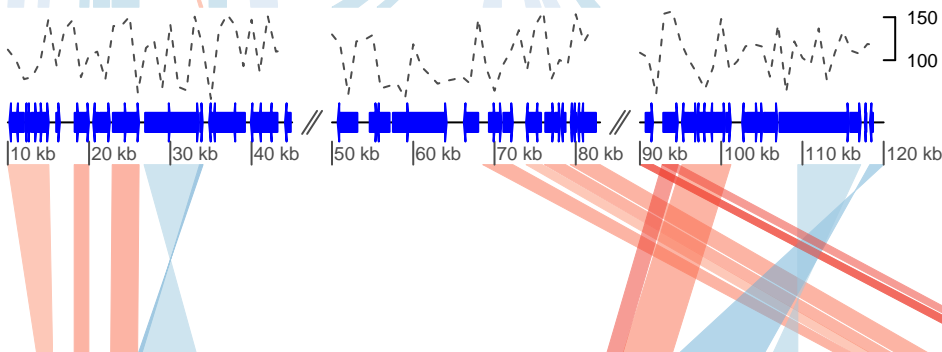
help("seg\_plot")

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

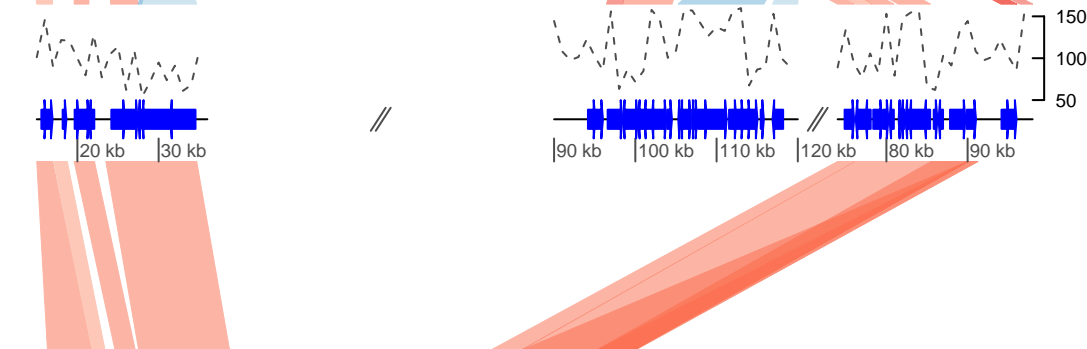
BB



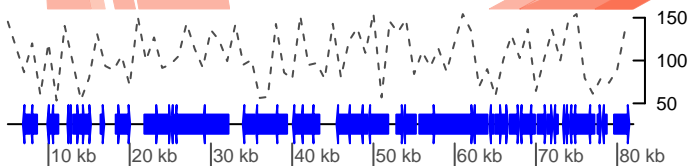
BG



BH

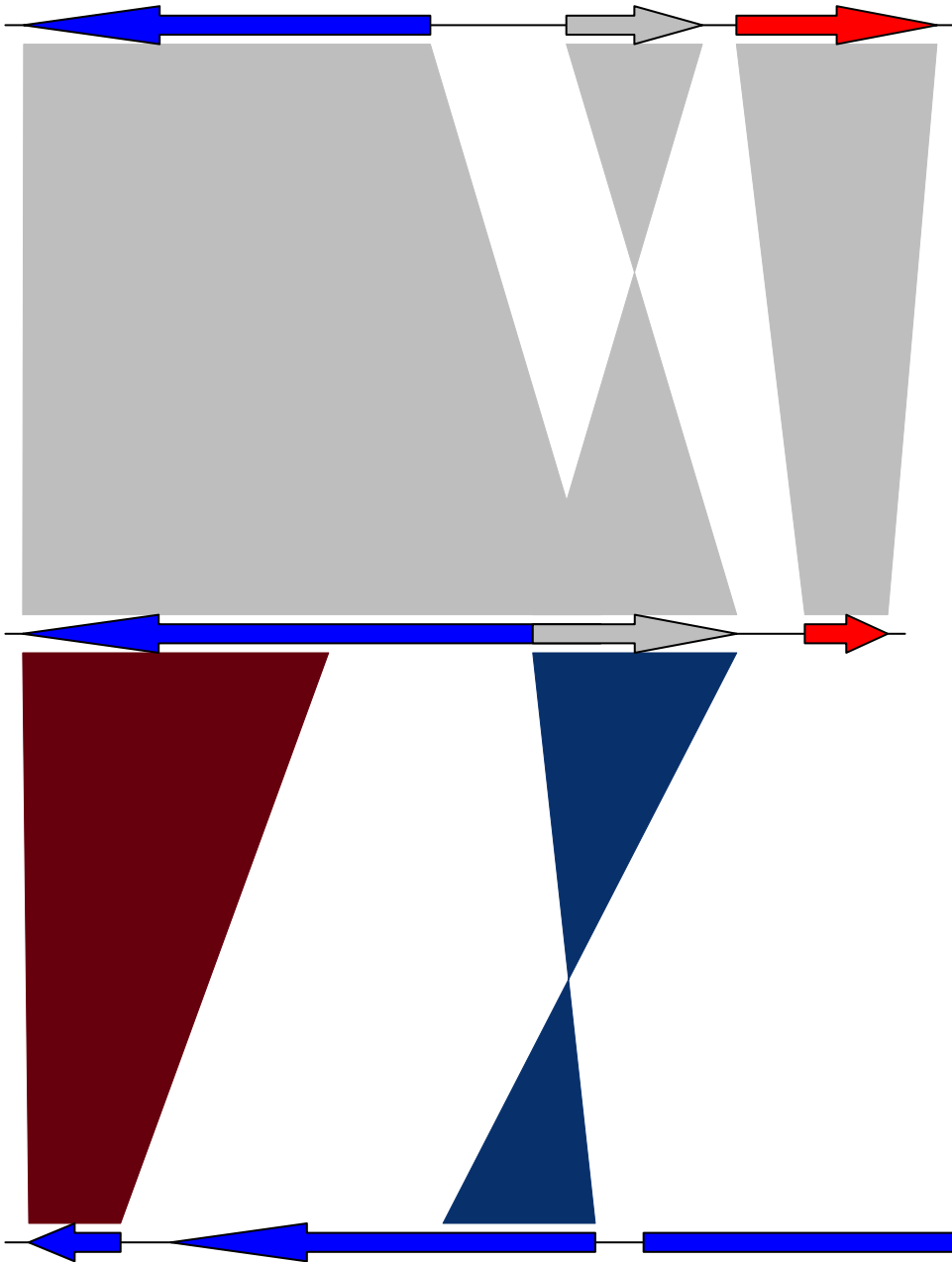


BQ



20 kb

help("seg\_plot")



help("three\_genes")

200 nt

