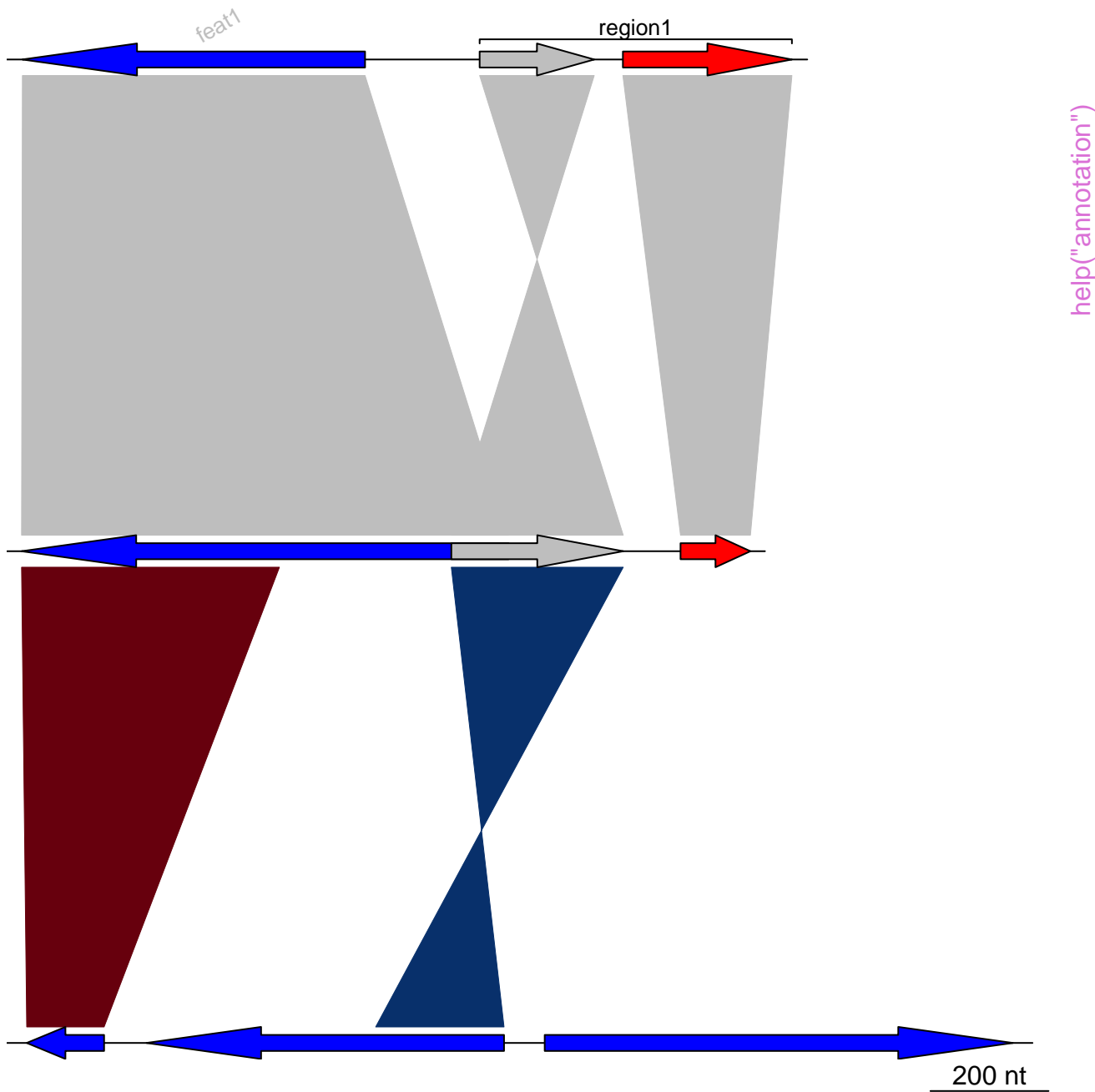
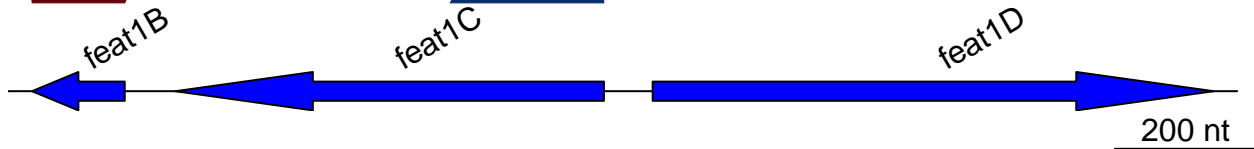
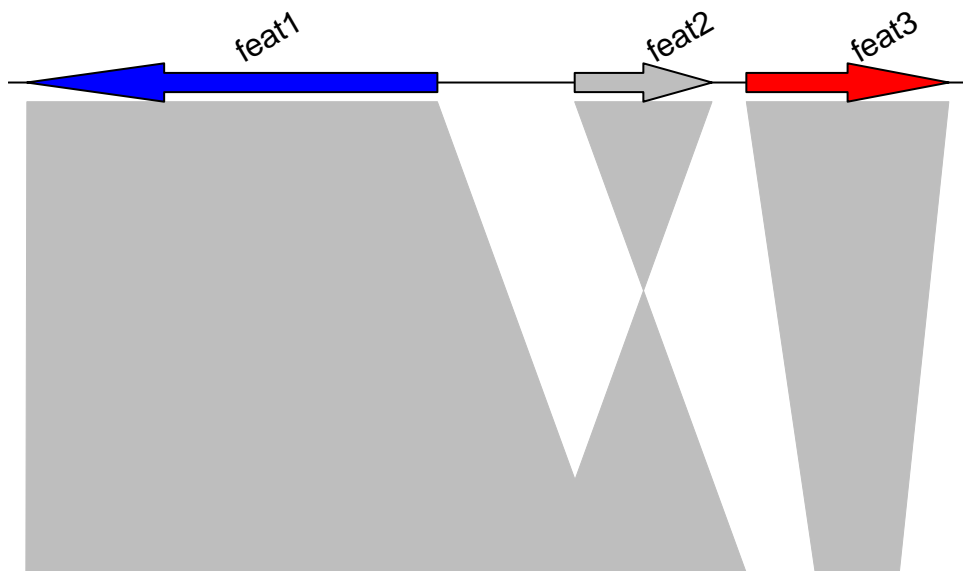
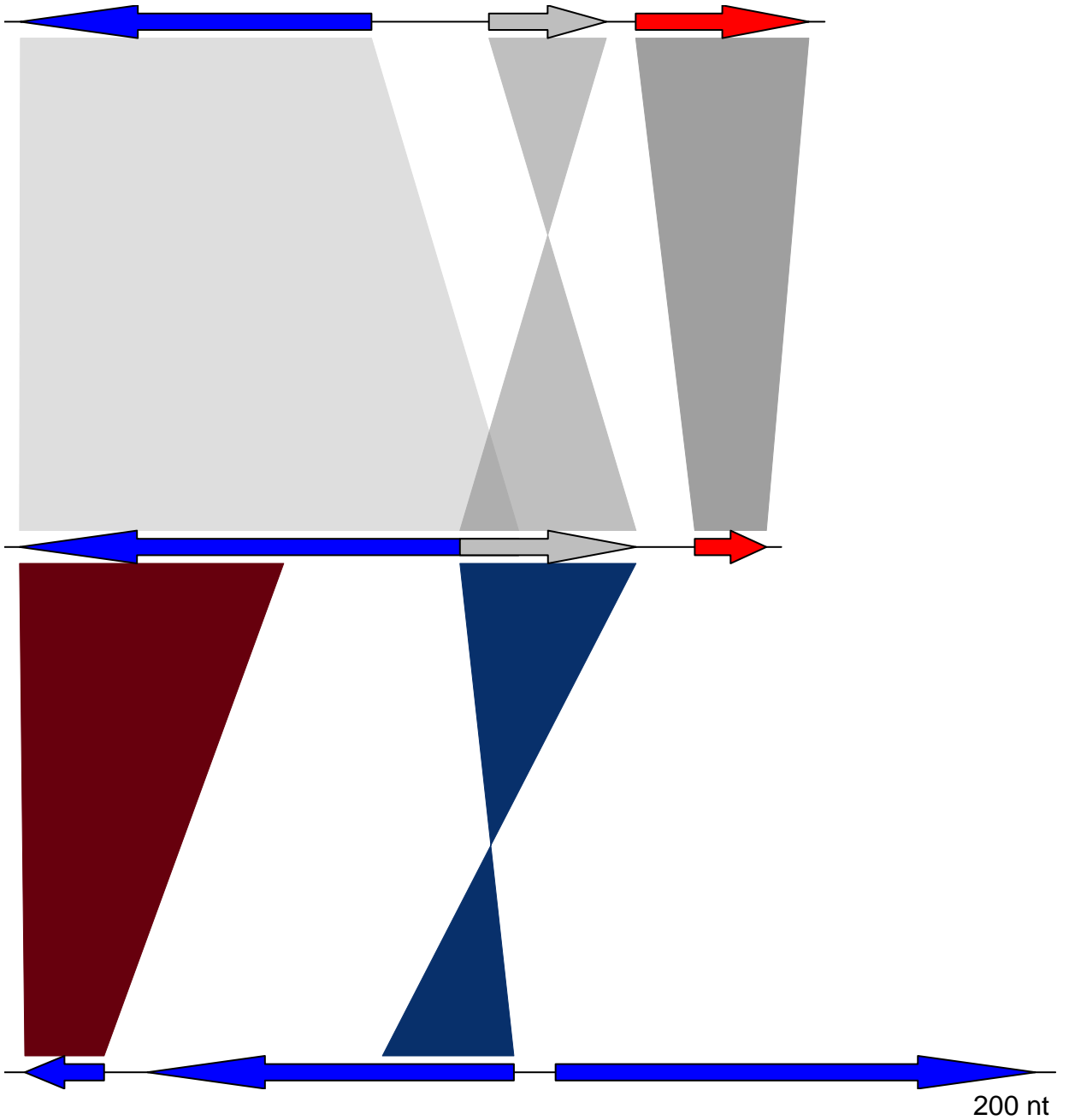


help("annotation")

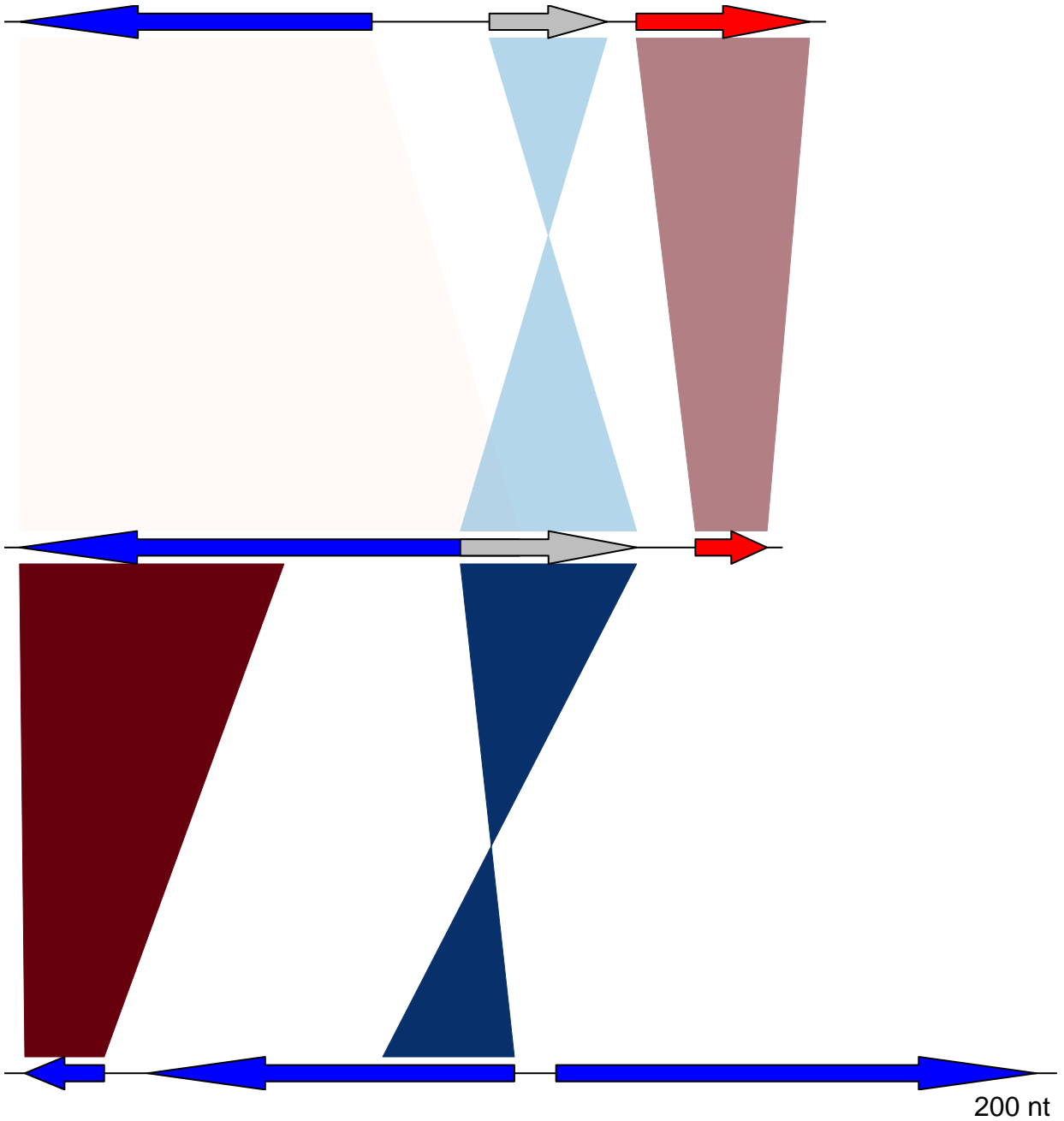




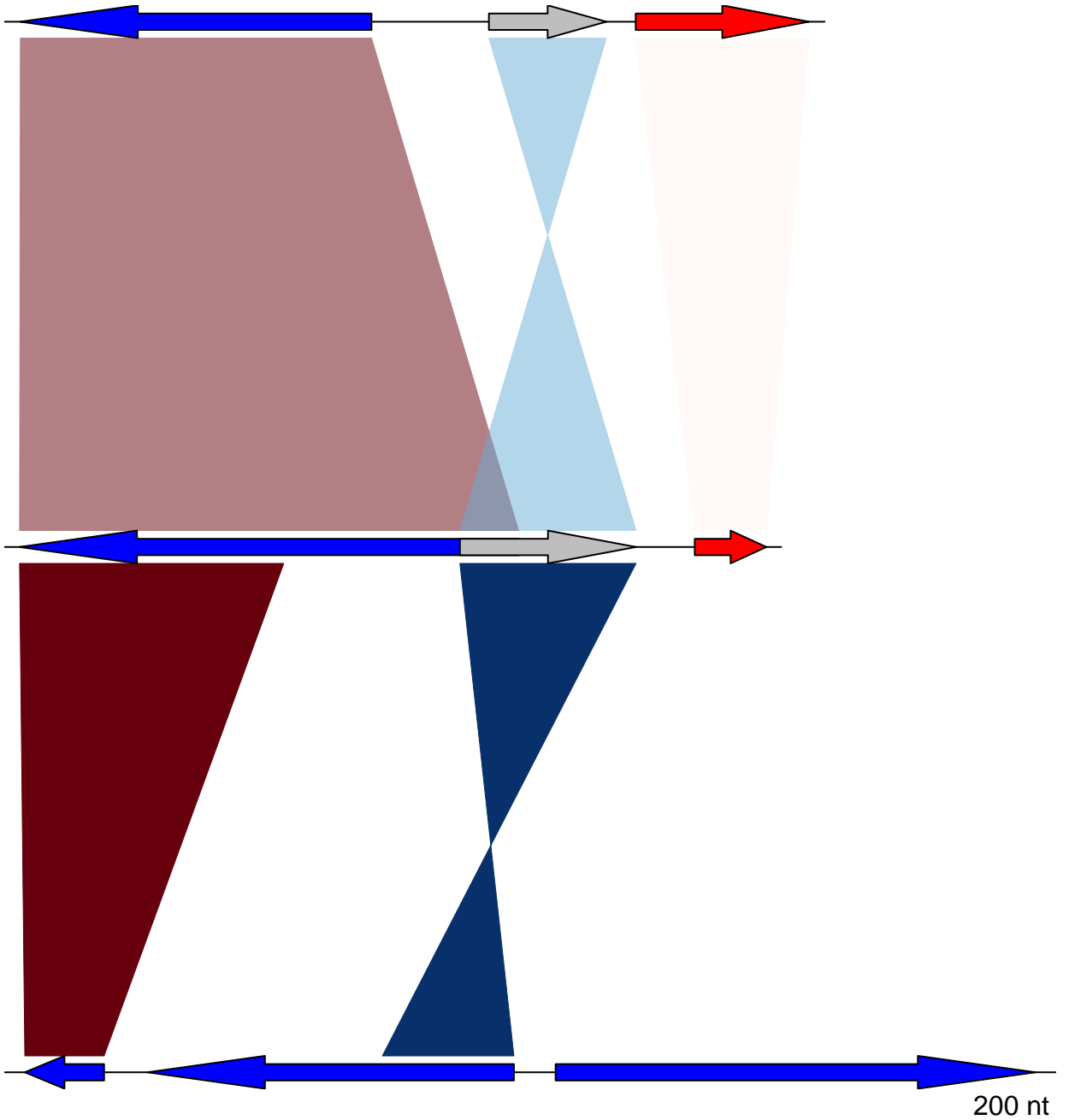
help("annotation")



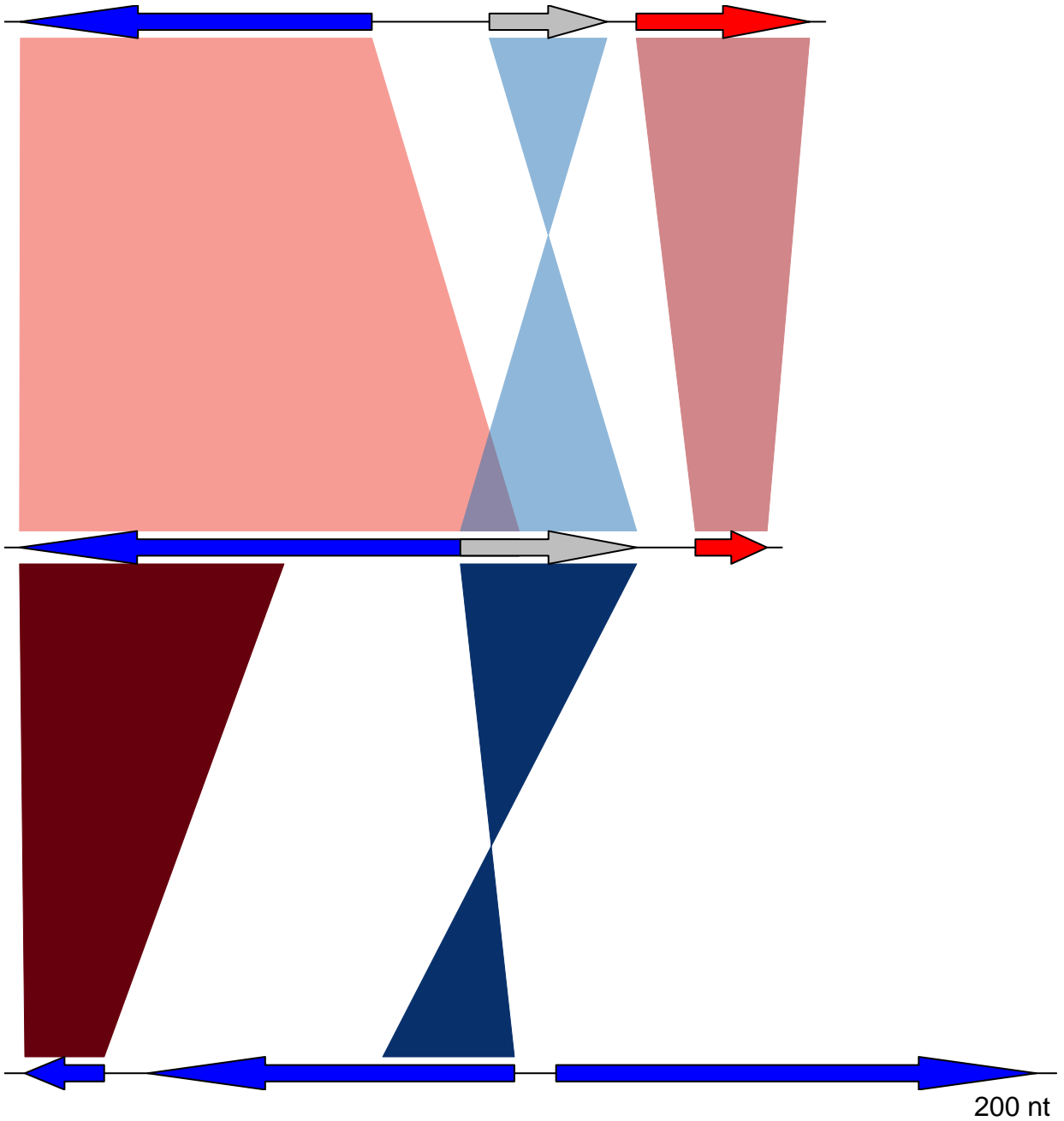
help("apply\_color\_scheme")



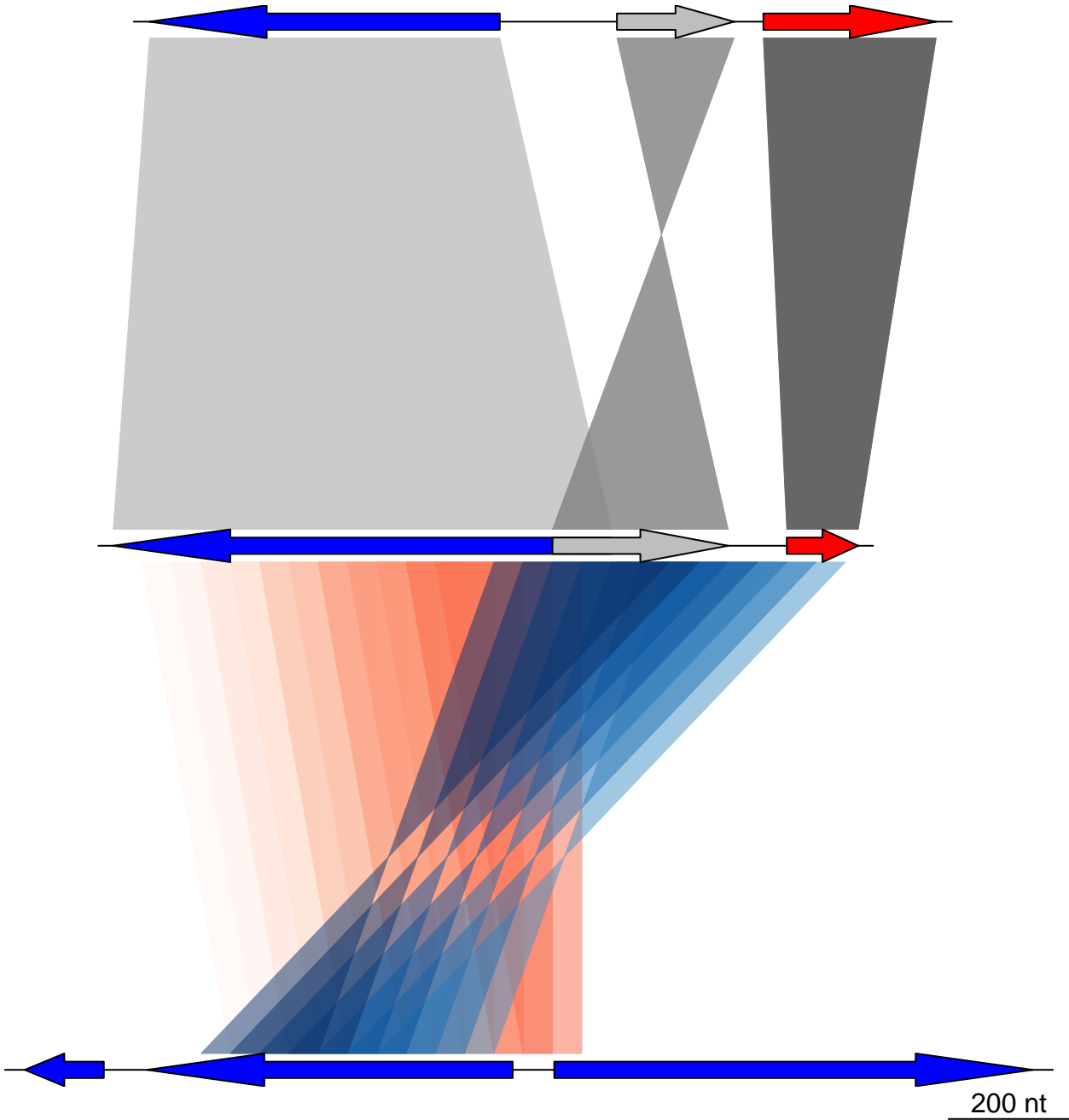
help("apply\_color\_scheme")



help("apply\_color\_scheme")

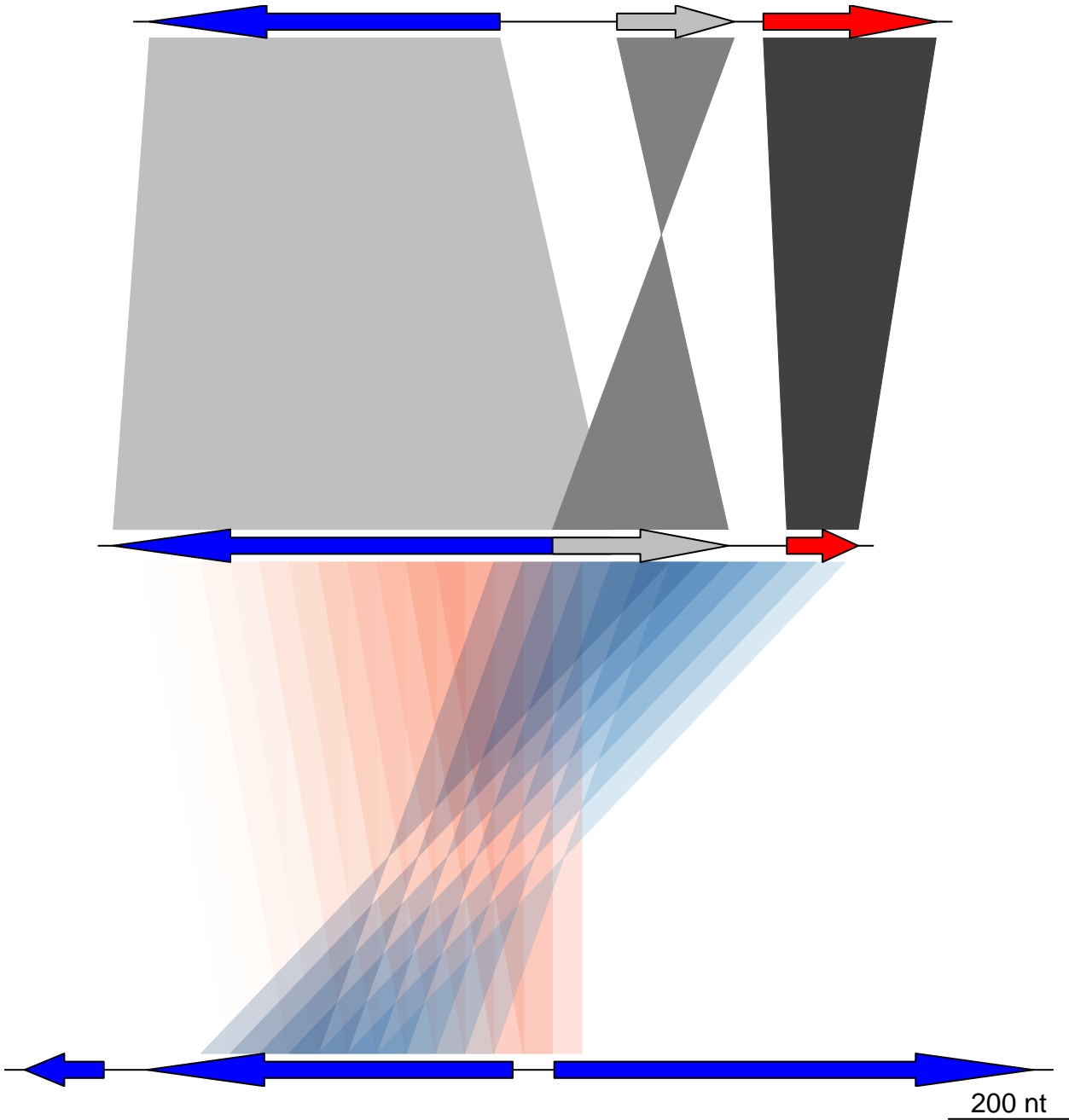


help("apply\_color\_scheme")

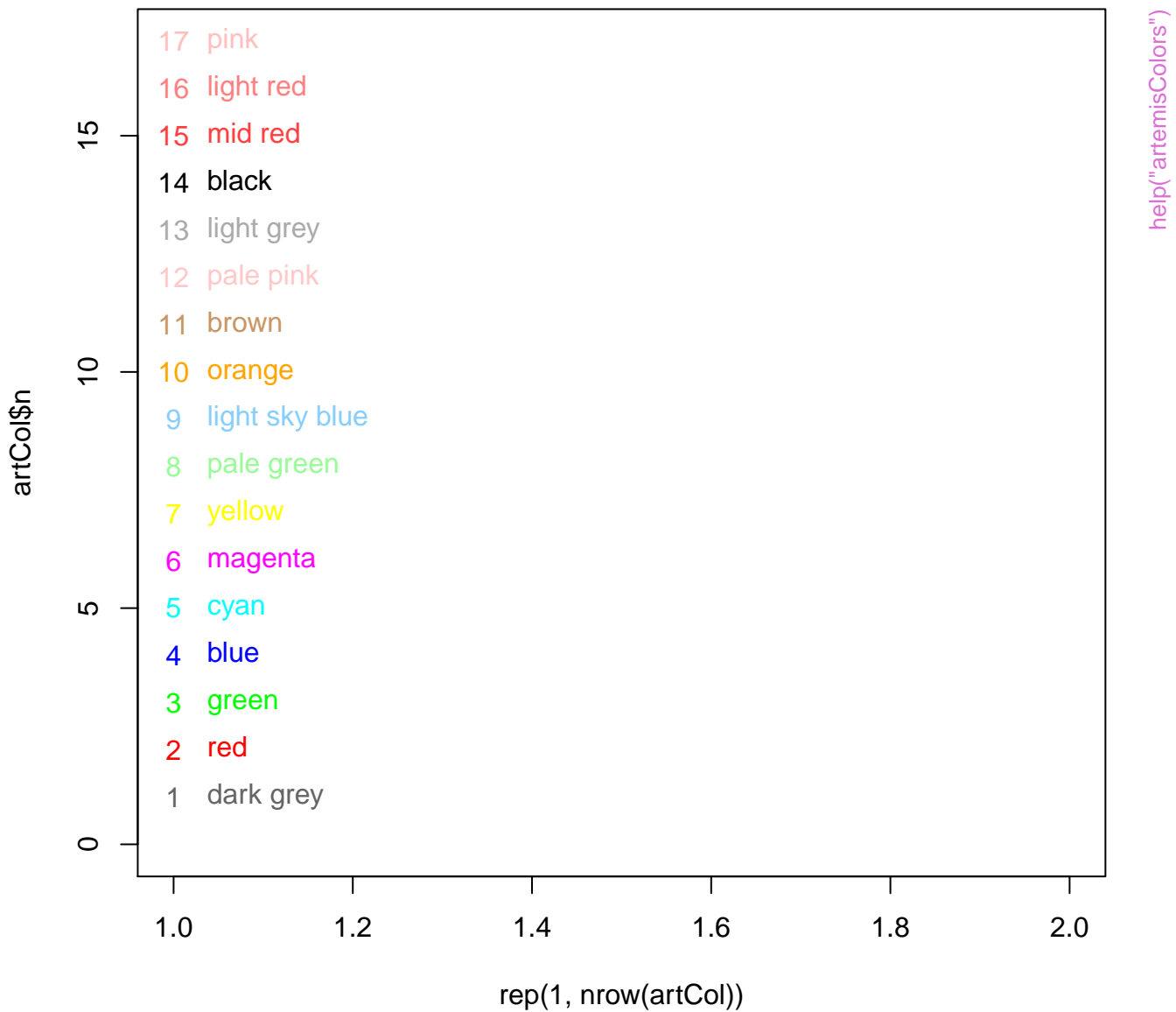


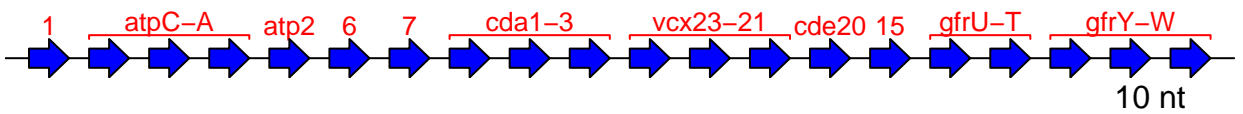
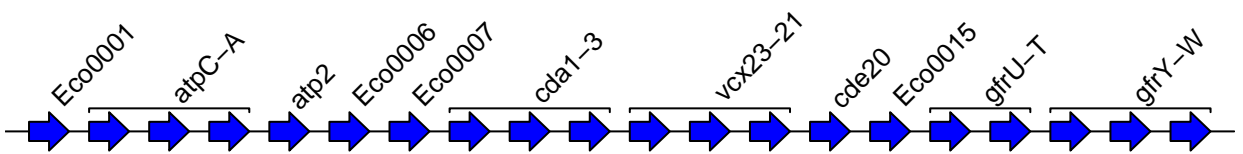
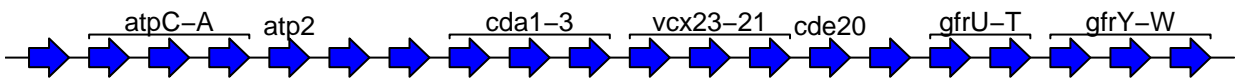
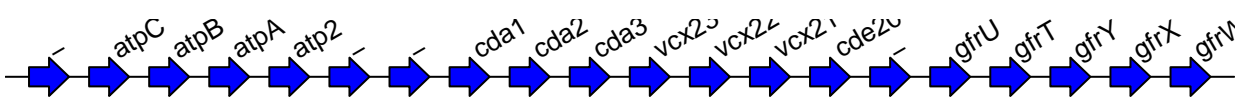
help("apply\_color\_scheme")





help("apply\_color\_scheme")





help("auto\_annotate")

BB

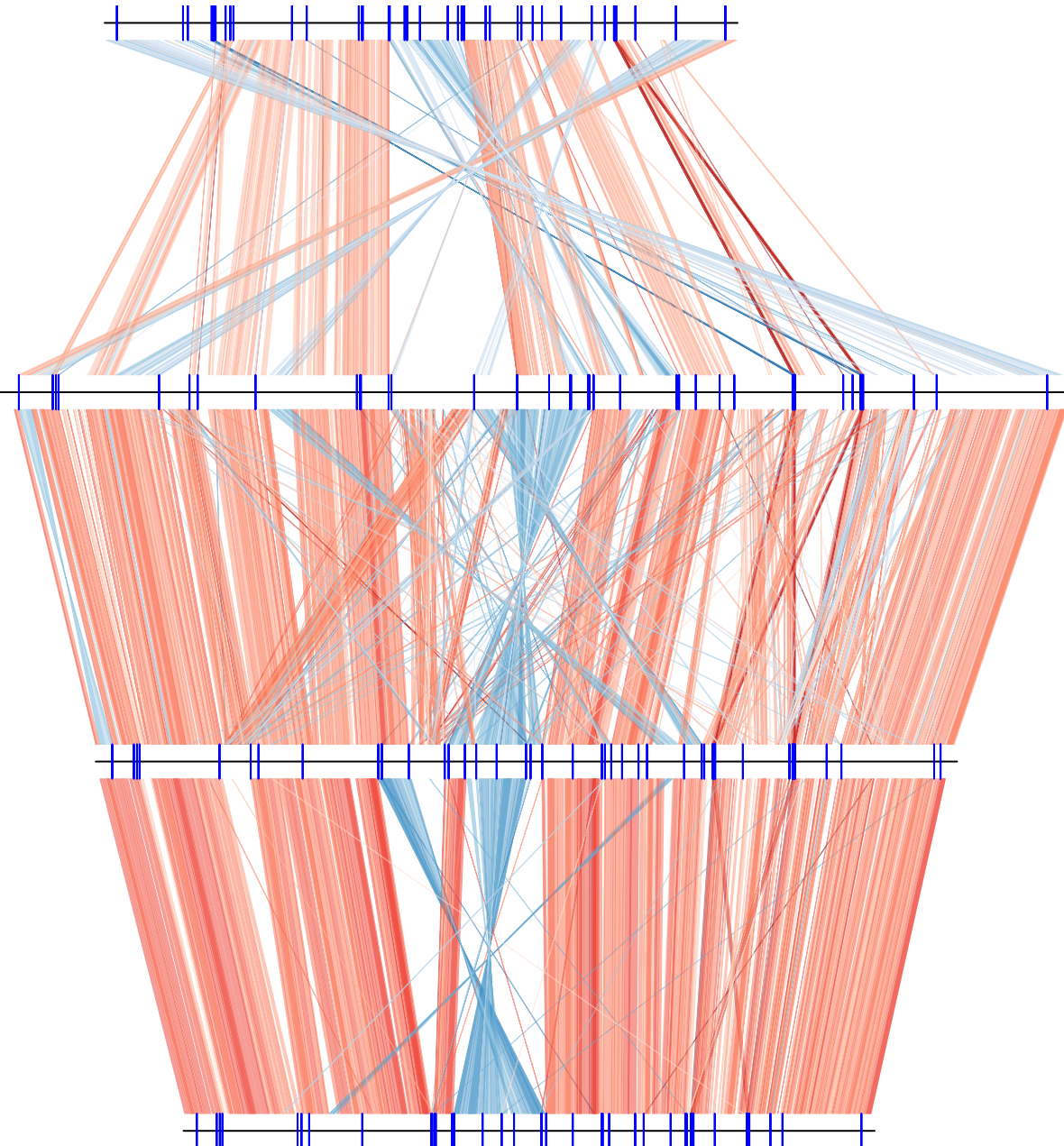
BG

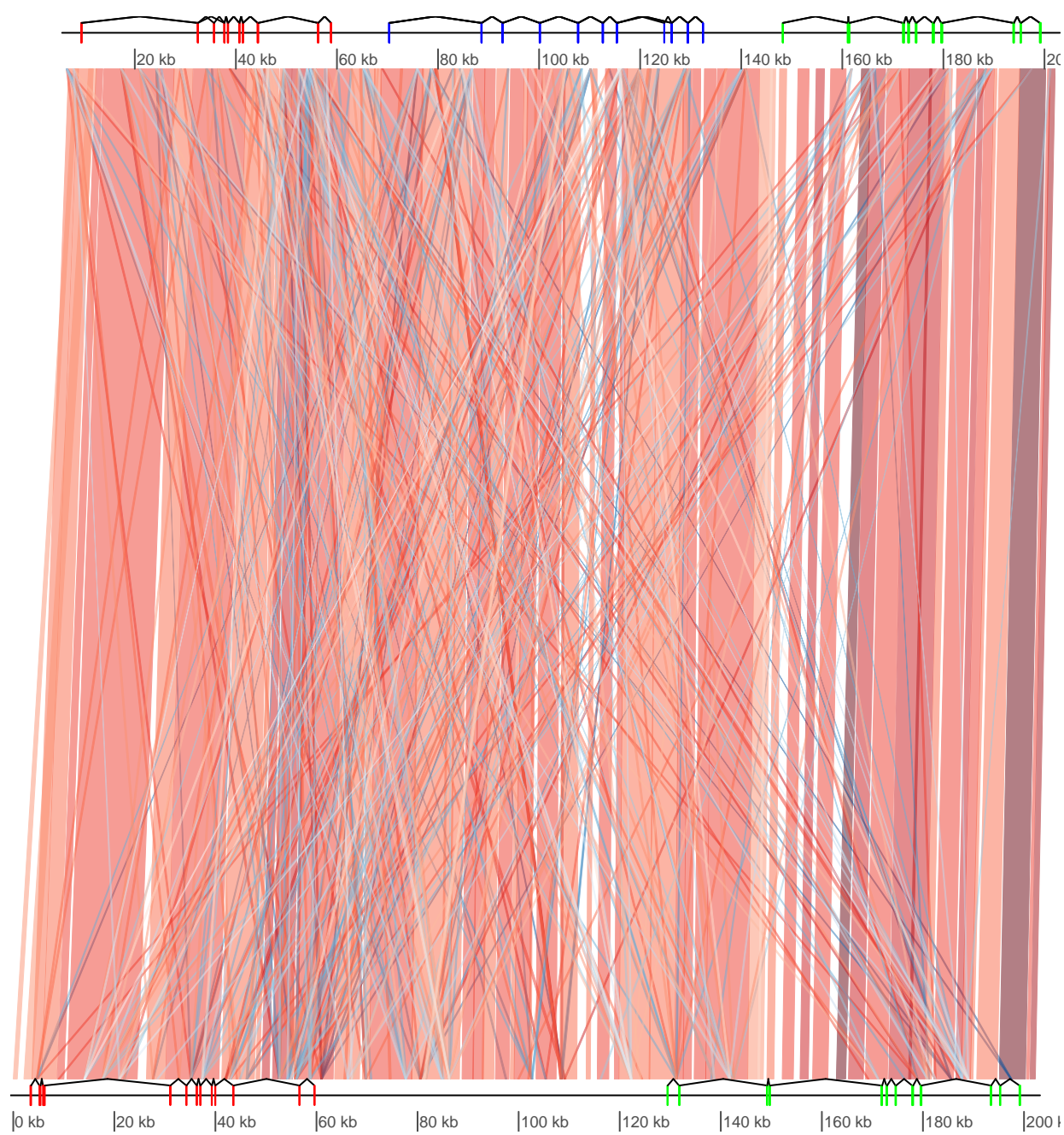
BH

BQ

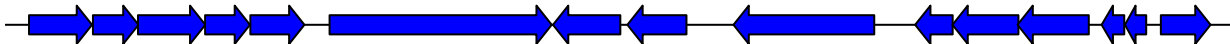
help("barto")

500 kb



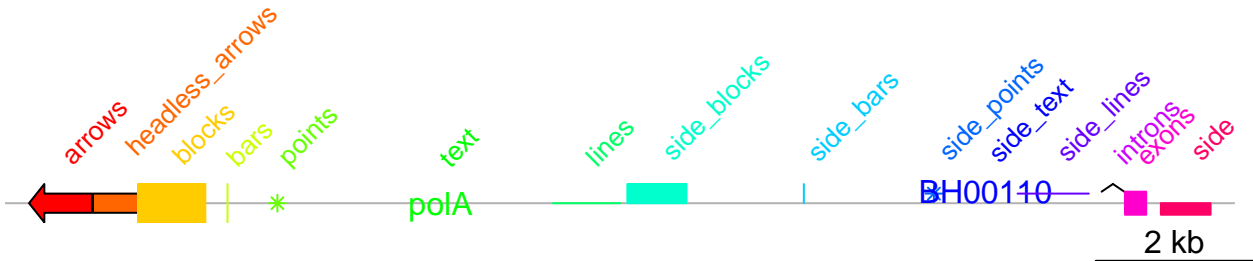
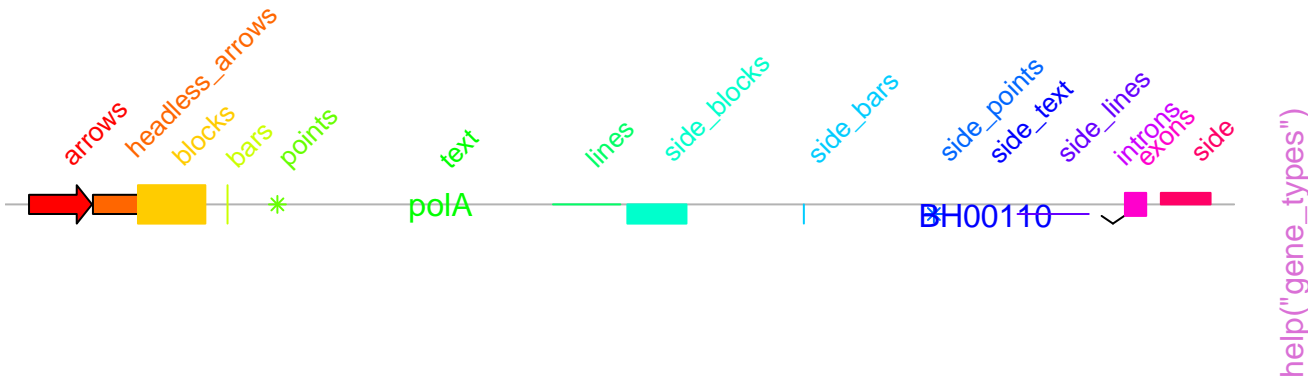


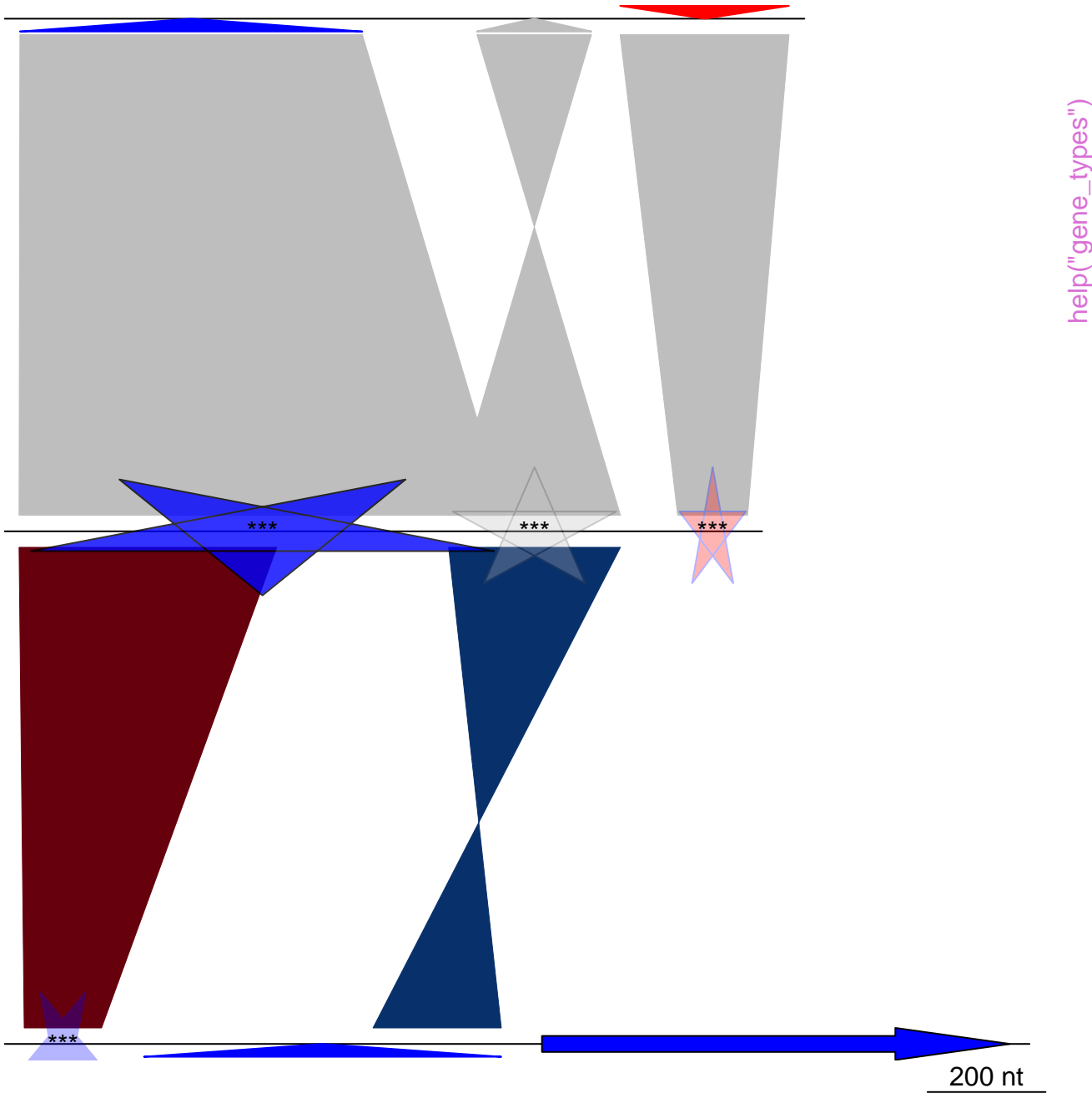
help("chrY\_subseg")



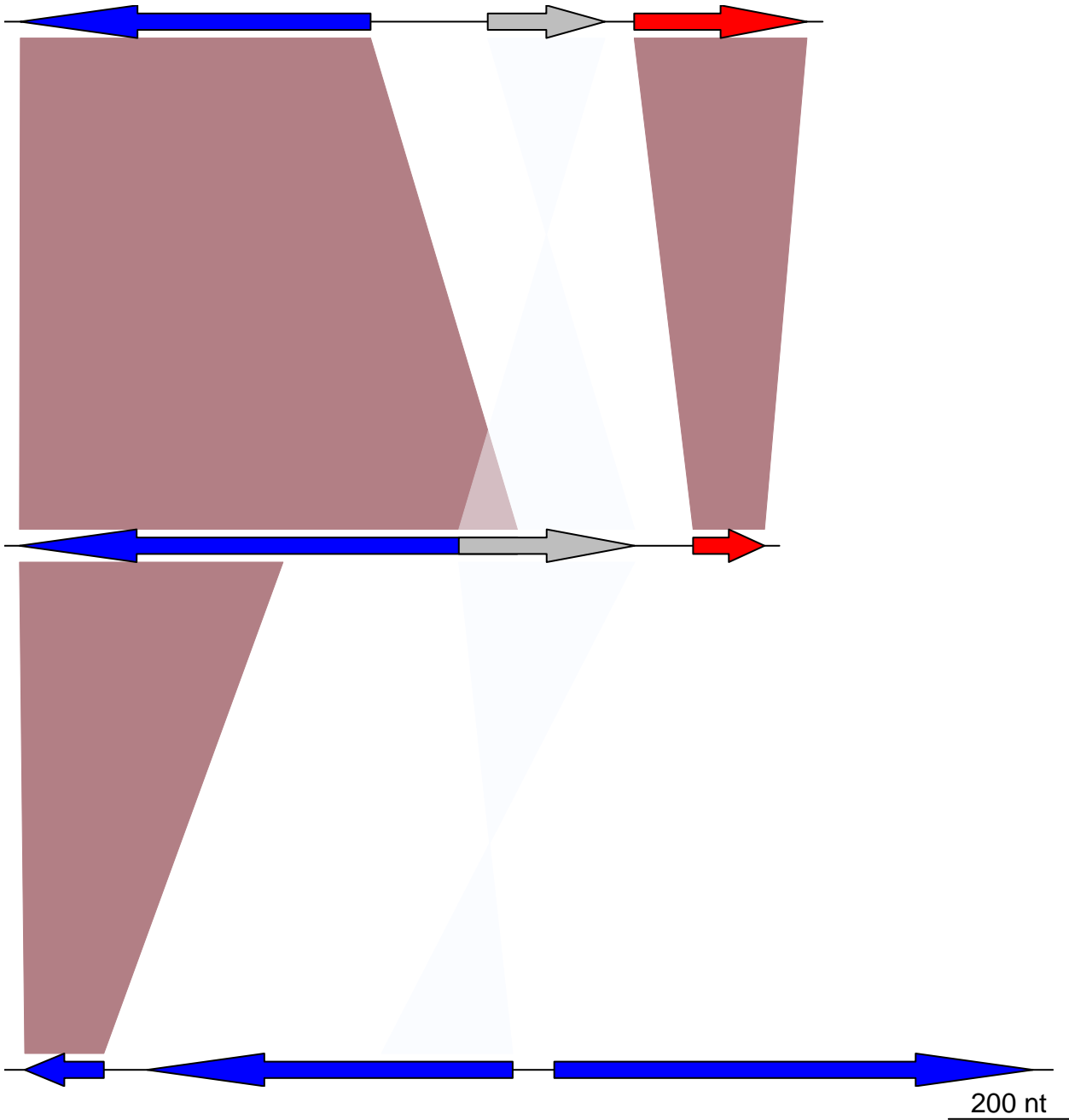
2 kb

help("gene\_types")









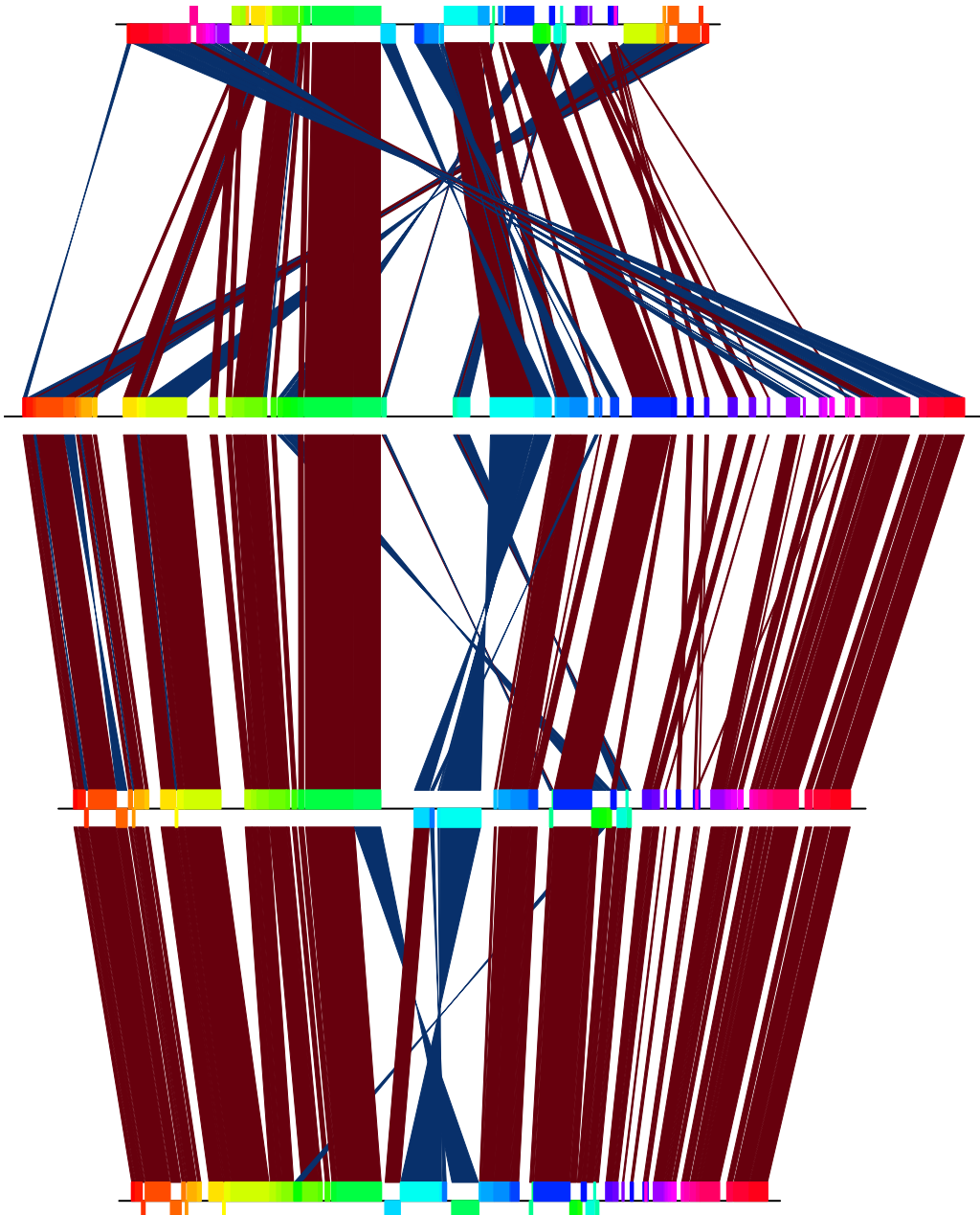
help("genoPlotR-package")

B\_bacilliformis

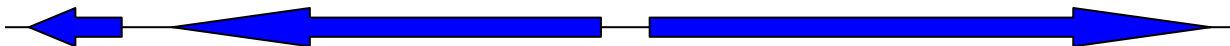
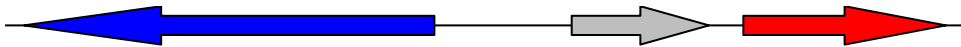
B\_grahamii

B\_henselae

B\_quintana

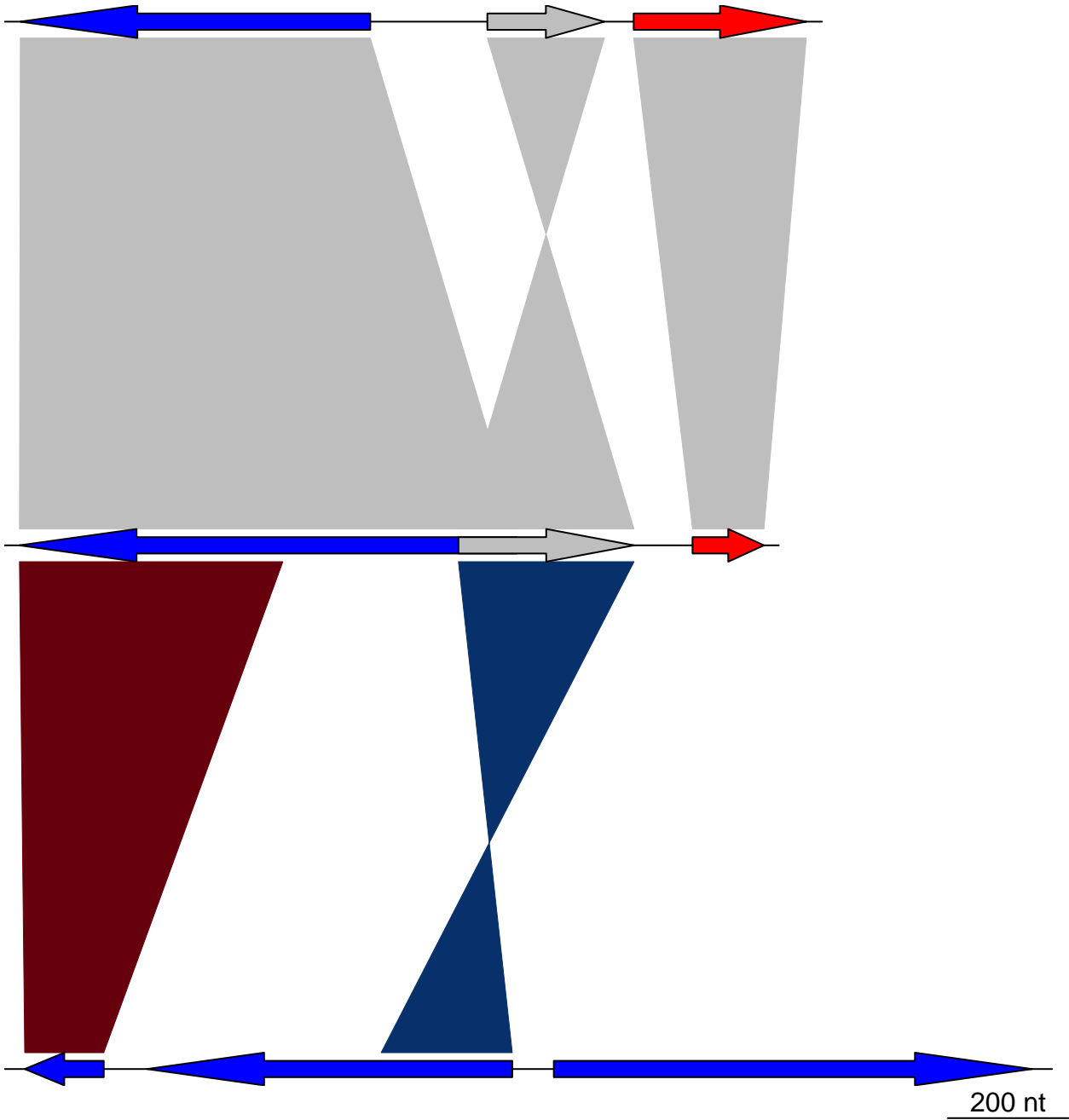


help("mauve.bbone")

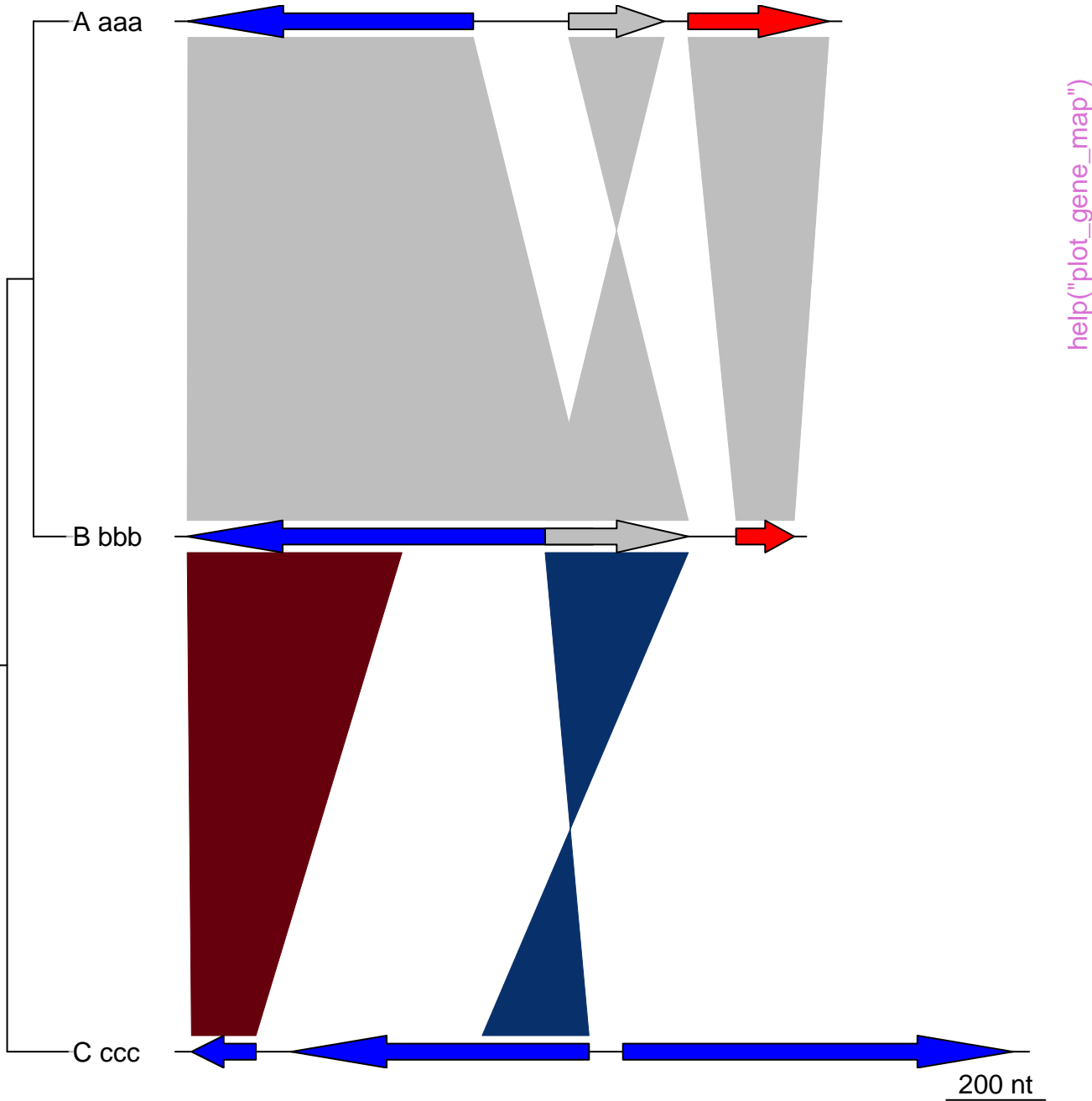


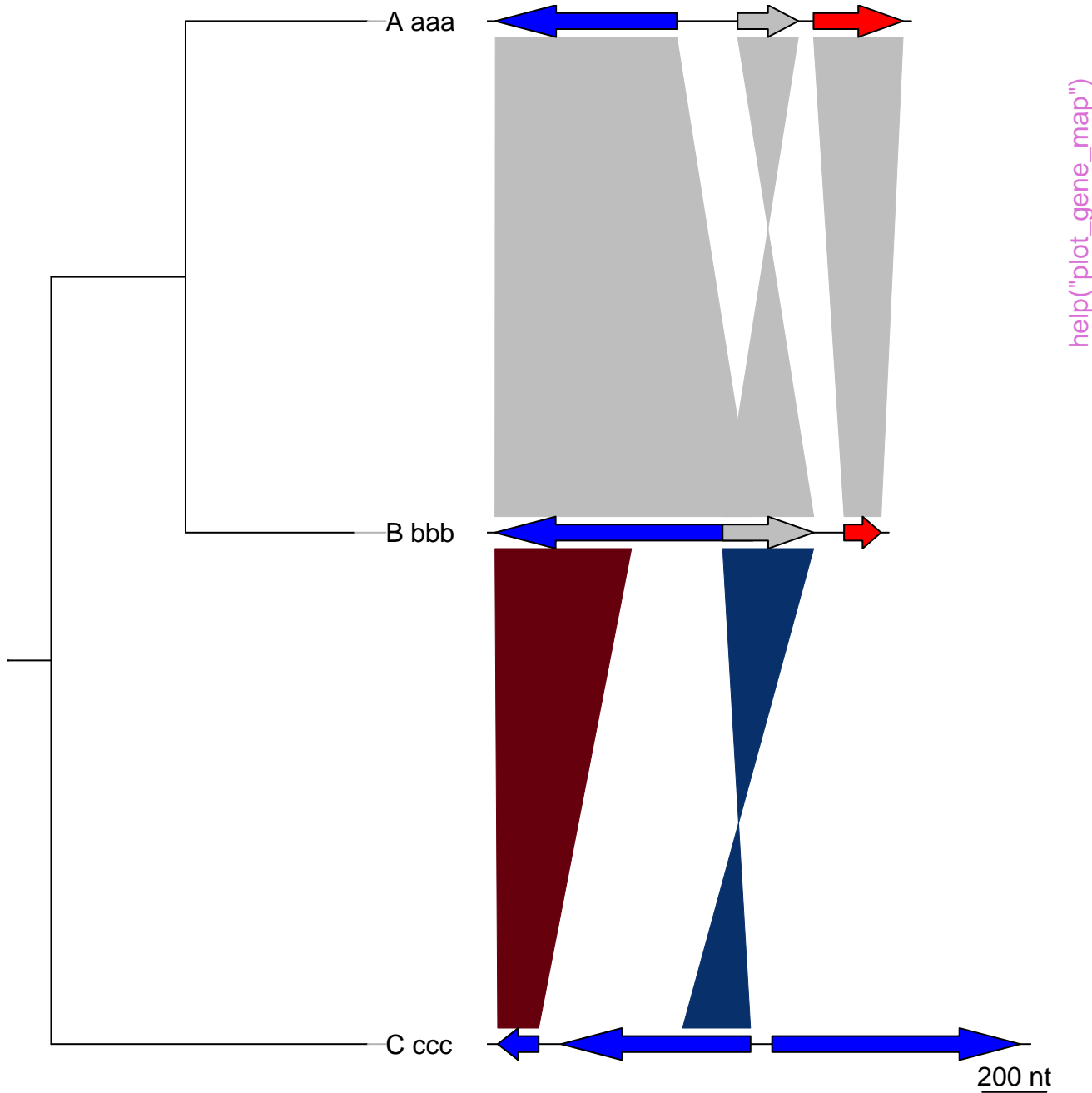
200 nt

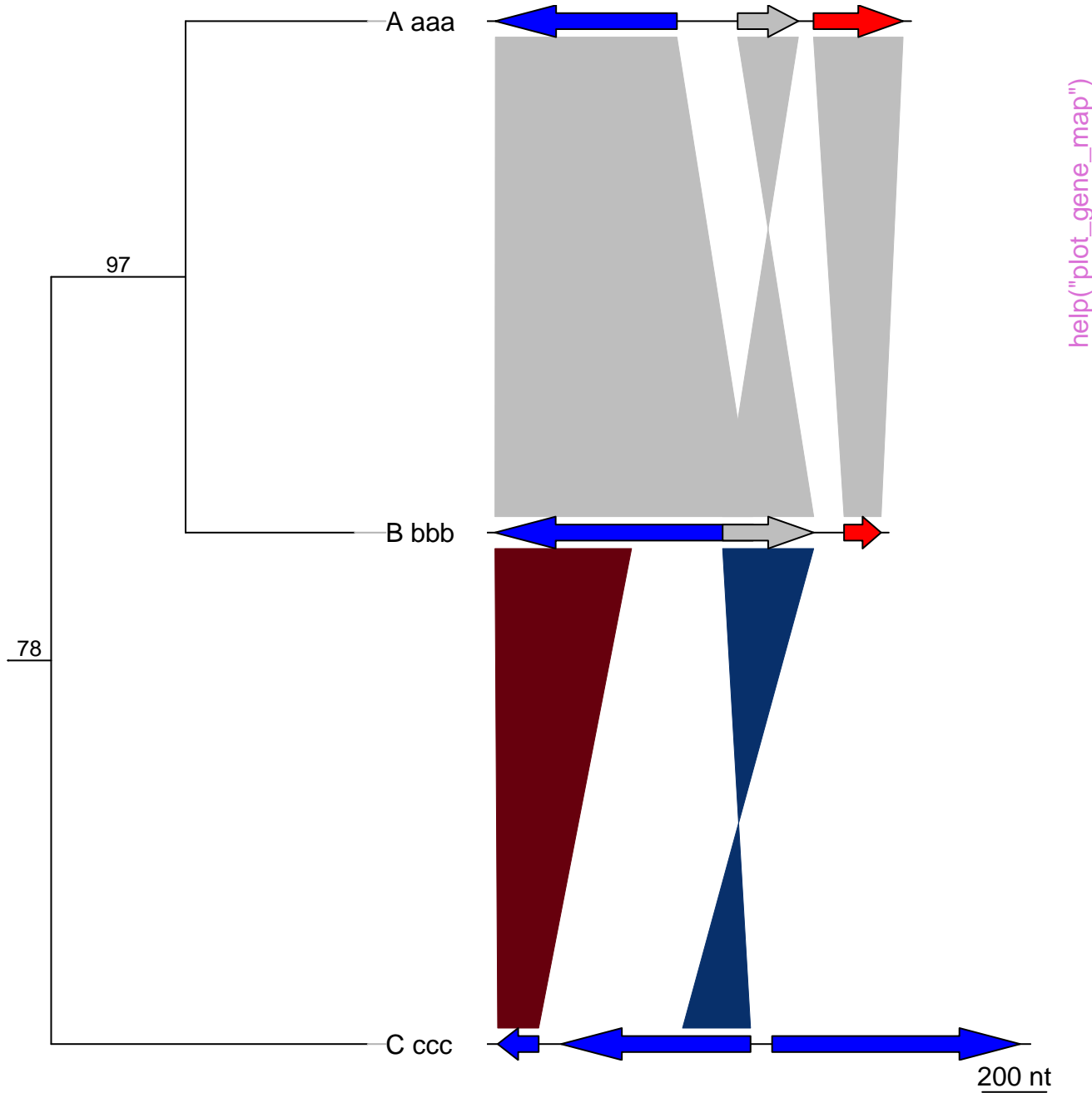
help("plot\_gene\_map")

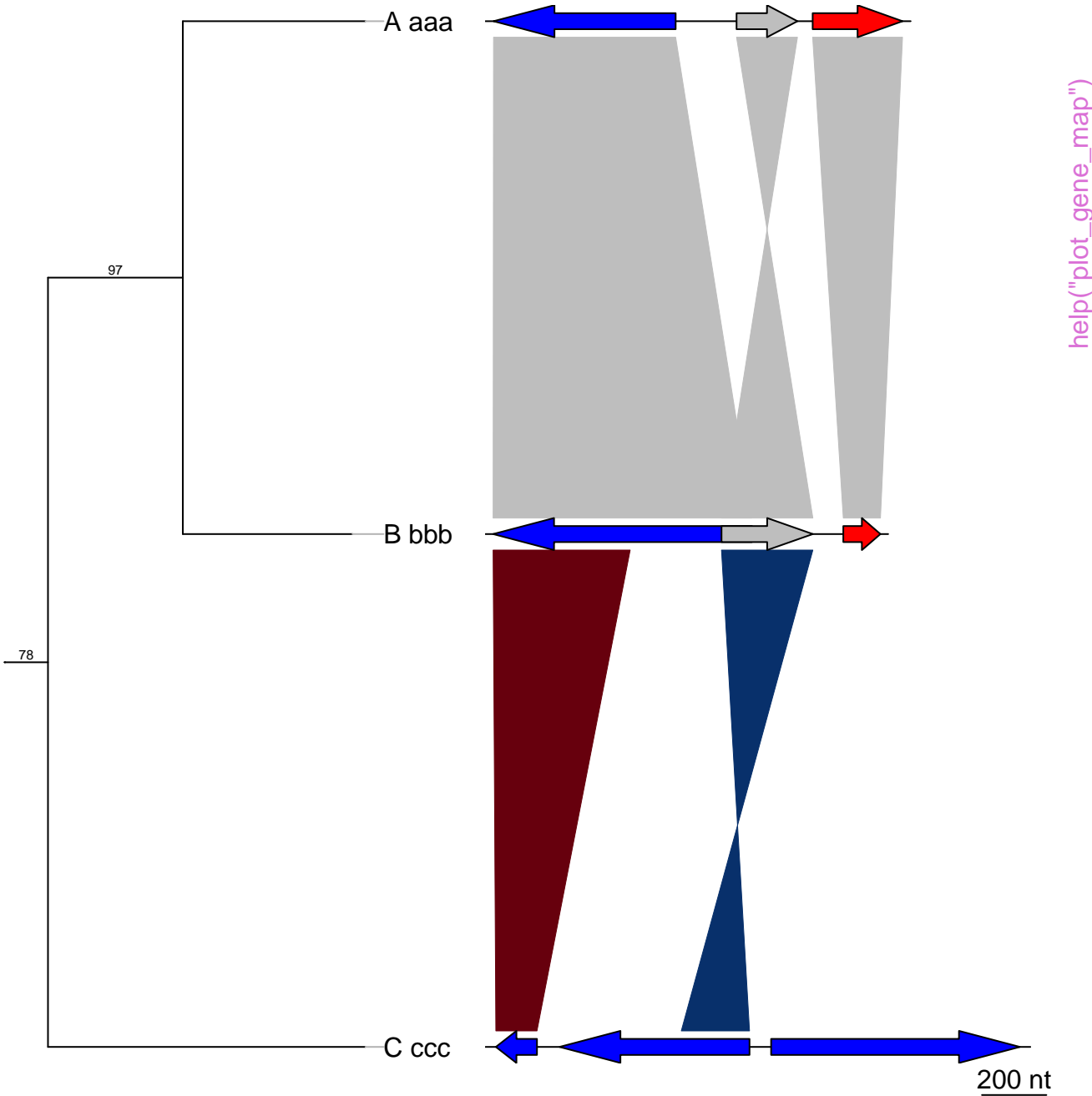


help("plot\_gene\_map")

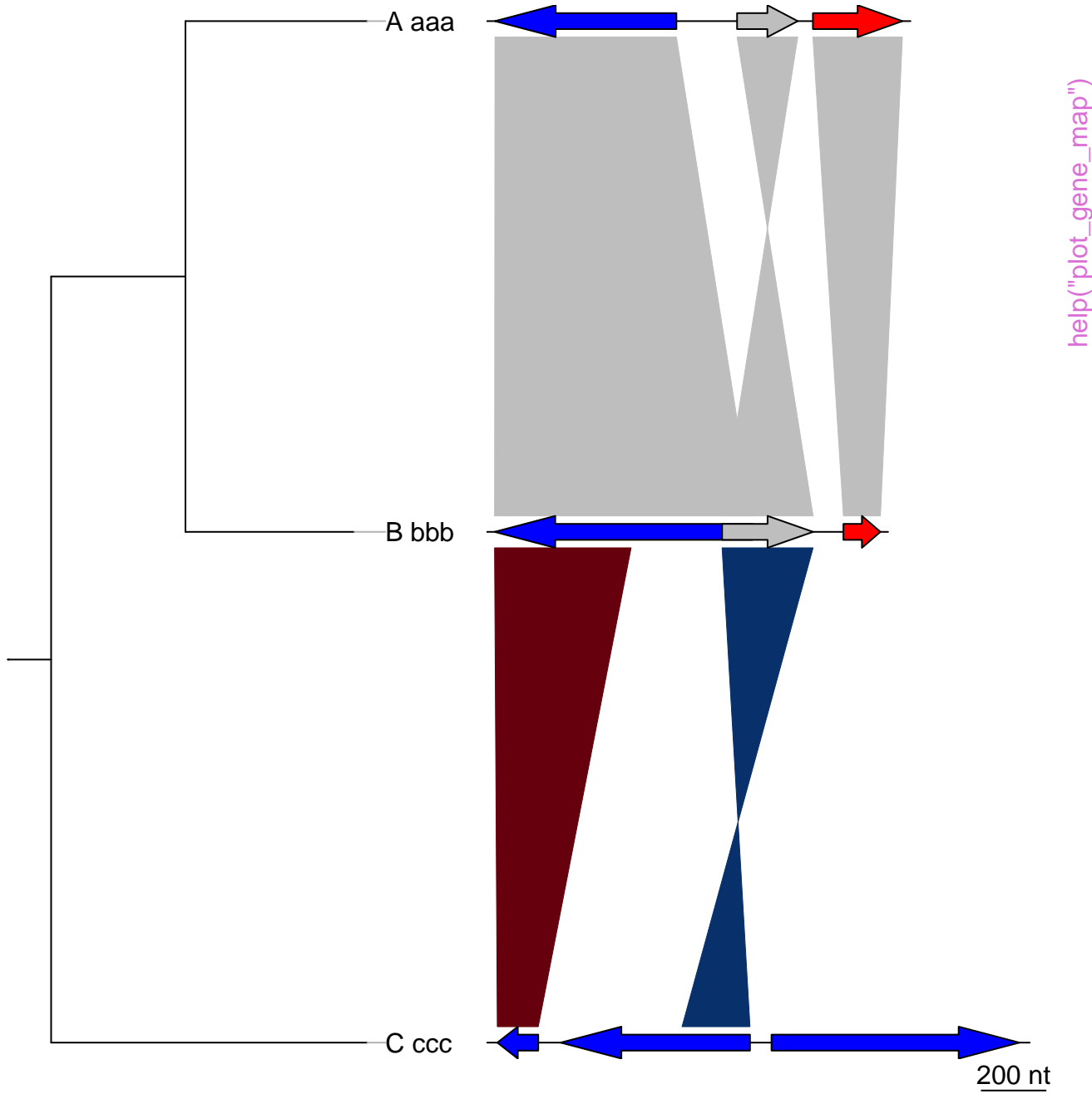


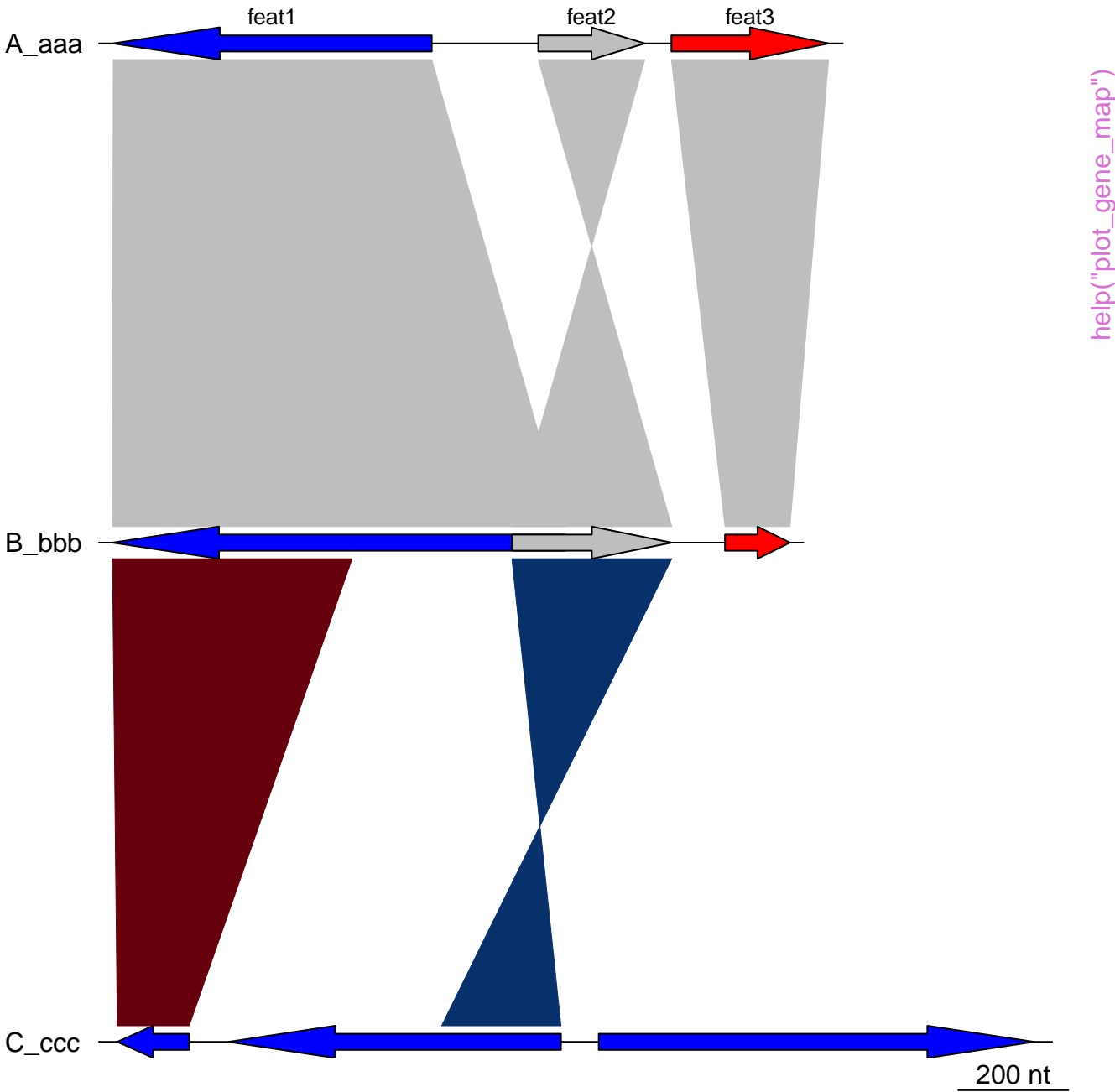


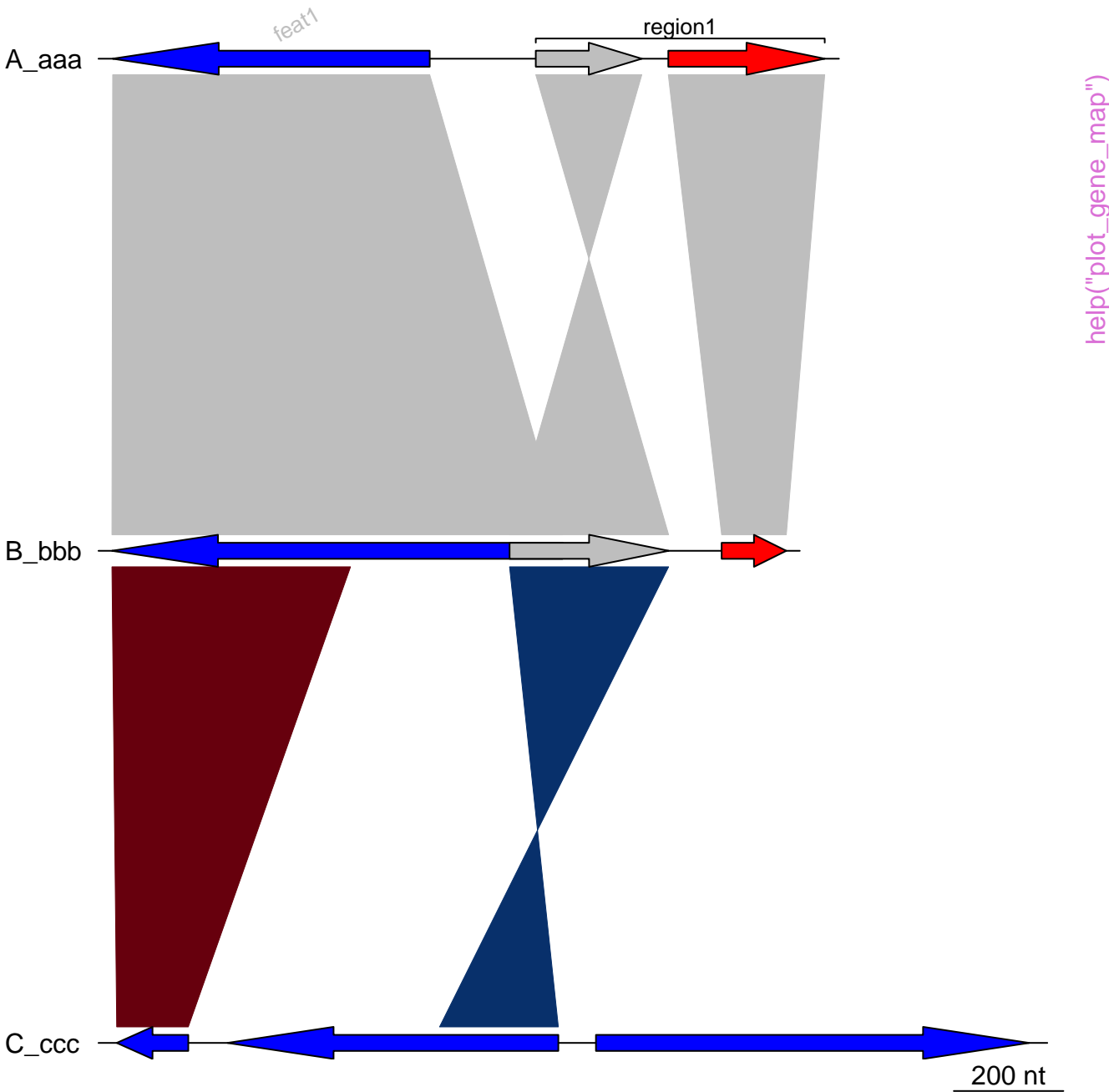


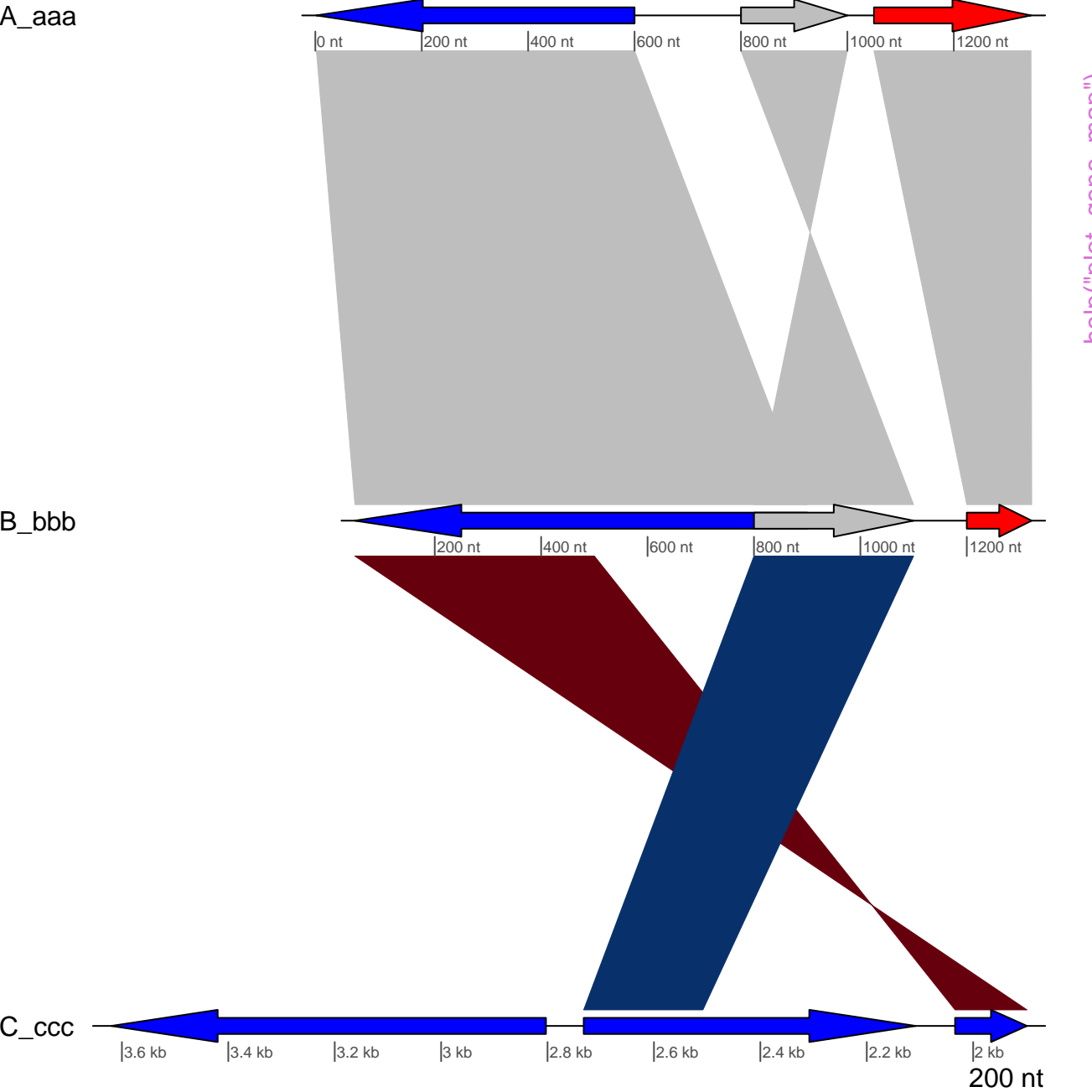


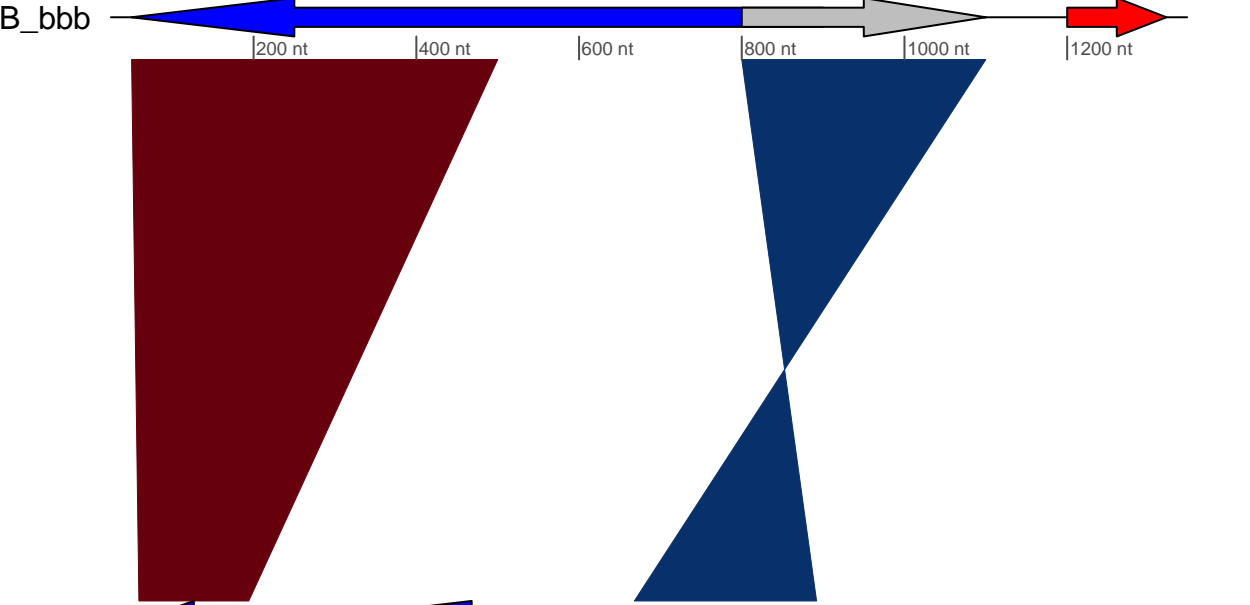
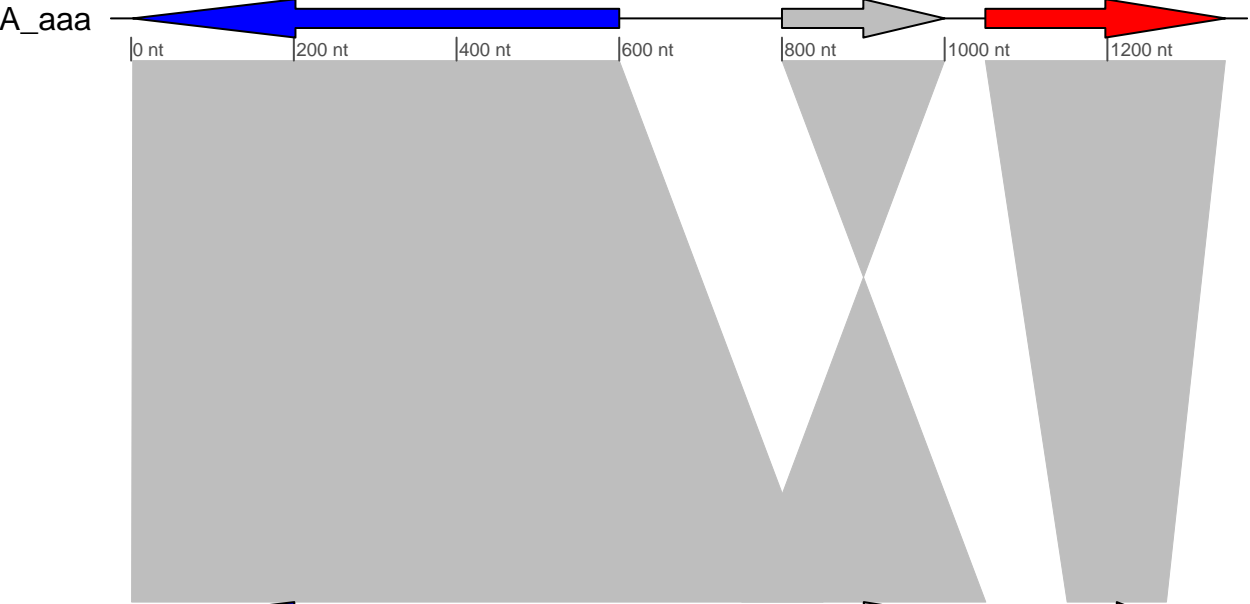








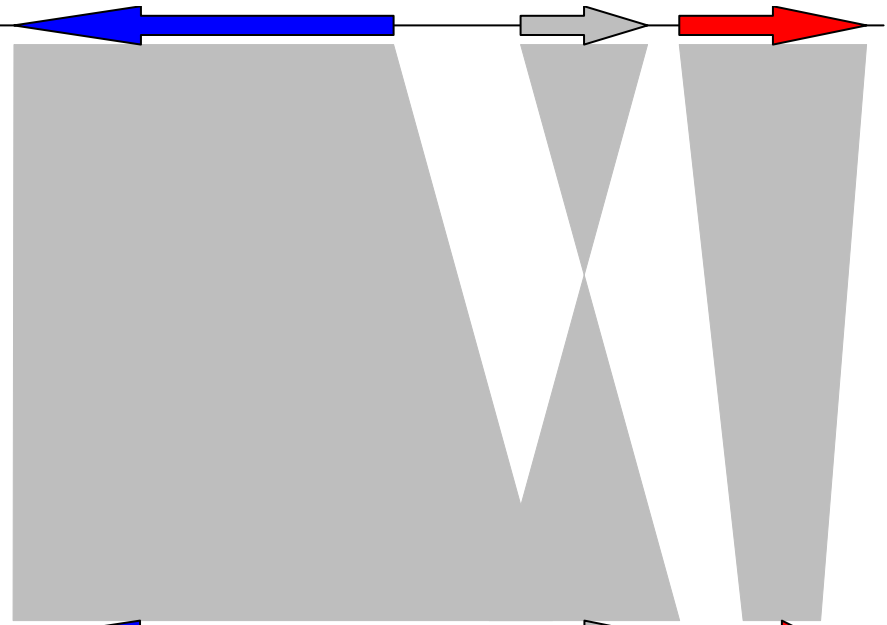




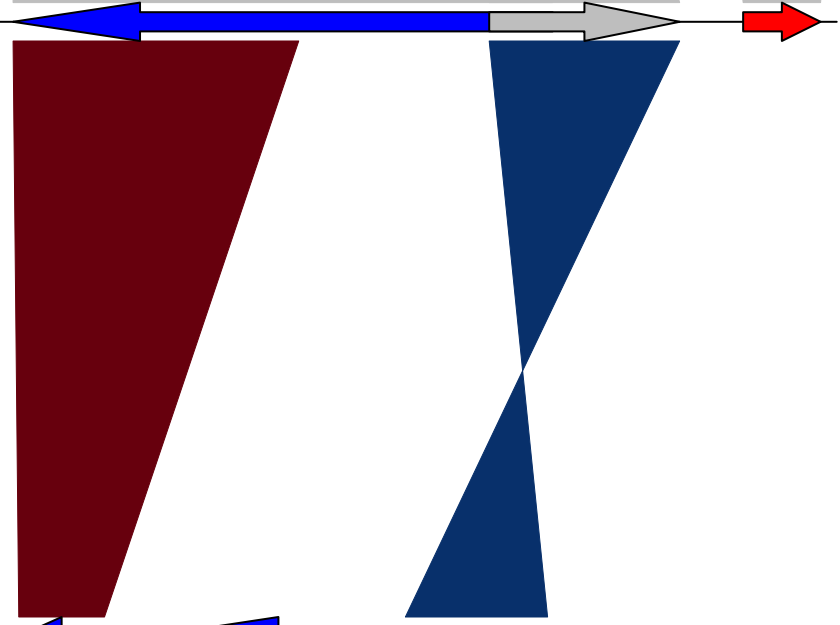
200 nt

help("plot\_gene\_map")

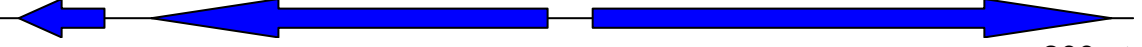
A\_aaa



B\_bbb



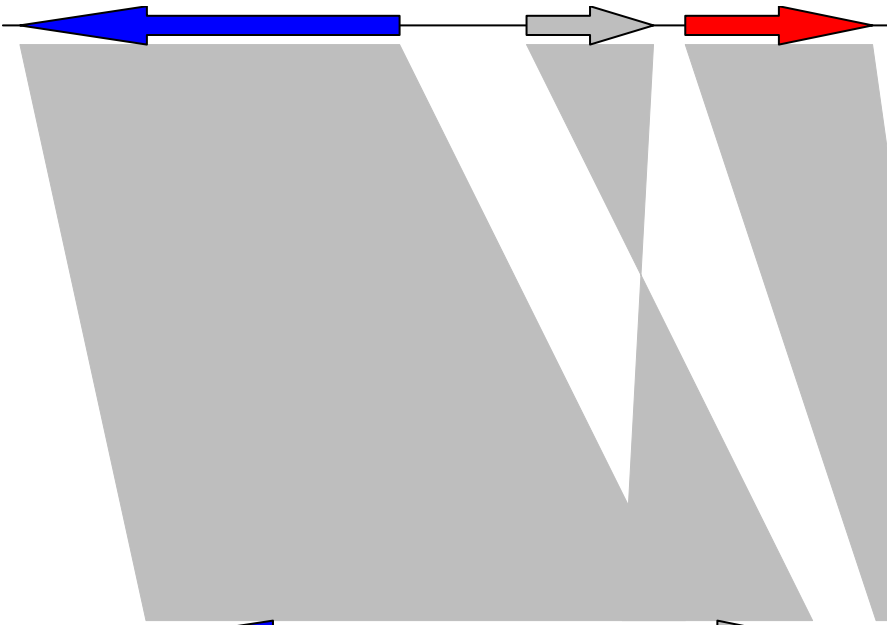
C\_ccc



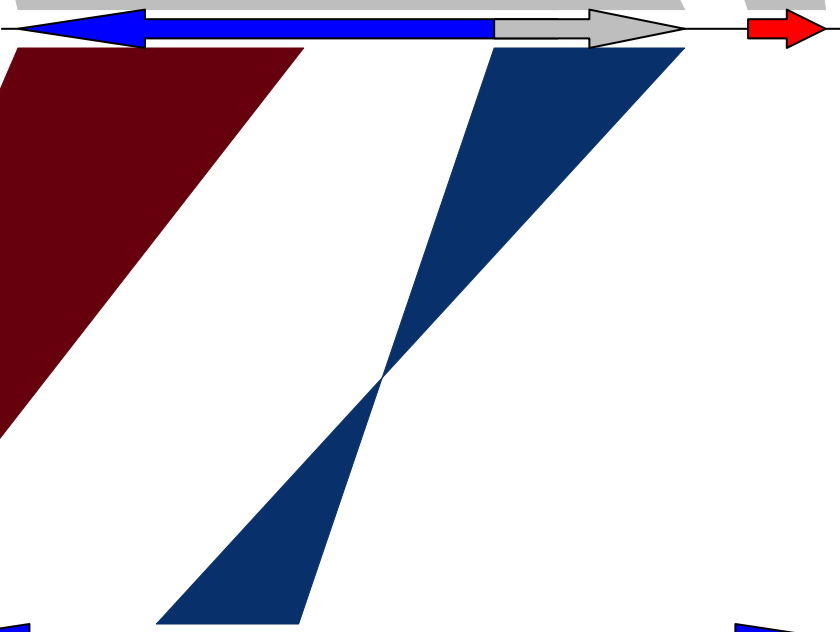
200 nt

help("plot\_gene\_map")

A\_aaa



B\_bbb



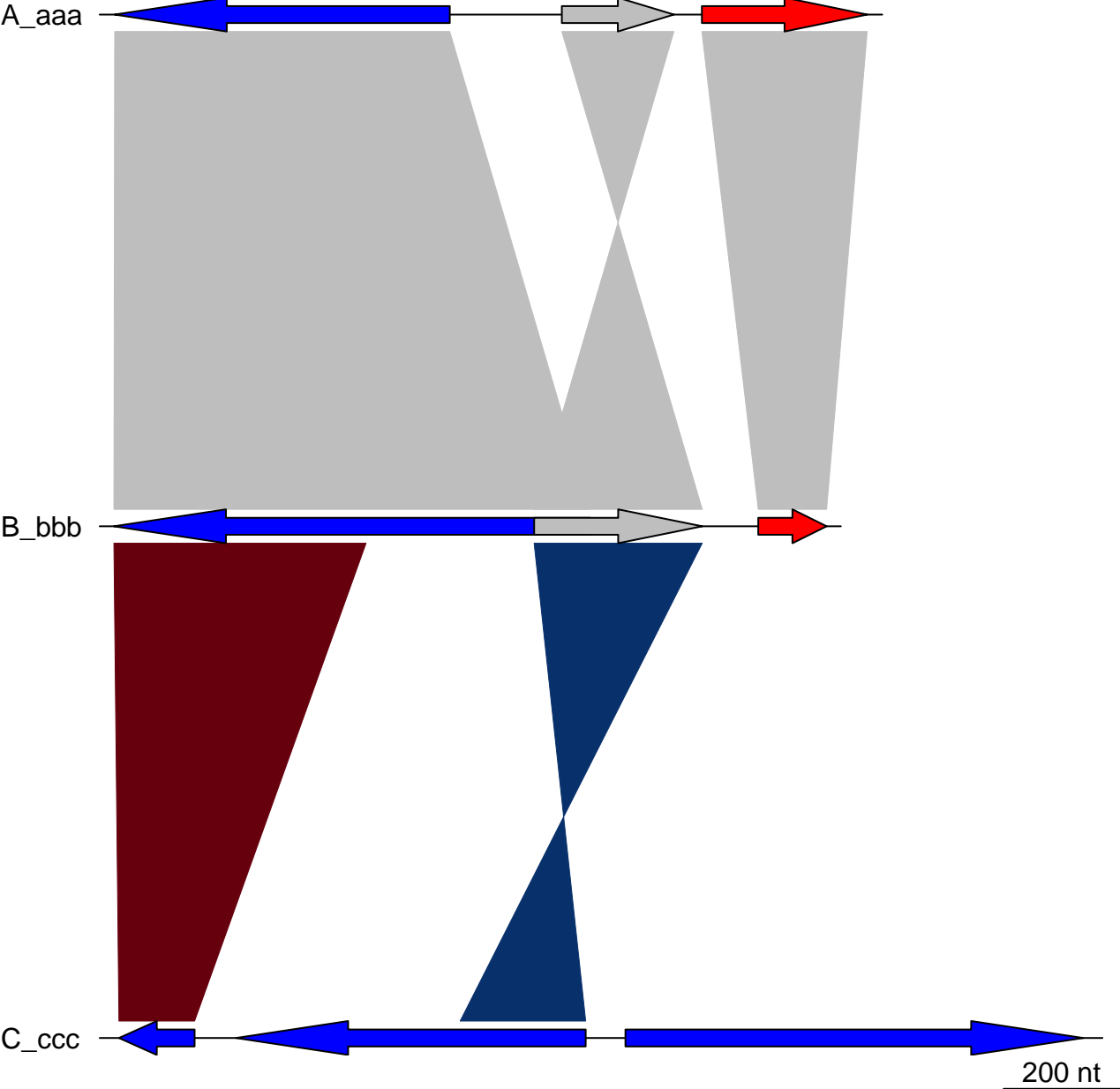
C\_ccc



200 nt

help("plot\_gene\_map")

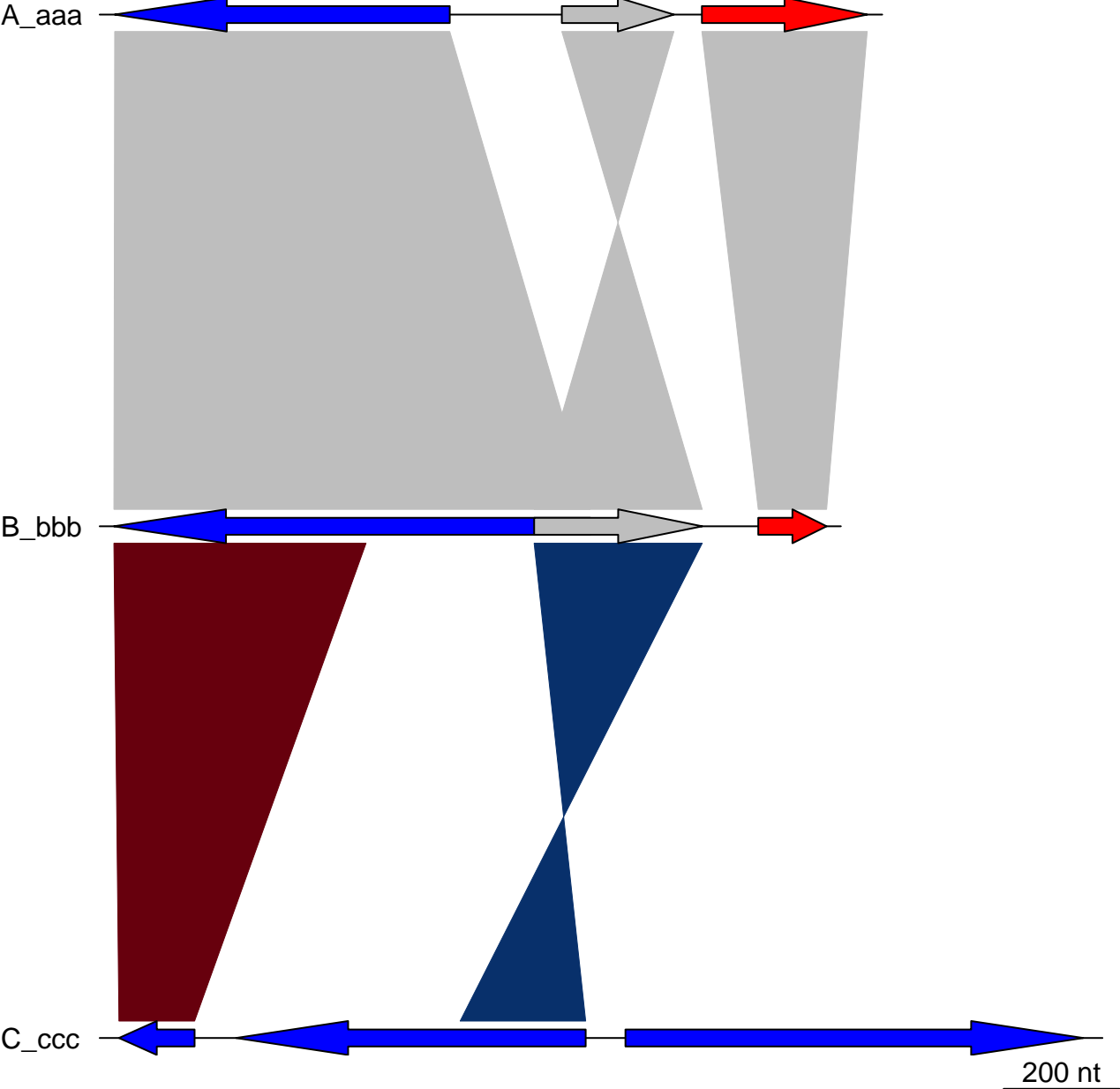
Comparison of A, B and C



help("plot\_gene\_map")

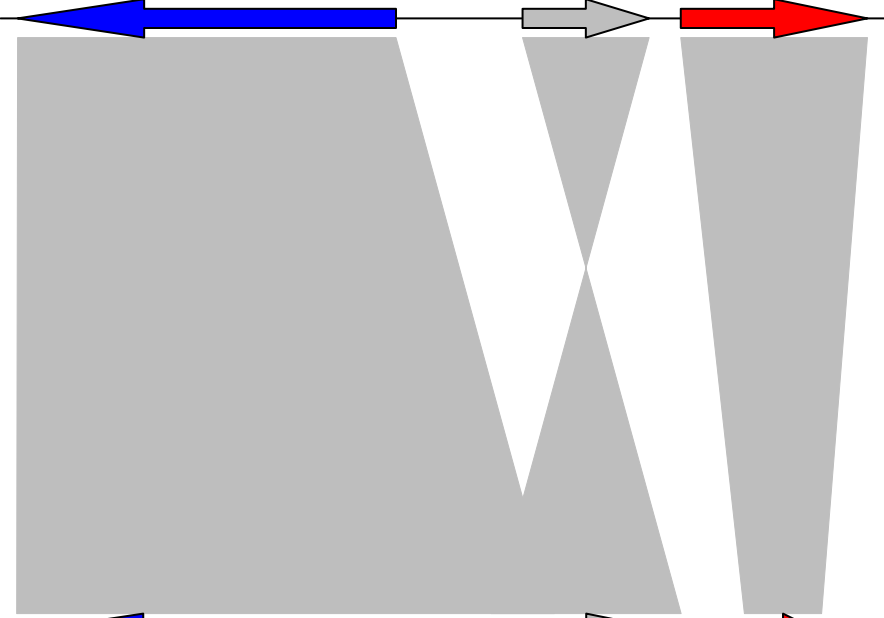


Comparison of A, B and C

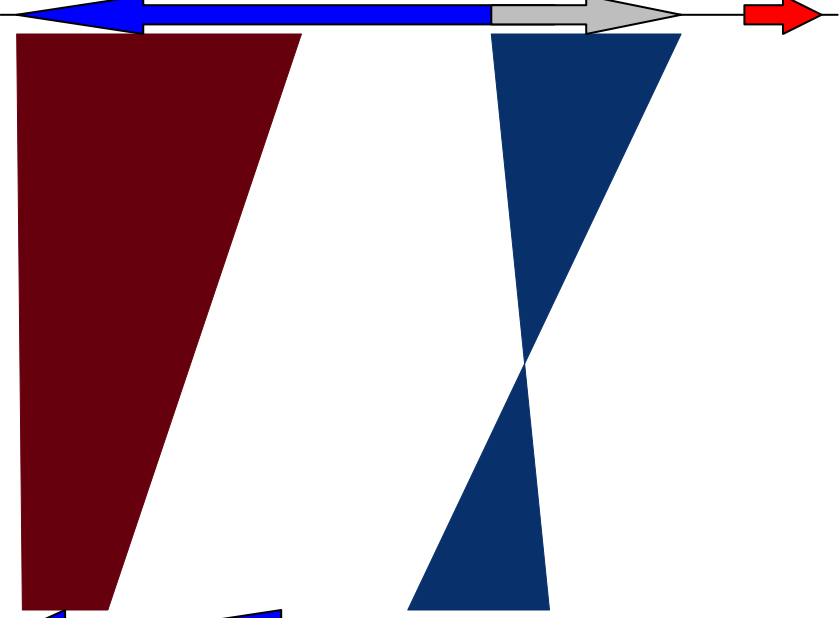


help("plot\_gene\_map")

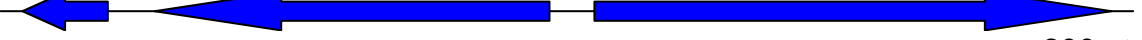
Huey



Dewey



Louie



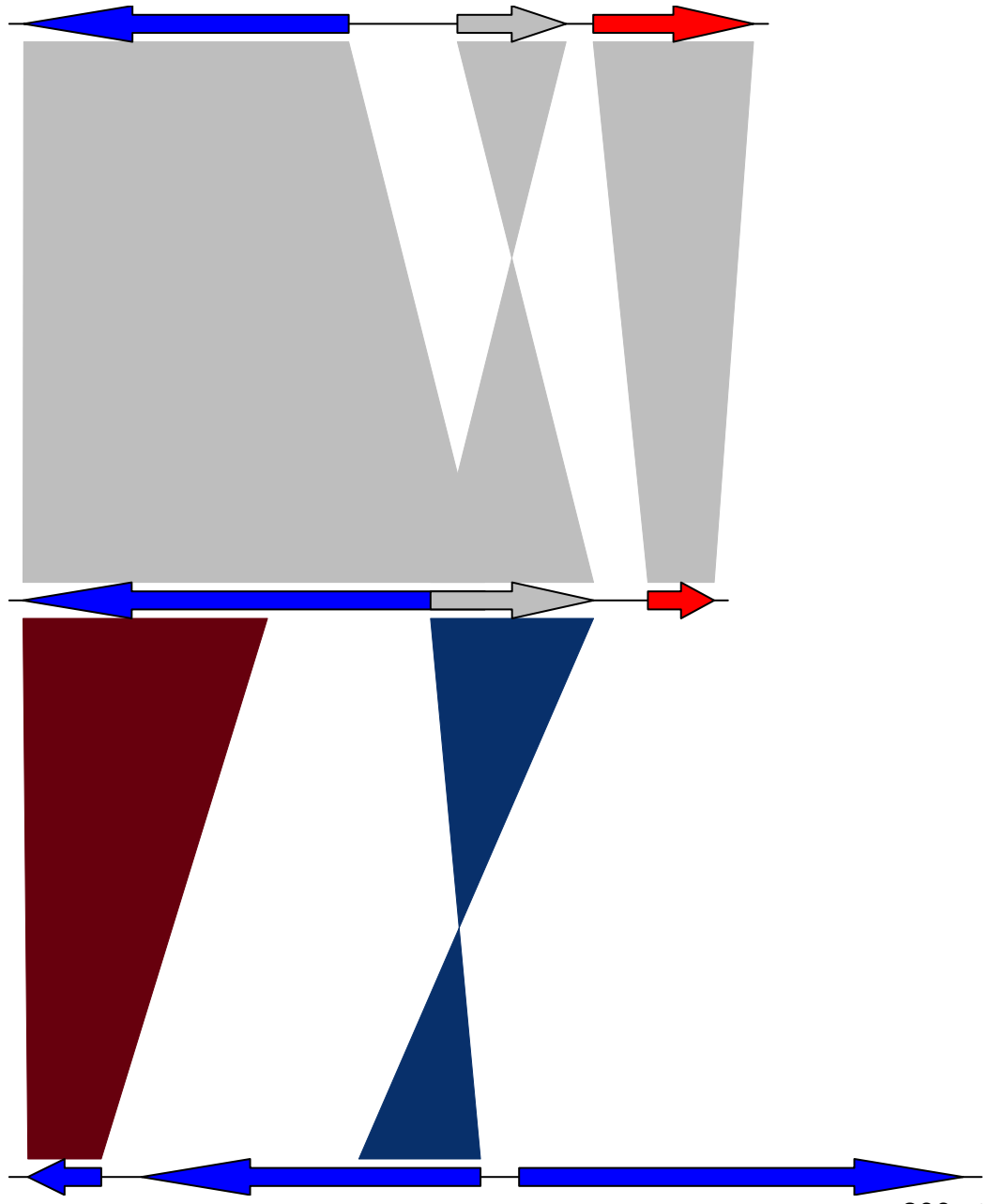
200 nt

help("plot\_gene\_map")

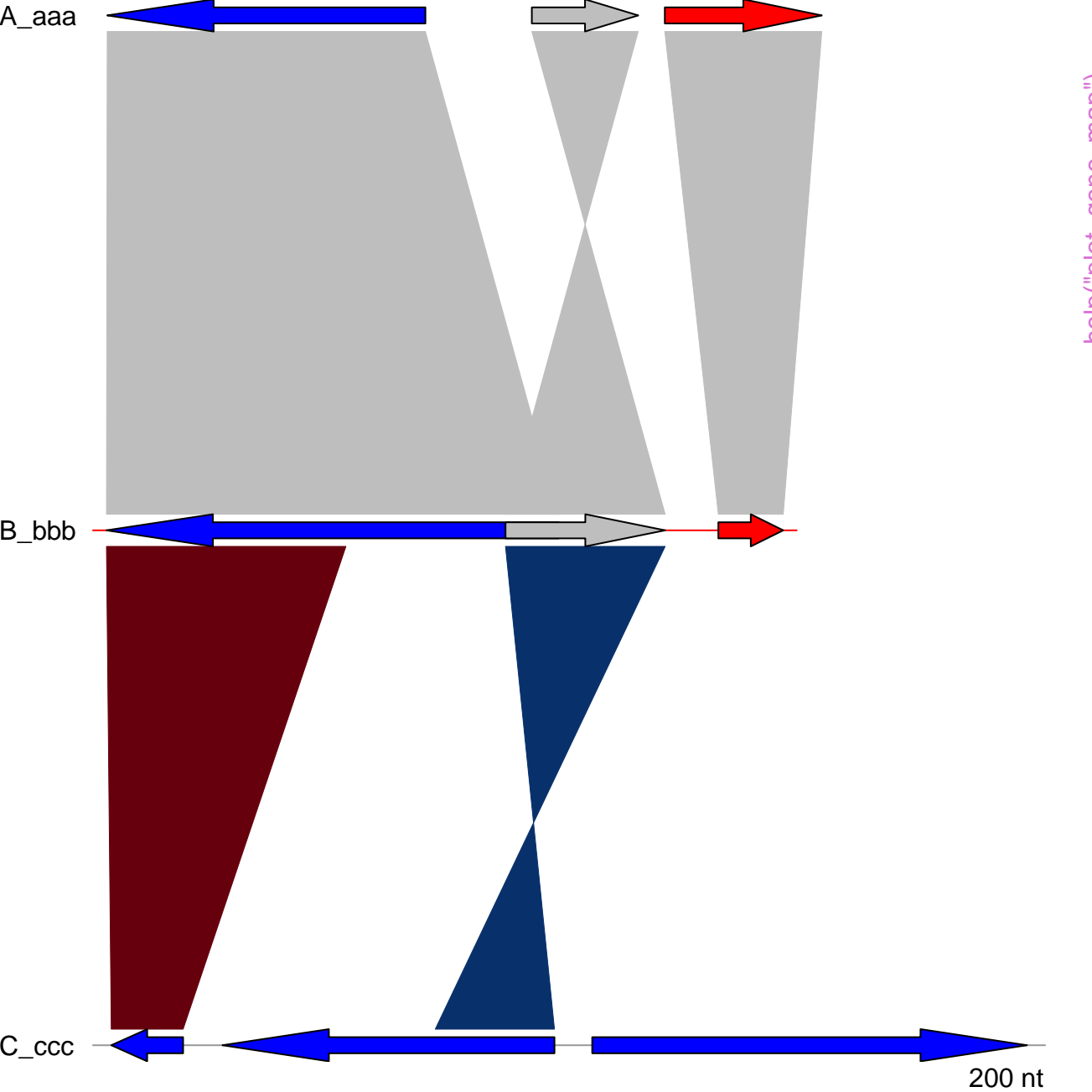
Huey

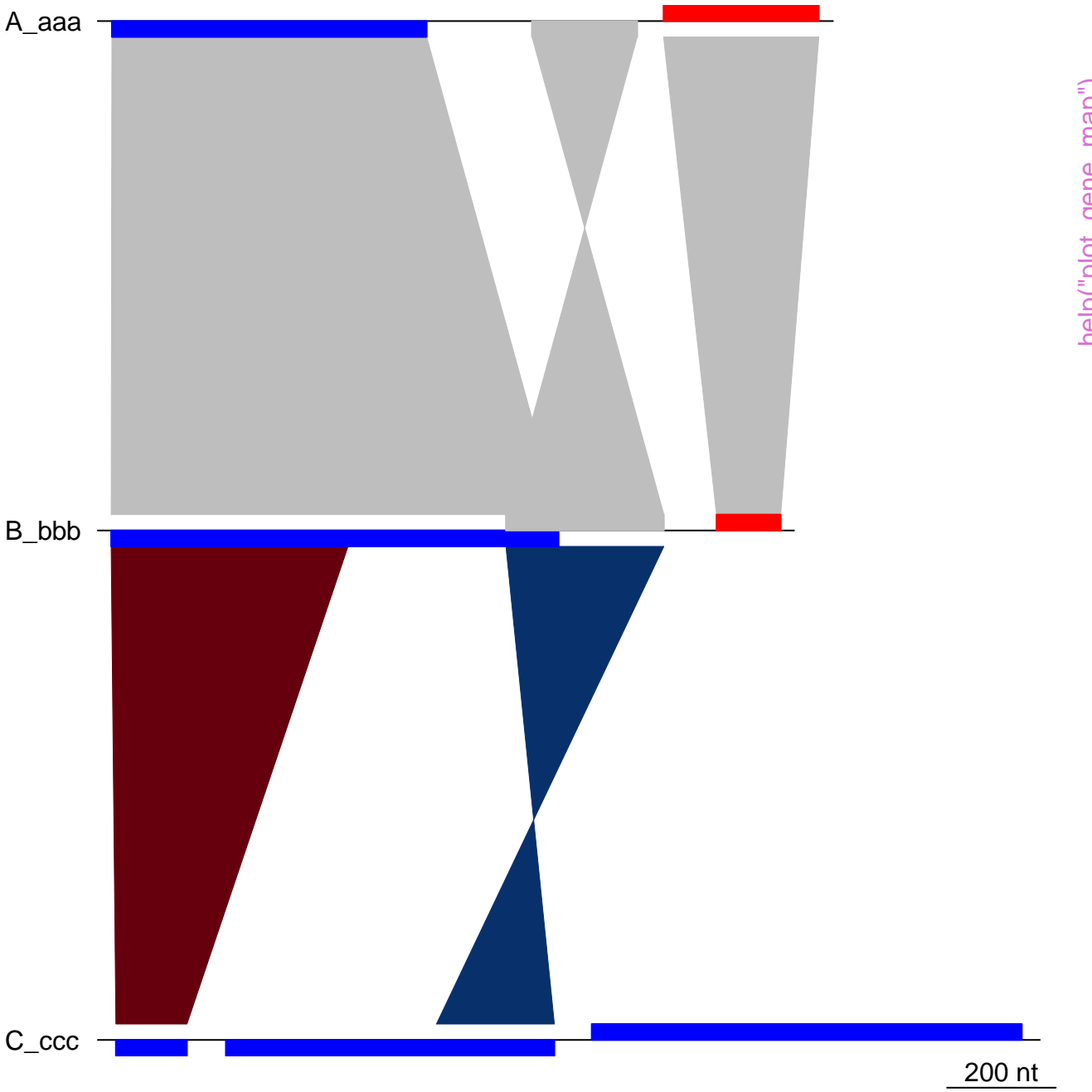
Dewey

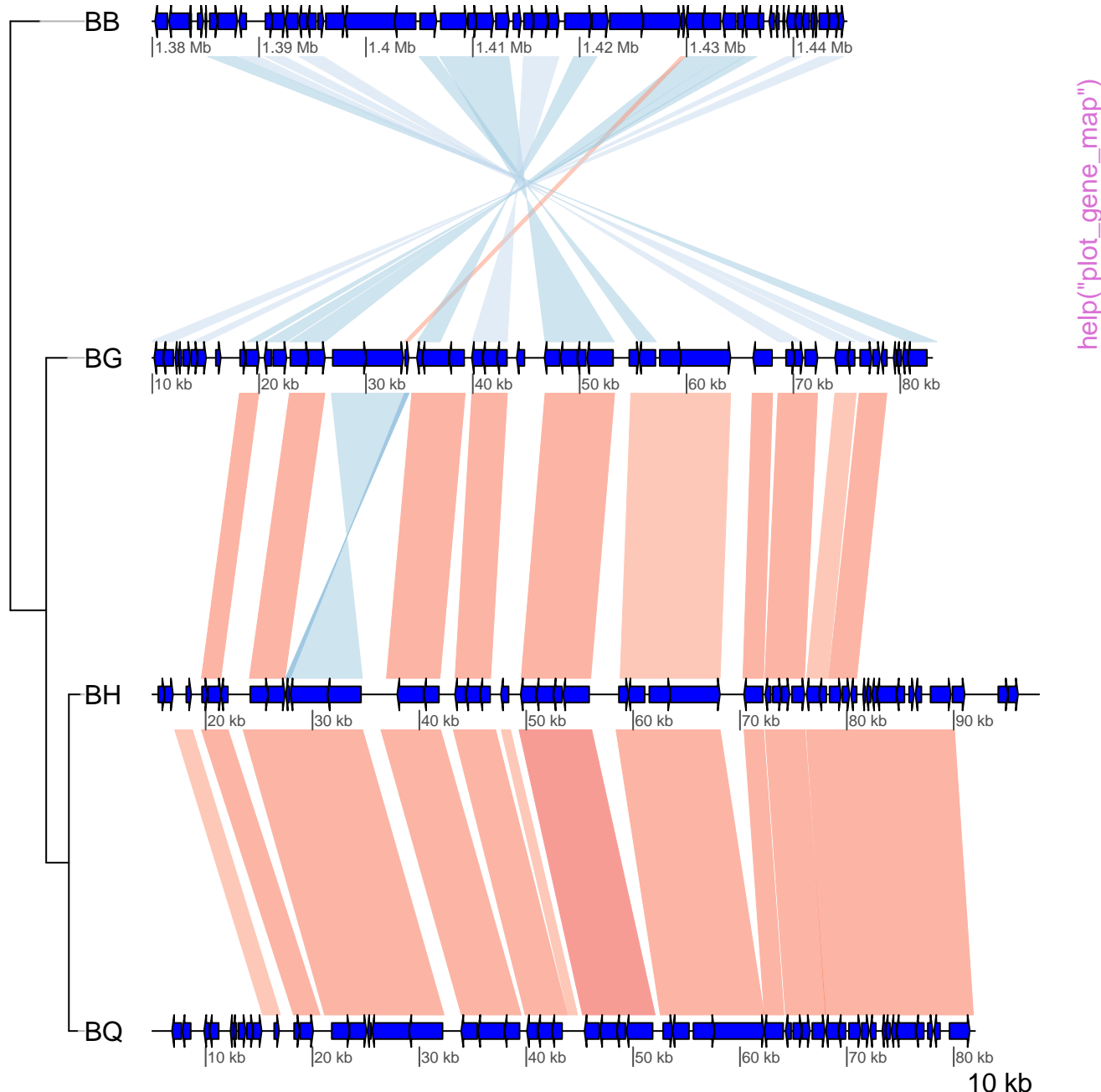
Louie

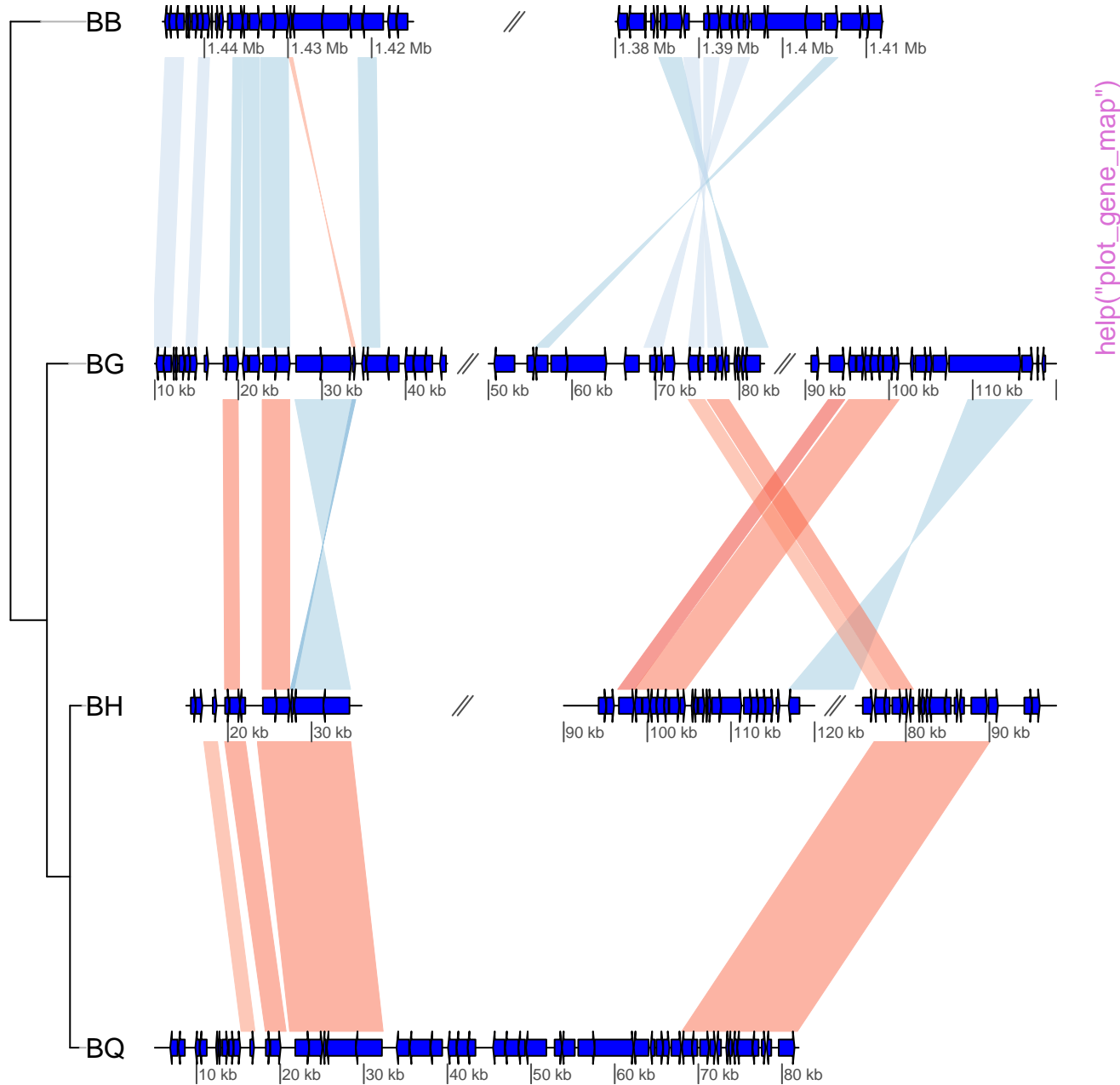


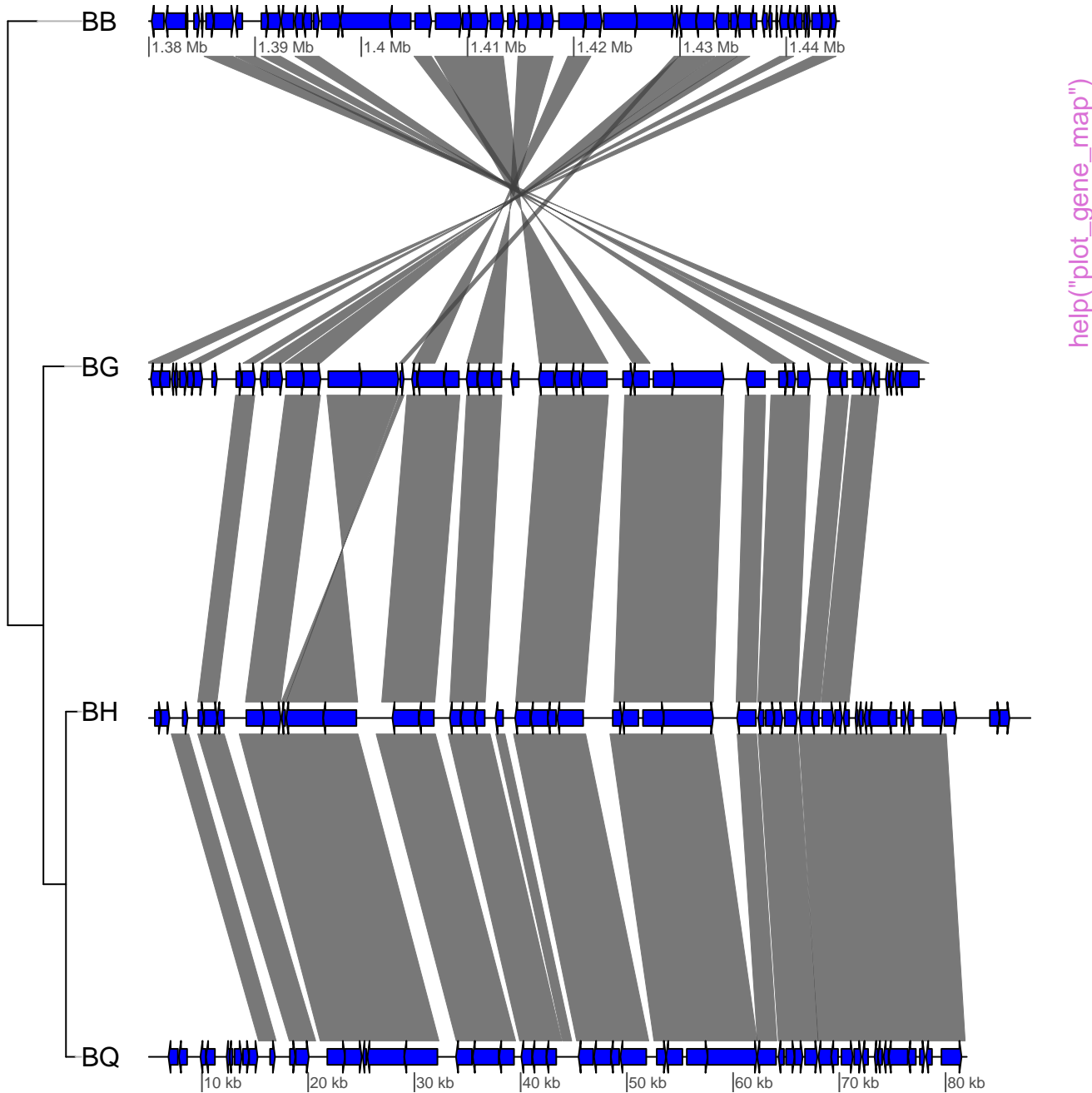
help("plot\_gene\_map")



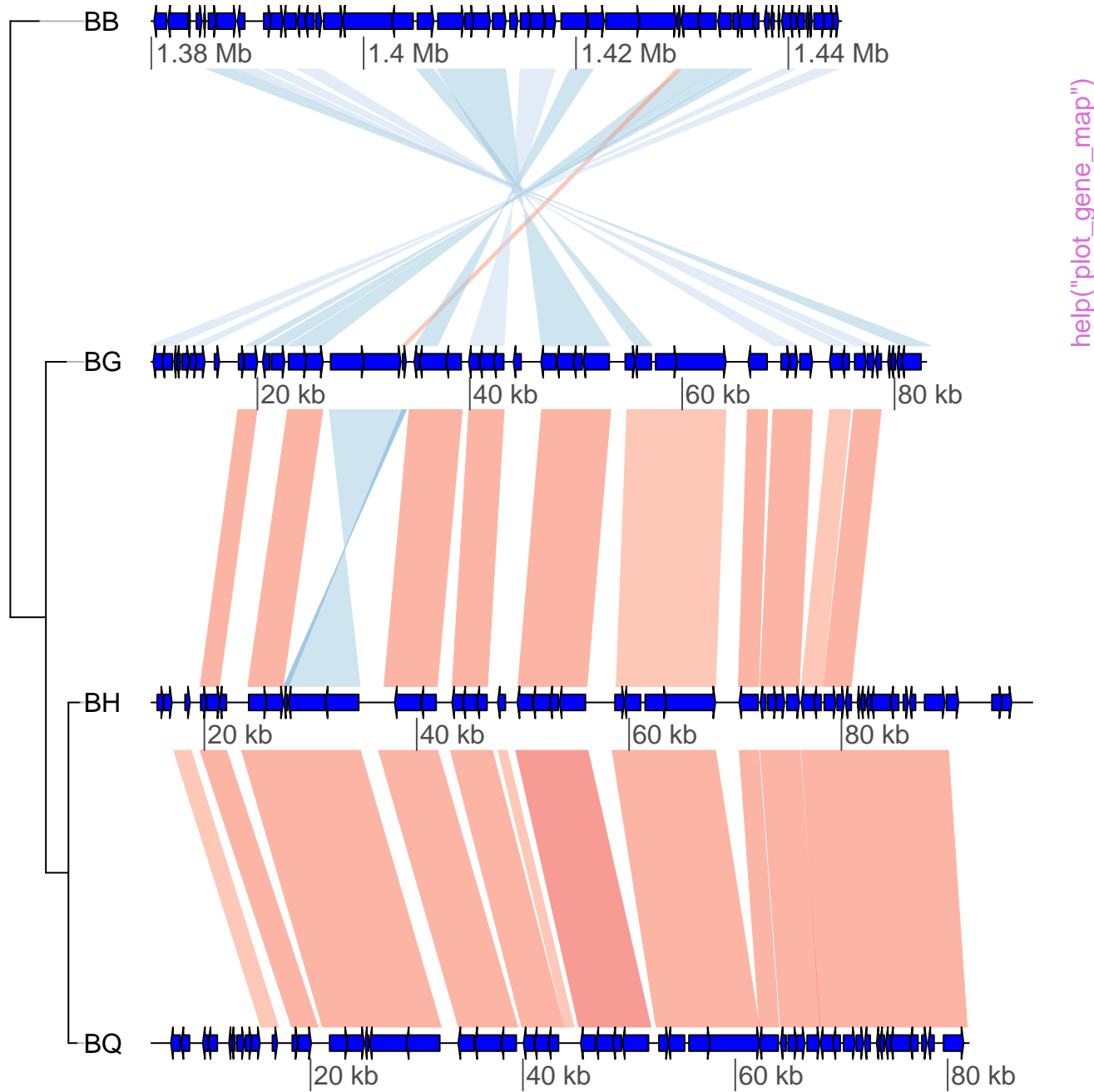




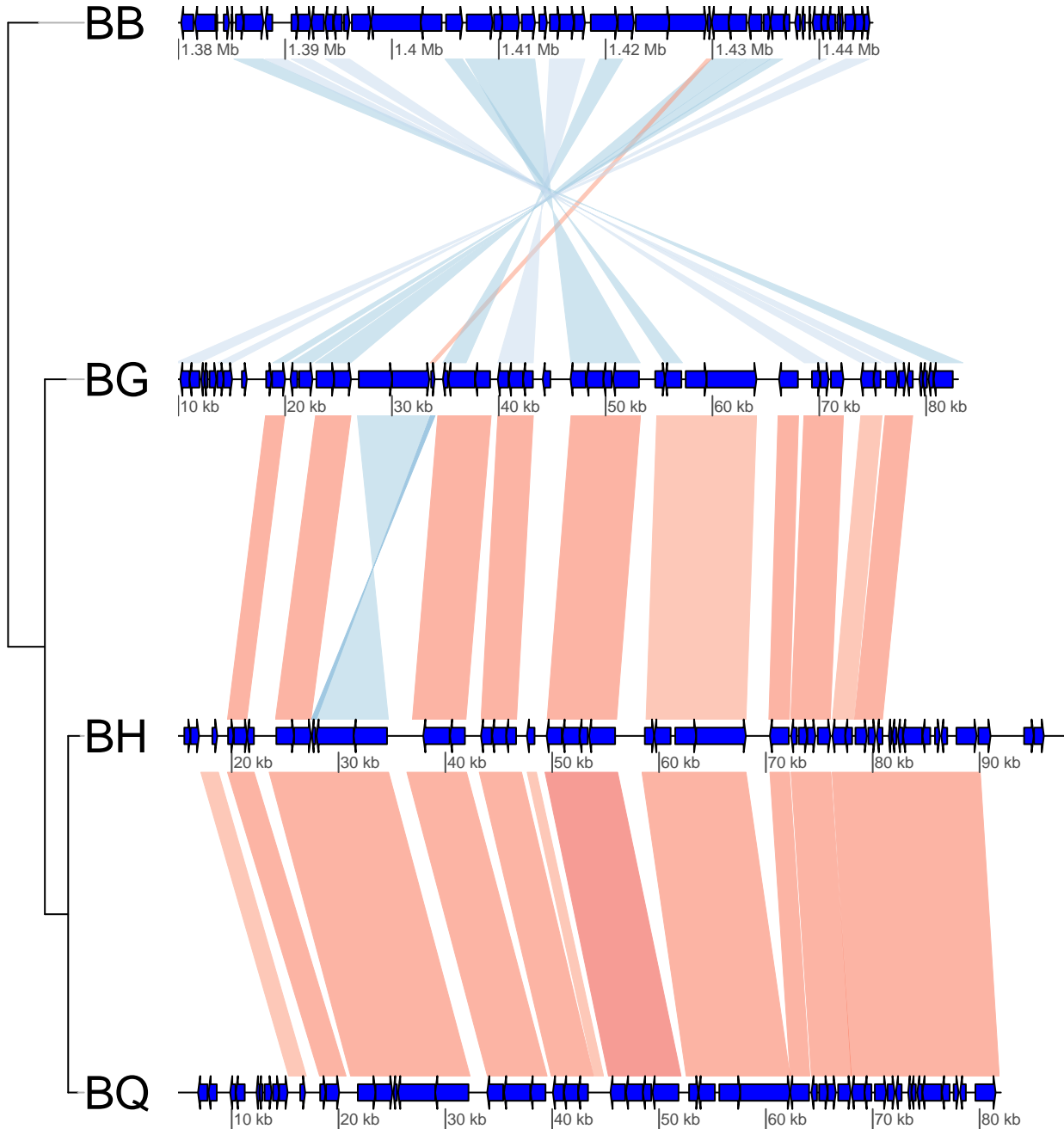


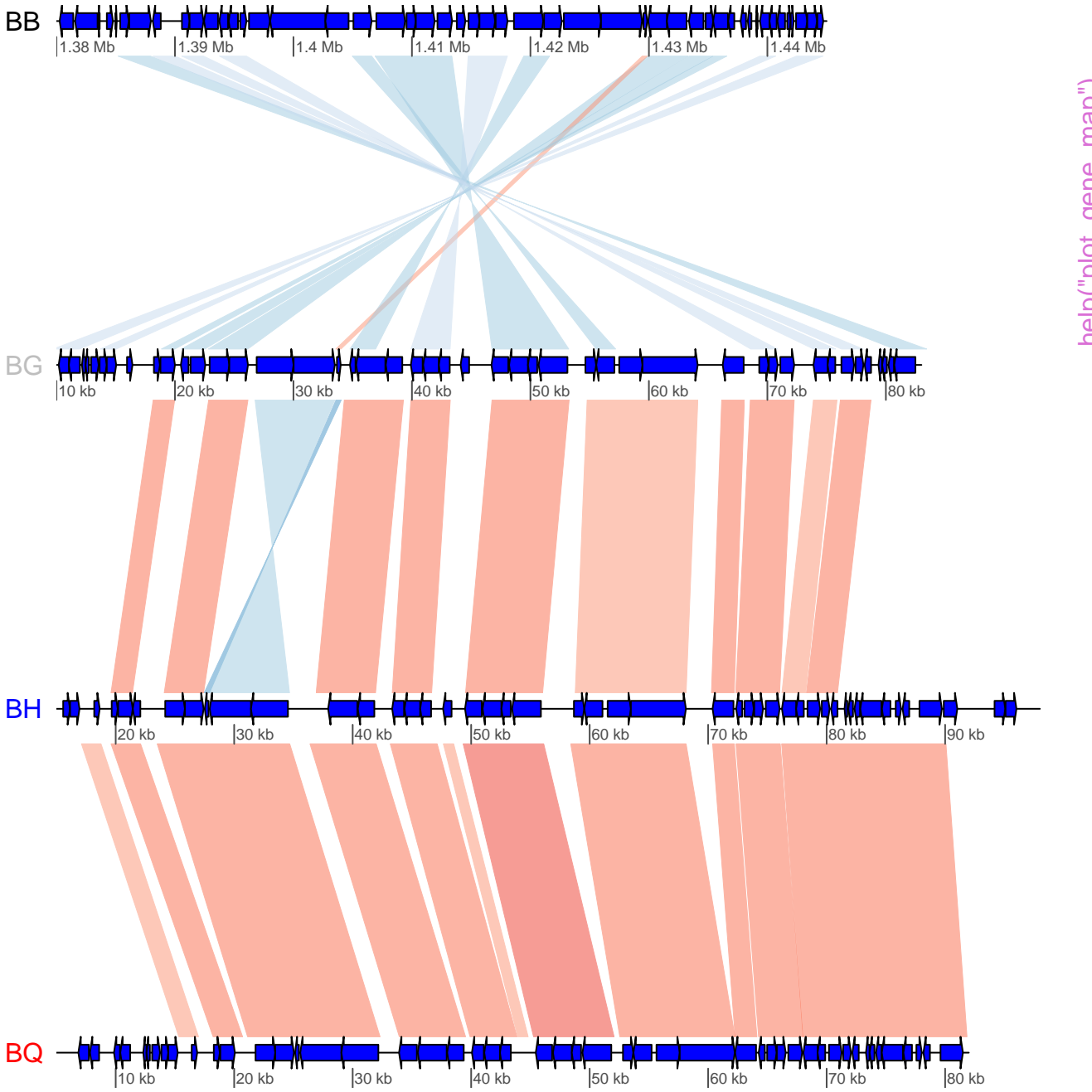




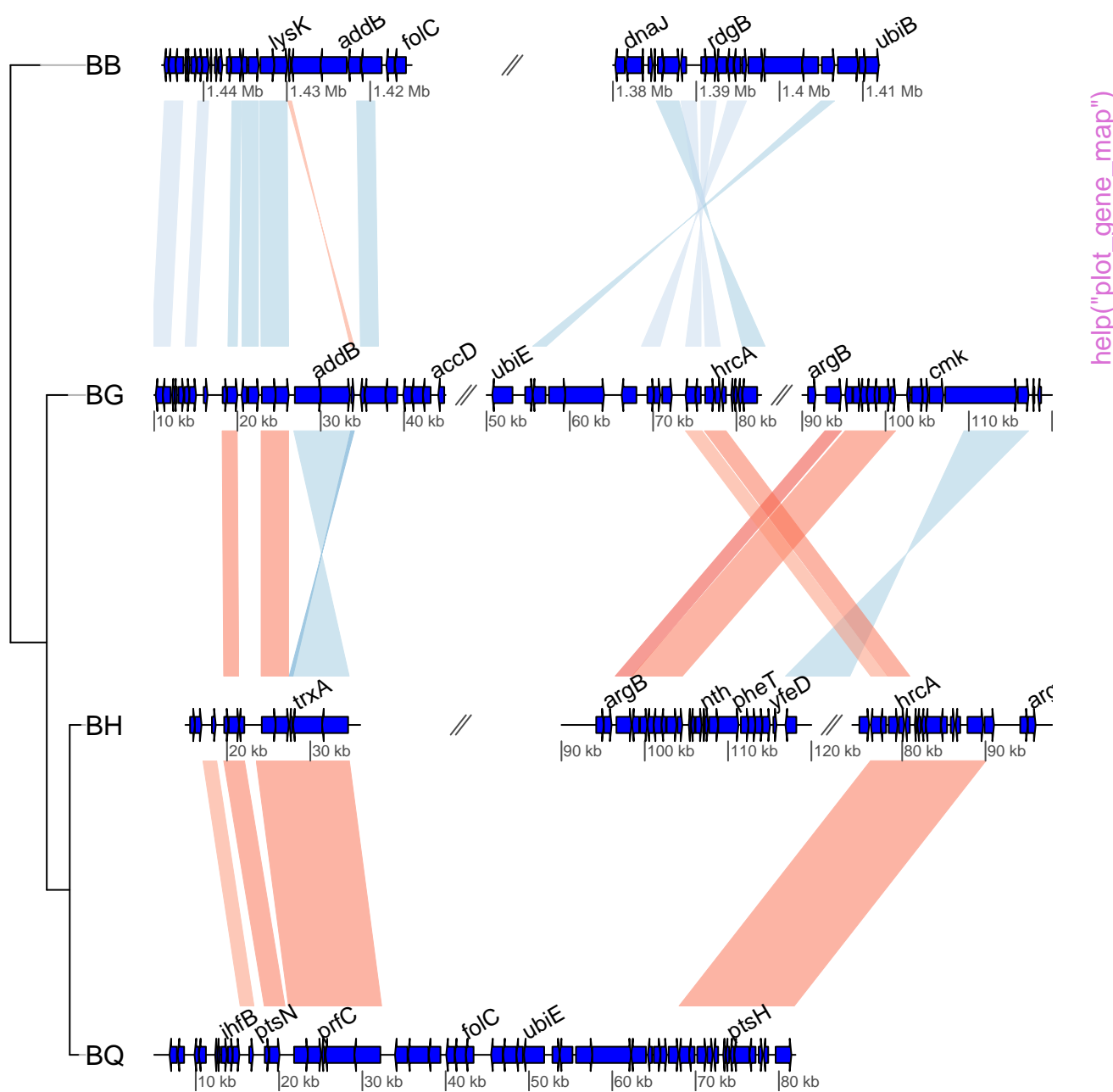


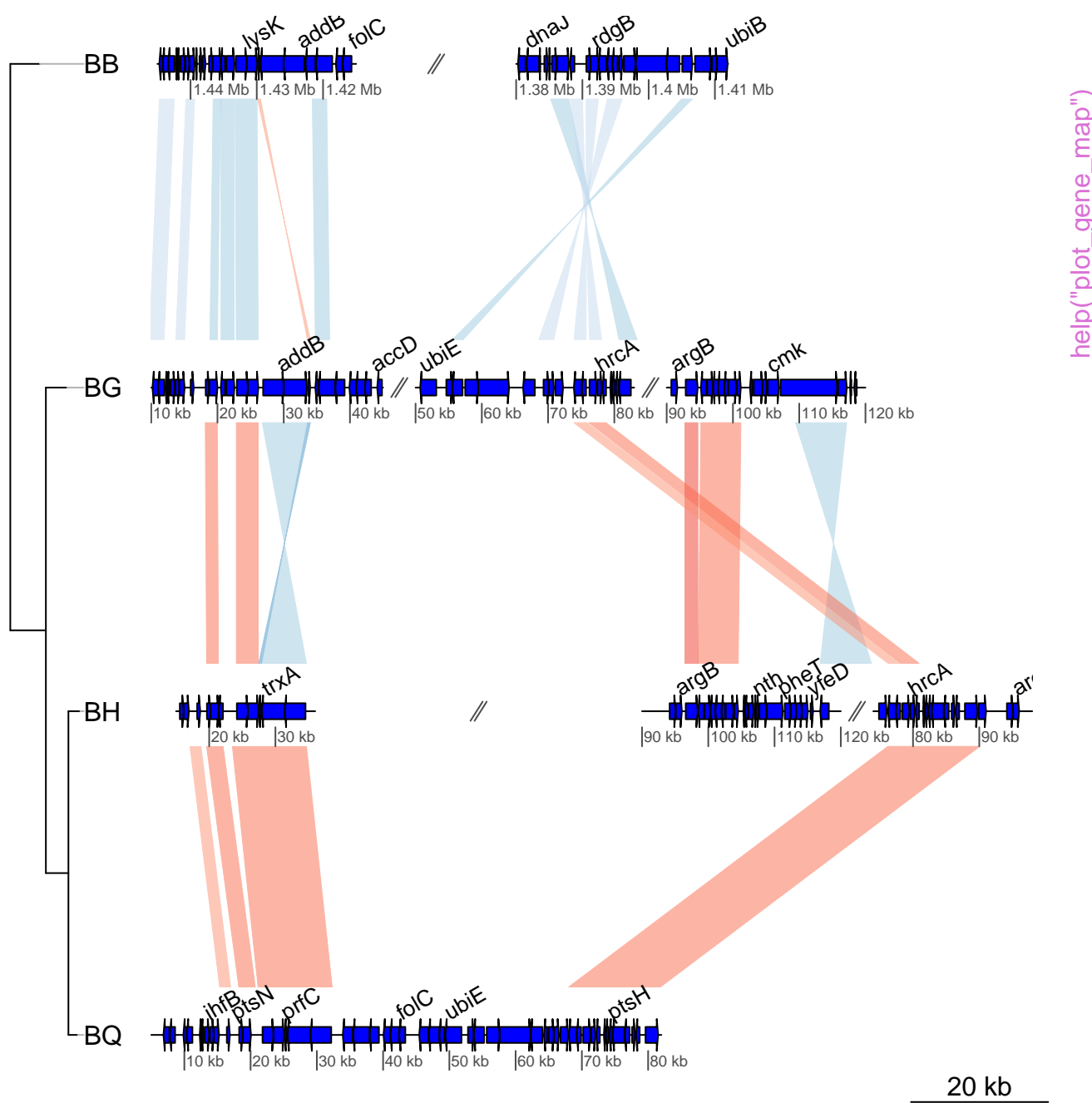
help("plot\_gene\_map")

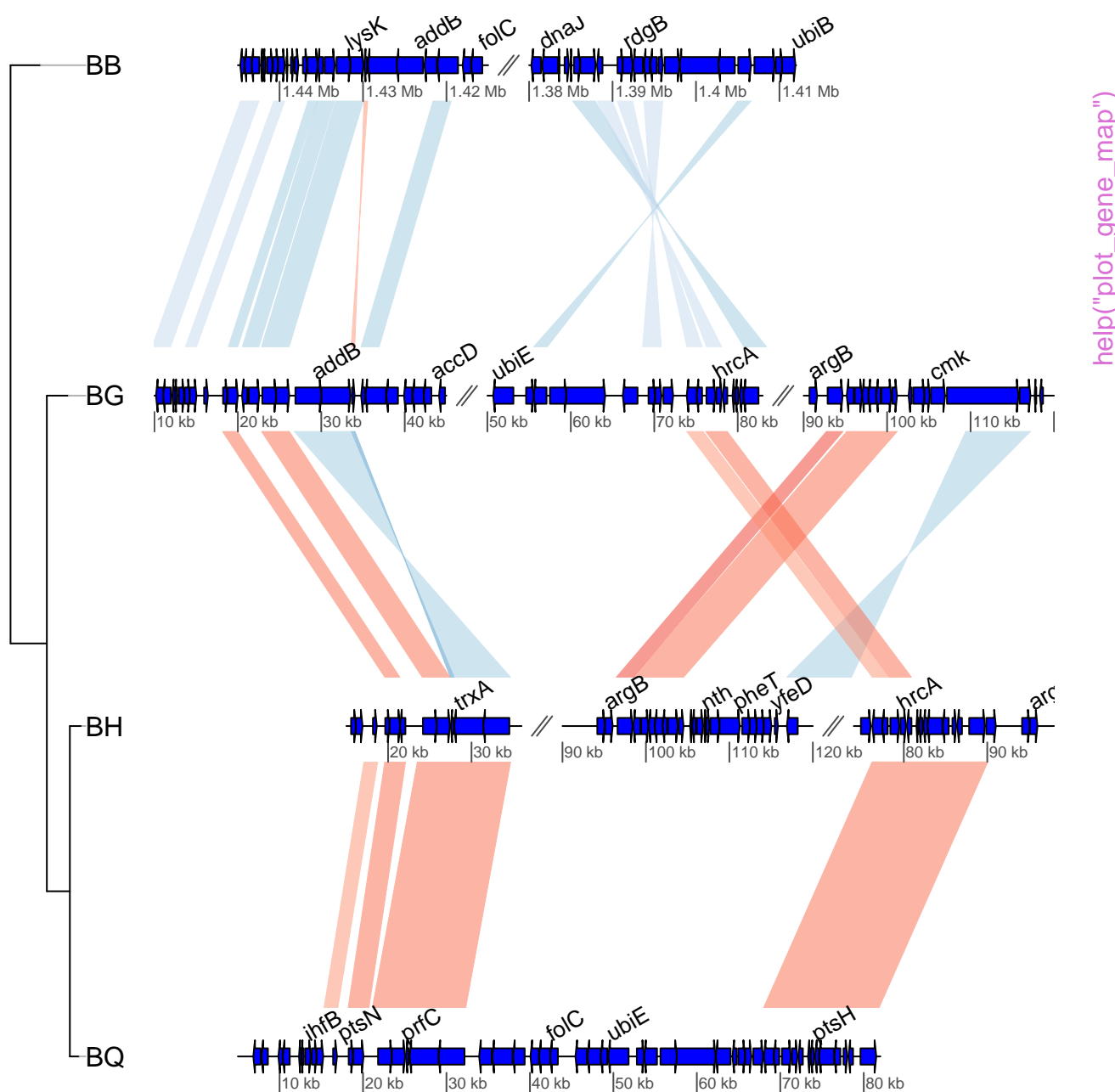




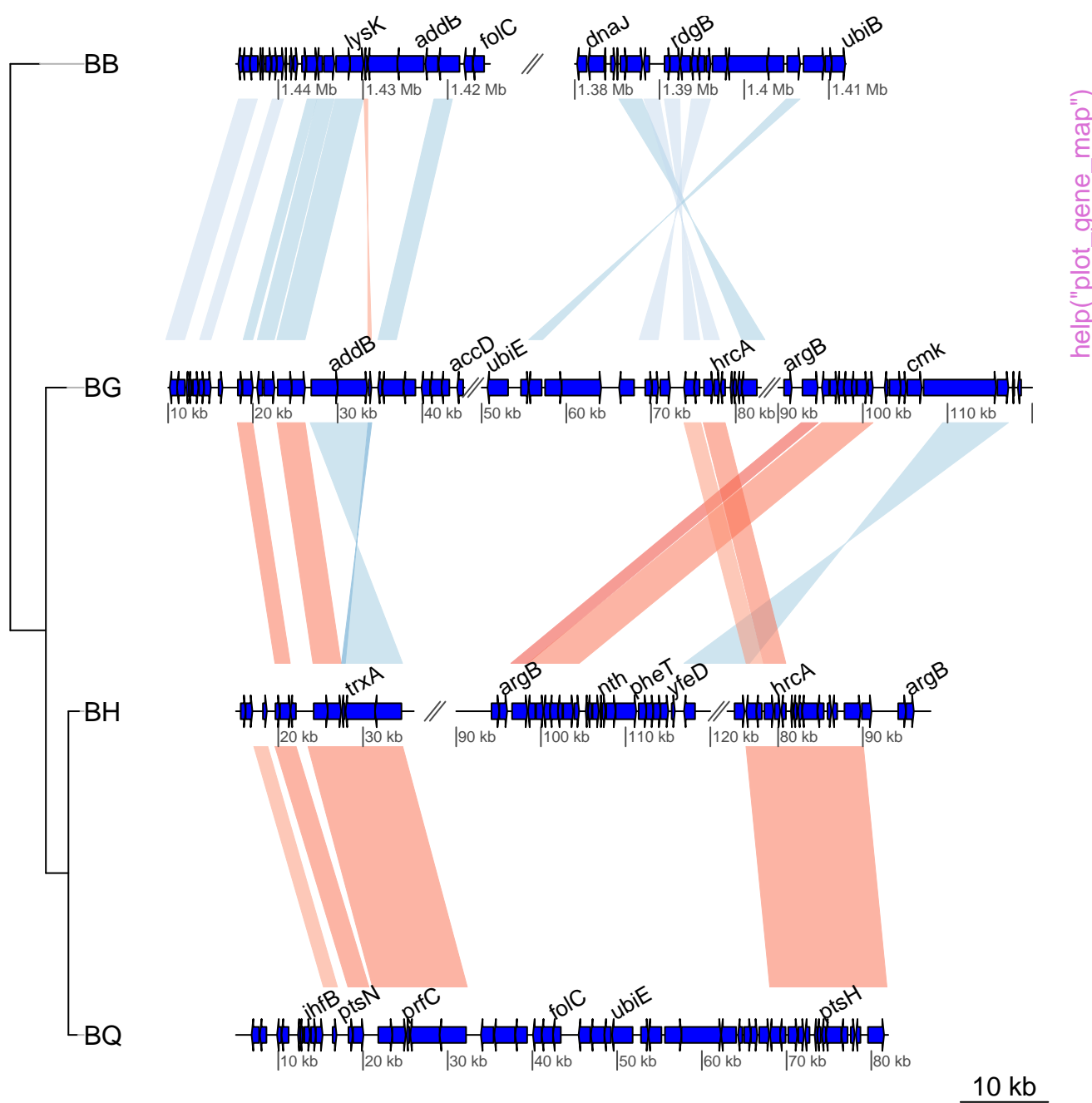
help("plot\_gene\_map")

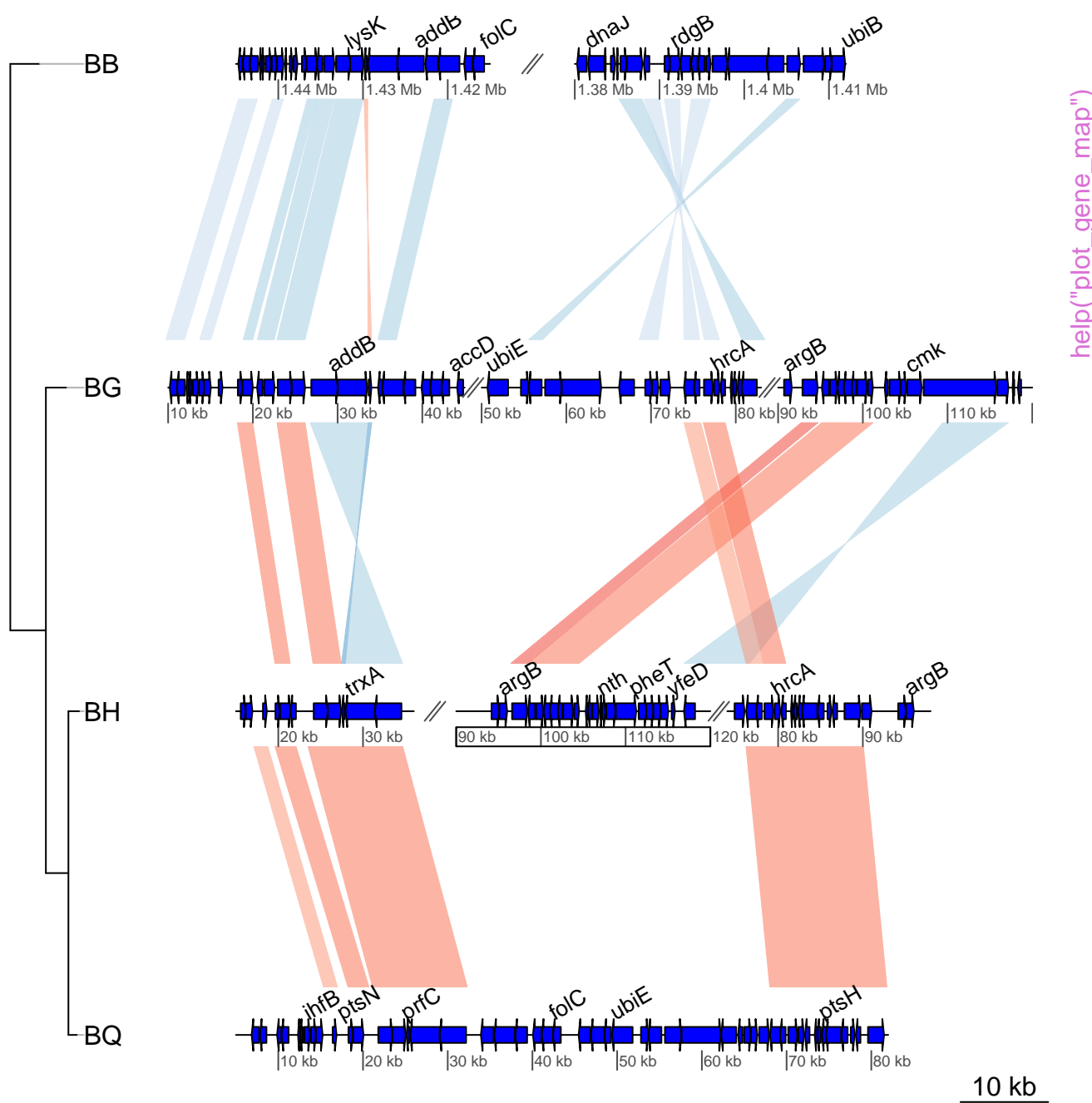




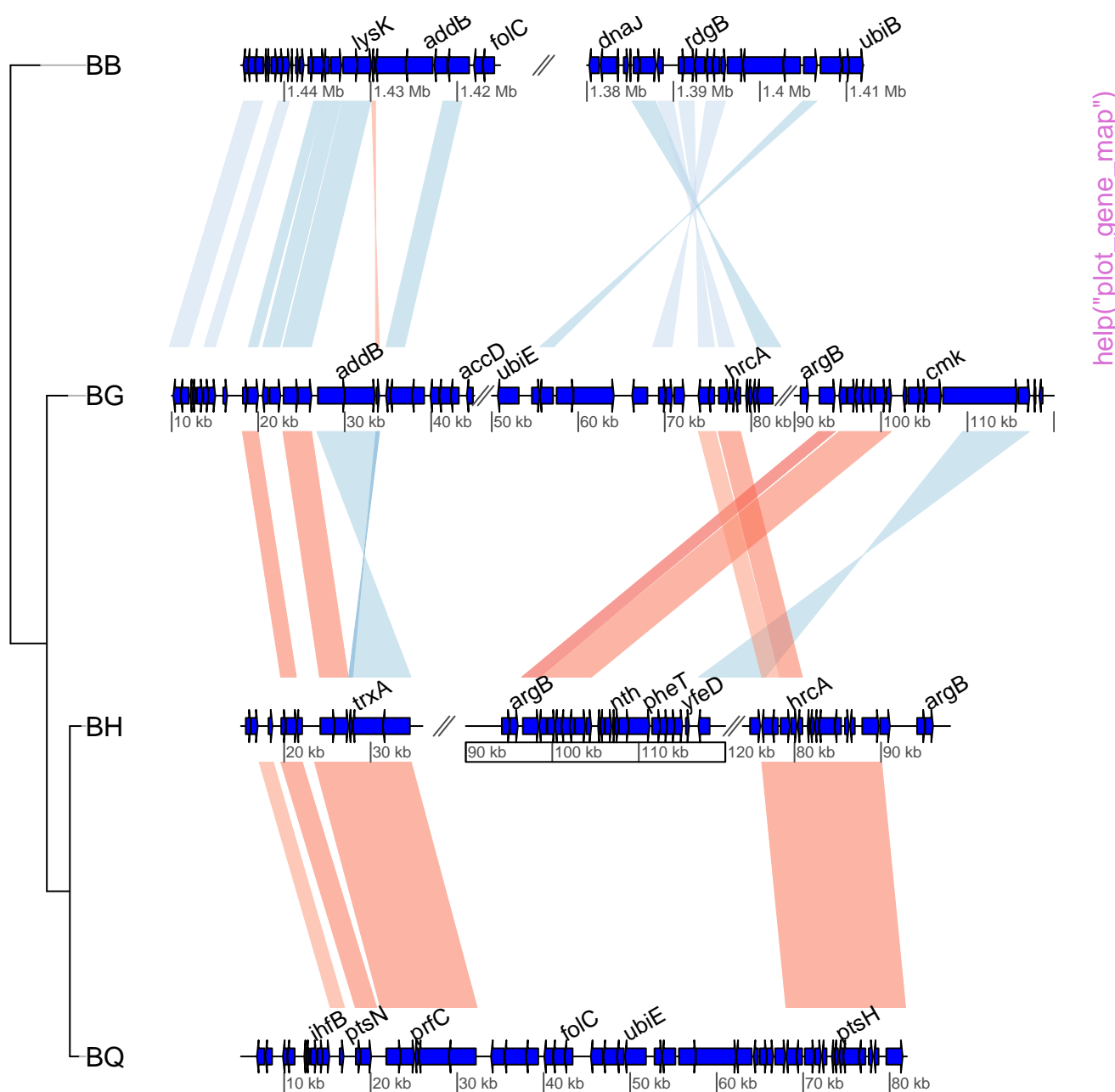


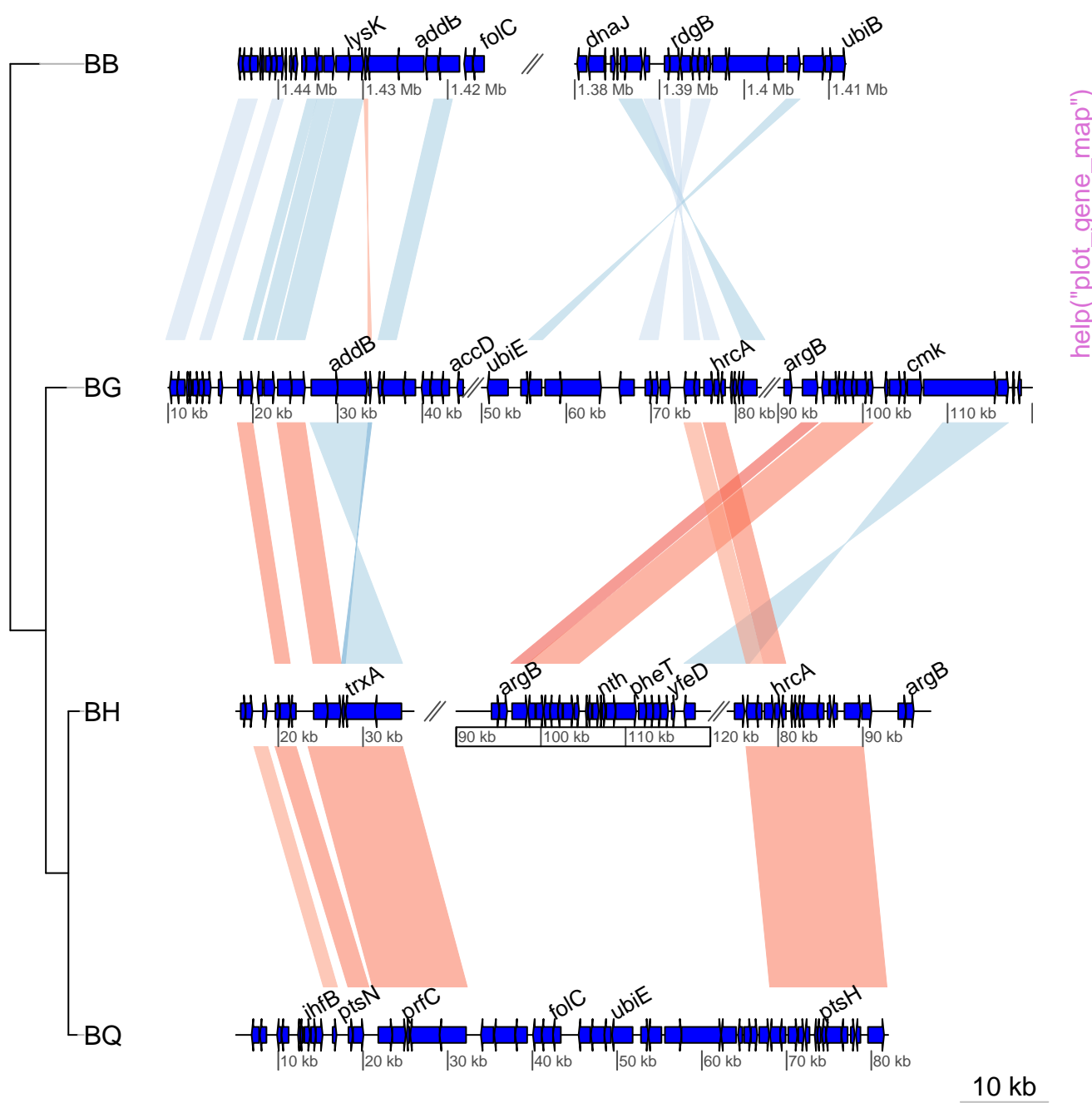
10 kb











geno

R

Plot

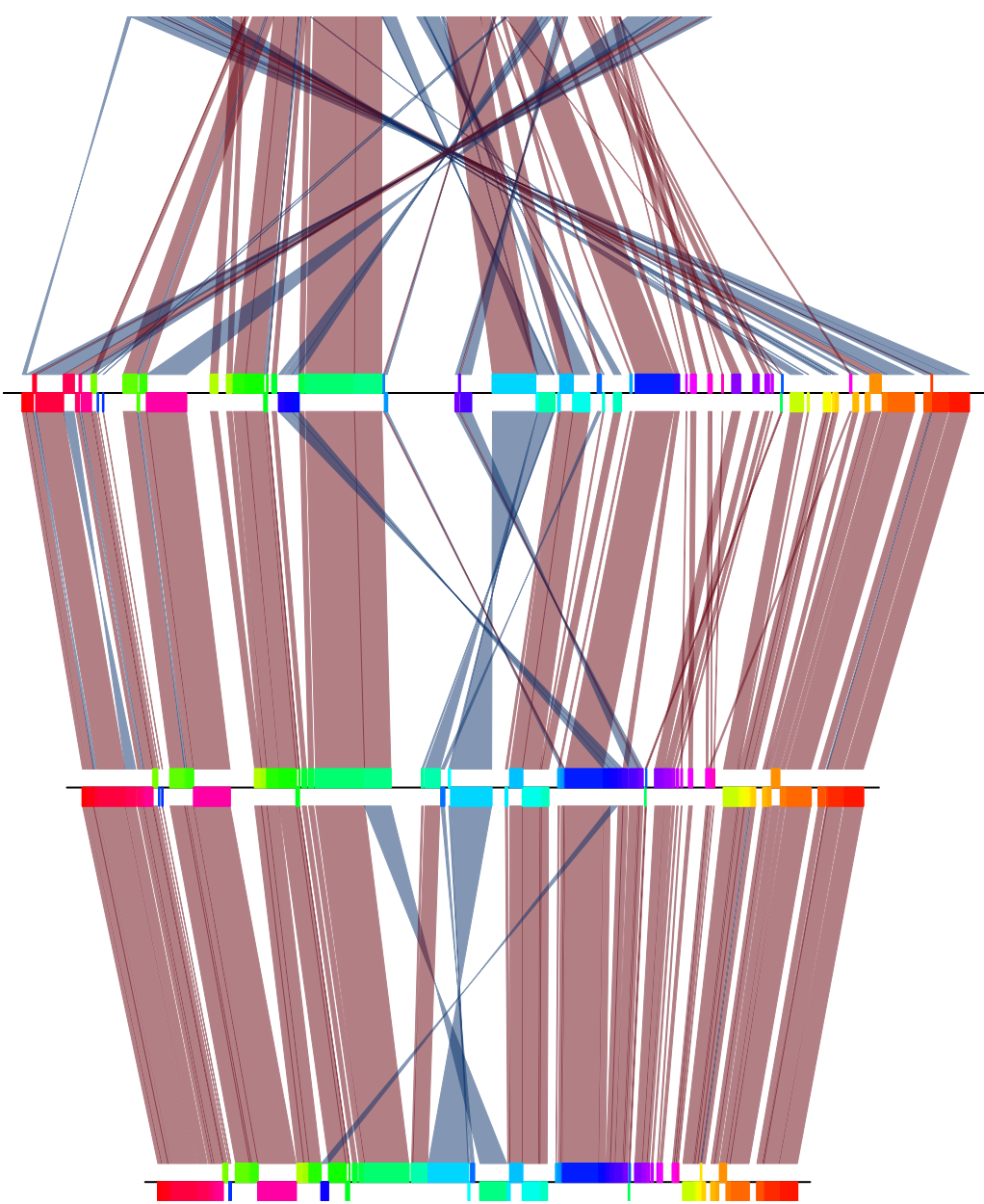
help("plot\_gene\_map")

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

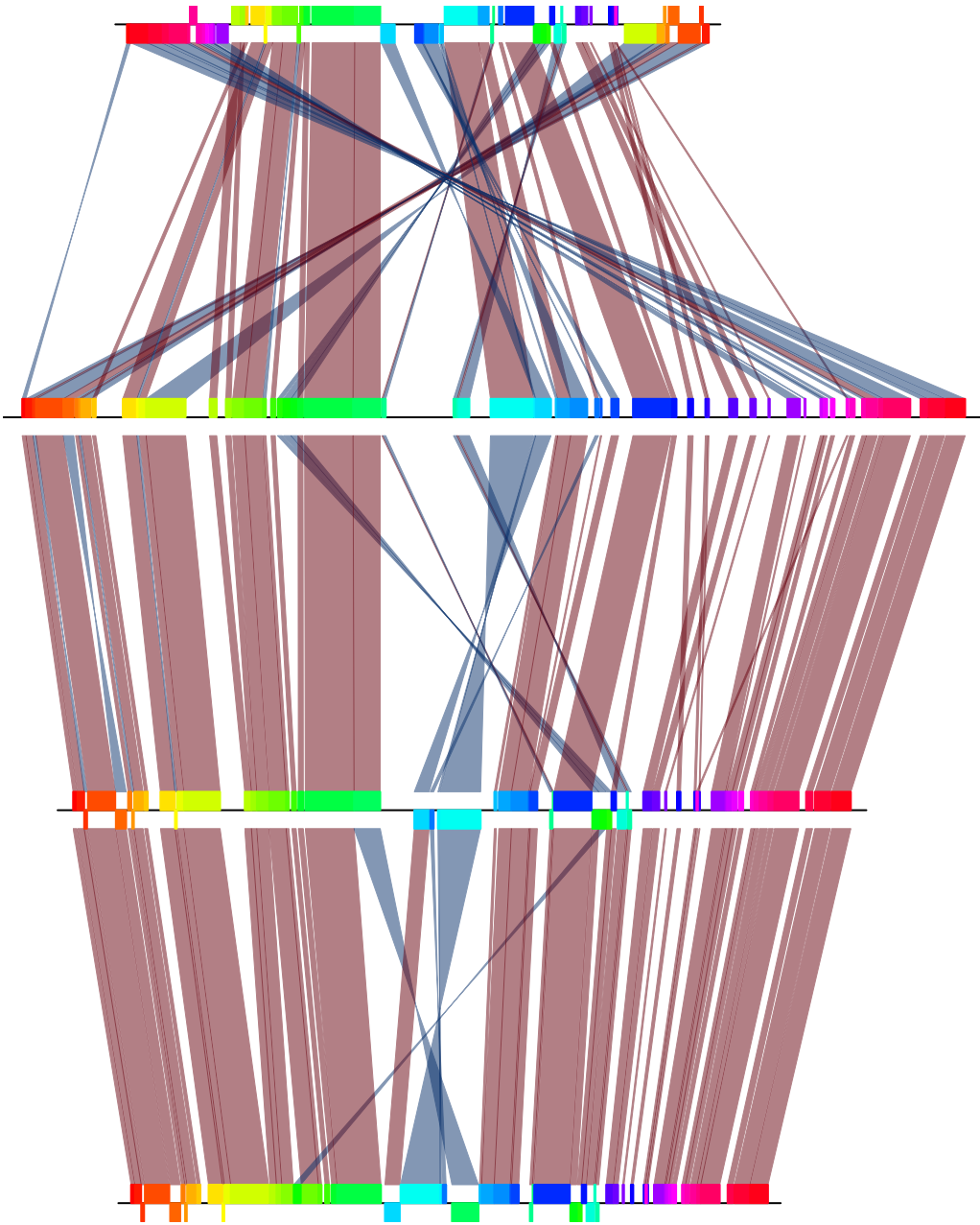
500 kb

B\_bacilliformis

B\_grahamii

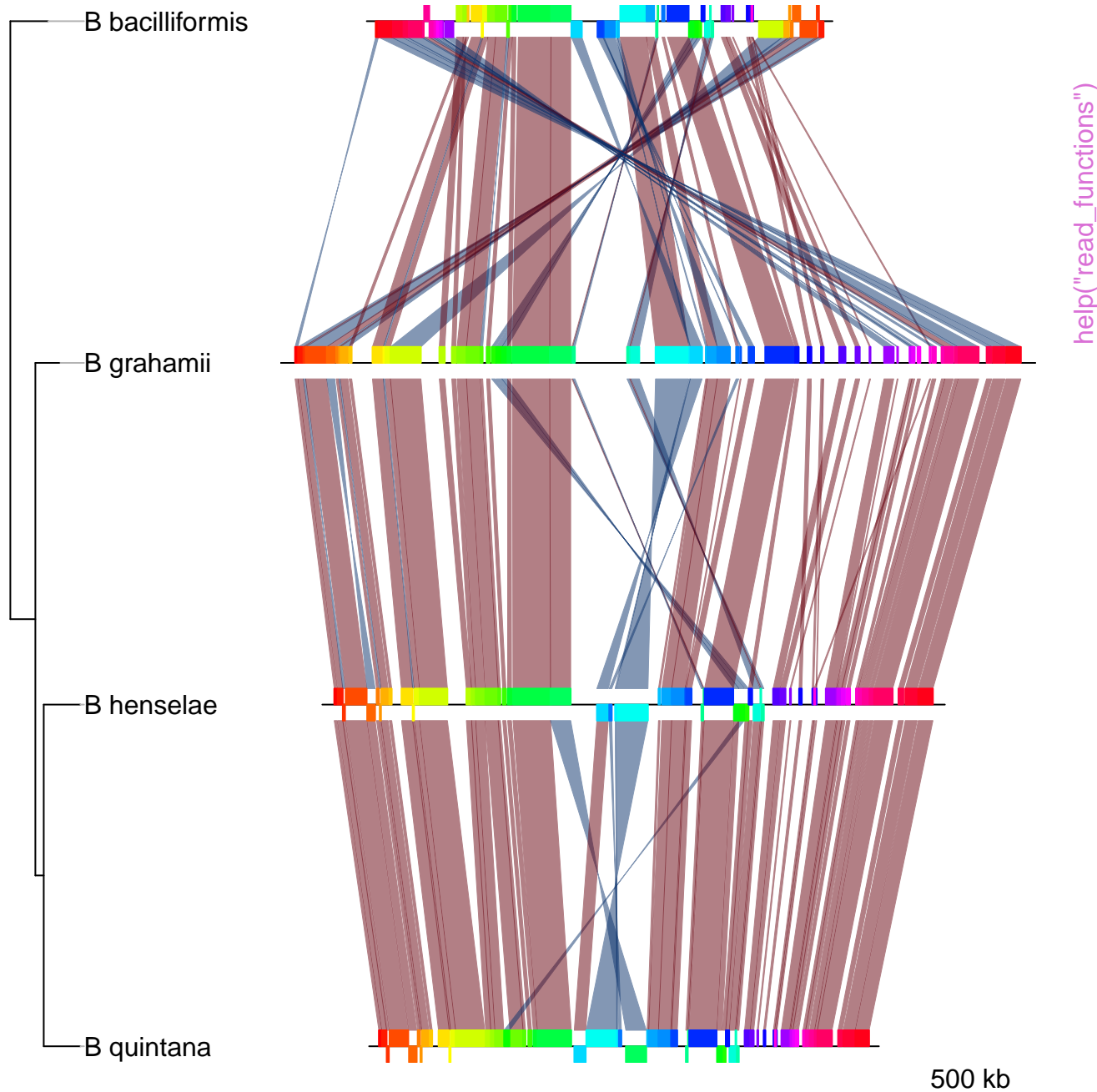
B\_henselae

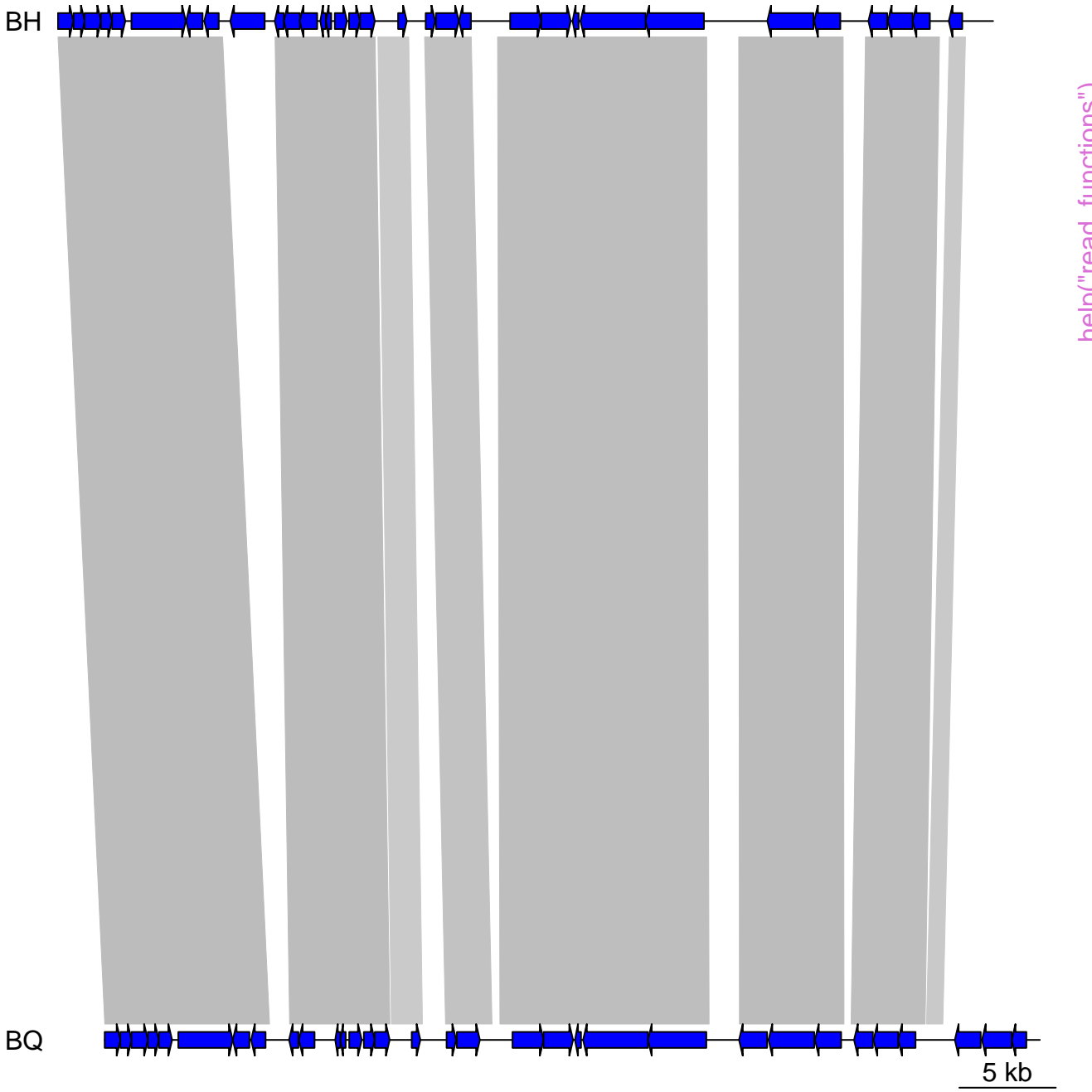
B\_quintana



help("read\_functions")

500 kb



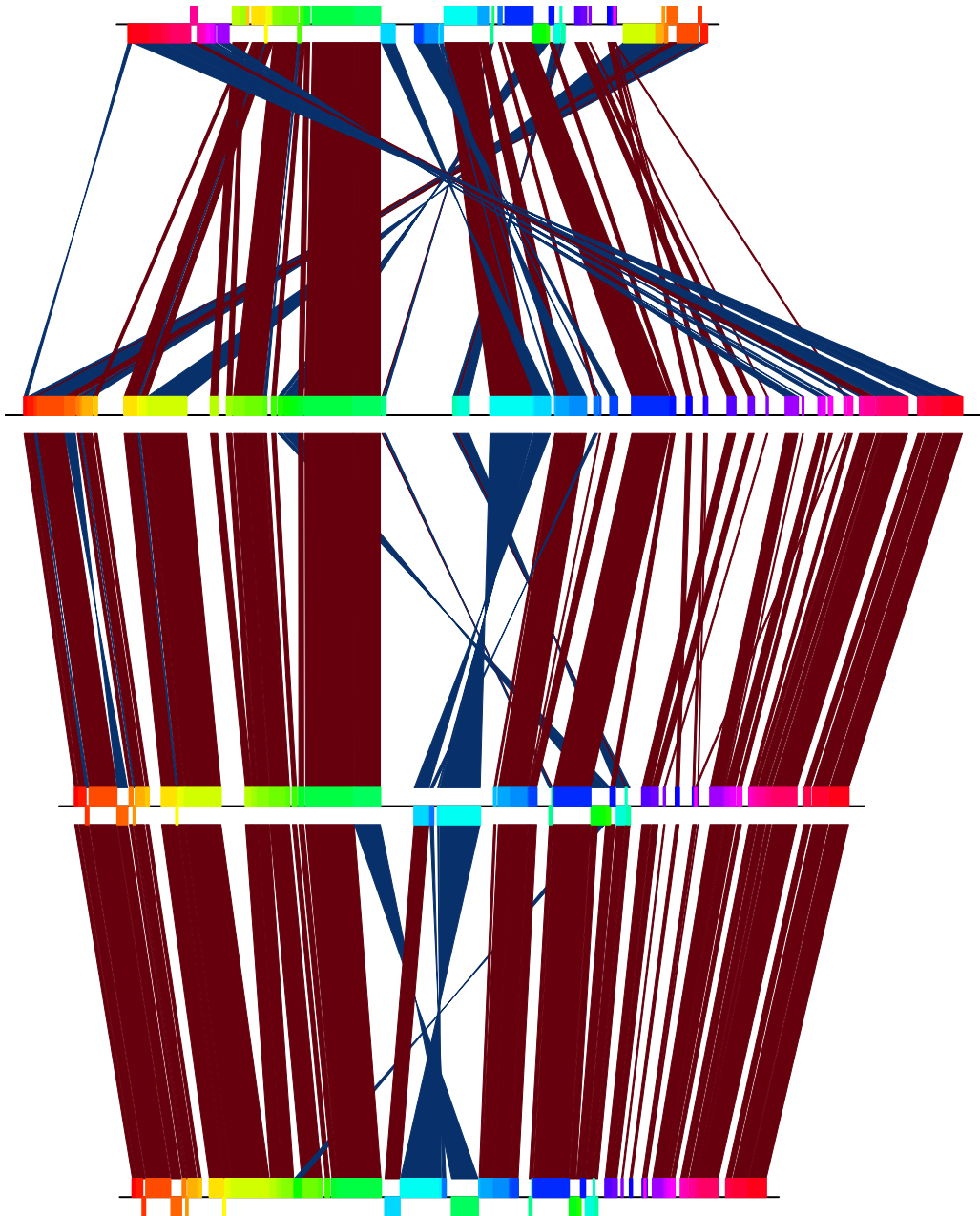


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("reverse")

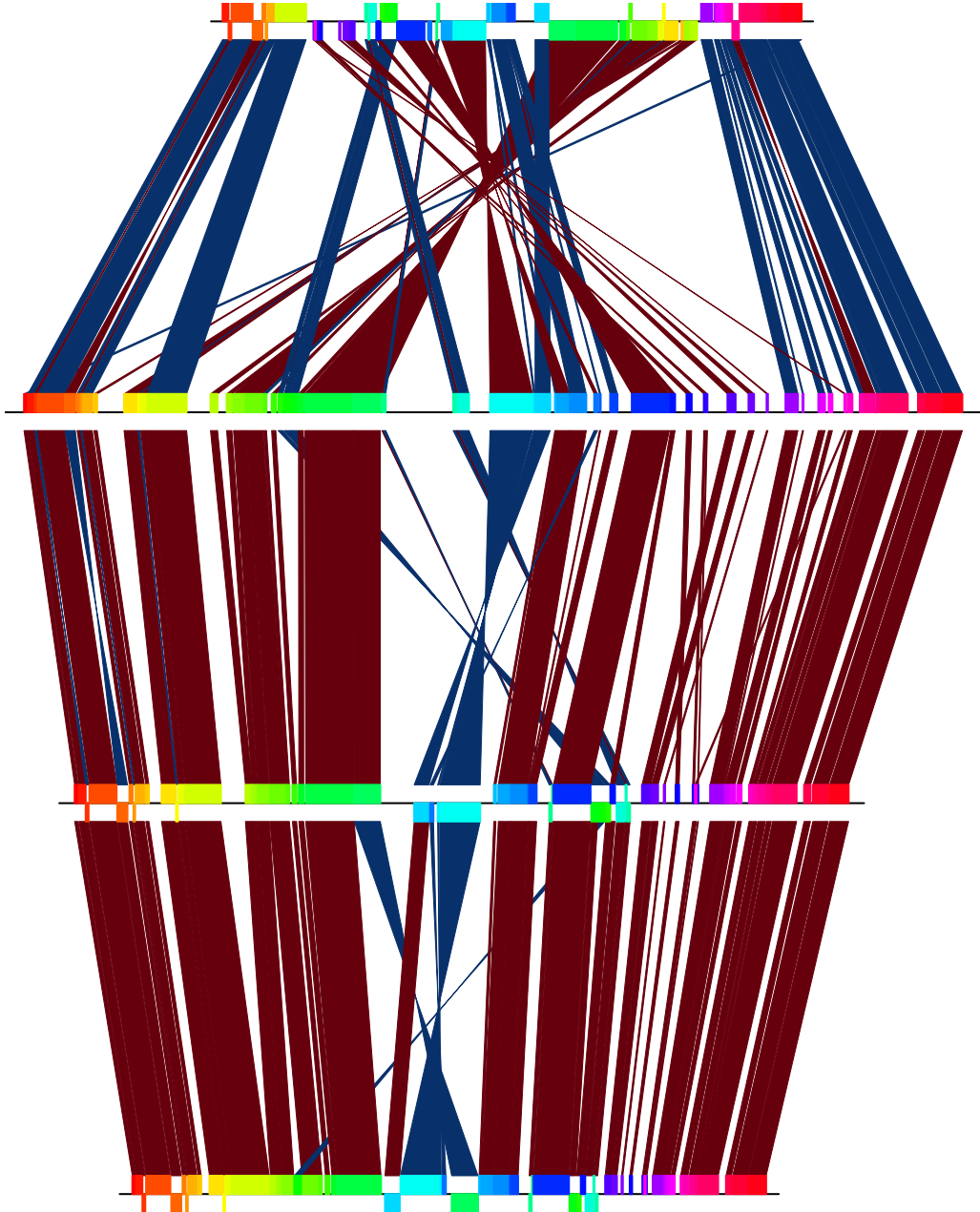


B\_bacilliformis

B\_grahamii

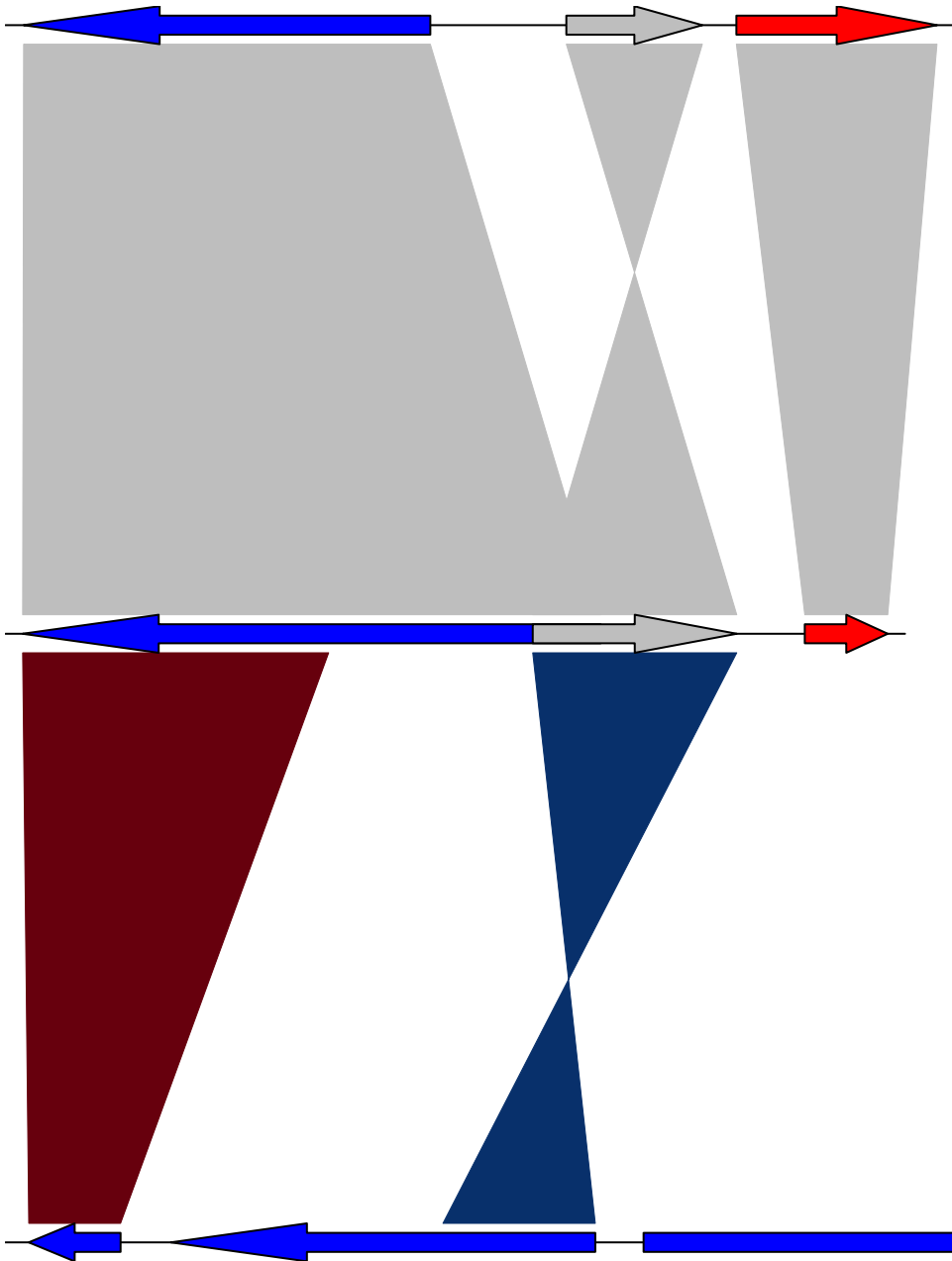
B\_henselae

B\_quintana



help("reverse")

500 kb



help("three\_genes")

200 nt

