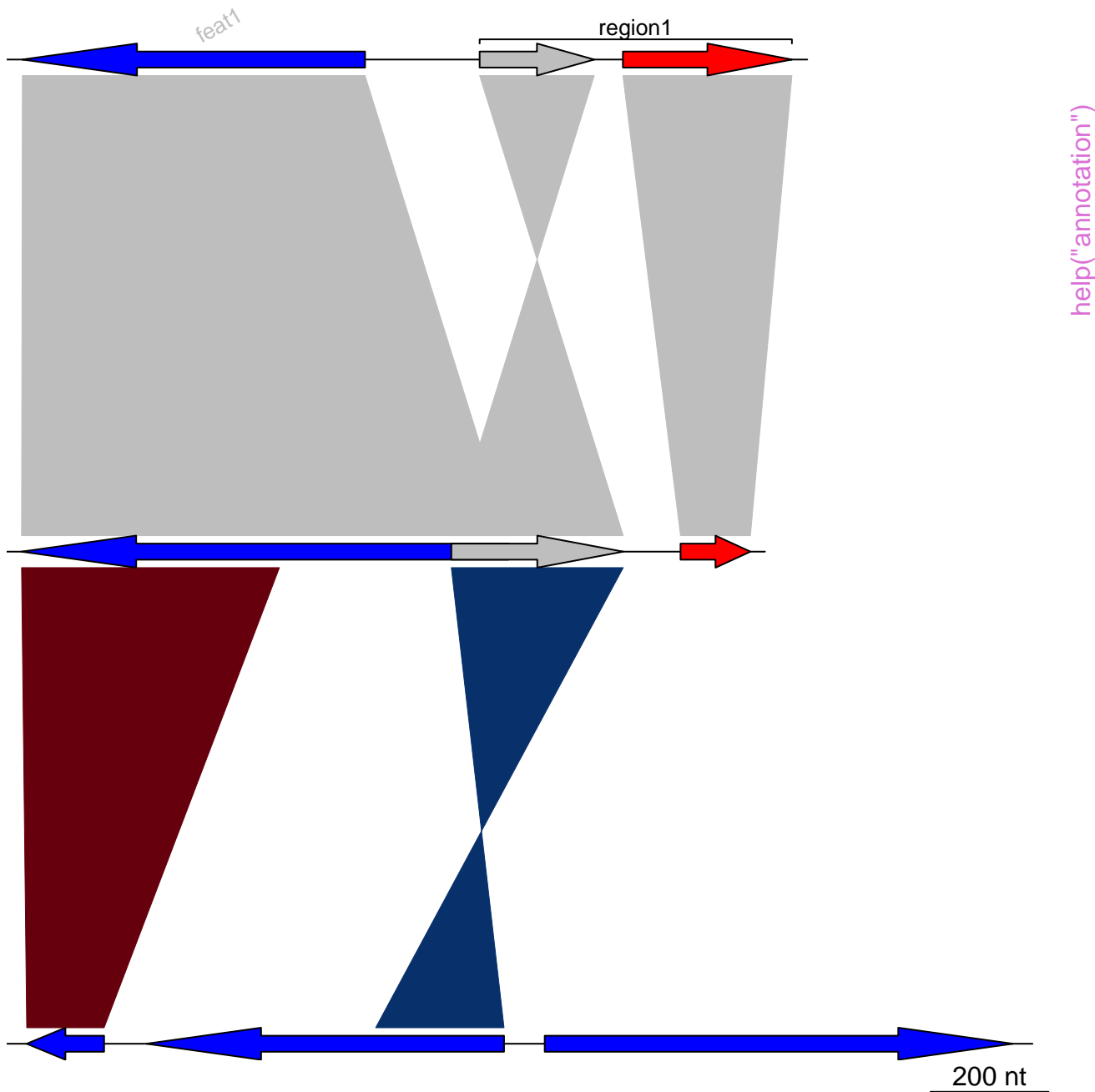
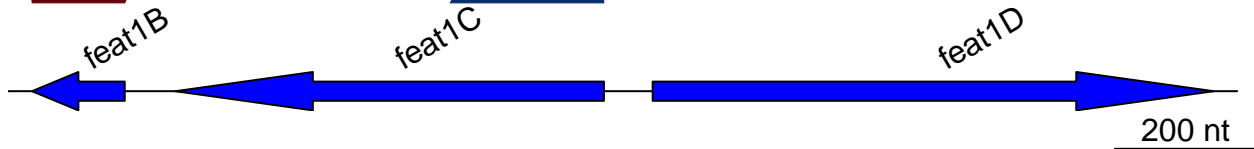
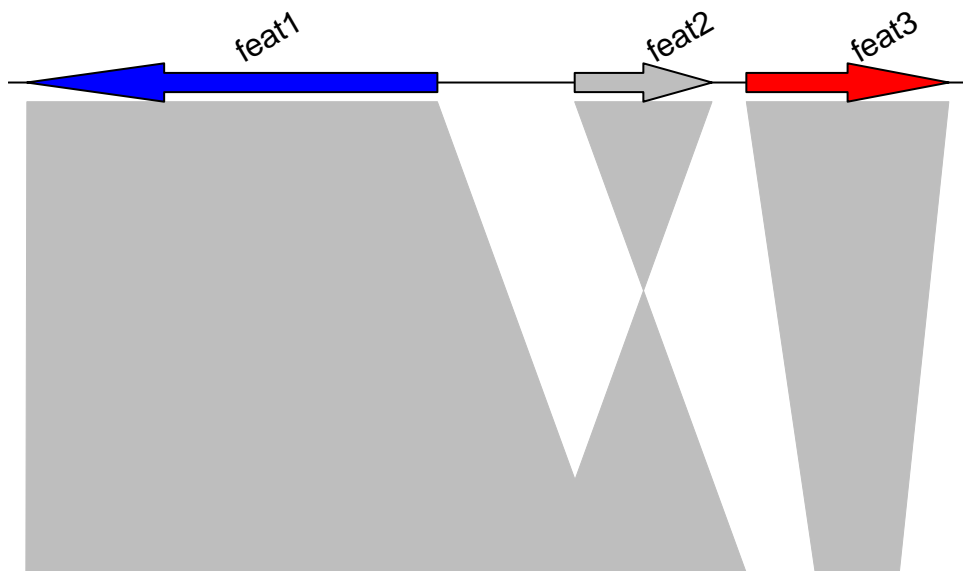


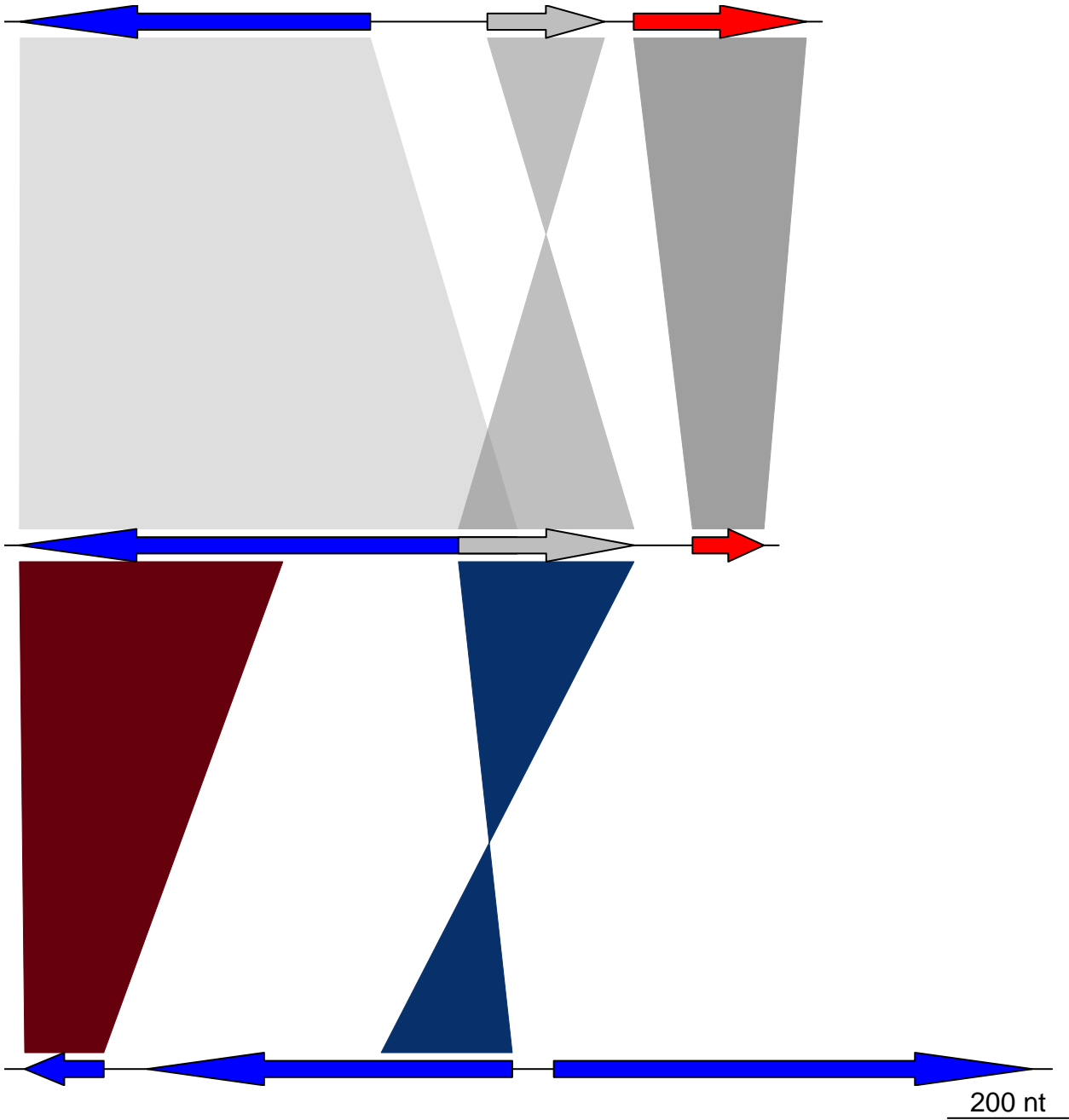
help("annotation")

200 nt

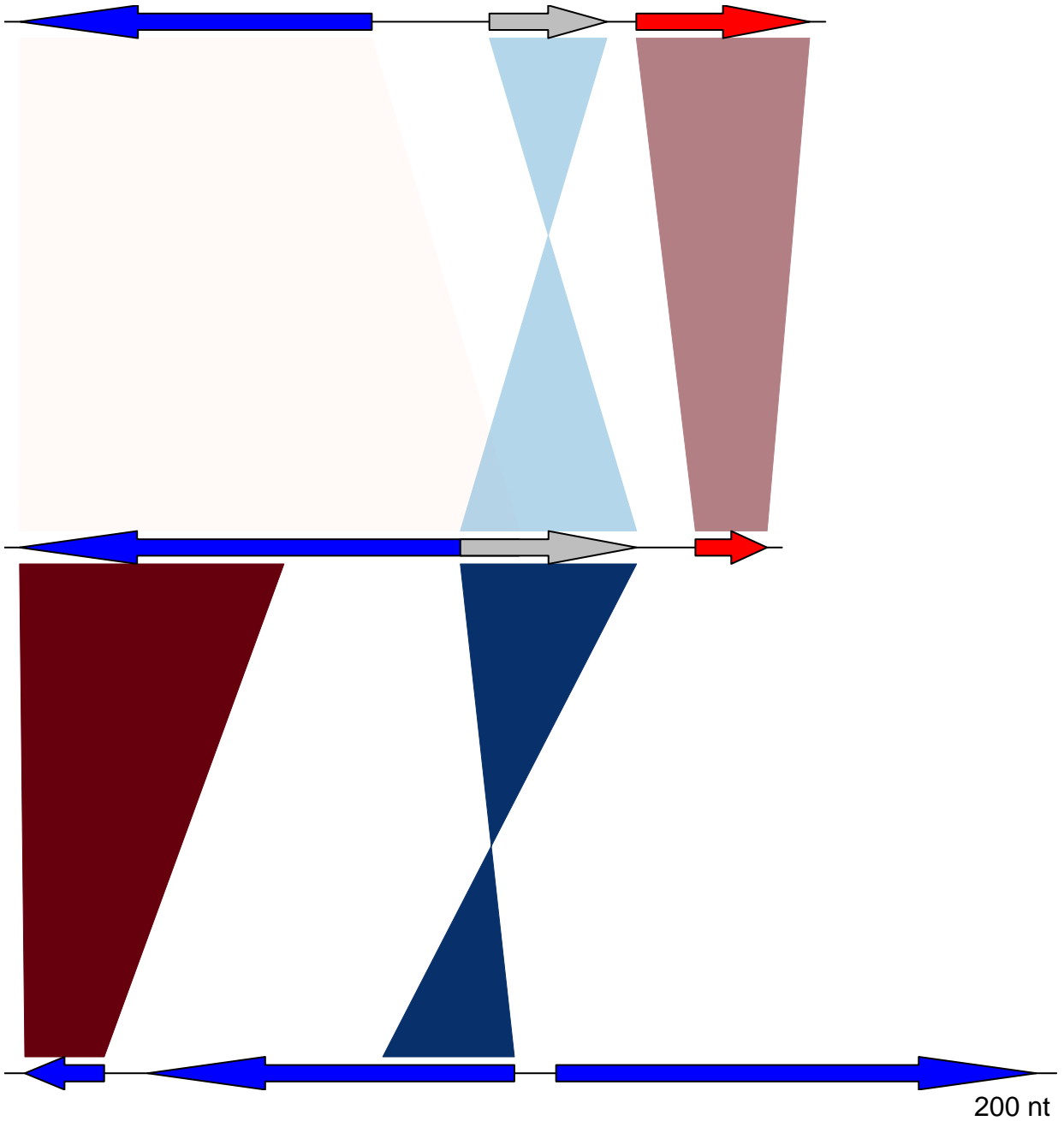




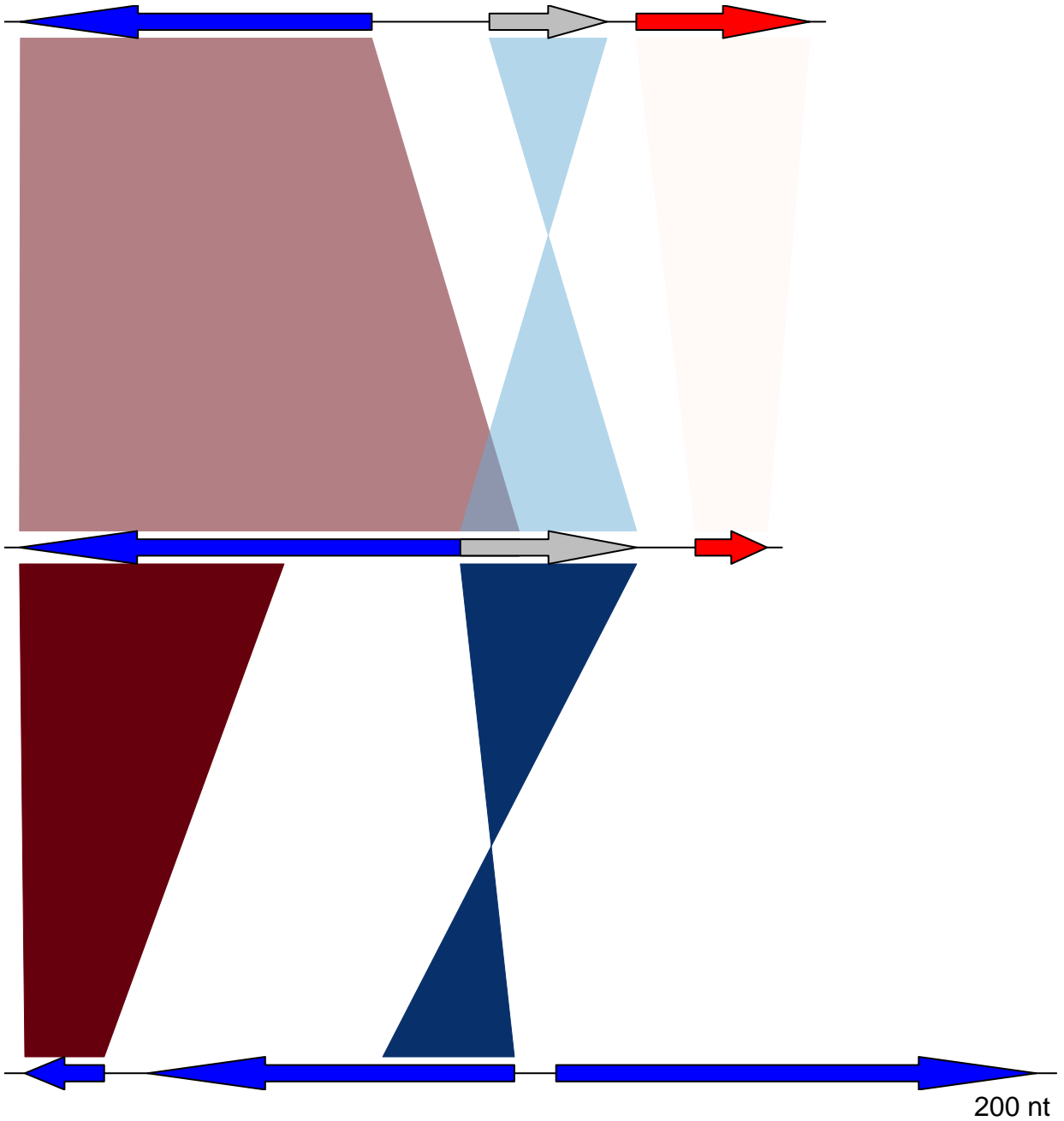
help("annotation")



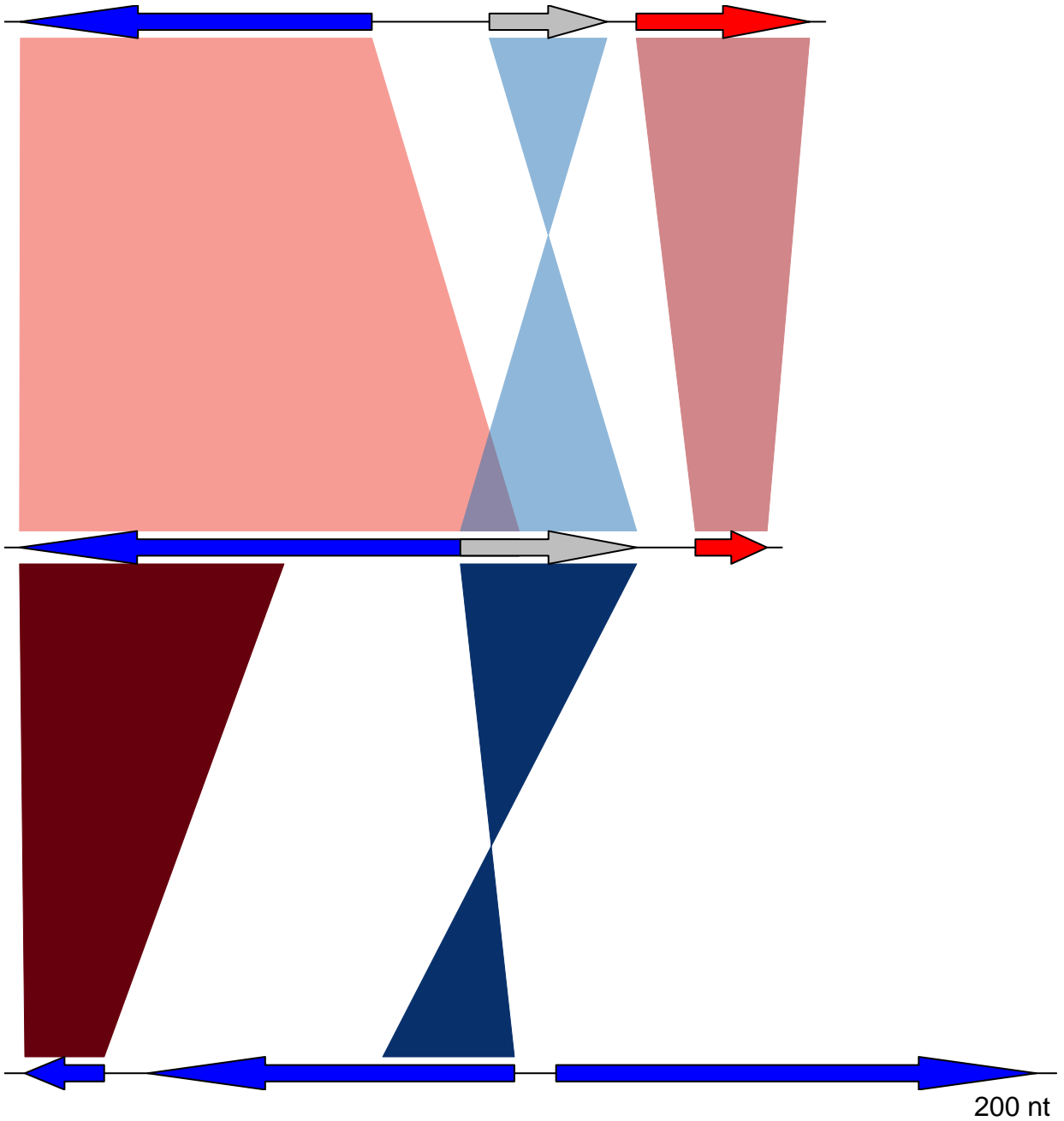
help("apply\_color\_scheme")



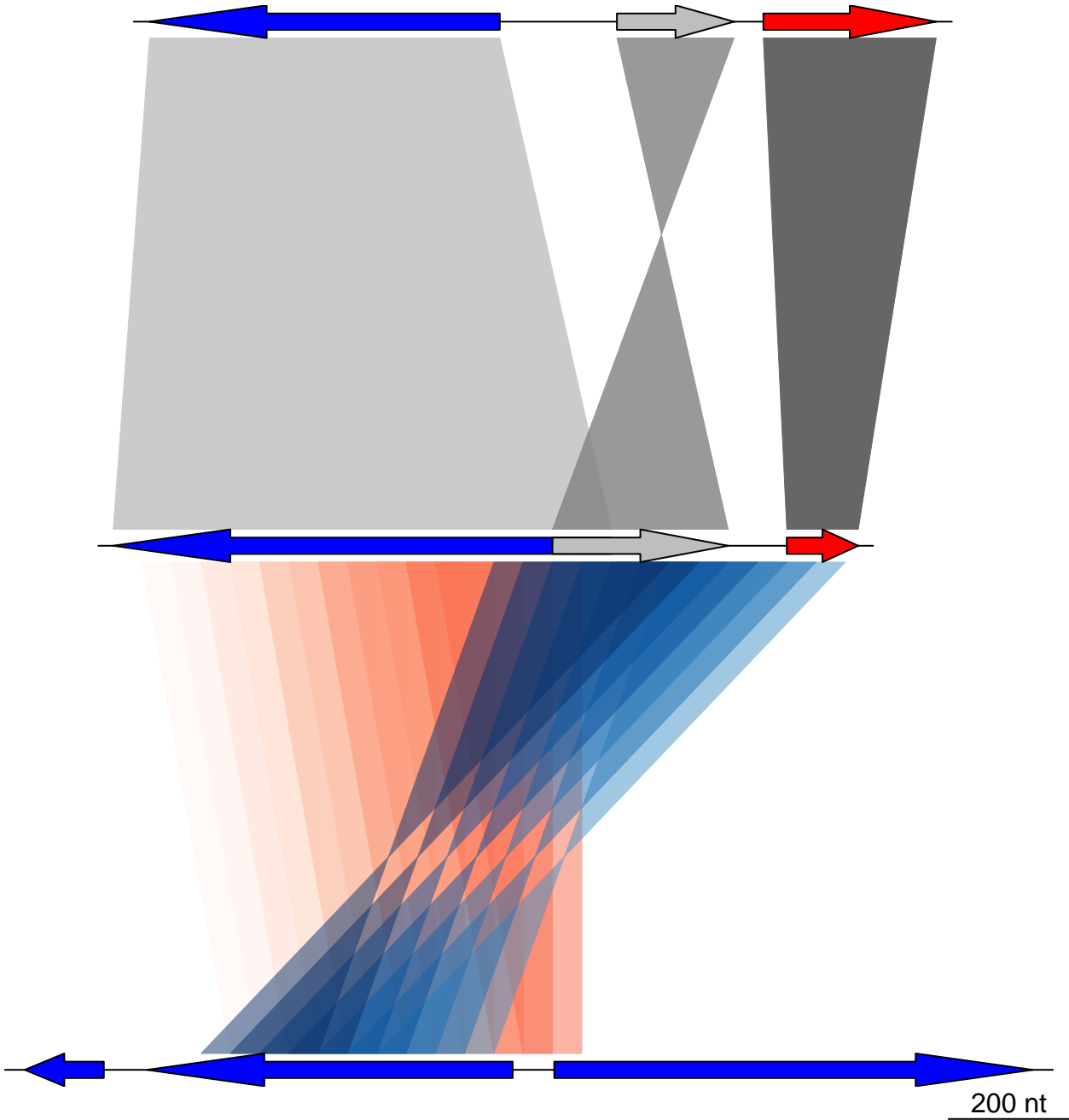
help("apply\_color\_scheme")



help("apply\_color\_scheme")

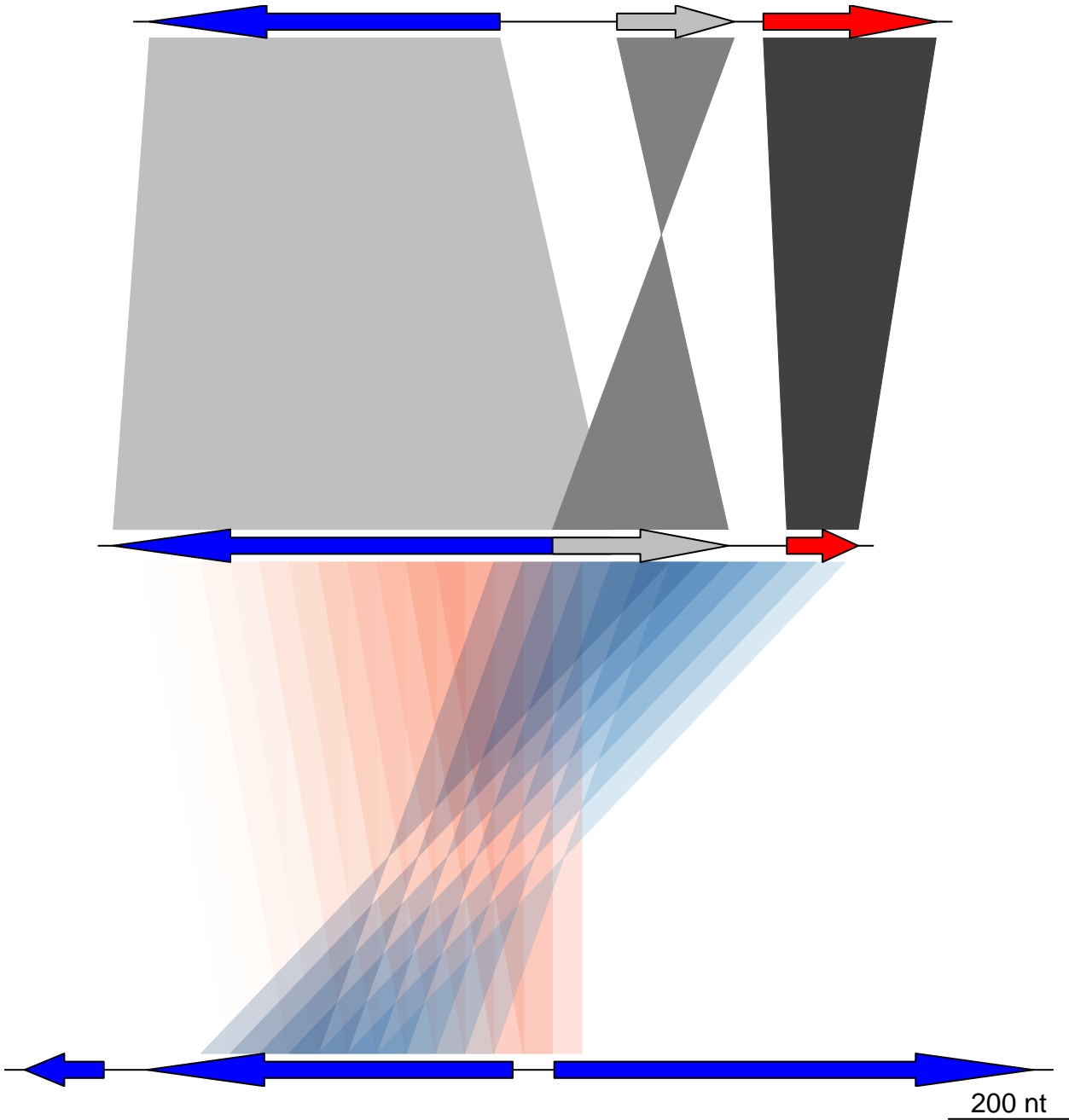


help("apply\_color\_scheme")

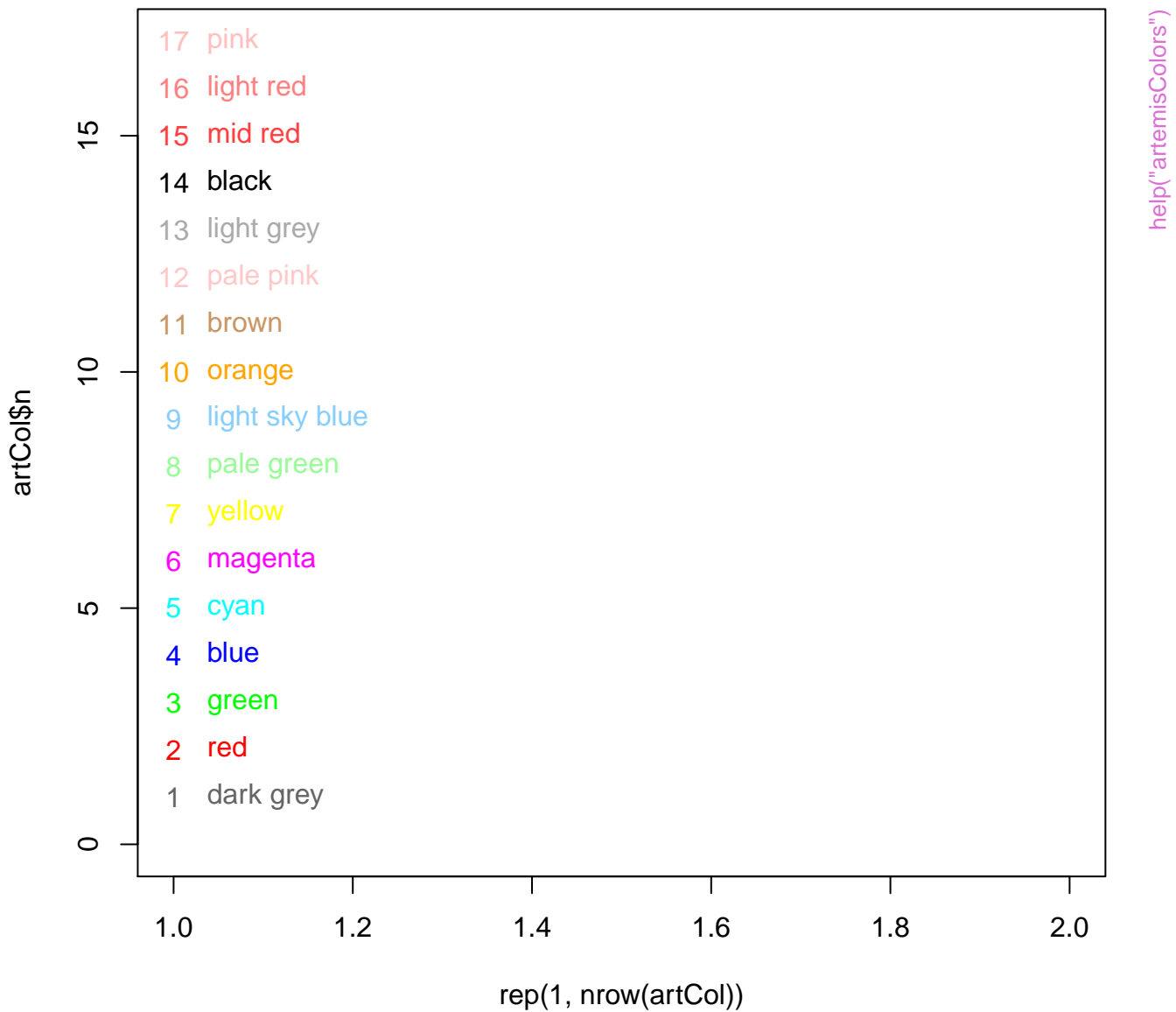


help("apply\_color\_scheme")





help("apply\_color\_scheme")



BB

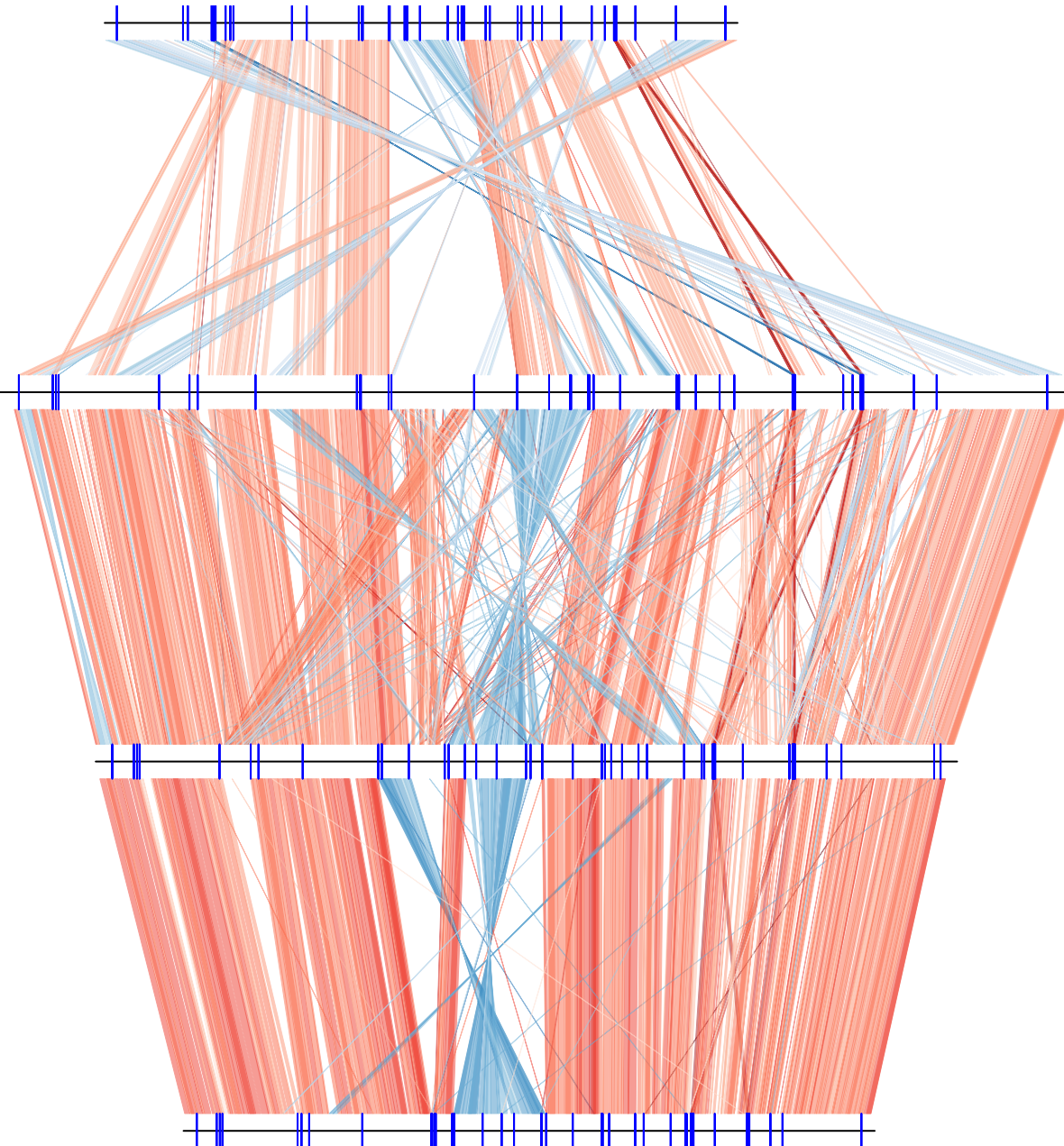
BG

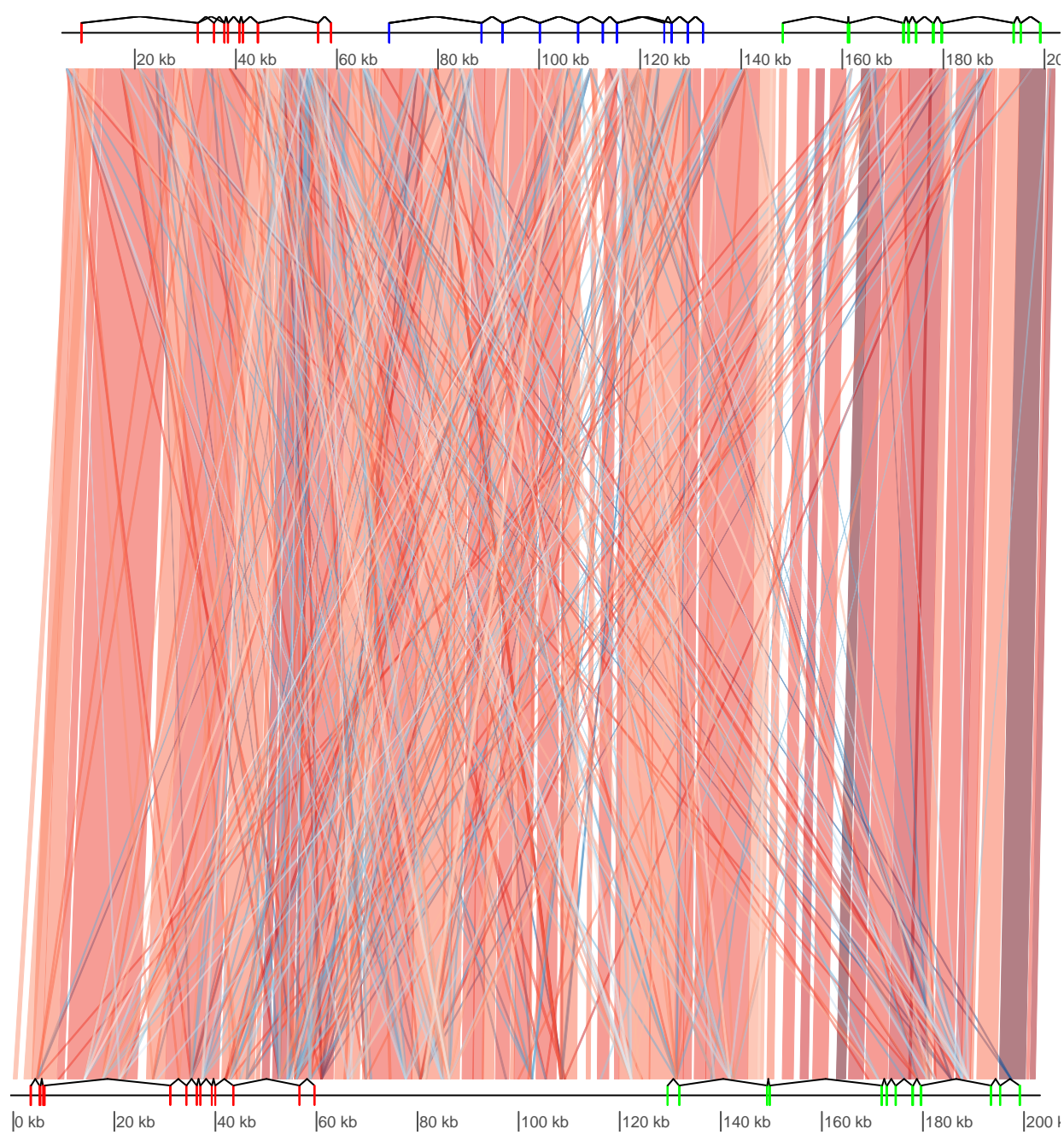
BH

BQ

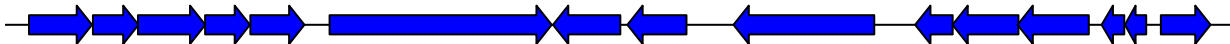
500 kb

help("barto")



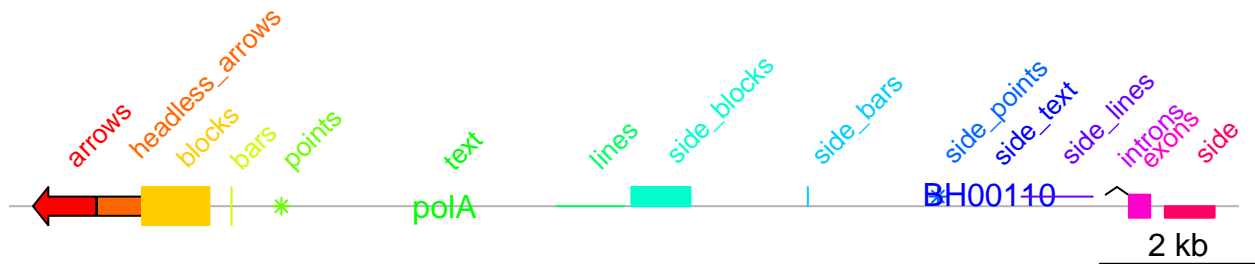
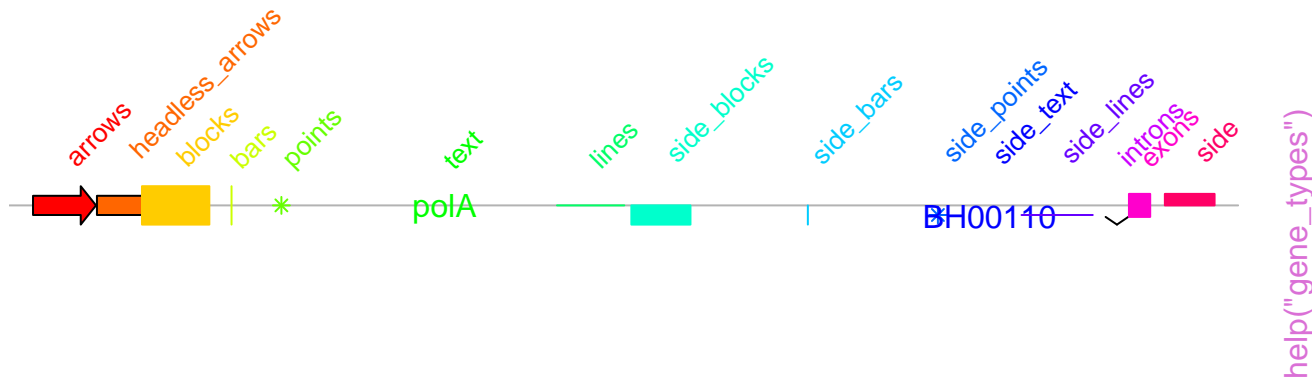


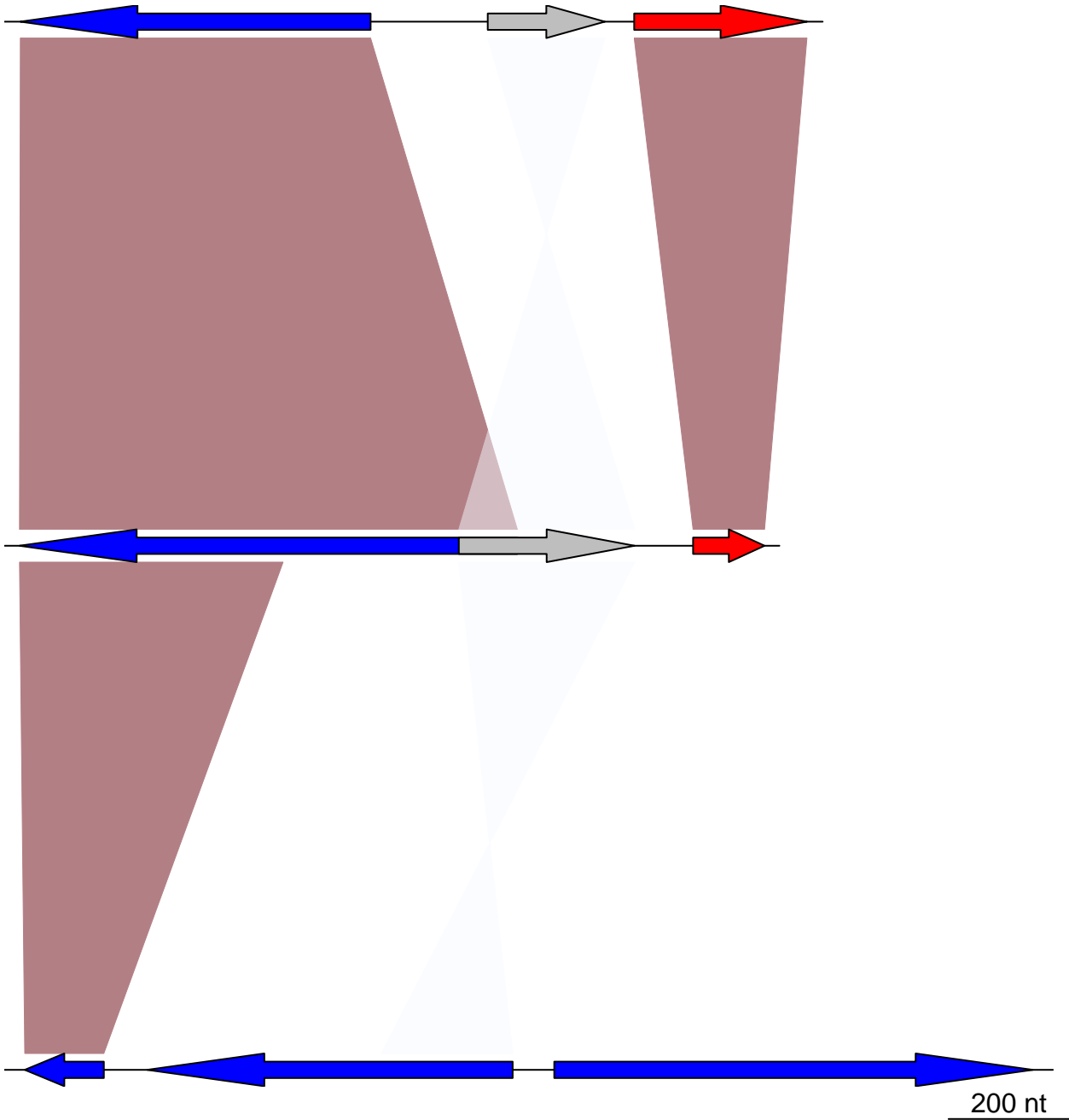
help("chrY\_subseg")



2 kb

help("gene\_types")





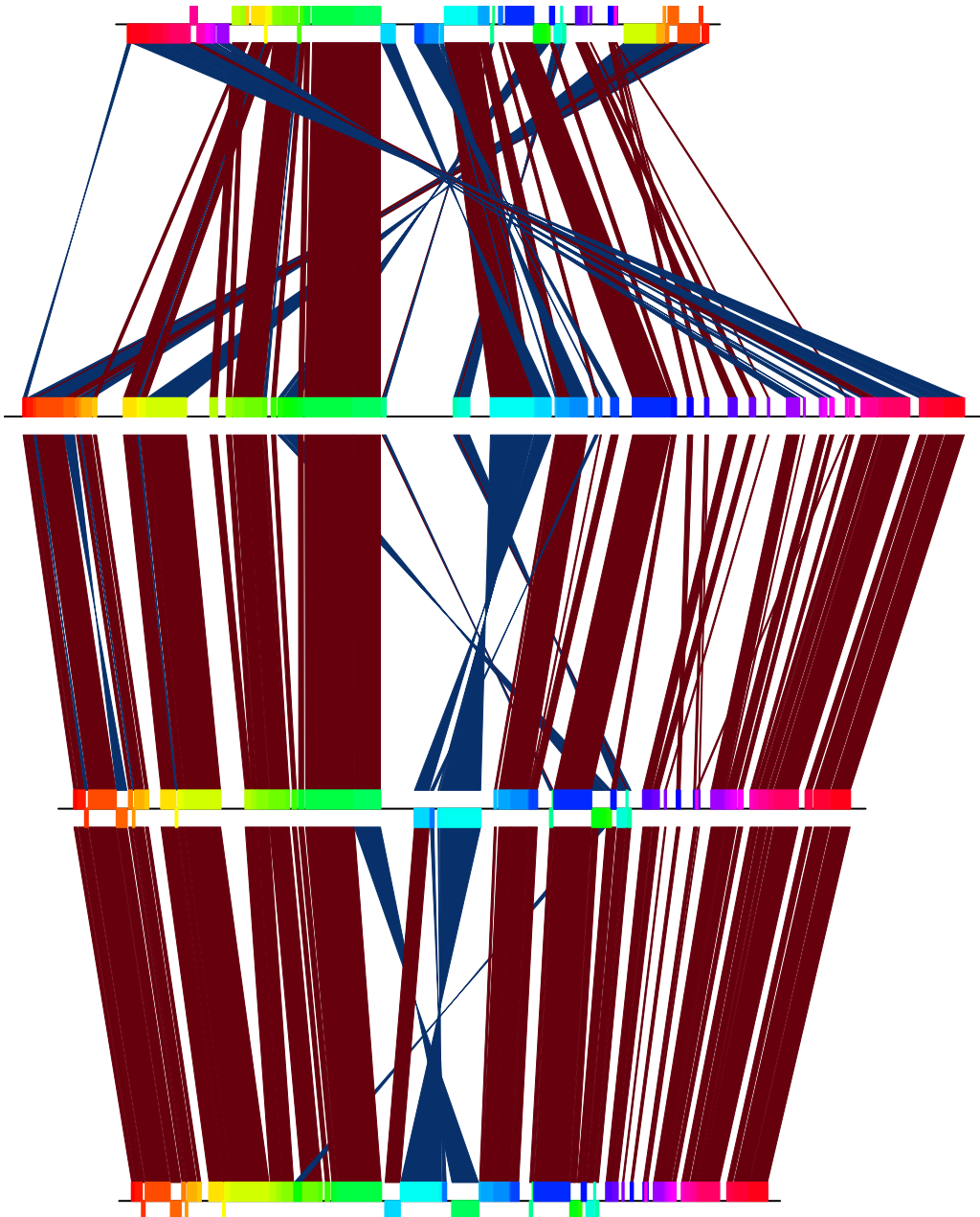
help("genoPlotR-package")

B\_bacilliformis

B\_grahamii

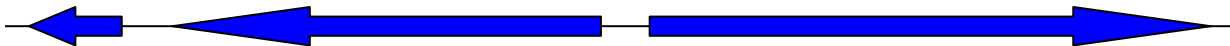
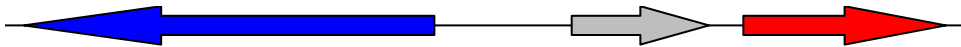
B\_henselae

B\_quintana



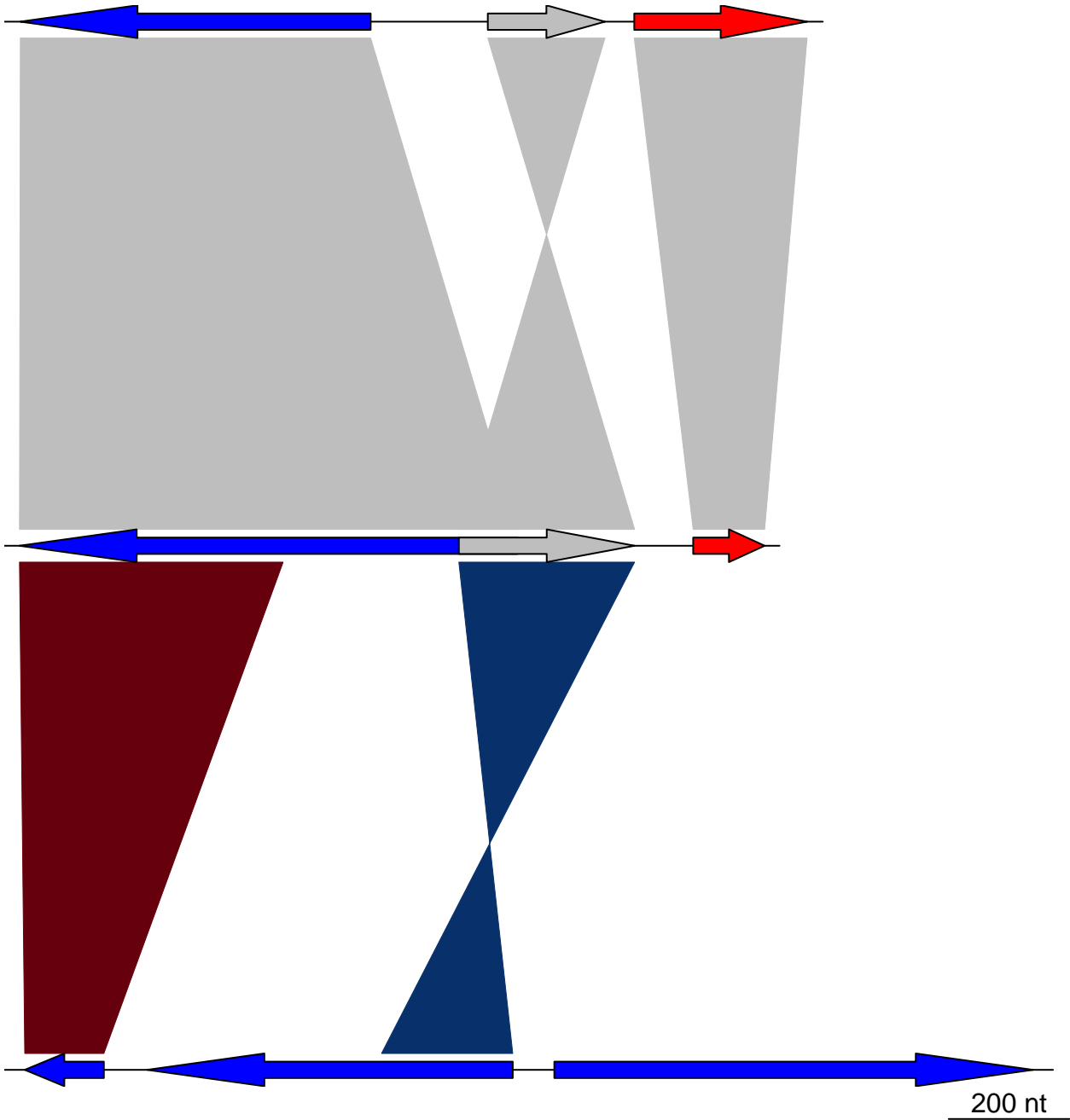
help("mauve.bbone")



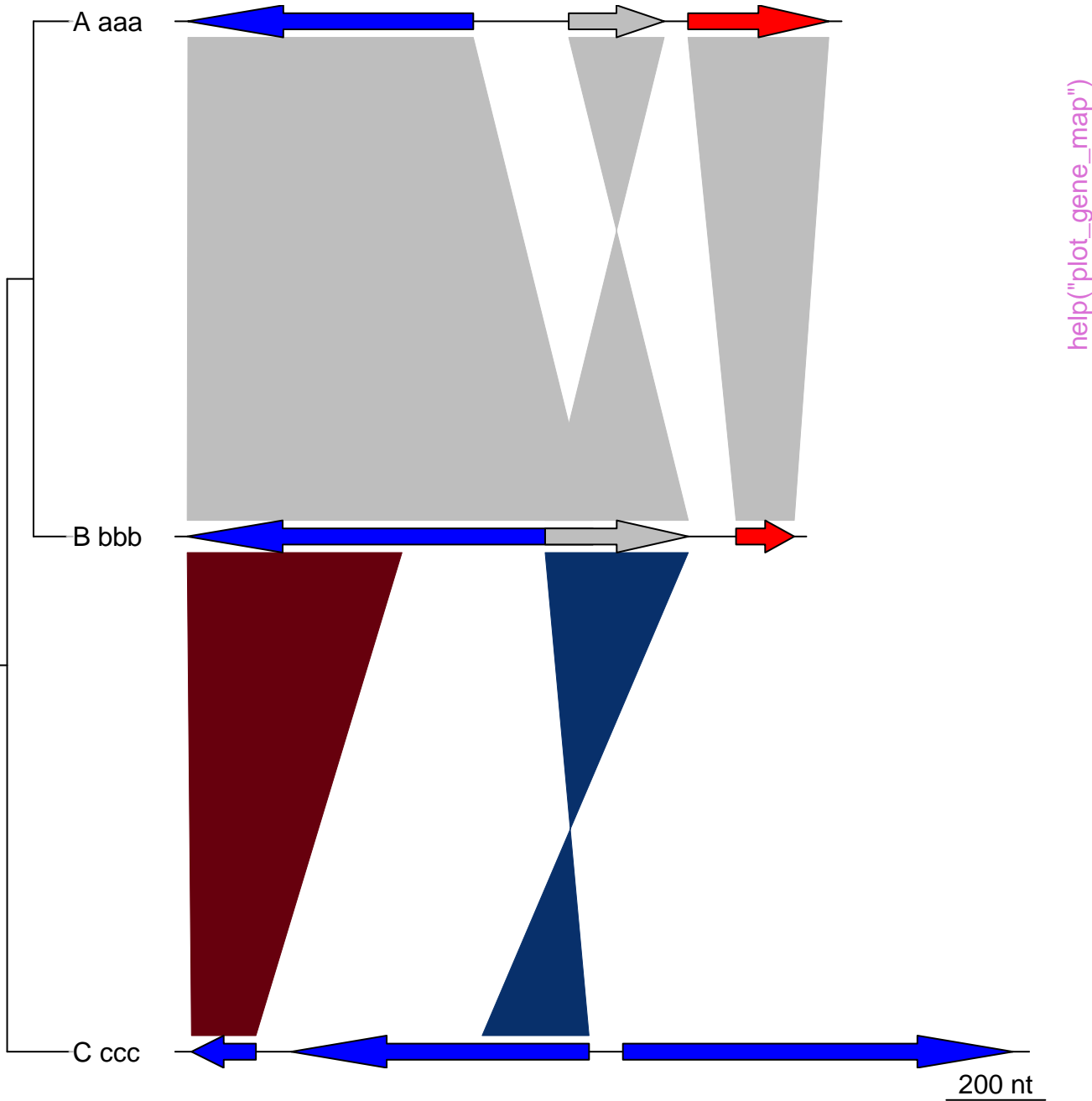


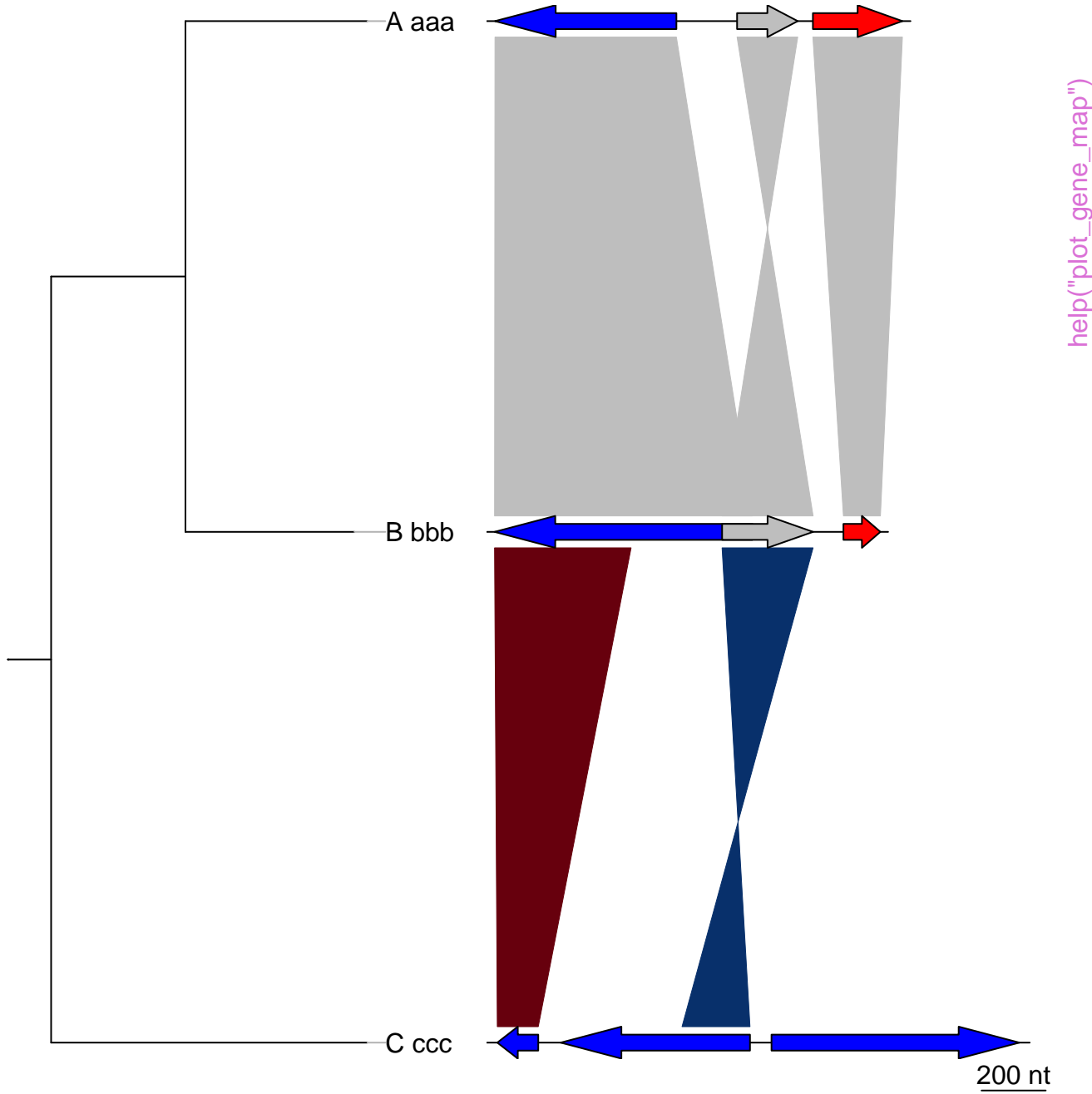
200 nt

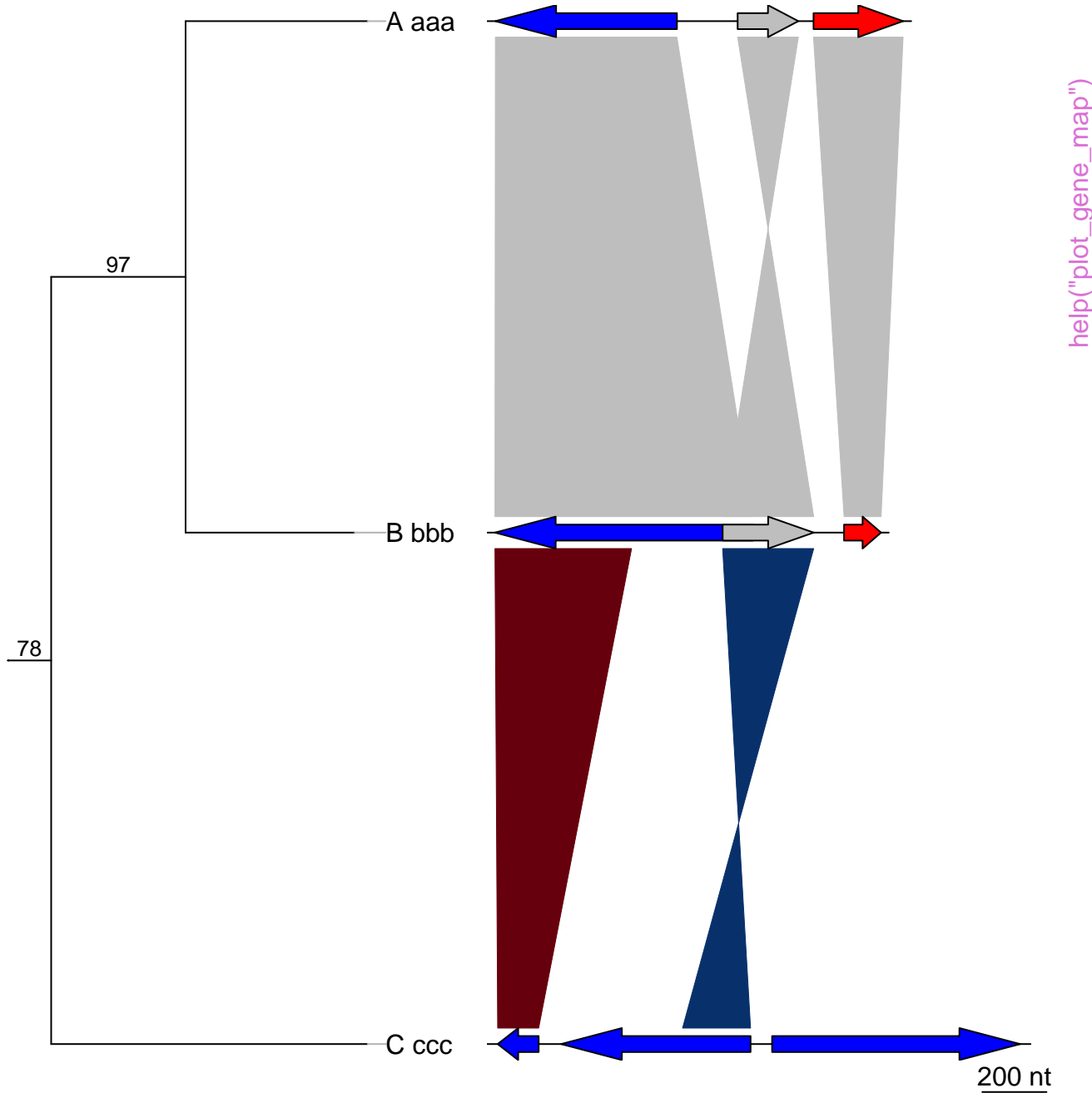
help("plot\_gene\_map")

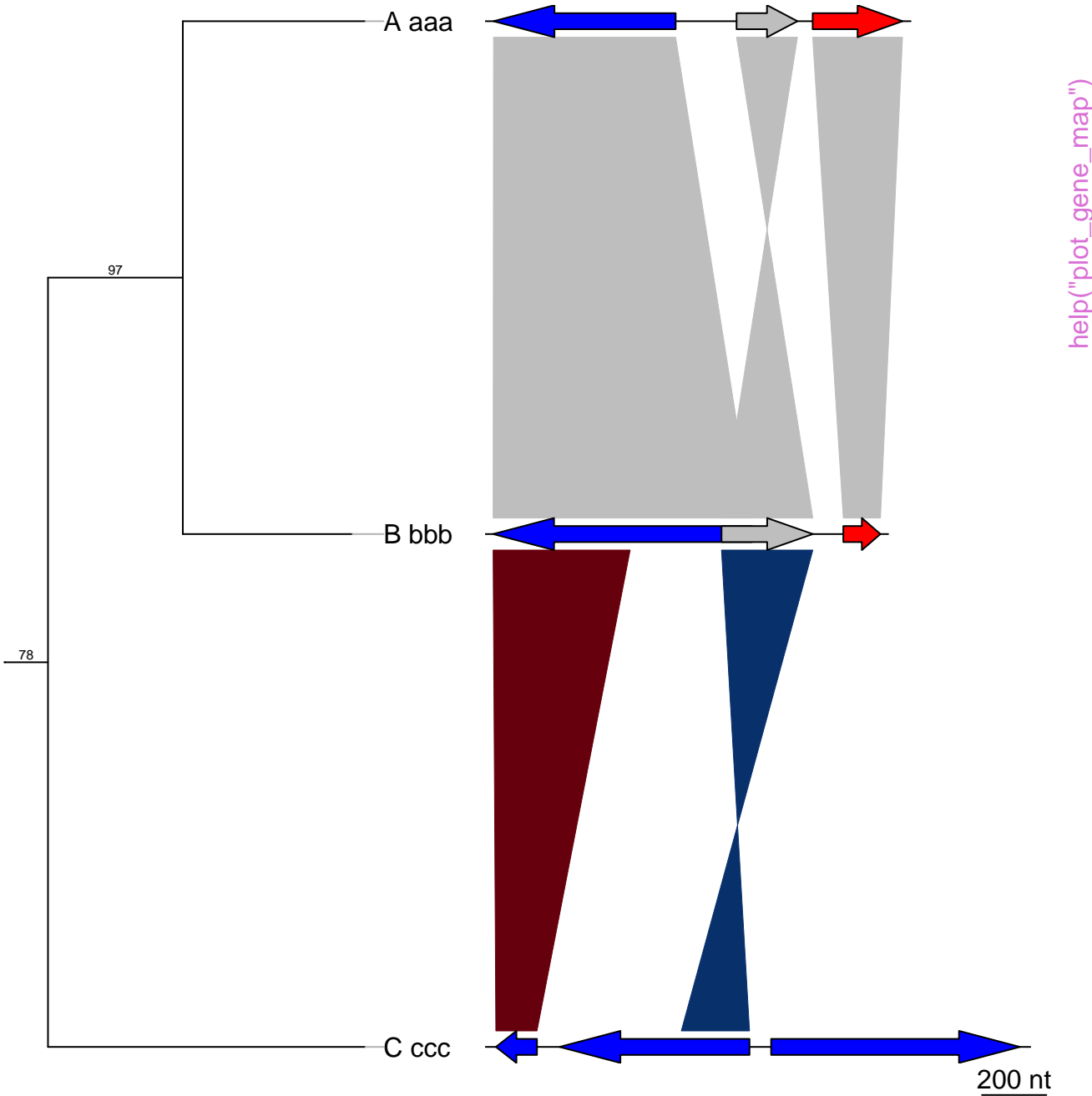


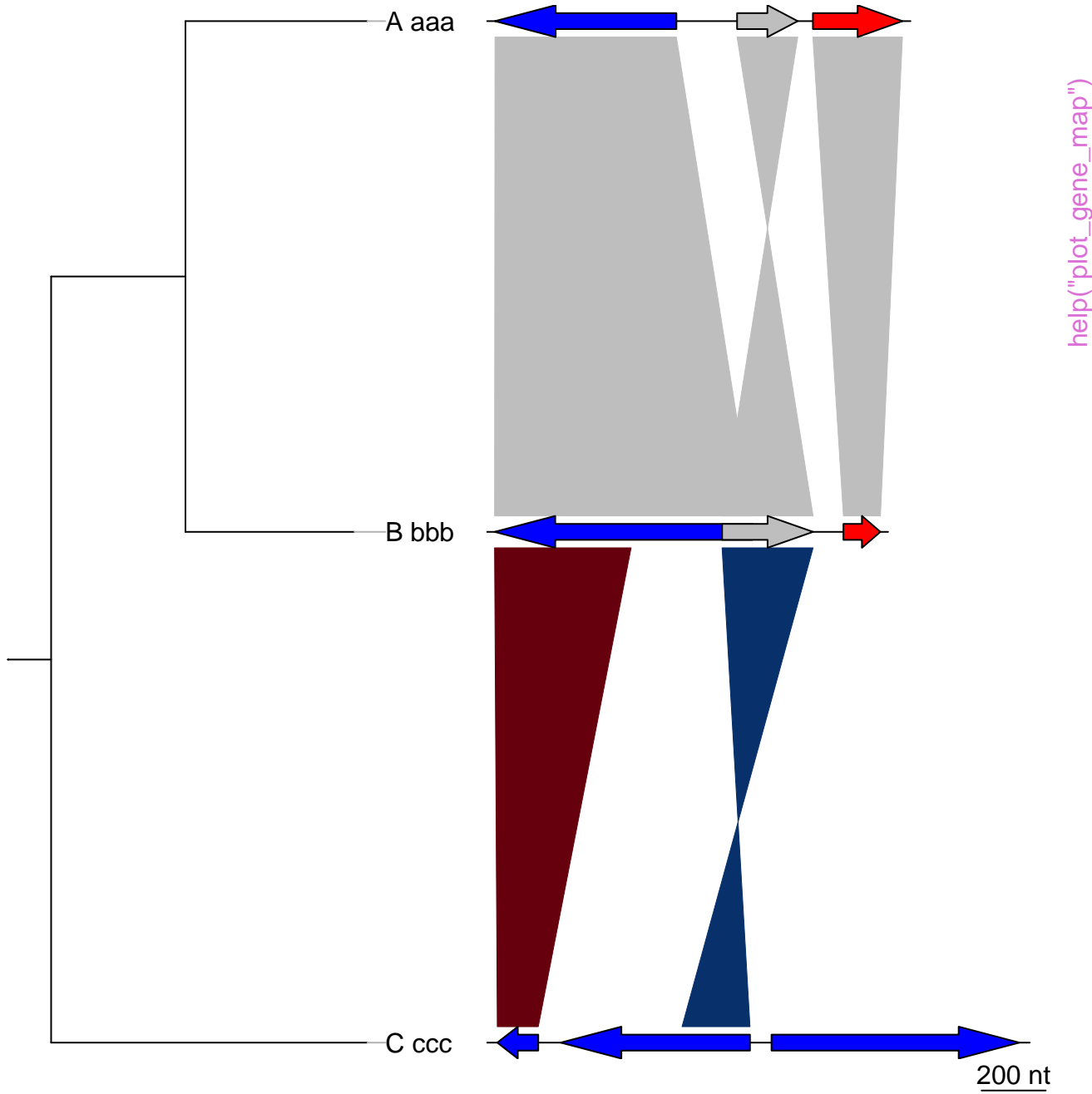
help("plot\_gene\_map")

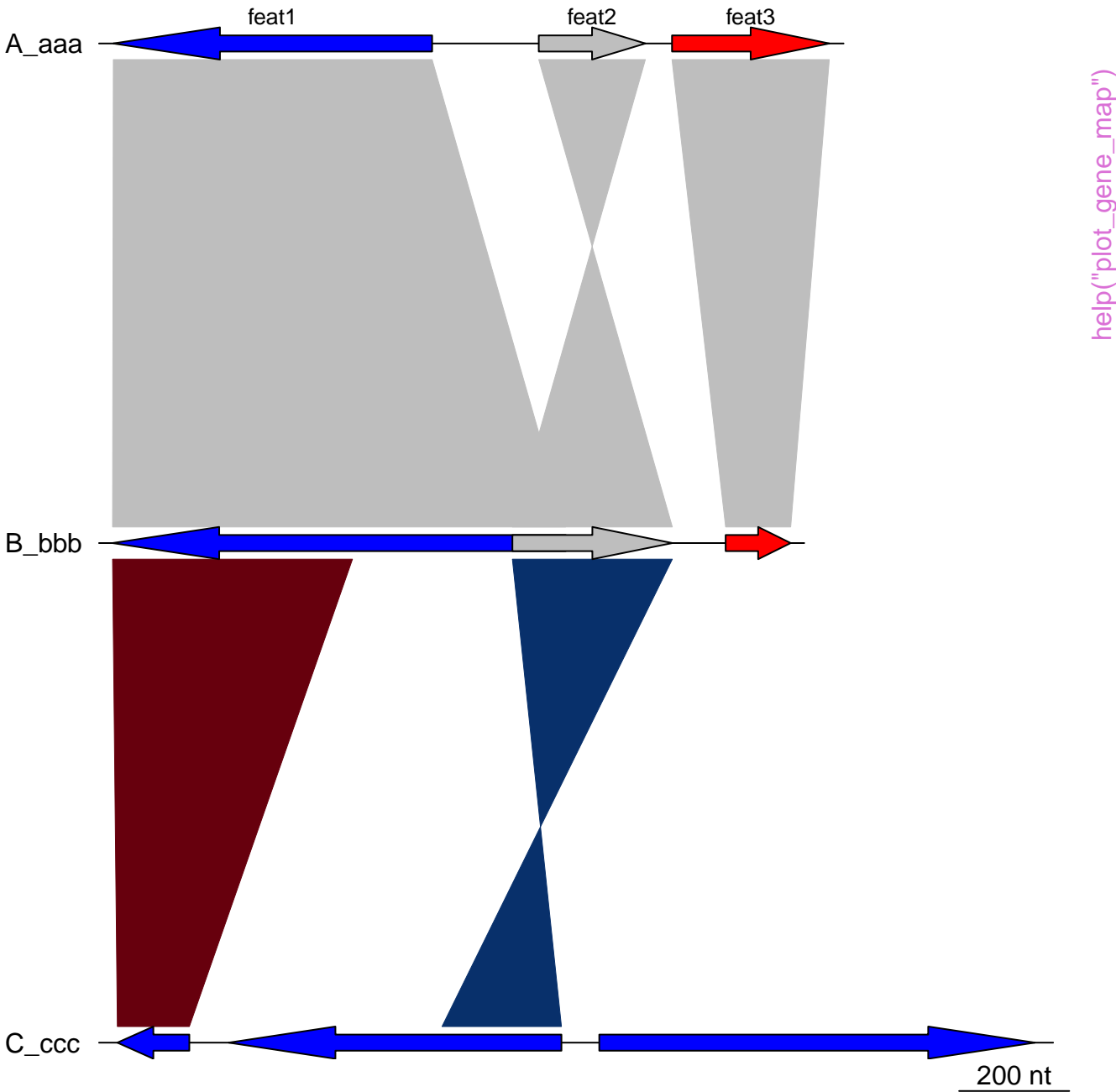




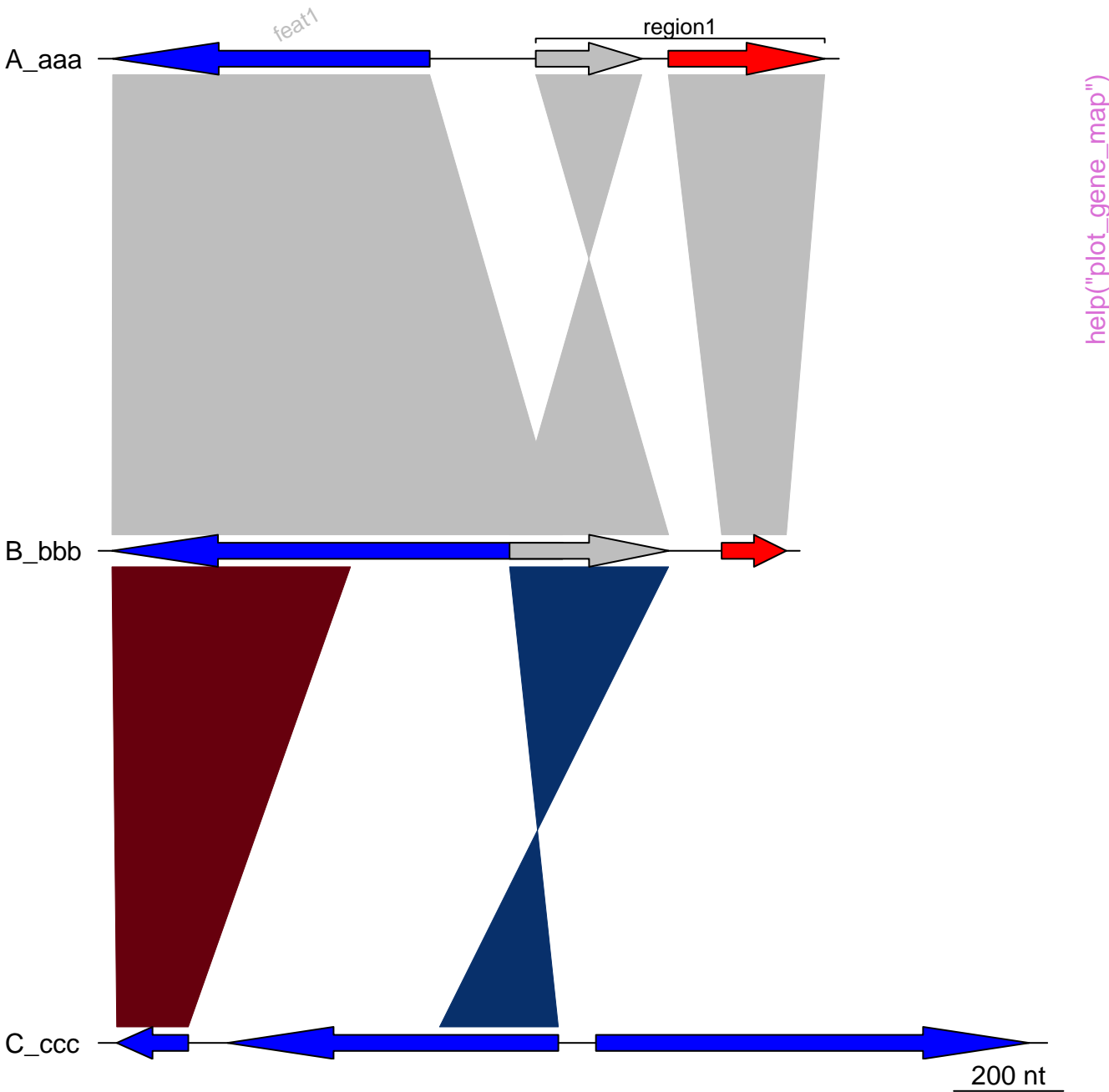


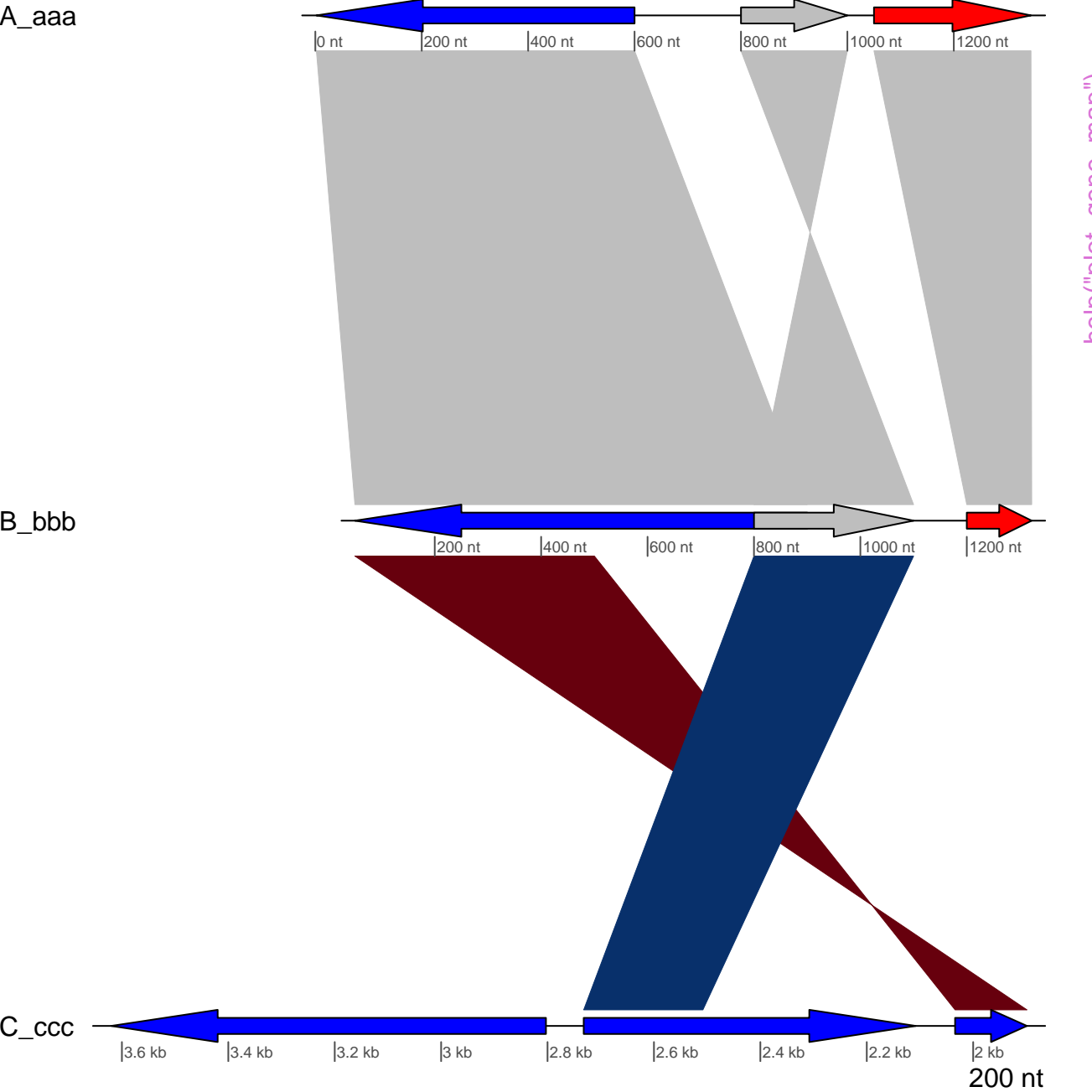


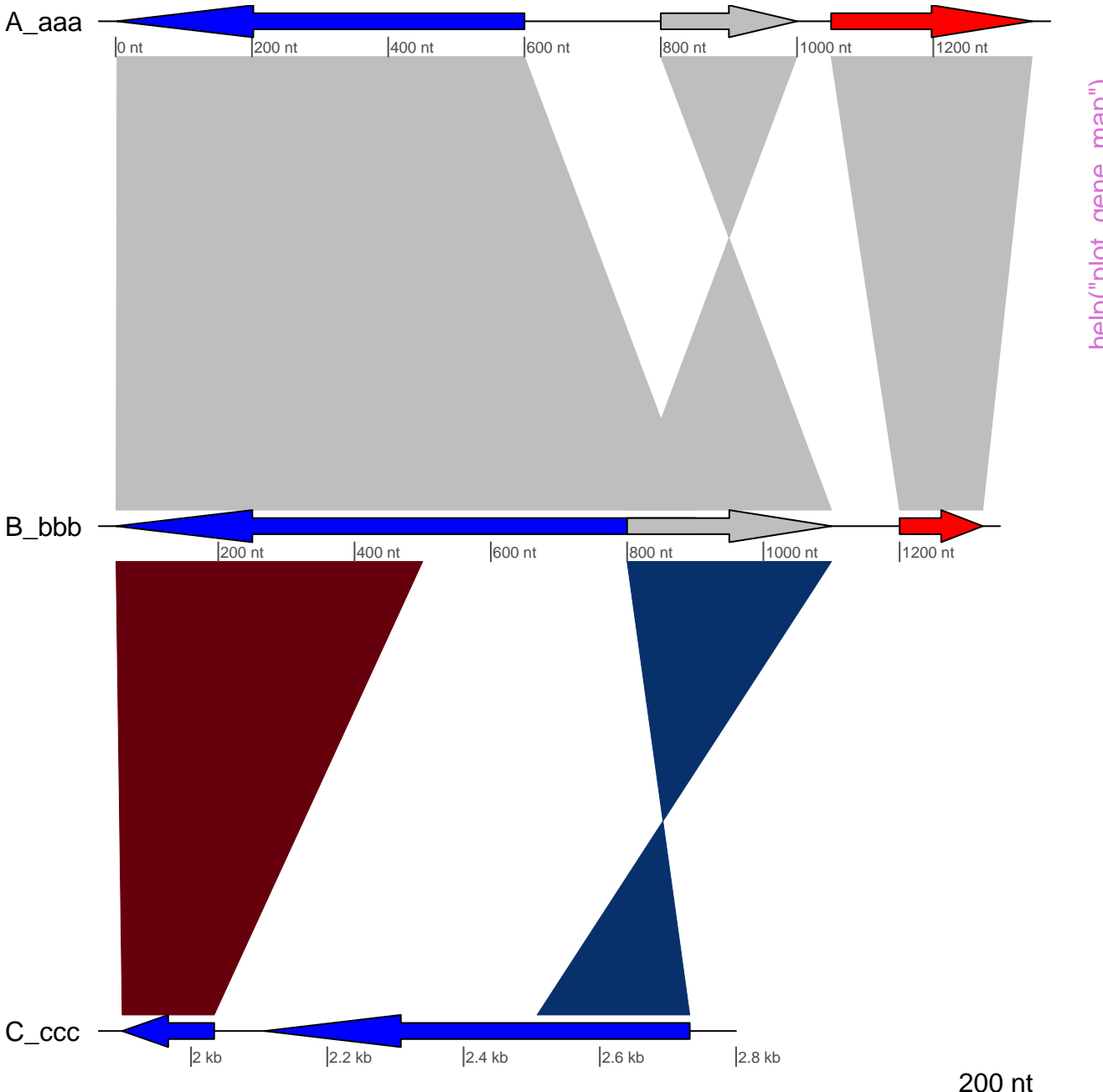




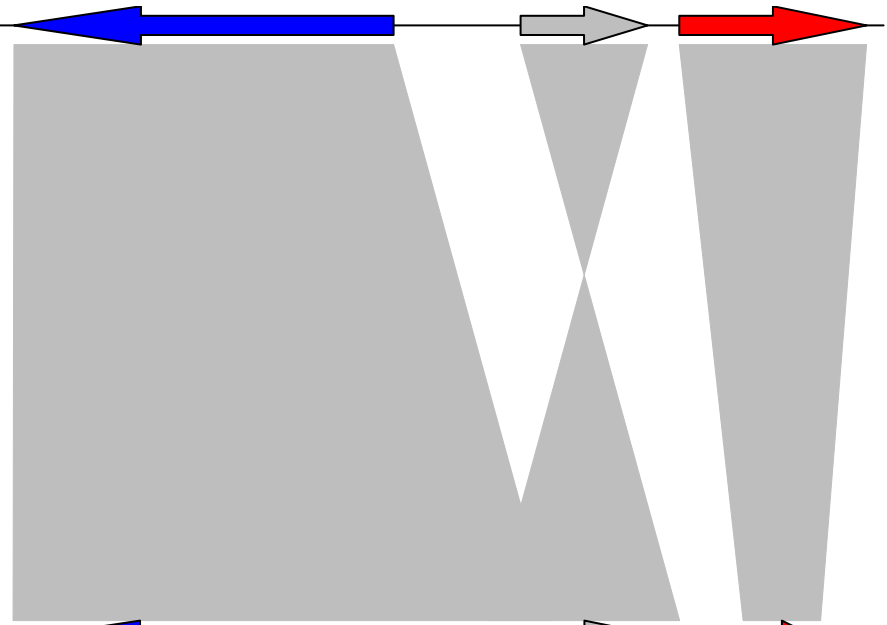




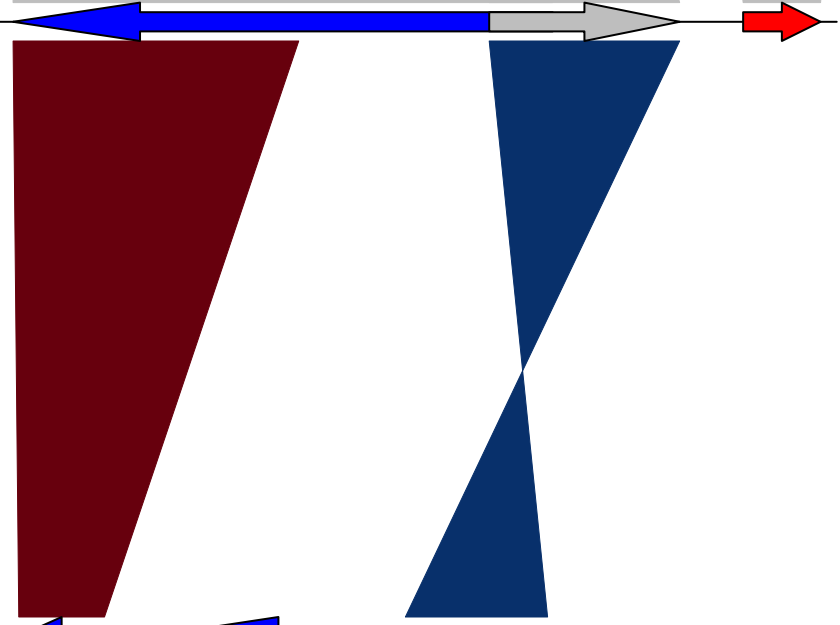




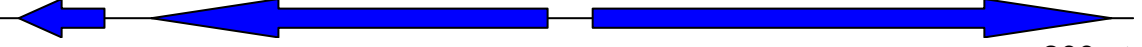
A\_aaa



B\_bbb



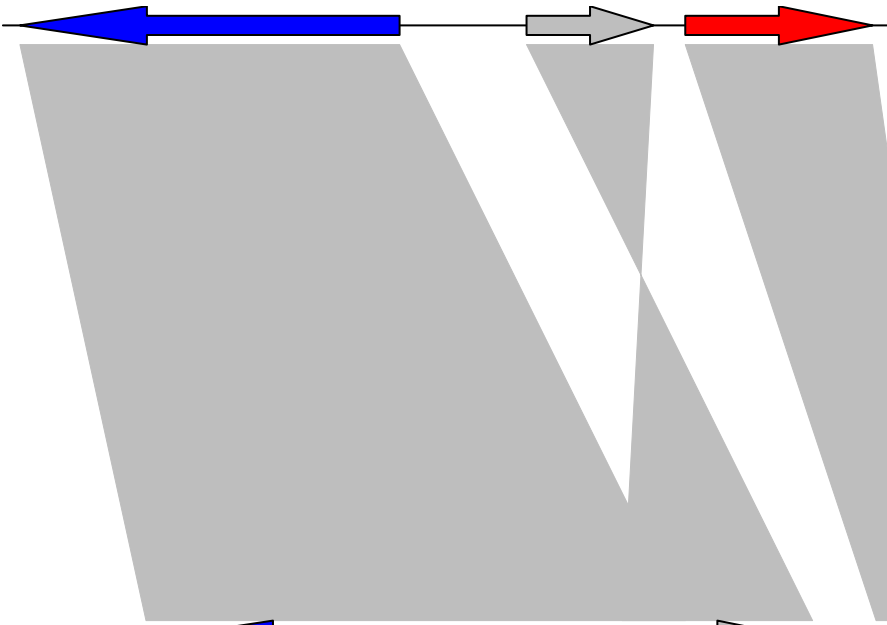
C\_ccc



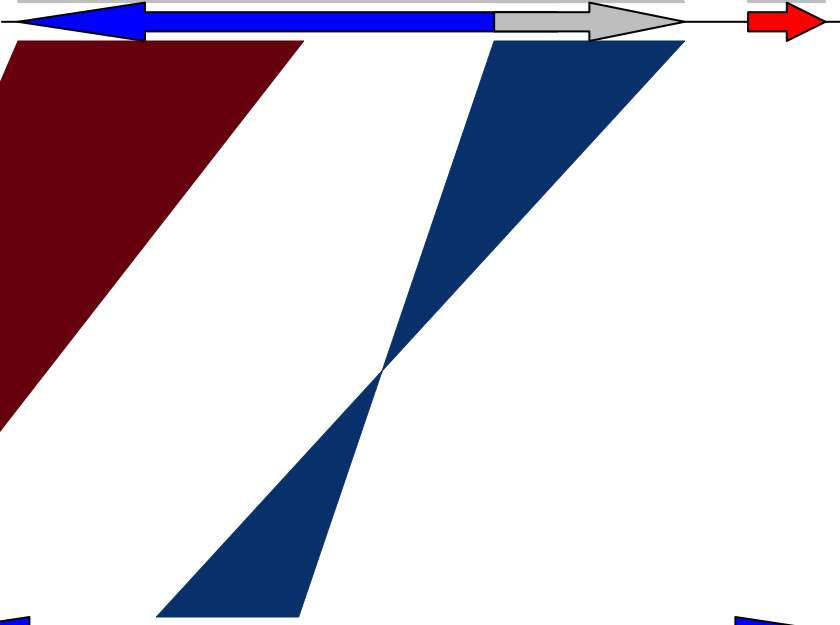
200 nt

help("plot\_gene\_map")

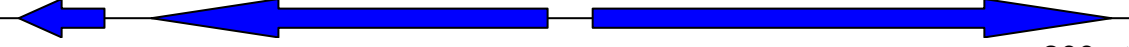
A\_aaa



B\_bbb



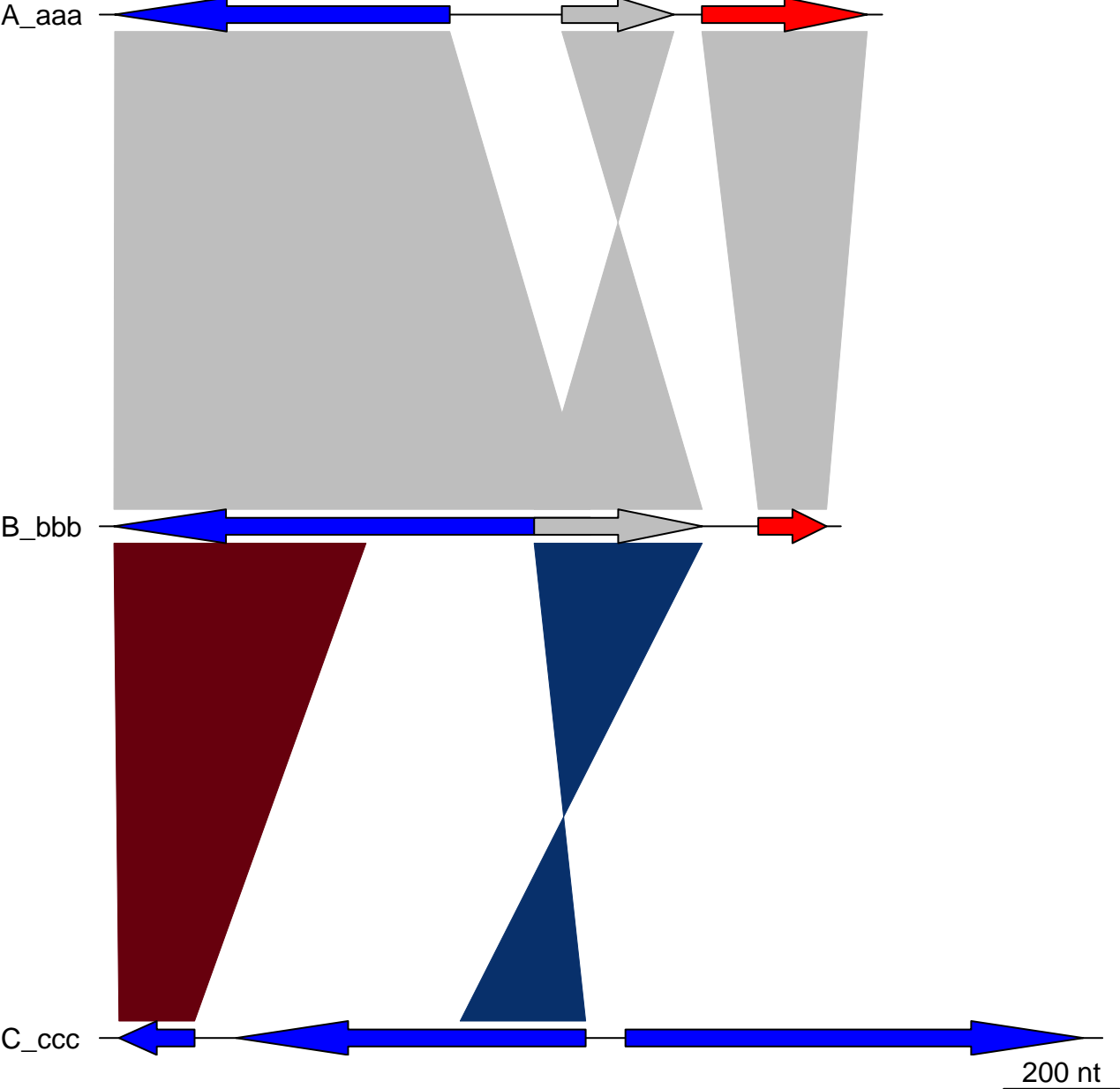
C\_ccc



200 nt

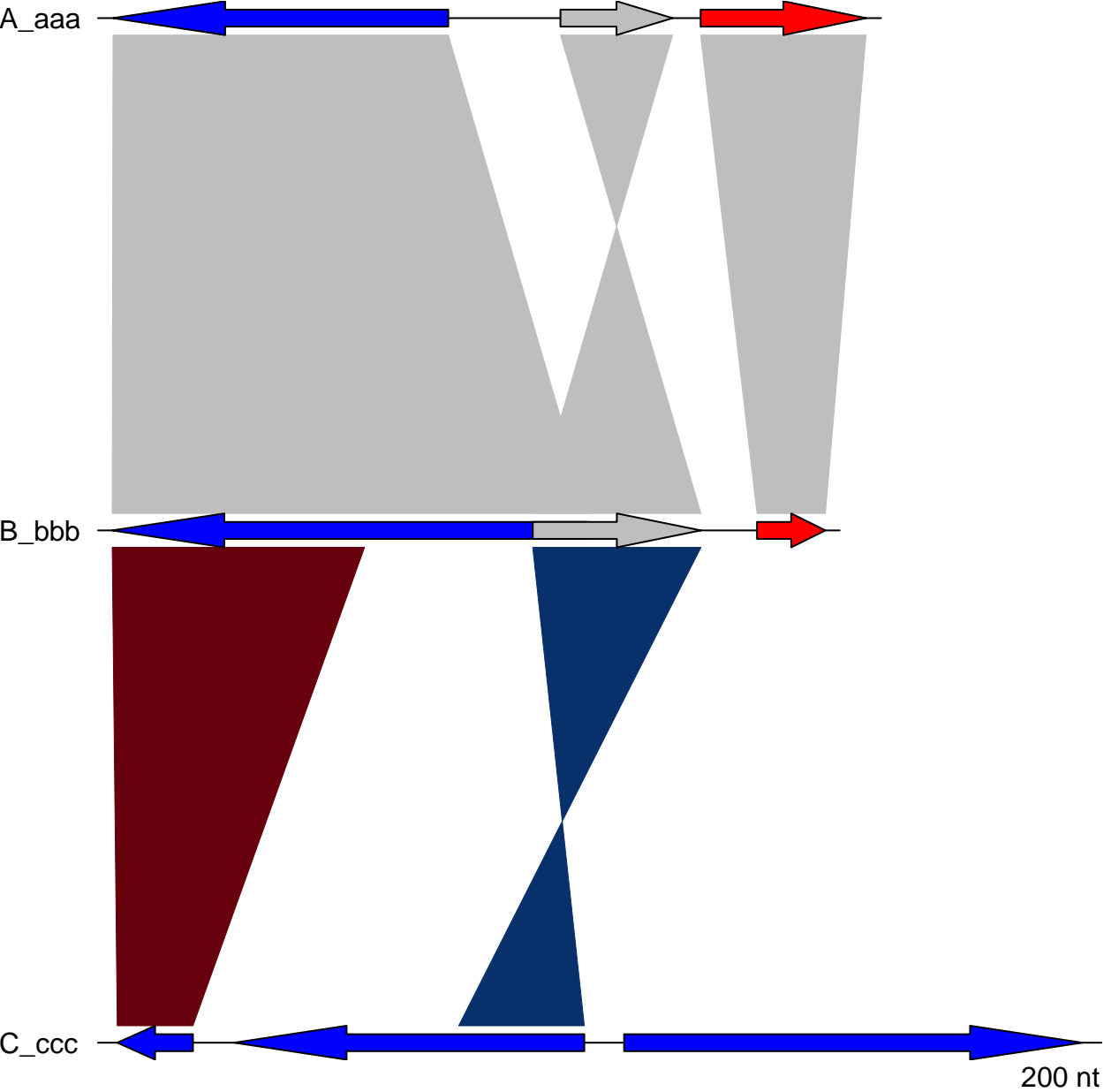
help("plot\_gene\_map")

Comparison of A, B and C



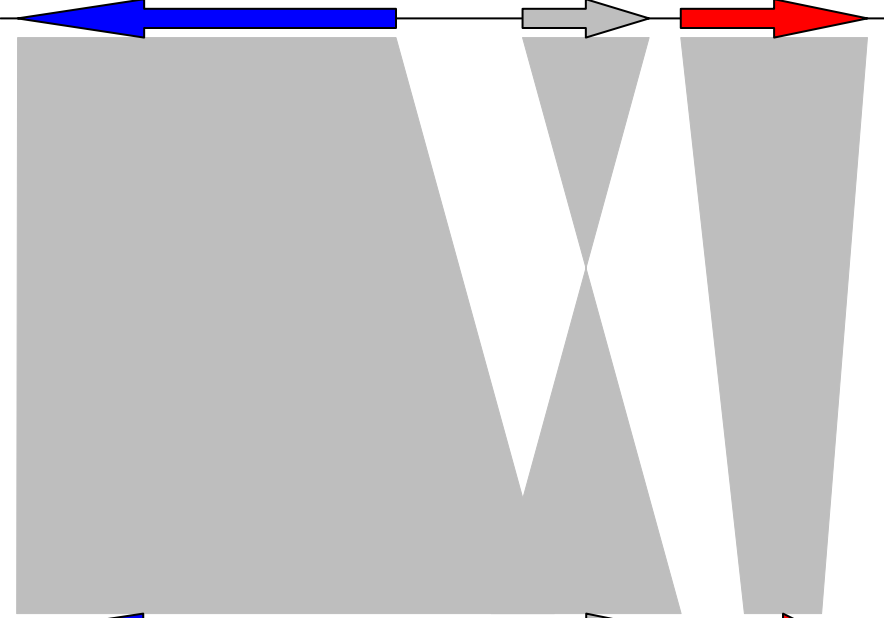
help("plot\_gene\_map")

Comparison of A, B and C

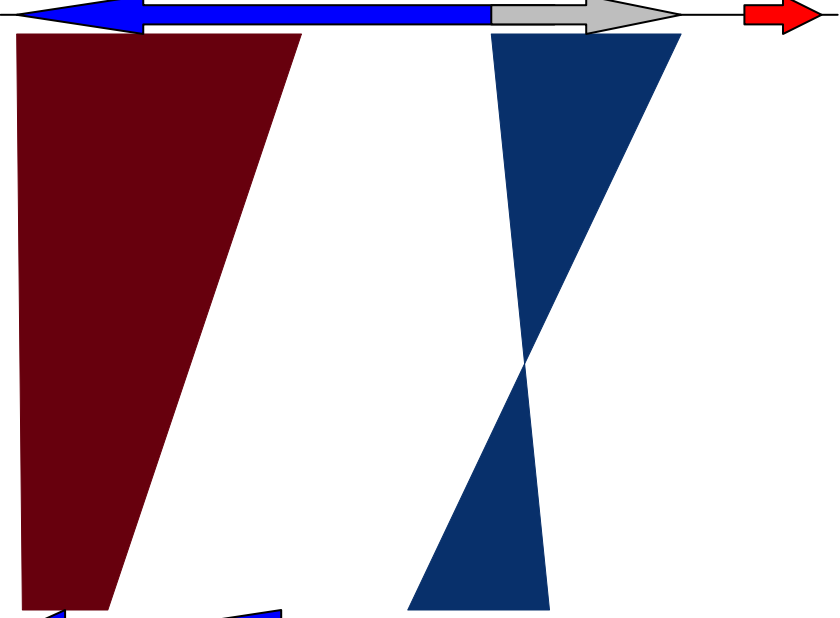


help("plot\_gene\_map")

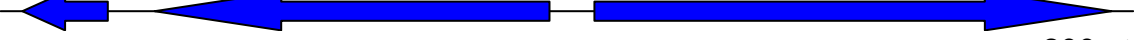
Huey



Dewey



Louie



200 nt

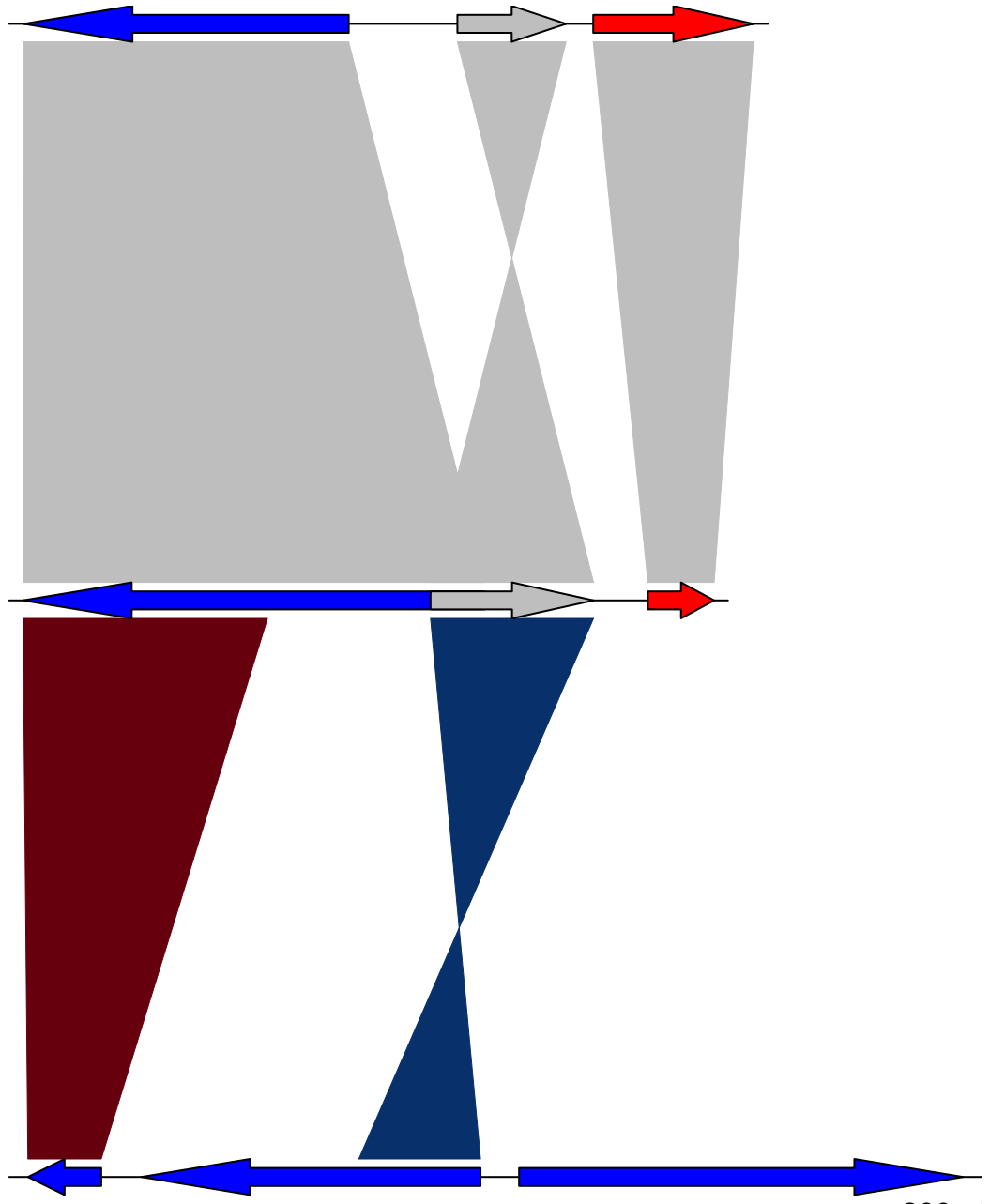
help("plot\_gene\_map")



Huey

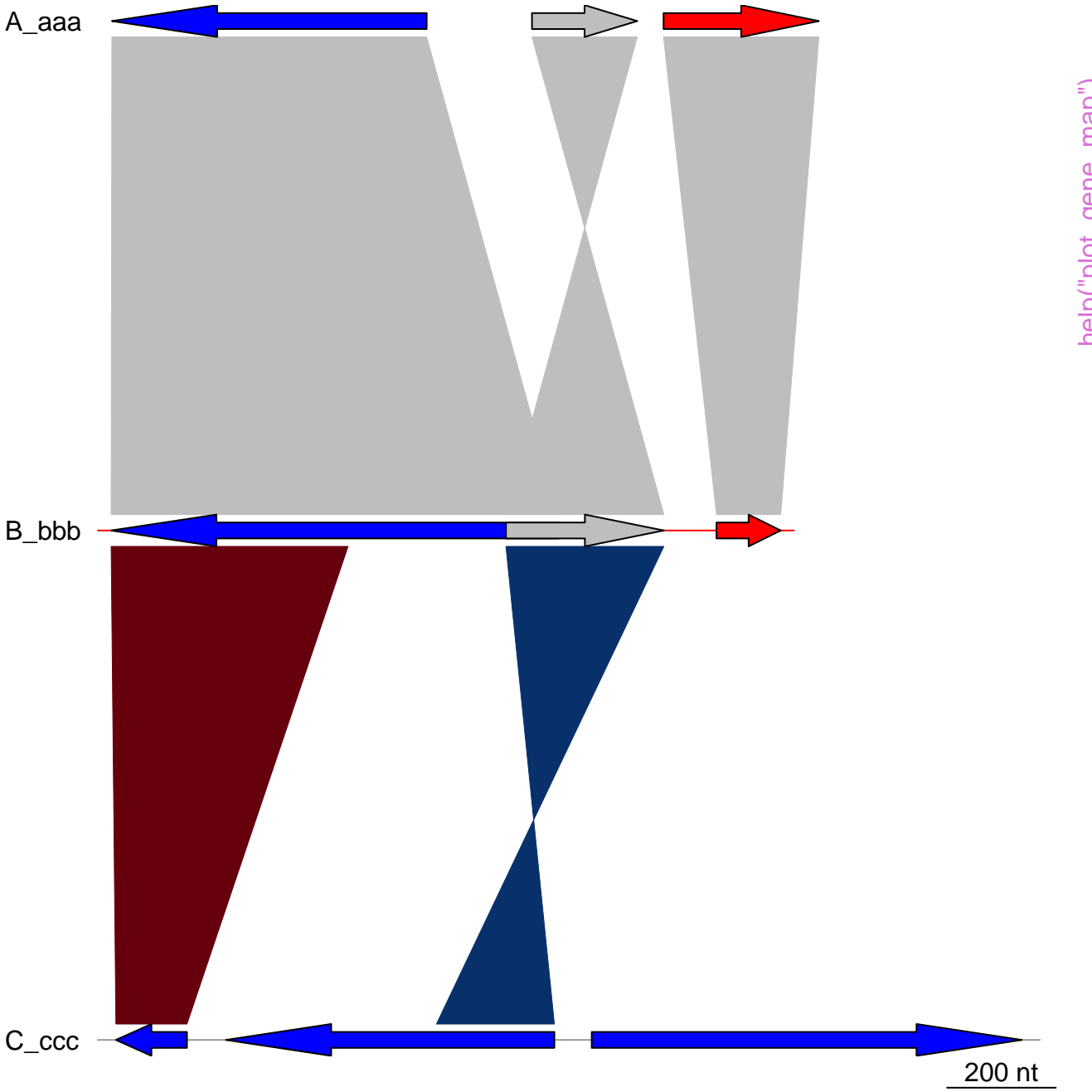
Dewey

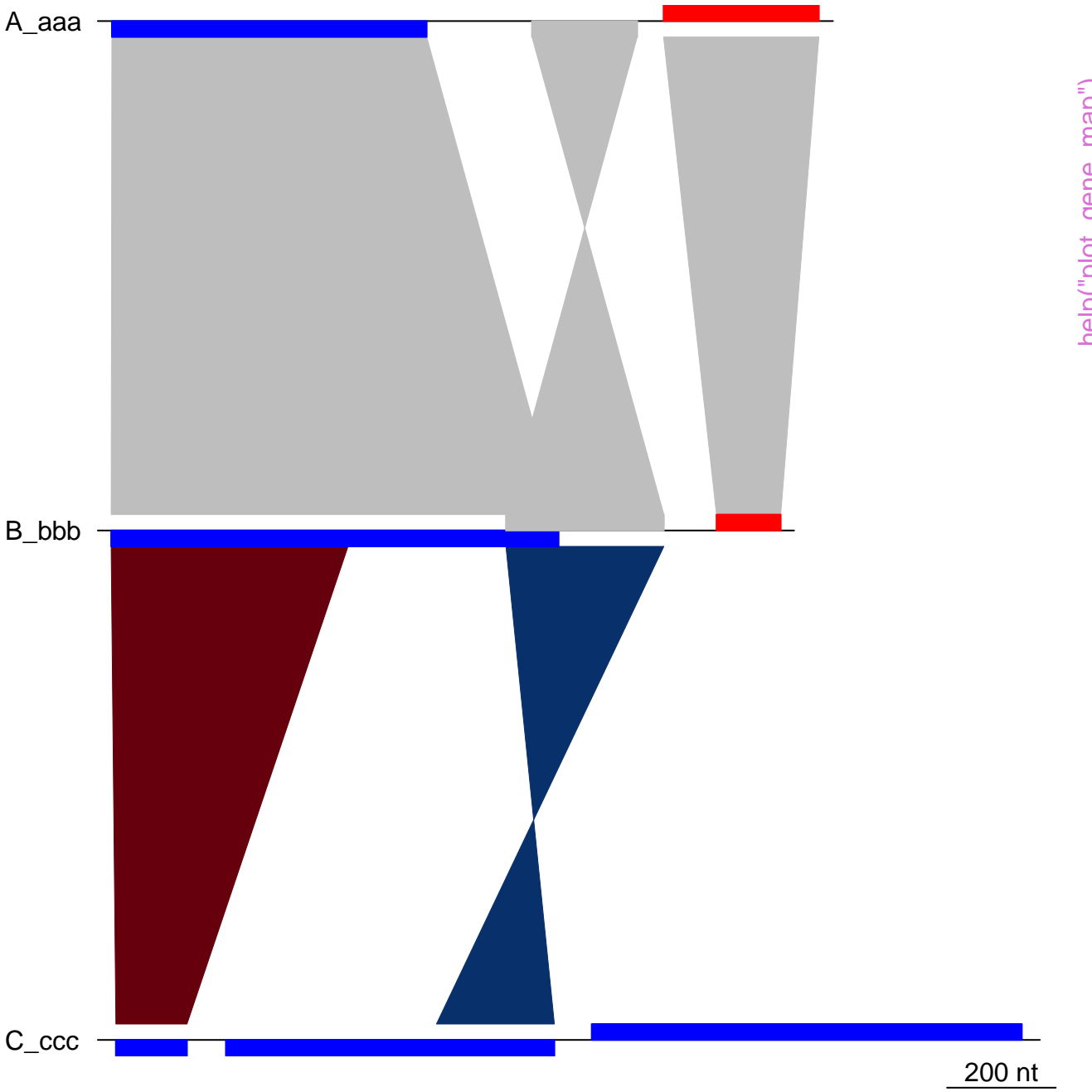
Louie

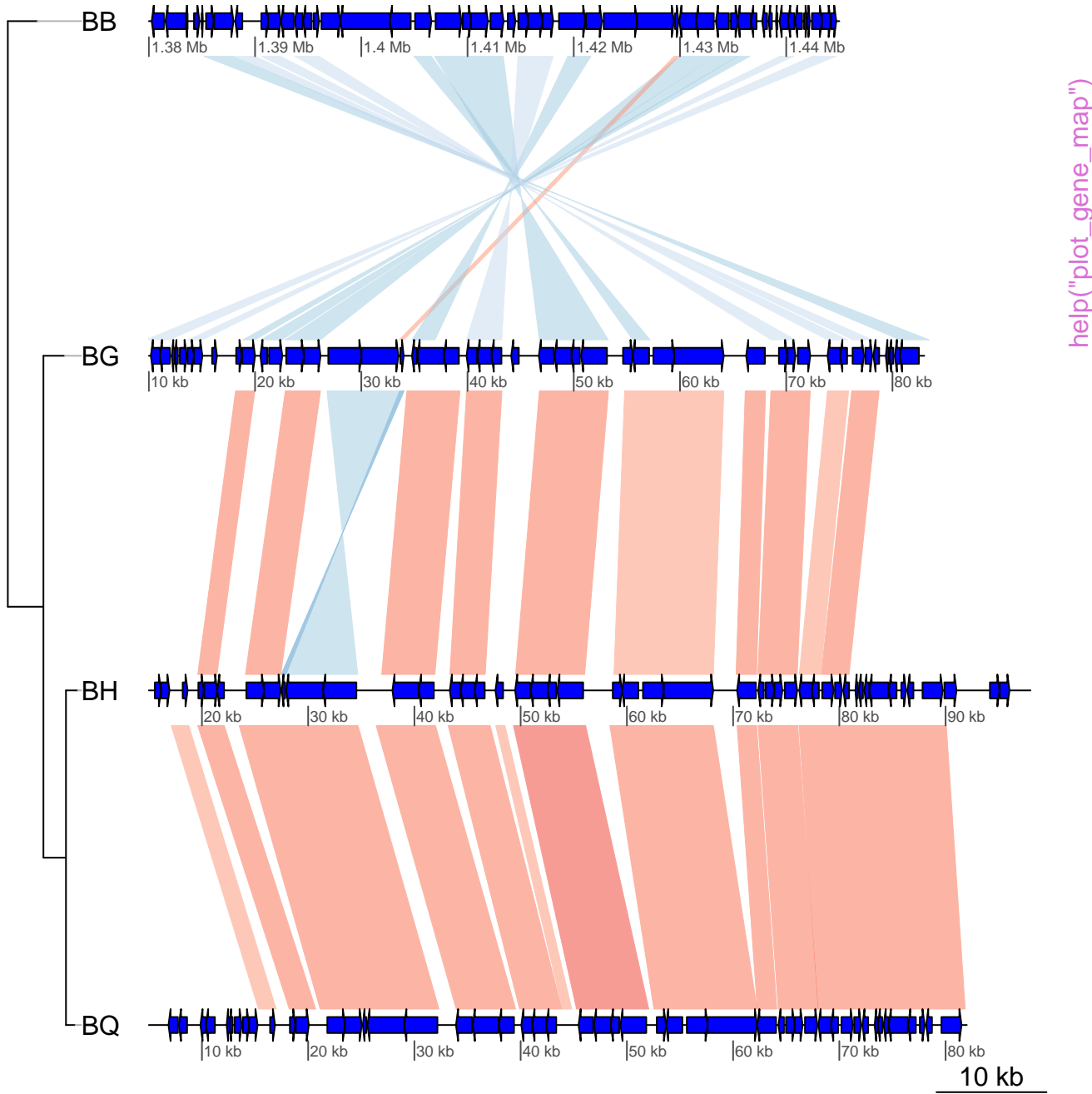


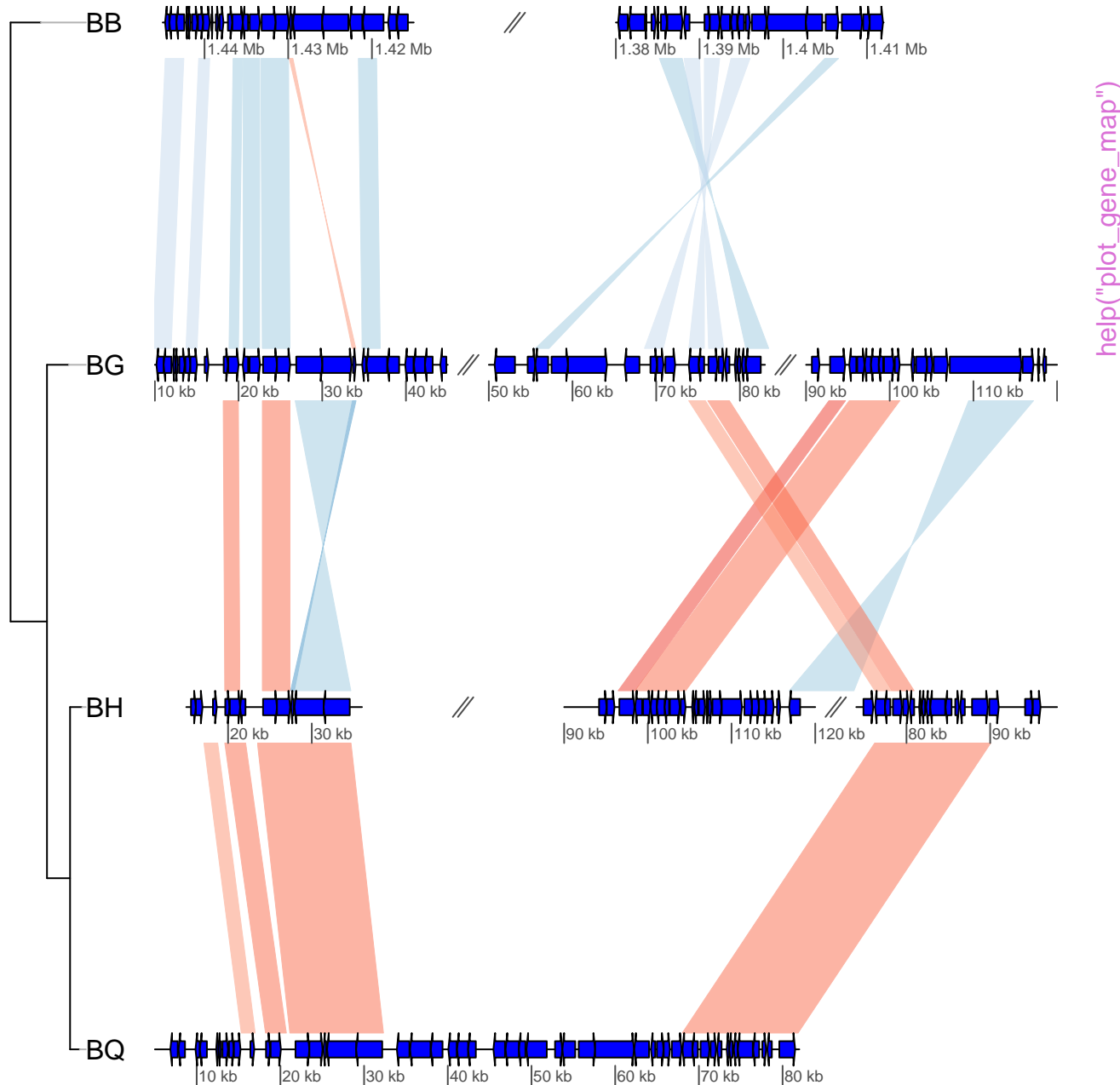
help("plot\_gene\_map")

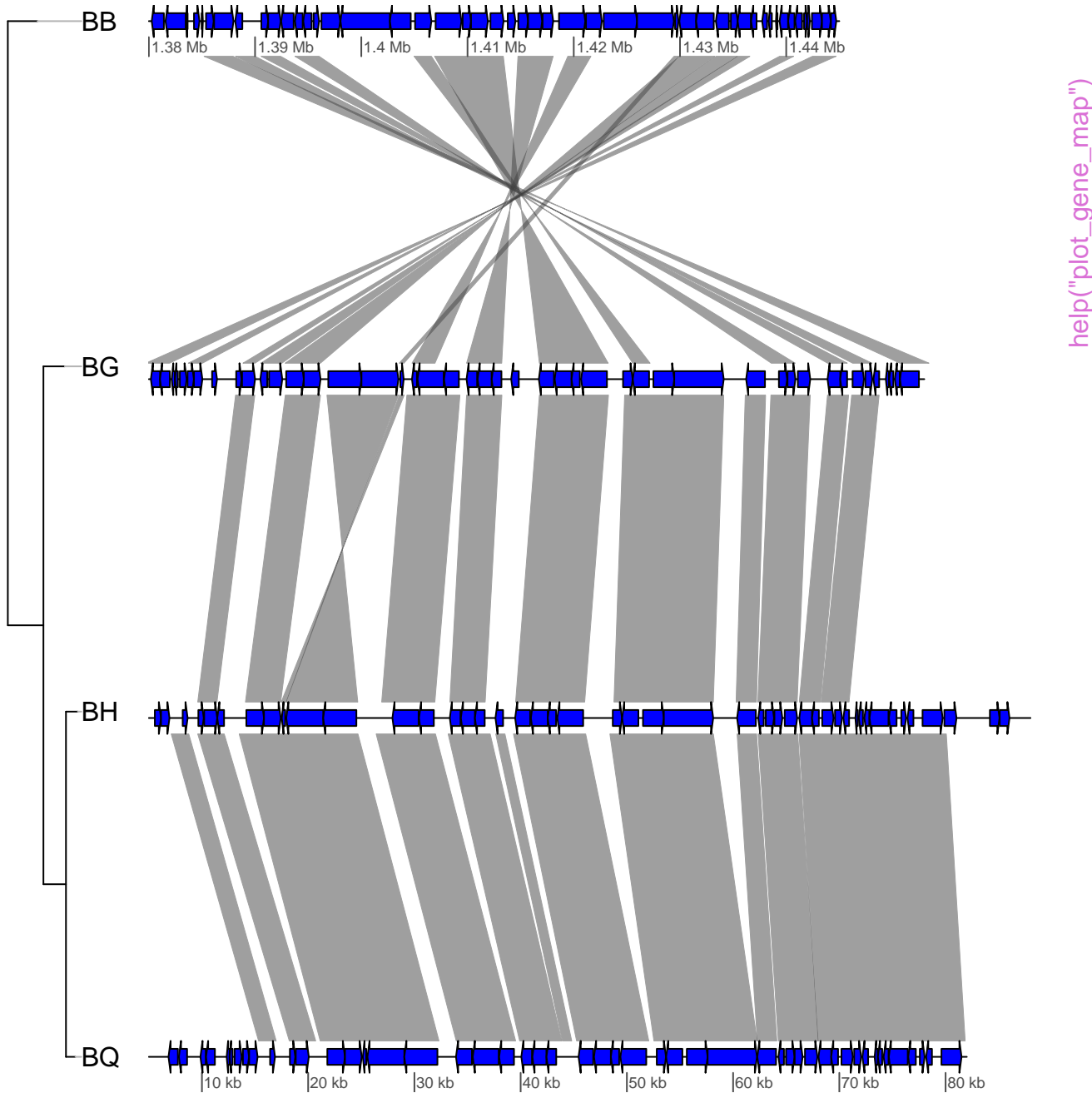
200 nt

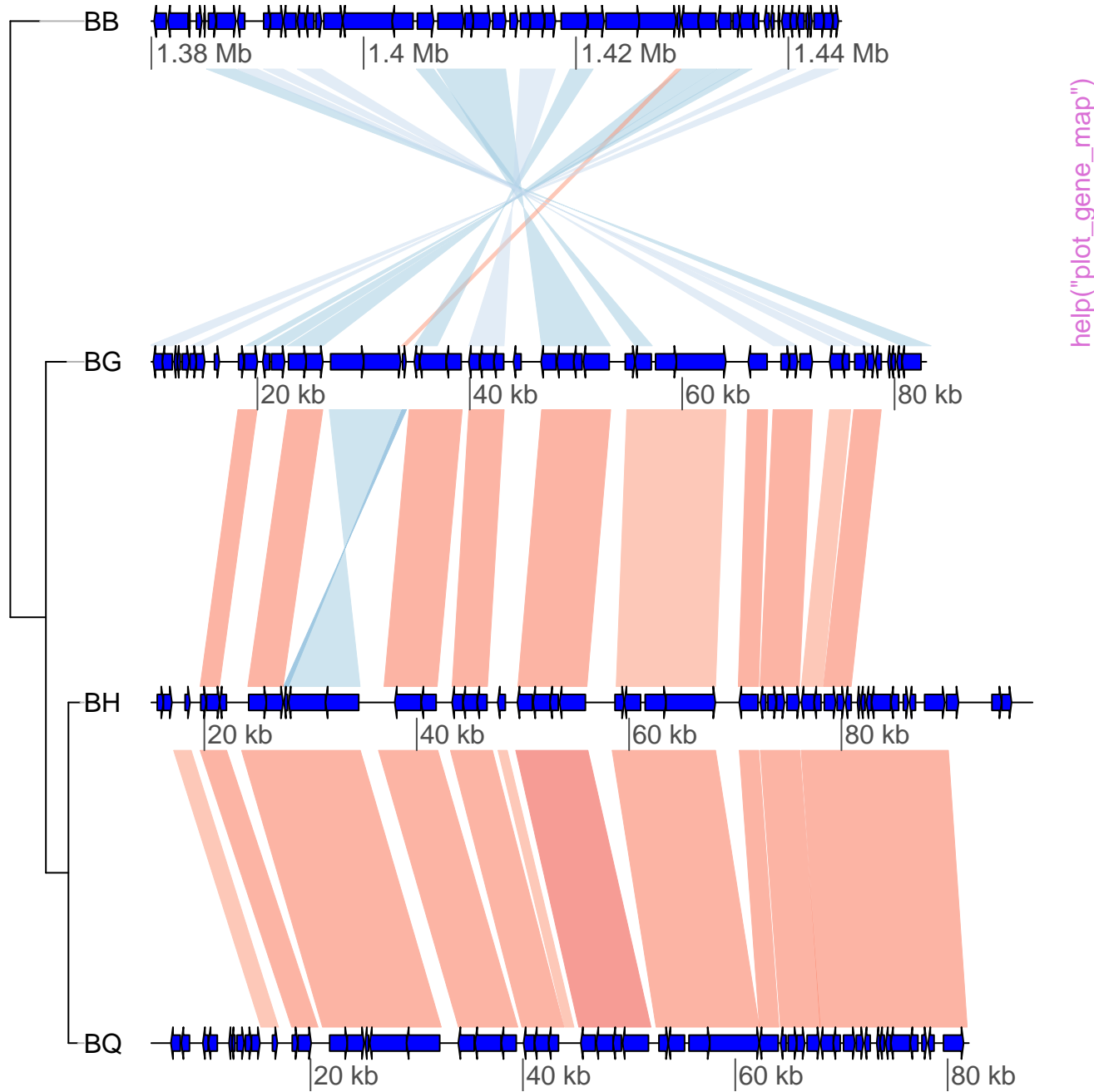




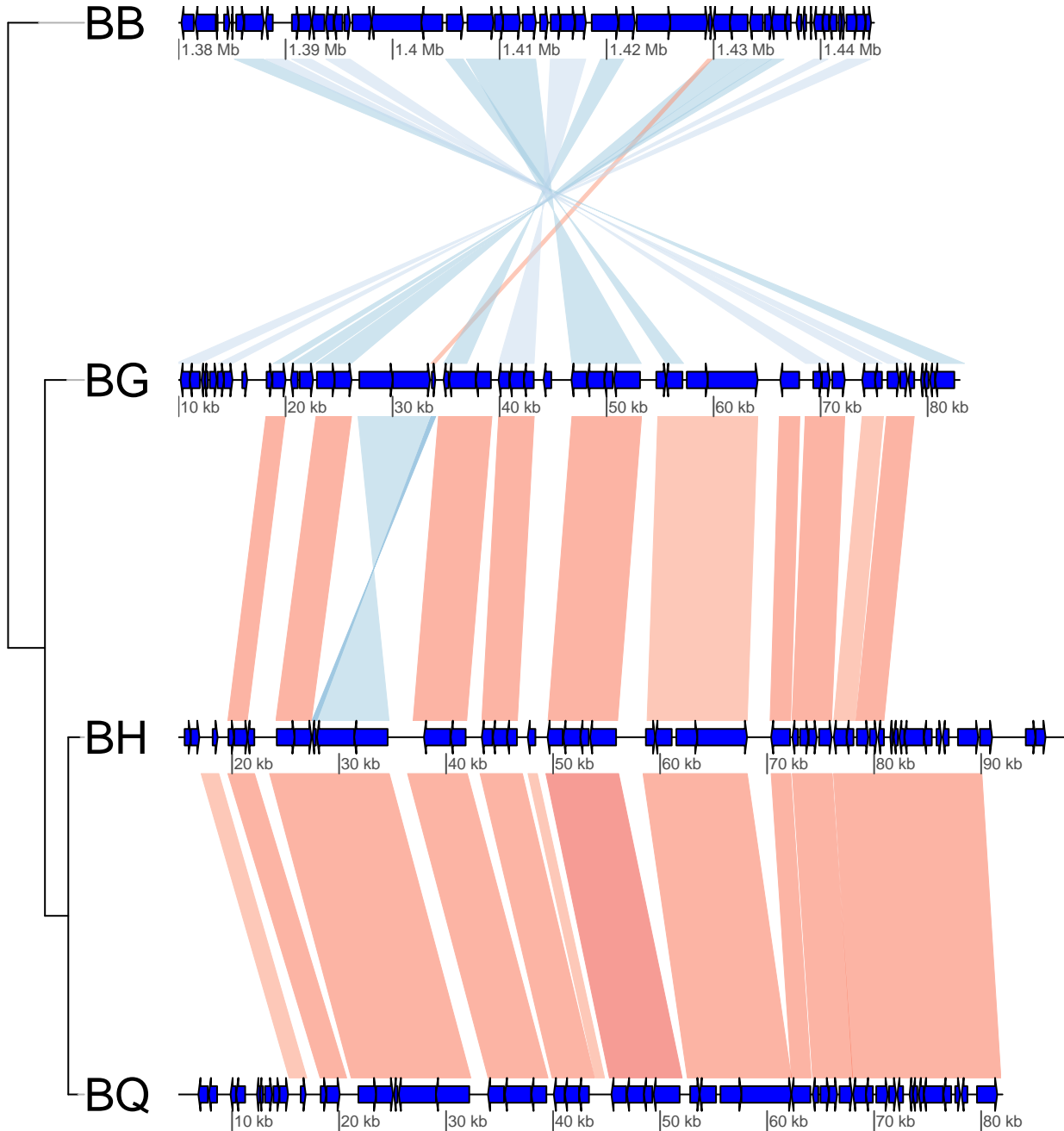




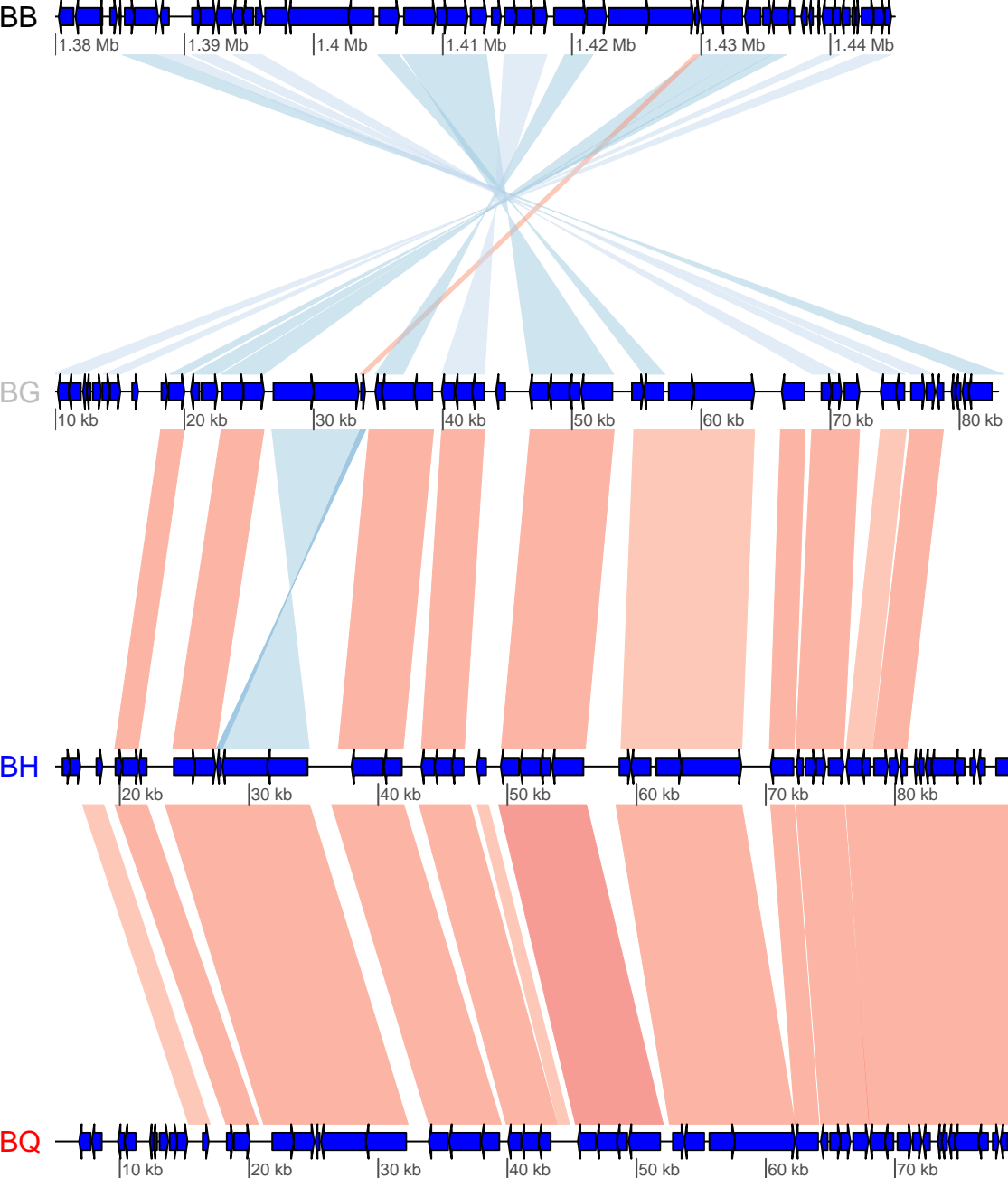




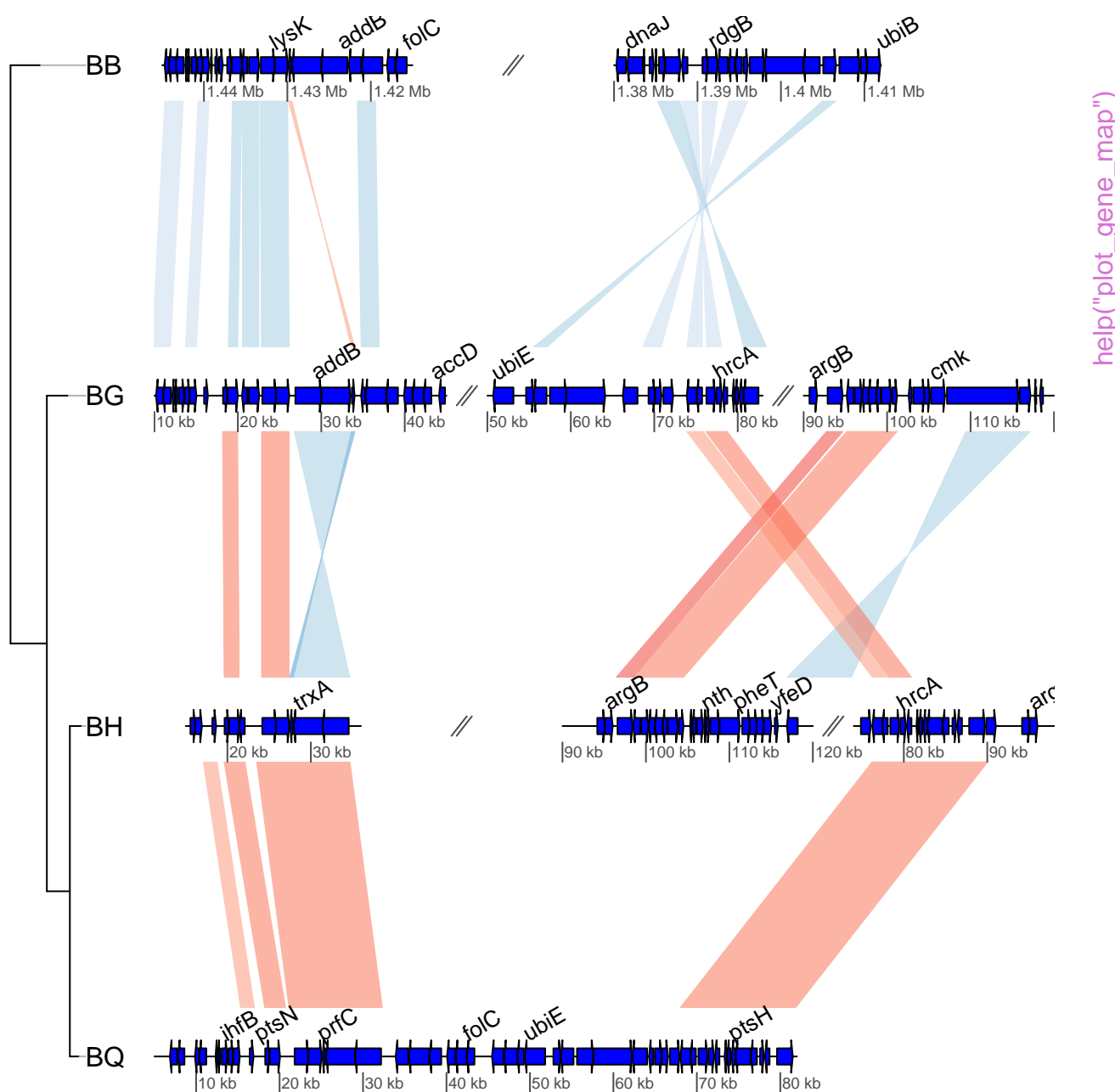
help("plot\_gene\_map")





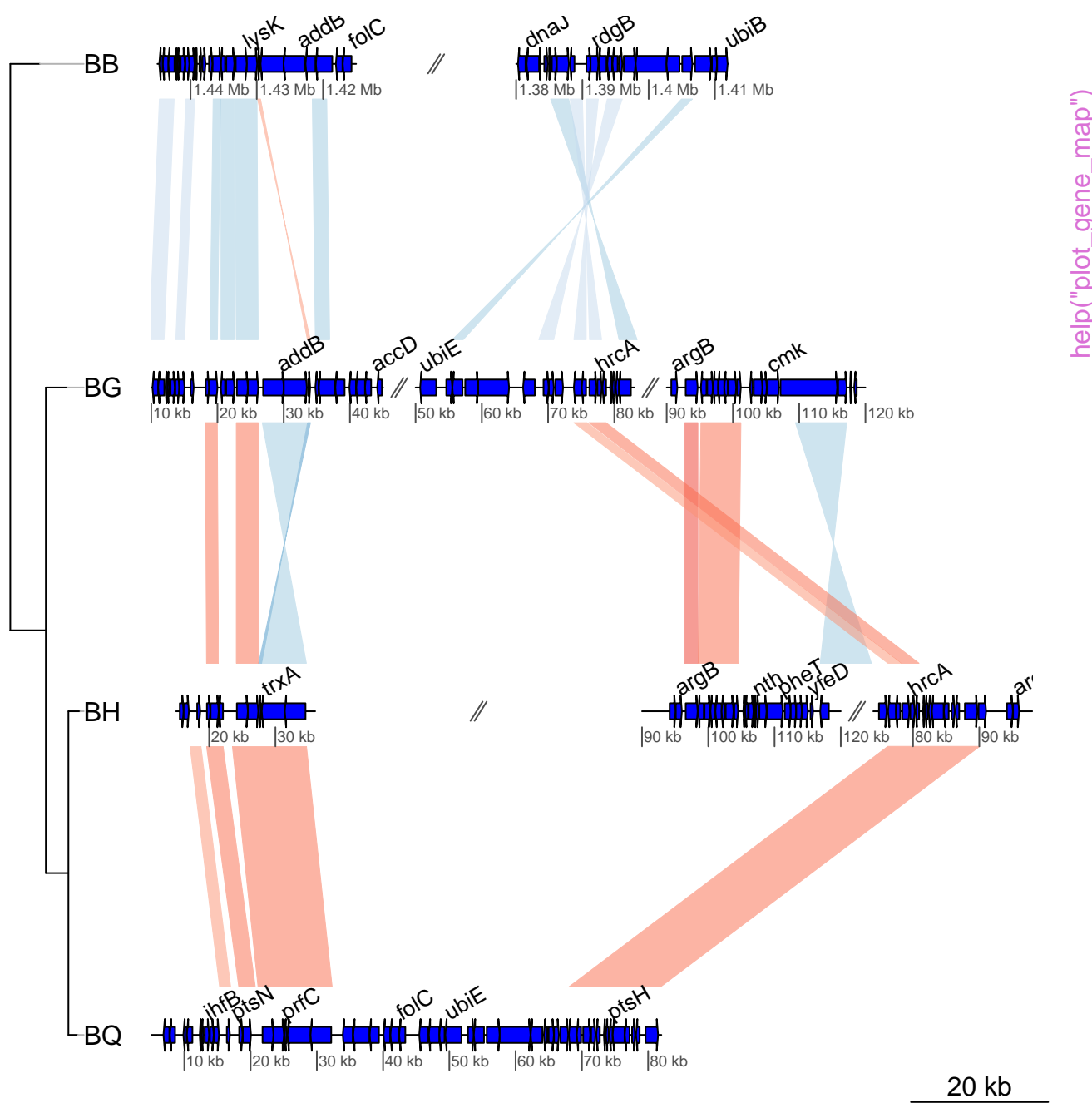


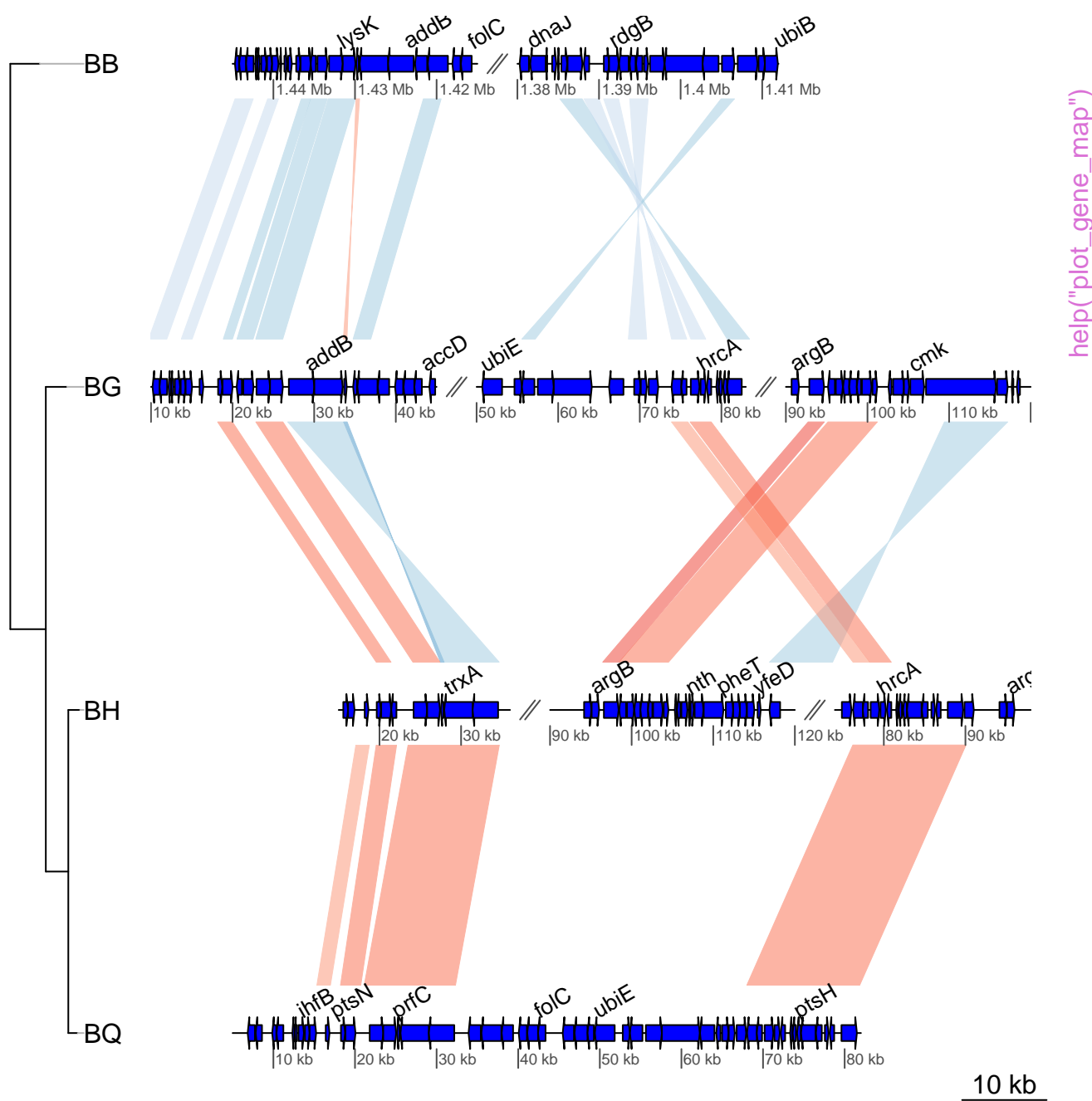
help("plot\_gene\_map")

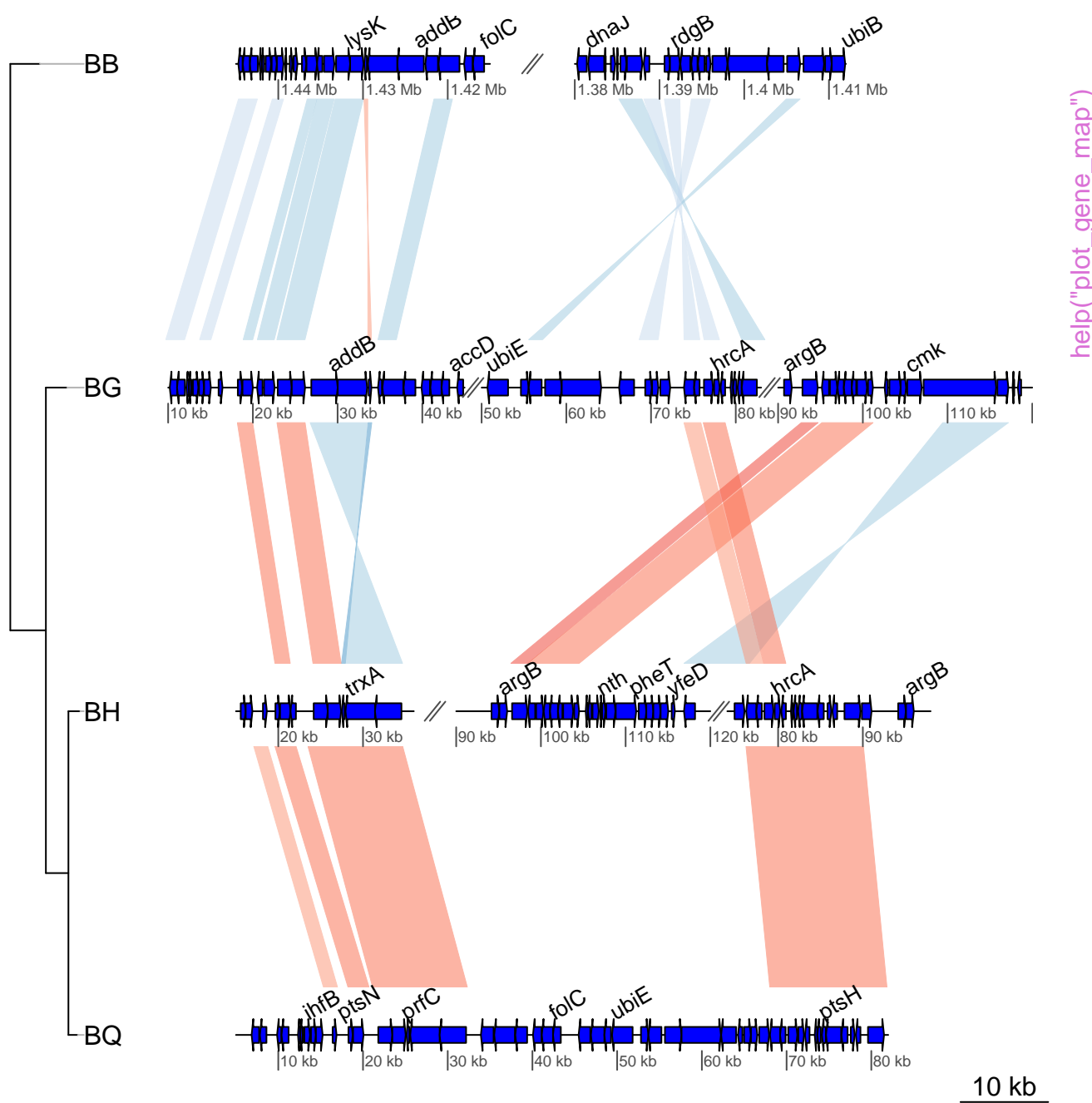


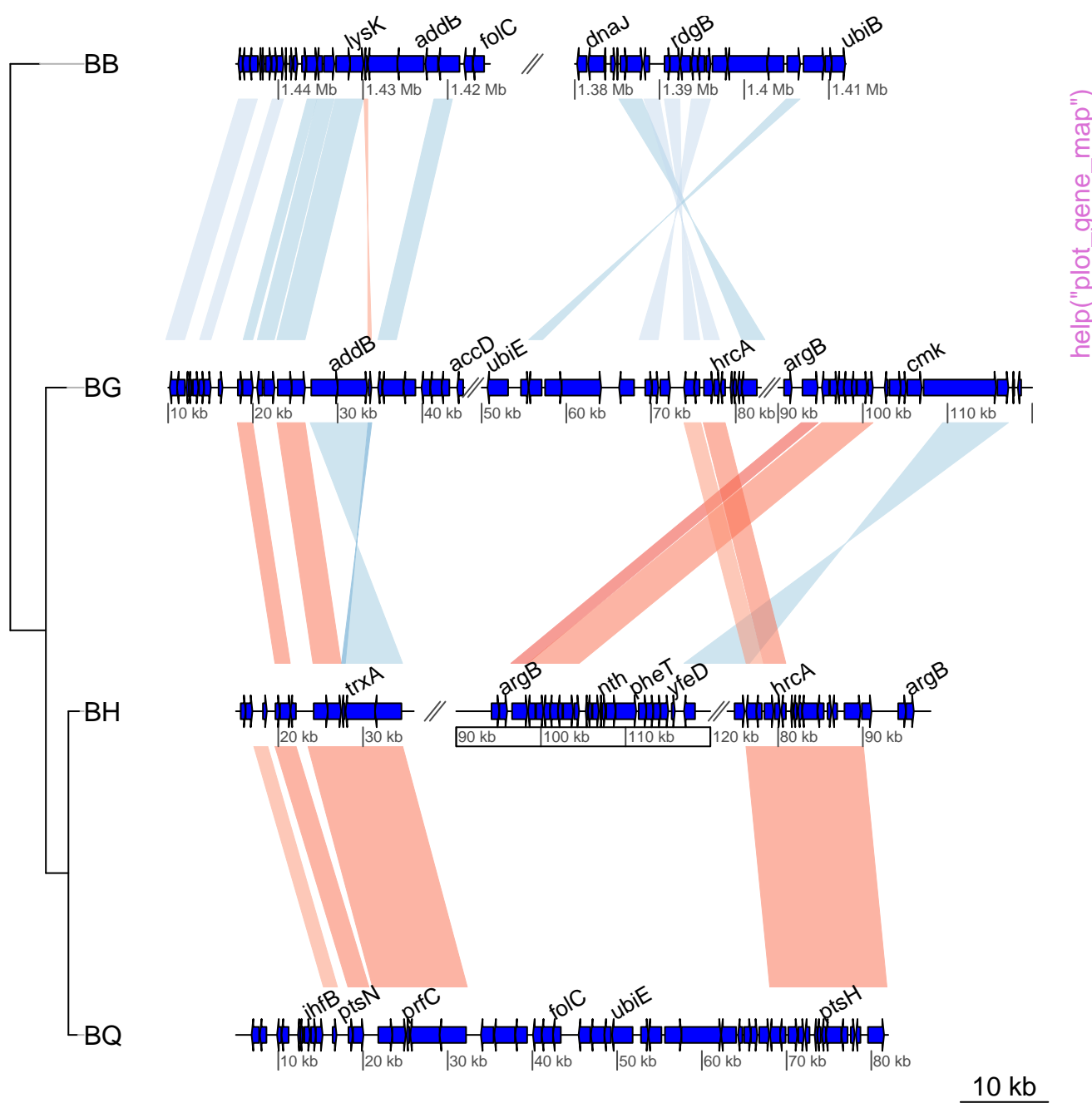
help("plot\_gene\_map")

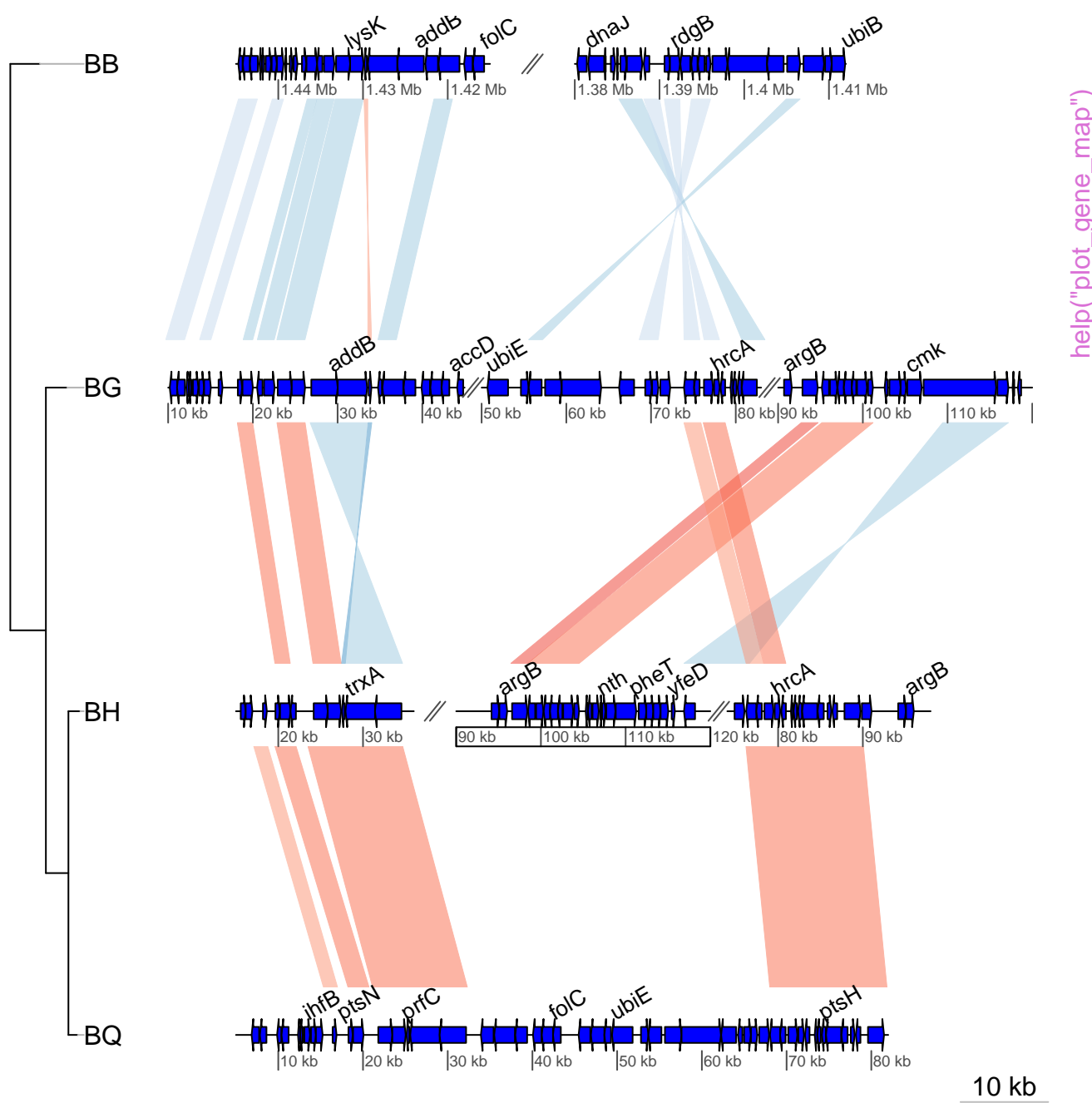
10 kb

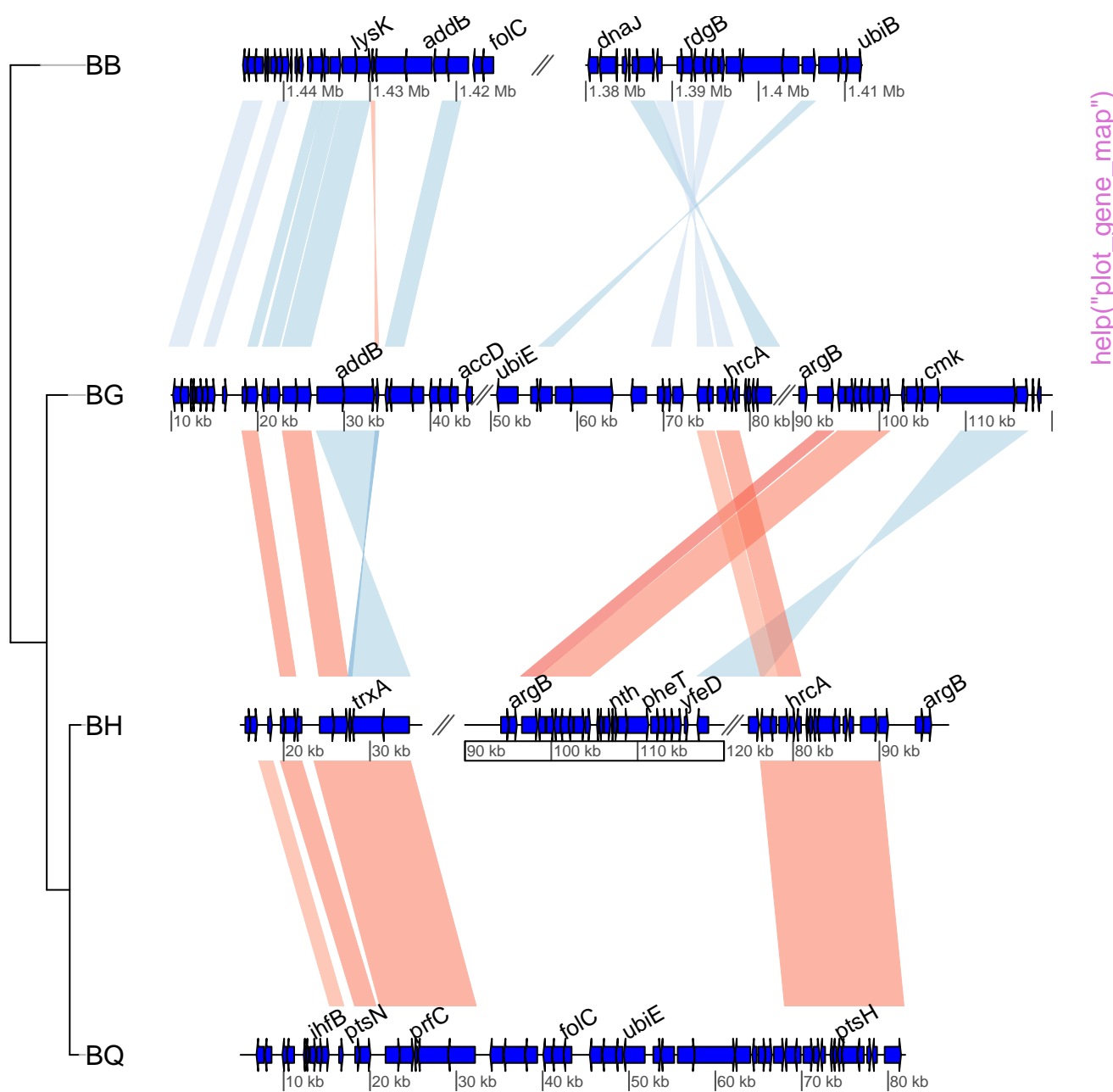














geno

R

Plot

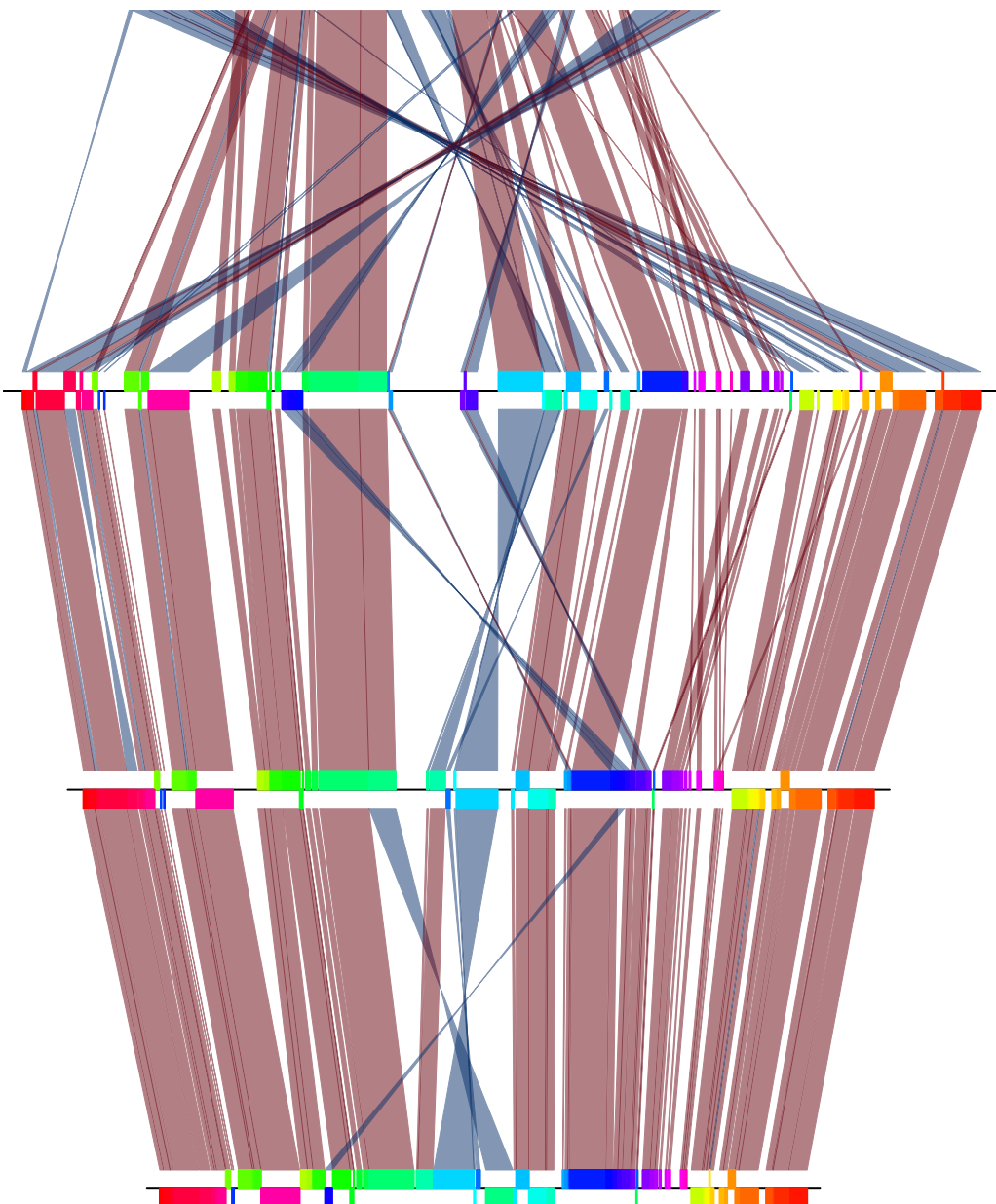
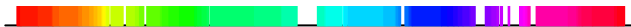
help("plot\_gene\_map")

B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("read\_functions")

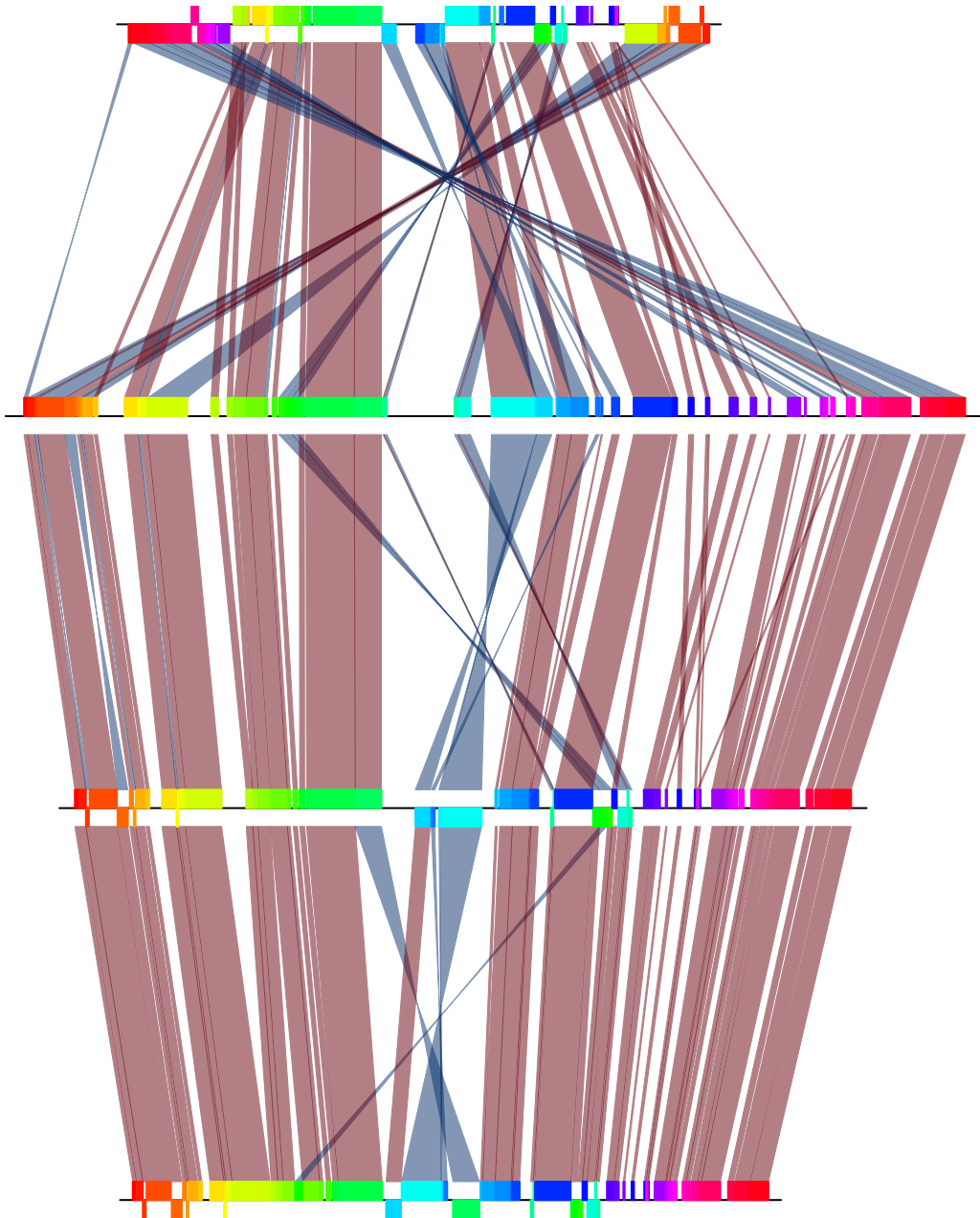
500 kb

B\_bacilliformis

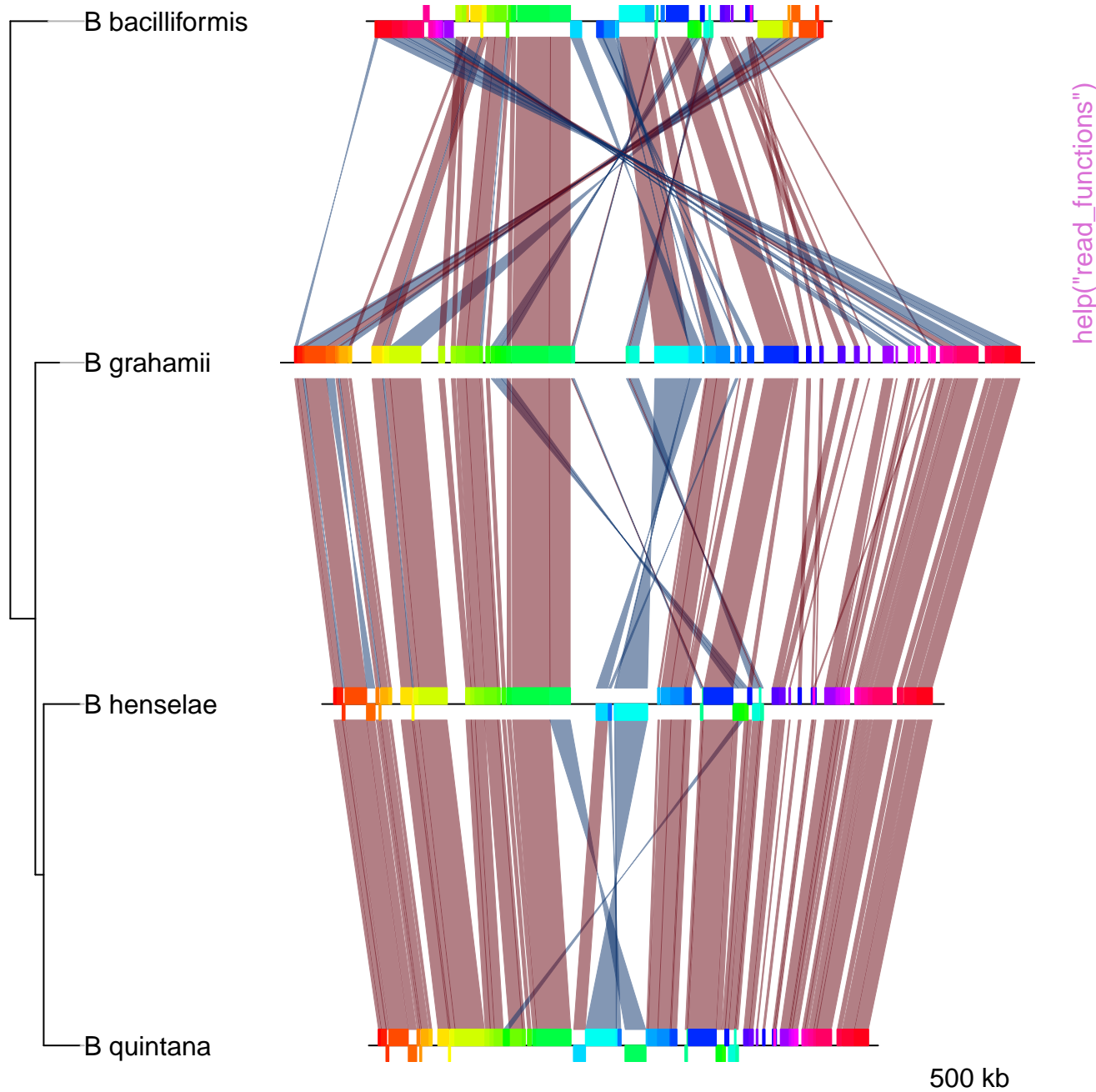
B\_grahamii

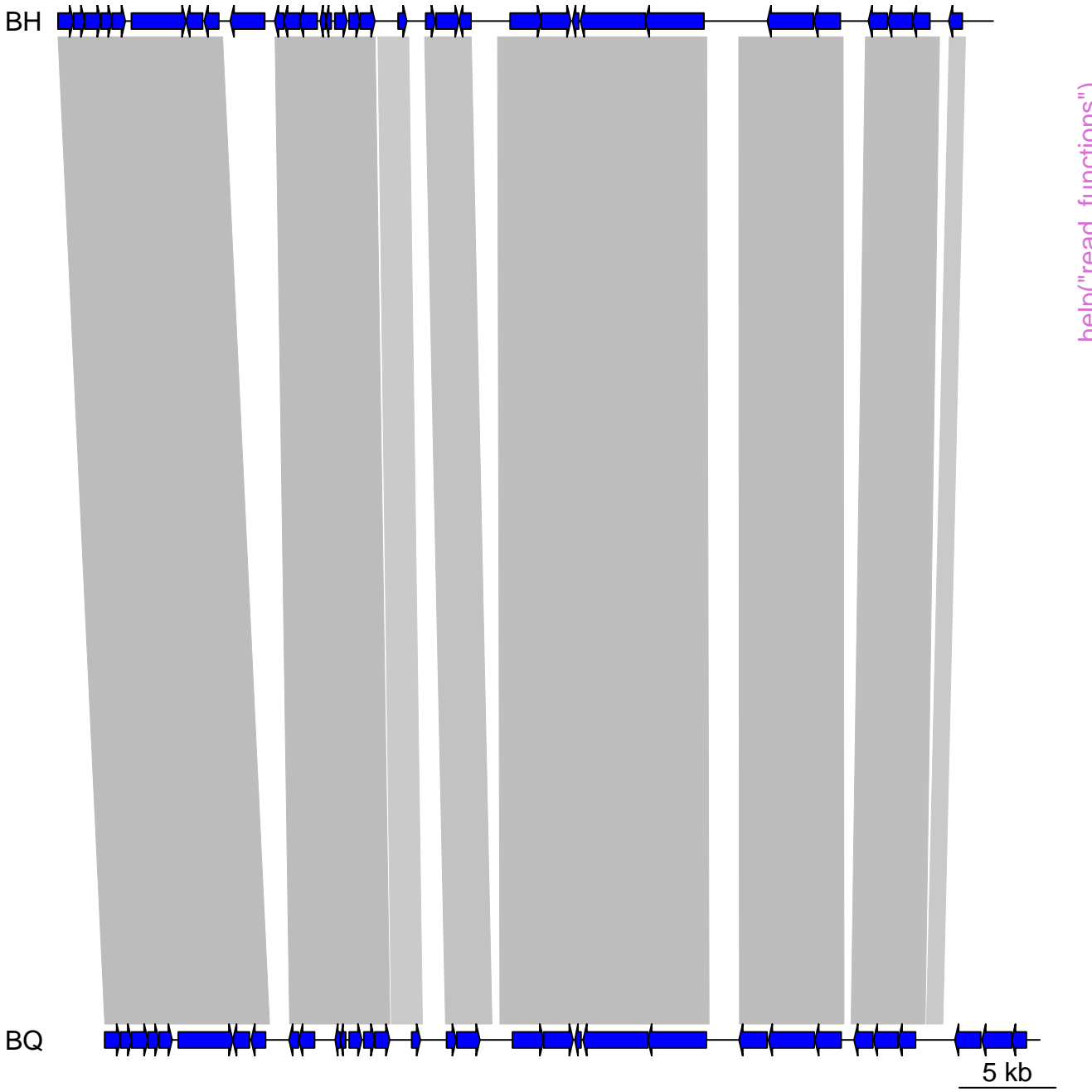
B\_henselae

B\_quintana



help("read\_functions")



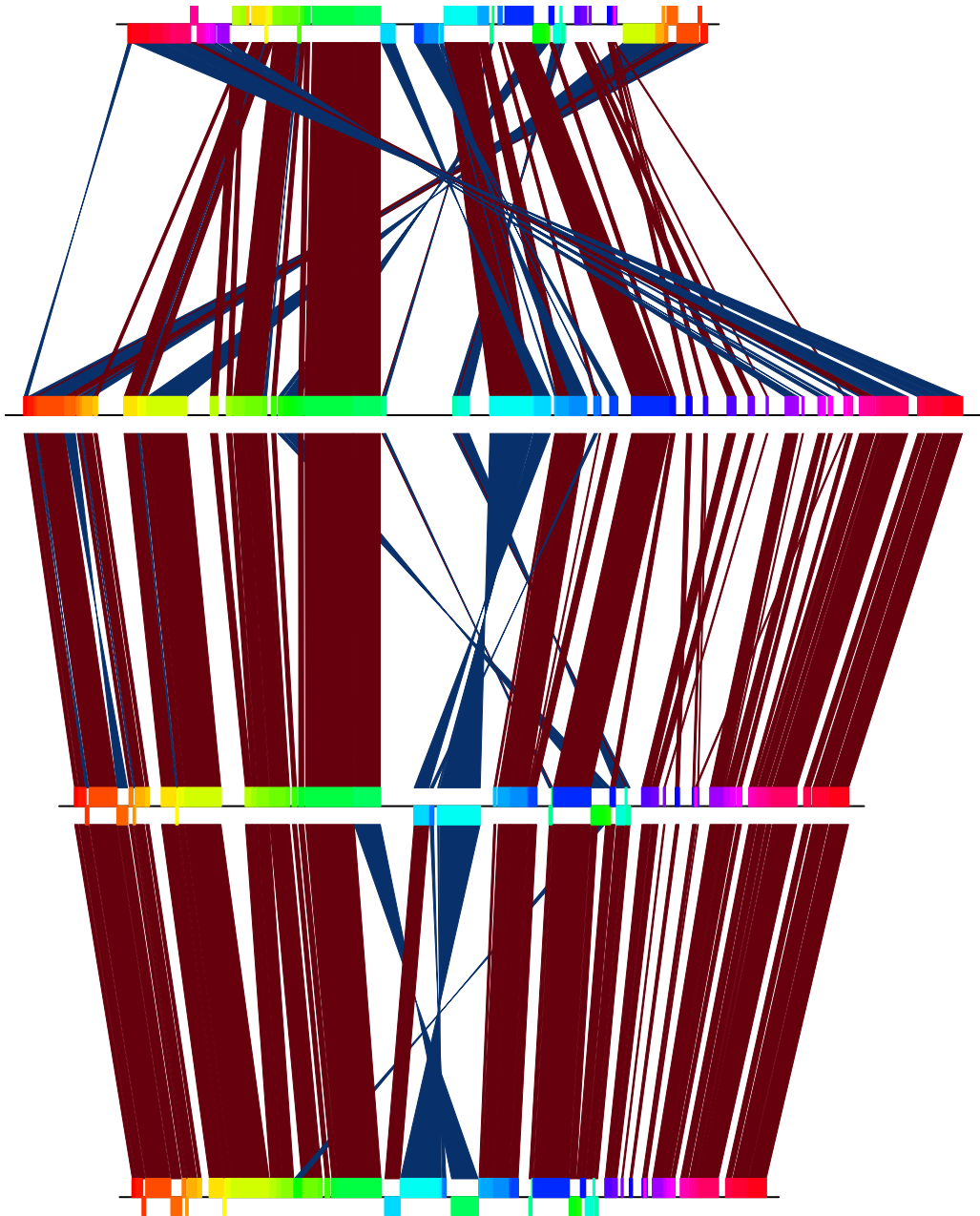


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



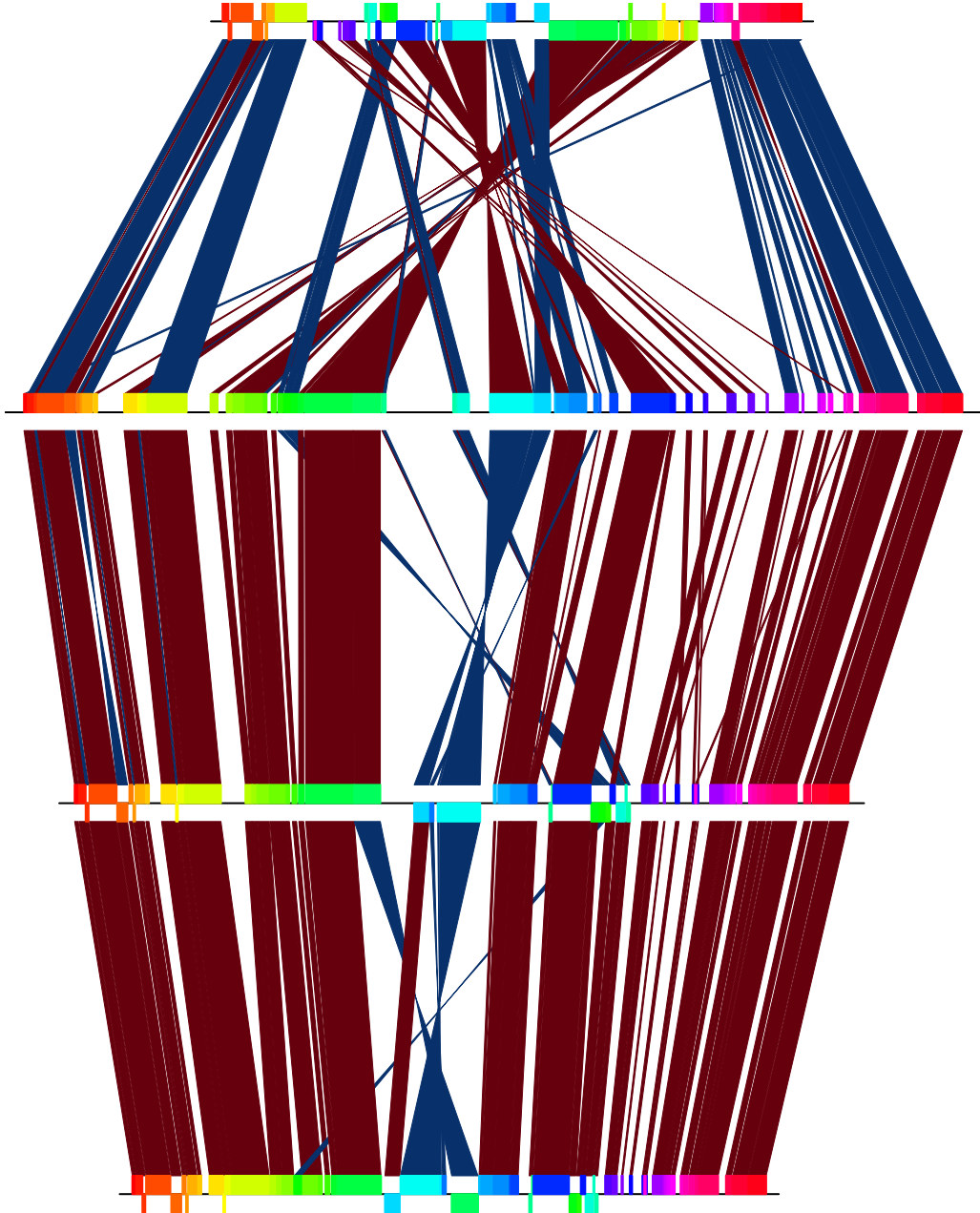
help("reverse")

B\_bacilliformis

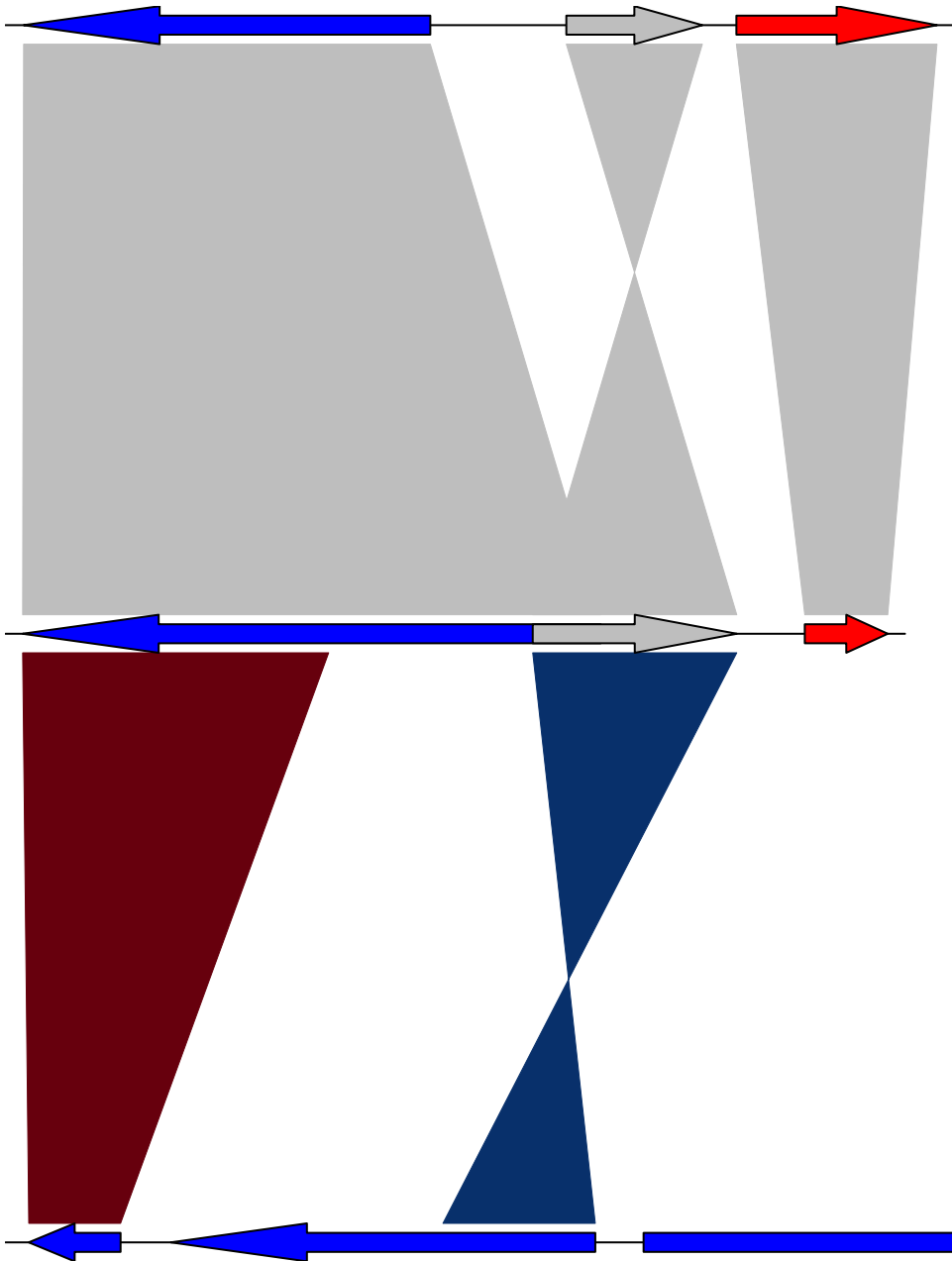
B\_grahamii

B\_henselae

B\_quintana



help("reverse")



help("three\_genes")

200 nt



