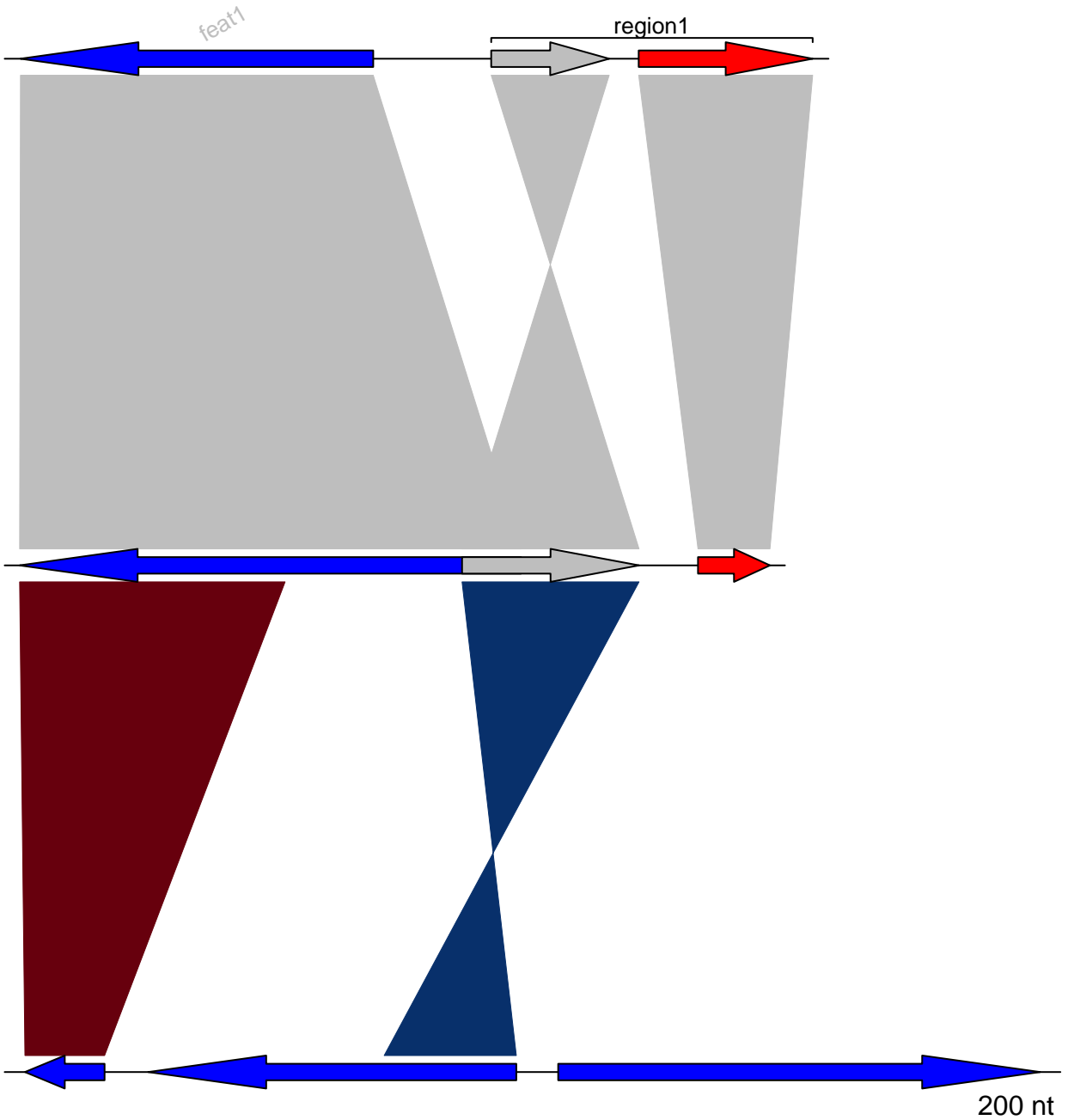


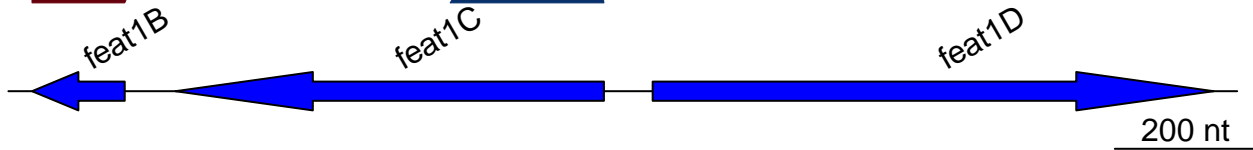
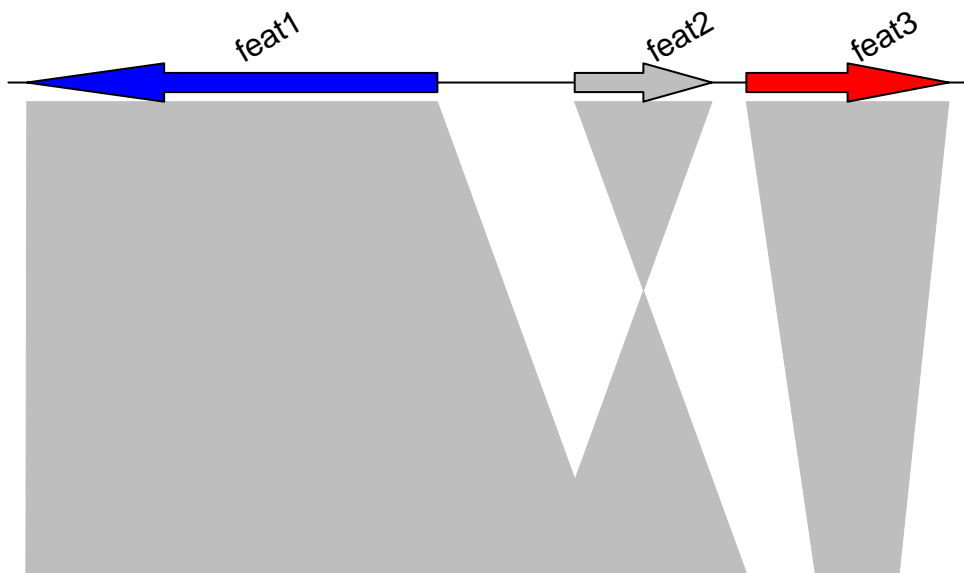
help("annotation")

200 nt

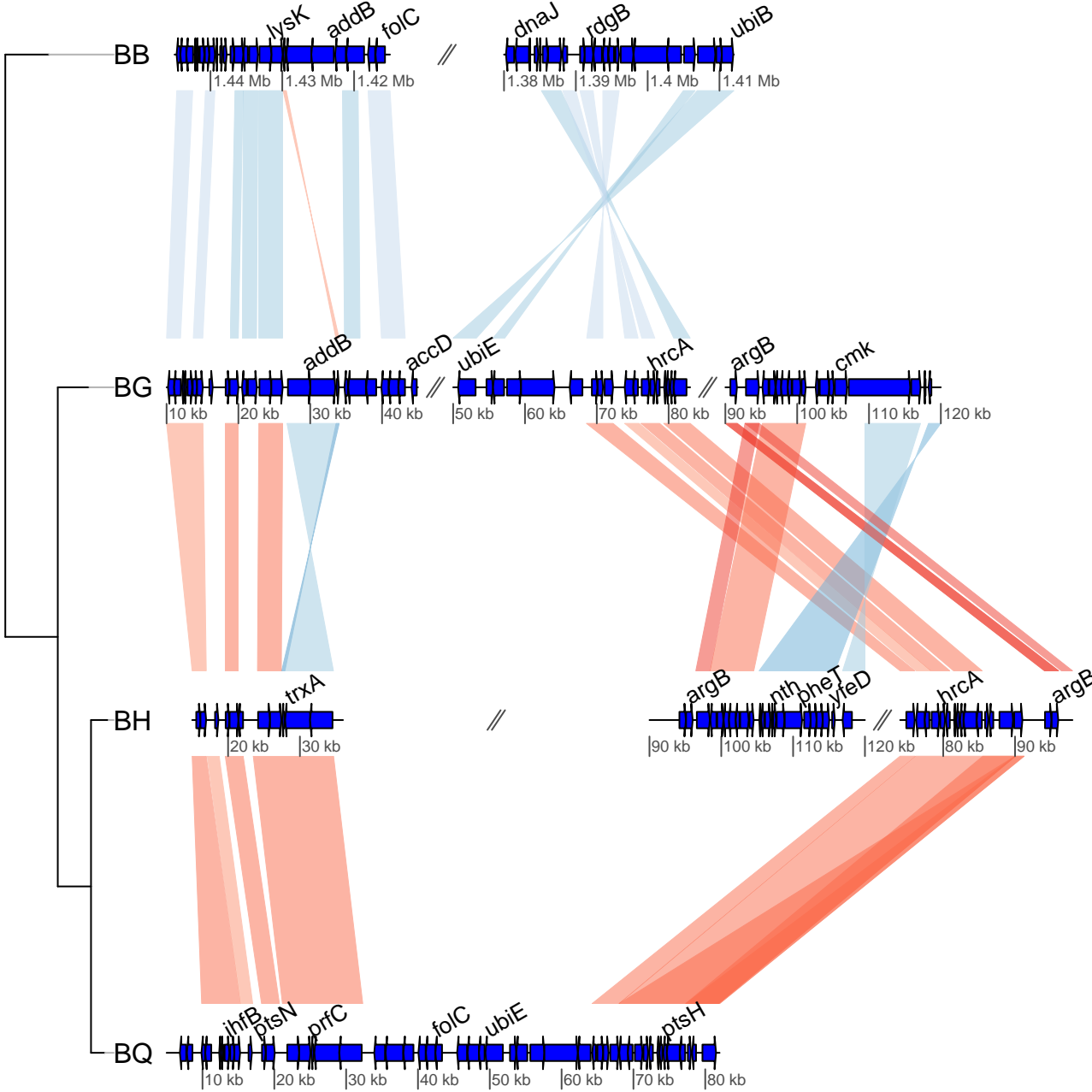


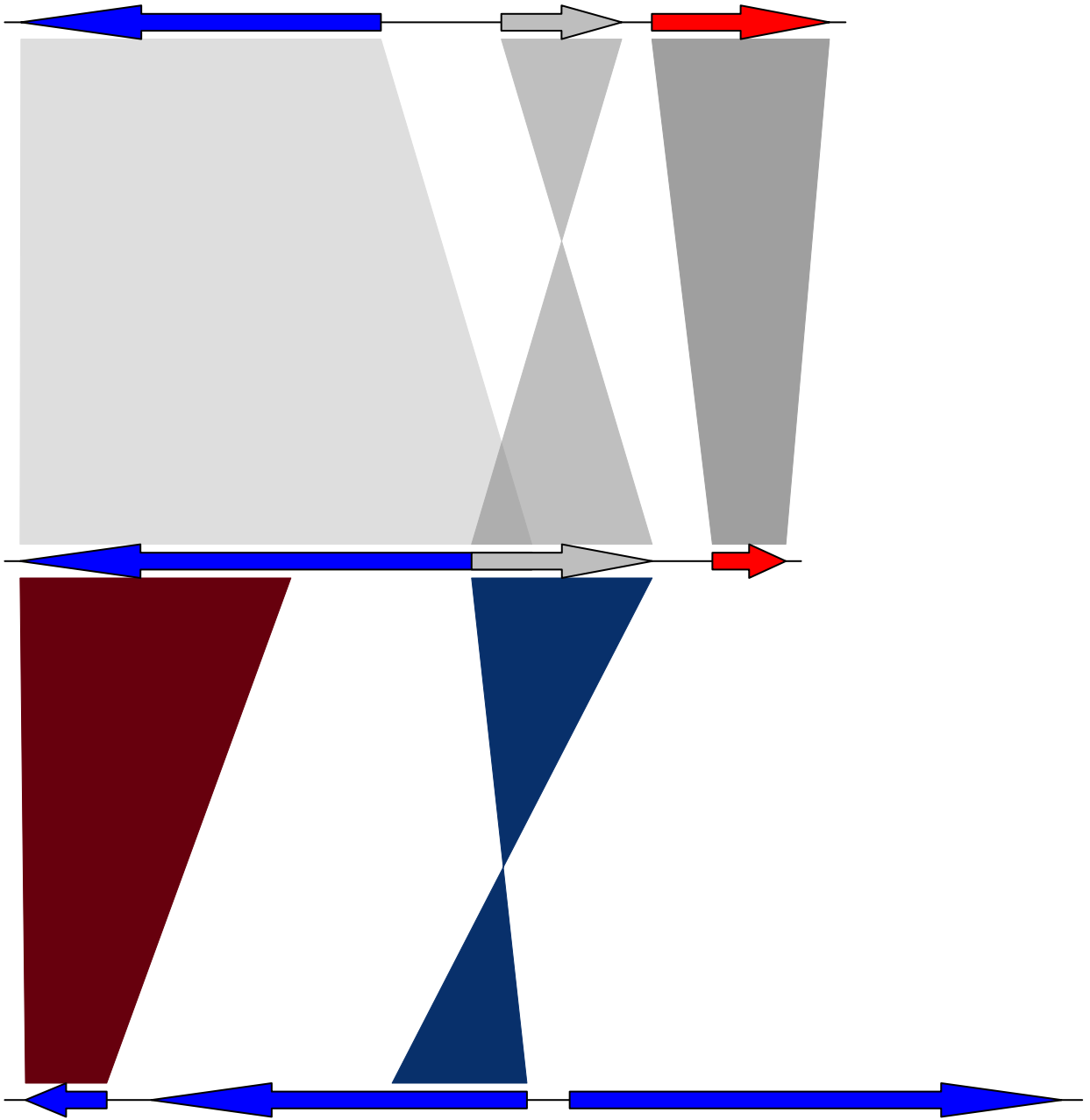
help("annotation")

200 nt



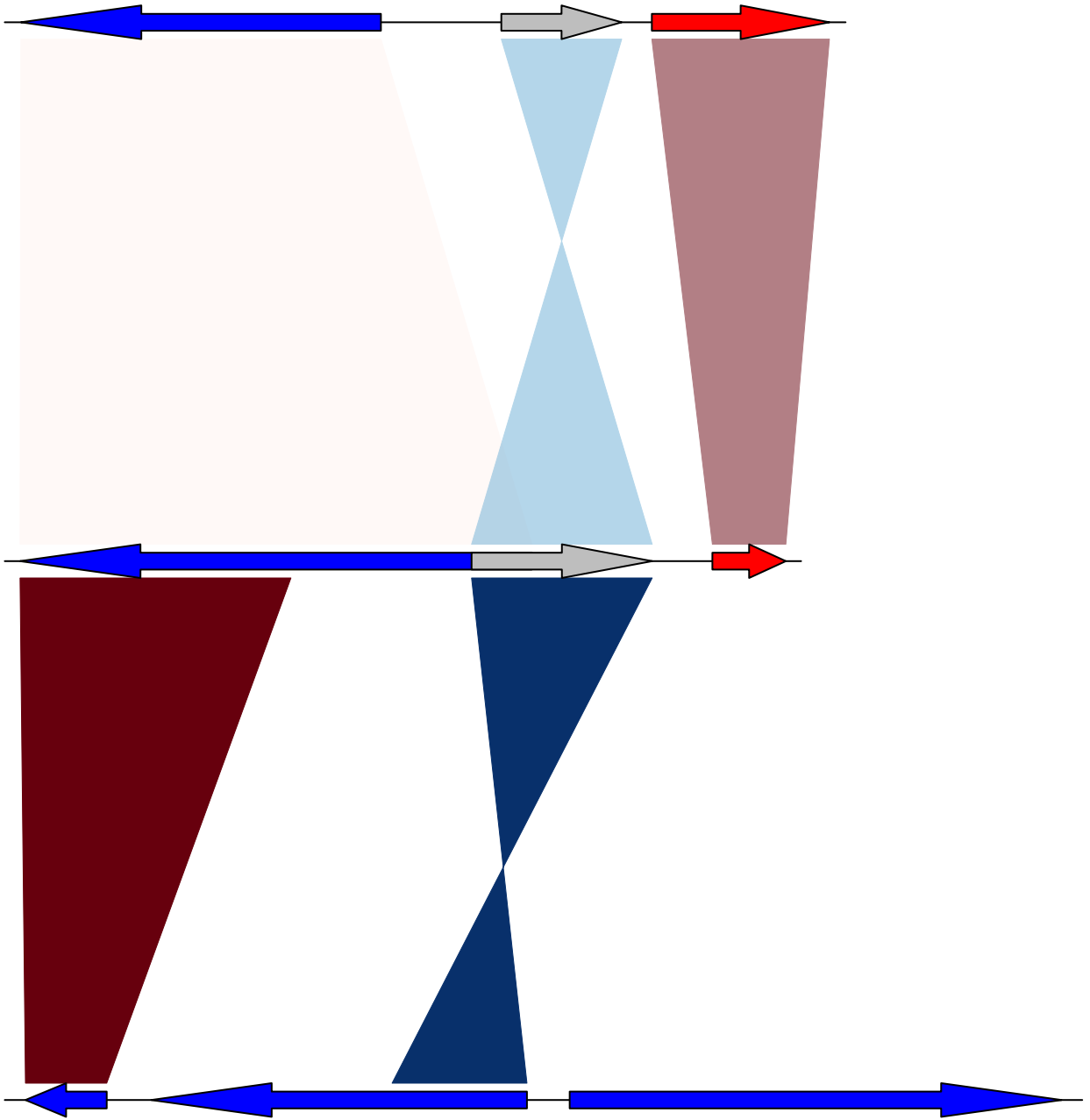
help("annotation")





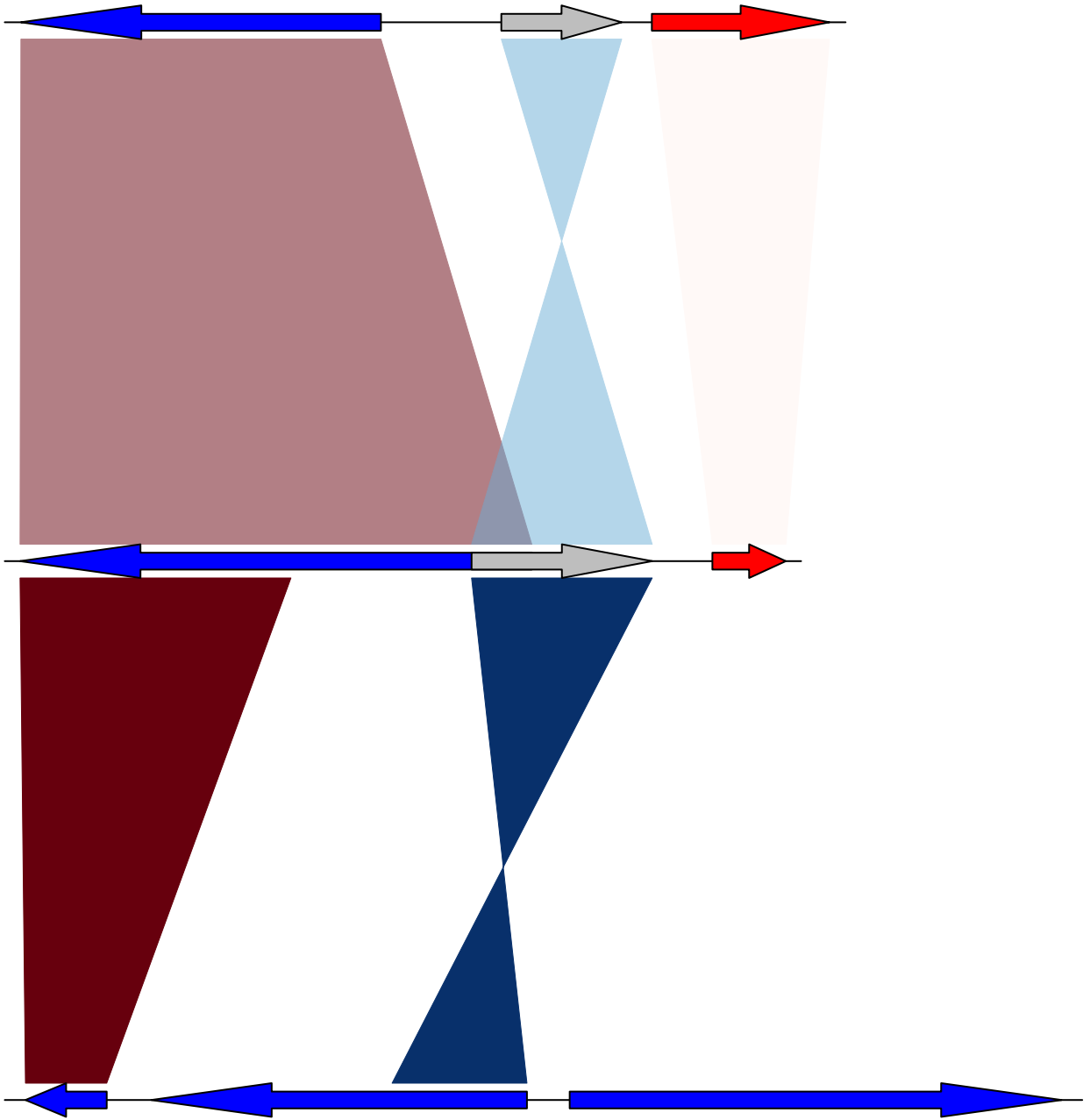
help("apply\_color\_scheme")

200 nt



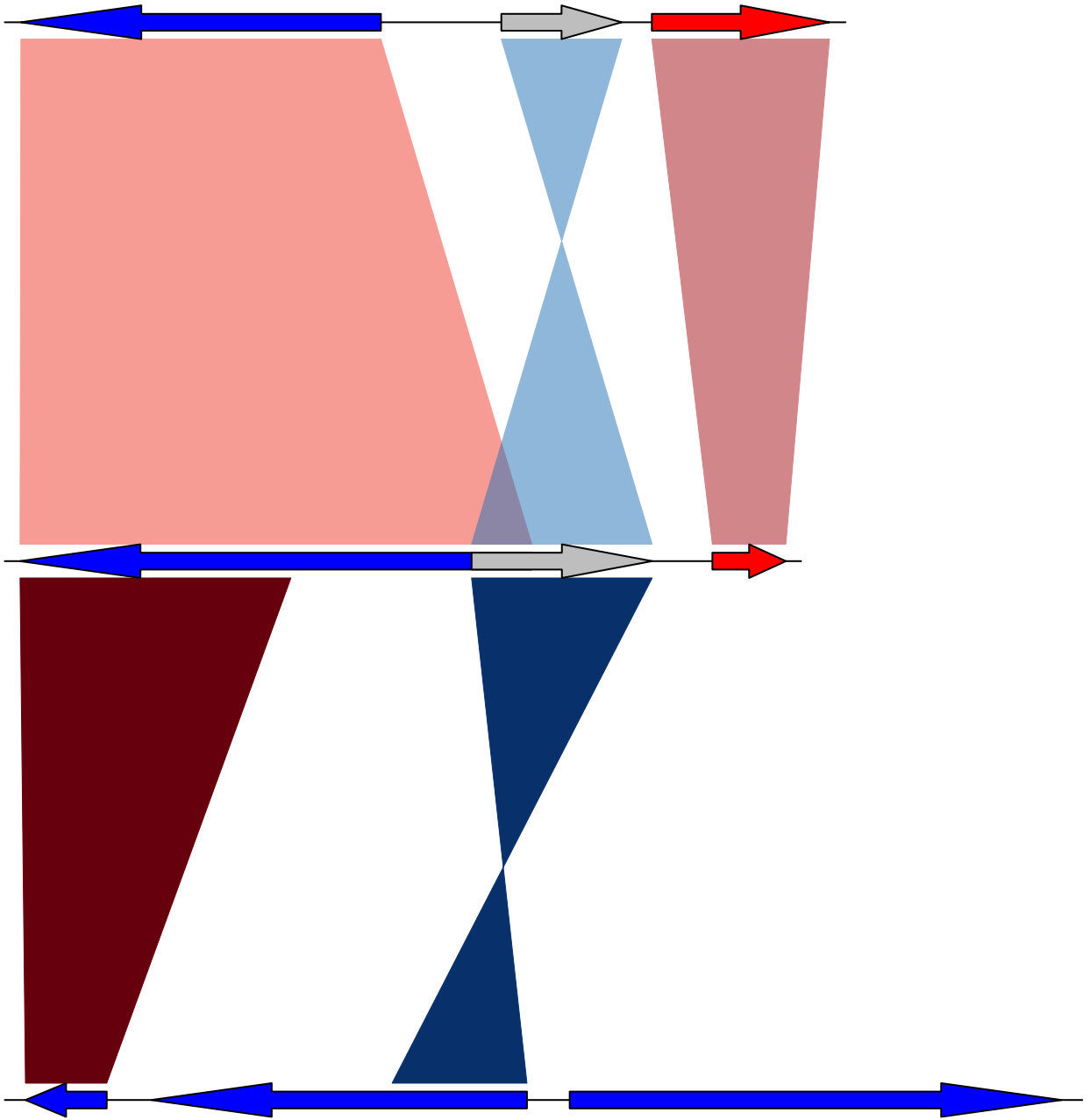
help("apply\_color\_scheme")

200 nt



help("apply\_color\_scheme")

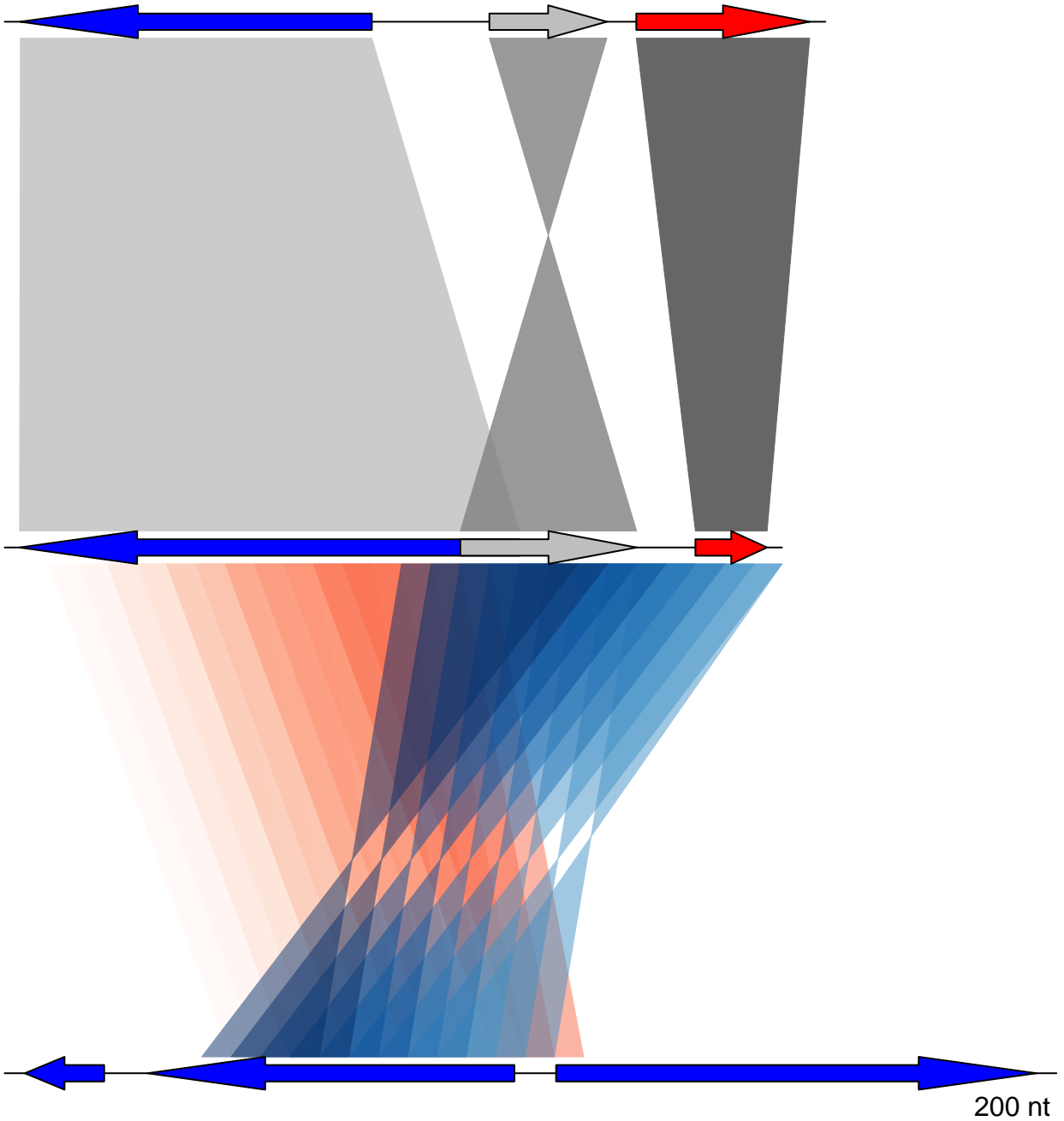
200 nt



help("apply\_color\_scheme")

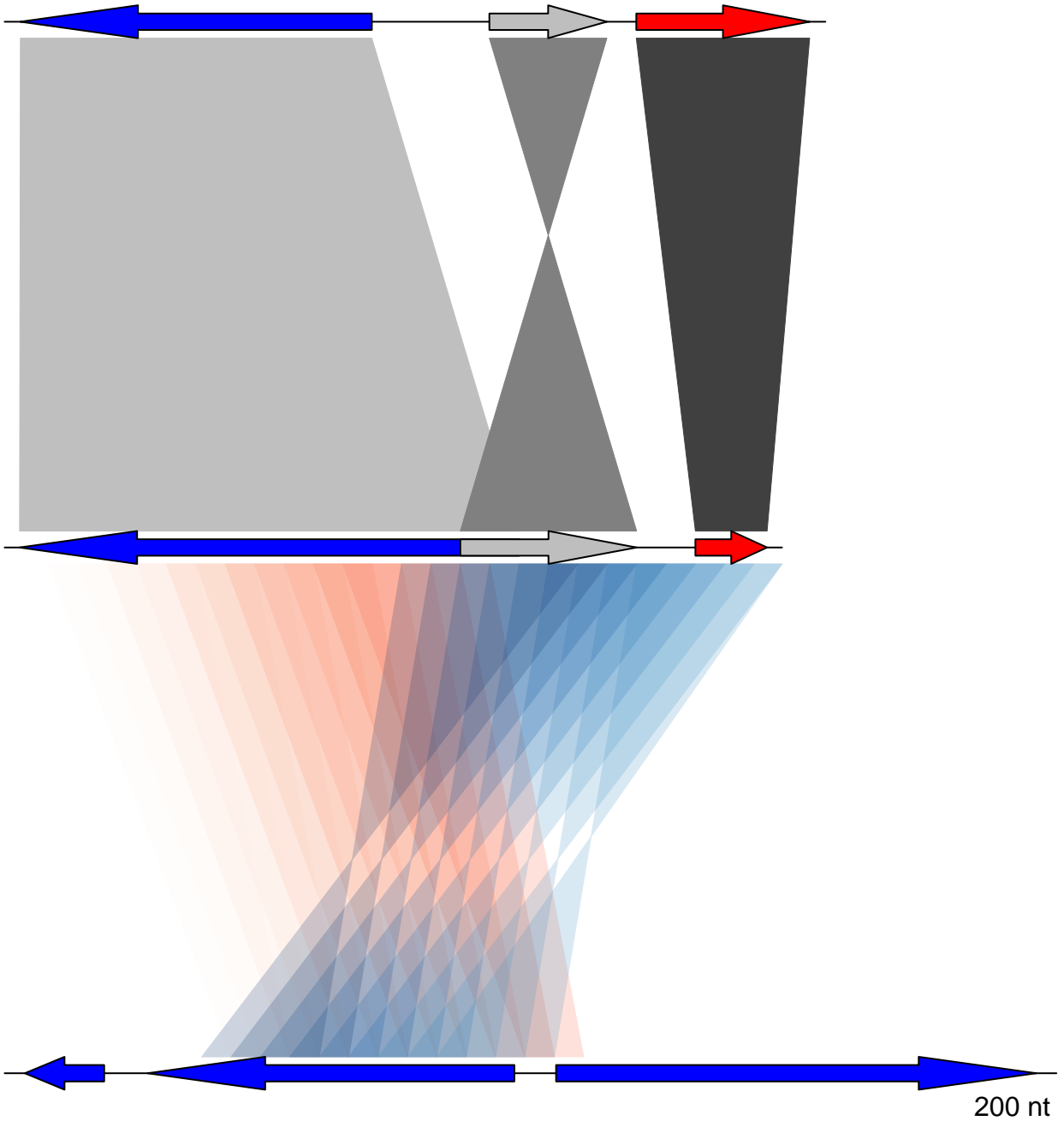
200 nt





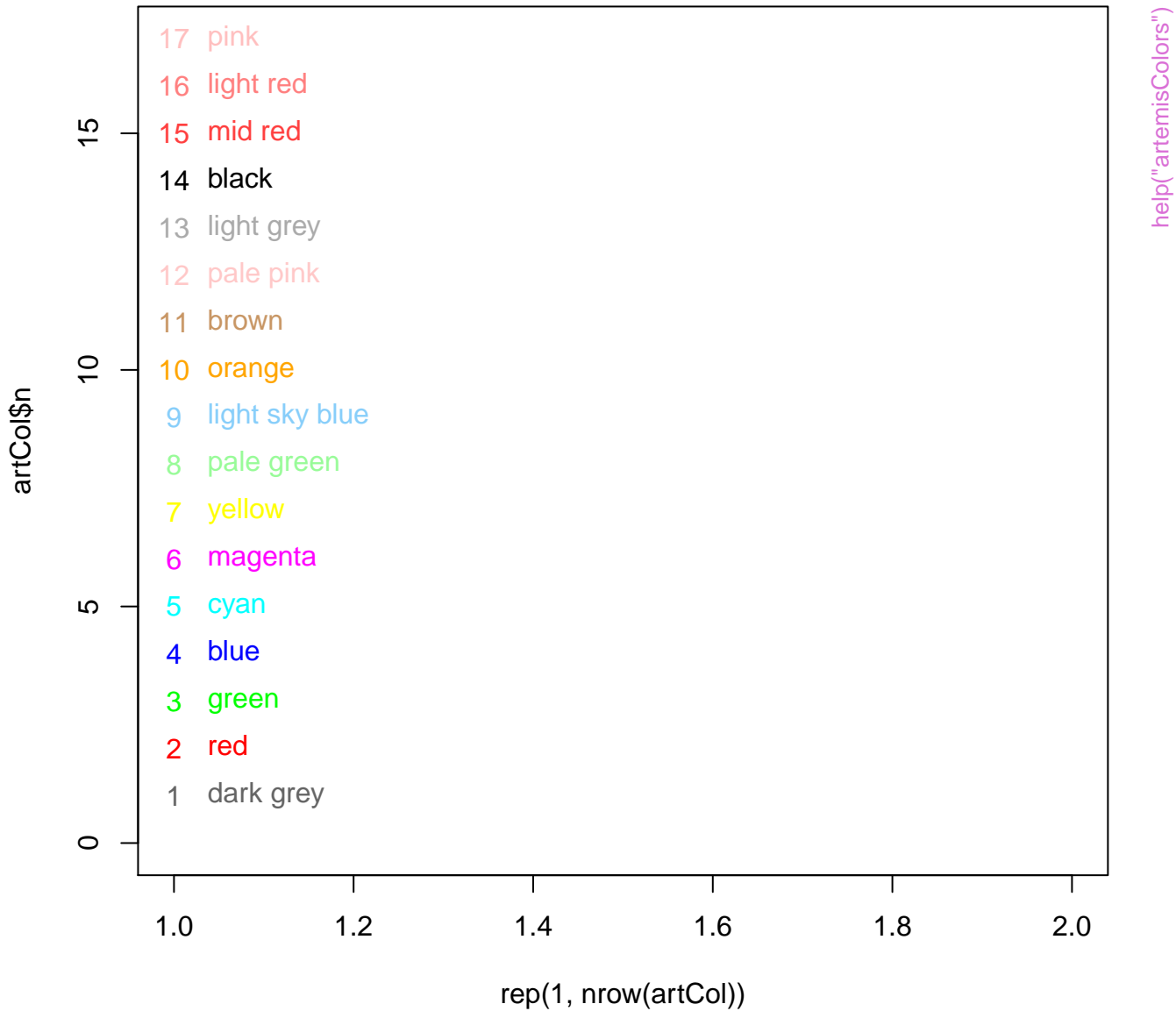
help("apply\_color\_scheme")

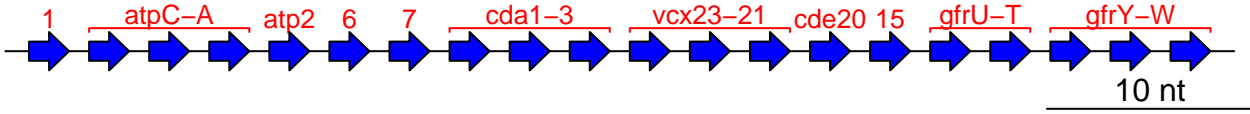
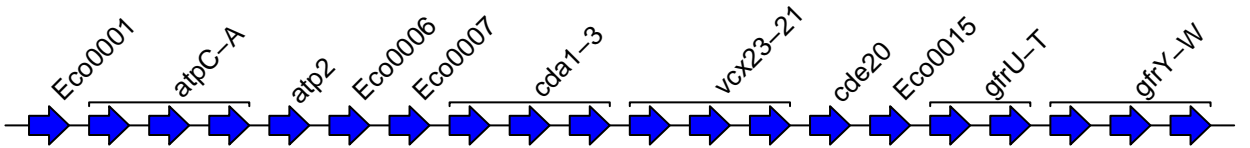
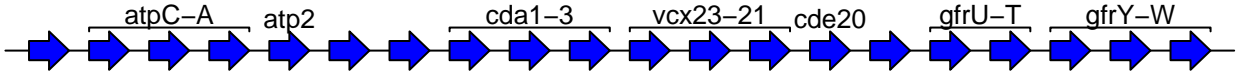
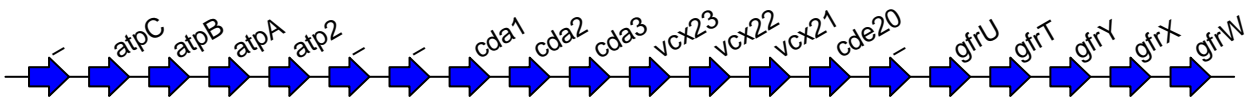
200 nt



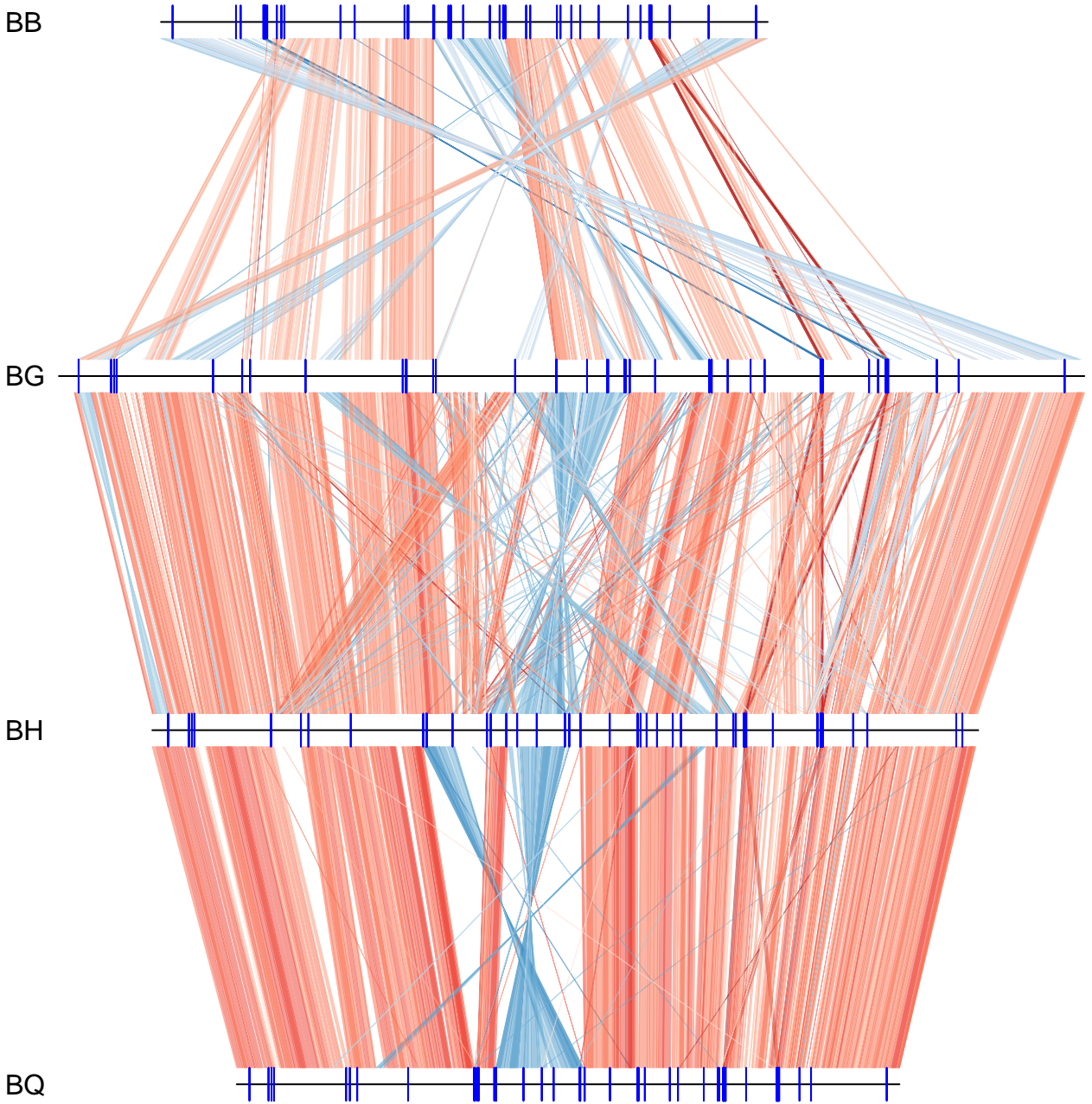
help("apply\_color\_scheme")

200 nt



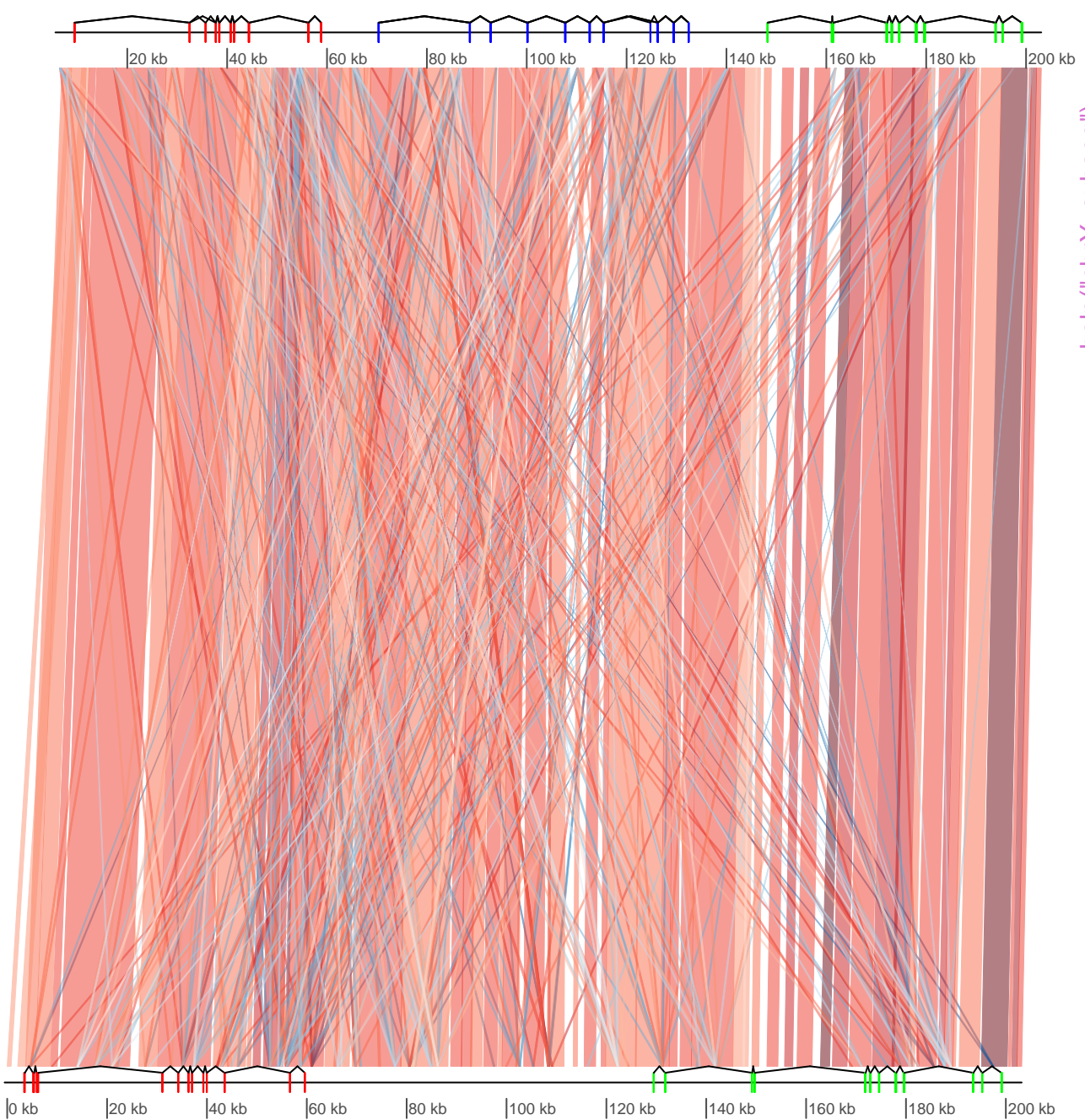


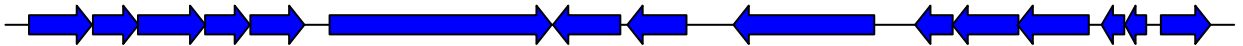
help("auto\_annotate")



help("barto")

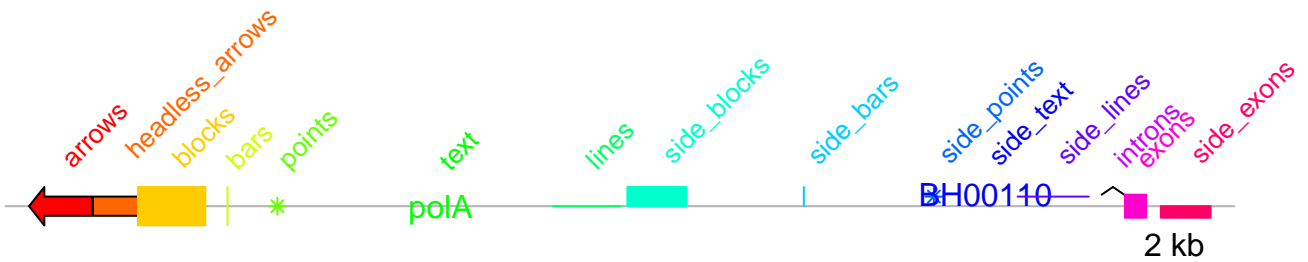
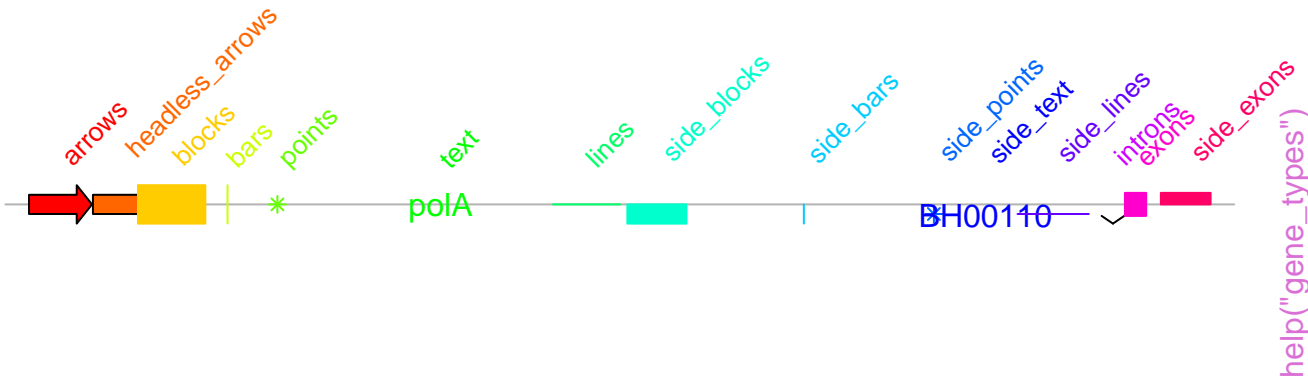
500 kb





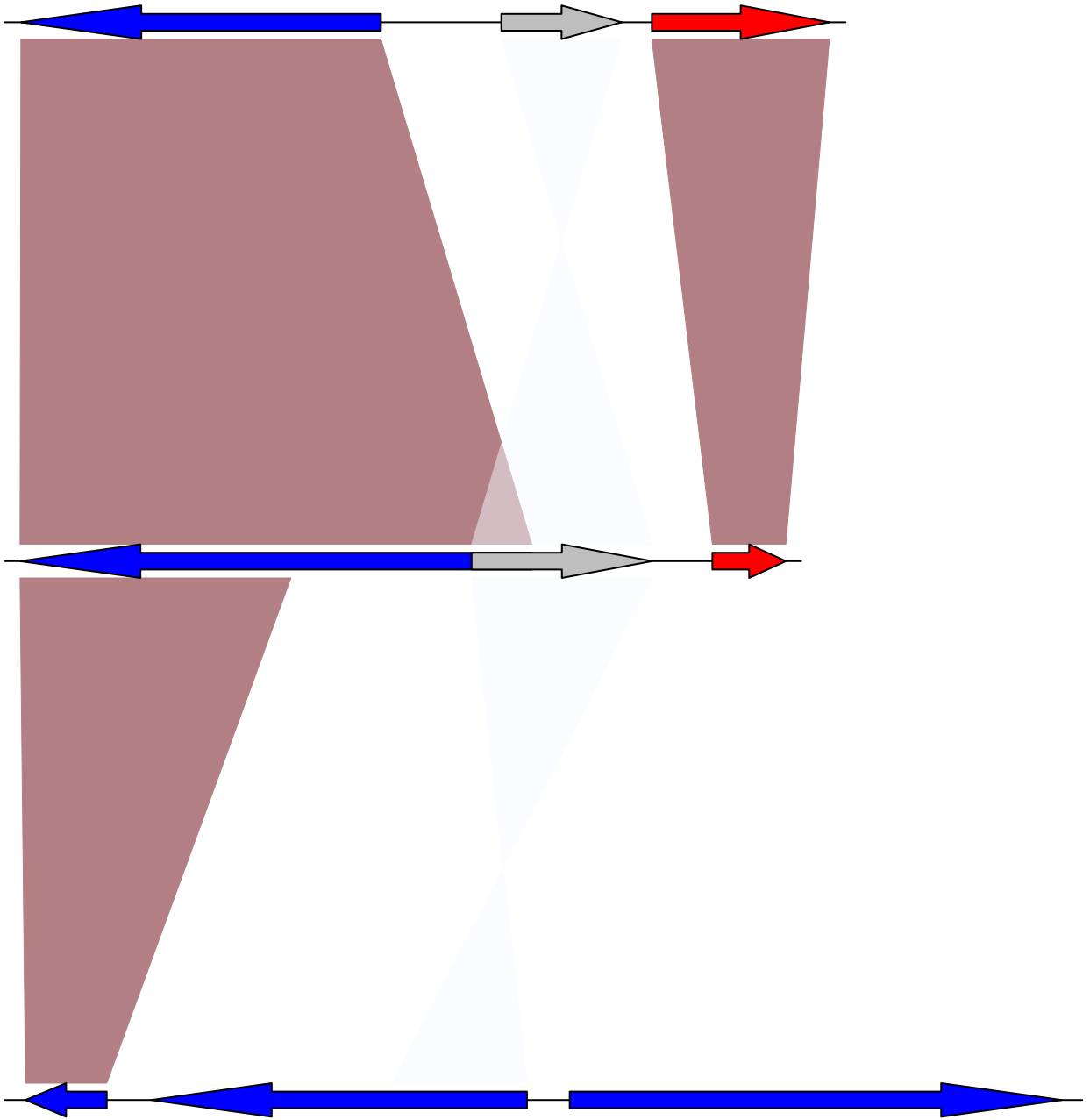
2 kb

help("gene\_types")









`help("genoPlotR-package")`

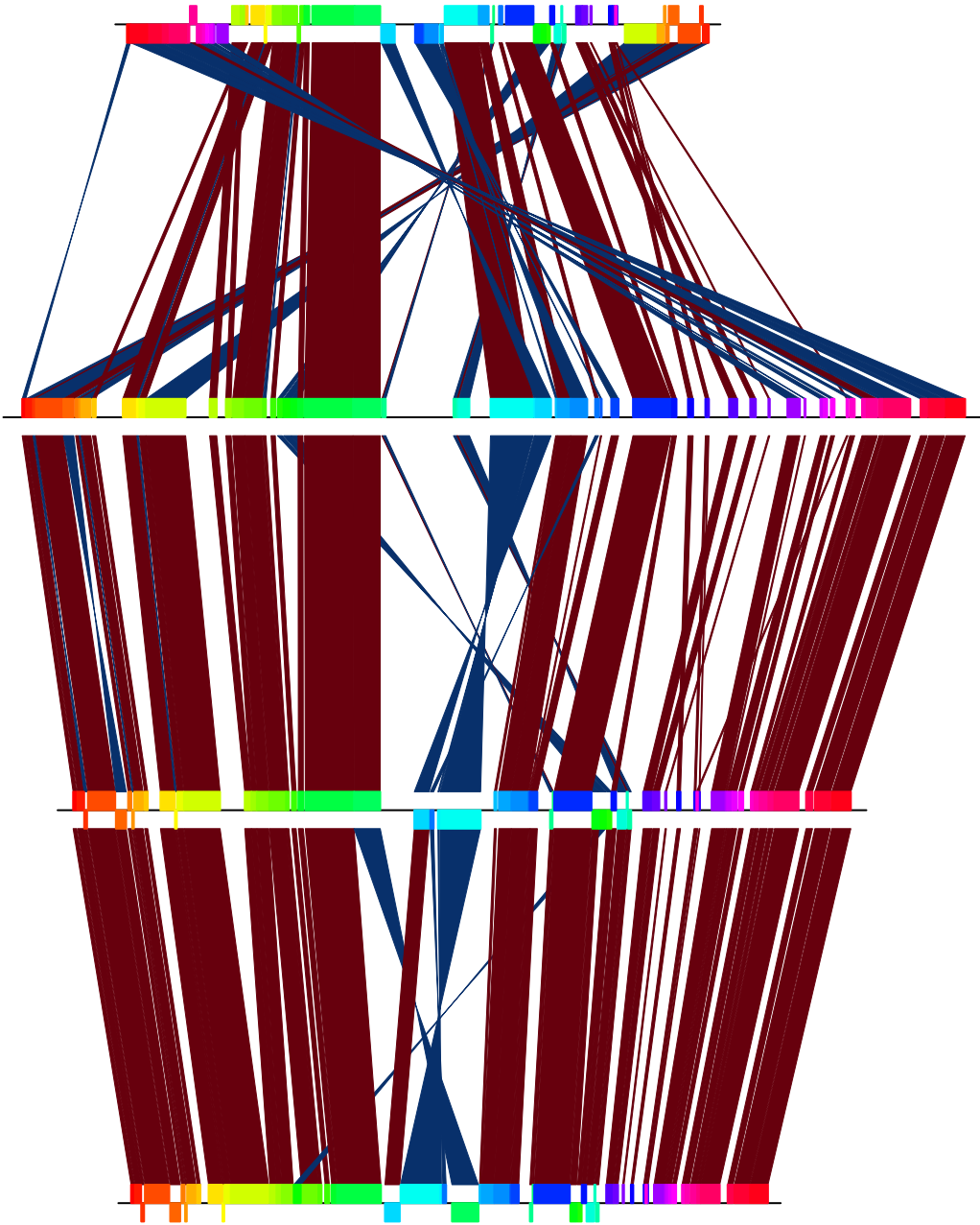
200 nt

B\_bacilliformis

B\_grahamii

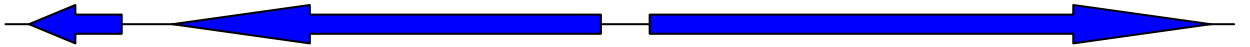
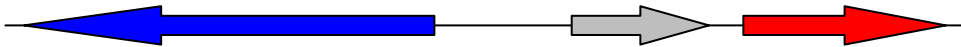
B\_henselae

B\_quintana



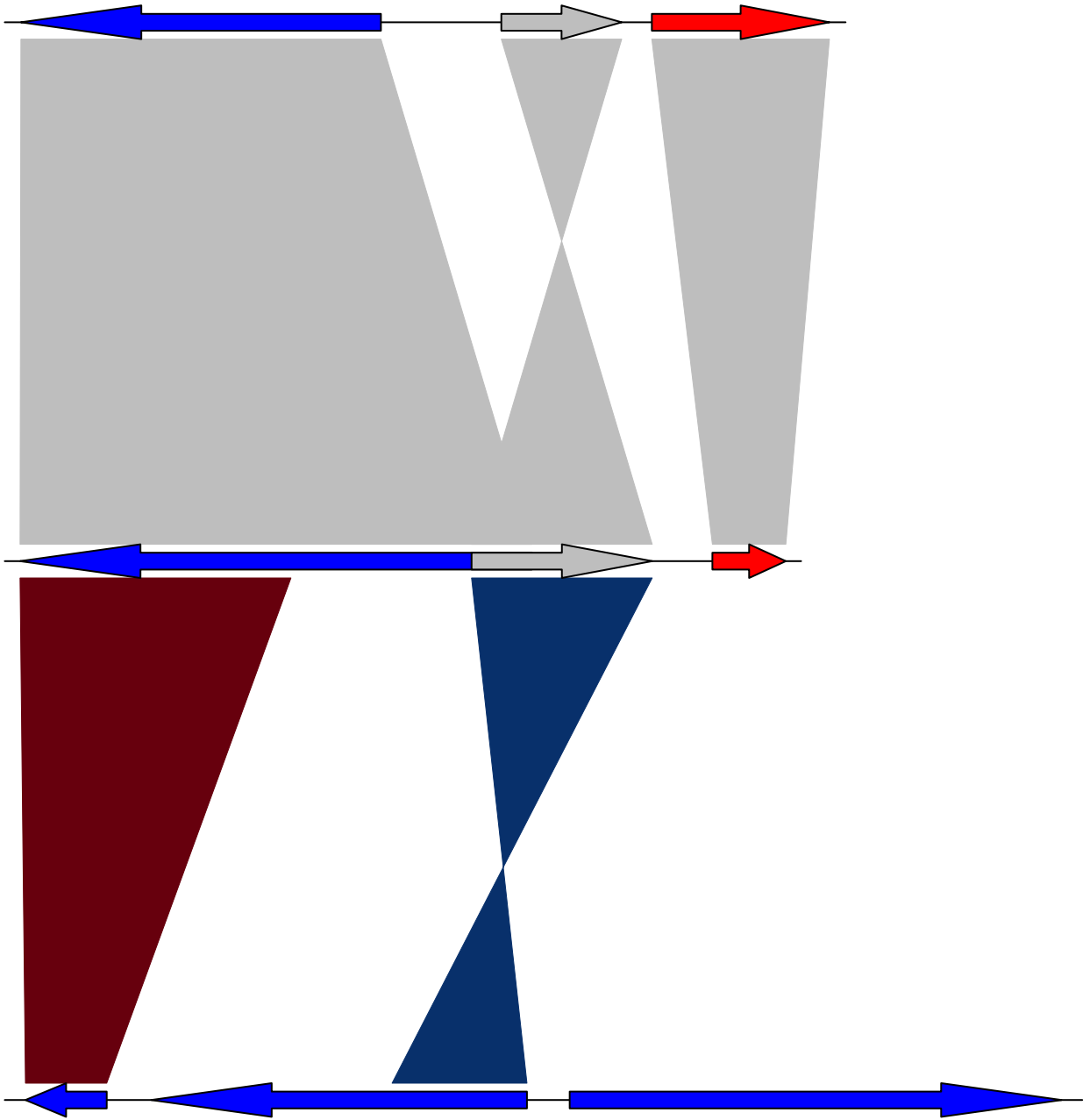
help("mauve\_bbone")

500 kb



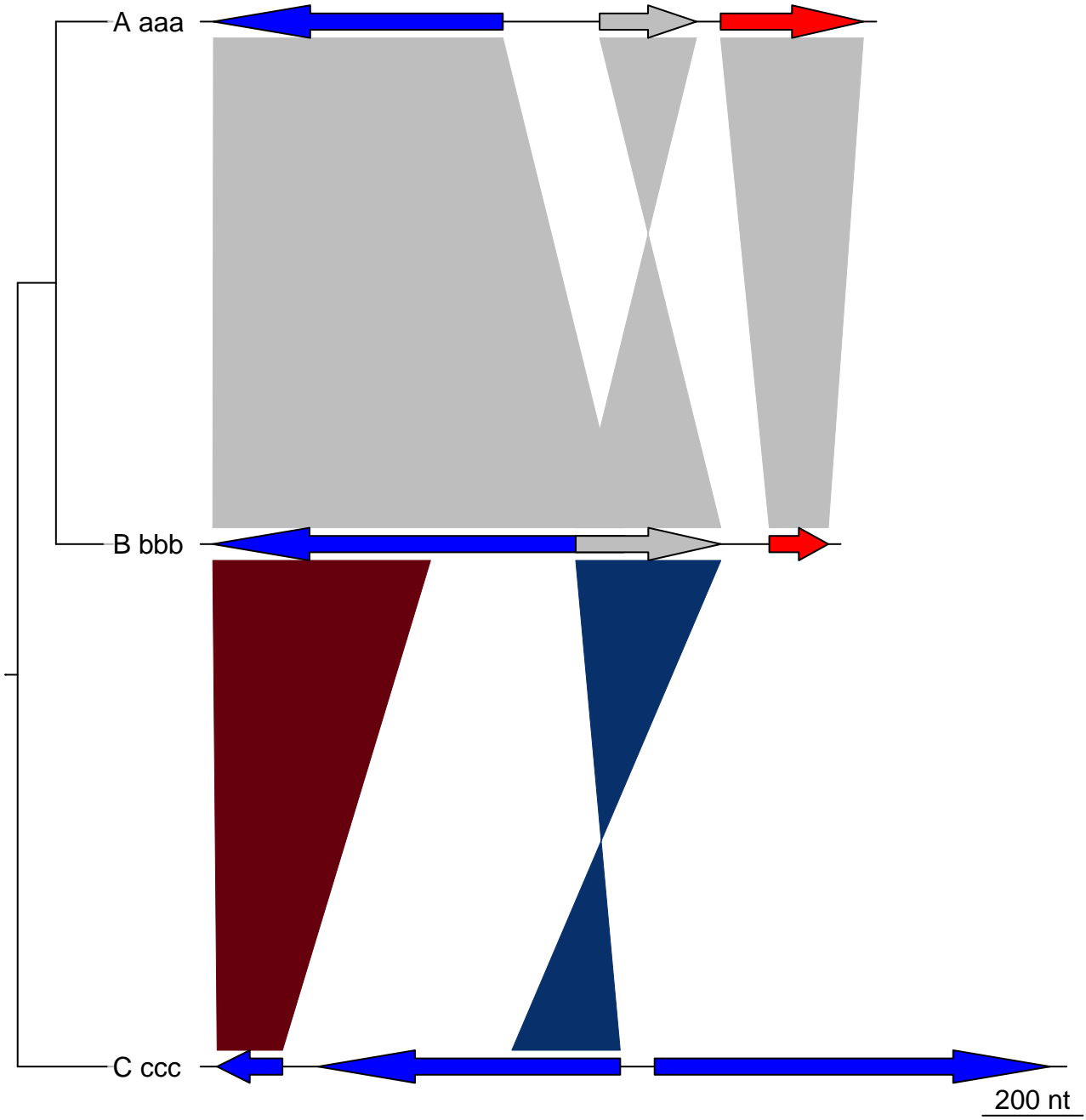
200 nt

help("plot\_gene\_map")



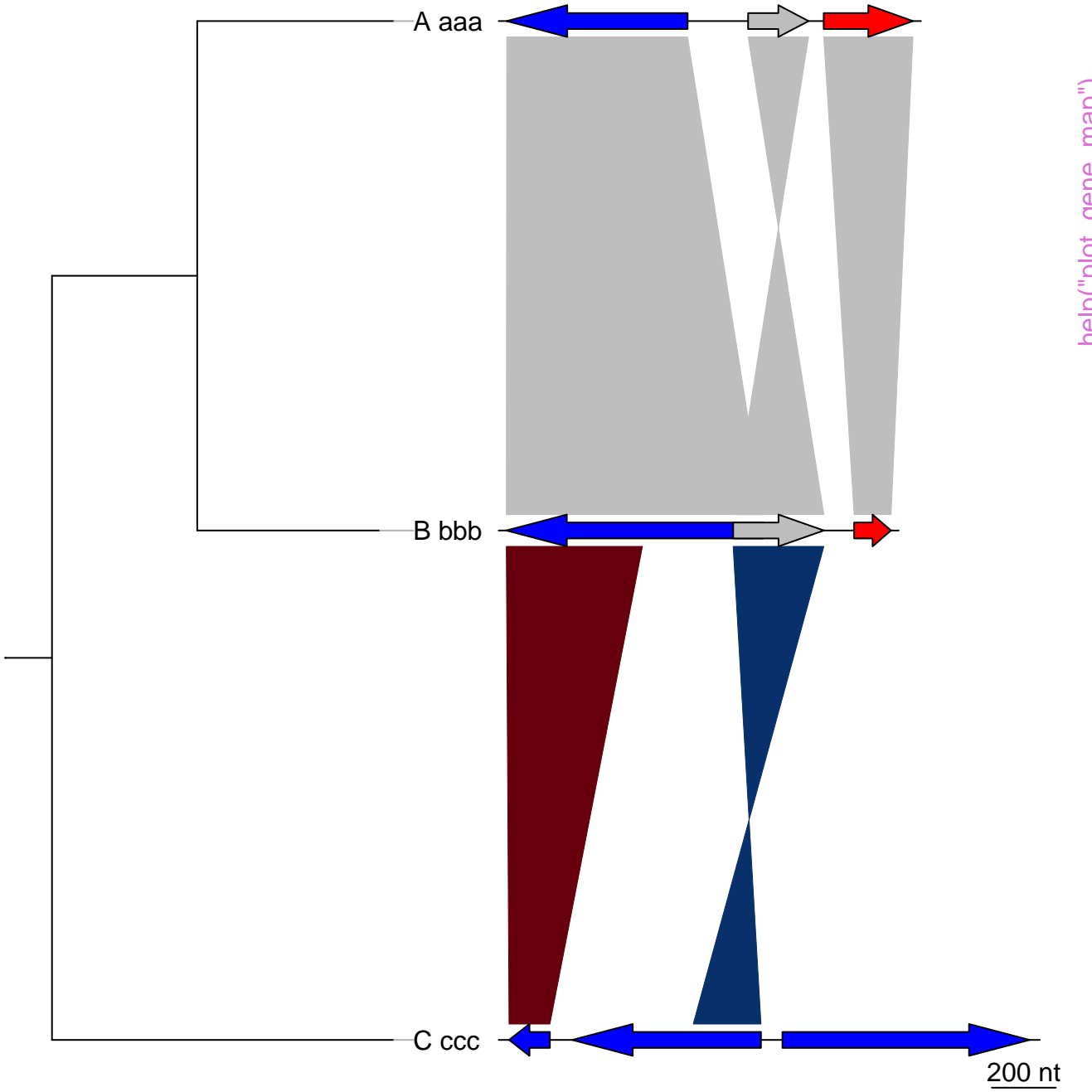
help("plot\_gene\_map")

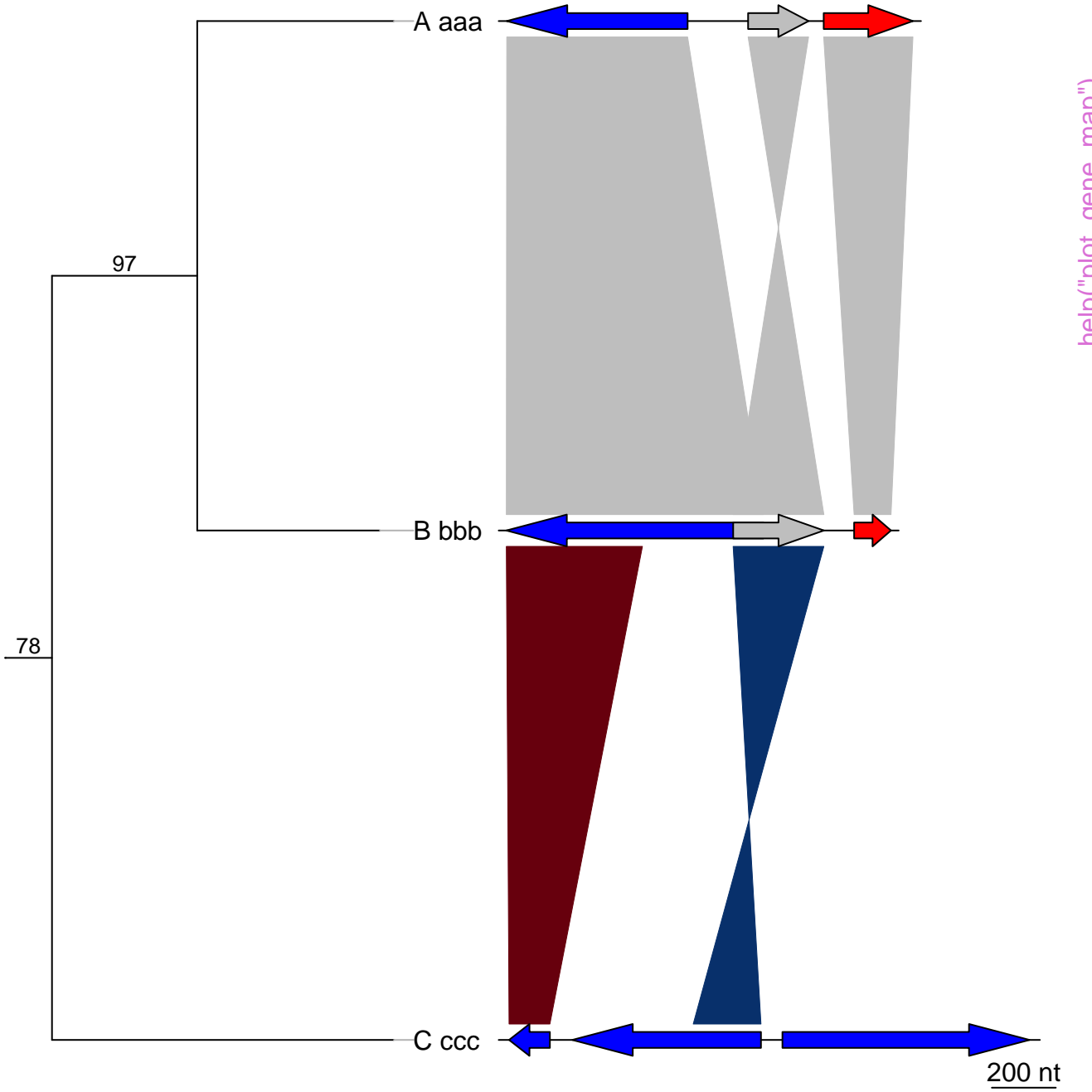
200 nt



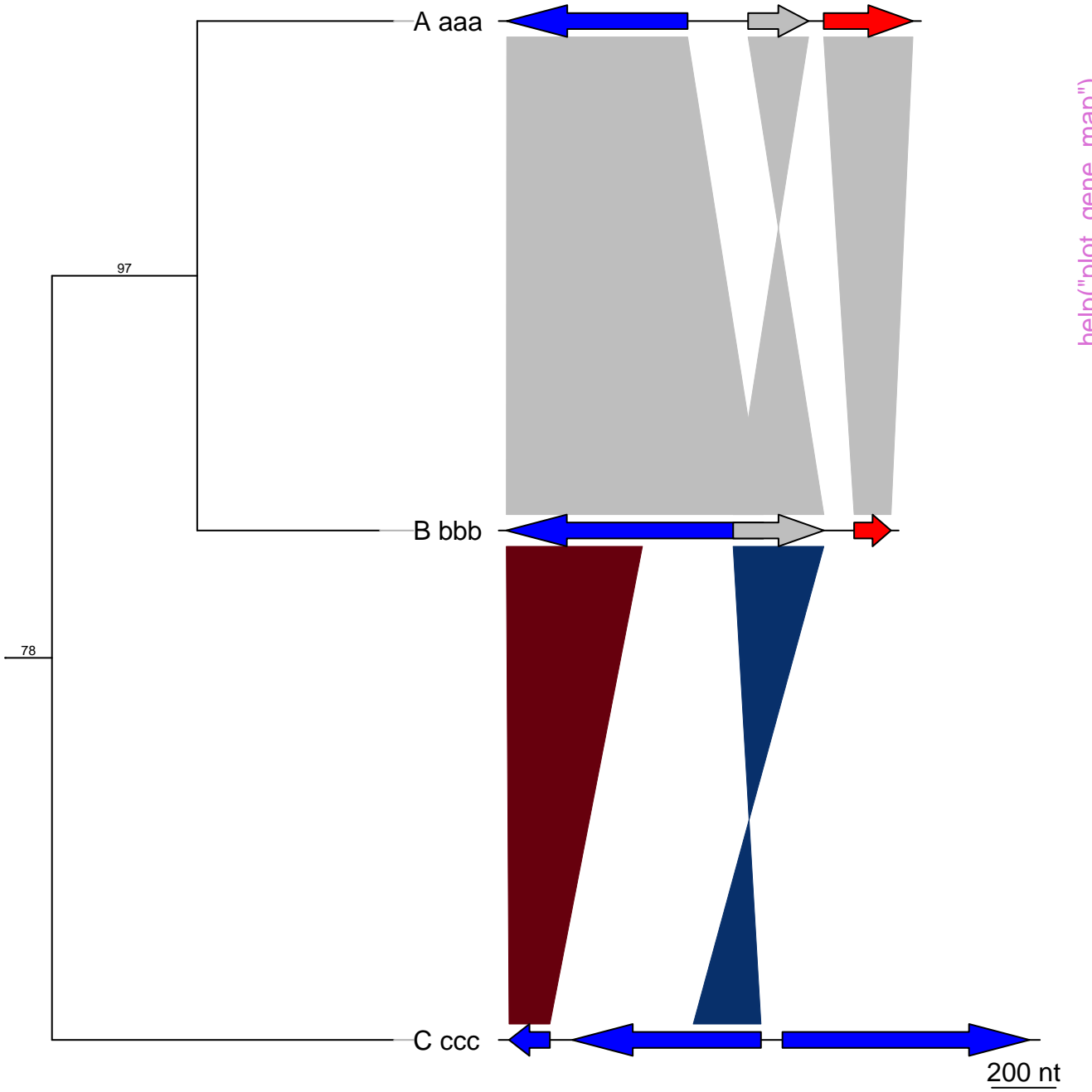
help("plot\_gene\_map")

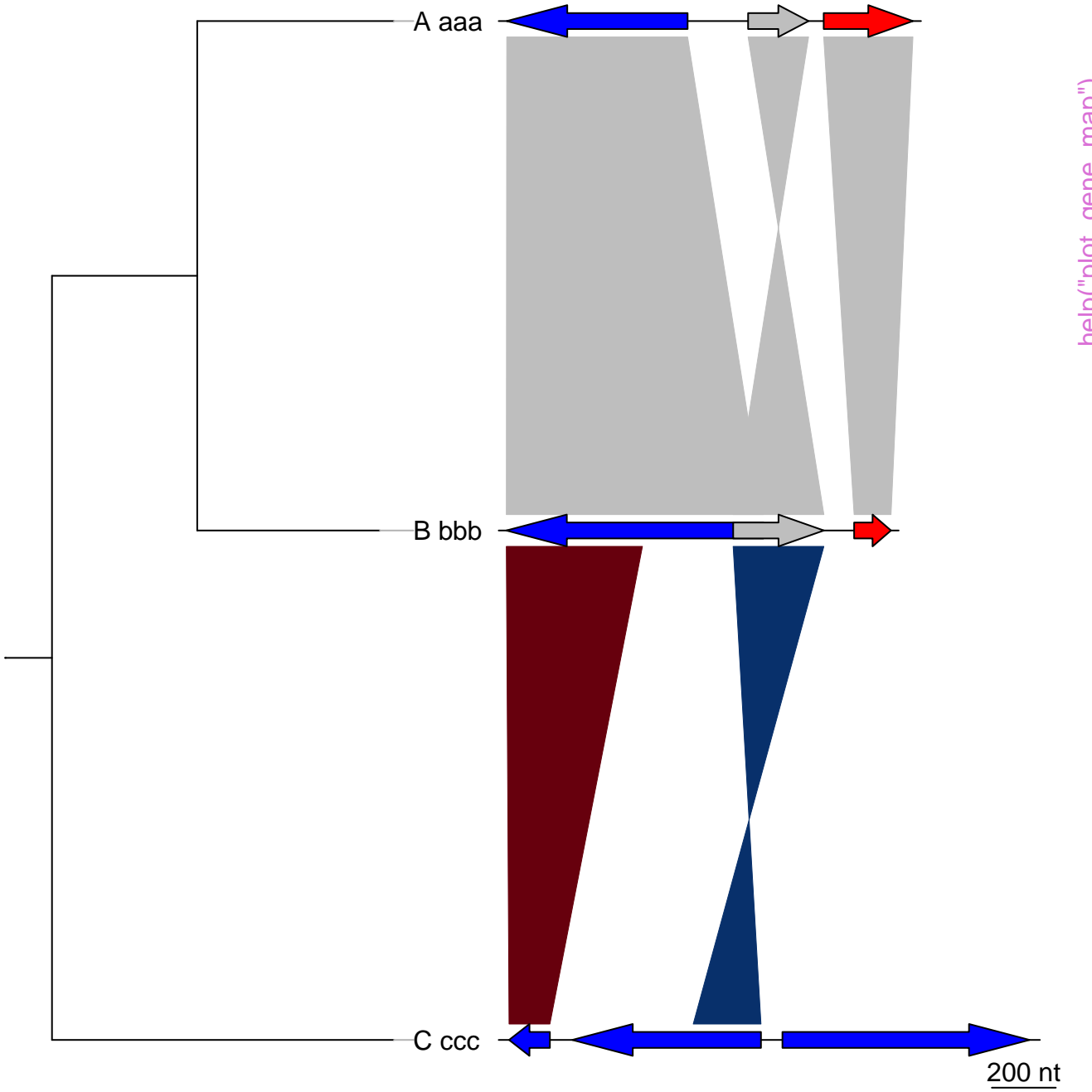
200 nt

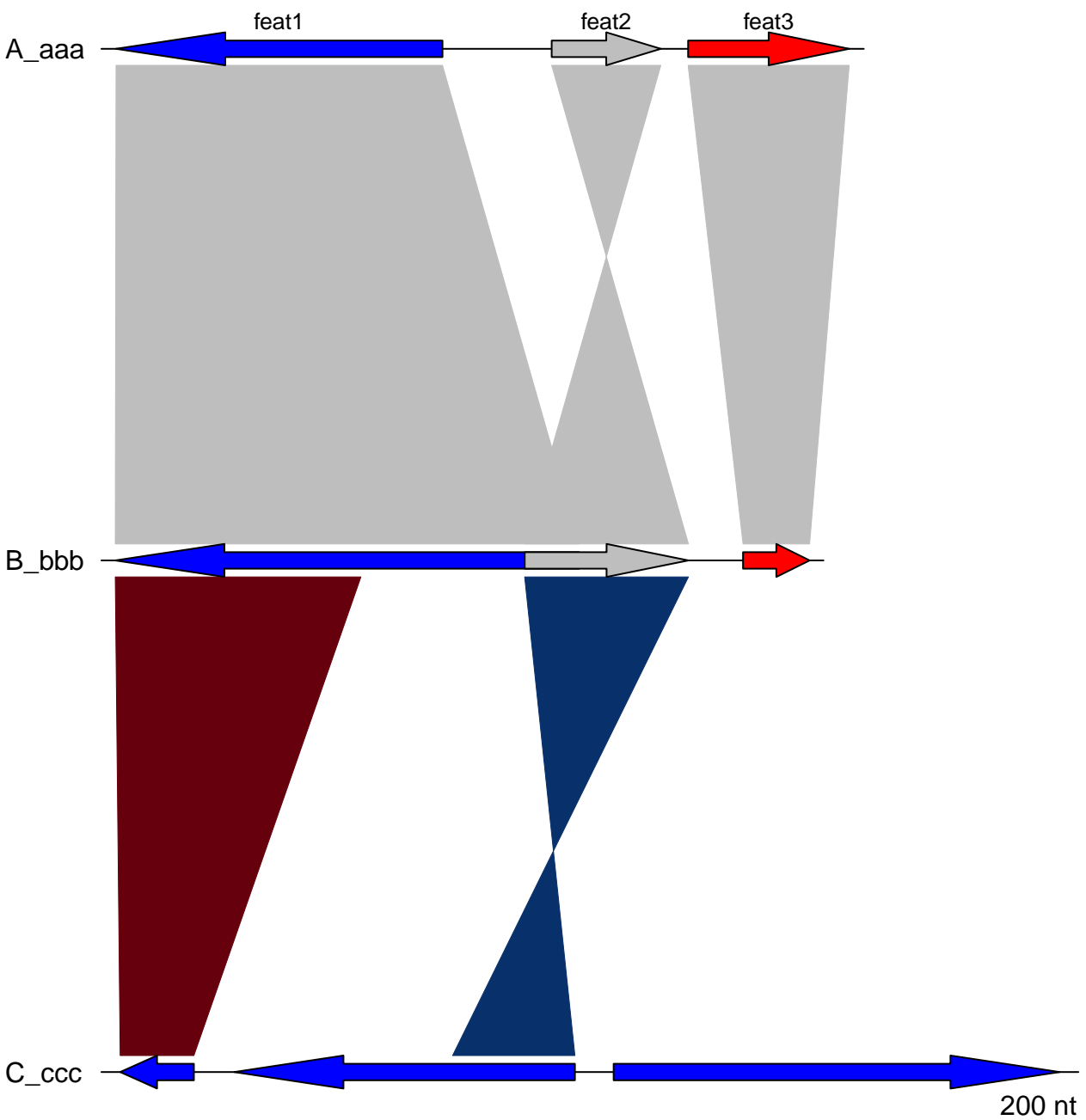




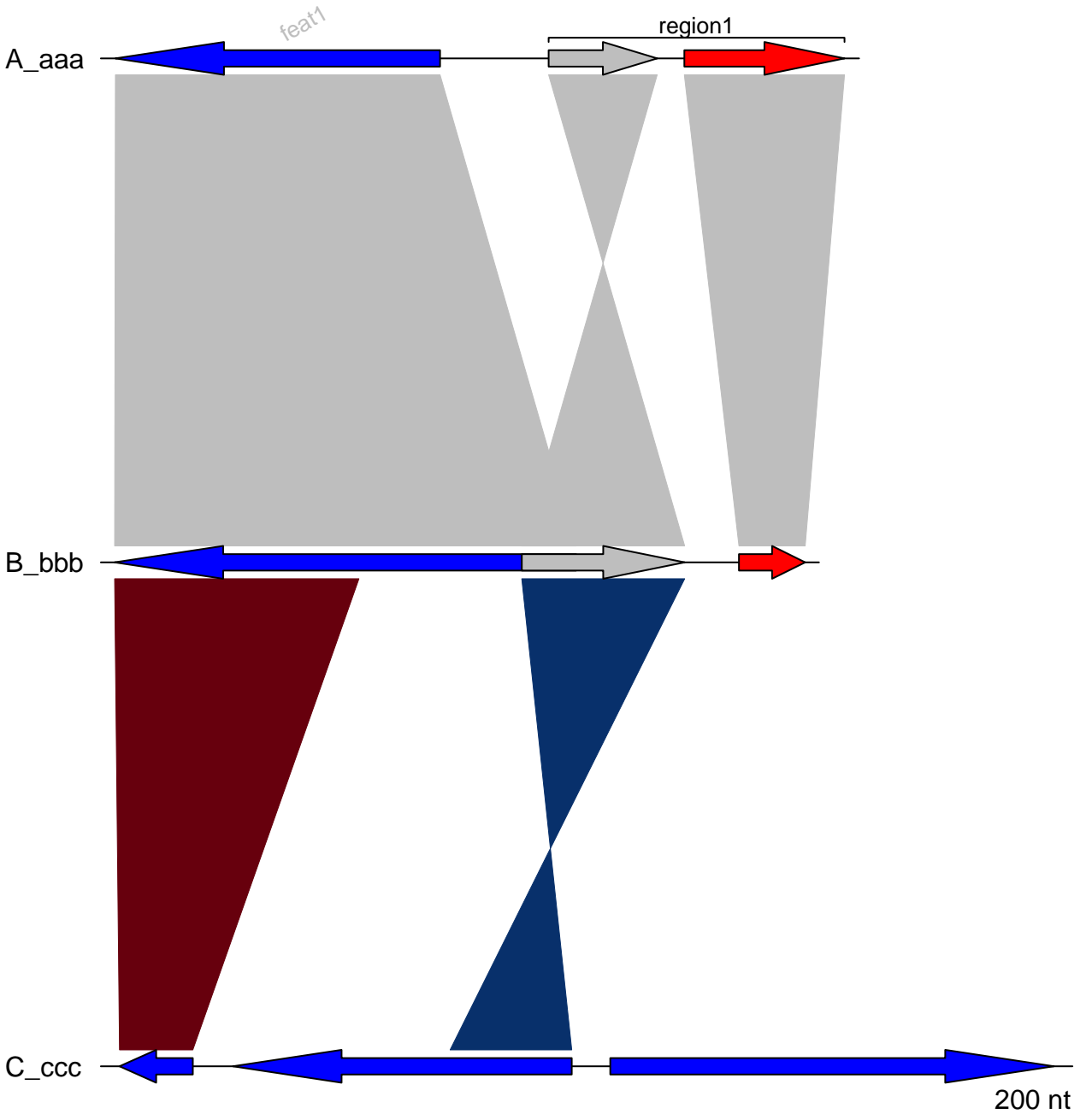






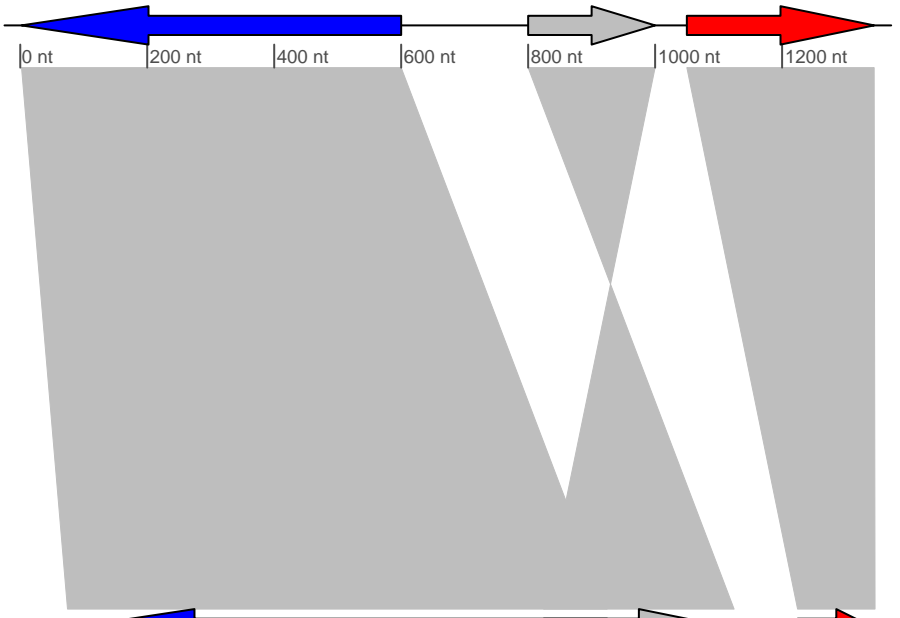


help("plot\_gene\_map")

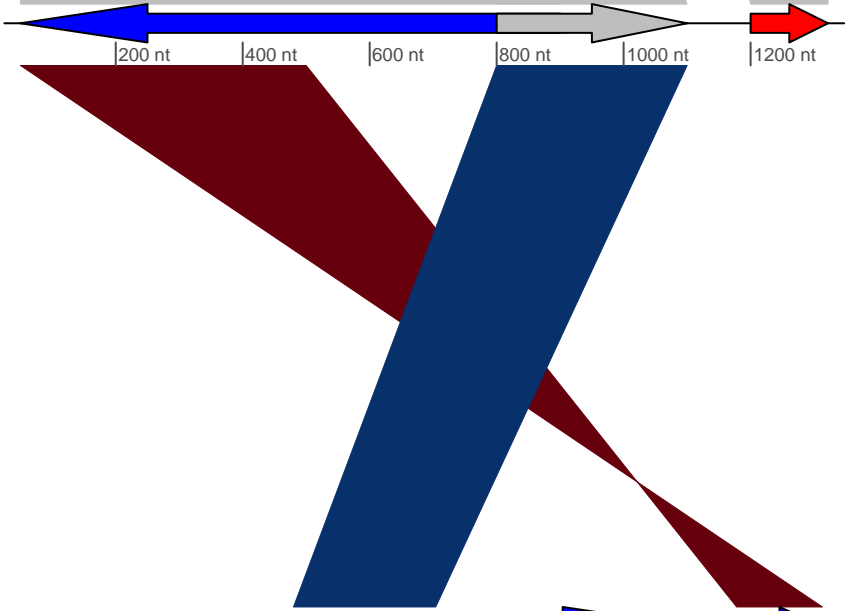


help("plot\_gene\_map")

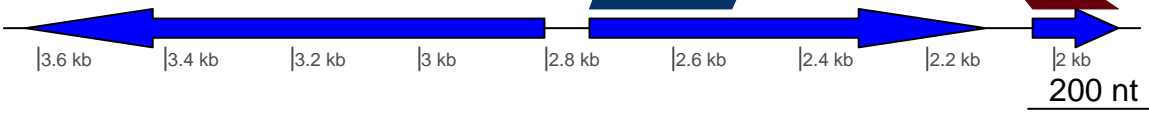
A\_aaa



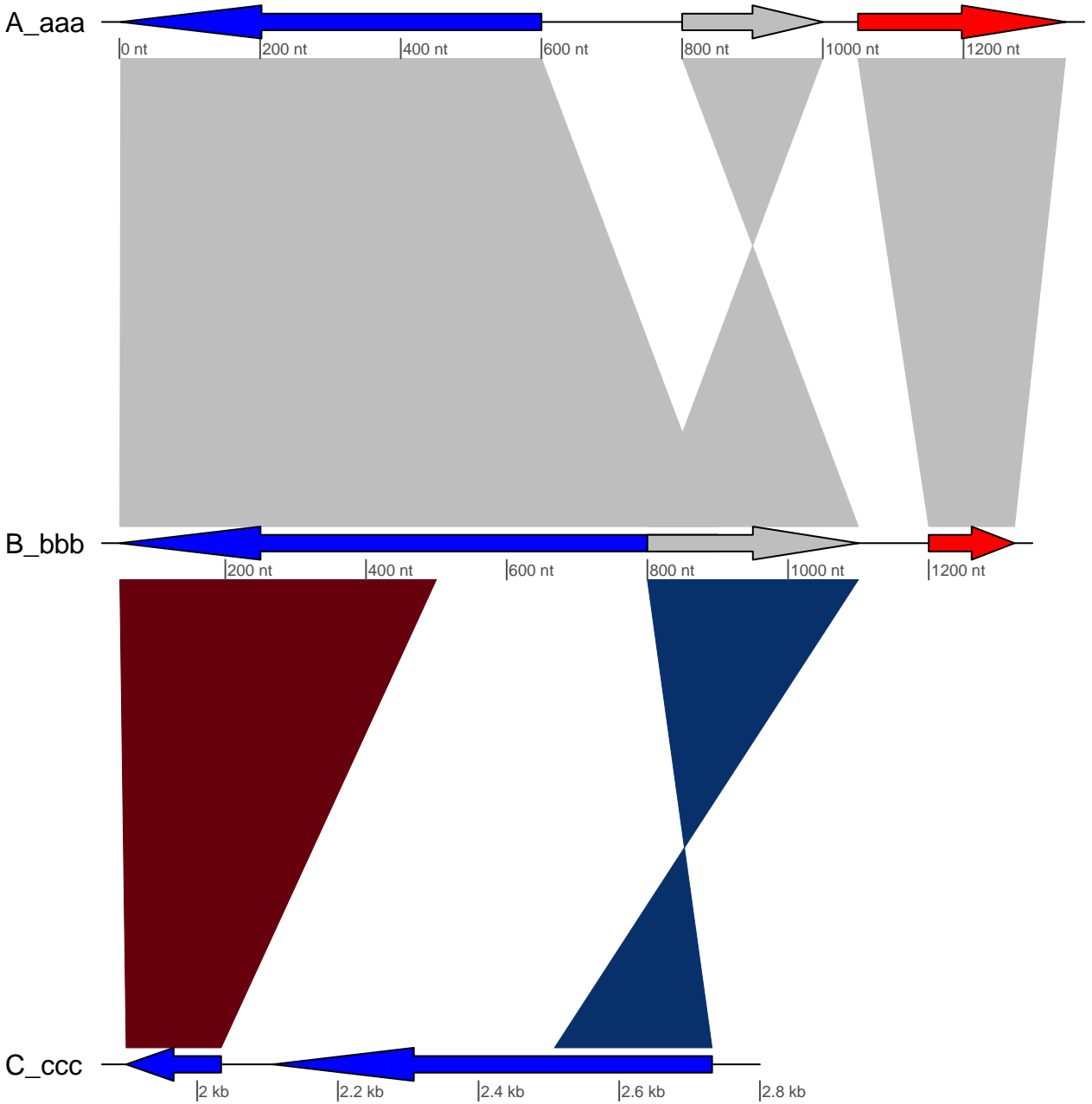
B\_bbb



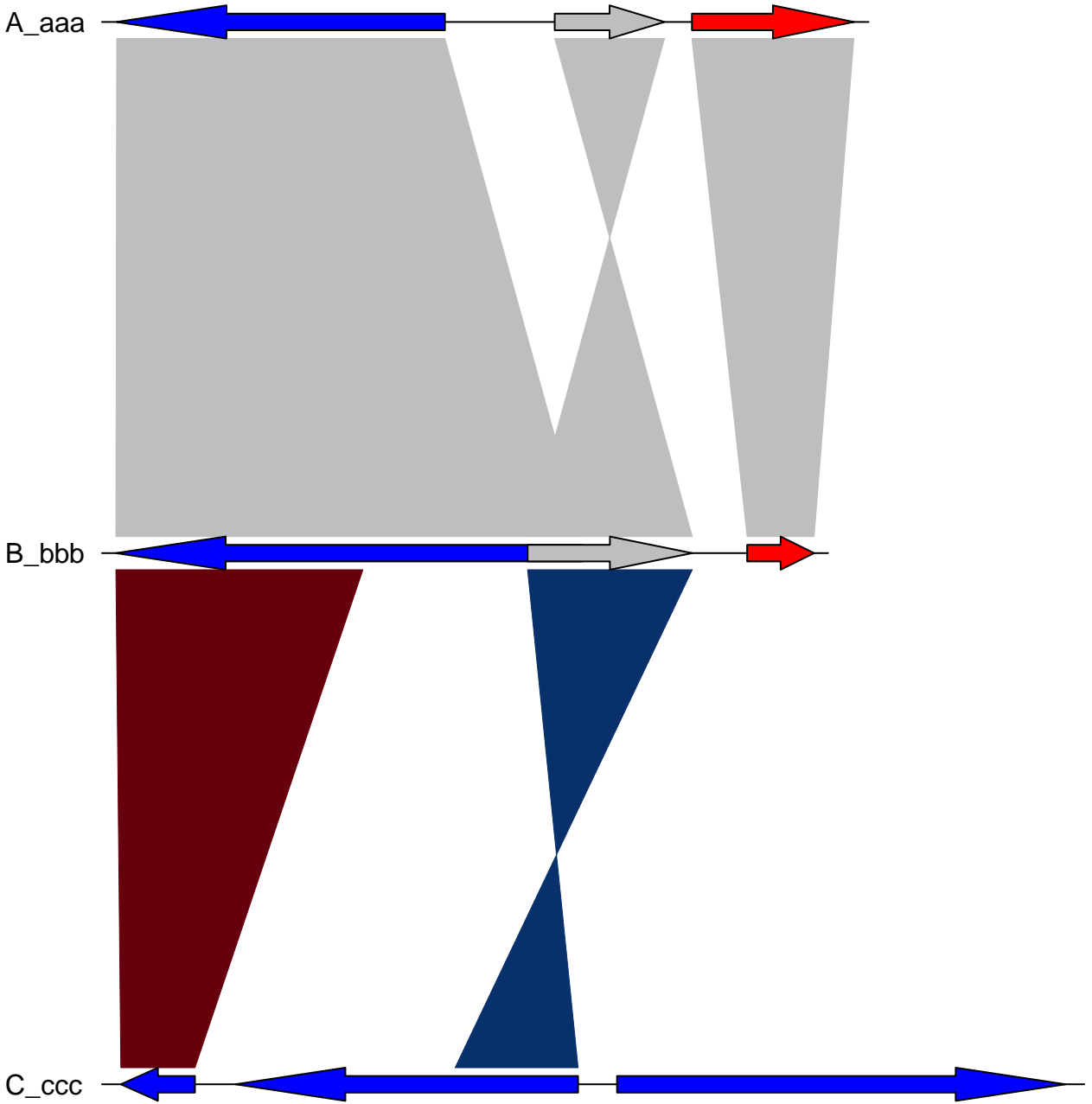
C\_ccc



help("plot\_gene\_map")

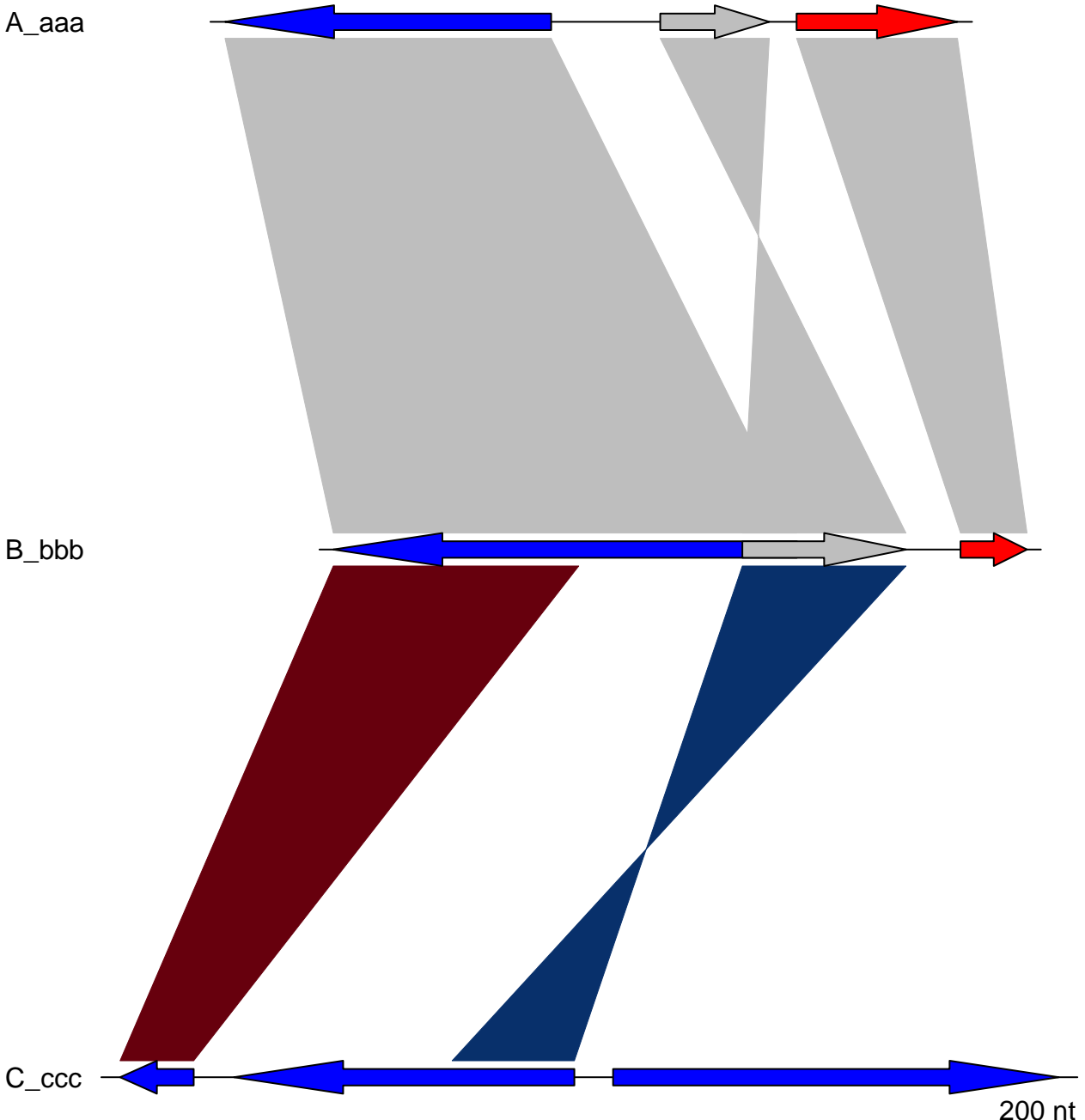


help("plot\_gene\_map")



help("plot\_gene\_map")

200 nt

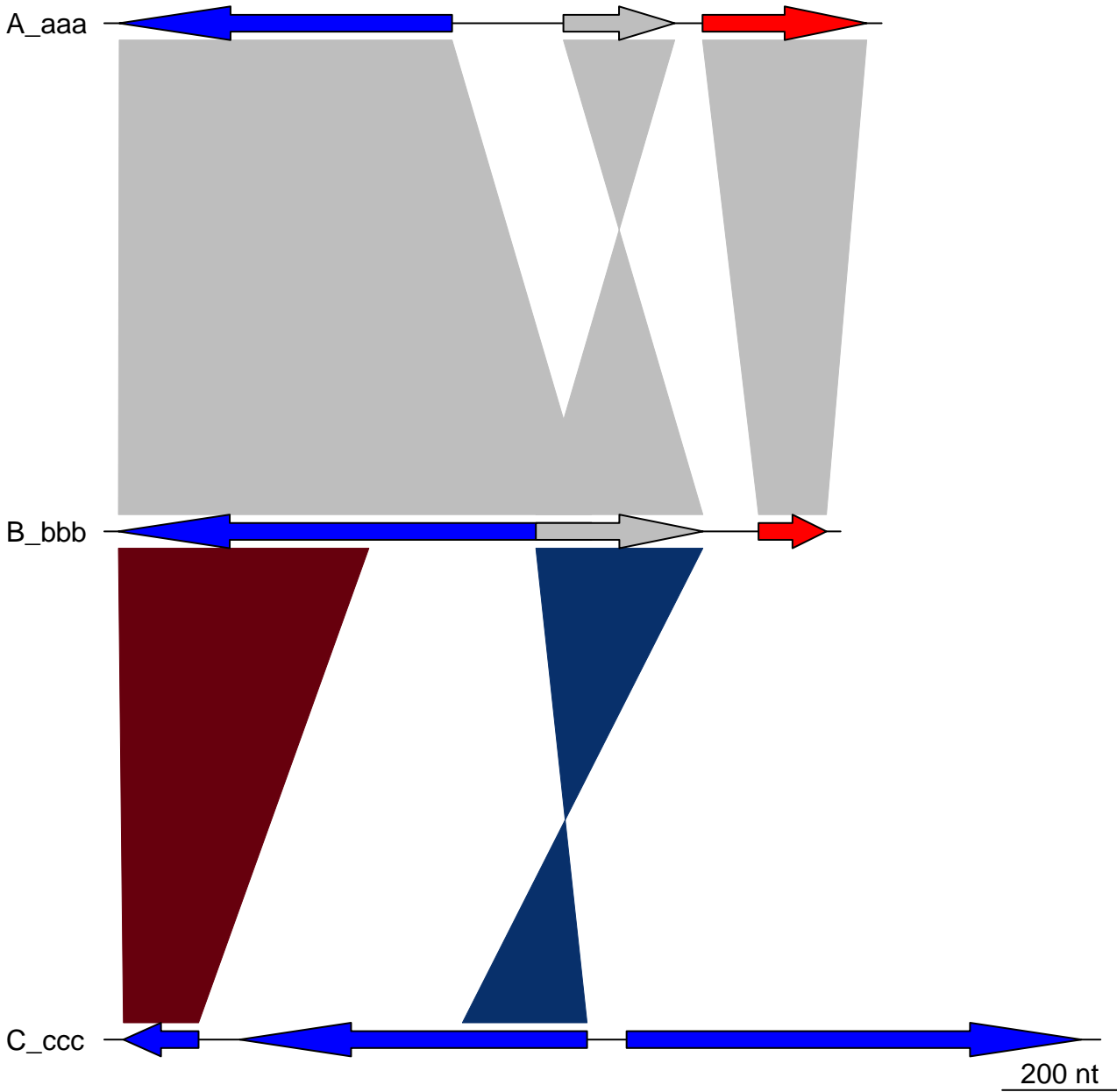


help("plot\_gene\_map")

200 nt



# Comparison of A, B and C



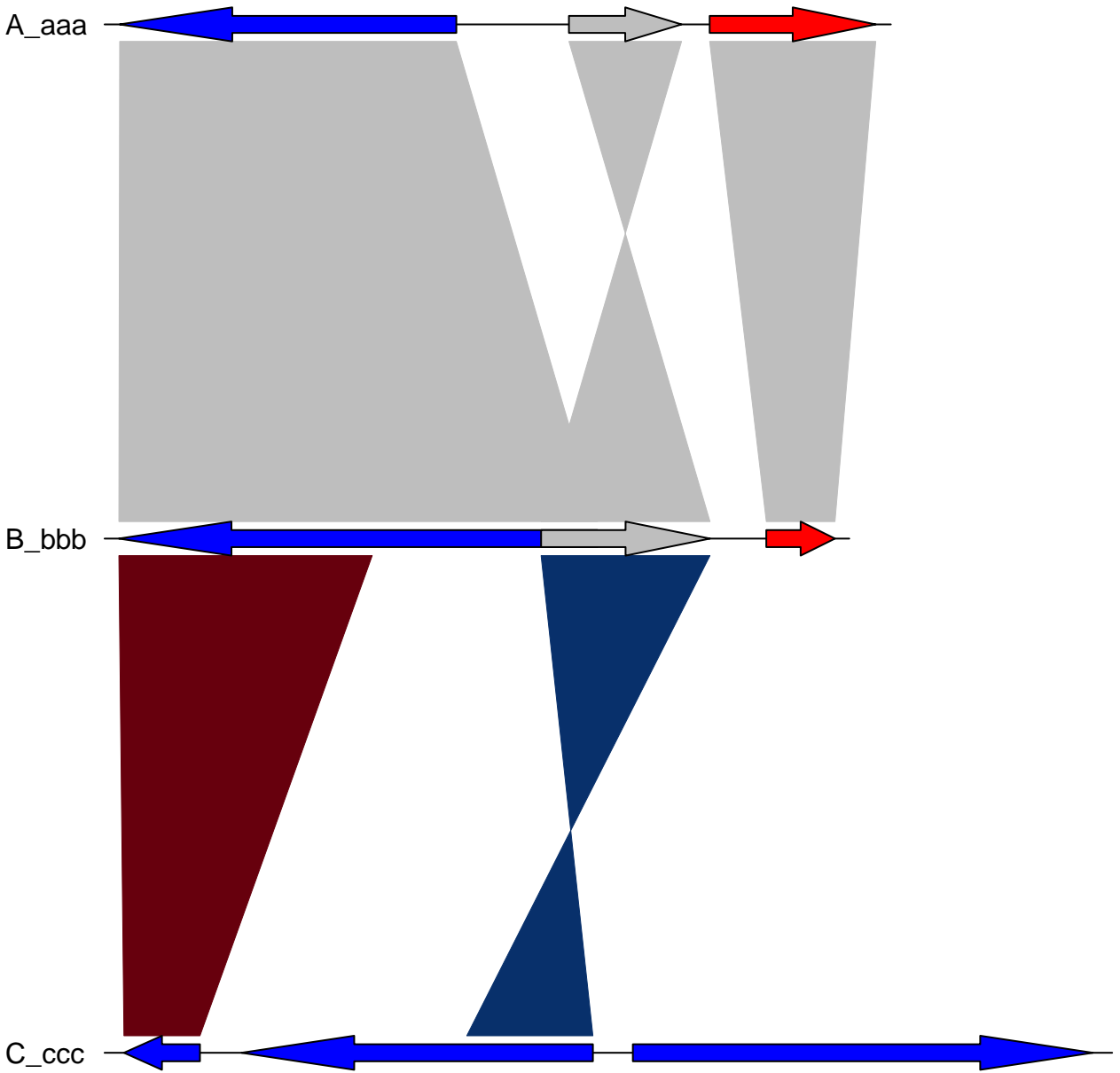
help("plot\_gene\_map")

# Comparison of A, B and C

A\_aaa

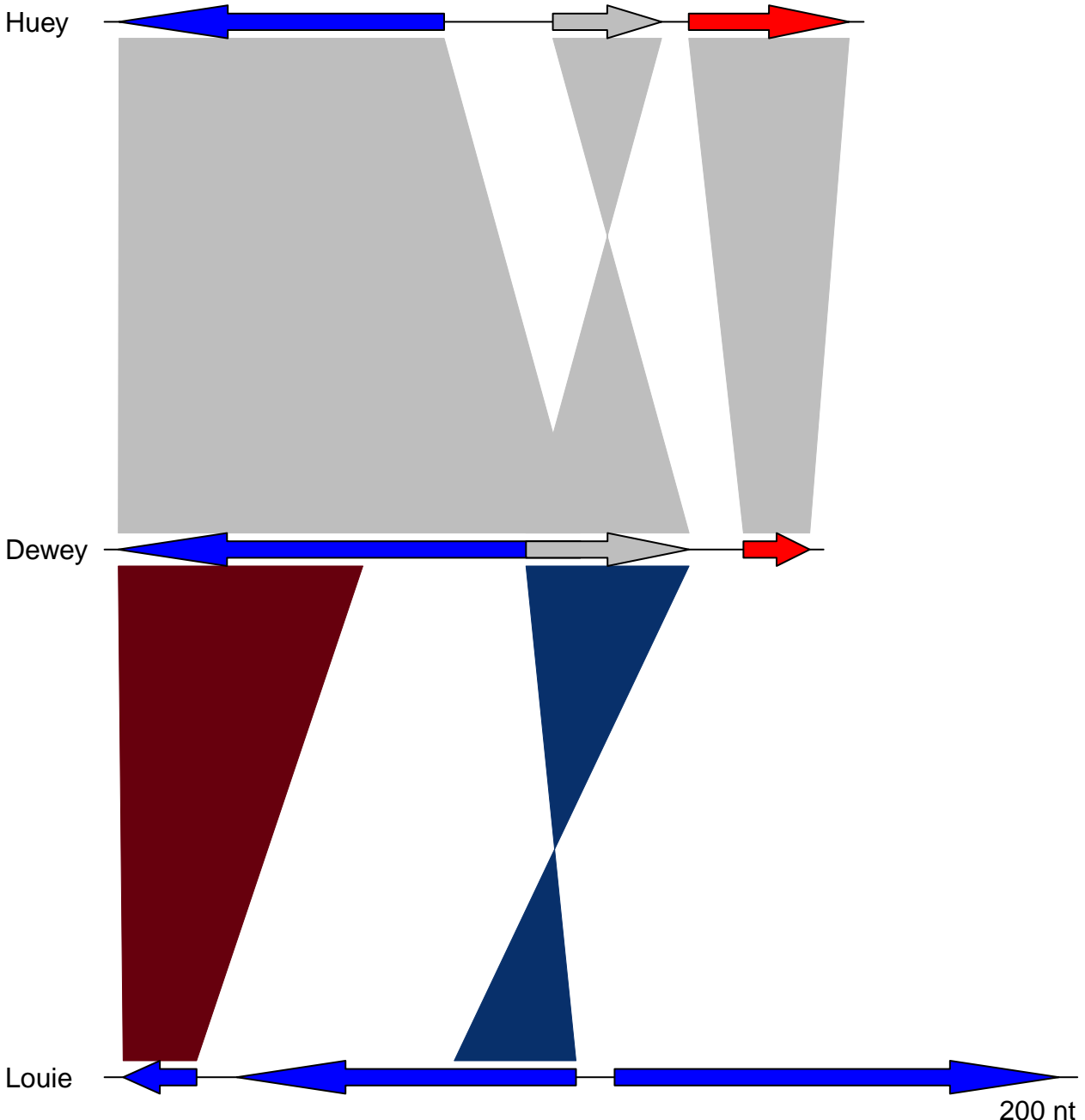
B\_bbb

C\_ccc

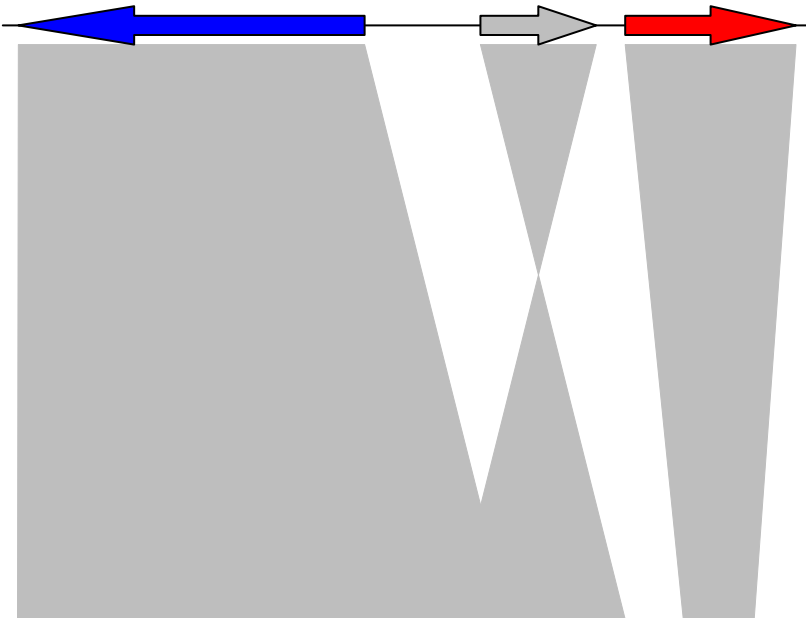


help("plot\_gene\_map")

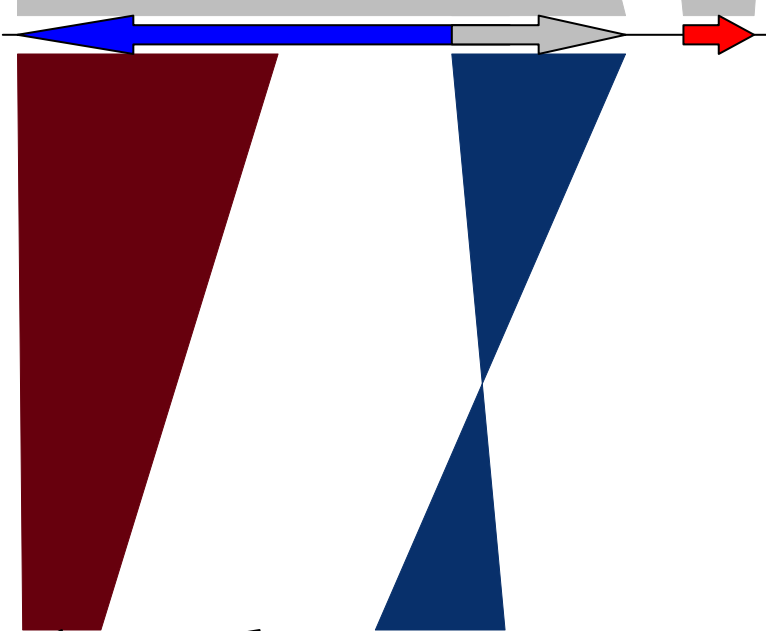
200 nt



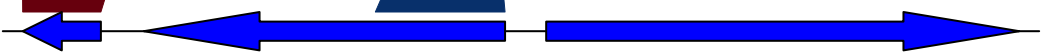
Huey



Dewey

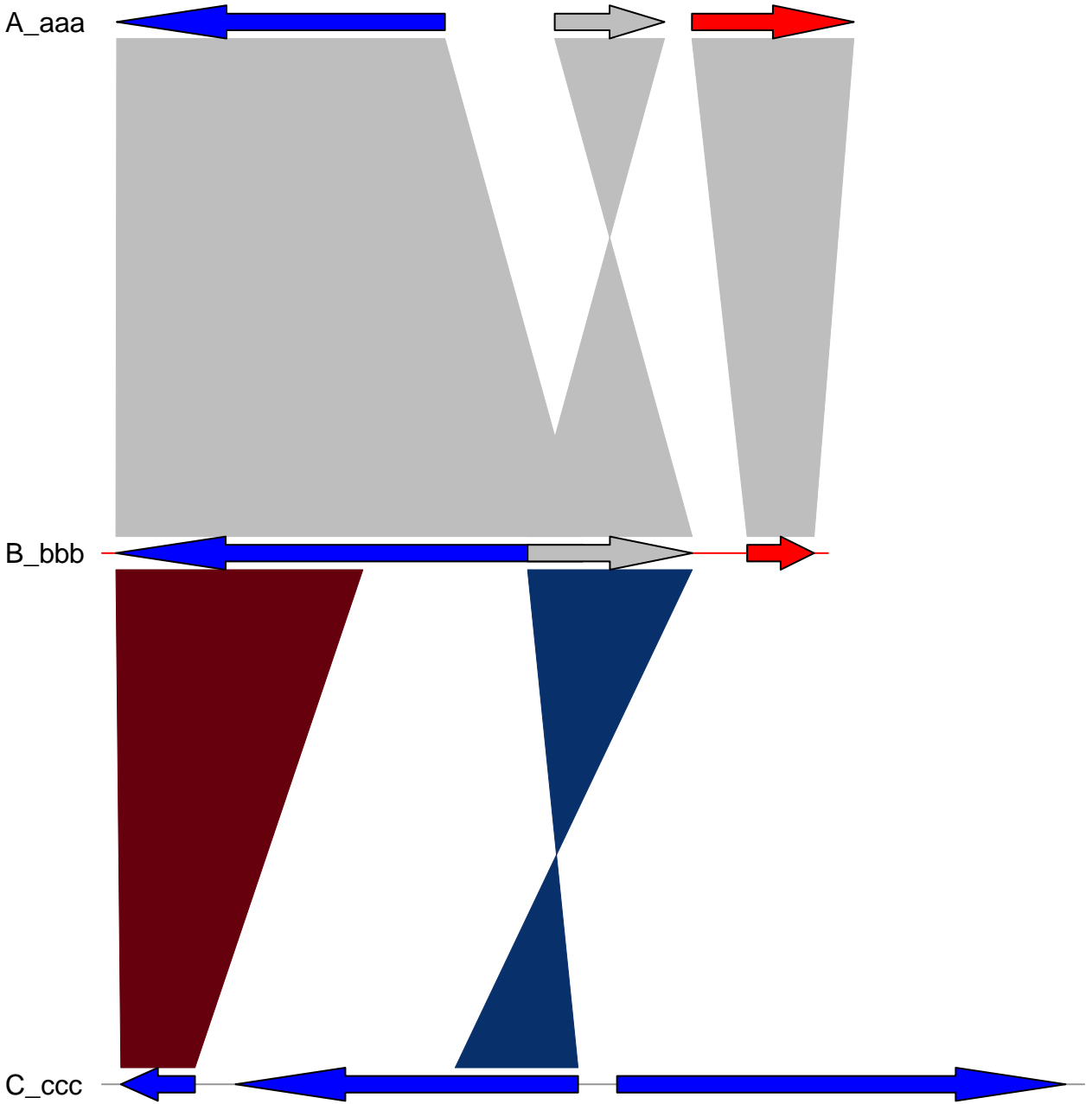


Louie



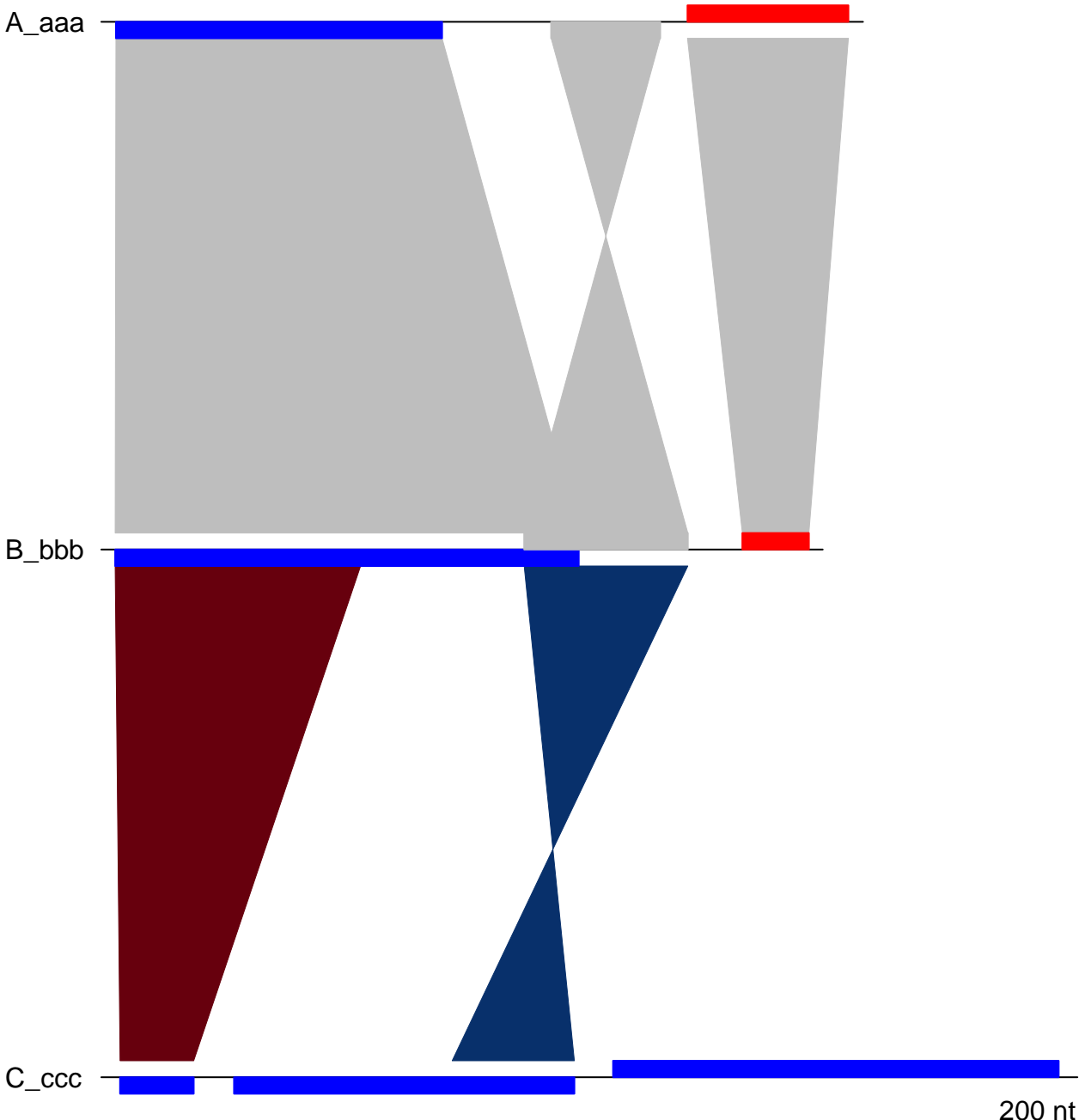
200 nt

help("plot\_gene\_map")

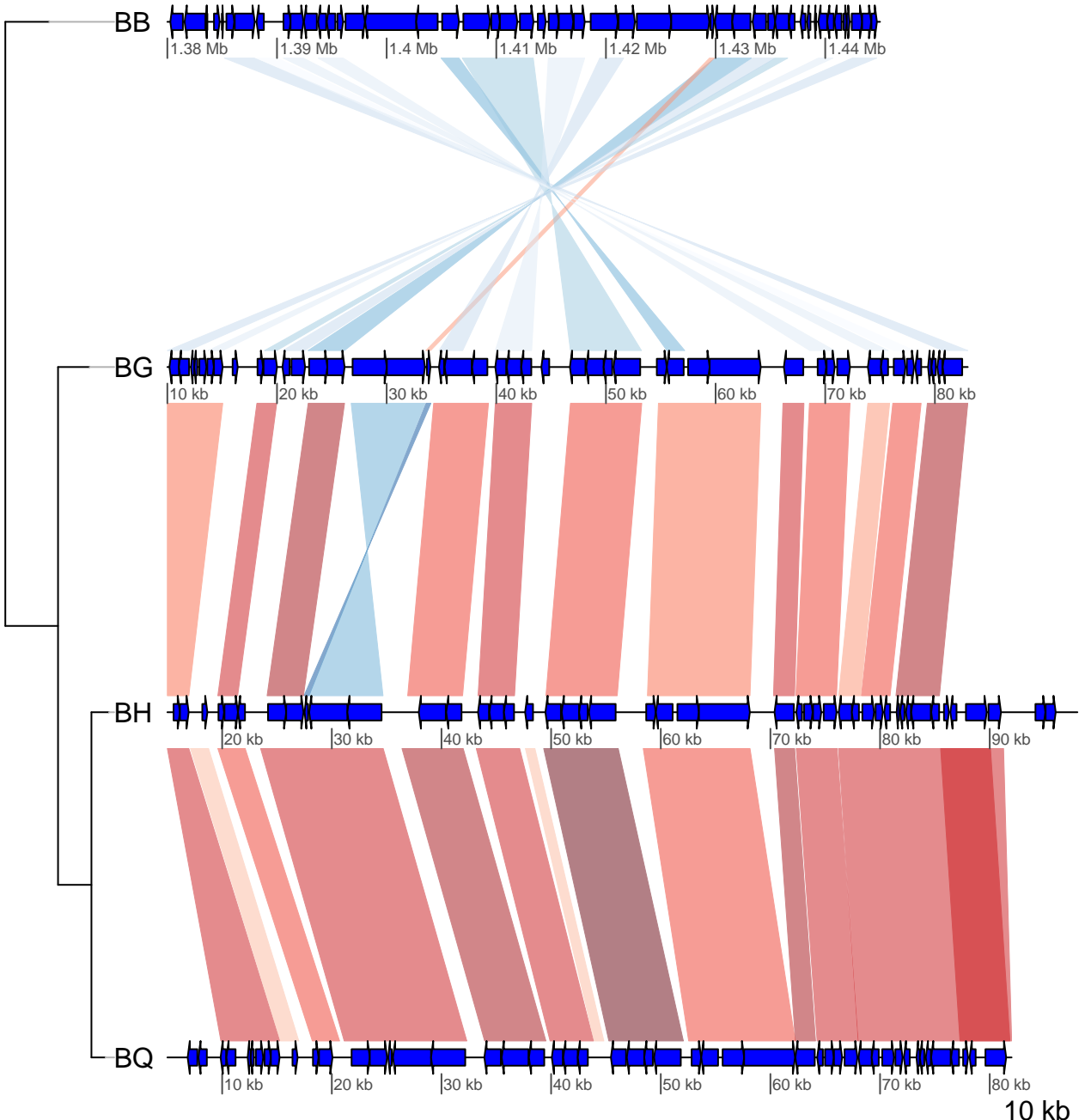


help("plot\_gene\_map")

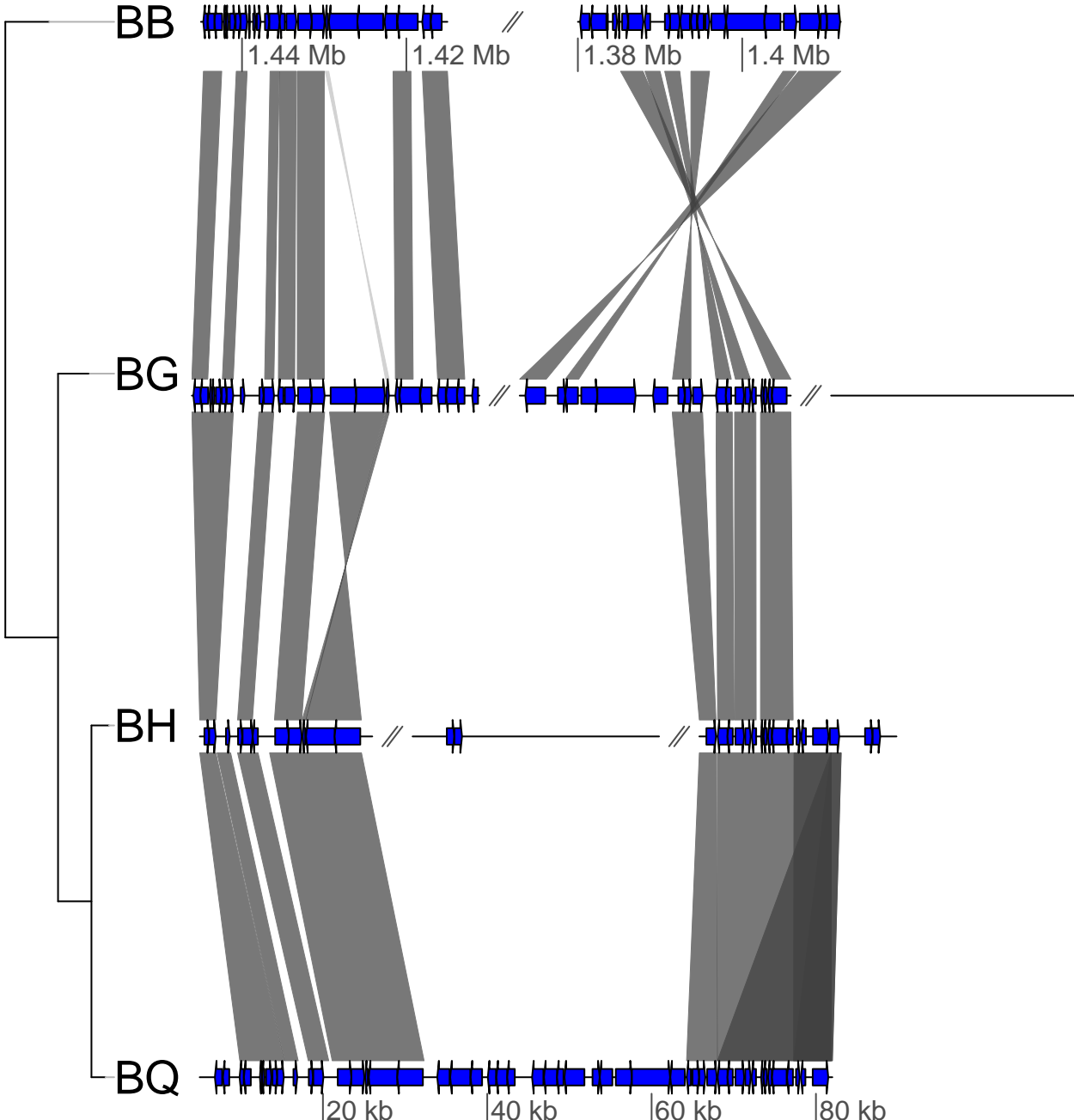
200 nt



help("plot\_gene\_map")

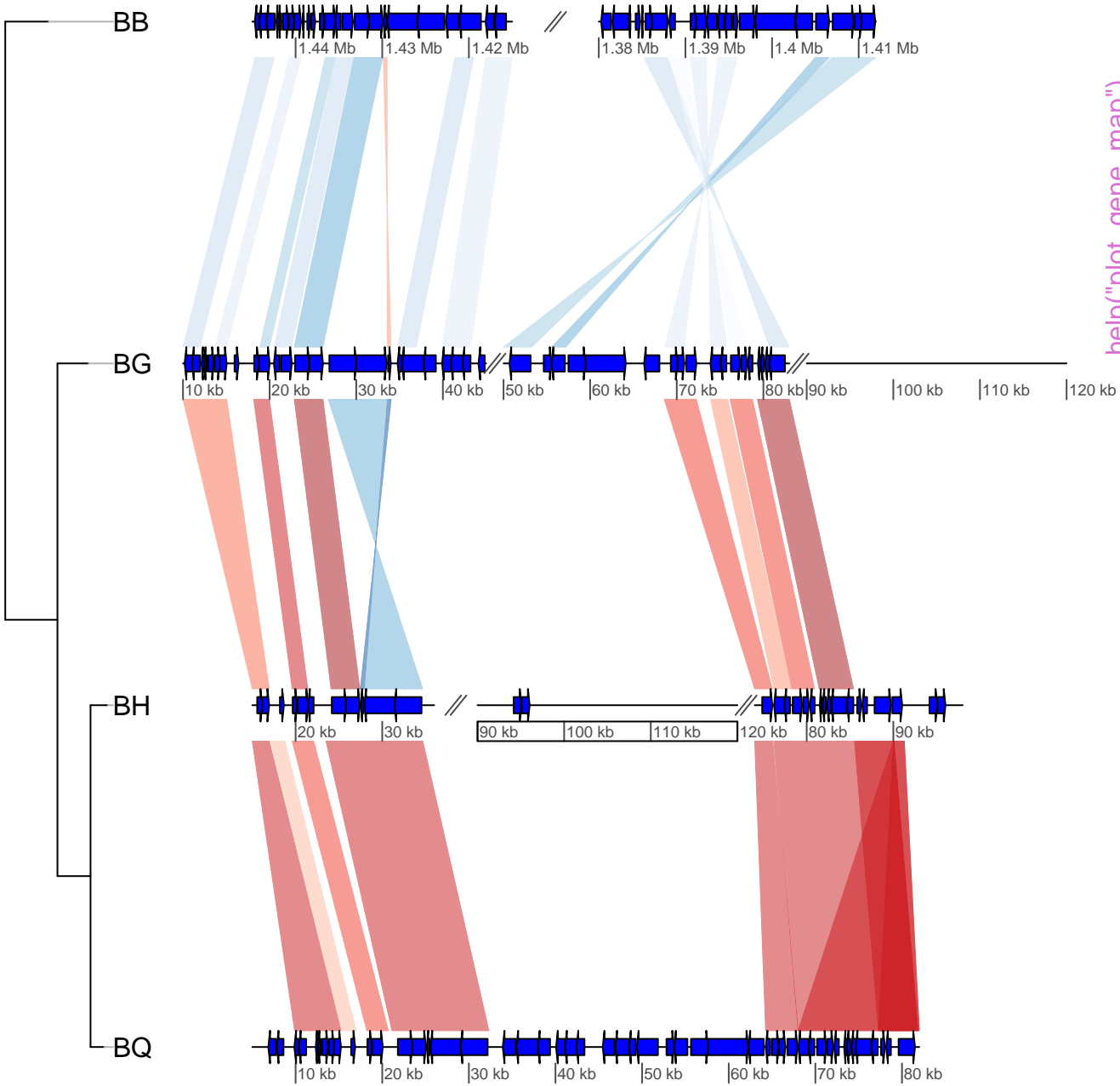


`help("plot_gene_map")`

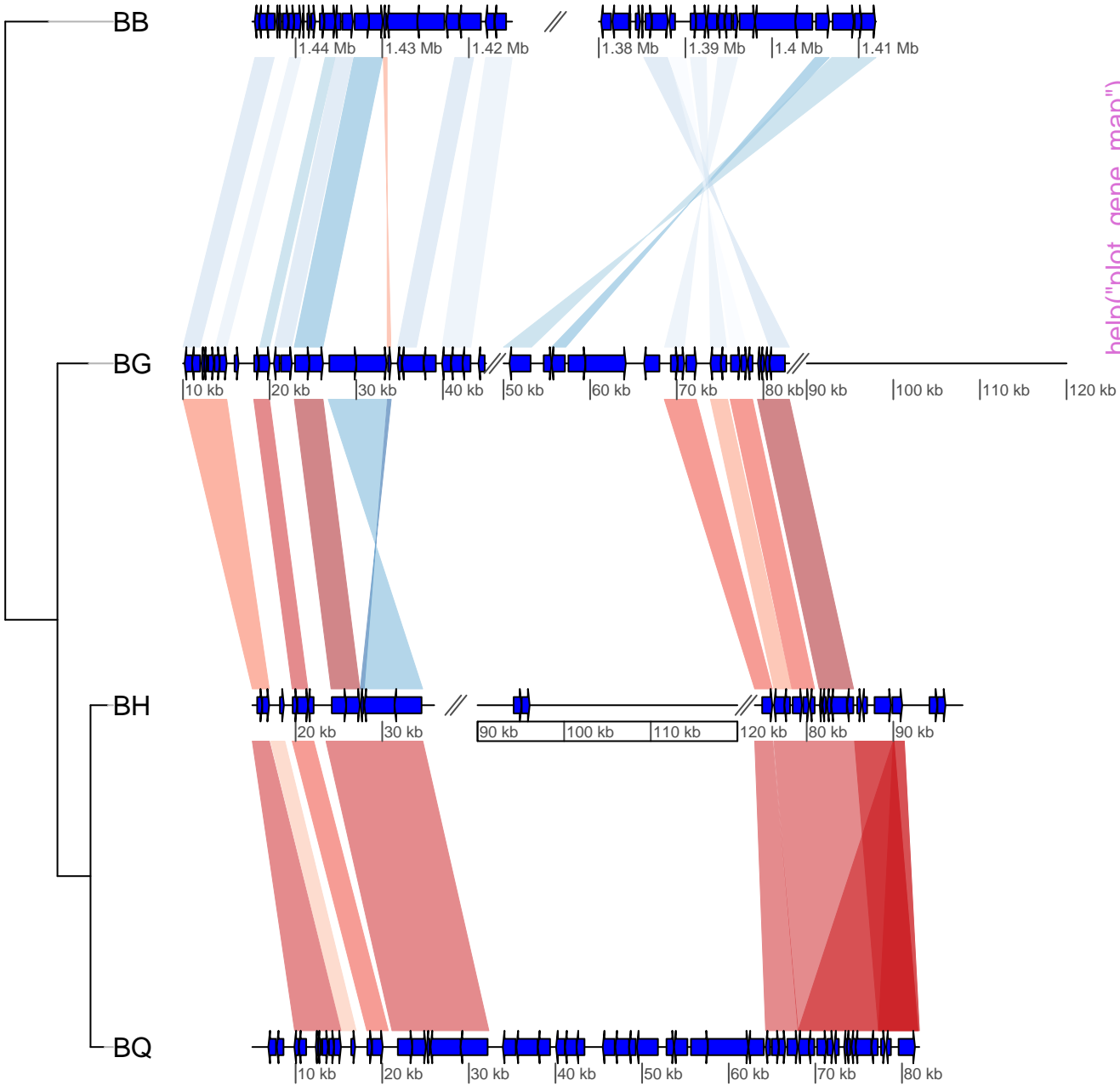


help("plot\_gene\_map")

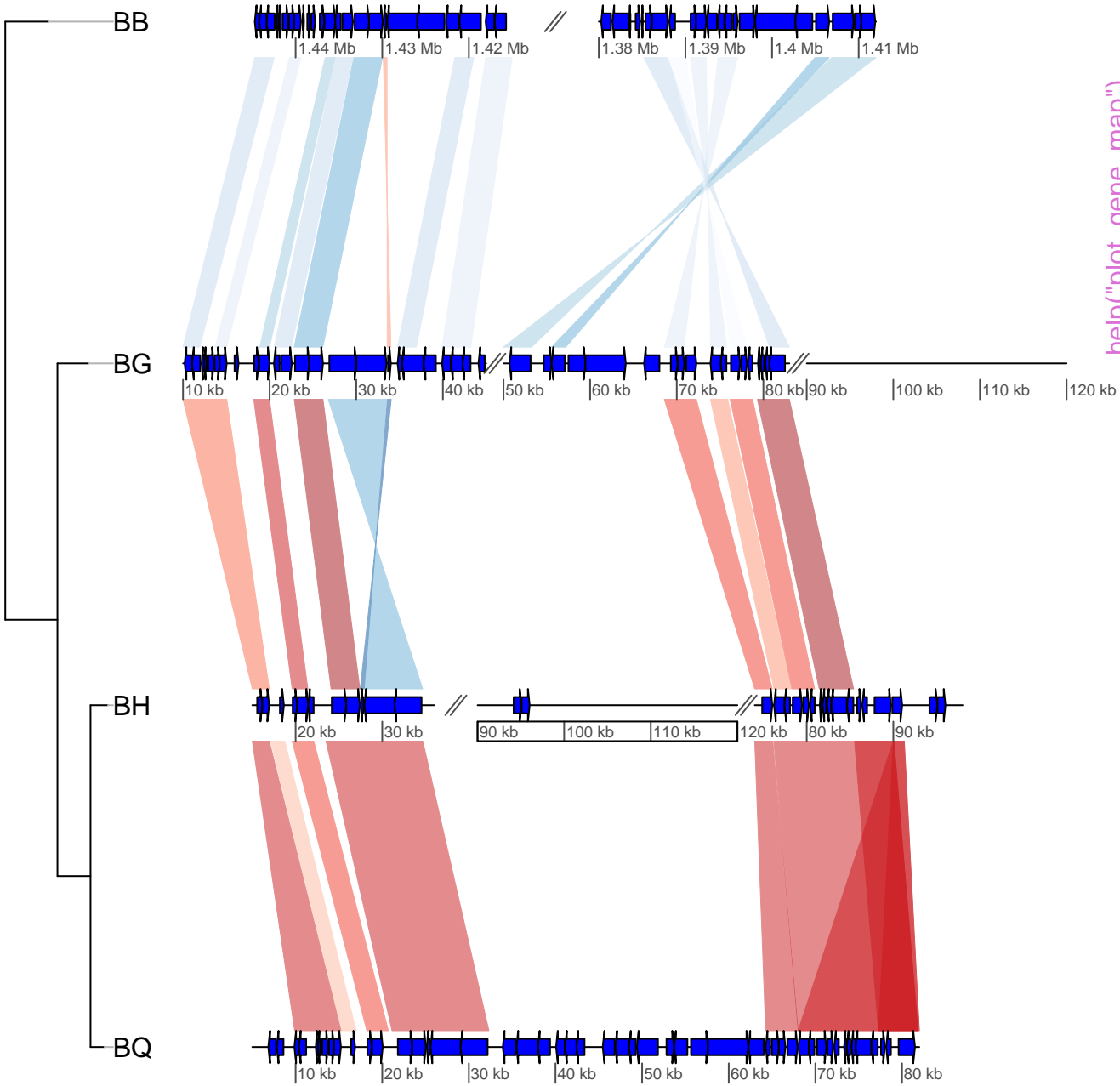




10 kb

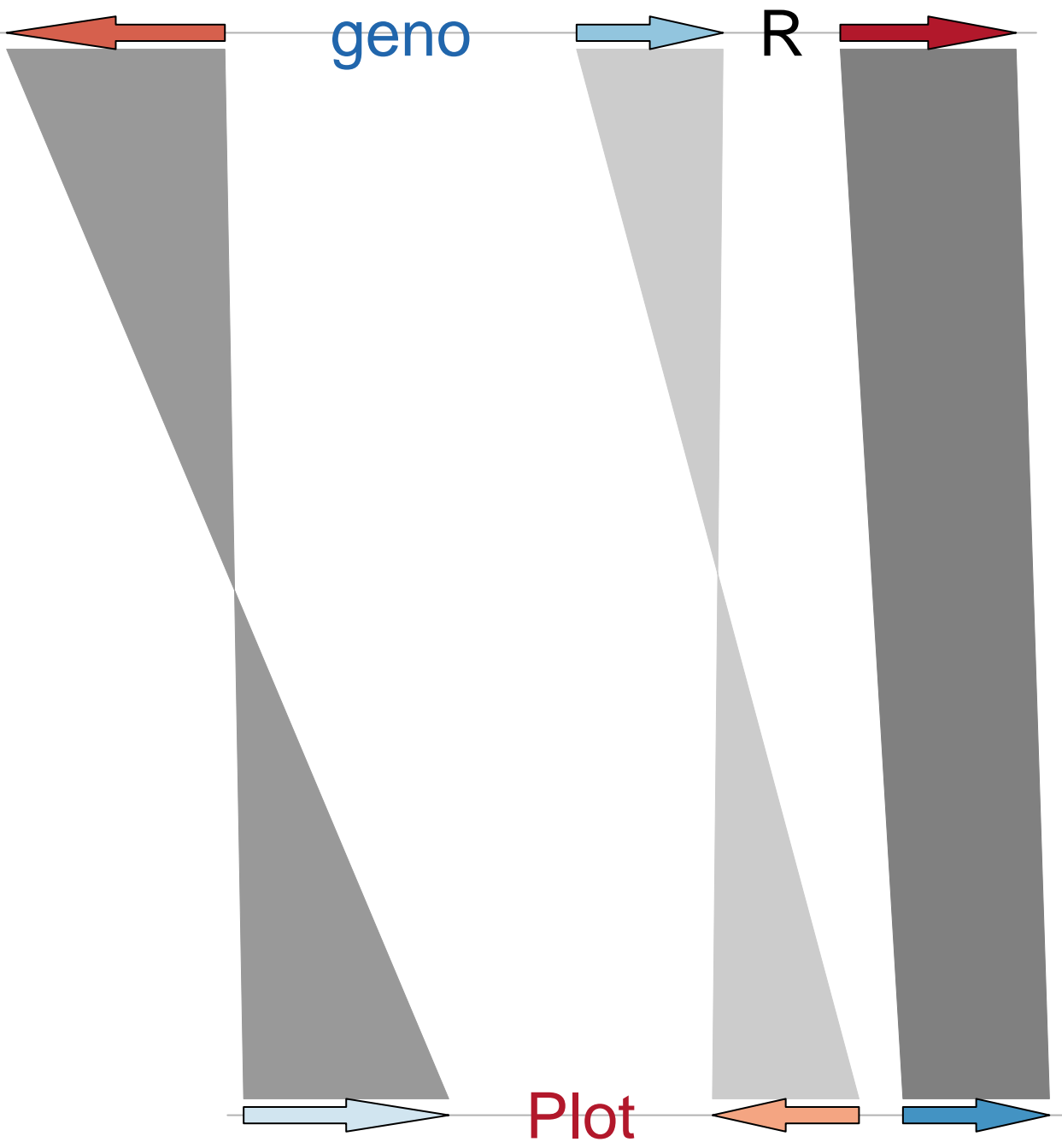


10 kb



help("plot\_gene\_map")

10 kb



B\_bacilliformis



B\_grahamii



B\_henselae

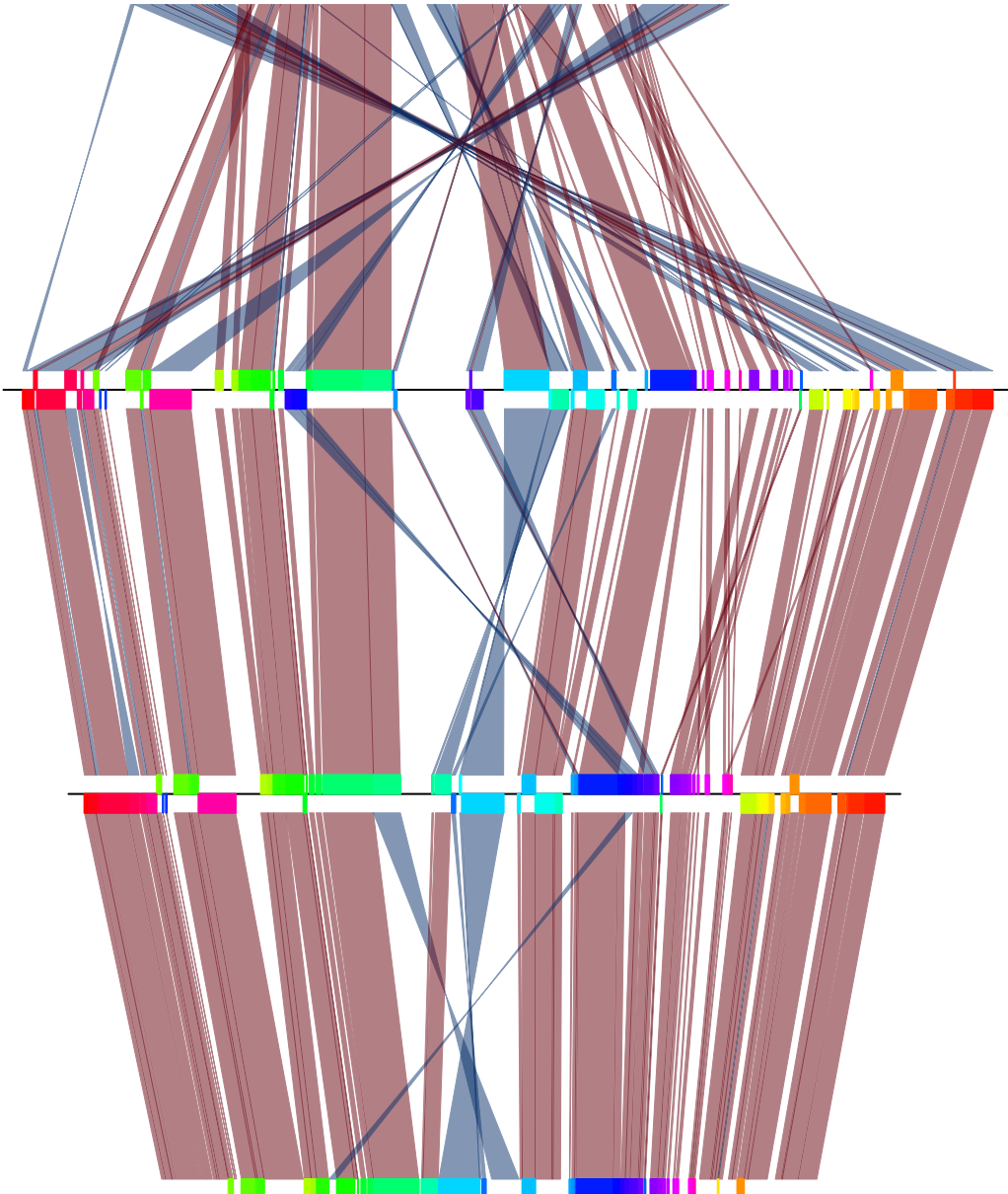


B\_quintana



help("read\_functions")

500 kb

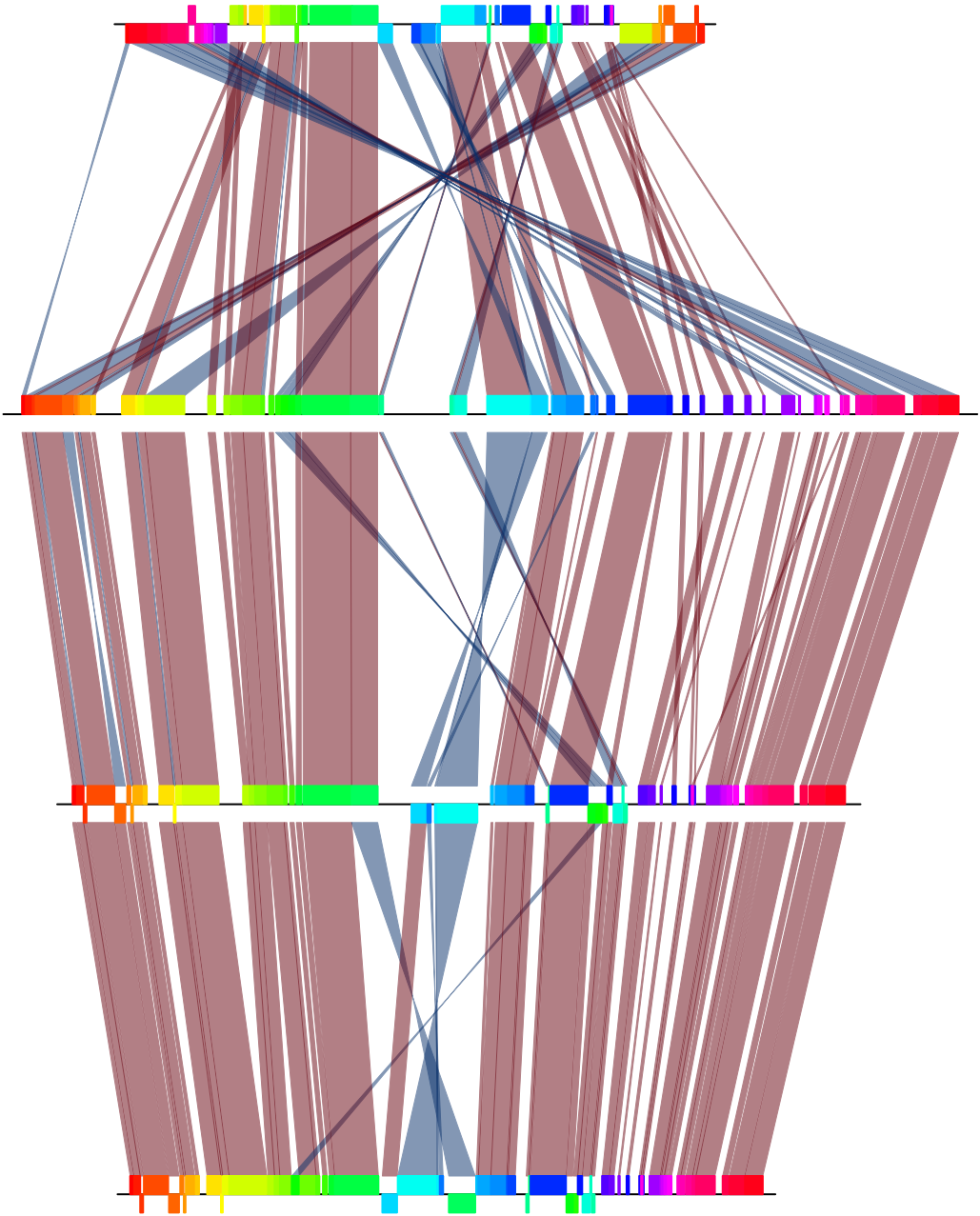


B\_bacilliformis

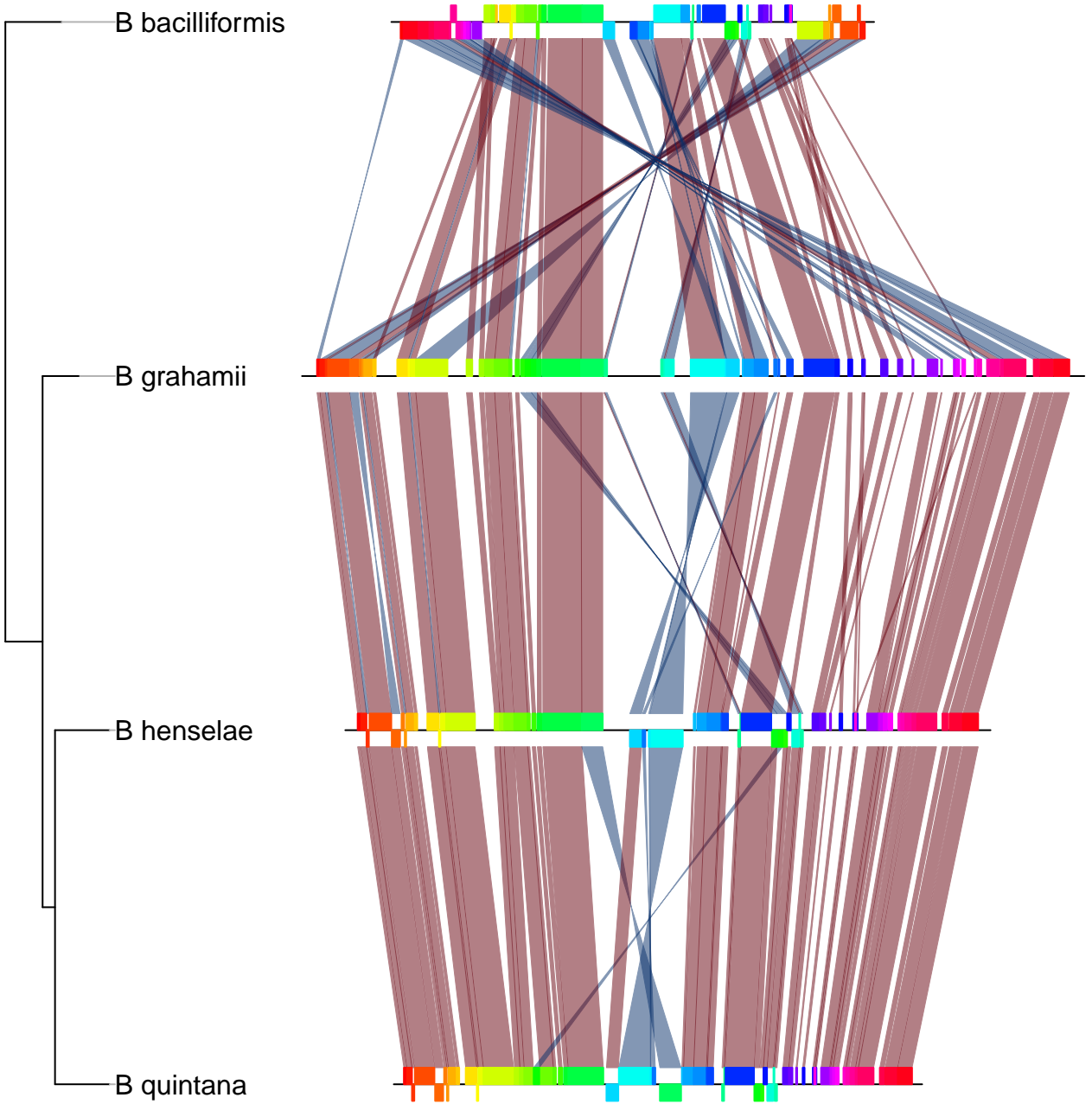
B\_grahamii

B\_henselae

B\_quintana



500 kb



*B. bacilliformis*

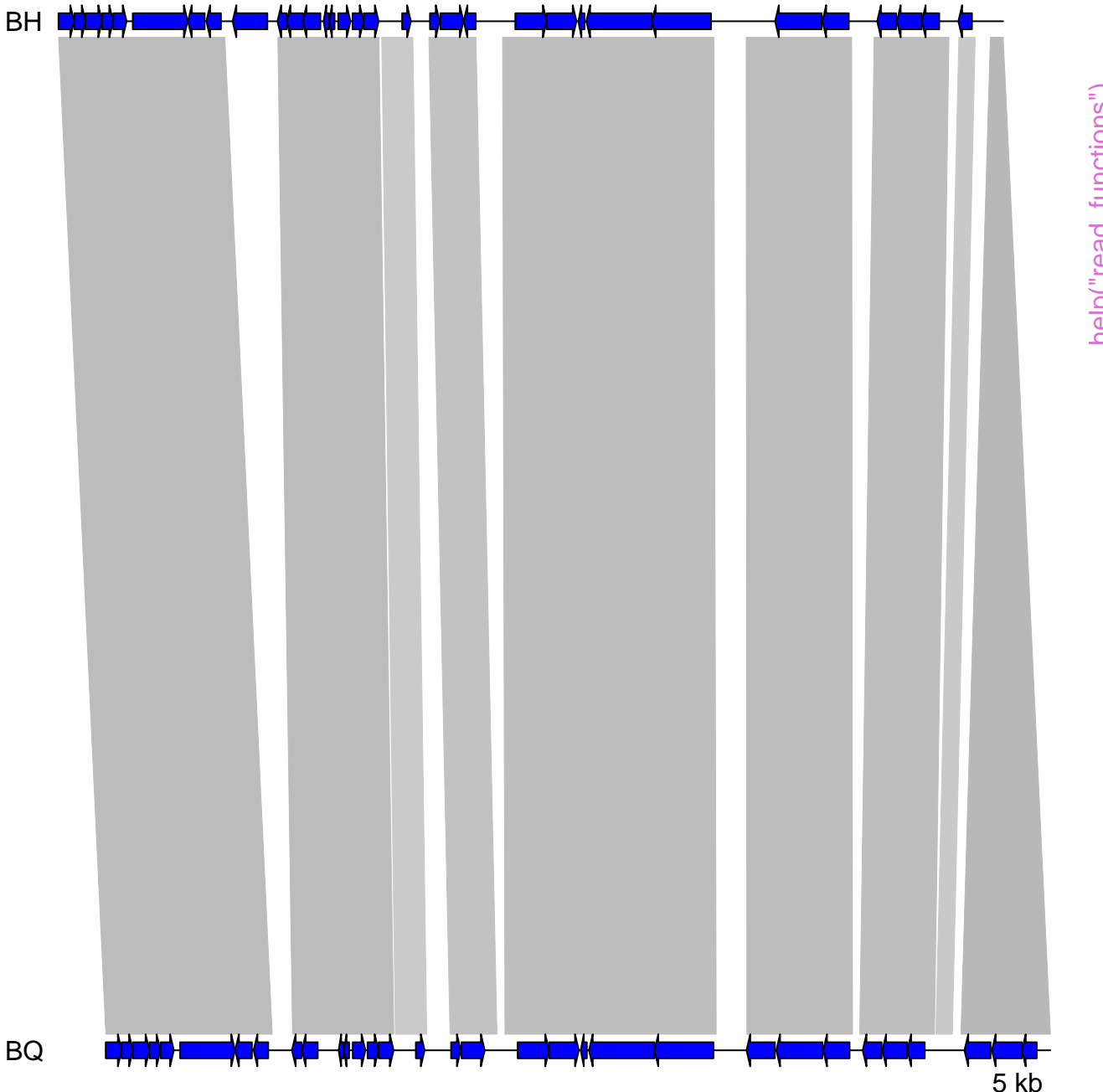
*B. grahamii*

*B. henselae*

*B. quintana*

500 kb

help("read\_functions")



BH

BQ

5 kb

help("read\_functions")

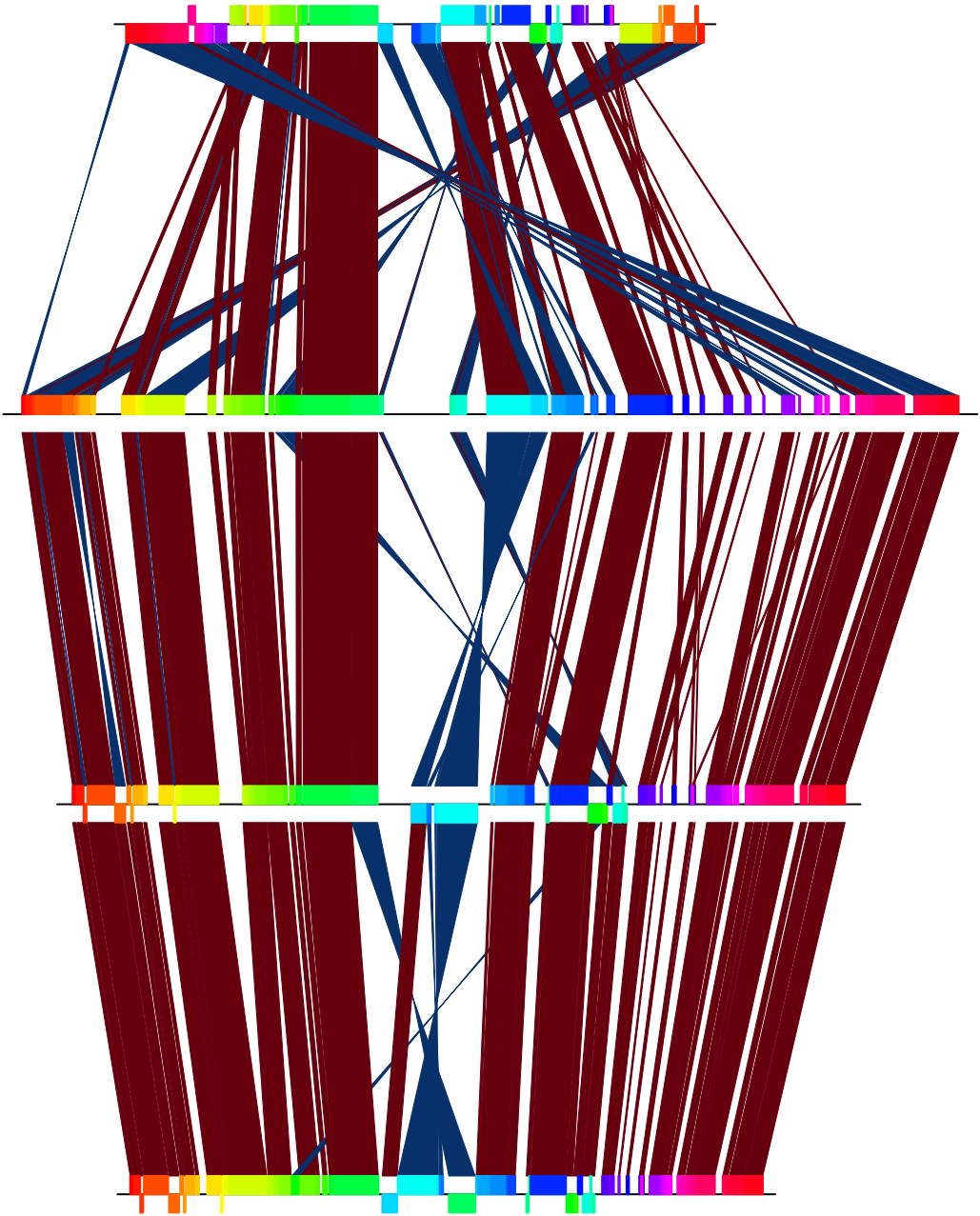


B\_bacilliformis

B\_grahamii

B\_henselae

B\_quintana



help("reverse")

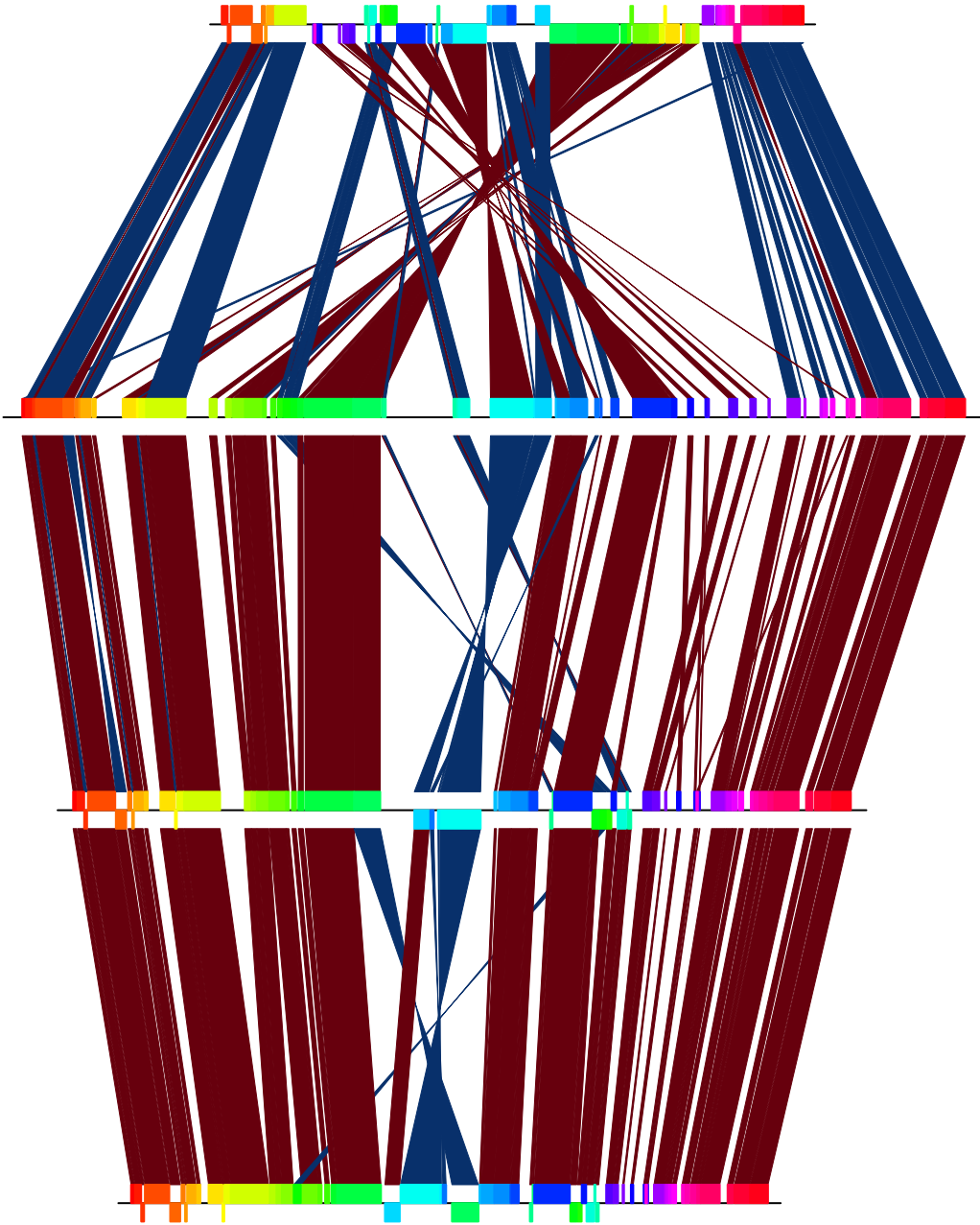
500 kb

B\_bacilliformis

B\_grahamii

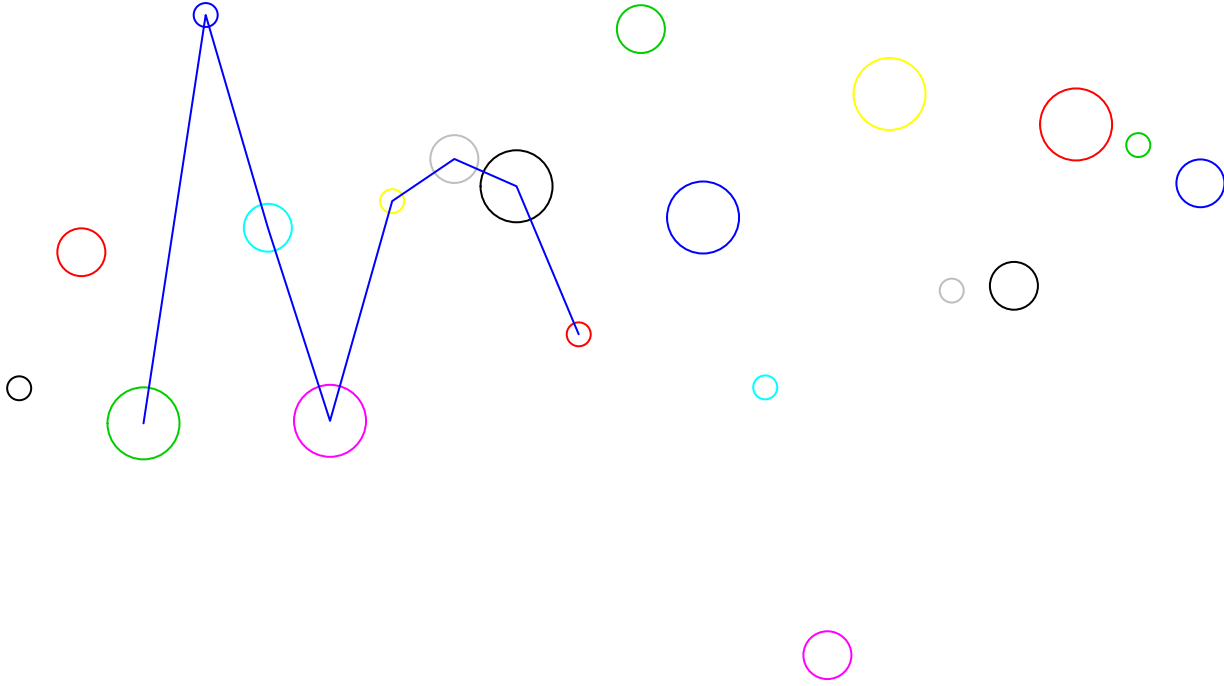
B\_henselae

B\_quintana

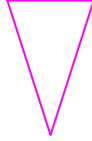
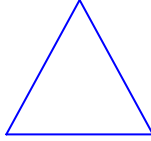


help("reverse")

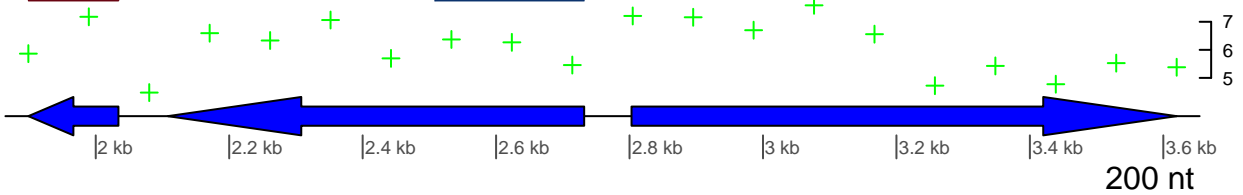
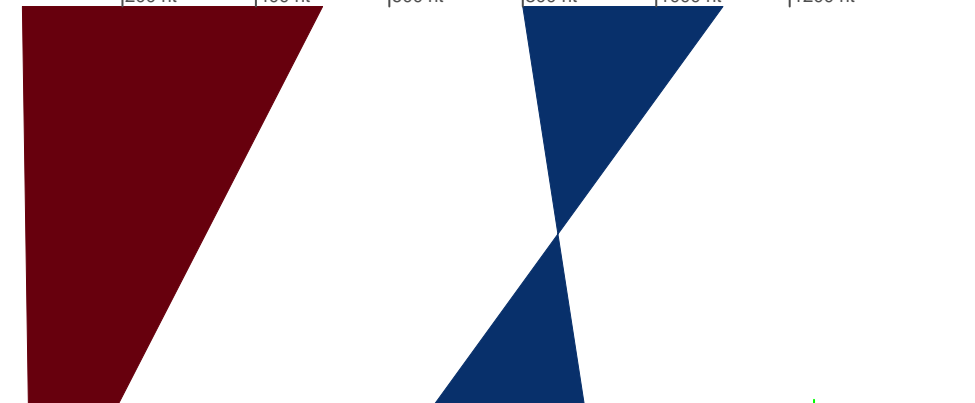
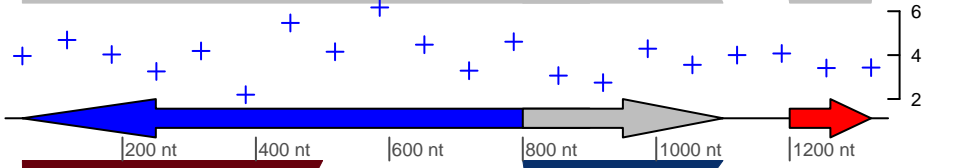
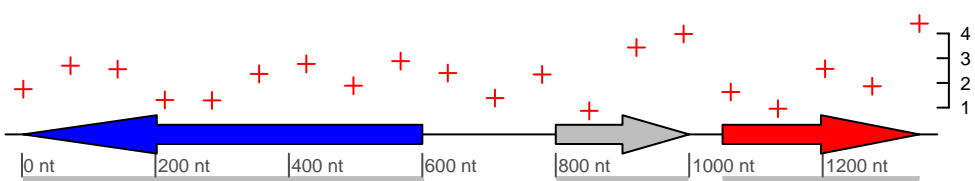
500 kb



help("seg\_plot")

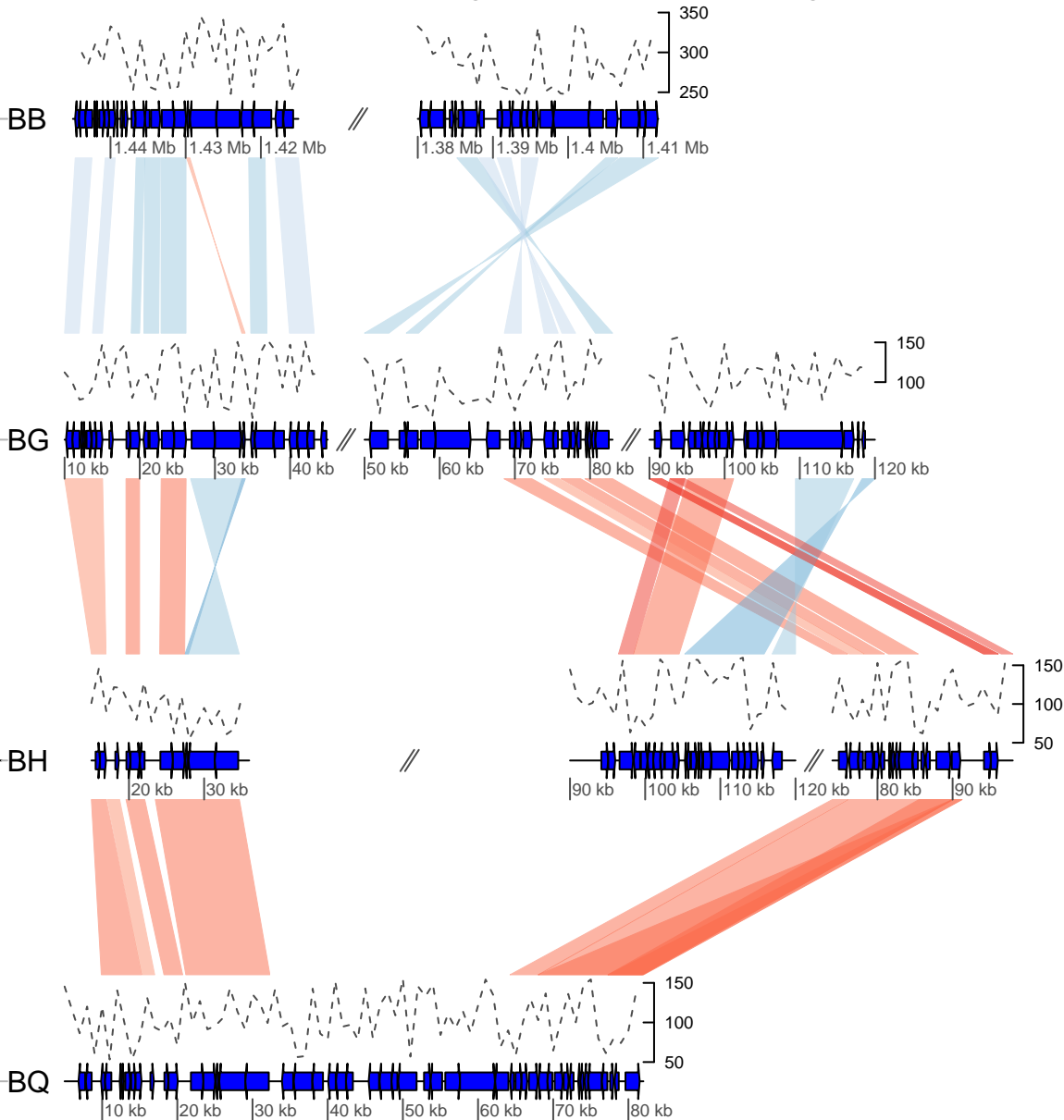


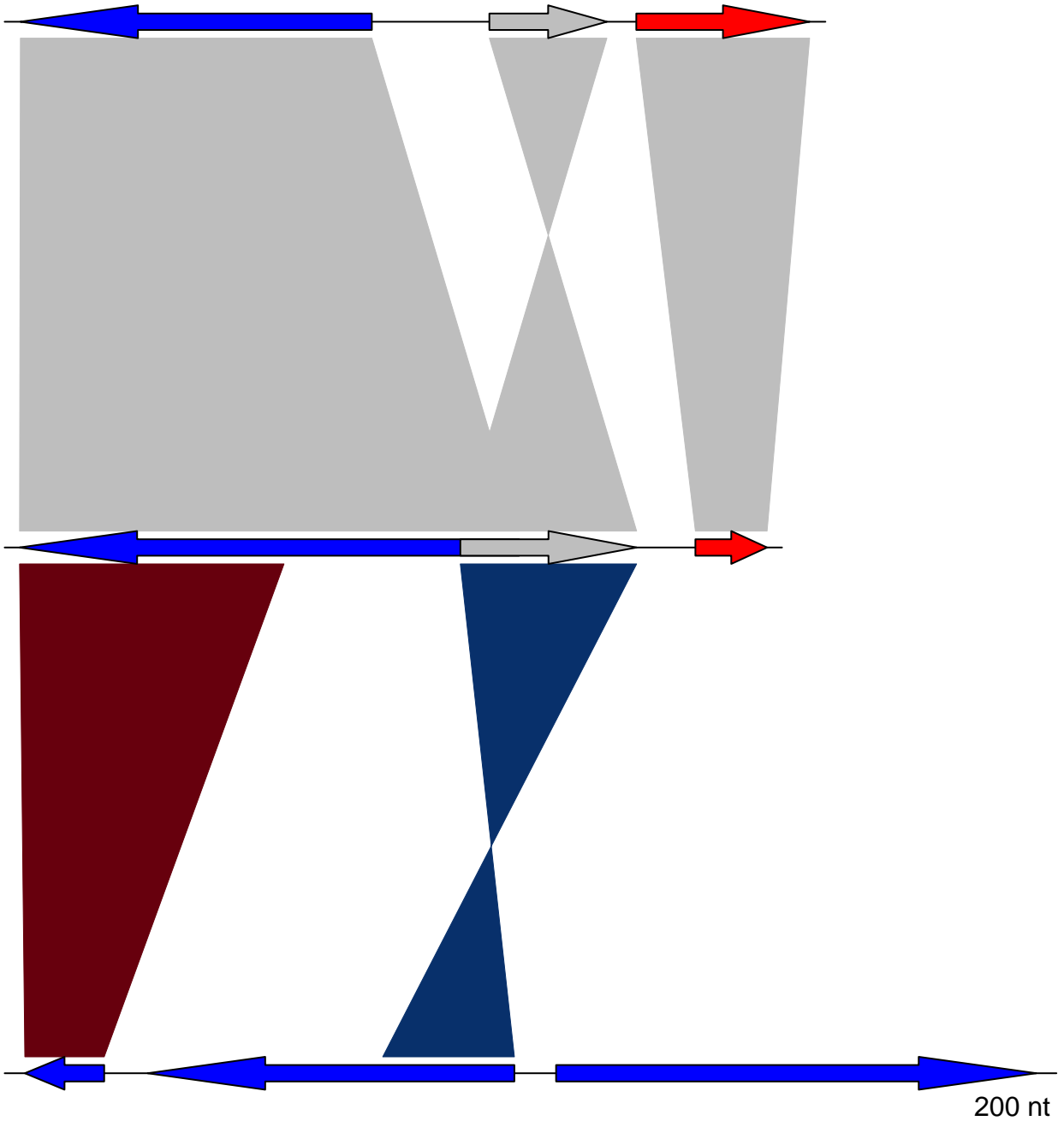
help("seg\_plot")



help("seg\_plot")

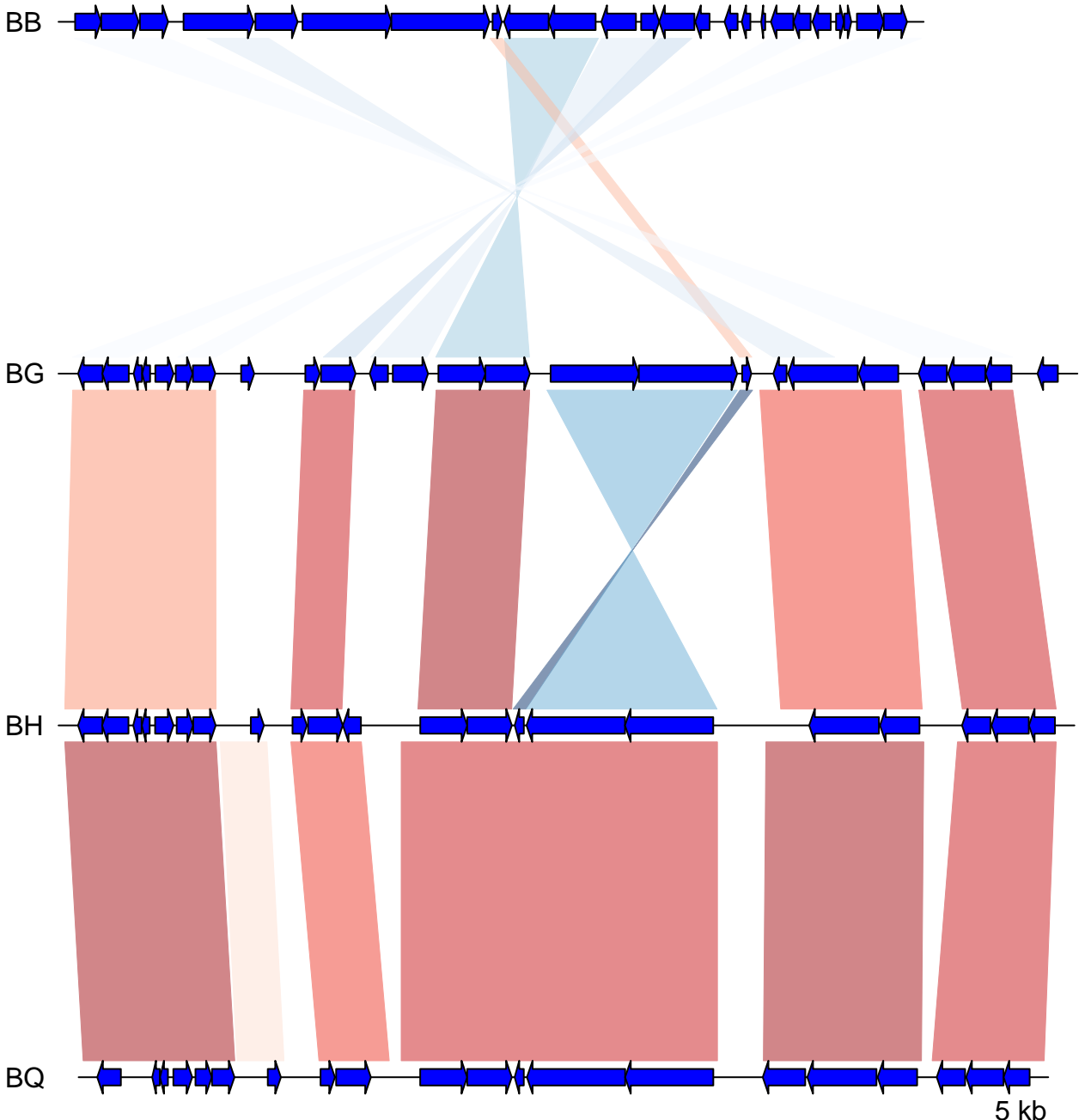
# Random plots for the same segment in 4 *Bartonella* genomes





help("three\_genes")

200 nt



help("trim")

5 kb