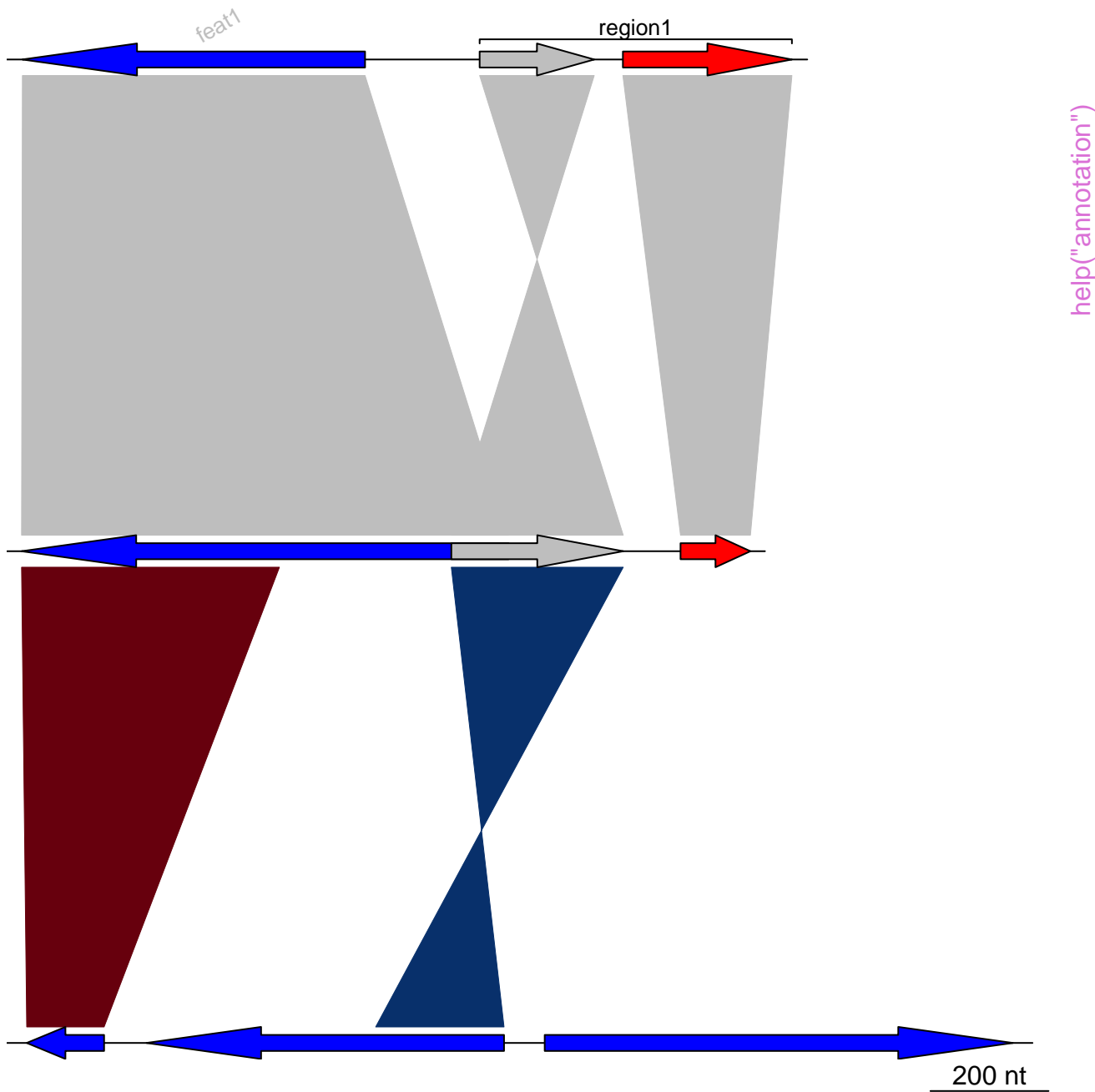
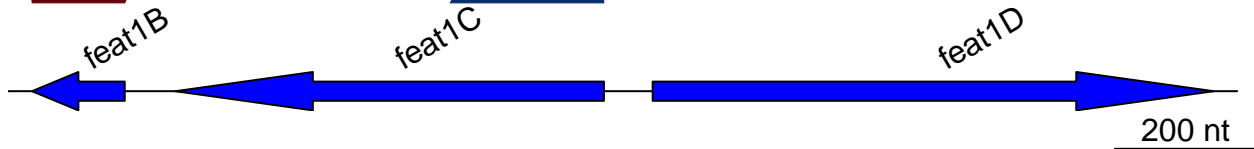
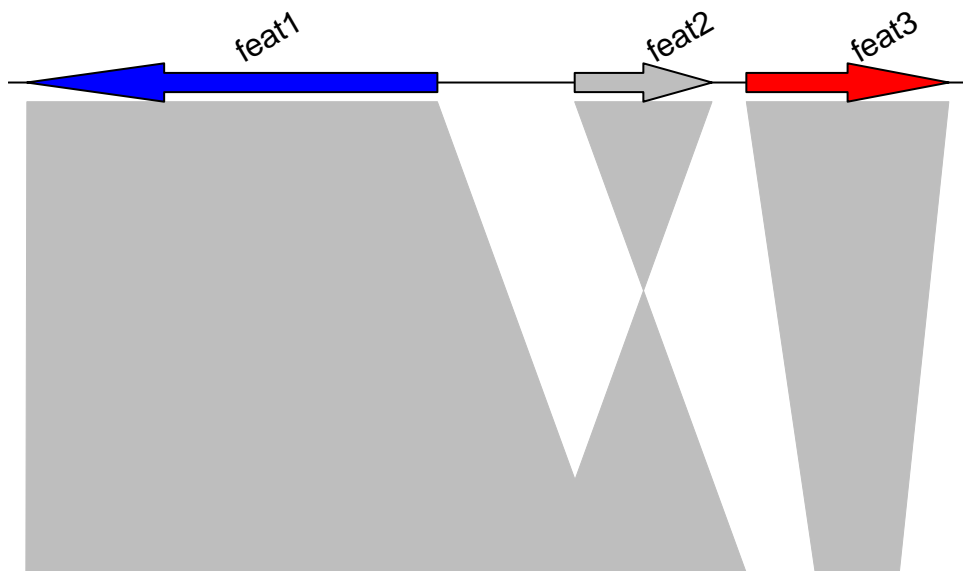


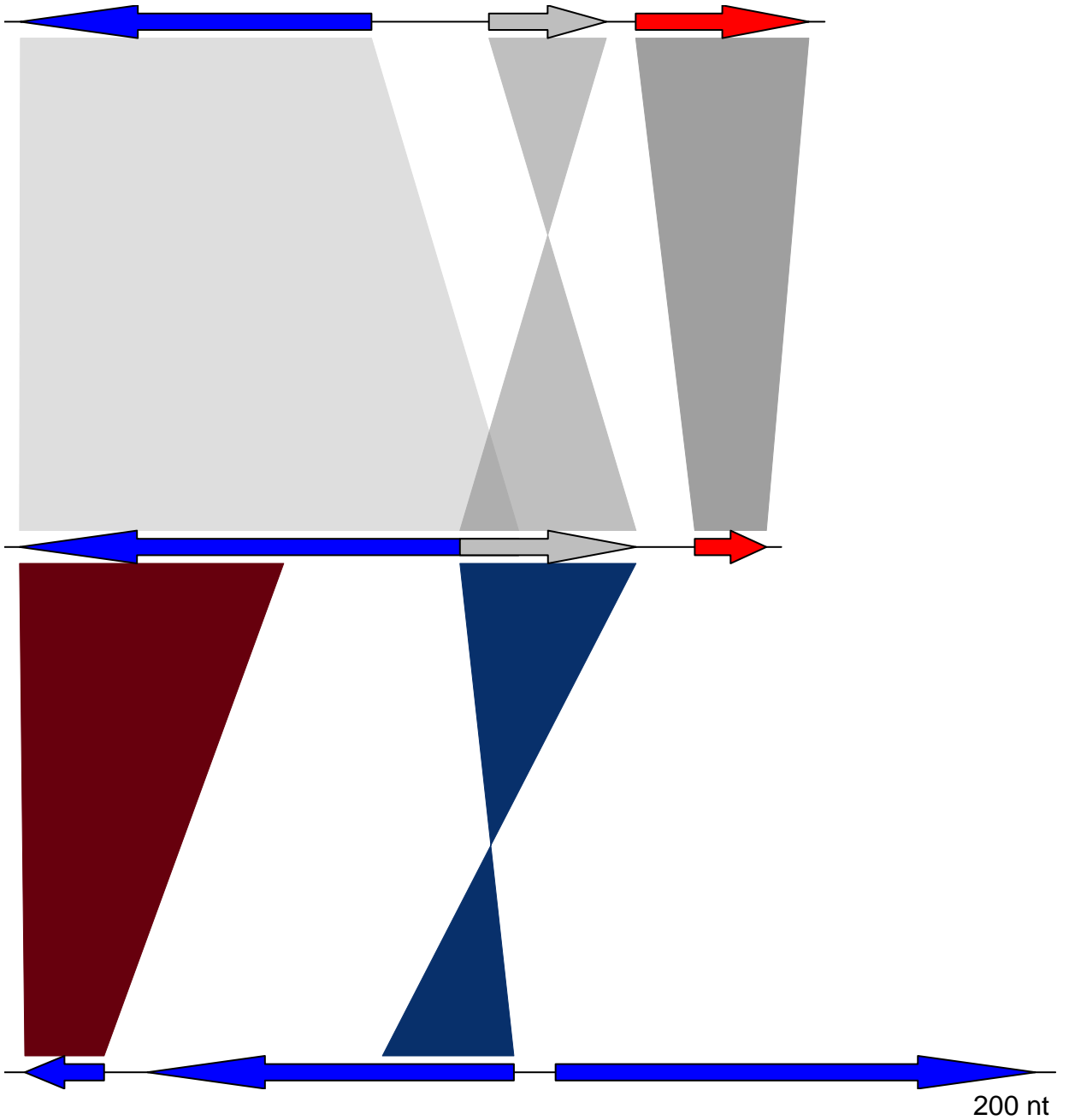
200 nt

help("annotation")

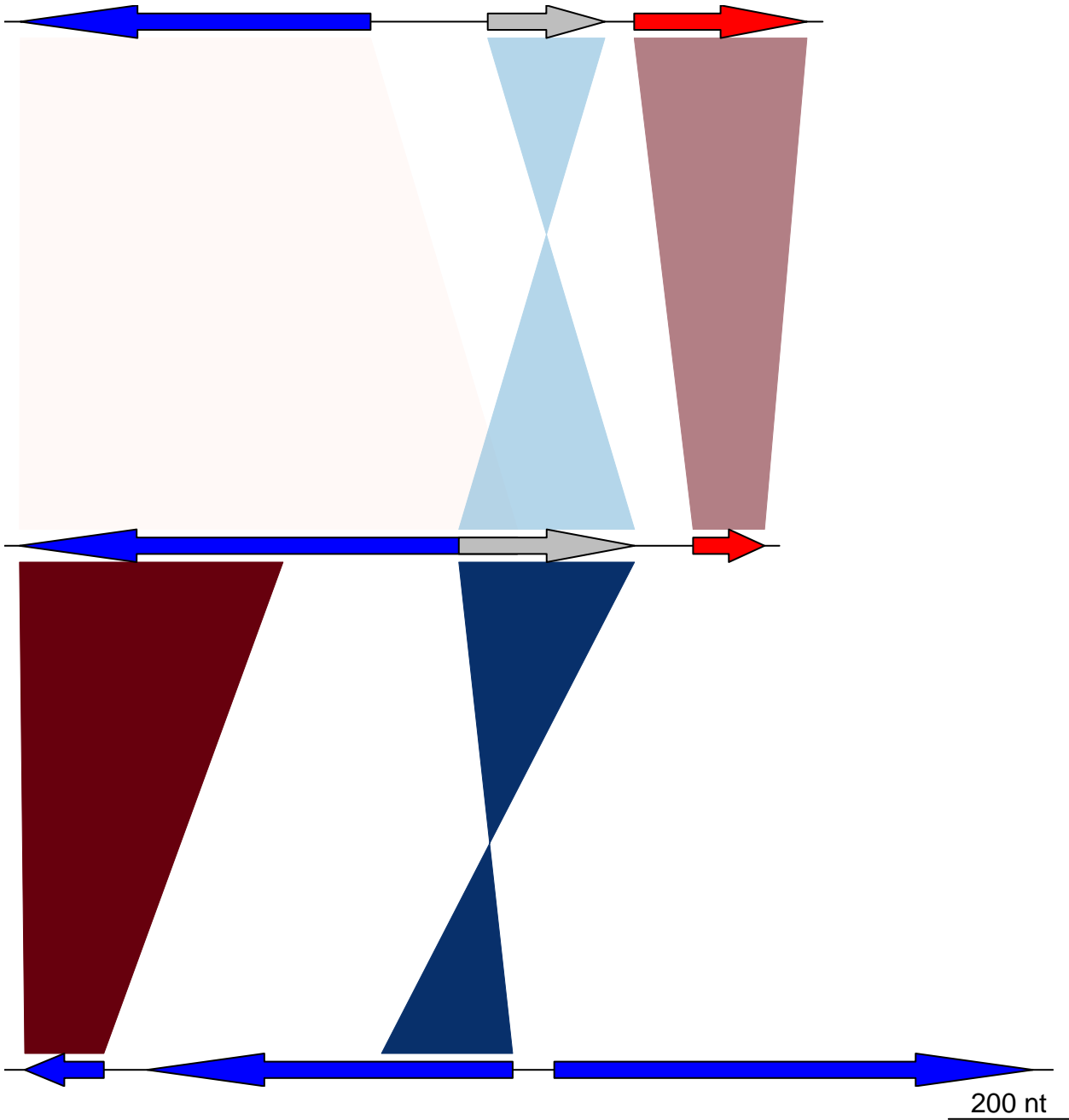




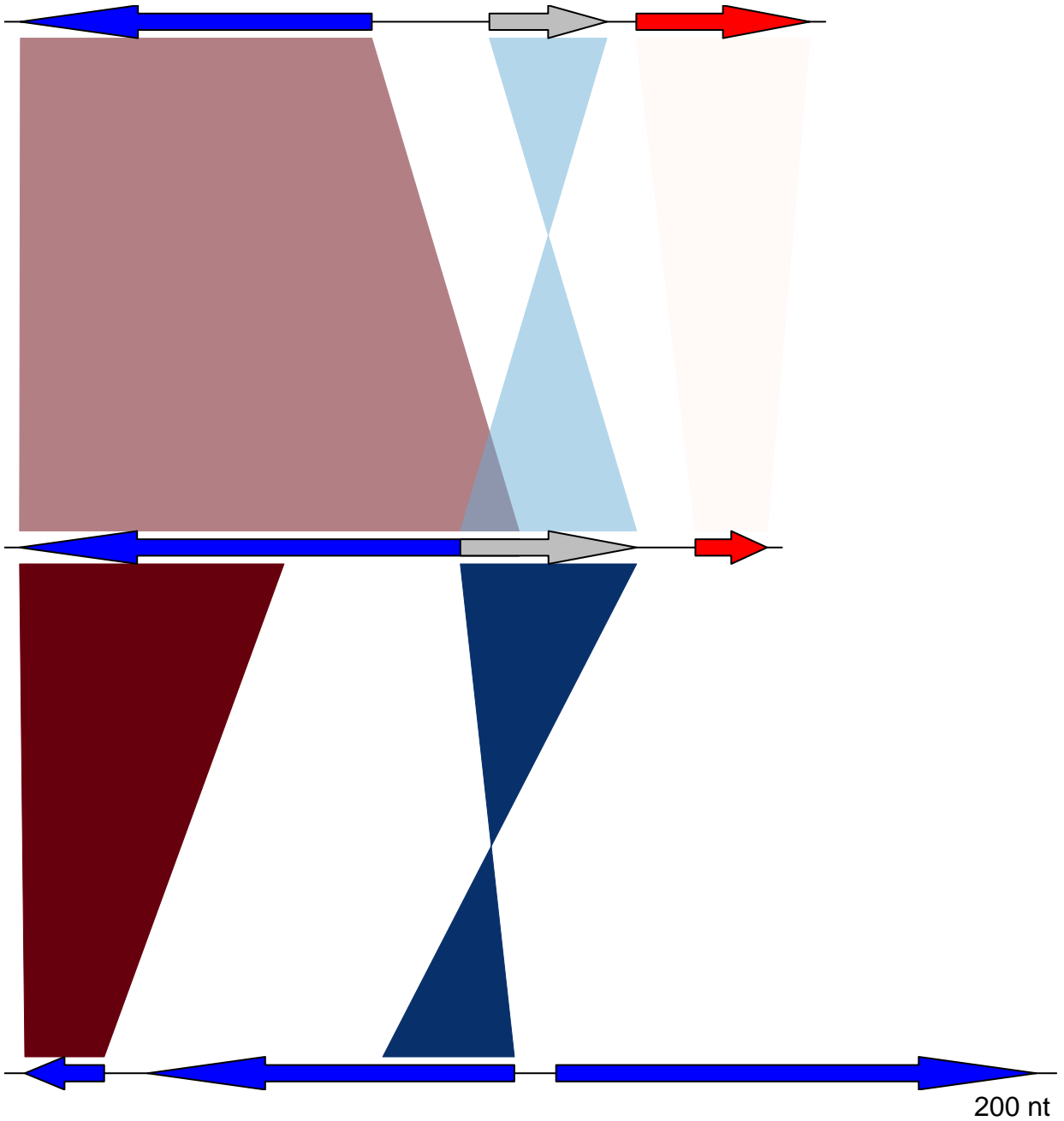
help("annotation")



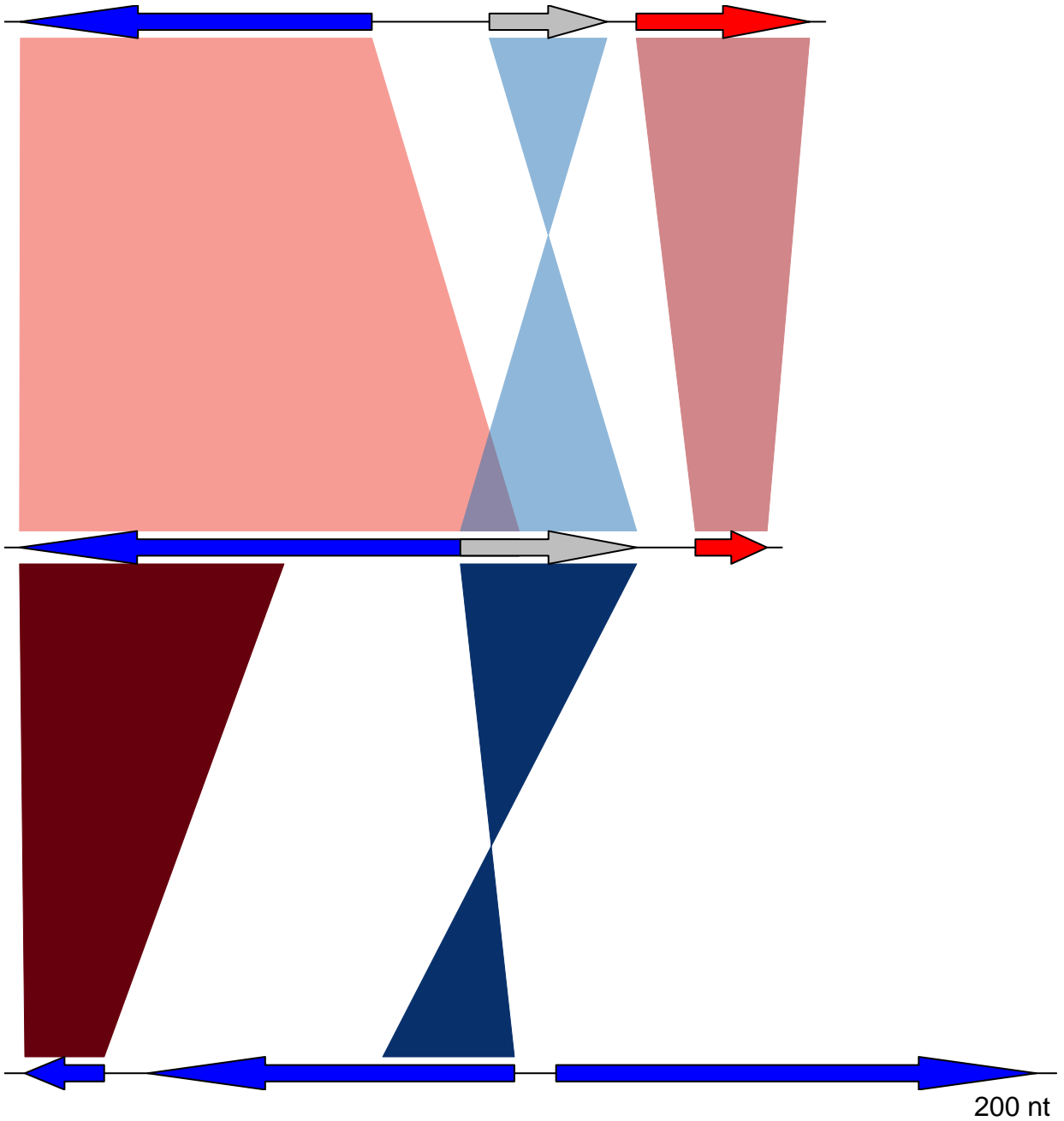
help("apply_color_scheme")



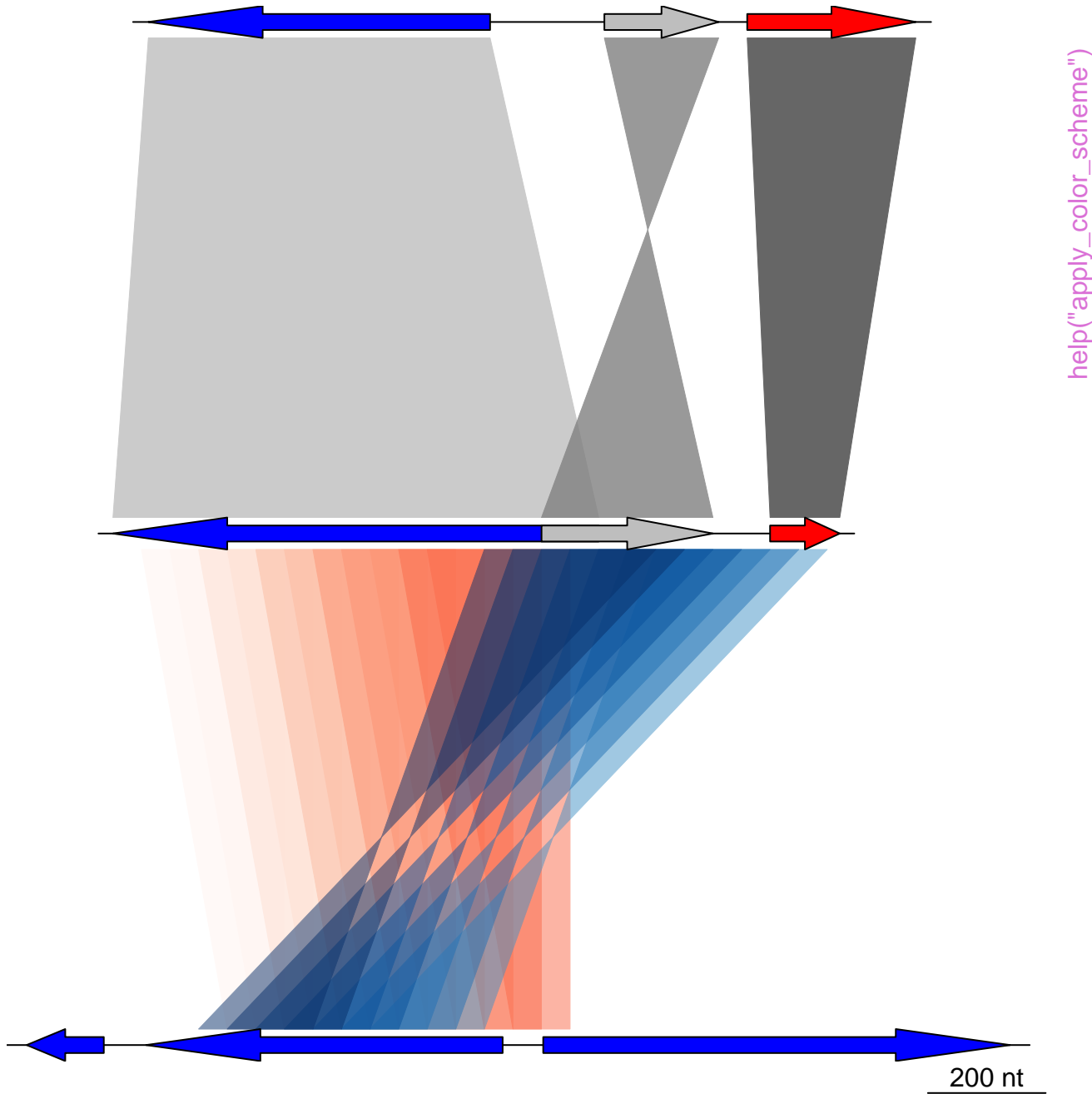
`help("apply_color_scheme")`

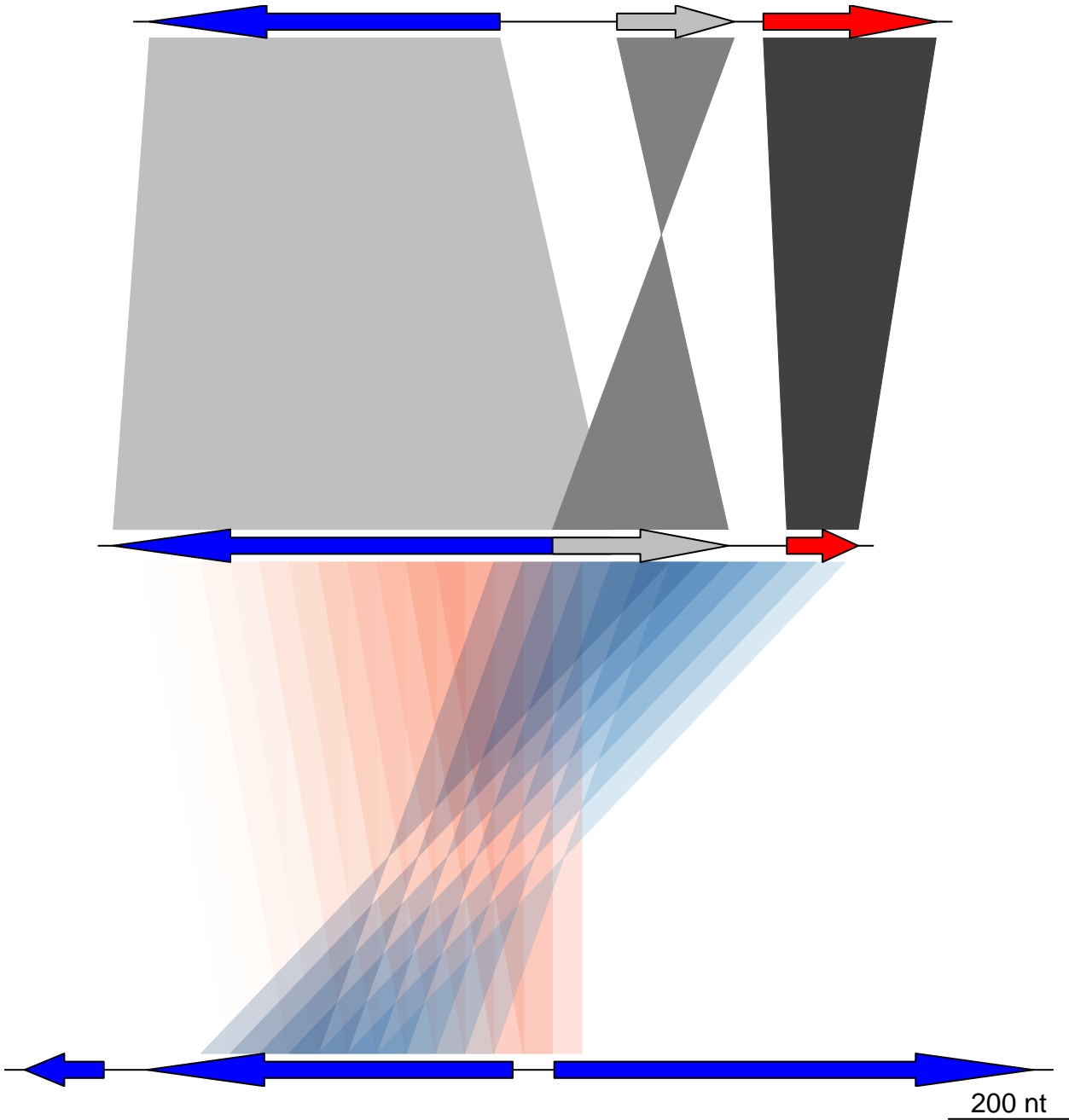


help("apply_color_scheme")

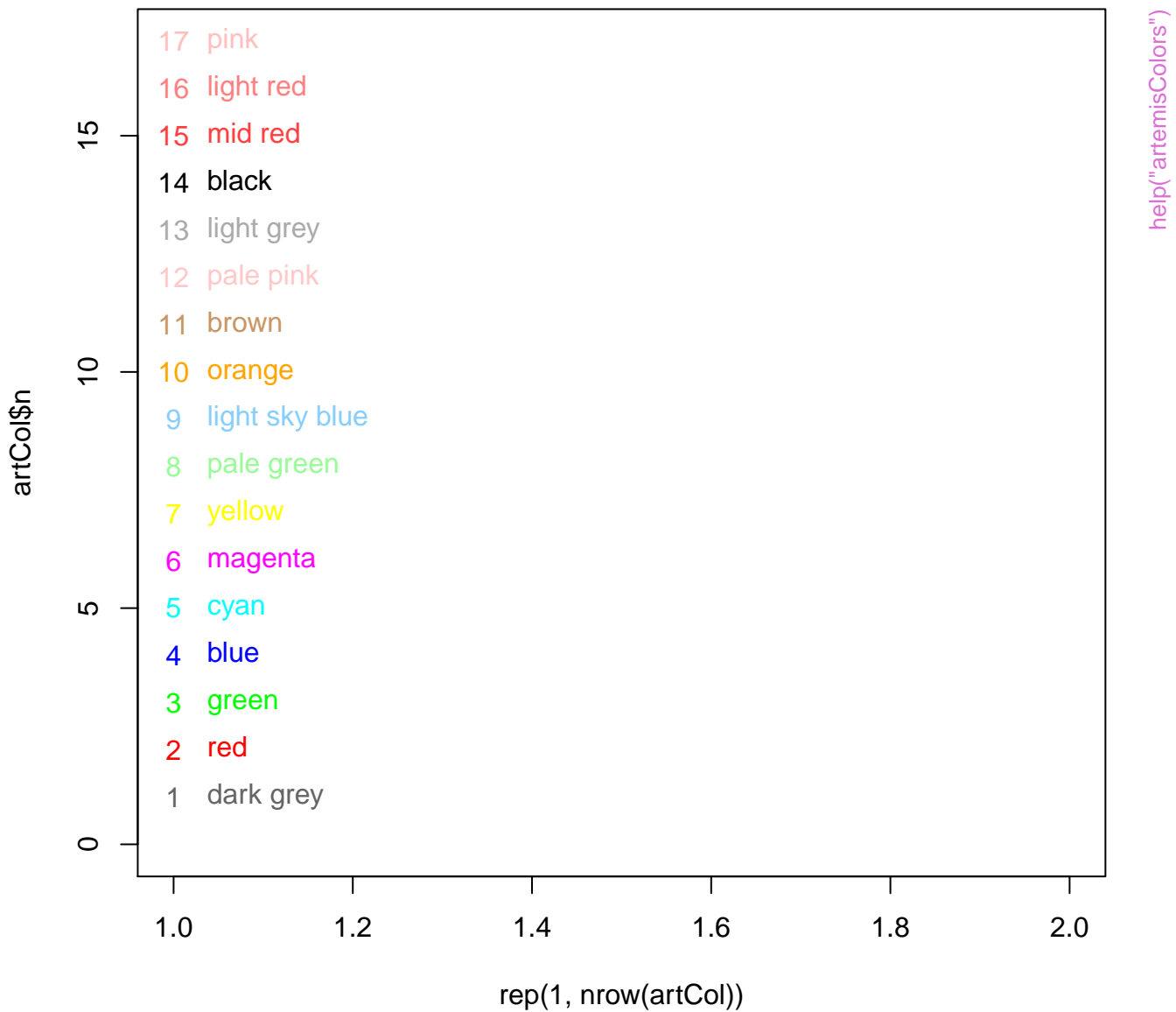


help("apply_color_scheme")





help("apply_color_scheme")



BB

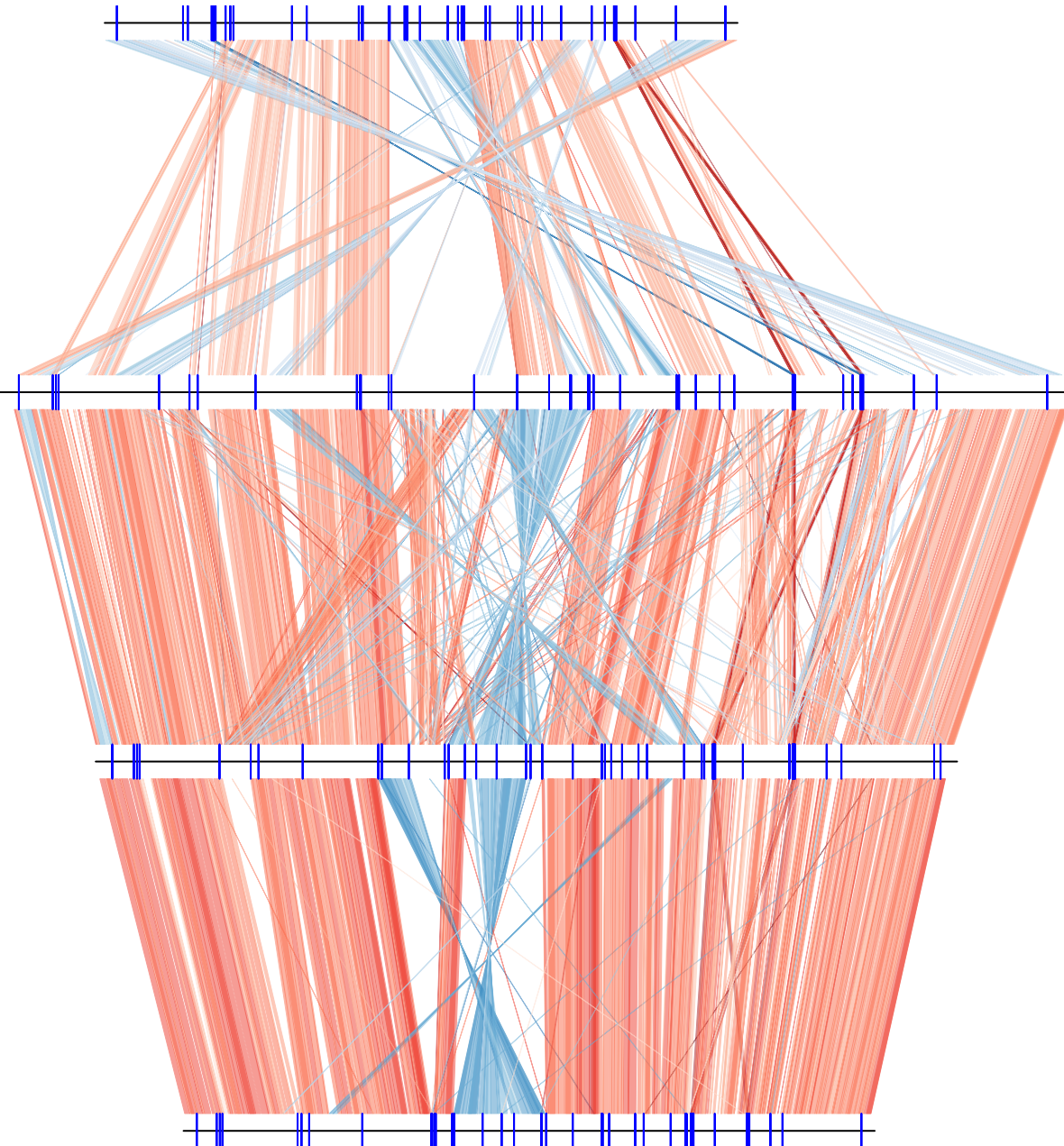
BG

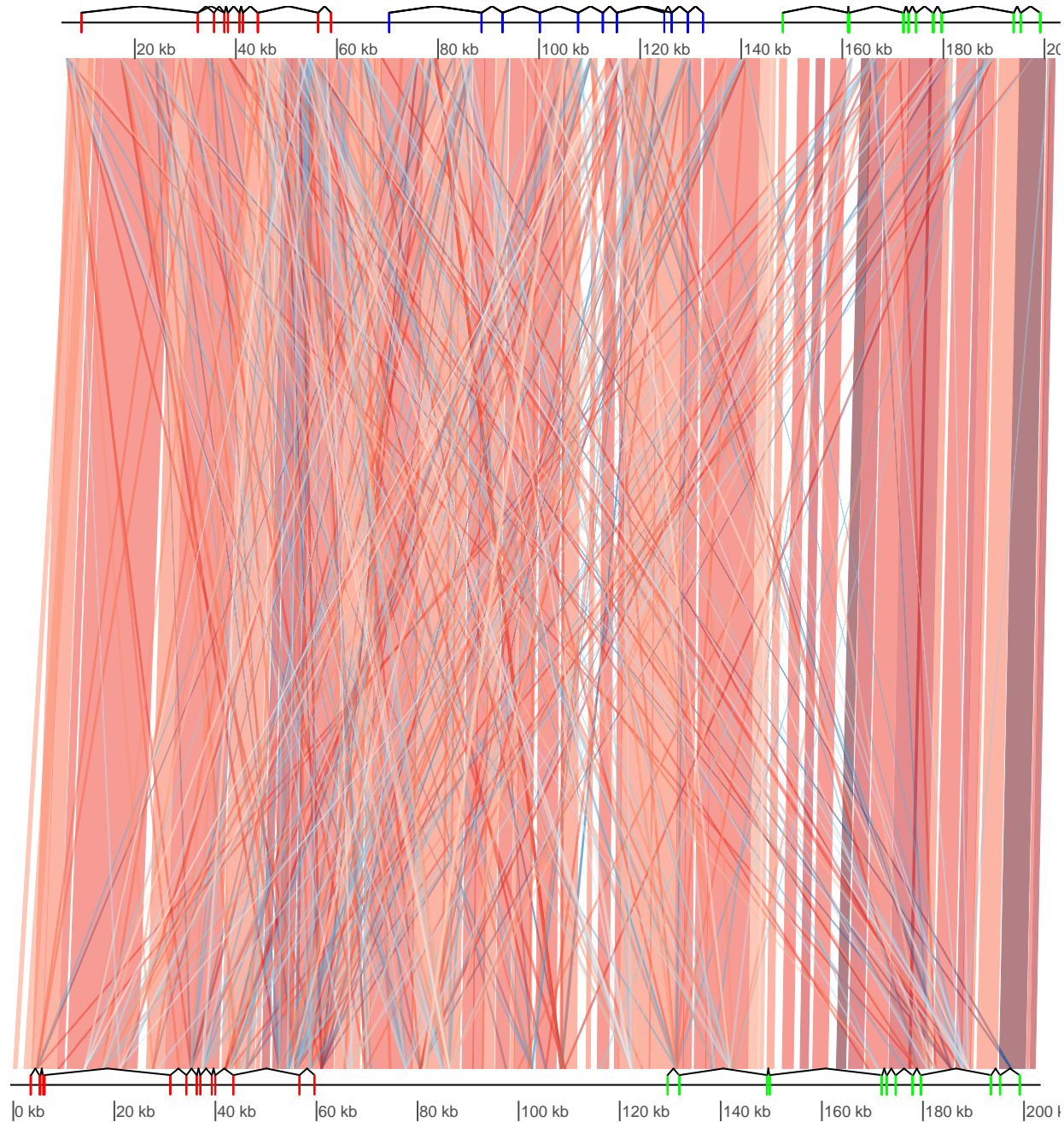
BH

BQ

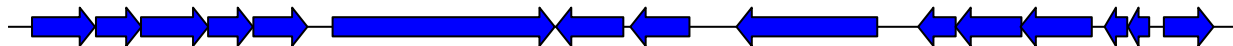
500 kb

help("barto")



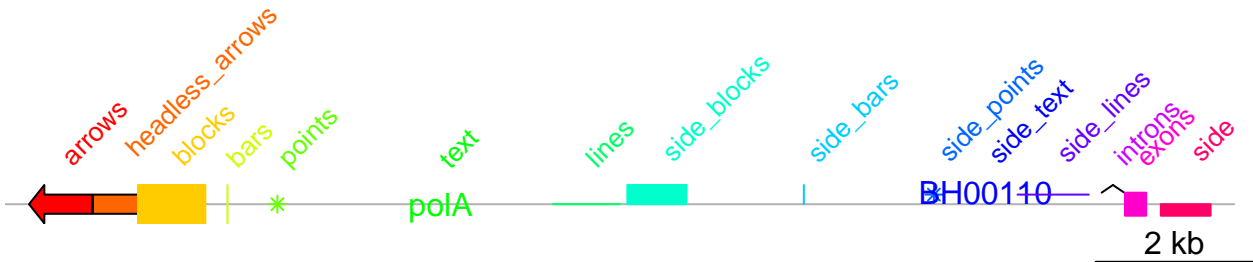
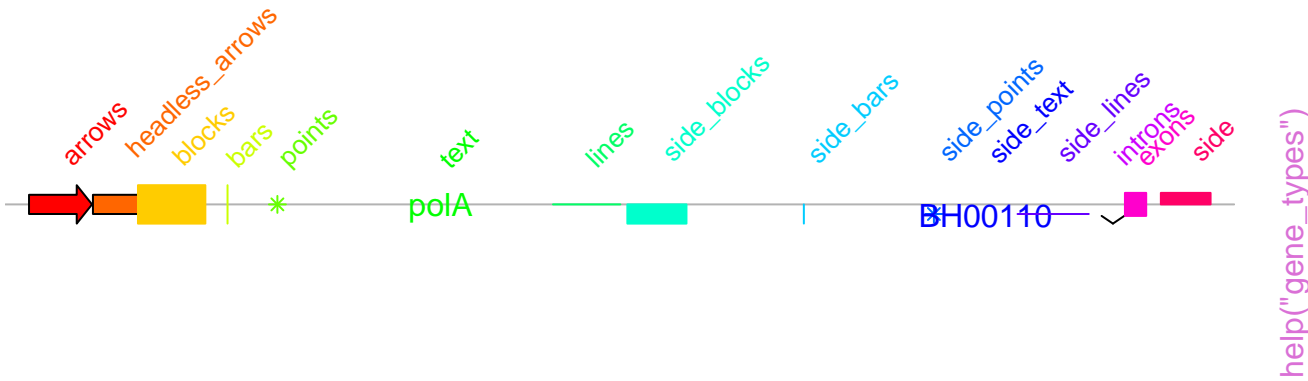


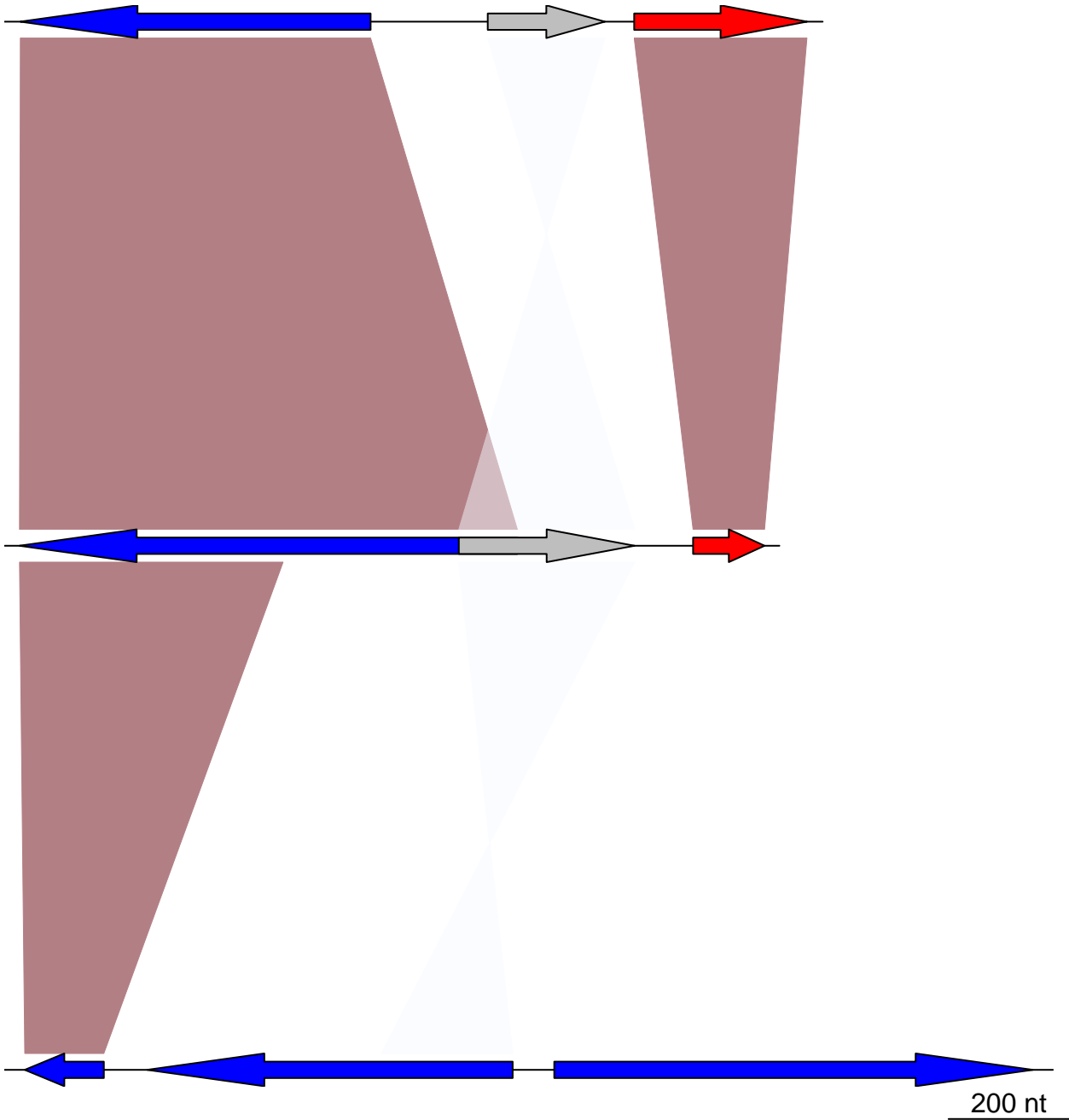
help("chrY_subseg")



2 kb

help("gene_types")





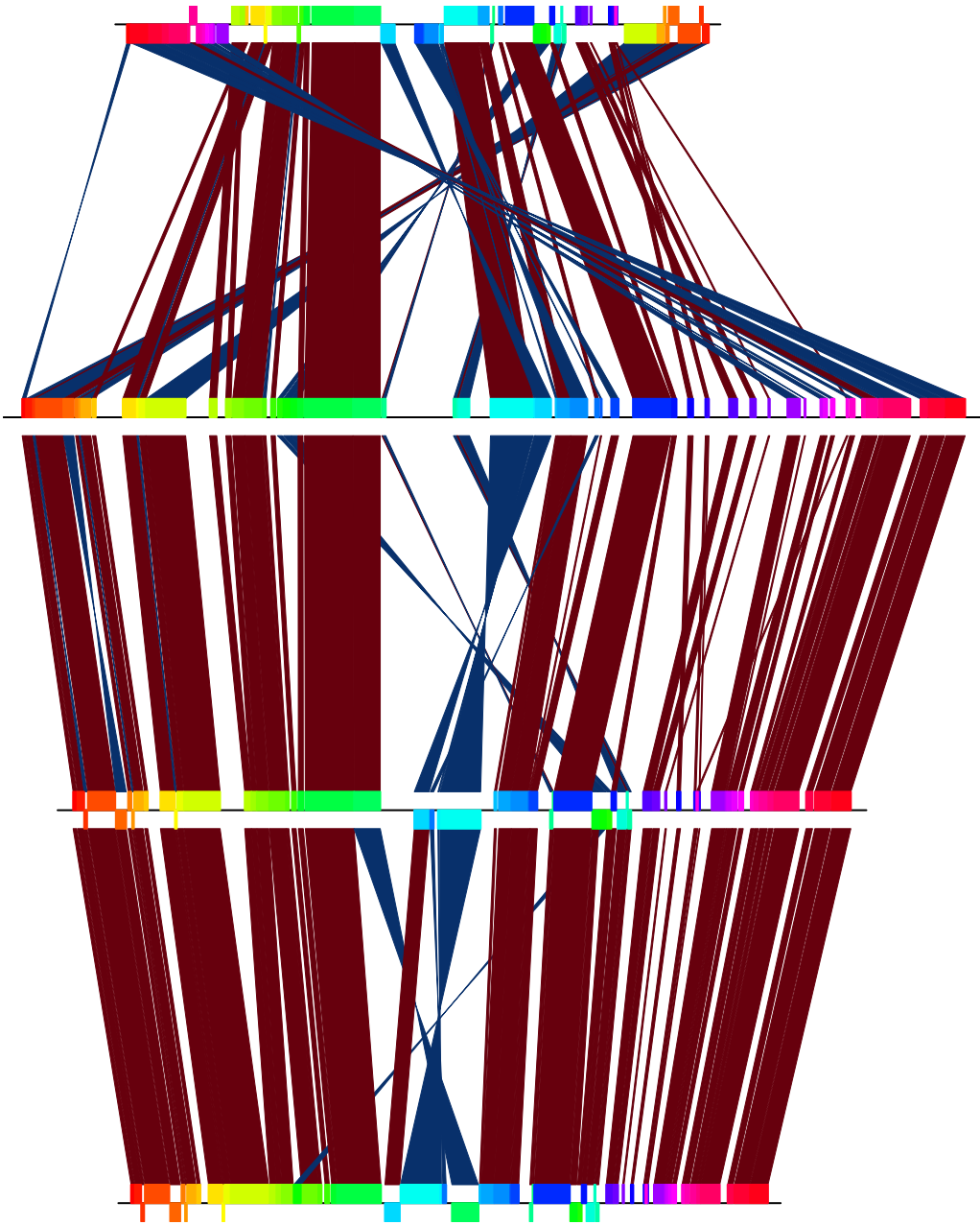
help("genoPlotR-package")

B_bacilliformis

B_grahamii

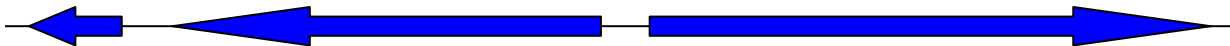
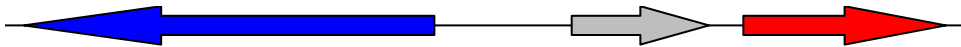
B_henselae

B_quintana



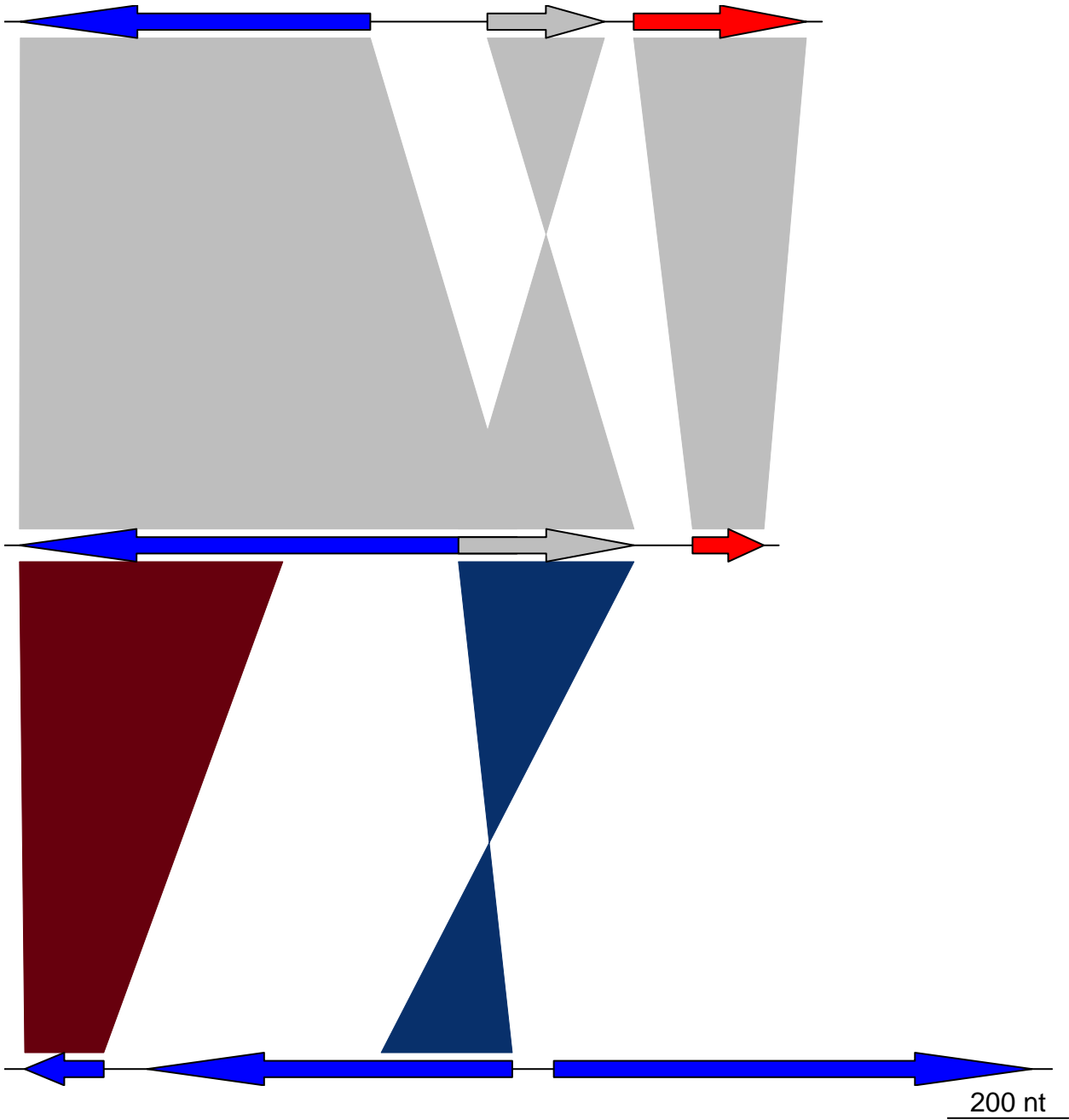
help("mauve.bbone")

500 kb

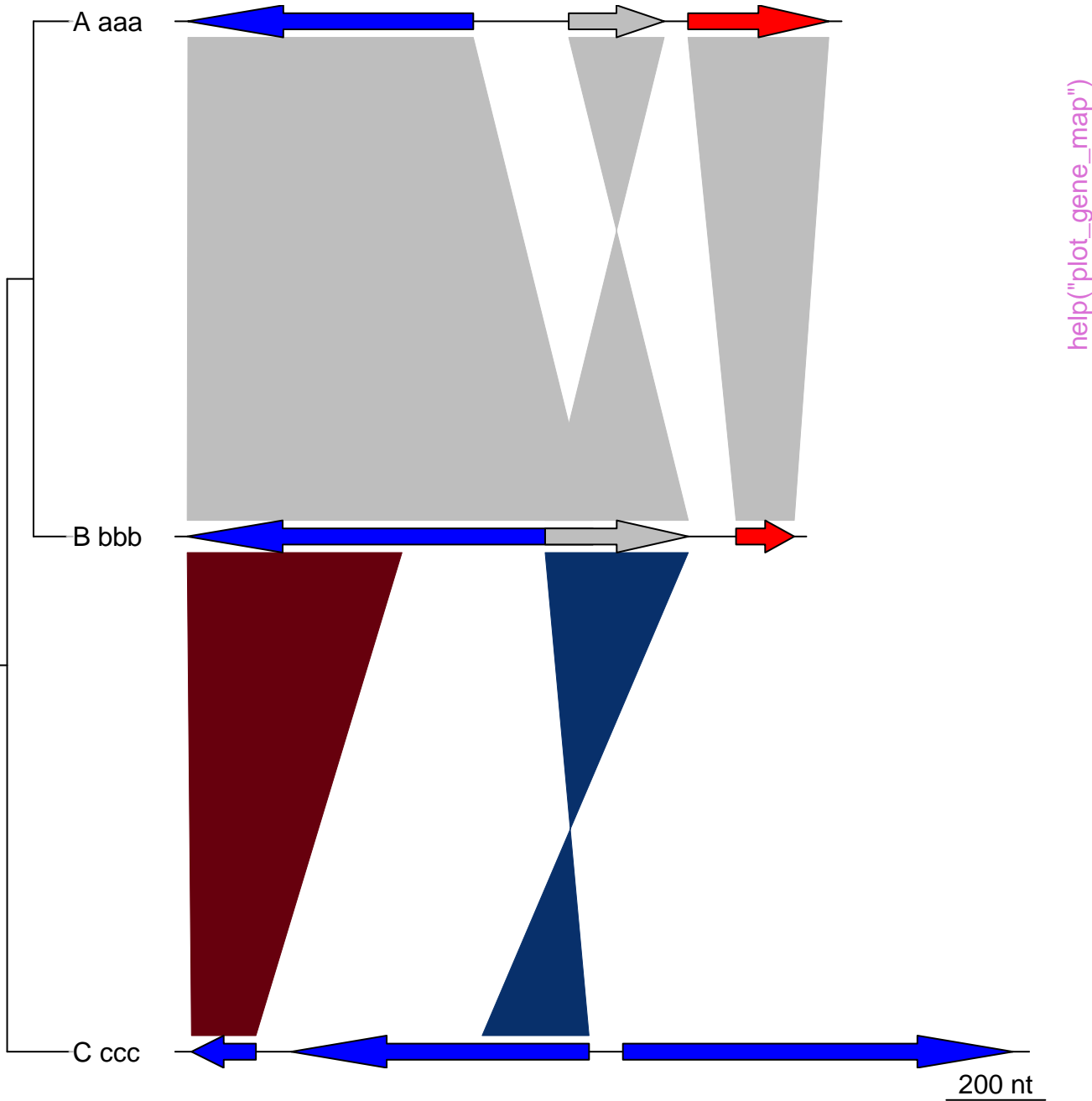


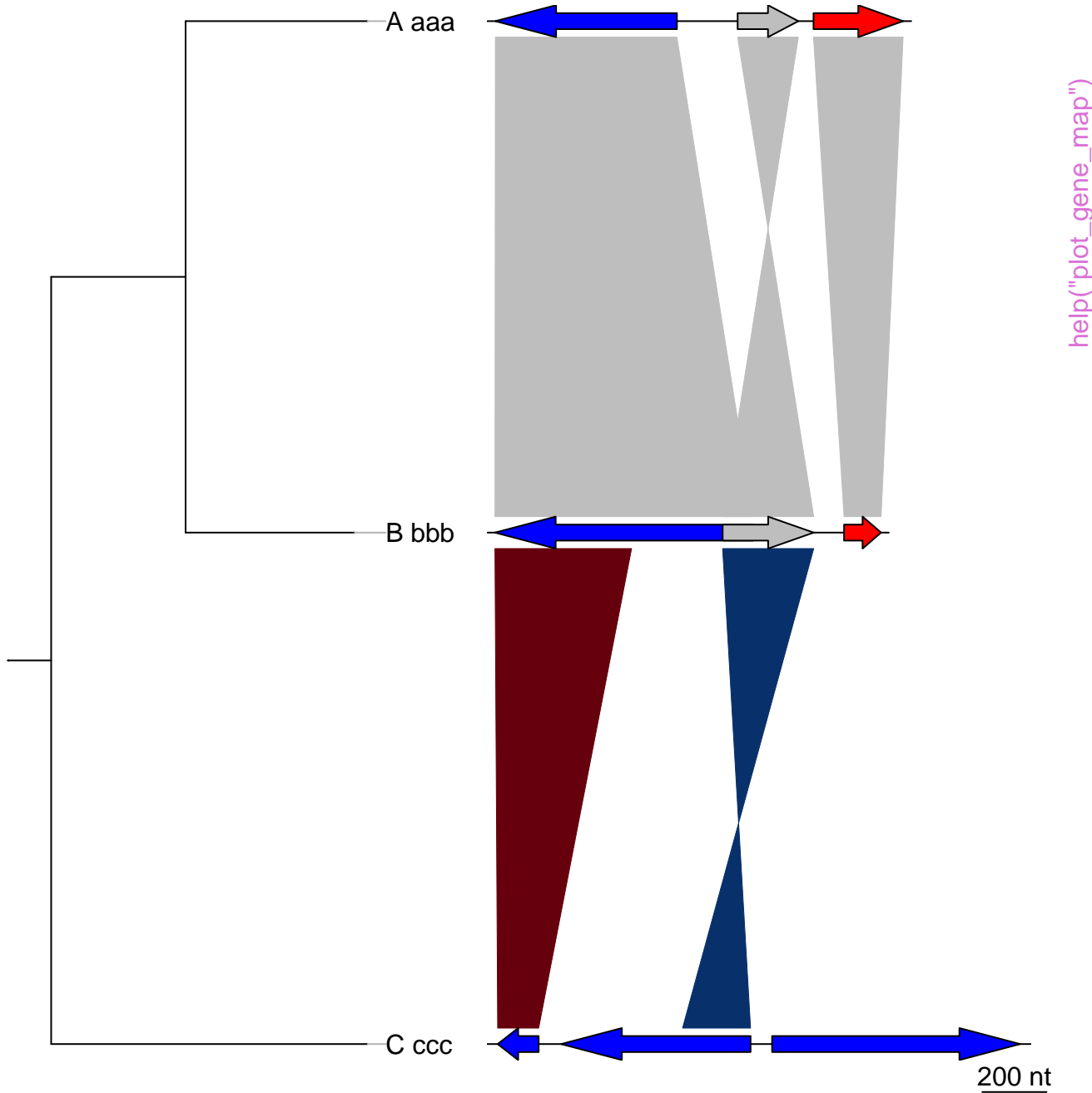
200 nt

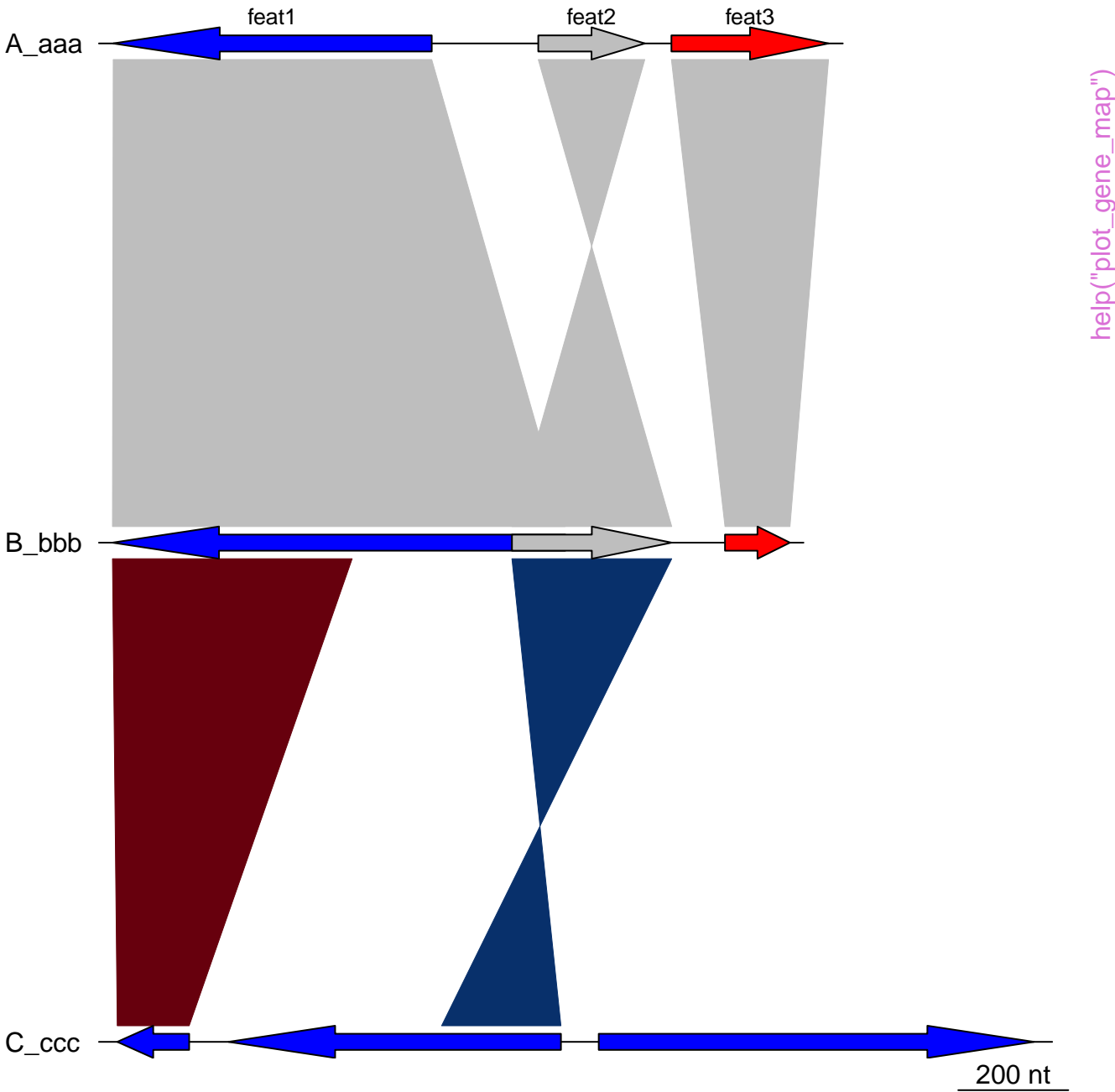
help("plot_gene_map")

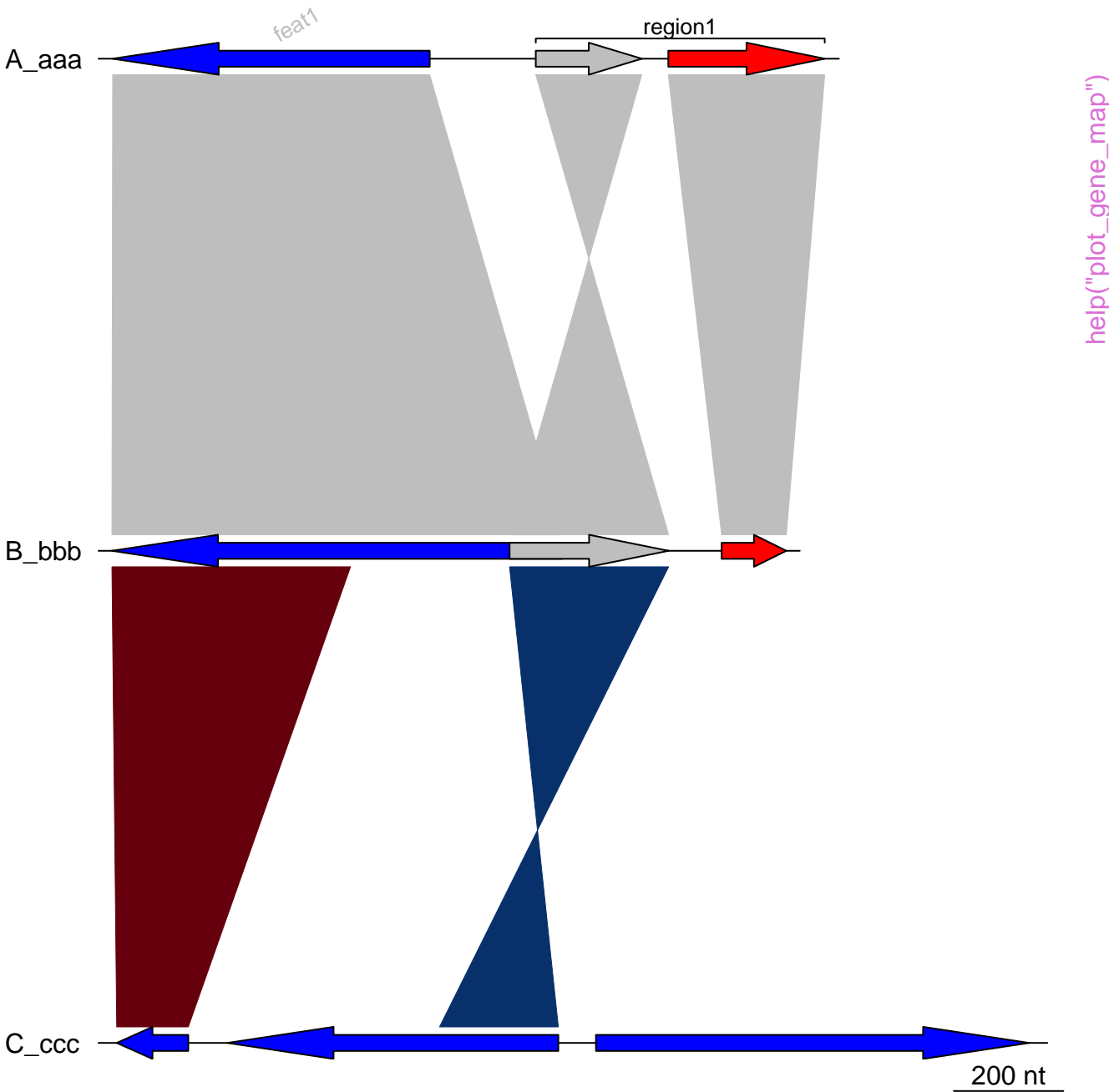


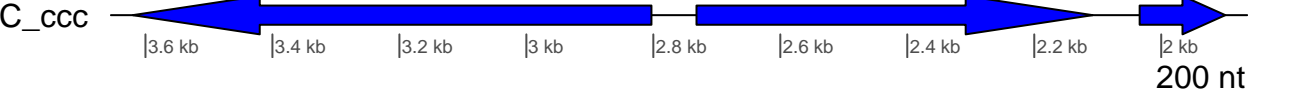
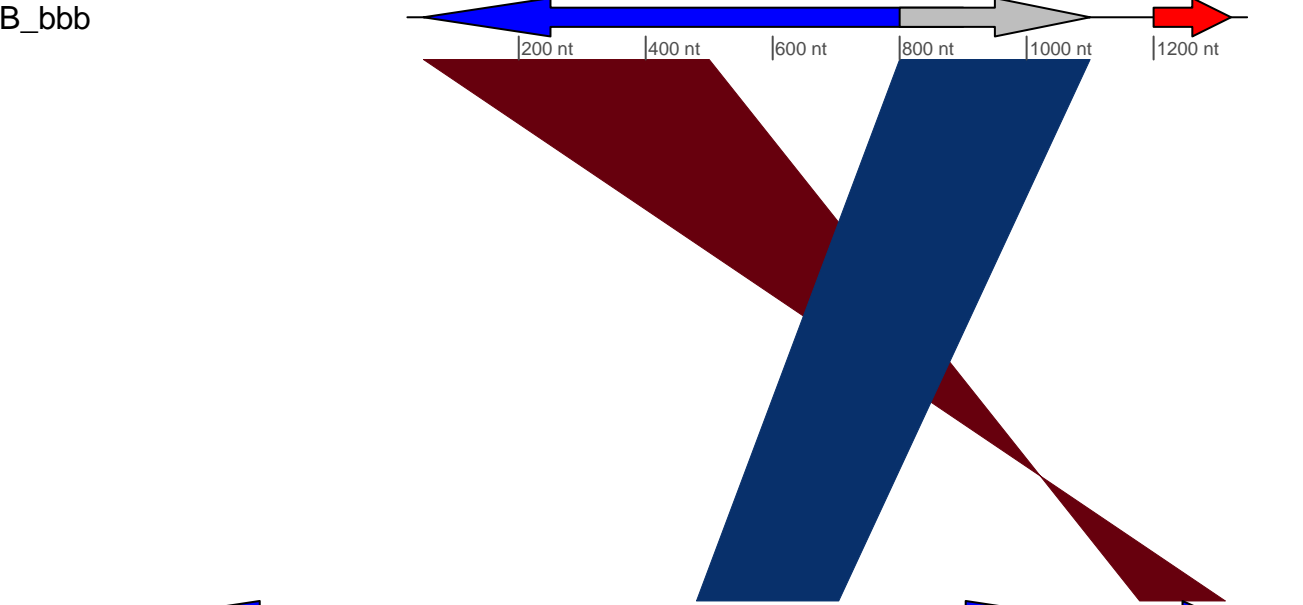
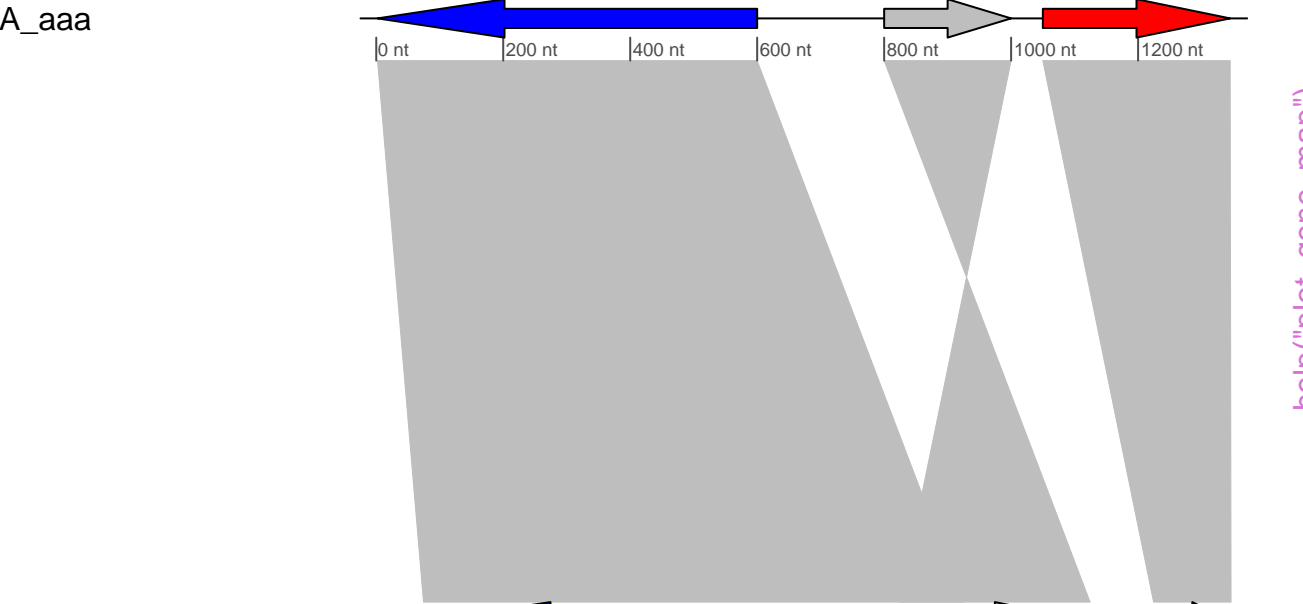
help("plot_gene_map")

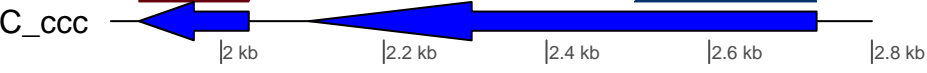
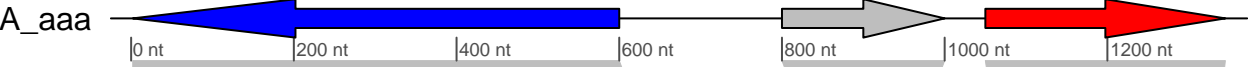








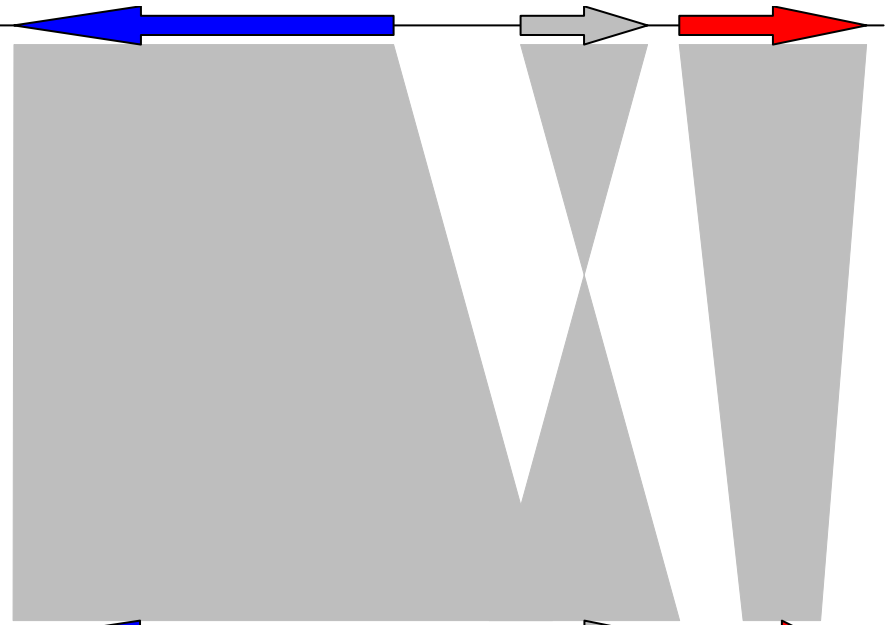




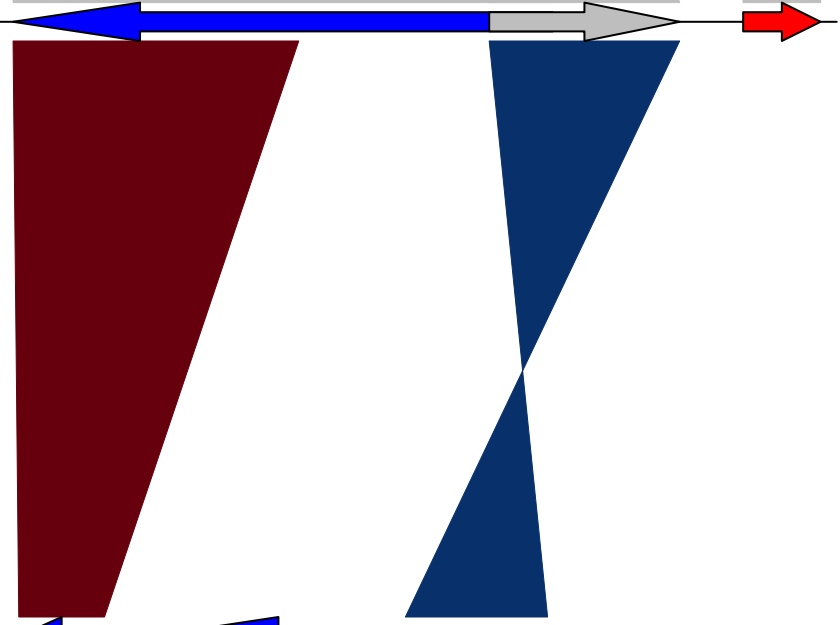
200 nt

help("plot_gene_map")

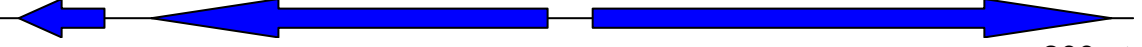
A_aaa



B_bbb



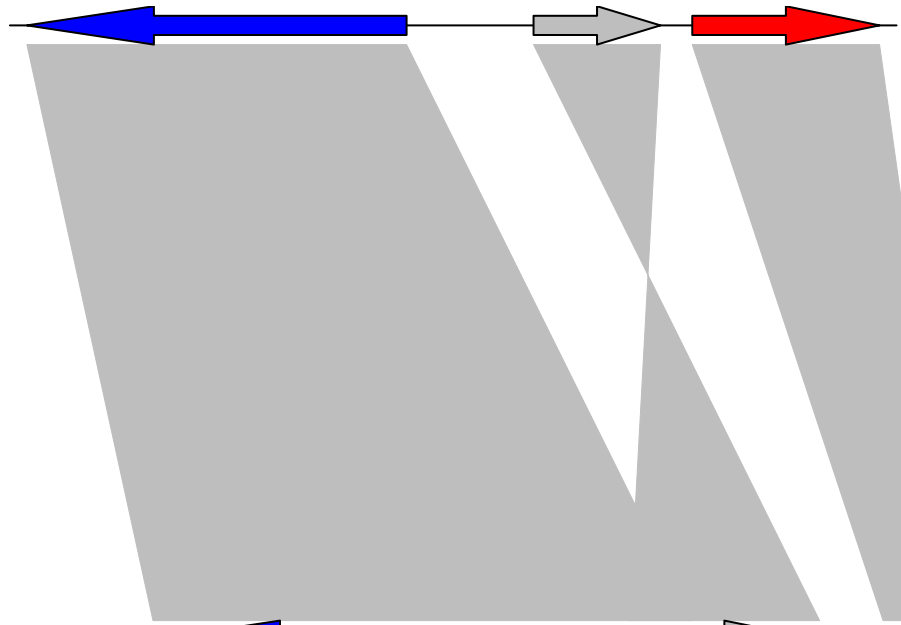
C_ccc



200 nt

help("plot_gene_map")

A_aaa



B_bbb



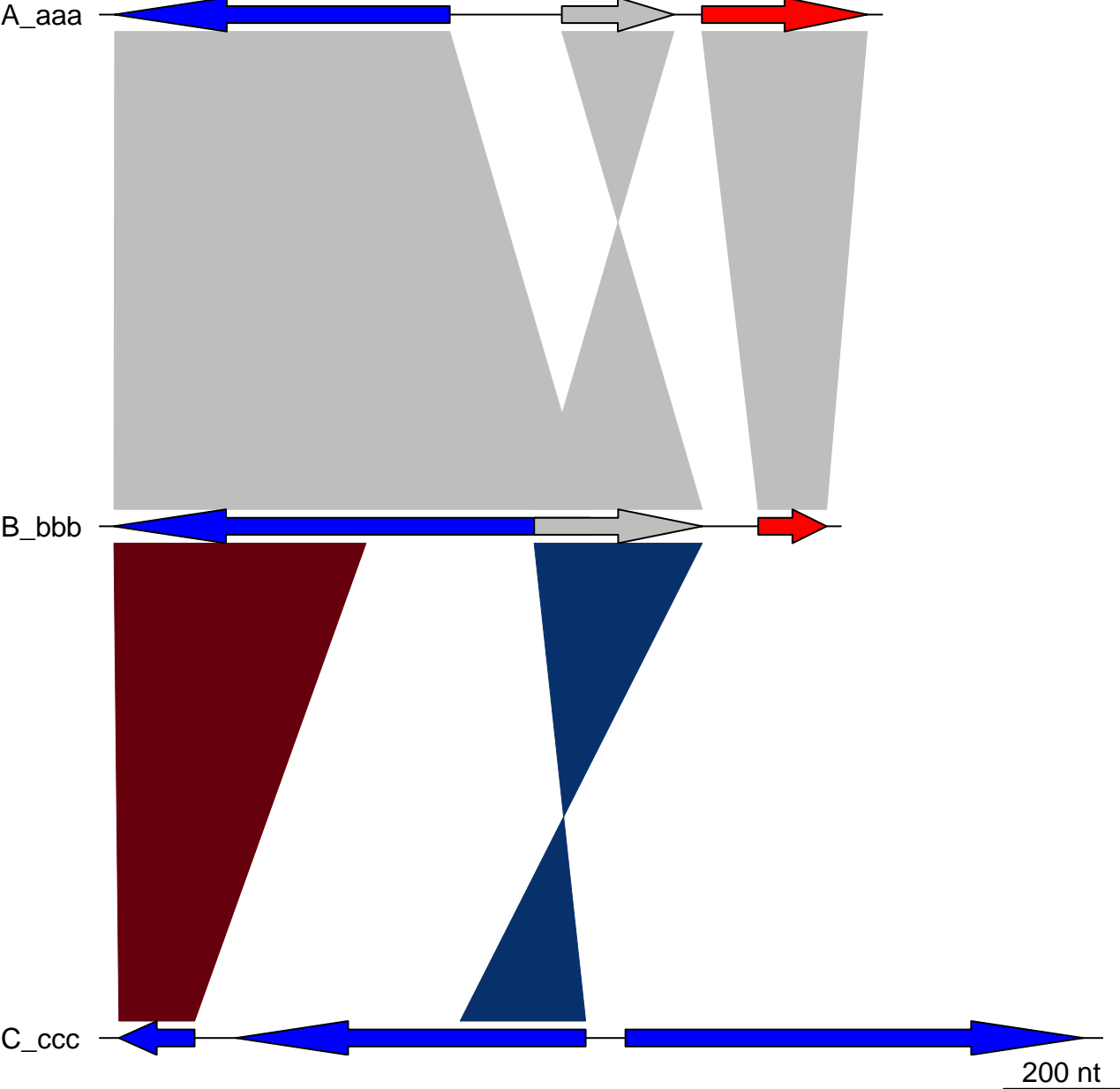
C_ccc



200 nt

help("plot_gene_map")

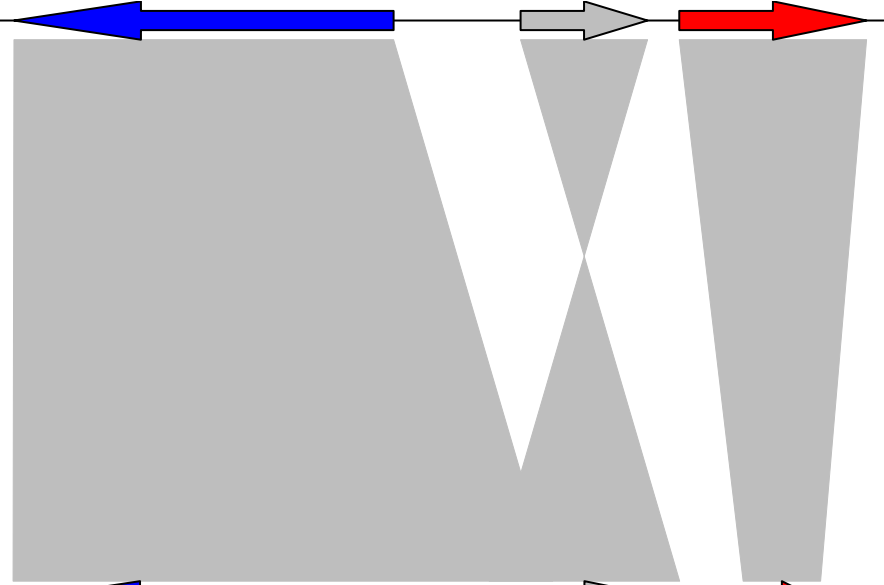
Comparison of A, B and C



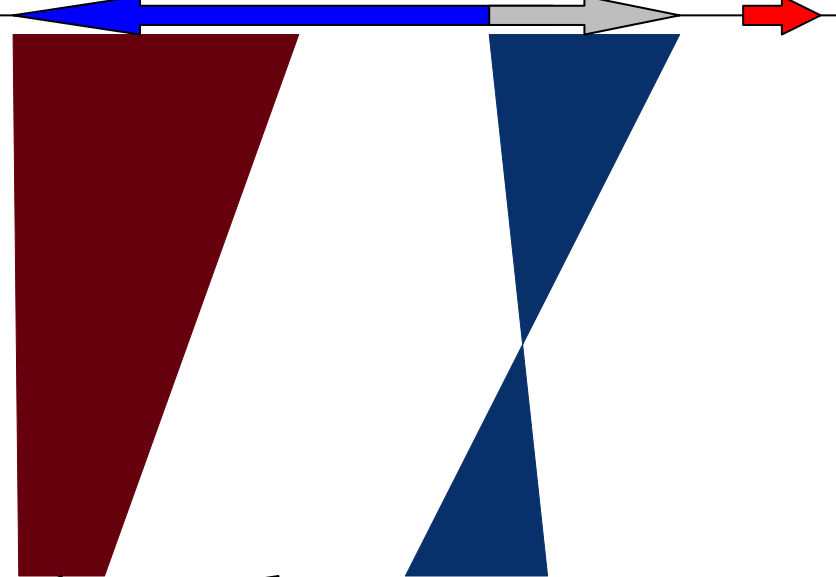
help("plot_gene_map")

Comparison of A, B and C

A_aaa



B_bbb



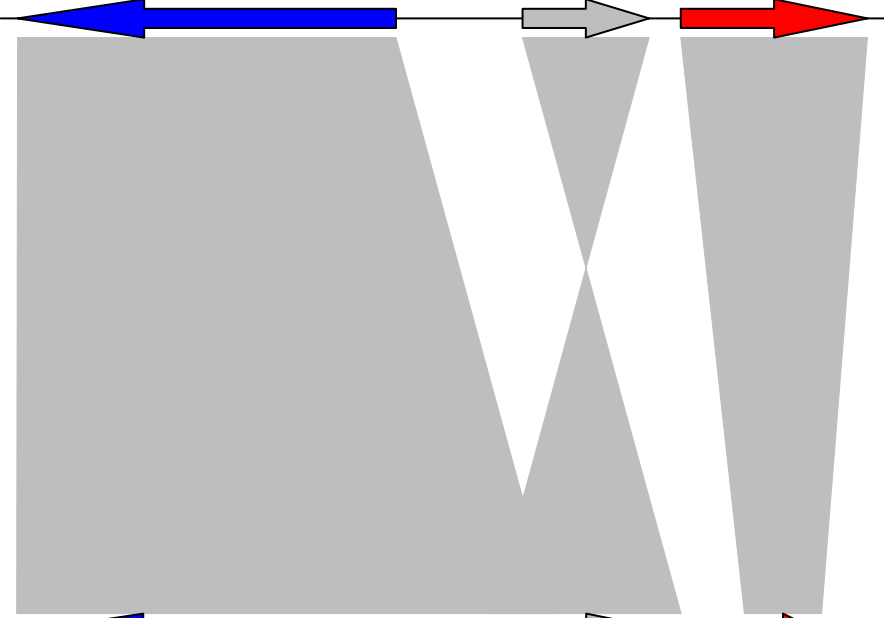
C_ccc



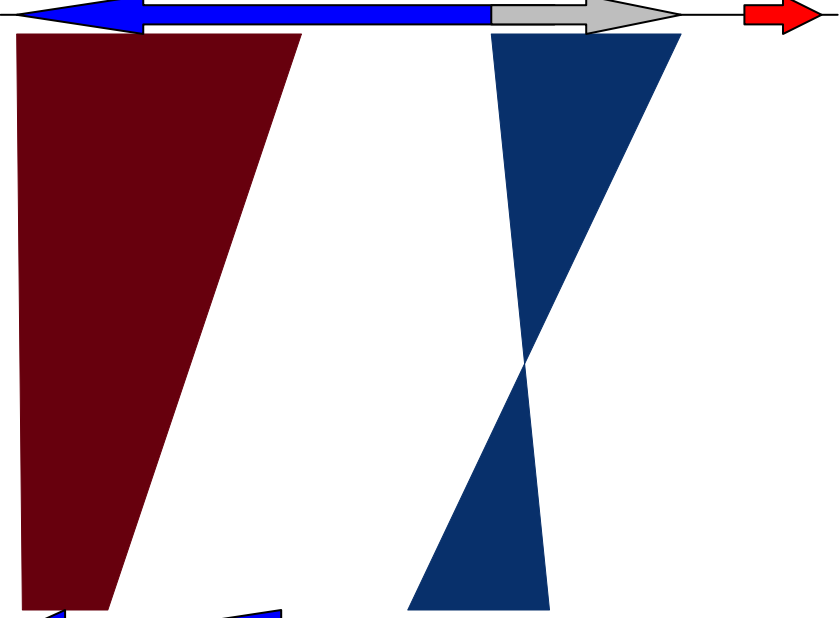
200 nt

help("plot_gene_map")

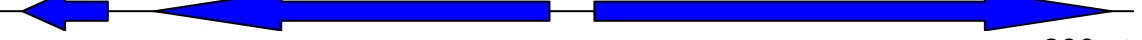
Huey



Dewey



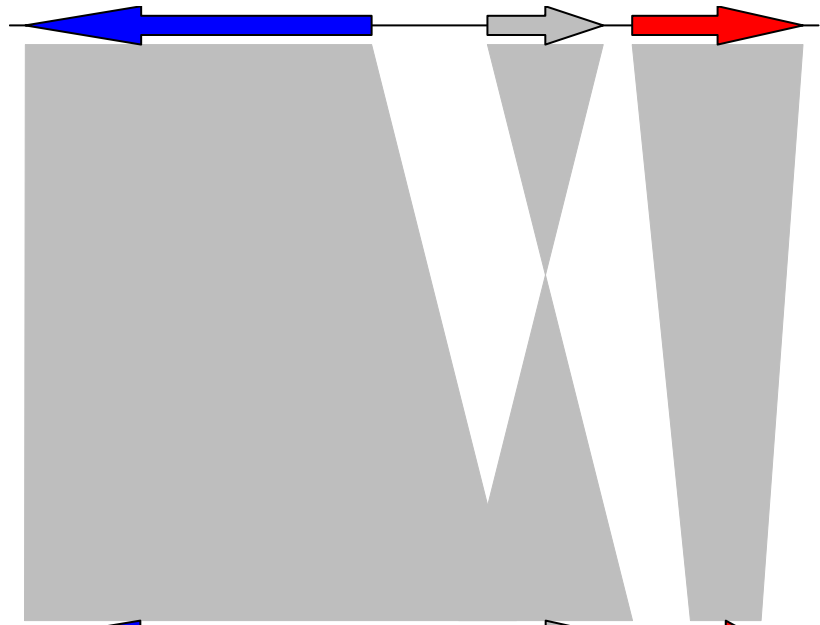
Louie



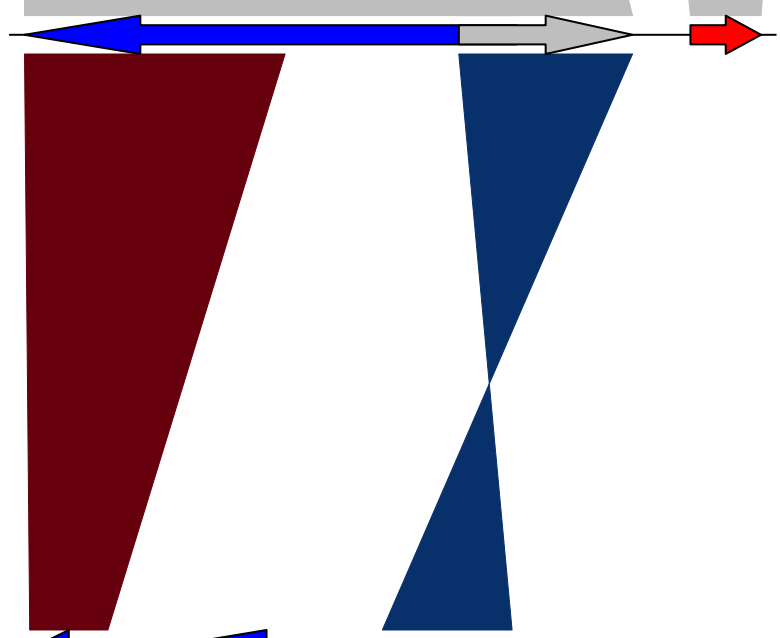
200 nt

help("plot_gene_map")

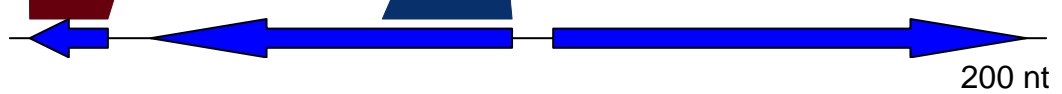
Huey



Dewey

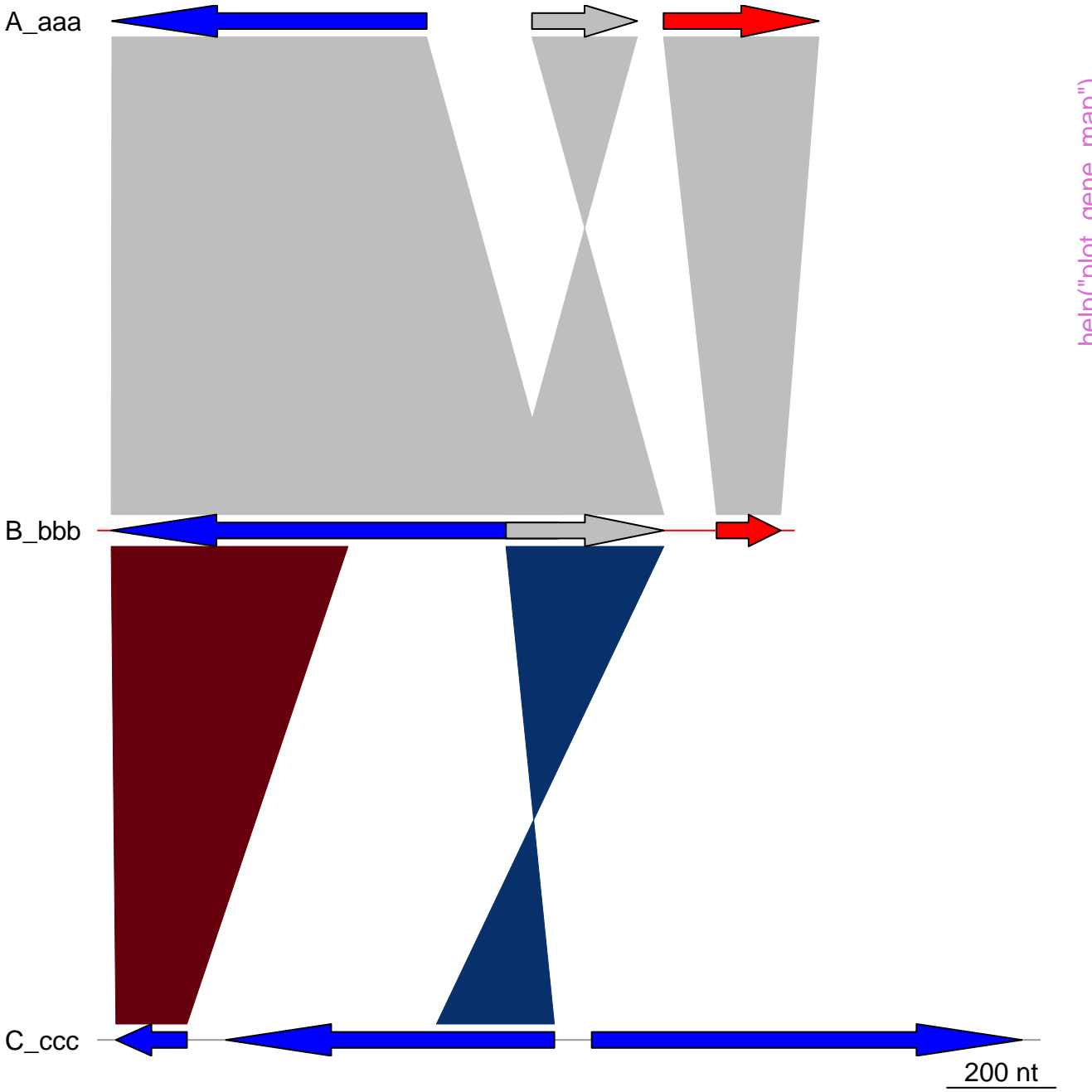


Louie



200 nt

help("plot_gene_map")



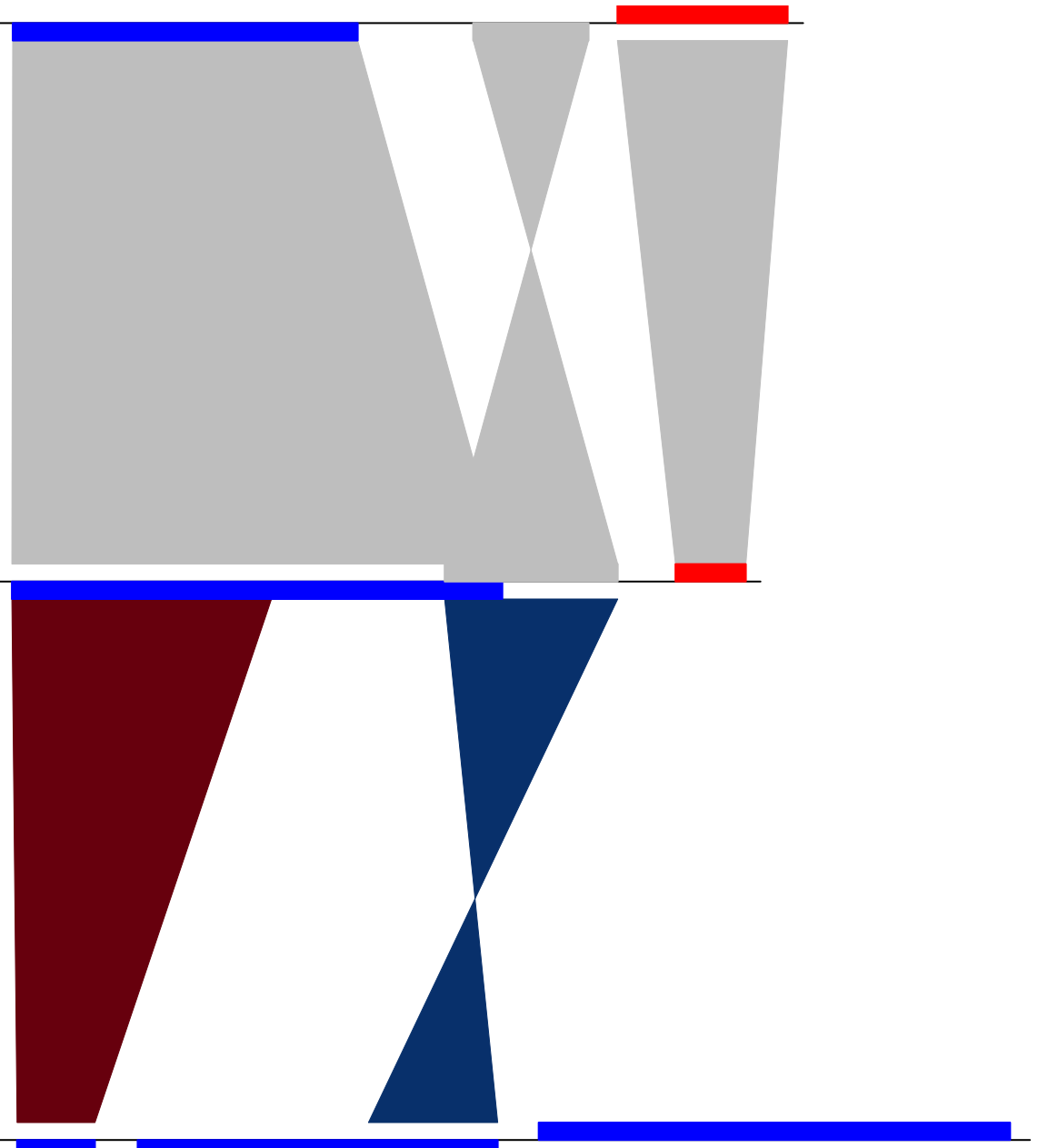
A_aaa

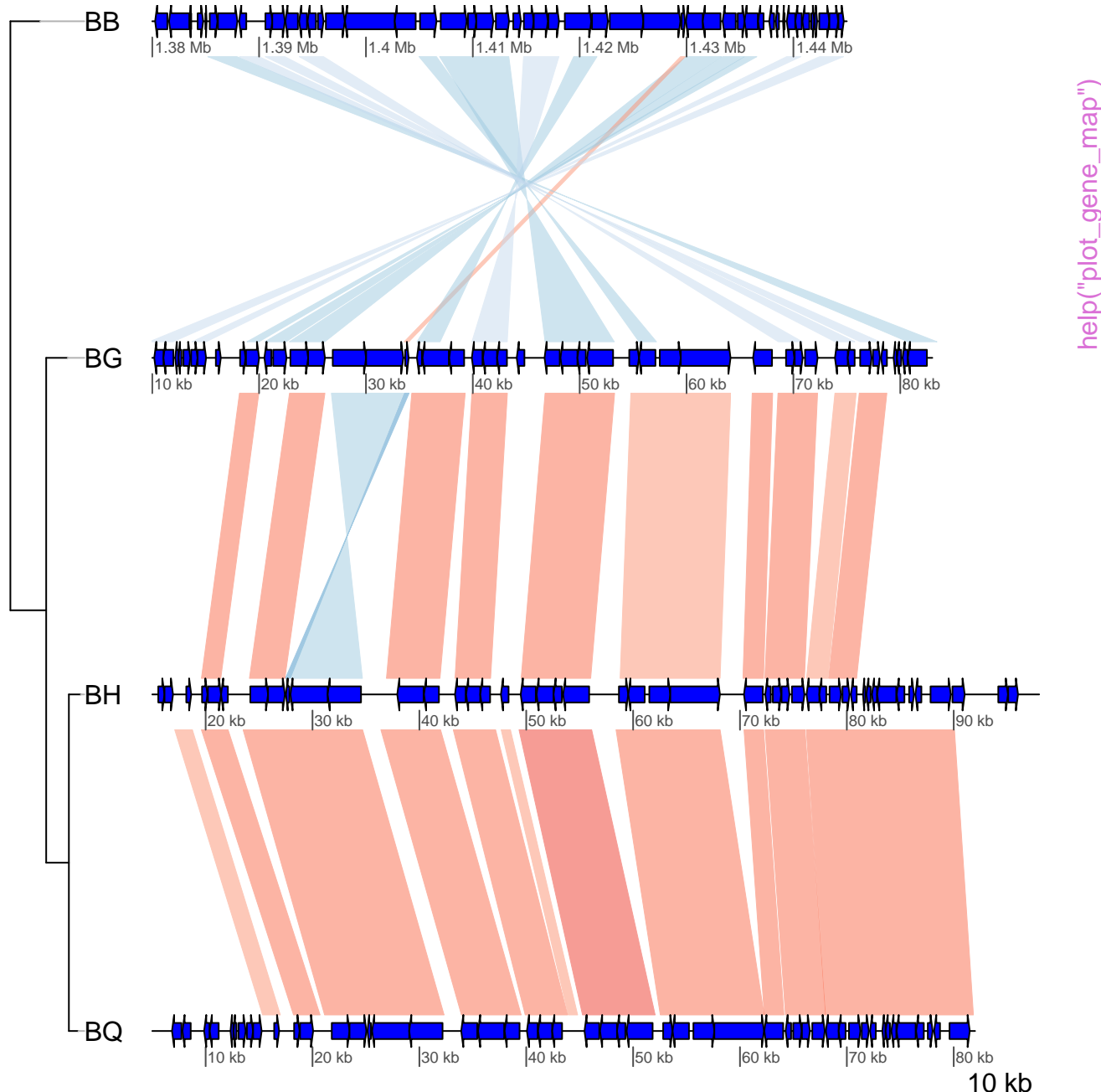
B_bbb

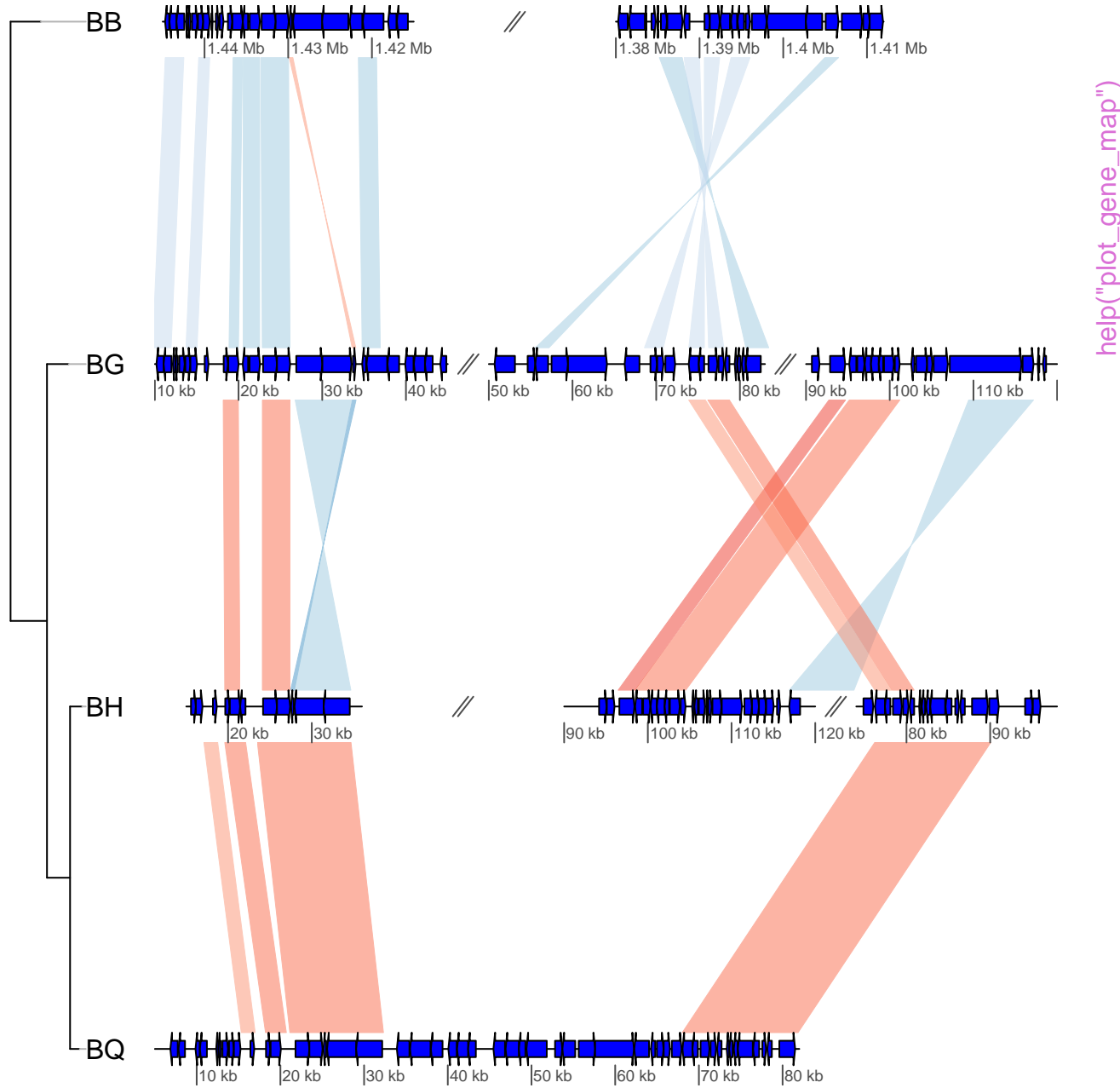
C_ccc

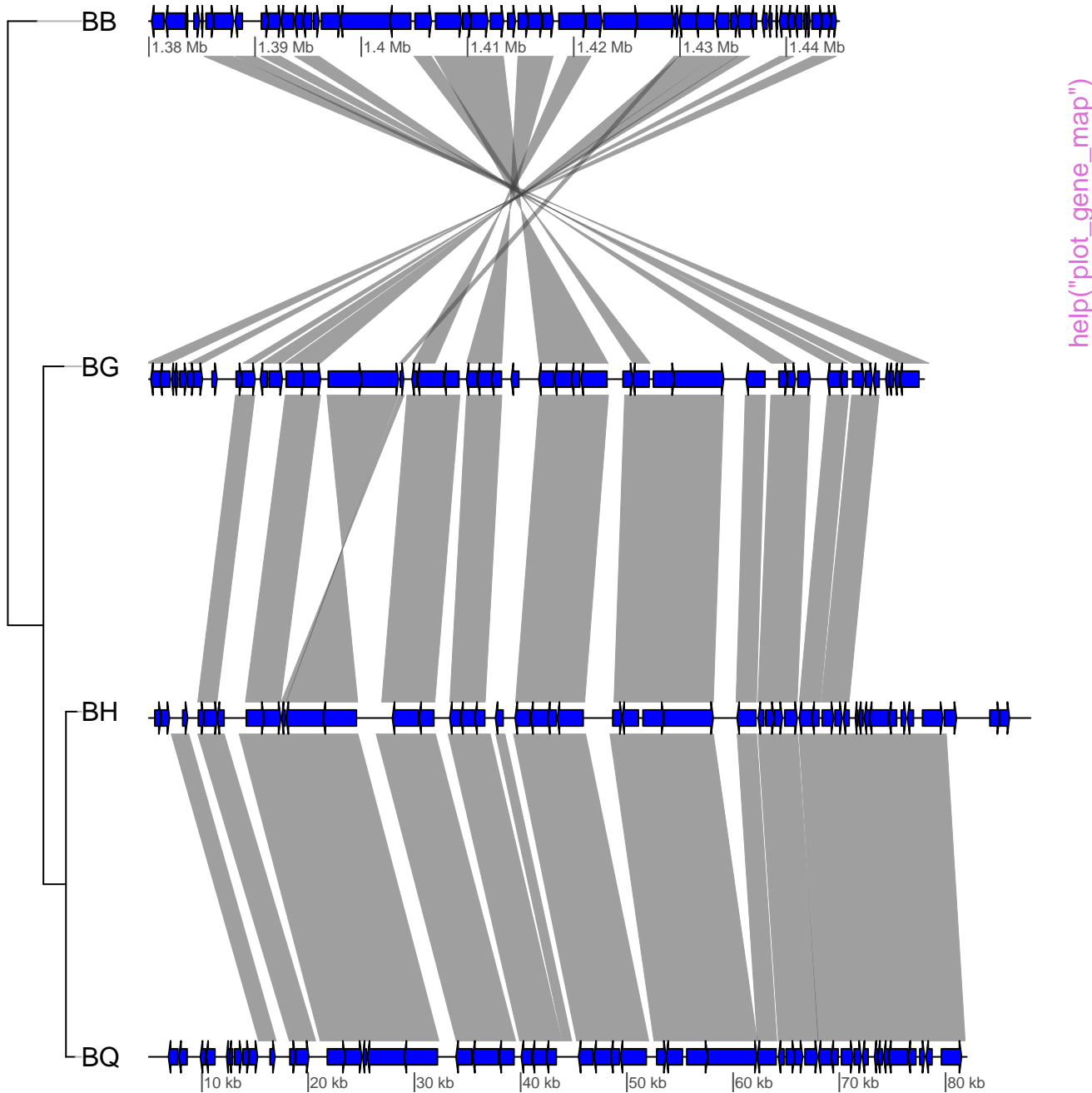
help("plot_gene_map")

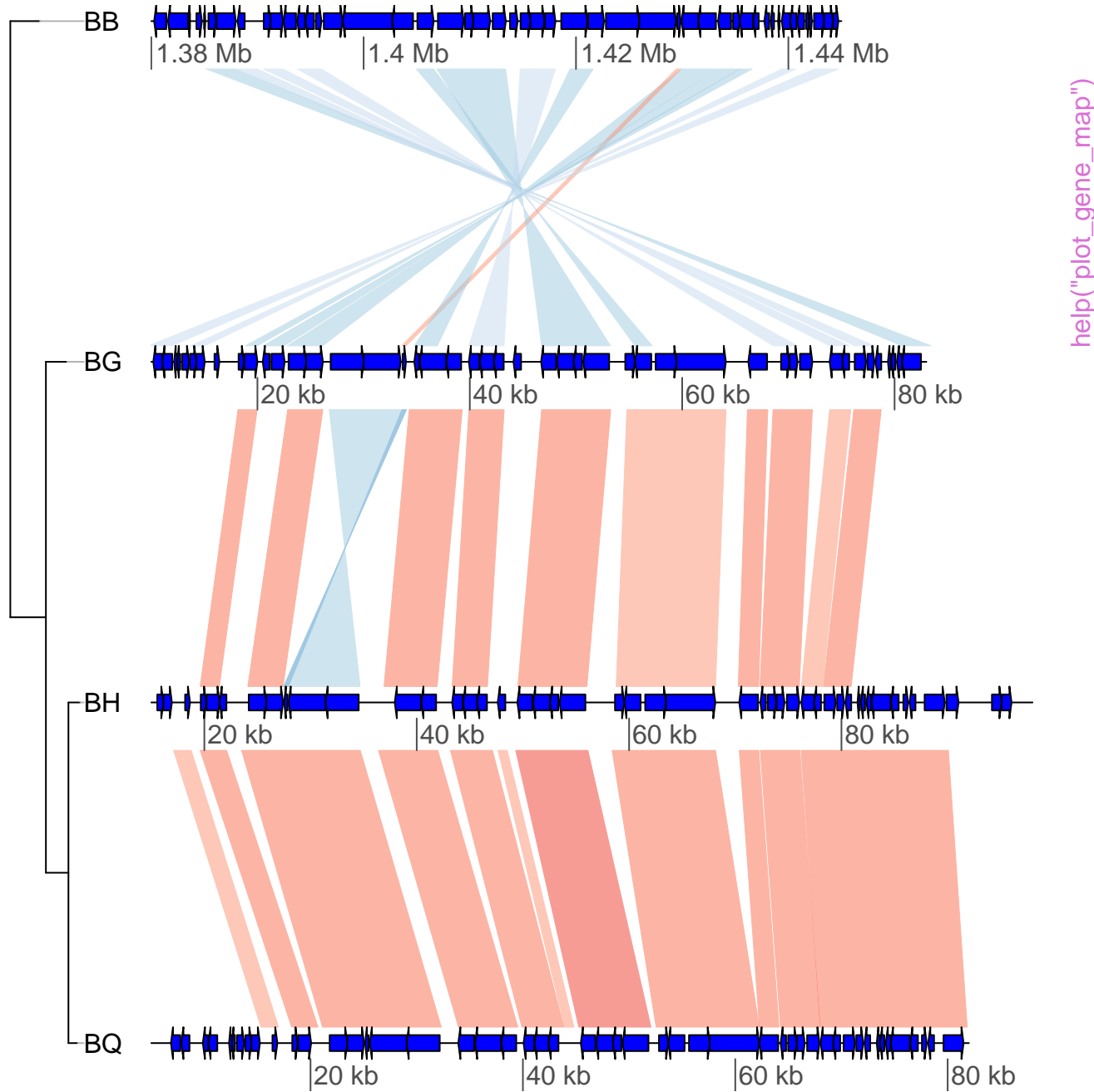
200 nt

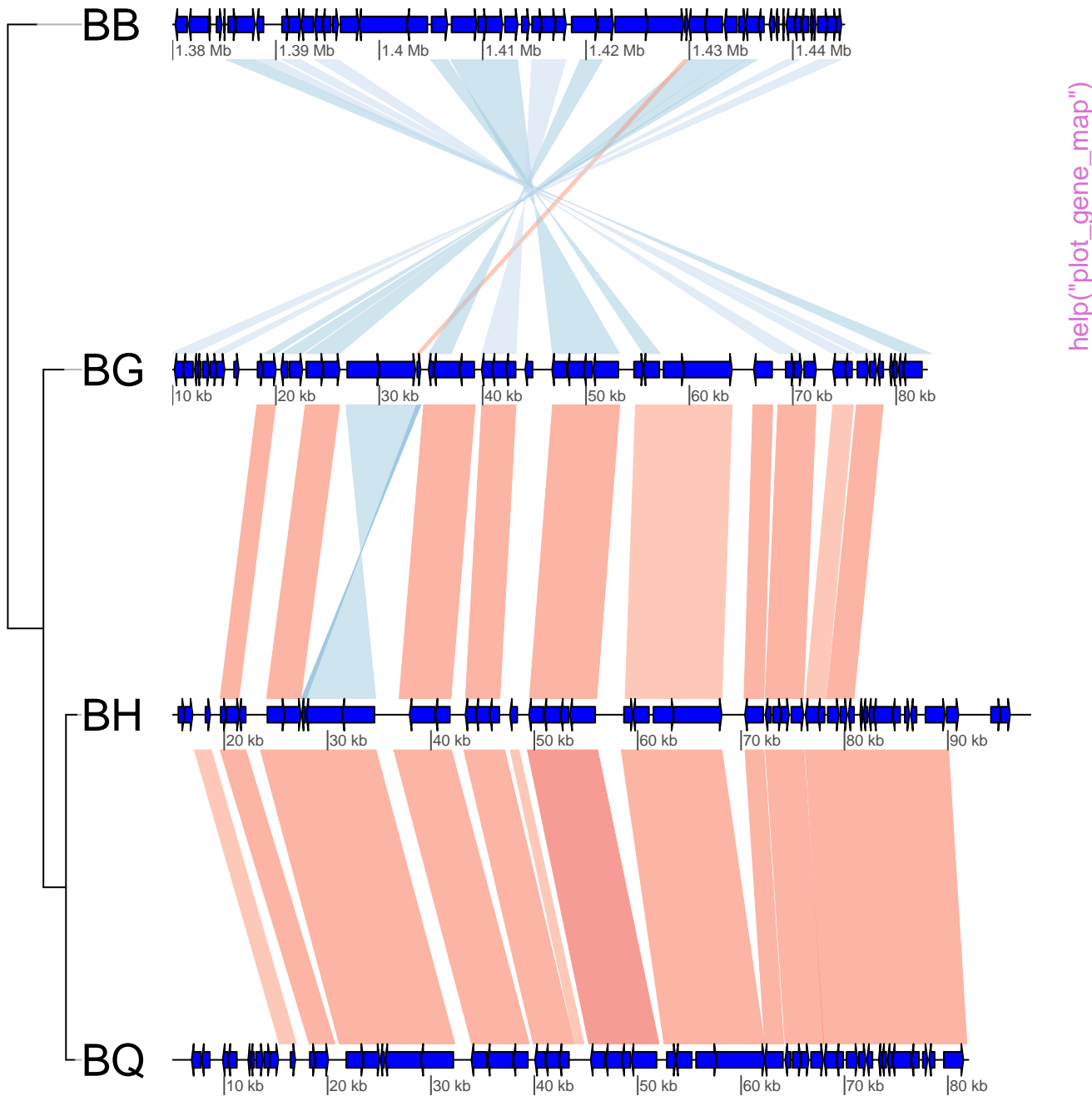


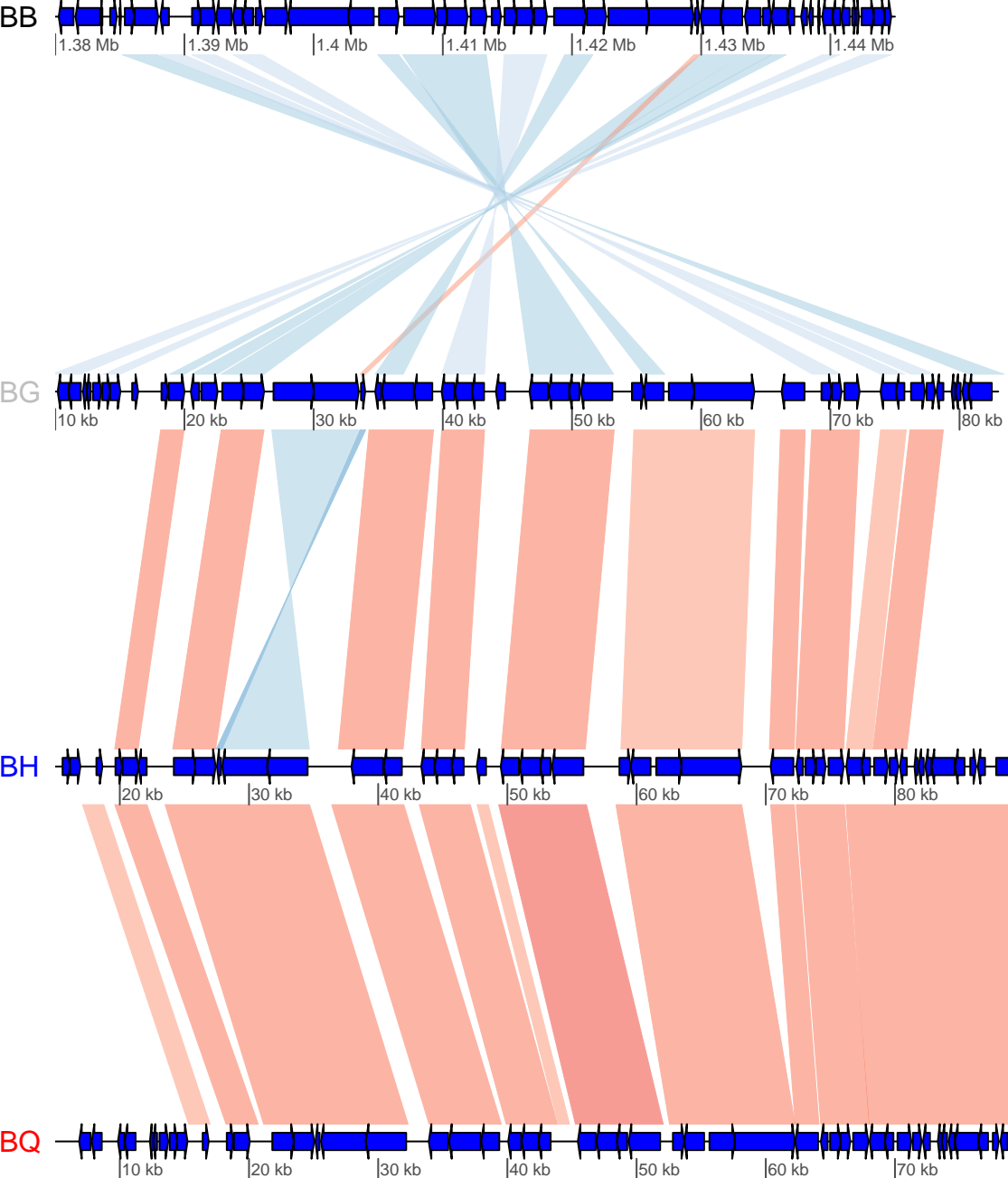




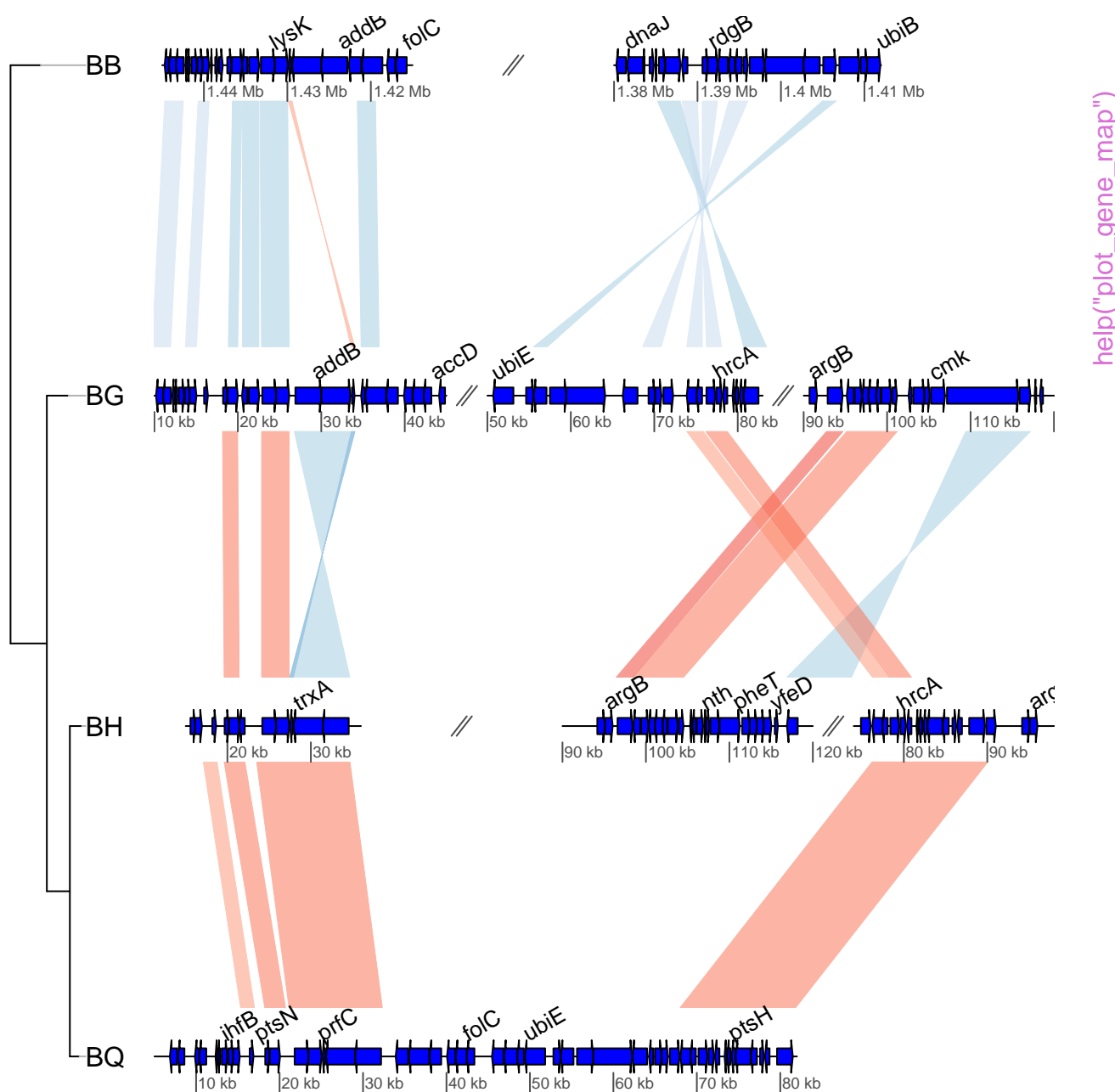




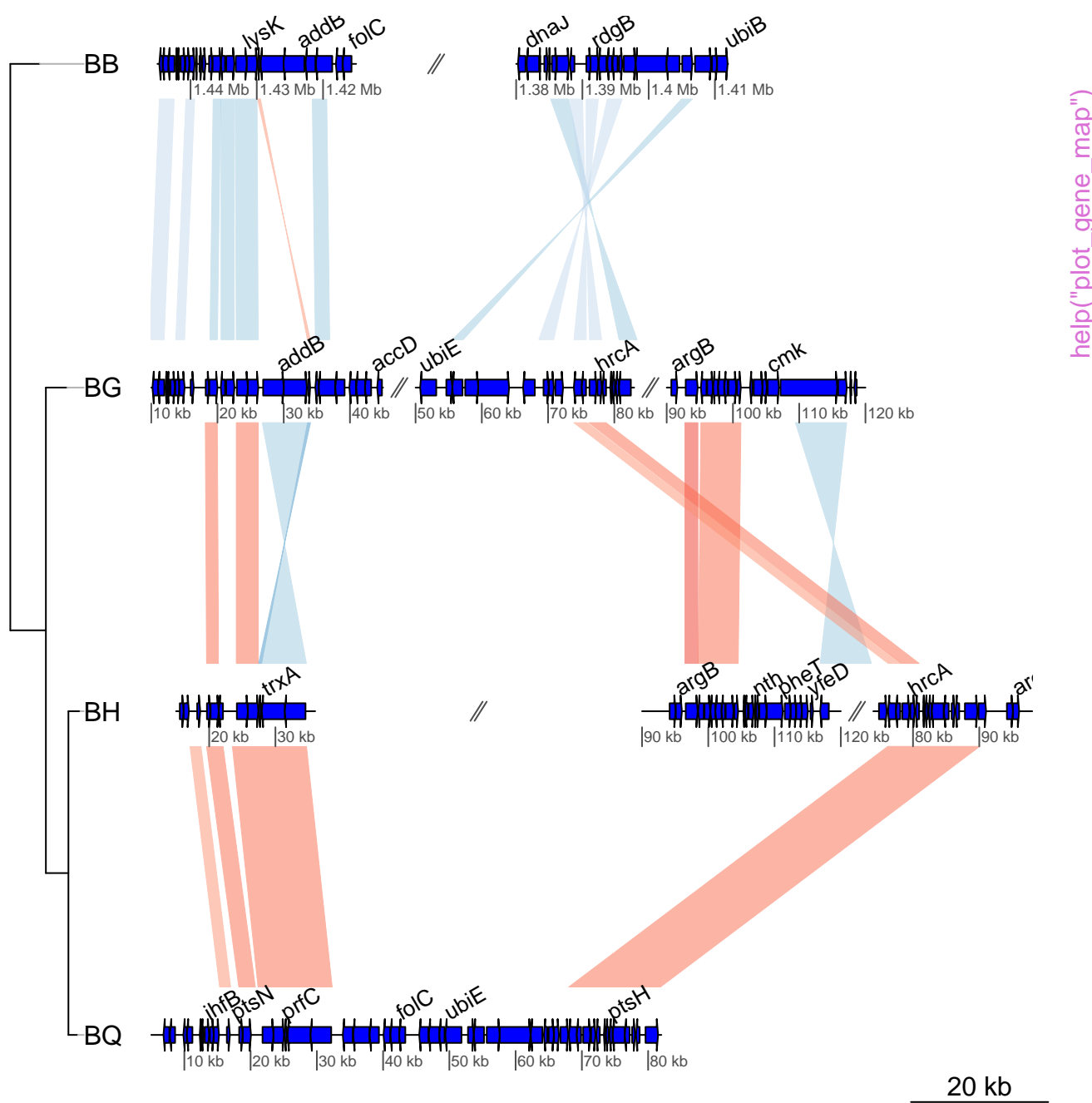


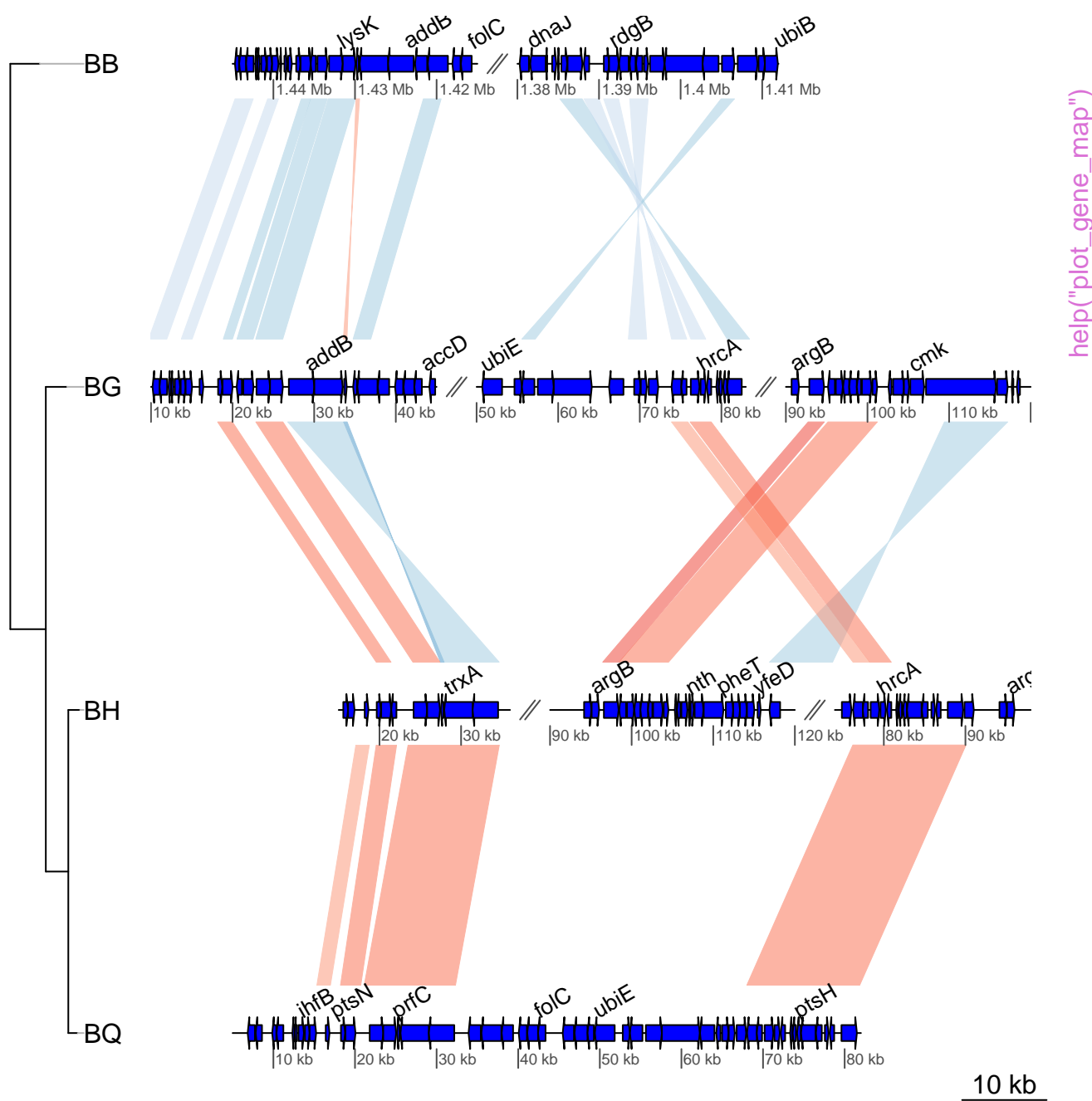


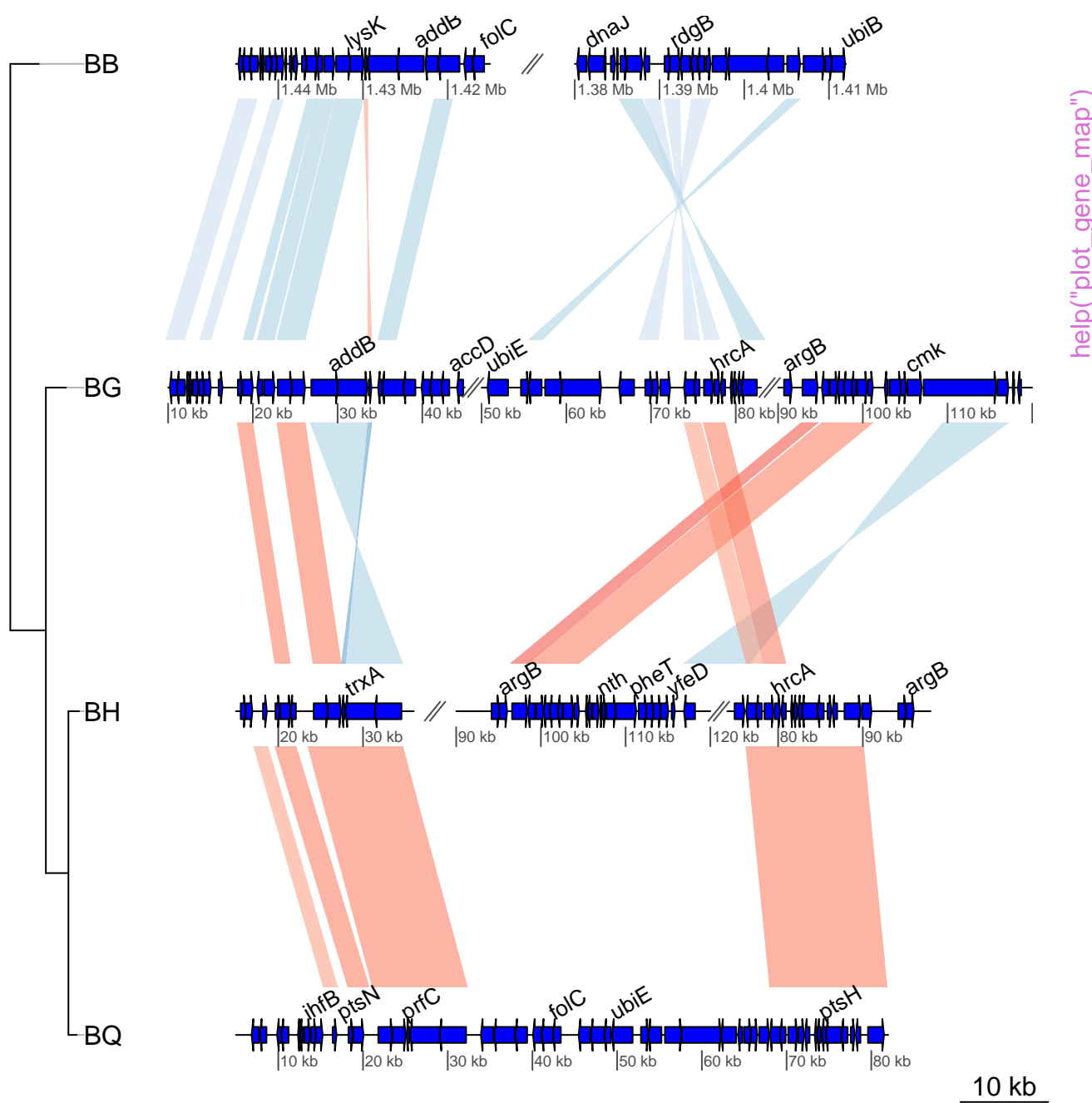
help("plot_gene_map")

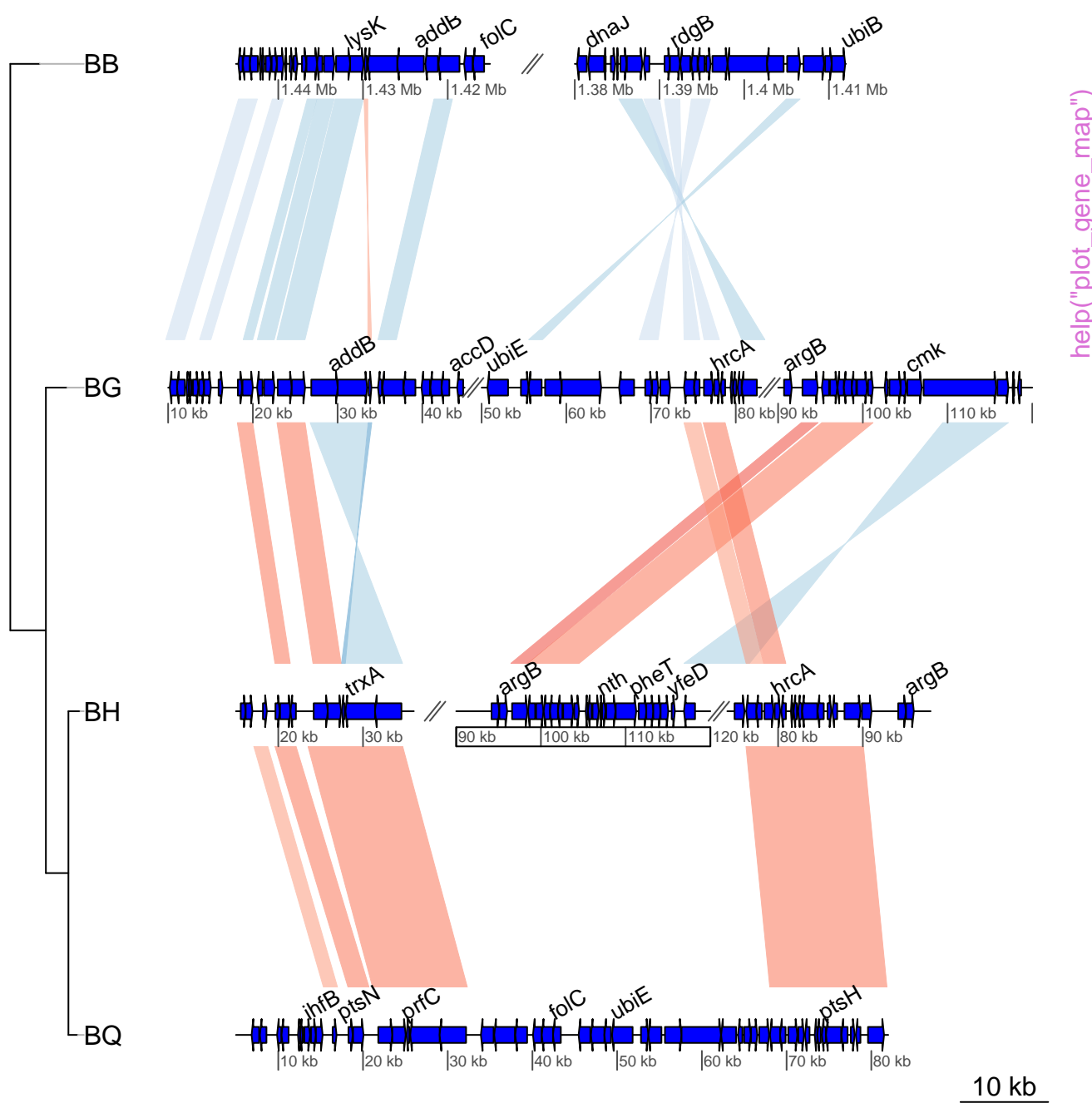


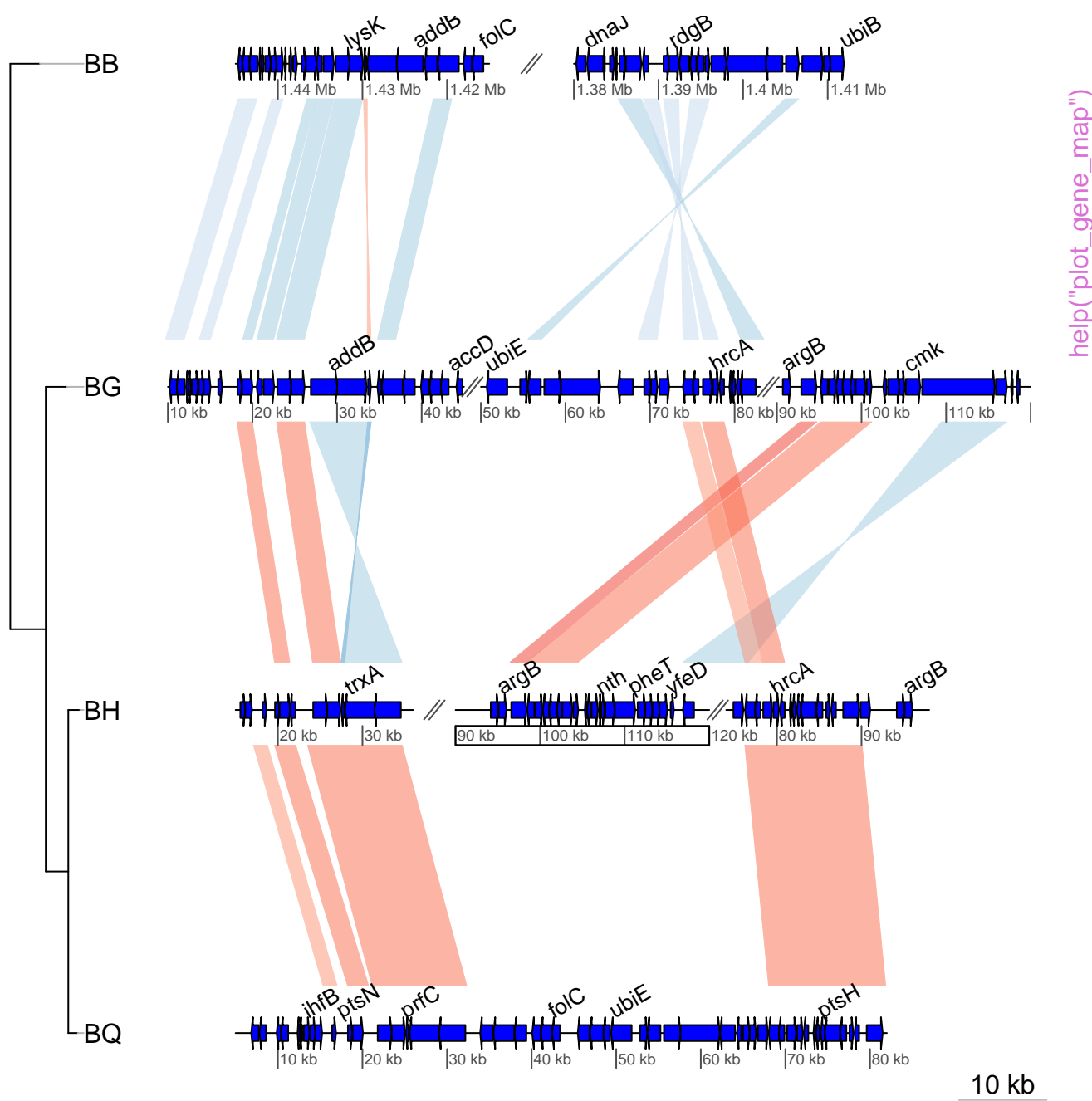
help("plot_gene_map")

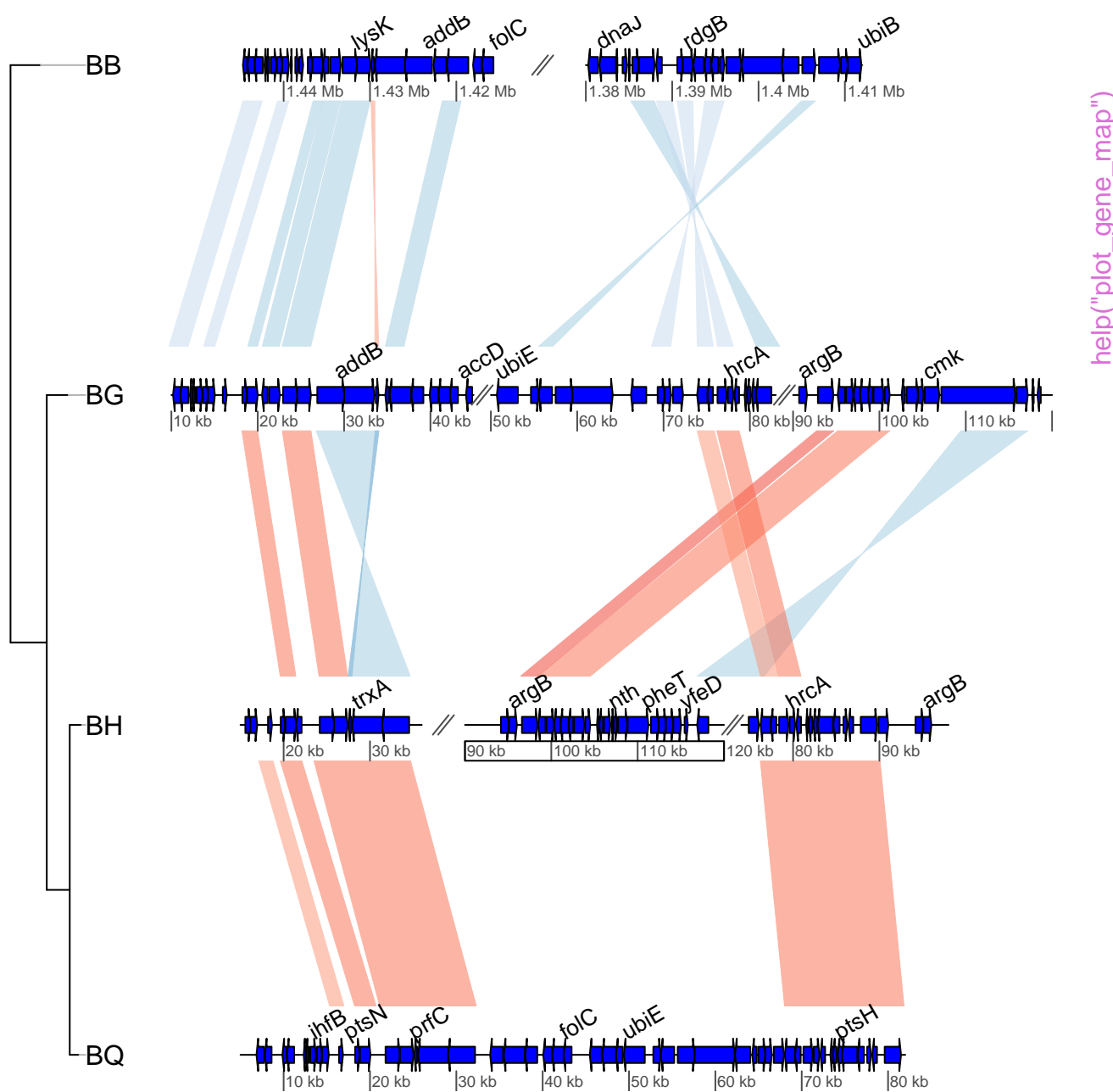












geno

R

Plot

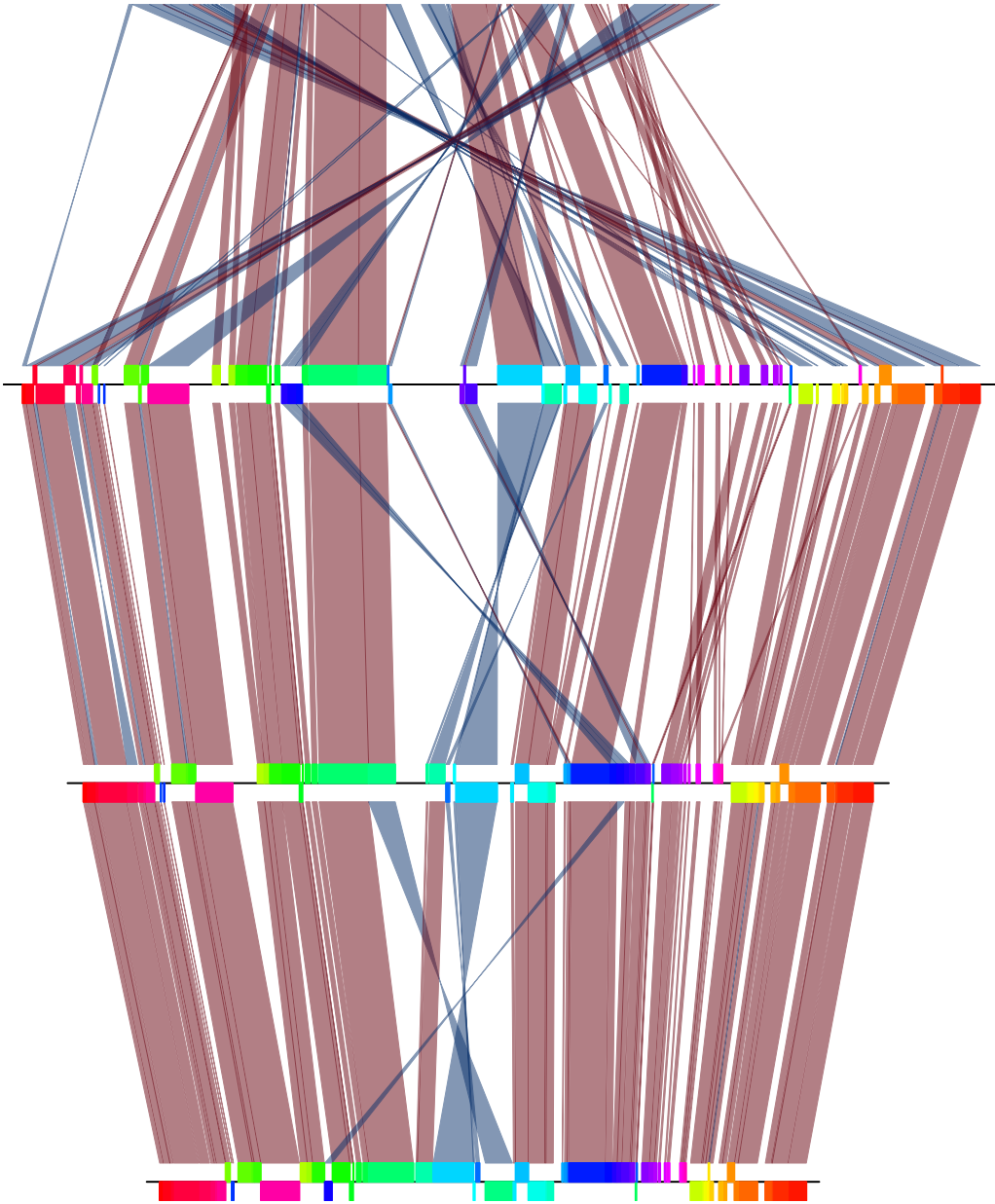
help("plot_gene_map")

B_bacilliformis

B_grahamii

B_henselae

B_quintana



help("read_functions")

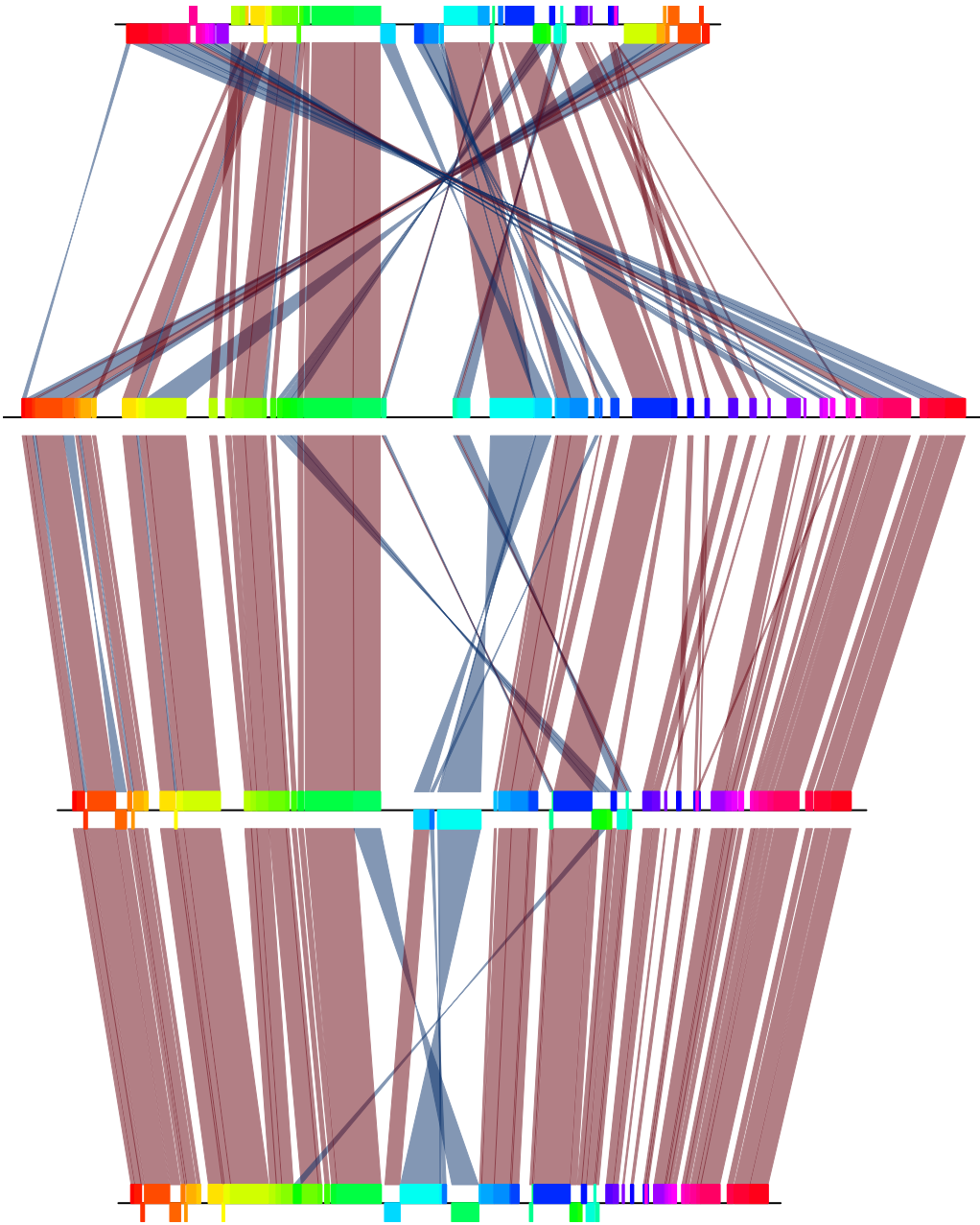
500 kb

B_bacilliformis

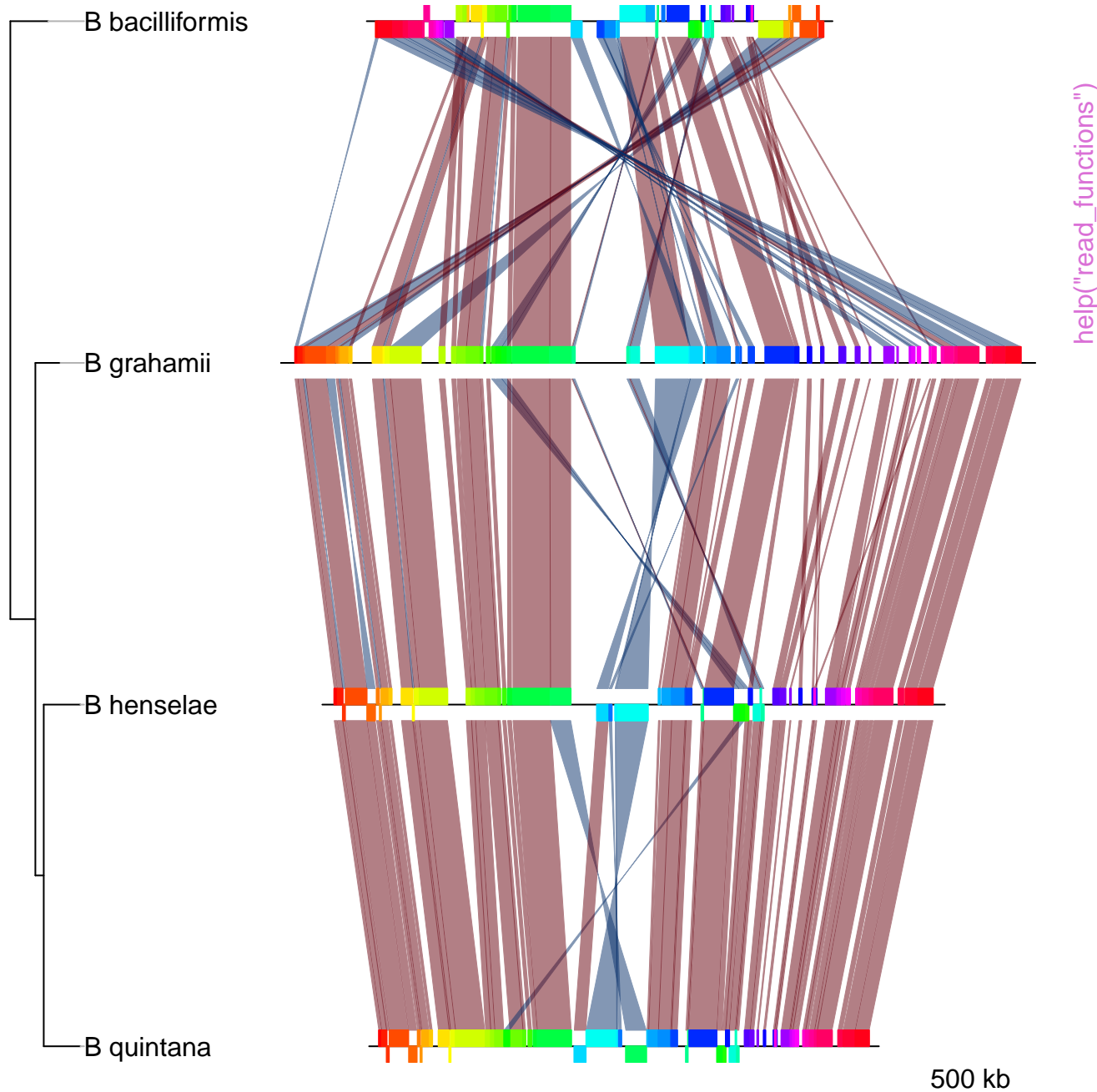
B_grahamii

B_henselae

B_quintana

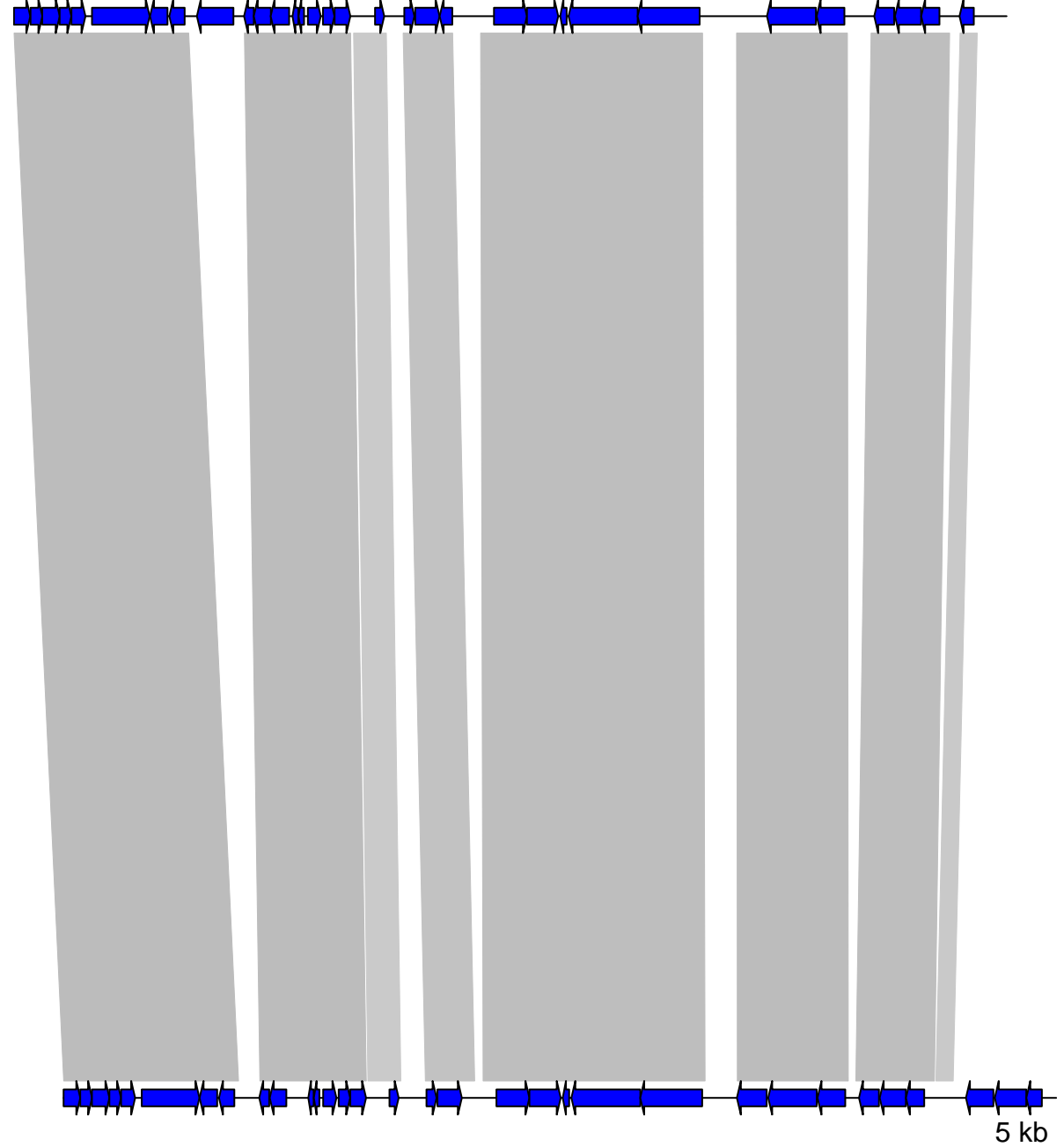


help("read_functions")



BH

BQ



help("read_functions")

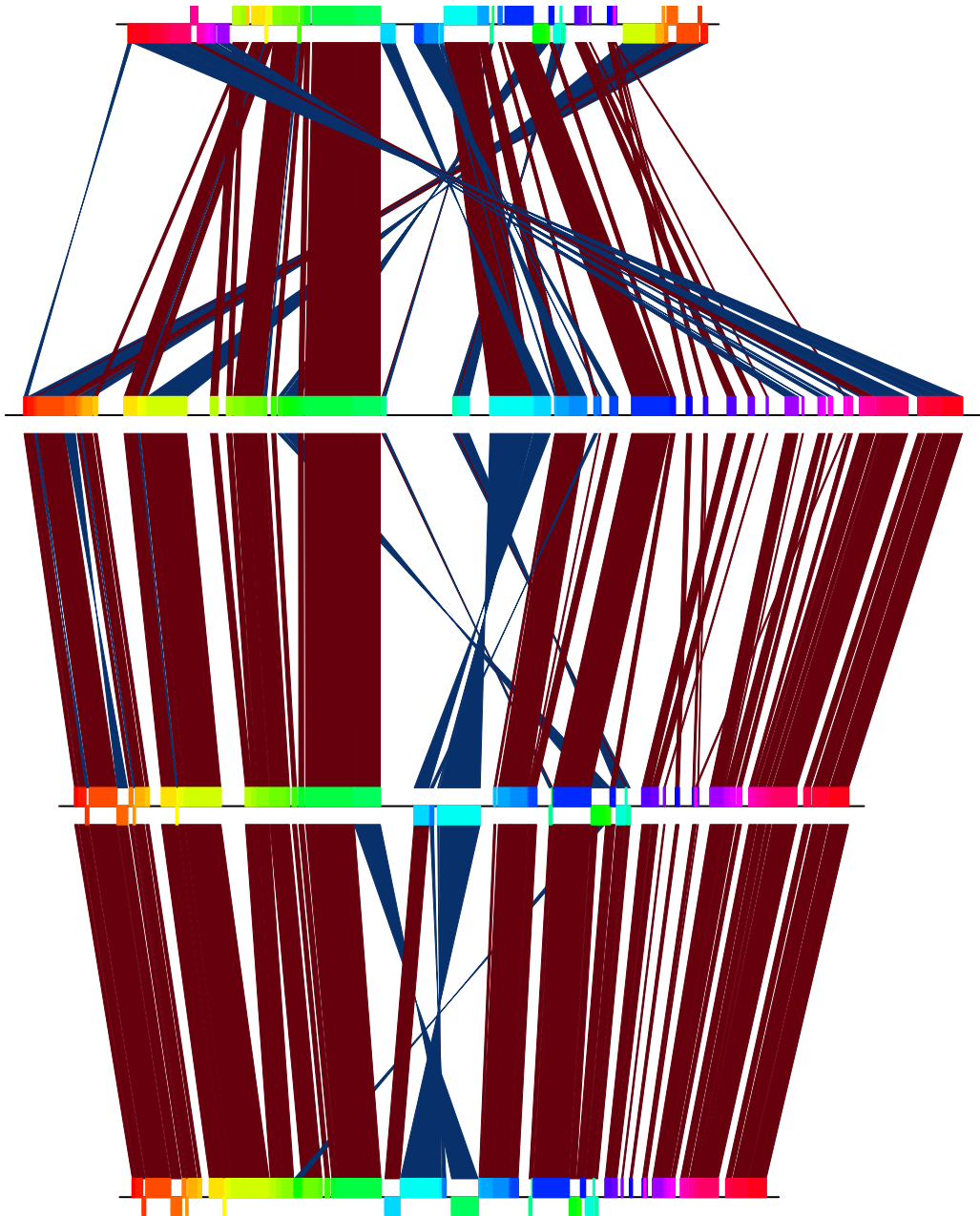
5 kb

B_bacilliformis

B_grahamii

B_henselae

B_quintana



help("reverse")

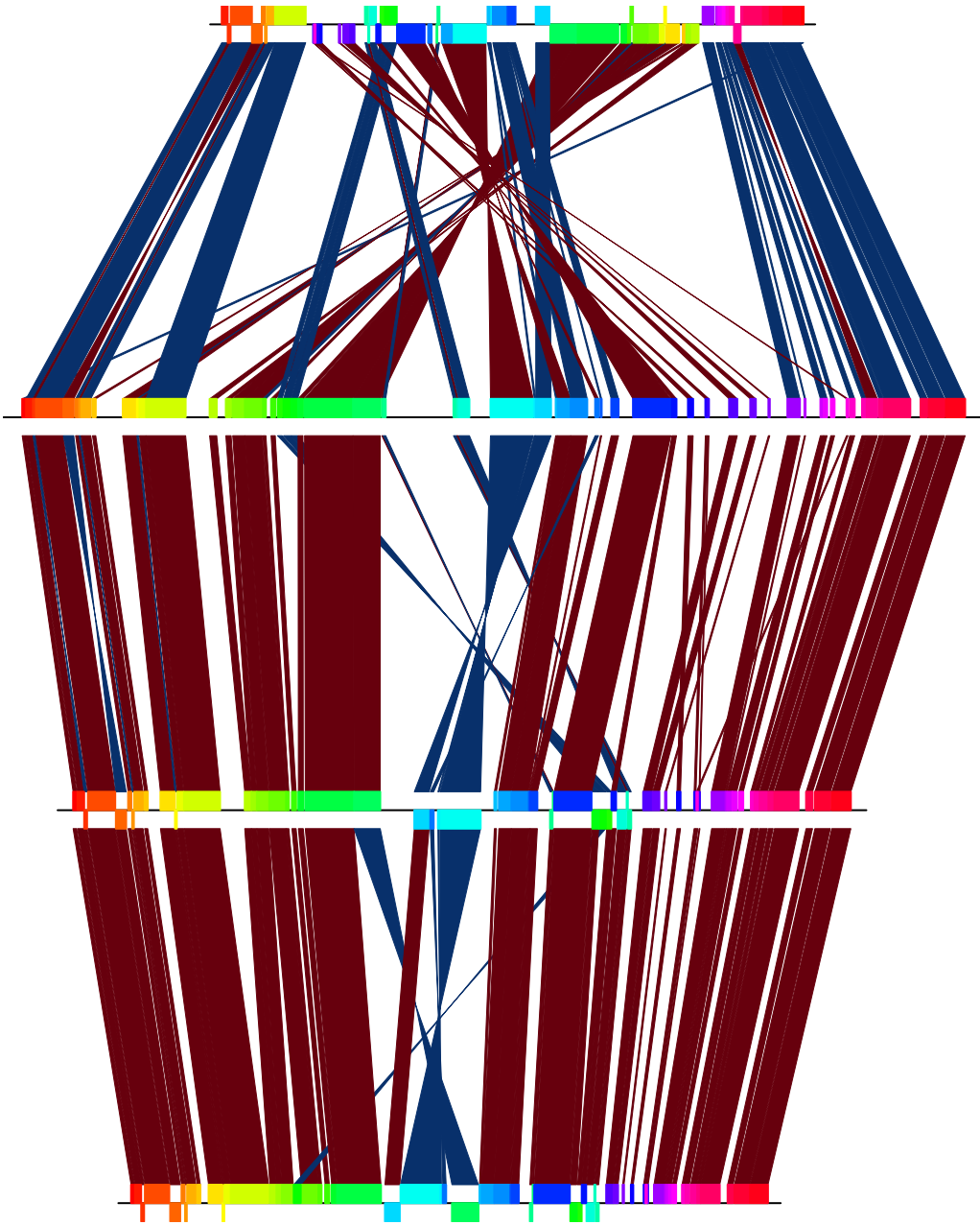
500 kb

B_bacilliformis

B_grahamii

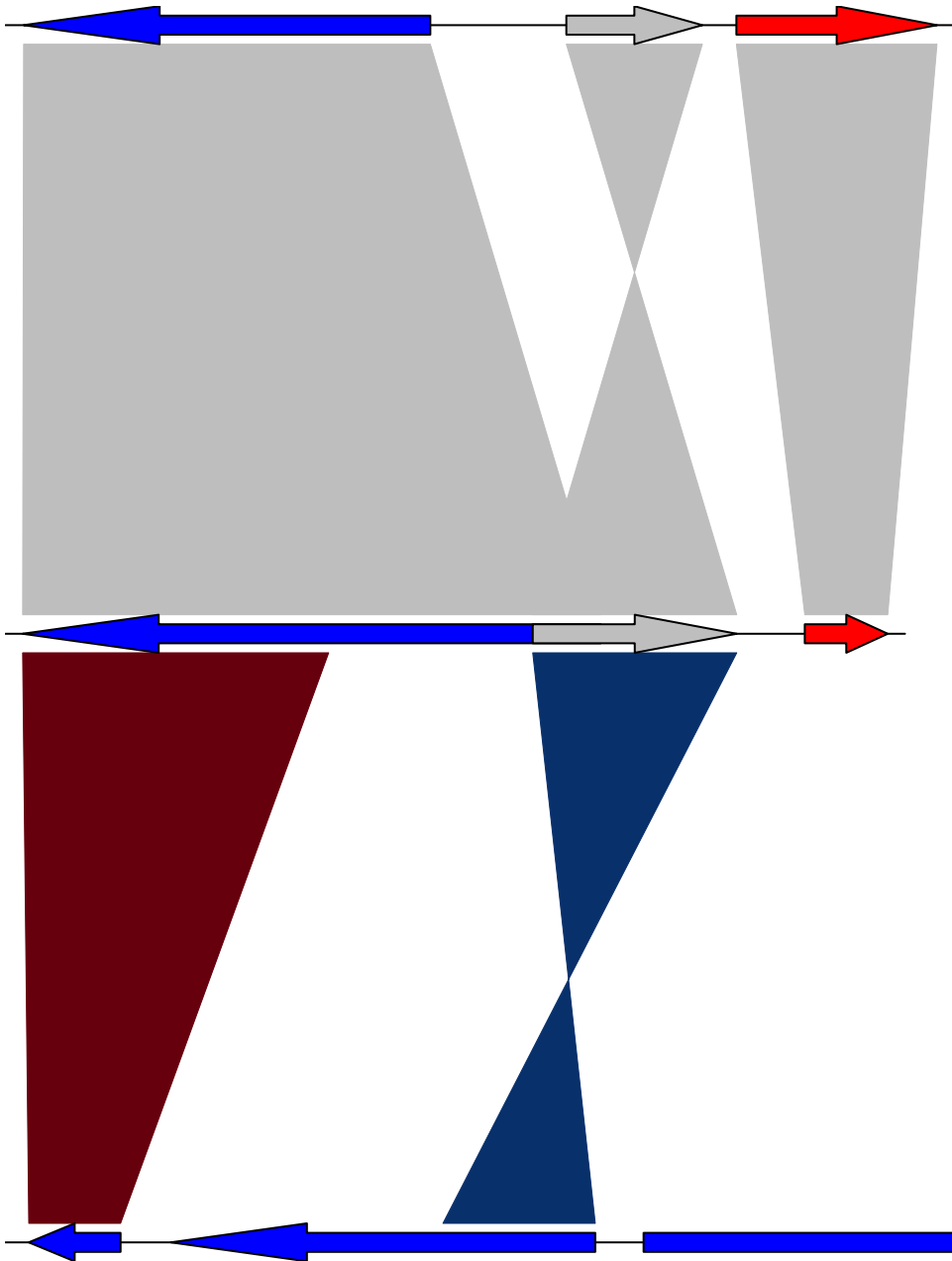
B_henselae

B_quintana



help("reverse")

500 kb



help("three_genes")

200 nt

