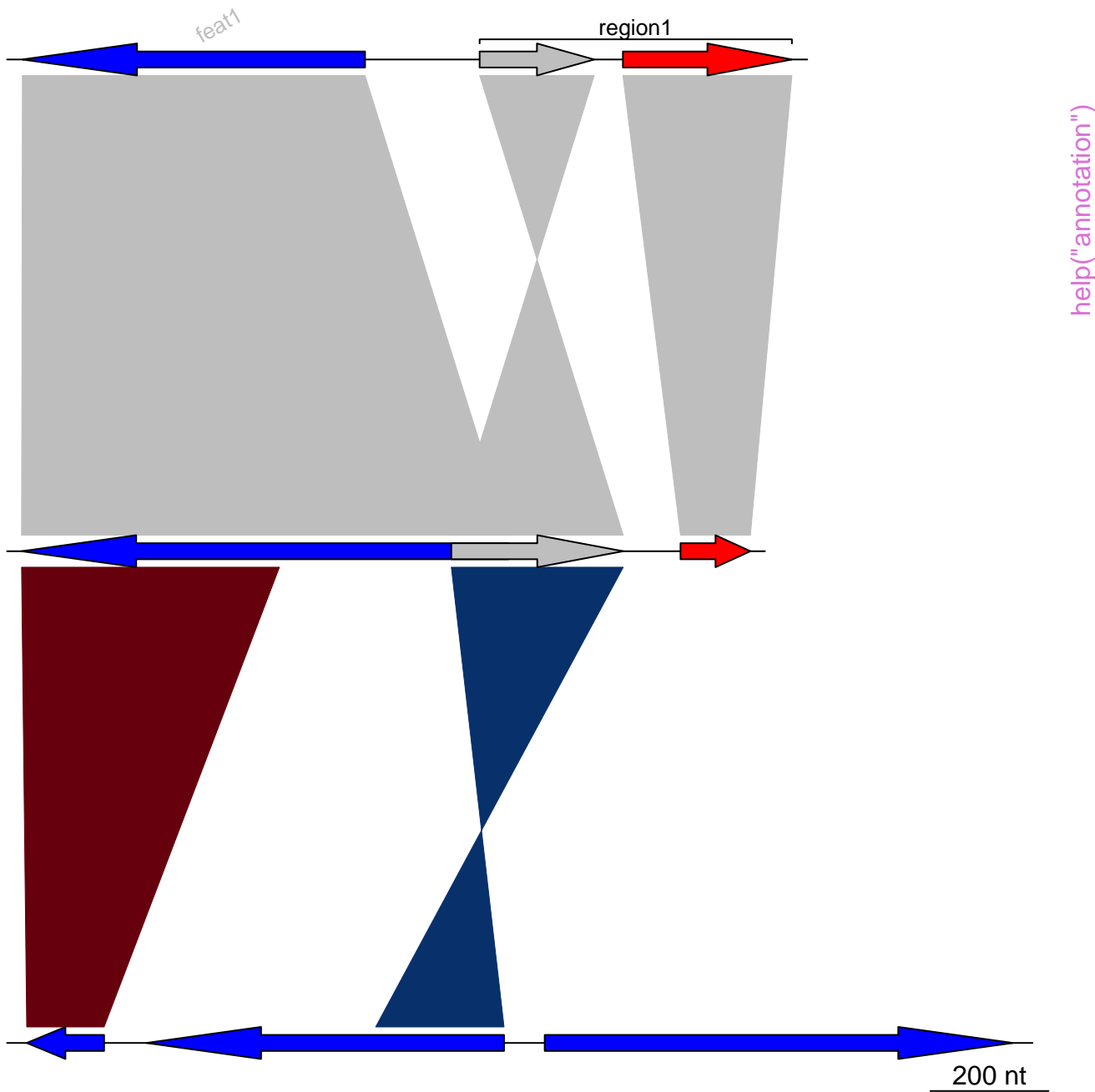
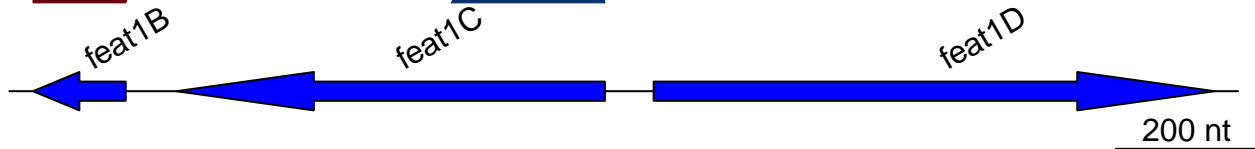
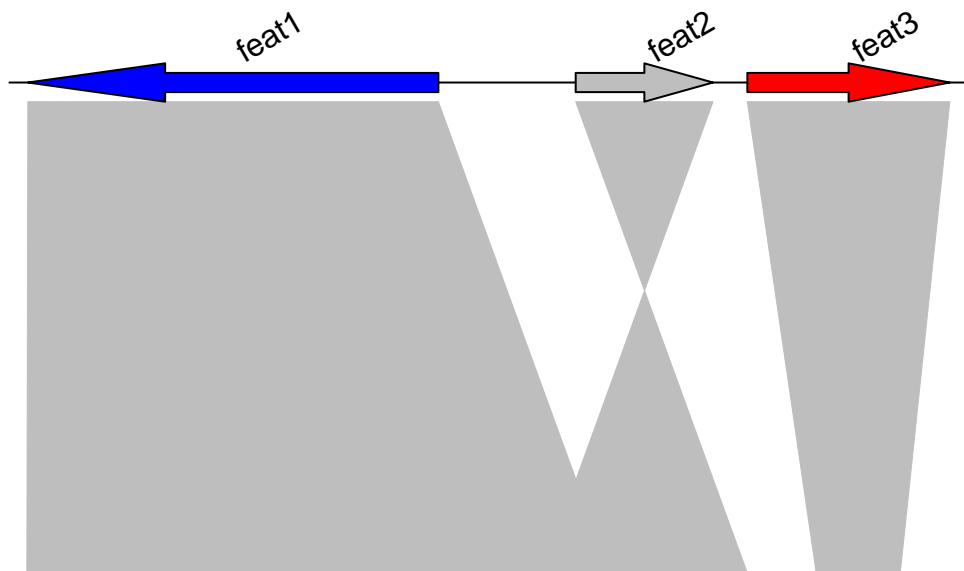


200 nt

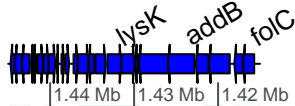
help("annotation")



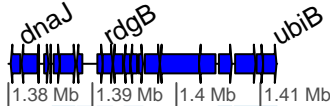


help("annotation")

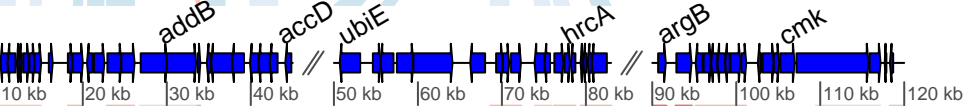
BB



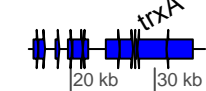
//



BG



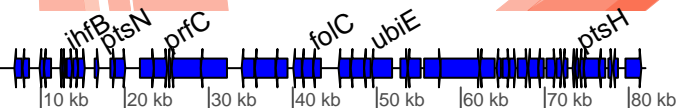
BH



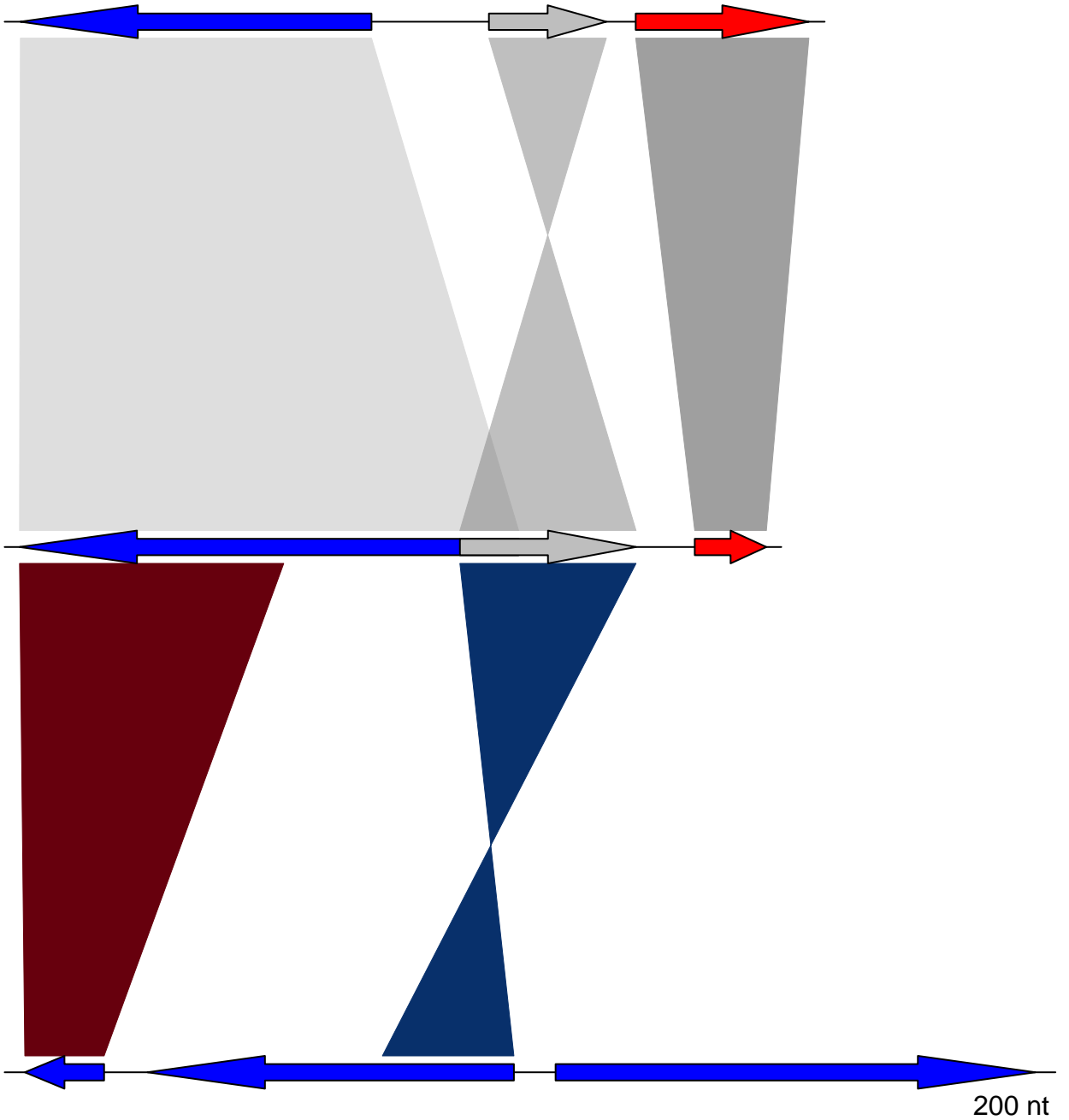
//



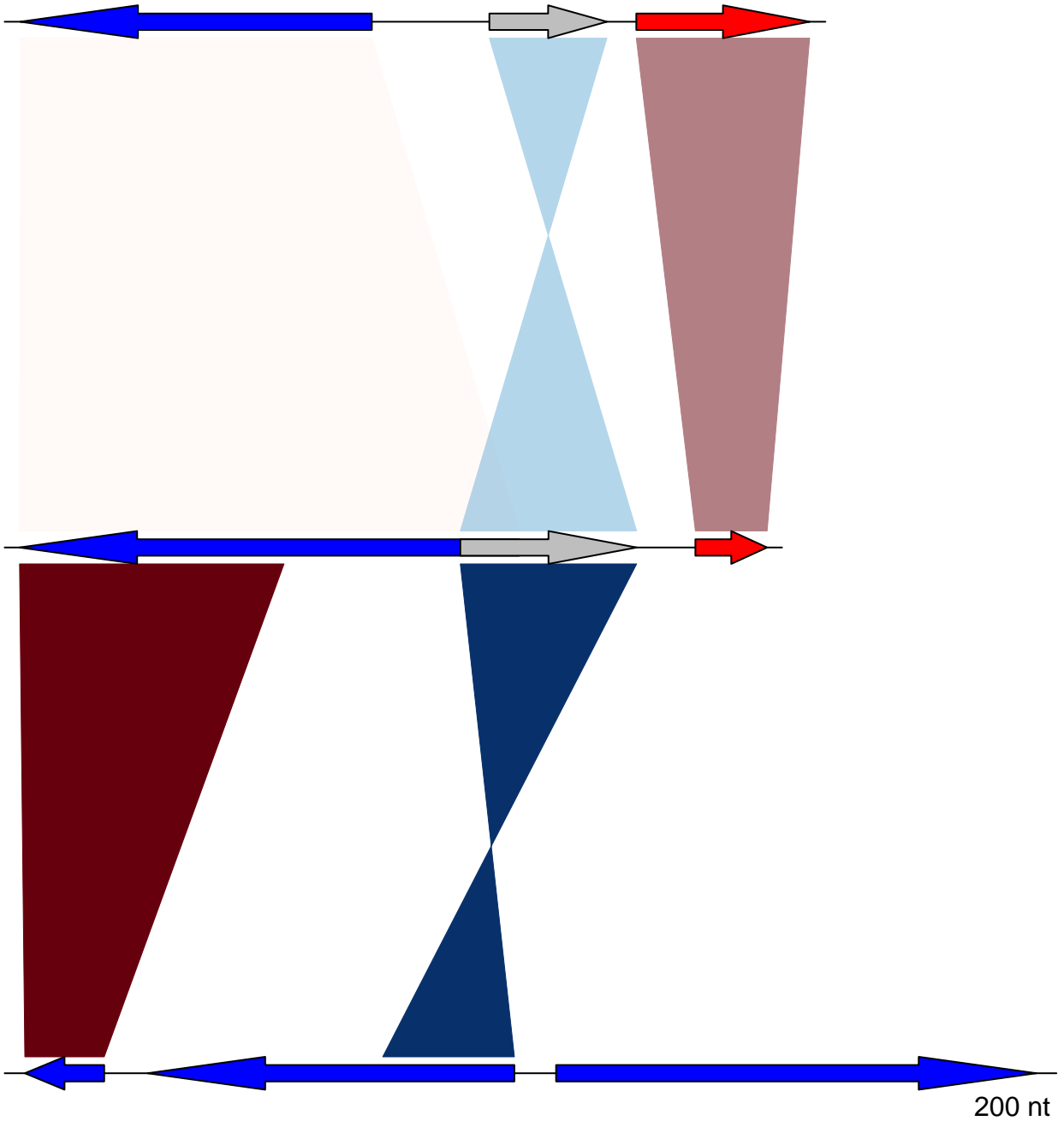
BQ



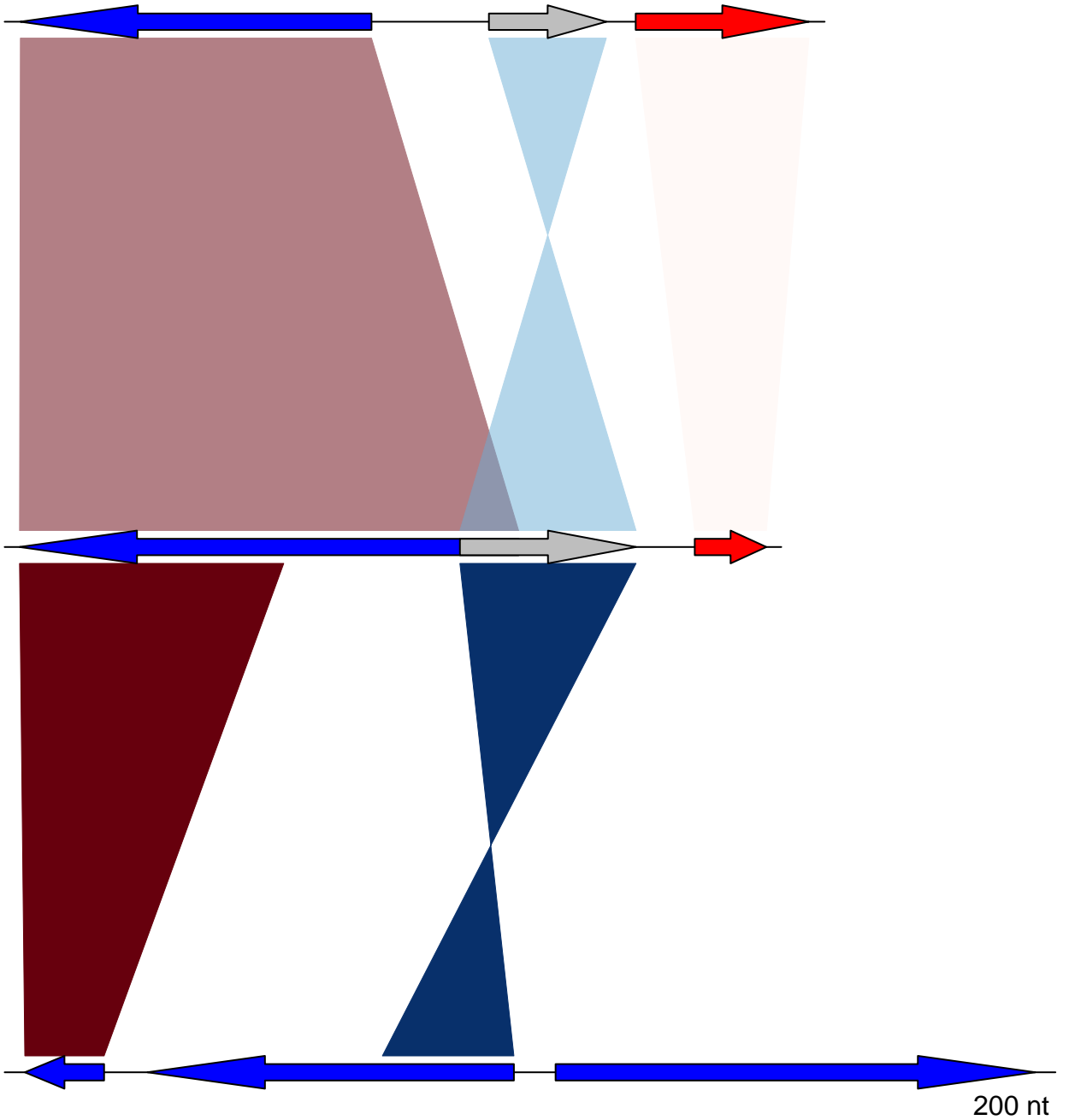
20 kb



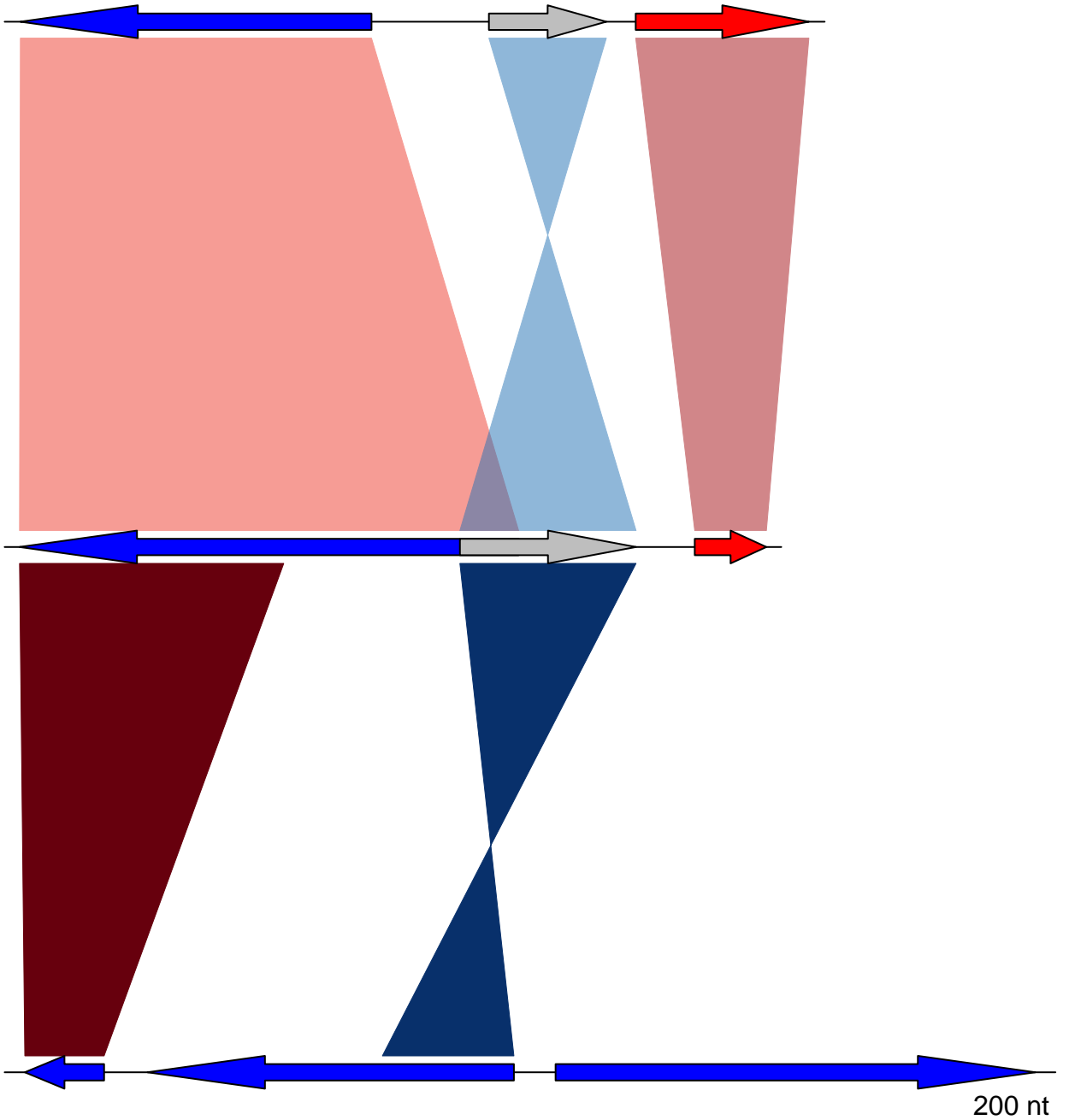
help("apply_color_scheme")



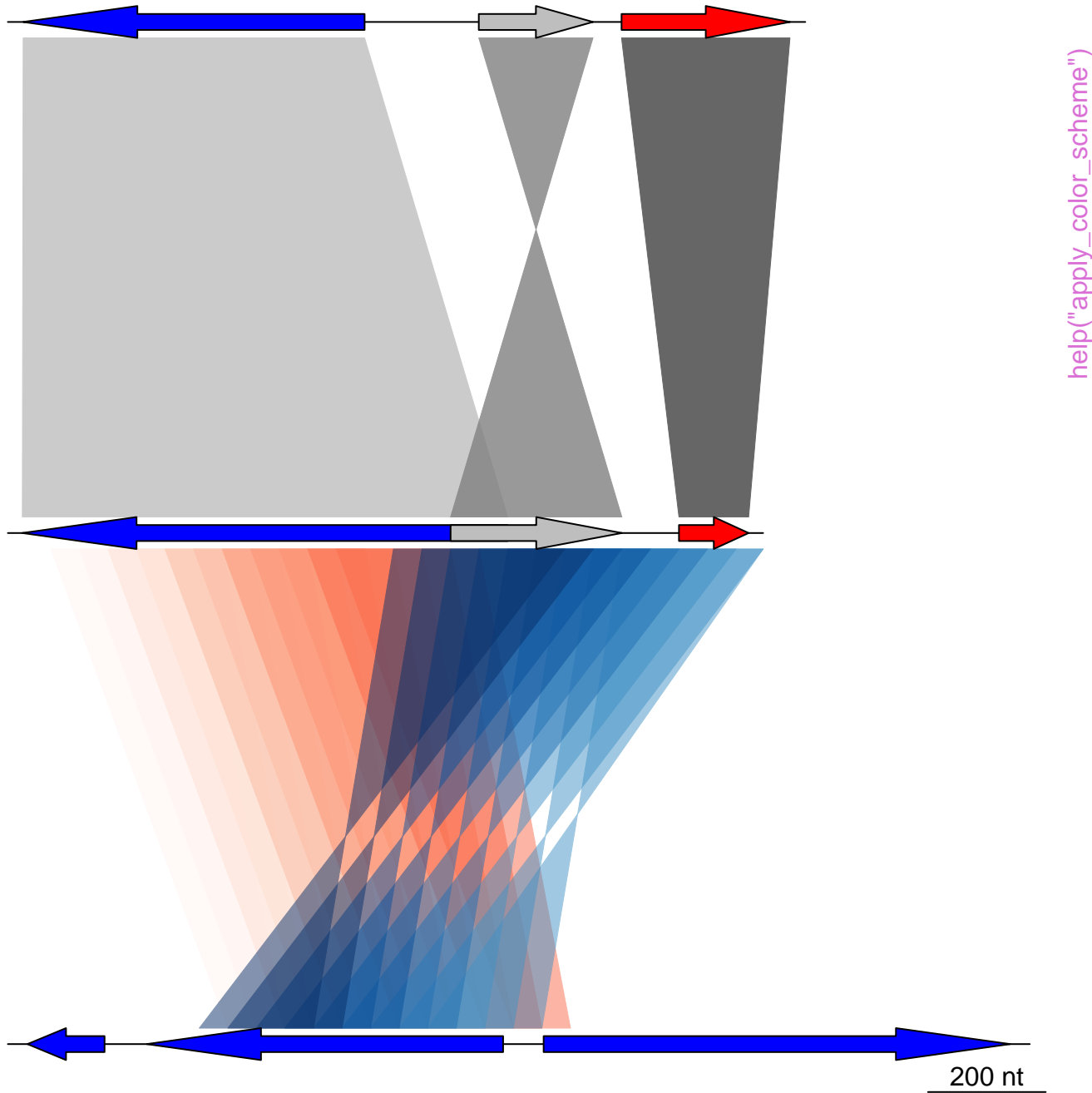
help("apply_color_scheme")

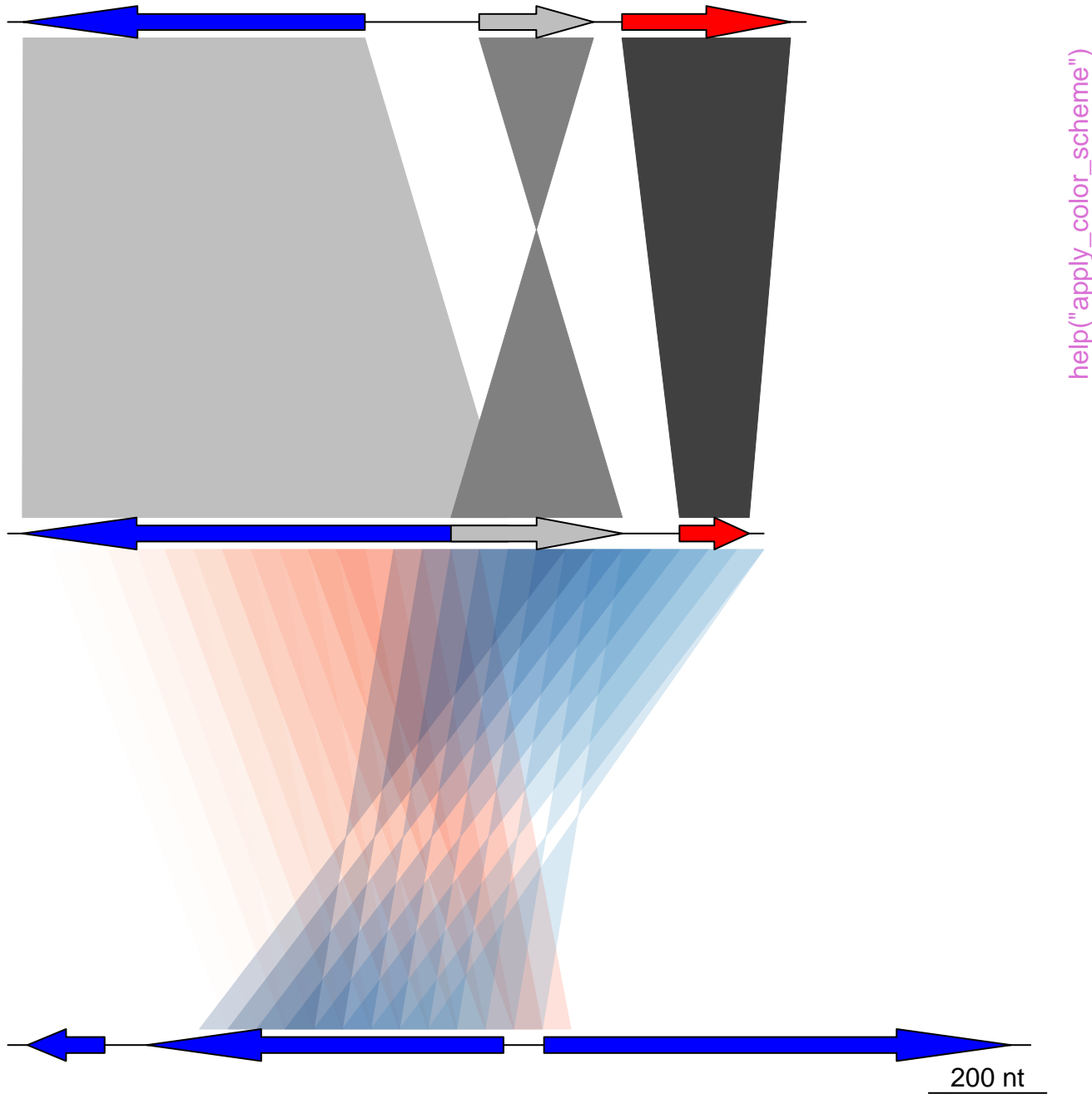


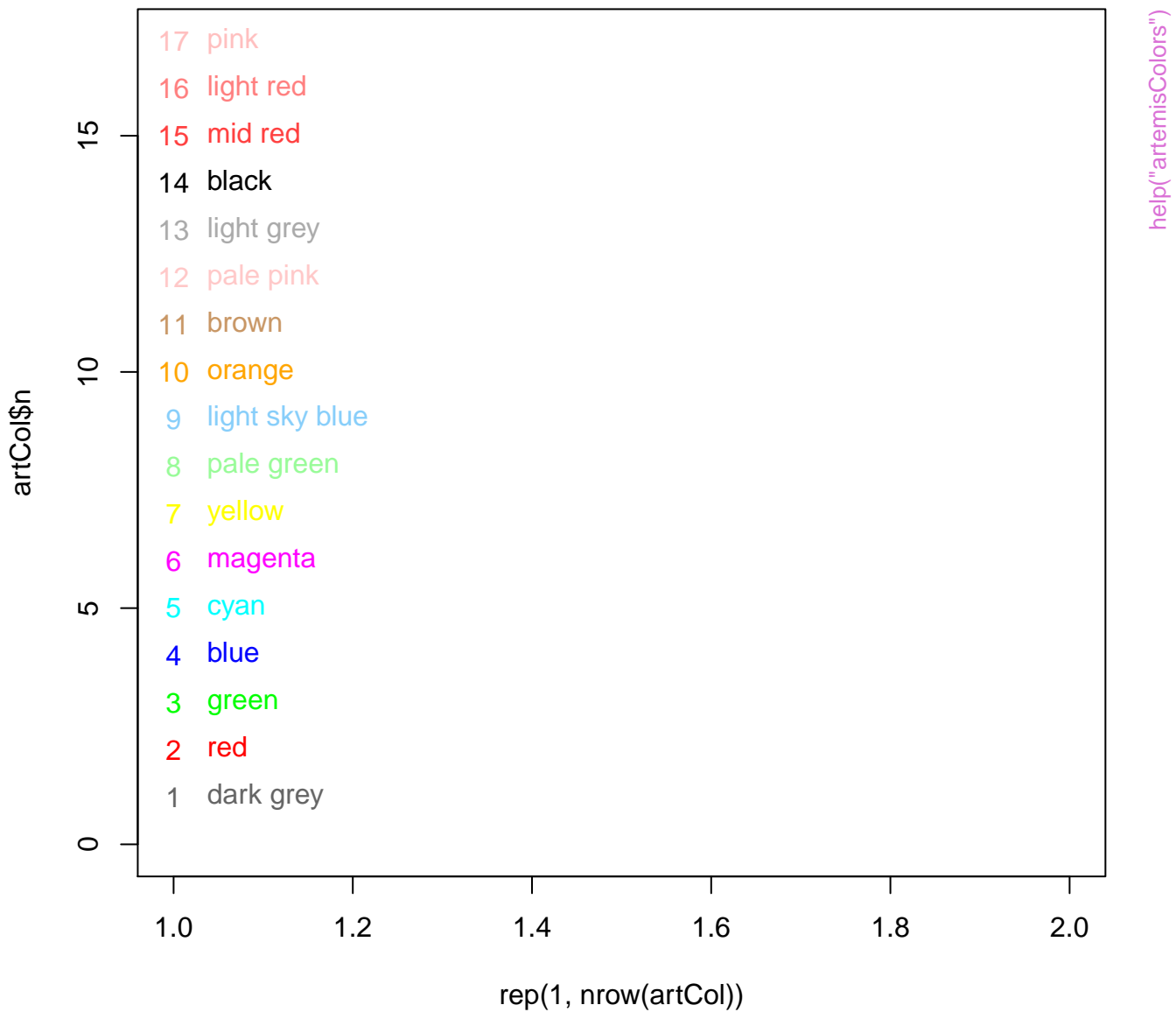
help("apply_color_scheme")

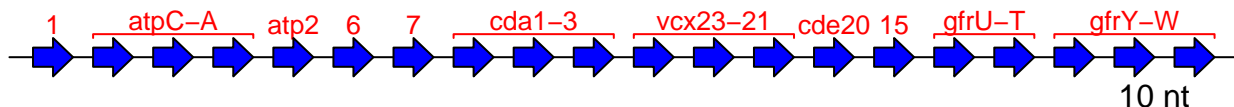
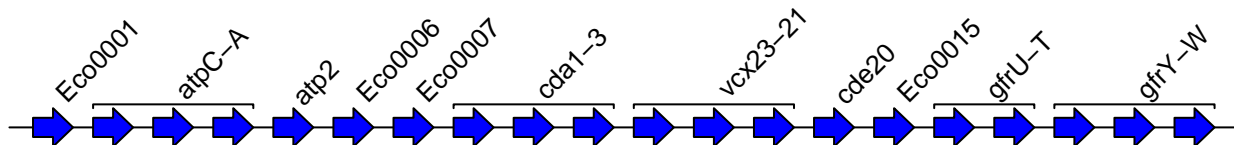
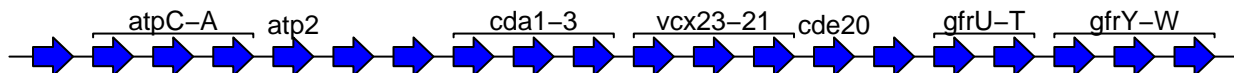
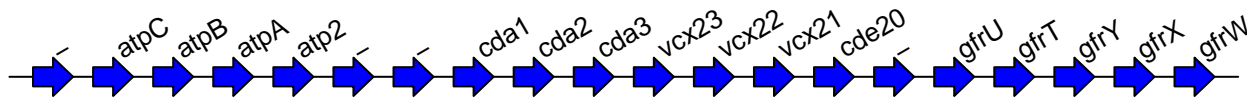


help("apply_color_scheme")









help("auto_annotate")

BB

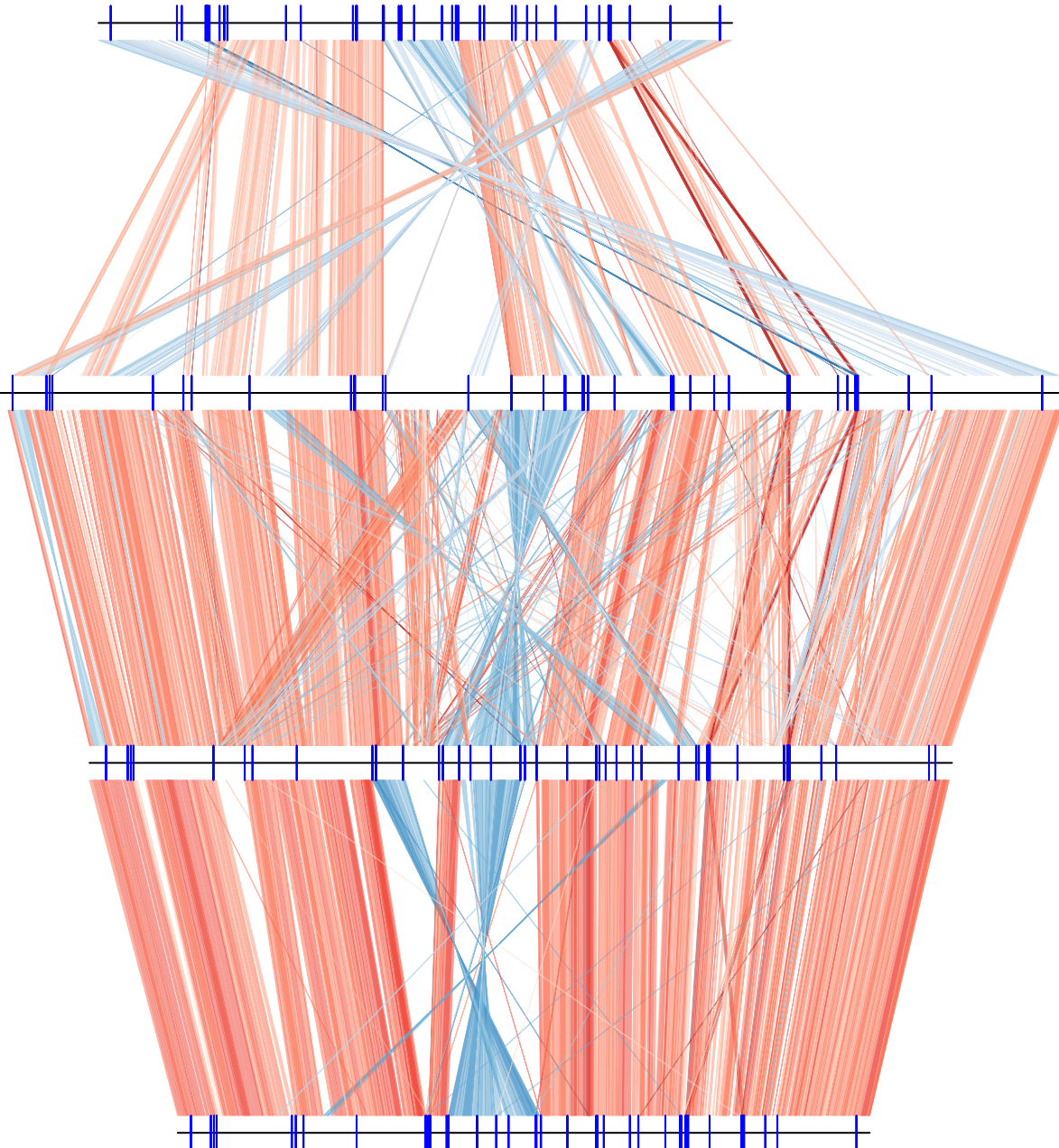
BG

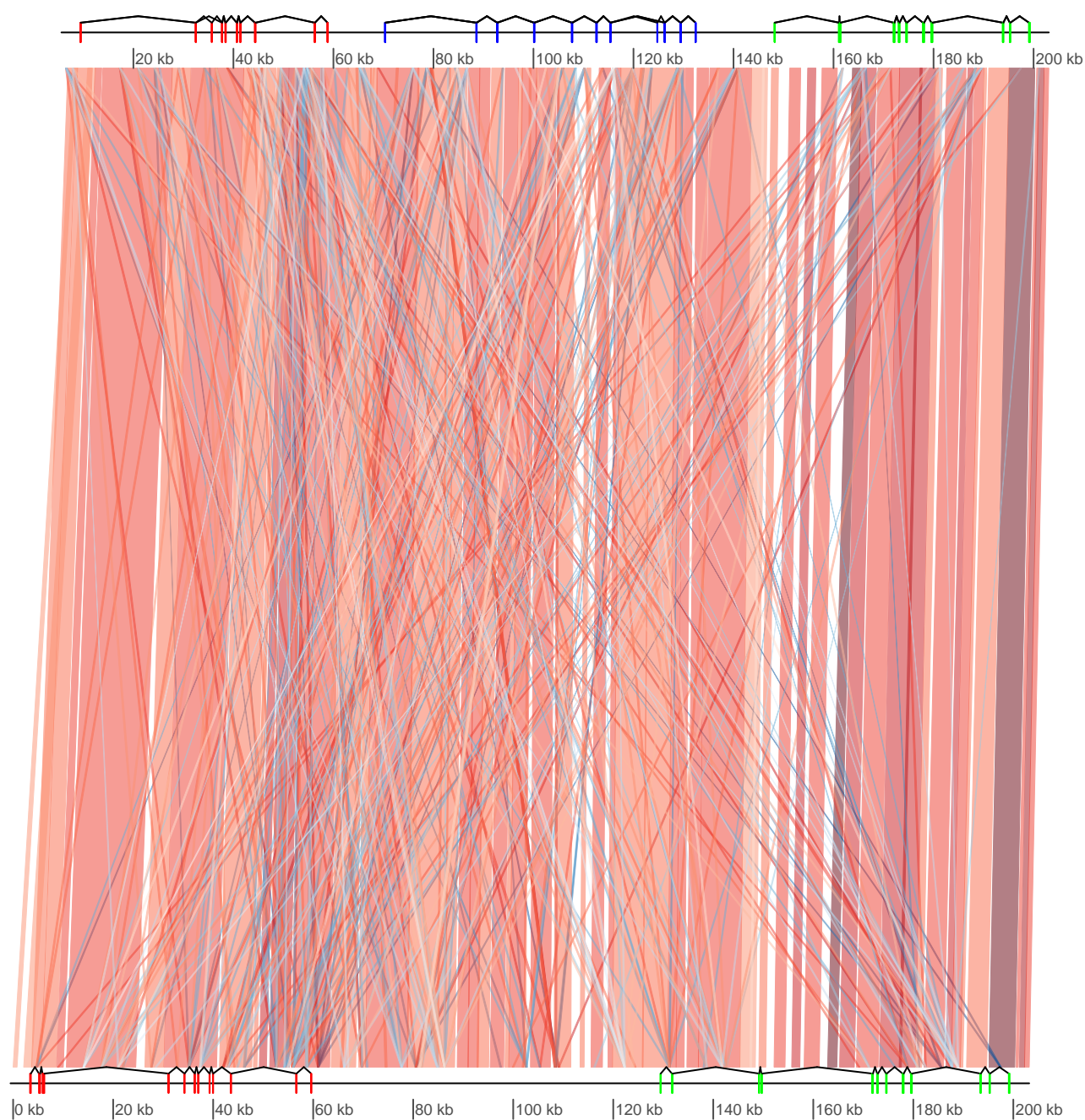
BH

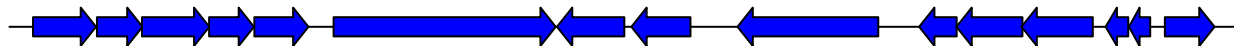
BQ

help("barto")

500 kb

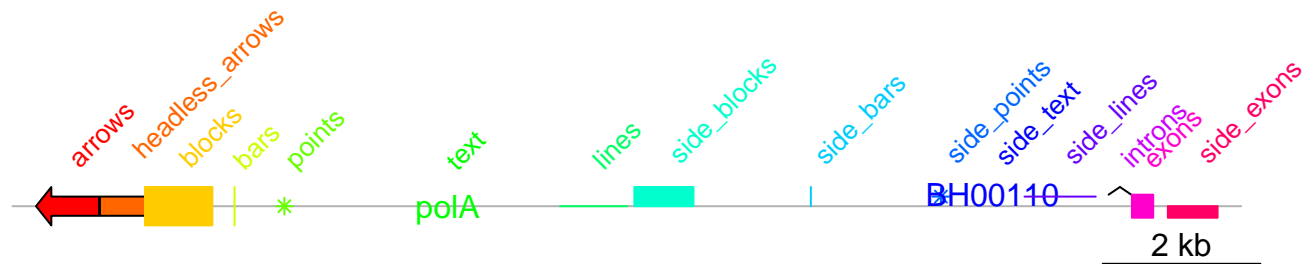
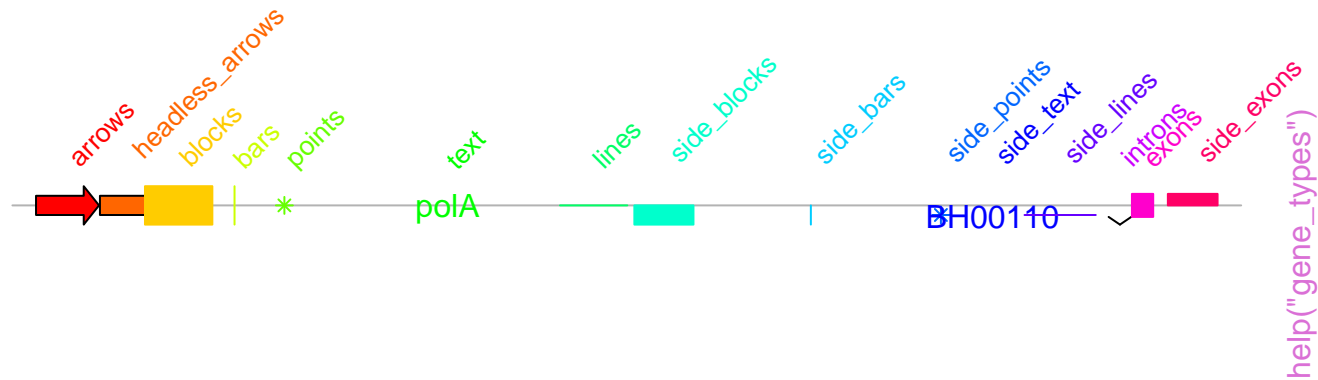


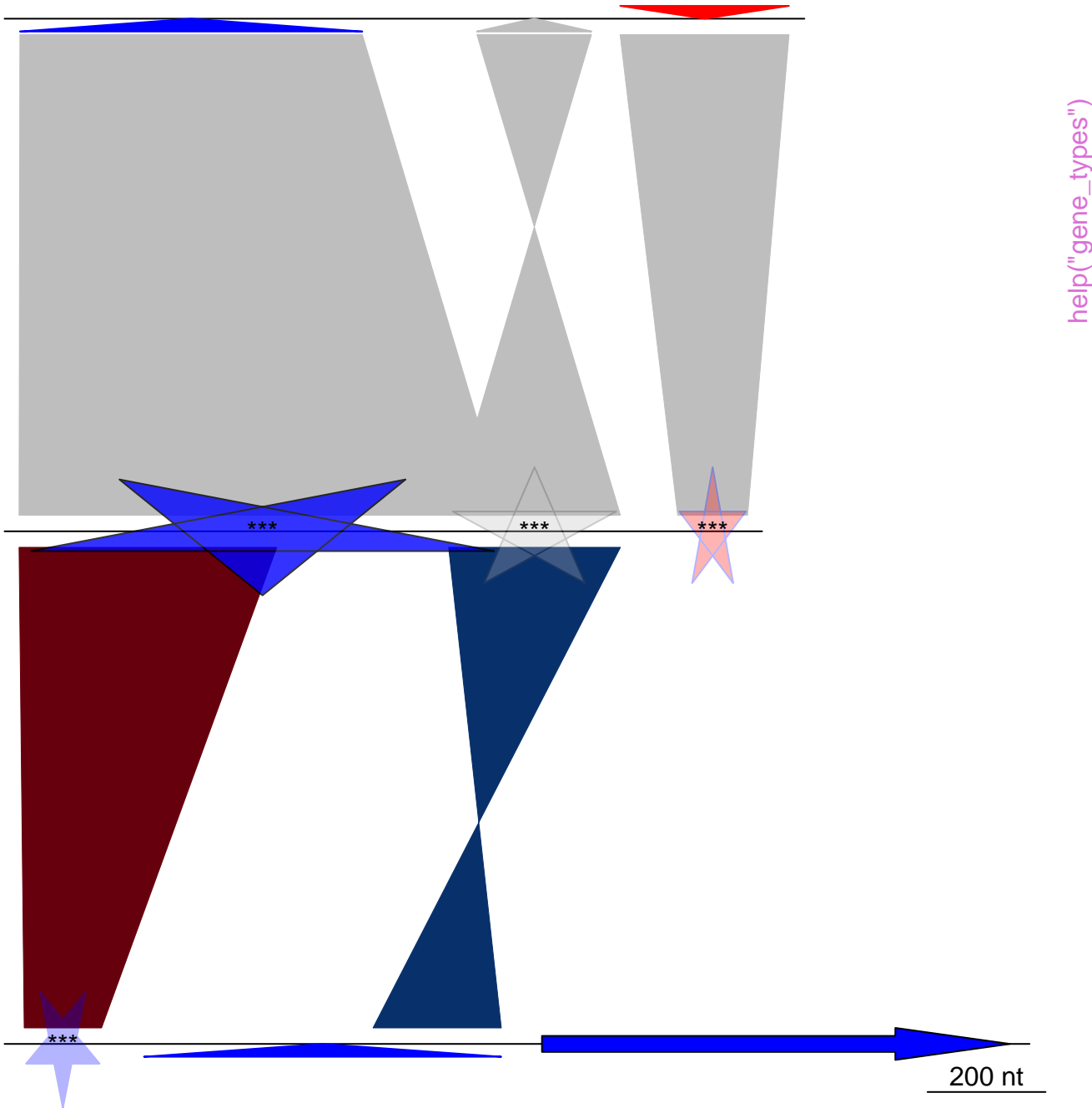


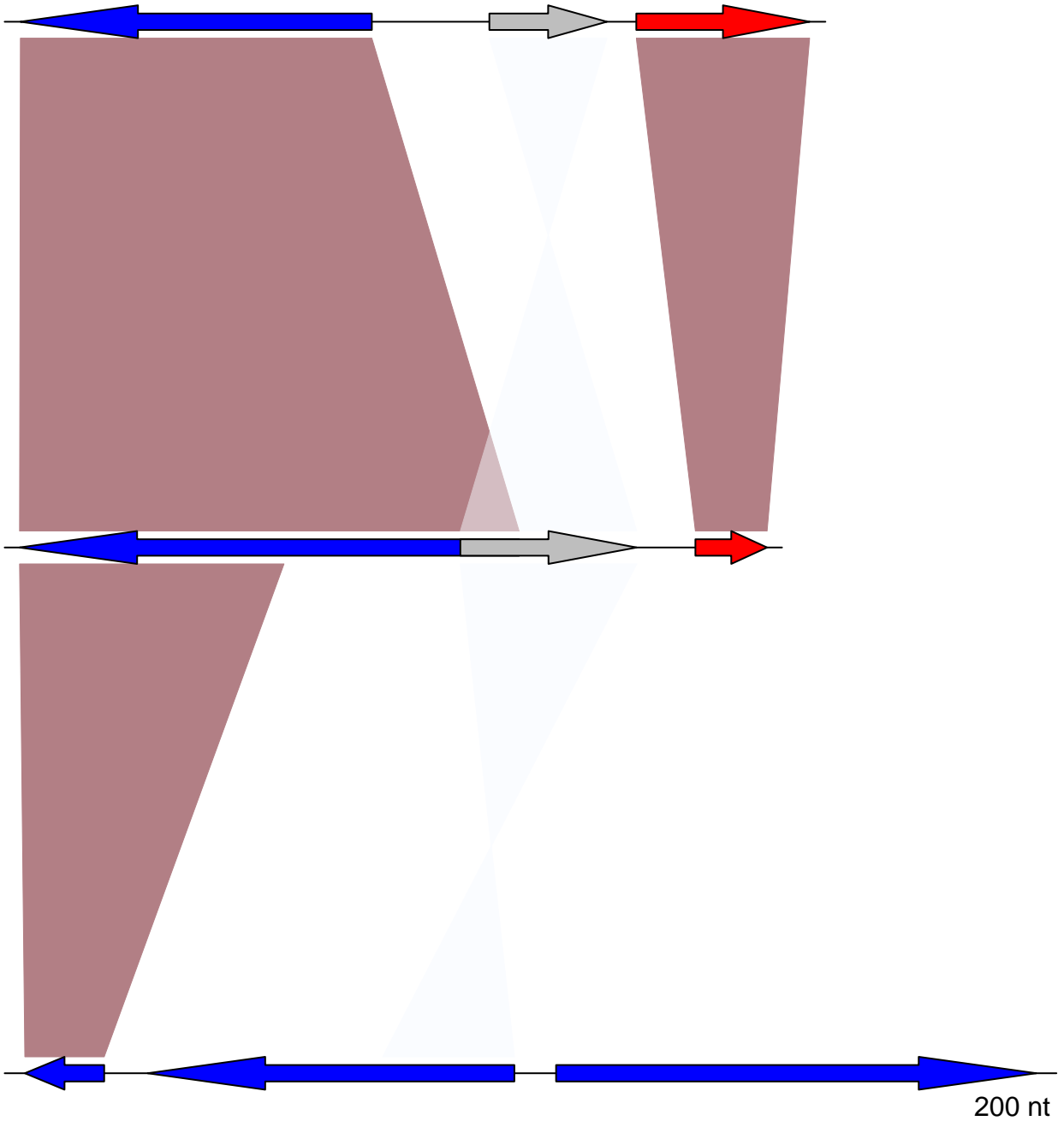


2 kb

help("gene_types")







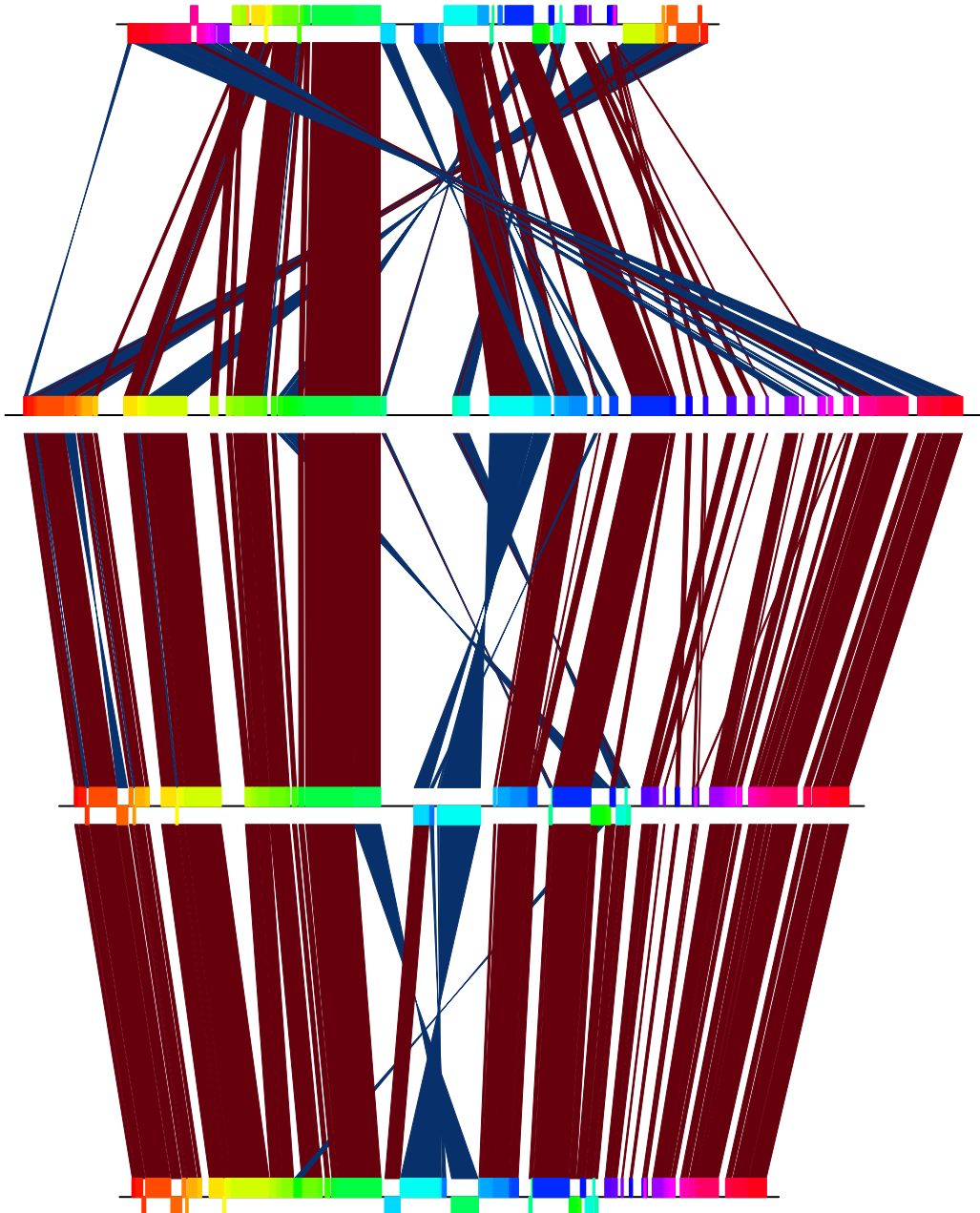
help("genoPlotR-package")

B_bacilliformis

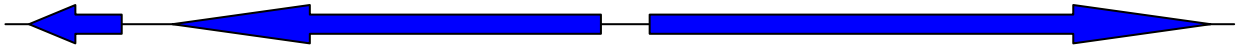
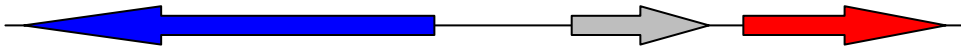
B_grahamii

B_henselae

B_quintana

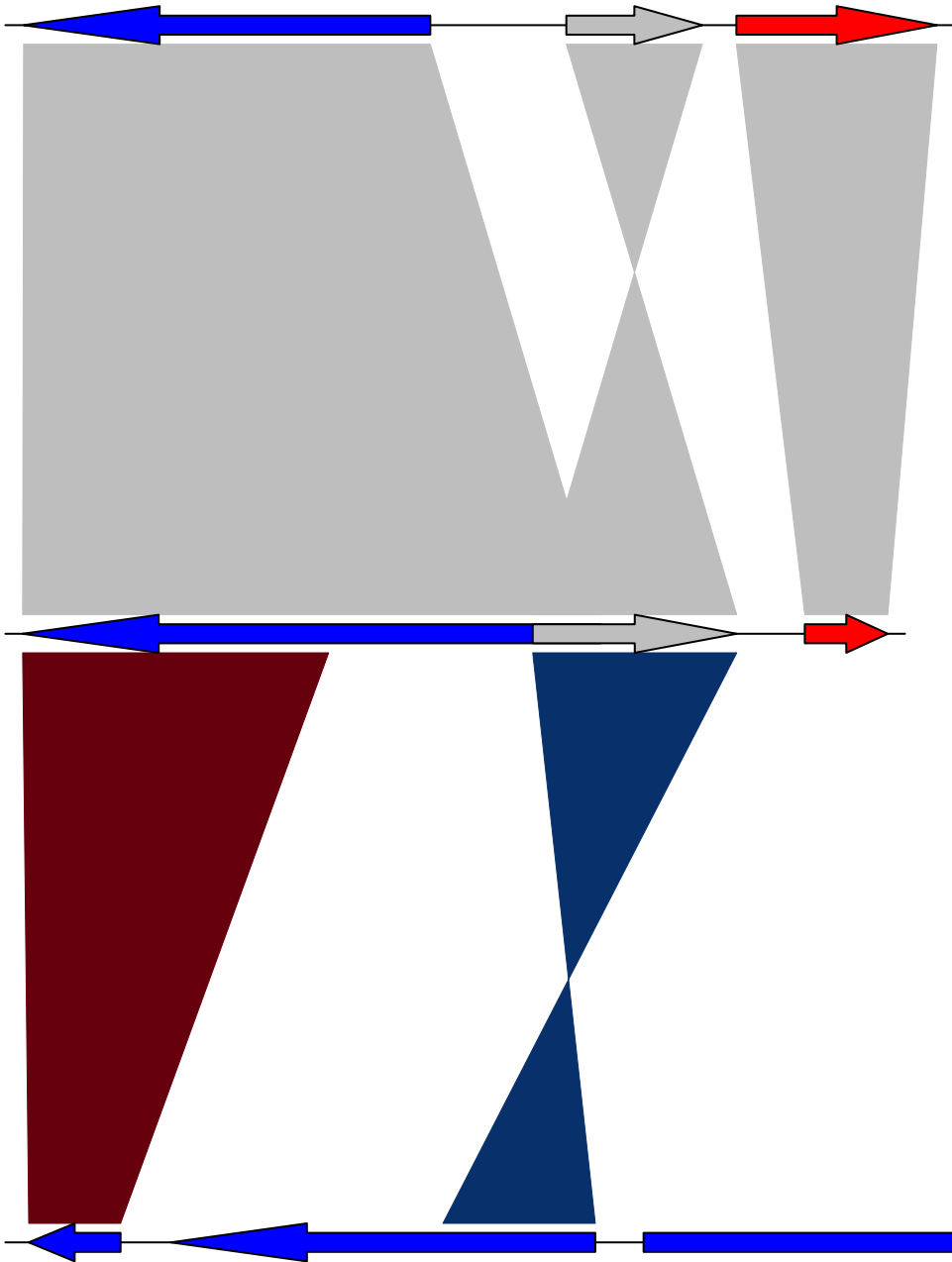


help("mauve.bbone")



200 nt

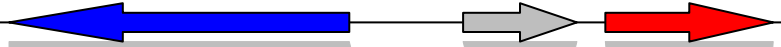
help("plot_gene_map")



help("plot_gene_map")

200 nt

A aaa



B bbb

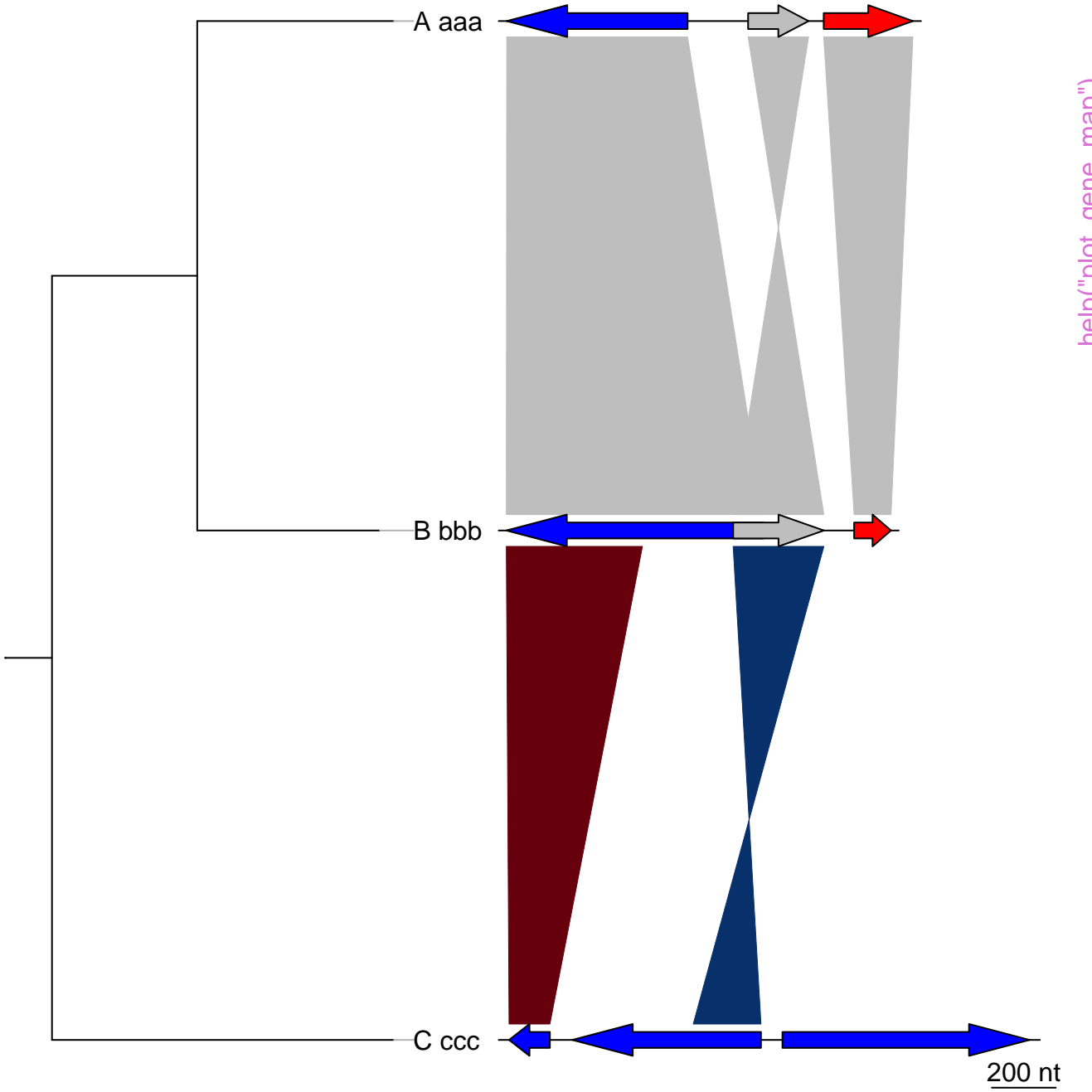


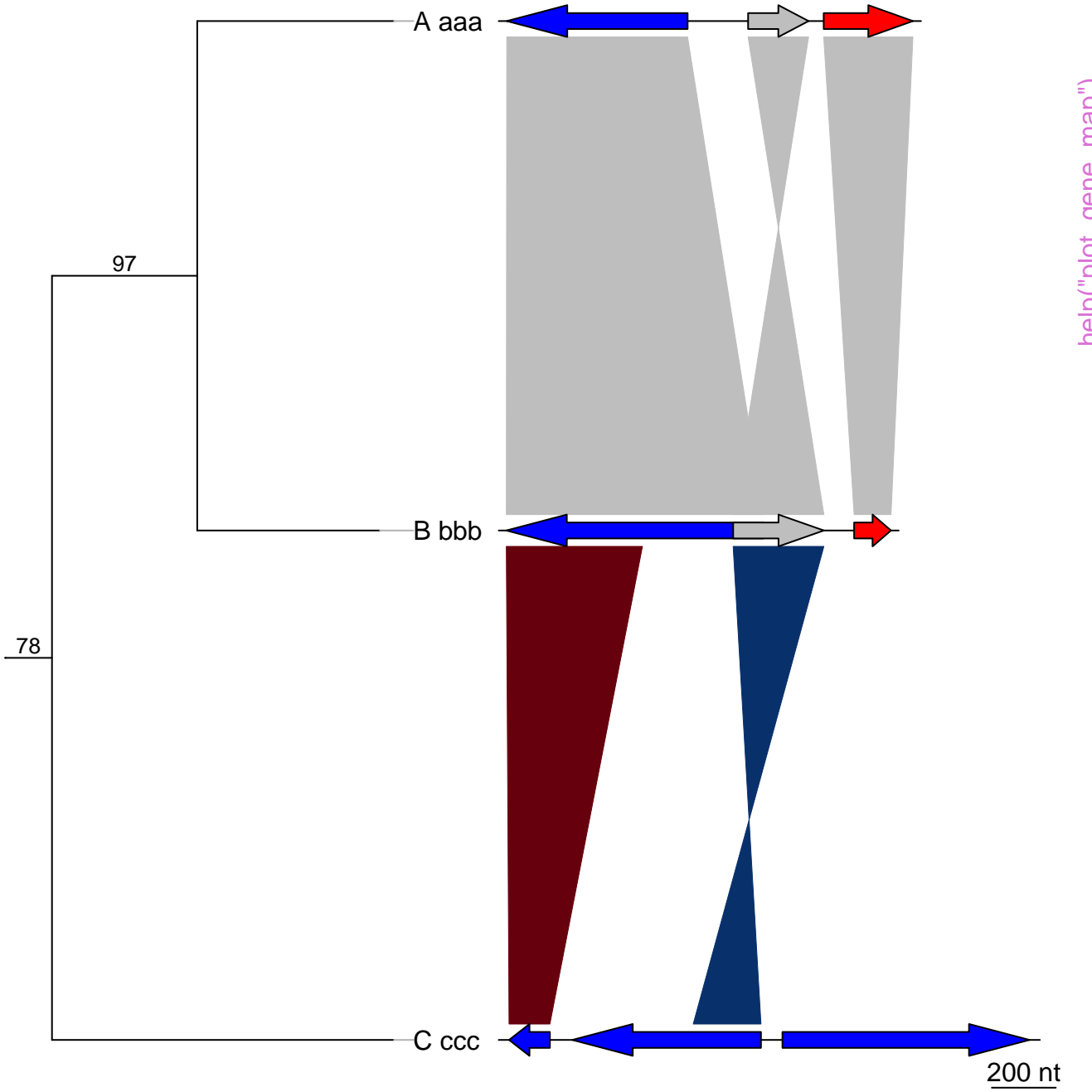
C ccc

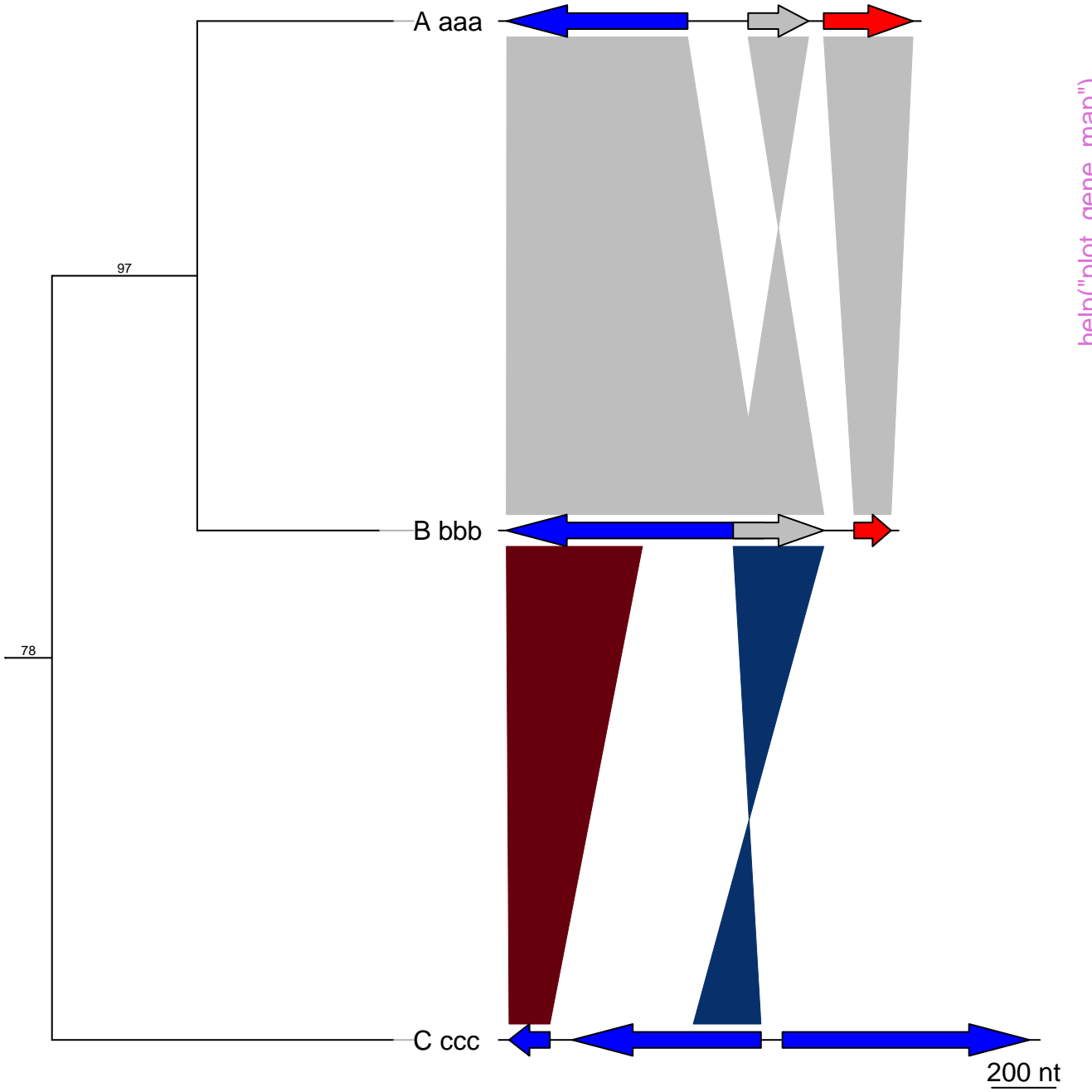


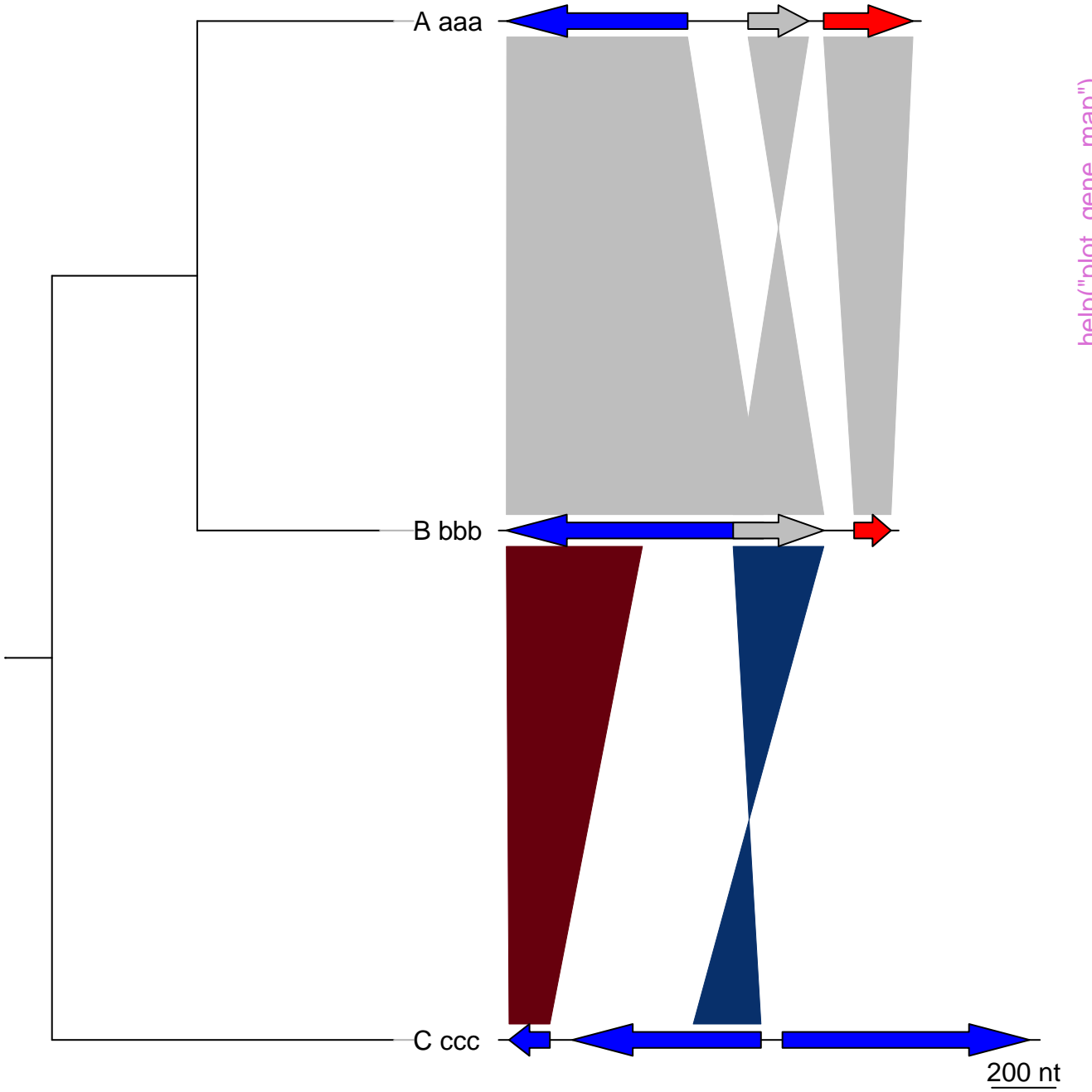
200 nt

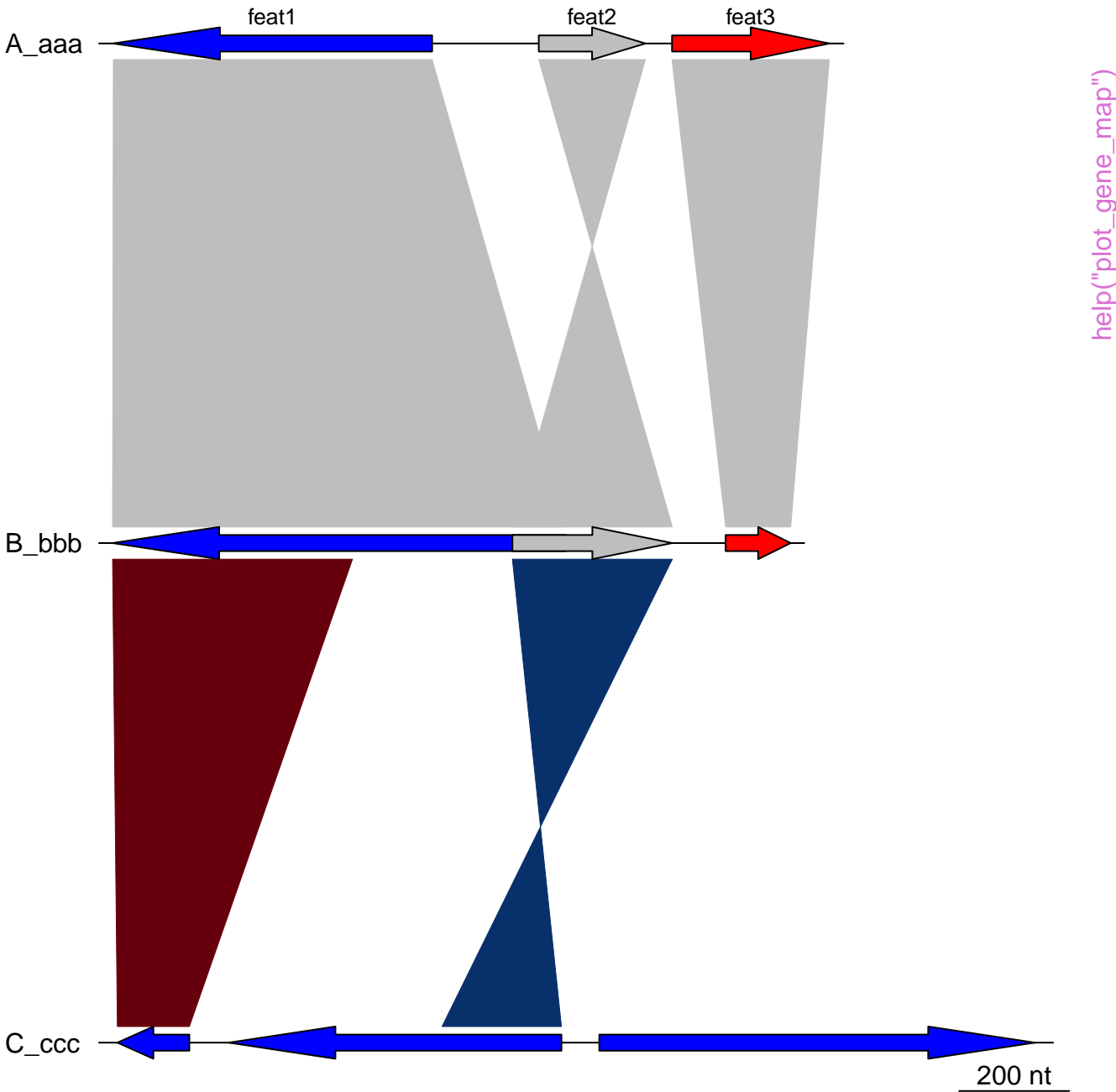
help("plot_gene_map")

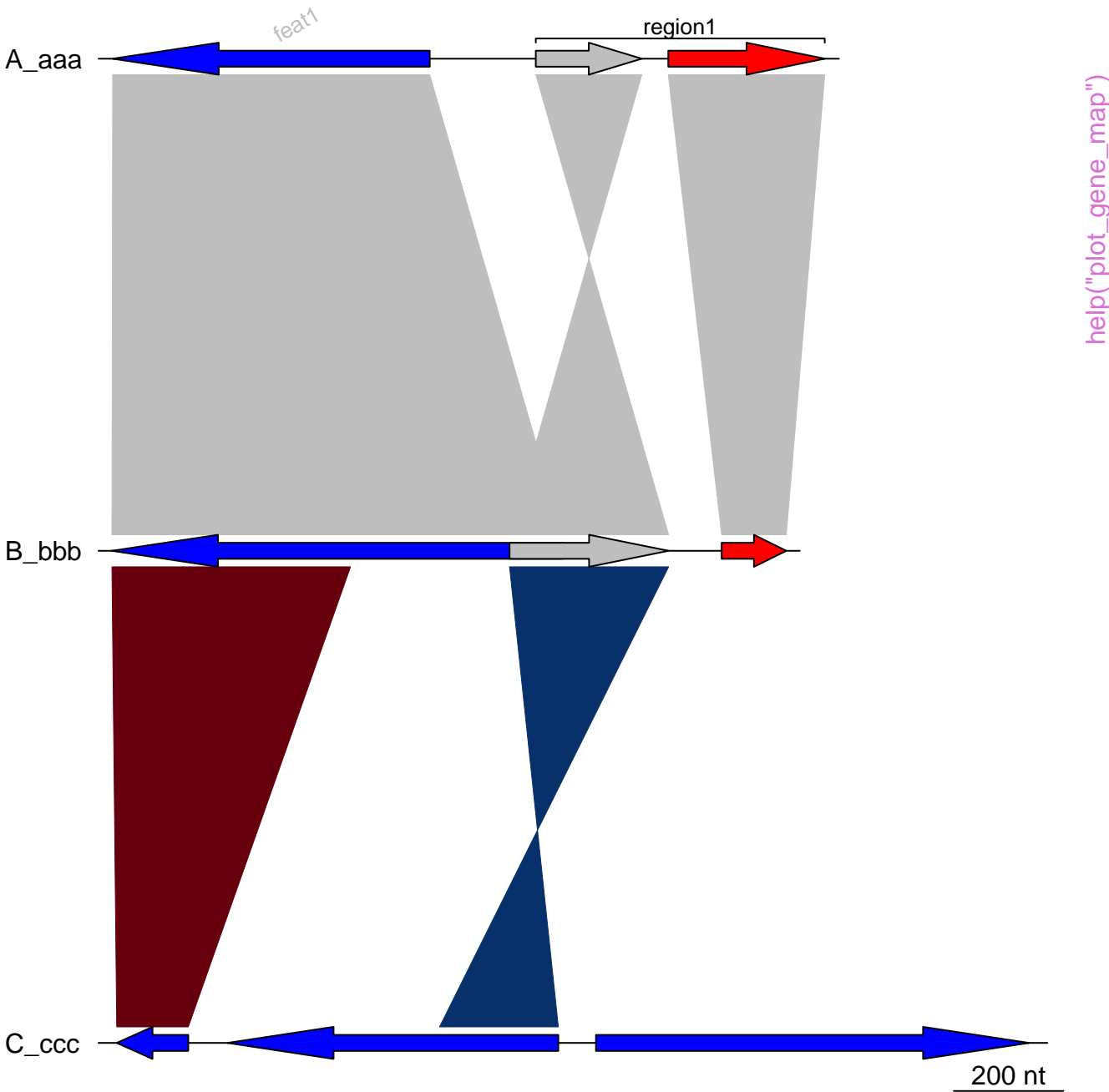




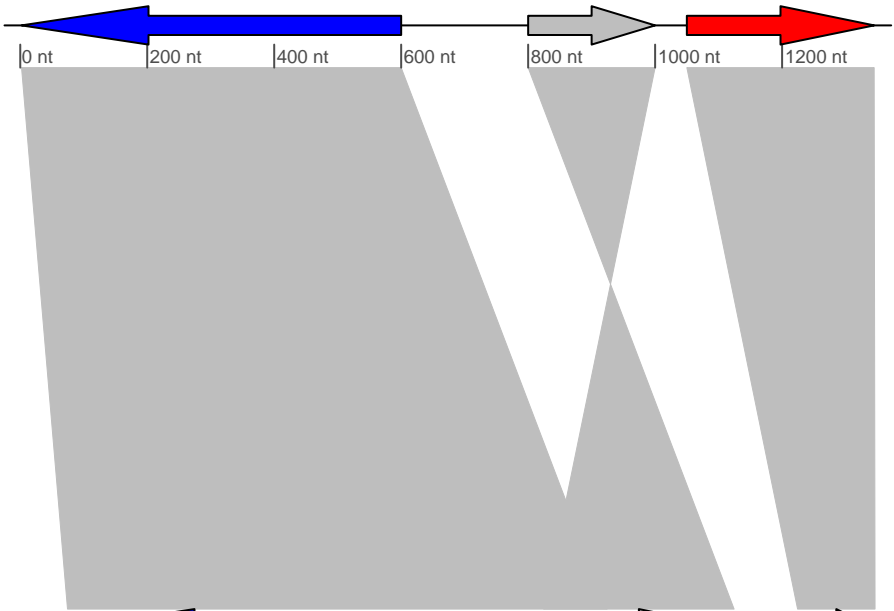






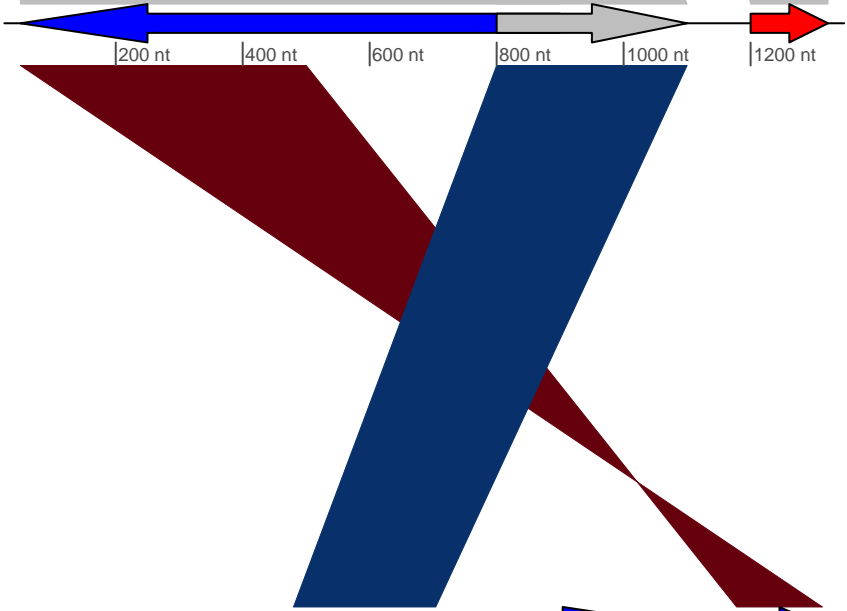


A_aaa

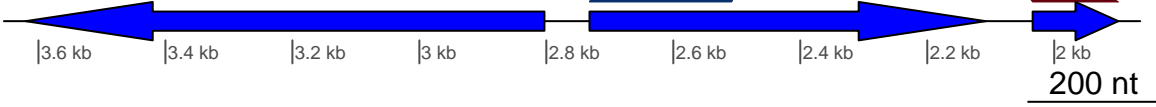


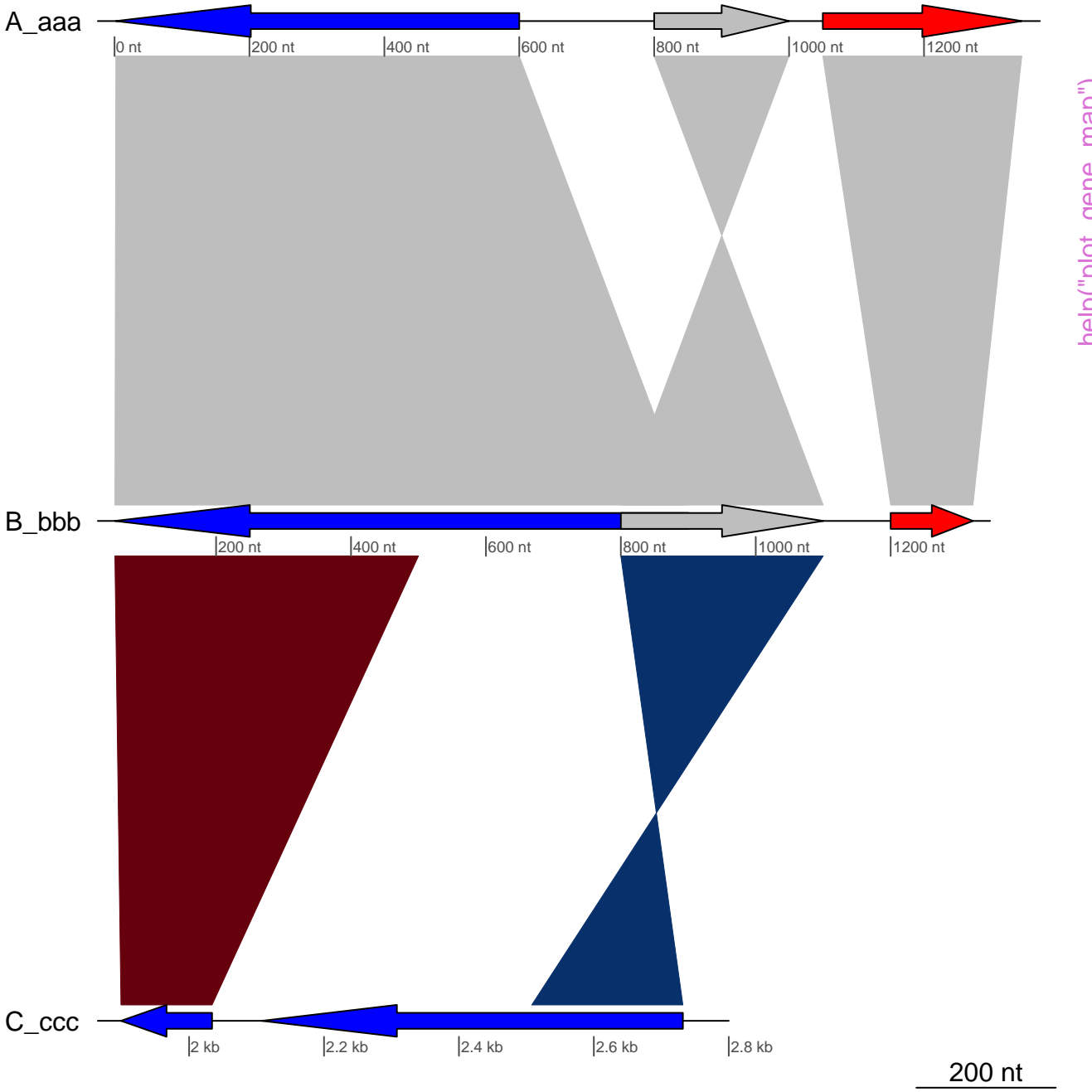
help("plot_gene_map")

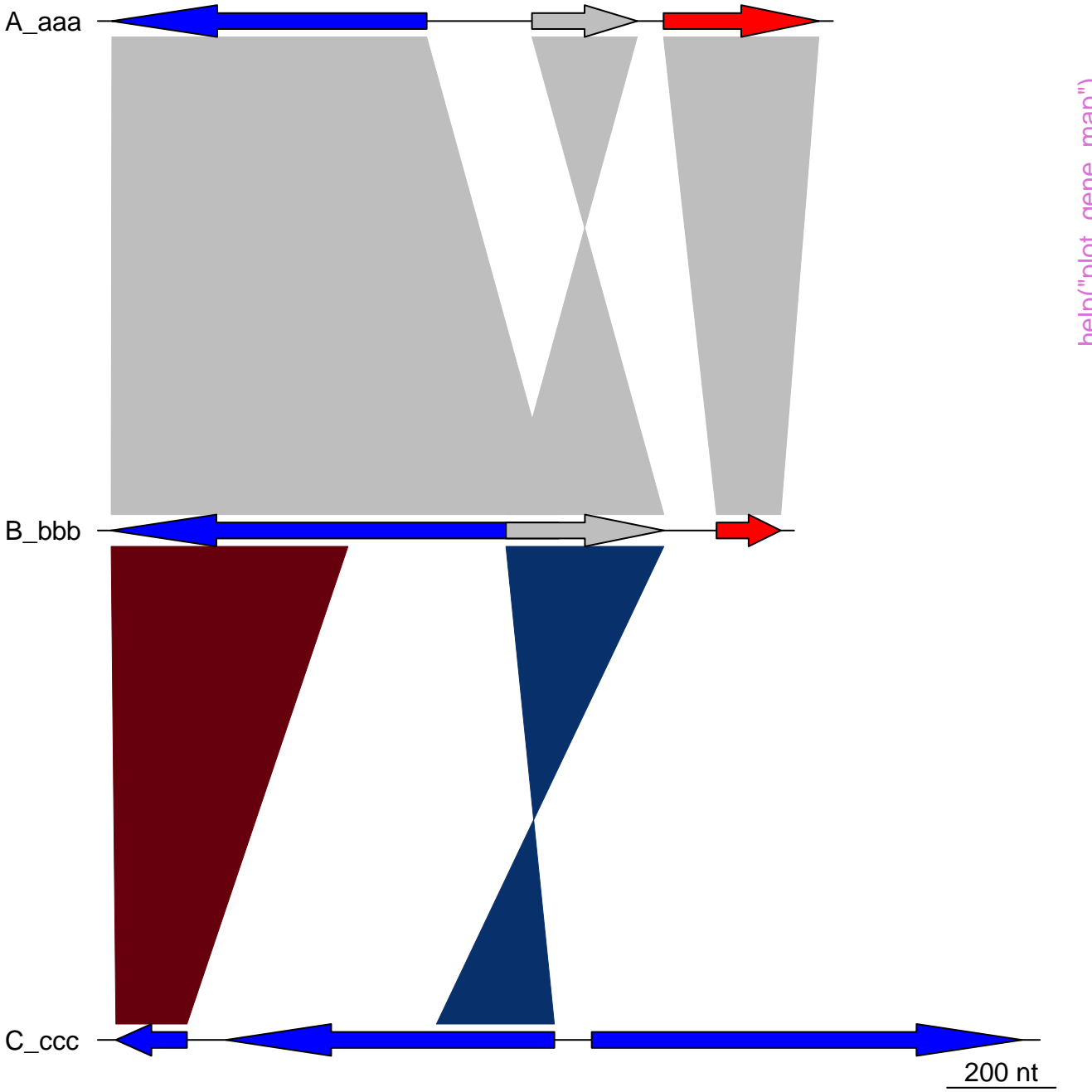
B_bbb



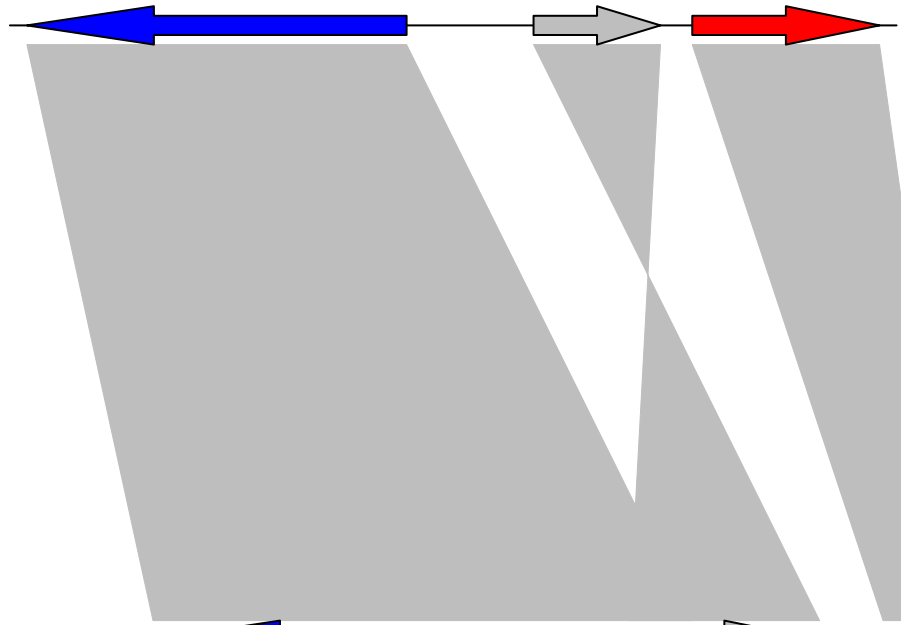
C_ccc



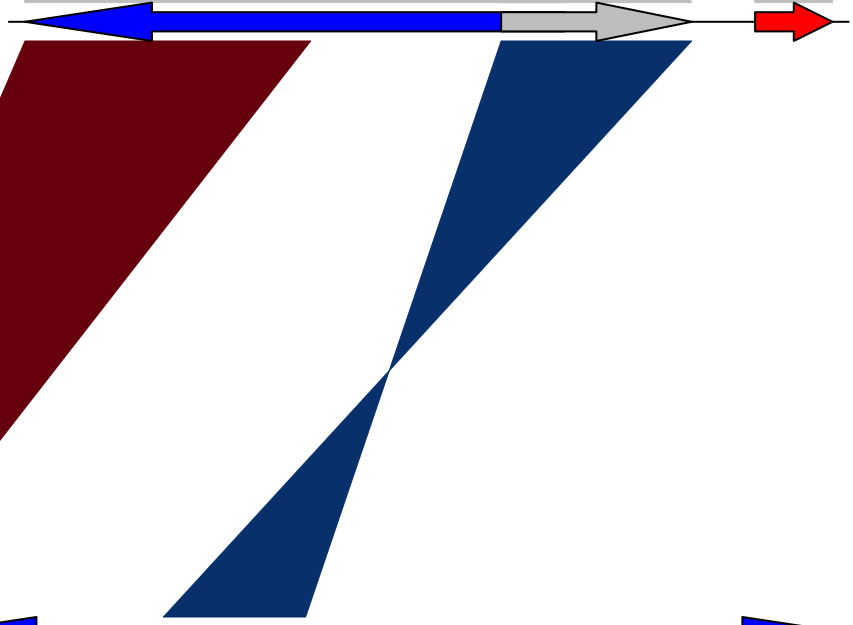




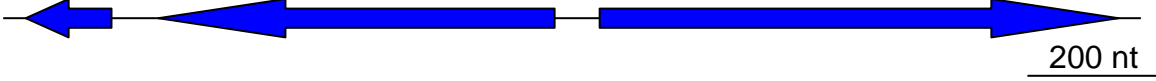
A_aaa



B_bbb



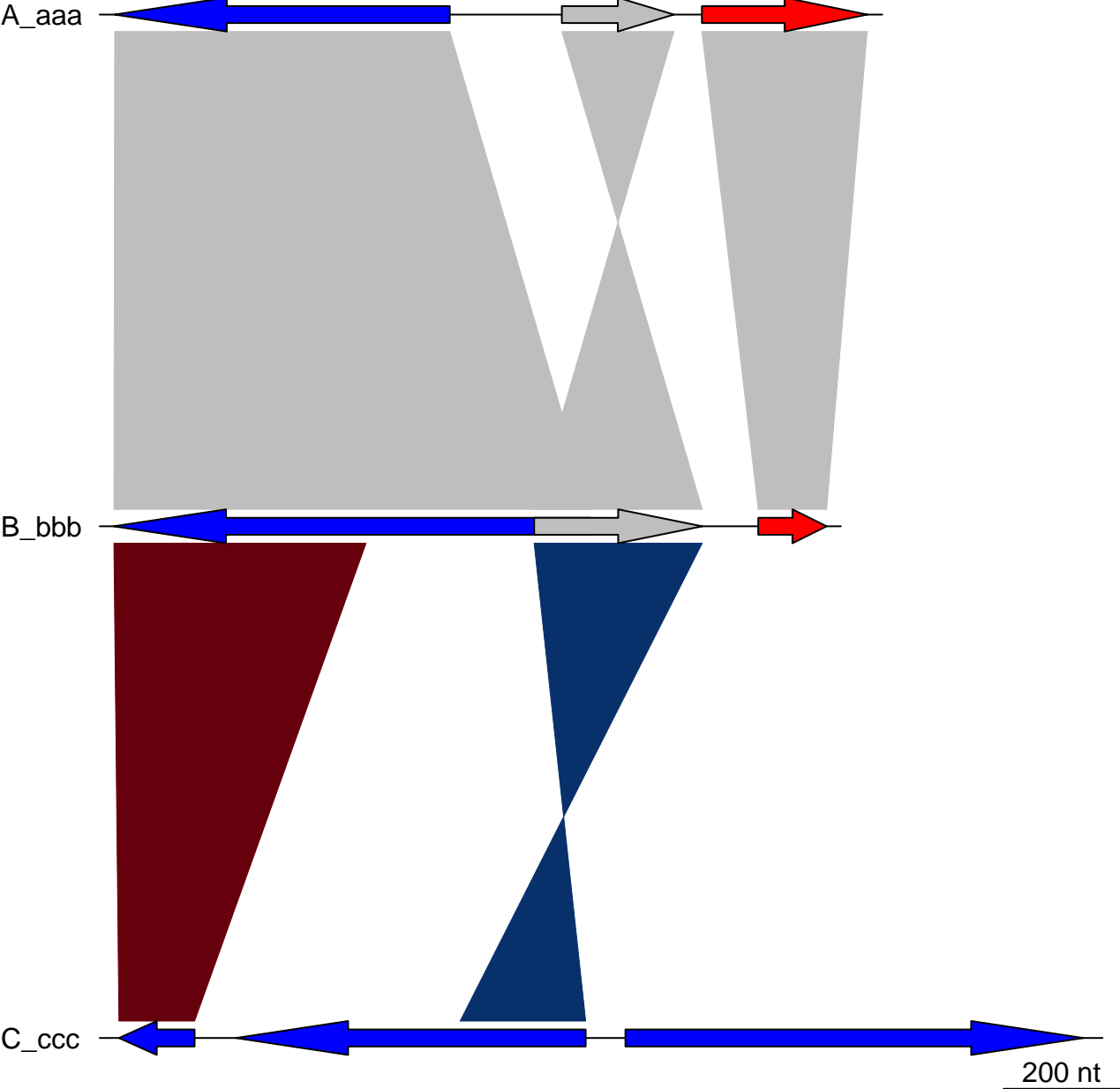
C_ccc



200 nt

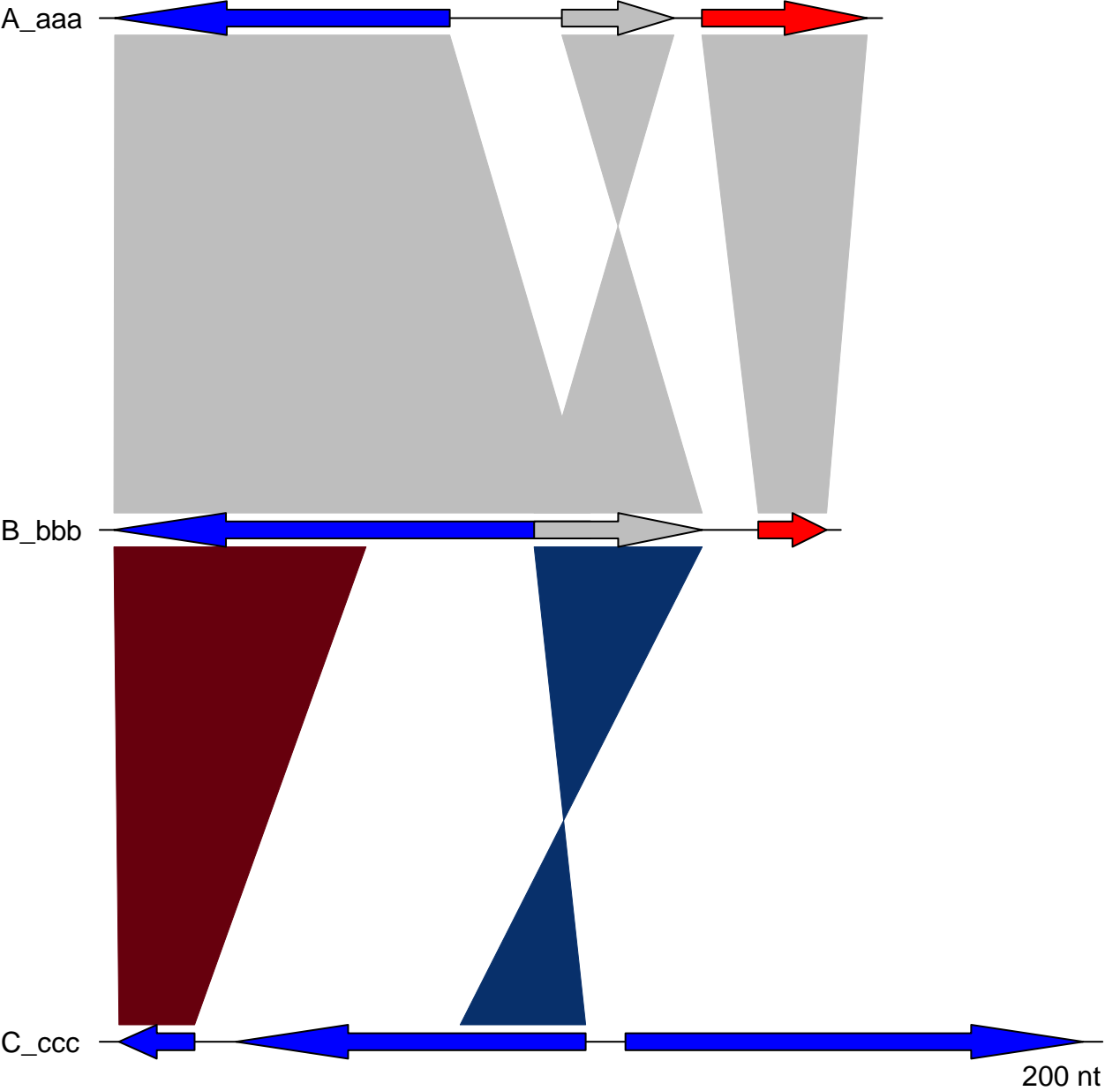
help("plot_gene_map")

Comparison of A, B and C

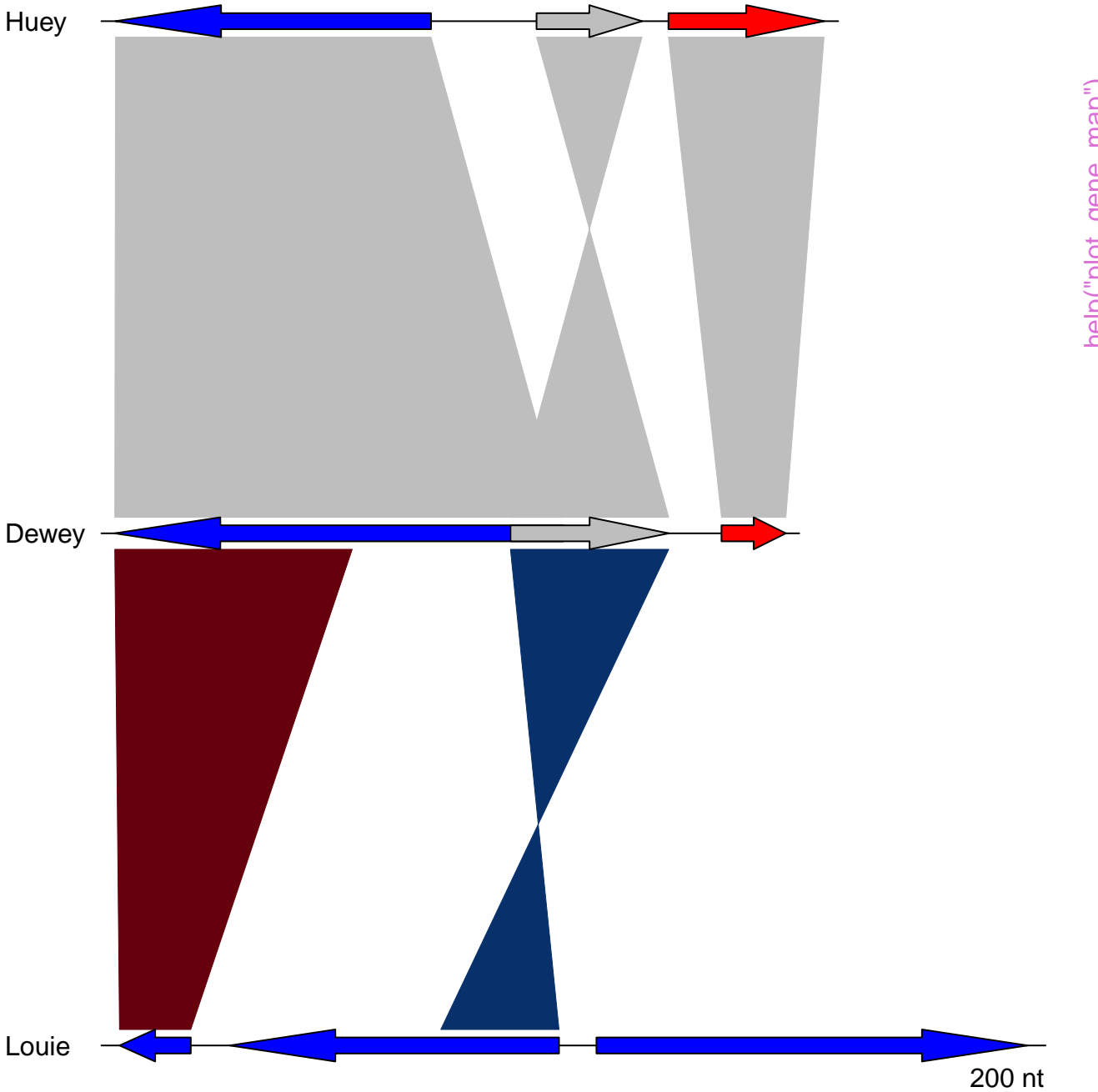


help("plot_gene_map")

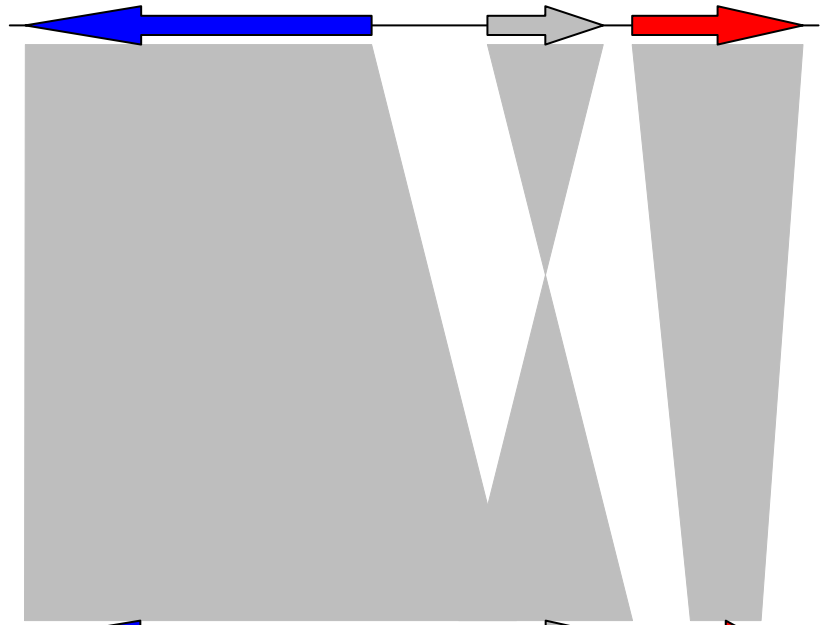
Comparison of A, B and C



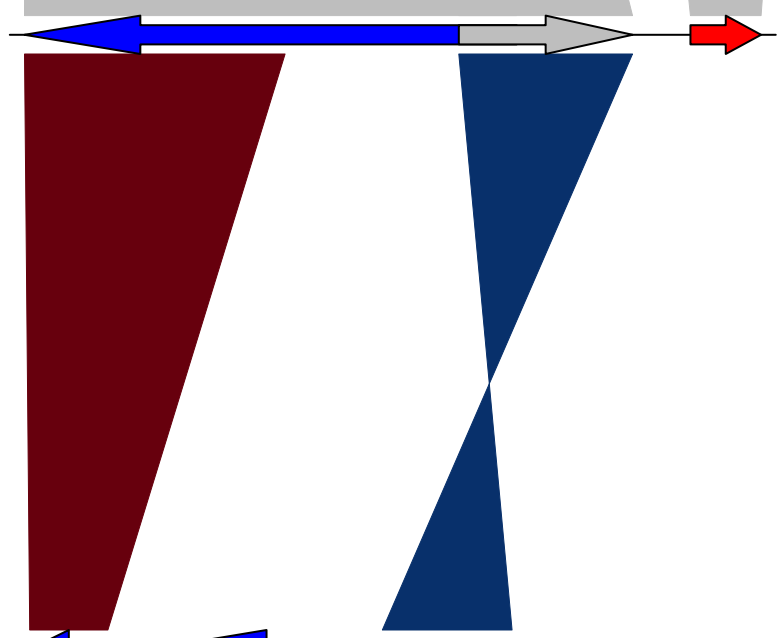
help("plot_gene_map")



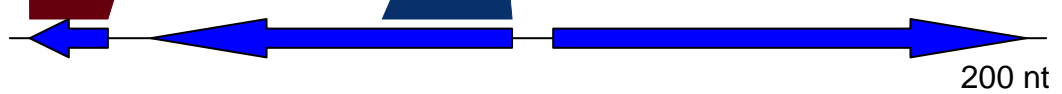
Huey



Dewey

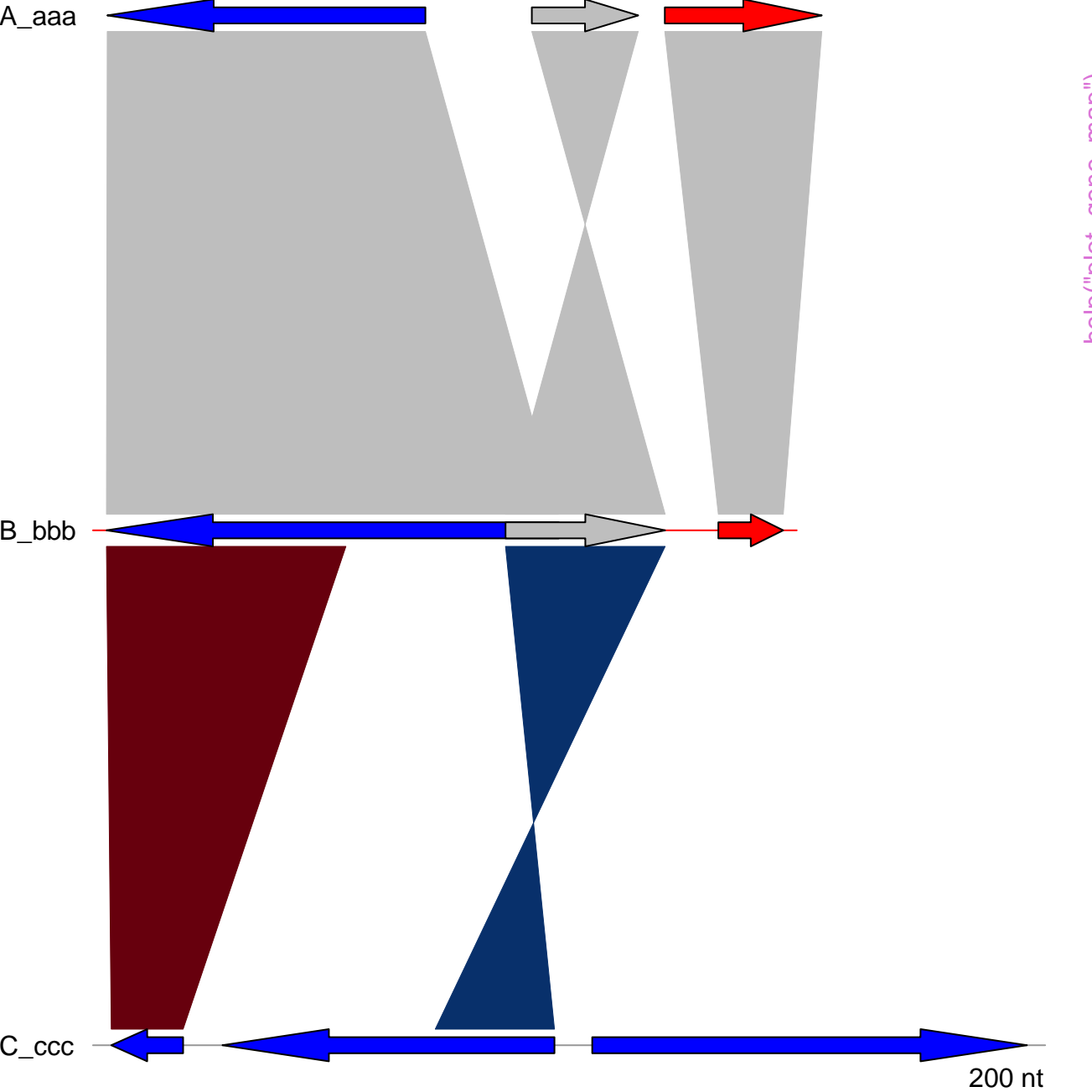


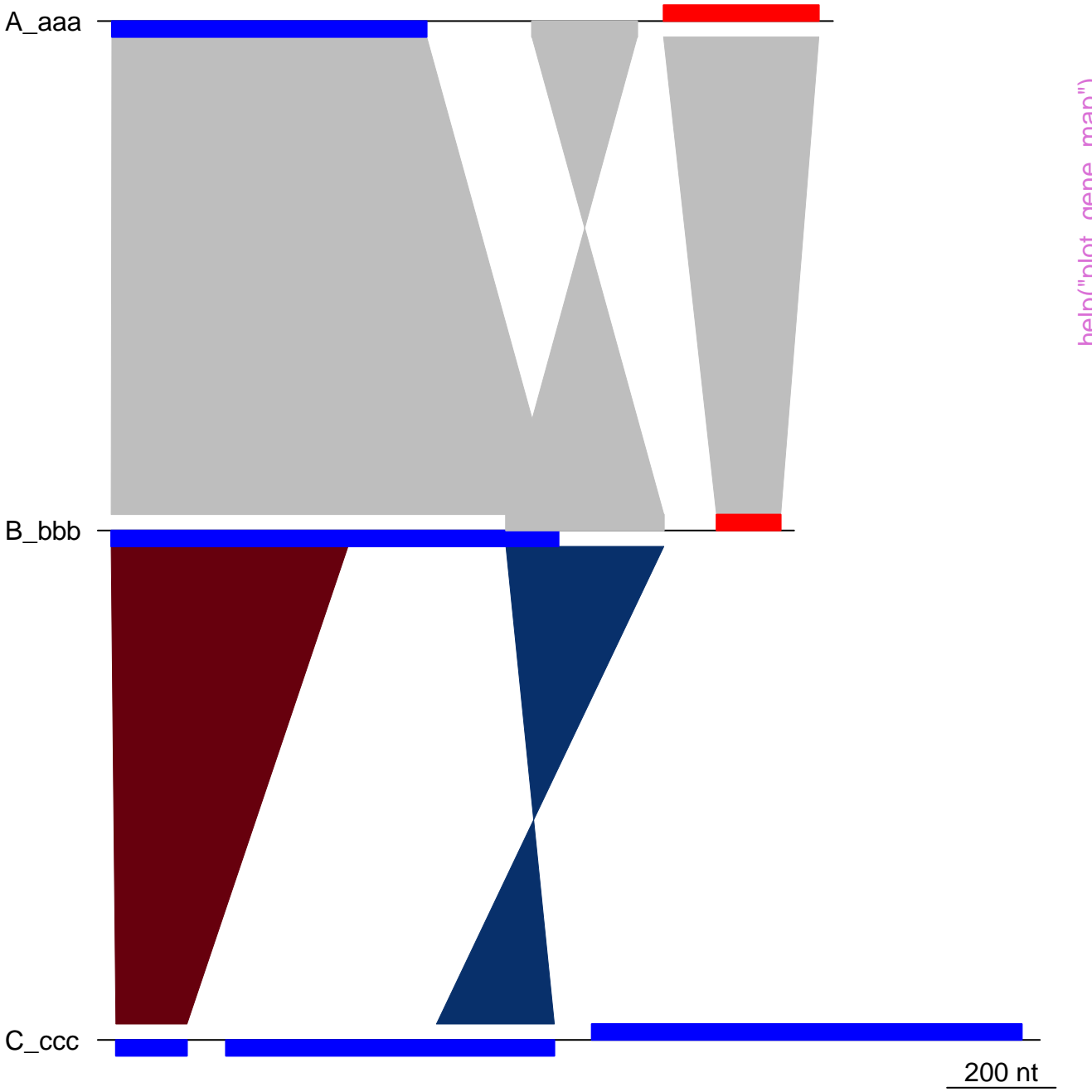
Louie



200 nt

help("plot_gene_map")





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

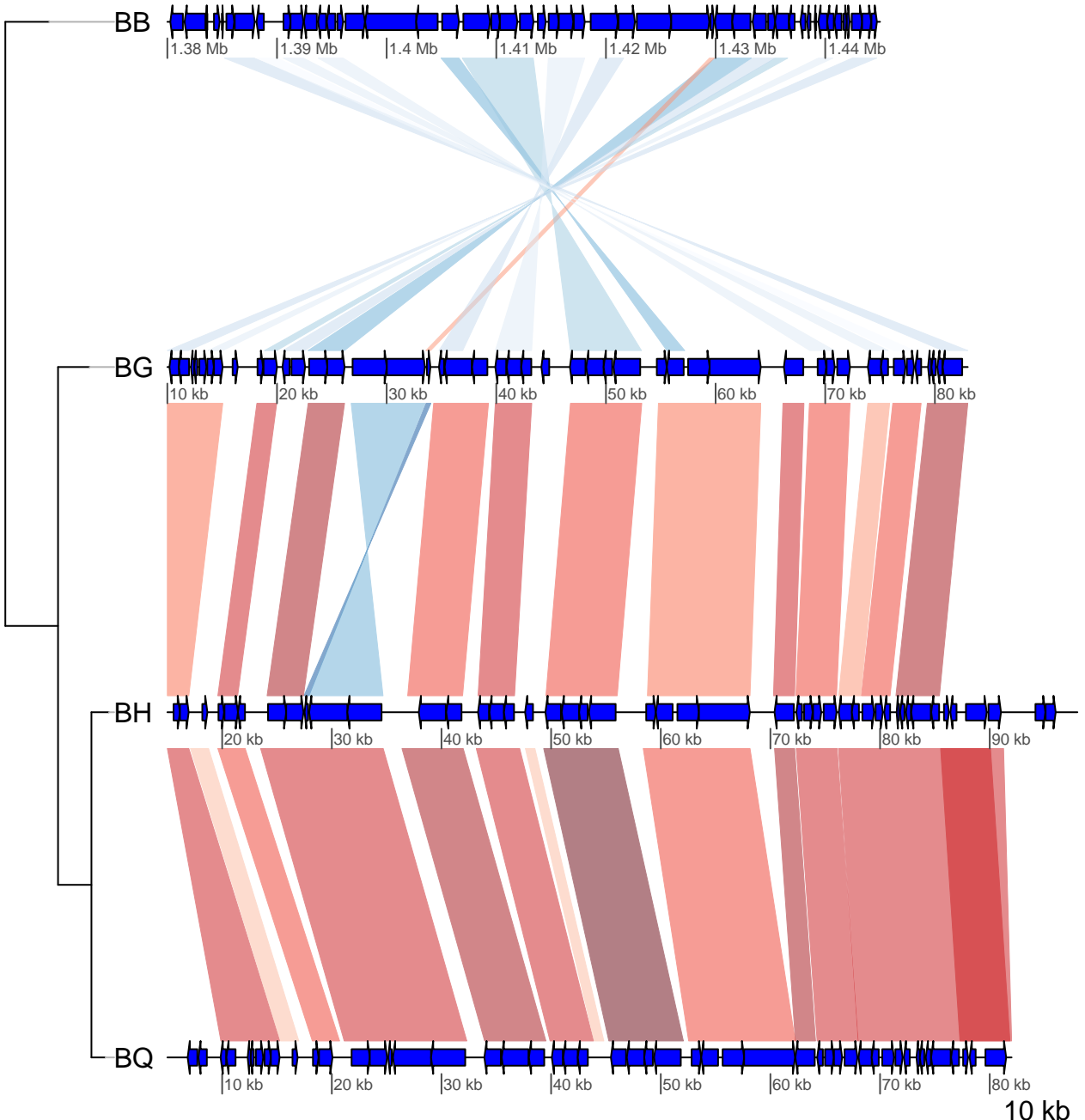
BG 10 kb 20 kb 30 kb 40 kb 50 kb 60 kb 70 kb 80 kb

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

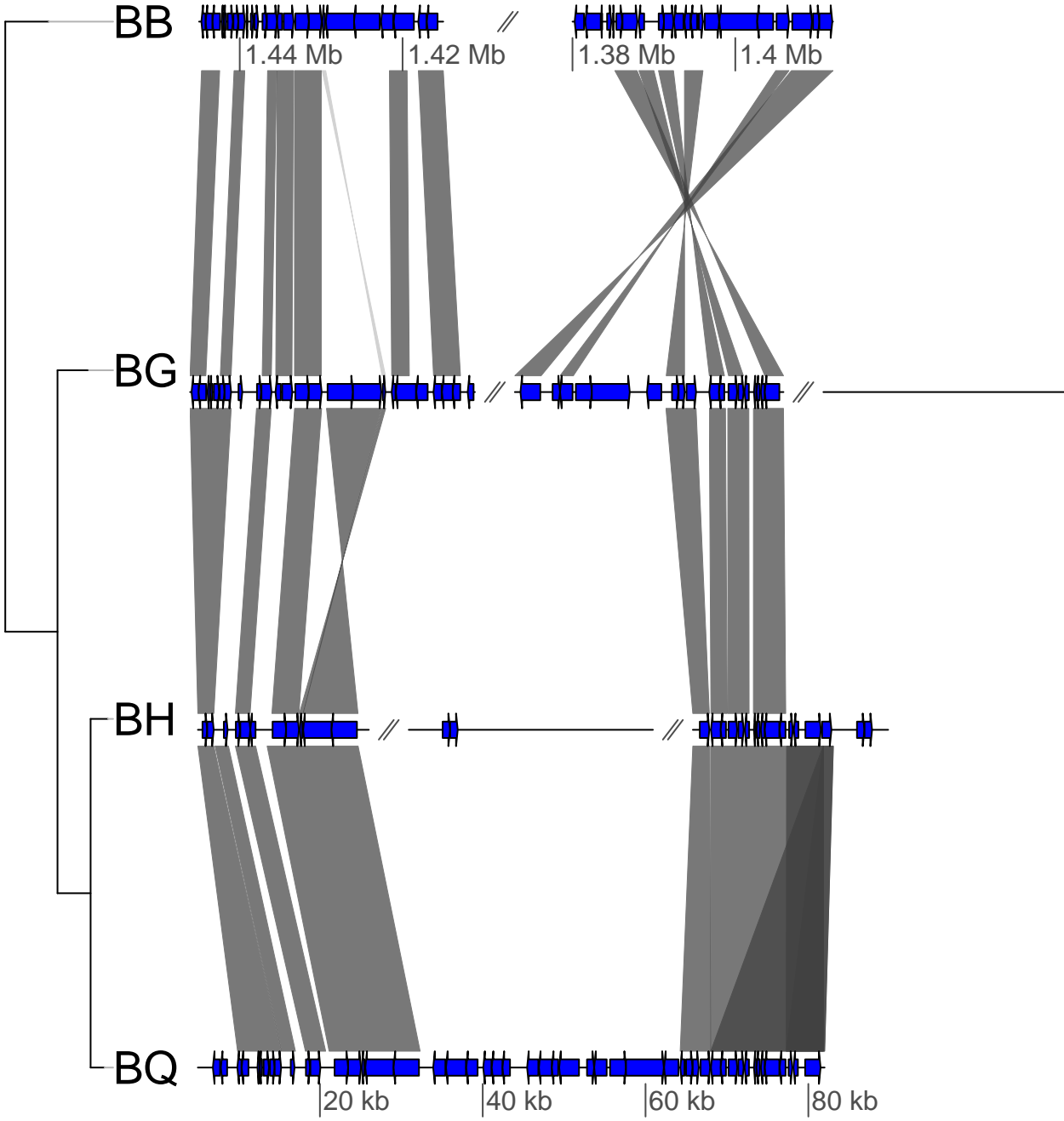
20 kb

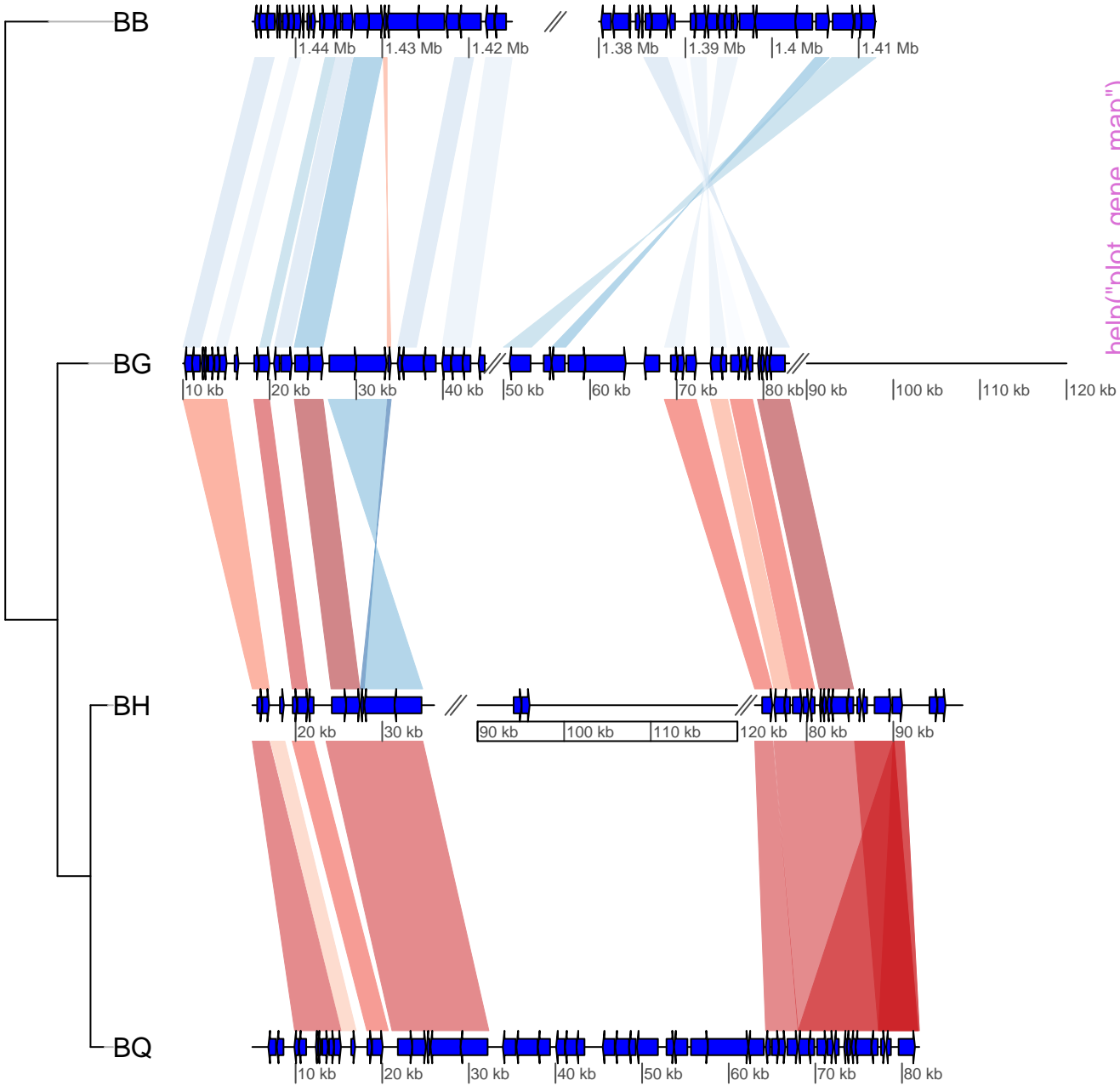
40 kb

60 kb

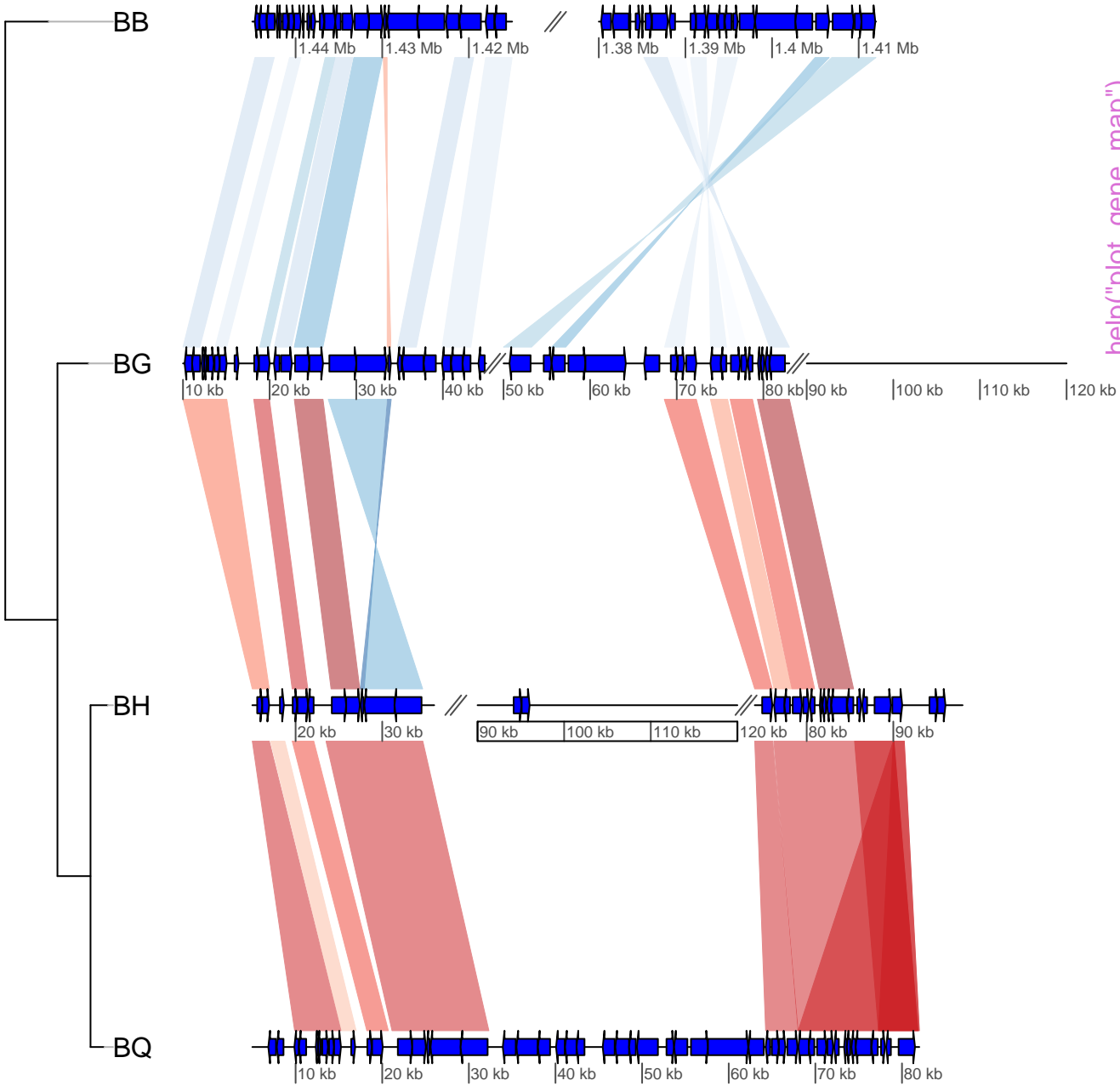
80 kb

help("plot_gene_map")

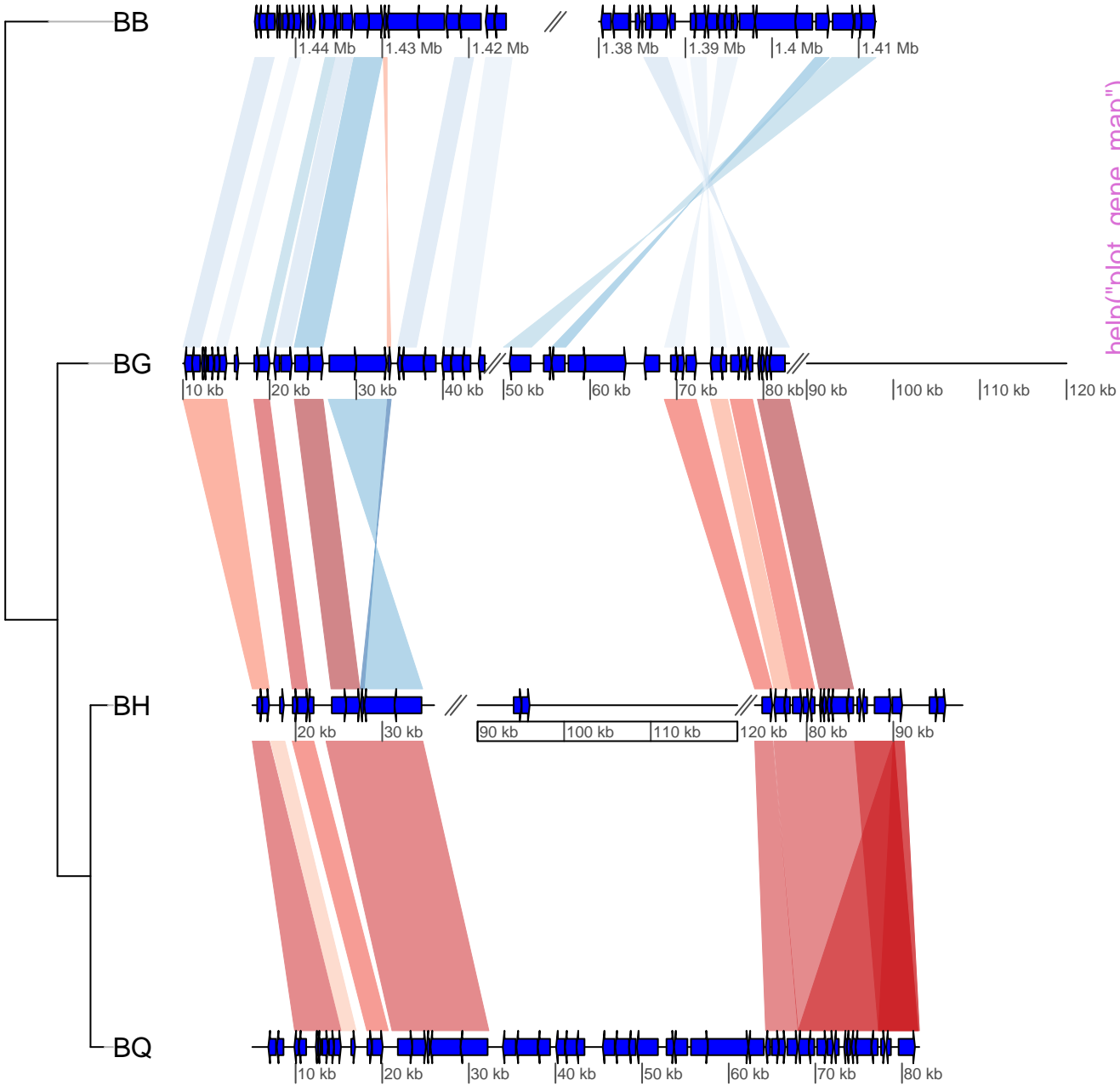




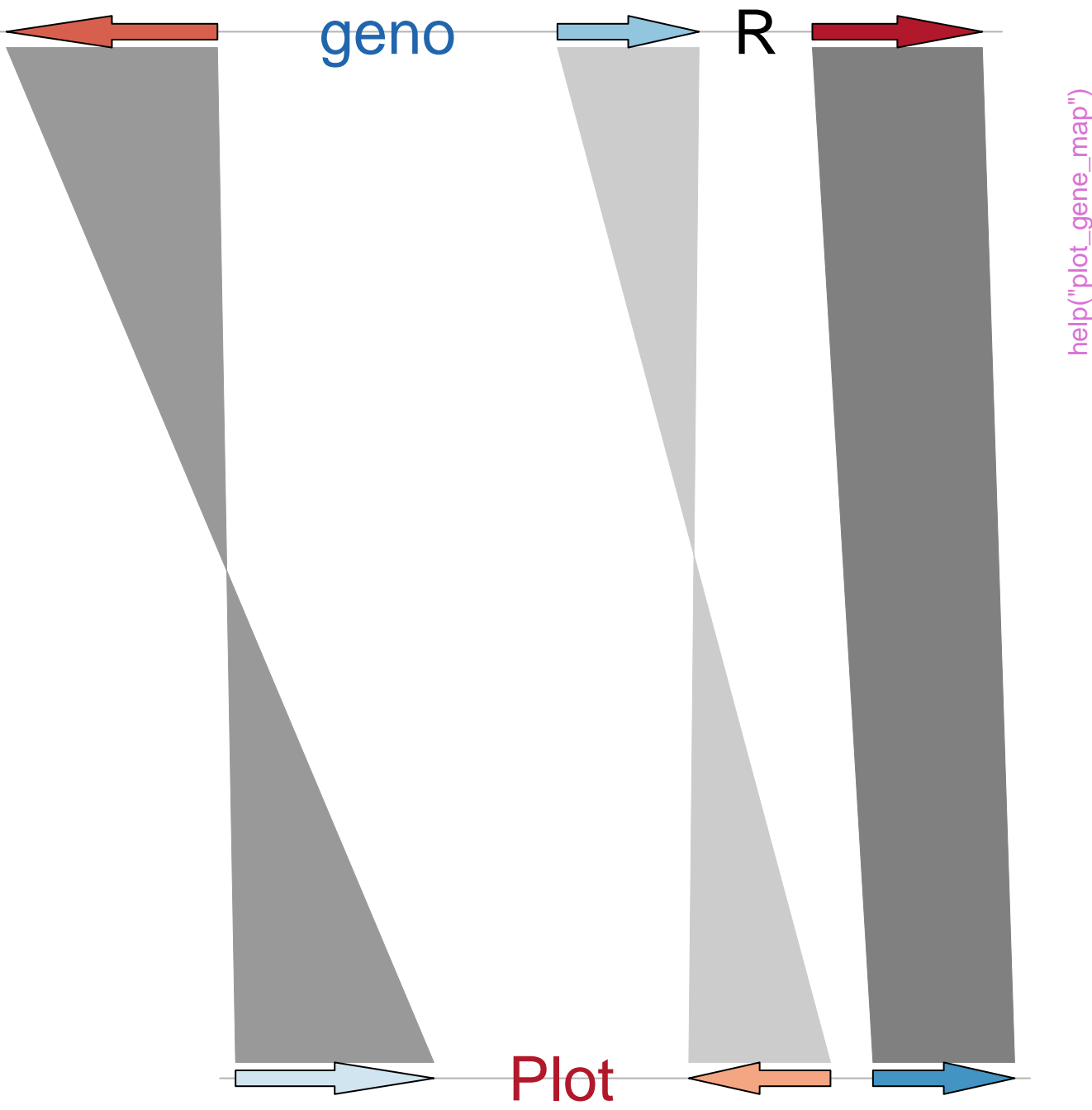
10 kb



help("plot_gene_map")



10 kb

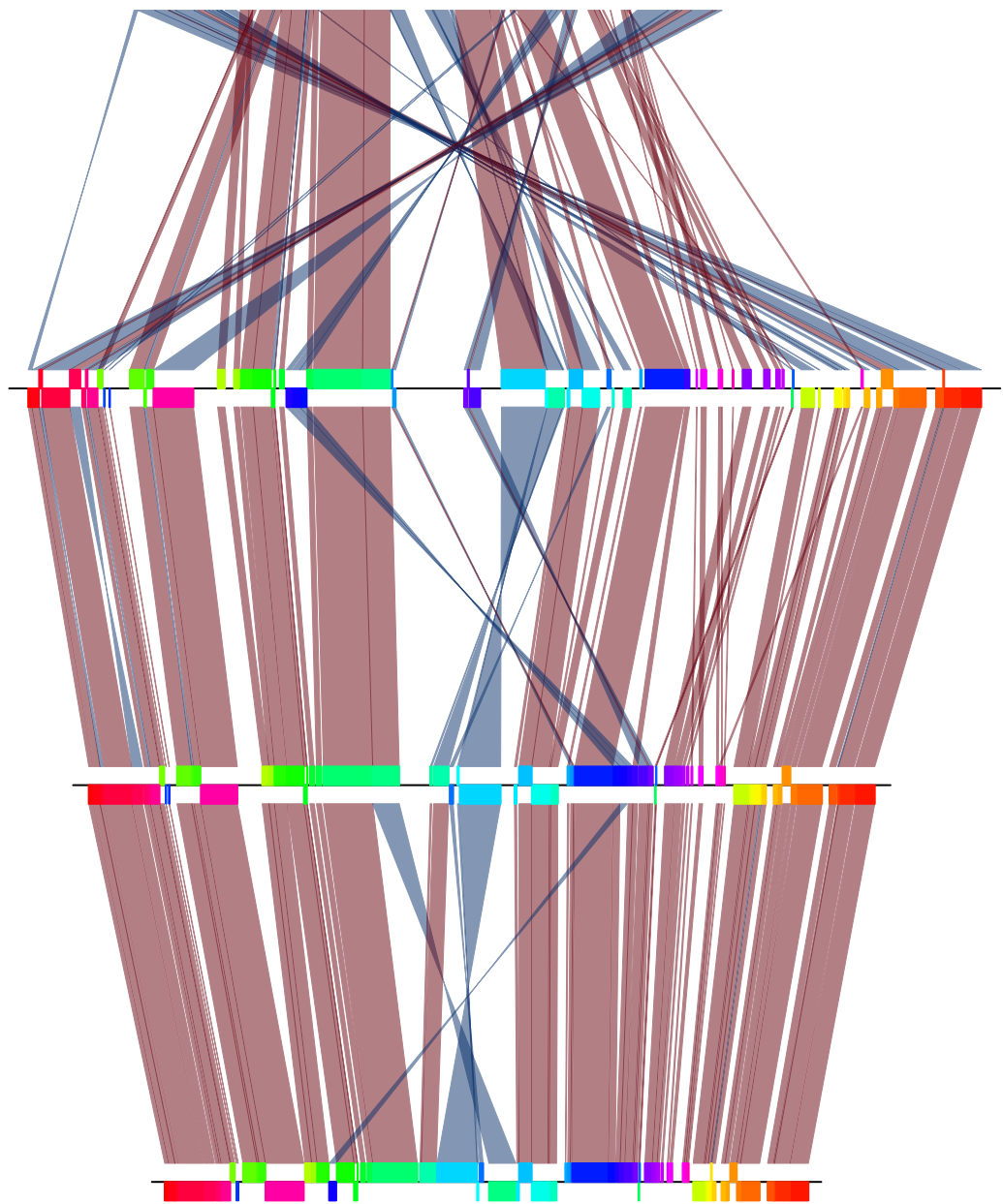
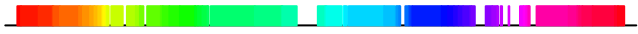


B_bacilliformis

B_grahamii

B_henselae

B_quintana



help("read_functions")

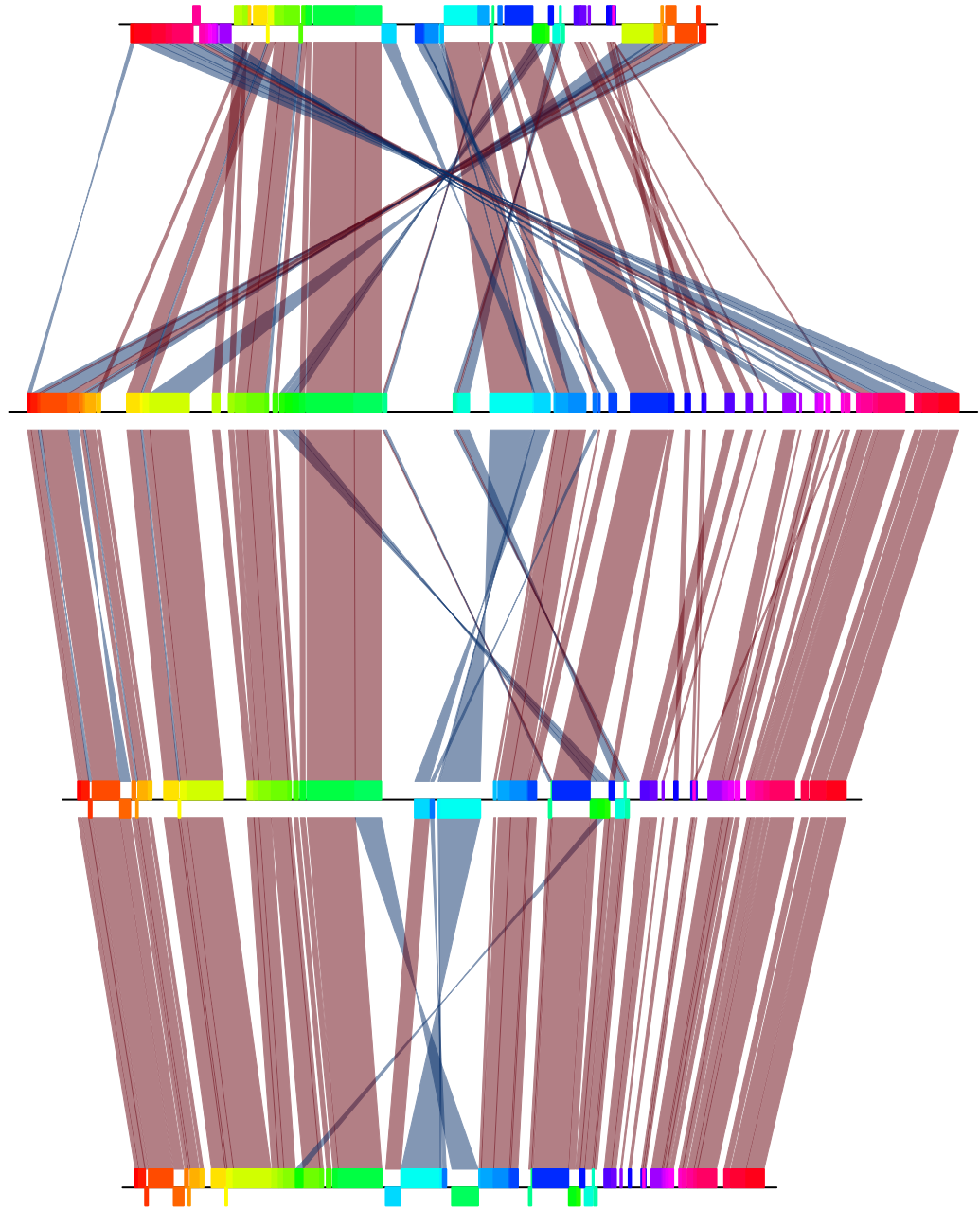
500 kb

B_bacilliformis

B_grahamii

B_henselae

B_quintana



help("read_functions")

B. bacilliformis

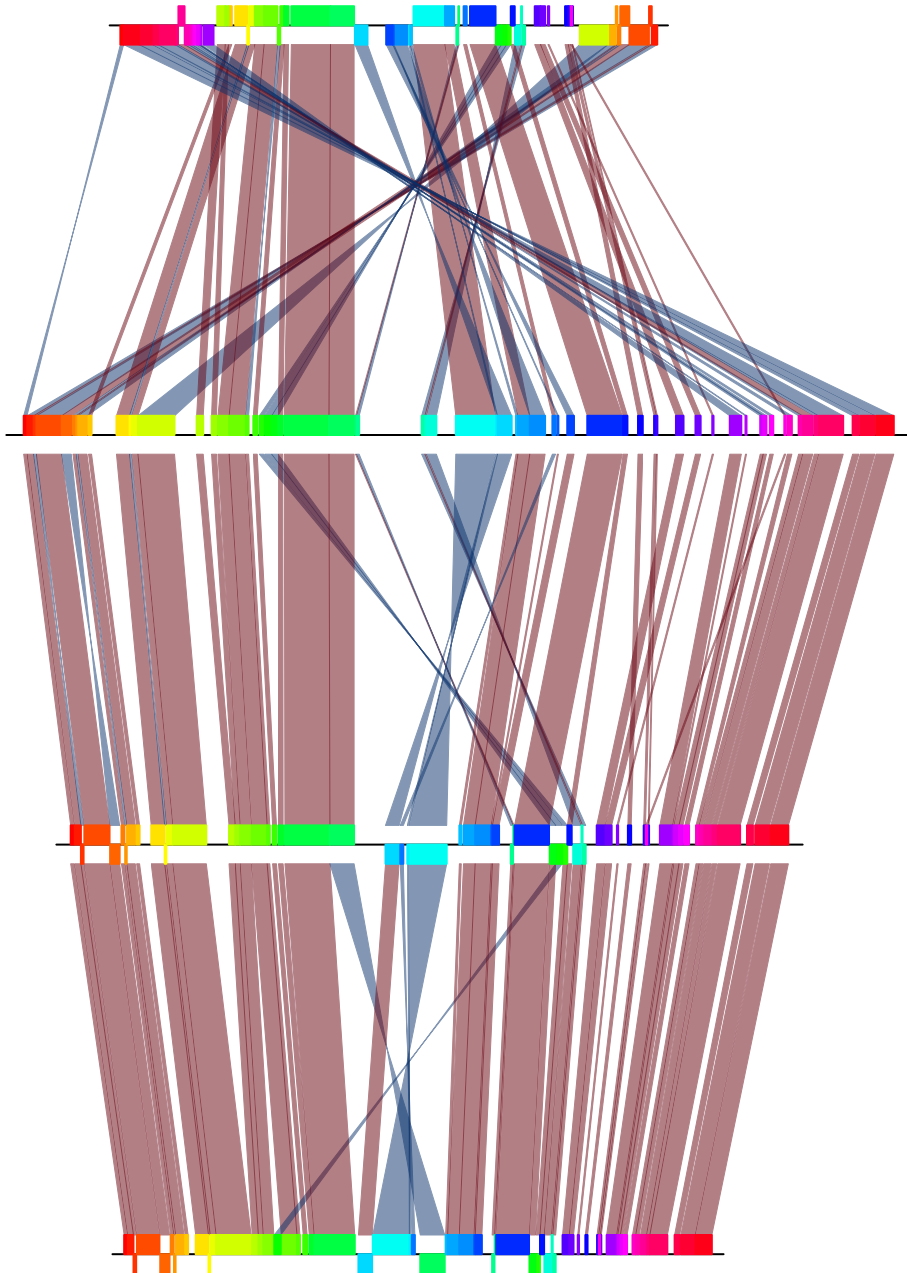
B. grahamii

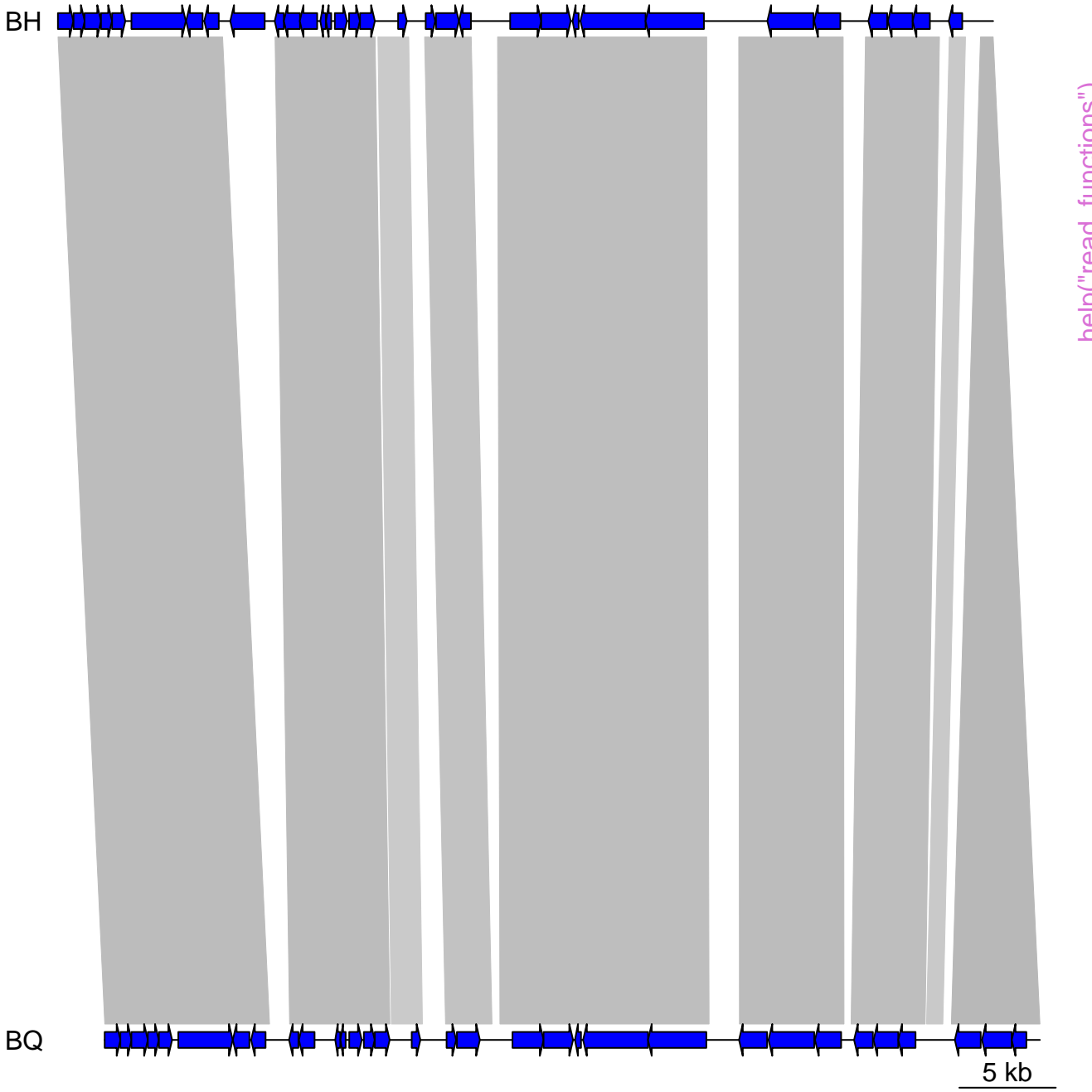
B. henselae

B. quintana

help("read_functions")

500 kb



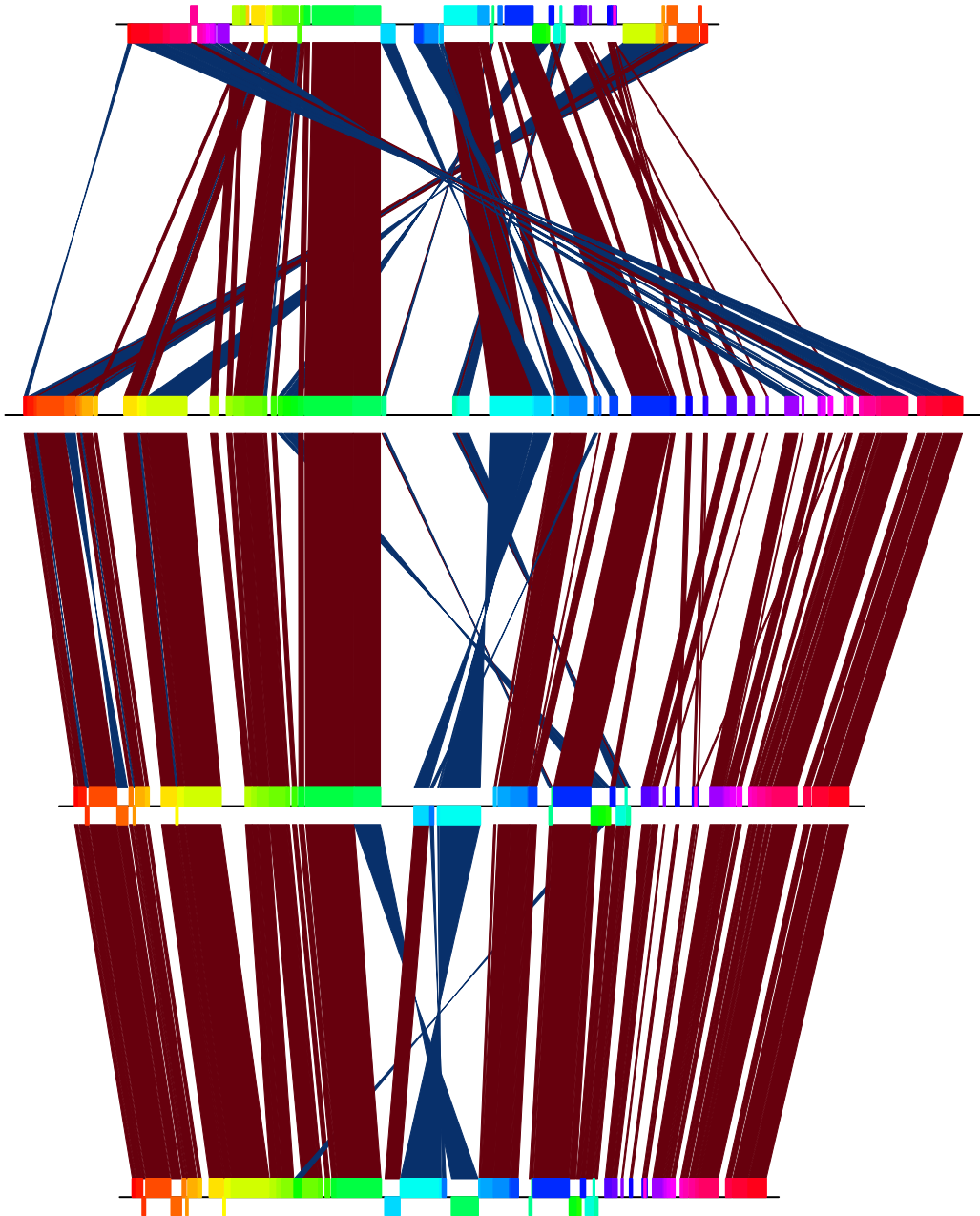


B_bacilliformis

B_grahamii

B_henselae

B_quintana



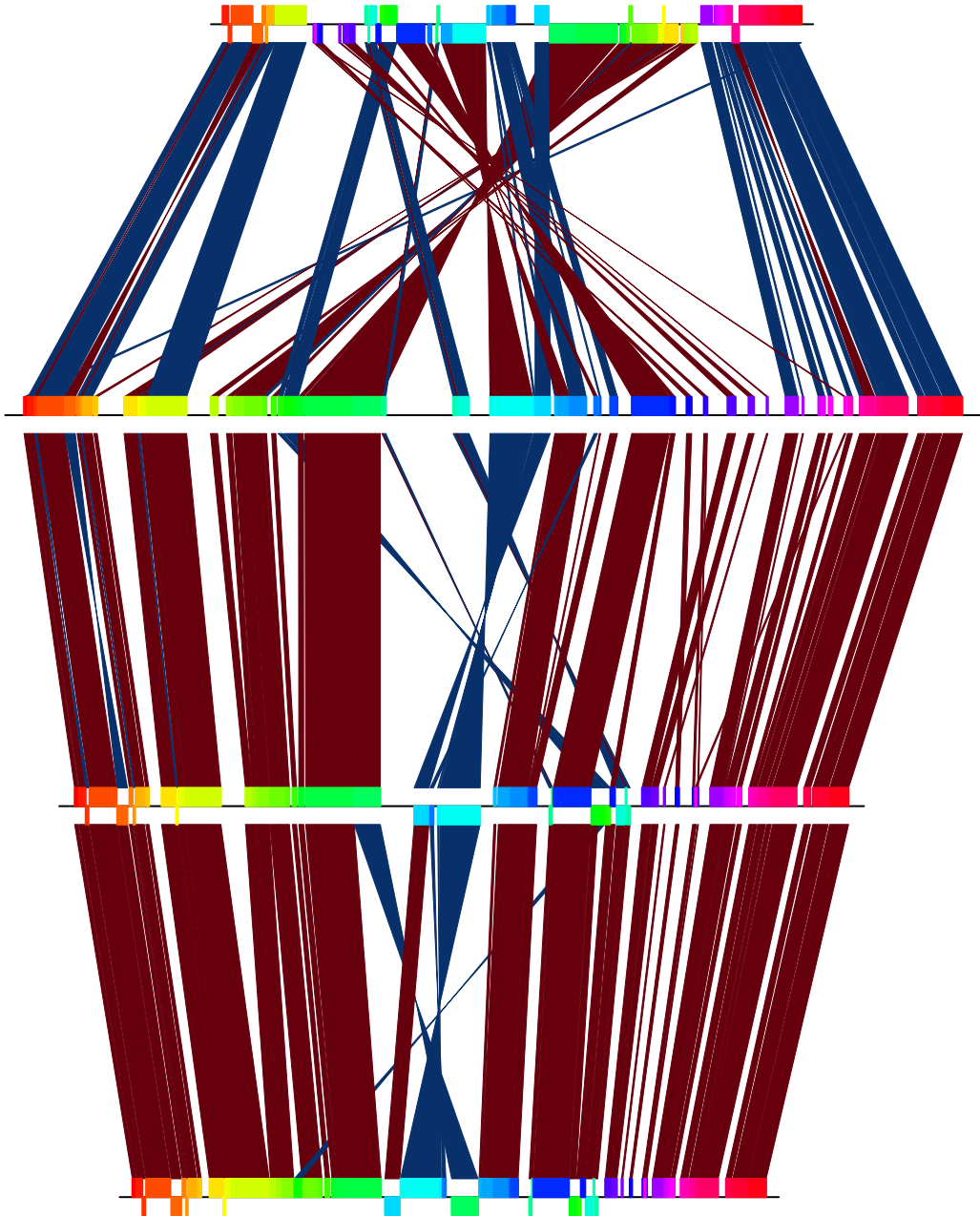
help("reverse")

B_bacilliformis

B_grahamii

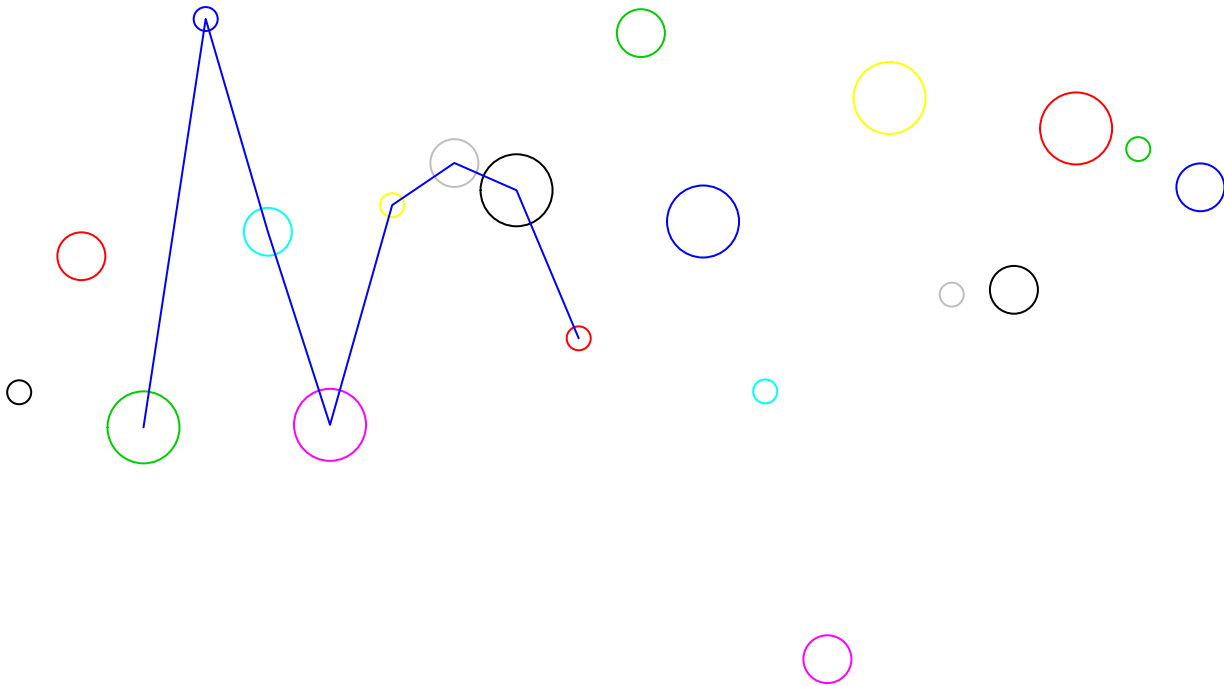
B_henselae

B_quintana

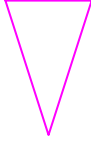
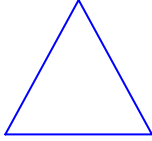


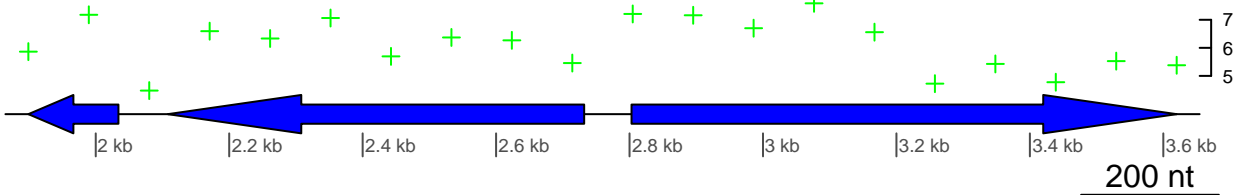
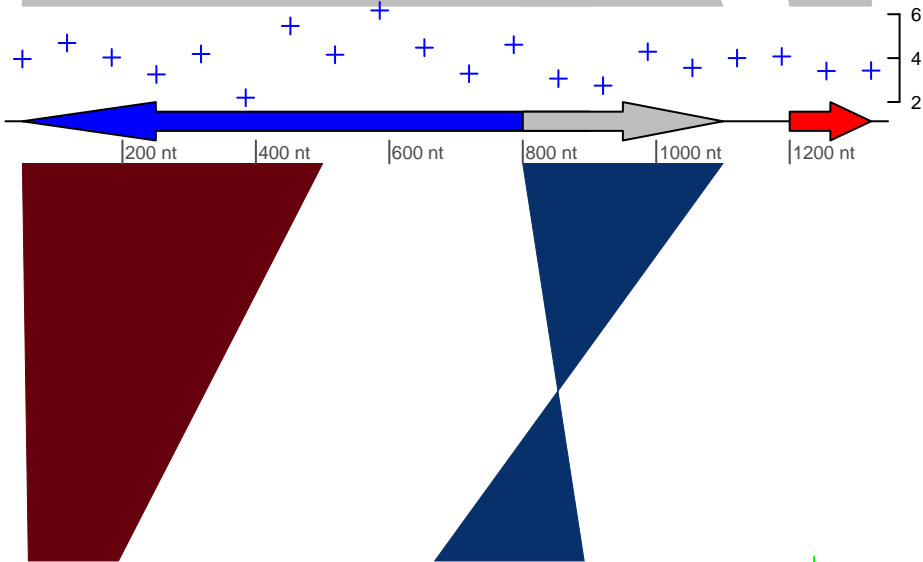
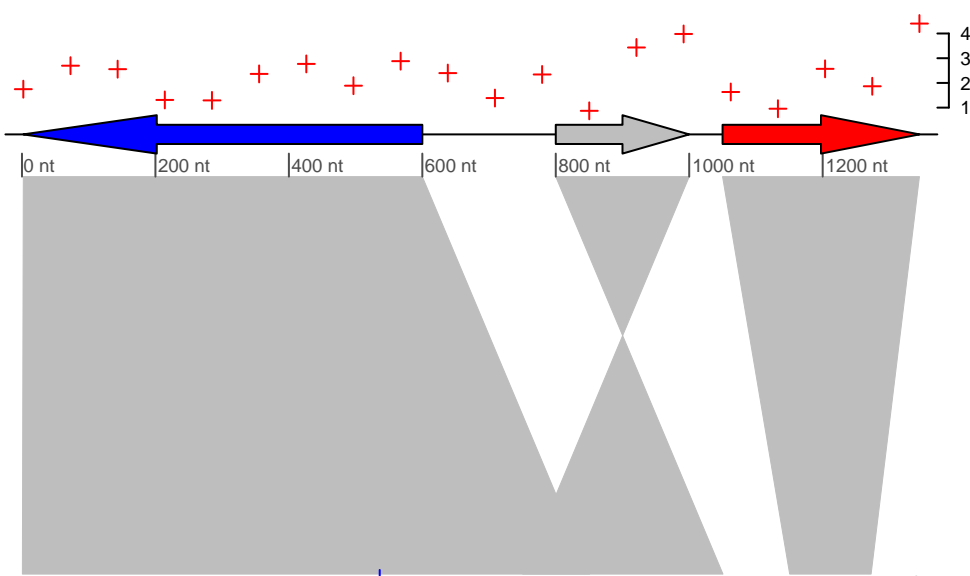
help("reverse")

500 kb



help("seg_plot")



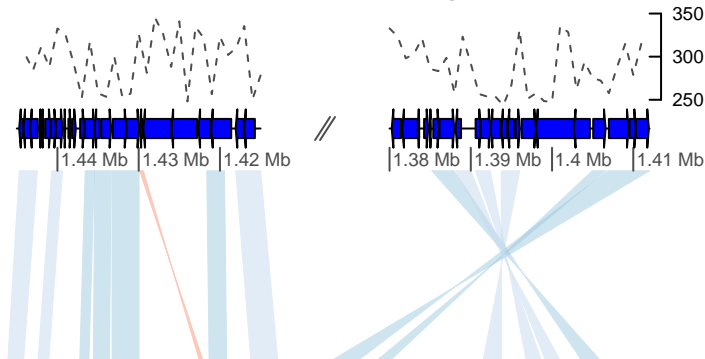


help("seg_plot")

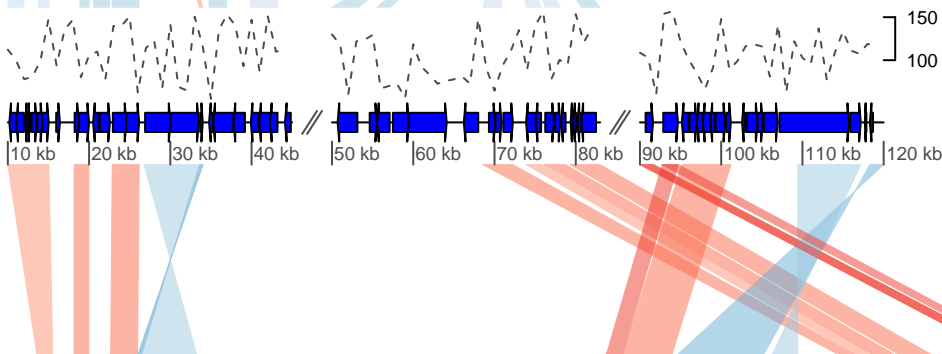
Random plots for the same segment in 4 *Bartonella* genomes

help("seg_plot")

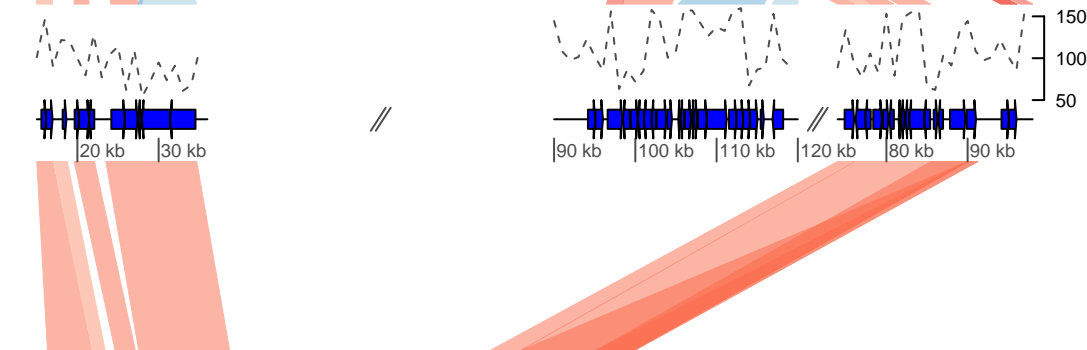
BB



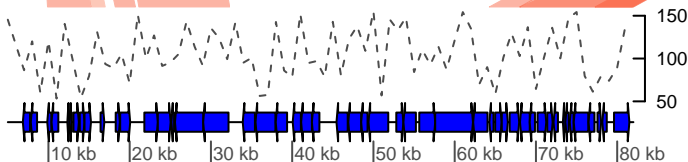
BG



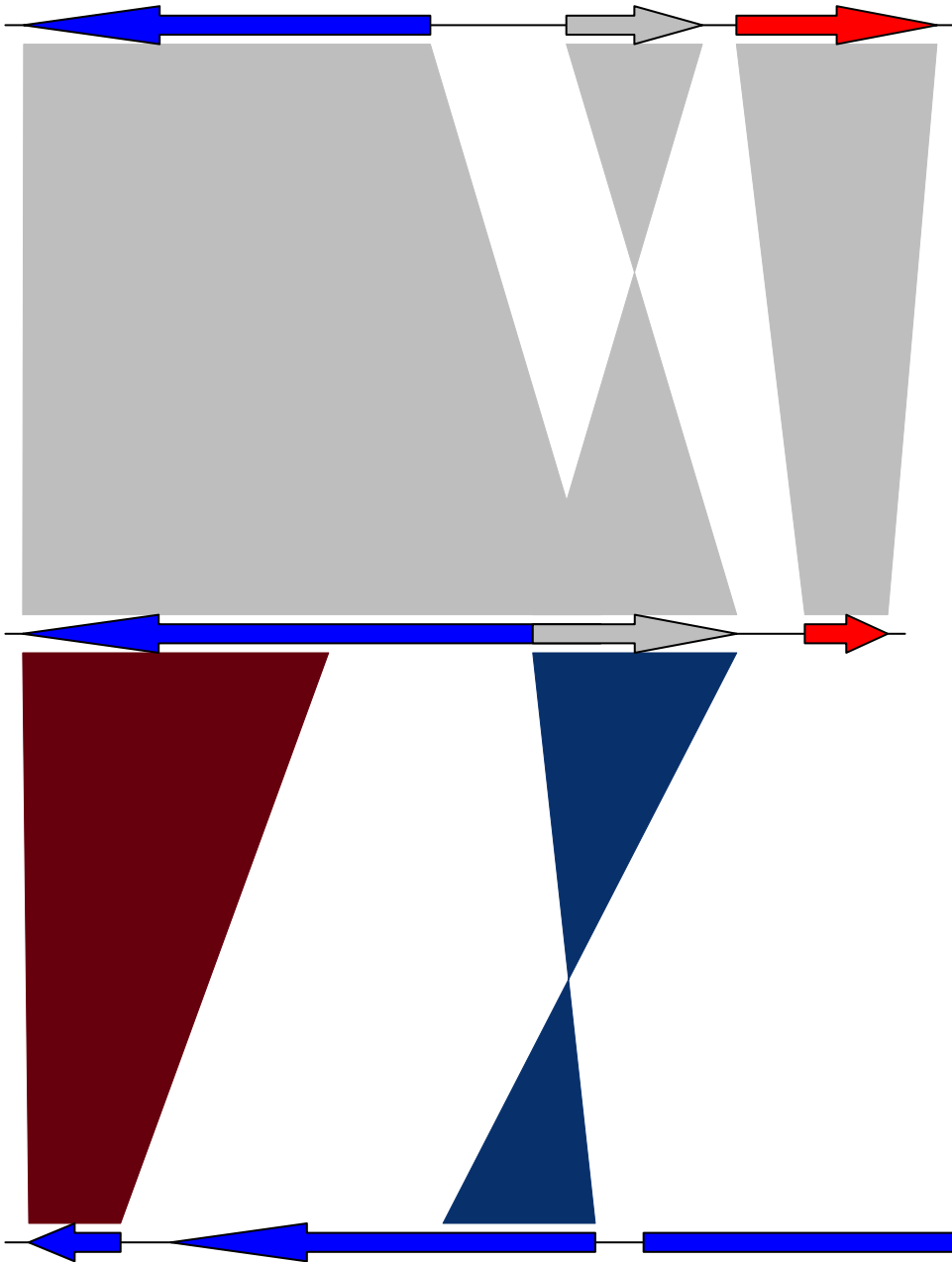
BH



BQ



20 kb



help("three_genes")

200 nt

