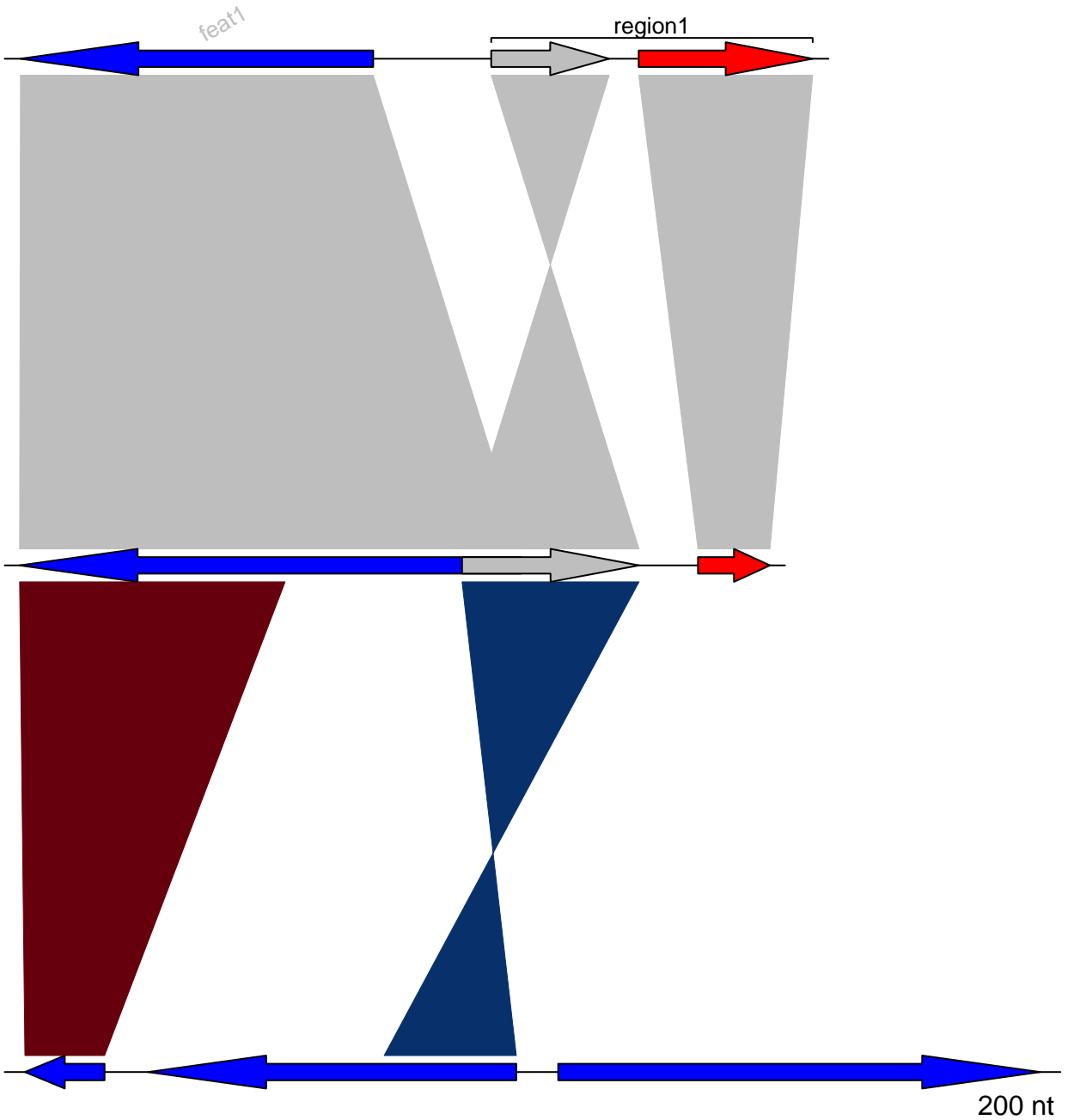
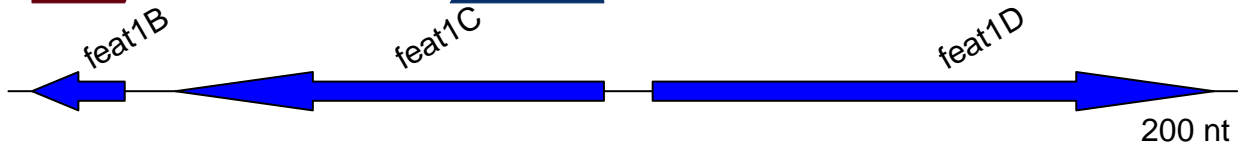
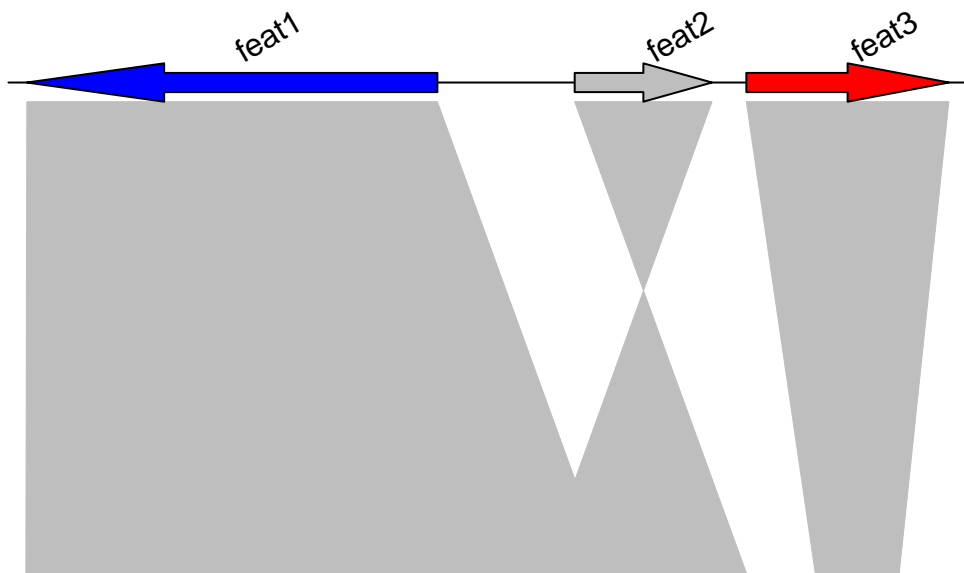


help("annotation")

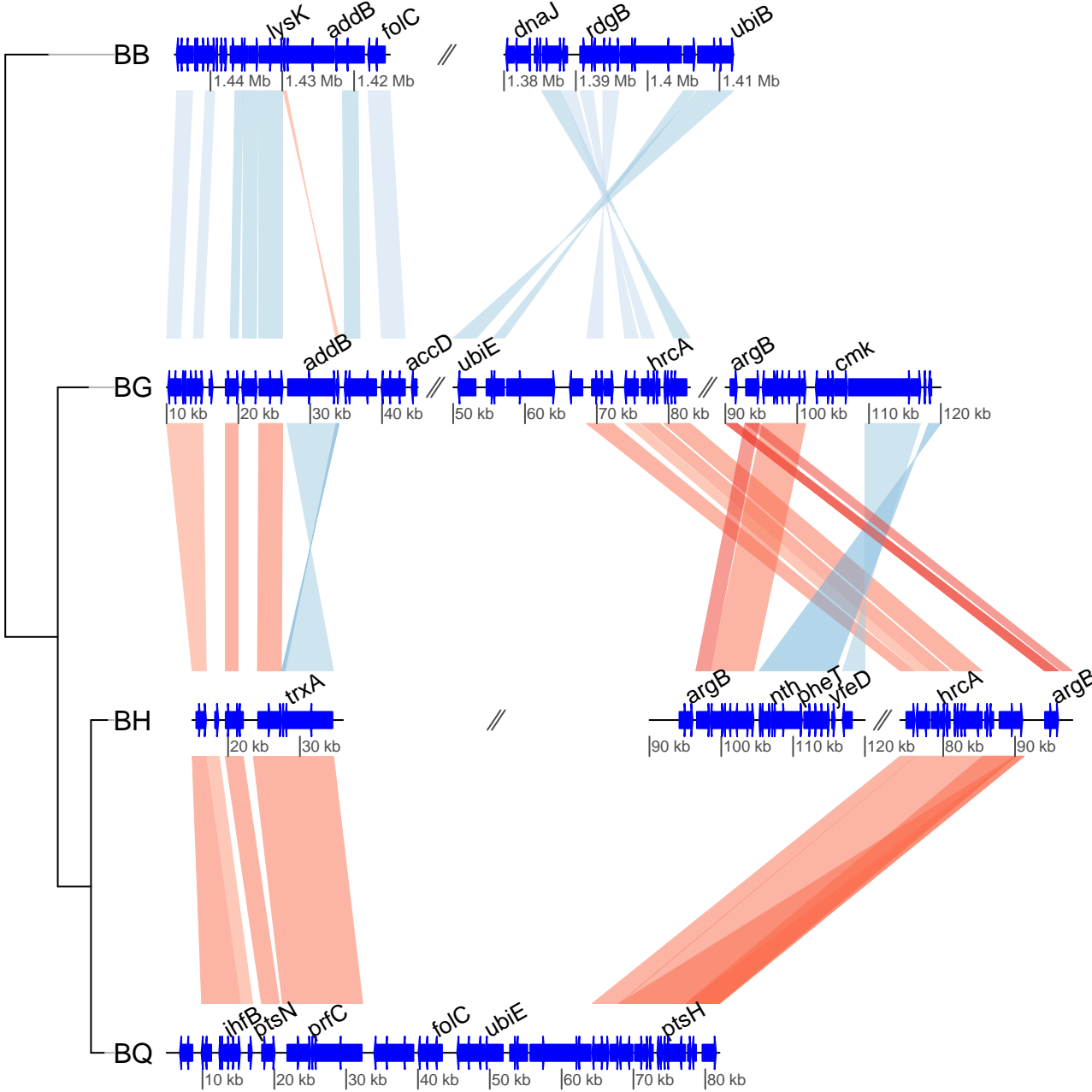


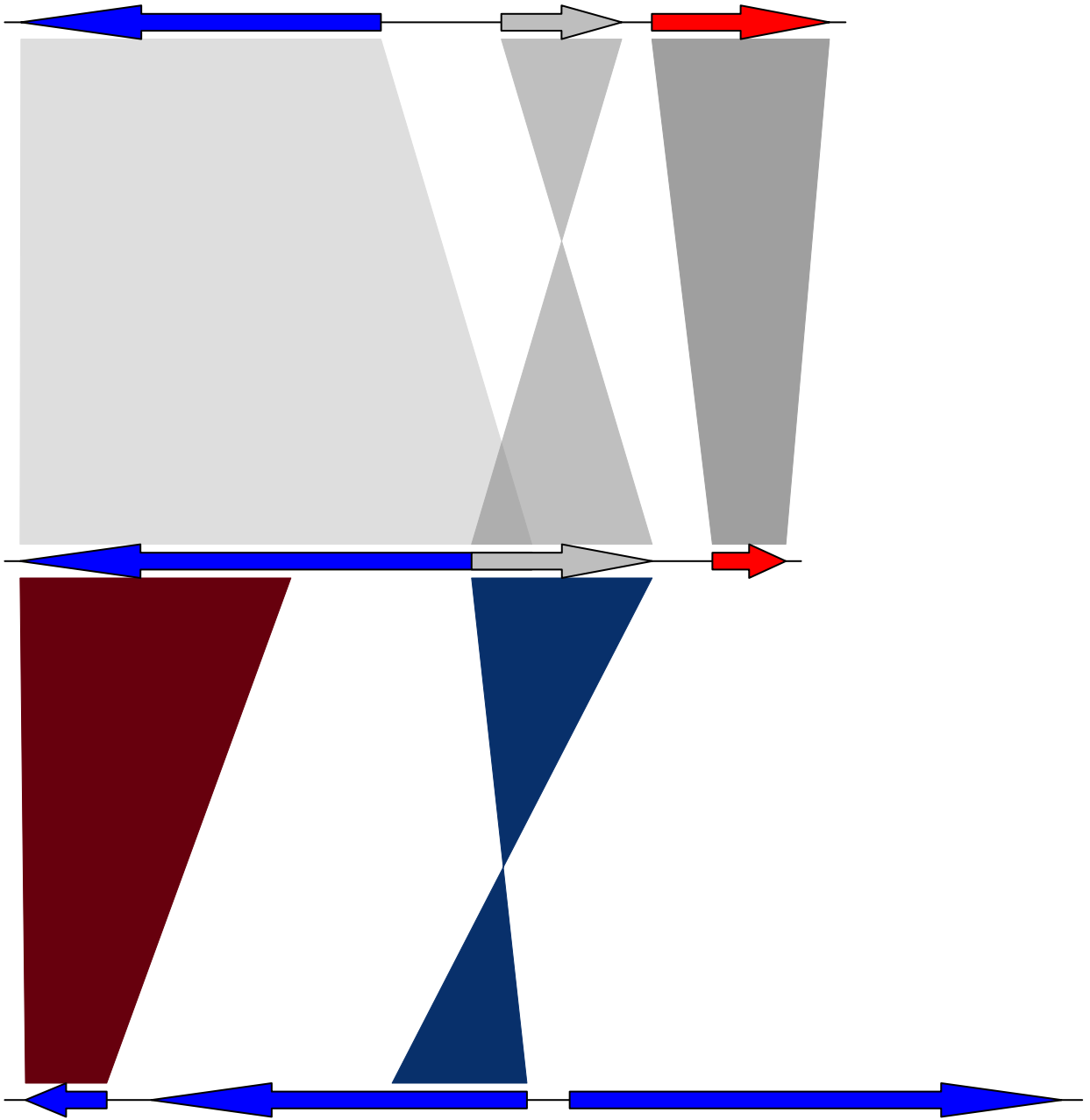
help("annotation")

200 nt



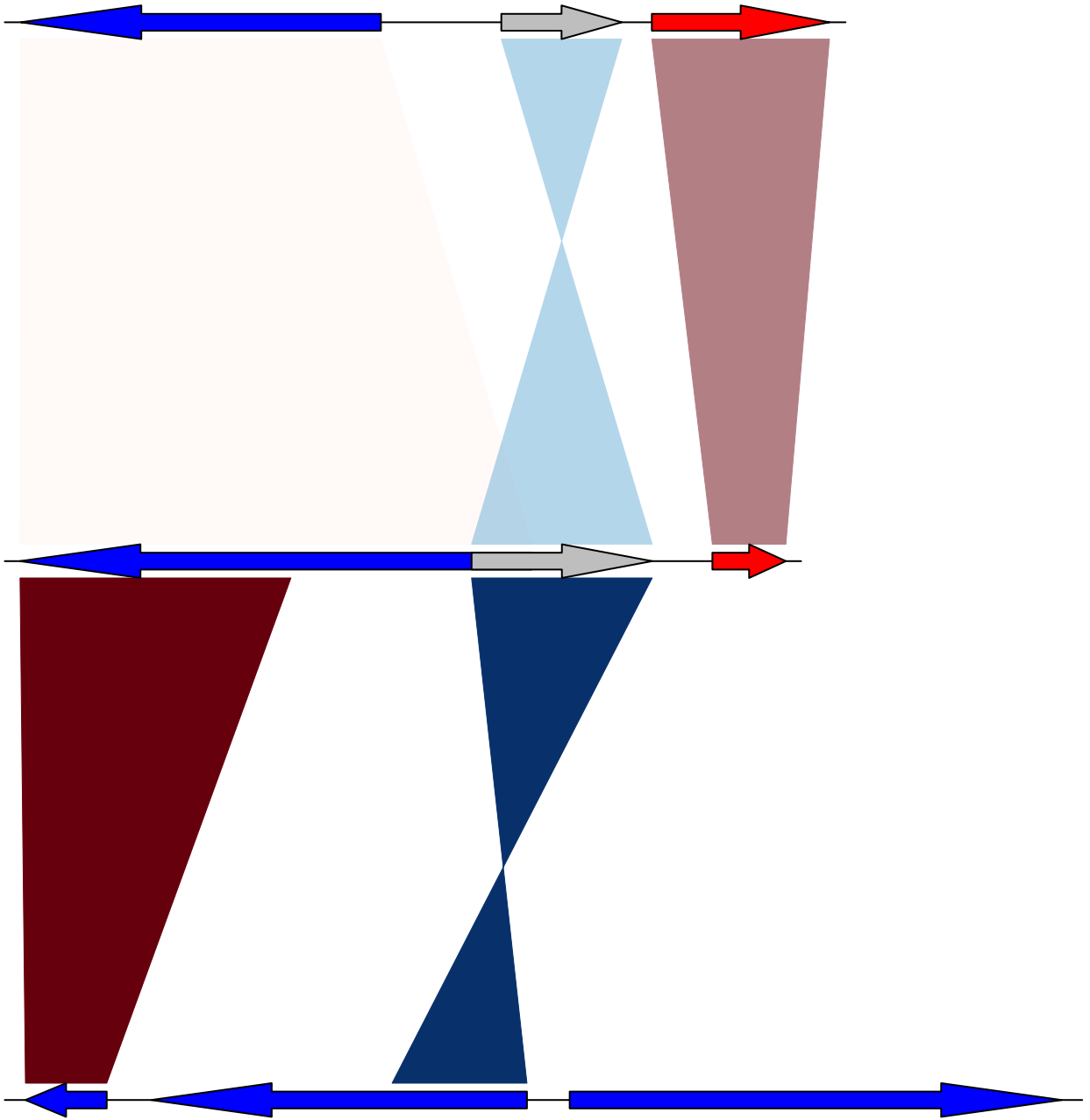
help("annotation")





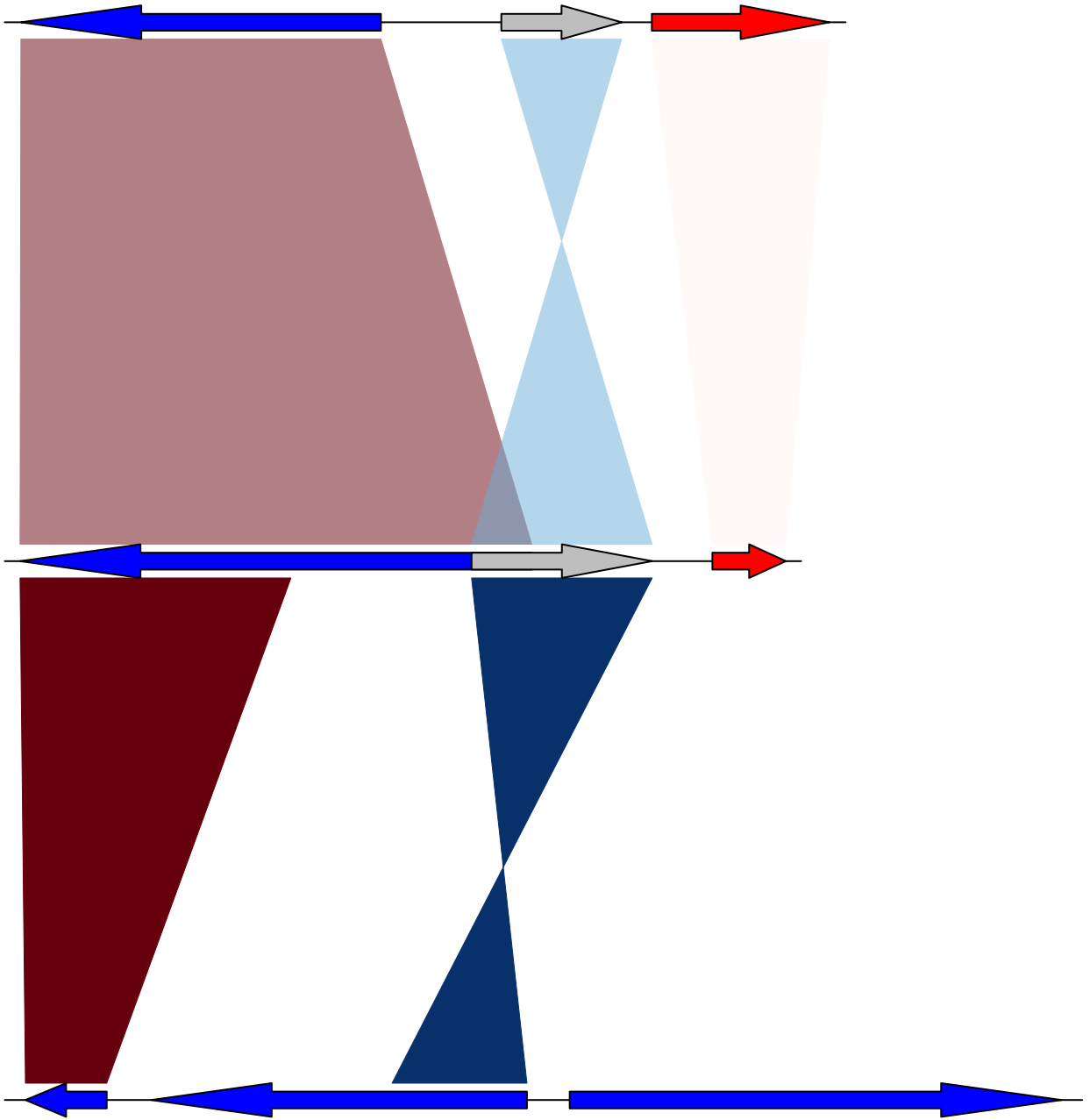
help("apply_color_scheme")

200 nt



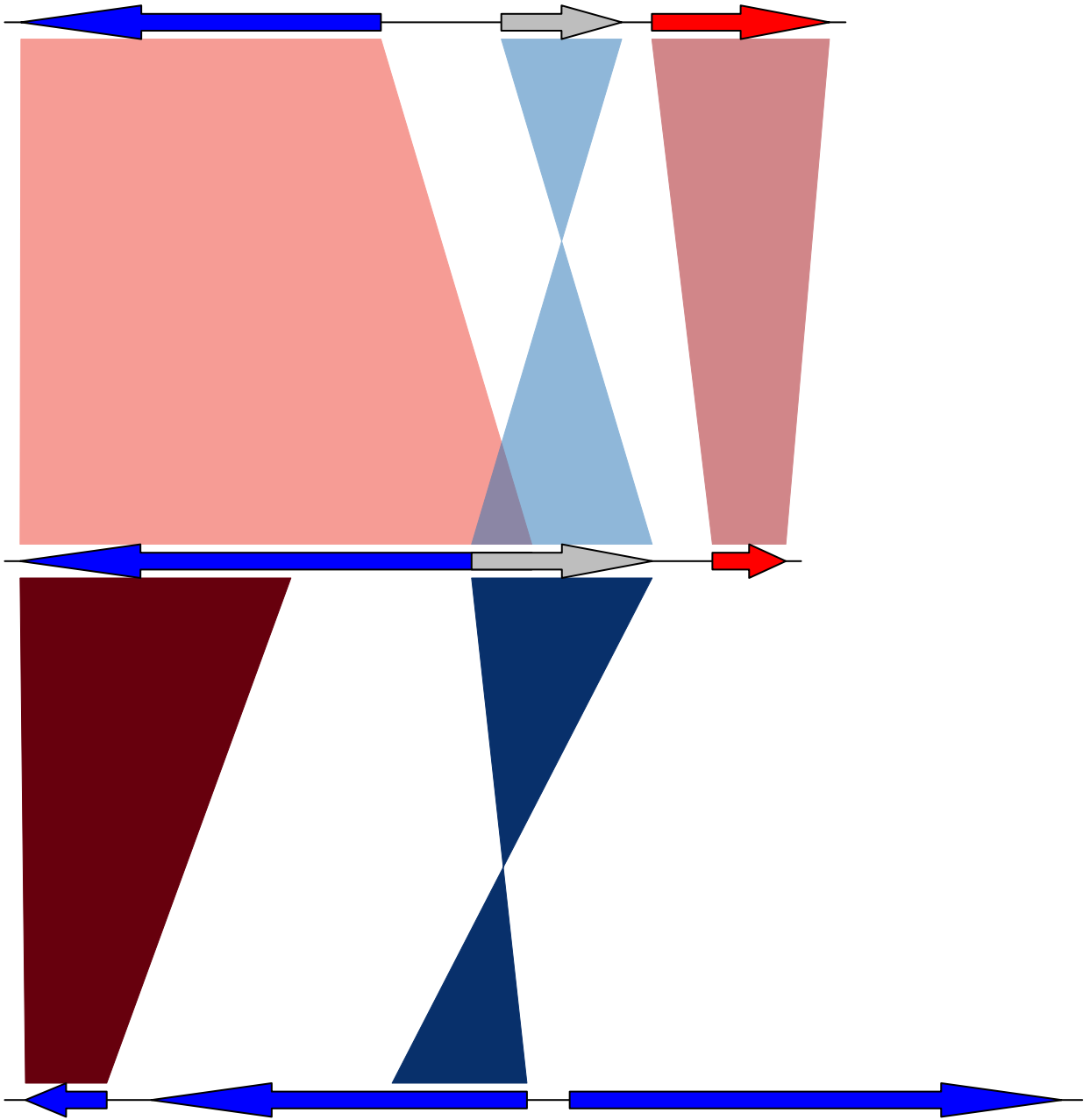
help("apply_color_scheme")

200 nt



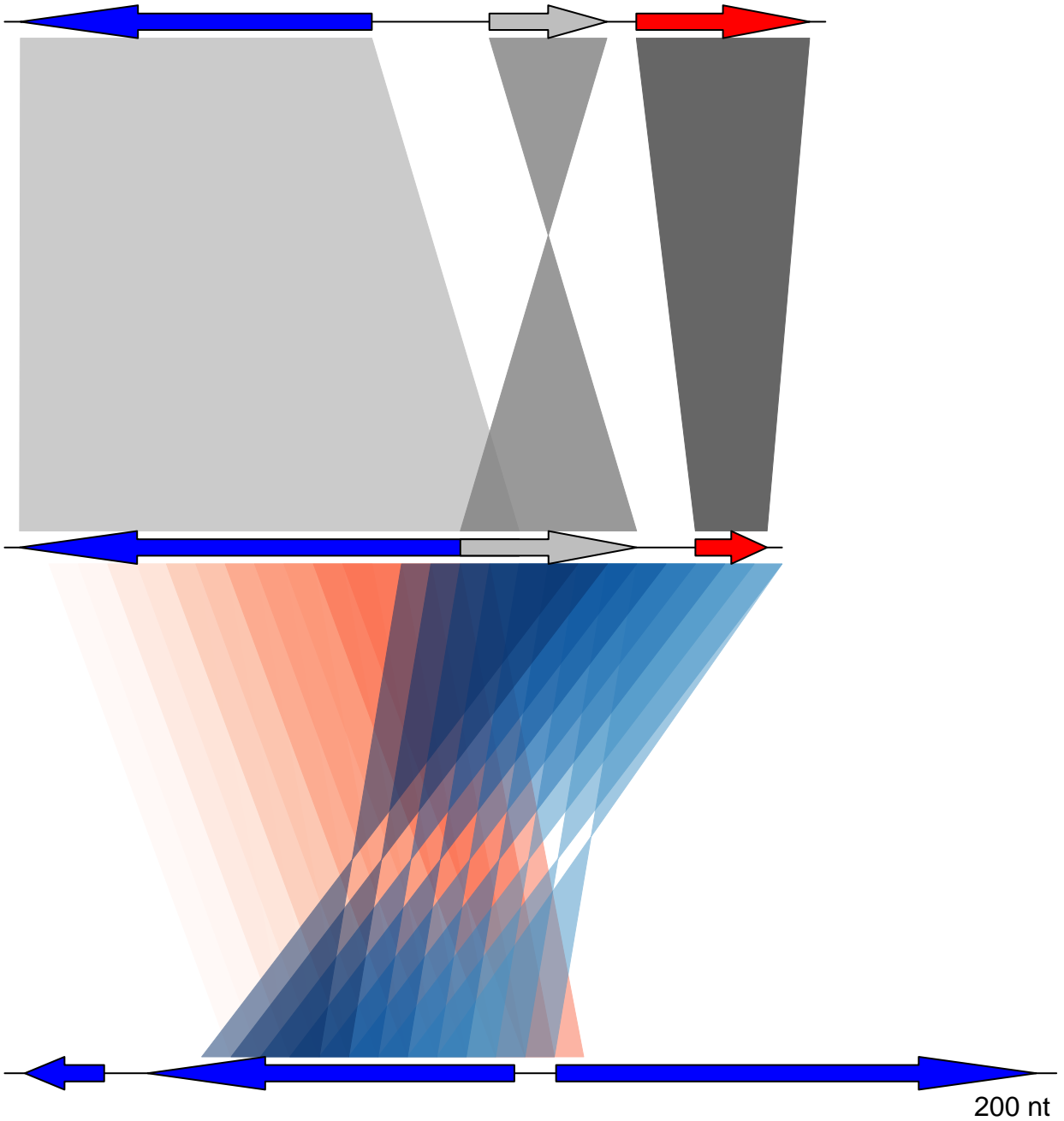
help("apply_color_scheme")

200 nt



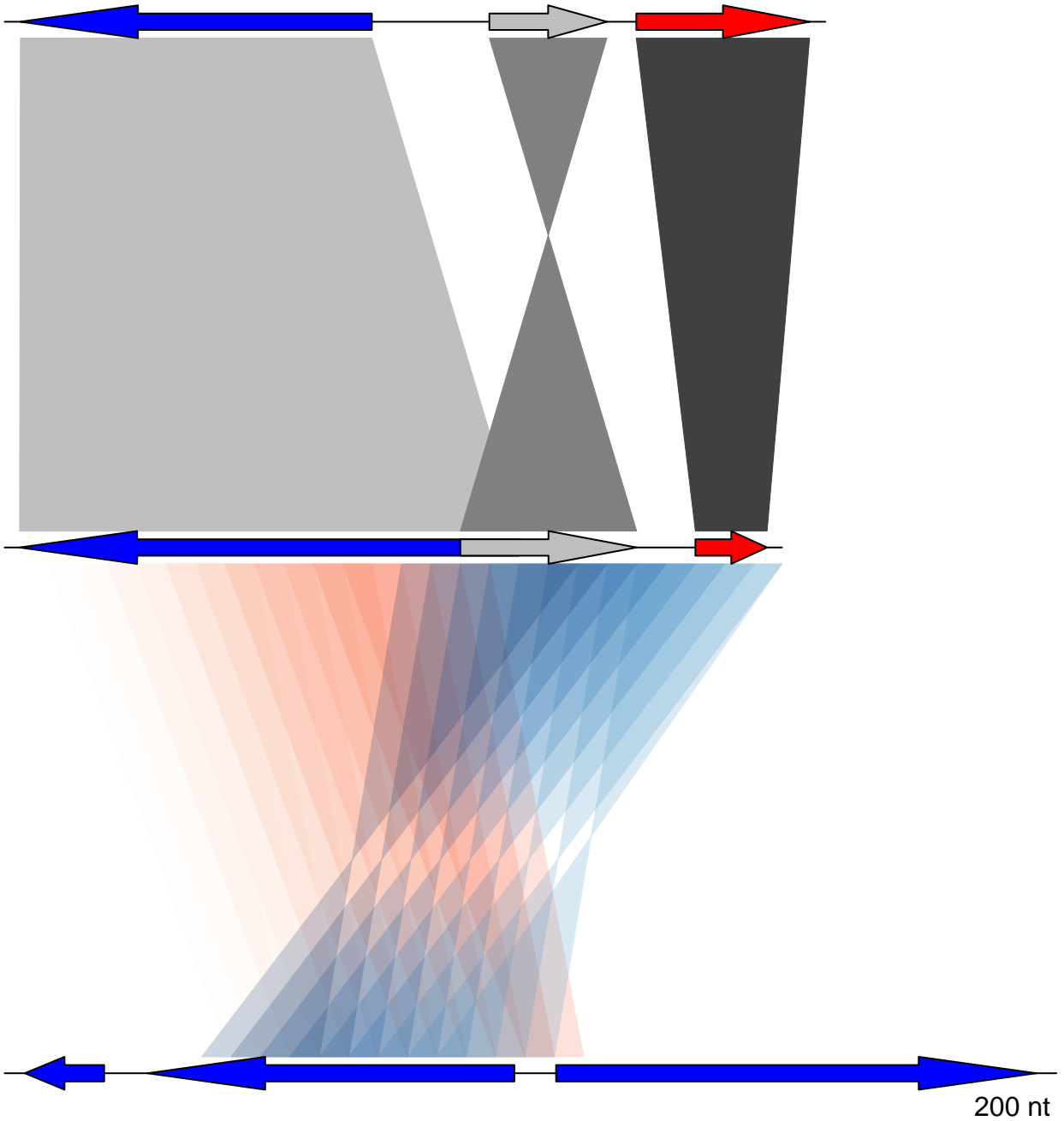
help("apply_color_scheme")

200 nt



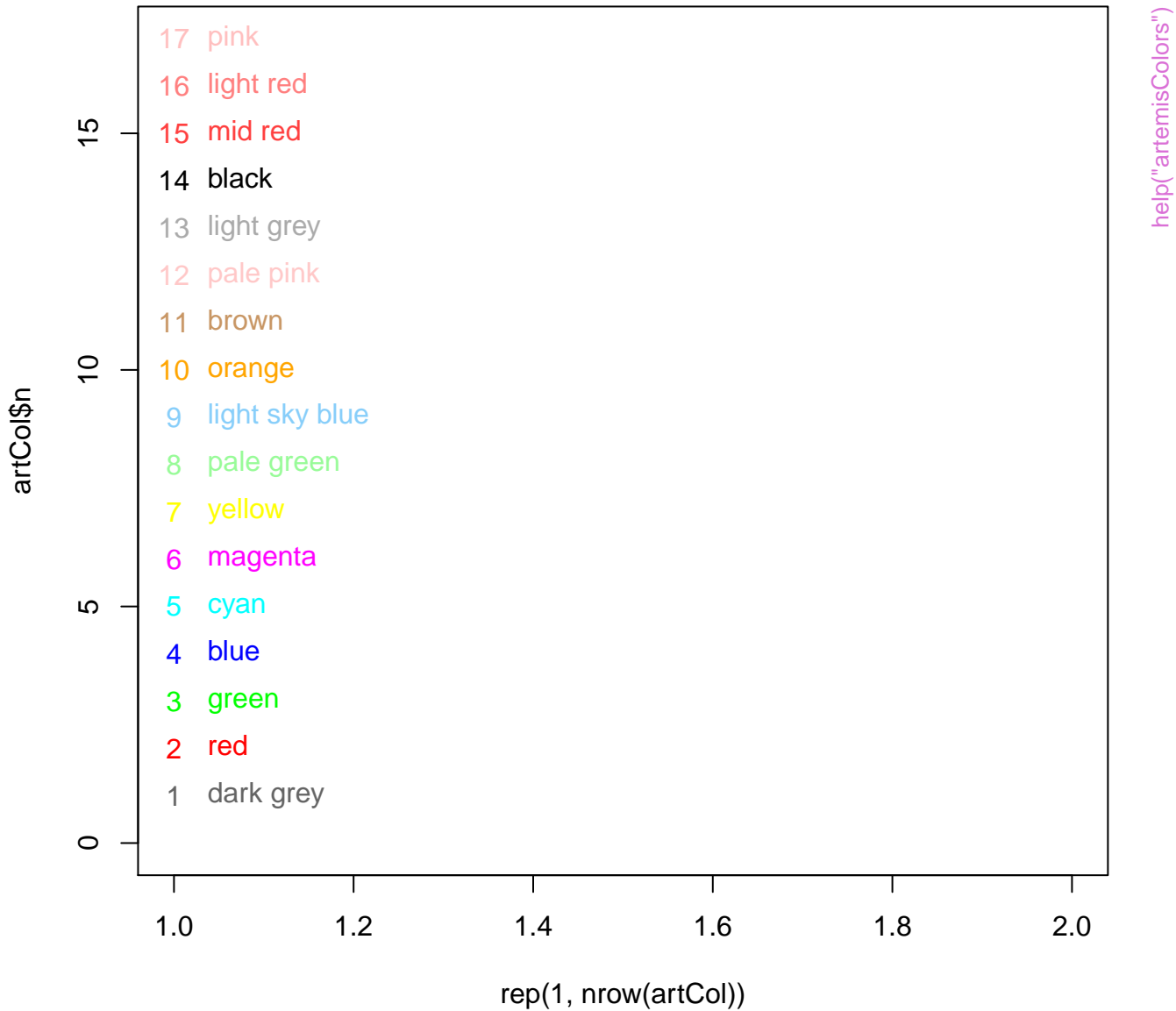
help("apply_color_scheme")

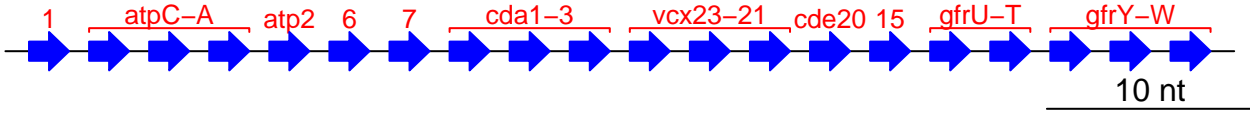
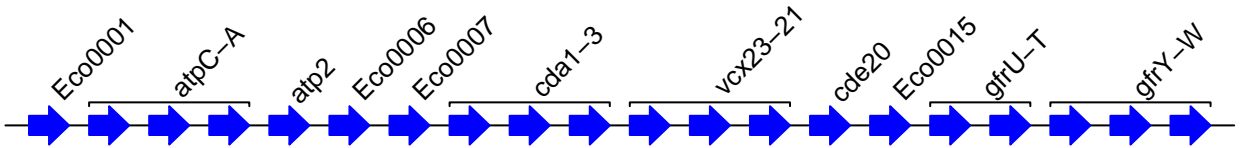
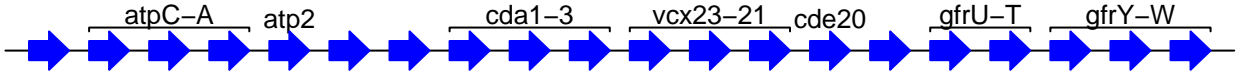
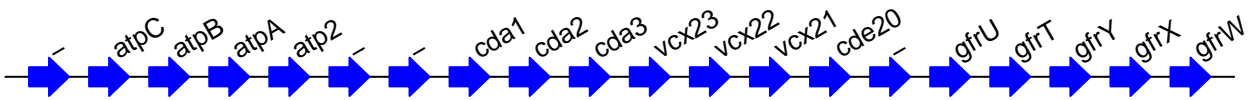
200 nt



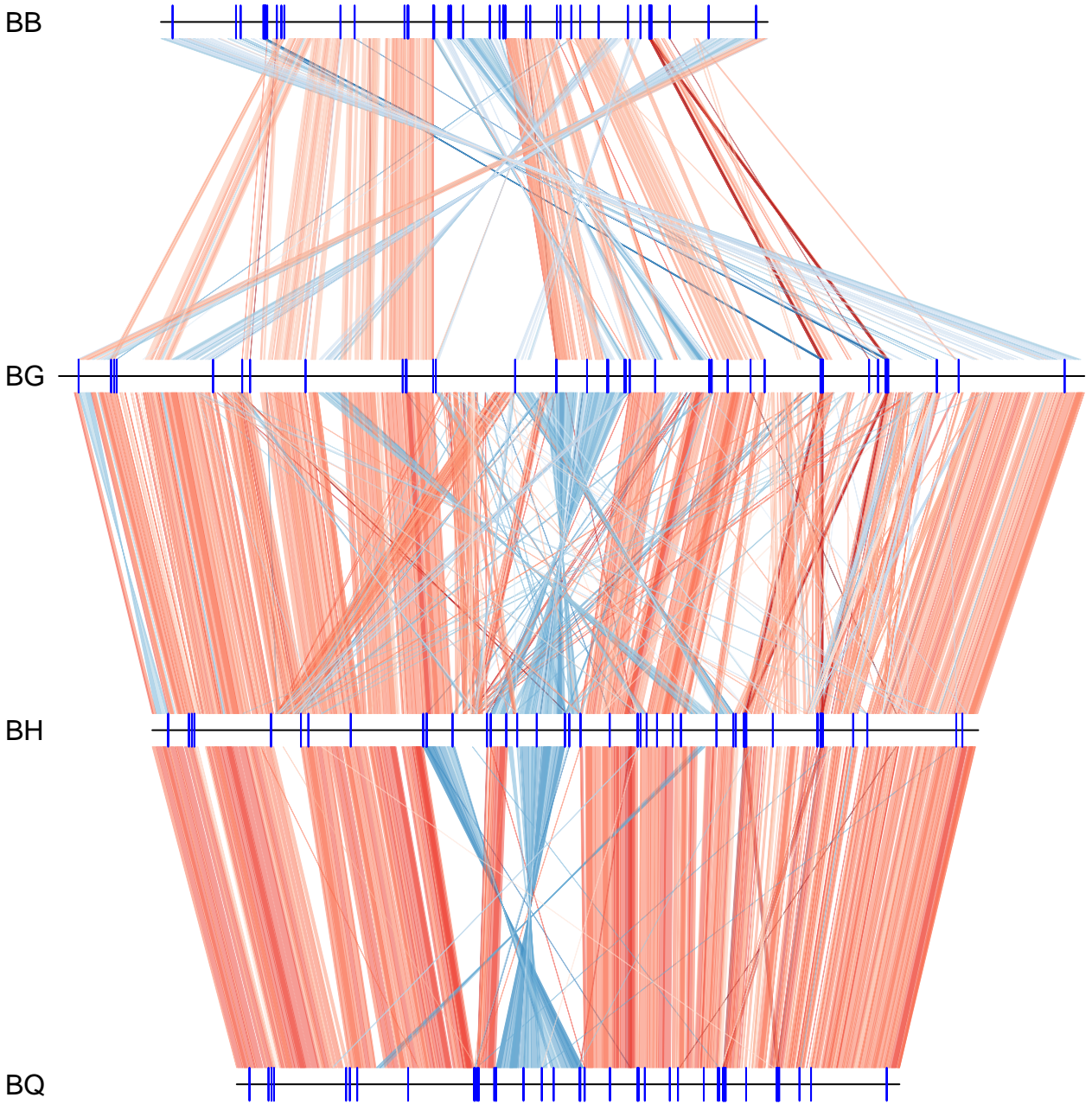
help("apply_color_scheme")

200 nt



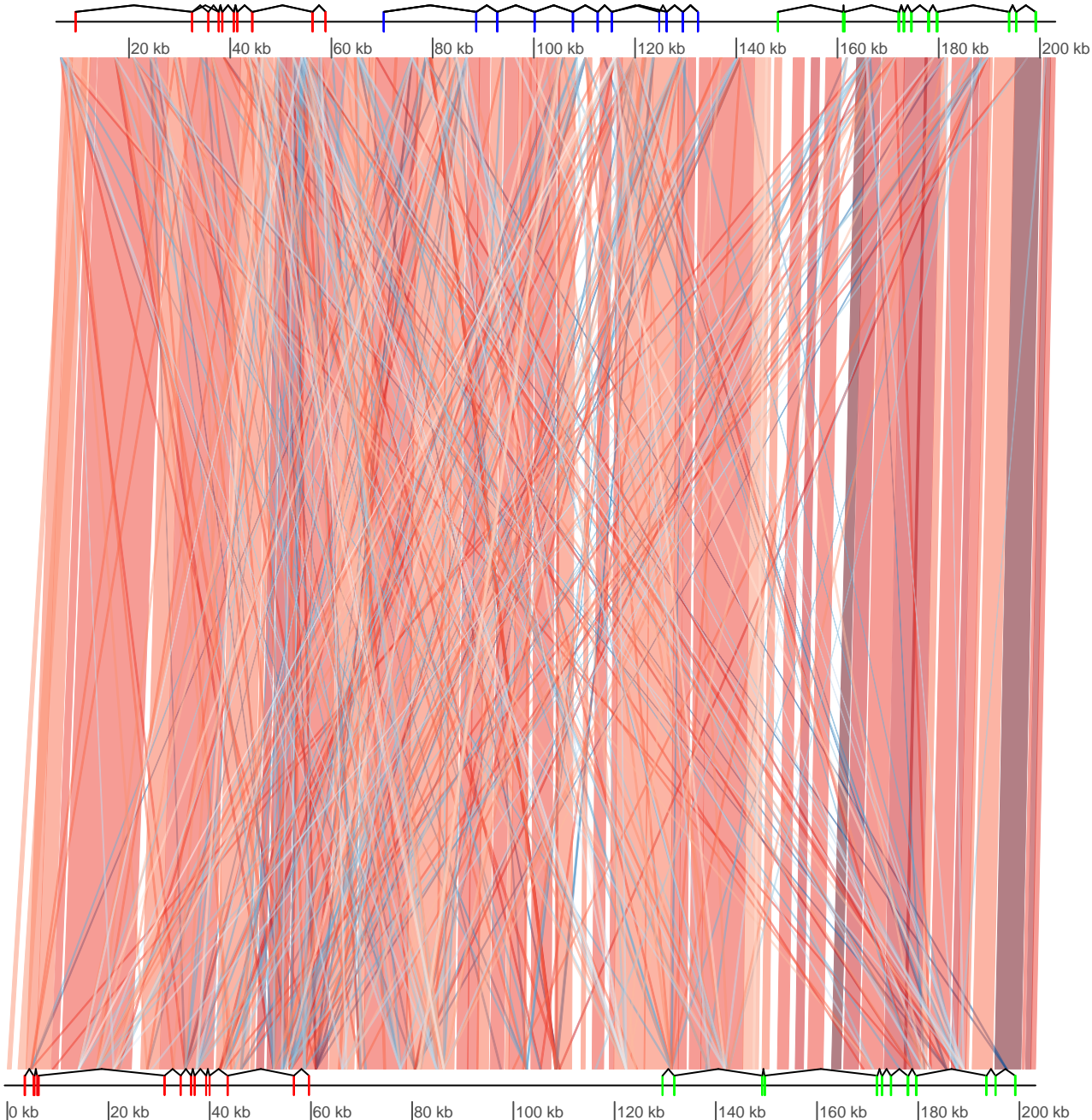


help("auto_annotate")



help("barto")

500 kb

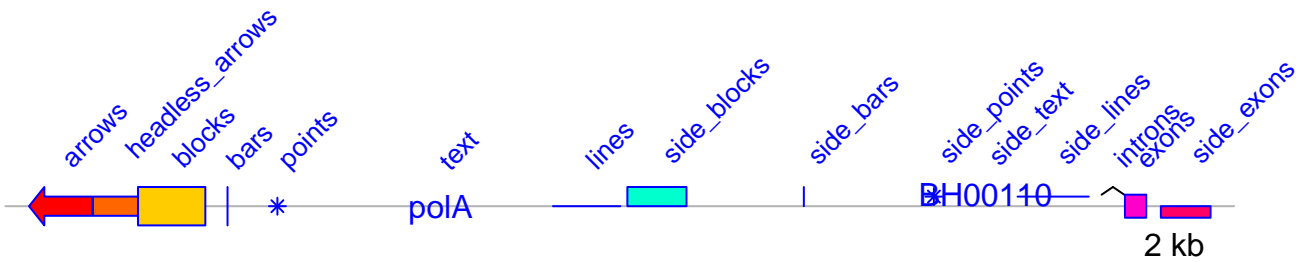
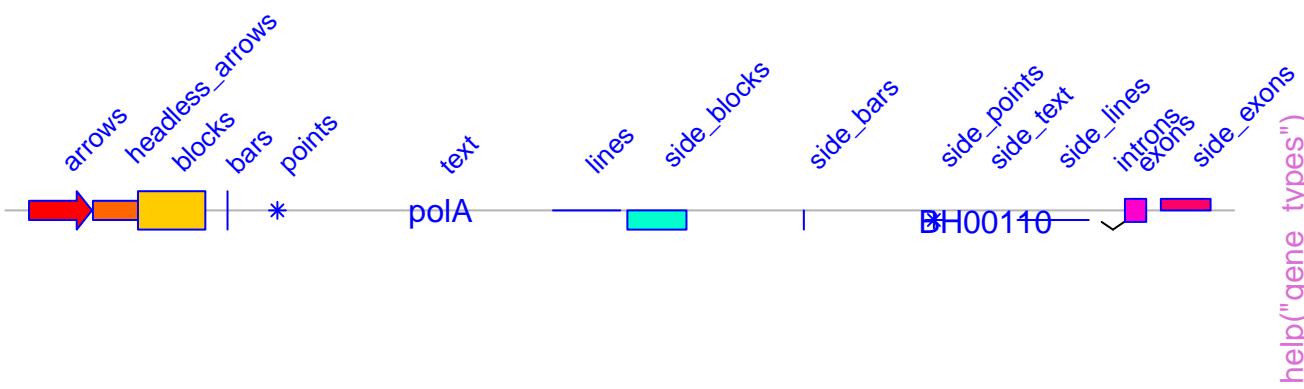


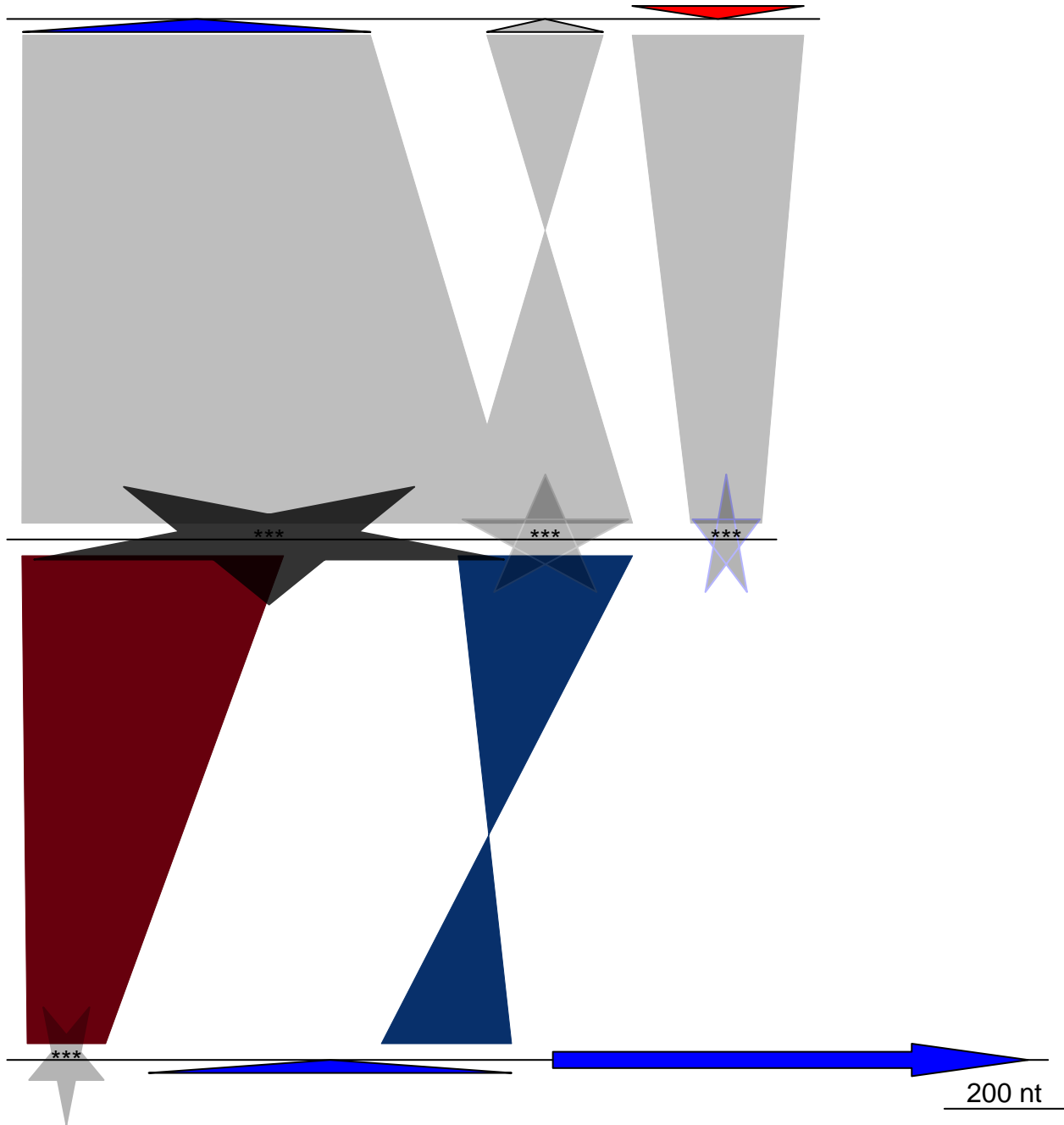
help("chrY_subseg")



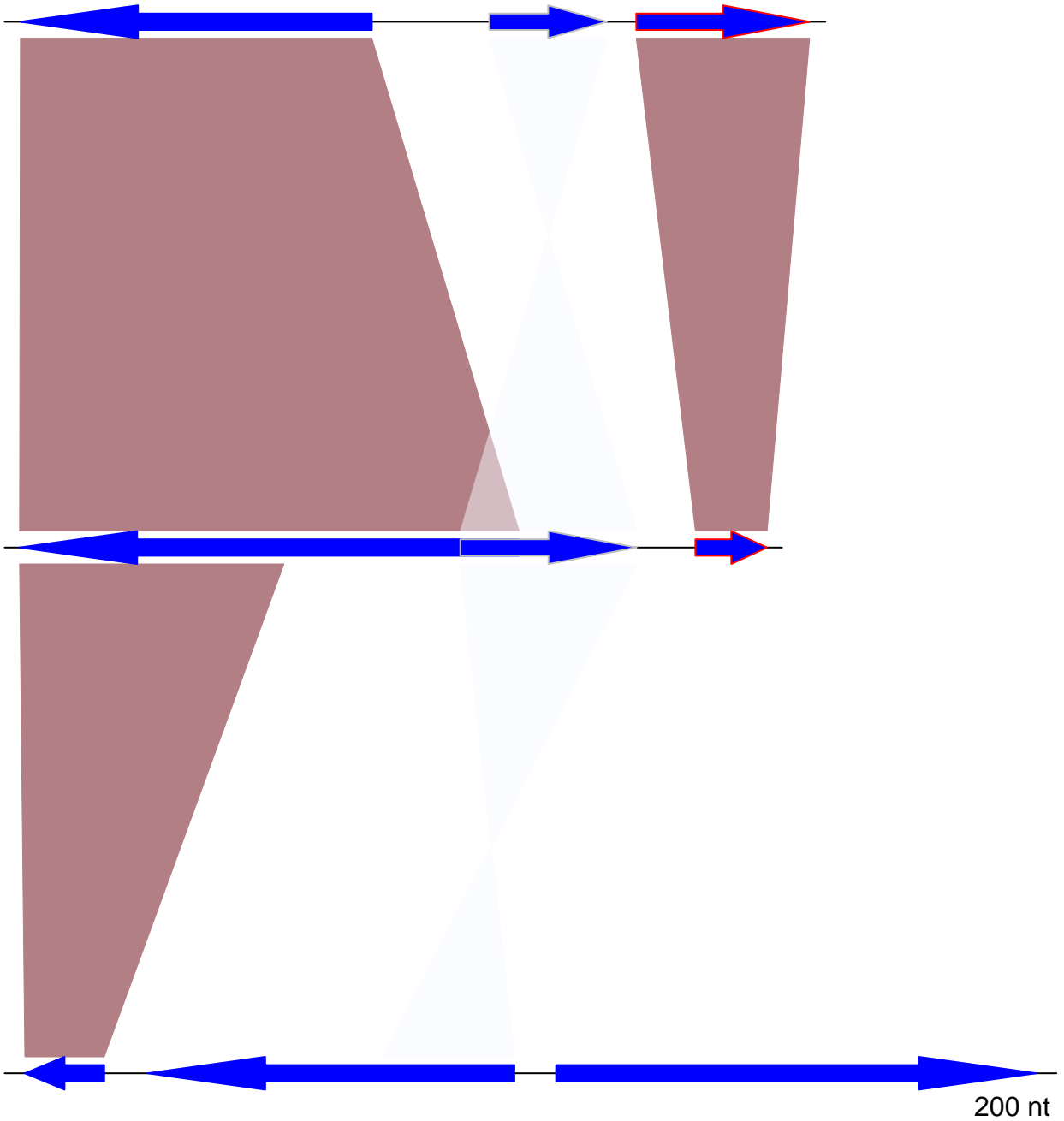
2 kb

help("gene_types")





help("gene_types")



help("genoPlotR-package")

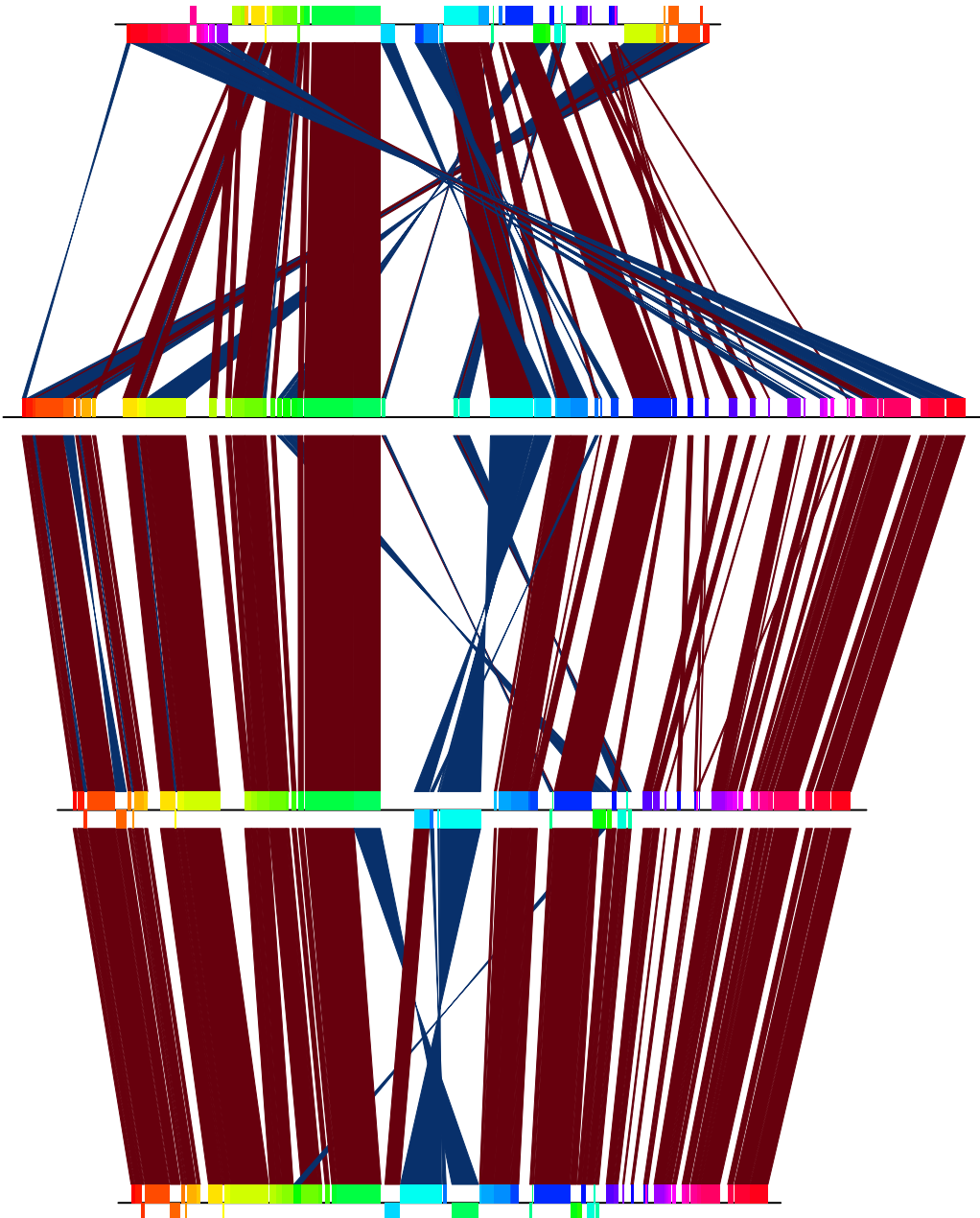
200 nt

B_bacilliformis

B_grahamii

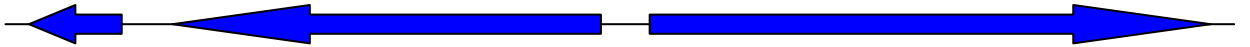
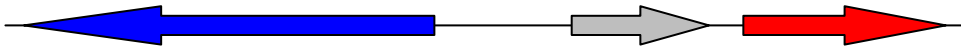
B_henselae

B_quintana



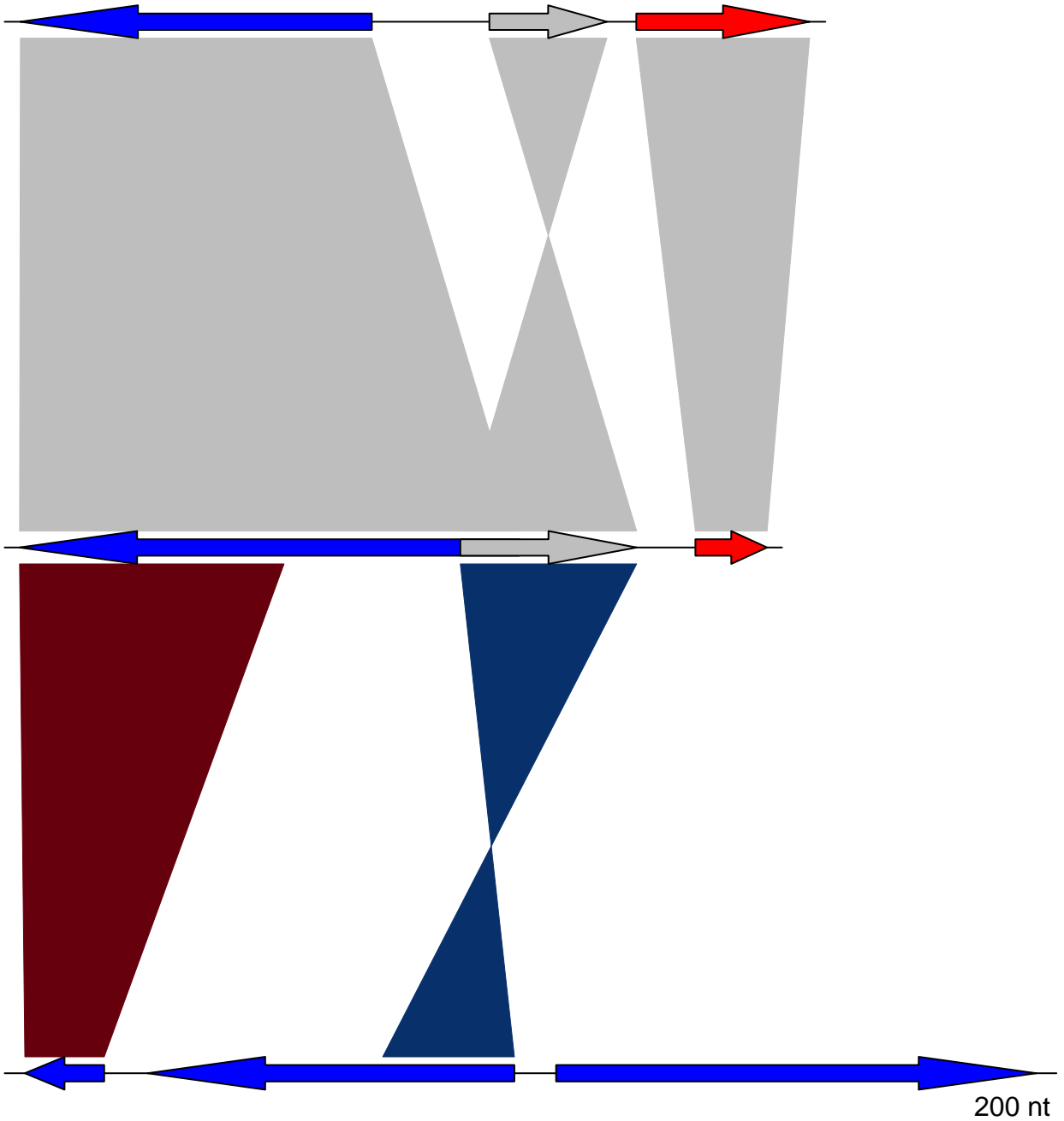
help("mauve.bbone")

500 kb



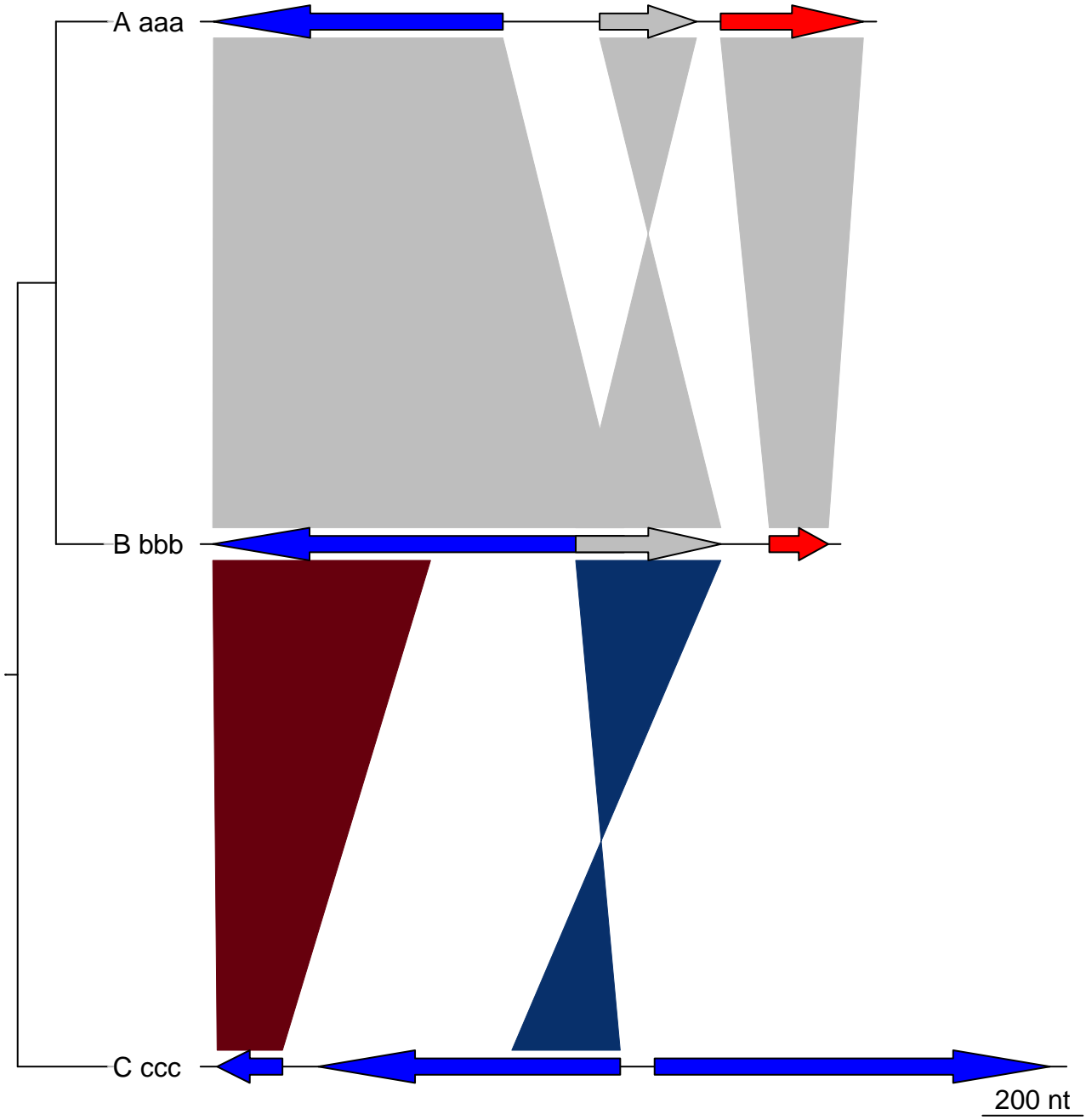
200 nt

help("plot_gene_map")

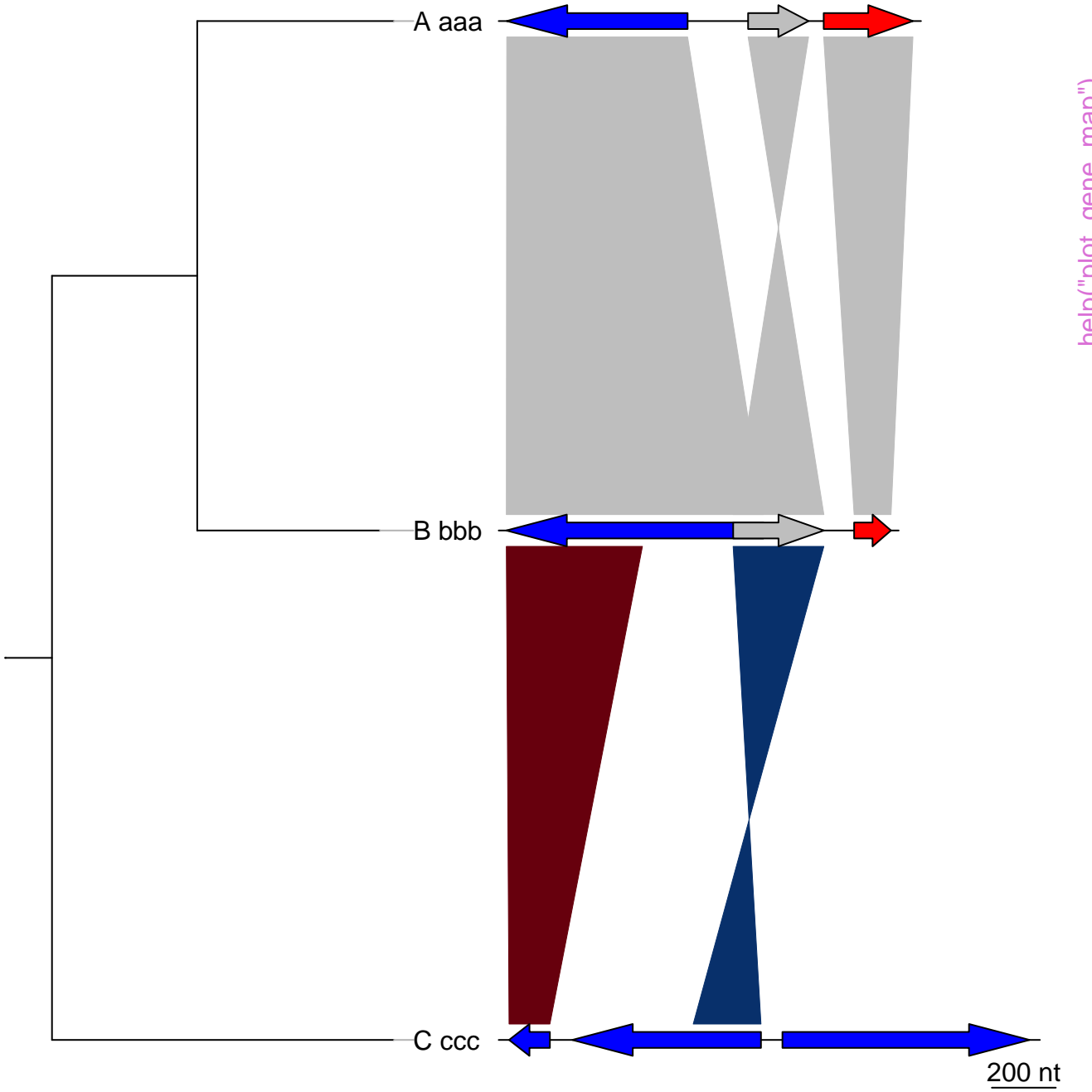


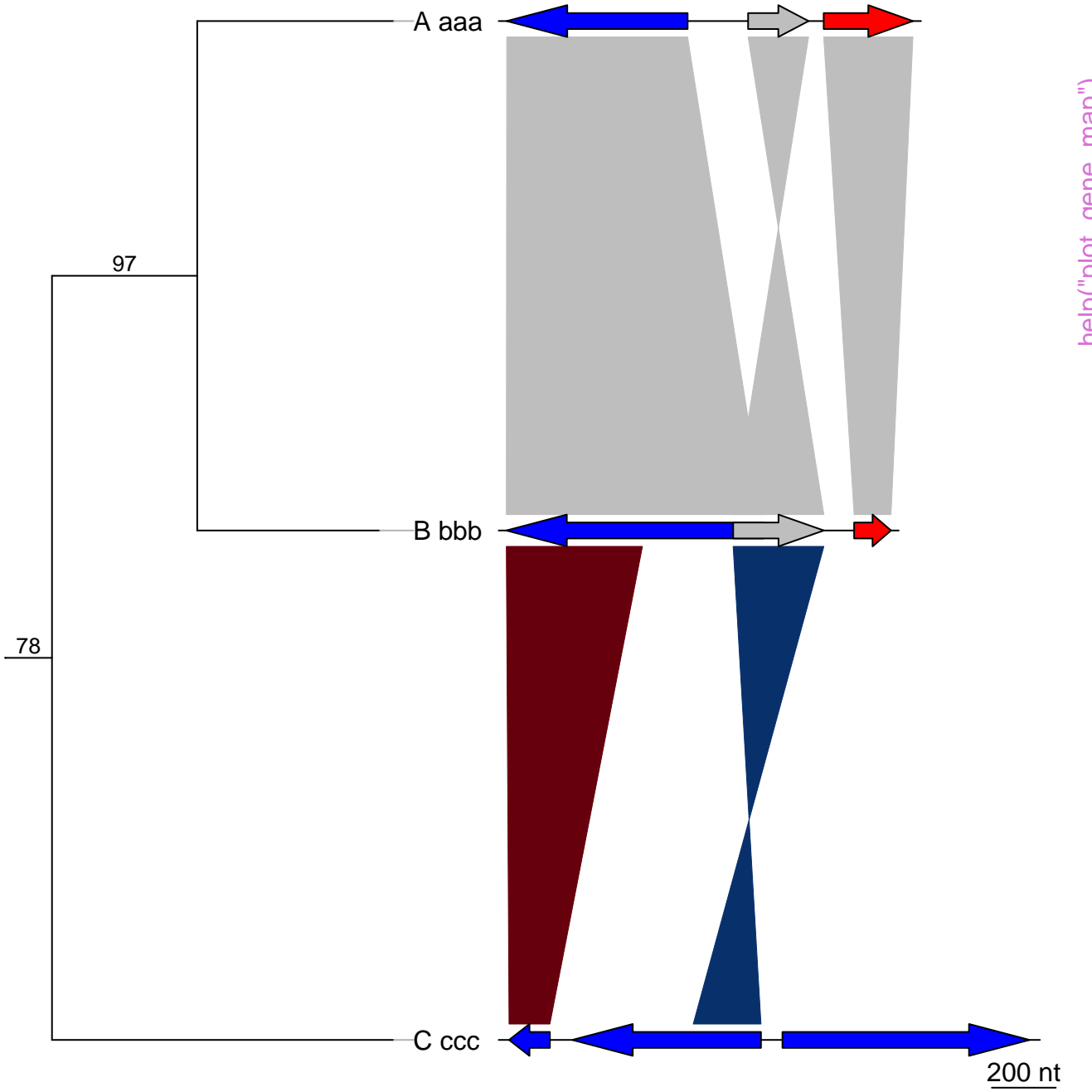
help("plot_gene_map")

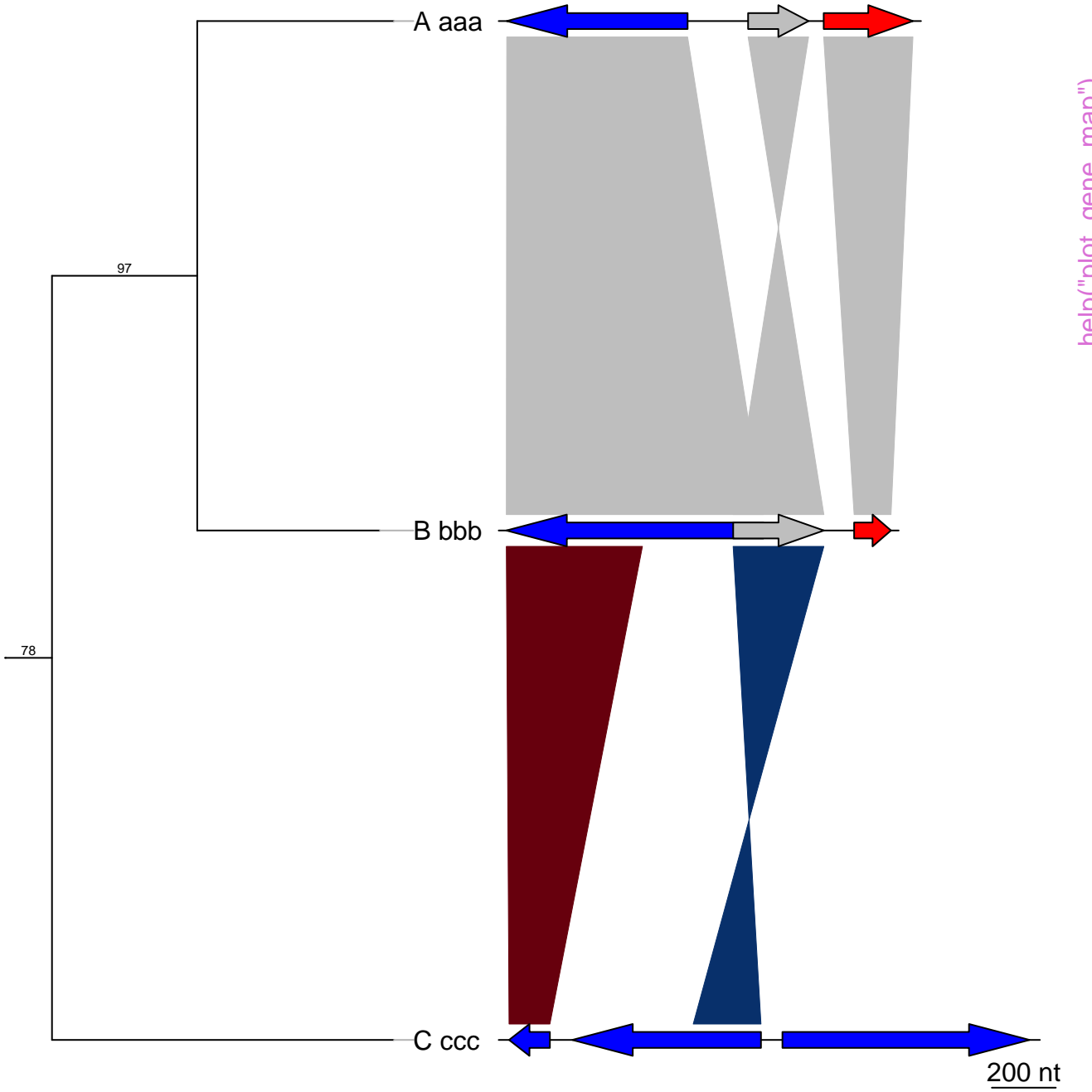
200 nt

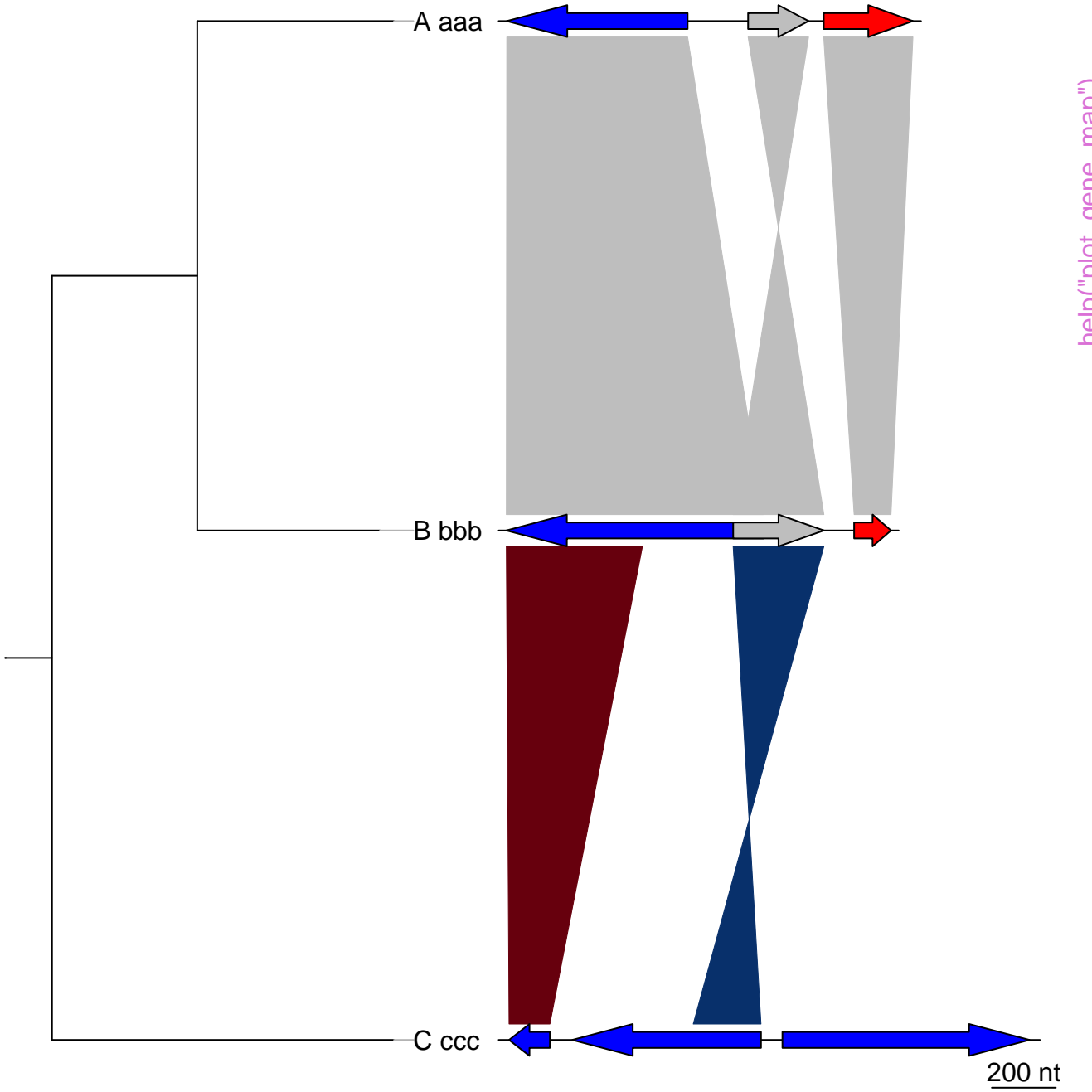


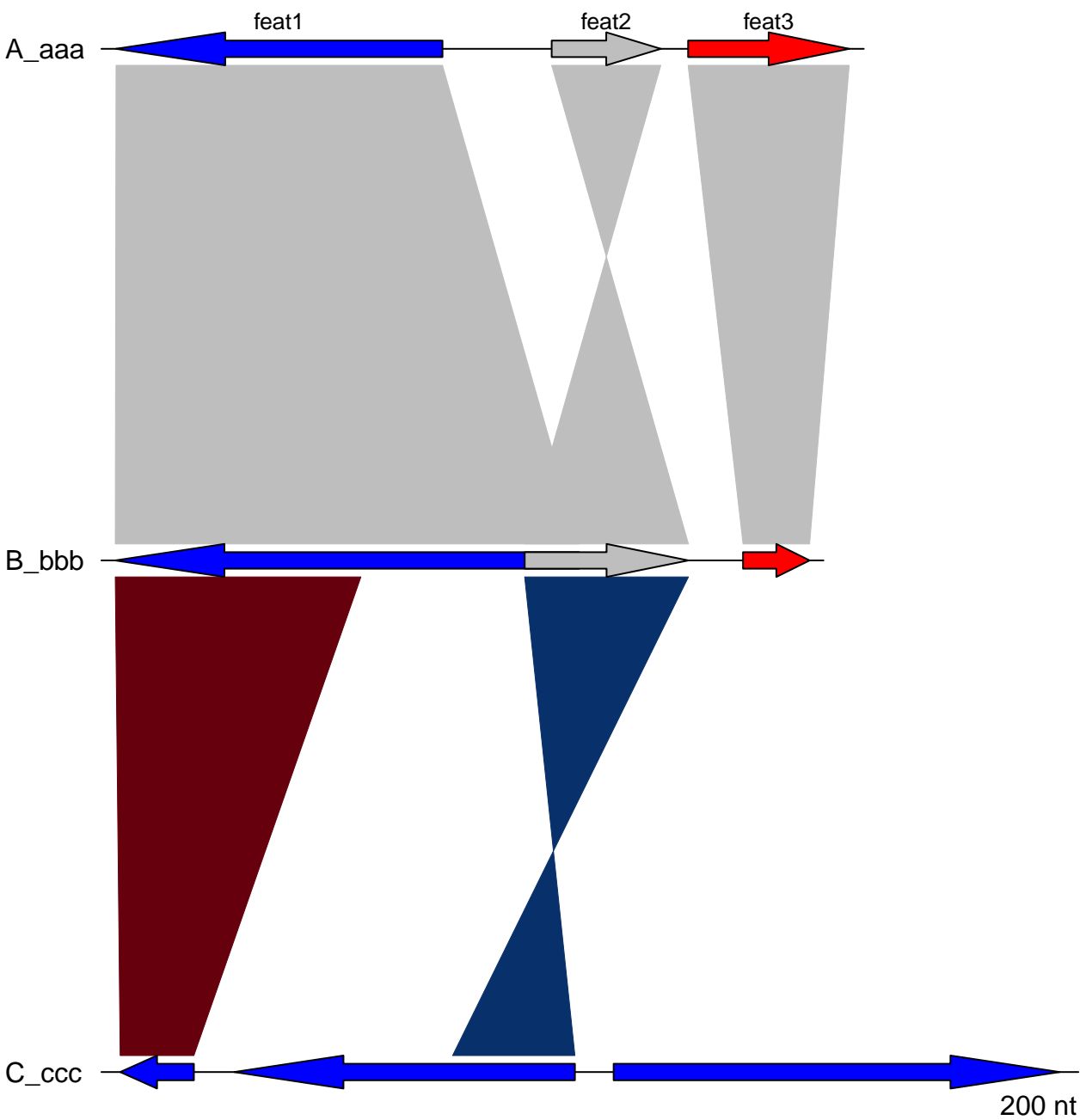
help("plot_gene_map")



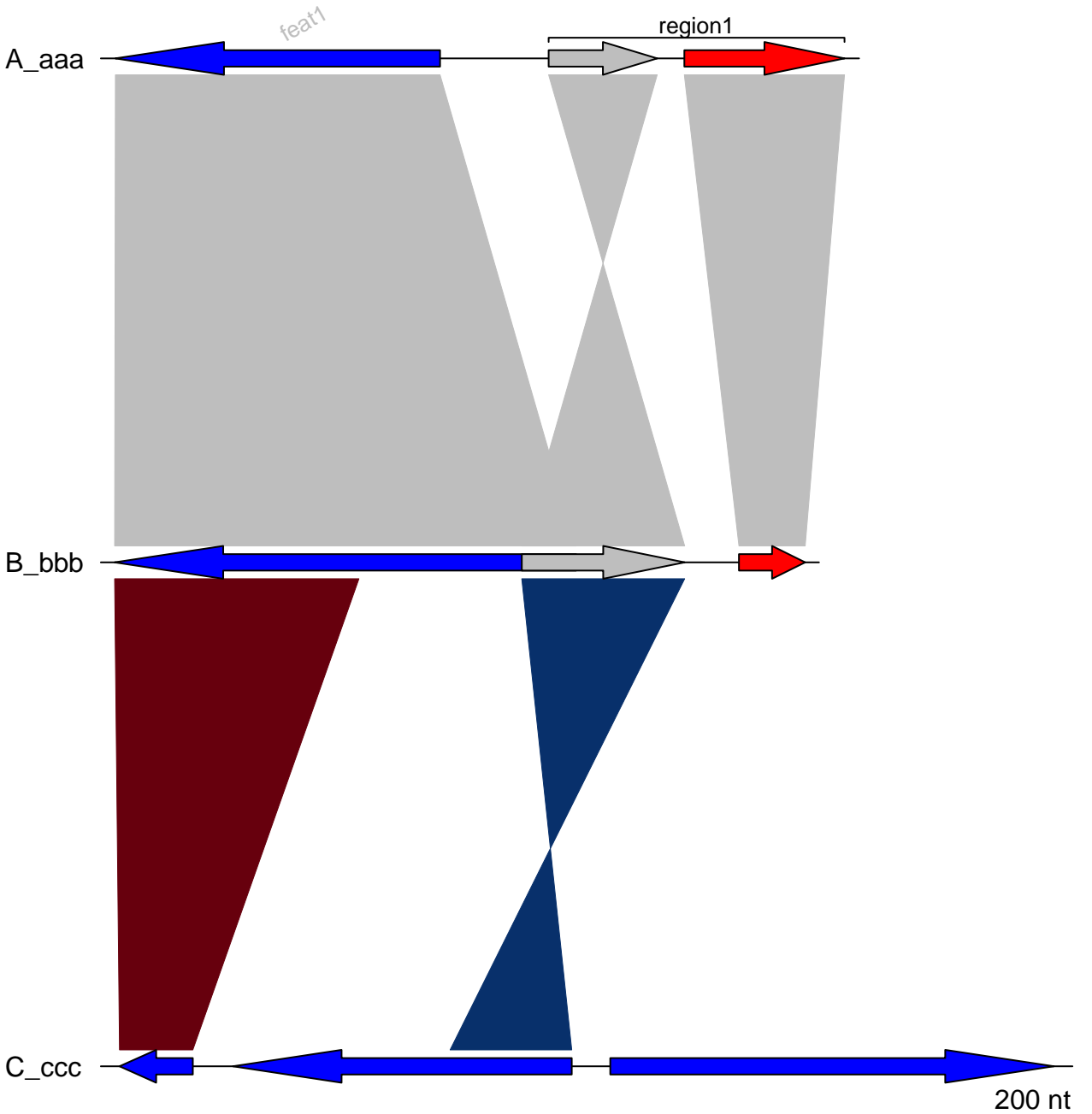






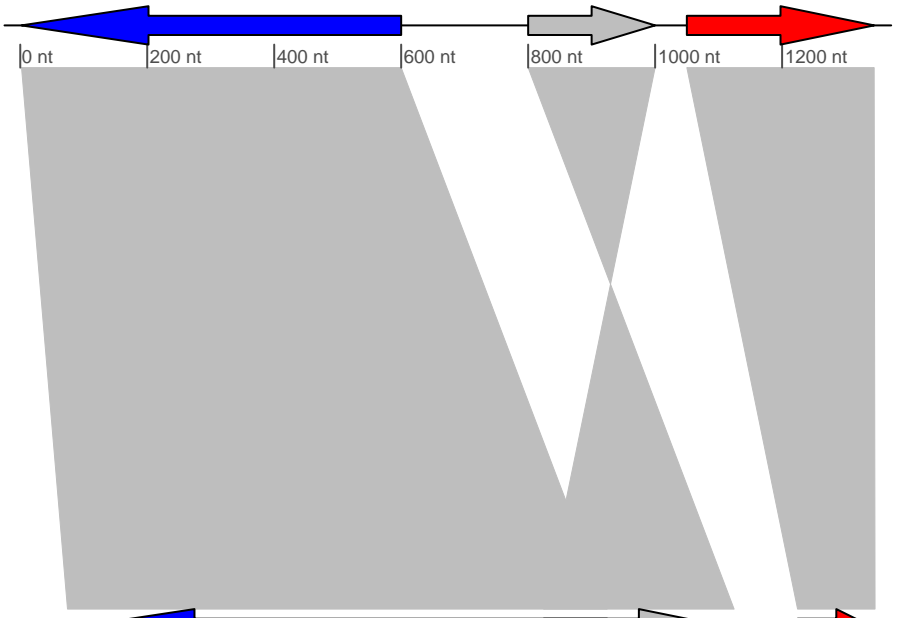


help("plot_gene_map")

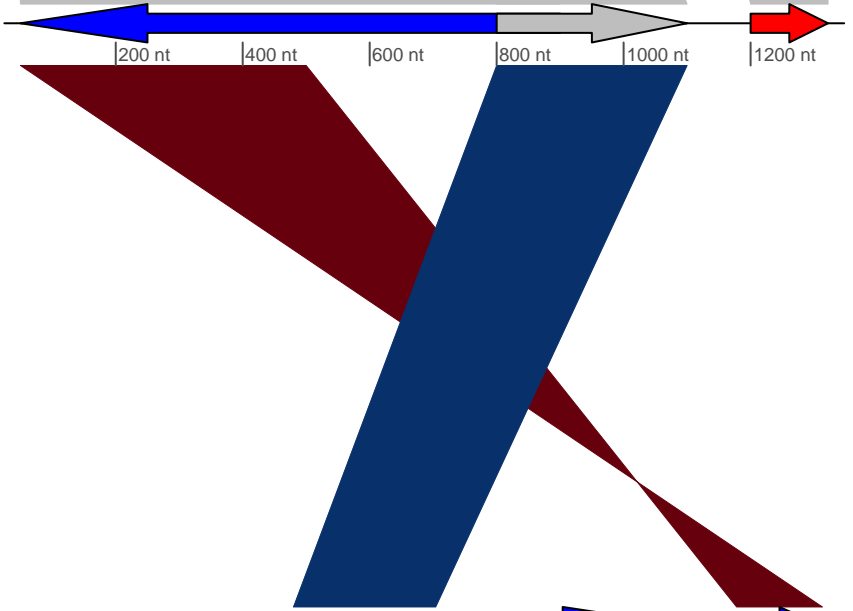


help("plot_gene_map")

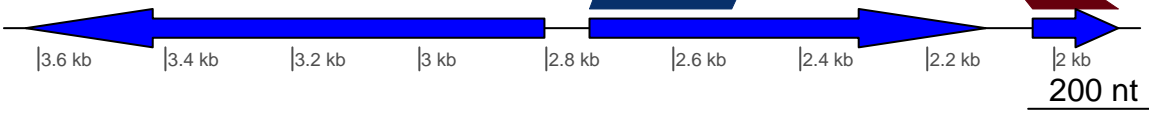
A_aaa



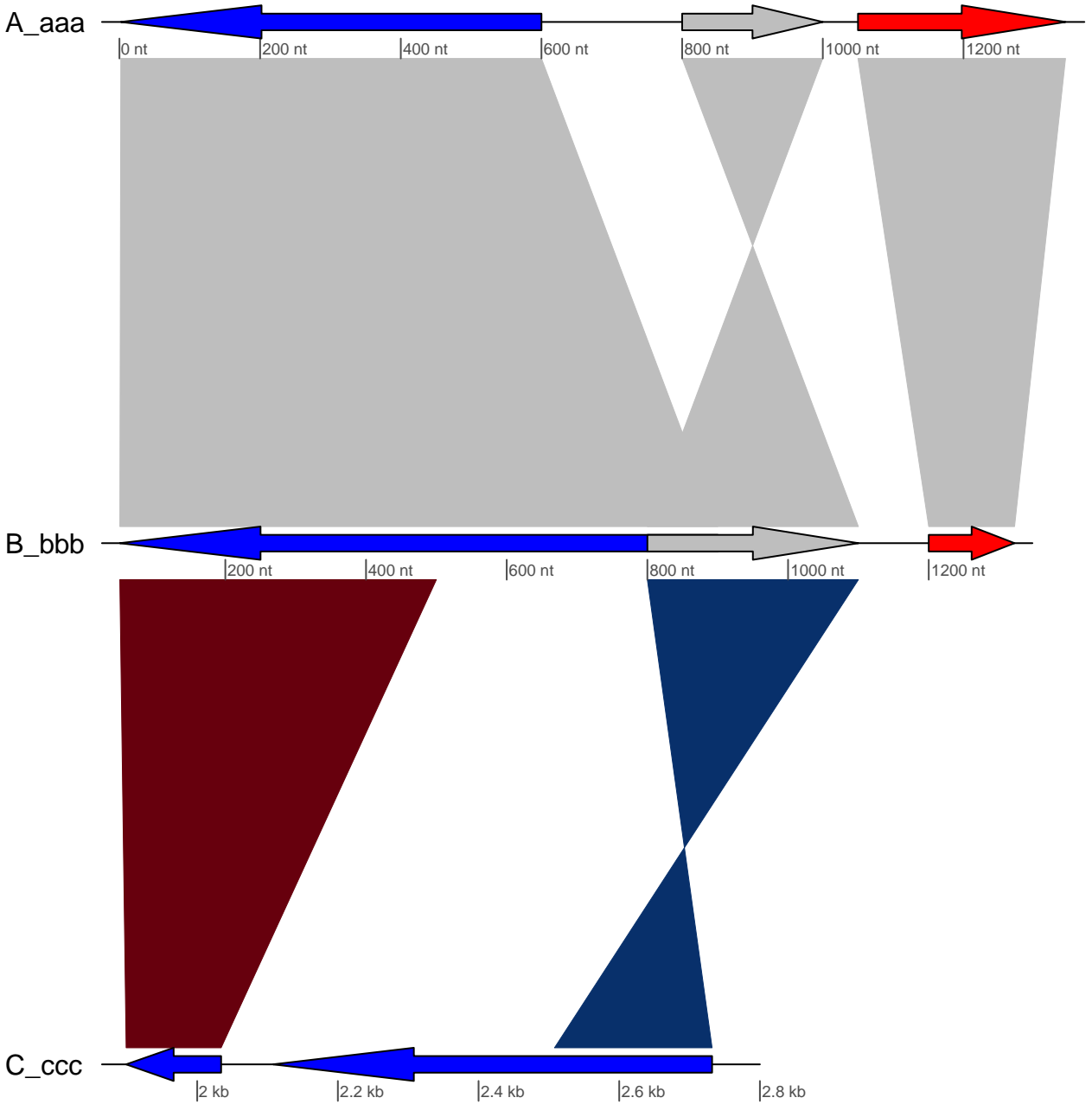
B_bbb



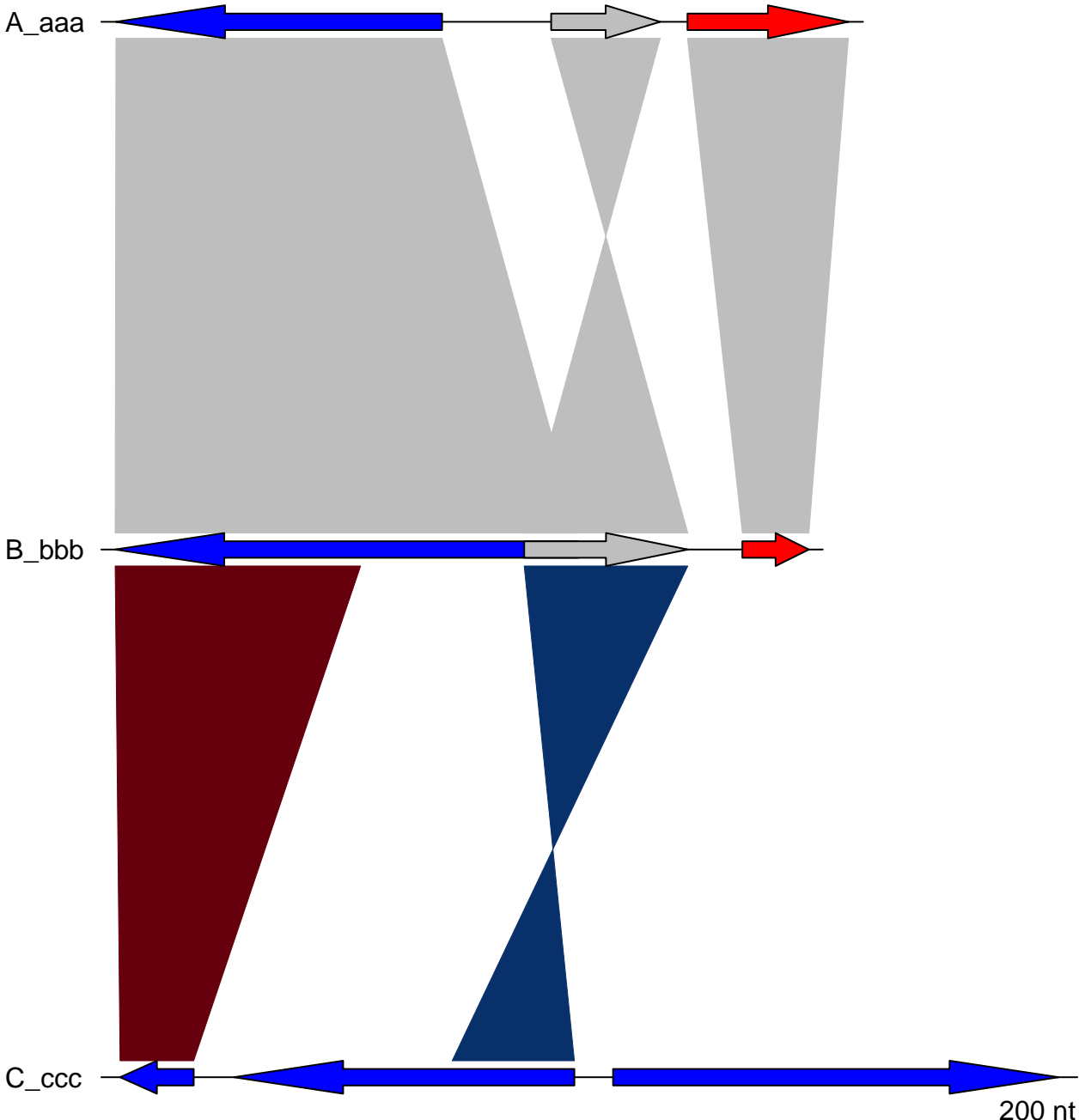
C_ccc



help("plot_gene_map")

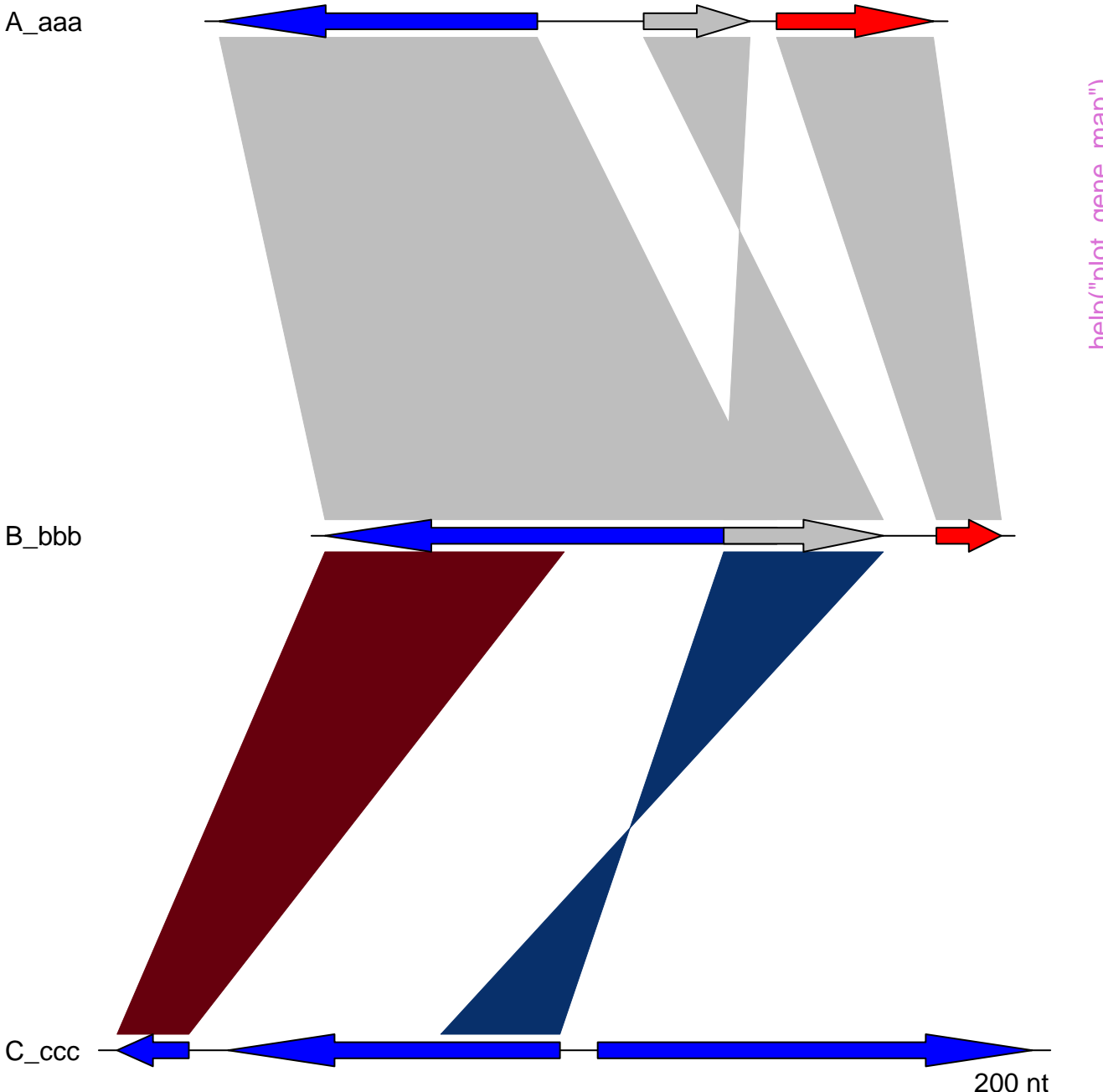


help("plot_gene_map")

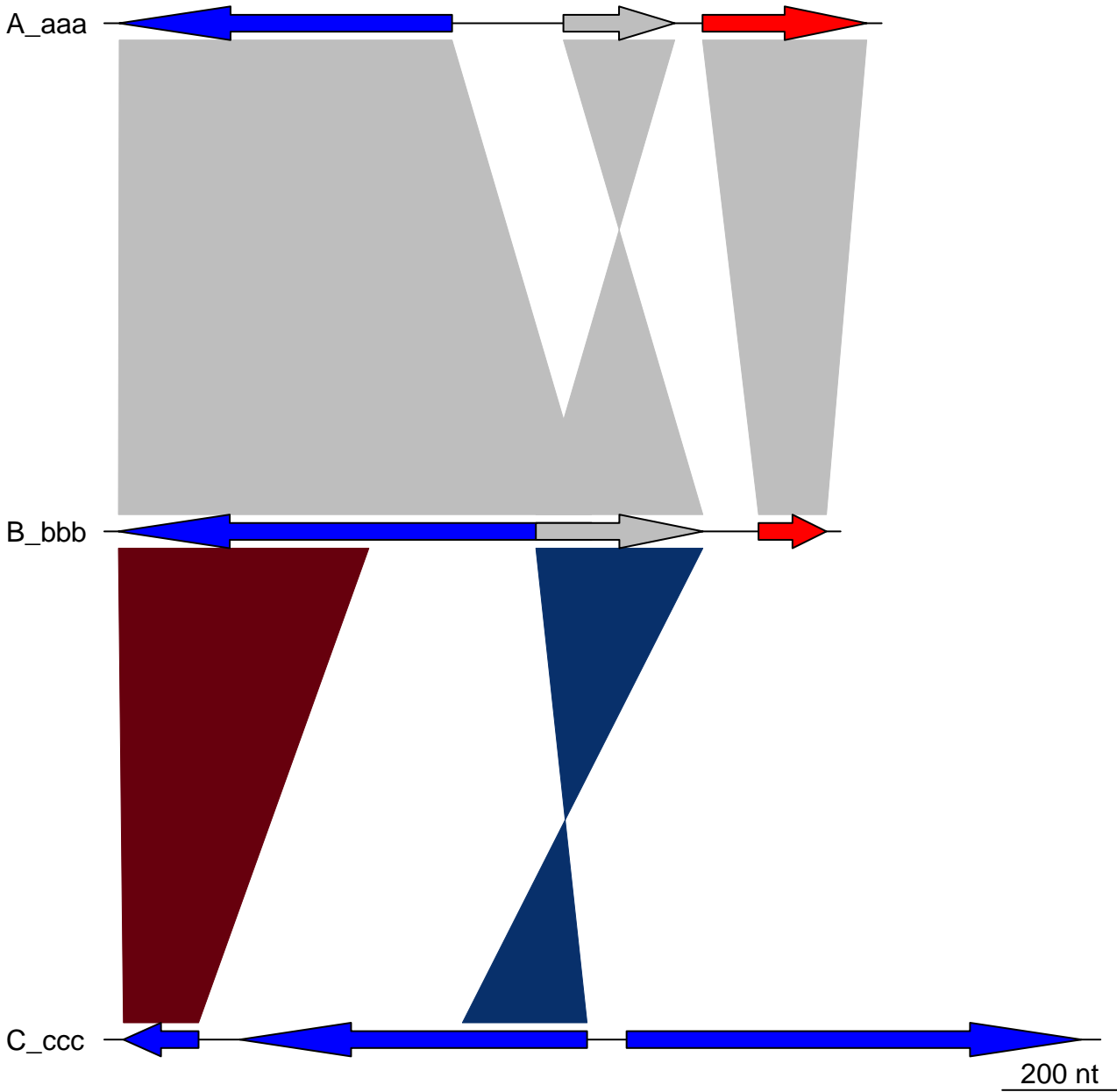


help("plot_gene_map")

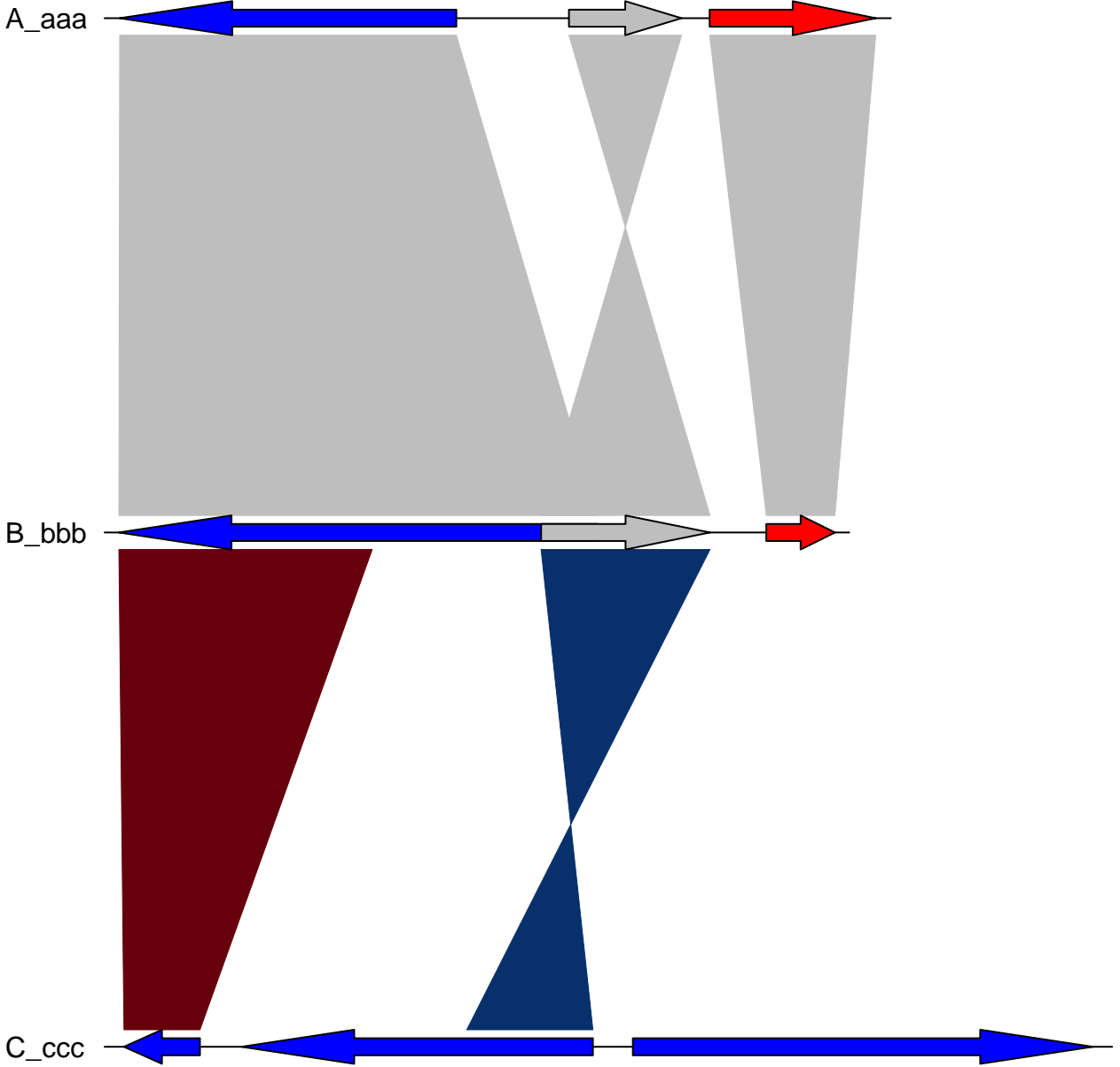
200 nt



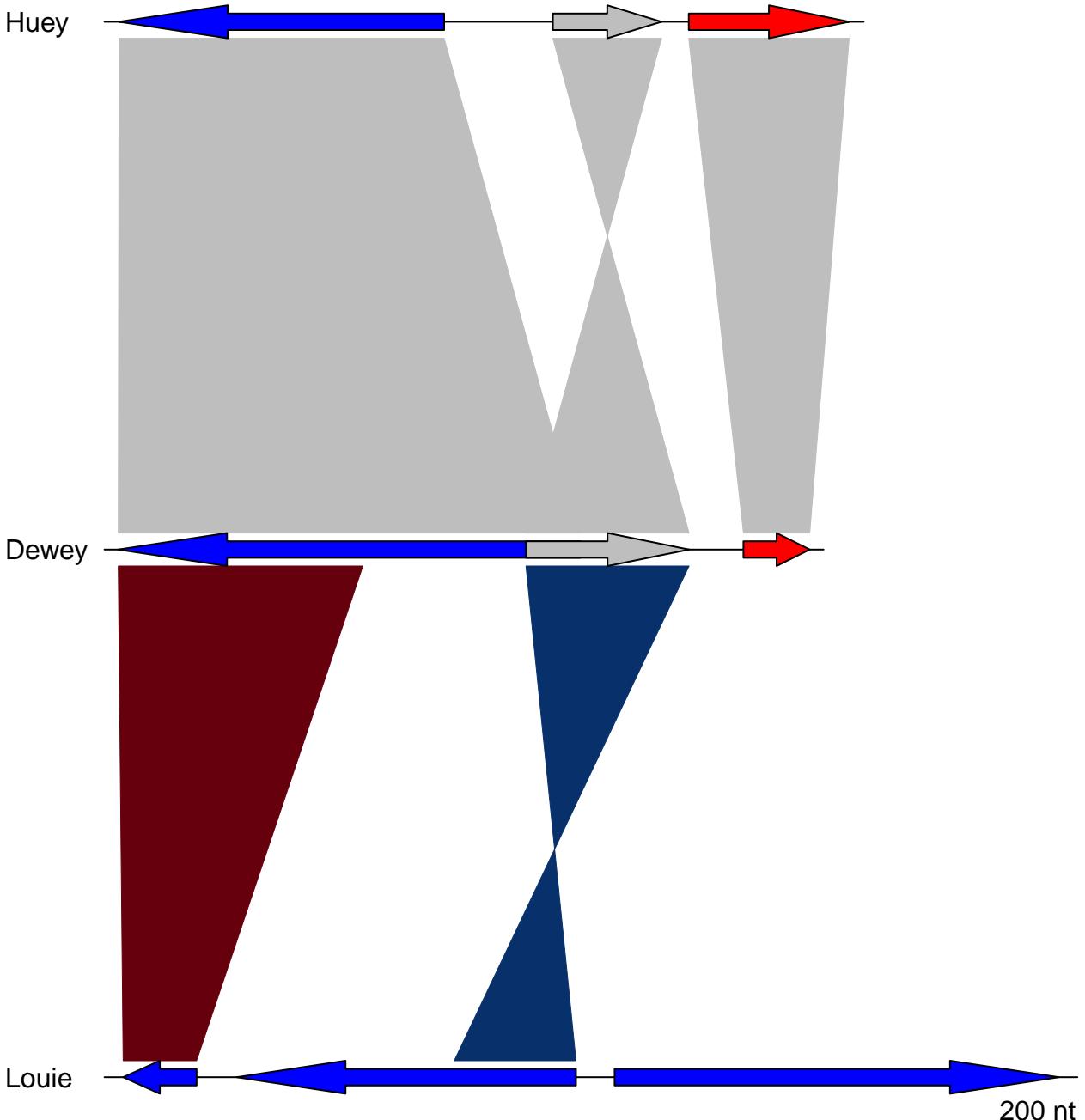
Comparison of A, B and C



Comparison of A, B and C



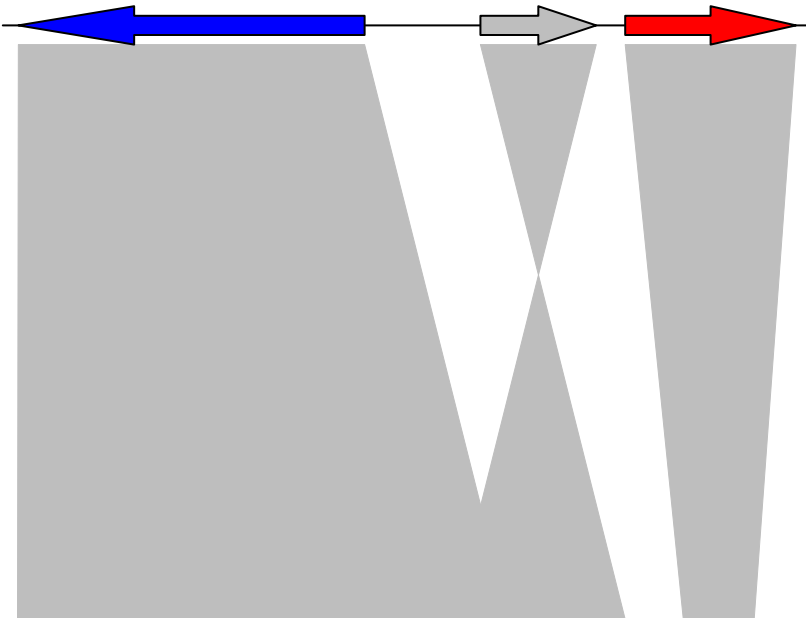
help("plot_gene_map")



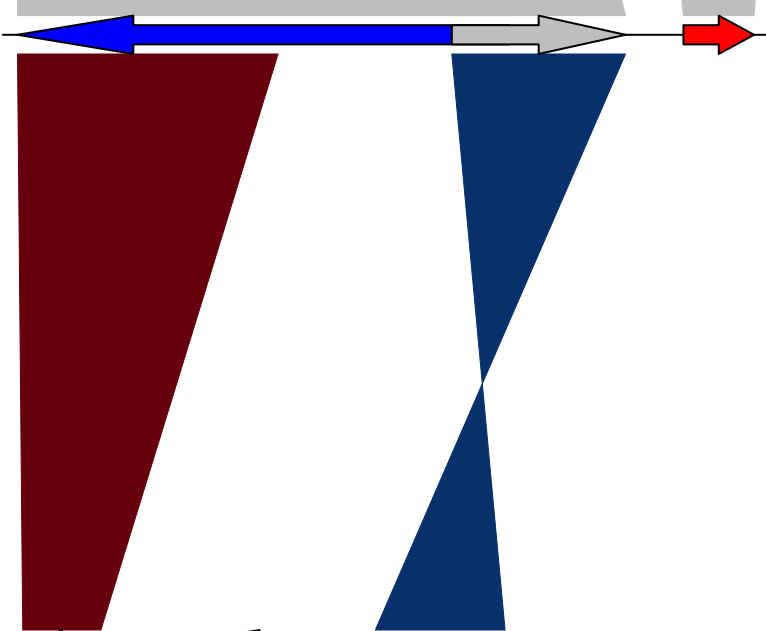
help("plot_gene_map")

200 nt

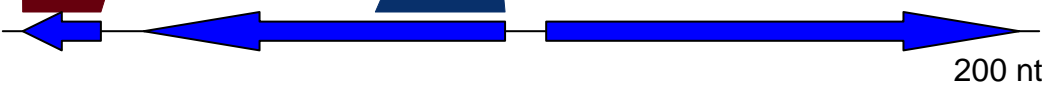
Huey



Dewey

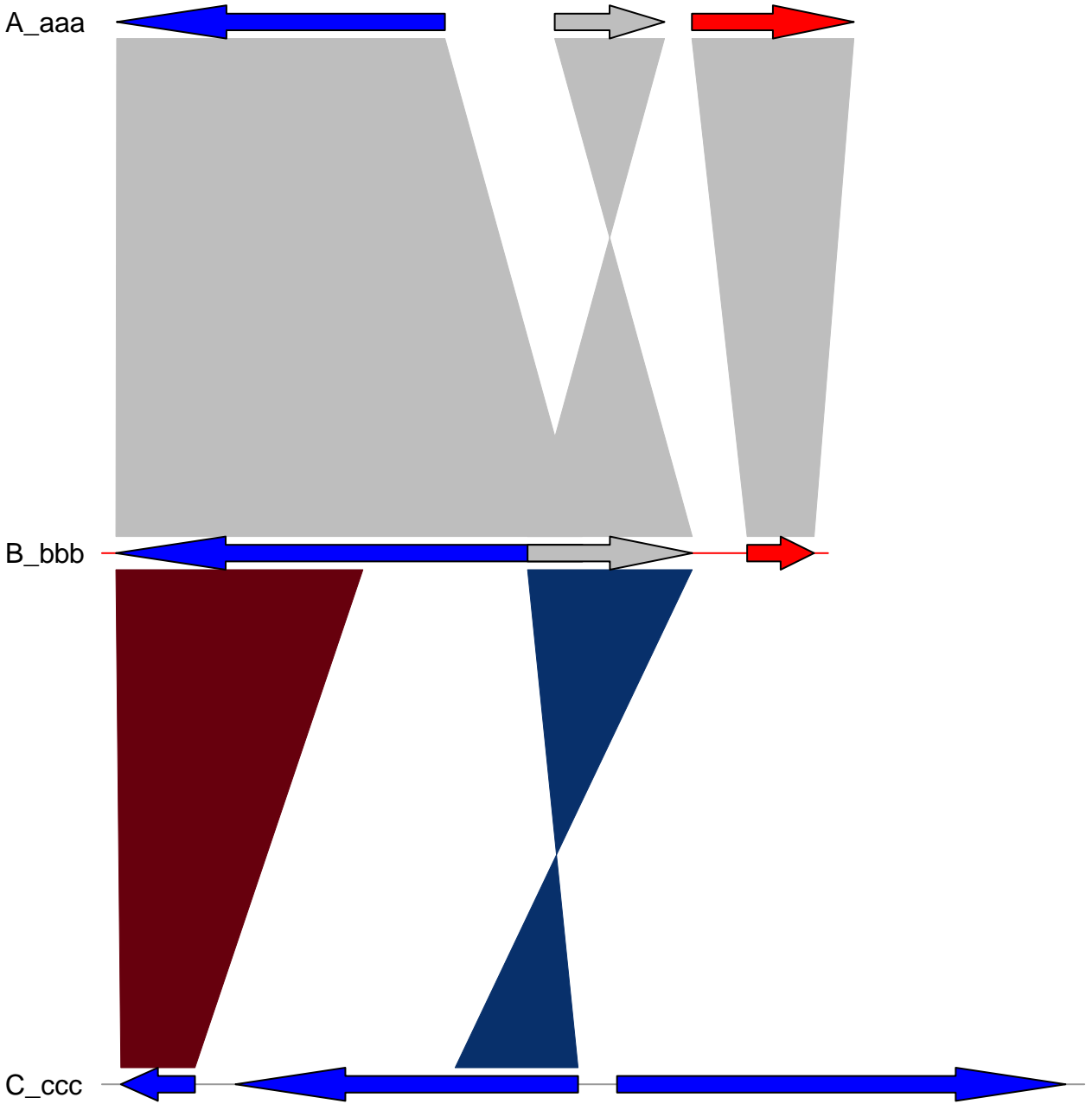


Louie



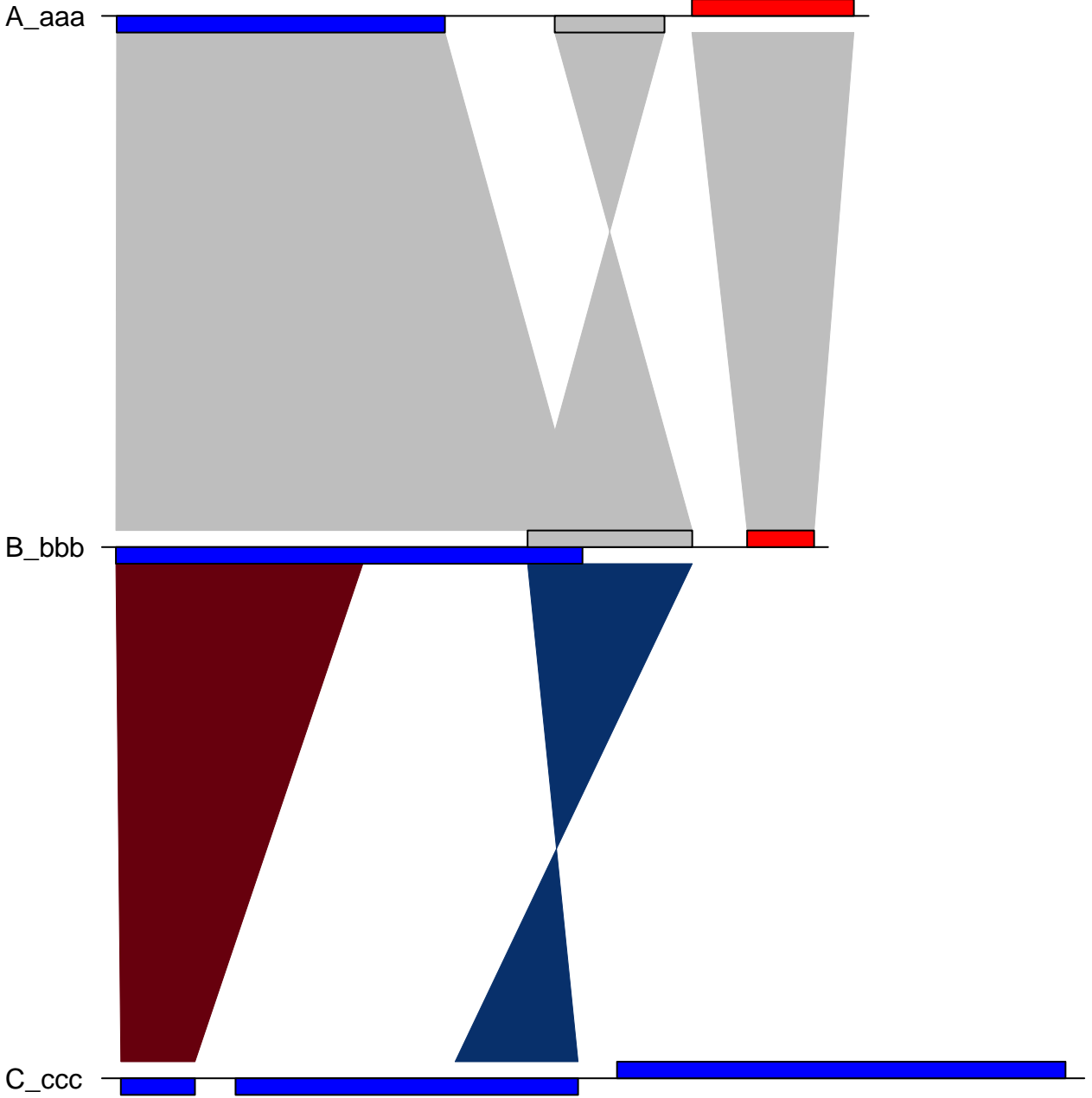
200 nt

help("plot_gene_map")



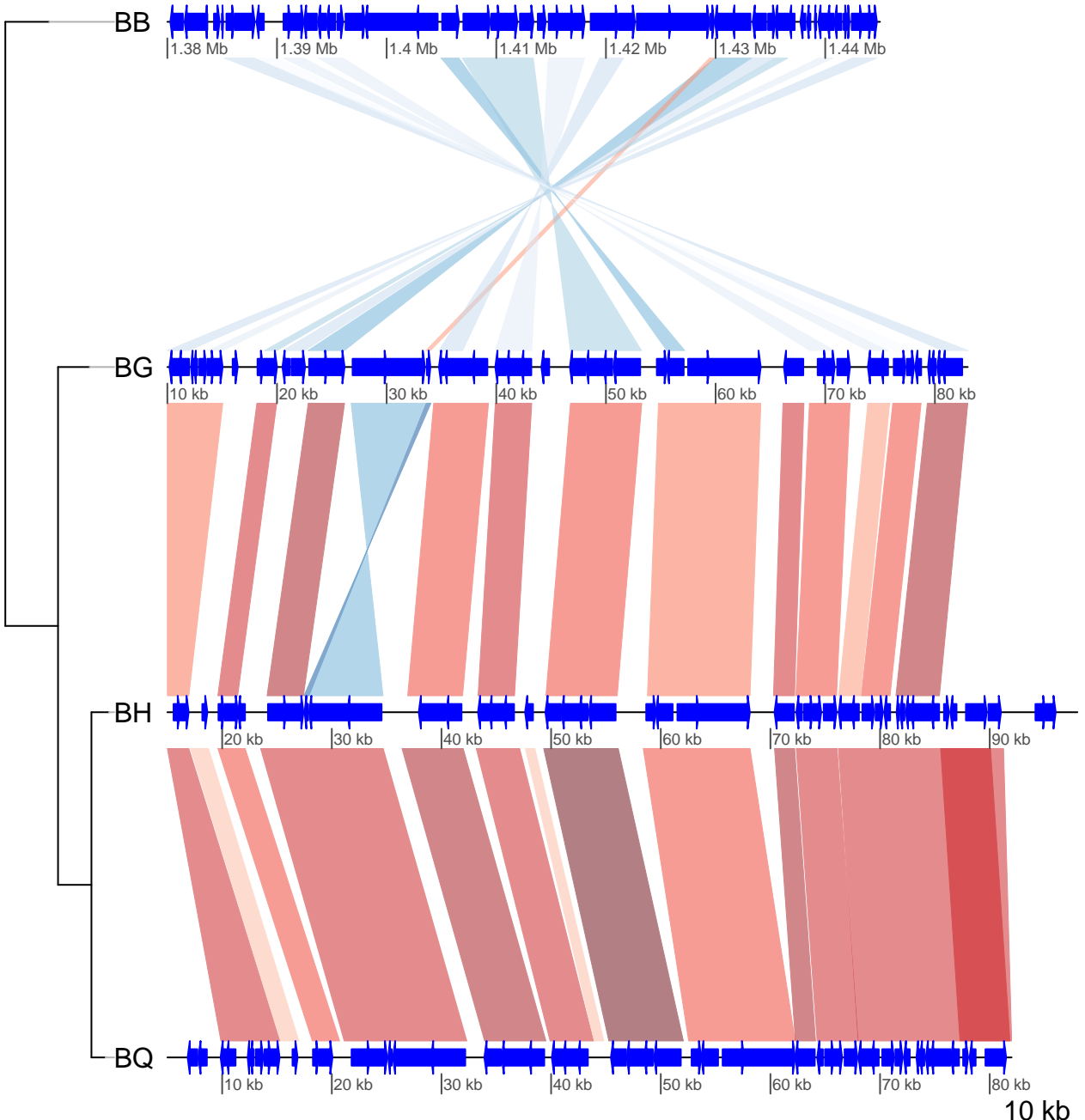
help("plot_gene_map")

200 nt

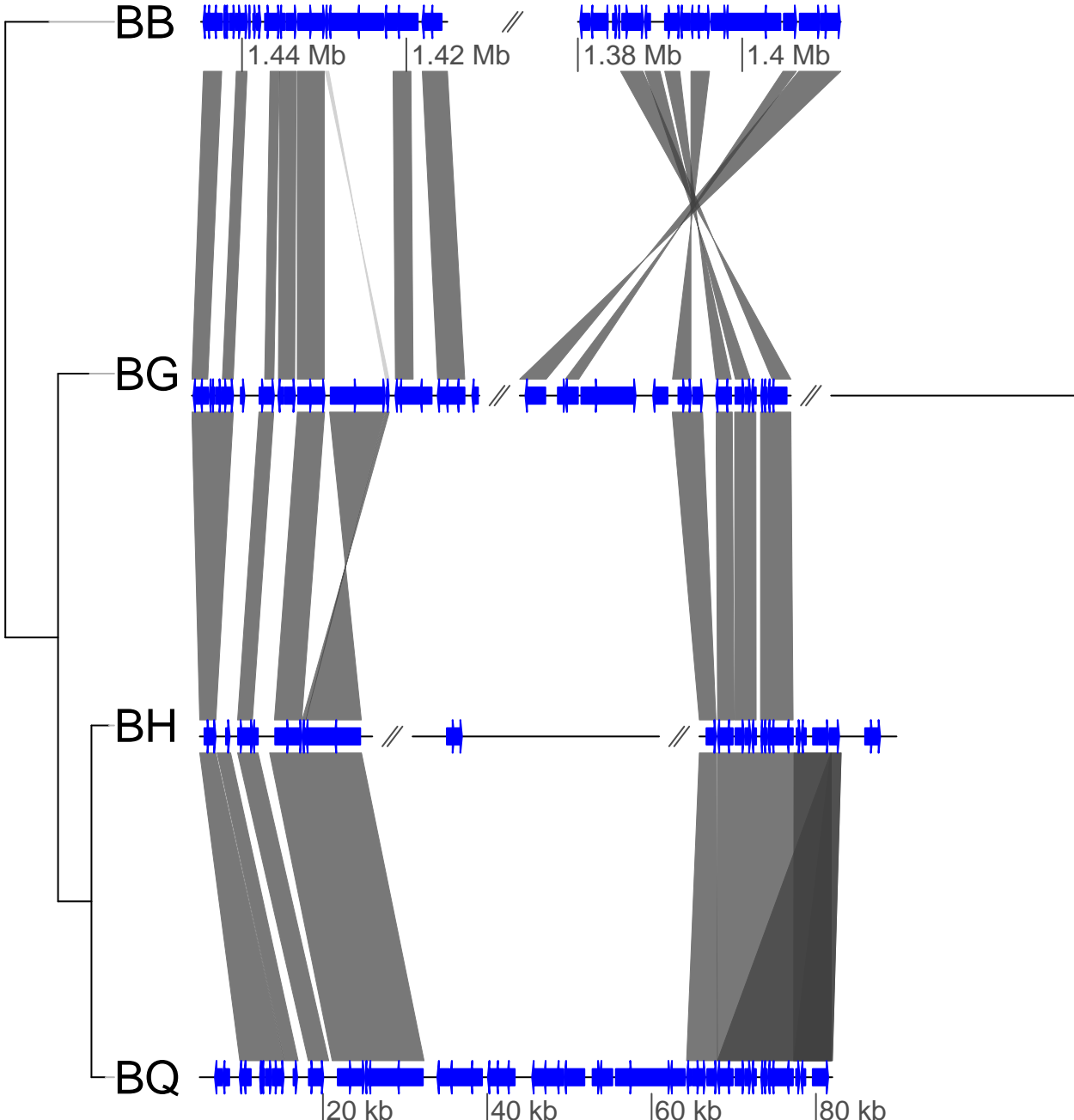


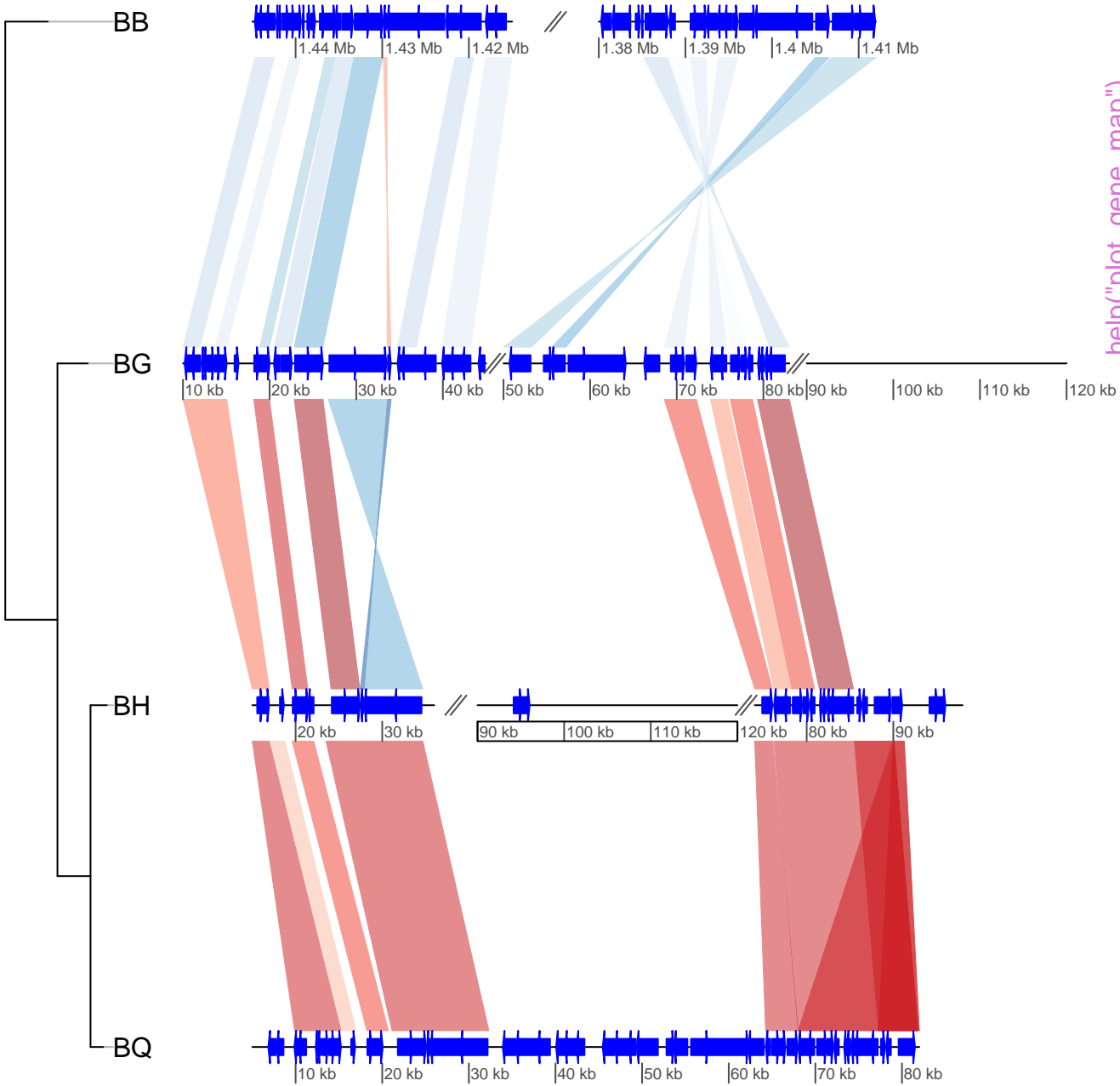
help("plot_gene_map")

200 nt

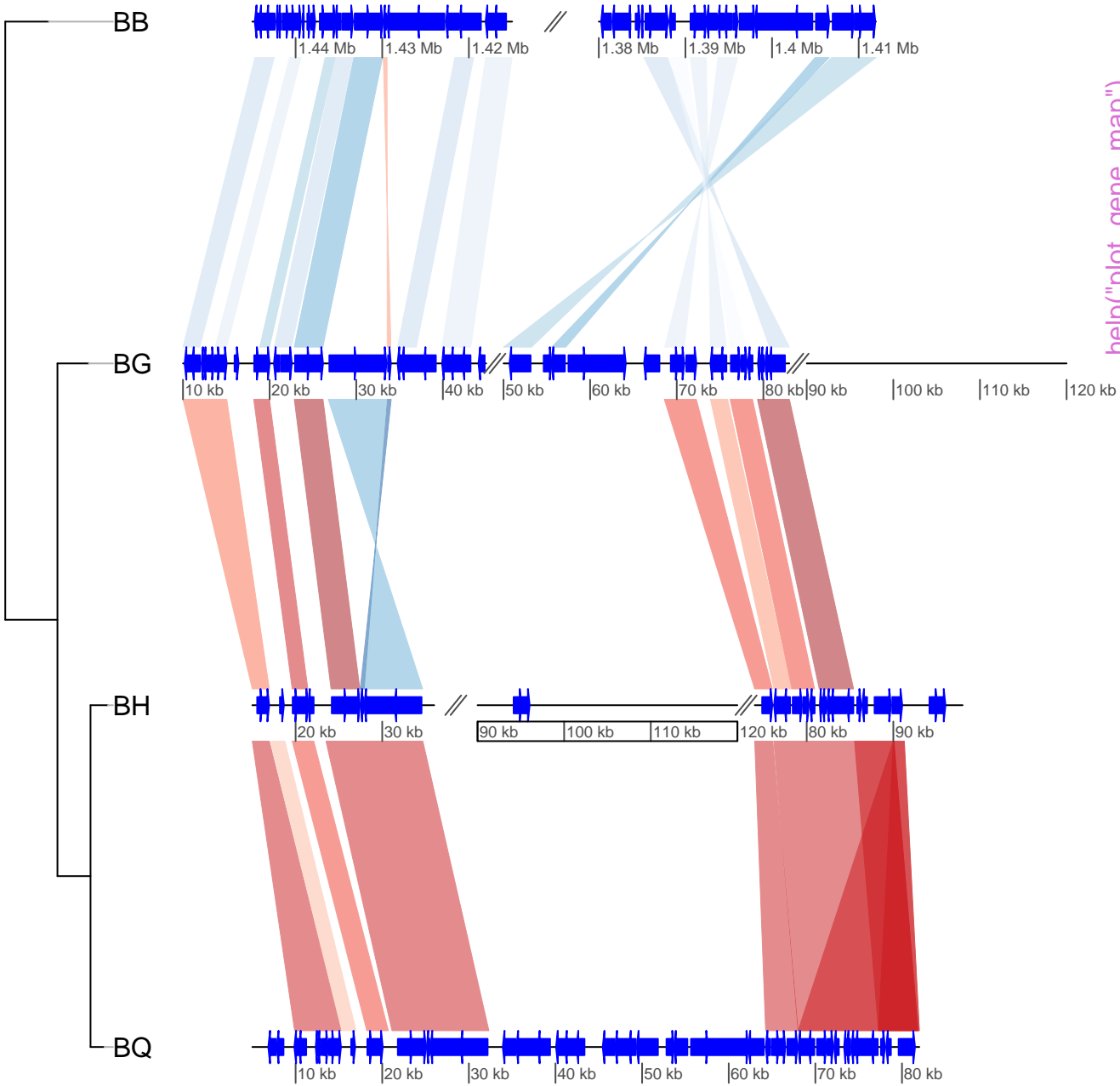


help("plot_gene_map")



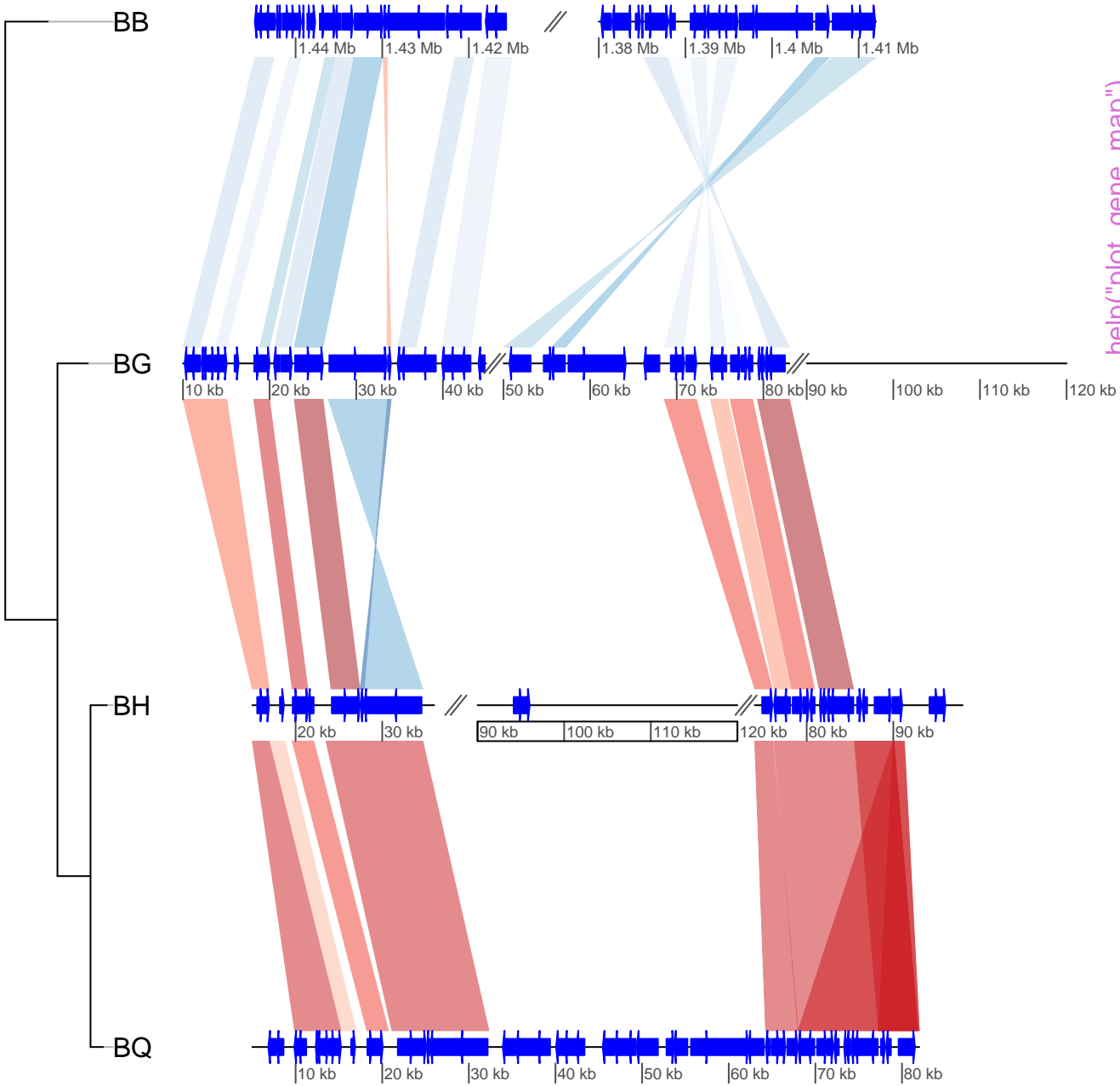


10 kb

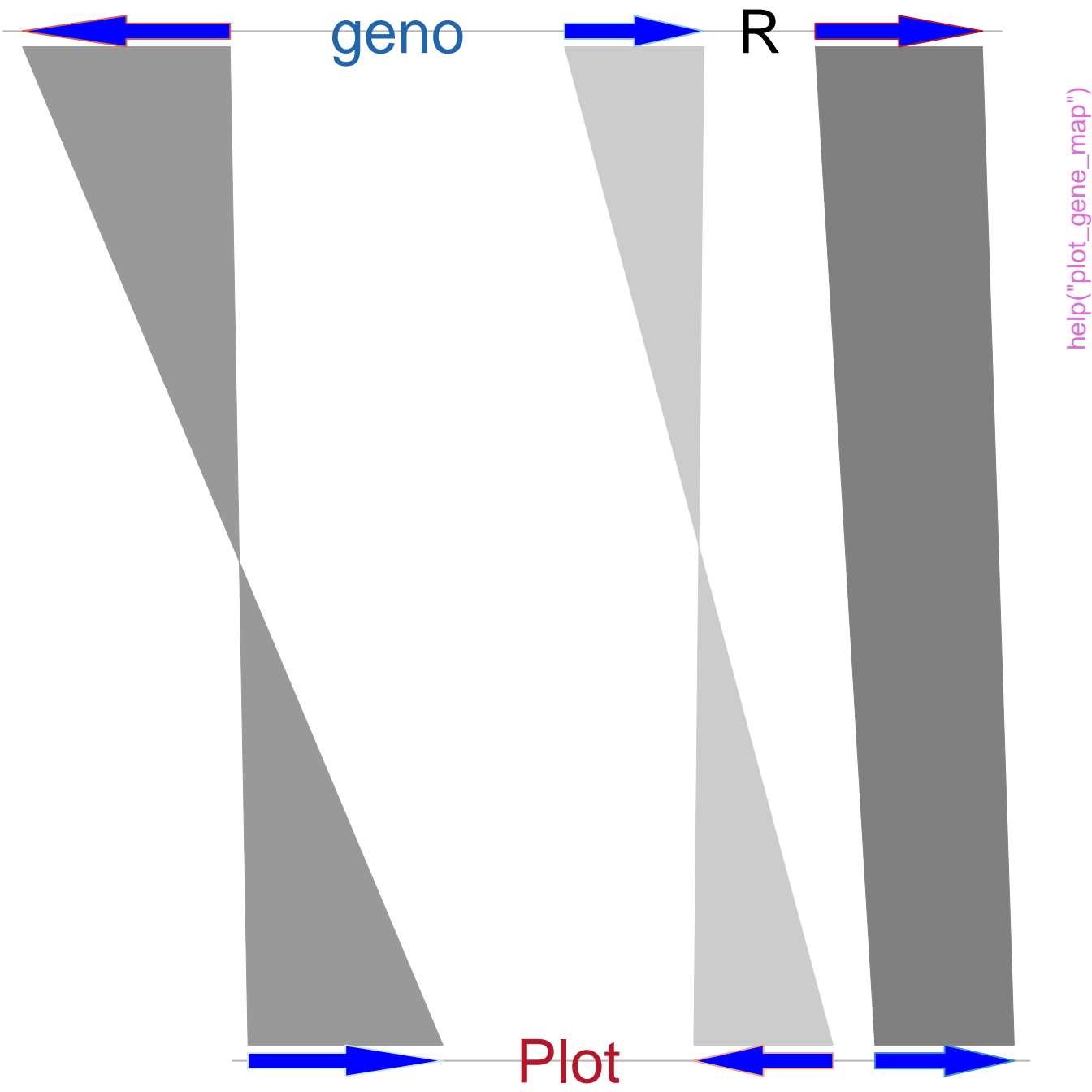


help("plot_gene_map")

10 kb



10 kb

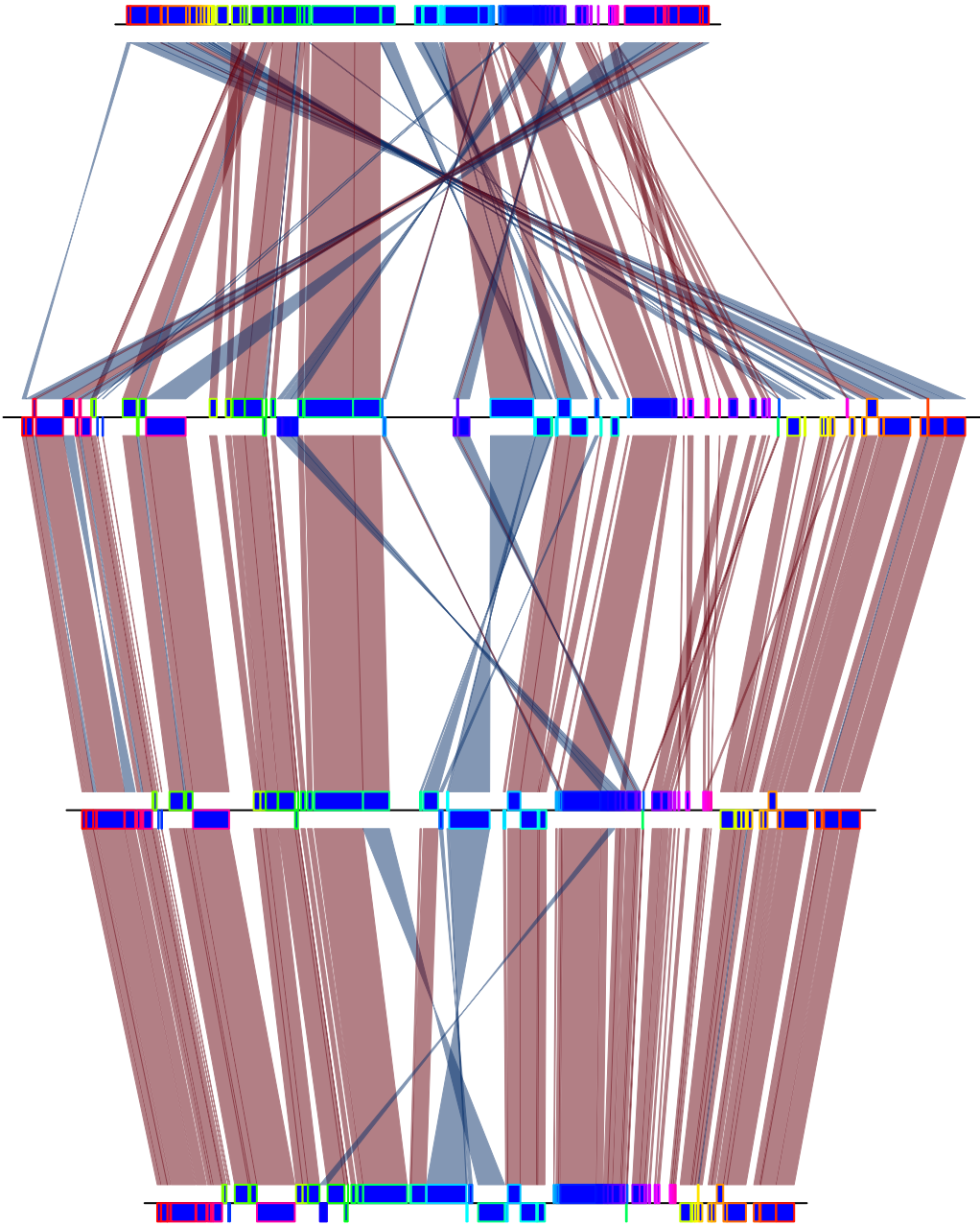


B_bacilliformis

B_grahamii

B_henselae

B_quintana



help("read_functions")

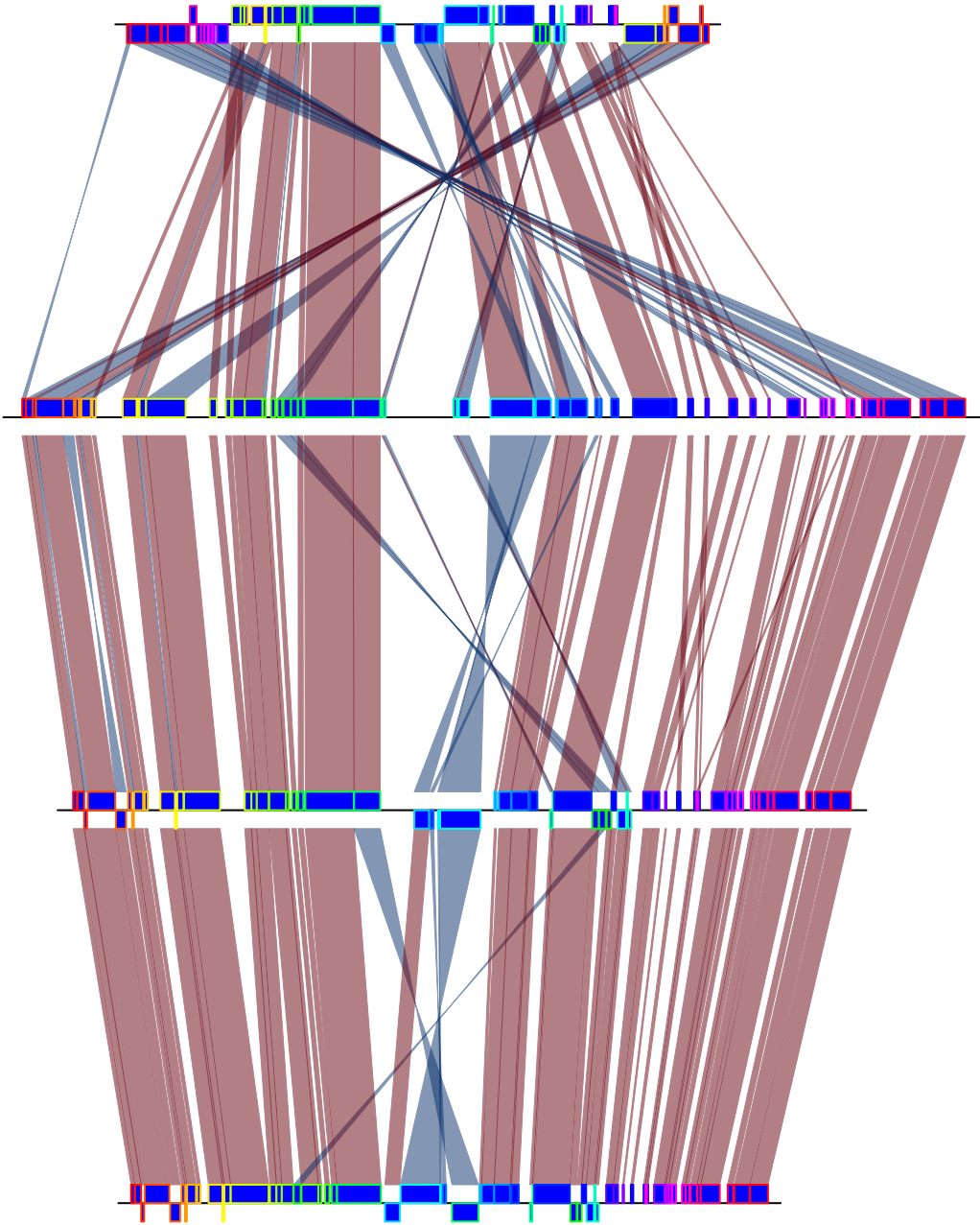
500 kb

B_bacilliformis

B_grahamii

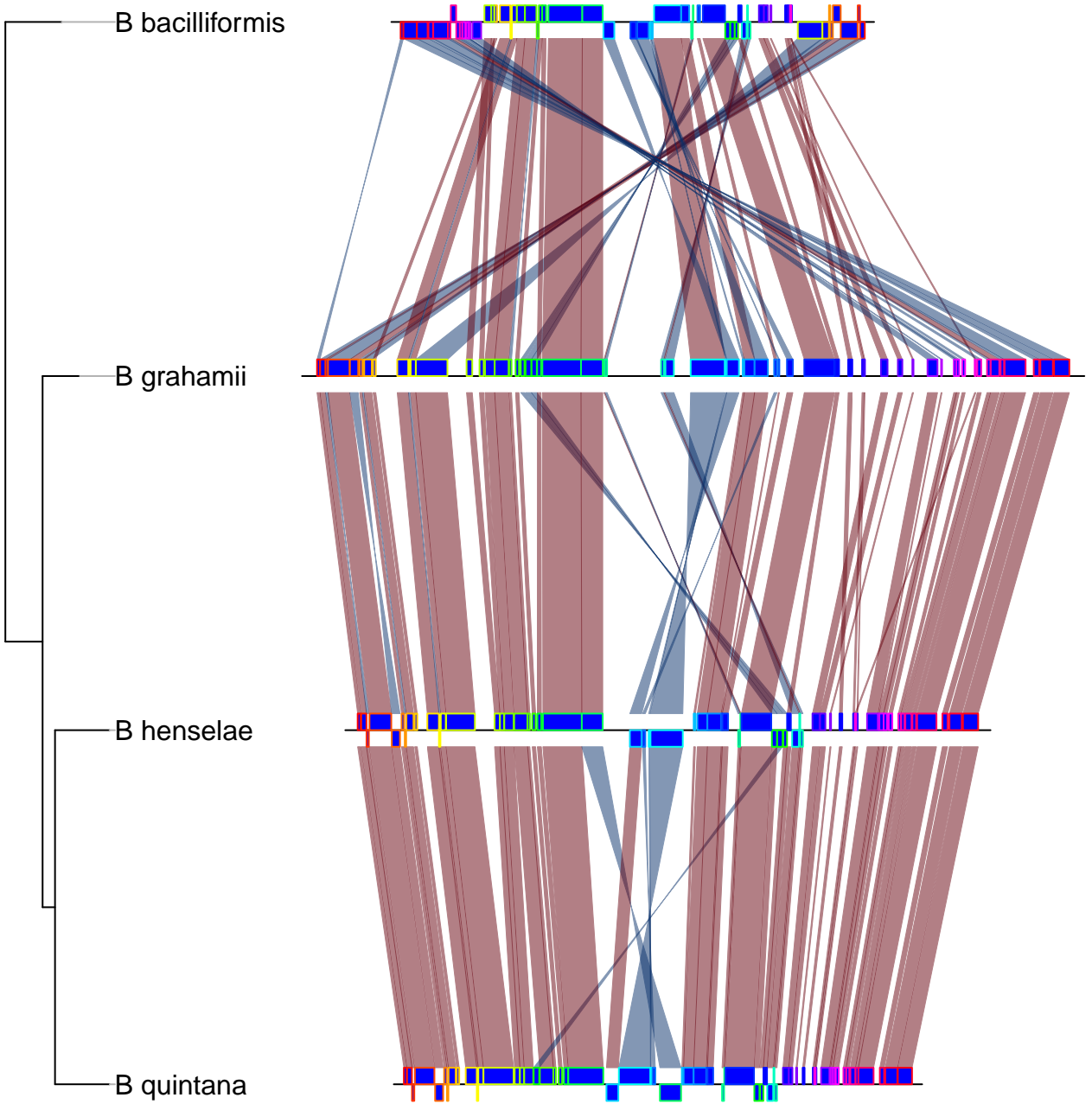
B_henselae

B_quintana



help("read_functions")

500 kb



B. bacilliformis

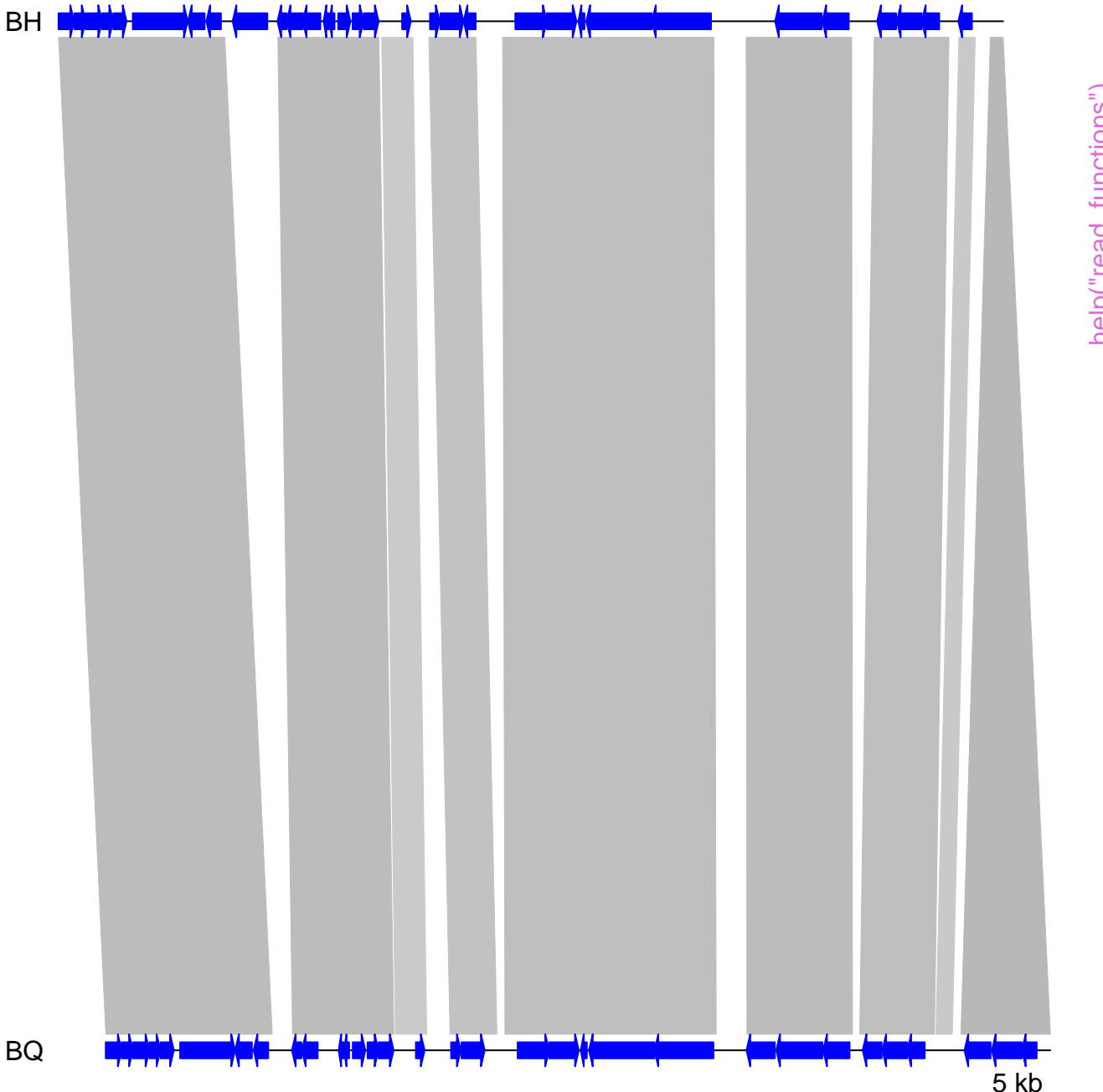
B. grahamii

B. henselae

B. quintana

500 kb

help("read_functions")



BH

BQ

5 kb

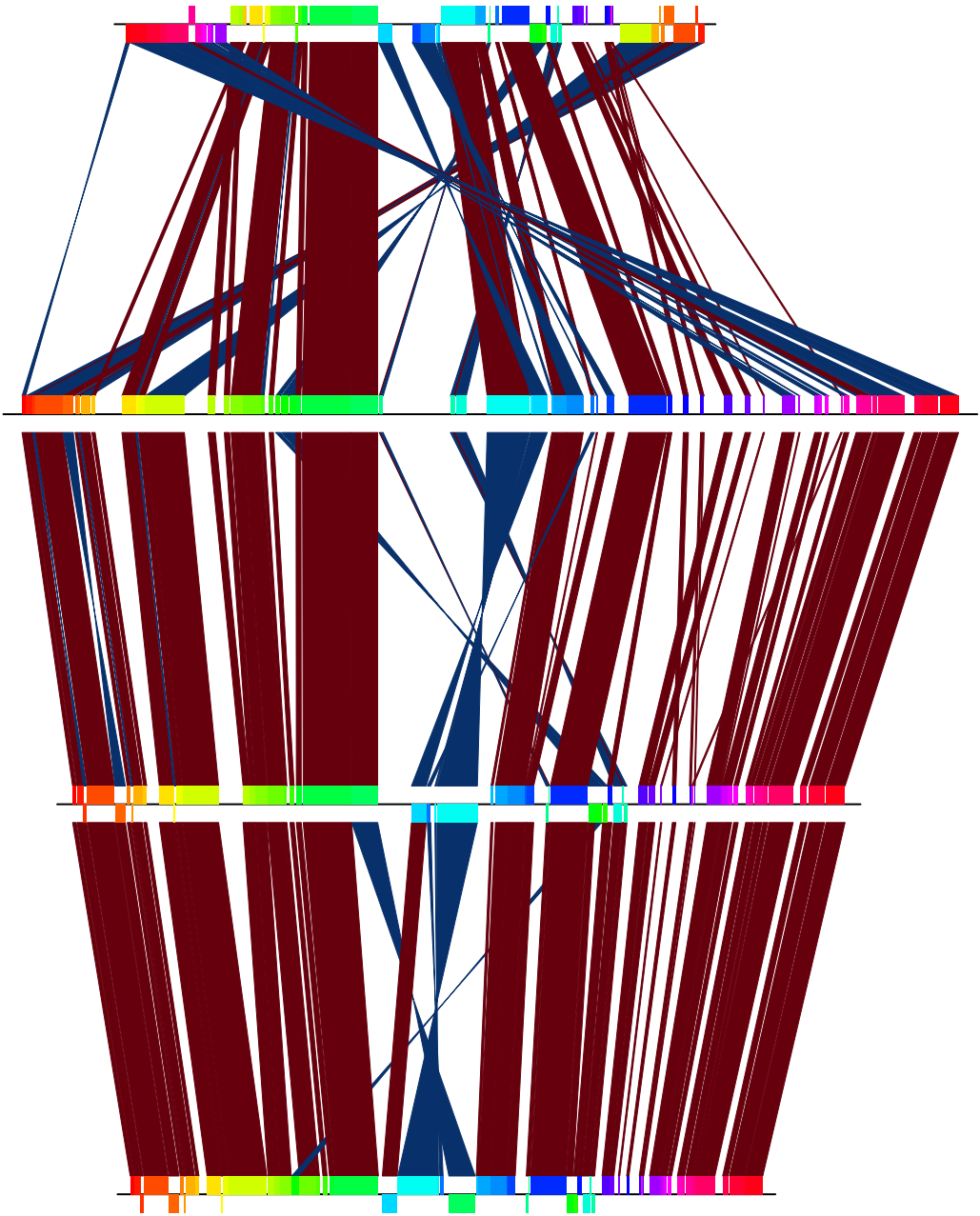
help("read_functions")

B_bacilliformis

B_grahamii

B_henselae

B_quintana



help("reverse")

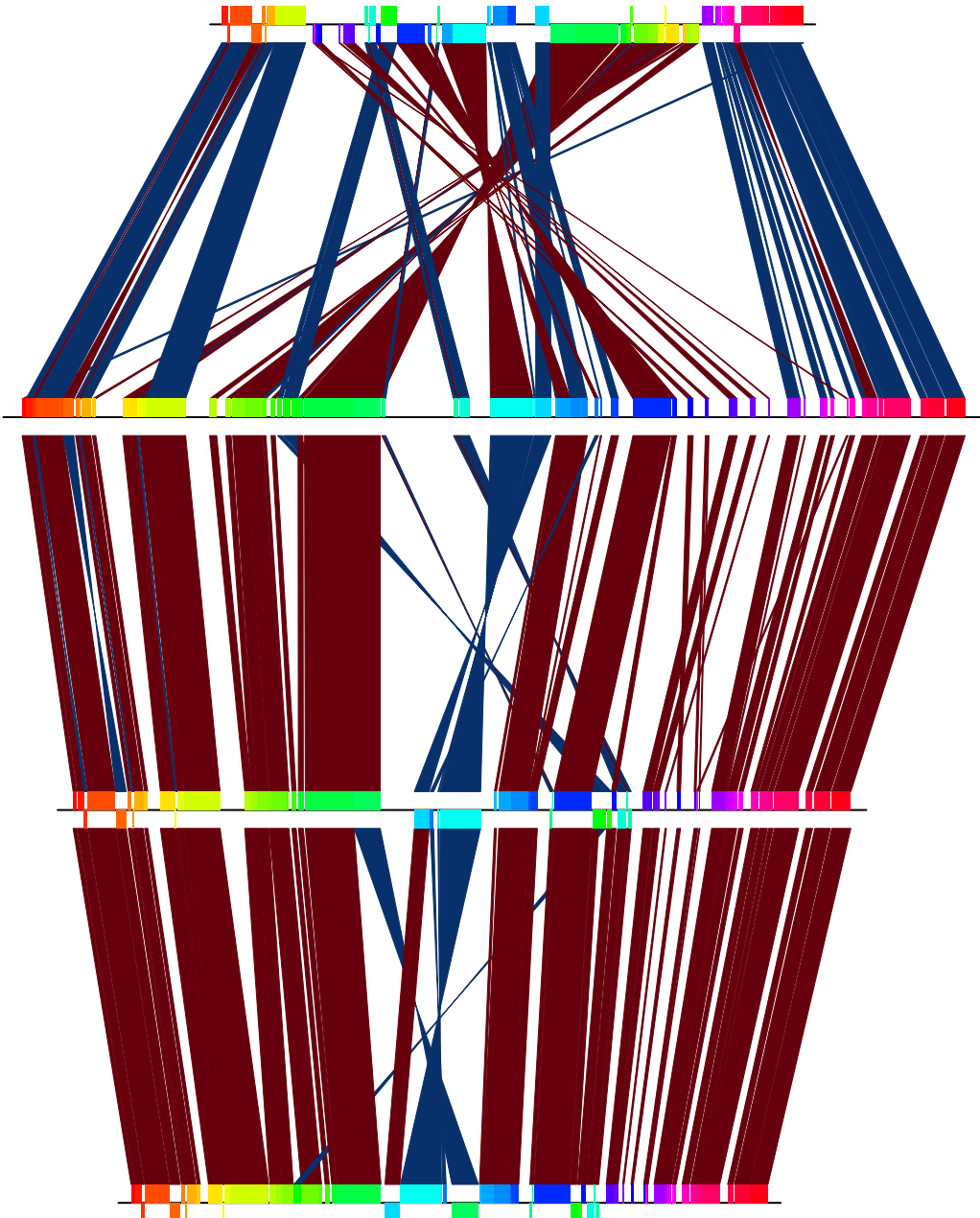
500 kb

B_bacilliformis

B_grahamii

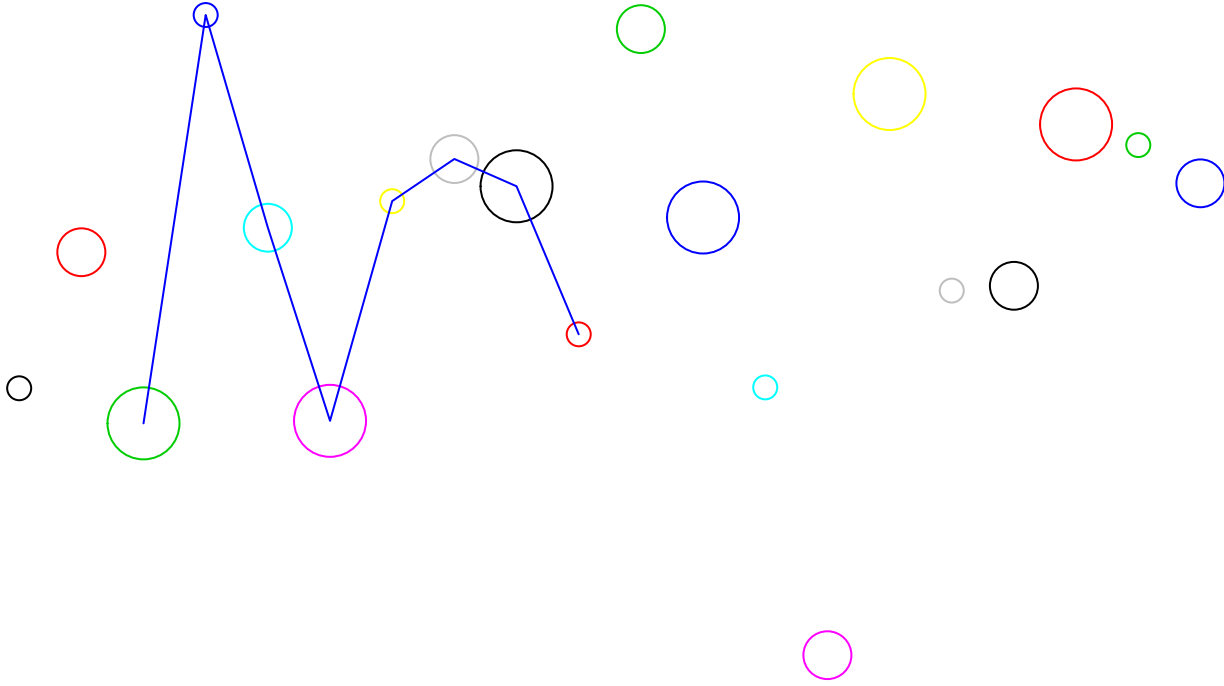
B_henselae

B_quintana

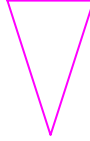
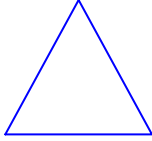


help("reverse")

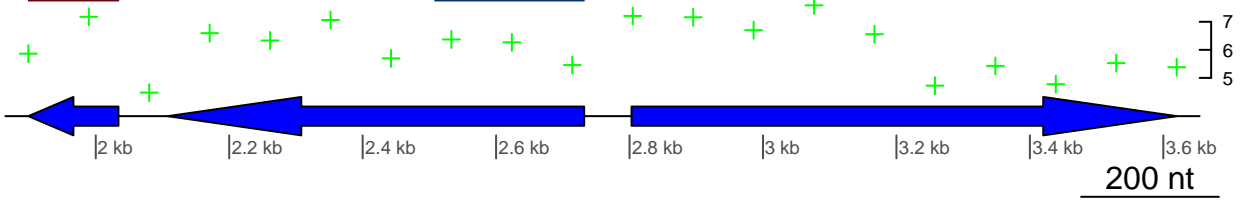
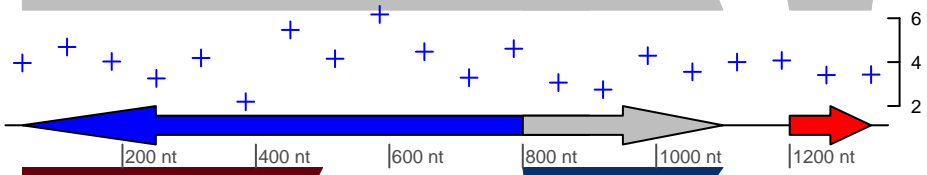
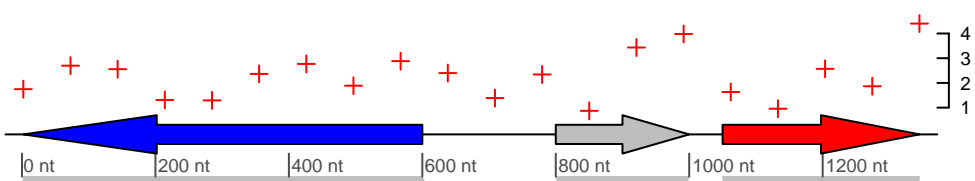
500 kb



help("seg_plot")

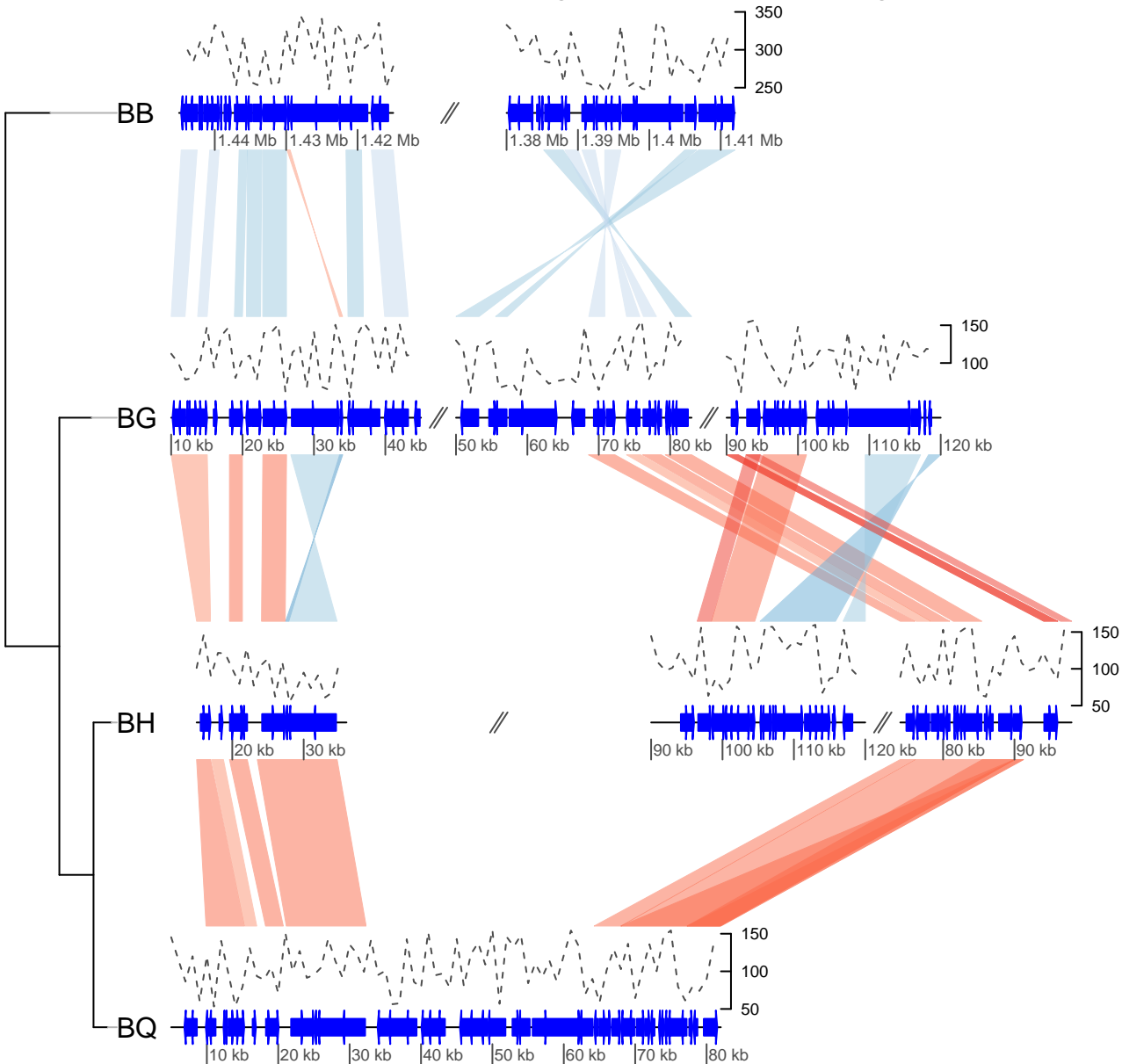


help("seg_plot")



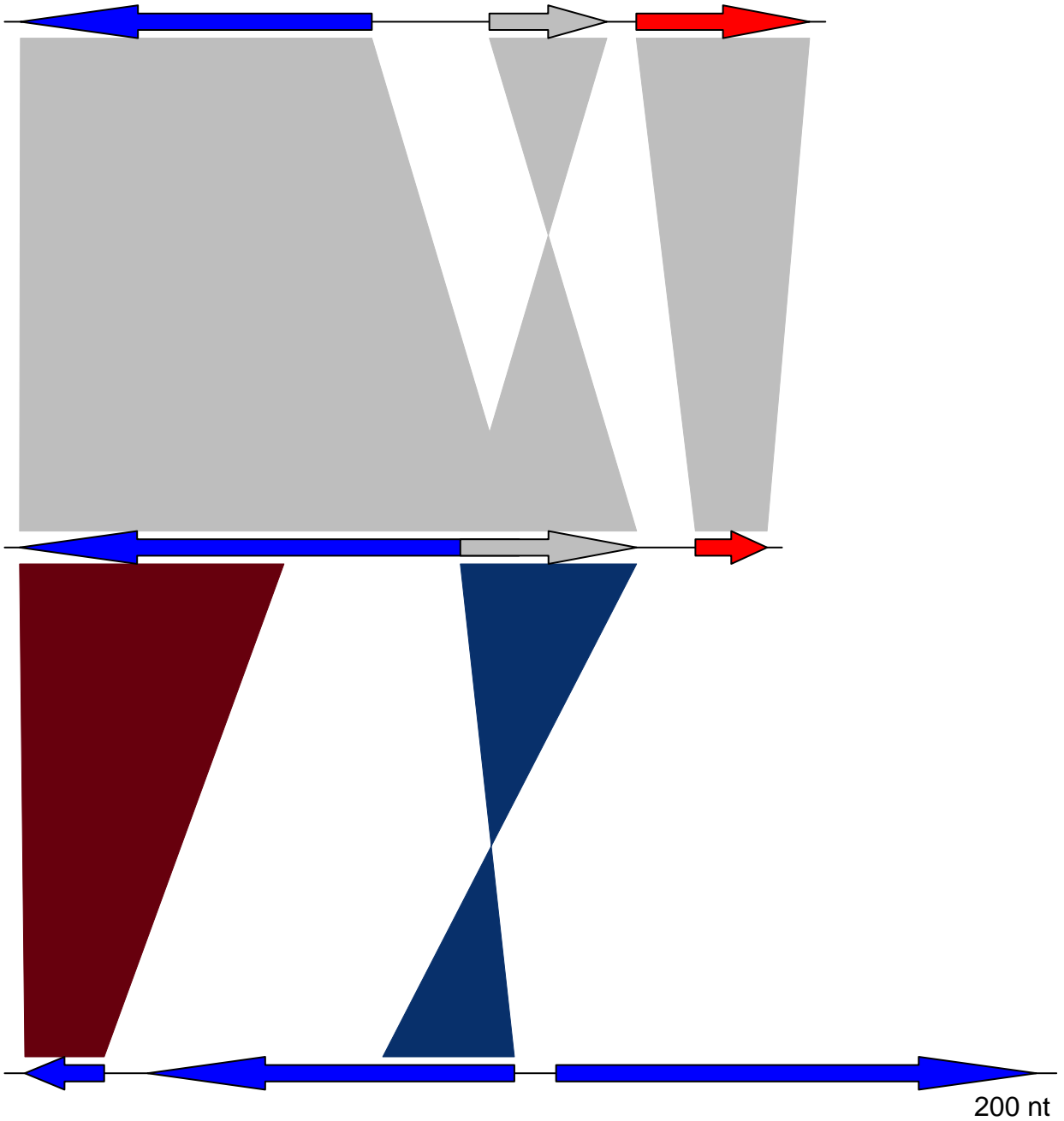
help("seg_plot")

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



help("seg_plot")

20 kb



help("three_genes")

200 nt

