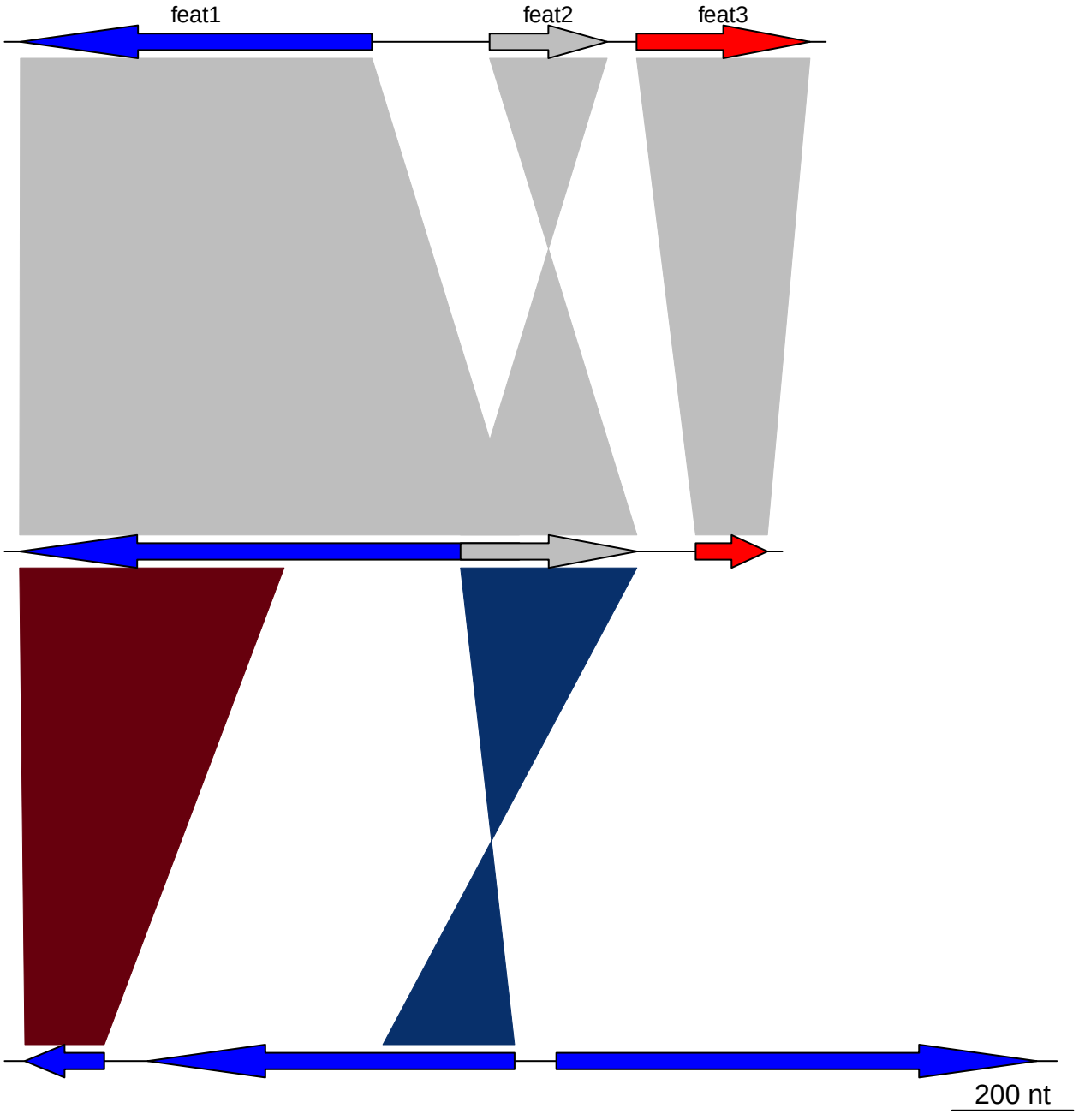
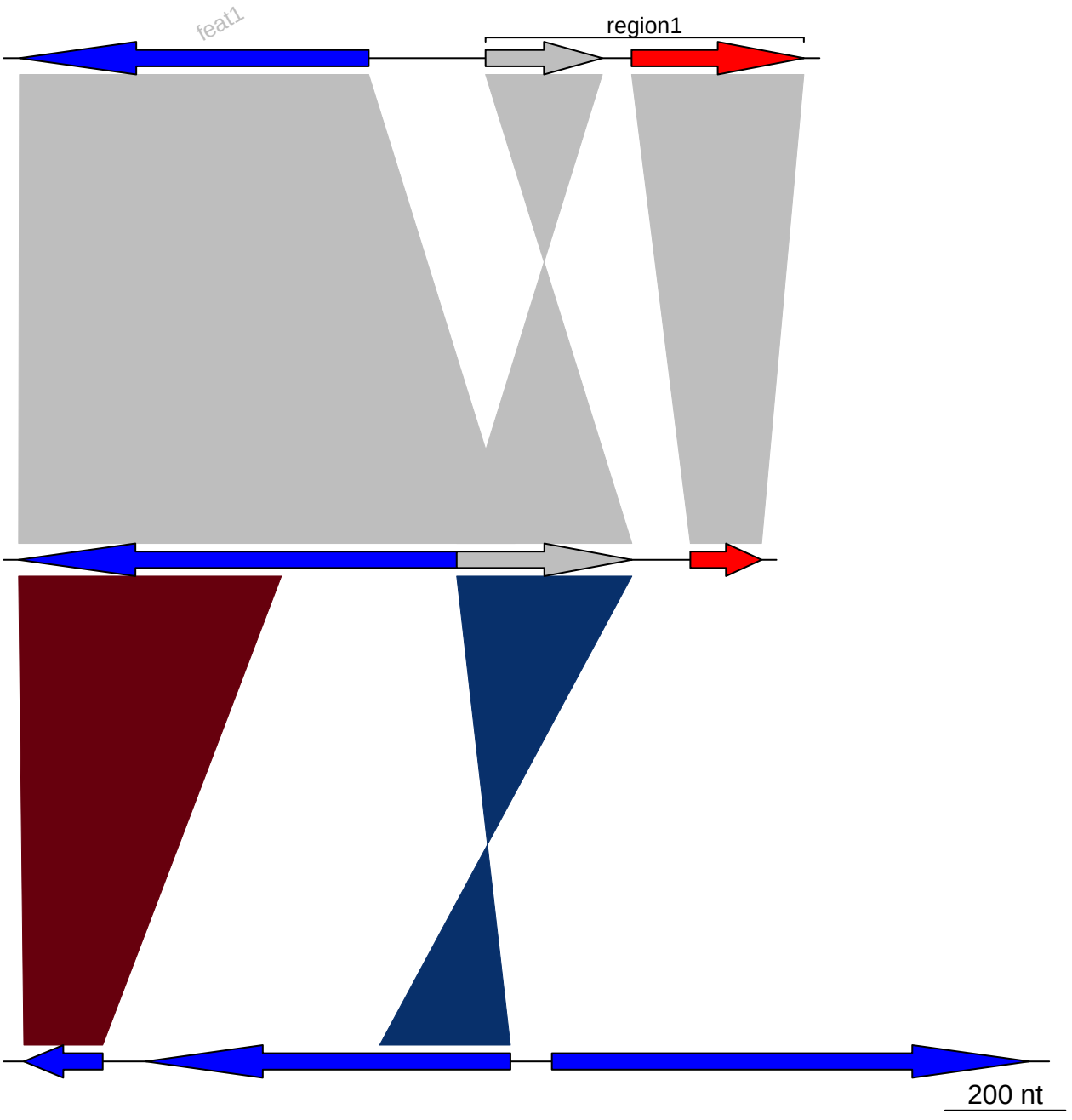
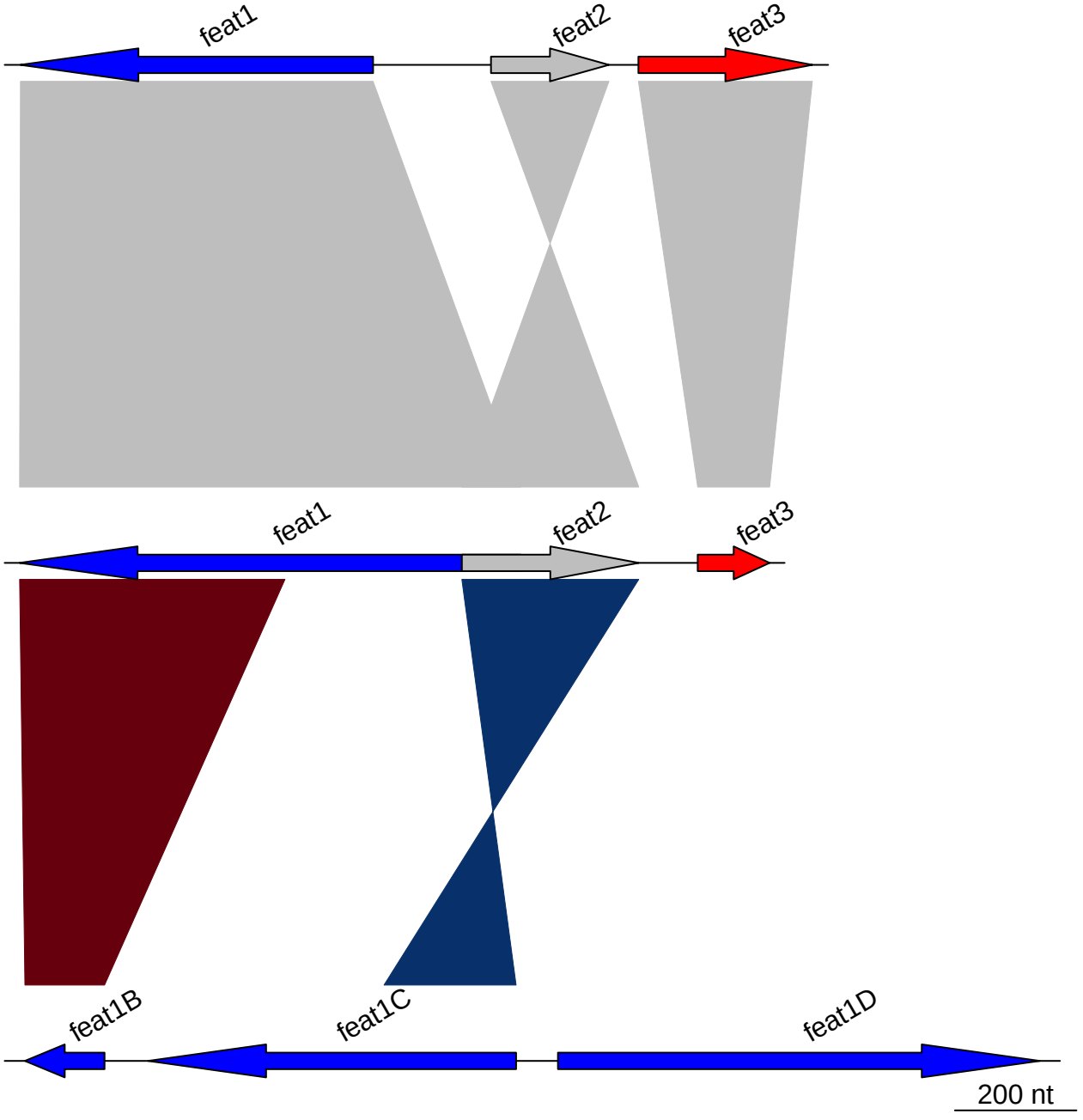


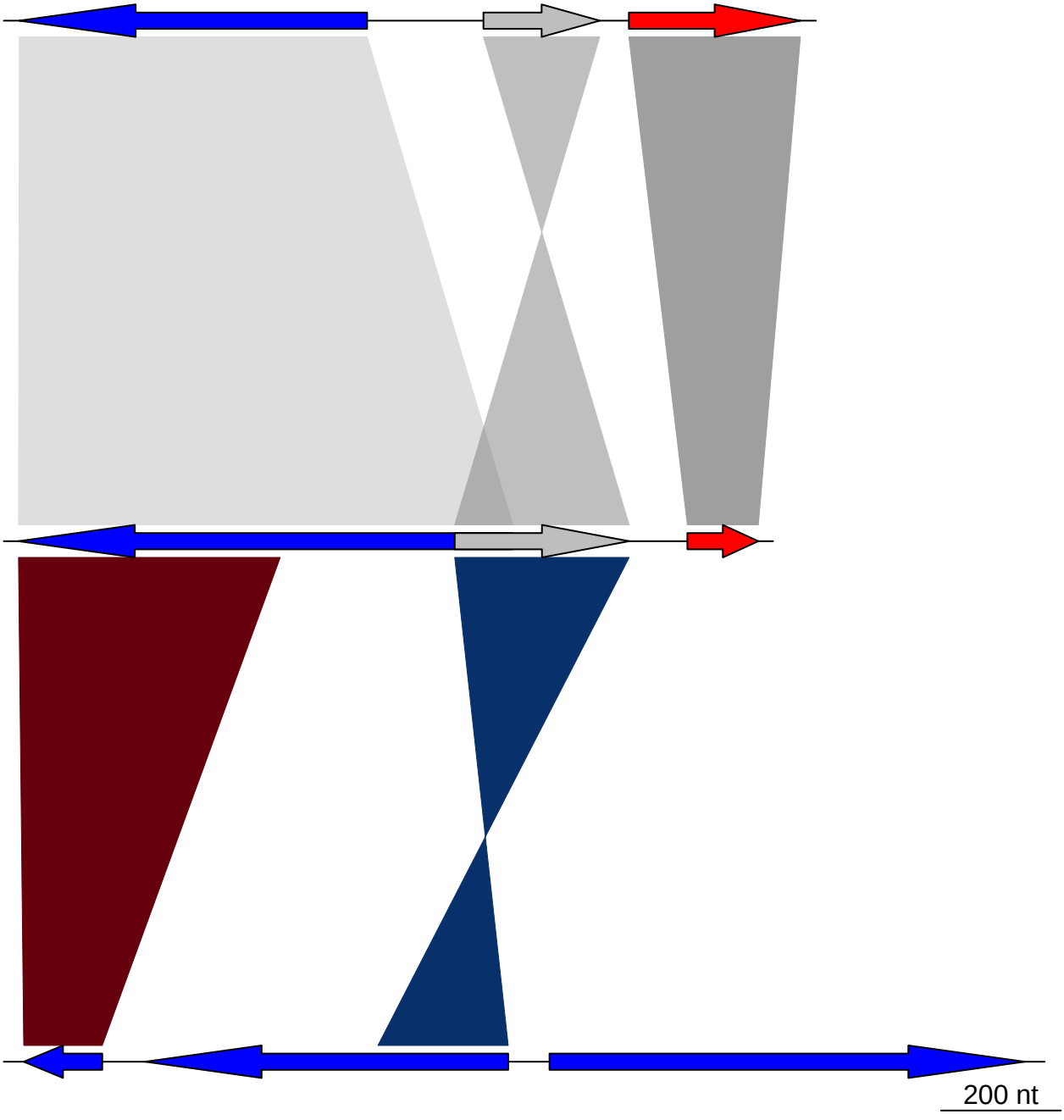
help("annotation")



help("annotation")



help("annotation")


help("apply_color_scheme")
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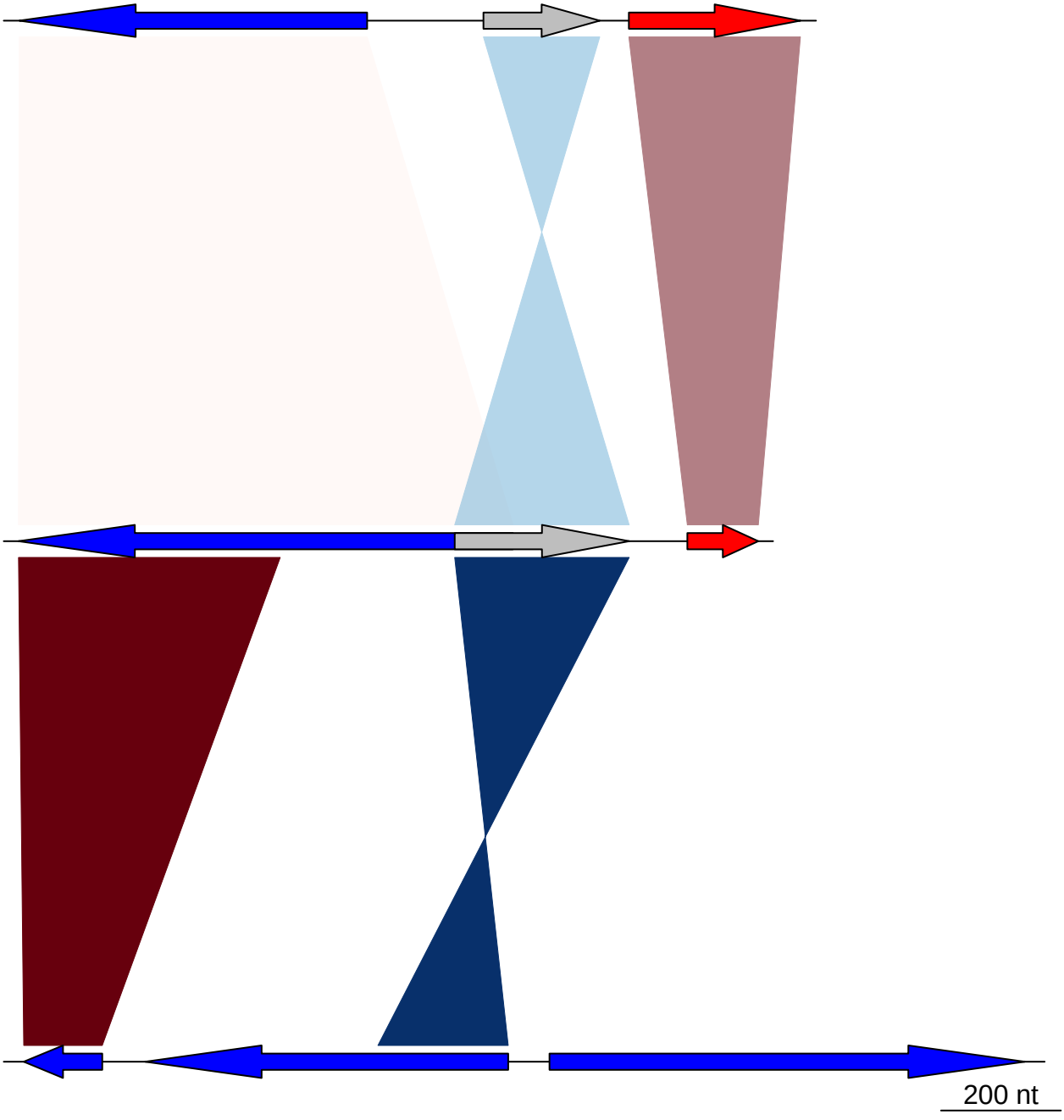
help("apply_color_scheme")
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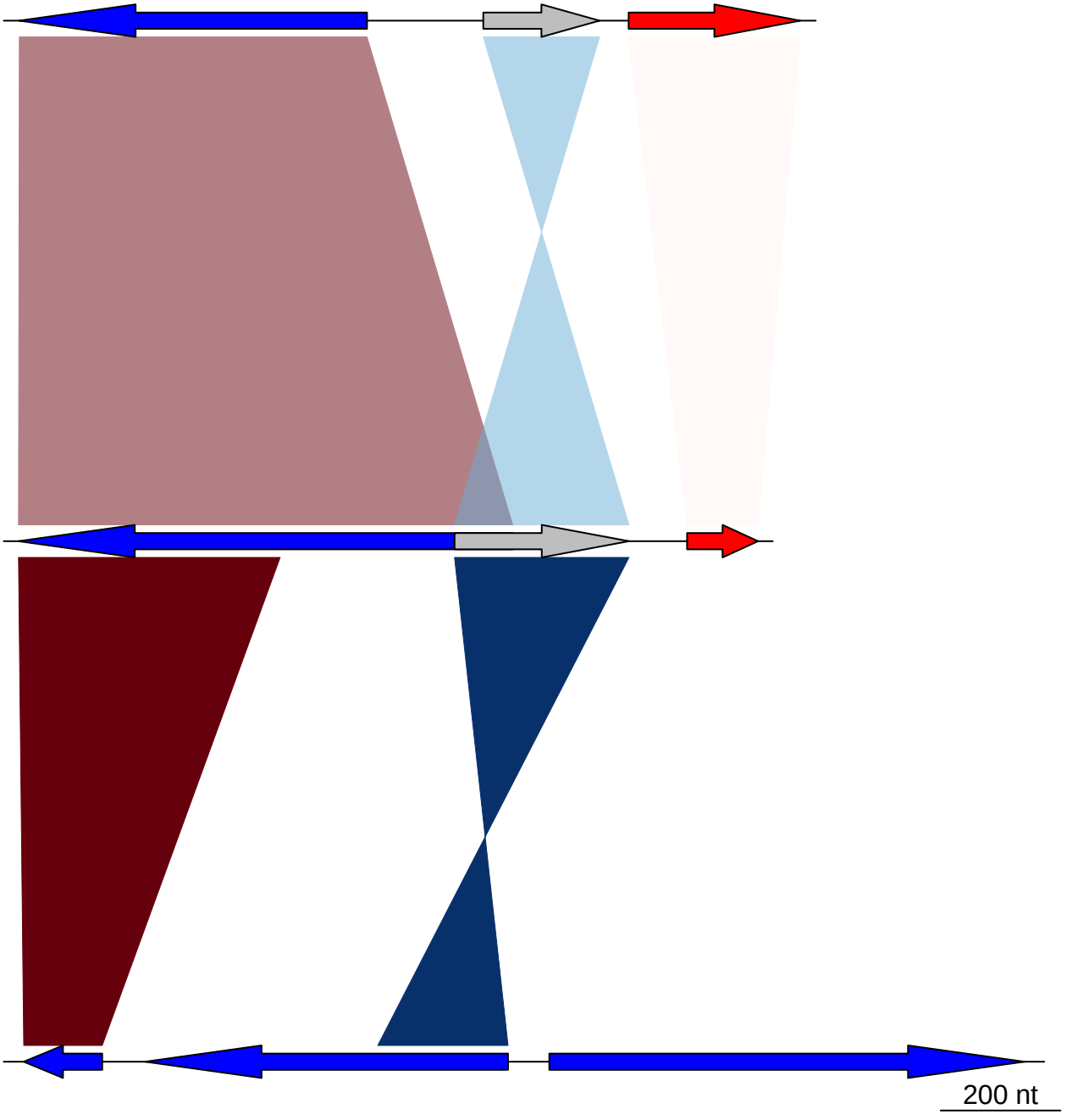
help("apply_color_scheme")
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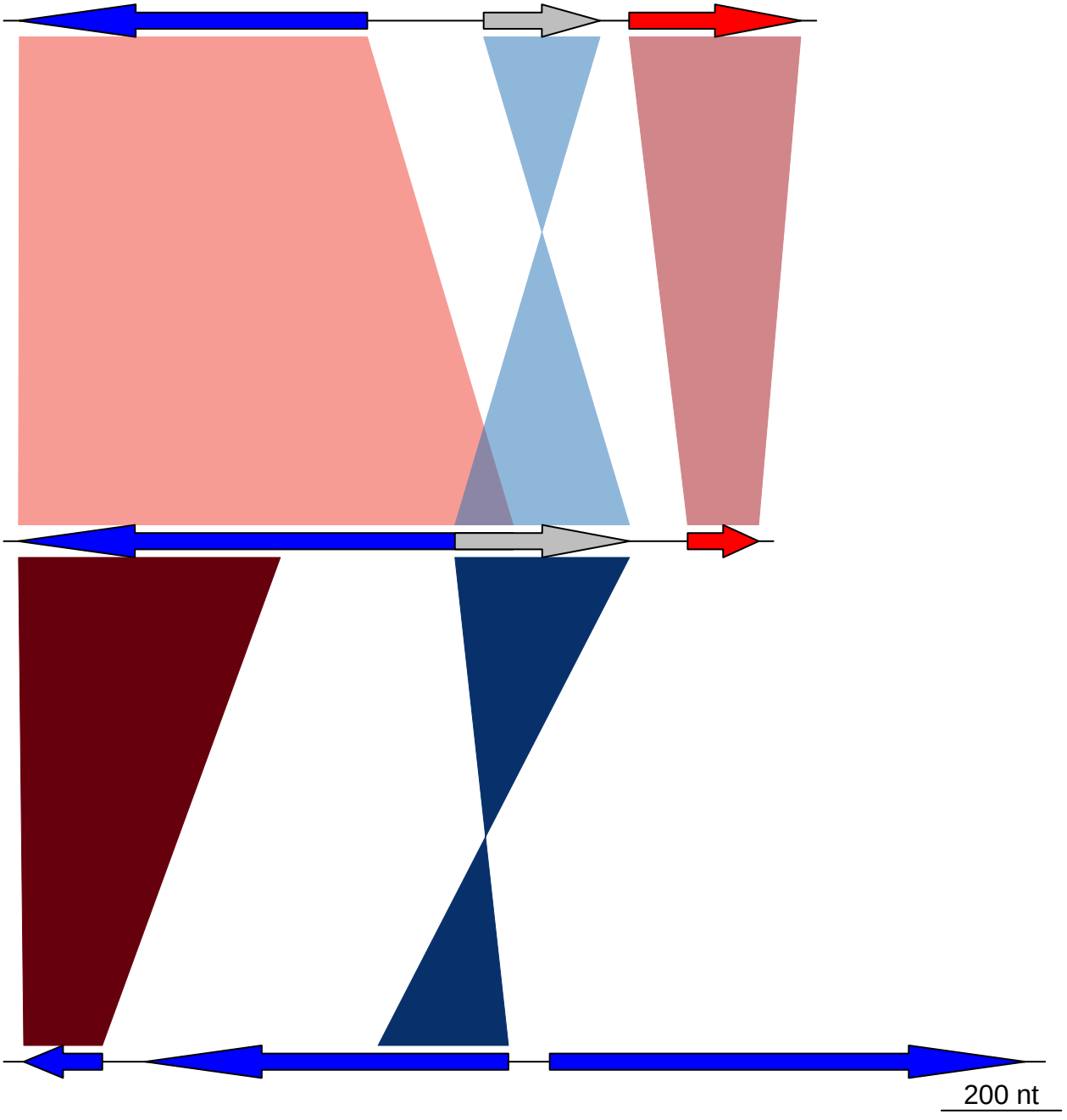
help("apply_color_scheme")
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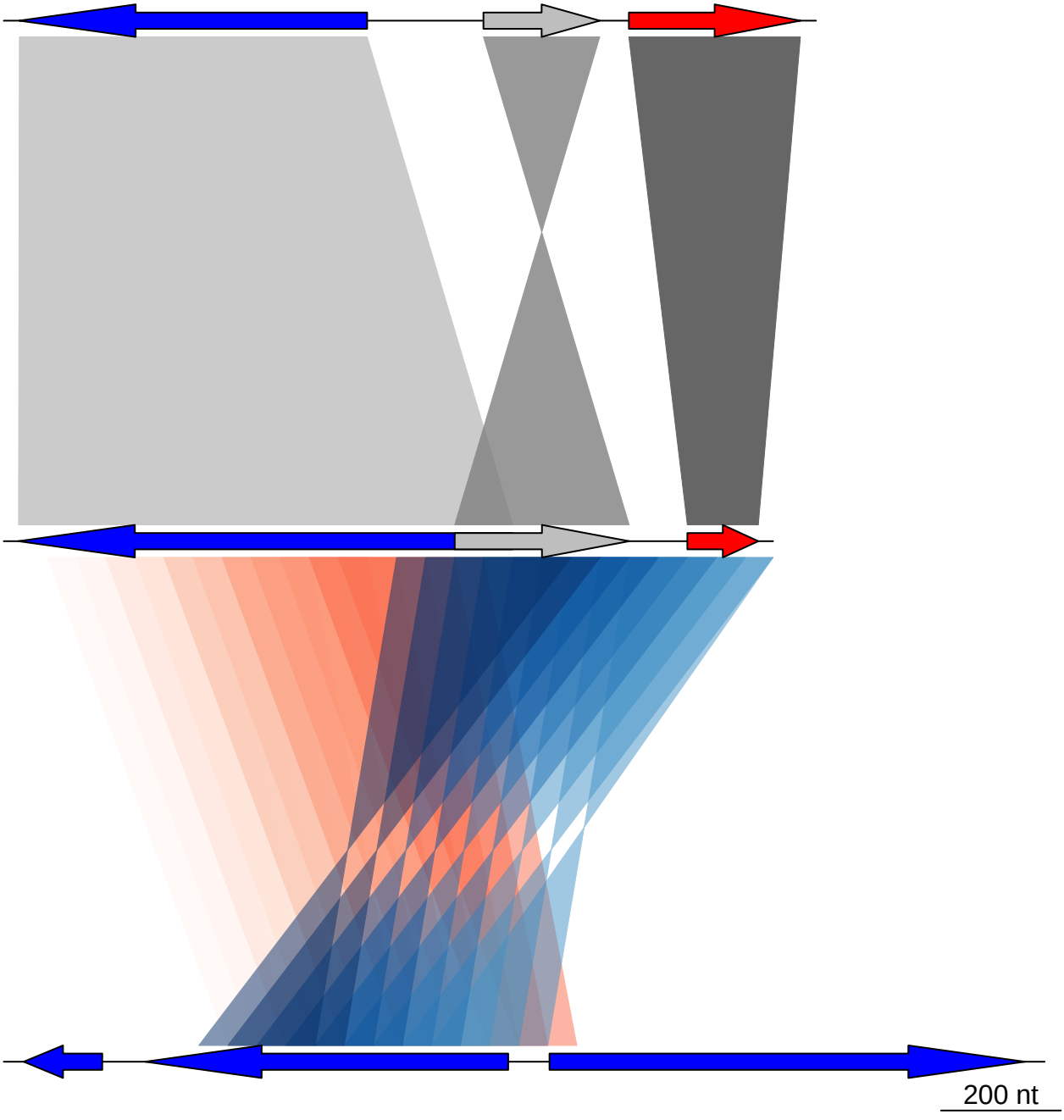
help("apply_color_scheme")
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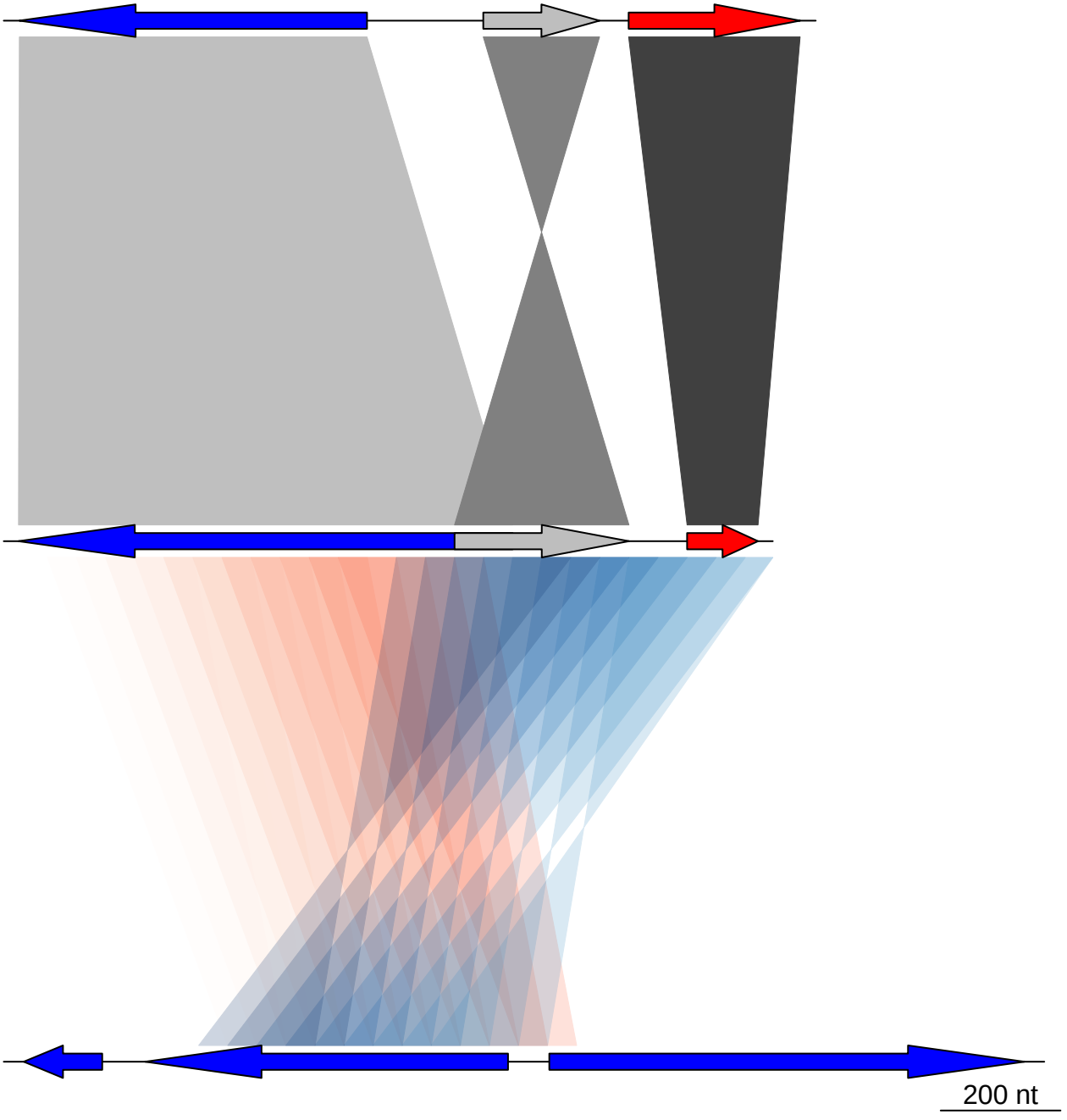
help("apply_color_scheme")
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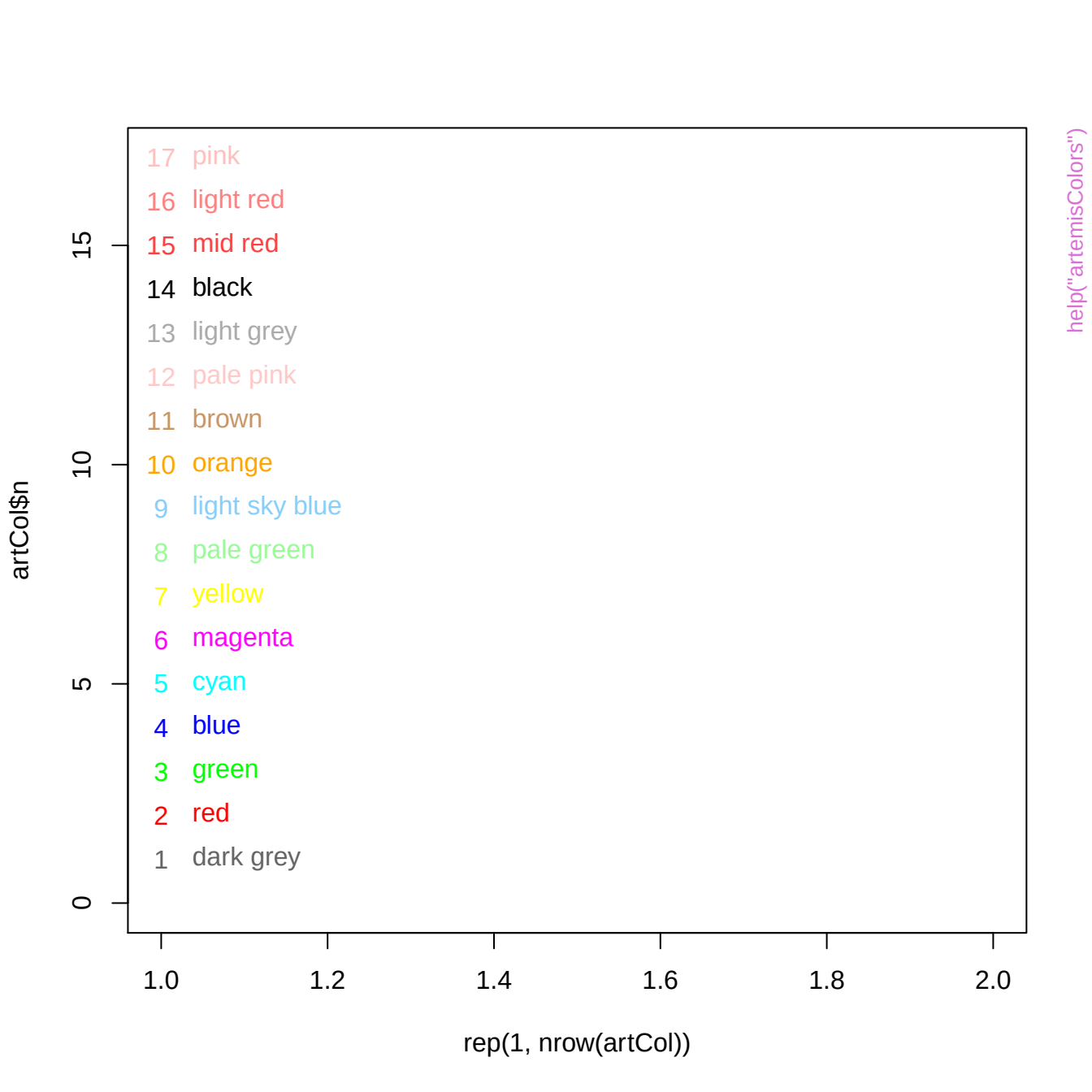
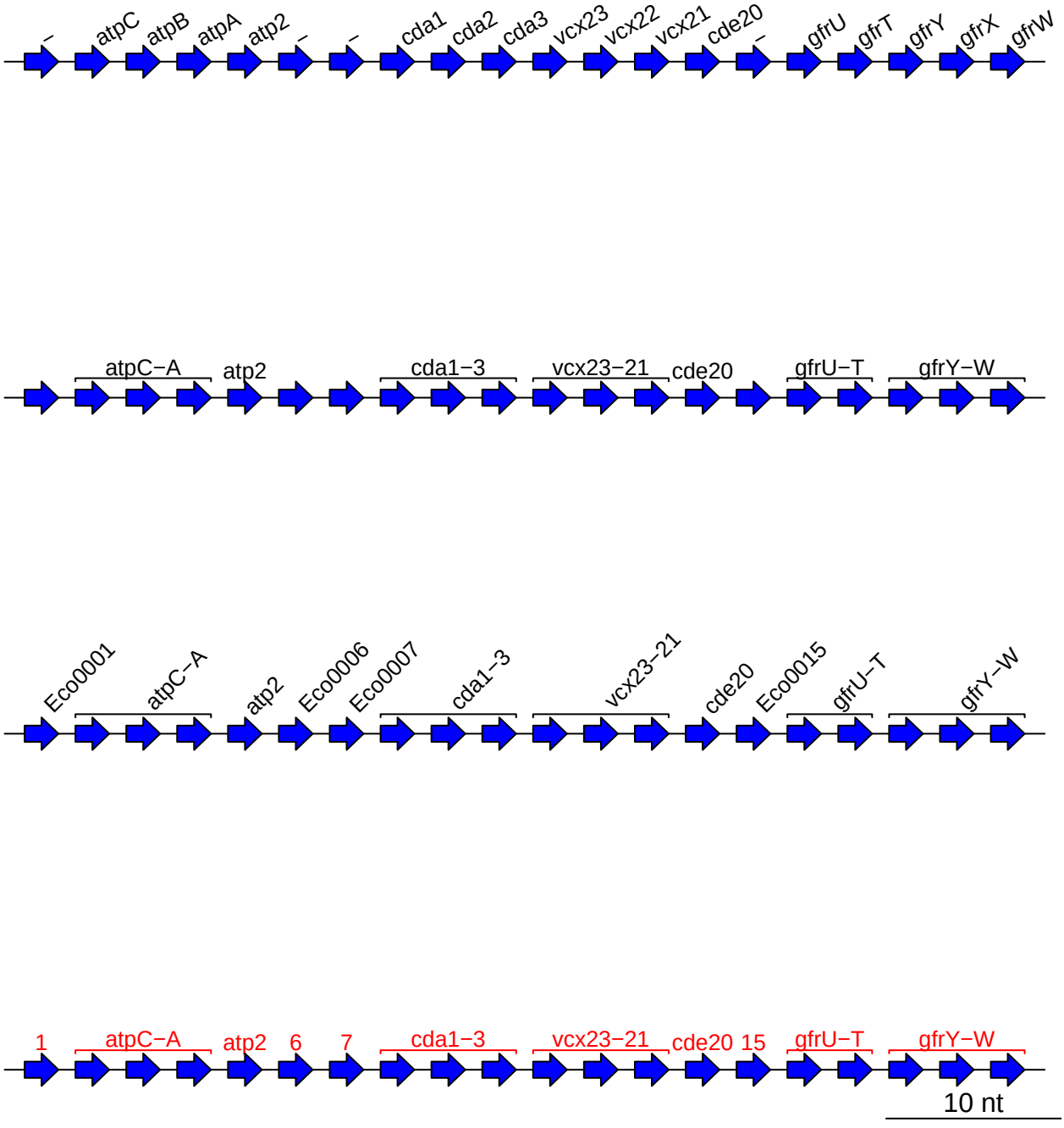
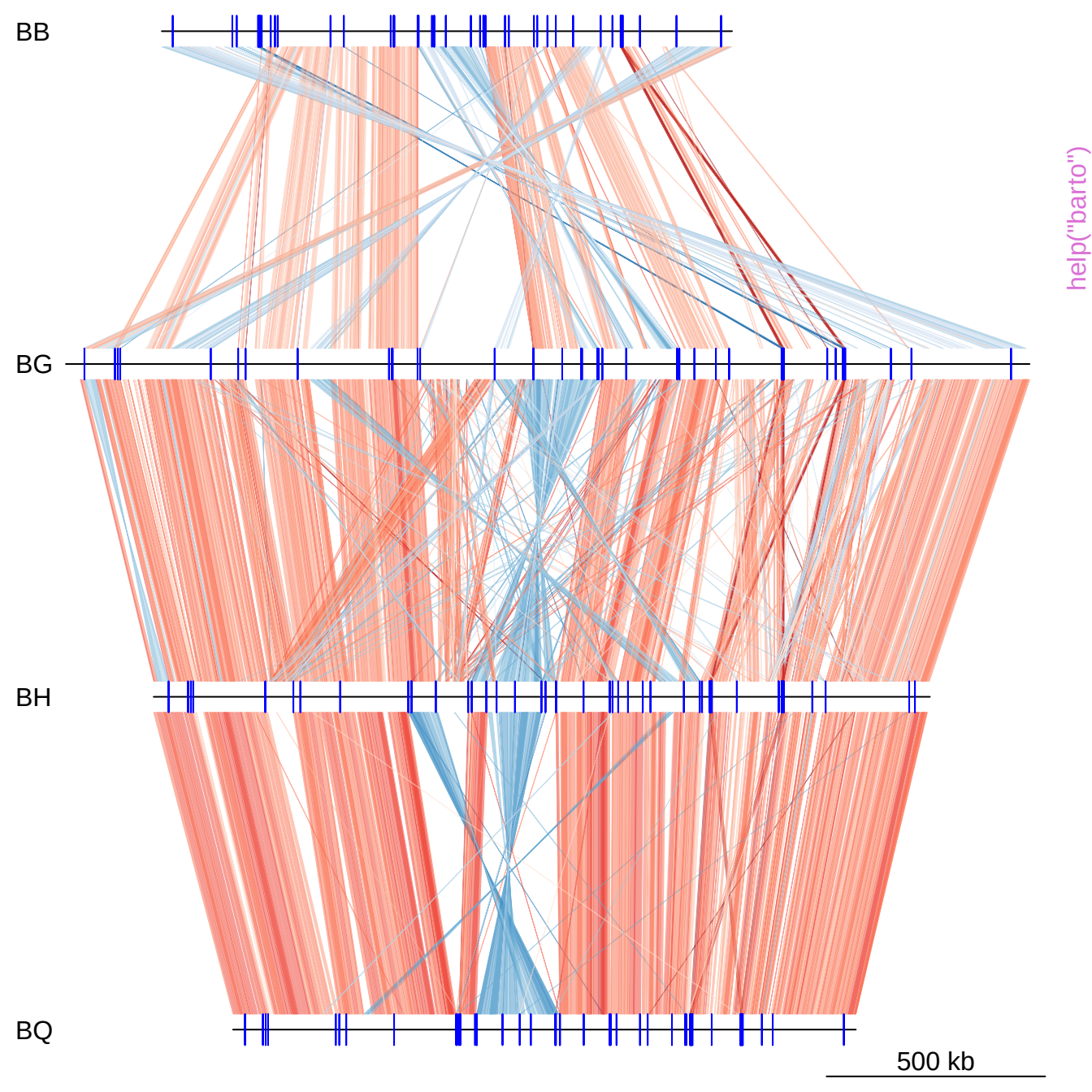

17 pink
16 light red
15 mid red
14 black
13 light grey
12 pale pink
11 brown
10 orange
9 light sky blue
8 pale green
7 yellow
6 magenta
5 cyan
4 blue
3 green
2 red
1 dark grey
0
5
10
15
artCol$n
1.0
1.2
1.4
1.6
1.8
2.0
rep(1, nrow(artCol))
help("artemisColors")



help("auto_annotate")


BB
BG
BH
BQ
help("barto")
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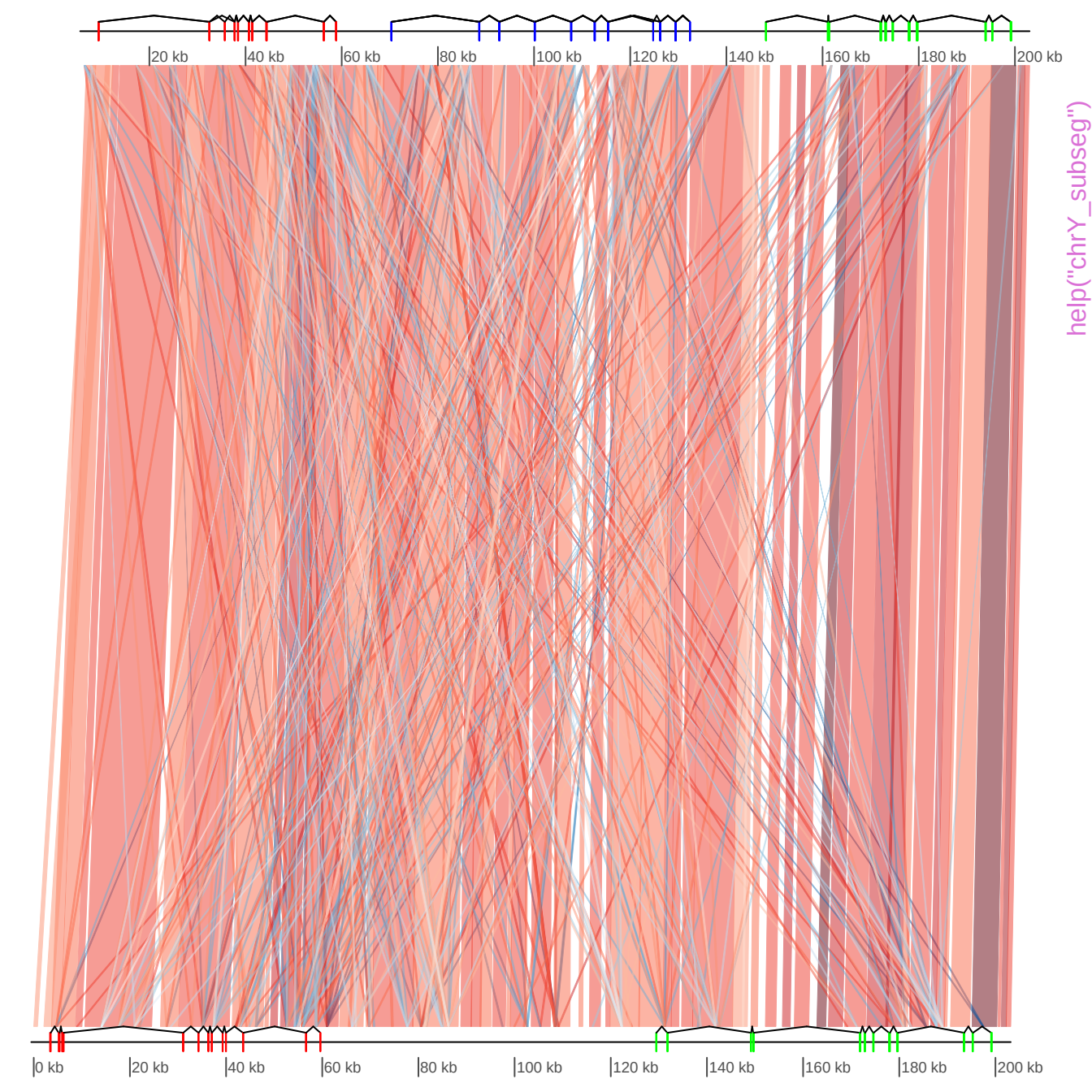
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200 kb
help("chrY_subseg")
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100 kb
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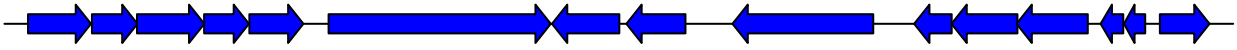
160 kb
180 kb
200 kb

help("gene_types")



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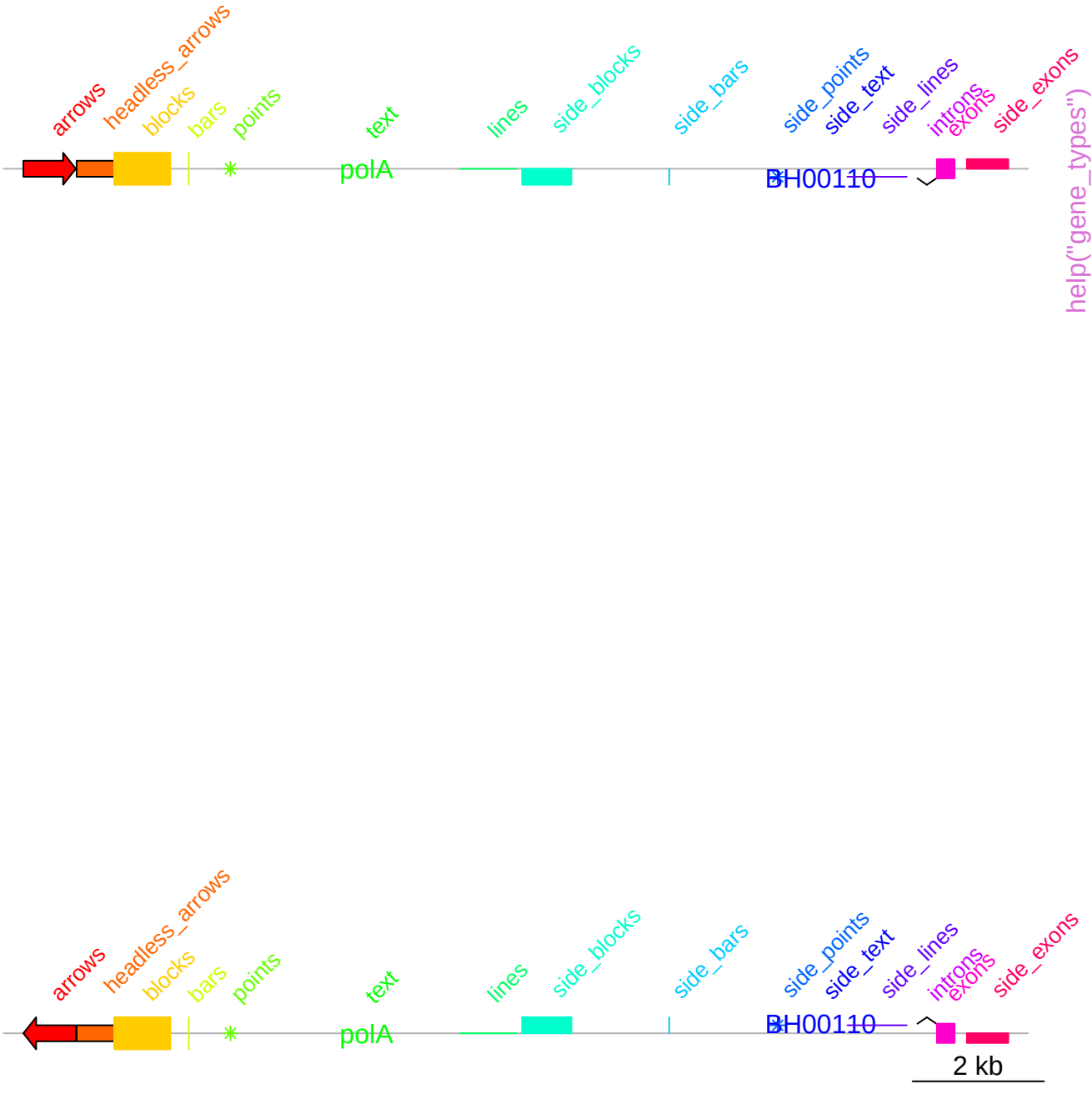
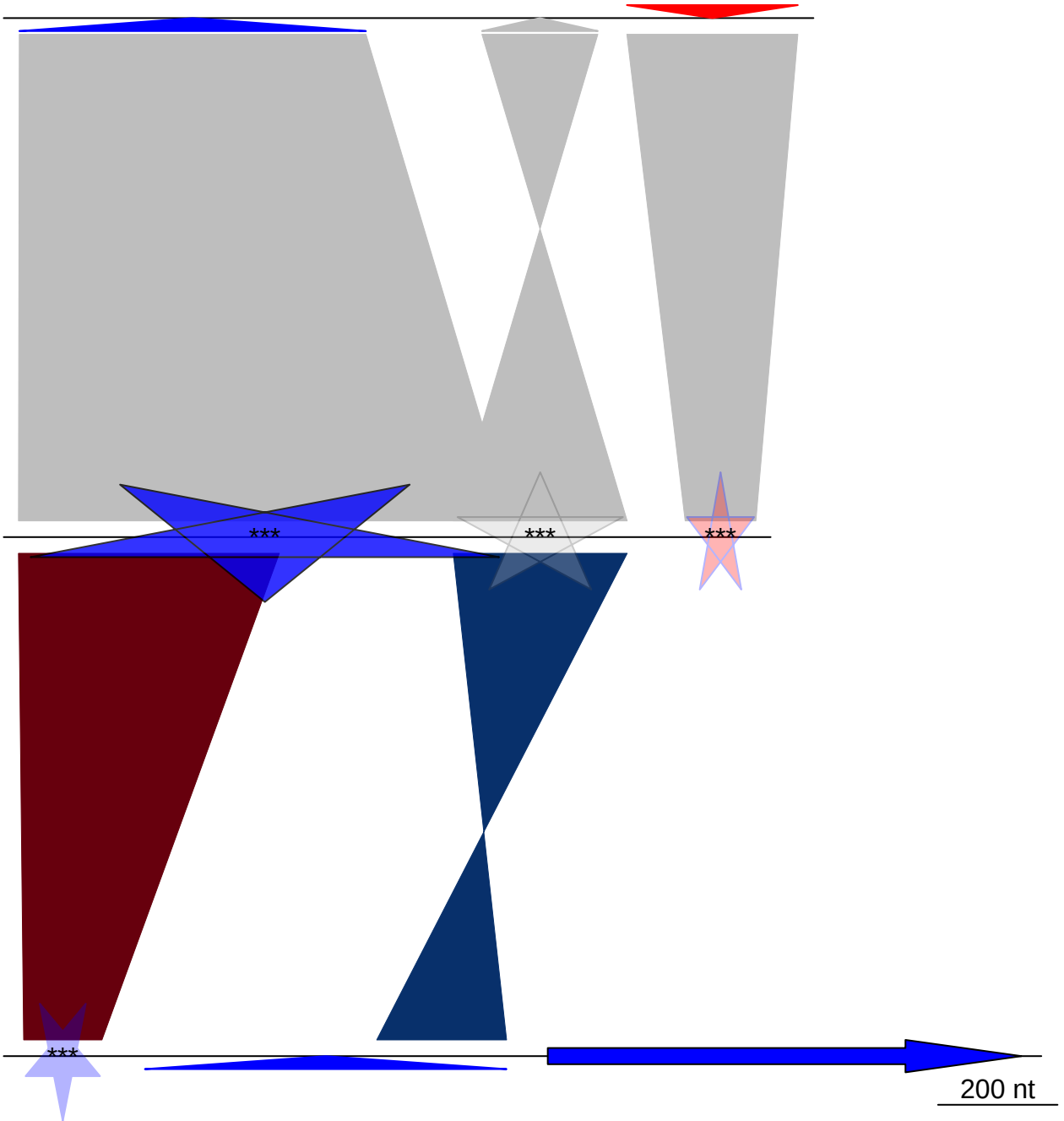

arrows
headless_arrows
blocks
bars
points
text
lines
side_blocks
side_bars
side_points
side_text
side_lines
introns
exons
side_exons
help("gene_types")
polA
BH00110
2 kb


help("gene_types")
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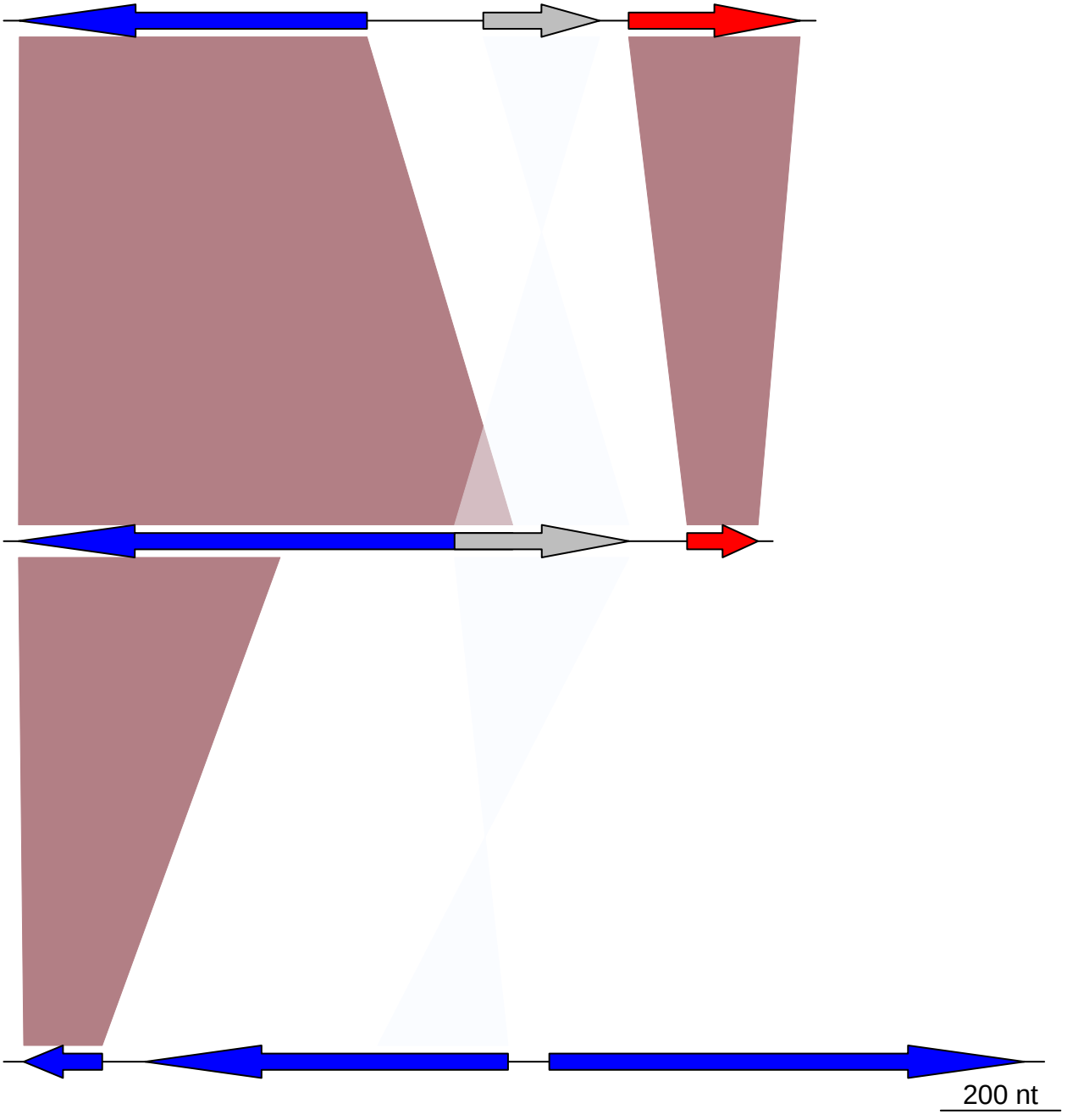
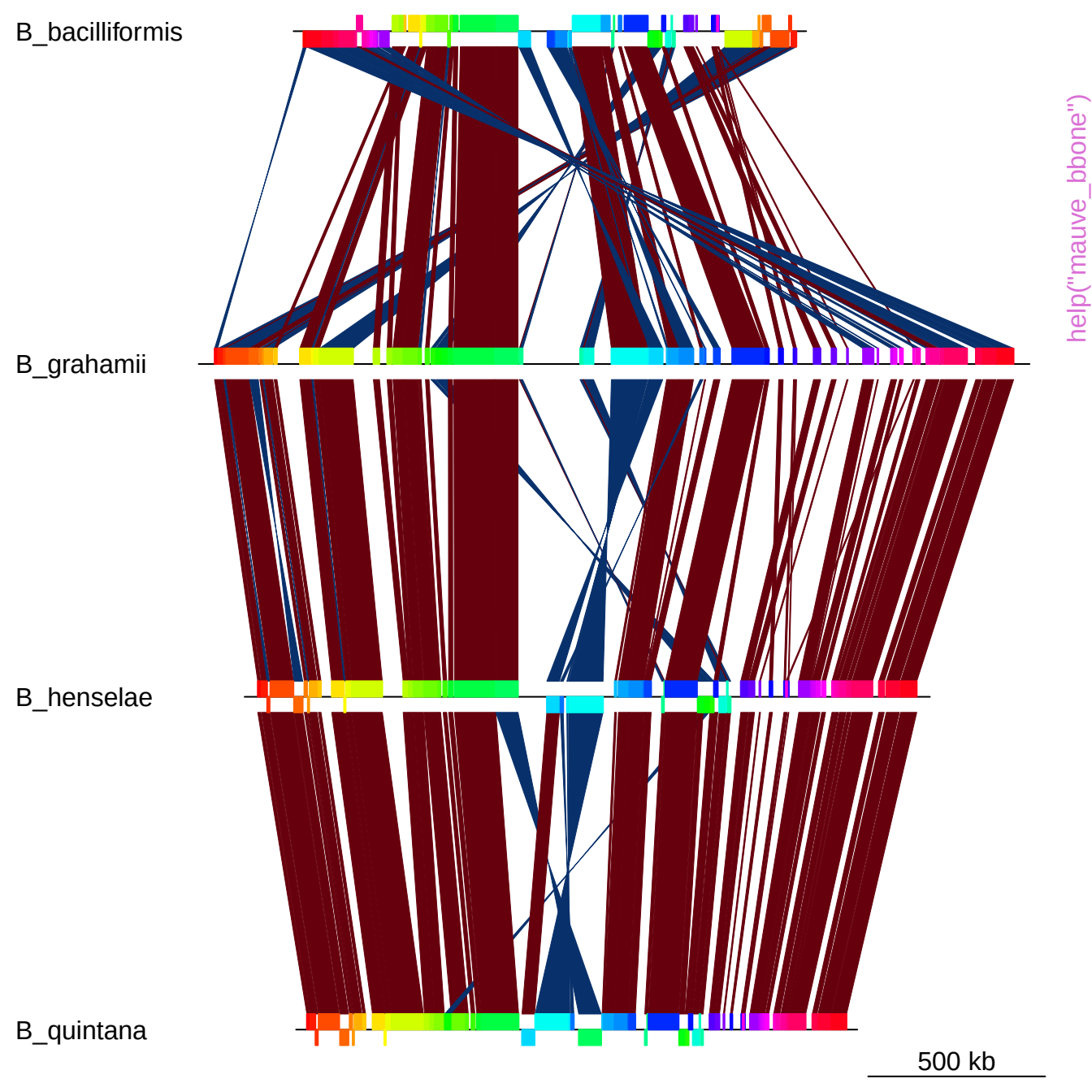
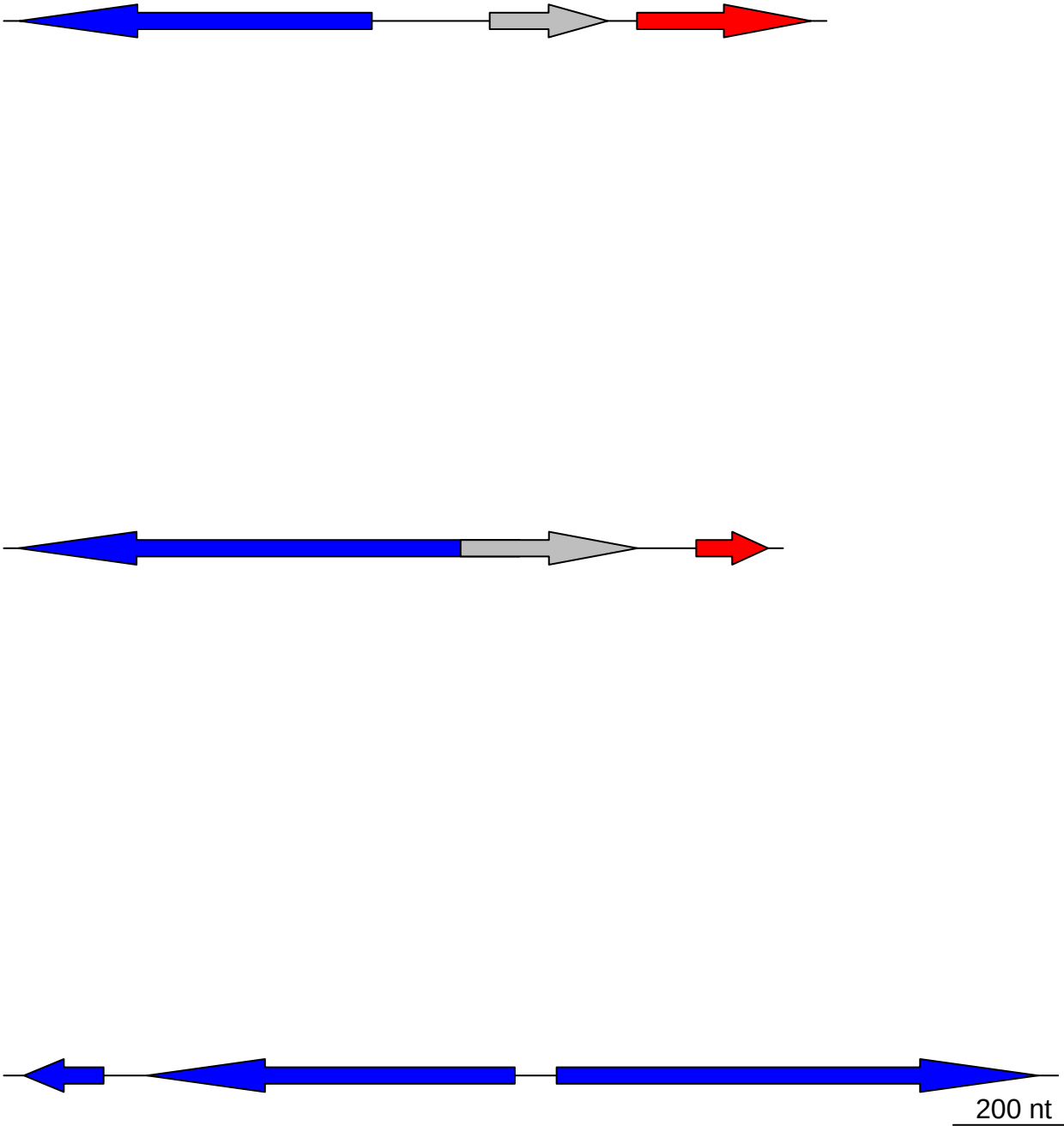
***
***
***
200 nt

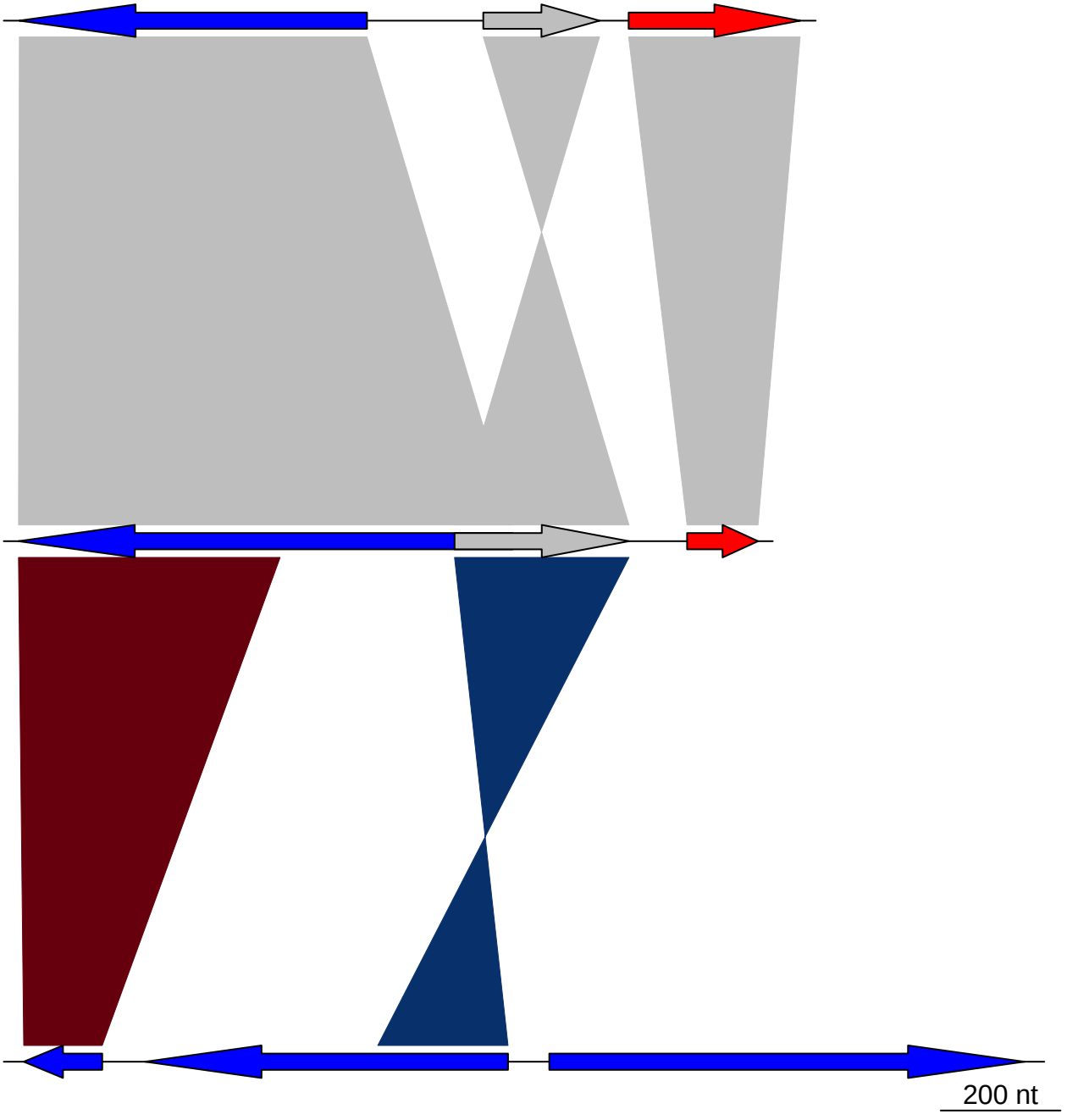


help("genoPlotR-package")


B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("mauve_bbone")



help("plot_gene_map")


help("plot_gene_map")
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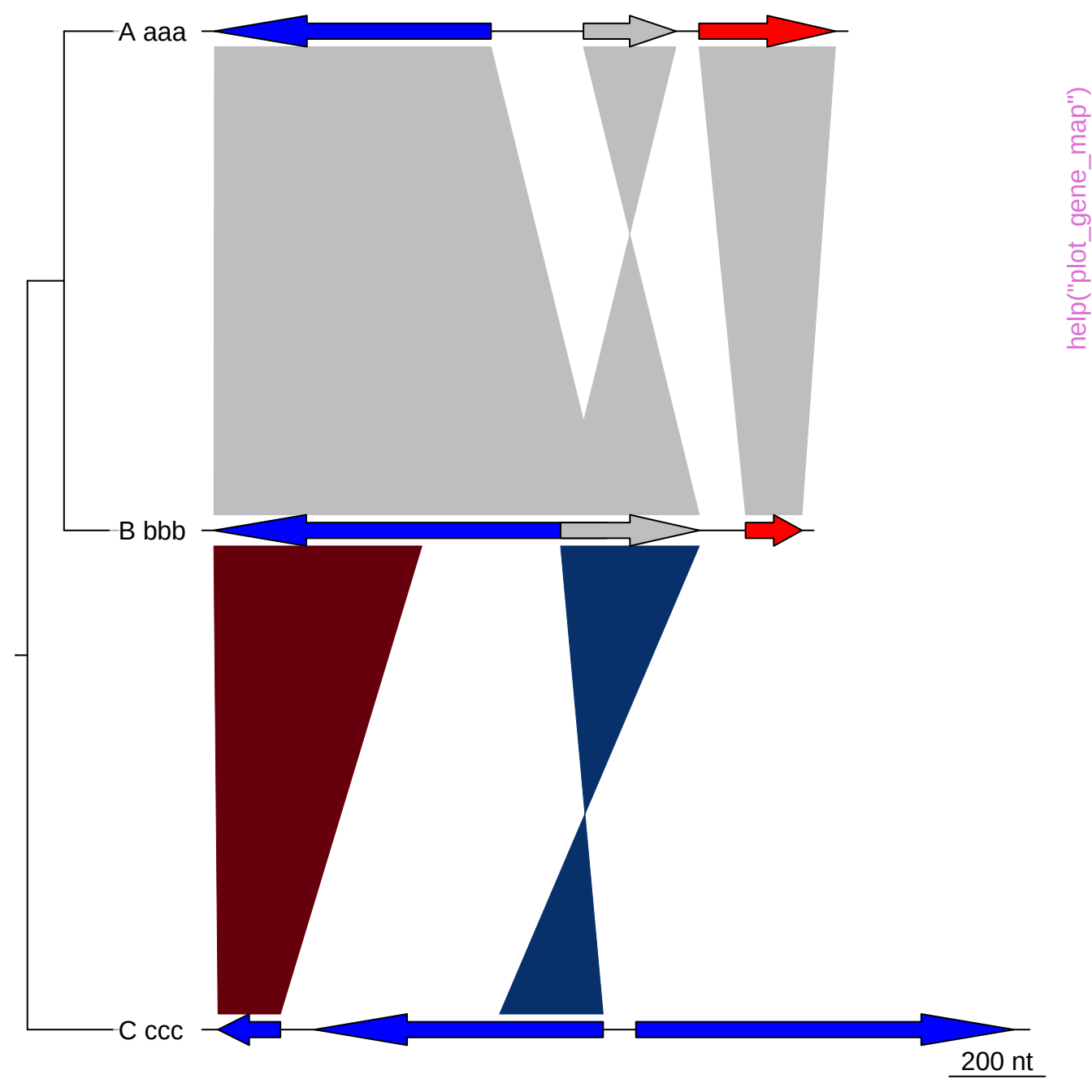
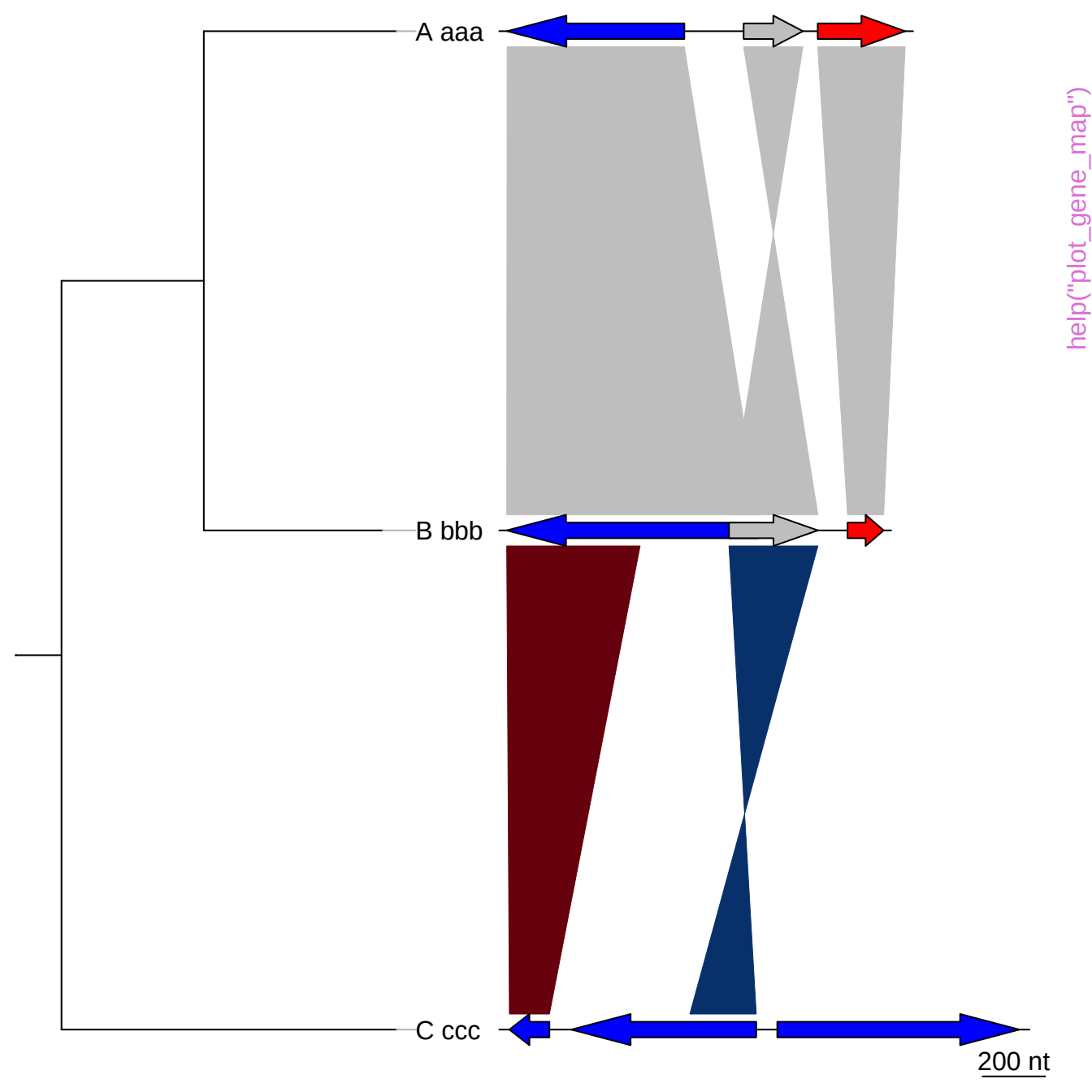
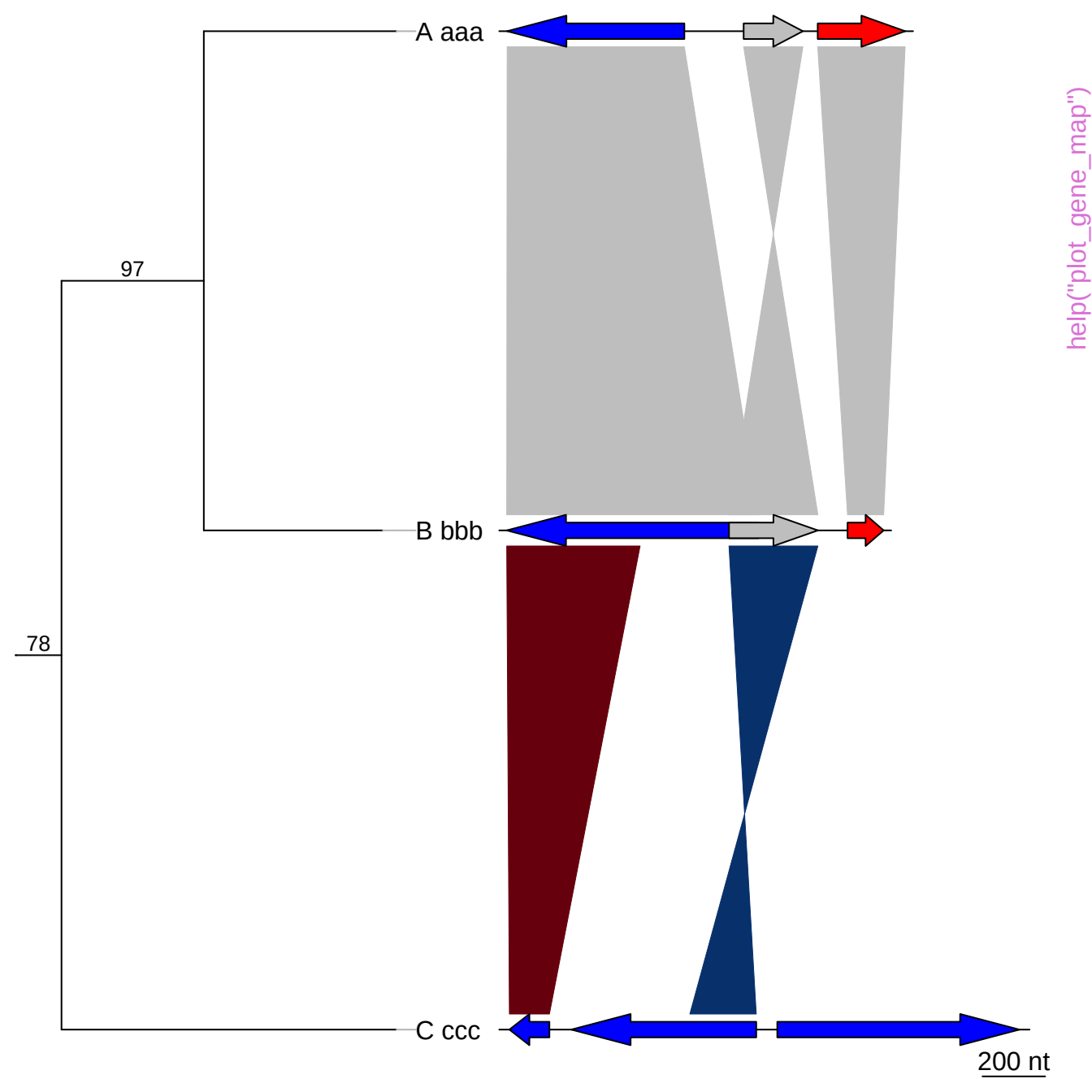
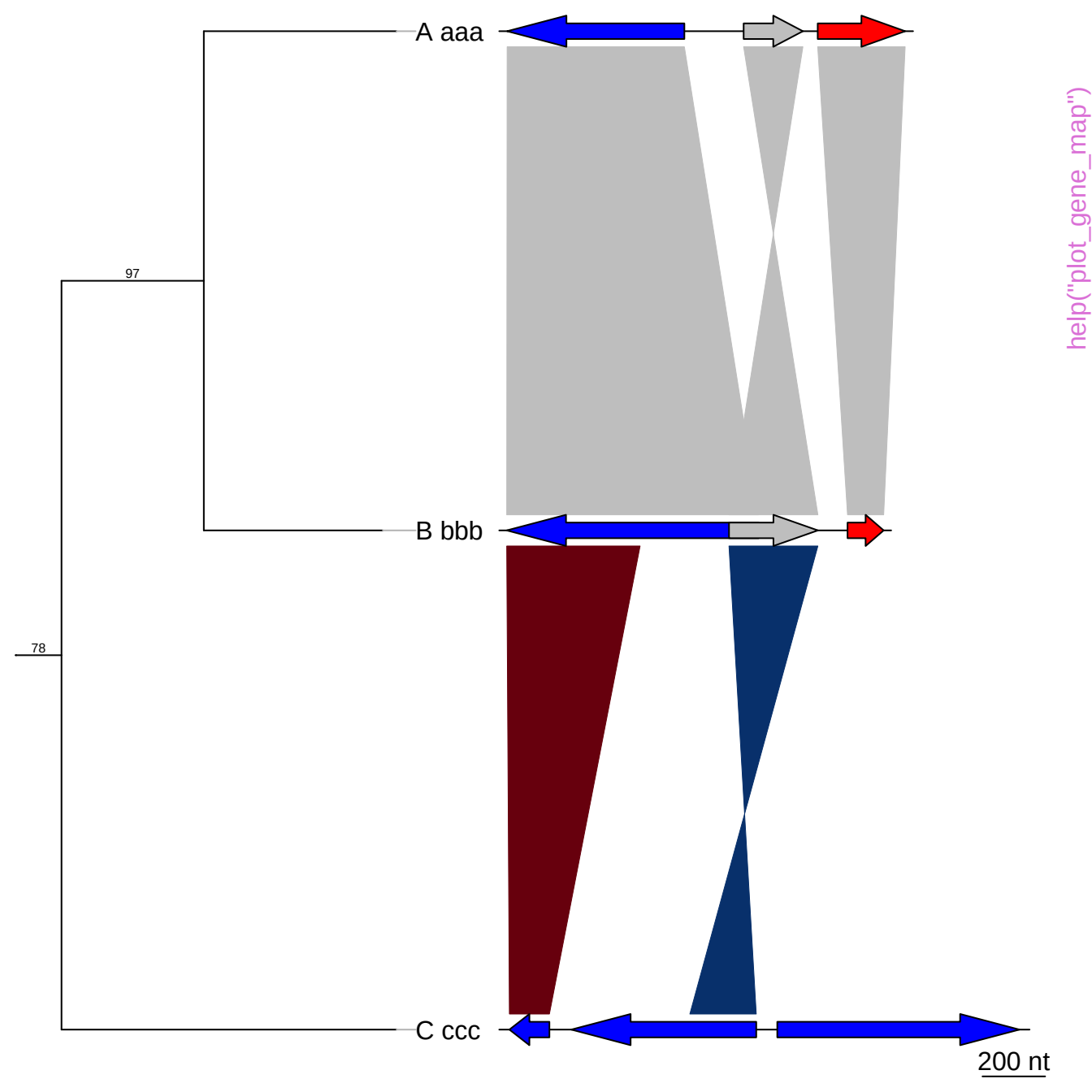
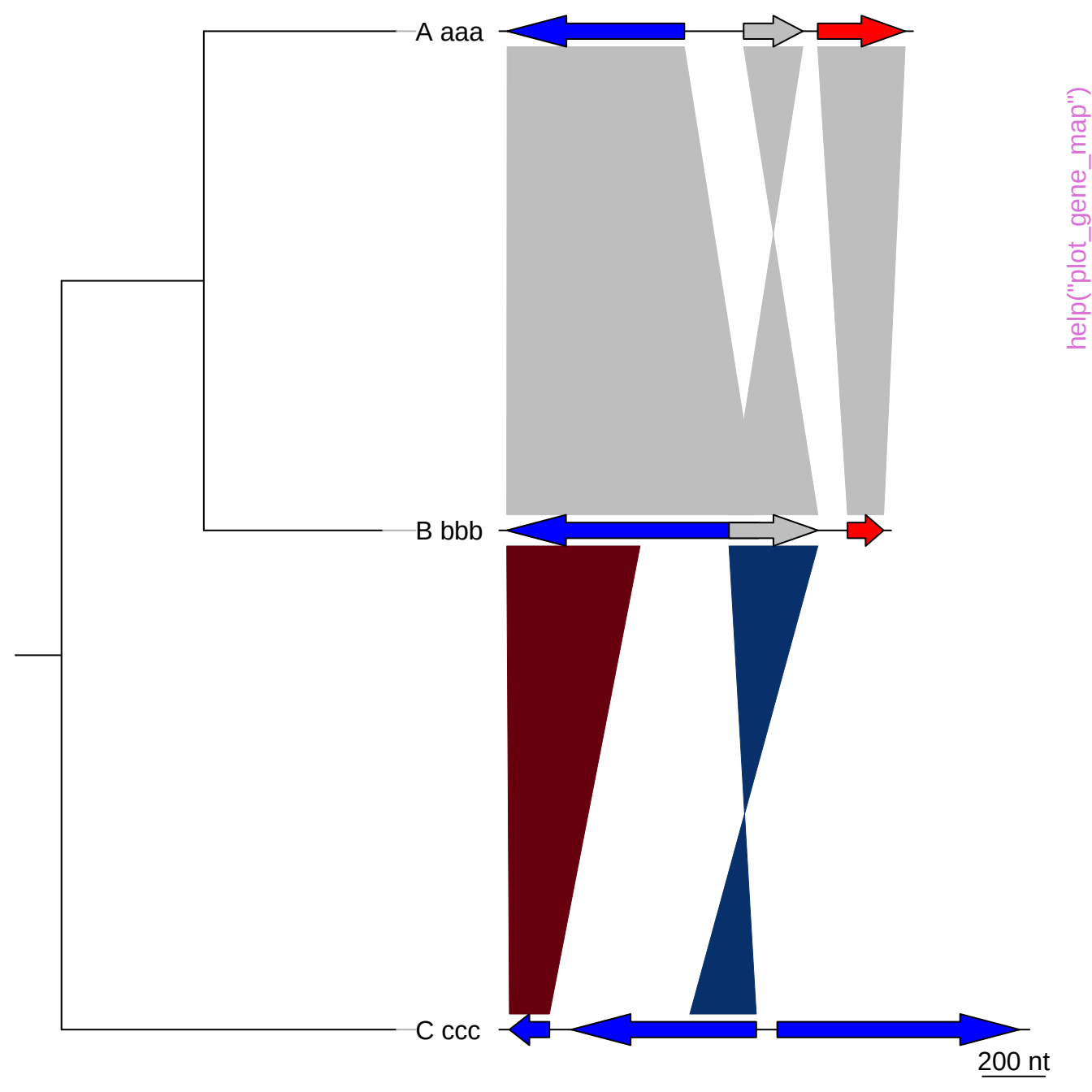
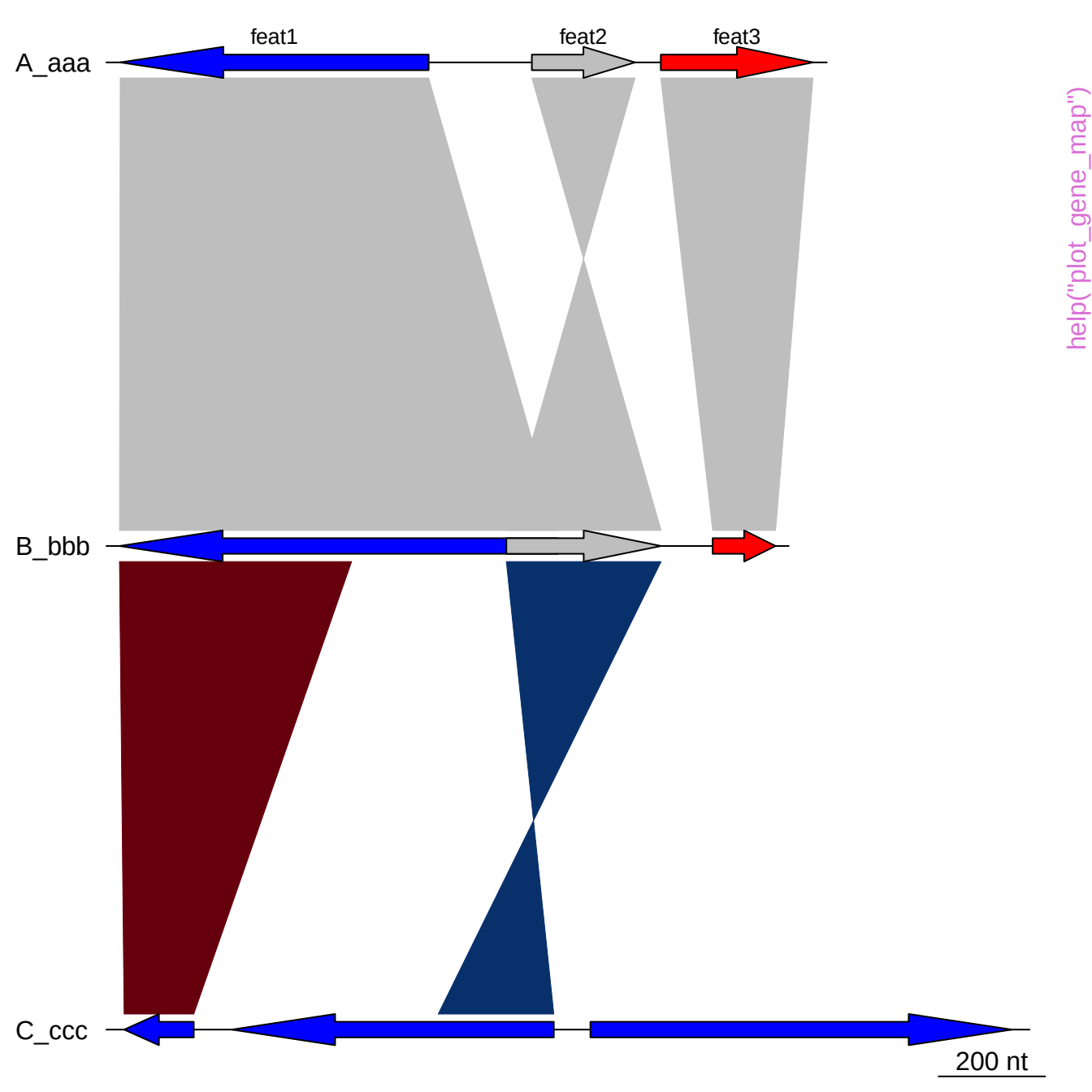

A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")


A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")


A aaa
B bbb
C ccc
97
78
200 nt
help("plot_gene_map")


A aaa
B bbb
C ccc
97
78
200 nt
help("plot_gene_map")


A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")


feat1
feat2
feat3
A_aaa
B_bbb
C_ccc
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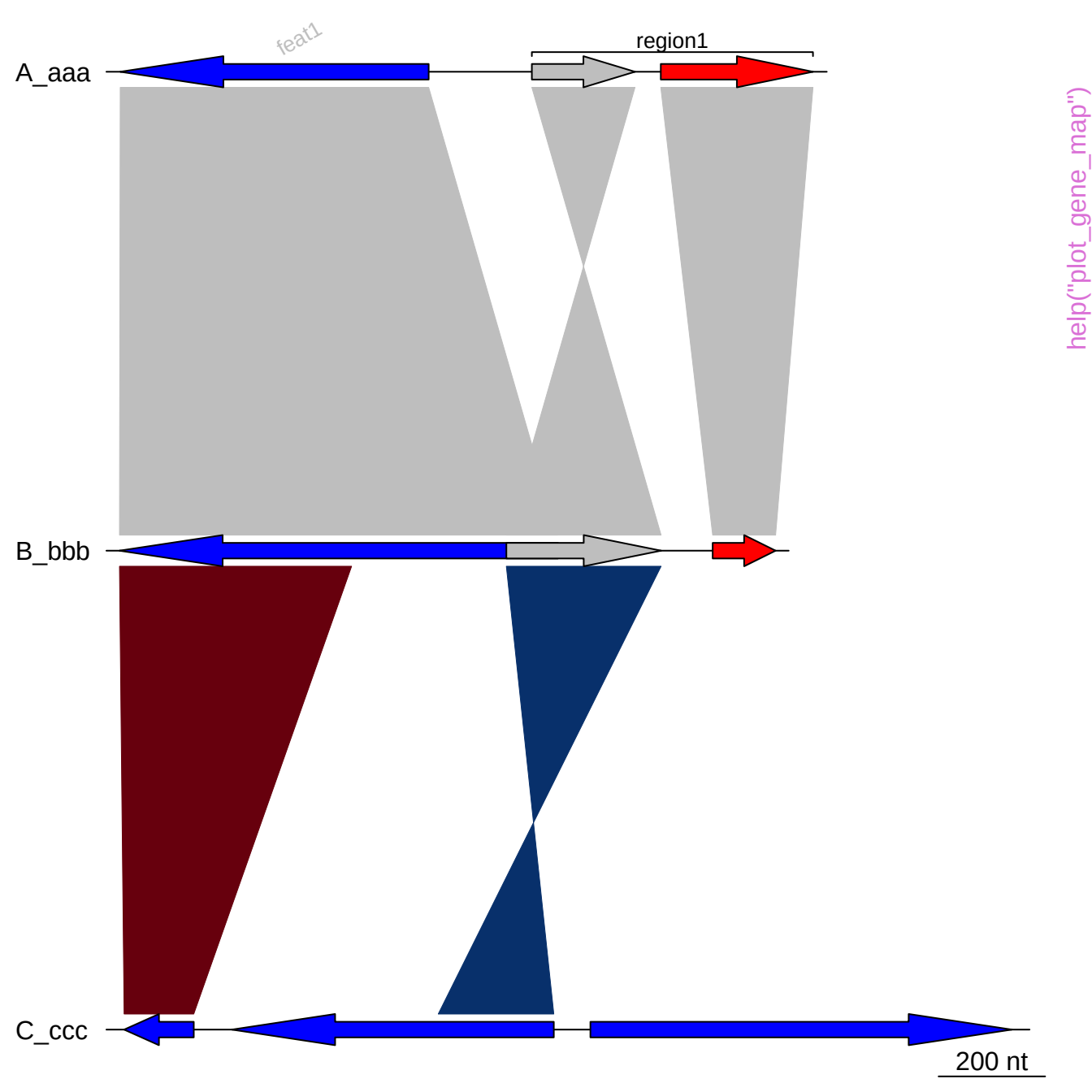
feat1
region1
A_aaa
B_bbb
C_ccc
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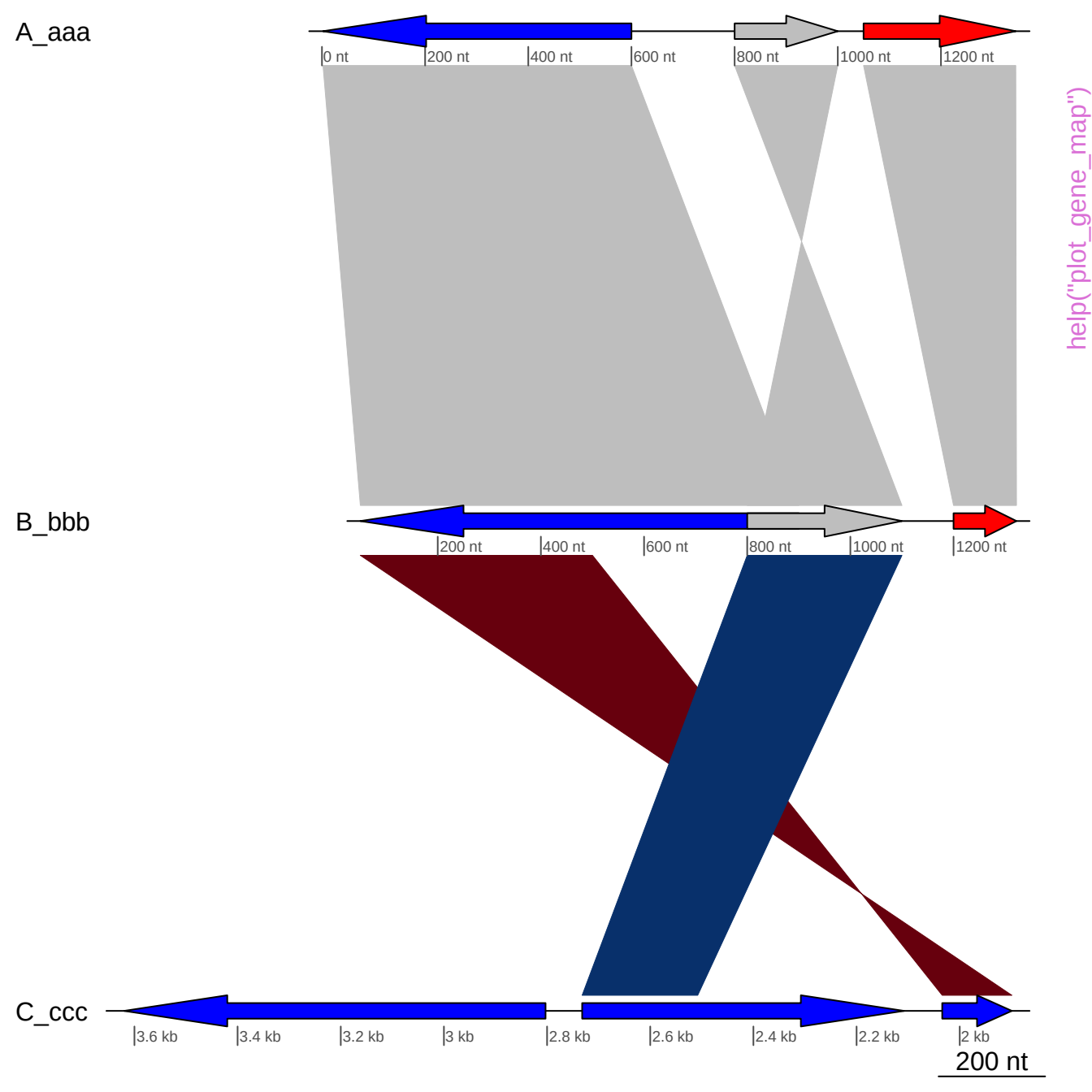
help("plot_gene_map")


A_aaa
0 nt
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
B_bbb
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
C_ccc
3.6 kb
3.4 kb
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3 kb
2.8 kb
2.6 kb
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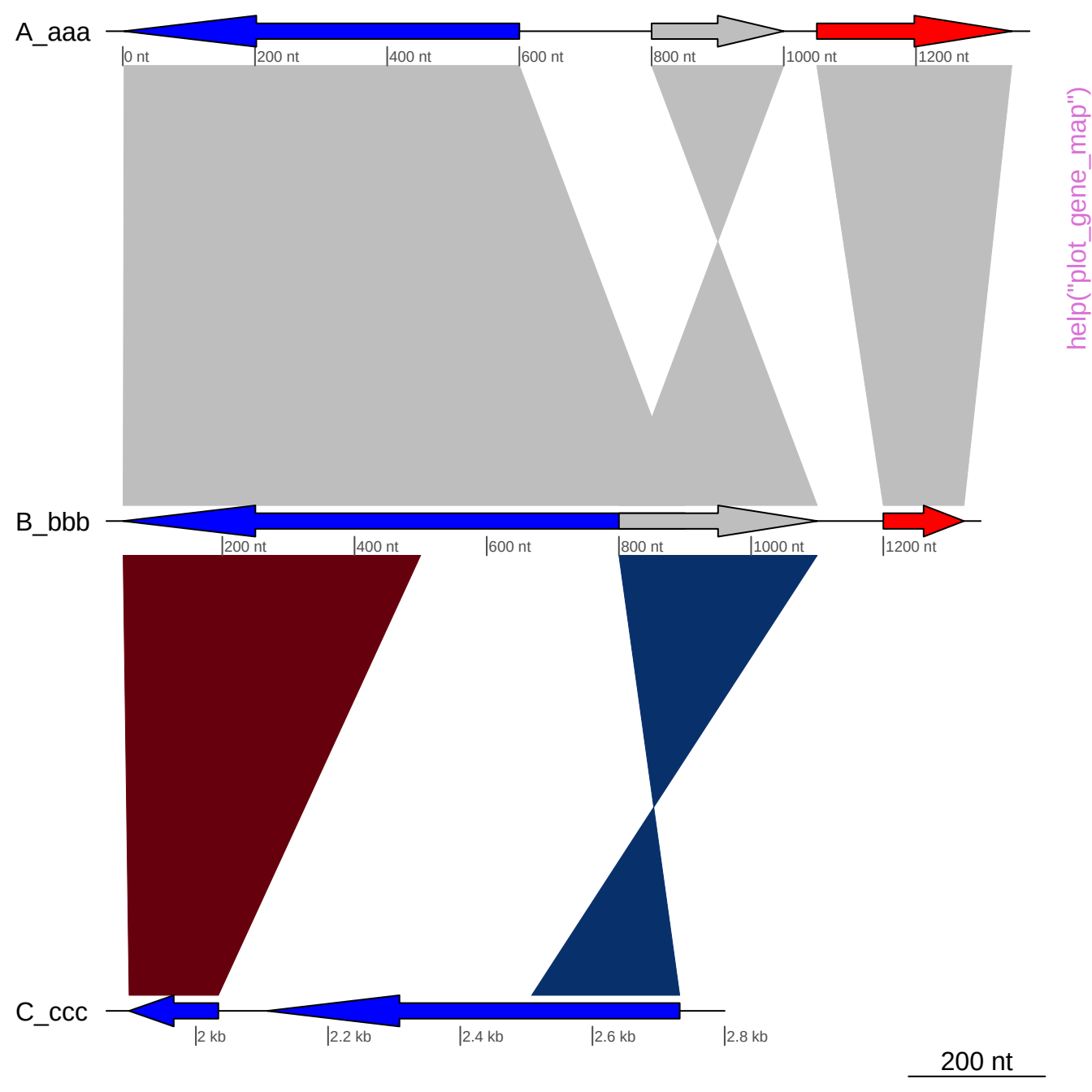
help("plot_gene_map")


A_aaa
0 nt
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
B_bbb
200 nt
400 nt
600 nt
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1000 nt
1200 nt
C_ccc
2 kb
2.2 kb
2.4 kb
2.6 kb
2.8 kb
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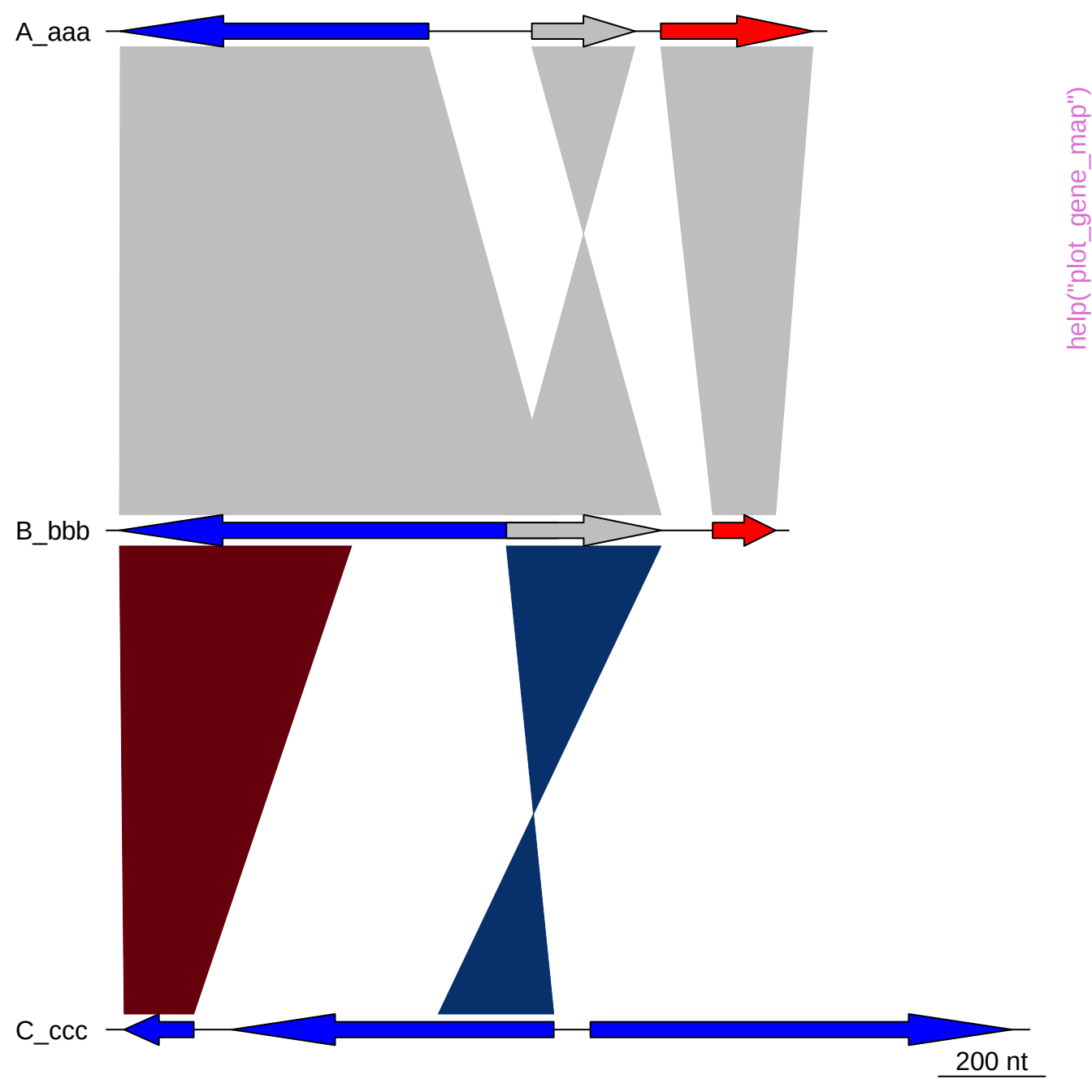
help("plot_gene_map")


A_aaa
B_bbb
C_ccc
200 nt
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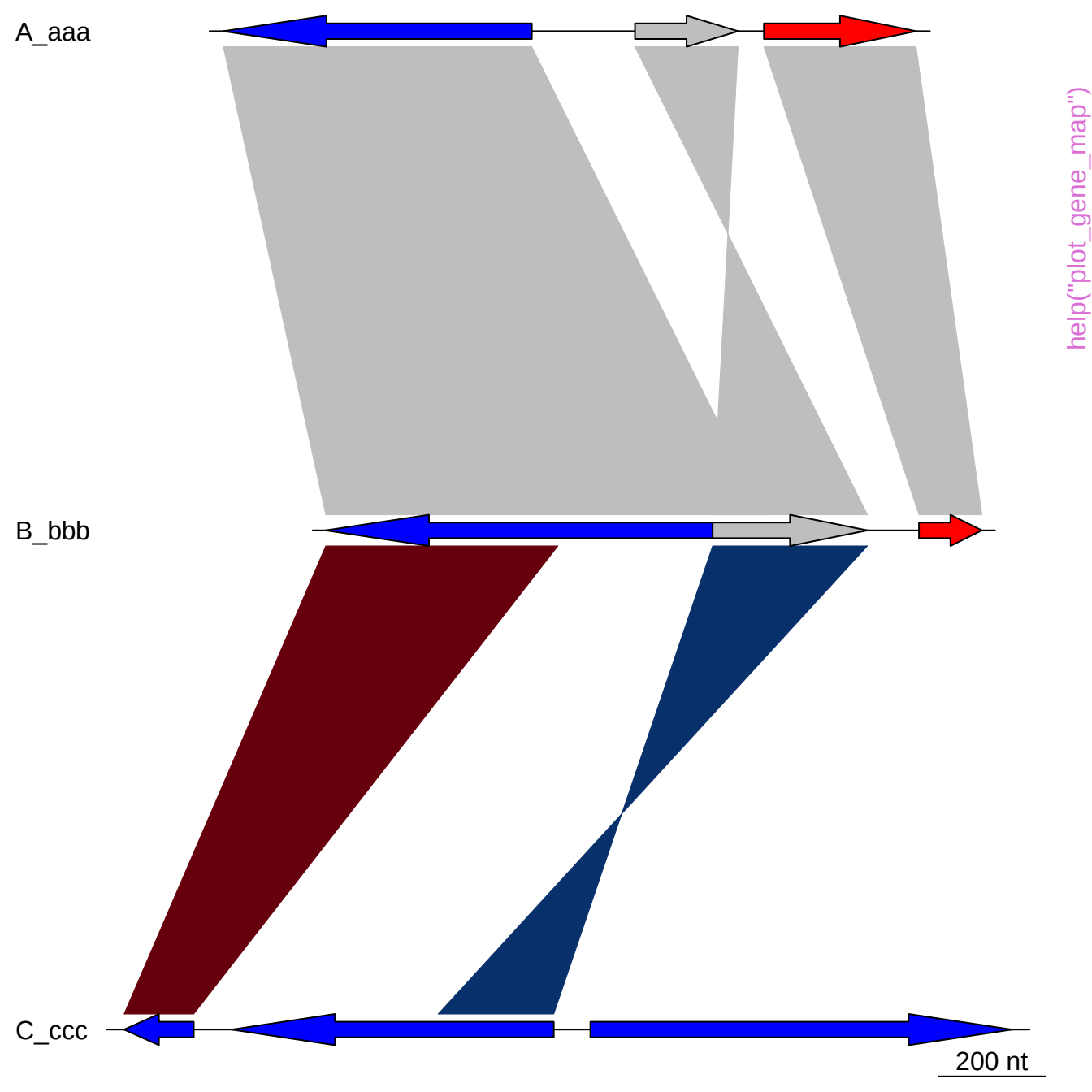
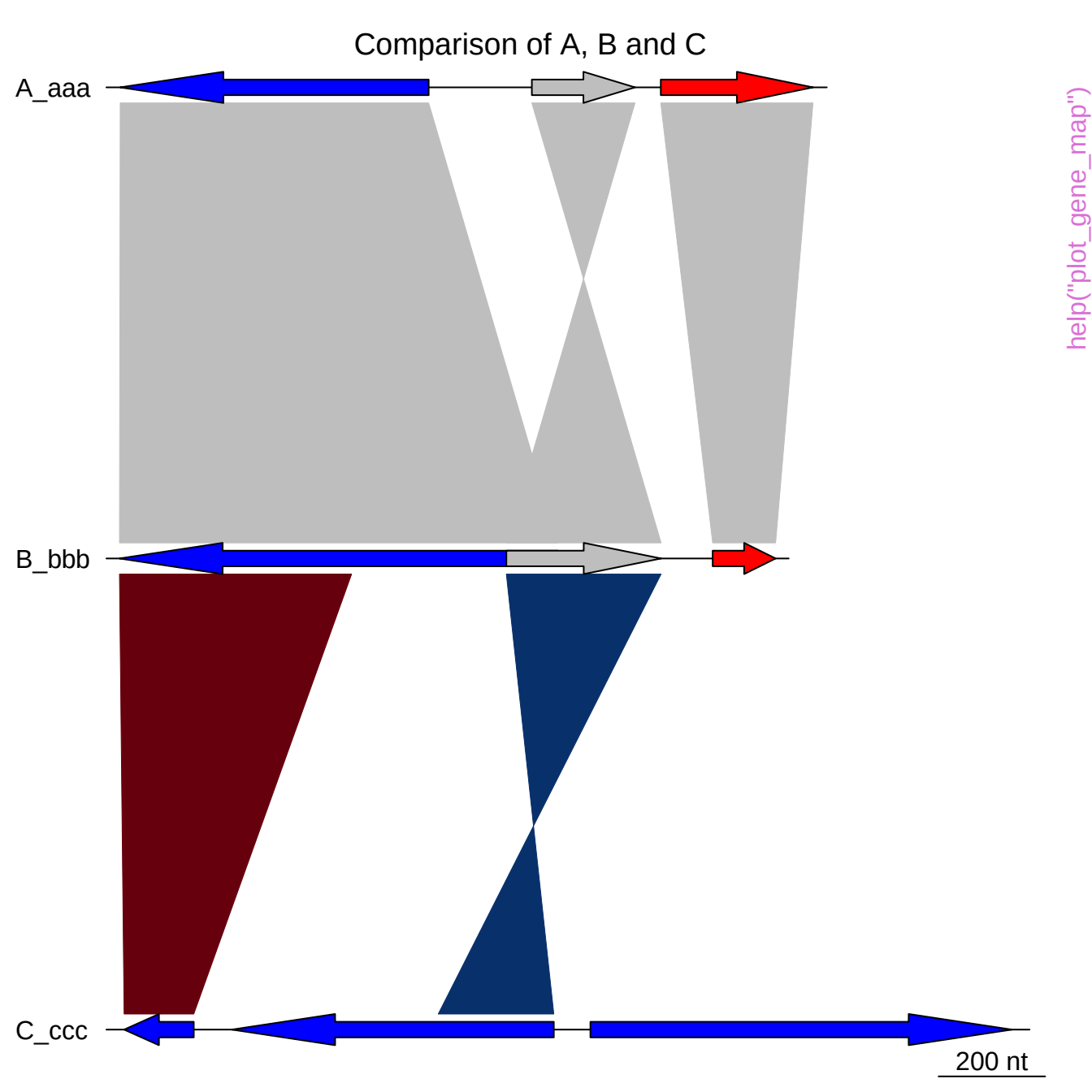
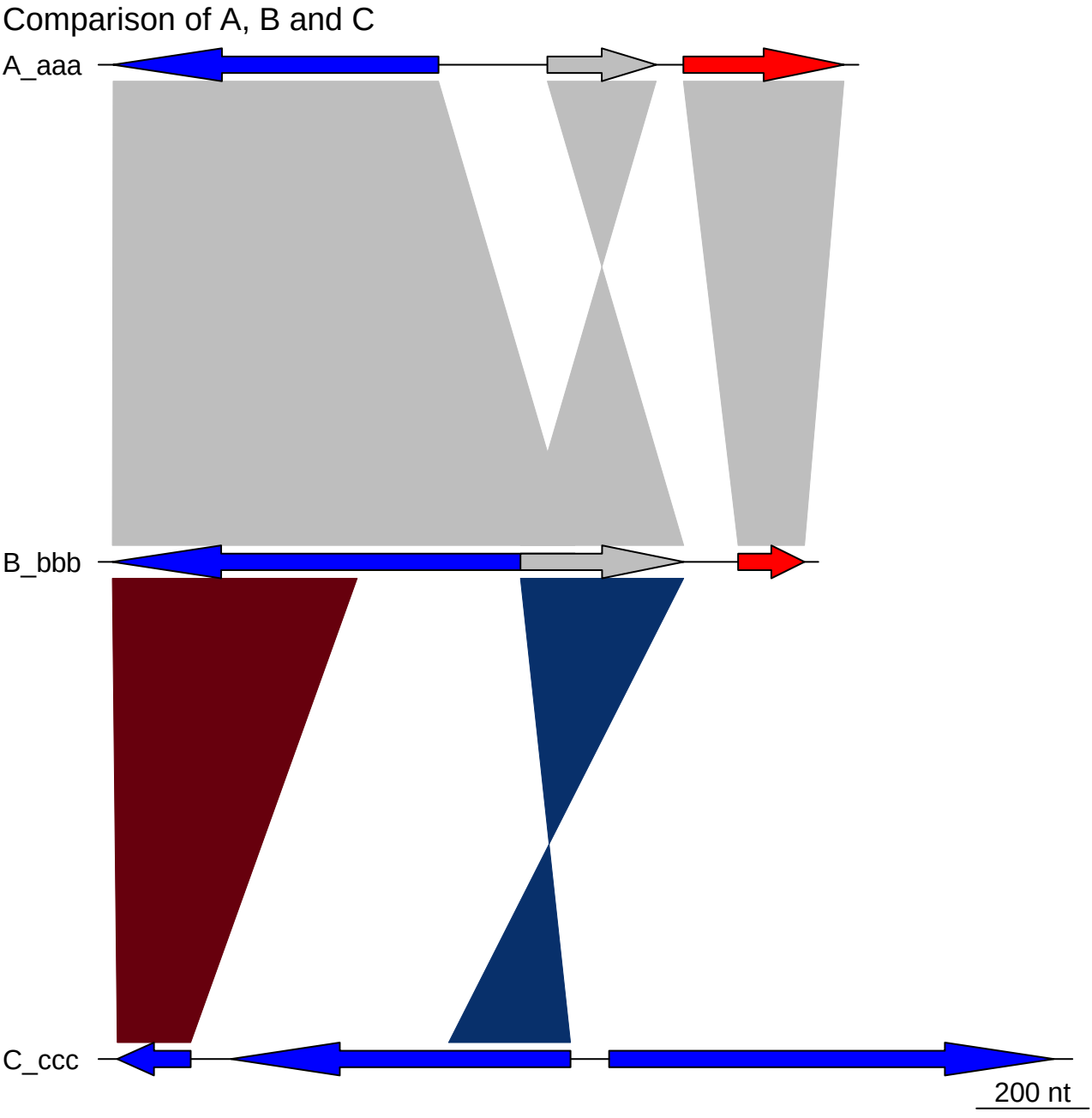
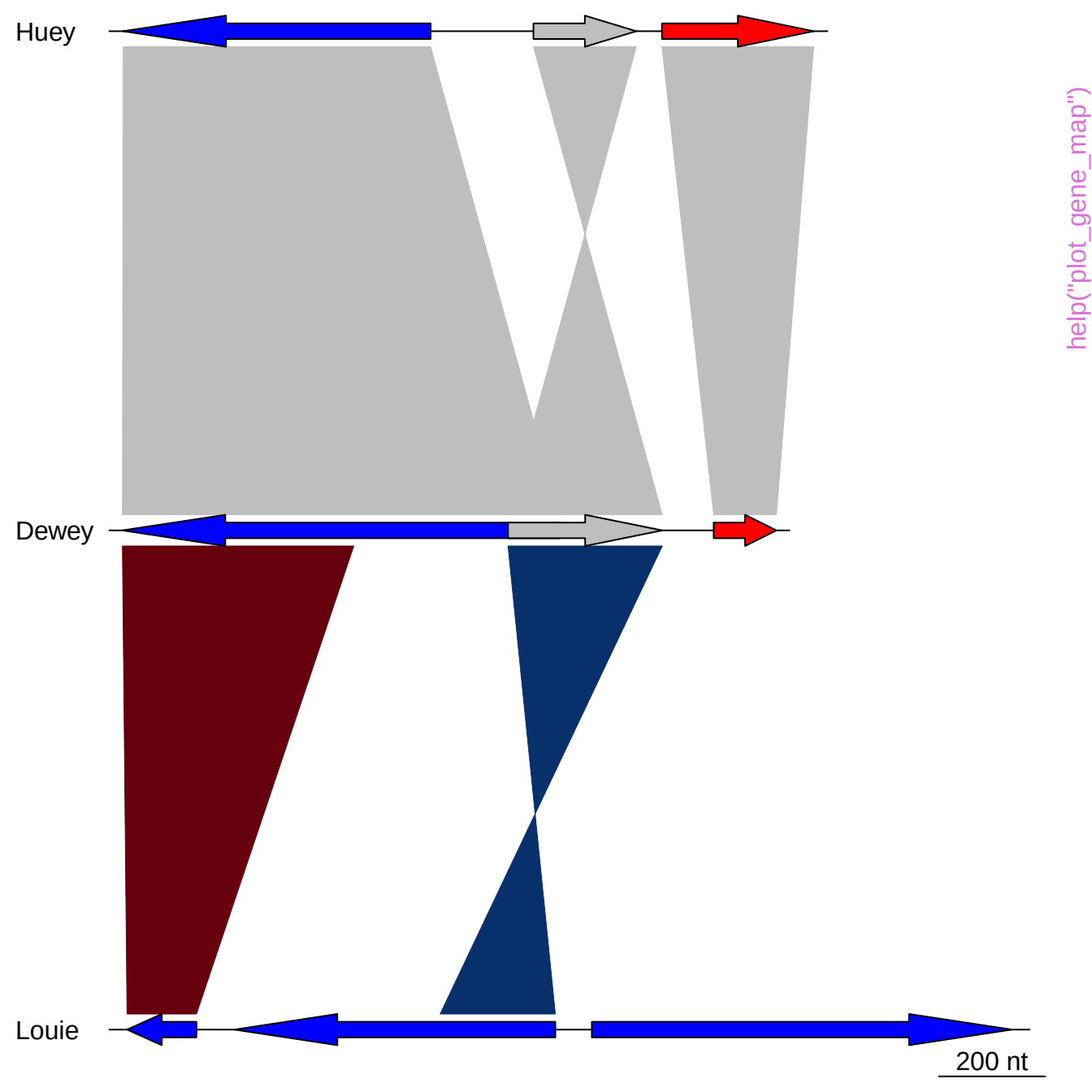
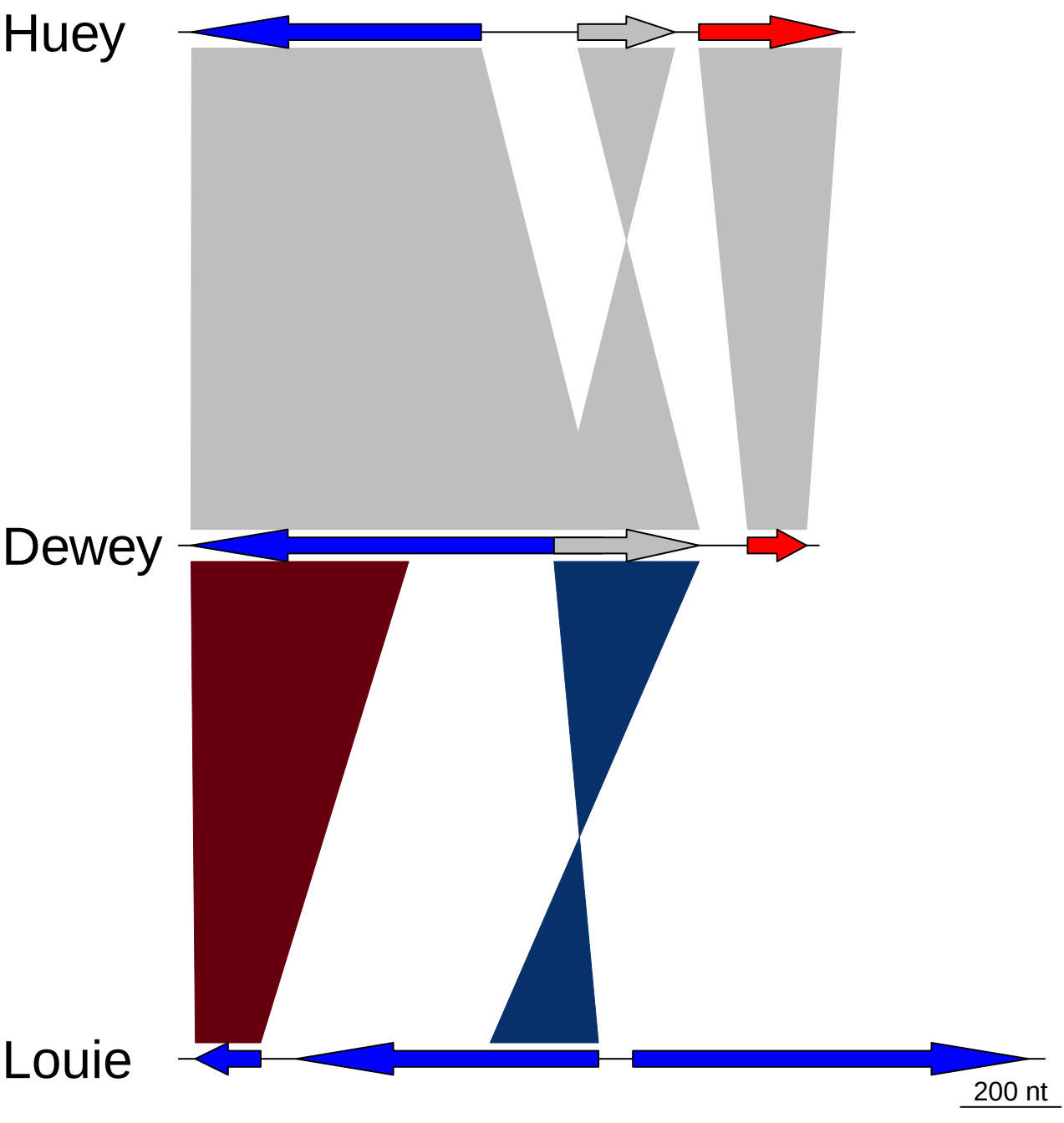
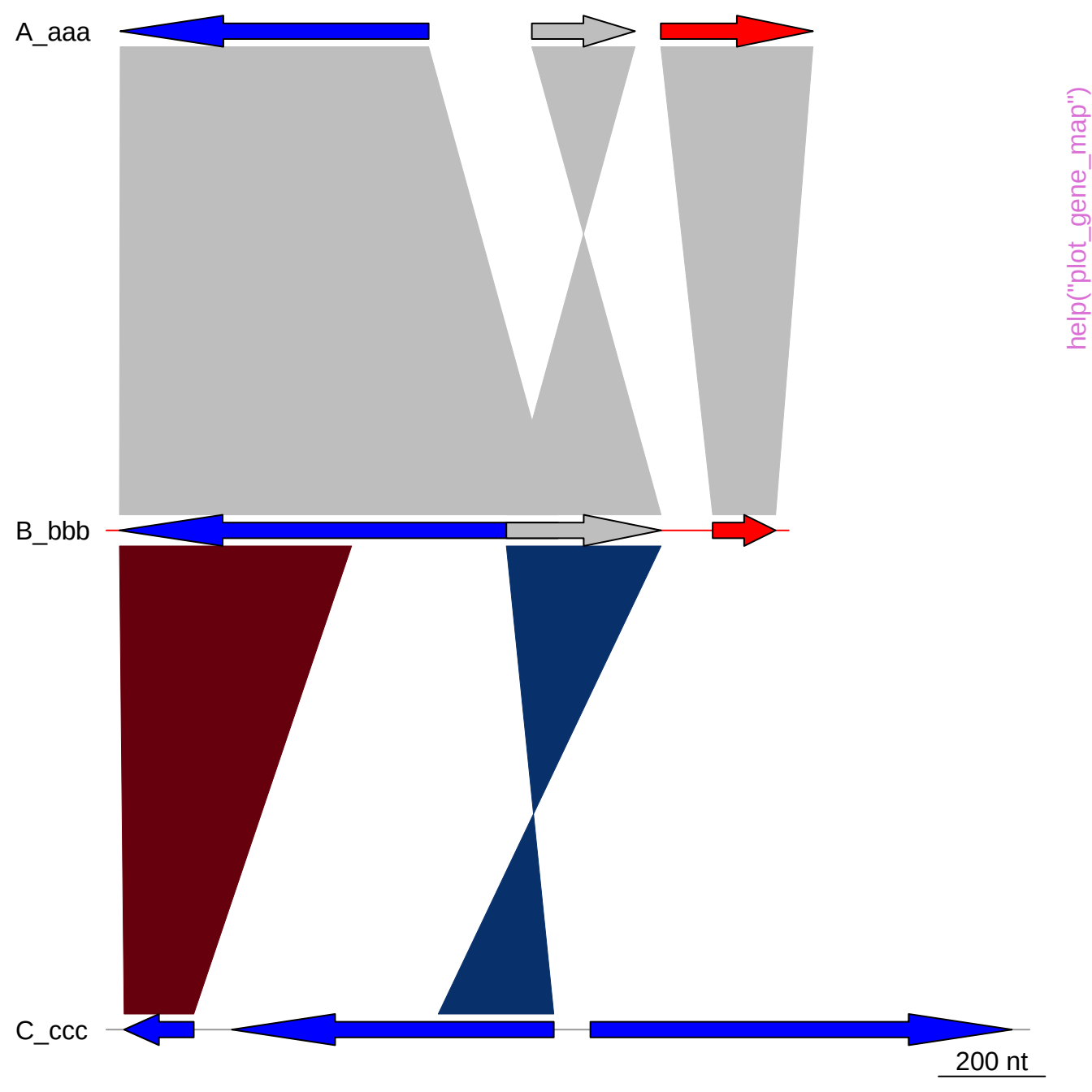

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

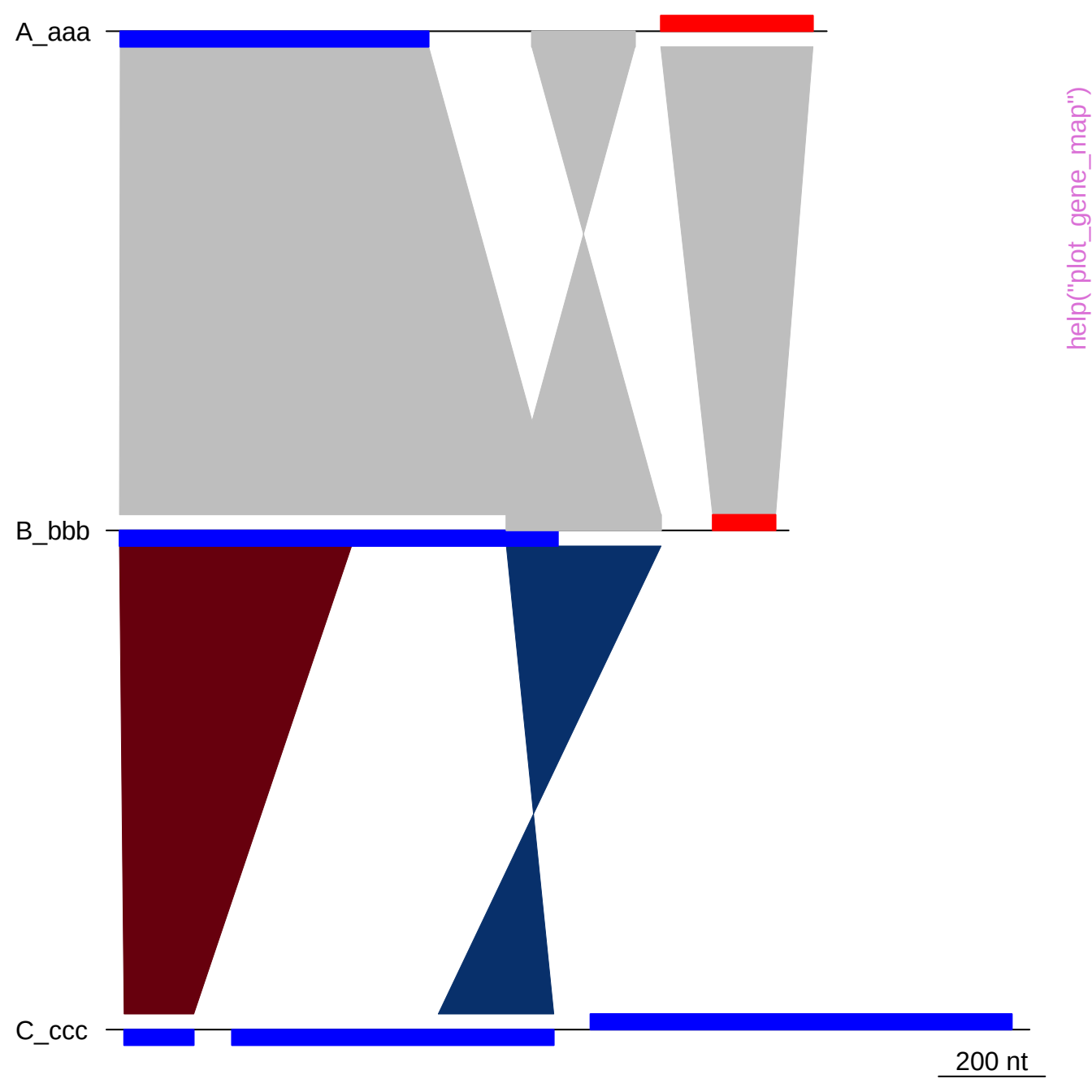

Comparison of A, B and C
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

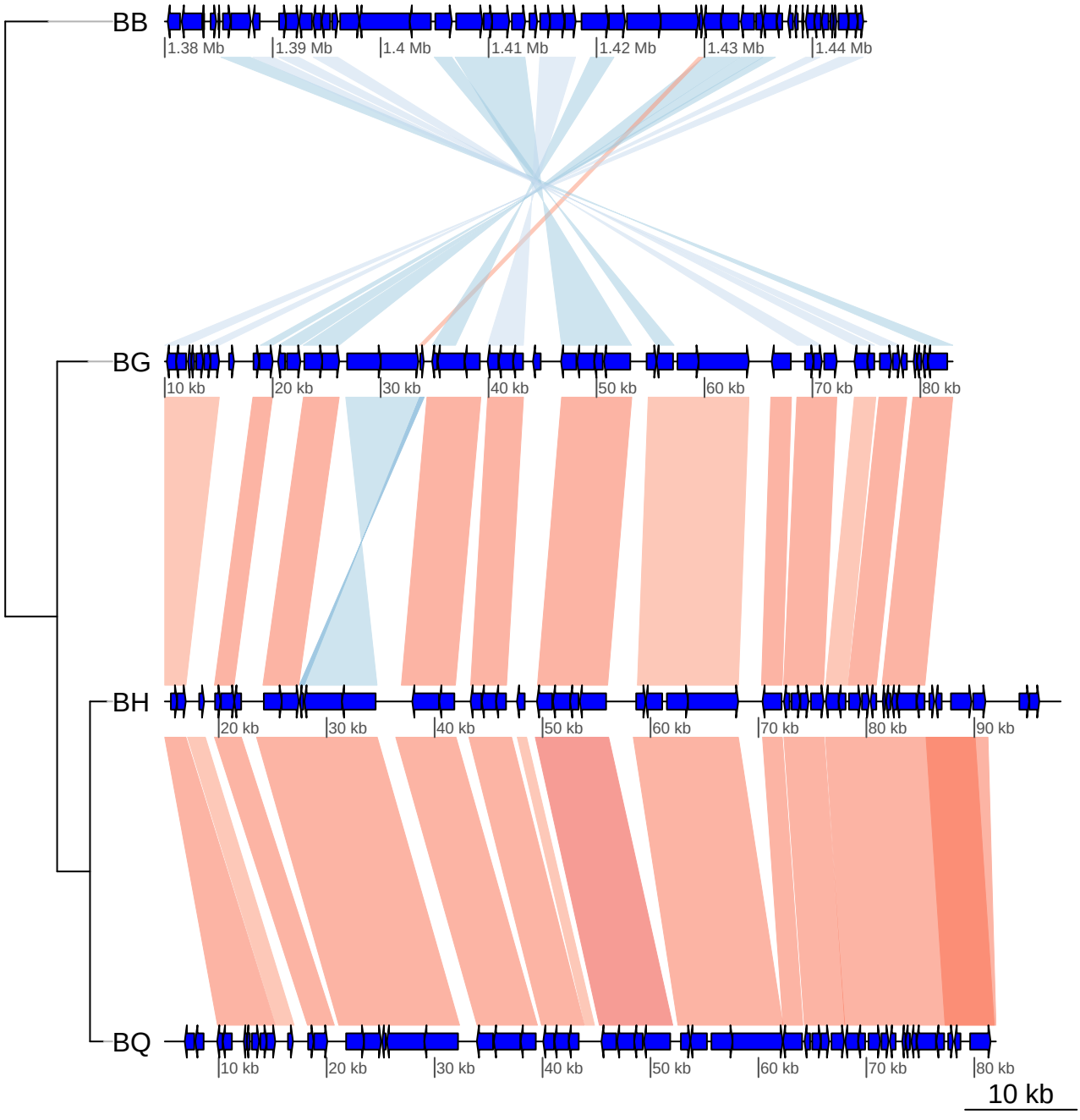

Comparison of A, B and C
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")


Huey
Dewey
Louie
200 nt
help("plot_gene_map")


Huey
Dewey
Louie
200 nt
help("plot_gene_map")


A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")


A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")


BB
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1.41 Mb
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1.43 Mb
1.44 Mb
BG
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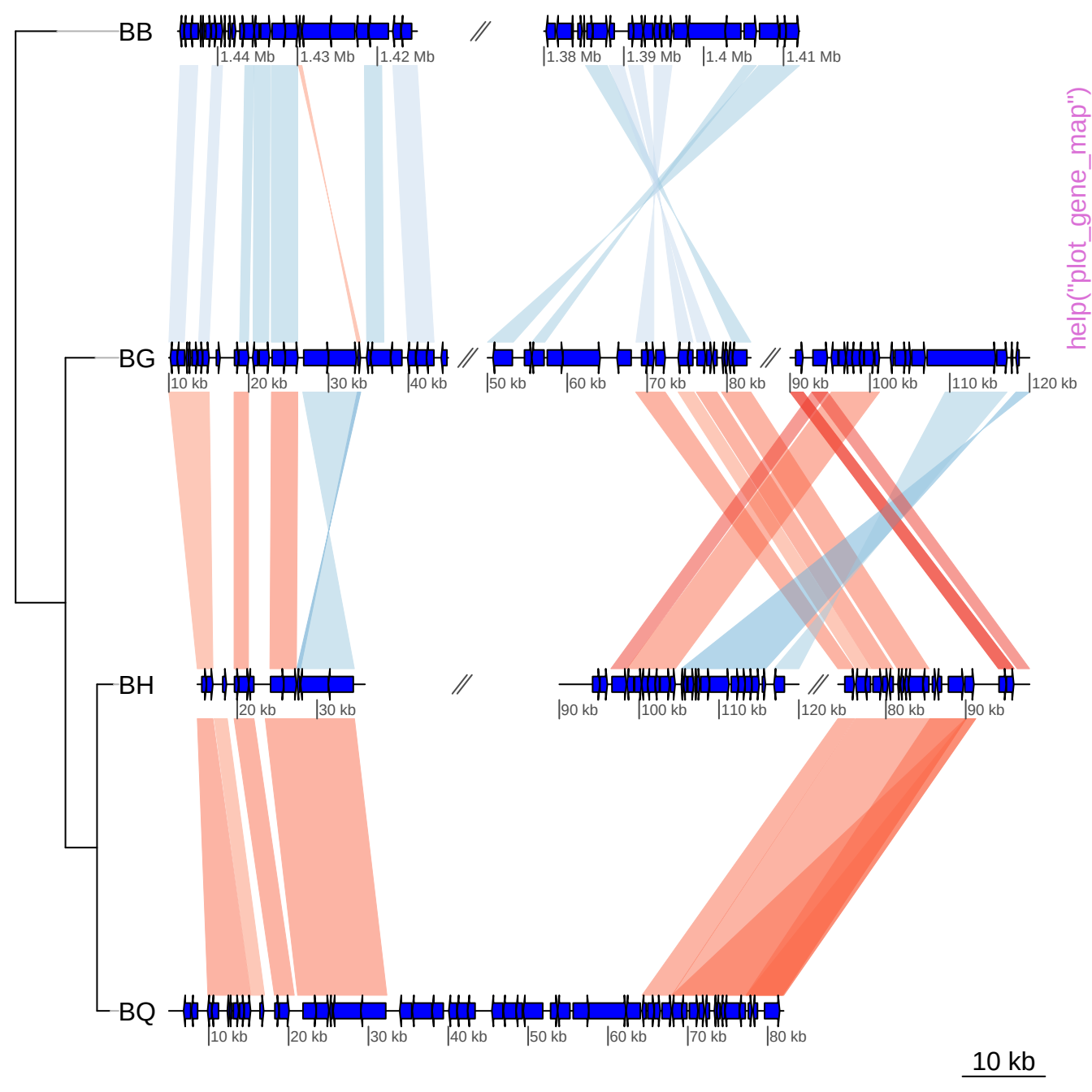
help("plot_gene_map")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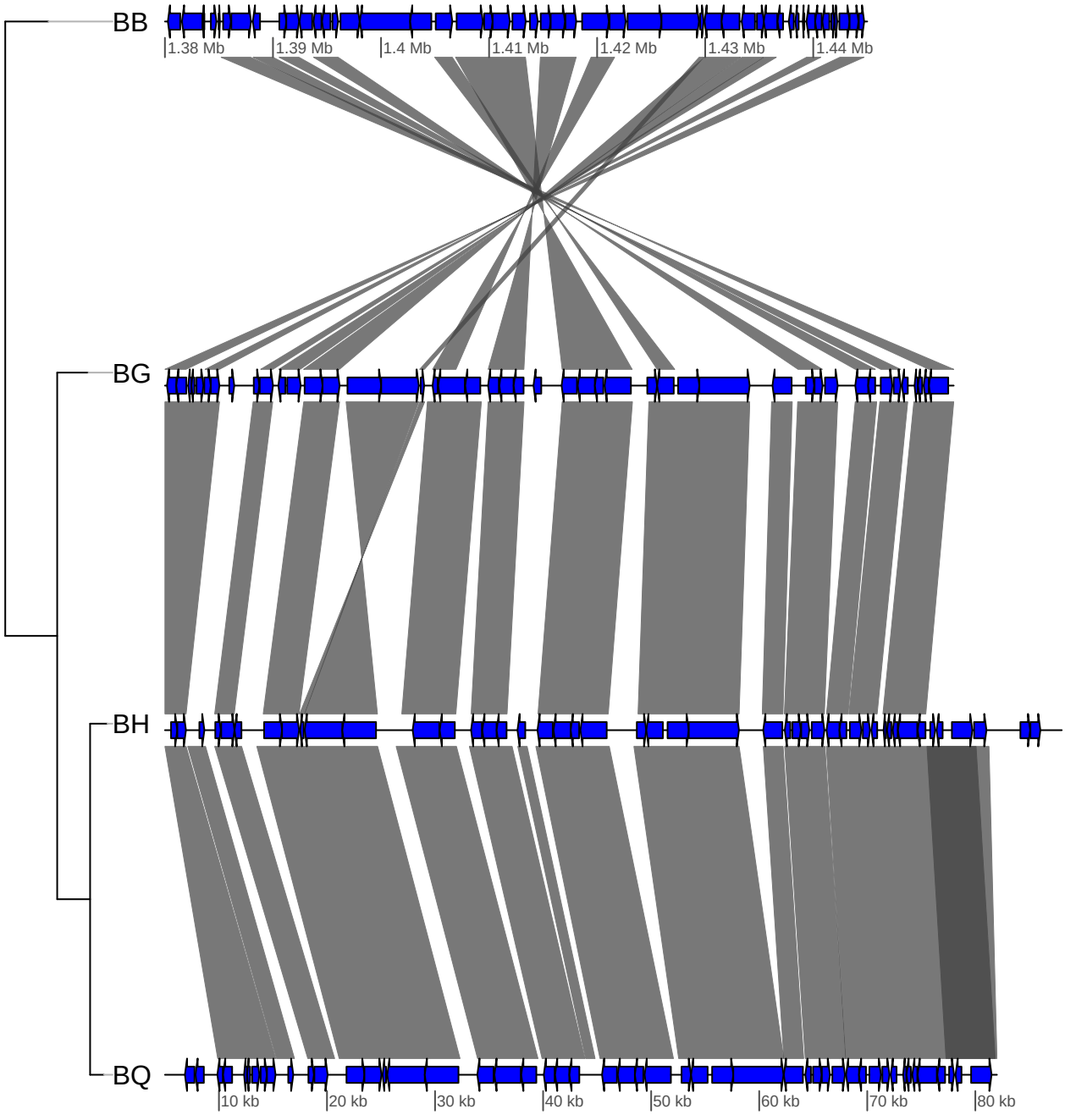
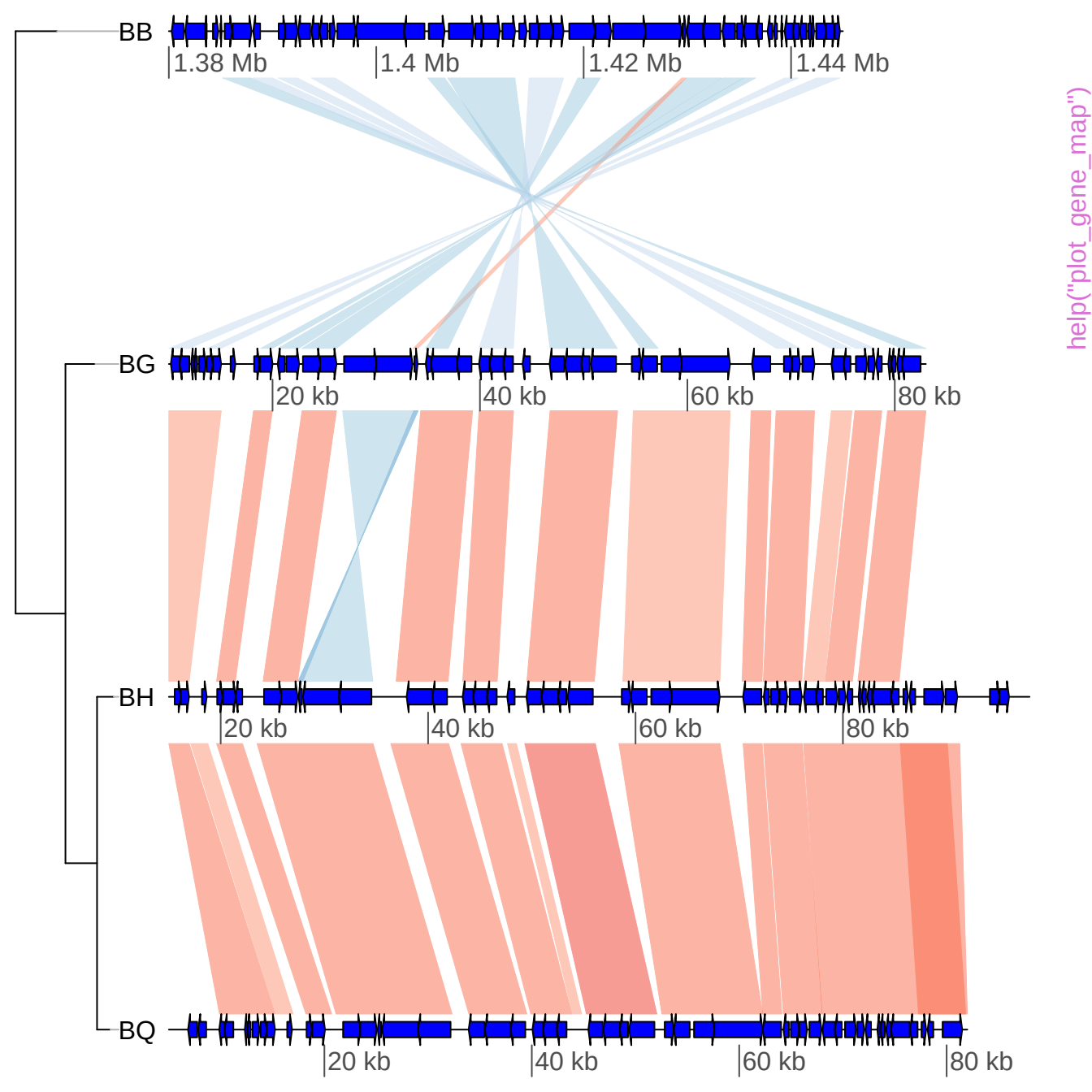


help("plot_gene_map")


BB
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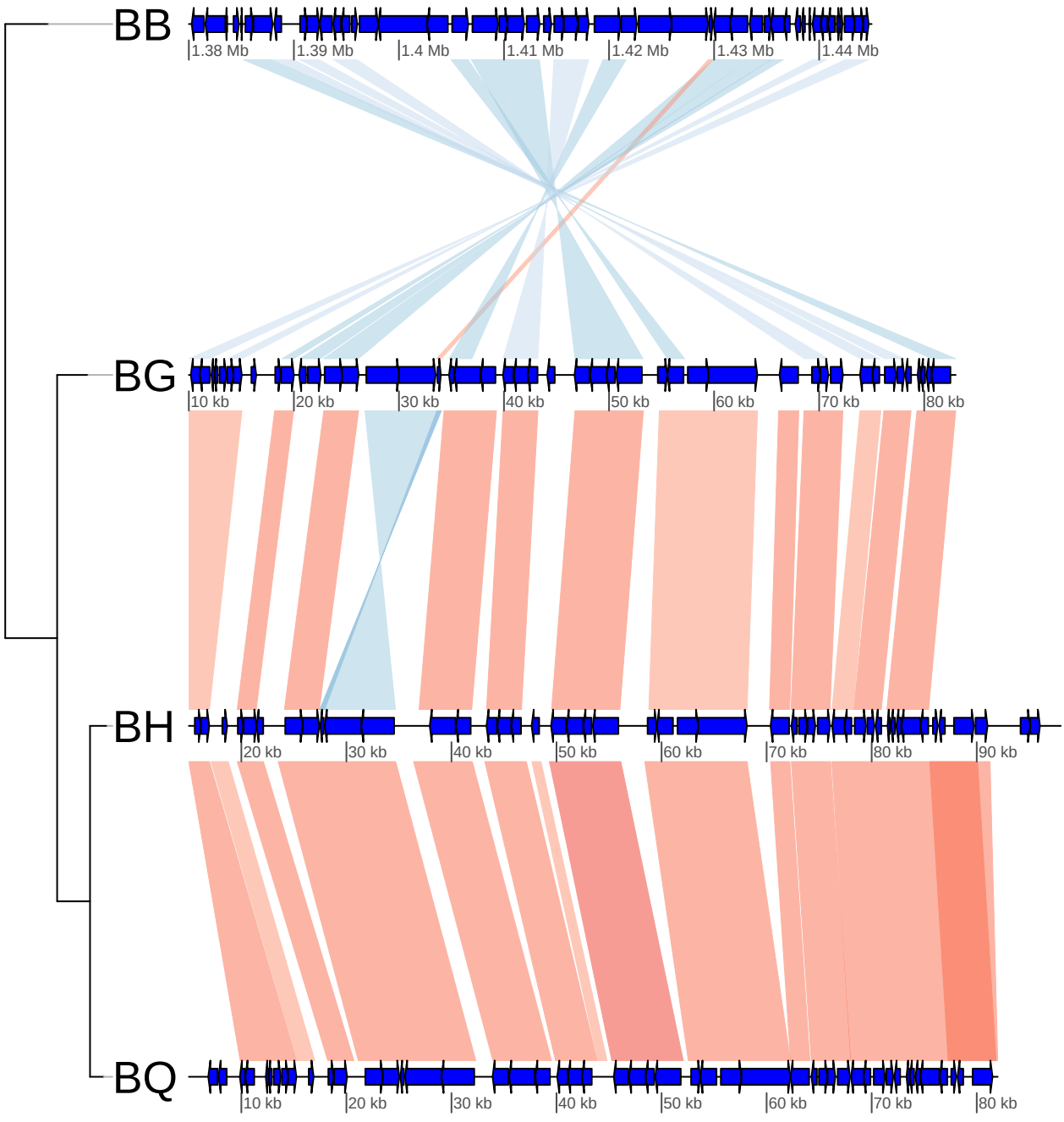
help("plot_gene_map")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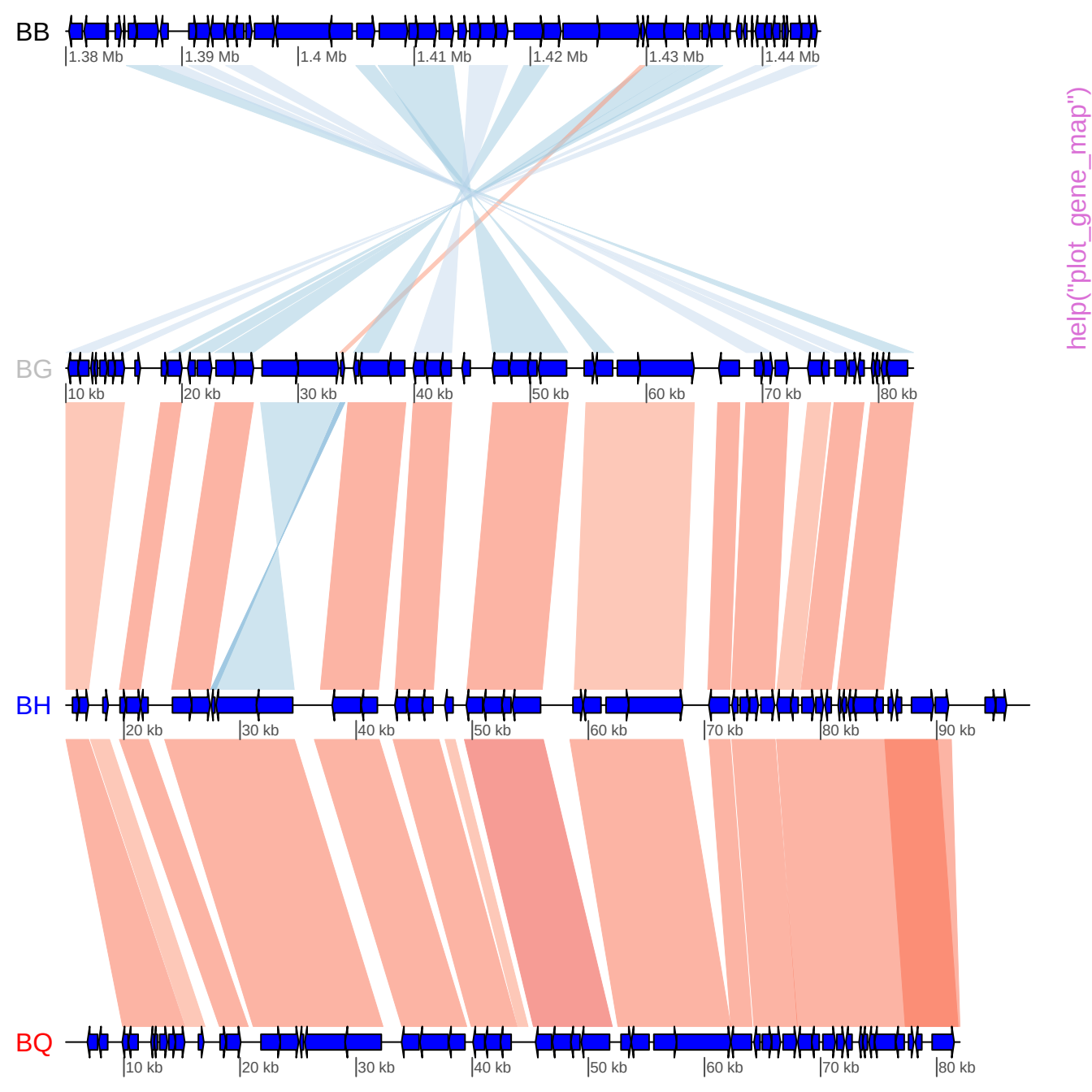
BB
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BQ
10 kb
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40 kb
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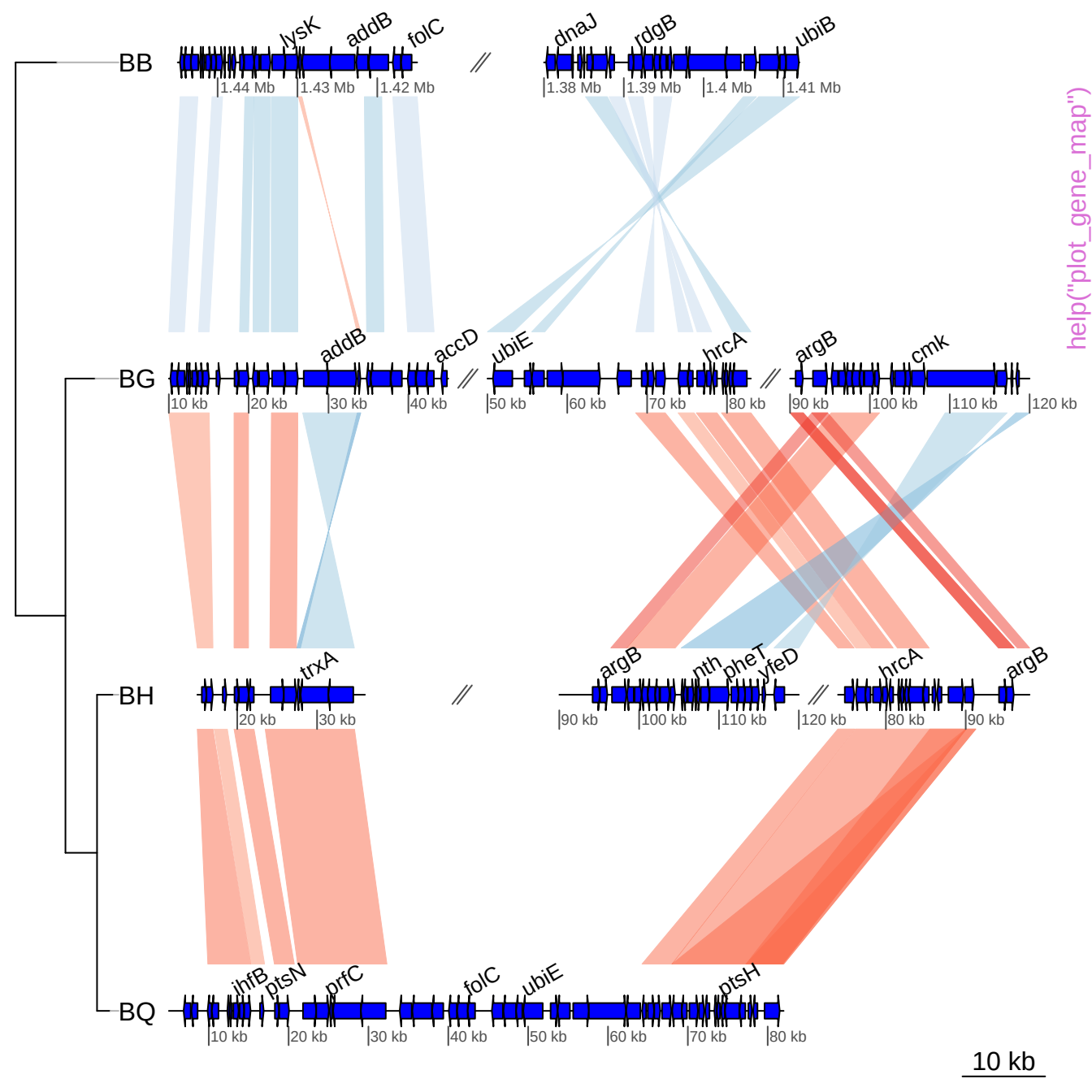
80 kb
help("plot_gene_map")


BB
lysK
addB
folC
1.44 Mb
1.43 Mb
1.42 Mb
dnaJ
rdgB
ubiB
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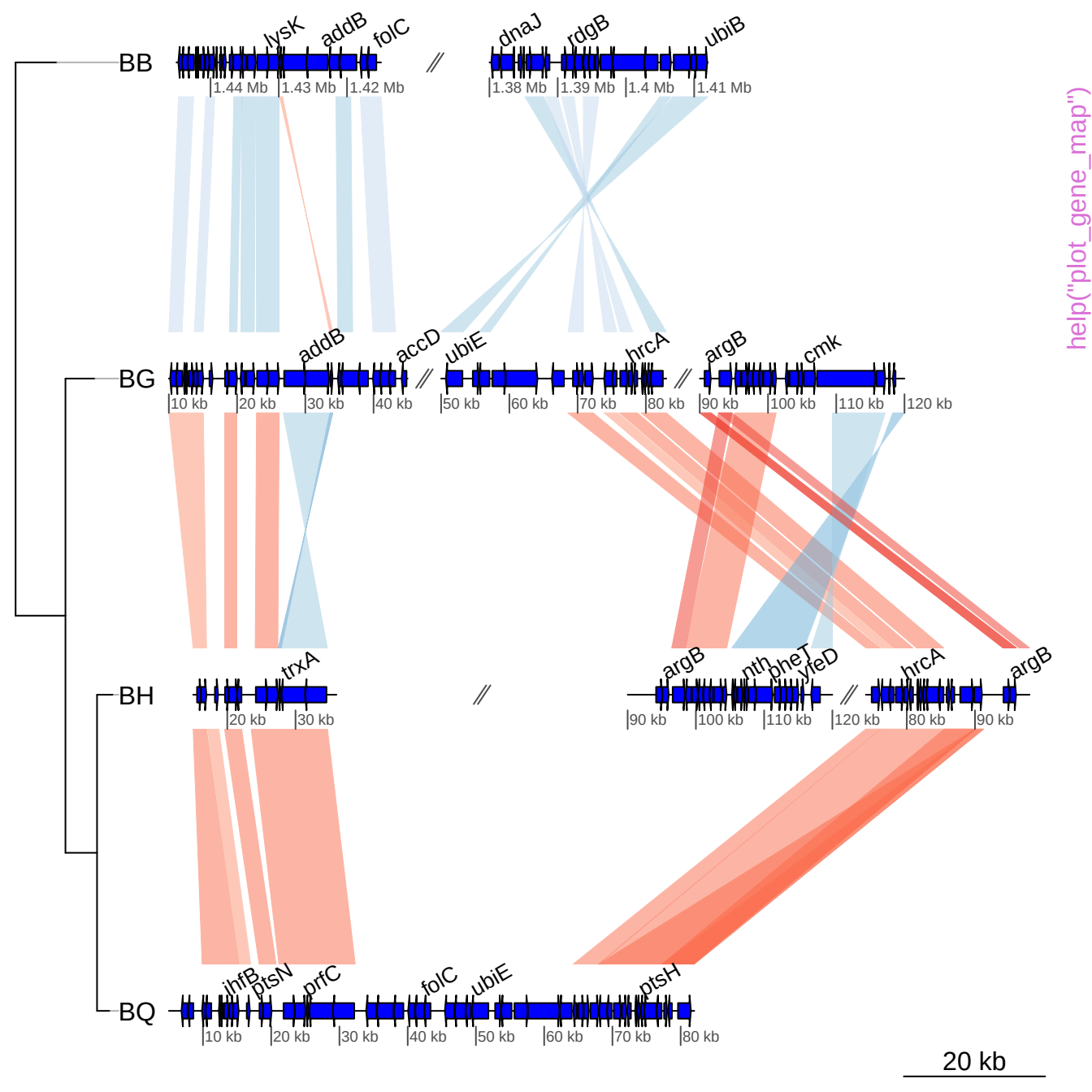
help("plot_gene_map")
10 kb


BB
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folC
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ubiB
1.44 Mb
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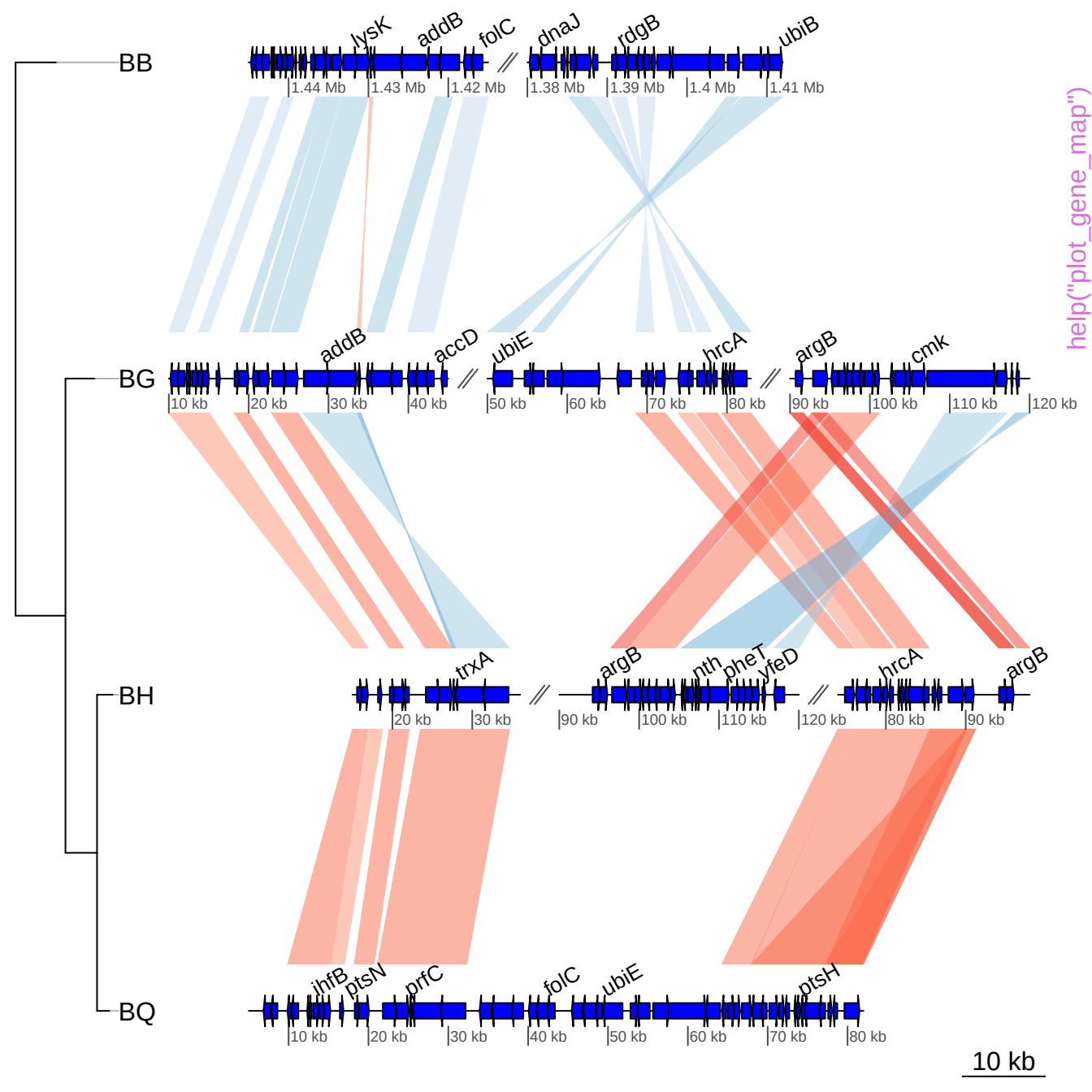
help("plot_gene_map")


BB
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help("plot_gene_map")
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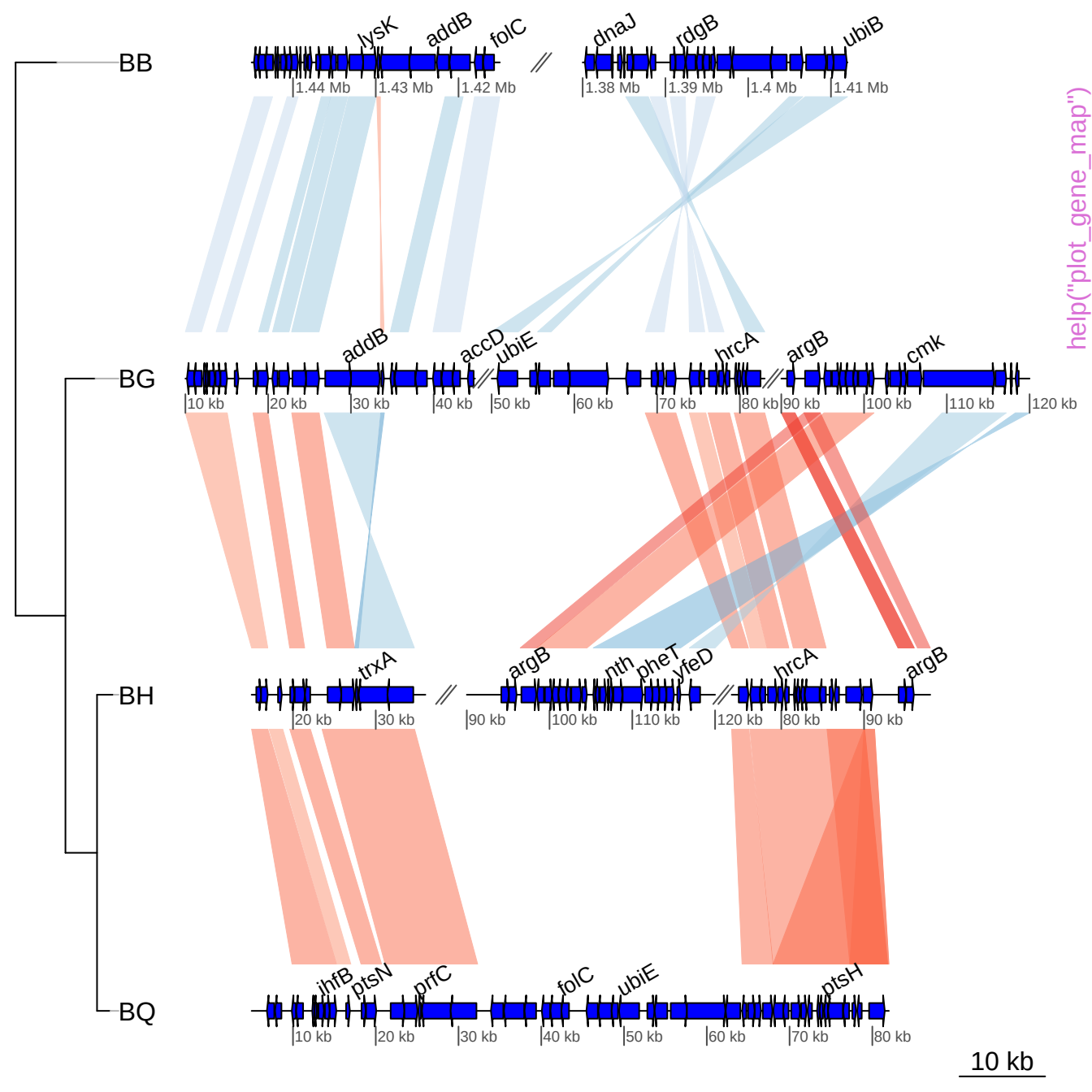
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help("plot_gene_map")
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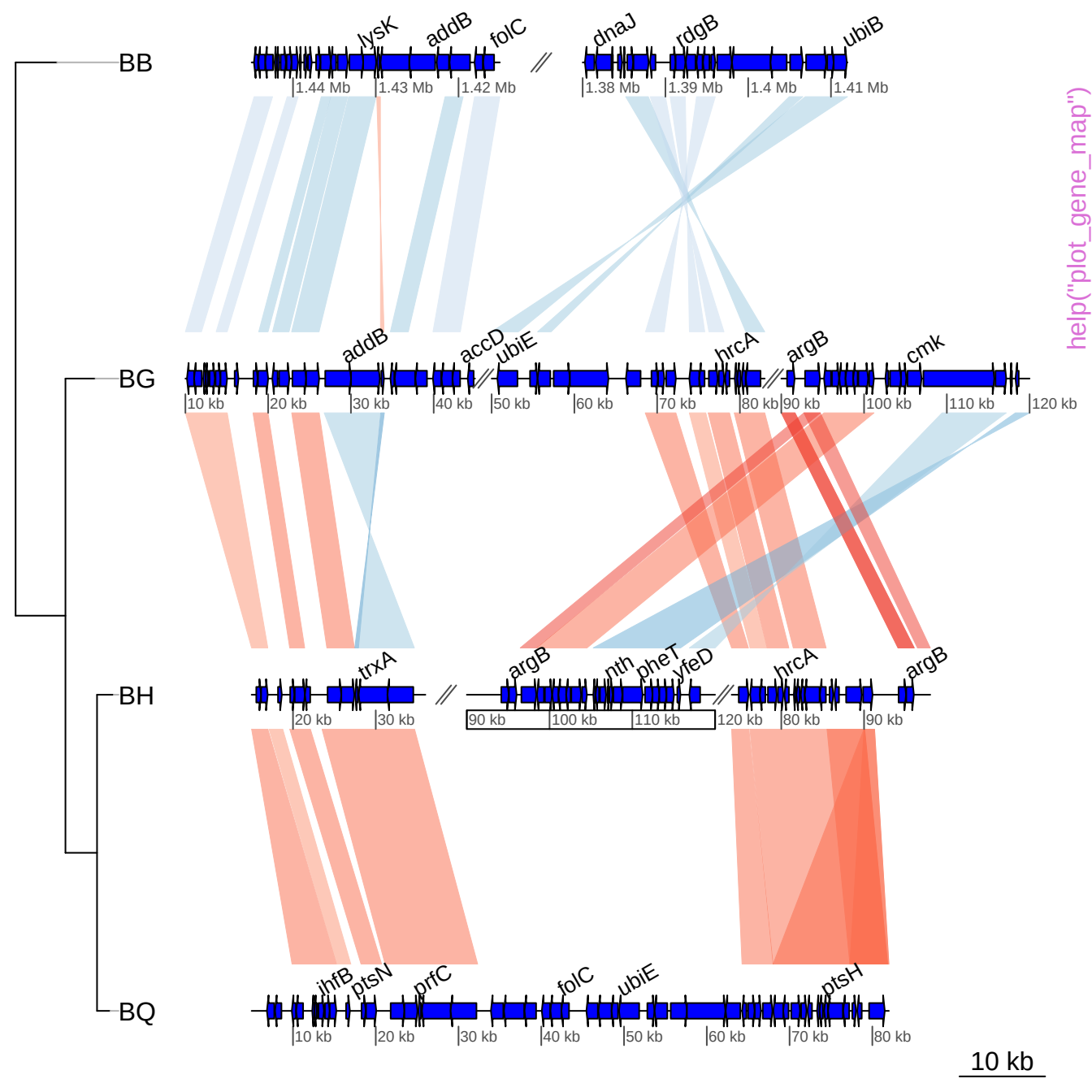
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help("plot_gene_map")
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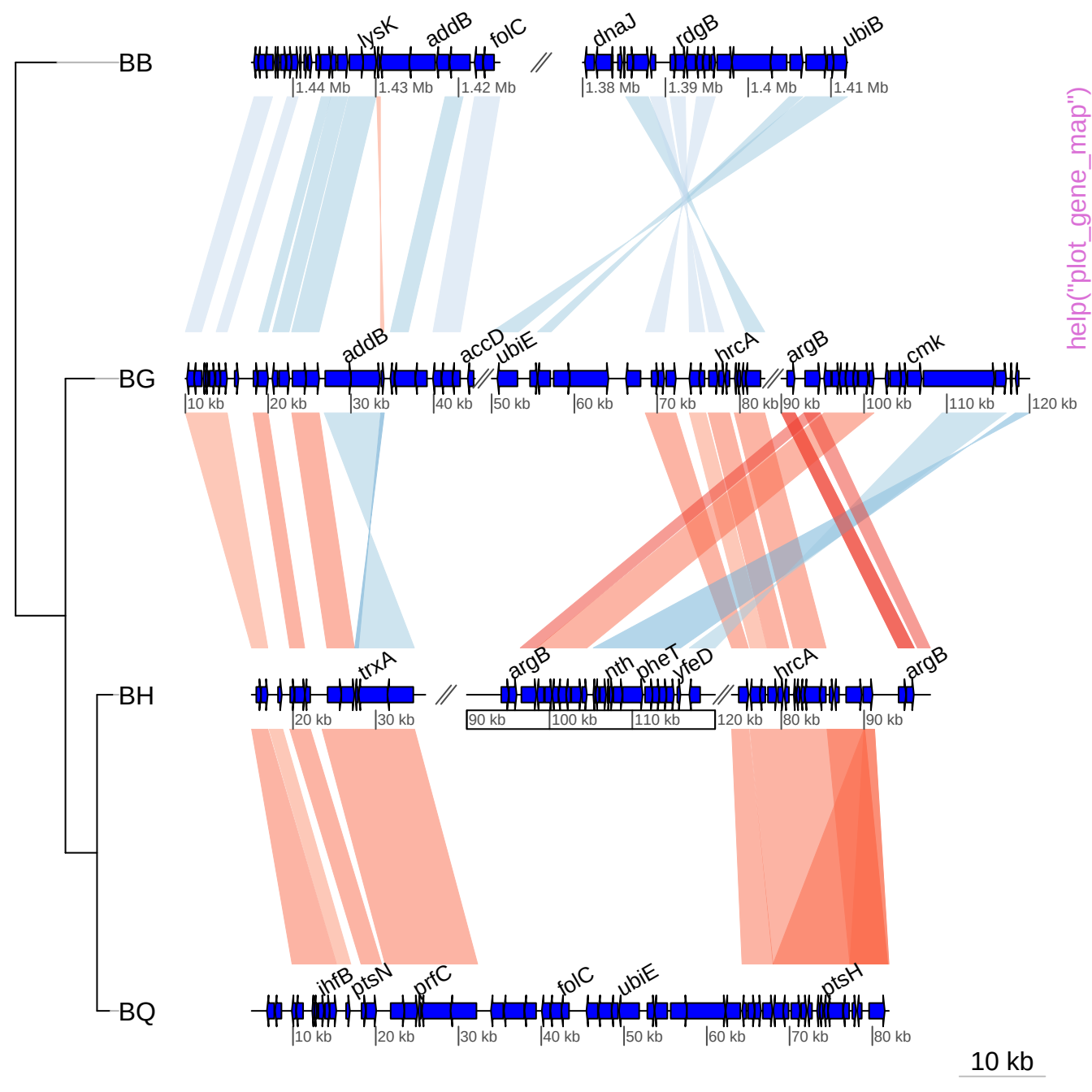
BB
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folC
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rdgB
ubiB
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help("plot_gene_map")
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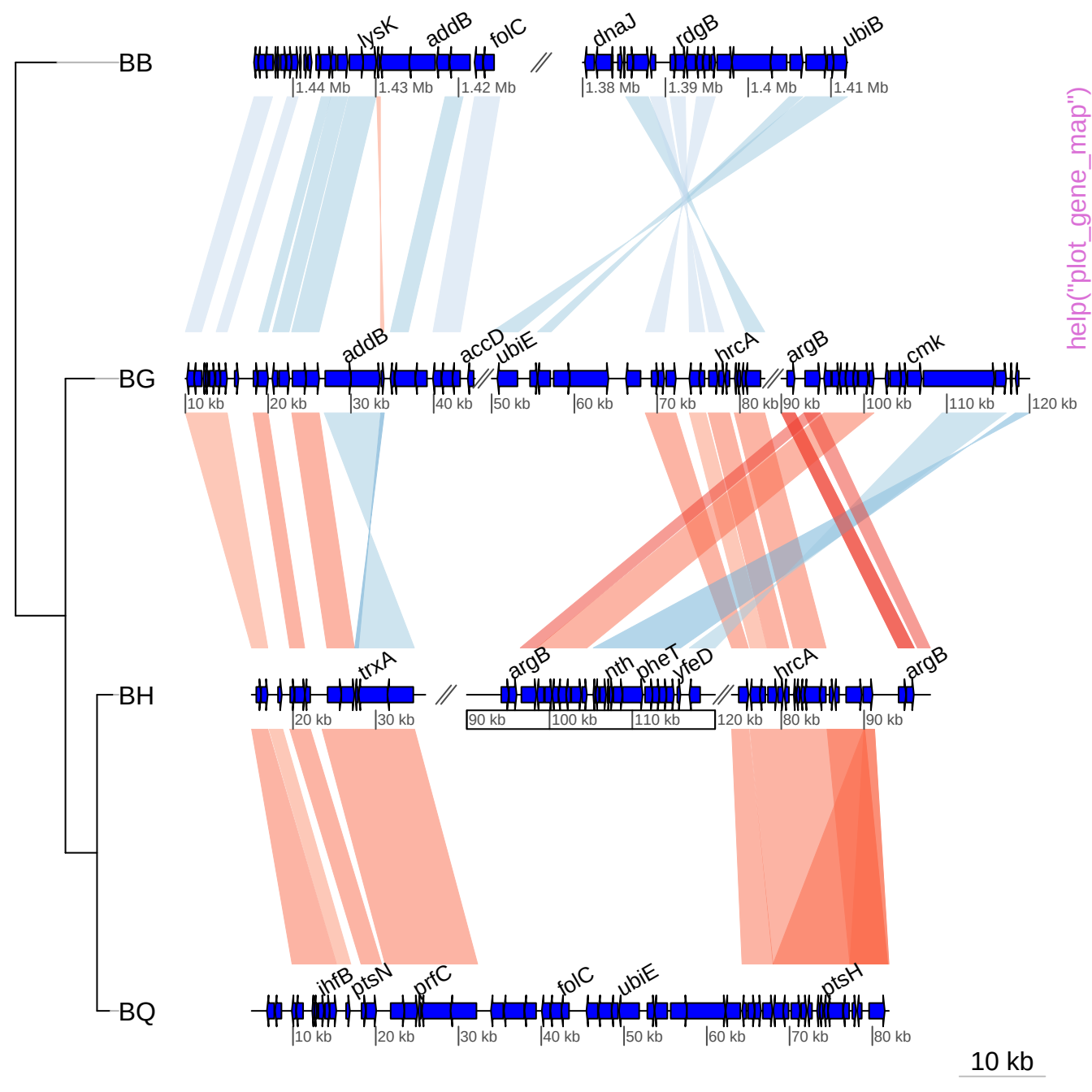
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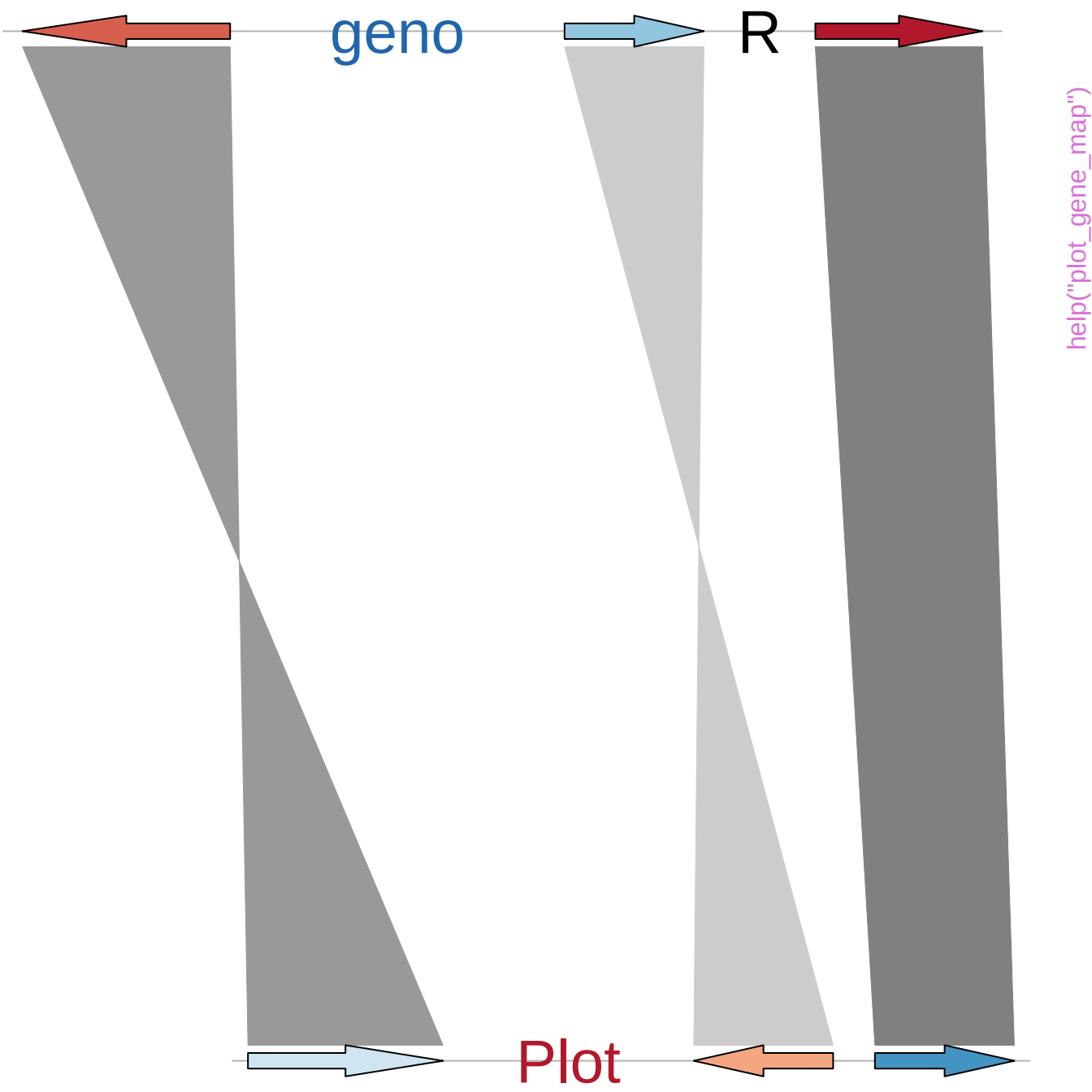
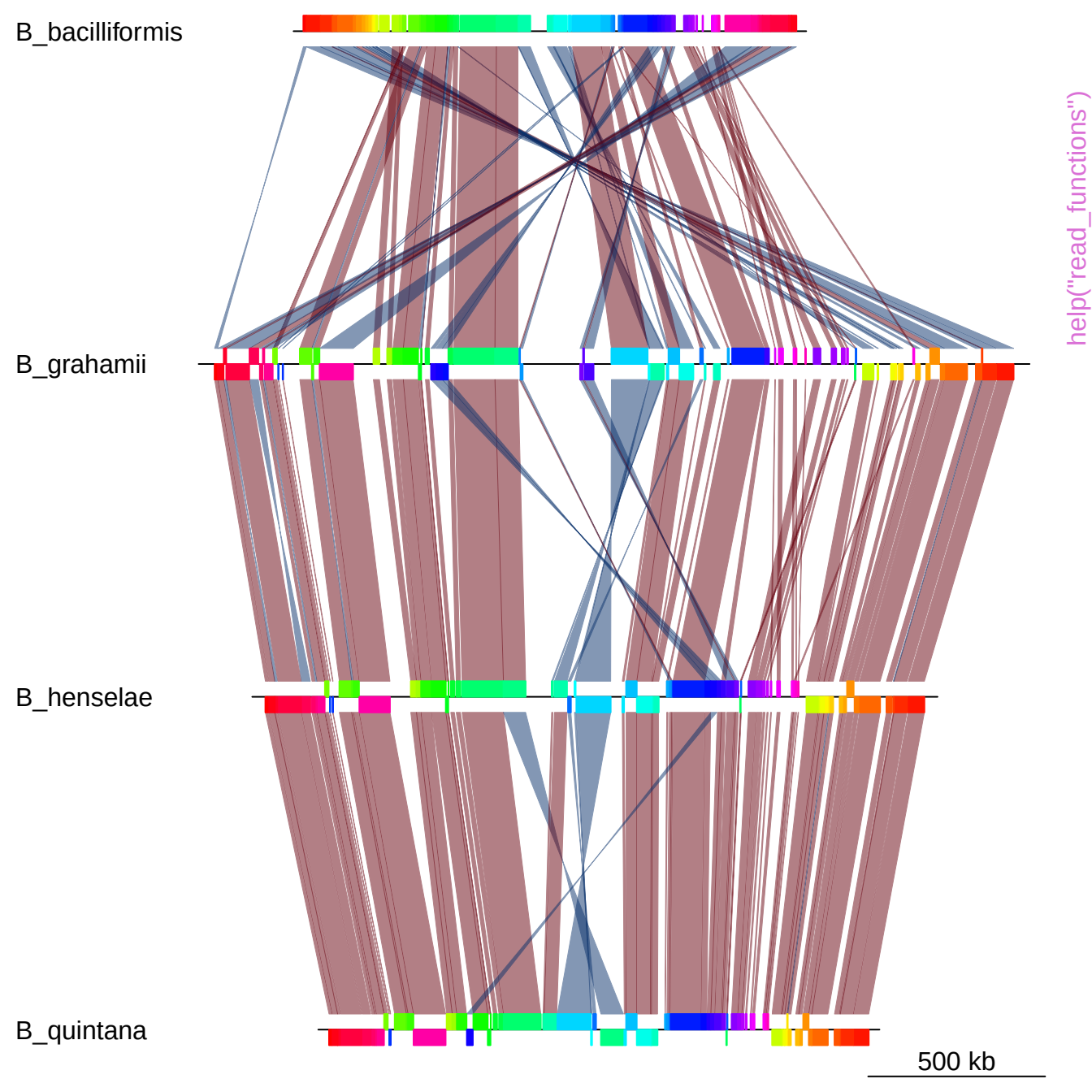
help("plot_gene_map")
10 kb


geno
R
Plot
help("plot_gene_map")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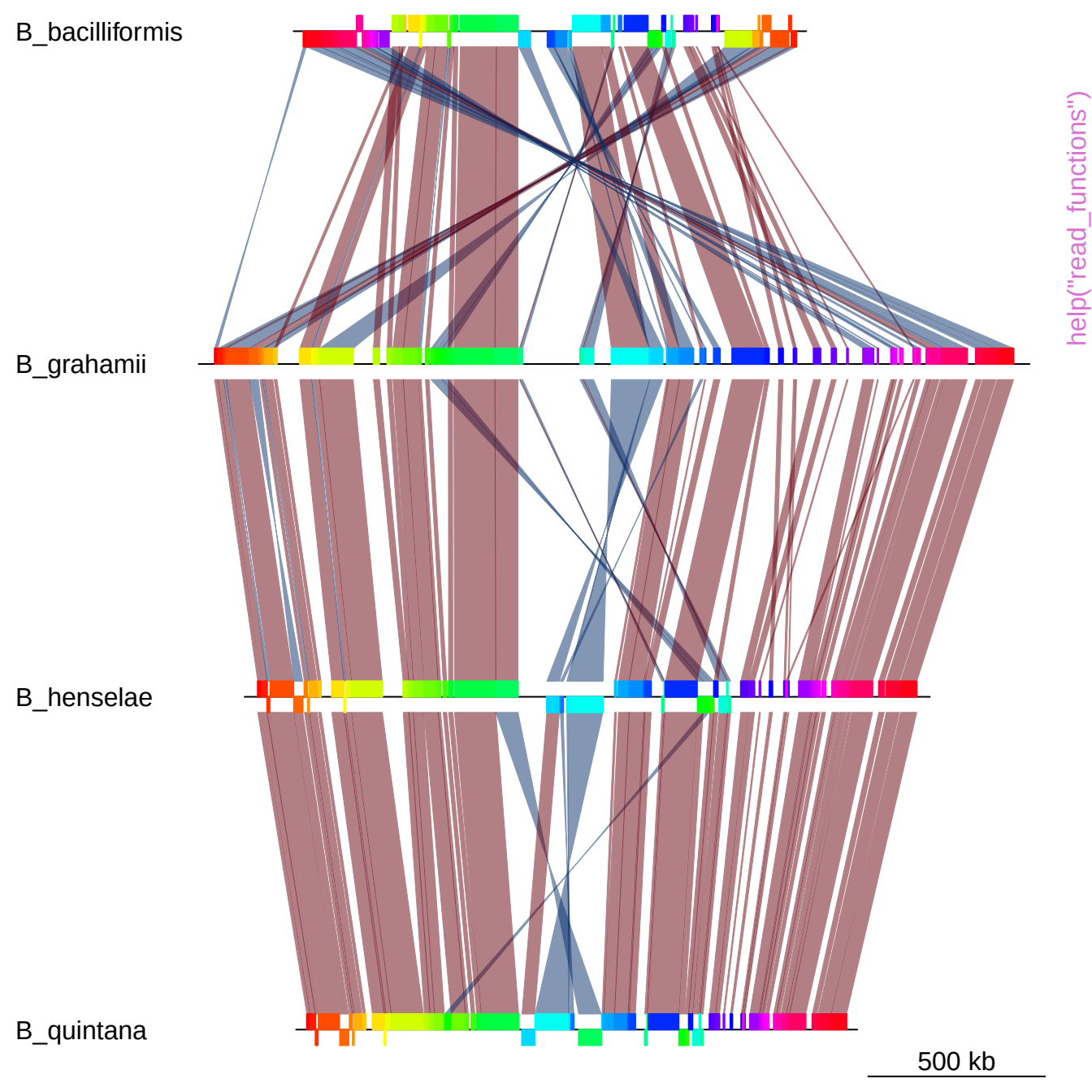
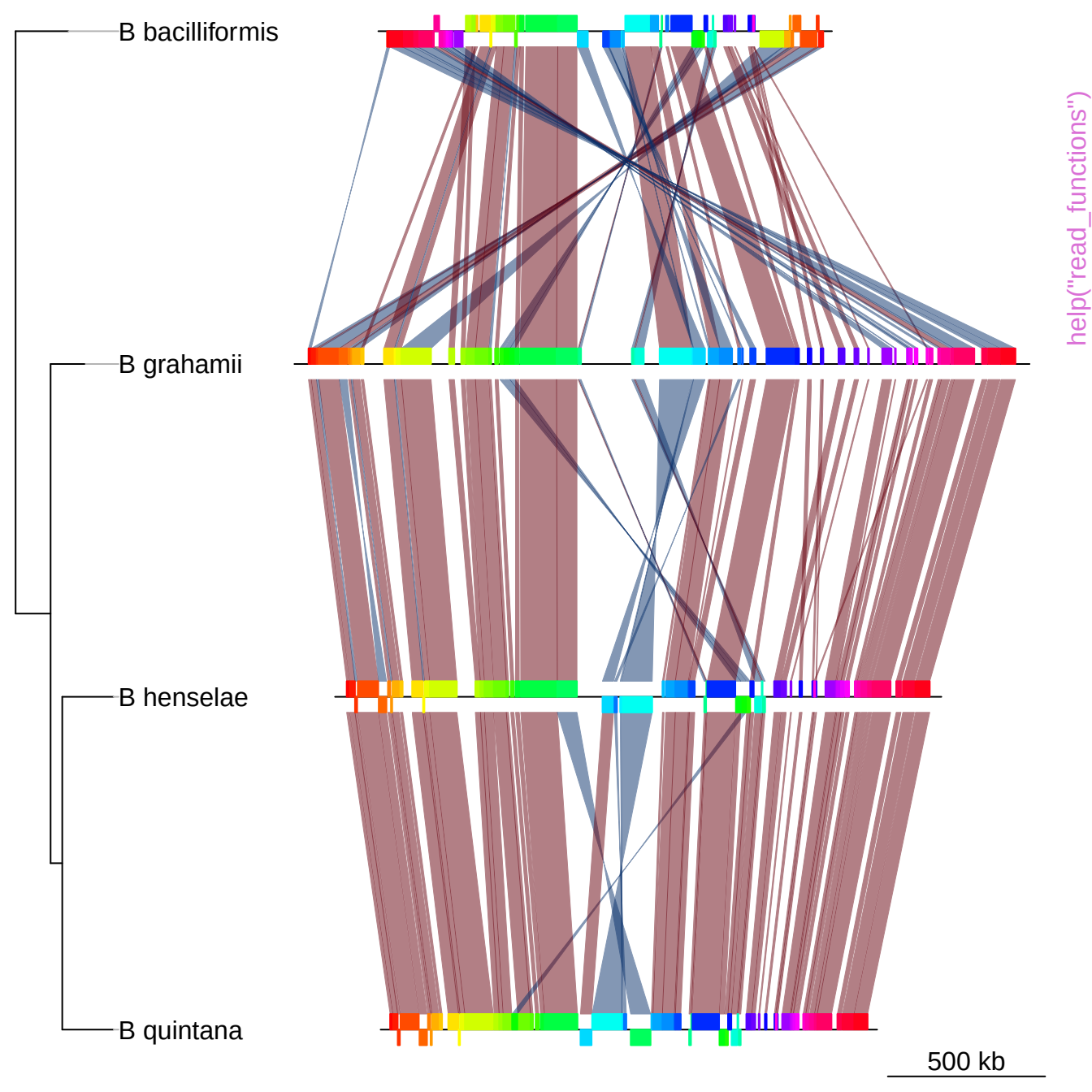
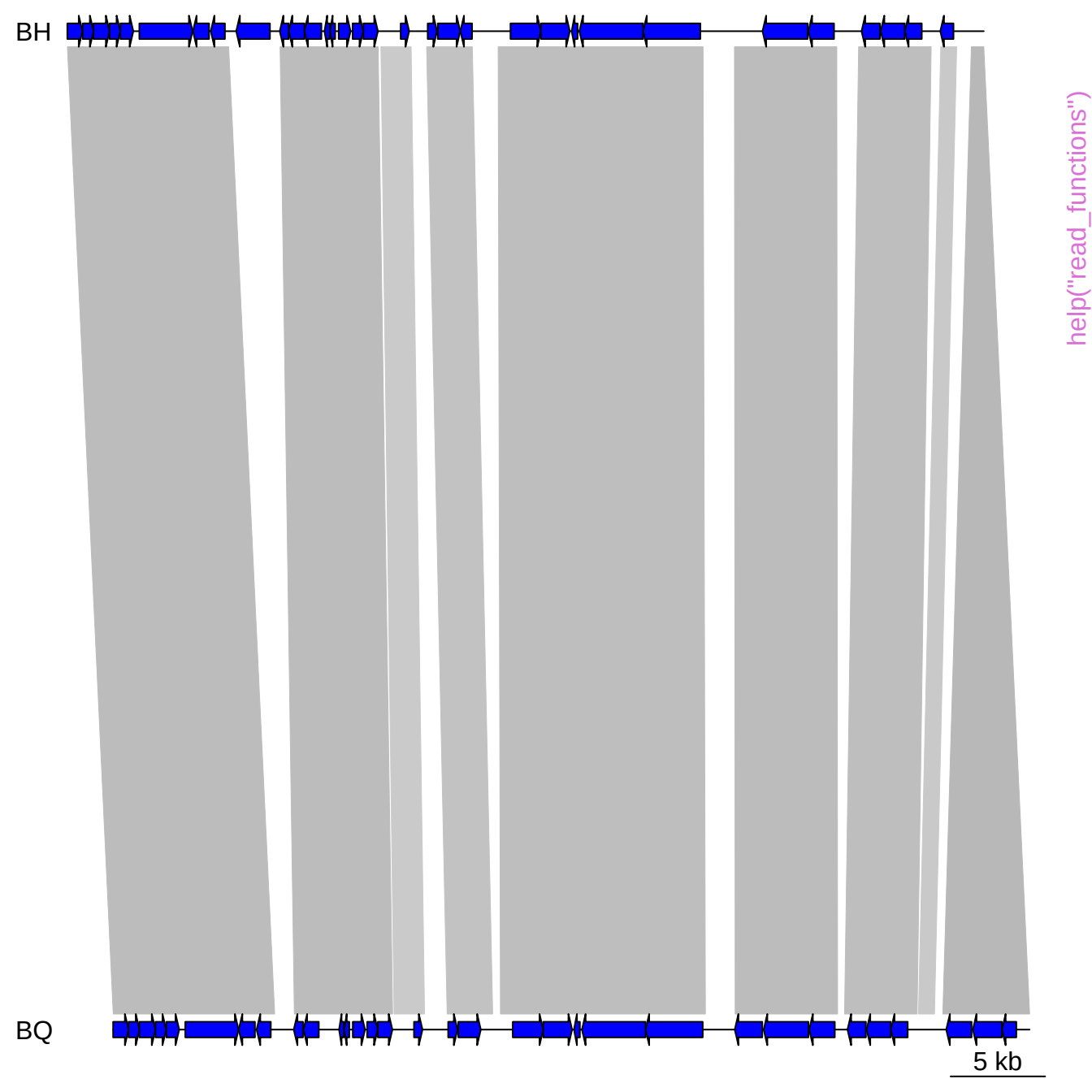
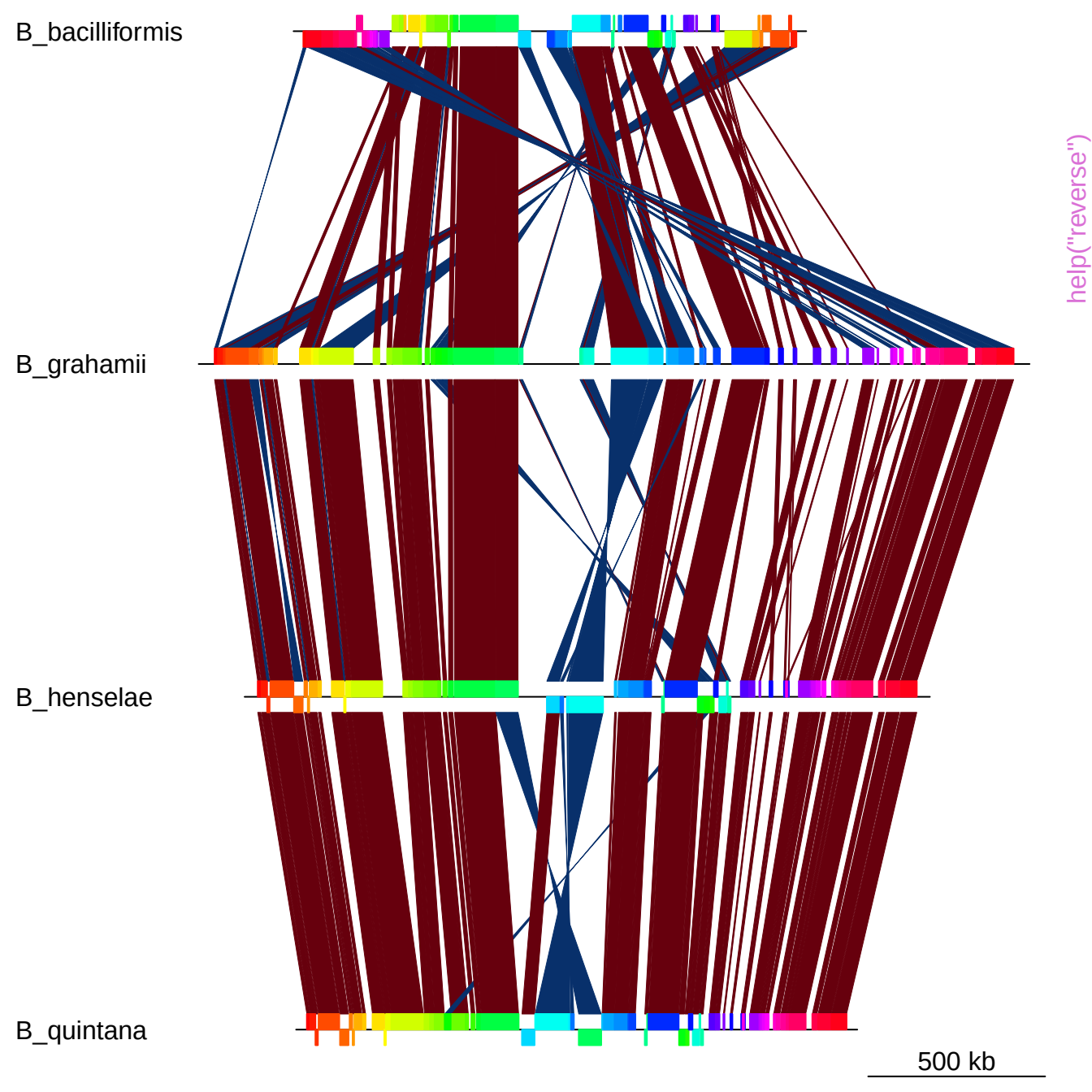
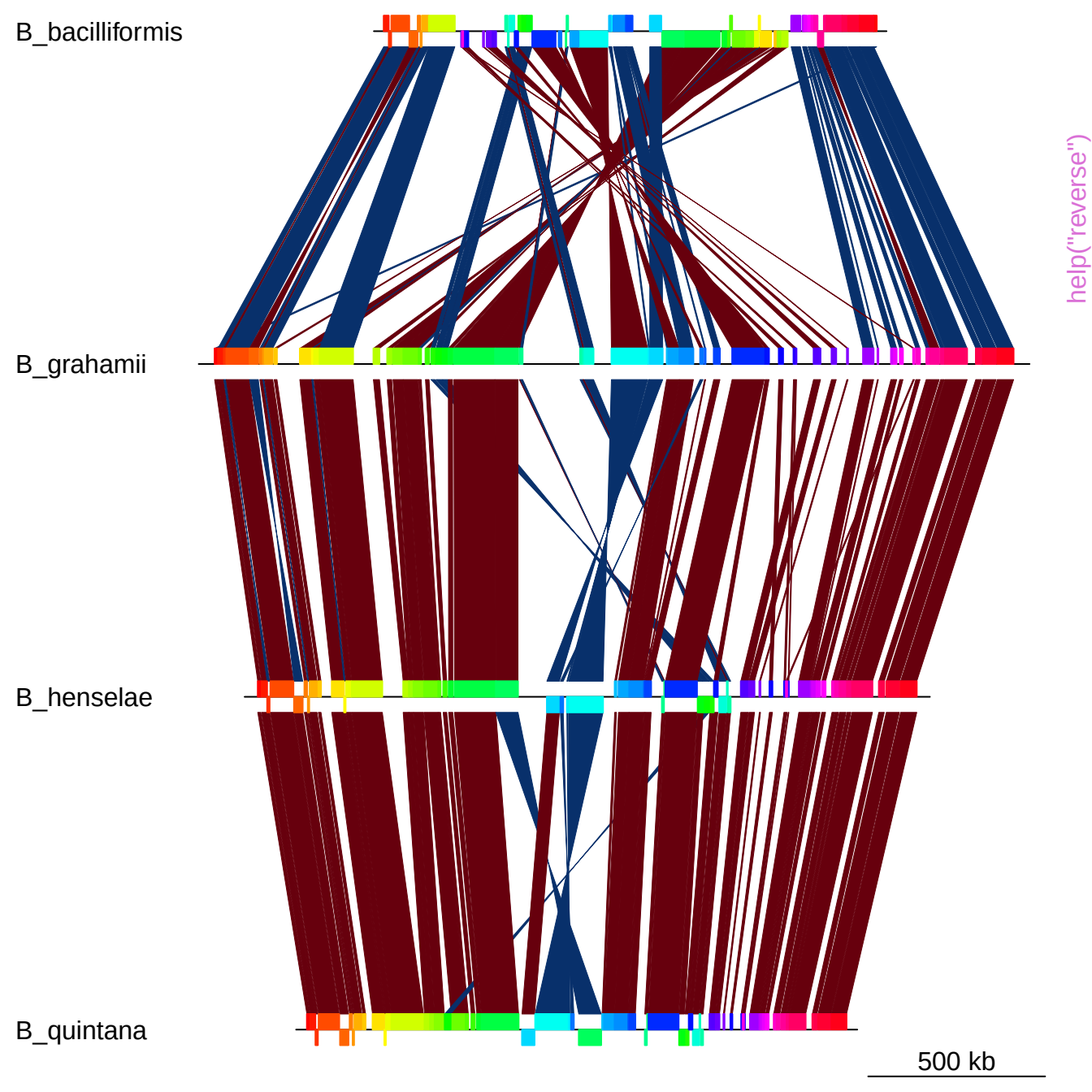
B_grahamii
B_henselae
B_quintana
500 kb
help("read_functions")

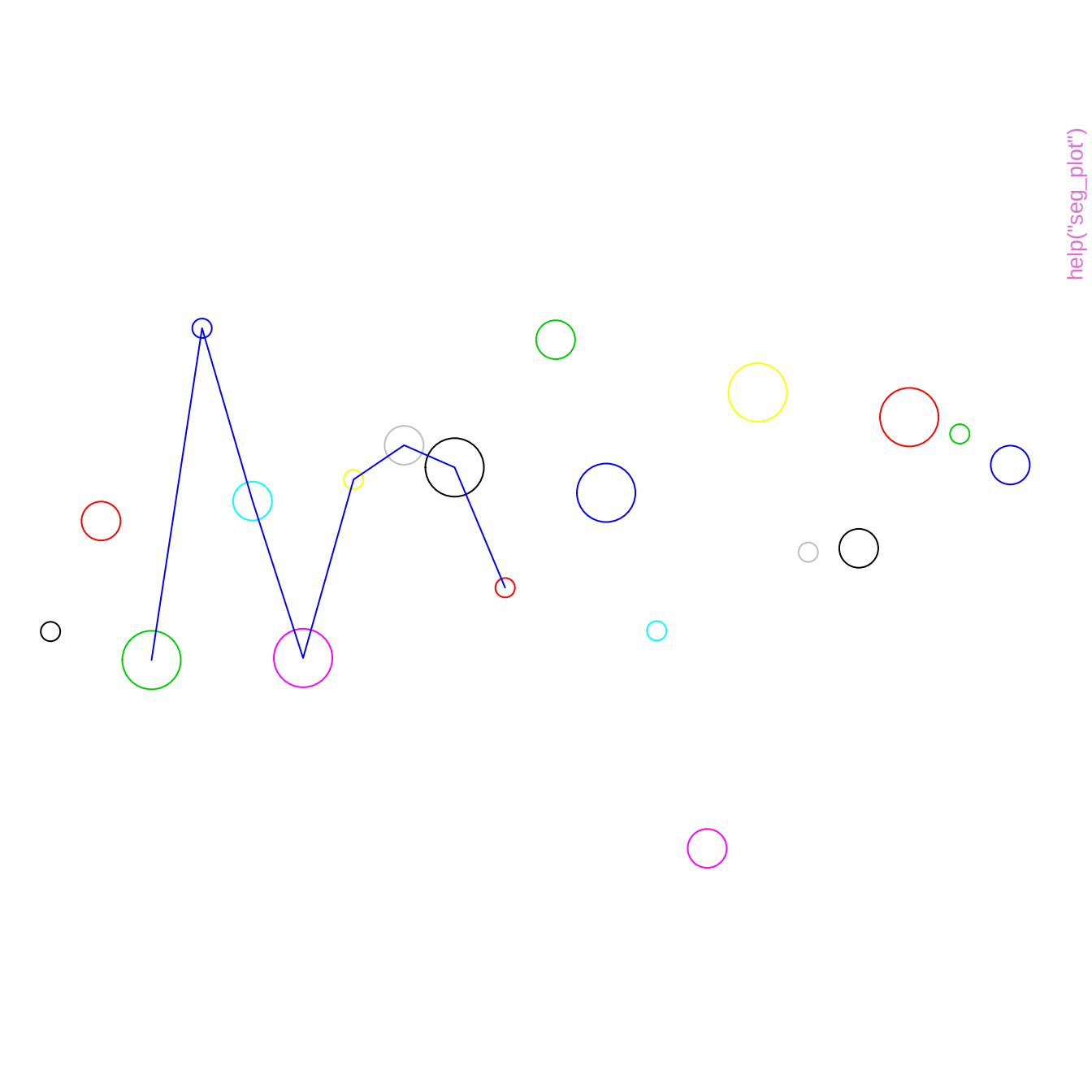

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("read_functions")

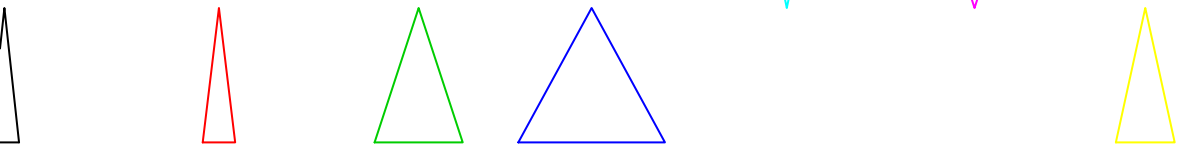

B bacilliformis
B grahamii
B henselae
B quintana
500 kb
help("read_functions")


BH
BQ
5 kb
help("read_functions")

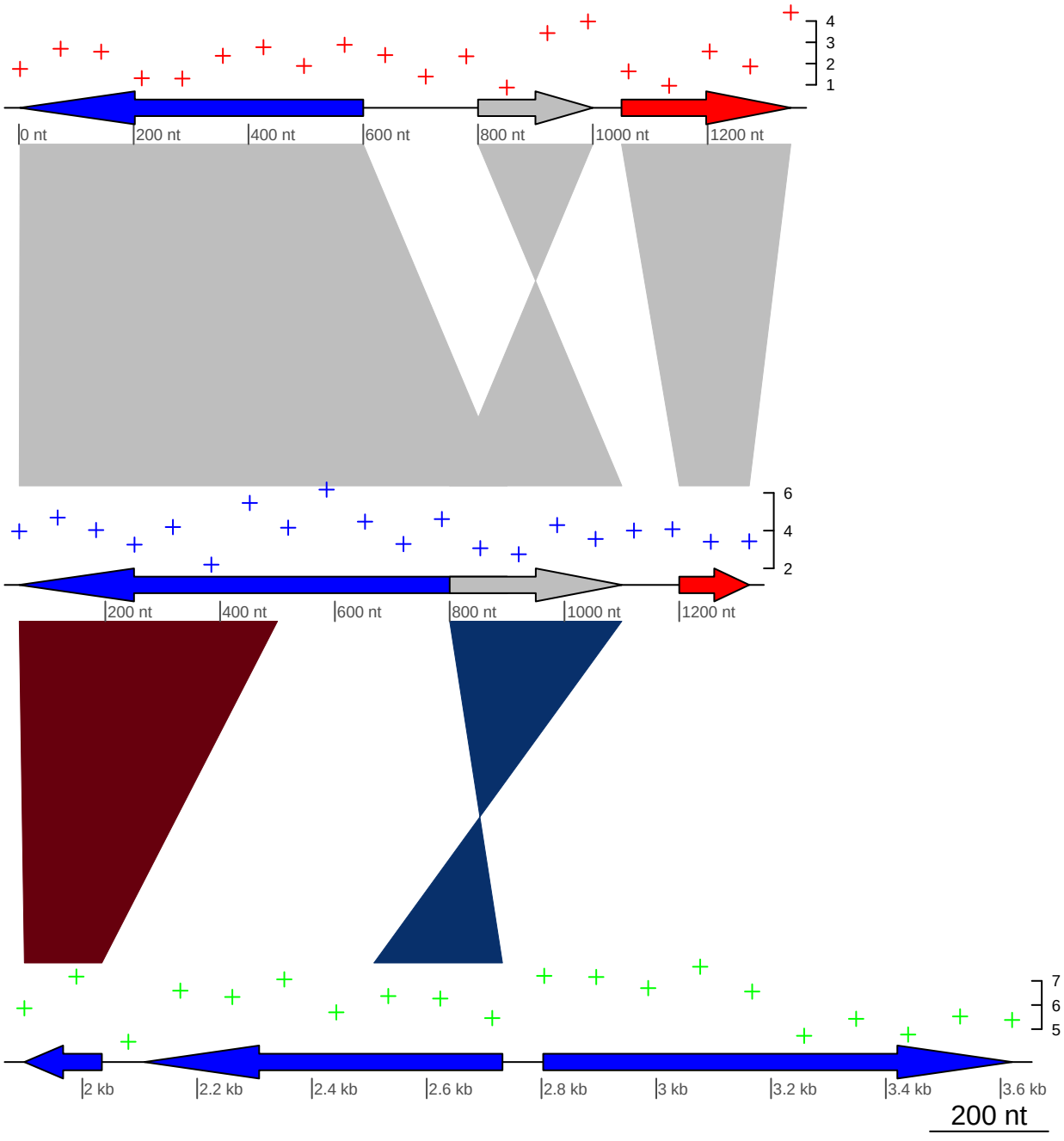

B_bacilliformis
B_grahamii
B_henselae
B_quintana
help("reverse")
500 kb


B_bacilliformis
B_grahamii
B_henselae
B_quintana
help("reverse")
500 kb


help("seg_plot")

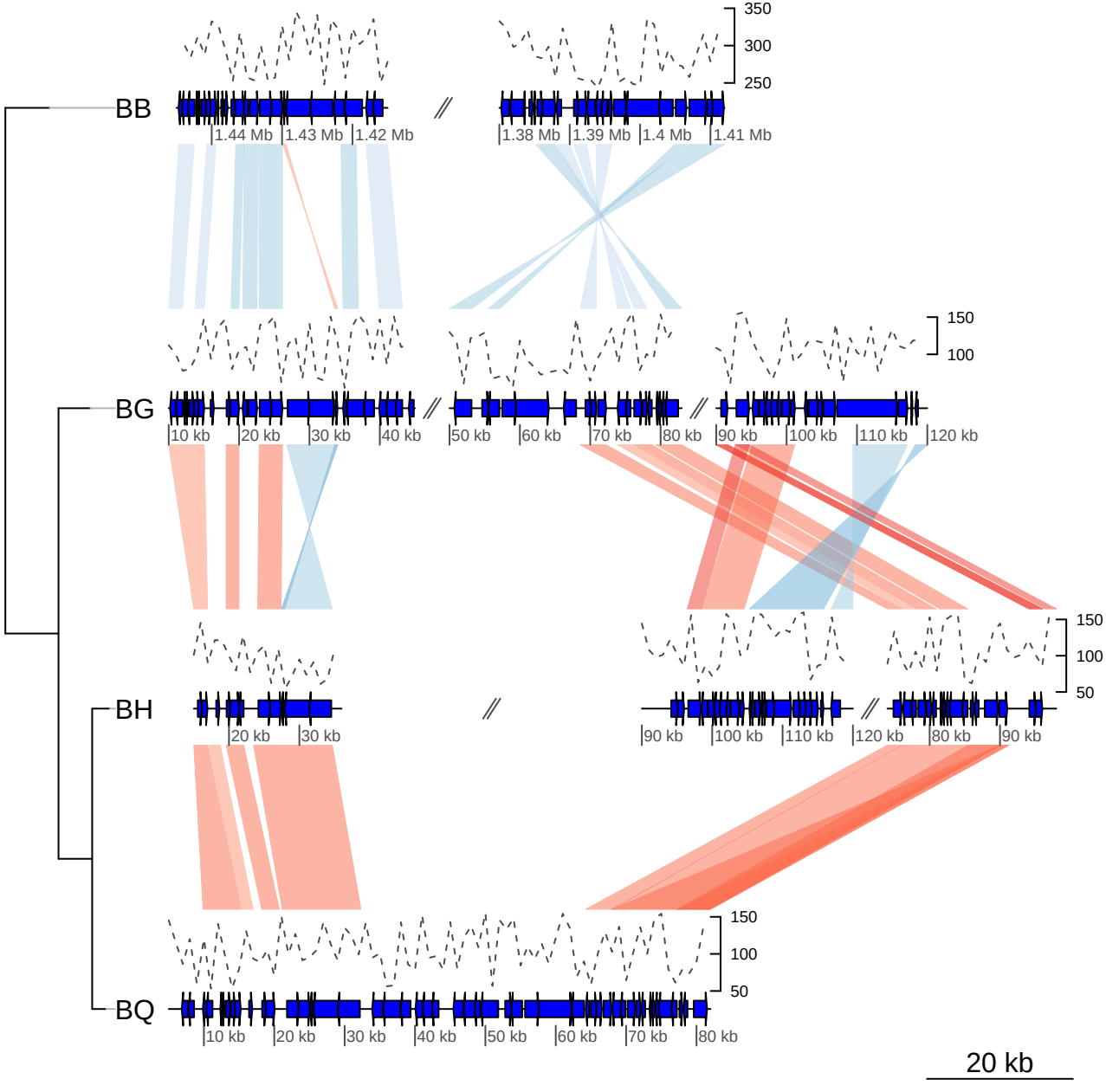


help("seg_plot")

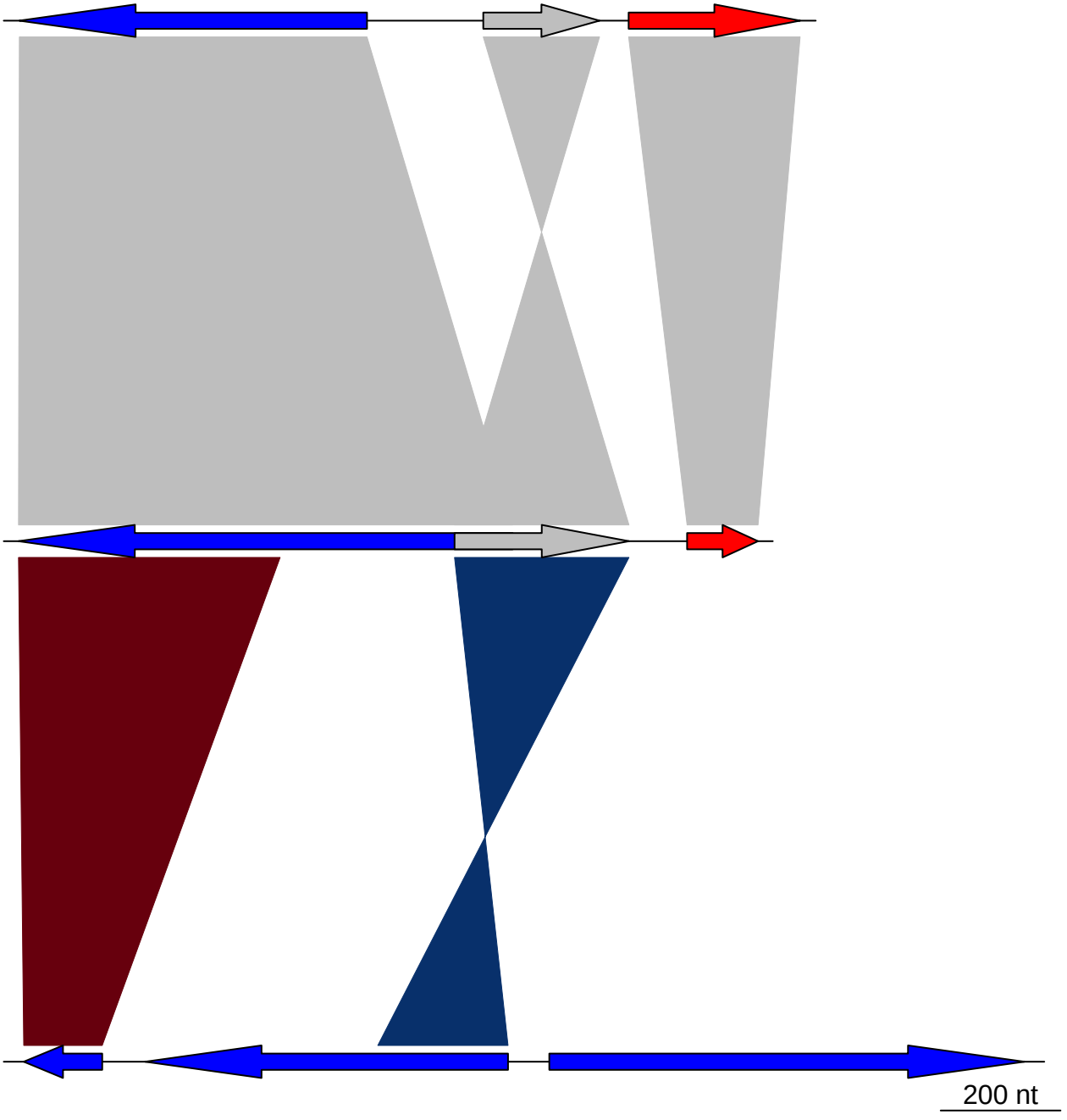


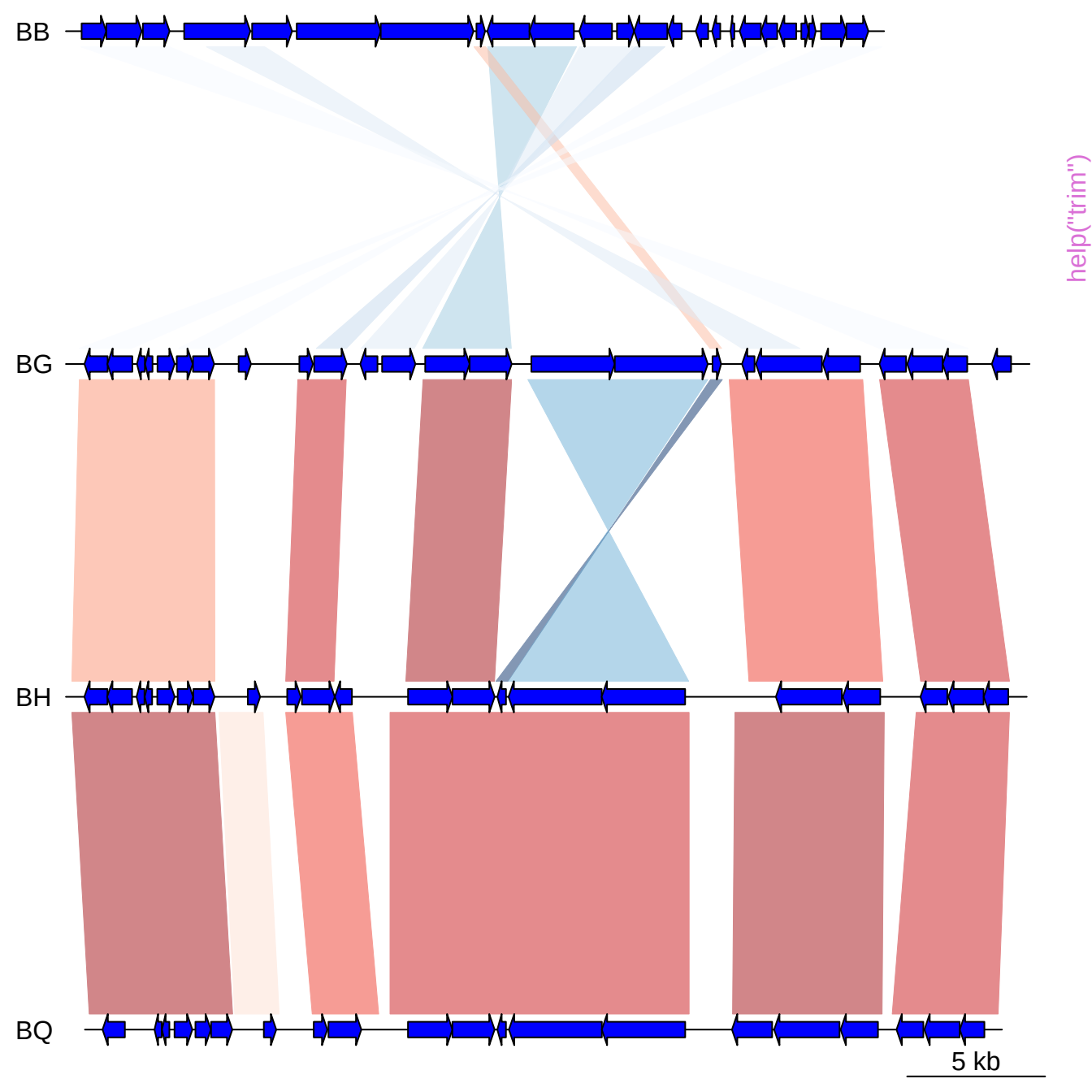
help("seg_plot")

Random plots for the same segment in 4 Bartonella genomes



help("seg_plot")


help("three_genes")
200 nt


BB
BG
BH
BQ
5 kb
help("trim")