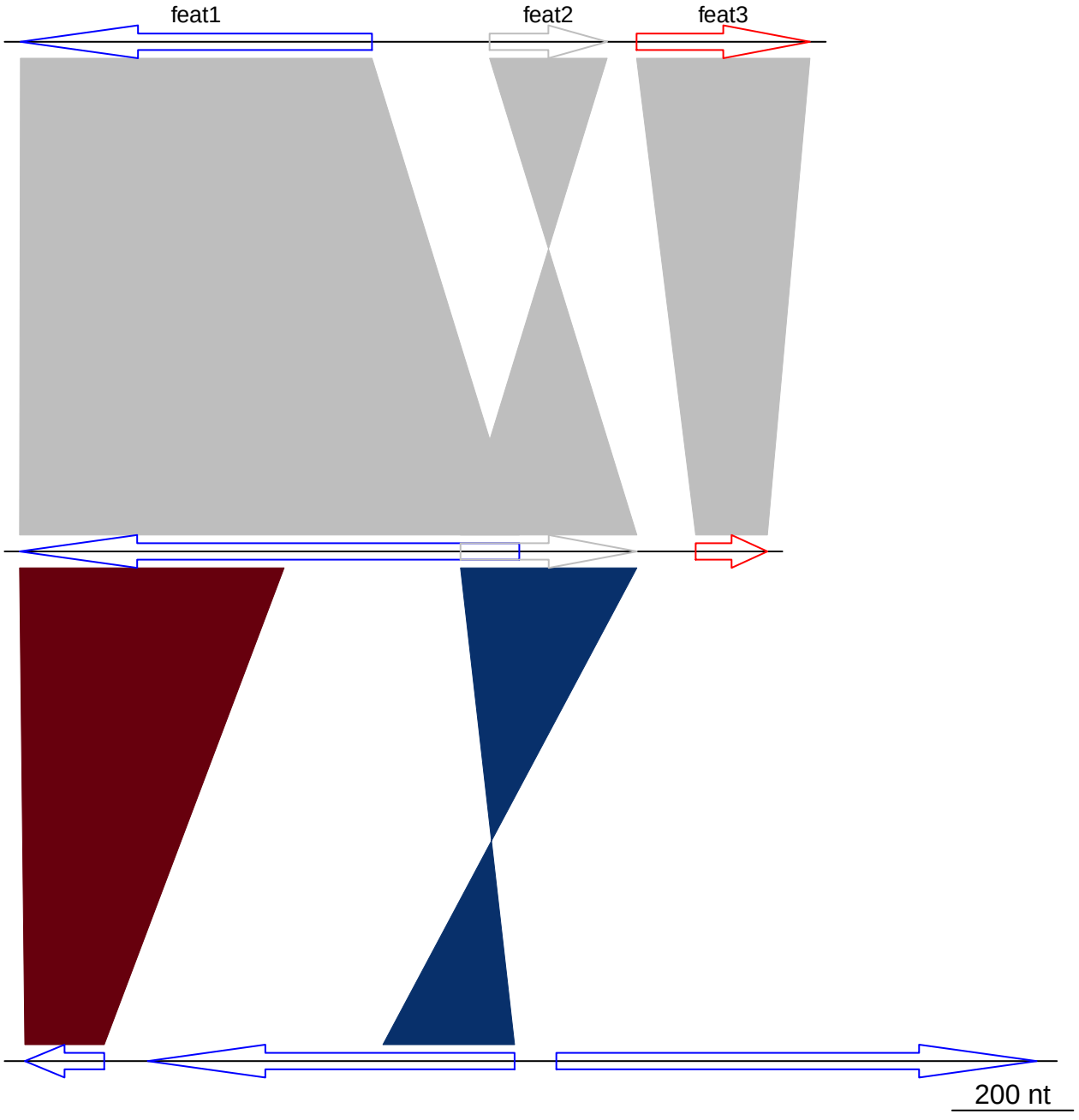
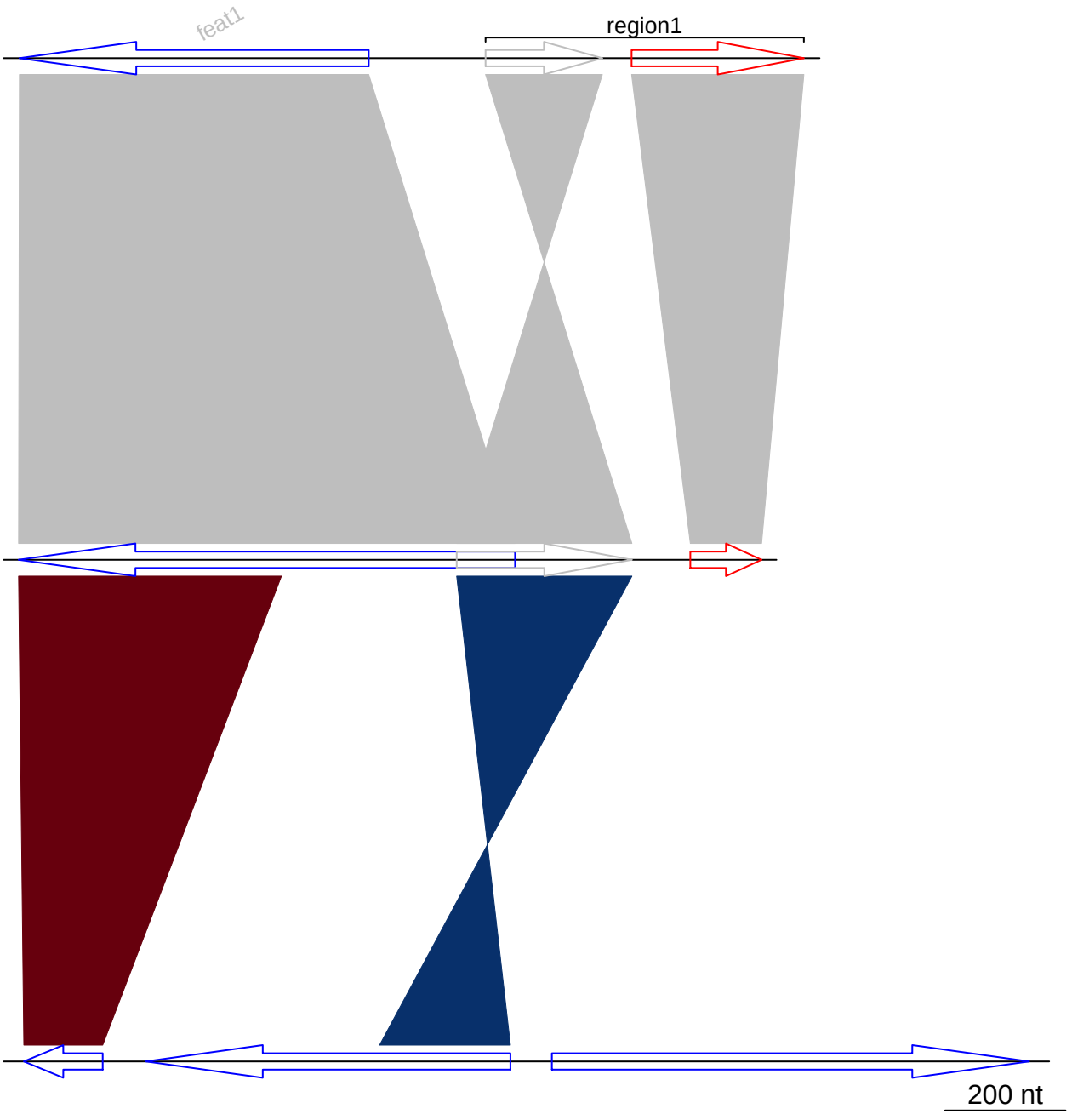
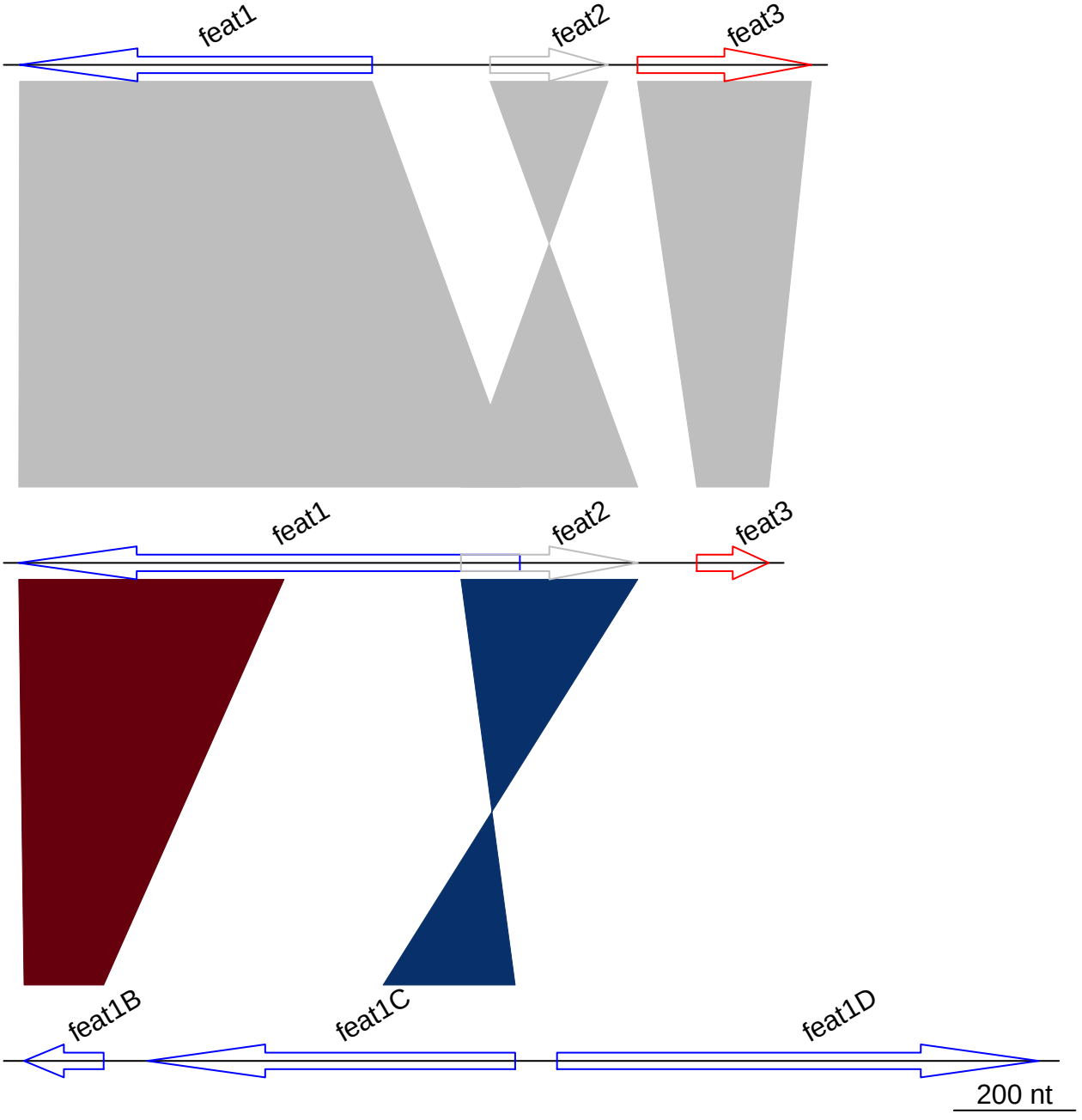


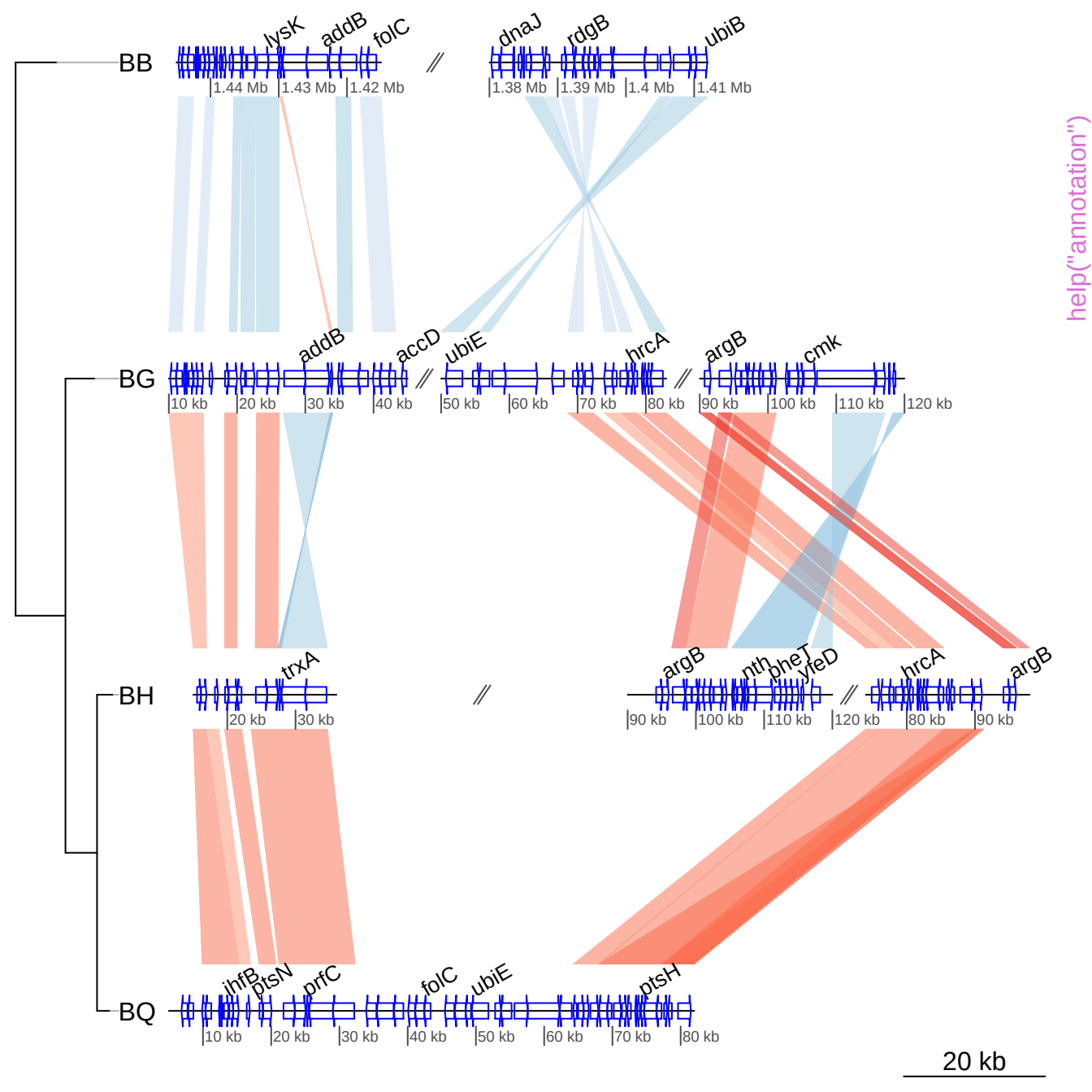
help("annotation")



help("annotation")



help("annotation")


BB
lysK
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folC
dnaJ
rdgB
ubiB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
BG
addB
accD
ubiE
hrcA
argB
cmk
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
100 kb
110 kb
120 kb
BH
trxA
argB
nth
pheT
yfeD
hrcA
argB
20 kb
30 kb
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100 kb
110 kb
120 kb
80 kb
90 kb
BQ
ihfB
ptsN
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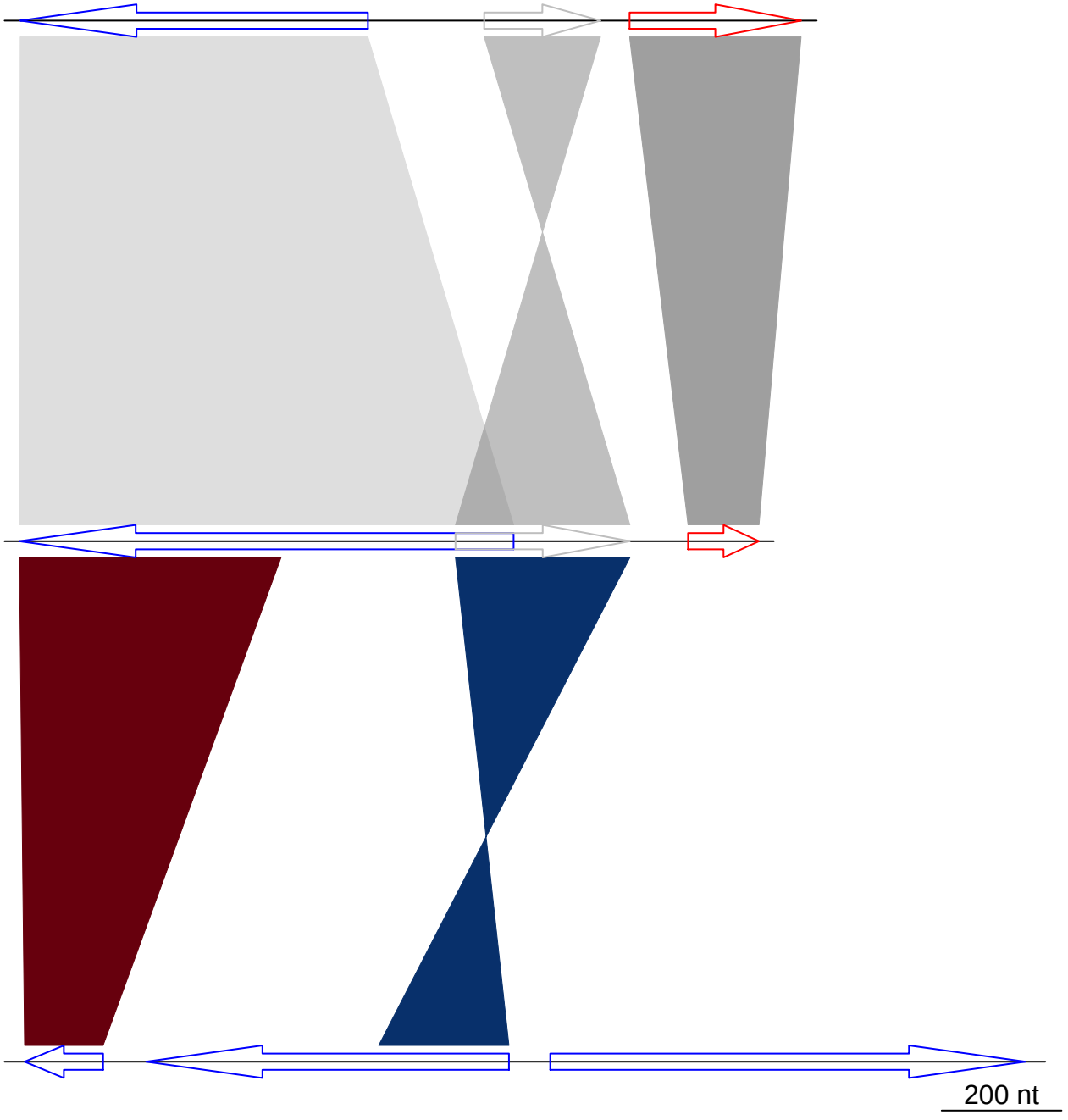
help("annotation")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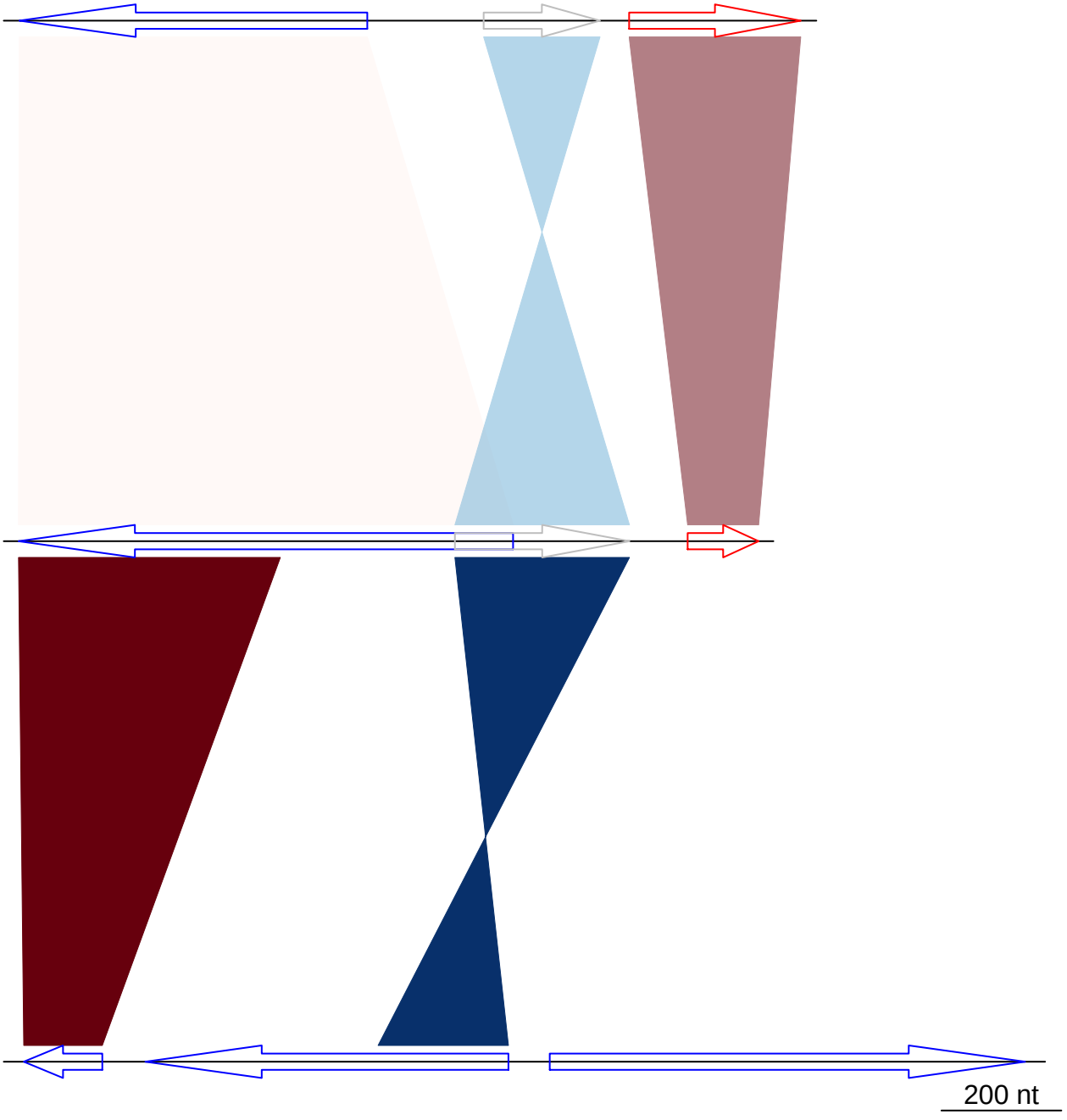
200 nt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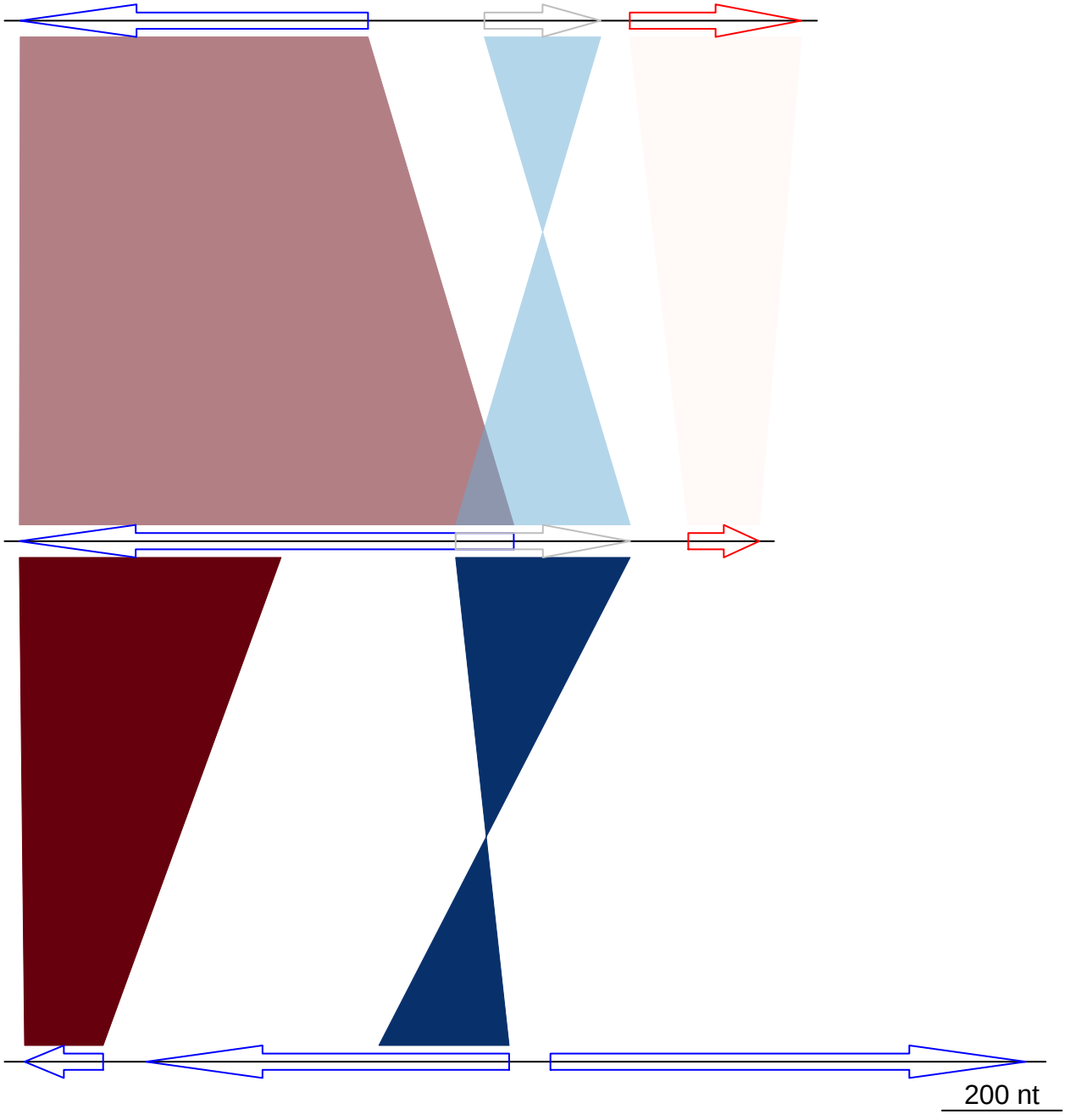
help("apply_color_scheme")
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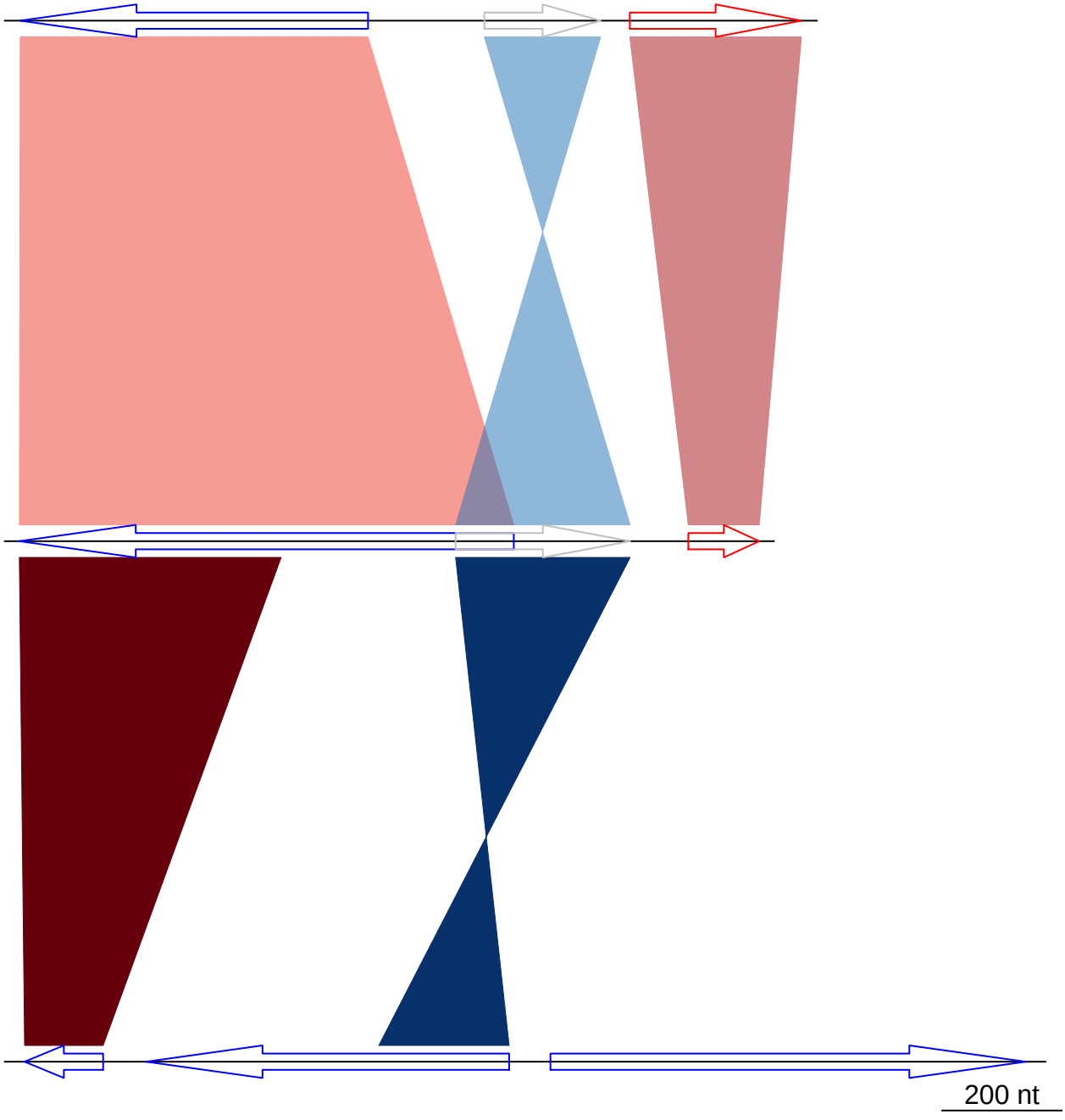
help("apply_color_scheme")
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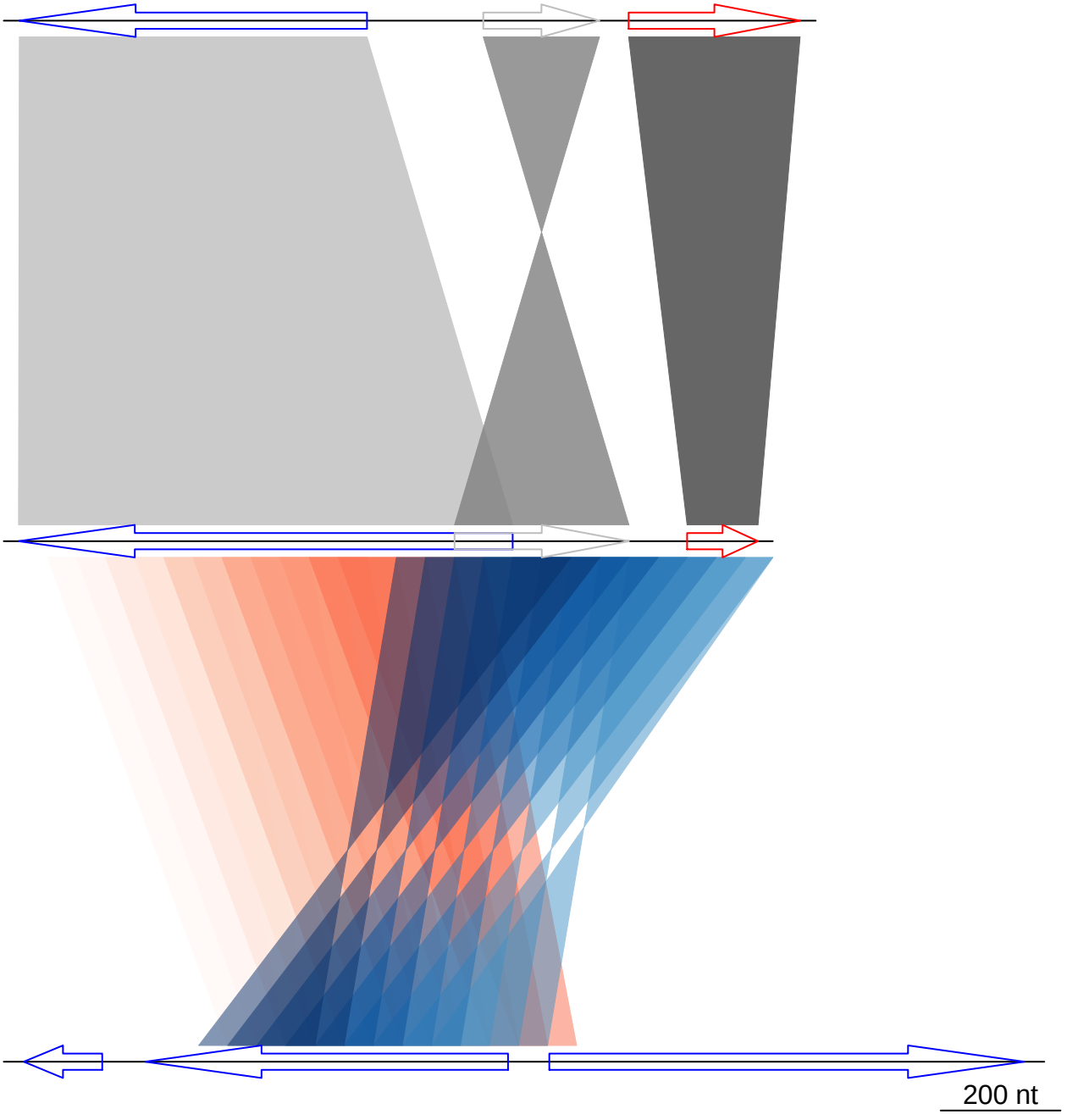
help("apply_color_scheme")
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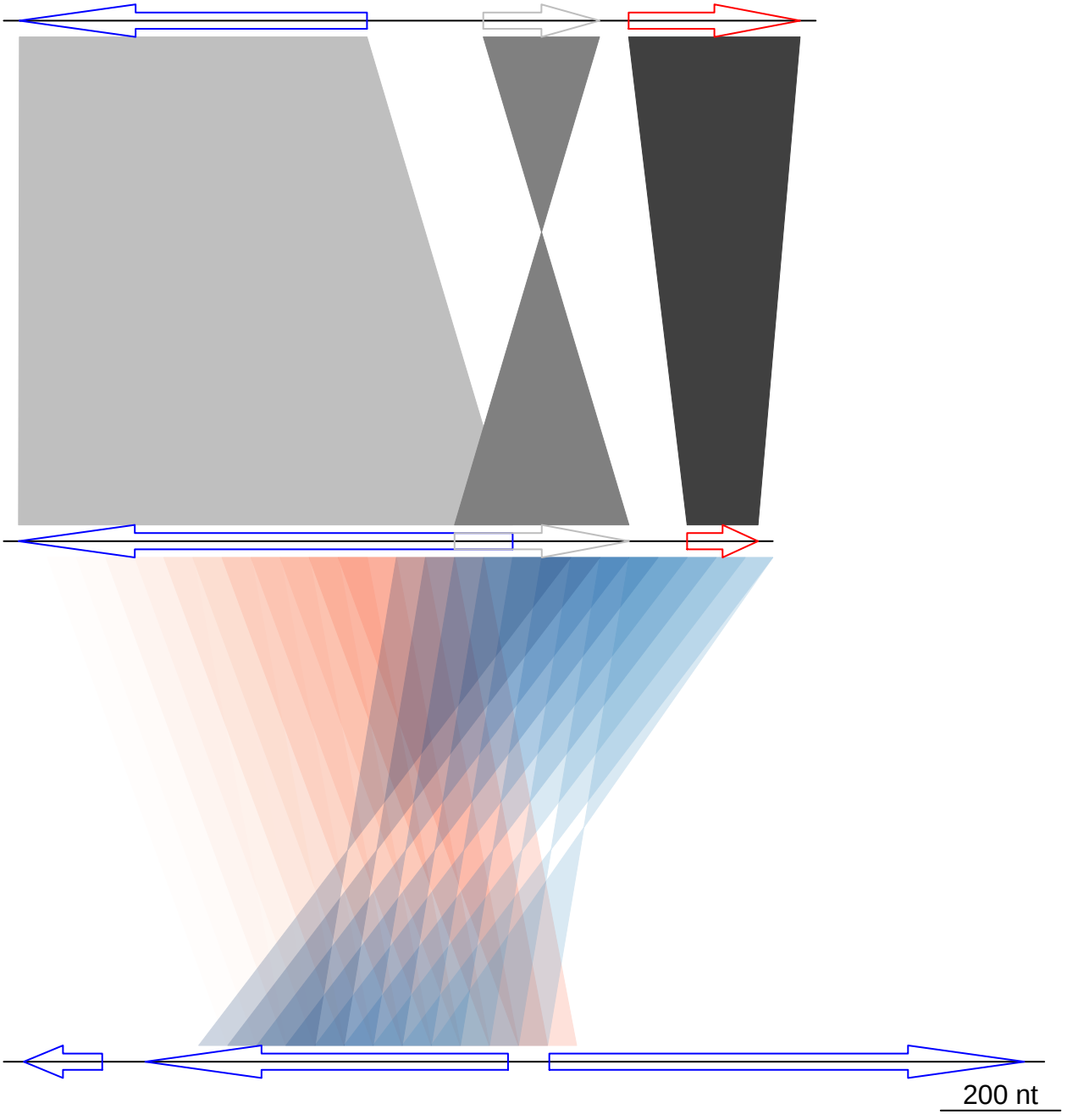
help("apply_color_scheme")
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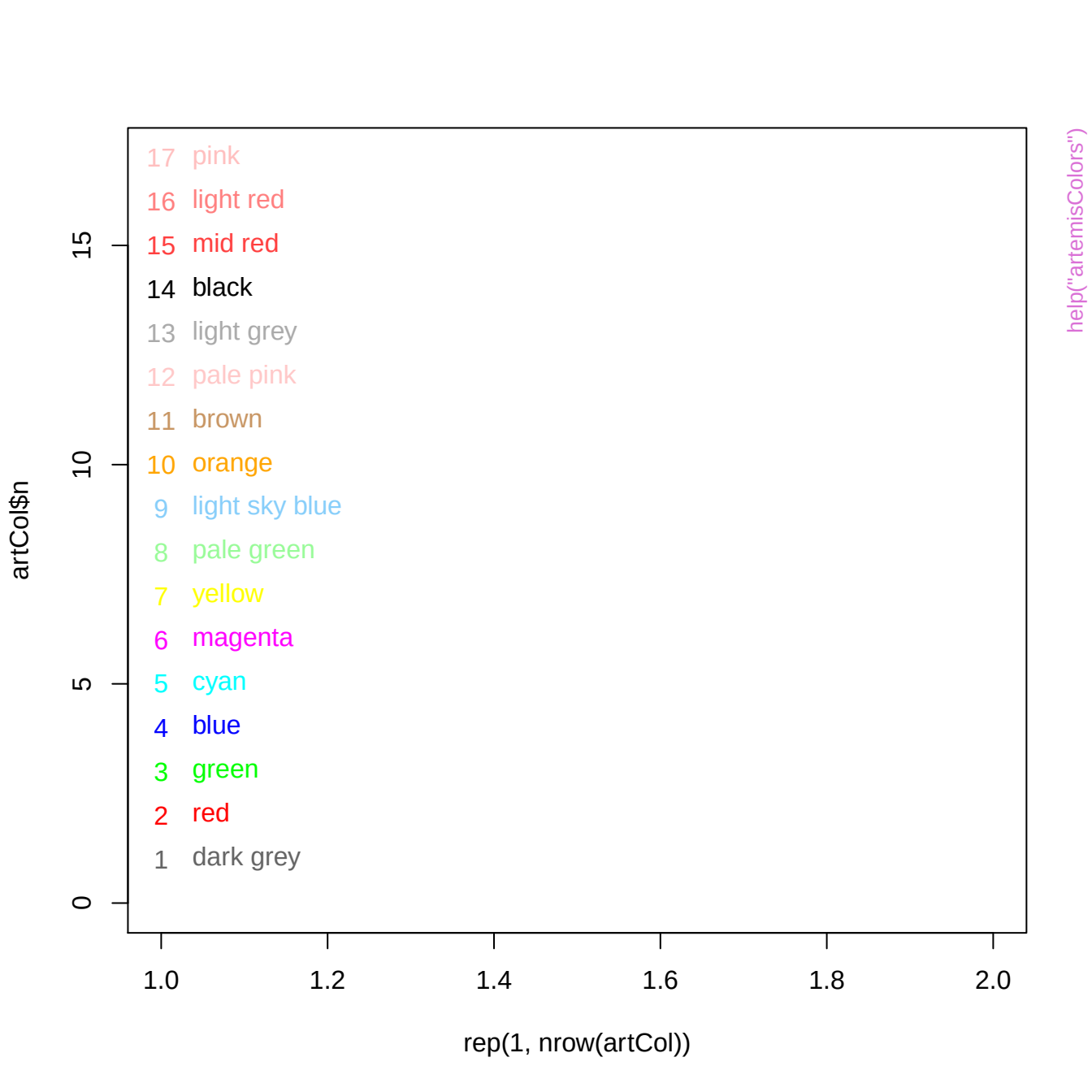
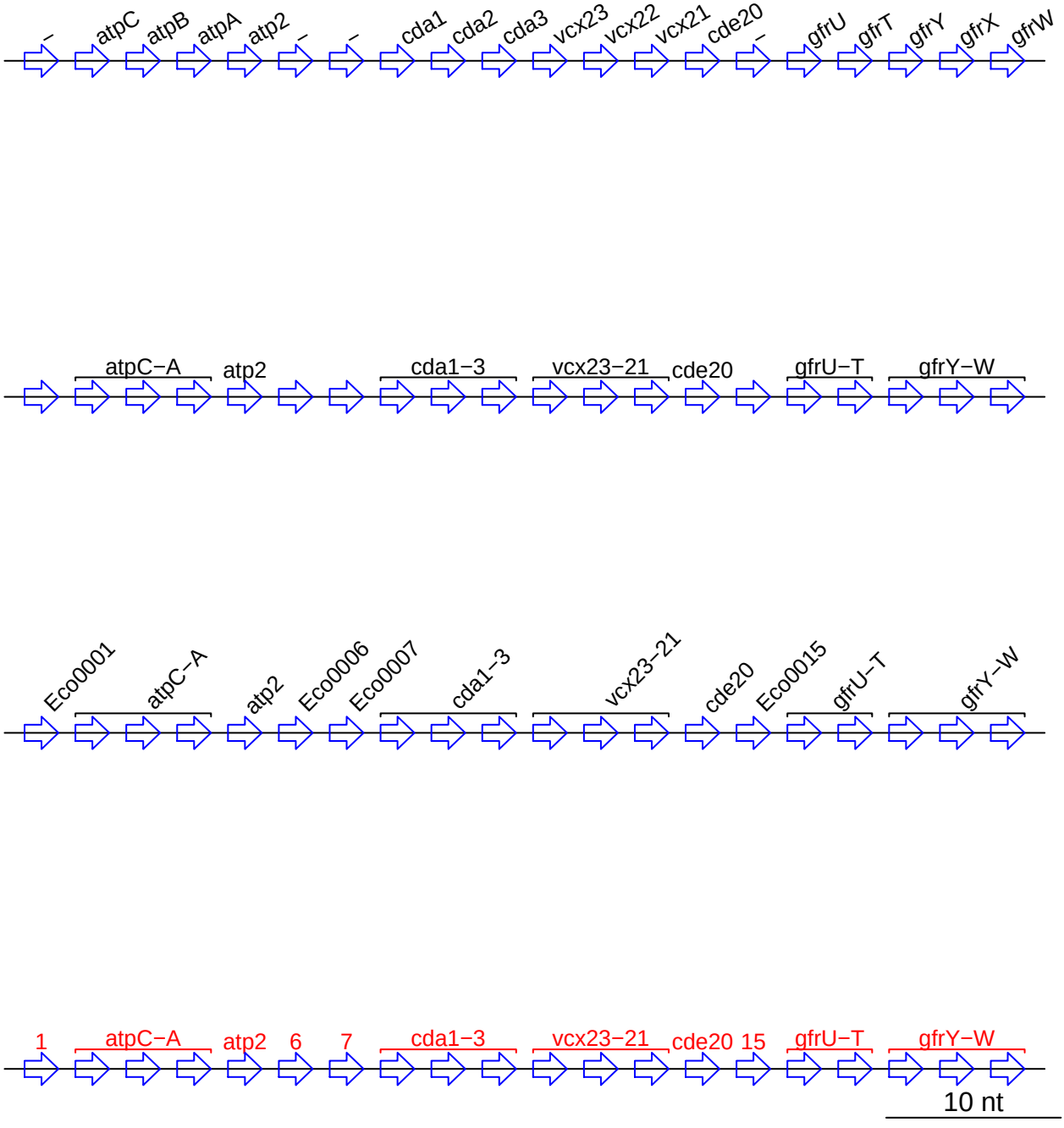
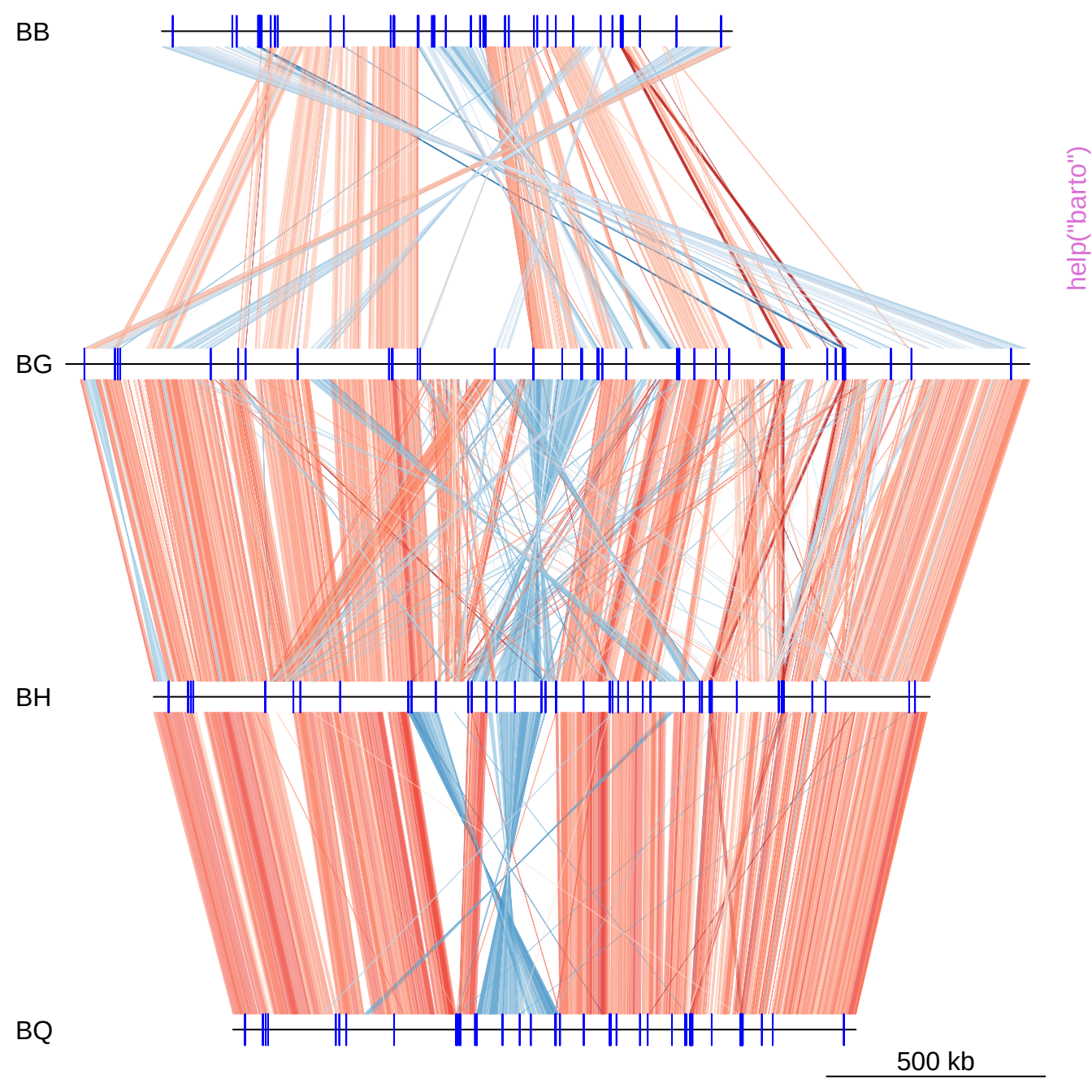
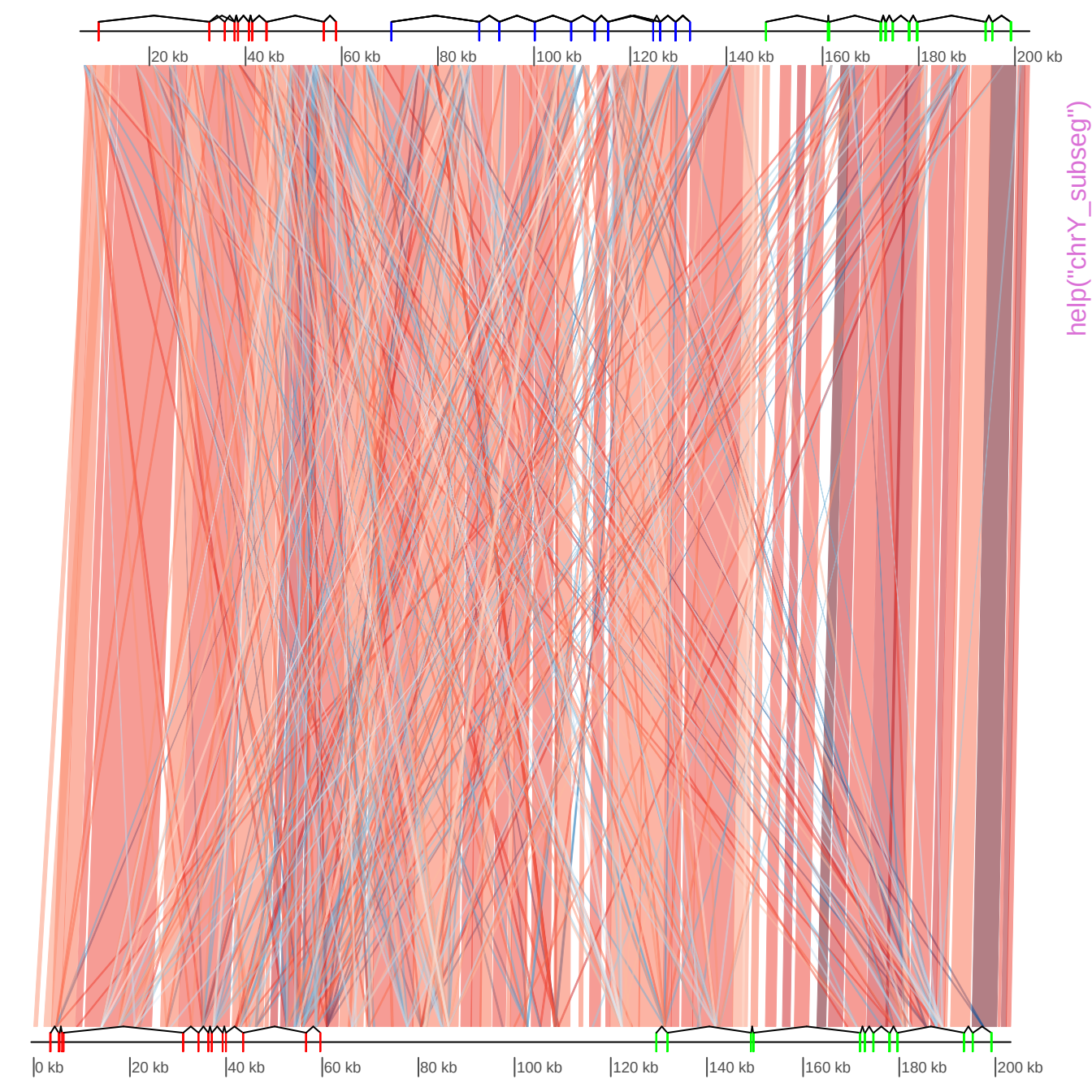

17 pink
16 light red
15 mid red
14 black
13 light grey
12 pale pink
11 brown
10 orange
9 light sky blue
8 pale green
7 yellow
6 magenta
5 cyan
4 blue
3 green
2 red
1 dark grey
0
5
10
15
artCol$n
1.0
1.2
1.4
1.6
1.8
2.0
rep(1, nrow(artCol))
help("artemisColors")



help("auto_annotate")


BB
BG
BH
BQ
help("barto")
500 kb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120 kb
140 kb
160 kb
180 kb
200 kb
help("chrY_subseg")
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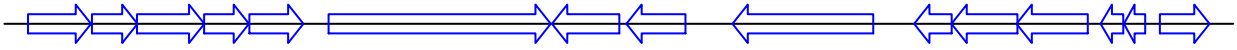
40 kb
60 kb
80 kb
100 kb
120 kb
140 kb
160 kb
180 kb
200 kb

help("gene_types")



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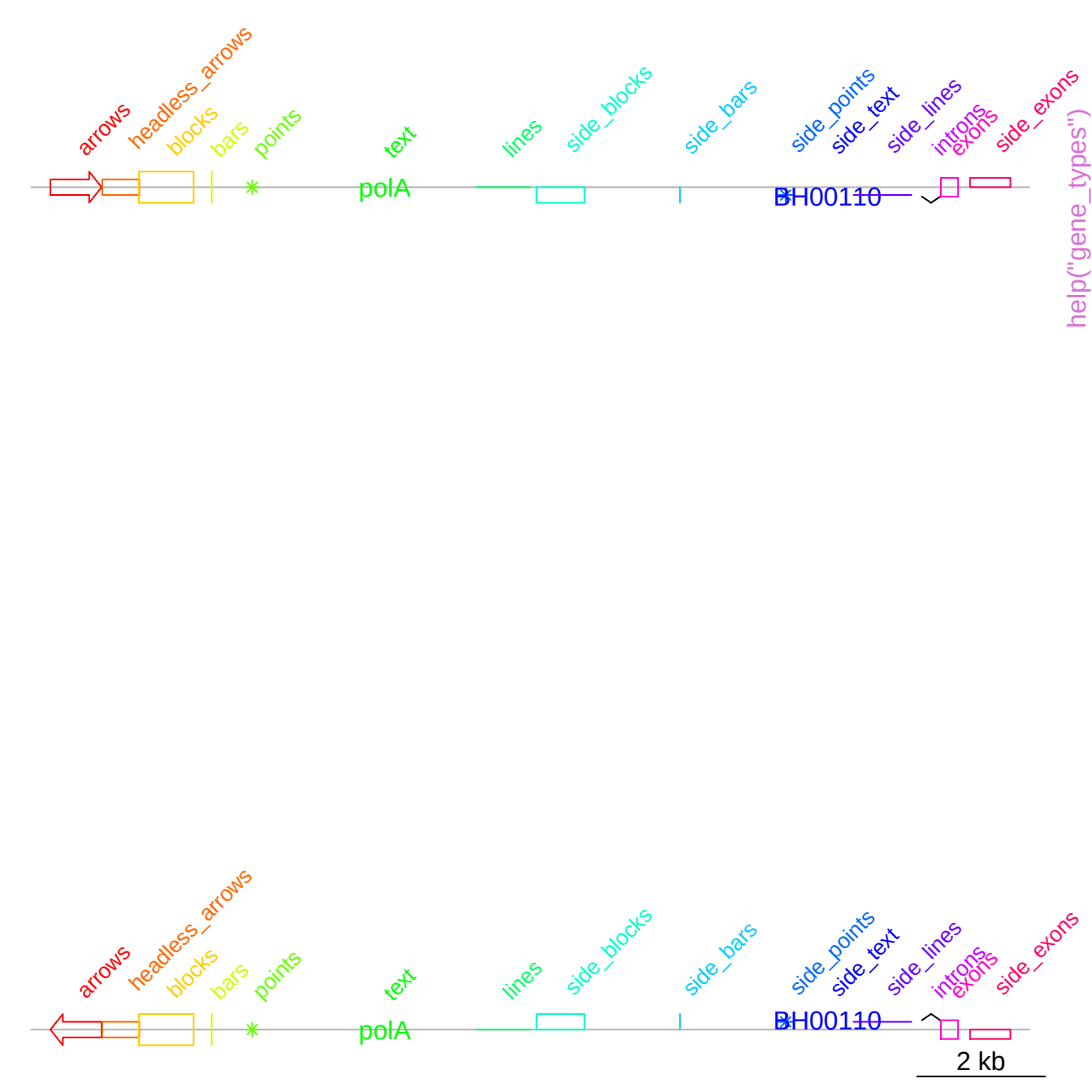
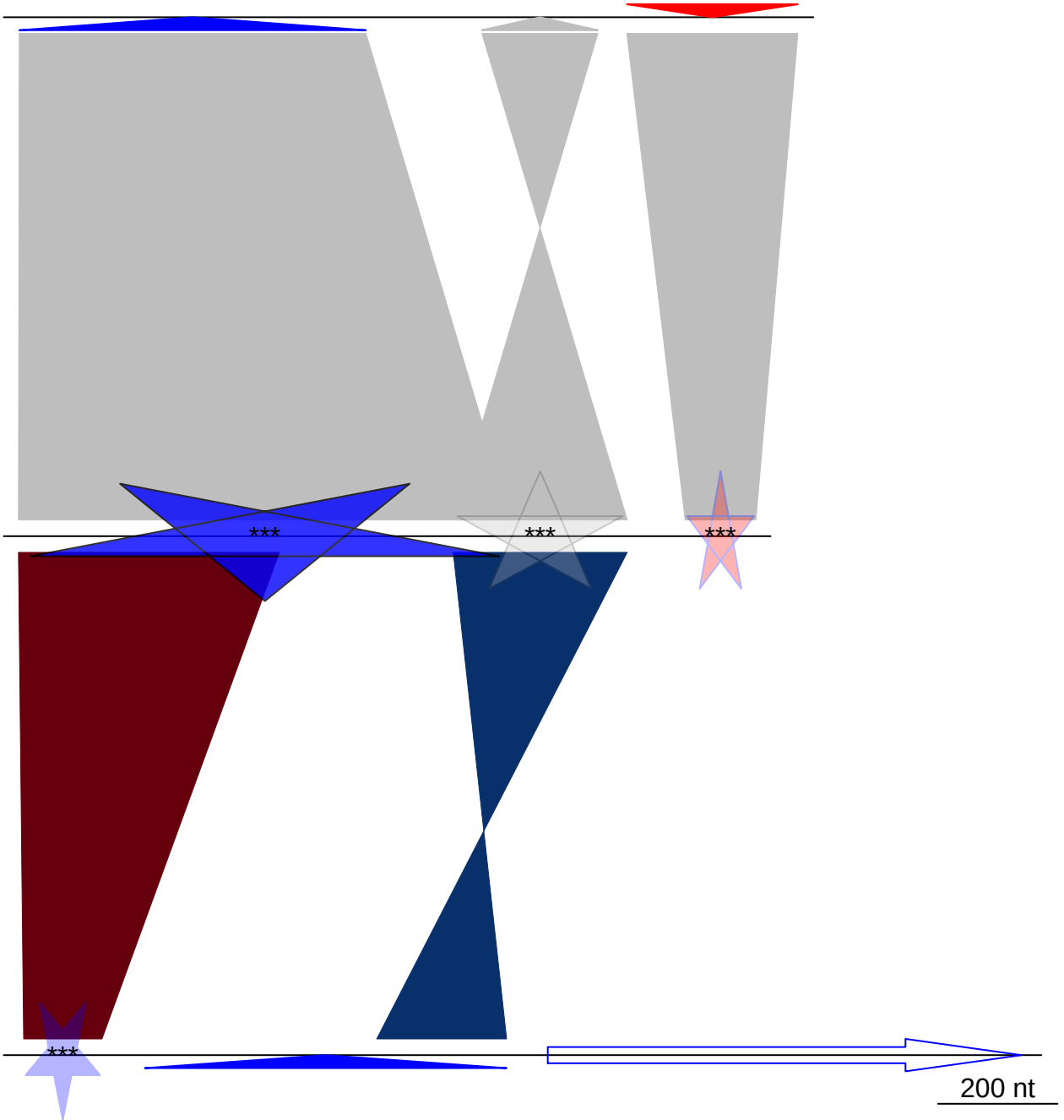

arrows
headless_arrows
blocks
bars
points
text
lines
side_blocks
side_bars
side_points
side_text
side_lines
introns
exons
side_exons
help("gene_types")
polA
BH00110
2 kb


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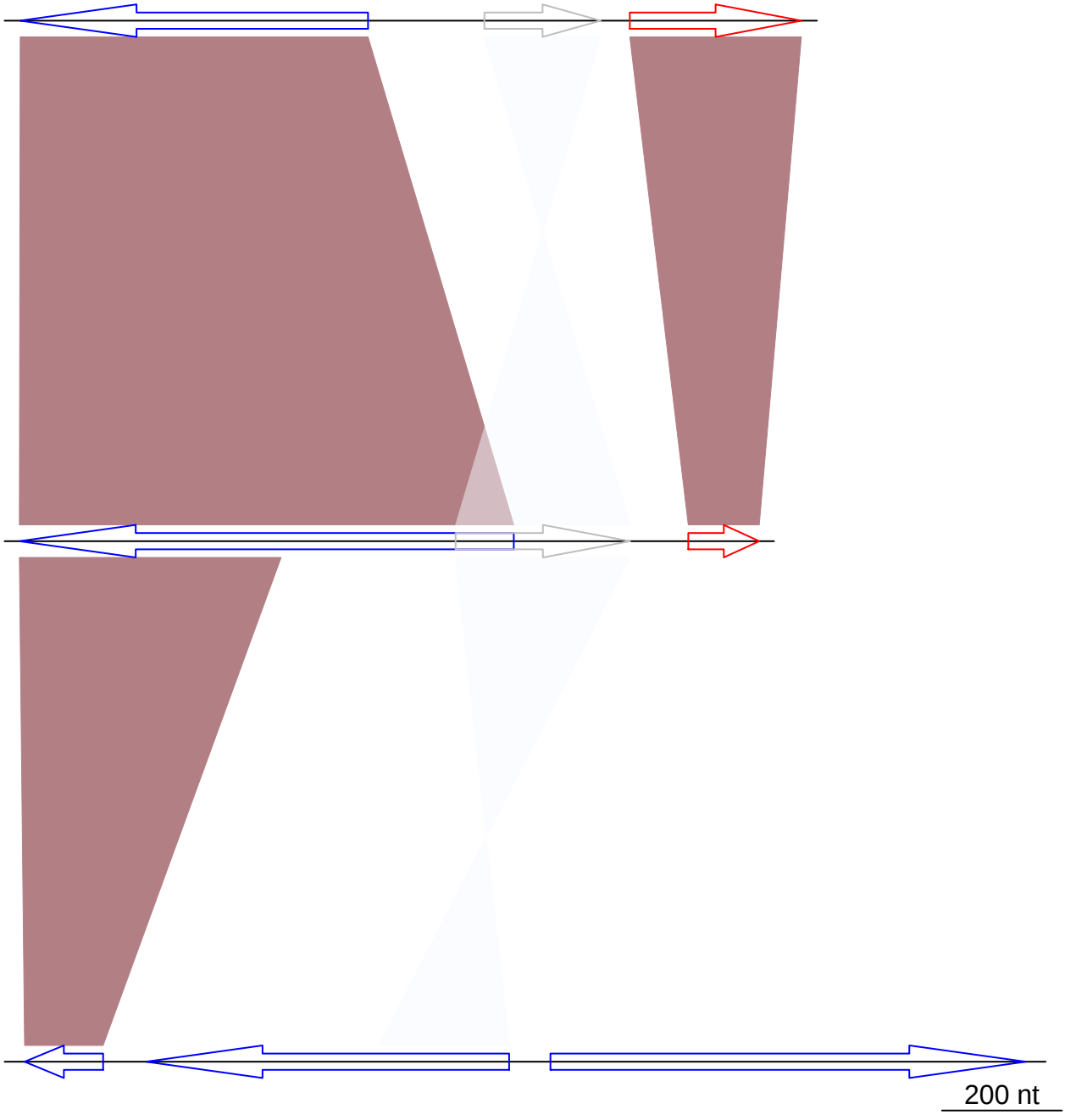
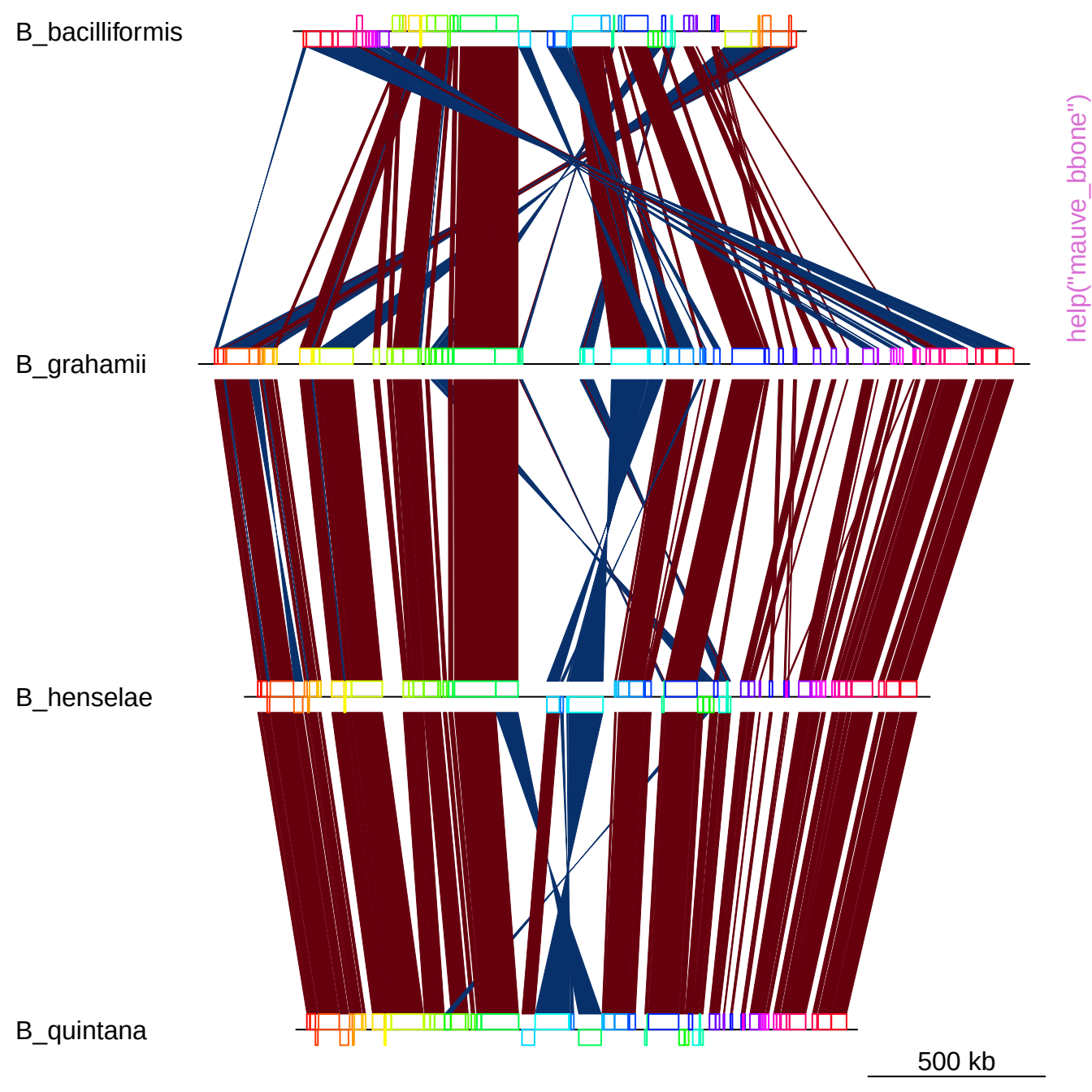
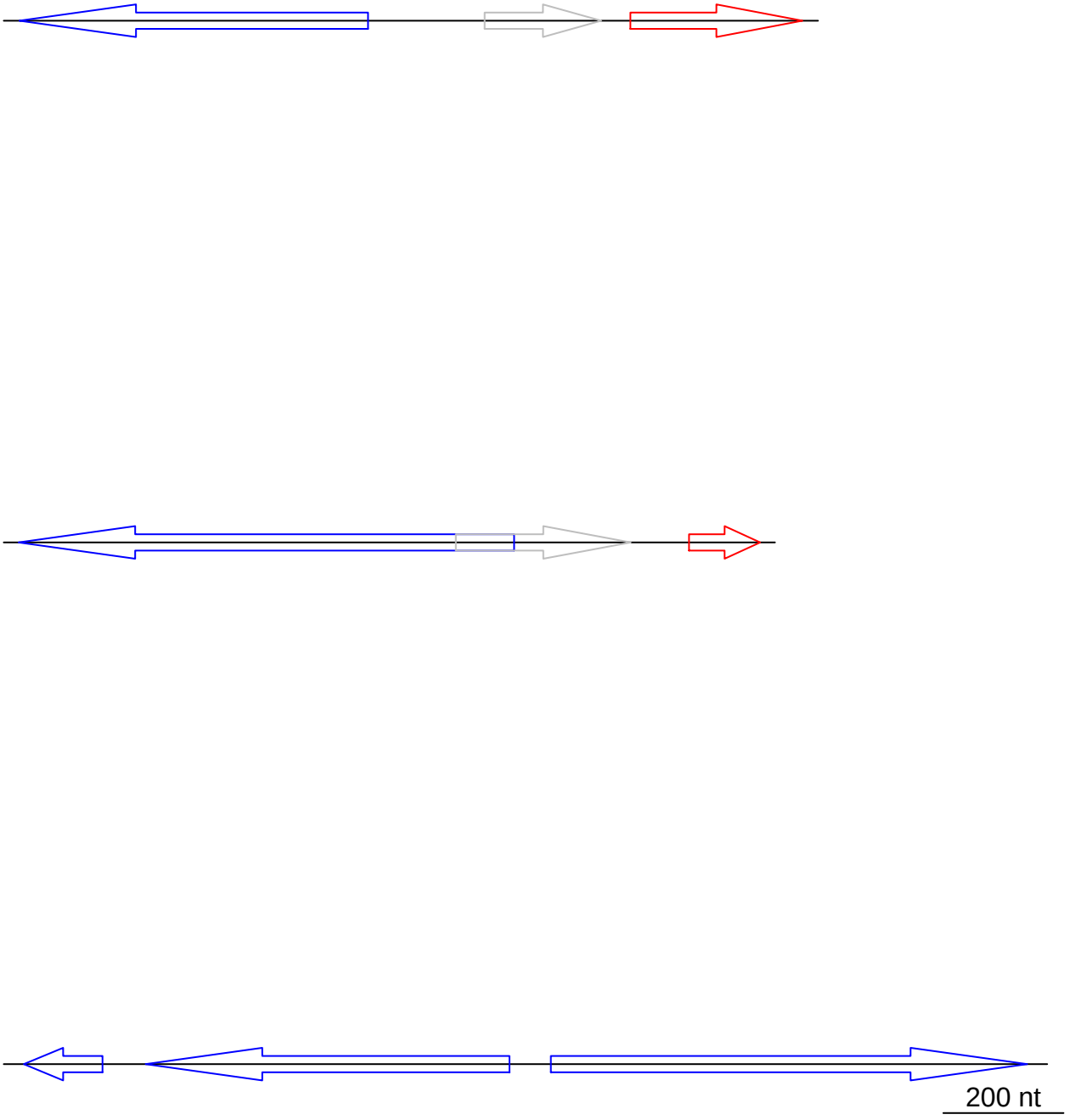
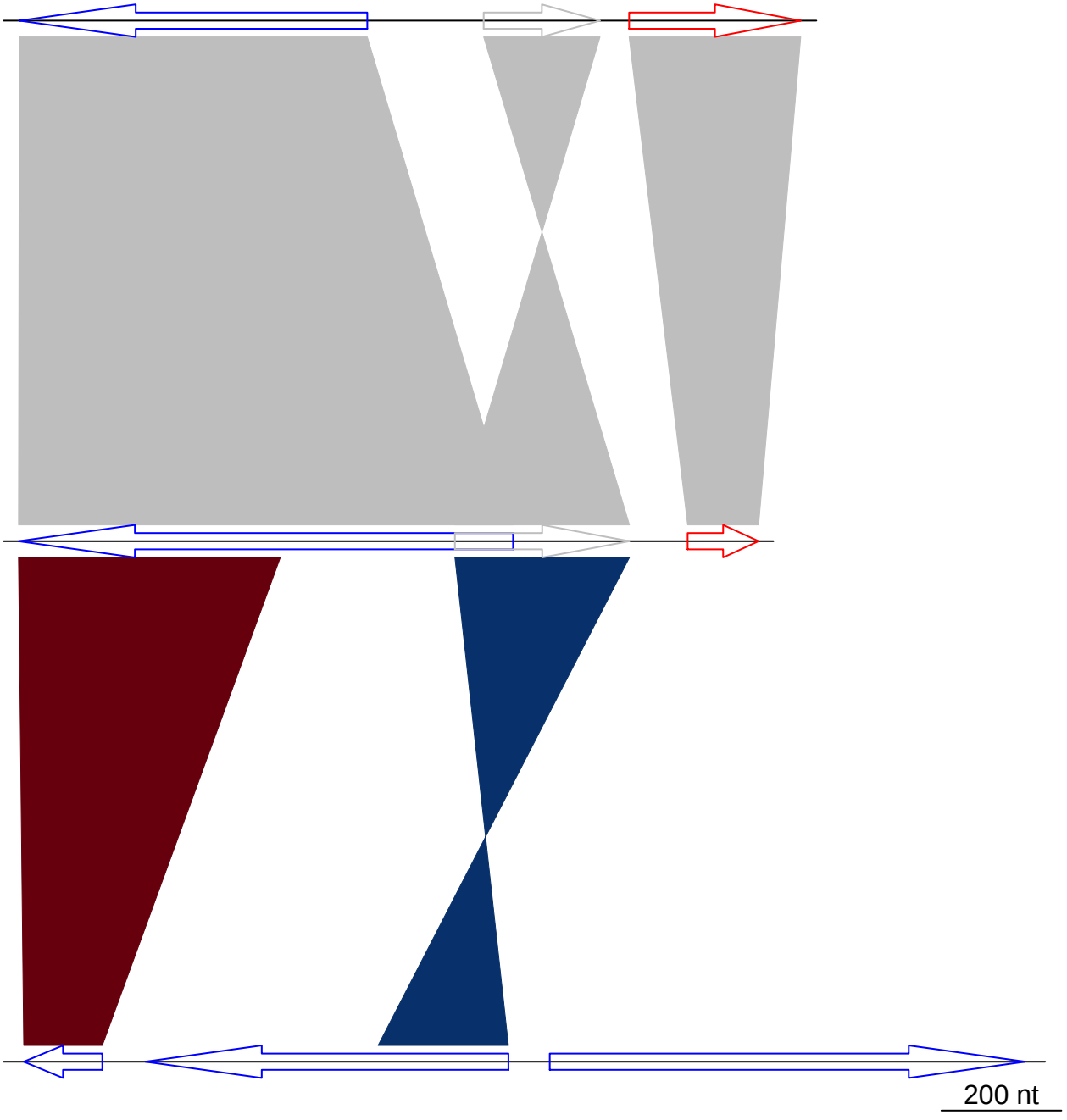
***
***
200 nt

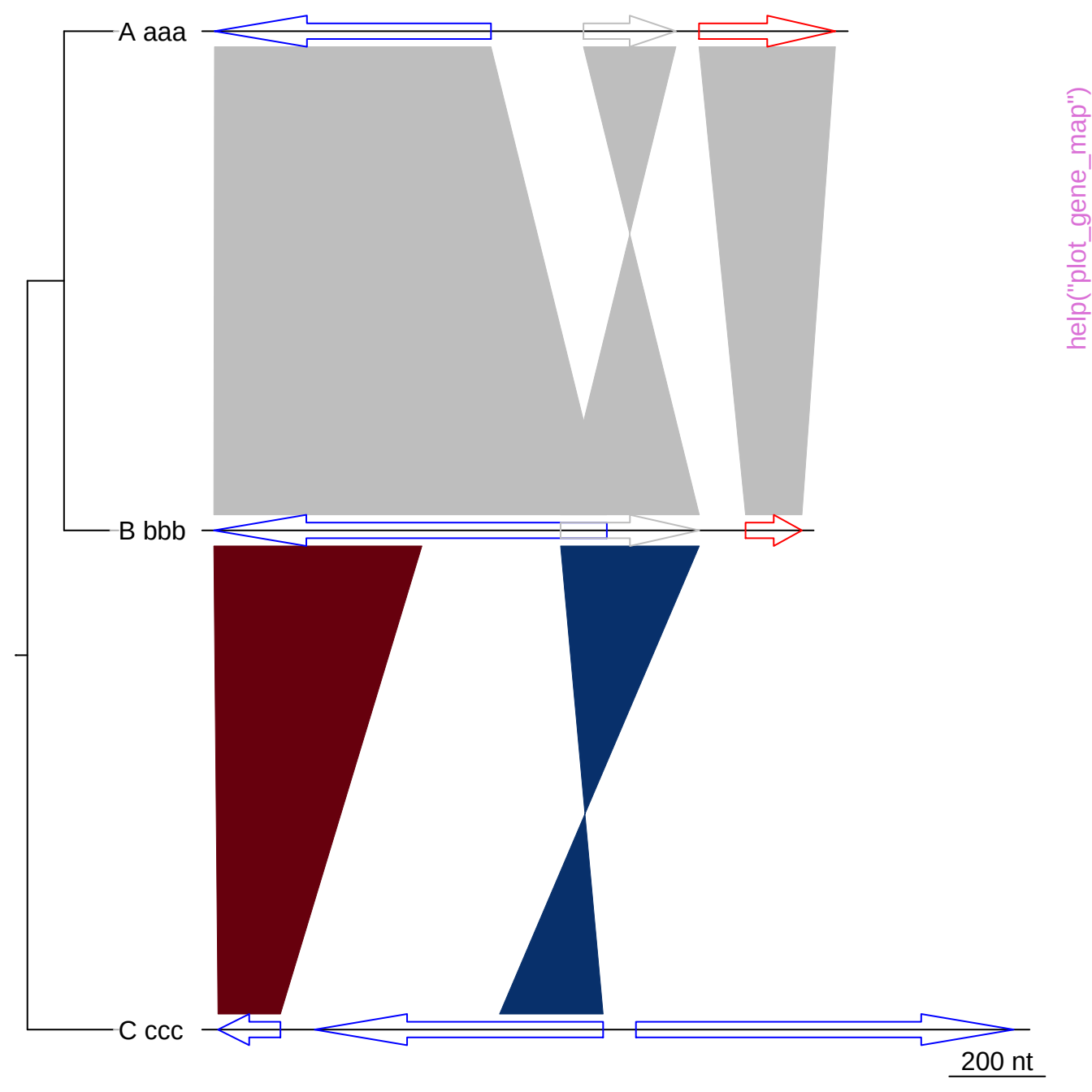


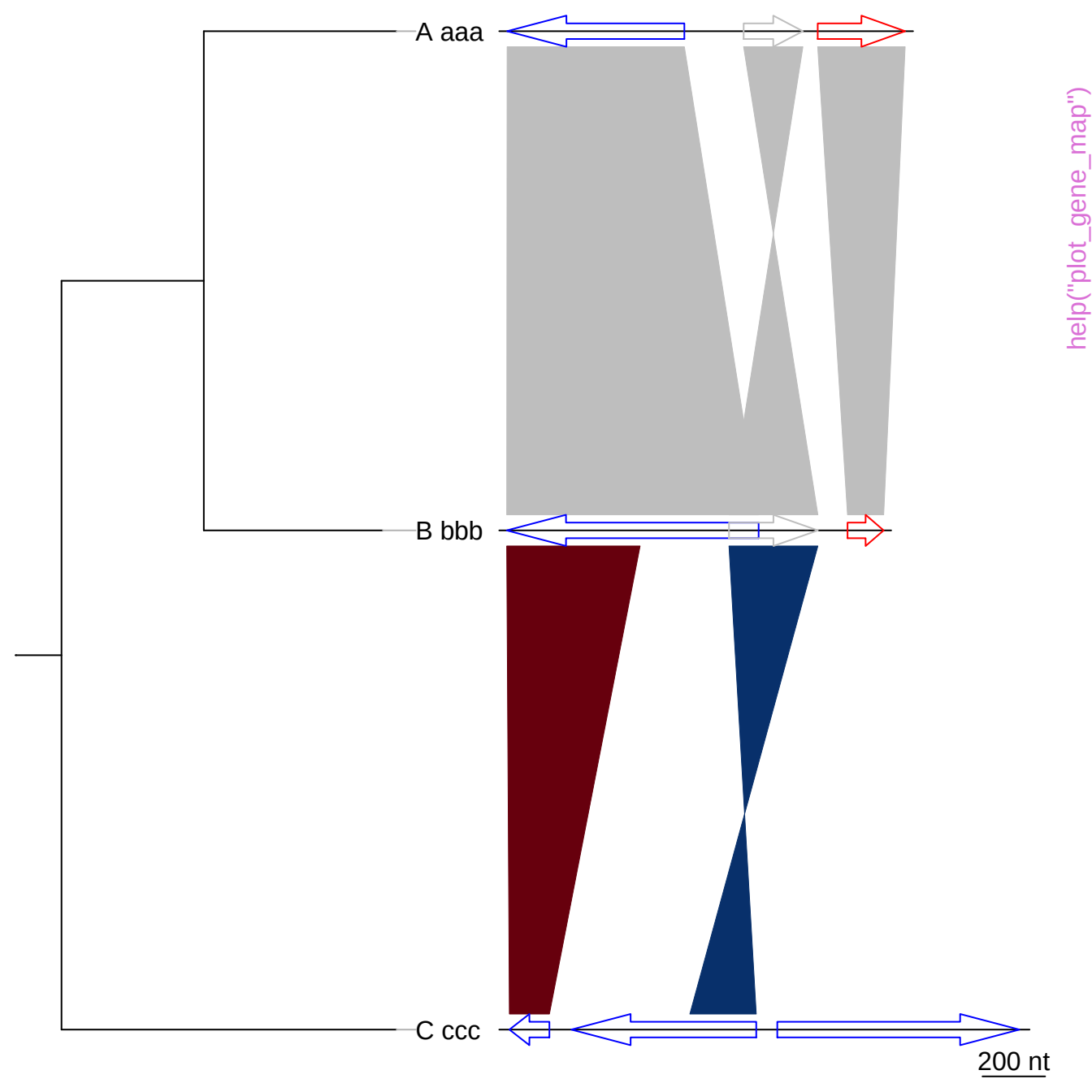
help("genoPlotR-package")

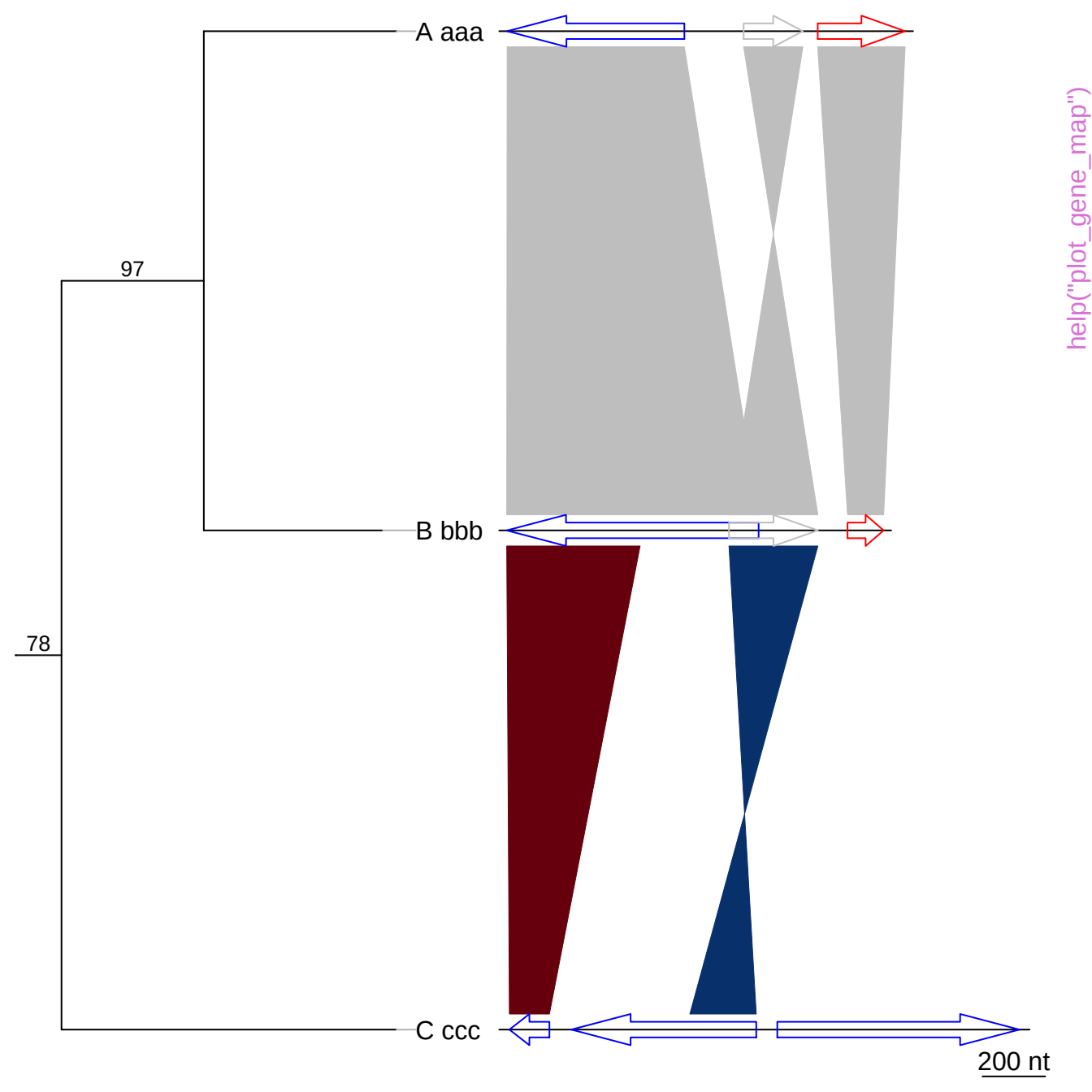

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("mauve_bbone")

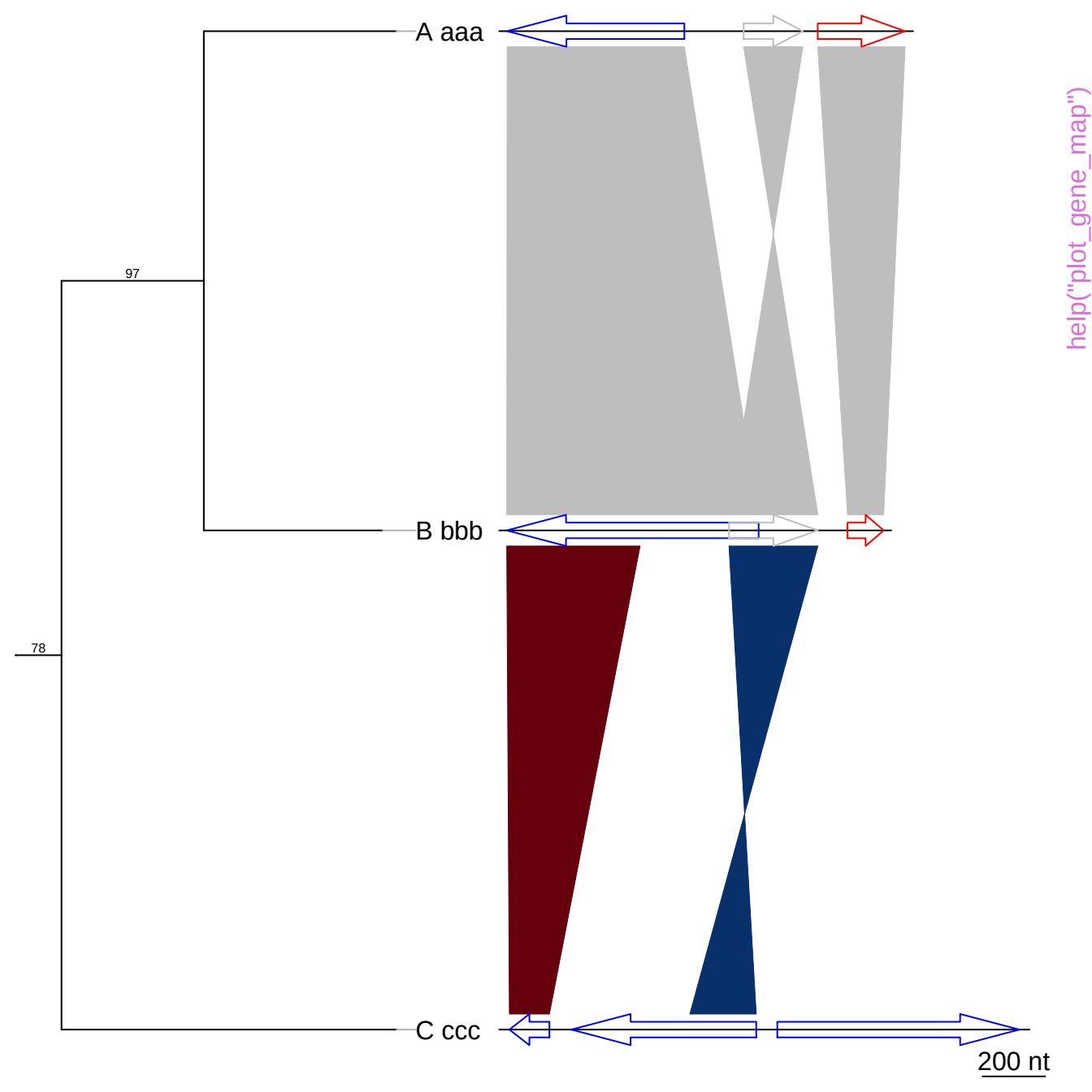

help("plot_gene_map")
200 nt

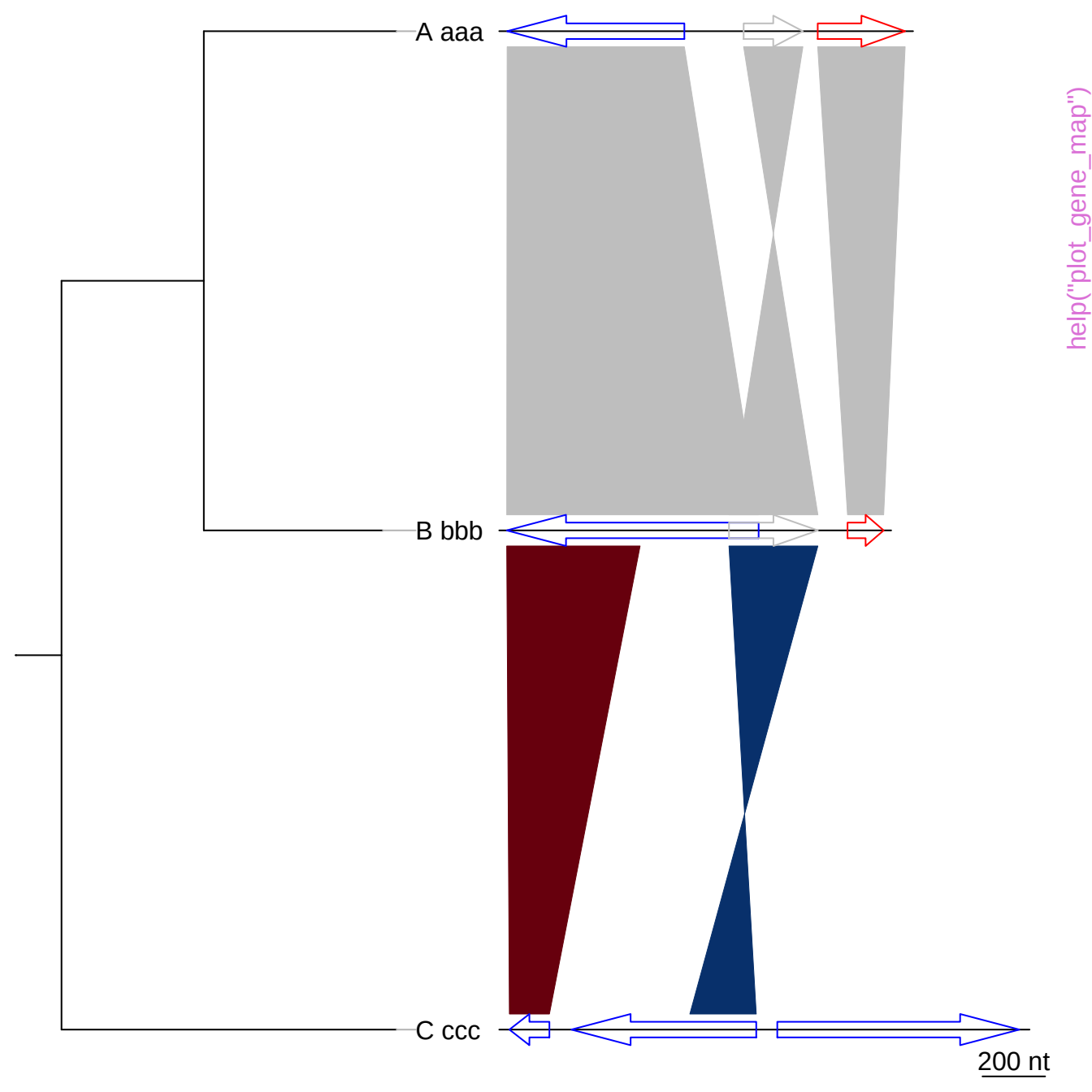

help("plot_gene_map")
200 nt

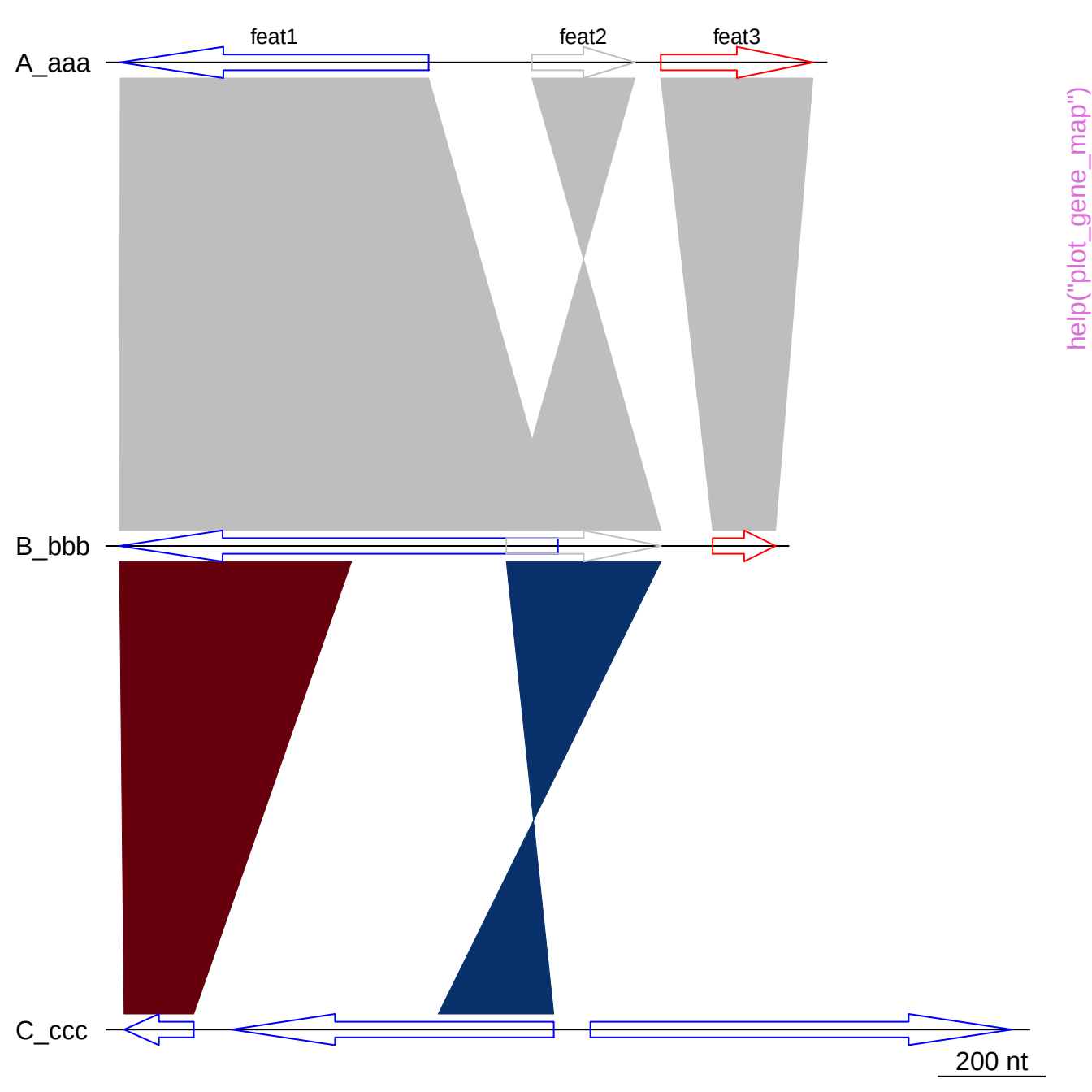

A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")

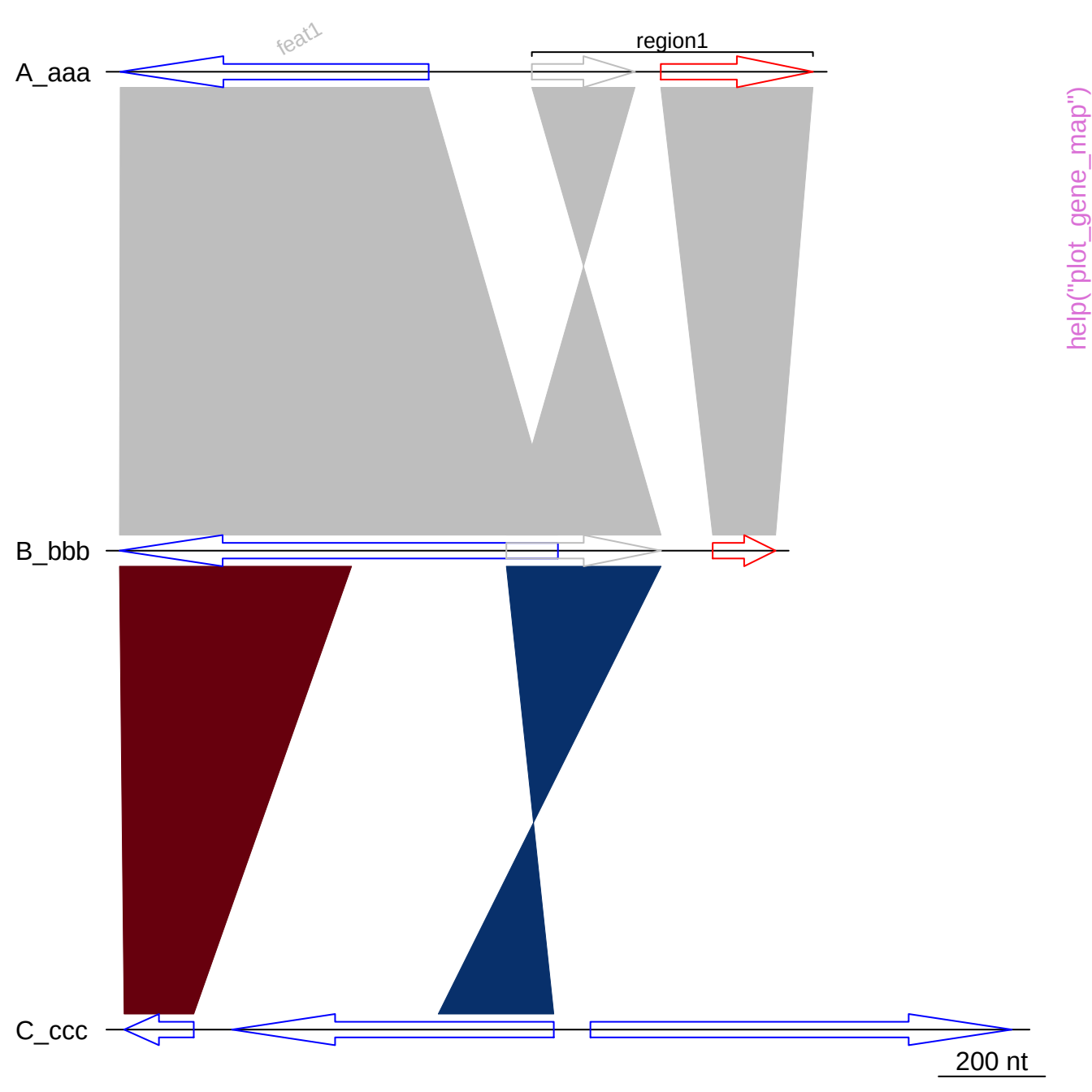

A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")


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
200 nt
help("plot_gene_map")


feat1
region1
A_aaa
B_bbb
C_ccc
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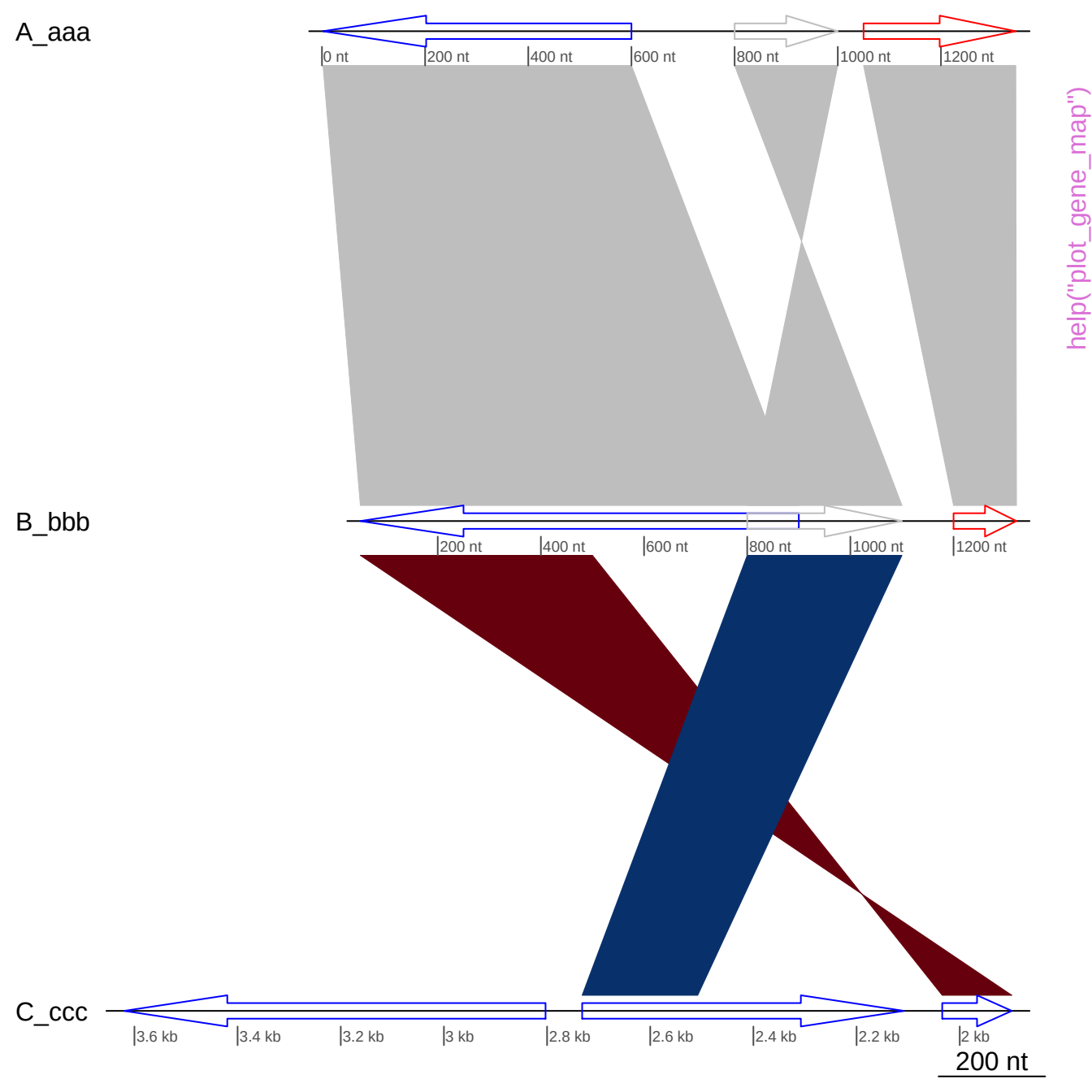
help("plot_gene_map")


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
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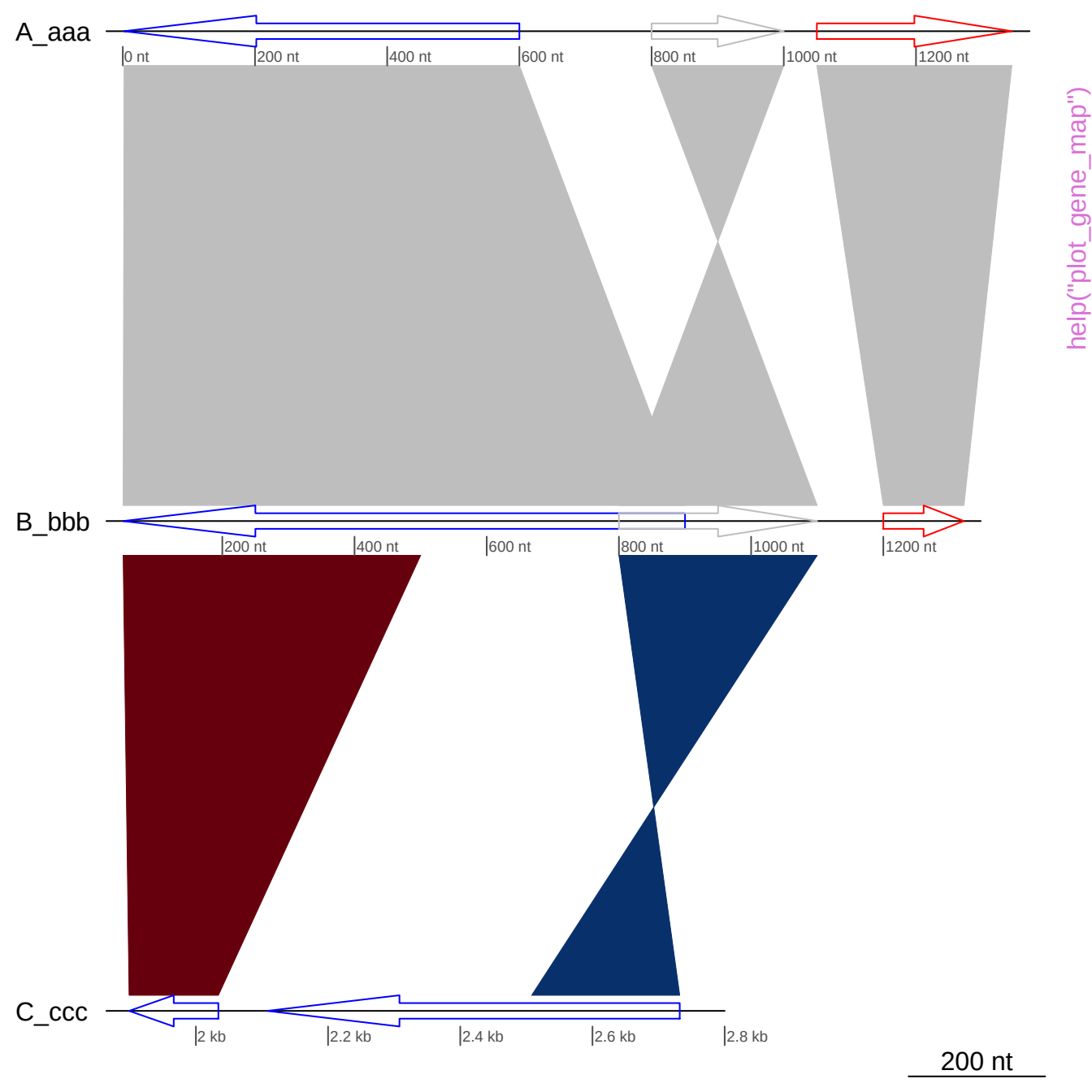
help("plot_gene_map")


A_aaa
0 nt
200 nt
400 nt
600 nt
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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
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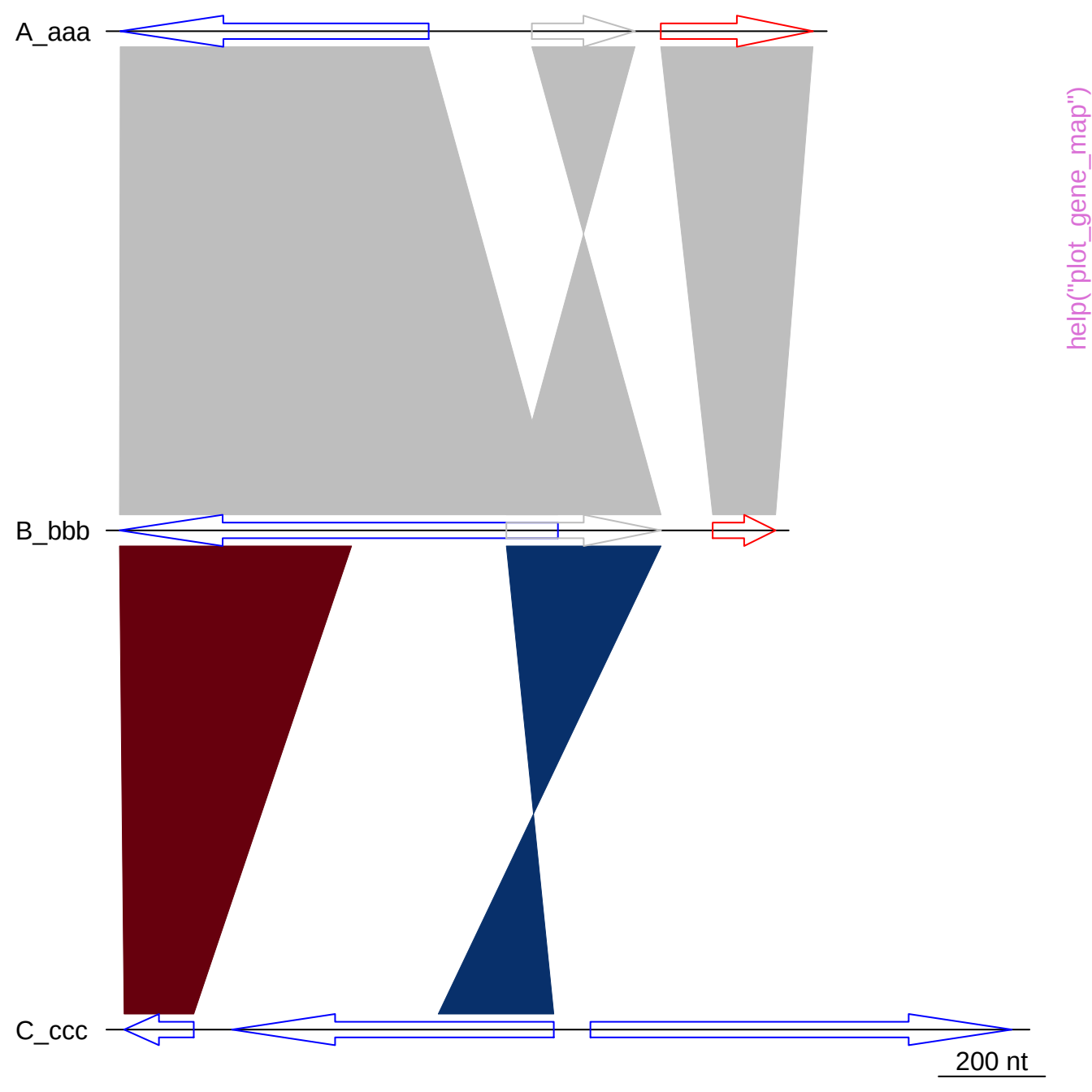
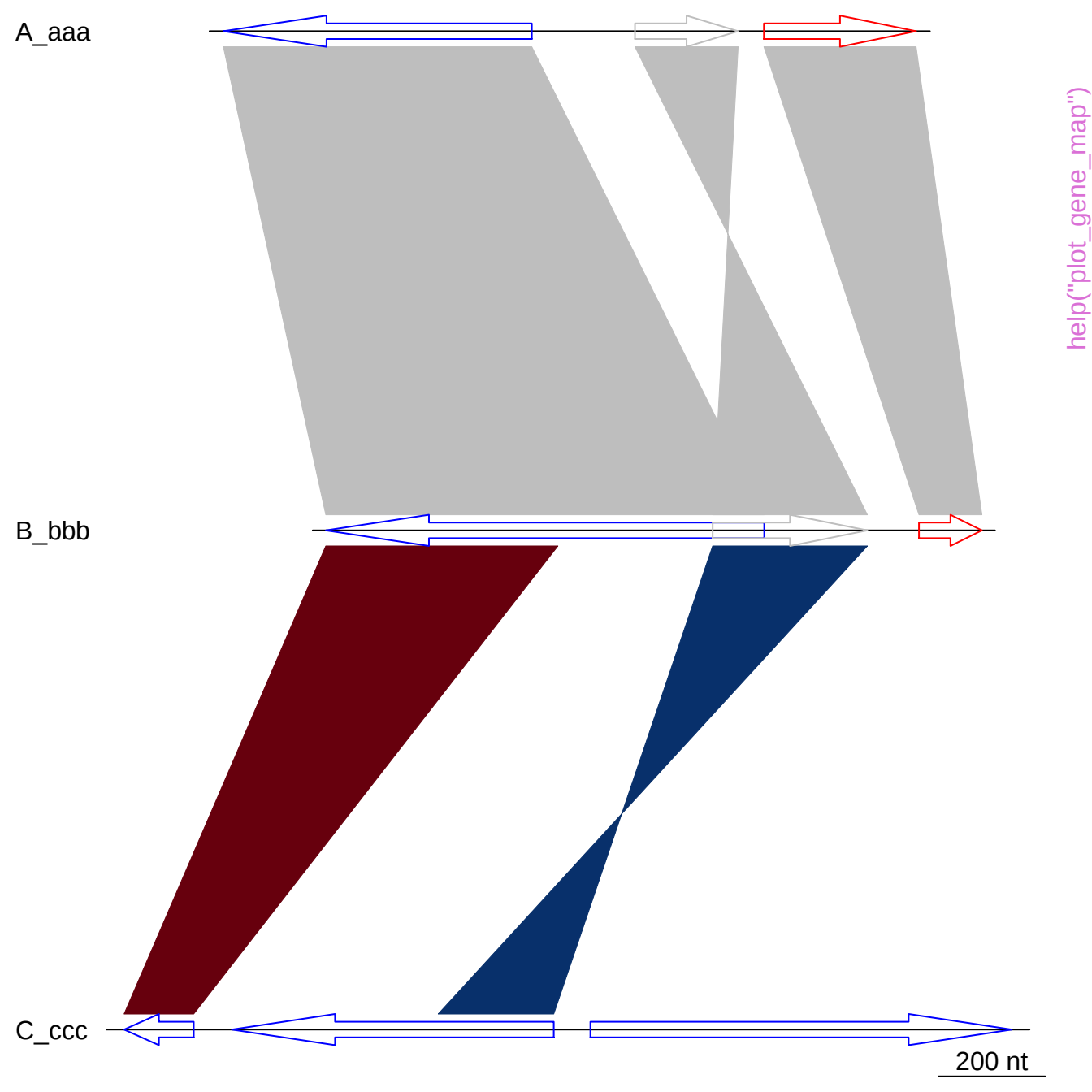
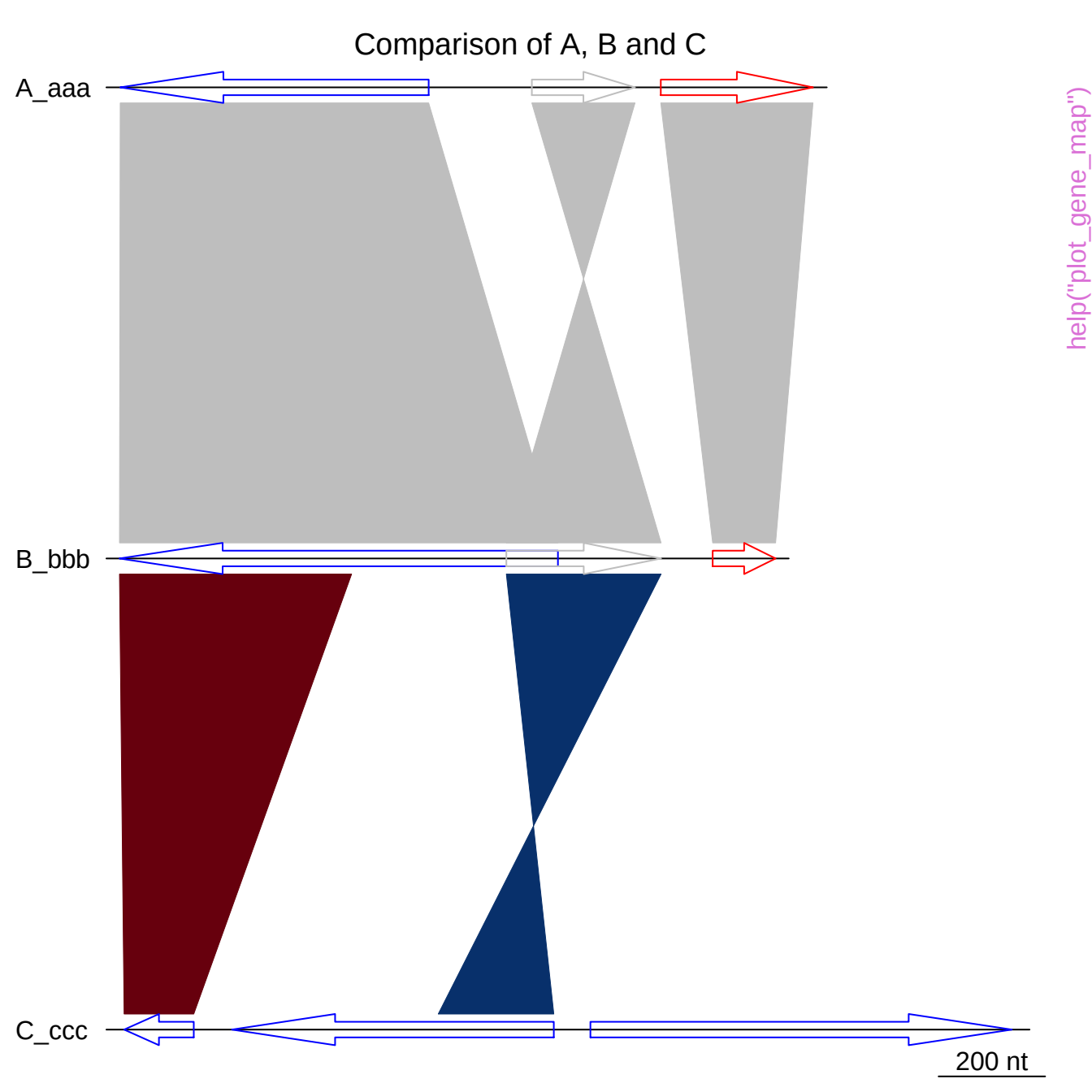
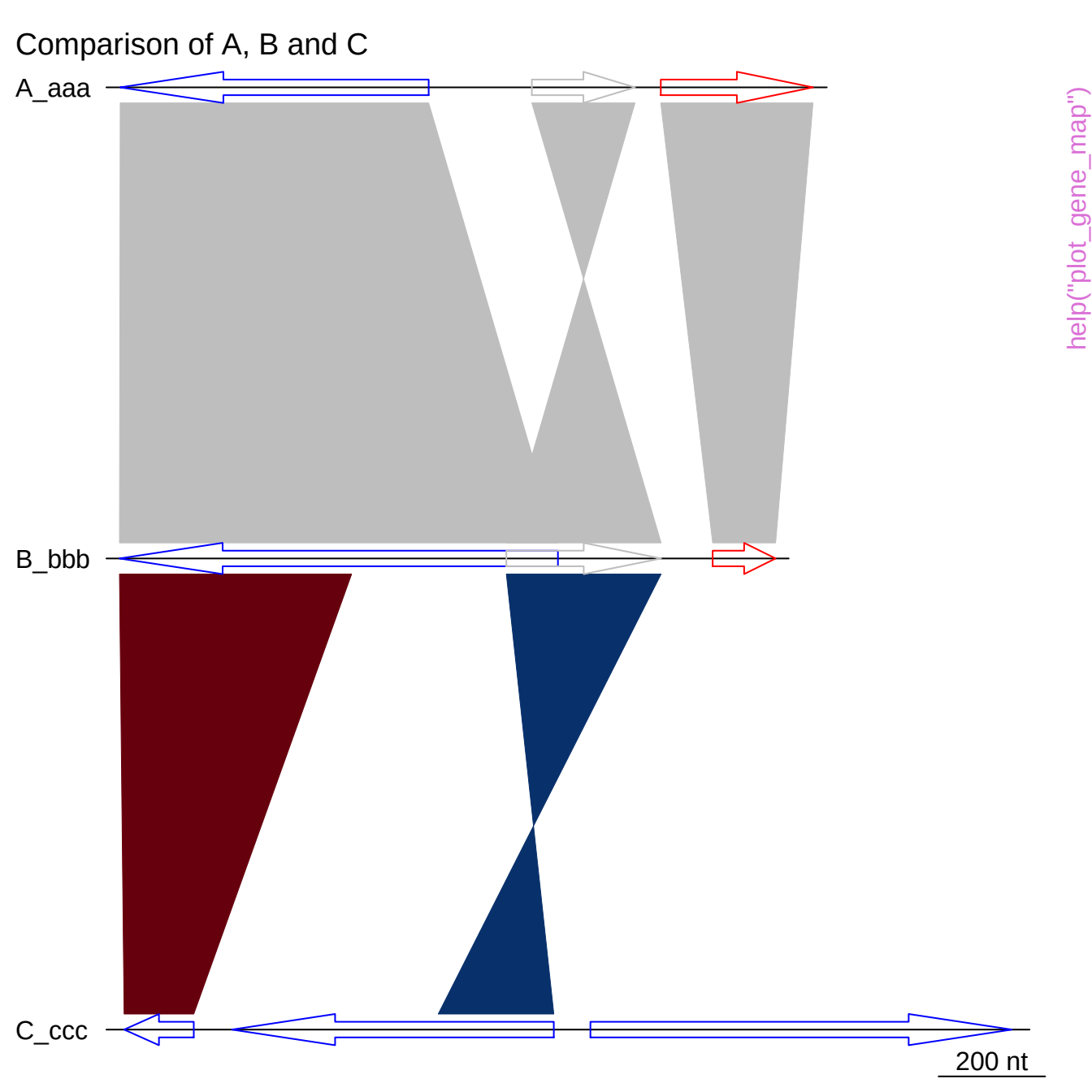
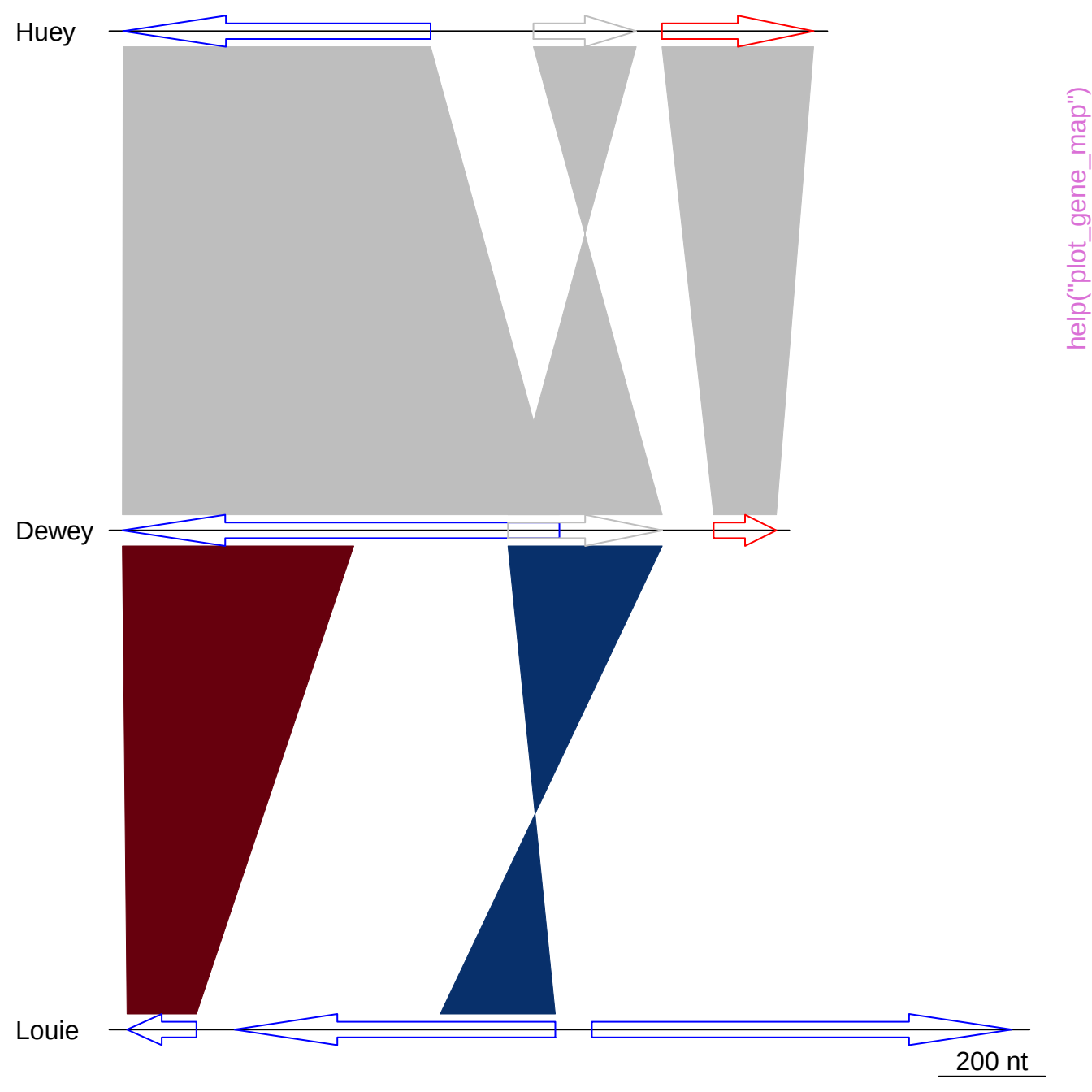
2.6 kb
2.8 kb
200 nt
help("plot_gene_map")

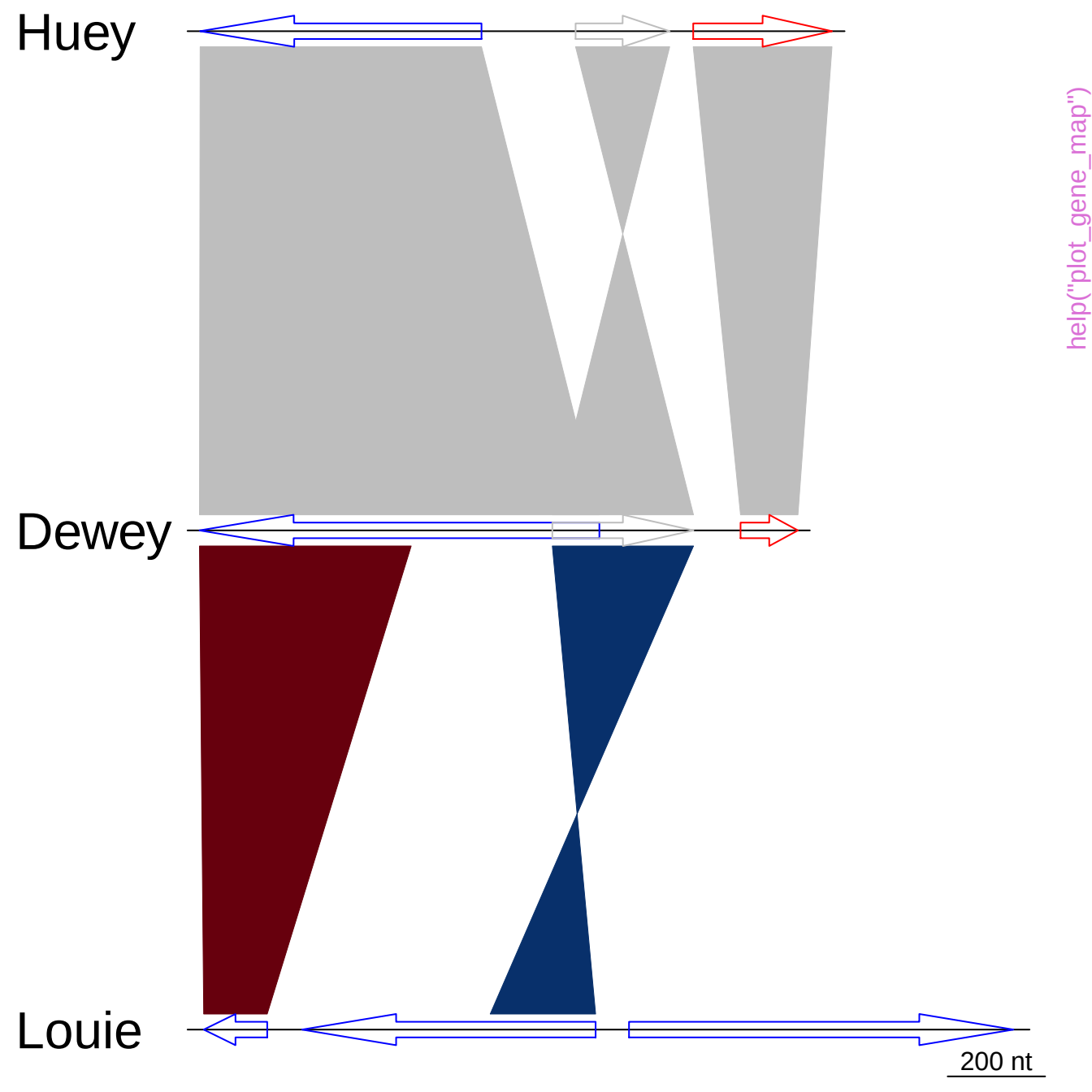

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

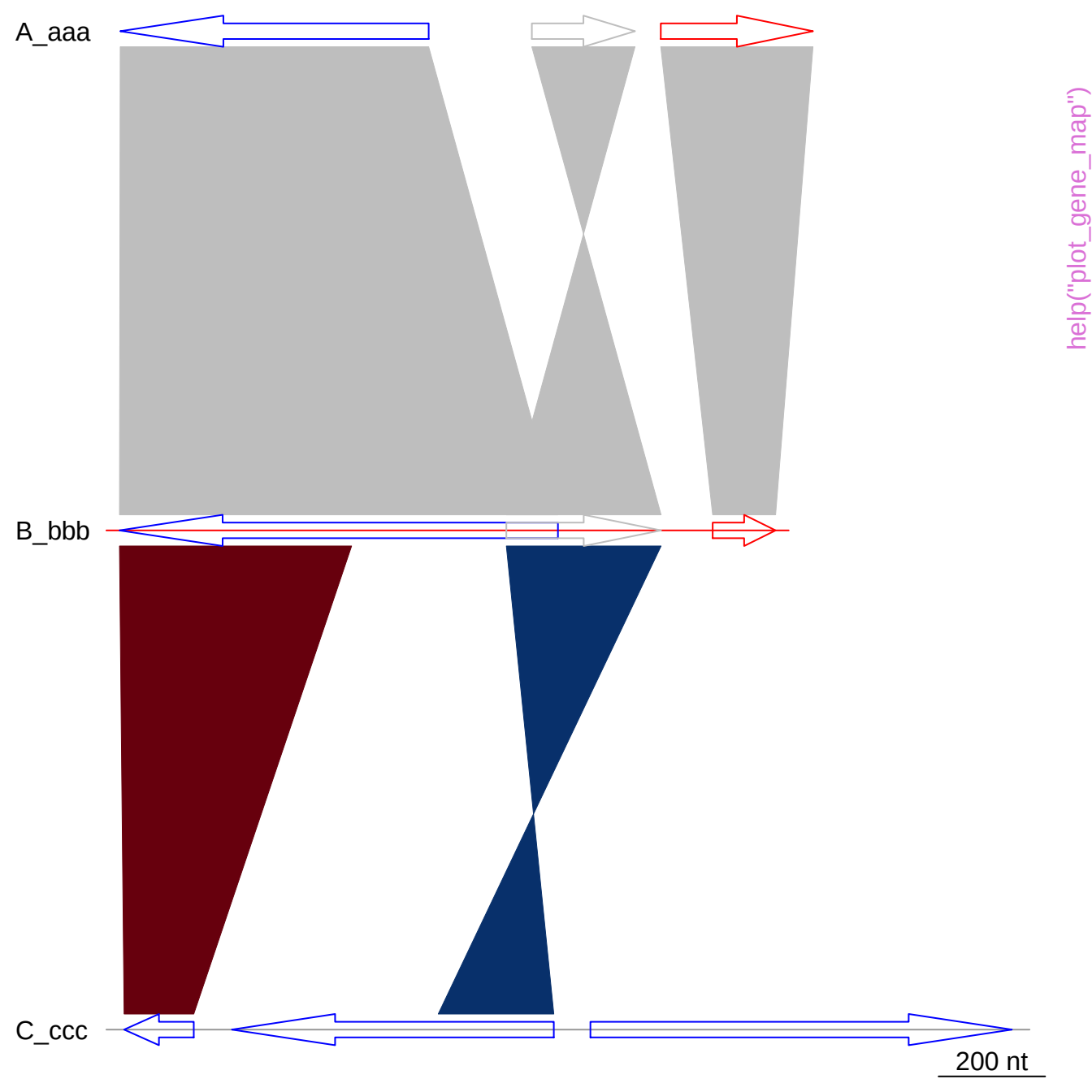

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

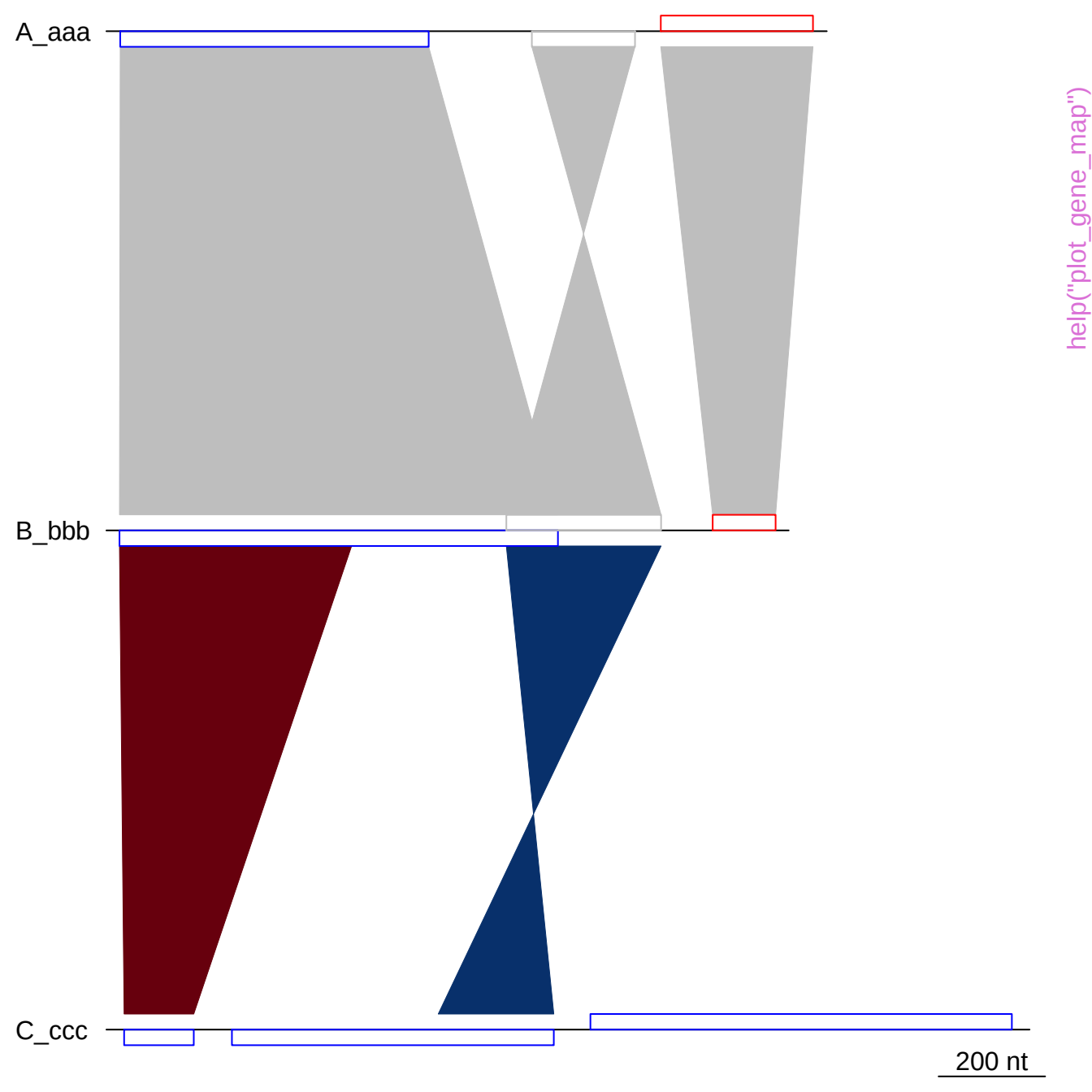

Comparison of A, B and C
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")


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
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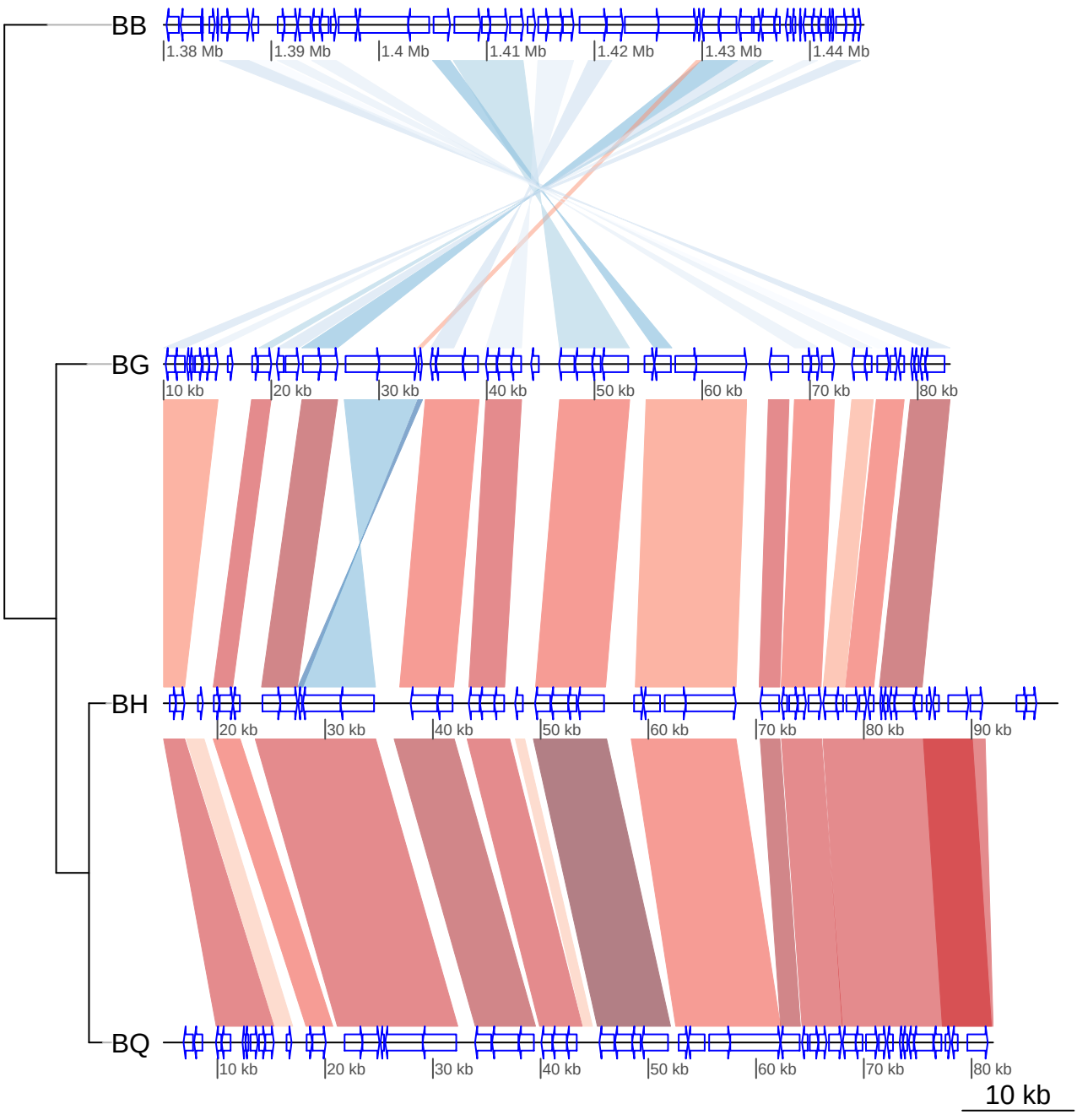
help("plot_gene_map")


BB
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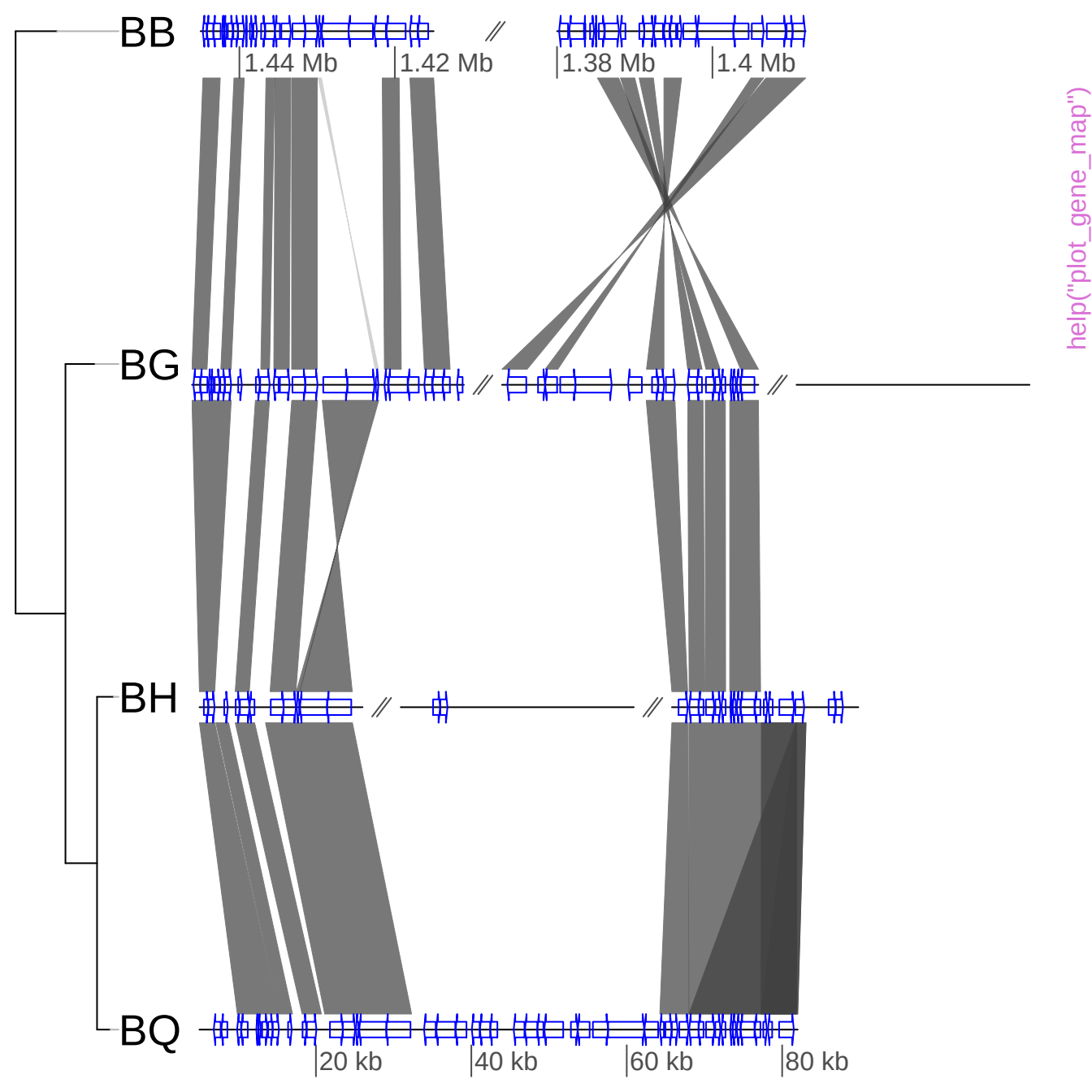
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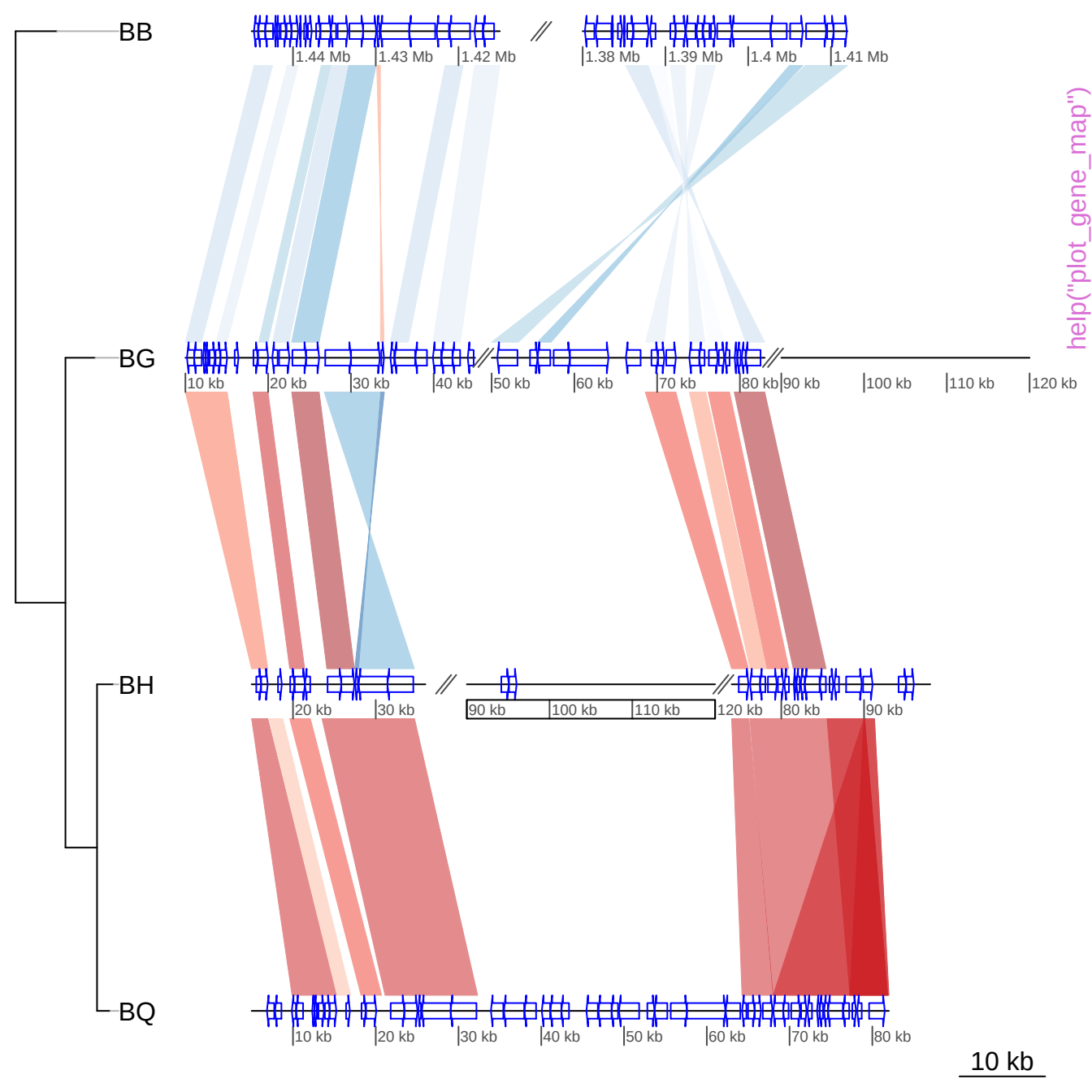
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90 kb
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110 kb
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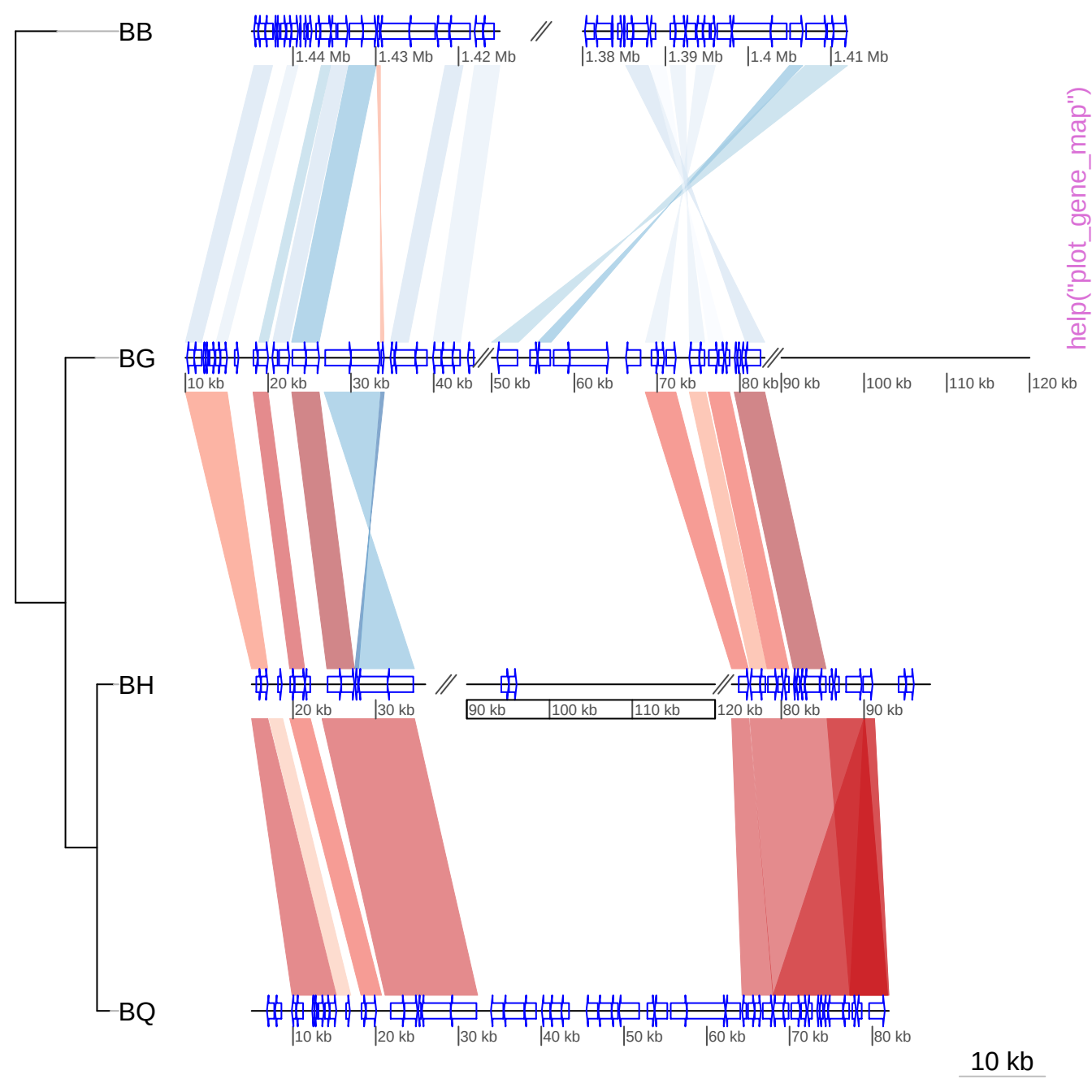
help("plot_gene_map")


BB
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120 kb
80 kb
90 kb
BQ
10 kb
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40 kb
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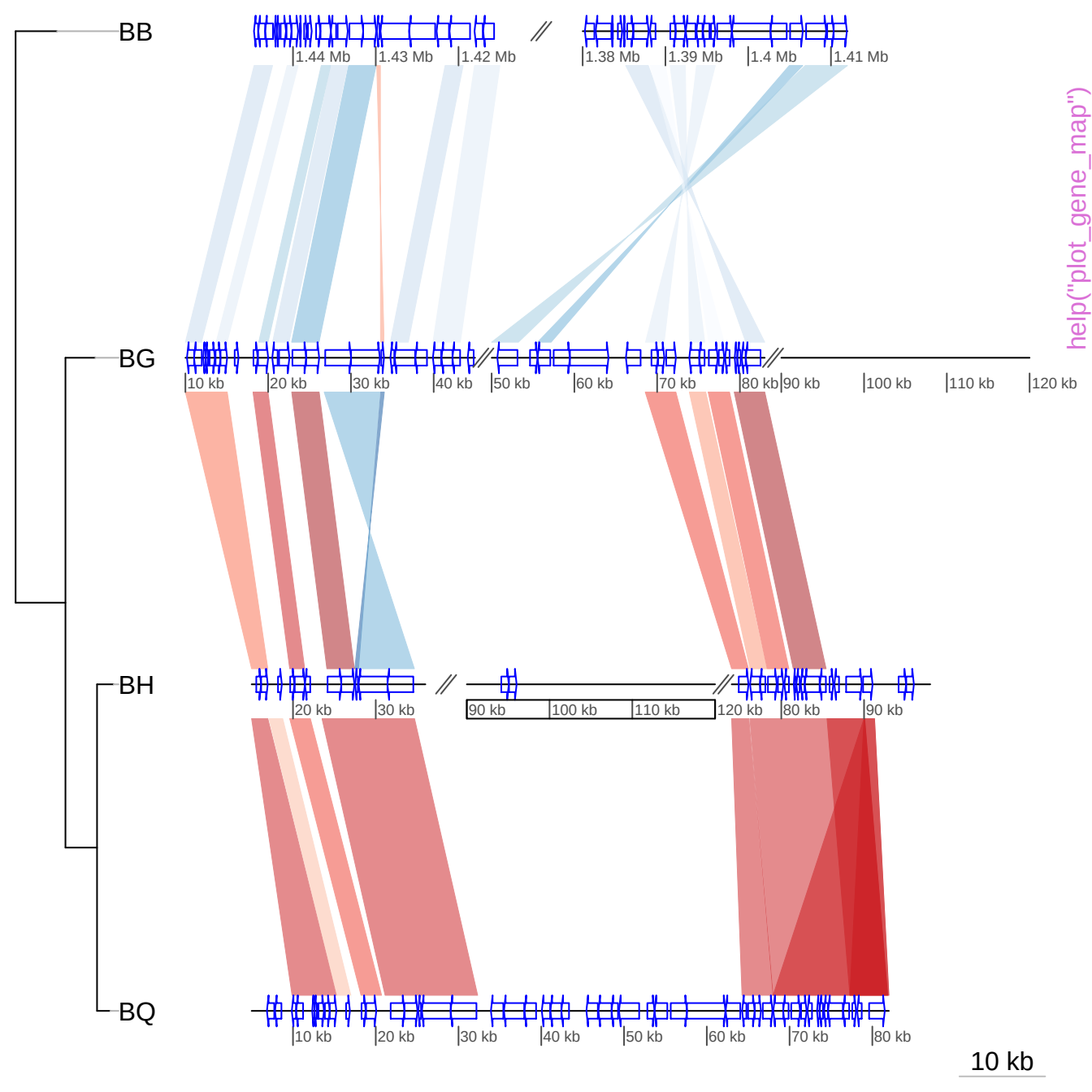
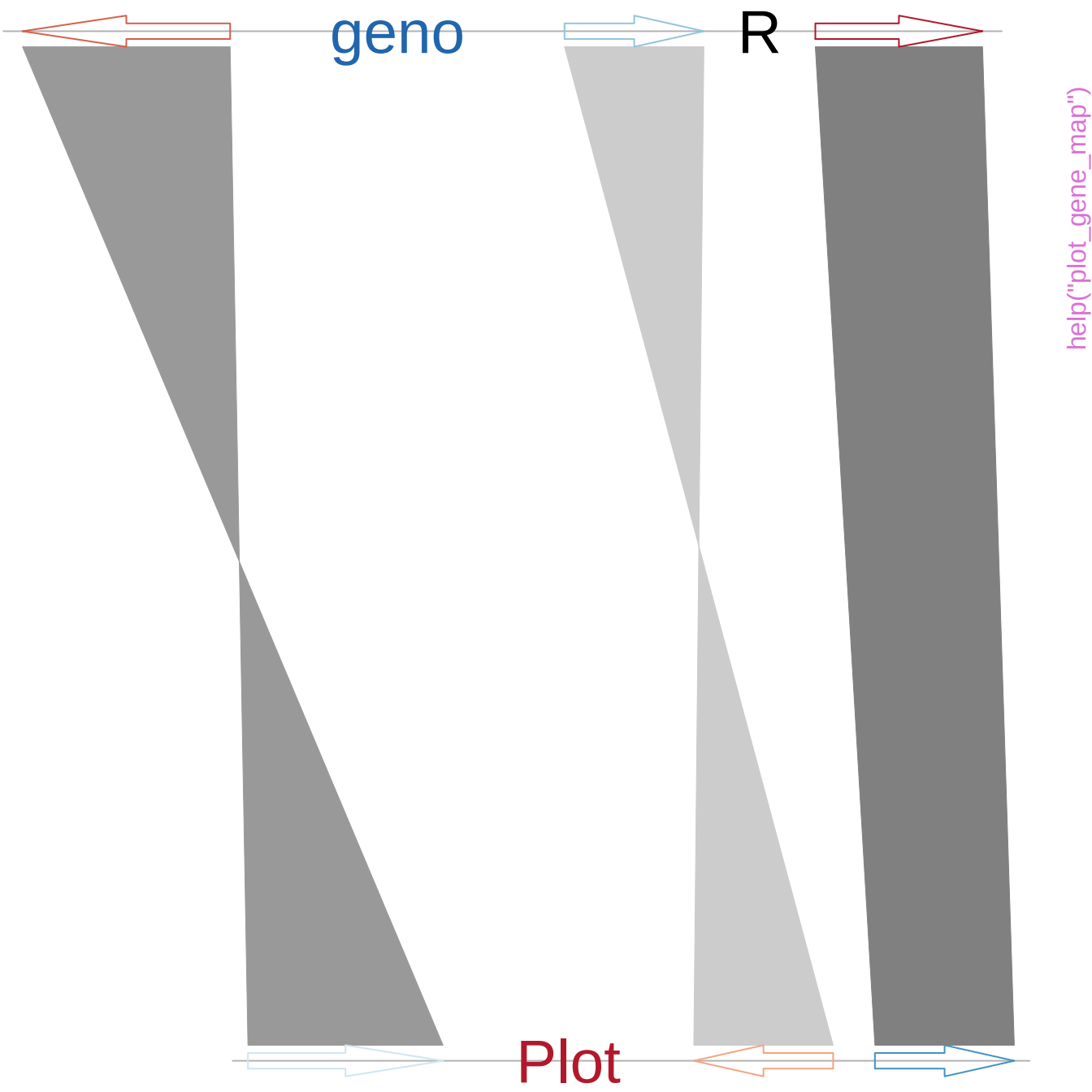
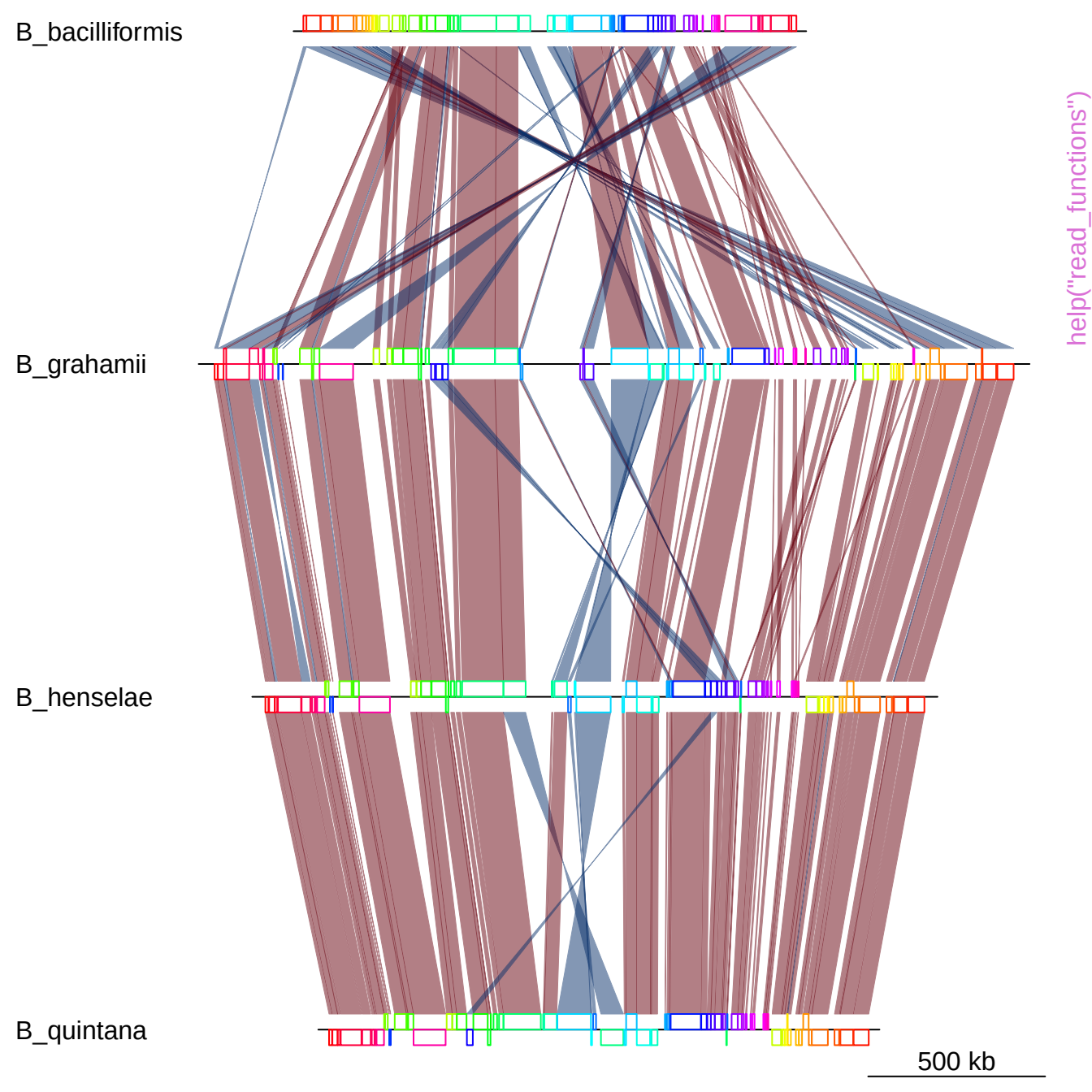
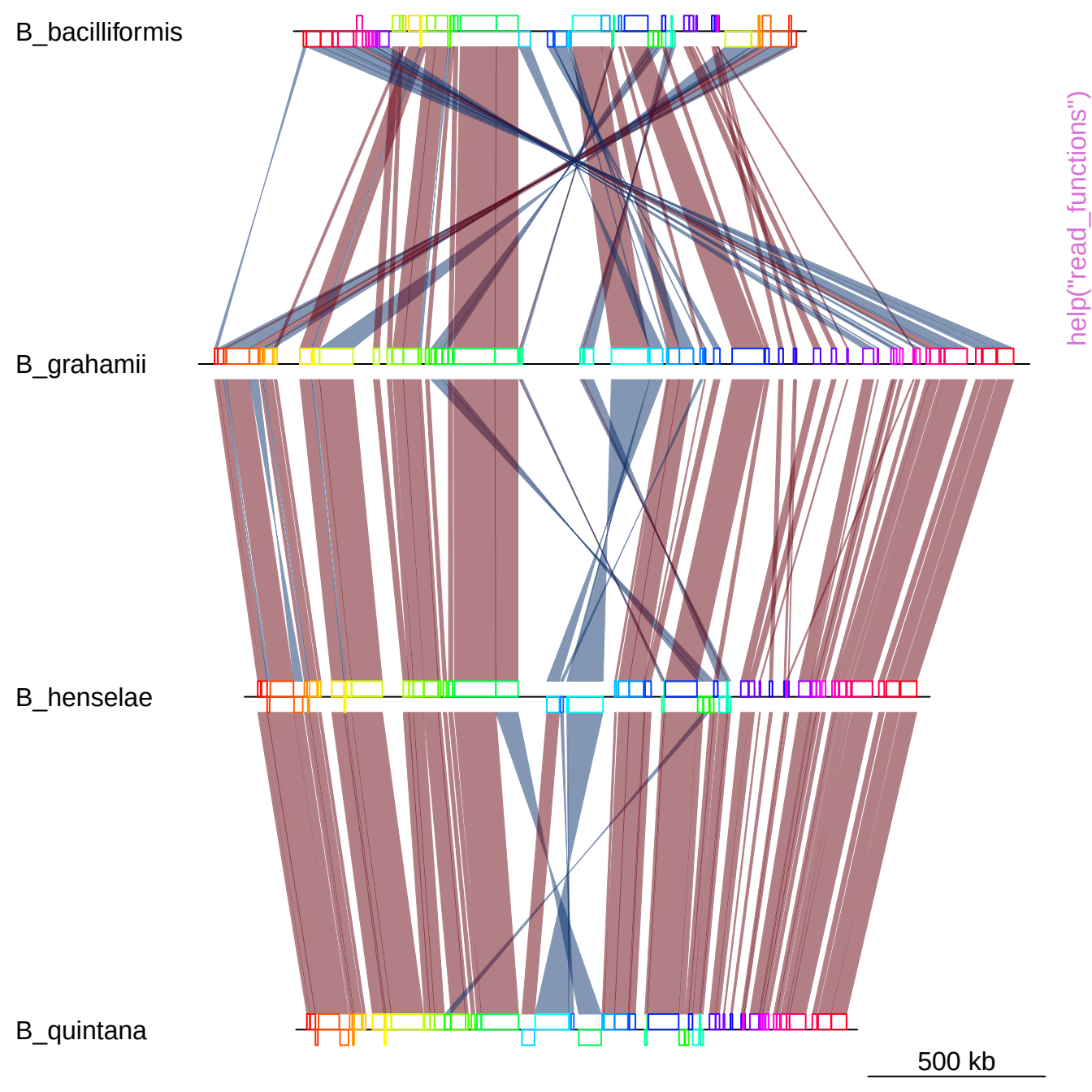
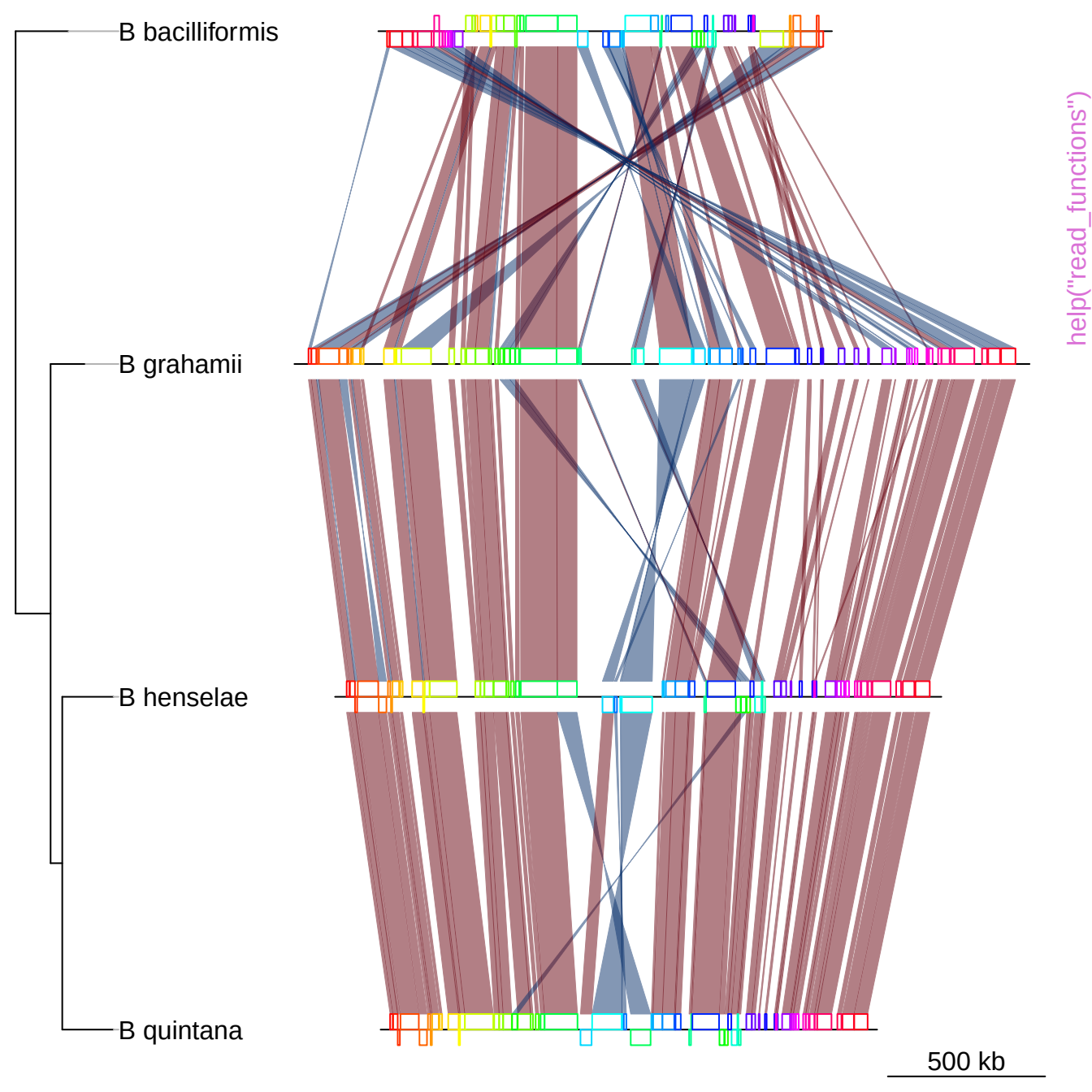
70 kb
80 kb
10 kb
help("plot_gene_map")

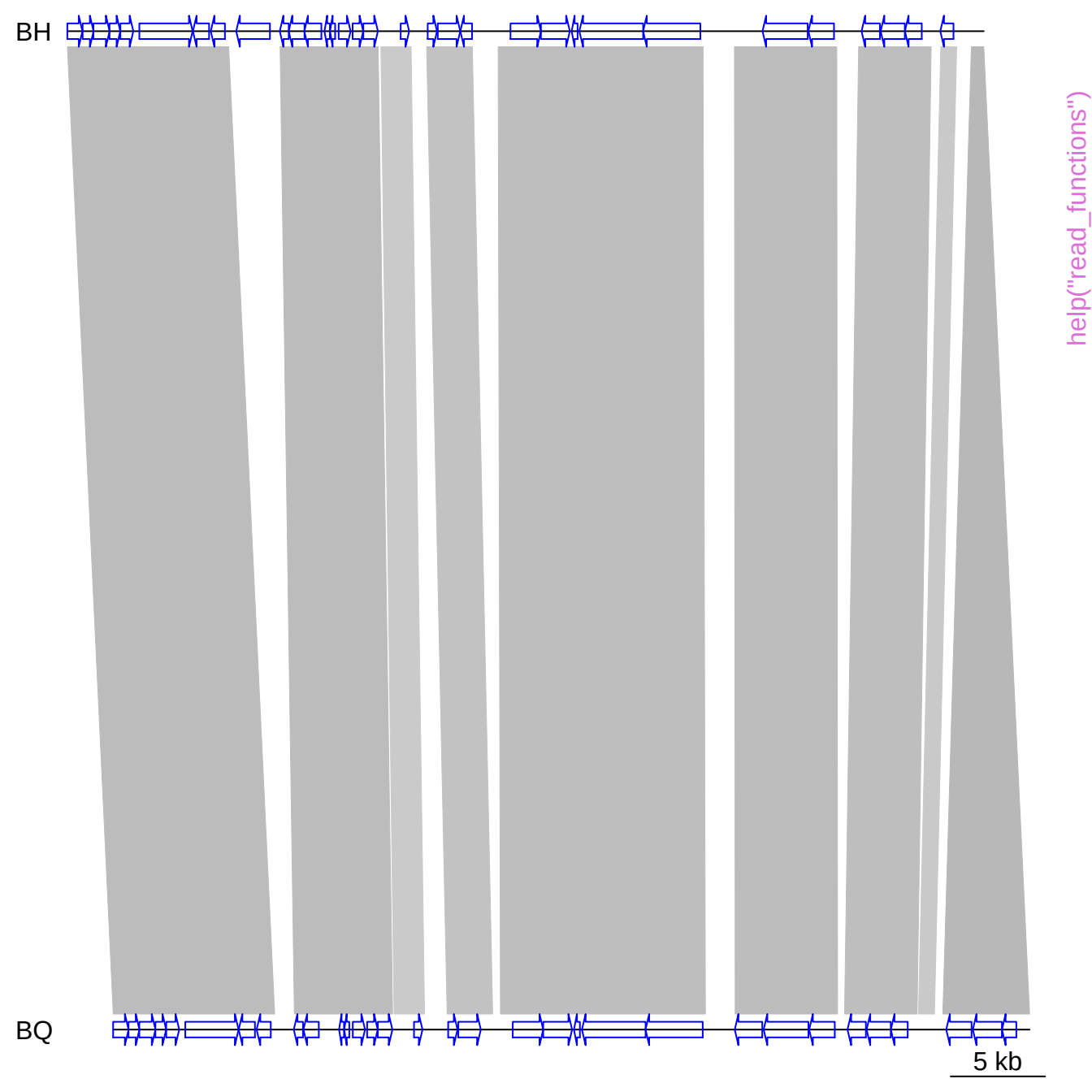

BB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
BG
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
100 kb
110 kb
120 kb
BH
20 kb
30 kb
90 kb
100 kb
110 kb
120 kb
80 kb
90 kb
BQ
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
10 kb
help("plot_gene_map")

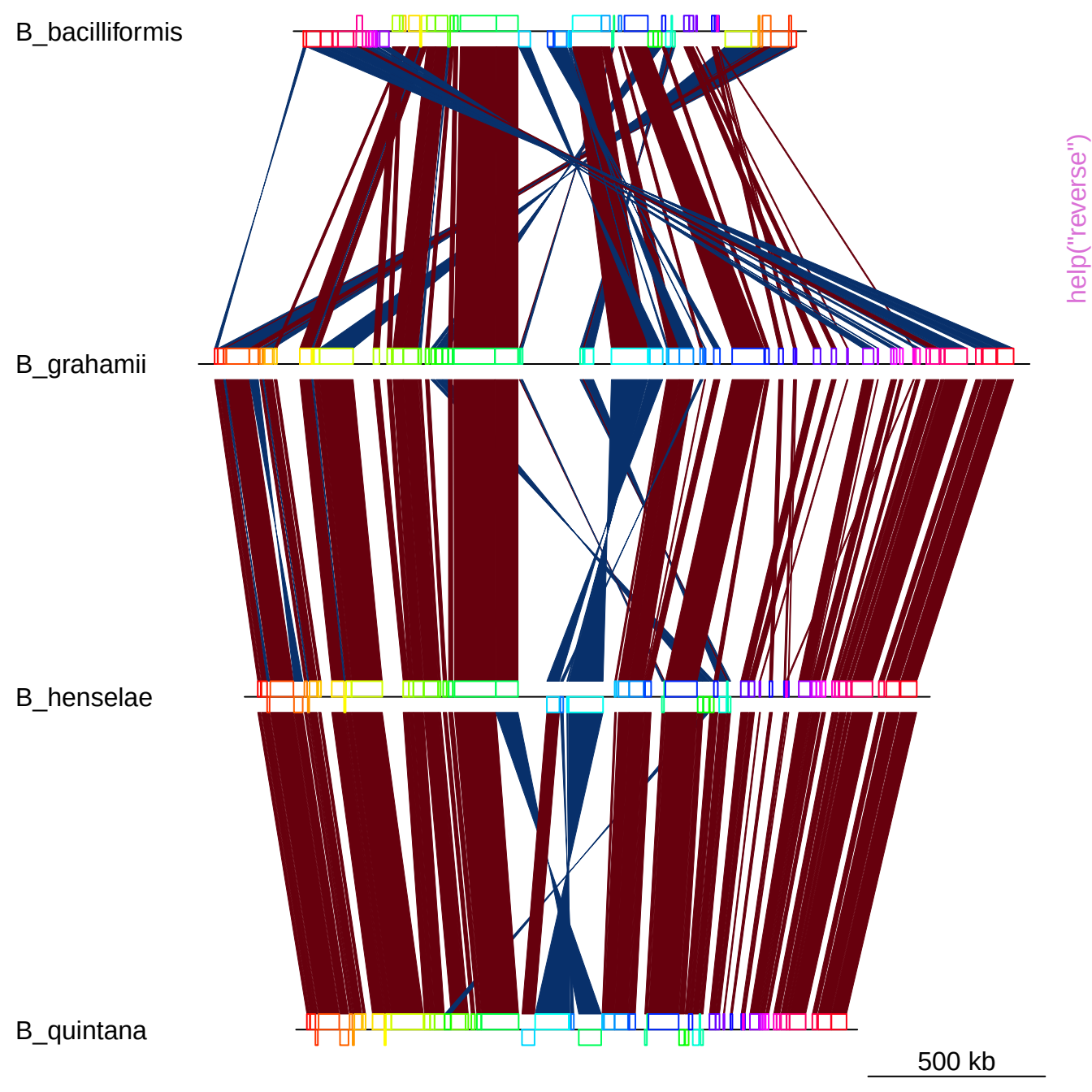

geno
R
Plot
help("plot_gene_map")

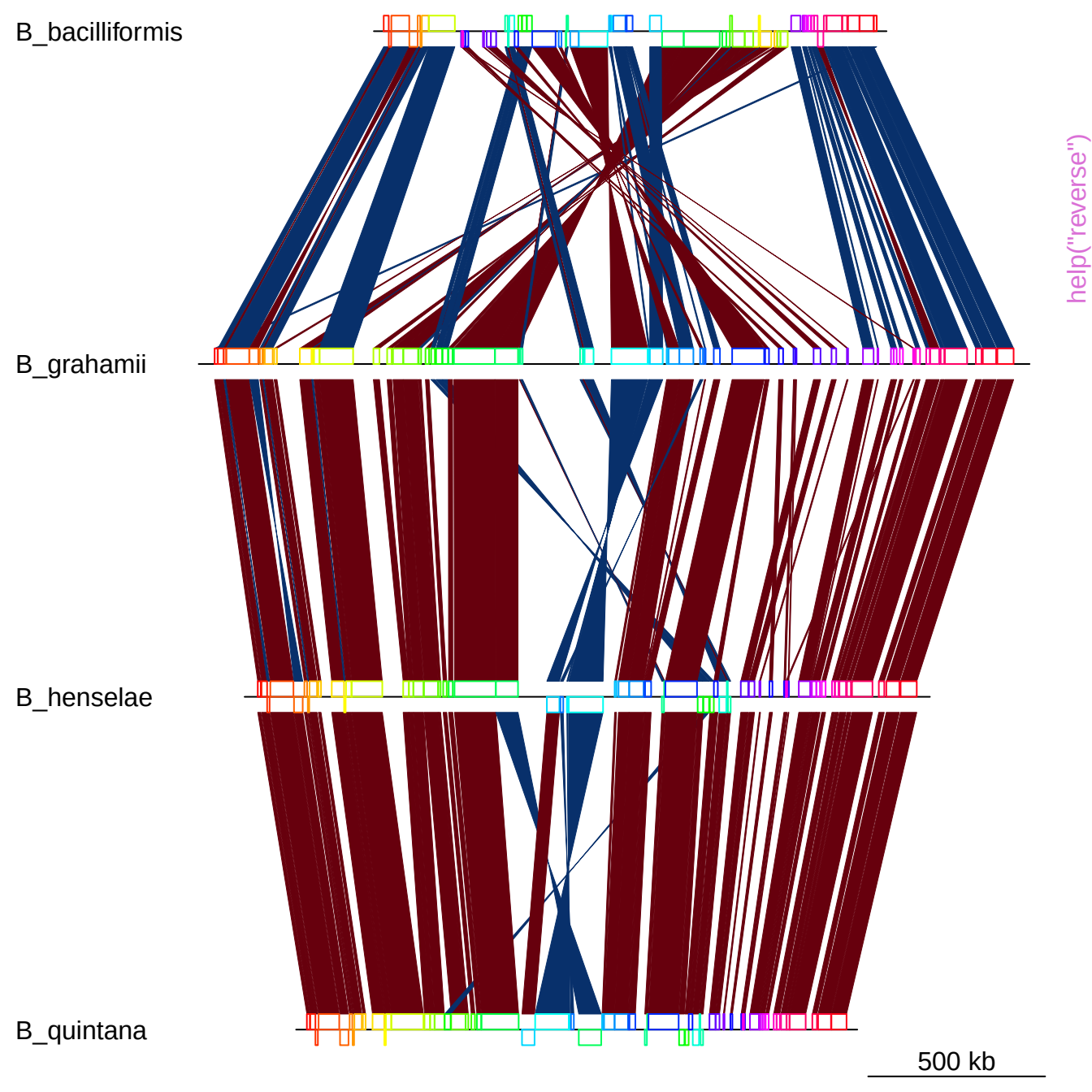

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("read_functions")

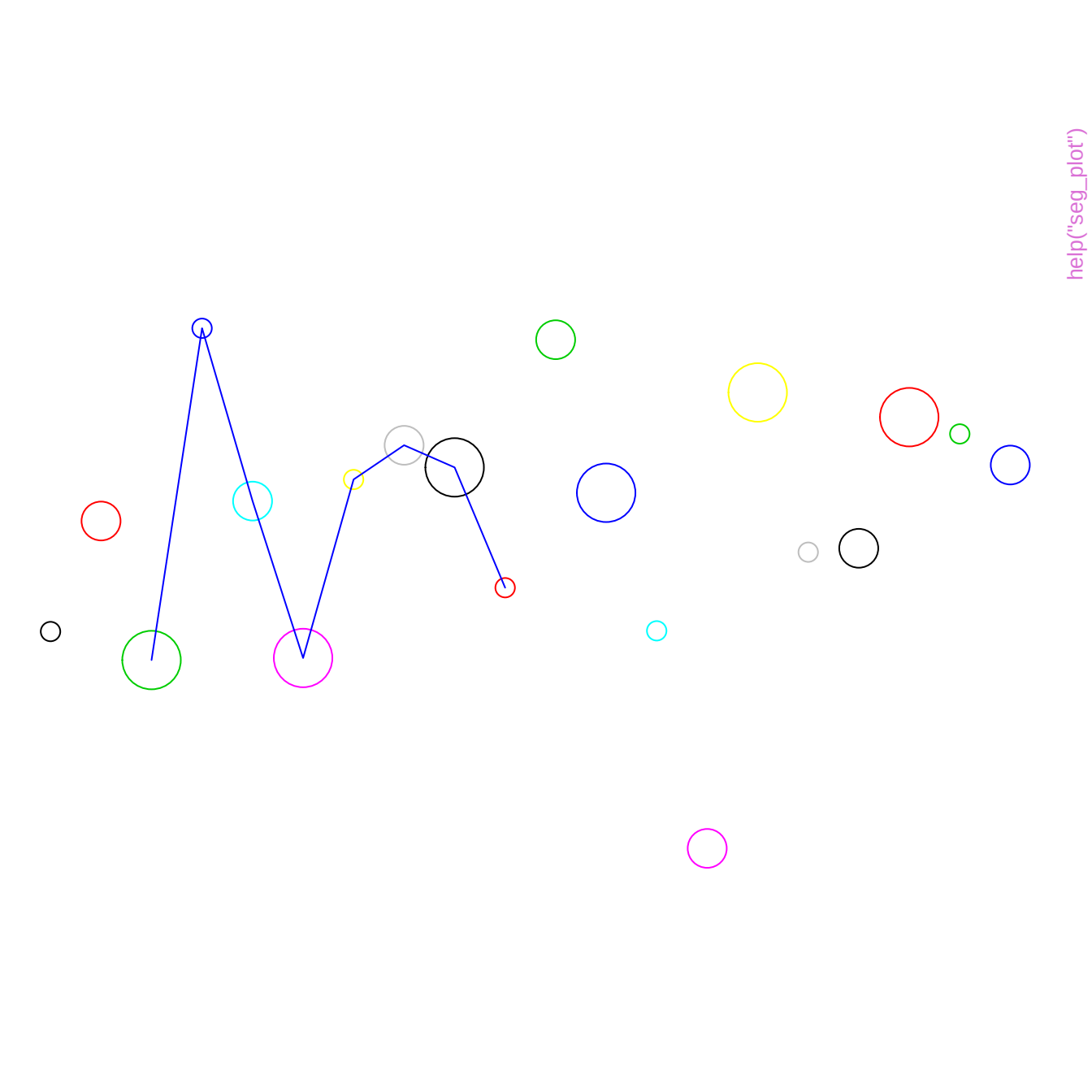

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("read_functions")

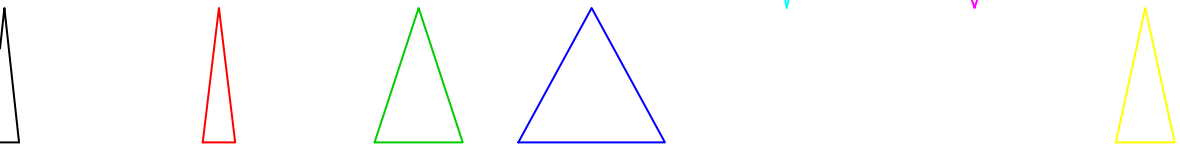

B bacilliformis
B grahamii
B henselae
B quintana
500 kb
help("read_functions")


BH
BQ
5 kb
help("read_functions")

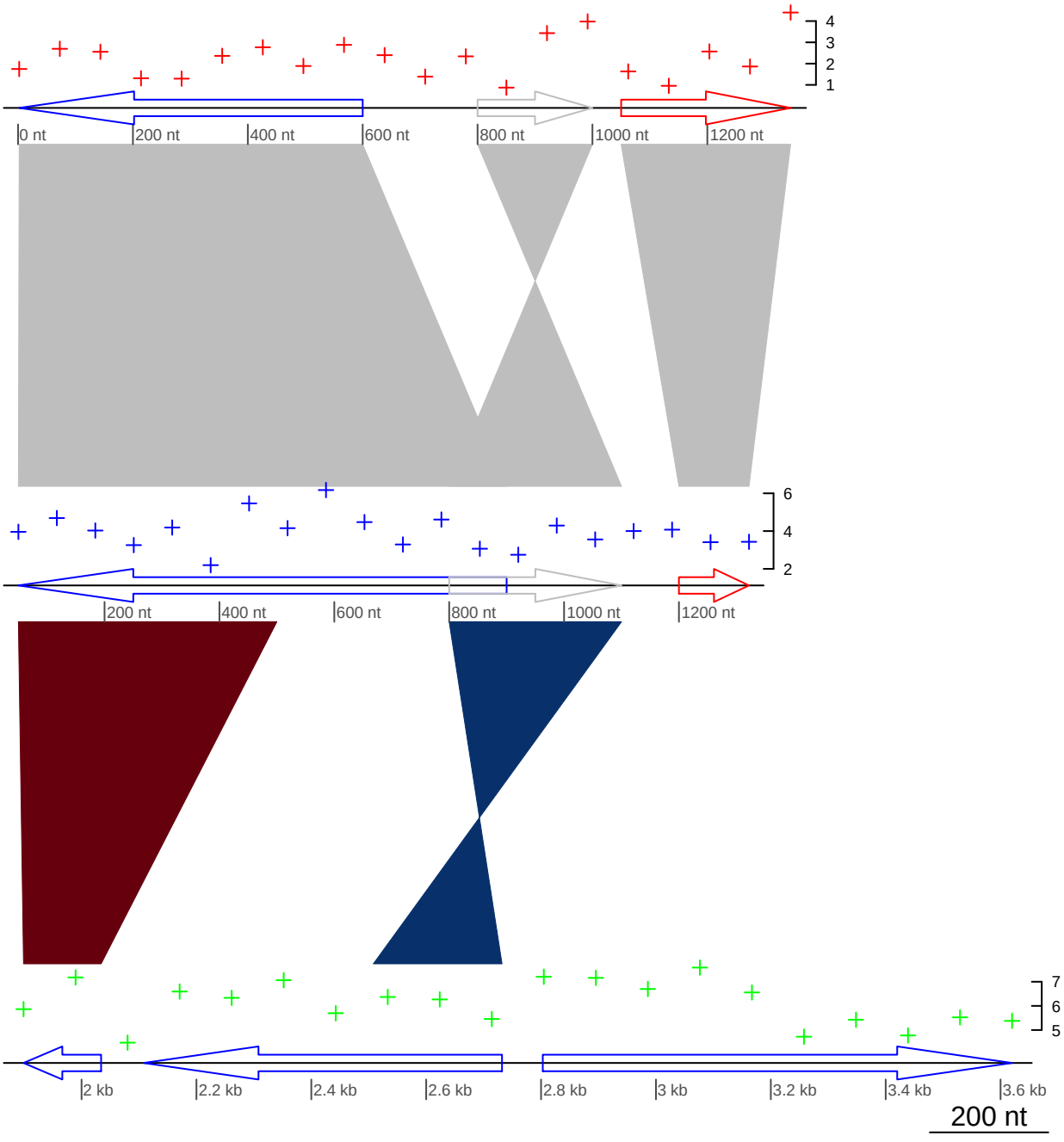

B_bacilliformis
B_grahamii
B_henselae
B_quintana
help("reverse")
500 kb


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


help("seg_plot")

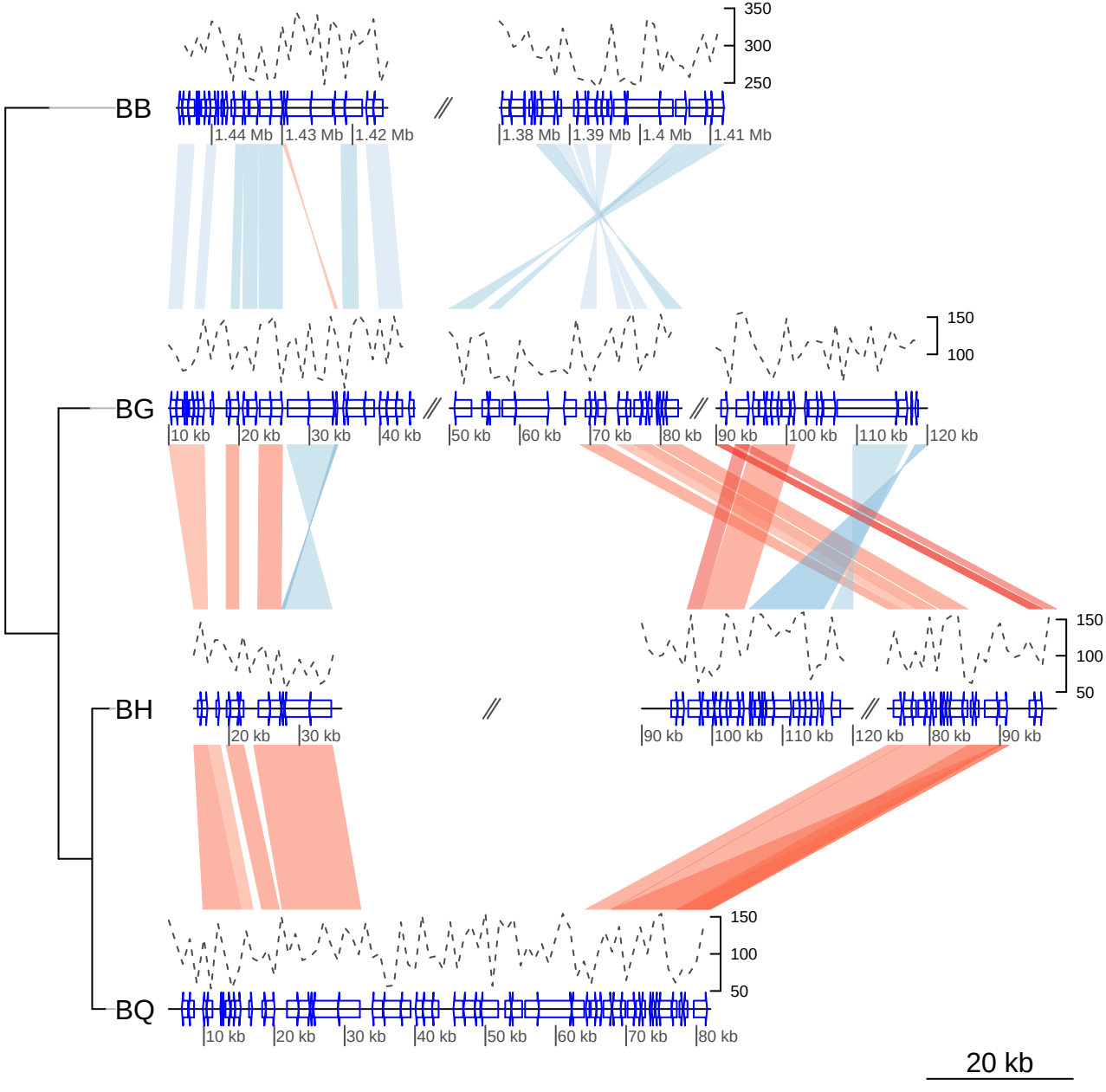


help("seg_plot")

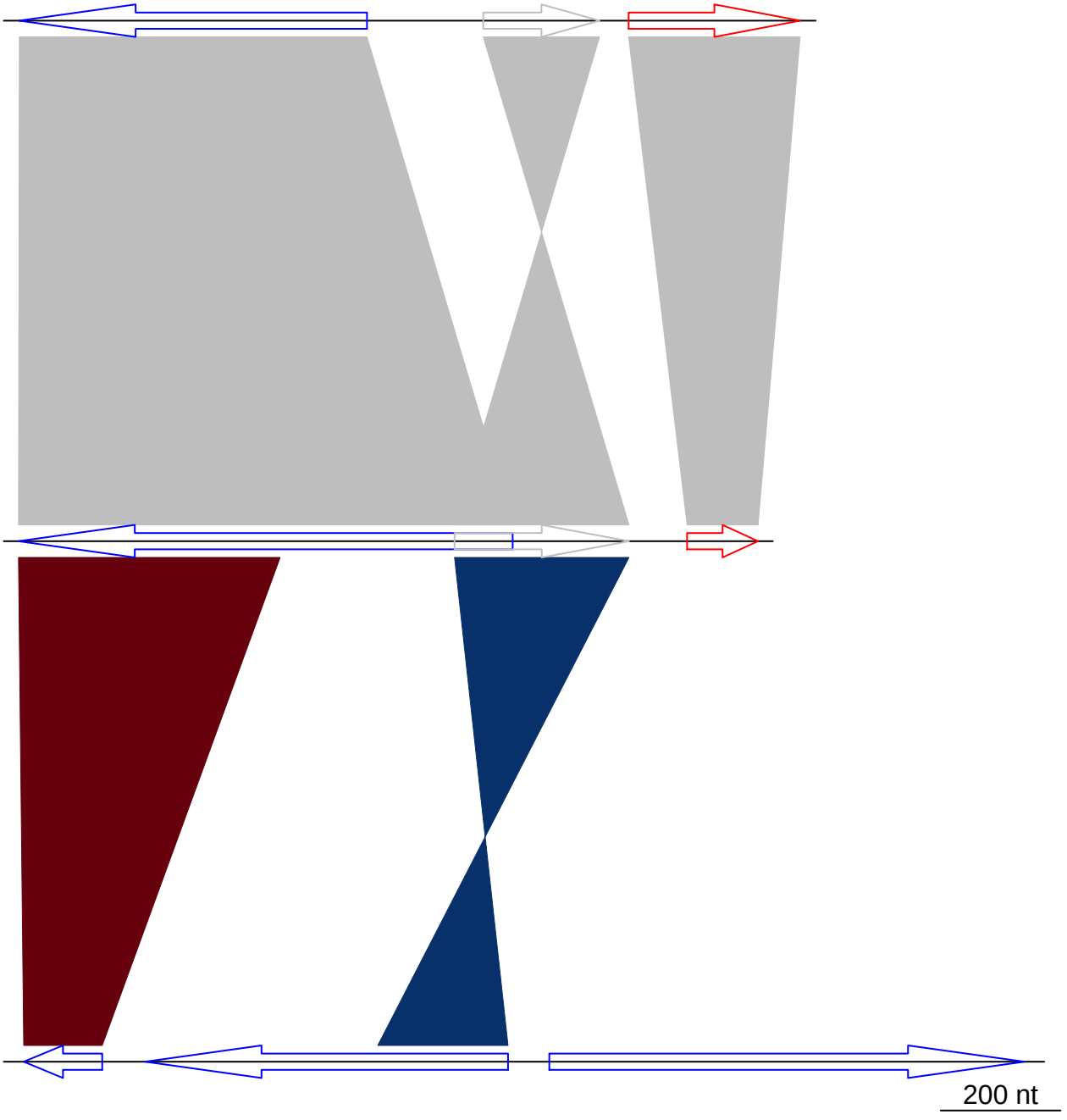


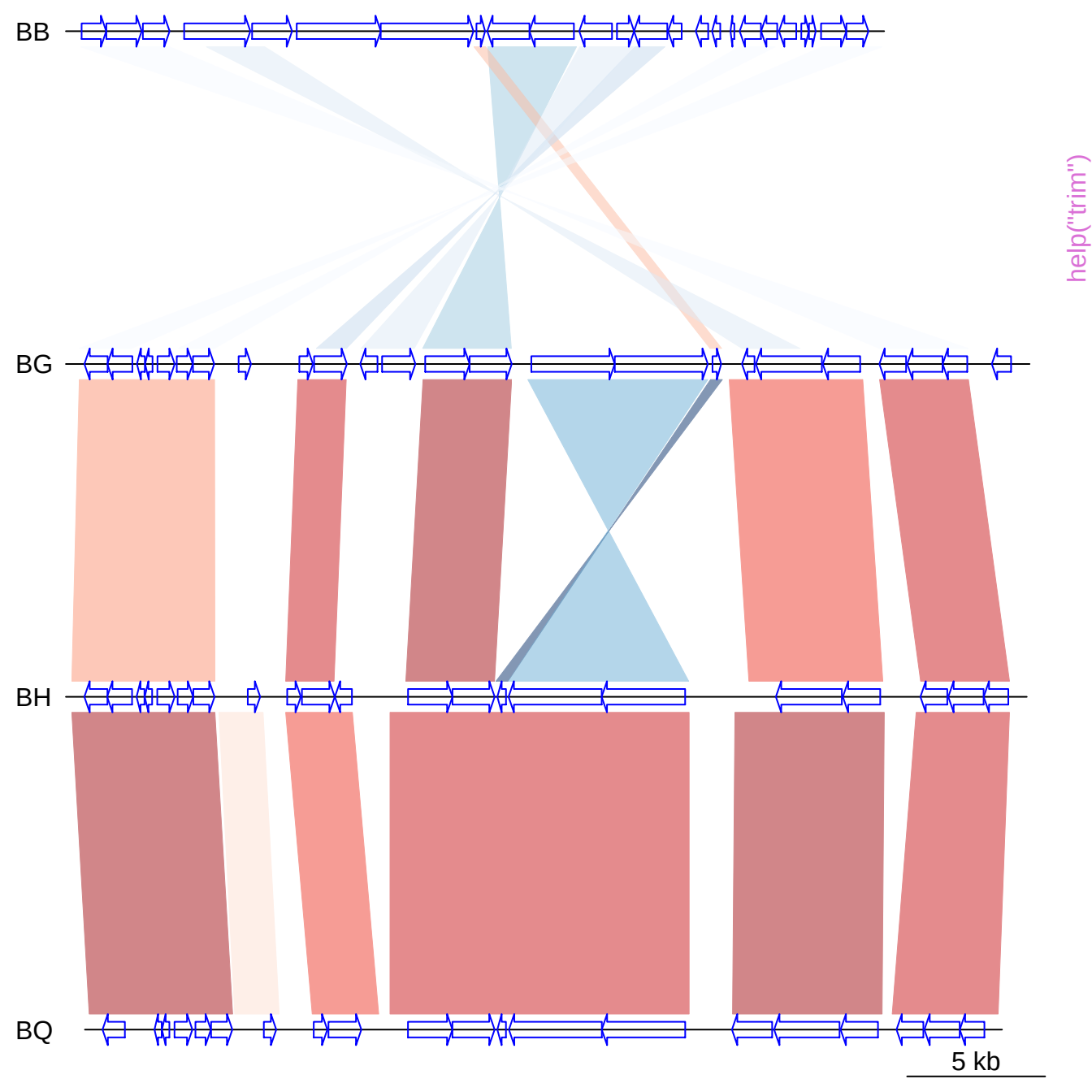
help("seg_plot")

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")