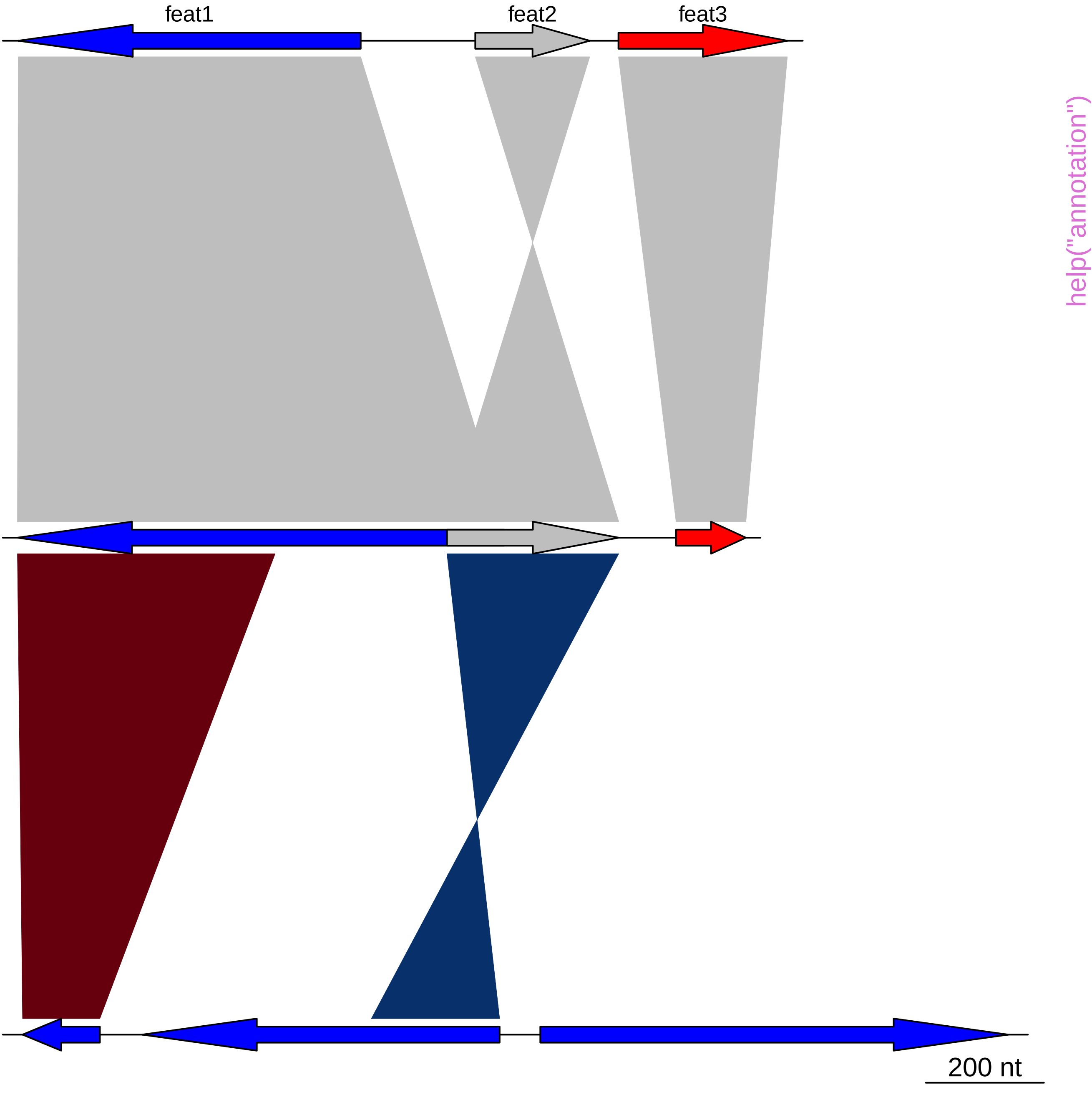
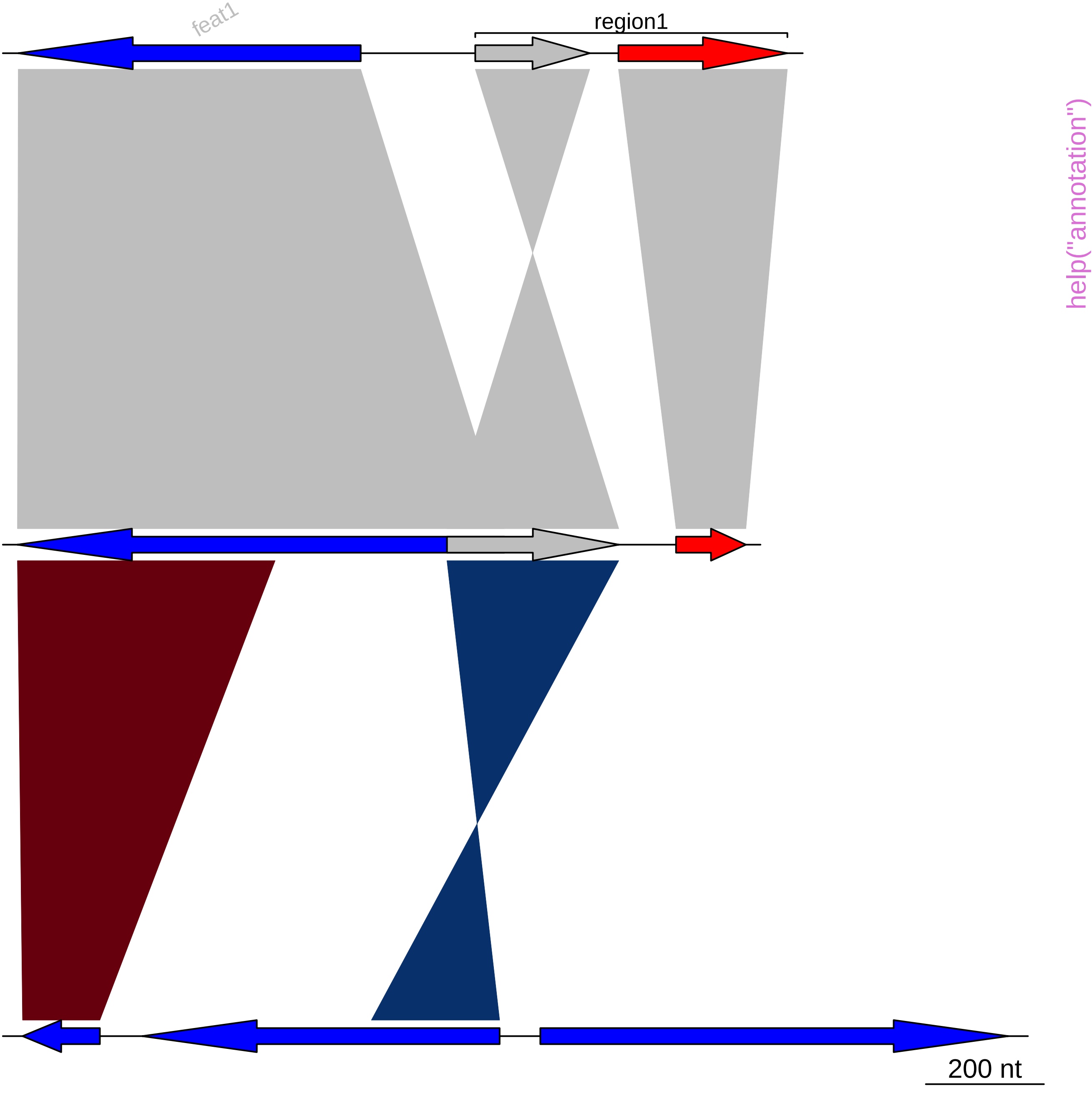
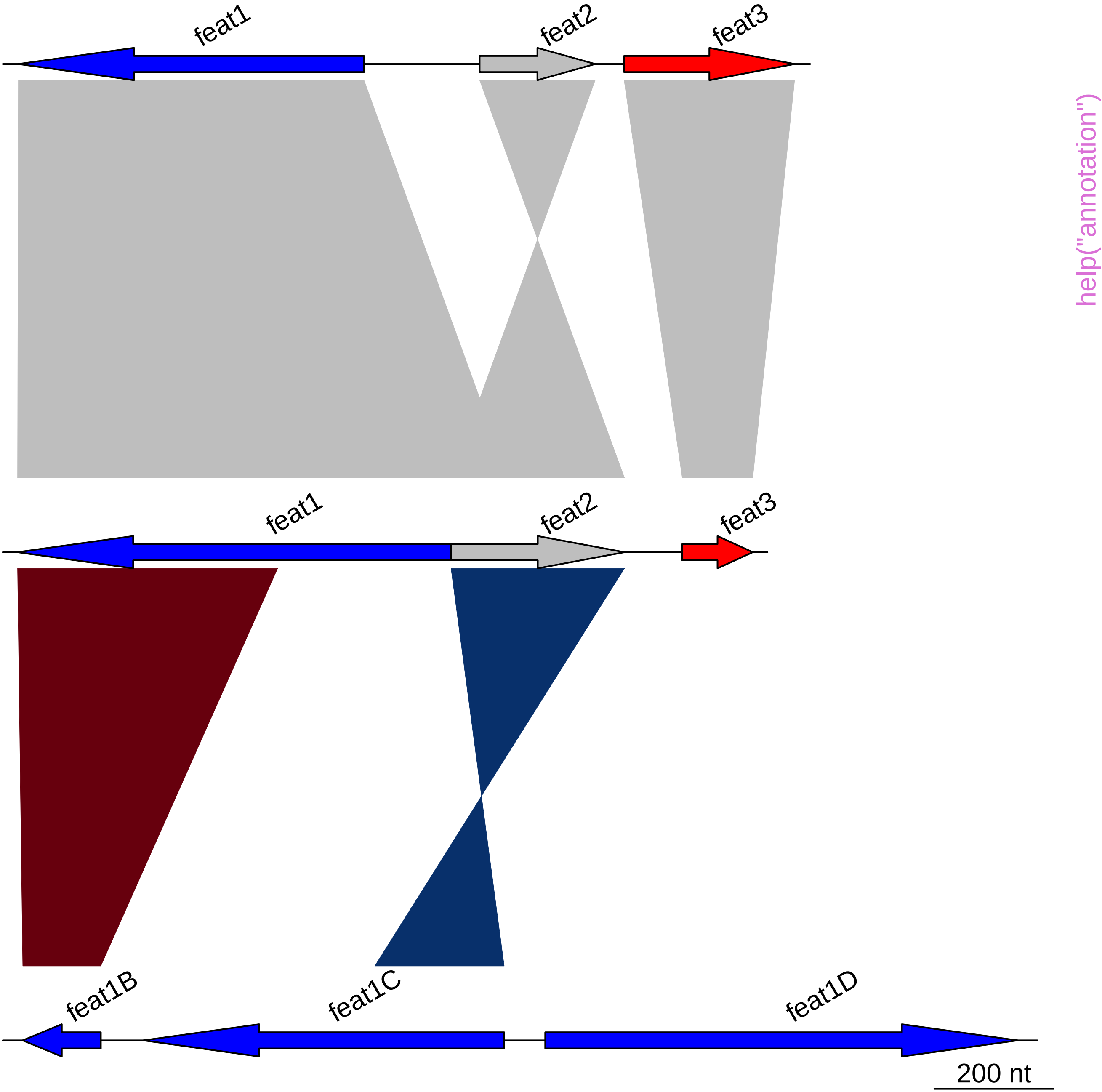
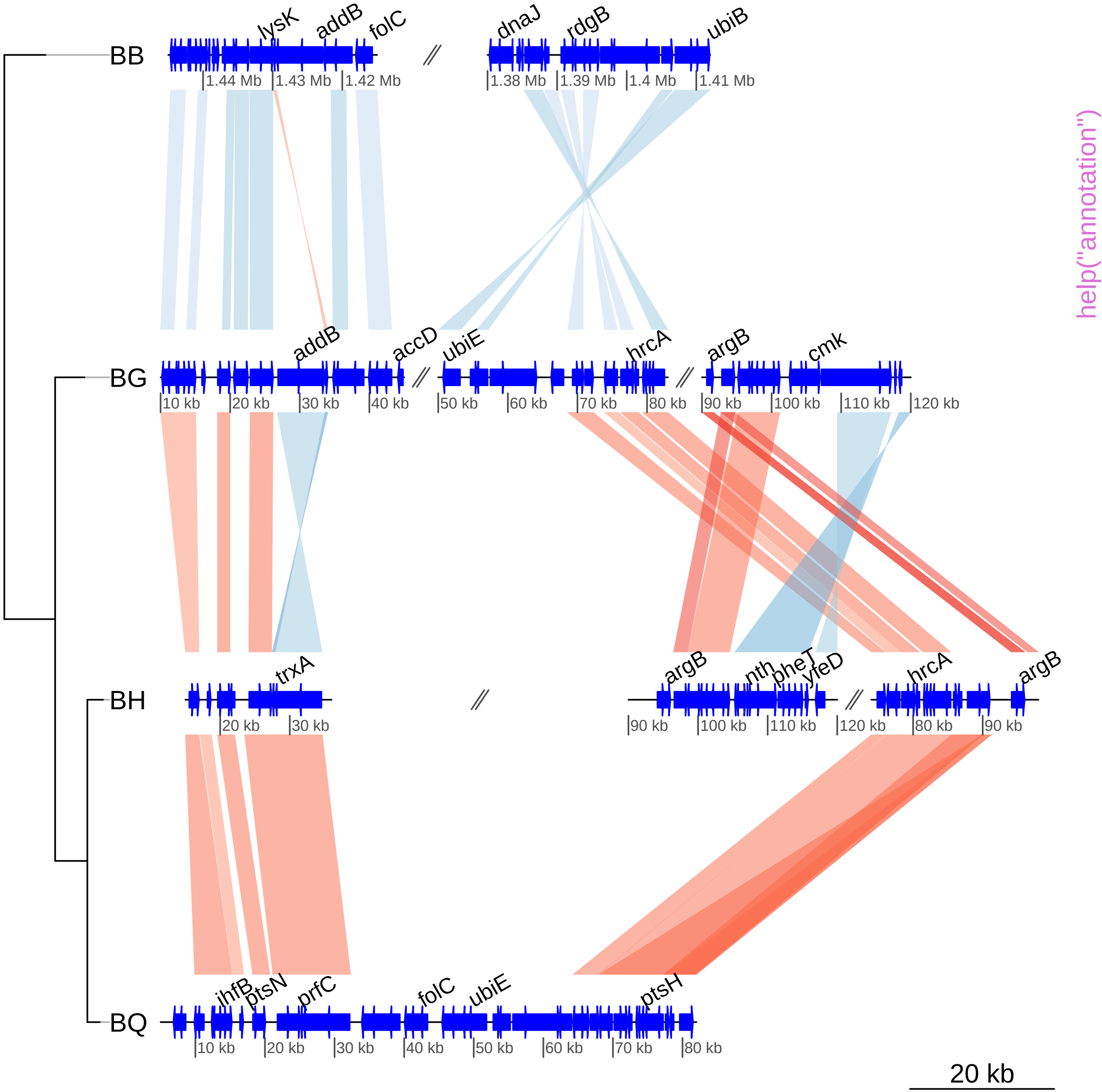
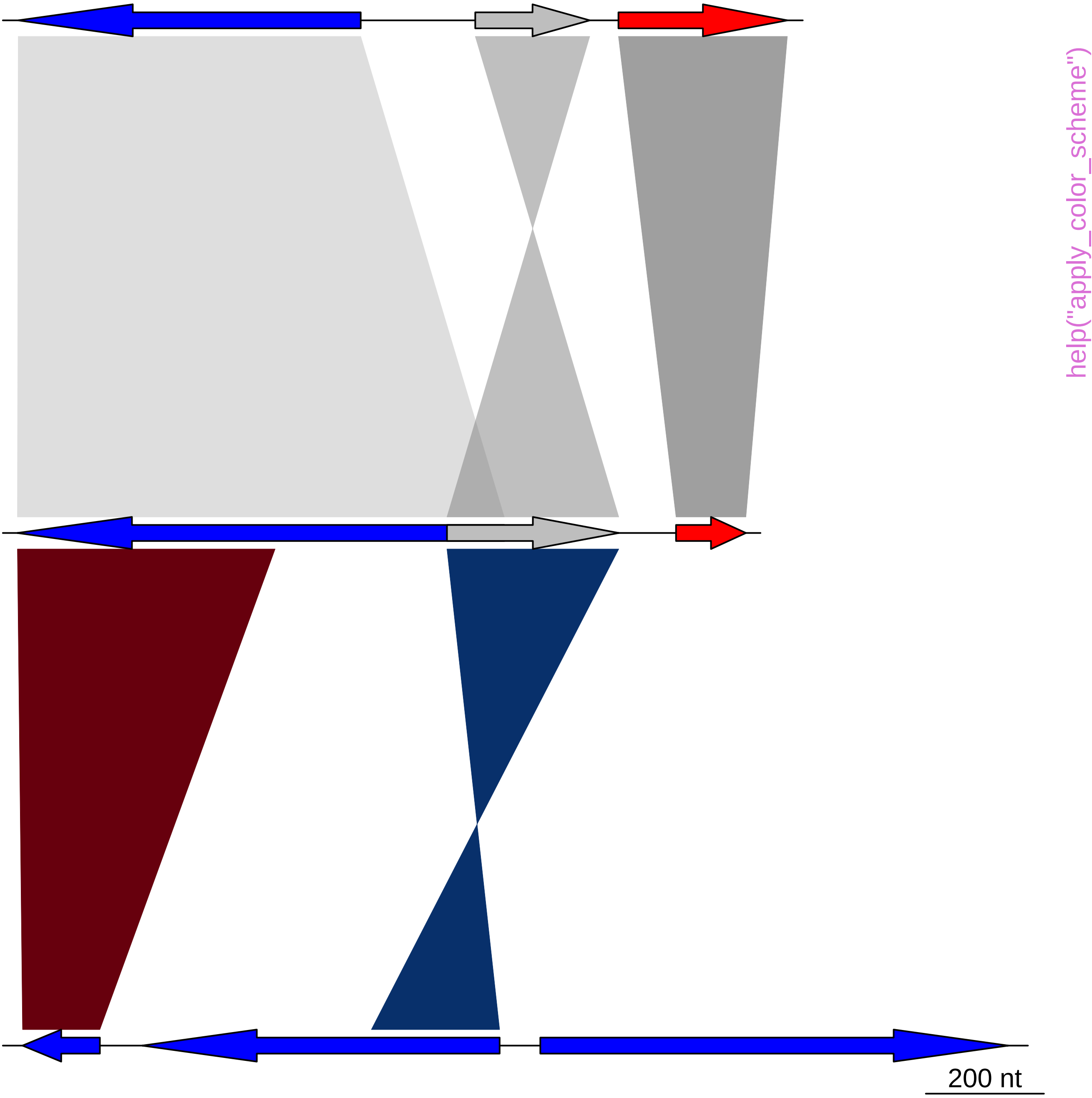
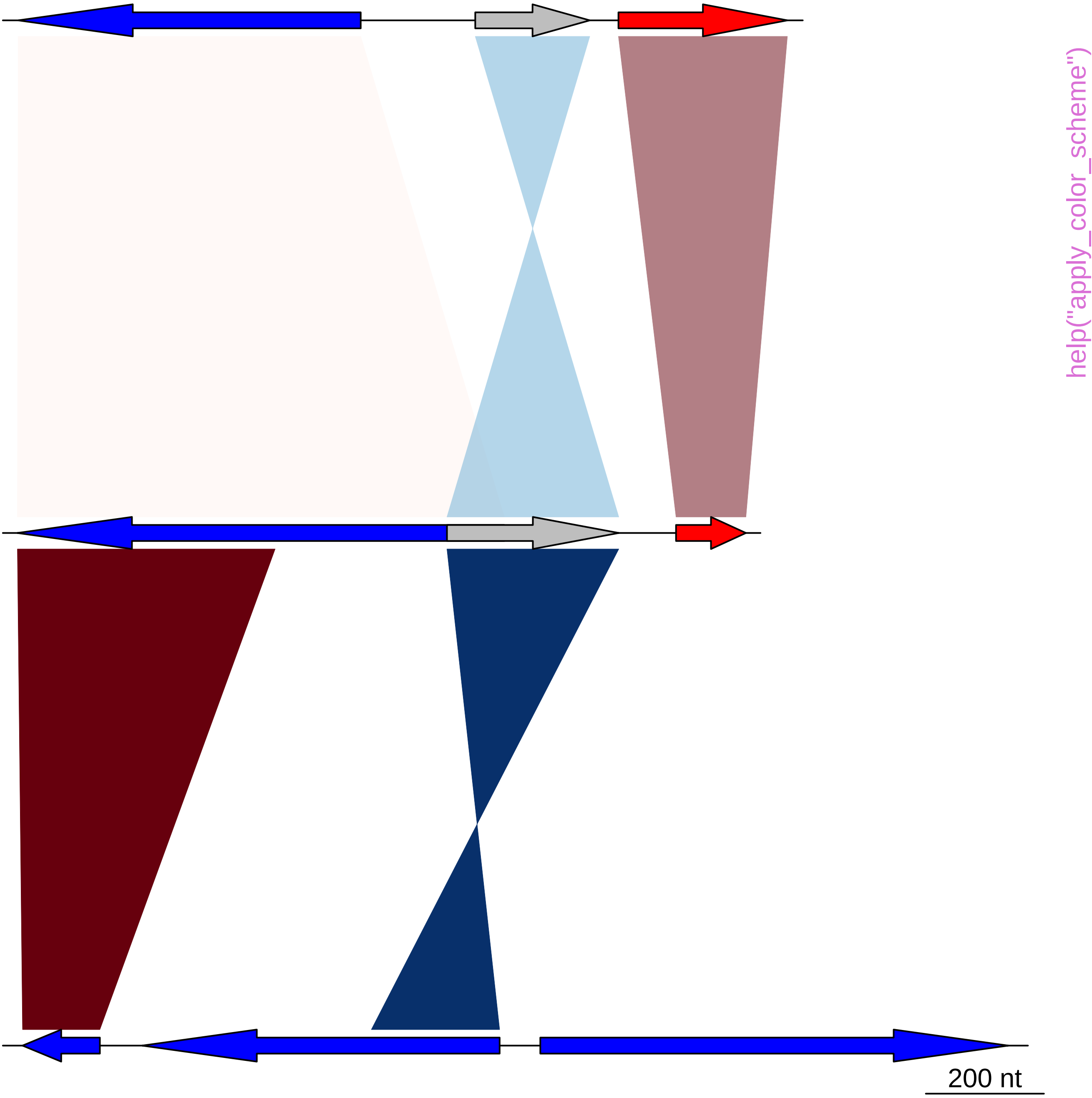

feat1
feat2
feat3
200 nt
help("annotation")

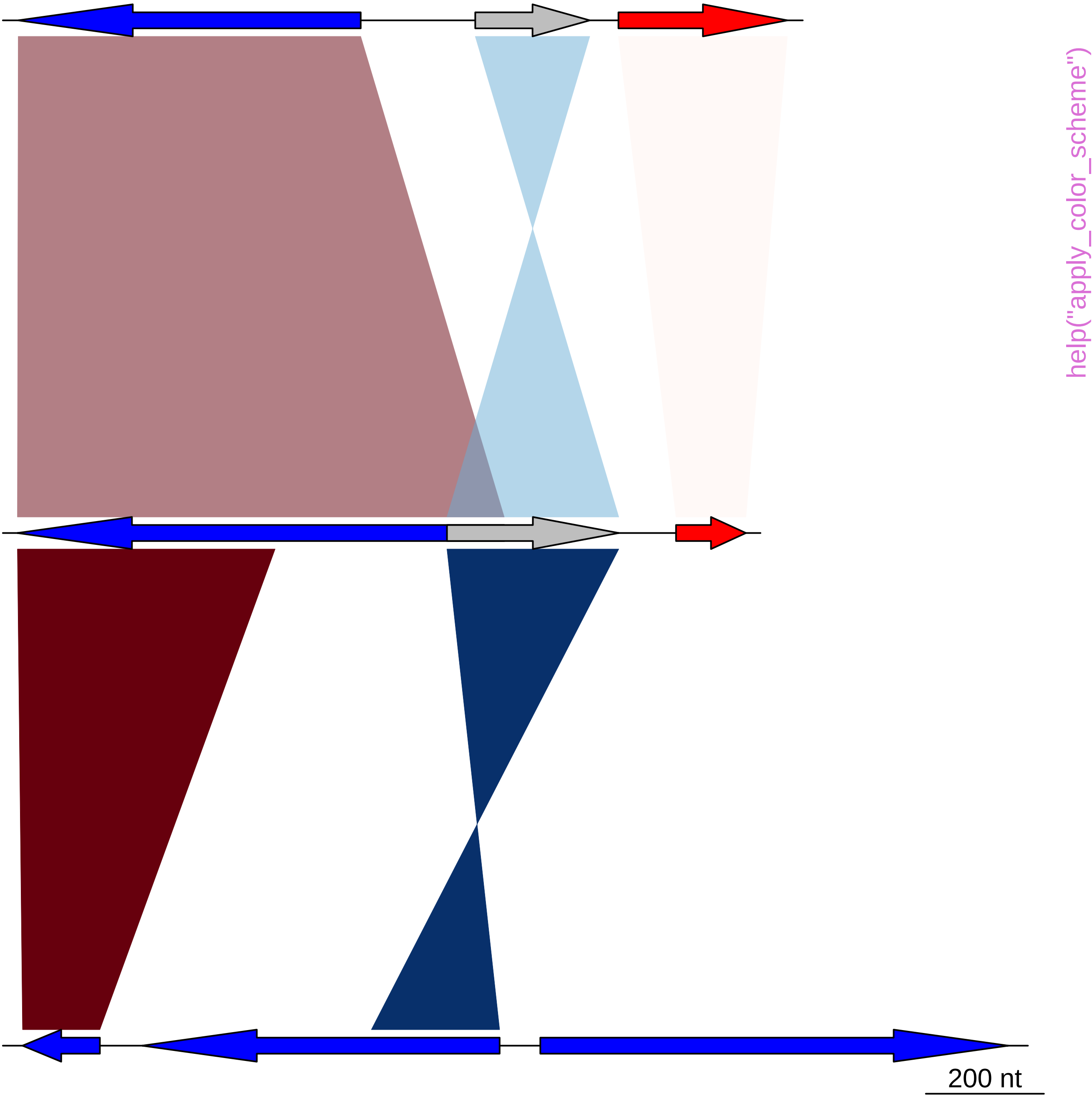

feat1
region1
help("annotation")
200 nt

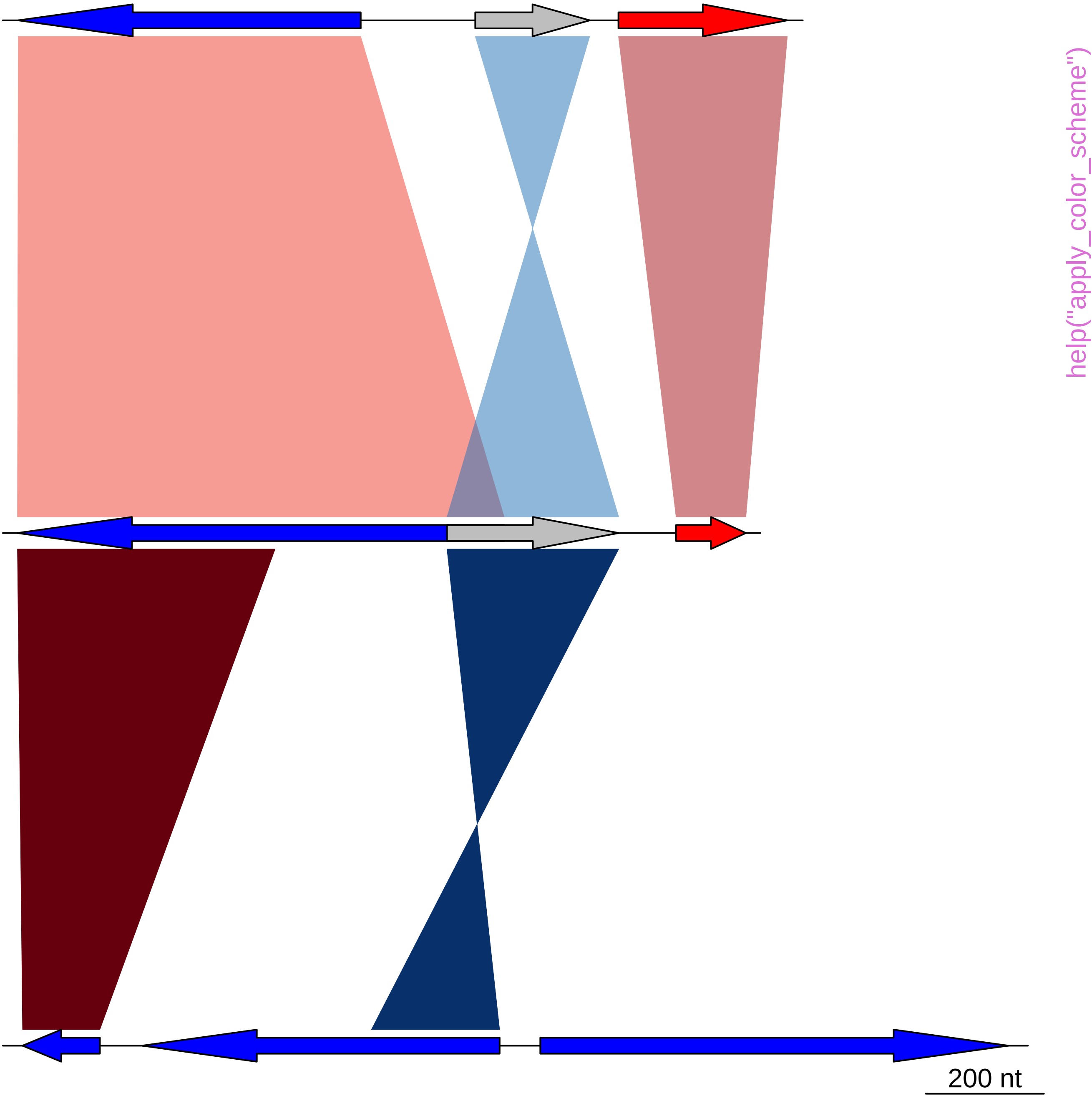

feat1
feat2
feat3
feat1
feat2
feat3
feat1B
feat1C
feat1D
200 nt
help("annotation")

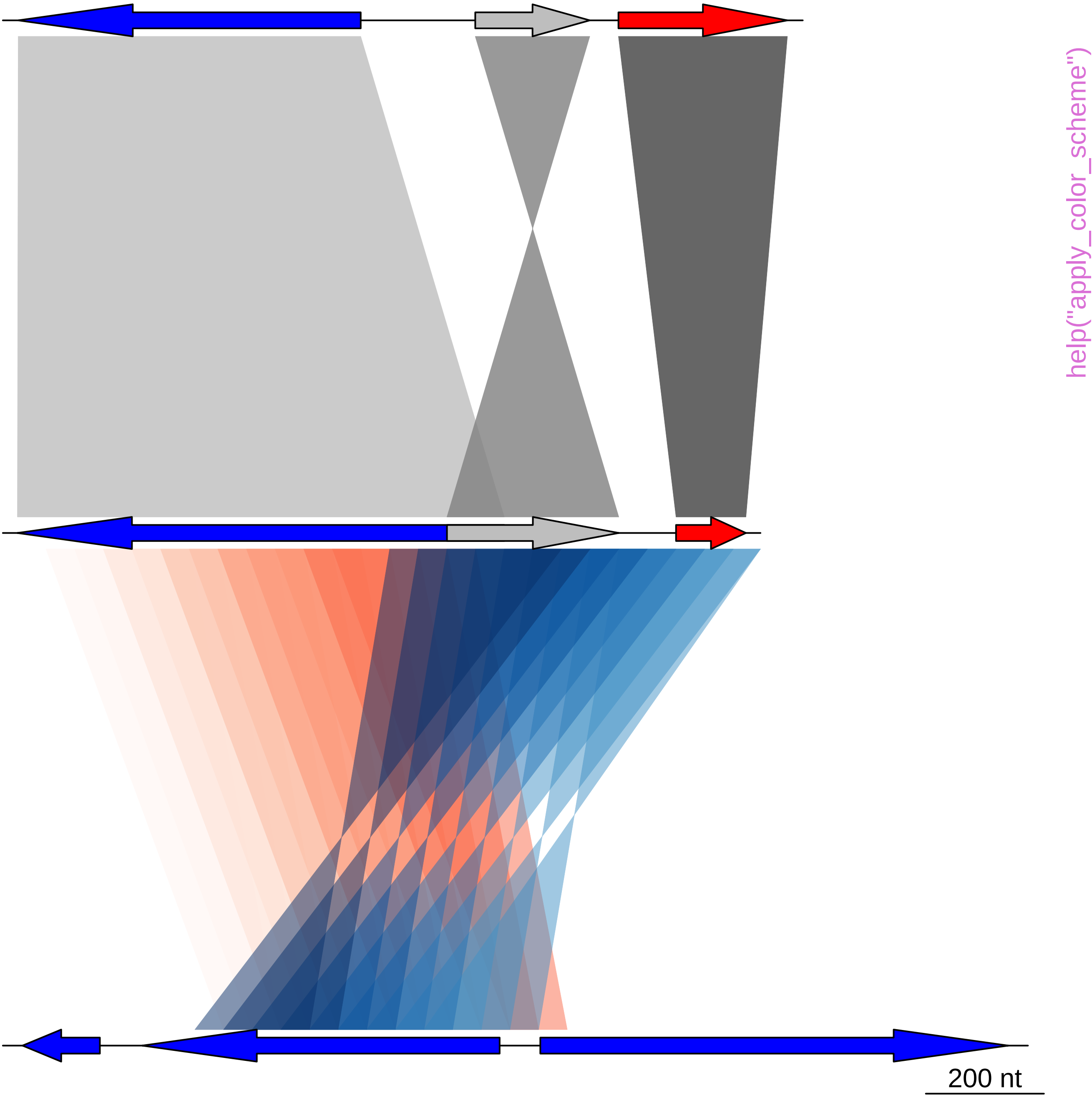

BB
lysK
addB
folC
dnaJ
rdgB
ubiB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
BG
addB
accD
ubiE
hrcA
argB
cmk
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
100 kb
110 kb
120 kb
BH
trxA
argB
nth
pheT
yfeD
hrcA
argB
20 kb
30 kb
90 kb
100 kb
110 kb
120 kb
80 kb
90 kb
BQ
ihfB
ptsN
prfC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

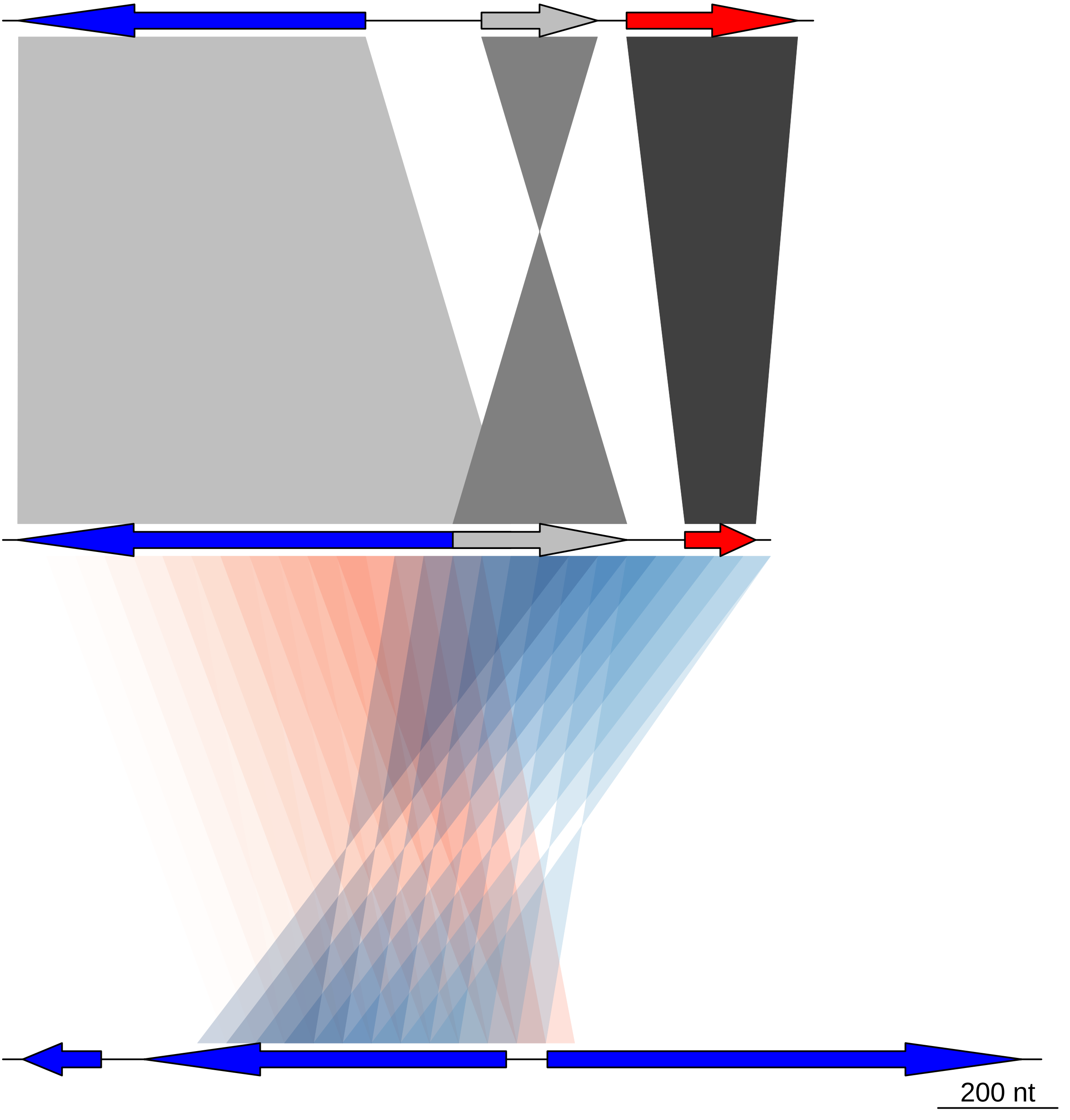

help("apply_color_scheme")
200 nt

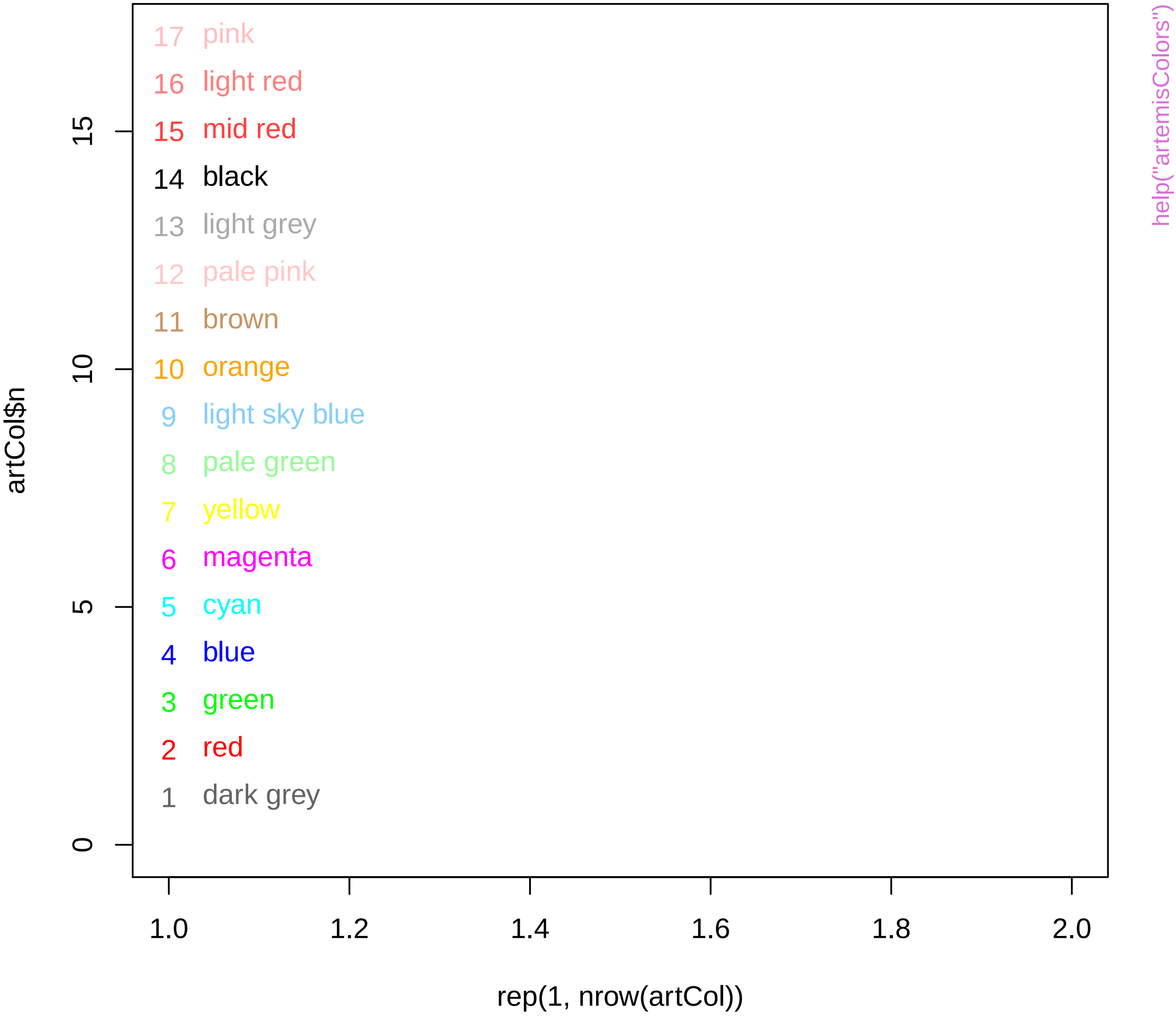

help("apply_color_scheme")
200 nt

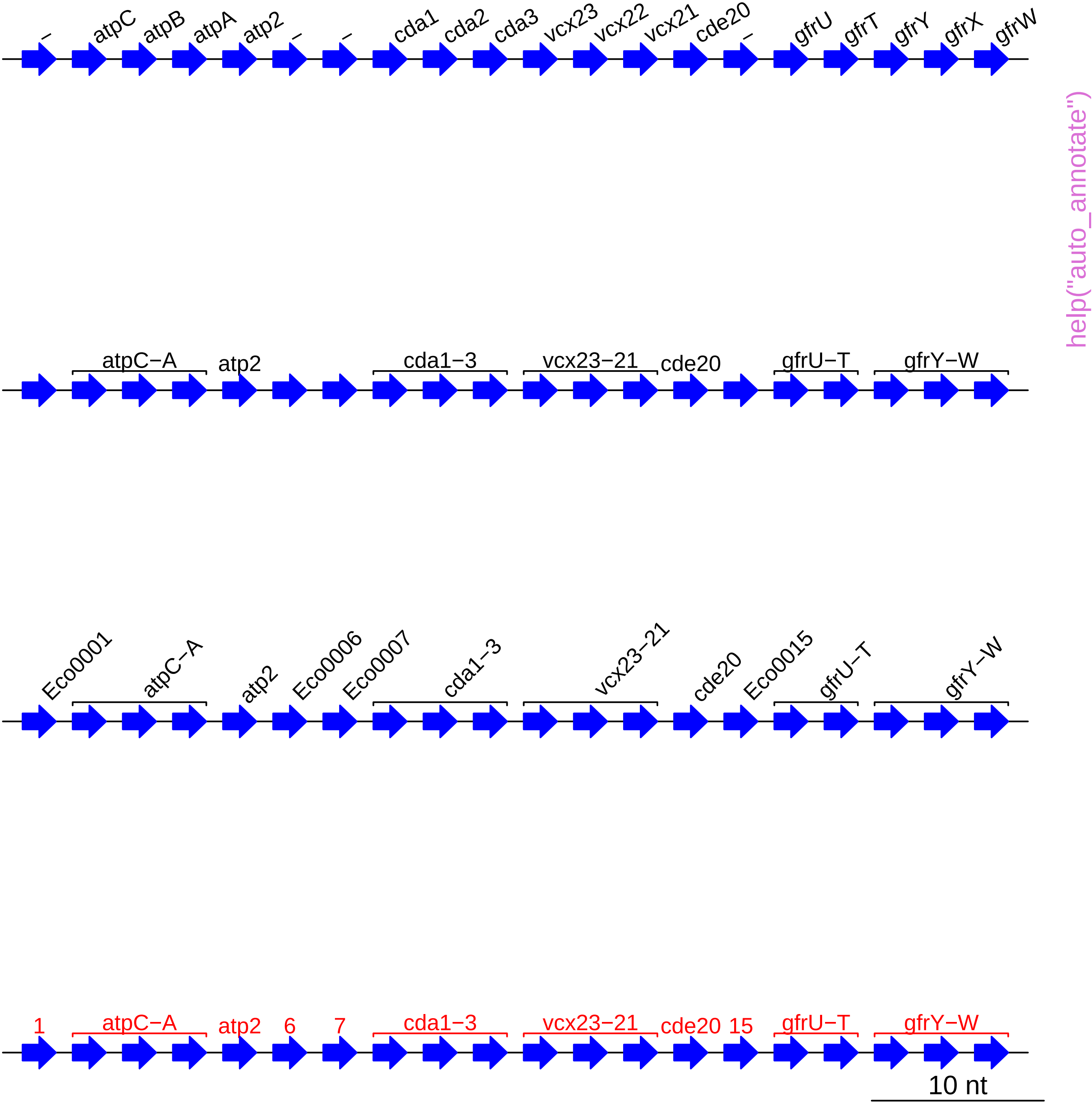

help("apply_color_scheme")
200 nt

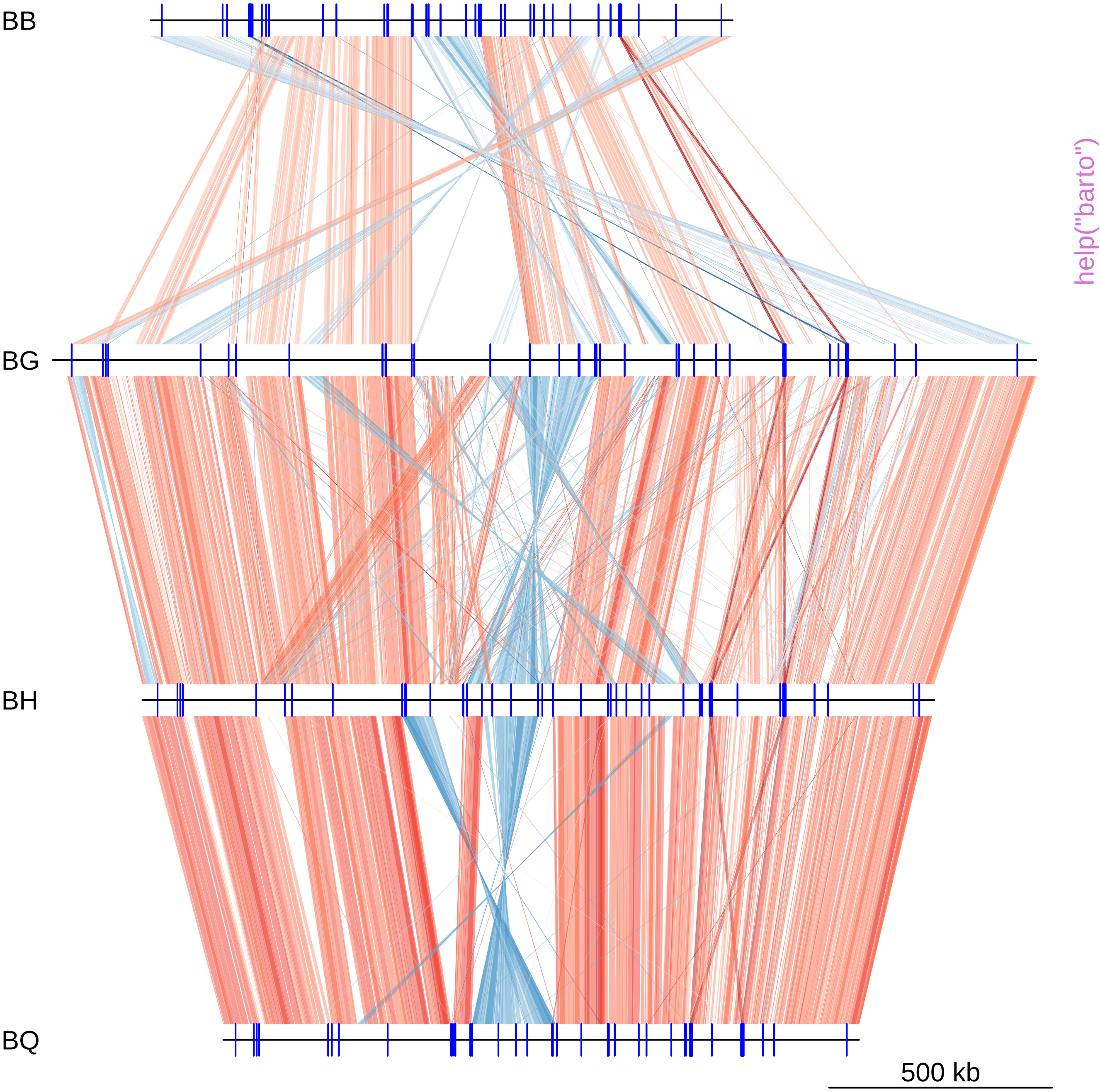

help("apply_color_scheme")
200 nt

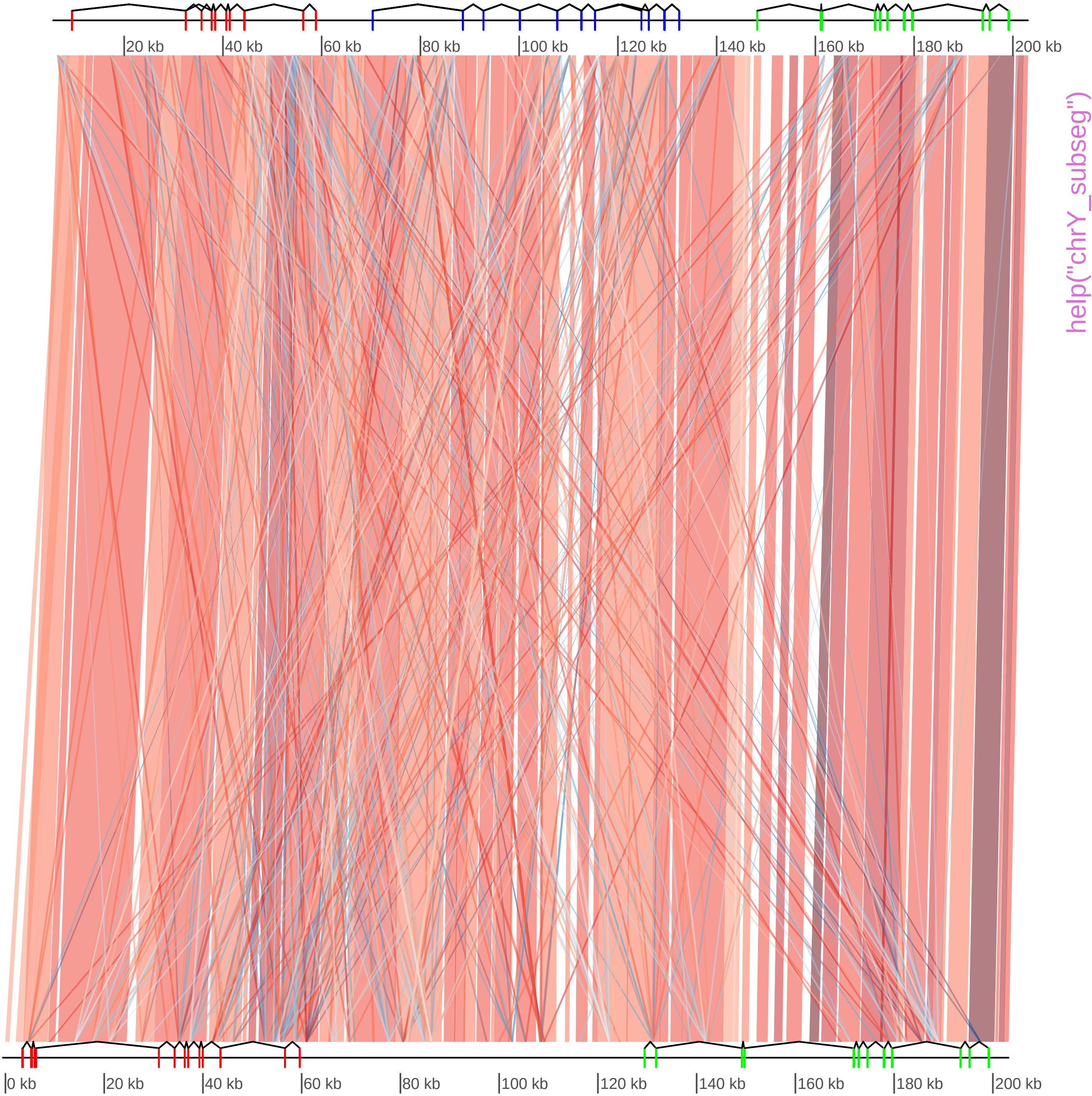

200 nt
help("apply_color_scheme")

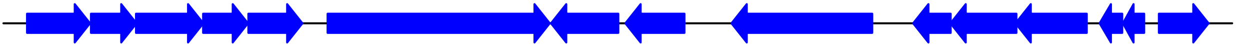

200 nt
help("apply_color_scheme")


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")

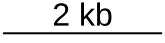

–
atpC
atpB
atpA
atp2
–
–
cda1
cda2
cda3
vcx23
vcx22
vcx21
cde20
–
gfrU
gfrT
gfrY
gfrX
gfrW
help("auto_annotate")
atpC−A
atp2
cda1−3
vcx23−21
cde20
gfrU−T
gfrY−W
Eco0001
atpC−A
atp2
Eco0006
Eco0007
cda1−3
vcx23−21
cde20
Eco0015
gfrU−T
gfrY−W
1
atpC−A
atp2
6
7
cda1−3
vcx23−21
cde20
15
gfrU−T
gfrY−W
10 nt

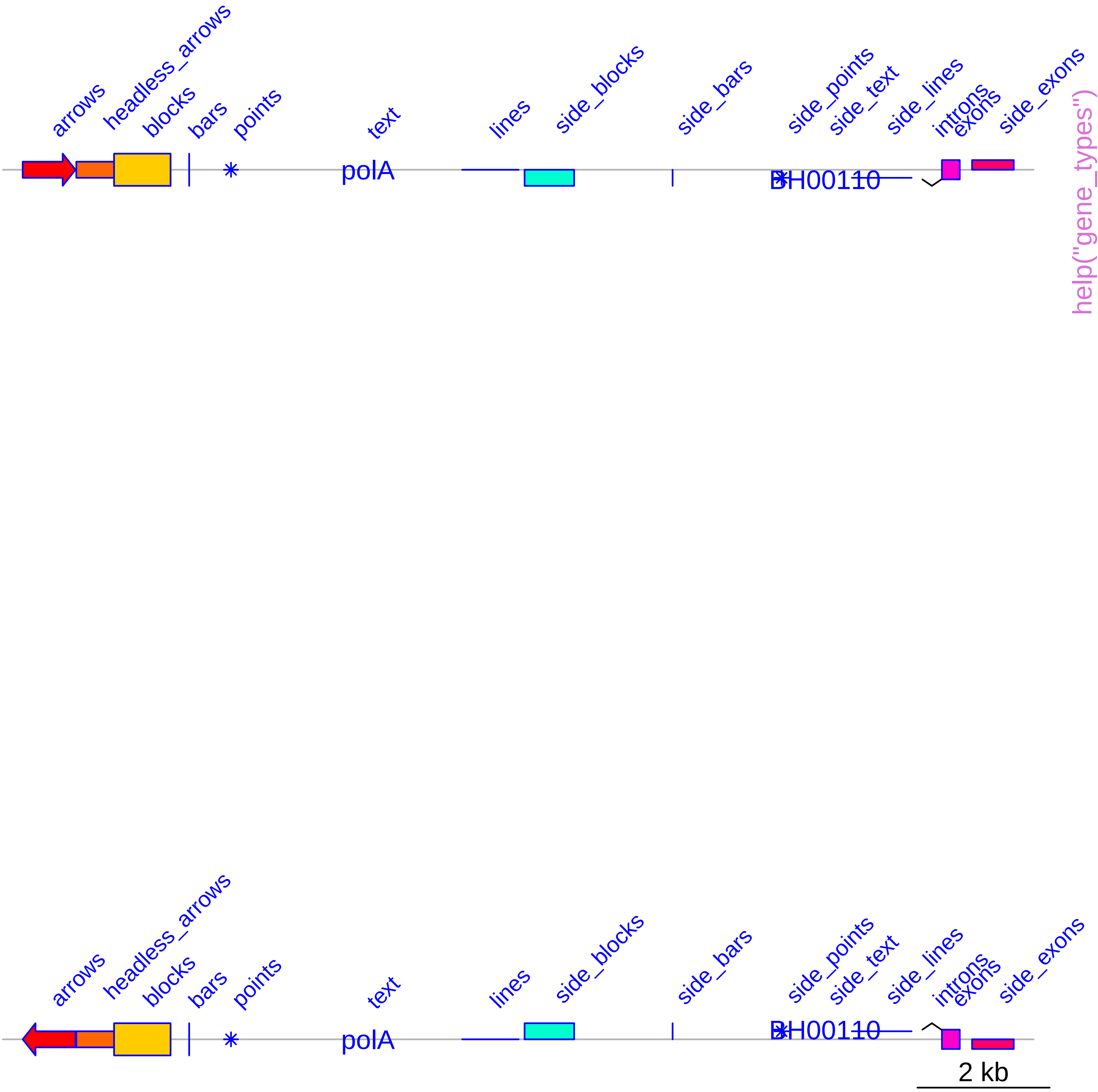

BB
BG
BH
BQ
500 kb
help("barto")

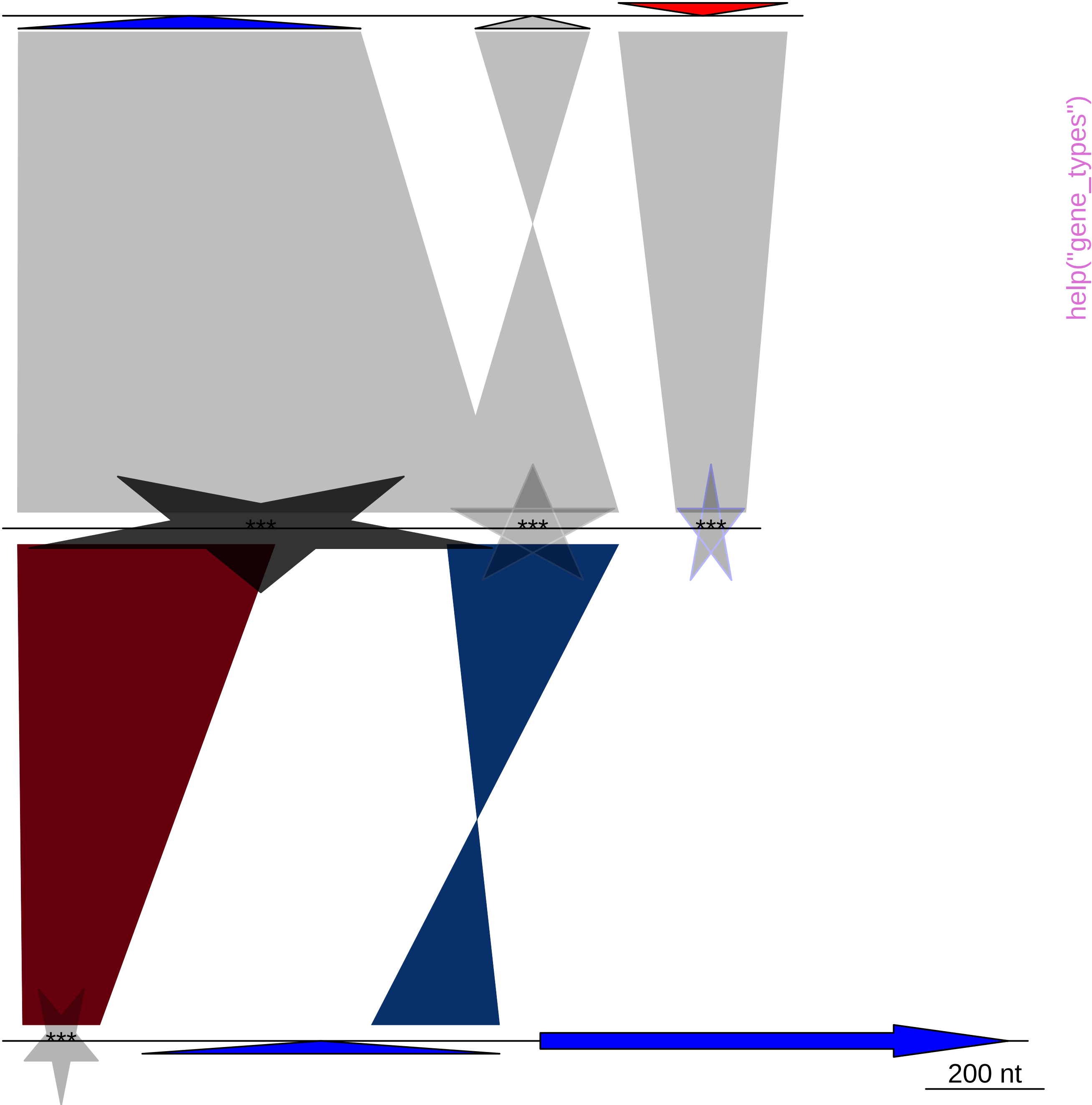

20 kb
40 kb
60 kb
80 kb
100 kb
120 kb
140 kb
160 kb
180 kb
200 kb
help("chrY_subseg")
0 kb
20 kb
40 kb
60 kb
80 kb
100 kb
120 kb
140 kb
160 kb
180 kb
200 kb

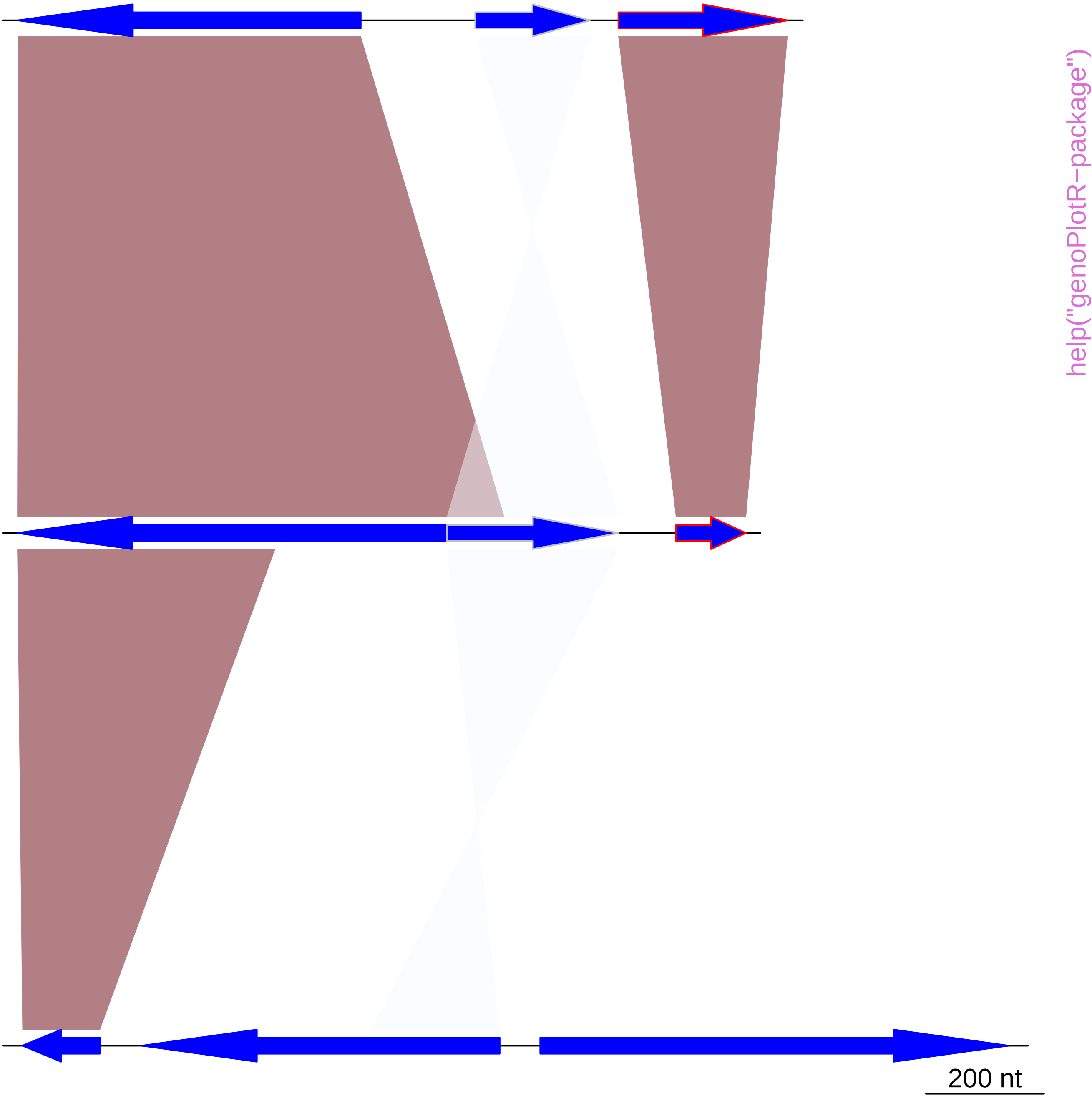


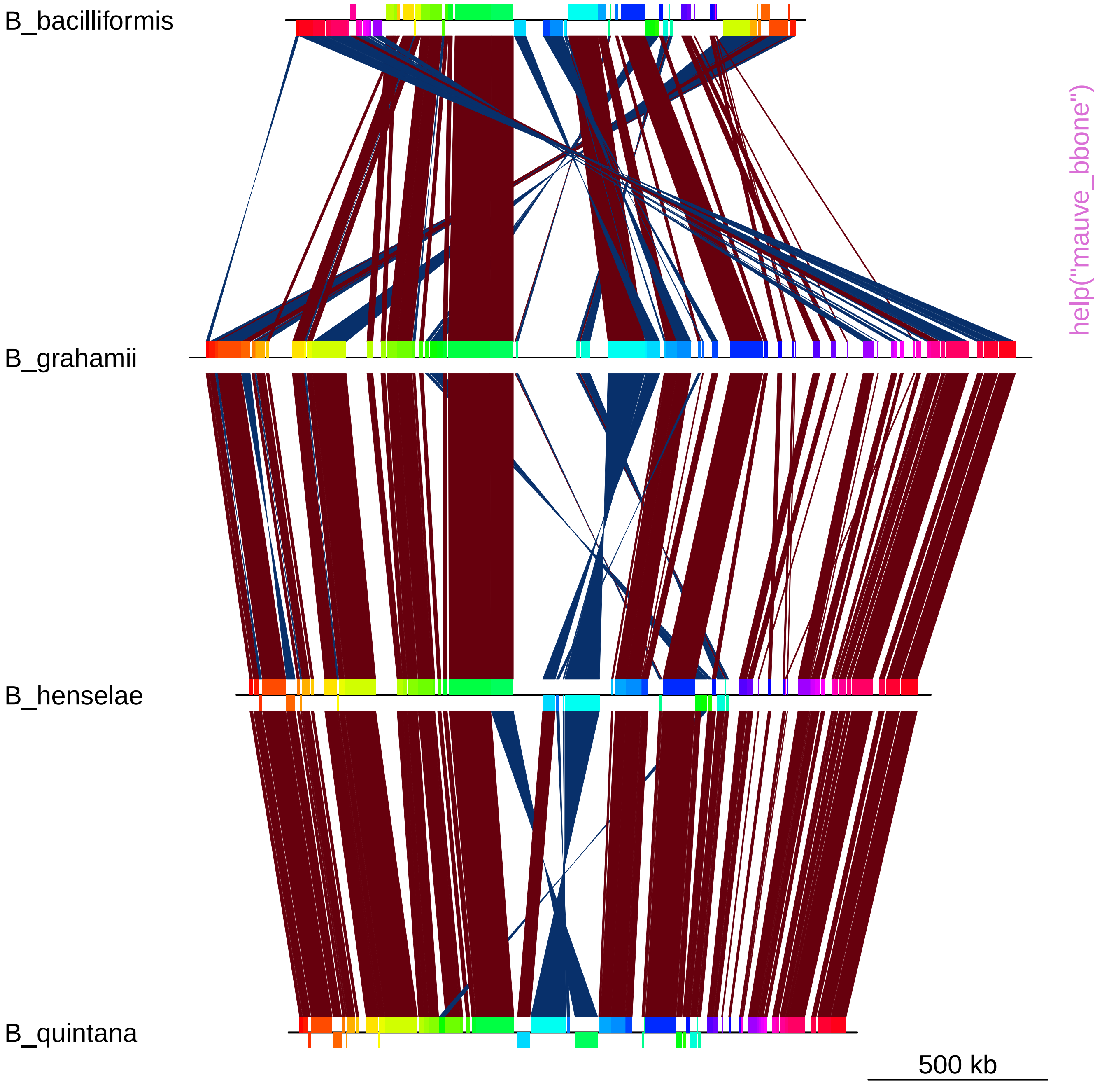
help("gene_types")

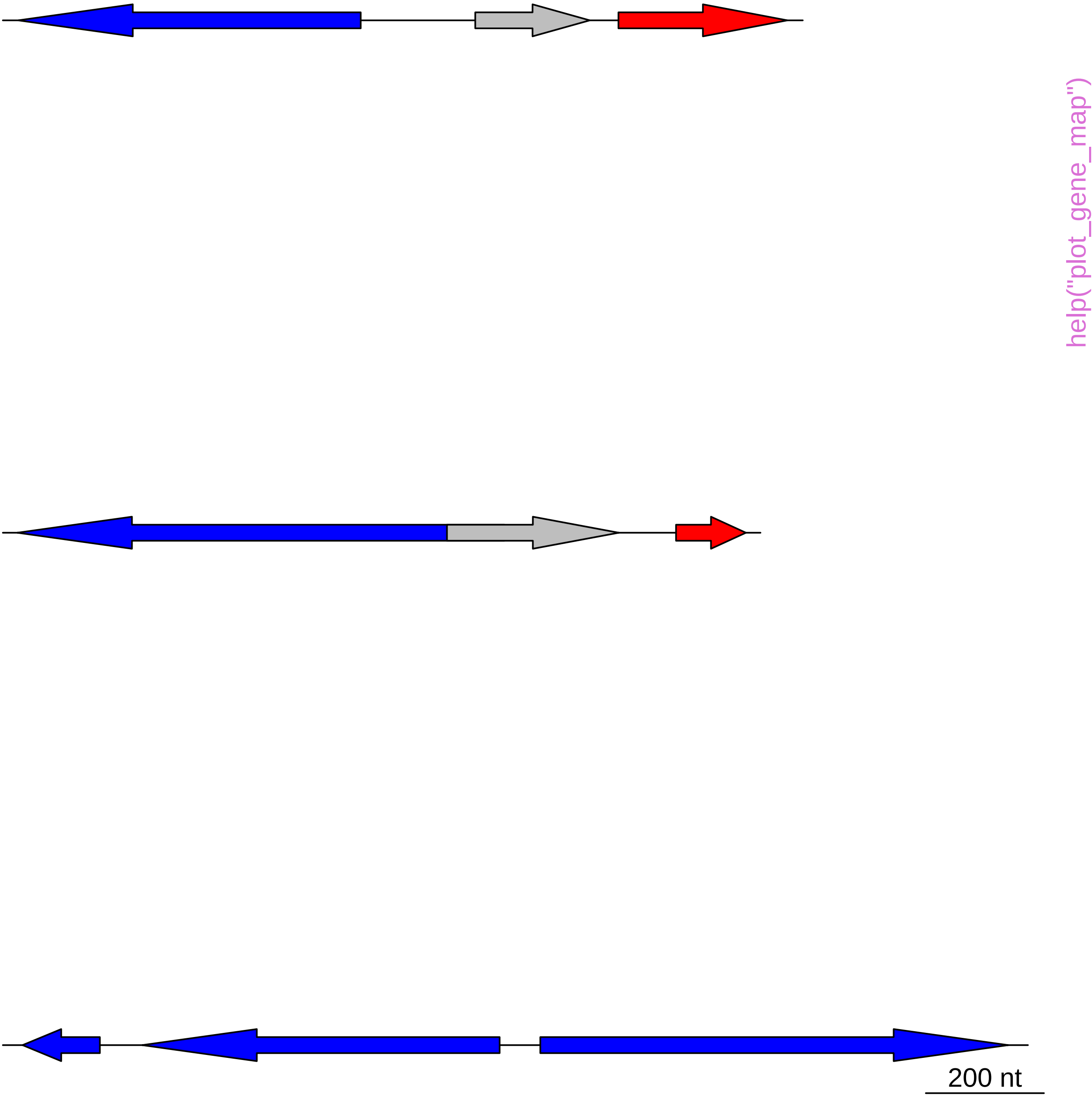

2 kb

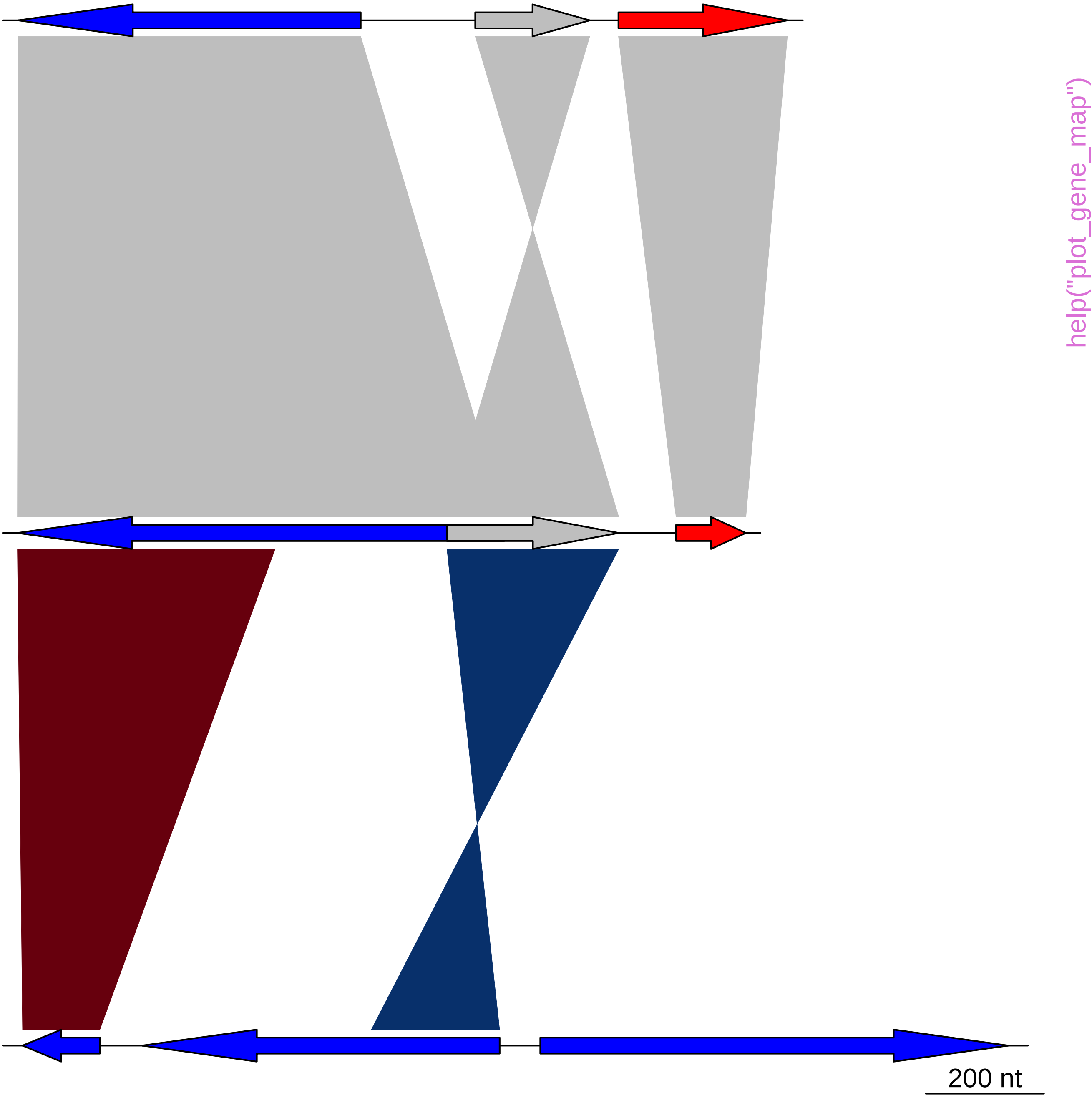

arrows
headless_arrows
blocks
bars
points
text
lines
side_blocks
side_bars
side_points
side_text
side_lines
introns
exons
side_exons
polA
BH00110
help("gene_types")
arrows
headless_arrows
blocks
bars
points
text
lines
side_blocks
side_bars
side_points
side_text
side_lines
introns
exons
side_exons
polA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

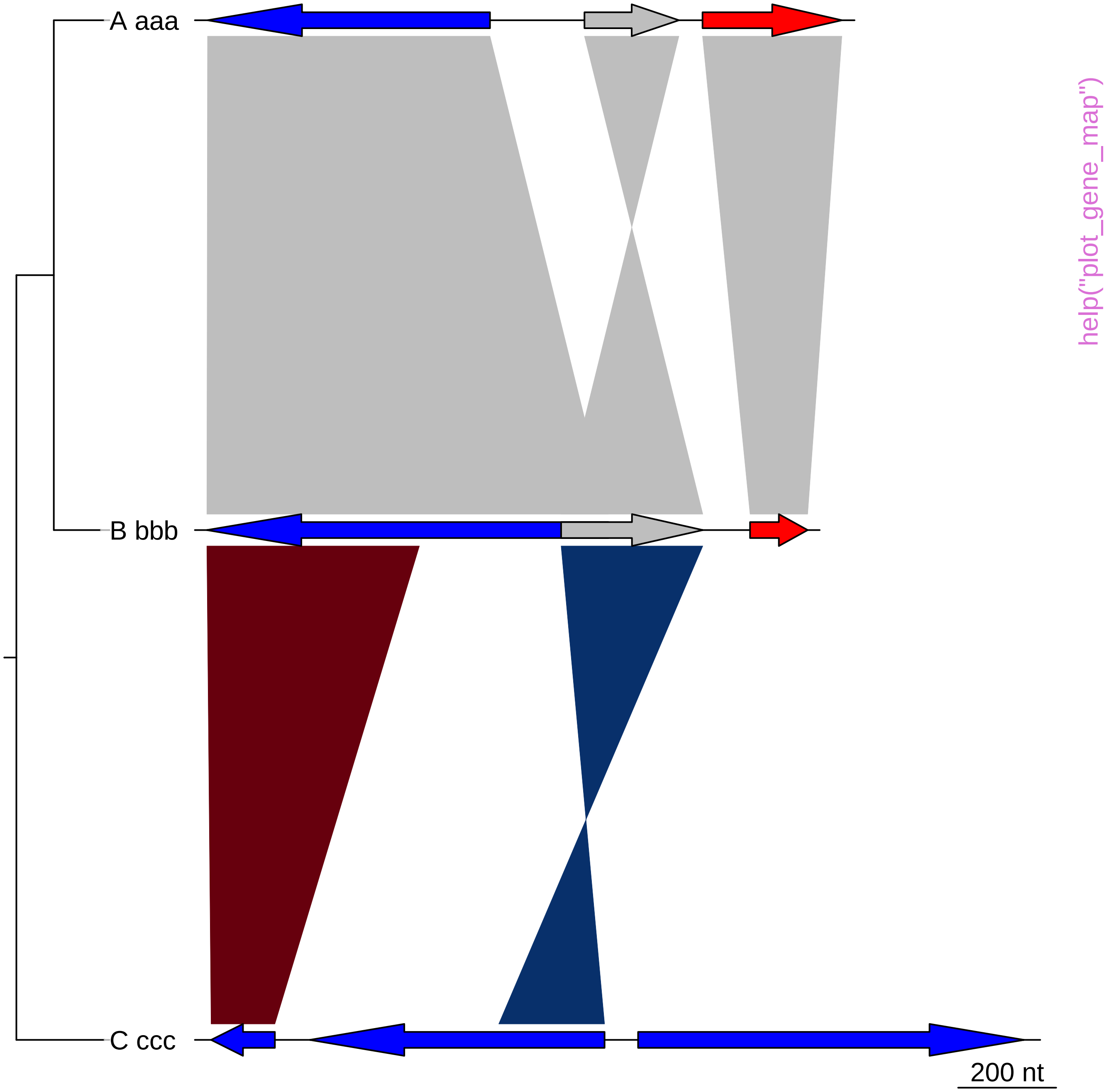

***
***
***
***
200 nt
help("gene_types")

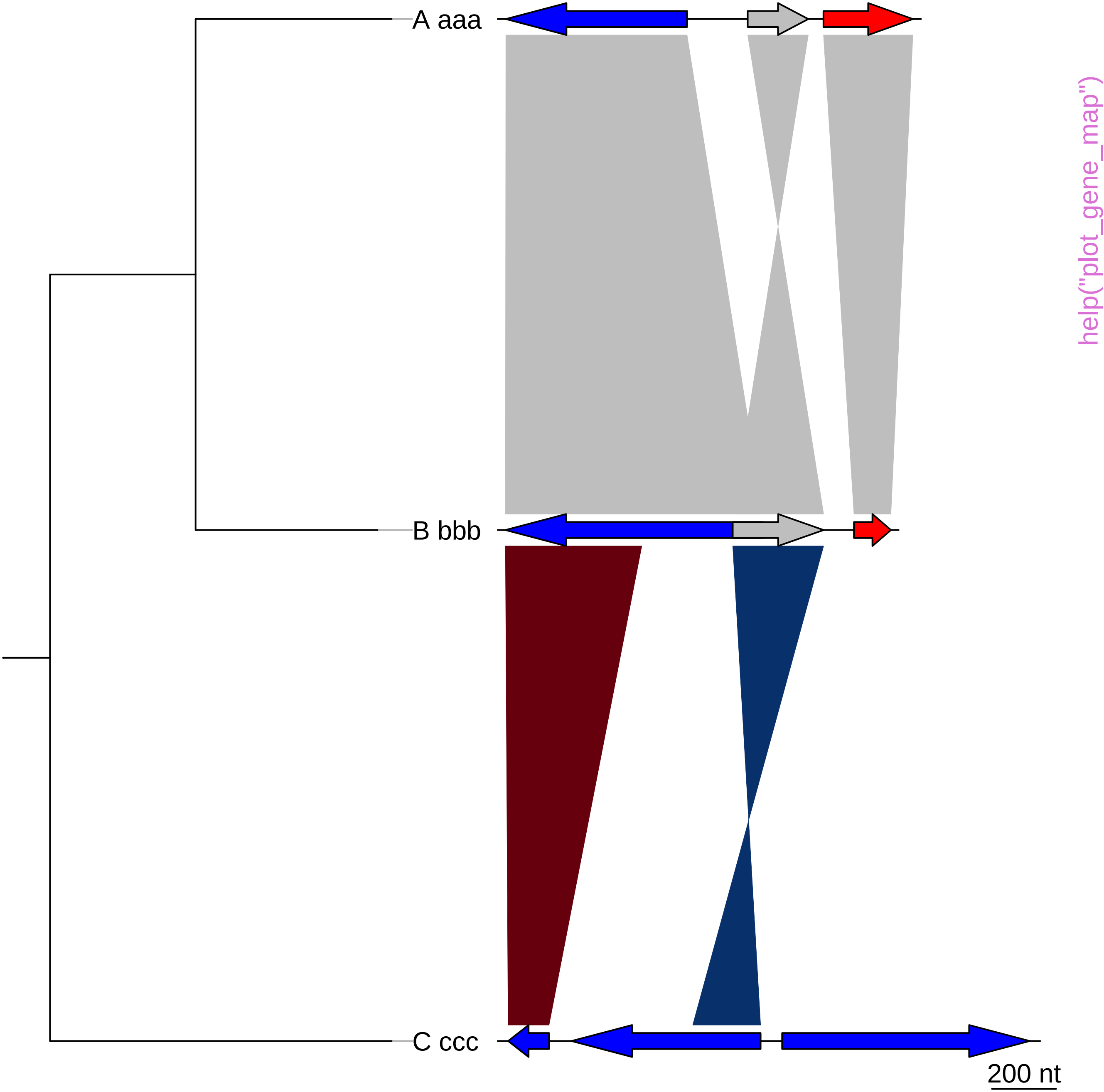

200 nt
help("genoPlotR-package")

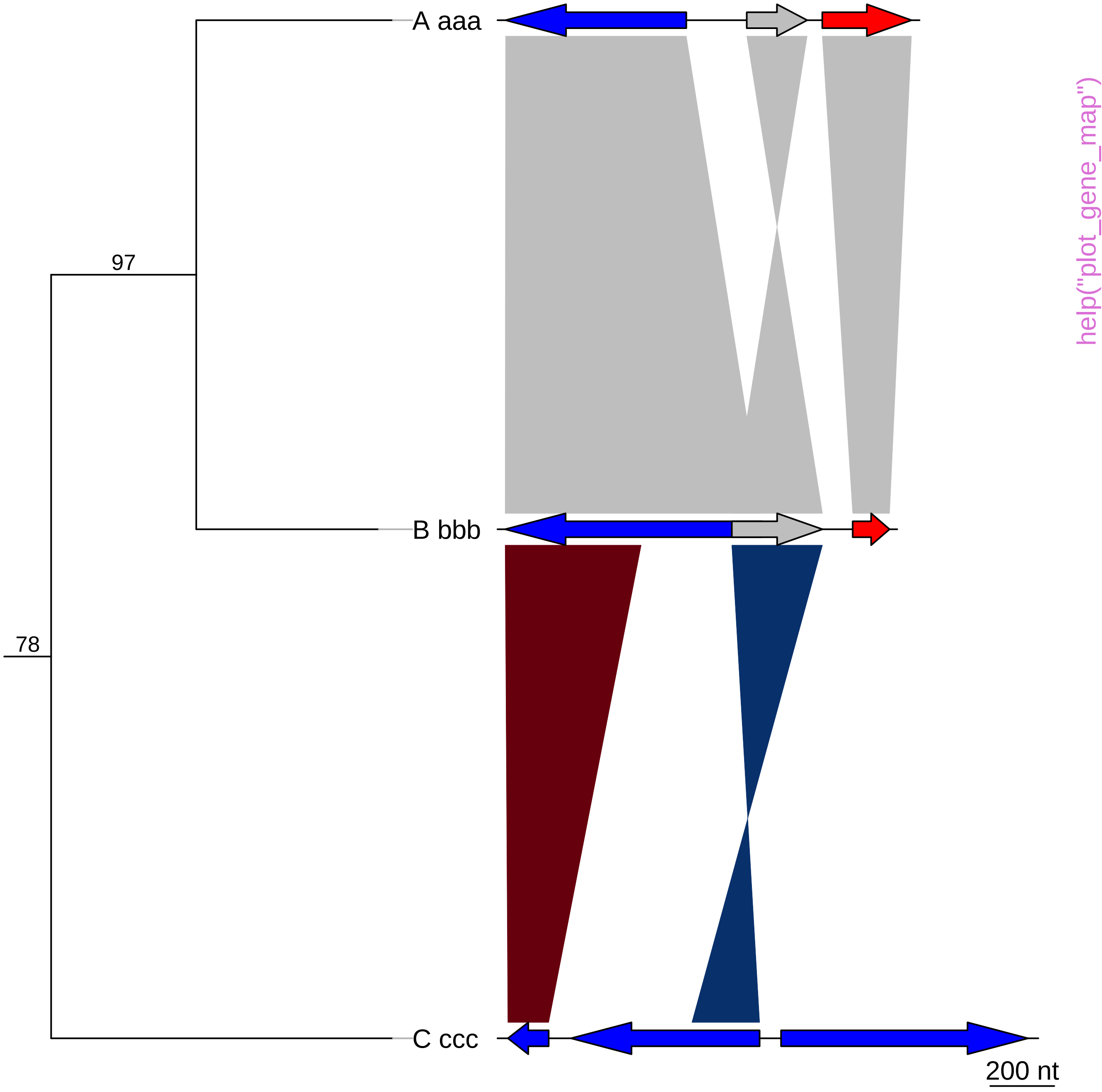

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("mauve_bbone")

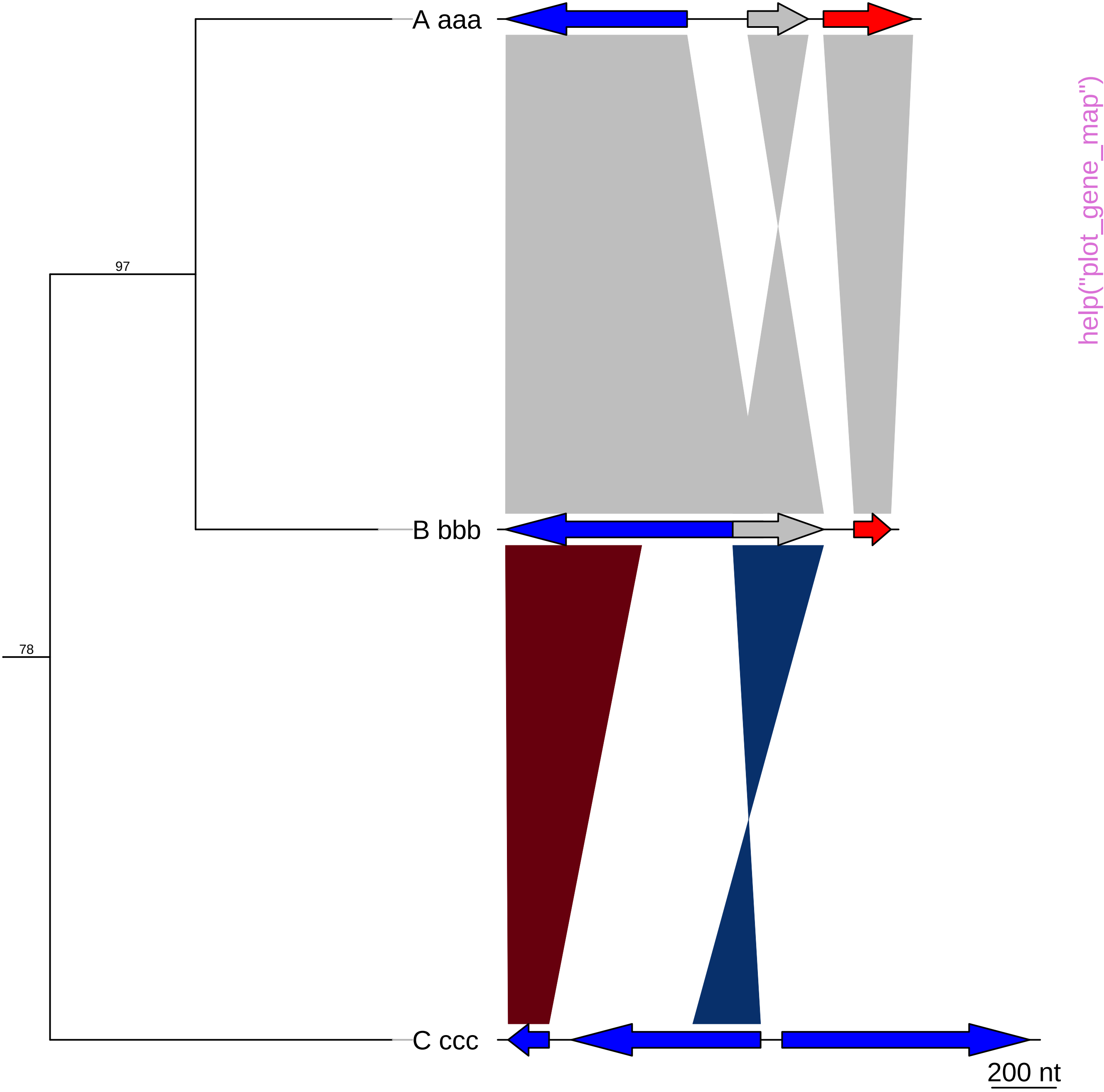

help("plot_gene_map")
200 nt

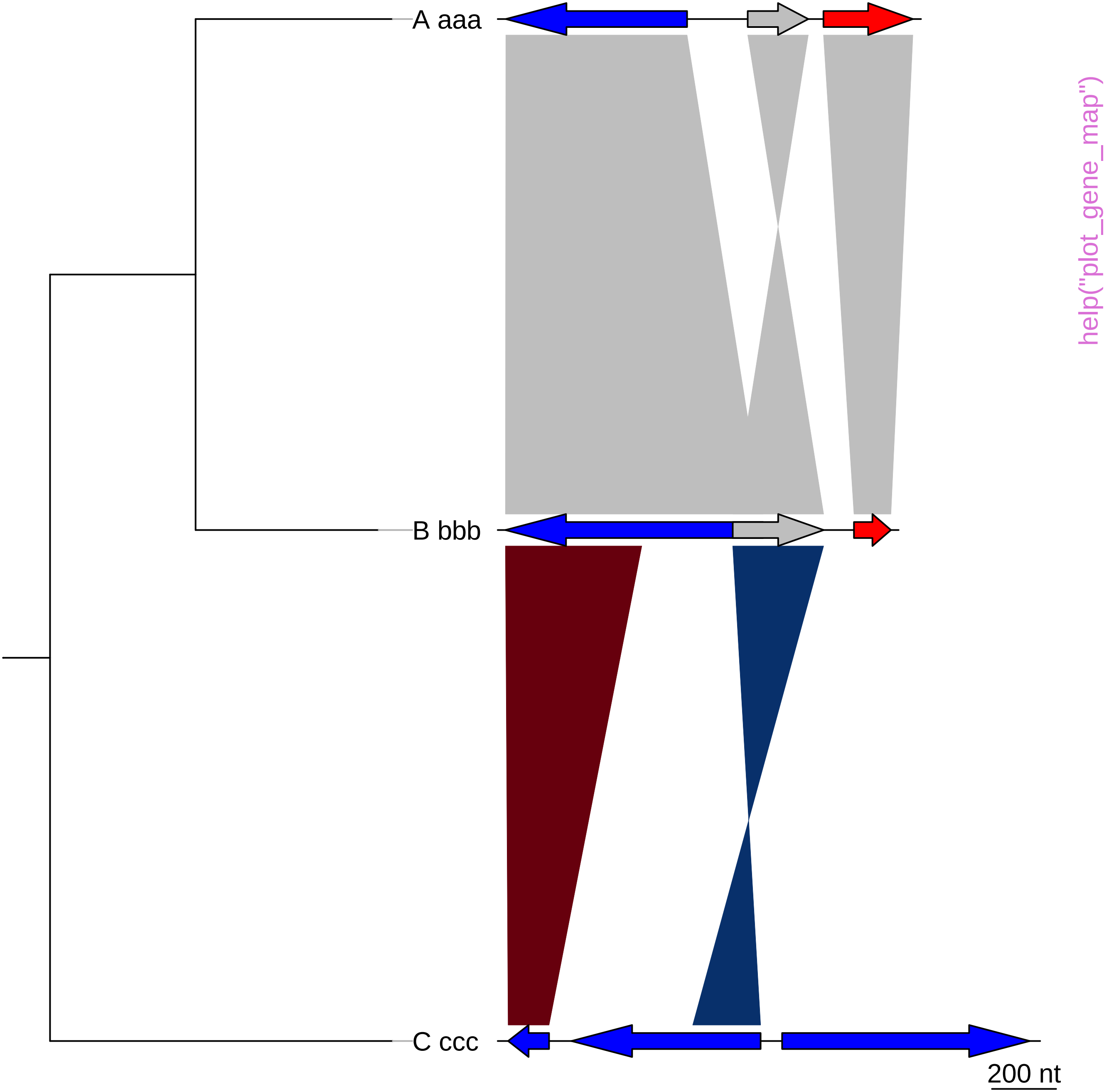

help("plot_gene_map")
200 nt

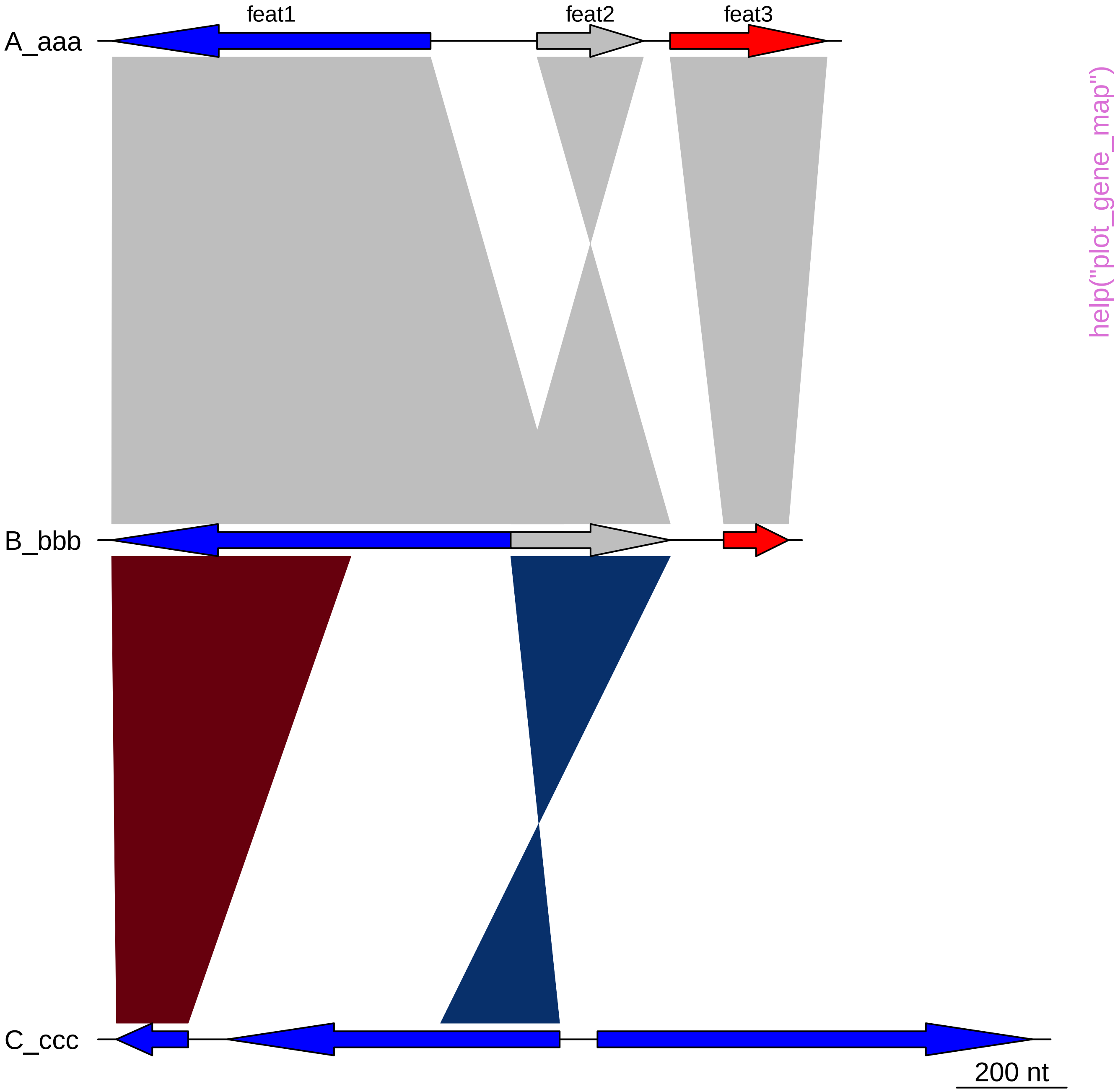

A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")

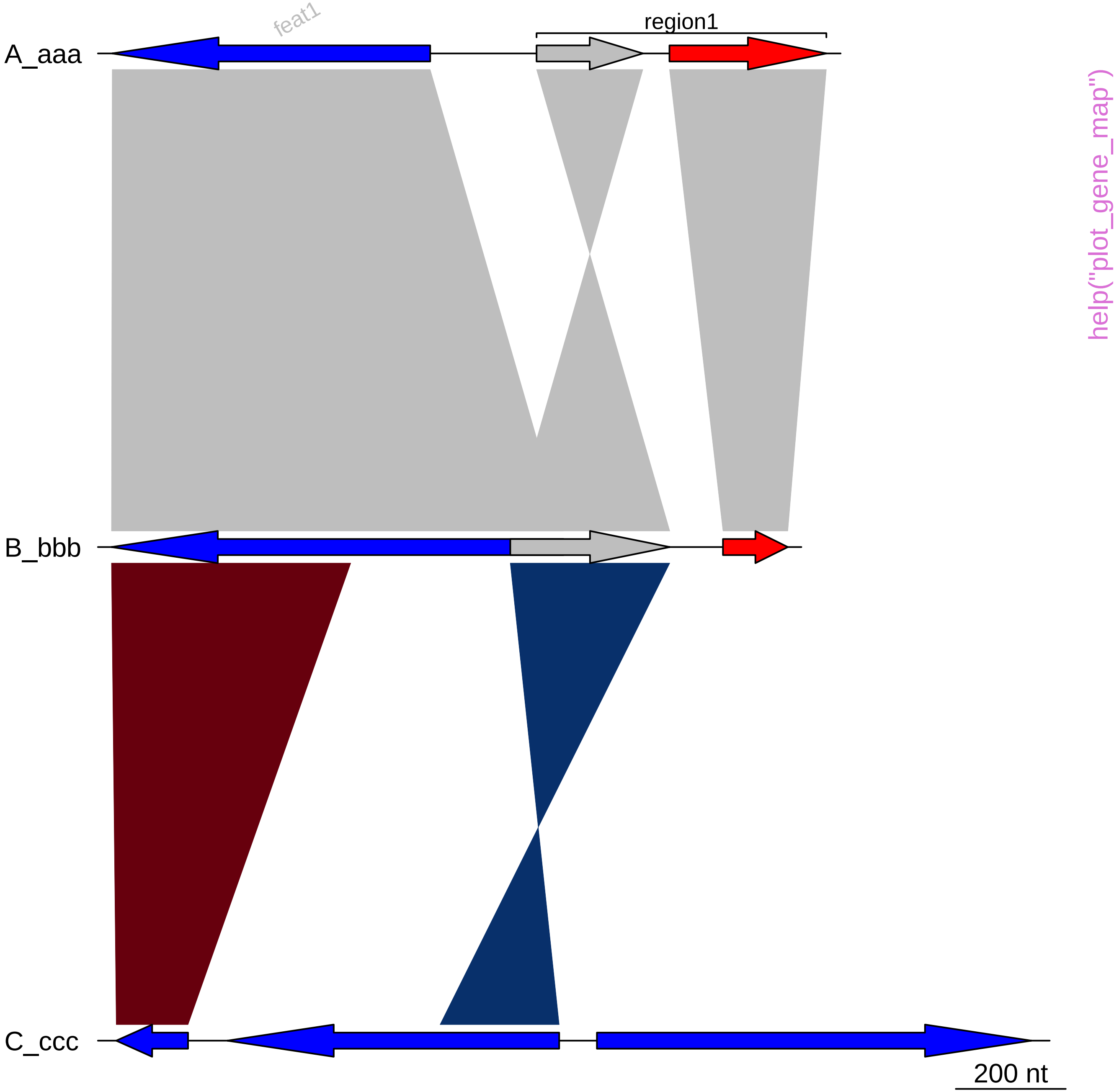

A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")

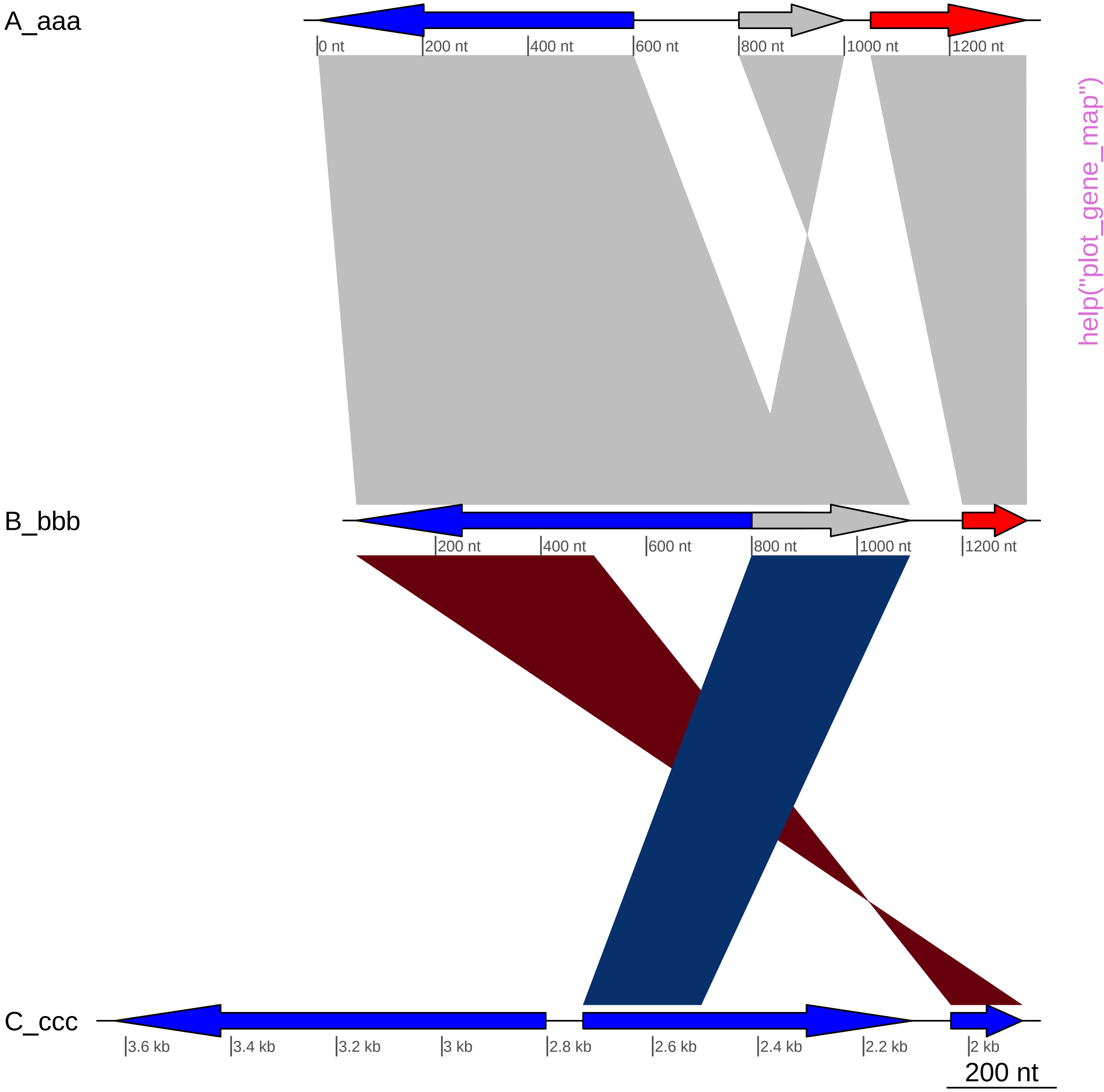

A aaa
97
B bbb
78
C ccc
200 nt
help("plot_gene_map")

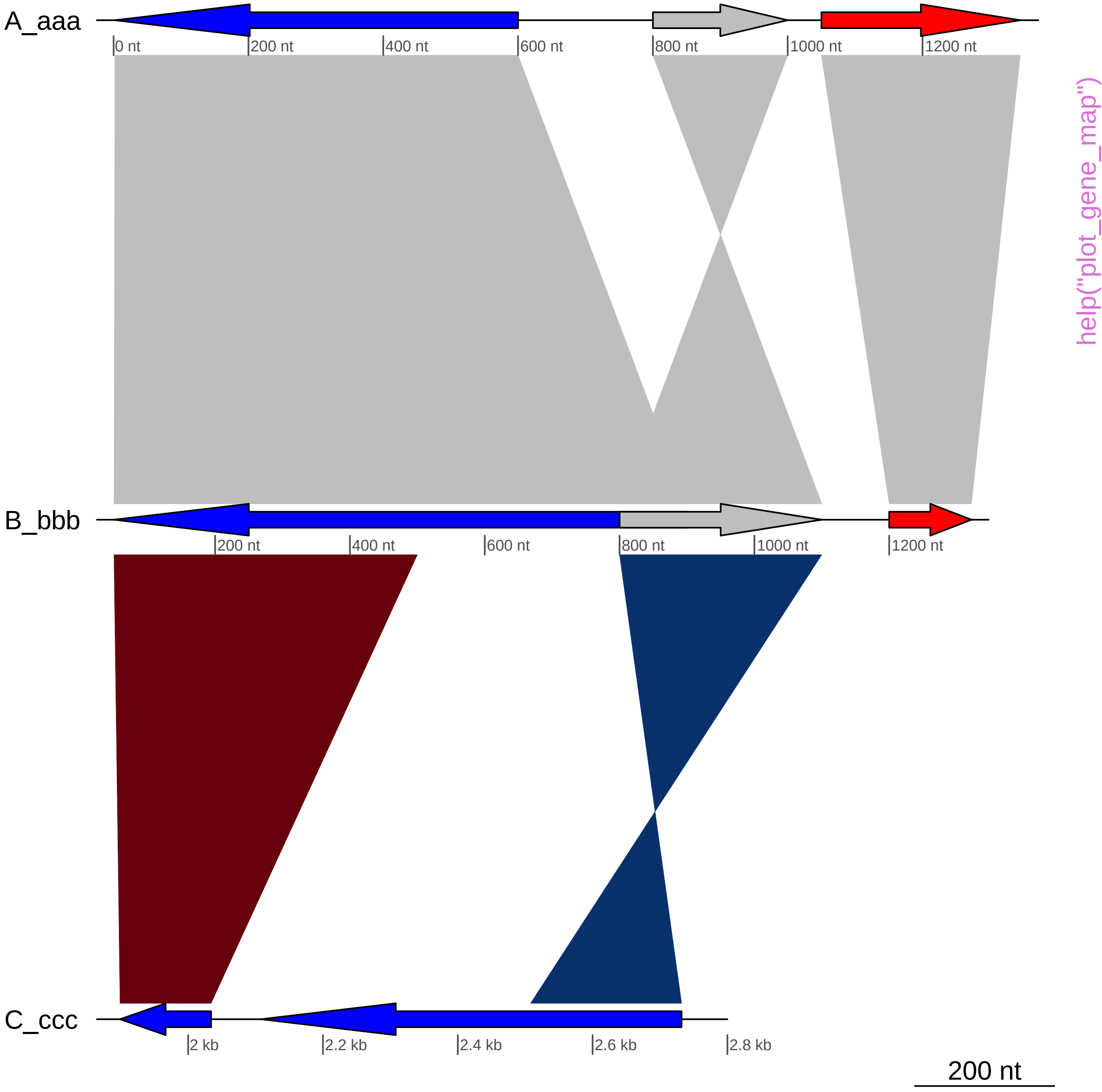

A aaa
B bbb
C ccc
97
78
200 nt
help("plot_gene_map")

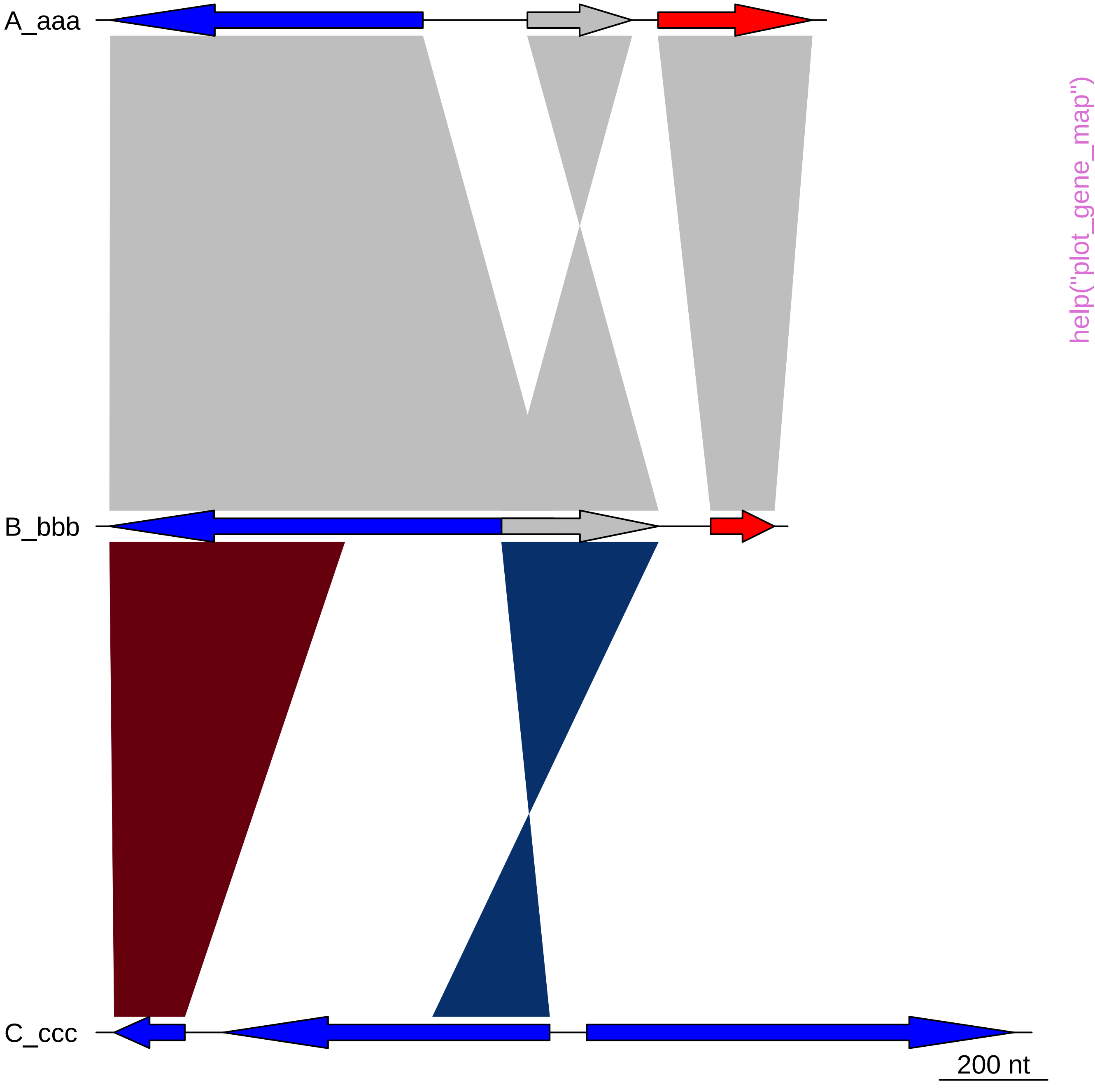

A aaa
B bbb
C ccc
200 nt
help("plot_gene_map")

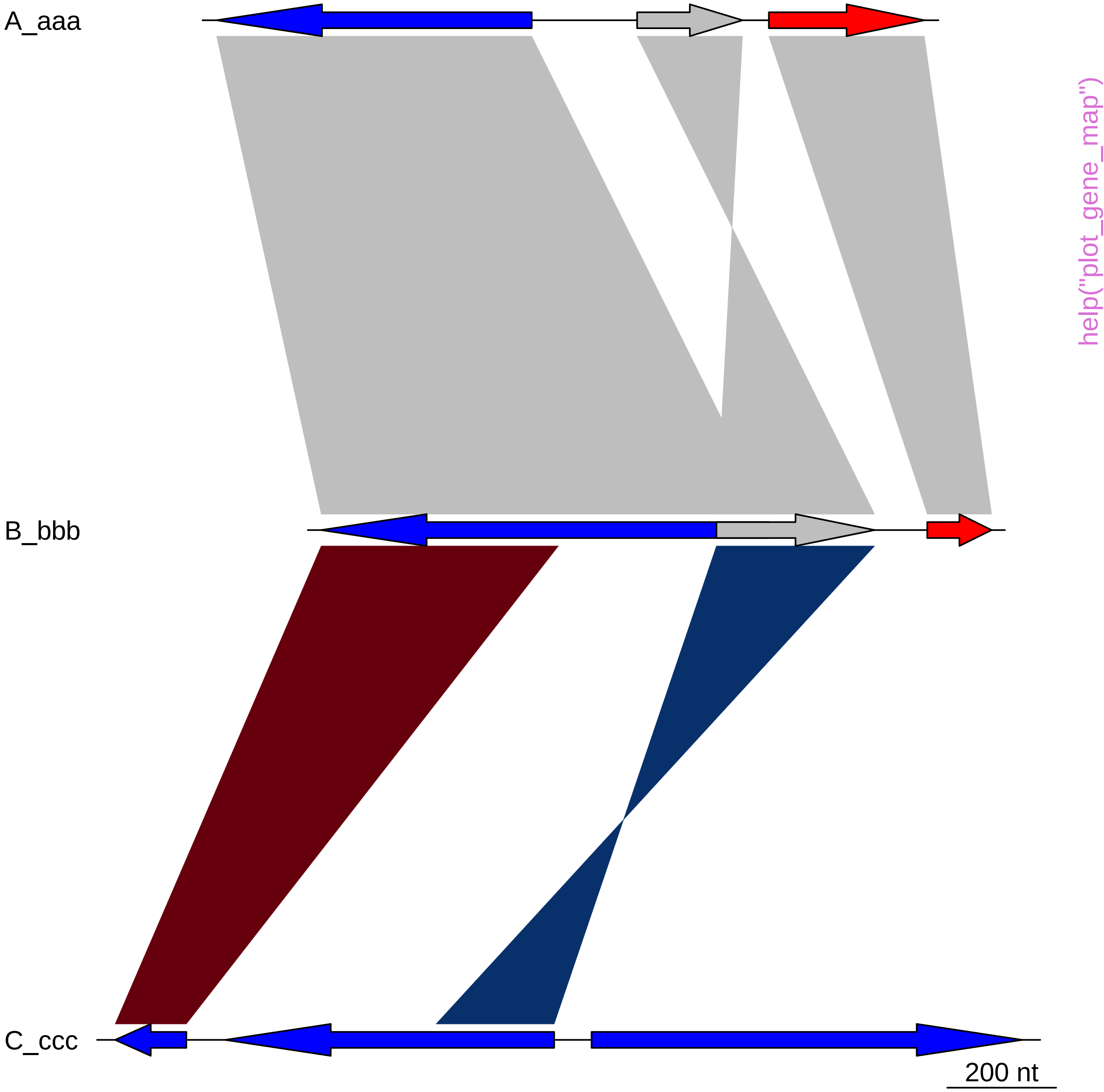

feat1
feat2
feat3
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

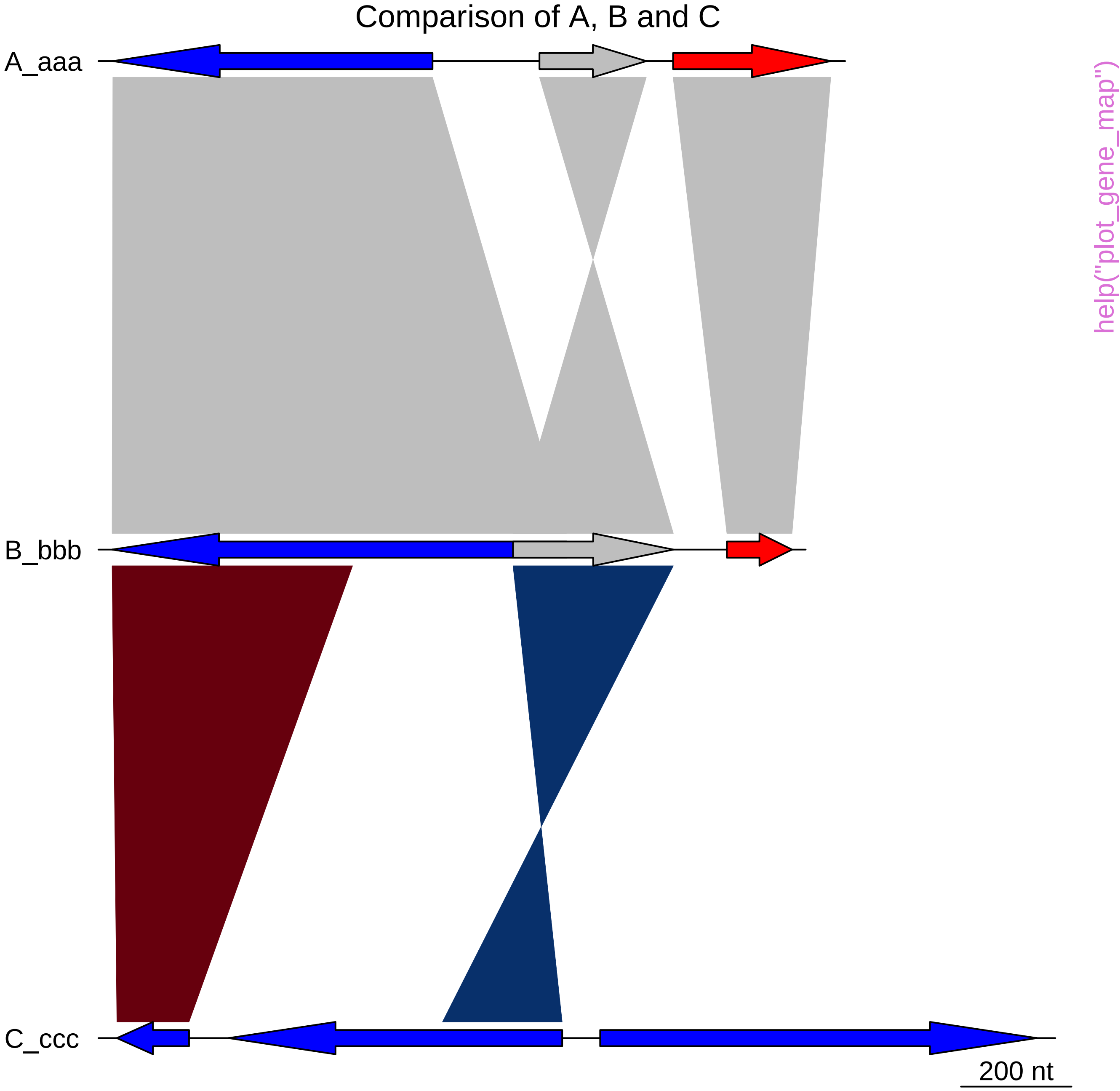

feat1
region1
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

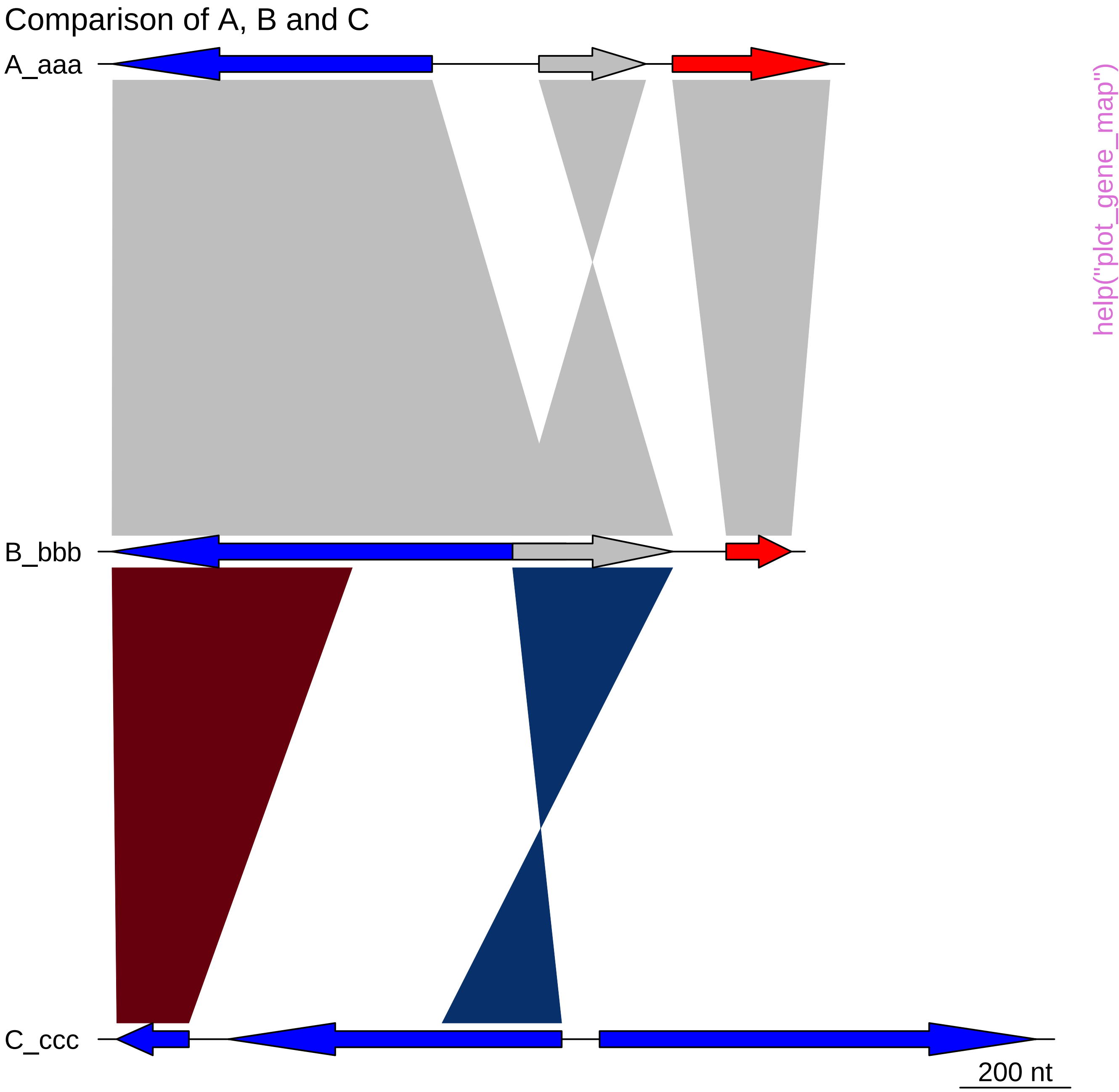

A_aaa
0 nt
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
B_bbb
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
C_ccc
3.6 kb
3.4 kb
3.2 kb
3 kb
2.8 kb
2.6 kb
2.4 kb
2.2 kb
2 kb
200 nt
help("plot_gene_map")

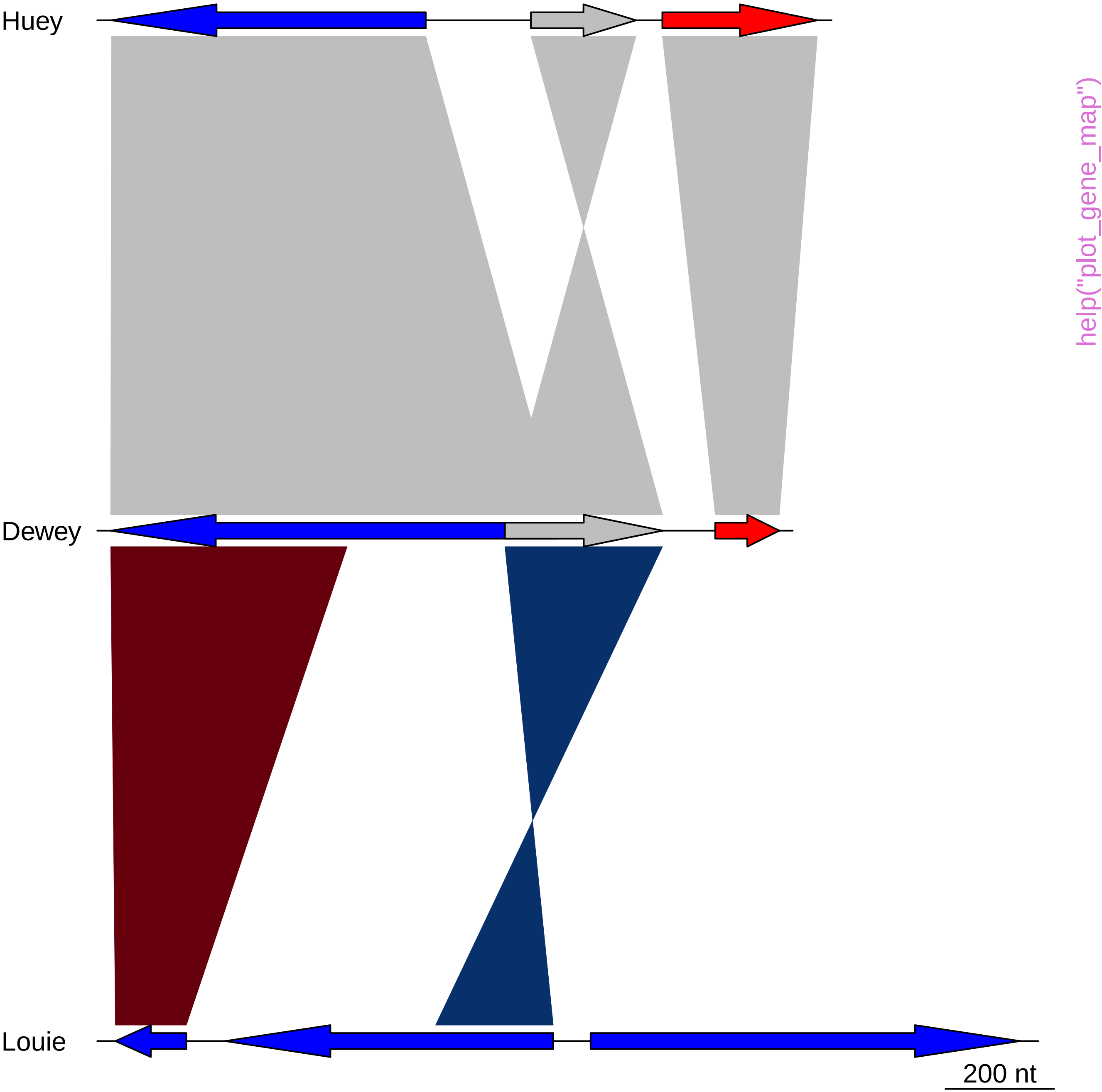

A_aaa
0 nt
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
B_bbb
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
C_ccc
2 kb
2.2 kb
2.4 kb
2.6 kb
2.8 kb
200 nt
help("plot_gene_map")

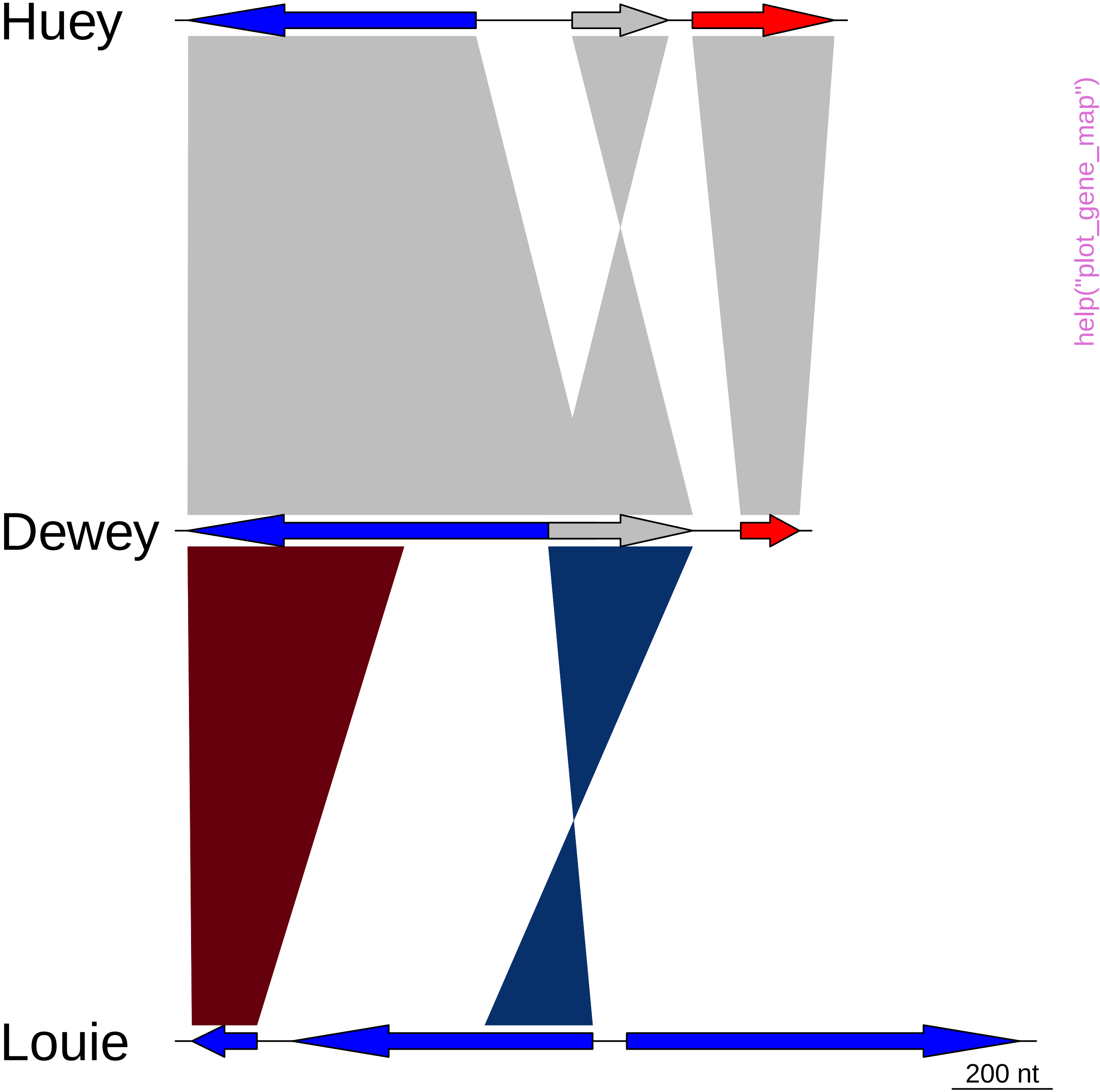

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

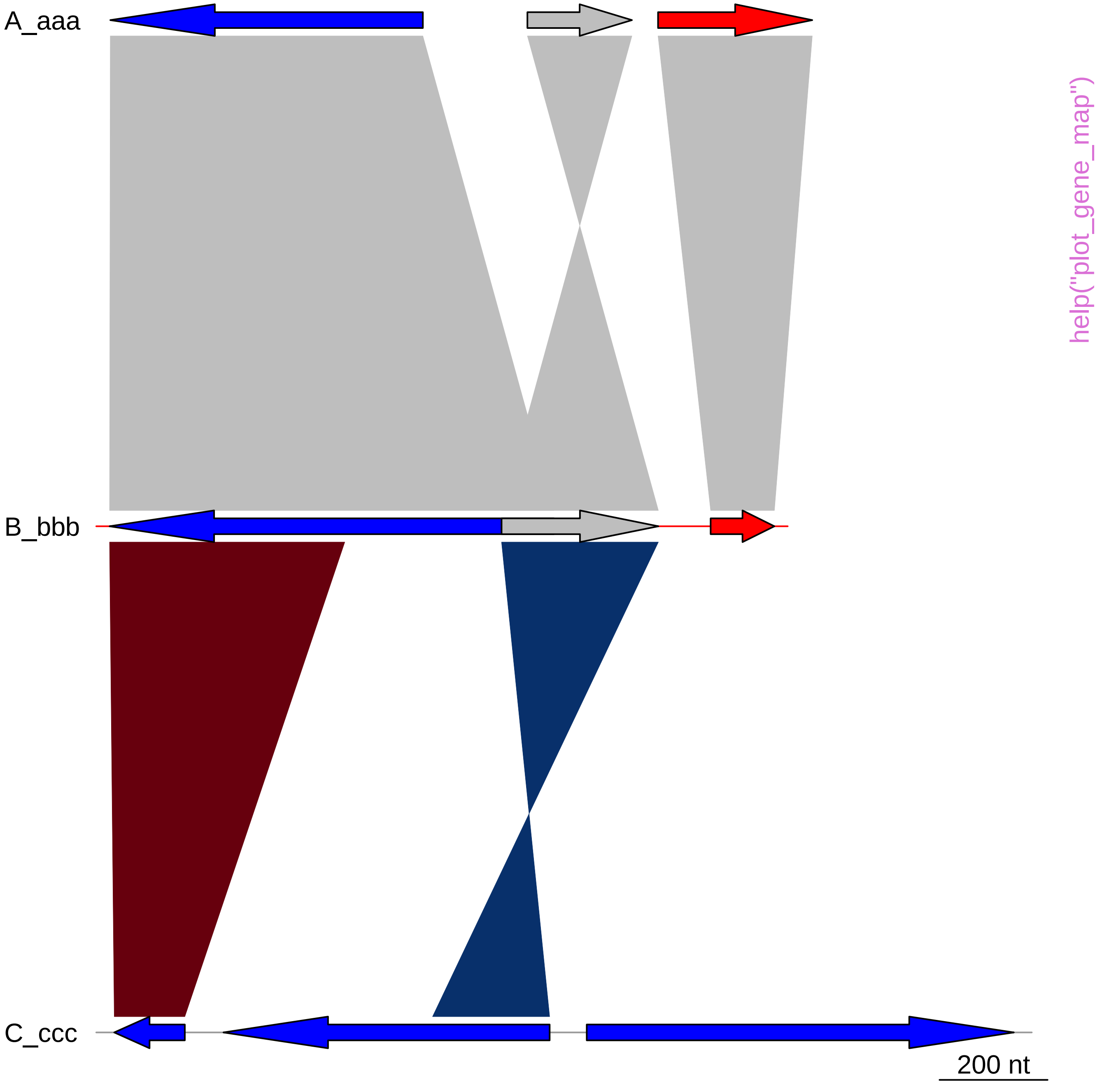

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

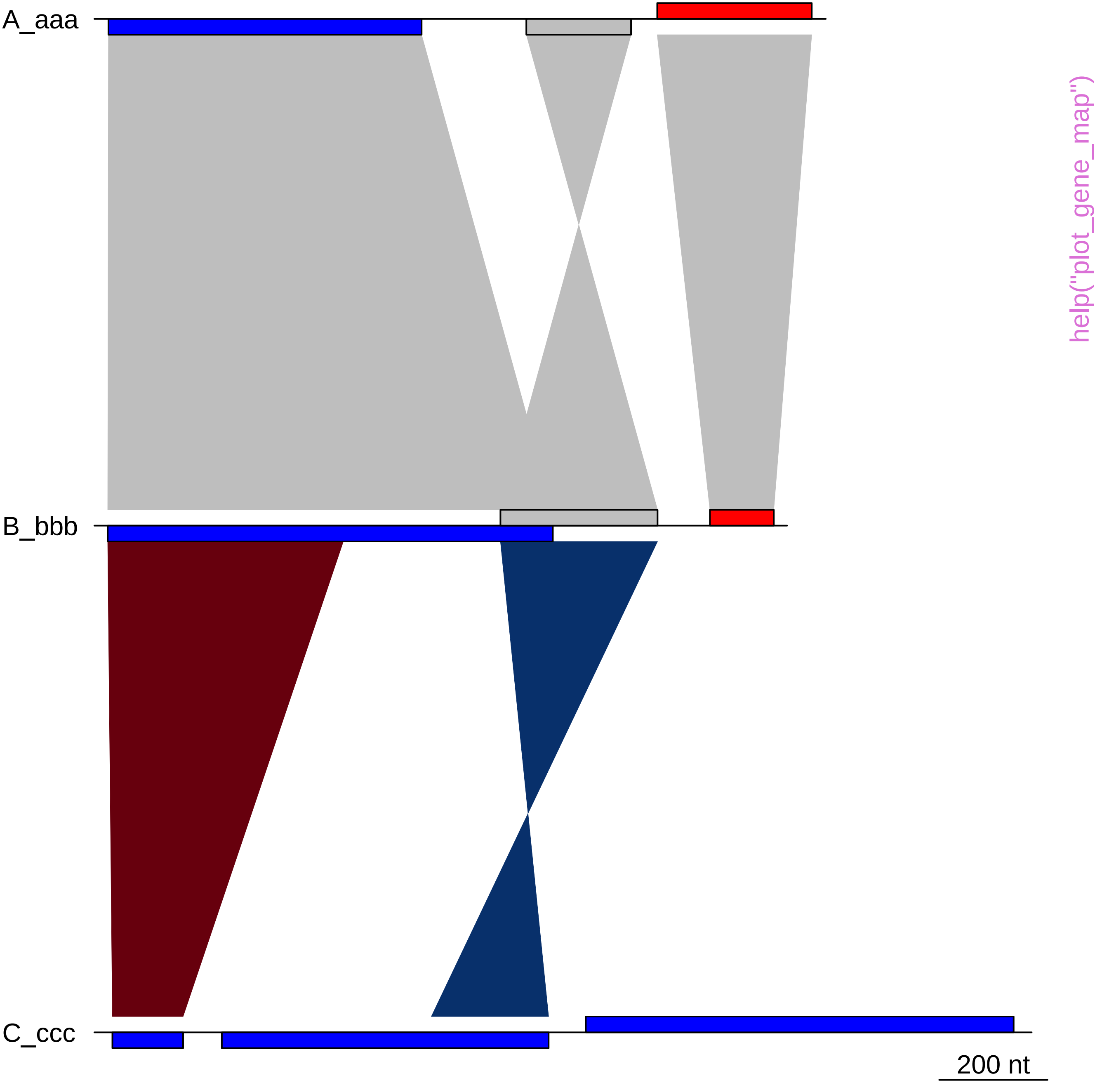

Comparison of A, B and C
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

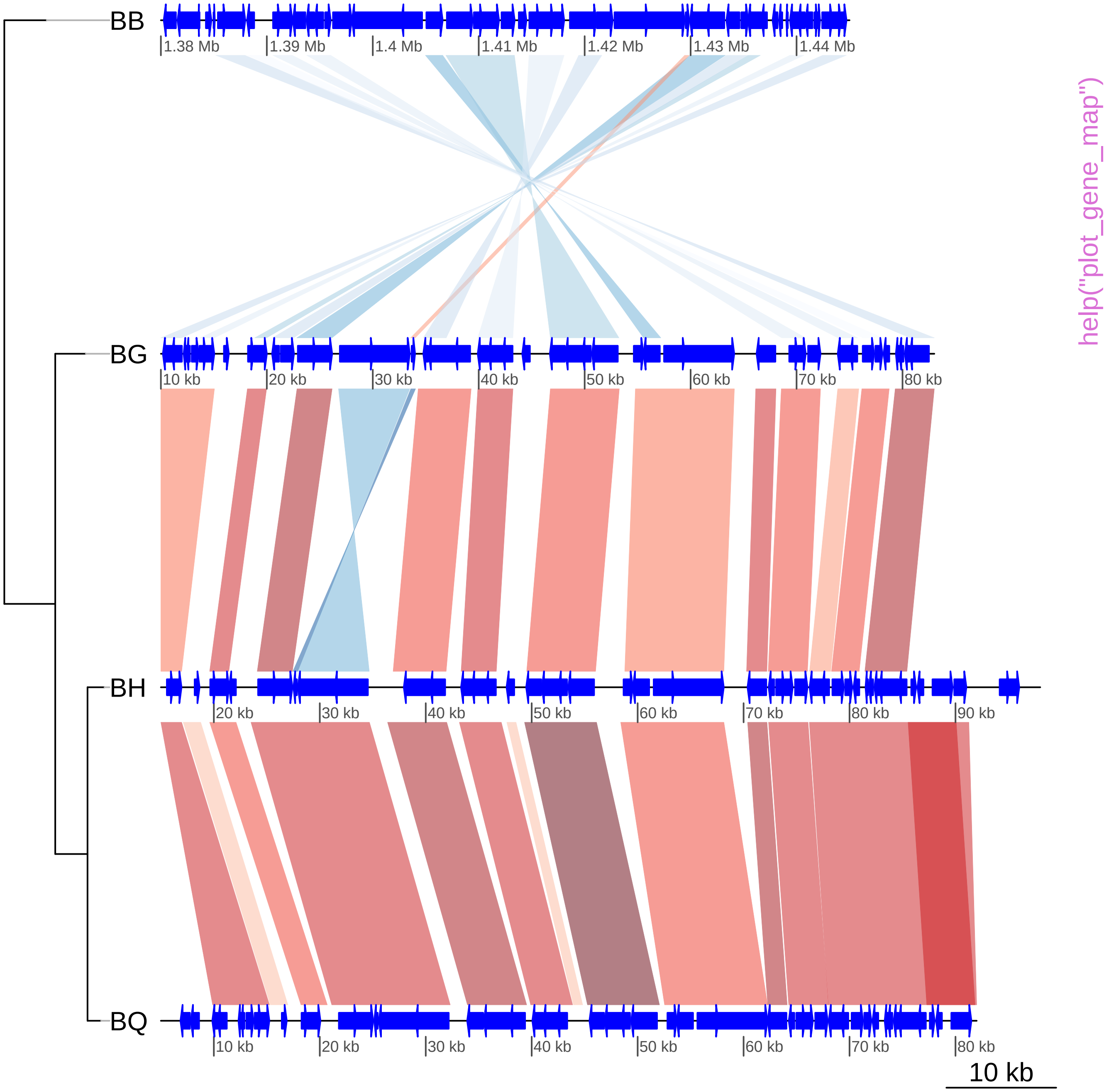

Comparison of A, B and C
A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")


Huey
Dewey
Louie
200 nt
help("plot_gene_map")

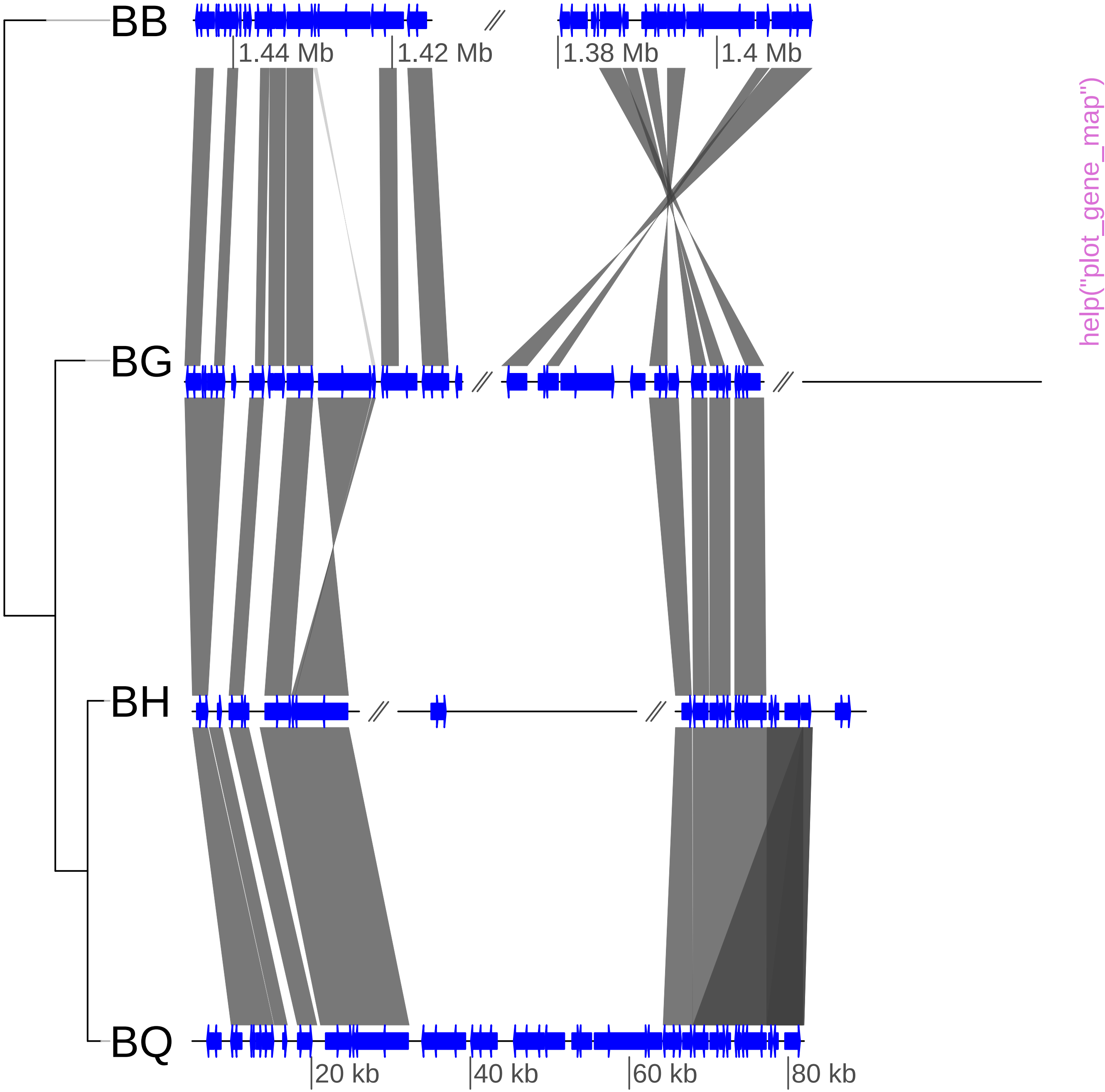

Huey
Dewey
Louie
200 nt
help("plot_gene_map")

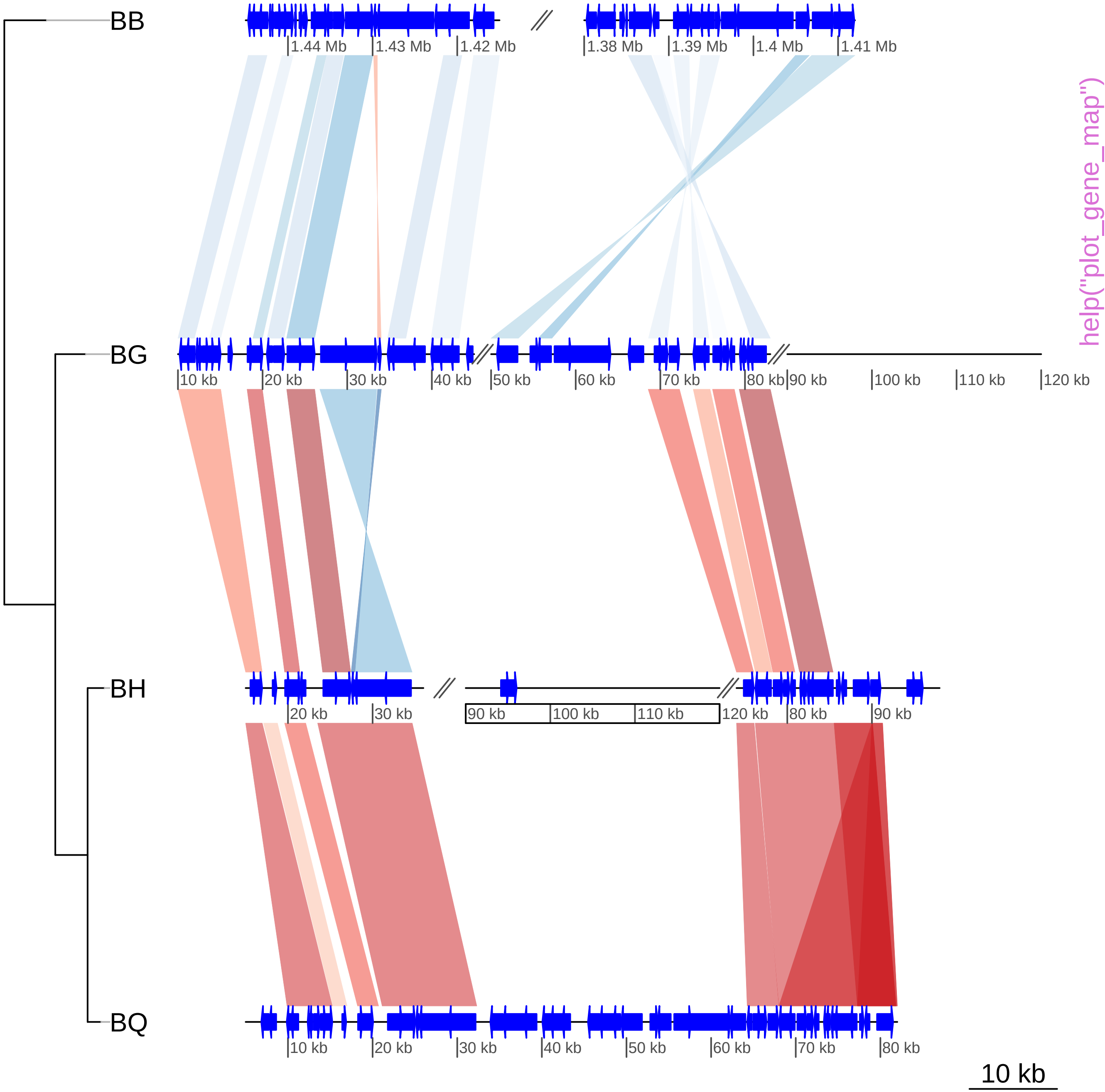

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

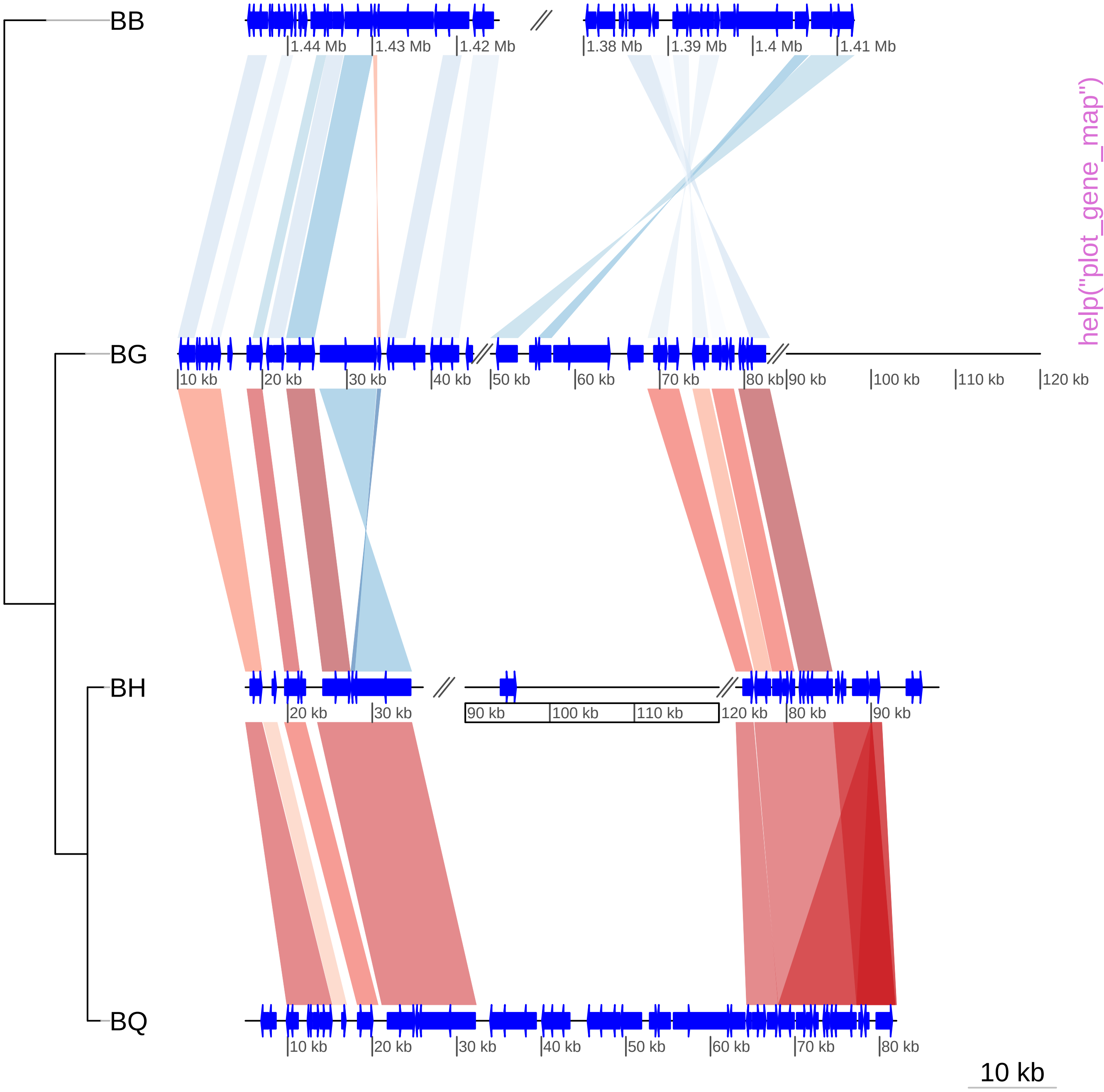

A_aaa
B_bbb
C_ccc
200 nt
help("plot_gene_map")

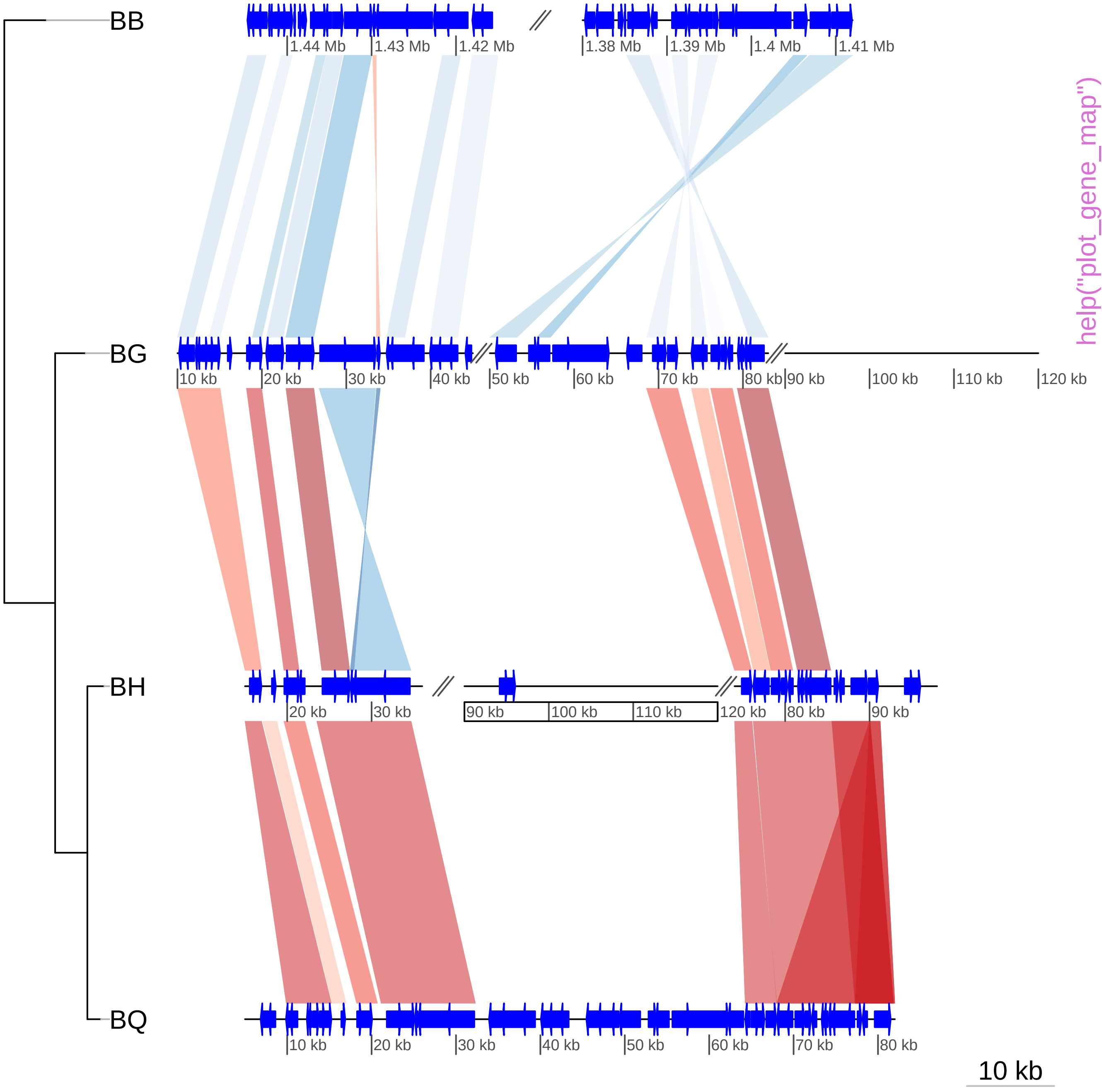


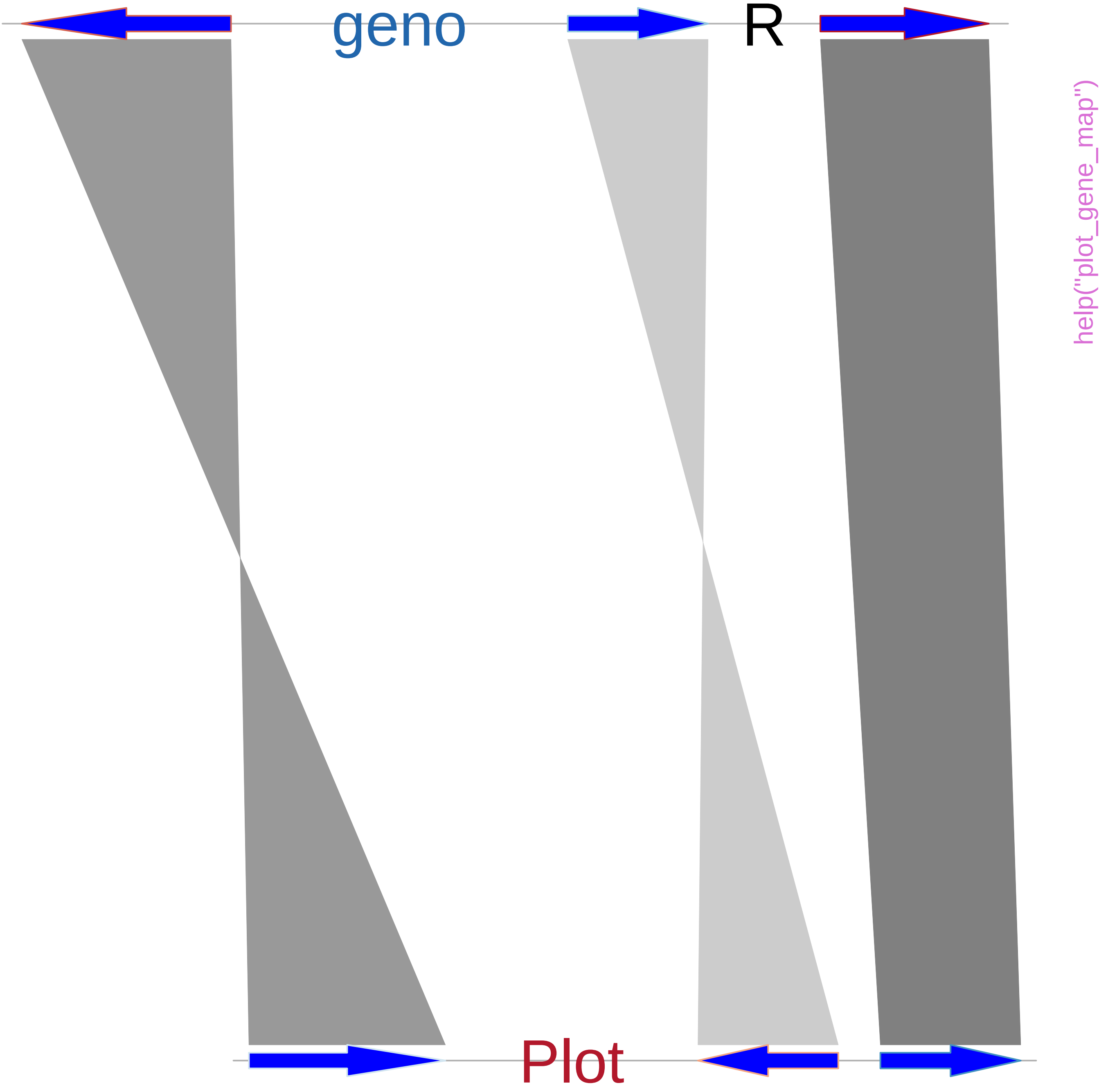
BB
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
1.42 Mb
1.43 Mb
1.44 Mb
BG
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
BH
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
BQ
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
10 kb
help("plot_gene_map")

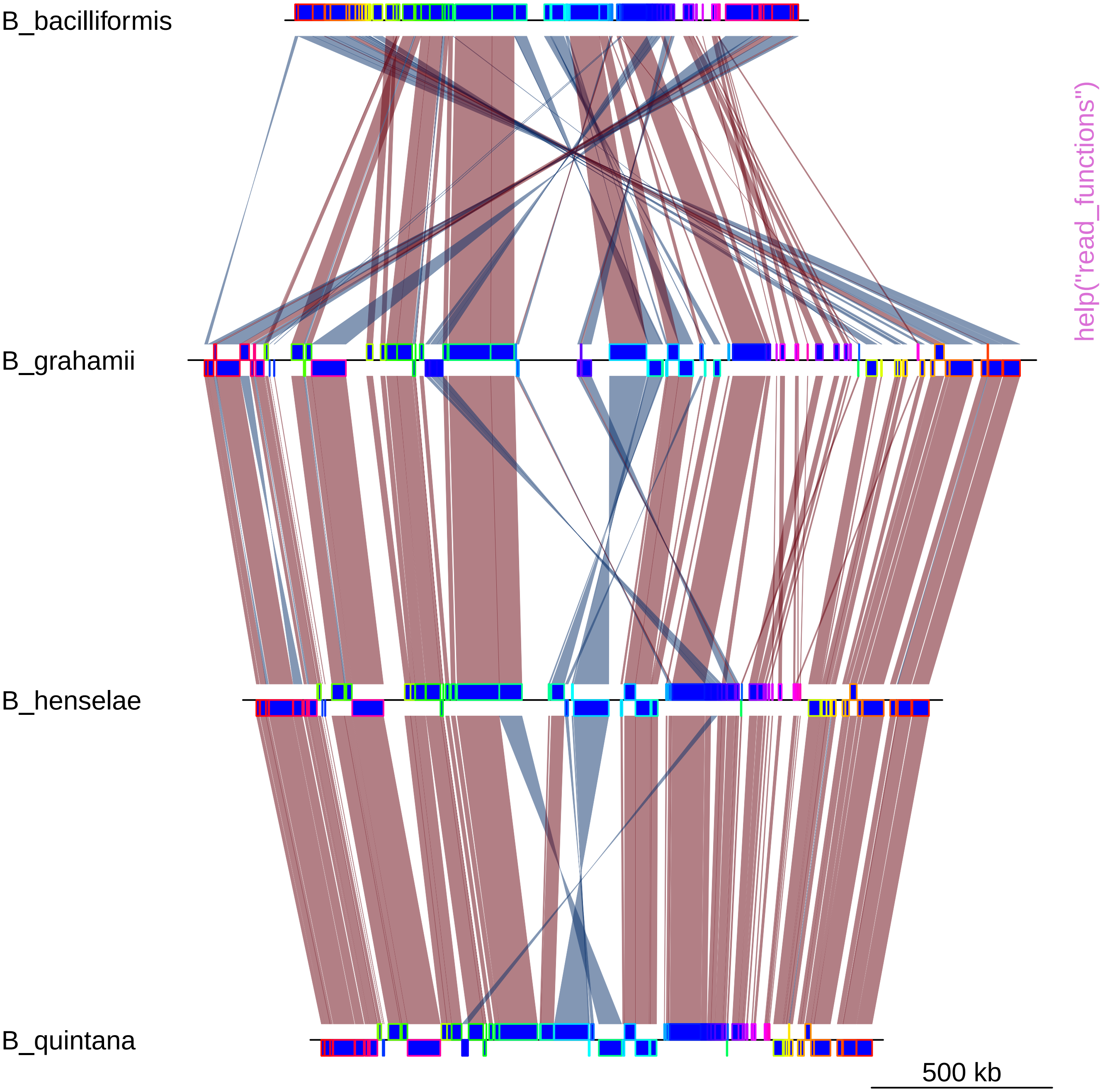

BB
1.44 Mb
1.42 Mb
1.38 Mb
1.4 Mb
BG
BH
BQ
20 kb
40 kb
60 kb
80 kb
help("plot_gene_map")

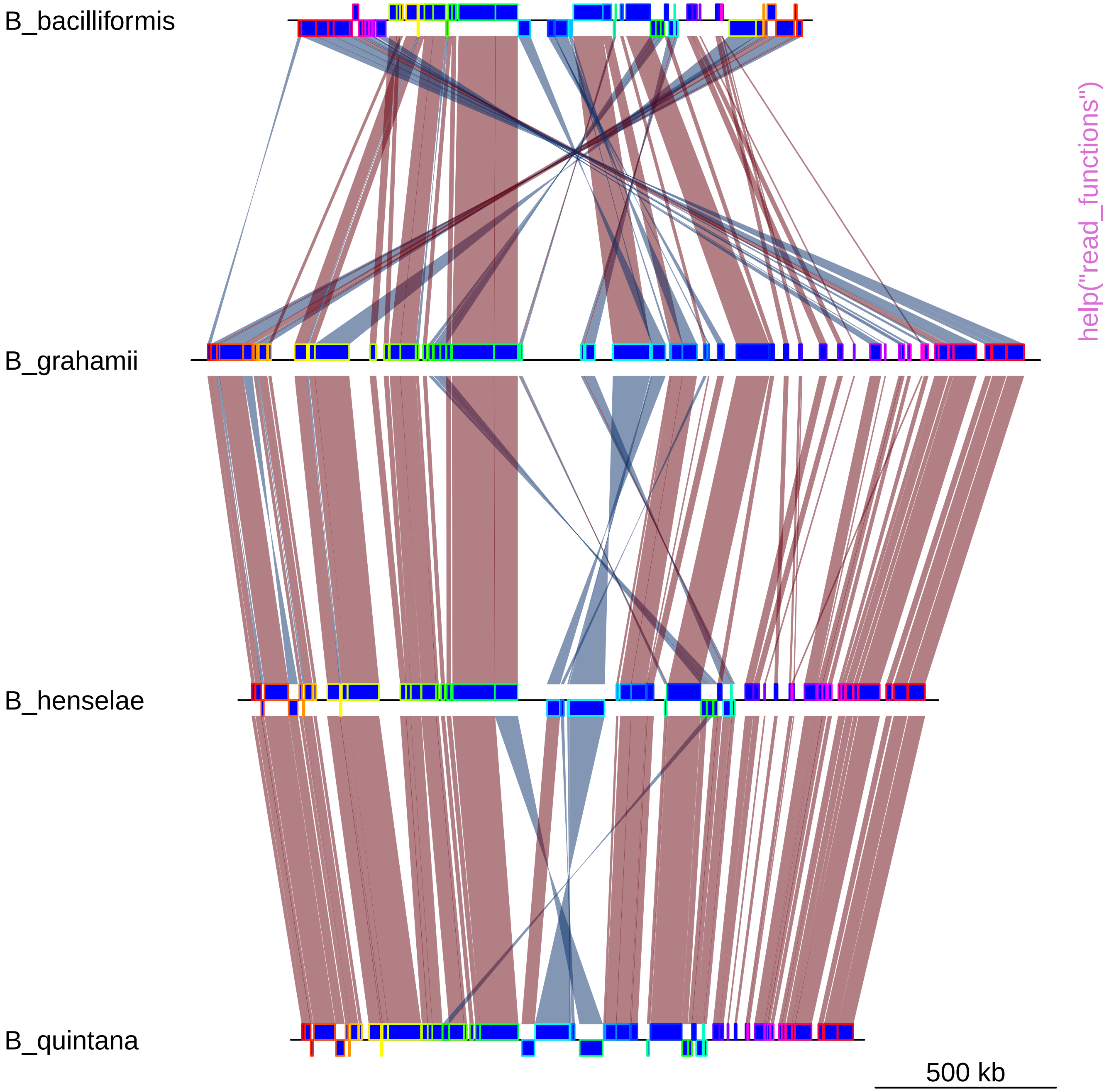

BB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
BG
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
100 kb
110 kb
120 kb
BH
20 kb
30 kb
90 kb
100 kb
110 kb
120 kb
80 kb
90 kb
BQ
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
10 kb
help("plot_gene_map")

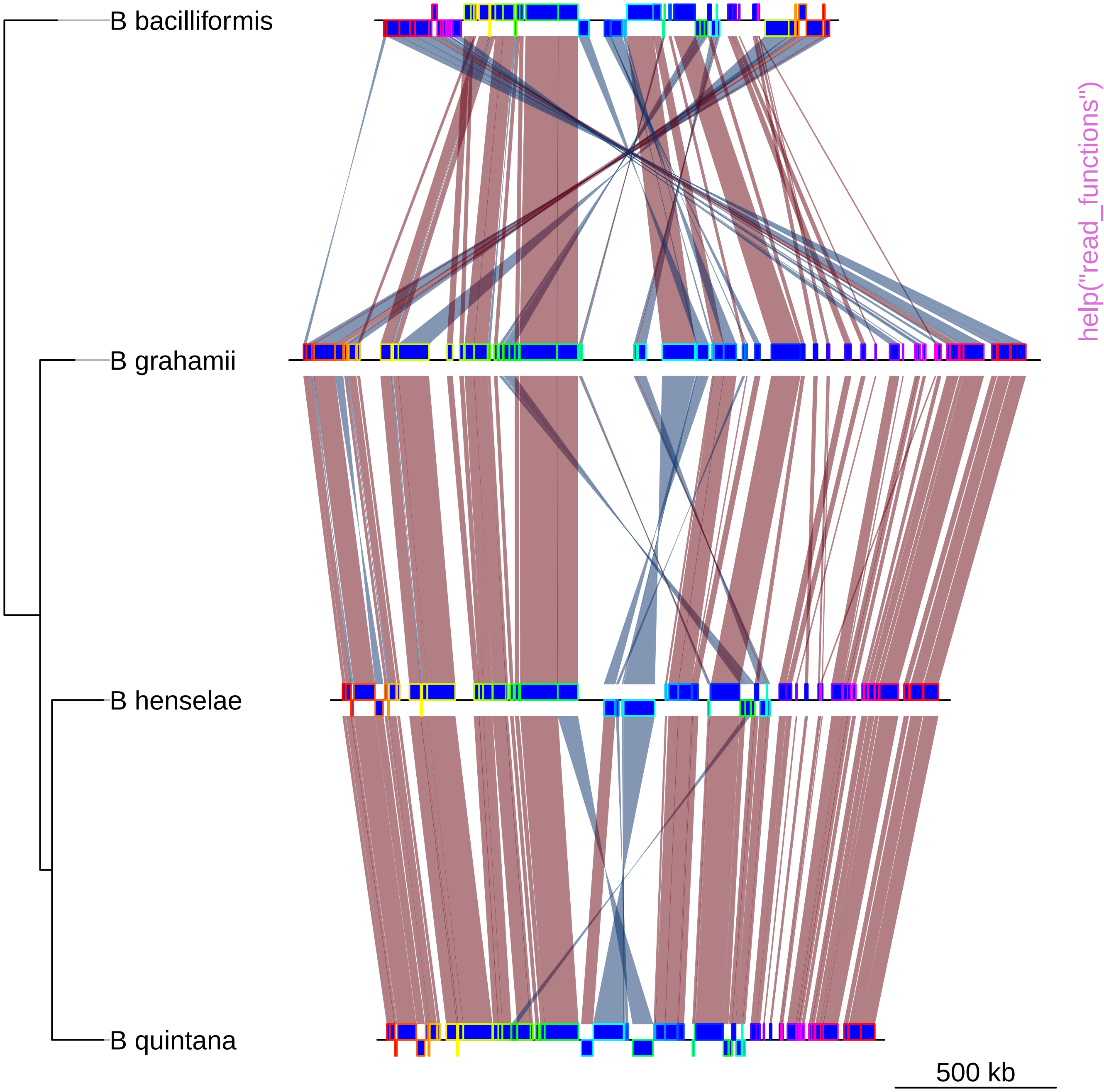

BB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
BG
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
100 kb
110 kb
120 kb
BH
20 kb
30 kb
90 kb
100 kb
110 kb
120 kb
80 kb
90 kb
BQ
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
10 kb
help("plot_gene_map")

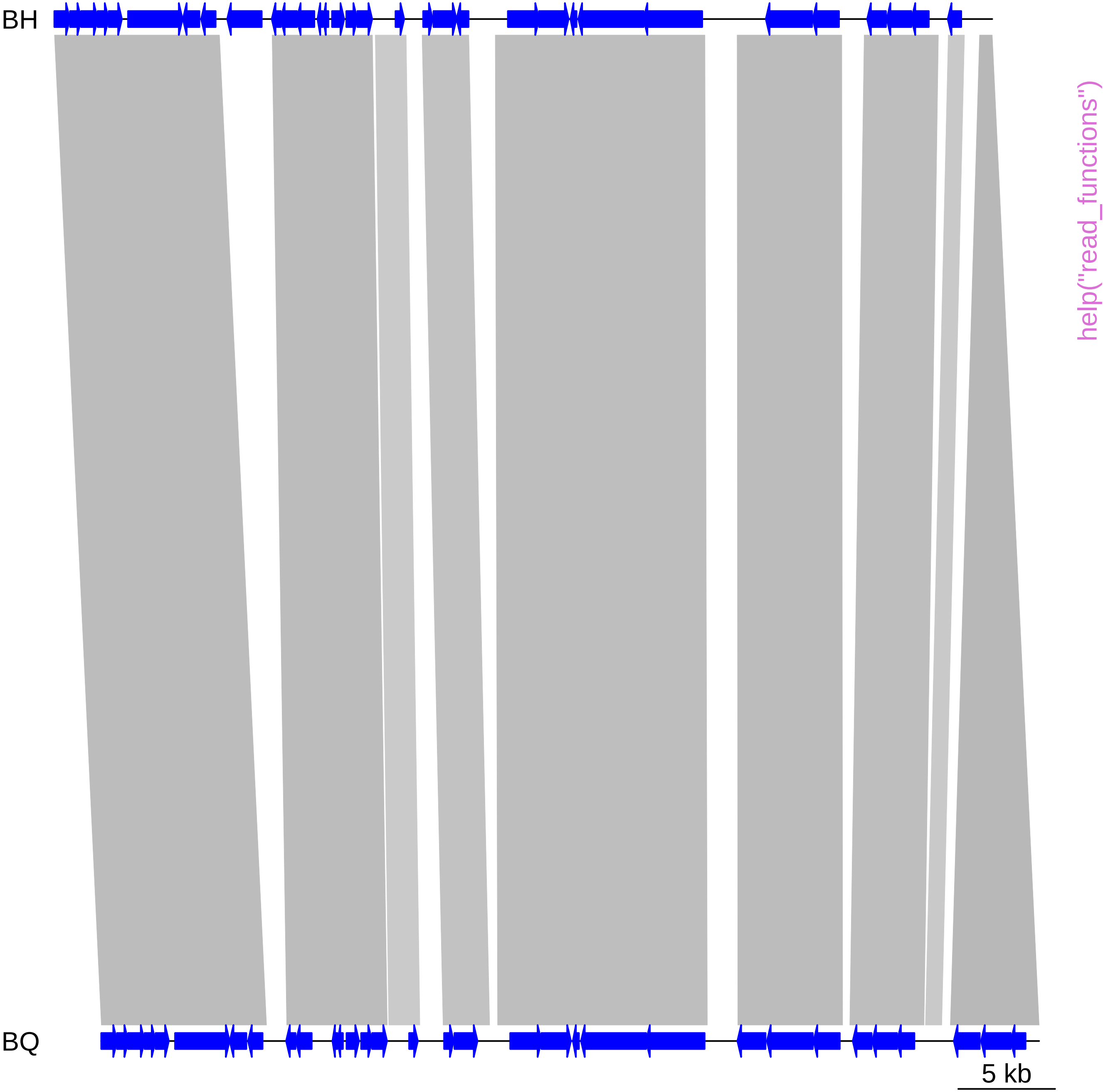

BB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
BG
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
90 kb
100 kb
110 kb
120 kb
BH
20 kb
30 kb
90 kb
100 kb
110 kb
120 kb
80 kb
90 kb
BQ
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
10 kb
help("plot_gene_map")

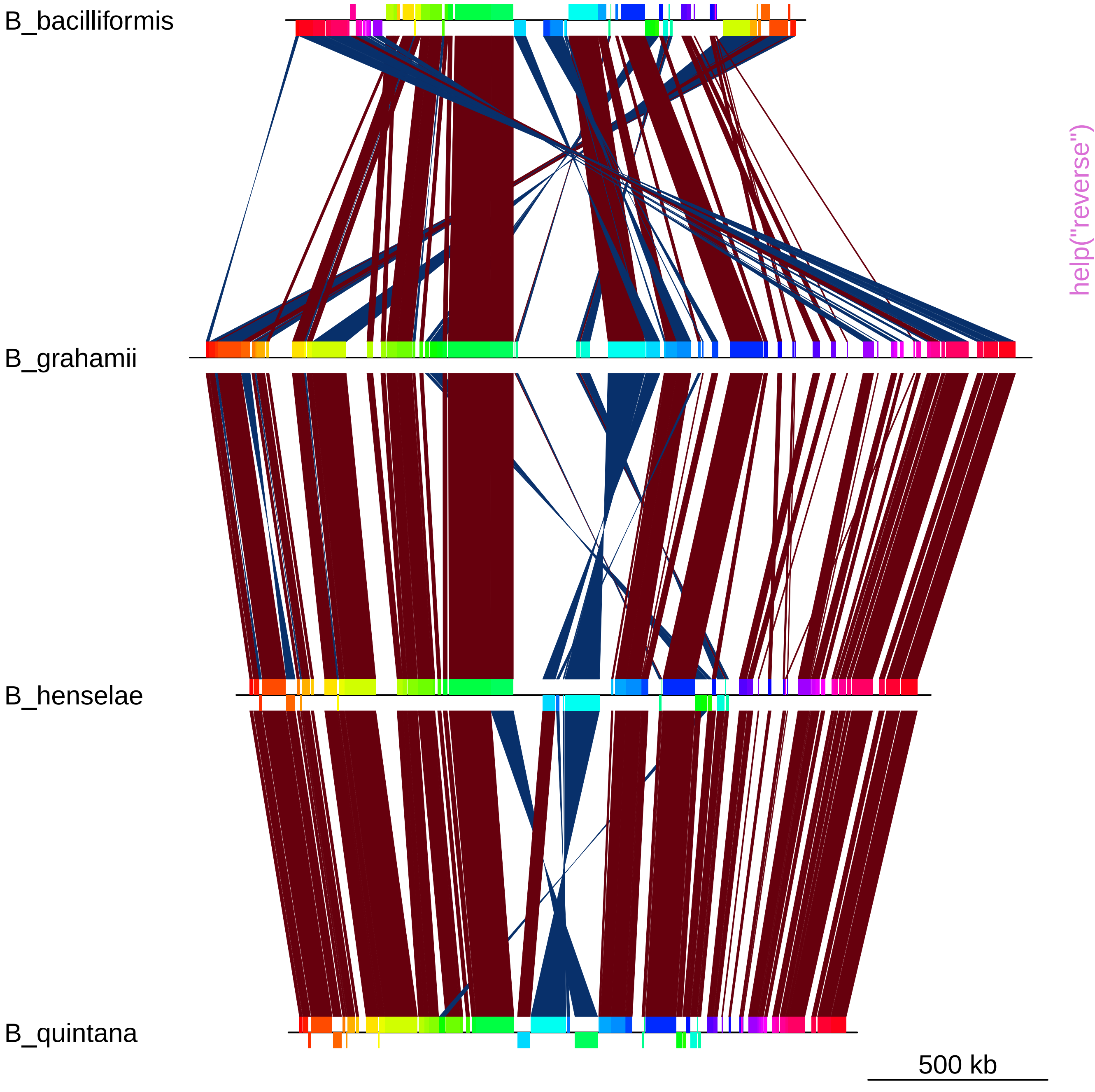

geno
R
Plot
help("plot_gene_map")

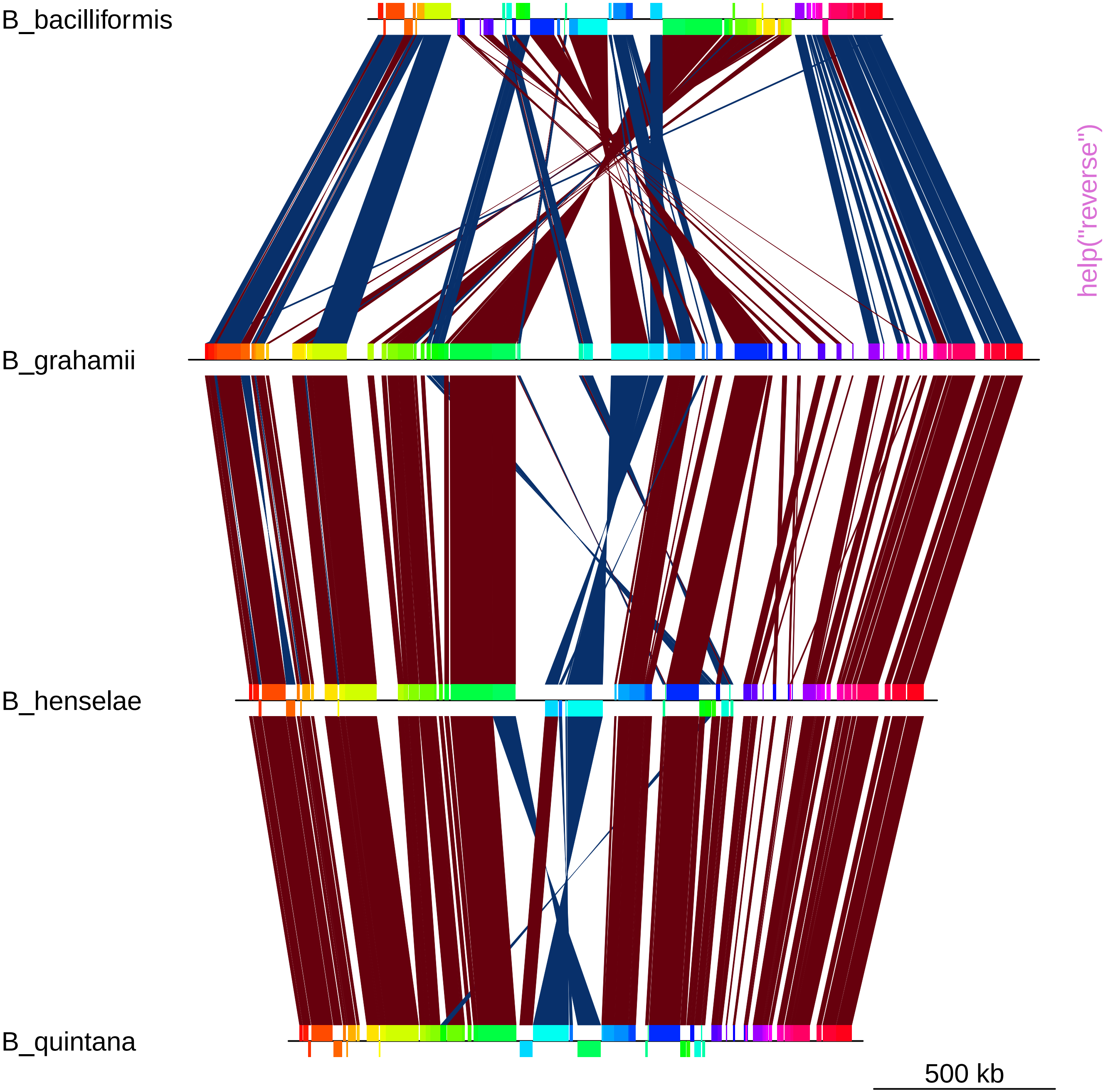

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("read_functions")

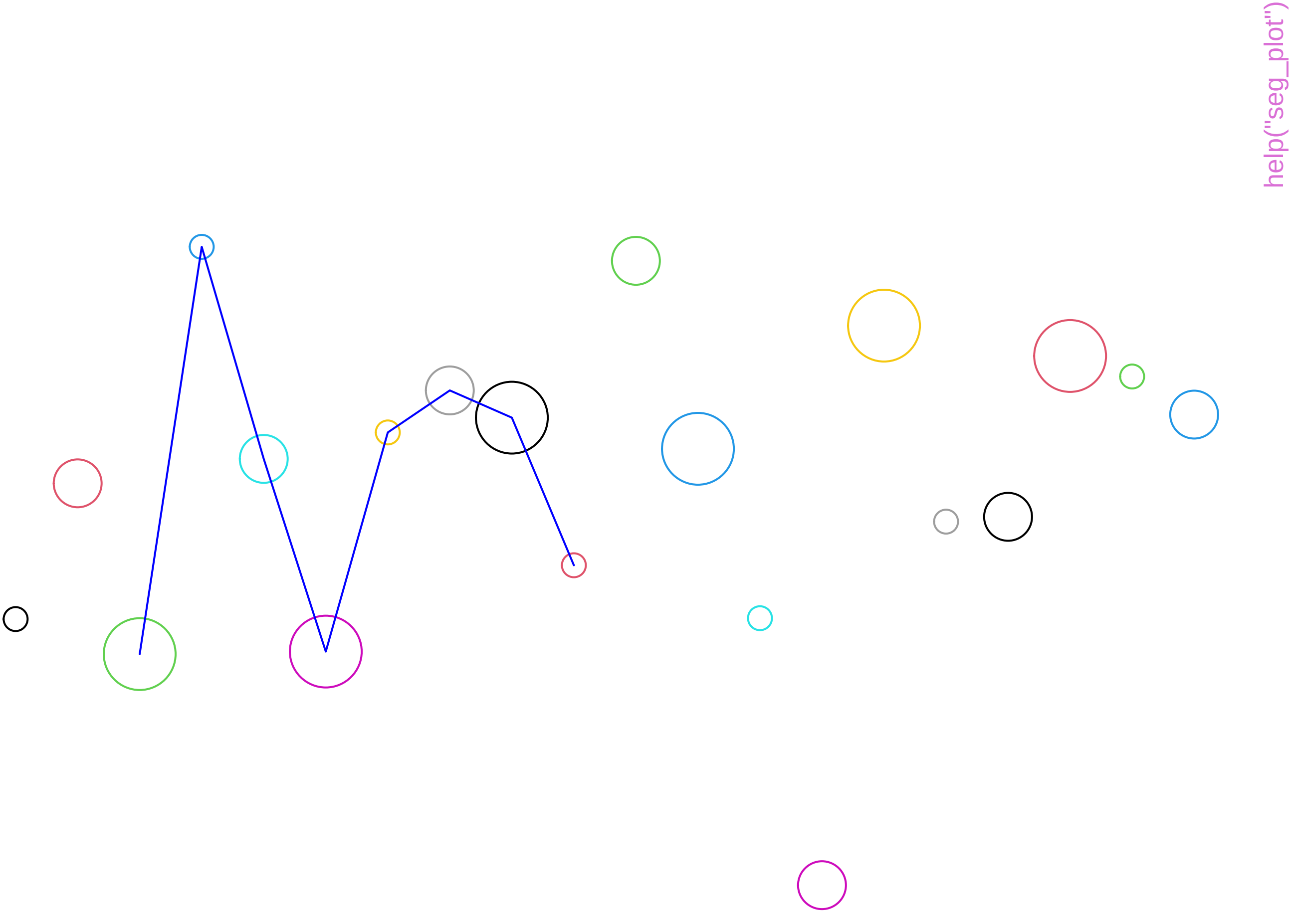

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("read_functions")

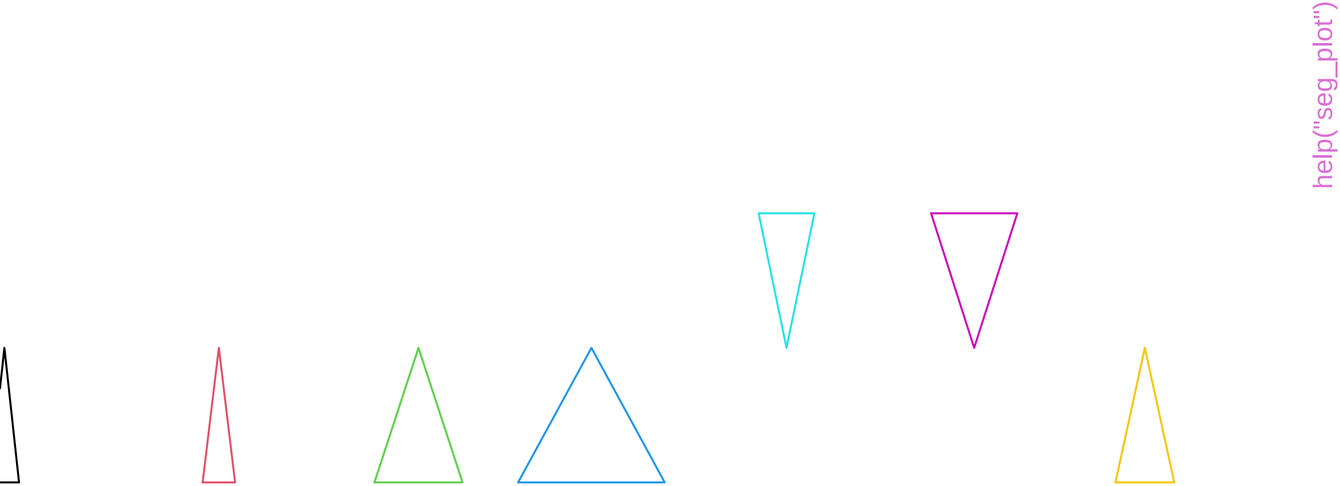

B bacilliformis
B grahamii
B henselae
B quintana
500 kb
help("read_functions")

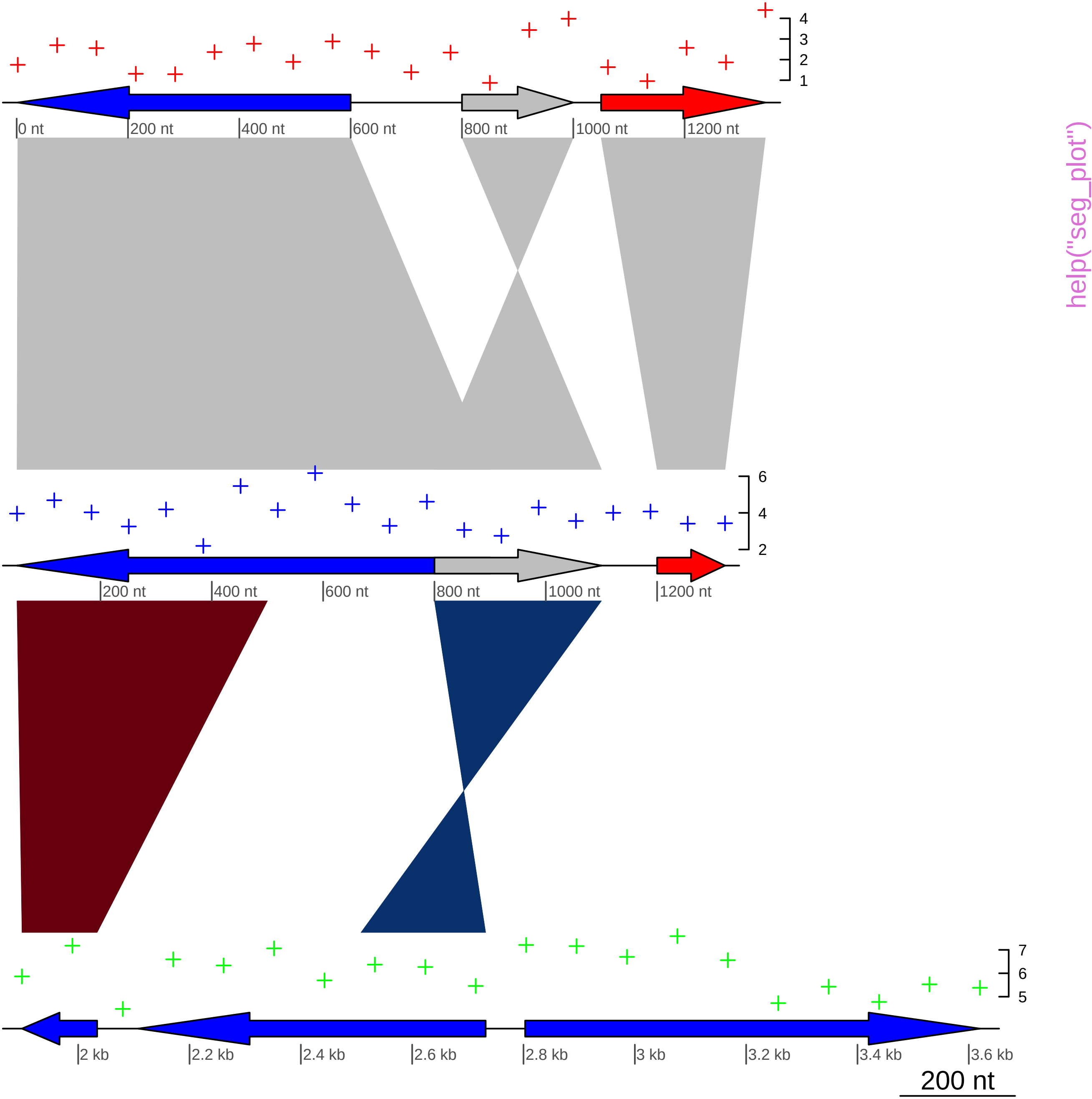

BH
BQ
5 kb
help("read_functions")


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

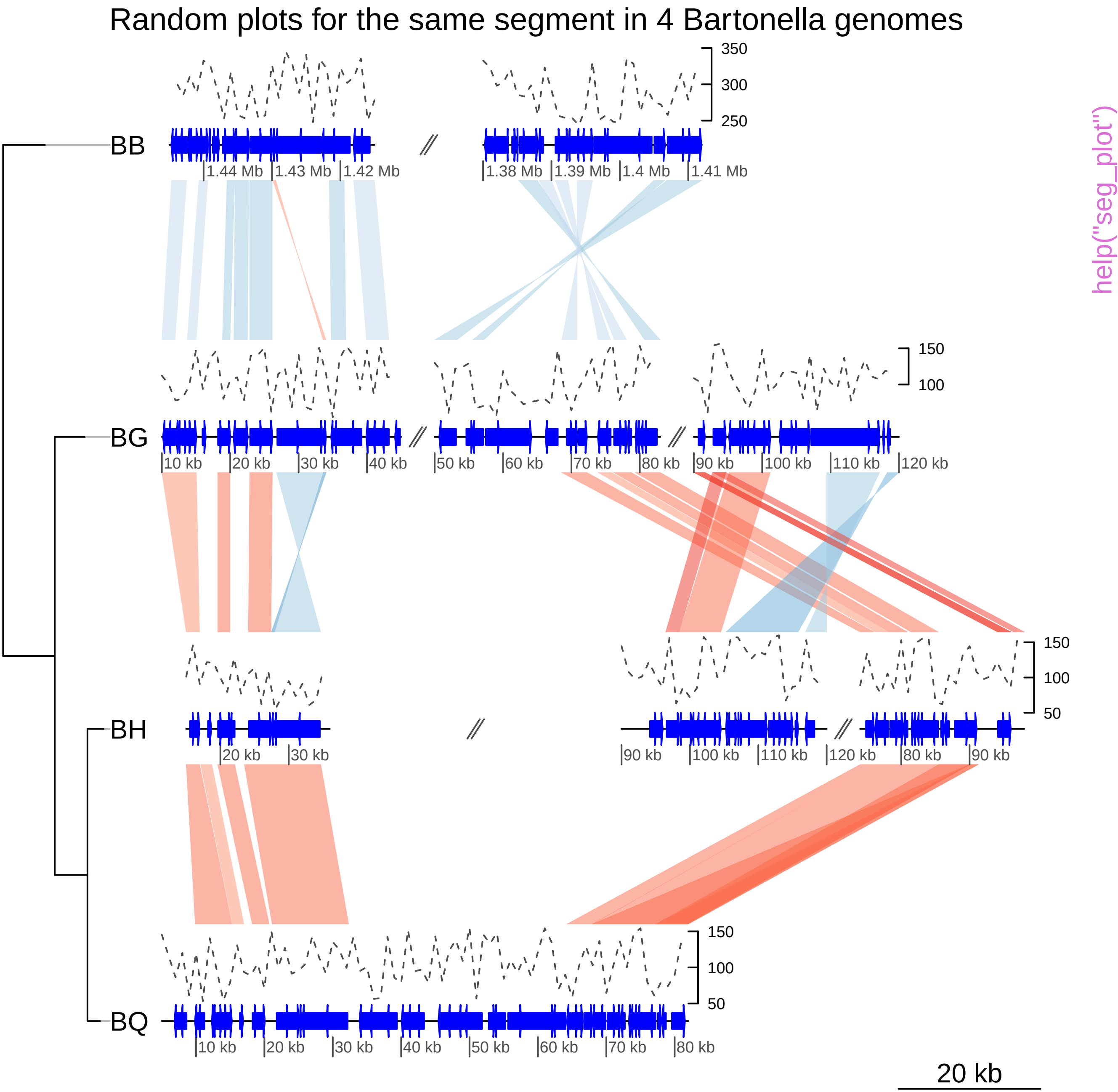

B_bacilliformis
B_grahamii
B_henselae
B_quintana
500 kb
help("reverse")

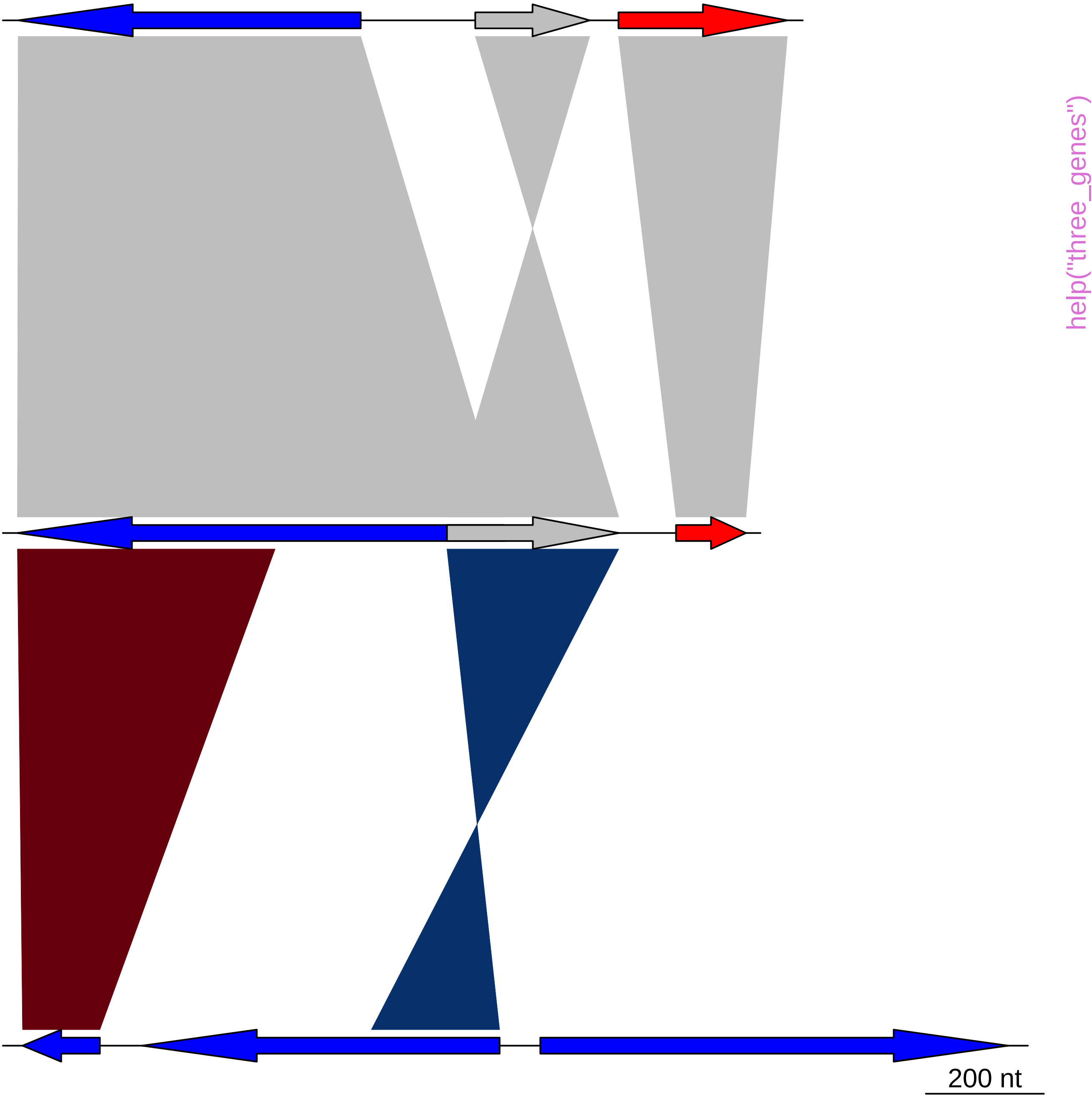

help("seg_plot")

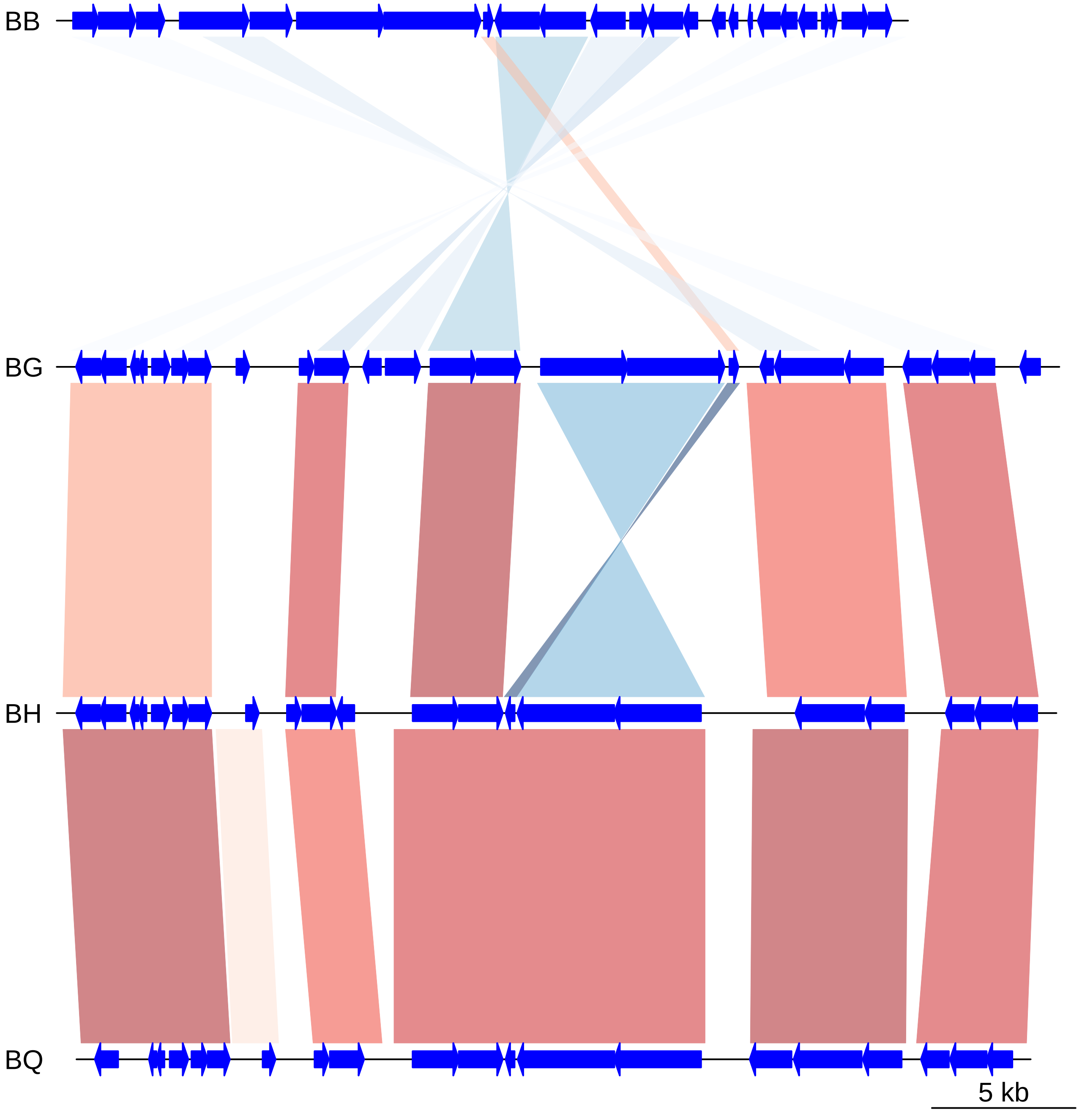

help("seg_plot")



4
3
2
1
0 nt
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
help("seg_plot")
6
4
2
200 nt
400 nt
600 nt
800 nt
1000 nt
1200 nt
7
6
5
2 kb
2.2 kb
2.4 kb
2.6 kb
2.8 kb
3 kb
3.2 kb
3.4 kb
3.6 kb
200 nt


Random plots for the same segment in 4 Bartonella genomes
350
300
250
BB
1.44 Mb
1.43 Mb
1.42 Mb
1.38 Mb
1.39 Mb
1.4 Mb
1.41 Mb
150
100
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
150
100
50
BH
20 kb
30 kb
90 kb
100 kb
110 kb
120 kb
80 kb
90 kb
150
100
50
BQ
10 kb
20 kb
30 kb
40 kb
50 kb
60 kb
70 kb
80 kb
20 kb
help("seg_plot")


help("three_genes")
200 nt



help("trim")