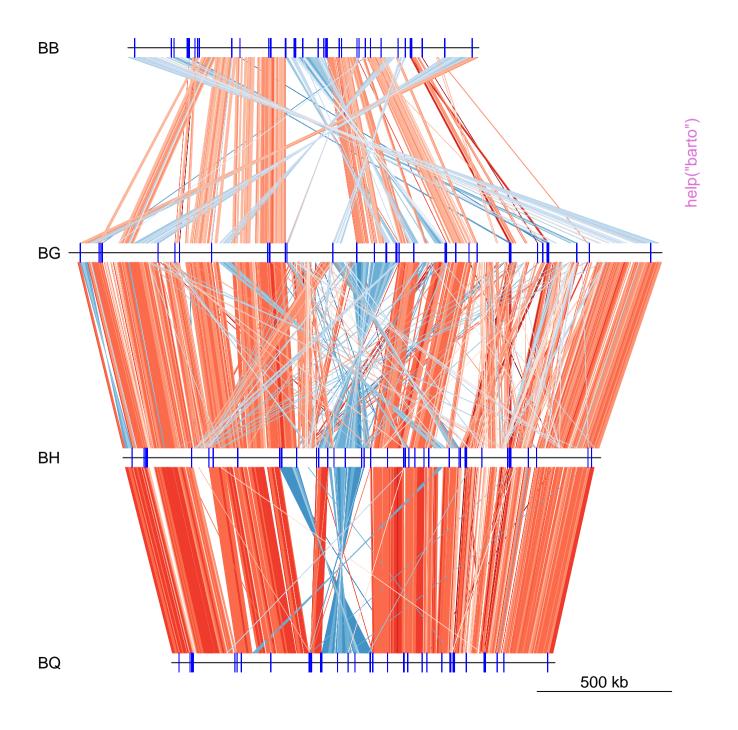
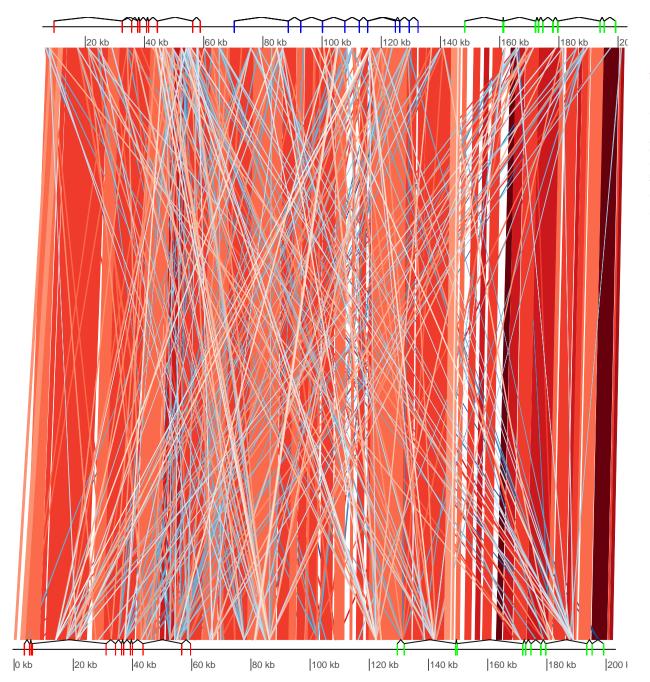


help("annotation")

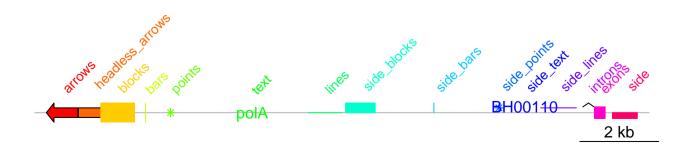
help("apply\_color\_scheme")



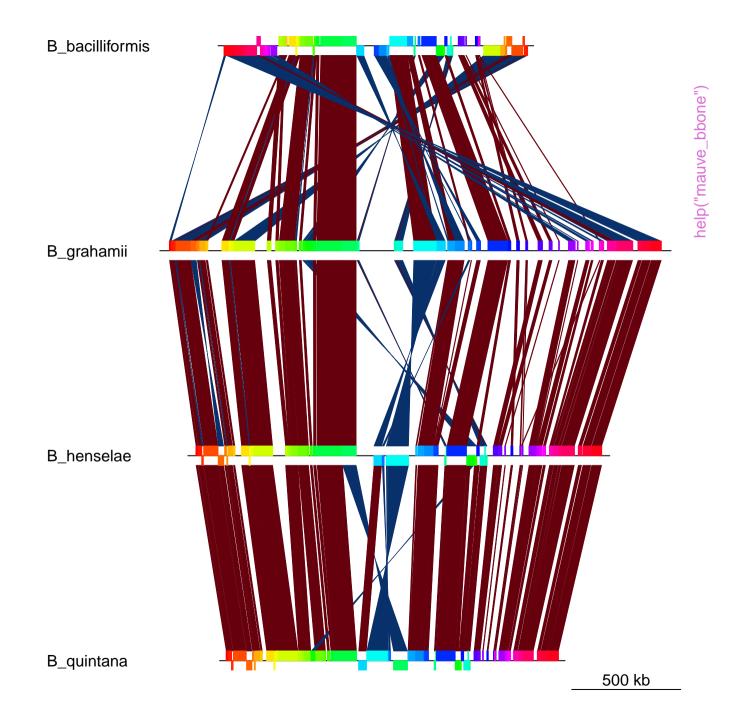


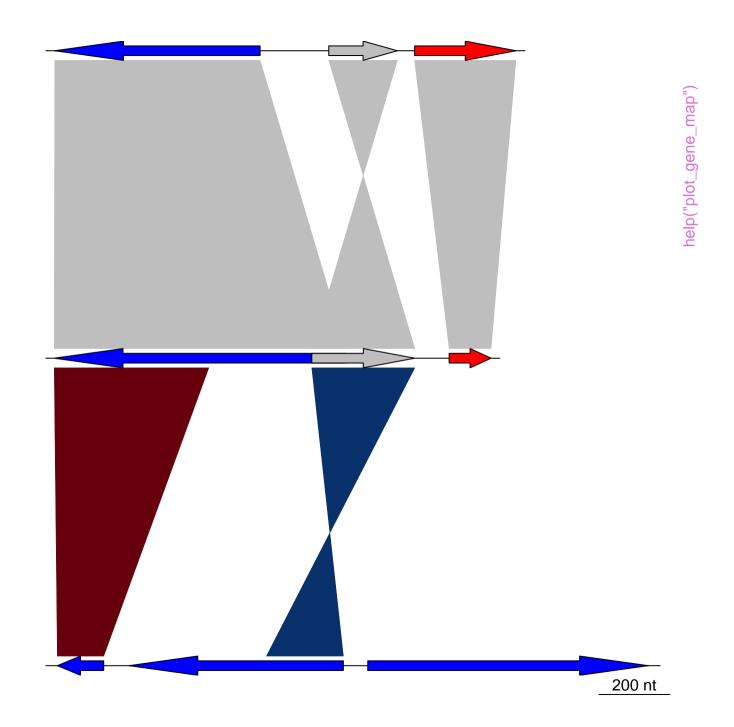
help("chrY\_subseg")

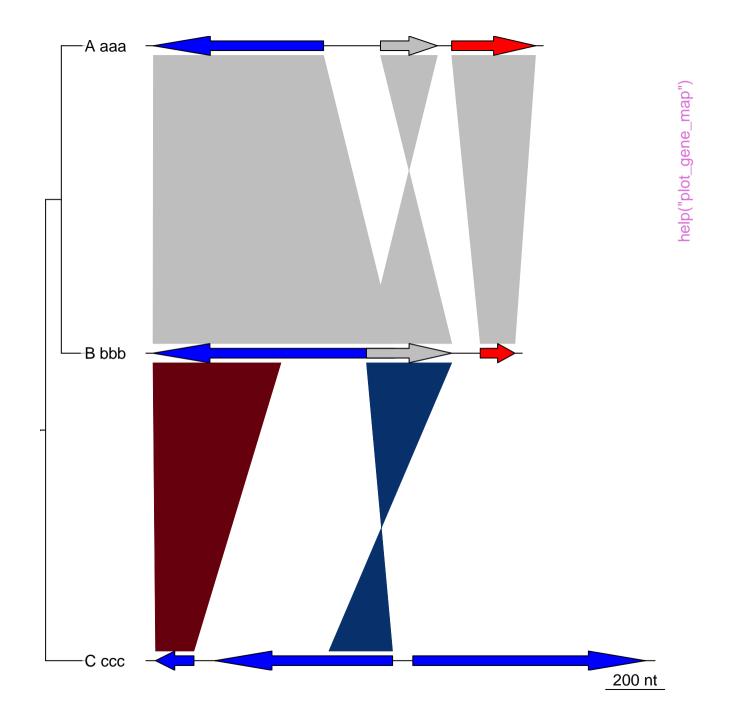


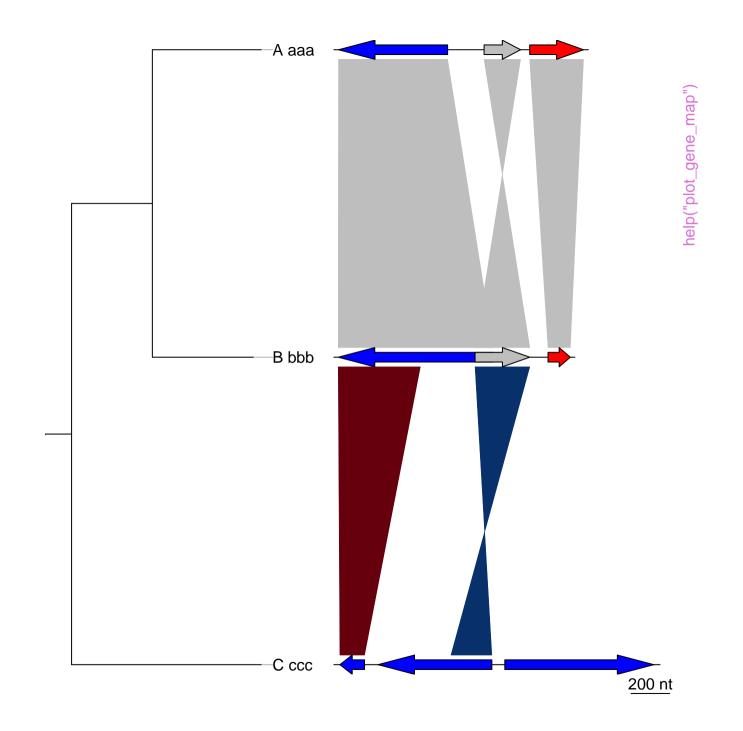


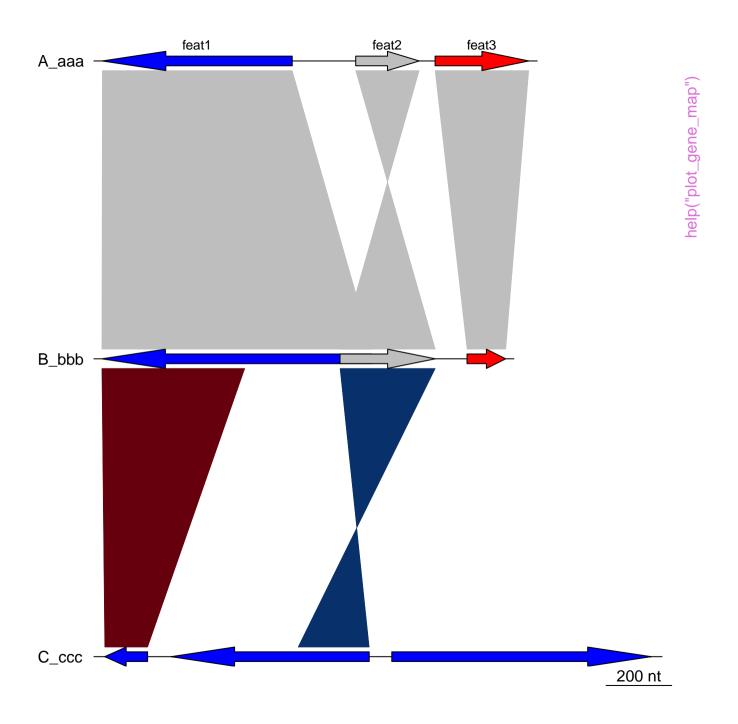
help("genoPlotR-package")

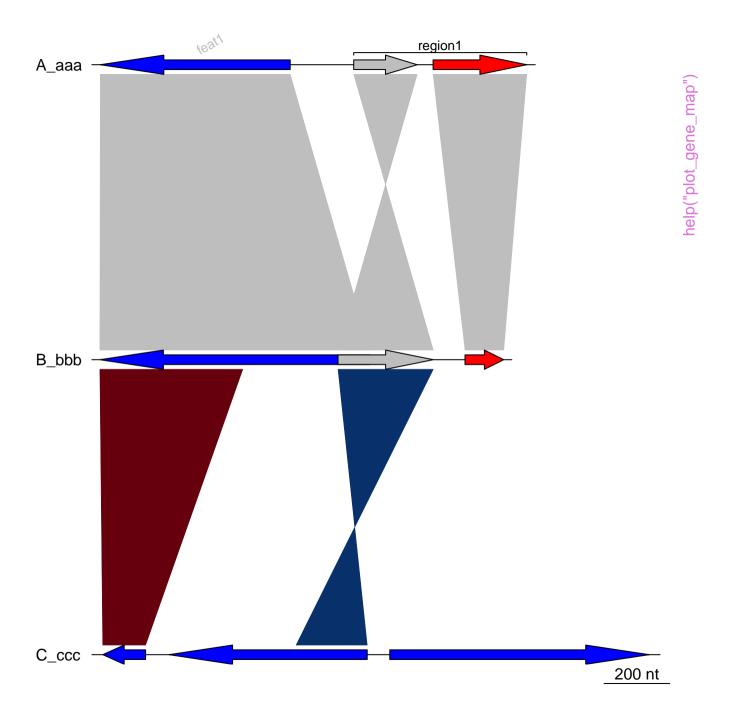


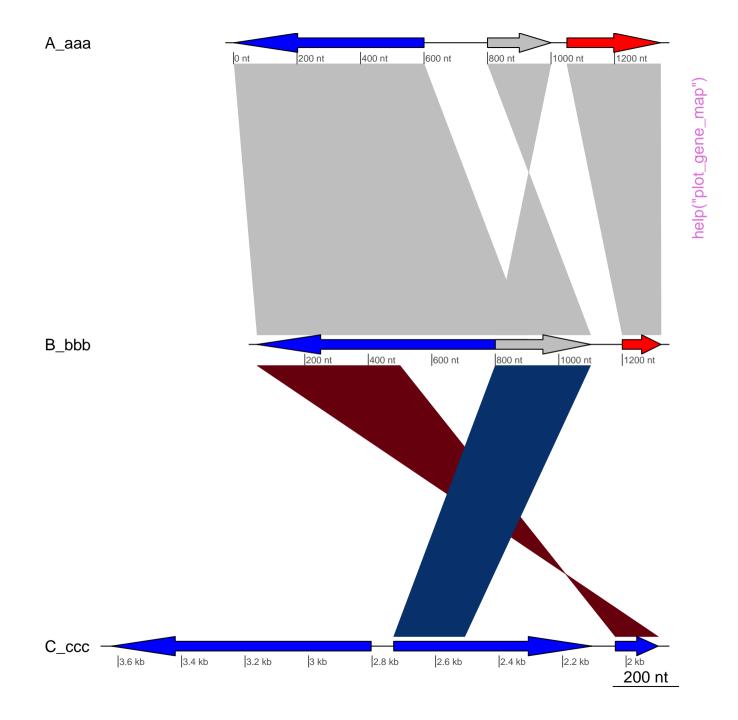


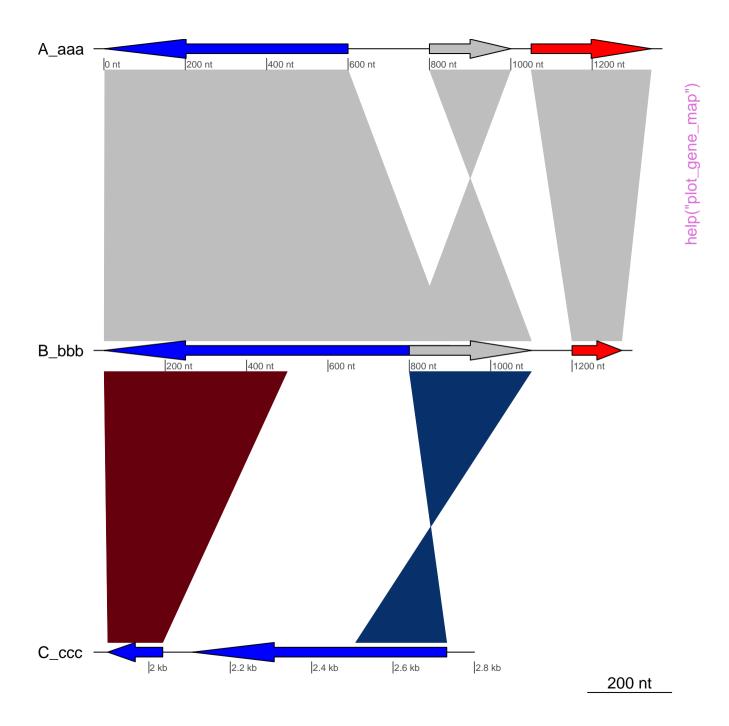


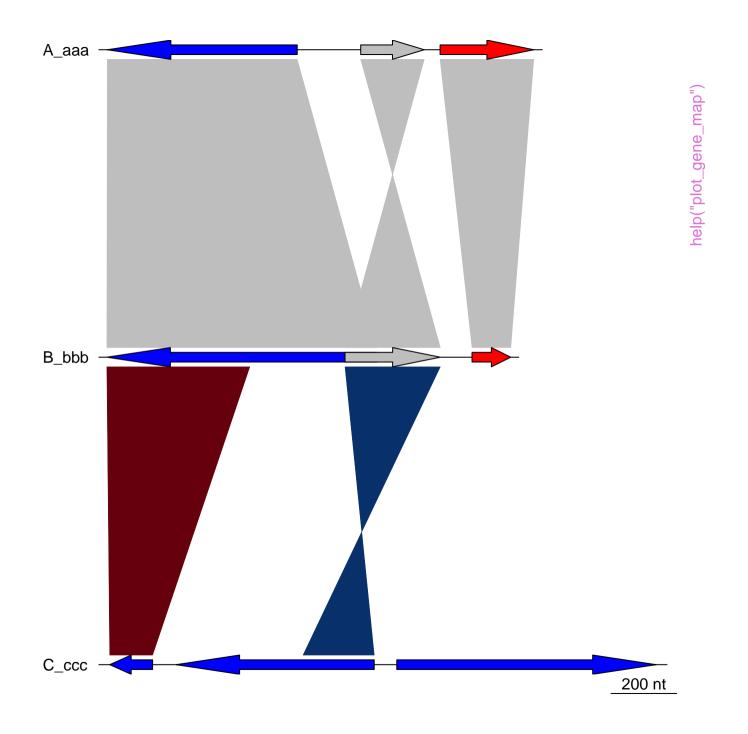


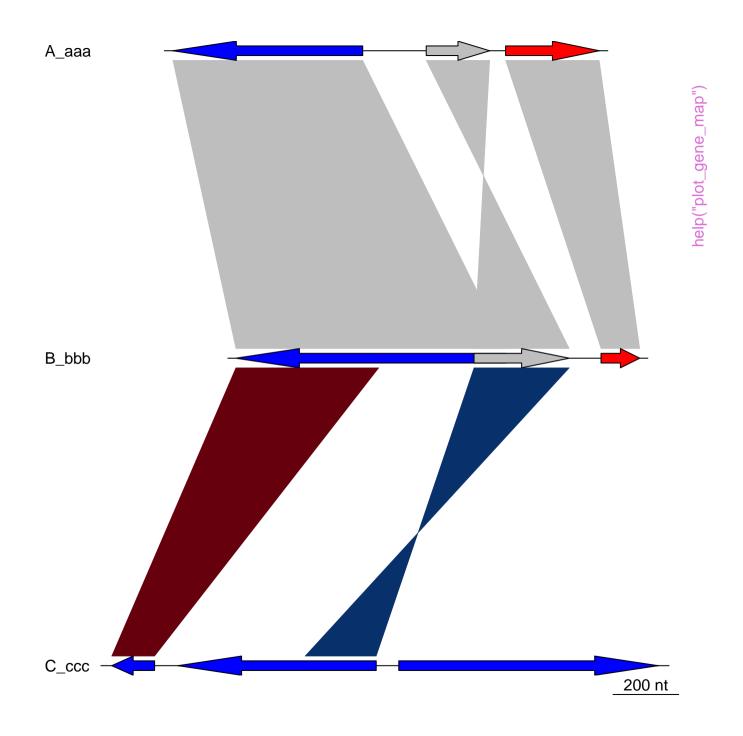


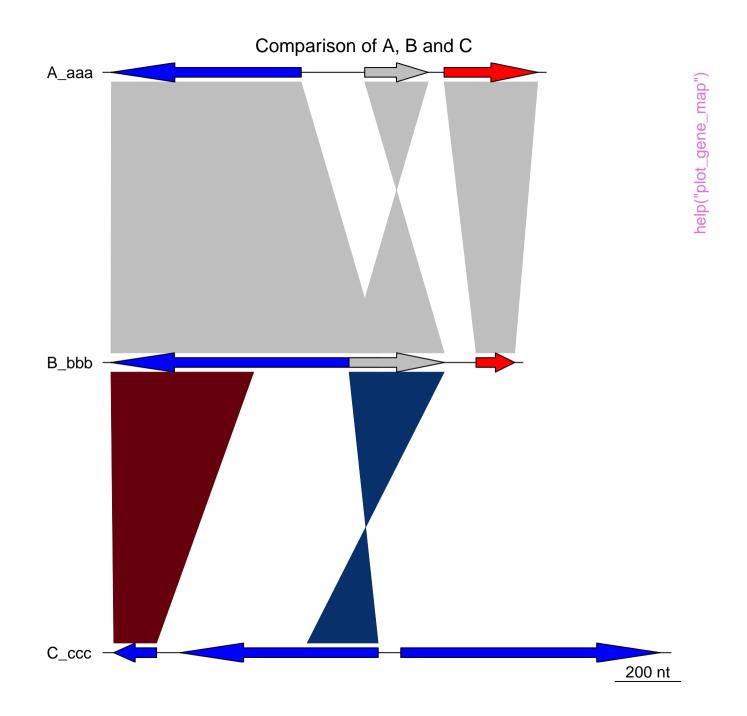


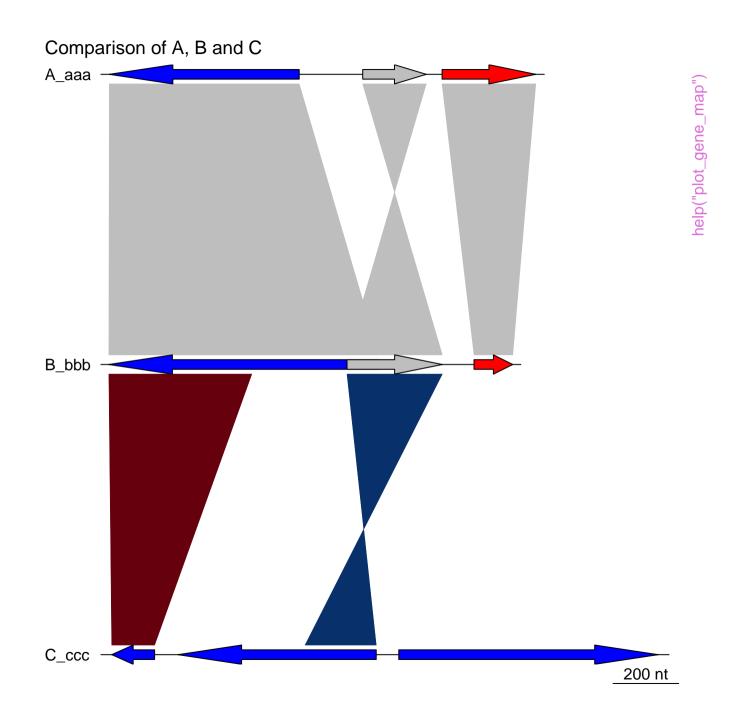


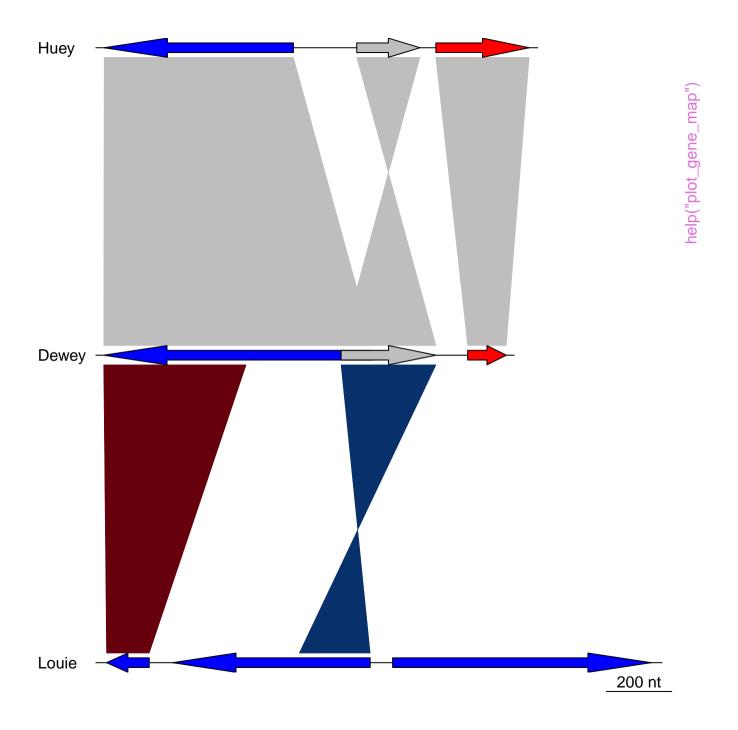


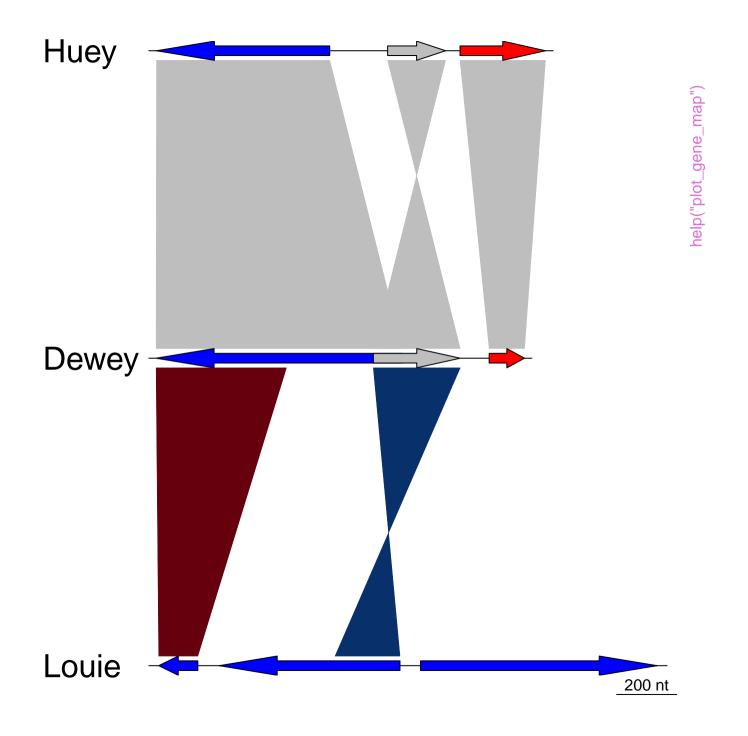


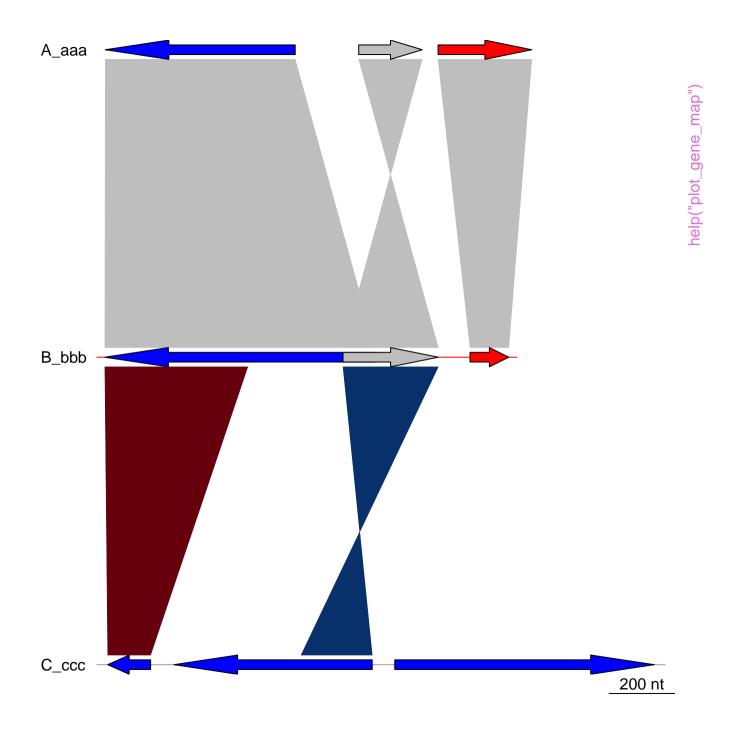


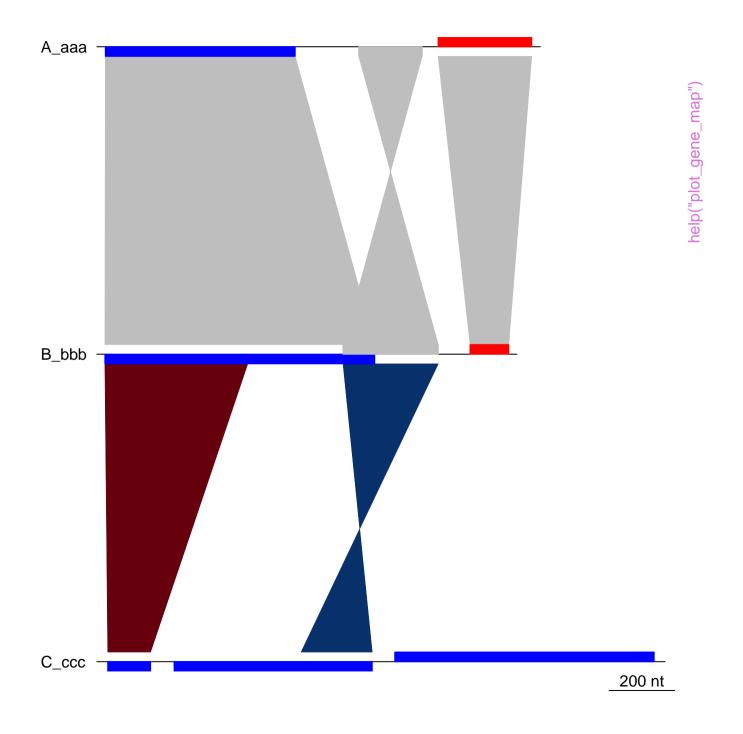


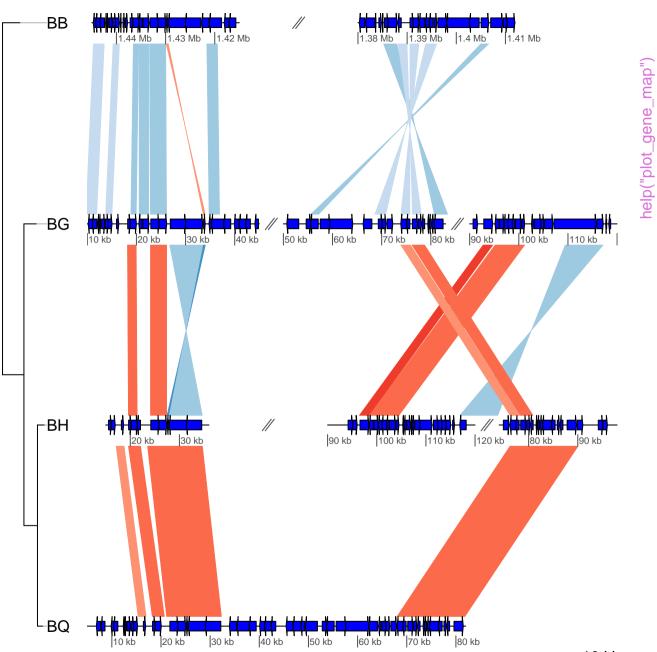


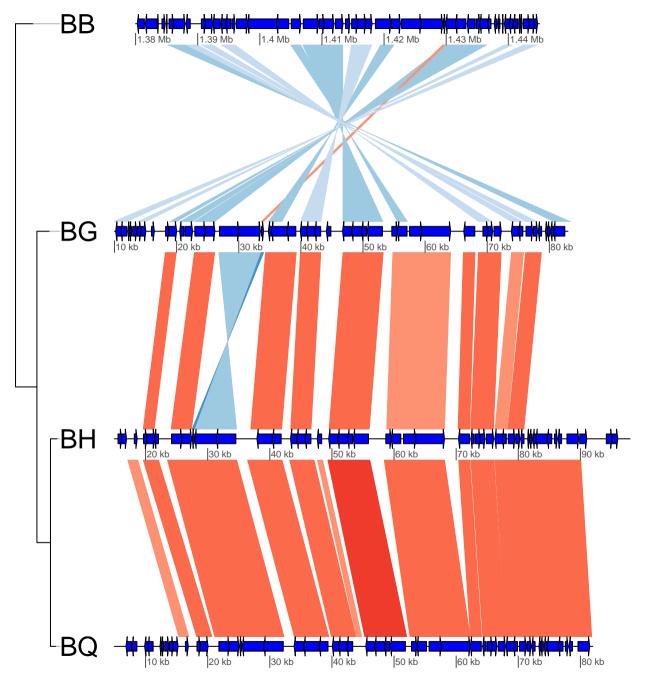










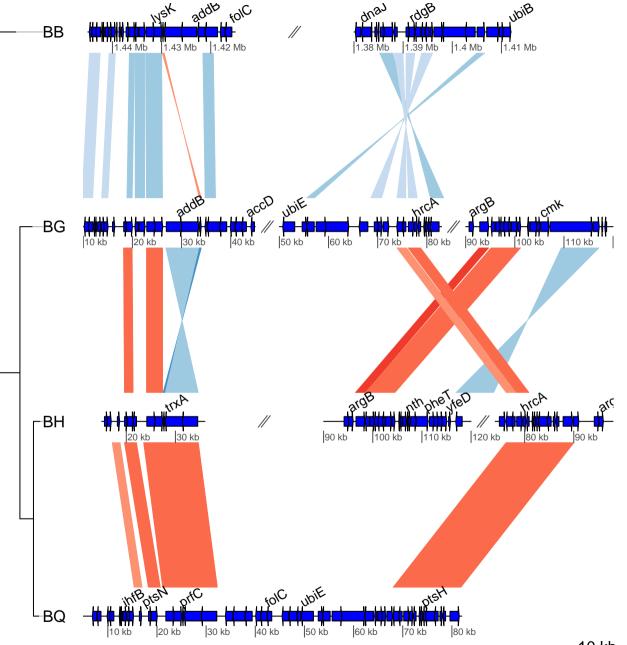


50 kb

40 kb

30 kb

10 kb 20 kb



help("plot\_gene\_map")

