

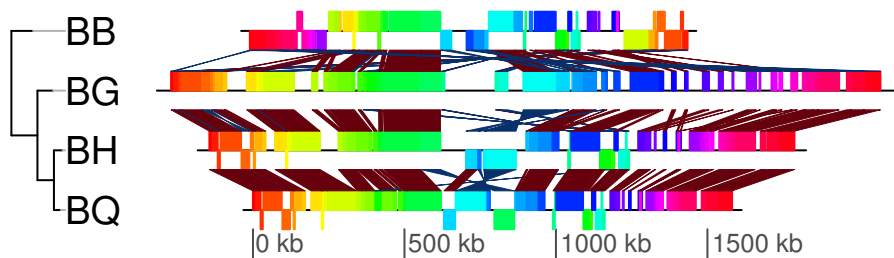
A

```

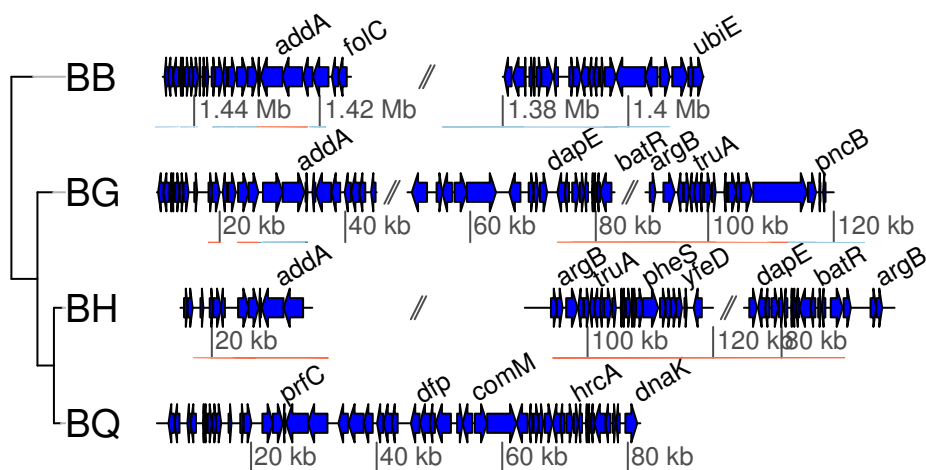
dna_seg1 <- read_dna_seg_from_tab("myTab1.tab")
dna_seg2 <- read_dna_seg_from_file("myGbk.gbk")
dna_seg3 <- read_dna_seg_from_file("myEmbl.embl")
comp1 <- read_comparison_from_tab("myTab2.tab")
comp2 <- read_comparison_from_blast("myBlast.blast")
tree <- newick2phylog("(A:2,(B:1,C:0.5):0.8);")
plot_gene_map(dna_segs=list(dna_seg1, dna_seg2, dna_seg3),
               comparisons=list(comp1, comp2), tree=tree)

```

B



C



D

