

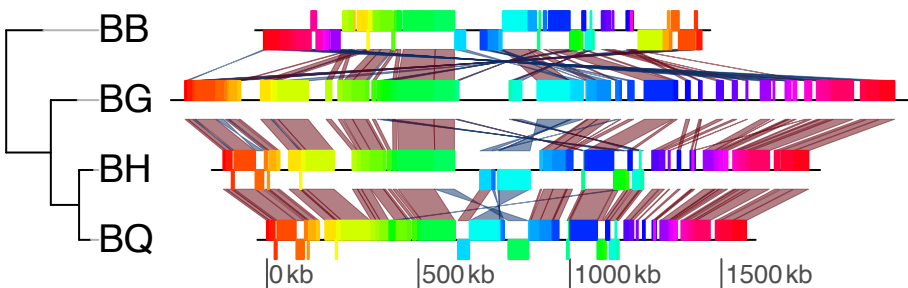
**A**

```

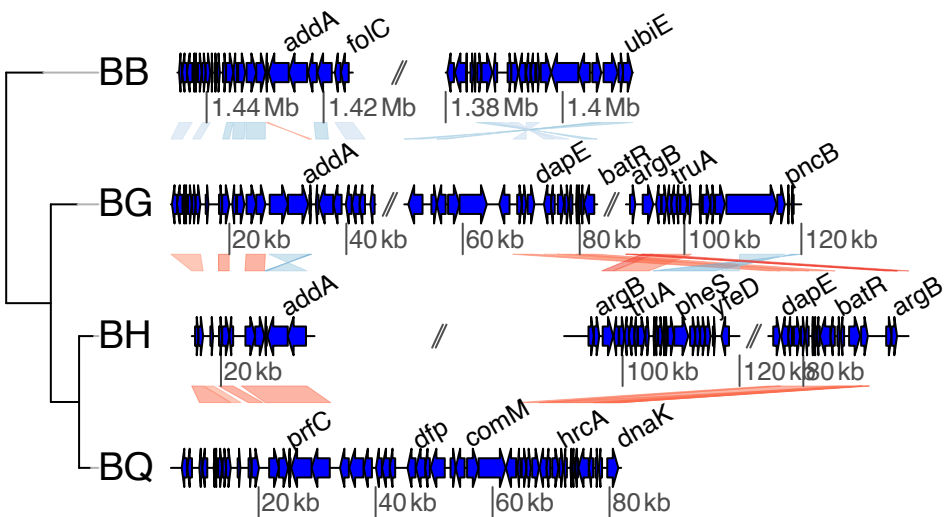
dna_seg1<-read_dna_seg_from_file("myGbk.gbk")
comp1<-read_comparison_from_blast("myBlast.blast")
tree<-newick2phylog("(A:2,(B:1,C:0.5):0.8);")
plot_gene_map(dna_segs=list(dna_seg1,dna_seg2,dna_seg3),
  comparisons=list(comp1,comp2),tree=tree)

```

**B**



**C**



**D**

