

A

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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)

```

