NPD

Micro-synteny analysis using sub genomic regions (50 kbps)n from Fungi Ensembl database. The input files are results from the progressive alignment using the Mauve software. Install packages:

```
install.packages("ade4")
install.packages("grid")
install.packages("genoPlotR")
```

"'Call packages from library

```
library(ade4)
```

```
## Warning: package 'ade4' was built under R version 4.1.1
```

```
library(grid)
library(genoPlotR)
```

Call .backbone file from directory

```
bone_file <- "/Users/lavinialavin/Desktop/Ejemplos R/Genomica/npd_alin_7jun.backbone"
```

"'Determine the reference genome (longest genome is used as reference, in this case N. crassa genome)

```
bbone <- read_mauve_backbone(bone_file, ref=6, gene_type = "side_blocks", header = TRUE, filter_low = 0
```

Labels dna_segs objects using the species names.

```
names <- c("B_bas", "M_ory", "M_bru", "M_maj", "M_rob", "M_acr", "M_ril", "M_alb", "M_ani", "M_gui", "T
names(bbone$dna_segs)<-names
```

Attach objects to the bbone file.

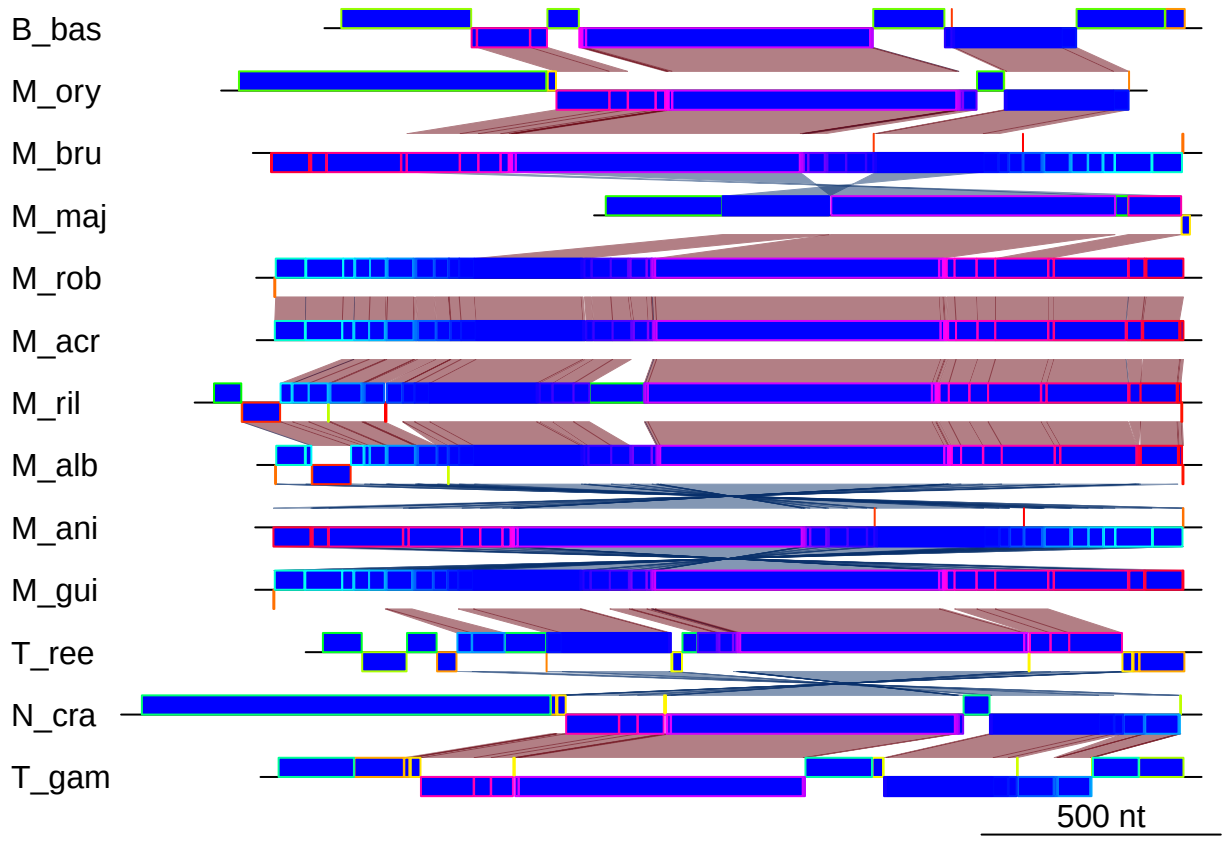
```
dna_segs<-(bbone$dna_segs)
comparisons<-(bbone$comparisons)
```

Calculate the genome lengths.

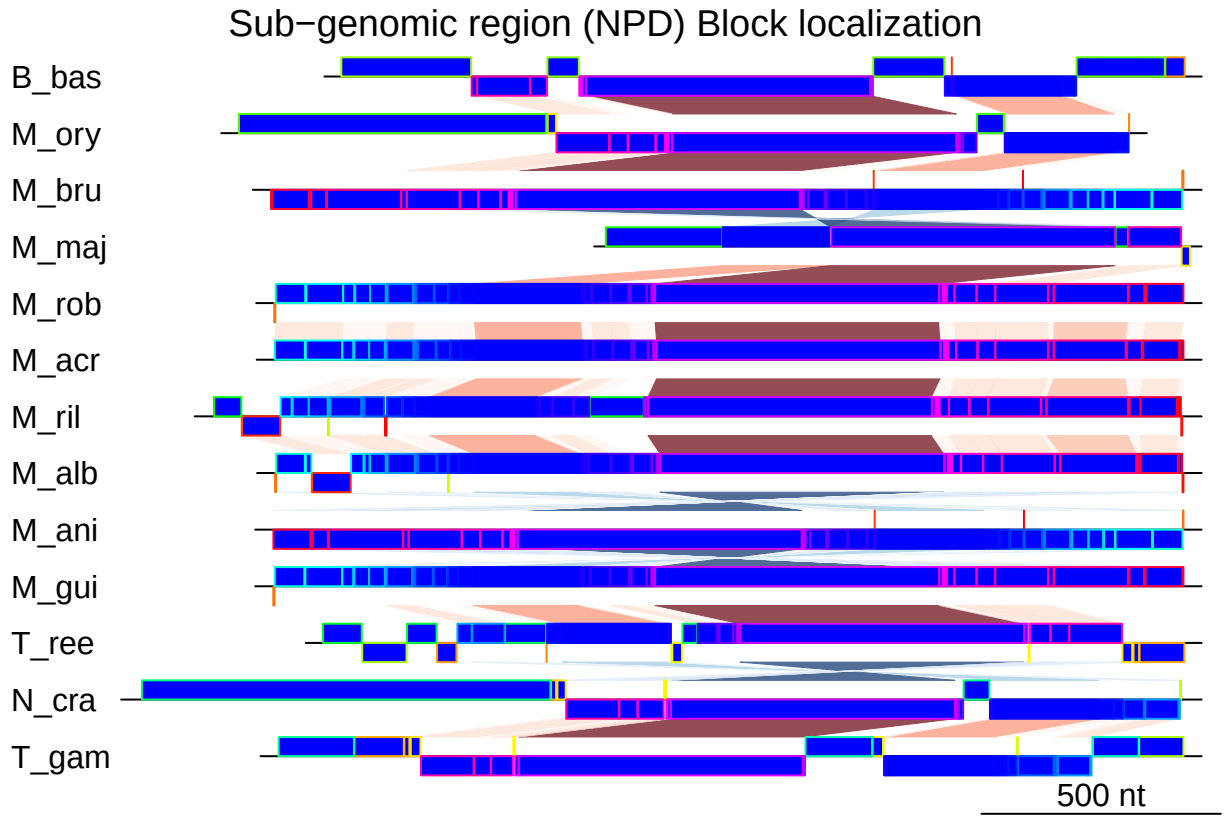
```
for (i in 1:length(bbone$comparisons)){
  cmp <- bbone$comparisons[[i]]
  bbone$comparisons[[i]]$length <-
    abs(cmp$end1 - cmp$start1) + abs(cmp$end2 - cmp$start2)
}
```

Initial plot, illustrates the comparison on the identified blocks.

```
plot_gene_map(dna_segs=bbone$dna_segs, comparisons=bbone$comparisons)
```




```
plot_gene_map(dna_segs=bbone$dna_segs,
              comparisons=bbone$comparisons,
              global_color_scheme=c("length", "increasing", "red_blue", 0.7),
              override_color_schemes=TRUE, main="Sub-genomic region (NPD) Block localization  ", scale="
```



Phylogenetic reconstruction using the .guide_tree file. Call file from directory.

```
tree<- "/Users/lavinialavin/Desktop/Ejemplos R/Genomica/npd_alin_7jun.guidetree"
```

Using the calculated distances from each node, the tree is reconstructed; to do this you have to copy-paste the distances from the file .guide_tree and label each sequence with the corresponding name of each species.

```
tree_demo <- newick2phylog("(M_maj:0.200819,(M_ory:0.256736,(N_cra:0.294616,(B_bas:0.230773,((T_gam:0.1
```

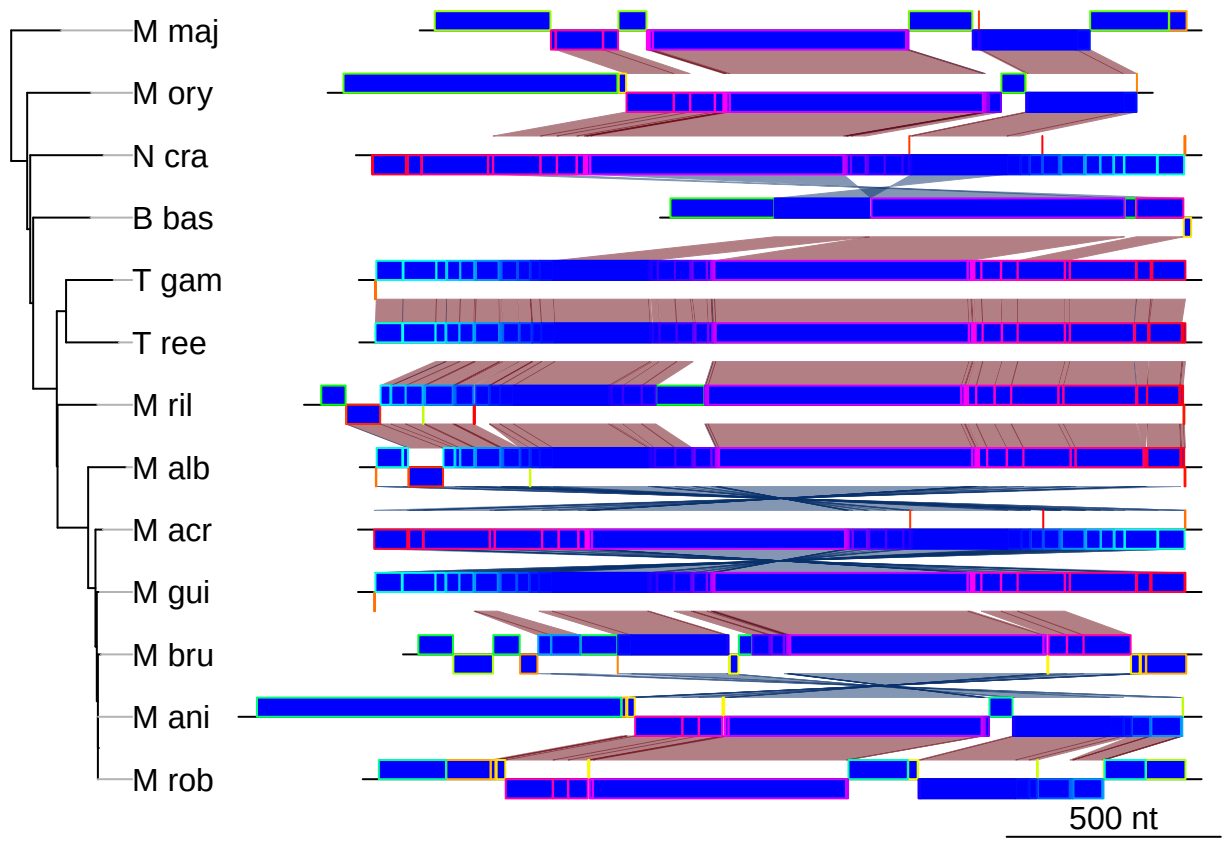
```
names <- c("M_maj", "M_ory", "N_cra", "B_bas", "T_gam", "T_ree", "M_ril", "M_alb","M_acr", "M_gui", "M_
names(dna_segs) <- names
```

Label “leaves”

```
tree_str <- readLines(tree_demo)
for (i in 1:length(names)){   tree_str <- gsub(paste("seq", i, sep=""), names[i], tree_str) }
tree <- newick2phylog(tree_demo)
```

Plot

```
plot_gene_map(dna_segs=dna_segs, comparisons=bbone$comparisons, tree=tree_demo)
```



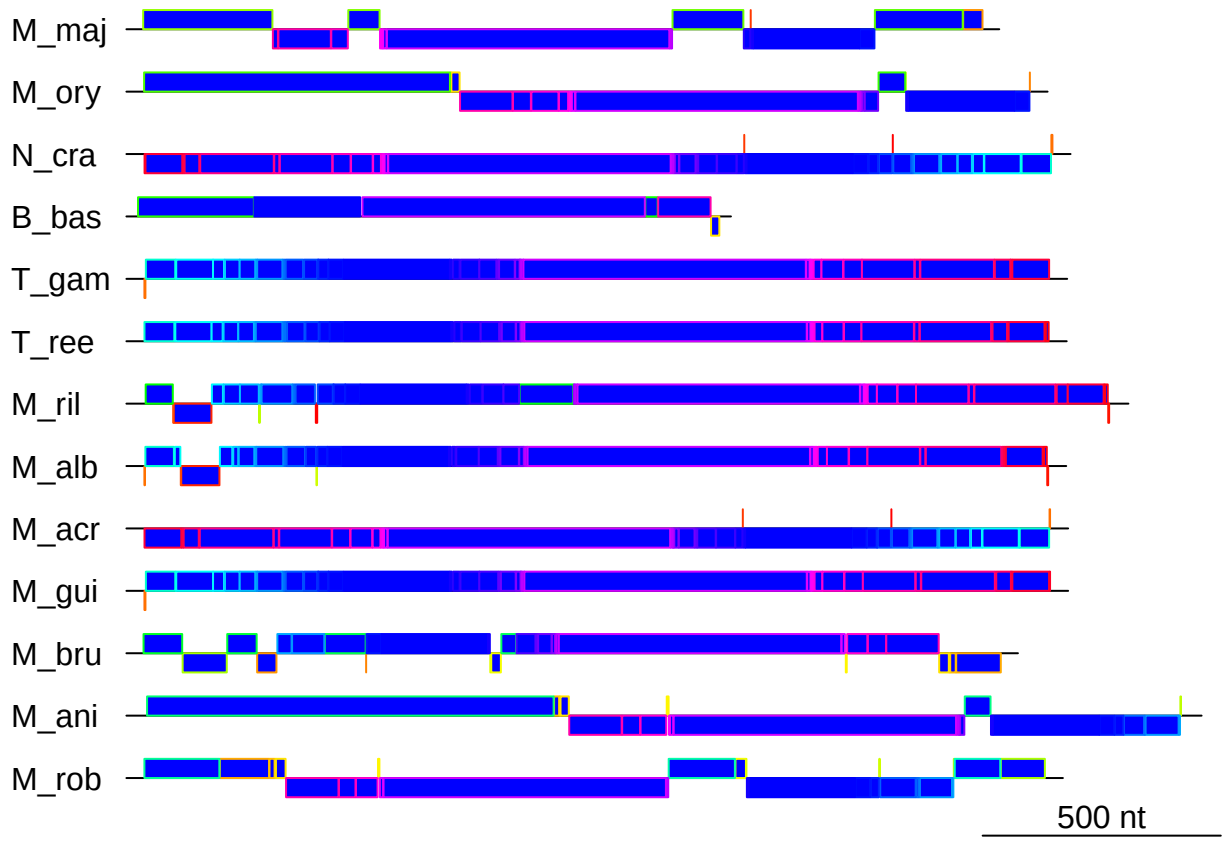
Delimit the sub-genomic regions with the xlims function.

```
xlims <- list(c( 1000, 2000, 3000, 17000),
              c(1000, 20000, 30000, 49000 ),
              c( 1000,20000,  30000, 49000),
              c(10000,  20000, 30000,  49000),
              c(10000, 20000, 30000, 49000),
              c( 10000,   20000, 30000,  49000),
              c( 10000, 20000, 30000, 49000),
              c( 10000, 20000, 30000, 49000),
              c(1000,20000, 30000,  49000 ),
              c(10000, 20000, 30000, 49000),
              c(10000, 20000, 30000, 49000),
              c(10000, 20000, 30000, 49000),
              c(10000, 20000, 30000, 49000))
```

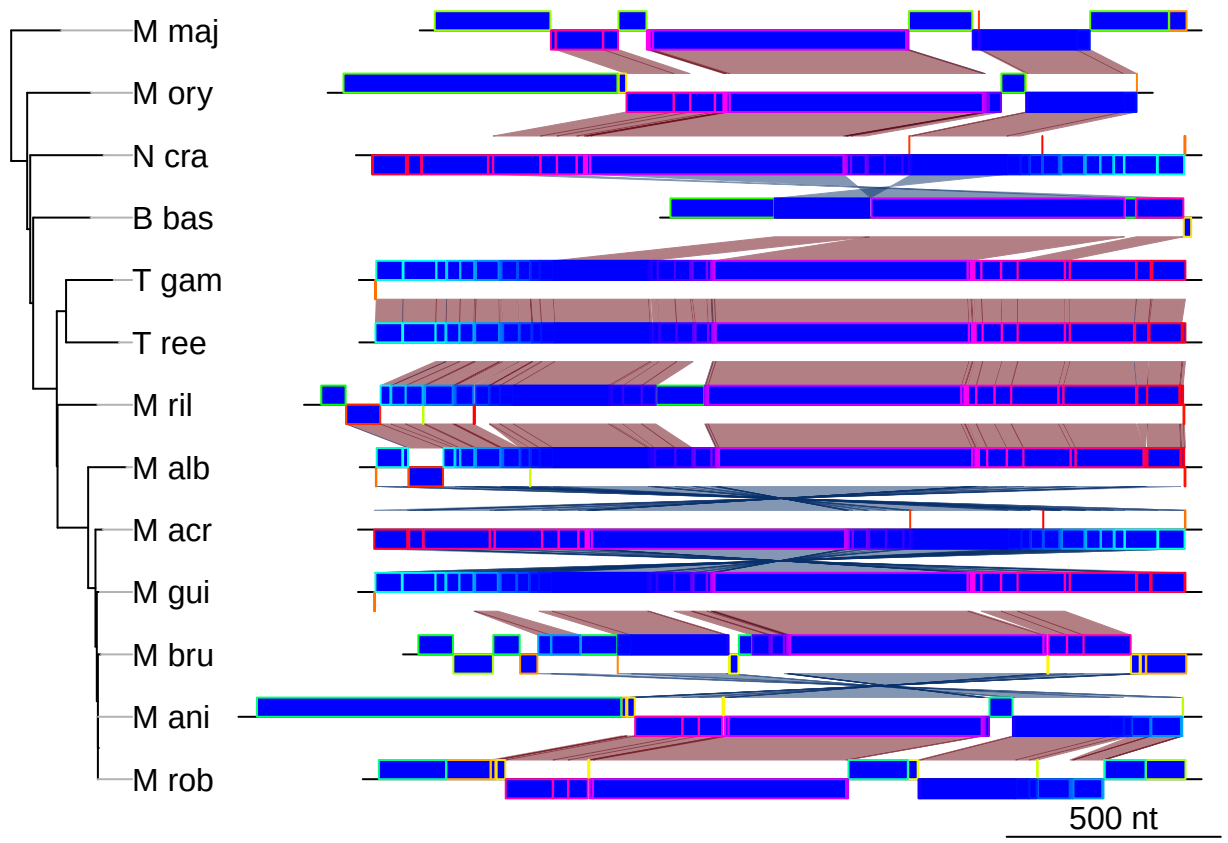
Plot on the compared genes using the whole subgenomic region (xlims=null)

```
plot_gene_map(dna_segs, comparisons = NULL,
              tree = NULL,
              tree_width = NULL,
              tree_branch_labels_cex = NULL,
              tree_scale = FALSE,
              legend = NULL,
              annotations = NULL,
              annotation_height = 1,
```

```
            annotation_cex = 0.8,
            seg_plots=NULL, # user-defined plots seg_plot_height=3, # height of plots (in lines) seg_
            xlims = NULL,
            offsets = NULL,
            minimum_gap_size = 0.05,
            fixed_gap_length = FALSE,
            limit_to_longest_dna_seg = TRUE,
            main = NULL,
            main_pos = "centre",
            dna_seg_labels = NULL,
            dna_seg_label_cex=1,
            dna_seg_label_col="black",
            gene_type = NULL,
            arrow_head_len = 200,
            dna_seg_line = TRUE,
            scale = TRUE,
            n_scale_ticks=7,
            scale_cex=0.6,
            global_color_scheme = c("auto", "auto", "blue_red", 0.5), override_color_schemes = FALSE,
            plot_new=TRUE,
            debug = 0)
```




```
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons, tree = tree_demo)
```



Calculate the diferences among blocks identified by Mauve.

```
df1 <- data.frame(name=c("feat1", "feat2", "feat3"), start=c(18000, 22000, 24000),
                  end=c(20000, 23000, 30000), strand=c(-1, 1, -1), col=c("red", "pink", "grey"))
dna_seg1 <- dna_seg(df1)
str(dna_seg1)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 1 -1
##  $ col      : chr  "red" "pink" "grey"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df2 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(15000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, 1, -1), col=c(
dna_seg2 <- dna_seg(df2)
str(dna_seg2)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
```

```
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  15000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 1 -1
##  $ col      : chr  "blue" "grey" "grey"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df3 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep

dna_seg3 <- dna_seg(df3)
str(dna_seg3)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "blue" "blue" "blue"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df4 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep

dna_seg4 <- dna_seg(df4)
str(dna_seg4)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "green" "green" "green"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df5 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
```

```
dna_seg5 <- dna_seg(df5)
str(dna_seg5)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "yellow" "yellow" "yellow"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df6 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(5000, 10000, 24000), end=c(20000, 23000, 25000), strand=c(-1, -1, 1), col=rep

dna_seg6 <- dna_seg(df6)
str(dna_seg6)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  5000 10000 24000
##  $ end      : num  20000 23000 25000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "cyan" "cyan" "cyan"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df7 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(20000, 22000, 30000), end=c(25000, 30000, 40000), strand=c(-1, -1, 1), col=re

dna_seg7 <- dna_seg(df7)
str(dna_seg7)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  20000 22000 30000
##  $ end      : num  25000 30000 40000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "pink" "pink" "pink"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
```

```
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df8 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
dna_seg8 <- dna_seg(df8)
str(dna_seg8)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "tan" "tan" "tan"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df9 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
dna_seg9 <- dna_seg(df9)
str(dna_seg9)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "violet" "violet" "violet"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df10 <- data.frame(name=c("feat1", "feat2", "feat3"),
                  start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
dna_seg10 <- dna_seg(df10)
str(dna_seg10)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "green4" "green4" "green4"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
```

```
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df11 <- data.frame(name=c("feat1", "feat2", "feat3"),
                   start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
dna_seg11 <- dna_seg(df11)
str(dna_seg11)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "purple" "purple" "purple"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df12 <- data.frame(name=c("feat1", "feat2", "feat3"),
                   start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
dna_seg12 <- dna_seg(df12)
str(dna_seg12)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "purple" "purple" "purple"
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
df13 <- data.frame(name=c("feat1", "feat2", "feat3"),
                   start=c(18000, 22000, 24000), end=c(20000, 23000, 30000), strand=c(-1, -1, 1), col=rep
dna_seg13 <- dna_seg(df13)
str(dna_seg13)
```

```
## Classes 'dna_seg' and 'data.frame':  3 obs. of  11 variables:
##  $ name     : chr  "feat1" "feat2" "feat3"
##  $ start    : num  18000 22000 24000
##  $ end      : num  20000 23000 30000
##  $ strand   : num  -1 -1 1
##  $ col      : chr  "purple" "purple" "purple"
```

```
##  $ fill     : chr  "blue" "blue" "blue"
##  $ lty      : num  1 1 1
##  $ lwd      : num  1 1 1
##  $ pch      : num  8 8 8
##  $ cex      : num  1 1 1
##  $ gene_type: chr  "arrows" "arrows" "arrows"
```

```
dna_segs <- list(dna_seg1, dna_seg2, dna_seg3, dna_seg4, dna_seg5, dna_seg6, dna_seg7, dna_seg8, dna_seg
```

Calculate comparisons among blocks, center the interest gene (25 kbp)

```
df4 <- data.frame(start1=dna_seg1$start, end1=dna_seg1$end,
                  start2=dna_seg2$start,
                  end2=dna_seg2$end)
comparison1 <- comparison(df4)
df5 <- data.frame(start1=c(20000, 38000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison2 <- comparison(df5)

comparisons <- list(comparison1, comparison2)
df5 <- data.frame(start1=c(20000, 38000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison2 <- comparison(df5)

df9 <- data.frame(start1=c(20000, 38000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison4 <- comparison(df9)

df3 <- data.frame(start1=c(10000, 20000), end1=c(15000, 30000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison5 <- comparison(df3)

df2 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison6 <- comparison(df2)


df2 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison6 <- comparison(df2)
```

```
df7 <- data.frame(start1=c(30000, 34000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))

comparison3 <- comparison(df7)

df10 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison8 <- comparison(df10)


df11 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison9 <- comparison(df11)


df6 <- data.frame(start1=c(5000, 10000), end1=c(10000, 20000),
                   start2=c(18000, 20000),
                   end2=c(20000, 30000),
                   col=c("#67000D", "#08306B"))
comparison10 <- comparison(df6)


df1 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison7 <- comparison(df1)
df3 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison3 <- comparison(df3)
df12 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison12 <- comparison(df12)
df13 <- data.frame(start1=c(20000, 18000), end1=c(35000, 41000),
                  start2=c(18000, 20000),
                  end2=c(20000, 30000),
                  col=c("#67000D", "#08306B"))
comparison13 <- comparison(df13)
```

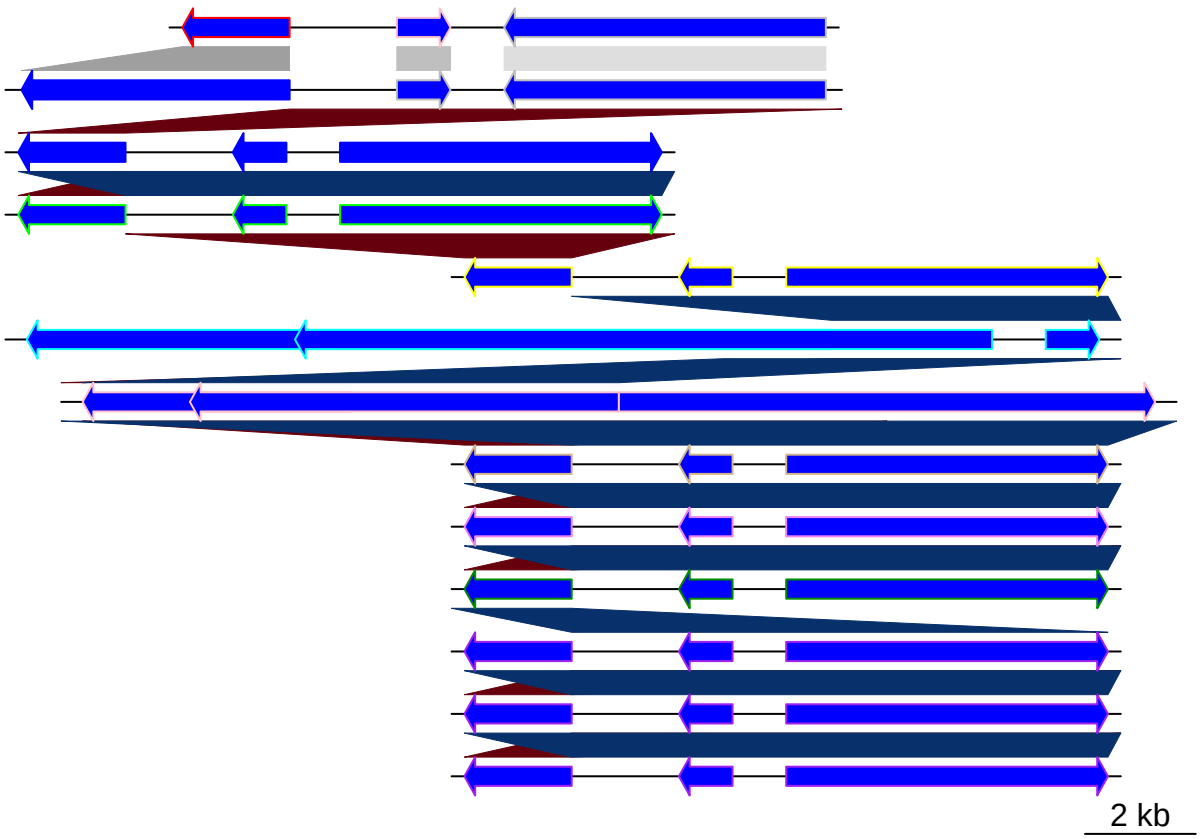
A new object is generated using the calculated comparisons.

```
comparisons <- list(comparison1, comparison2, comparison3, comparison4, comparison5, comparison6, compa

comparisons[[1]]$col <- apply_color_scheme(c(0.6, 0.5, 0.4), "red")
```

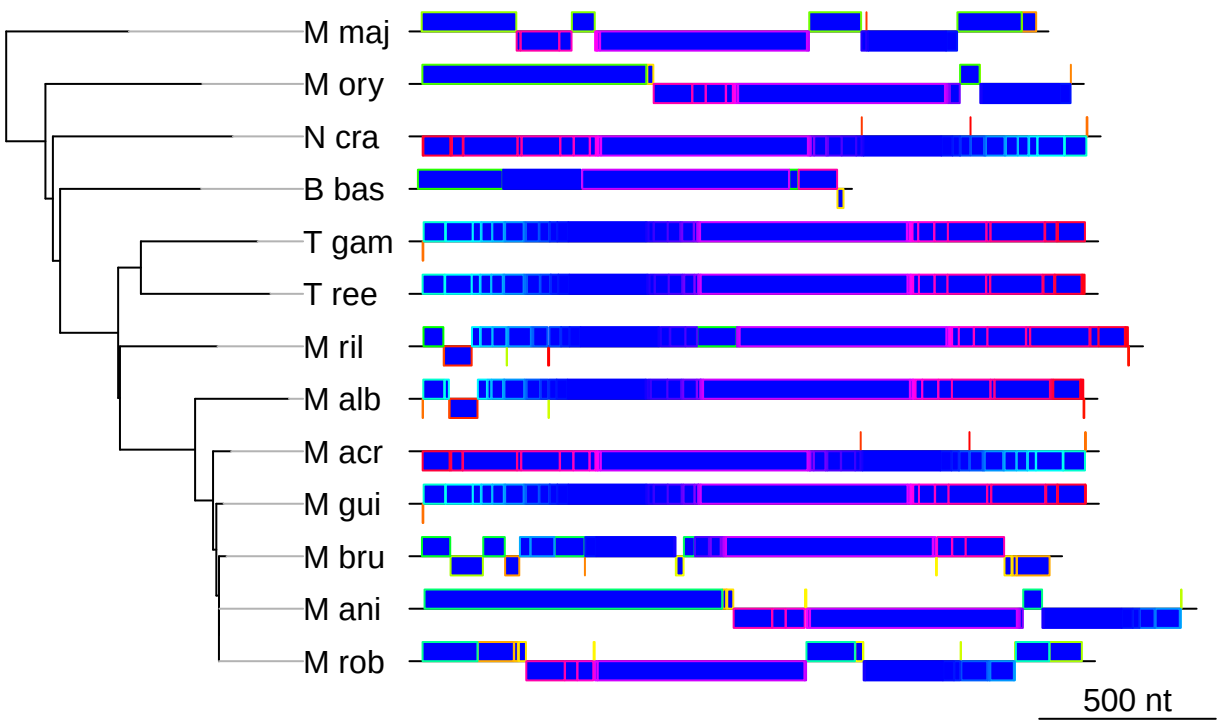
Plot without names or block labels, arrows indicate the different LCBs.

```
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons)
```




```
names(dna_segs)<- names
names(dna_segs=dna_segs) <-names
names(bbone$dna_segs) <- names

mid_pos <- middle(dna_segs[[1]])
annot <- annotation(x1=c(mid_pos[1], dna_segs[[1]]$end[2]),
                    x2=c(NA, dna_segs[[1]]$end[11]), text=c(dna_segs[[1]]$name[1], "region1"), rot=c(30
plot_gene_map(bbone$dna_seg, comparisons=comparisons,
              annotations=annot, annotation_height=1.3, tree=tree_demo, tree_width=2, main="Comparison
```



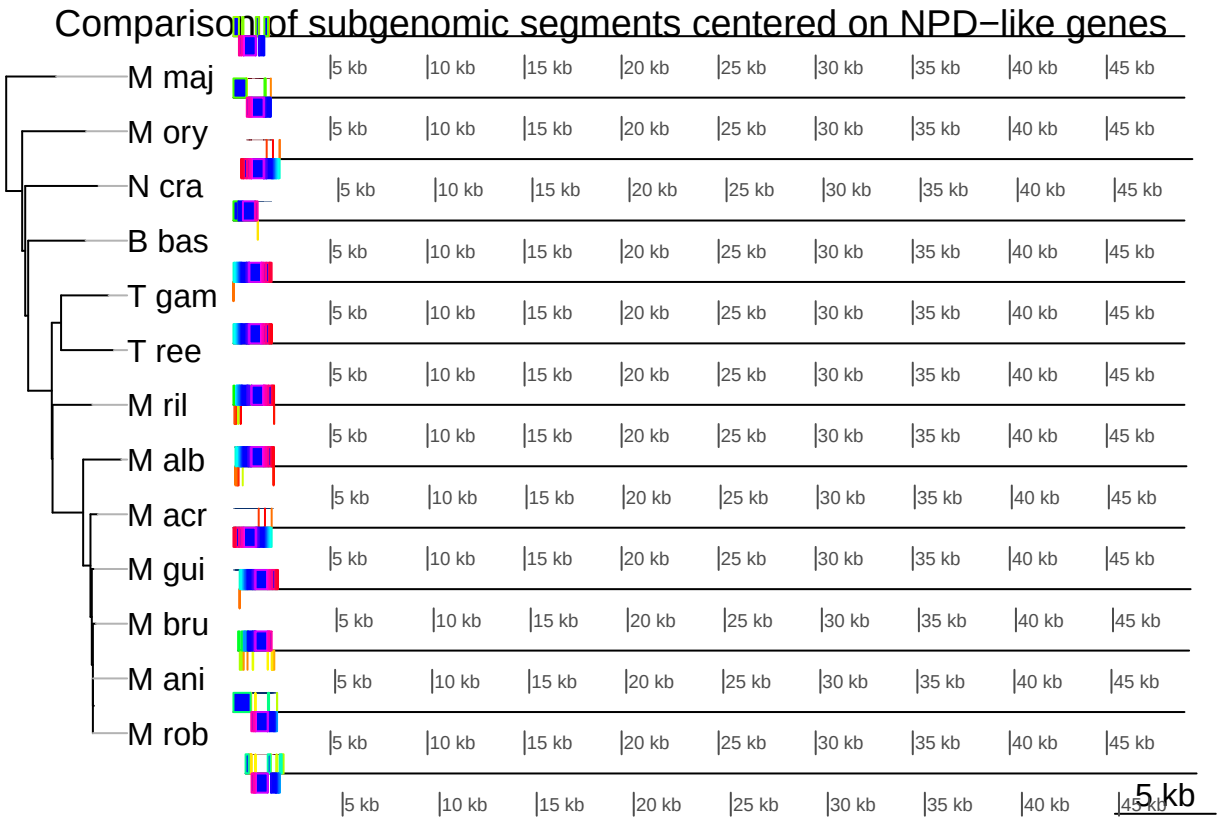
To delimit the sub genomic region of interest the xlims function is used. This xlims function contains the 50kbp sub genomic region of each species.

```
xlims <- list(c( 1,  49000),
              c(1, 49000 ),
              c( 1, 49000),
              c(1,  49000),
              c(1, 49000),
              c(1, 49000),
              c(1, 49000),
              c(1, 49000),
              c(1, 49000),
              c(1, 49000),
              c(1, 49000),
              c( 1, 49000),
              c(1, 49000),
              c(1,49000))
annots <- lapply(bbone$dna_segs, function(x){
  mid <- middle(x)
  annot <- annotation(x1=mid, text=x$name, rot=13)
  idx <- grep("^[^B]", annot$text, perl=TRUE)
  annot[idx[idx %% 4 == 0],]})
```

Plot without annotations (block-annotations).

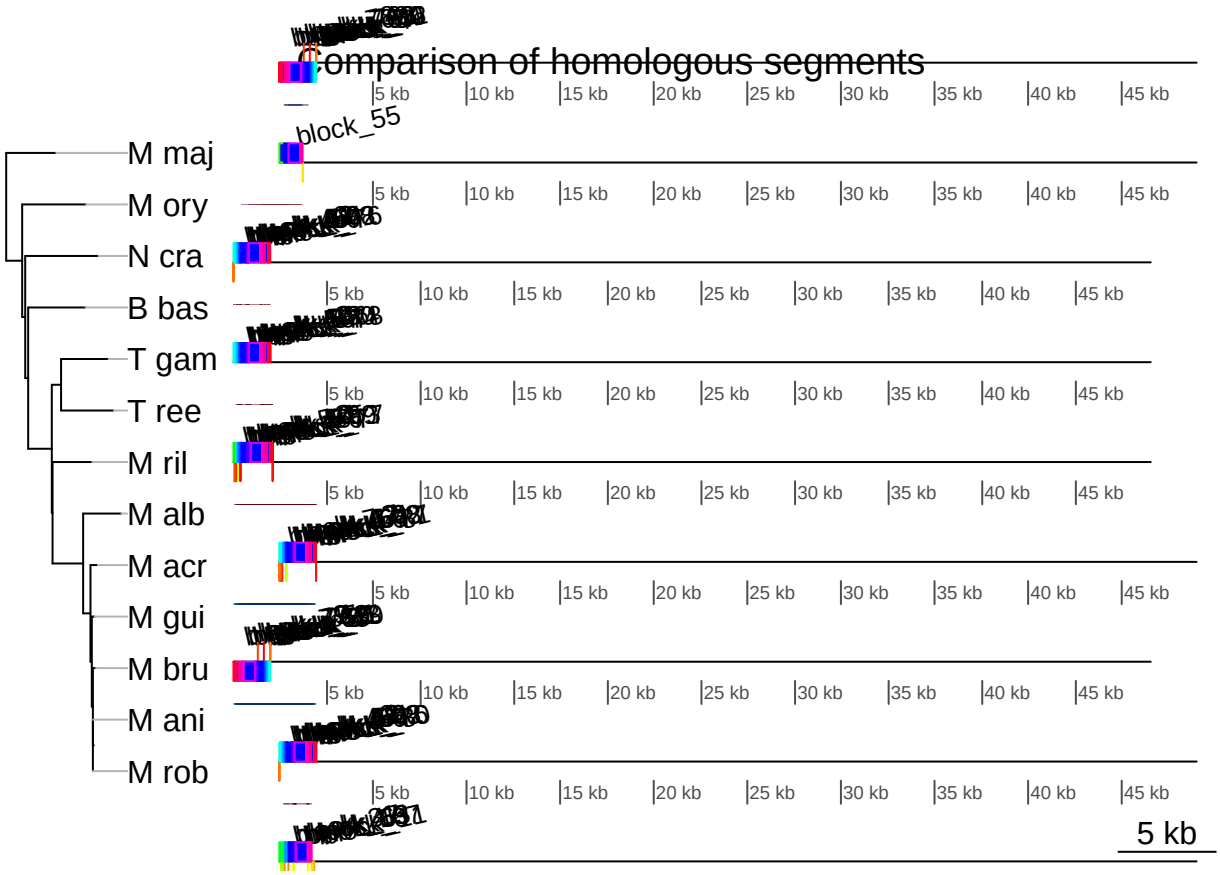
```
plot_gene_map(bbone$dna_segs, bbone$comparisons, tree=tree_demo,
              xlims=xlims,
```

```
            limit_to_longest_dna_seg=FALSE,
            dna_seg_scale=TRUE, scale=TRUE,
            main="Comparison of subgenomic segments centered on NPD-like genes")
```



Plot with block annotations, this shows each identified block by Mauve.

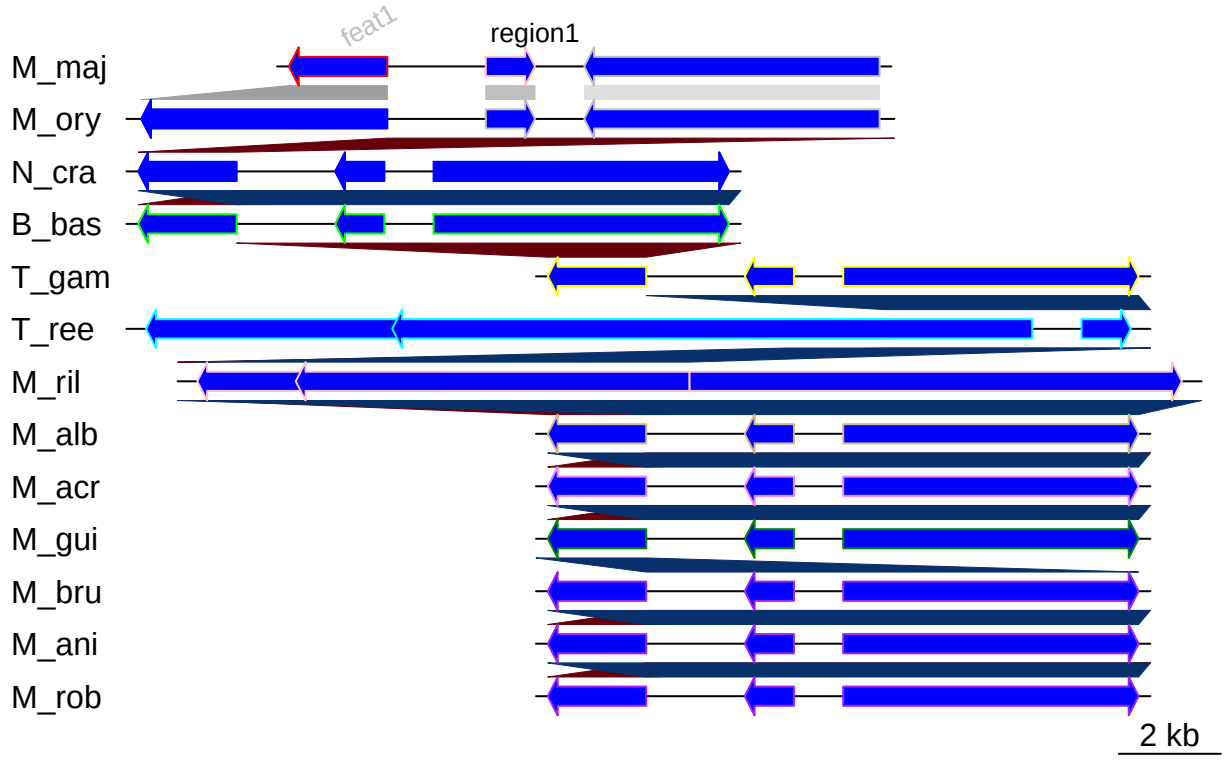
```
plot_gene_map(bbone$dna_segs, bbone$comparisons, tree=tree_demo, annotations =  annots,
              xlims=xlims,
              limit_to_longest_dna_seg=TRUE,
              dna_seg_scale=TRUE, scale=TRUE,
              main="Comparison of homologous segments")
```



Plot without the reconstructed phylogenetic tree, this shows the arrows that are indicative for each block of interest.

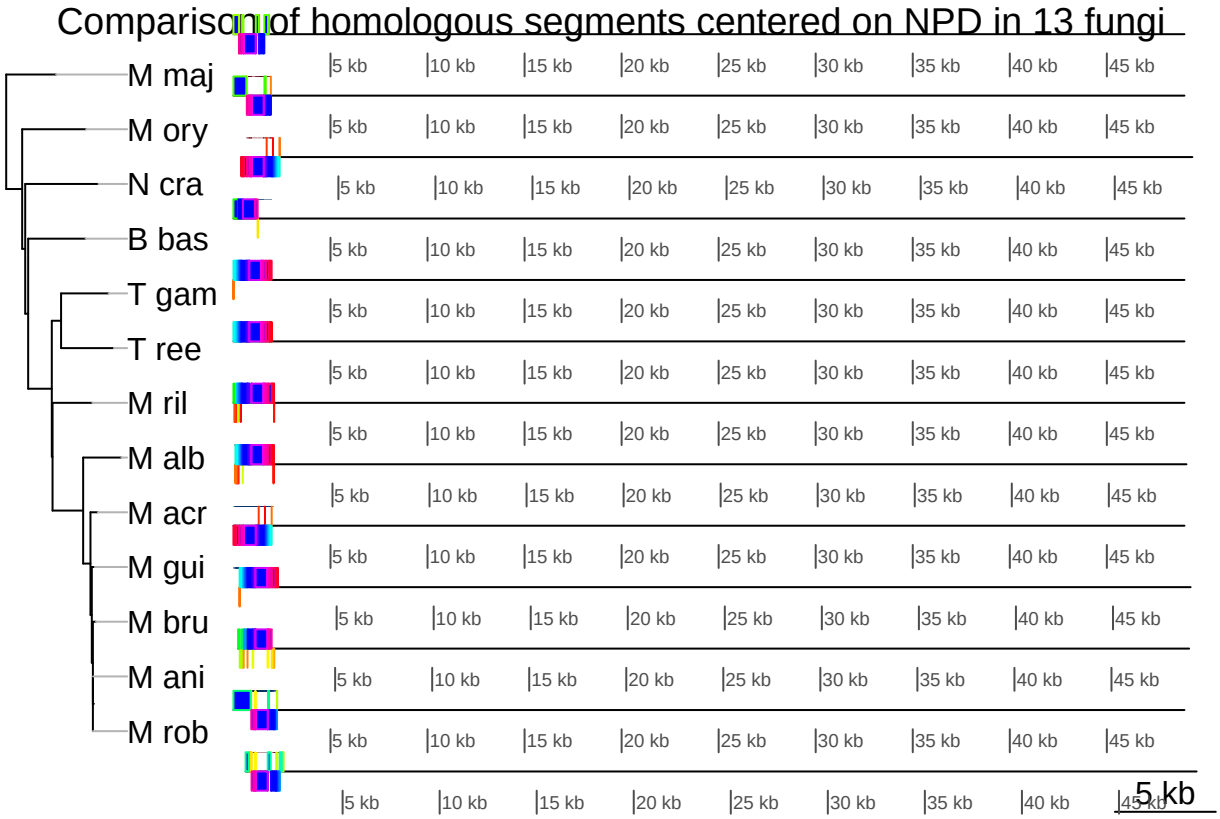
```
plot_gene_map(dna_segs=dna_segs, comparisons=comparisons,
                  annotations=annot, annotation_height=1.3,

                main="Comparison of subgenomic regions centered on NPD")
```



Plot that identifies the LCBs, the phylogenetic reconstruction and the comparisons between the 50kbp sub genomic regions.

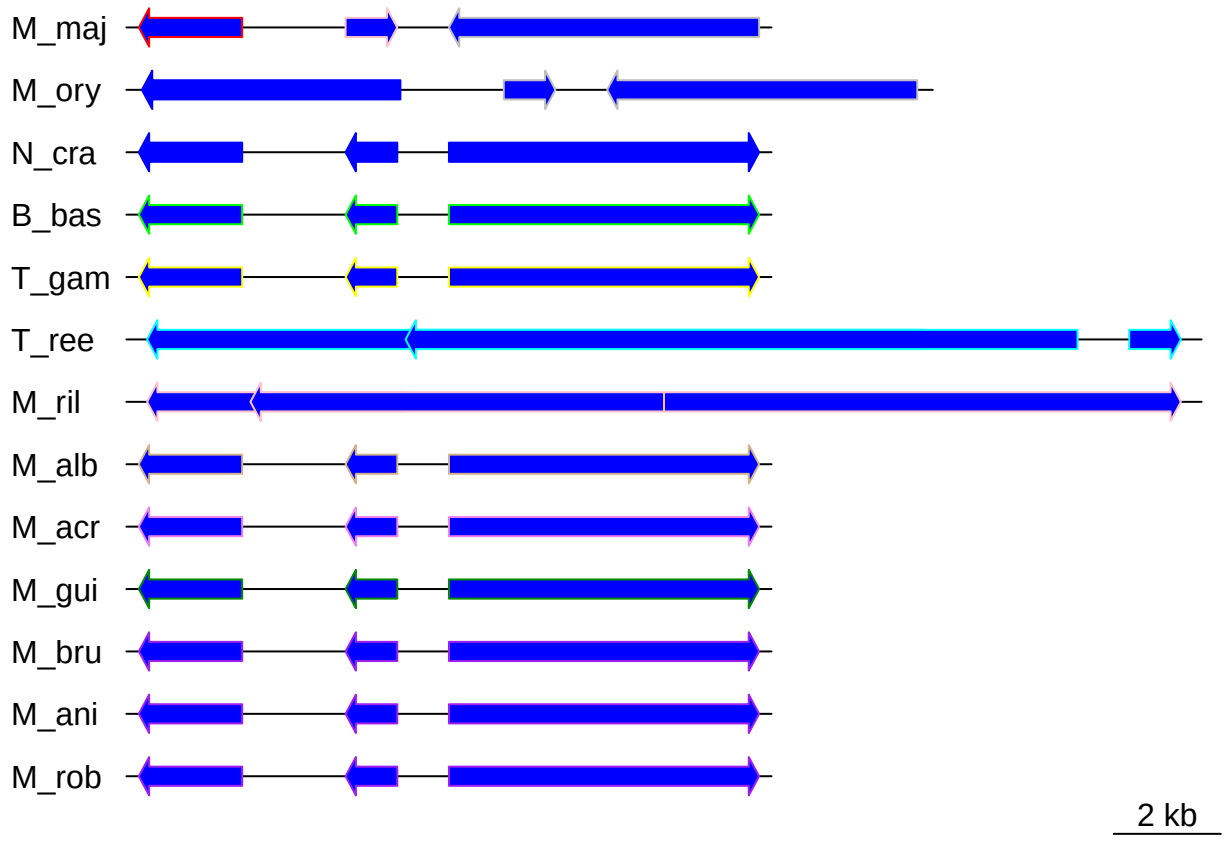
```
plot_gene_map(bbone$dna_segs, bbone$comparisons, tree = tree_demo,
          xlims=xlims,
     limit_to_longest_dna_seg=FALSE,
         dna_seg_scale=TRUE, scale=TRUE,
              main="Comparison of homologous segments centered on NPD in 13 fungi")
```



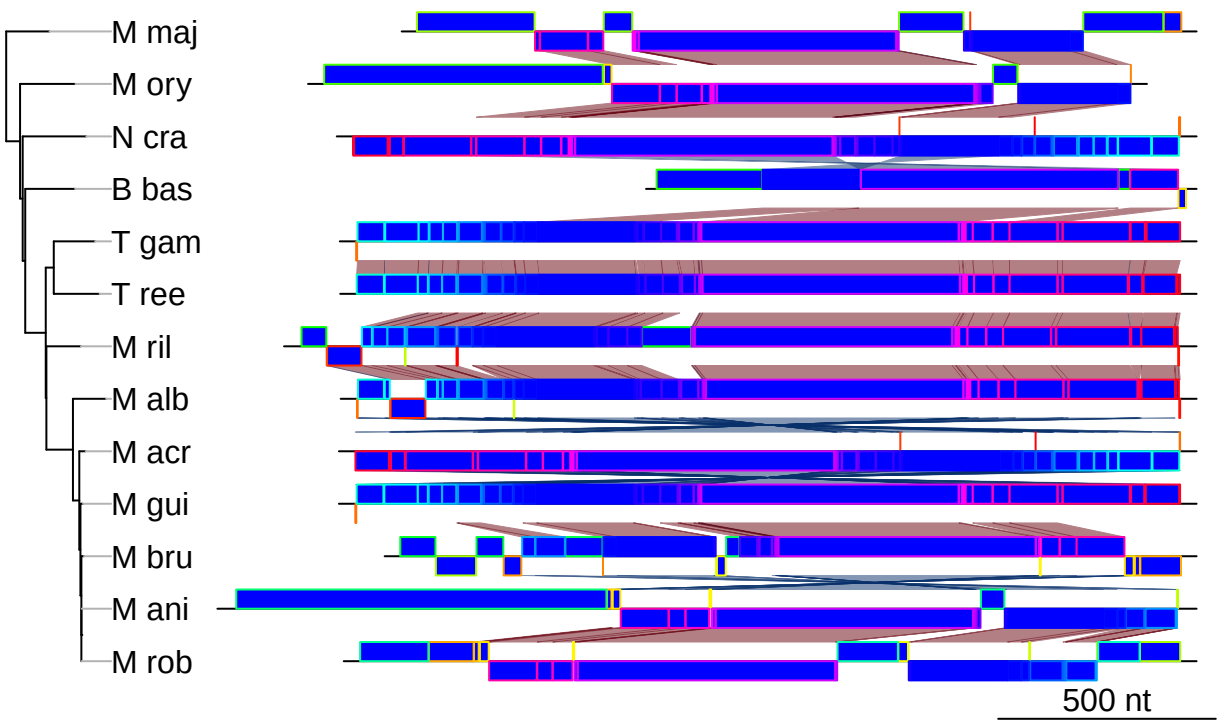
Plot that shows only the arrows that are indicative of the LCBs.

```
plot_gene_map(dna_segs,
              comparisons = NULL,
              tree = NULL,
              tree_width = NULL,
              tree_branch_labels_cex = NULL,
              tree_scale = FALSE,
              legend = NULL,
              annotations = NULL,
              annotation_height = 1,
              annotation_cex = 0.8,
              seg_plots=NULL,     # user-defined plots
              seg_plot_height=3, # height of plots (in lines)
              seg_plot_height_unit="lines", # unit of preceding
              seg_plot_yaxis=3, # if non-null or non false, ticks
              seg_plot_yaxis_cex=scale_cex,
              xlims = NULL,
              offsets = NULL,
              minimum_gap_size = 0.05,
              fixed_gap_length = FALSE,
              limit_to_longest_dna_seg = TRUE,
              main = NULL,
              main_pos = "centre",
              dna_seg_labels = NULL,
              dna_seg_label_cex=1,
              dna_seg_label_col="black",
```

```
              gene_type = NULL,
              arrow_head_len = 200,
              dna_seg_line = TRUE,
              scale = TRUE,
              dna_seg_scale =FALSE,
              n_scale_ticks=7,
              scale_cex=0.6,
              global_color_scheme = c("auto", "auto", "blue_red", 0.5),
              override_color_schemes = FALSE,
              plot_new=TRUE,
              degub=0)
```

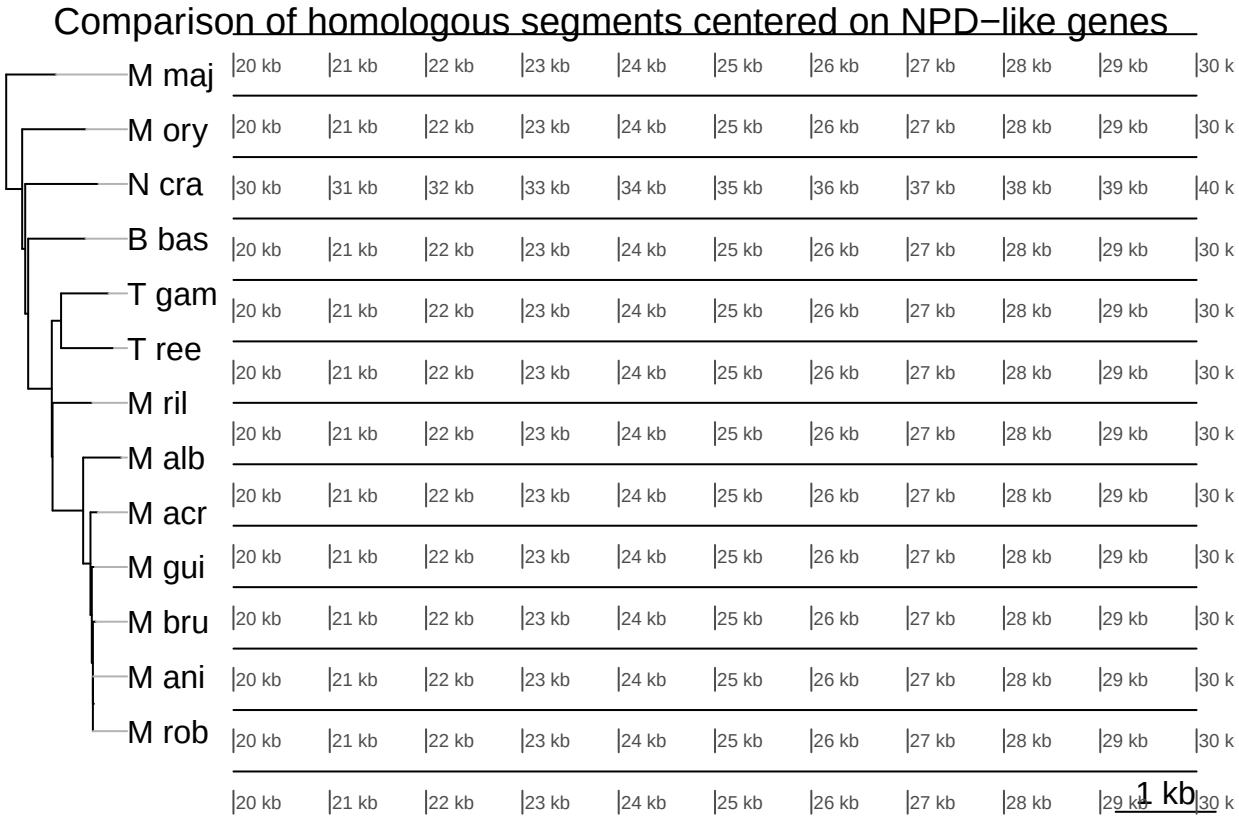



```
plot_gene_map(bbone$dna_segs, bbone$comparisons,
              annotations=annot, annotation_height=1.3,
              tree=tree_demo, tree_width=1,
              main="Comparison of homologous segments centered on NPD-like genes")
```



To delimit the regions used to calculate the synteny, you can use the xlims function centering on the specific localization of the gene of interest to get a better view of the sub genomic context of each species.

```
xlims <- list(c(20000,  30000),
              c(20000, 30000 ),
              c( 30000, 40000),
              c(20000,  30000),
              c(20000,  30000),
              c(20000,  30000),
              c(20000,  30000),
              c(20000,  30000),
              c(20000, 30000),
              c( 20000, 30000),
              c( 20000, 30000),
              c(20000, 30000),
              c(20000, 30000))
plot_gene_map(bbone$dna_segs, bbone$comparisons, tree=tree_demo,
              xlims=xlims,
              limit_to_longest_dna_seg=FALSE,
              dna_seg_scale=TRUE, scale=TRUE,
              main="Comparison of homologous segments centered on NPD-like genes")
```


Comparison of homologous segments centered on NPD−like genes
M maj
M ory
N cra
B bas
T gam
T ree
M ril
M alb
M acr
M gui
M bru
M ani
M rob
20 kb
21 kb
22 kb
23 kb
24 kb
25 kb
26 kb
27 kb
28 kb
29 kb
30 kb
31 kb
32 kb
33 kb
34 kb
35 kb
36 kb
37 kb
38 kb
39 kb
40 kb
1 kb