Plotting C victoriae RiPP regions with transposons

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```
knitr::opts_chunk$set(echo = TRUE)
```

Run Lastz and convert text output into DNAcomp files for plotting in genoPlotR libary

Exampe lastz run:

lastz Cvic_tig07.fasta Cvic_tig16.fasta –entropy
–format=general:name1,strand1,start1,end1,length1,name2,strand2,start2+,end2+,length2,score,identity
–markend –gfextend –nochain –gapped –step=1 –strand=both –output=Tig07_Tig16_out_nogap.txt
–identity=90 –continuity=80 –matchcount=1000

```
library(genoPlotR)
```

```
## Loading required package: ade4
```

```
## Loading required package: grid
```

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------------------------------------------
```

```
## v ggplot2 3.3.0     v purrr   0.3.3
## v tibble  2.1.3     v dplyr   0.8.5
## v tidyr   1.0.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
raw_ident_comp<-read.delim("Cvictig07vstig16_nochain80_2kb.txt")
write_delim(raw_ident_comp,"Cvic07_Cvic16ident_80_2kb.comp",delim = "\t")

Chr_comp<-read_comparison_from_tab("Cvic07_Cvic16ident_80_2kb.comp", header=T)
Chr_comp$direction<-Chr_comp$strand
```

Need to make file for important gene locations, i.e. RiPP genes, Copper Amine Oxidase

Exported gff file from Geneious and edited manually in excel to make genes and transposon .seg files

Make DNA alignment (comparisons) into a list

```
Componly<-list(Chr_comp)
```

Set X lims for whole chromosomes

```
start.second=1
end.second=316216
start.main=1600000
end.main=2111100
xlims1 <- list(c(start.main, end.main), c(start.second, end.second))
```

Set X lims for figure 2C

```
start.second=160000
end.second=316216
start.main=2000000
end.main=2111100
xlims2 <- list(c(start.main, end.main), c(start.second, end.second))
```

Plot everything with TEs

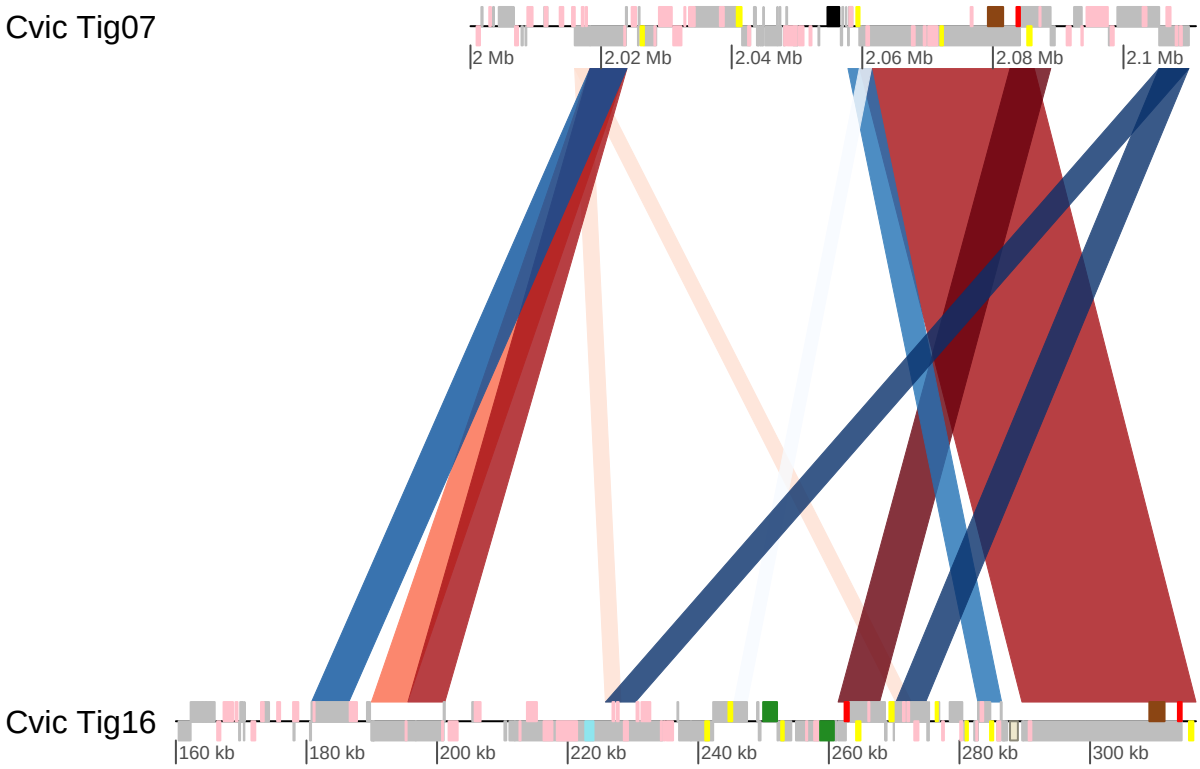
```
CV07.annot.TE<-data.frame(read.delim("Tig07_gene_TE.segs", sep="\t", header=F))
names(CV07.annot.TE)<-c("name","start","end","strand","col","fill","gene_type")
CV07.gene_TE.seg<-dna_seg(CV07.annot.TE)

CV16.annot.TE<-data.frame(read.delim("Tig16_gene_TE.segs", sep = "\t", header = F))
names(CV16.annot.TE)<-c("name","start","end","strand","col", "fill","gene_type")
CV16.gene_TE.seg<-dna_seg(CV16.annot.TE)

GenesandTEs<-list(CV07.gene_TE.seg,CV16.gene_TE.seg)
names(GenesandTEs)<- c("Cvic Tig07","Cvic Tig16")
Componly<-list(Chr_comp)


plot_gene_map(dna_segs = GenesandTEs , comparisons = Componly, gene_type = "side_blocks",
              global_color_scheme = c("identity", "auto","red_blue",0.8),
              dna_seg_scale = T, xlims=xlims2, scale=F,
              main = "A",main_pos = "left",plot_new = T, legend = T)
```

A




```
cairo_pdf(paste0("FigureXX.pdf"), width = 5, height = 2)
pushViewport(viewport(layout=grid.layout(1,1, heights=unit(c(1,1), rep("null",1))), name="Synteny betwe
## Panel A
pushViewport(viewport(layout.pos.row = 1, name="panelC"))
plot_gene_map(dna_segs = GenesandTEs ,
              comparisons = Componly,
              gene_type = "side_blocks", dna_seg_scale= T,
              scale=F, xlims=xlims2,
              global_color_scheme = c("identity","auto","blue_red", 0.8), main="C", main_pos="left", leg
dev.off()
```

```
## pdf
##   2
```