Compartments

```
wd <- "/home/mcabrera/Desktop/MN/p53/"
samples <- readRDS(paste0(wd,"samples.rds"))
results <- paste0(wd,"results/HCT116/")  #path where the clean files are

knitr::opts_chunk$set(dev = "pdf",
                      dpi = 300,
                      # echo = FALSE, #to print code or not
                      cache = TRUE,
                      root.dir = paste0(results))
getwd()
```

```
## [1] "/home/mcabrera/Desktop/MN/p53/scripts/HiC/Plotting"
```

```
packages <- c("ggforce","ggfortify","dendextend","colormap","paletteer", "ggthemes","scico","reshape","
invisible(lapply(packages, library, character.only = TRUE))

colors_samples=c("#fde725ff", "#37b578ff","#21908dff","#31668dff","#43377fff","#440154ff")
color_A_B_Compartments=c("#881010","#23447f")
color_heatmap_compartments <- colorRamp2(breaks = c(-0.5,0,0.5), colors = c("#23447f", "snow1","#881010

load(paste0(results,"HiC/Compartments.RData"))
```

Fig 16C: Percentage of 100kb genomic regions defined as A or B compartments for each time point.

```
table_AB <- data.frame(apply(data.frame(Compartments.gr)[- grep("NULL", Compartments.gr$all_compartments
colnames(table_AB) <-  sub("Category_", "", colnames(table_AB))

head(table_AB)
```

```
##   Nut.0h_compartment_category Nut.1h_compartment_category
## A                       16025                       16746
## B                       11220                       10499
##   Nut.4h_compartment_category Nut.7h_compartment_category
## A                       16500                       16260
## B                       10745                       10985
##   Nut.10h_compartment_category Nut.24h_compartment_category
## A                        14888                        15208
## B                        12357                        12037
# Nut.0h Nut.1h Nut.4h Nut.7h Nut.10h Nut.24h
# A  16025  16746  16500  16260   14888   15208
# B  11220  10499  10745  10985   12357   12037

table_AB$compartment <- rownames(table_AB)
```

```
table_AB$compartment <- factor(table_AB$compartment, levels=c("A","B"))

table_AB %>% melt(id.vars = "compartment") %>%
        mutate(variable=factor(variable,levels=unique(rev(variable))))%>%
        ggplot(aes(y = variable, x = value, fill = compartment)) +
          geom_col() +
          geom_text(aes(label = paste0(round(value/nrow(data.frame(Compartments.gr)[- grep("NULL", Compa
          theme_classic()+
          theme(axis.text.y=element_text(size=rel(1), angle=0),
                axis.text.x=element_text(size=rel(1)))+
          scale_fill_manual(values=c(color_A_B_Compartments))+
        scale_x_continuous(breaks = seq(0, nrow(data.frame(Compartments.gr)), by = 5000), expand = c(0,0
        xlab("")+
        ylab("")+
  labs(title='A/B genome distribution of all samples',
        subtitle=paste0('n=',nrow(data.frame(Compartments.gr)[- grep("NULL", Compartments.gr$all_compartm
  theme(plot.subtitle=element_text(size=8, face='italic', color='grey50'))+
    geom_vline(xintercept=table_AB$Category_Nut.0h[2], color="white")
```


16C-1.pdf
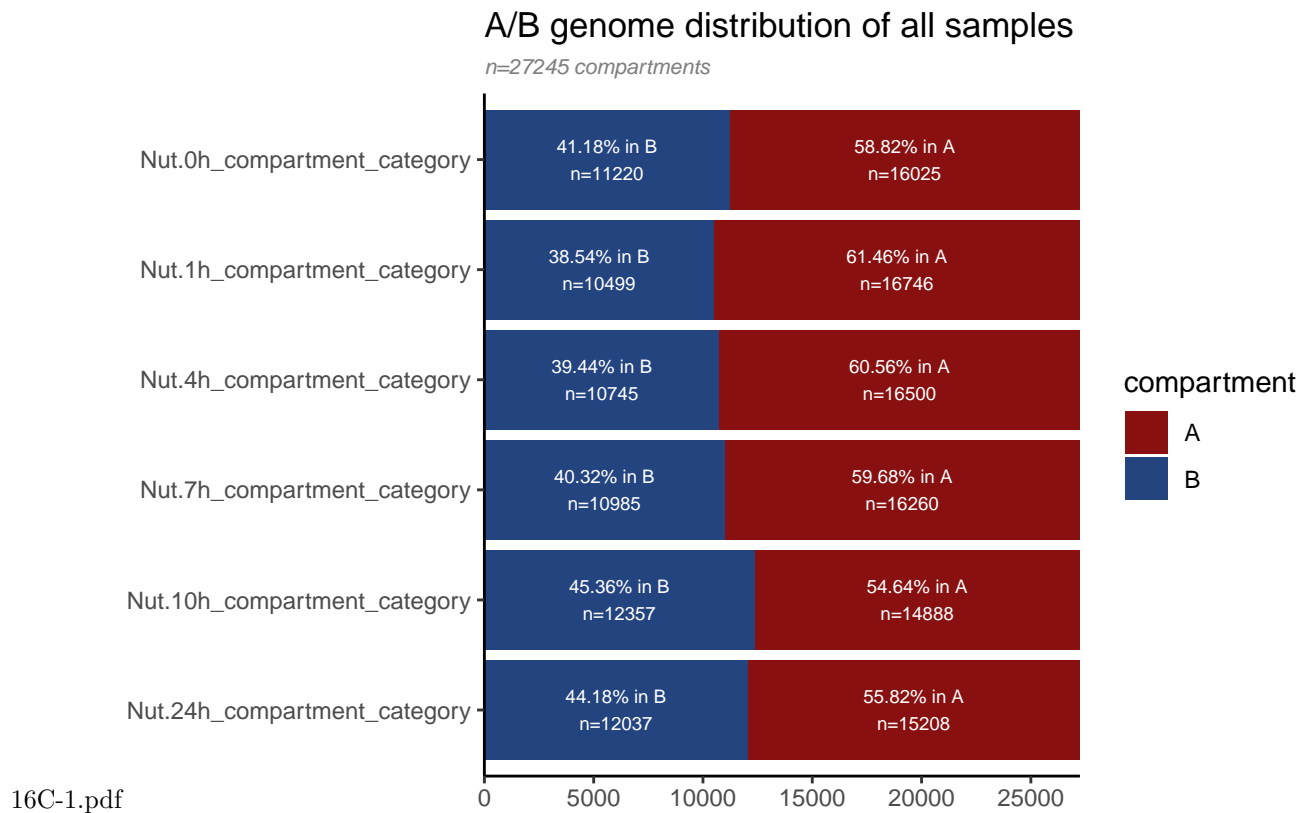
Fig 16 D: Percentage of compartment categories according to their dynamics along p53 activation. Dynamic compartments are defined as those that change compartment between any two time points

```r
static_dynamic_compartments <- data.frame(sort(table(data.frame(Compartments.gr)[- grep("NULL", Compartm

colnames(static_dynamic_compartments) <- c("Category", "Total_number")

static_dynamic_compartments$Category <- as.character(static_dynamic_compartments$Category)
static_dynamic_compartments[nrow(static_dynamic_compartments) + 1,] = c('static', sum(static_dynamic_co
static_dynamic_compartments$Category <- as.factor(static_dynamic_compartments$Category)
static_dynamic_compartments$Category <- factor(static_dynamic_compartments$Category, levels = c("static
static_dynamic_compartments$Total_number <- as.integer(static_dynamic_compartments$Total_number)

ggplot(static_dynamic_compartments[1:3,], aes(x="", y = Total_number, fill=Category)) +
        geom_bar(position="stack",stat="identity",width = 0.2 )+
        scale_fill_manual(values=c("#881010","black", "#23447f"))+
        ggtitle(paste0("Out of the total ",nrow(data.frame(Compartments.gr)[- grep("NULL", Compartments
  labs(title = "Genomic distribution of the compartments", subtitle = "Divided by stable and switching")
        xlab("")+
        ylab("Number of compartments")+
        theme_ipsum() +
        theme_classic()+
        theme_minimal()+
        theme(legend.position="bottom")+
        theme(axis.ticks.x=element_blank())+
        geom_text(aes(label = paste0(Category,"\n",Total_number," \n (",round((Total_number/nrow(data.f
```

Genomic distribution of the compartments
Divided by stable and switching
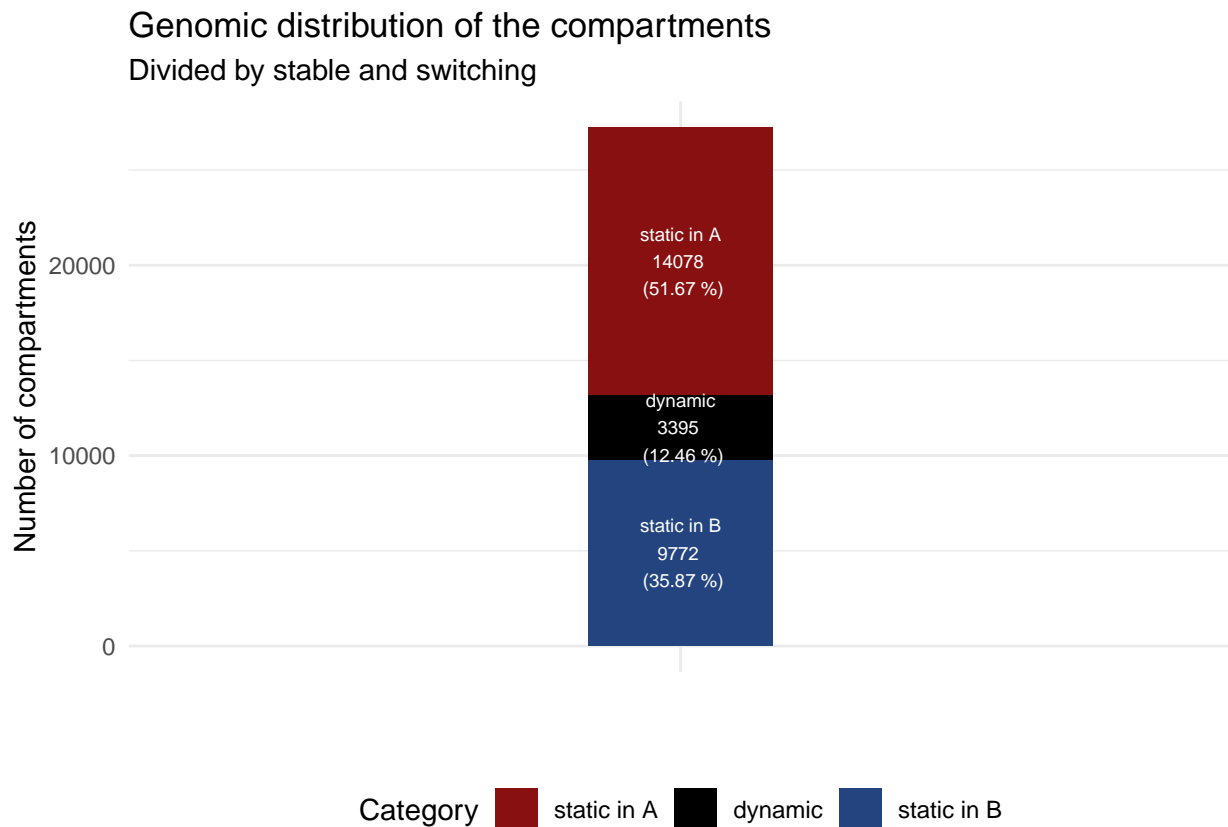
Fig 16E Compartment scores of the dynamic compartments in response to p53 activation, with each row representing a 100kb bin and each column representing a time point.

```r
compartments_Freq <- data.frame(sort(table(data.frame(Compartments.gr)$all_compartments_combinations),d
compartments_Freq$order_combinations <- seq(1:nrow(compartments_Freq)) # we add the frequency rank as I

Compartments.gr$Frequency_combinations = compartments_Freq$Freq[match(as.character(data.frame(Compartmen

Compartments.gr$order_combinations = compartments_Freq$order_combinations[match(data.frame(Compartments

dynamic_compartments_Freq <- data.frame(sort(table(data.frame(Compartments.gr)[! grepl("NULL", Compartme

dynamics_Freq_ordered <- data.frame(Compartments.gr)[Compartments.gr$all_compartments_state=="dynamic" &

dynamics_Freq_ordered$Percentage_Freq = dynamic_compartments_Freq$Percentage[match(dynamics_Freq_ordere

dynamics_Freq_ordered$types <-as.character(

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-B-B-B-B-B", 'DMSO specific activati

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-A-A-A-A-A", 'p53 specific activatio

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-A-B-B-B-B", 'p53 1h specific activa

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-B-A-A-A-A", 'p53 1h specific inacti

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-B-A-B-B-B", 'p53 4h specific activa

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-A-B-A-A-A", 'p53 4h specific inacti

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-B-B-A-B-B", 'p53 7h specific activa

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-A-A-B-A-A", 'p53 4h specific inacti

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-B-B-B-A-B", 'p53 10h specific activ

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-A-A-A-B-A", 'p53 10h specific inact

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-B-B-B-B-A", 'p53 24h specific activ

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-A-A-A-A-B", 'p53 24h specific inact

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-A-A-A-B-B" | dynamics_Freq_ordered$

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-B-B-B-A-A" | dynamics_Freq_ordered$

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "B-B-B-B-A-A", 'Late activation',

    ifelse(dynamics_Freq_ordered$all_compartments_combinations == "A-A-A-A-B-B", 'Late inactivation','H

# dynamics_Freq_ordered$types[dynamics_Freq_ordered$Percentage_Freq <9] <- "<10%"
```

```
Compartments_types_freq <- data.frame(sort(table(dynamics_Freq_ordered$types),decreasing = T))
Compartments_types_freq$type_freq <- Compartments_types_freq$Freq*100/nrow(dynamics_Freq_ordered)
# Compartments_types_freq$name_freq <- as.character(Compartments_types_freq$Var1)
Compartments_types_freq$name_freq[Compartments_types_freq$type_freq <5] <- "<5%"

dynamics_Freq_ordered$heatmap = Compartments_types_freq$type_freq[match(dynamics_Freq_ordered$types,Comp
dynamics_Freq_ordered$heatmap_types = Compartments_types_freq$name_freq[match(dynamics_Freq_ordered$typ

dynamics_Freq_ordered <- dynamics_Freq_ordered[order(dynamics_Freq_ordered$heatmap, decreasing = T),]

dynamics_Freq_ordered$caca <- paste0(dynamics_Freq_ordered$heatmap_types,"\n",round(dynamics_Freq_ordere

Heatmap(as.matrix(dynamics_Freq_ordered[,c(samples)]),column_title = "Heatmap dynamic regions", column_
cluster_rows = F, show_row_names = F,row_split=factor(dynamics_Freq_ordered$types, levels = c("Early act
row_title_rot = 0,row_title_gp = gpar(col = c("black"),fontsize=5),row_gap = unit(1.5, "mm")
,border = FALSE,border_gp = gpar(col = "black", lwd = 2),
cluster_columns=F,col = color_heatmap_compartments)
```
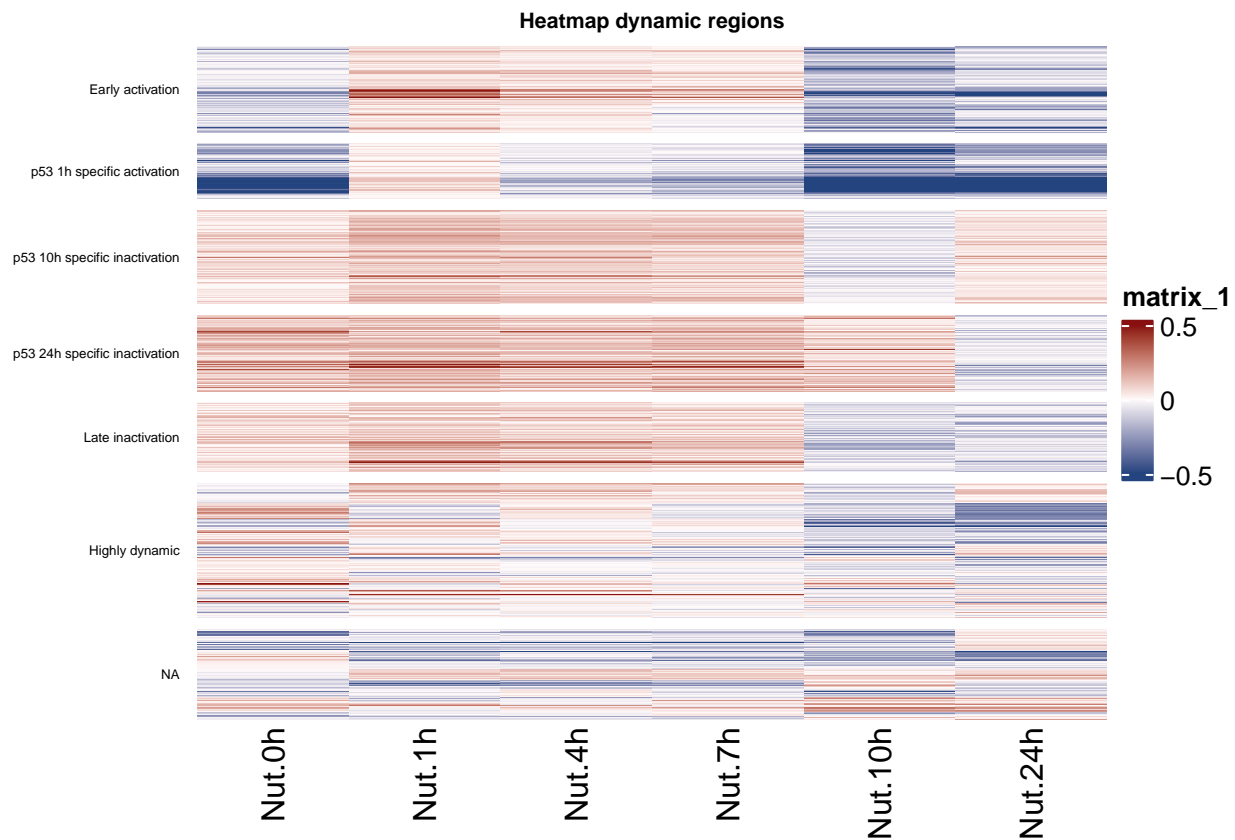

Heatmap dynamic regions

Fig 17A: Correlation plot resultant from Pearson's residuals Chi-square test of independence for the contingency table time-course vs. compartment category

```
# Chi-square test examines whether rows and columns of a contingency table are statistically significan
## rows are the different variables, values are the frequencies of the variables done by each category
A_B_distribution <- sapply(data.frame(Compartments.gr)[- grep("NULL", Compartments.gr$all_compartments_

colnames(A_B_distribution) <- samples

chisq <- chisq.test(A_B_distribution)
print(chisq)
```

```
##
##  Pearson's Chi-squared test
##
## data:  A_B_distribution
## X-squared = 410.52, df = 5, p-value < 2.2e-16
```

```
corrplot(chisq$residuals, is.cor = FALSE,tl.col="black", method="circle",col=colorRampPalette(c("#23447
```
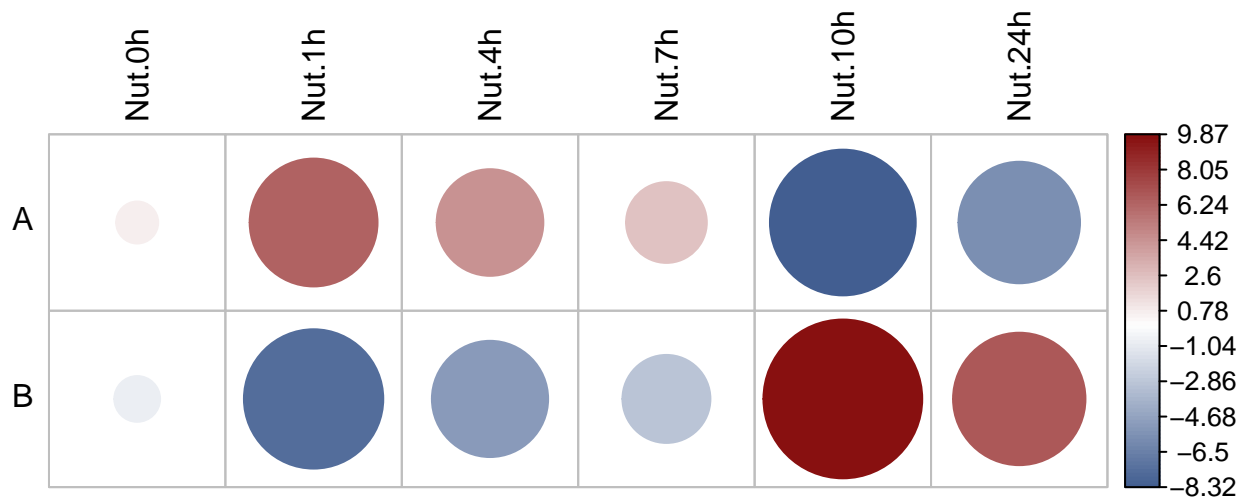


```
# contrib <- 100*chisq$residuals^2/chisq$statistic
# round(contrib)
# corrplot(contrib, is.cor=FALSE)
```

#Fig 17B: Variation of eigenvector values along a 50 Mb genomic region of chromosome 12.

```
region <- melt(data.frame(Compartments.gr)[! grepl("NULL", Compartments.gr$all_compartments_combinations
region$colour <- ifelse(region$value < 0,"negative","positive")

ggplot(region,aes(start,value))+
  geom_bar(stat="identity",position="identity",aes(fill = colour),size=10)+
  scale_fill_manual(values=c(positive="#881010",negative="#23447f"))+
  theme_classic()+
  ylim(-1,1)+
  xlab("Genomic position (in bp) of the chromosome 12")+
  facet_wrap_paginate(. ~ variable, nrow = 6, ncol = 1)
```
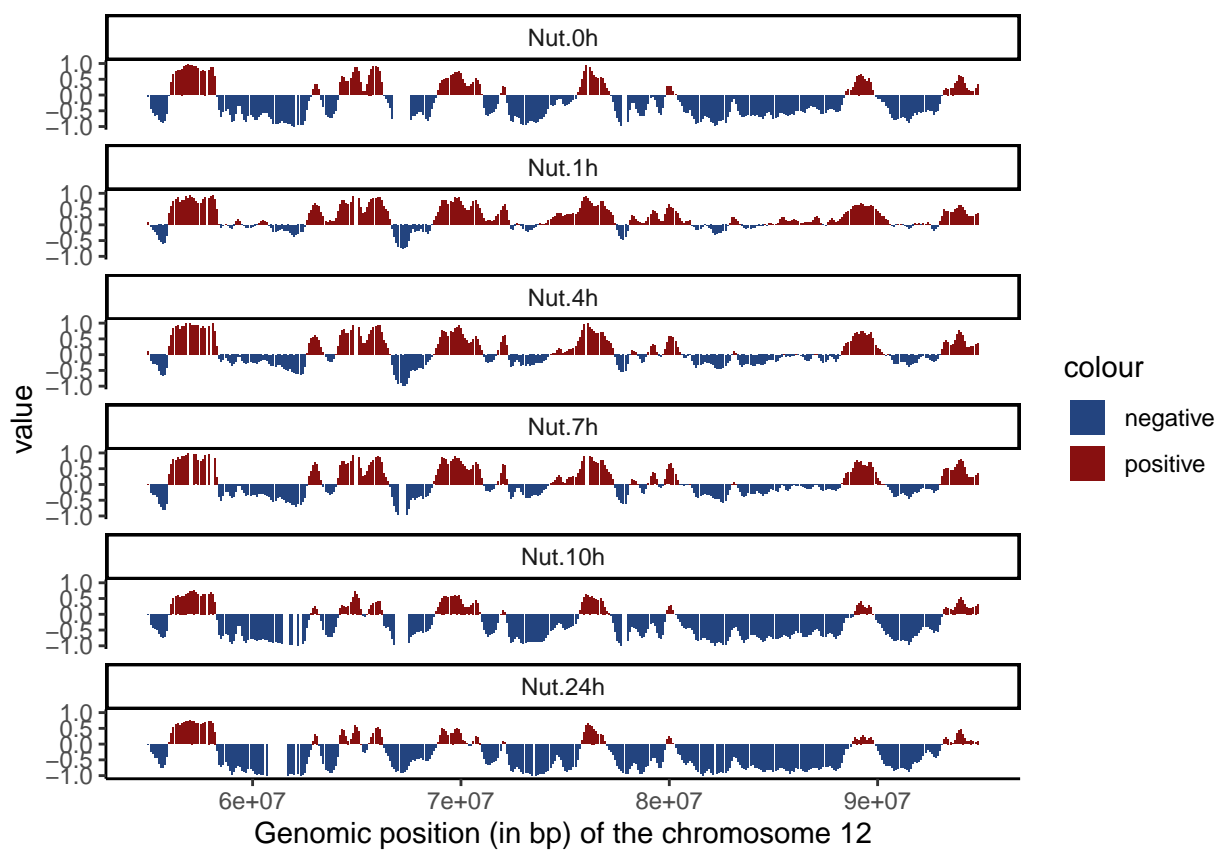
Figure 1: caca

Extra figures not added in the thesis