

HiC_Compartments_Figure1

Fig1.Compartment dynamics across TP53 activation —

```
load(paste0(data,"Compartments.RData"))
```

Fig1D.Fraction of genomic regions divided by stable (in A compartment or B compartment) and switching compartment residency during p53 activation —

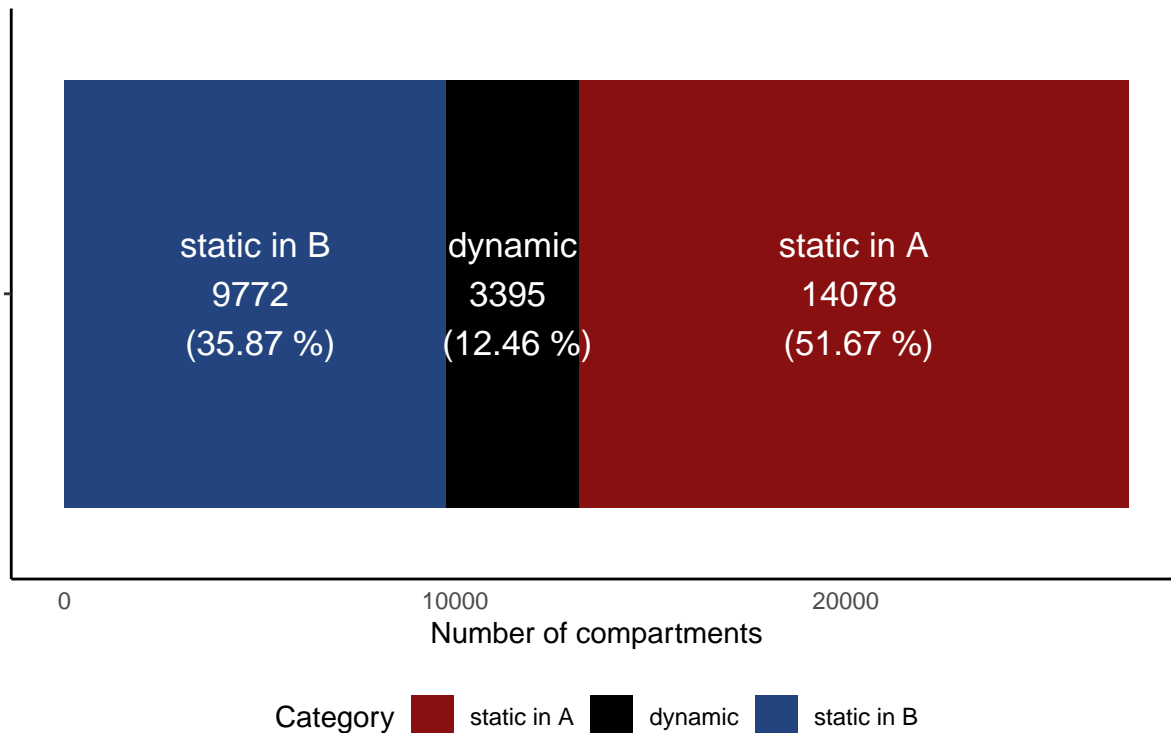
```
static_dynamic_compartments <- data.frame(sort(table(data.frame(Compartments.gr)[- grep("NULL", Compartments.gr)],
colnames(static_dynamic_compartments) <- c("Category", "Total_number")

static_dynamic_compartments$Category <- as.character(static_dynamic_compartments$Category)
static_dynamic_compartments[nrow(static_dynamic_compartments) + 1,] = c('static', sum(static_dynamic_compartments$Total_number))
static_dynamic_compartments$Category <- as.factor(static_dynamic_compartments$Category)
static_dynamic_compartments$Category <- factor(static_dynamic_compartments$Category, levels = c("static", "switching"))
static_dynamic_compartments$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 = 0.9 )+
  scale_fill_manual(values=c("#881010","black", "#23447f"))+
  ggtitle(paste0("Out of the total ",nrow(data.frame(Compartments.gr)[- grep("NULL", Compartments.gr)])))+
  labs(title = "Genomic distribution of the compartments", subtitle = "Divided by stable and switching",
  xlab(""),
  ylab("Number of compartments")+
  theme_ipsum() +
  theme_classic()+
  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.frame(Compartments.gr)[- grep("NULL", Compartments.gr)])))))
  coord_flip()
```

Genomic distribution of the compartments

Divided by stable and switching



```
compartments_Freq <- data.frame(sort(table(data.frame(Compartments.gr)$combinations),decreasing = T))
compartments_Freq$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(Compartments.gr)$combinations),compartments_Freq$order_combinations)]

dynamic_compartments_Freq <- data.frame(sort(table(data.frame(Compartments.gr)[! grepl("NULL", Compartments.gr$Frequency_combinations)],decreasing = T))
dynamic_compartments_Freq$Percentage <- round(dynamic_compartments_Freq$Freq/nrow(data.frame(Compartments.gr)[! grepl("NULL", Compartments.gr$Frequency_combinations)]))
dynamic_compartments_Freq$colors <- as.character(ifelse(grepl('^A', dynamic_compartments_Freq$Var1) & dynamic_compartments_Freq$Percentage >= 1, "static in A", "static in B"))
dynamic_compartments_Freq$labels <- as.character(ifelse(dynamic_compartments_Freq$Percentage >= 1, dynamic_compartments_Freq$Percentage, "static in B"))

ggplot(dynamic_compartments_Freq, aes(x="",y=Percentage,fill=Var1)) +
  geom_bar(position="stack",stat="identity",width = 1,color="black") +
  scale_fill_manual(values = dynamic_compartments_Freq$colors) +
  labs(title = "Switching compartments distribution of all compartments",subtitle = "Divided by a",
  xlab("")+
  ylab("% of switching compartments")+
  theme_ipsum() +
  theme_classic()+
  theme(axis.ticks.x=element_blank())+
  theme(aspect.ratio = 2.5)+
  scale_y_continuous(expand = c(0,0))+
  geom_text(aes(label = paste0(Percentage, " %")),position = position_stack(vjust = .5), color="white")
```

```
# geom_text(data = dynamic_compartments_Freq[dynamic_compartments_Freq$Percentage >= 1,], color = "white", size = 10, fontweight = "bold",
ggtitle(""))
```

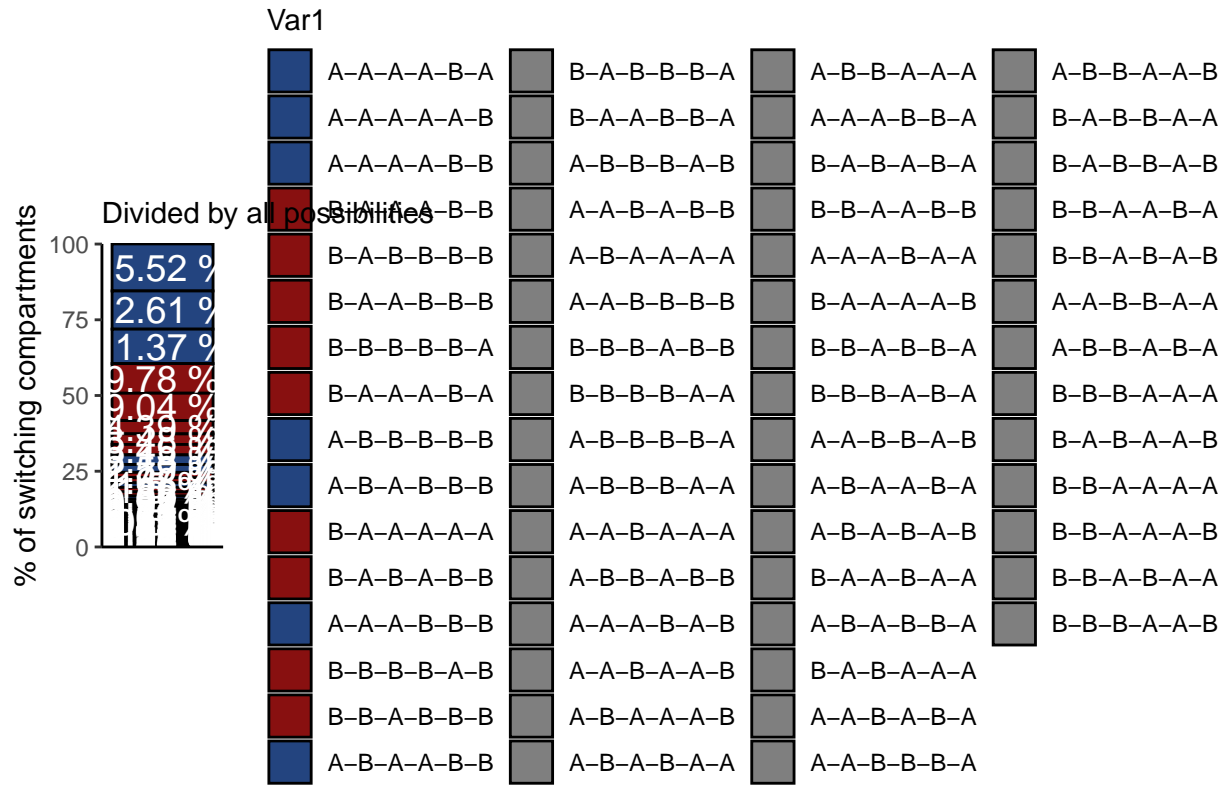


Fig1E. Compartment score heatmap of the dynamic regions agrupated by patterns of temporal compartment changes.

```
dynamics_Freq_ordered <- data.frame(Compartments.gr)[Compartments.gr$state_Compartments=="dynamic" & !grepl("A", Compartments.gr$state_Compartments)]
dynamics_Freq_ordered$Percentage_Freq = dynamic_compartments_Freq$Pe[match(dynamics_Freq_ordered$combinations, dynamic_compartments_Freq$combinations)]
dynamics_Freq_ordered$types <- as.character(
  ifelse(dynamics_Freq_ordered$combinations == "A-B-B-B-B-B", 'DMSO specific activation',
  ifelse(dynamics_Freq_ordered$combinations == "B-A-A-A-A-A", 'p53 specific activation',
  ifelse(dynamics_Freq_ordered$combinations == "B-A-B-B-B-B", 'p53 1h specific activation',
  ifelse(dynamics_Freq_ordered$combinations == "A-B-A-A-A-A", 'p53 1h specific inactivation',
  ifelse(dynamics_Freq_ordered$combinations == "B-B-A-B-B-B", 'p53 4h specific activation',
  ifelse(dynamics_Freq_ordered$combinations == "A-A-B-A-A-A", 'p53 4h specific inactivation',
  ifelse(dynamics_Freq_ordered$combinations == "B-B-B-A-B-B", 'p53 7h specific activation',
  ifelse(dynamics_Freq_ordered$combinations == "A-A-A-B-A-A", 'p53 4h specific inactivation',
```

```

ifelse(dynamics_Freq_ordered$combinations == "B-B-B-B-A-B", 'p53 10h specific activation',
ifelse(dynamics_Freq_ordered$combinations == "A-A-A-A-B-A", 'p53 10h specific inactivation',
ifelse(dynamics_Freq_ordered$combinations == "B-B-B-B-B-A", 'p53 24h specific activation',
ifelse(dynamics_Freq_ordered$combinations == "A-A-A-A-A-B", 'p53 24h specific inactivation',
ifelse(dynamics_Freq_ordered$combinations == "B-A-A-A-B-B" | dynamics_Freq_ordered$combinations ==
ifelse(dynamics_Freq_ordered$combinations == "A-B-B-B-A-A" | dynamics_Freq_ordered$combinations ==
ifelse(dynamics_Freq_ordered$combinations == "B-B-B-B-A-A", 'Late activation',
ifelse(dynamics_Freq_ordered$combinations == "A-A-A-A-B-B", 'Late inactivation','Highly dynamic'))))

# 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$name_freq[match(dynamics_Freq_ordered$types

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_order

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 ac
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)

```

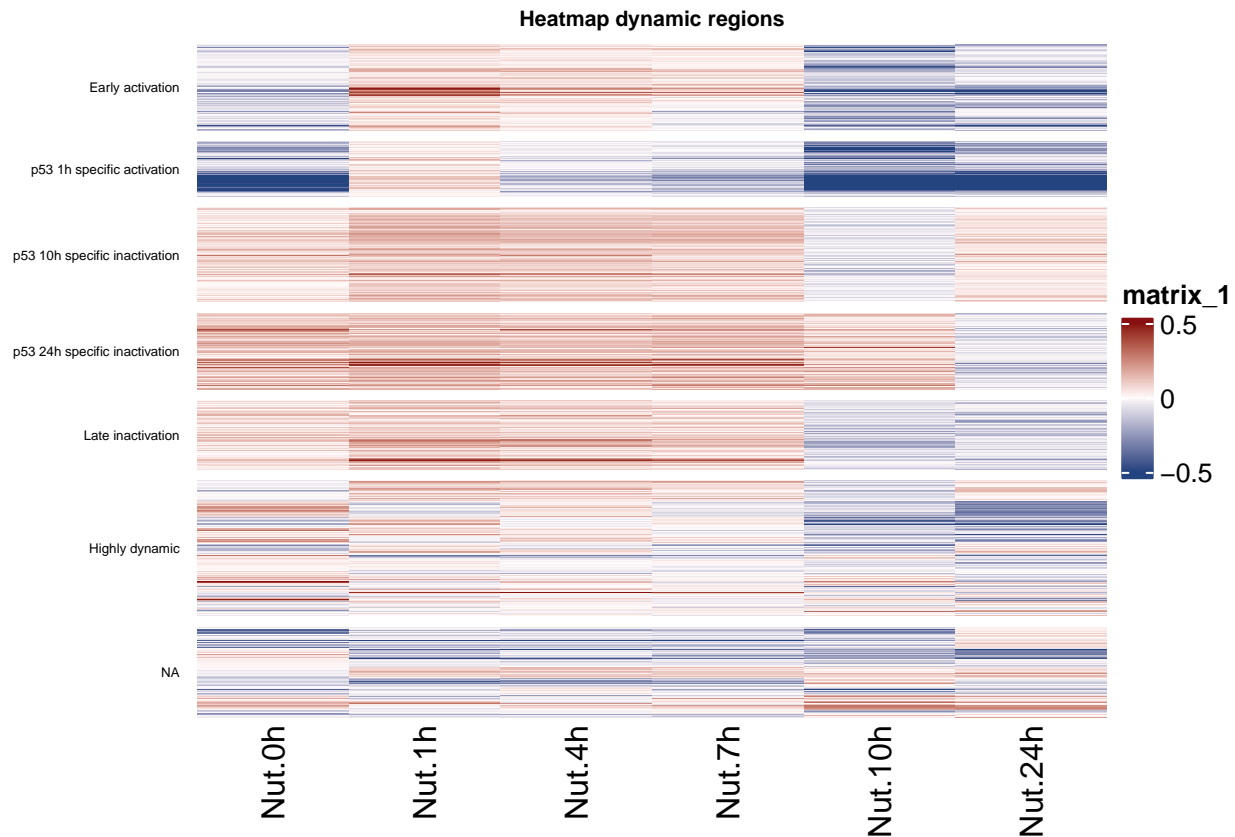


Fig1F. Transformation of the Hi-C map on the basis of the PC1 values of a PCA on the Hi-C correlation matrix (100 kb resolution) across six time points of TP53 activation. PC1 values for A and B compartments are shown in x and y colours.

```
region <- melt(data.frame(Compartments.gr)[! grepl("NULL", Compartments.gr$combinations) & data.frame(C
region$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)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
```

```
## i Please use `linewidth` instead.
```

```
## Warning: Removed 57 rows containing missing values (`geom_bar()`).
```

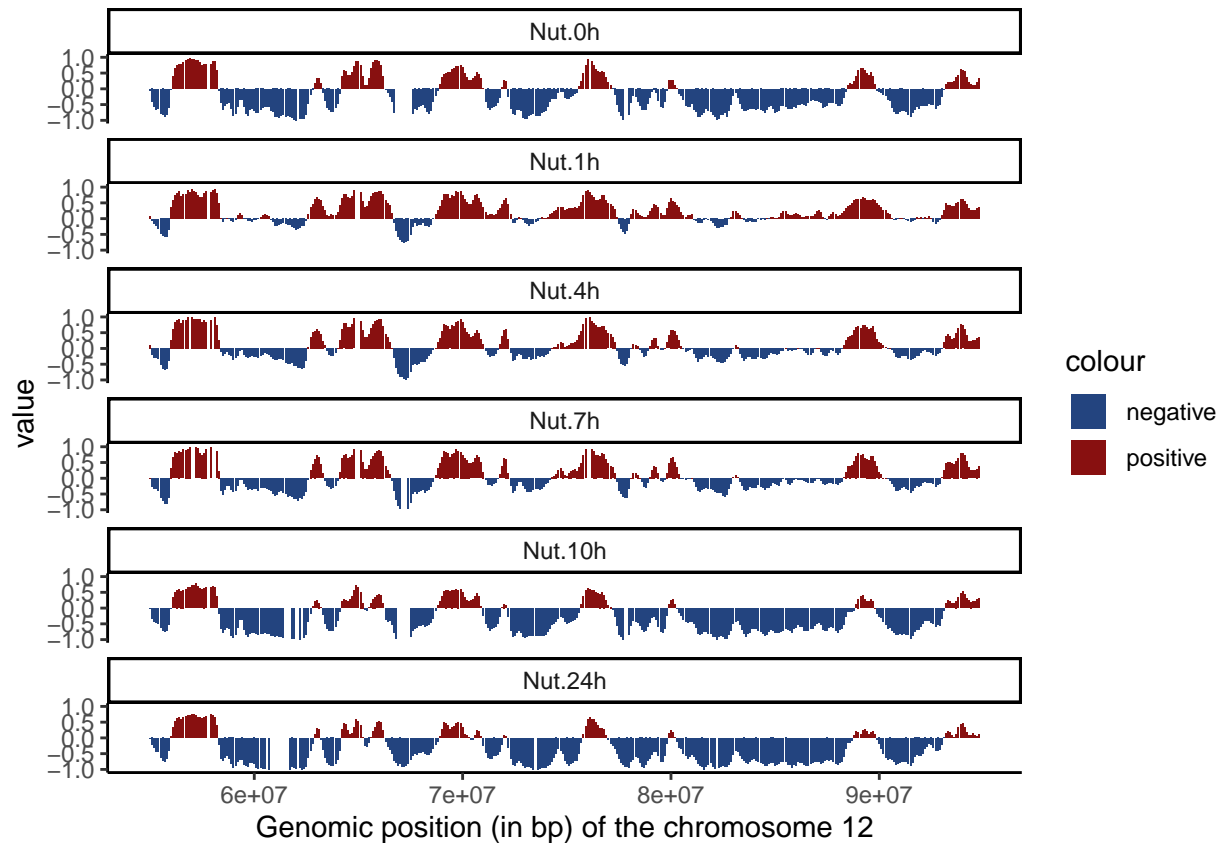
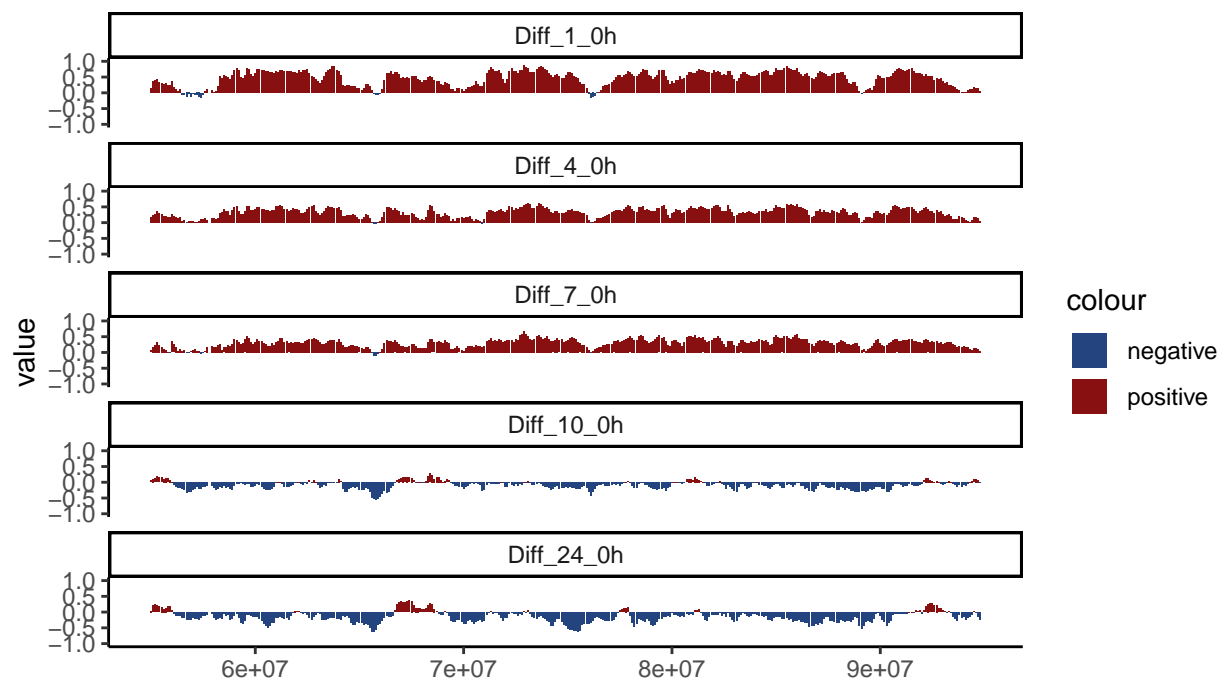


Fig1G.Differential of f (The two tendencies of early activation and late inactivation are highlighted)

```
Compartments.gr$Diff_1_0h <- Compartments.gr$Nut.1h - Compartments.gr$Nut.0h
Compartments.gr$Diff_4_0h <- Compartments.gr$Nut.4h - Compartments.gr$Nut.0h
Compartments.gr$Diff_7_0h <- Compartments.gr$Nut.7h - Compartments.gr$Nut.0h
Compartments.gr$Diff_10_0h <- Compartments.gr$Nut.10h - Compartments.gr$Nut.0h
Compartments.gr$Diff_24_0h <- Compartments.gr$Nut.24h - Compartments.gr$Nut.0h

diff_region <- melt(data.frame(Compartments.gr)[! grepl("NULL", Compartments.gr$combinations) & data.frame(
diff_region$colour <- ifelse(diff_region$value < 0,"negative","positive")

ggplot(diff_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)
```



Genomic position (in bp) of the chromosome 12

END ————— #