

HiC_Compartments_SupplFig1

SupplFig1 —

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

SupplFig1C.Fraction of genome in A and B compartment of all time points.
Y-axis match the temporal status of p53 activation.

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

head(table_AB)

##   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

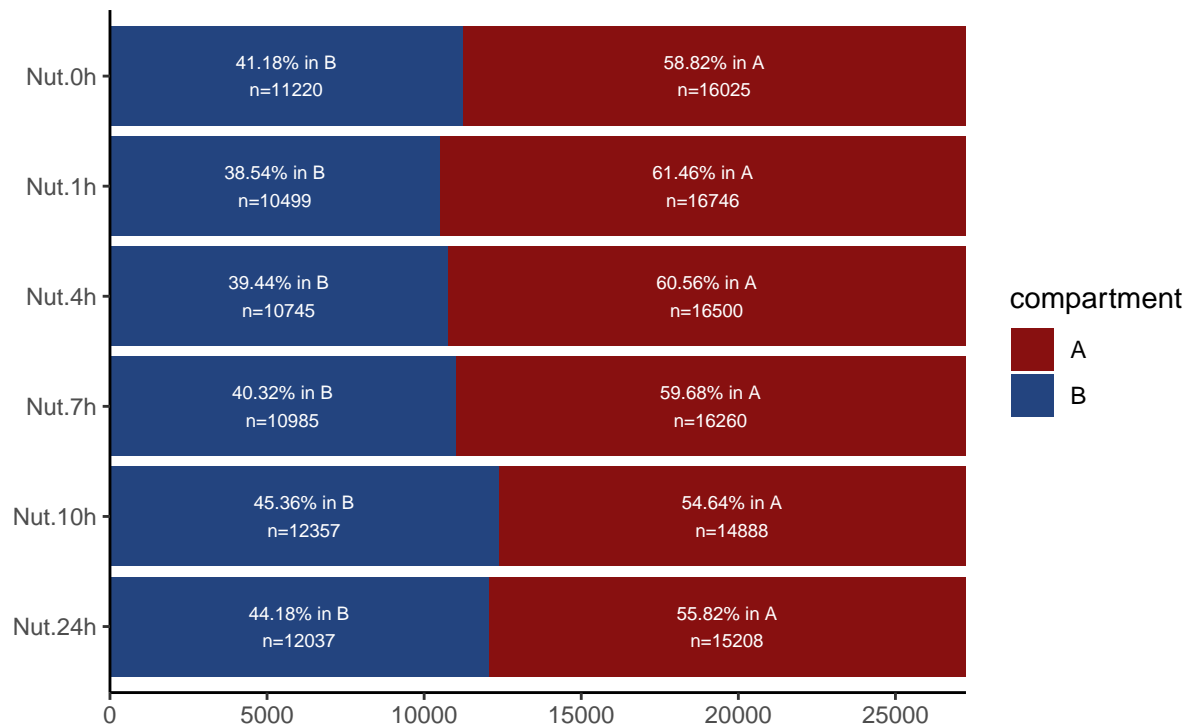
# Nut.0h Nut.1h Nut.4h Nut.7h Nut.10h Nut.24h
# A  16025  16746  16500  16260   14888   15208
# B   11220   10499   10745   10985   12357   12037

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", Comp
    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$combination
    theme(plot.subtitle=element_text(size=8, face='italic', color='grey50'))+
    geom_vline(xintercept=table_AB$Category_Nut.0h[2], color="white")
```

A/B genome distribution of all samples

n=27245 compartments

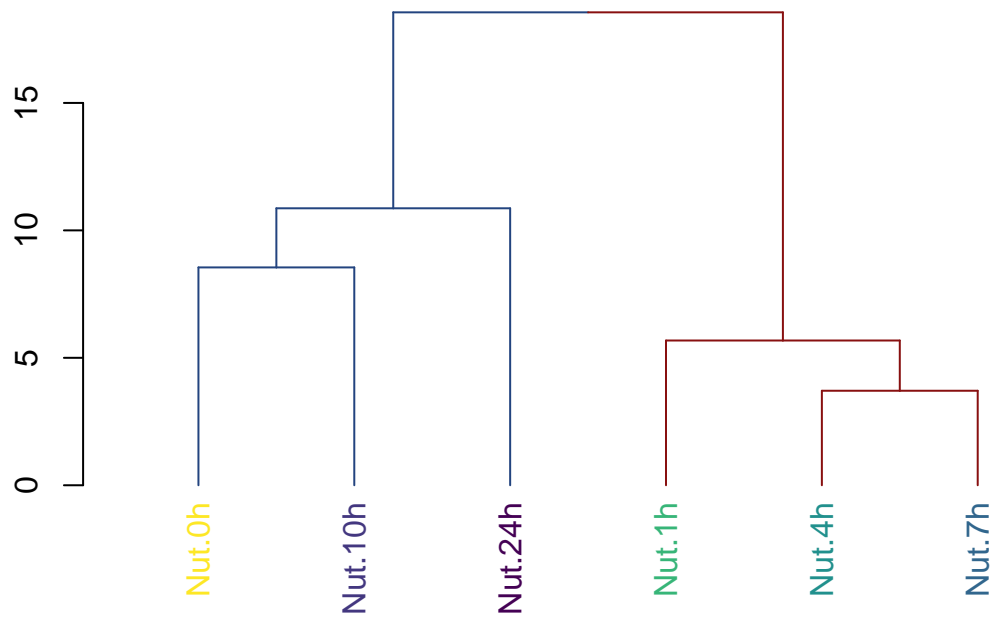


SupplFig1E.Hierachical clustering according to dynamic compartment

```
# Perform hierarchical cluster analysis.
dend <- t(data.frame(Compartments.gr)[!grepl("NULL",Compartments.gr$combinations) & grepl("dynamic", Compartments.gr$combinations),])
  dist(method = "euclidean") %>% hclust(method="ward.D2") %>% sort %>% as.dendrogram()

dend %>%
  set("branches_k_color", value = c("#23447f", "#881010"), k=2) %>%
  set("labels_col", value = c("#fde725ff", "#43377fff", "#440154ff", "#37b578ff", "#21908dff", "#31668dff"),
  plot(horiz=FALSE, axes=TRUE, main="Hierarchical cluster of all the compartment with values in all samples")
```

Hierarchical cluster of all the compartment with values in all sample



SupplFig1F.Heatmap of the non dynamic compartments

```
Heatmap(as.matrix(data.frame(Compartments.gr)[!grepl("NULL",Compartments.gr$combinations) & !grepl("dyna
```

