

R Notebook

```
#['#b2182b', '#ef8a62', '#fddbc7', '#f7f7f7', '#d1e5f0', '#67a9cf', '#2166ac']

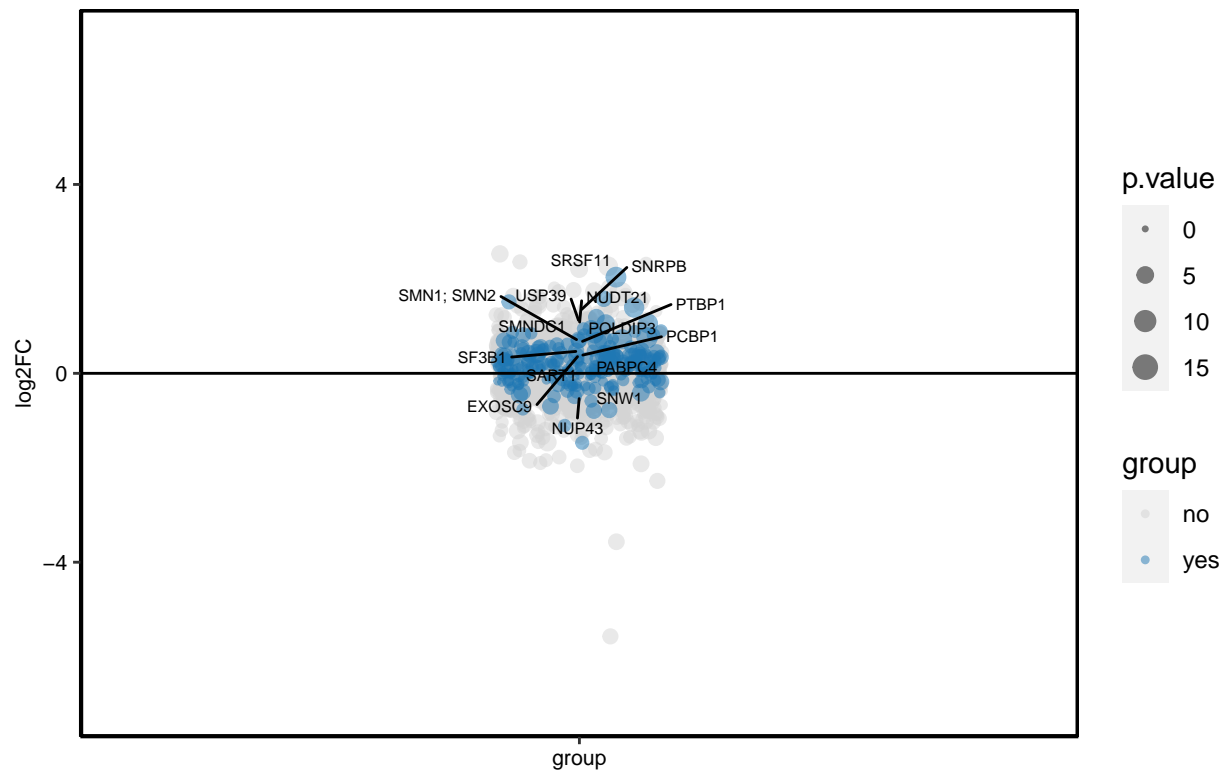
data <- read.csv('InputChromatin_GSK_vs_DMSO.csv')
data$Score <- abs(data$Score)
data <- data[order(data$p.value, decreasing = TRUE),]

#DMSO_color <- '#d4d4d4'
#GSK_color <- '#008837'
#MS023_color <- '#7b3294'

data$df <- 'group'
terms <- c('Transport of Mature', 'RNA transport', 'Spliceosome', 'mRNA splicing', 'mRNA surveillance',
data$pathways <- paste(data$Molecular.Function, data$KEGG.Pathways, data$Reactome.Pathways, sep = ';')

data$transport <- ifelse(grepl(paste(terms, collapse='|'), data$pathways, ignore.case = TRUE), "yes", "no")

data <- data[order(data$transport),]
ggplot(data, aes(x=df, y=GSK.DMSO, color = group, label = Gene.Symbol)) +
  geom_jitter(aes(size=p.value, alpha = group, colour = transport), width=0.1, height=0.1, shape = 20, alpha=0.5) +
  scale_color_manual(values= c('#d4d4d4', '#1f78b4')) +
  geom_text_repel(data = subset(data, transport == 'yes')[1:15,], aes(label=Gene.Symbol), size=2, color='black') +
  theme(legend.position = "right",
        axis.text.y = element_text(size=8, colour = "black"),
        axis.text.x = element_text(size=8, colour = "black"),
        axis.title.y = element_text(size=8, colour = "black"),
        axis.title.x = element_text(size=8, colour = "black"),
        panel.background = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"),
        panel.border = element_rect(colour = "black", fill=NA, size=1))+
  #geom_vline(xintercept=c(0), linetype="solid")+
  geom_hline(yintercept=c(0), linetype="solid")+
  #geom_hline(yintercept=c(4.4), linetype="dotted")+
  ylim(-7,7)+
  #scale_y_continuous(limits = c(0,20), expand = c(0, 0)) +
  labs(title="", x="", y = "log2FC")
```



```

#['#b2182b', '#ef8a62', '#fddbc7', '#f7f7f7', '#d1e5f0', '#67a9cf', '#2166ac']
data <- read.csv('polyA_backgroundsubtracted_GSK_vs_DMSO.csv')
data$Score <- abs(data$Score)
data <- data[order(data$p.value, decreasing = TRUE),]

#DMSO_color <- '#d4d4d4'
#GSK_color <- '#008837'
#MS023_color <- '#7b3294'

data$df <- 'group'
terms <- c('Transport of Mature', 'RNA transport', 'Spliceosome', 'mRNA splicing', 'mRNA surveillance',
data$pathways <- paste(data$Molecular.Function, data$KEGG.Pathways, data$Reactome.Pathways, sep = ';')

data$transport <- ifelse(grepl(paste(terms, collapse='|'), data$pathways, ignore.case = TRUE), "yes", "no")

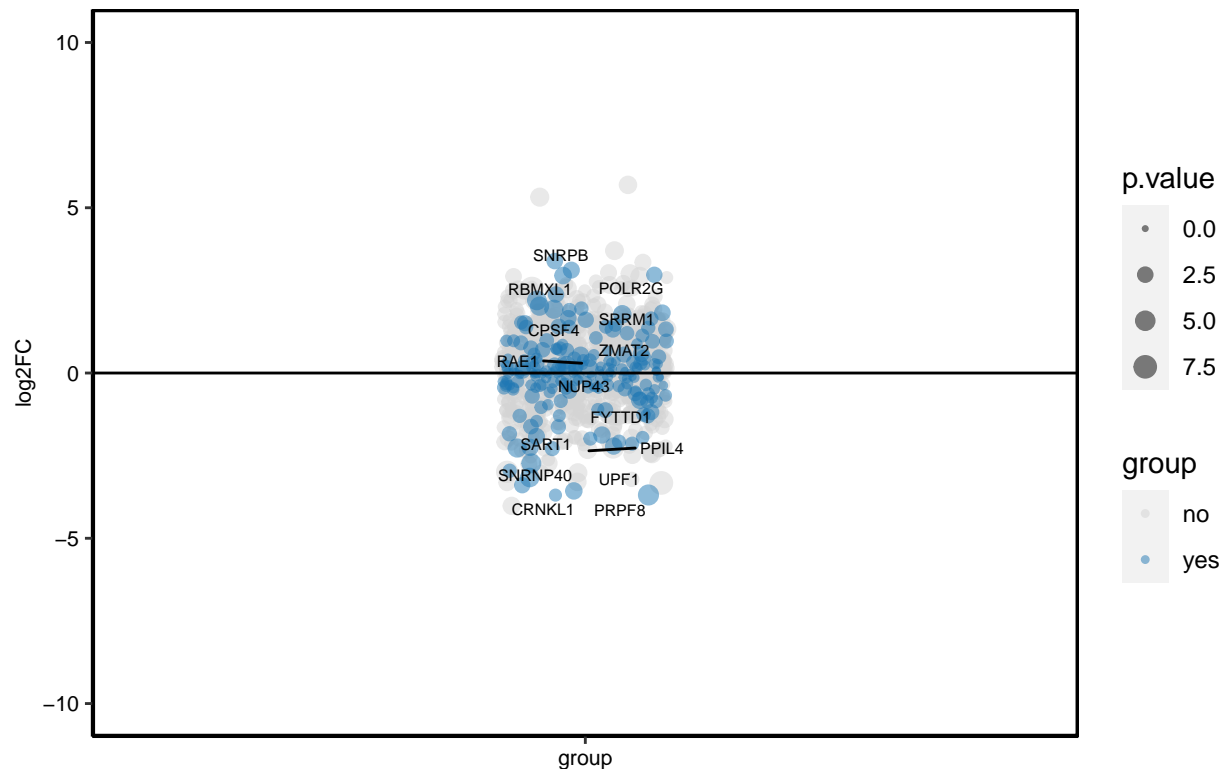
data <- data[order(data$transport),]
ggplot(data, aes(x=df, y=GSK.DMSO, color = group, label = Gene.Symbol)) +
  geom_jitter(aes(size=p.value, alpha = group, colour = transport), width=0.1, height=0.1, shape = 20, aes(
  scale_color_manual(values= c('#d4d4d4', '#1f78b4')) +
  geom_text_repel(data = subset(data, transport == 'yes')[1:15,], aes(label=Gene.Symbol), size=2, color=
  theme(legend.position = "right",
        axis.text.y = element_text(size=8, colour = "black"),
        axis.text.x = element_text(size=8, colour = "black"),
        axis.title.y = element_text(size=8, colour = "black"),
        axis.title.x = element_text(size=8, colour = "black"),
        panel.background = element_blank(),

```

```

panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),
axis.line = element_line(colour = "black"),
panel.border = element_rect(colour = "black", fill=NA, size=1))+
#geom_vline(xintercept=c(0), linetype="solid")+
geom_hline(yintercept=c(0), linetype="solid")+
#geom_hline(yintercept=c(4.4), linetype="dotted")+
ylim(-10,10)+
#scale_y_continuous(limits = c(0,20), expand = c(0, 0)) +
labs(title="", x="", y = "log2FC")

```



```

#['#b2182b', '#ef8a62', '#fddbc7', '#f7f7f7', '#d1e5f0', '#67a9cf', '#2166ac']

```

```

data <- read.csv('InputChromatin_MS023_vs_DMSO.csv')
data$Score <- abs(data$Score)
data <- data[order(data$p.value, decreasing = TRUE),]

```

```

#DMSO_color <- '#d4d4d4'
#GSK_color <- '#008837'
#MS023_color <- '#7b3294'

```

```

data$df <- 'group'
terms <- c('Transport of Mature', 'RNA transport', 'Spliceosome', 'mRNA splicing', 'mRNA surveillance',
data$pathways <- paste(data$Molecular.Function, data$KEGG.Pathways, data$Reactome.Pathways, sep = ';')

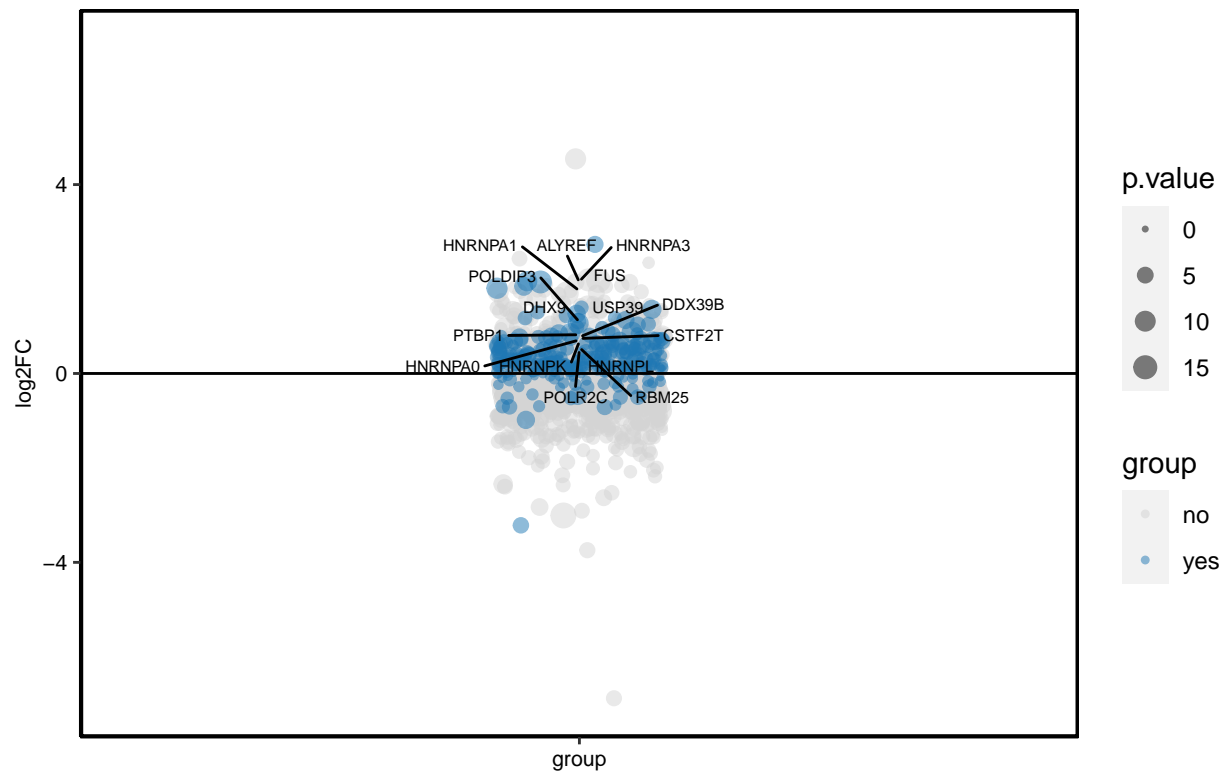
```

```

data$transport <- ifelse(grepl(paste(terms,collapse='|'), data$pathways, ignore.case = TRUE), "yes", "no")

data <- data[order(data$transport),]
ggplot(data, aes(x=df, y=MS023.DMSO, color = group, label = Gene.Symbol)) +
  geom_jitter(aes(size=p.value, alpha = group, colour = transport),width=0.1, height=0.1, shape = 20, alpha=0.5) +
  scale_color_manual(values= c('#d4d4d4', '#1f78b4')) +
  geom_text_repel(data = subset(data, transport == 'yes')[1:15,], aes(label=Gene.Symbol), size=2, color='black') +
  theme(legend.position = "right",
        axis.text.y = element_text(size=8, colour = "black"),
        axis.text.x = element_text(size=8, colour = "black"),
        axis.title.y = element_text(size=8, colour = "black"),
        axis.title.x = element_text(size=8, colour = "black"),
        panel.background = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"),
        panel.border = element_rect(colour = "black", fill=NA, size=1))+
  #geom_vline(xintercept=c(0), linetype="solid")+
  geom_hline(yintercept=c(0), linetype="solid")+
  #geom_hline(yintercept=c(4.4), linetype="dotted")+
  ylim(-7,7)+
  #scale_y_continuous(limits = c(0,20), expand = c(0, 0)) +
  labs(title="",x="", y = "log2FC")

```



```

#['#b2182b', '#ef8a62', '#fddbc7', '#f7f7f7', '#d1e5f0', '#67a9cf', '#2166ac']

data <- read.csv('polyA_backgroundsubtracted_MS023_vs_DMS0.csv')
data$Score <- abs(data$Score)
data <- data[order(data$p.value, decreasing = TRUE),]

#DMS0_color <- '#d4d4d4'
#GSK_color <- '#008837'
#MS023_color <- '#7b3294'

data$df <- 'group'
terms <- c('Transport of Mature', 'RNA transport', 'Spliceosome', 'mRNA splicing', 'mRNA surveillance',
data$pathways <- paste(data$Molecular.Function, data$KEGG.Pathways, data$Reactome.Pathways, sep = ';')

data$transport <- ifelse(grepl(paste(terms, collapse='|'), data$pathways, ignore.case = TRUE), "yes", "no")

data <- data[order(data$transport),]
ggplot(data, aes(x=df, y=MS023.DMS0, color = group, label = Gene.Symbol)) +
  geom_jitter(aes(size=p.value, alpha = group, colour = transport), width=0.1, height=0.1, shape = 20, aes(alpha=0.5)) +
  scale_color_manual(values= c('#d4d4d4', '#1f78b4')) +
  geom_text_repel(data = subset(data, transport == 'yes')[1:15,], aes(label=Gene.Symbol), size=2, color="black",
  theme(legend.position = "right",
        axis.text.y = element_text(size=8, colour = "black"),
        axis.text.x = element_text(size=8, colour = "black"),
        axis.title.y = element_text(size=8, colour = "black"),
        axis.title.x = element_text(size=8, colour = "black"),
        panel.background = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"),
        panel.border = element_rect(colour = "black", fill=NA, size=1))+
  #geom_vline(xintercept=c(0), linetype="solid")+
  geom_hline(yintercept=c(0), linetype="solid")+
  #geom_hline(yintercept=c(4.4), linetype="dotted")+
  ylim(-10,10)+
  #scale_y_continuous(limits = c(0,20), expand = c(0, 0)) +
  labs(title="", x="", y = "log2FC")

```

