

Comparison of Hot and Cold Tumors

Gepoliano Chaves (Ph. D.)

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To prepare material for this notebook I used notebooks ADRN-MES-Sengupta-Final.Rmd and “Survial MES.Rmd”.

1) Library installation

```
library(ggplot2)
library(GSVA)
library(GSVAdata)
library(data.table)
library(stringr)
library(tibble)
library(viridis)
library(expss)
library(ggpubr)
```

2) Gene Expression and GSVA

Load data-frames

```
GSE49711 <- readRDS("../..../Hypoxia_Paper/for loop MES/data/GSE49711.rds")
GSE49711_GeneMatrix <- as.matrix(GSE49711)
```

Load gene sets

```
cfDNA_PCA_gene_list <- getGmt("~/Desktop/Gepoliano/Analysis/cfDNA_genes_PCA.txt")
```

```
## Warning in readLines(con, ...): incomplete final line found on
## '~/Desktop/Gepoliano/Analysis/cfDNA_genes_PCA.txt'
```

```
## Warning in getGmt("~/Desktop/Gepoliano/Analysis/cfDNA_genes_PCA.txt"): 323
## record(s) contain duplicate ids: ADRN_Gene_List_373, ADRN_Gronigen, ...,
## WP_GLYCOLYSIS_AND_GLUconeogenesis_7, WP_GLYCOLYSIS_IN_SENESCENCE_Genes_4
```

Construct GSVA data-frame

```

# Needs to re-run this step if there are new gene sets
GSE49711_GSVA <- gsva(GSE49711_GeneMatrix,
                     cfDNA_PCA_gene_list,
                     min.sz=1, max.sz=Inf,
                     verbose=TRUE)

## Warning: useNames = NA is deprecated. Instead, specify either useNames = TRUE
## or useNames = TRUE.

## Warning in .filterFeatures(expr, method): 755 genes with constant expression
## values throughout the samples.

## Warning in .filterFeatures(expr, method): Since argument method!="ssgsea",
## genes with constant expression values are discarded.

## Warning in .gsva(expr, mapped.gset.idx.list, method, kcdf, rnaseq, abs.ranking,
## : Some gene sets have size one. Consider setting 'min.sz > 1'.

## Estimating GSVA scores for 314 gene sets.
## Estimating ECDFs with Gaussian kernels
## |

```

```

GSVA_GeneExpression_Matrix <- rbind(GSE49711_GSVA, GSE49711_GeneMatrix)

```

2) Process GSVA DF with Phenotype Scores

Previous chunk used was from notebook “Multiple Test Correction Kocak.Rmd”. Below we will transpose and Name Column with Sample Names

```

GSVA_GeneExpression_Matrix_t <- t(GSVA_GeneExpression_Matrix)
GSVA_GeneExpression_Matrix_t_df <- as.data.frame(GSVA_GeneExpression_Matrix_t)
GSVA_GeneExpression_Matrix_t_df["Sample_ID"] <- rownames(GSVA_GeneExpression_Matrix_t_df)

```

2.1) Inflammatory Response vs Hot

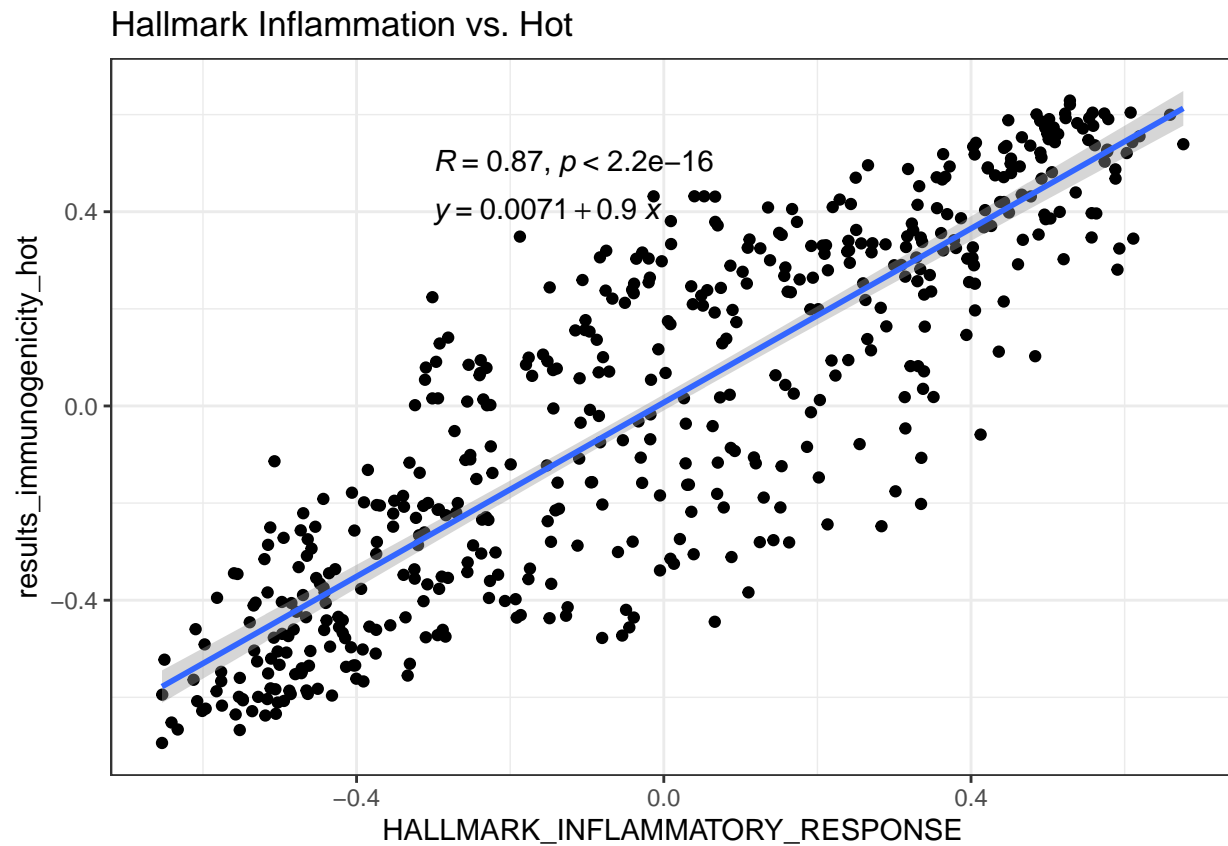
```

qplot(data = GSVA_GeneExpression_Matrix_t_df,
      HALLMARK_INFLAMMATORY_RESPONSE,
      results_immunogenicity_hot,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "results_immunogenicity_hot",
      main = "Hallmark Inflammation vs. Hot")+
  geom_smooth(method=lm)+
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4)+
  theme_bw()

```

```
## Warning: 'qplot()' was deprecated in ggplot2 3.4.0.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

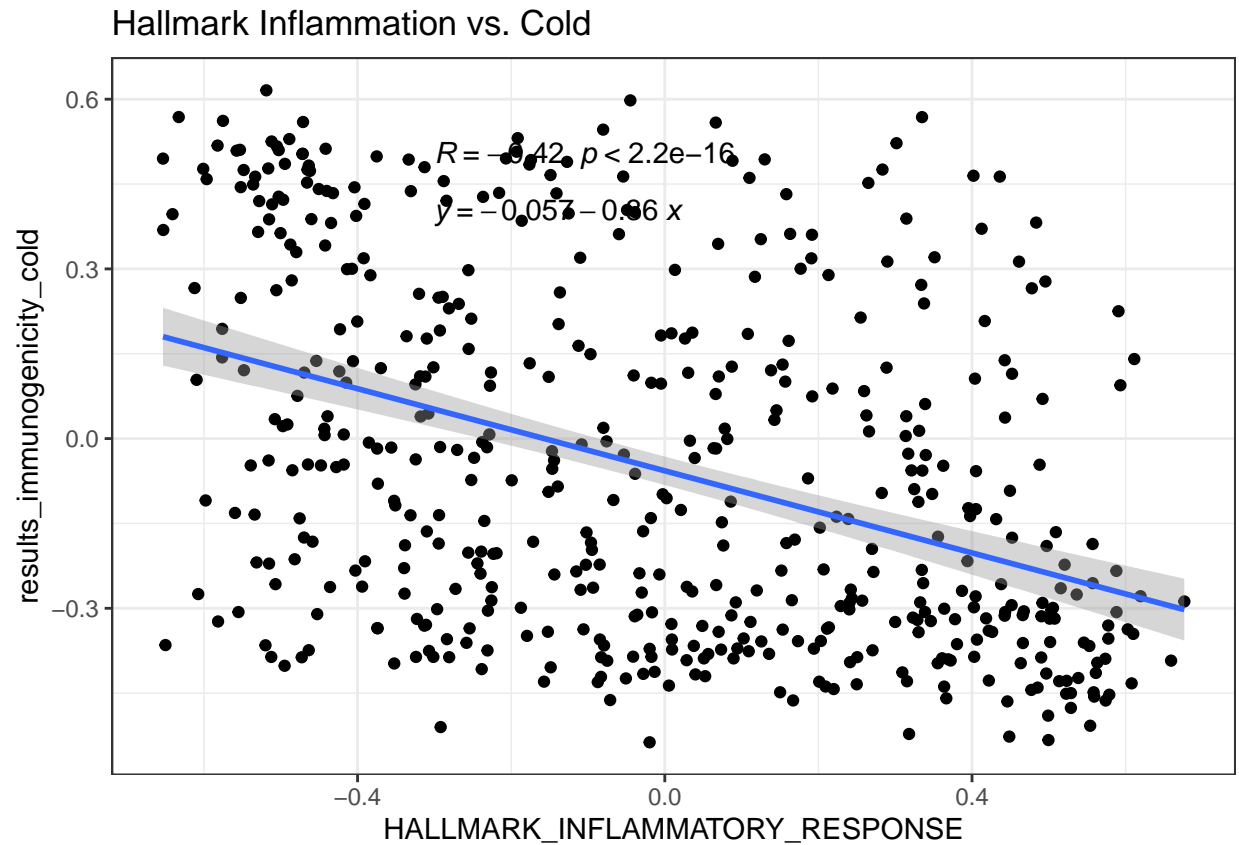
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.2) Inflammatory Response vs Cold

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      HALLMARK_INFLAMMATORY_RESPONSE,
      results_immunogenicity_cold,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "results_immunogenicity_cold",
      main = "Hallmark Inflammation vs. Cold")+
  geom_smooth(method=lm)+
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4)+
  theme_bw()
```

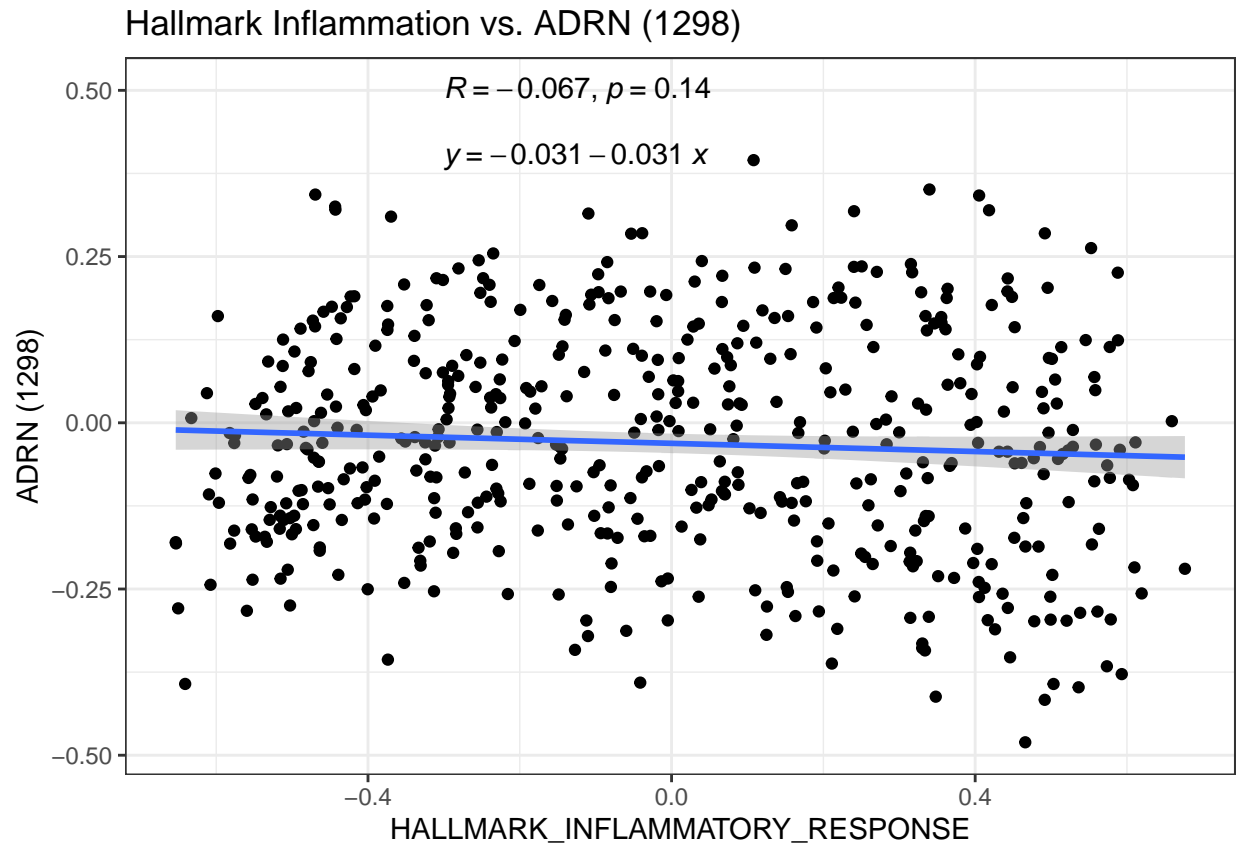
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.3) Inflammatory Response vs ADRN

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      HALLMARK_INFLAMMATORY_RESPONSE,
      List_RNA_Normoxia_ADRN_vs_MES_Up.txt,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "ADRN (1298)",
      main = "Hallmark Inflammation vs. ADRN (1298)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

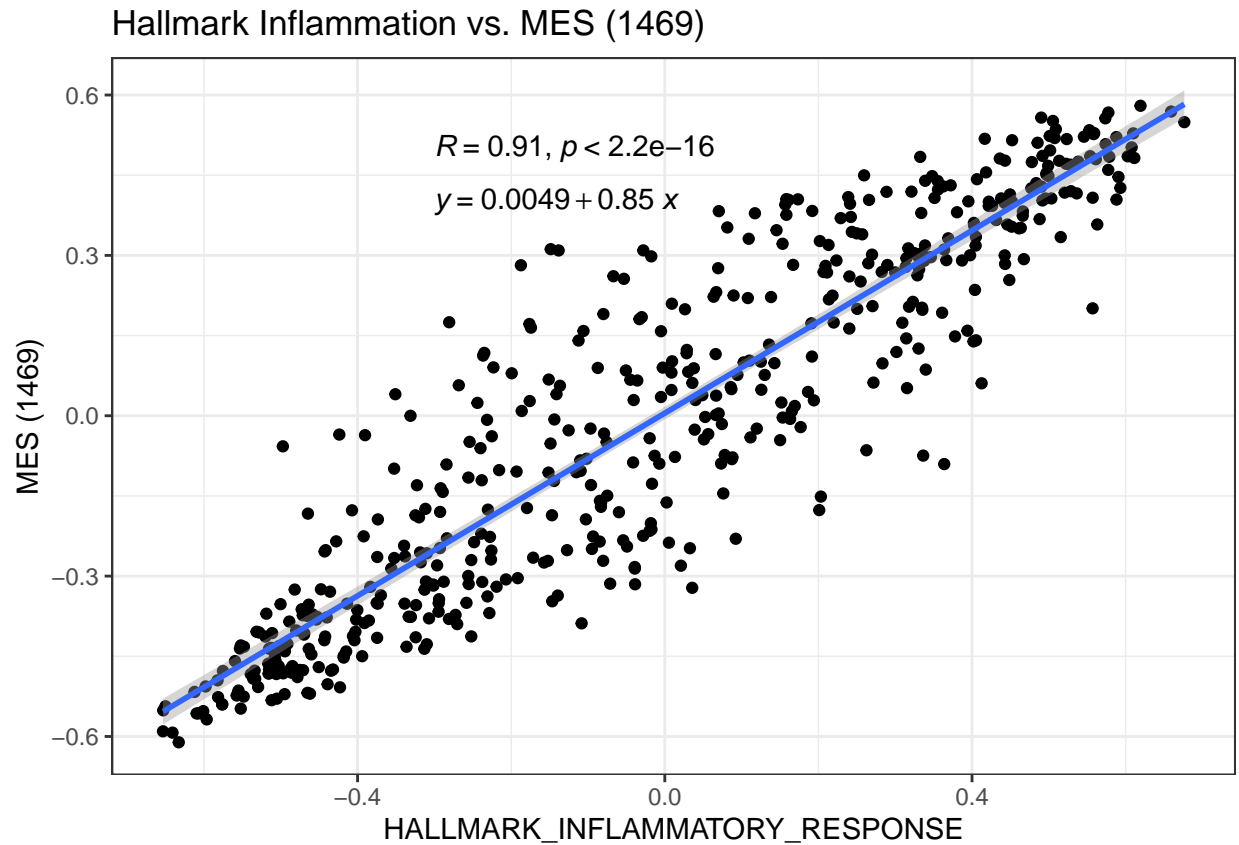
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.4) Inflammatory Response vs MES

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      HALLMARK_INFLAMMATORY_RESPONSE,
      List_RNA_Normoxia_ADRN_vs_MES_Down.txt,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "MES (1469)",
      main = "Hallmark Inflammation vs. MES (1469)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

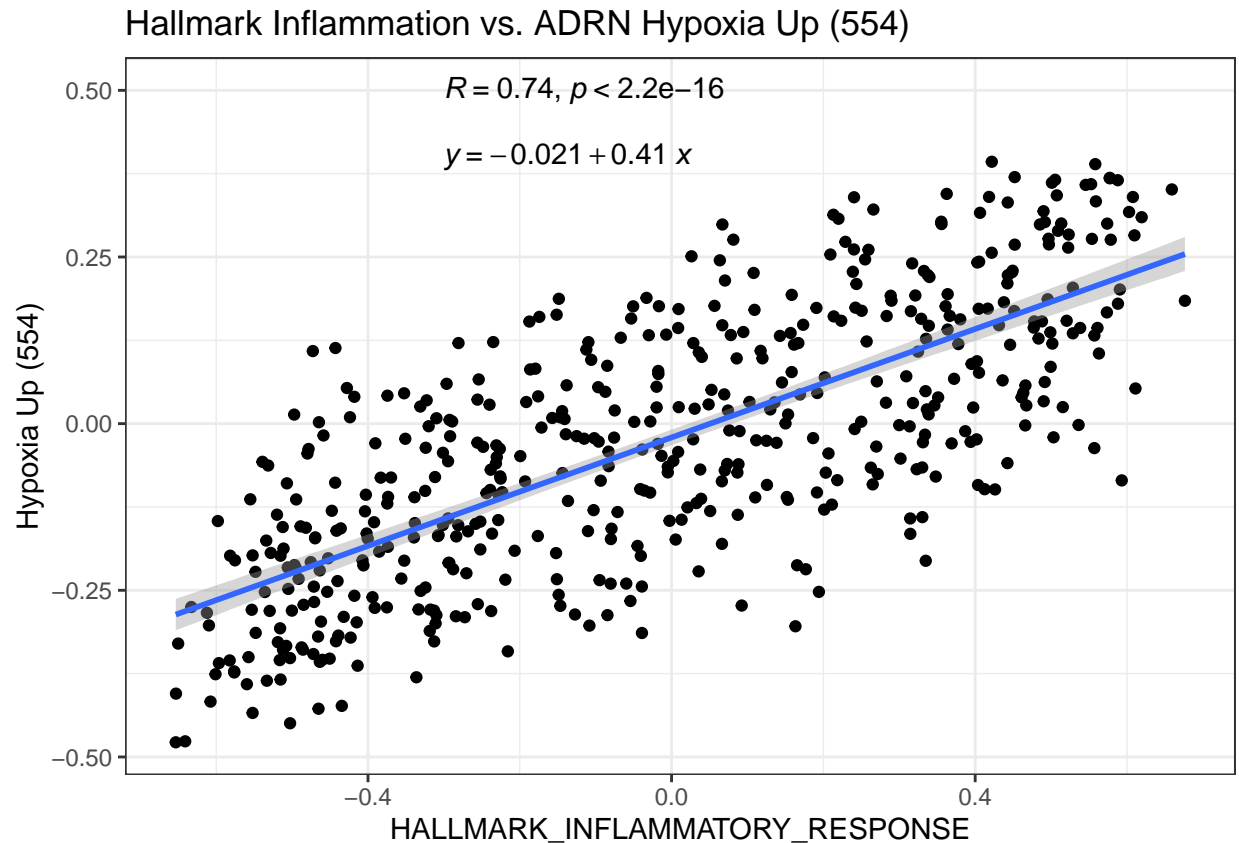
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.5) Inflammatory Response vs ADRN_Norm_vs_Hypo_Up_554.txt

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      HALLMARK_INFLAMMATORY_RESPONSE,
      ADRN_Norm_vs_Hypo_Up_554.txt,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "Hypoxia Up (554)",
      main = "Hallmark Inflammation vs. ADRN Hypoxia Up (554)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

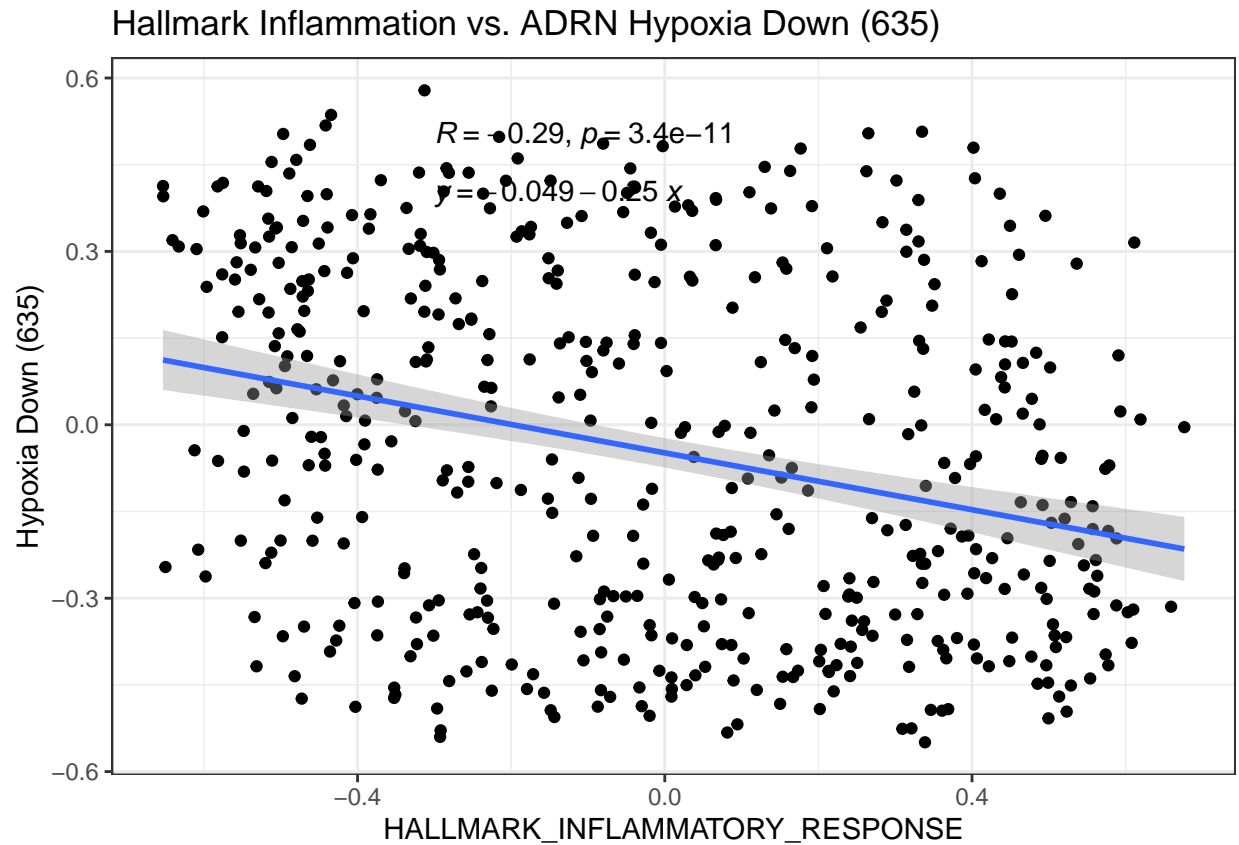
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.6) Inflammatory Response vs ADRN_Norm_vs_Hypo_Down_635.txt

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      HALLMARK_INFLAMMATORY_RESPONSE,
      ADRN_Norm_vs_Hypo_Down_635.txt,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "Hypoxia Down (635)",
      main = "Hallmark Inflammation vs. ADRN Hypoxia Down (635)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

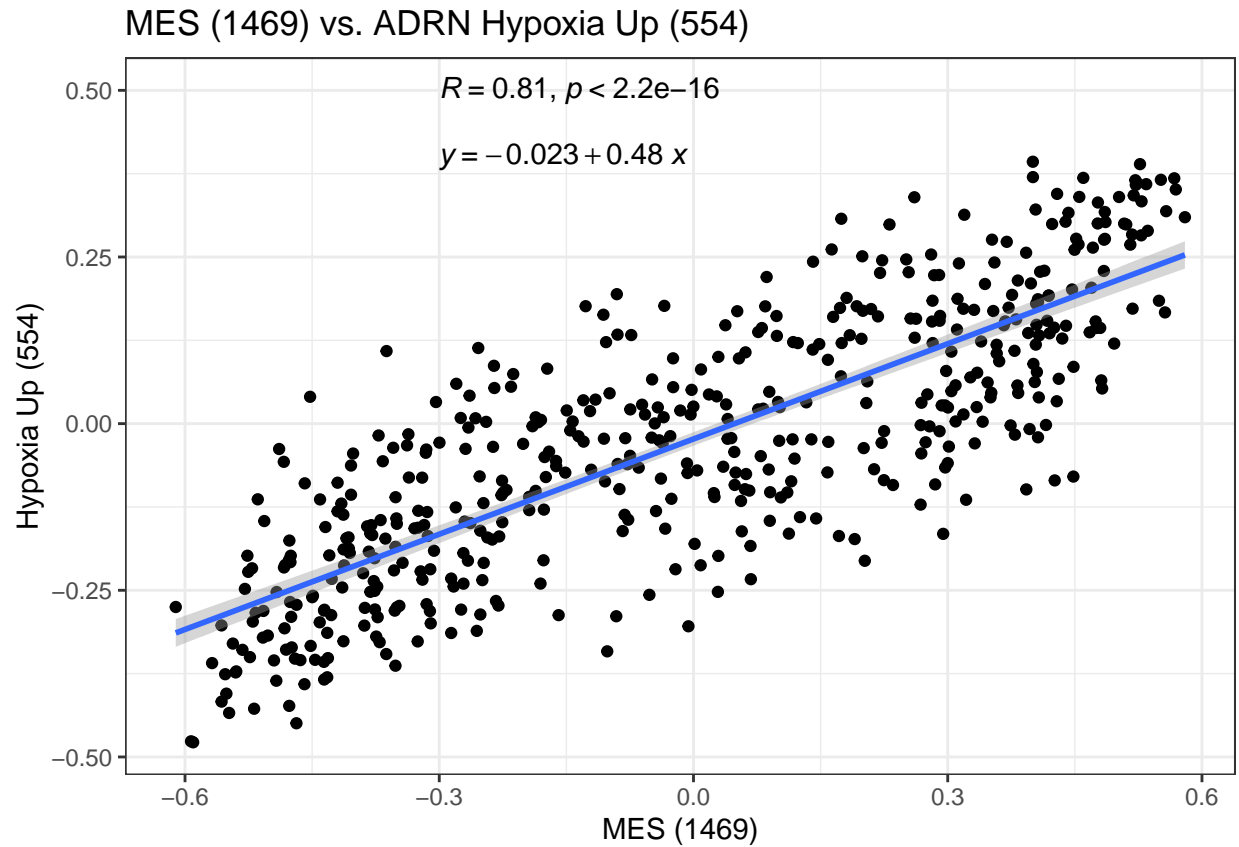
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.7) Check MES vs. Hypoxia Up

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      List_RNA_Normoxia_ADRN_vs_MES_Down.txt,
      ADRN_Norm_vs_Hypo_Up_554.txt,
      xlab = "MES (1469)",
      ylab = "Hypoxia Up (554)",
      main = "MES (1469) vs. ADRN Hypoxia Up (554)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

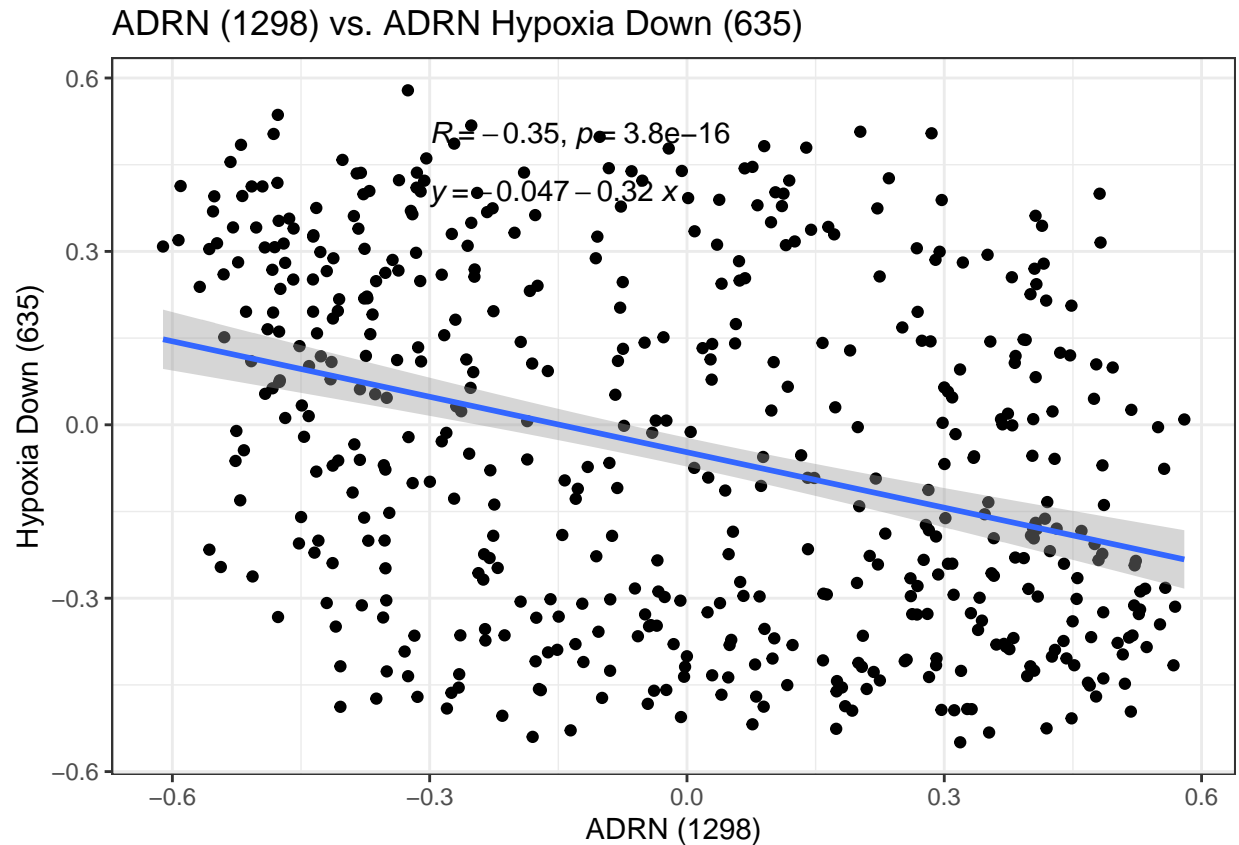
```
## 'geom_smooth()' using formula = 'y ~ x'
```

2.8) Check ADRN vs. Hypoxia Down

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      List_RNA_Normoxia_ADRN_vs_MES_Down.txt,
      ADRN_Norm_vs_Hypo_Down_635.txt,
      xlab = "ADRN (1298)",
      ylab = "Hypoxia Down (635)",
      main = "ADRN (1298) vs. ADRN Hypoxia Down (635)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

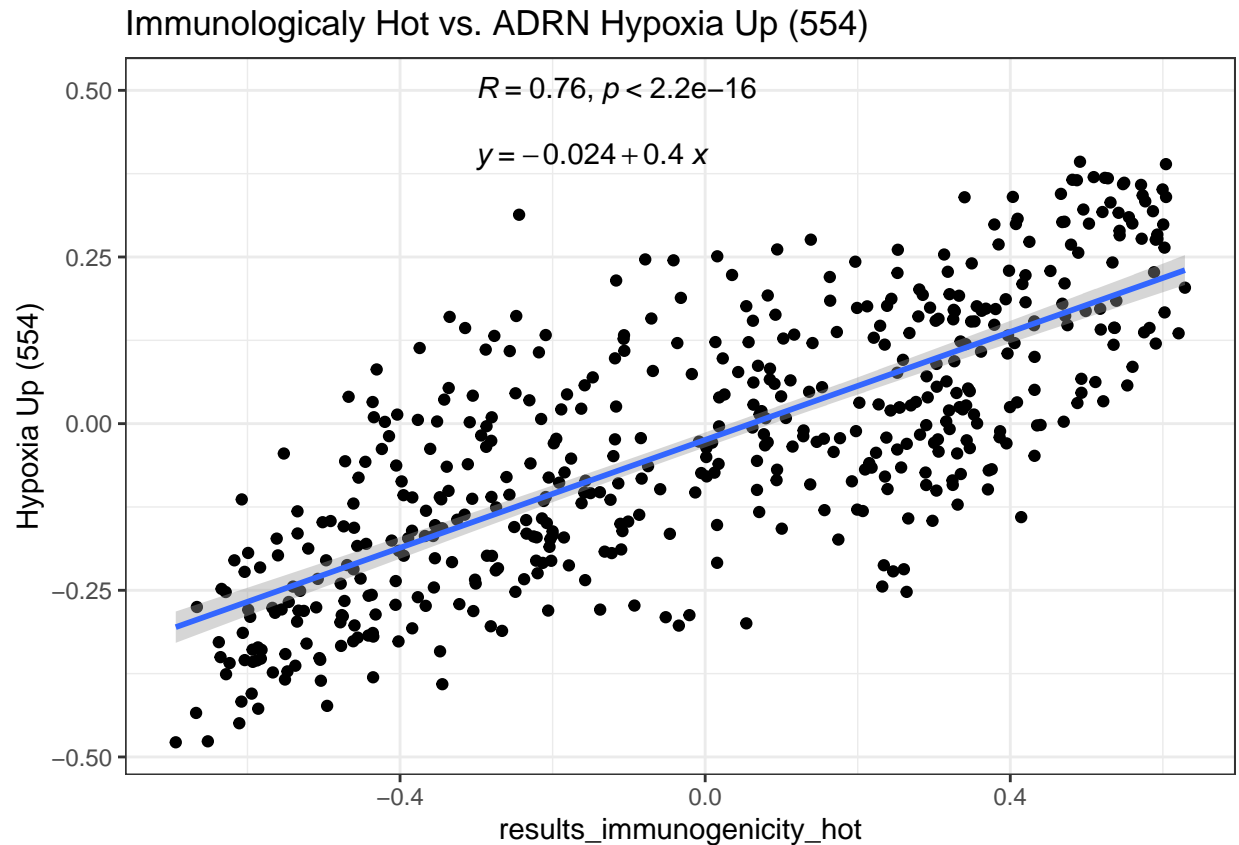
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.9) Check Hot vs. Hypoxia Up

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      results_immunogenicity_hot,
      ADRN_Norm_vs_Hypo_Up_554.txt,
      xlab = "results_immunogenicity_hot",
      ylab = "Hypoxia Up (554)",
      main = "Immunologically Hot vs. ADRN Hypoxia Up (554)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

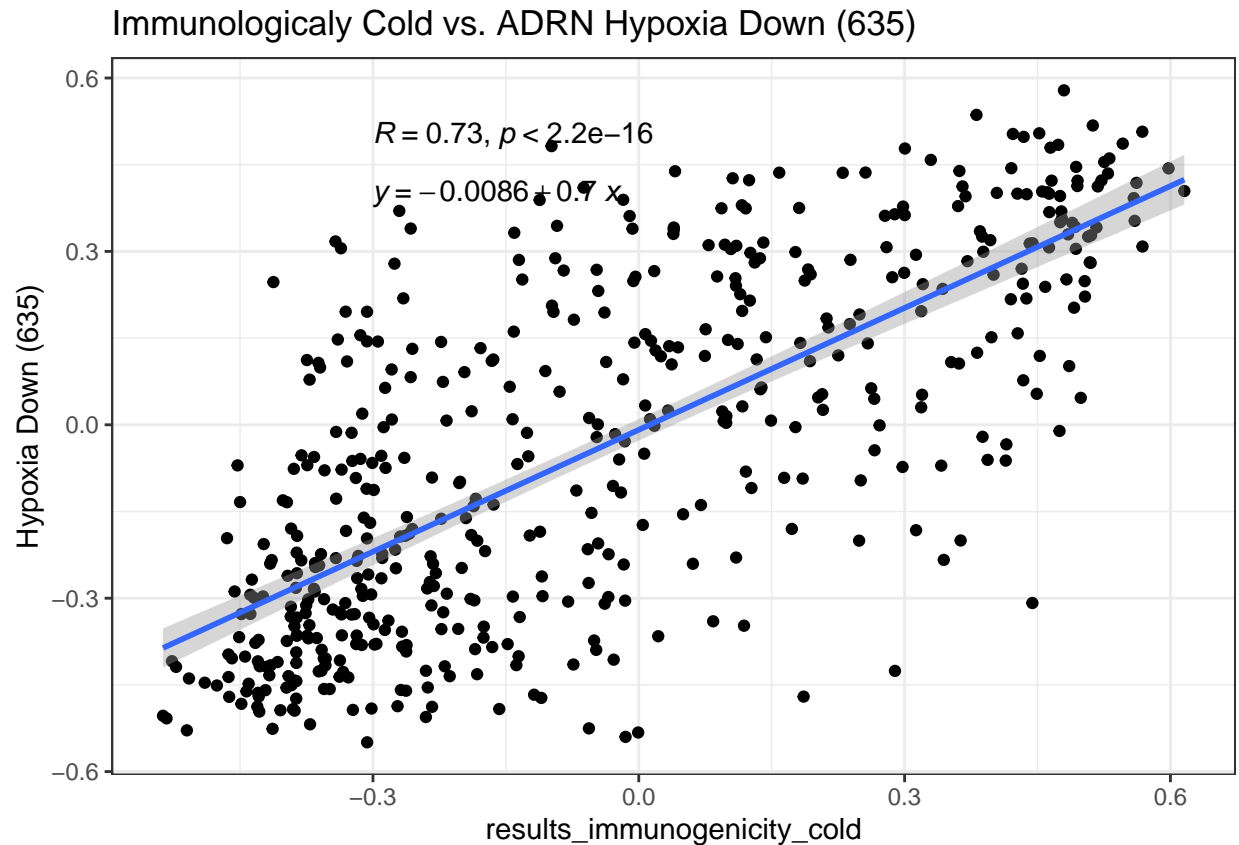
```
## 'geom_smooth()' using formula = 'y ~ x'
```



2.10) Check Cold vs. Hypoxia Down

```
qplot(data = GSVA_GeneExpression_Matrix_t_df,
      results_immunogenicity_cold,
      ADRN_Norm_vs_Hypo_Down_635.txt,
      xlab = "results_immunogenicity_cold",
      ylab = "Hypoxia Down (635)",
      main = "Immunologically Cold vs. ADRN Hypoxia Down (635)") +
  geom_smooth(method=lm) +
  stat_cor(label.x = (-.3), label.y = 0.5) +
  stat_regline_equation(label.x = (-.3), label.y = 0.4) +
  theme_bw()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



Correlation Matrix

```
r2_gse62564_gsva_genes_df <- t(r2_gse62564_GSVA_genes)
```

Select terms to be plotted

```
GSVA_GeneExpression_Matrix <- GSVA_GeneExpression_Matrix_t_df[,
  c("HALLMARK_INFLAMMATORY_RESPONSE",
    "results_immunogenicity_hot",
    "results_immunogenicity_cold",
    "List_RNA_Normoxia_ADRN_vs_MES_Up.txt",
    "List_RNA_Normoxia_ADRN_vs_MES_Down.txt",
    "ADRN_Norm_vs_Hypo_Up_554.txt",
    "ADRN_Norm_vs_Hypo_Down_635.txt", #, This
    # "MES_Norm_vs_Hypo.compCas_Up_287.txt"
    # "MES_Norm_vs_Hypo.compCas_Down_171.tx
    # "MES_Norm_vs_Hypo.compCas_Up_212.txt"
    # "MES_Norm_vs_Hypo.compCas_Down_103.tx
  )]
```

```

GSVA_GeneExpression_Matrix_df <- as.data.frame(GSVA_GeneExpression_Matrix)

GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Inflam_Response = HALL
GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hot = results_immunoge
GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Cold = results_immunoge
GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(ADRN_1298 = List_RNA_No
GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(MES_1469 = List_RNA_No
GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hypo_Up_554 = ADRN_Norm
GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hypo_Down_635 = ADRN_No

# GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hypo_UP_287 = MES_No
# GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hypo_DN_171 = MES_No
# GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hypo_UP_212 = MES_No
# GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% dplyr::rename(Hypo_DN_103 = MES_No

```

Make character, numeric

```
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.1.2
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:expss':
```

```
##
```

```
##      compute, contains, na_if, recode, vars, where
```

```
## The following objects are masked from 'package:maditr':
```

```
##
```

```
##      between, coalesce, first, last
```

```
## The following objects are masked from 'package:data.table':
```

```
##
```

```
##      between, first, last
```

```
## The following objects are masked from 'package:GSEABase':
```

```
##
```

```
##      intersect, setdiff, union
```

```
## The following object is masked from 'package:graph':
```

```
##
```

```
##      union
```

```
## The following object is masked from 'package:AnnotationDbi':
```

```
##
```

```
##      select
```

```
## The following objects are masked from 'package:IRanges':
```

```
##
```

```
##      collapse, desc, intersect, setdiff, slice, union
```

```
## The following objects are masked from 'package:S4Vectors':
##
##   first, intersect, rename, setdiff, setequal, union

## The following object is masked from 'package:Biobase':
##
##   combine

## The following objects are masked from 'package:BiocGenerics':
##
##   combine, intersect, setdiff, union

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

GSVA_GeneExpression_Matrix_df <- GSVA_GeneExpression_Matrix_df %>% mutate_if(is.character, as.numeric)
```

Calculate correlation

```
GSVA_GeneExpression_Matrix_cor_df <- cor(GSVA_GeneExpression_Matrix_df)
```

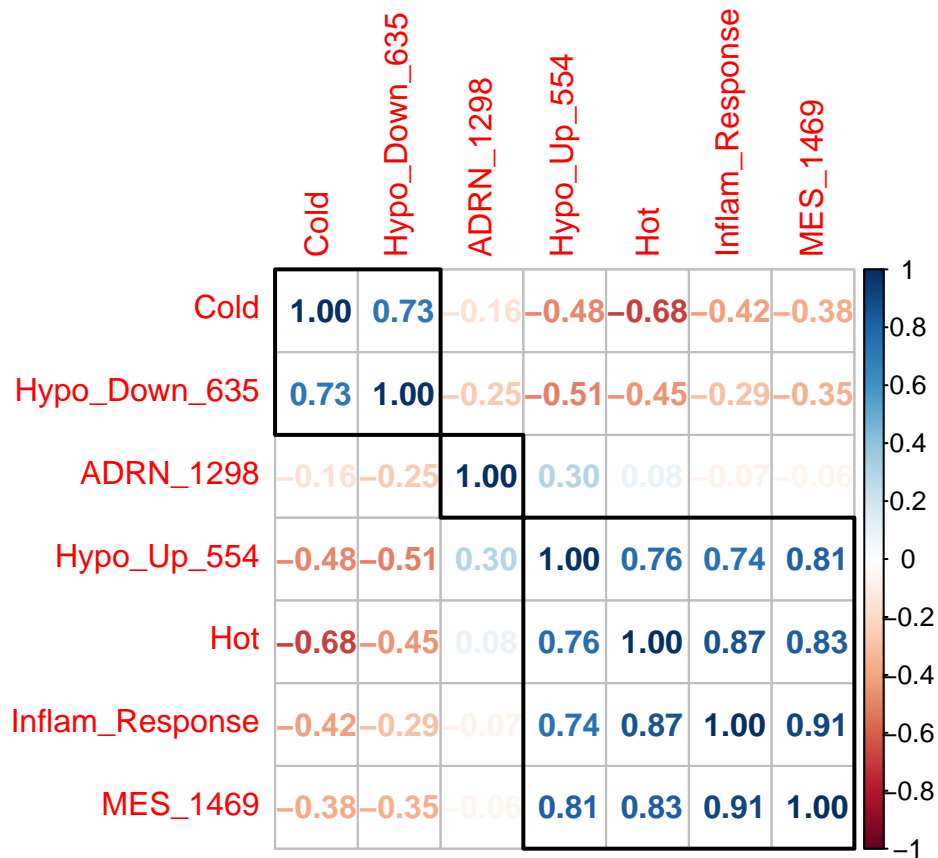
Plot correlation matrix

Plot with colorful number

```
library(corrplot )

## corrplot 0.92 loaded

corrplot(GSVA_GeneExpression_Matrix_cor_df, method = 'number', order="hclust", addrect = 3)
```



Plot circles

```

corrplot(GSVA_GeneExpression_Matrix_cor_df,
  type="lower",
  order="hclust",
  #method = c(pie),
  title = "Correlation Matrix Hot and Cold Tumors",
  tl.col = "black",
  #tl.offset=1,
  tl.srt = 45,
  addrect = 4,
  col=colorRampPalette(c("#053061",
    "#2166AC",
    "#4393C3",
    "#92C5DE",
    "#D1E5F0",
    "#FFFFFF",
    "#FDDBC7",
    "#F4A582",
    "#D6604D",
    "#B2182B",
    "#67001F"
  ))(200)
)

```

Correlation Matrix Hot and Cold Tumors

