User Guide

Step 1 :

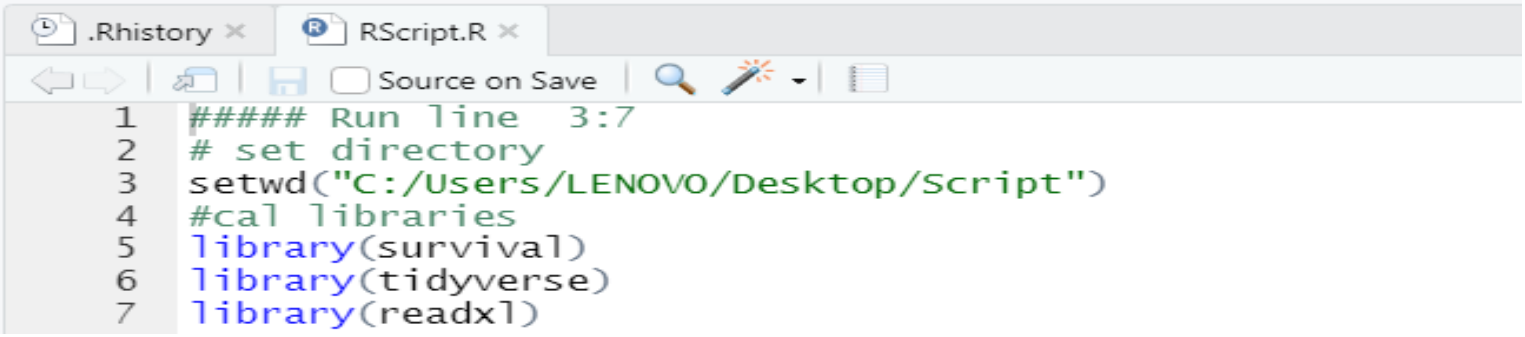
Creat a folder in your desktop and name it « Script »

Step 2 :

Download the csv files in the « Script » directory

Step3 :

Download the R script and open it with R studio



Step 4 :

Run lines 3 to 7

Step 5 :

Change the Gene symbole to your target gene symbol

Step 5 :

Run the Script

>> Result will be automaticly exported in txt files in the « Script « folder

1. Genetic Differencial Expression

Search your target gene in the lists

Import the over expressed and the under expressed gene list

```
# High prevalence data ------------------------------------------

#up_gene mean overexpressed genes
#down_gene mean underexpressed genes
#select and Run line 16 and line 17

down_gene <- read_csv("down_exp_high.csv")
up_gene  <- read_csv("up_exp_high.csv")

#Filter gene of interest // replace "APOOL" by the gene symbole
#select and Run line 22:31

x <- any(up_gene =="XRCC4")
y <-  any(down_gene =="XRCC4")
if (x==TRUE){
  exp_high <- "The gene is overexpressed"
} else if (y==TRUE) {
  exp_high <-"the gene is underexpressed"
} else {
  exp_high <-"The gene is not differencially expressed"
}
exp_high

#export the result
#run line 34 to download the result
write.table(exp_high,"expression_profile_high.txt")
```

Output options :

```
> exp_high
[1] "the gene is underexpressed"
```

```
> exp_medium
[1] "The gene is overexpressed"
```

```
> exp_medium_to_high
[1] "The gene is not differencially expressed"
```

2. Methylation of CpGs in the promoter

```
#methylation profile study
#replace the "LY6G5C"by your gene symbole and Rune line 39:41
promoter_methylation_high <- read_excel("promoter_methylation_high.xlsx")
cpg_met <- promoter_methylation_high %>%
  filter(gene =="XRCC4")
#result
cpg_met
#export result
write.table( cpg_met , "cpg_methylation_high.txt" , row.names=F , sep = ",")
```

Output options :

If there is methylated CpG s in the promoter region of the gene

```
# A tibble: 11 x 10
   gene  cpg        P.Value    B         logFC     UCSC_CpG_Islands_Name    Relation_to_UCSC_CpG_Island DMR   Regulatory_Feature_Name
   <chr> <chr>      <chr>      <chr>     <chr>     <chr>                    <chr>                       <chr> <chr>
 1 UXS1  cg21738971 0.00849828 -2.592215 5.22e-01  chr2:106809942-106811175 Island                      NA    2:106810524-106811161
 2 UXS1  cg09903262 0.02090364 -3.38008  4.86e-01  chr2:106809942-106811175 N_Shore                     NA    2:106809664-106809954
 3 UXS1  cg21149548 0.04949292 -4.11494  2.99e-01  chr2:106809942-106811175 Island                      NA    2:106810524-106811161
 4 UXS1  cg17912513 0.09457791 -4.646572 -1.64e-01 chr2:106809942-106811175 Island                      NA    2:106810524-106811161
 5 UXS1  cg01668174 0.11951348 -4.832349 -8.63e-02 chr2:106809942-106811175 Island                      NA    2:106810524-106811161
 6 UXS1  cg27654189 0.12496066 -4.867258 1.87e-01  chr2:106809942-106811175 Island                      NA    2:106810524-106811161
 7 UXS1  cg22712920 0.21377166 -5.272789 -8.58e-02 chr2:106809942-106811175 Island                      NA    2:106809664-106809954
 8 UXS1  cg00118342 0.55045112 -5.871039 9.31e-02  NA                       NA                          NA    2:106776749-106777628
 9 UXS1  cg23362669 0.58897033 -5.903569 5.93e-02  NA                       NA                          NA    2:106776749-106777628
10 UXS1  cg15341833 0.62831269 -5.932599 8.77e-02  NA                       NA                          NA    2:106776749-106777628
11 UXS1  cg07866464 0.64173542 -5.941609 -4.96e-02 chr2:106809942-106811175 Island                      NA    2:106810524-106811161
>
```

If there is no methylated CpG s

```
> #methylation profile study
> #replace the "LY6G5C"by your gene symbole and Rune line 39:41
> promoter_methylation_high <- read_excel("promoter_methylation_high.xlsx")
> cpg_met <- promoter_methylation_high %>%
+   filter(gene =="XRCC4")
> #result
> cpg_met
# A tibble: 0 x 9
# ... with 9 variables: gene <chr>, cpg <chr>, P.Value <chr>, B <chr>, logFC <chr>, UCSC_CpG_Islands_Name <chr>, Relation_to_UCSC_CpG_Island <chr>, DMR <chr>,
#   Regulatory_Feature_Group <chr>
>
```

3. Regulatory miRNAs

```
# Low prevalence -------------------------------------------------------------

#No expression data availbul



#methylation profile study
#replace the "LY6G5C"by your gene symbole and Rune line 39:41
promoter_methylation_low<- read_excel("promoter_methylation_low.xlsx")
cpg_met4 <- promoter_methylation_low %>%
  filter(gene =="UXS1")
#result
cpg_met4
#export result
write.table( cpg_met4 , "cpg_methylation_low.txt" , row.names=F , sep = ",")
```