RDS ICA

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## Importing Data and Libraries

#### Required files:

1. data\_all.csv - .csv file containing sample names in row 1 and gene names in column 1.
2. gene\_annotation.csv - .csv file containing gene names and their type and long names.
3. genelist\_72.csv - .csv files containing genes of interest to be included in analysis.
4. sample\_annotation.csv - .csv file containing sample names and their treatment groups.

#### Required installed libraries:

1. pheatmap

## Warning: package 'pheatmap' was built under R version 4.3.2

## [1] "Imported files!"

## Data Filtering

Extracting data from data\_all.csv with only genes listed in genelist\_72.csv into data\_filtered dataframe.

## [1] "1 duplicate(s) found in genelist.csv"

## [1] "40 gene(s) seleced from data\_all.csv for further processing."

## Data Processing

log scale the data into logdata dataframe.

## [1] "0 NA values in data\_filtered"

## [1] "Data log scaled."

## Extracting annotations and long names

Extracting gene type and treatment type annotations from sample\_annotation.csv and gene\_annotation.csv.  
Also renaming gene names into their long name for heatmap plots.

## [1] "All genes annotated with gene type"

## [1] "All samples annotated with treatment groups"

## [1] "All genes renamed to their long names"

## Heatmaps

