# Steps for EnrichR Analysis

## R Markdown - Enrichment anlalysis using EnrichR R package

* Summary
  + Input gene lists created from T-Test / EdgeR group comparison analysis (“Bladder mucosae surrounding cancer (Comparison) vs. Normal bladder mucosae (Baseline))
  + Short list genes based on group-decided criteria. FDR-adjusted p-value must be less than or equal to 0.01.
  + Run EnrichR on short listed gene list

## Import T-test results back into R so that we can shortlist further

## Filtering/shortlisting

* Short list genes based on group-decided criteria. FDR-adjusted p-value must be less than or equal to 0.01.
  + Only 273 genes after this filtering
* Export the short listed results for reference

## Clean gene names

* Currently, the gene names are in the form of "reporterid|genename". So need to split this.
* remove duplicates in the gene list
* remove NA values in the gene list
* print number of unique genes
  + Only 250 genes after cleaning which becomes the geneListFinal

## Load Databases for Enrichr R package , and check connection

* Load in the list of databases for which enrichment analysis will be run
  + Which comes from the “2023-EnrichR-Databases.txt" file

## Call function to run Enrichment

* Load R script into the environment which comes from file “functionEnrichment.R”
* Convert gene list to a dataframe to avoid errors with the “functionEnrichment.R”
* Call function on gene list created in previous step