

in file system



report

- report_main_template.Rmd
- Covariate_table.Rmd
- PCA_plot.Rmd



R_common

- basic_funcs.R
- basic_plots.R

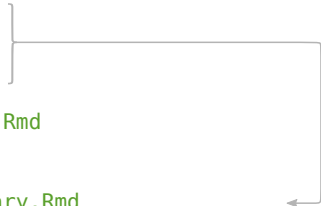


contrast

- contrast_main_template.Rmd
- Contrast_summary.Rmd
- Init_code.Rmd
- MA_plot.Rmd
- Result_table.Rmd

in config

```
report:
  defaults:
    contrast:
      - Init_code.Rmd
      - MA_plot.Rmd
  report_snippets:
    - Covariate_table.Rmd
    - PCA_plot.Rmd
    - contrast:
      - Contrast_summary.Rmd
      - __list__:
        - "5xFAD vs control in hip (2 months)"
        - "5xFAD vs control in cor (2 months)":
          - Init_code.Rmd
          - MA_plot.Rmd
          - Result_table.Rmd
```



Rmd snippet

```
# PCA plot
```

A PCA plot of all samples.

```
```${r PCA}
library(DESeq2)
dds <- readRDS(subset(file_tab, step=="DESeq2" & ...)$filename)
dds_trans <- normTransform(dds)
plotPCA(dds_trans, intgroup=configQCsamples_pca$annotation_col)
```
```