```
in file system
                              in config
                              report:
report
                                 defaults:
report main template.Rmd
                                   contrast:
Covariate table.Rmd
                                      - Init code.Rmd
PCA plot.Rmd
                                      - MA plot.Rmd
                                 report snippets:
    R common
                                   - Covariate table.Rmd
    basic funcs.R
                                   - PCA plot.Rmd
   - basic plots.R
                                   - contrast:
   contrast
                                      - "5xFAD vs control in hip (2 months)" 	<

    contrast main template.Rmd

                                      - "5xFAD vs control in cor (2 months)":
  - Init code.Rmd
                                        - Init code.Rmd
   - MA plot.Rmd
                                        - FilterByPval code.Rmd
   - FilterByPval code.Rmd
                                        - MA plot.Rmd
                                        - Result table.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" & ...)$filename)</pre>
 dds trans <- normTransform(dds)
 plotPCA(dds trans, intgroup=configQCsamples pca$annotation col)
```