

Generating_reports

```
library(MLEXPRESSO)
library(MLEXPRESSodata)
library(plyr)
```

Blah Blah datasets descriptions

```
condition.m <-ifelse(BRCA_methylation_chr17$SUBTYPE=="LumA","LumA","other")
condition.e <-ifelse(BRCA_mRNAseq_chr17$SUBTYPE=="LumA","LumA","other")

BRCA_methylation_chr17_gene <- aggregate_probes(BRCA_methylation_chr17)
test_met_brca <- calculate_test(BRCA_methylation_chr17_gene, condition.m, "ttest")
test_expr_brca <- calculate_test(BRCA_mRNAseq_chr17[, -1], condition.e, "lrt")

expression_100 <-test_expr_brca[order(test_expr_brca$pval, decreasing= F),]
expression_100 <- expression_100[c(1:100),]

methylation_100 <-test_met_brca[order(test_met_brca$pval, decreasing= F),]
methylation_100 <- methylation_100[c(1:100),]

x <- expression_100[which(expression_100$id %in% methylation_100$id),]

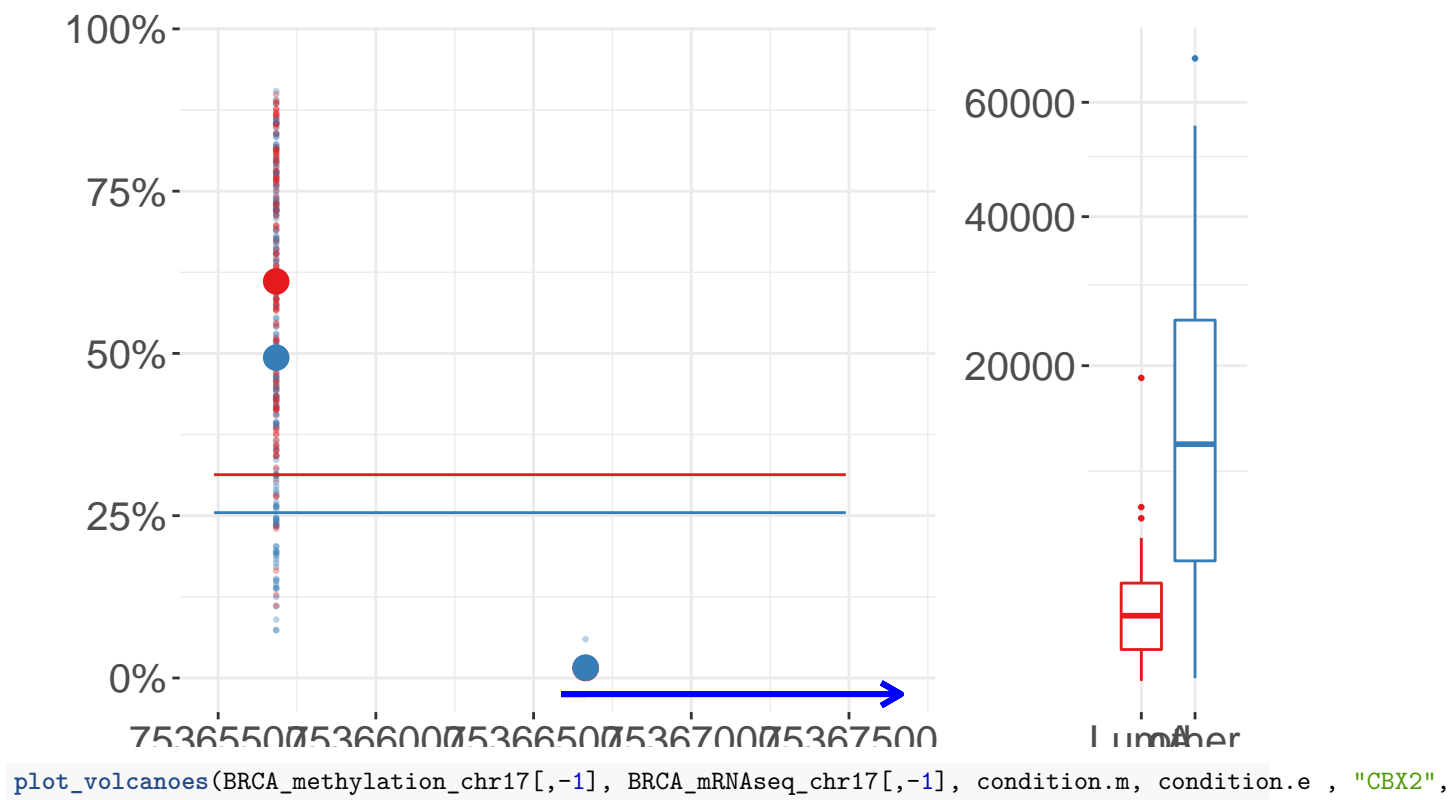
genes <- x$id
```

Function report_generate for generating reports:

```
report_generate(BRCA_mRNAseq_chr17[, -1], BRCA_methylation_chr17[, -1], condition.e, condition.m,
               test_expr_brca, test_met_brca, genes)

plot_gene(BRCA_methylation_chr17[, -1], BRCA_mRNAseq_chr17[, -1], condition.m, condition.e, "CBX2")
```

CBX2



| mean | mean | mean | mean | mean | mean | mean |
|-------|-------|-------|-------|-------|-------|-------|
| 0.23 | 0.13 | 0.06 | 0.03 | 0.01 | 0.005 | 0.002 |
| Luma | Luma | Luma | Luma | Luma | Luma | Luma |
| 307 | 891 | 1861 | 2457 | 3133 | | |
| 0.15 | 0.24 | 0.16 | 0.09 | 0.04 | 0.02 | 0.01 |
| other | other | other | other | other | other | other |
| 346 | 4187 | 12224 | 16689 | 25381 | | |

