

# Generating\_reports

```
library(MetExpR)
library(plyr)
```

Blah Blah datasets descriptions

```
expression_500 <- test_expr_brca[order(test_expr_brca$pval, decreasing= F),]
expression_500 <- expression_500[c(1:500),]
```

```
methylation_500 <- test_met_brca[order(test_met_brca$pval, decreasing= F),]
methylation_500 <- methylation_500[c(1:500),]
```

```
x <- expression_500[which(expression_500$id %in% methylation_500$id),]
```

```
genes <- x$id
```

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

Function report\_generate for generating reports:

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