

Vignette Title

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Package (Abstract?)

It is considered that the result of increased methylation is decreased gene expression. While, recent studies suggest that the relationship between methylation and expression is more complex than was previously thought. The package ... provides methods to test for differential expression and methylation by use of the negative binomial distribution and t-test. Additionally package ... allows to visualize results in a simple way.

Standard Workflow

In this vignette we will work with the data sets containing information about gene expression and methylation for patients with breast cancer. We will analyze differences in methylation and expression for patients with different subtypes of BRCA cancer.

Function `test_diff`

The main function of the package is `test_diff`. It allows to find differences between genes methylation or expression, taking into account additional information about samples.

Methylation

Methylation is a process by which methyl groups are added to the DNA molecule. It can change the activity of a DNA without changing the sequence. DNA methylation typically acts to repress gene transcription. But there exist situations in which adding the methyl groups intensify it. DNA methylation is associated with a lots of key processes including genomic imprinting, repression of transposable elements, aging and carcinogenesis. In our work we want to bind methylation process and carcinogenesis.

BRCA_methylation_chr17 data set

In this section, we will work with the methylation level data from TCGA database. Package contains BRCA_methylation_chr17 dataset. BRCA_methylation_chr17 contains information about methylation of CpG islands located on 17th chromosome for patients with breast cancer. Rows of this data set correspond to patients, more precisely, to samples taken from patients. First column SUBTYPE corresponds to a subtype of BRCA cancer, next columns correspond to CpG islands. Values inside the table indicate the methylation level of CpG island for specified sample.

```
library(MetExprR)
```

```
##
```

```
head(BRCA_methylation_chr17)[1:5,1:4]
```

```
##                SUBTYPE cg00021527 cg00031162 cg00032227
## TCGA-A1-A0SD-01A-11D-A112-05    LumA 0.03781858 0.7910348 0.006391233
## TCGA-A2-A04N-01A-11D-A112-05    LumA 0.01437552 0.7359370 0.008752293
## TCGA-A2-A04P-01A-31D-A032-05    Basal 0.01360124 0.6967802 0.009442039
## TCGA-A2-A04Q-01A-21D-A032-05    Basal 0.01525656 0.5341244 0.014674247
## TCGA-A2-A04T-01A-21D-A032-05    Basal 0.01167384 0.7378100 0.012251559
```

Data preparation

In this analysis we would like to find genes with different methylation level. At first we need to use function `map_to_gene`, which generates new data frame with CpG islands mapped to genes.

```
BRCA_methylation_chr17_gen <- map_to_gene(BRCA_methylation_chr17[, -1])
head(BRCA_methylation_chr17_gen)[1:5, 1:4]
```

```
##                AANAT    AARSD1    AATF    AATK
## TCGA-A1-A0SD-01A-11D-A112-05 0.7148533 0.8625816 0.24294092 0.7835302
## TCGA-A2-A04N-01A-11D-A112-05 0.5850106 0.8355825 0.21367129 0.8466190
## TCGA-A2-A04P-01A-31D-A032-05 0.4495537 0.8786166 0.03277413 0.3417919
## TCGA-A2-A04Q-01A-21D-A032-05 0.7120650 0.8819490 0.03460160 0.7264985
## TCGA-A2-A04T-01A-21D-A032-05 0.6010397 0.7739978 0.02501599 0.6276399
```

Function `test_diff` allows us to test for differences between the base means for two or more conditions.

In this case we have two conditions, connected with subtypes of breast cancer.

Before we go to the testing, we need to define condition values for each sample. We would like to test for differences between LumA subtype and other subtypes of breast cancer, so we create vector, which each element corresponds to a sample. Our division into this two group relies on numbers of occurrences of each subtype. The LumA subtype is the most common, in case of breast cancer.

```
condition <- ifelse(BRCA_methylation_chr17$SUBTYPE=="LumA", "LumA", "other")
head(condition, 8)
```

```
## [1] "LumA" "LumA" "other" "other" "other" "other" "LumA" "other"
```

T-test

One of the most used tools for testing differences between values is t-test. The null hypothesis we have consider, is that means in two groups are equal. To use it in `test_diff` function, we set value of parameter `test` on "ttest".

```
test.mety <- test_diff(BRCA_methylation_chr17_gen, condition, test="ttest")
```

As a result we obtain a data frame with columns corresponds to: id of gene, mean, logarithm of fold change, p-value for t-test, adjusted p-value (BH method). For more information about customizing this function see the help page for `test_diff`.

```
head(test.mety)
```

```
##           id      mean  log2.fold      pval      padj
## ICAM2      ICAM2 0.3330801 -0.15151320 3.754116e-17 3.063359e-14
## RILP       RILP 0.3341447 -0.05073691 2.575168e-13 1.050668e-10
## PIPOX      PIPOX 0.3647812  0.11505558 5.360053e-12 1.196885e-09
## TNFSF12    TNFSF12 0.2485025 -0.13412855 5.867083e-12 1.196885e-09
## CD7        CD7 0.8127112  0.09822690 1.641919e-11 2.679612e-09
## KSR1       KSR1 0.5549808  0.19973400 2.054467e-11 2.794075e-09
```

Expression

Gene expression is the process by which information from a gene is used in the synthesis of proteins. The process of gene expression is used by all known life.

BRCA_mRNAseq_chr17 data set

In this section we will use data set `BRCA_mRNAseq_chr17`, which contains information about gene expression. This data set contains per-gene read counts computed for genes from 17th chromosome for 100 patients with breast cancer. Rows of this data set correspond to samples taken from patients. First column `SUBTYPE` corresponds to a subtype of BRCA cancer, next columns correspond to genes.

```
BRCA_mRNAseq_chr17[1:5,1:5]
```

```
##           SUBTYPE AANAT AARSD1 AATF AATK
## TCGA-A1-AOSB-01A-11R-A144-07 Normal      9  2354 2870 317
## TCGA-A1-AOSD-01A-11R-A115-07 LumA       2  1846 5656 312
## TCGA-A1-AOSE-01A-11R-A084-07 LumA      11  3391 9522 736
## TCGA-A1-AOSF-01A-11R-A144-07 LumA       0  2169 4625 169
## TCGA-A1-AOSG-01A-11R-A144-07 LumA       1  2273 3473  92
```

Negative binomial test

Negative binomial test, which uses negative binomial distribution is an another tool for finding differential expression between our conditions.

As in the t-test we also need a description of the samples, which we keep in a vector, whose elements correspond to different groups.

In our example we will test for differential expression between groups with LumA breast cancer subtype and other subtypes of that cancer. Again we will use vector `conditions`, which consist of two values corresponds to subtype of breast cancer: LumA and other.

```
condition<-ifelse(BRCA_mRNAseq_chr17$SUBTYPE=="LumA","LumA","other")
head(condition,8)
```

```
## [1] "other" "LumA" "LumA" "LumA" "LumA" "LumA" "other" "LumA"
```

For using negative binomial test, in function `test_diff` we set value "nbinom" for parameter `test`. Evaluation for nbinorm may take a few minutes.

```
test.expr <- test_diff(BRCA_mRNAseq_chr17[, -1], condition, test="nbinom")
```

As a result we obtain the following data frame:

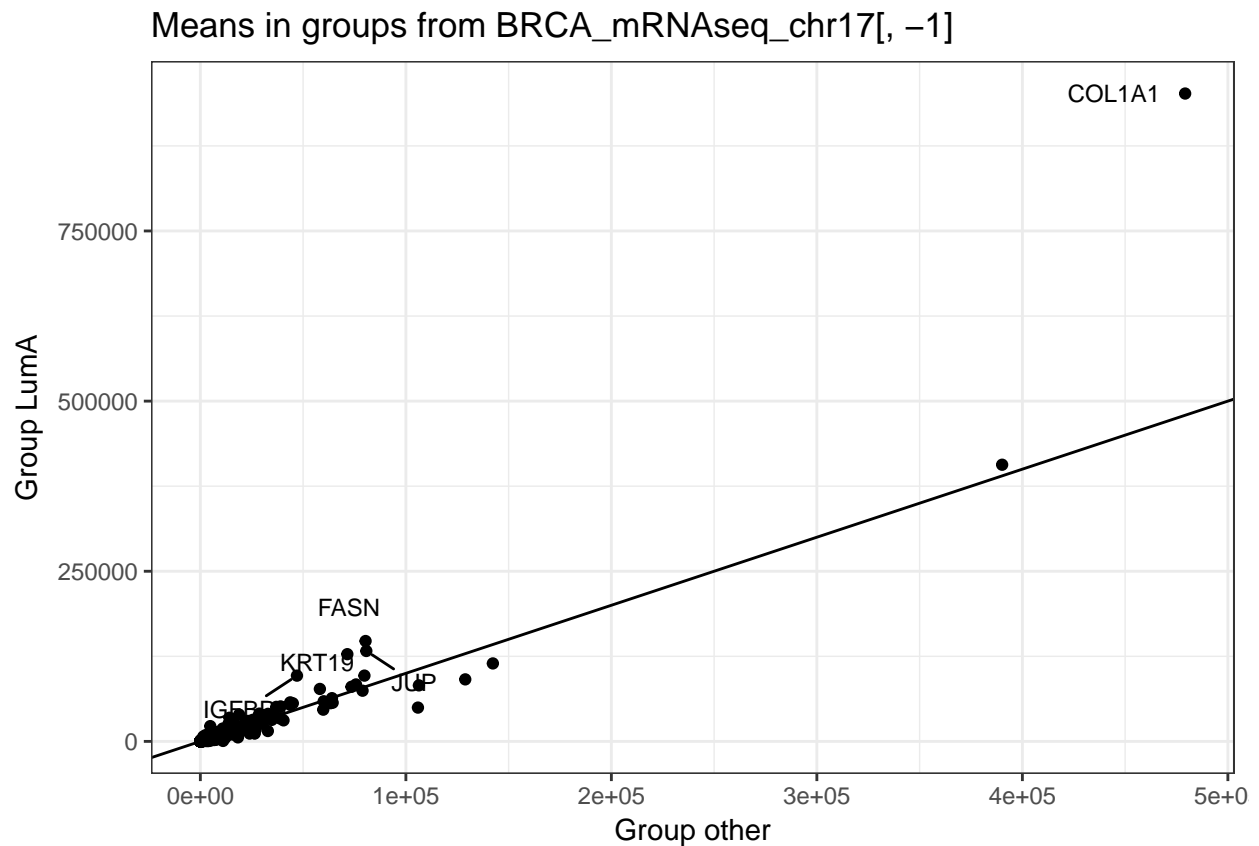
```
head(test.expr)
```

##	id	mean	log2.fold	pval	padj
## 1	AANAT	3.455436	-0.40216187	0.9453634	0.9920531
## 2	AARSD1	2779.448414	0.07427334	0.6627296	0.8992428
## 3	AATF	6750.269650	-0.13313947	0.6864598	0.9111193
## 4	AATK	352.805108	-0.02272566	0.8051408	0.9585881
## 5	ABCA5	1933.257431	0.07031881	0.5837682	0.8489059
## 6	ABCA6	689.547294	0.44680041	0.1289441	0.3857753

Visualization

em_plot

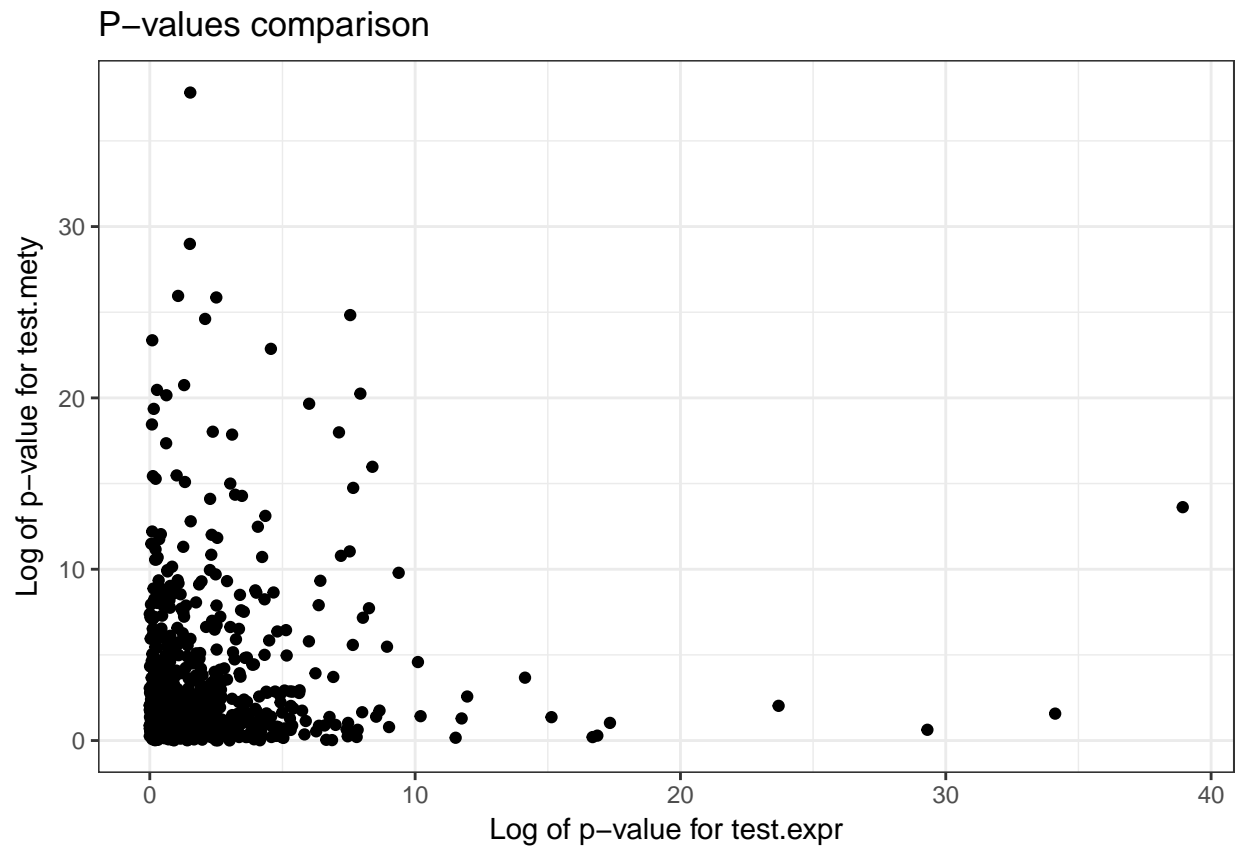
```
em_plot(BRCA_mRNAseq_chr17[, -1], condition, names=5)
```



log-log p-value

Firstly, we want to visualise the p-values for expression and methylation from negative binomial test and t-test respectively.

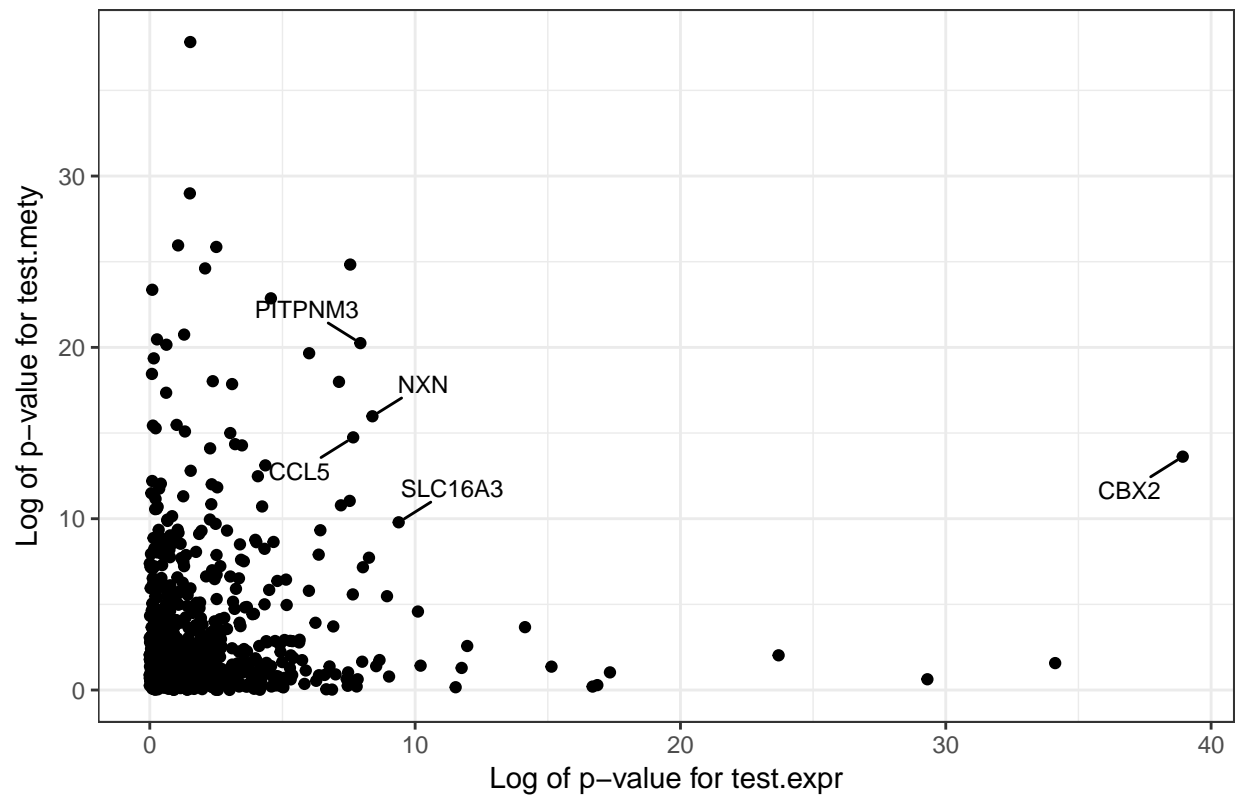
```
p_values_plot(test.expr, test.mety)
```



Additionally, **names** parameter allows to mark genes with sum of p-values for methylation and expression, lower than given value. Value of parameter **names** defines, number of genes to label.

```
p_values_plot(test.expr, test.mety, names = 5)
```

P-values comparison



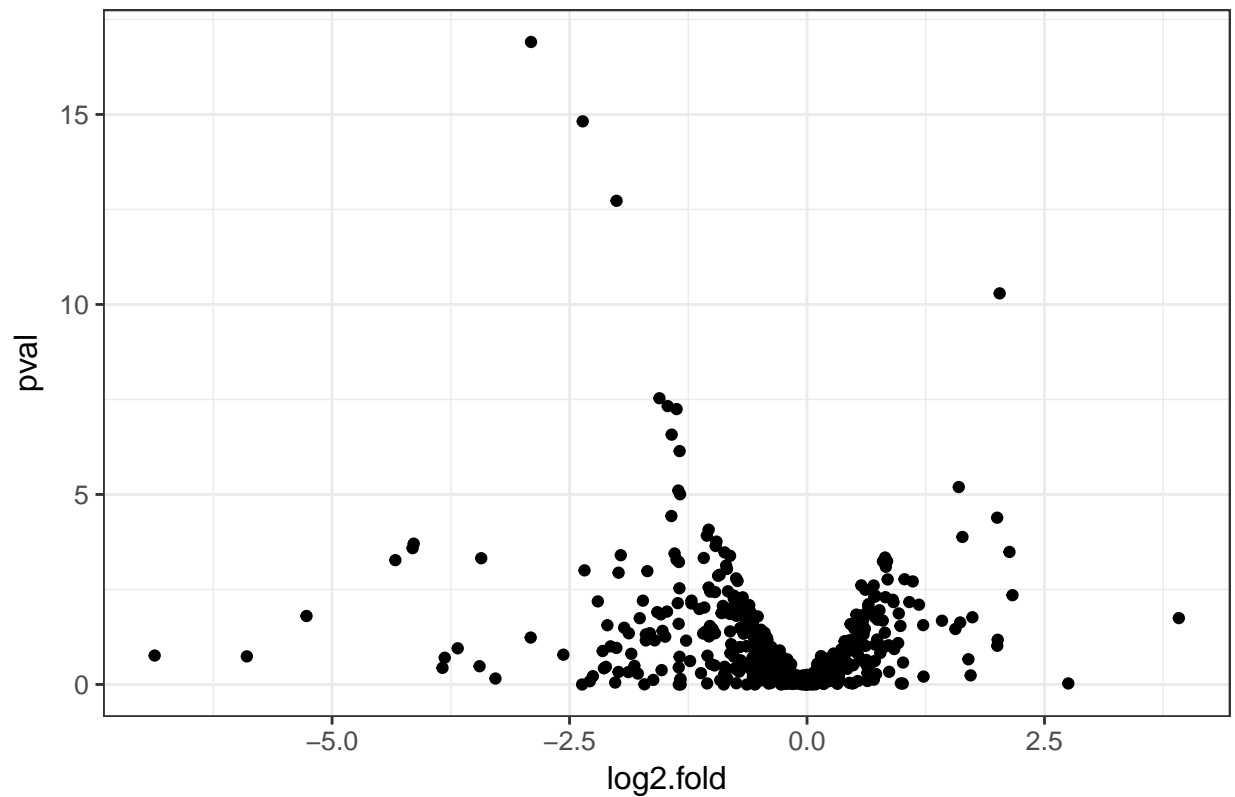
To read more about `p_values_plot` (e.g other ways to labeling genes) see help page for that function.

Volcano plot

For identify changes in our data sets we use a volcano plot - some type of scatter-plot. It plots logarithm of p-value versus logarithm of fold-change on the y and x axes, respectively.

```
volcano_plot(test.expr)
```

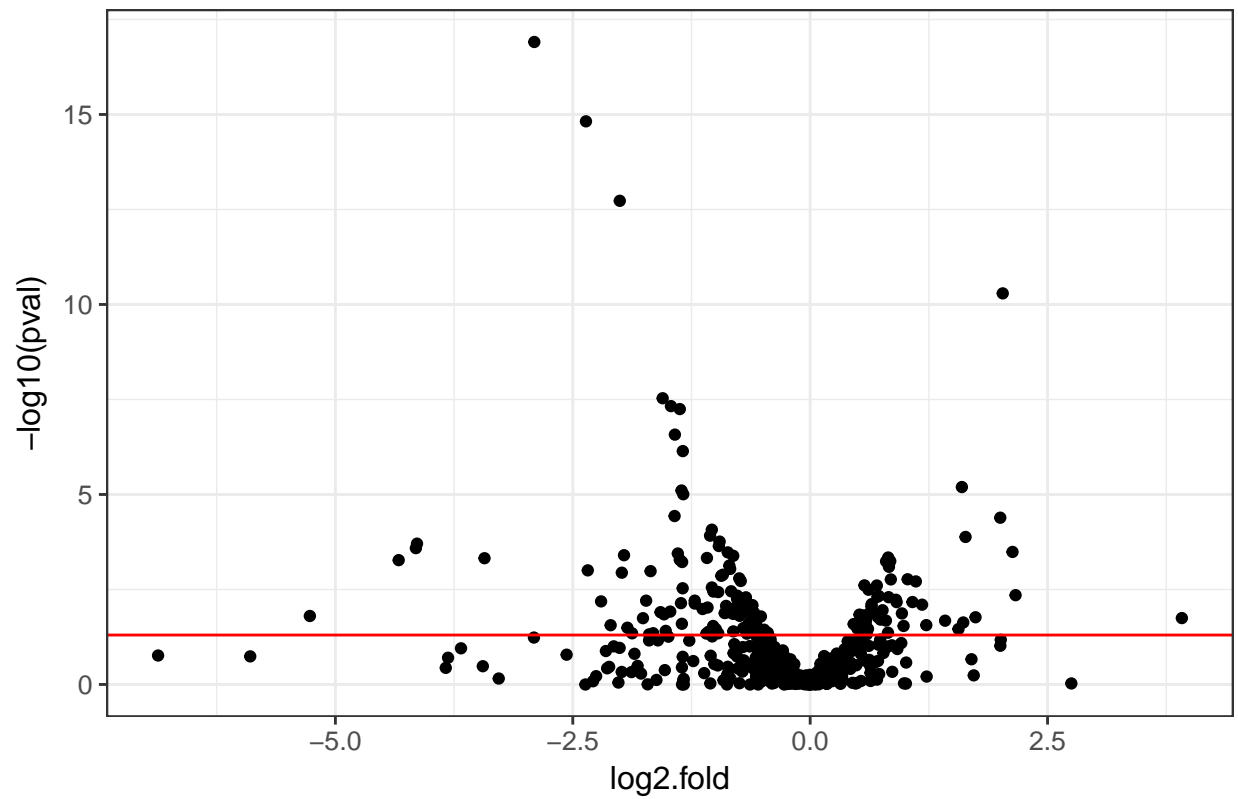
Volcano plot of structure(list(id = c("AANAT", "AARSD1", "AATF", "AA"



Function `volcano_plot` has parameters that allow to better analyze the results: `line` and `names`. The `line` parameter allows to set the horizontal line on plot on selected value. The `names` parameter signs choosen number of genes with the lowest p-value.

```
volcano_plot(test.expr, line = 0.05)
```

Volcano plot of structure(list(id = c("AANAT", "AARSD1", "AATF", "AA

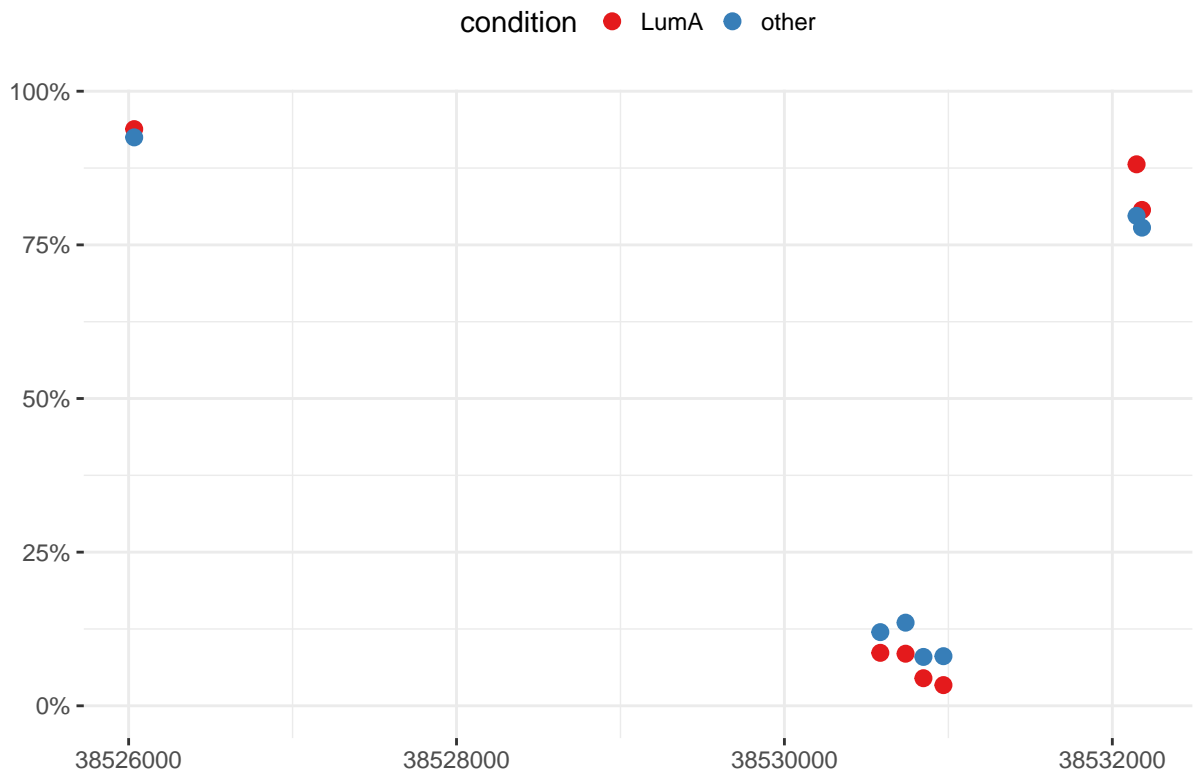


```
volcano_plot(test.expr, names = 10)
```



```
## 'select()' returned 1:many mapping between keys and columns
```

Methylation of gene BRCA1

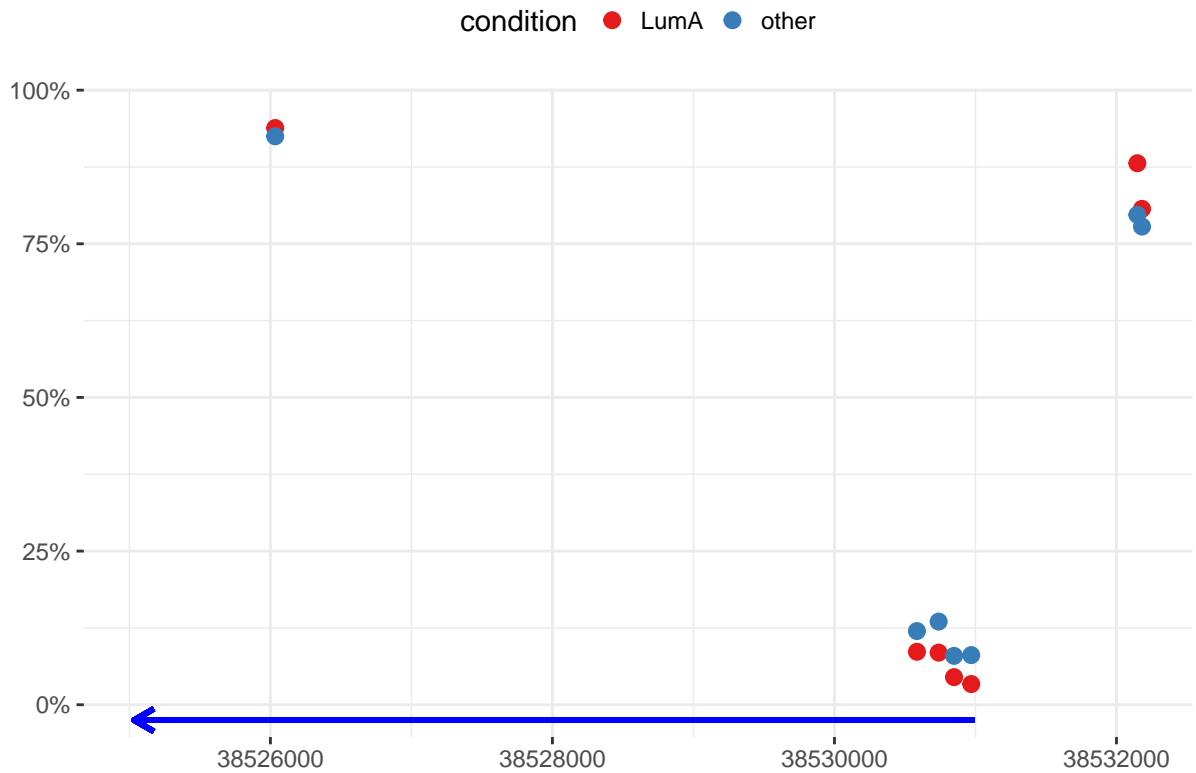


```
genereg_vs_met(BRCA_methylation_chr17, condition, "BRCA1", show_gen=TRUE)
```

```
## 'select()' returned 1:1 mapping between keys and columns
```

```
## 'select()' returned 1:many mapping between keys and columns
```

Methylation of gene BRCA1



```
## 'select()' returned 1:1 mapping between keys and columns
## 'select()' returned 1:many mapping between keys and columns
## Warning: Removed 1 rows containing missing values (geom_point).
```

Methylation of gene BRCA1

