Wykresy - volcanoplots

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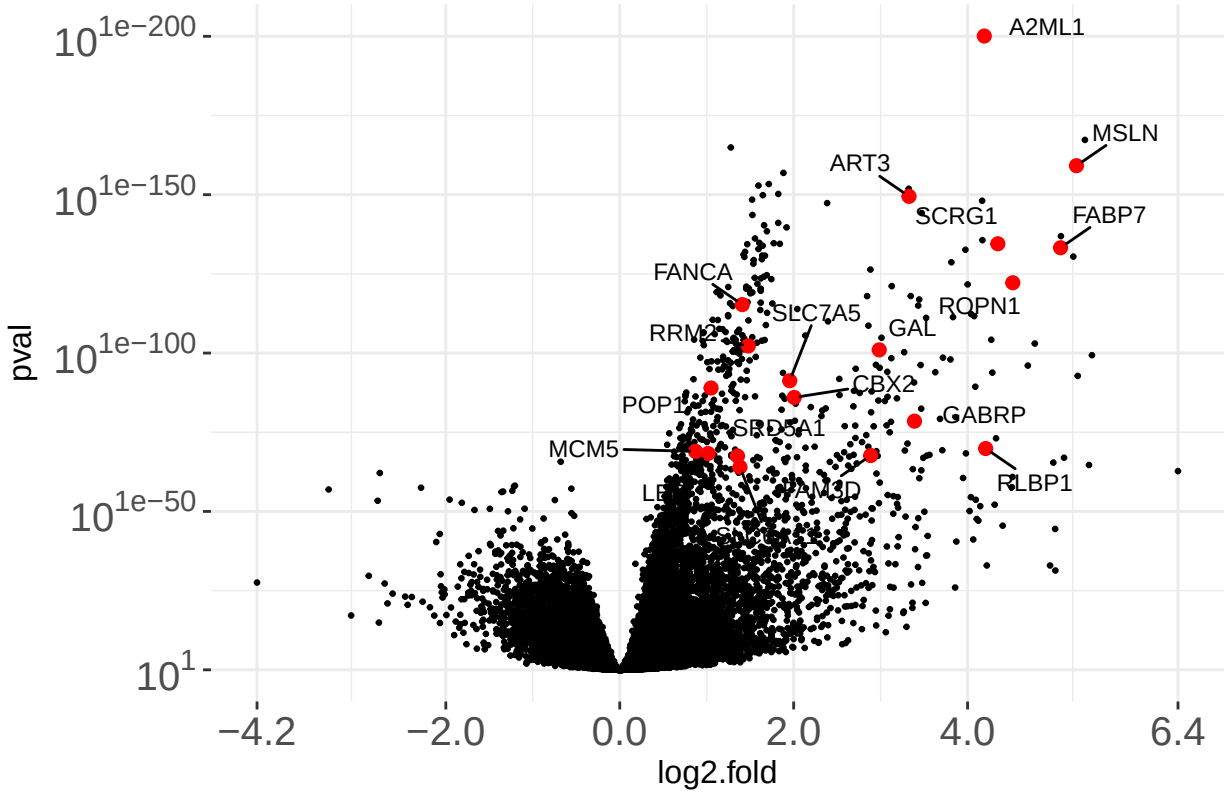
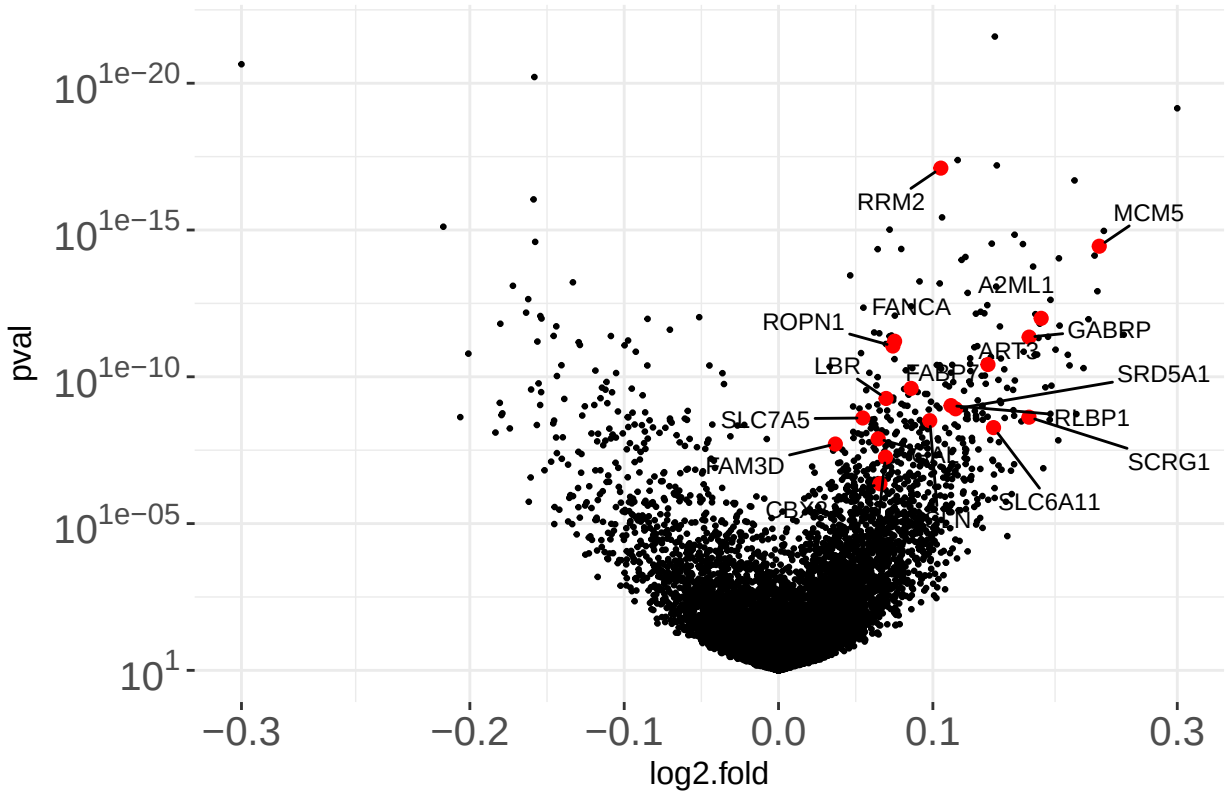
Weźmy pierwsze 500 genów o najbardziej zróżnicowanej ekspresji i metylacji.

##

W obu zbiorach danych powtarza się 19 genów.

Volcanoploty





Dane dla genów z volcanoplotów

```
genes<-genes[1:3]
plot <- list()
for (i in 1:length(genes)){
  #plot[[i]] <- genereg_vs_met(BRCA_methylation_all[,-1], condition.m, gene="BRCA2")

   plot[[i]] <- visual_volc(condition.e, condition.m, BRCA_methylation_all[,-1],BRCA_mRNAseq_all[,-1], g


  }
```

A2ML1

Expression (cpm)

	min	1st Q	med	mean	3rd Q	max	count
LumA	19.3	74.5	95.8	142.9	136.5	3122.2	359
other	26.6	93.4	215	2516.4	1186.2	75020.3	377

Methylation

	min	1st Q	med	mean	3rd Q	max	count
LumA	0.2	0.7	0.8	0.7	0.8	0.9	139
other	0.1	0.4	0.5	0.5	0.8	0.9	153

MSLN

Expression (cpm)

	min	1st Q	med	mean	3rd Q	max	count
LumA	0	7.2	14.4	195.1	30.2	23631.9	359
other	0	5.5	21.1	2466.8	360.3	221515.9	377

Methylation

	min	1st Q	med	mean	3rd Q	max	count
LumA	0.6	0.9	0.9	0.9	0.9	0.9	139
other	0.3	0.7	0.9	0.8	0.9	1	153

ART3

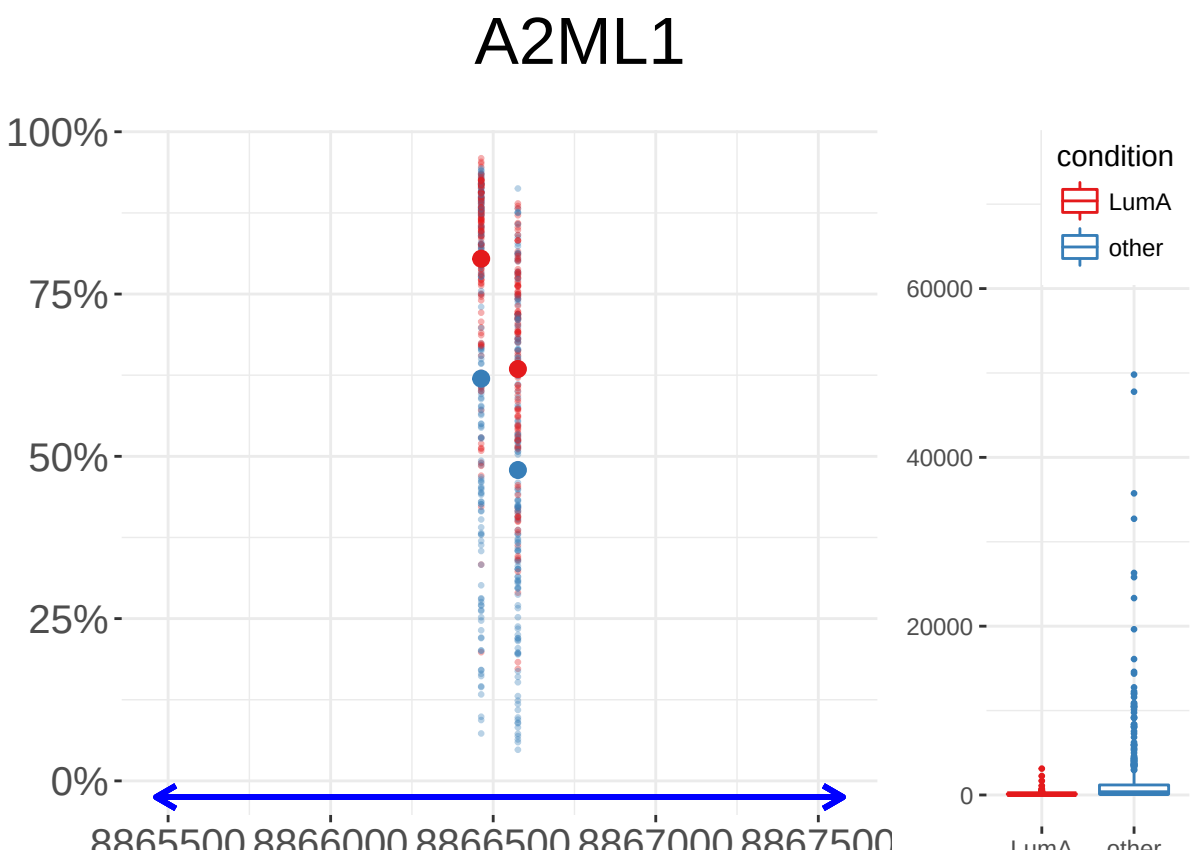
Expression (cpm)

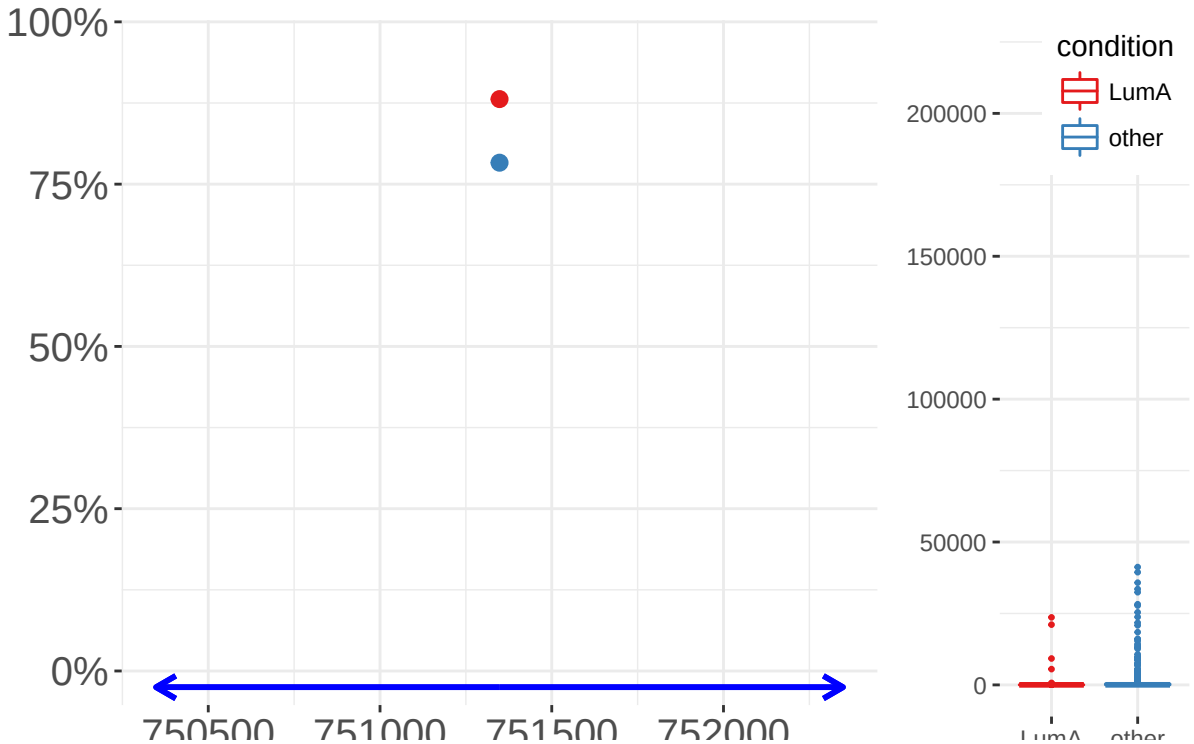
	min	1st Q	med	mean	3rd Q	max	count
LumA	54.9	154.9	201.9	238.9	272.5	3089.2	359
other	62.7	152.9	241.1	2425	597.8	67834.8	377

Methylation

	min	1st Q	med	mean	3rd Q	max	count
LumA	0.3	0.7	0.8	0.8	0.8	0.9	139
other	0.1	0.5	0.7	0.6	0.8	0.9	153

Wizytówki dla metylacji




MSLN
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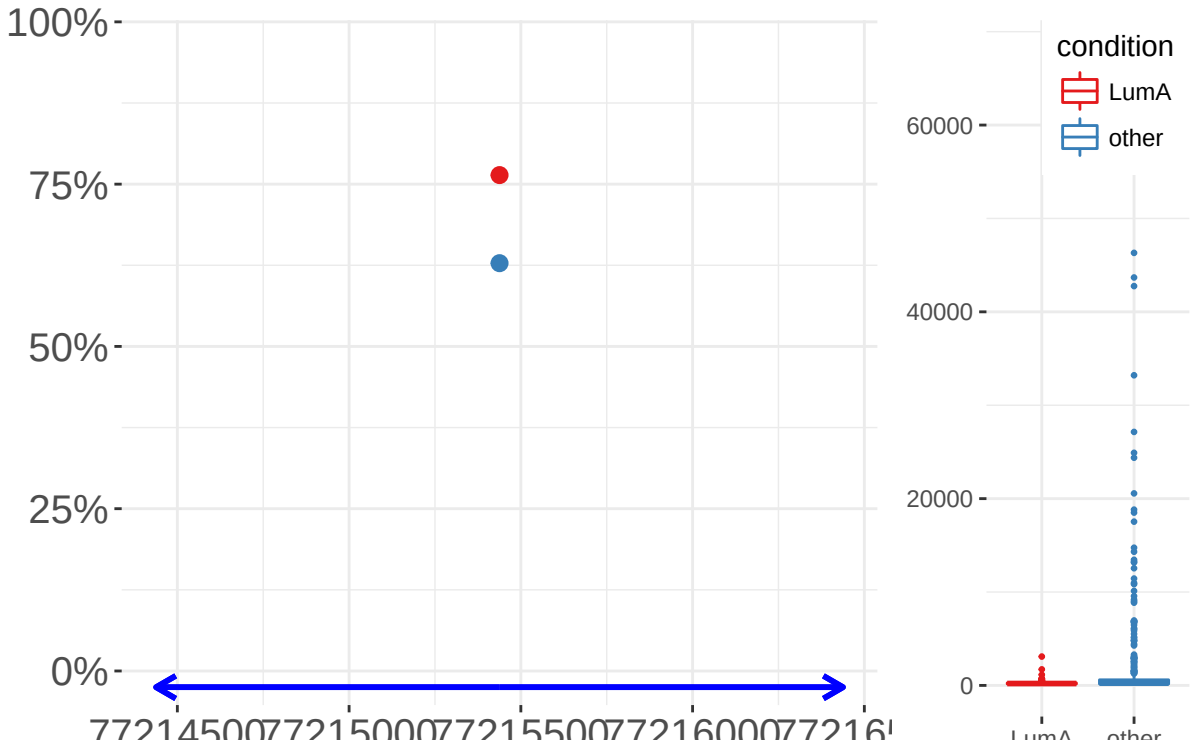
75%
50%
25%
0%
750500
751000
751500
752000
condition
LumA
other
200000
150000
100000
50000
0

ART3


100%
75%
50%
25%
0%
77214500
77215000
77215500
77216000
77216
condition
LumA
other
60000
40000
20000
0
LumA
other