

Homework two report

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ABSTRACT

According to the result obtained from the following analysis, transcription activator B plays a more important role in cancer.

Results

Quality Control

To check if there exists any microarray chips that perform abnormally, I first briefly visualized the distribution of expression level for each chip in Relative Log Expression Level(REL) with the package *Oligo*.¹ It is revealed that the total expression level among these chips are approximately the same. Consequently, I can make sure that all microarray data are reliable and can be applied to subsequent analysis.

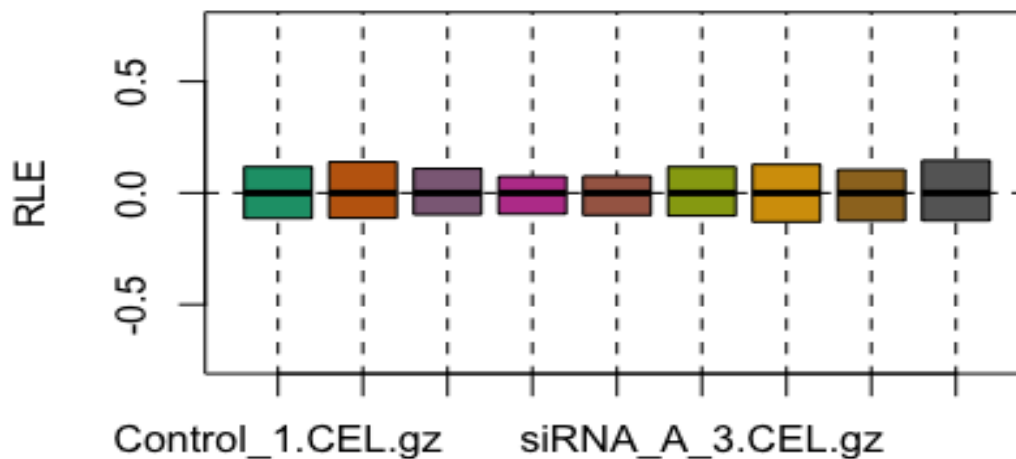


Figure 1. Relative Log Expression Level(REL) for each chip

Differential Expression Gene Analysis

Rawdata retrieved from chips are read in with the package *Affy*, and are pretreated using *rma* algorithm, which are proved to have a better performance in enhancing the signal from Perfect Match(PM) probes².

By respectively comparing the data retrieved from transcription-activator-A-knocked out(abbreviated as sample A below) and transcription-activator-B-knocked out(abbreviated as sample B below) samples with data from control samples, a Differential Expression Gene Analysis has been performed. Result shows that more genes are differentially expressed in samples treated with siRNA B. The threshold of differential expression is determined by $abs(logFC) > 1.5$ and $adj.P.value < 0.05$ so as to remove as much false positive results as possible. The result are drawn as volcanoplots listed below. After figuring out the number of significantly expressed genes respectively in sample A and B, I found that sample B contains dramatically higher number of differential expressed genes.

group	sample A	sample B
number	7	264

Table 1. number of significantly expressed genes

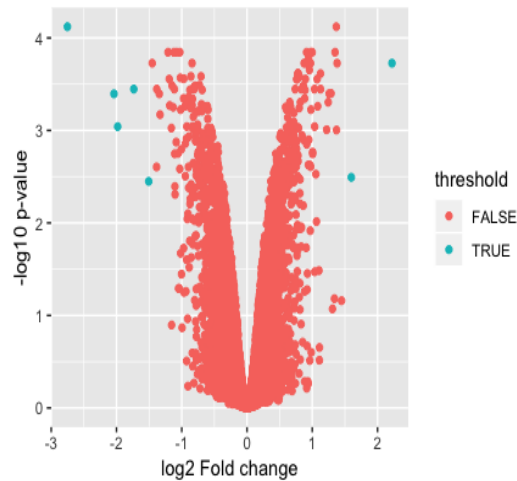


Figure 2. volcanoplot of sample A

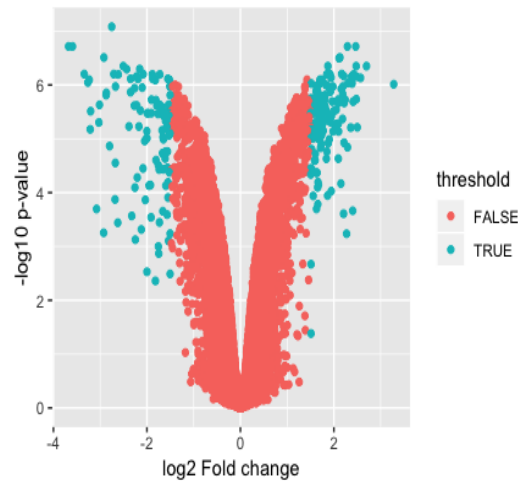


Figure 3. volcanoplot of sample B

Probable Impact of Transcription Activator B on Cancer

After clustering the differential expressed genes obtained in the previous step by Genetic Oncology(GO) Analysis and Kegg Analysis, I found that the transcription activator B plays a role in cancer probably through interfering cell cycle

0.0.1 Genetic Oncology(GO) Analysis

0.0.2 Kegg Analysis

0.0.3 GSEA Analysis

A/B Gene Hypothesis

- First item
- Second item

Topical subheadings are allowed.

Discussion

The Discussion should be succinct and must not contain subheadings.

Methods

Topical subheadings are allowed. Authors must ensure that their Methods section includes adequate experimental and characterization data necessary for others in the field to reproduce their work.

References

1. <https://blog.csdn.net/u014801157/article/details/66974577>. Accessed March 27, 2017.
2. <https://www.jianshu.com/p/db8b915a27e9>. Accessed May 7, 2018.
3. Hao, Z., AghaKouchak, A., Nakhjiri, N. & Farahmand, A. Global integrated drought monitoring and prediction system (GIDMaPS) data sets. *figshare* <http://dx.doi.org/10.6084/m9.figshare.853801> (2014).

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For data citations of datasets uploaded to e.g. *figshare*, please use the `howpublished` option in the bib entry to specify the platform and the link, as in the `Hao:gidmaps:2014` example in the sample bibliography file.

Acknowledgements (not compulsory)

Acknowledgements should be brief, and should not include thanks to anonymous referees and editors, or effusive comments. Grant or contribution numbers may be acknowledged.

Author contributions statement

Must include all authors, identified by initials, for example: A.A. conceived the experiment(s), A.A. and B.A. conducted the experiment(s), C.A. and D.A. analysed the results. All authors reviewed the manuscript.

Additional information

To include, in this order: **Accession codes** (where applicable); **Competing interests** (mandatory statement).

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