生信文章修改甲基化测序

2024-05-23

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1 摘要

Whole-genome DNA methylation analysis in liver tissue of offspring of Zuogui pill (ZGP)-intervened GD rats, trying to find evidence for ZGP effect on epigenetics and potential pathways

Then, 92 DM-related differentially methylated genes were identified. They were mainly enriched in glycometabolism, receptors on the membrane, and protein kinases and their regulators by GO analysis as well as in MAPK pathway by KEGG analysis.

A core **network involved in PI3K/AKT signaling was obtained.** The effect of ZGP on eugenics in the offspring of GD rats may be achieved by affecting the liver methylation of the offspring, with **PI3K/AKT pathway as one of targets.**

- differentially methylated regions (DMRs) identification
- Bismark was used for aligning clean reads to reference genome
- profiles of extracted methylation sites were analyzed by **methylKit** to perform calling DMR between Model and Model-Cure group, with $|delta| > 0.3$, FDR < 0.05, and annotate DMRs-related genes by Rattus norvegicus genome

2 前言

3 材料和方法

3.1 材料

3.2 方法

Mainly used method:

- R version 4.4.0 (2024-04-24); Other R packages (eg., `dplyr` and `ggplot2`) used for statistic analysis or data visualization.

4 分析结果

5 结论

6 附：分析流程

- 许凯霞需求
- 浙江百越 4 例 WGBS 信息采集与分析

Table 1 (下方表格) 为表格 unnamed chunk 10 概览。

(对应文件为 Figure+Table/unnamed-chunk-10.csv)

> 注：表格共有 12 行 29 列，以下预览的表格可能省略部分数据；含有 1 个唯一 'Sample'。

1. Sample: 样本名称。
2. Lib: 文库名称。
3. Total Reads: 总的读取数（reads）。
4. Mapped Reads: 成功比对到参考基因组的读取数。
5. Mapped Ratio: 成功比对的读取数占总读取数的比例。
6. Unique Reads: 成功比对且唯一比对的读取数。
7. Unique Ratio: 唯一比对的读取数占总读取数的比例。
8. PE Unique Reads: 成对读取（paired-end reads）中唯一比对的读取数。
9. PE Unique Ratio: 成对读取中唯一比对的读取数占总读取数的比例。
10. Unmapped Reads: 未成功比对的读取数。
11. Unmapped Ratio: 未成功比对的读取数占总读取数的比例。
12. Mutimapped Reads: 成功比对但多重比对的读取数。
13. Mutimapped Ratio: 多重比对的读取数占总读取数的比例。
14. Discarded Reads: 被丢弃的读取数。
15. Top Strand: 比对到正链（top strand）的读取数。
16. Bottom Strand: 比对到负链（bottom strand）的读取数。
17. Total C: 总的 C 位点数。
18. mCG: 甲基化的 CG 位点数。
19. mCHG: 甲基化的 CHG 位点数。
20. mCHH: 甲基化的 CHH 位点数。
21. mUn: 甲基化的未识别位点数。
22. unmCG: 未甲基化的 CG 位点数。
23. unmCHG: 未甲基化的 CHG 位点数。
24. unmCHH: 未甲基化的 CHH 位点数。
25. unmUn: 未甲基化的未识别位点数。
26. CG level: CG 位点的甲基化水平。
27. CHG level: CHG 位点的甲基化水平。
28. CHH level: CHH 位点的甲基化水平。
29. Un level: 未识别位点的甲基化水平。

Table 1: Unnamed chunk 10

Sample	Lib	Total ...	Mapped...	Mapped...	Unique...	Unique...	PE Uni...	PE Uni...	Unmapp...	...
Model-1	220614...	32393432	21860820	67.49%	19692844	60.79%	19692844	60.8%	10532612	...
Model-1	220614...	33843456	22773076	67.29%	20512426	60.61%	20512426	60.6%	11070380	...
Model-1	220614...	31845426	21656537	68.01%	19489323	61.20%	19489323	61.2%	10188889	...

Sample	Lib	Total ...	Mapped...	Mapped...	Unique...	Unique...	PE Uni...	PE Uni...	Unmapp...	...
Model-1	220614...	28307315	18847140	66.58%	17005125	60.07%	17005125	60.1%	9460175	...
Model-1	220614...	34022926	24091817	70.81%	21689901	63.75%	21689901	63.8%	9931109	...
Model-1	220614...	35655498	25208927	70.70%	22696324	63.65%	22696324	63.7%	10446571	...
Model-1	220614...	33196722	23690173	71.36%	21306552	64.18%	21306552	64.2%	9506549	...
Model-1	220614...	28994735	20309191	70.04%	18310831	63.15%	18310831	63.2%	8685544	...
Model-1	220711...	9785946	7364737	75.26%	6611903	67.57%	6611903	67.6%	2421209	...
Model-1	220711...	10175734	7663477	75.31%	6881304	67.62%	6881304	67.6%	2512257	...
Model-1	220711...	9709125	7332078	75.52%	6576371	67.73%	6576371	67.7%	2377047	...
Model-1	220711...	8564409	6370360	74.38%	5727736	66.88%	5727736	66.9%	2194049	...