表观线_高级分析

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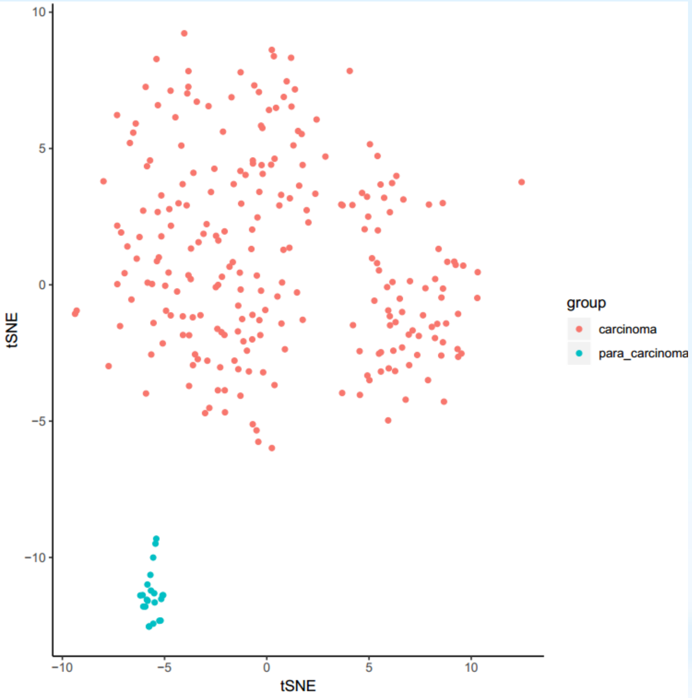
■ T-sne降维算法展示样本分组



结果展示


结果
文献应用
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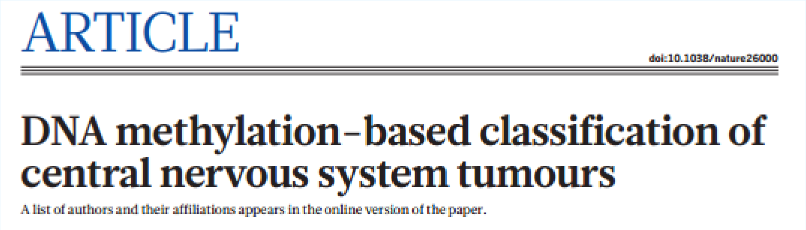
参考文献


ARTICLE

doi:10.1038/nature26000

DNA methylation-based classification of central nervous system tumours

A list of authors and their affiliations appears in the online version of the paper.

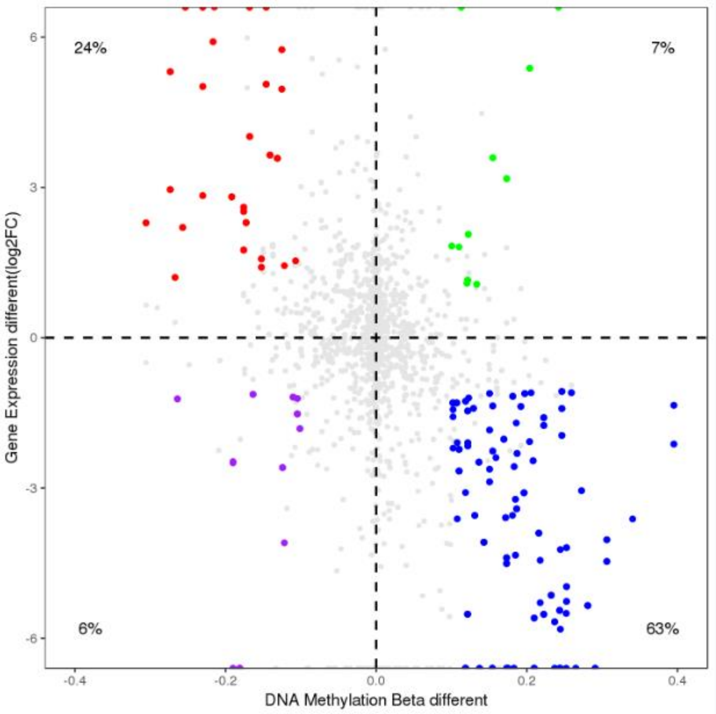
适用项目

850K、捕获测序、WGBS

注意事项

更适用单细胞测序，多样本

■ Methyl&RNA的关联分析_1



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参考文献


Li et al. *Cell Death Discovery* (2018)4:36
DOI 10.1038/s41420-018-0033-x

Cell Death Discovery

ARTICLE Open Access

Novel biomarker *ZCCHC13* revealed by integrating DNA methylation and mRNA expression data in non-obstructive azoospermia

Zhiming Li[1,2], Shuai Chen[1], Yufeng Yang[2], Xuan Zhuang[2,3] and Chi-Meng Tzeng[1,4,5]

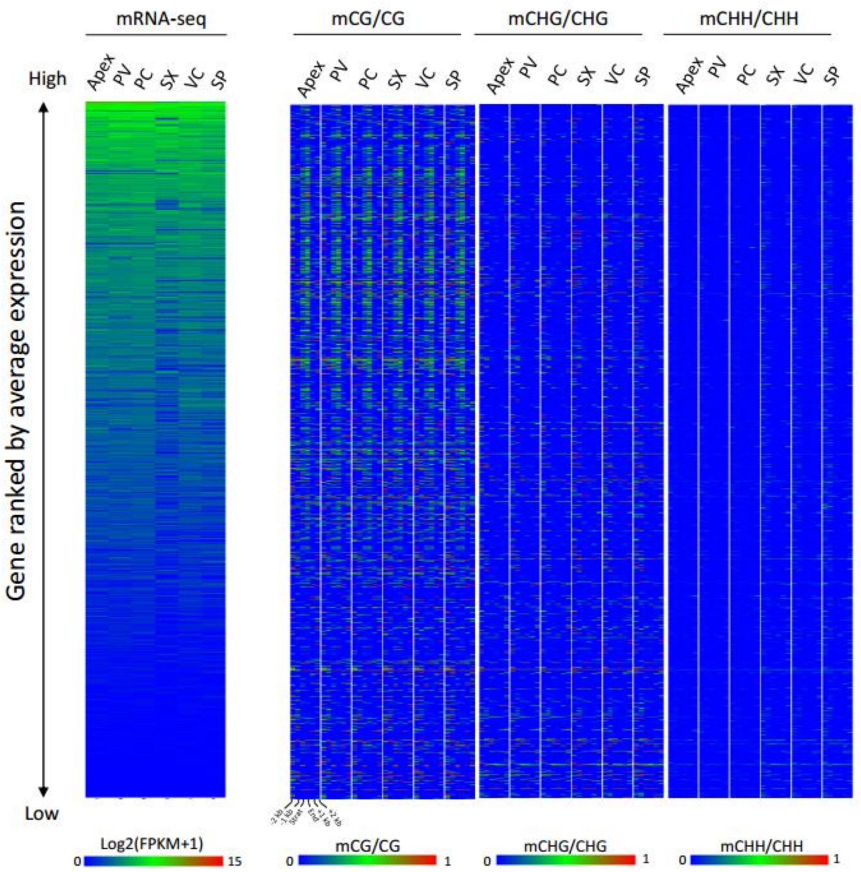
适用项目

850K、捕获测序、WGBS、MeDIP-seq

注意事项

关联的方式很多可通过基因关联也可通过位点关联，基因关联可与mRNA、lncRNA、mRNA&lncRNA关联。

■ Methyl&RNA的关联分析_2



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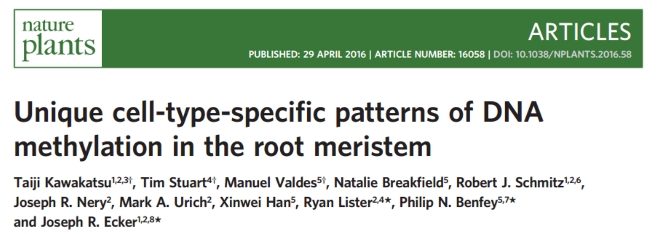
参考文献


nature plants

ARTICLES

PUBLISHED: 29 APRIL 2016 | ARTICLE NUMBER: 16058 | DOI: 10.1038/NPLANTS.2016.58

Unique cell-type-specific patterns of DNA methylation in the root meristem

Taiji Kawakatsu[1,2,3†], Tim Stuart[4†], Manuel Valdes[5†], Natalie Breakfield[5], Robert J. Schmitz[1,2,6], Joseph R. Nery[2], Mark A. Urich[2], Xinwei Han[5], Ryan Lister[2,4*], Philip N. Benfey[5,7*] and Joseph R. Ecker[1,2,8*]

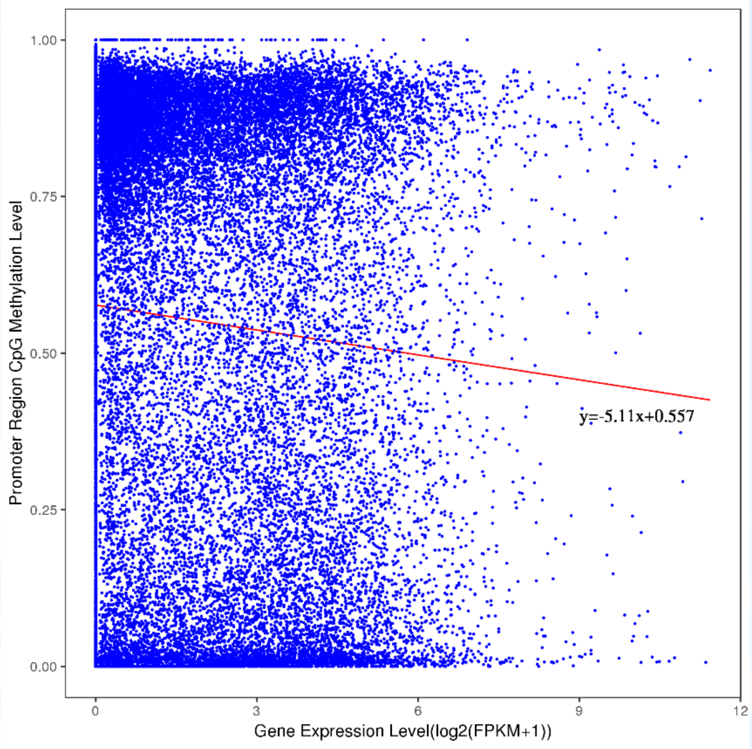
适用项目

WGBS、捕获测序

注意事项

捕获测序的CHG、CHH水平的甲基化位点信息不多

■ Methyl&RNA的关联分析_3



结果展示

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参考文献

SCIENTIFIC REPORTS

OPEN

Genome-wide methylation analysis identified sexually dimorphic methylated regions in hybrid tilapia

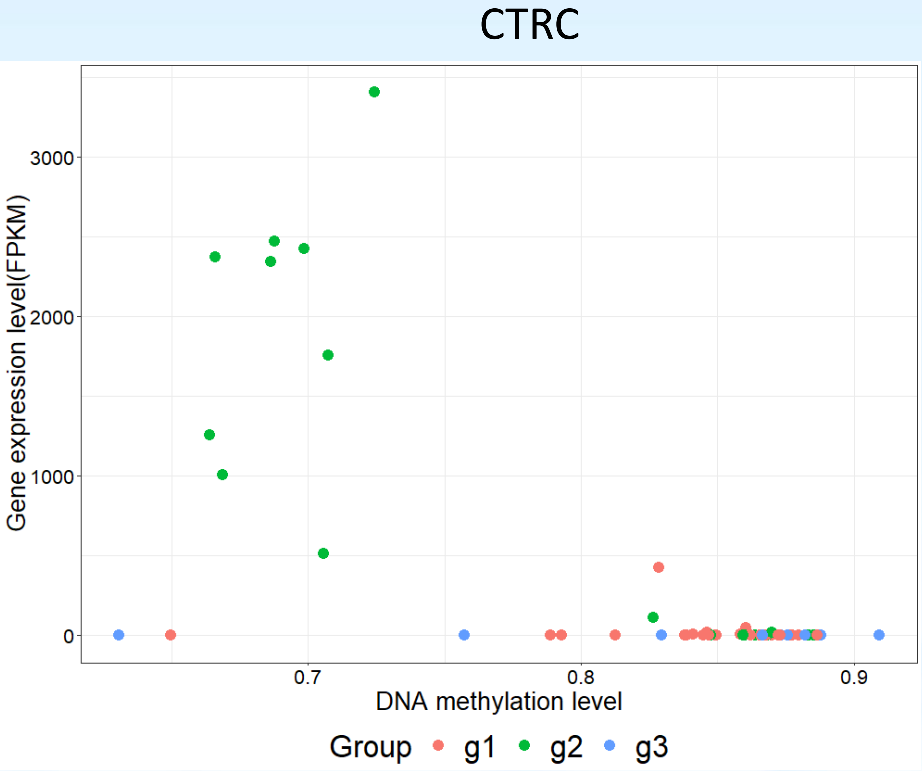
适用项目

WGBS、捕获测序

注意事项

甲基化值推荐取启动子区的CG位点甲基化均值，一般包括TSS200,TSS1000,TSS1500。

■ 特定基因的甲基化程度与基因表达关联



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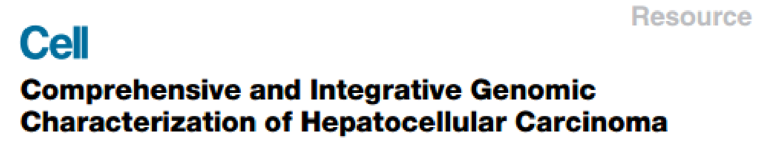
参考文献


Resource

Cell

Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma

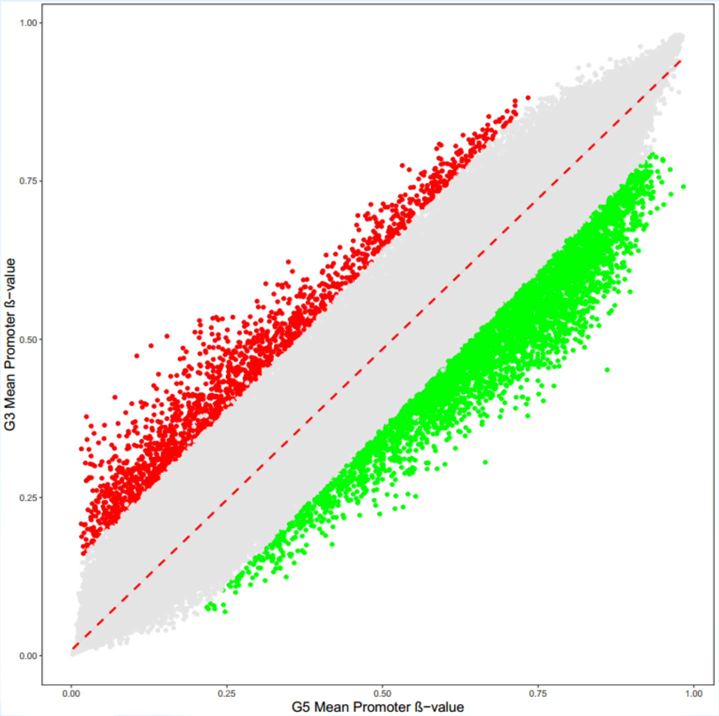
适用项目

850K、捕获测序、WGBS

注意事项

取基因启动子区（TSS200、TSS1500）位点的甲基化均值与对应基因的表达量进行关联

■ 组间启动子区甲基化展示



结果展示

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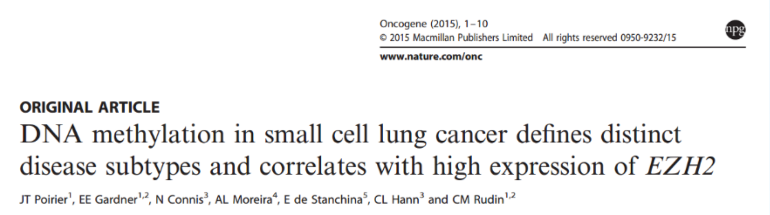
参考文献



Oncogene (2015), 1–10
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www.nature.com/onc

ORIGINAL ARTICLE

DNA methylation in small cell lung cancer defines distinct disease subtypes and correlates with high expression of *EZH2*

JT Poirier[1], EE Gardner[1,2], N Connis[3], AL Moreira[4], E de Stanchina[5], CL Hann[3] and CM Rudin[1,2]

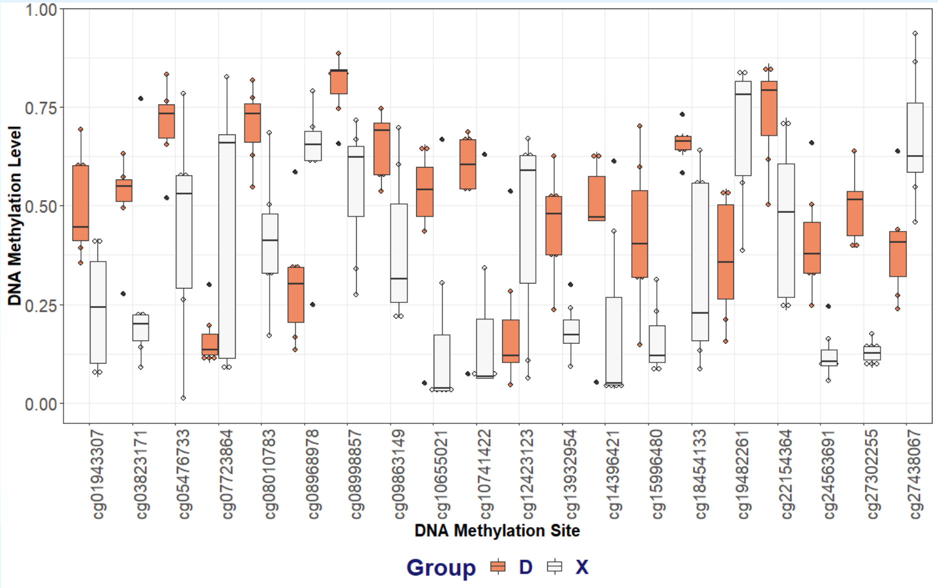
适用项目

850K、捕获测序、WGBS

注意事项

默认取位于TSS200和TSS1500的位点作图

■ 展示top20显著差异的位点



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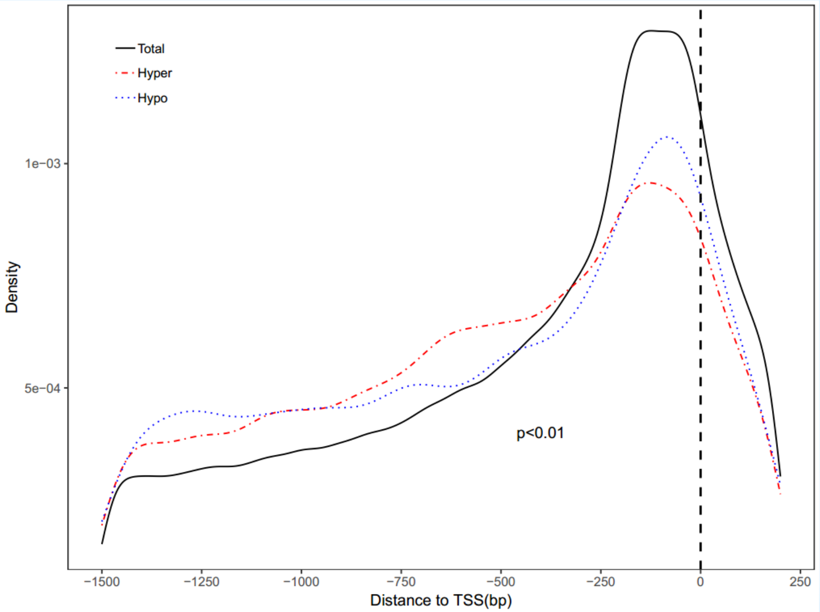
适用项目

850K、捕获测序、WGBS

注意事项

■ TSS区域高低甲基化位点密度曲线图



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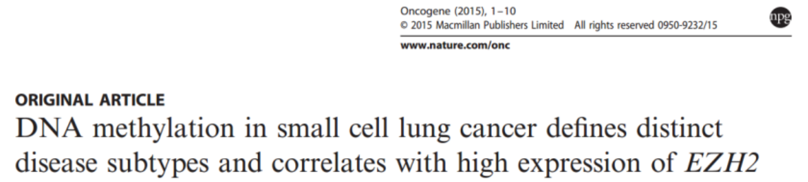

Oncogene (2015), 1–10
© 2015 Macmillan Publishers Limited All rights reserved 0950-9232/15
www.nature.com/onc

ORIGINAL ARTICLE

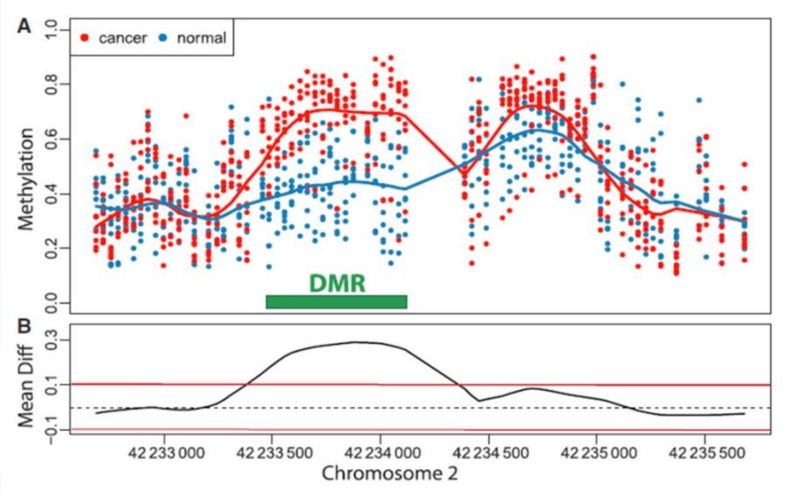
DNA methylation in small cell lung cancer defines distinct disease subtypes and correlates with high expression of *EZH2*

适用项目

850K、捕获测序、WGBS

注意事项

■ 差异甲基化区域（DMR）



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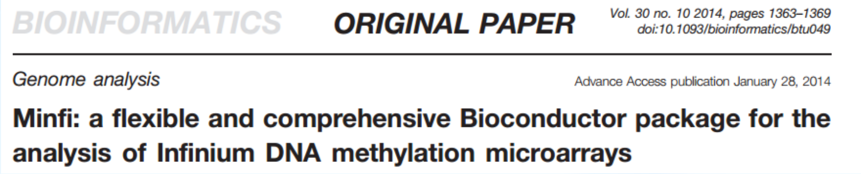

BIOINFORMATICS ORIGINAL PAPER Vol. 30 no. 10 2014, pages 1363–1369
doi:10.1093/bioinformatics/btu049

Genome analysis Advance Access publication January 28, 2014

Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays

适用项目

850K、捕获测序、WGBS

注意事项

bumphunter算法寻找真正的差异甲基化区域

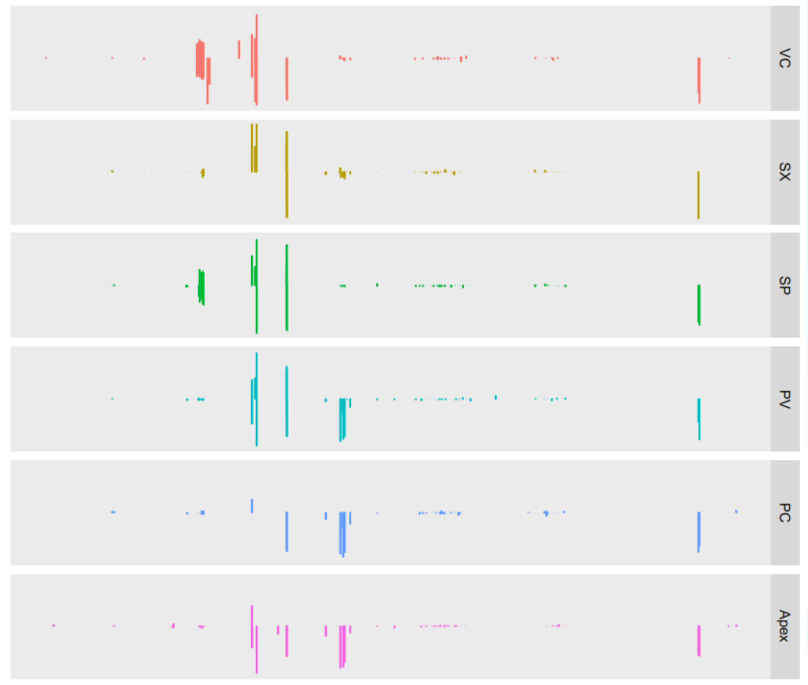
■ 差异甲基化区域（DMR)

表头	表头注释	结果展示
name	基因名称	GSTTP1
annotation	基因编号、转录本编号	NM_001039498 NM_015371 NR_003081
description	DMR与基因的位置关系	promoter
strand	基因正负链信息	-
geneL	基因长度	6663
chr	染色体信息	chr22
start	DMR的起始位置	24348549
end	DMR的终止位置	24348715
value	甲基化差异程度（Δβ)	-0.083935488
p.value	P值	0.013294287

注：表中每一行对应一个DMR（一张图），默认出图按照|value|＞0.1，p.value＜0.05，description位于promoter或5‘UTR区域，避免chr位于X、Y染色体的前5行出图。Tips：若按此条件筛选过滤掉了所有条目，可根据实际情况适当调整部分参数。

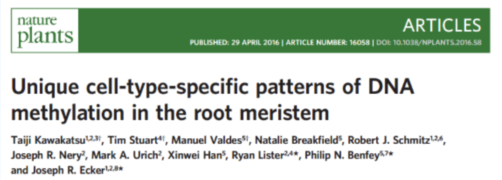
■ 特定基因CG位点甲基化程度展示

PtBRX-A（130个CG位点）



结果展示

参考文献



nature plants ARTICLES

PUBLISHED: 29 APRIL 2016 | ARTICLE NUMBER: 16058 | DOI: 10.1038/NPLANTS.2016.58

Unique cell-type-specific patterns of DNA methylation in the root meristem

Taiji Kawakatsu[1,2,3†], Tim Stuart[4†], Manuel Valdes[5†], Natalie Breakfield[5], Robert J. Schmitz[1,2,6], Joseph R. Nery[2], Mark A. Urich[2], Xinwei Han[5], Ryan Lister[2,4*], Philip N. Benfey[5,7*] and Joseph R. Ecker[1,2,8*]

适用项目

850K、捕获测序、WGBS

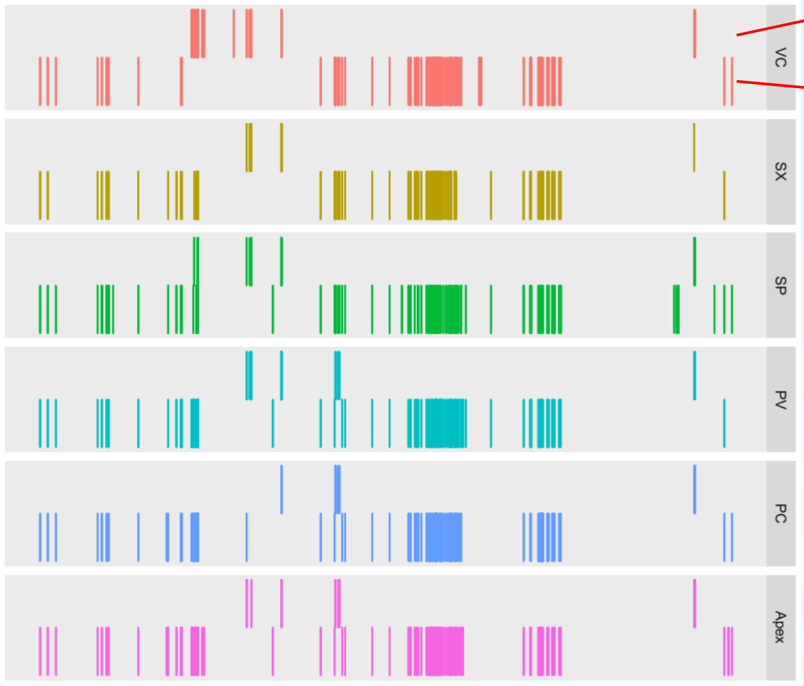
注意事项

1：峰高代表甲基化程度

2：每个样本上下两个方向代表正负链

■ 特定基因CG位点是否甲基化展示

PtBRX-A（130个CG位点）

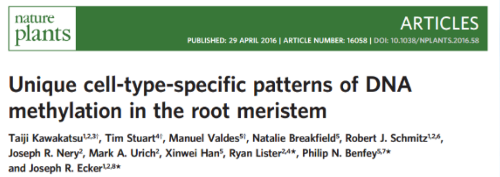


甲基化程度值＞0.3，认为该位点发生了甲基化

甲基化程度值＜0.3，认为该位点未发生甲基化

结果展示

参考文献


nature plants

ARTICLES

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Unique cell-type-specific patterns of DNA methylation in the root meristem

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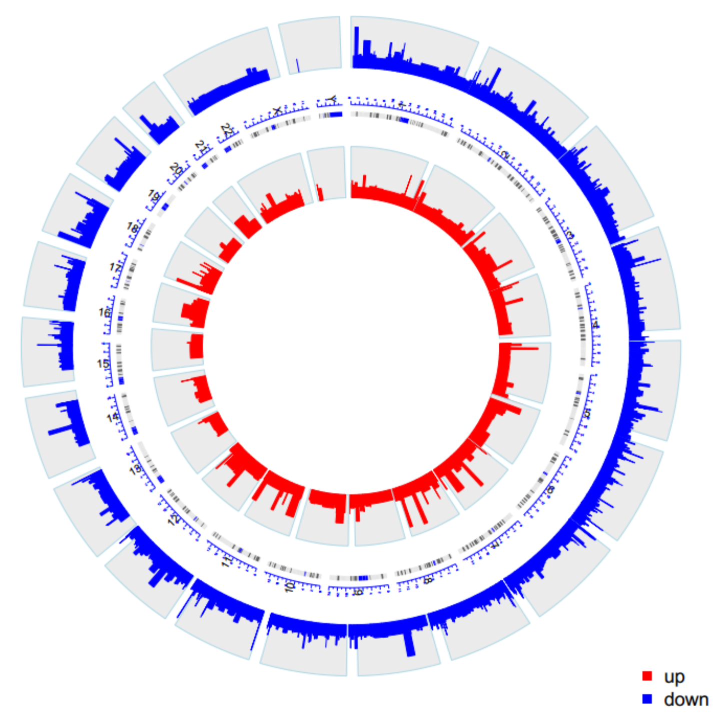
适用项目

850K、捕获测序、WGBS

注意事项

图 7 数字代表了染色体编号，红色代表了高甲基化的点，蓝色代表低甲基化点。数据采用FDR＜0.01各组样本的均值。(4)

■ 圈图展示差异甲基化在染色体上的分布



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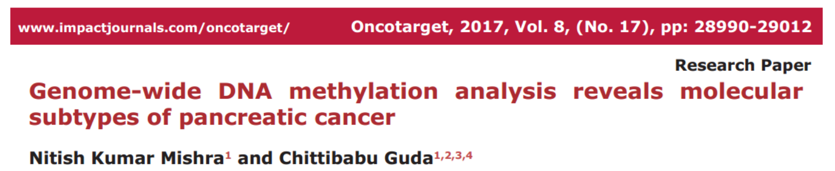

www.impactjournals.com/oncotarget/ Oncotarget, 2017, Vol. 8, (No. 17), pp: 28990-29012

Research Paper

Genome-wide DNA methylation analysis reveals molecular subtypes of pancreatic cancer

Nitish Kumar Mishra[1] and Chittibabu Guda[1,2,3,4]

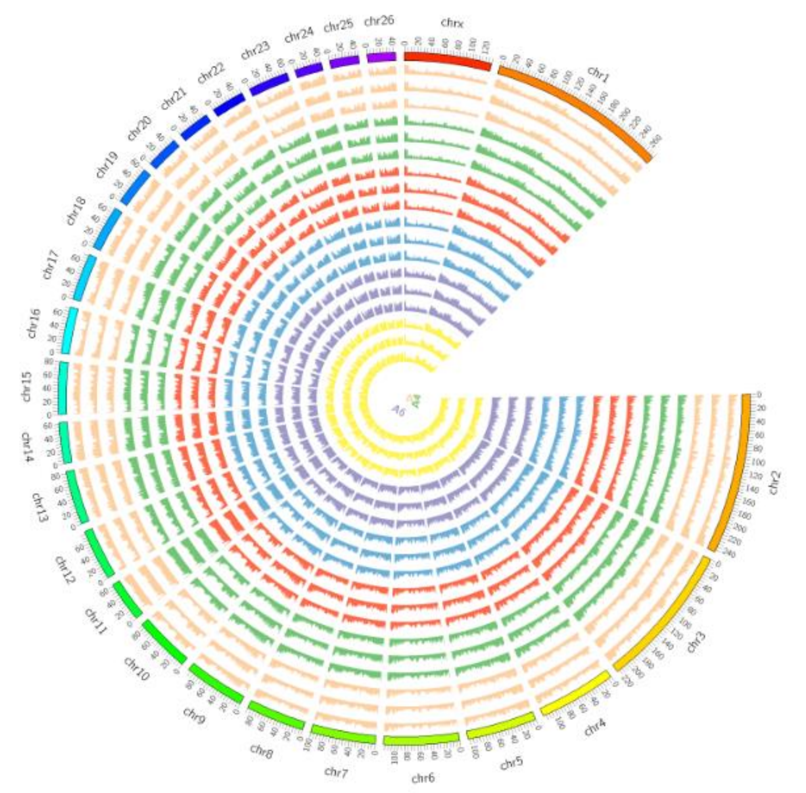
适用项目

850K、捕获测序、WGBS

注意事项

无

■ 圈图展示样本CG、CHG、CHH下不同染色体的甲基化程度



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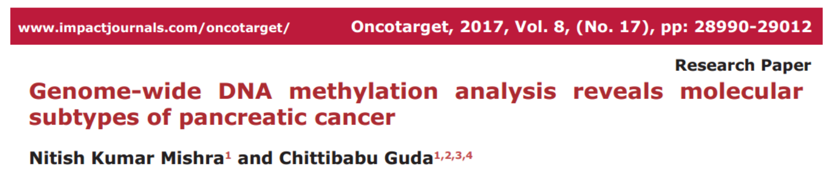
www.impactjournals.com/oncotarget/ Oncotarget, 2017, Vol. 8, (No. 17), pp: 28990-29012

Research Paper

Genome-wide DNA methylation analysis reveals molecular subtypes of pancreatic cancer

Nitish Kumar Mishra[1] and Chittibabu Guda[1,2,3,4]

适用项目

MeDIP-seq

注意事项

以峰高展示甲基化的程度

■ 圈图展示样本CG、CHG、CHH下不同染色体的甲基化程度

结果展示


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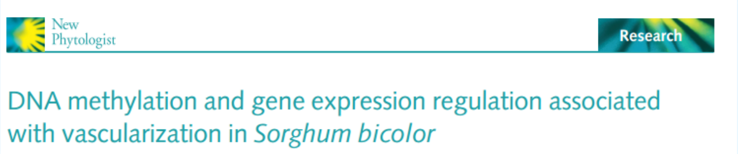
参考文献


New Phytologist
Research

DNA methylation and gene expression regulation associated with vascularization in *Sorghum bicolor*

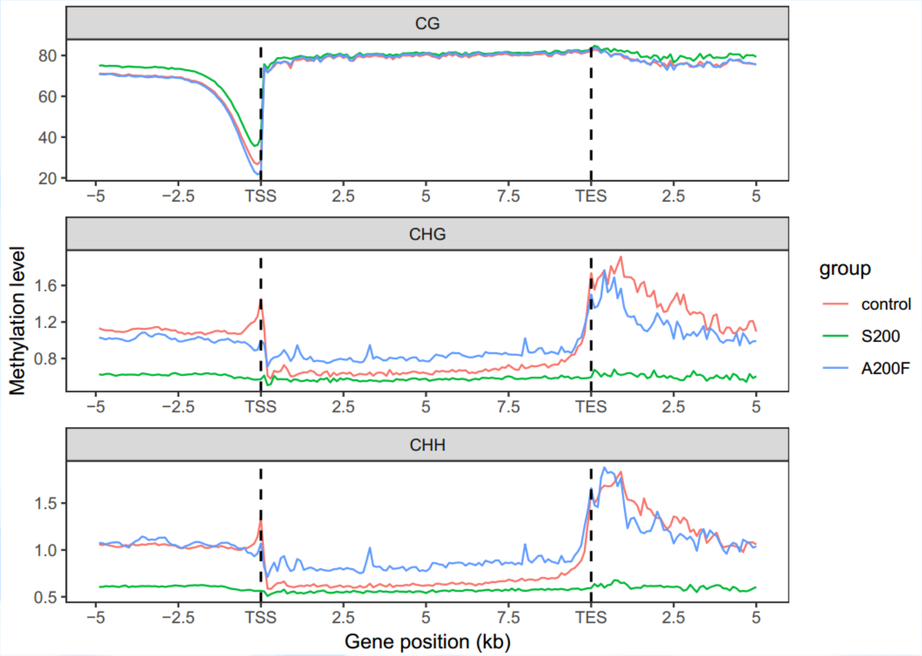
适用项目

850K、捕获测序、WGBS

注意事项

以不同颜色展示甲基化的程度

■ 所有基因甲基化趋势变化展示



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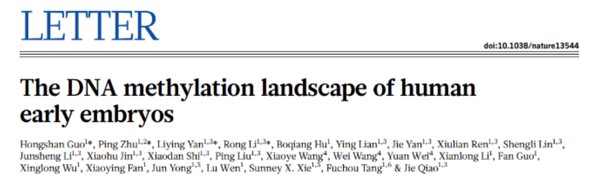


LETTER

doi:10.1038/nature13544

The DNA methylation landscape of human early embryos

Hongshan Guo[1]*, Ping Zhu[1,2]*, Liying Yan[1,3]*, Rong Li[1,3]*, Boqiang Hu[1], Ying Lian[1,3], Jie Yan[1,3], Xiulian Ren[1,3], Shengli Lin[1,3], Junsheng Li[1,3], Xiaohu Jin[1,3], Xiaodan Shi[1,3], Ping Liu[1,3], Xiaoye Wang[4], Wei Wang[4], Yuan Wei[4], Xianlong Li[1], Fan Guo[1], Xinglong Wu[1], Xiaoying Fan[1], Jun Yong[1,5], Lu Wen[1], Sunney X. Xie[1,5], Fuchou Tang[1,6] & Jie Qiao[1,3]

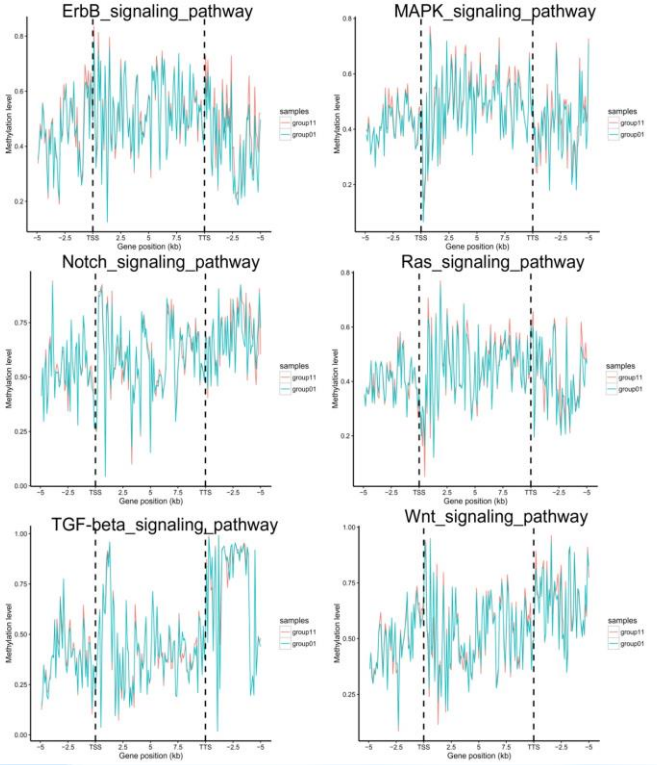
适用项目

850K、 捕获测序、WGBS

注意事项

捕获测序的CHG、CHH水平的甲基化位点信息不多，每个水平的图也可分开展示。

■ 信号通路的甲基化趋势变化展示



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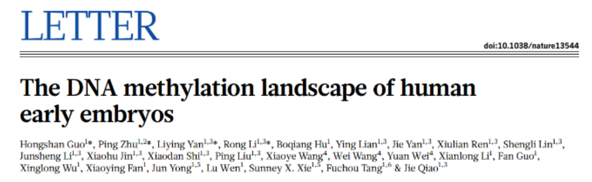
LETTER

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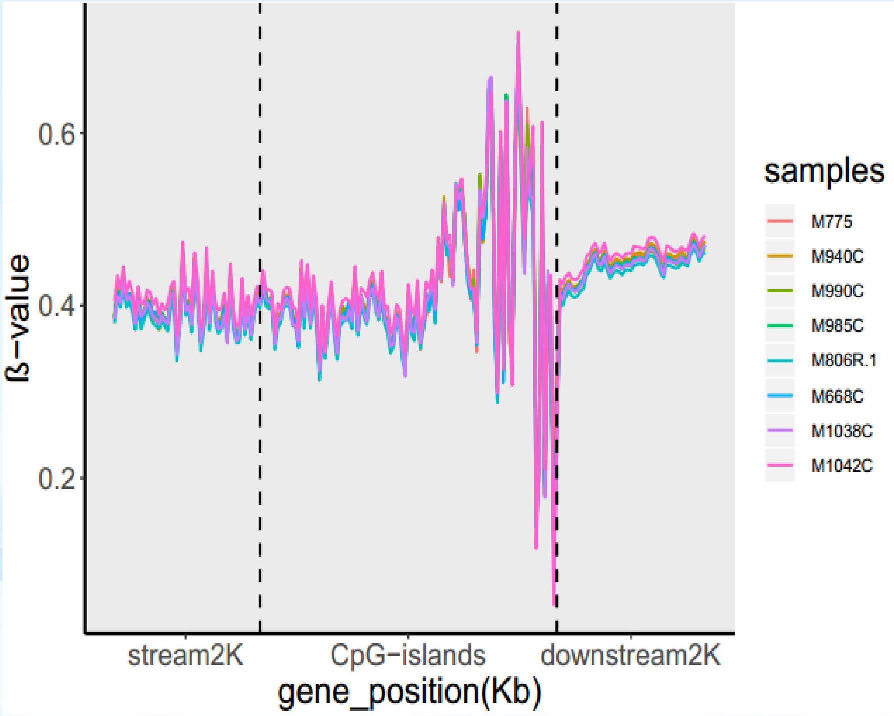
适用项目

850K、捕获测序、WGBS

注意事项

需客户指定通路

■ CGI上下游2K的甲基化走势分析



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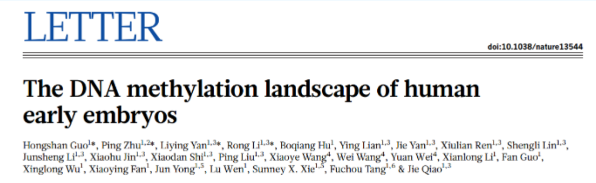
LETTER

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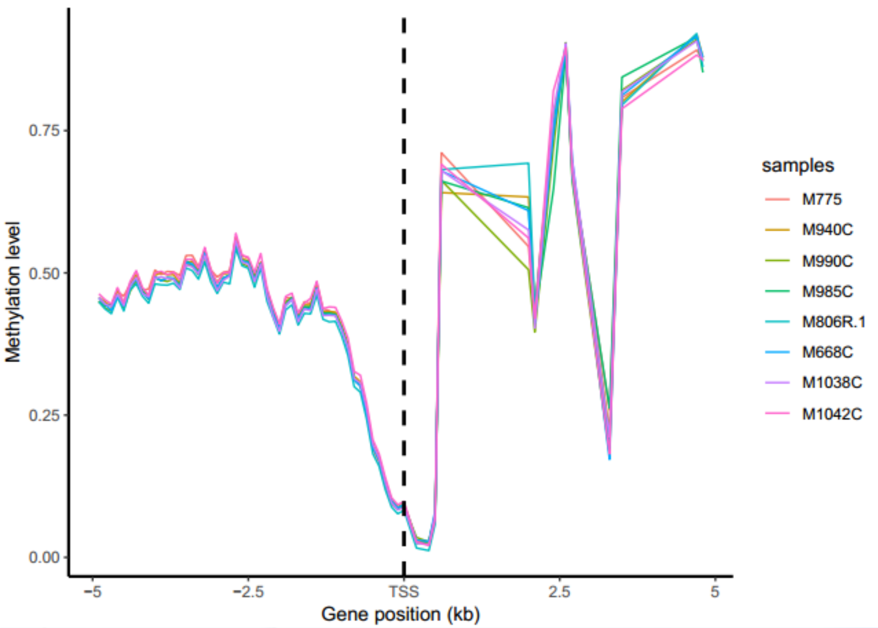
适用项目

850K、捕获测序、WGBS

注意事项

■ miRNA转录起始位点上下游5K的甲基化走势分析



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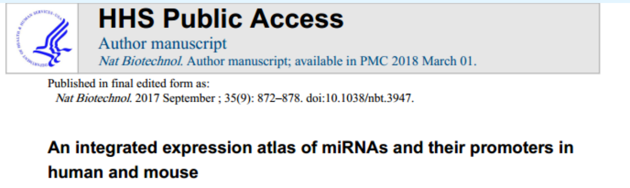

HHS Public Access
Author manuscript
Nat Biotechnol. Author manuscript; available in PMC 2018 March 01.

Published in final edited form as:
Nat Biotechnol. 2017 September ; 35(9): 872–878. doi:10.1038/nbt.3947.

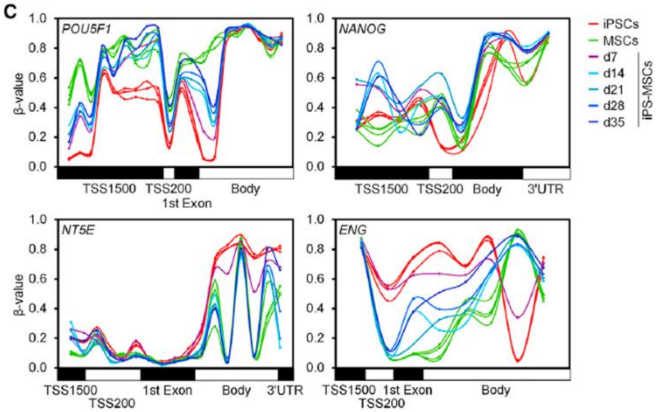
An integrated expression atlas of miRNAs and their promoters in human and mouse

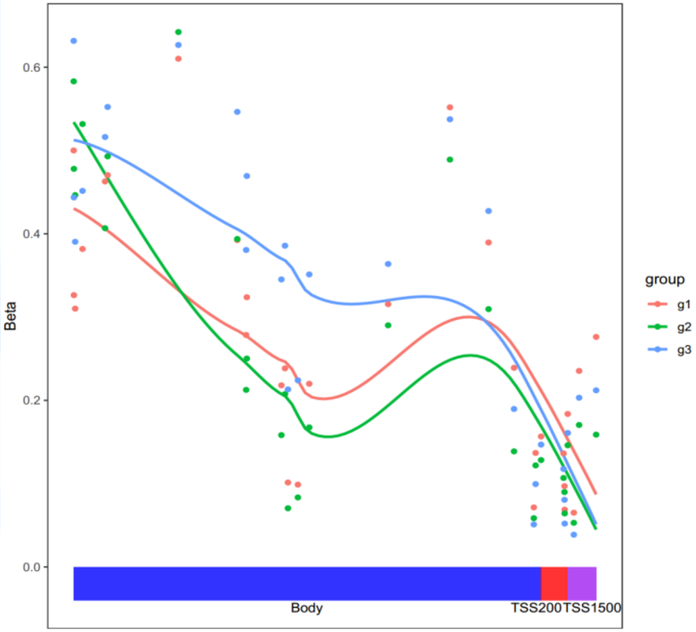
适用项目

850K、捕获测序、WGBS

注意事项

■ 特定基因的甲基化程度走走势图





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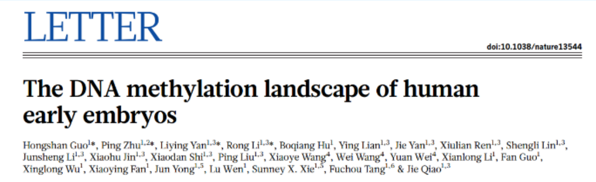

LETTER

doi:10.1038/nature13544

The DNA methylation landscape of human early embryos

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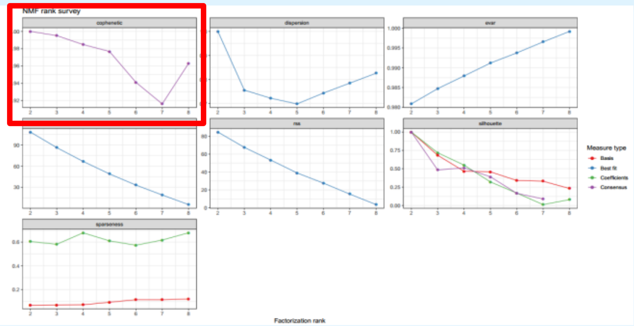
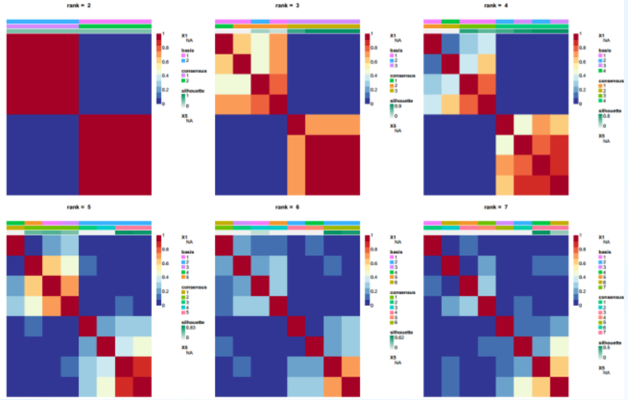
适用项目

850K、捕获测序、WGBS

注意事项

■ 基于甲基化数据肿瘤亚型分析





结果展示

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文献应用
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参考文献

ARTICLE

doi:10.1038/nature16965

Genomic analyses identify molecular subtypes of pancreatic cancer

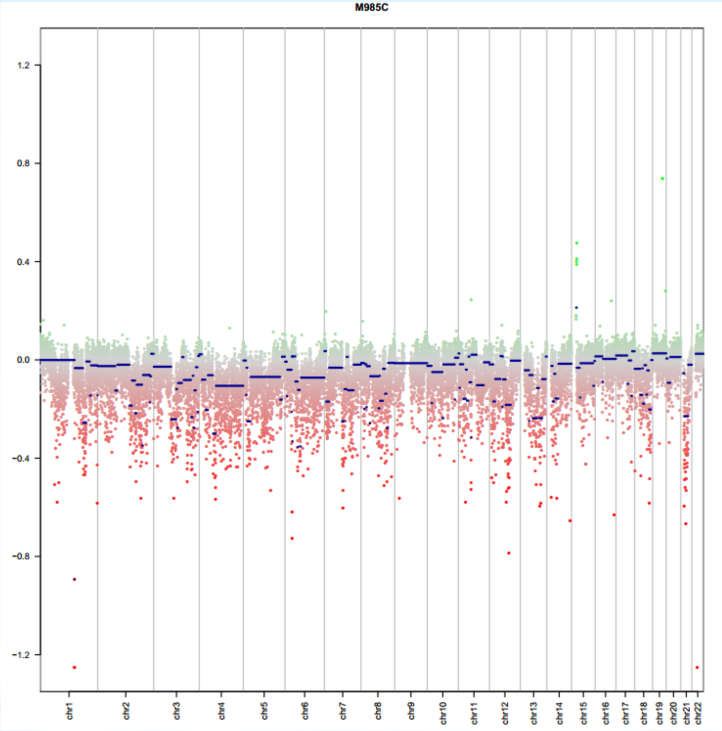
适用项目

850K、捕获测序、WGBS、MeDIP-seq

注意事项

多见于单细胞测序分析，适用于样本数多的项目

■ 基于甲基化芯片对的CNV分析



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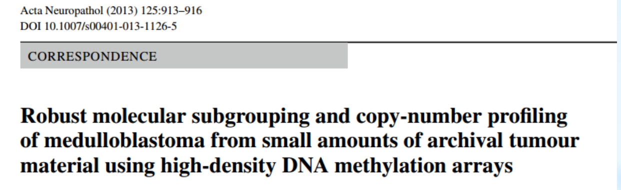
参考文献


Acta Neuropathol (2013) 125:913–916
DOI 10.1007/s00401-013-1126-5

CORRESPONDENCE

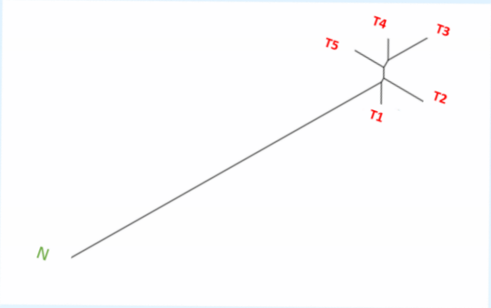
Robust molecular subgrouping and copy-number profiling of medulloblastoma from small amounts of archival tumour material using high-density DNA methylation arrays

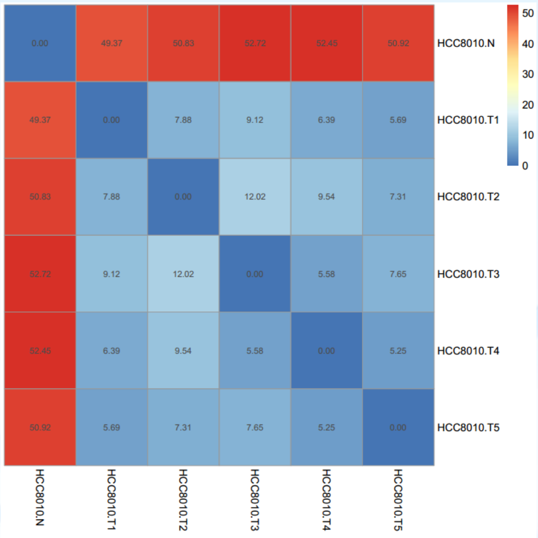
适用项目

850K、450K

注意事项

■ 基于甲基化数据的克隆演化





	HCC8010.N	HCC8010.T1	HCC8010.T2	HCC8010.T3	HCC8010.T4	HCC8010.T5
HCC8010.N	0.00	49.37	50.83	52.72	52.45	50.92
HCC8010.T1	49.37	0.00	7.88	9.12	6.39	5.69
HCC8010.T2	50.83	7.88	0.00	12.02	9.54	7.31
HCC8010.T3	52.72	9.12	12.02	0.00	5.58	7.65
HCC8010.T4	52.45	6.39	9.54	5.58	0.00	5.25
HCC8010.T5	50.92	5.69	7.31	7.65	5.25	0.00

结果展示

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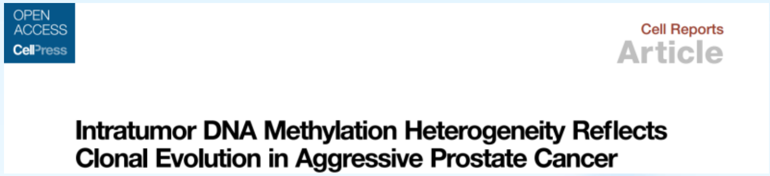
参考文献



OPEN ACCESS
CellPress

Cell Reports
Article

Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer

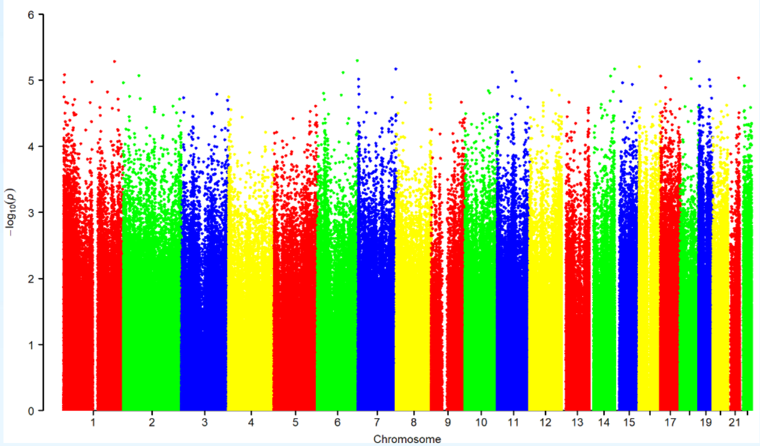
适用项目

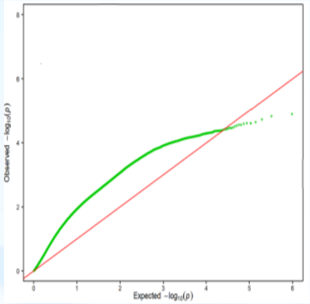
850K、捕获测序、WGBS

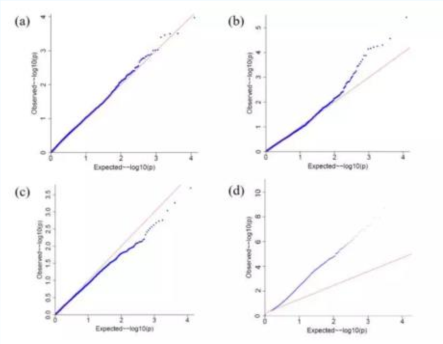
注意事项

用于分析的位点筛选标准可自定义

■ EWAS







结果展示

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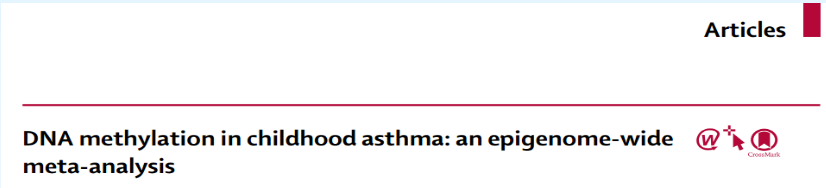


Articles

DNA methylation in childhood asthma: an epigenome-wide meta-analysis

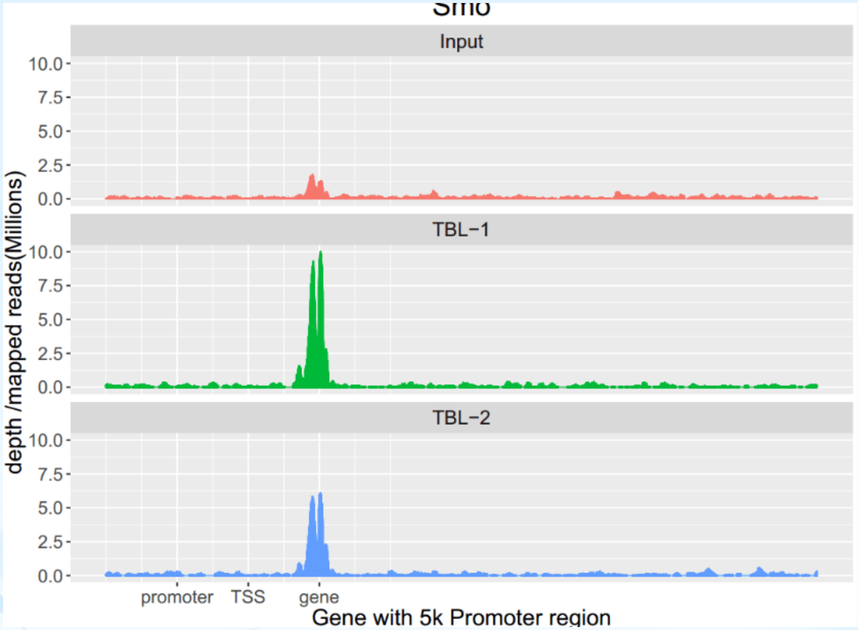
适用项目

850K、捕获测序、WGBS

注意事项

对样本数有要求

■ 特定基因的覆盖深度统计



结果展示


结果
文献应用
read.me

参考文献


Cell

Master Transcription Factors and Mediator Establish Super-Enhancers at Key Cell Identity Genes

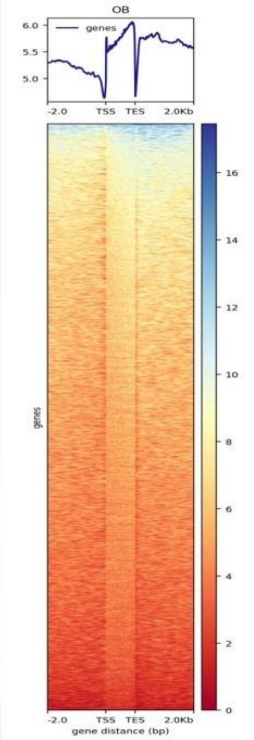
适用项目

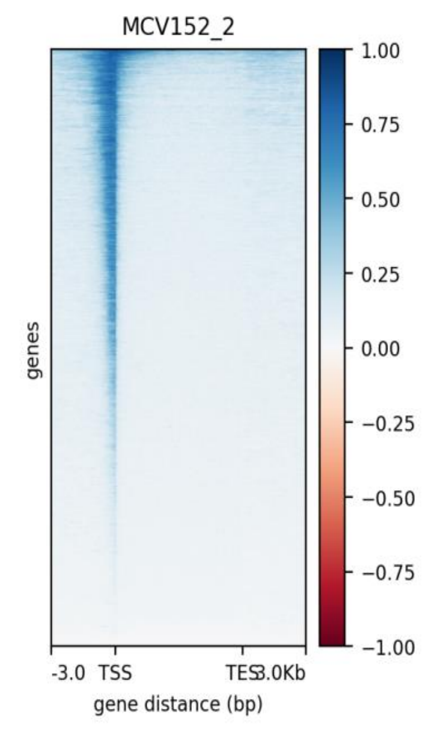
ChIP-seq

注意事项

相比于IGV或上传UCSC看，更加科学

■ 所有基因附近的平均信号分布图和热图





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文献应用
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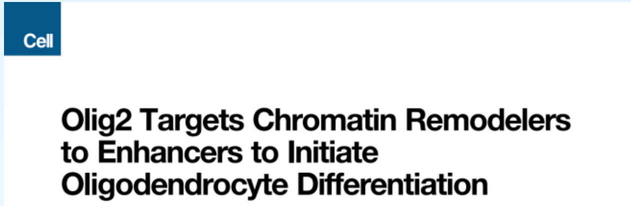
参考文献



Cell

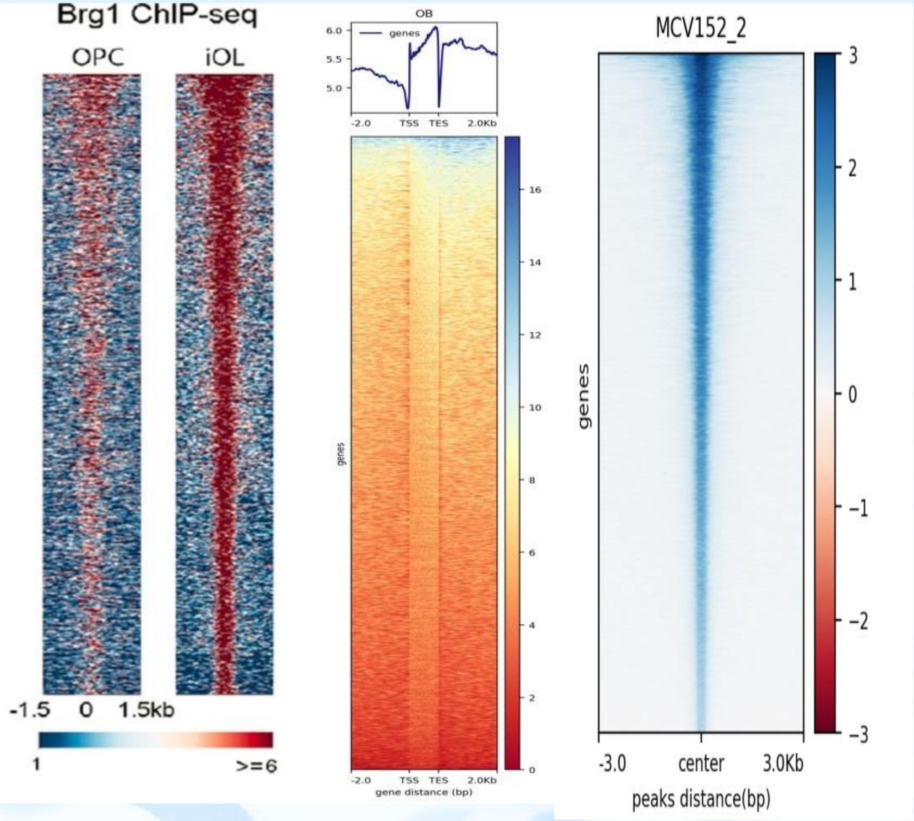
Olig2 Targets Chromatin Remodelers to Enhancers to Initiate Oligodendrocyte Differentiation

适用项目

ChIP-seq

注意事项

■ peak的峰中心热图



结果展示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文献应用
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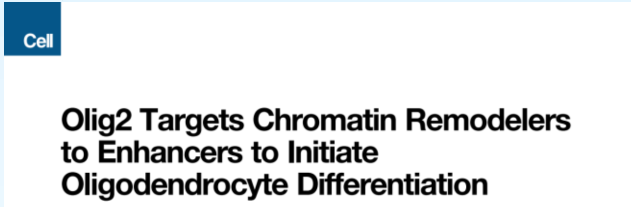
参考文献


Cell

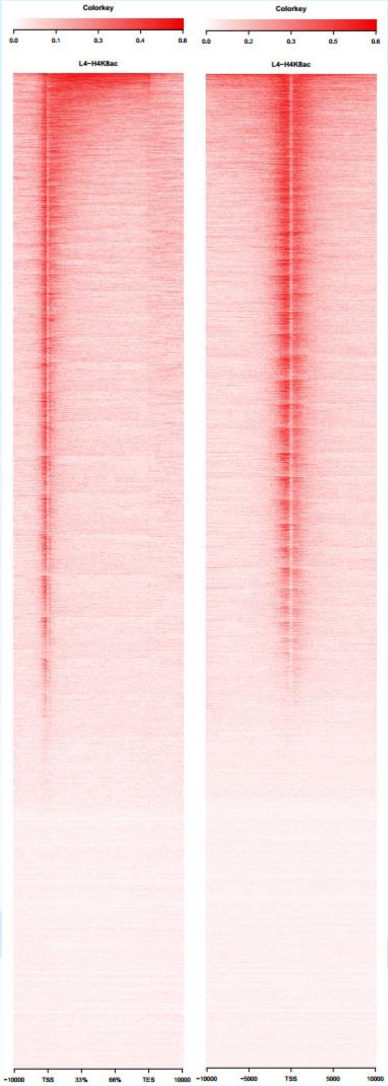
Olig2 Targets Chromatin Remodelers to Enhancers to Initiate Oligodendrocyte Differentiation

适用项目

ChIP-seq

注意事项

■ Reads在基因上的平均信号分布图



结果展示

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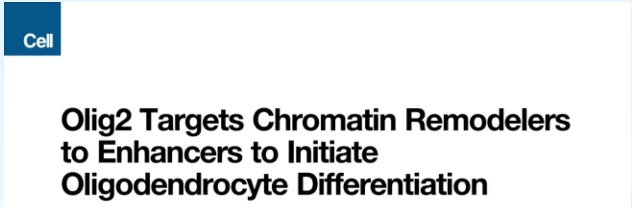
参考文献



Cell

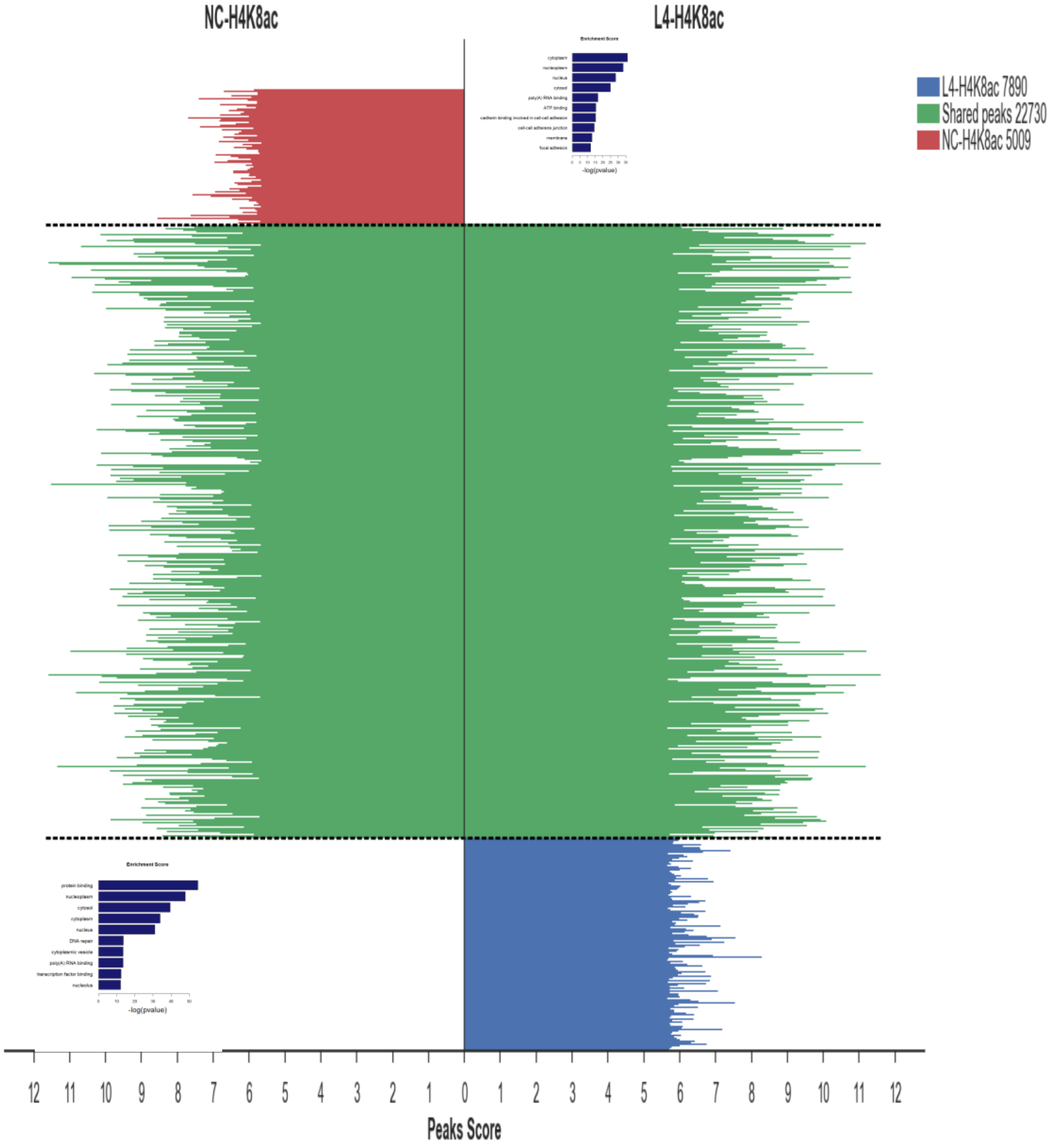
Olig2 Targets Chromatin Remodelers to Enhancers to Initiate Oligodendrocyte Differentiation

适用项目

ChIP-seq

注意事项

■ 不同样本的peaks score统计



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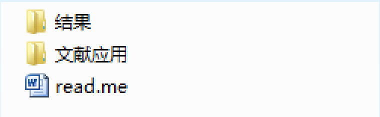

结果

文献应用

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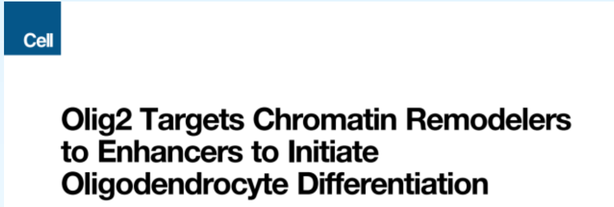
参考文献



Cell

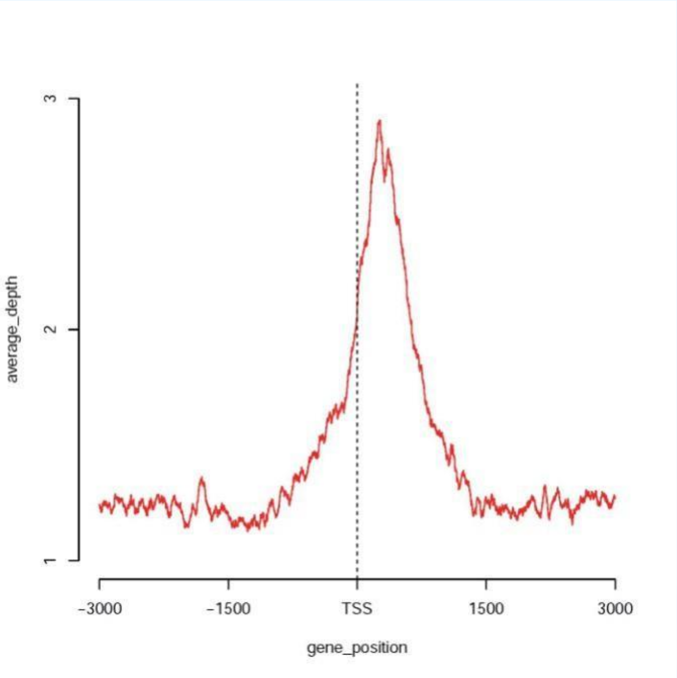
Olig2 Targets Chromatin Remodelers to Enhancers to Initiate Oligodendrocyte Differentiation

适用项目

ChIP-seq

注意事项

■ 所有基因TSS上下游depth统计图



结果展示


结果
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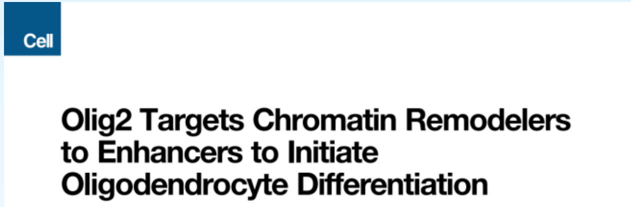
参考文献



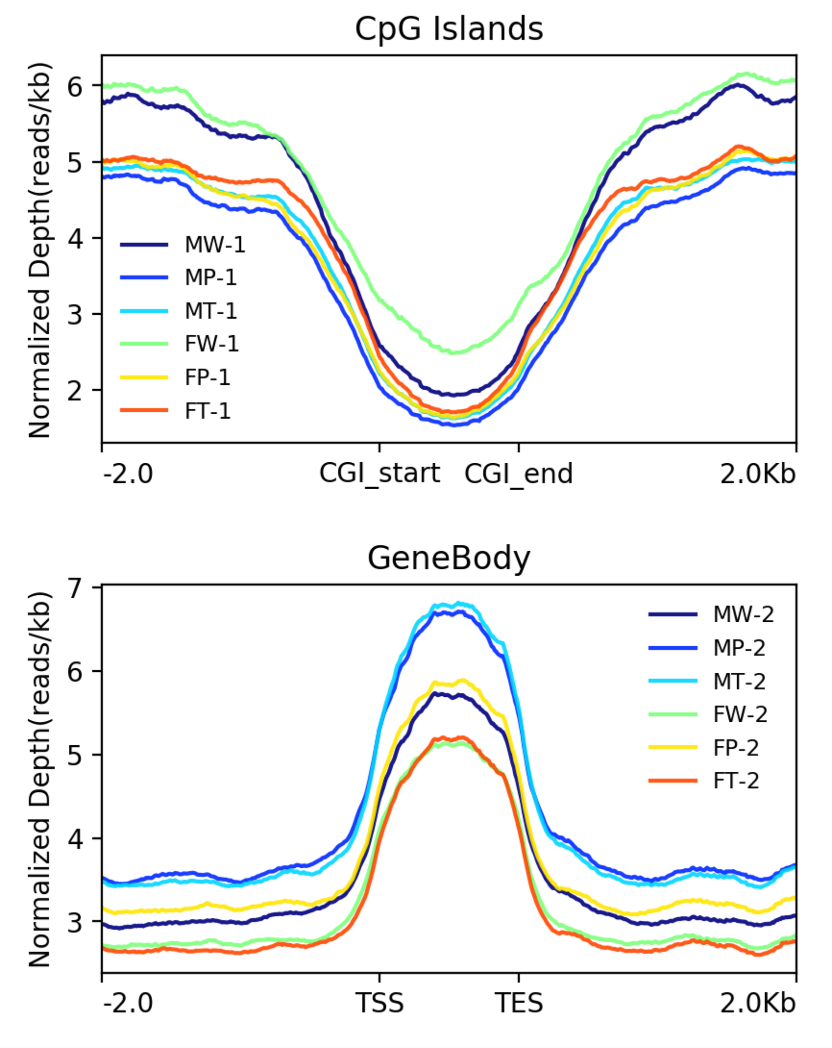
Olig2 Targets Chromatin Remodelers to Enhancers to Initiate Oligodendrocyte Differentiation

适用项目

ChIP-seq

注意事项

■ 样本在基因和CpG岛不同功能区域的reads覆盖程度统计



结果展示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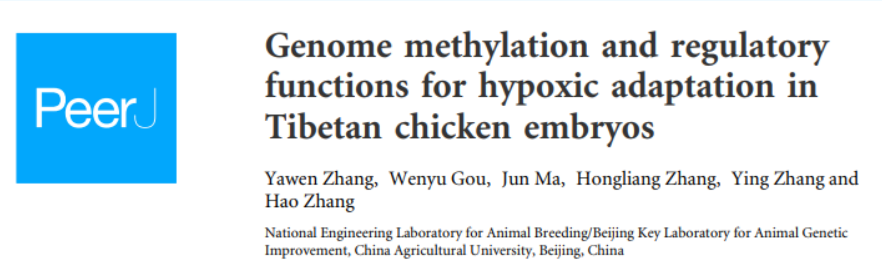
PeerJ

Genome methylation and regulatory functions for hypoxic adaptation in Tibetan chicken embryos

Yawen Zhang, Wenyu Gou, Jun Ma, Hongliang Zhang, Ying Zhang and Hao Zhang

National Engineering Laboratory for Animal Breeding/Beijing Key Laboratory for Animal Genetic Improvement, China Agricultural University, Beijing, China

适用项目

MeDIP-seq

注意事项

伯豪生物
SHBIO