Whole Genome Bisulfite Sequencing

DNA methylation is an epigenetic mechanism that occurs by the addition of a methyl group to cytosine nucleotides in DNA. This modification often alters the function and expression of the affected genes. Whole genome bisulfite sequencing (WGBS) is used to convert non-methylated cytosines to uracil, leaving the methylated cytosines to be identified by sequencing on a genome-wide scale.

Why Novogene?

Extensive experience with over 3000 projects

Industry-leading data quality guarantee

In house pipeline to meet different analysis requirement

Find out more: novogene.com

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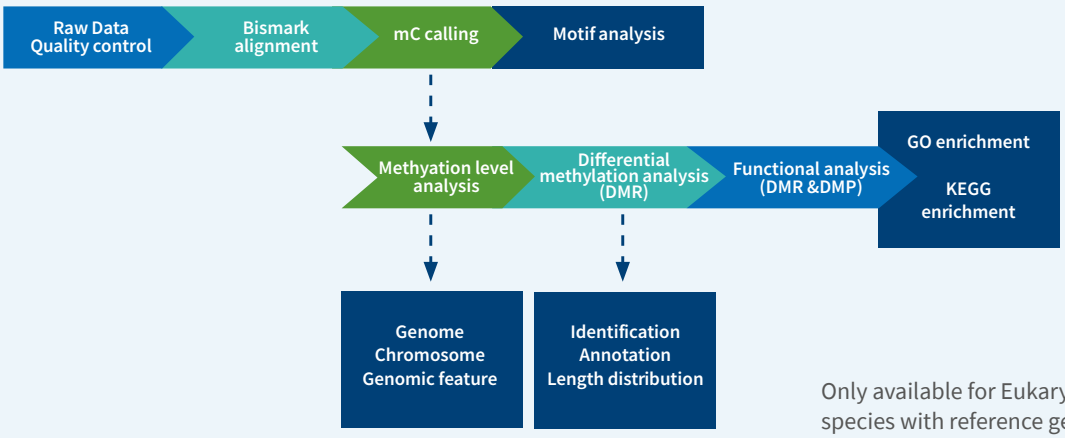
Sample requirements

Sample Type	Amount	Volume	Concentration	Purity
Genomic DNA	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	OD260/280≥ 2.0 OD260/230 ≥ 2.0 No degradation No contamination

Sequencing parameters

Platform	Read length	Recommended sequencing depth	Data quality	Turnaround time
Illumina NovaSeq 6000	Pair-end 150	Recommended: ≥ 30X	Q30 ≥ 85%.	Express service with only 25 working days from library preparation to data delivery. <24 samples & WOBI

Analysis pipeline



Only available for Eukaryotic diploid species with reference genome

Publications using Novogene's expertise

Cell Death & Disease, 2020.
LncRNA MNX1-AS1 promotes progression of intrahepatic cholangiocarcinoma through the MNX1/Hippo axis

bioRxiv, 2020.
Pou5f3 and Sox19b select gene expression repertoire at Zygotic Genome Activation

Molecular Cell, 2019.
Co-transcriptional Loading of RNA Export Factors Shapes the Human Transcriptome

PNAS, 2019.
Coupling of COPII vesicle trafficking to nutrient availability by the IRE1α-XBP1s axis

Cell, 2017.
A Natural Allele of a Transcription Factor in Rice Confers Broad-Spectrum Blast Resistance

Nucleic Acids Research, 2020.
The m6A reader YTHDF1 promotes ovarian cancer progression via augmenting EIF3C translation

HEPATOLOGY, 2017.
RNA N6-methyladenosine methyltransferase-like 3 promotes liver cancer progression through YTHDF2-dependent posttranscriptional silencing of SOCS2

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Case study

DNA methylation is not involved in dietary restriction induced lifespan extension in adult Drosophila.

Lian et al., 2018. Genetics Research. DOI: 10.1017/S0016672317000064.

Research objective:

To explore whether DNA methylation is the underlying cause of the lifespan extension observed in Drosophila under dietary restriction.

Sample collection:

DNA collected from flies under dietary restriction and fully fed conditions.

Sequencing strategy:

PE150 on the Illumina Hiseq 2500 platform.

Data amount:

> 11 Gb (> 34X) raw data per sample.

Results (partial results shown)

1.

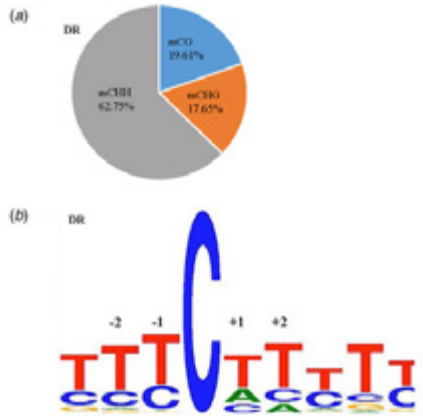

Figure 1
DNA methylation pattern between (a) dietary restricted and (b) fully fed flies.

2.

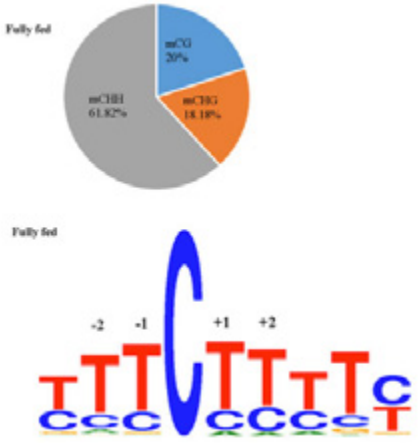

Figure 2
Sequence characteristics near mCHH* sites. (a) dietary restricted flies; (b) fully fed flies.

3.

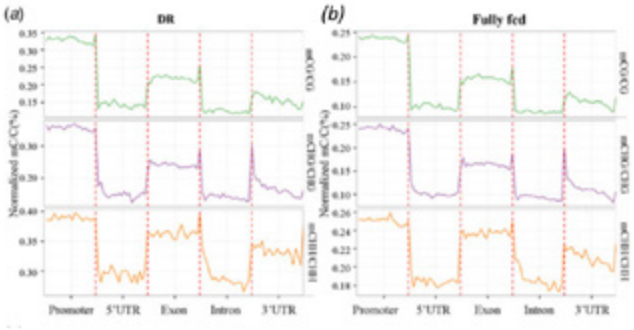

Figure 3
The average cytosine methylation density for each context (mCG, mCHG, mCHH*) within each genomic feature. (a) dietary restricted and (b) fully fed flies.

Conclusions

With the help of Novogene, this study showed no significant change in the methylation of DNA in dietary restricted Drosophila when compared with fully fled flies. This suggests that DNA methylation does not contribute to the lifespan extension observed in dietary restricted flies and that some other epigenetic mechanism, such as histone modification, may be involved.

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