Questionnaire for Data Processing, Analysis, and Interpretation for

WGBS or **Targeted methylation seq**

## Study Objectives: Please specify the aim of the project.

## **Project Background: Brief description of the project.**

## **Choose the appropriate experiment type**

**Whole Genome Bisulfite Sequencing (WGBS)**

**Targeted methylation sequencing**

## Expected deliverables: Please choose the deliverables below and/or specify any additional items/requirements

Please specify the species below

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| --- | --- | --- |
| Standard species | Human (Homo sapiens) | Hg38 |
| Hg19(GRCh37) |
| Mouse (Mus musculus) | mm10 (GRCm38) |
| Others |  |  |

## Standard deliverables:

|  |  |  |
| --- | --- | --- |
| **Analysis Item** | **Y/N** | **If yes, any specific requirements?** |
| Sequencing quality control: FastQC |  |  |
| Sequence alignment raw files: bam |  |
| Remove duplicate reads (Not recommended for Targeted methylation experiment, such as TruSeq Methyl Capture EPIC) |  |
| Summary report of alignment, methylation extractor stats |  |
| CpG cytosine report |  |
| Differential Analysis and Quality assessment:   1. Differentially Methylation analysis (CpG) 2. Differentially Methylation base Annotations and Annotation plot 3. Histogram for percent methylation distribution 4. Histogram of CpG coverage 5. Sample correlation Plot (Pearson correlation) 6. Sample Hierarchical clustering (ward’s method) 7. PCA Analysis and PCA screen plot |  |  |

## Clearly specify experimental design to FOR differentially methylation analysis

For example:

Group A vs. Group B

Group A: Sample 1, 2, 3

Group B: Sample 4, 5, 6

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| --- |
|  |

\*If any specific version of genome sequence, annotation file, or software/packages/tools for data analyze is needed, please specify it below:

|  |
| --- |
|  |

## Customized deliverables **(each item is an additional charge and may affect turnaround time, please request specific pricing from PM team)**:

|  |  |  |
| --- | --- | --- |
| **Analysis Item** | **Y/N** | **If yes, any specific requirements?** |
| Differentially Methylation analysis with non CpG context (i.e CHH, CHG) |  |  |
| Differentially Methylated **Region** with MethylKit (CpG only) |  |  |

If any other customized analysis item(s) is needed, please provide the detailed requirements below, our bioinformatics team will evaluate the feasibility.

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## **Sequencing details: Eg. Sequencing primer detail etc.**

## References: Please attach and or provide links of the relevant references as per your project