3. Bioinformatics Analysis

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| **Standard Analysis** |
| Data quality control (filtering reads containing adapter or with low quality; Q20, Q30, error rate distribution, GC distribution, total bases) |
| Alignment to reference genome (mapping rate, sequencing depth, reads coverage) |
| Quality controls for 5-mC identification (MspI digestion efficiency analysis and BS conversion rate) |
| mCs detection, methylation level calculation |
| (1) Methylation level and frequency distribution in different sequence context (CG, CHG, CHH)  (2) Methylation level and frequency distribution in different functional elements (promoter, 5'UTR, exon, intron, 3'UTR) |
| Differentially methylated regions (DMRs), Differentially Methylated Promoter (DMPs)  detection and annotation |
| Function enrichment (Gene Ontology and KEGG Pathway) of DMR-associated genes and DMP-associated genes |
| Visualization of BS seq data |