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) |
| Mapping onto reference genome(mapping rate,duplication rate, sequencing depth, reads coverage) |
| 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 chromosomes  (3) Methylation level and frequency distribution in different functional elements (promoter, 5'UTR, exon, intron, 3'UTR) |
| Differentially Methylated Site(DMS) detection |
| 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 |