3. Bioinformatics Analysis

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| **Standard Analysis of mRNA & lncRNA (for Species with Reference)** | | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | | |
| Mapping Clean Reads to Reference Genome and Transcript Prediction | | |
| Structural Analysis | Alternative Splicing (**AS**) Quantification and Differential Expression Analysis (**Only for Compared Groupings)** | |
| SNP/InDel Detection and Annotation Analysis | |
| lncRNA prediction | Transcript Assembly | |
| Filtering of Candidate lncRNA | |
| Transcript Expression Quantification | | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | | |
| Differential Expression Analysis (**Only for Compared Groupings**) | | |
| LncRNA Target Gene Prediction | | Co-location Prediction of lncRNA and mRNA |
| Co-expression Prediction of lncRNA and mRNA |
| Functional Analysis of **Differentially Expressed mRNA and Differentially Expressed lncRNA Targeting Genes** (**Only for Compared Groupings** | | Gene Ontology (**GO**) Enrichment Analysis |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |
| Transcription Factors Functional Annotation analysis |
| Protein Protein Interaction Analysis |
| Fusion Gene Analysis | | |

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| **Standard Analysis of CircRNA (for Species with Reference)** | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | |
| Mapping Clean Reads to Reference Genome | |
| circRNA Identification | Length Distribution of circRNAs |
| Sources of circRNAs |
| Distribution of circRNA on the Chromosomes |
| Transcript Expression Quantification | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | |
| Differential Expression Analysis (**Only for Compared Groupings**) | |
| Functional Analysis of **Differentially Expressed circRNA Source Genes** (**Only for Compared Groupings**) | Gene Ontology (**GO**) Enrichment Analysis |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |
| CircRNA Target Gene Prediction | |

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| **Standard Analysis of miRNA** | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | |
| Summary of Length Distribution | |
| Common and Specific Sequence Summary | |
| Mapping Clean Reads to Reference Genome | |
| Functional Classification and Annotation of small RNA | Identification Known miRNA |
| Non-coding Transcripts Annotation |
| Repeat Sequence Annotation  (Annotation of the reference genome should be provided) |
| Exon and Intron Annotation |
| Novel miRNA Prediction |
| miRNA Base Edit | |
| miRNA Family Analysis | |
| miRNA Expression Quantification | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | |
| Differential Expression Analysis (**Only for Compared Groupings**) | |
| Target Gene Prediction of Known and Novel miRNA | |
| Functional Analysis of **Differentially Expressed miRNA Genes** (**Only for Compared Groupings**) | Gene Ontology (**GO**) Enrichment Analysis |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |