3. Bioinformatics Analysis

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| **Standard Analysis for lncRNA & mRNA** | |
| **QC** | 1. Data Quality Control: filtering reads containing adapter or with low quality |
| 1. Statistics of Data Production and Quality |
| 1. Alignment with reference genome |
| **lncRNA prediction** | 1. Reference based reconstruction of transcripts |
| 1. Filtering of candidate lncRNA |
| **Structure analysis** | 1. Alternative splicing analysis |
| 1. SNP/Indel calling |
| 3．LncRNA target gene prediction |
| 4. Fusion Gene Analysis (for tumor sample and cancer cell line of human/mouse only) |
| **Expression quantification analysis** | 1. Expression quantification analysis for mRNA and lncRNA (two or more groups of samples) |
| 1. Correlation analysis (For biological replicates only) |
| 1. Differential expression analysis for mRNA and lncRNA (two or more groups of samples) |
| 1. GO enrichment analysis of differentially expressed coding genes |
| 1. KEGG enrichment analysis differentially expressed coding genes |
| 1. Network analysis of protein-protein interactions of differential mRNA |
| 1. Enrichment analysis of differentially expressed lncRNA target genes |
| **lncRNA**  **mRNA**  **comparative analysis** | 1. Structural comparison between lncRNA and mRNA |
| 2. Expression comparison between lncRNA and mRNA |
| 3. Conservation comparison between lncRNA and mRNA (For a few animal species only) |
| 4.lncRNA-mRNA network analysis |

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| **Standard Analysis for circular RNA** | |
| **QC** | 1. Data Quality Control: filtering reads containing adapter or with low quality |
| 1. Statistics of Data Production and Quality |
| 1. Alignment with Reference Genome |
| **circRNA**  **Identification** | 1. Length Distribution of circRNAs |
| 1. Sources of circRNAs |
| 1. Distribution of circRNA in the Chromosomes |
| **Differential Expression of circRNAs** | 1. Expression Quantification Analysis of circRNAs |
| 1. TPM Distribution of circRNAs |
| 1. Differential Expression Analysis of circRNAs (>2 sample groups) |
| **Enrichment Analysis** | 1. GO Enrichment Analysis |
| 1. KEGG Enrichment Analysis |
| **Prediction of miRNA targets** | 1. Finding miRNA targets from circRNAs |

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| **Standard Analysis for small RNA** |
| Data Quality Control: filtering reads containing adapter or with low quality |
| Summarize the length distribution of small RNA |
| Analyze common and specific sequences between two samples |
| Align small RNA to reference genome |
| Identify known miRNA |
| Identify rRNA, tRNA, snRNA, snoRNA and Non-coding RNA |
| Identify repeat associated small RNAs (repeat annotation information of the reference genome should be provided) |
| Align small RNA to mRNA, exon and intron |
| Predict novel miRNAs and their secondary structures by Mireap from unannotated small RNAs |
| Analyze the expression pattern of known miRNAs |
| Analyze the base bias of miRNA |
| Classify and annotate of small RNAs |
| Analyze correlation of miRNA expression among samples (≥2 samples) |
| Analyze differentially expressed miRNA and cluster analysis among samples (≥2 samples) |
| Predict target gene of miRNA |
| Gene ontology analysis of DEGs and pathway enrichment analysis of DEGs |

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| **Advanced Association Analysis** | |
| **LncRNA vs mRNA** | Interaction analysis of lncRNA targeted gene and mRNA |
| **LncRNA vs miRNA** | Homology analysis of lncRNA and pro-miRNA |
| Targeting relation analysis between lncRNA and mRNA |
| Interaction analysis of differential miRNA and its targeted lncRNA |
| **miRNA vs mRNA** | Interaction relation analysis between differential mRNA and miRNA |
| Interaction analysis of differential miRNA and its targeted mRNA |
| **circular RNA vs mRNA** | Interaction analysis of circRNA and its source gene |
| **circular RNA vs miRNA** | Targeting relation analysis of differential circRNA and miRNA |
| **LncRNA vs miRNA vs mRNA** | Interaction analysis of miRNA, lncRNA and mRNA |
| **circular RNA vs miRNA vs mRNA** | Interaction analysis of circRNA, lncRNA and mRNA |