1. Bioinformatics Analysis

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| ***De novo* Standard Analysis (Species without Reference)** | |
| Data Quality Control: Filtering reads containing adapter or uncertain nucleotides or of low quality, and statistic summary of data quality | |
| *De novo* Transcriptome Assembly | |
| Gene Functional Annotation | |
| GO, COG, KEGG Classification | |
| Coding Sequence (**CDS**) Prediction | |
| Structural Analysis | SNP/InDel Detection and Annotation Analysis |
| Simple Sequence Repeats (SSR) Analysis |
| Gene Expression Quantification | |
| Correlation Analysis Between Groups (**Only for Samples with biological replicates**) | |
| Differential Expression Analysis (**Only for Grouping with control samples**) | |
| Functional Analysis of **Differentially Expressed Genes** (DEGs) (**Only for Grouping with control samples**) | Gene Ontology (**GO**) Enrichment Analysis |
| Kyoto Encyclopedia of Genes and Genomes (**KEGG**) Pathway Enrichment Analysis |
| Protein Protein Interaction Analysis |