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| **Standard Analysis (for Species with Reference)** | |
| 1. Data quality control | |
| 2. Identification, clustering and correction of full-length transcripts | |
| 3. Mapping reads to reference genome | |
| 5. Prediction and annotation (GO, Swiss-Prot) of novel transcripts | |
| 8. Structural Analysis of Isoforms | Fusion transcript analysis |
| Alternative splicing |
| Alternative polyadenylation |
| TTS & TSS prediction |
| 7. Transcription factor analysis | |
| 8. lncRNA prediction | |
| 9. Differential expression analysis (Only for Compared Groupings) | Isoform quantification and differential expression analysis |
| GO enrichment |
| KEGG enrichment |

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| **Standard analysis (for Species without Reference)** | |
| 1. Data quality control | |
| 2. Identification, cluster and correction of full-length transcripts | |
| 3. Simple Sequence Repeat (SSR) analysis | |
| 4. Functional annotation (via Nr, Nt, KEGG, GO, KOG, Swiss-Prot and Pfam databases) | |
| 5. Transcription factor analysis (only for plants and animals species) | |
| 6. Differential expression analysis (Only for Compared Groupings) | Isoform quantification and differential expression analysis |
| GO enrichment |
| KEGG enrichment |