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| **Standard analysis**  **(Full-length transcriptome with reference genome)** |
| 1. Data quality control |
| 2. Identification, cluster and correction of full-length transcripts |
| 3. Mapping reads to reference genome |
| 4. Alternative splicing |
| 5. Prediction and annotation (GO, Swissprot) of novel gene and novel trasnscript |
| 6. Fusion transcript analysis |
| 7. Alternative polyadenylation |
| 8.Comparation of transcript in samples (two or more samples) |
| 9.lncRNA prediction |
| 10. Transcription factor analysis |
| **Standard analysis**  **(Full-length transcriptome without reference genome)** |

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| 1. Data quality control |
| 2. Identification, cluster and correction of full-length transcripts |
| 3. SSR analysis |
| 4. Transcript functional annotation using seven databases ( Nr, Nt, KEGG, GO, KOG, Swissprot, Pfam ) |
| 6. Transcription Factor analysis (plants and animals only) |
| 7. Comparation of transcript in samples (two or more samples) |