# ### All the softwares we used are free and open source, and we have cited every software in our manuiscript.

# A README file gene annotation

## Genome annotation

1. hisat\_samtools\_run.sh, Shell script for aligning RNA-seq file to reference.
2. Trinity\_GG\_denovo.sh, Shell script to both Denovo and genome-guided assembles rna-seq data using Trinity software.
3. PASA\_align\_run.sh , Shell script to running PASA.
4. ab\_homo\_pipe.sh, Shell script for performing ab initio and homologous prediction. Augustus and TBLASTN were performed in the pipeline geta <https://github.com/chenlianfu/geta>.
5. evm\_run.sh, Shell script for integrating ab initio, transcriptome-based and homology-based evidences to final consensus gene sets using EvidenceModeler.
6. PASA\_update.sh, Shell script for updating alternatively spliced isoforms.