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

1. **Genome analyses**
2. TE annotation: we performed command ‘perl EDTA.pl --genome genome.fasta --sensitive 1 -anno 1’ implemented in EDTA software to annotate TE.

## Genome annotation

1. 1hisat\_samtools\_run.sh-Script to align RNA-seq file to reference.
2. 2Trinity\_GG\_denovo.sh-Script to perform rna-seq data assmble based on both Denovo and genome-guided methods using Trinity software.
3. 3PASA\_align\_run.sh -Script to run PASA.
4. 4ab\_homo\_pipe.sh-Script to perform ab initio and homologous prediction. Augustus and TBLASTN were performed in the pipeline geta <https://github.com/chenlianfu/geta>
5. 5evm\_run.sh, Script to integrate ab initio, transcriptome-based and homology-based evidences to the final consensus gene set using EvidenceModeler.
6. 6PASA\_update.sh, Script to update alternatively spliced isoforms.

# 2.Variant-calling

## Call\_SNP

(1) 1trimmomatic.sh - Script to use Trimmomatic to filter raw reads.

(2) 2bwa&picard.sh – Script to use BWA to map reads to reference genome, use SAMtools to sort the alignment results and use Picard to mark PCR duplicate.

(3) 3GATK-HaplotypeCaller.sh, 4GATK-Combinegvcf.sh and 5GATK-GenotypeGVCFs.sh - Scripts to use GATK to perform SNP and Indel calling.

(4) 6summary-coverage\_ratio.sh, 6summary-depth.sh, 6summary-mapping\_ratio.sh – Scripts to summary statistics of whole genome re-sequencing data.

(5) filter – Scripts to performe multiple filtering steps to only retain high-quality SNPs for downstream analysis.

(6) filter/ 12SNPfilter5-bedfile\_create - Scripts to use SNPable to mask the genome.

## Call\_Indel

1. 1seperate-Indel.sh - Script to use Vcftools to separate Indel from raw vcf-format files.
2. filter - Scripts to performe multiple filtering steps to only retain high-quality Indels for downstream analysis.

## Call\_SV

1. 1call\_SV1.sh, 2call\_SV2.sh, 3call\_SV3.sh – Scripts to use Delly to call SV.
2. 4merge\_filter.sh – Script to performe multiple filtering steps to only retain high-quality SVs for downstream analysis.

# 3.Population\_genetics

1. 1structure.sh - Script to perform structure analyses.
2. 2NJ.sh - Script to perform phylogenetic analyses.
3. 3pi-24pops.sh - Script to calculate genetic diversity of each population.
4. 4pi&dxy\_NS.sh - Script to calculate genetic diversity of intra-group and inter-group.
5. 5Fst&TajimaD.sh - Script to calculate Fst and Tajima’s D of each group.
6. 6IBD&IBE.sh - Scripts to perform IBD, IBE, pIBD and pIBE analyses.
7. 7PSMC - Scripts to perform PSMC analyses.
8. 8LD.sh – Script to estimate and compare the pattern of LD among different groups.

# 4.Local adaptation

1. 1LFMM\_onebio.sh - Scripts to perform LFMM analyses.
2. 2manhattan.sh - Scripts to convert pvalue to qvalue and make manhatton plots.
3. 3cor\_plot.R - Scripts to calculate the correlation between environmental variables.
4. 4RDA.R - Scripts to perform RDA analyses.
5. 5pk\_beagle\_eff.sh - Scripts to annote the vcf-format file.
6. 6IHS.sh - Scripts to calculate iHS value.
7. 7supp\_picture\_plot.R - Scripts to make Supplementary Fig. 12.

**5. Call\_ATAC\_peak**

(1) 1.atac\_trim\_reads.sh - Script to use Trimmomatic to filter raw reads.

(2) 2.atac\_index.sh - Script to use Bowtie2 to build the reference index.

(3) 3.atac\_bowtie\_rmdup.sh - Script to use Bowtie2 to map reads to reference genome, use SAMtools to sort the alignment results and use Picard to remove PCR duplicates.

(4) 4.atac\_insertsize.sh - Scripts to summary insrtsize of ATAC data.

(5) 5.macs\_call\_peak.sh - Scripts to use MACS2 to call ATAC peak and gain the location of peaks.

**6.RONA**

(1) 1RONA\_calculate.R - Scripts to calculate RONA of each climate model.

(2) 2aveRONA\_plot.R - Scripts to make plots using ave\_RONA.

(3) 3MODELS\_cor.R - Scripts to calculate the correlation among the RONA calculated by 4 climate models.

(4) 4RONA\_ave\_weightedSE.R - Scripts to calculate the SE across 4 climate models.

**7.Genetic offset**

1. 1GF.R - Scripts to make GFanalyses (environment\_variables-RANK;PC-plot;offset-calculate).

### 19 climate variables for example

1. 2 genetic\_offset-plot.R - Scripts to make genetic\_offset plots.
2. 3migrant\_offset.R - Scripts to assess the metrics of forward, reverse and local genetic offset.
3. 4future\_forward\_dist.R - Scripts to estimate the forward genetic offset by assuming that populations have different migration capacity (100km,250km,500km,1000km,unlimited).
4. 5offset\_cor.R - Scripts to calculate the correlation among the genetic offset calculated by 4 climate models.