

docker: rocesv/plantina-chiplike

## Epigenetic files processing

Preprocess - *trim\_galore*

Mapping - *bowtie2*

Filter - *samtools/picard*

Calling - *macs2*

Format - *bedtools*

SRA+PCSD

10 marks

*A.thaliana*: 130

*O.sativa*: 63

*Z.mays*: 96

**Table S1**

## Peaks and signal tracks

Correlations - *deepTools*

**Figure S2**

## Inter-species CS: hiHMM

Annotation - *ChromHMM*

**Figure 1**

Overlap enrich. - *LOLA*

**Figure 2-4**

F. enrich. - *clusterProfiler*

**Figure 3; S3-4**

## Application: Paralog modelling

Replicate two published models in *A.thaliana* including new CS-metrics

**Figure 5  
Table S3**

Ezoe *et al.*, 2021

LR RImpt., Wilcox

LR Evaluation  
(ROC,PR)

Filters and Prediction\*

Cusack *et al.*, 2021

RF FImpt. Top Variables

SVM Evaluation  
(ROC, PR)

Experimental Validation\*; **Figure 7**

## Whole Genome Alignments

WGA - *lastz CNEr\*\**

Format - *lavToPsl,  
maf-cover\*\**

Chaining - *axtChain,  
chainMergeSort\*\**

Improve - *RepeatFiller,  
chainCleaner*

Netting - *chainNet,  
netSyntenic, netToAxt\*\**

Bidirectional WGA  
using Kent+Hiller  
tools to improve  
sensitivity

CNEs  
.netAxt files

WGA LiftOver  
pipeline\*\*

docker: rocesv/compcnes

Format - *deepTools*

Mapping - *STAR*

Preprocess - *trim\_galore*

EBI-ATLAS

*A.thaliana*: 118

*O.sativa*: 43

*Z.mays*: 411

**Table S2**

## RNA-seq files processing

## LECIF Functional Conservation

Preprocess input - *LECIF*

Split data - *LECIF*

Training/tuning - *LECIF*

Score prediction - *LECIF*

Conservation - CNEs,  
*PhastCons-PlantRegMap*

CS similarity- *R,  
philentropy*

Genetic variability- *LOLA*

Bidirectional  
LECIF functional  
conservation  
score

At vs Os  
At vs Zm  
Os vs At  
Os vs Zm  
Zm vs At  
Zm vs Os

**Figure 6  
Table S4**

## Resource: Database

Search

Genome Browser

LOLA enrichments

Public DB  
tracks available  
for future  
applications

