

A

CAGE sequence tags  
(fastq)Map to reference  
(BWA, HISAT2)

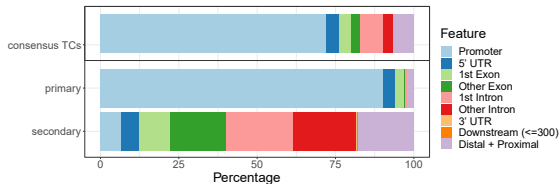
BAM

Coverage and  
visualization  
CTSS count and  
clustering (CAGER)

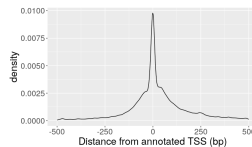
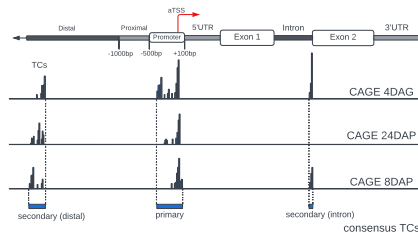
BedGraph

TCs  
(tag clusters)Definition of  
consensus TCs  
across stagesPromoter architecture  
analysis and clustering  
(seqArchR)Clusters of primary and  
secondary consensus  
promotersGO-term annotation  
(GOMAP, Enricher)Tissue specificity of  
gene expression  
(calculate tau values)Positioned motif analysis and  
footprintDB plant search (RSAT)Epigenetic profiles  
Overlap with TEs5'UTR analysis to  
search for TOR targets  
(calculate TOP scores)

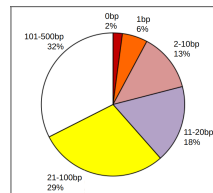
C



B



E



D

