

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 stages

Promoter architecture
analysis and clustering
(seqArchR)

Clusters of primary and
secondary consensus
promoters

GO-term annotation
(GOMAP, Enricher)

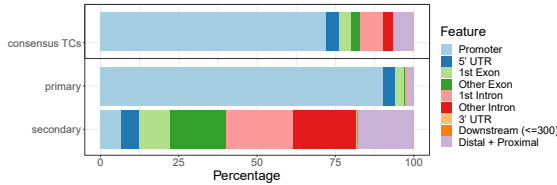
Tissue specificity of
gene expression
(calculate tau values)

Epigenetic profiles
Overlap with TEs

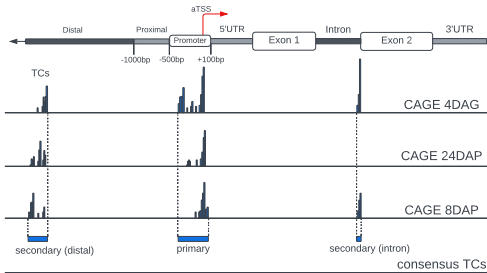
Positioned motif analysis and
footprintDB plant search (RSAT)

5'UTR analysis to
search for TOR targets
(calculate TOP scores)

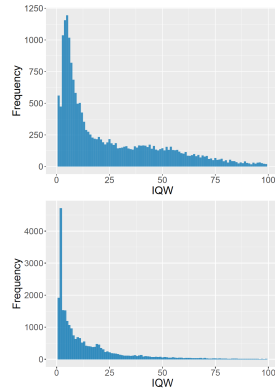
C



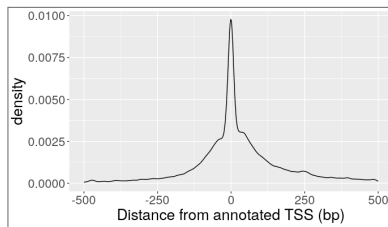
B



D



E



F

