

Genome
assembly data

FASTA files

TransposonPSI

Detection of TEs by ancient
homology

RepeatModeler

Detection of repetitive
DNA, makes consensus
sequences

LTRharvest

Detection of LTR-RTs

Clustering (80%
sequence similarity)

CD-HIT-EST

LTRdigest

Detecting LTR-RT specific
features

Removal of non-
TE genes

BLASTX against known non-
TE proteins

Scripts for clustering
sequences

Provided by Dr. Ning Jiang

Additional
classification

HMM profiles, BLASTX

RepeatClassifier

Classification

