Total RNA extraction
Magnetic beads capture mRNA fragments
Ligated with 5′ adapters
Biotinylated random primers
Reverse transcription
PCR amplification
Degradome library construction
Sequencing (Illumina HiSeq 2000 platform)
Raw reads
Data filtering
Clean tags
Annotation and classification of tags
Rfam
Genbank
PolyN identification
Reference genes
Tags from mRNAs (annotated as cDNA)
Identification of cleavage sites
miRNA-target pairs
T-plot & Functional annotation
Analysis of degradome sequencing data