

BrainSeq non-coding RNAs

- Novel (structured) small ncRNAs
 - Binned the human-mouse alignment
 - Trained a classification method to discriminate between the bins in CDS, ncRNA, and UTRs
 - Each window is represented with nucleotide conservation, secondary structure conservation/stability, Aminoacid conservation, GC content, median RNA-Seq expression, ...
 - ncRNAs: (tRNA, miRNA, rRNA, snoRNA, snRNA, ...)
 - List of regions on wiki with high ncRNA score from the classifier (chr1-chr13 for now)
 - High sec. structure stability,
 - Expression > TAR threshold in at least one region.
 - A BED file with 3 added columns for ncRNA, CDS, UTR columns
 - Overlap with novel and differentially expressed TARs
 - Still trying to figure out a way to look for long ncRNAs
- Another approach (With Minfeng)
 - Generate a large database of ncRNAs (miRBase, RFAM, GENCODE, AceView, ...)
 - Identify the ncRNA genes with differential expression