* AnnoSINE\_v2:

python AnnoSINE\_v2 -t 24 3 In\_genome/hg38.fa Outdir/Human

python AnnoSINE\_v2 -t 24 3 In\_genome/danRer11.fa Outdir/Fish

python AnnoSINE\_v2 -t 24 3 In\_genome/mm39.fa Outdir/Mouse

* SINE-Finder:

Python SINEFinder.py In\_genome/hg38.fa

Python SINEFinder.py In\_genome/danRer11.fa

Python SINEFinder.py In\_genome/mm39.fa

* RepeatMakser:

RepeatMasker -e ncbi -pa 24 -q -no\_is -norna -nolow -div 40 -cutoff 225 -lib Dfam\_DB.fa In\_genome/hg38.fa -dir RM\_res\_human > RepeatMasker\_human

RepeatMasker -e ncbi -pa 24 -q -no\_is -norna -nolow -div 40 -cutoff 225 -lib Dfam\_DB.fa In\_genome/danRer11.fa -dir RM\_res\_fish > RepeatMasker\_fish

RepeatMasker -e ncbi -pa 24 -q -no\_is -norna -nolow -div 40 -cutoff 225 -lib Dfam\_DB.fa In\_genome/mm39.fa -dir RM\_res\_mouse > RepeatMasker\_mouse

* The standard UCSC annotations used in the paper:

#human

Dec. 2013 (GRCh38/hg38)

https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/

hg38.fa.out.gz - RepeatMasker .out file. RepeatMasker was run with the

-s (sensitive) setting.

June 20 2013 (open-4-0-3) version of RepeatMasker

RepBase library: RELEASE 20130422

https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/hg38.fa.out.gz

# mouse

Jun. 2020 (GRCm39/mm39)

https://hgdownload.soe.ucsc.edu/goldenPath/mm39/bigZips/

mm39.fa.out.gz - RepeatMasker .out file. RepeatMasker was run with the

-s (sensitive) setting.

February 01 2017 (open-4-0-8) 1.332 version of RepeatMasker

RepBase library: Dfam\_Consensus RELEASE 20181026

CC RepBase RELEASE 20181026;

https://hgdownload.soe.ucsc.edu/goldenPath/mm39/bigZips/mm39.fa.out.gz

# zebrafish

May 2017 (GRCz11/danRer11)

https://hgdownload.soe.ucsc.edu/goldenPath/danRer11/bigZips/

danRer11.fa.out.gz - RepeatMasker .out file. RepeatMasker was run with the

-s (sensitive) setting.

January 31 2015 (open-4-0-5) version of RepeatMasker

RepBase library: RELEASE 20140131

https://hgdownload.soe.ucsc.edu/goldenPath/danRer11/bigZips/danRer11.fa.out.gz