* AnnoSINE\_v2:

Mode1:

python AnnoSINE\_v2 -a 1 -t 24 1 In\_genome/hg38.fa Outdir/Fish

python AnnoSINE\_v2 -a 1 -t 24 1 In\_genome/danRer11.fa Outdir/Fish

python AnnoSINE\_v2 -a 1 -t 24 1 In\_genome/mm39.fa Outdir/Fish

Mode2:

python AnnoSINE\_v2 -a 1 -t 24 2 In\_genome/hg38.fa Outdir/Fish

python AnnoSINE\_v2 -a 1 -t 24 2 In\_genome/danRer11.fa Outdir/Fish

python AnnoSINE\_v2 -a 1 -t 24 2 In\_genome/mm39.fa Outdir/Fish

Mode3:

python AnnoSINE\_v2 -a 1 -t 24 3 In\_genome/hg38.fa Outdir/Fish

python AnnoSINE\_v2 -a 1 -t 24 3 In\_genome/danRer11.fa Outdir/Fish

python AnnoSINE\_v2 -a 1 -t 24 3 In\_genome/mm39.fa Outdir/Fish

* 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 standardannotations used in the paper:

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

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

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