

## Small RNA analysis software

Name	Version	Description	Main Parameter
Bowtie	bowtie-0.12.9	for mapping	-v 0 -k 1
miREvo	miREvo_v1.1	Modify mirdeep2 for known miRNA analysis ;	-i -r -M -m -k -p 10 -g 50000
mirdeep2 ViennaRNA	mirdeep2_0_0_5 ViennaRNA-2.1.1	IntegrationmiREvo and mirdeep2 for novel miRNA prediction ; ViennaRNA for mirdeep2 internal call	quantifier.pl -p -m -r -y -g 0 -T 10 default
srna-tools-cli	<a href="http://srna-tools.cm.p.uea.ac.uk/">http://srna-tools.cm.p.uea.ac.uk/</a>	for plant TAS prediction	--tool phasing --abundance 3 --pval 0.001 --minsize 20 --maxsize 26 --trrna
RepeatMasker	open-4.0.3	for repeat analysis , based on RepBase18.07 , using trf and irf	-species -nolow -no_is -norna -pa 8
miRanda	miRanda-3.3a	animal target prediction	-sc 140 -en 10 -scale 4 -strict -out
psRobot	psRobot_v1.2	plant target prediction	-s -t -o -p 5
DEseq2	1.12.0	for Biological repeats analysis	padj<0.05
DEGSeq	1.2.2	for no Biological repeats analysis	qvalue<0.01  log2foldchange >1
EdgeR	3.2.4	for special circumstances analysis	padj<0.05  log2foldchange >1
GOSeq/topGO	Release 2.12	GO enrichment	enrichmentMethod: Wallenius; padjust:BH
KOBAS	V3.0	KEGG enrichment	blastx 1e-10; padjust:BH