

## Software List

Tools	Version	Description	Linkages
Trinity	v2.5.1	A Full-length transcriptome assembly tool from RNA-Seq data without a reference genome	<a href="https://github.com/trinityrnaseq/trinityrnaseq/wiki">https://github.com/trinityrnaseq/trinityrnaseq/wiki</a>
TransDecoder	v5.0.0	An tool for identifying candidate coding regions within transcript sequences	<a href="http://sourceforge.net/projects/transdecoder/">http://sourceforge.net/projects/transdecoder/</a>
MISA	v1.0	A MicroSatellite identification tool	<a href="http://pgrc.ipk-gatersleben.de/misa/misa.html">http://pgrc.ipk-gatersleben.de/misa/misa.html</a>
BLAST	v2.2.31	Basic Local Alignment Search Tool	<a href="http://blast.ncbi.nlm.nih.gov/Blast.cgi">http://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
KOBAS2.0	v2.0	A software to identify statistically significantly enriched pathways using hypergeometric test	<a href="http://kobas.cbi.pku.edu.cn/help.do">http://kobas.cbi.pku.edu.cn/help.do</a>
HMMER	v3.1b	A tool for	<a href="http://hmmer.org/">http://hmmer.org/</a>

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	2	searching sequence databases for sequence homologs, and for making sequence alignments	
RSEM	v1.2.1 9	An accurate tool for quantifying transcript abundances from RNA- Seq data	<a href="http://deweylab.github.io/RSEM/">http://deweylab.github.io/RSEM/</a>
TGICL	v2.1	A software system for fast clustering of large EST datasets	<a href="http://www.tigr.org/tdb/tgi/software/">http://www.tigr.org/tdb/tgi/software/</a>
cd-hit-est	v4.6.1	A very widely used program for clustering and comparing protein or nucleotide sequences.	<a href="http://weizhongli-lab.org/cd-hit/">http://weizhongli-lab.org/cd-hit/</a>
Blast2GO	v2.5	A bioinformatic s platform for high-quality protein function prediction and	<a href="https://www.blast2go.com/">https://www.blast2go.com/</a>

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		functional analysis of genomic datasets.	
STAR	v2.6.0b	An ultrafast universal RNA-seq aligner	<a href="https://github.com/alexdobin/STAR">https://github.com/alexdobin/STAR</a>
GATK	v3.2.2	A wide variety of tools with a primary focus on variant discovery and genotyping	<a href="https://software.broadinstitute.org/gatk/">https://software.broadinstitute.org/gatk/</a>
DESeq2	v1.6.3	An R package for RNA-Seq Differential Expression Analysis based on a model using the negative binomial distribution	<a href="http://www.bioconductor.org/packages/release/bioc/html/DESeq.html">http://www.bioconductor.org/packages/release/bioc/html/DESeq.html</a>
edgeR	v3.8.6	edgeR: a Bioconductor package for differential expression analysis of digital gene expression data	<a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2796818/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2796818/</a>
topGO	v2.28.0	An R package for gene ontology	<a href="http://www.bioconductor.org/packages/release/bioc/html/topGO.html">http://www.bioconductor.org/packages/release/bioc/html/topGO.html</a>

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		enrichment analysis	
		An open source software	
Cytoscape	v3.6.1	platform for visualizing complex networks	<a href="http://www.cytoscape.org/">http://www.cytoscape.org/</a>

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