Tool	Citation	Link
Trimmomatic	Bolger, A. M., *et.al.,* 2014 Trimmomatic: A flexible trimmer for Illumina Sequence Data. *Bioinformatics*, btu170	http://www.usadellab.org/cms/?page=trimmomatic
Cutadapt	Marcel Martin Cutadapt Removes Adapter Sequences From High-Throughput Sequencing Reads EMBnet. Journal Bioinformatics in Action	https://cutadapt.readthedocs.io/en/stable/
HISAT2	Daehwan Kim *et.al.,* 2019 Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. Nature Biotechnology **37:** 907–915	http://www.ccb.jhu.edu/software/hisat/index.shtml
SAMtools	Li *et.al.,* 2009 The Sequence Alignment/Map format and SAMtools	http://samtools.sourceforge.net
BEDTools	Quinlan *et.al.,*2010 BEDTools: a flexible suite of utilities for comparing genomic features	https://bedtools.readthedocs.io/en/latest/content/installation.html
DESeq2	Love MI, Huber W, Anders S et.al., 2014 Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15, 550.	https://bioconductor.org/packages/release/bioc/html/DESeq2.html
Trinity	Grabherr *et.al.,* 2011 Trinity: reconstructing a full-length transcriptome without a genome from RNA-Seq data Nat Biotechnol. **29(7):** 644–652	https://github.com/trinityrnaseq/trinityrnaseq.github.io/blob/master/deprecated/index.asciidoc
RSEM	Li *et.al.,* 2011 RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome BMC Bioinformatics 12, Article number: 323	https://github.com/deweylab/RSEM
Salmon	R Patro *et.al.,* 2017 Salmon provides fast and bias-aware quantification of transcript expression Nat Methods volume 14, pages417–419	https://salmon.readthedocs.io/en/latest/salmon.html
Edge R	M. D. Robinson *et.al.,* 2010 edgeR: a Bioconductor package for differential expression analysis of digital gene expression data Bioinformatics **26(1) :** 139-140	https://bioconductor.org/packages/release/bioc/html/edgeR.html
NR/NT NCBI blast database	National Center for Biotechnology Information *et.al.,* 2015 Database resources of the National Center for Biotechnology Information	https://blast.ncbi.nlm.nih.gov/Blast.cgi
limma	M.E.Ritchie *et.al.,* limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Research, **43(7)**, e47. doi	http://www.bioconductor.org/packages/release/bioc/html/limma.html
bioDBnet (biological DataBasenetwork)	U. Mudunuri *et.al.,* 2009 bioDBnet: the biological database network Bioinformatics, **25(4):** 555–556	https://biodbnet-abcc.ncifcrf.gov/db/db2db.php

Affymetrix	N. Jiang *et.al.,*2008 Methods for evaluating gene expression from Affymetrix microarray datasets BMC Bioinformatics, 284	https://www.affymetrix.com/analysis/netaffx/xmlquery_ex.affx?netaffx=wtgene_transcript
GEOquery	S. Davis *et.al.,* 2007 GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor Bioinformatics, **23(14):** 1846–1847	http://www.bioconductor.org/packages/2.8/bioc/html/GEOquery.html
Array Express	H. Parkinson *et.al.,* 2007 ArrayExpress—a public database of microarray experiments and gene expression profiles Nucleic Acids Research **35:** 747-750	http://www.ebi.ac.uk/arrayexpress/
Plant Trait Ontology database	Xiang Z *et.al.,*2011 Ontobee: A Linked Data Server and Browser for Ontology Terms. Proceedings of the 2nd International Conference on Biomedical Ontologies (ICBO), Buffalo, NY, USA. Pages 279-281	http://www.ontobee.org/ontology/TO
KEGG API (Application Programming Interface)	Kanehisa *et.al.,* 2000 KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Res. **28:** (27-30).	https://www.kegg.jp/kegg/rest/keggapi.html
Cytoscape	Gustavsen JA, Pai S, Isserlin R et al. RCy3: Network biology using Cytoscape from within R [version 3; peer review: 3 approved]. F1000Research 2019, 8:1774	https://cytoscape.org/
g:Profiler	J Reimand *et.al.,*2007 g:Profiler—a web-based toolset for functional profiling of gene lists from large-scale experiments	https://biit.cs.ut.ee/gprofiler/gost
EatupTF tool	S Shim *et.al.,* 2020 EAT-UpTF: Enrichment Analysis Tool for Upstream Transcription Factors of a Group of Plant Genes	http://chromatindynamics.snu.ac.kr:8080/EatupTF
Heatmaply	Galili, *et.al.,* 2017 "heatmaply: an R package for creating interactive cluster heatmaps for online publishing." Bioinformatics. 10.1093	http://cran.r-project.org/package=heatmaply
ATTED-II	Obayashi *et.al.,* 2018 ATTED-II in 2018: A Plant Coexpression Database Based on Investigation of Statistical Property of the Mutual Rank Index. Plant Cell Physiology, 59, e3	https://atted.jp/
AraNet v2	T Lee *et.al.,* 2015 AraNet v2: an improved database of co-functional gene networks for the study of Arabidopsis thaliana and 27 other nonmodel plant species Nucleic Acids Res	http://www.inetbio.org/aranet
TAIR (The Arabidopsis Information Resource)	S. Y. Rhee *et.al.,*2003 The Arabidopsis Information Resource (TAIR): a model organism database providing a centralized, curated gateway to Arabidopsis biology, research materials and community Nucleic Acids Res 31(1): 224-228	http://arabidopsis.org/
UpSetR	J.R. Conway *et.al.,* 2017UpSetR: An R Package for the Visualization of Intersecting Sets and their Properties Bioinformatics Volume **33(18):** 2938–2940	https://github.com/hms-dbmi/UpSetR/

Metascape	Zhou *et.al.,* 2019 Metascape provides a biologist-oriented resource for the analysis of systems-level datasets Nature Commun.**10(1):** 1523	https://metascape.org/gp/index.html
AraCyc	Lukas A *et.al.,* 2003 AraCyc: A Biochemical Pathway Database for Arabidopsis Plant Physiol **132(2):** 453-460	http://www.arabidopsis.org/tools/aracyc
WikiPathways	Martens M *et.al.,* 2021 WikiPathways: connecting communities Nucleic Acids Research, **(D1):** D613–D621	https://www.wikipathways.org/
Tableau public desktop (Version 2020.4,)		https://public.tableau.com/en-us/s/
Flourish studio		https://app.flourish.studio/