Table S3: Miscellaneous tools for omics data analysis and visualization.

Tools	Description	URL	Pro/Con	Reference
GEPIA2	A web-server for large scale expression profiling and analysis. It encompasses 198,619 isoforms and 84 cancer subtypes. It has extended gene expression quantification from the gene level to the transcript level, and supports analysis of a specific cancer subtype, and comparison between subtypes.	http://gepia2.cancer-pku.cn/	**Pro:** It provides an interactive interface for convenient exploration of the large datasets for multiple analyses i.e.. survival, differential gene expression, clustering dimensionality reduction, etc. **Con:** Data taken from limited resources, i.e. TCGA and GTEX.	[94]
SCUDO	It is an online tool for the analysis of gene expression profiles for diagnostic and classification purposes.	http://www.cosbi.eu/scudo	**Pro:** It is quite tool since it relies only on the relative ordering of the gene expression values within each profile, and not on the values themselves.	[95]

			Con: Dataset size is limited.	
ChIP-Array2	Tool for integrating multi-omics dataset for constructing gene regulatory network	http://jjwanglab.org/chip-array	**Con:** Website is not working and not updated after it's development in 2015.	[96]
DeAnnCNV	Tool for detection of CNV in whole-exome sequencing data. It has mainly two modules: (i) one for detection and visualization of CNVs from each sample, as well as detecting shared CNVs among multiple patients; (ii) second for the annotation of the detected CNVs and the associated genes.	http://mcg.ustc.edu.cn/db/cnv/	Pro: User-friendly web-based tool that is capable of systematic detection and annotation of CNVs from Whole Exome sequencing (WES) data. User can upload files in tar.gz format for analyses. **Con**: It not upgraded after it's development in 2015.	[97]
Sniplay3	Web-based tool for detection, management, and analysis of genetic variants. It has functionalities for management of next generation data in terms of data filtering, analysis and visualization. In addition, it has functionalities for genomic annotation of SNP, diversity analysis, haplotype reconstruction and network, linkage	http://sniplay.southgreen.fr	**Pro:** It has ability to handle the standard VCF format as input files and allows genomic annotation of SNP, diversity analysis, haplotype reconstruction and network, linkage disequilibrium, GWAS, population stratification, distance tree	[98]

	disequilibrium, etc.		analysis in an interactive manner. **Con**: All tools and workflows are incorporated into the Galaxy framework. One should have knowledge of galaxy to install and work with this tool.	
varFish	It is web application for the quality control, filtering, prioritization, analysis of DNA variants of rare diseases. Besides, it also allows user-based annotation of DNA variants.	https://varfish-kiosk.bihealth.org	**Pro:** The laboratory notebook features of the varFish promote collaborative analysis of cases within a center and the re-analysis of variants at multiple points in time.	[99]
Oviz-Bio	A web tool for interactive cancer genomic data visualization. It provides various types of visualization of common cancer mutation types, like annotation and signatures of small scale mutations, haplotype view and focal clusters of copy number variations, split-reads	https://bio.oviz.org/	**Pro:** It allows various types of input file formats, i.e., VCF, MAF and BED, TSV and CSV.	[100]

	alignment and heatmap view of structural variations.			
Cancer3D 2.0	Tool for interactive analysis of the 3D pattern of cancer mutations. It allows analyzing cancer missense mutations in the context of structures of proteins they are found in and in relation to patients' clinical data. It maintains a total of 1,457,702 mutations mapped onto 18,425 unique proteins from 9079 samples for 32 cancer types.	http://www.cancer3d.org	**Pro:** User-friendly interface to analyze cancer mutations in the context of their three-dimensional structures with clinical features of patients. **Con:** There are limited sources of data, i.e. TCGA consortium and NCI Data Commons only.	[101]
FireBrowse	Tool for analyzing, visualizing the multi-omics data for all cancer types. It allows analyses of multi-omics and clinical profiles of samples among samples of a TCGA-cancer particular cohort.	http://firebrowse.org/	**Pro:** User-friendly web-interface allows comparison among samples of a selected cancer cohort. **Con:** It is only capable of displaying pre-calculated results. Data is obtained only from the TCGA project.	[102]