Supplemental Table 1. Open Source Data Analysis Tools

Supported Omics Data Types	Open Source Omics Analytic Tool	Web-Based	Computer-Based

Multi-omics	• Galaxy usegalaxy.org
	  ○ In addition to genomics analyses, Galaxy is used for epigenomic, proteomic, transcriptomic, and metabolomic analyses
	  ○ Galaxy also supports the Galaxy ToolShed (toolshed.g2.bx.psu.edu) which is a repository of analytical tools and workflows developed by Galaxy community members
		X	

	• 3Omics 3omics.cmdm.tw ○ Visualization tool that assists with the integration of transcriptomic, proteomic and metabolomic data	X	

Genomic	• shinyGAStool github.com/kordk/shinyGAStool
	  ○ Facilitates candidate gene association studies
	  ○ Accessible on Windows or requires R
			X

Epigenomic	• EpiExplorer epiexplorer.mpi-inf.mpg.de
	  ○ Facilitates interactive exploration of large epigenomic datasets
	  ○ Facilitates filtering genomic regions for the identification and prioritization of candidate regions
		X	

	• VisR visrsoftware.github.io
	  ○ Framework for analyzing sequencing data
	  ○ Accessible on Mac OS X, Linux and Windows
	  ○ Requires R
			X

Transcriptomic	• Differential Expression Interactive Visual Analysis (DEIVA) github.com/Hypercubed/DEIVA
	  ○ Visual analytical tool
	  ○ Assists researchers to identify and locate genes
		X	

	• ExpressionDB github.com/5c077/ExpressionDB/wiki
	  ○ Available for use online or in RStudio
	  ○ Facilitates exploring, visualizing and sharing GE data
	  ○ Accessible for RNA-seq or microarray data
		X	X

	• Shiny Transcriptome Analysis Resource Tool (START) App github.com/jminnier/STARTapp
	  ○ Facilitates RNA-seq upload, analysis and visualization
	  ○ Requires R
			X

	• VisR visrsoftware.github.io		X
Proteomic	• MixProTool wsslearning.shinyapps.io/MixProTool ○ Facilitates data analysis and visualization	X	
	• OpenMS openms.de ○ Supported on Windows, Linux, and Mac OS systems		X
	• Trans-Proteomic Pipeline tools.proteomecenter.org/software.php ○ Available for use on Linux and Windows systems and can build on Mac OS X		X

Metabolomic	• MetaboAnalyst 4.0 metaboanalyst.ca
	  ○ Free repository of tools for analyzing high-throughput metabolomics data
	  ○ Accepts data input from NMR, LC-MS, or GC-MS
	  ○ The companion R package, MetaboAnalystR, assists with reproducible data analysis
		X	X

	• OpenMS openms.de/metabolomics ○ Facilitates metabolite quantification and identification		X
	• XCMS Online xcmsonline.scripps.edu ○ Facilitates statistical analysis of LC-MS and GC-MS data	X	
Microbiome	• Integrated Microbiome Analysis Pipeline (iMAP) github.com/tmbuza/iMAP ○ Facilitates data analysis, integration and visualization		X

	• MicrobiomeAnalyst microbiomeanalyst.ca
	  ○ Facilitates data filtering, transformation, and analysis
	  ○ Facilitates interactive data visualization
		X	

Note. Abbreviations: NMR = nuclear magnetic resonance spectroscopy; LC-MS = liquid chromatography-mass spectrometry; GC-MS = gas chromatography-mass spectrometry