Resources for Biological Discovery from RNAseq Data

R (RStudio)	www.rstudio.com	windows-style environment for R, Shiny apps
iDEP	bioinformatics.sdstate.edu/idep	web interface for PCA, clustering, DEgenes (R tools)
Heatmapper	www2.heatmapper.ca/expression	heatmap with clustering
Panther	pantherdb.org	GO term, pathway enrichment in DE genes
	Nature Protocols: www.nature.com/articles/s41596-019-0128-8	
DAVID	david.ncifcrf.gov	GO term, pathway enrichment in DE genes
	Nature Protocols: www.nature.com/articles/nprot.2008.211	
Reactome	reactome.org	pathway enrichment in DE genes, expression overlay
	bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-017-1559-2	
GSEA/MSig*	software.broadinstitute.org/gsea	gene set enrichment across full log2FC
	User guide: software.broadinstitute.org/gsea/doc/GSEAUserGuideFrame.html	
Ingenuity†	www.qiagenbioinformatics.com/products/ingenuity-pathway-analysis/	
	Tutorials: qiagen.force.com/KnowledgeBase/KnowledgeIPAPage	

General Resources for RNAseq

Overview	chagall.med.cornell.edu/RNASEQcourse/Intro2RNAseq.pdf	
Galaxy	usegalaxy.org	web-based NGS analysis tools
BRC BioIT	biohpc.cornell.edu	high-performance servers*, workshops at Cornell

* login required
† license required (contact WCM Library: library.weill.cornell.edu/node/1050)