

Materials List for

# *In Silico* Identification and Characterization of circRNAs During Host-Pathogen Interactions

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## URL

jove.com/video/64565

## Materials

Name	Company	Catalog Number	Comments
Bedtools	GitHub	<a href="https://github.com/arq5x/bedtools2/">https://github.com/arq5x/bedtools2/</a>	Referring to section 4.1.2. Needed for Circr.
BWA	Burrows-Wheeler Aligner	<a href="http://bio-bwa.sourceforge.net/">http://bio-bwa.sourceforge.net/</a>	Referring to section 2.1.1 and 2.1.2. Needed to run CIRIquant, and to index the genome
Circr	GitHub	<a href="https://github.com/bicciatolab/Circr">https://github.com/bicciatolab/Circr</a>	Referring to section 4. Use to predict the miRNA binding sites
CIRIquant	GitHub	<a href="https://github.com/bioinfo-biols/CIRIquant">https://github.com/bioinfo-biols/CIRIquant</a>	Referring to section 2.1.3. To predict circRNAs
ClusterProfiler	GitHub	<a href="https://github.com/YuLab-SMU/clusterProfiler">https://github.com/YuLab-SMU/clusterProfiler</a>	Referring to section 7. For GO and KEGG functional enrichment
CPU	Intel	Intel(R) Xeon(R) CPU E5-2620 V2 @ 2.10 GHz Cores: 6-core CPU Memory: 65 GB Graphics card: NVIDIA GK107GL (QUADRO K2000)	Specifications used to run this entire protocol.
Cytoscape	Cytoscape	<a href="https://cytoscape.org/download.html">https://cytoscape.org/download.html</a>	Referring to section 5.2. Needed to plot ceRNA network
FastQC	Babraham Bioinformatics	<a href="https://www.bioinformatics.babraham.ac.uk/projects/fastqc/">https://www.bioinformatics.babraham.ac.uk/projects/fastqc/</a>	Referring to section 1.2.1. Quality checking on Fastq files
HISAT2		<a href="http://daehwankimlab.github.io/hisat2/">http://daehwankimlab.github.io/hisat2/</a>	Referring to section 2.1.1 and 2.1.2. Needed to run CIRIquant, and to index the genome
Linux	Ubuntu 20.04.5 LTS (Focal Fossa)	<a href="https://releases.ubuntu.com/focal/">https://releases.ubuntu.com/focal/</a>	Needed to run the entire protocol. Other Ubuntu versions may still be valid to carry out the protocol.
miRanda		<a href="http://www.microrna.org/microrna/getDownloads.do">http://www.microrna.org/microrna/getDownloads.do</a>	Referring to section 4.1.2. Needed for Circr
Pybedtools	pybedtools 0.8.2	<a href="https://pypi.org/project/pybedtools/">https://pypi.org/project/pybedtools/</a>	Needed for BED file genomic manipulation
Python	Python 2.7 and 3.6 or abover	<a href="https://www.python.org/downloads/">https://www.python.org/downloads/</a>	To run necessary library modules

R	The Comprehensive R Archive Network	<a href="https://cran.r-project.org/">https://cran.r-project.org/</a>	To manipulate dataframes
RNAhybrid	BiBiServ	<a href="https://bibiserv.cebitec.uni-bielefeld.de/rnahybrid">https://bibiserv.cebitec.uni-bielefeld.de/rnahybrid</a>	Referring to section 4.1.2. Needed for Circr
RStudio	RStudio	<a href="https://www.rstudio.com/">https://www.rstudio.com/</a>	A workspace to run R
samtools	SAMtools	<a href="http://www.htslib.org/">http://www.htslib.org/</a>	Referring to section 2.1.2. Needed to run CIRIquant
StringTie	Johns Hopkins University: Center for Computational Biology	<a href="http://ccb.jhu.edu/software/stringtie/index.shtml">http://ccb.jhu.edu/software/stringtie/index.shtml</a>	Referring to section 2.1.2. Needed to run CIRIquant
TargetScan	GitHub	<a href="https://github.com/nsoranzo/targetscan">https://github.com/nsoranzo/targetscan</a>	Referring to section 4.1.2. Needed for Circr