

### R/Bioconductor packages:

```
source("https://bioconductor.org/biocLite.R")
biocLite("ChIPQC")
biocLite("TxDb.Hsapiens.UCSC.hg38.knownGene")
biocLite("DiffBind")
biocLite("ChIPseeker")
biocLite("GenomicRanges")
biocLite("chipenrich")
biocLite("ChIPpeakAnno")
biocLite("rGREAT")
biocLite("DiffBind")
biocLite("Rcade")
biocLite("DiffHiC")
biocLite("biomaRt")
```

SPP

```
require(devtools)
devtools::install_github('hms-dbmi/spp', build_vignettes = FALSE)
```

### Other tools:

Fastqc v0.11.5

[https://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc\\_v0.11.5.zip](https://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.5.zip)

Cutadapt

```
pip install --upgrade cutadapt
```

BWA 0.7.16a

<https://sourceforge.net/projects/bio-bwa/files/bwa-0.7.16a.tar.bz2/download>

IGV 2.3 and IGV tools

[http://data.broadinstitute.org/igv/projects/downloads/IGV\\_2.3.97.zip](http://data.broadinstitute.org/igv/projects/downloads/IGV_2.3.97.zip)

[http://data.broadinstitute.org/igv/projects/downloads/igvtools\\_2.3.95.zip](http://data.broadinstitute.org/igv/projects/downloads/igvtools_2.3.95.zip)

bowtie2 2.3.3

[https://sourceforge.net/projects/bowtie-bio/files/bowtie2/2.3.3/bowtie2-2.3.3-linux-x86\\_64.zip/download](https://sourceforge.net/projects/bowtie-bio/files/bowtie2/2.3.3/bowtie2-2.3.3-linux-x86_64.zip/download)

STAR 2.5.3a

<https://github.com/alexdobin/STAR/archive/2.5.3a.tar.gz>

MACS2

```
pip install --upgrade MACS2
```

Bedtools 2.26

<https://github.com/arq5x/bedtools2/releases/download/v2.26.0/bedtools-2.26.0.tar.gz>