1. NGS QC Toolkit (v2.3.3)

https://www.mybiosoftware.com/ngs-qc-toolkit-v2-3-3-toolkit-for-the-quality-control-qc-of-next-generation-sequencing-ngs-data.html

NGSQCToolkit\_/QC/IlluQC.pl -pe %s %s adaptor A -l 50 -s 20 -o %s -t 2'%(file\_list[i], file\_list[i+1], out\_dir)

2. FastQC

<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>

[fastqc, "-o", outdir, "-d", temp\_dir, "-f", format, "-t", threads] + files

(" ").join(command\_line\_list) + "\n"

3. multiQC

https://multiqc.info/docs/#flat--interactive-plots

multiqc ./datadir

4. Hisat (v2-2.1.0)

http://www.ccb.jhu.edu/software/hisat/index.shtml

'hisat2 -p 8 --dta -x %s -1 %s -2 %s -S %s%s.sam'%(ref\_name, file\_name[i], file\_name[i+1], out\_dir, file\_name[i].split('/')[2].split('\_')[0])

5. edgeR (v3.10)

<https://bioconductor.org/packages/release/bioc/html/edgeR.html>

nor.data <- normalizeCounts(fil.data ,group=sample.group, method="TMM")

6. pheatmap (v1.0.12)

<https://cran.r-project.org/web/packages/pheatmap/pheatmap.pdf>

pheatmap(input.data,scale="row",show\_rownames=T,cex=1,annotation\_col=group.data,border\_color=FALSE, cluster\_cols = FALSE)

7. GO enrichment analysis (clusterprofiler : v3.1, org.At.tair.db : v3.9)

<https://bioconductor.riken.jp/packages/3.1/bioc/html/clusterProfiler.html>

<https://bioconductor.riken.jp/packages/release/data/annotation/html/org.At.tair.db.html>

enrichGO(gene = “DEG ID list”, OrgDb = "org.At.tair.db",keyType = "TAIR",ont = "GO type", universe = keys(org.At.tair.db), pAdjustMethod = "BH", pvalueCutoff = 0.05, qvalueCutoff = 0.05)