**Software List:**

Python 2.7

expHTS – experimental High Throughput Sequencing

<https://github.com/msettles/expHTS>

to install module, download and within the directory

python setup.py install

**Preprocessing**:

Python 2.7

Modules: argparse, optparse, distutils

bowtie2 - contaminant screening

<http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>

Super-Deduper – Identify and remove PCR duplicates

<https://github.com/dstreett/Super-Deduper>

Sickle – Trim low quality regions

<https://github.com/dstreett/sickle> [ forked version ]

Scythe – Identify and remove adapters in SE reads

<https://github.com/ucdavis-bioinformatics/scythe>

FLASH2 – Join overlapping reads, identify and remove adapter in PE reads

<https://github.com/dstreett/FLASH2>

**Mapping**:

Python 2.7

bwa mem – map reads to a reference

<http://sourceforge.net/projects/bio-bwa/files/>

samtools – processing of sam/bam files

<http://www.htslib.org/>

**Read Counting:**

Python 2.7

HTSeq-0.6.1 htseq\_count – Count reads occurrences within genes

<http://www-huber.embl.de/users/anders/HTSeq/>

**Analysis of differential expression:**

R 3.3.0 or greater

<http://www.r-project.org/>

RStudio

https://www.rstudio.com/

R Package: optparse, parallel, tools from cran

R Package: ShortRead, EdgeR from bioconductor

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