

Goal:

FASTQ

Outputs:

Subsample to 2M reads

seqtk sample

[*_subsample.fastq.gz](#)

Basic QC

[fastqc](#)

[*_subsample_fastqc.html](#)

Check contaminants

fastq_screen

[*_subsample_screen.html](#)

Trim adapter

bbduk

[*_subsample_bbduk.fastq](#)

Classify reads

centrifuge

[*_centrifuge_classification.tsv](#)

Visualisation

krona

[*_centrifuge_krona.html](#)

