



Quality Control:

FastQC/MultiQC, Cutadapt

Sequencing

Paired-end Reads
FASTQ

Merge Reads:
Flash2

Merged Reads
FASTQ

Aligner:
BWA

Aligned Reads
SAM/BAM

Filter:
SAMtools, AWK

Filtered Reads
SAM/BAM

Collapser:

Collapser: FASTX-Toolkit

Collapsed Reads
FASTA

Reference Genome
FASTA