

Step 1: User inputs sequencing reads (fastq) and primer and adapter sequences

Sequencing Reads
(fastq)

Primers & Adapters
CTCGGCATTCCTGT...
GATCTATTATACTCC...

Step 2: FastQC

- Detect Phred offset
- Search for sequence tags

Steps 3 & 4: Process sequencing reads

Cutadapt
• Trim sequence primers
and adapters

Prinseq
• Trim low quality bases
• Remove short sequences
low complexity and
redundant reads

Step 5: Output quality controlled sequencing reads

Clean Sequencing Reads
(fastq)