

Step 1: User supplies 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

Step 3: Process sequencing reads

Cutadapt & Prinseq

- Trim sequence primers and adapters
- Trim low quality bases
- Remove short, low complexity, and redundant reads

Step 4: Output quality controlled sequencing reads

Preprocessed Sequencing Reads
(fastq)