FASTX Toolkit (implemented in C)

* FASTQ-to-FASTA converter - Convert FASTQ files to FASTA files
* FASTQ Information - Chart Quality Statistics and Nucleotide Distribution
* FASTQ/A Collapser - Collapsing identical sequences in a FASTQ/A file into a single sequence (while maintaining reads counts)
* FASTQ/A Trimmer - Shortening reads in a FASTQ or FASTQ files (removing barcodes or noise)
* FASTQ/A Renamer - Renames the sequence identifiers in FASTQ/A file
* FASTQ/A Clipper - Removing sequencing adapters / linkers
* FASTQ/A Reverse-Complement - Producing the Reverse-complement of each sequence in a FASTQ/FASTA file
* FASTQ/A Barcode splitter- Splitting a FASTQ/FASTA files containing multiple samples
* FASTA Formatter - Changes the width of sequences line in a FASTA file
* FASTA Nucleotide Changer - Converts FASTA sequences from/to RNA/DNA
* FASTQ Quality Filter - Filters sequences based on quality
* FASTQ Quality Trimmer- Trims (cuts) sequences based on quality
* FASTQ Masker - Masks nucleotides with 'N' (or other character) based on quality

fastq-tools (implemented in C)

* *fastq-sort* : sort fastq entries by various keys
* *fastq-grep* : match sequences against regular expressions
* *fastq-kmers* : count k-mer occurrences
* *fastq-match* : (smith-waterman) local sequence alignment
* *fastq-qual* : tabulate quality scores
* *fastq-sample* : randomly sample reads, with or without replacement
* *fastq-uniq* : count duplicate reads
* *fastq-qualadj* : adjust quality scores by a fixed offset

sqt - SeQuencing Tools (<https://bitbucket.org/marcelm/sqt>, implemented in Python)

* sqt-coverage -- Compute per-reference statistics such as coverage and GC content
* sqt-fastqmod -- FASTQ modifications: shorten, subset, reverse complement, quality trimming
* sqt-fastastats -- Compute N50, min/max length, GC content etc. of a FASTA file
* sqt-qualityguess -- Guess quality encoding of one or more FASTA files
* sqt-globalalign -- Compute a global or semiglobal alignment of two strings
* sqt-chars -- Count length of the first word given on the command line
* sqt-sam-cscq -- Add the CS and CQ tags to a SAM file with colorspace reads
* sqt-fastamutate -- Add substitutions and indels to sequences in a FASTA file
* sqt-fastaextract -- Efficiently extract one or more regions from an indexed FASTA file
* sqt-translate -- Replace characters in FASTA files (like the 'tr' command)
* sqt-sam-fixn -- Replace all non-ACGT characters within reads in a SAM file
* sqt-sam-insertsize -- Mean and standard deviation of paired-end insert sizes
* sqt-sam-set-op -- Set operations (union, intersection, ...) on SAM/BAM files
* sqt-bam-eof -- Check for the End-Of-File marker in compressed BAM files
* sqt-checkfastqpe -- Check whether two FASTQ files contain correctly paired paired-end data

ea-utils (FASTQ processing utilities,<http://code.google.com/p/ea-utils/>)

NGS QC Toolkit (<http://www.nipgr.res.in/ngsqctoolkit.html>)

seqtk (<https://github.com/lh3/seqtk>)