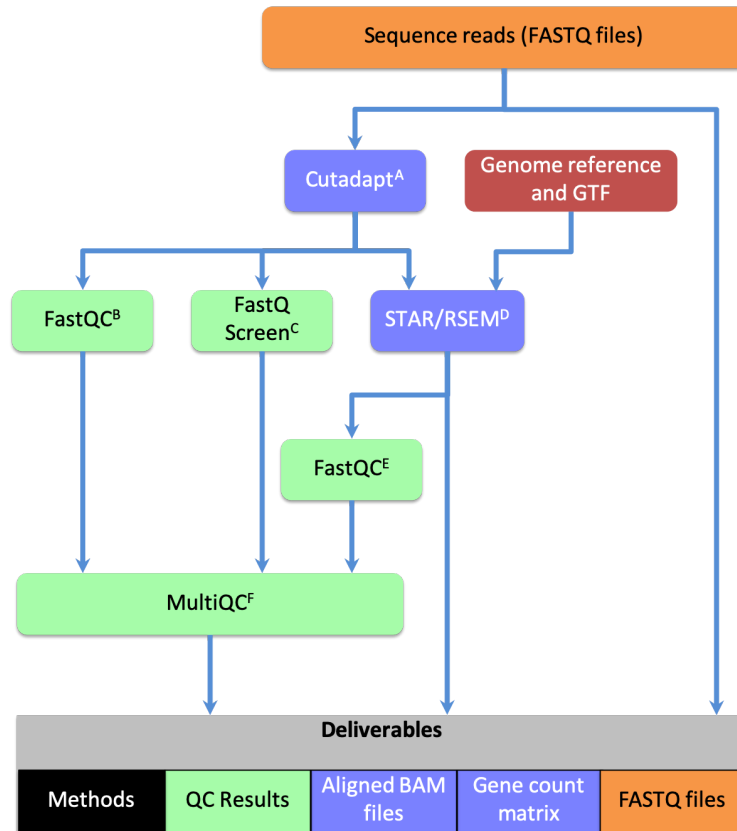


RNA-Seq Methods

Note: this is just a sample excerpt and should not be used for publication; the actual method details will be included in your results.



- A. Reads were trimmed to remove adapters and low quality basecalls using Cutadapt (v2.3) [1]. (Options: --nextseq-trim 13 -u 3 -m 20 --trim-n -a AGATCGGAAGAG -A AGATCGGAAGAG)
- B. FastQC (v0.11.8) was used to examine the quality of sequence data [2].
- C. FastQ Screen (v0.13.0) / Bowtie2 (v2.3.5) were used to assess sample contamination [3,4].
- D. Reads were mapped to the reference genome using STAR (v2.6.1b) with and assigned count estimates to genes with RSEM (v1.3.1) [5,6]. Alignment options followed ENCODE standards for RNA-seq [7]. STAR/RSEM used reference genome Ensembl GRCh38 with GTF GRCh38.98 [8].
- E. FastQC was run on the aligned reads and results were aggregated using MultiQC (v1.7) [2,9].

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