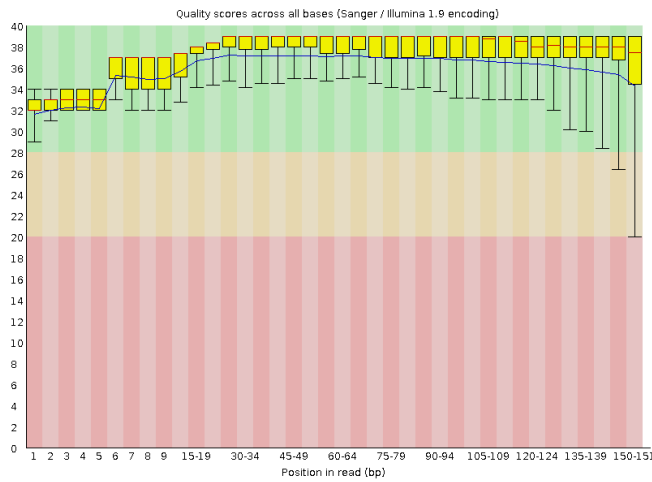# FastQC Quality Results

1 Basic Statistics

Filename: 04-D15-22373-HT-Nextera-Myeloid-Val1-Repeat_S4_L001_R1_001.fastq.gz

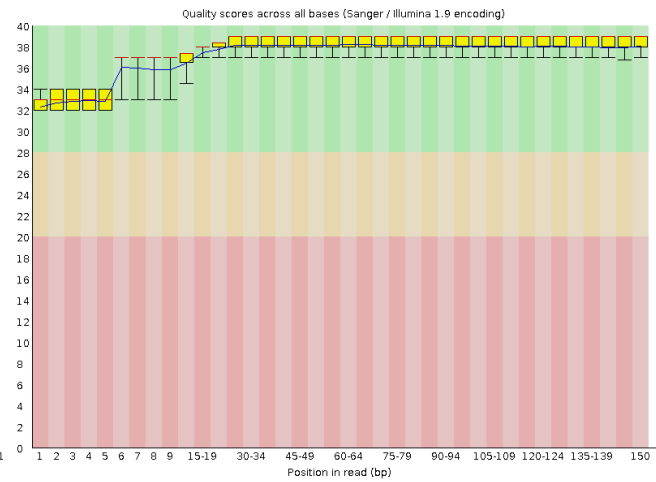**File type:** Conventional base calls

Encoding: Sanger / Illumina 1.9

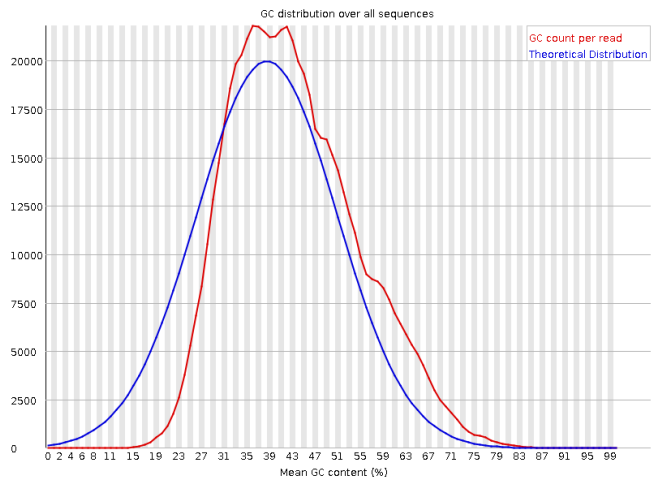|	Before trimming	After trimming
Total Sequences	616751	310338
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	43	40

2 FastQC

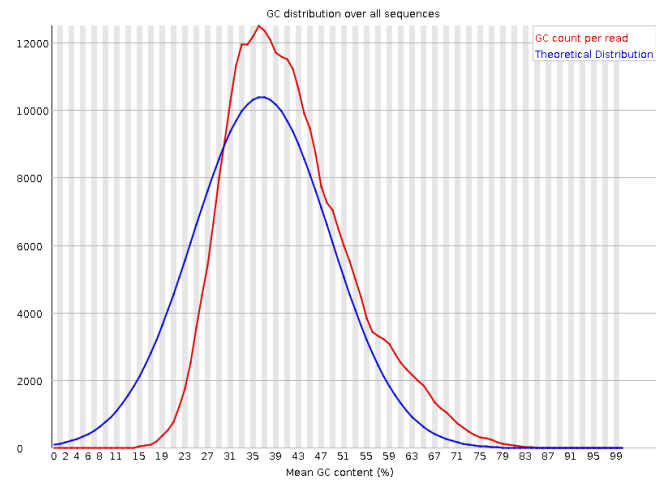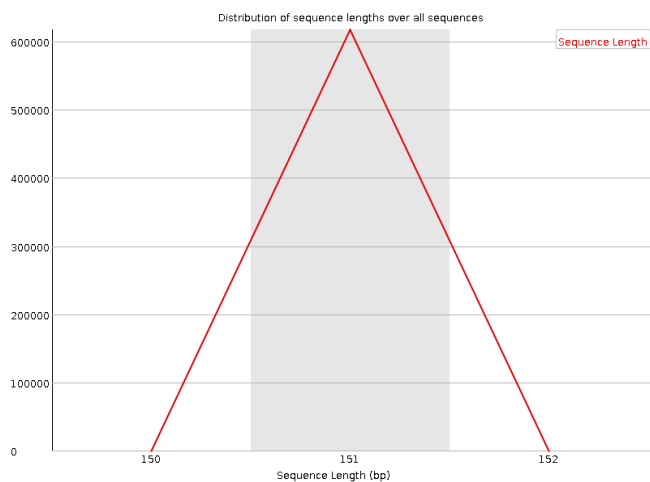

(a) Per base sequence quality BEFORE trimming
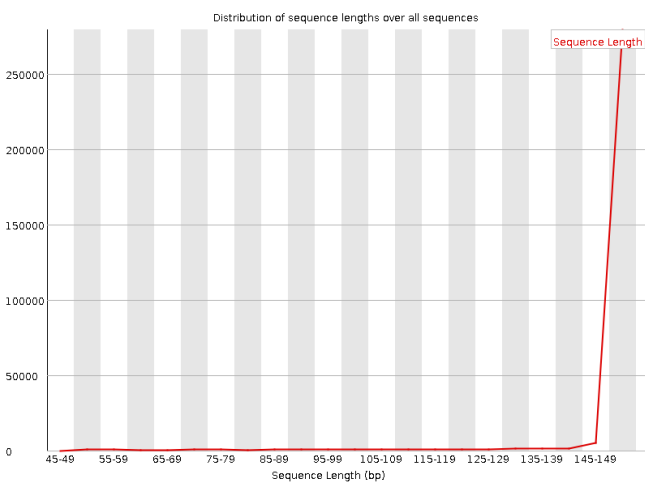

(b) Per base sequence quality AFTER trimming PASS

(c) Per sequence GC content BEFORE trimming

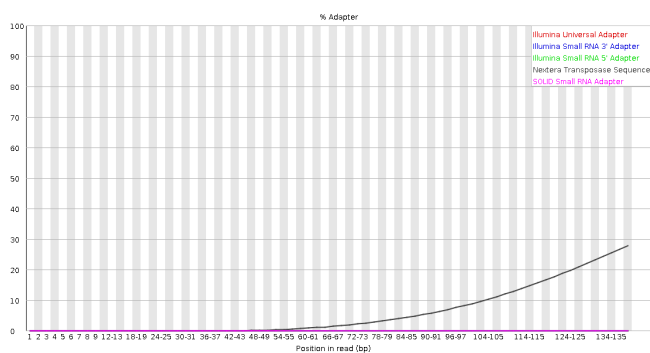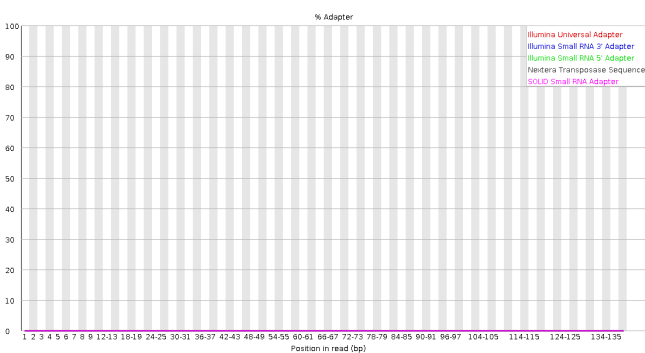
(d) Per sequence GC content AFTER trimming FAIL

(e) Sequence Length Distribution BEFORE trimming

(f) Sequence Length Distribution AFTER trimming WARN

(g) Adapter content BEFORE trimming

(h) Adapter content AFTER trimming PASS

3 BamStats

04-D15-22373-HT-Nextera-Myeloid-Val1-Repeat_S4_L001_R1_2373-HT-Nextera-Myeloid-Val1-Repeat_S4_L001_R1_2373-HT-