Sample Quality Results

1   Basic Statistics

Sample: 08-D15-08791-AD-Nextera-Myeloid-Val1-Repeat_S8_L001

File type: Conventional base calls

Encoding: Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	1075635	583098
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	42	39

2   FastQC

Figure 1: Per base sequence quality

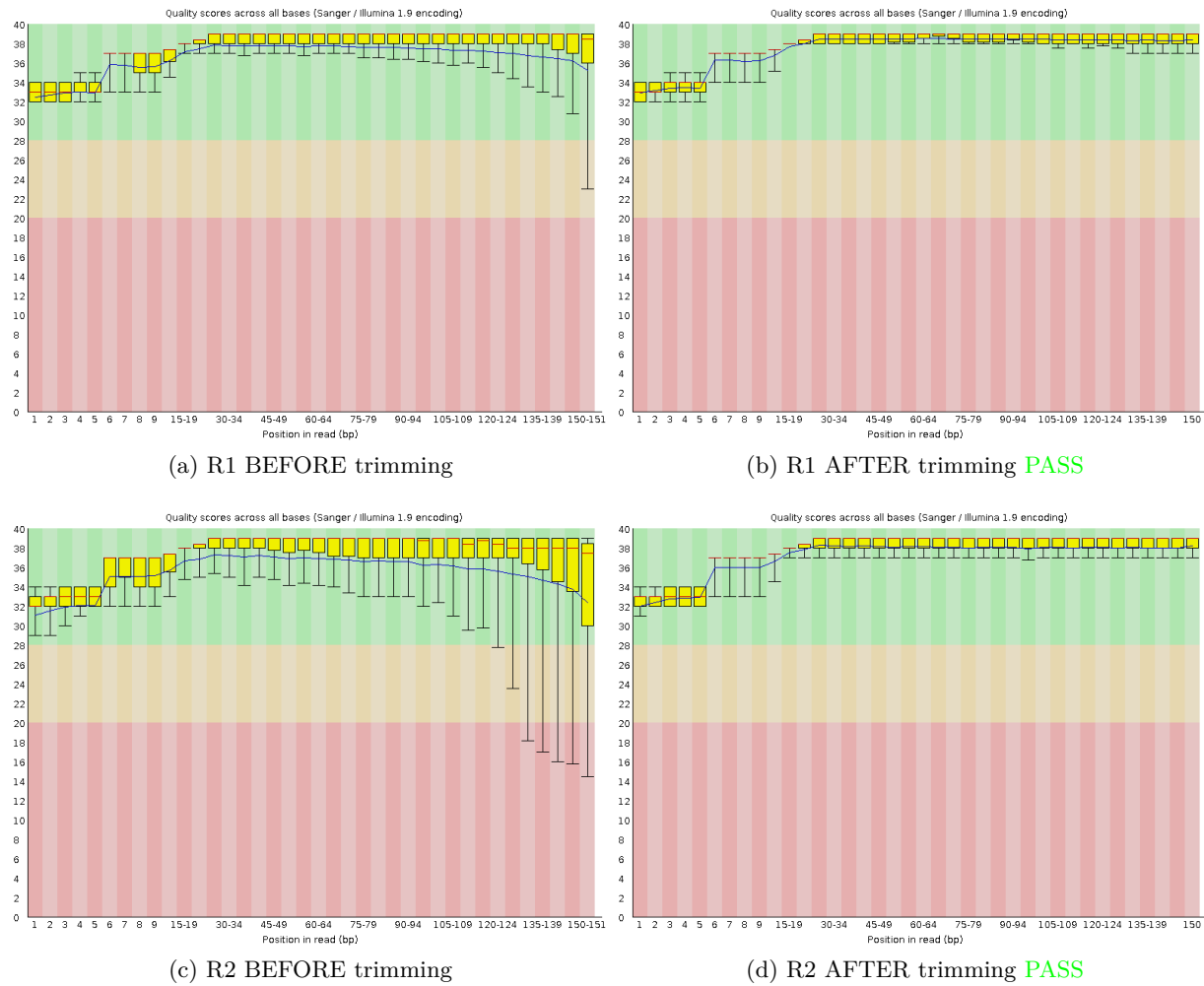(a) R1 BEFORE trimming

(b) R1 AFTER trimming PASS

(c) R2 BEFORE trimming
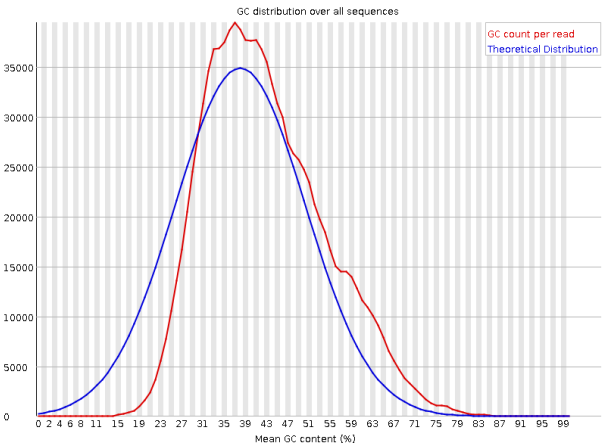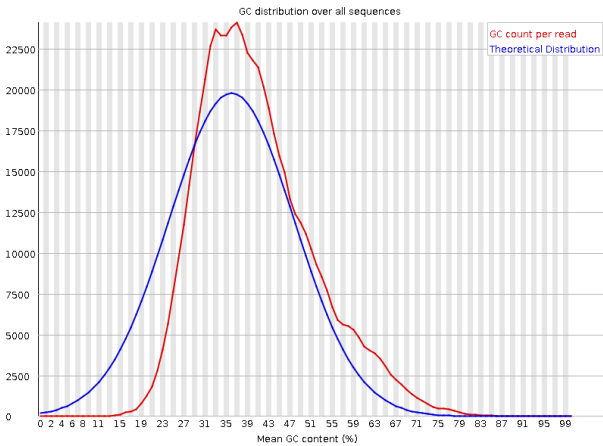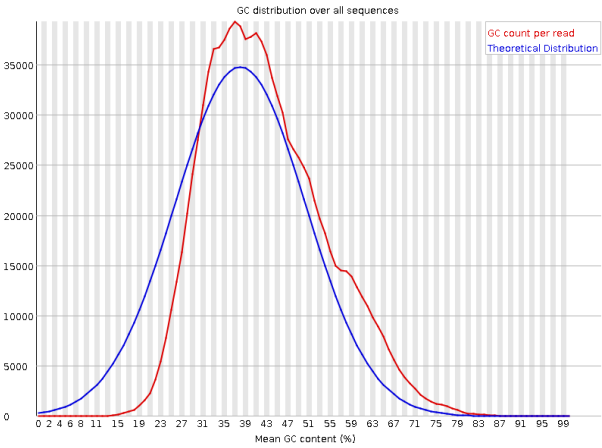

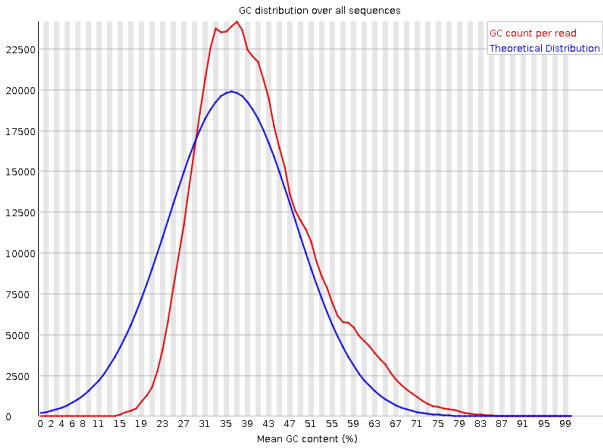(d) R2 AFTER trimming PASS

Figure 2: Per sequence GC content

(a) R1 BEFORE trimming

(b) R1 AFTER trimming FAIL

(c) R2 BEFORE trimming

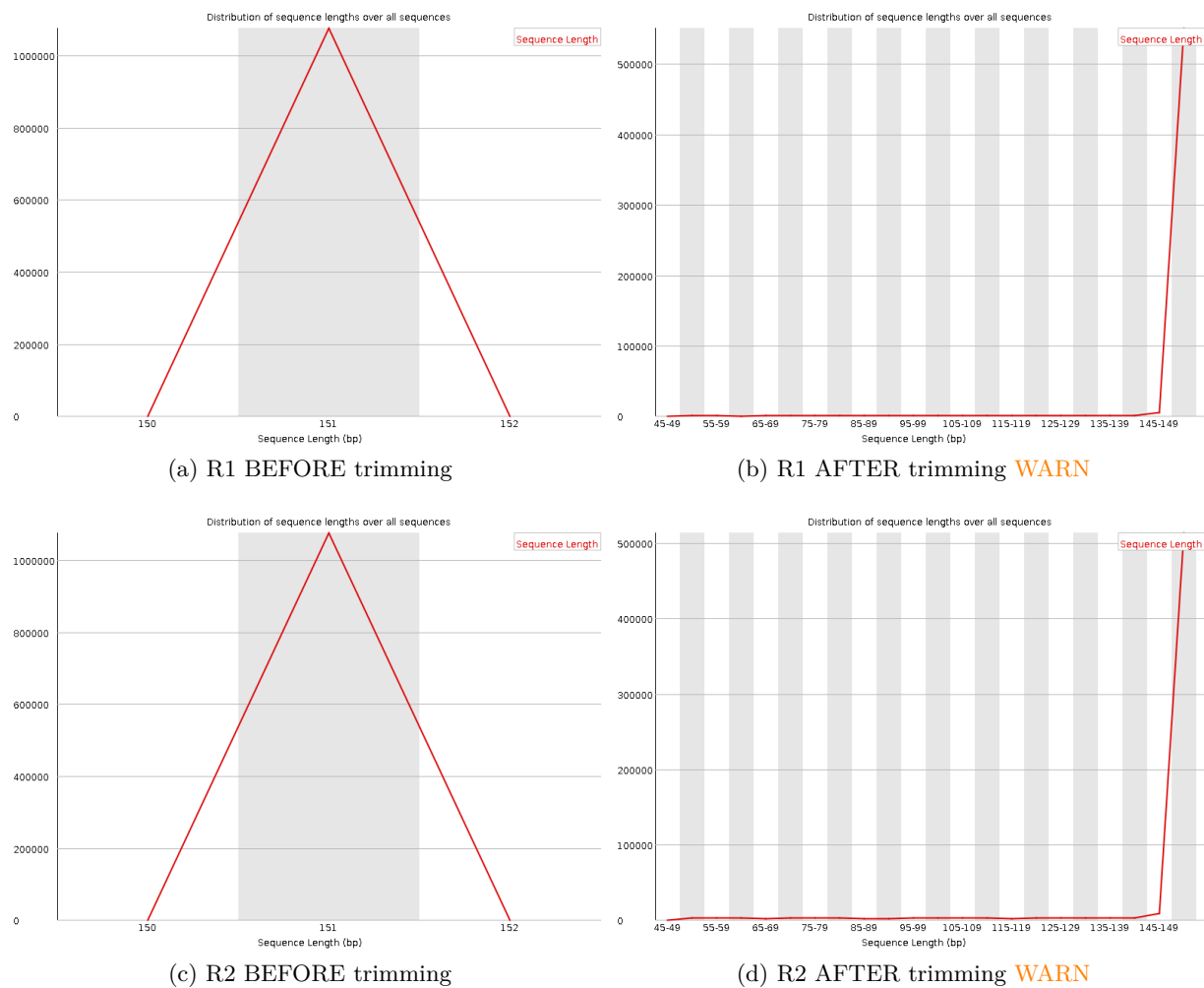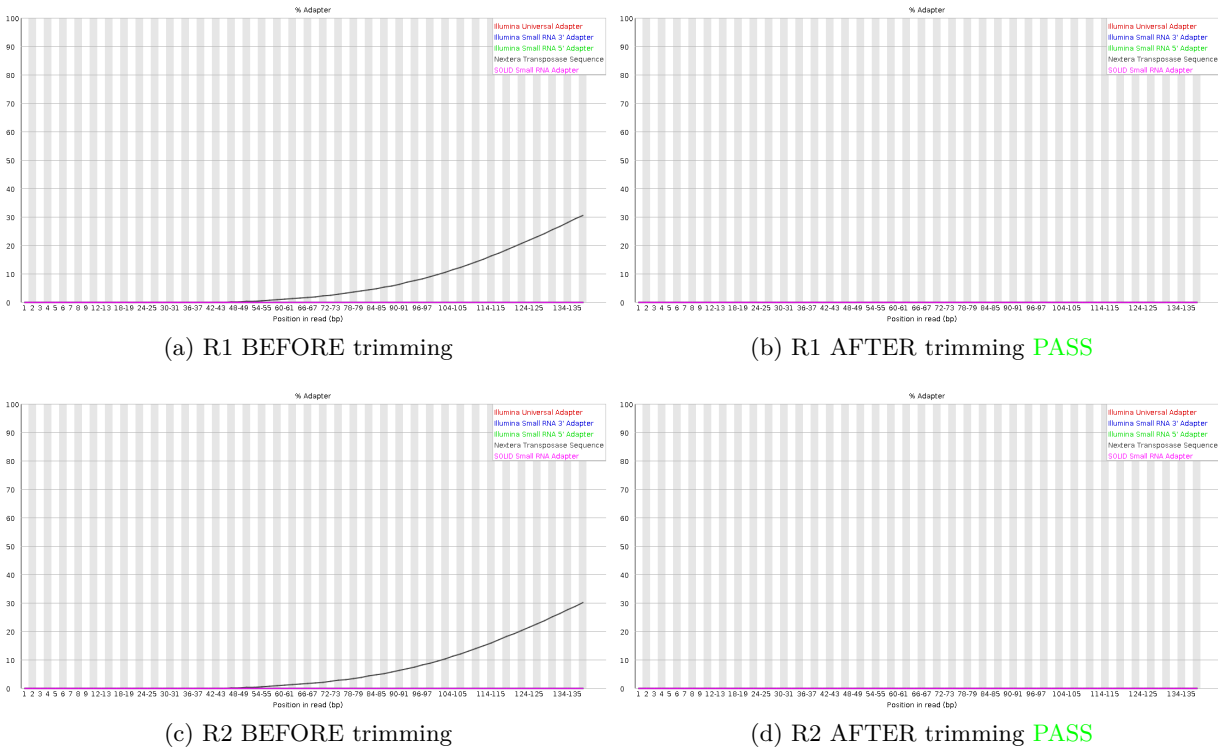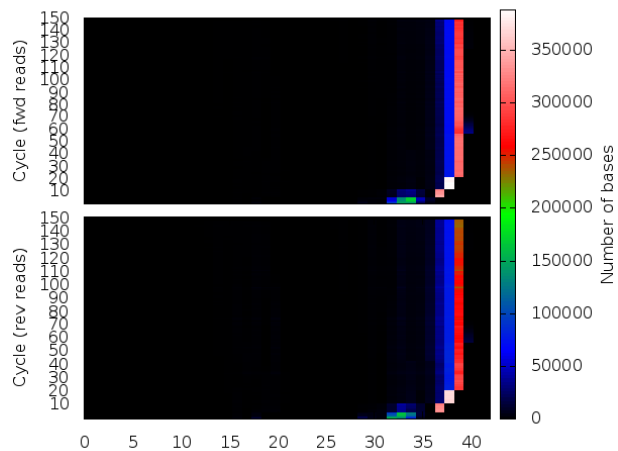(d) R2 AFTER trimming FAIL

Figure 3: Sequence Length Distribution

(a) R1 BEFORE trimming

(b) R1 AFTER trimming WARN

(c) R2 BEFORE trimming

(d) R2 AFTER trimming WARN

Figure 4: Adapter Content

(a) R1 BEFORE trimming

(b) R1 AFTER trimming PASS

(c) R2 BEFORE trimming

(d) R2 AFTER trimming PASS

3 BamStats

(a) Base quality per cycle

(b) Fragment size

(c) Quality per cycle

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