Sample Quality Results

1 Basic Statistics

Sample: 17-D13-42537-RB-Nextera-Myeloid-Val1-Repeat__S17__L001

File type: Conventional base calls

Encoding: Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	796529	453945
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	43	41

2 FastQC

Figure 1: Per base sequence quality

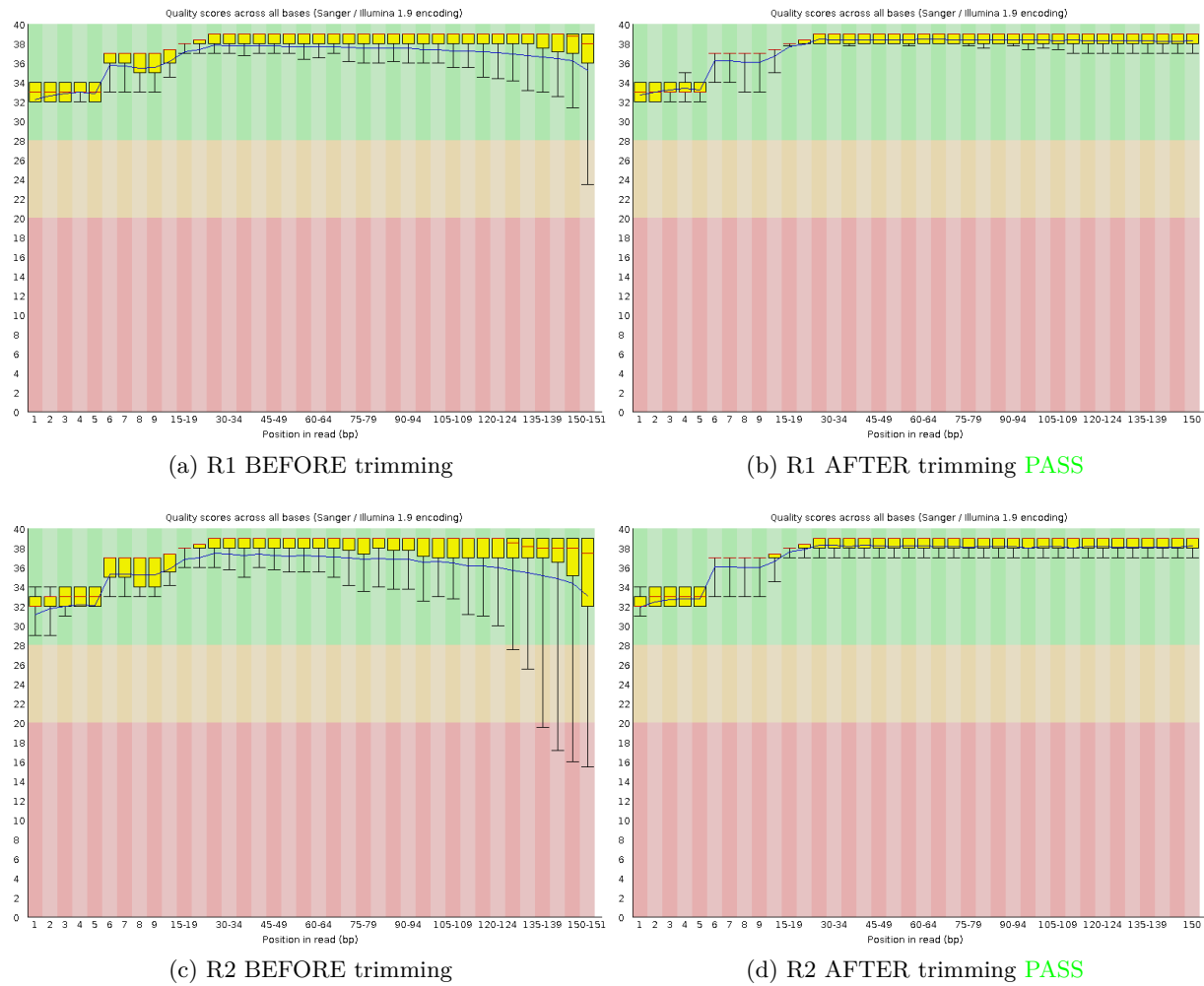(a) R1 BEFORE trimming

(b) R1 AFTER trimming PASS

(c) R2 BEFORE trimming
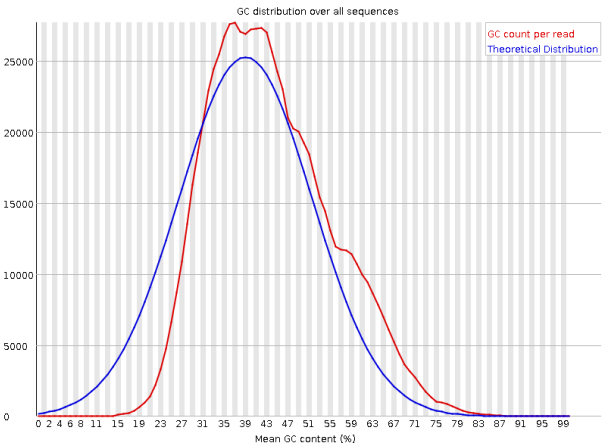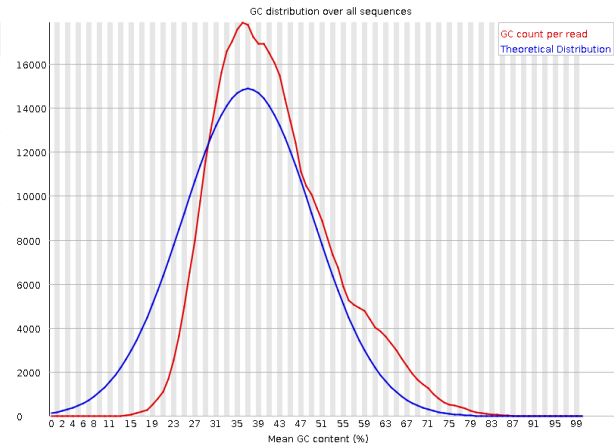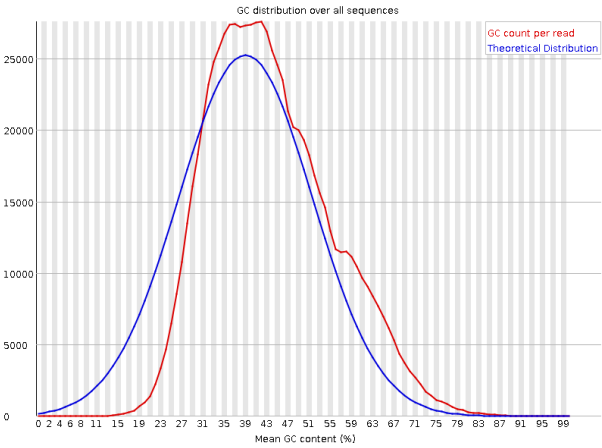

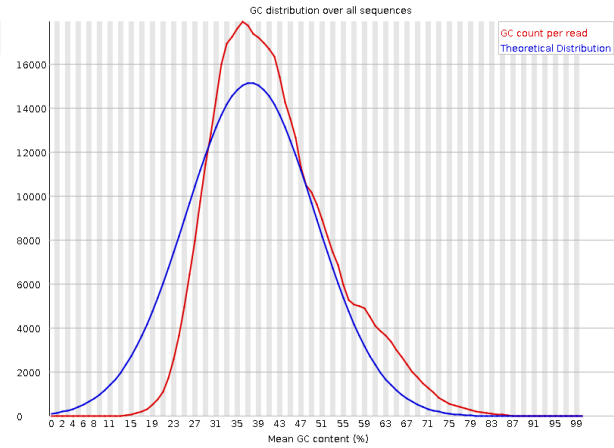(d) R2 AFTER trimming PASS

Figure 2: Per sequence GC content
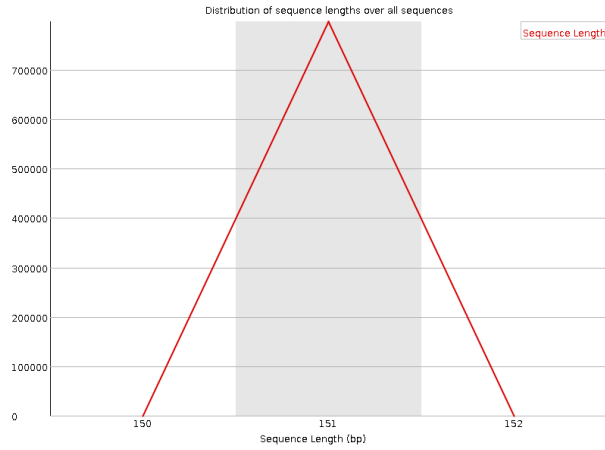

(a) R1 BEFORE trimming

(b) R1 AFTER trimming FAIL

(c) R2 BEFORE trimming
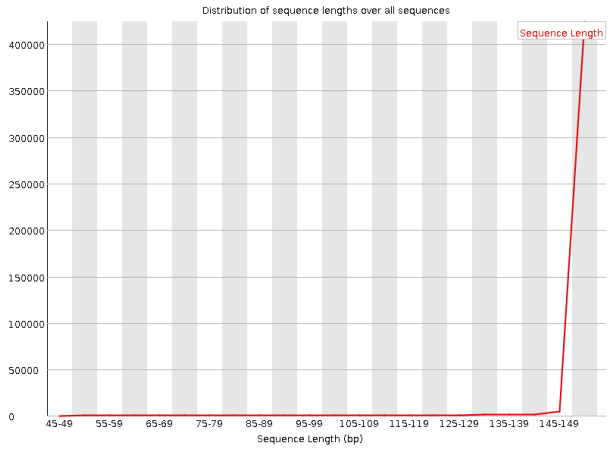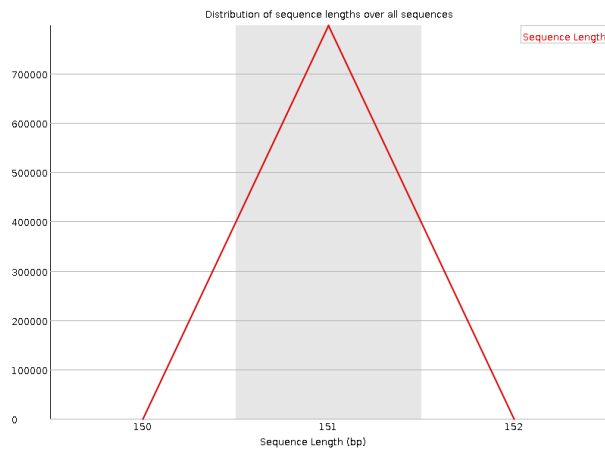

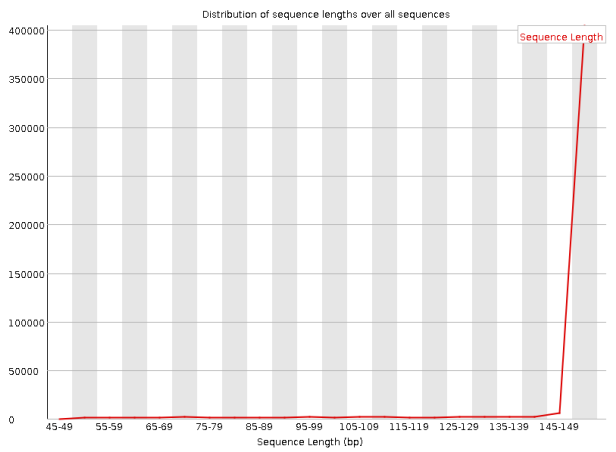(d) R2 AFTER trimming WARN

Figure 3: Sequence Length Distribution

(a) R1 BEFORE trimming

(b) R1 AFTER trimming WARN

(c) R2 BEFORE trimming
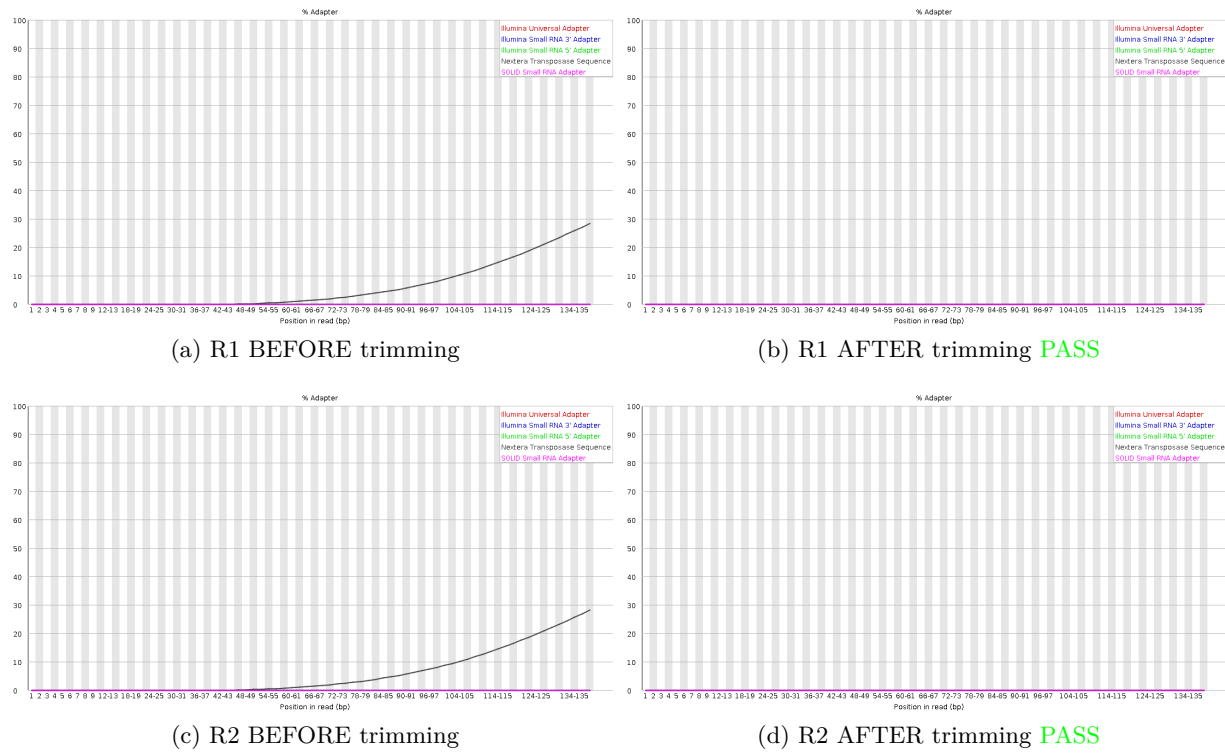
(d) R2 AFTER trimming WARN

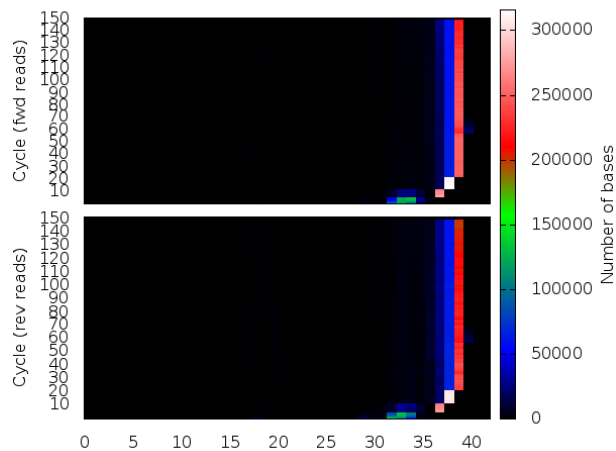Figure 4: Adapter Content

(a) R1 BEFORE trimming

(b) R1 AFTER trimming PASS
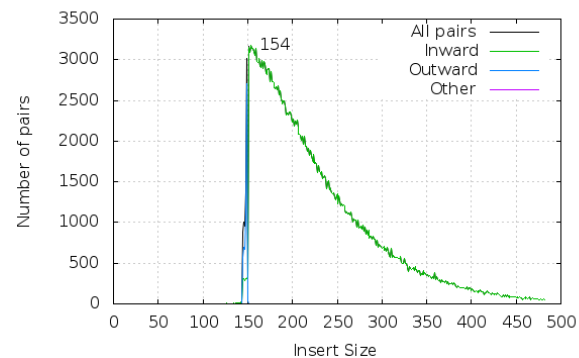

(c) R2 BEFORE trimming

(d) R2 AFTER trimming PASS

3 BamStats

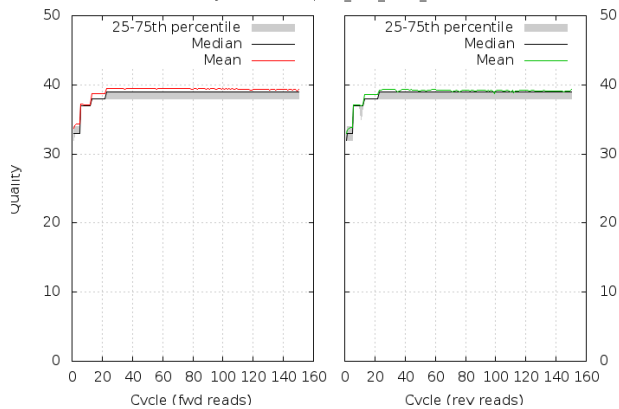2537-RB-Nextera-Myeloid-Val1-Repeat_S17_L001_.bwa.drm.sorted.bam.sta

(a) Base quality per cycle

D13-42537-RB-Nextera-Myeloid-Val1-Repeat_S17_L001_.bwa.drm.sorted.b

(b) Fragment size

17-D13-42537-RB-Nextera-Myeloid-Val1-Repeat_S17_L001_.bwa.drm.sorted.bam.stats

(c) Quality per cycle