Sample Quality Results

1 Basic Statistics

Sample: 12-D15-50424-LB-Nextera-Myeloid-Val1-Repeat__S12__L001

File type: Conventional base calls

Encoding: Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	986534	527371
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	41	39

2 FastQC

Figure 1: Per base sequence quality

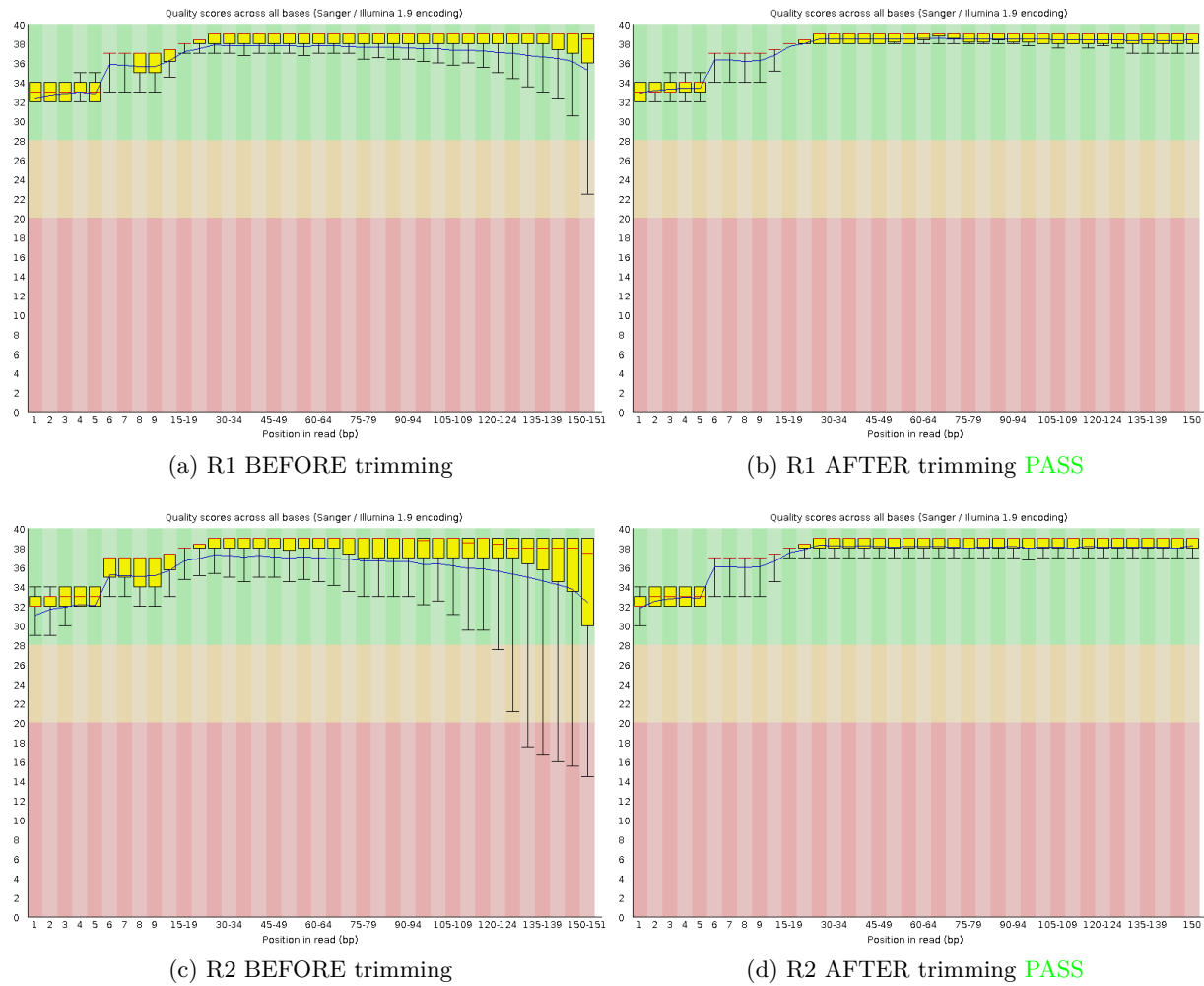(a) R1 BEFORE trimming

(b) R1 AFTER trimming PASS

(c) R2 BEFORE trimming

(d) R2 AFTER trimming PASS

Figure 2: Per sequence GC content

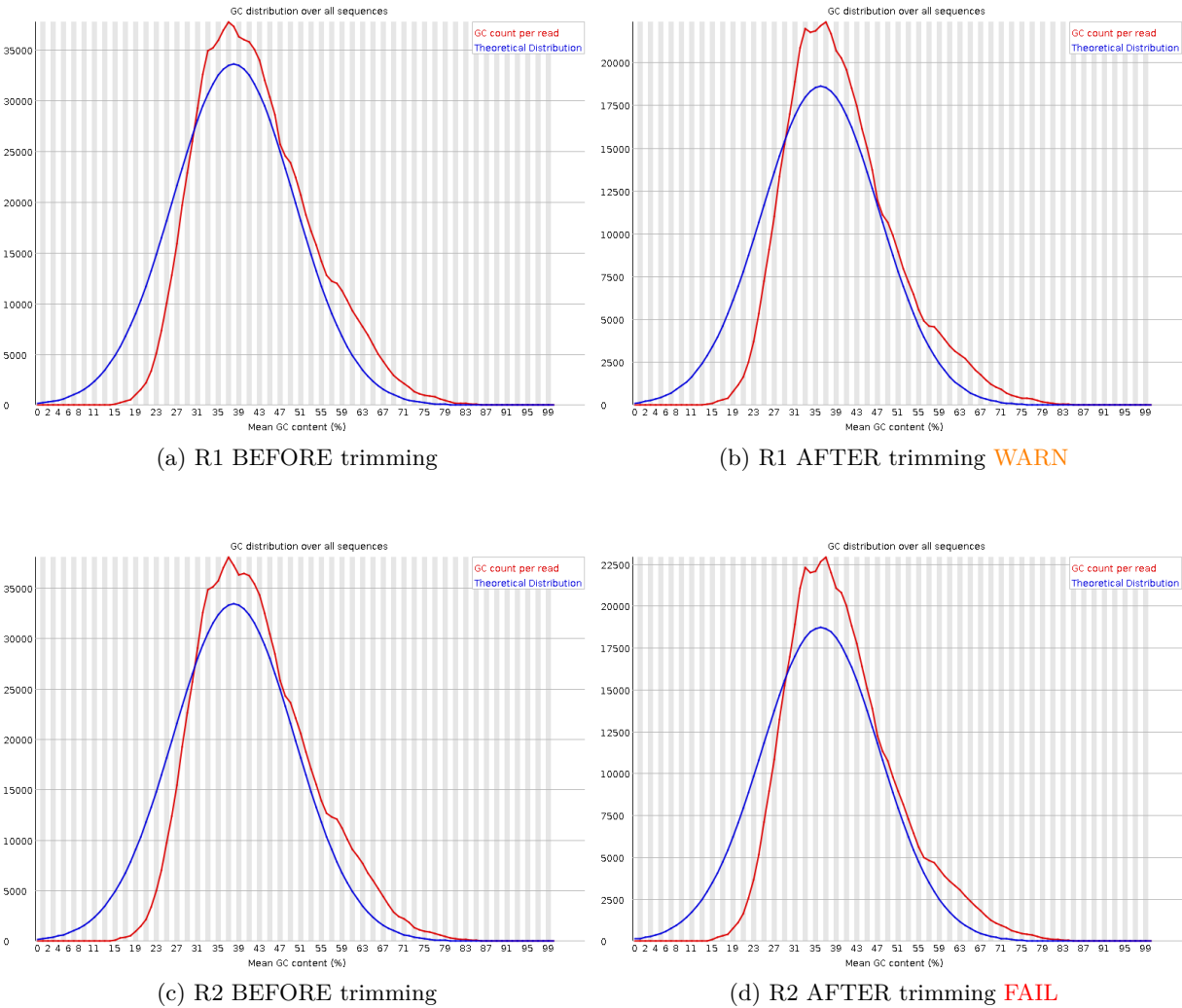(a) R1 BEFORE trimming

(b) R1 AFTER trimming WARN

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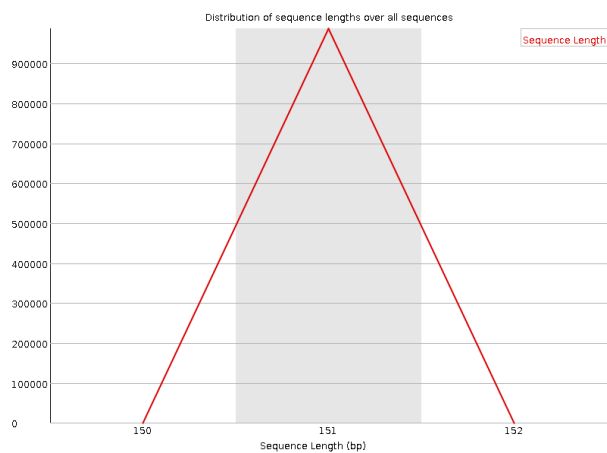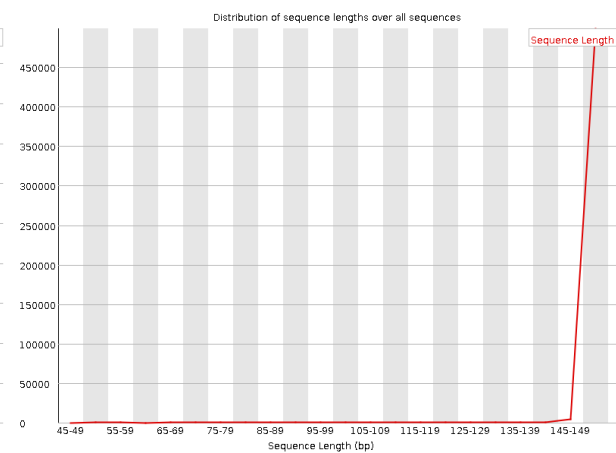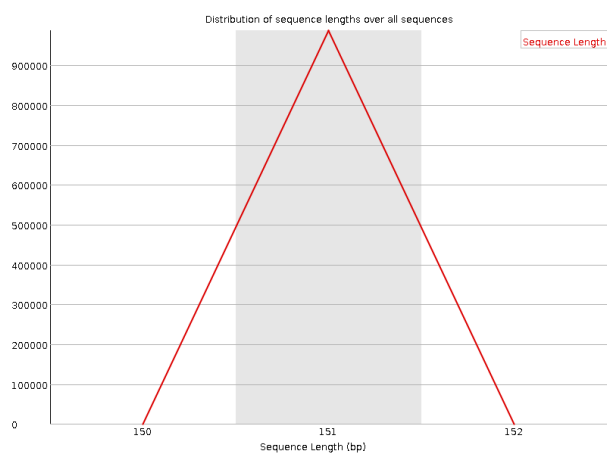
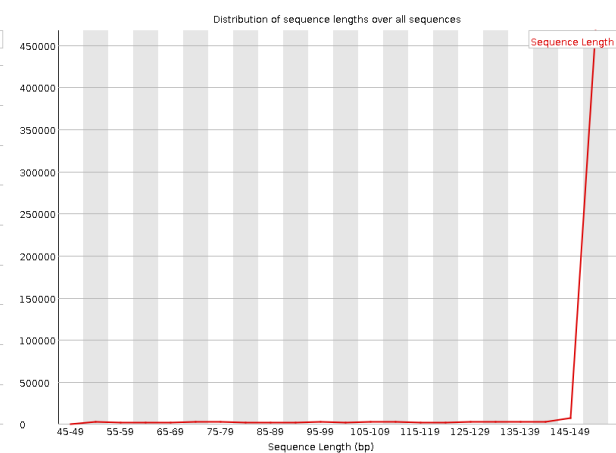(d) R2 AFTER trimming FAIL

Figure 3: Sequence Length Distribution

(a) R1 BEFORE trimming

(b) R1 AFTER trimming WARN

(c) R2 BEFORE trimming

(d) R2 AFTER trimming WARN
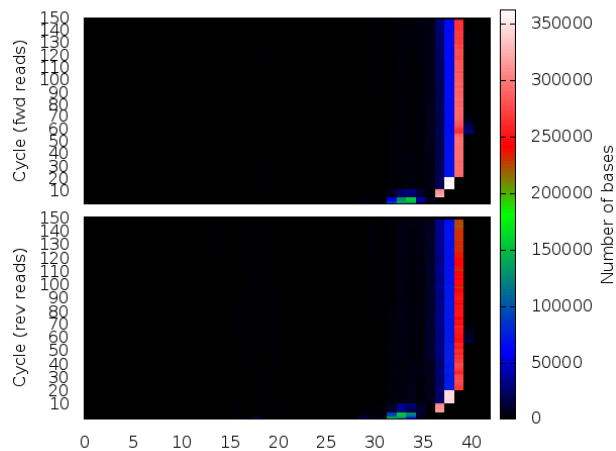
Figure 4: Adapter Content

(a) R1 BEFORE trimming

(b) R1 AFTER trimming PASS
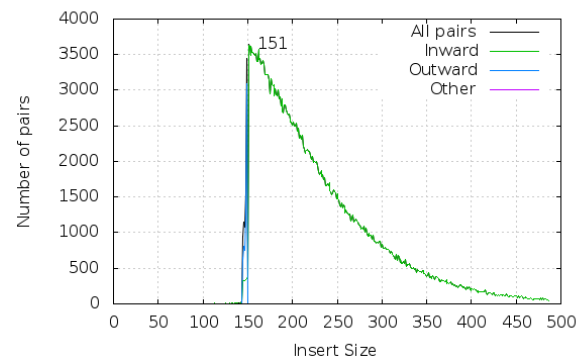
(c) R2 BEFORE trimming

(d) R2 AFTER trimming PASS
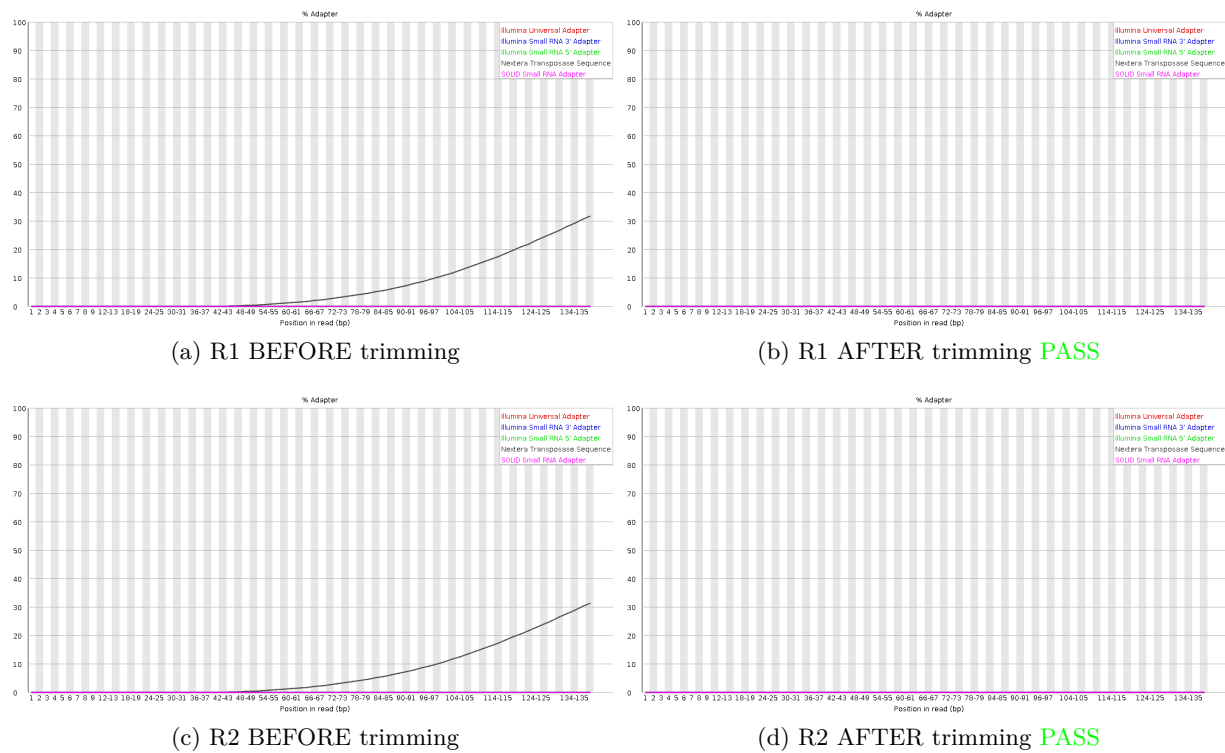
3 BamStats

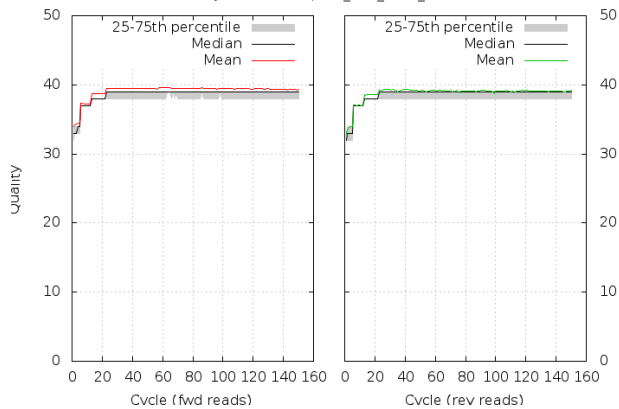0424-LB-Nextera-Myeloid-Val1-Repeat_S12_L001_.bwa.drm.sorted.bam.sta

(a) Base quality per cycle

D15-50424-LB-Nextera-Myeloid-Val1-Repeat_S12_L001_.bwa.drm.sorted.b

(b) Fragment size

12-D15-50424-LB-Nextera-Myeloid-Val1-Repeat_S12_L001_.bwa.drm.sorted.bam.stats

(c) Quality per cycle