

Sample Quality Results

1 Basic Statistics

Sample: 24-D15-26810-FM-Nextera-Myeloid-Val1-Repeat_S24_L001

File type: Conventional base calls

Encoding: Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	689976	307753
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	43	40

2 FastQC

Figure 1: Per base sequence quality

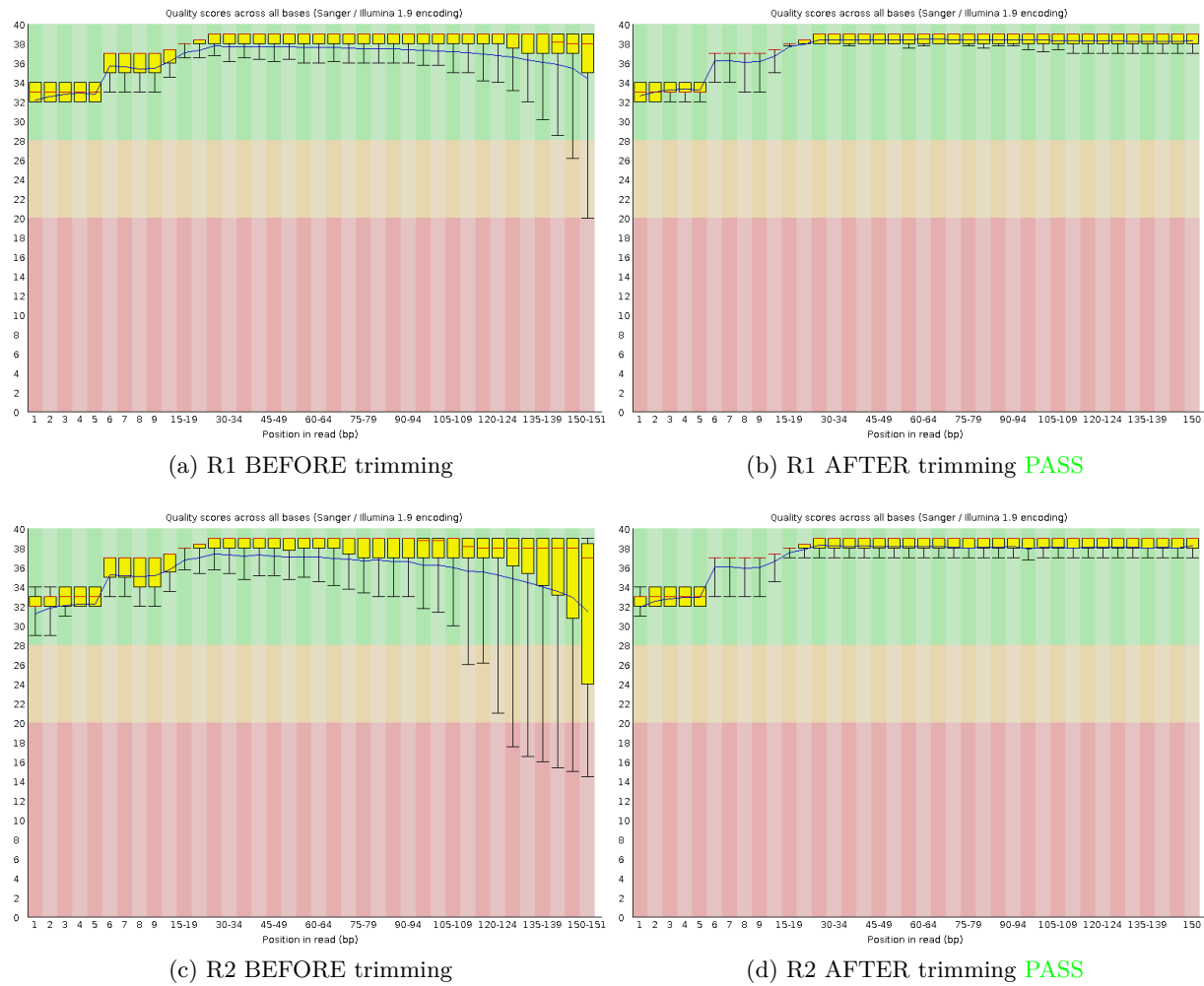
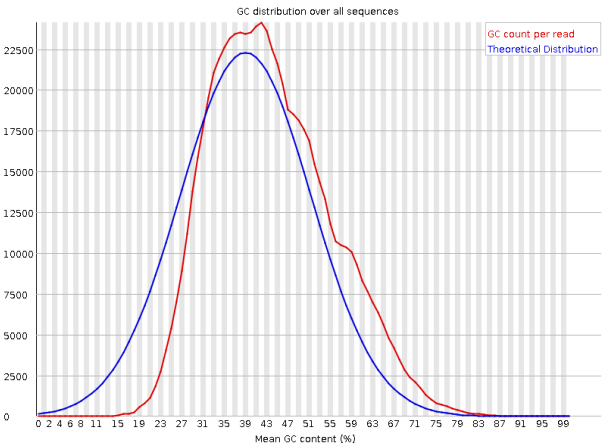
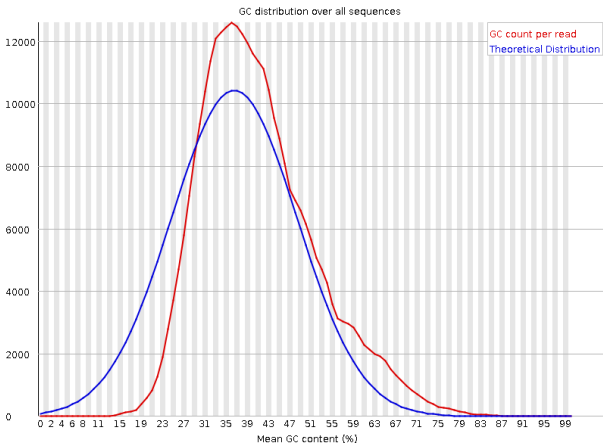


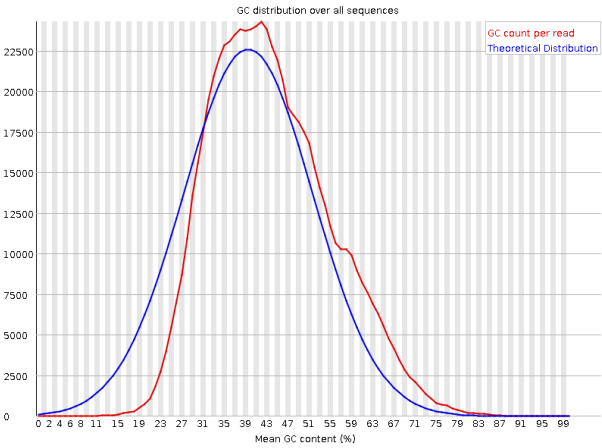
Figure 2: Per sequence GC content



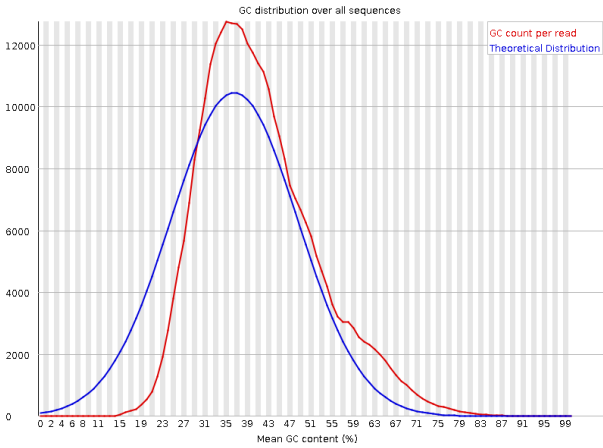
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **FAIL**

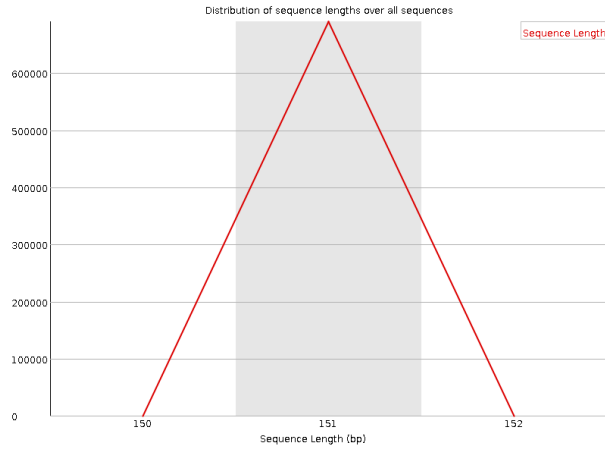


(c) R2 BEFORE trimming

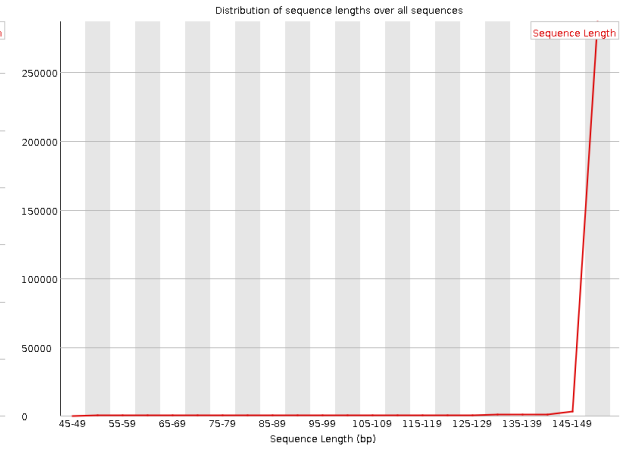


(d) R2 AFTER trimming **FAIL**

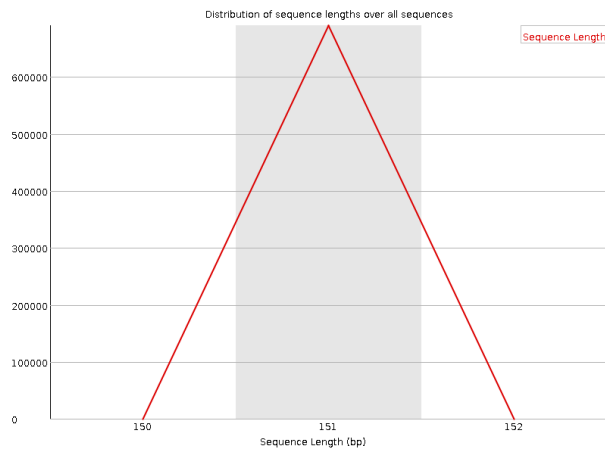
Figure 3: Sequence Length Distribution



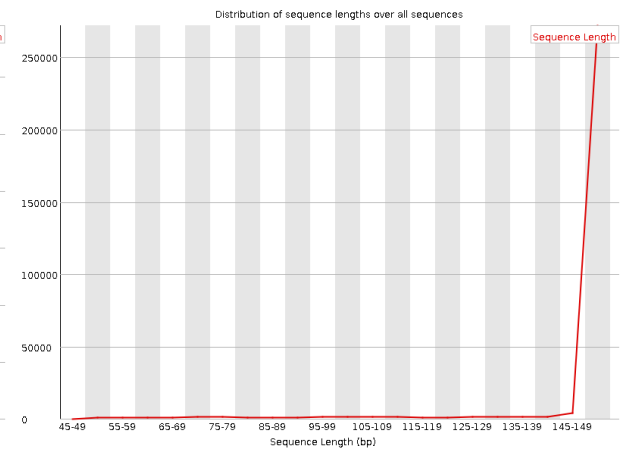
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **WARN**

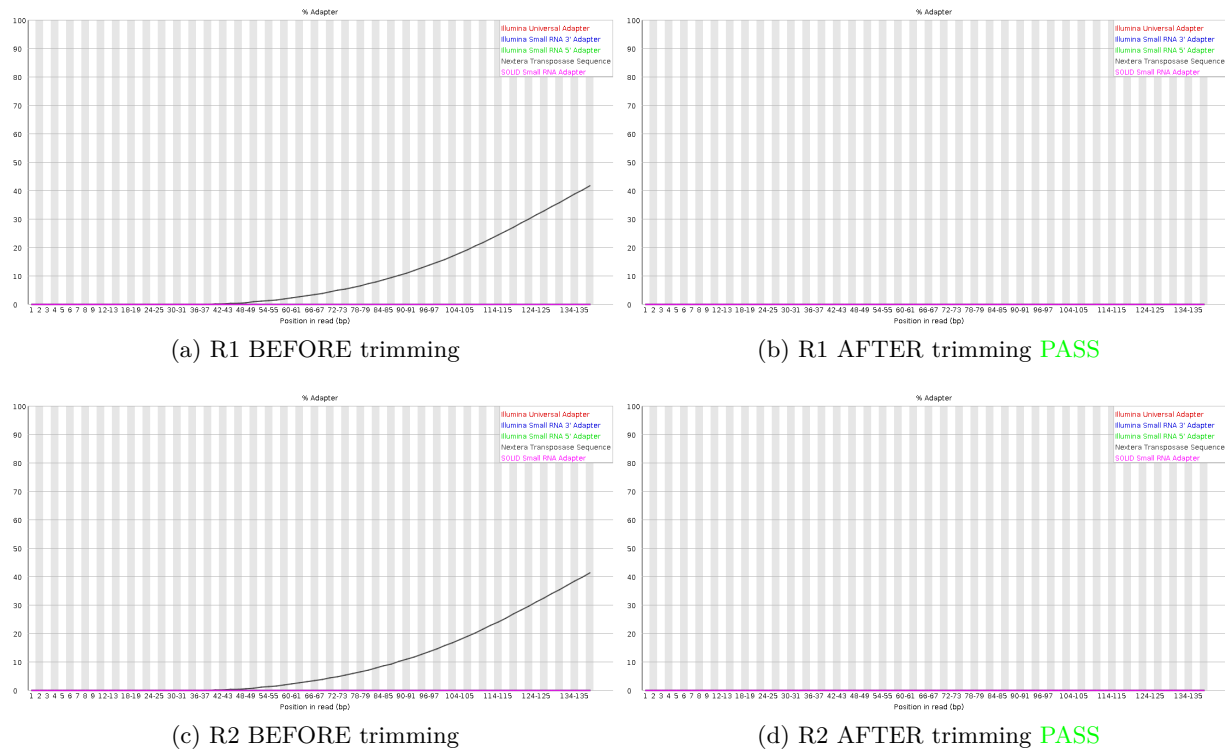


(c) R2 BEFORE trimming



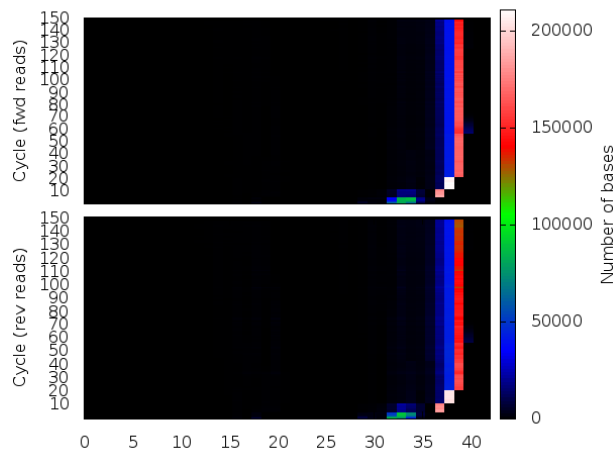
(d) R2 AFTER trimming **WARN**

Figure 4: Adapter Content



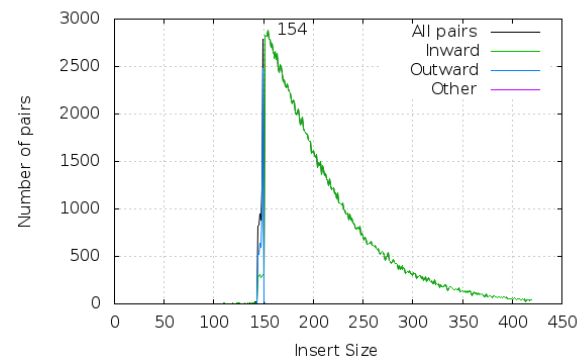
3 BamStats

5810-FM-Nextera-Myeloid-Val1-Repeat_S24_L001_.bwa.drm.sorted.bam.stat



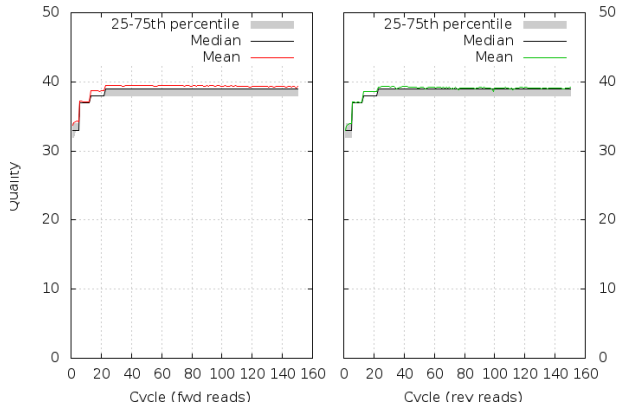
(a) Base quality per cycle

D15-26810-FM-Nextera-Myeloid-Val1-Repeat_S24_L001_.bwa.drm.sorted.b



(b) Fragment size

24-D15-26810-FM-Nextera-Myeloid-Val1-Repeat_S24_L001_.bwa.drm.sorted.bam.stats



(c) Quality per cycle