

# Sample Quality Results

## 1 Basic Statistics

**Sample:** 21-D14-30832-BY-Nextera-Myeloid-Val1-Repeat\_S21\_L001

**File type:** Conventional base calls

**Encoding:** Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	889481	502022
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	43	41

## 2 FastQC

Figure 1: Per base sequence quality

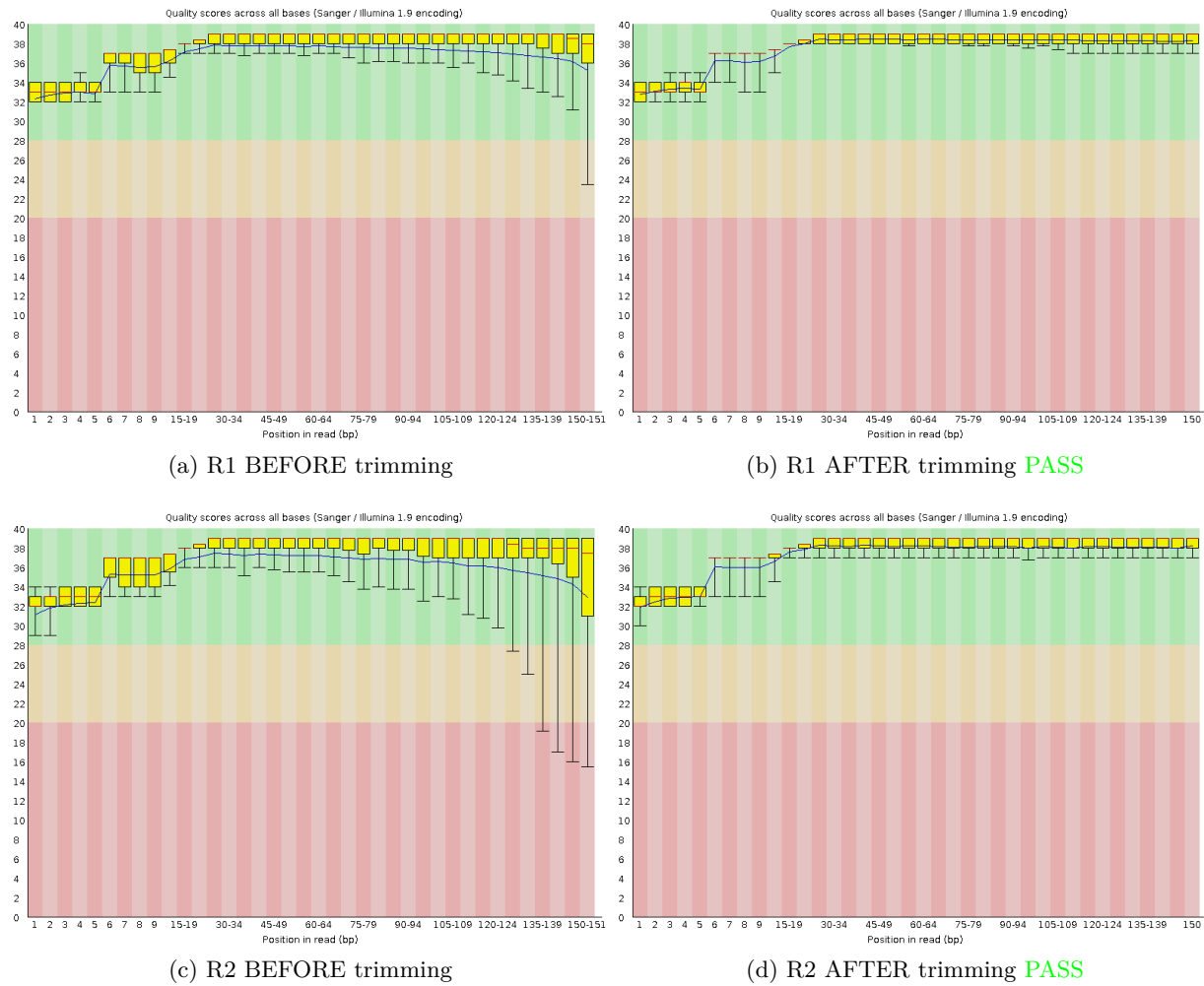
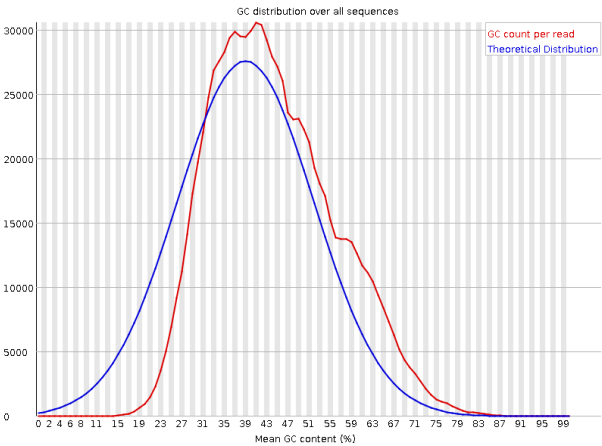
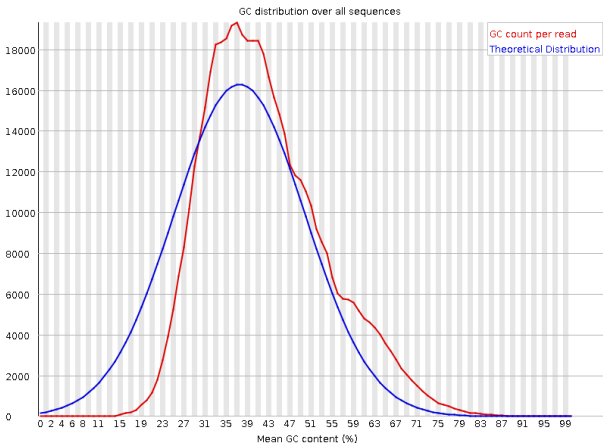


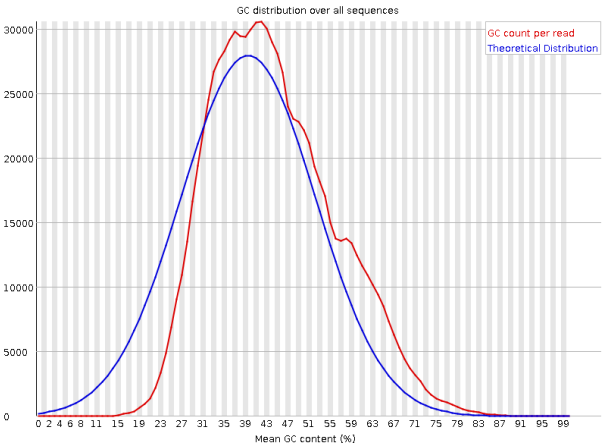
Figure 2: Per sequence GC content



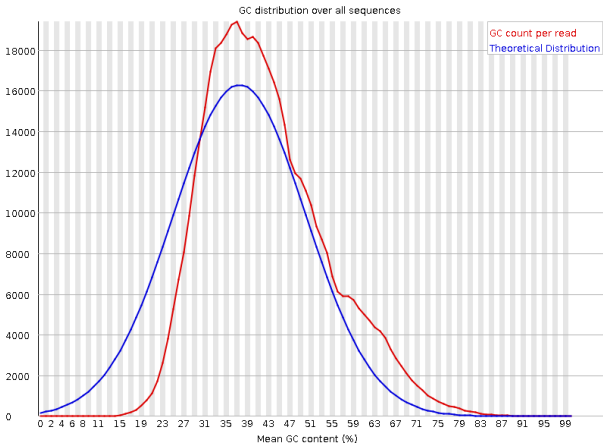
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **FAIL**

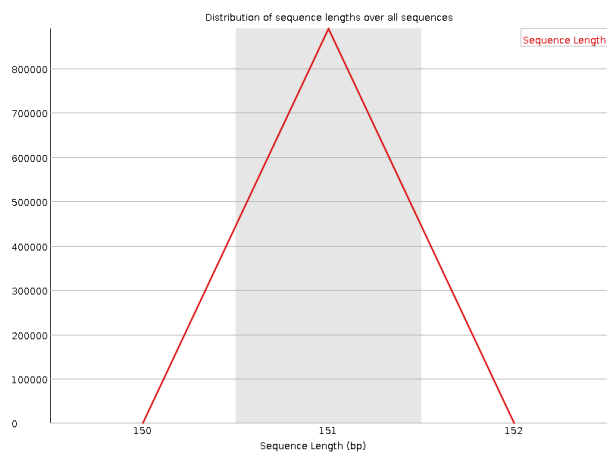


(c) R2 BEFORE trimming

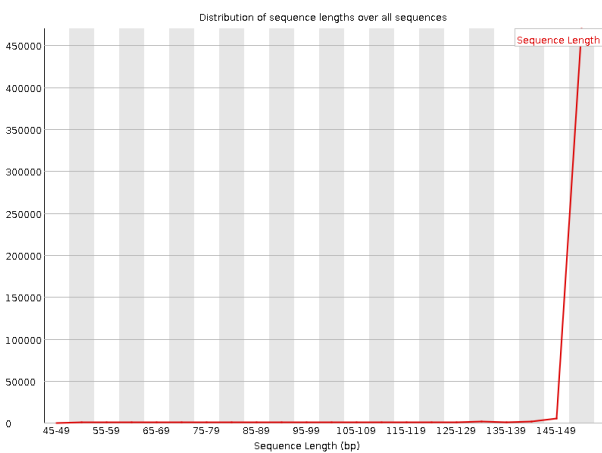


(d) R2 AFTER trimming **FAIL**

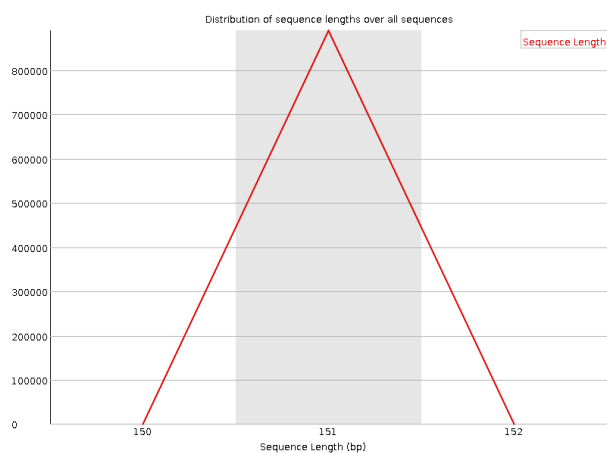
Figure 3: Sequence Length Distribution



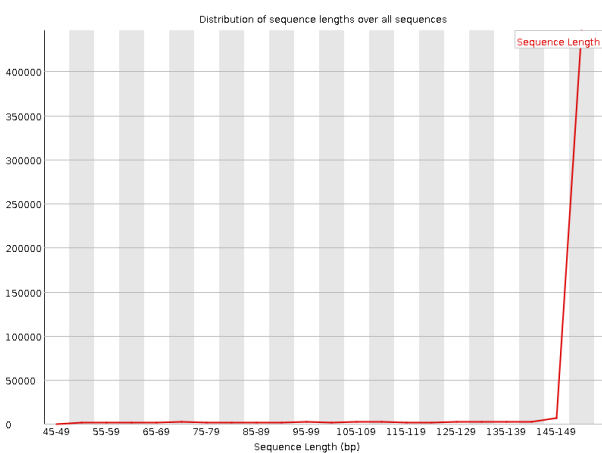
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **WARN**

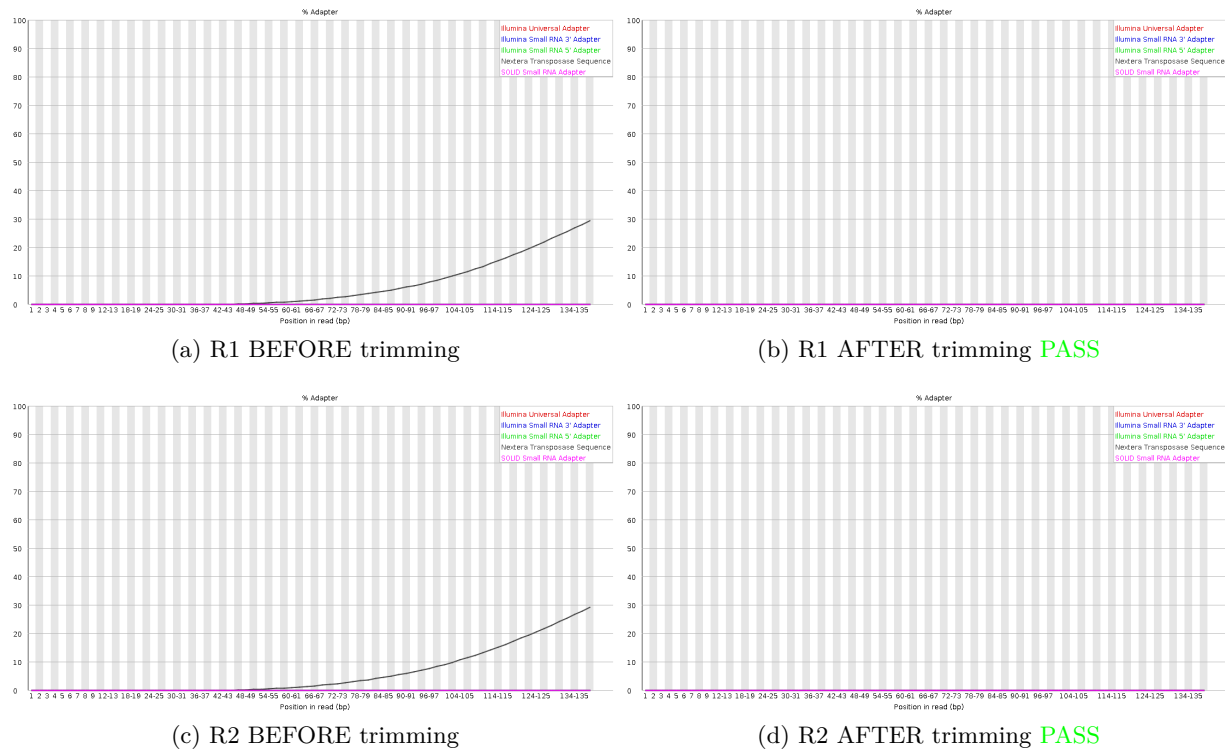


(c) R2 BEFORE trimming



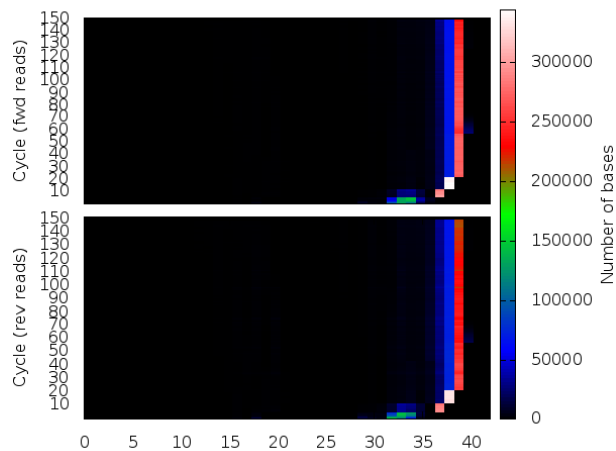
(d) R2 AFTER trimming **WARN**

Figure 4: Adapter Content



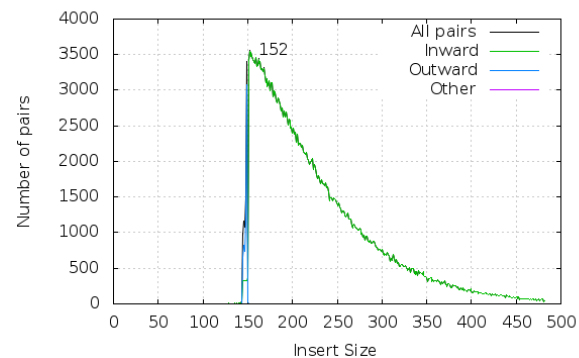
### 3 BamStats

0832-BY-Nextera-Myeloid-Va11-Repeat\_S21\_L001\_.bwa.drm.sorted.bam.stat



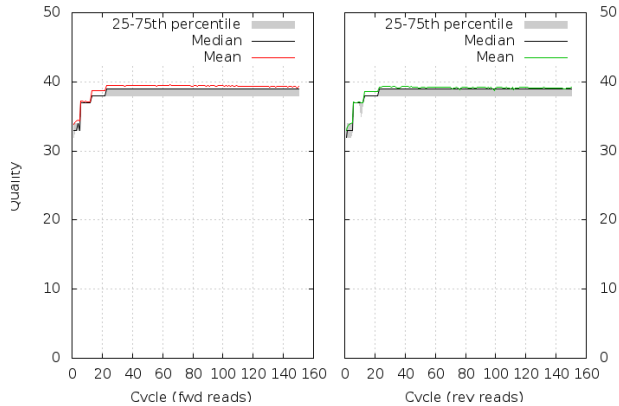
(a) Base quality per cycle

D14-30832-BY-Nextera-Myeloid-Va11-Repeat\_S21\_L001\_.bwa.drm.sorted.ba



(b) Fragment size

21-D14-30832-BY-Nextera-Myeloid-Va11-Repeat\_S21\_L001\_.bwa.drm.sorted.bam.stat



(c) Quality per cycle