# Sample Quality Results

## 1 Basic Statistics

**Sample:** 23-D15-02217-LT-Nextera-Myeloid-Val1-Repeat_S23_L001

**File type:** Conventional base calls

**Encoding:** Sanger / Illumina 1.9

|  | Before trimming | After trimming |
|---|---|---|
| Total Sequences | 729037 | 371874 |
| Sequences flagged as poor quality | 0 | 0 |
| Sequence length | 151 | 50-150 |
| %GC | 43 | 40 |

## 2 FastQC

Figure 1: Per base sequence quality



(a) R1 BEFORE trimming
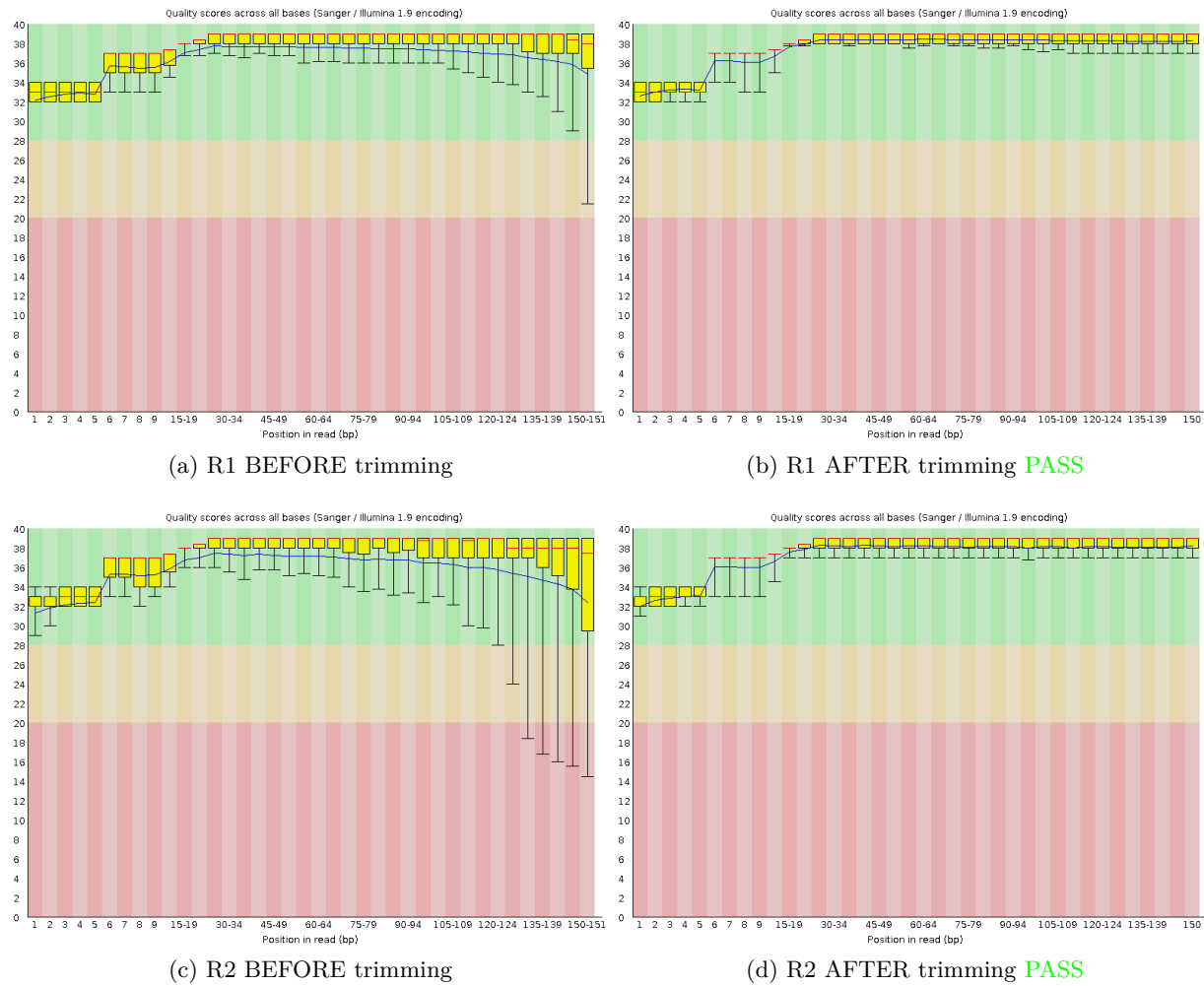


(b) R1 AFTER trimming PASS



(c) R2 BEFORE trimming
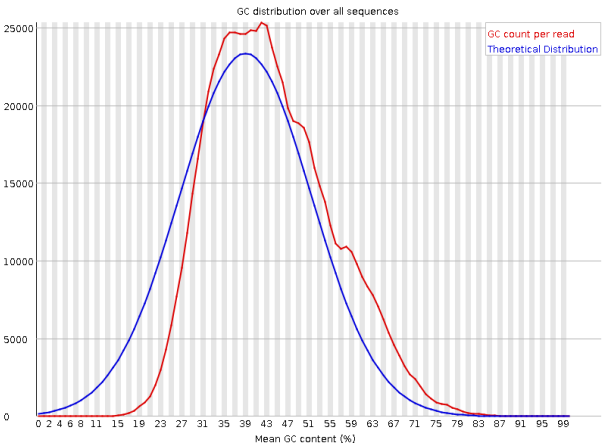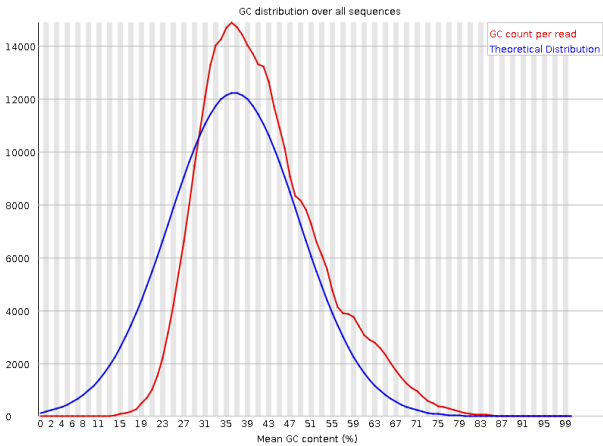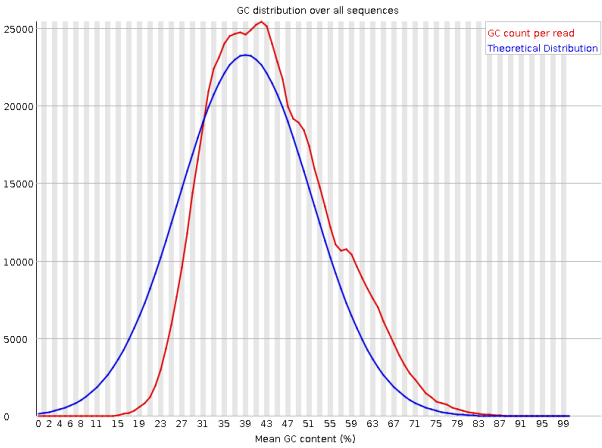


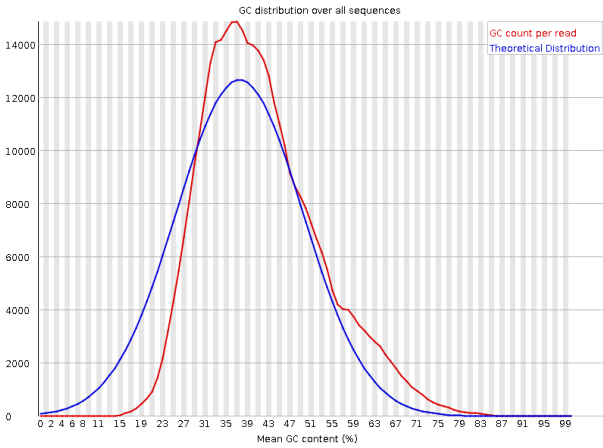(d) R2 AFTER trimming PASS

Figure 2: Per sequence GC content
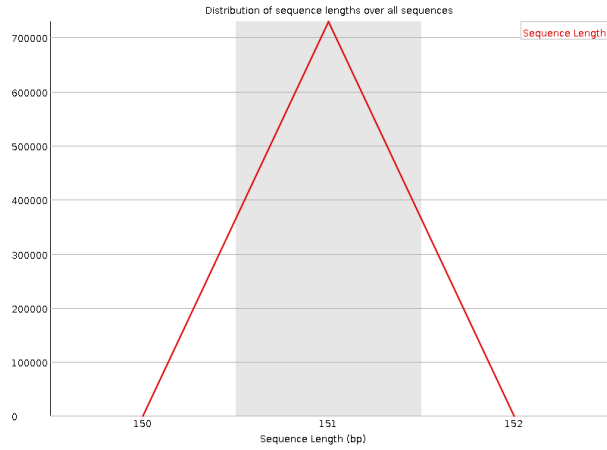


(a) R1 BEFORE trimming

(b) R1 AFTER trimming FAIL

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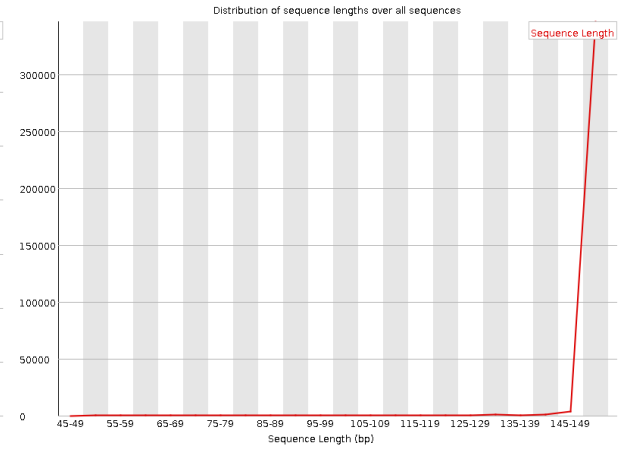
(d) R2 AFTER trimming WARN

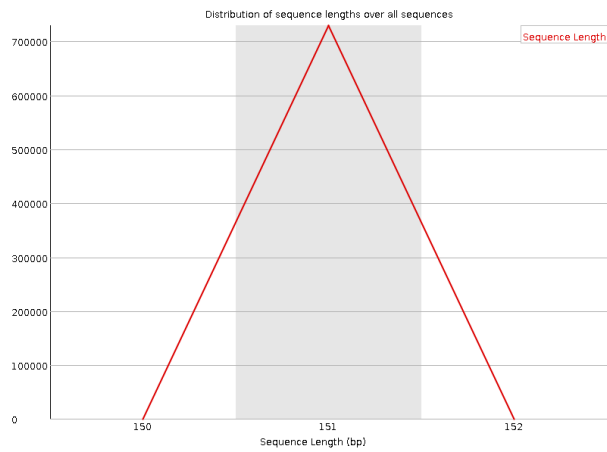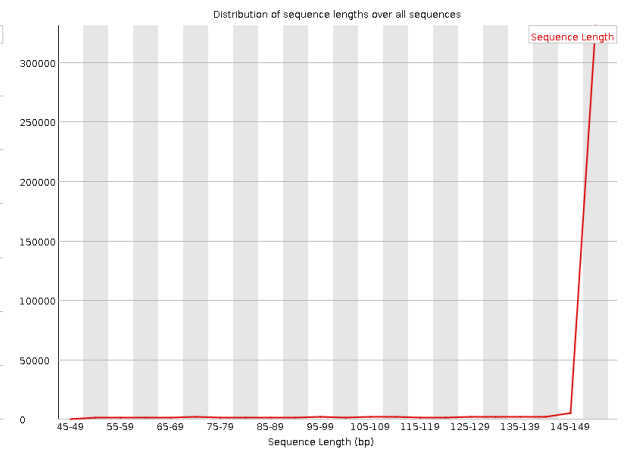Figure 3: Sequence Length Distribution



(a) R1 BEFORE trimming



(b) R1 AFTER trimming WARN



(c) R2 BEFORE trimming
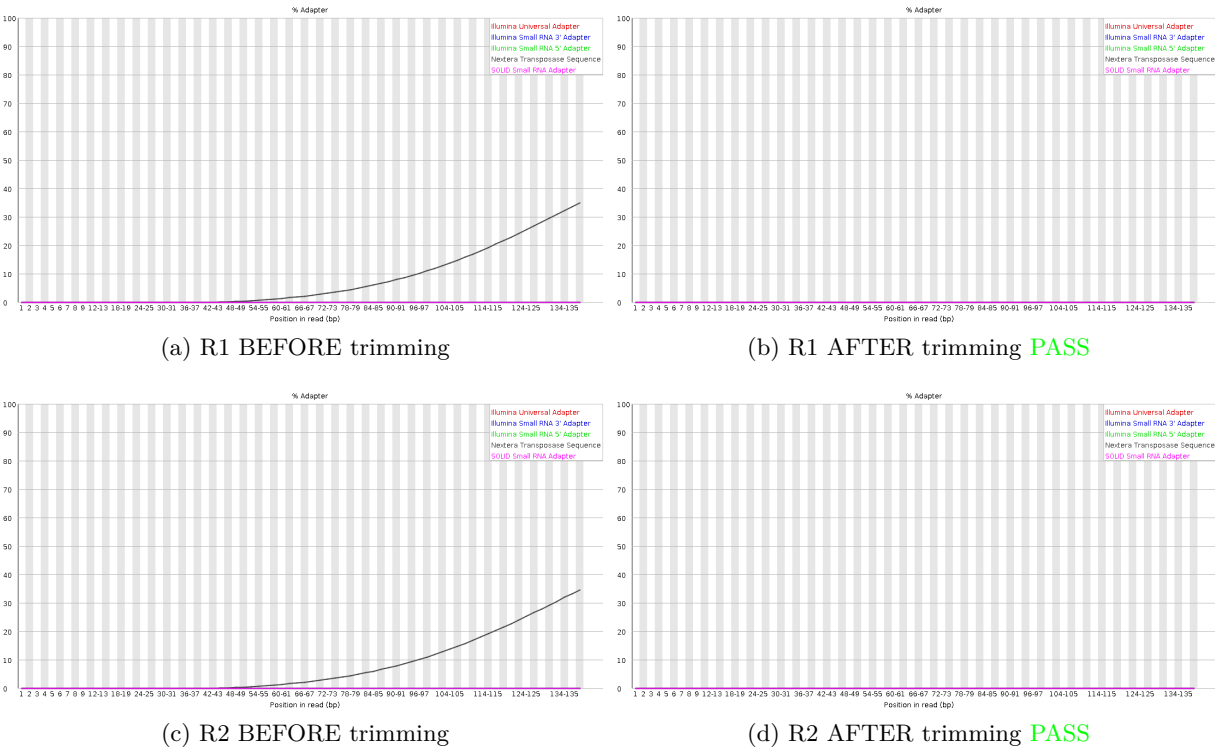


(d) R2 AFTER trimming WARN
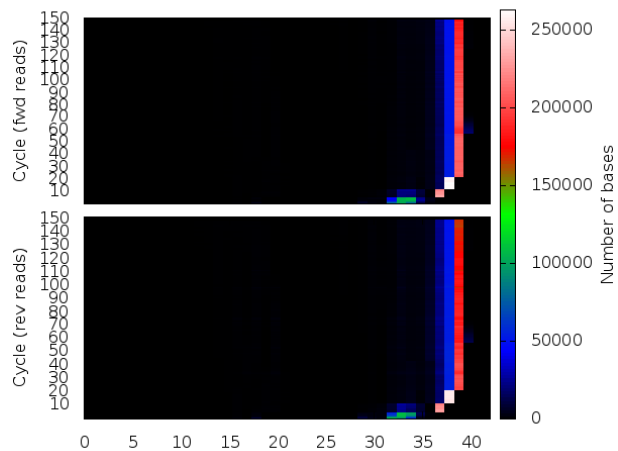
Figure 4: Adapter Content


(a) R1 BEFORE trimming


(b) R1 AFTER trimming PASS
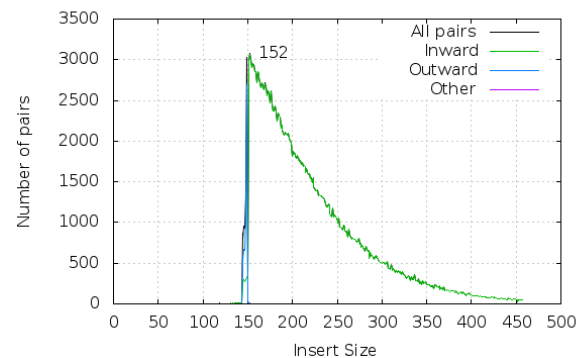

(c) R2 BEFORE trimming


(d) R2 AFTER trimming PASS

# 3 BamStats

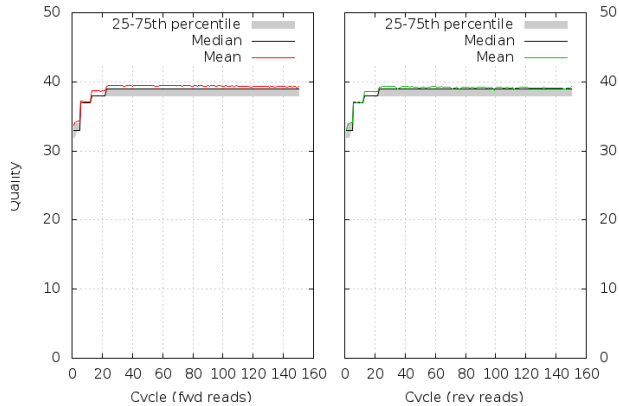2217-LT-Nextera-Myeloid-Val1-Repeat_S23_L001_.bwa.drm.sorted.bam.sta

(a) Base quality per cycle

-D15-02217-LT-Nextera-Myeloid-Val1-Repeat_S23_L001_.bwa.drm.sorted.ba

(b) Fragment size

23-D15-02217-LT-Nextera-Myeloid-Val1-Repeat_S23_L001_.bwa.drm.sorted.bam.stats

(c) Quality per cycle