

# Sample Quality Results

## 1 Basic Statistics

**Sample:** 04-D15-22373-HT-Nextera-Myeloid-Val1-Repeat\_S4\_L001

**File type:** Conventional base calls

**Encoding:** Sanger / Illumina 1.9

|                                   | Before trimming | After trimming |
|-----------------------------------|-----------------|----------------|
| Total Sequences                   | 616751          | 310338         |
| Sequences flagged as poor quality | 0               | 0              |
| Sequence length                   | 151             | 50-150         |
| %GC                               | 43              | 40             |

## 2 FastQC

Figure 1: Per base sequence quality

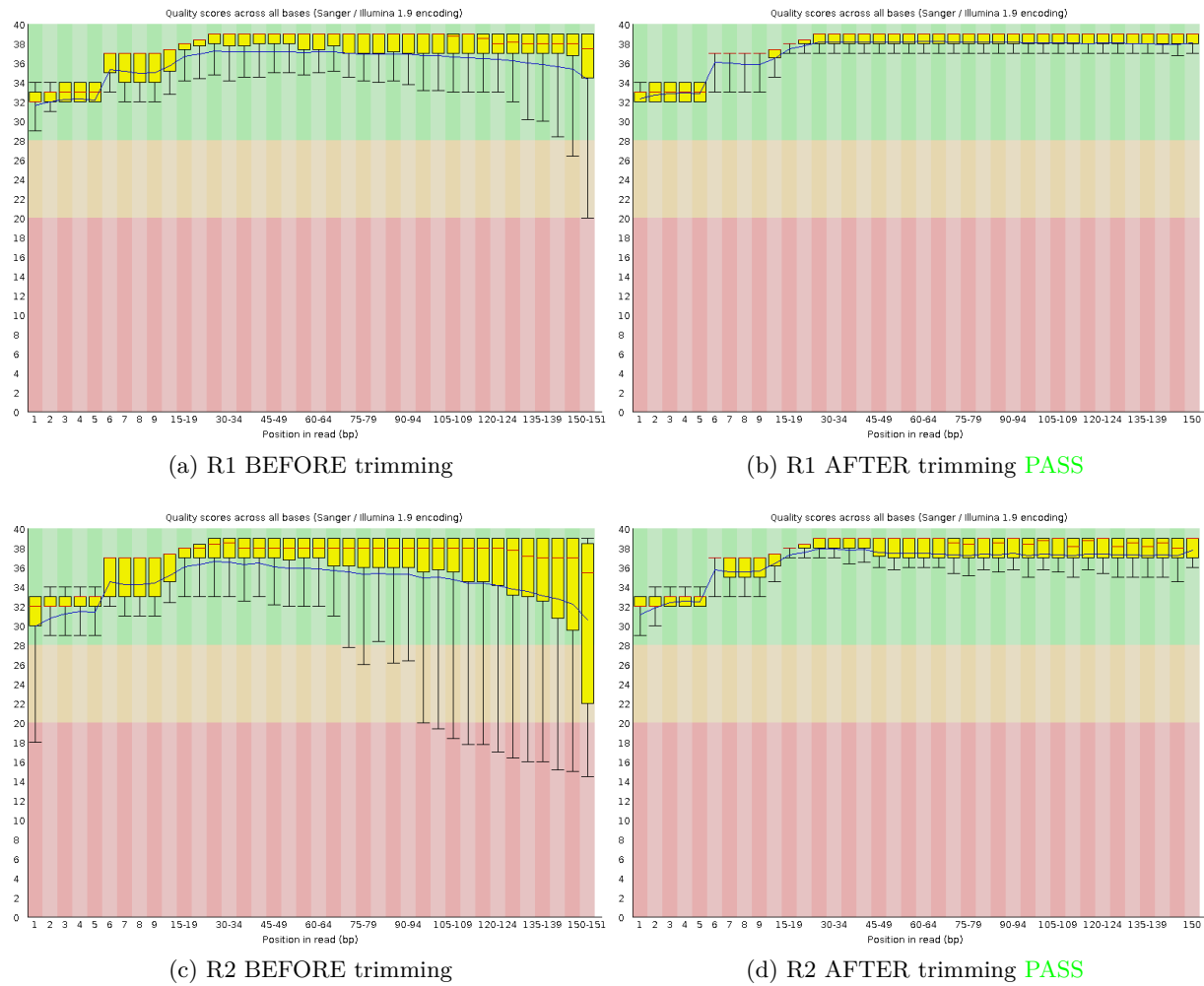
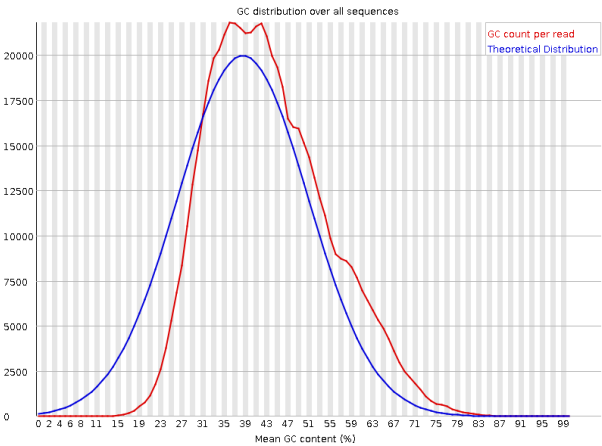
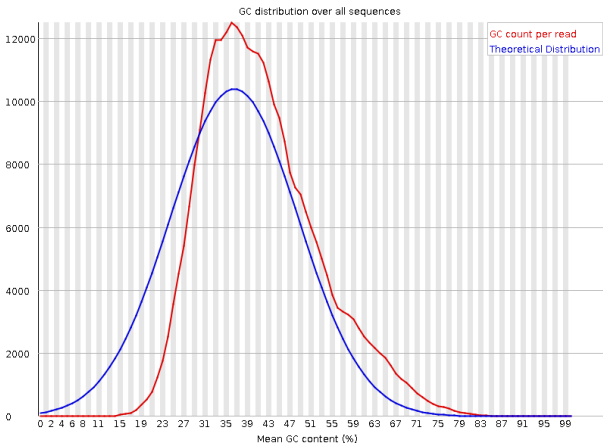


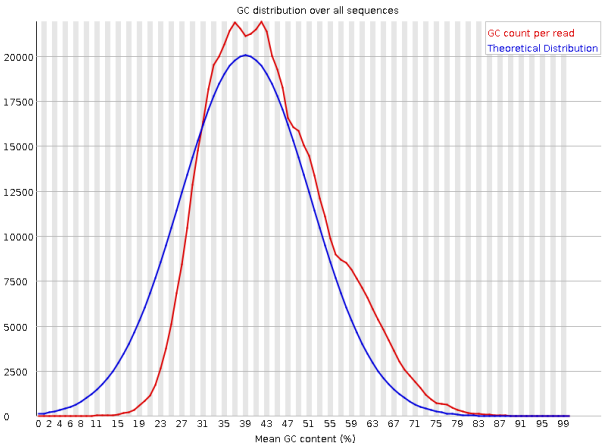
Figure 2: Per sequence GC content



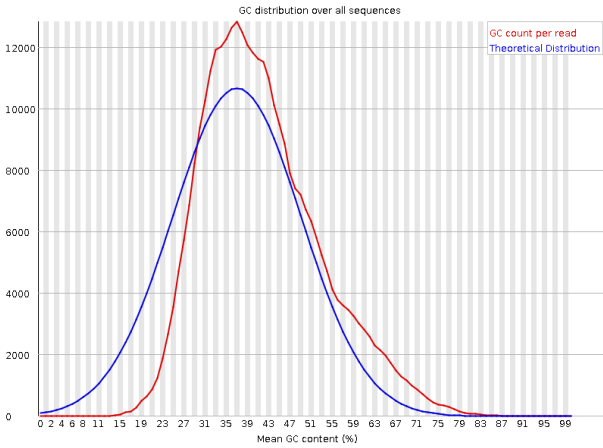
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **FAIL**

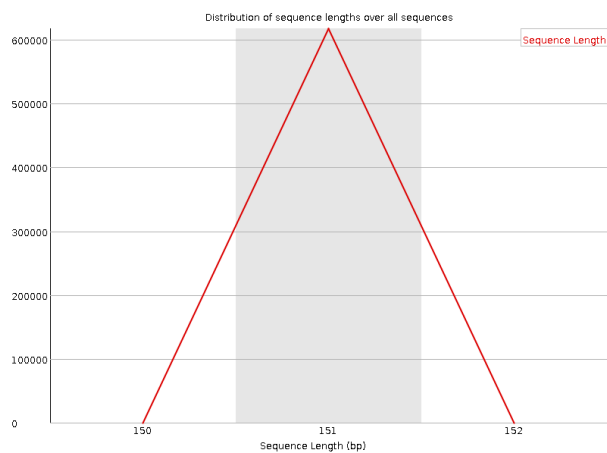


(c) R2 BEFORE trimming

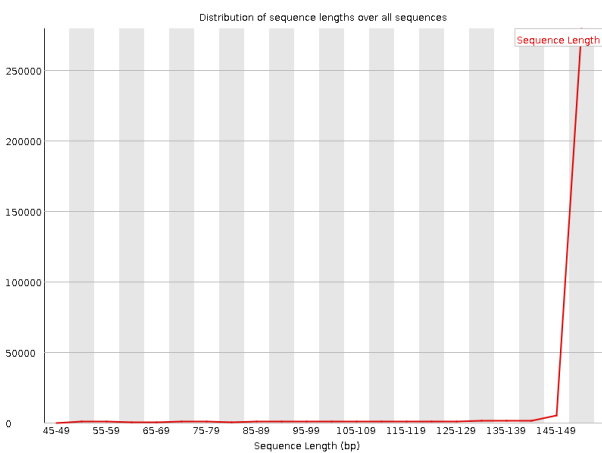


(d) R2 AFTER trimming **FAIL**

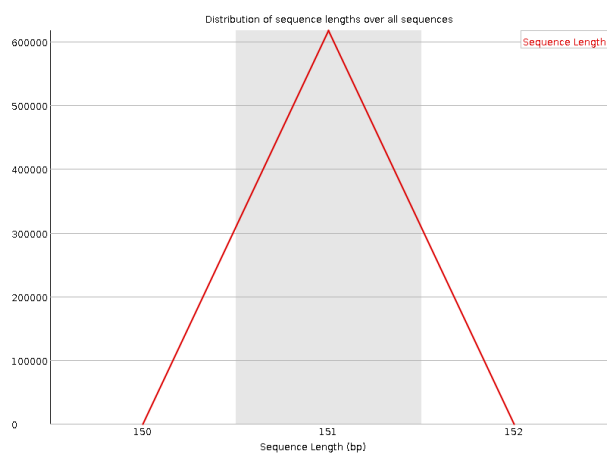
Figure 3: Sequence Length Distribution



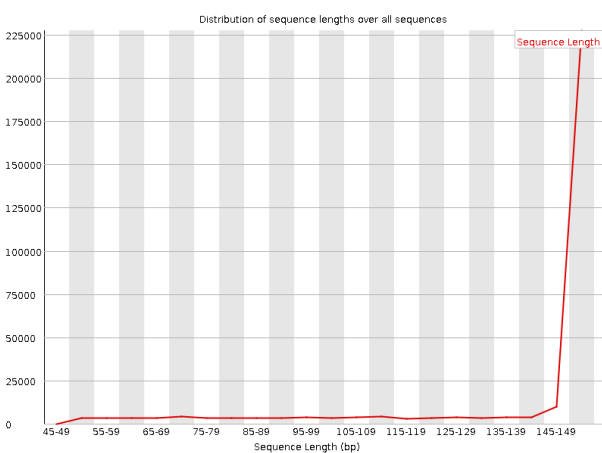
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **WARN**

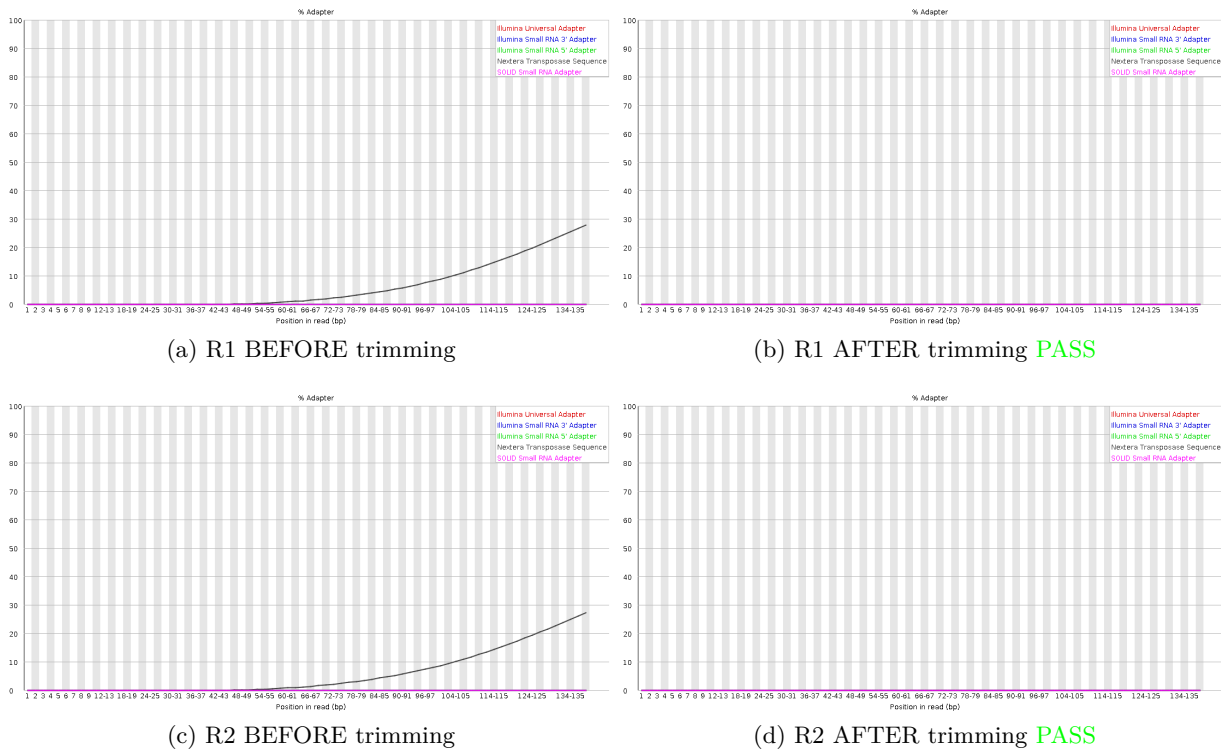


(c) R2 BEFORE trimming



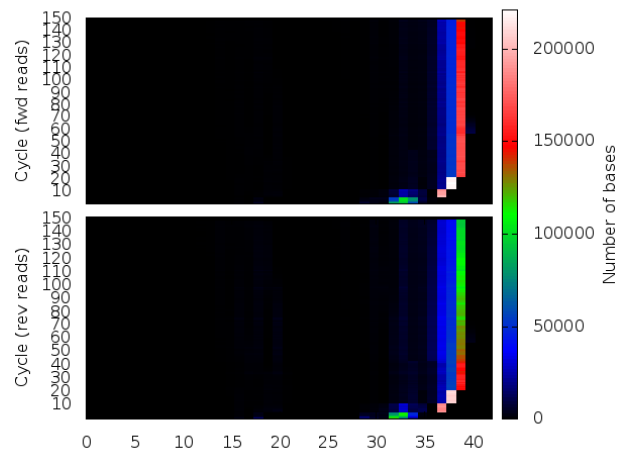
(d) R2 AFTER trimming **WARN**

Figure 4: Adapter Content



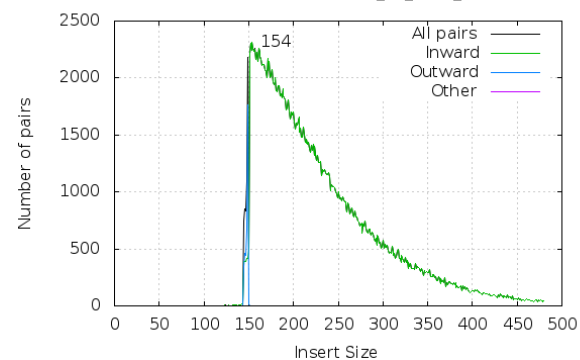
### 3 BamStats

2373-HT-Nextera-Myeloid-Va11-Repeat\_S4\_L001\_.bwa.drm.sorted.bam.stat



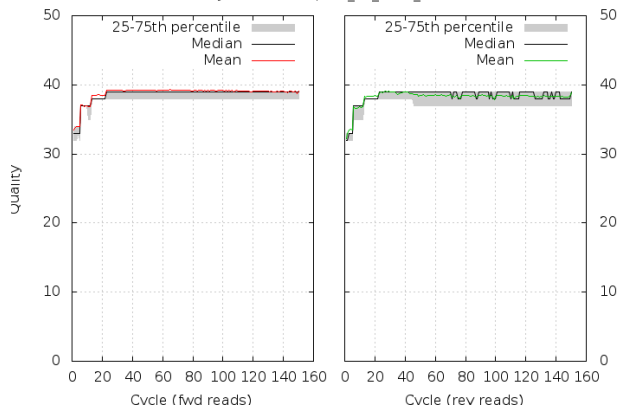
(a) Base quality per cycle

-D15-2373-HT-Nextera-Myeloid-Va11-Repeat\_S4\_L001\_.bwa.drm.sorted.ba



(b) Fragment size

04-D15-2373-HT-Nextera-Myeloid-Va11-Repeat\_S4\_L001\_.bwa.drm.sorted.bam.stats



(c) Quality per cycle