

# Sample Quality Results

## 1 Basic Statistics

**Sample:** 10-D15-04183-CS-Nextera-Myeloid-Val1-Repeat\_S10\_L001

**File type:** Conventional base calls

**Encoding:** Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	1062507	568534
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	43	41

## 2 FastQC

Figure 1: Per base sequence quality

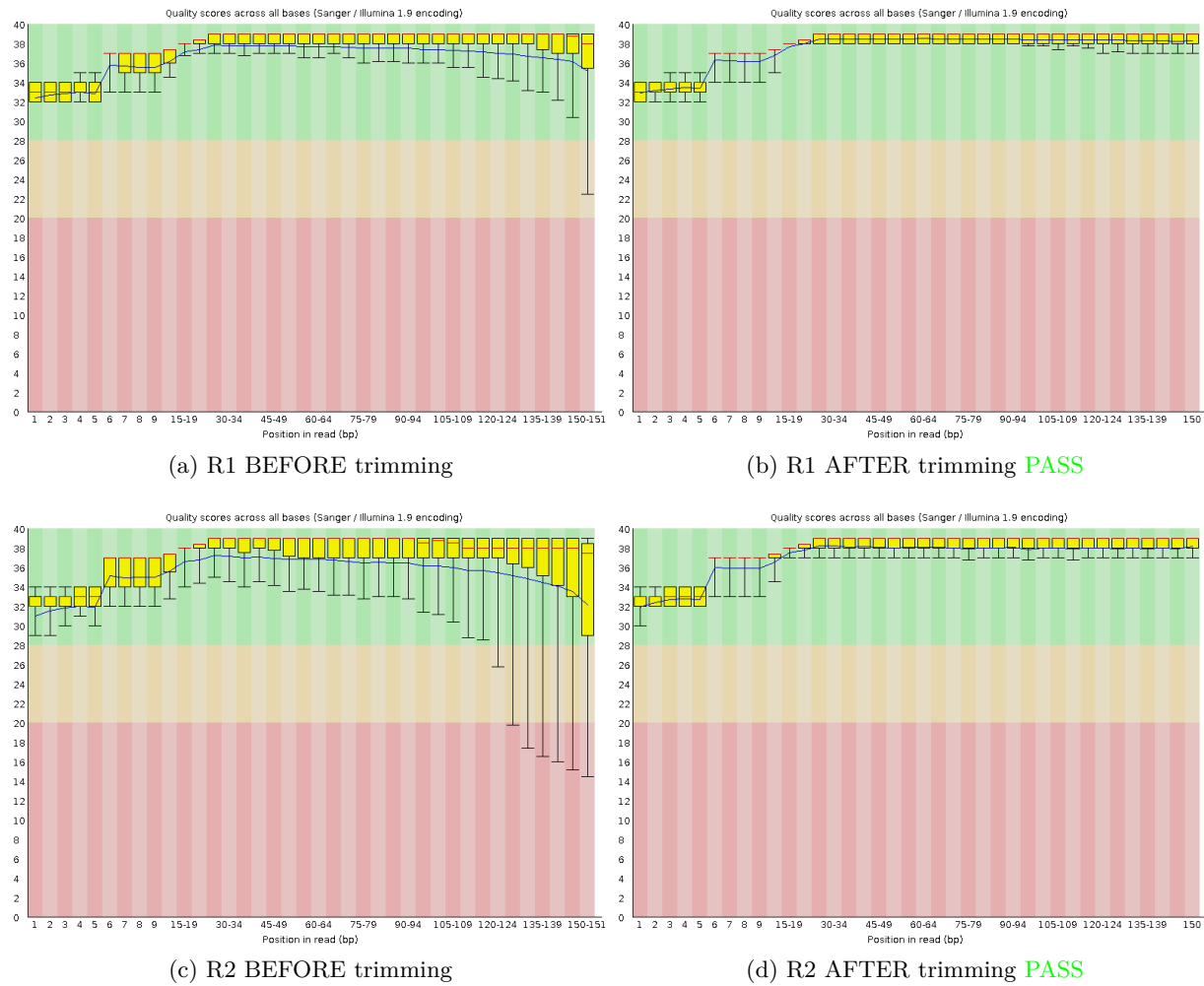


Figure 2: Per sequence GC content

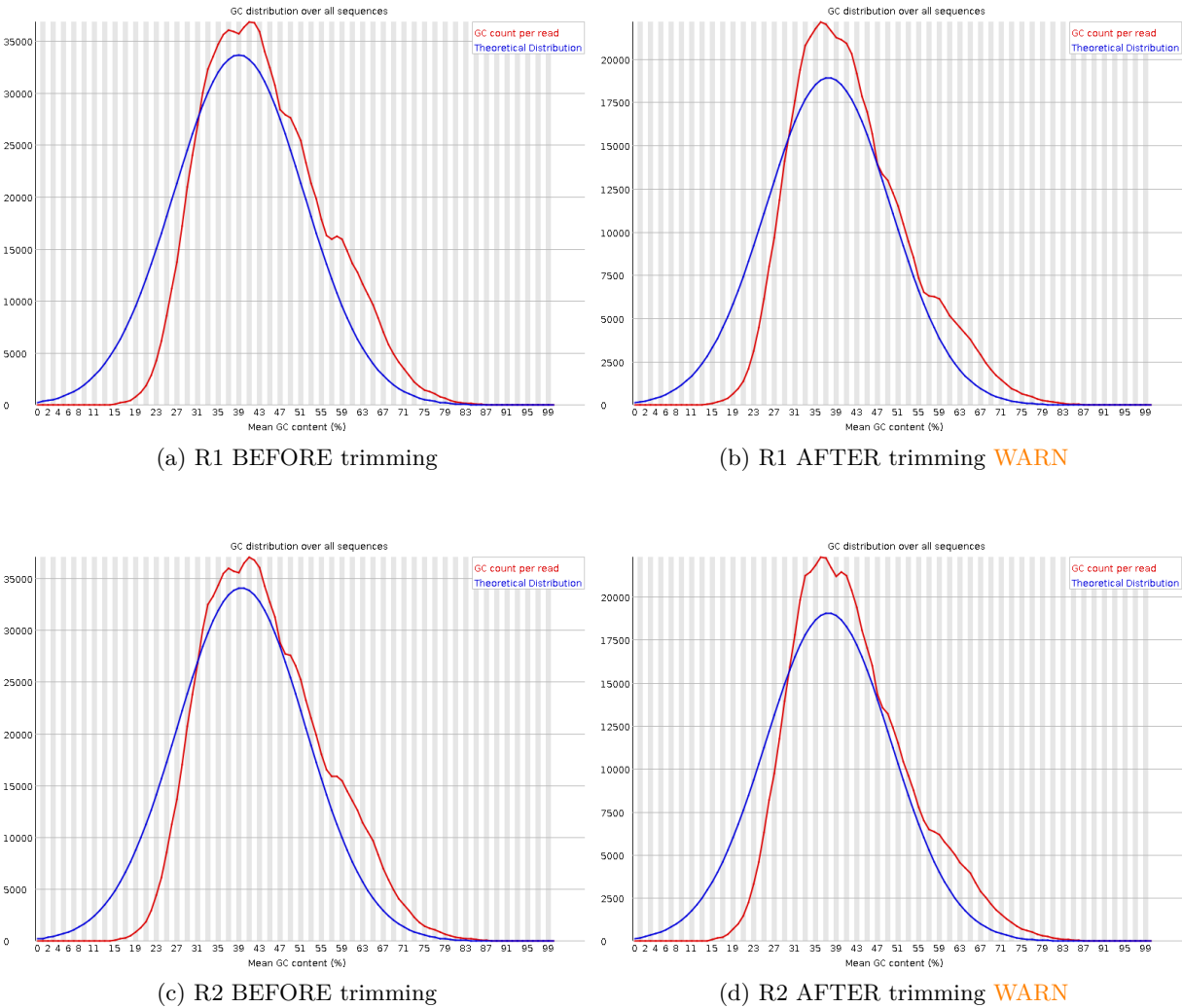
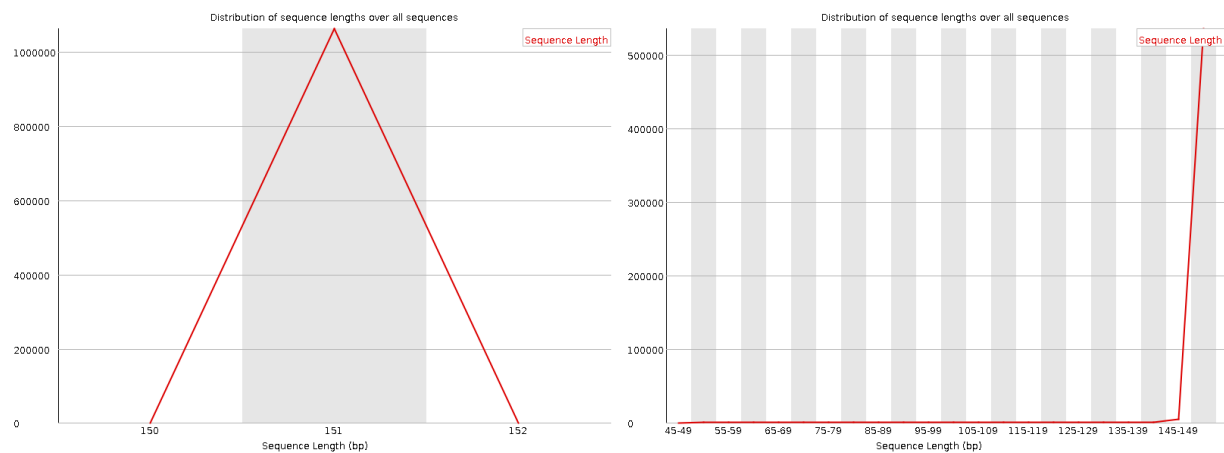
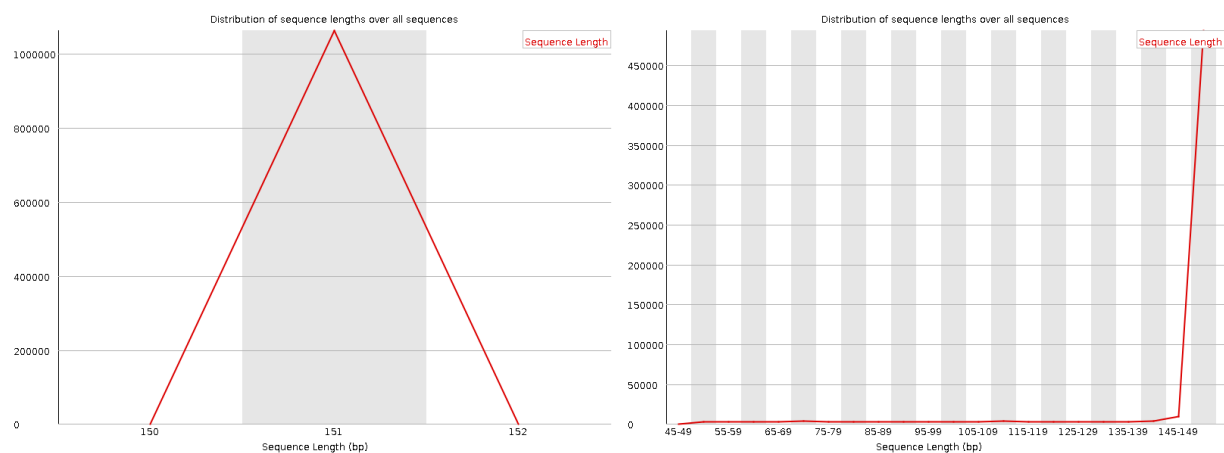


Figure 3: Sequence Length Distribution



(a) R1 BEFORE trimming

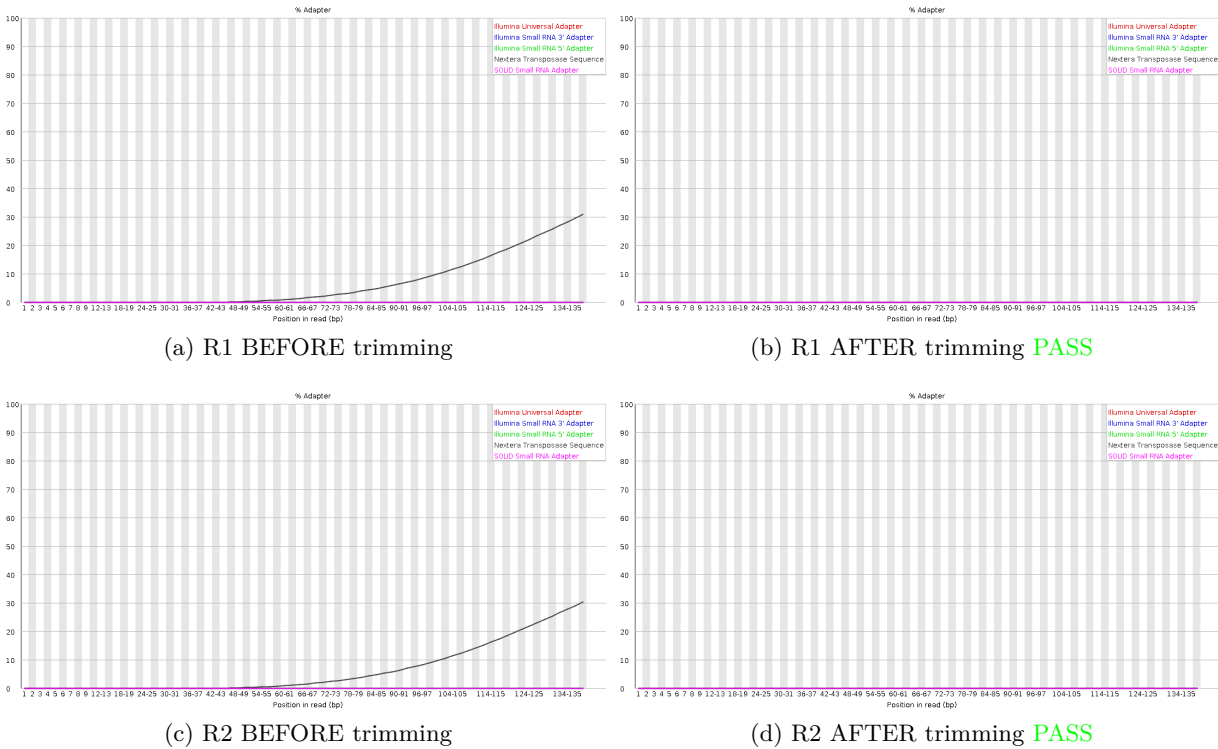
(b) R1 AFTER trimming **WARN**



(c) R2 BEFORE trimming

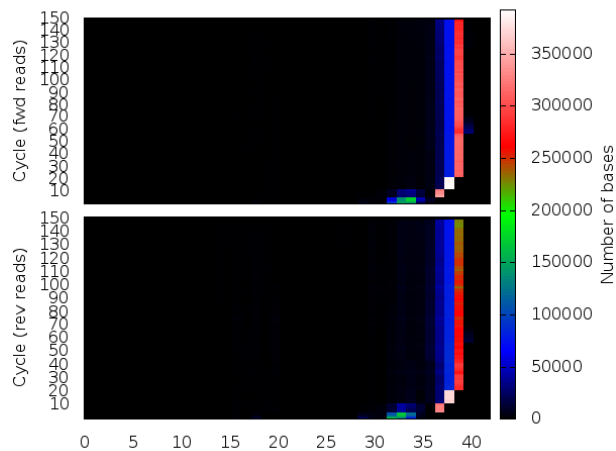
(d) R2 AFTER trimming **WARN**

Figure 4: Adapter Content



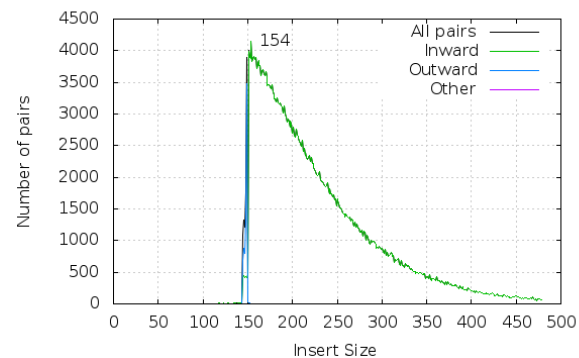
### 3 BamStats

4183-CS-Nextera-Myeloid-Val1-Repeat\_S10\_L001\_.bwa.drm.sorted.bam.sta



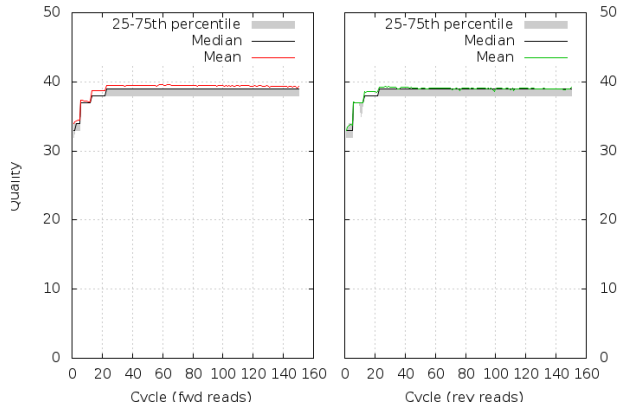
(a) Base quality per cycle

D15-04183-CS-Nextera-Myeloid-Val1-Repeat\_S10\_L001\_.bwa.drm.sorted.b



(b) Fragment size

10-D15-04183-CS-Nextera-Myeloid-Val1-Repeat\_S10\_L001\_.bwa.drm.sorted.bam.stats



(c) Quality per cycle