

Sample Quality Results

1 Basic Statistics

Sample: 14-D14-45300-CB-Nextera-Myeloid-Val1-Repeat_S14_L001

File type: Conventional base calls

Encoding: Sanger / Illumina 1.9

	Before trimming	After trimming
Total Sequences	624614	344026
Sequences flagged as poor quality	0	0
Sequence length	151	50-150
%GC	43	40

2 FastQC

Figure 1: Per base sequence quality

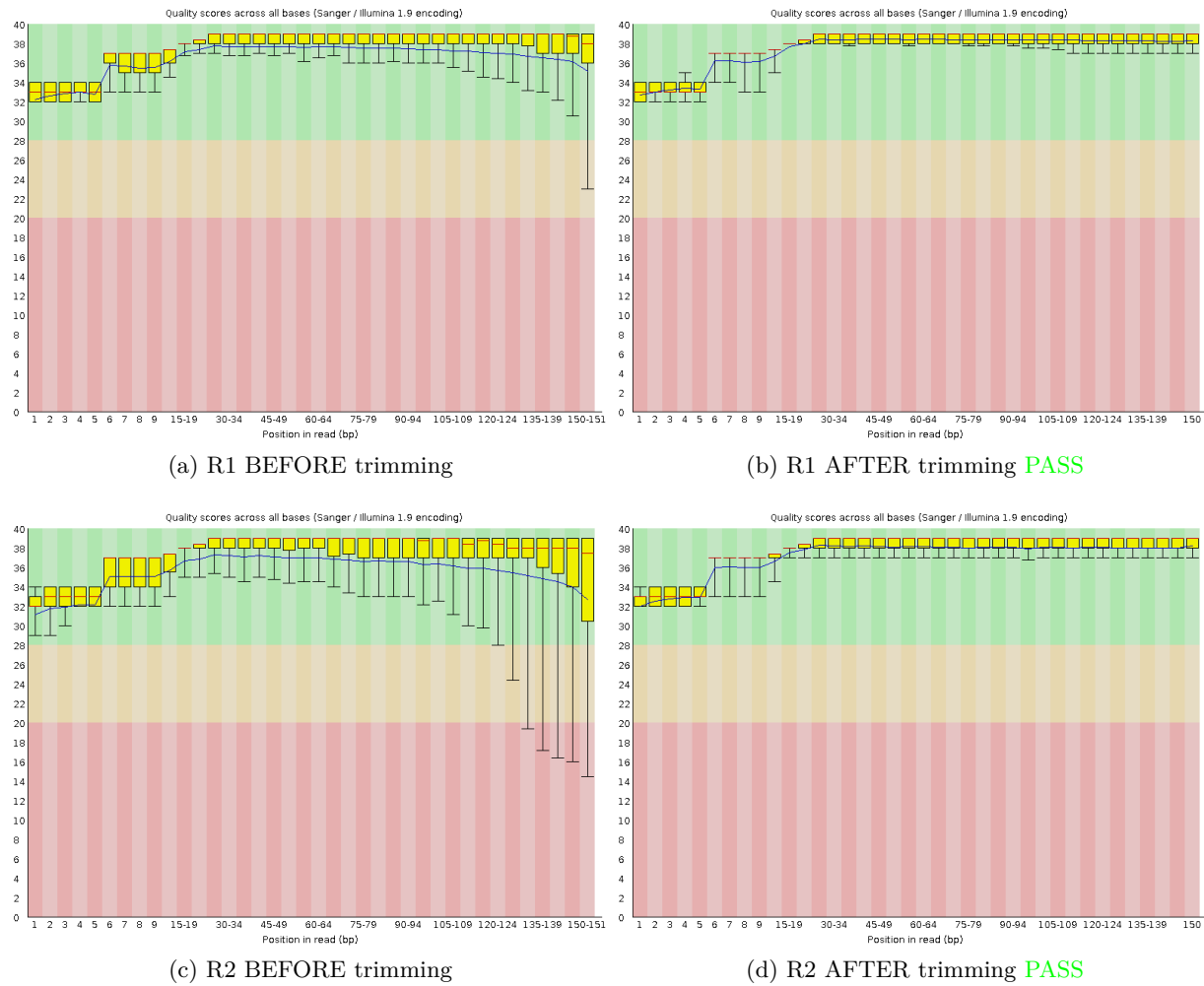
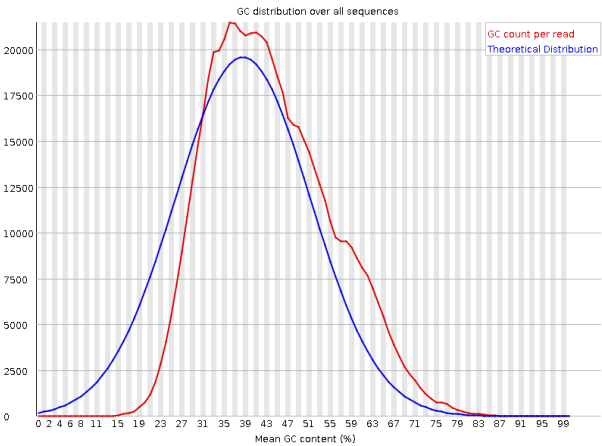
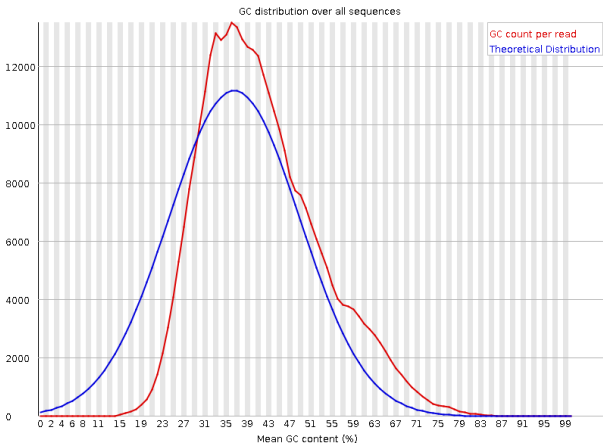


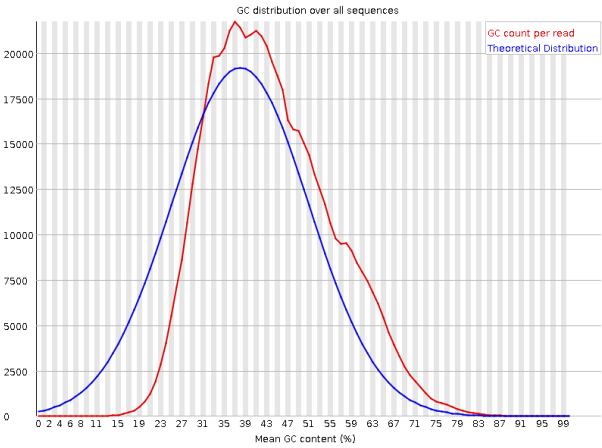
Figure 2: Per sequence GC content



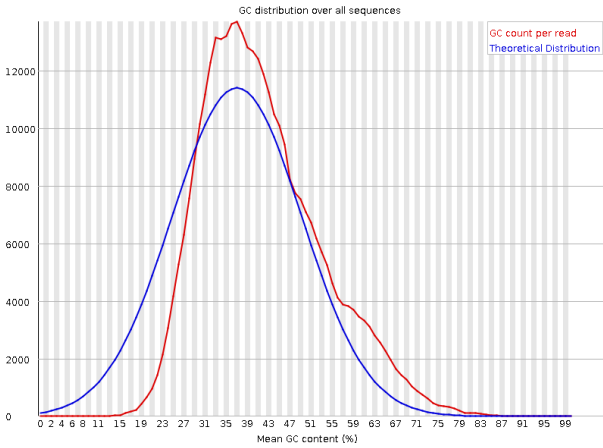
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **FAIL**

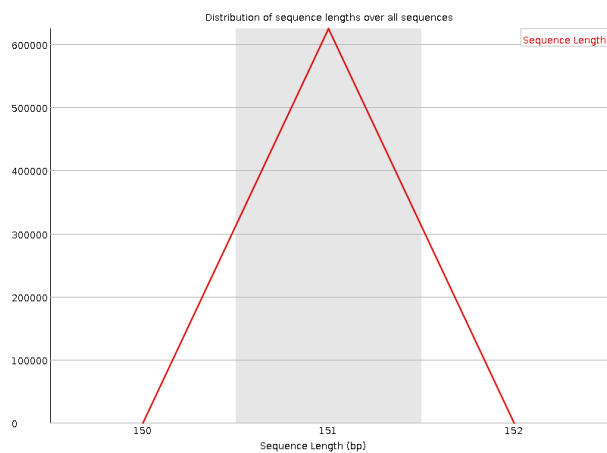


(c) R2 BEFORE trimming

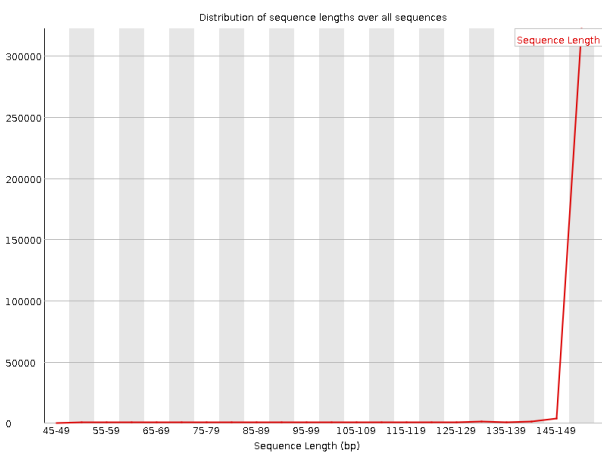


(d) R2 AFTER trimming **FAIL**

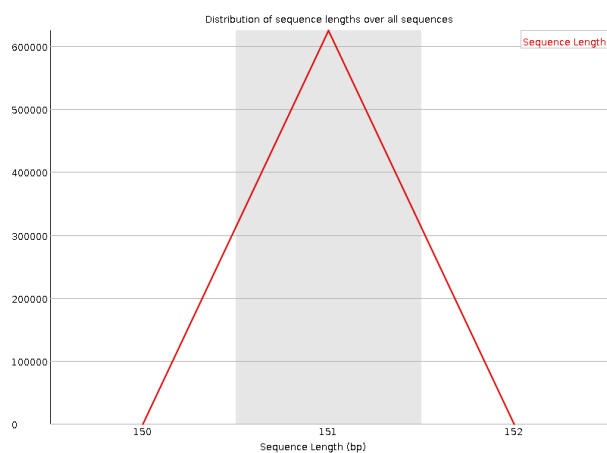
Figure 3: Sequence Length Distribution



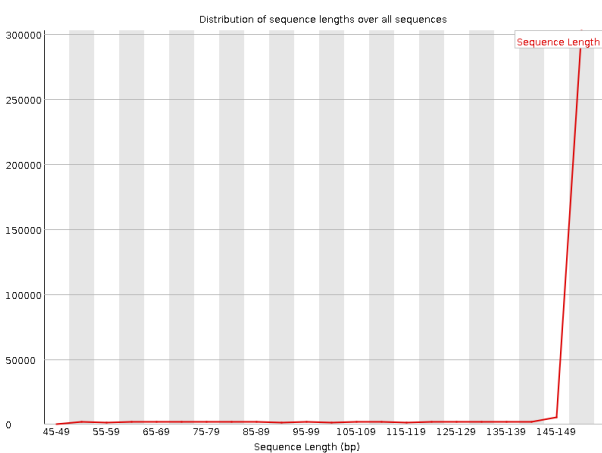
(a) R1 BEFORE trimming



(b) R1 AFTER trimming **WARN**

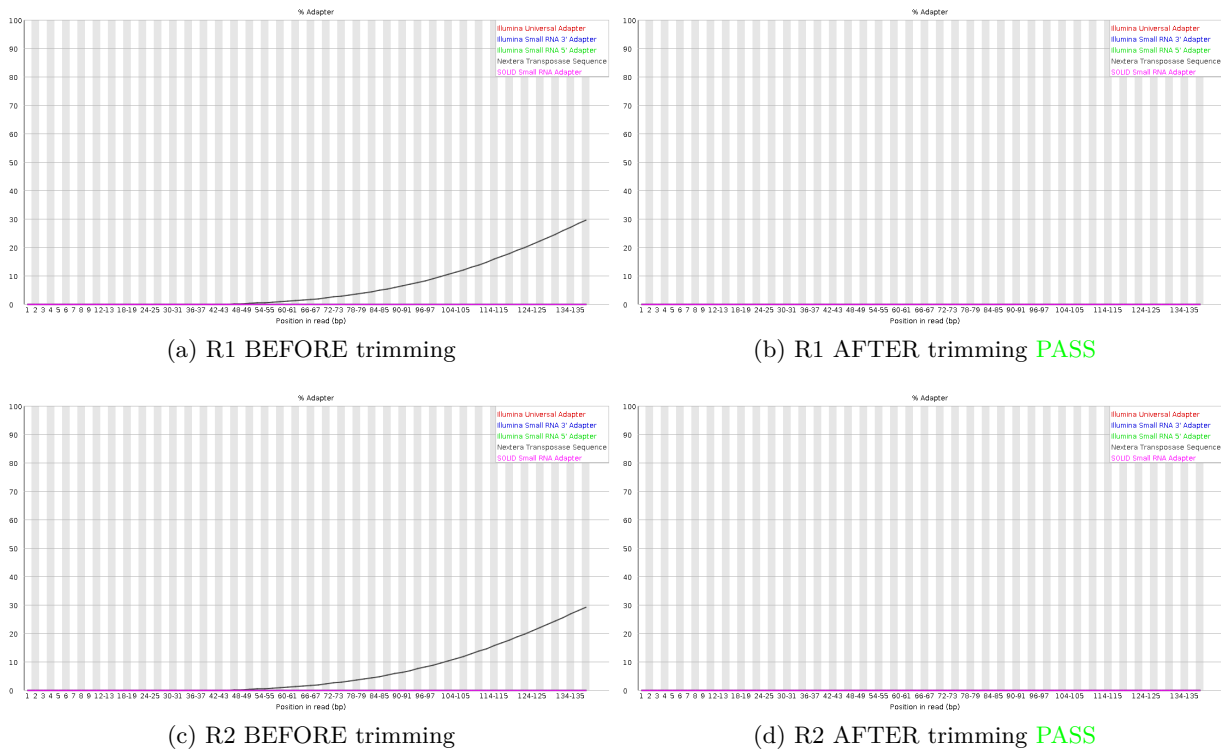


(c) R2 BEFORE trimming

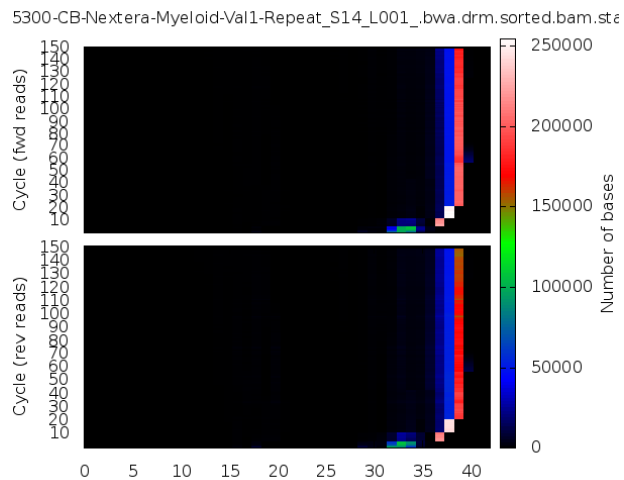


(d) R2 AFTER trimming **WARN**

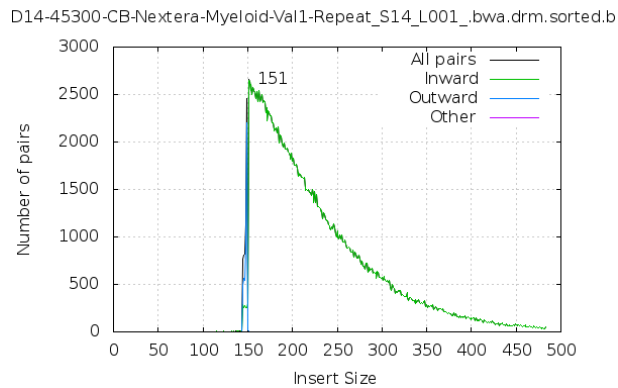
Figure 4: Adapter Content



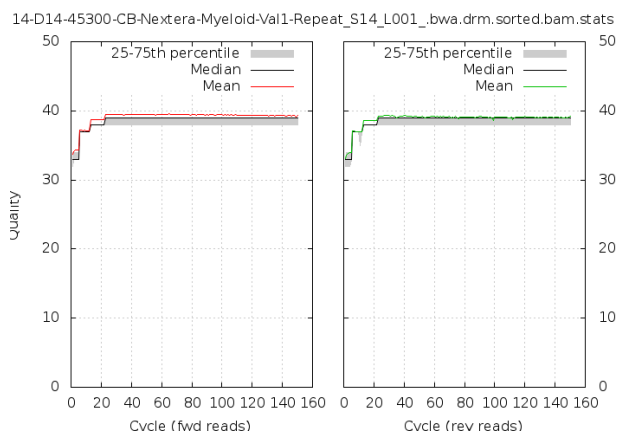
3 BamStats



(a) Base quality per cycle



(b) Fragment size



(c) Quality per cycle