Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/08/17 06:00:38

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam results/mapped/q10/hiv.sorted.dedup.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa mem data/reference.fasta data/miseq/SRR961514_1.fastq data/miseq/SRR961514_2.fastq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 17 06:00:38 EDT 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	results/mapped/q10/hiv.sorted.dedup.bam

2. Summary

2.1. Globals

Reference size	9,719
Number of reads	664,162
Mapped reads	664,155 / 100%
Unmapped reads	7 / 0%
Mapped paired reads	664,155 / 100%
Mapped reads, first in pair	331,716 / 49.95%
Mapped reads, second in pair	332,439 / 50.05%
Mapped reads, both in pair	664,154 / 100%
Mapped reads, singletons	1 / 0%
Secondary alignments	0
Supplementary alignments	7,479 / 1.13%
Read min/max/mean length	30 / 251 / 213.87
Duplicated reads (estimated)	655,075 / 98.63%
Duplication rate	97.92%
Clipped reads	133,380 / 20.08%

2.2. ACGT Content

Number/percentage of A's	50,130,024 / 36.69%
Number/percentage of C's	23,785,718 / 17.41%
Number/percentage of T's	30,109,656 / 22.04%
Number/percentage of G's	32,590,410 / 23.86%
Number/percentage of N's	12,694 / 0.01%

GC Percentage	41.27%

2.3. Coverage

Mean	14,087.0627
Standard Deviation	6,017.9624

2.4. Mapping Quality

Mean Mapping Quality	57.54

2.5. Insert size

Mean	350.66
Standard Deviation	347.82
P25/Median/P75	185 / 297 / 443

2.6. Mismatches and indels

General error rate	4.05%
Mismatches	5,229,973
Insertions	47,028
Mapped reads with at least one insertion	6.53%
Deletions	72,601
Mapped reads with at least one deletion	8.65%
Homopolymer indels	55.9%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

		bases	coverage	deviation
K03455.1	9719	136912162	14,087.0627	6,017.9624

3. Results : Coverage across reference

Coverage across reference
hiv.sorted.dedup.bam

4. Results : Coverage Histogram

Coverage Histogram
hiv.sorted.dedup.bam
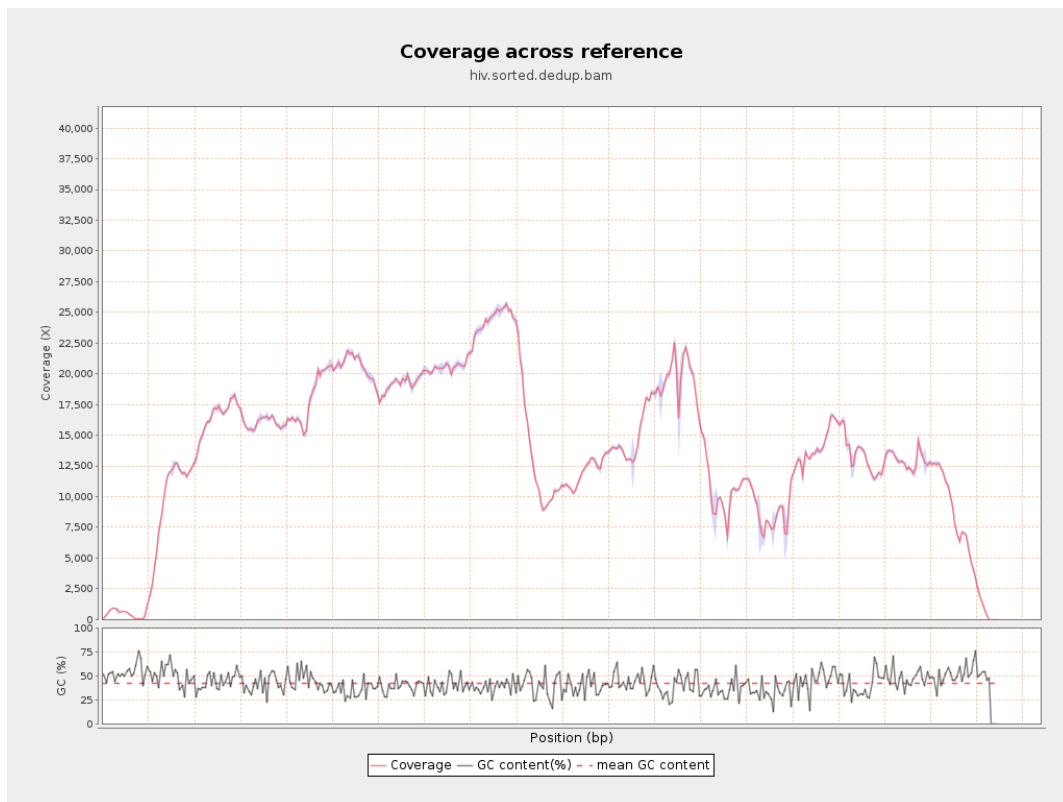
5. Results : Coverage Histogram (0-50X)
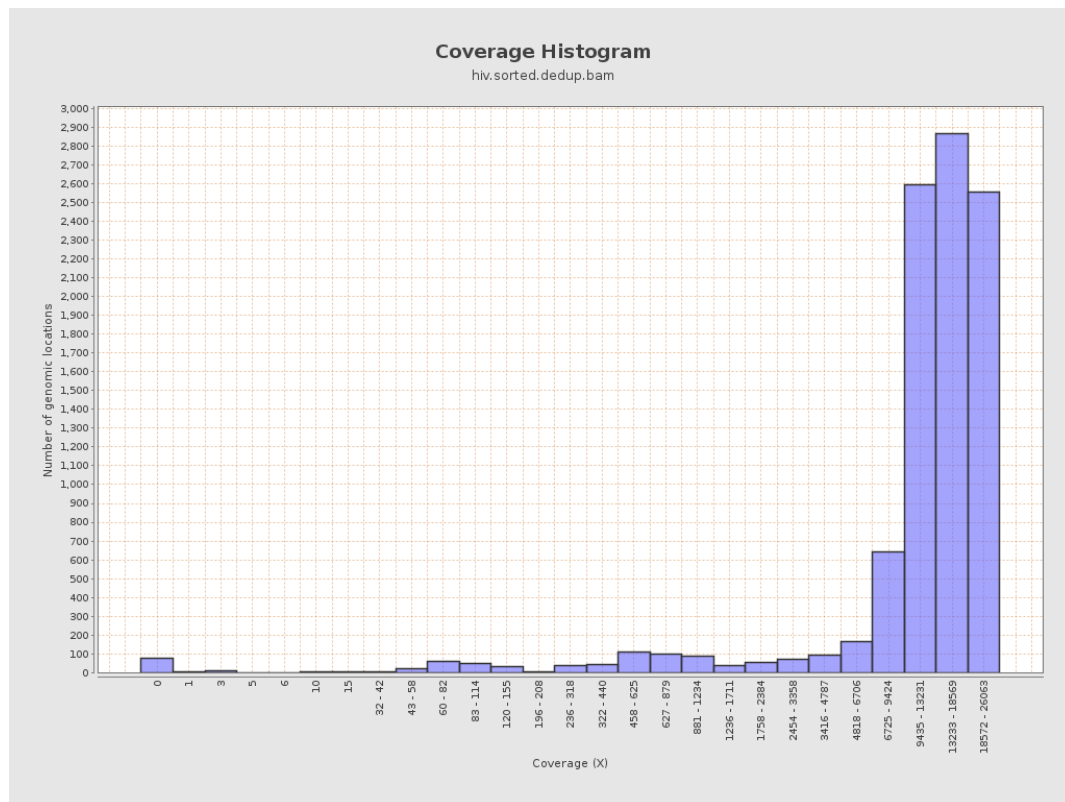
Coverage Histogram (0-50X)
hiv.sorted.dedup.bam
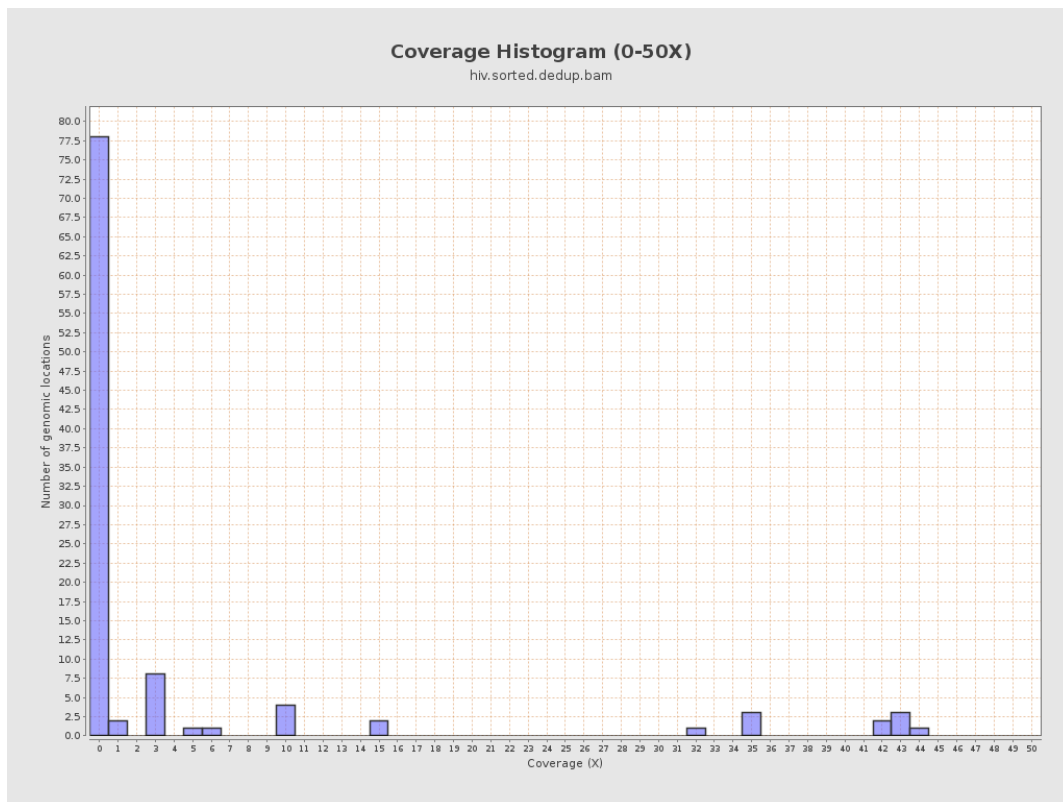
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
hiv.sorted.dedup.bam
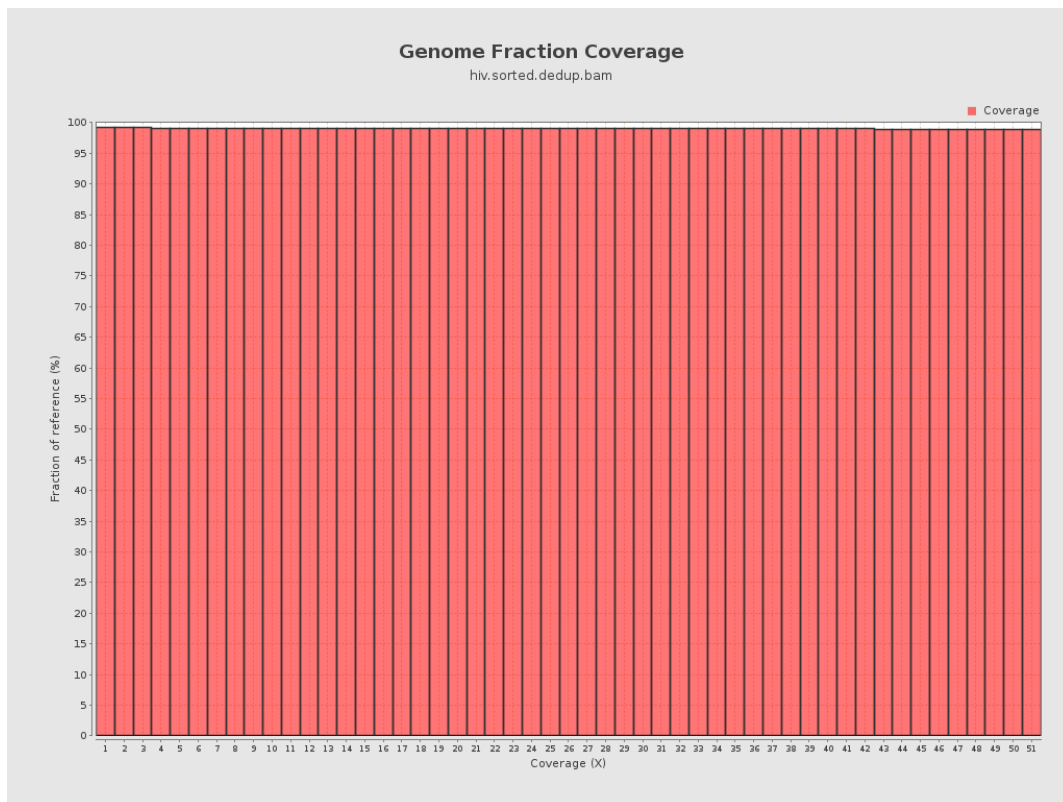
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
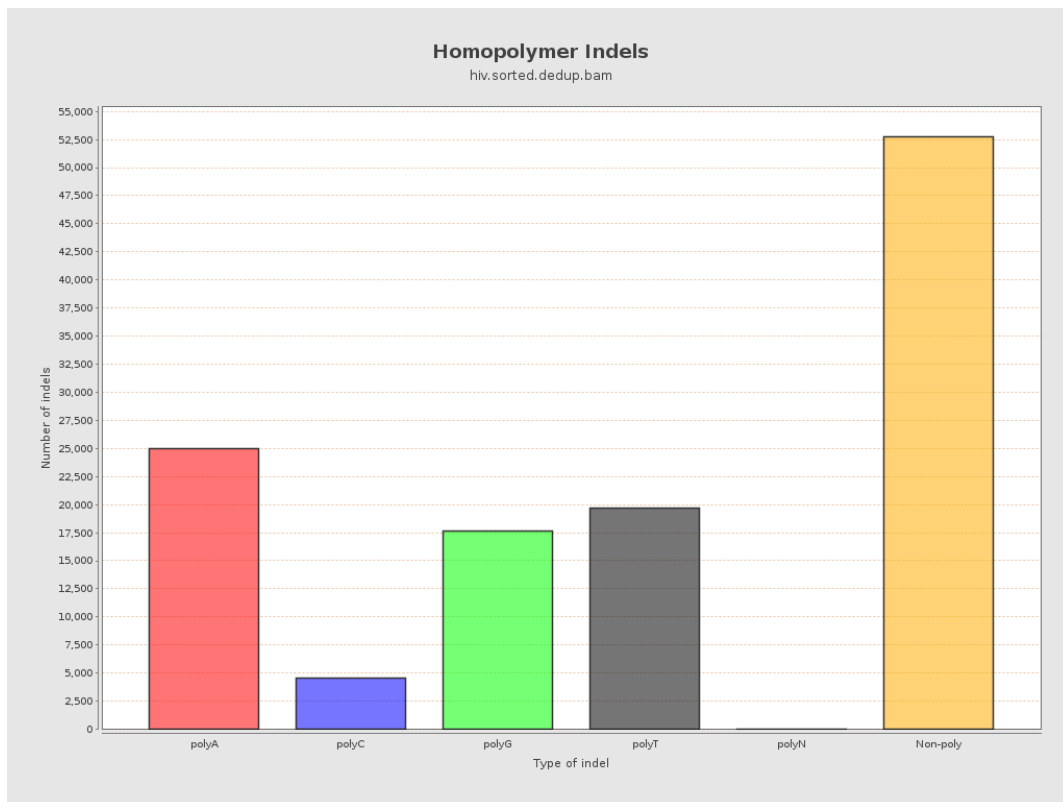hiv.sorted.dedup.bam
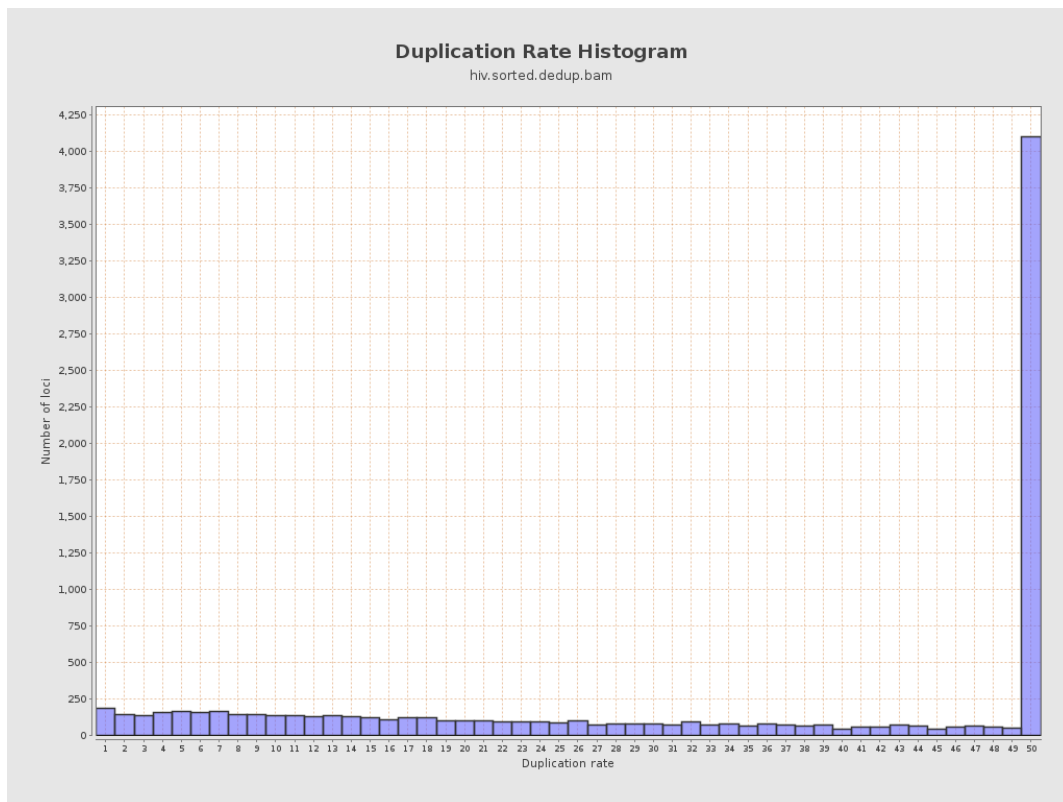
8. Results : Mapped Reads Nucleotide Content
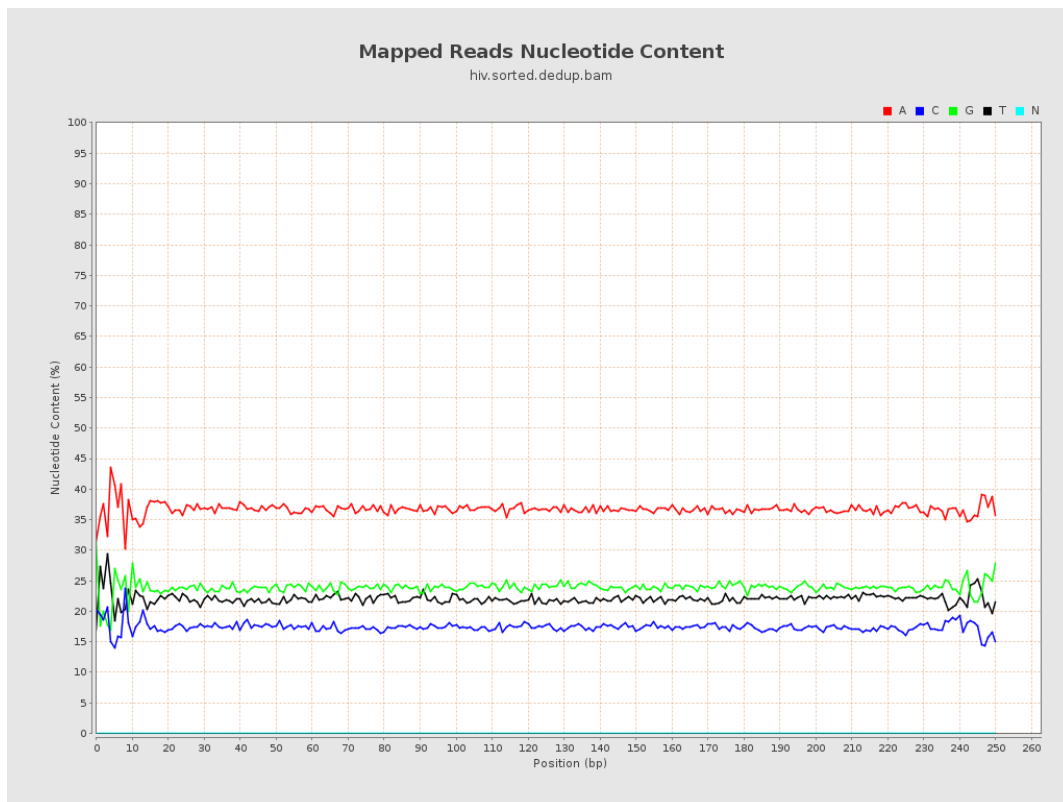
9. Results : Mapped Reads GC-content Distribution
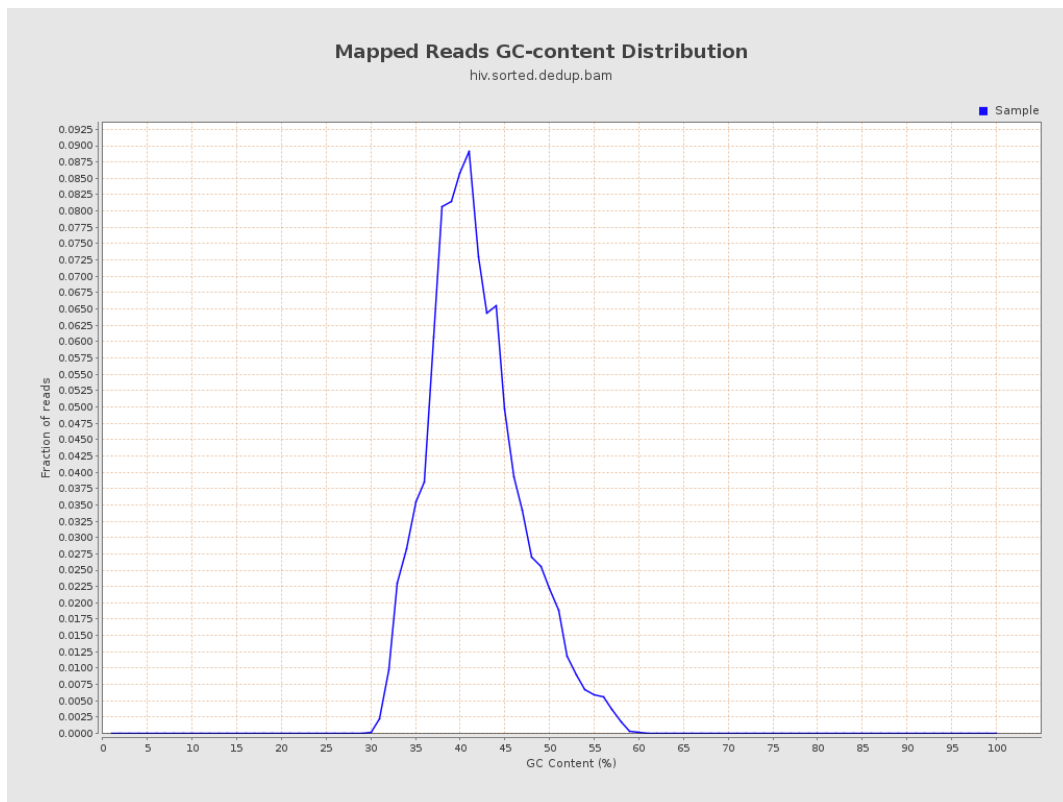
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
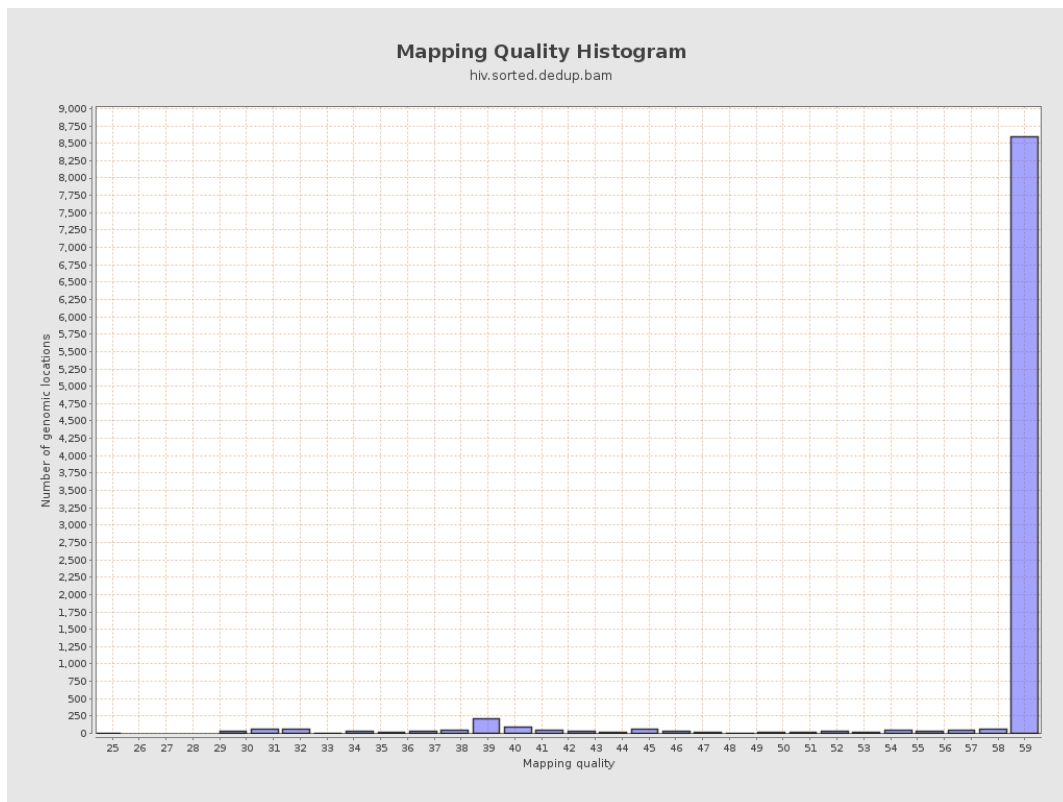hiv.sorted.dedup.bam
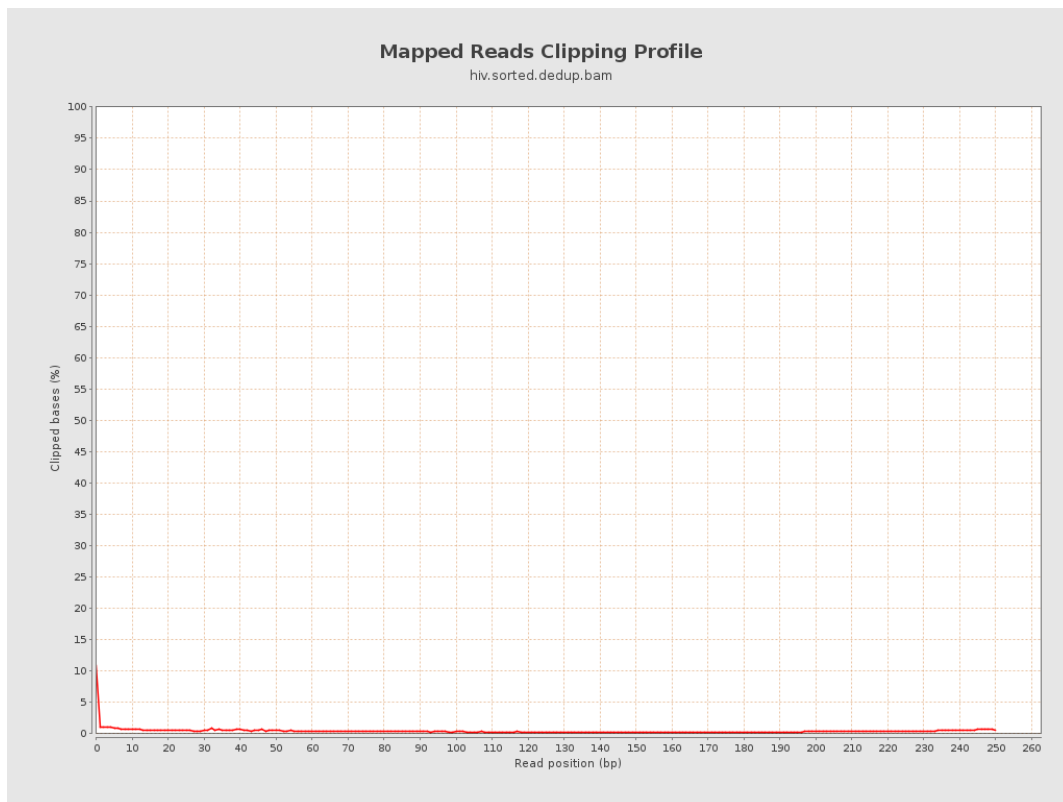
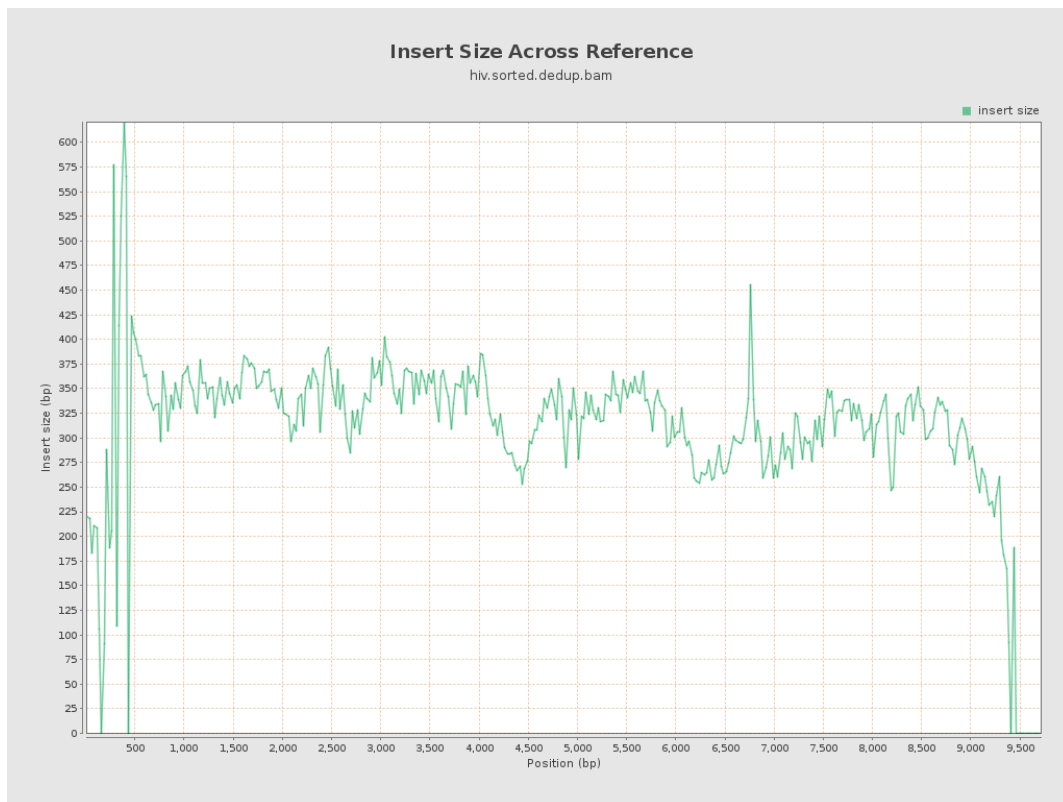# 11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference
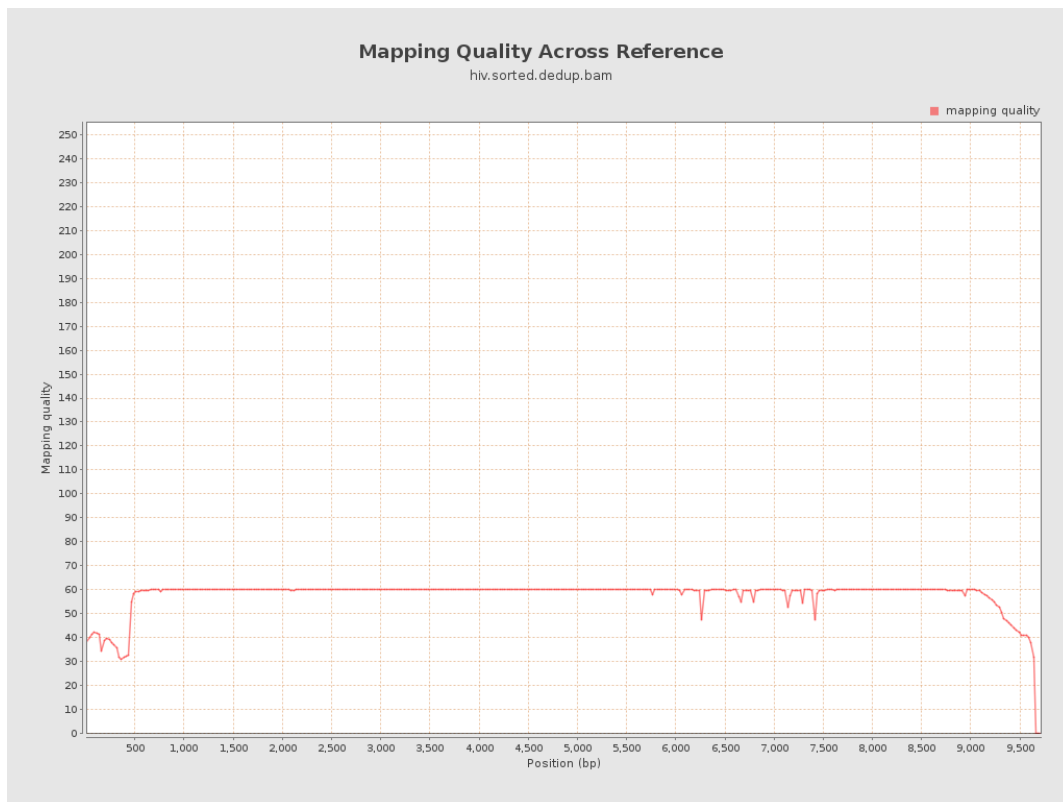
13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram