Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/08/17 06:01:09

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam results/mapped/q30/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 06:01:08 EDT 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	results/mapped/q30/hiv.sorted.dedup.bam

2. Summary

2.1. Globals

Reference size	9,719
Number of reads	662,117
Mapped reads	662,109 / 100%
Unmapped reads	8 / 0%
Mapped paired reads	662,109 / 100%
Mapped reads, first in pair	330,755 / 49.95%
Mapped reads, second in pair	331,354 / 50.04%
Mapped reads, both in pair	662,108 / 100%
Mapped reads, singletons	1 / 0%
Secondary alignments	0
Supplementary alignments	7,051 / 1.06%
Read min/max/mean length	30 / 251 / 213.93
Duplicated reads (estimated)	653,070 / 98.63%
Duplication rate	98.01%
Clipped reads	132,144 / 19.96%

2.2. ACGT Content

Number/percentage of A's	50,039,164 / 36.71%
Number/percentage of C's	23,716,771 / 17.4%
Number/percentage of T's	30,039,714 / 22.04%
Number/percentage of G's	32,500,768 / 23.85%
Number/percentage of N's	12,471 / 0.01%

GC Percentage	41.25%

2.3. Coverage

Mean	14,054.0492
Standard Deviation	6,045.9557

2.4. Mapping Quality

Mean Mapping Quality	57.95

2.5. Insert size

Mean	349.11
Standard Deviation	336.4
P25/Median/P75	185 / 297 / 443

2.6. Mismatches and indels

General error rate	4.04%
Mismatches	5,208,516
Insertions	46,514
Mapped reads with at least one insertion	6.47%
Deletions	72,242
Mapped reads with at least one deletion	8.63%
Homopolymer indels	56.04%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

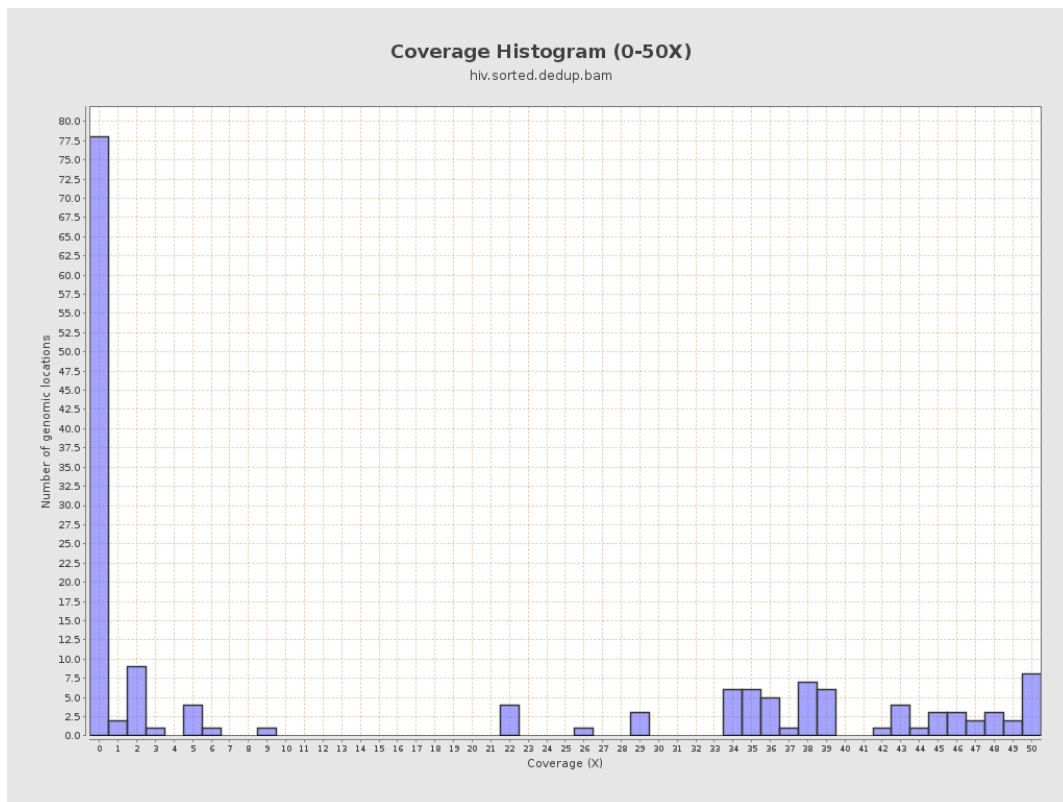|		bases	coverage	deviation
K03455.1	9719	136591304	14,054.0492	6,045.9557

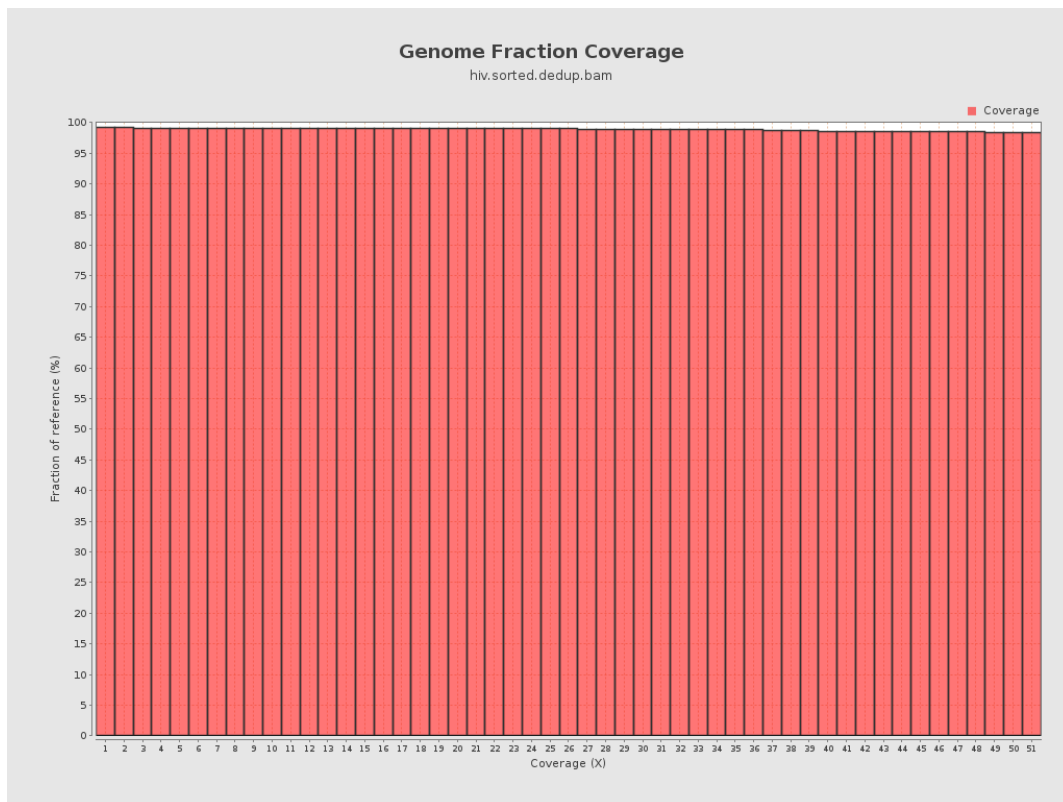# 3. Results : Coverage across reference

4. Results : Coverage Histogram

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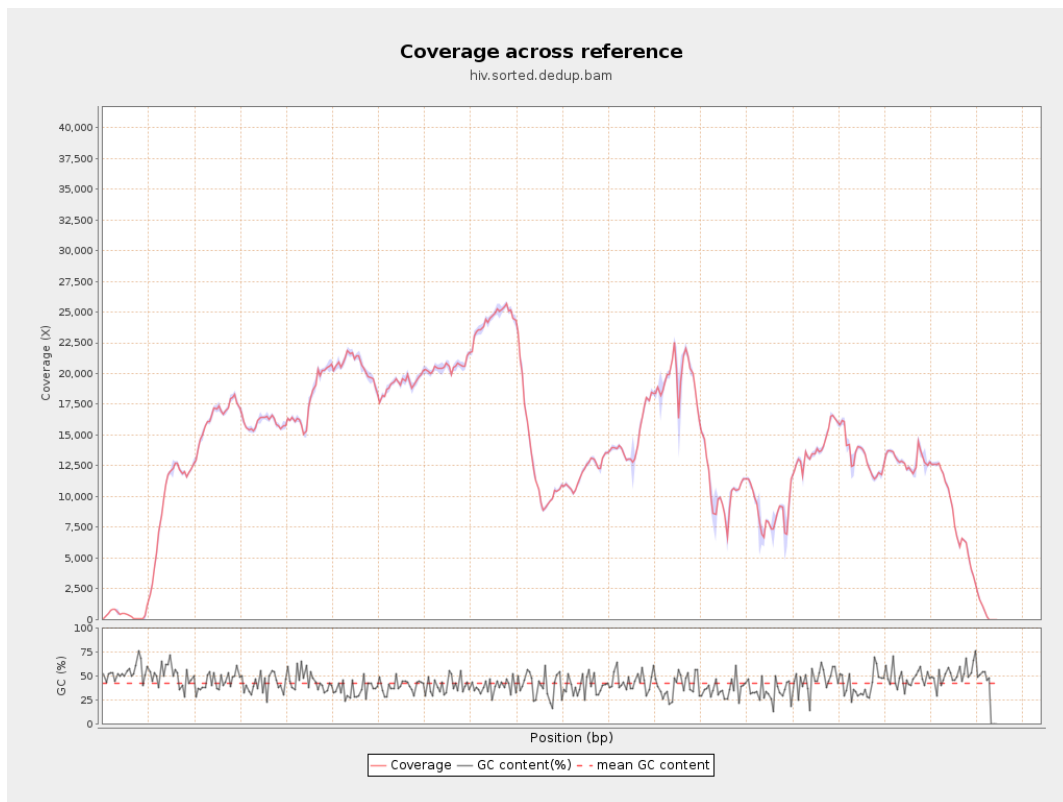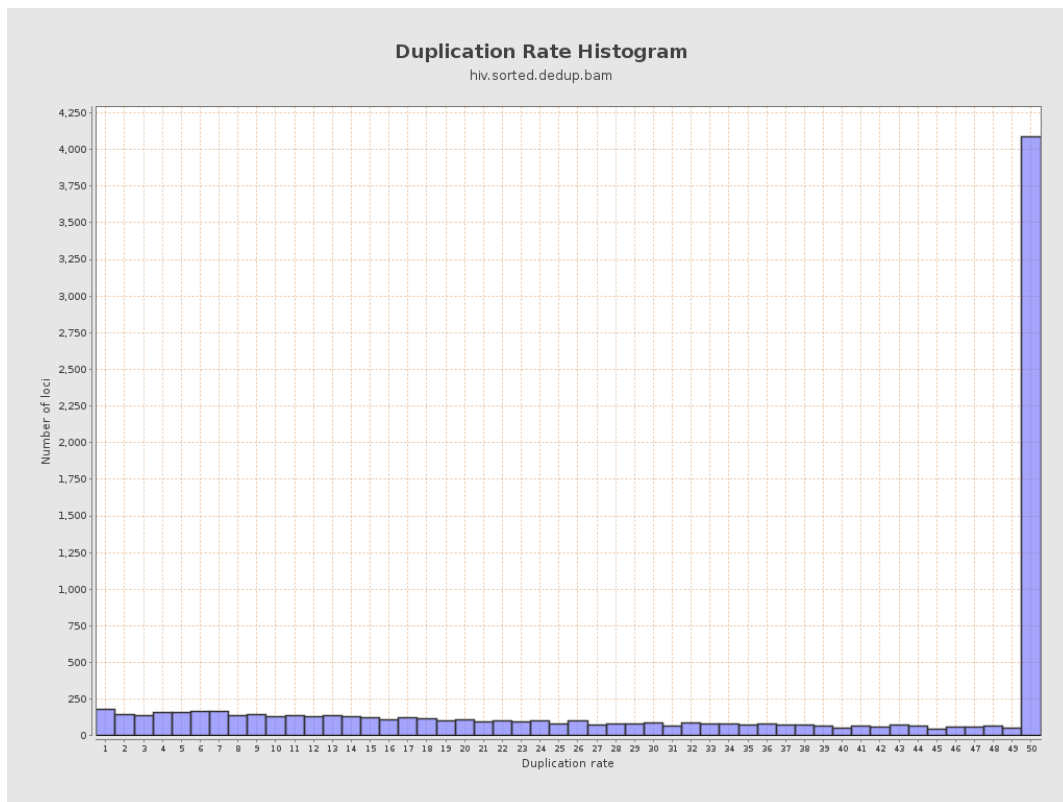
5. Results : Coverage Histogram (0-50X)
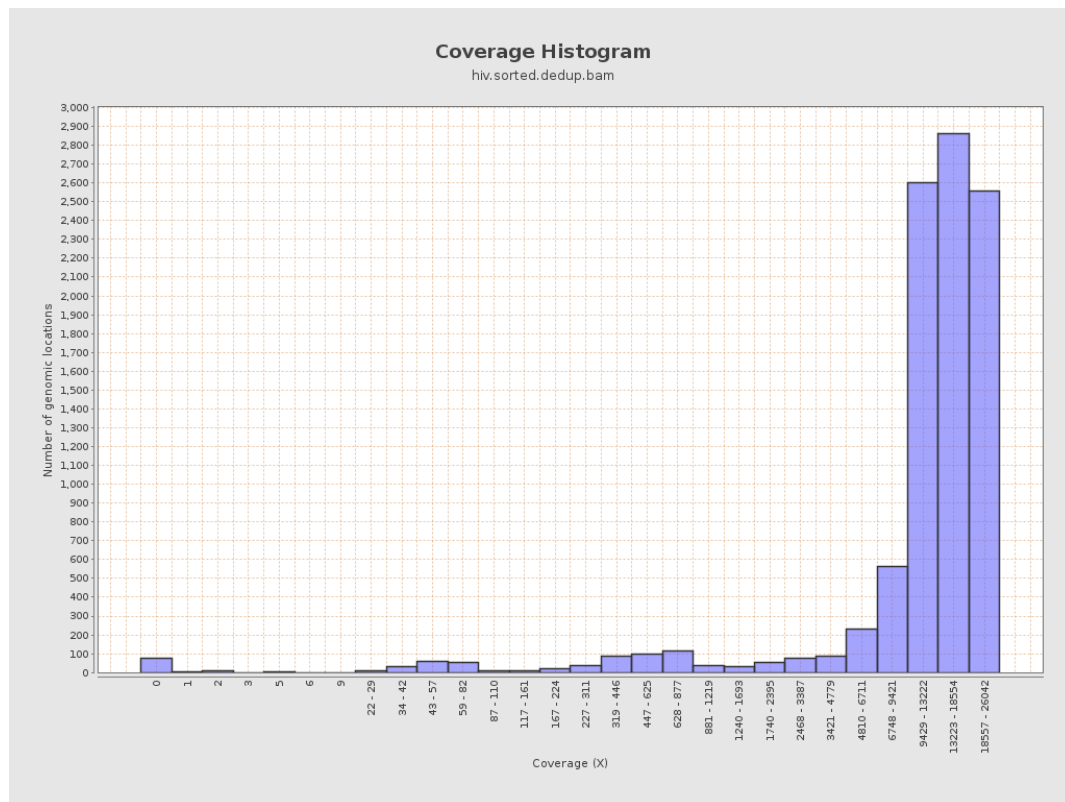
Coverage Histogram (0-50X)
hiv.sorted.dedup.bam

6. Results : Genome Fraction Coverage

Genome Fraction Coverage
hiv.sorted.dedup.bam

7. Results : Duplication Rate Histogram
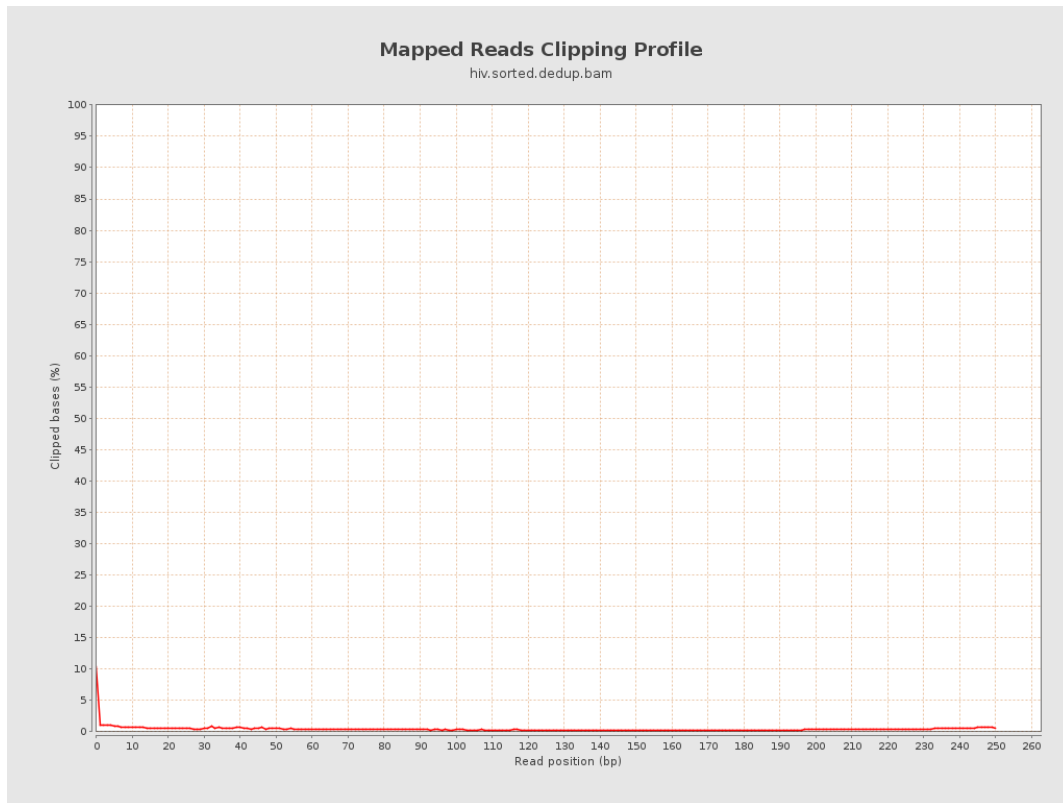

Duplication Rate Histogram
hiv.sorted.dedup.bam

8. Results : Mapped Reads Nucleotide Content
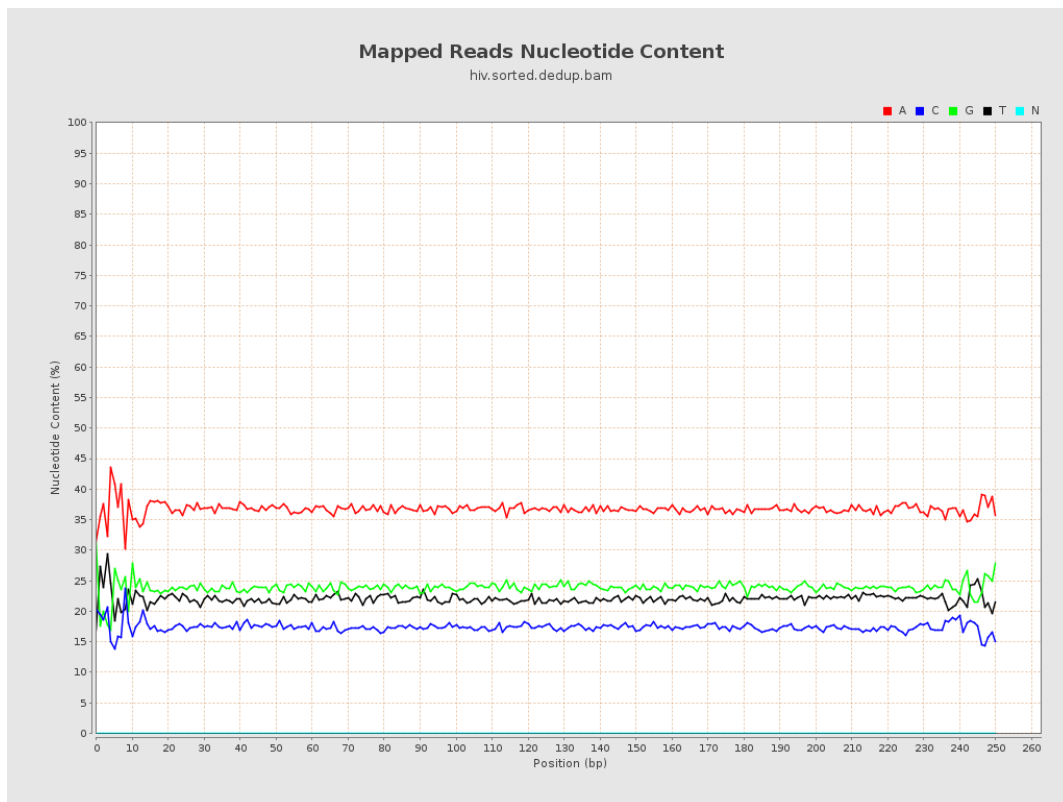
9. Results : Mapped Reads GC-content Distribution
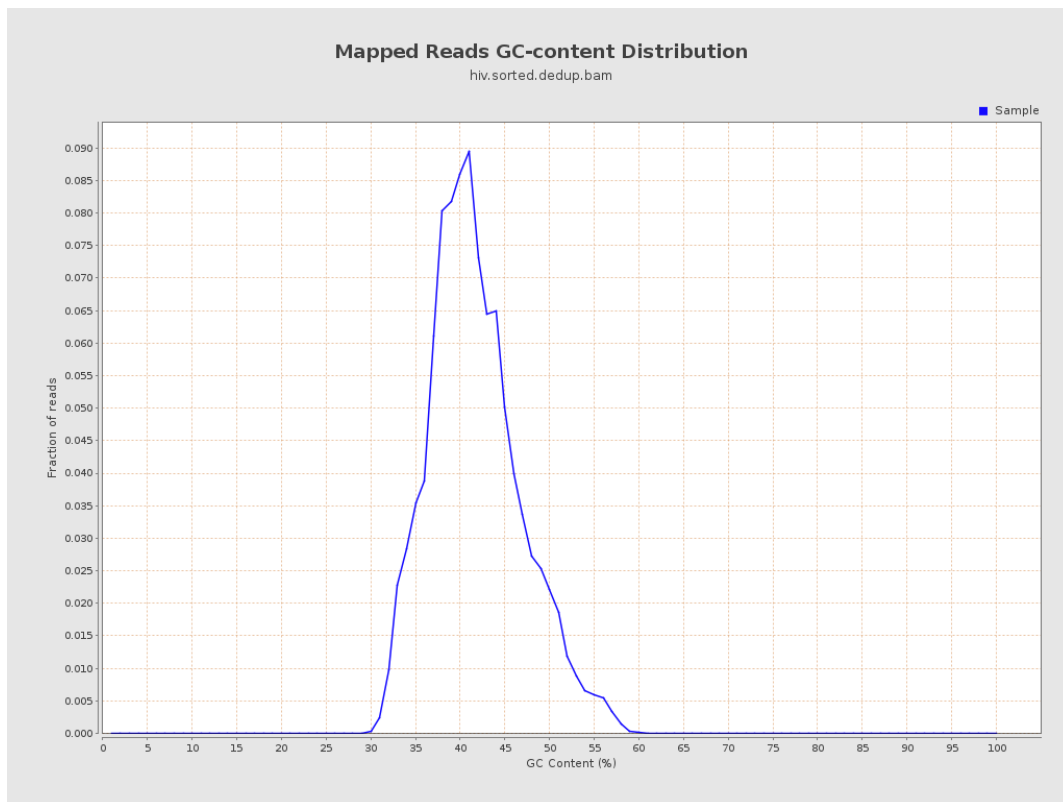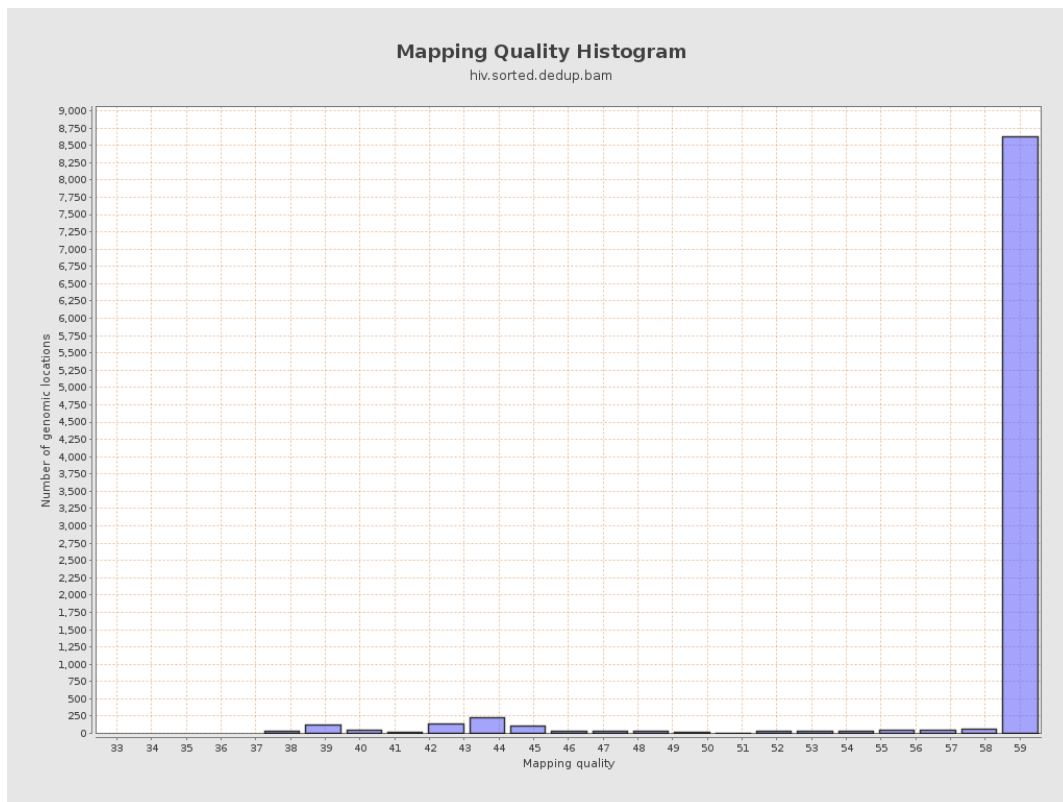
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
hiv.sorted.dedup.bam

11. Results : Homopolymer Indels
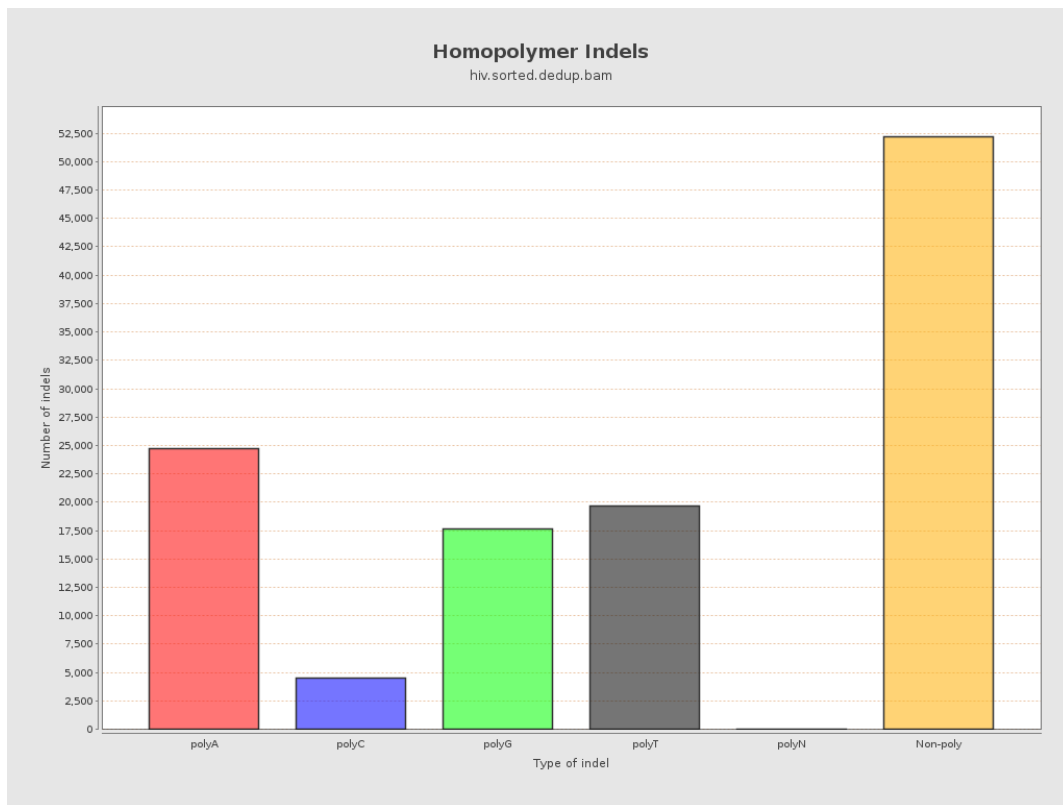
Homopolymer Indels
hiv.sorted.dedup.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
hiv.sorted.dedup.bam

13. Results : Mapping Quality Histogram
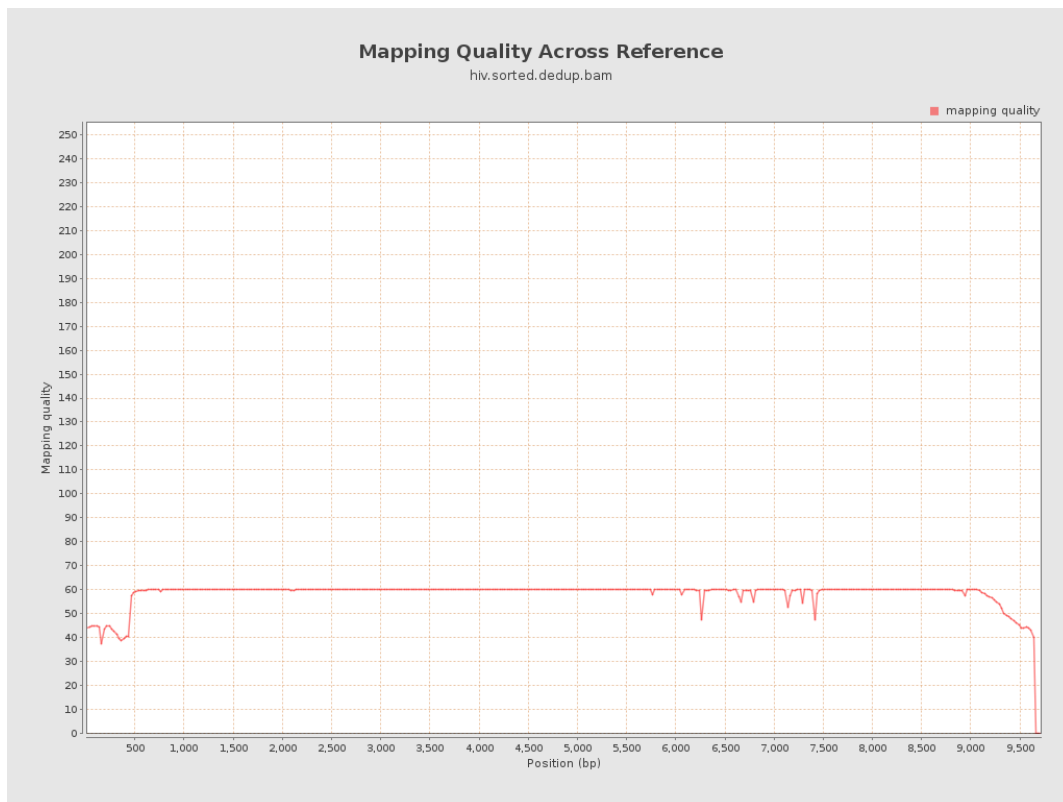
Mapping Quality Histogram
hiv.sorted.dedup.bam

14. Results : Insert Size Across Reference
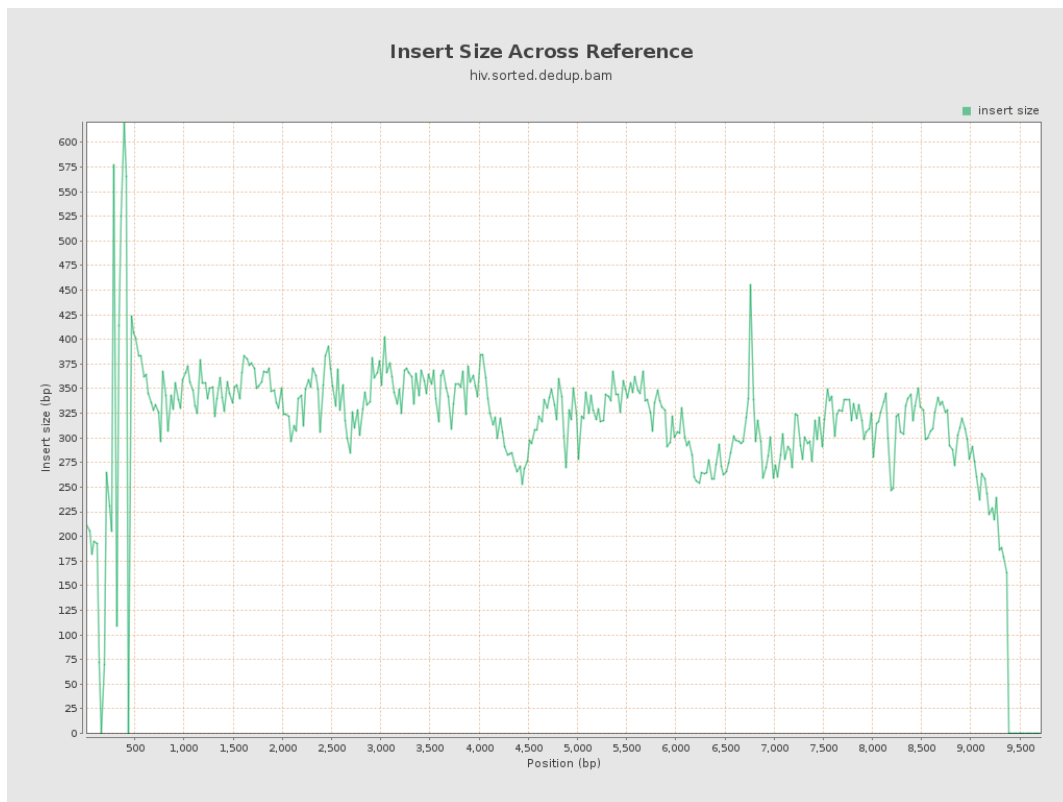
15. Results : Insert Size Histogram