

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/08/17 06:01:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam results/mapped/q0/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 06:01:03 EDT 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	results/mapped/q0/hiv.sorted.dedup.b am

2. Summary

2.1. Globals

Reference size	9,719
Number of reads	675,303
Mapped reads	669,451 / 99.13%
Unmapped reads	5,852 / 0.87%
Mapped paired reads	669,451 / 99.13%
Mapped reads, first in pair	334,355 / 49.51%
Mapped reads, second in pair	335,096 / 49.62%
Mapped reads, both in pair	669,442 / 99.13%
Mapped reads, singletons	9 / 0%
Secondary alignments	0
Supplementary alignments	7,889 / 1.17%
Read min/max/mean length	30 / 251 / 212.14
Duplicated reads (estimated)	660,116 / 97.75%
Duplication rate	98.14%
Clipped reads	135,381 / 20.05%

2.2. ACGT Content

Number/percentage of A's	50,296,537 / 36.63%
Number/percentage of C's	23,953,177 / 17.44%
Number/percentage of T's	30,271,844 / 22.04%
Number/percentage of G's	32,799,129 / 23.89%
Number/percentage of N's	12,786 / 0.01%

GC Percentage	41.33%
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2.3. Coverage

Mean	14,159.747
Standard Deviation	5,895.0338

2.4. Mapping Quality

Mean Mapping Quality	55.96
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2.5. Insert size

Mean	353.67
Standard Deviation	388.13
P25/Median/P75	183 / 296 / 443

2.6. Mismatches and indels

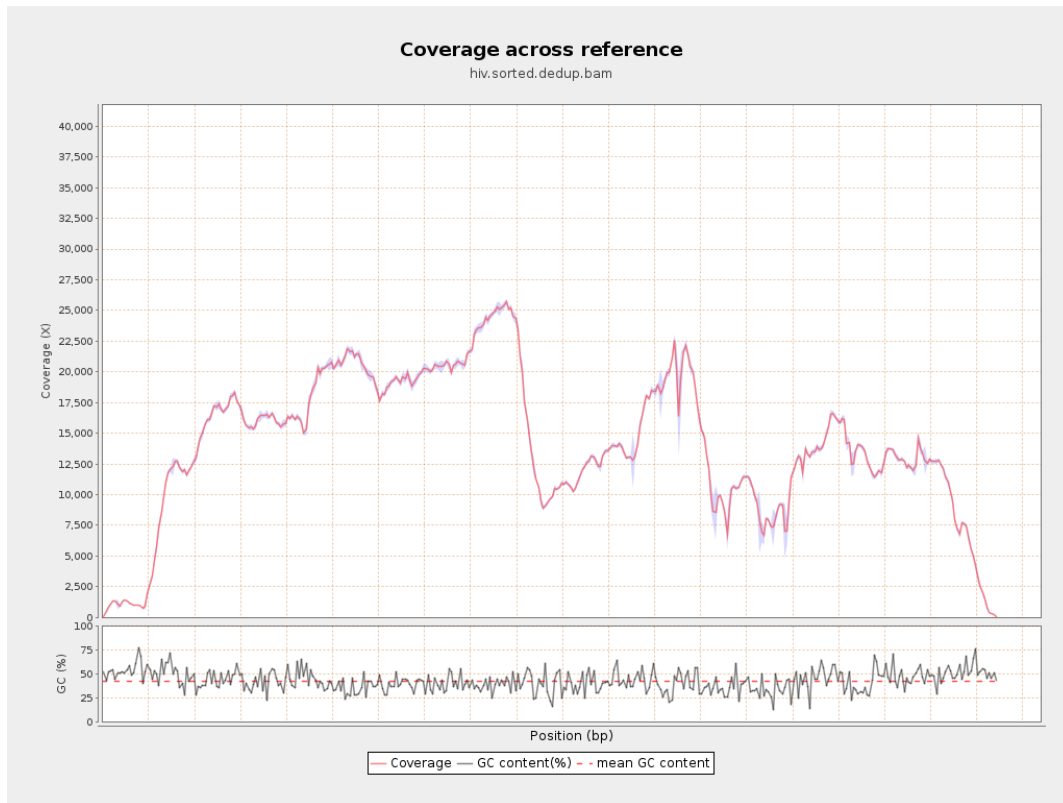
General error rate	4.05%
Mismatches	5,259,697
Insertions	47,642
Mapped reads with at least one insertion	6.57%
Deletions	73,012
Mapped reads with at least one deletion	8.64%
Homopolymer indels	55.59%

2.7. Chromosome stats

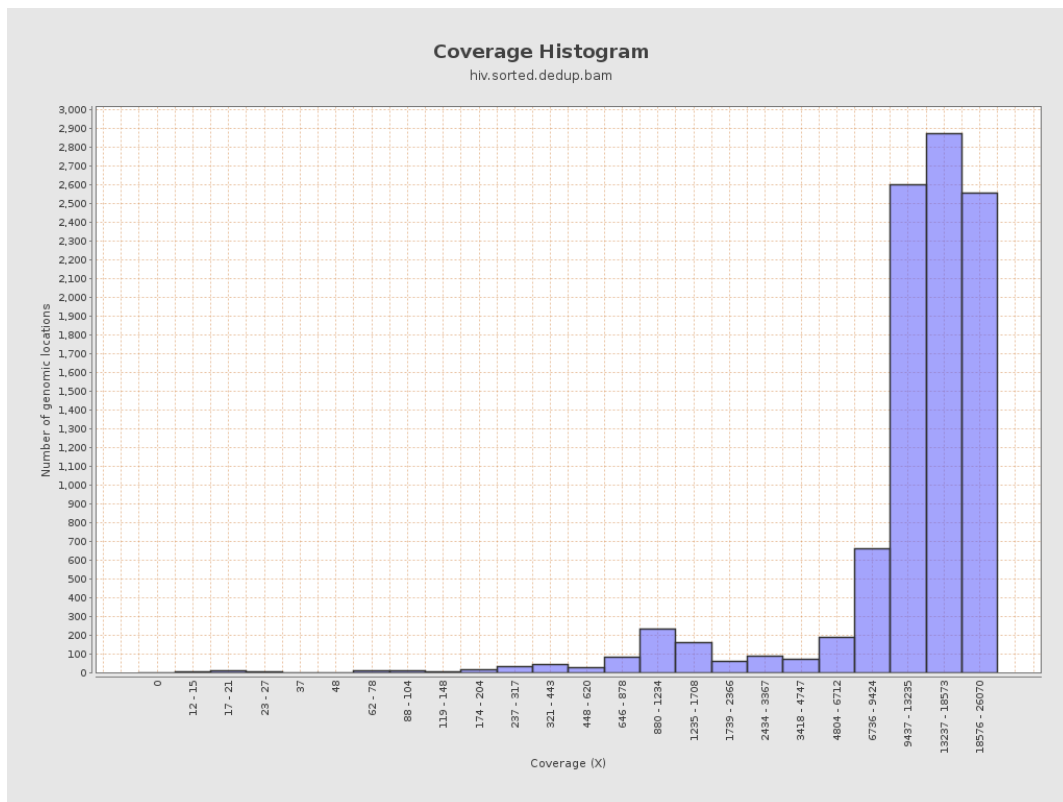
Name	Length	Mapped	Mean	Standard
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		bases	coverage	deviation
K03455.1	9719	137618581	14,159.747	5,895.0338

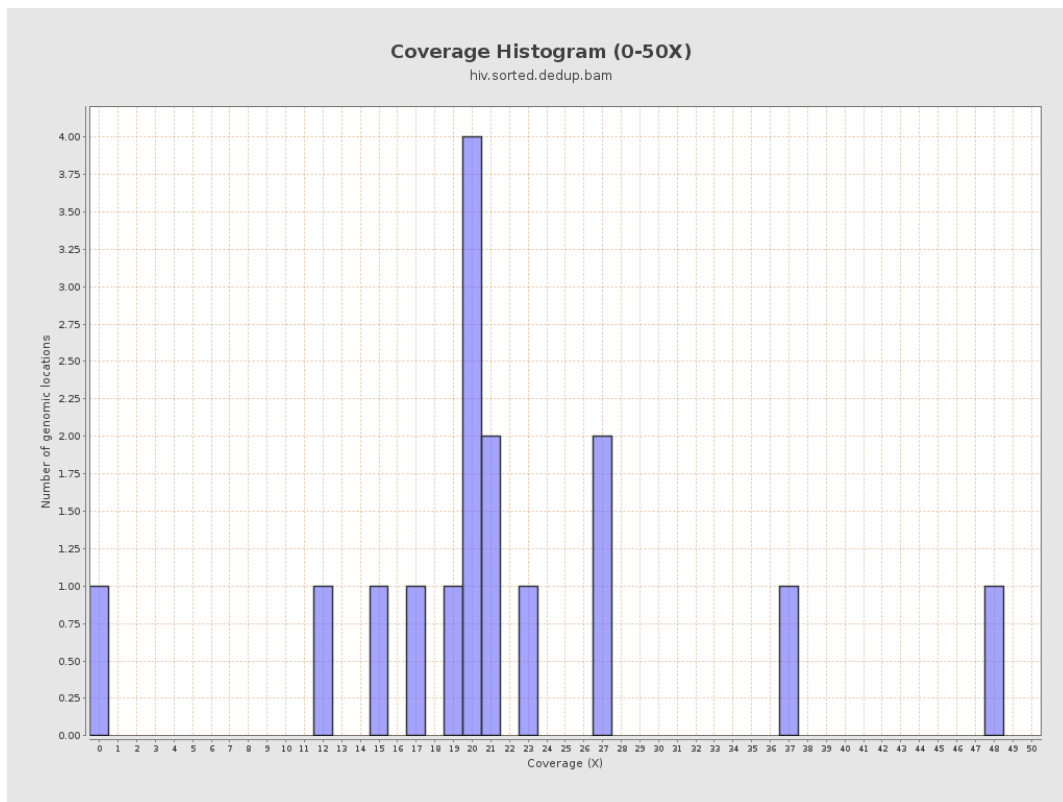
3. Results : Coverage across reference



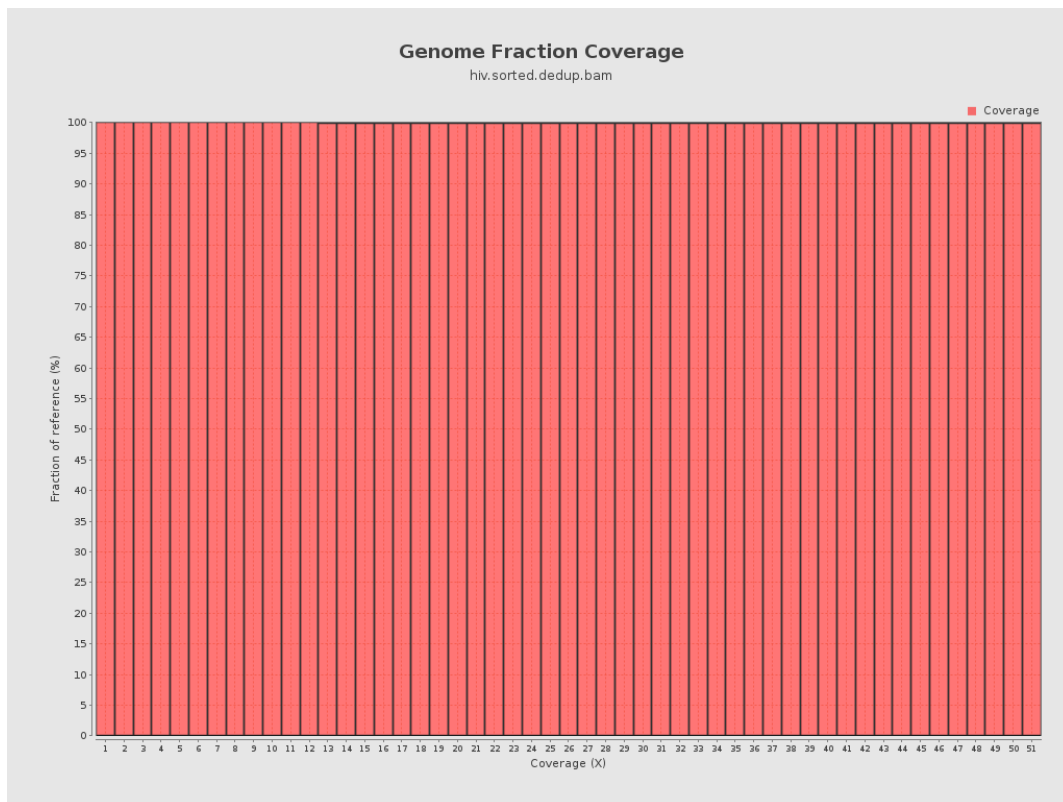
4. Results : Coverage Histogram



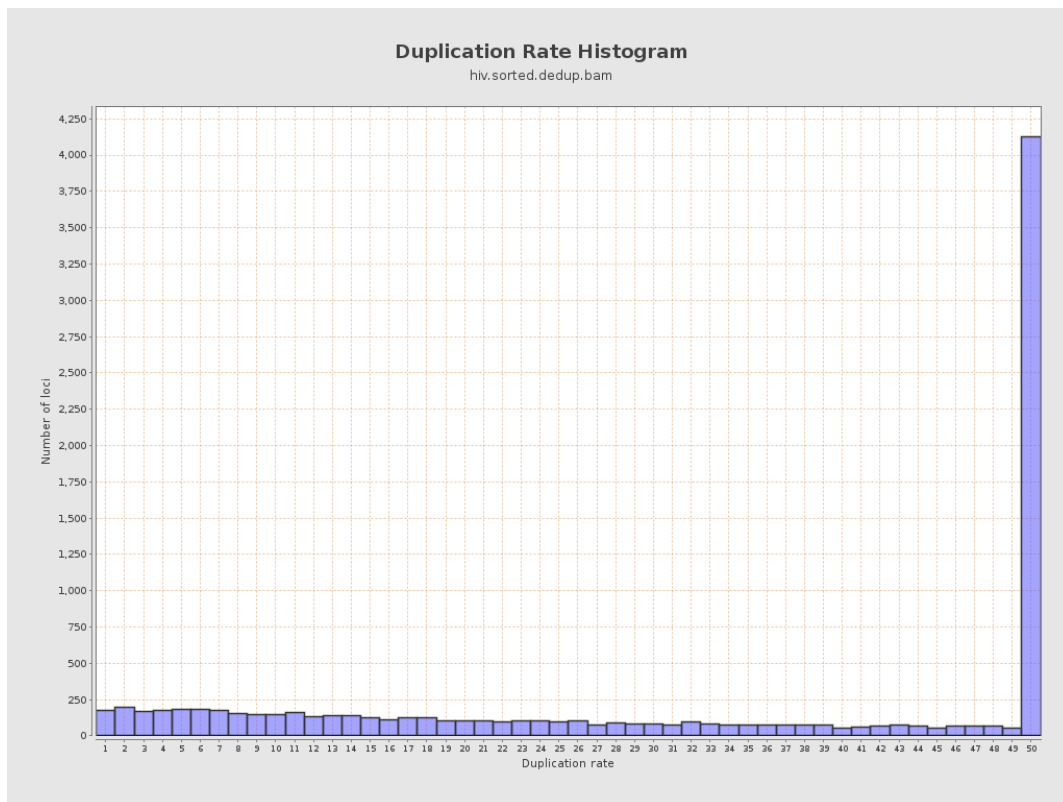
5. Results : Coverage Histogram (0-50X)



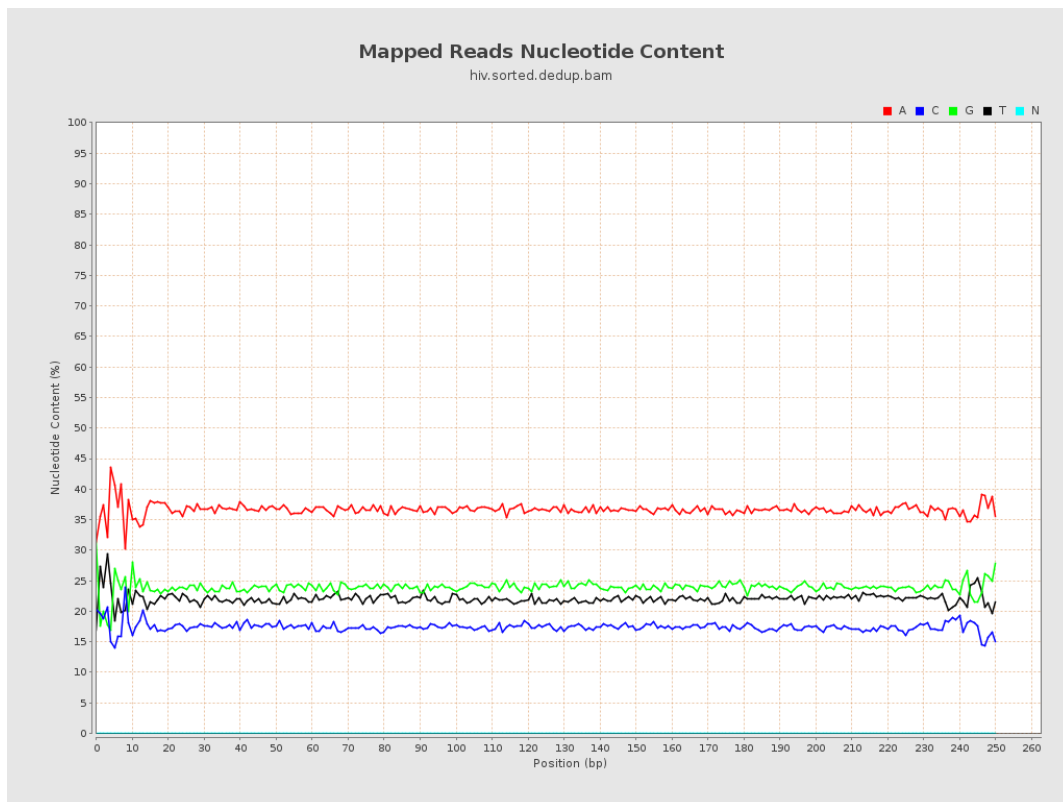
6. Results : Genome Fraction Coverage



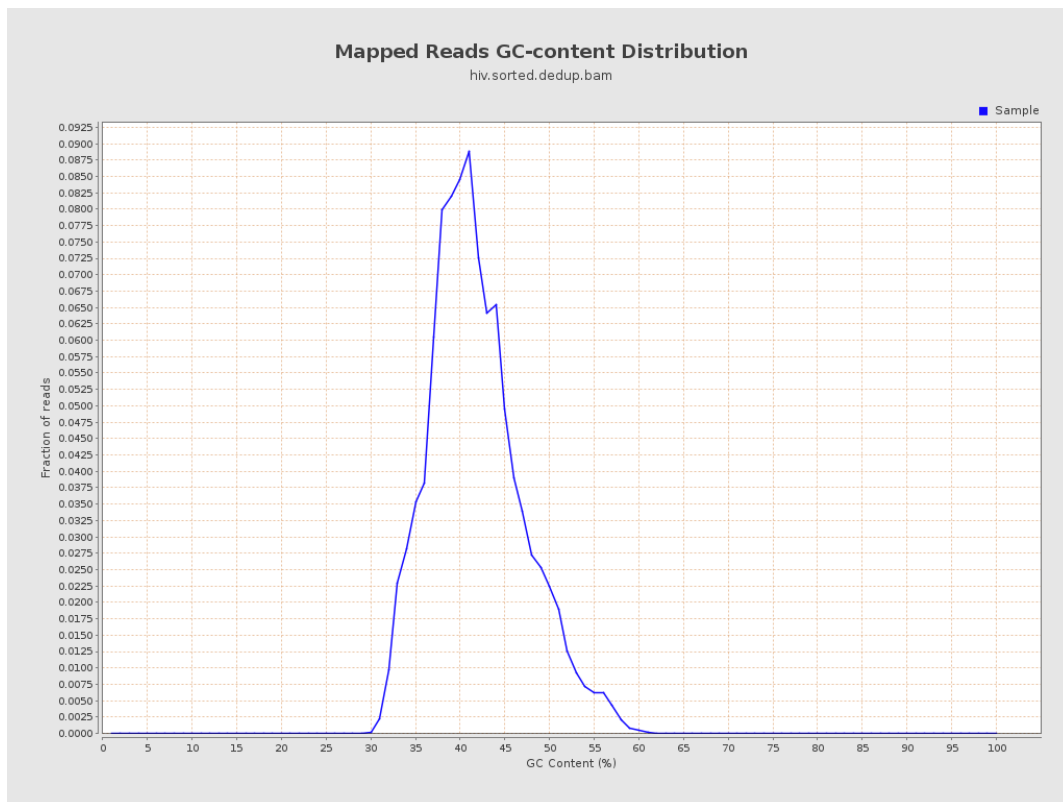
7. Results : Duplication Rate Histogram



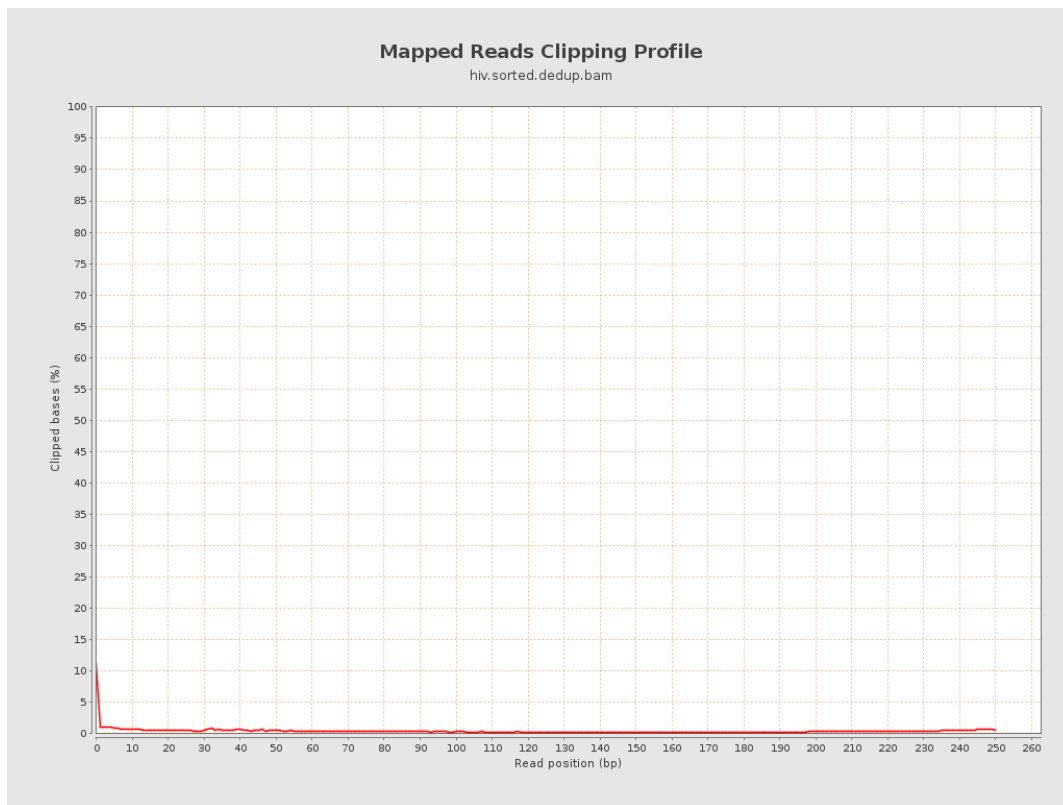
8. Results : Mapped Reads Nucleotide Content



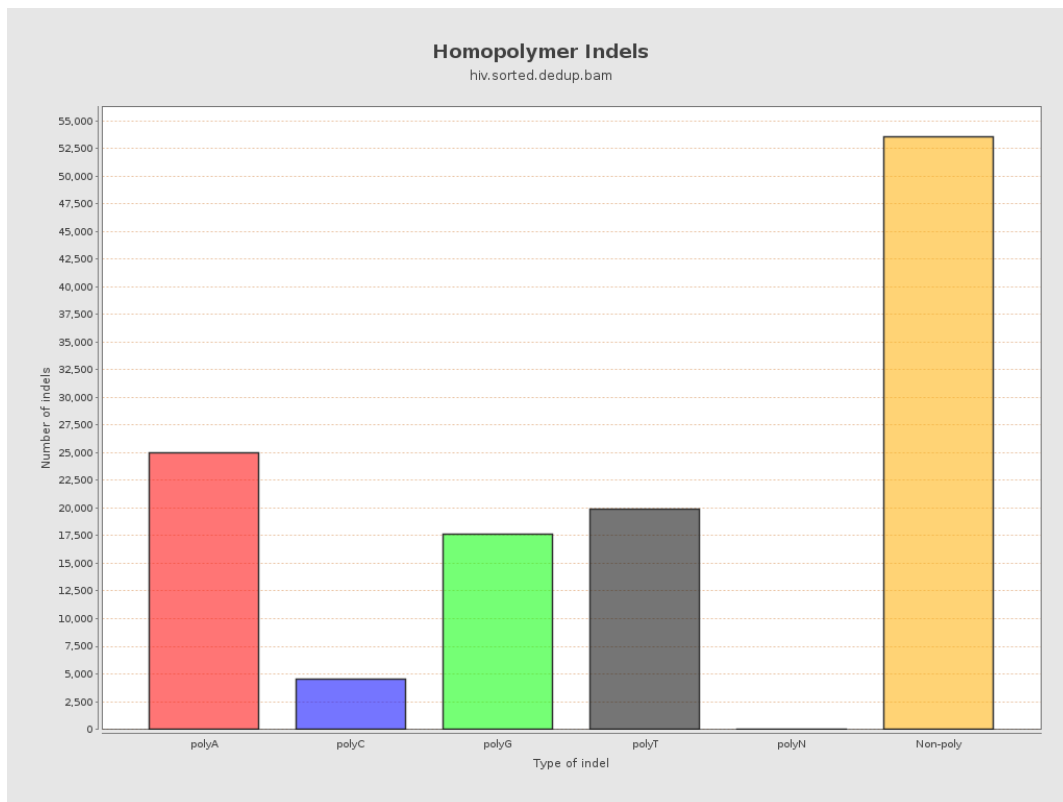
9. Results : Mapped Reads GC-content Distribution



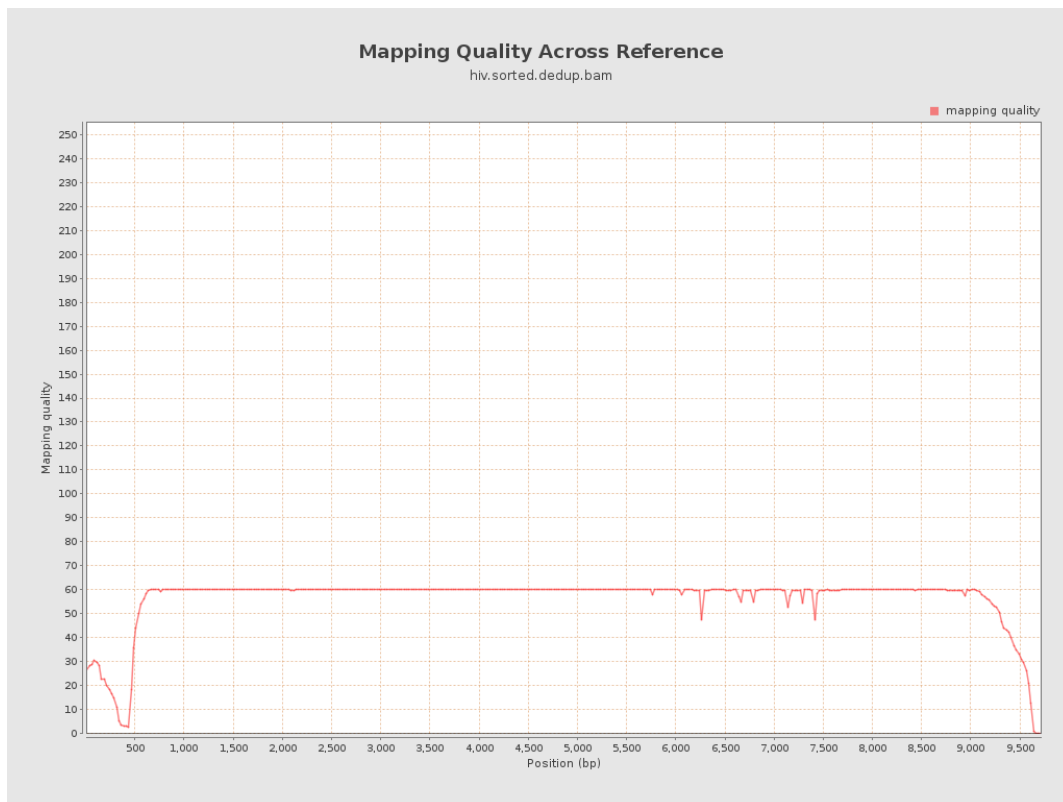
10. Results : Mapped Reads Clipping Profile



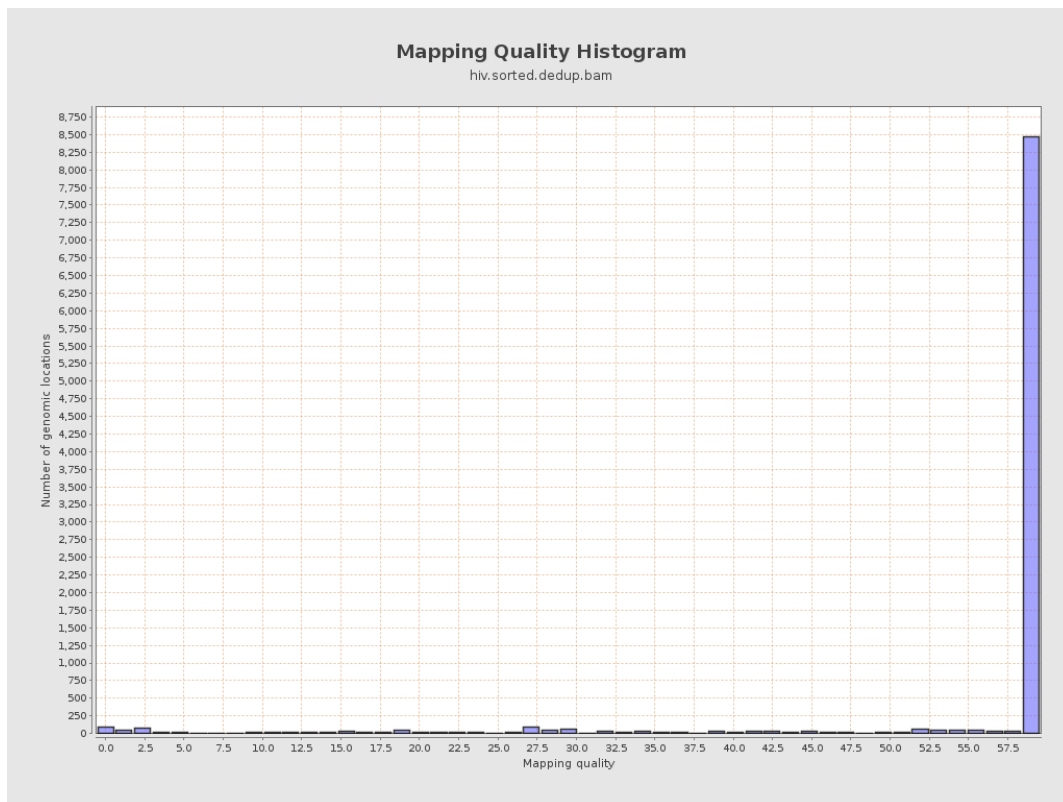
11. Results : Homopolymer Indels



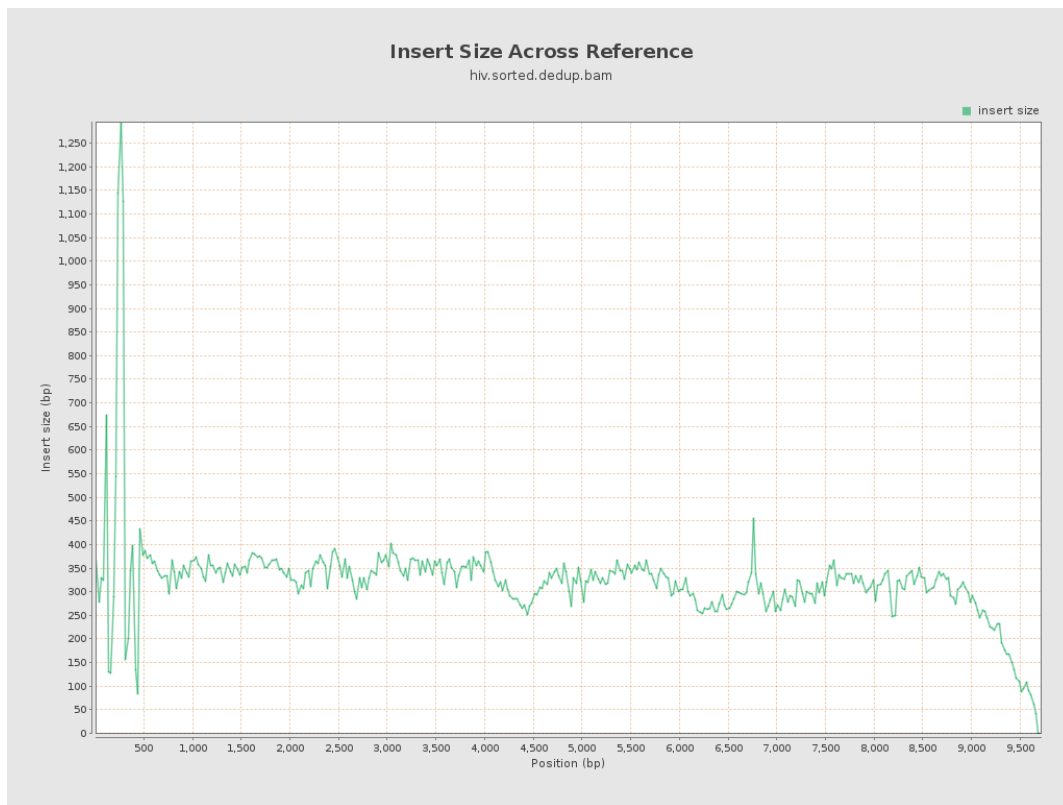
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

