Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:54:19

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397
O
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397O .nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\t SM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_591/02-FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_591_S158_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_591/02-FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_591_S158_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:54:18 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	124,433,763
Mapped reads	117,172,252 / 94.16%
Unmapped reads	7,261,511 / 5.84%
Mapped paired reads	117,172,252 / 94.16%
Mapped reads, first in pair	58,759,665 / 47.22%
Mapped reads, second in pair	58,412,587 / 46.94%
Mapped reads, both in pair	114,763,393 / 92.23%
Mapped reads, singletons	2,408,859 / 1.94%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	19,941,917 / 16.03%
Clipped reads	26,399,895 / 21.22%

2.2. ACGT Content

Number/percentage of A's	5,008,972,077 / 30.81%
Number/percentage of C's	3,122,097,561 / 19.2%
Number/percentage of T's	5,018,721,302 / 30.87%
Number/percentage of G's	3,110,160,955 / 19.13%
Number/percentage of N's	89,681 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	52.3087
Standard Deviation	391.4011

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Insert size

Mean	226,127.08
Standard Deviation	2,256,832.1
P25/Median/P75	328 / 434 / 570

2.6. Mismatches and indels

General error rate	2.4%
Mismatches	360,118,875
Insertions	10,692,866
Mapped reads with at least one insertion	8.21%
Deletions	10,965,378
Mapped reads with at least one deletion	8.31%
Homopolymer indels	56.21%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1296765766	43.6264	115.3269

| LT669789.1 | 36598175 | 1929789130 | 52.7291 | 402.032 |
LT669790.1	30422129	1683774716	55.347	380.3842
LT669791.1	52758100	2722770252	51.6086	342.1612
LT669792.1	28376109	1461487930	51.5042	436.2785
LT669793.1	33388210	1622947997	48.6084	276.2511
LT669794.1	50579949	2491525314	49.2592	334.7993
LT669795.1	49795044	3092528522	62.1051	588.1633

3. Results : Coverage across reference

Coverage across reference
3970.nodup.bam
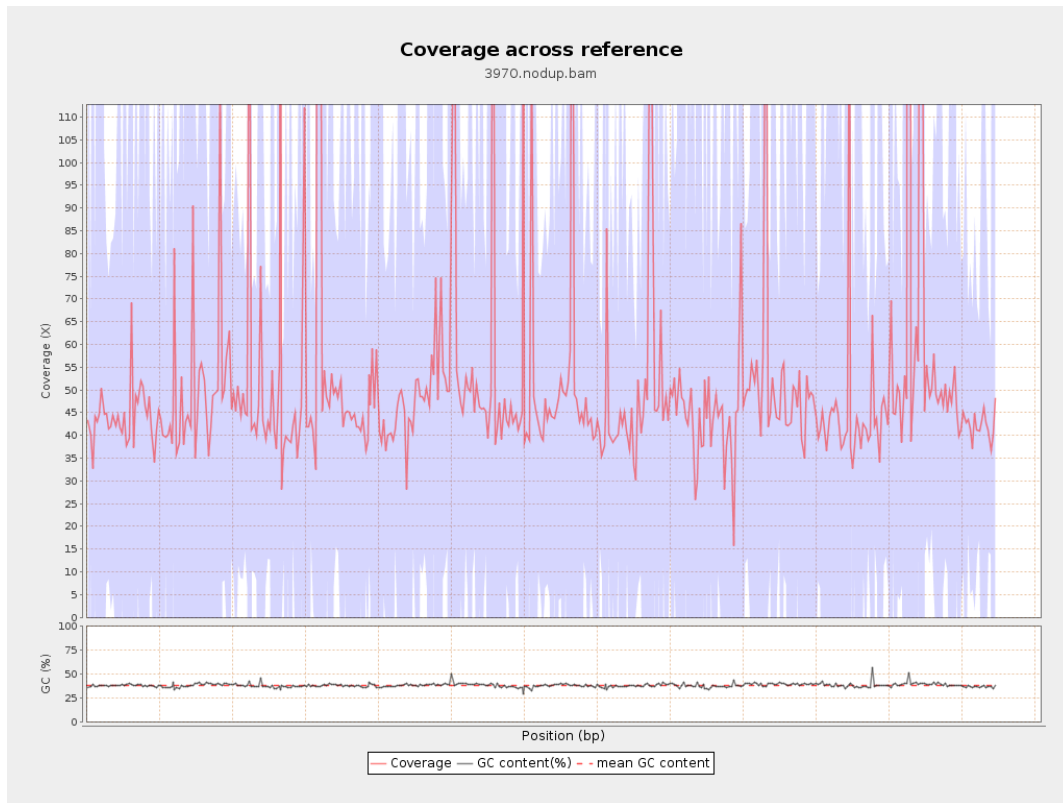
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
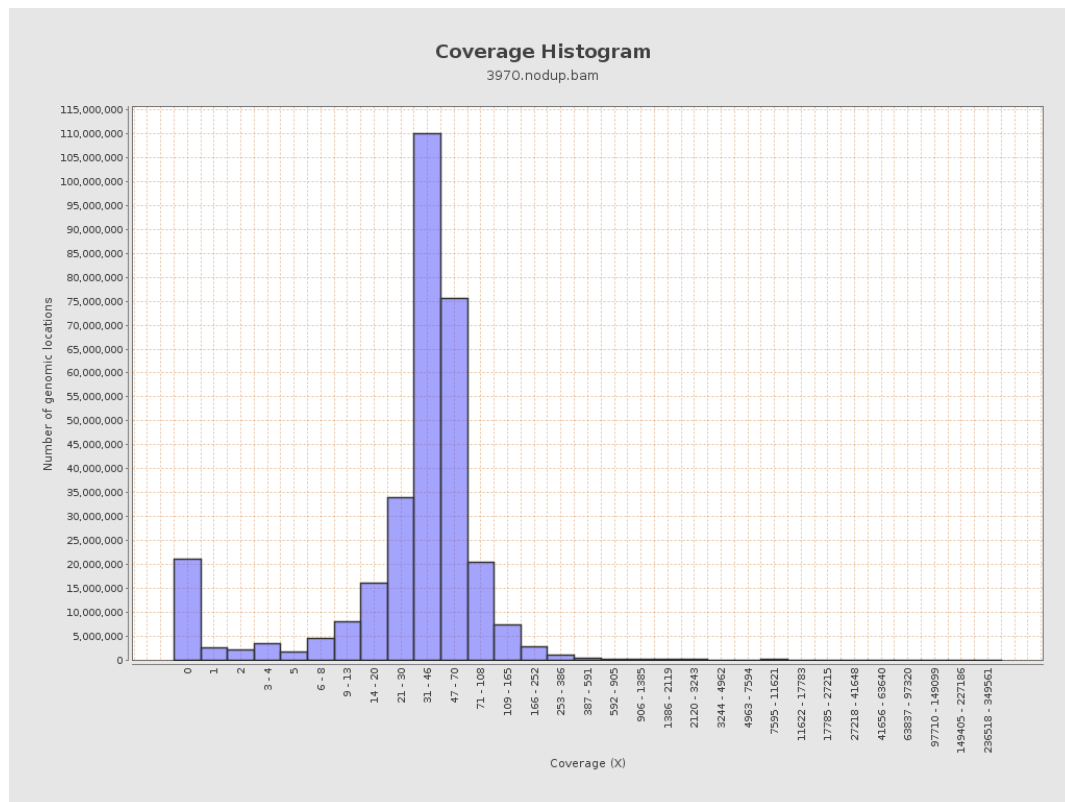
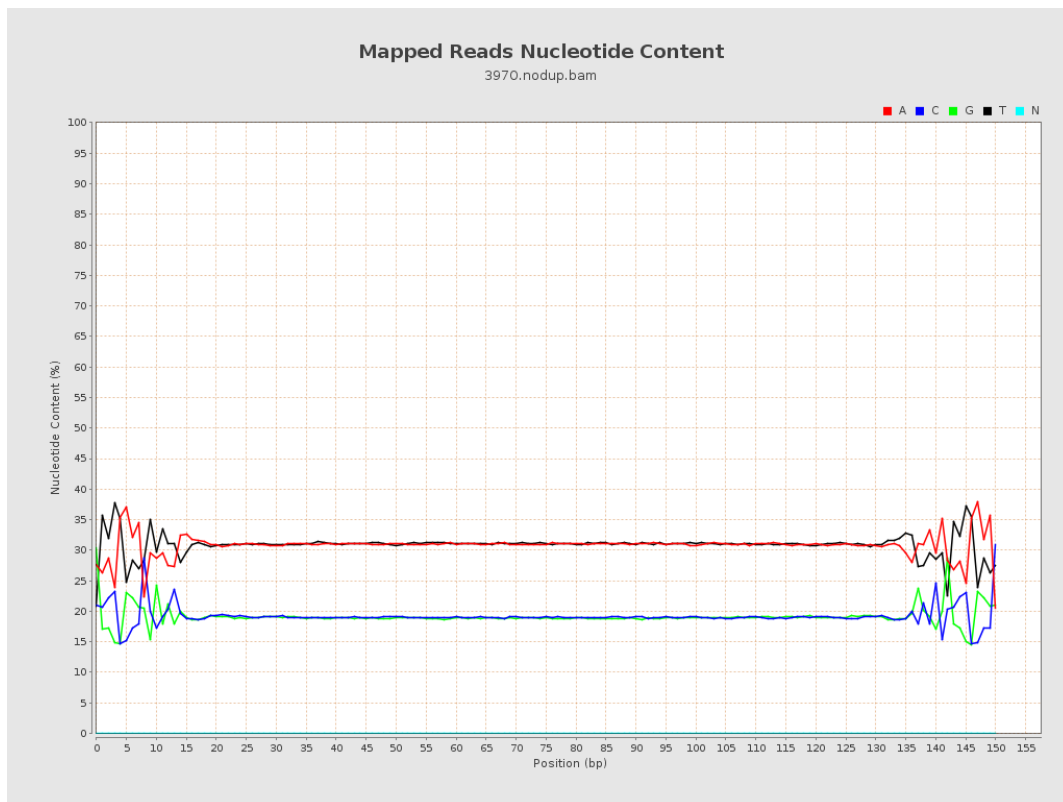Coverage Histogram (0-50X)
3970.nodup.bam
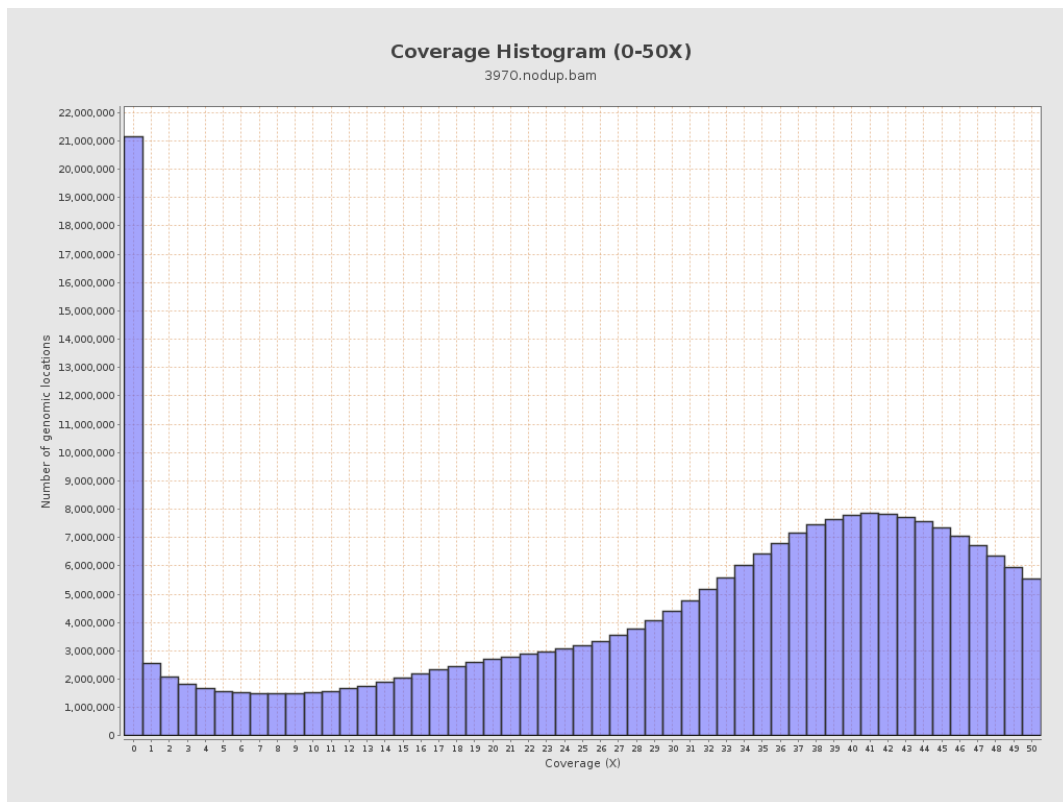
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
3970.nodup.bam
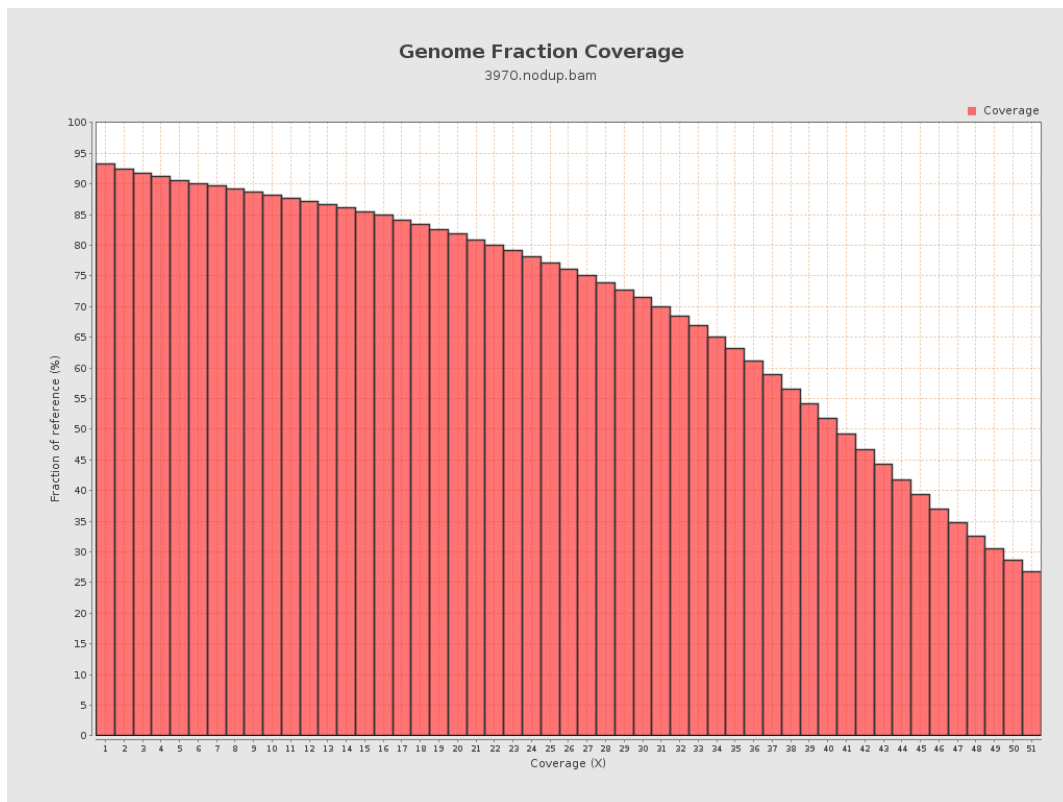
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
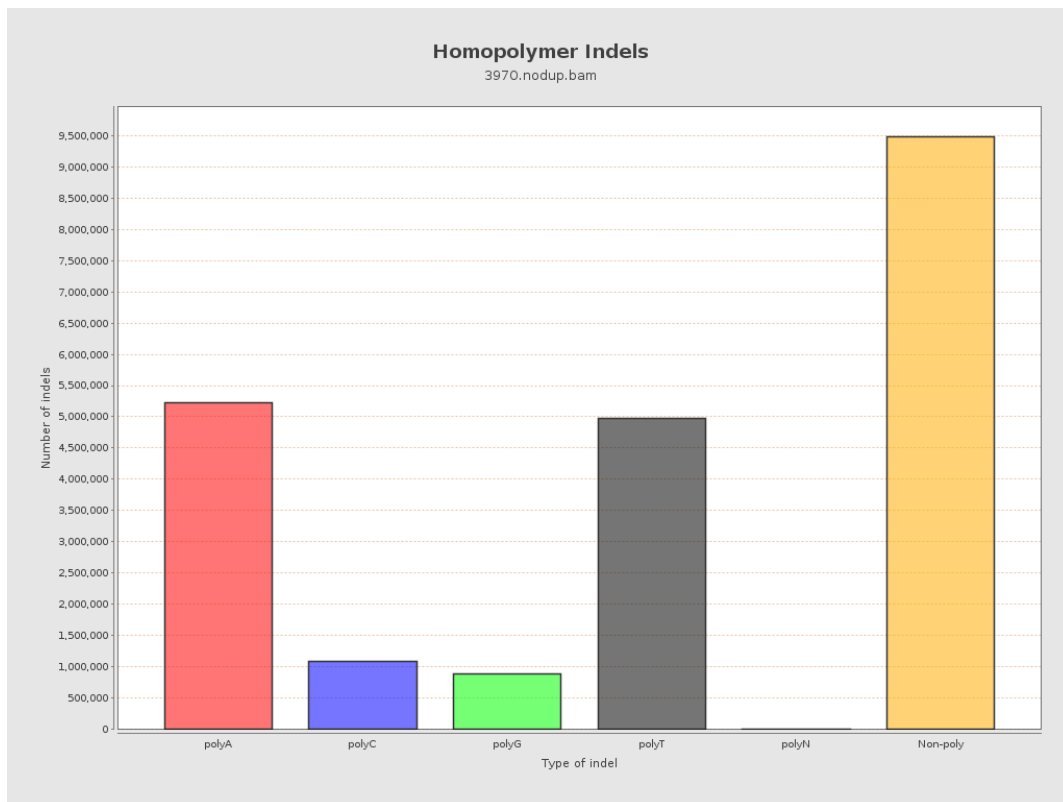3970.nodup.bam
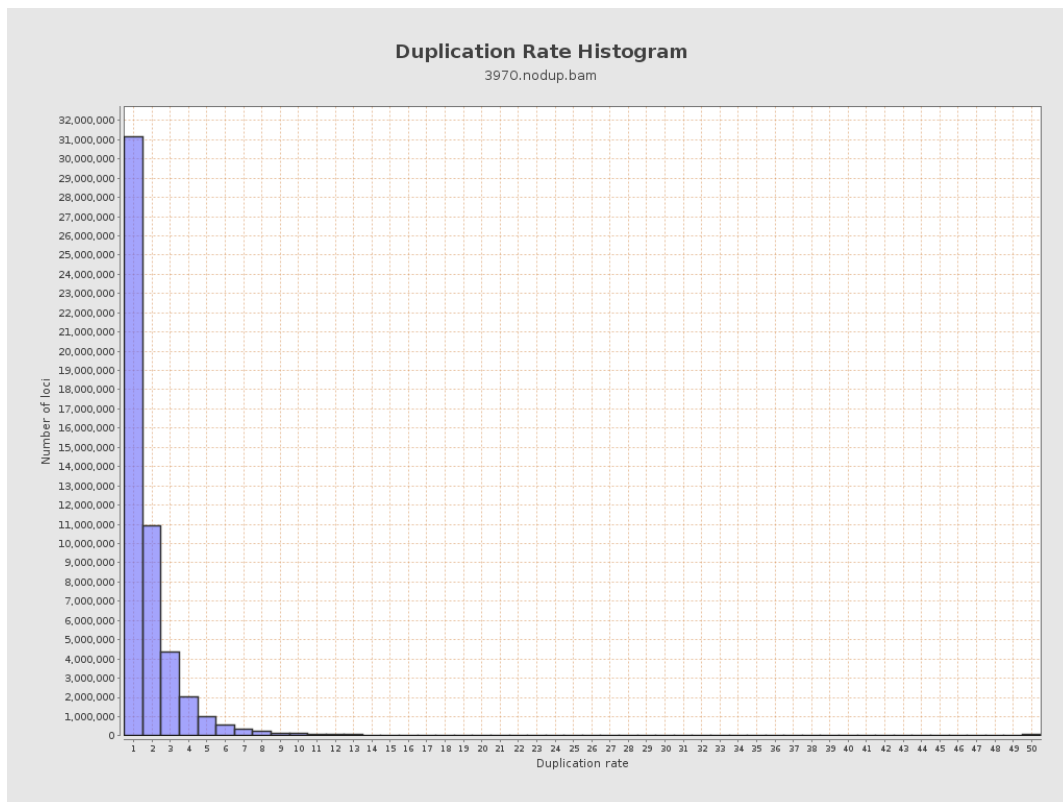
8. Results : Mapped Reads Nucleotide Content
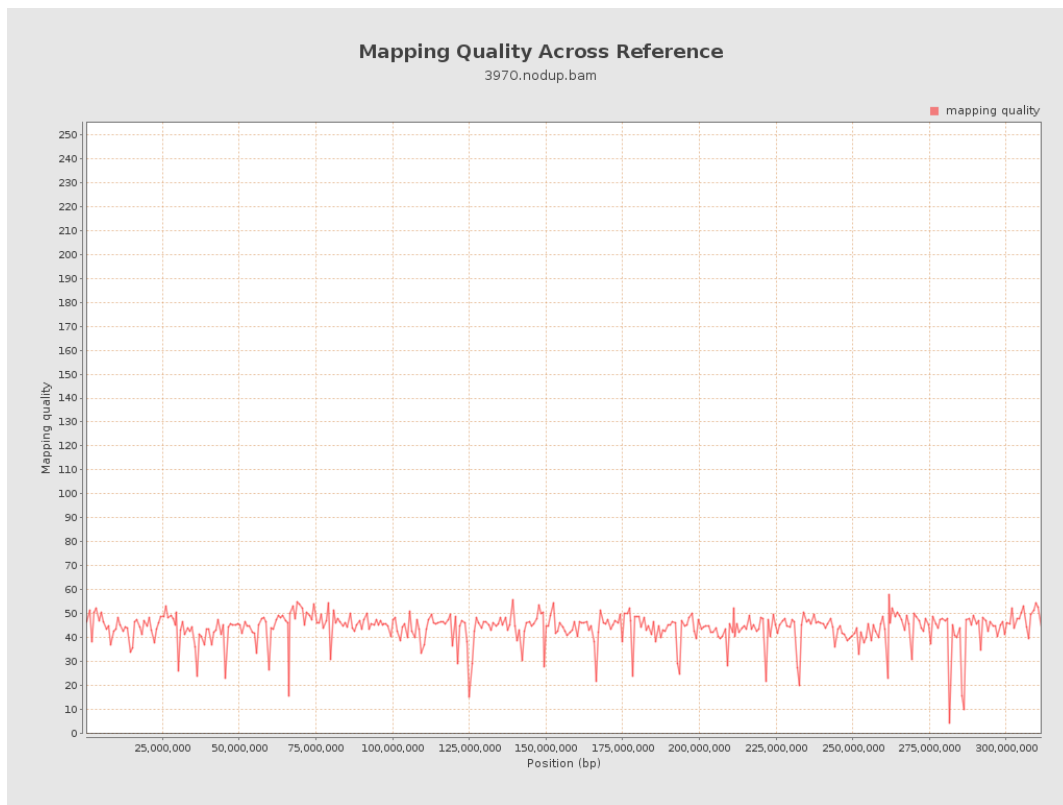
9. Results : Mapped Reads GC-content Distribution
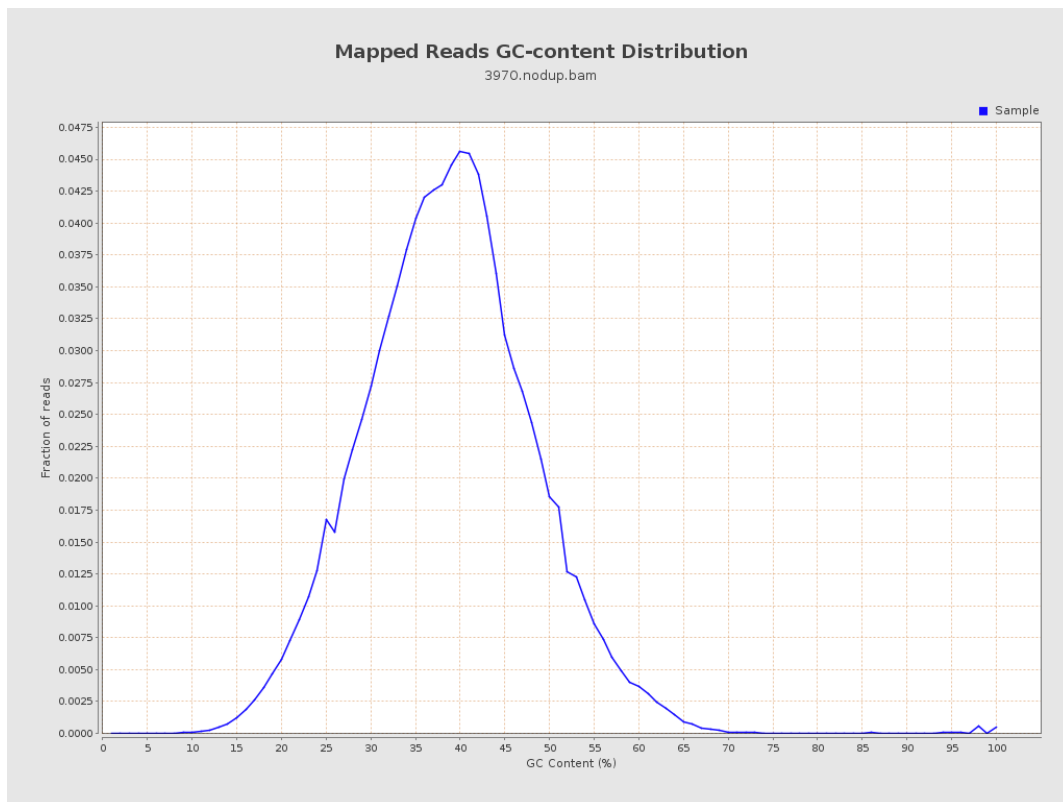
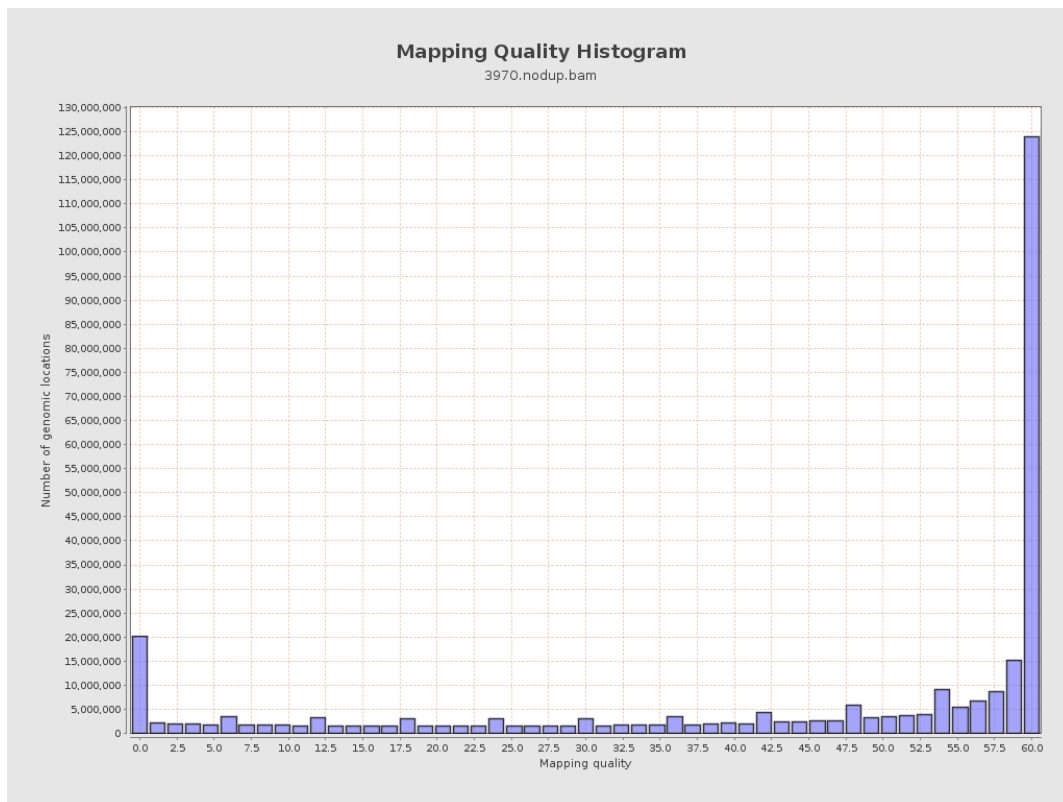# 10. Results : Mapped Reads Clipping Profile
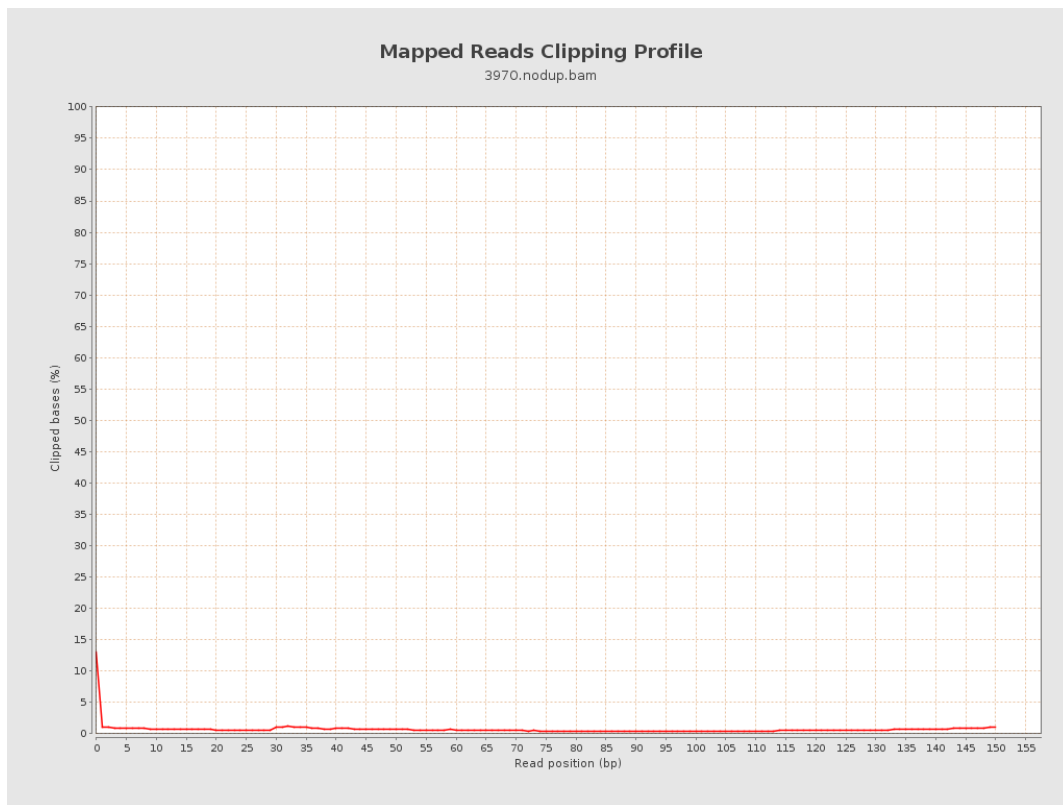
11. Results : Homopolymer Indels

Homopolymer Indels
3970.nodup.bam

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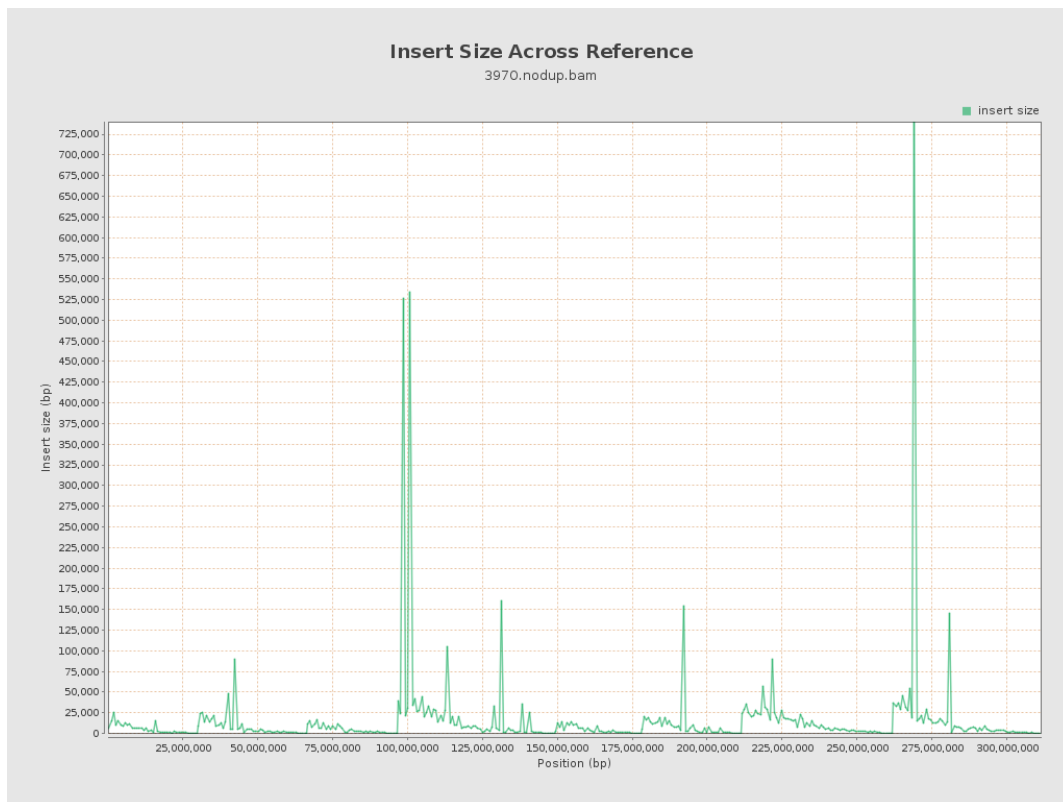
13. Results : Mapping Quality Histogram

Mapping Quality Histogram
3970.nodup.bam

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
3970.nodup.bam