Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/956.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/956.nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_574/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_574_S141_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_574/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_574_S141_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:08 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	51,777,314
Mapped reads	49,562,047 / 95.72%
Unmapped reads	2,215,267 / 4.28%
Mapped paired reads	49,562,047 / 95.72%
Mapped reads, first in pair	24,851,327 / 48%
Mapped reads, second in pair	24,710,720 / 47.72%
Mapped reads, both in pair	48,802,246 / 94.25%
Mapped reads, singletons	759,801 / 1.47%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	6,782,913 / 13.1%
Clipped reads	11,015,077 / 21.27%

2.2. ACGT Content

Number/percentage of A's	2,123,536,834 / 30.73%
Number/percentage of C's	1,333,324,004 / 19.3%
Number/percentage of T's	2,126,510,264 / 30.77%
Number/percentage of G's	1,326,591,120 / 19.2%
Number/percentage of N's	49,657 / 0%
GC Percentage	38.49%

2.3. Coverage

Mean	22.2294
Standard Deviation	184.3065

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Insert size

Mean	202,645.97
Standard Deviation	2,103,475.98
P25/Median/P75	315 / 410 / 528

2.6. Mismatches and indels

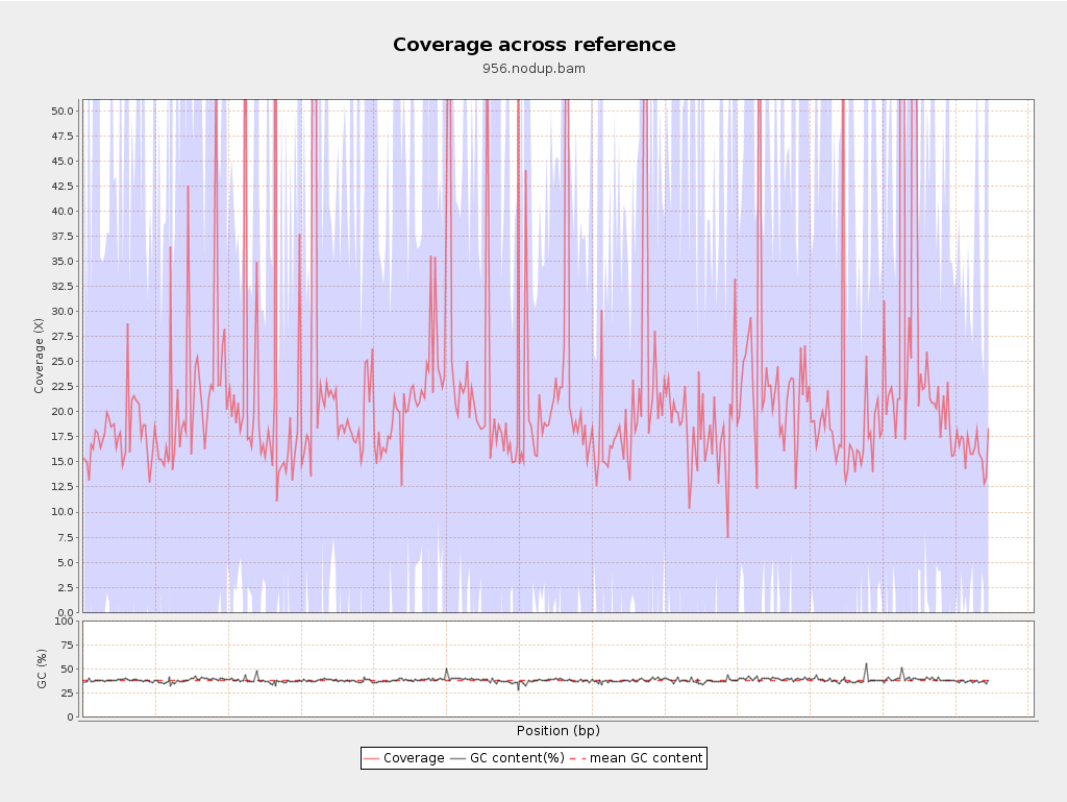
General error rate	2.48%
Mismatches	159,709,079
Insertions	4,433,705
Mapped reads with at least one insertion	8.09%
Deletions	4,668,699
Mapped reads with at least one deletion	8.39%
Homopolymer indels	55.56%

2.7. Chromosome stats

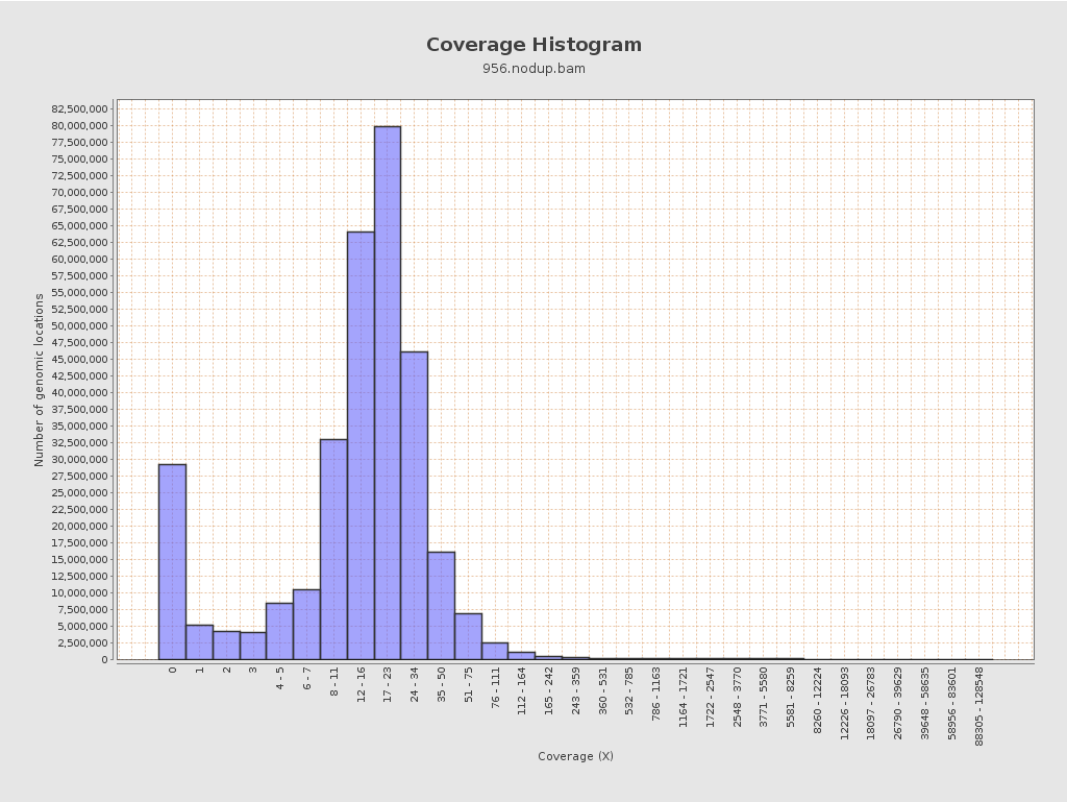
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	519407252	17.4741	43.8542

LT669789.1	36598175	846943753	23.1417	203.5821
LT669790.1	30422129	668410250	21.9712	144.4381
LT669791.1	52758100	1164620250	22.0747	136.8175
LT669792.1	28376109	608931978	21.4593	211.2052
LT669793.1	33388210	694304826	20.7949	127.1464
LT669794.1	50579949	1092037835	21.5903	164.9439
LT669795.1	49795044	1332957906	26.7689	290.6441

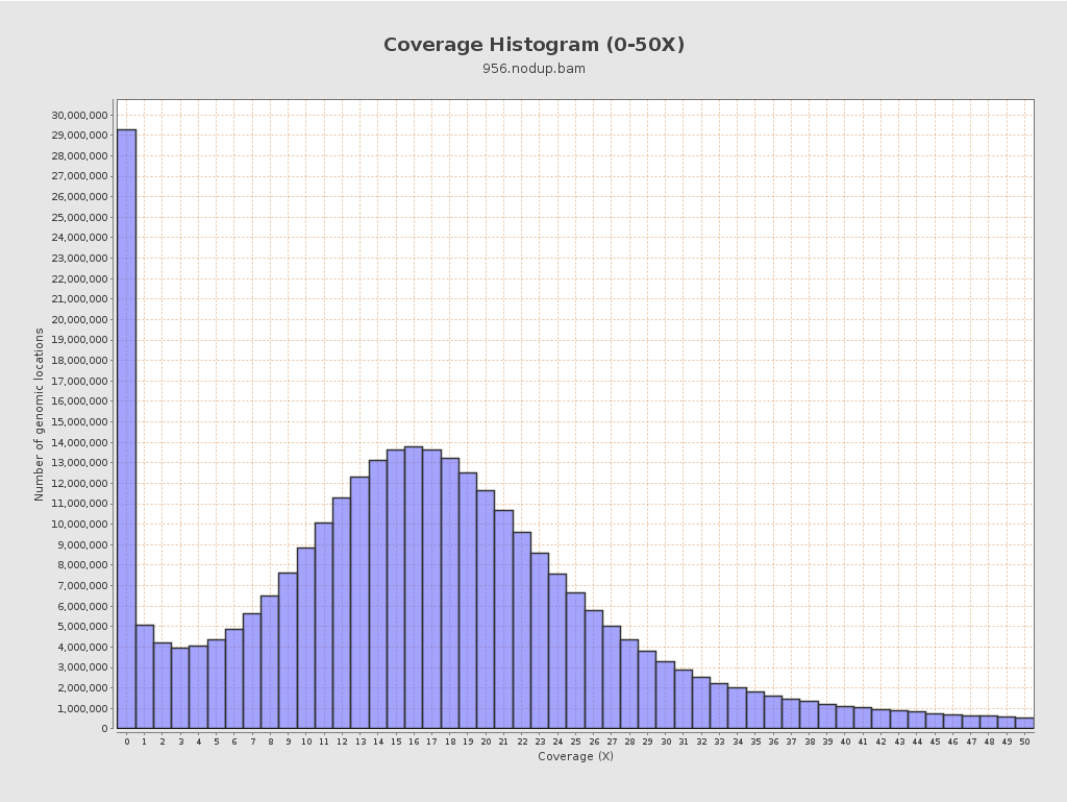
3. Results : Coverage across reference



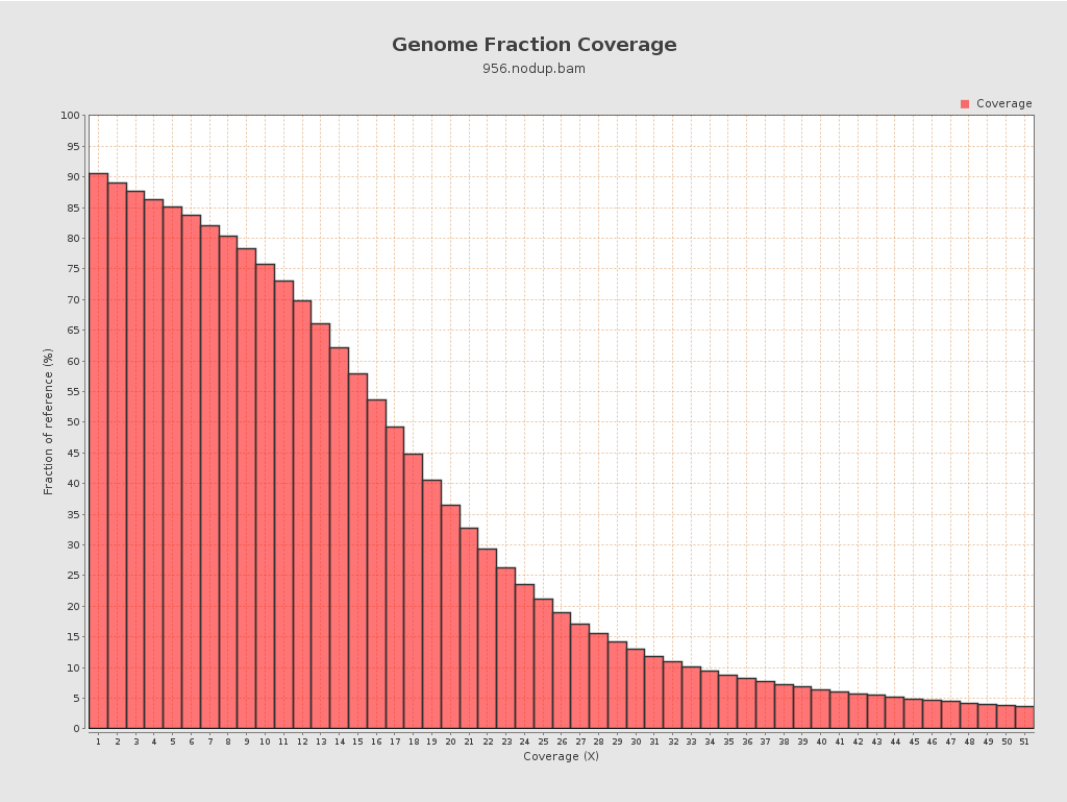
4. Results : Coverage Histogram



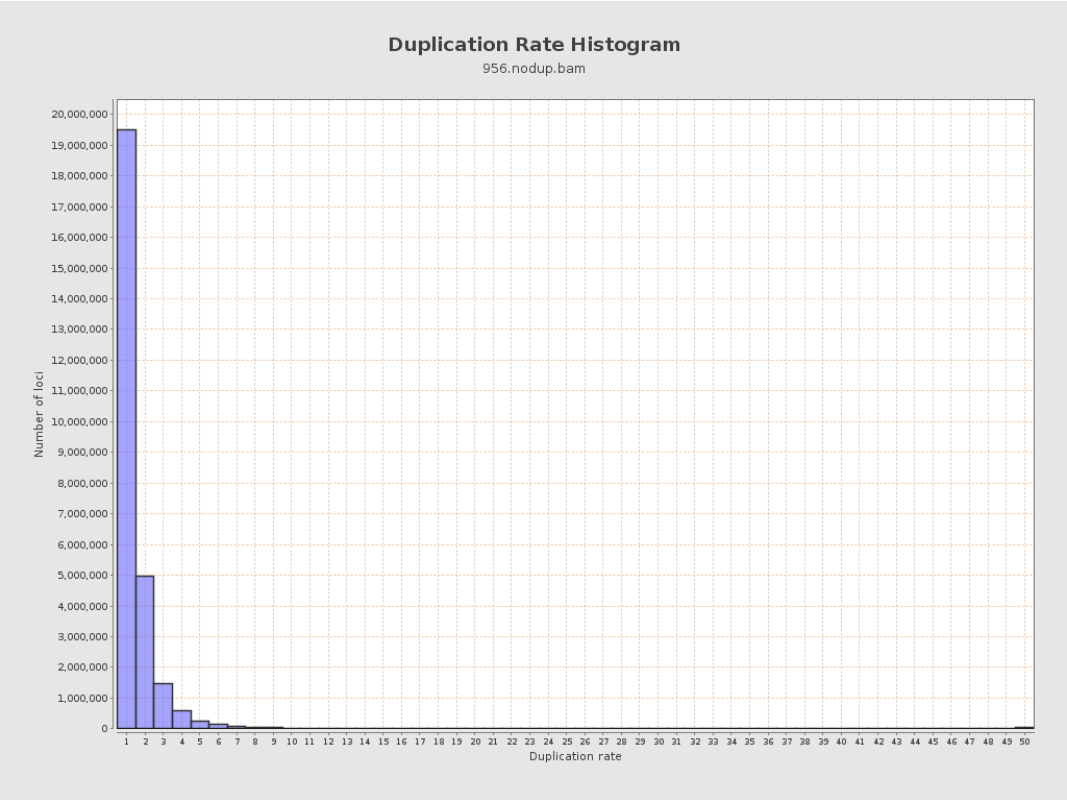
5. Results : Coverage Histogram (0-50X)



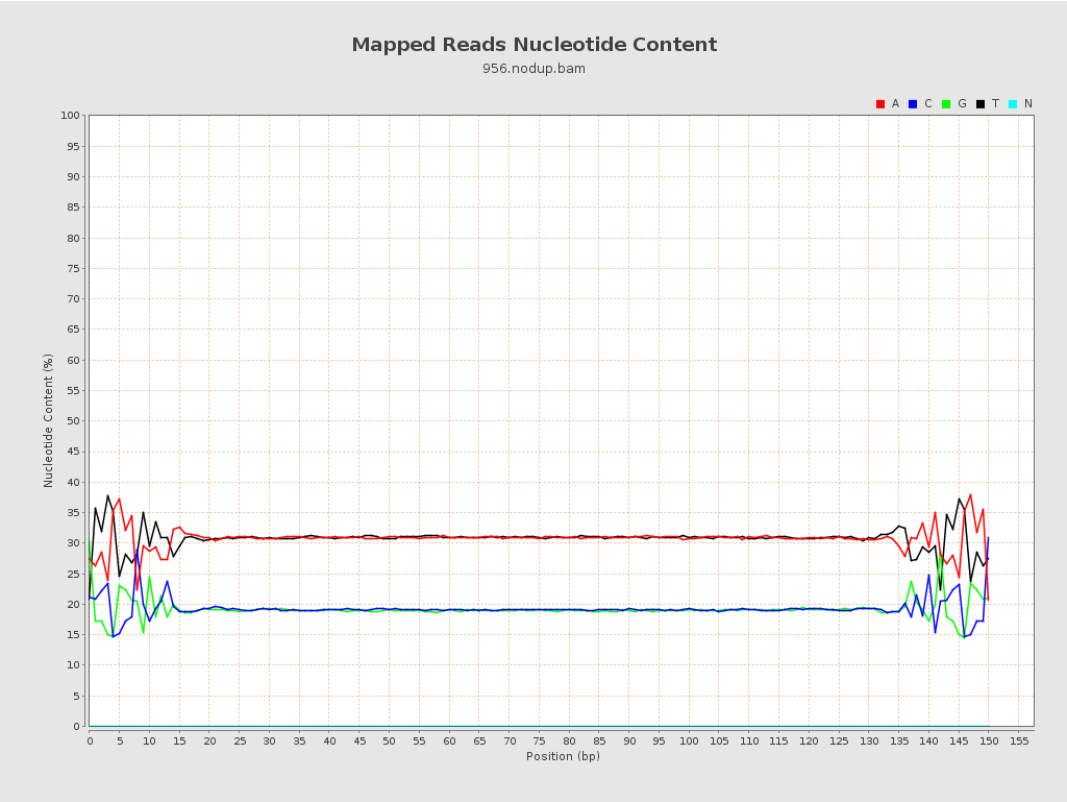
6. Results : Genome Fraction Coverage



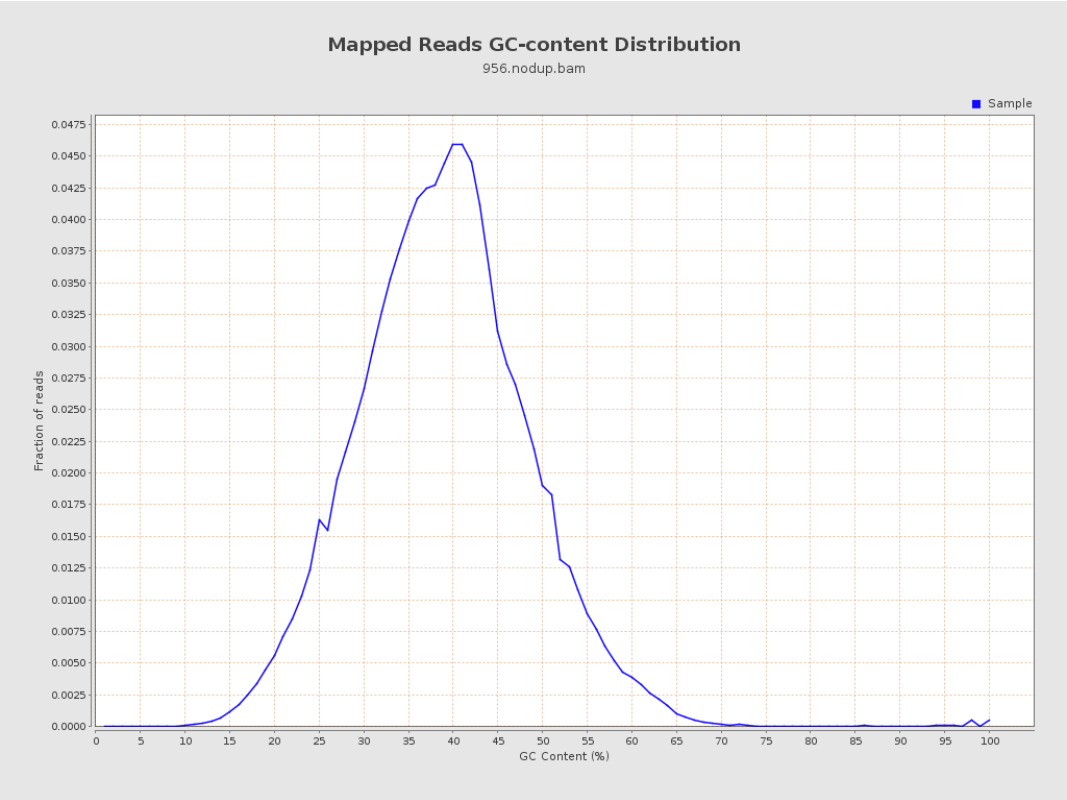
7. Results : Duplication Rate Histogram



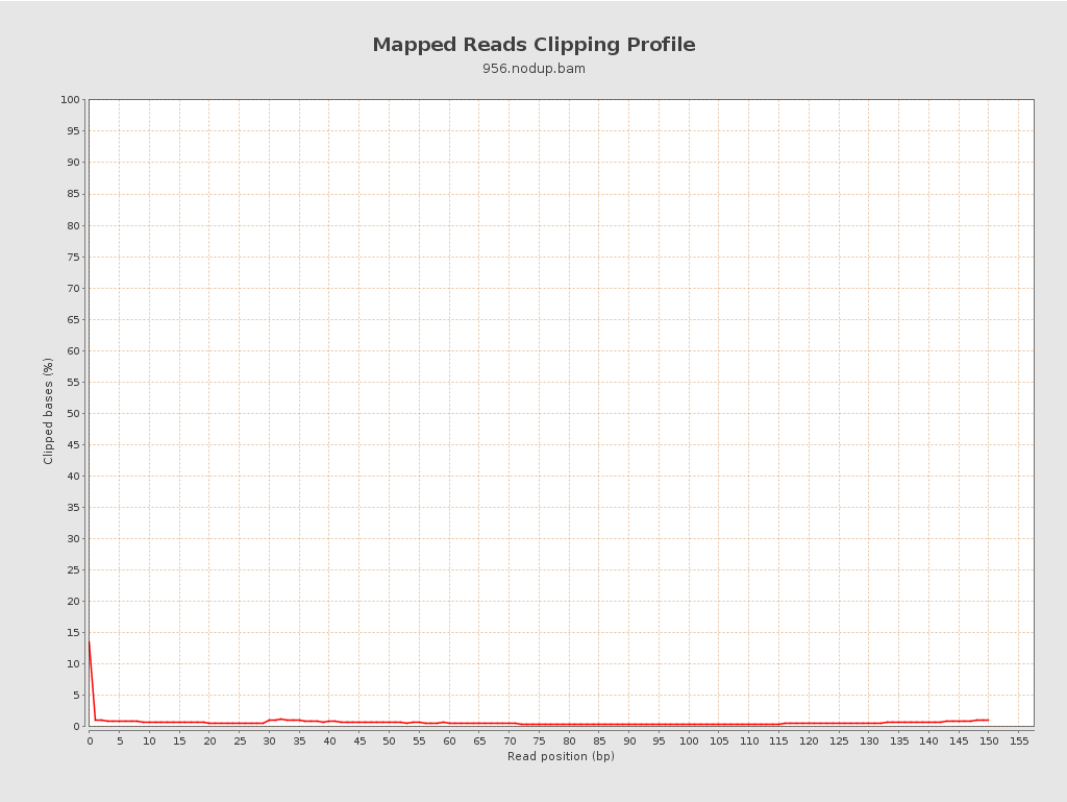
8. Results : Mapped Reads Nucleotide Content



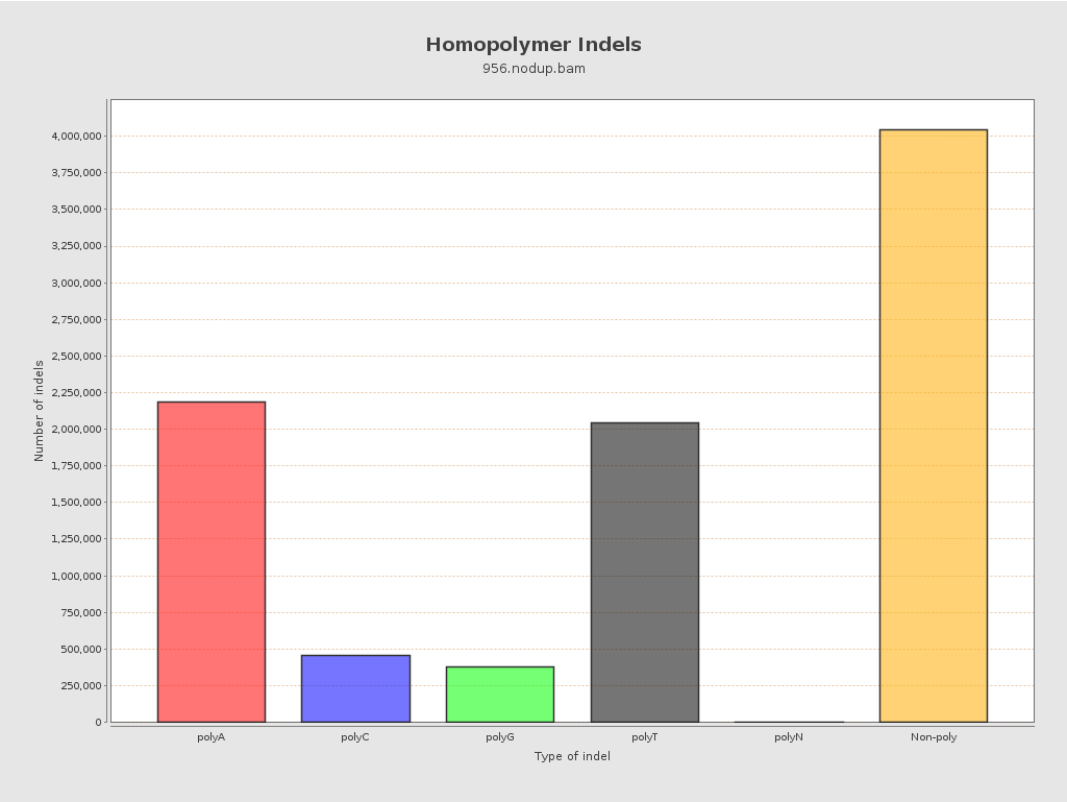
9. Results : Mapped Reads GC-content Distribution



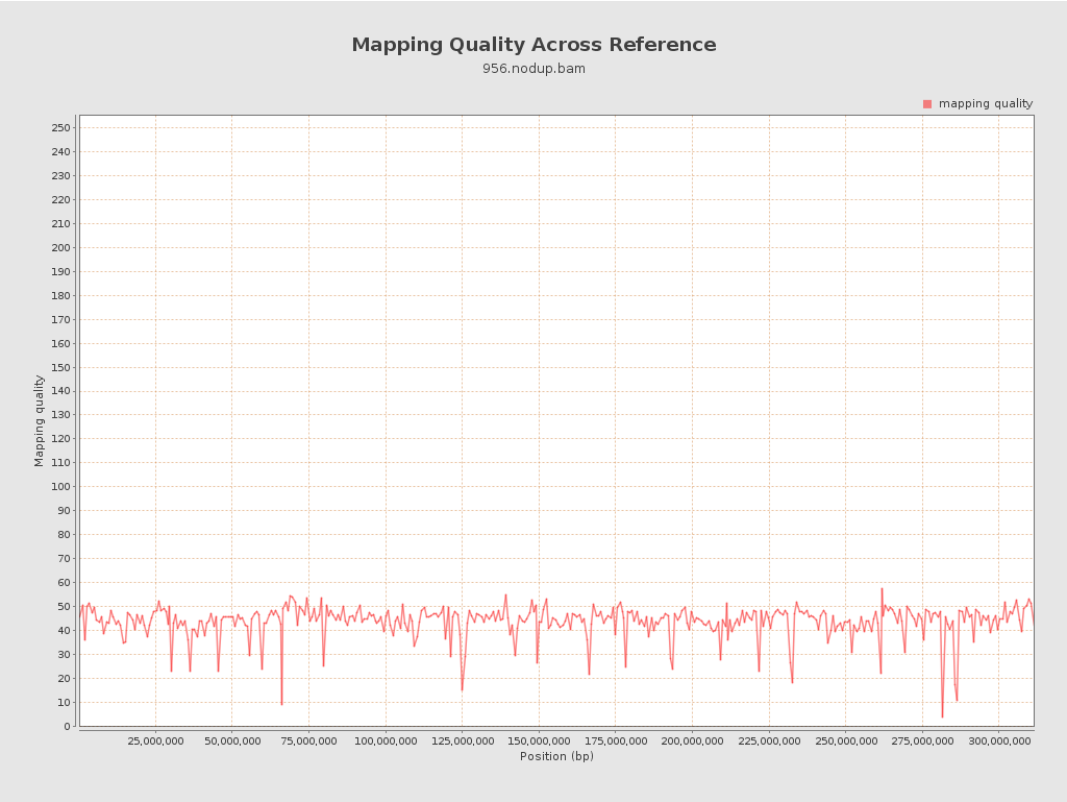
10. Results : Mapped Reads Clipping Profile



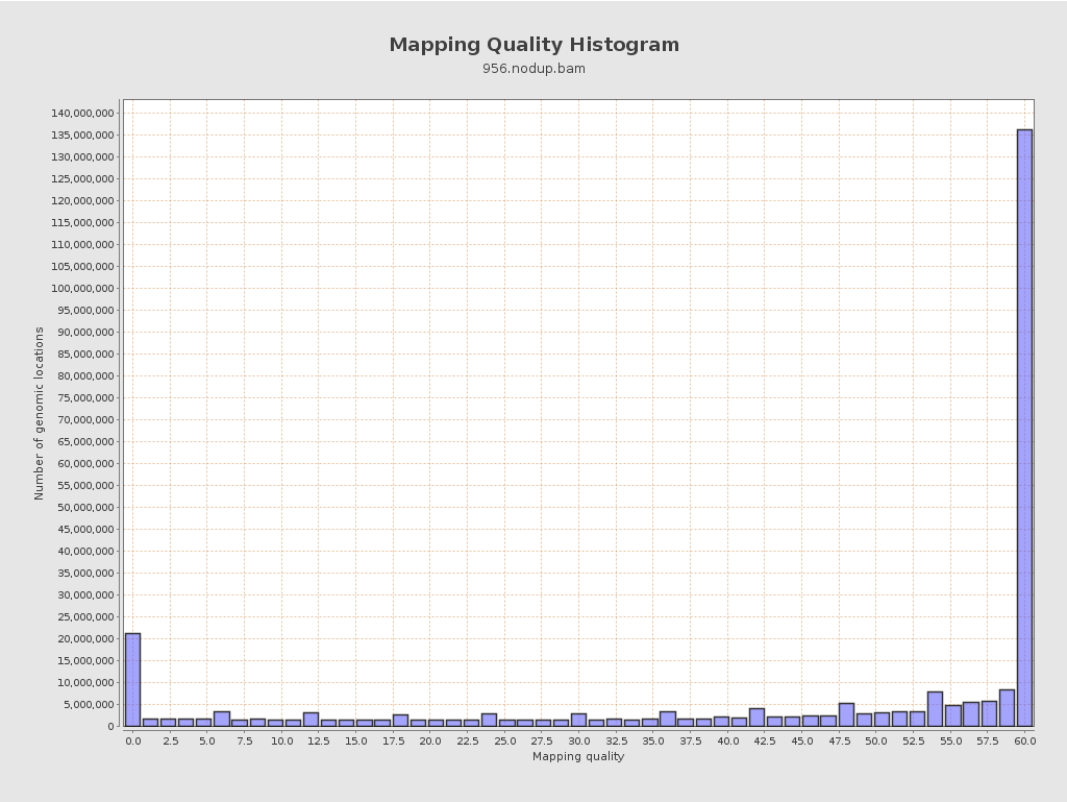
11. Results : Homopolymer Indels



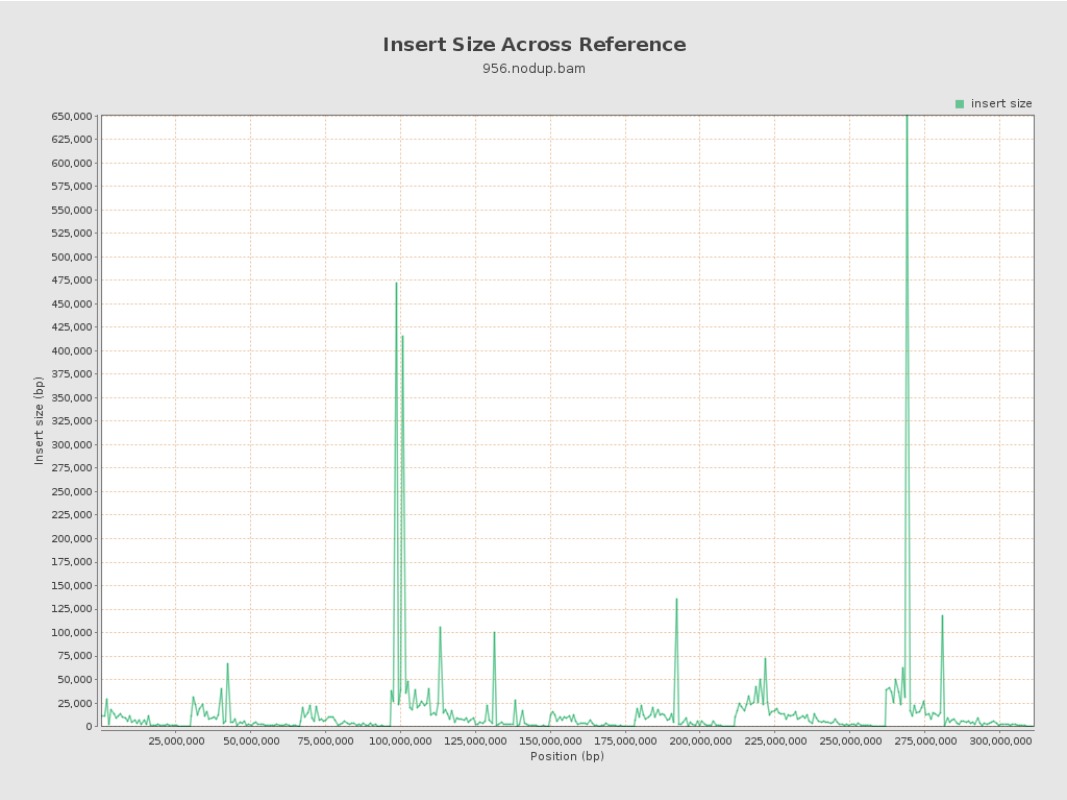
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram