Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/908.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/908.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_205/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_205_S286_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_205/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_205_S286_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	55,652,303
Mapped reads	52,598,026 / 94.51%
Unmapped reads	3,054,277 / 5.49%
Mapped paired reads	52,598,026 / 94.51%
Mapped reads, first in pair	26,356,467 / 47.36%
Mapped reads, second in pair	26,241,559 / 47.15%
Mapped reads, both in pair	51,659,606 / 92.83%
Mapped reads, singletons	938,420 / 1.69%
Read min/max/mean length	30 / 151 / 148.04
Duplicated reads (flagged)	7,132,460 / 12.82%
Clipped reads	11,852,161 / 21.3%

2.2. ACGT Content

Number/percentage of A's	2,239,625,253 / 30.69%
Number/percentage of C's	1,409,244,220 / 19.31%
Number/percentage of T's	2,242,239,641 / 30.73%
Number/percentage of G's	1,405,745,788 / 19.27%
Number/percentage of N's	27,575 / 0%
GC Percentage	38.58%

2.3. Coverage

Mean	23.476
Standard Deviation	200.0827

2.4. Mapping Quality

Mean Mapping Quality	43.74

2.5. Insert size

Mean	222,959.88
Standard Deviation	2,229,278.69
P25/Median/P75	311 / 410 / 536

2.6. Mismatches and indels

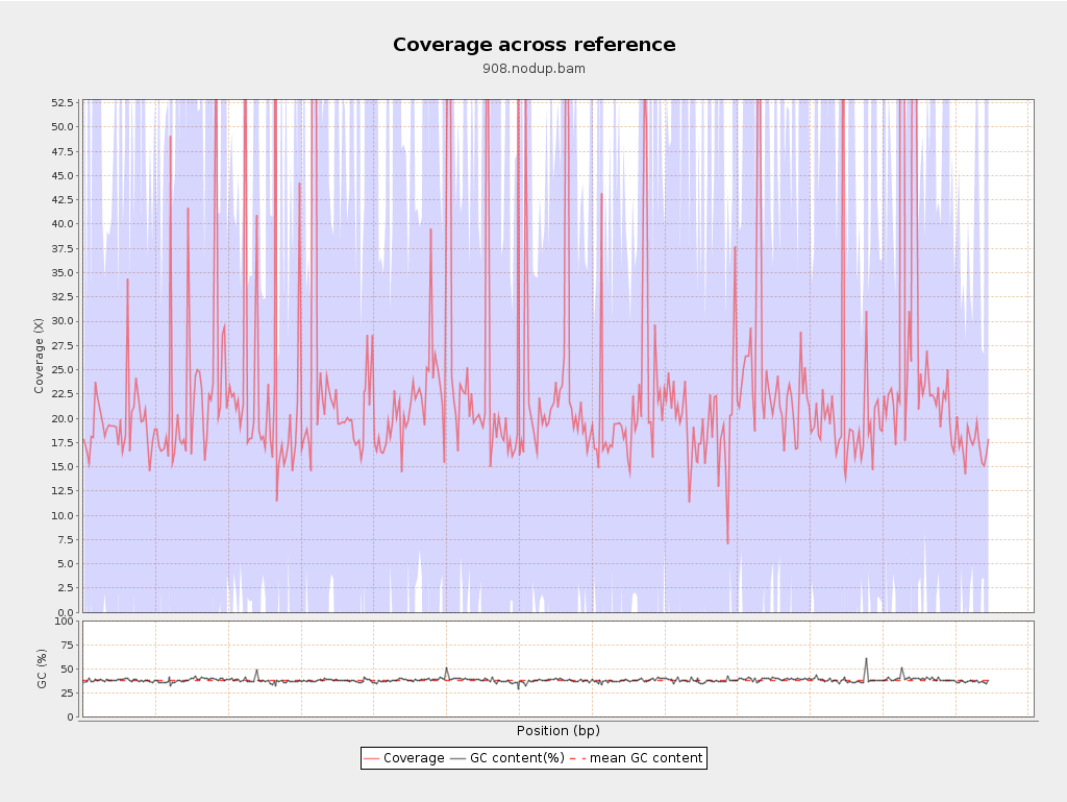
General error rate	2.32%
Mismatches	155,984,003
Insertions	4,871,268
Mapped reads with at least one insertion	8.34%
Deletions	5,065,952
Mapped reads with at least one deletion	8.54%
Homopolymer indels	55.7%

2.7. Chromosome stats

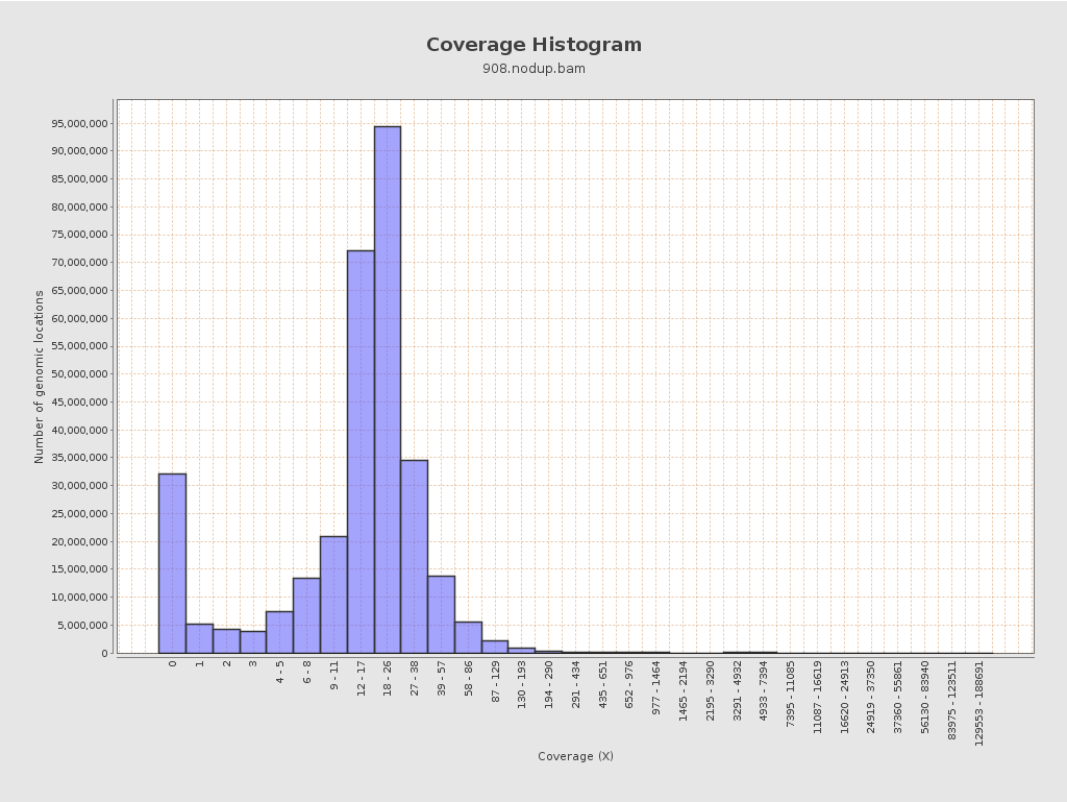
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	570437426	19.1909	66.0918

LT669789.1	36598175	874336745	23.8902	219.9306
LT669790.1	30422129	725921247	23.8616	167.6661
LT669791.1	52758100	1211010206	22.954	179.0587
LT669792.1	28376109	647432230	22.8161	205.8142
LT669793.1	33388210	716521050	21.4603	95.2094
LT669794.1	50579949	1162430711	22.982	192.8332
LT669795.1	49795044	1408030027	28.2765	305.3177

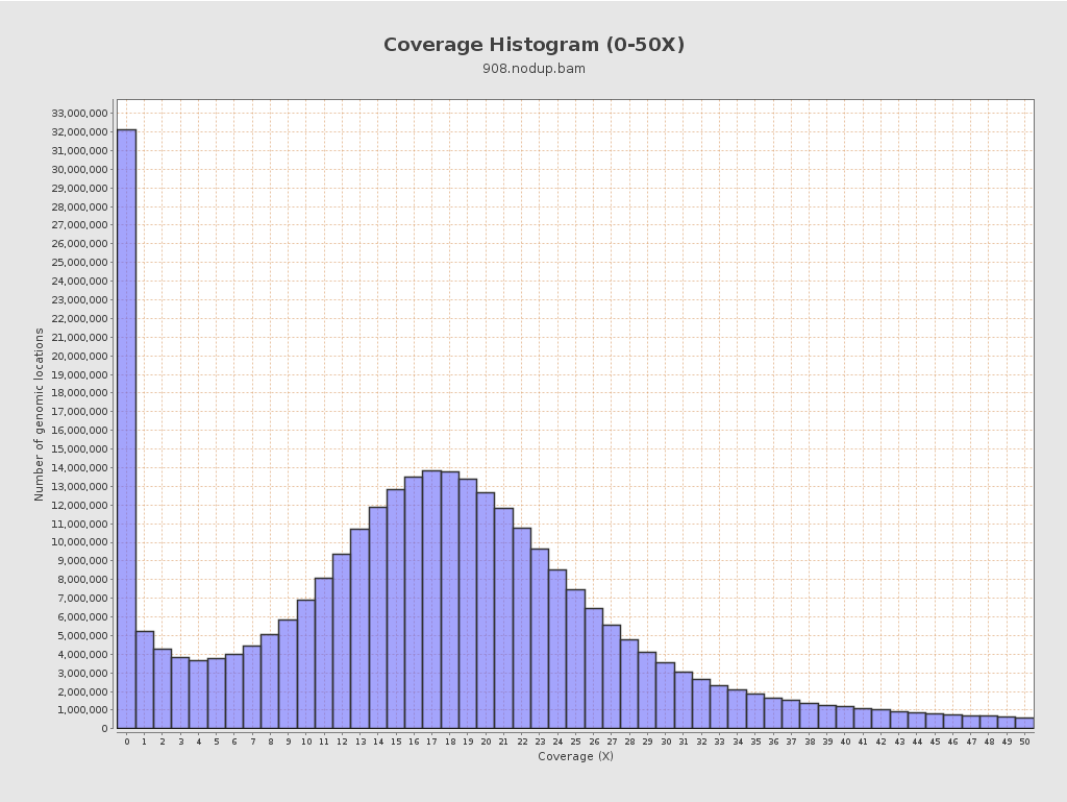
3. Results : Coverage across reference



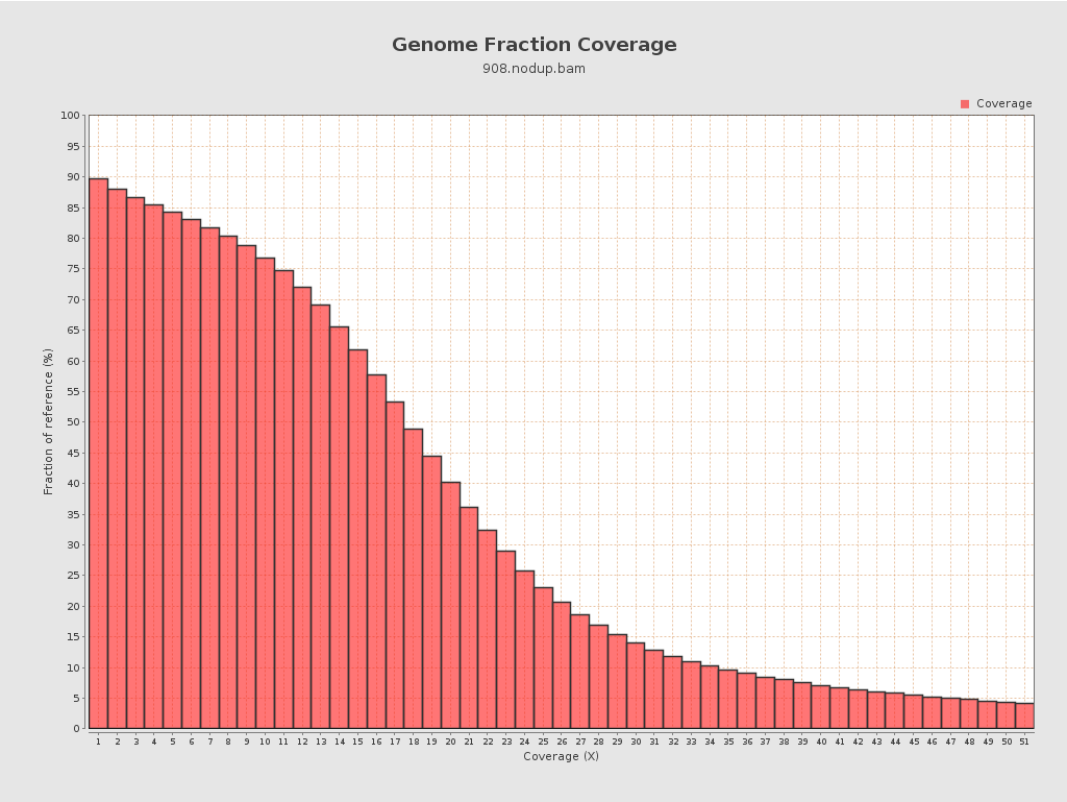
4. Results : Coverage Histogram



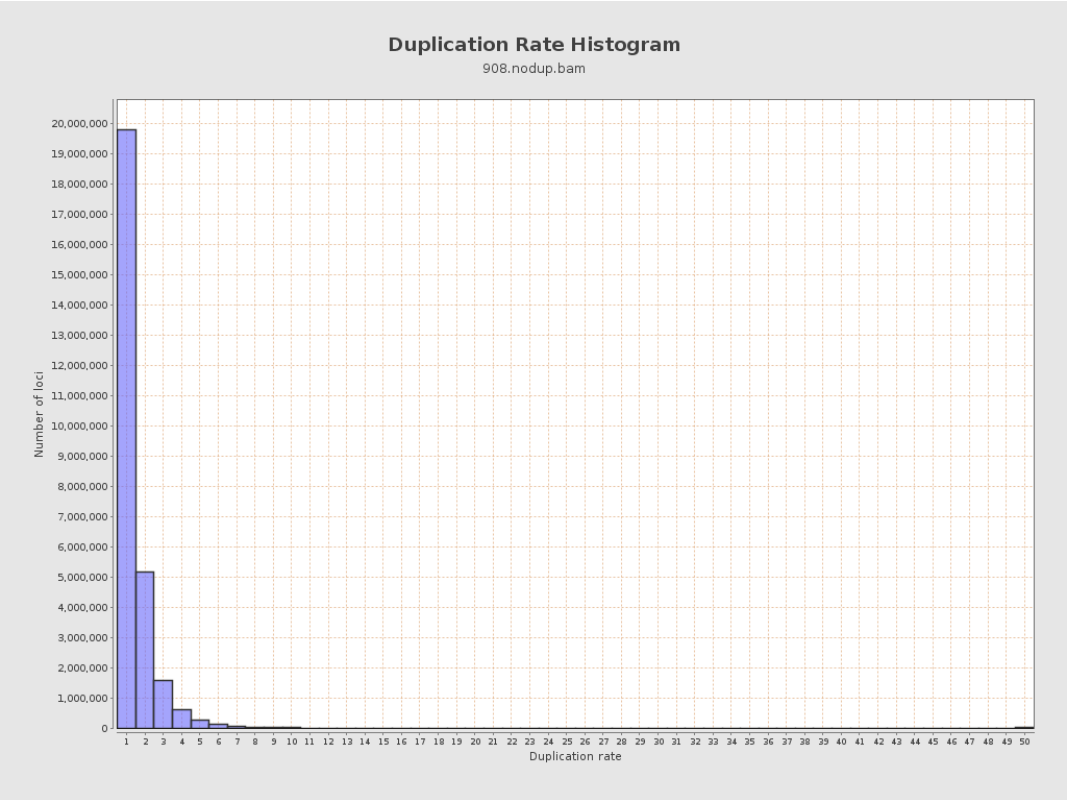
5. Results : Coverage Histogram (0-50X)



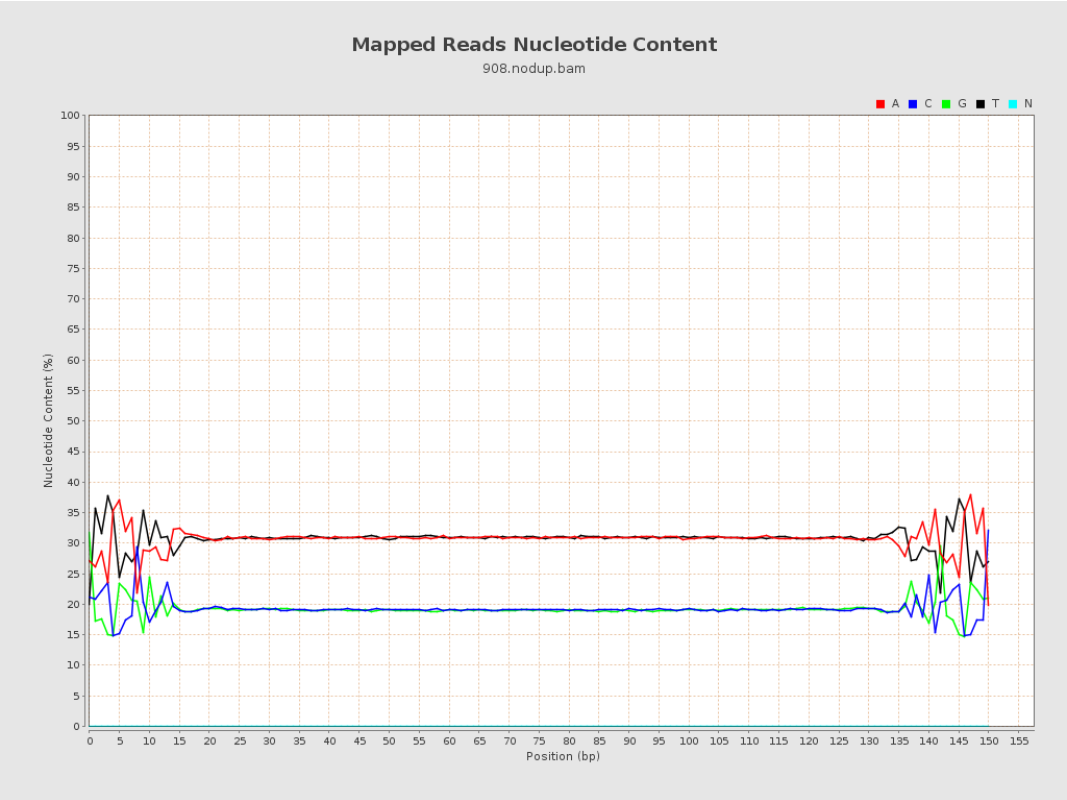
6. Results : Genome Fraction Coverage



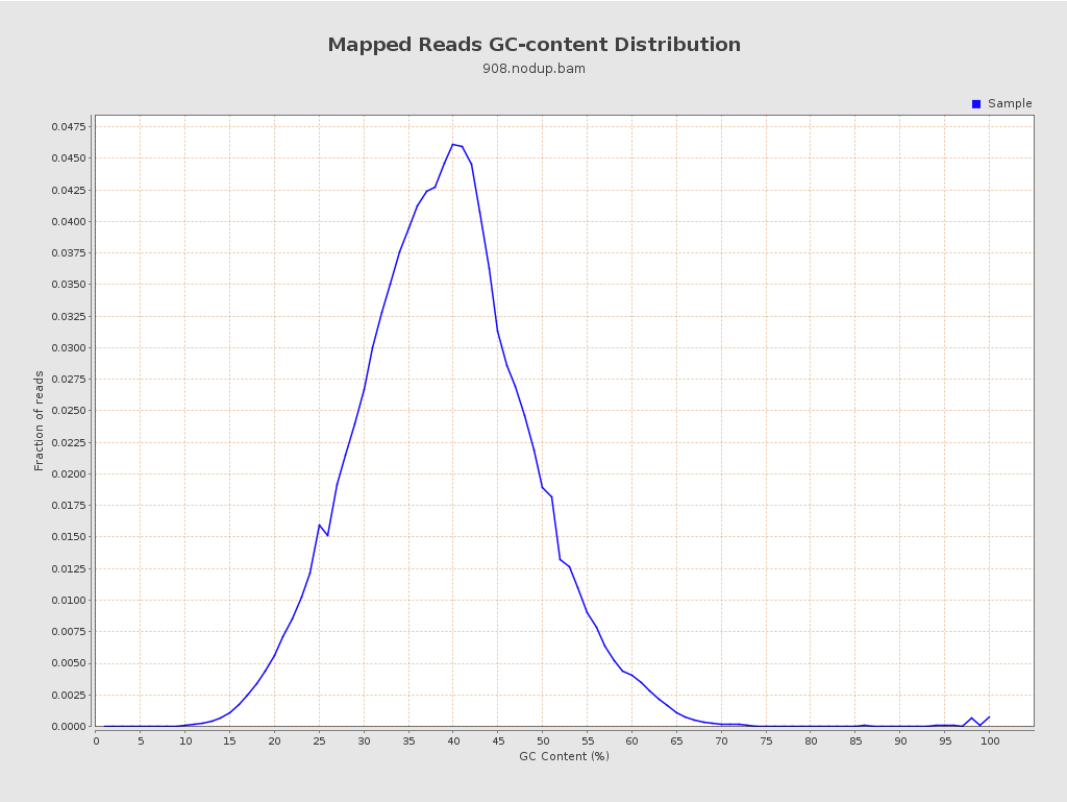
7. Results : Duplication Rate Histogram



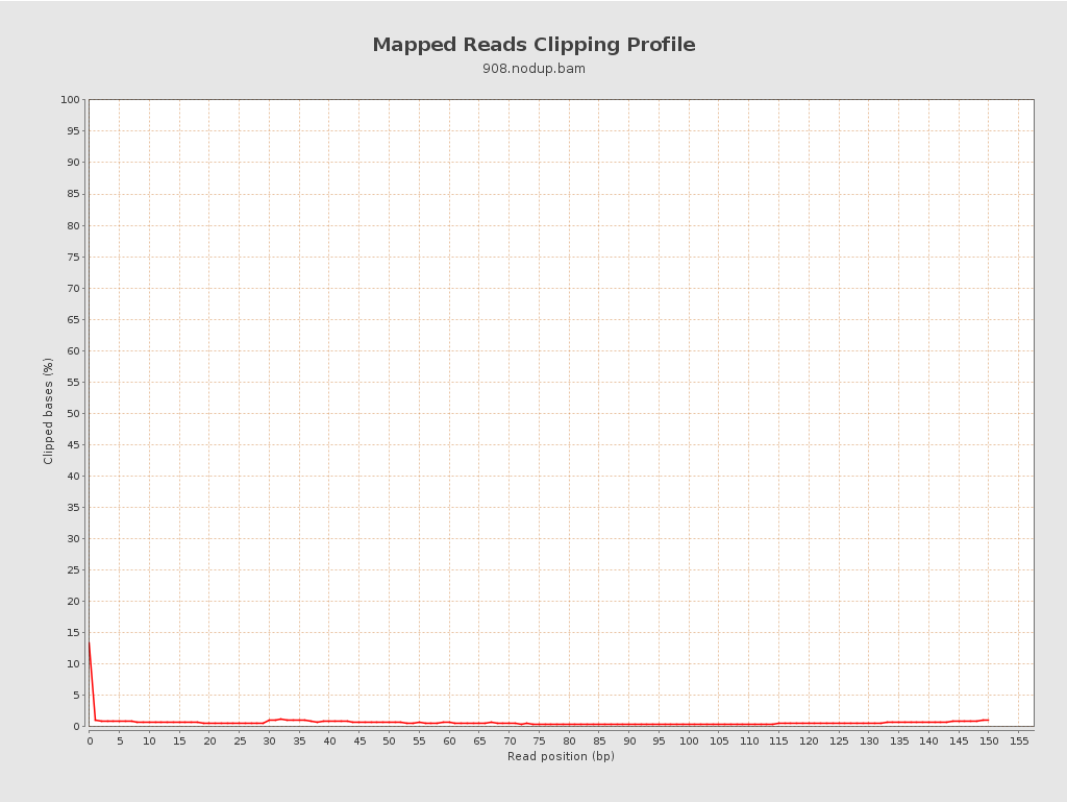
8. Results : Mapped Reads Nucleotide Content



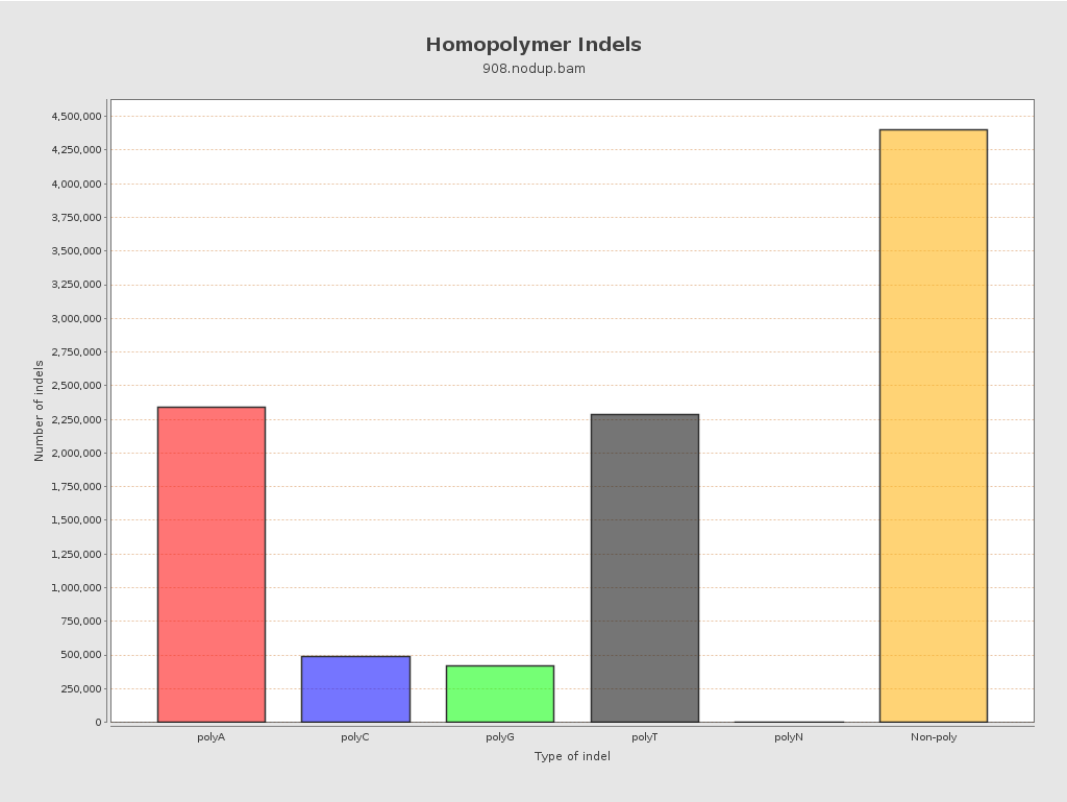
9. Results : Mapped Reads GC-content Distribution



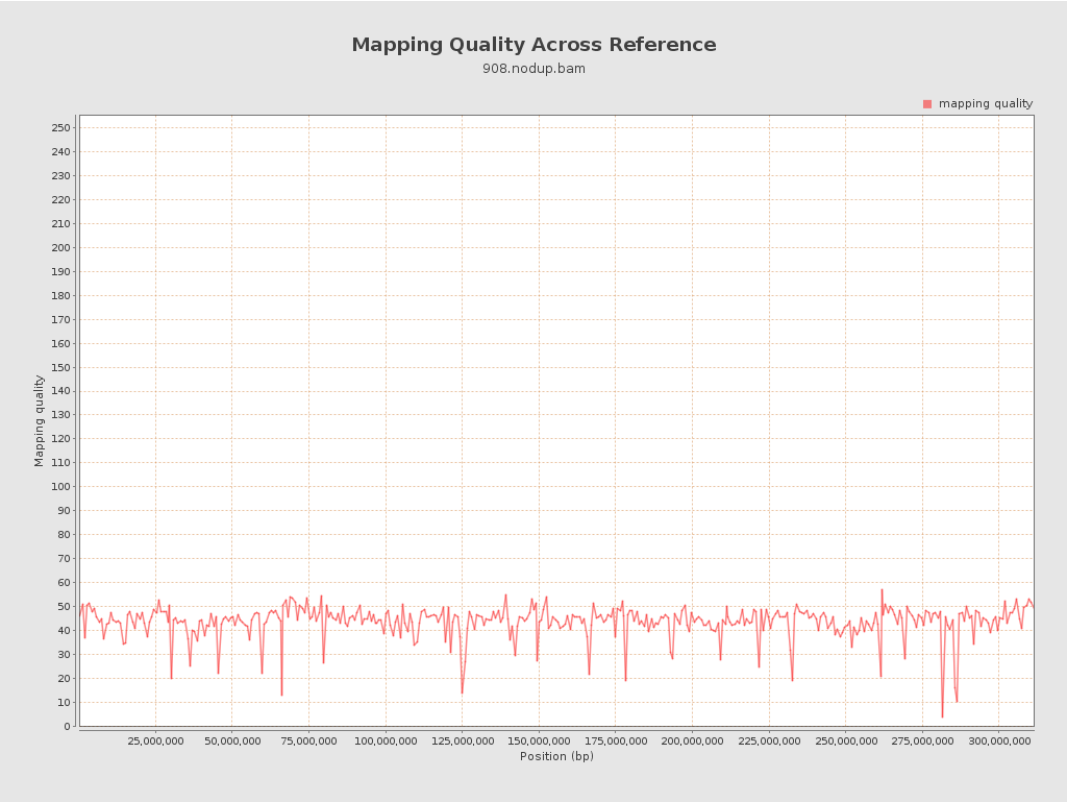
10. Results : Mapped Reads Clipping Profile



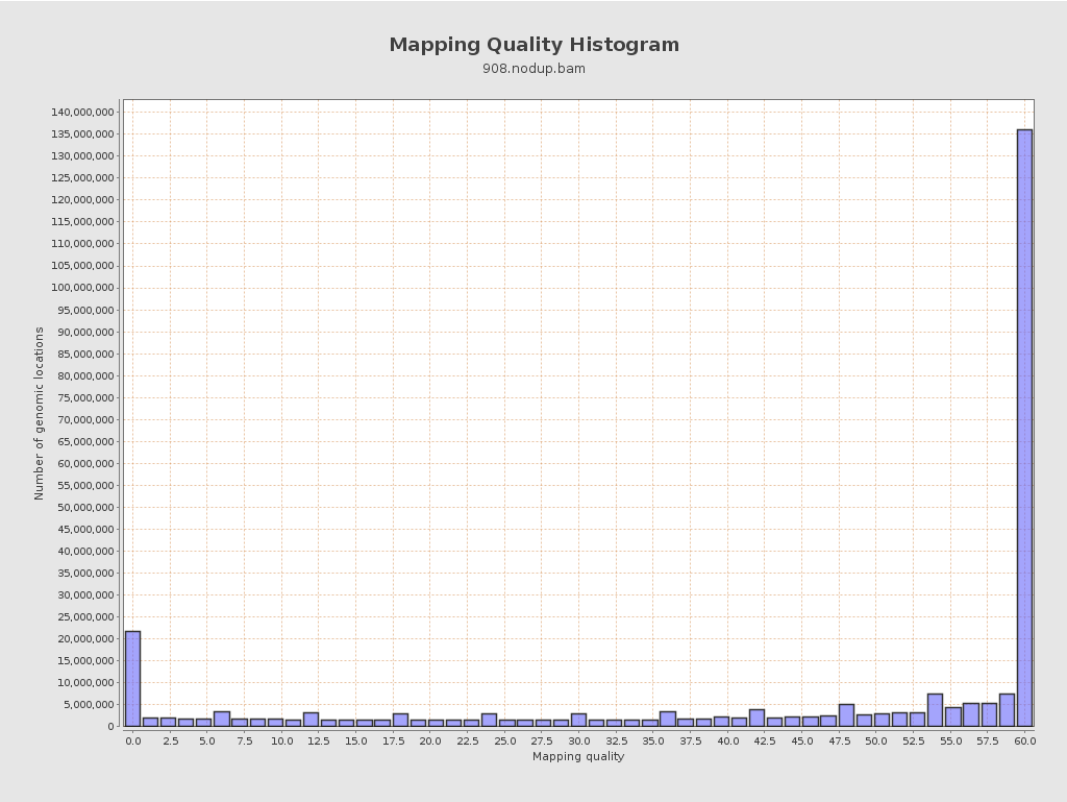
11. Results : Homopolymer Indels



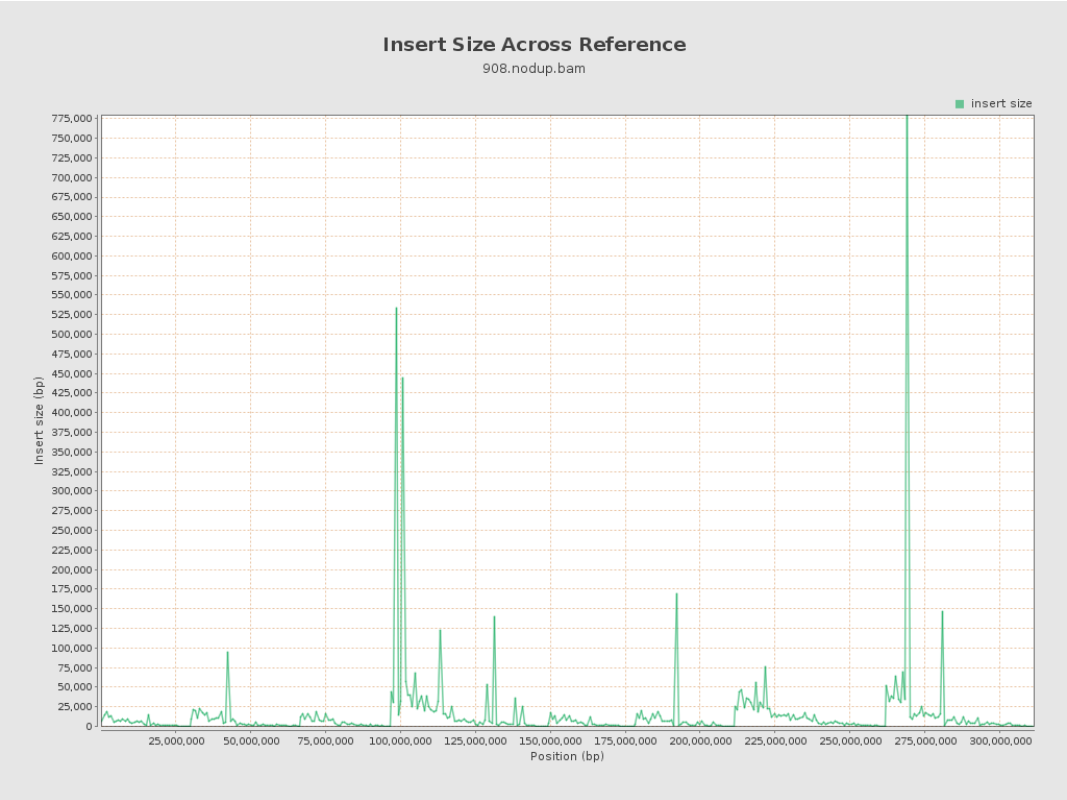
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram