Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1108
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1108 .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_235/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_235_S316_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_235/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_235_S316_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:44 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	76,208,459
Mapped reads	71,282,074 / 93.54%
Unmapped reads	4,926,385 / 6.46%
Mapped paired reads	71,282,074 / 93.54%
Mapped reads, first in pair	35,719,711 / 46.87%
Mapped reads, second in pair	35,562,363 / 46.66%
Mapped reads, both in pair	69,673,225 / 91.42%
Mapped reads, singletons	1,608,849 / 2.11%
Read min/max/mean length	30 / 151 / 148.01
Duplicated reads (flagged)	10,372,379 / 13.61%
Clipped reads	16,488,088 / 21.64%

2.2. ACGT Content

Number/percentage of A's	3,044,429,109 / 30.94%
Number/percentage of C's	1,876,079,919 / 19.06%
Number/percentage of T's	3,046,441,014 / 30.96%
Number/percentage of G's	1,874,420,823 / 19.05%
Number/percentage of N's	36,710 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	31.6636
Standard Deviation	234.0093

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Insert size

Mean	244,927.43
Standard Deviation	2,349,434.83
P25/Median/P75	327 / 427 / 550

2.6. Mismatches and indels

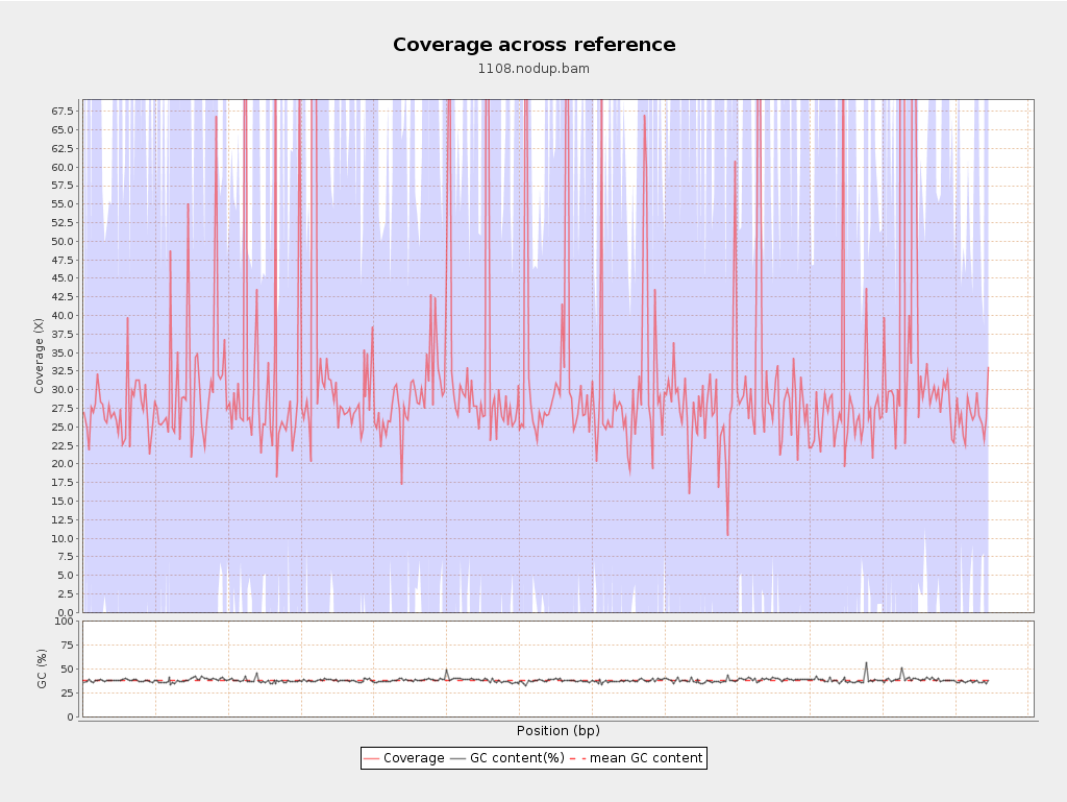
General error rate	2.34%
Mismatches	211,135,050
Insertions	6,885,160
Mapped reads with at least one insertion	8.66%
Deletions	6,924,296
Mapped reads with at least one deletion	8.59%
Homopolymer indels	56.4%

2.7. Chromosome stats

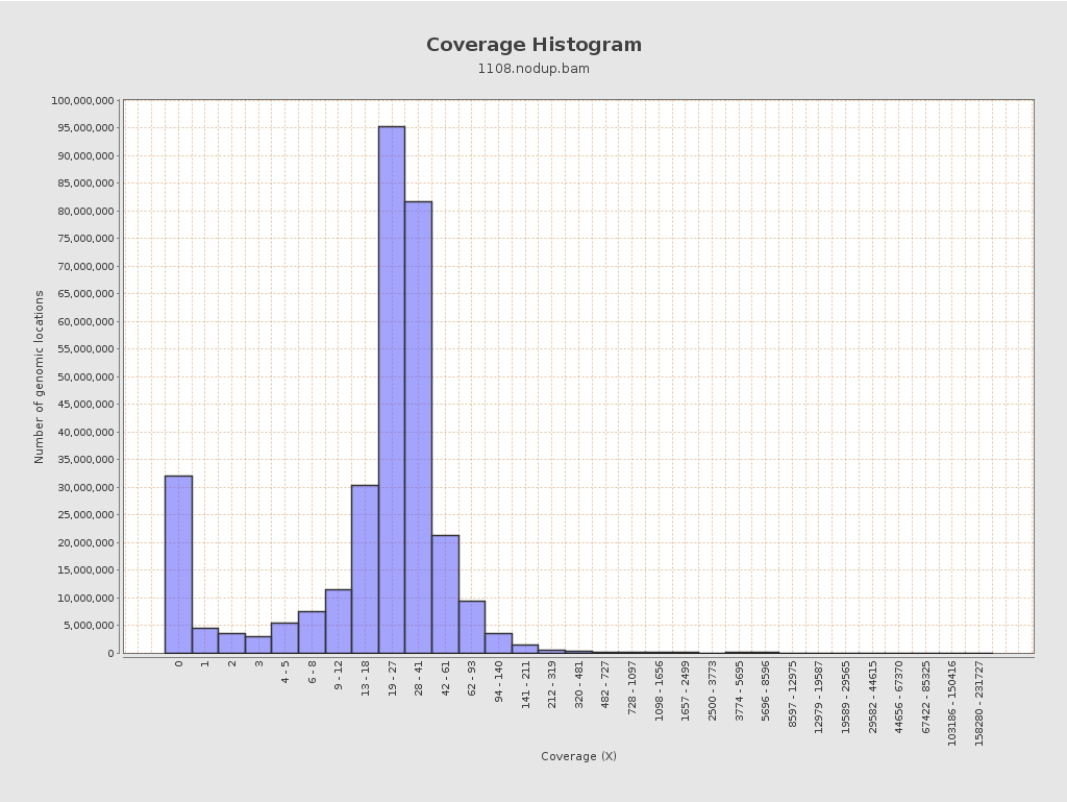
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	803193508	27.0214	76.7787

LT669789.1	36598175	1172162991	32.0279	243.7449
LT669790.1	30422129	1079463092	35.4828	262.9976
LT669791.1	52758100	1638044794	31.0482	218.2799
LT669792.1	28376109	901016354	31.7526	281.4776
LT669793.1	33388210	984355374	29.4821	133.6282
LT669794.1	50579949	1504416800	29.7433	197.9256
LT669795.1	49795044	1785043808	35.8478	325.3182

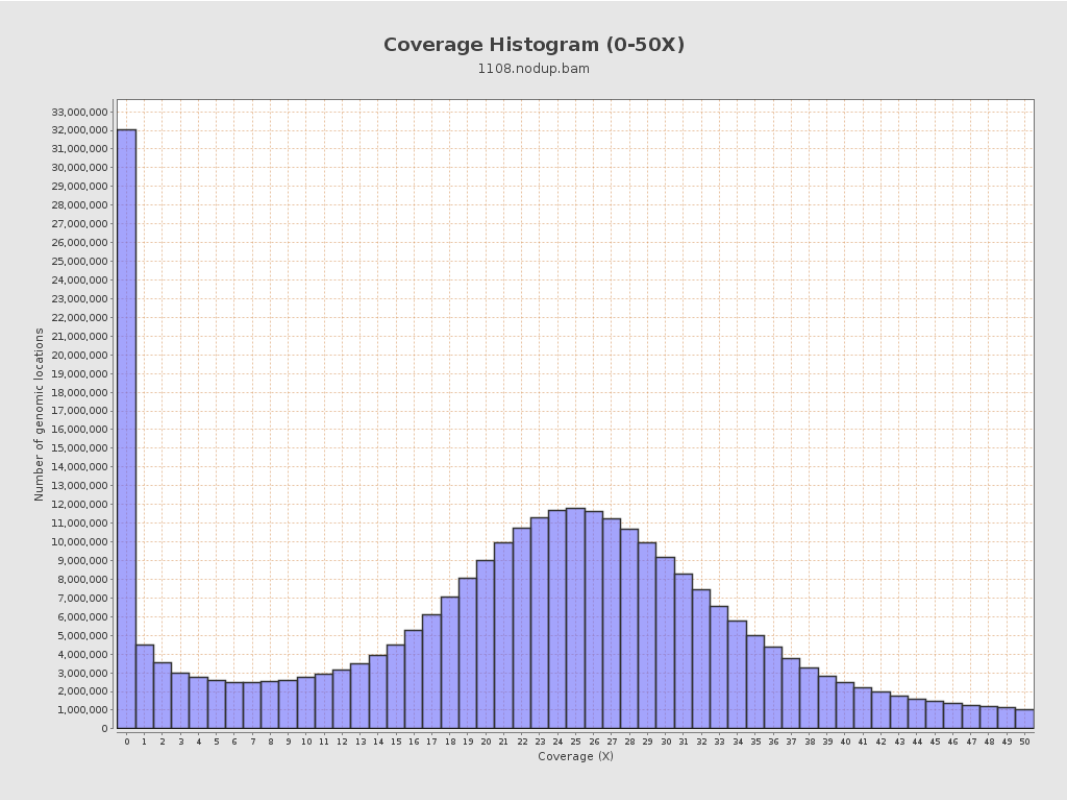
3. Results : Coverage across reference



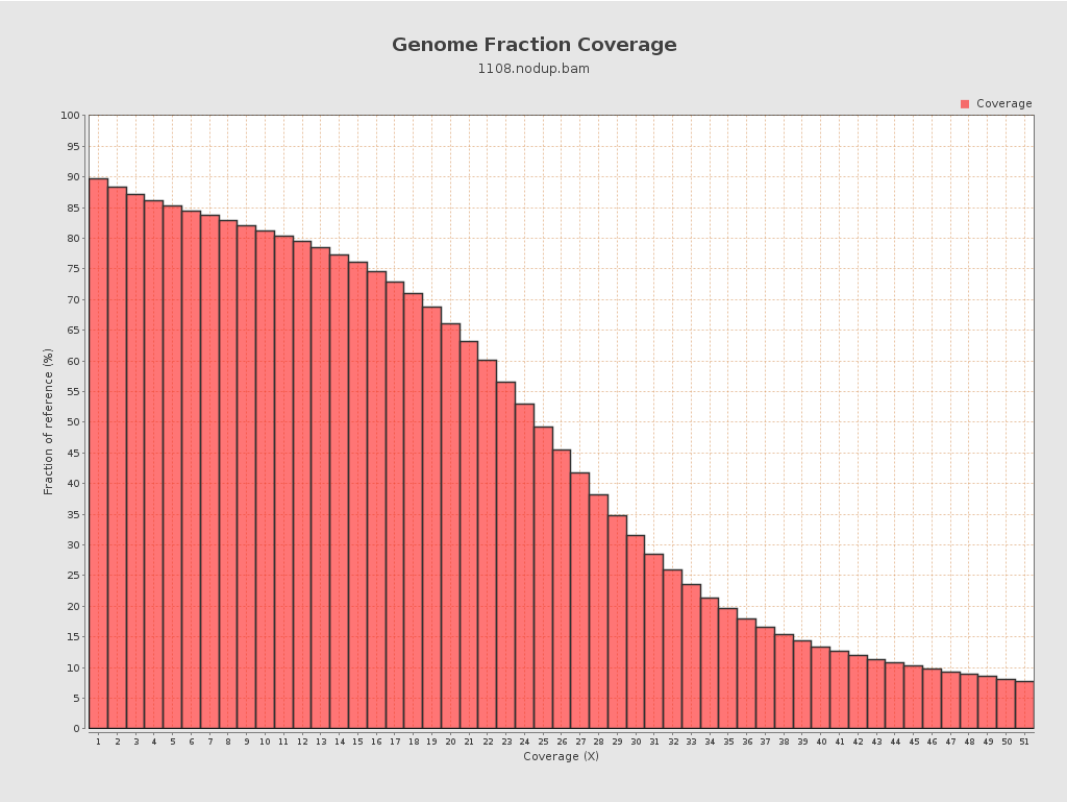
4. Results : Coverage Histogram



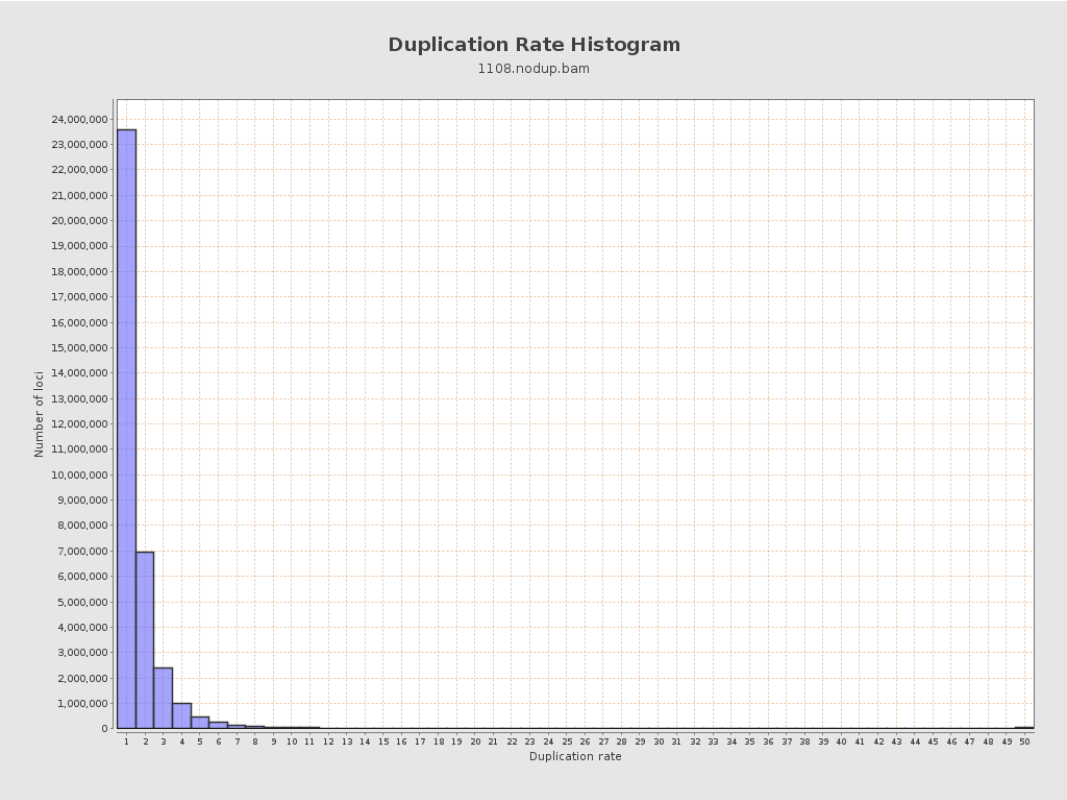
5. Results : Coverage Histogram (0-50X)



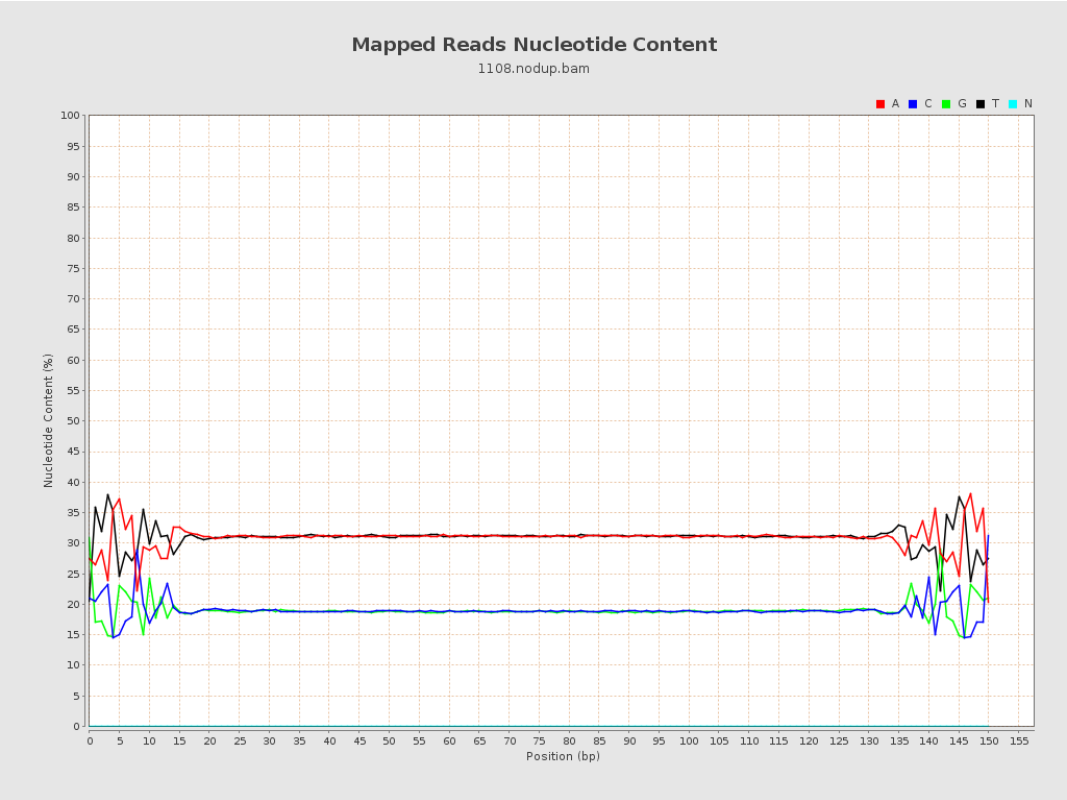
6. Results : Genome Fraction Coverage



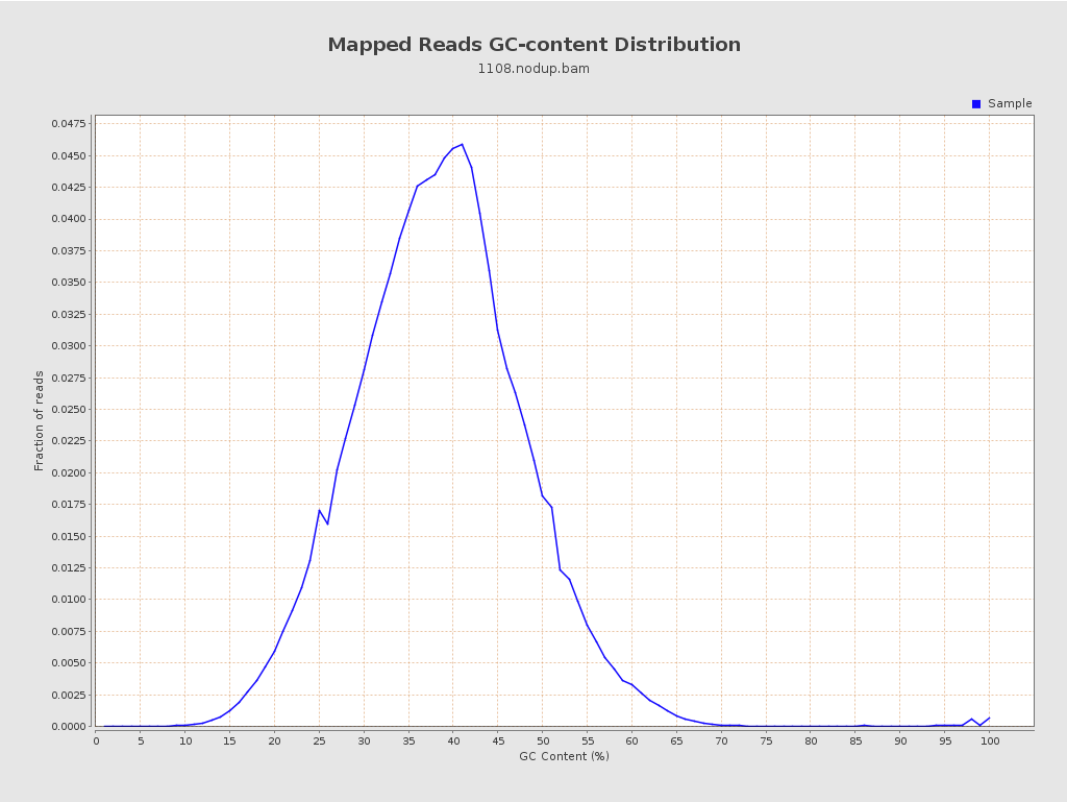
7. Results : Duplication Rate Histogram



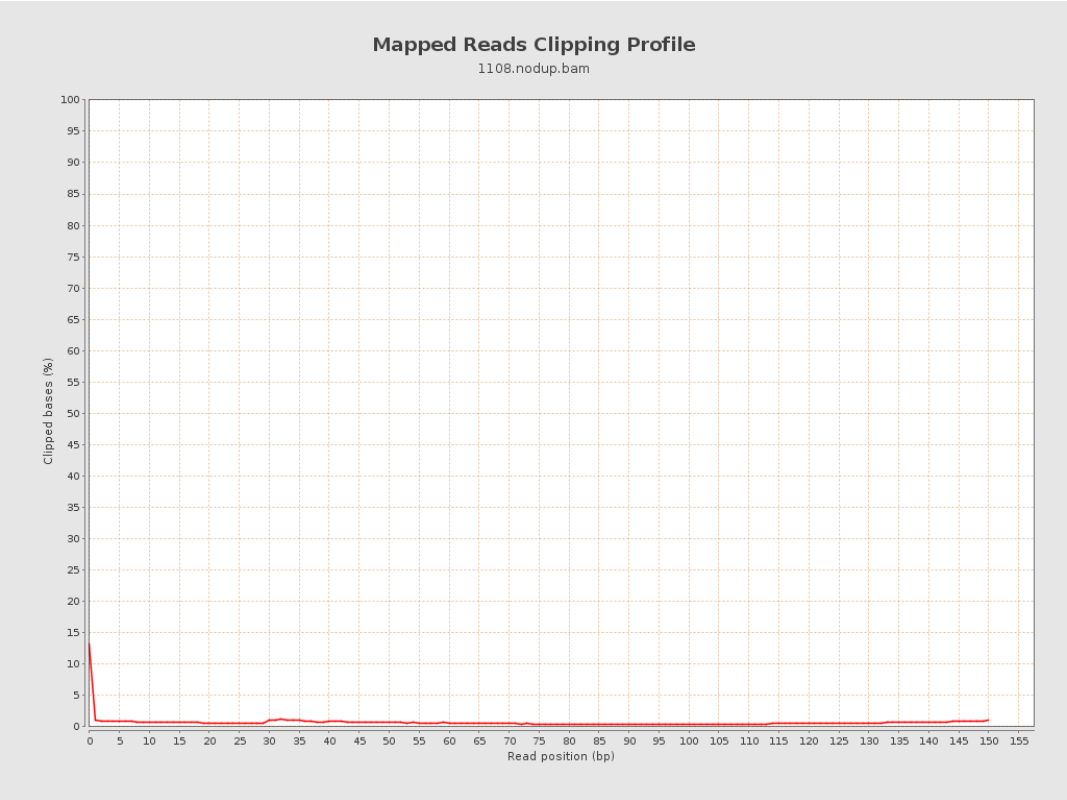
8. Results : Mapped Reads Nucleotide Content



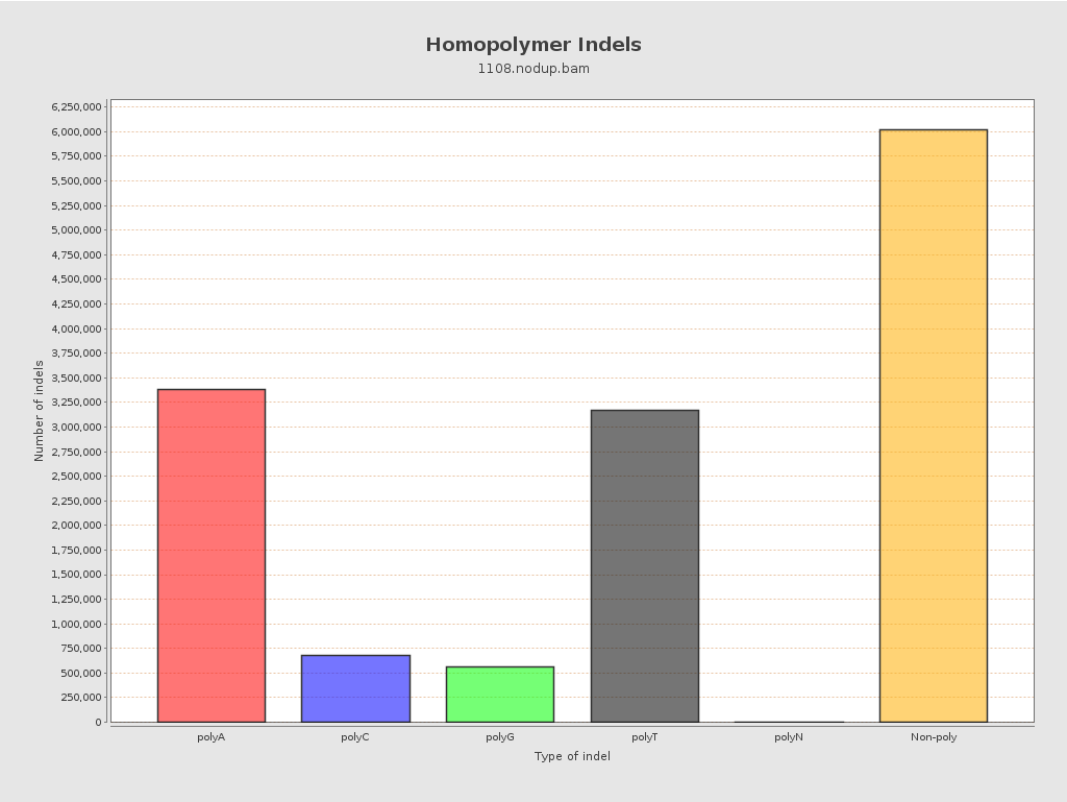
9. Results : Mapped Reads GC-content Distribution



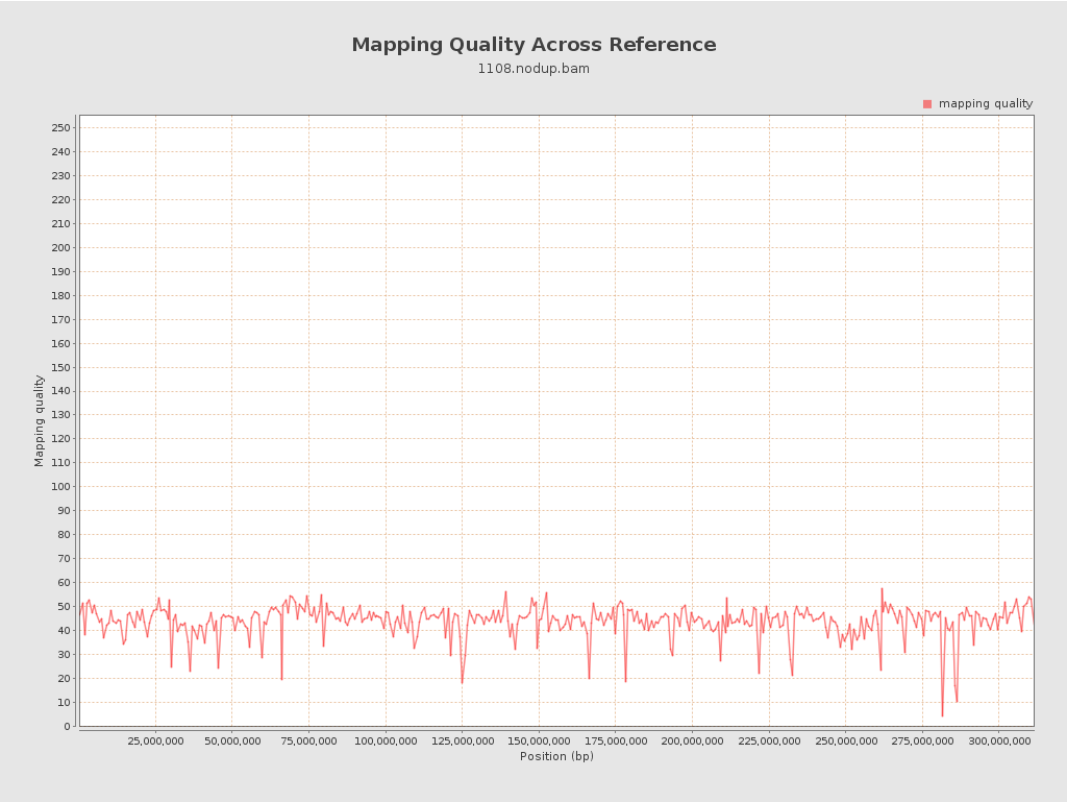
10. Results : Mapped Reads Clipping Profile



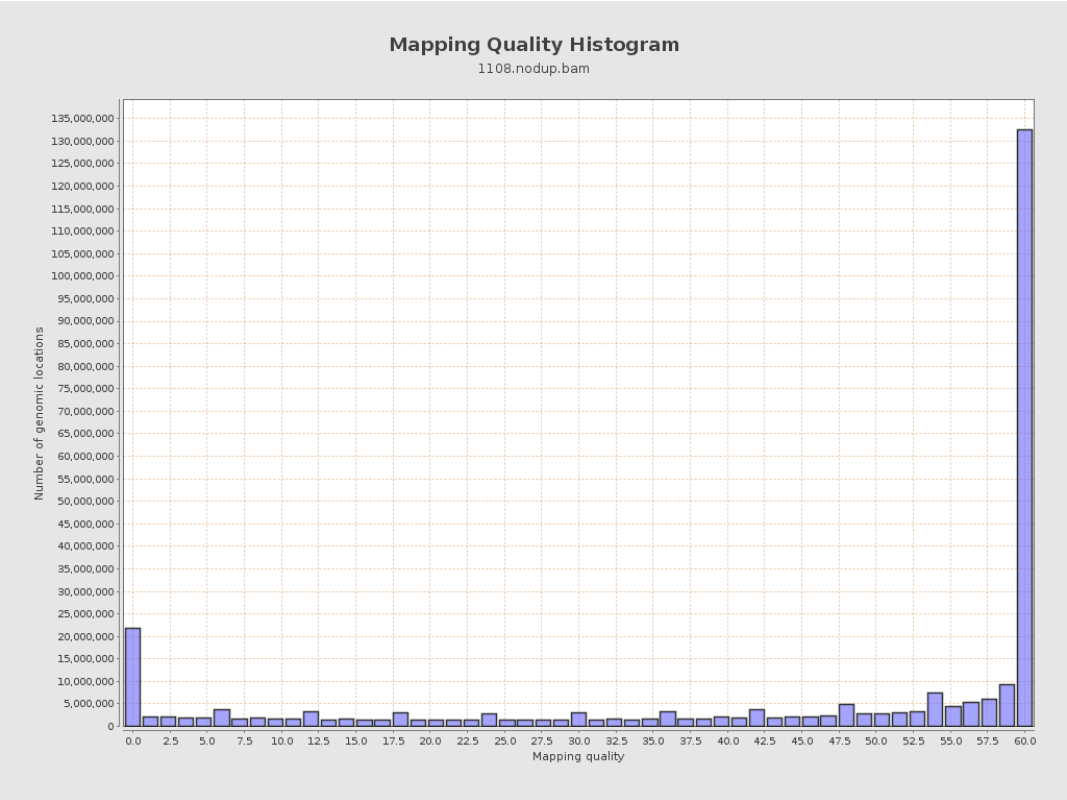
11. Results : Homopolymer Indels



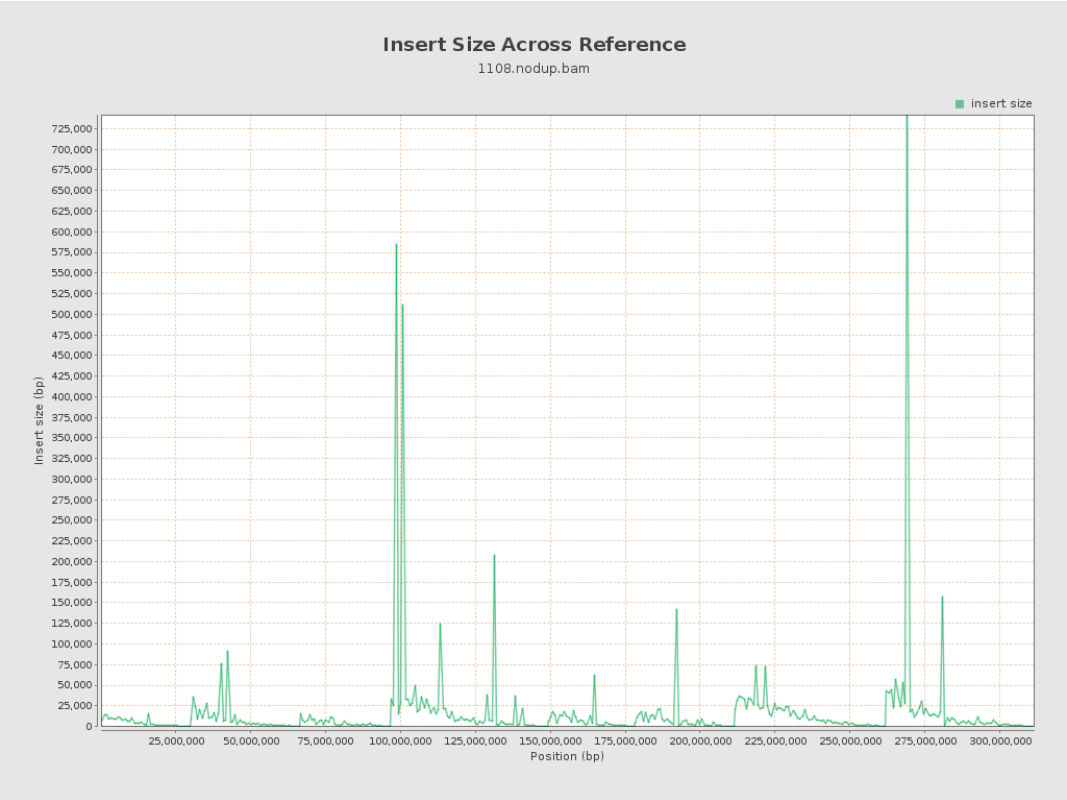
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram