Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1102
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1102 .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_272/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_272_S353_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_272/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_272_S353_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:10 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,935,553
Mapped reads	54,295,542 / 90.59%
Unmapped reads	5,640,011 / 9.41%
Mapped paired reads	54,295,542 / 90.59%
Mapped reads, first in pair	27,207,207 / 45.39%
Mapped reads, second in pair	27,088,335 / 45.2%
Mapped reads, both in pair	52,449,899 / 87.51%
Mapped reads, singletons	1,845,643 / 3.08%
Read min/max/mean length	30 / 151 / 147.94
Duplicated reads (flagged)	9,207,450 / 15.36%
Clipped reads	13,638,293 / 22.75%

2.2. ACGT Content

Number/percentage of A's	2,286,646,004 / 30.94%
Number/percentage of C's	1,406,448,230 / 19.03%
Number/percentage of T's	2,288,364,336 / 30.97%
Number/percentage of G's	1,408,218,014 / 19.06%
Number/percentage of N's	28,110 / 0%
GC Percentage	38.09%

2.3. Coverage

Mean	23.7761
Standard Deviation	251.8365

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Insert size

Mean	271,664.93
Standard Deviation	2,517,820.36
P25/Median/P75	310 / 408 / 534

2.6. Mismatches and indels

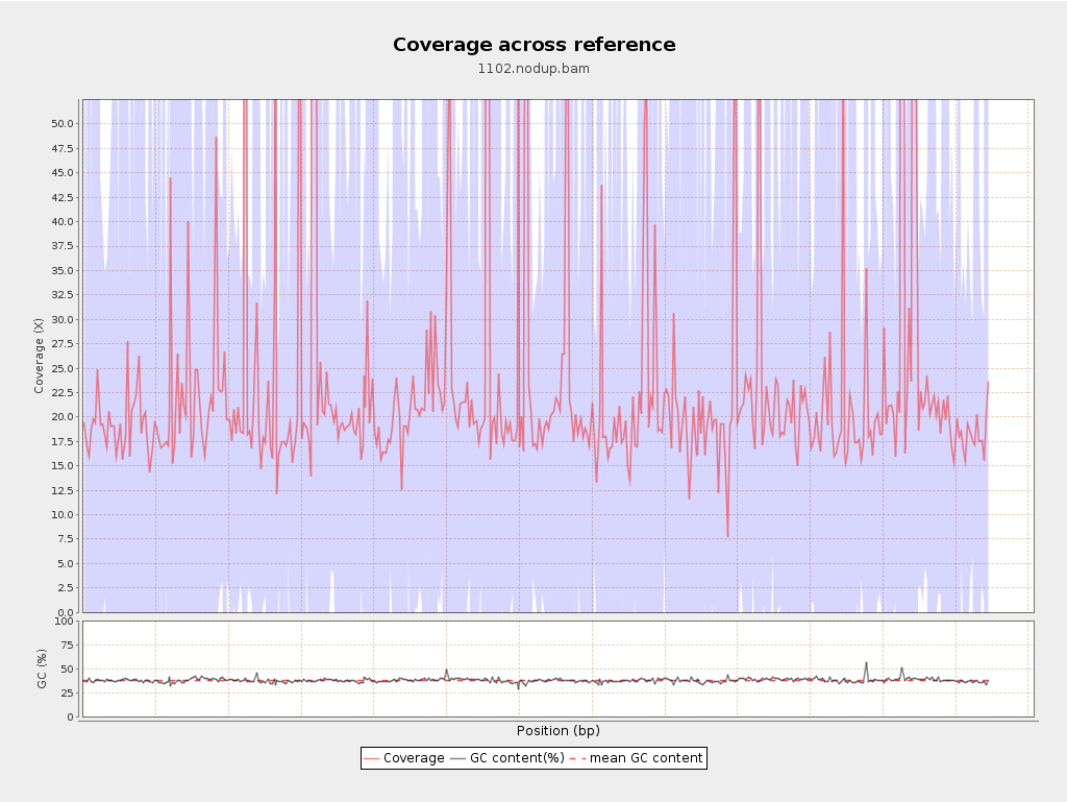
General error rate	2.43%
Mismatches	163,905,676
Insertions	5,652,457
Mapped reads with at least one insertion	9.25%
Deletions	5,325,718
Mapped reads with at least one deletion	8.69%
Homopolymer indels	57.57%

2.7. Chromosome stats

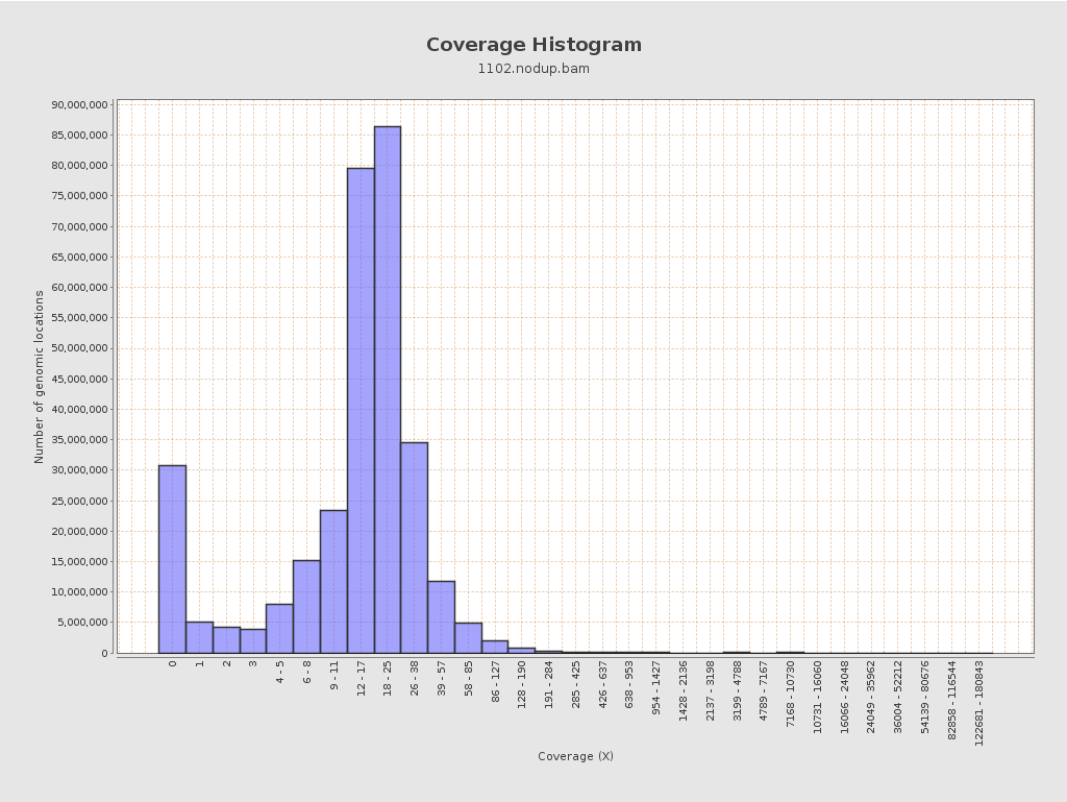
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	562914705	18.9378	103.5813

LT669789.1	36598175	883861792	24.1504	259.0551
LT669790.1	30422129	923831794	30.3671	378.3638
LT669791.1	52758100	1241987495	23.5412	279.3782
LT669792.1	28376109	677931728	23.8909	241.5952
LT669793.1	33388210	716340329	21.4549	191.808
LT669794.1	50579949	1114636227	22.0371	190.6141
LT669795.1	49795044	1288115910	25.8684	275.9494

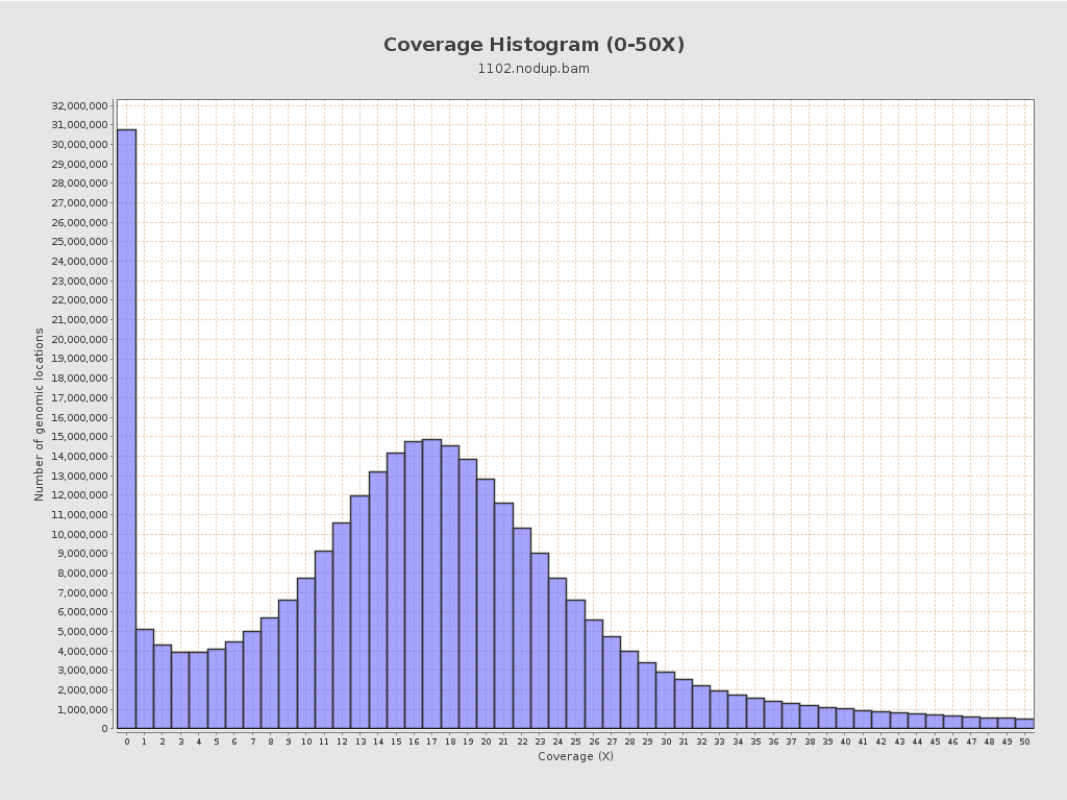
3. Results : Coverage across reference



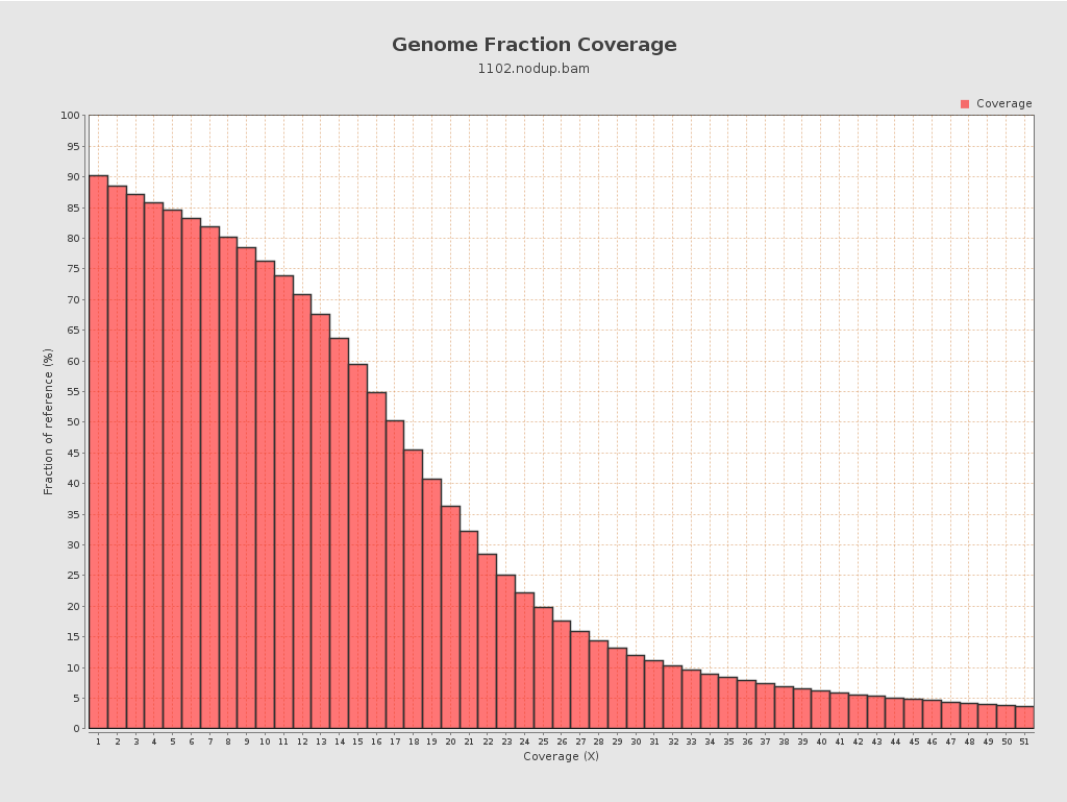
4. Results : Coverage Histogram



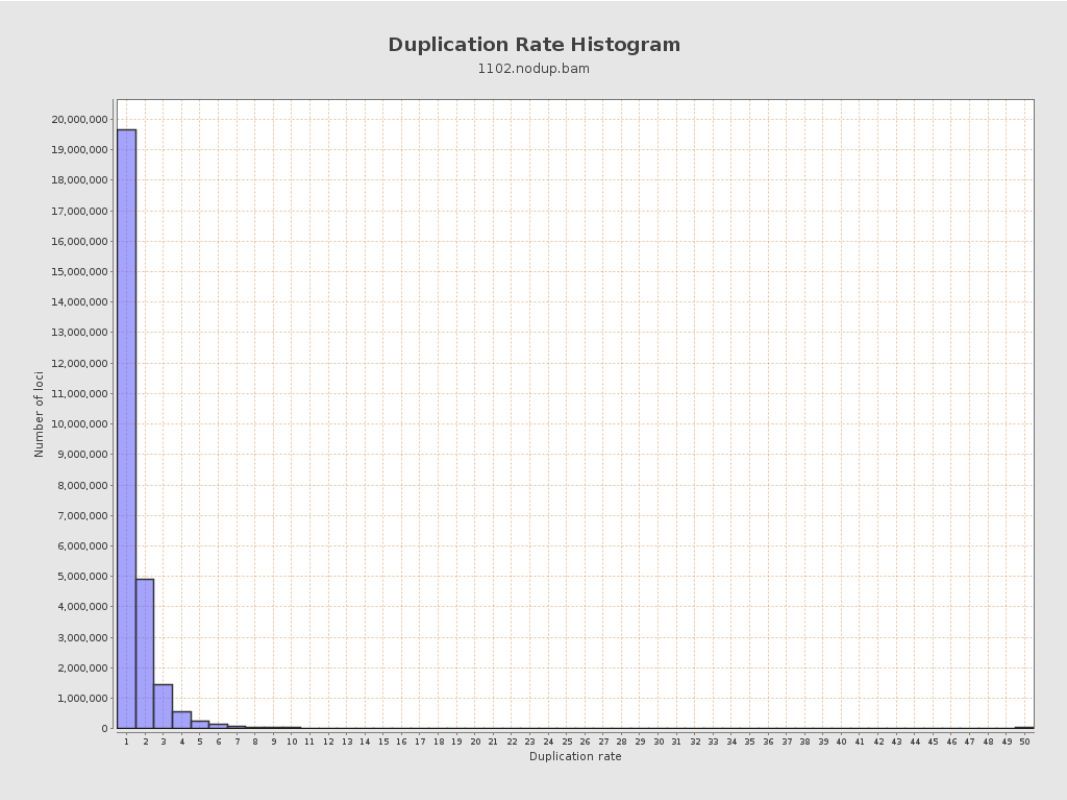
5. Results : Coverage Histogram (0-50X)



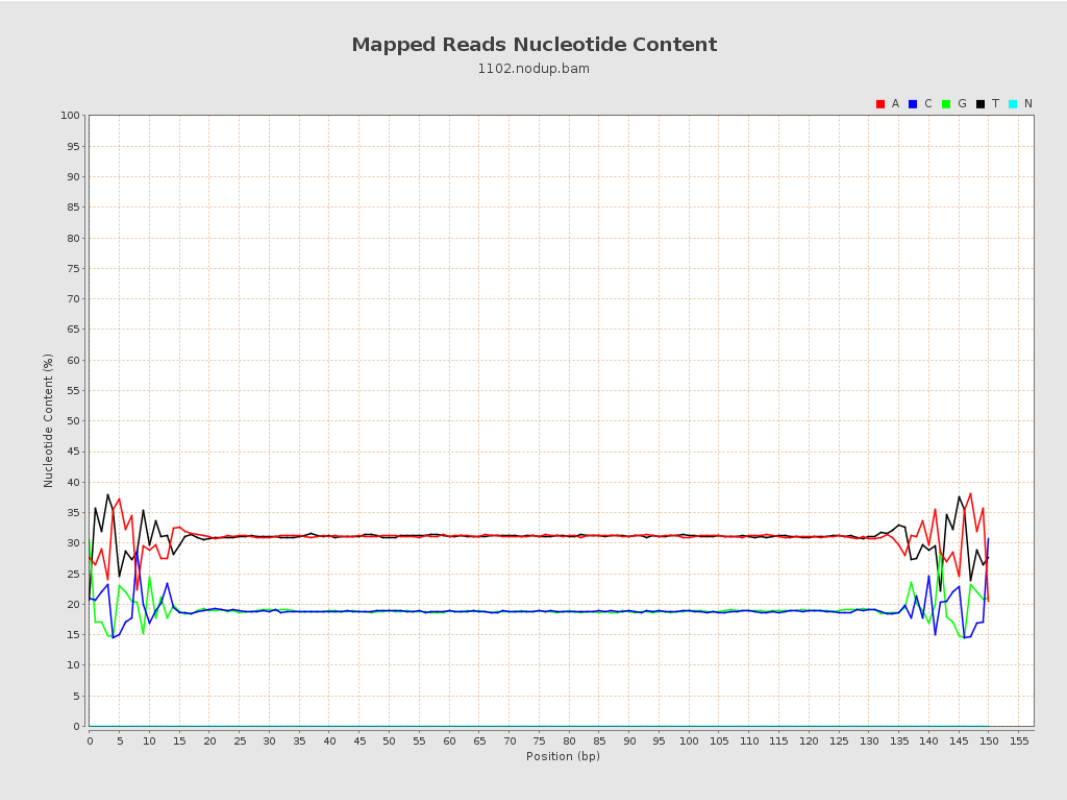
6. Results : Genome Fraction Coverage



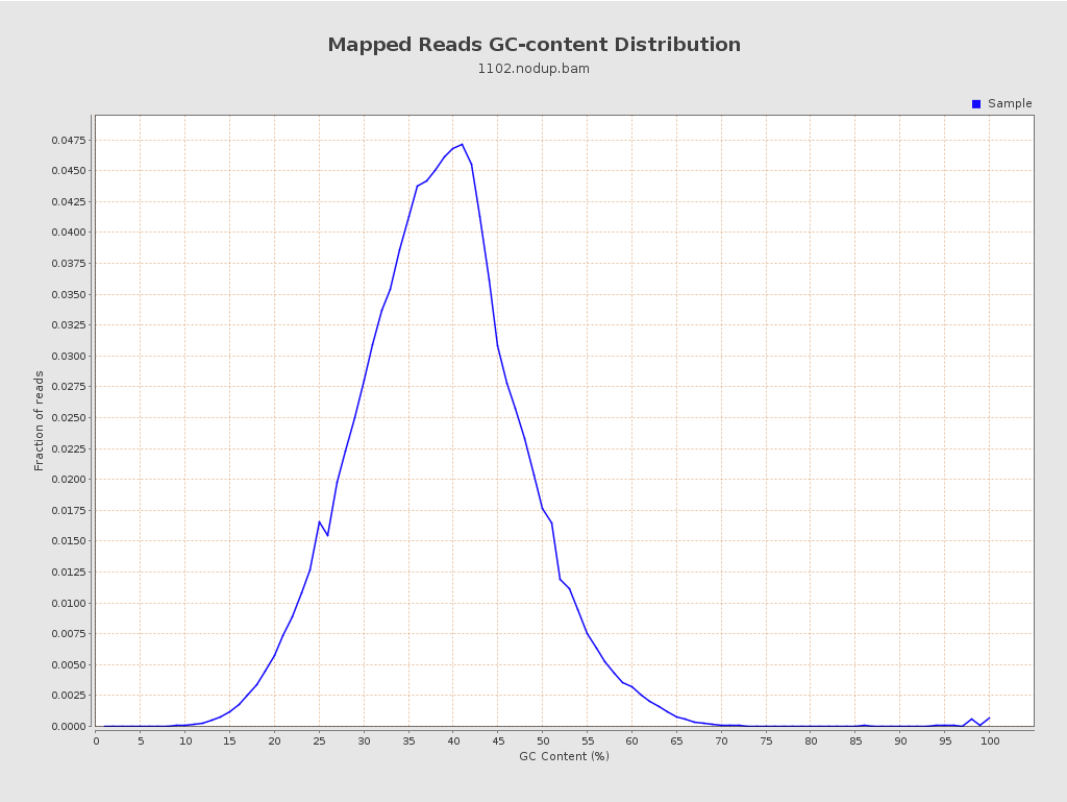
7. Results : Duplication Rate Histogram



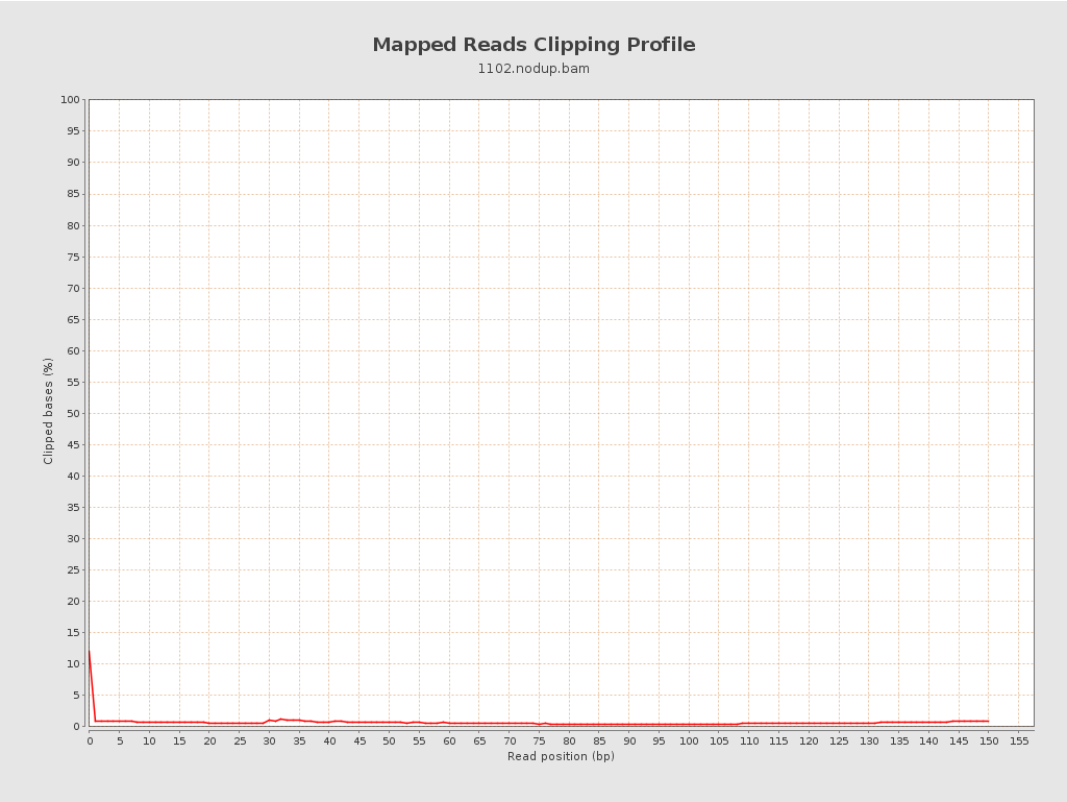
8. Results : Mapped Reads Nucleotide Content



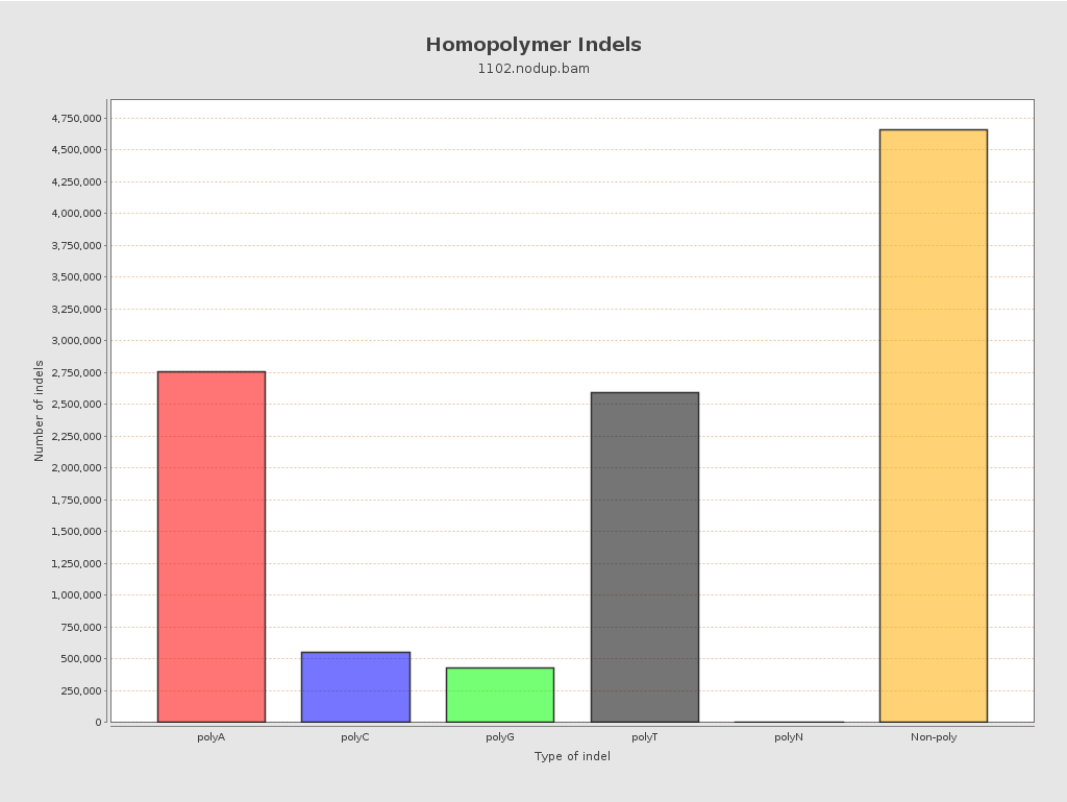
9. Results : Mapped Reads GC-content Distribution



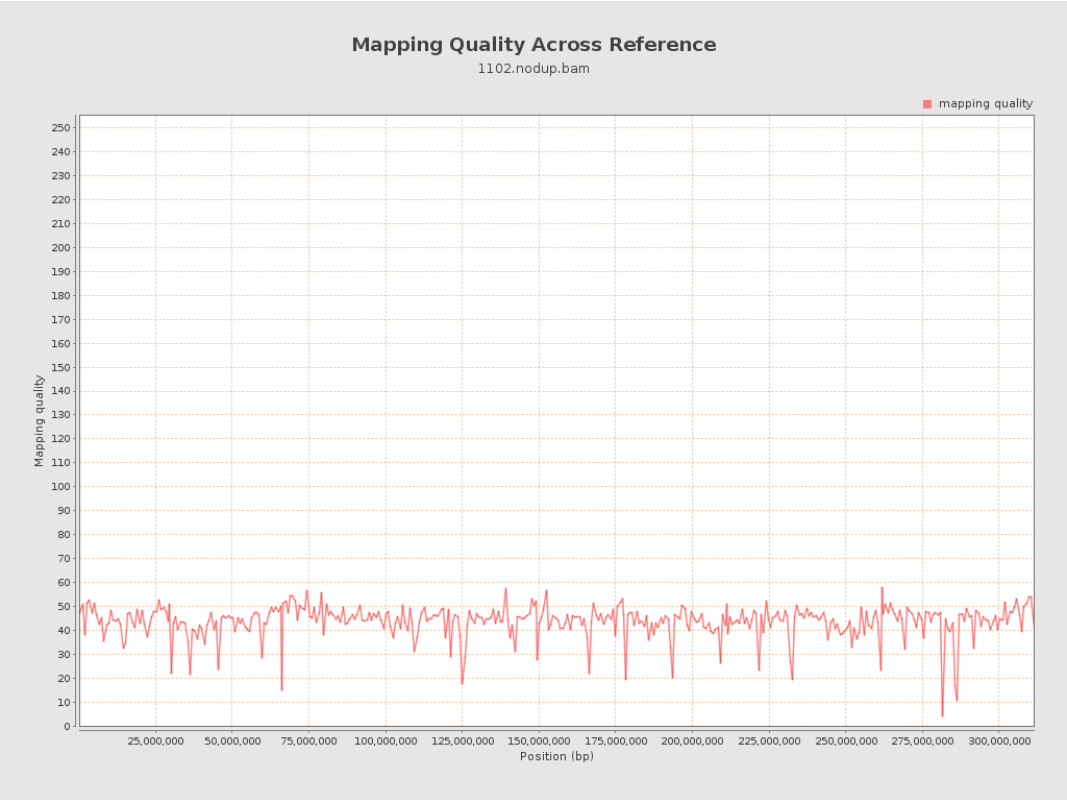
10. Results : Mapped Reads Clipping Profile



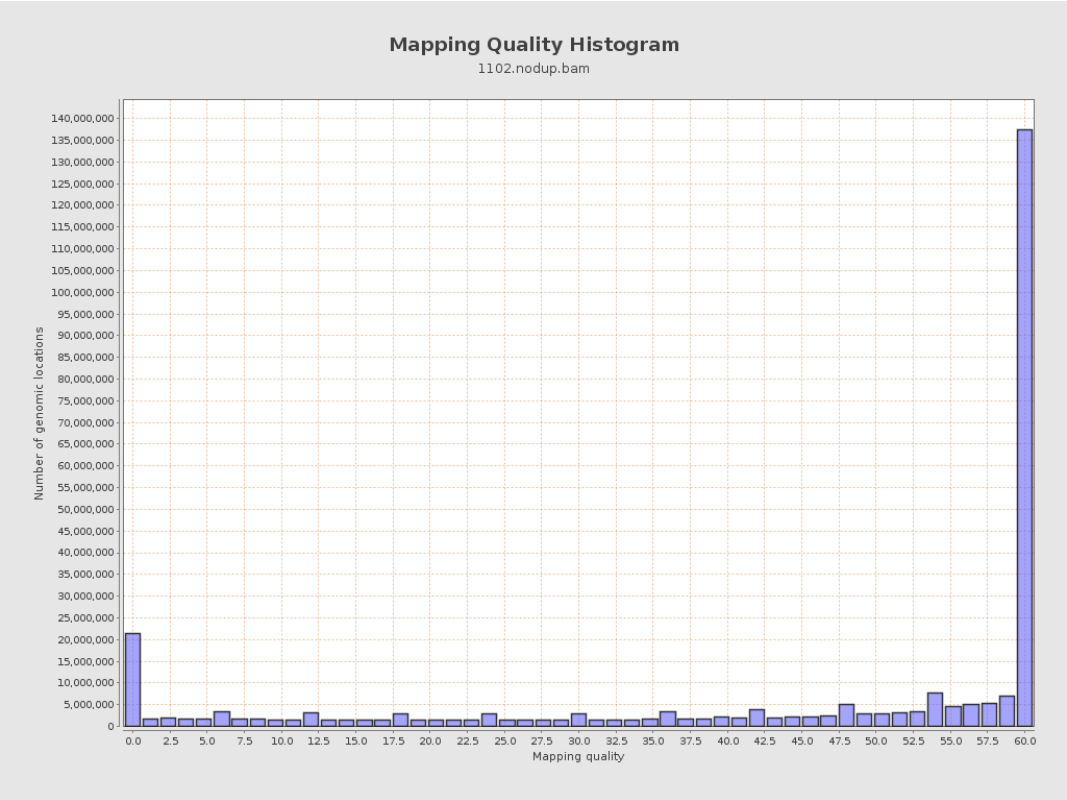
11. Results : Homopolymer Indels



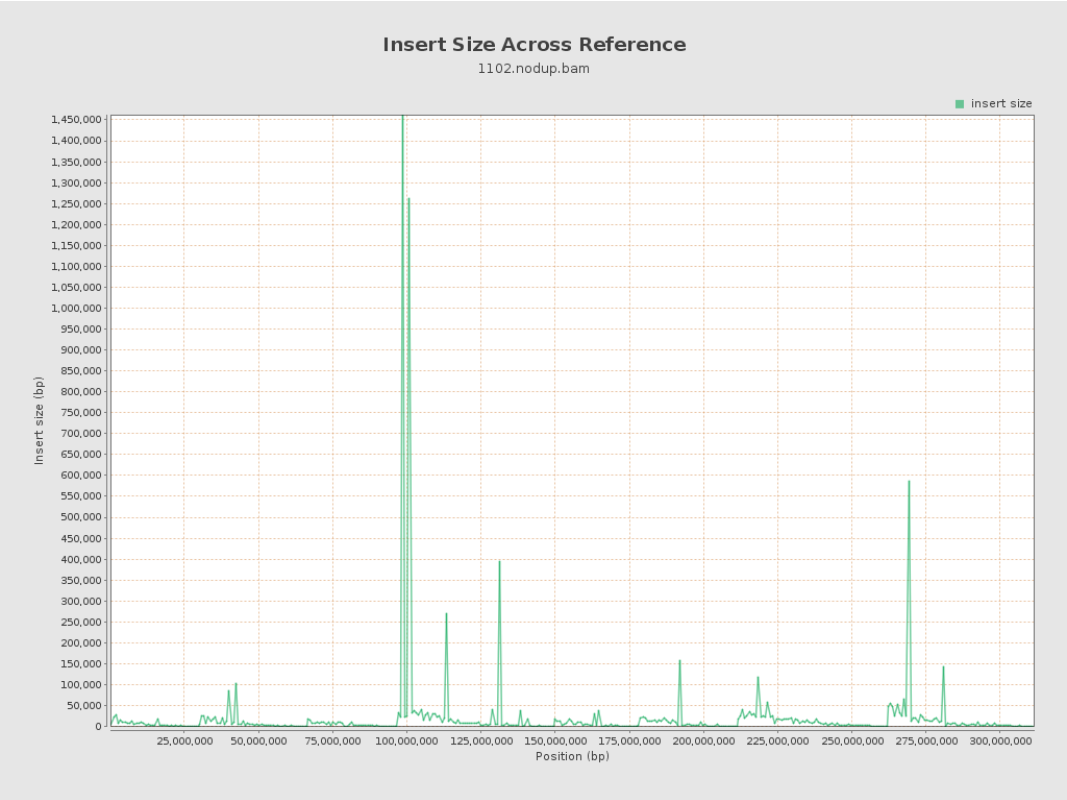
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram