Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:39:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1022
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1022 .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_211/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_211_S292_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_211/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_211_S292_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:39:35 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	88,338,620
Mapped reads	84,257,871 / 95.38%
Unmapped reads	4,080,749 / 4.62%
Mapped paired reads	84,257,871 / 95.38%
Mapped reads, first in pair	42,218,541 / 47.79%
Mapped reads, second in pair	42,039,330 / 47.59%
Mapped reads, both in pair	82,891,098 / 93.83%
Mapped reads, singletons	1,366,773 / 1.55%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	12,399,945 / 14.04%
Clipped reads	18,840,815 / 21.33%

2.2. ACGT Content

Number/percentage of A's	3,613,268,961 / 30.85%
Number/percentage of C's	2,246,308,263 / 19.18%
Number/percentage of T's	3,613,102,837 / 30.85%
Number/percentage of G's	2,238,939,800 / 19.12%
Number/percentage of N's	43,611 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	37.6786
Standard Deviation	304.1587

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Insert size

Mean	209,692.11
Standard Deviation	2,152,580.43
P25/Median/P75	305 / 401 / 523

2.6. Mismatches and indels

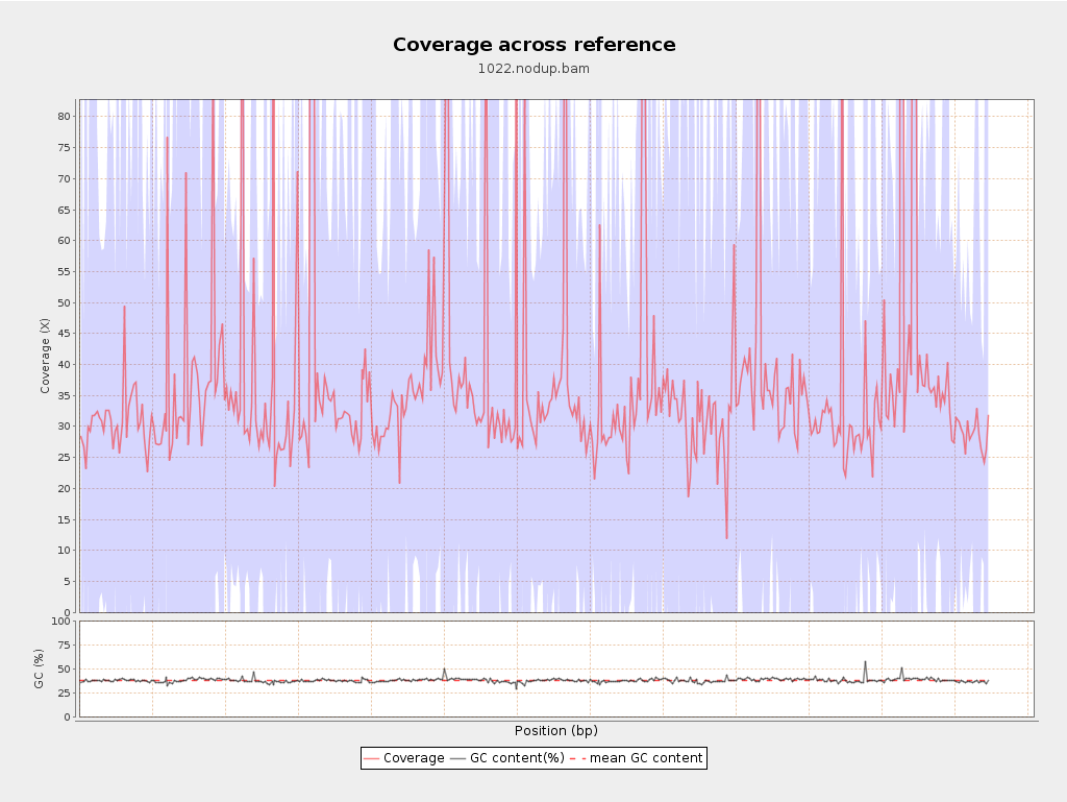
General error rate	2.34%
Mismatches	253,348,282
Insertions	7,678,225
Mapped reads with at least one insertion	8.22%
Deletions	8,107,990
Mapped reads with at least one deletion	8.55%
Homopolymer indels	56.23%

2.7. Chromosome stats

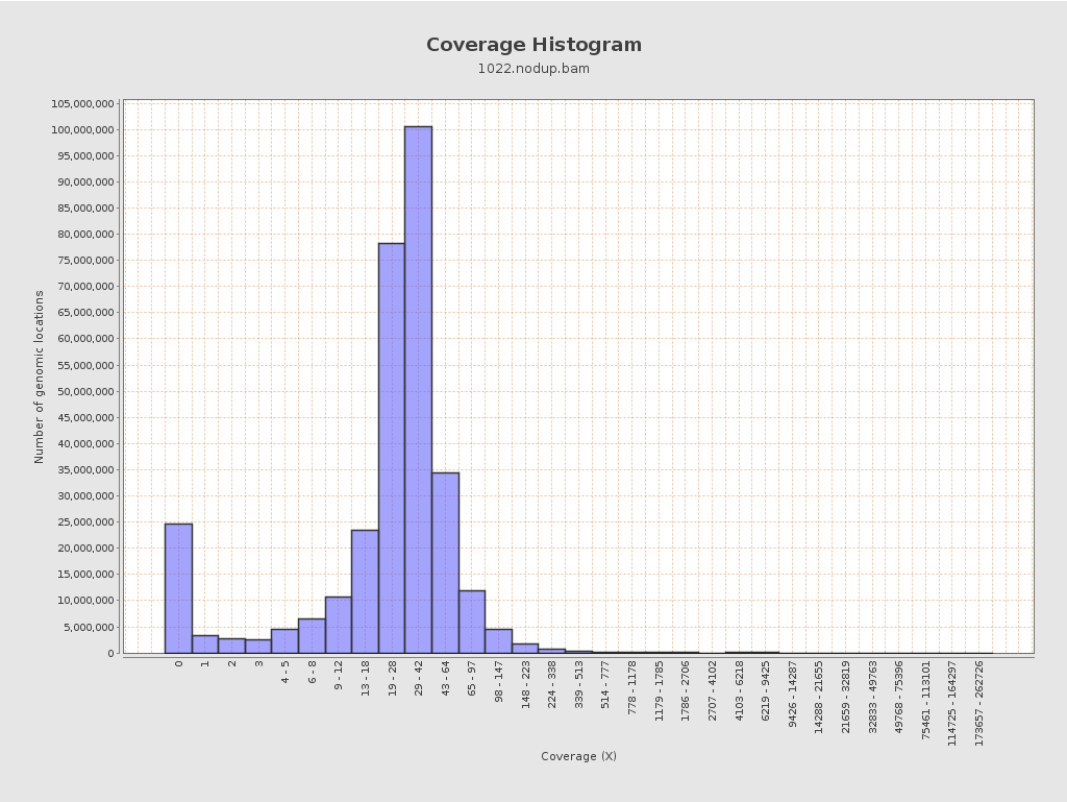
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	907558176	30.5325	77.2572

LT669789.1	36598175	1417463811	38.7305	313.3865
LT669790.1	30422129	1178791058	38.7478	283.6474
LT669791.1	52758100	1954593057	37.0482	230.249
LT669792.1	28376109	1038092318	36.5833	311.7315
LT669793.1	33388210	1182259336	35.4095	211.6099
LT669794.1	50579949	1834922781	36.2777	289.5027
LT669795.1	49795044	2228561607	44.7547	476.7567

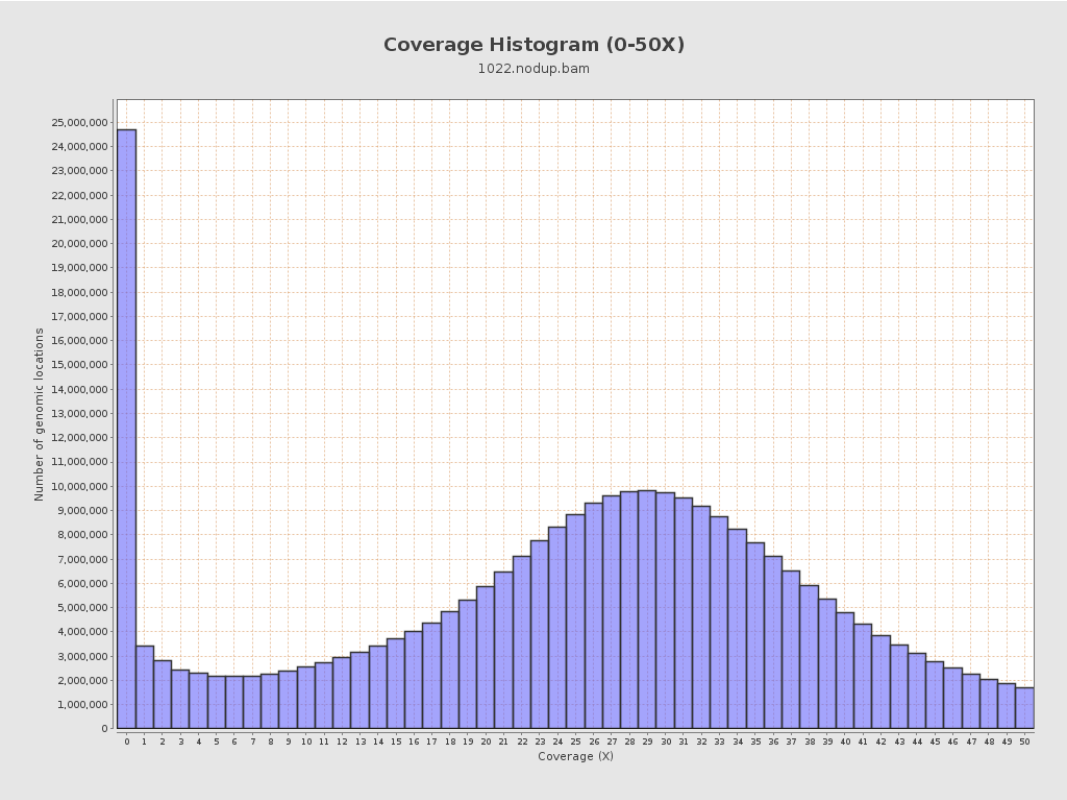
3. Results : Coverage across reference



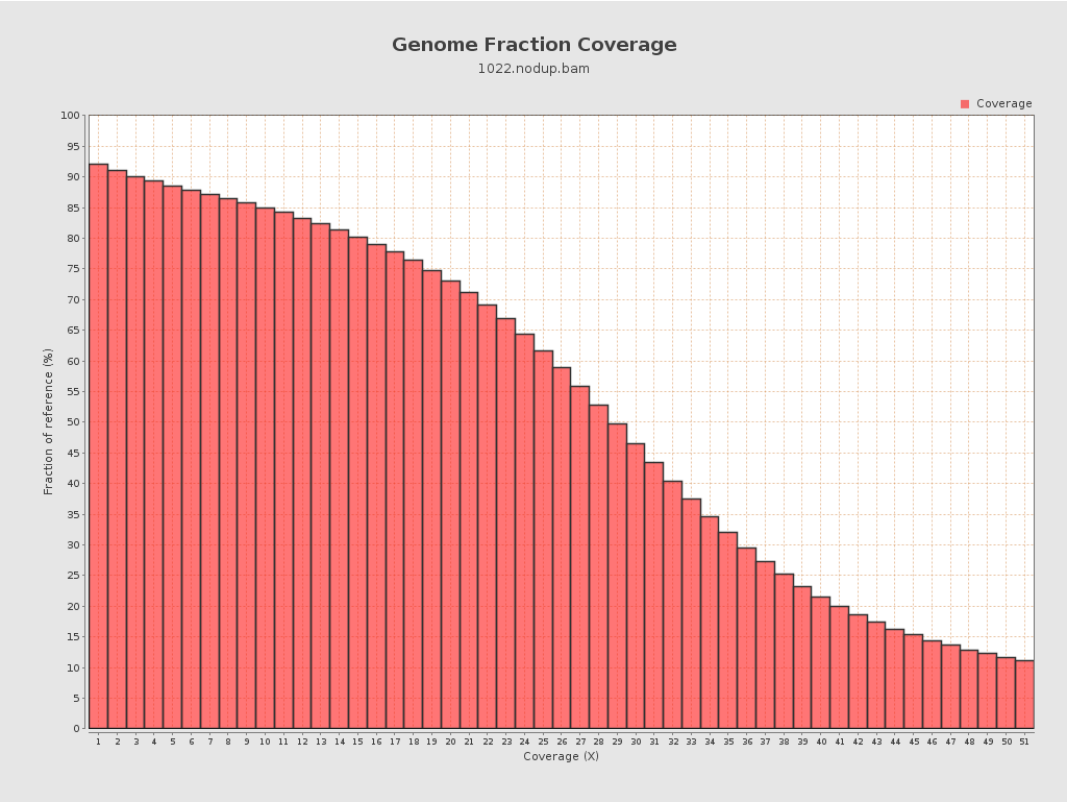
4. Results : Coverage Histogram



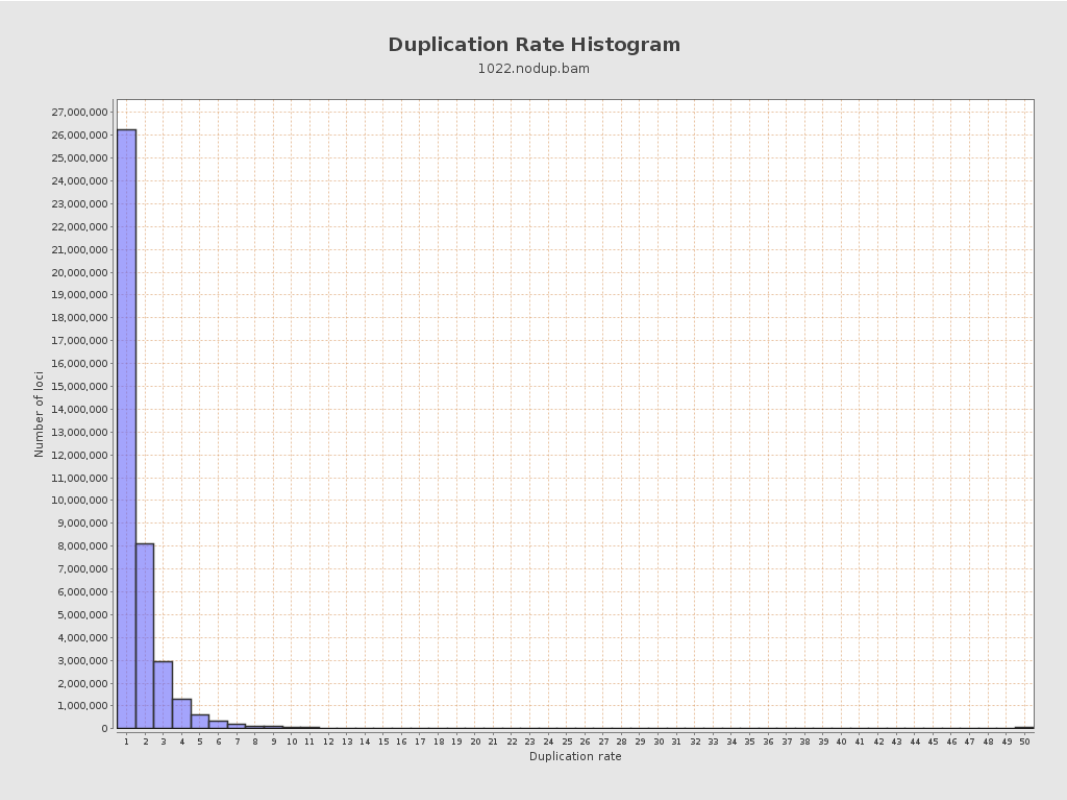
5. Results : Coverage Histogram (0-50X)



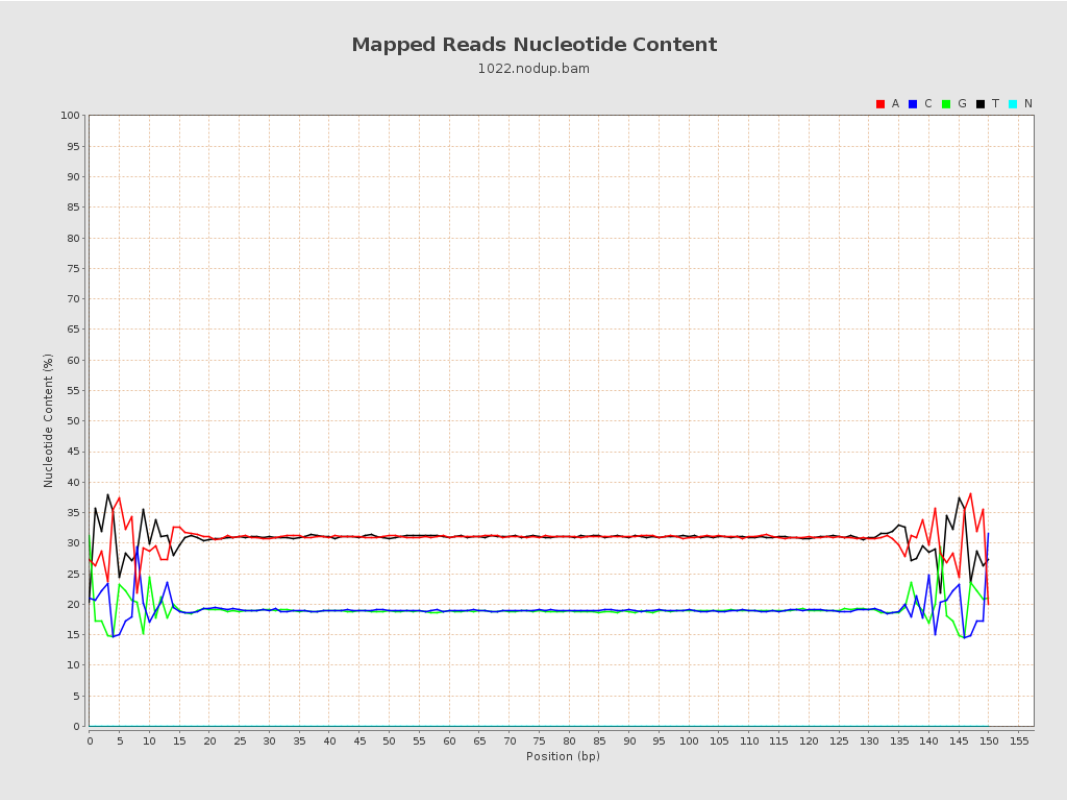
6. Results : Genome Fraction Coverage



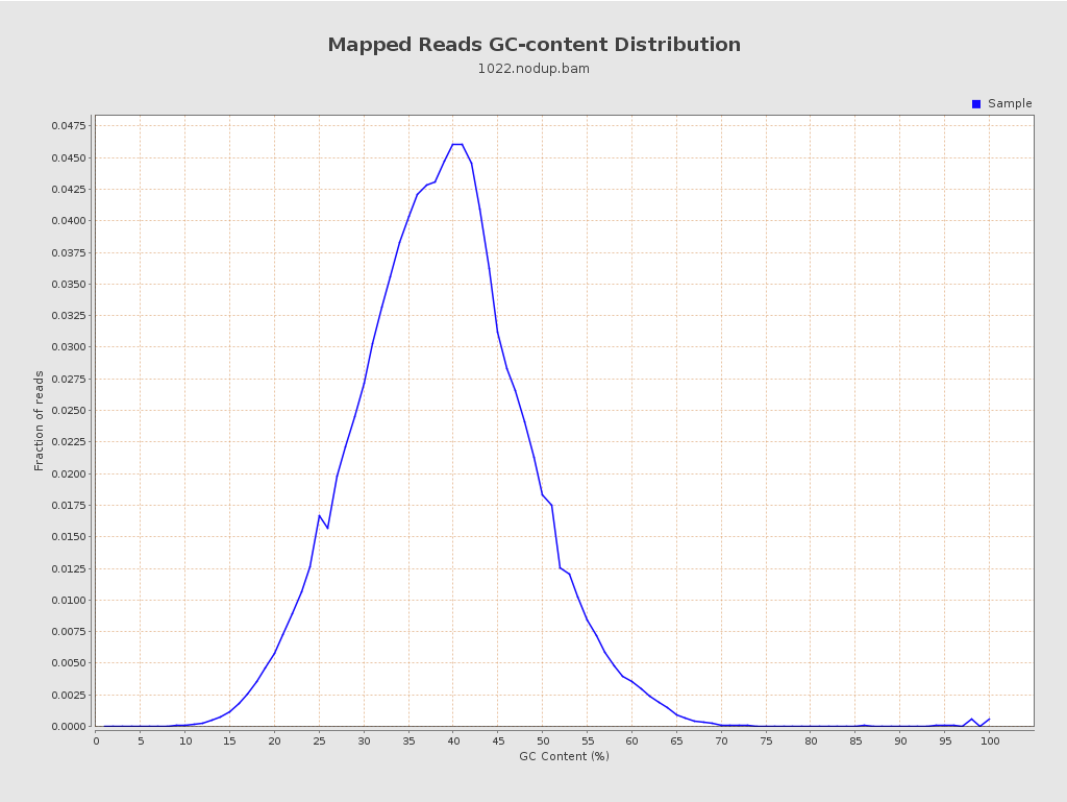
7. Results : Duplication Rate Histogram



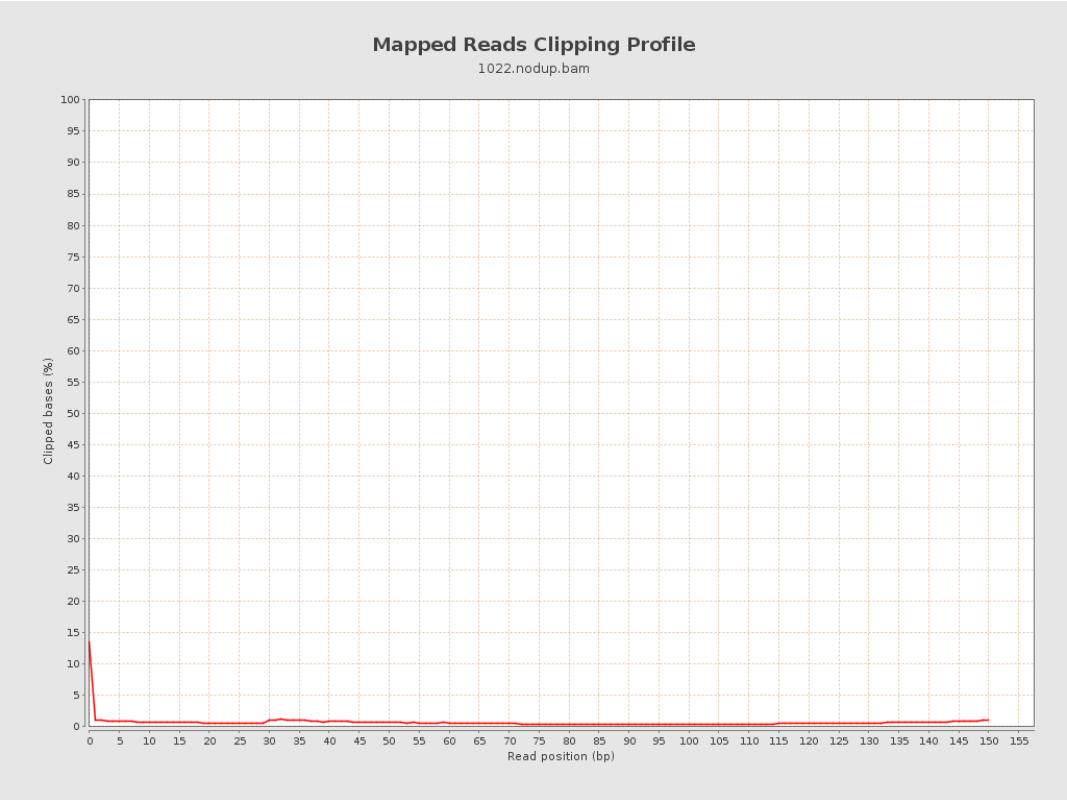
8. Results : Mapped Reads Nucleotide Content



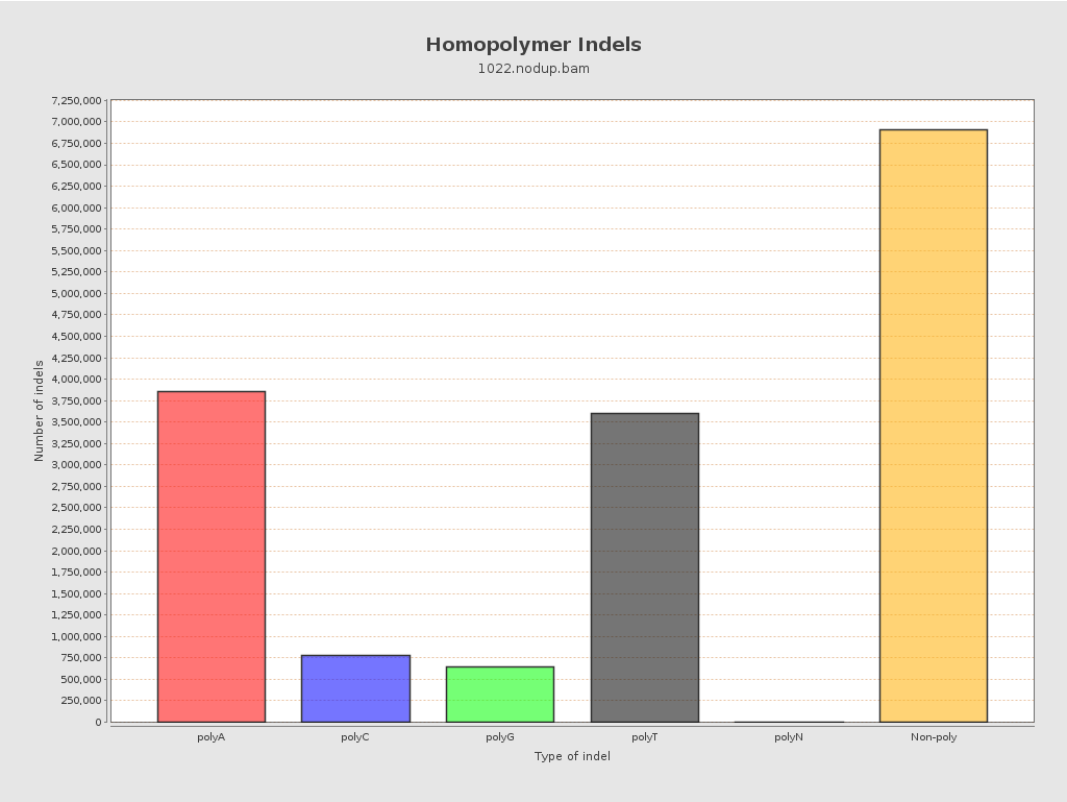
9. Results : Mapped Reads GC-content Distribution



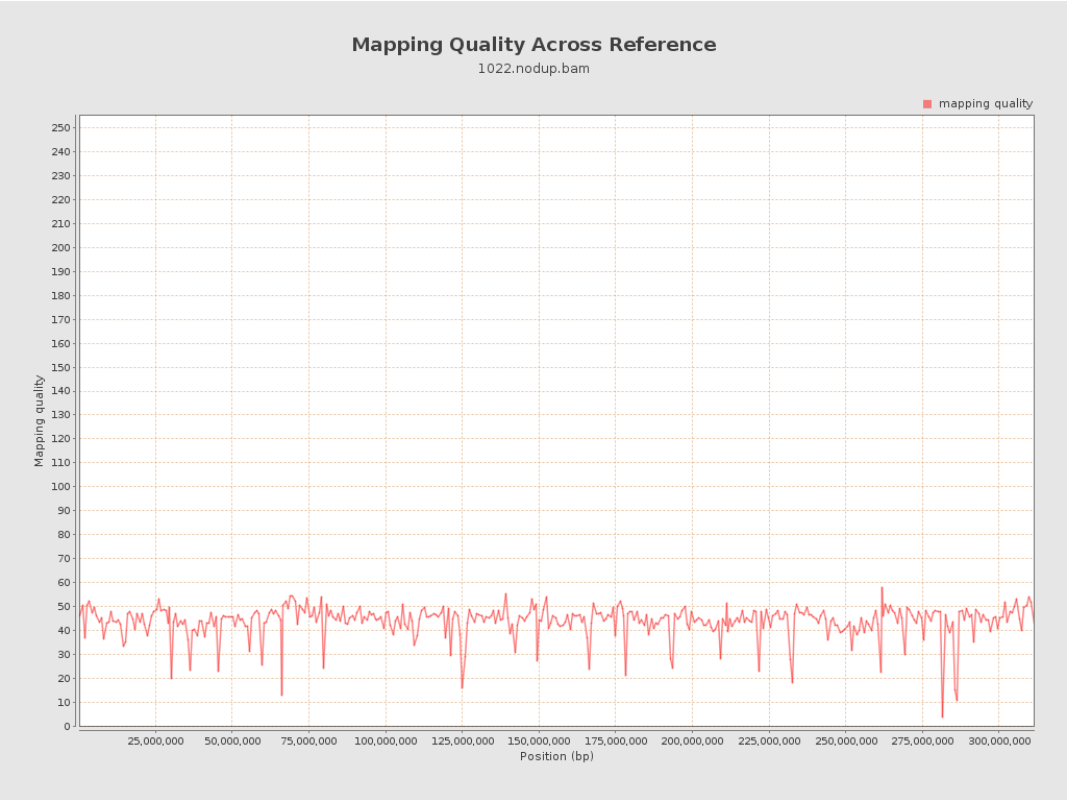
10. Results : Mapped Reads Clipping Profile



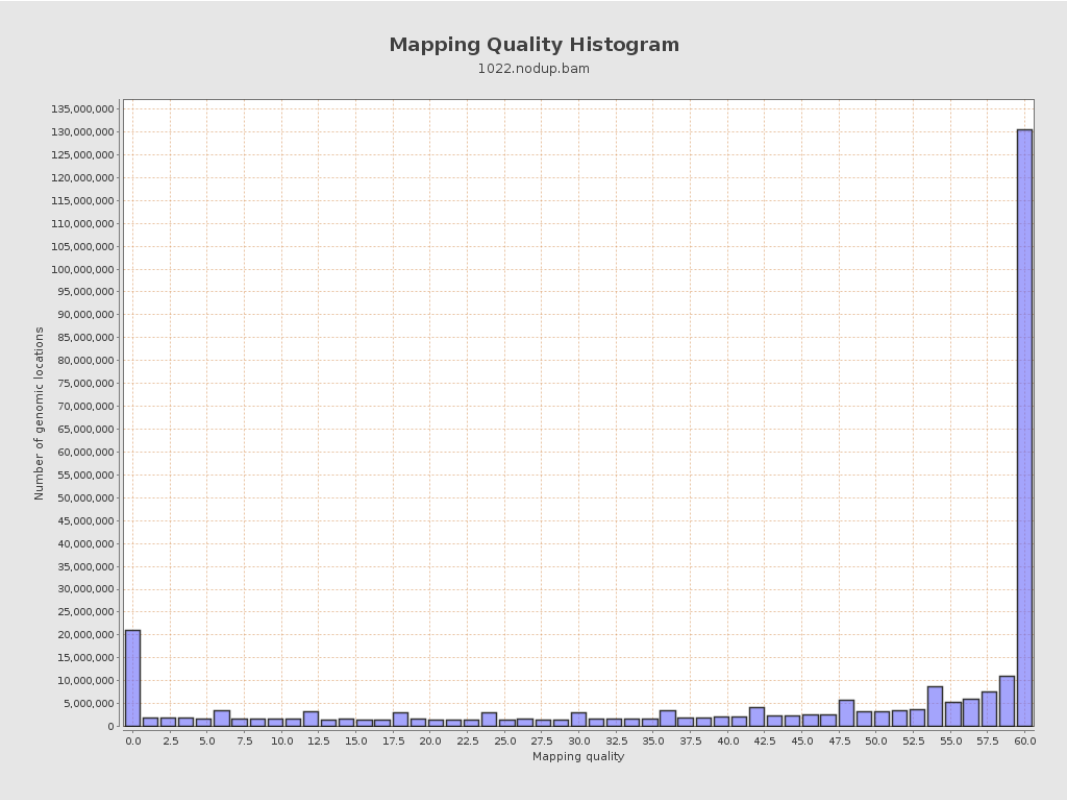
11. Results : Homopolymer Indels



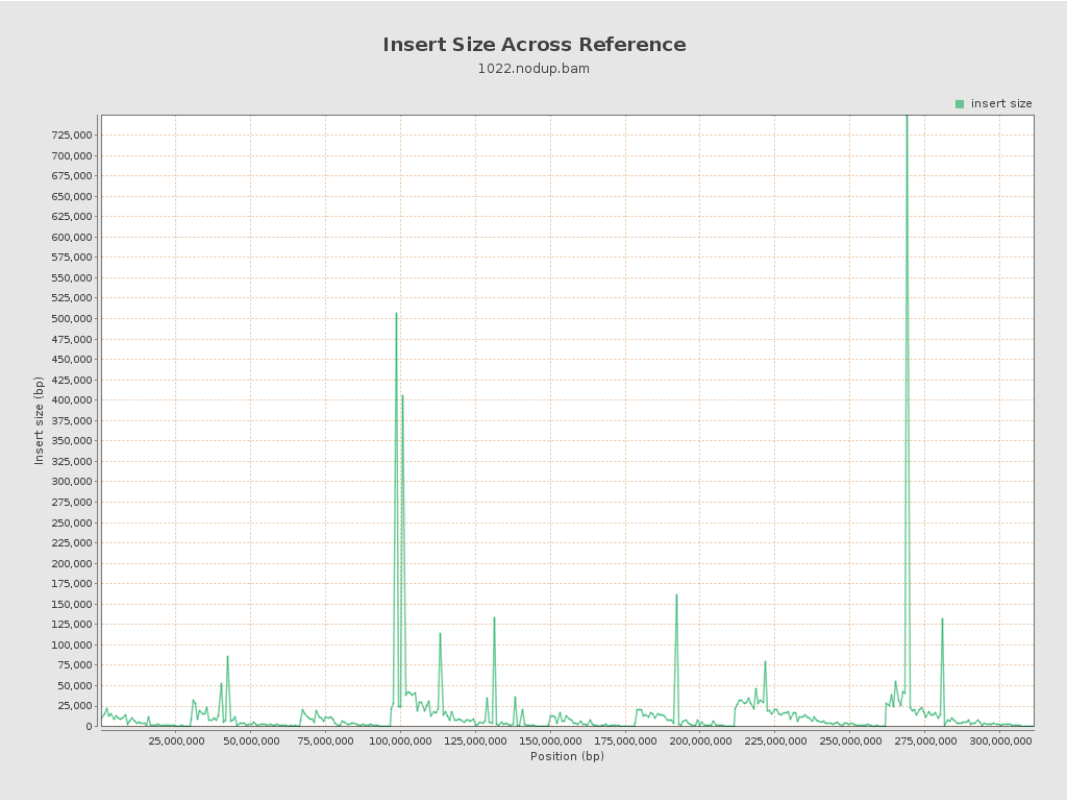
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram