Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:39:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/638.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/638.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_226/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_226_S307_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_226/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_226_S307_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:39:06 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	88,784,280
Mapped reads	81,516,732 / 91.81%
Unmapped reads	7,267,548 / 8.19%
Mapped paired reads	81,516,732 / 91.81%
Mapped reads, first in pair	40,830,544 / 45.99%
Mapped reads, second in pair	40,686,188 / 45.83%
Mapped reads, both in pair	79,166,159 / 89.17%
Mapped reads, singletons	2,350,573 / 2.65%
Read min/max/mean length	30 / 151 / 148.04
Duplicated reads (flagged)	14,416,090 / 16.24%
Clipped reads	19,688,486 / 22.18%

2.2. ACGT Content

Number/percentage of A's	3,450,681,917 / 30.92%
Number/percentage of C's	2,128,698,033 / 19.07%
Number/percentage of T's	3,451,140,423 / 30.92%
Number/percentage of G's	2,131,137,878 / 19.09%
Number/percentage of N's	40,835 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	35.9077
Standard Deviation	341.2716

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Insert size

Mean	251,521.11
Standard Deviation	2,407,972.59
P25/Median/P75	315 / 414 / 539

2.6. Mismatches and indels

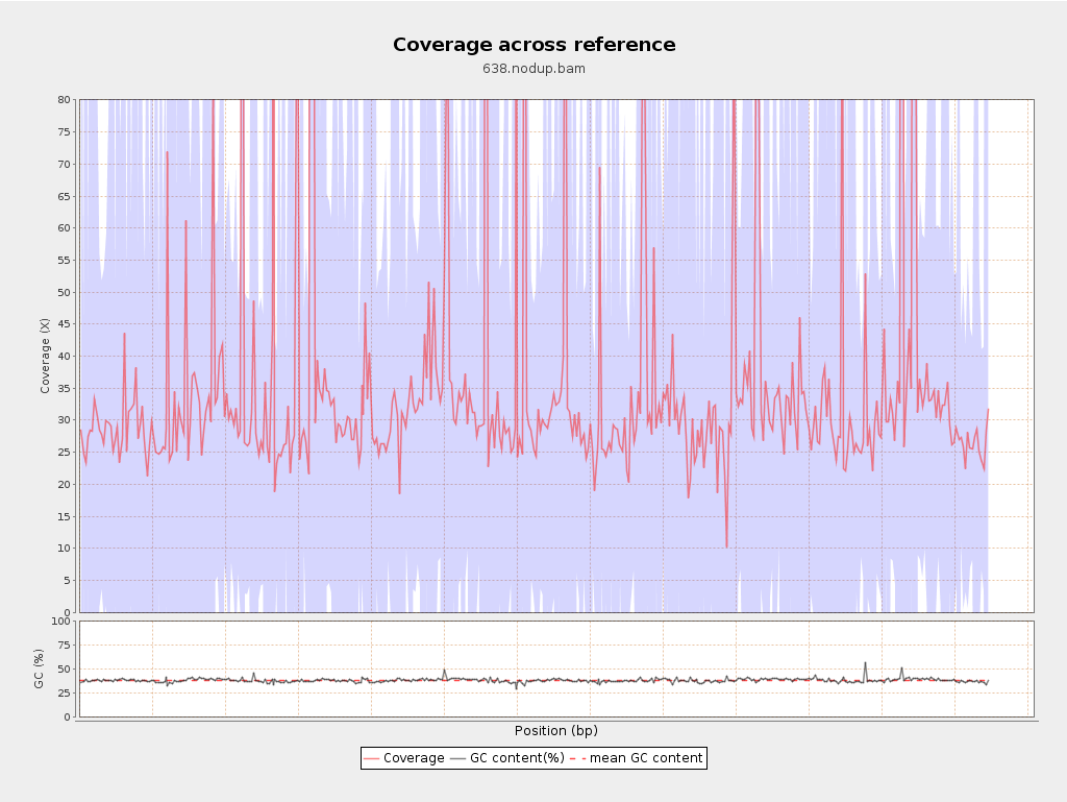
General error rate	2.37%
Mismatches	242,646,443
Insertions	8,004,579
Mapped reads with at least one insertion	8.75%
Deletions	7,701,938
Mapped reads with at least one deletion	8.4%
Homopolymer indels	57.41%

2.7. Chromosome stats

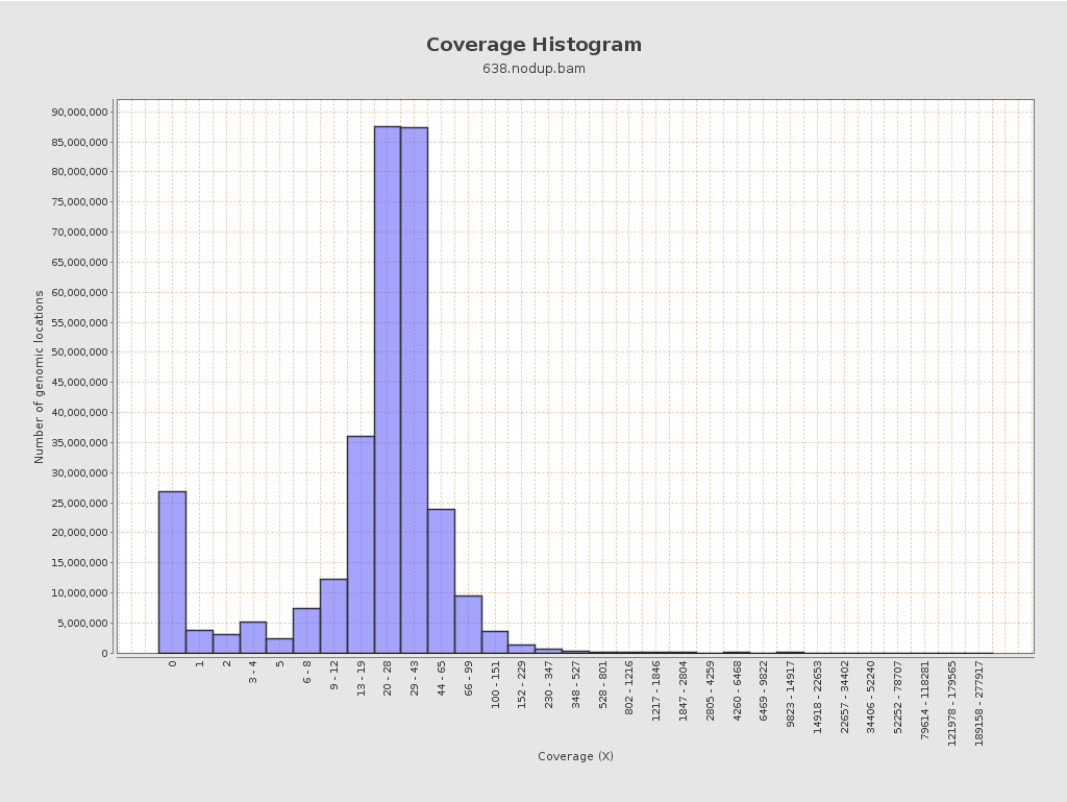
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	841964249	28.3257	126.3739

LT669789.1	36598175	1334028471	36.4507	349.259
LT669790.1	30422129	1286919247	42.3021	455.5221
LT669791.1	52758100	1887251429	35.7718	350.989
LT669792.1	28376109	1016294997	35.8152	368.3553
LT669793.1	33388210	1098015153	32.8863	226.147
LT669794.1	50579949	1728975701	34.183	259.6044
LT669795.1	49795044	1996911669	40.1026	438.4802

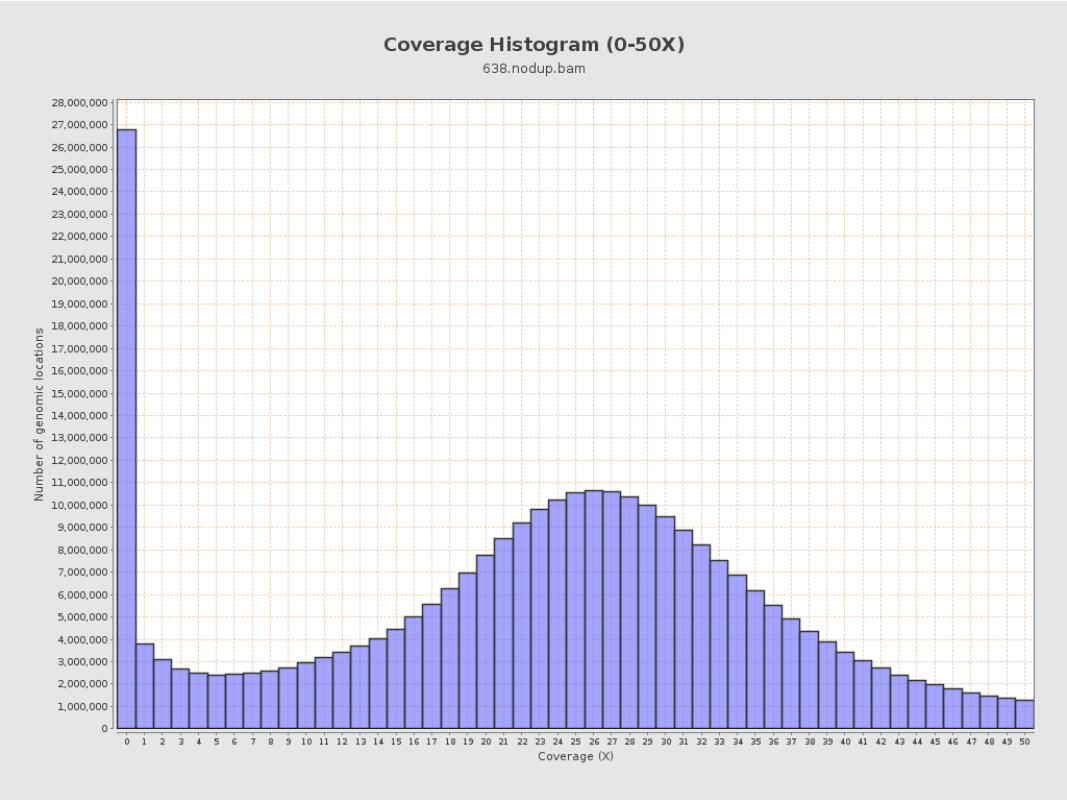
3. Results : Coverage across reference



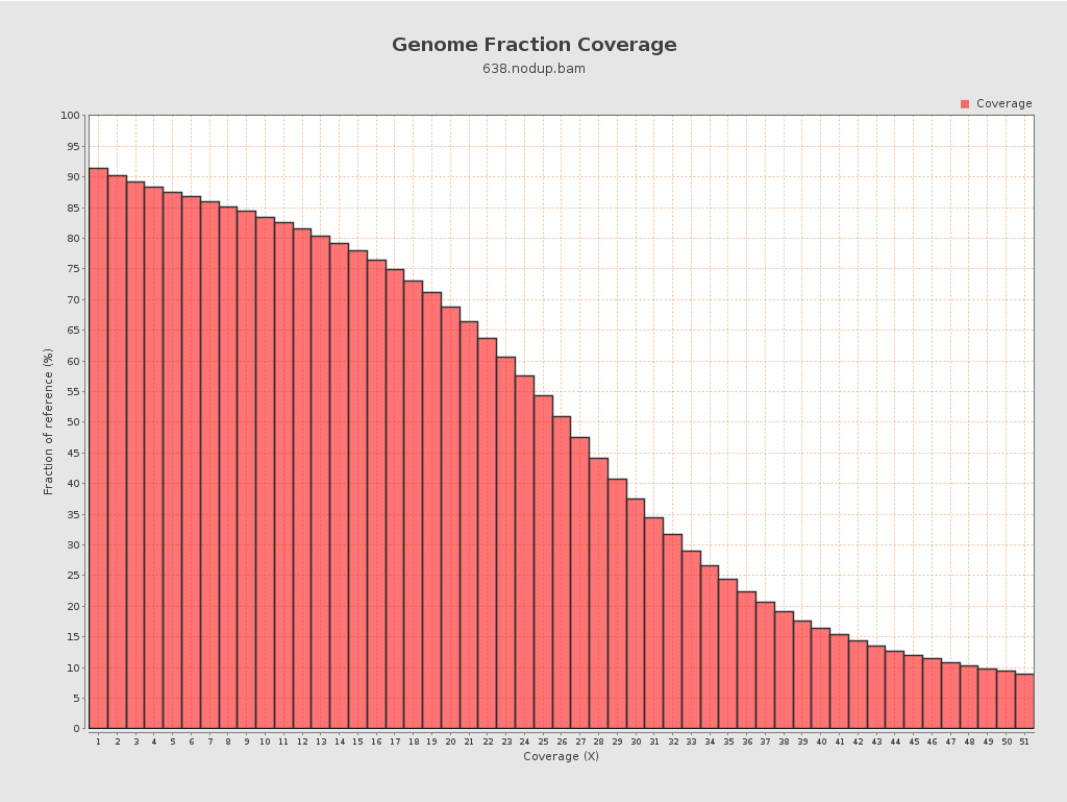
4. Results : Coverage Histogram



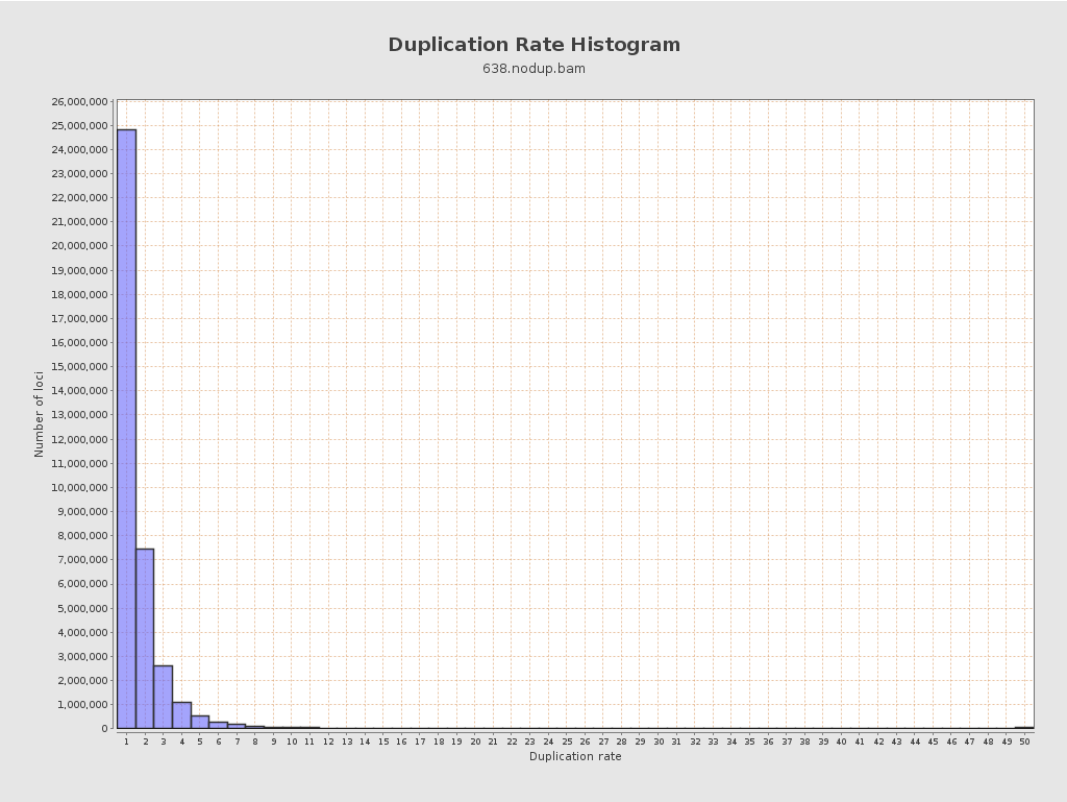
5. Results : Coverage Histogram (0-50X)



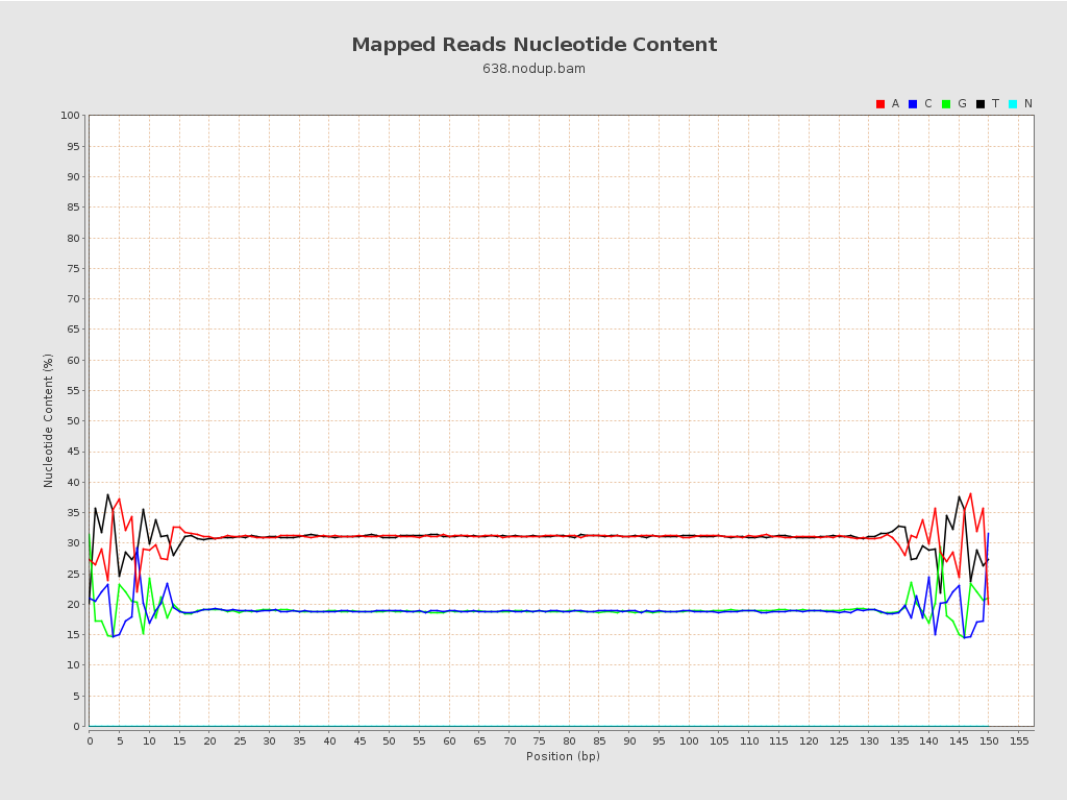
6. Results : Genome Fraction Coverage



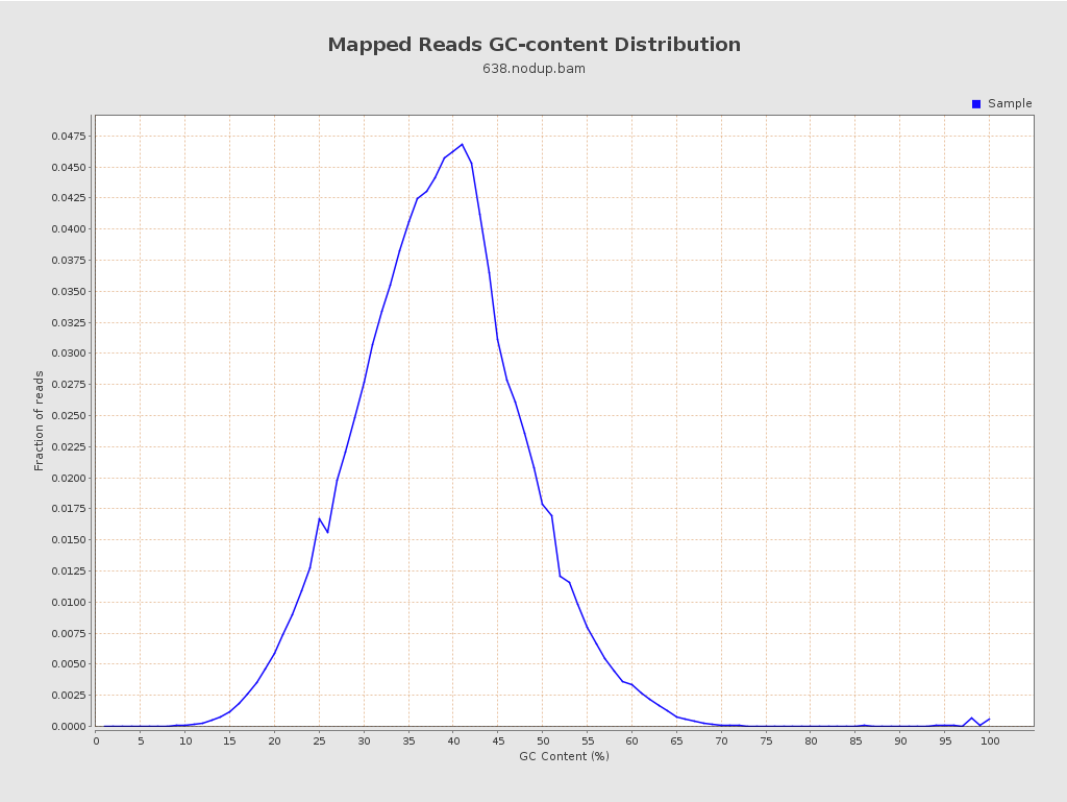
7. Results : Duplication Rate Histogram



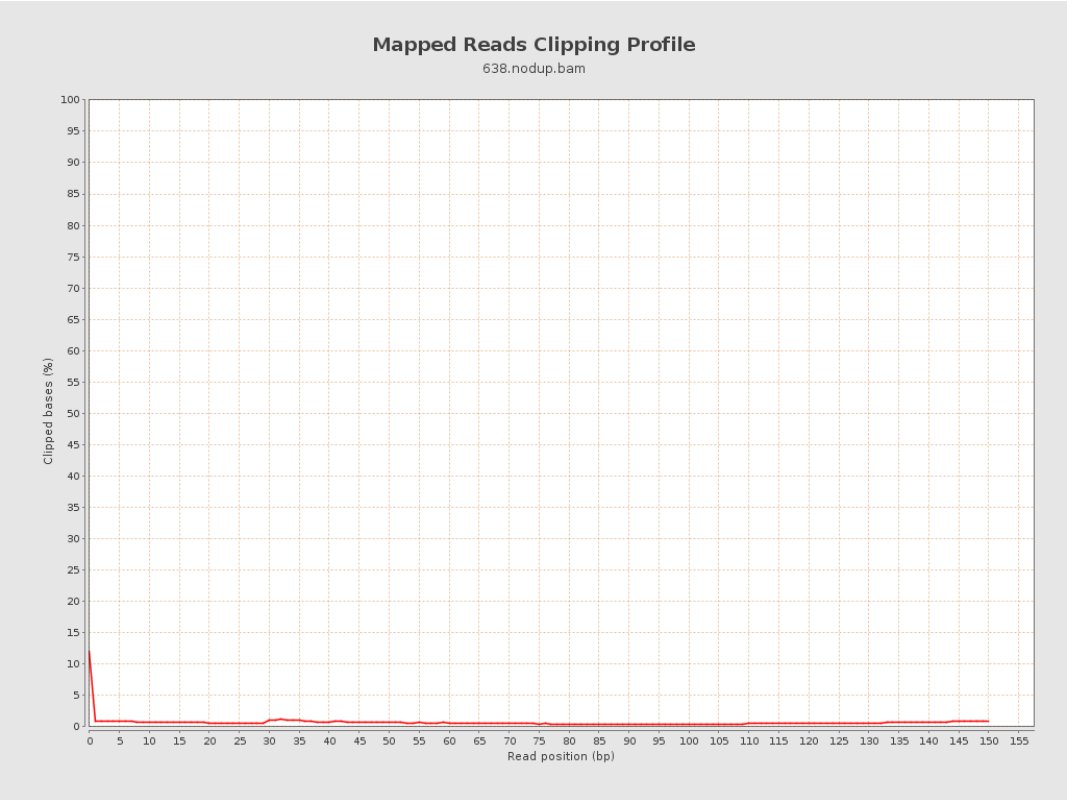
8. Results : Mapped Reads Nucleotide Content



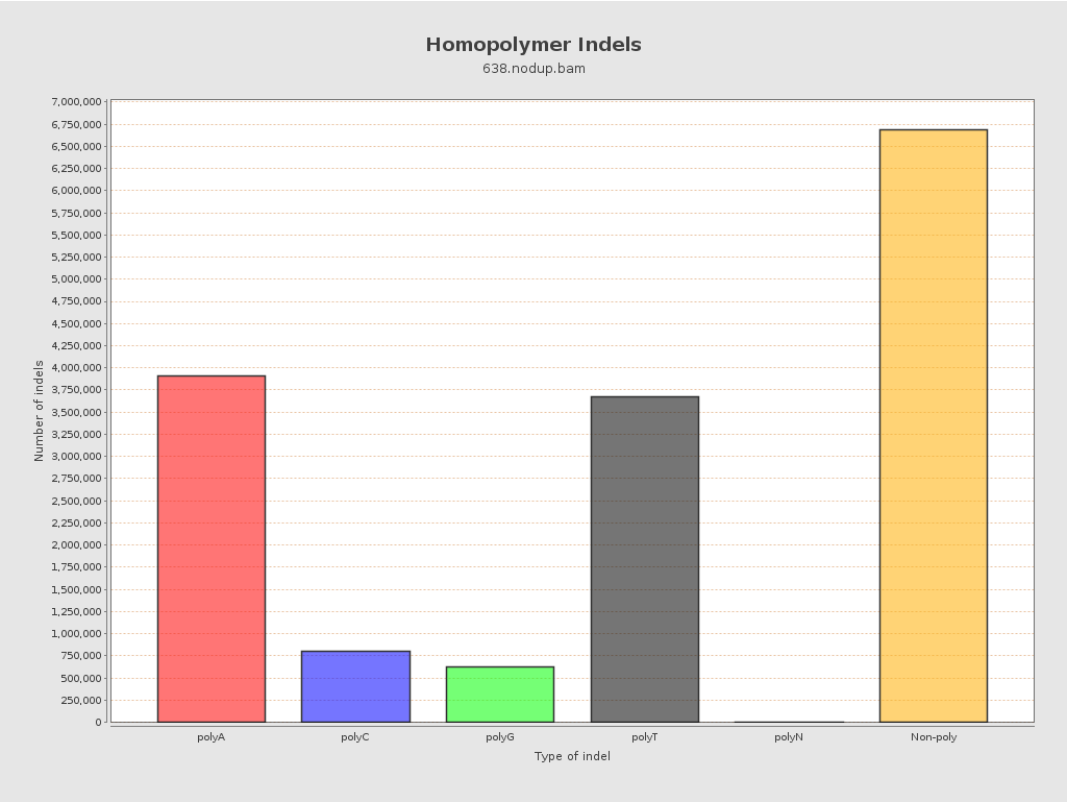
9. Results : Mapped Reads GC-content Distribution



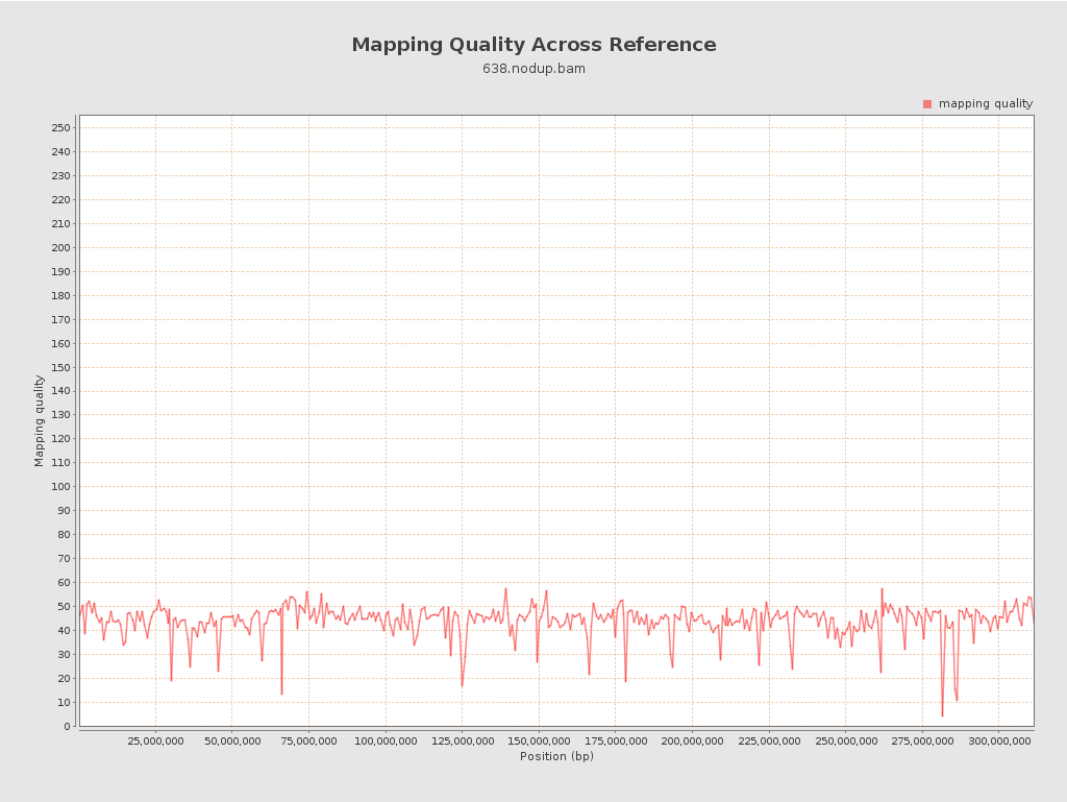
10. Results : Mapped Reads Clipping Profile



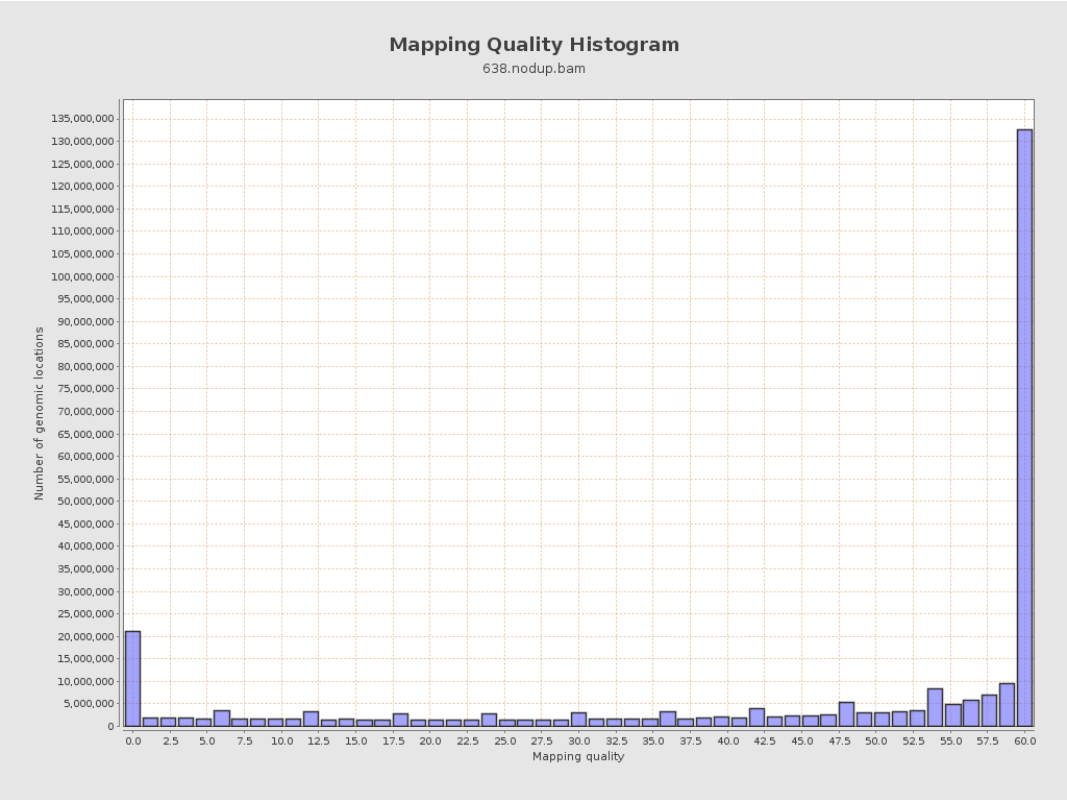
11. Results : Homopolymer Indels



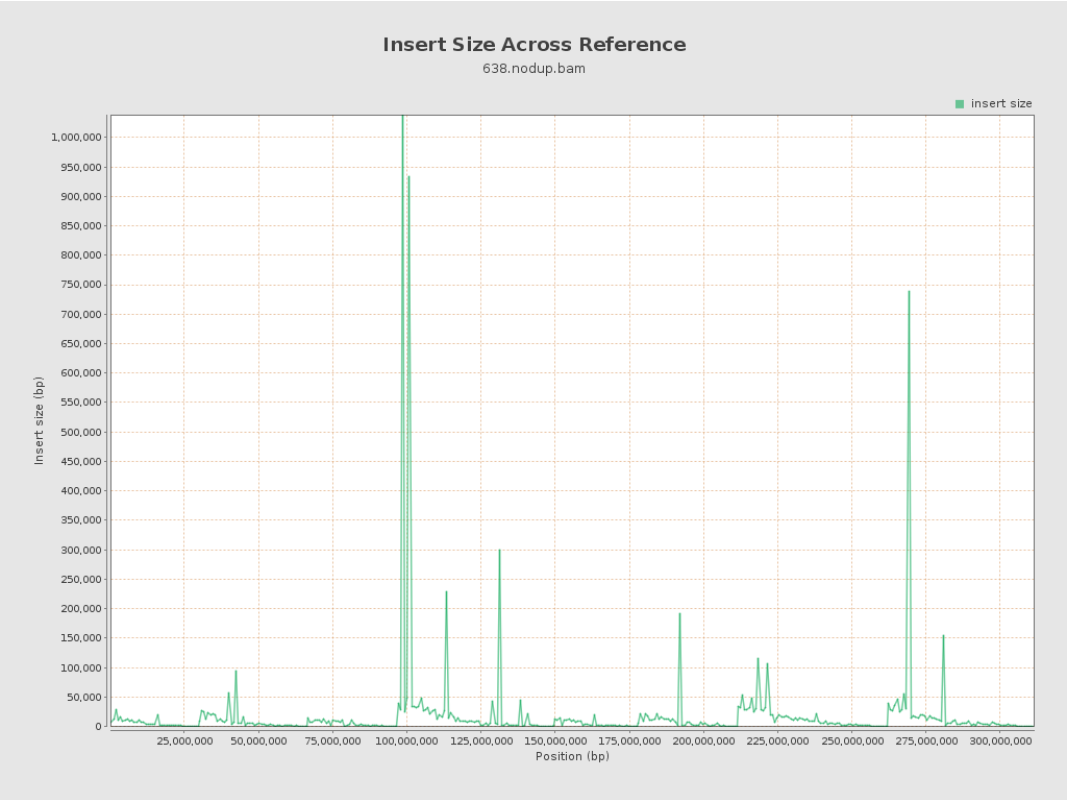
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram