Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/135
1
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1351 .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_429/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_429_S404_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_429/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_429_S404_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:58 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,836,597
Mapped reads	63,175,661 / 94.52%
Unmapped reads	3,660,936 / 5.48%
Mapped paired reads	63,175,661 / 94.52%
Mapped reads, first in pair	31,639,067 / 47.34%
Mapped reads, second in pair	31,536,594 / 47.18%
Mapped reads, both in pair	62,002,665 / 92.77%
Mapped reads, singletons	1,172,996 / 1.76%
Read min/max/mean length	30 / 151 / 148.31
Duplicated reads (flagged)	9,260,741 / 13.86%
Clipped reads	13,014,110 / 19.47%

2.2. ACGT Content

Number/percentage of A's	2,731,702,883 / 30.91%
Number/percentage of C's	1,687,983,243 / 19.1%
Number/percentage of T's	2,734,672,017 / 30.95%
Number/percentage of G's	1,682,038,896 / 19.04%
Number/percentage of N's	30,750 / 0%
GC Percentage	38.14%

2.3. Coverage

Mean	28.4261
Standard Deviation	208.7782

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Insert size

Mean	227,568.17
Standard Deviation	2,257,418.11
P25/Median/P75	365 / 476 / 623

2.6. Mismatches and indels

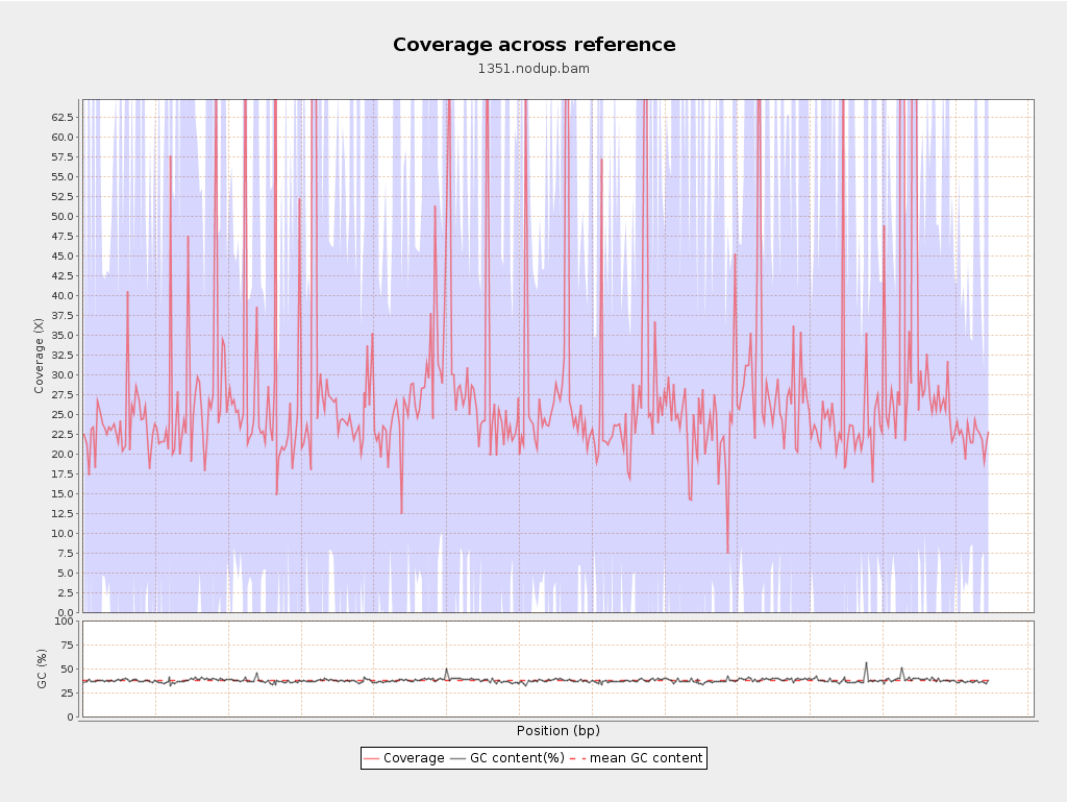
General error rate	2.2%
Mismatches	178,602,108
Insertions	5,649,080
Mapped reads with at least one insertion	8.05%
Deletions	5,868,352
Mapped reads with at least one deletion	8.28%
Homopolymer indels	56.79%

2.7. Chromosome stats

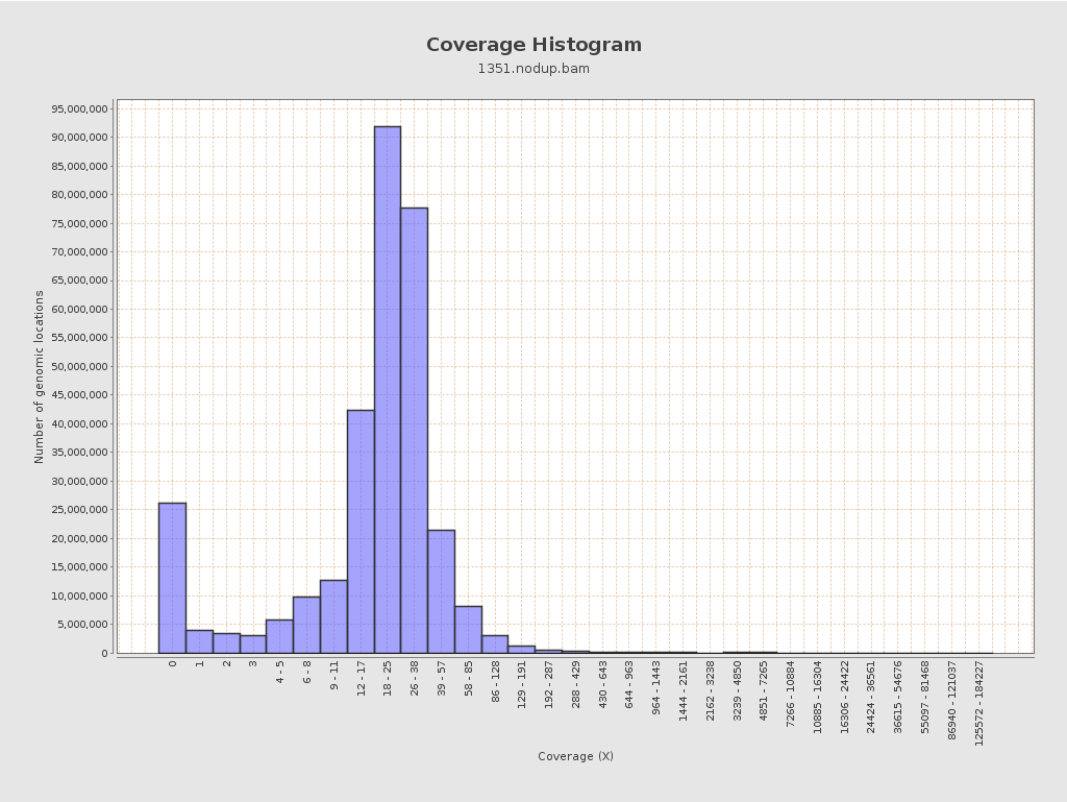
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	693846717	23.3427	49.2989

LT669789.1	36598175	1045520981	28.5676	208.786
LT669790.1	30422129	892177068	29.3266	189.0115
LT669791.1	52758100	1480171176	28.0558	159.665
LT669792.1	28376109	785936551	27.6971	244.0675
LT669793.1	33388210	890031510	26.6571	156.5965
LT669794.1	50579949	1374885518	27.1824	174.2354
LT669795.1	49795044	1696202651	34.0637	330.4468

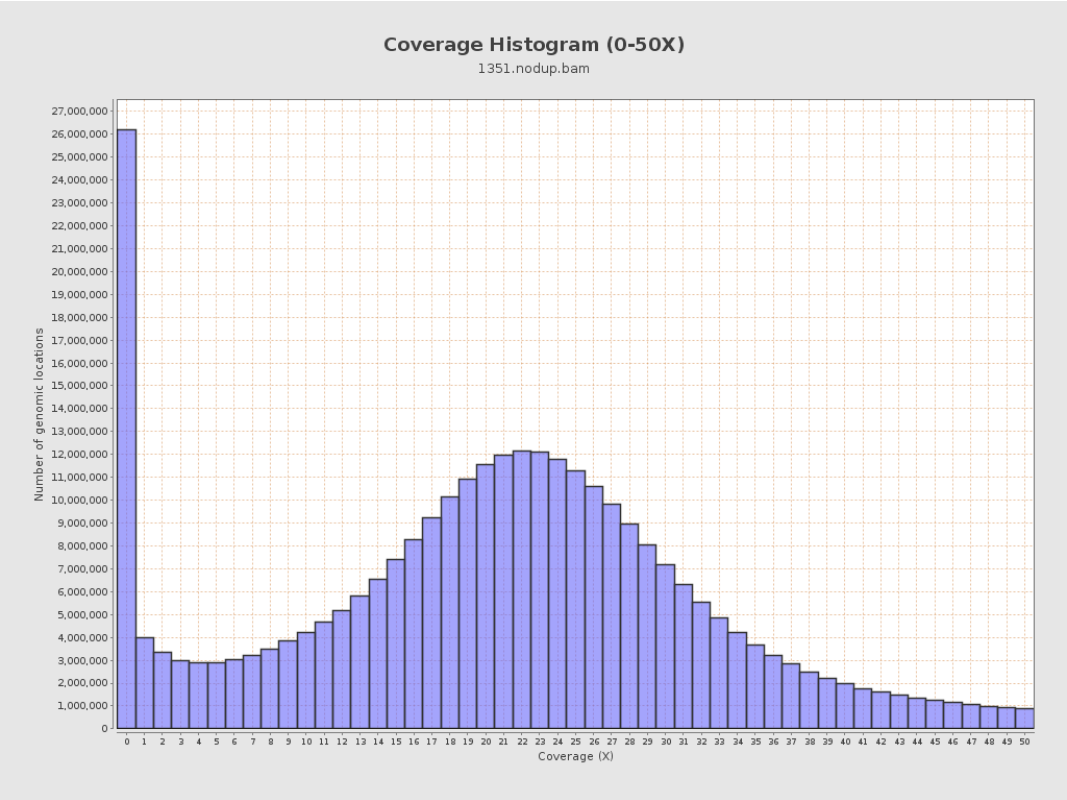
3. Results : Coverage across reference



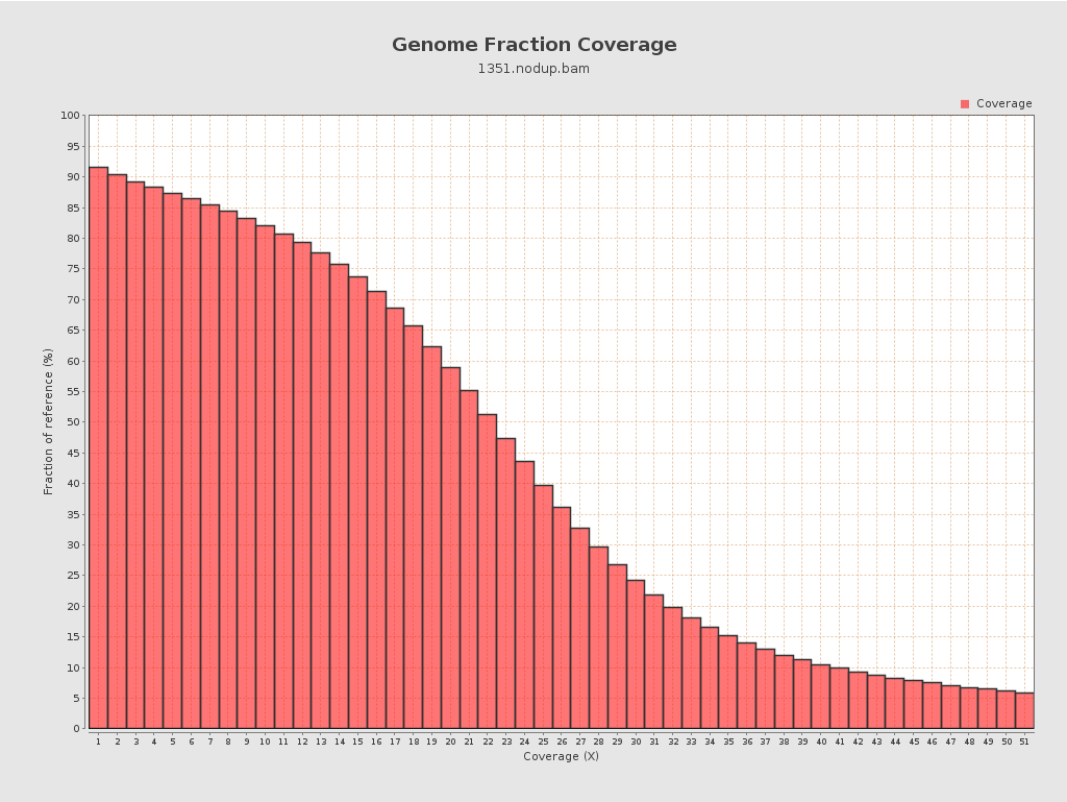
4. Results : Coverage Histogram



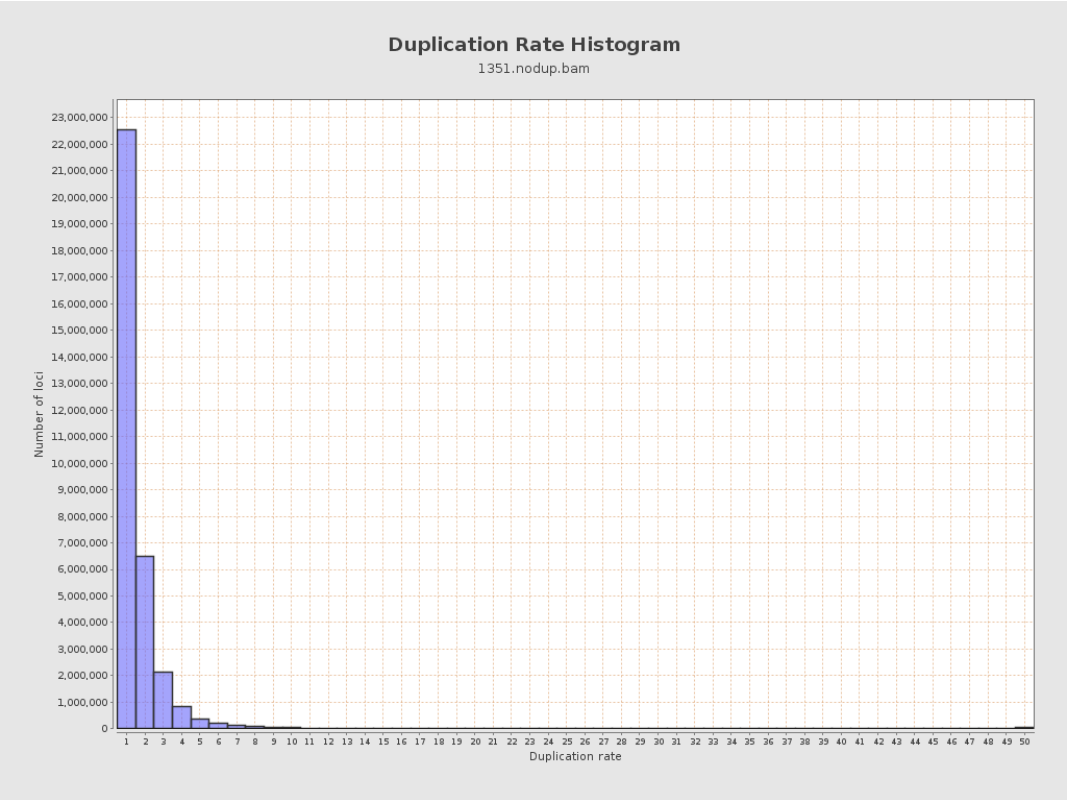
5. Results : Coverage Histogram (0-50X)



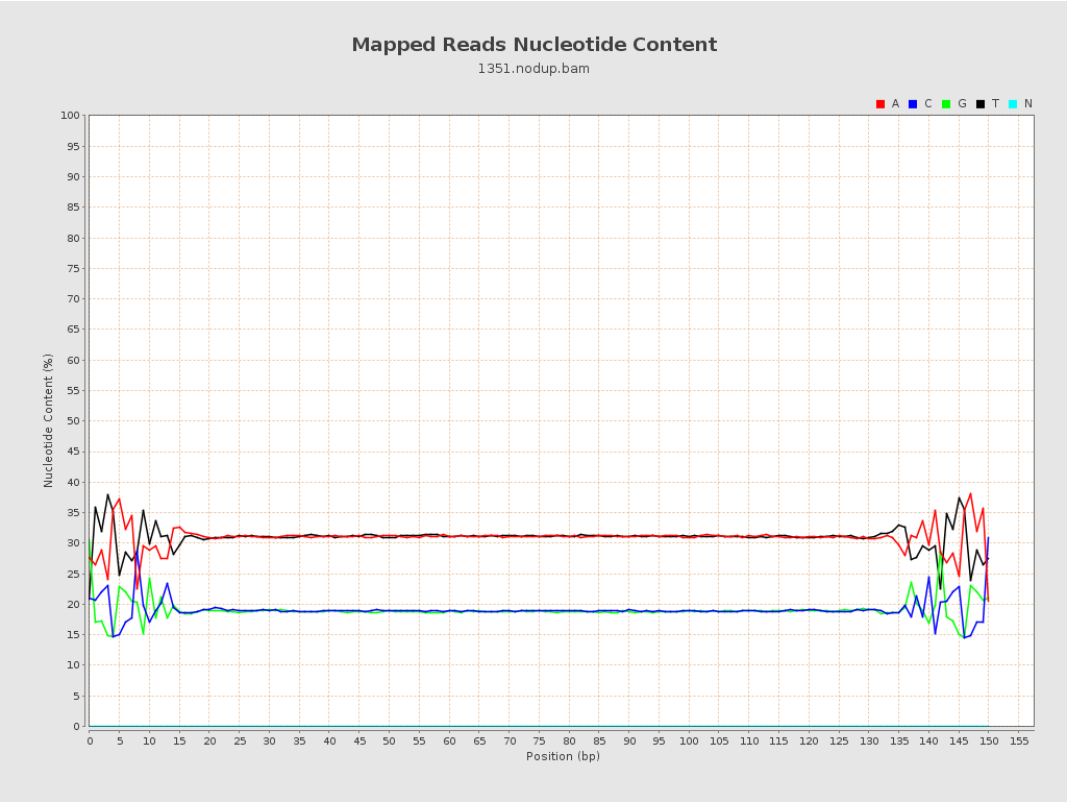
6. Results : Genome Fraction Coverage



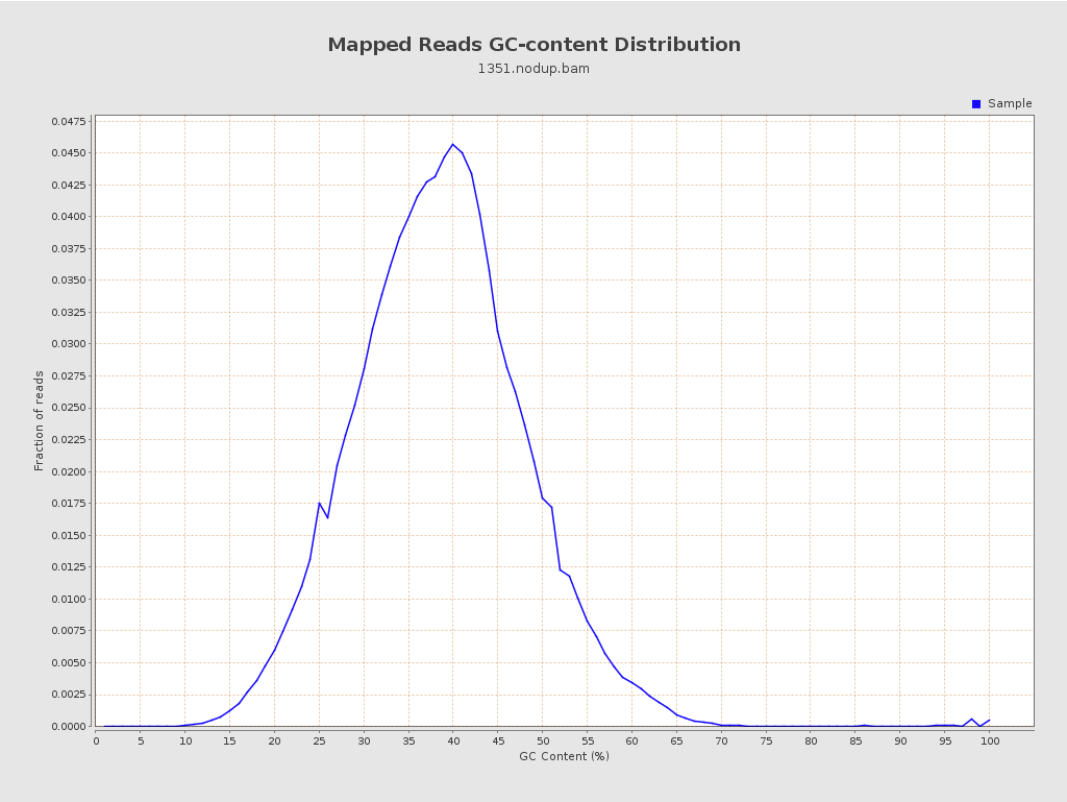
7. Results : Duplication Rate Histogram



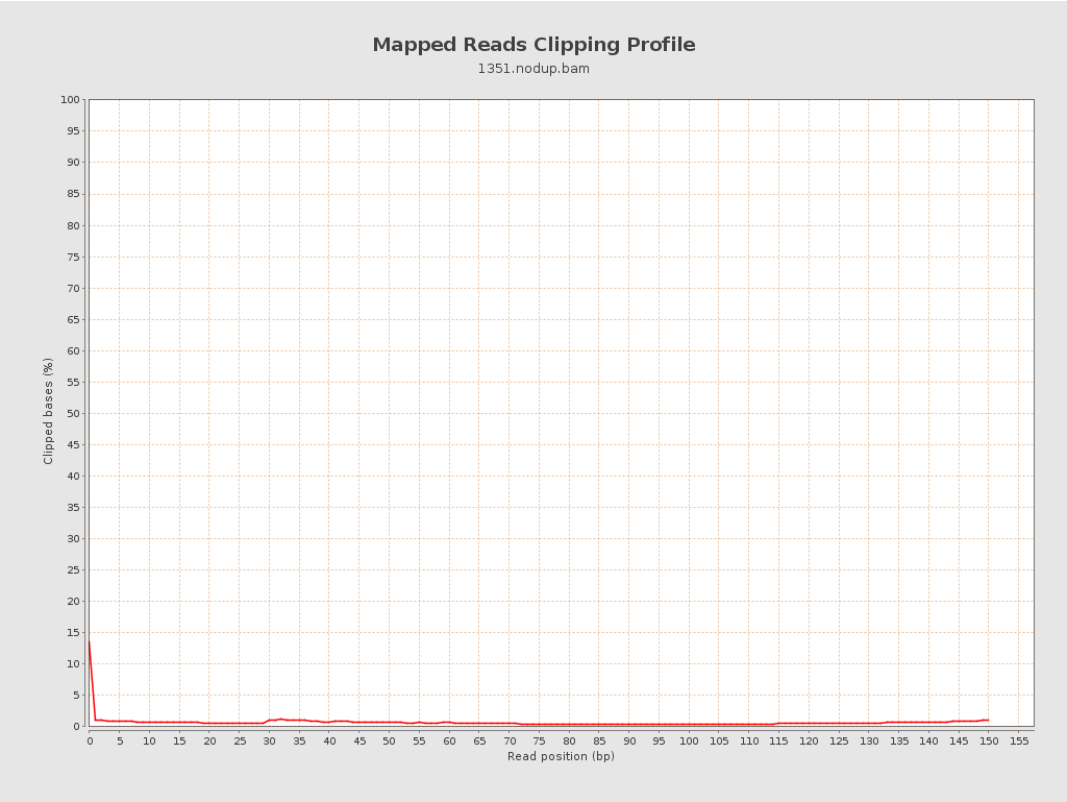
8. Results : Mapped Reads Nucleotide Content



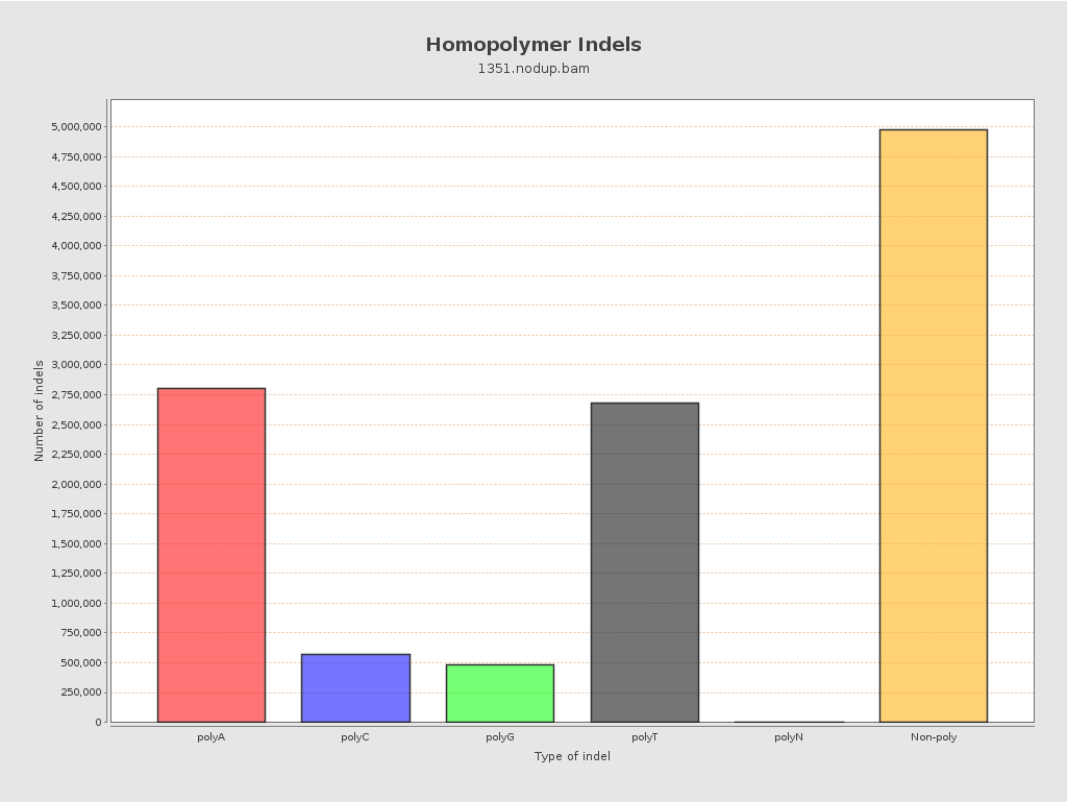
9. Results : Mapped Reads GC-content Distribution



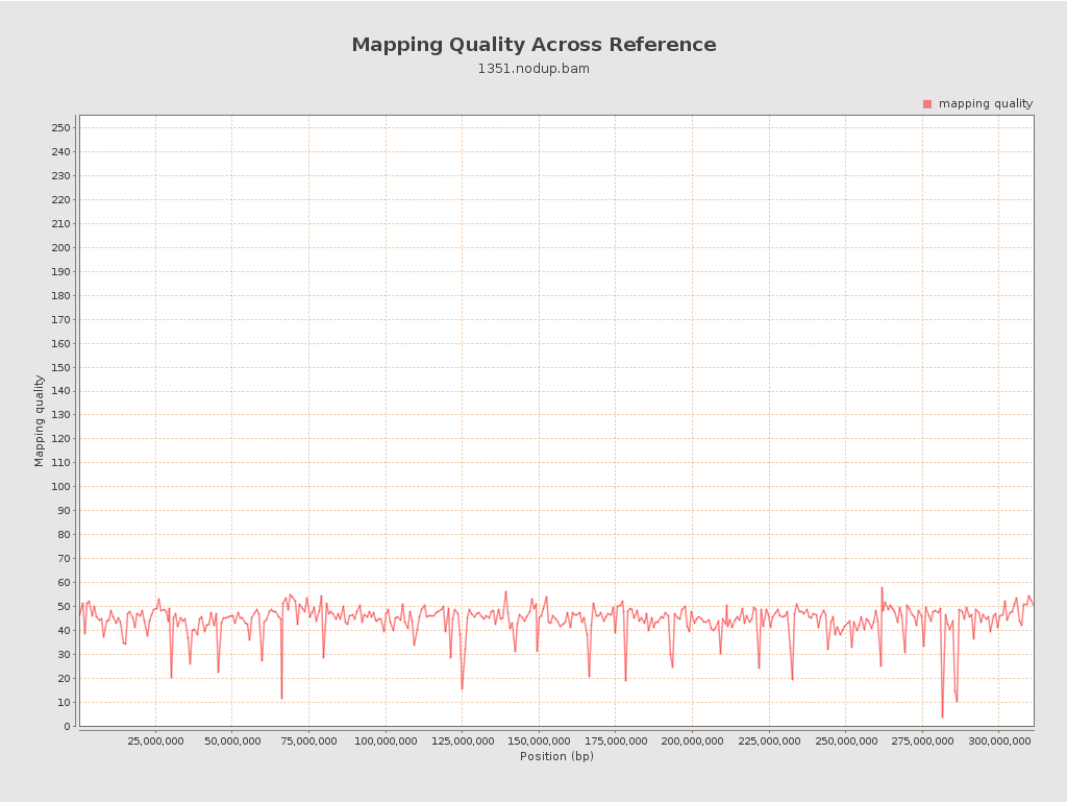
10. Results : Mapped Reads Clipping Profile



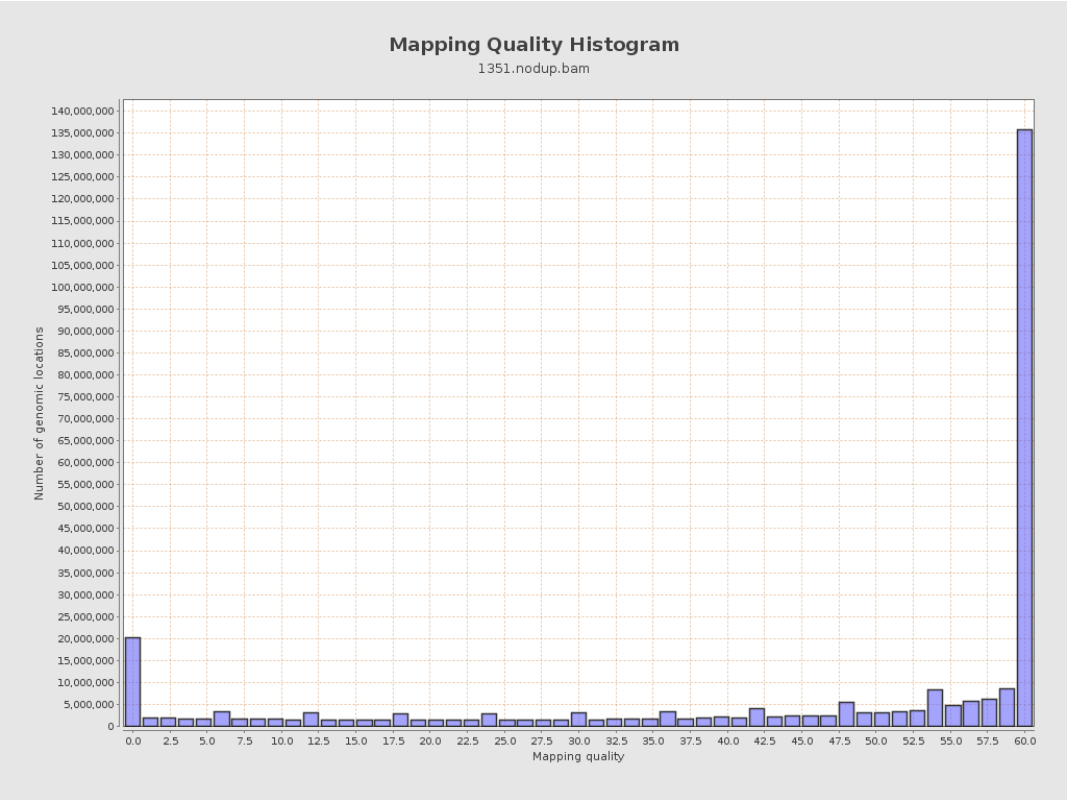
11. Results : Homopolymer Indels



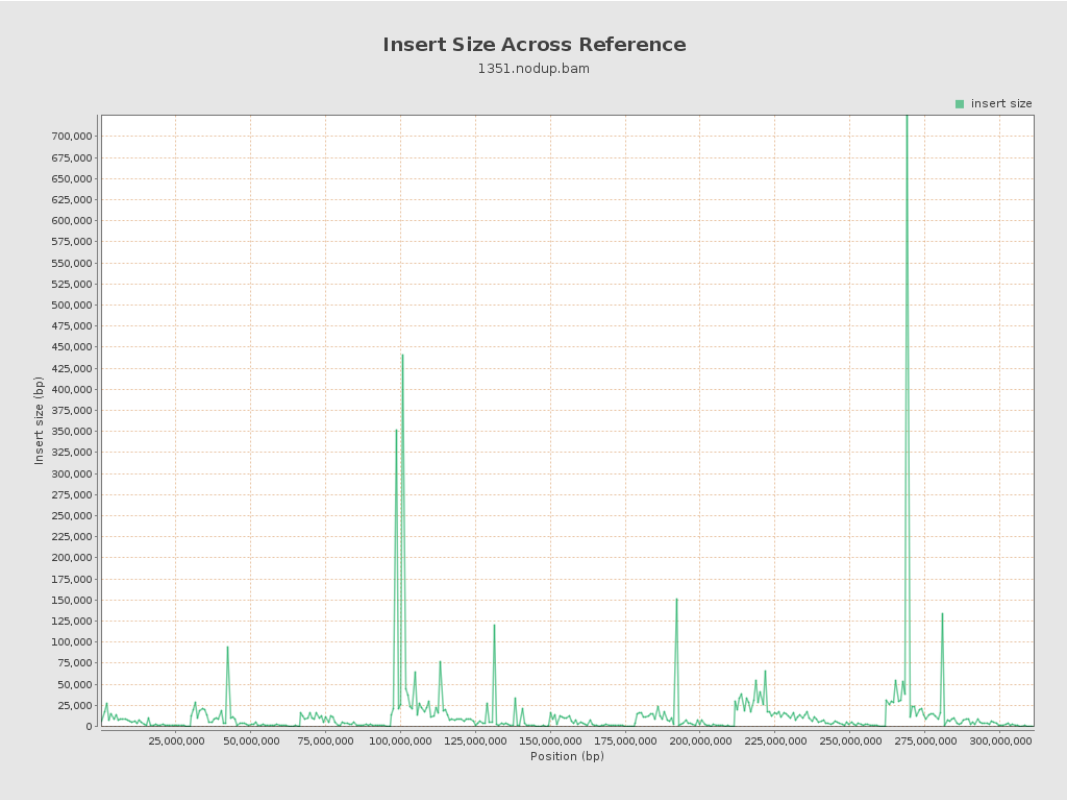
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram