Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1458
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1458 .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_232/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_232_S313_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_232/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_232_S313_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,557,496
Mapped reads	66,445,036 / 91.58%
Unmapped reads	6,112,460 / 8.42%
Mapped paired reads	66,445,036 / 91.58%
Mapped reads, first in pair	33,290,854 / 45.88%
Mapped reads, second in pair	33,154,182 / 45.69%
Mapped reads, both in pair	64,897,642 / 89.44%
Mapped reads, singletons	1,547,394 / 2.13%
Read min/max/mean length	30 / 151 / 147.99
Duplicated reads (flagged)	9,327,336 / 12.86%
Clipped reads	15,797,245 / 21.77%

2.2. ACGT Content

Number/percentage of A's	2,814,218,018 / 30.77%
Number/percentage of C's	1,755,702,271 / 19.2%
Number/percentage of T's	2,820,763,657 / 30.84%
Number/percentage of G's	1,754,829,047 / 19.19%
Number/percentage of N's	34,187 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	29.4276
Standard Deviation	243.7936

2.4. Mapping Quality

Mean Mapping Quality	43.45

2.5. Insert size

Mean	247,523.45
Standard Deviation	2,364,228.9
P25/Median/P75	316 / 417 / 549

2.6. Mismatches and indels

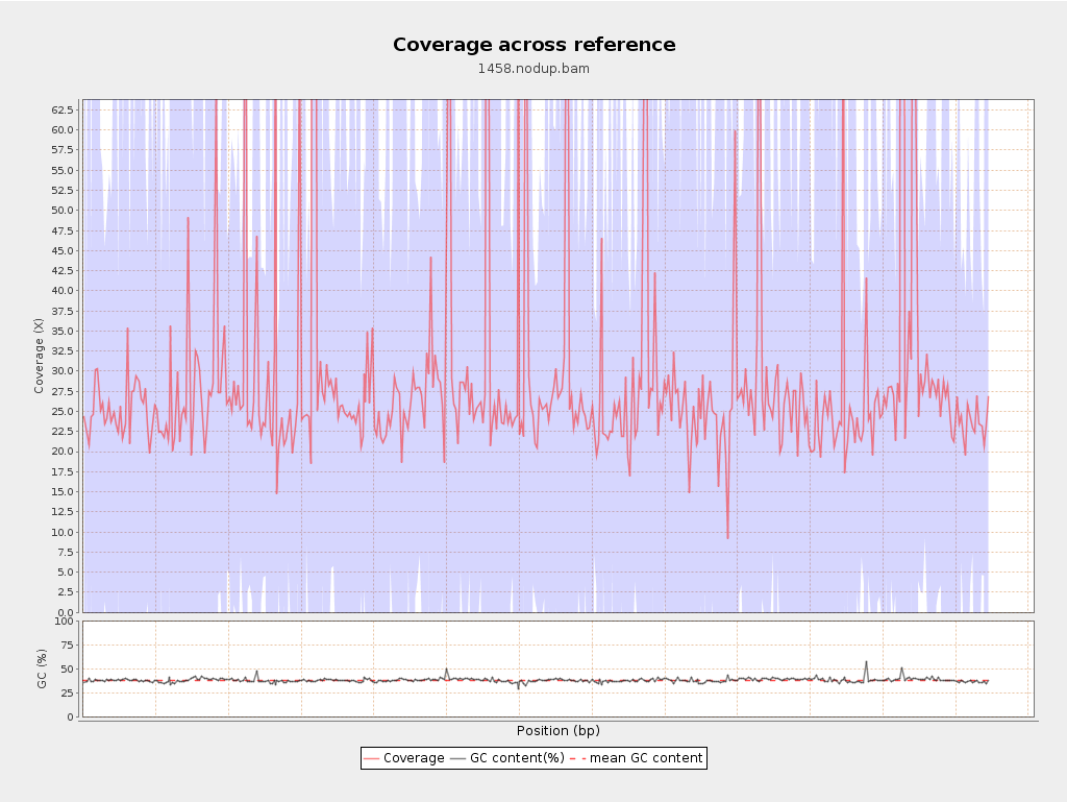
General error rate	2.4%
Mismatches	201,396,351
Insertions	6,461,675
Mapped reads with at least one insertion	8.71%
Deletions	6,575,570
Mapped reads with at least one deletion	8.75%
Homopolymer indels	56.05%

2.7. Chromosome stats

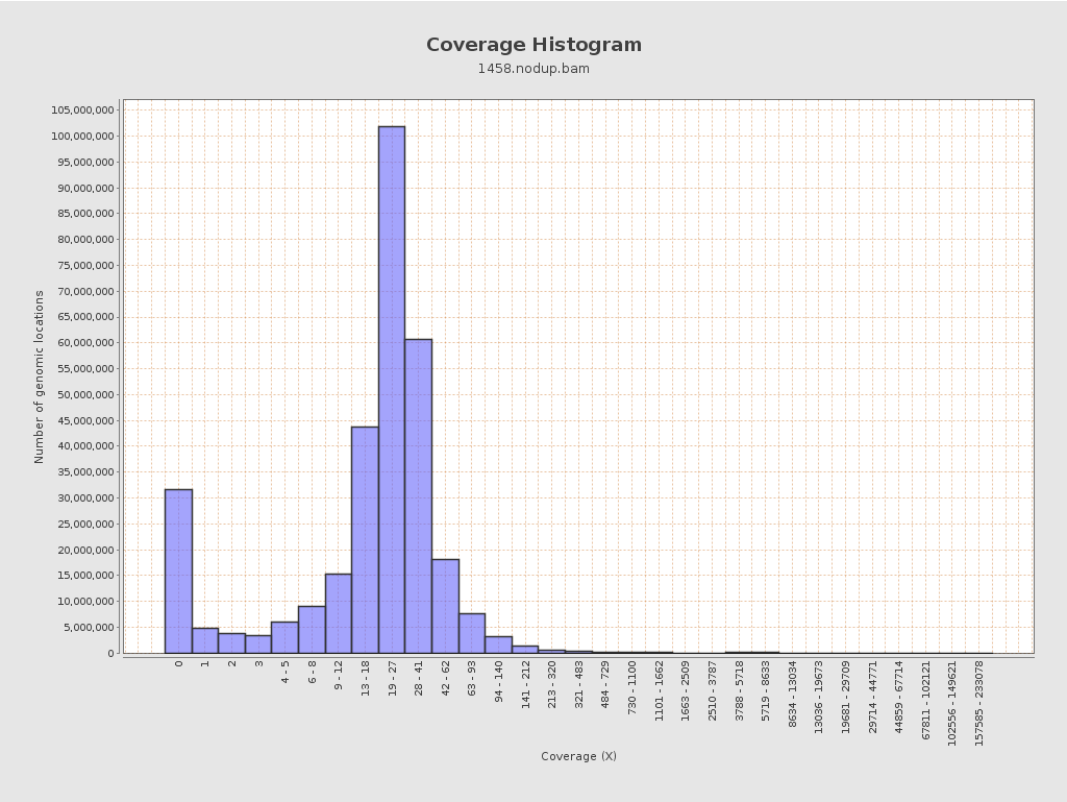
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	739660325	24.884	90.7466

LT669789.1	36598175	1087019192	29.7015	253.4667
LT669790.1	30422129	994696222	32.6965	260.1208
LT669791.1	52758100	1529626308	28.9932	238.3807
LT669792.1	28376109	836252091	29.4703	262.7926
LT669793.1	33388210	936981468	28.0632	212.4404
LT669794.1	50579949	1383908423	27.3608	205.4519
LT669795.1	49795044	1662722843	33.3913	325.2149

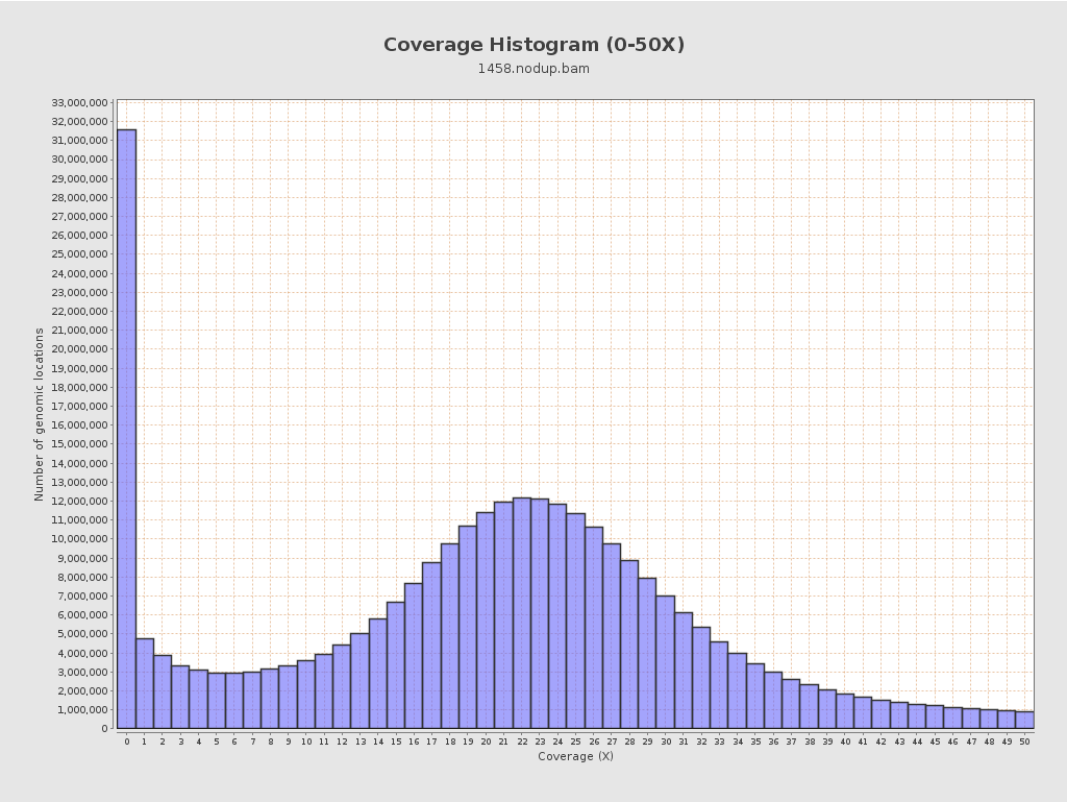
3. Results : Coverage across reference



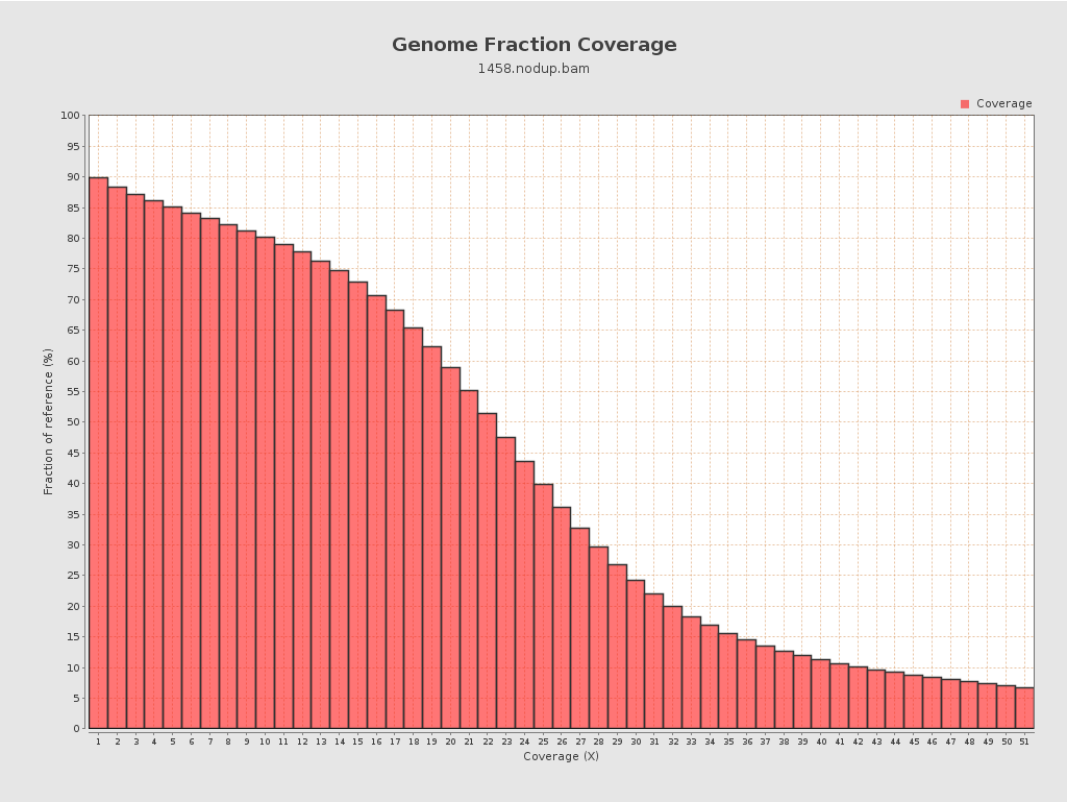
4. Results : Coverage Histogram



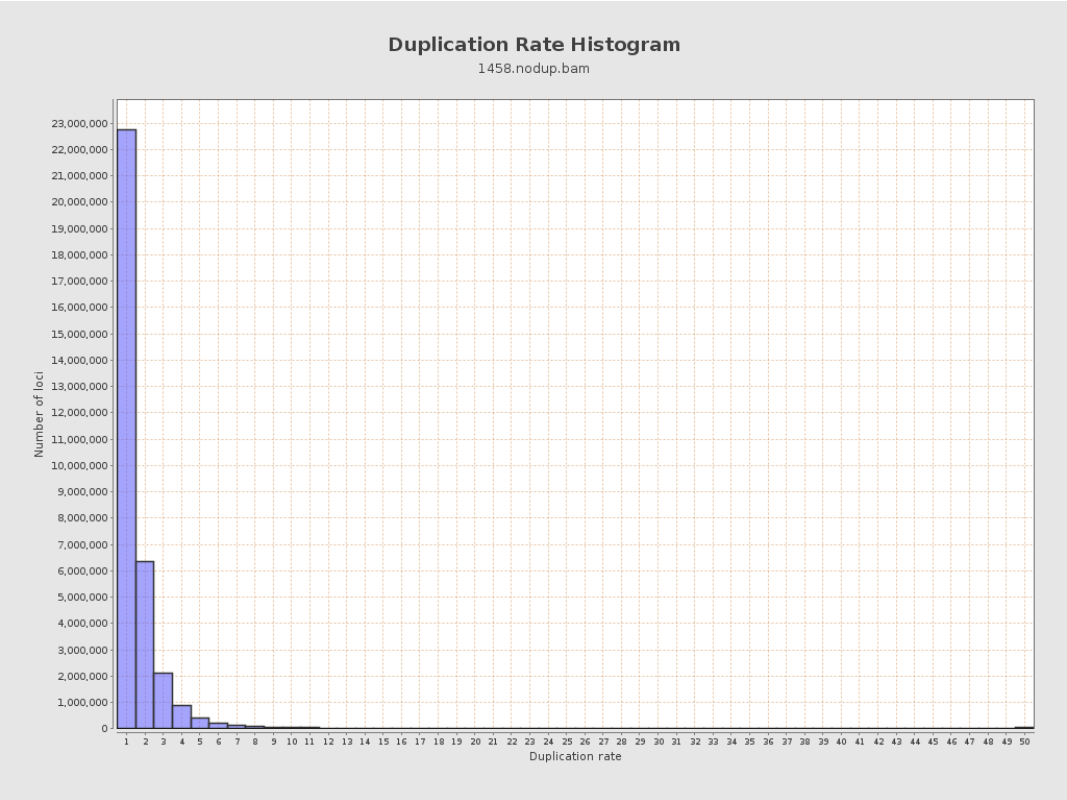
5. Results : Coverage Histogram (0-50X)



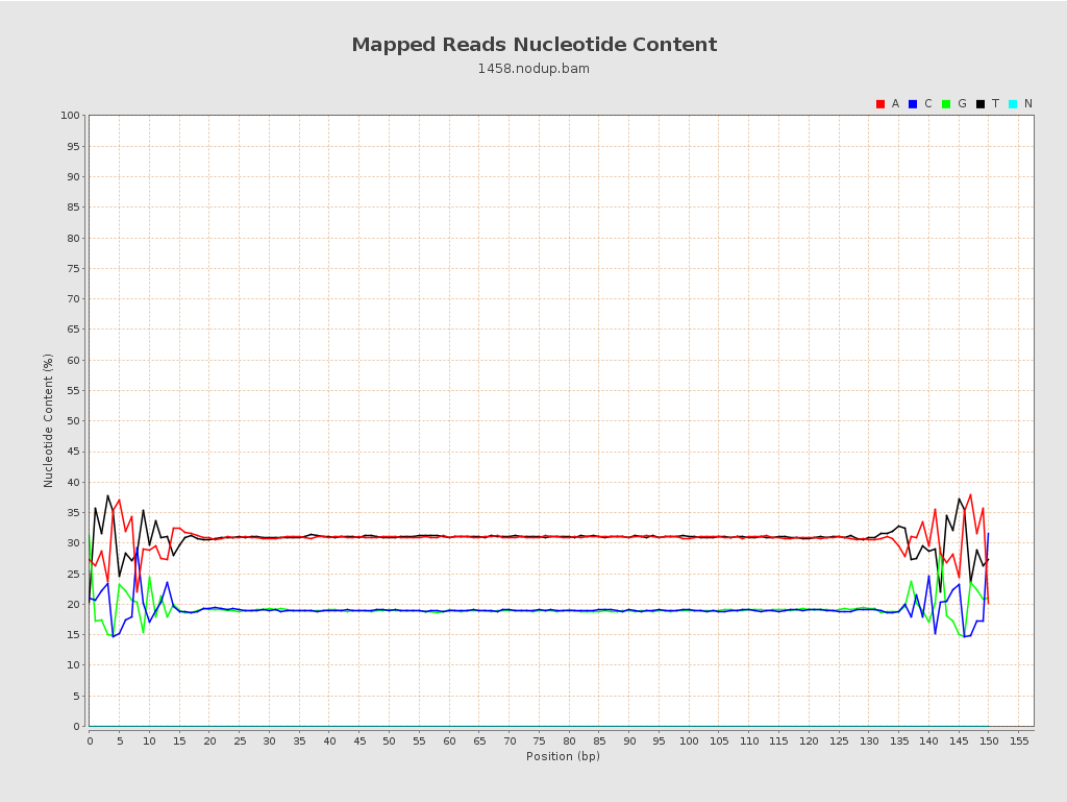
6. Results : Genome Fraction Coverage



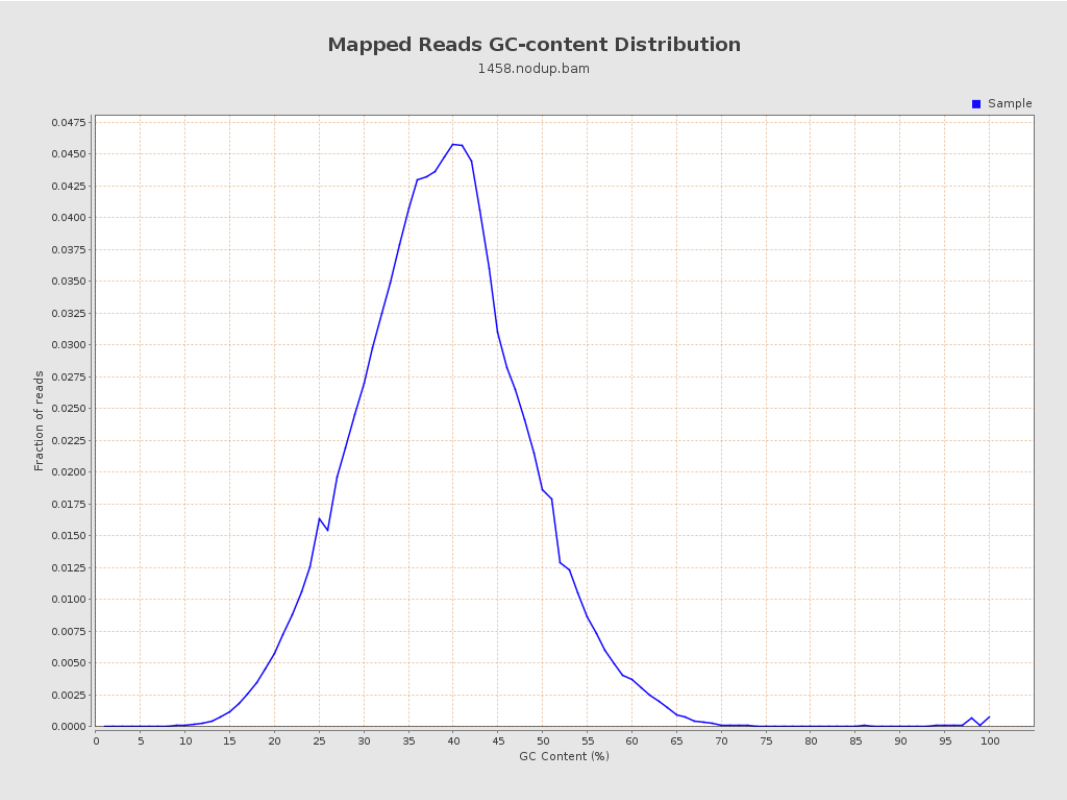
7. Results : Duplication Rate Histogram



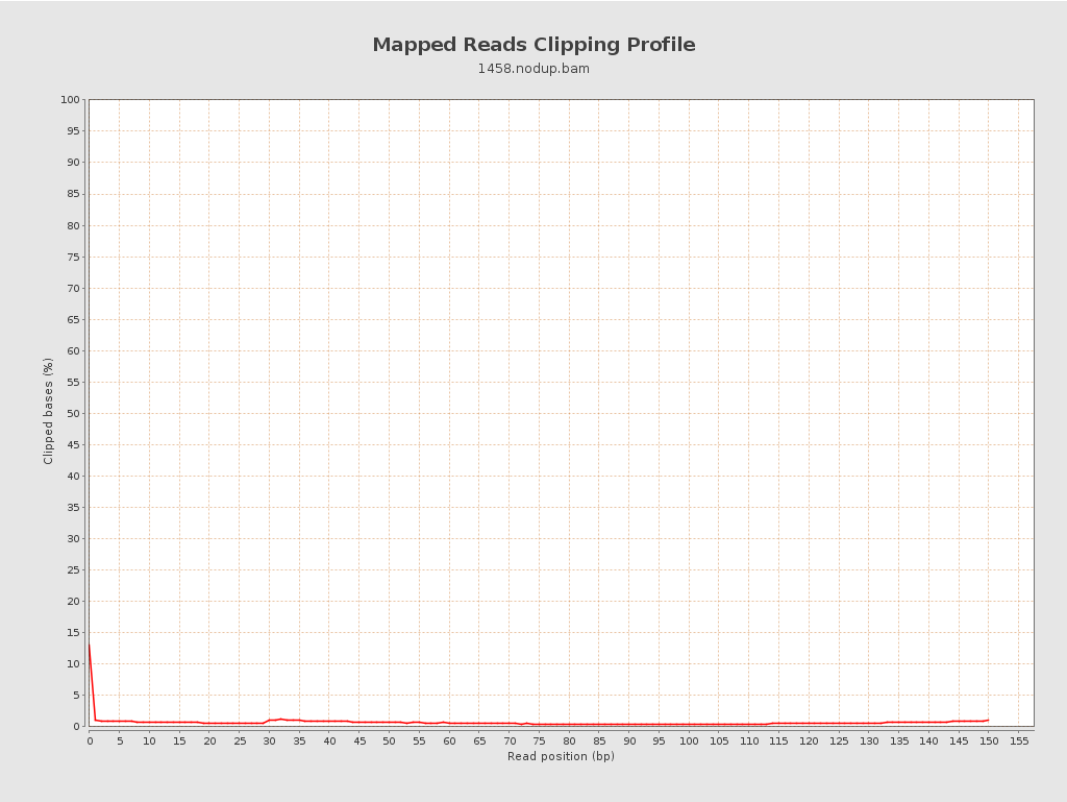
8. Results : Mapped Reads Nucleotide Content



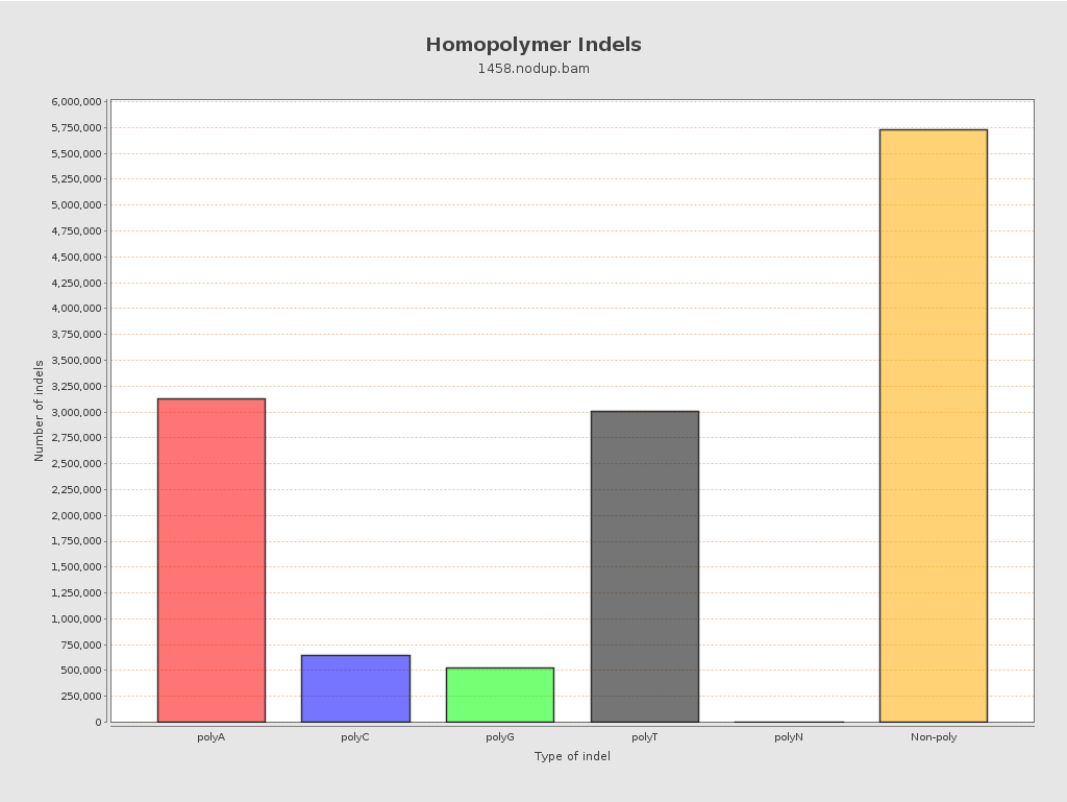
9. Results : Mapped Reads GC-content Distribution



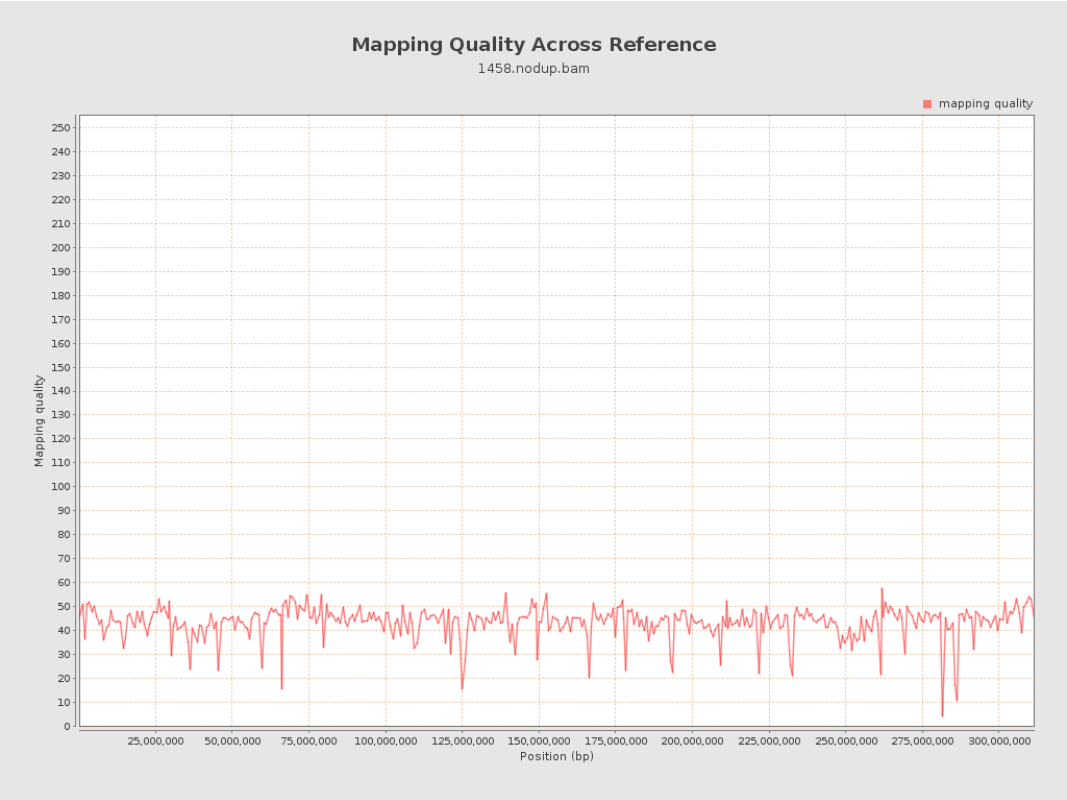
10. Results : Mapped Reads Clipping Profile



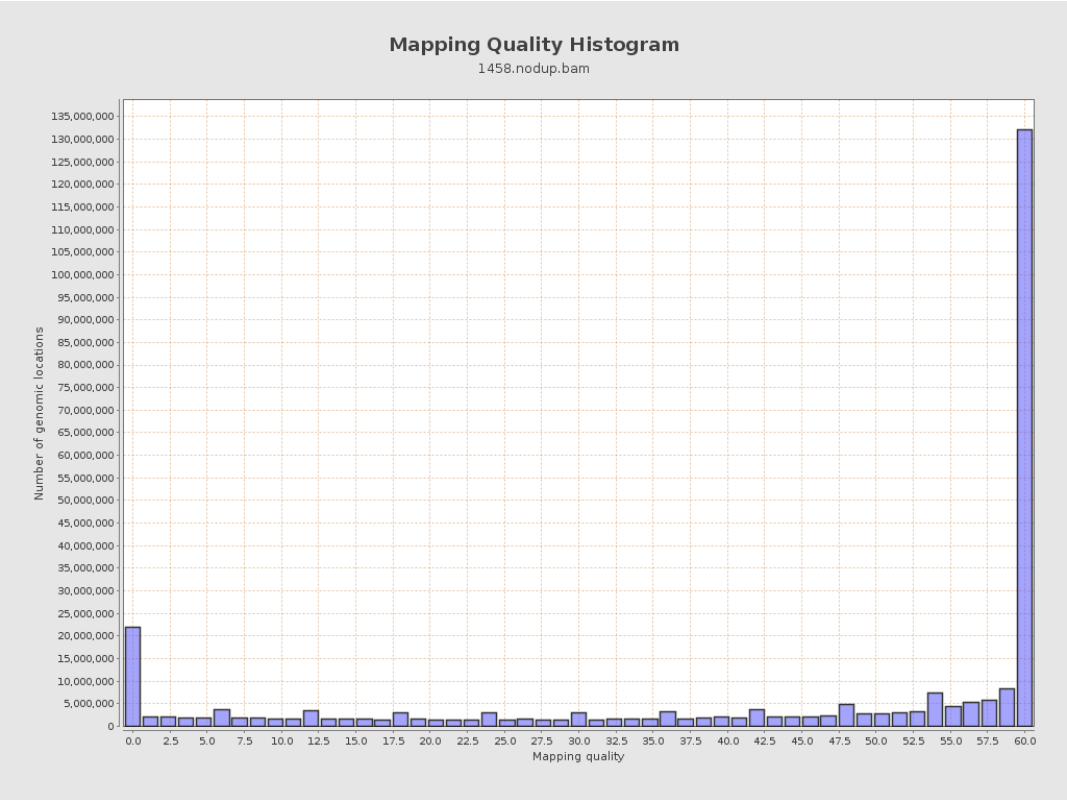
11. Results : Homopolymer Indels



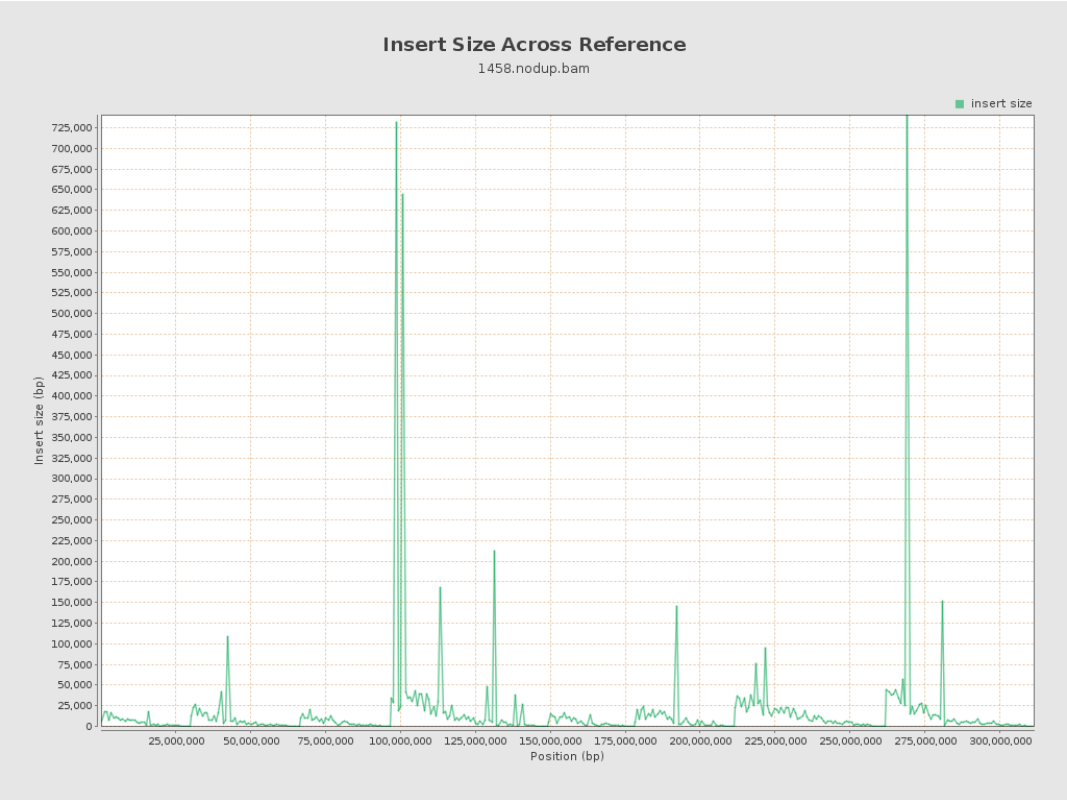
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram