Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1438
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1438 .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_583/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_583_S150_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_583/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_583_S150_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:25 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	53,899,783
Mapped reads	51,493,345 / 95.54%
Unmapped reads	2,406,438 / 4.46%
Mapped paired reads	51,493,345 / 95.54%
Mapped reads, first in pair	25,820,238 / 47.9%
Mapped reads, second in pair	25,673,107 / 47.63%
Mapped reads, both in pair	50,650,770 / 93.97%
Mapped reads, singletons	842,575 / 1.56%
Read min/max/mean length	30 / 151 / 148.23
Duplicated reads (flagged)	7,203,837 / 13.37%
Clipped reads	11,435,509 / 21.22%

2.2. ACGT Content

Number/percentage of A's	2,216,547,109 / 30.91%
Number/percentage of C's	1,370,581,509 / 19.11%
Number/percentage of T's	2,216,916,624 / 30.92%
Number/percentage of G's	1,366,488,111 / 19.06%
Number/percentage of N's	51,970 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	23.0653
Standard Deviation	182.1054

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Insert size

Mean	200,351.64
Standard Deviation	2,108,667.25
P25/Median/P75	317 / 414 / 534

2.6. Mismatches and indels

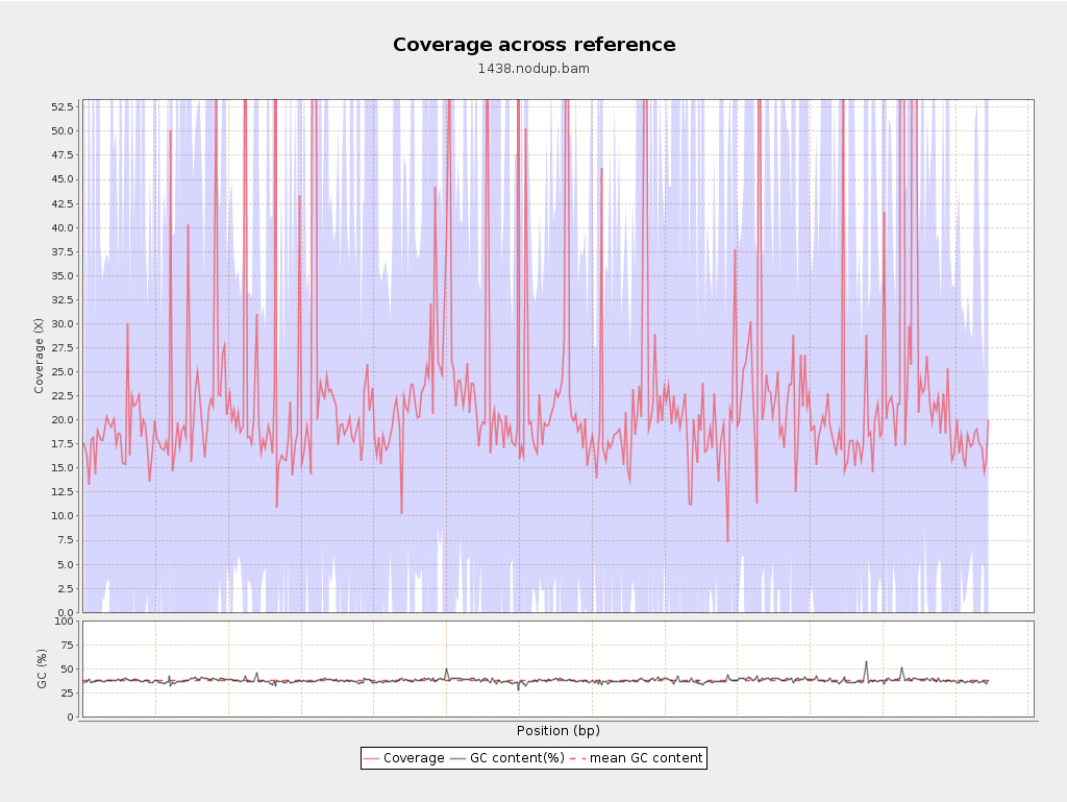
General error rate	2.42%
Mismatches	161,358,063
Insertions	4,517,271
Mapped reads with at least one insertion	7.93%
Deletions	4,679,530
Mapped reads with at least one deletion	8.12%
Homopolymer indels	56.33%

2.7. Chromosome stats

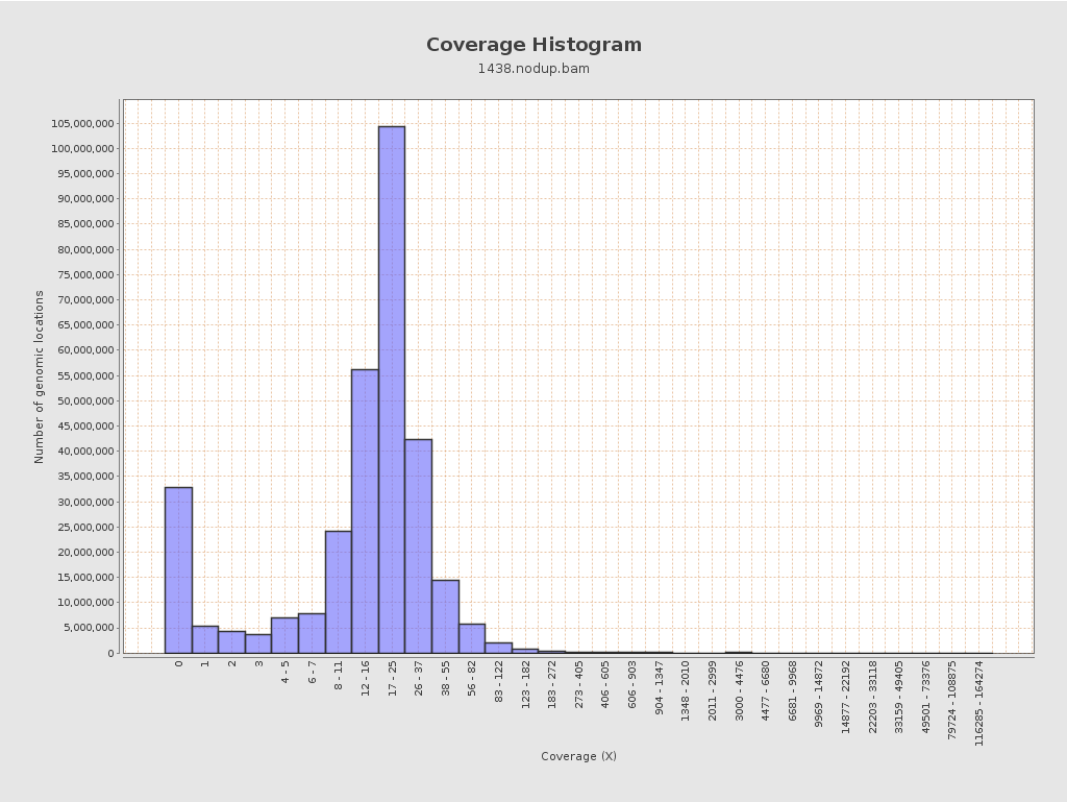
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	547748585	18.4276	39.3194

LT669789.1	36598175	854134445	23.3382	178.2993
LT669790.1	30422129	721544540	23.7178	159.2682
LT669791.1	52758100	1213378841	22.9989	128.4852
LT669792.1	28376109	639380703	22.5324	197.6204
LT669793.1	33388210	723328081	21.6642	134.5512
LT669794.1	50579949	1113493156	22.0145	153.0063
LT669795.1	49795044	1375120483	27.6156	303.4132

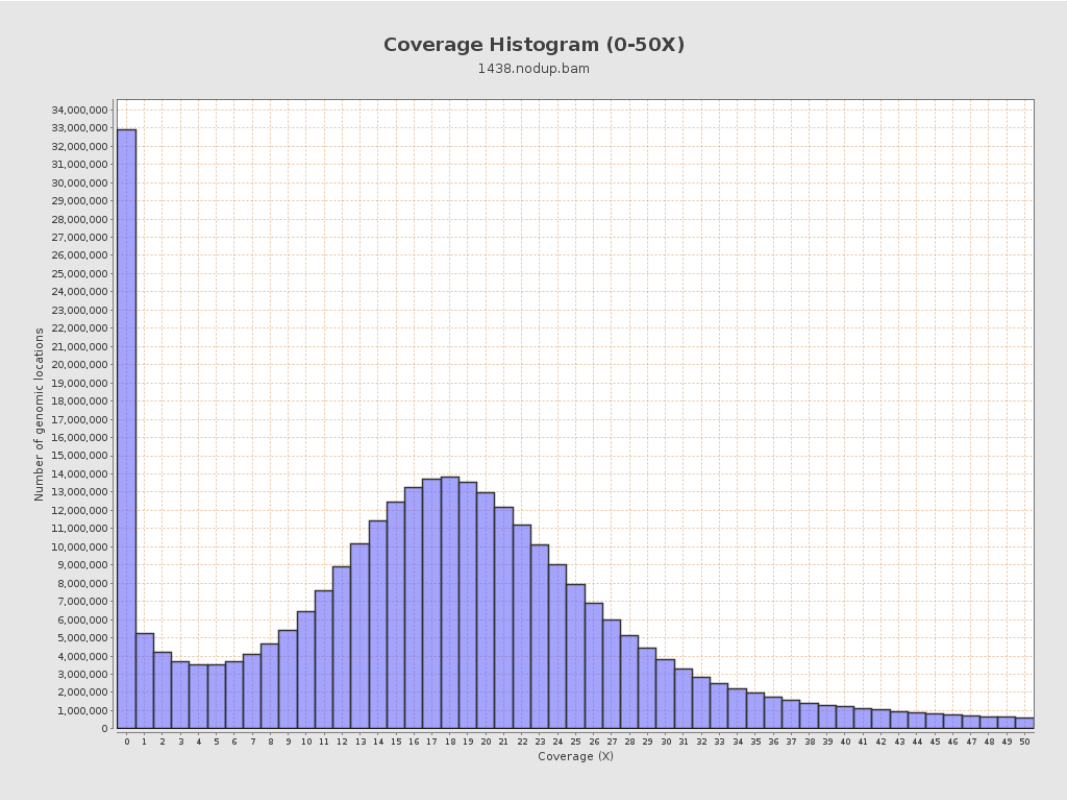
3. Results : Coverage across reference



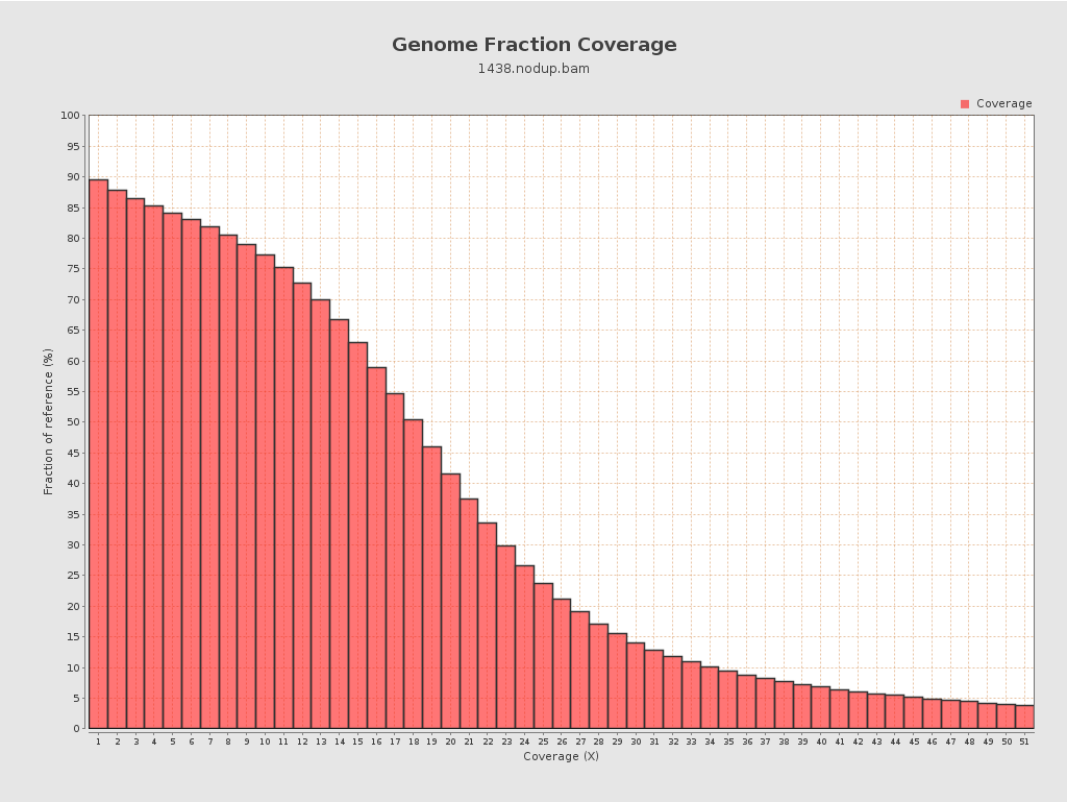
4. Results : Coverage Histogram



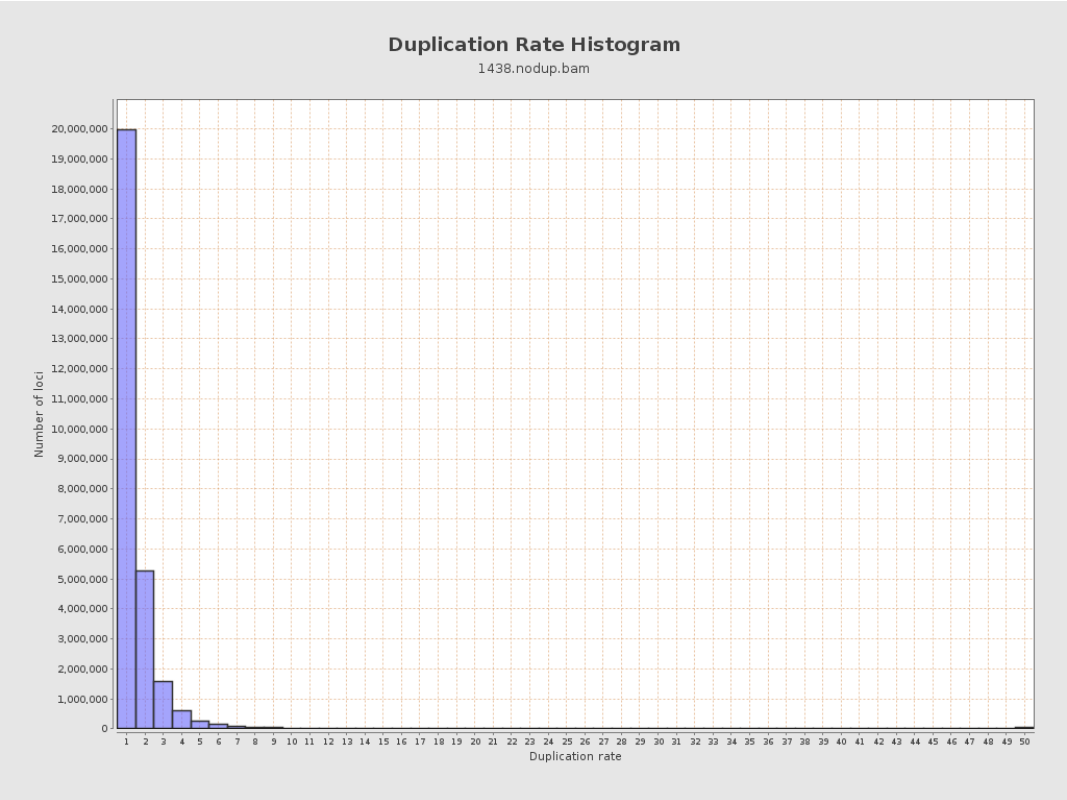
5. Results : Coverage Histogram (0-50X)



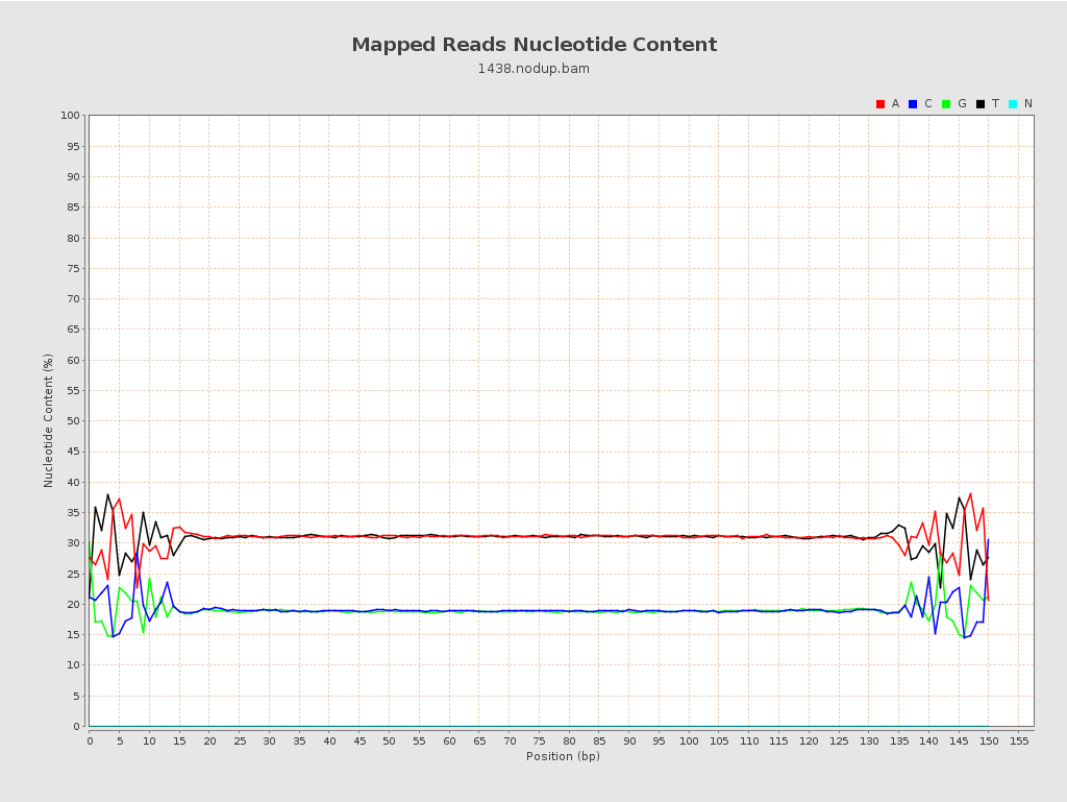
6. Results : Genome Fraction Coverage



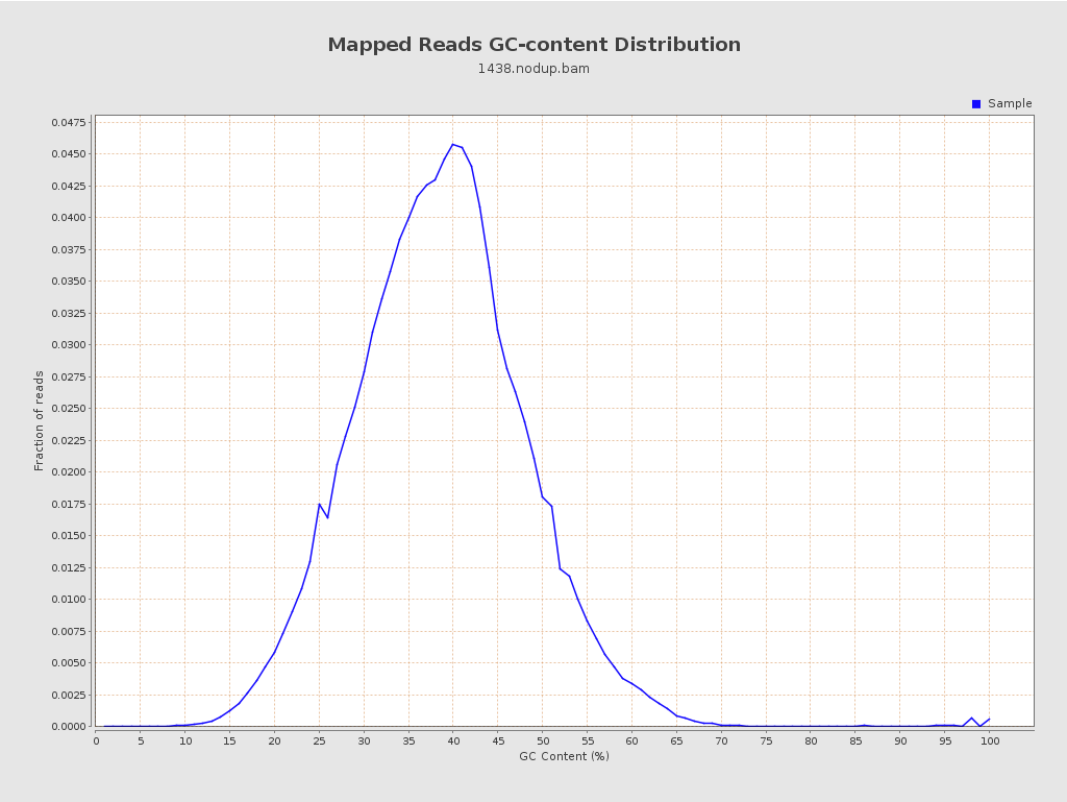
7. Results : Duplication Rate Histogram



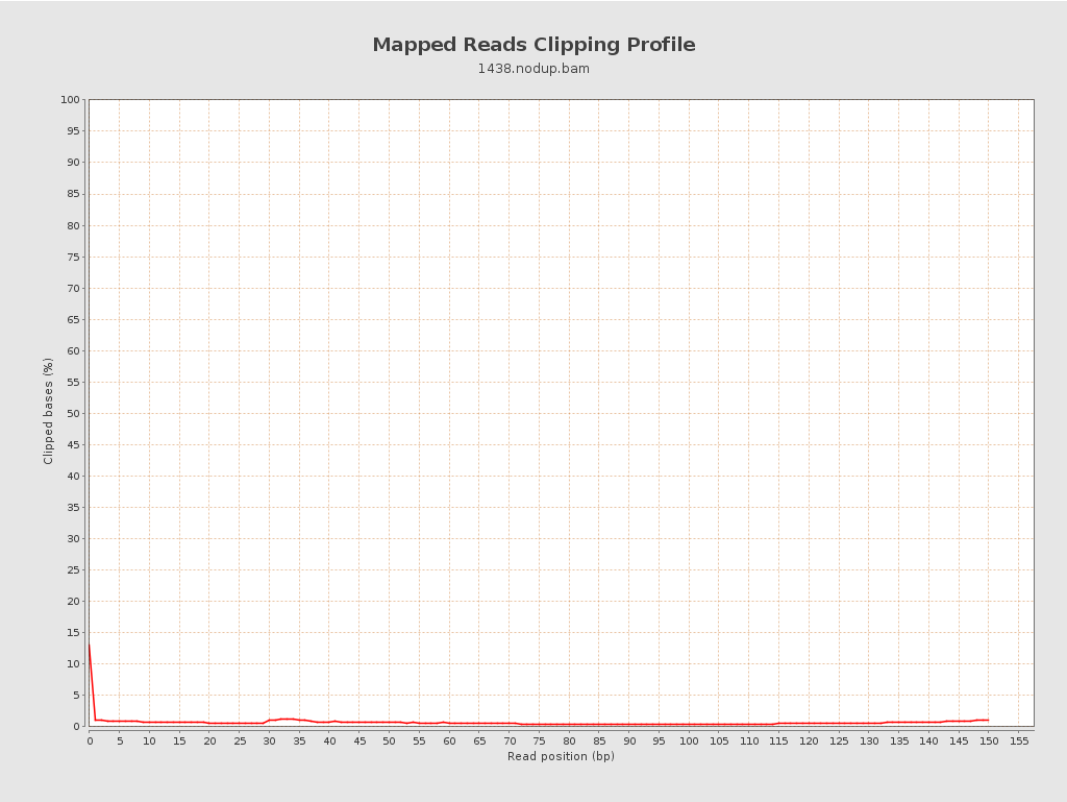
8. Results : Mapped Reads Nucleotide Content



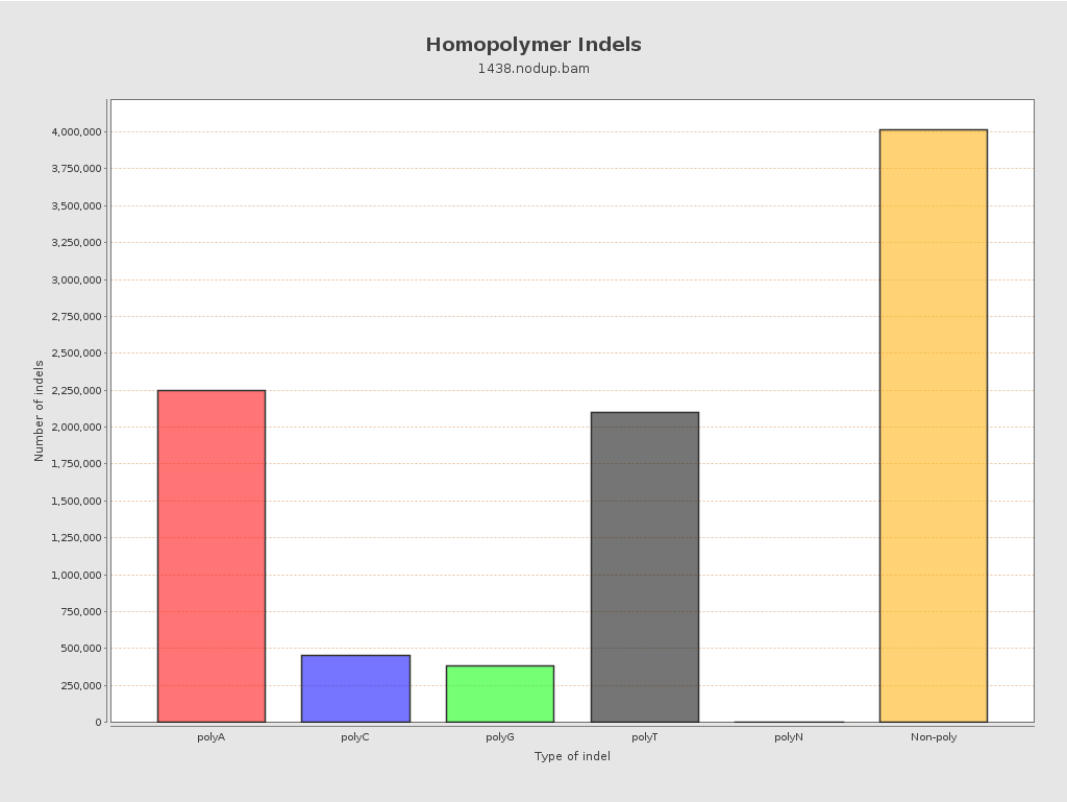
9. Results : Mapped Reads GC-content Distribution



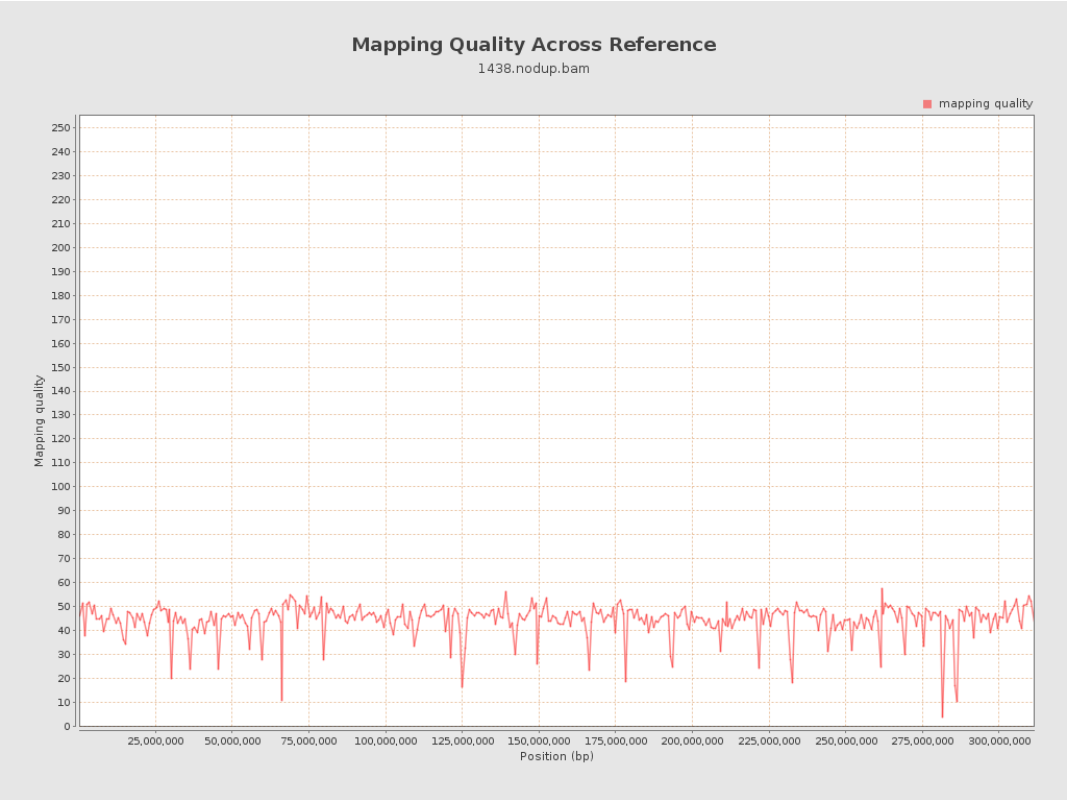
10. Results : Mapped Reads Clipping Profile



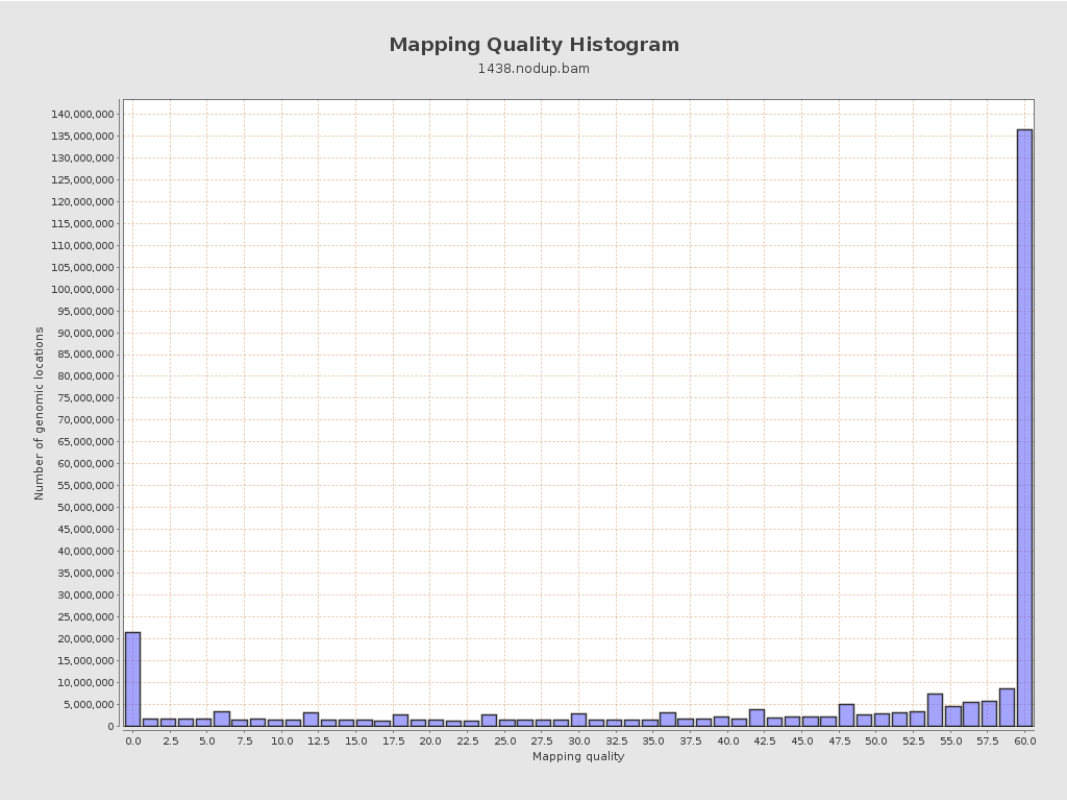
11. Results : Homopolymer Indels



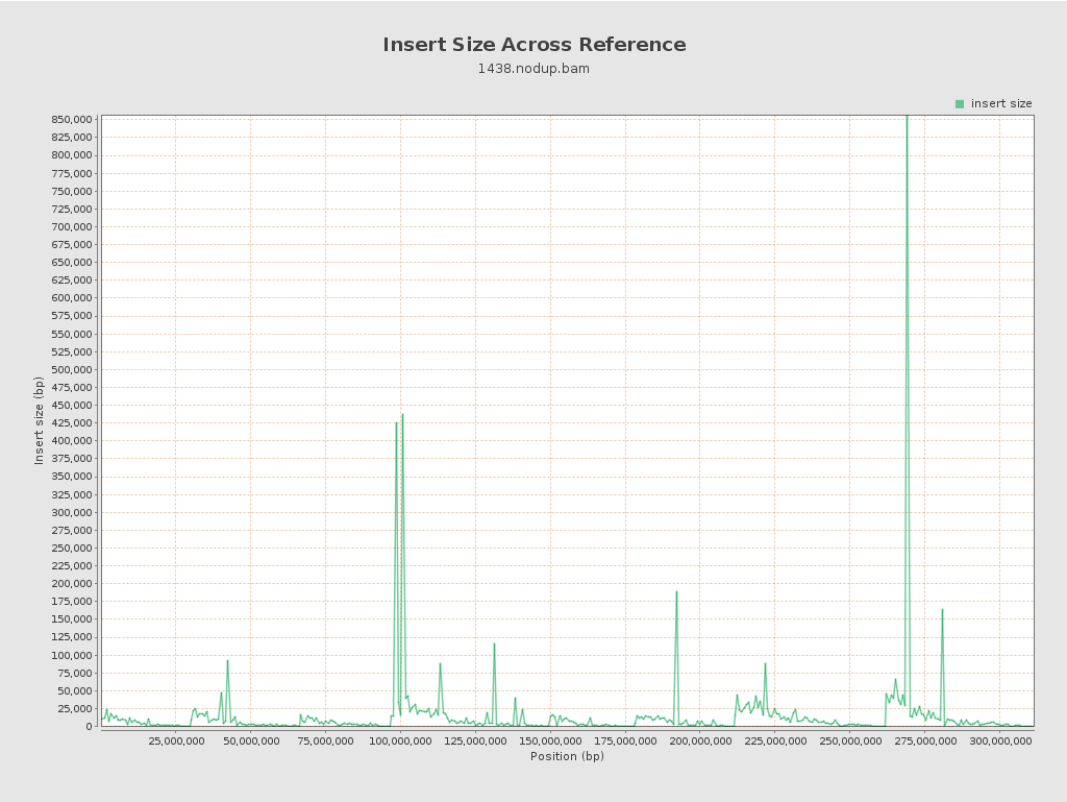
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram