Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1439
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1439 .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_533/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_533_S100_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_533/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_533_S100_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:26:45 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,299,962
Mapped reads	57,210,800 / 93.33%
Unmapped reads	4,089,162 / 6.67%
Mapped paired reads	57,210,800 / 93.33%
Mapped reads, first in pair	28,701,053 / 46.82%
Mapped reads, second in pair	28,509,747 / 46.51%
Mapped reads, both in pair	55,895,673 / 91.18%
Mapped reads, singletons	1,315,127 / 2.15%
Read min/max/mean length	30 / 151 / 148.27
Duplicated reads (flagged)	8,254,507 / 13.47%
Clipped reads	13,226,828 / 21.58%

2.2. ACGT Content

Number/percentage of A's	2,448,963,665 / 30.93%
Number/percentage of C's	1,513,434,541 / 19.11%
Number/percentage of T's	2,449,122,305 / 30.93%
Number/percentage of G's	1,506,783,413 / 19.03%
Number/percentage of N's	56,576 / 0%
GC Percentage	38.14%

2.3. Coverage

Mean	25.4725
Standard Deviation	192.4516

2.4. Mapping Quality

Mean Mapping Quality	44.24

2.5. Insert size

Mean	222,545.63
Standard Deviation	2,242,823.51
P25/Median/P75	322 / 419 / 540

2.6. Mismatches and indels

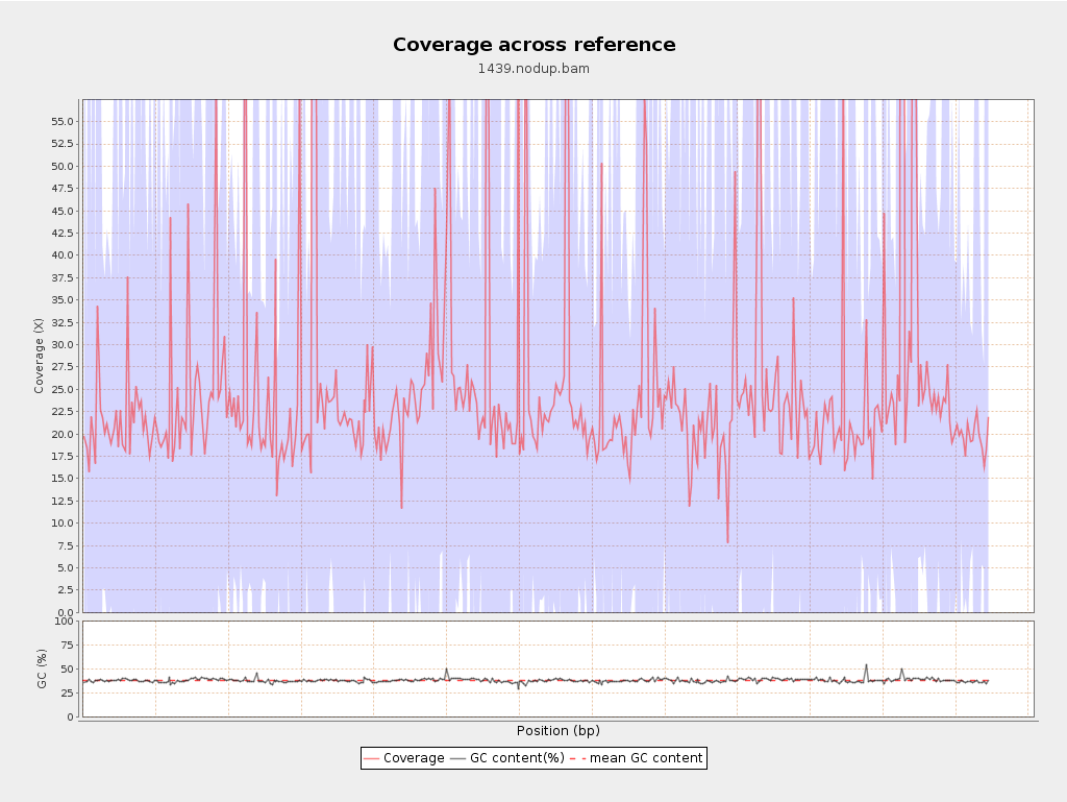
General error rate	2.5%
Mismatches	183,561,867
Insertions	5,279,057
Mapped reads with at least one insertion	8.29%
Deletions	5,321,637
Mapped reads with at least one deletion	8.27%
Homopolymer indels	56.66%

2.7. Chromosome stats

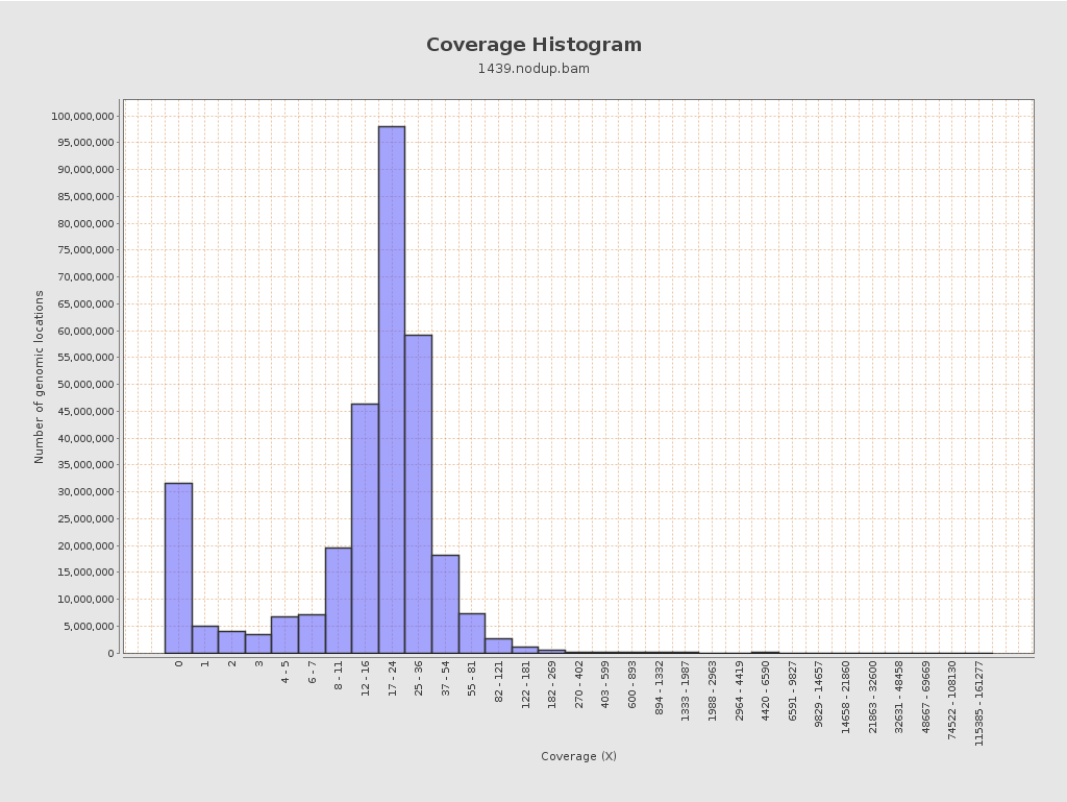
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	626595031	21.0802	57.2473

LT669789.1	36598175	936006108	25.5752	195.5878
LT669790.1	30422129	832974558	27.3805	216.2752
LT669791.1	52758100	1342048753	25.4378	174.7001
LT669792.1	28376109	717913630	25.2999	234.3691
LT669793.1	33388210	776104363	23.2449	108.0812
LT669794.1	50579949	1227277499	24.2641	171.3803
LT669795.1	49795044	1479387203	29.7095	267.9723

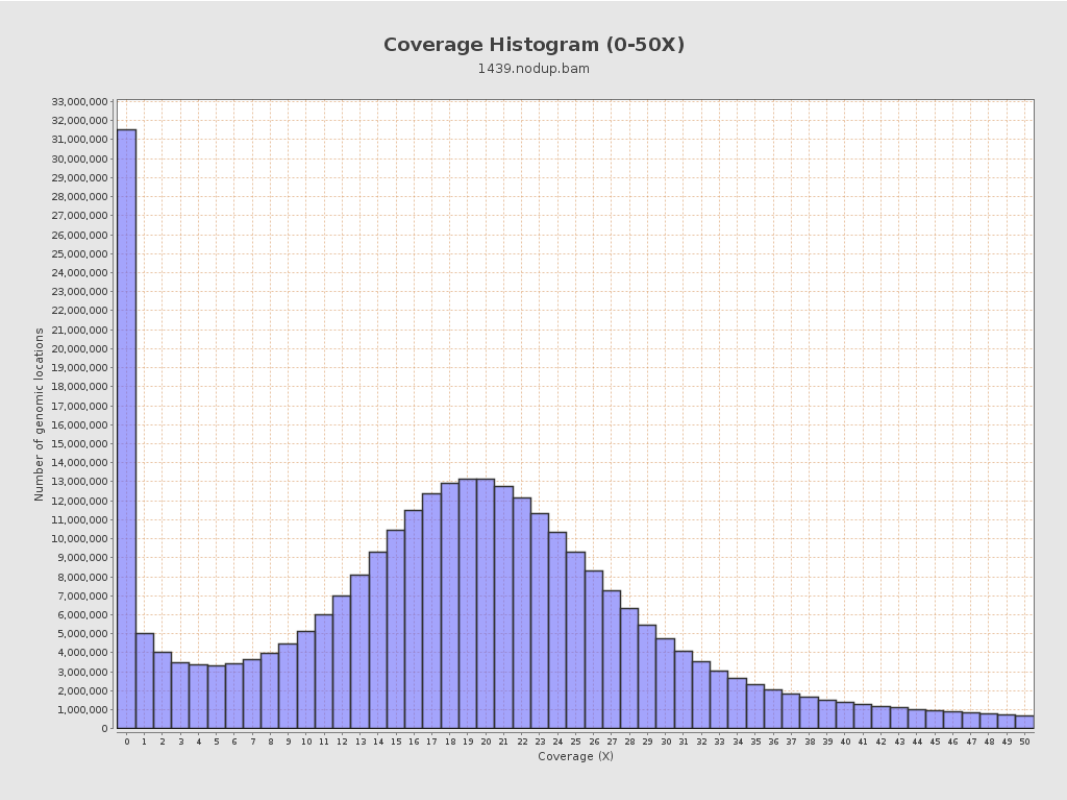
3. Results : Coverage across reference



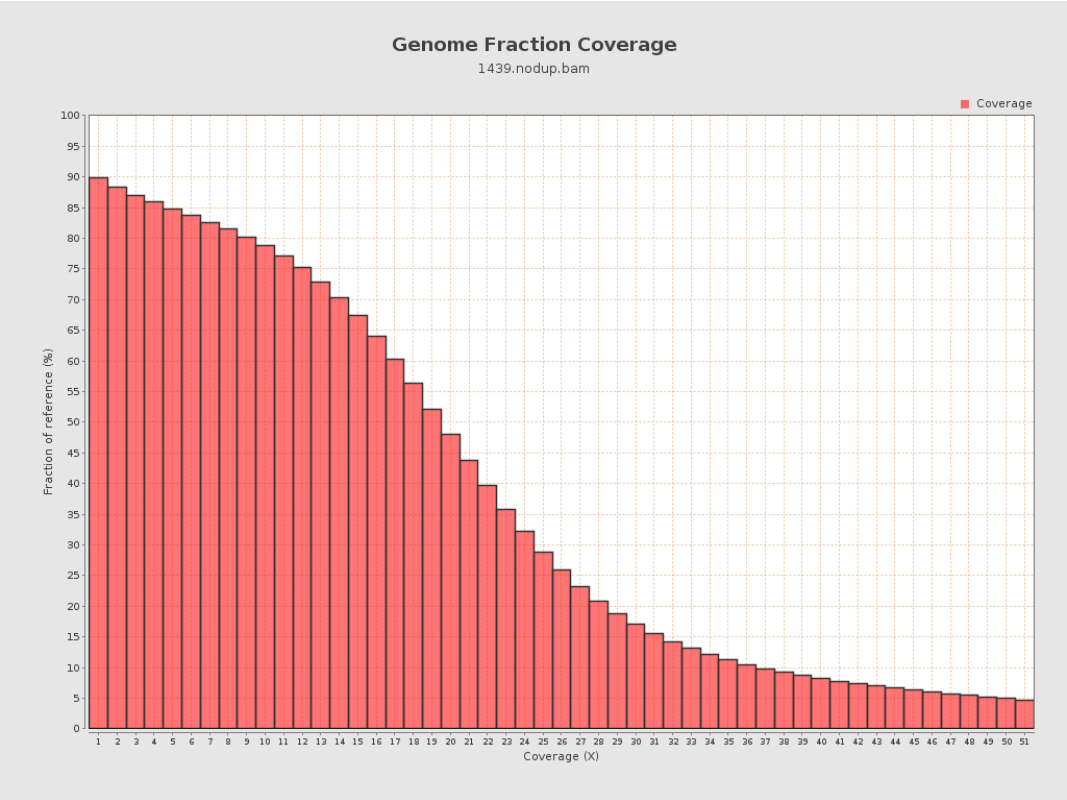
4. Results : Coverage Histogram



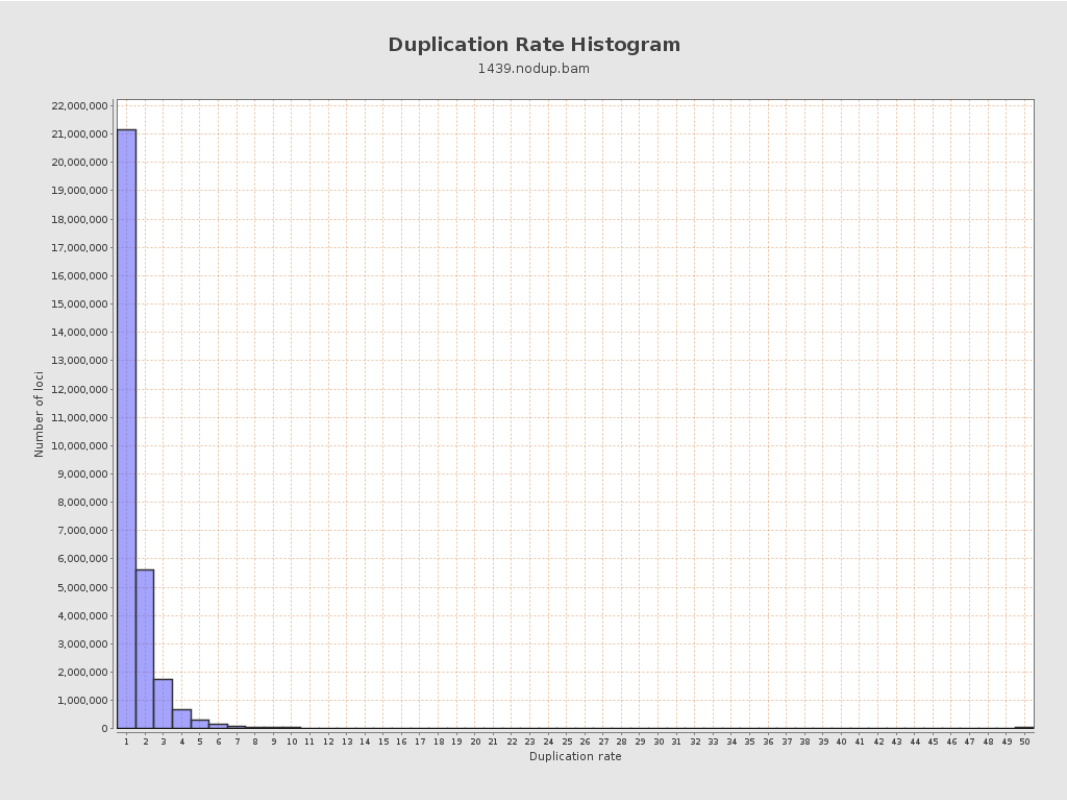
5. Results : Coverage Histogram (0-50X)



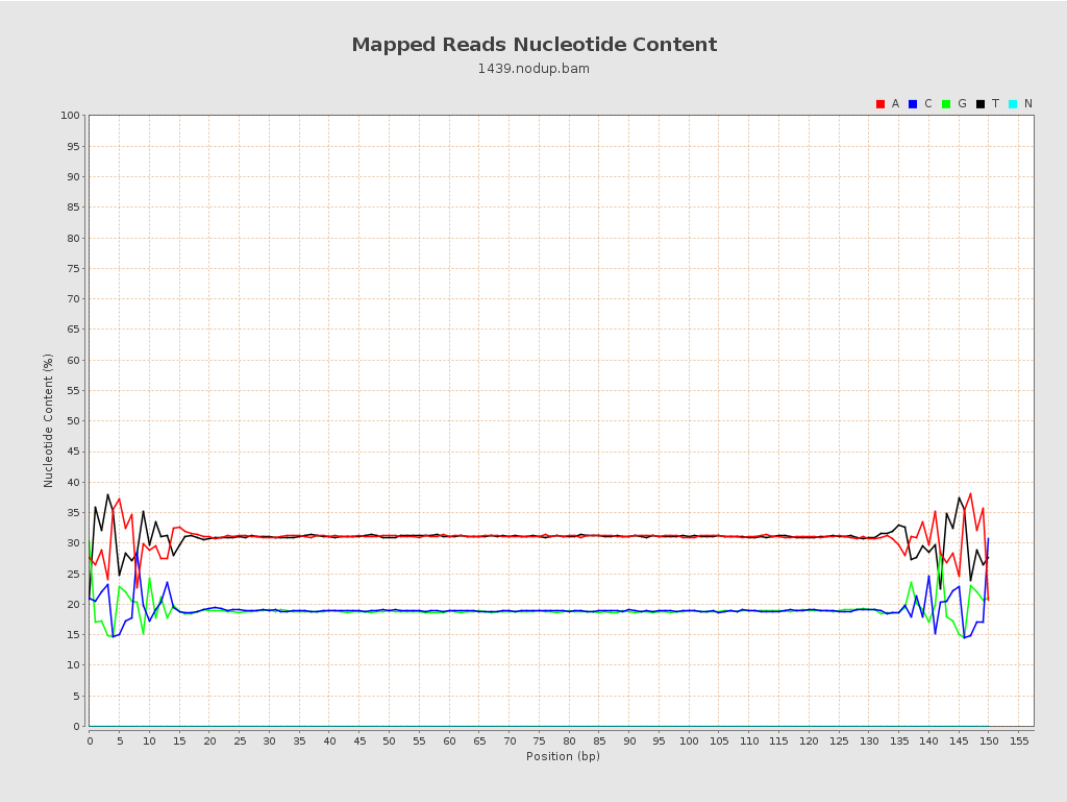
6. Results : Genome Fraction Coverage



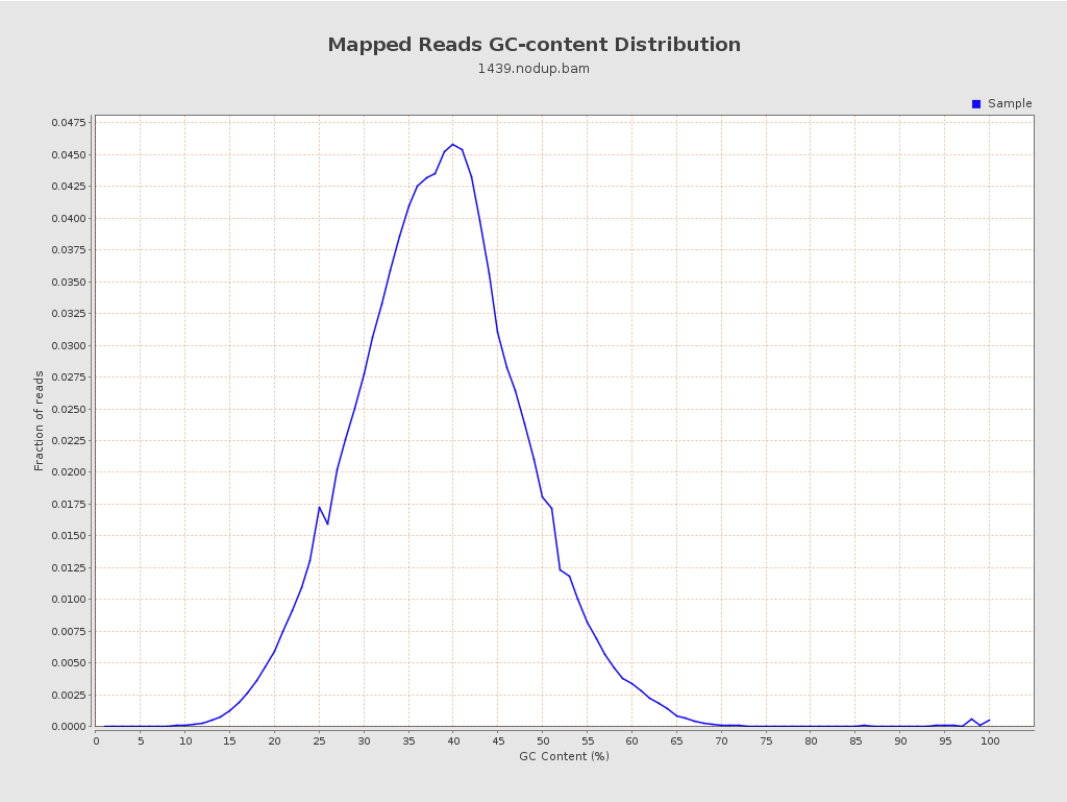
7. Results : Duplication Rate Histogram



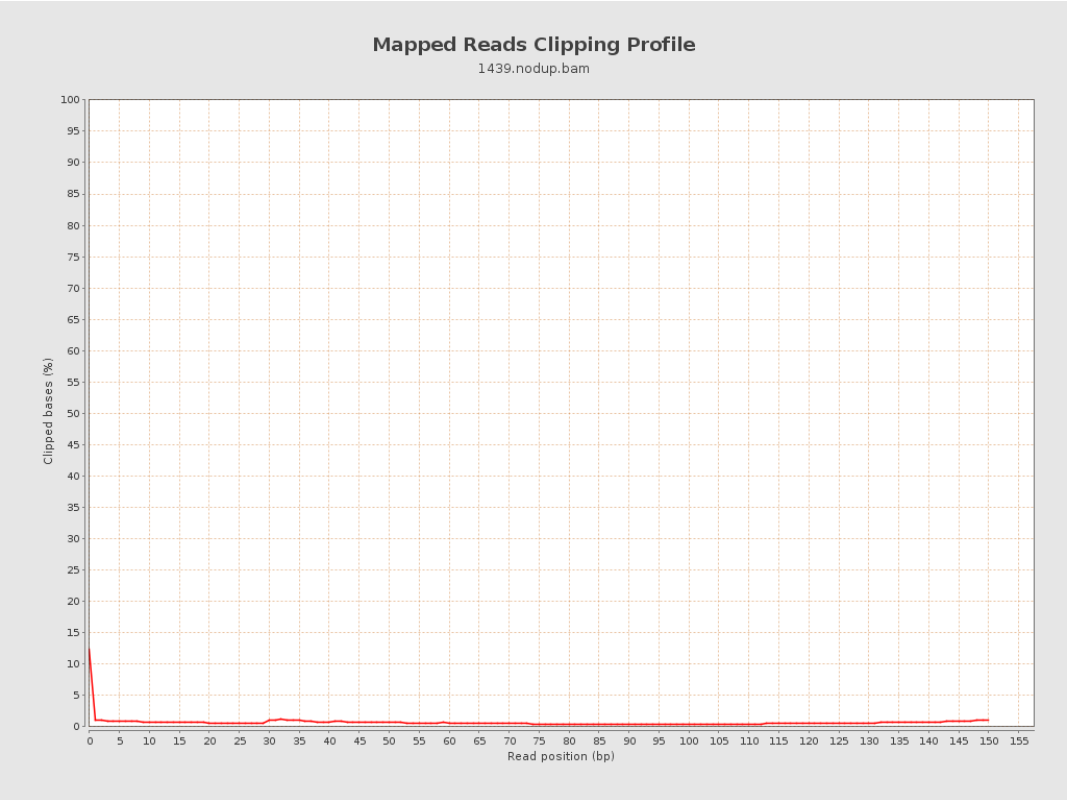
8. Results : Mapped Reads Nucleotide Content



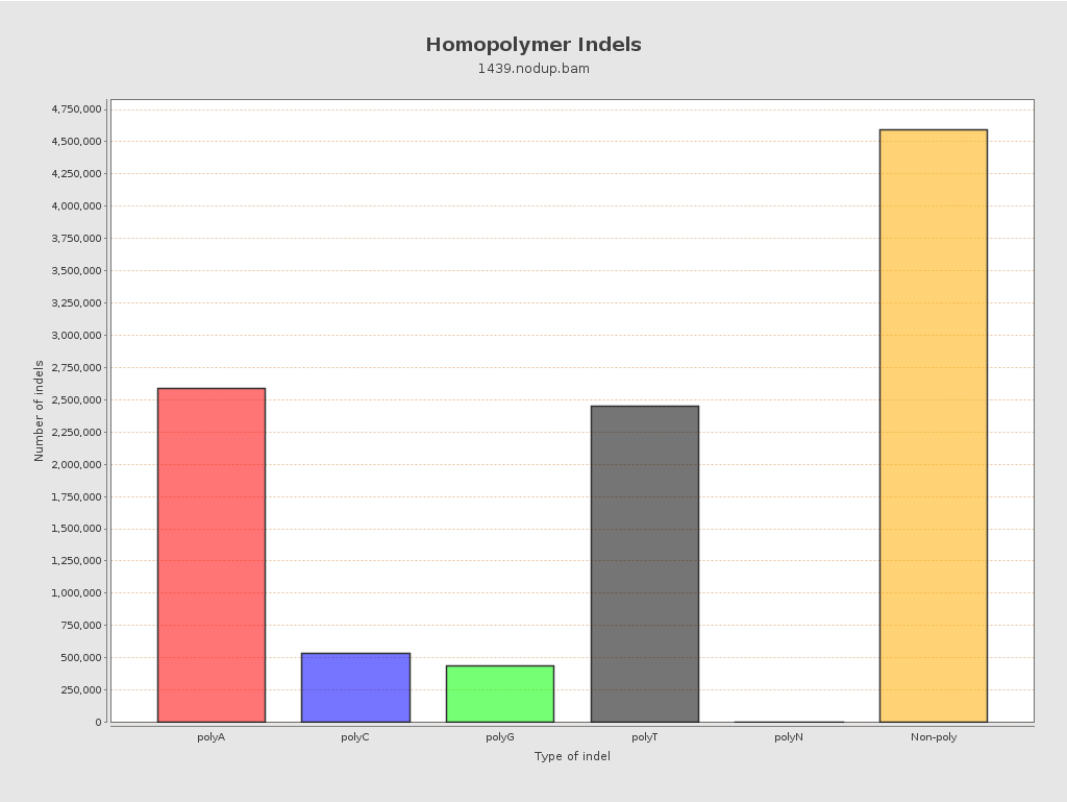
9. Results : Mapped Reads GC-content Distribution



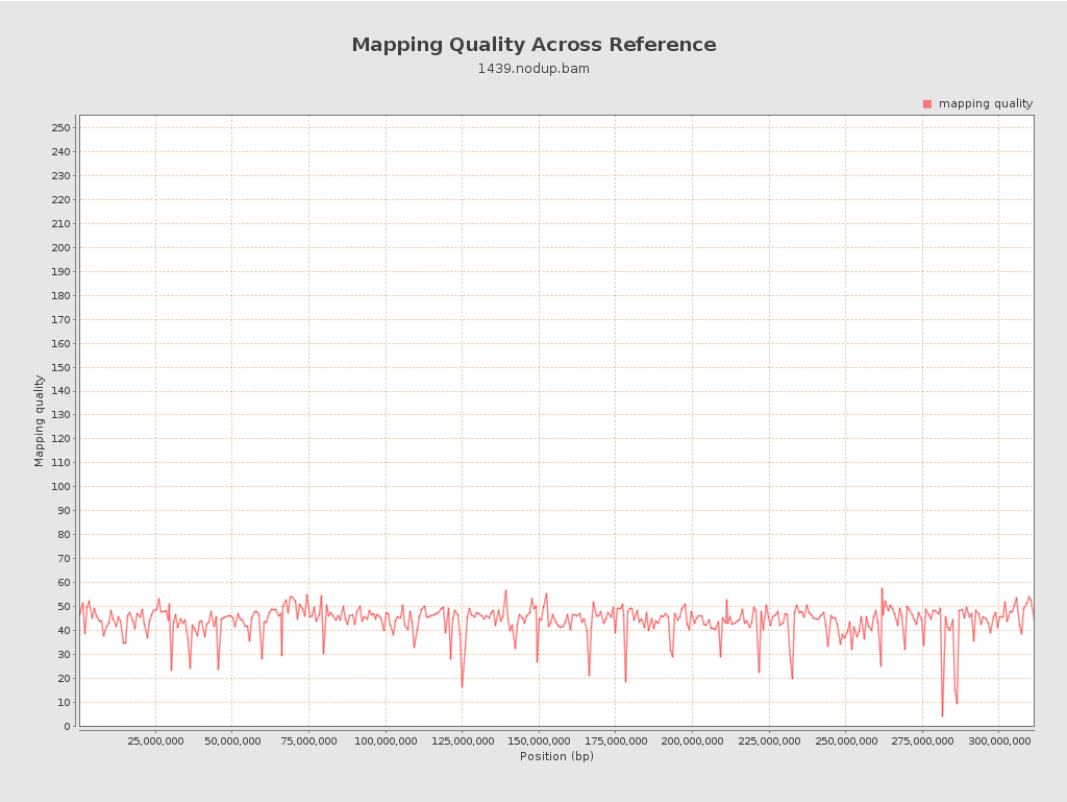
10. Results : Mapped Reads Clipping Profile



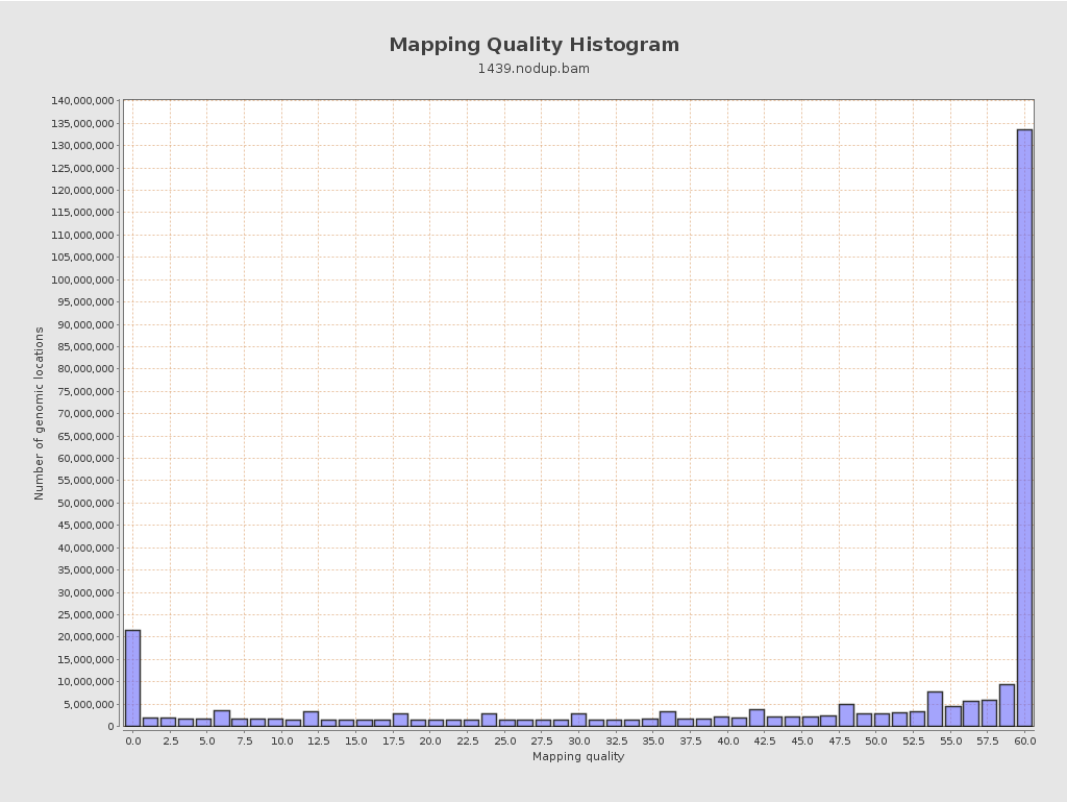
11. Results : Homopolymer Indels



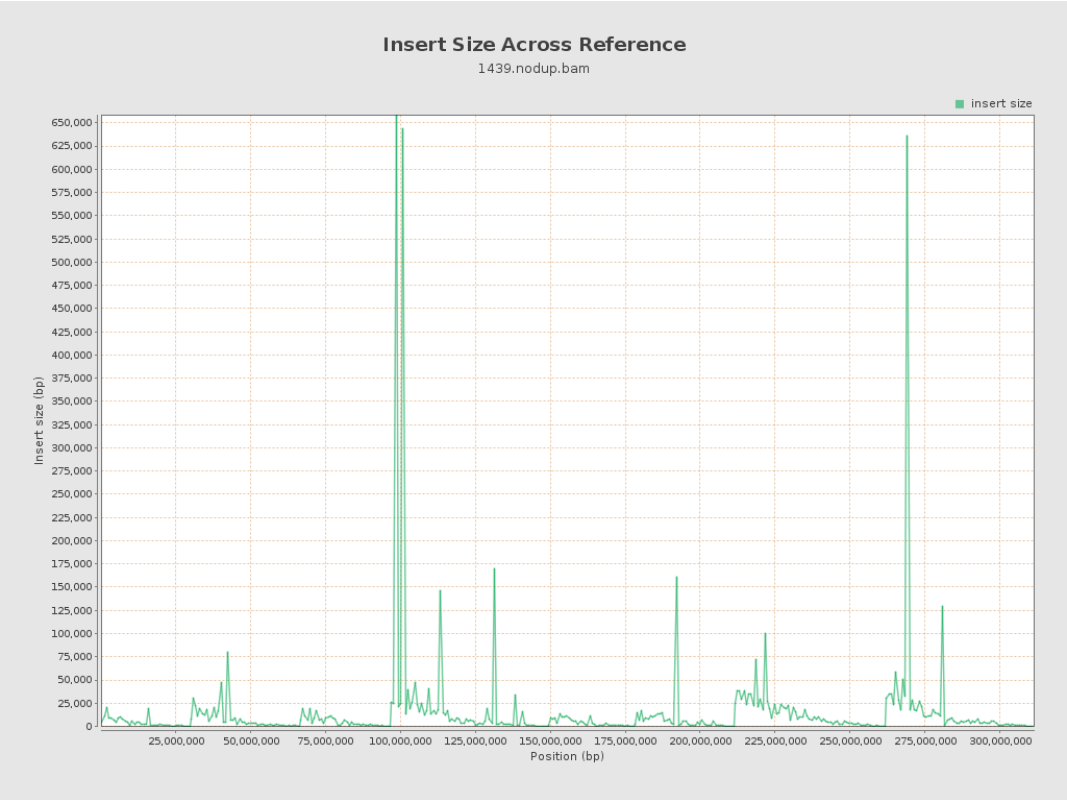
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram