Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/439.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/439.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_557/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_557_S124_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_557/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_557_S124_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:22 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,114,670
Mapped reads	63,524,515 / 93.26%
Unmapped reads	4,590,155 / 6.74%
Mapped paired reads	63,524,515 / 93.26%
Mapped reads, first in pair	31,867,832 / 46.79%
Mapped reads, second in pair	31,656,683 / 46.48%
Mapped reads, both in pair	62,118,276 / 91.2%
Mapped reads, singletons	1,406,239 / 2.06%
Read min/max/mean length	30 / 151 / 148.25
Duplicated reads (flagged)	9,506,301 / 13.96%
Clipped reads	14,649,962 / 21.51%

2.2. ACGT Content

Number/percentage of A's	2,716,693,197 / 30.86%
Number/percentage of C's	1,683,991,545 / 19.13%
Number/percentage of T's	2,721,257,448 / 30.92%
Number/percentage of G's	1,680,003,190 / 19.09%
Number/percentage of N's	61,507 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	28.316
Standard Deviation	224.8923

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Insert size

Mean	215,971.44
Standard Deviation	2,210,705.56
P25/Median/P75	309 / 402 / 518

2.6. Mismatches and indels

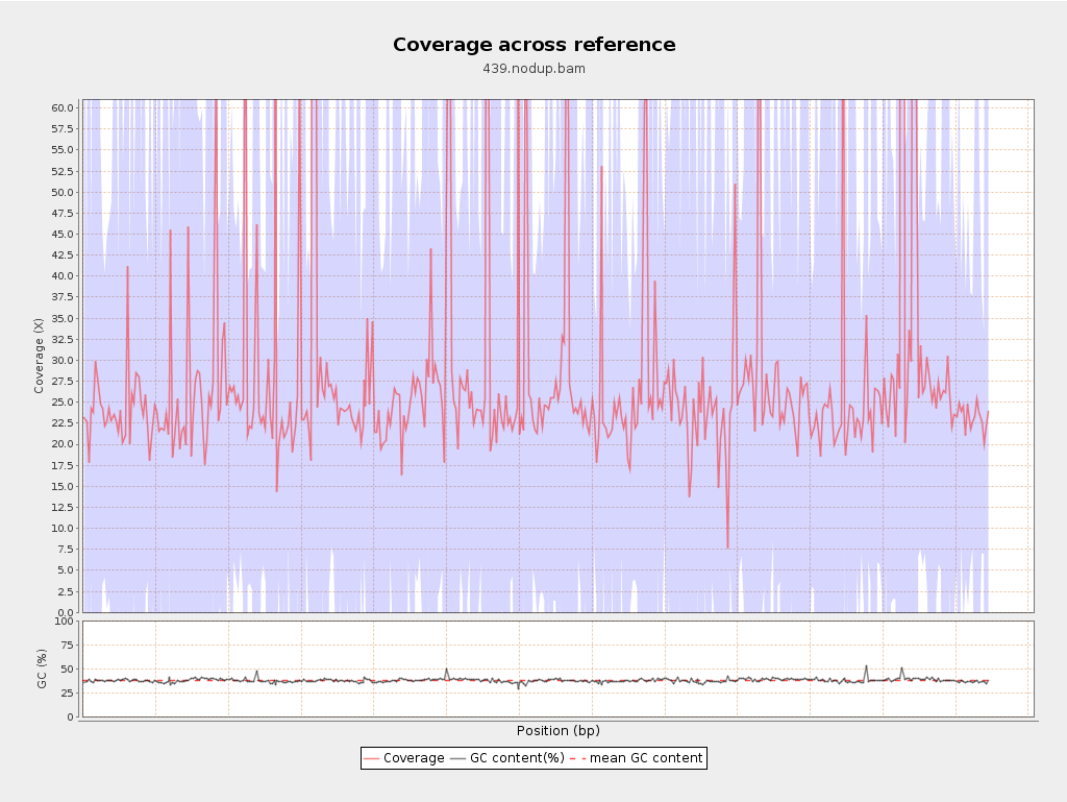
General error rate	2.55%
Mismatches	208,045,437
Insertions	5,939,048
Mapped reads with at least one insertion	8.39%
Deletions	5,998,352
Mapped reads with at least one deletion	8.37%
Homopolymer indels	55.76%

2.7. Chromosome stats

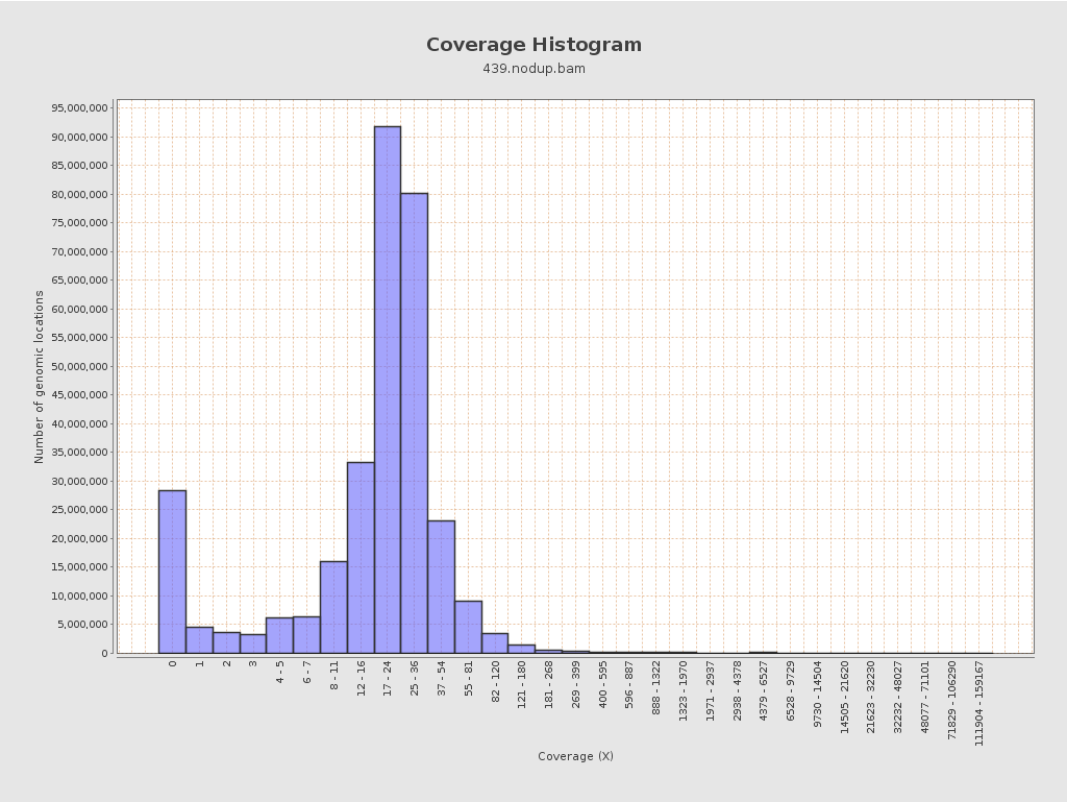
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	710028921	23.8871	87.236

LT669789.1	36598175	1025202734	28.0124	244.1621
LT669790.1	30422129	940123550	30.9026	235.7973
LT669791.1	52758100	1453128582	27.5432	222.6083
LT669792.1	28376109	795644045	28.0392	228.5205
LT669793.1	33388210	870740450	26.0793	148.5152
LT669794.1	50579949	1347454211	26.6401	203.8703
LT669795.1	49795044	1682143574	33.7813	308.0314

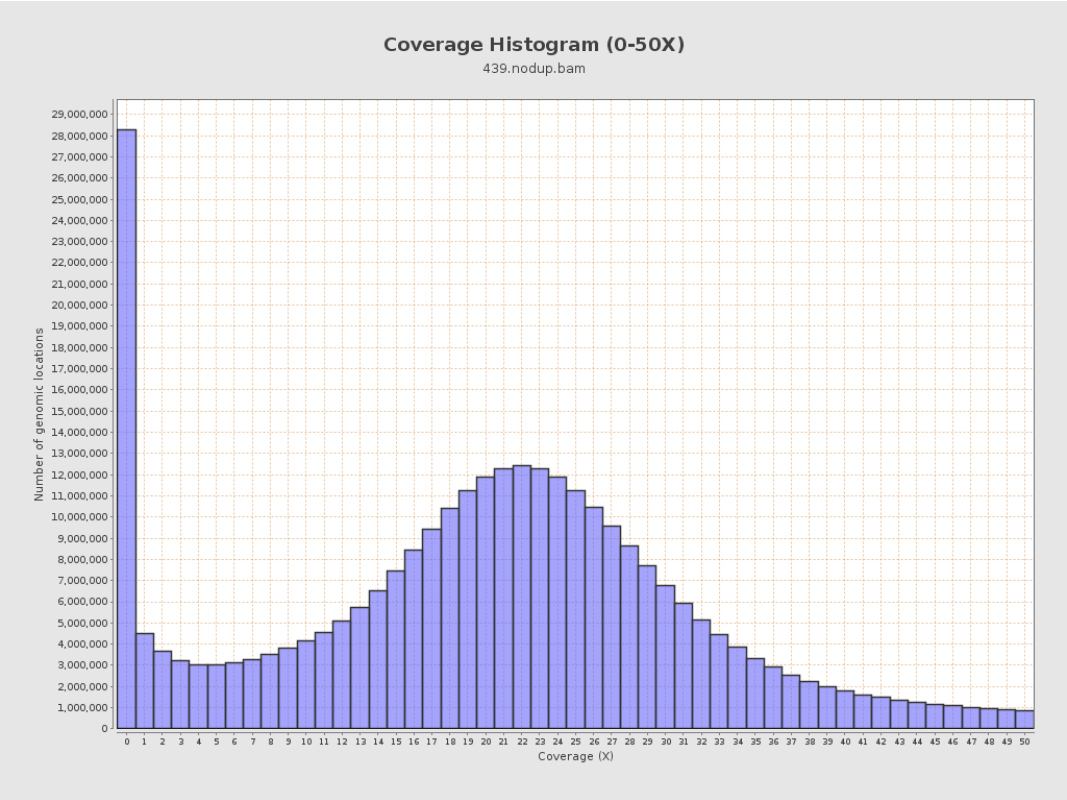
3. Results : Coverage across reference



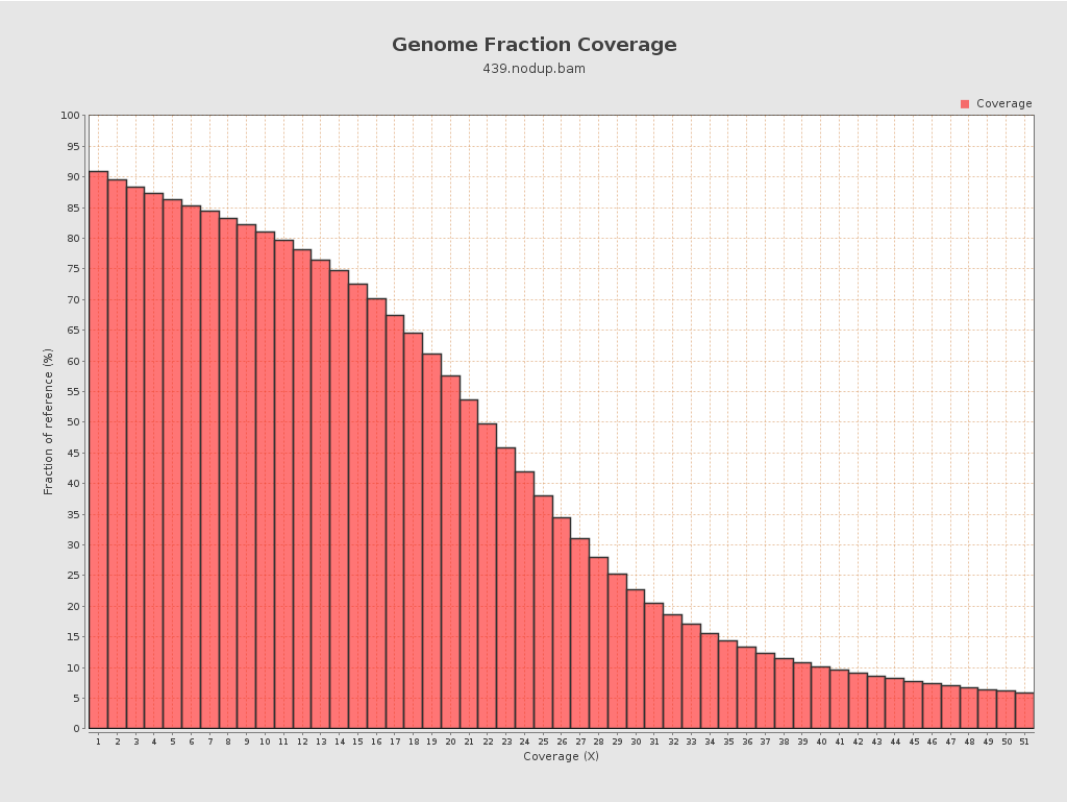
4. Results : Coverage Histogram



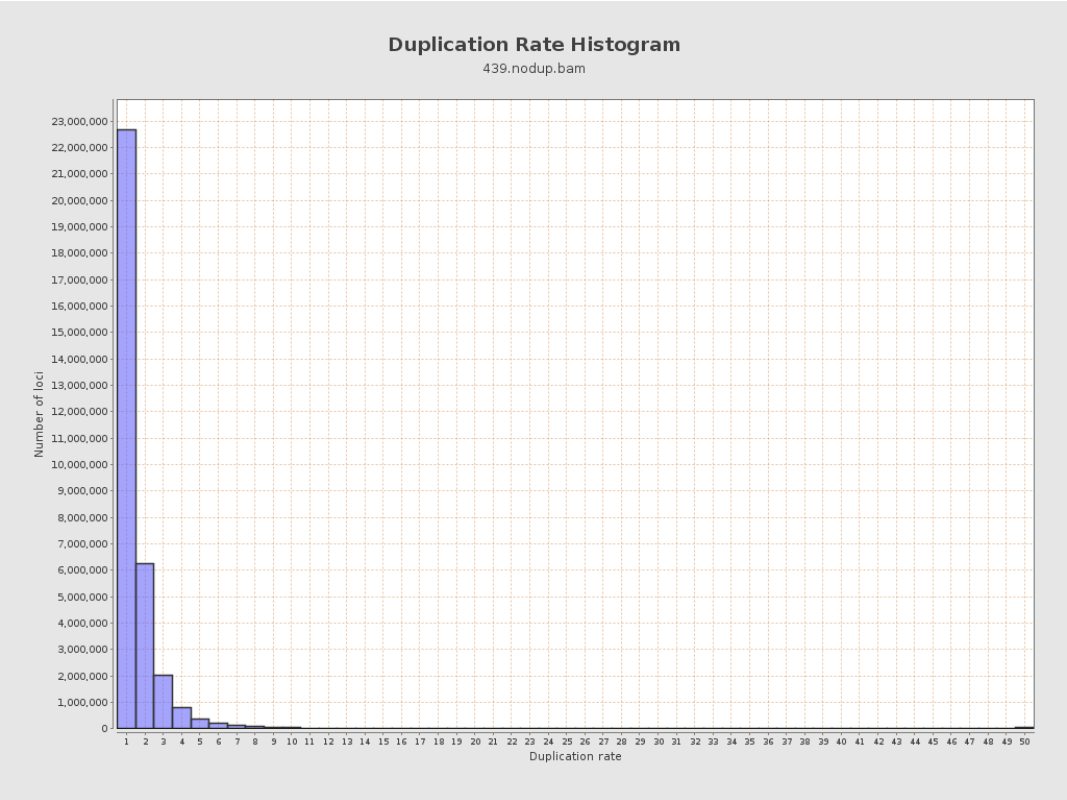
5. Results : Coverage Histogram (0-50X)



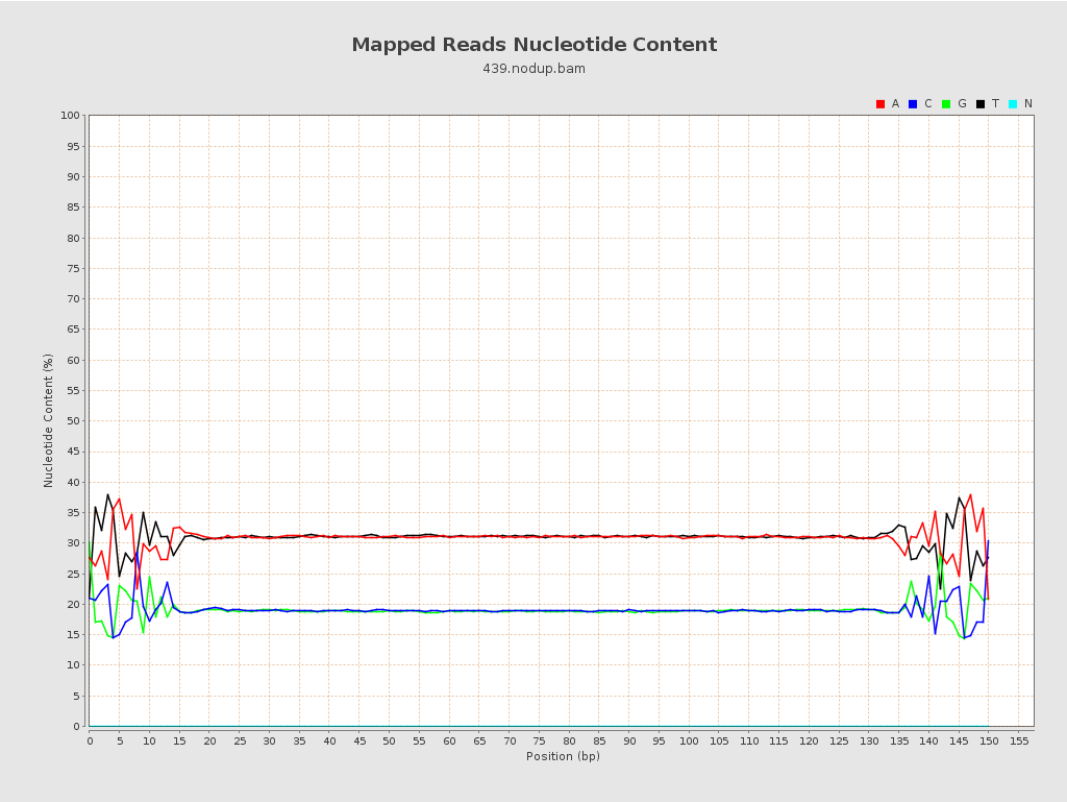
6. Results : Genome Fraction Coverage



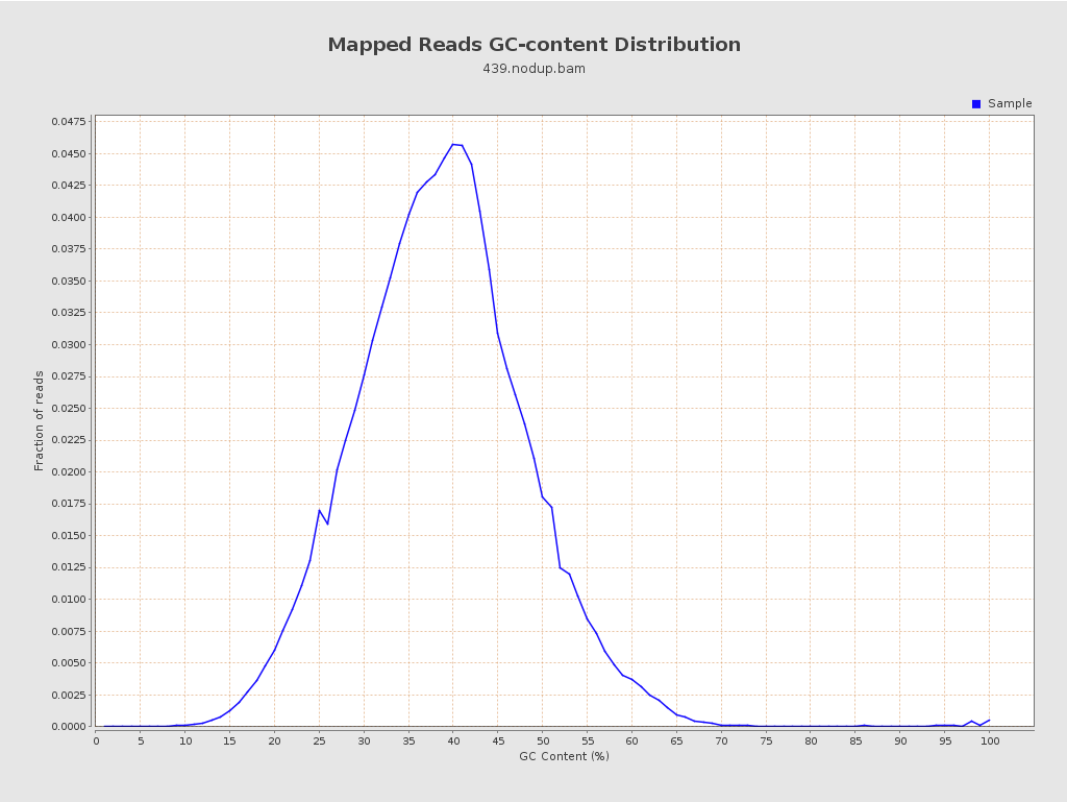
7. Results : Duplication Rate Histogram



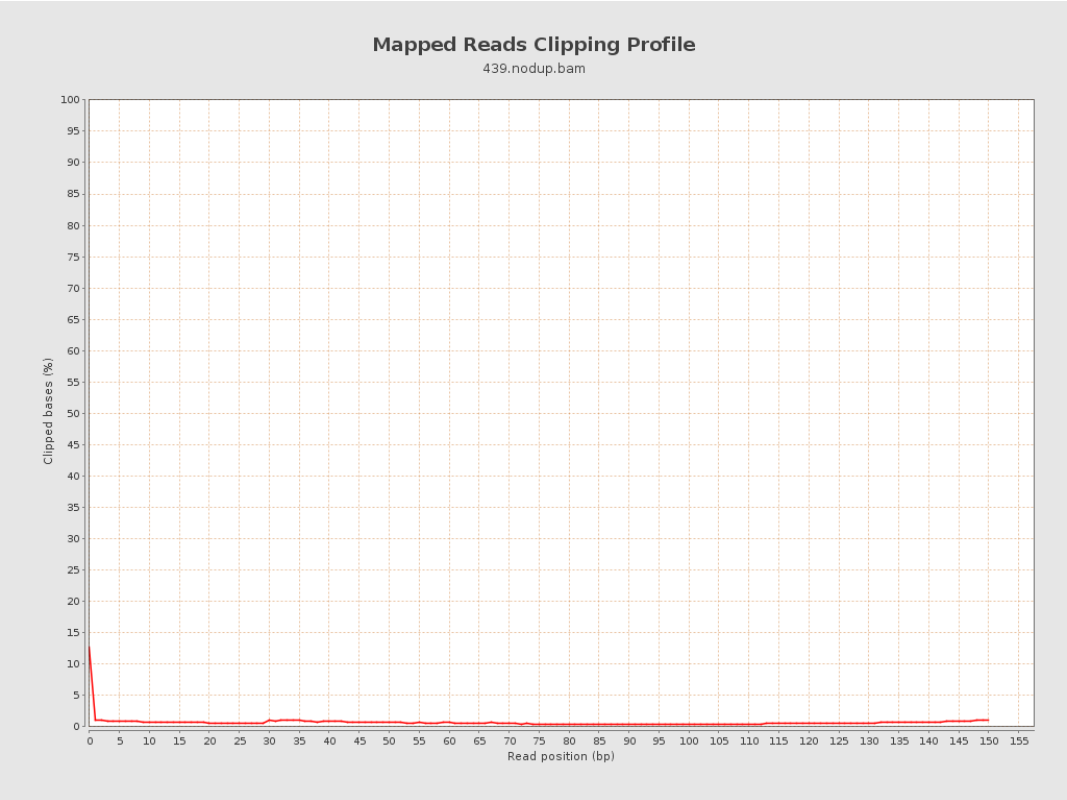
8. Results : Mapped Reads Nucleotide Content



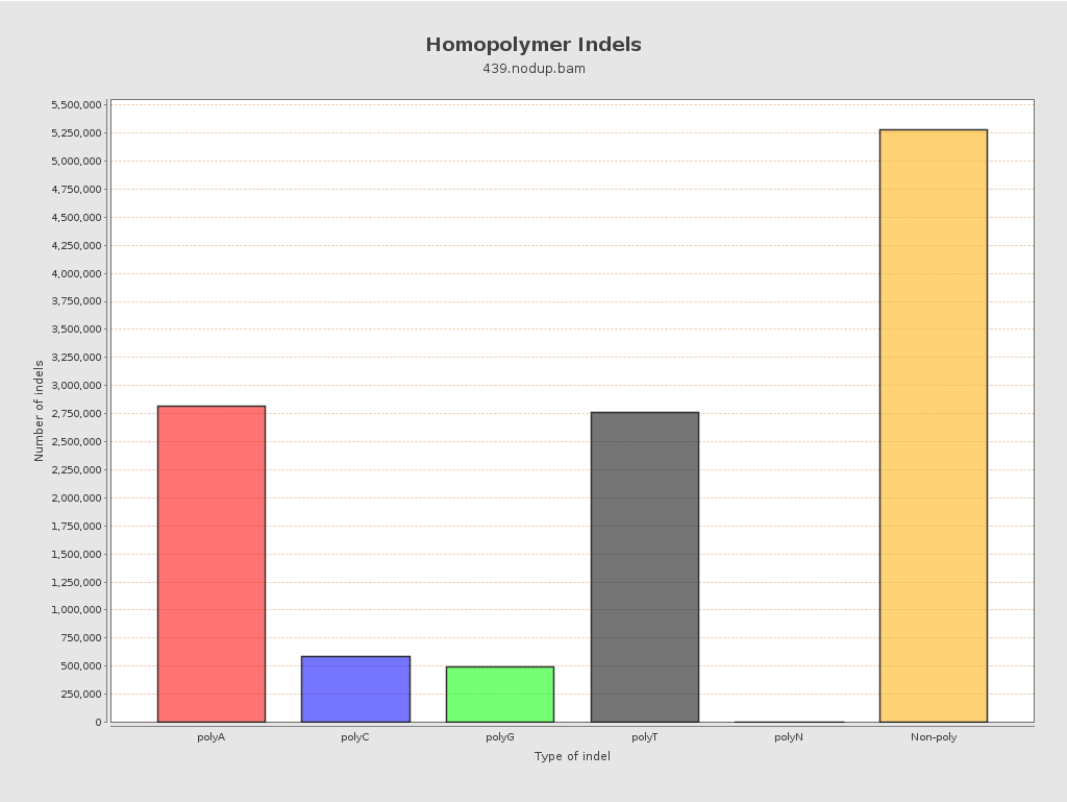
9. Results : Mapped Reads GC-content Distribution



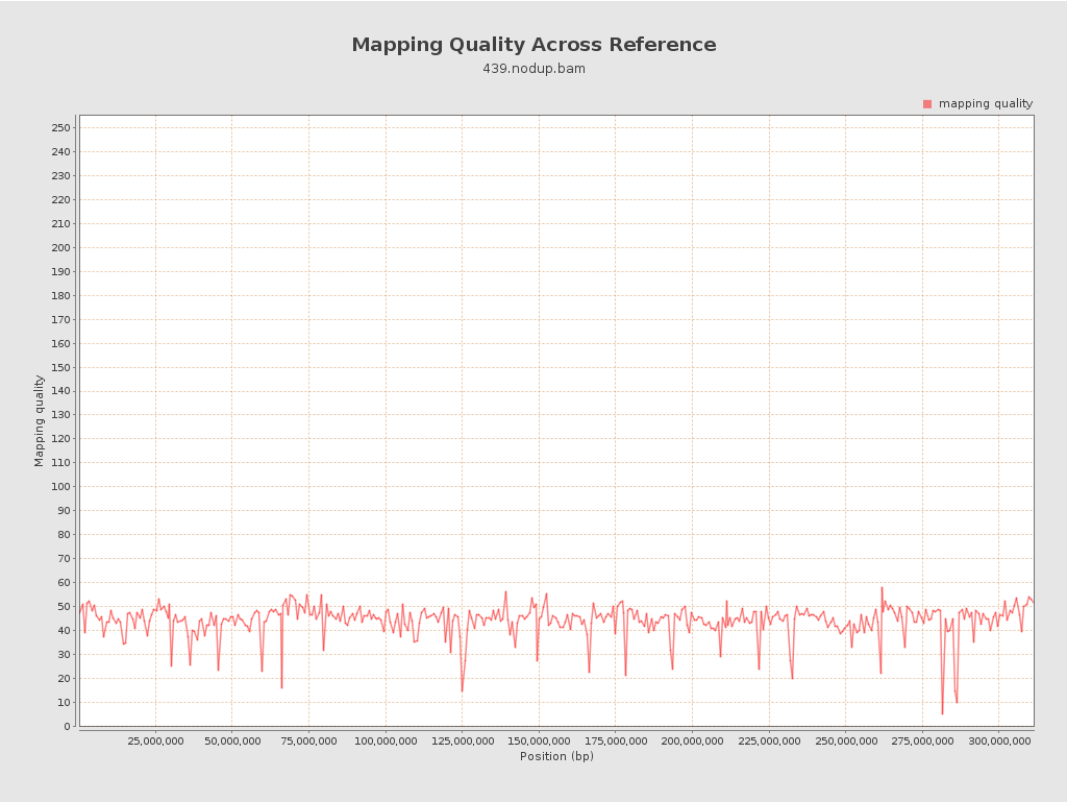
10. Results : Mapped Reads Clipping Profile



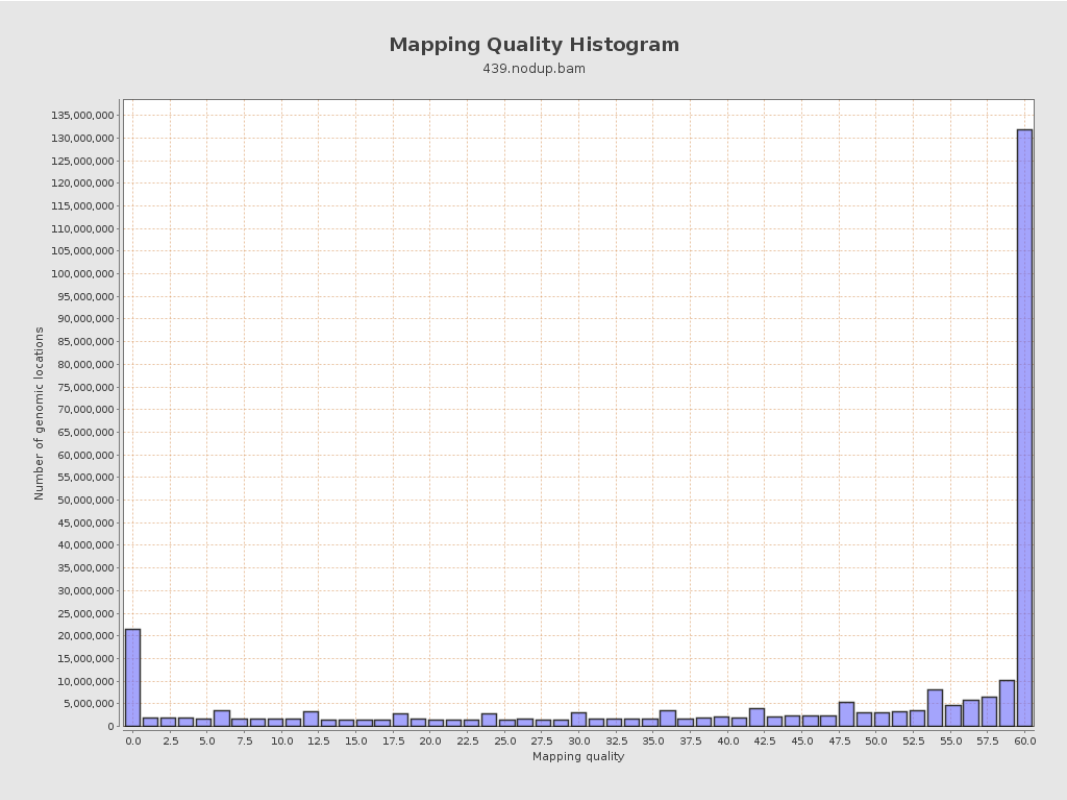
11. Results : Homopolymer Indels



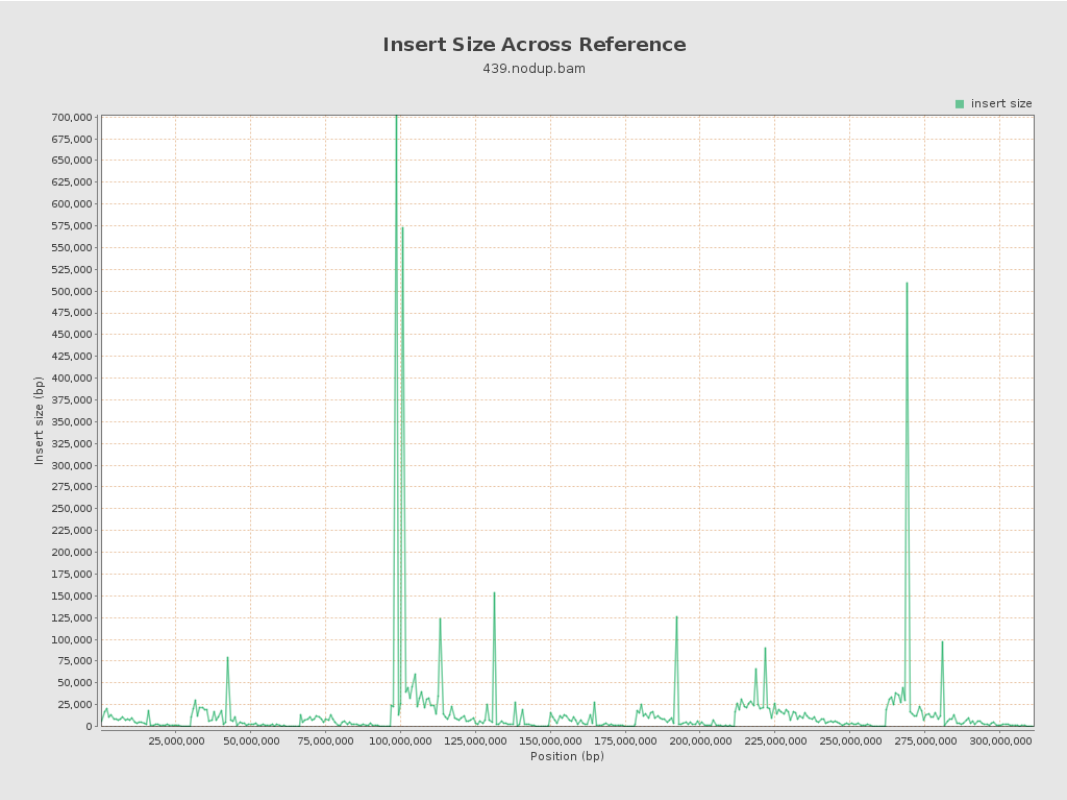
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram