Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/539.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/539.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_131/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_131_S221_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_131/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_131_S221_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:47 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,091,798
Mapped reads	73,285,413 / 91.5%
Unmapped reads	6,806,385 / 8.5%
Mapped paired reads	73,285,413 / 91.5%
Mapped reads, first in pair	36,661,637 / 45.77%
Mapped reads, second in pair	36,623,776 / 45.73%
Mapped reads, both in pair	71,172,025 / 88.86%
Mapped reads, singletons	2,113,388 / 2.64%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	14,116,491 / 17.63%
Clipped reads	17,302,630 / 21.6%

2.2. ACGT Content

Number/percentage of A's	3,113,227,227 / 30.88%
Number/percentage of C's	1,927,436,493 / 19.12%
Number/percentage of T's	3,115,332,537 / 30.91%
Number/percentage of G's	1,924,116,781 / 19.09%
Number/percentage of N's	39,575 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	32.429
Standard Deviation	292.2066

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Insert size

Mean	241,445.98
Standard Deviation	2,354,242.82
P25/Median/P75	306 / 400 / 521

2.6. Mismatches and indels

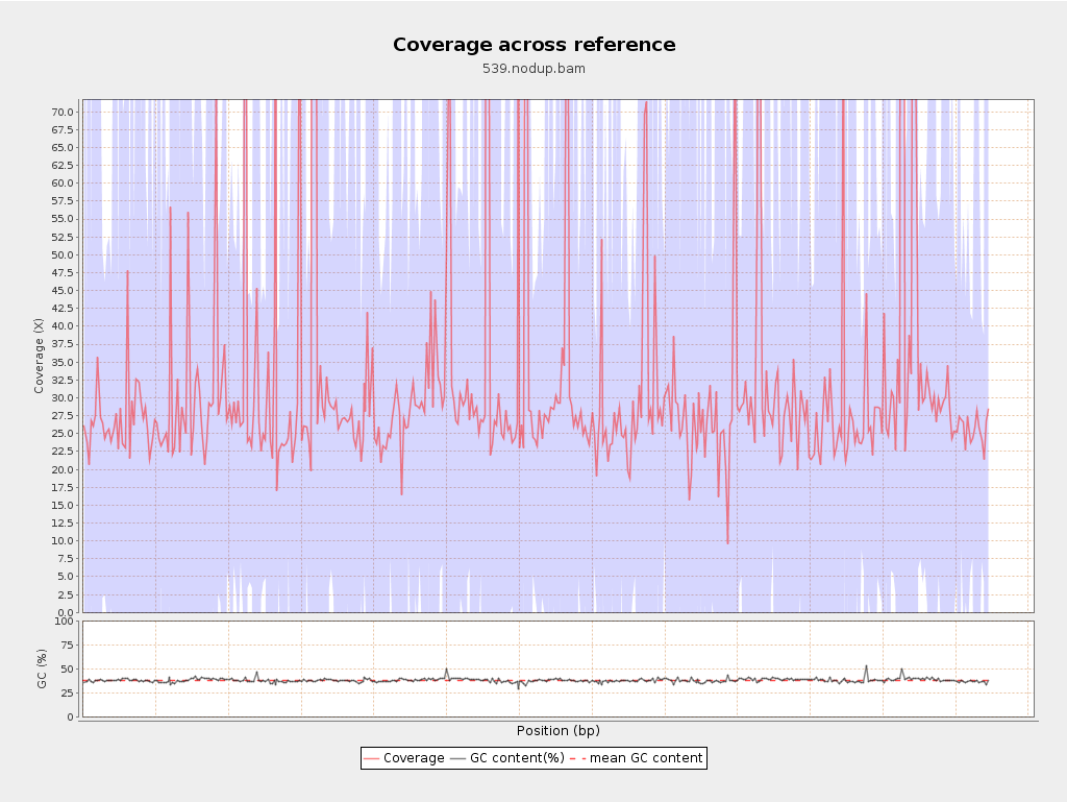
General error rate	2.45%
Mismatches	227,012,567
Insertions	7,284,768
Mapped reads with at least one insertion	8.88%
Deletions	7,050,079
Mapped reads with at least one deletion	8.52%
Homopolymer indels	56.87%

2.7. Chromosome stats

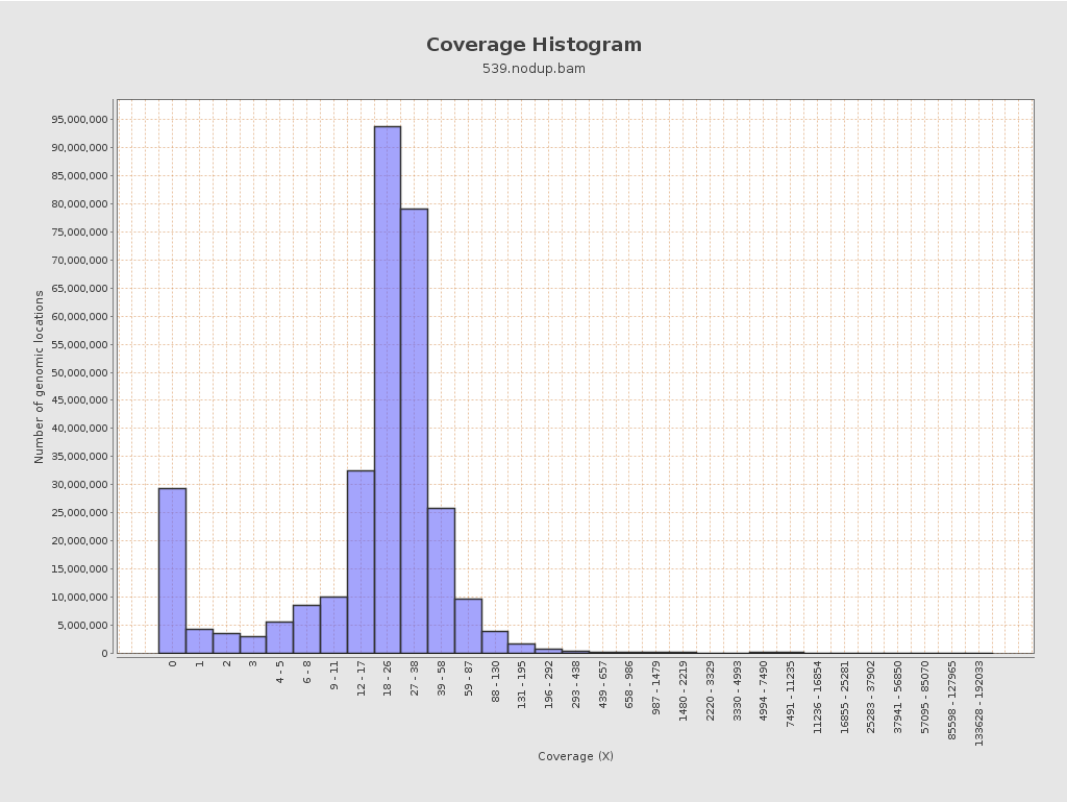
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	790177395	26.5835	112.9051

LT669789.1	36598175	1190222161	32.5214	308.5964
LT669790.1	30422129	1179721970	38.7784	415.1501
LT669791.1	52758100	1684950264	31.9373	310.5421
LT669792.1	28376109	925915127	32.6301	313.4272
LT669793.1	33388210	974386313	29.1835	188.785
LT669794.1	50579949	1533633748	30.321	258.2061
LT669795.1	49795044	1827237842	36.6952	318.7976

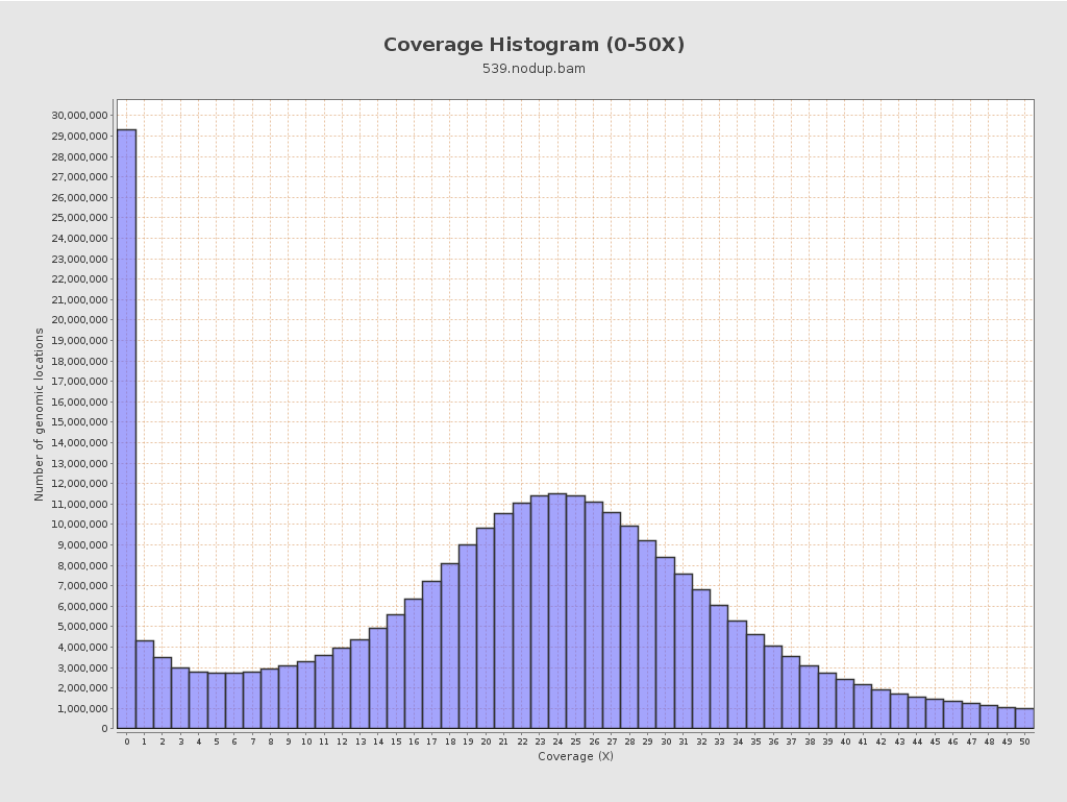
3. Results : Coverage across reference



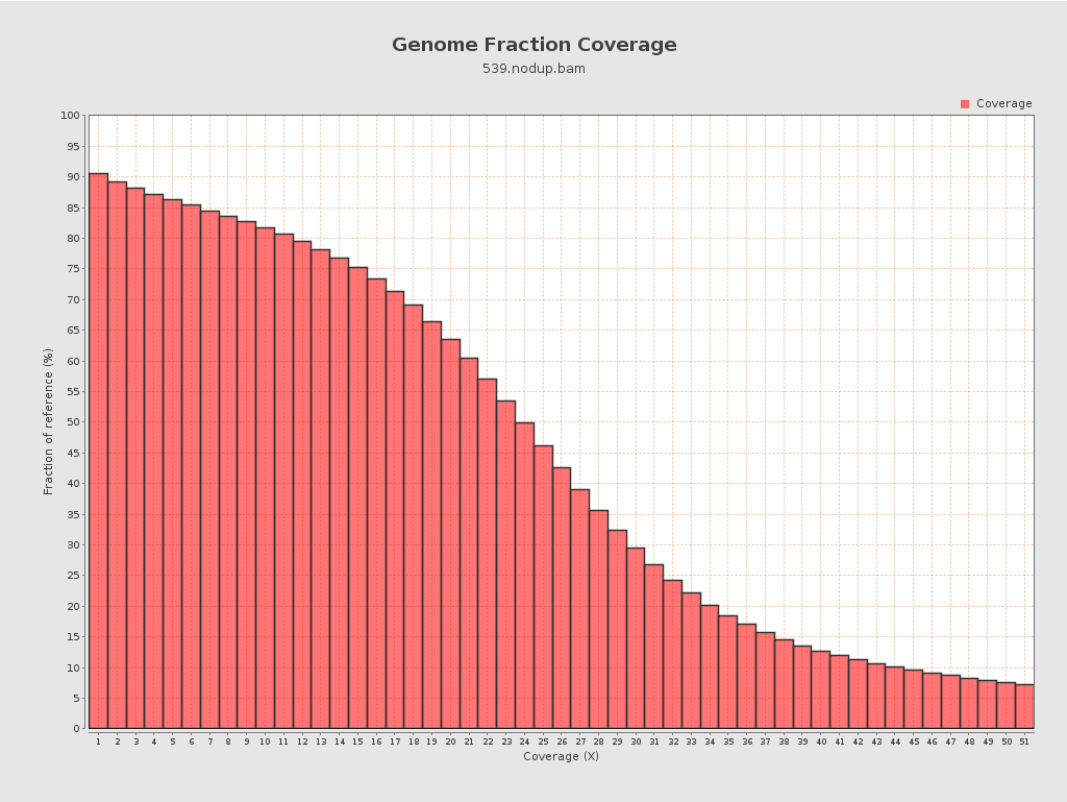
4. Results : Coverage Histogram



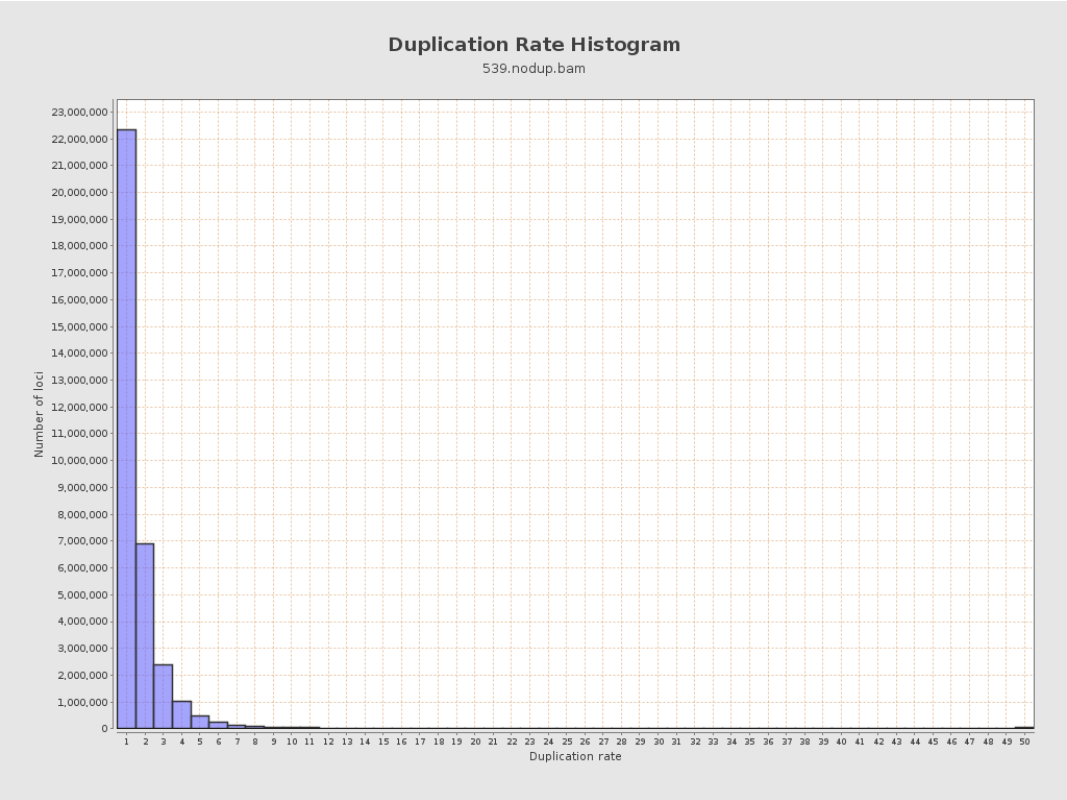
5. Results : Coverage Histogram (0-50X)



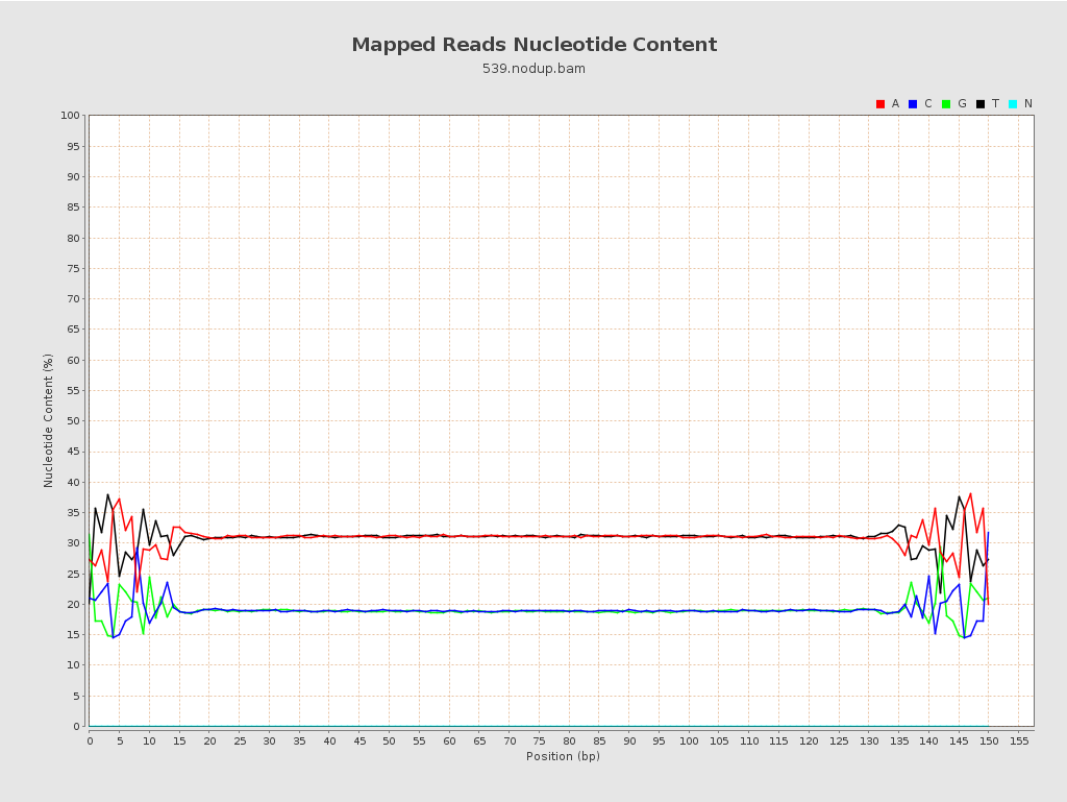
6. Results : Genome Fraction Coverage



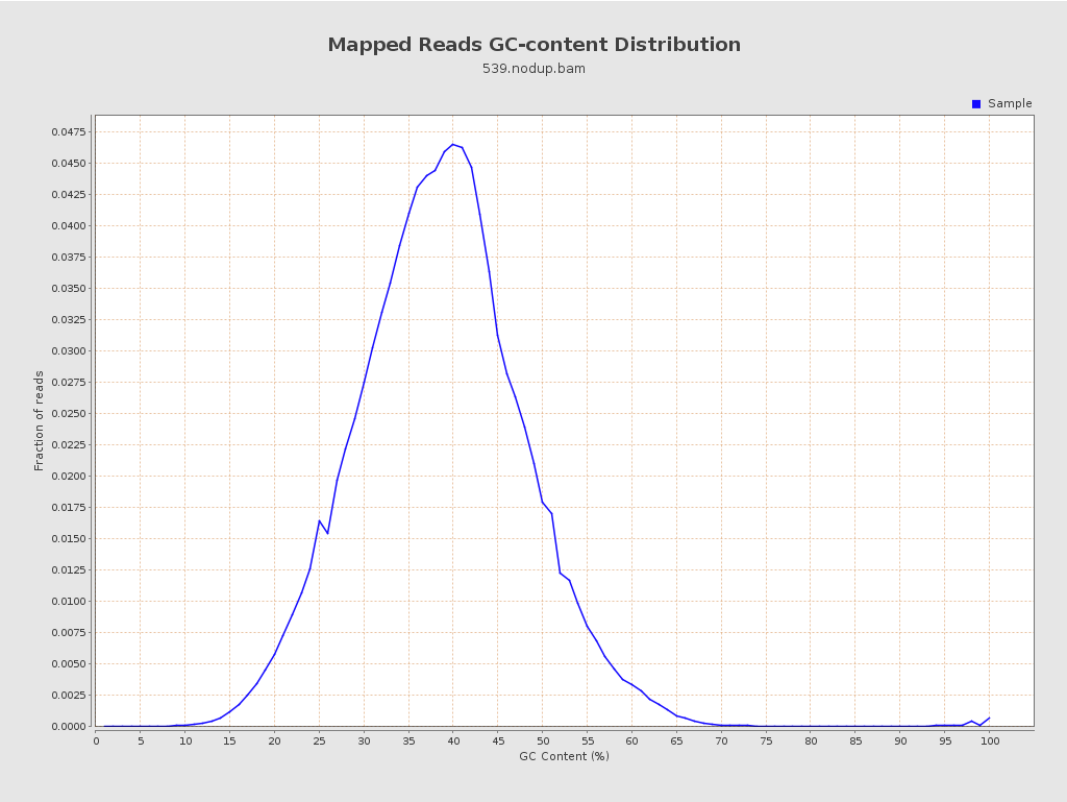
7. Results : Duplication Rate Histogram



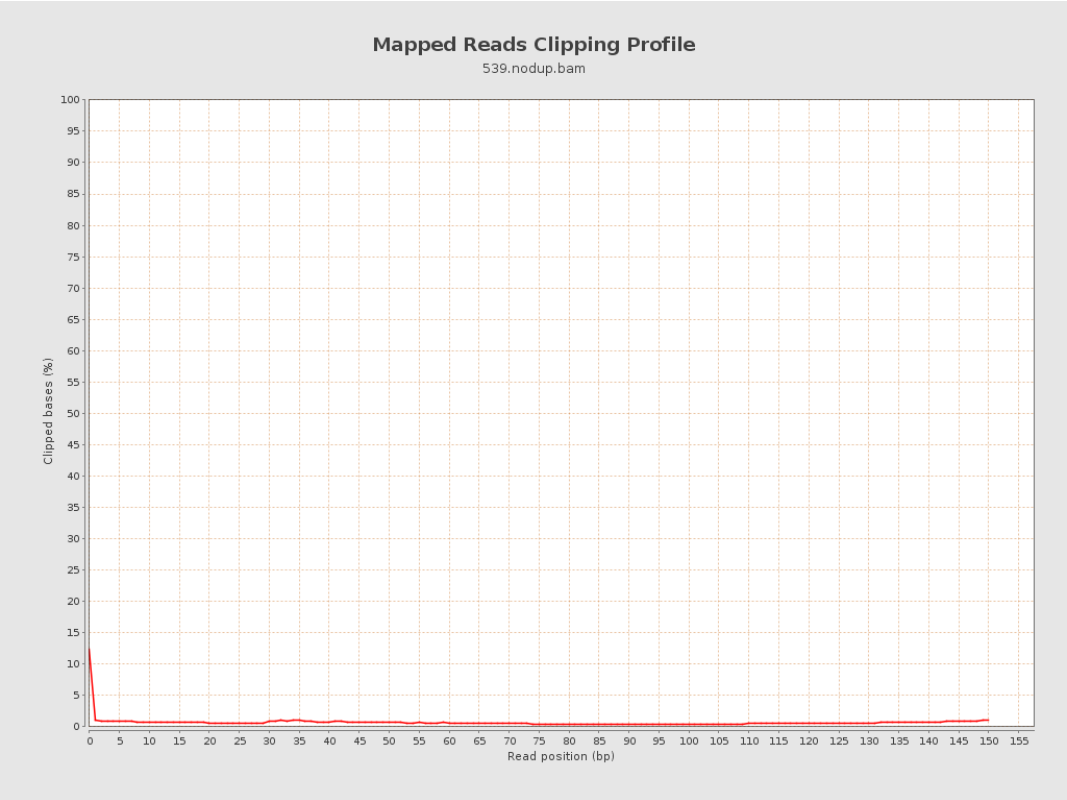
8. Results : Mapped Reads Nucleotide Content



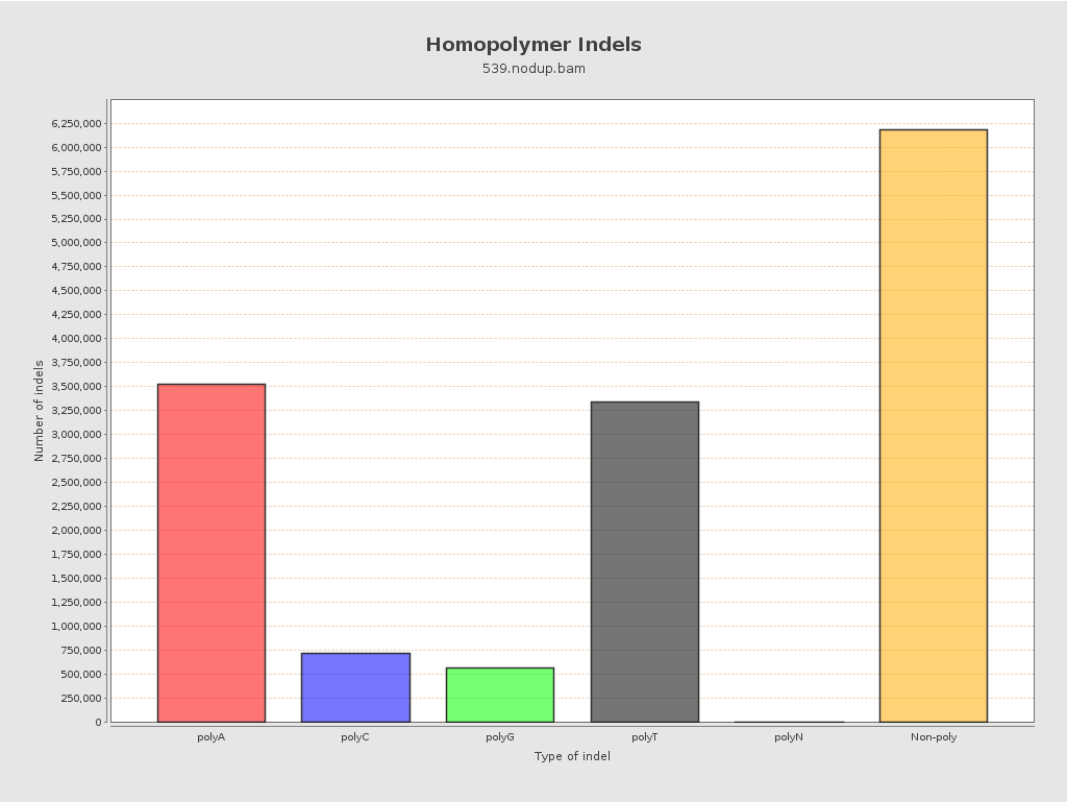
9. Results : Mapped Reads GC-content Distribution



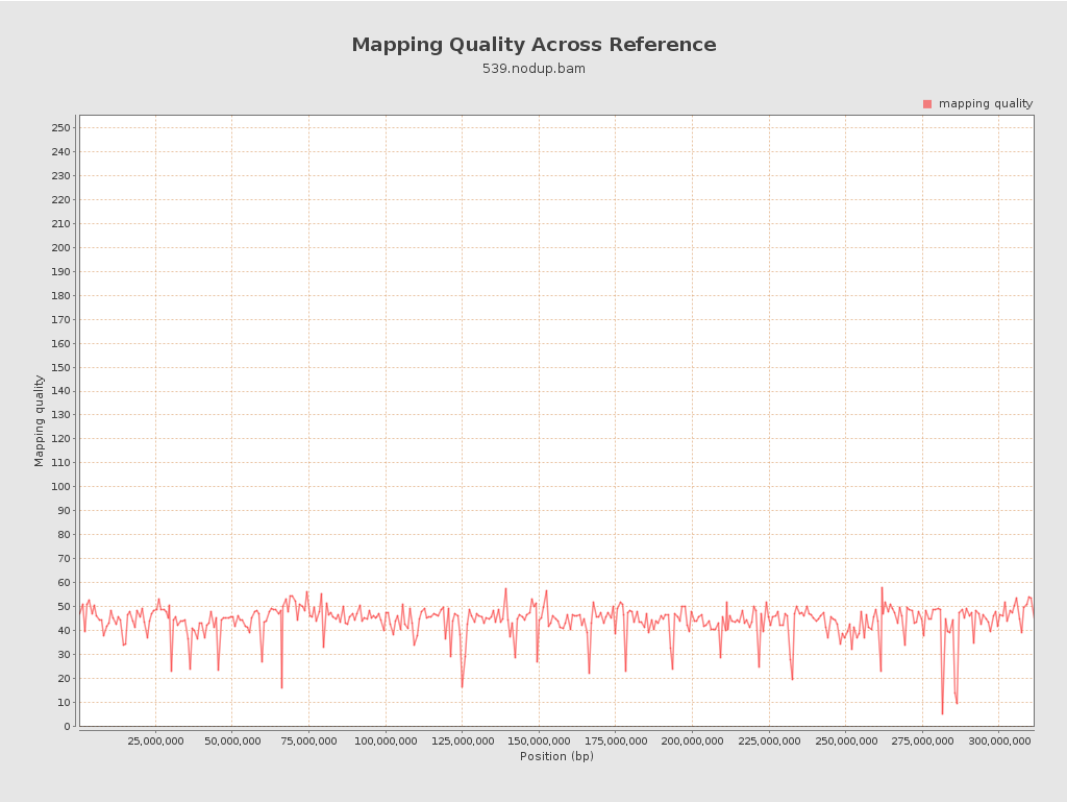
10. Results : Mapped Reads Clipping Profile



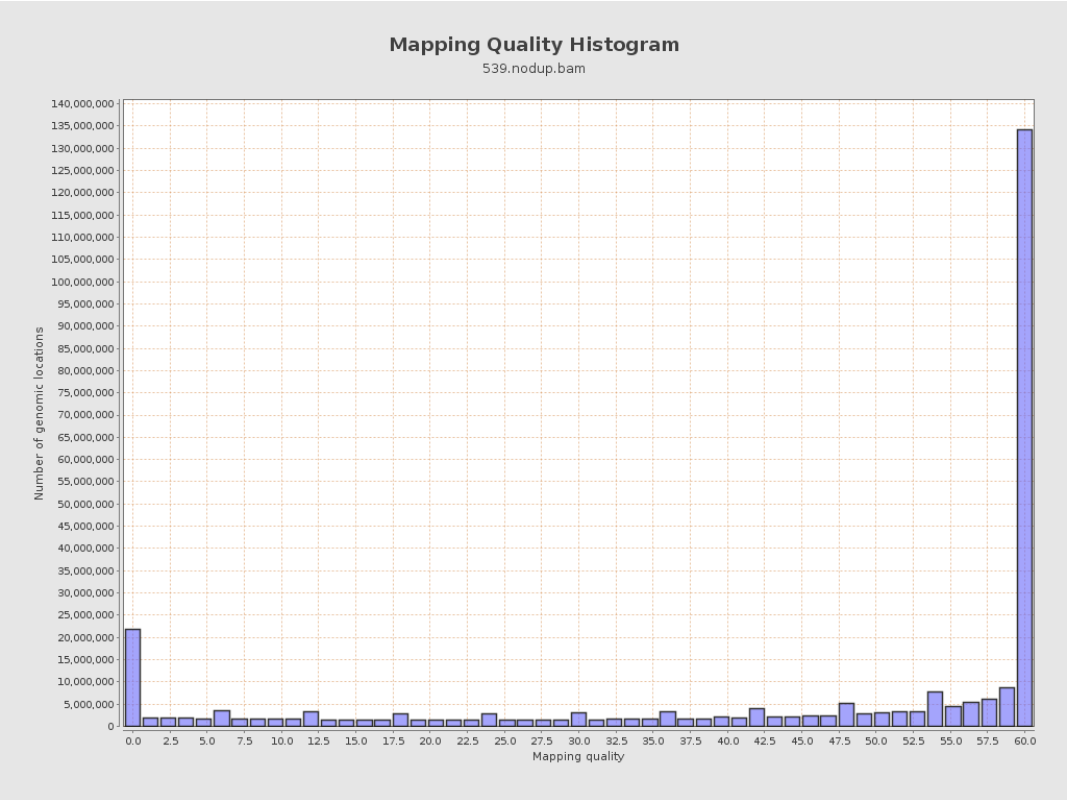
11. Results : Homopolymer Indels



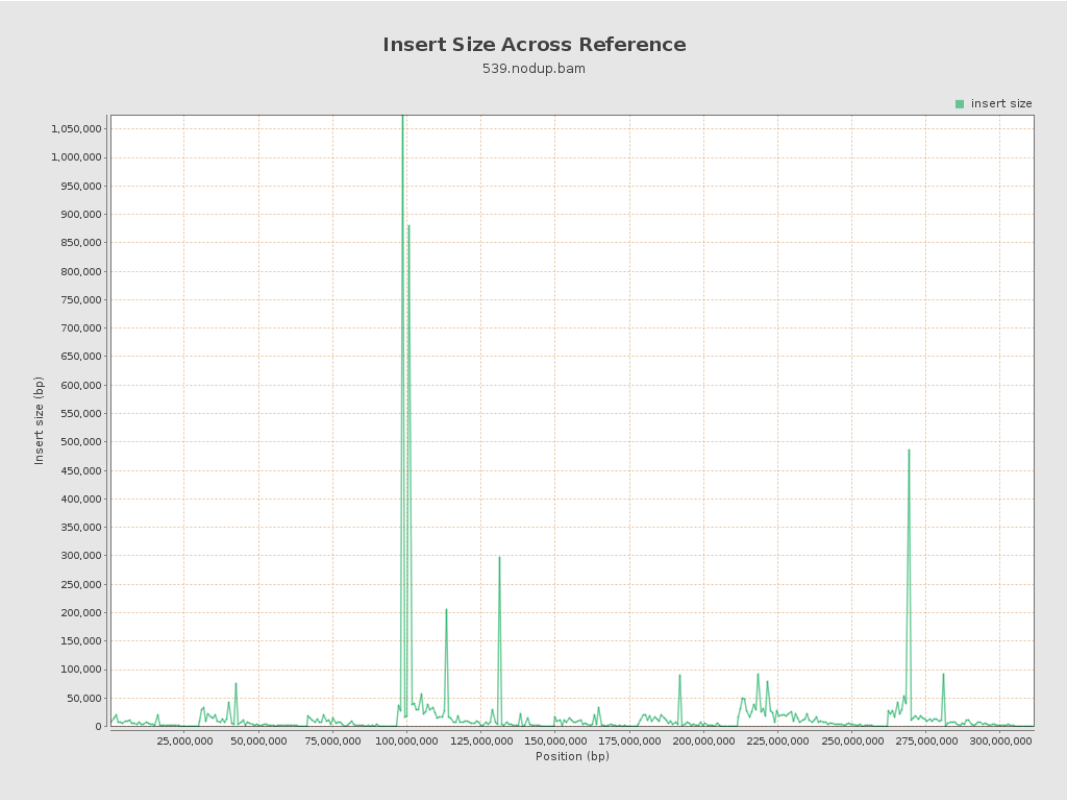
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram