

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/101
0
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1010 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_541/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_541_S108_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_541/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_541_S108_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:50 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	77,721,855
Mapped reads	71,855,396 / 92.45%
Unmapped reads	5,866,459 / 7.55%
Mapped paired reads	71,855,396 / 92.45%
Mapped reads, first in pair	36,044,022 / 46.38%
Mapped reads, second in pair	35,811,374 / 46.08%
Mapped reads, both in pair	70,065,248 / 90.15%
Mapped reads, singletons	1,790,148 / 2.3%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	13,084,304 / 16.83%
Clipped reads	17,215,865 / 22.15%

2.2. ACGT Content

Number/percentage of A's	3,053,205,527 / 30.85%
Number/percentage of C's	1,893,354,474 / 19.13%
Number/percentage of T's	3,058,653,386 / 30.91%
Number/percentage of G's	1,890,146,579 / 19.1%
Number/percentage of N's	70,628 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	31.8343
Standard Deviation	263.5828

2.4. Mapping Quality

Mean Mapping Quality	44.09
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2.5. Insert size

Mean	231,829.76
Standard Deviation	2,305,360.52
P25/Median/P75	315 / 413 / 533

2.6. Mismatches and indels

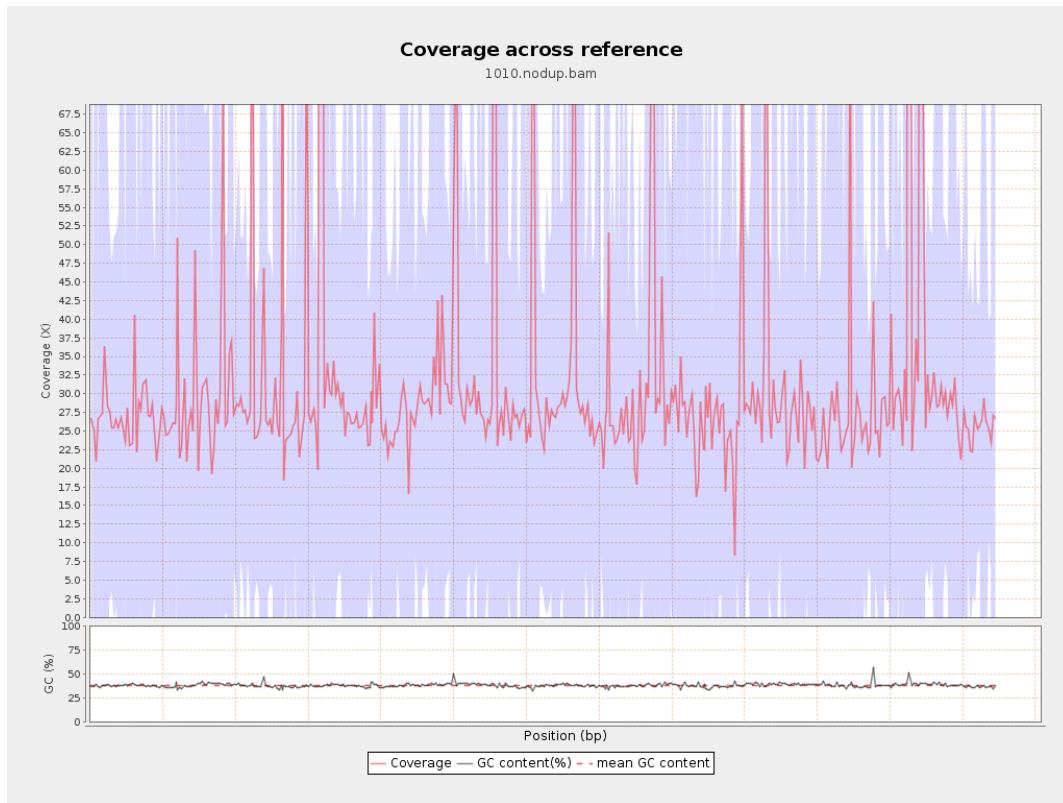
General error rate	2.54%
Mismatches	233,212,694
Insertions	6,731,134
Mapped reads with at least one insertion	8.39%
Deletions	6,734,228
Mapped reads with at least one deletion	8.31%
Homopolymer indels	56.35%

2.7. Chromosome stats

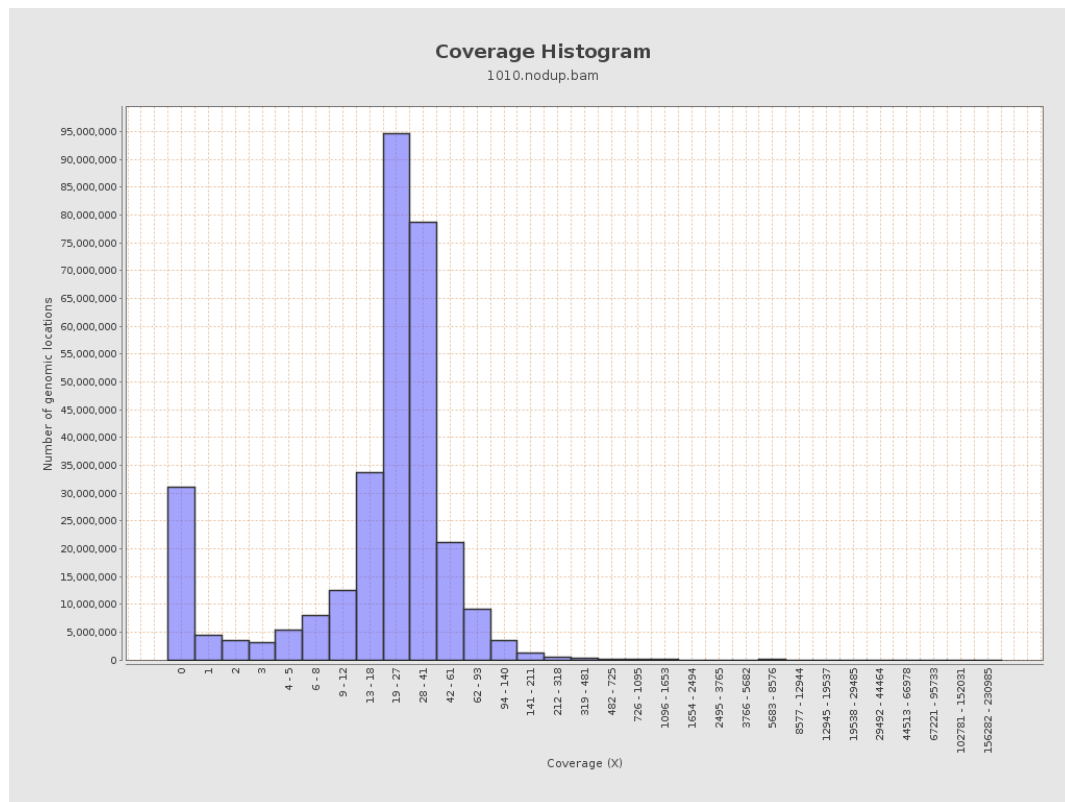
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	795721323	26.77	92.4808

LT669789.1	36598175	1153466119	31.517	269.5084
LT669790.1	30422129	1118722452	36.7733	318.513
LT669791.1	52758100	1649528517	31.2659	253.7347
LT669792.1	28376109	895878556	31.5716	255.2416
LT669793.1	33388210	1002031113	30.0115	242.3617
LT669794.1	50579949	1476512689	29.1917	208.2941
LT669795.1	49795044	1829043469	36.7314	354.2405

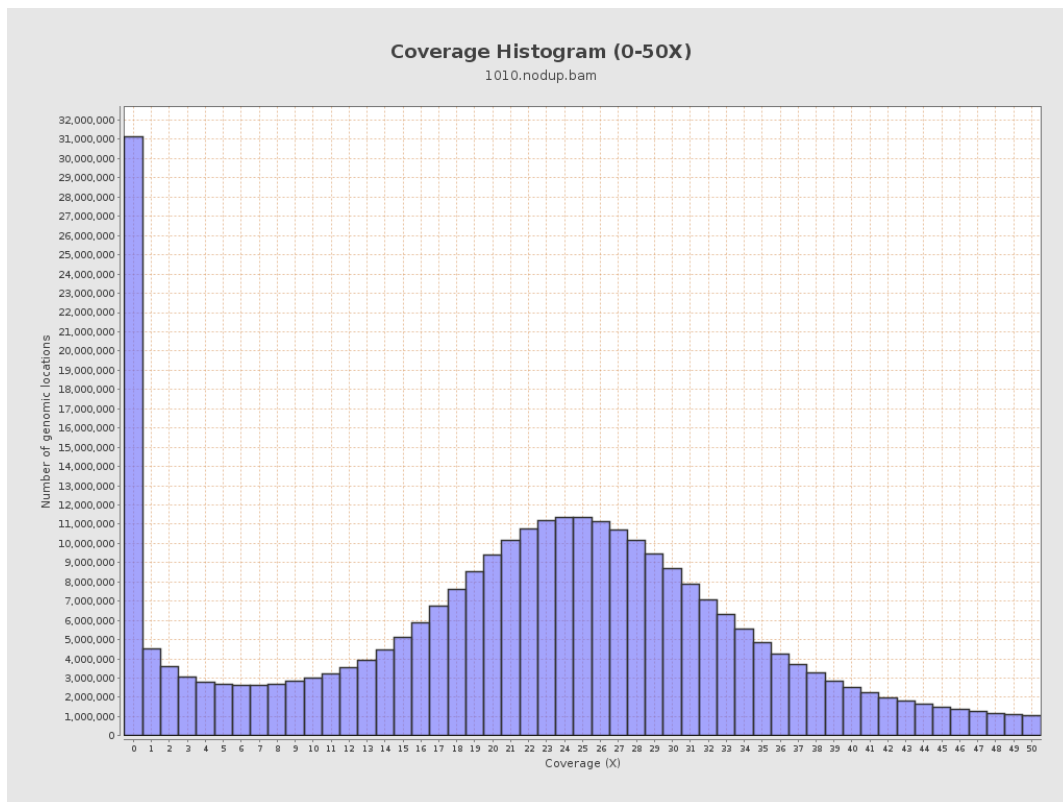
3. Results : Coverage across reference



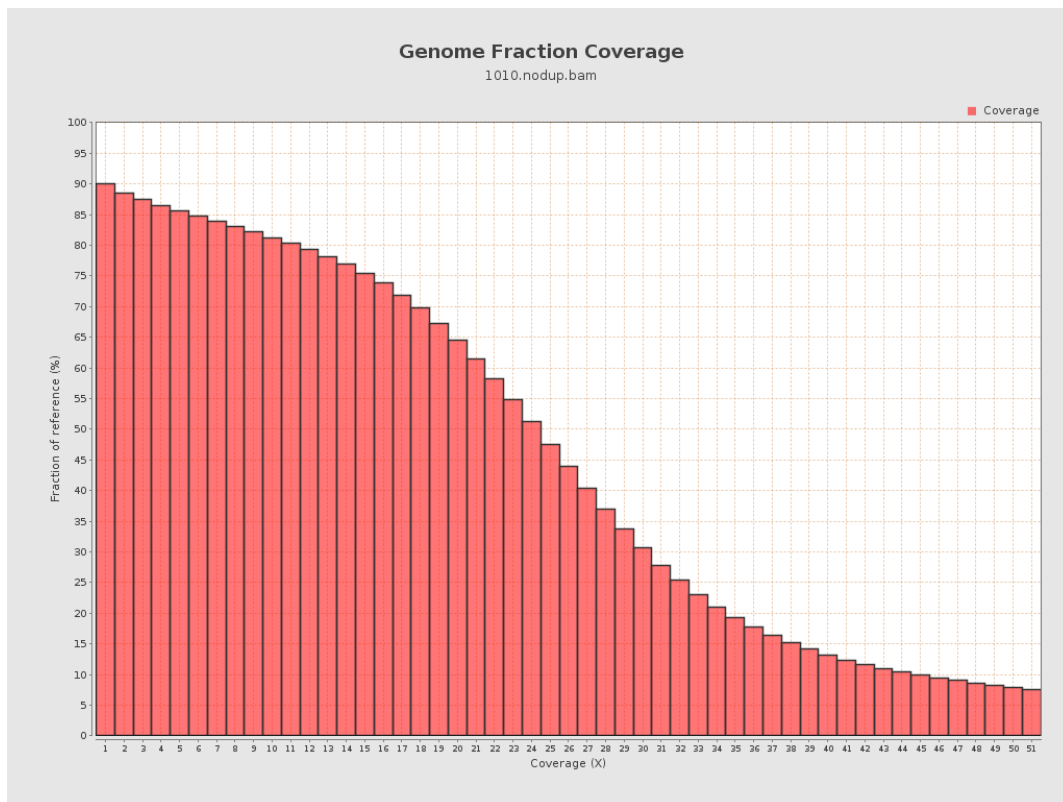
4. Results : Coverage Histogram



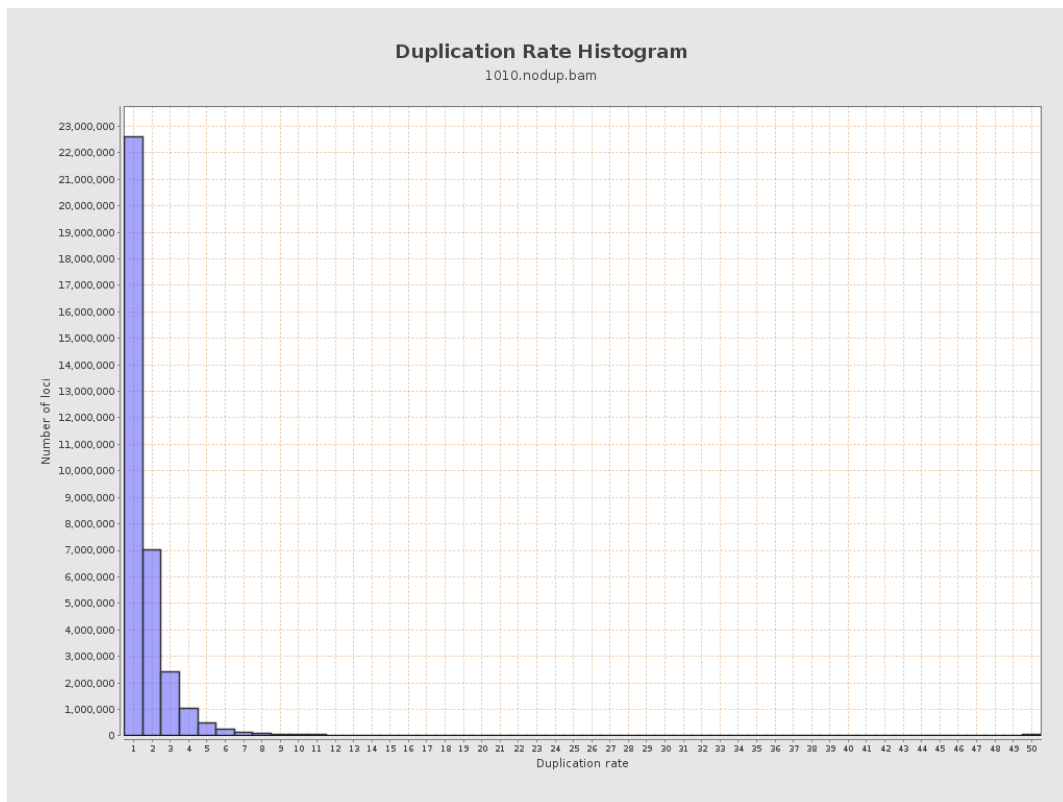
5. Results : Coverage Histogram (0-50X)



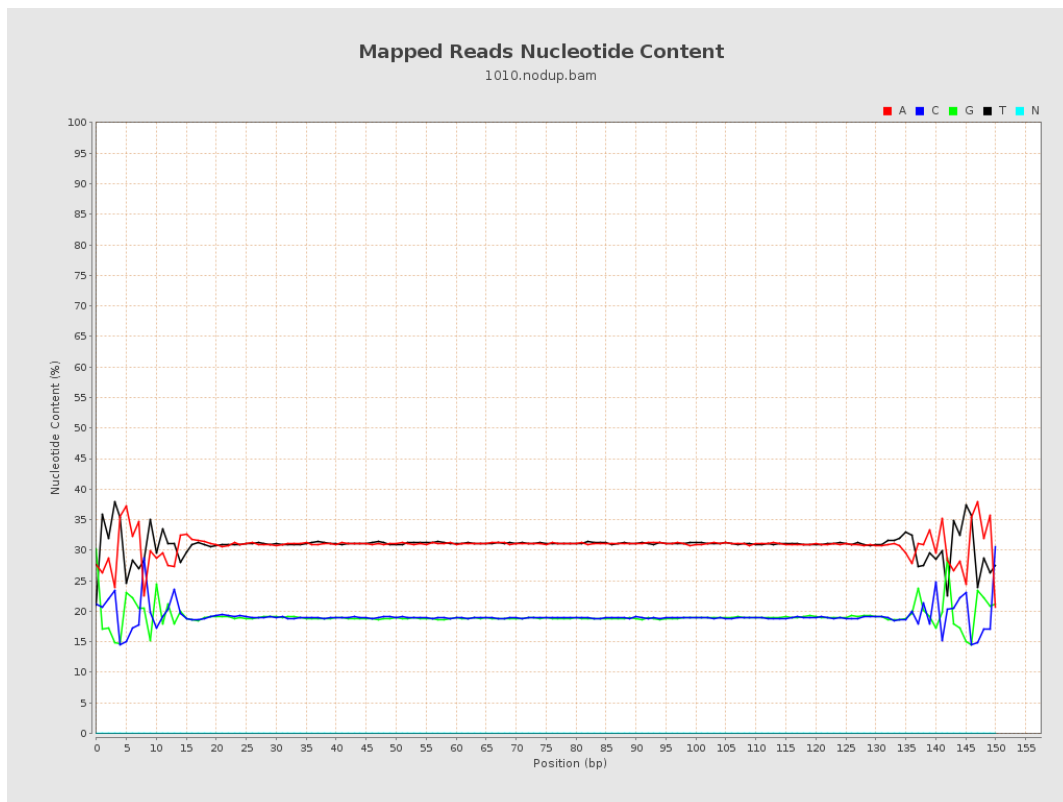
6. Results : Genome Fraction Coverage



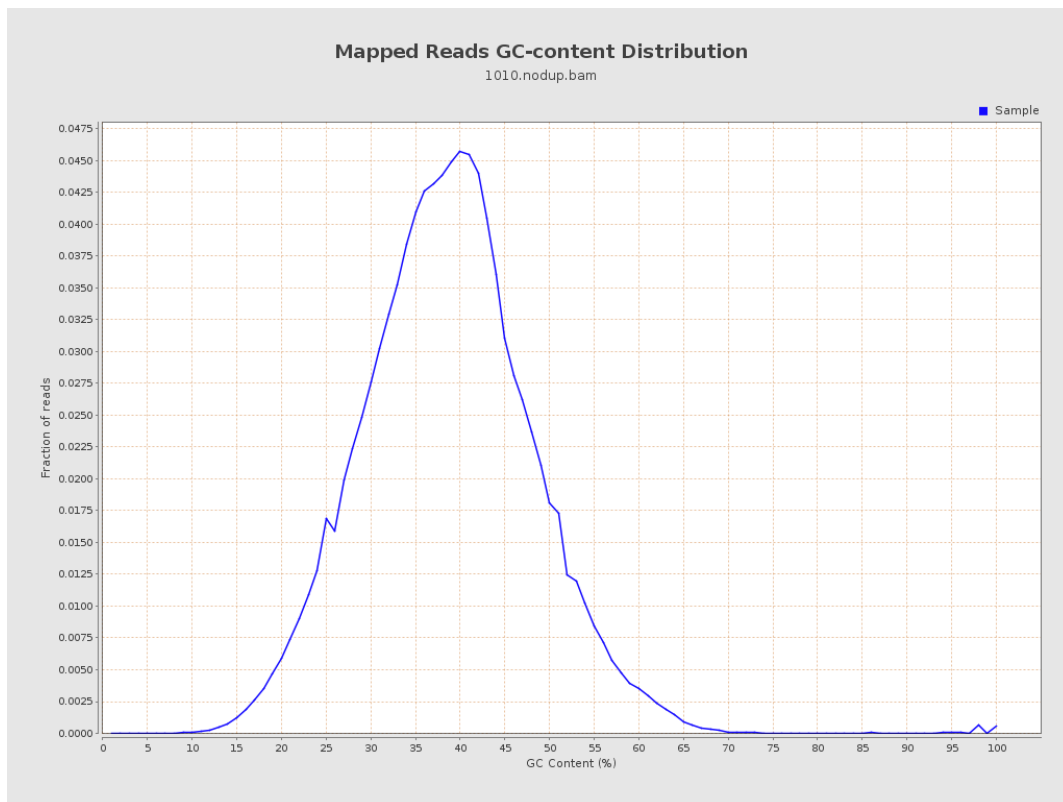
7. Results : Duplication Rate Histogram



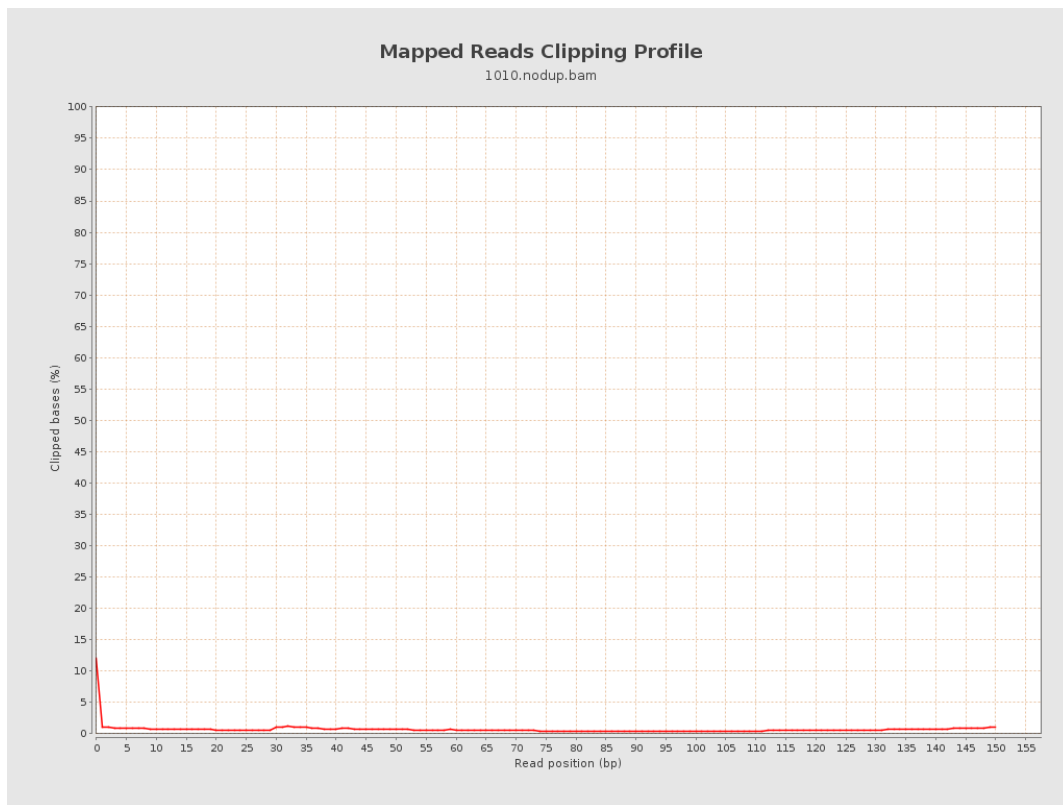
8. Results : Mapped Reads Nucleotide Content



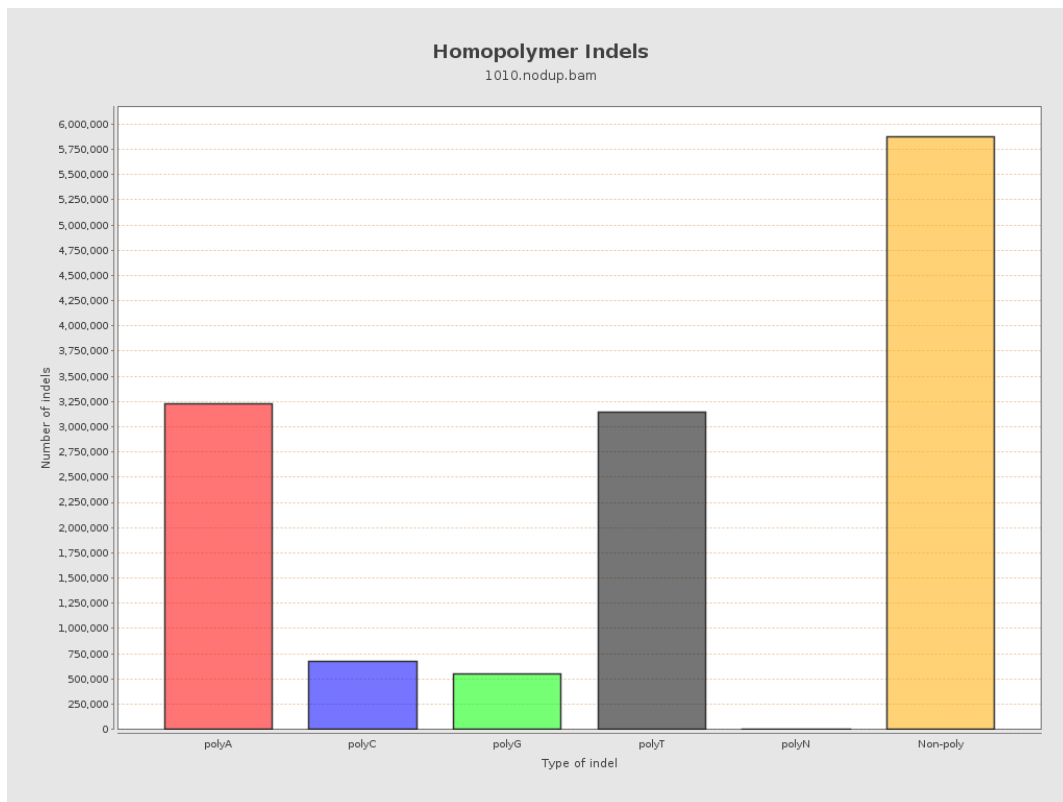
9. Results : Mapped Reads GC-content Distribution



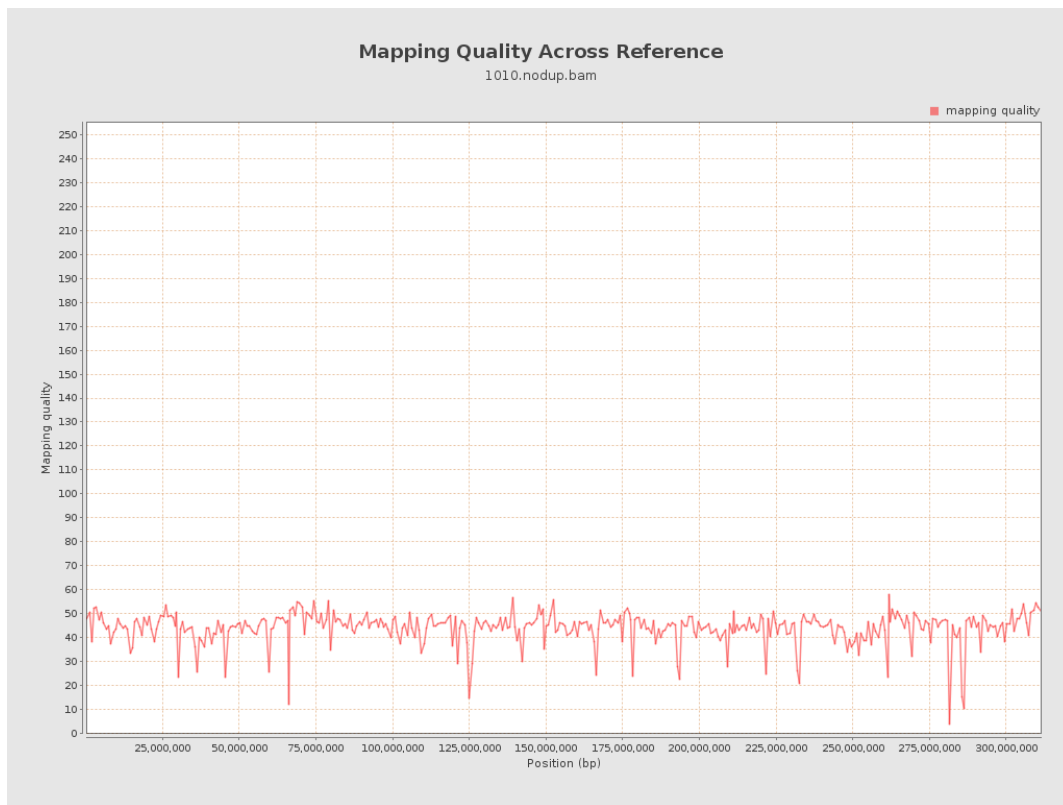
10. Results : Mapped Reads Clipping Profile



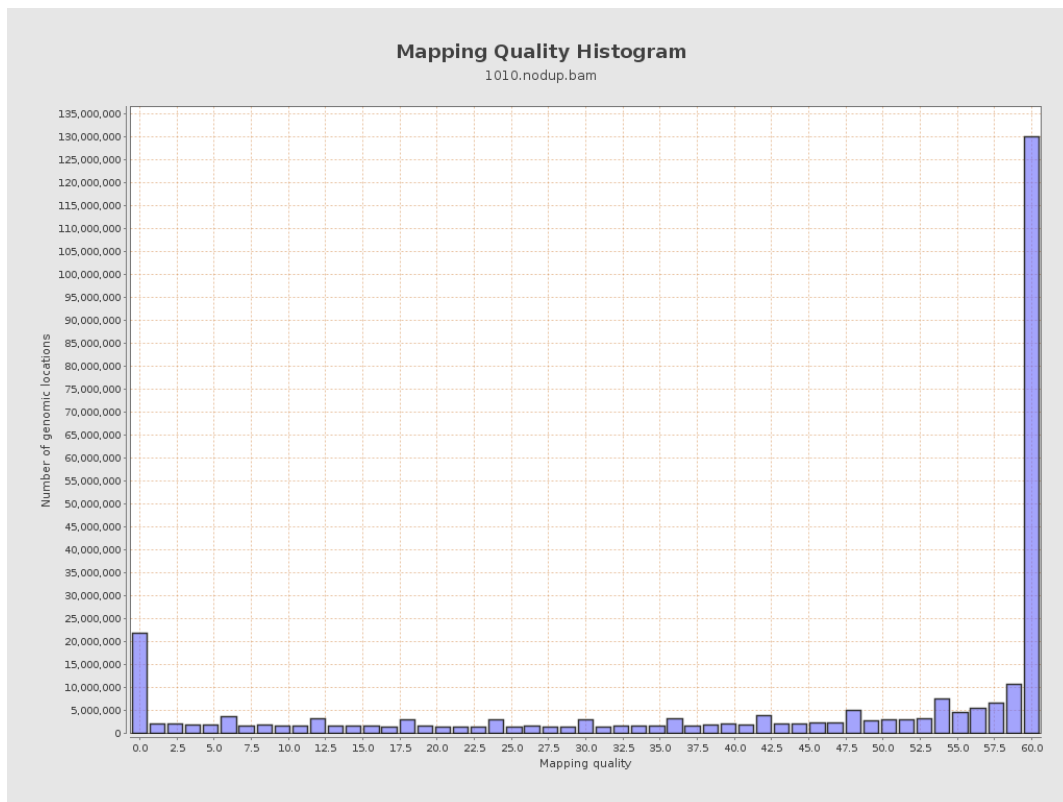
11. Results : Homopolymer Indels



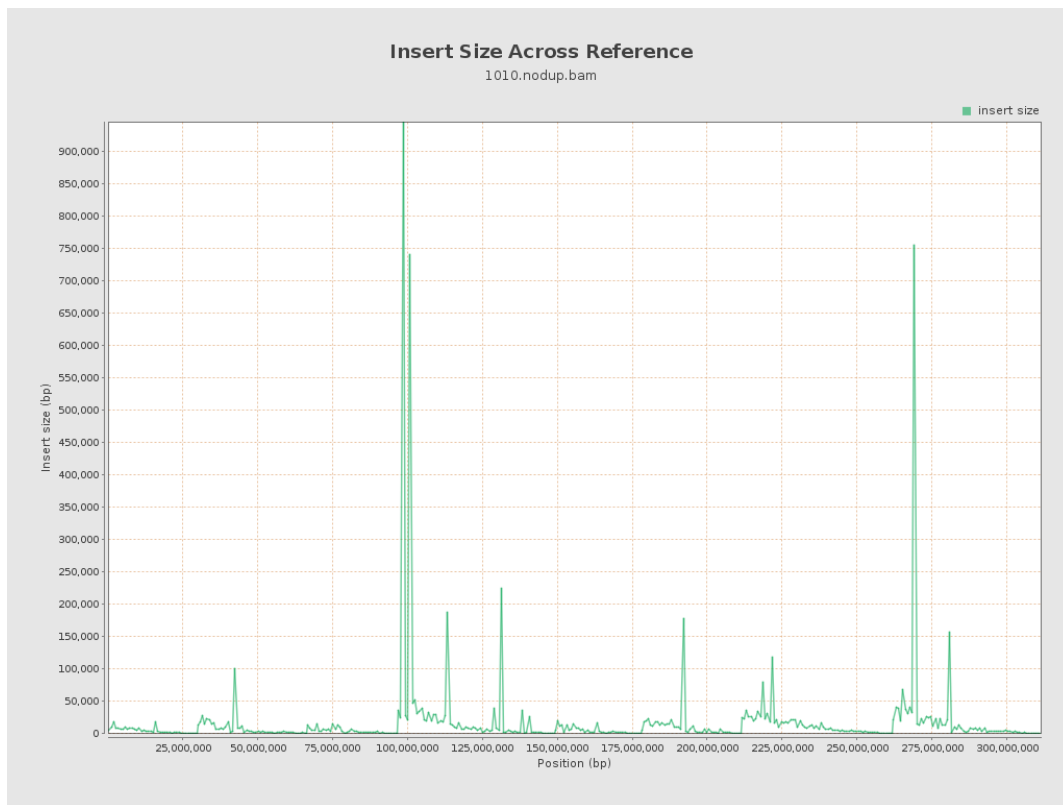
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

