

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/141
0
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1410 .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_450/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_450_S425_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_450/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_450_S425_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:31:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	73,186,094
Mapped reads	59,941,852 / 81.9%
Unmapped reads	13,244,242 / 18.1%
Mapped paired reads	59,941,852 / 81.9%
Mapped reads, first in pair	29,982,324 / 40.97%
Mapped reads, second in pair	29,959,528 / 40.94%
Mapped reads, both in pair	58,704,660 / 80.21%
Mapped reads, singletons	1,237,192 / 1.69%
Read min/max/mean length	30 / 151 / 148.57
Duplicated reads (flagged)	9,032,699 / 12.34%
Clipped reads	13,738,749 / 18.77%

2.2. ACGT Content

Number/percentage of A's	2,542,462,774 / 30.82%
Number/percentage of C's	1,581,776,228 / 19.17%
Number/percentage of T's	2,547,247,081 / 30.88%
Number/percentage of G's	1,577,957,165 / 19.13%
Number/percentage of N's	27,556 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	26.5416
Standard Deviation	218.2832

2.4. Mapping Quality

Mean Mapping Quality	43.55
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2.5. Insert size

Mean	237,367.26
Standard Deviation	2,298,499.87
P25/Median/P75	347 / 455 / 597

2.6. Mismatches and indels

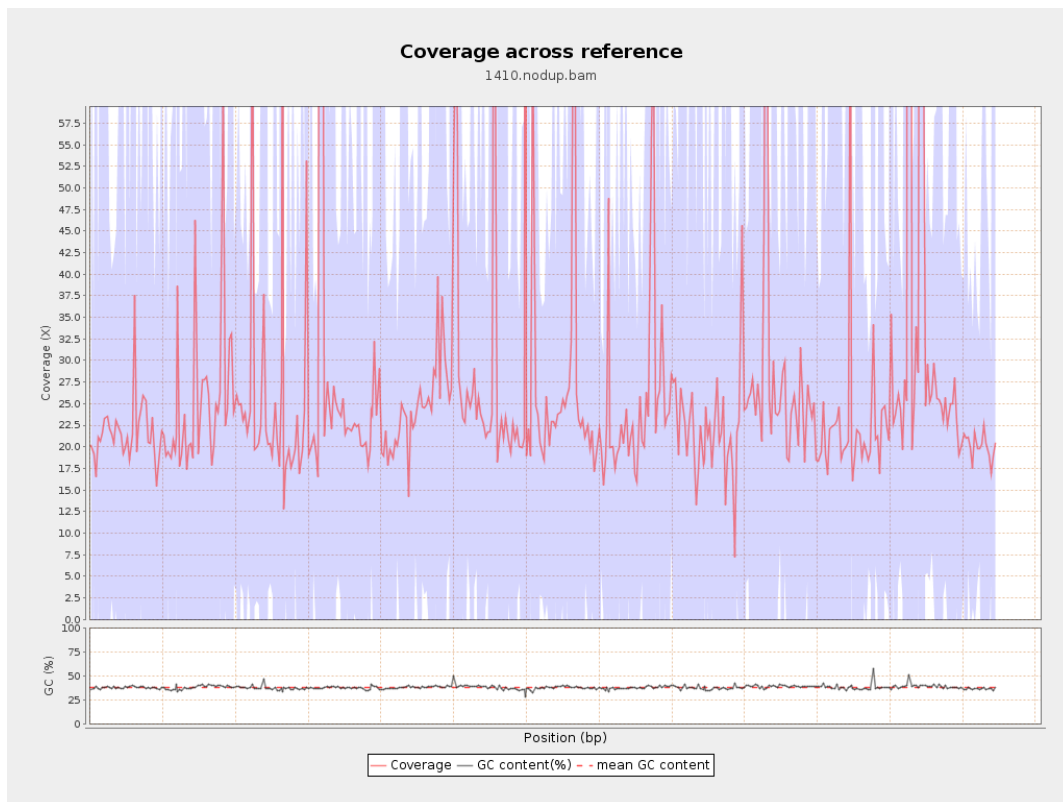
General error rate	2.38%
Mismatches	181,552,606
Insertions	5,490,902
Mapped reads with at least one insertion	8.23%
Deletions	5,789,496
Mapped reads with at least one deletion	8.57%
Homopolymer indels	56.17%

2.7. Chromosome stats

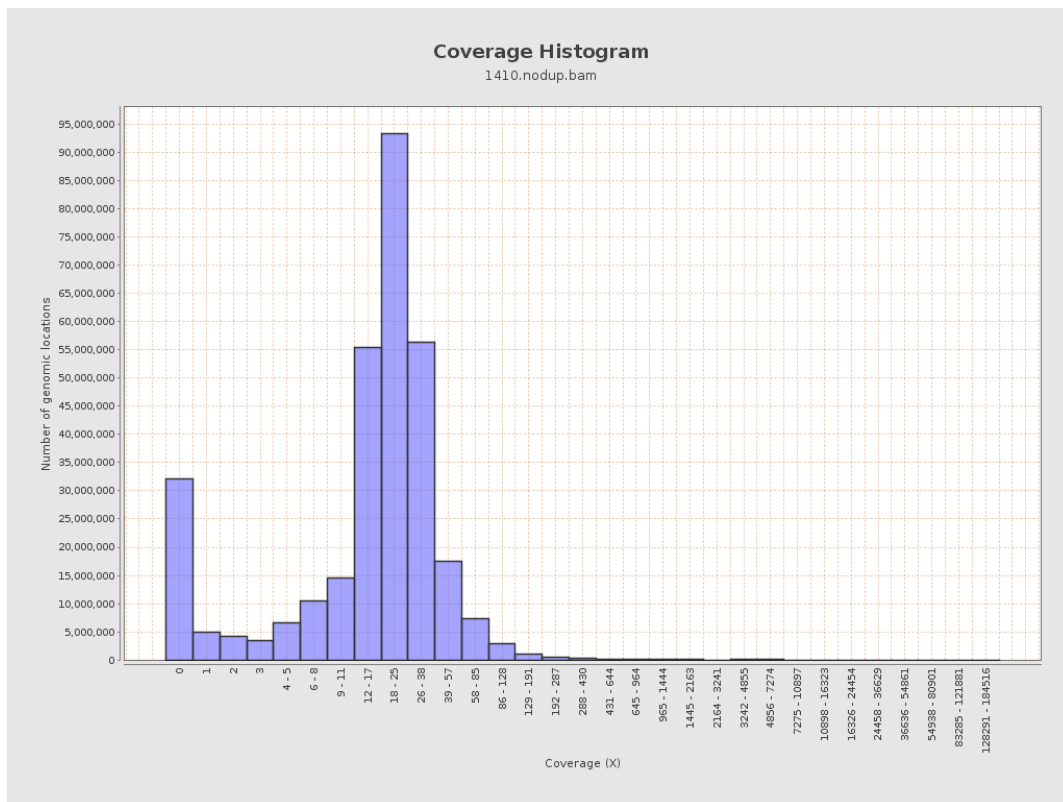
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	635041702	21.3644	60.1587

LT669789.1	36598175	958841839	26.1992	194.8267
LT669790.1	30422129	842299726	27.6871	205.7683
LT669791.1	52758100	1374318141	26.0494	167.1901
LT669792.1	28376109	733774928	25.8589	211.1311
LT669793.1	33388210	819667826	24.5496	200.2406
LT669794.1	50579949	1282957253	25.3649	188.3628
LT669795.1	49795044	1624563606	32.625	352.526

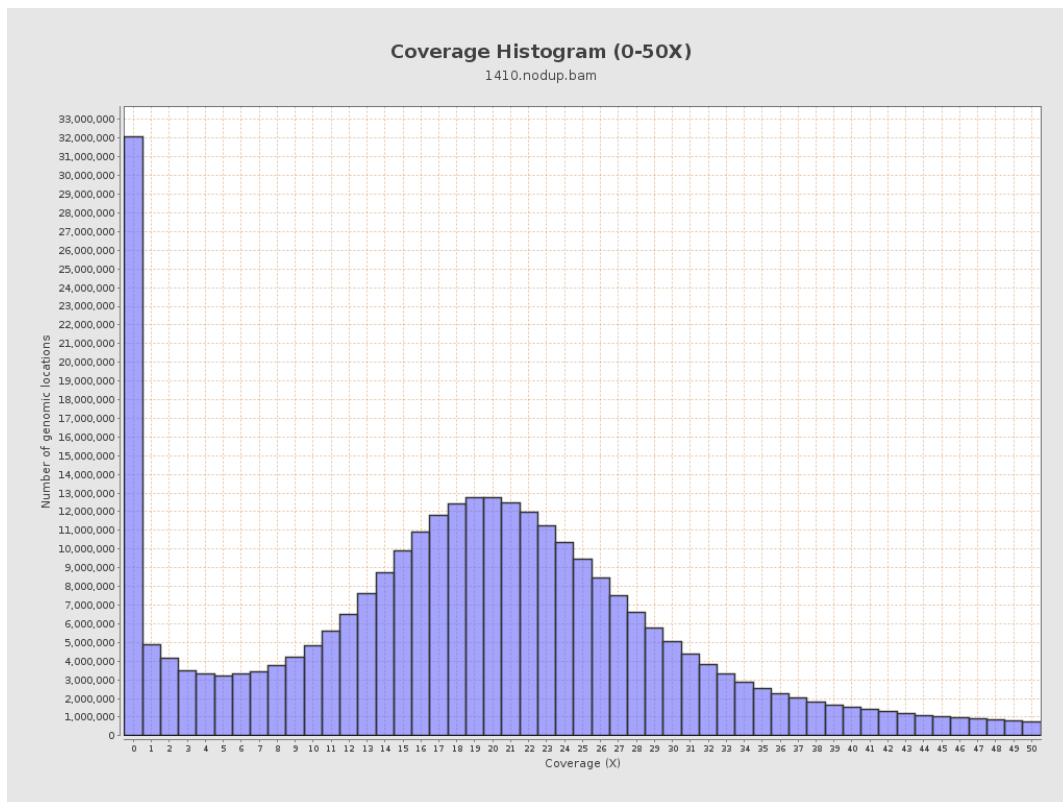
3. Results : Coverage across reference



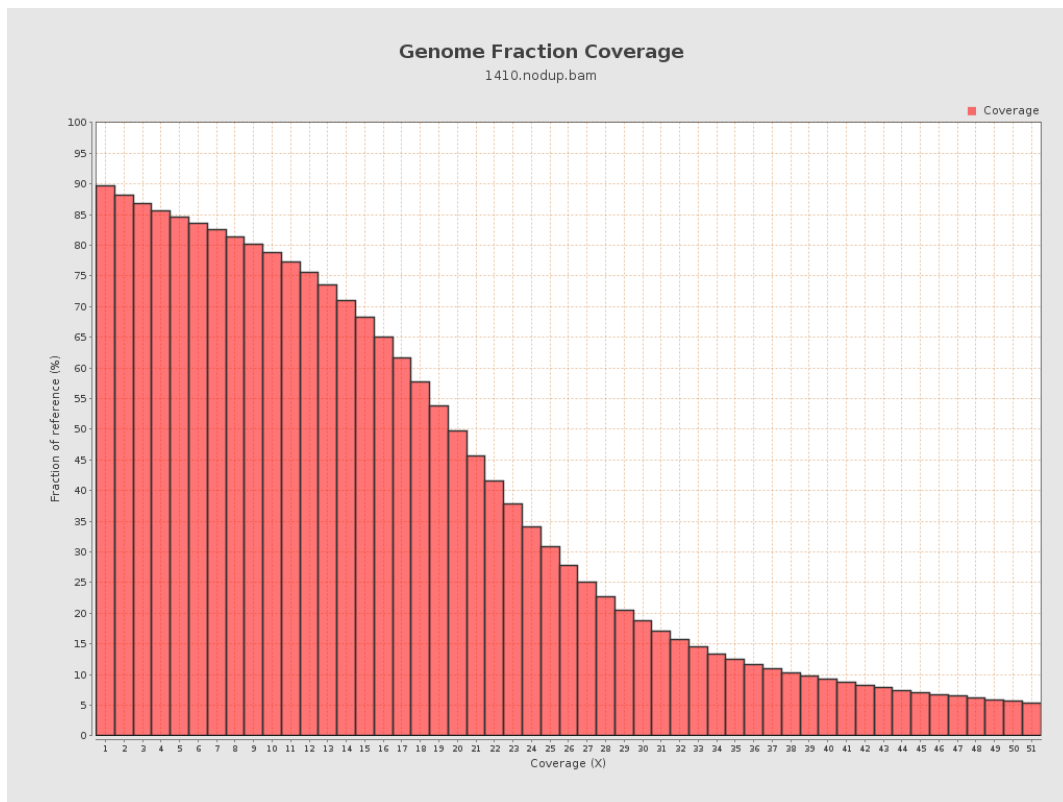
4. Results : Coverage Histogram



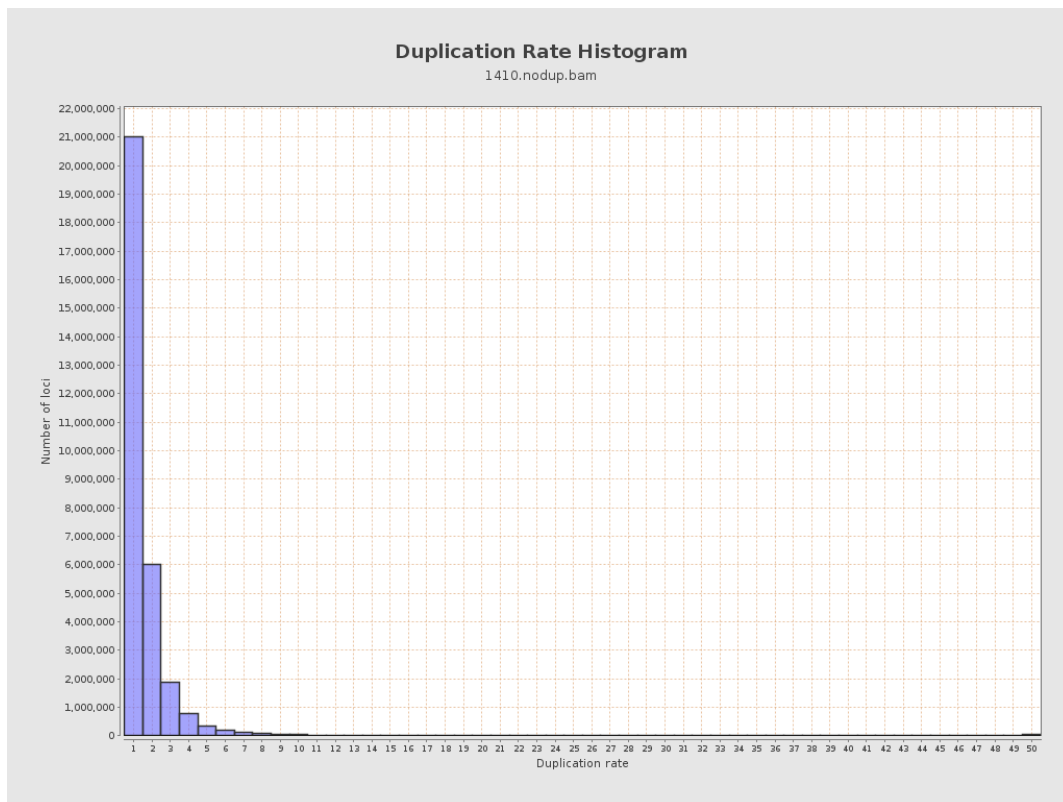
5. Results : Coverage Histogram (0-50X)



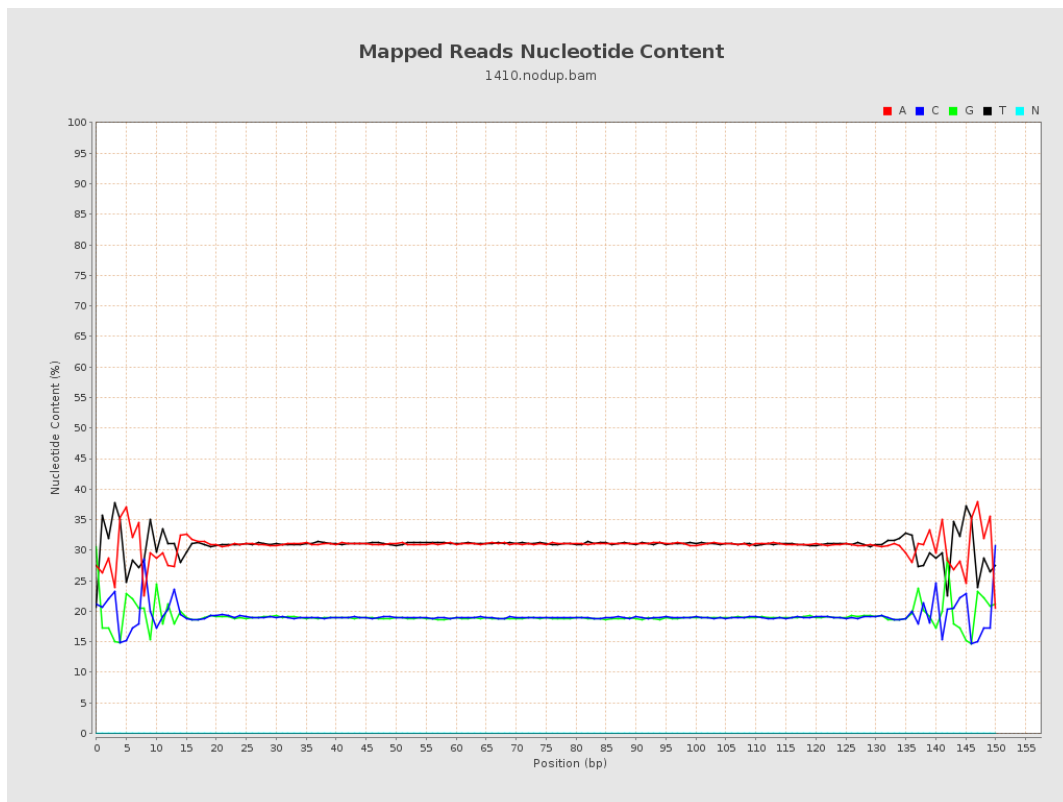
6. Results : Genome Fraction Coverage



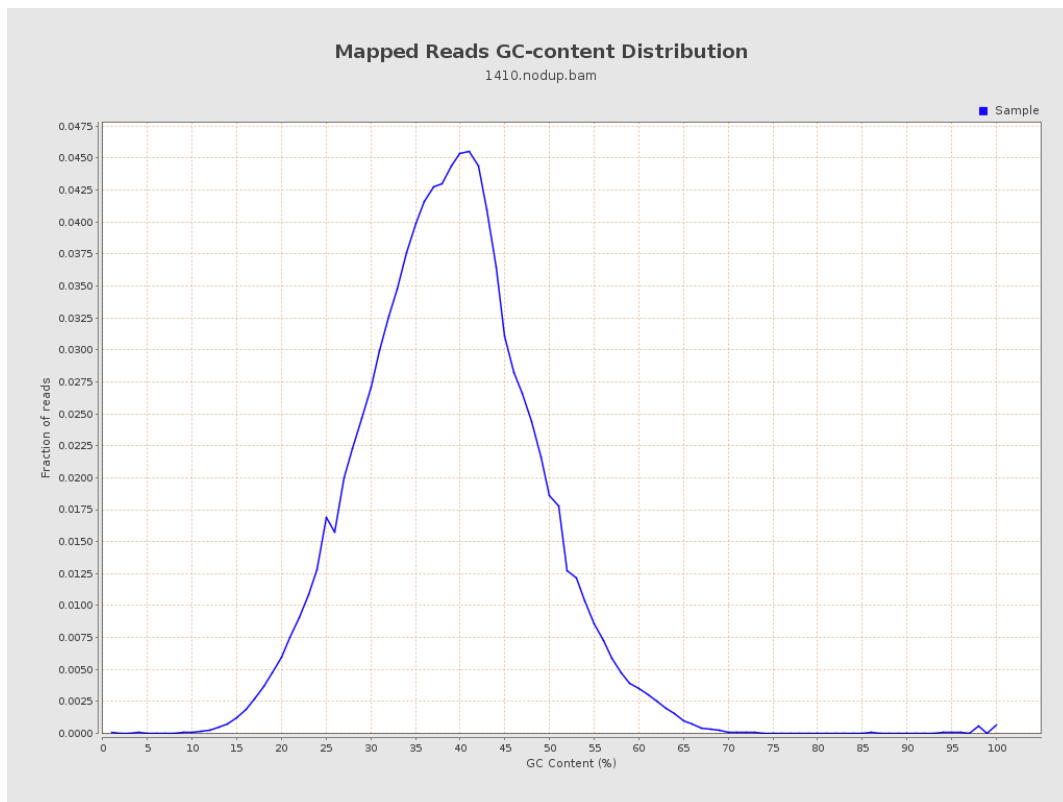
7. Results : Duplication Rate Histogram



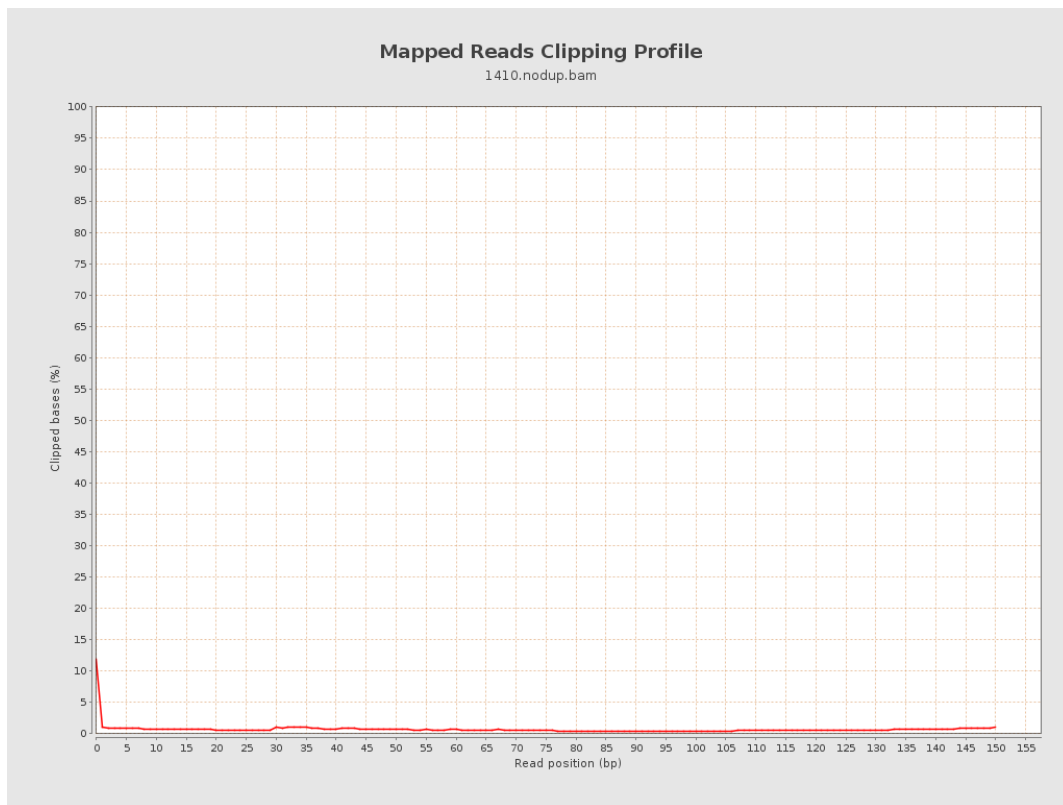
8. Results : Mapped Reads Nucleotide Content



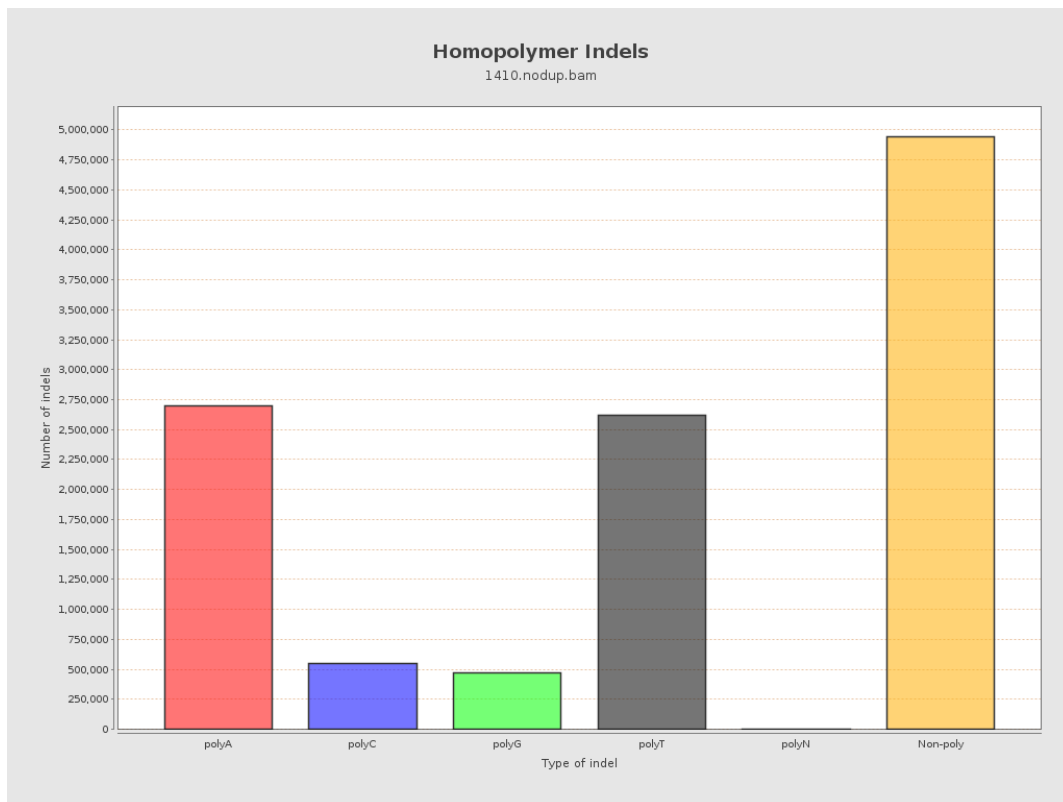
9. Results : Mapped Reads GC-content Distribution



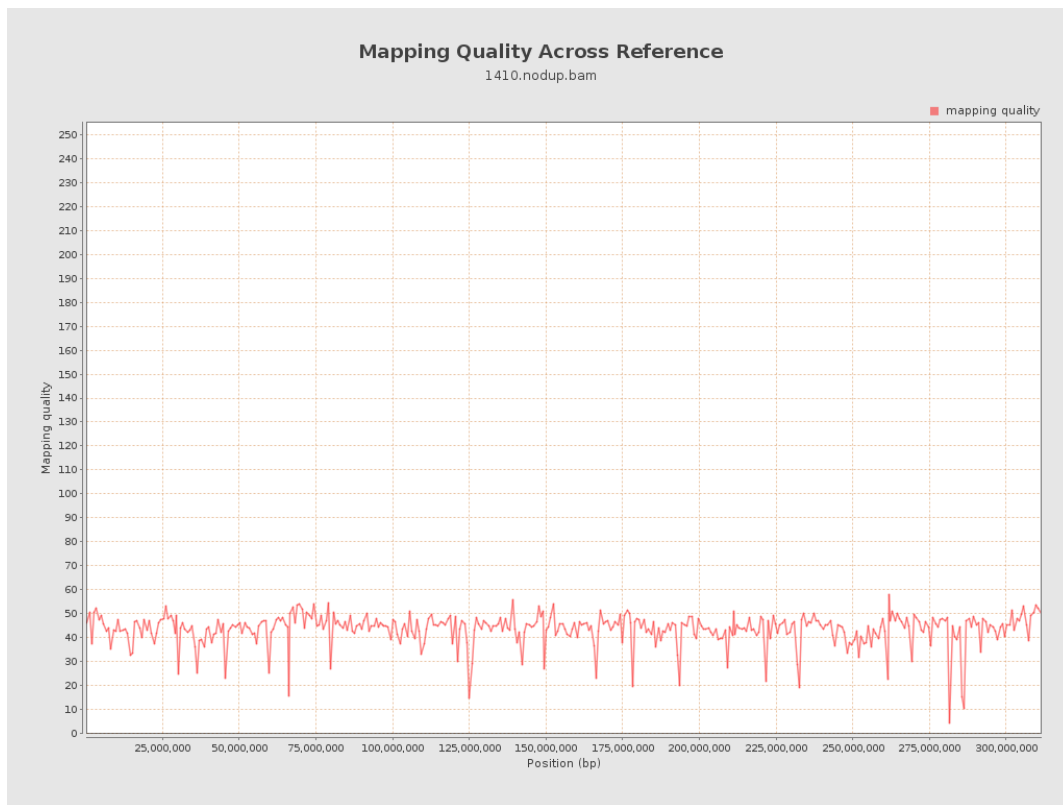
10. Results : Mapped Reads Clipping Profile



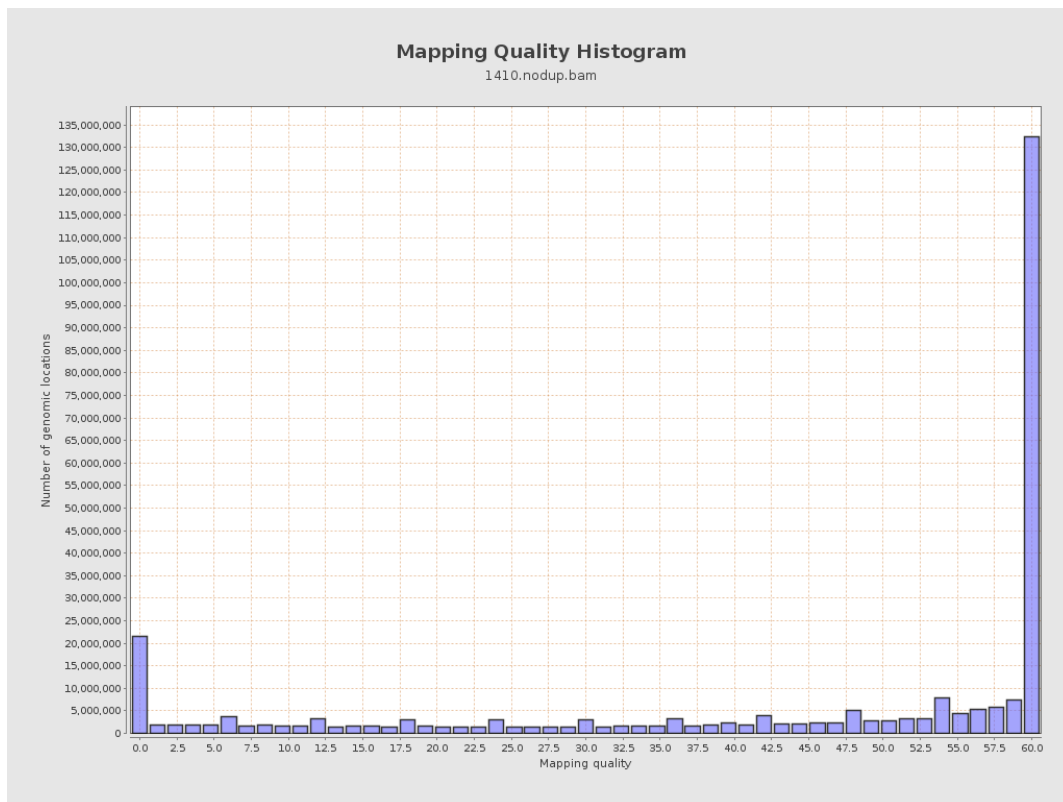
11. Results : Homopolymer Indels



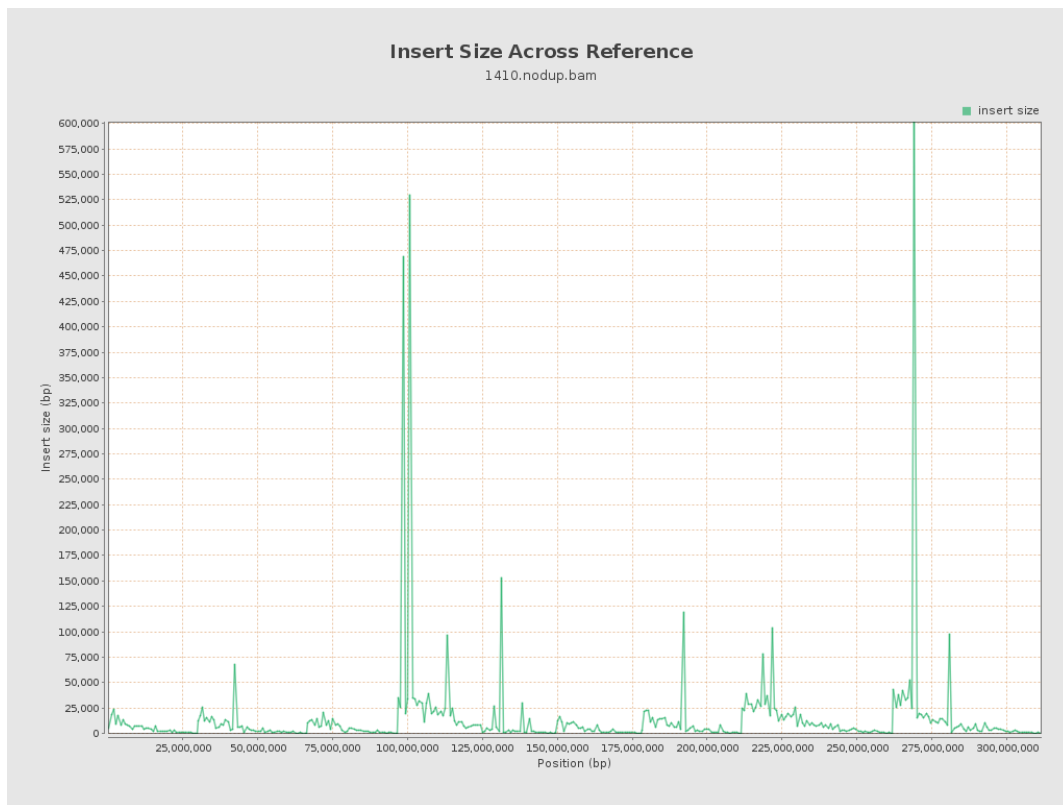
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

