Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1365
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1365 .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_440/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_440_S415_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_440/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_440_S415_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:38:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,732,404
Mapped reads	79,168,292 / 92.34%
Unmapped reads	6,564,112 / 7.66%
Mapped paired reads	79,168,292 / 92.34%
Mapped reads, first in pair	39,695,948 / 46.3%
Mapped reads, second in pair	39,472,344 / 46.04%
Mapped reads, both in pair	76,927,575 / 89.73%
Mapped reads, singletons	2,240,717 / 2.61%
Read min/max/mean length	30 / 151 / 147.99
Duplicated reads (flagged)	14,255,173 / 16.63%
Clipped reads	18,653,745 / 21.76%

2.2. ACGT Content

Number/percentage of A's	3,362,015,194 / 30.86%
Number/percentage of C's	2,083,046,571 / 19.12%
Number/percentage of T's	3,367,281,279 / 30.91%
Number/percentage of G's	2,080,946,727 / 19.1%
Number/percentage of N's	36,823 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	35.0478
Standard Deviation	317.7453

2.4. Mapping Quality

Mean Mapping Quality	43.87

2.5. Insert size

Mean	267,005.83
Standard Deviation	2,480,128.81
P25/Median/P75	350 / 461 / 608

2.6. Mismatches and indels

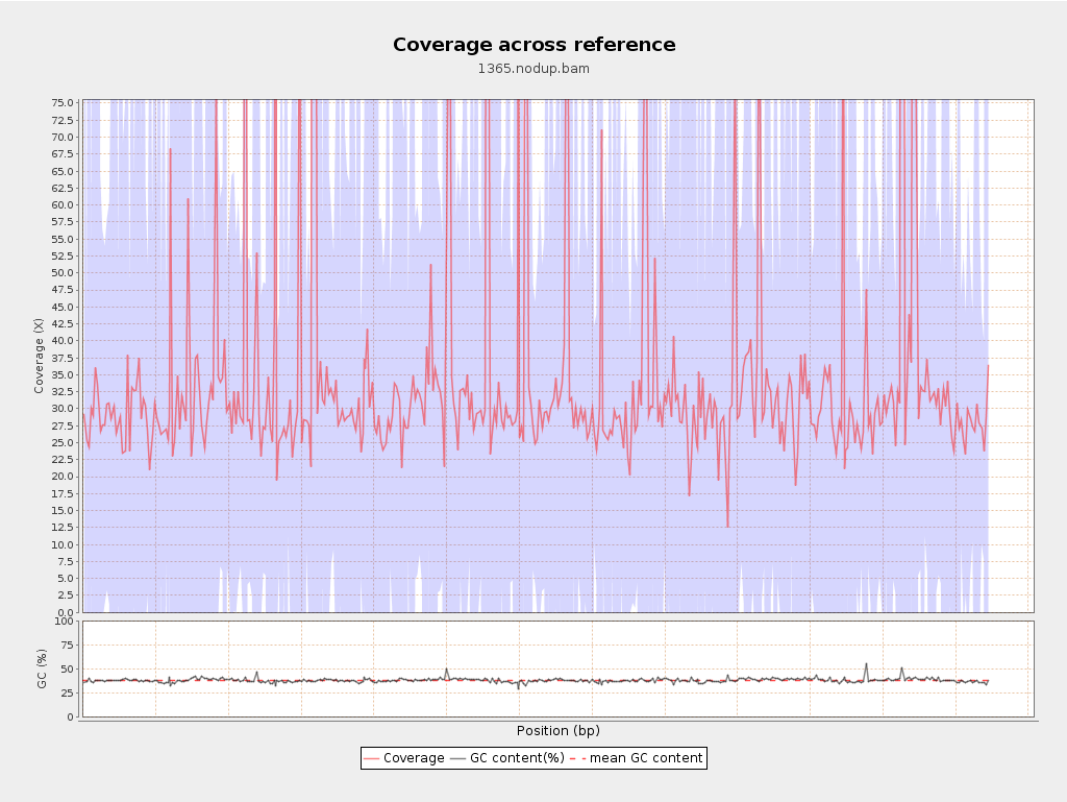
General error rate	2.4%
Mismatches	240,012,104
Insertions	7,897,422
Mapped reads with at least one insertion	8.92%
Deletions	7,739,667
Mapped reads with at least one deletion	8.66%
Homopolymer indels	56.64%

2.7. Chromosome stats

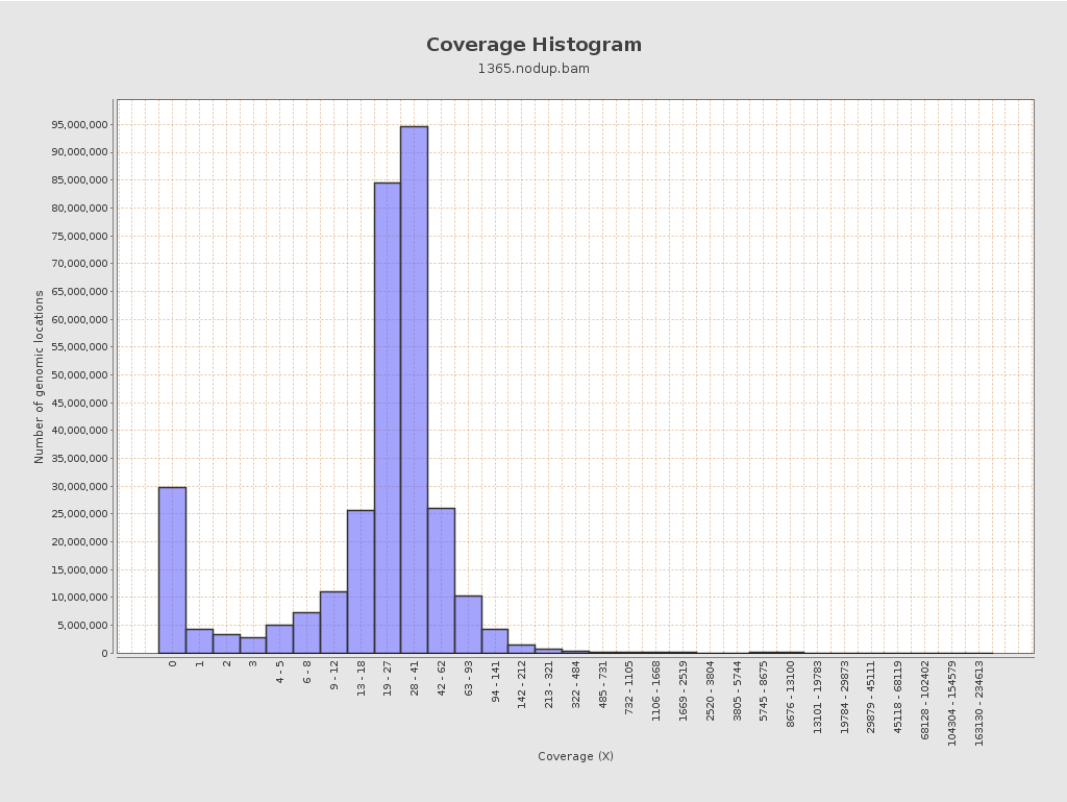
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	856311725	28.8084	125.5611

LT669789.1	36598175	1317682550	36.0041	352.0287
LT669790.1	30422129	1242913921	40.8556	396.9111
LT669791.1	52758100	1804125186	34.1962	325.7853
LT669792.1	28376109	993315142	35.0053	320.5409
LT669793.1	33388210	1081526193	32.3925	203.4081
LT669794.1	50579949	1675670003	33.1291	276.5791
LT669795.1	49795044	1950834091	39.1773	398.2632

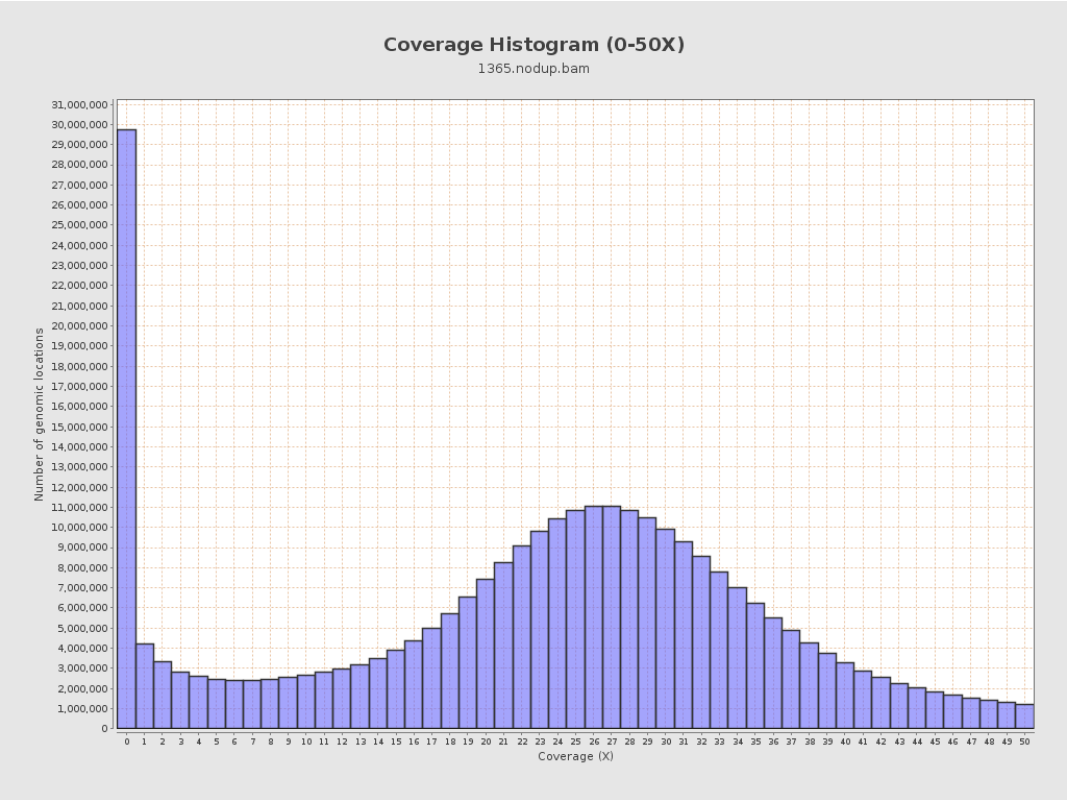
3. Results : Coverage across reference



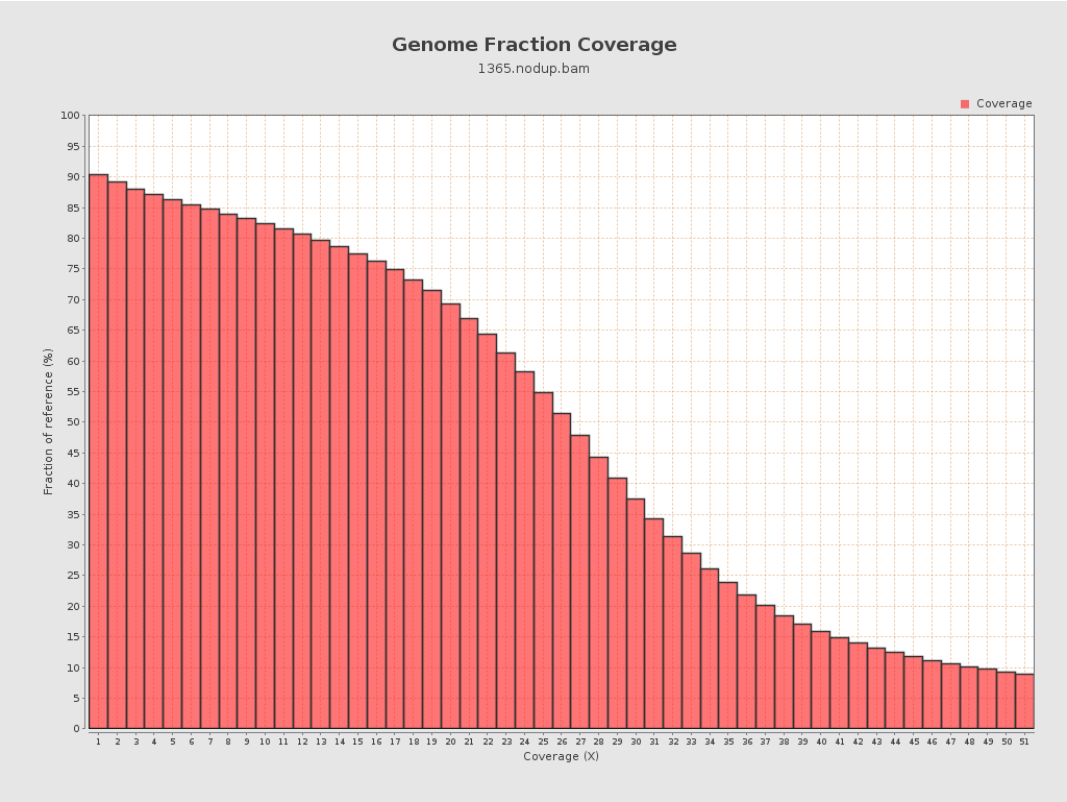
4. Results : Coverage Histogram



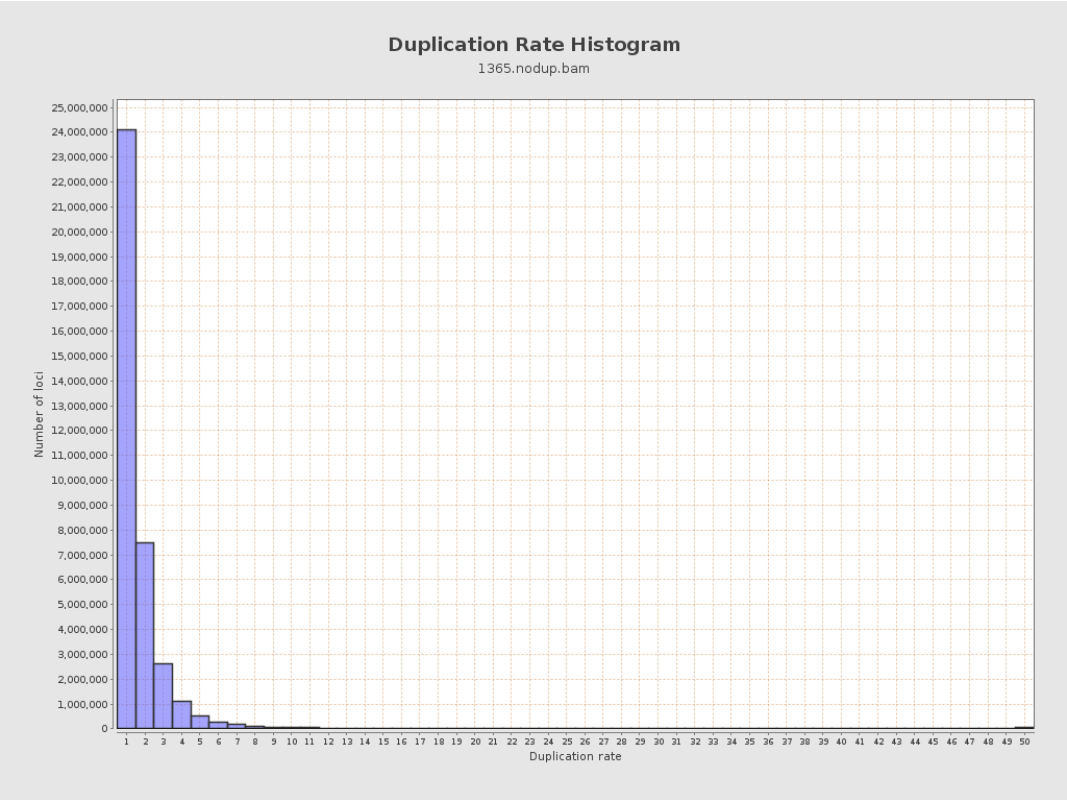
5. Results : Coverage Histogram (0-50X)



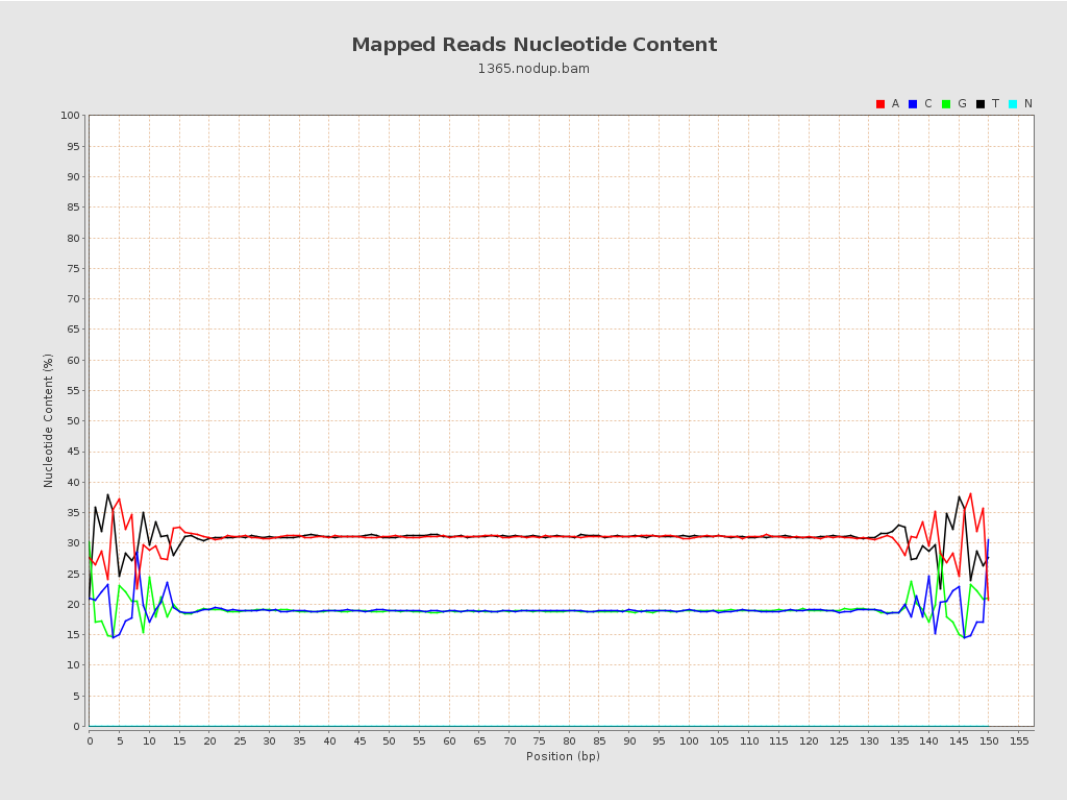
6. Results : Genome Fraction Coverage



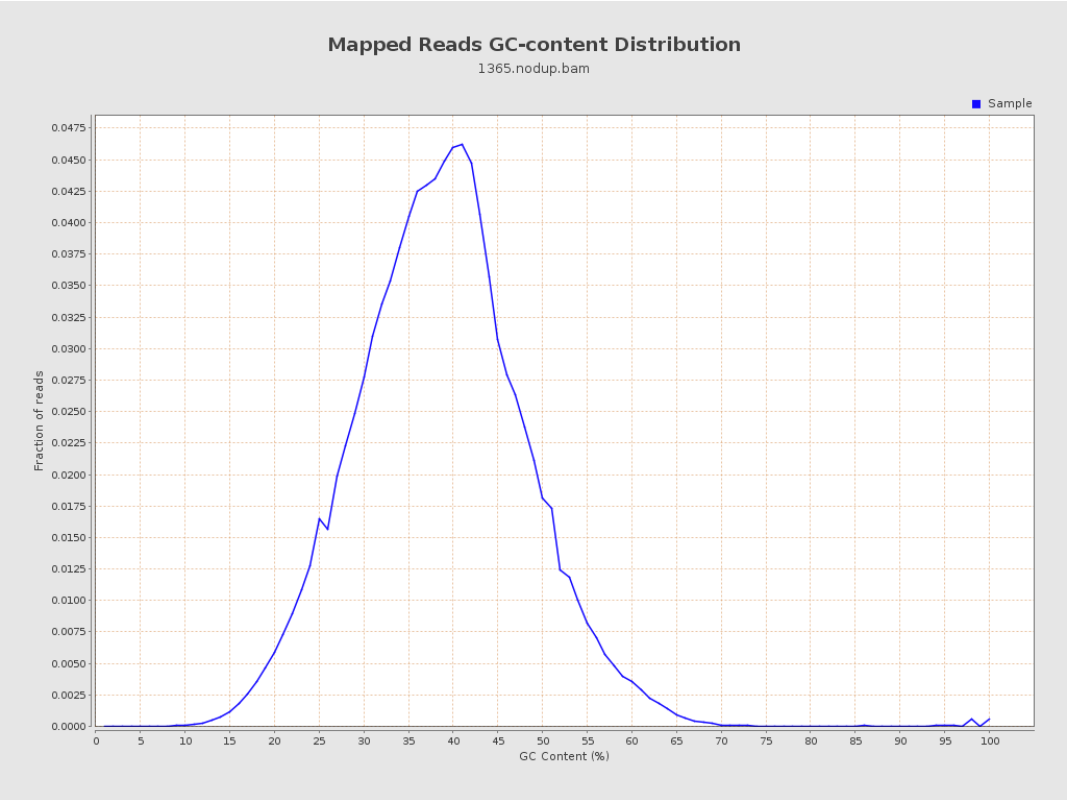
7. Results : Duplication Rate Histogram



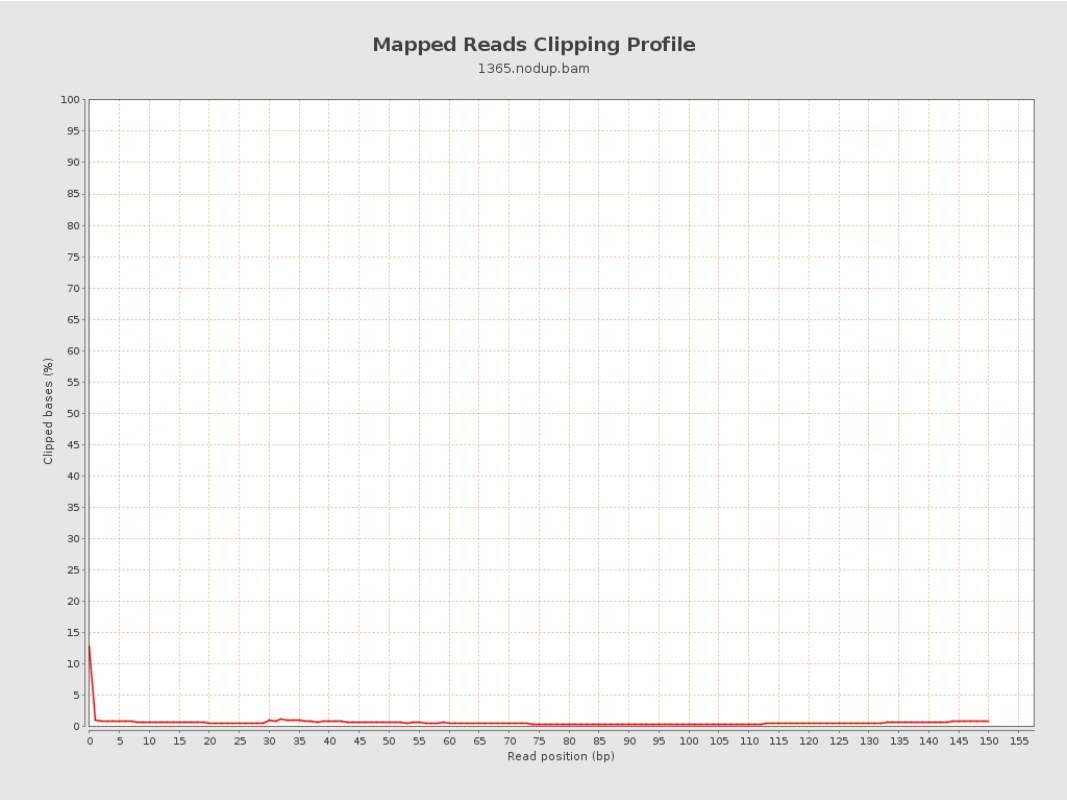
8. Results : Mapped Reads Nucleotide Content



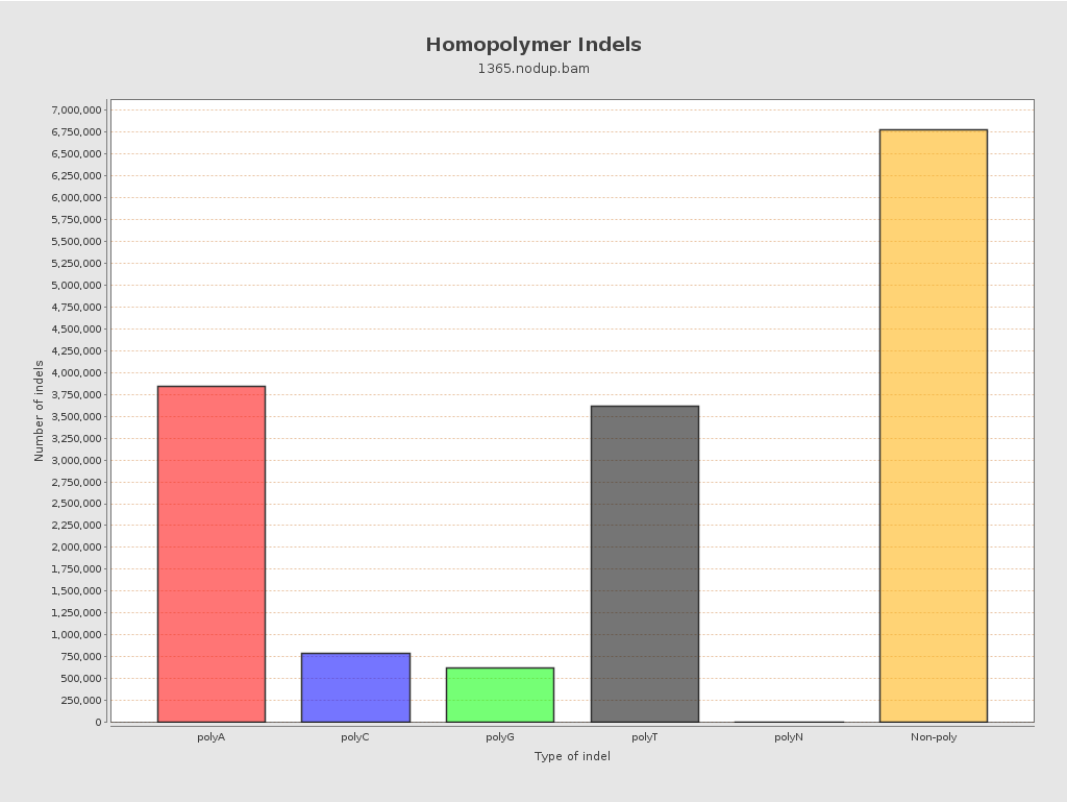
9. Results : Mapped Reads GC-content Distribution



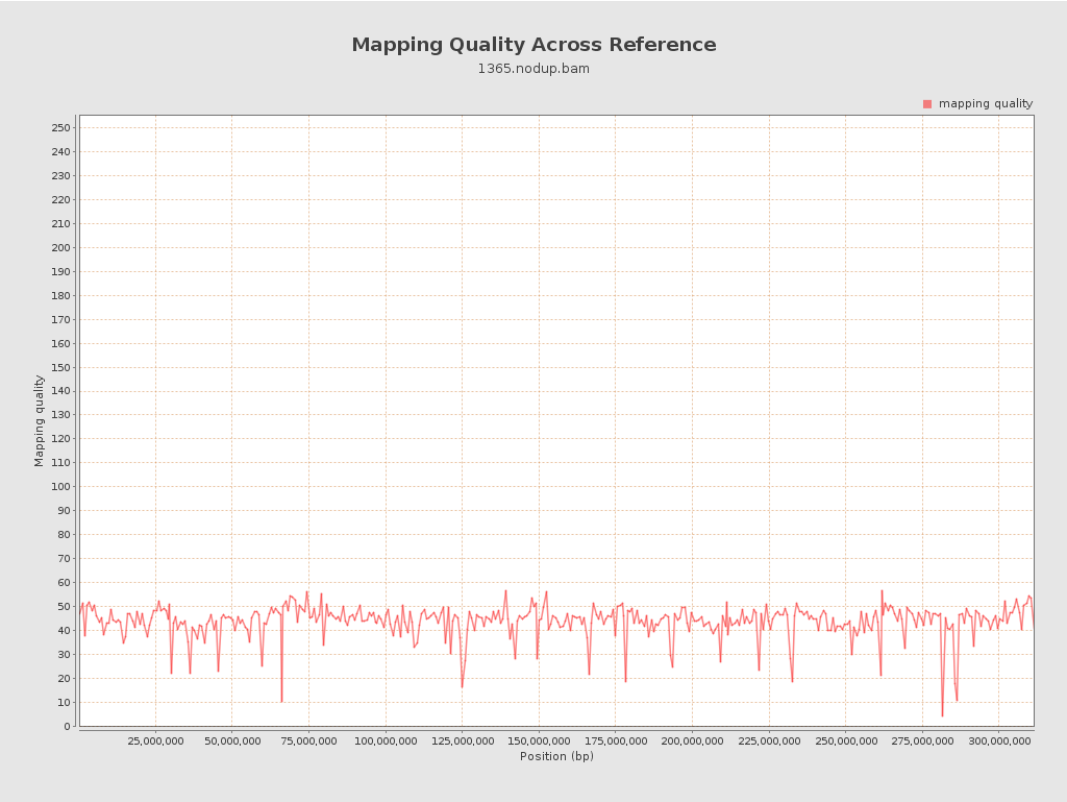
10. Results : Mapped Reads Clipping Profile



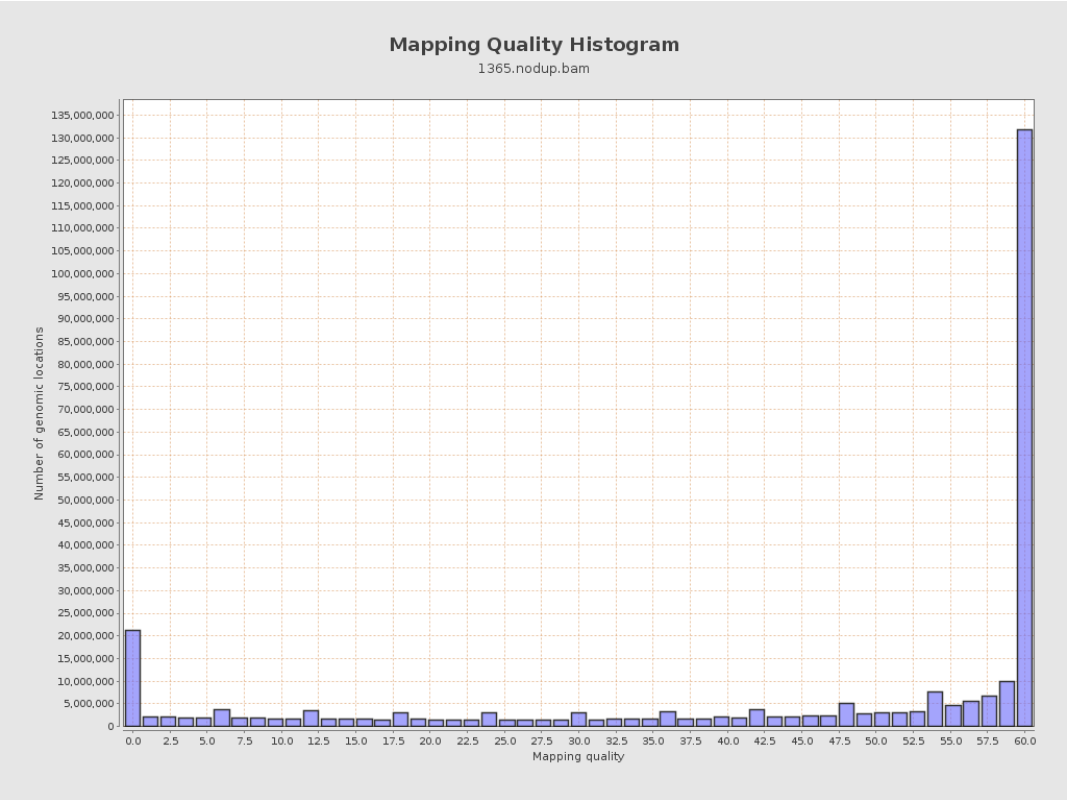
11. Results : Homopolymer Indels



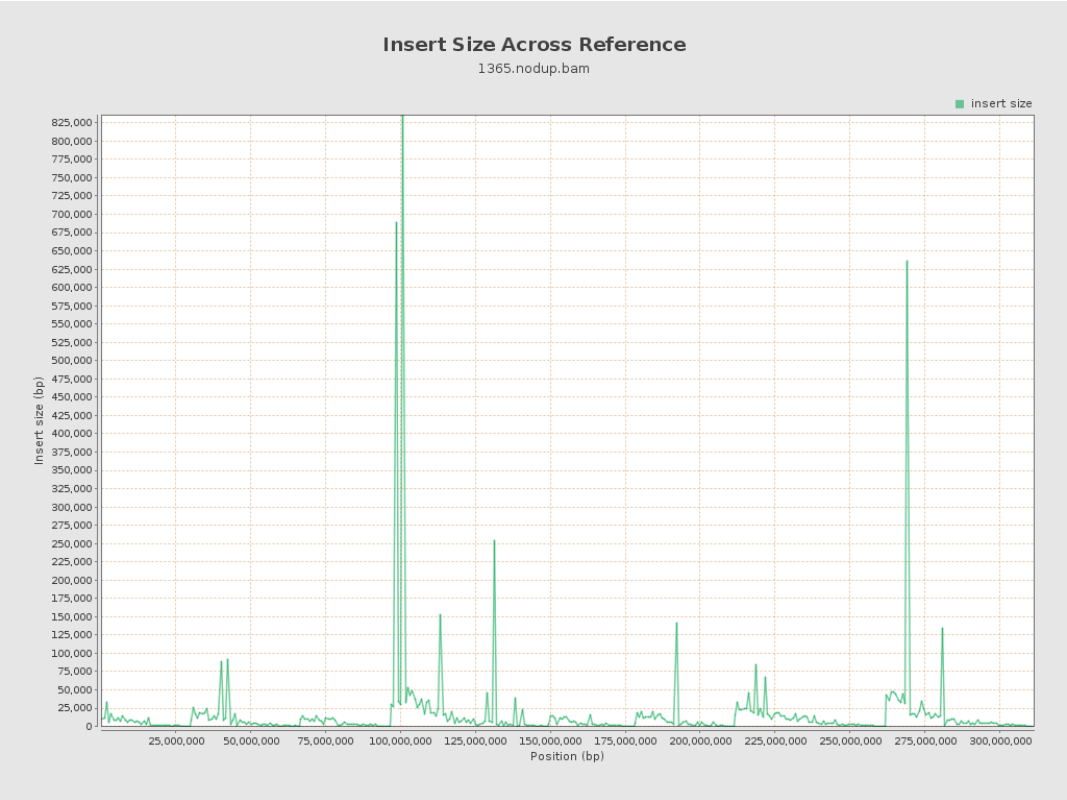
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram