Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/431.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/431.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_168/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_168_S258_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_168/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_168_S258_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:13 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,283,900
Mapped reads	68,370,466 / 94.59%
Unmapped reads	3,913,434 / 5.41%
Mapped paired reads	68,370,466 / 94.59%
Mapped reads, first in pair	34,172,960 / 47.28%
Mapped reads, second in pair	34,197,506 / 47.31%
Mapped reads, both in pair	67,155,220 / 92.9%
Mapped reads, singletons	1,215,246 / 1.68%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	11,137,214 / 15.41%
Clipped reads	14,833,563 / 20.52%

2.2. ACGT Content

Number/percentage of A's	2,938,191,522 / 30.85%
Number/percentage of C's	1,823,050,774 / 19.14%
Number/percentage of T's	2,943,828,668 / 30.91%
Number/percentage of G's	1,820,103,623 / 19.11%
Number/percentage of N's	37,140 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	30.6461
Standard Deviation	238.3014

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Insert size

Mean	218,642.7
Standard Deviation	2,219,950.86
P25/Median/P75	301 / 392 / 510

2.6. Mismatches and indels

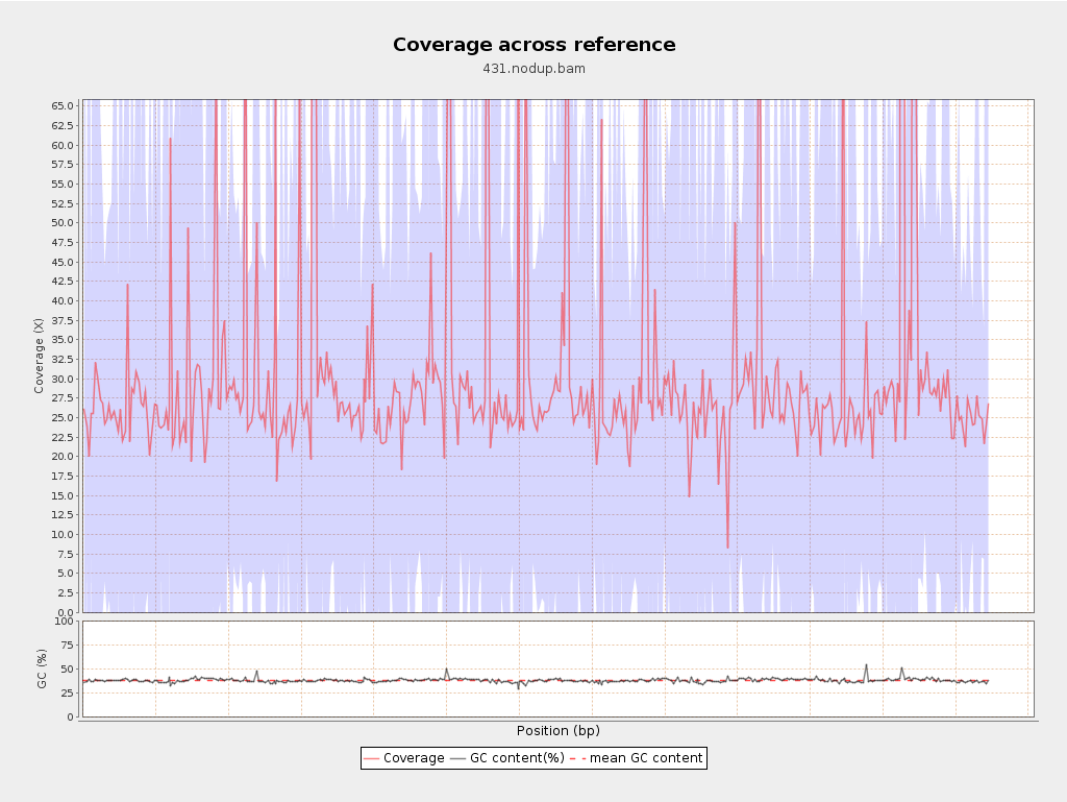
General error rate	2.34%
Mismatches	204,927,489
Insertions	6,515,656
Mapped reads with at least one insertion	8.56%
Deletions	6,655,046
Mapped reads with at least one deletion	8.61%
Homopolymer indels	55.51%

2.7. Chromosome stats

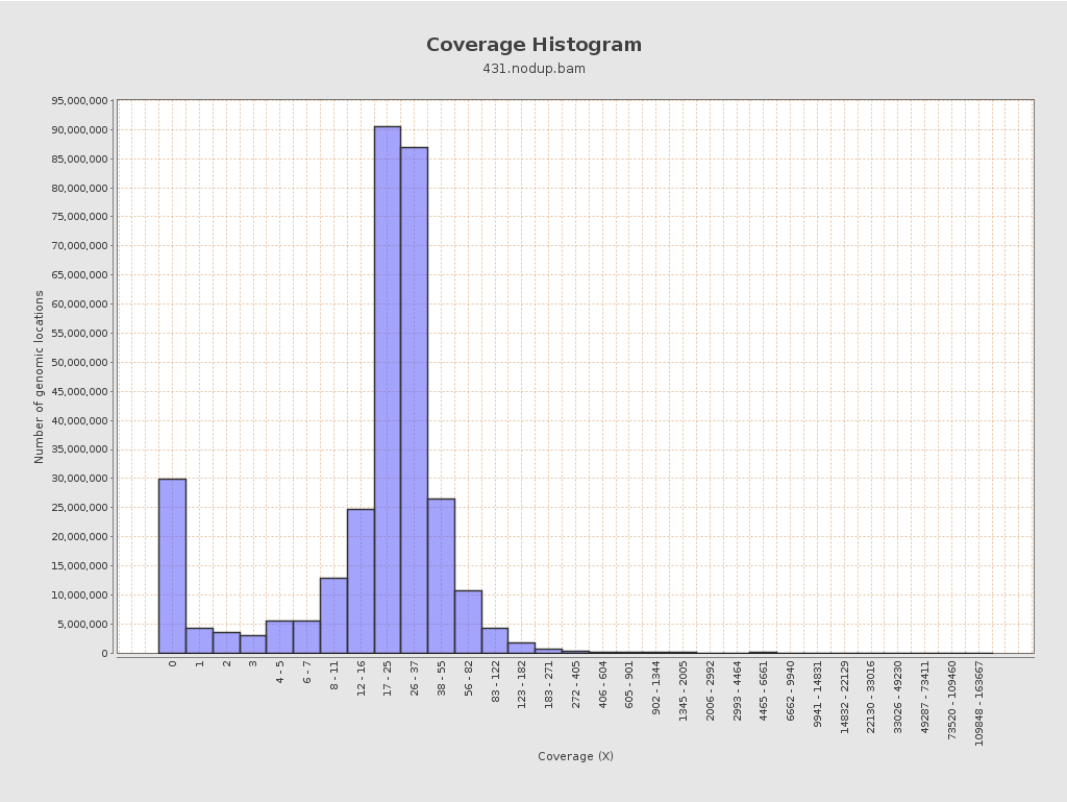
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	773761389	26.0312	87.7713

LT669789.1	36598175	1122651114	30.6751	260.9508
LT669790.1	30422129	1008350322	33.1453	224.3161
LT669791.1	52758100	1573994551	29.8342	233.1908
LT669792.1	28376109	870882609	30.6907	278.9618
LT669793.1	33388210	950210855	28.4595	159.0488
LT669794.1	50579949	1456343028	28.7929	214.0412
LT669795.1	49795044	1794410637	36.0359	323.2741

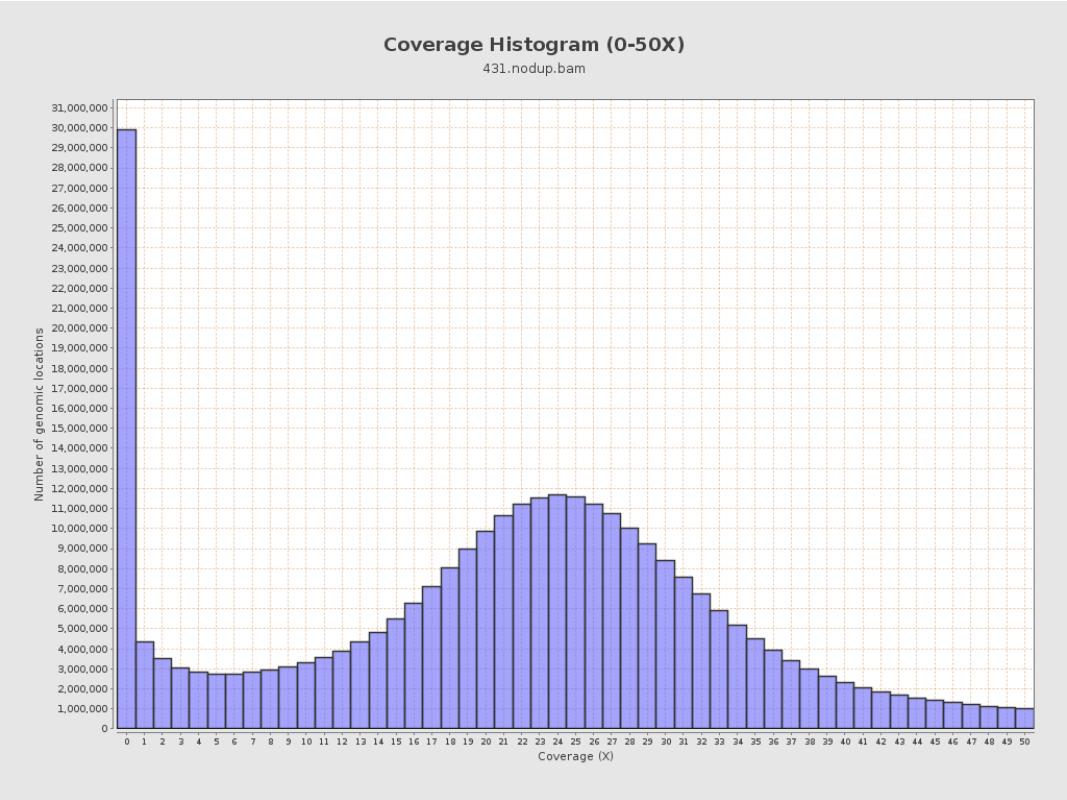
3. Results : Coverage across reference



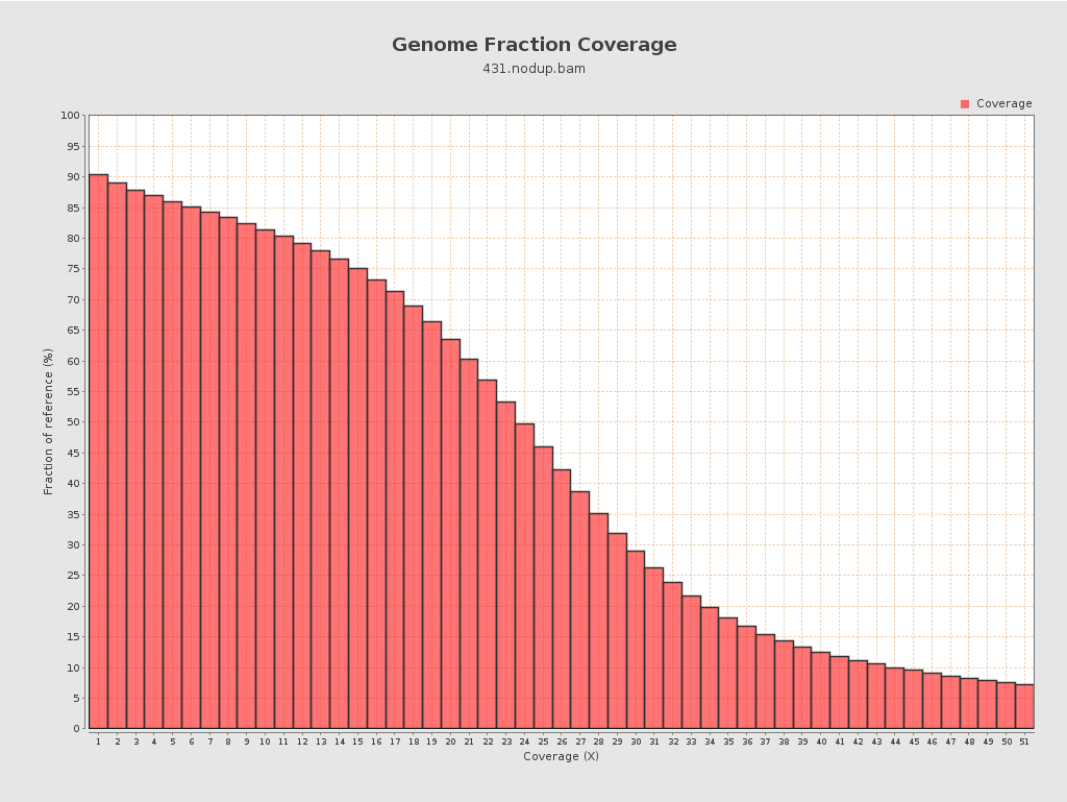
4. Results : Coverage Histogram



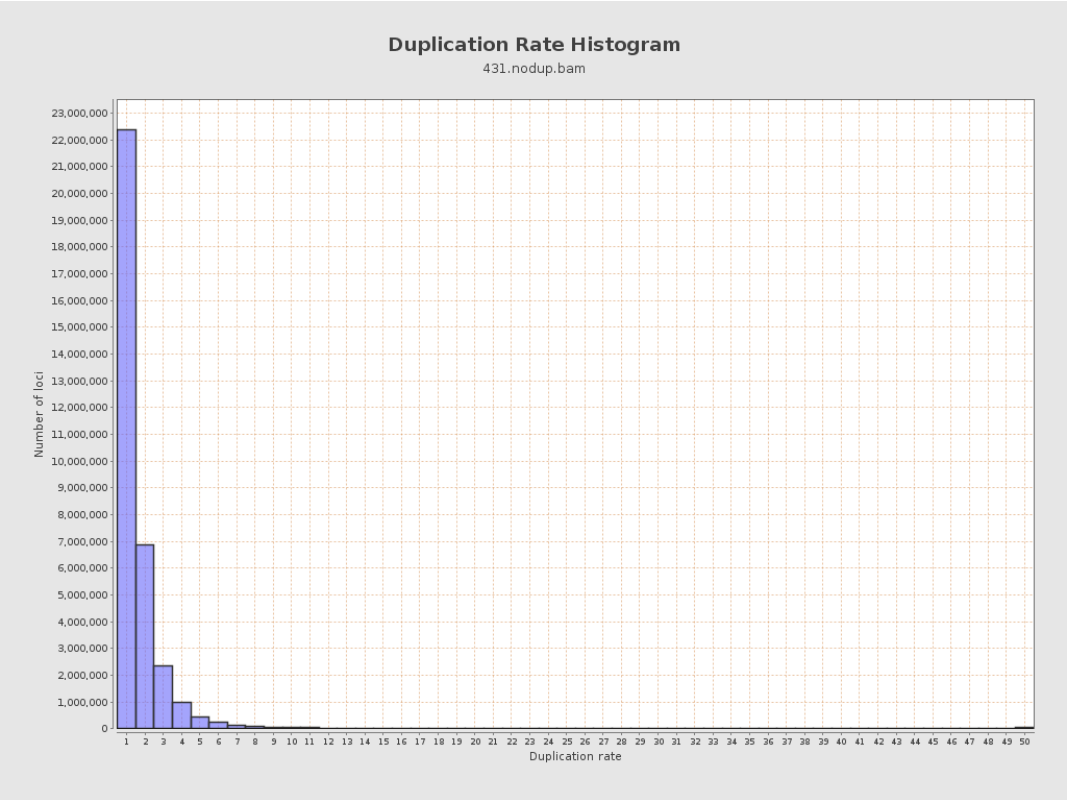
5. Results : Coverage Histogram (0-50X)



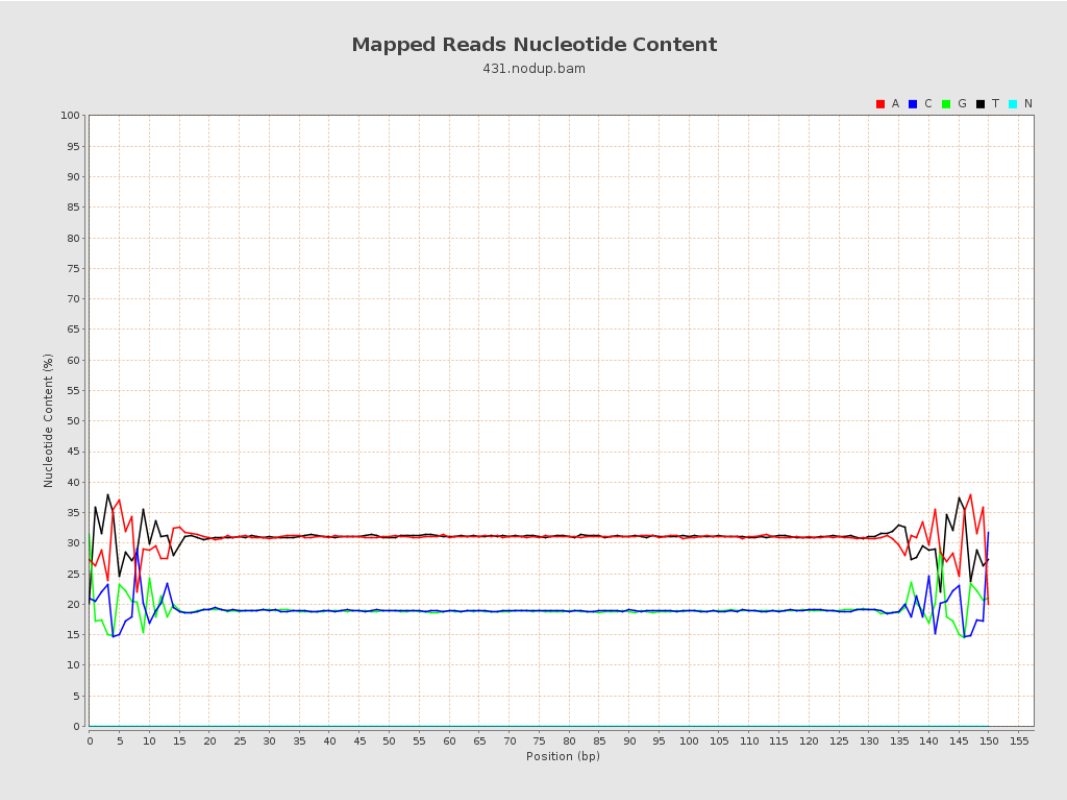
6. Results : Genome Fraction Coverage



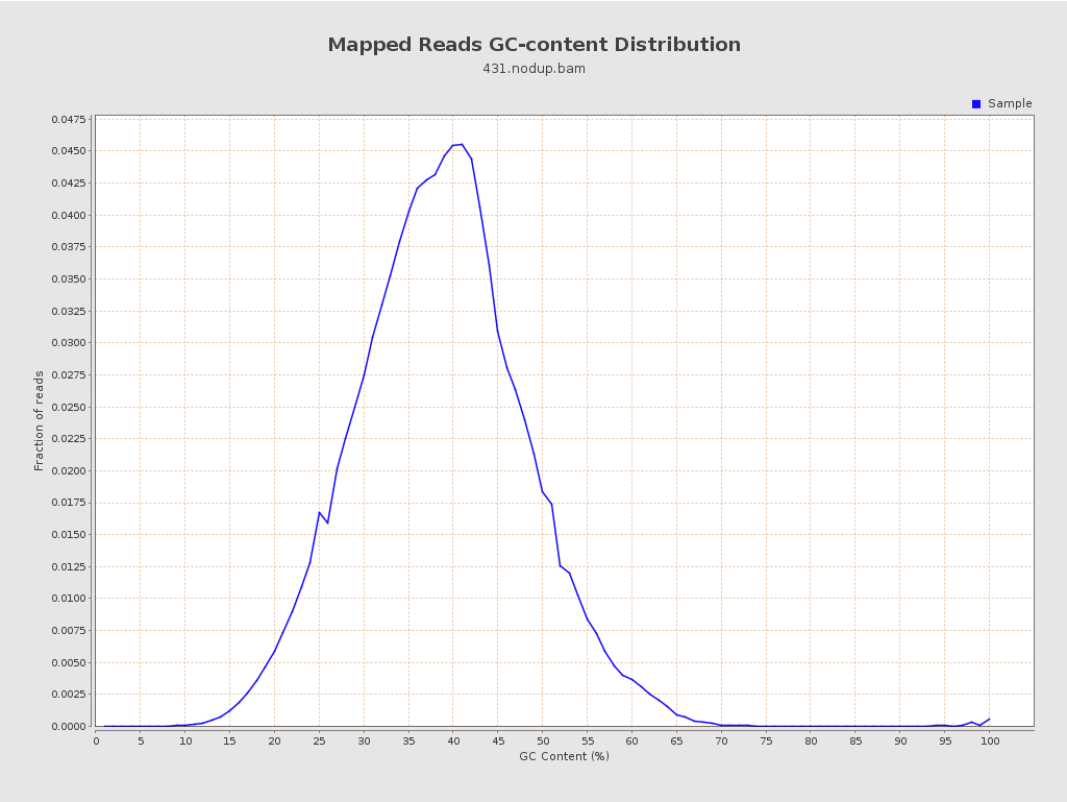
7. Results : Duplication Rate Histogram



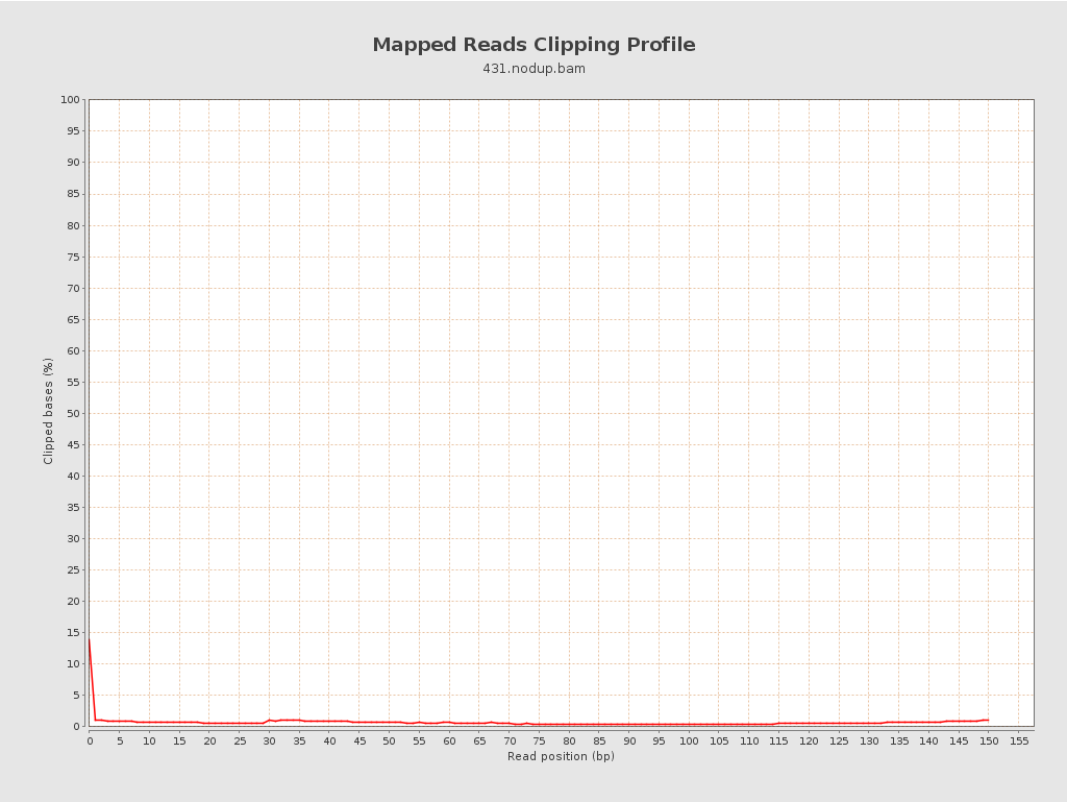
8. Results : Mapped Reads Nucleotide Content



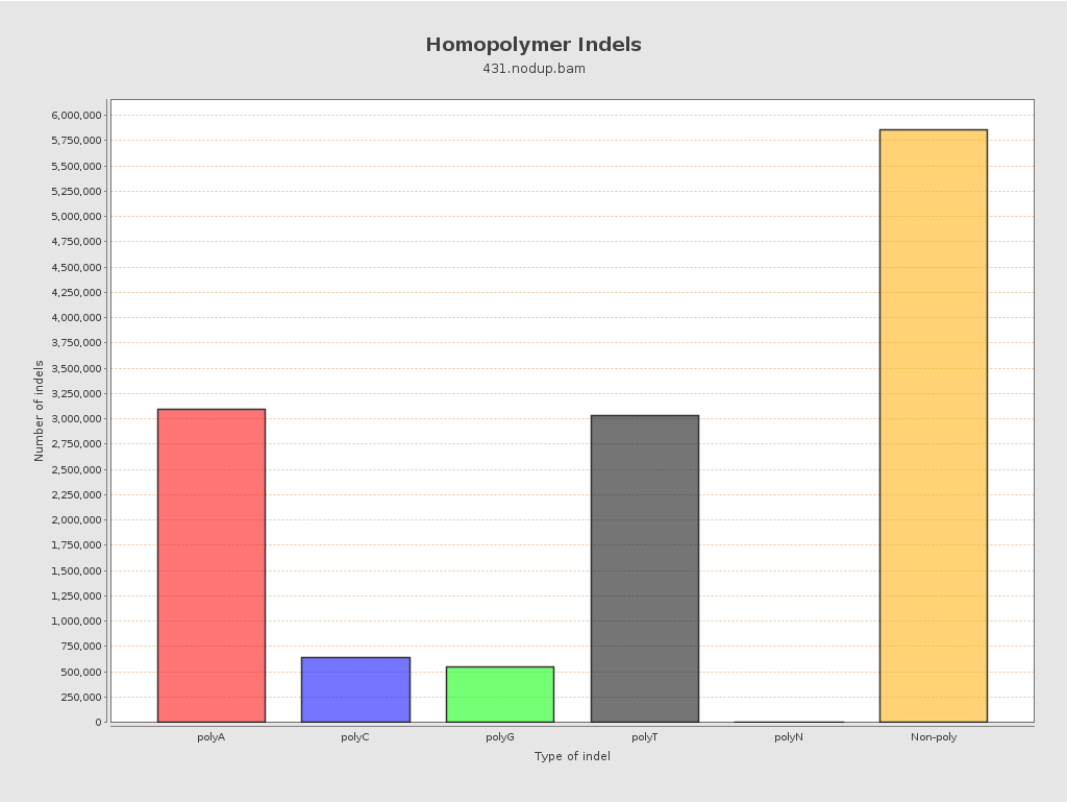
9. Results : Mapped Reads GC-content Distribution



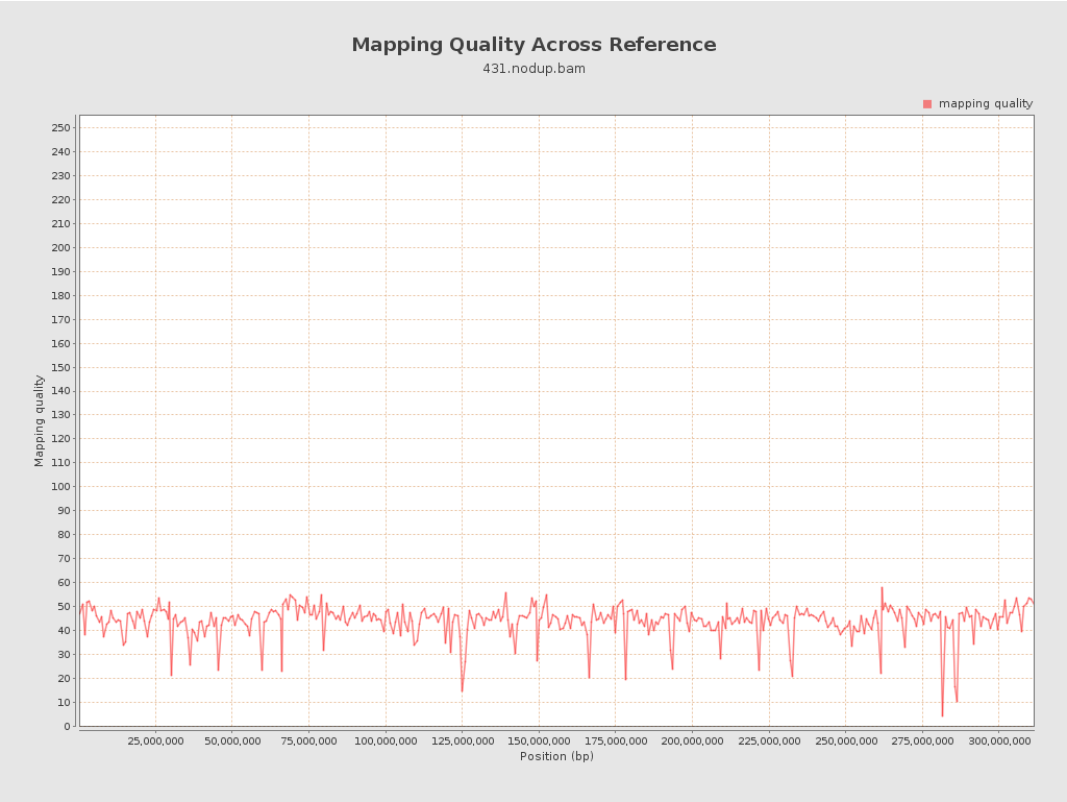
10. Results : Mapped Reads Clipping Profile



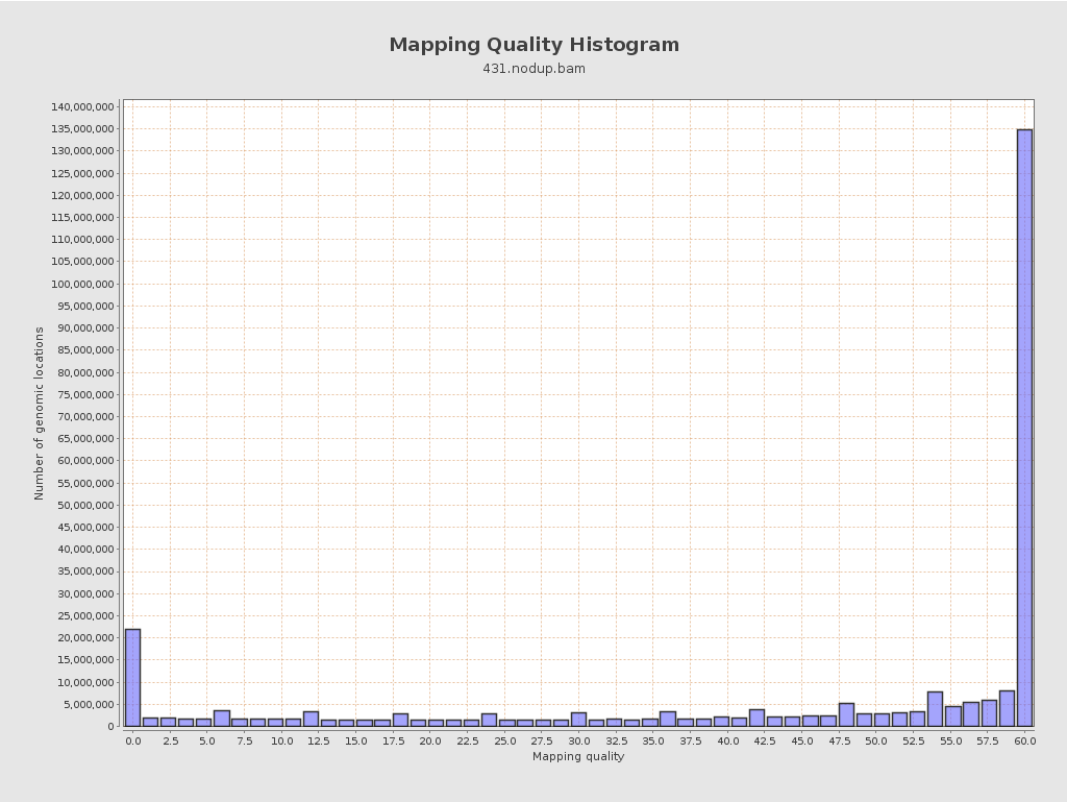
11. Results : Homopolymer Indels



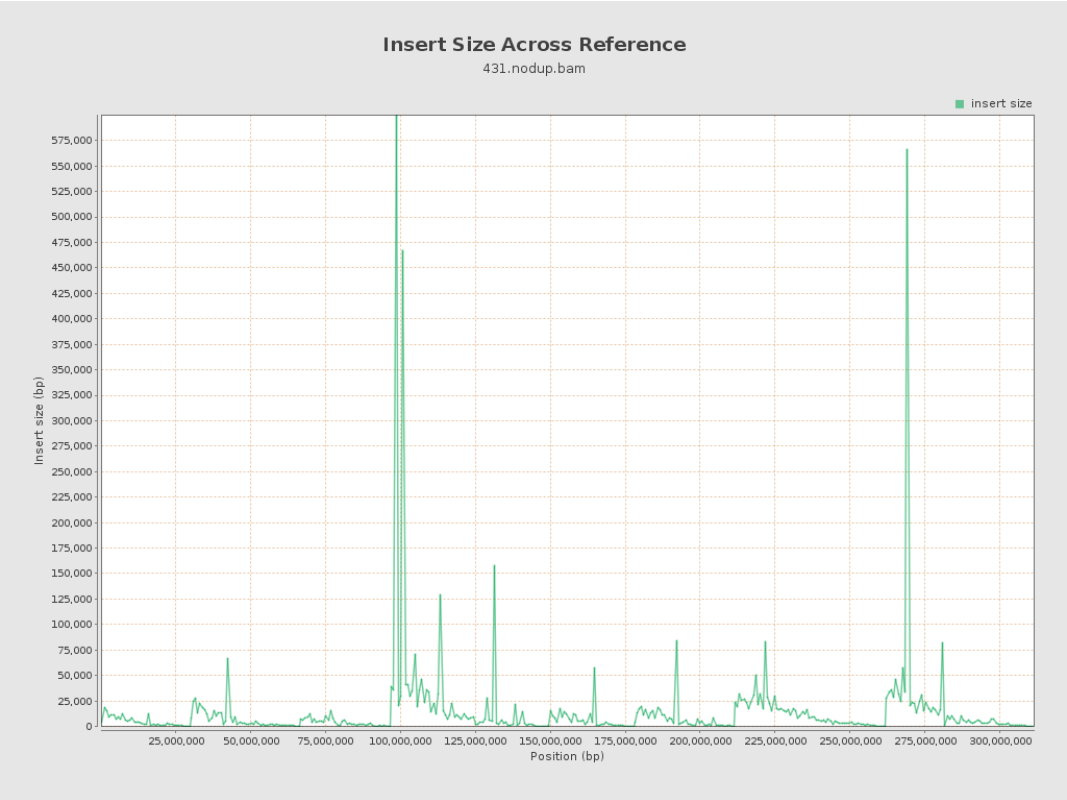
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram