Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:42:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/436.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/436.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_236/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_236_S317_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_236/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_236_S317_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:42:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	98,812,952
Mapped reads	92,384,360 / 93.49%
Unmapped reads	6,428,592 / 6.51%
Mapped paired reads	92,384,360 / 93.49%
Mapped reads, first in pair	46,278,338 / 46.83%
Mapped reads, second in pair	46,106,022 / 46.66%
Mapped reads, both in pair	90,299,130 / 91.38%
Mapped reads, singletons	2,085,230 / 2.11%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	15,843,233 / 16.03%
Clipped reads	20,975,271 / 21.23%

2.2. ACGT Content

Number/percentage of A's	3,945,095,885 / 30.88%
Number/percentage of C's	2,443,496,779 / 19.13%
Number/percentage of T's	3,946,944,214 / 30.9%
Number/percentage of G's	2,438,504,412 / 19.09%
Number/percentage of N's	48,169 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	41.0929
Standard Deviation	336.5928

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Insert size

Mean	231,234.05
Standard Deviation	2,296,648.63
P25/Median/P75	317 / 416 / 540

2.6. Mismatches and indels

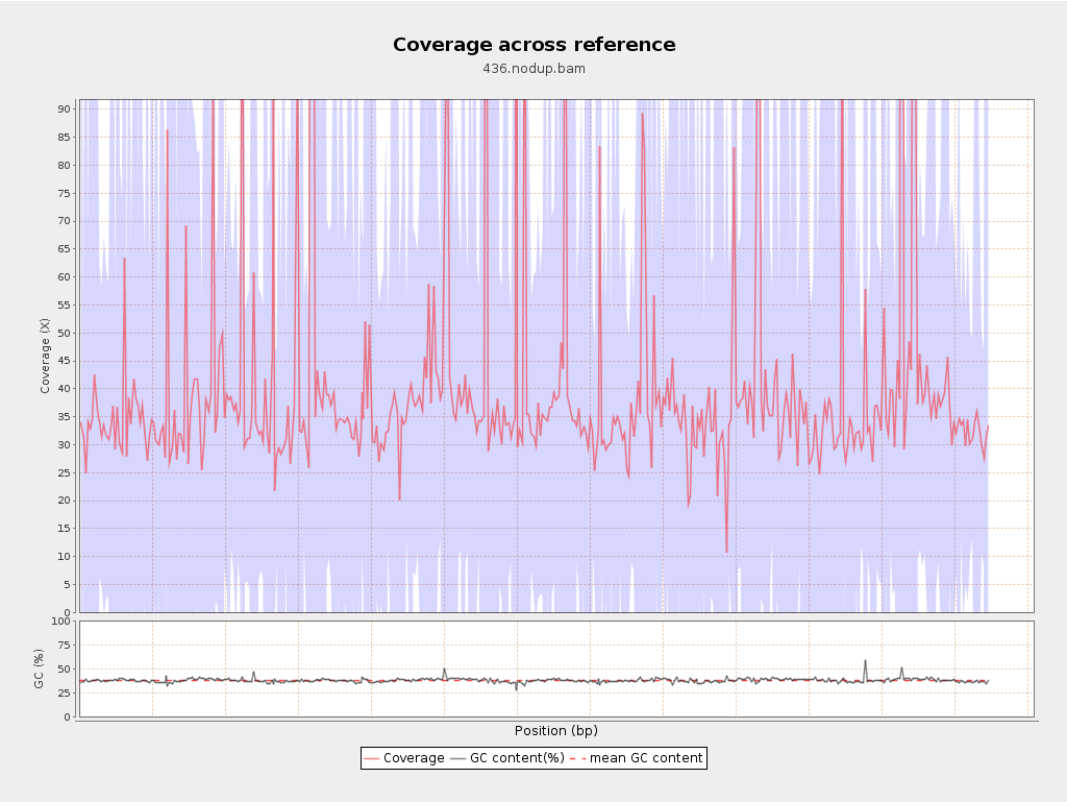
General error rate	2.27%
Mismatches	266,340,293
Insertions	8,662,658
Mapped reads with at least one insertion	8.41%
Deletions	8,630,435
Mapped reads with at least one deletion	8.27%
Homopolymer indels	56.56%

2.7. Chromosome stats

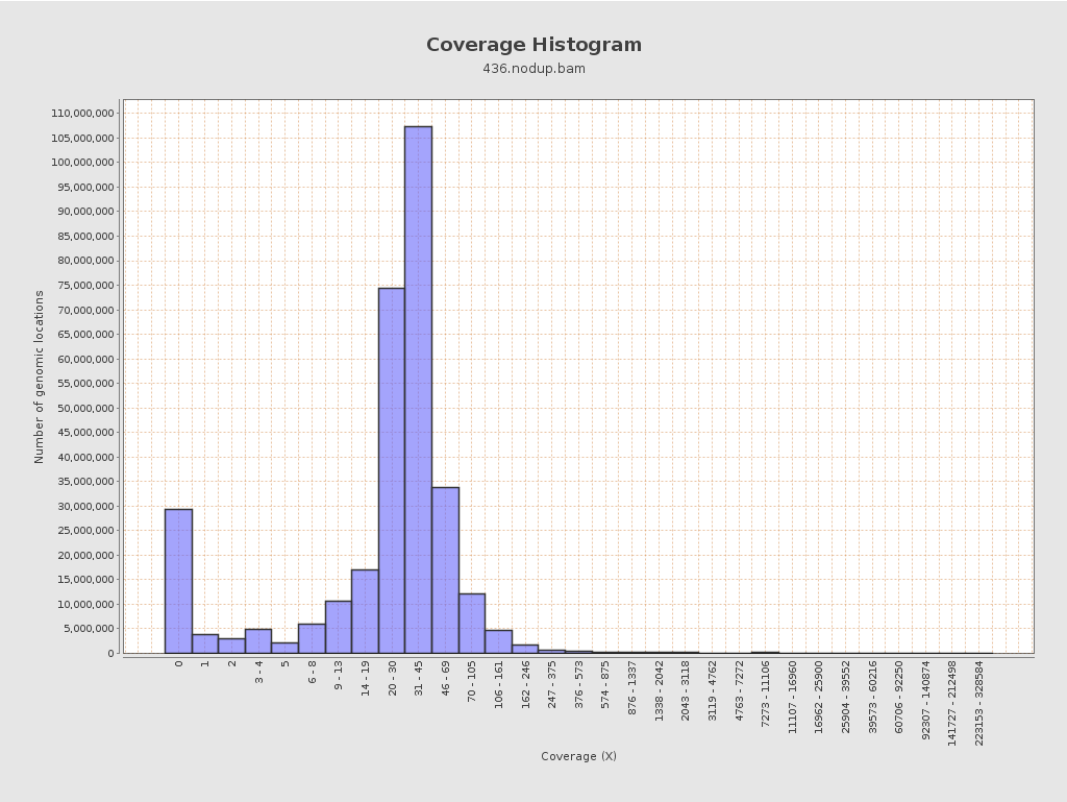
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1011273752	34.0217	113.6219

LT669789.1	36598175	1490855708	40.7358	348.5467
LT669790.1	30422129	1393226518	45.7965	388.5352
LT669791.1	52758100	2137457933	40.5143	313.0186
LT669792.1	28376109	1164376193	41.0337	369.6543
LT669793.1	33388210	1242169931	37.2038	181.2788
LT669794.1	50579949	1953908021	38.6301	295.7826
LT669795.1	49795044	2413001460	48.4587	476.5899

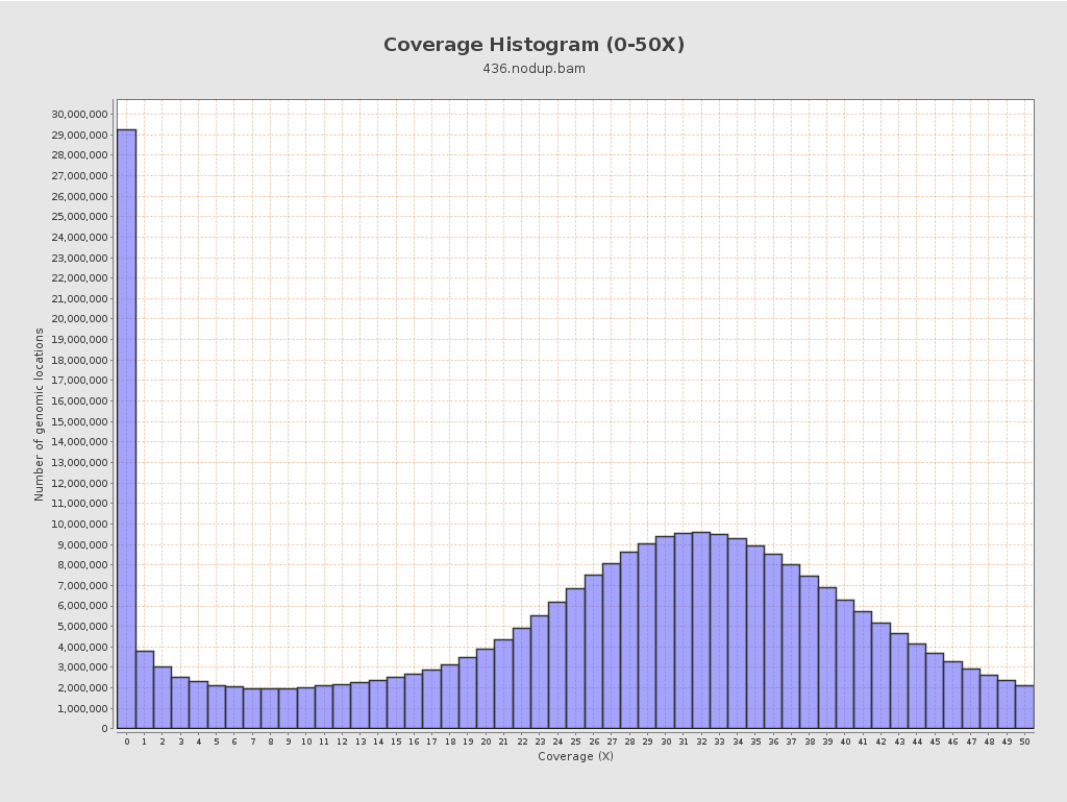
3. Results : Coverage across reference



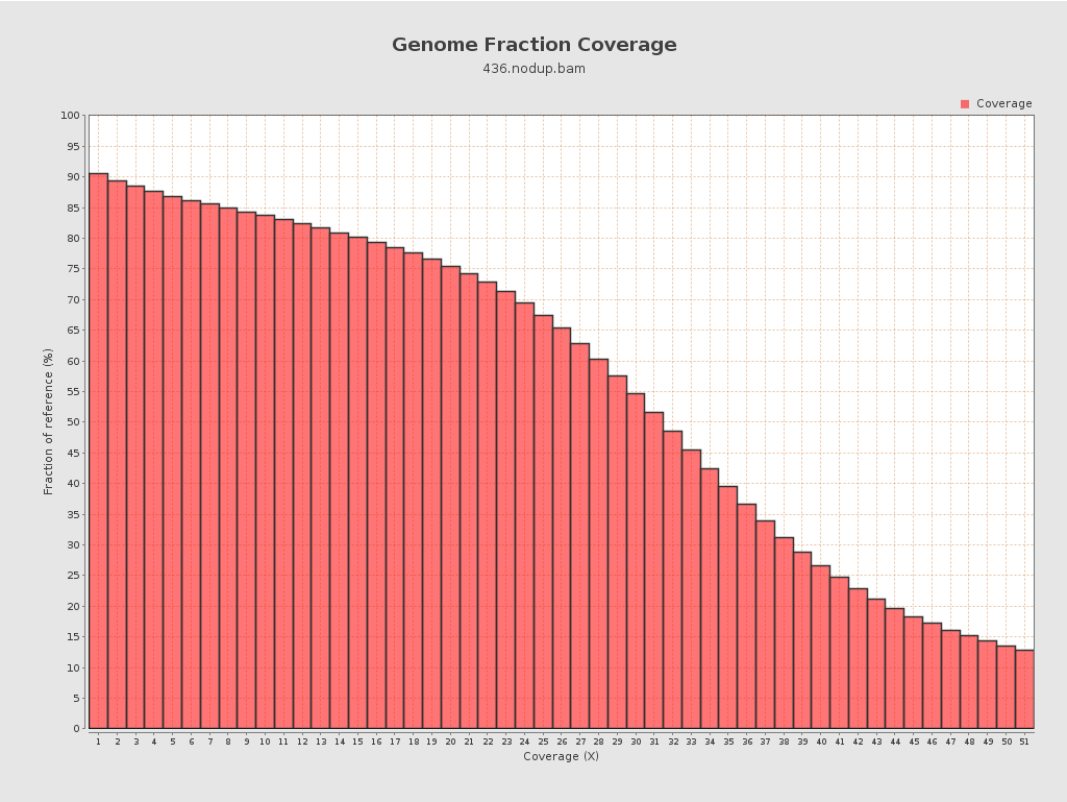
4. Results : Coverage Histogram



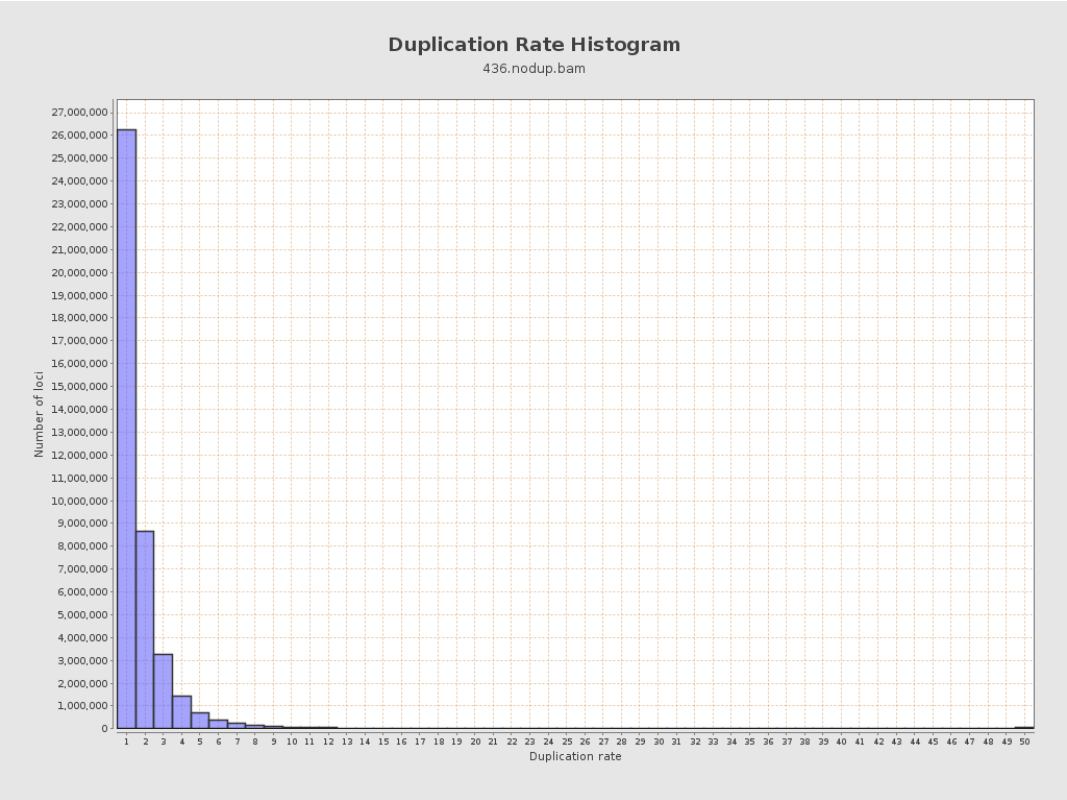
5. Results : Coverage Histogram (0-50X)



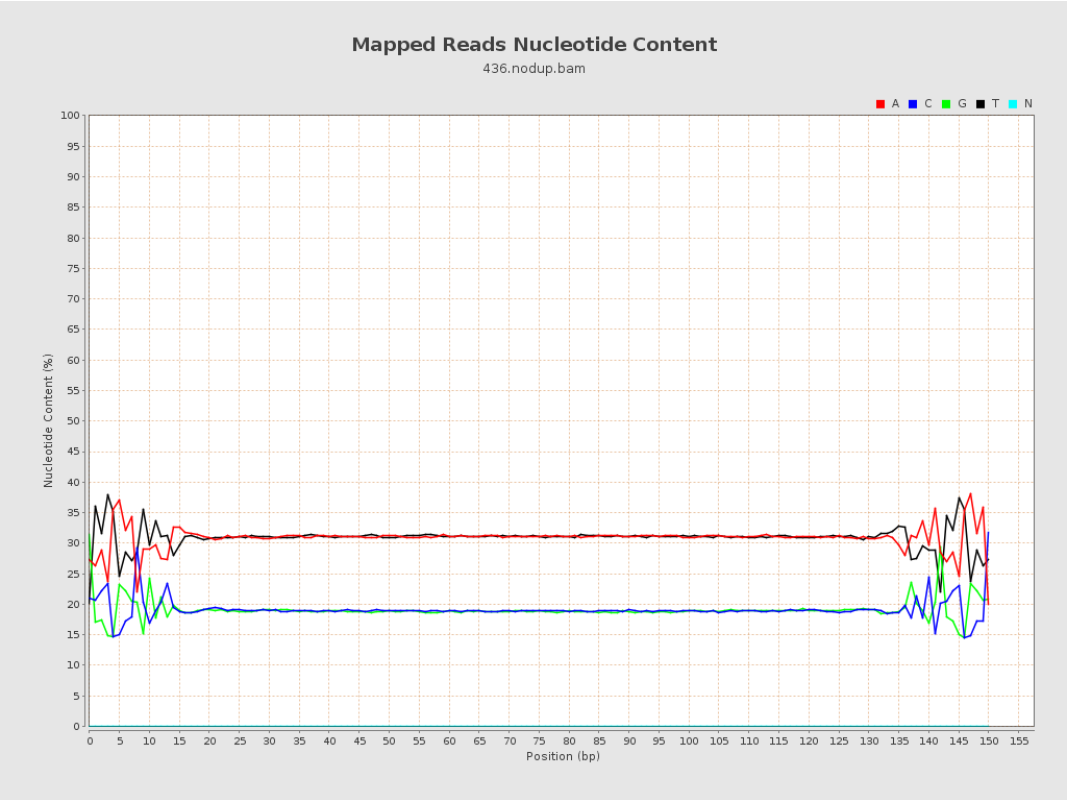
6. Results : Genome Fraction Coverage



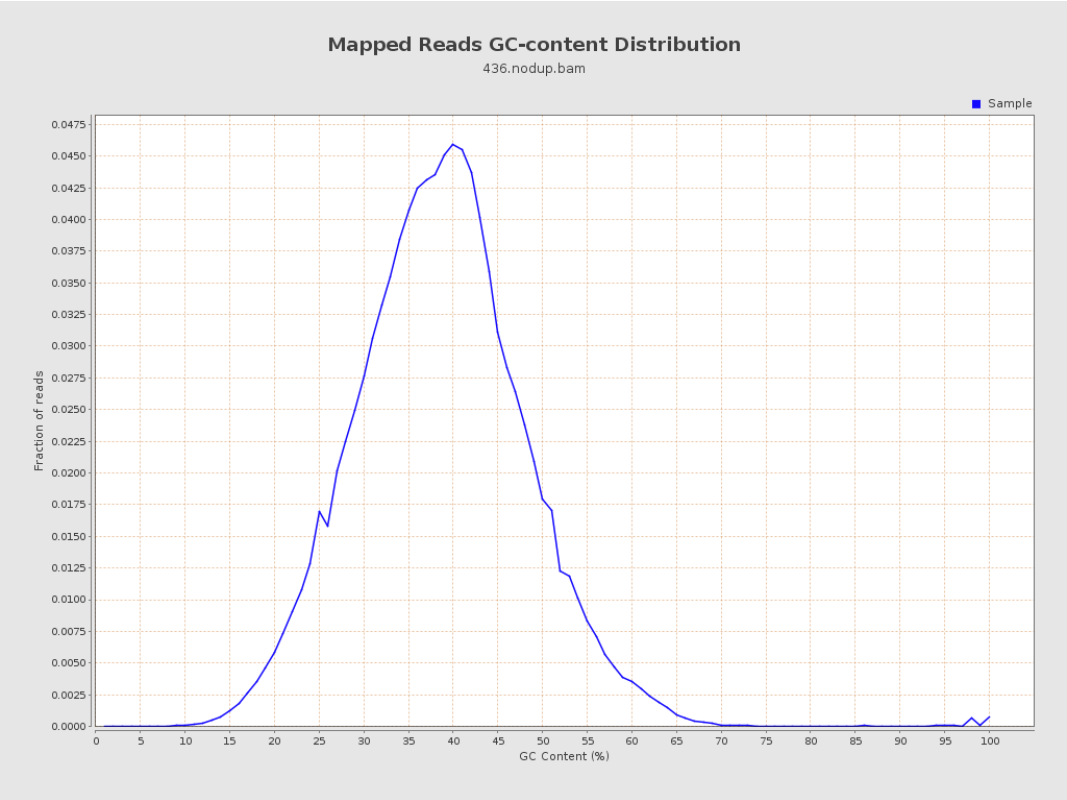
7. Results : Duplication Rate Histogram



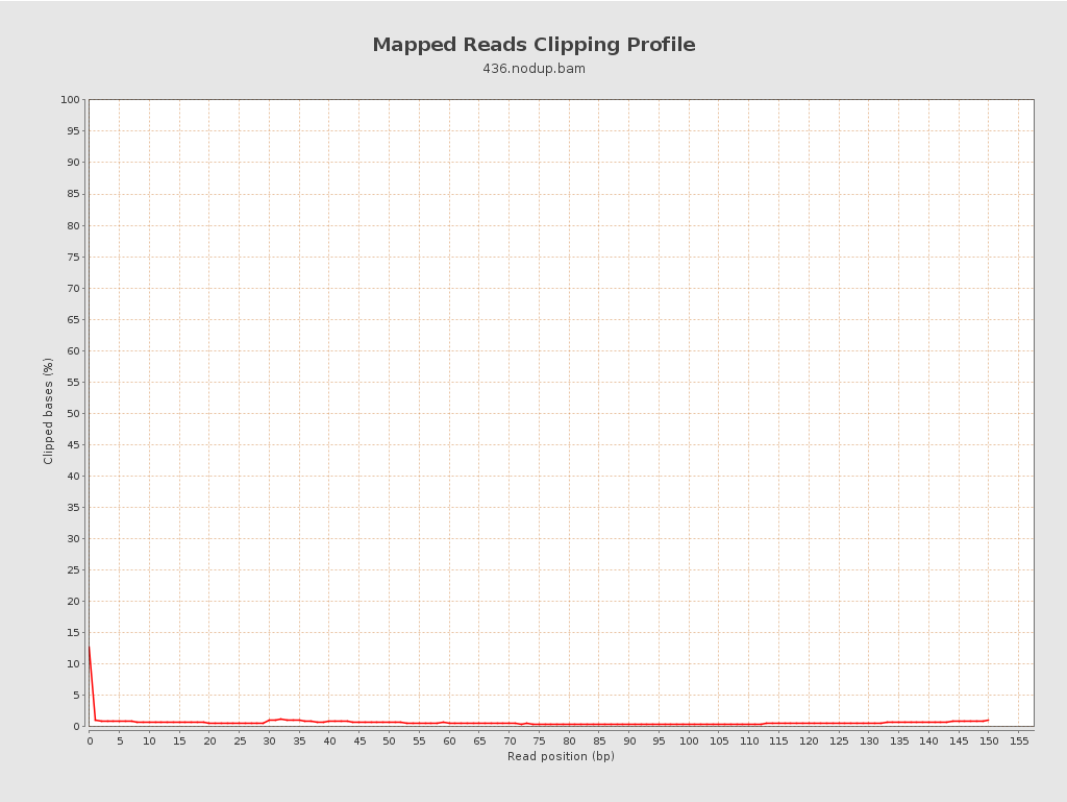
8. Results : Mapped Reads Nucleotide Content



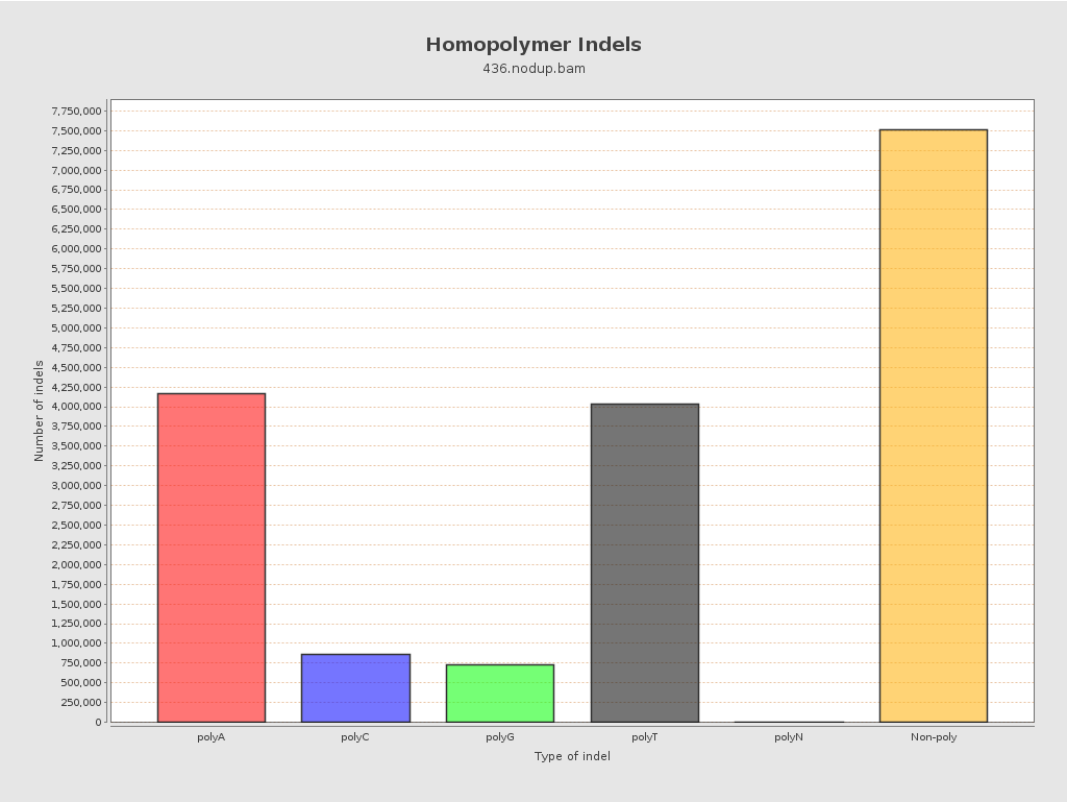
9. Results : Mapped Reads GC-content Distribution



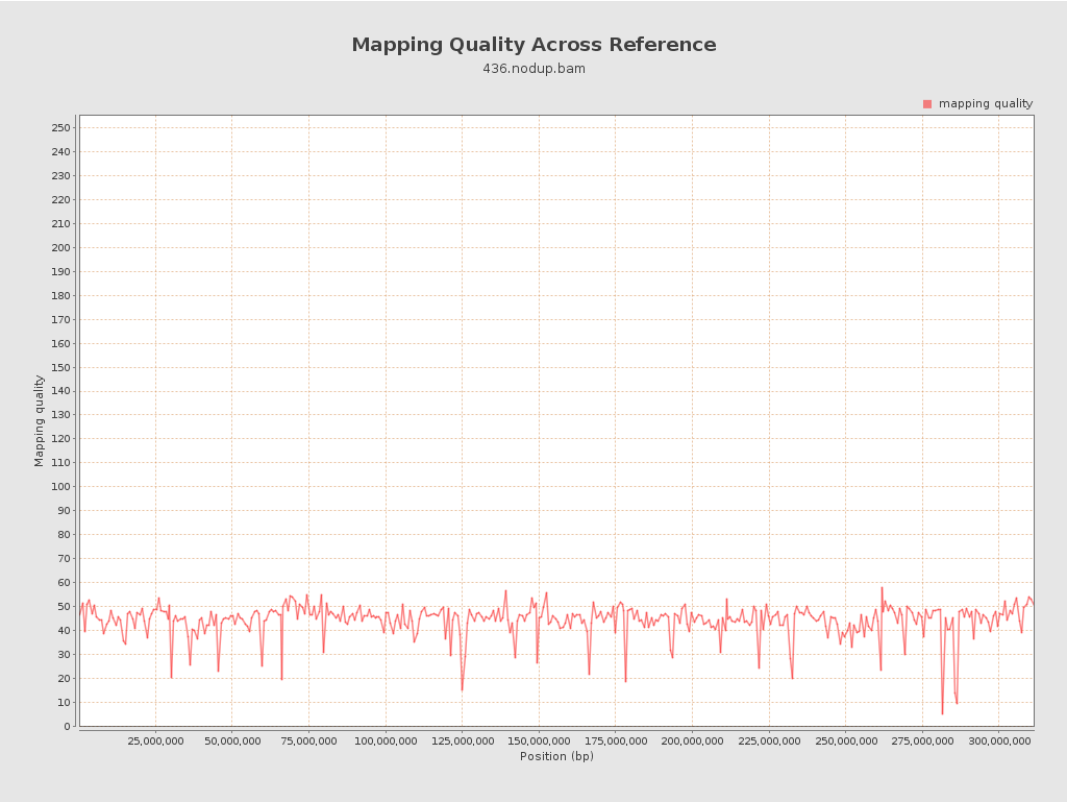
10. Results : Mapped Reads Clipping Profile



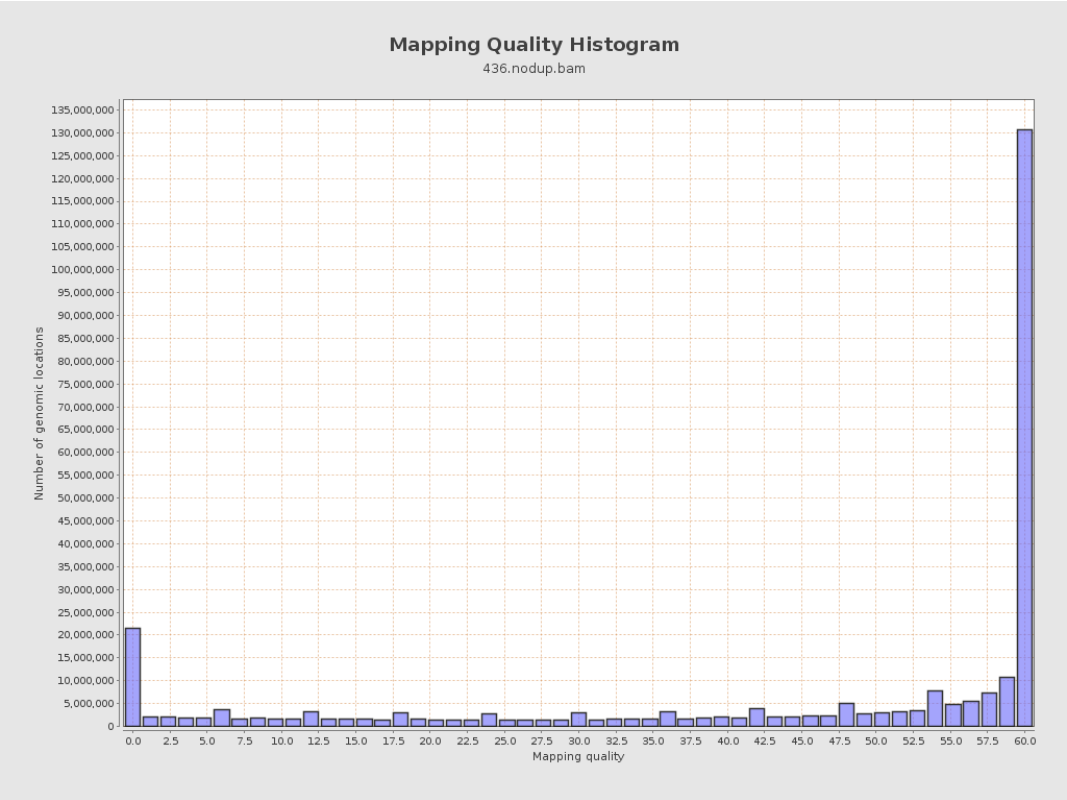
11. Results : Homopolymer Indels



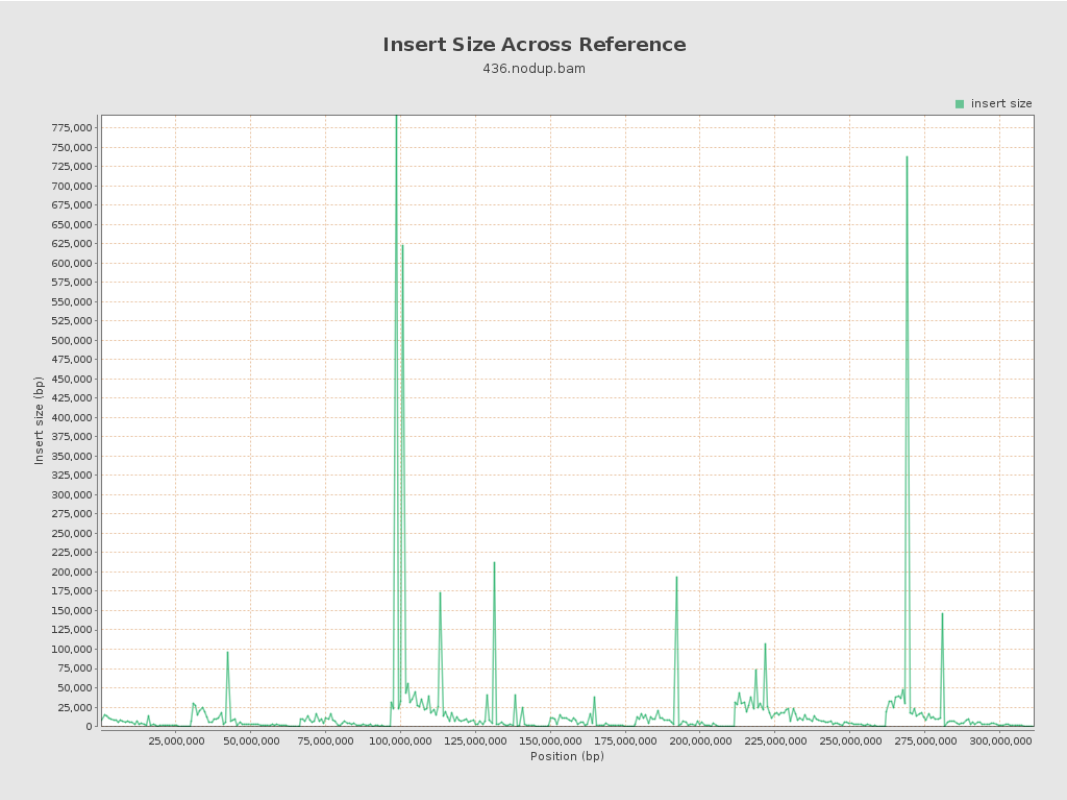
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram