Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/435.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/435.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_186/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_186_S276_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_186/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_186_S276_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	52,087,549
Mapped reads	48,309,306 / 92.75%
Unmapped reads	3,778,243 / 7.25%
Mapped paired reads	48,309,306 / 92.75%
Mapped reads, first in pair	24,161,135 / 46.39%
Mapped reads, second in pair	24,148,171 / 46.36%
Mapped reads, both in pair	47,075,183 / 90.38%
Mapped reads, singletons	1,234,123 / 2.37%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	7,572,569 / 14.54%
Clipped reads	10,821,702 / 20.78%

2.2. ACGT Content

Number/percentage of A's	2,070,578,013 / 30.97%
Number/percentage of C's	1,272,617,965 / 19.03%
Number/percentage of T's	2,071,332,652 / 30.98%
Number/percentage of G's	1,272,304,711 / 19.03%
Number/percentage of N's	26,616 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	21.513
Standard Deviation	169.4097

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Insert size

Mean	248,708.9
Standard Deviation	2,390,886.48
P25/Median/P75	337 / 441 / 580

2.6. Mismatches and indels

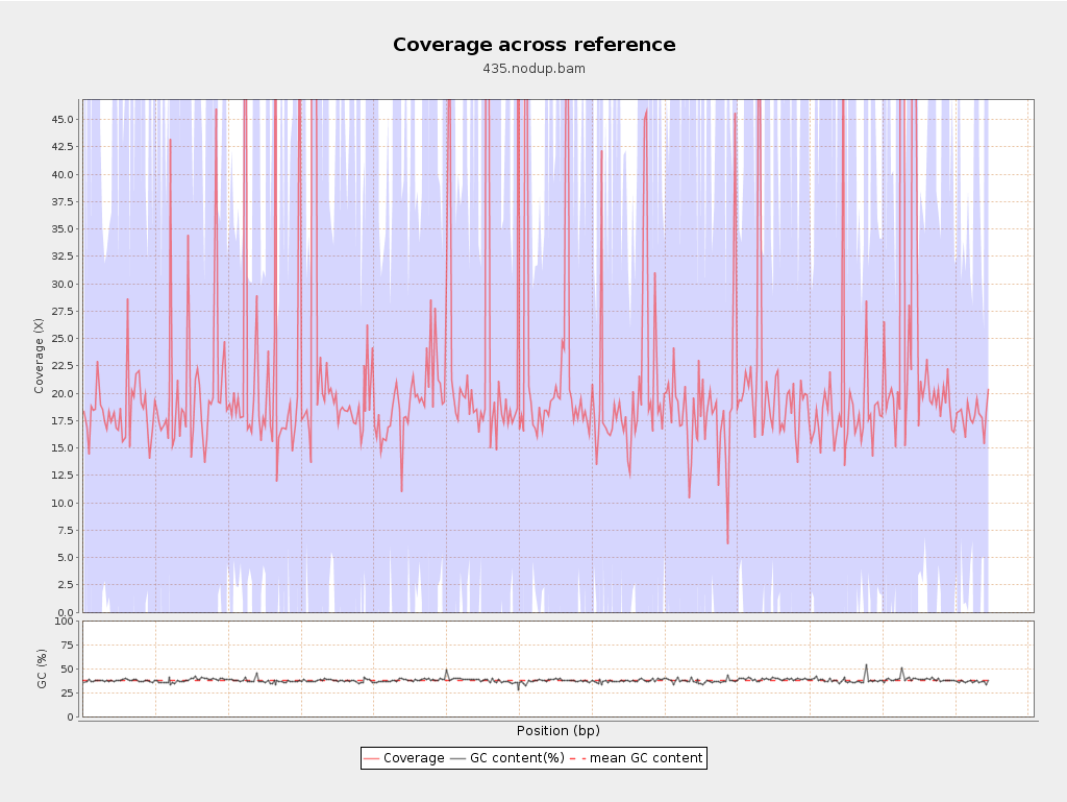
General error rate	2.33%
Mismatches	143,006,914
Insertions	4,667,827
Mapped reads with at least one insertion	8.64%
Deletions	4,616,517
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56.71%

2.7. Chromosome stats

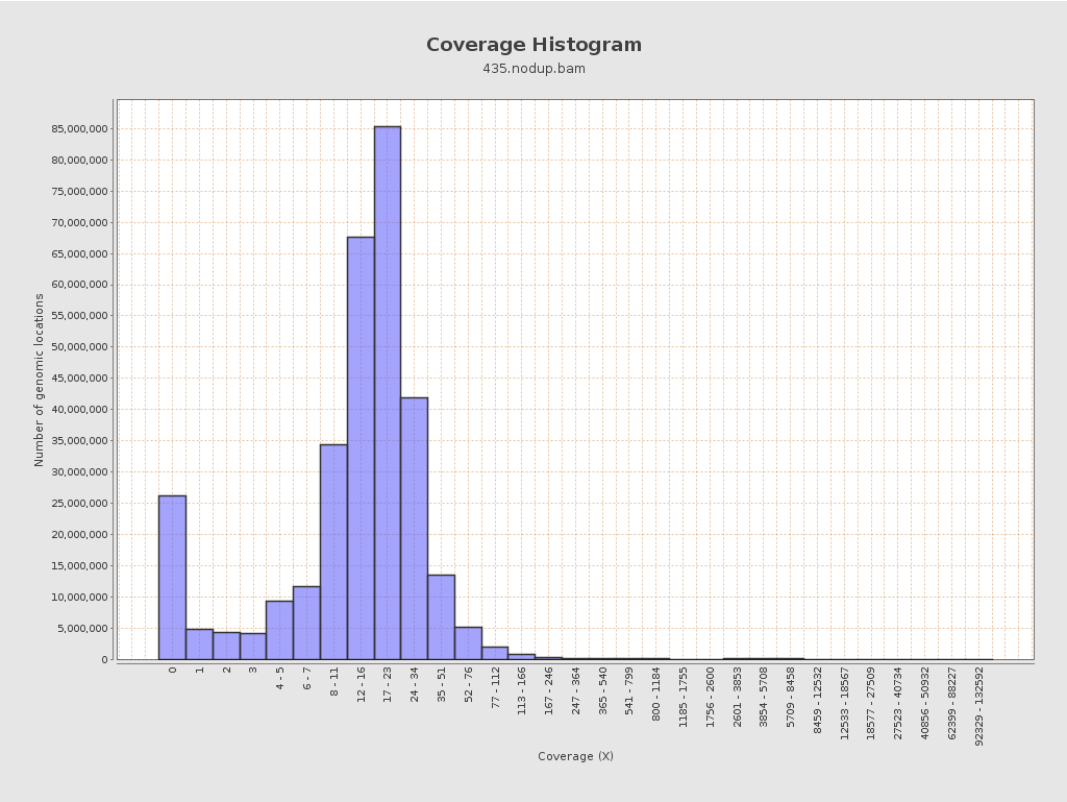
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	542429819	18.2487	62.6518

LT669789.1	36598175	789129155	21.562	178.0084
LT669790.1	30422129	758808193	24.9426	220.4705
LT669791.1	52758100	1110153563	21.0423	173.4502
LT669792.1	28376109	619854963	21.8443	183.9478
LT669793.1	33388210	659464180	19.7514	115.6424
LT669794.1	50579949	1013811567	20.0437	142.902
LT669795.1	49795044	1210718505	24.314	208.3144

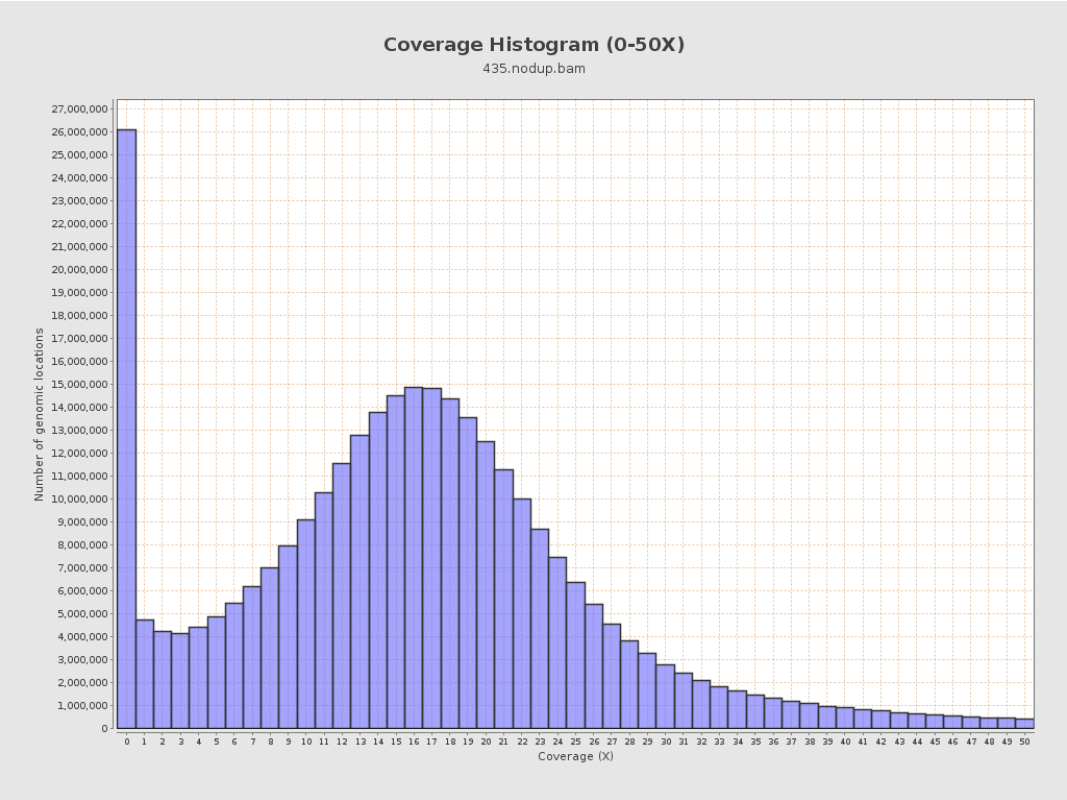
3. Results : Coverage across reference



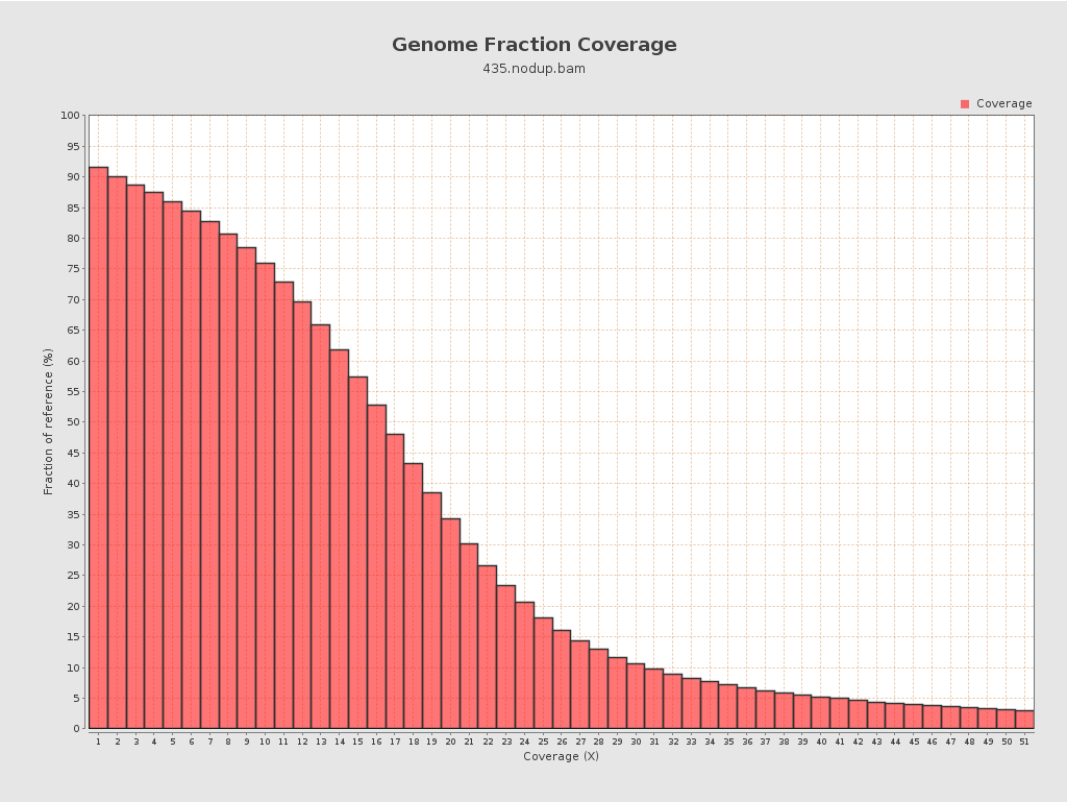
4. Results : Coverage Histogram



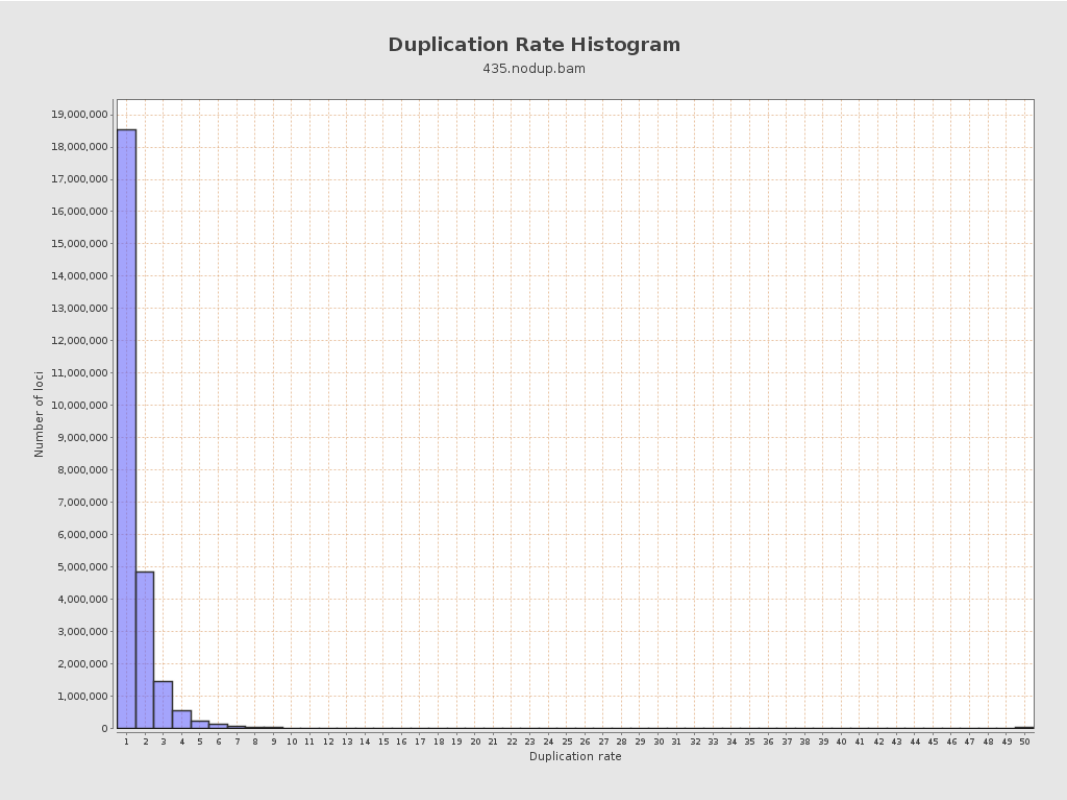
5. Results : Coverage Histogram (0-50X)



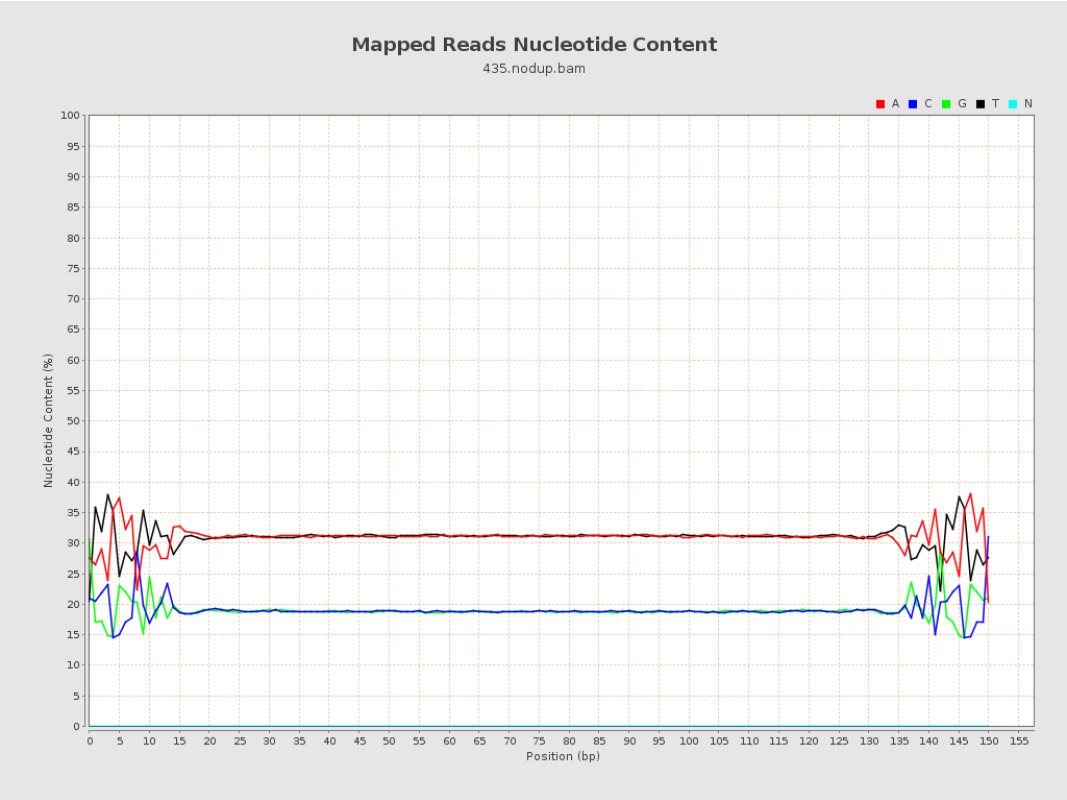
6. Results : Genome Fraction Coverage



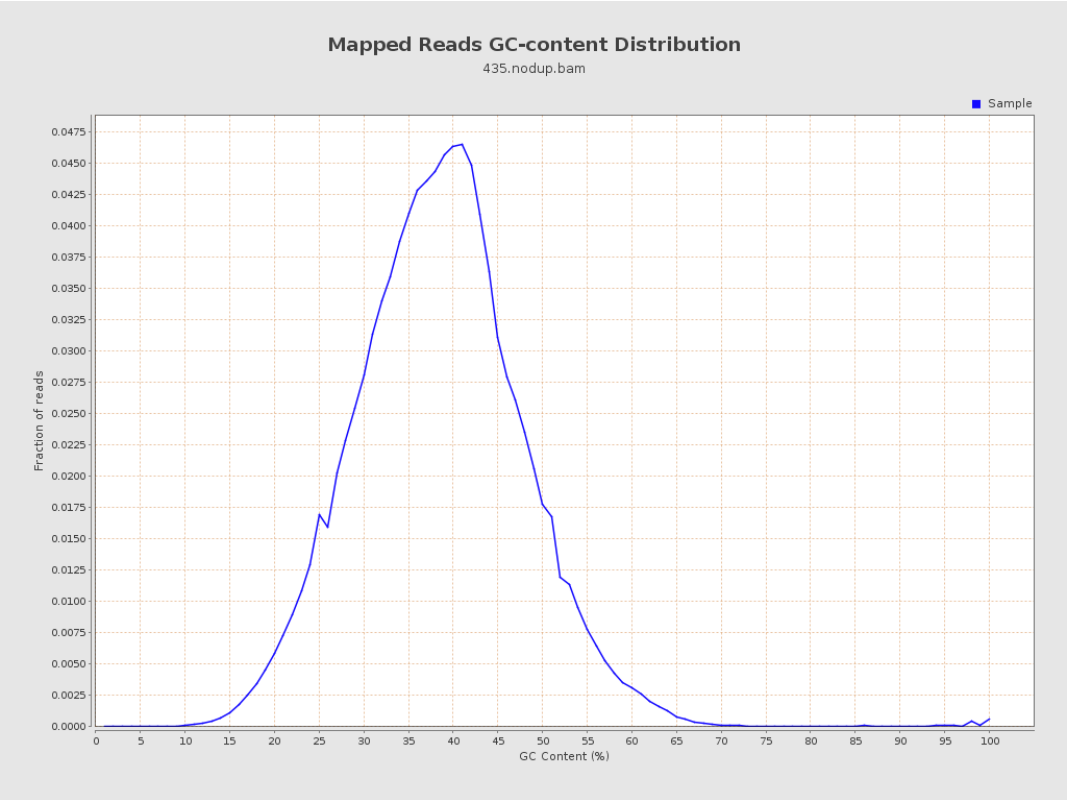
7. Results : Duplication Rate Histogram



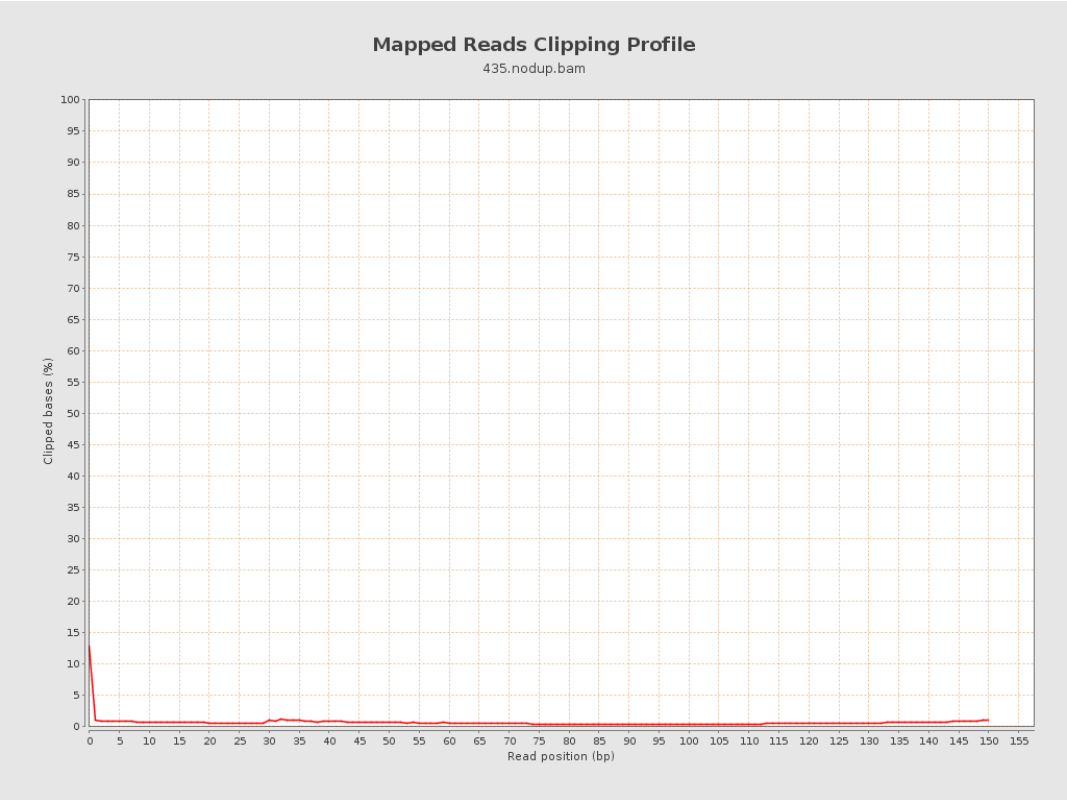
8. Results : Mapped Reads Nucleotide Content



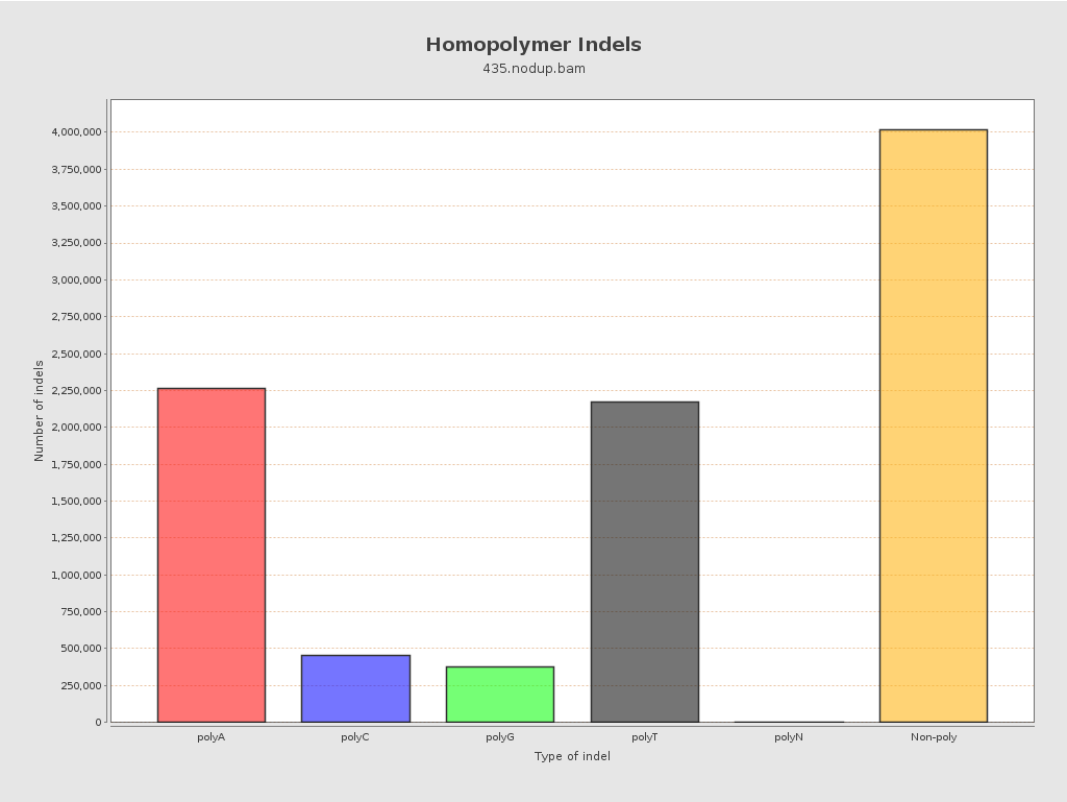
9. Results : Mapped Reads GC-content Distribution



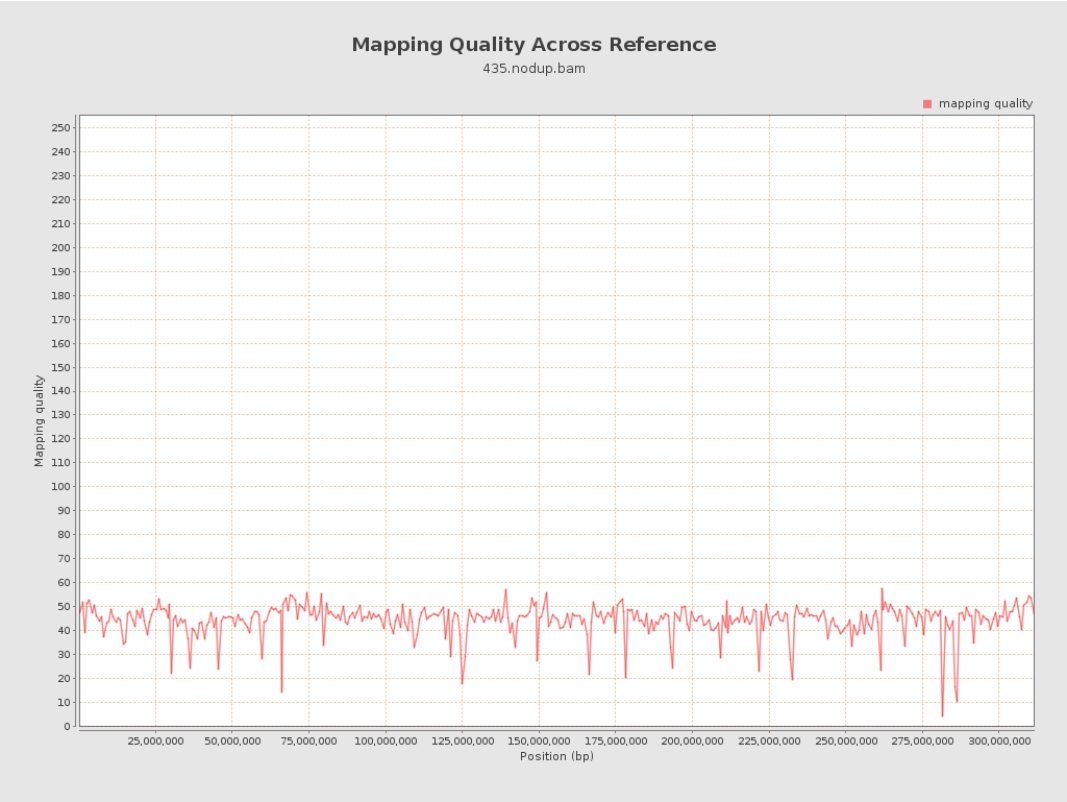
10. Results : Mapped Reads Clipping Profile



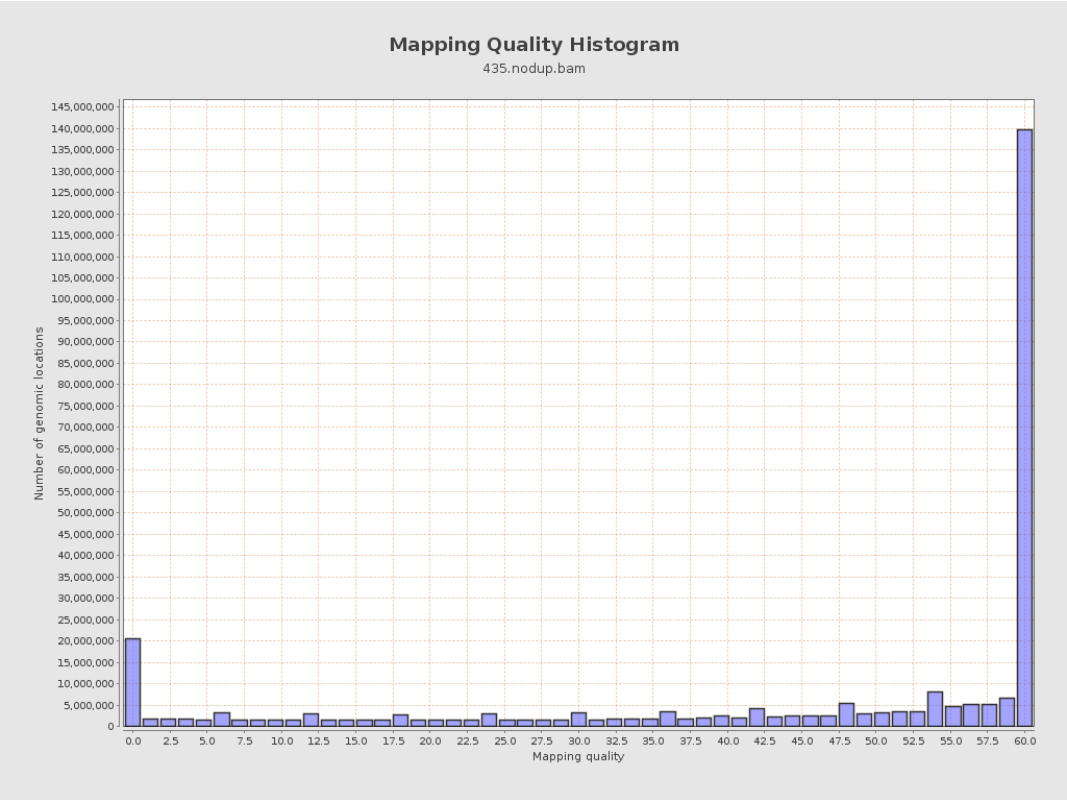
11. Results : Homopolymer Indels



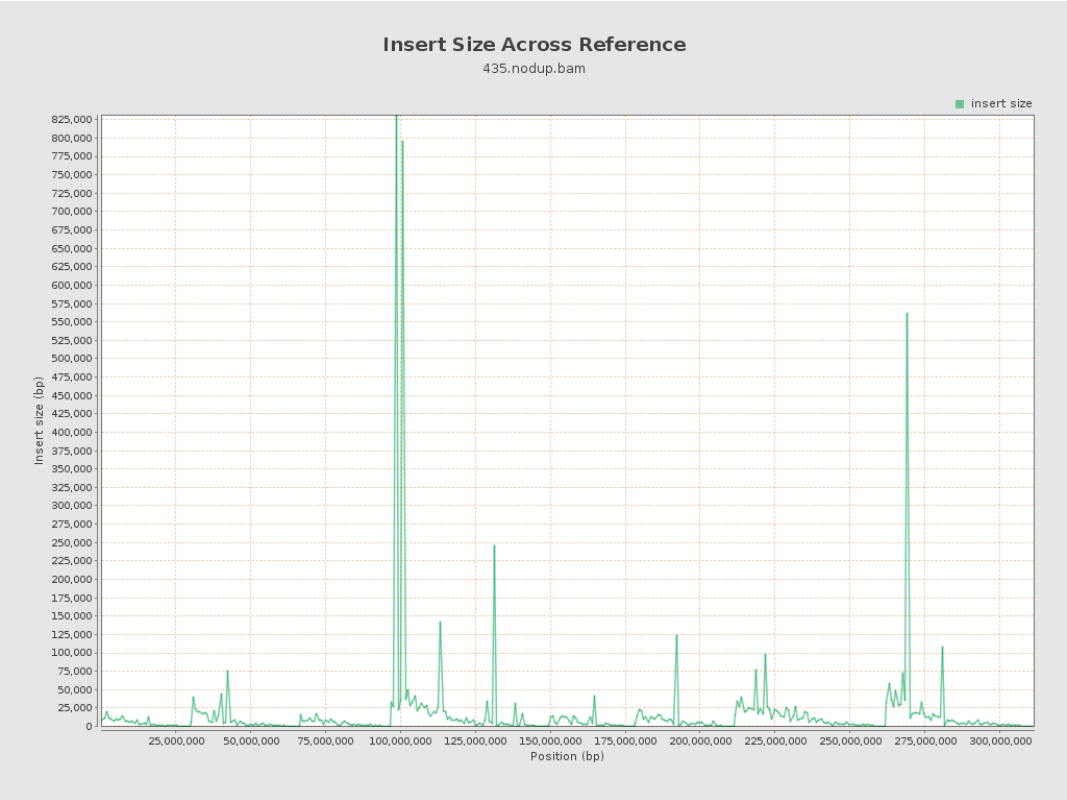
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram