Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/424.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/424.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_228/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_228_S309_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_228/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_228_S309_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:17 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	77,622,296
Mapped reads	70,920,812 / 91.37%
Unmapped reads	6,701,484 / 8.63%
Mapped paired reads	70,920,812 / 91.37%
Mapped reads, first in pair	35,541,481 / 45.79%
Mapped reads, second in pair	35,379,331 / 45.58%
Mapped reads, both in pair	68,814,602 / 88.65%
Mapped reads, singletons	2,106,210 / 2.71%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	11,599,095 / 14.94%
Clipped reads	16,853,486 / 21.71%

2.2. ACGT Content

Number/percentage of A's	3,015,492,778 / 30.99%
Number/percentage of C's	1,850,179,359 / 19.01%
Number/percentage of T's	3,016,294,195 / 31%
Number/percentage of G's	1,848,573,315 / 19%
Number/percentage of N's	35,982 / 0%
GC Percentage	38.01%

2.3. Coverage

Mean	31.3037
Standard Deviation	283.4638

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Insert size

Mean	244,461.22
Standard Deviation	2,362,255.53
P25/Median/P75	319 / 420 / 549

2.6. Mismatches and indels

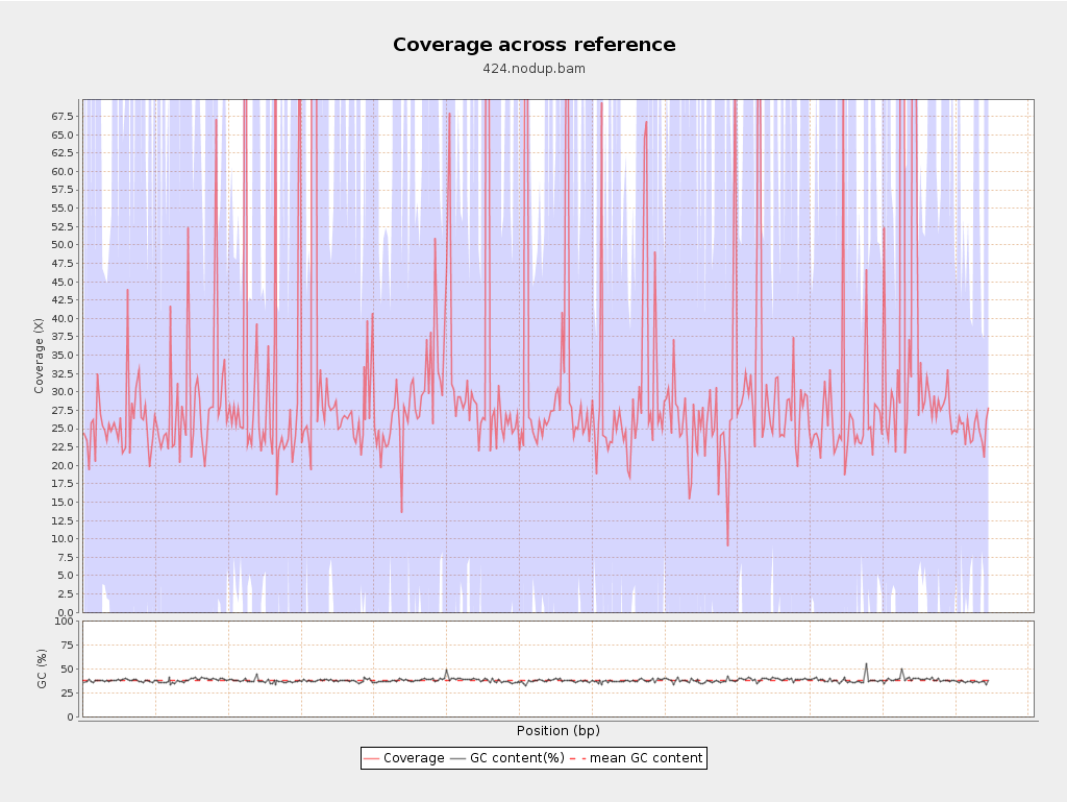
General error rate	2.33%
Mismatches	207,582,016
Insertions	6,945,777
Mapped reads with at least one insertion	8.74%
Deletions	6,701,981
Mapped reads with at least one deletion	8.41%
Homopolymer indels	57.4%

2.7. Chromosome stats

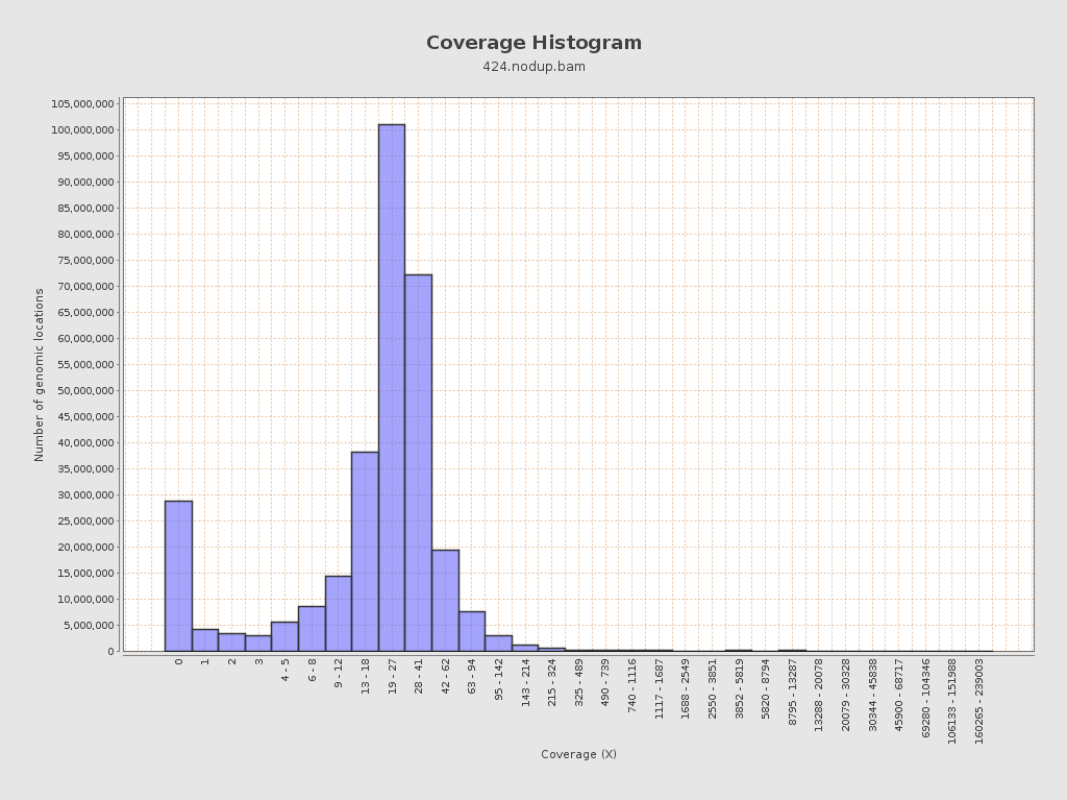
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	758188019	25.5073	100.3308

LT669789.1	36598175	1123367693	30.6946	267.6739
LT669790.1	30422129	1137757021	37.399	393.3503
LT669791.1	52758100	1636559340	31.0201	284.434
LT669792.1	28376109	897345635	31.6233	325.4622
LT669793.1	33388210	950115463	28.4566	189.027
LT669794.1	50579949	1476169500	29.1849	229.3739
LT669795.1	49795044	1776040062	35.667	355.1503

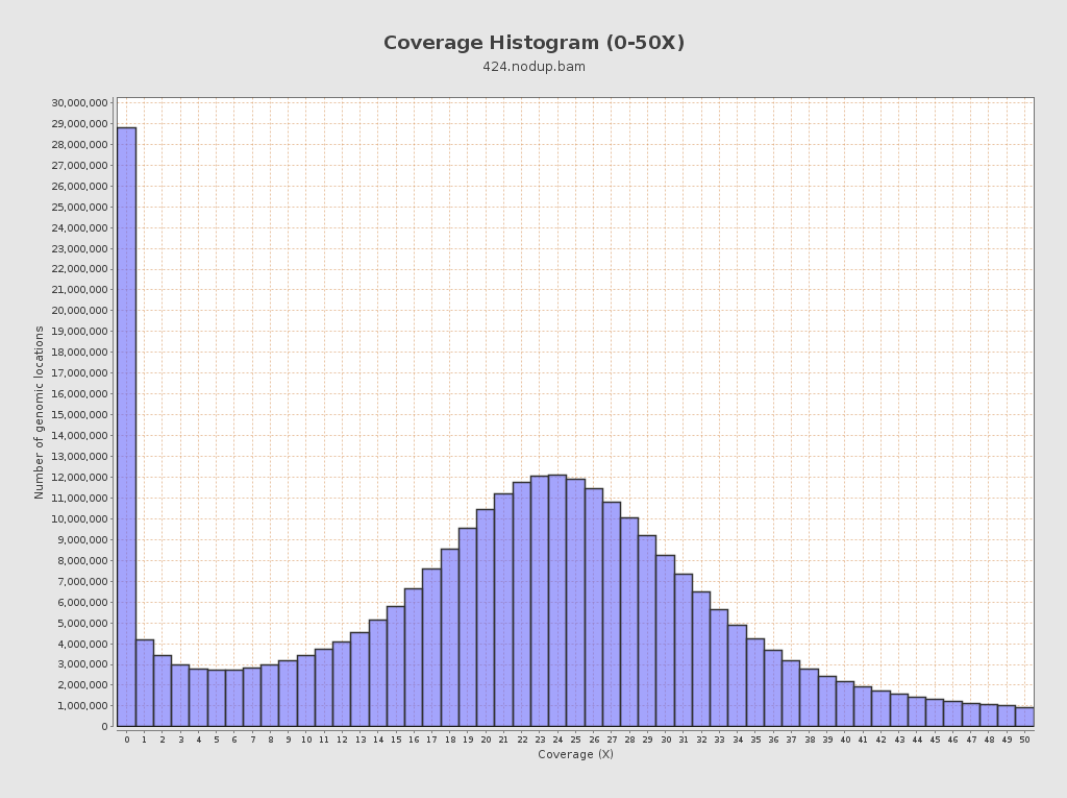
3. Results : Coverage across reference



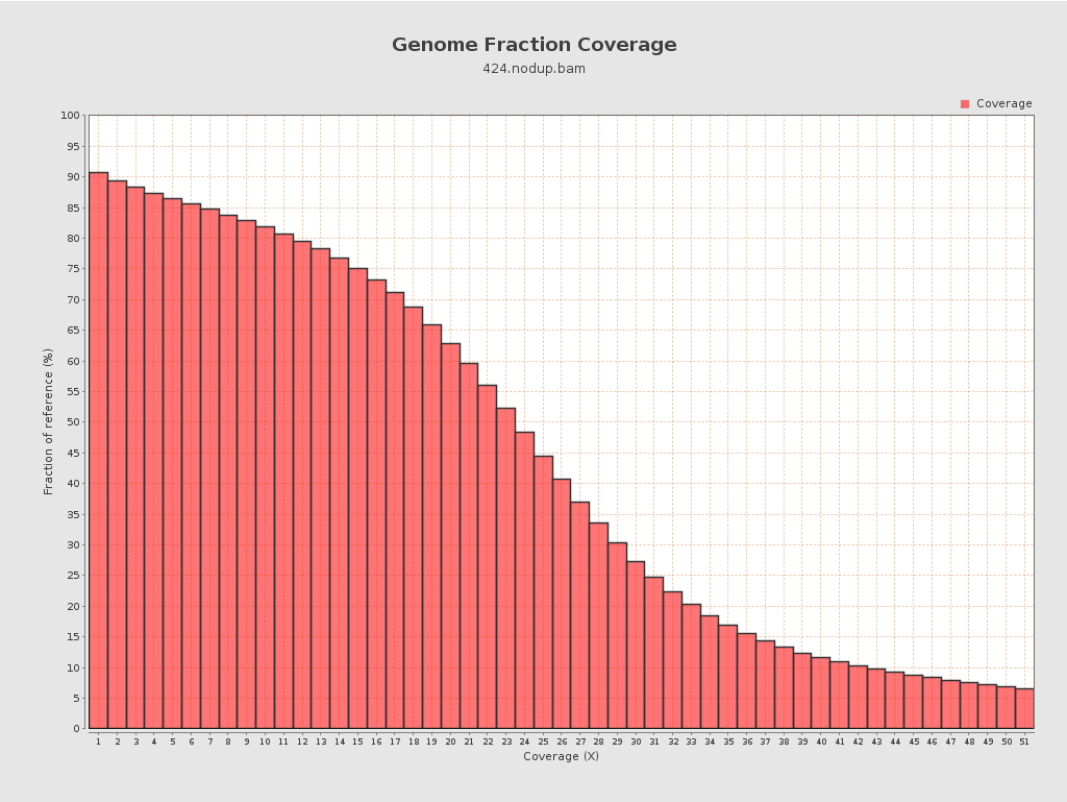
4. Results : Coverage Histogram



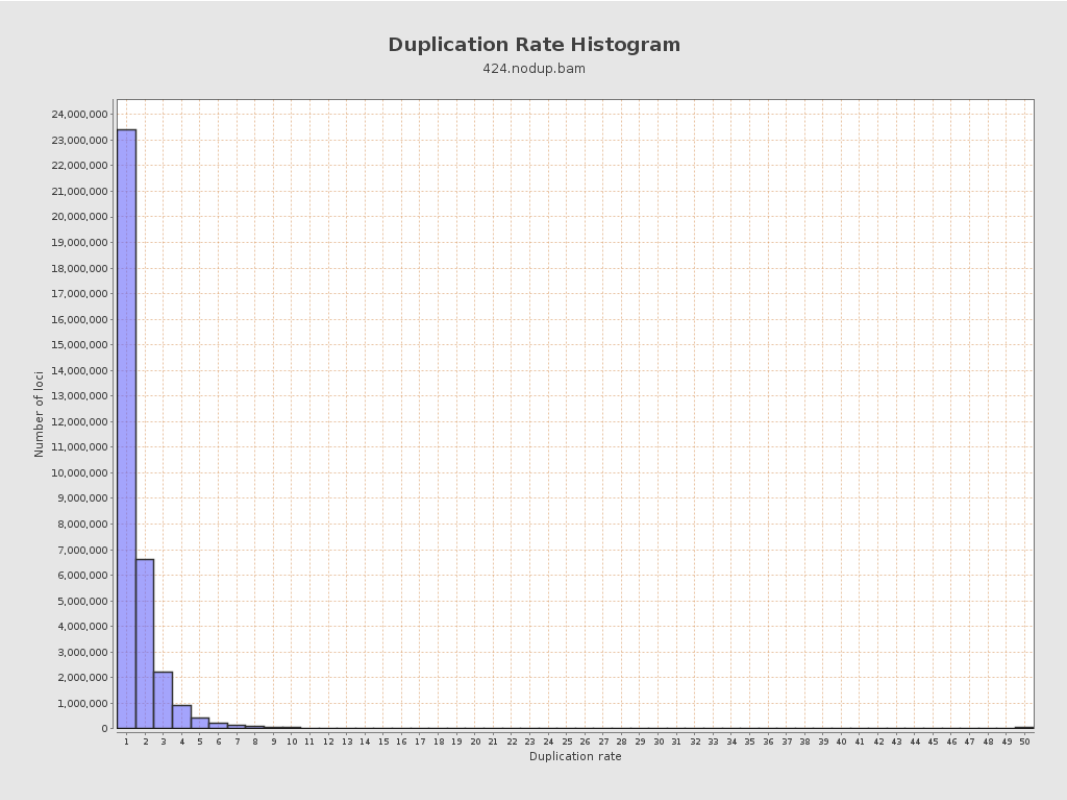
5. Results : Coverage Histogram (0-50X)



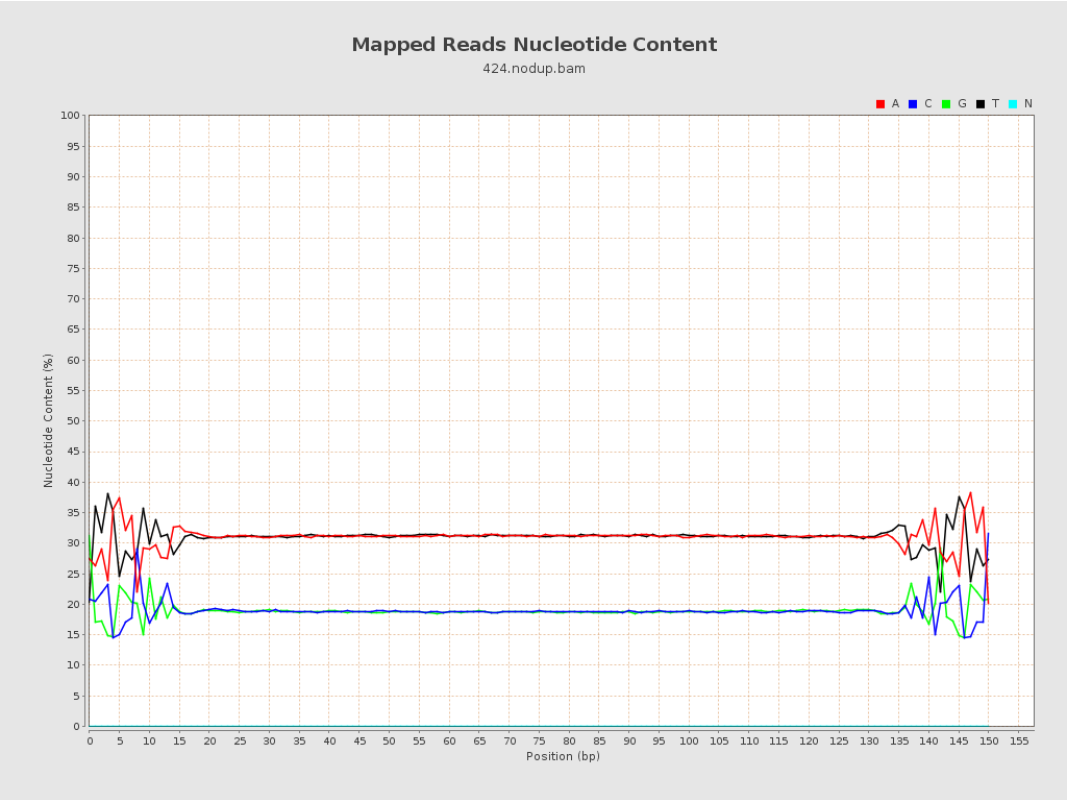
6. Results : Genome Fraction Coverage



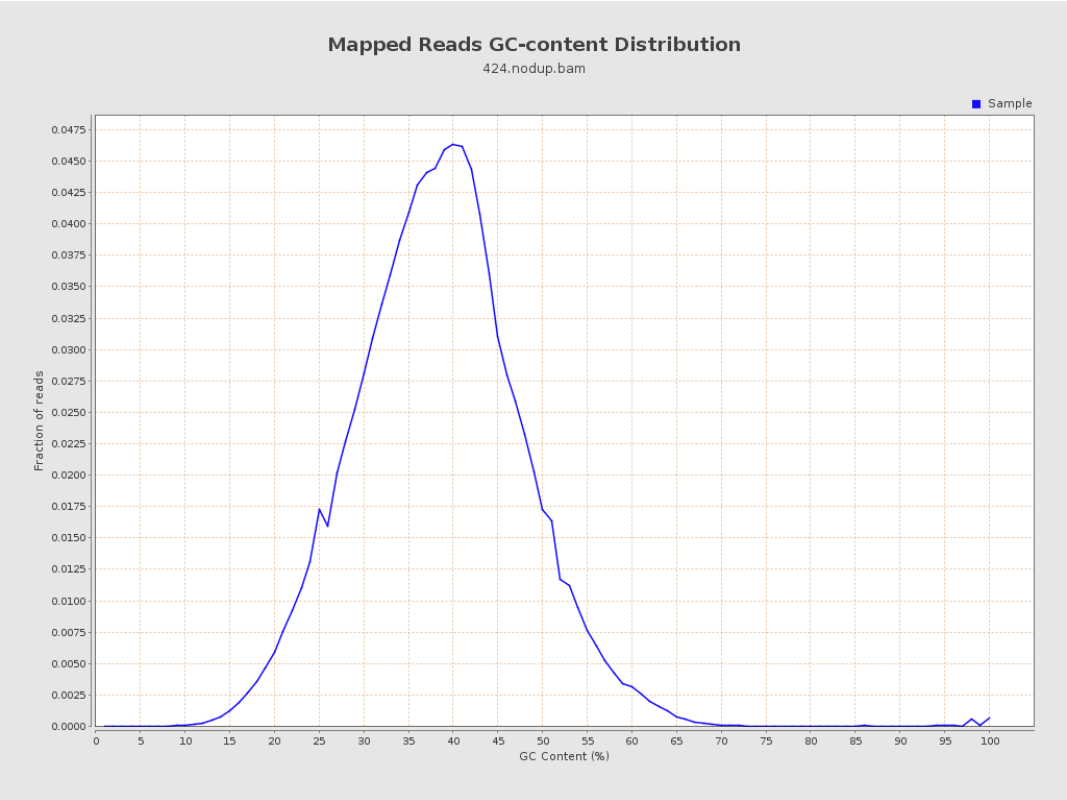
7. Results : Duplication Rate Histogram



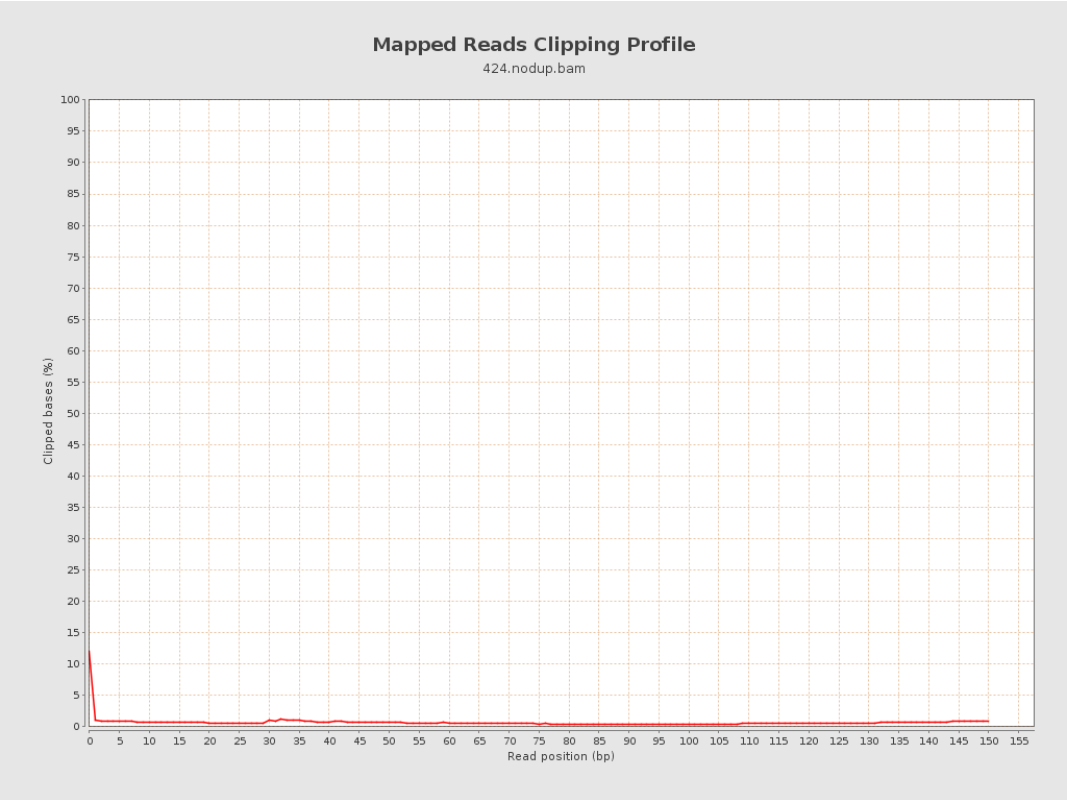
8. Results : Mapped Reads Nucleotide Content



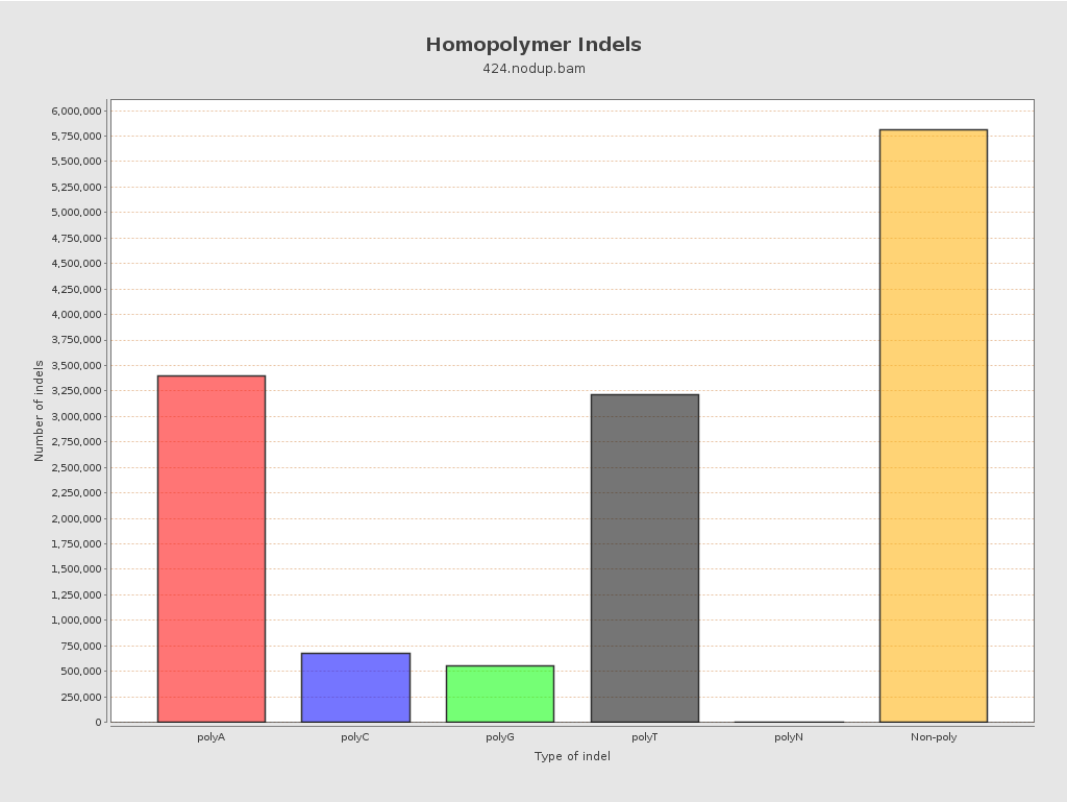
9. Results : Mapped Reads GC-content Distribution



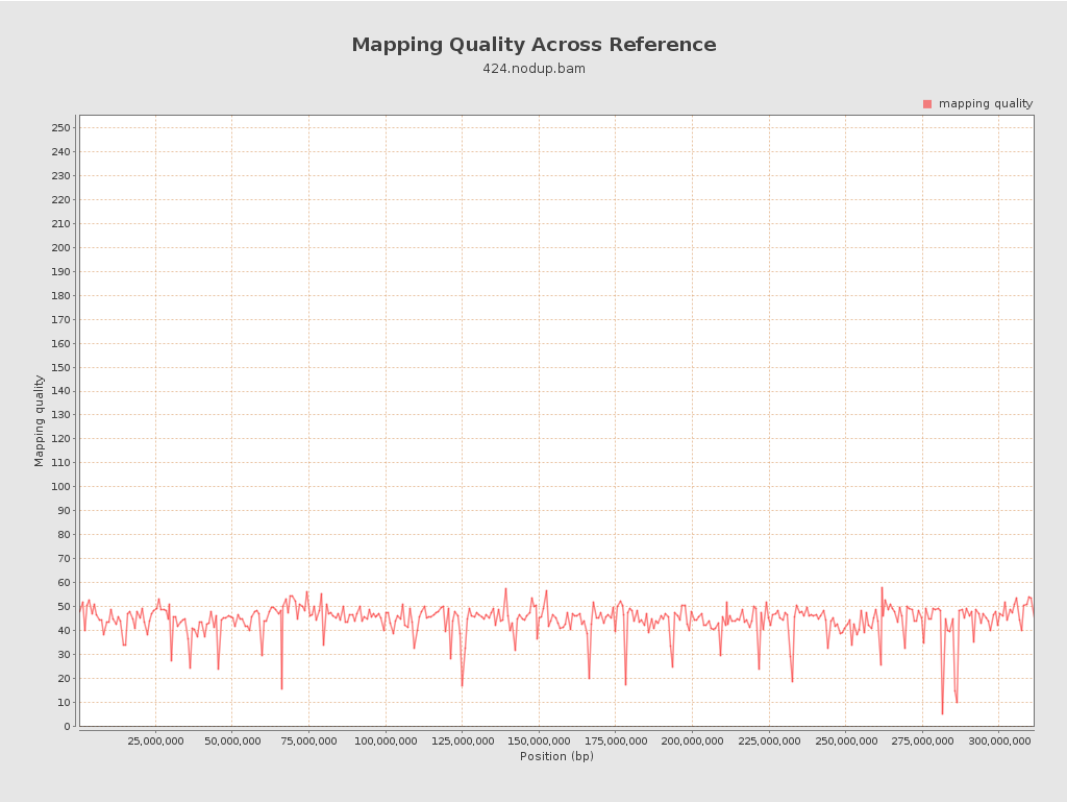
10. Results : Mapped Reads Clipping Profile



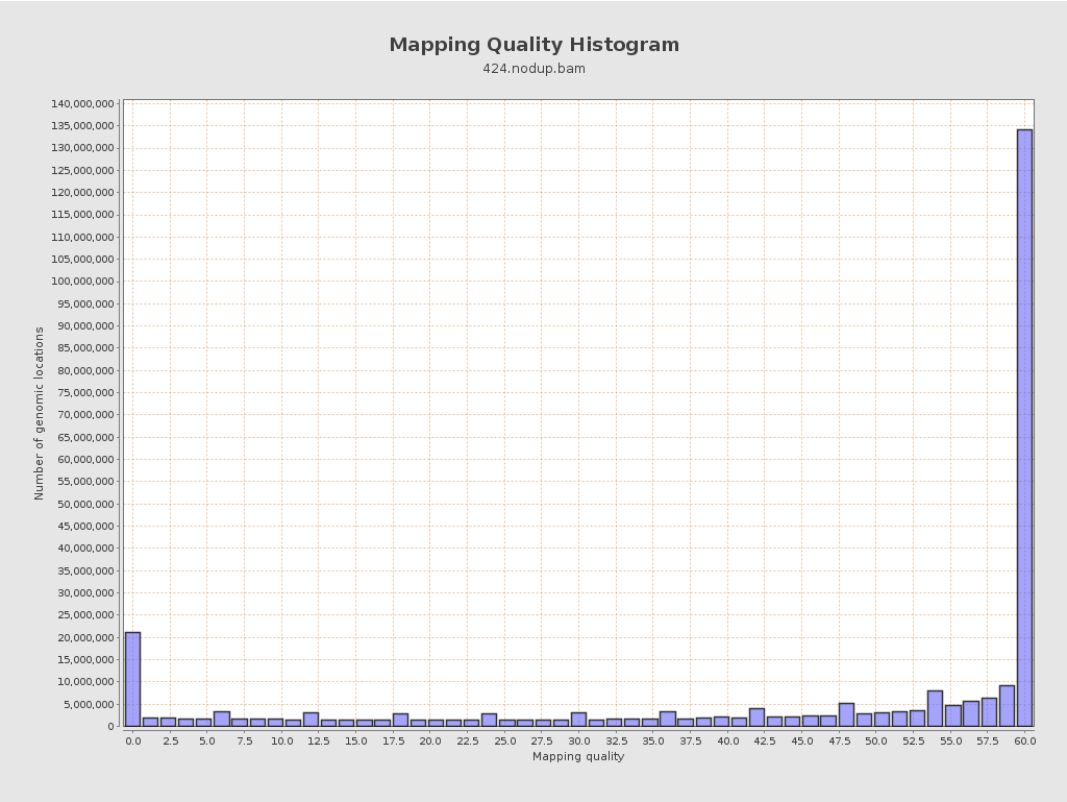
11. Results : Homopolymer Indels



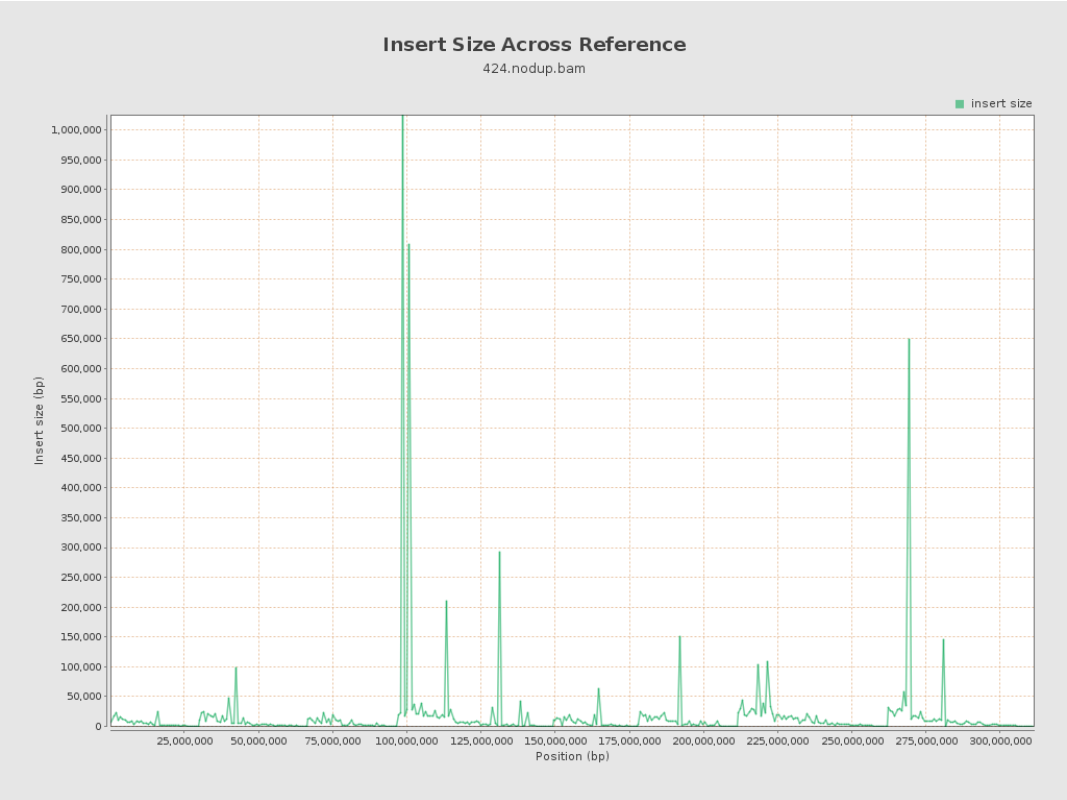
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram