Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1423
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1423 .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_285/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_285_S366_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_285/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_285_S366_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:31:57 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,762,409
Mapped reads	66,594,144 / 92.8%
Unmapped reads	5,168,265 / 7.2%
Mapped paired reads	66,594,144 / 92.8%
Mapped reads, first in pair	33,379,511 / 46.51%
Mapped reads, second in pair	33,214,633 / 46.28%
Mapped reads, both in pair	64,903,127 / 90.44%
Mapped reads, singletons	1,691,017 / 2.36%
Read min/max/mean length	30 / 151 / 147.93
Duplicated reads (flagged)	10,036,782 / 13.99%
Clipped reads	15,991,172 / 22.28%

2.2. ACGT Content

Number/percentage of A's	2,822,010,310 / 30.84%
Number/percentage of C's	1,750,545,061 / 19.13%
Number/percentage of T's	2,826,106,335 / 30.89%
Number/percentage of G's	1,751,582,498 / 19.14%
Number/percentage of N's	34,064 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	29.4419
Standard Deviation	250.021

2.4. Mapping Quality

Mean Mapping Quality	43.55

2.5. Insert size

Mean	256,031.76
Standard Deviation	2,415,130.86
P25/Median/P75	319 / 419 / 546

2.6. Mismatches and indels

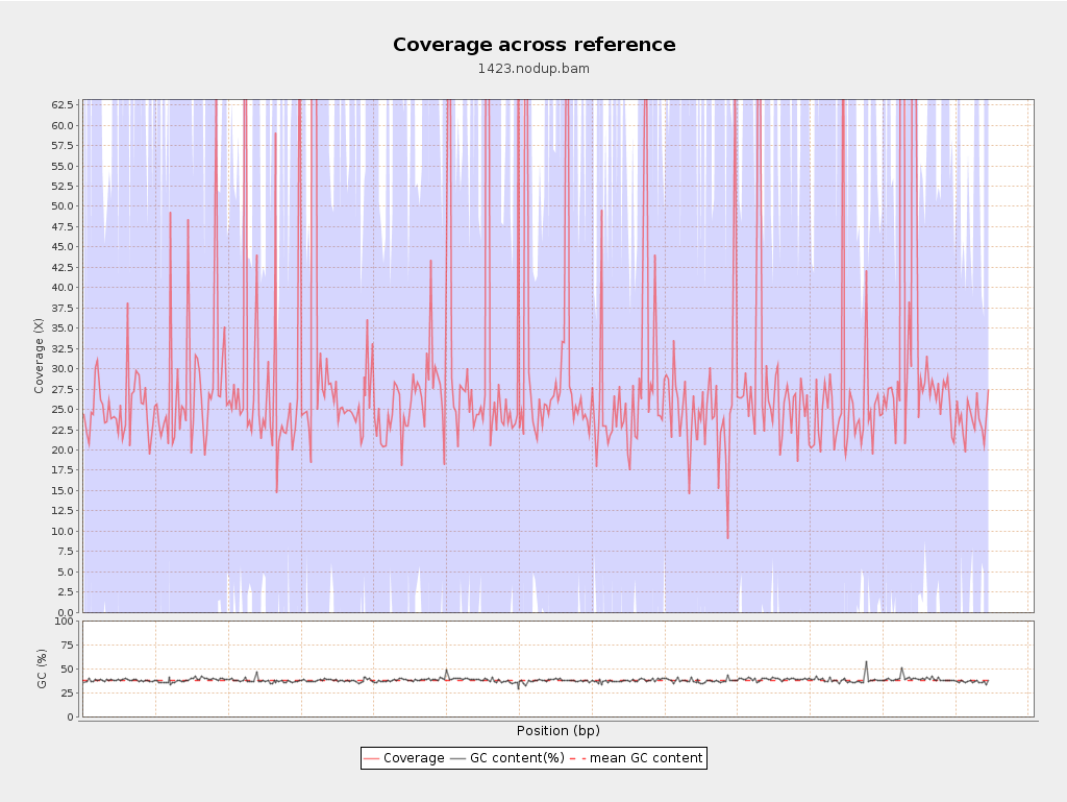
General error rate	2.42%
Mismatches	203,043,473
Insertions	6,538,436
Mapped reads with at least one insertion	8.77%
Deletions	6,585,193
Mapped reads with at least one deletion	8.74%
Homopolymer indels	56.25%

2.7. Chromosome stats

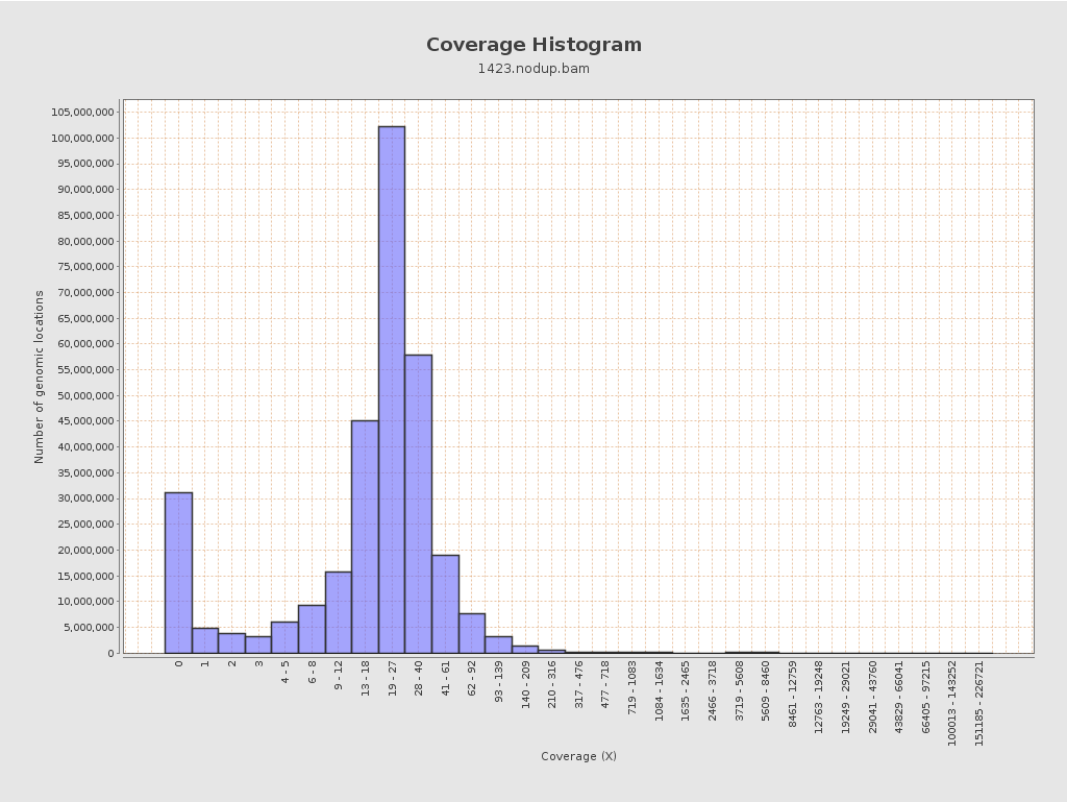
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	740525274	24.9131	98.1844

LT669789.1	36598175	1081193204	29.5423	254.4948
LT669790.1	30422129	1035455886	34.0363	304.5176
LT669791.1	52758100	1515606261	28.7275	254.6918
LT669792.1	28376109	843092304	29.7113	250.276
LT669793.1	33388210	908559816	27.212	212.3473
LT669794.1	50579949	1401780849	27.7142	218.4857
LT669795.1	49795044	1649132308	33.1184	313.0812

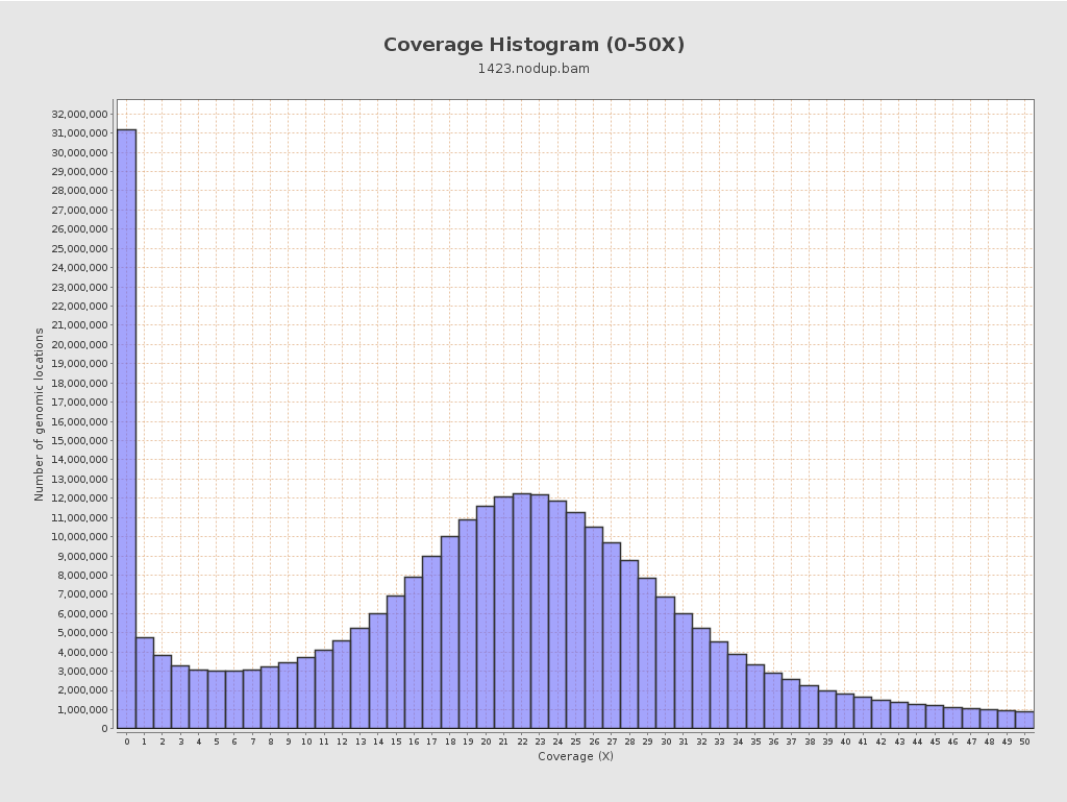
3. Results : Coverage across reference



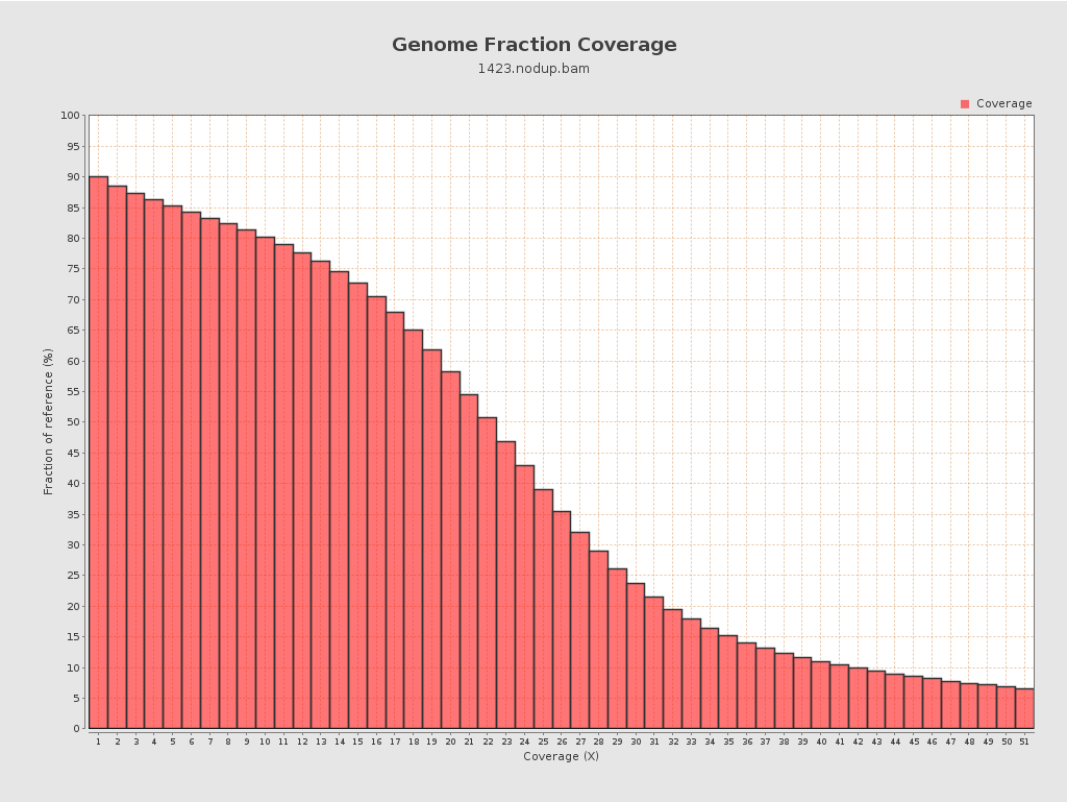
4. Results : Coverage Histogram



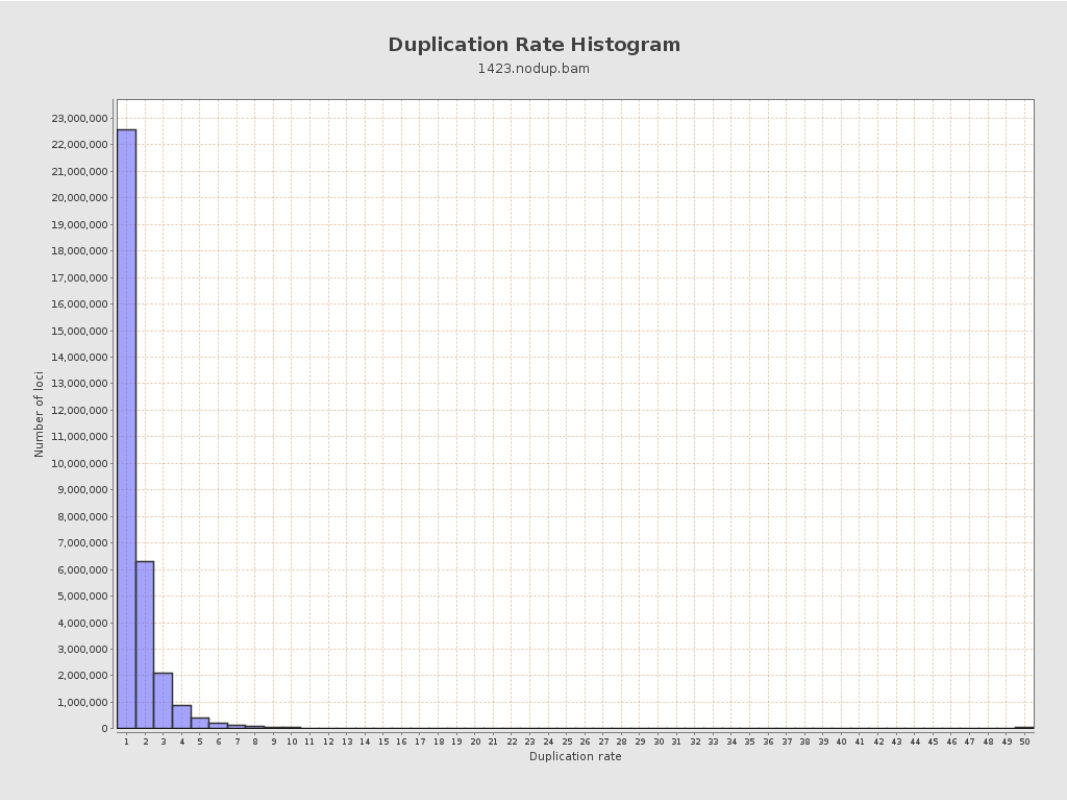
5. Results : Coverage Histogram (0-50X)



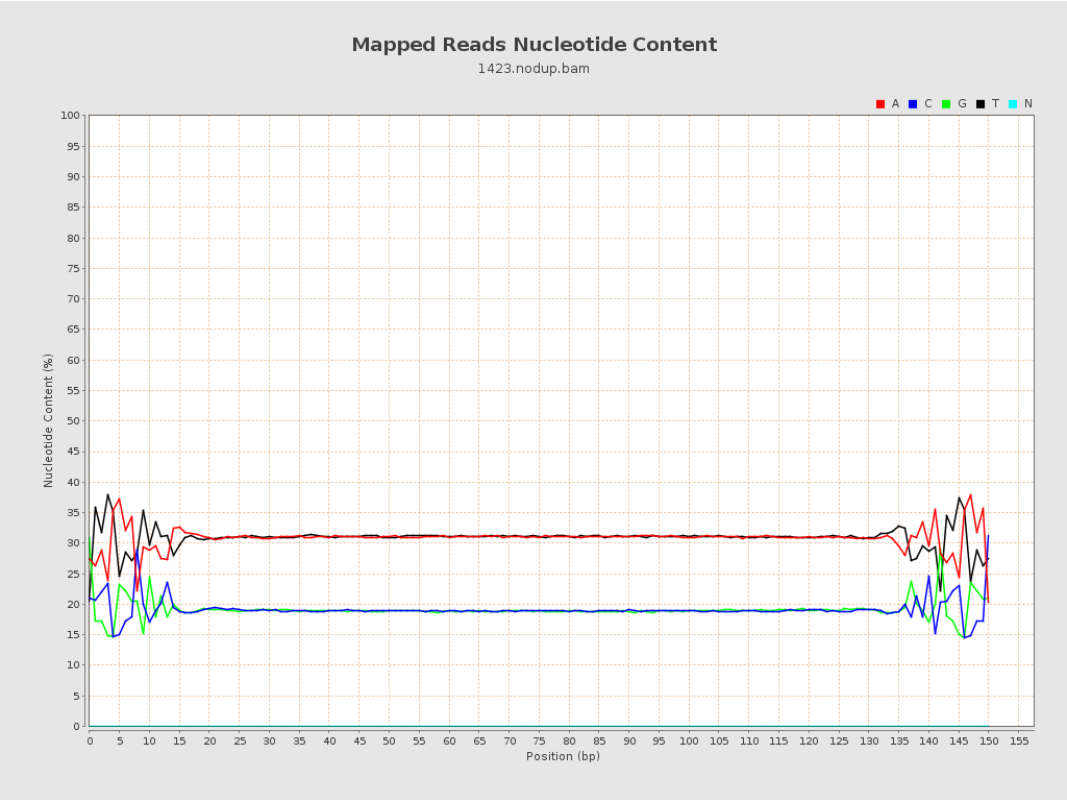
6. Results : Genome Fraction Coverage



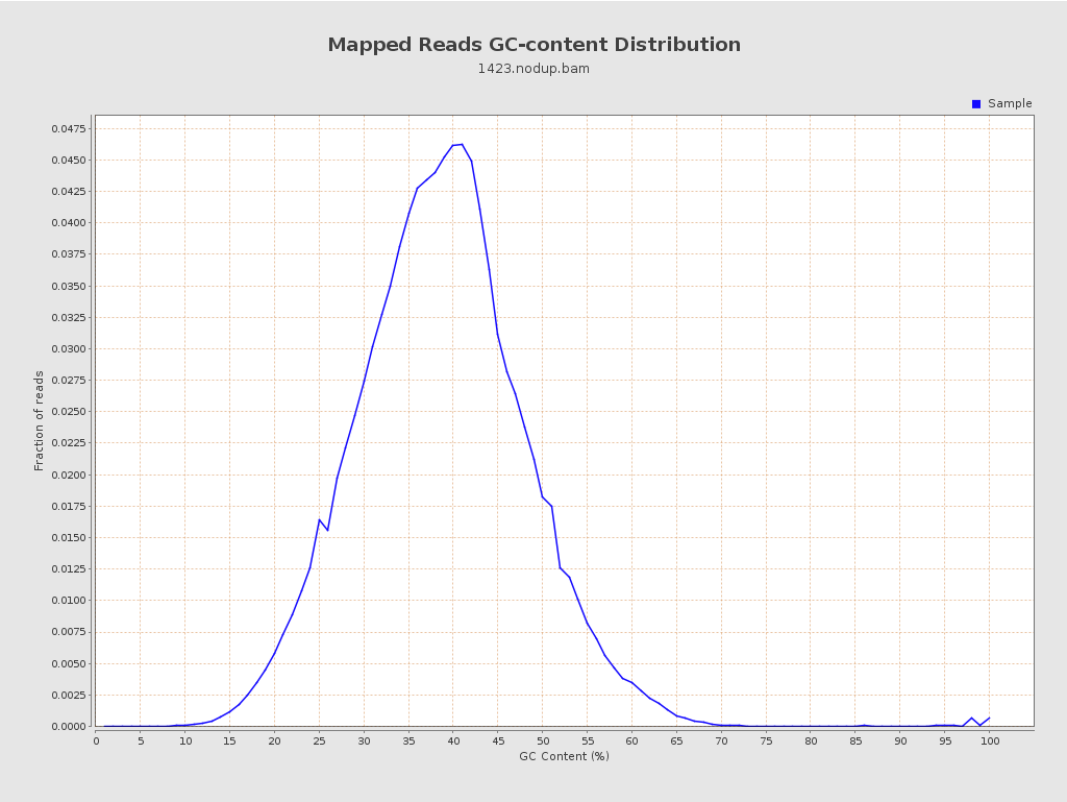
7. Results : Duplication Rate Histogram



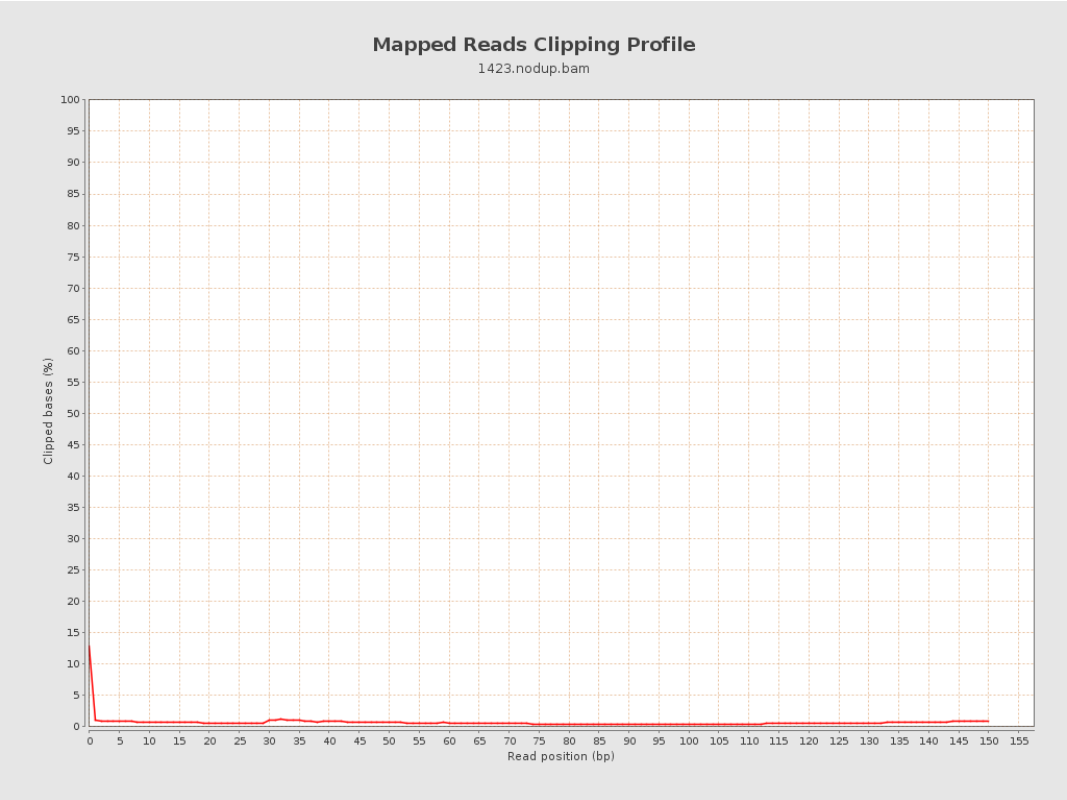
8. Results : Mapped Reads Nucleotide Content



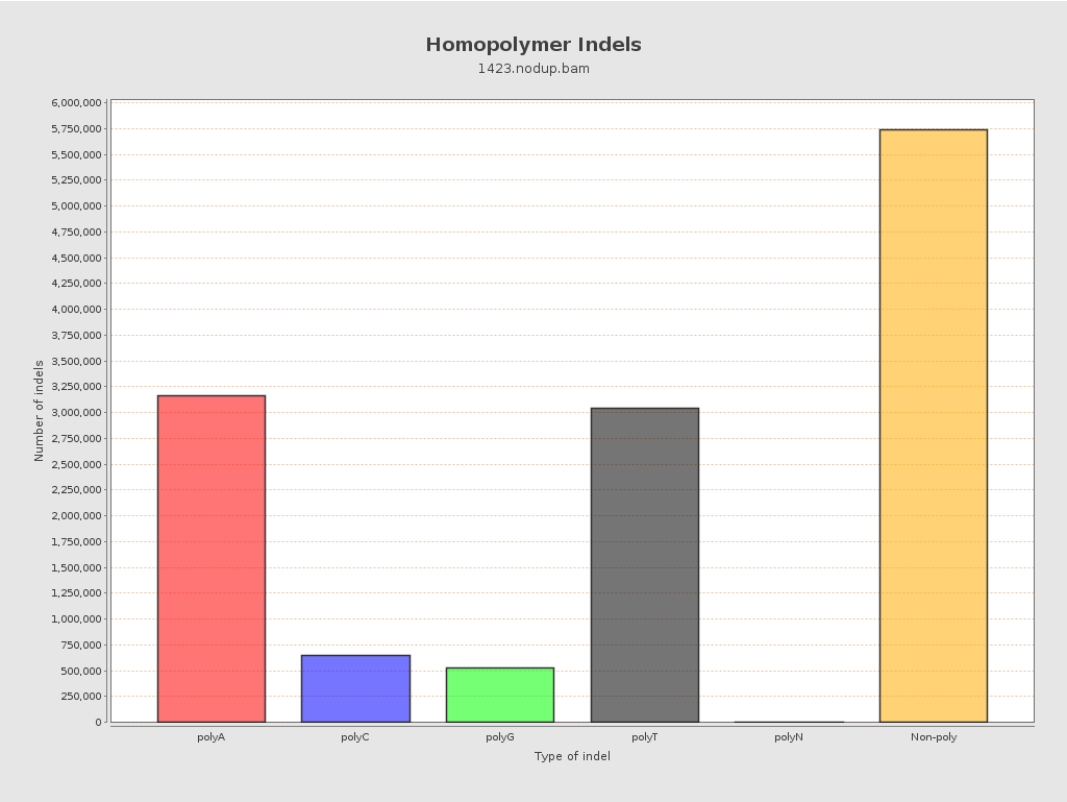
9. Results : Mapped Reads GC-content Distribution



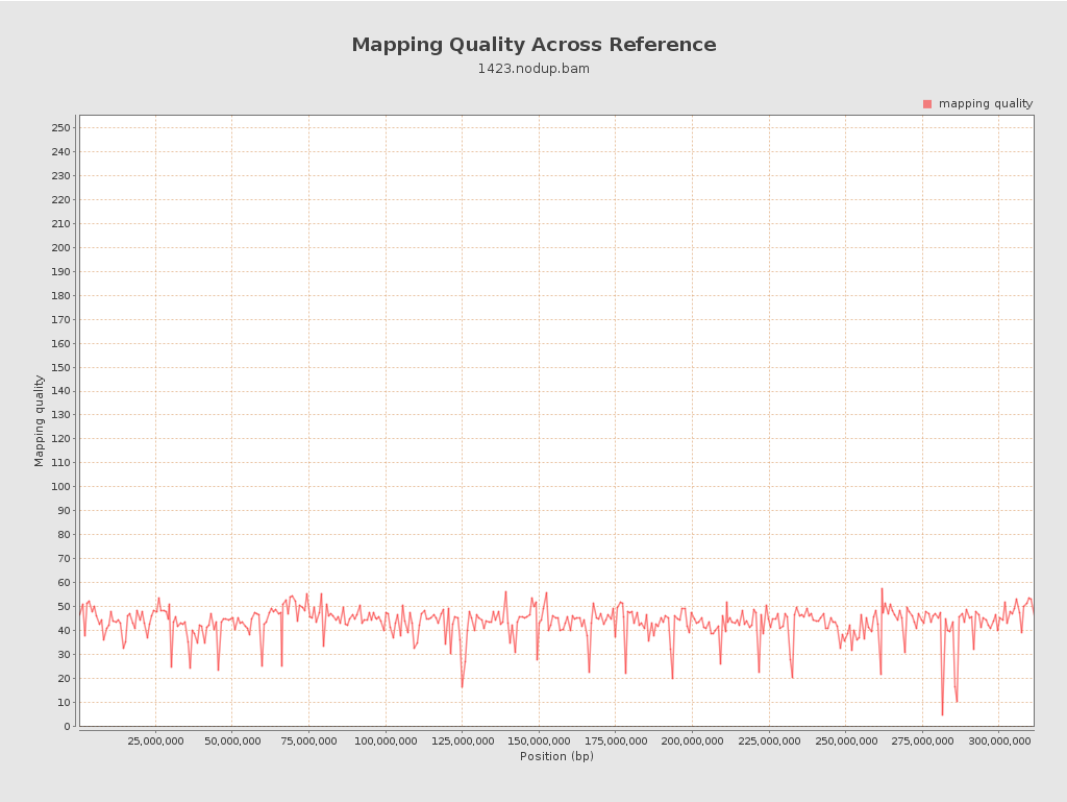
10. Results : Mapped Reads Clipping Profile



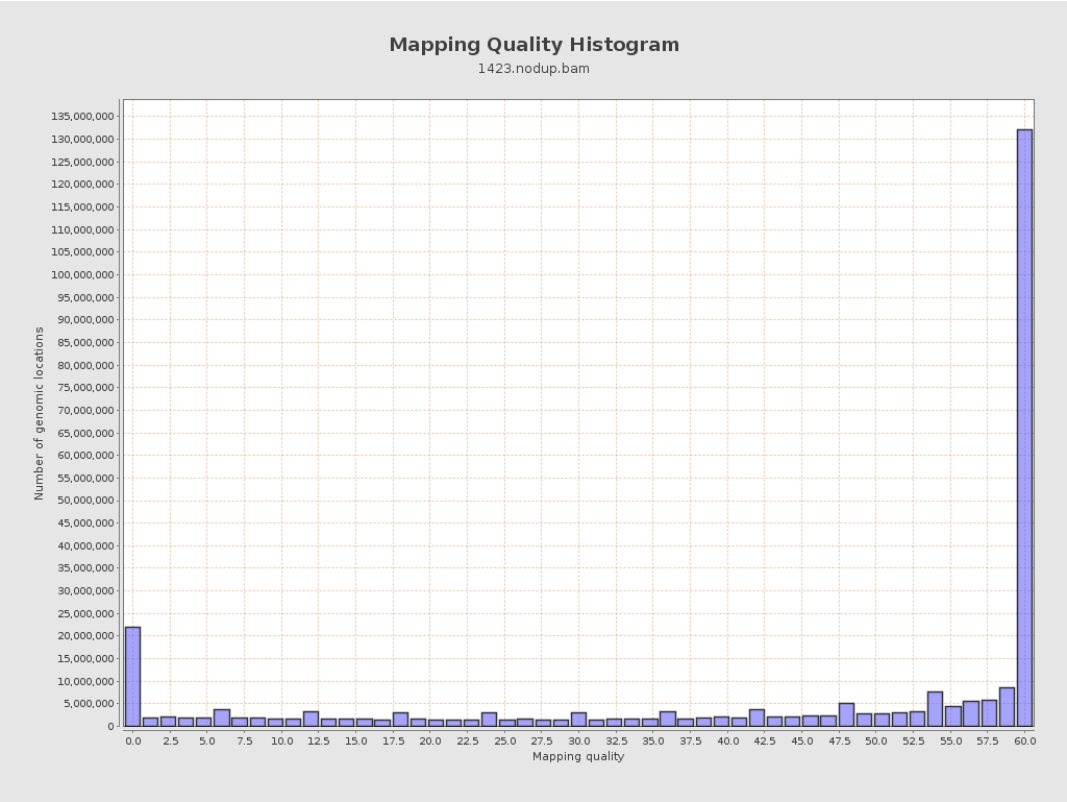
11. Results : Homopolymer Indels



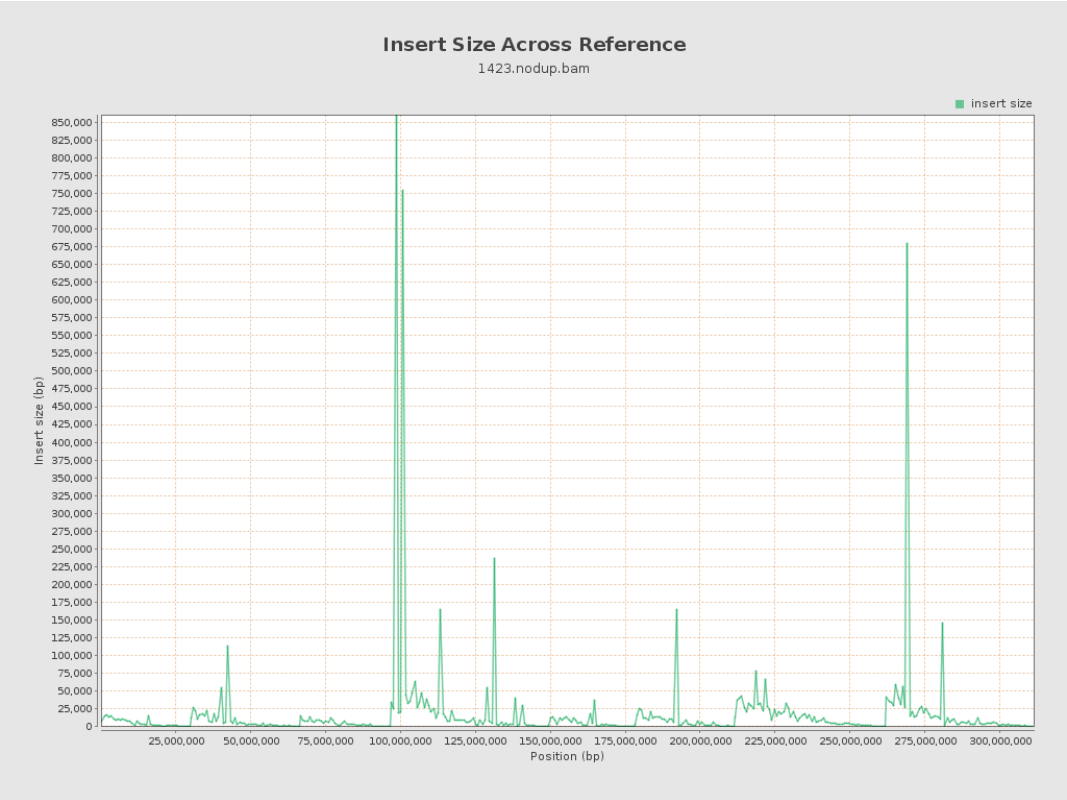
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram