Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1420
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1420 .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_489/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_489_S464_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_489/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_489_S464_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:24 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,289,843
Mapped reads	63,272,139 / 92.65%
Unmapped reads	5,017,704 / 7.35%
Mapped paired reads	63,272,139 / 92.65%
Mapped reads, first in pair	31,667,399 / 46.37%
Mapped reads, second in pair	31,604,740 / 46.28%
Mapped reads, both in pair	62,015,148 / 90.81%
Mapped reads, singletons	1,256,991 / 1.84%
Read min/max/mean length	30 / 151 / 148.38
Duplicated reads (flagged)	8,973,776 / 13.14%
Clipped reads	12,897,718 / 18.89%

2.2. ACGT Content

Number/percentage of A's	2,743,892,111 / 30.97%
Number/percentage of C's	1,687,501,407 / 19.05%
Number/percentage of T's	2,745,904,614 / 30.99%
Number/percentage of G's	1,682,655,848 / 18.99%
Number/percentage of N's	29,036 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	28.5002
Standard Deviation	193.3027

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Insert size

Mean	223,593.58
Standard Deviation	2,246,502.62
P25/Median/P75	362 / 469 / 613

2.6. Mismatches and indels

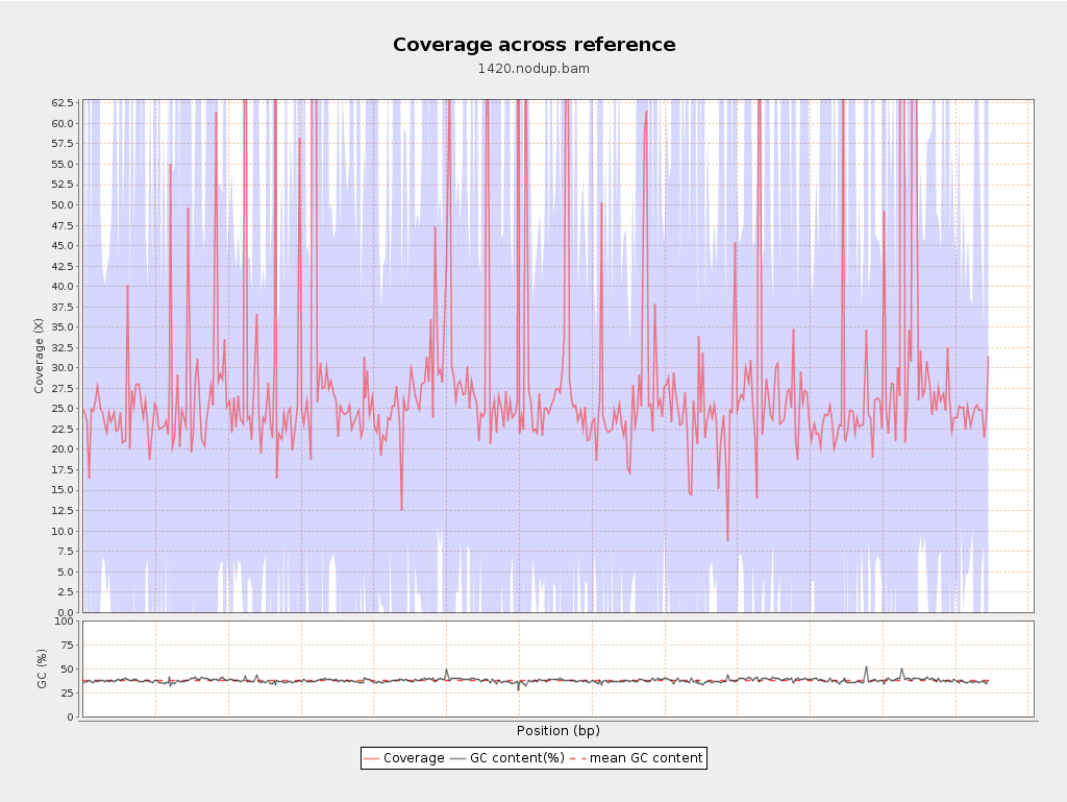
General error rate	2.24%
Mismatches	182,149,316
Insertions	5,705,671
Mapped reads with at least one insertion	8.12%
Deletions	5,814,007
Mapped reads with at least one deletion	8.17%
Homopolymer indels	56.87%

2.7. Chromosome stats

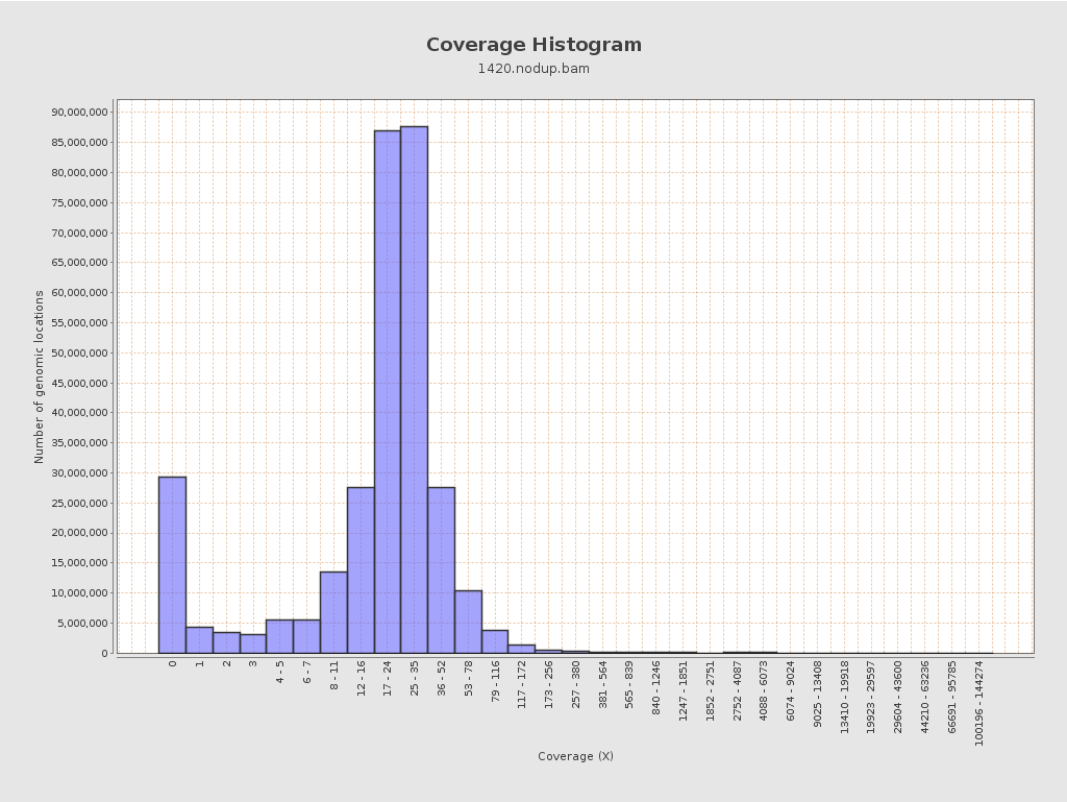
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	719582671	24.2085	62.3365

LT669789.1	36598175	1054301717	28.8075	211.0253
LT669790.1	30422129	932434084	30.6499	195.246
LT669791.1	52758100	1472122508	27.9033	156.4208
LT669792.1	28376109	810909889	28.5772	219.4341
LT669793.1	33388210	877166918	26.2718	142.6222
LT669794.1	50579949	1334026490	26.3746	159.3545
LT669795.1	49795044	1681314906	33.7647	287.523

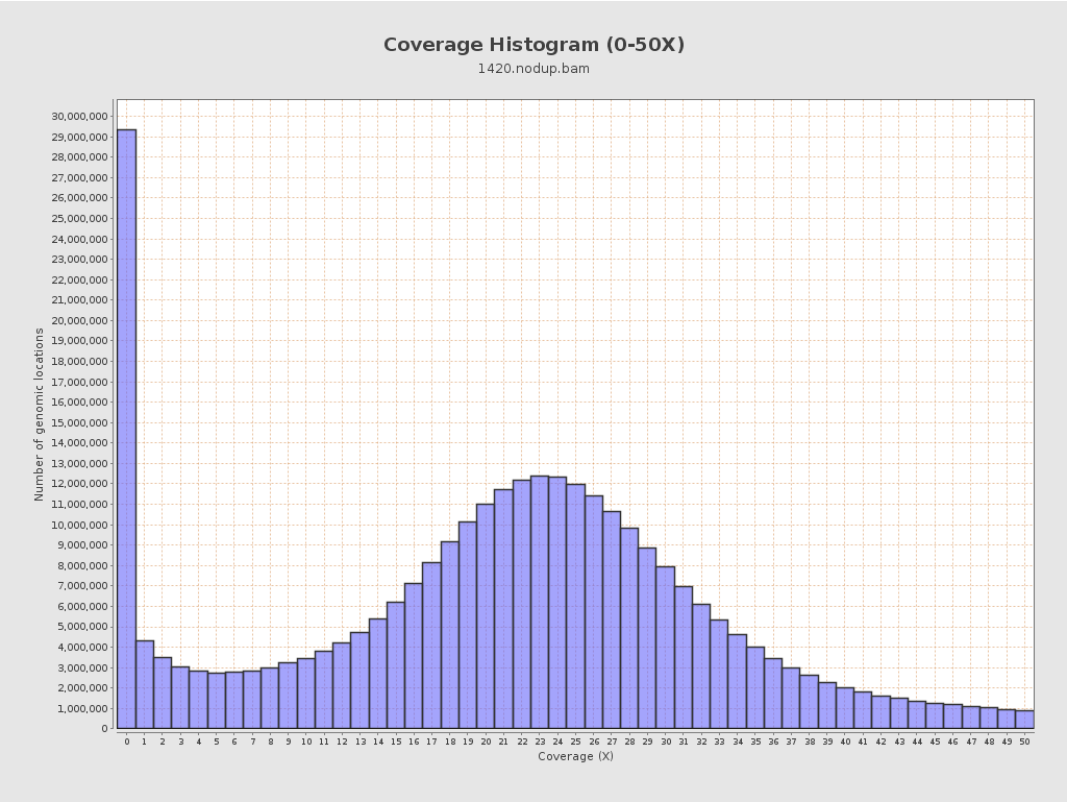
3. Results : Coverage across reference



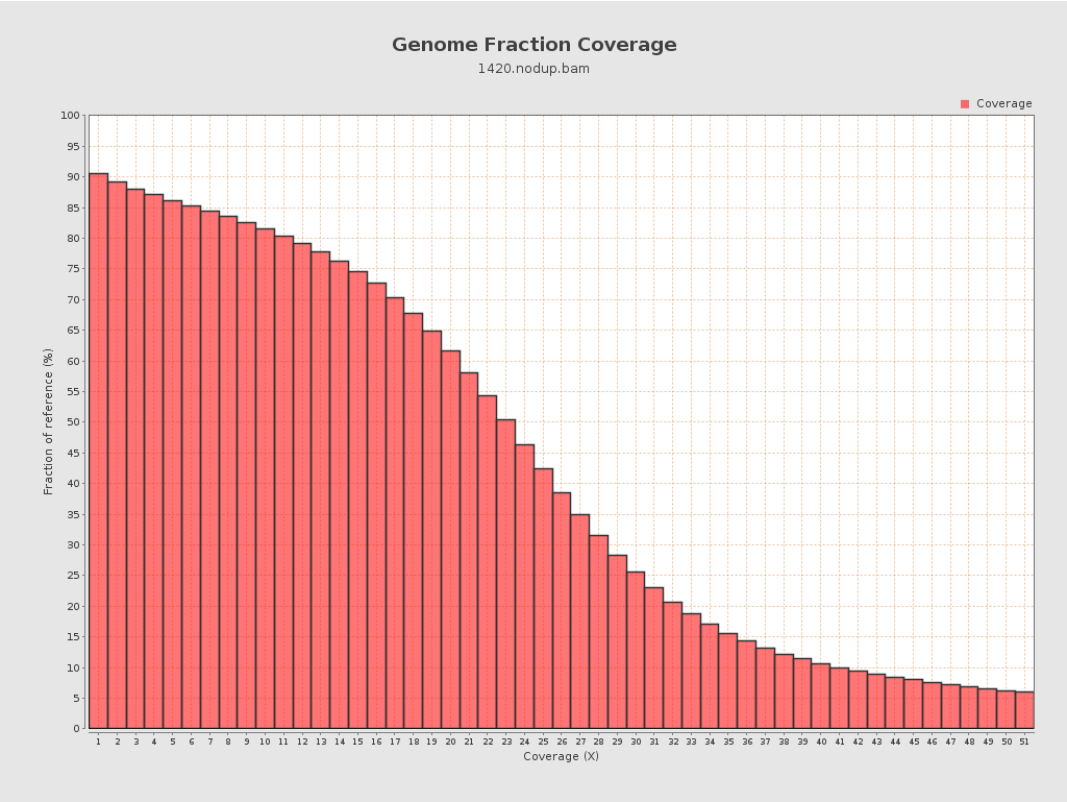
4. Results : Coverage Histogram



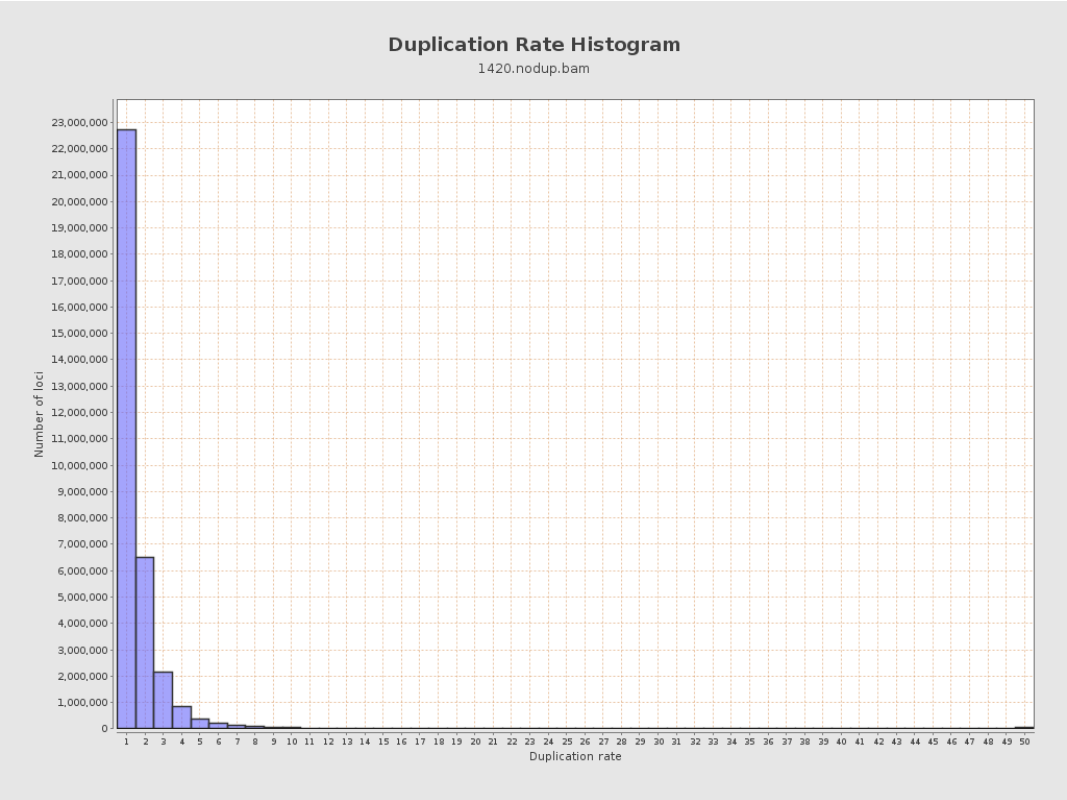
5. Results : Coverage Histogram (0-50X)



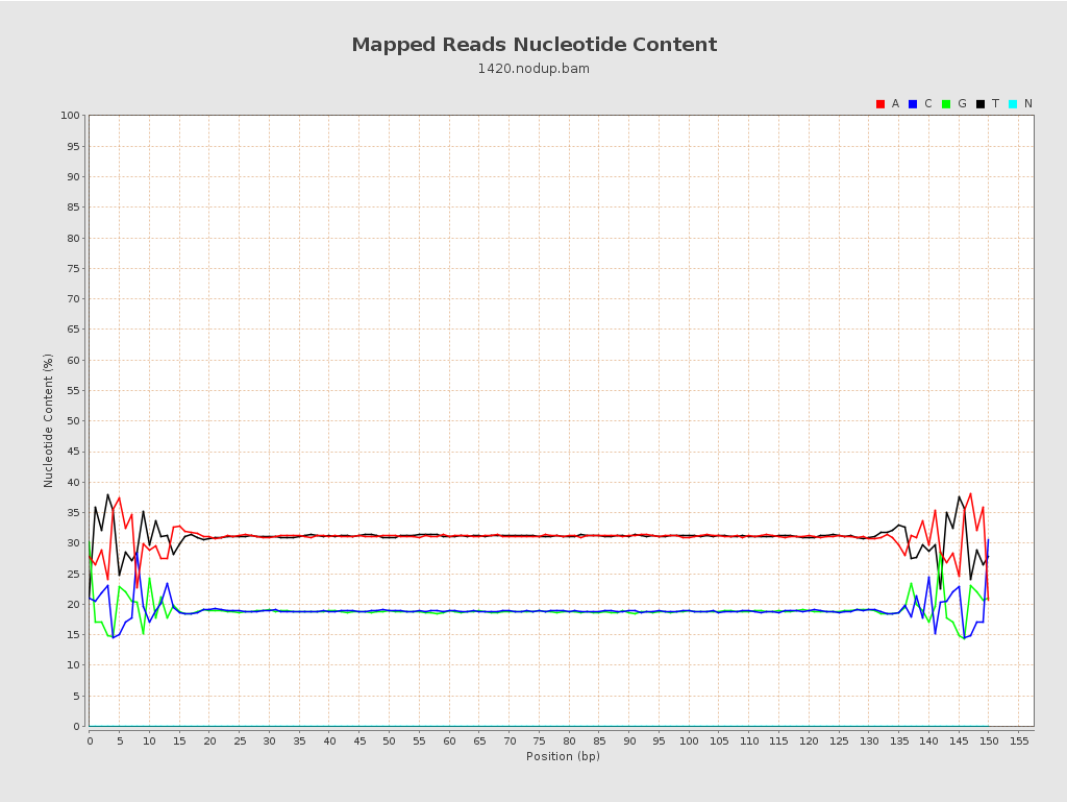
6. Results : Genome Fraction Coverage



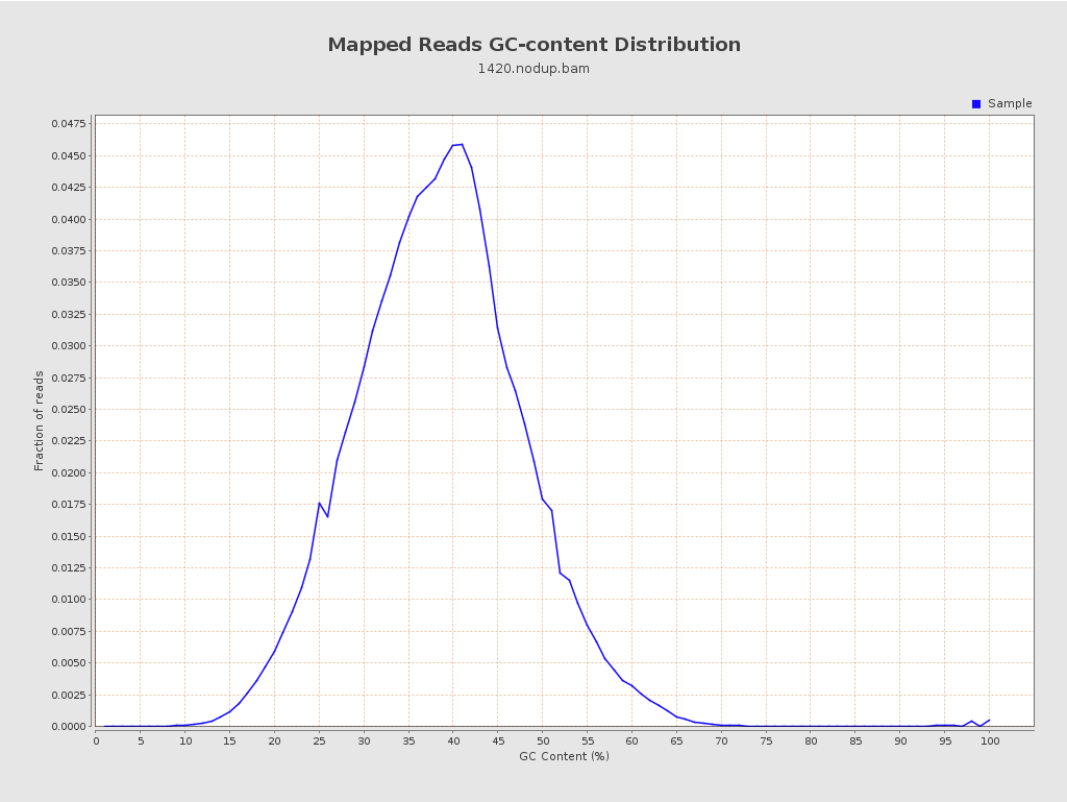
7. Results : Duplication Rate Histogram



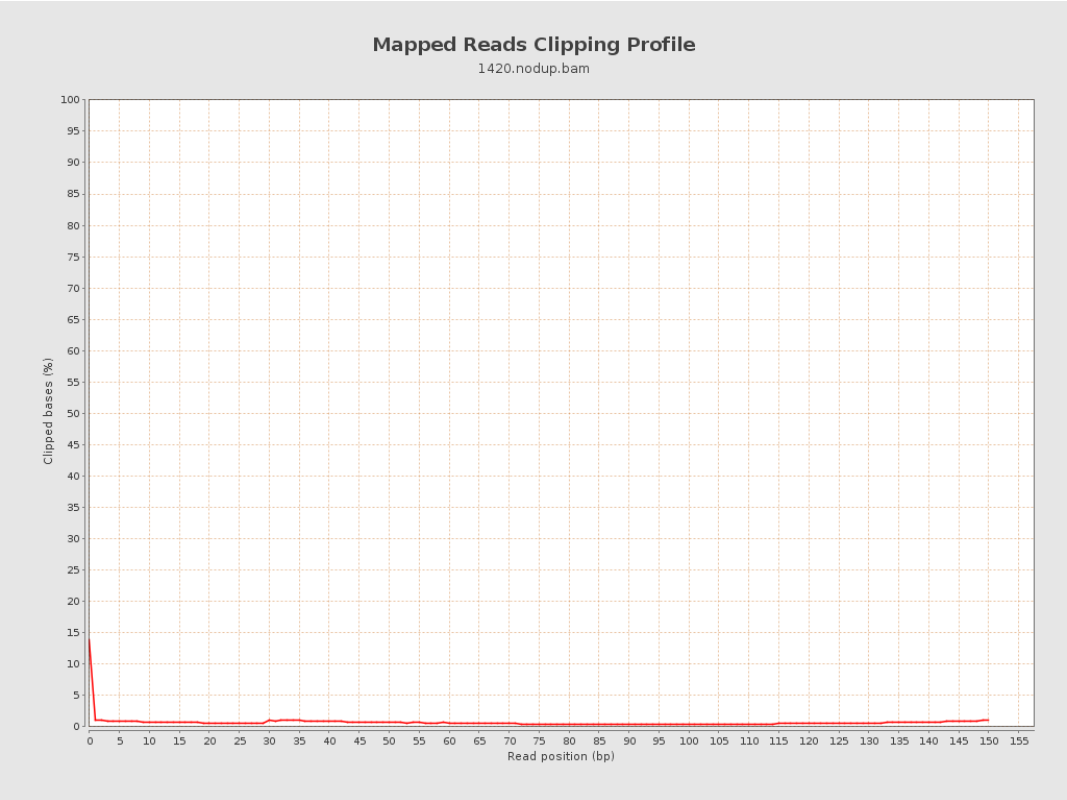
8. Results : Mapped Reads Nucleotide Content



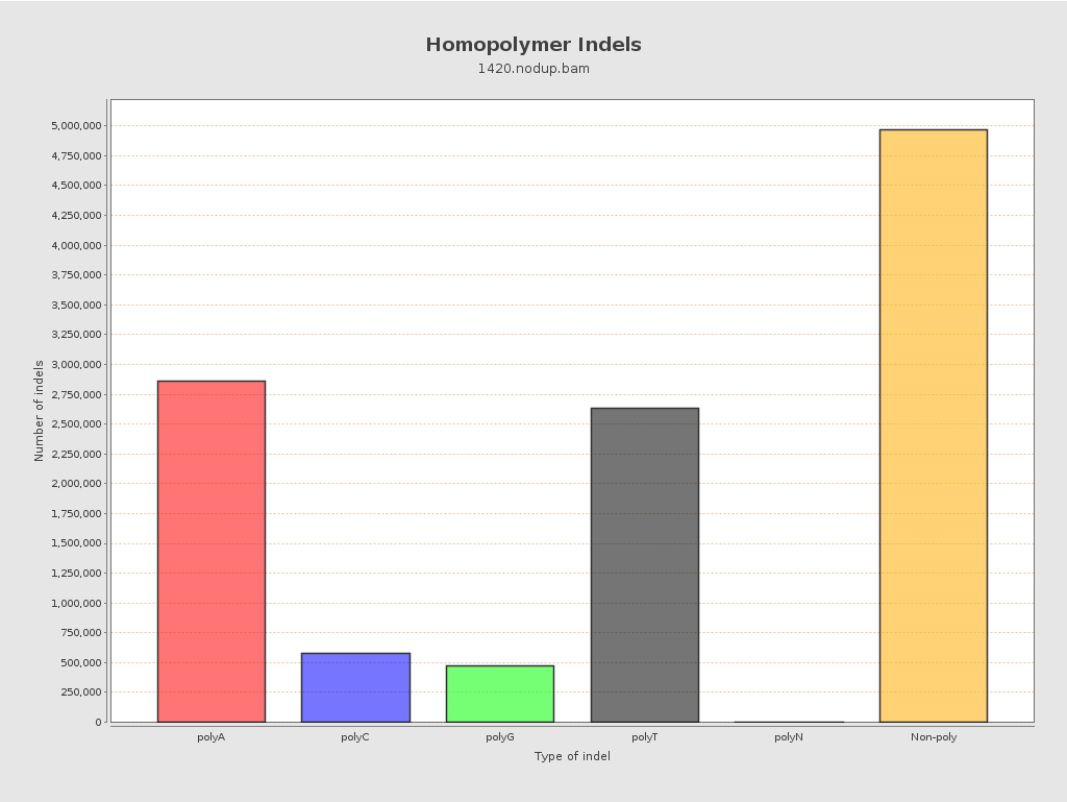
9. Results : Mapped Reads GC-content Distribution



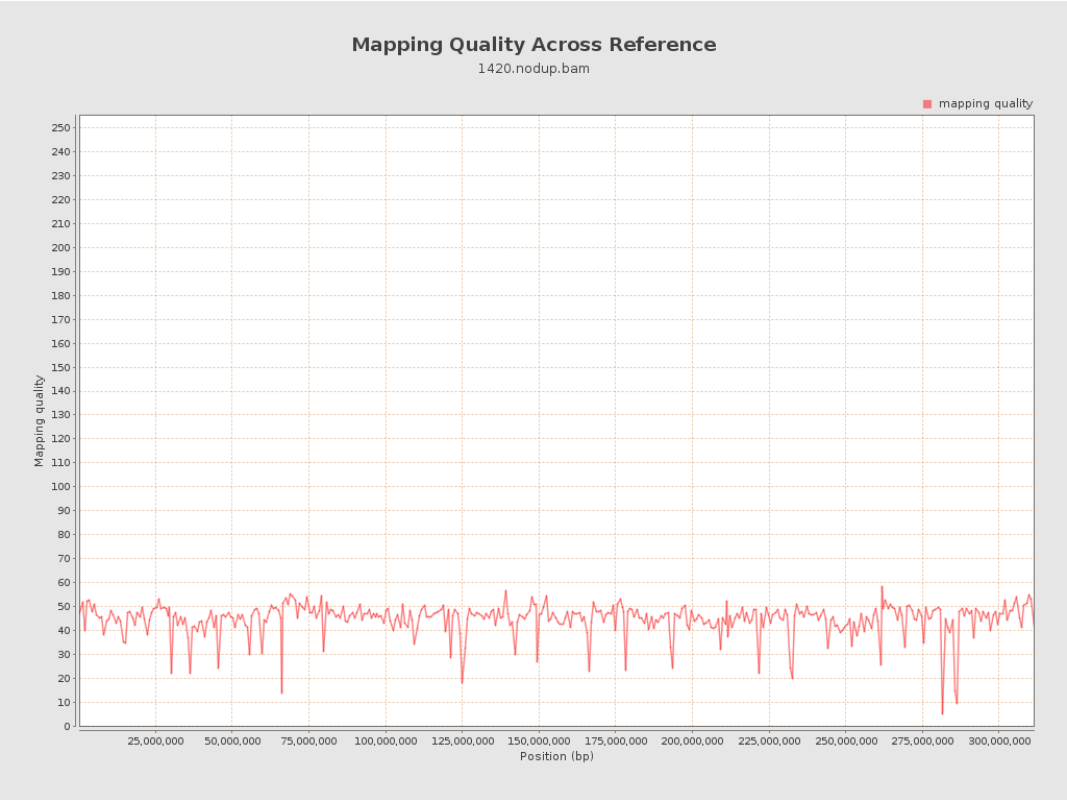
10. Results : Mapped Reads Clipping Profile



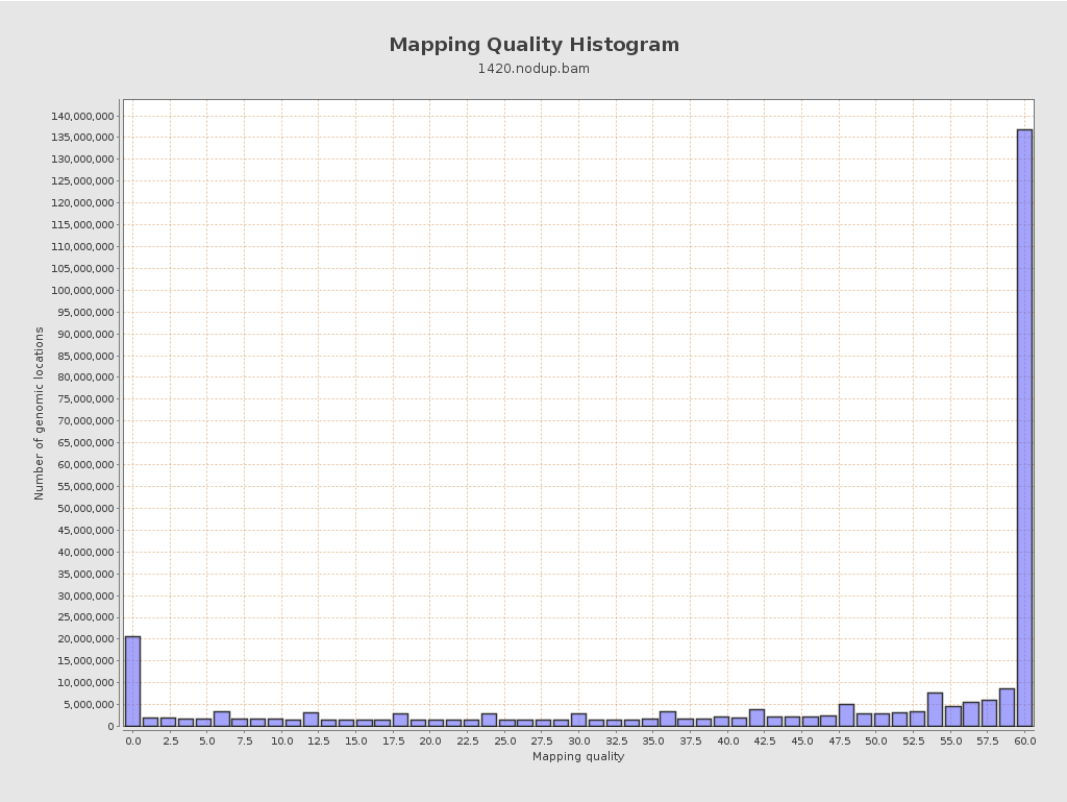
11. Results : Homopolymer Indels



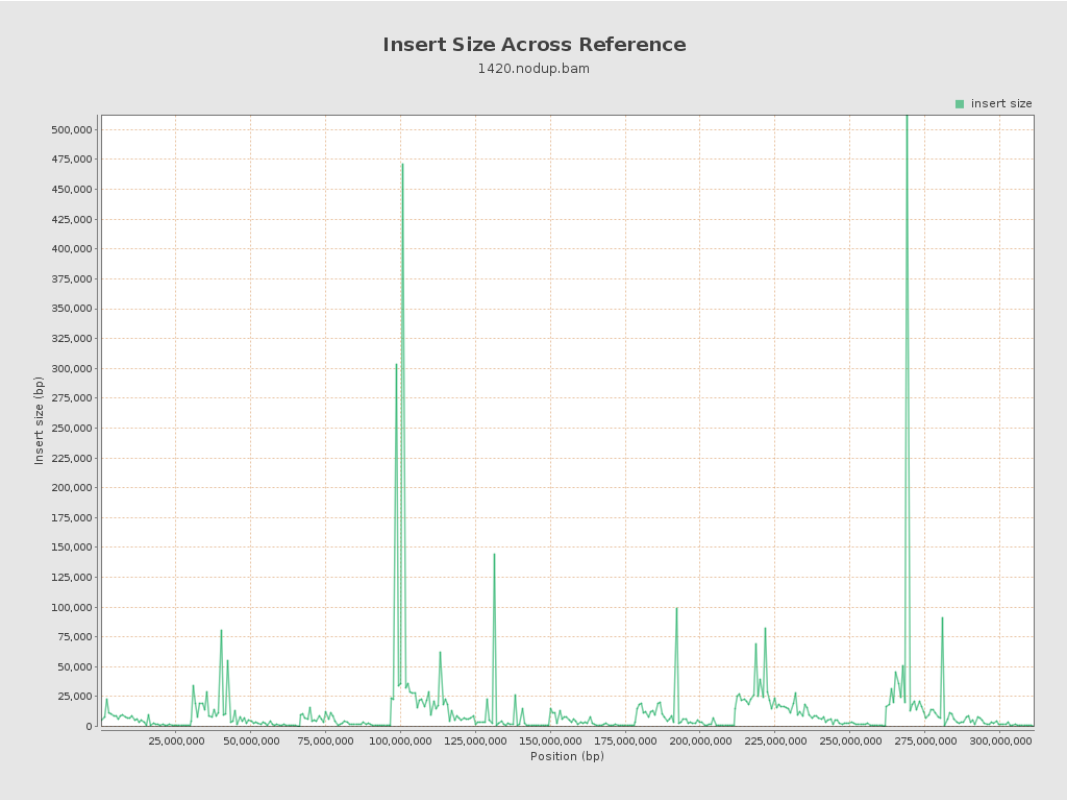
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram