Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/420.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/420.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_148/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_148_S238_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_148/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_148_S238_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:40:04 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	90,239,515
Mapped reads	85,991,268 / 95.29%
Unmapped reads	4,248,247 / 4.71%
Mapped paired reads	85,991,268 / 95.29%
Mapped reads, first in pair	43,075,147 / 47.73%
Mapped reads, second in pair	42,916,121 / 47.56%
Mapped reads, both in pair	84,579,653 / 93.73%
Mapped reads, singletons	1,411,615 / 1.56%
Read min/max/mean length	30 / 151 / 148.12
Duplicated reads (flagged)	14,545,171 / 16.12%
Clipped reads	18,429,519 / 20.42%

2.2. ACGT Content

Number/percentage of A's	3,704,943,250 / 30.91%
Number/percentage of C's	2,288,800,269 / 19.1%
Number/percentage of T's	3,707,857,776 / 30.94%
Number/percentage of G's	2,283,352,688 / 19.05%
Number/percentage of N's	50,964 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	38.557
Standard Deviation	272.1824

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Insert size

Mean	211,086.45
Standard Deviation	2,172,244.58
P25/Median/P75	312 / 409 / 538

2.6. Mismatches and indels

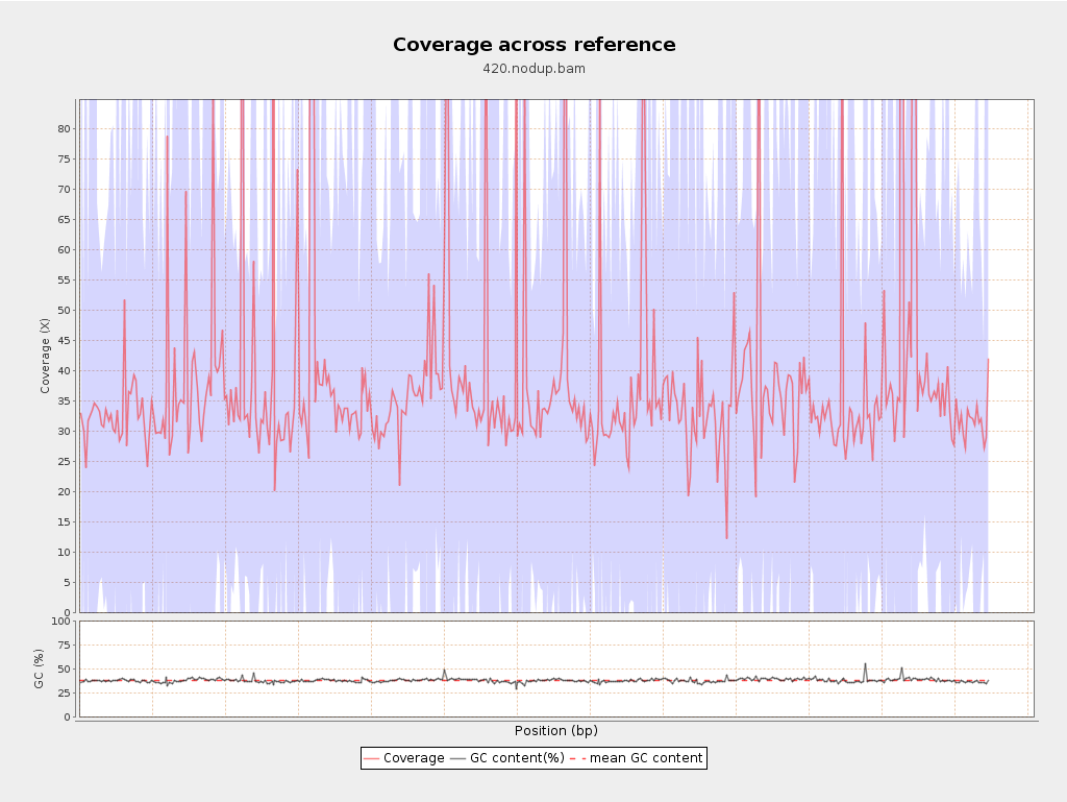
General error rate	2.22%
Mismatches	244,344,107
Insertions	7,874,355
Mapped reads with at least one insertion	8.25%
Deletions	8,120,579
Mapped reads with at least one deletion	8.4%
Homopolymer indels	56.44%

2.7. Chromosome stats

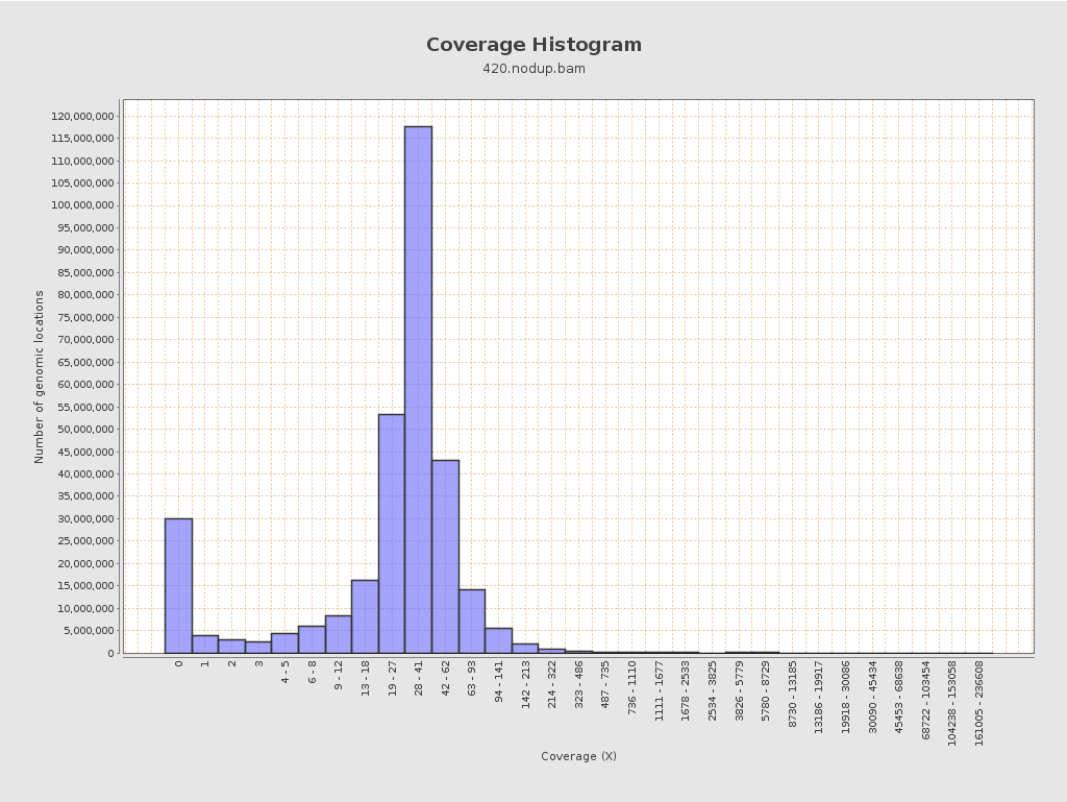
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	962091179	32.3671	77.1682

LT669789.1	36598175	1469062378	40.1403	320.4732
LT669790.1	30422129	1230095270	40.4342	240.4203
LT669791.1	52758100	1980389690	37.5372	220.9686
LT669792.1	28376109	1078450191	38.0056	299.0166
LT669793.1	33388210	1210526202	36.2561	207.8397
LT669794.1	50579949	1848228855	36.5407	240.5329
LT669795.1	49795044	2237145231	44.9271	398.5023

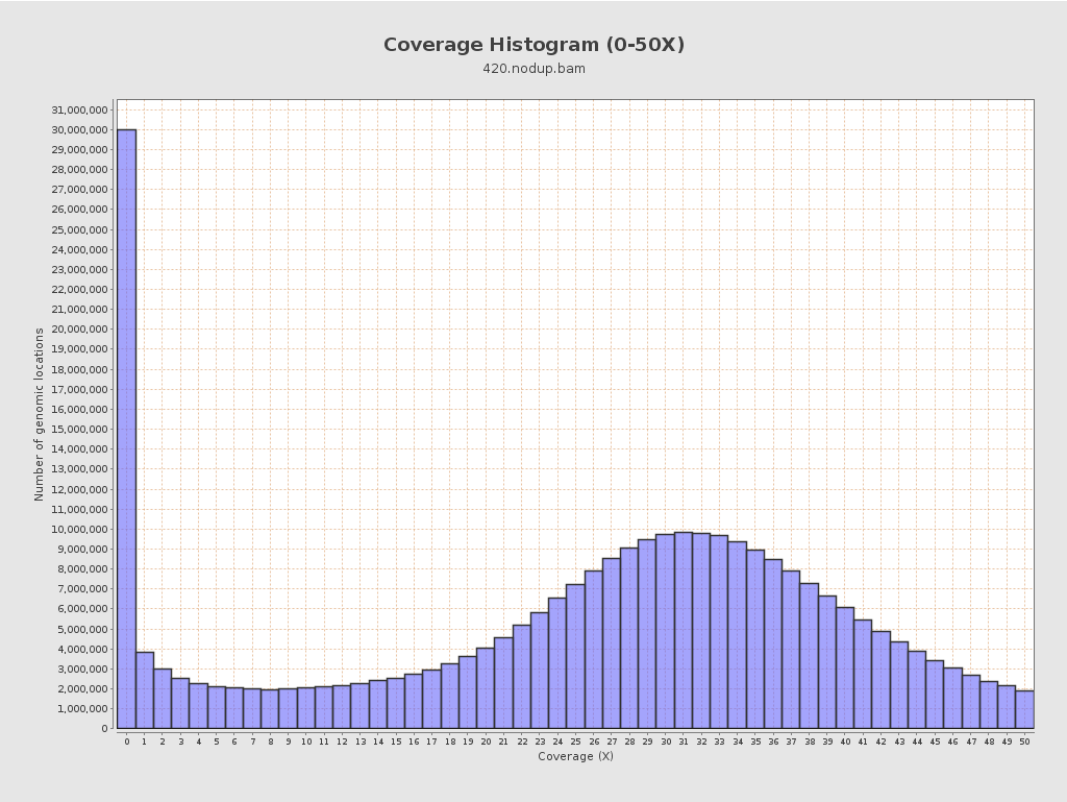
3. Results : Coverage across reference



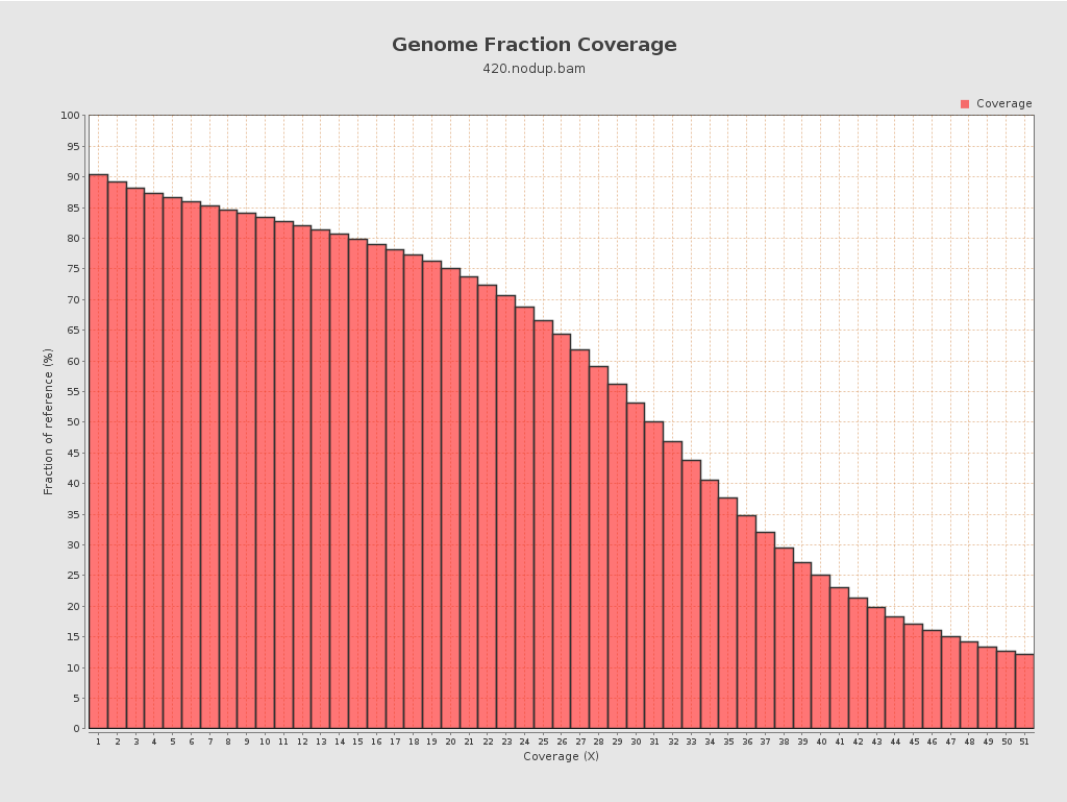
4. Results : Coverage Histogram



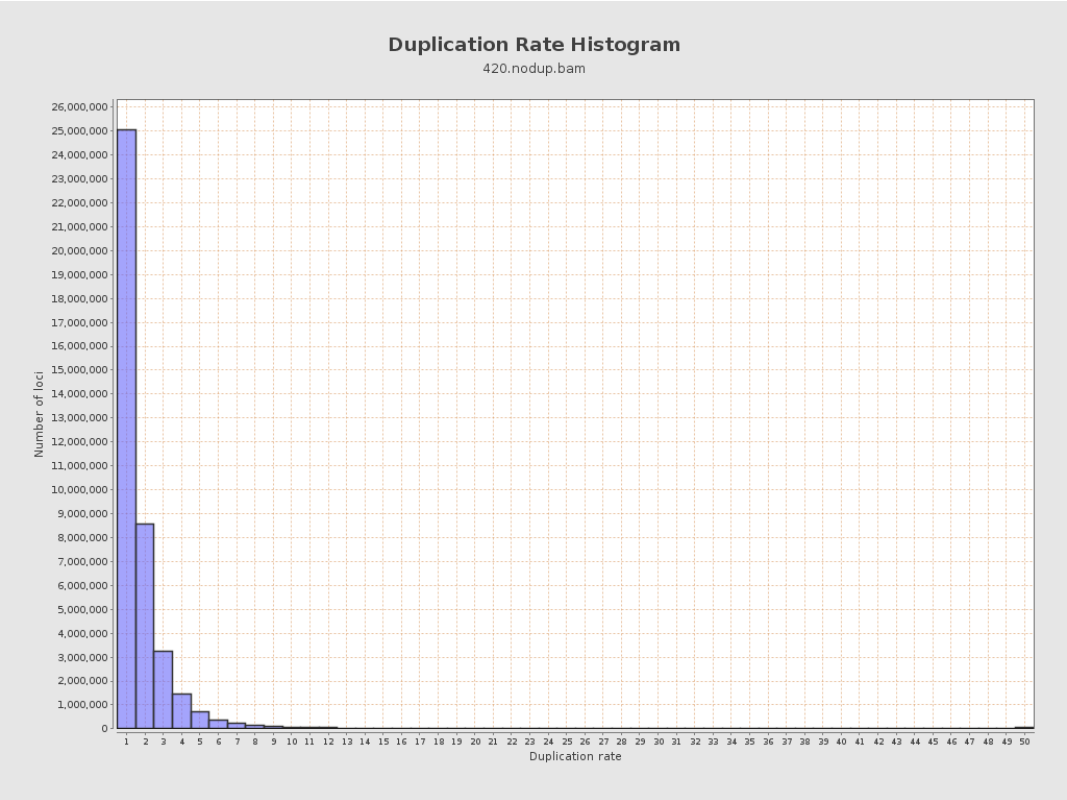
5. Results : Coverage Histogram (0-50X)



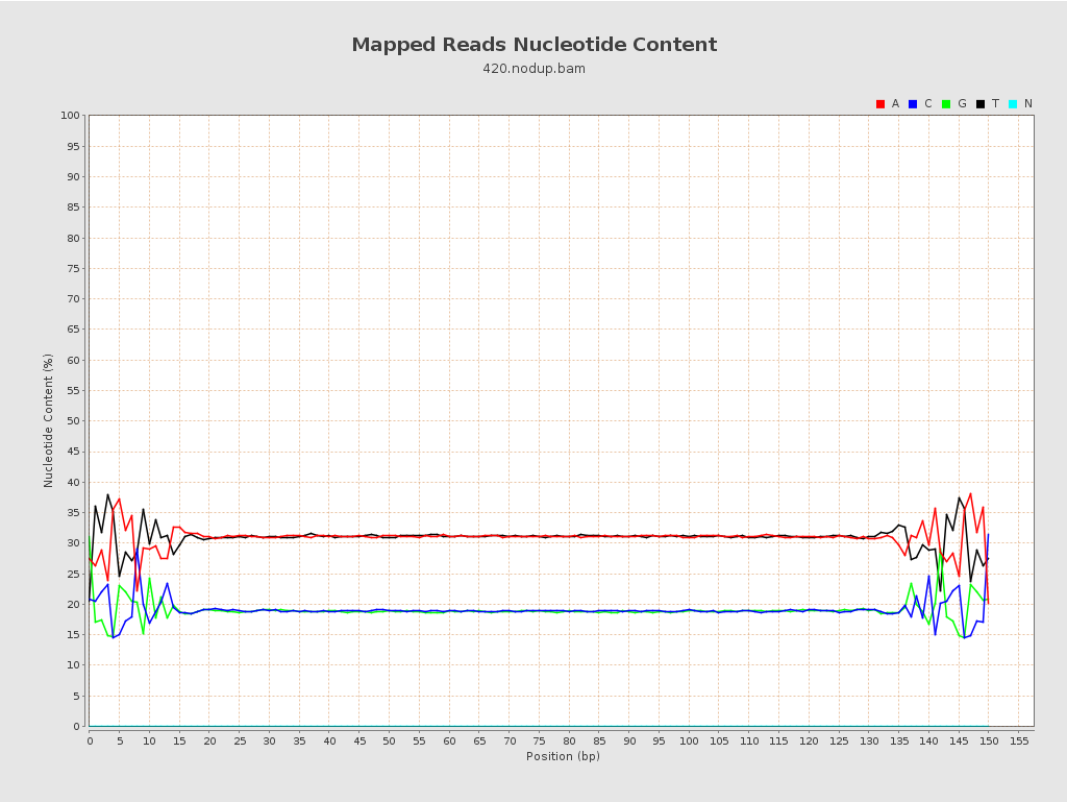
6. Results : Genome Fraction Coverage



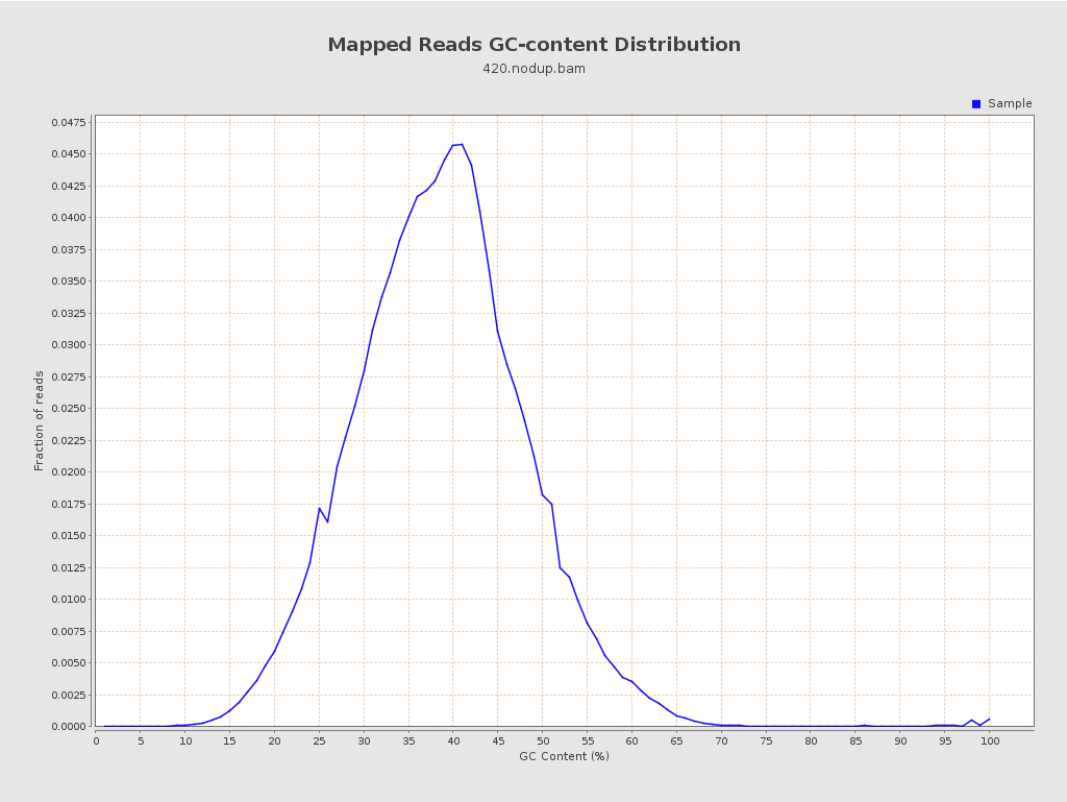
7. Results : Duplication Rate Histogram



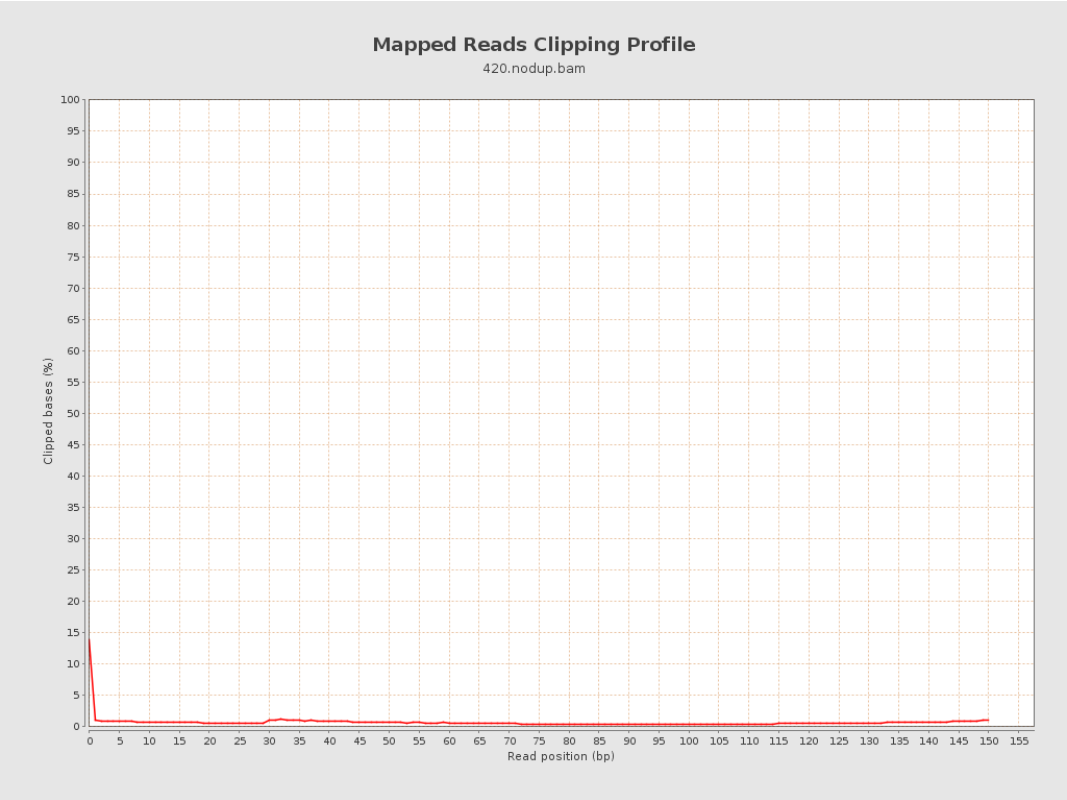
8. Results : Mapped Reads Nucleotide Content



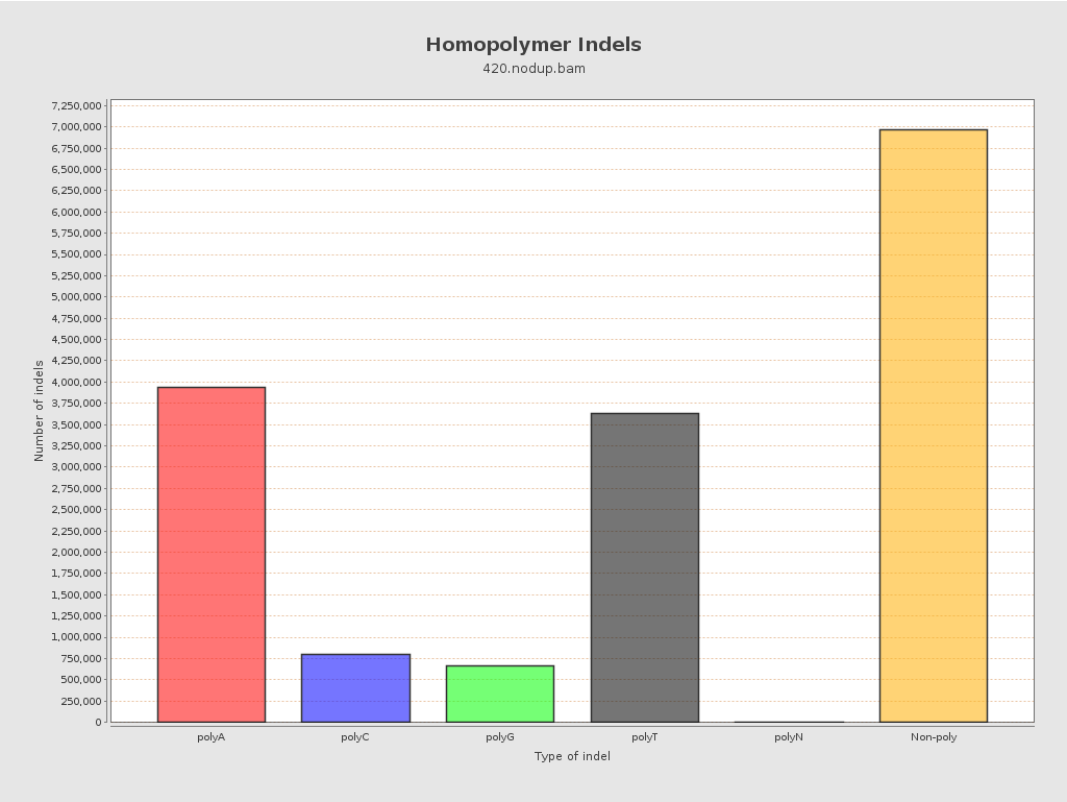
9. Results : Mapped Reads GC-content Distribution



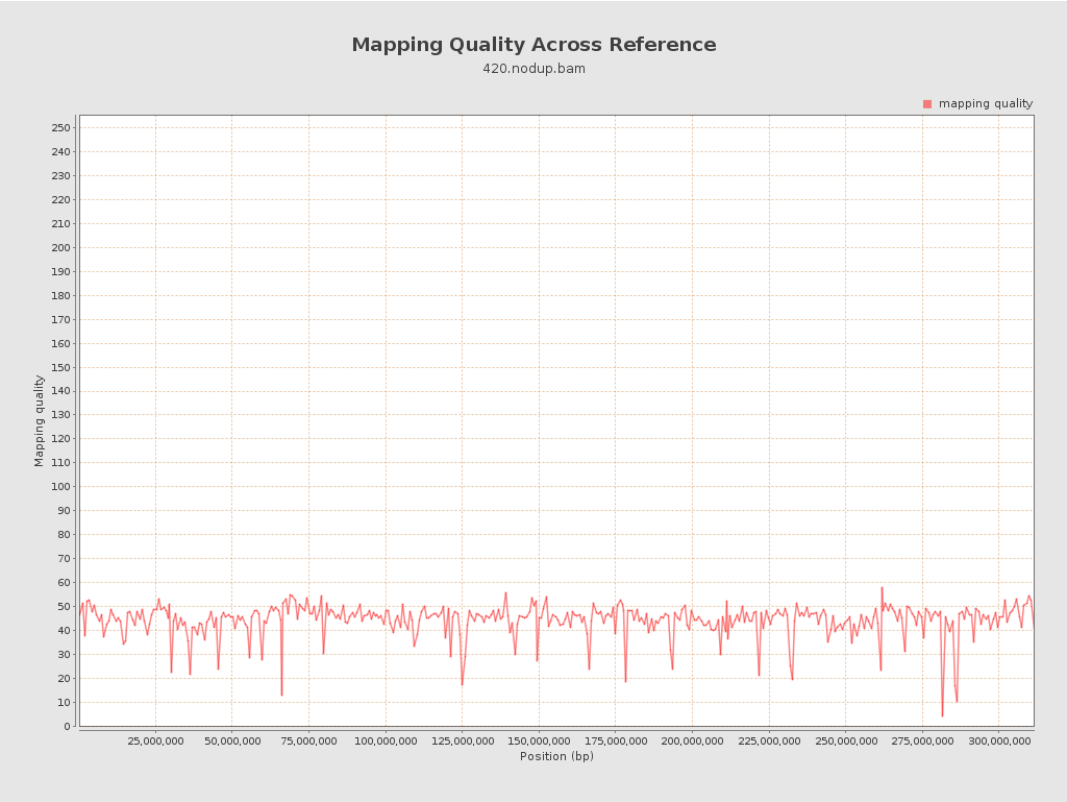
10. Results : Mapped Reads Clipping Profile



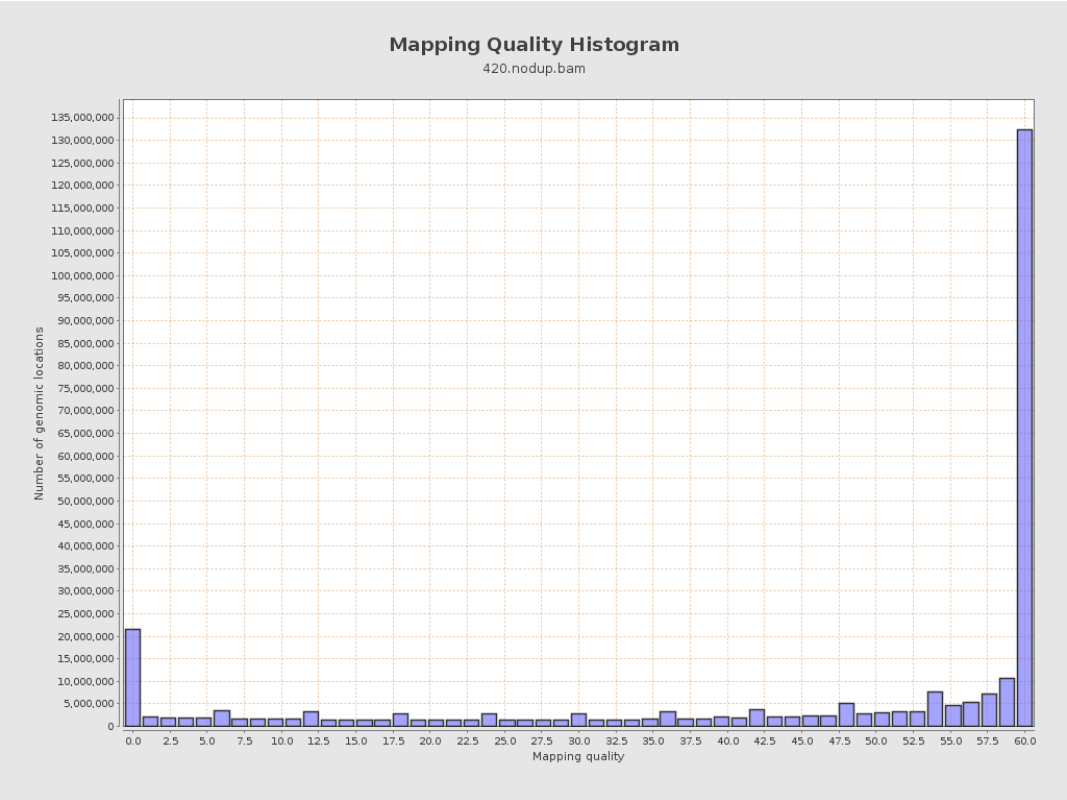
11. Results : Homopolymer Indels



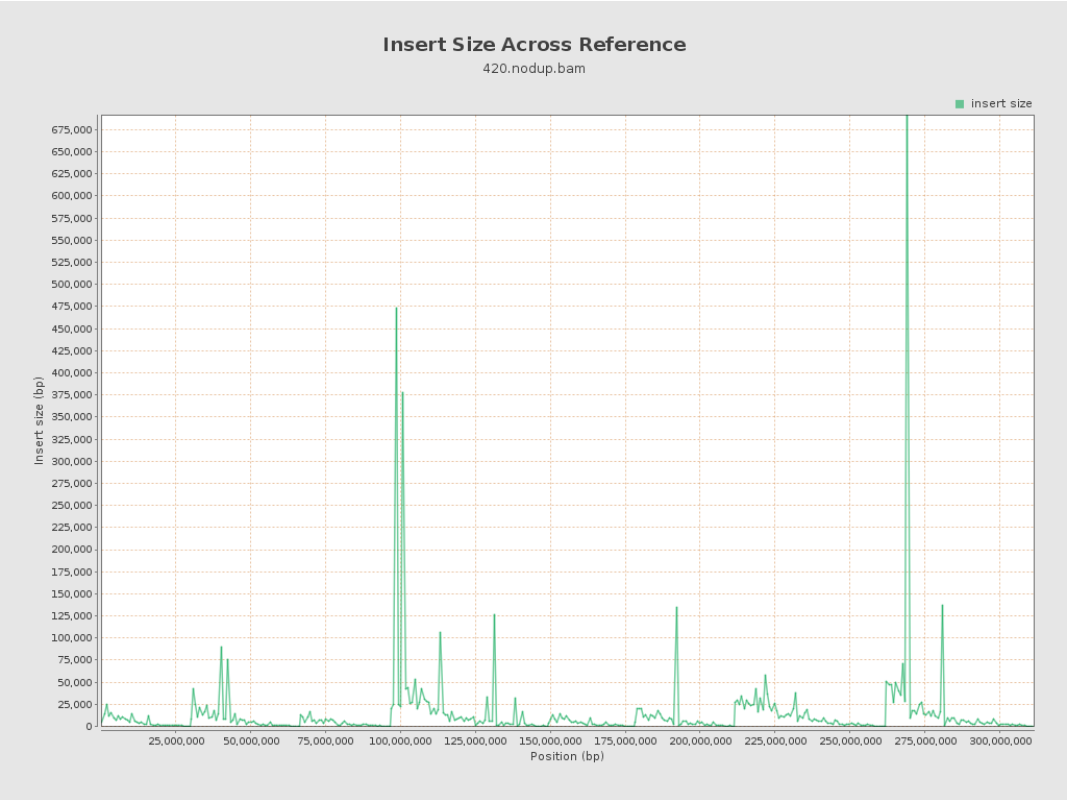
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram