Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/421.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/421.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_277/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_277_S358_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_277/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_277_S358_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	73,660,402
Mapped reads	68,013,347 / 92.33%
Unmapped reads	5,647,055 / 7.67%
Mapped paired reads	68,013,347 / 92.33%
Mapped reads, first in pair	34,053,085 / 46.23%
Mapped reads, second in pair	33,960,262 / 46.1%
Mapped reads, both in pair	66,204,468 / 89.88%
Mapped reads, singletons	1,808,879 / 2.46%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	11,327,825 / 15.38%
Clipped reads	16,101,800 / 21.86%

2.2. ACGT Content

Number/percentage of A's	2,887,818,683 / 30.89%
Number/percentage of C's	1,786,156,487 / 19.1%
Number/percentage of T's	2,891,636,738 / 30.93%
Number/percentage of G's	1,784,320,792 / 19.08%
Number/percentage of N's	33,609 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	30.0803
Standard Deviation	270.646

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Insert size

Mean	241,018.77
Standard Deviation	2,344,376.59
P25/Median/P75	317 / 416 / 538

2.6. Mismatches and indels

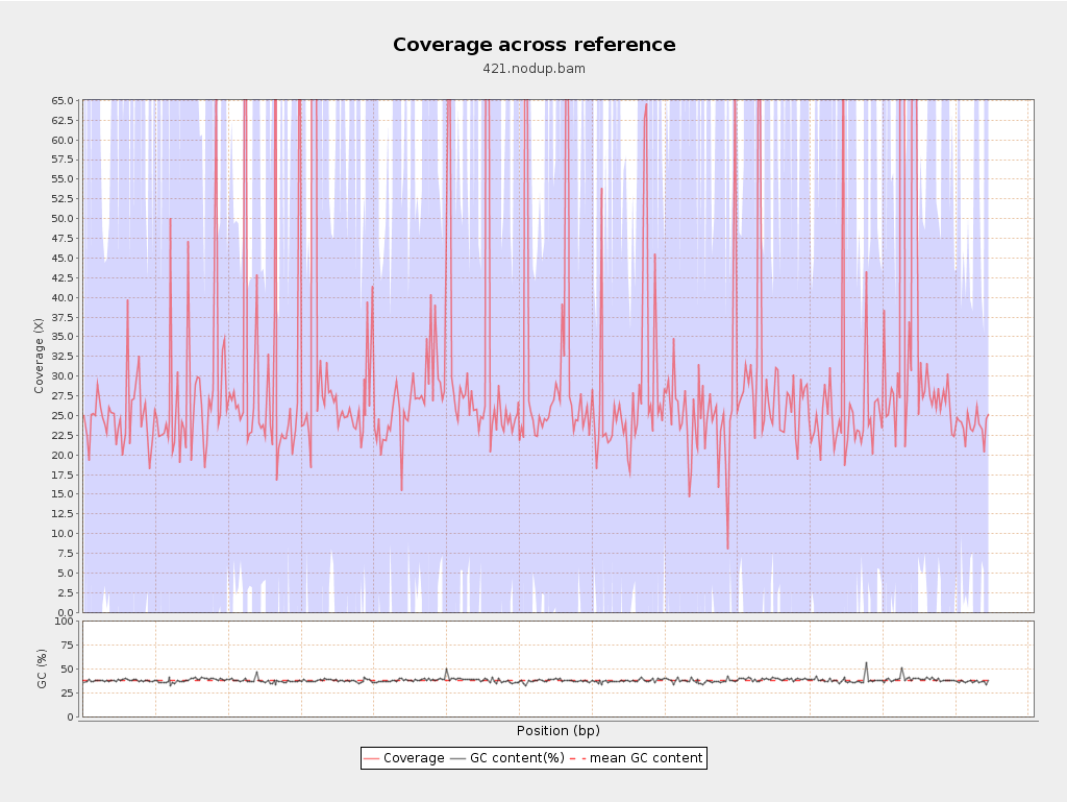
General error rate	2.36%
Mismatches	202,845,467
Insertions	6,597,278
Mapped reads with at least one insertion	8.67%
Deletions	6,472,336
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.72%

2.7. Chromosome stats

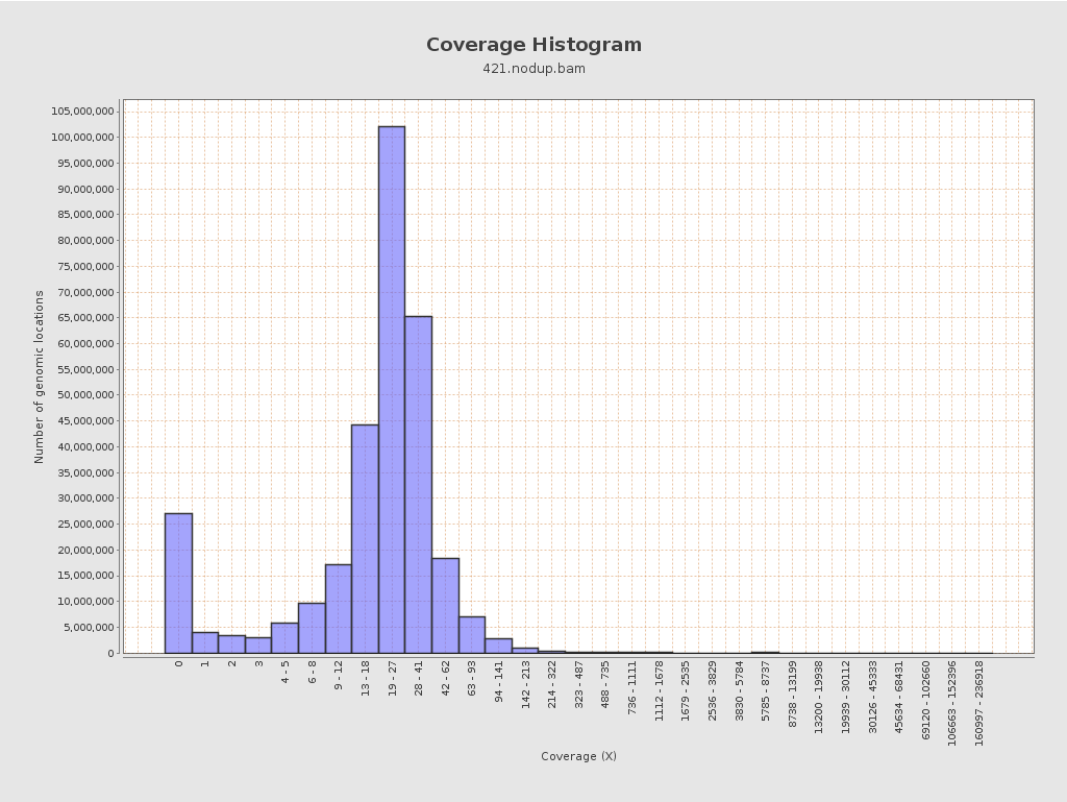
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	732580336	24.6458	96.0809

LT669789.1	36598175	1087991893	29.728	268.8503
LT669790.1	30422129	1067402312	35.0864	337.8921
LT669791.1	52758100	1566514154	29.6924	267.011
LT669792.1	28376109	848878596	29.9153	293.3793
LT669793.1	33388210	909967426	27.2542	171.6506
LT669794.1	50579949	1412905621	27.9341	209.4922
LT669795.1	49795044	1748048720	35.1049	375.5712

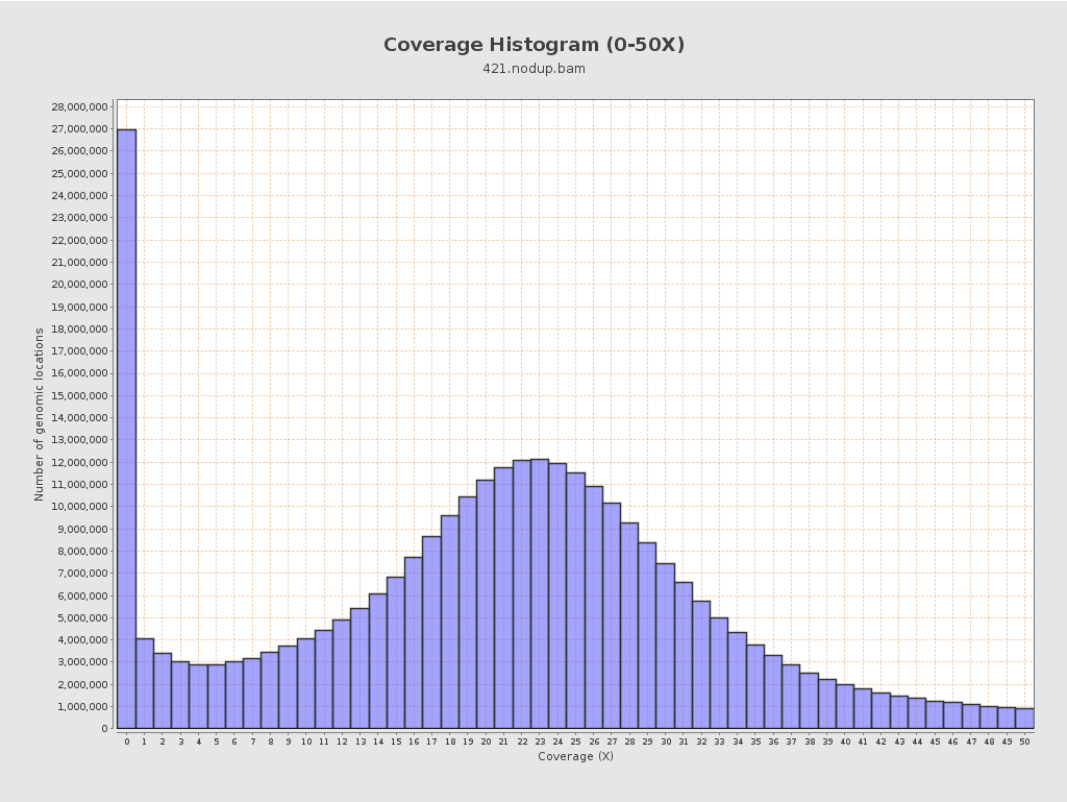
3. Results : Coverage across reference



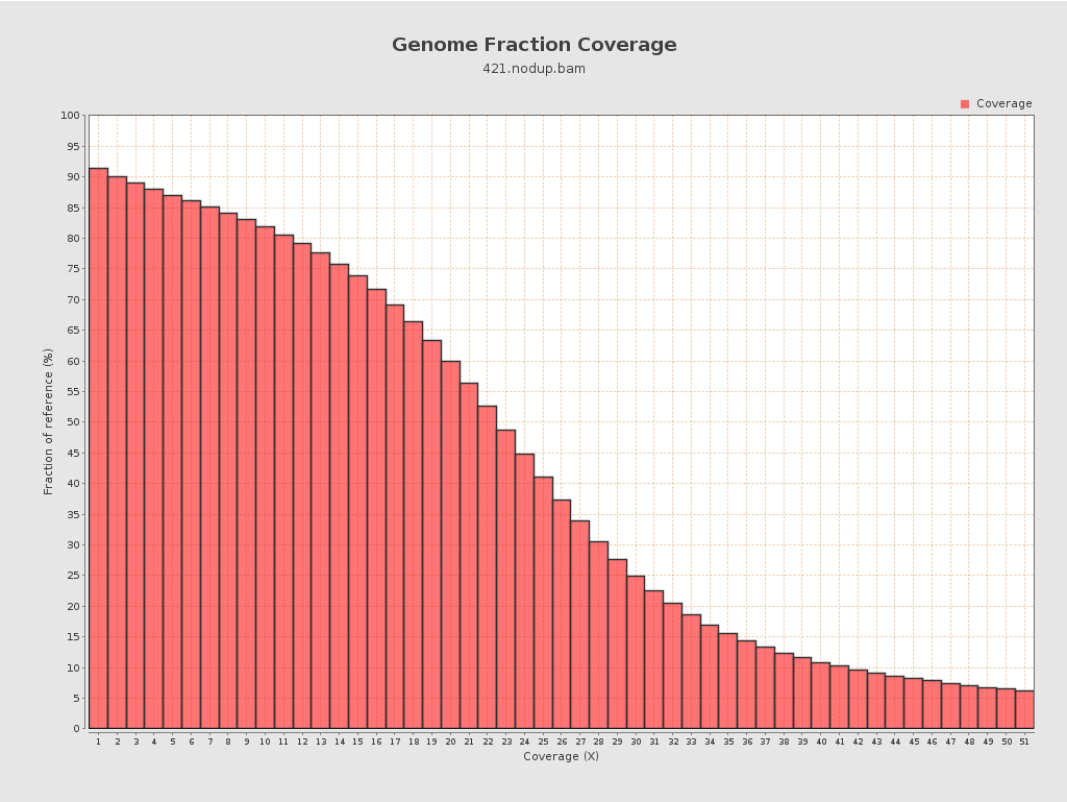
4. Results : Coverage Histogram



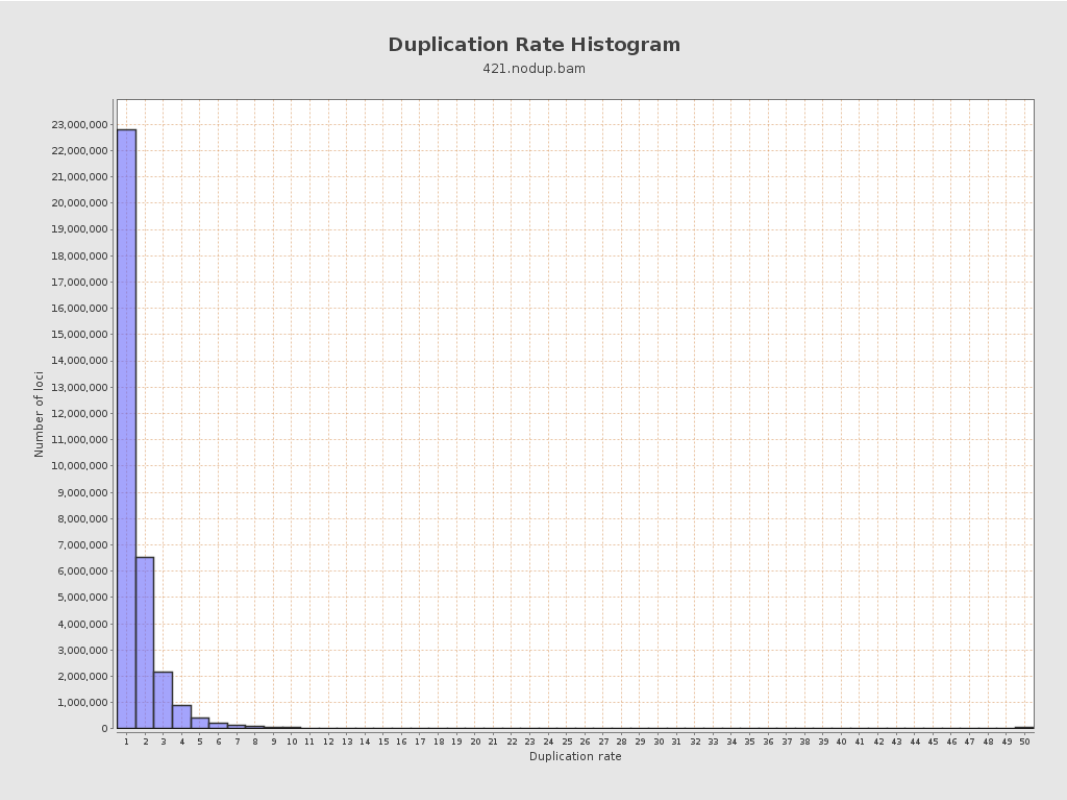
5. Results : Coverage Histogram (0-50X)



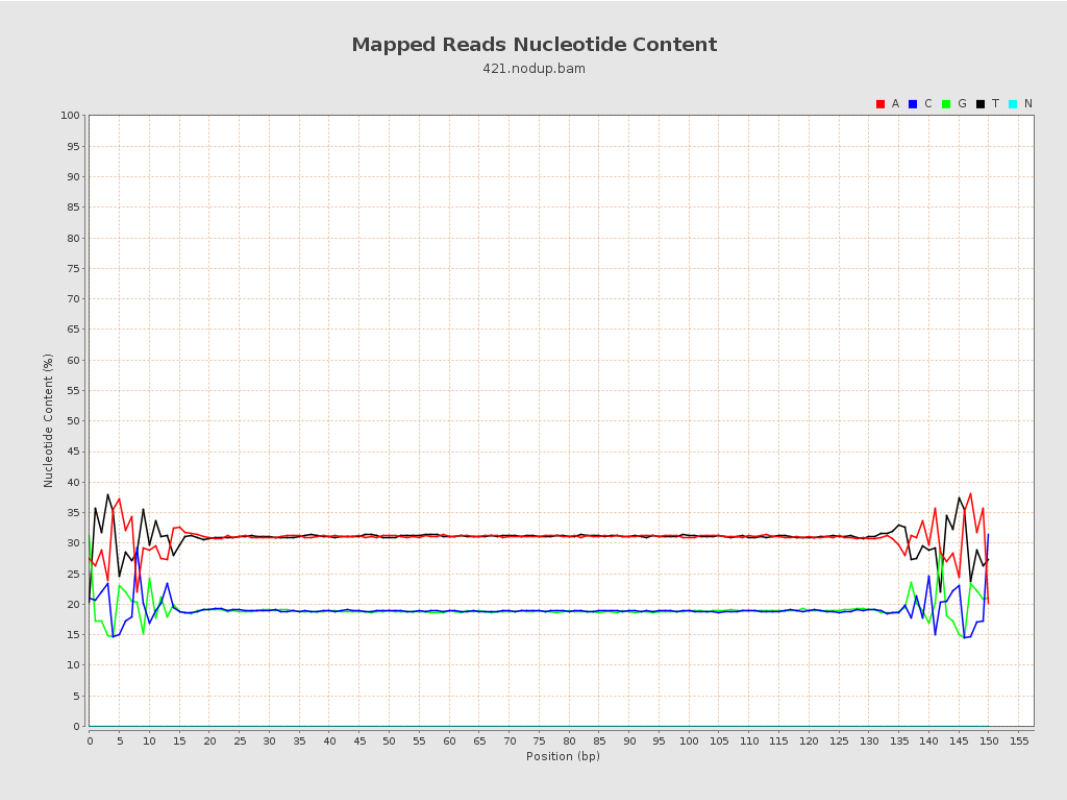
6. Results : Genome Fraction Coverage



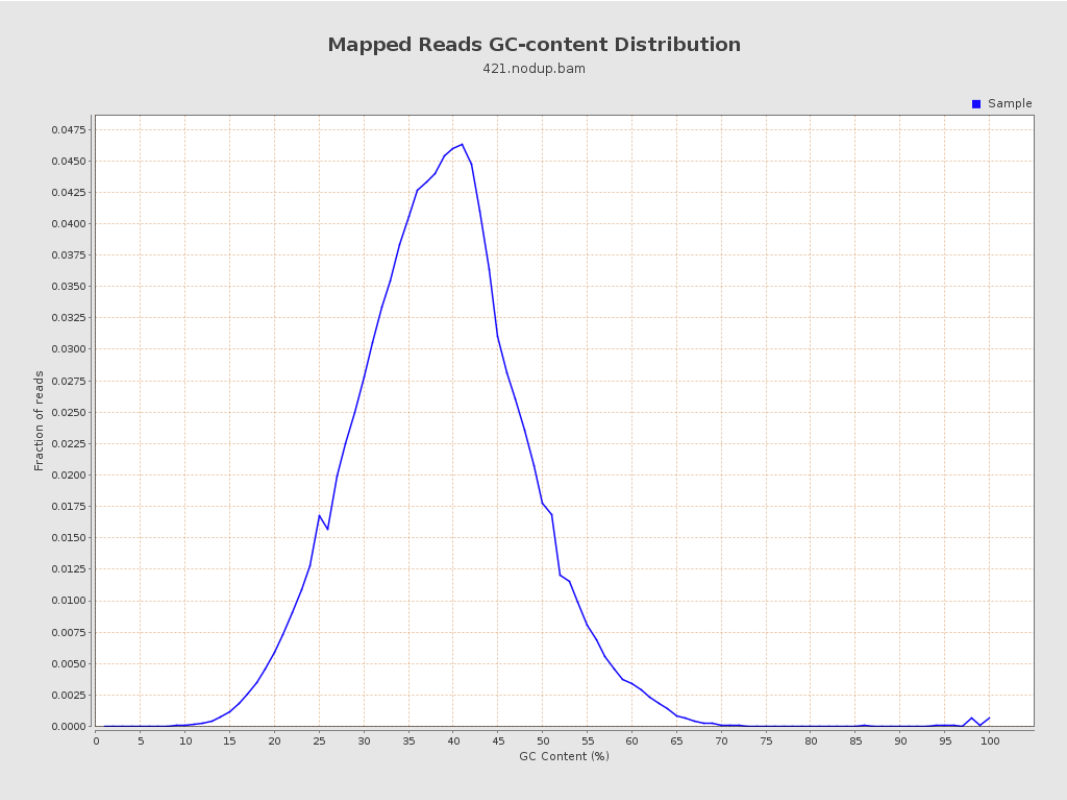
7. Results : Duplication Rate Histogram



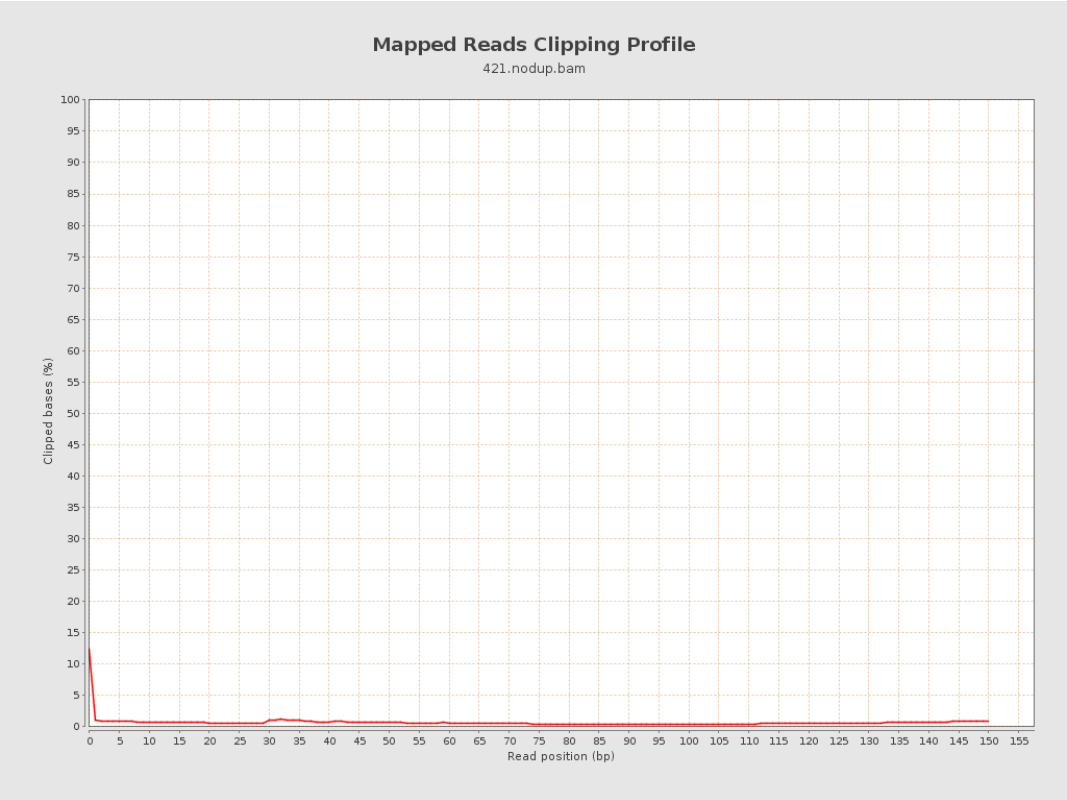
8. Results : Mapped Reads Nucleotide Content



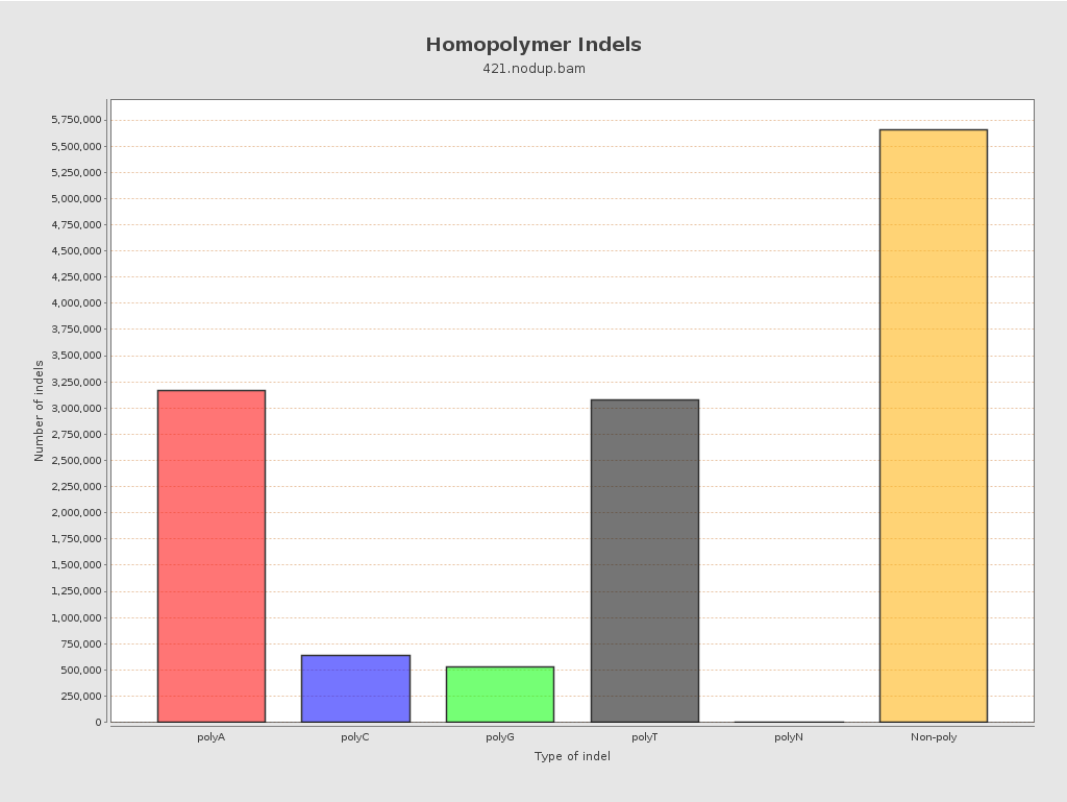
9. Results : Mapped Reads GC-content Distribution



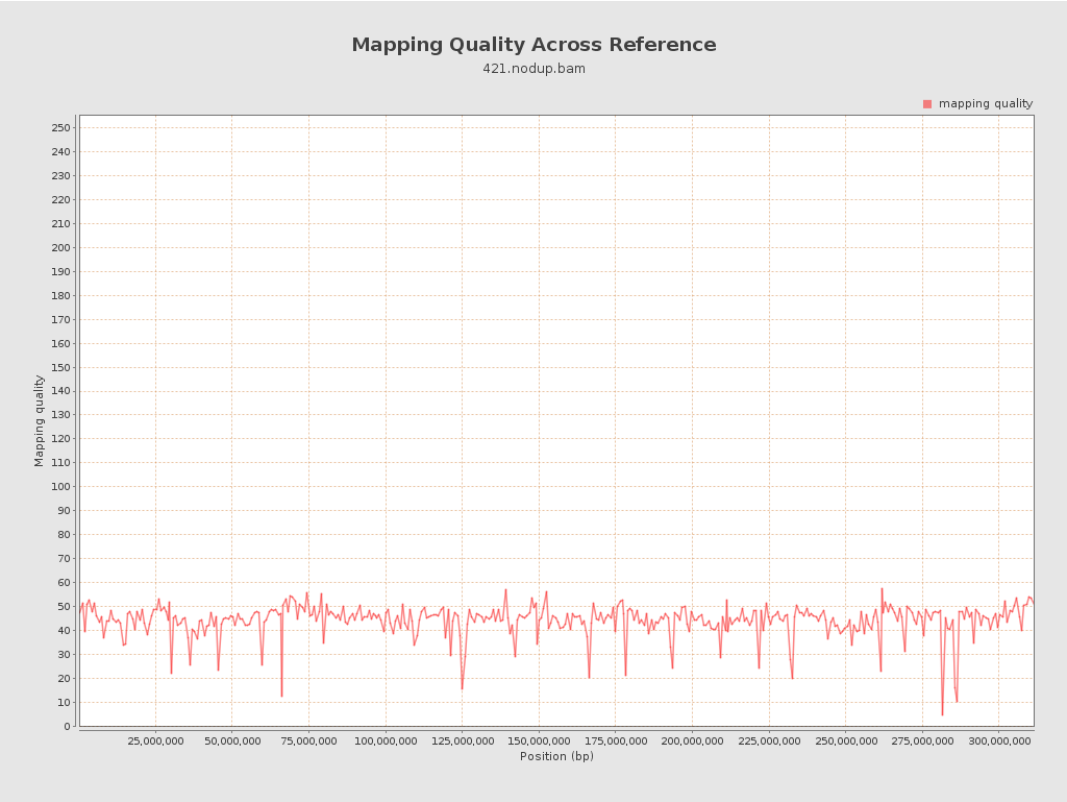
10. Results : Mapped Reads Clipping Profile



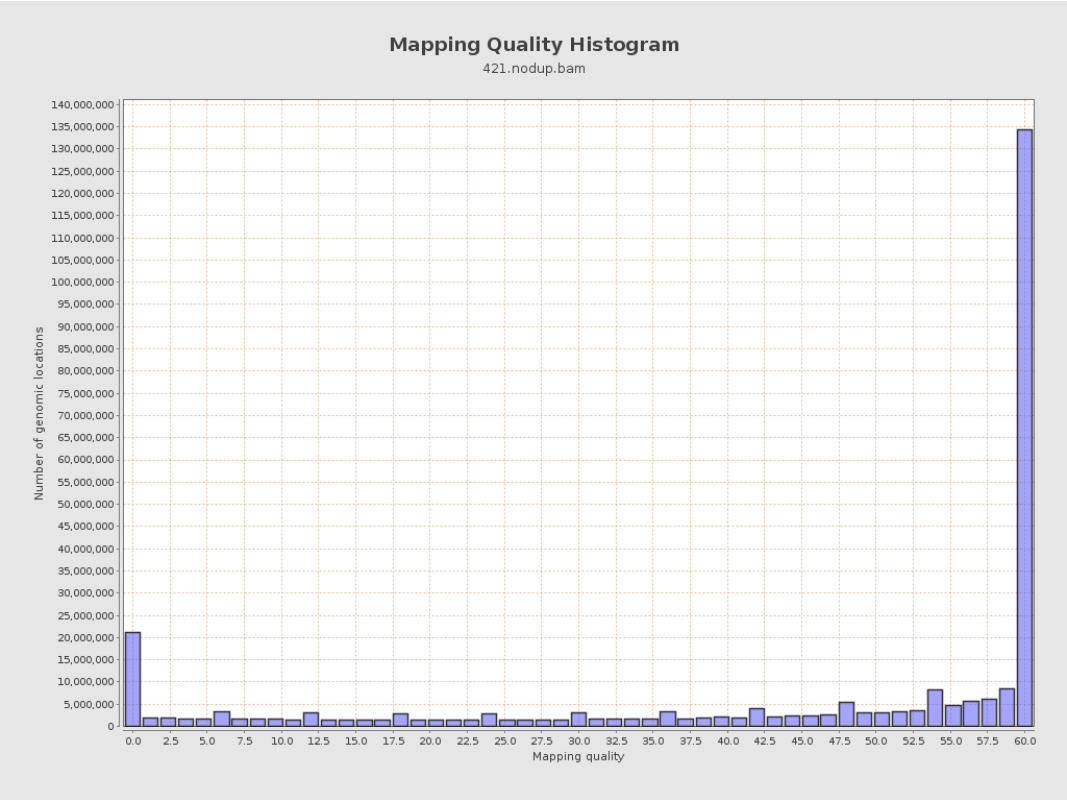
11. Results : Homopolymer Indels



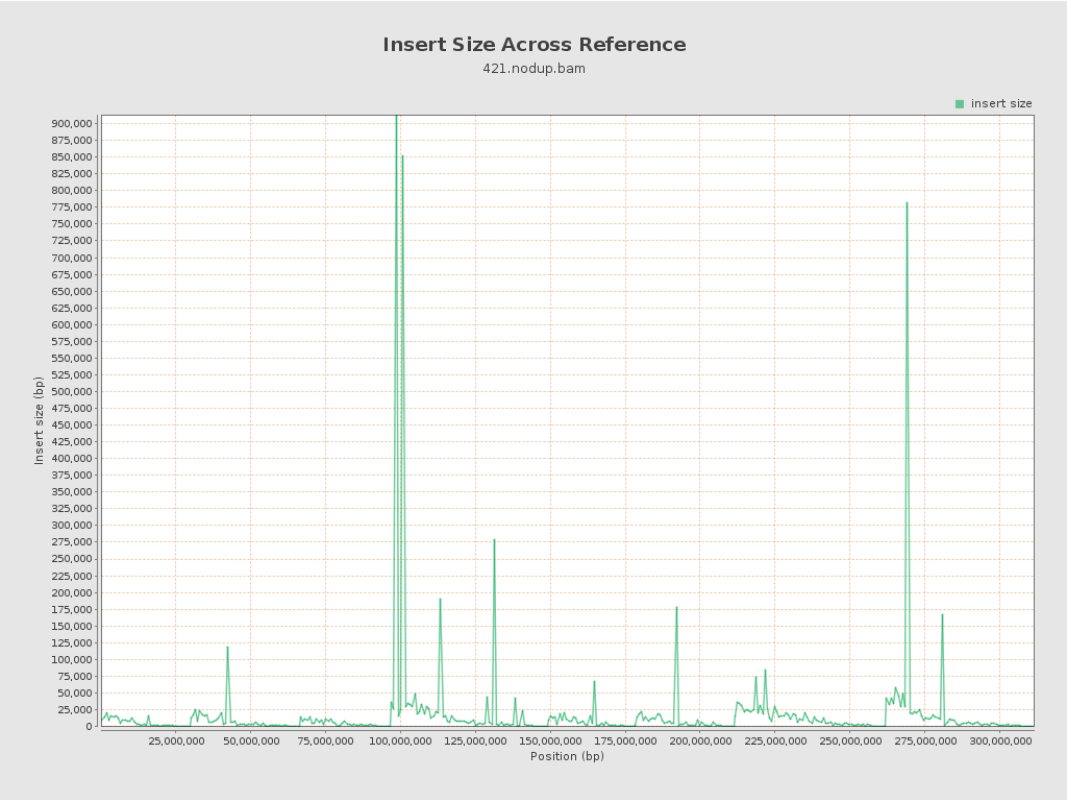
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram