Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/520.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/520.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_453/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_453_S428_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_453/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_453_S428_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:40:51 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	92,740,267
Mapped reads	86,915,546 / 93.72%
Unmapped reads	5,824,721 / 6.28%
Mapped paired reads	86,915,546 / 93.72%
Mapped reads, first in pair	43,526,907 / 46.93%
Mapped reads, second in pair	43,388,639 / 46.79%
Mapped reads, both in pair	84,921,667 / 91.57%
Mapped reads, singletons	1,993,879 / 2.15%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	15,285,195 / 16.48%
Clipped reads	18,961,105 / 20.45%

2.2. ACGT Content

Number/percentage of A's	3,729,311,689 / 30.91%
Number/percentage of C's	2,302,766,637 / 19.09%
Number/percentage of T's	3,736,575,370 / 30.97%
Number/percentage of G's	2,295,643,559 / 19.03%
Number/percentage of N's	41,842 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	38.812
Standard Deviation	326.2542

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Insert size

Mean	237,402.64
Standard Deviation	2,328,704.21
P25/Median/P75	331 / 435 / 574

2.6. Mismatches and indels

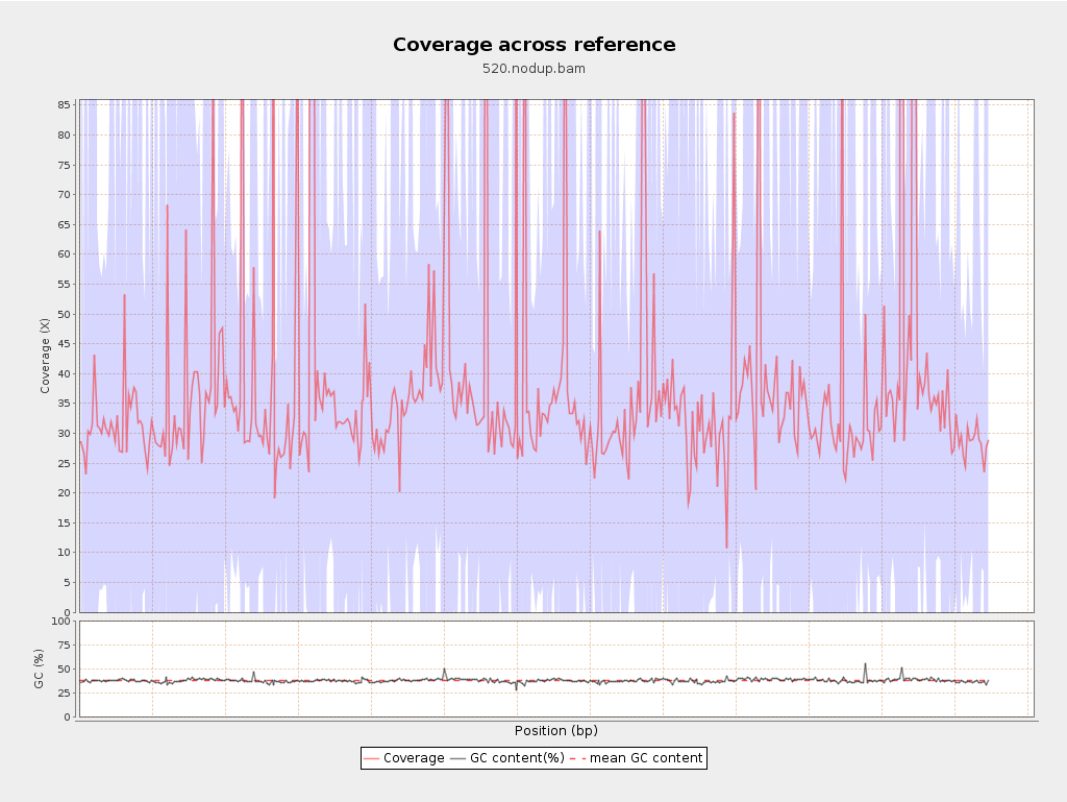
General error rate	2.27%
Mismatches	251,614,360
Insertions	8,272,361
Mapped reads with at least one insertion	8.52%
Deletions	8,273,003
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.8%

2.7. Chromosome stats

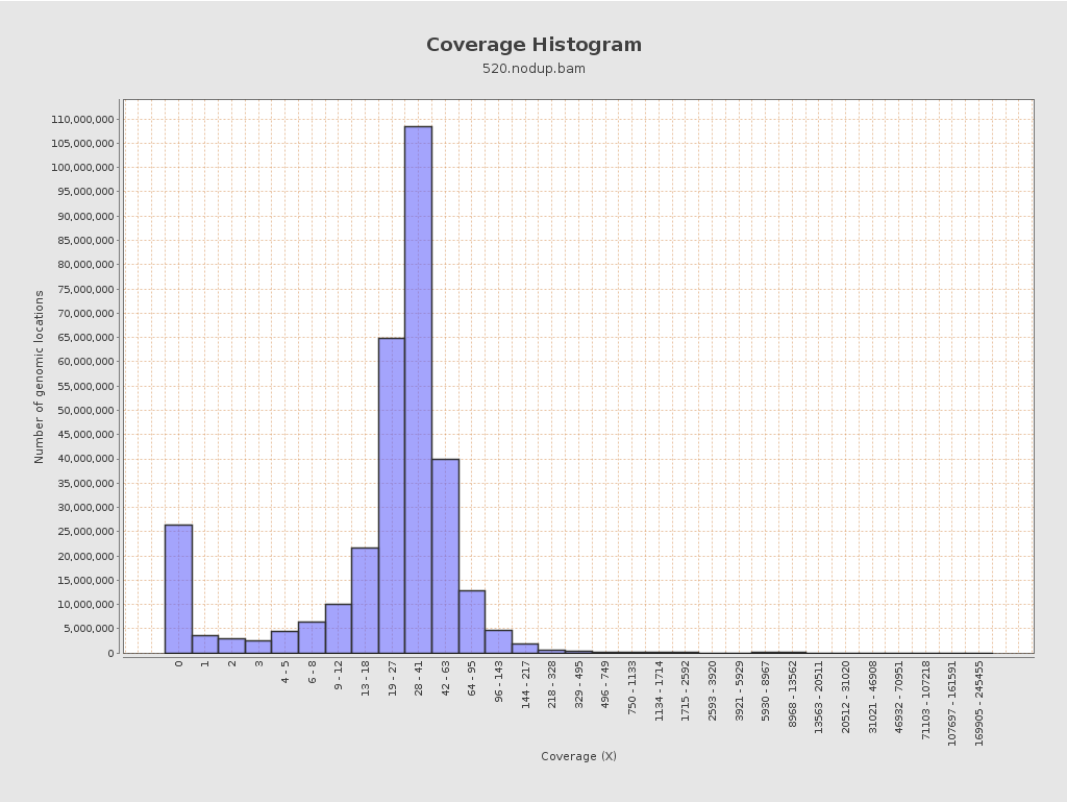
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	923394565	31.0653	108.1544

LT669789.1	36598175	1420152369	38.8039	346.5797
LT669790.1	30422129	1306412302	42.9428	382.7799
LT669791.1	52758100	2049430280	38.8458	310.5541
LT669792.1	28376109	1082579286	38.1511	332.7889
LT669793.1	33388210	1196421620	35.8337	224.6446
LT669794.1	50579949	1847154164	36.5195	278.6719
LT669795.1	49795044	2269905534	45.585	450.8508

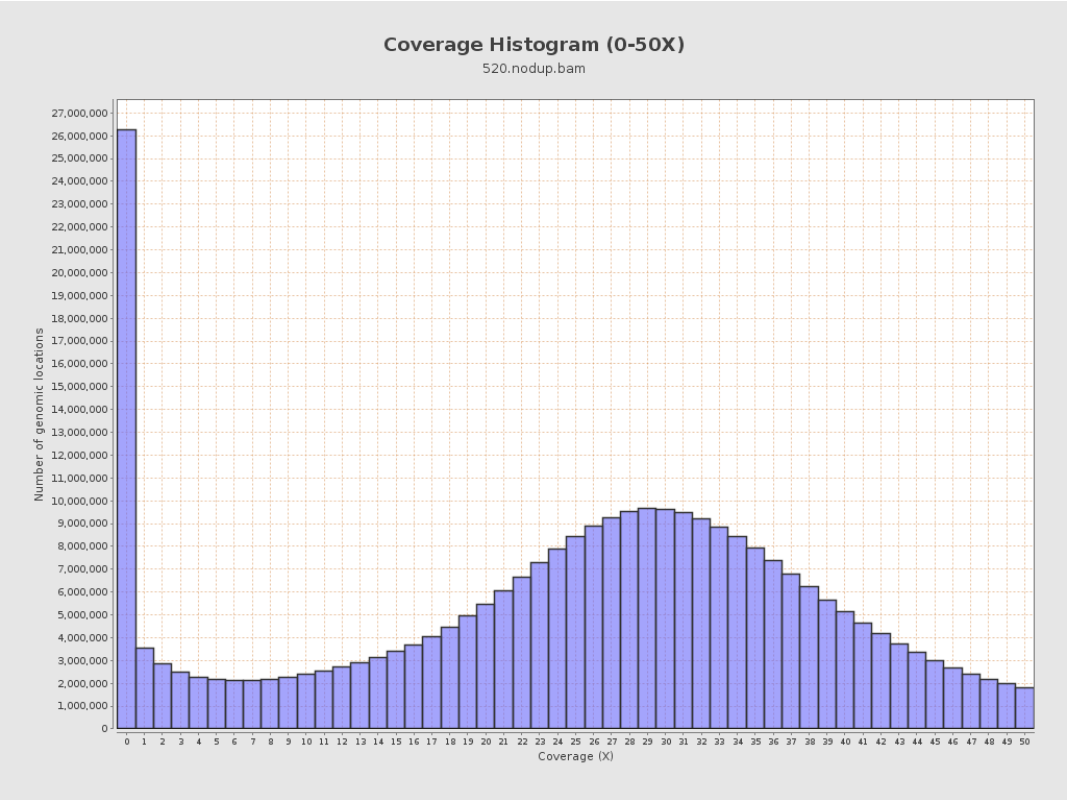
3. Results : Coverage across reference



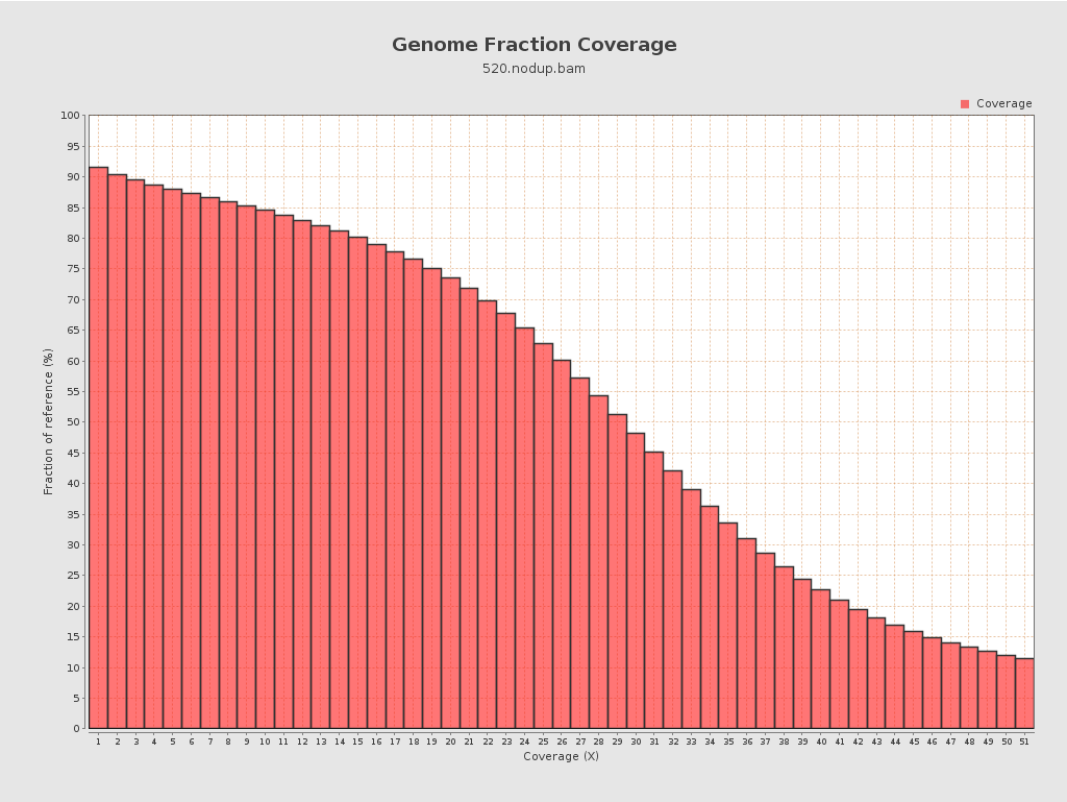
4. Results : Coverage Histogram



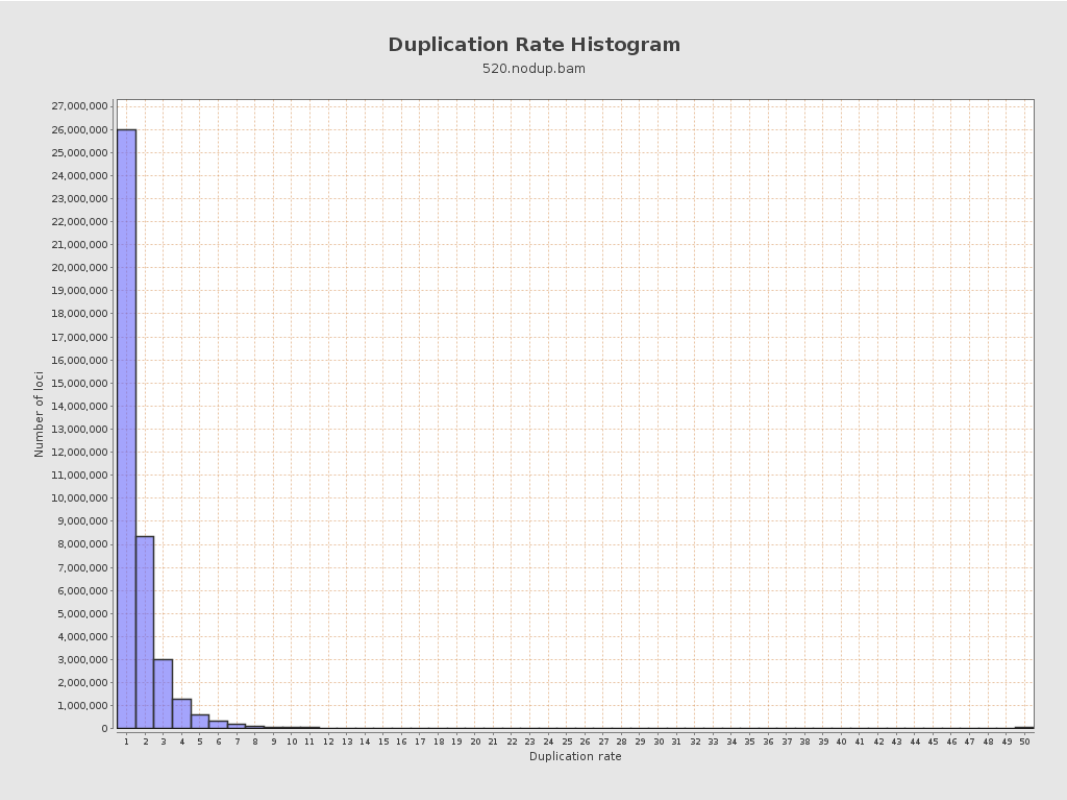
5. Results : Coverage Histogram (0-50X)



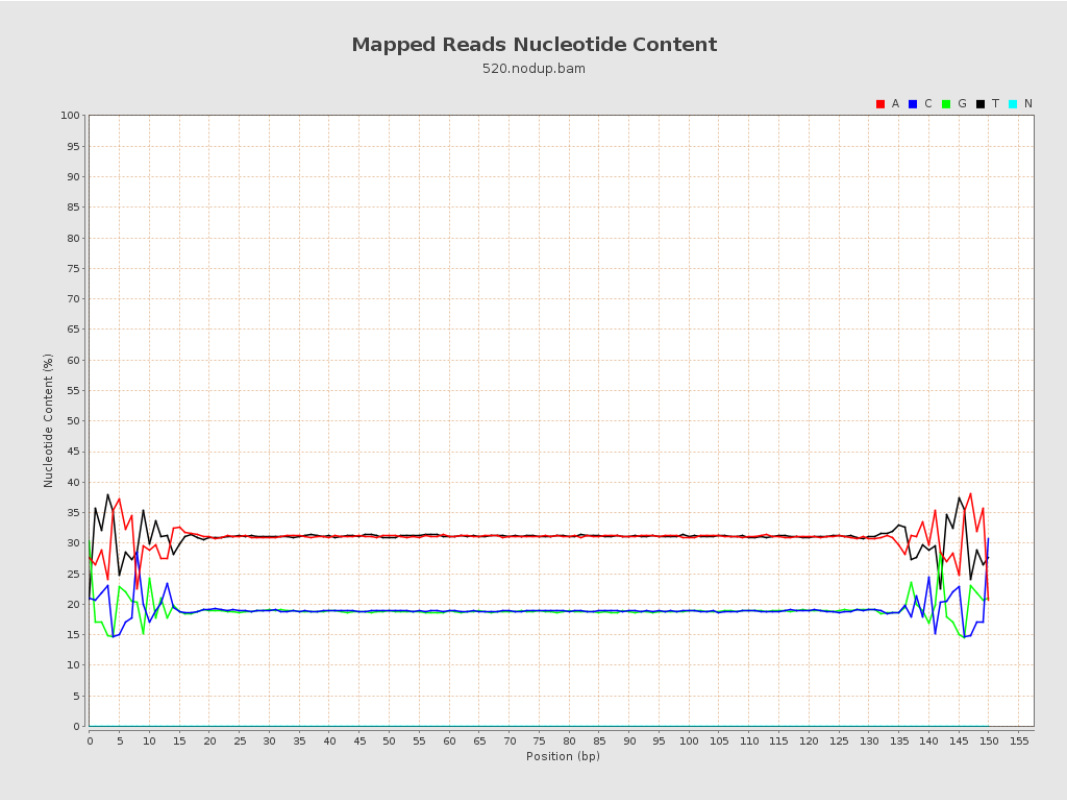
6. Results : Genome Fraction Coverage



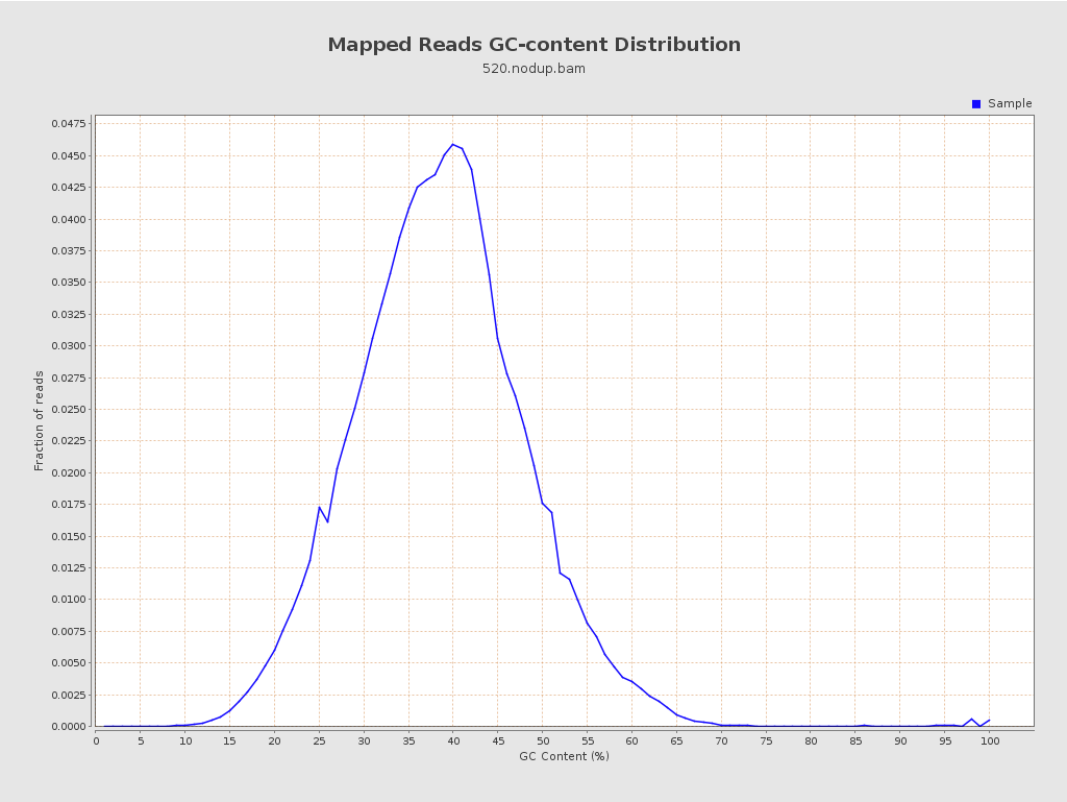
7. Results : Duplication Rate Histogram



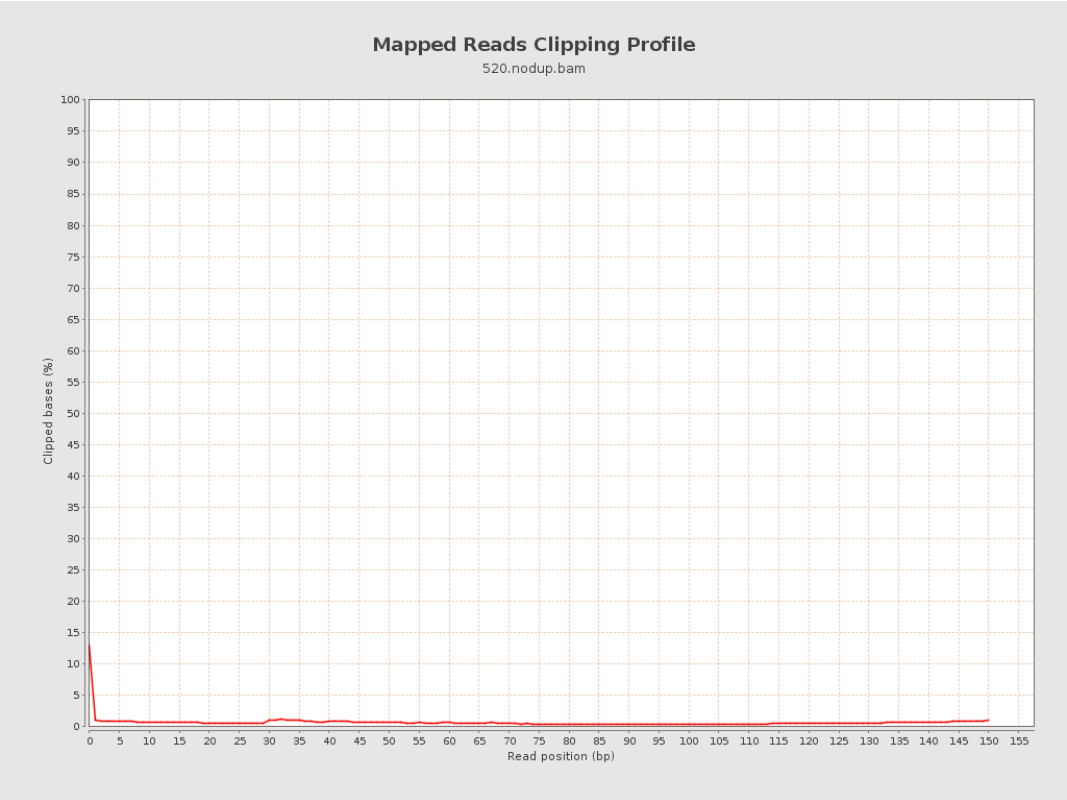
8. Results : Mapped Reads Nucleotide Content



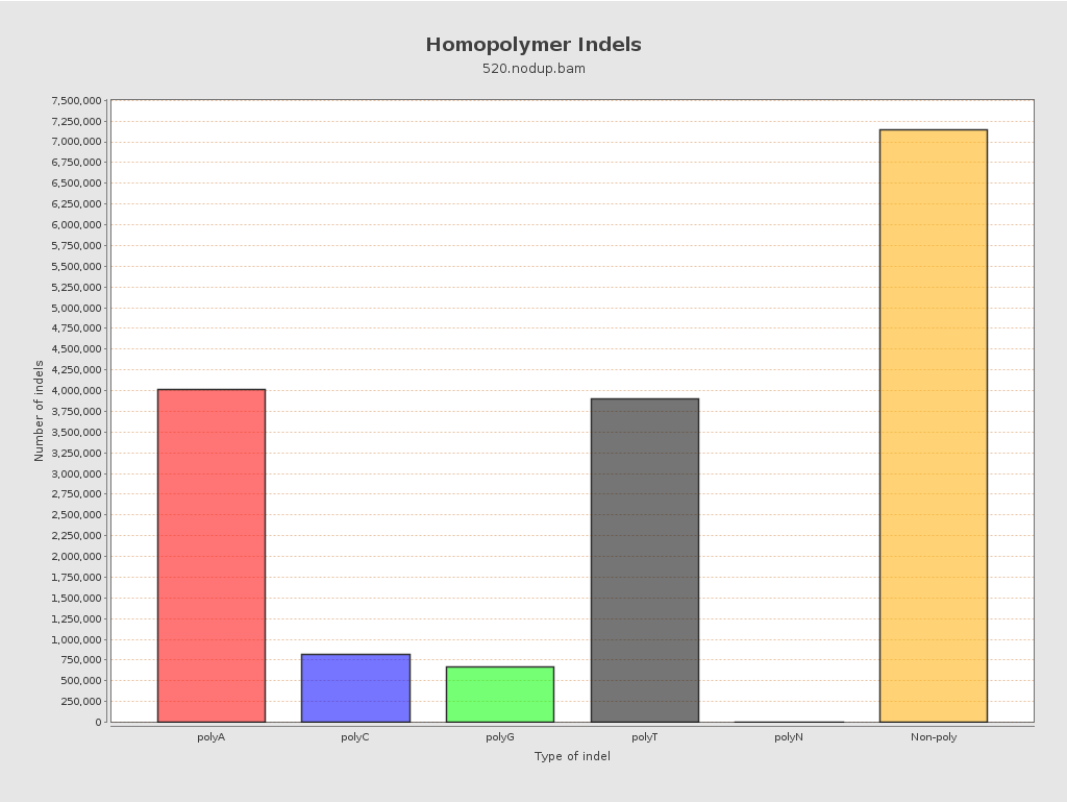
9. Results : Mapped Reads GC-content Distribution



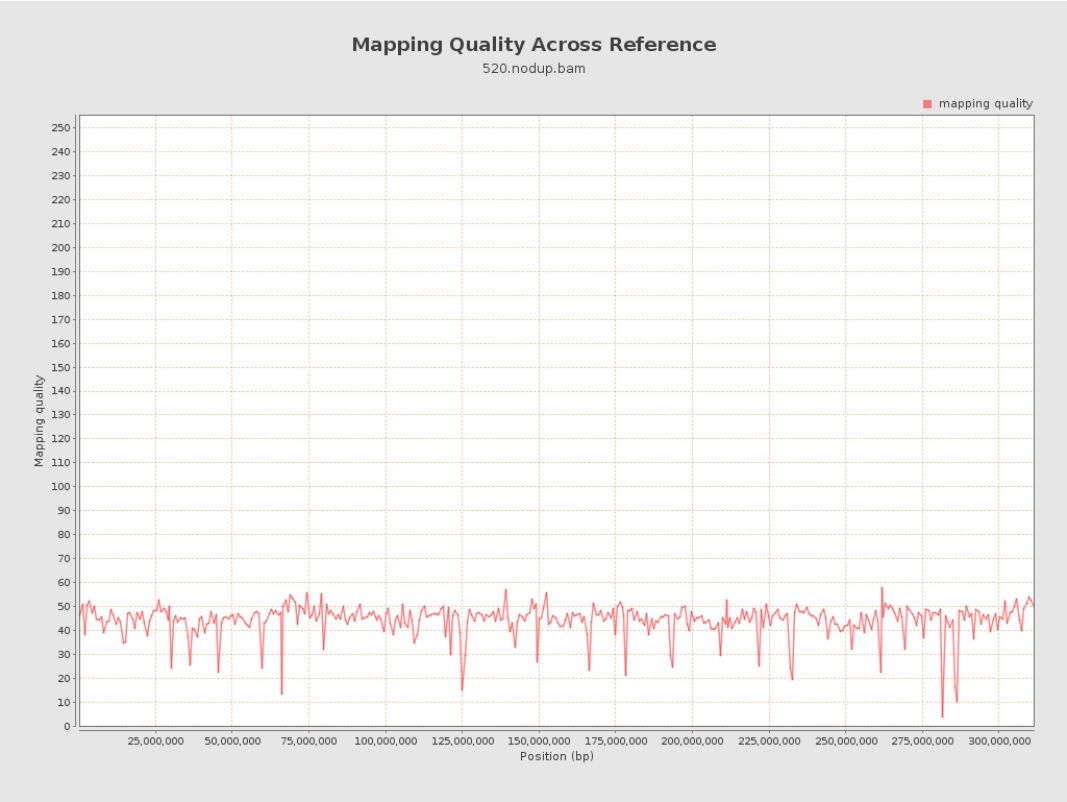
10. Results : Mapped Reads Clipping Profile



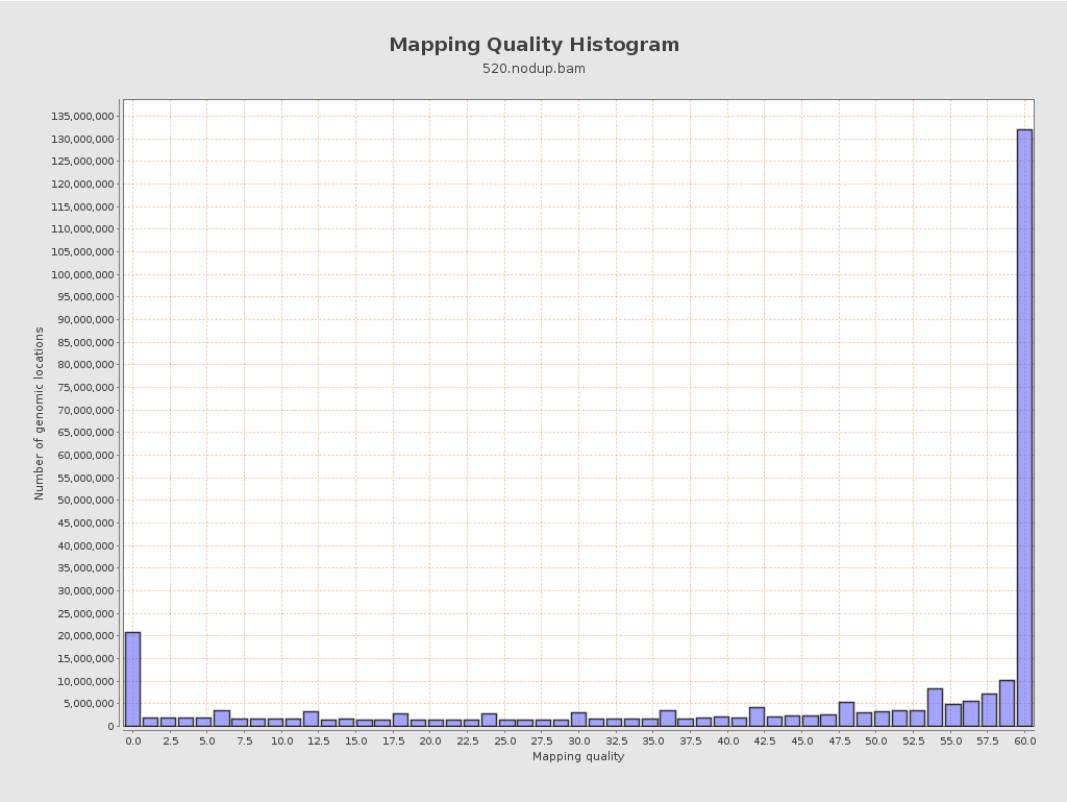
11. Results : Homopolymer Indels



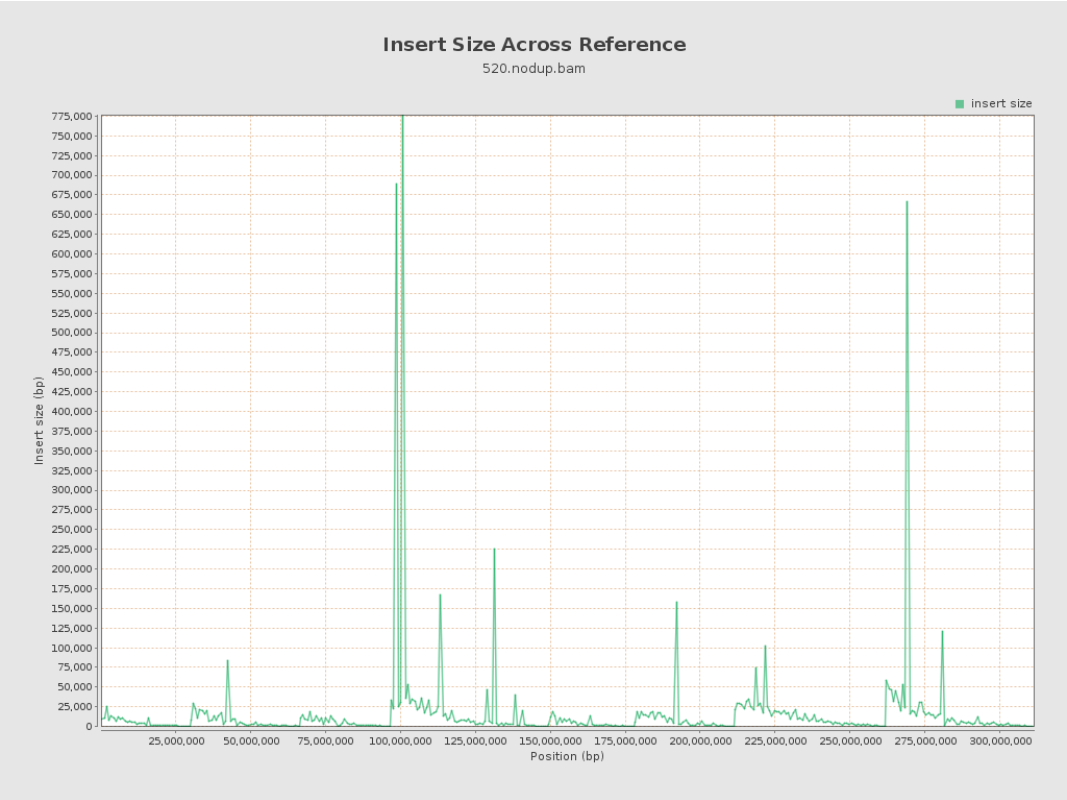
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram