Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/994.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/994.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_116/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_116_S206_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_116/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_116_S206_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:14 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	77,967,170
Mapped reads	73,198,238 / 93.88%
Unmapped reads	4,768,932 / 6.12%
Mapped paired reads	73,198,238 / 93.88%
Mapped reads, first in pair	36,658,367 / 47.02%
Mapped reads, second in pair	36,539,871 / 46.87%
Mapped reads, both in pair	71,777,017 / 92.06%
Mapped reads, singletons	1,421,221 / 1.82%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	12,109,641 / 15.53%
Clipped reads	15,752,761 / 20.2%

2.2. ACGT Content

Number/percentage of A's	3,145,576,647 / 30.88%
Number/percentage of C's	1,951,938,216 / 19.16%
Number/percentage of T's	3,145,369,692 / 30.87%
Number/percentage of G's	1,944,988,743 / 19.09%
Number/percentage of N's	42,115 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	32.7745
Standard Deviation	257.2123

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Insert size

Mean	225,320.21
Standard Deviation	2,244,981.32
P25/Median/P75	327 / 427 / 558

2.6. Mismatches and indels

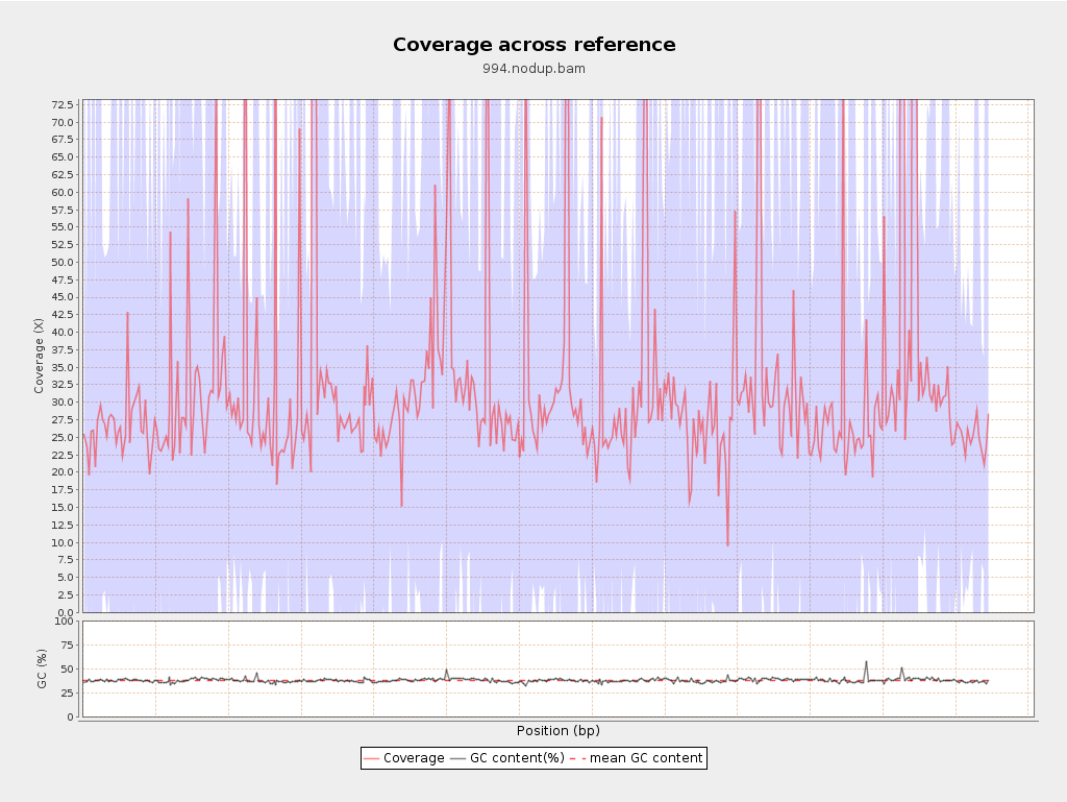
General error rate	2.24%
Mismatches	210,230,141
Insertions	6,652,686
Mapped reads with at least one insertion	8.18%
Deletions	6,854,610
Mapped reads with at least one deletion	8.32%
Homopolymer indels	56.81%

2.7. Chromosome stats

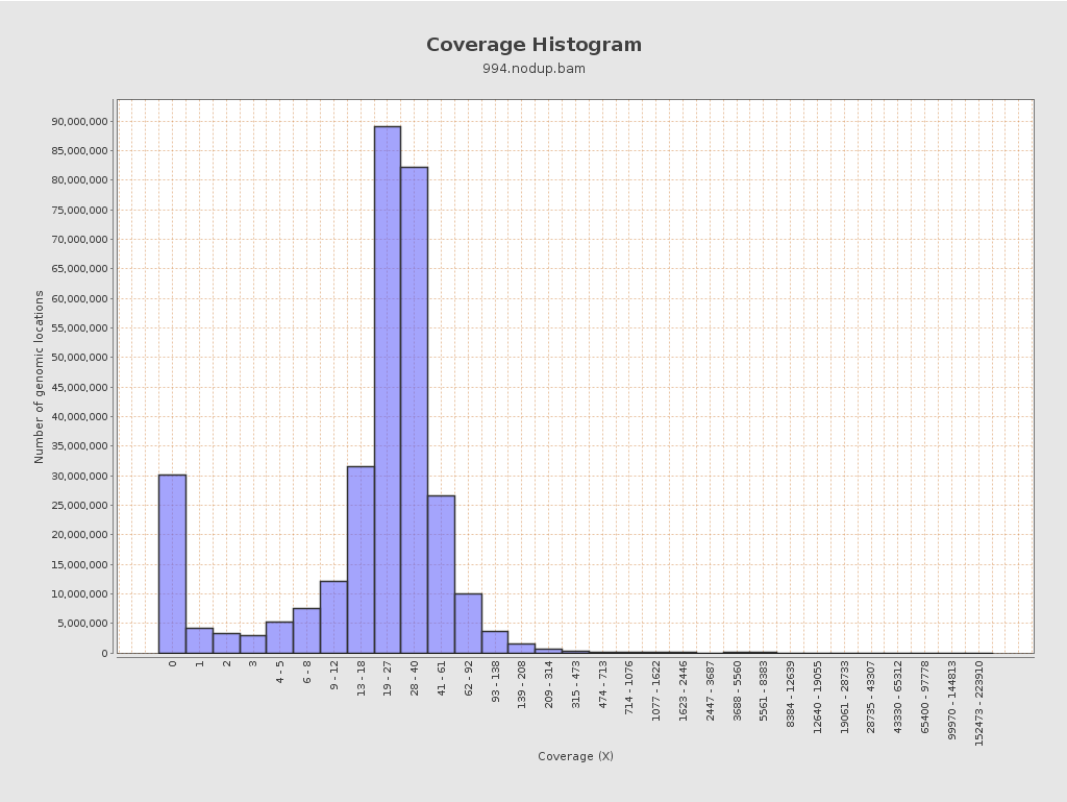
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	781078196	26.2774	67.3914

LT669789.1	36598175	1209184024	33.0395	250.9344
LT669790.1	30422129	1062230131	34.9164	246.56
LT669791.1	52758100	1718594341	32.575	199.3086
LT669792.1	28376109	900463368	31.7332	272.6986
LT669793.1	33388210	1027814463	30.7838	189.0737
LT669794.1	50579949	1573353654	31.1063	212.4944
LT669795.1	49795044	1941180961	38.9834	416.5881

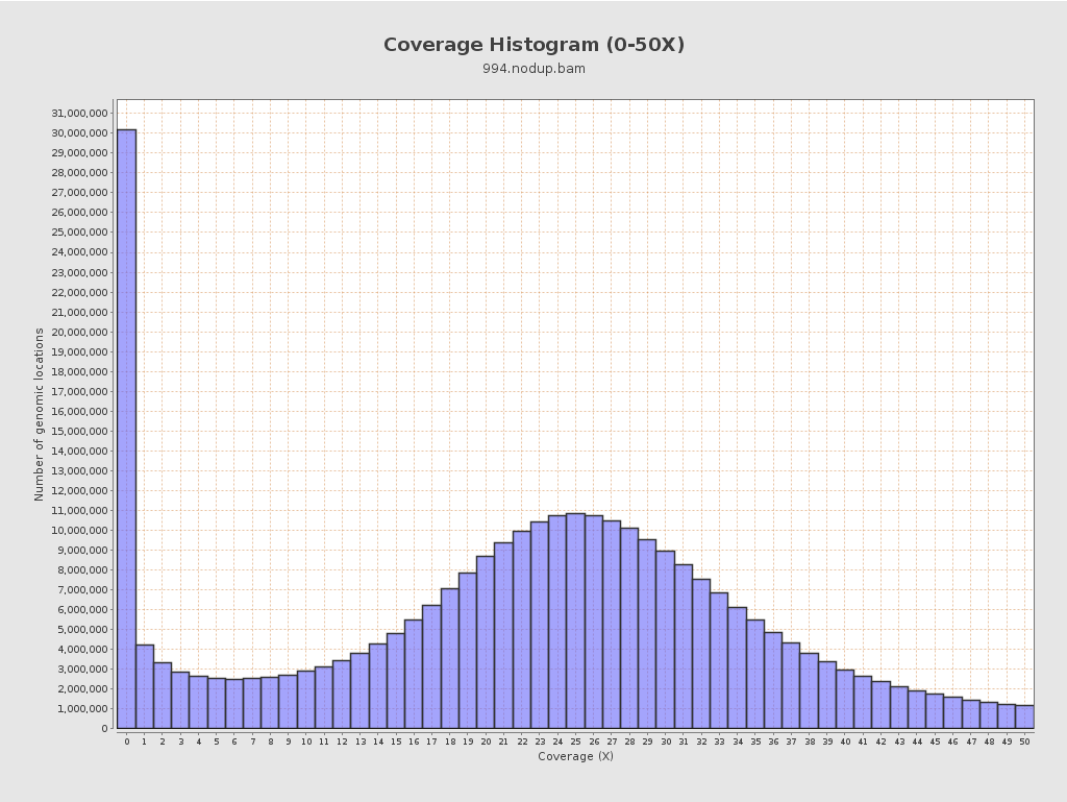
3. Results : Coverage across reference



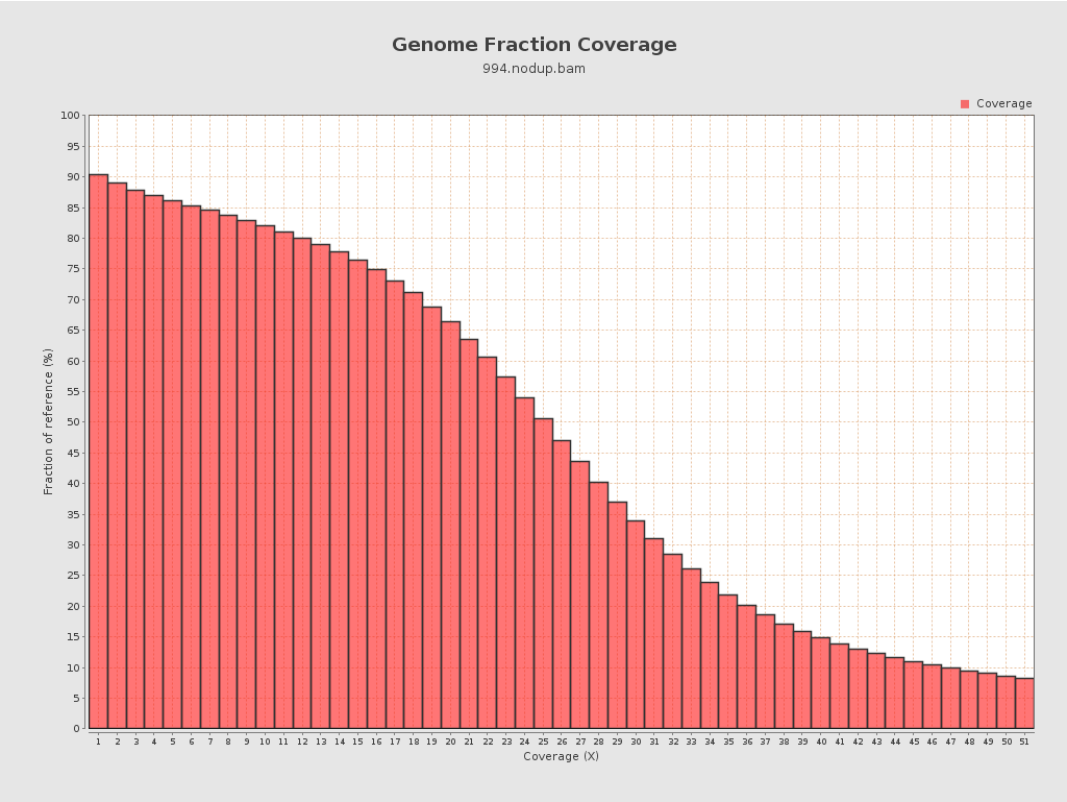
4. Results : Coverage Histogram



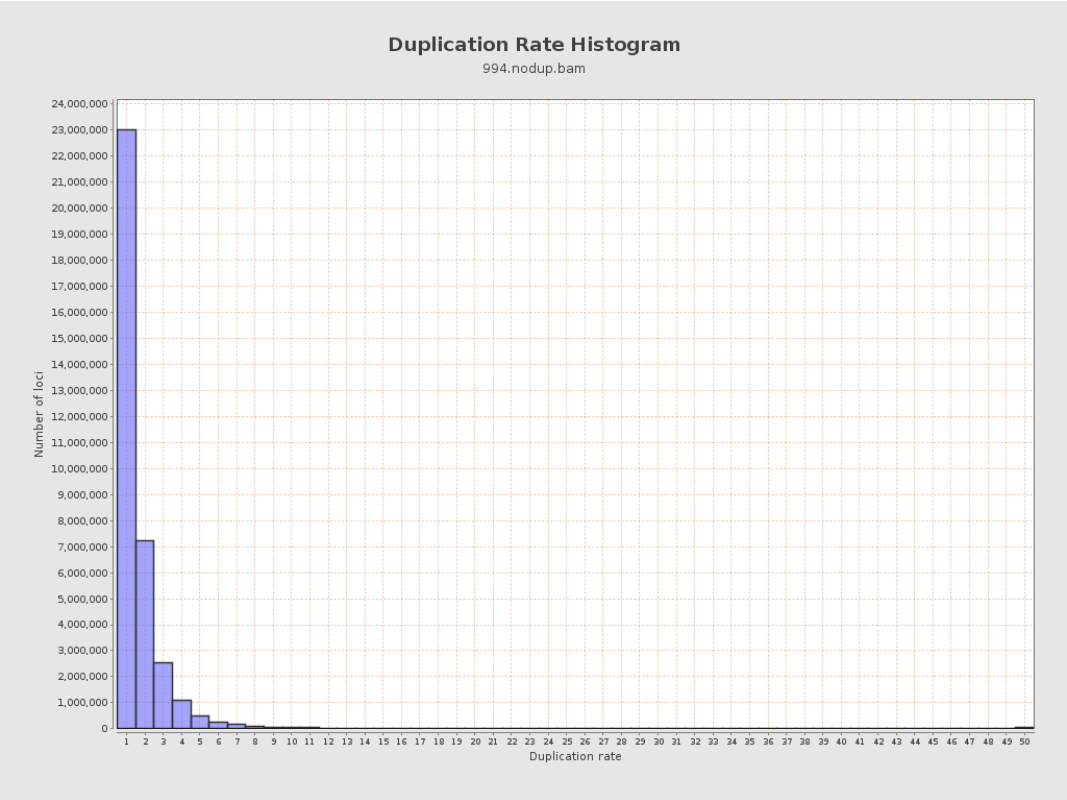
5. Results : Coverage Histogram (0-50X)



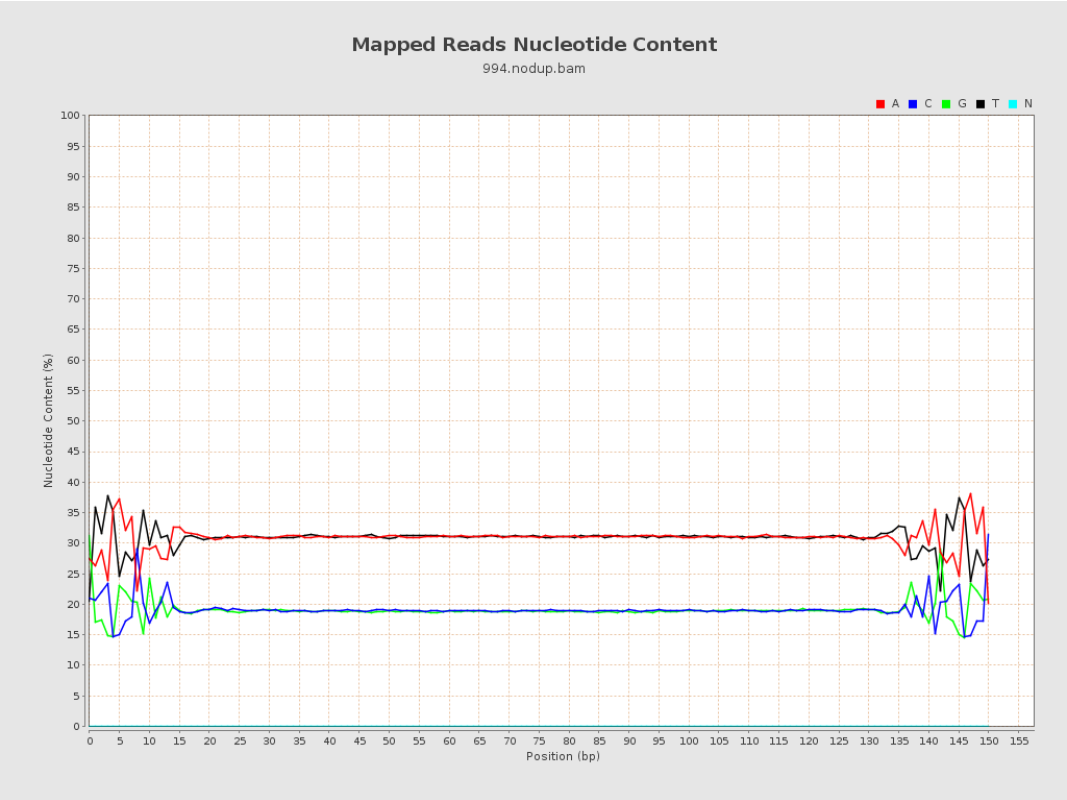
6. Results : Genome Fraction Coverage



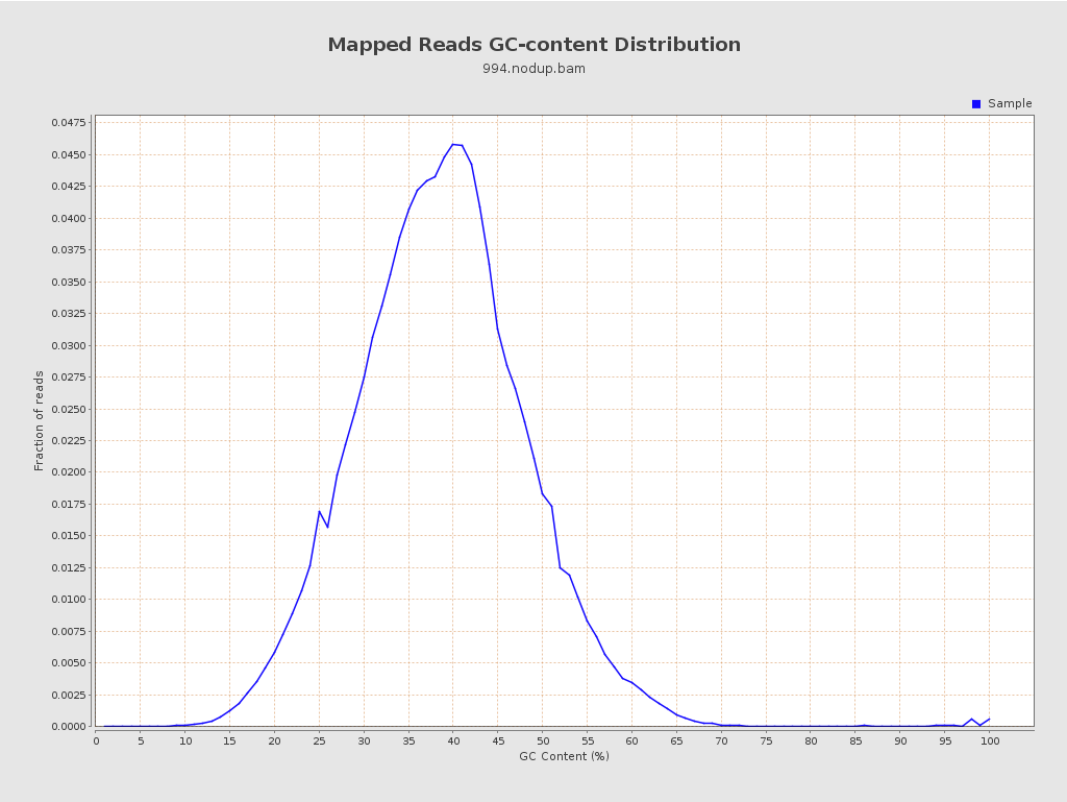
7. Results : Duplication Rate Histogram



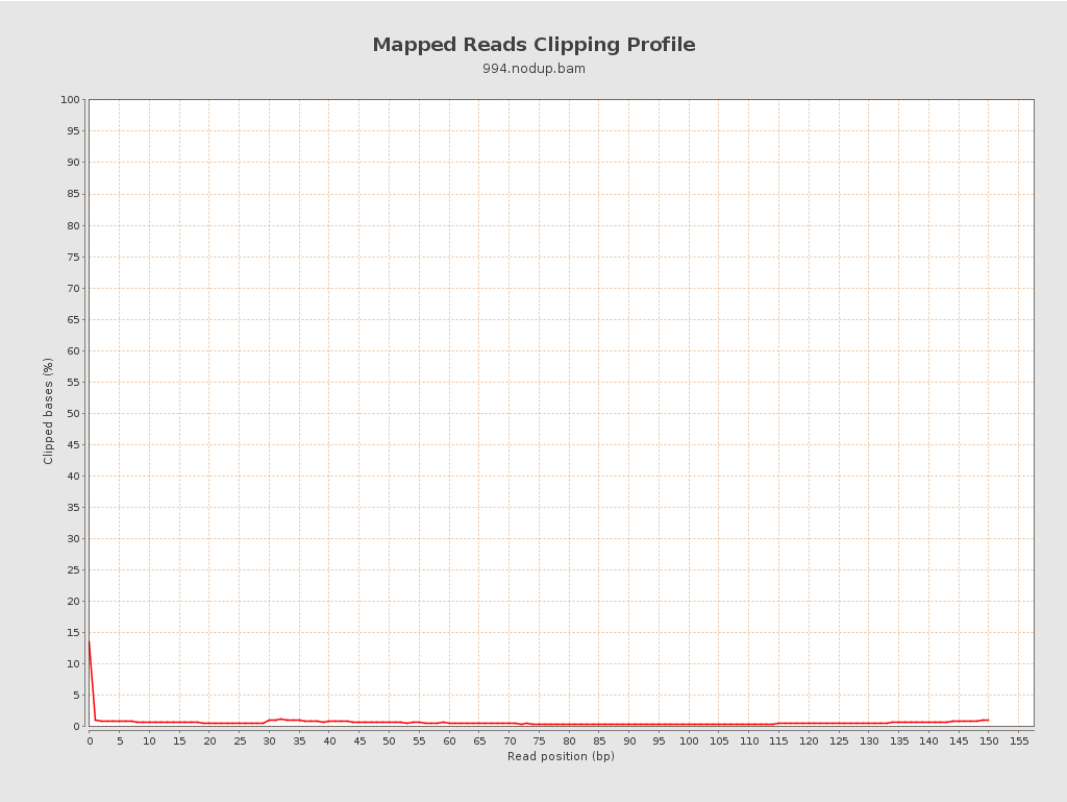
8. Results : Mapped Reads Nucleotide Content



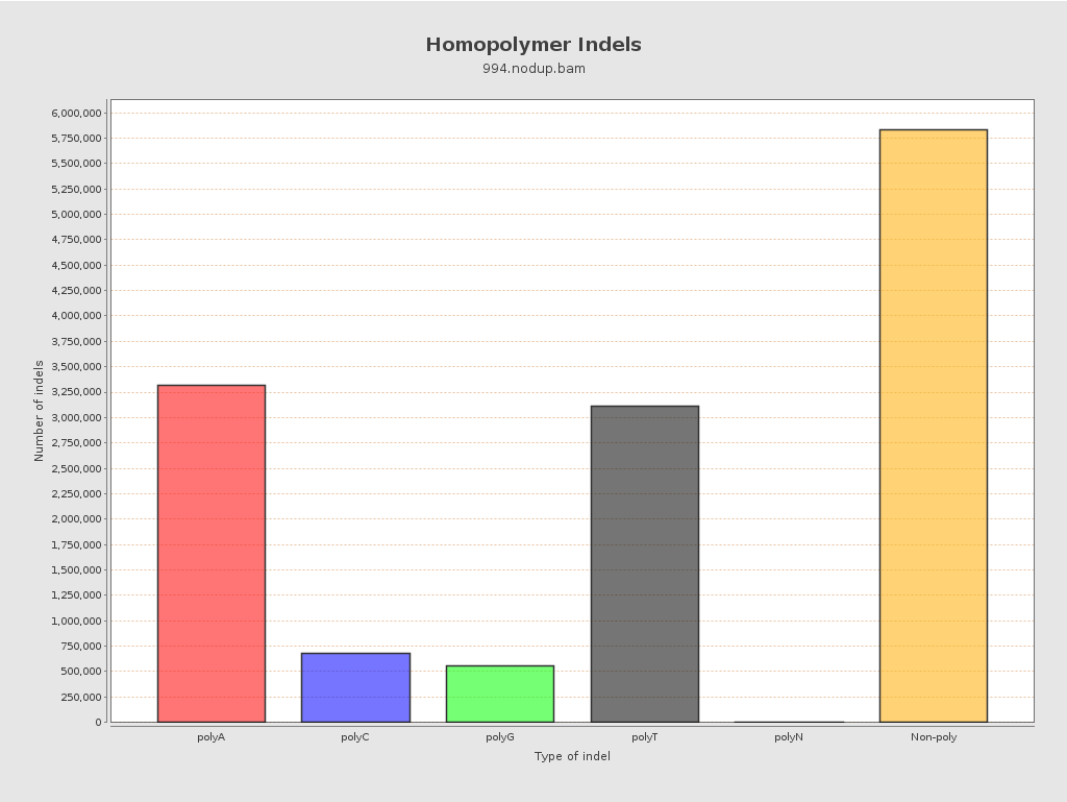
9. Results : Mapped Reads GC-content Distribution



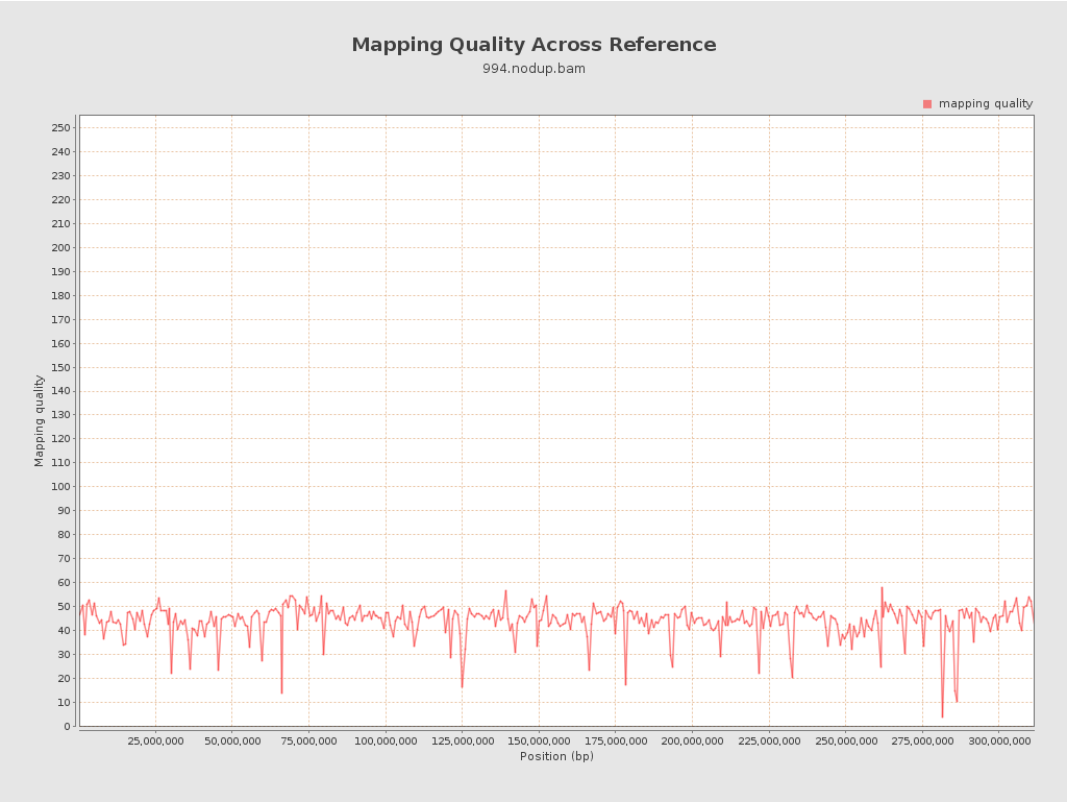
10. Results : Mapped Reads Clipping Profile



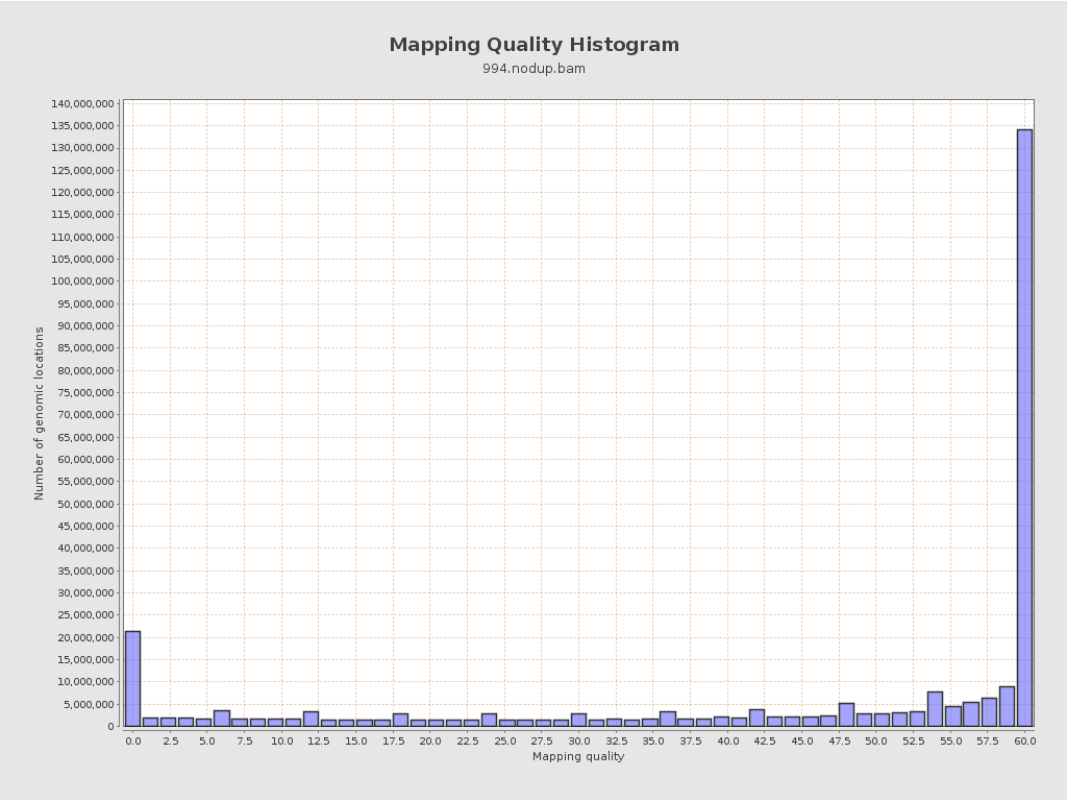
11. Results : Homopolymer Indels



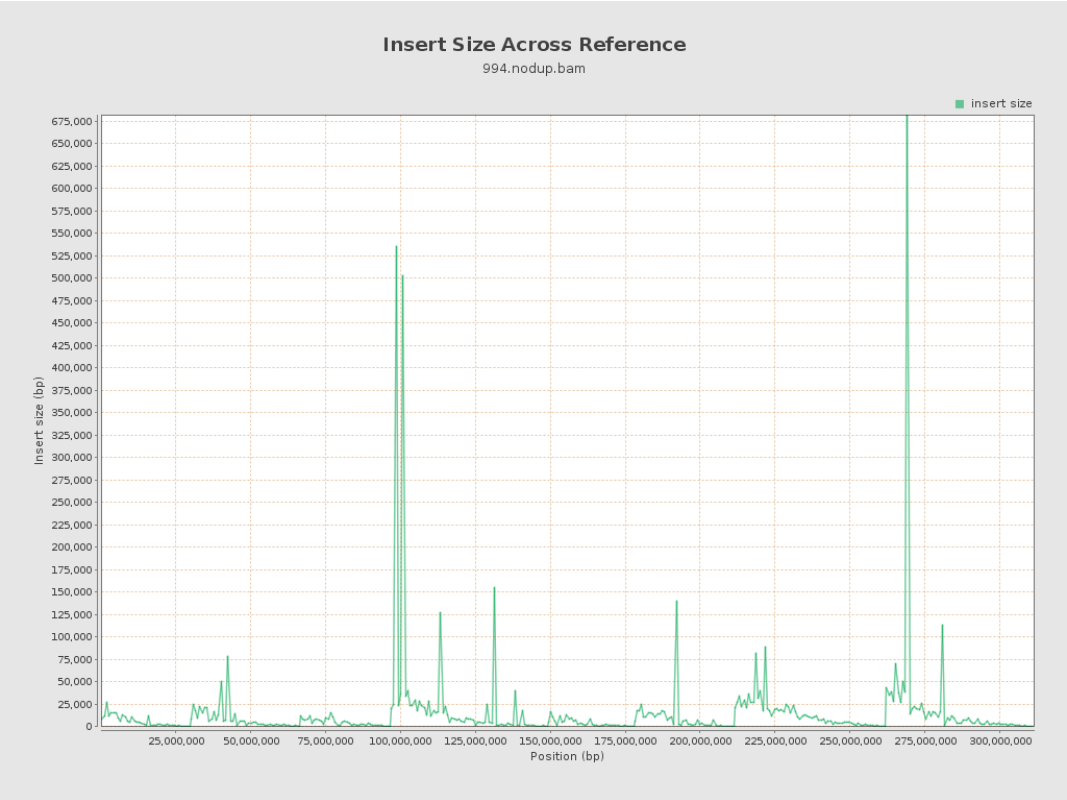
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram