Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/978.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/978.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_245/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_245_S326_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_245/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_245_S326_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	81,635,706
Mapped reads	75,070,943 / 91.96%
Unmapped reads	6,564,763 / 8.04%
Mapped paired reads	75,070,943 / 91.96%
Mapped reads, first in pair	37,595,366 / 46.05%
Mapped reads, second in pair	37,475,577 / 45.91%
Mapped reads, both in pair	73,026,998 / 89.45%
Mapped reads, singletons	2,043,945 / 2.5%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	12,448,745 / 15.25%
Clipped reads	17,636,955 / 21.6%

2.2. ACGT Content

Number/percentage of A's	3,181,445,265 / 30.88%
Number/percentage of C's	1,969,604,420 / 19.12%
Number/percentage of T's	3,186,955,654 / 30.94%
Number/percentage of G's	1,963,660,542 / 19.06%
Number/percentage of N's	38,917 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	33.1396
Standard Deviation	302.6406

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Insert size

Mean	231,417.23
Standard Deviation	2,313,982.88
P25/Median/P75	298 / 393 / 510

2.6. Mismatches and indels

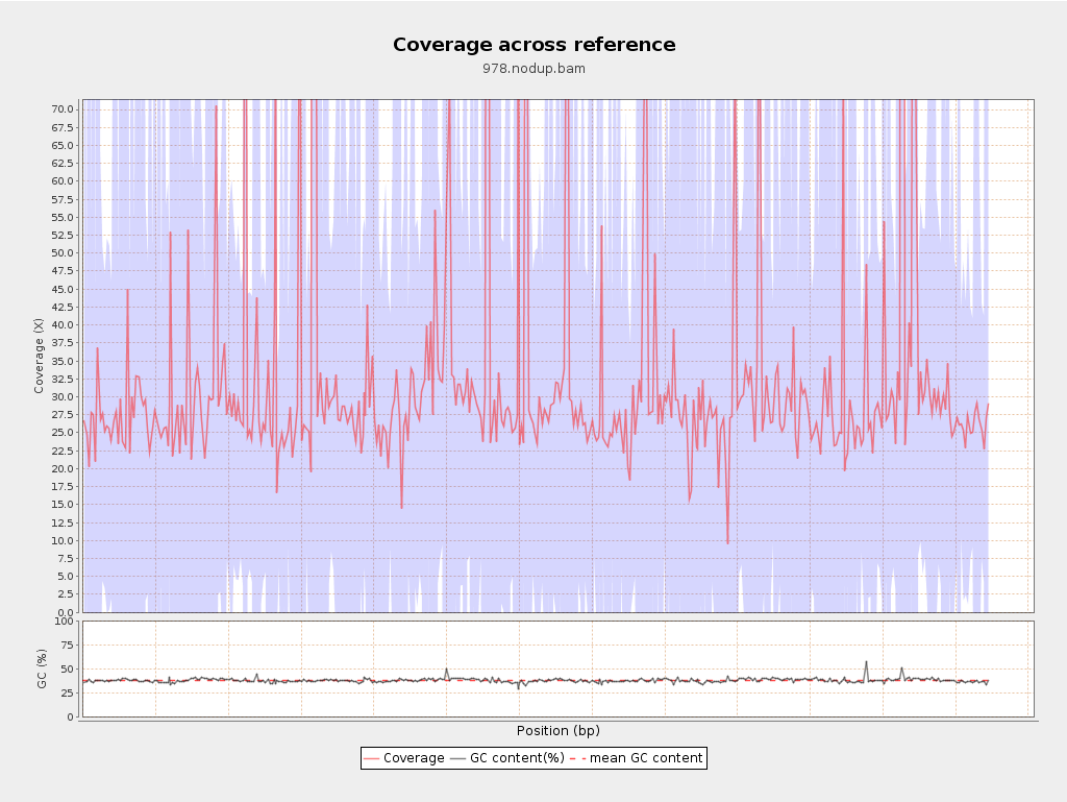
General error rate	2.26%
Mismatches	212,186,529
Insertions	7,218,803
Mapped reads with at least one insertion	8.59%
Deletions	6,927,713
Mapped reads with at least one deletion	8.21%
Homopolymer indels	57.71%

2.7. Chromosome stats

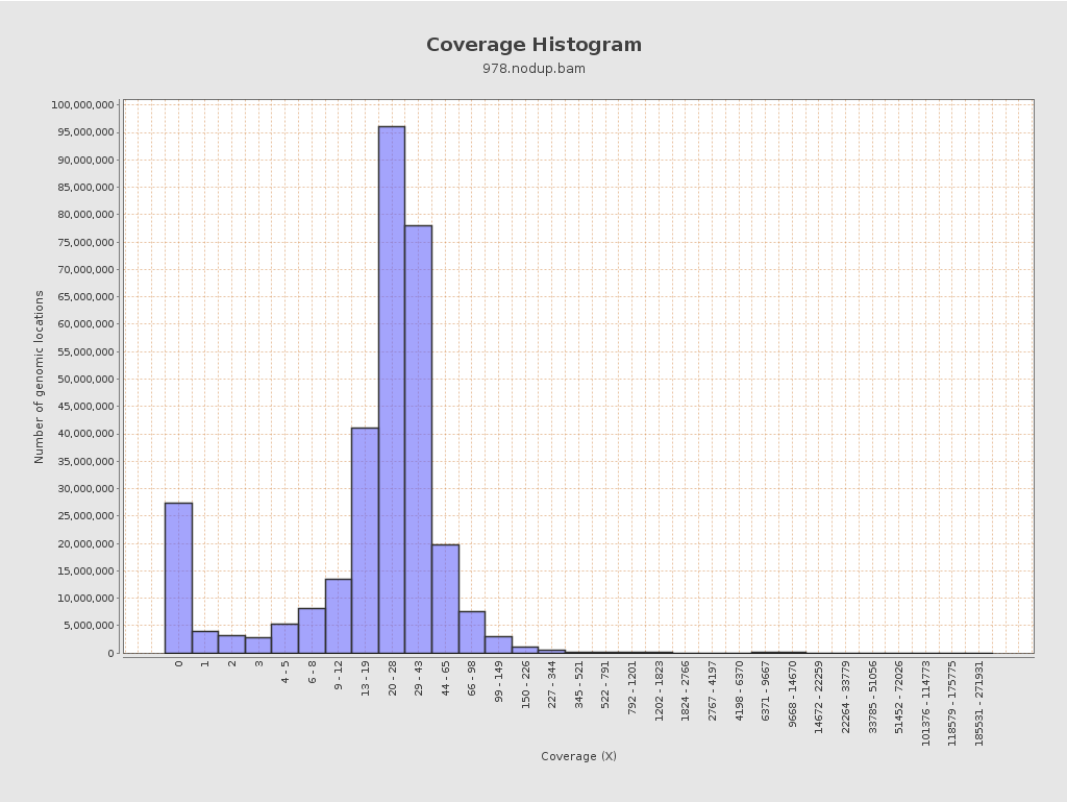
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	802674933	27.004	111.1886

LT669789.1	36598175	1192661502	32.588	297.6149
LT669790.1	30422129	1187051176	39.0193	412.6263
LT669791.1	52758100	1746945795	33.1124	315.4696
LT669792.1	28376109	941767674	33.1888	314.7285
LT669793.1	33388210	1000517173	29.9662	195.7278
LT669794.1	50579949	1543089510	30.5079	227.3771
LT669795.1	49795044	1912989812	38.4173	395.6597

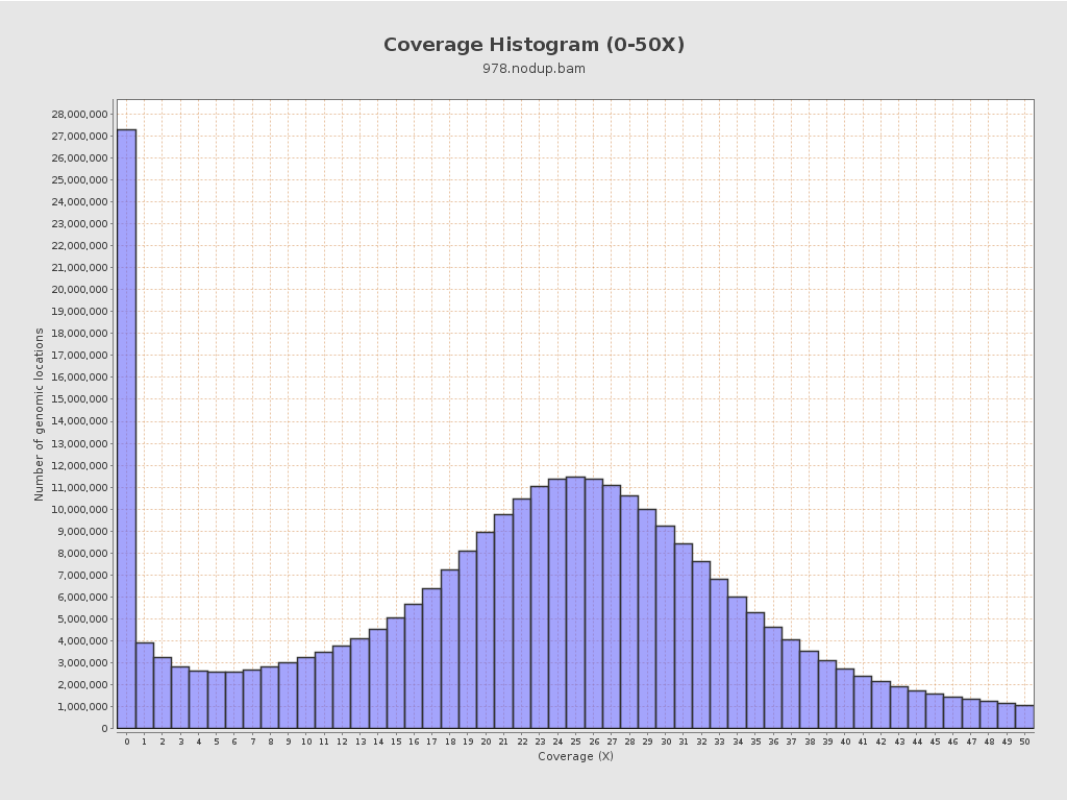
3. Results : Coverage across reference



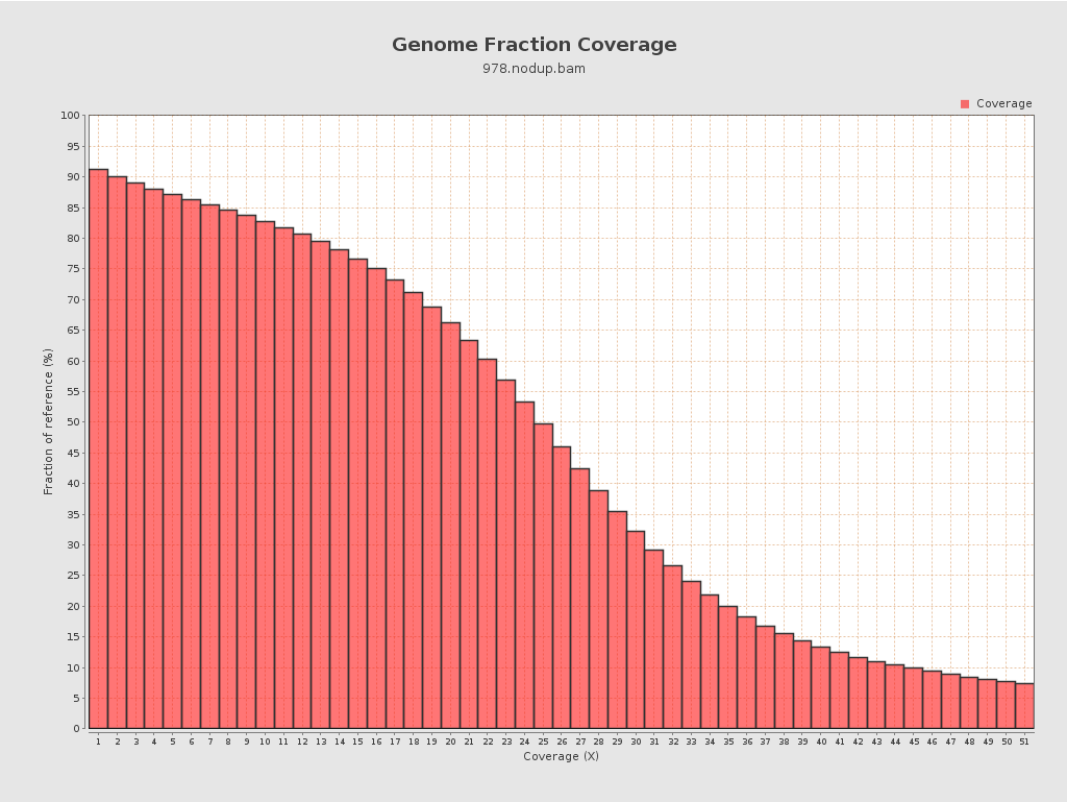
4. Results : Coverage Histogram



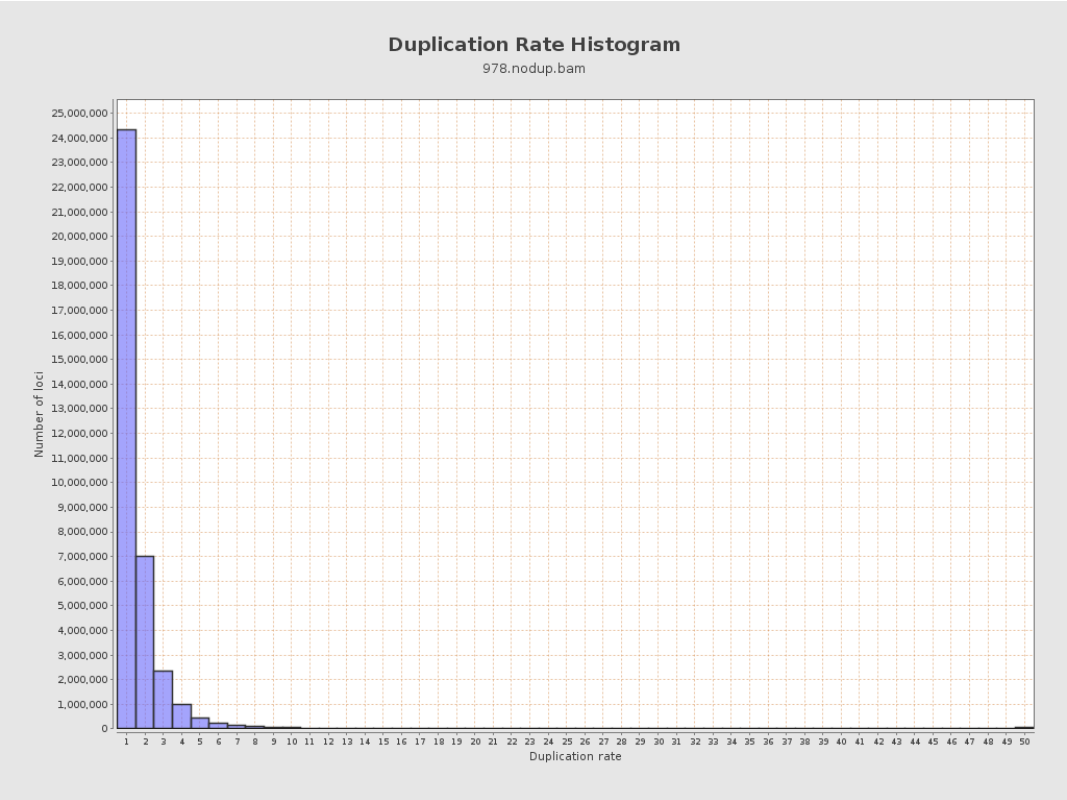
5. Results : Coverage Histogram (0-50X)



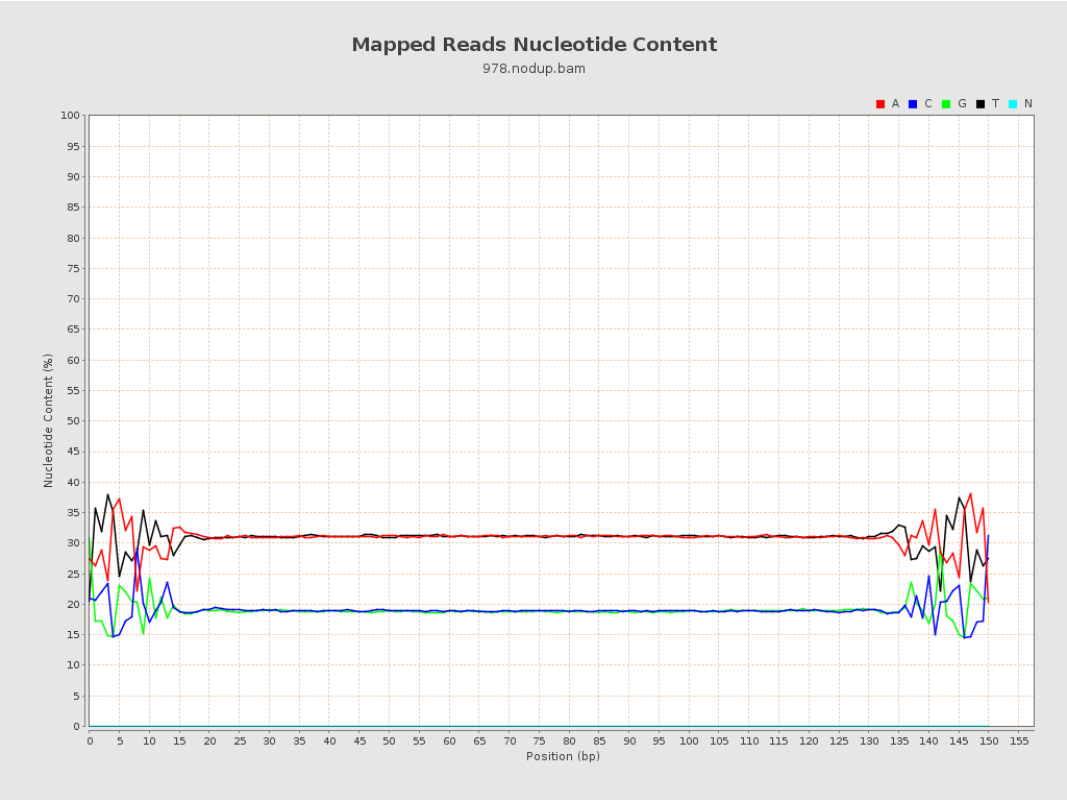
6. Results : Genome Fraction Coverage



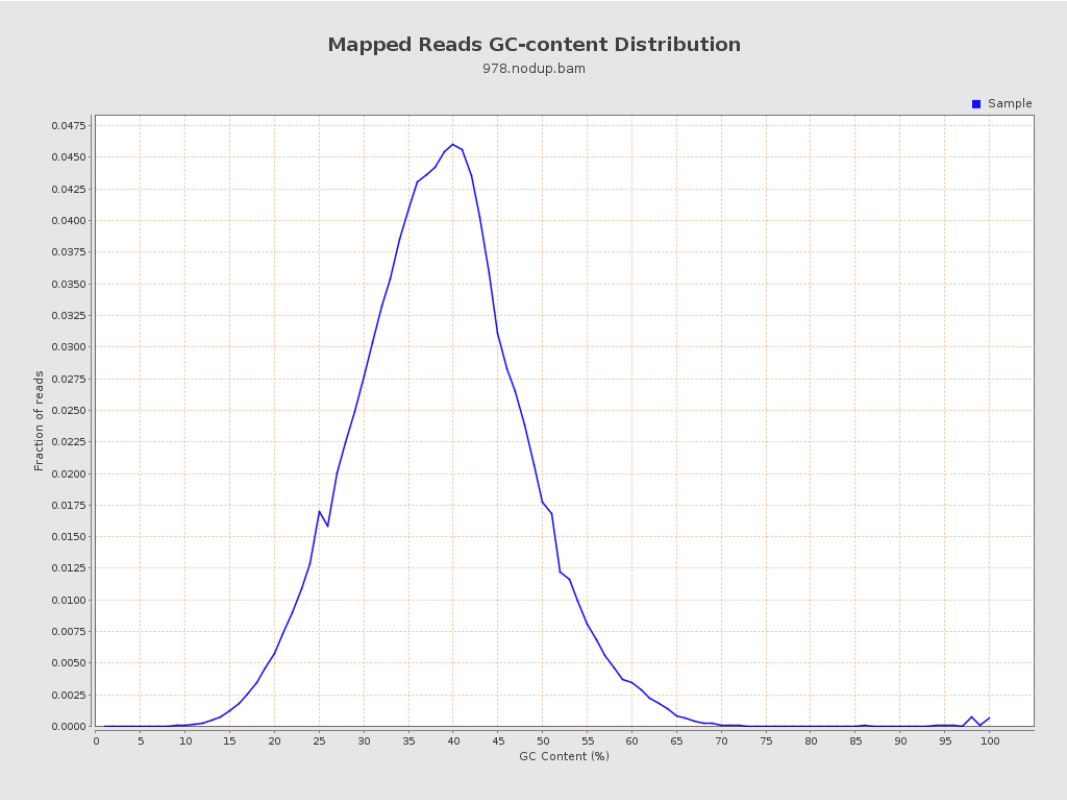
7. Results : Duplication Rate Histogram



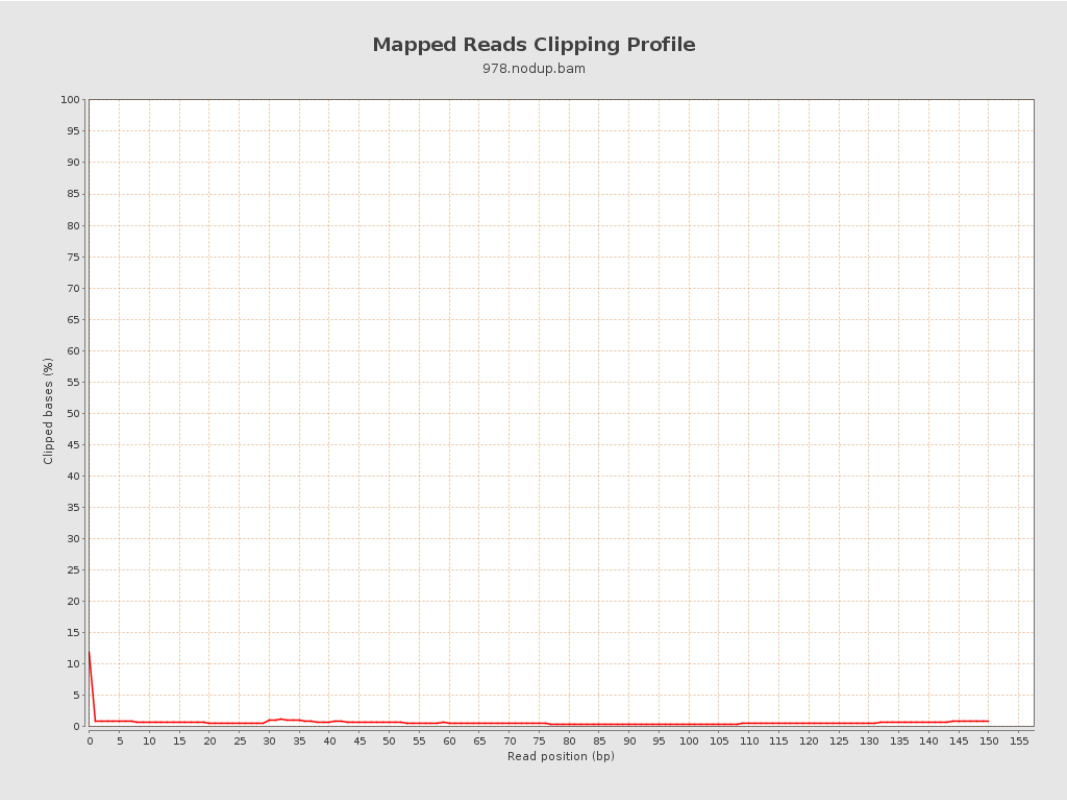
8. Results : Mapped Reads Nucleotide Content



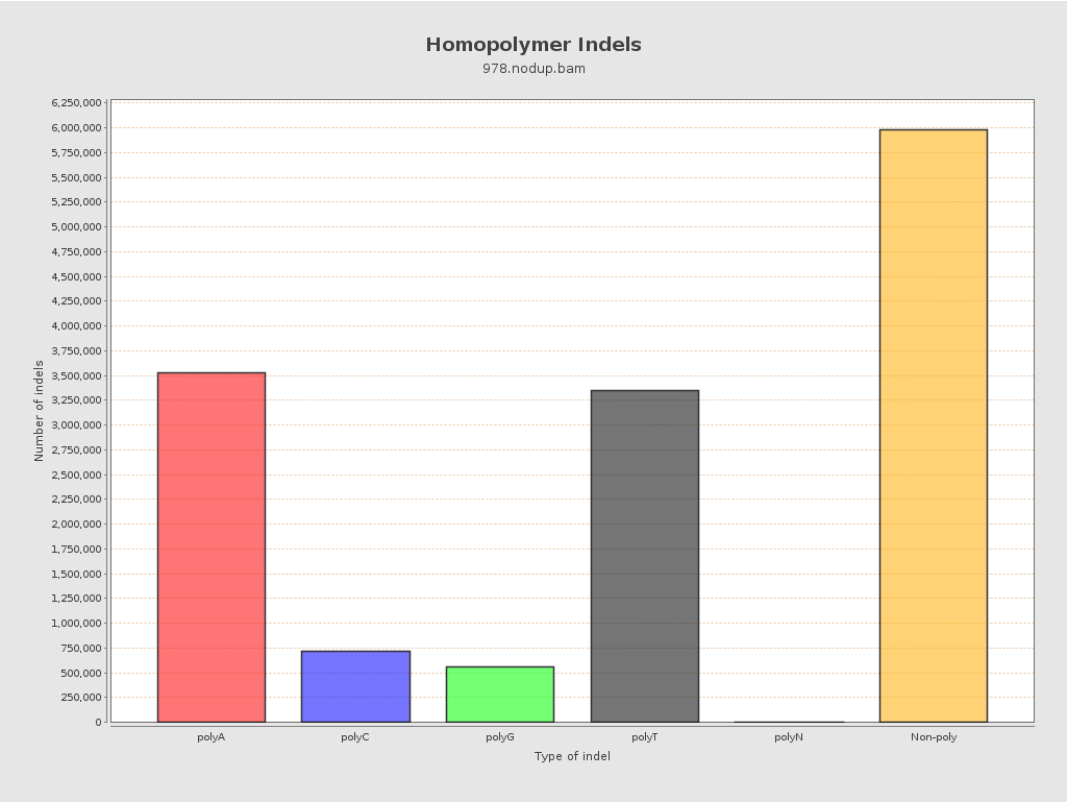
9. Results : Mapped Reads GC-content Distribution



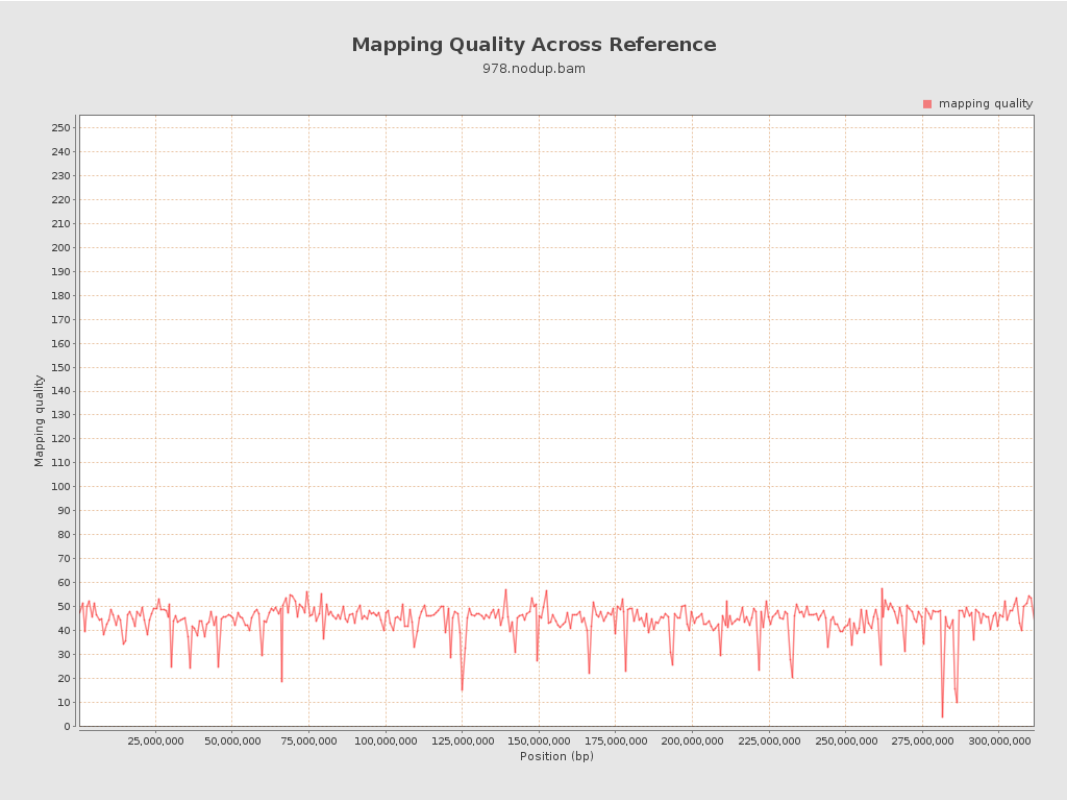
10. Results : Mapped Reads Clipping Profile



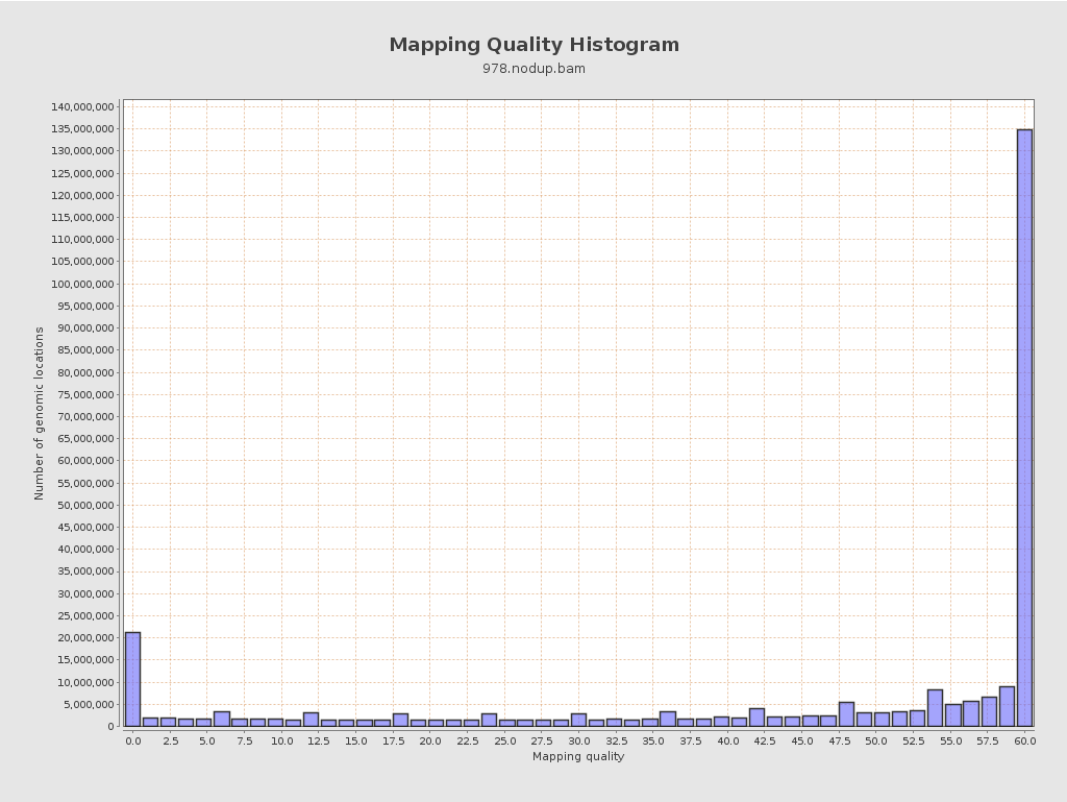
11. Results : Homopolymer Indels



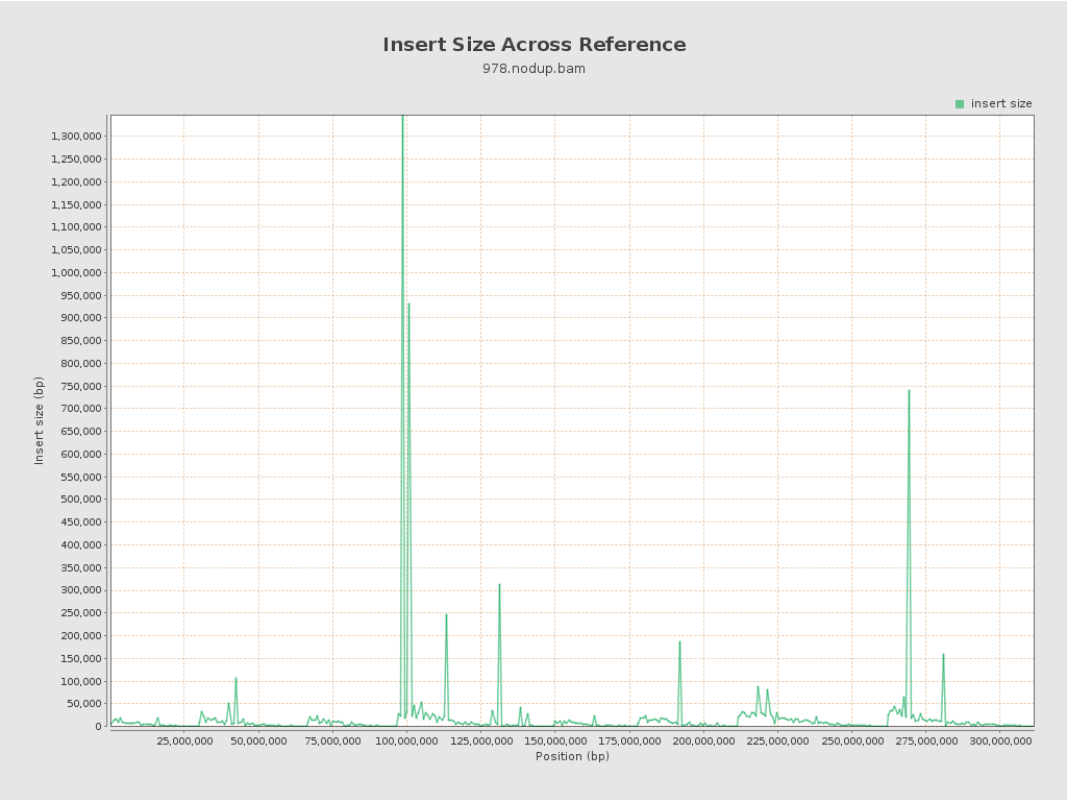
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram