Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:25:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/975.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/975.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_404/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_404_S379_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_404/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_404_S379_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:25:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	49,723,301
Mapped reads	46,745,197 / 94.01%
Unmapped reads	2,978,104 / 5.99%
Mapped paired reads	46,745,197 / 94.01%
Mapped reads, first in pair	23,391,386 / 47.04%
Mapped reads, second in pair	23,353,811 / 46.97%
Mapped reads, both in pair	45,727,375 / 91.96%
Mapped reads, singletons	1,017,822 / 2.05%
Read min/max/mean length	30 / 151 / 148.26
Duplicated reads (flagged)	6,909,506 / 13.9%
Clipped reads	9,867,357 / 19.84%

2.2. ACGT Content

Number/percentage of A's	2,008,376,150 / 30.78%
Number/percentage of C's	1,256,718,065 / 19.26%
Number/percentage of T's	2,010,069,544 / 30.81%
Number/percentage of G's	1,249,203,353 / 19.15%
Number/percentage of N's	21,713 / 0%
GC Percentage	38.41%

2.3. Coverage

Mean	20.9881
Standard Deviation	174.8618

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Insert size

Mean	237,174.49
Standard Deviation	2,303,105.86
P25/Median/P75	361 / 467 / 607

2.6. Mismatches and indels

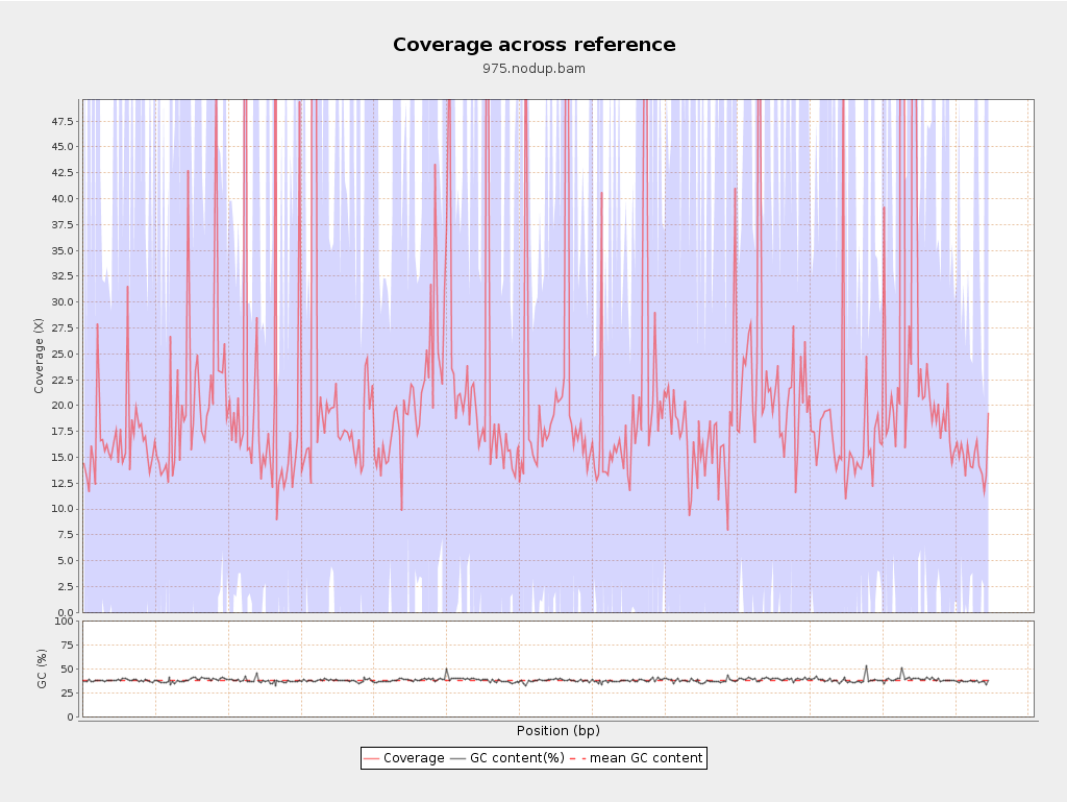
General error rate	2.32%
Mismatches	139,518,382
Insertions	4,377,089
Mapped reads with at least one insertion	8.43%
Deletions	4,398,251
Mapped reads with at least one deletion	8.39%
Homopolymer indels	57%

2.7. Chromosome stats

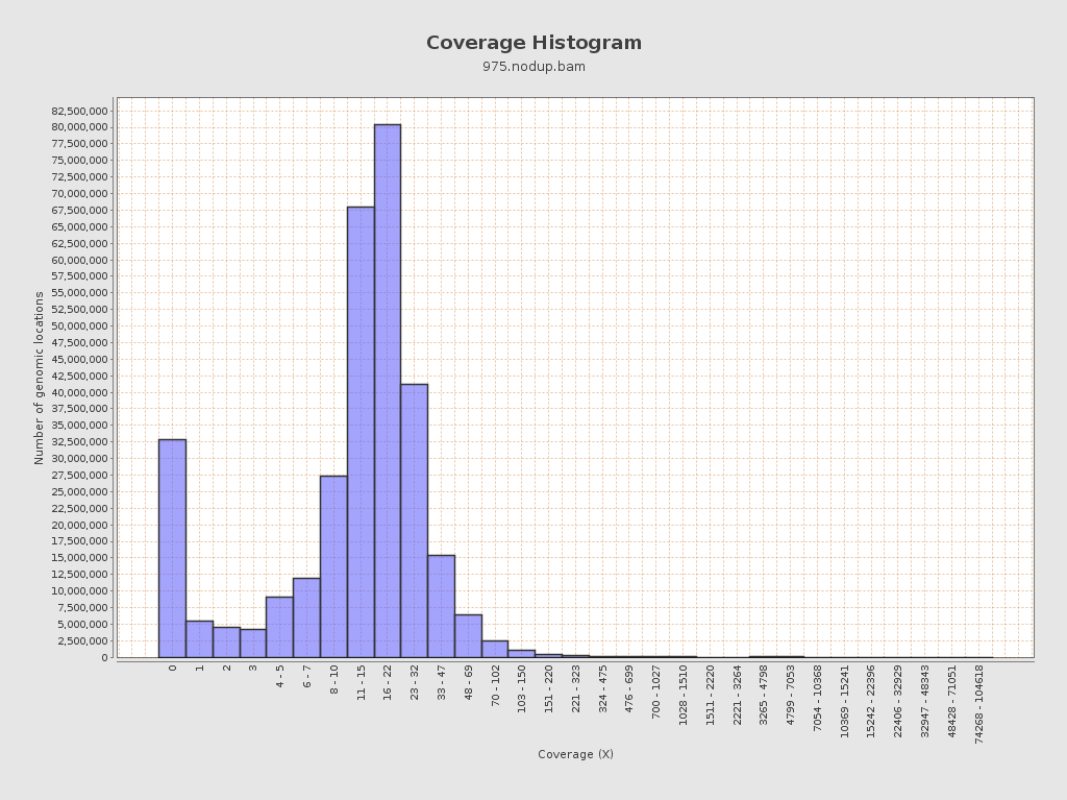
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	482166446	16.2213	49.7076

LT669789.1	36598175	798134814	21.808	189.2959
LT669790.1	30422129	677524702	22.2708	199.0818
LT669791.1	52758100	1115795854	21.1493	151.5222
LT669792.1	28376109	572196760	20.1647	214.9103
LT669793.1	33388210	650055030	19.4696	131.6821
LT669794.1	50579949	1034974725	20.4622	162.6051
LT669795.1	49795044	1209922982	24.2981	224.0125

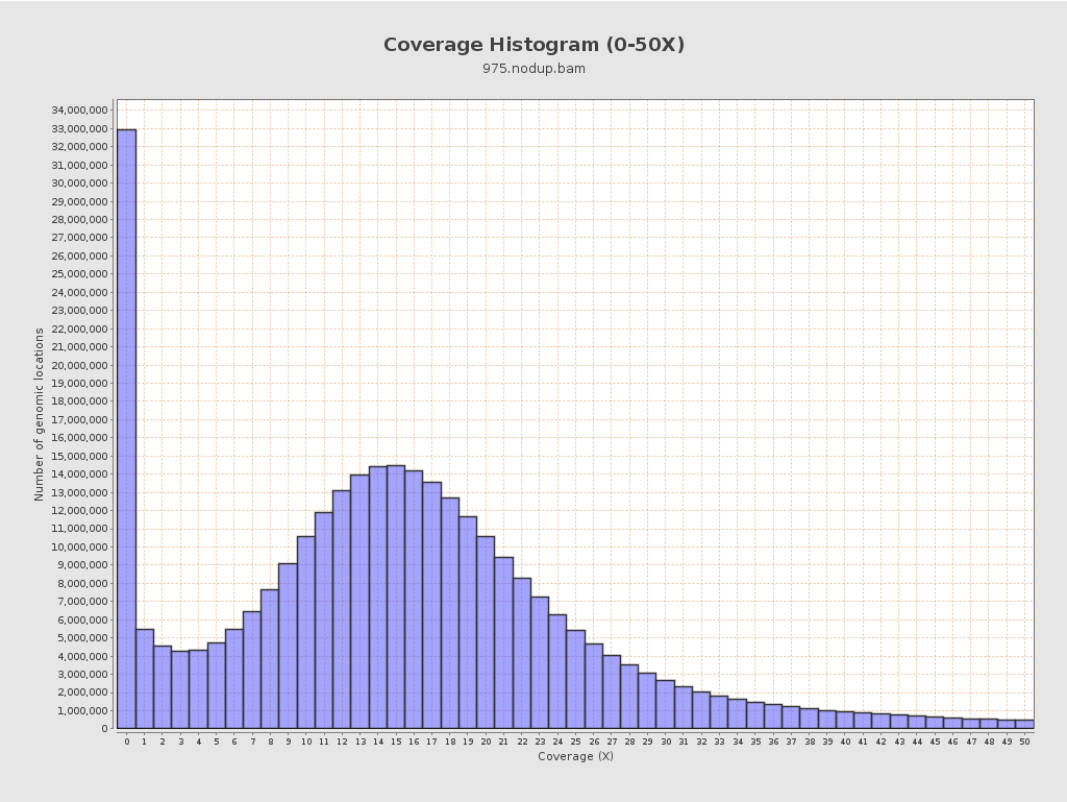
3. Results : Coverage across reference



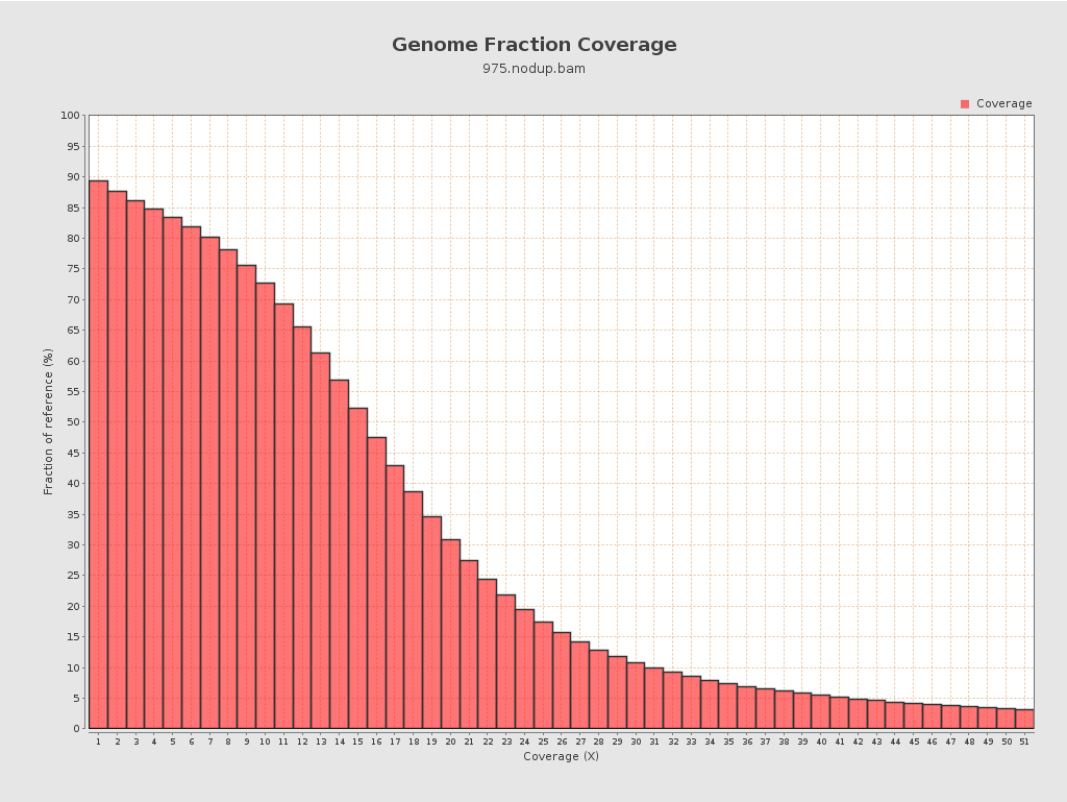
4. Results : Coverage Histogram



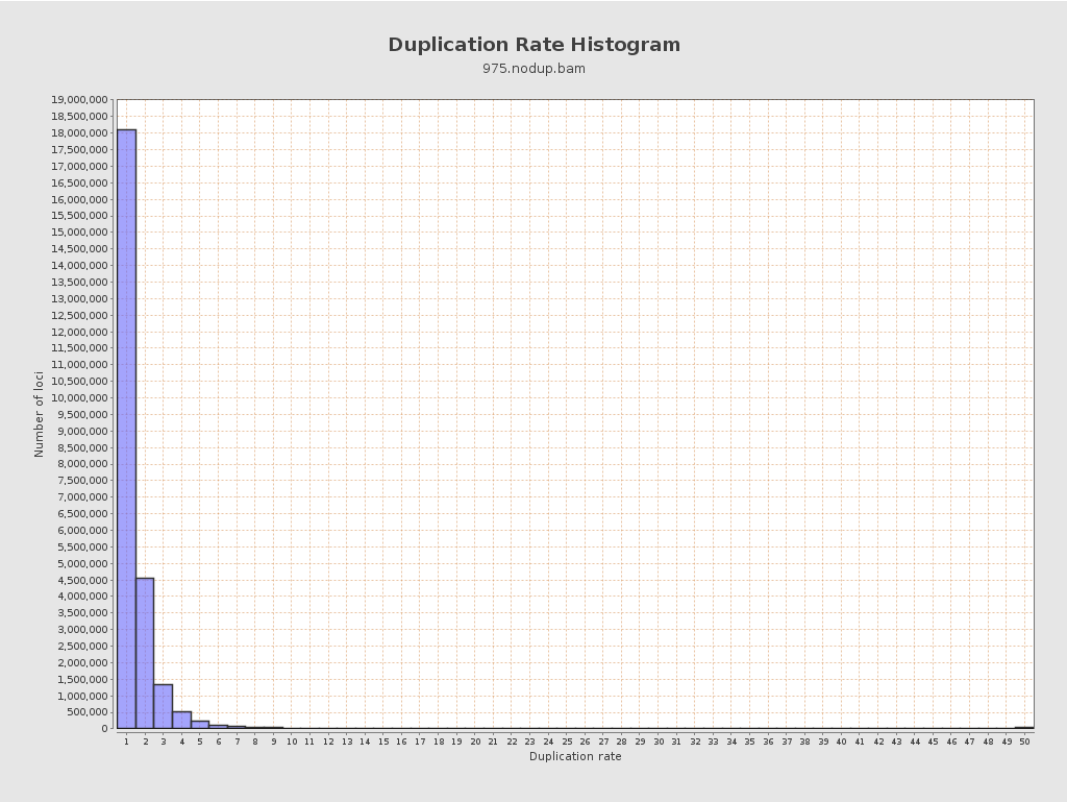
5. Results : Coverage Histogram (0-50X)



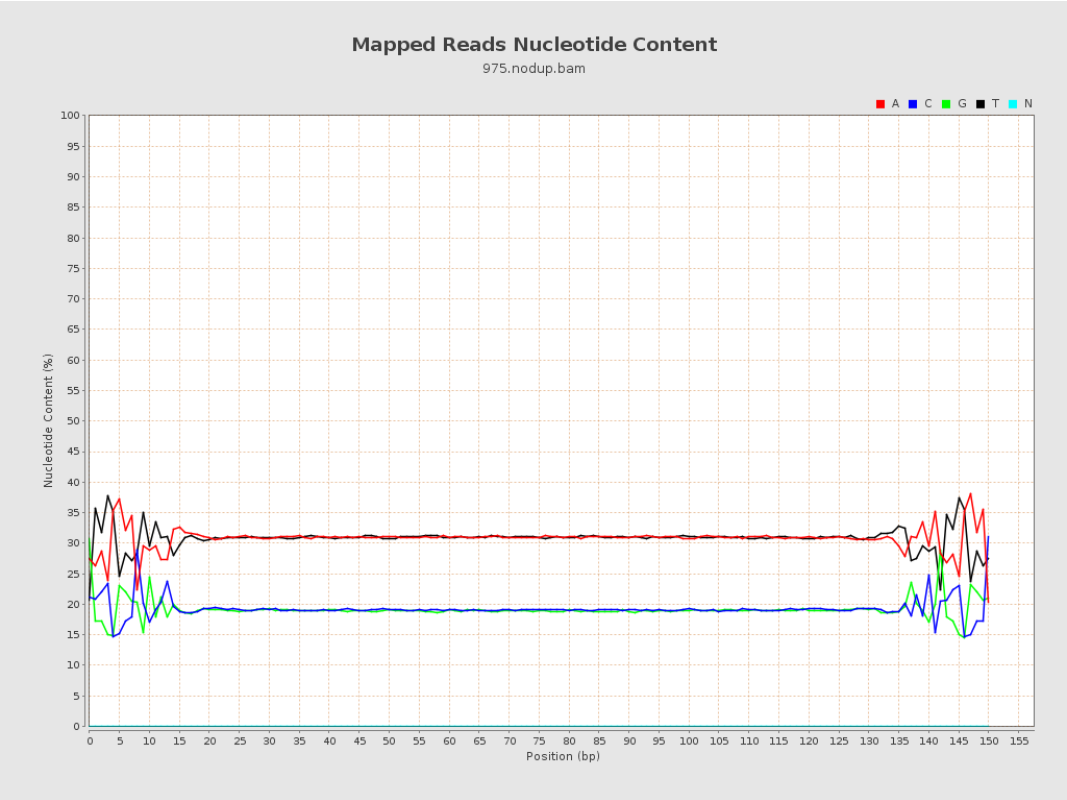
6. Results : Genome Fraction Coverage



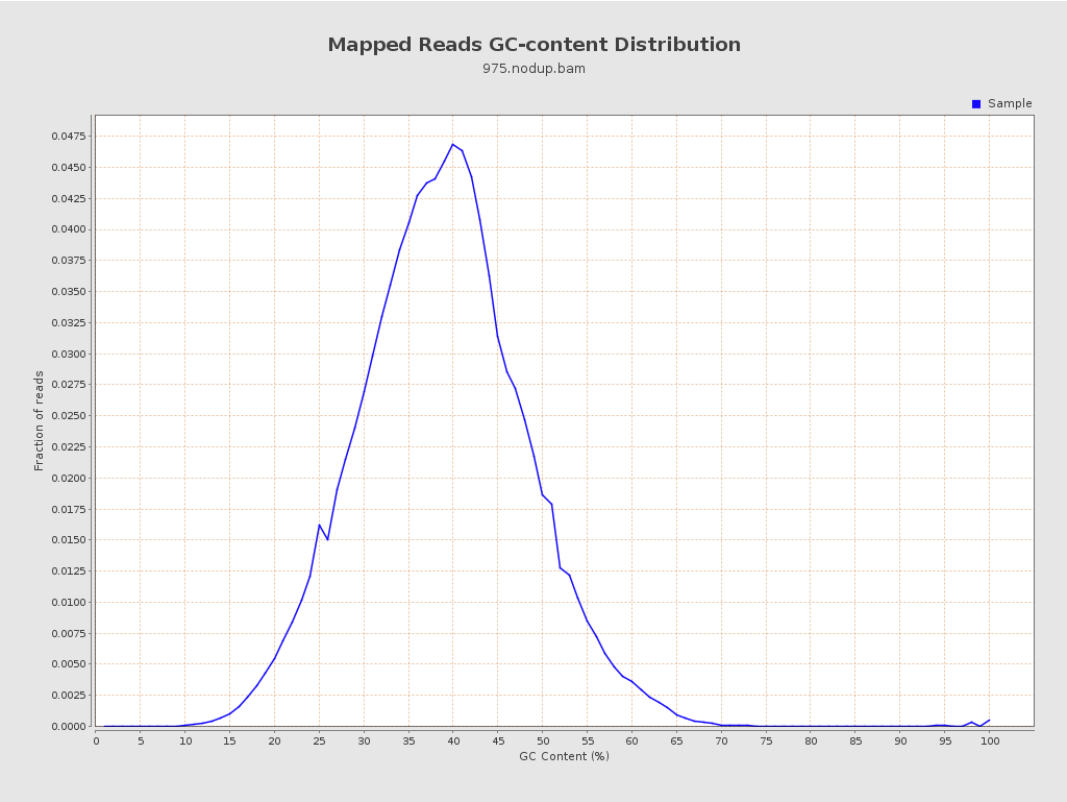
7. Results : Duplication Rate Histogram



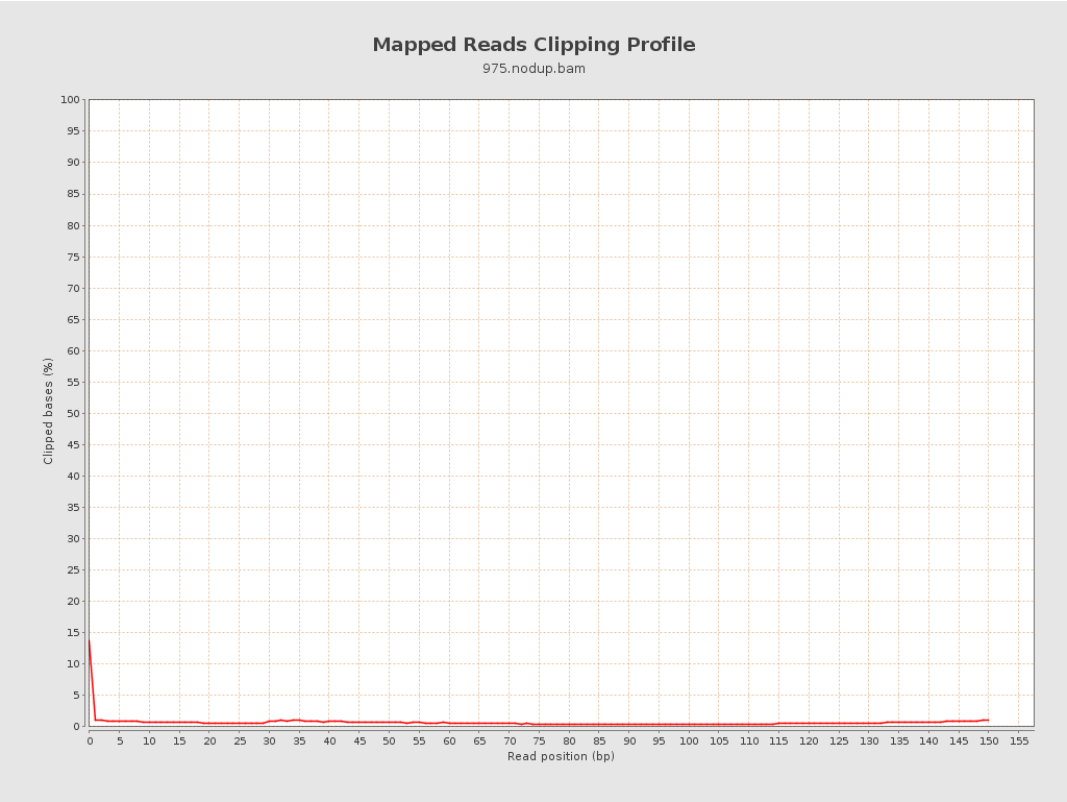
8. Results : Mapped Reads Nucleotide Content



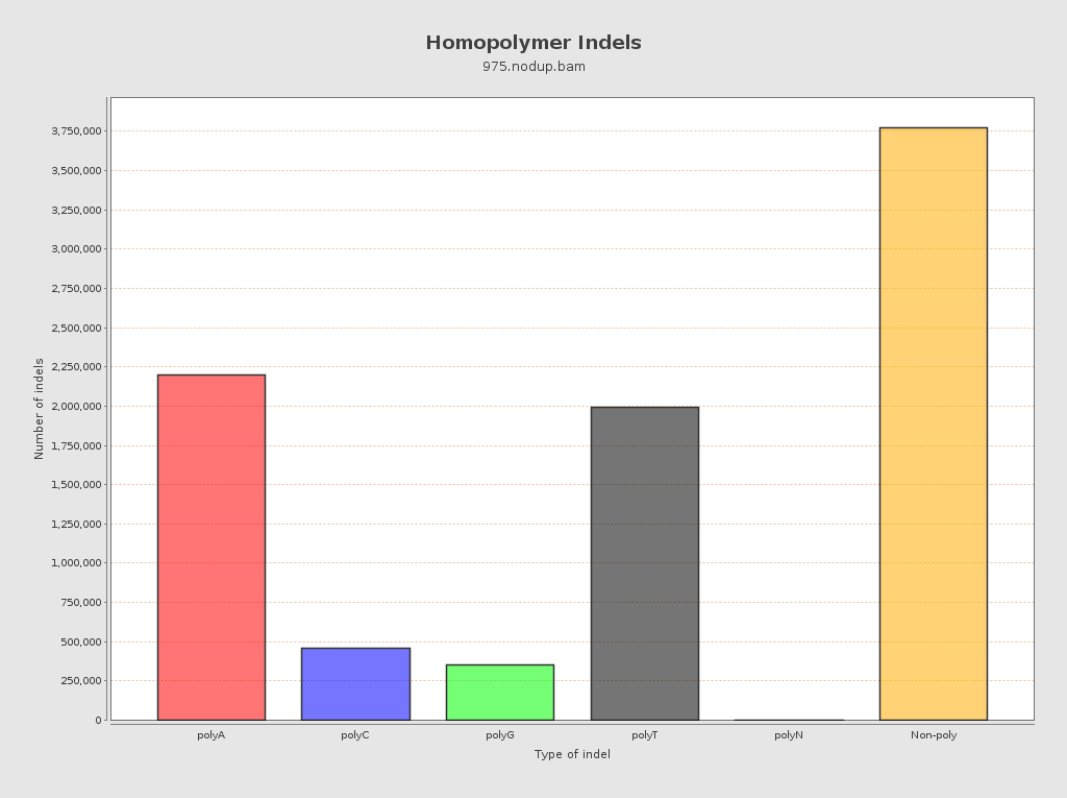
9. Results : Mapped Reads GC-content Distribution



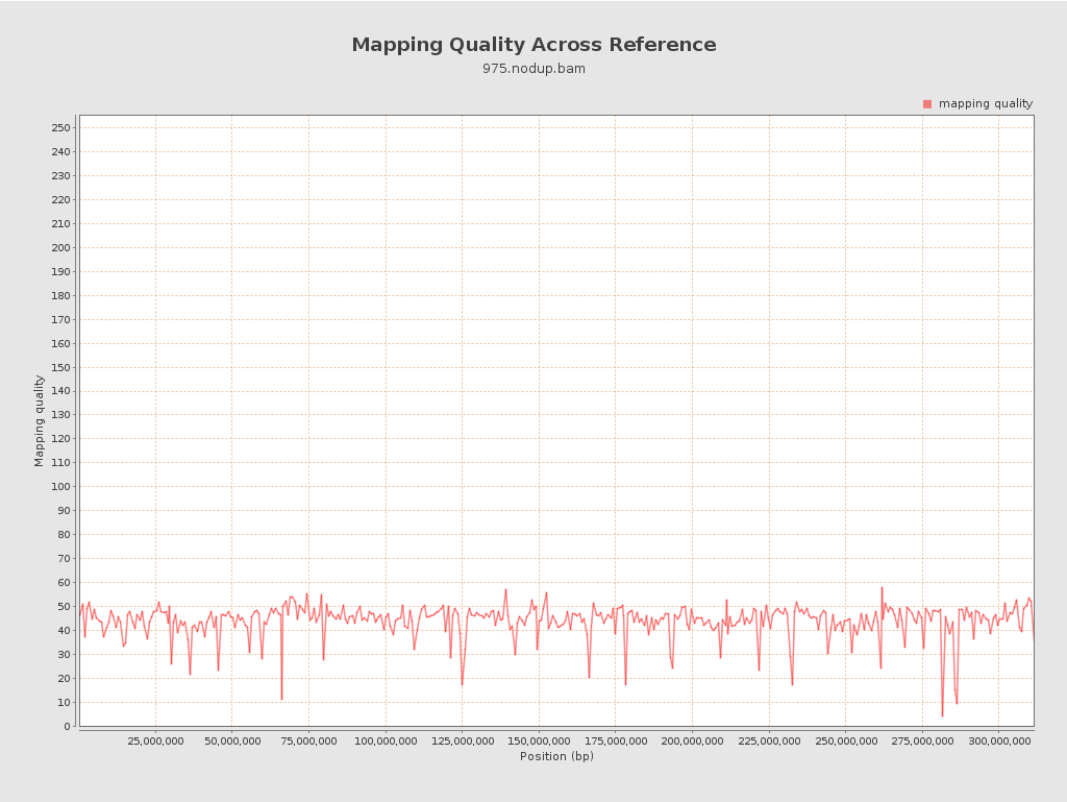
10. Results : Mapped Reads Clipping Profile



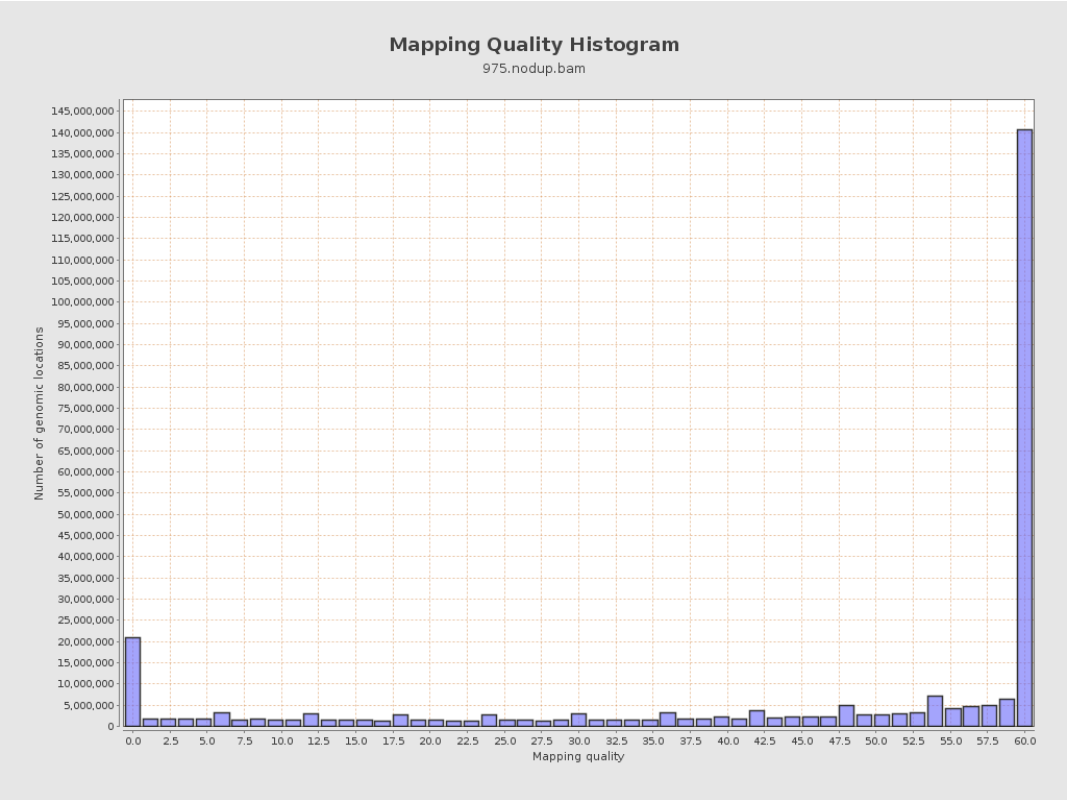
11. Results : Homopolymer Indels



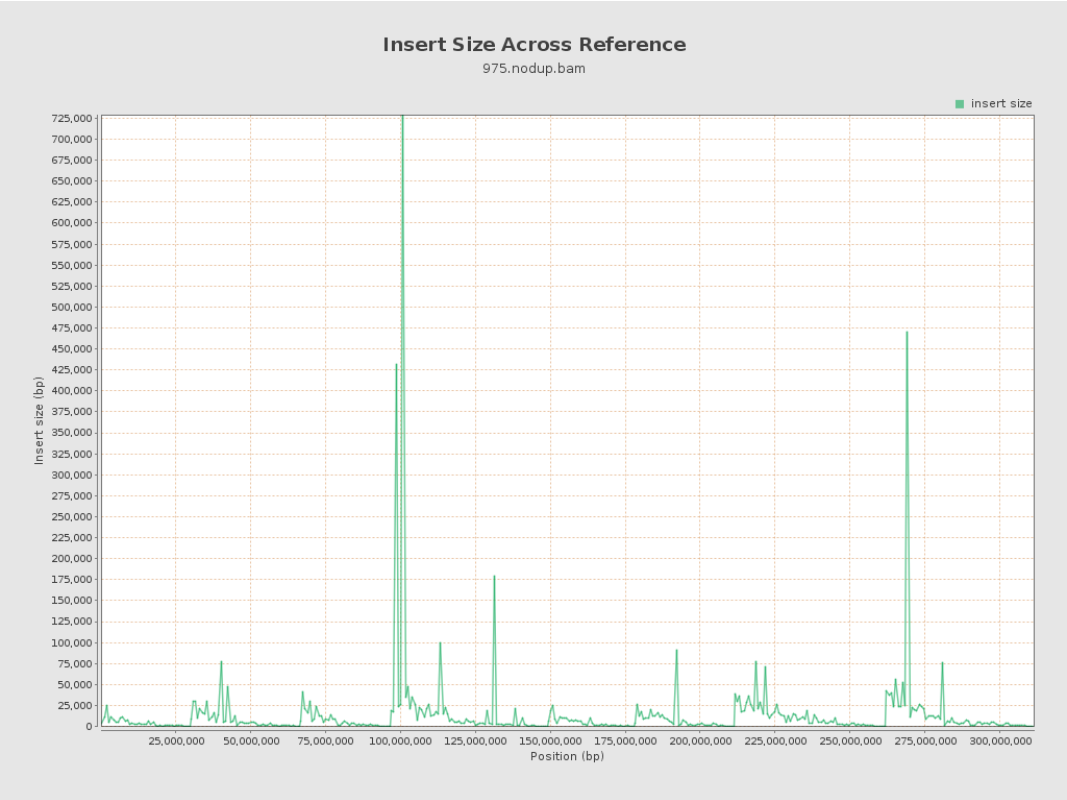
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram