Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/997.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/997.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_105/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_105_S195_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_105/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_105_S195_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	69,689,138
Mapped reads	65,647,552 / 94.2%
Unmapped reads	4,041,586 / 5.8%
Mapped paired reads	65,647,552 / 94.2%
Mapped reads, first in pair	32,878,521 / 47.18%
Mapped reads, second in pair	32,769,031 / 47.02%
Mapped reads, both in pair	64,299,724 / 92.27%
Mapped reads, singletons	1,347,828 / 1.93%
Read min/max/mean length	30 / 151 / 148.29
Duplicated reads (flagged)	10,742,537 / 15.41%
Clipped reads	13,687,896 / 19.64%

2.2. ACGT Content

Number/percentage of A's	2,842,720,401 / 31.03%
Number/percentage of C's	1,742,509,252 / 19.02%
Number/percentage of T's	2,839,854,535 / 30.99%
Number/percentage of G's	1,737,407,043 / 18.96%
Number/percentage of N's	38,046 / 0%
GC Percentage	37.98%

2.3. Coverage

Mean	29.4735
Standard Deviation	207.8772

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Insert size

Mean	217,641.72
Standard Deviation	2,216,534.79
P25/Median/P75	335 / 432 / 556

2.6. Mismatches and indels

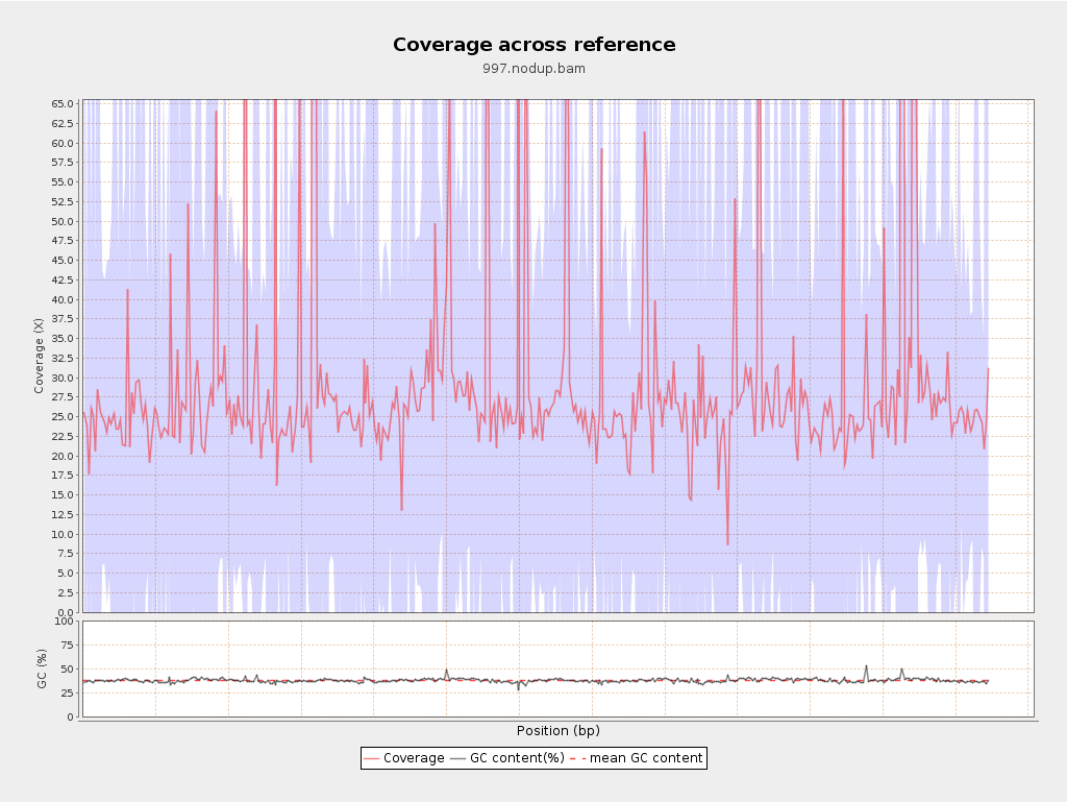
General error rate	2.21%
Mismatches	185,331,818
Insertions	6,041,106
Mapped reads with at least one insertion	8.27%
Deletions	6,060,537
Mapped reads with at least one deletion	8.22%
Homopolymer indels	57.5%

2.7. Chromosome stats

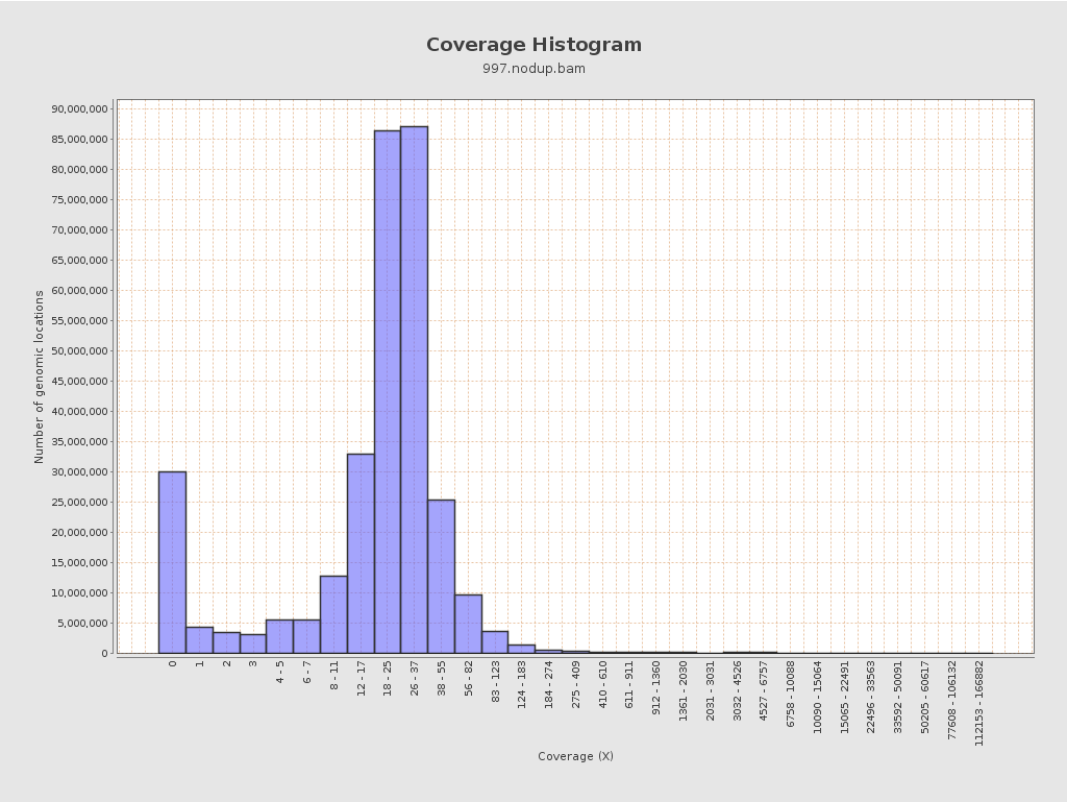
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	735630860	24.7484	62.4499

LT669789.1	36598175	1096407105	29.958	225.8694
LT669790.1	30422129	988305382	32.4864	243.7701
LT669791.1	52758100	1526300357	28.9302	180.1702
LT669792.1	28376109	845361000	29.7913	234.1461
LT669793.1	33388210	898889746	26.9224	112.8508
LT669794.1	50579949	1402183837	27.7221	181.517
LT669795.1	49795044	1692114442	33.9816	294.3294

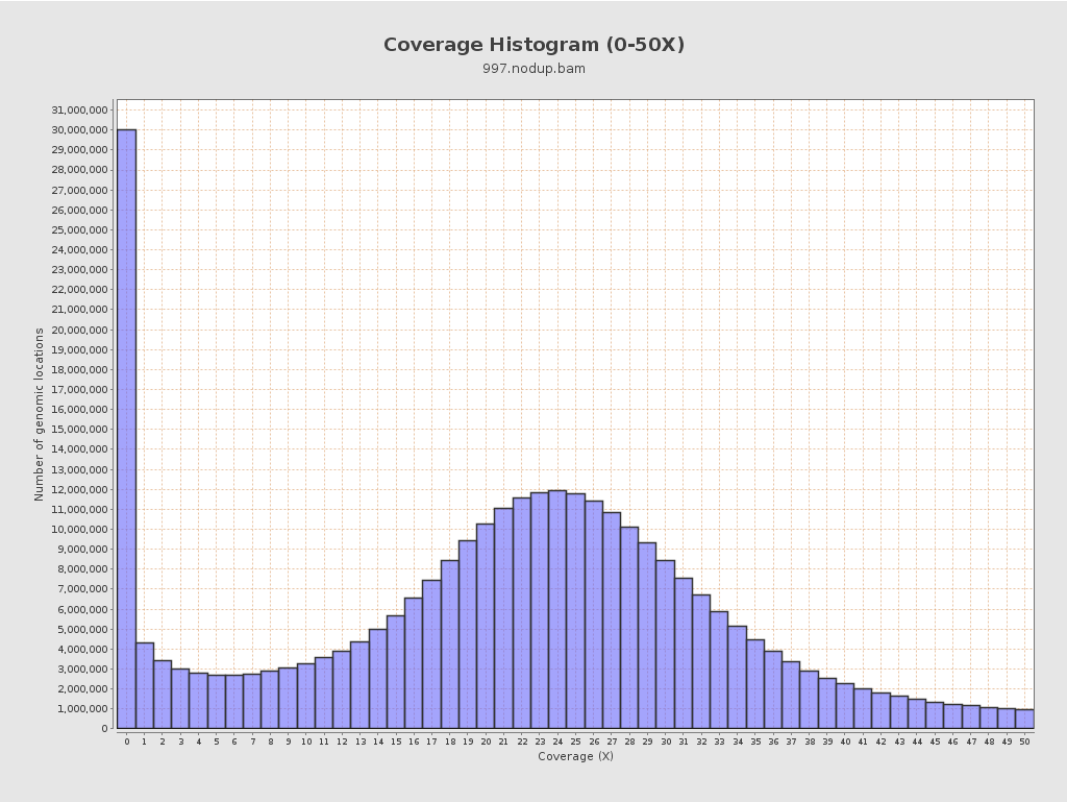
3. Results : Coverage across reference



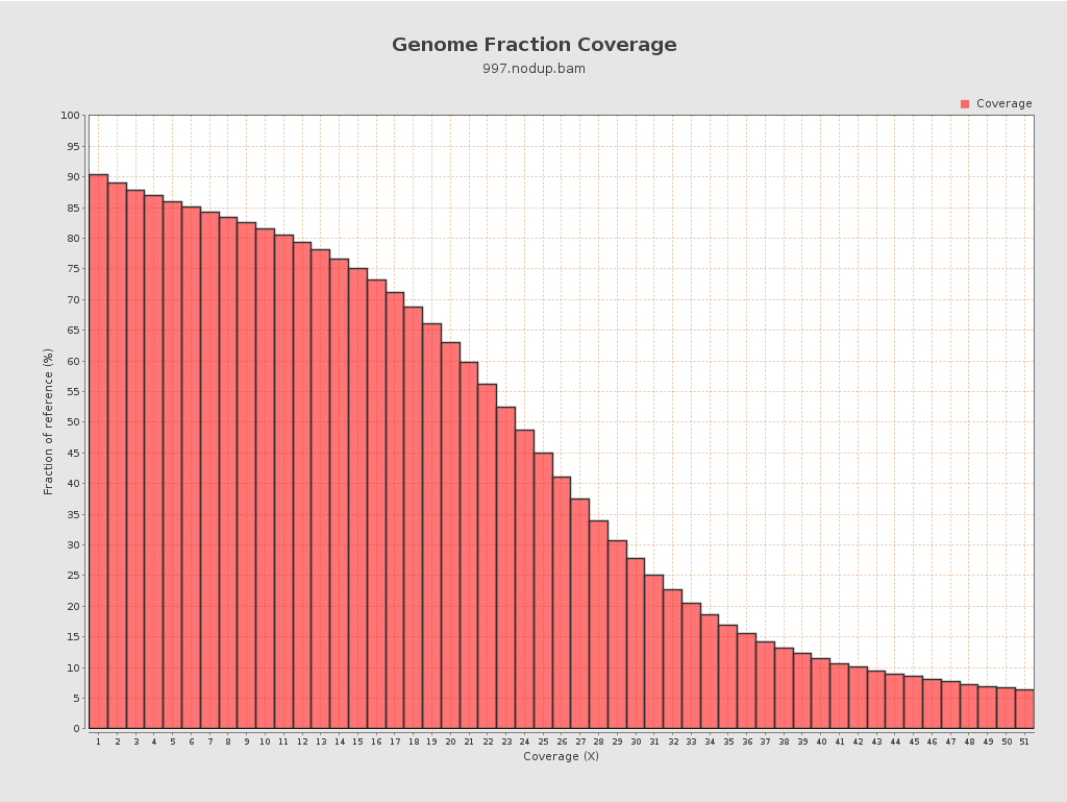
4. Results : Coverage Histogram



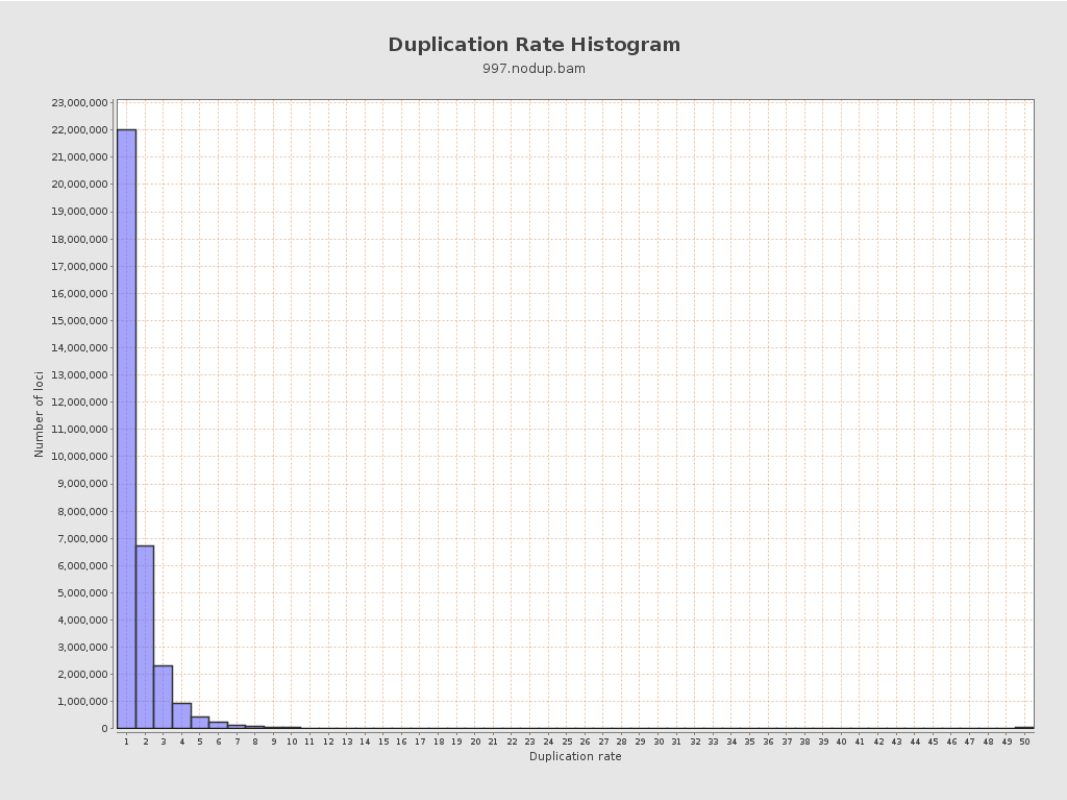
5. Results : Coverage Histogram (0-50X)



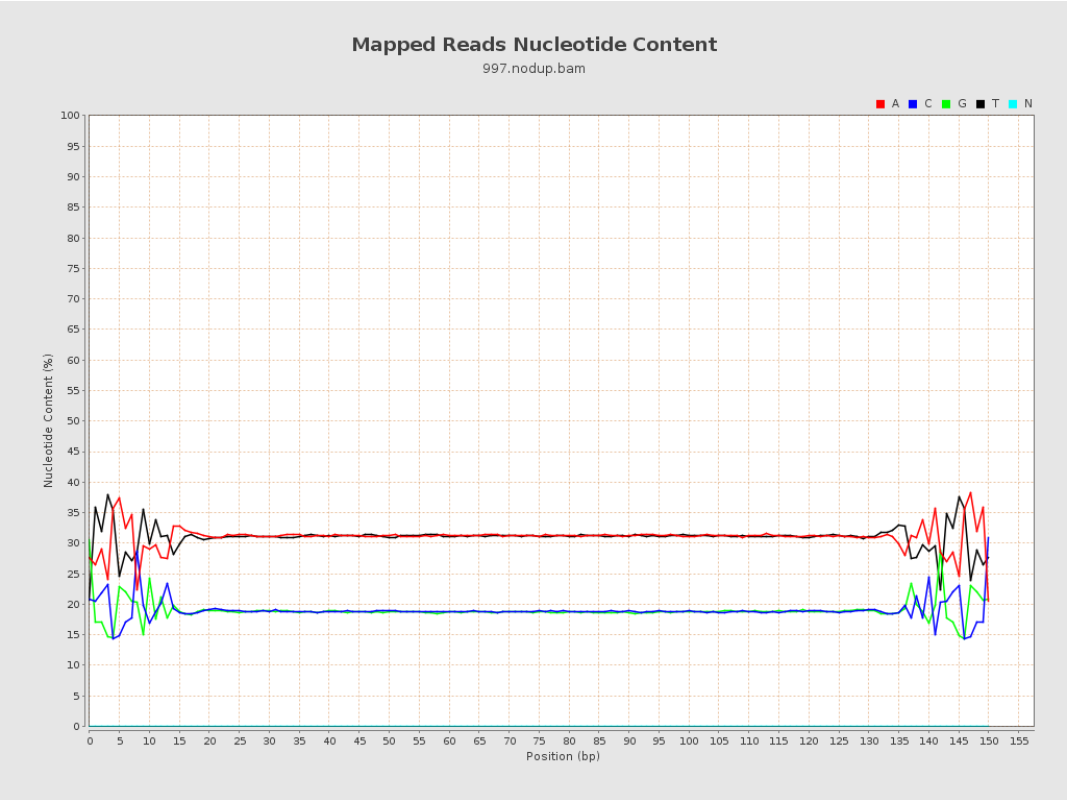
6. Results : Genome Fraction Coverage



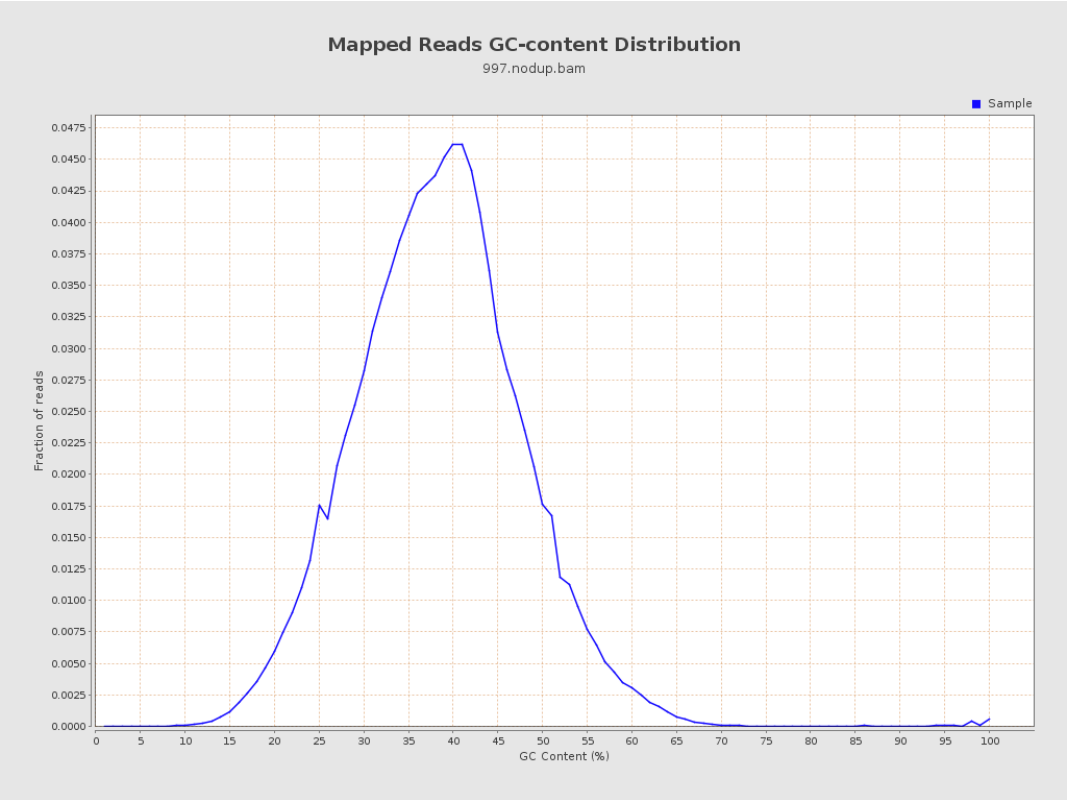
7. Results : Duplication Rate Histogram



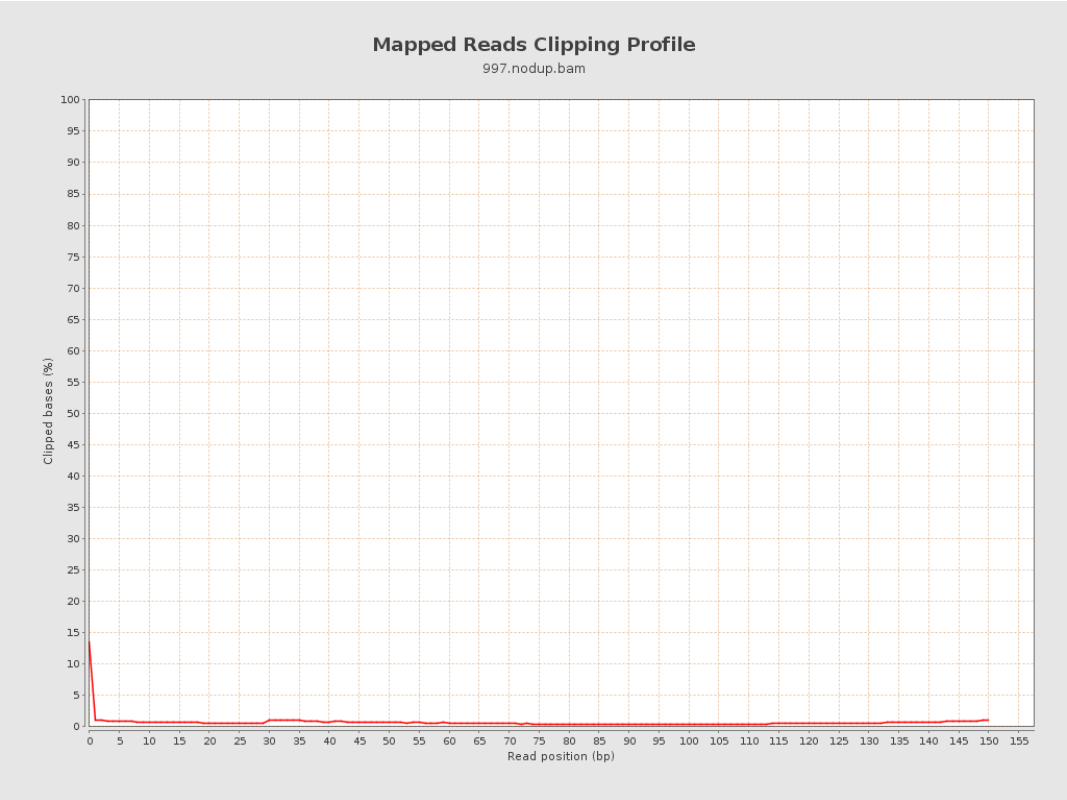
8. Results : Mapped Reads Nucleotide Content



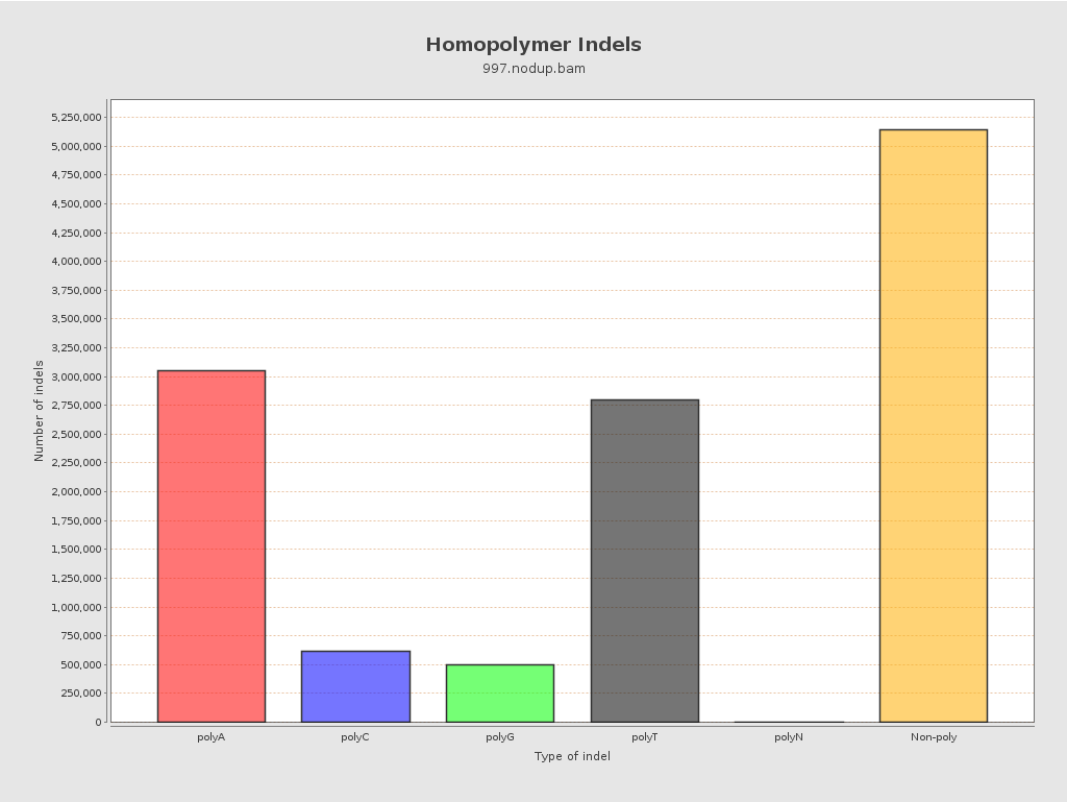
9. Results : Mapped Reads GC-content Distribution



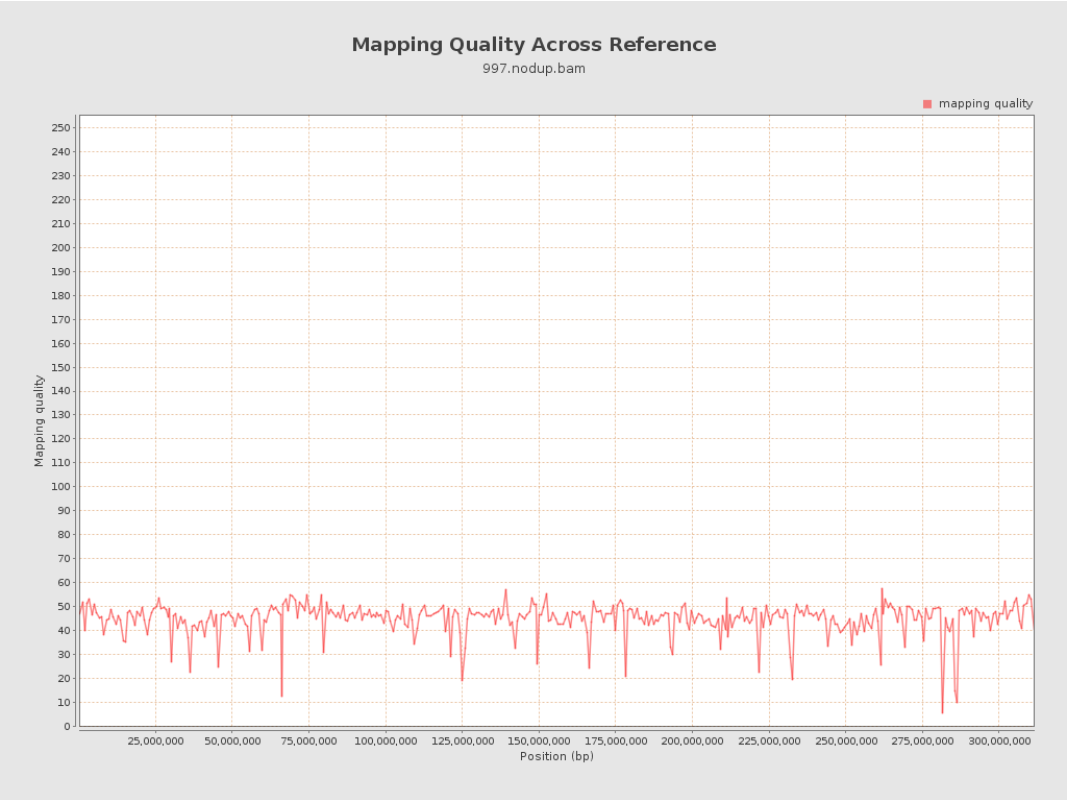
10. Results : Mapped Reads Clipping Profile



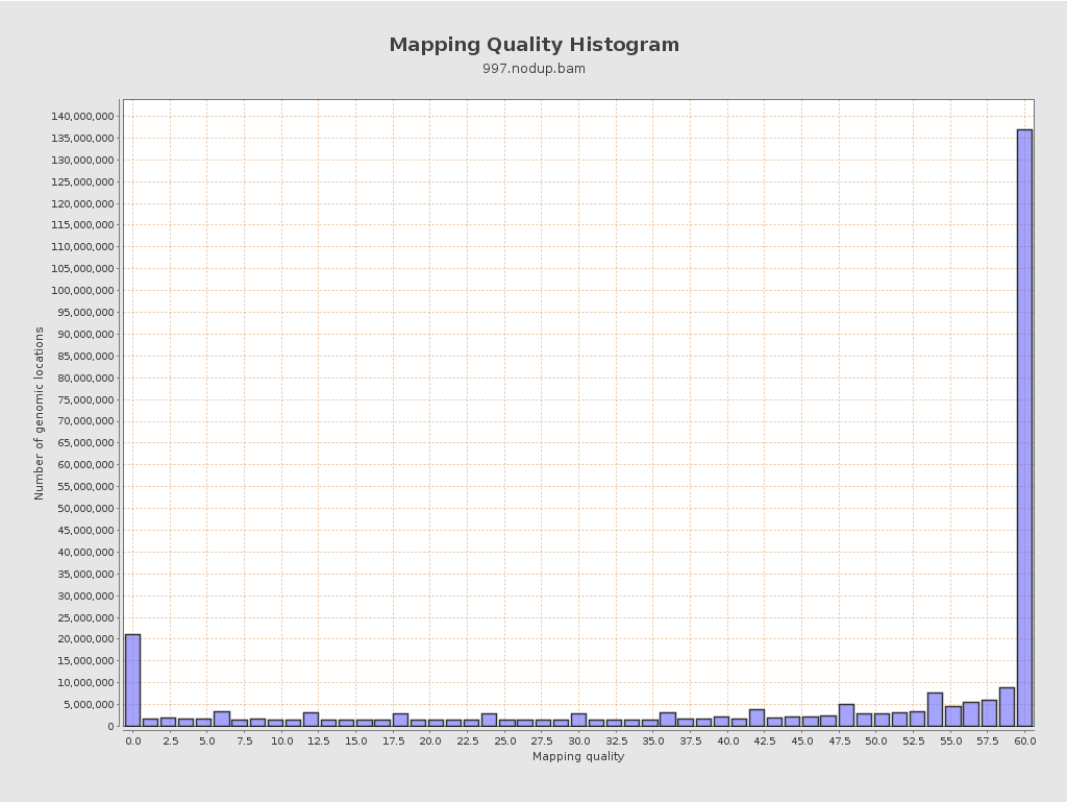
11. Results : Homopolymer Indels



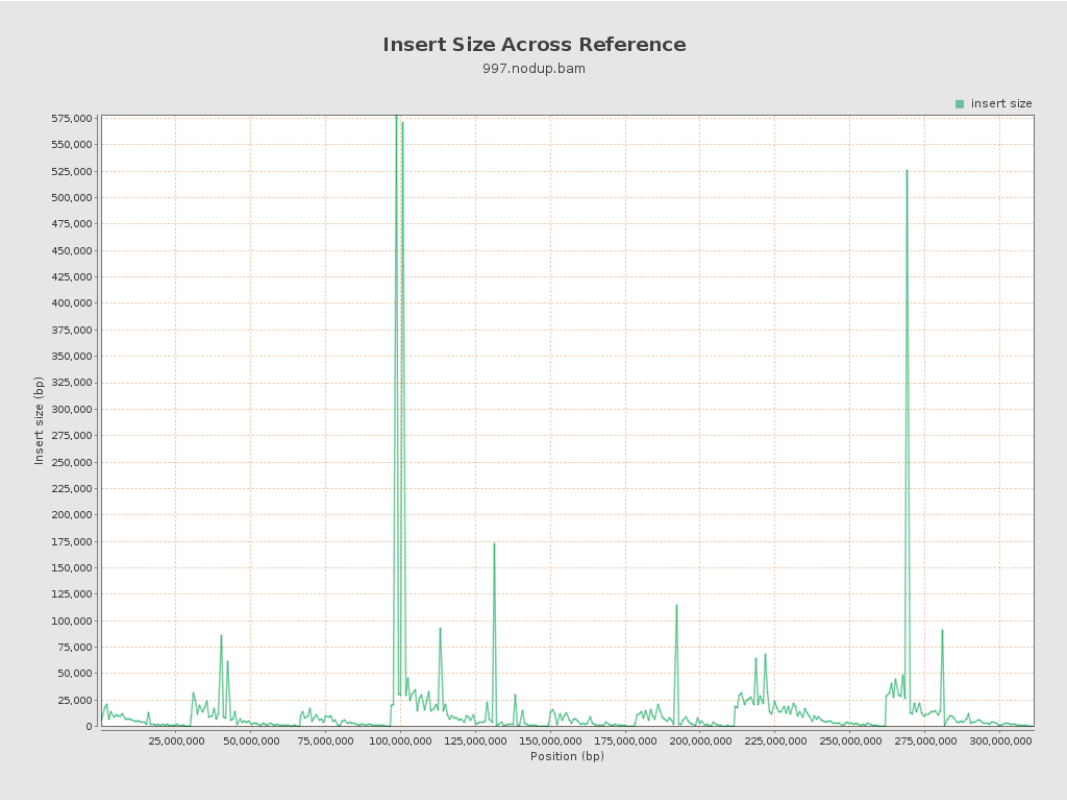
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram