Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:41:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/597.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/597.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_458/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_458_S433_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_458/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_458_S433_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:41:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	89,602,009
Mapped reads	83,521,470 / 93.21%
Unmapped reads	6,080,539 / 6.79%
Mapped paired reads	83,521,470 / 93.21%
Mapped reads, first in pair	41,822,064 / 46.68%
Mapped reads, second in pair	41,699,406 / 46.54%
Mapped reads, both in pair	81,553,243 / 91.02%
Mapped reads, singletons	1,968,227 / 2.2%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	14,290,210 / 15.95%
Clipped reads	18,238,096 / 20.35%

2.2. ACGT Content

Number/percentage of A's	3,579,040,996 / 30.86%
Number/percentage of C's	2,220,882,210 / 19.15%
Number/percentage of T's	3,587,309,727 / 30.93%
Number/percentage of G's	2,210,210,121 / 19.06%
Number/percentage of N's	39,728 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	37.3108
Standard Deviation	303.6815

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Insert size

Mean	239,667.17
Standard Deviation	2,335,885.98
P25/Median/P75	341 / 448 / 592

2.6. Mismatches and indels

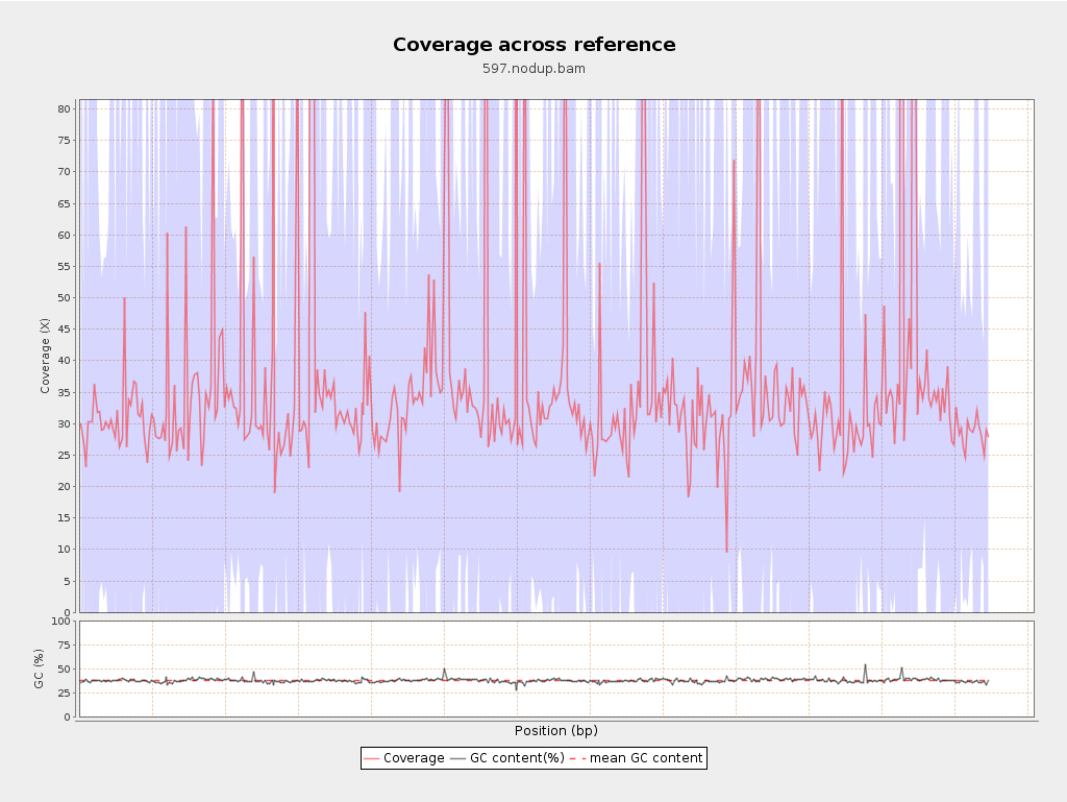
General error rate	2.29%
Mismatches	243,775,496
Insertions	7,936,621
Mapped reads with at least one insertion	8.51%
Deletions	7,948,352
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.69%

2.7. Chromosome stats

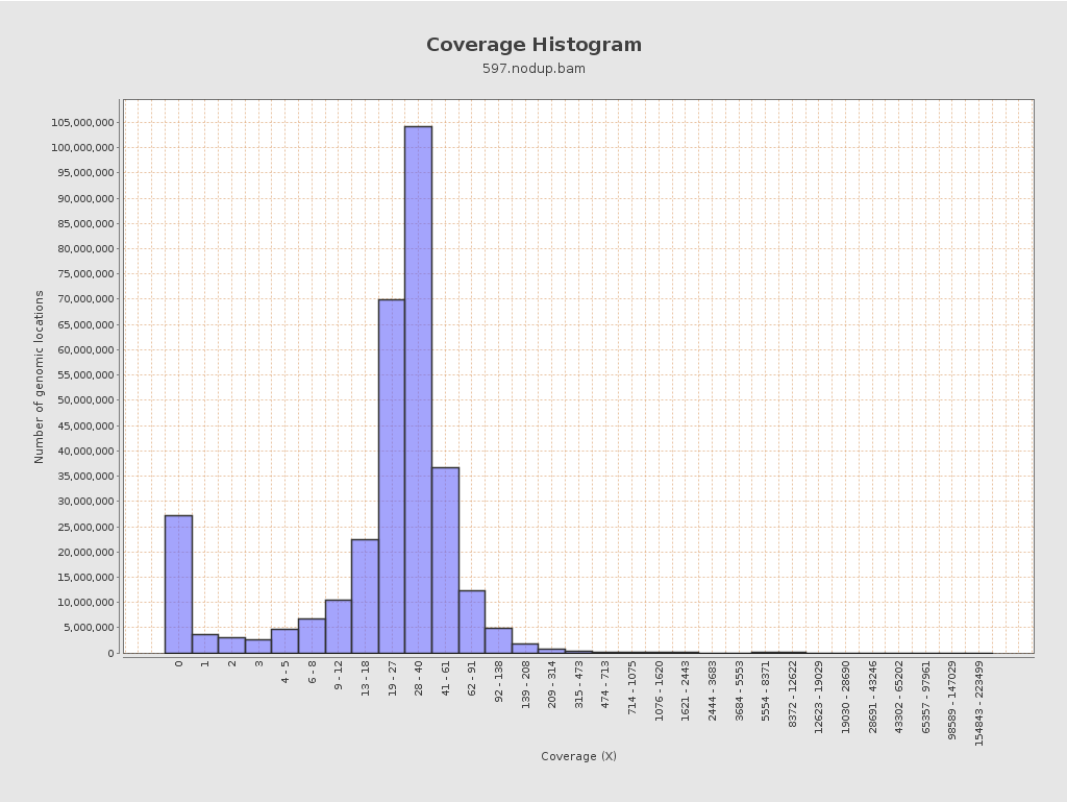
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	905035615	30.4476	97.8652

LT669789.1	36598175	1355507204	37.0376	317.3076
LT669790.1	30422129	1250528778	41.1059	342.5757
LT669791.1	52758100	1938773294	36.7484	280.7284
LT669792.1	28376109	1044994874	36.8266	309.5989
LT669793.1	33388210	1140441845	34.157	206.0464
LT669794.1	50579949	1764858917	34.8925	251.8581
LT669795.1	49795044	2227481950	44.733	441.1726

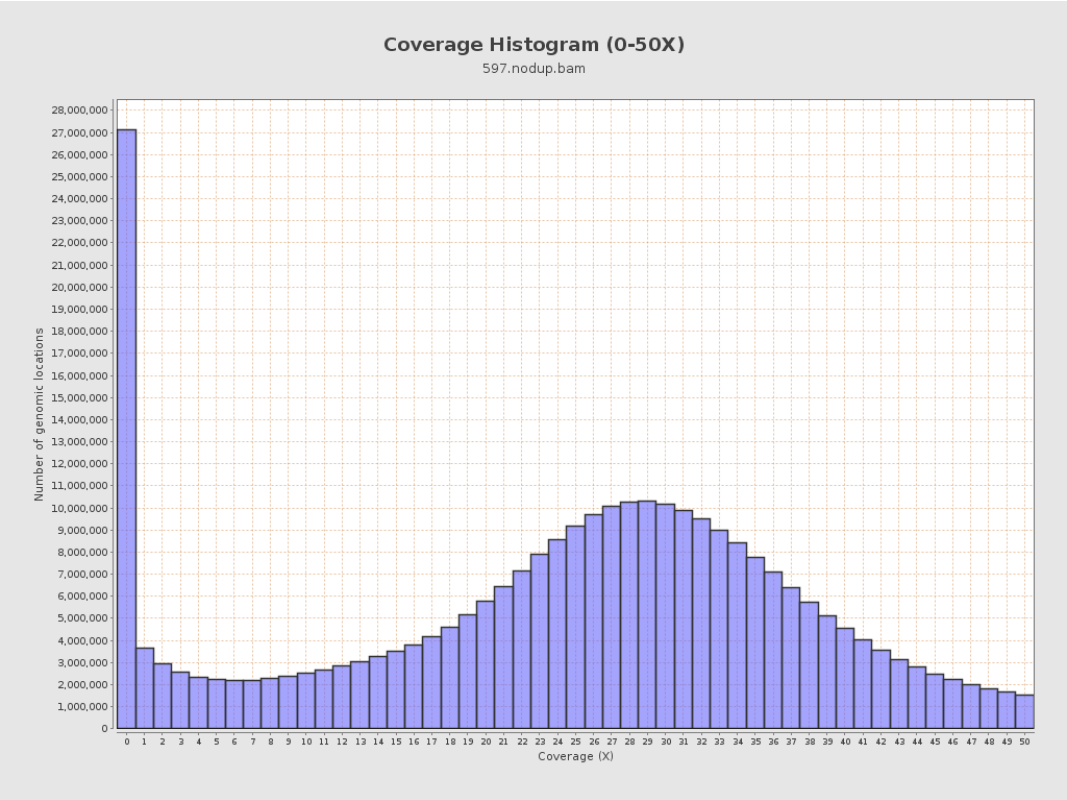
3. Results : Coverage across reference



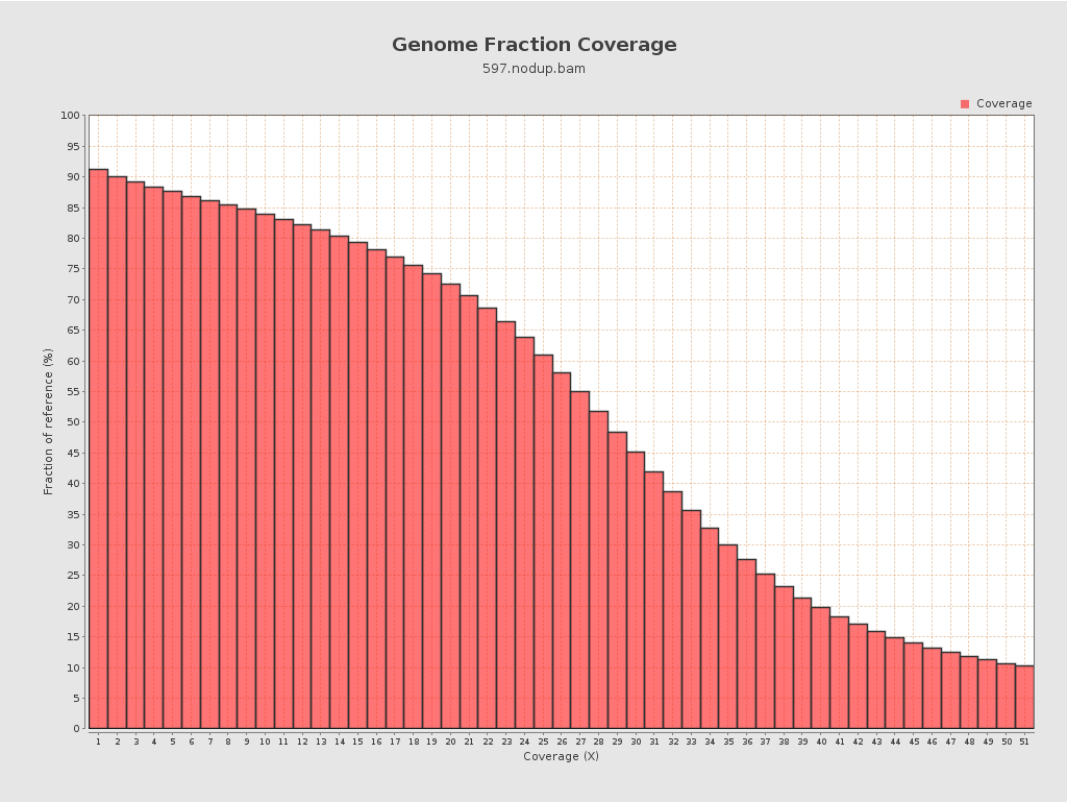
4. Results : Coverage Histogram



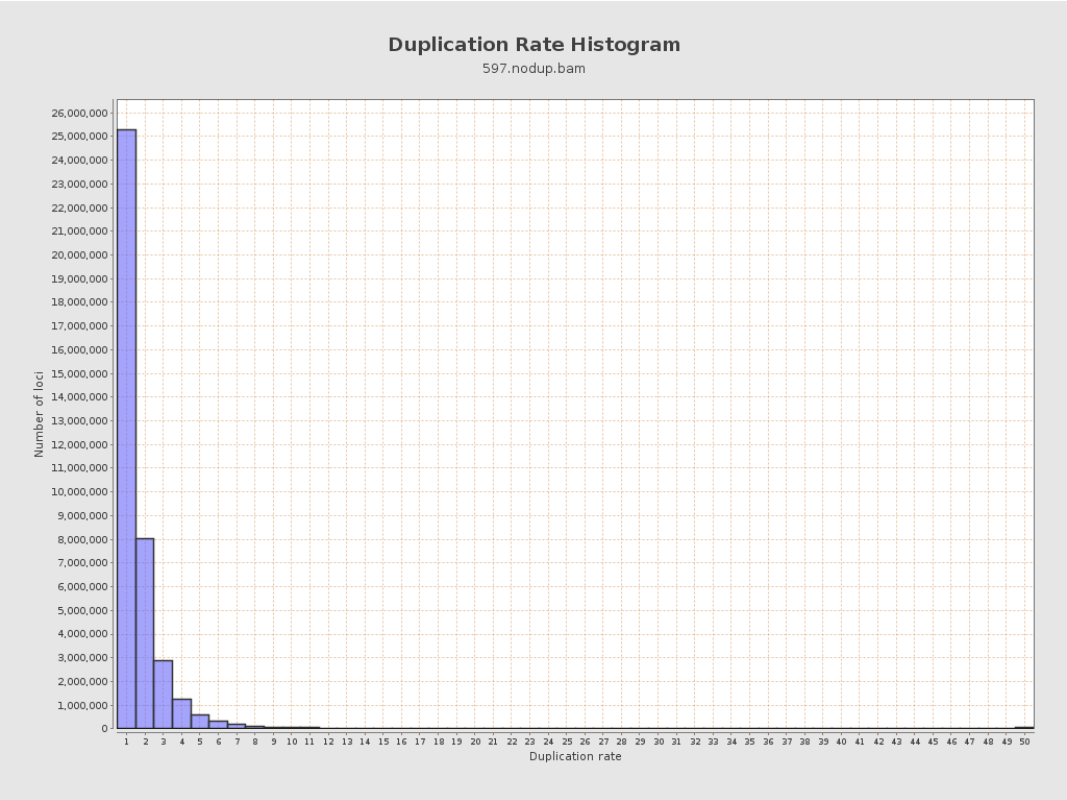
5. Results : Coverage Histogram (0-50X)



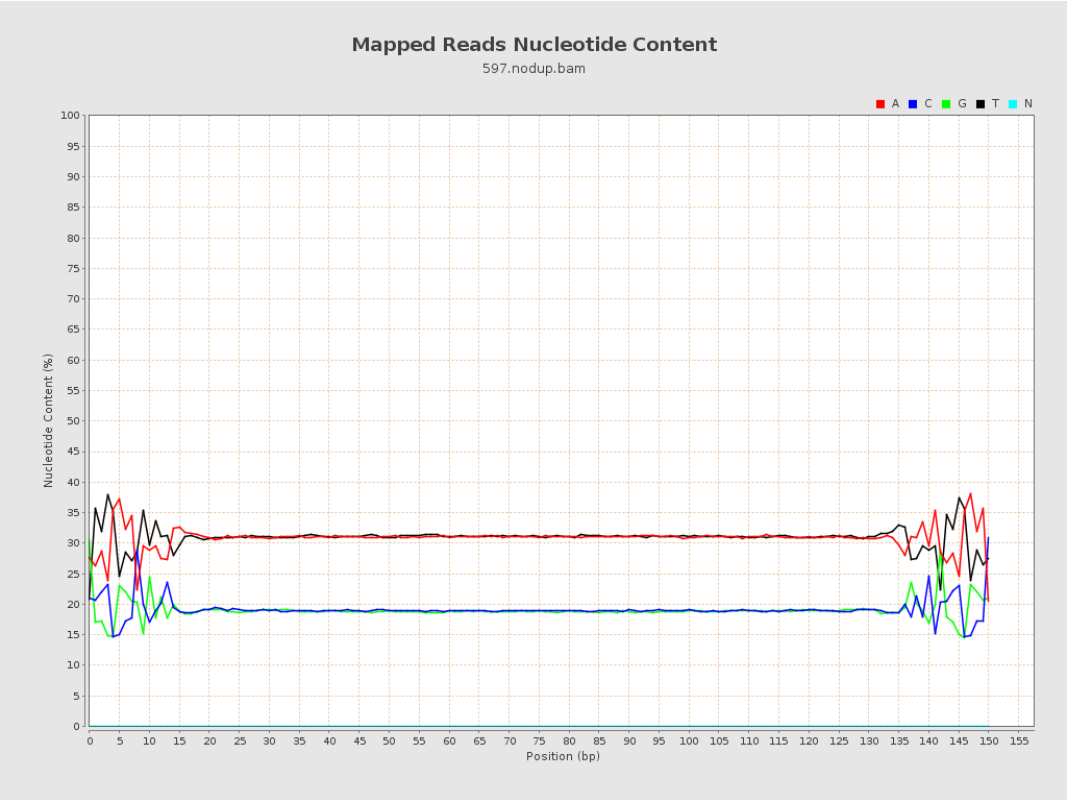
6. Results : Genome Fraction Coverage



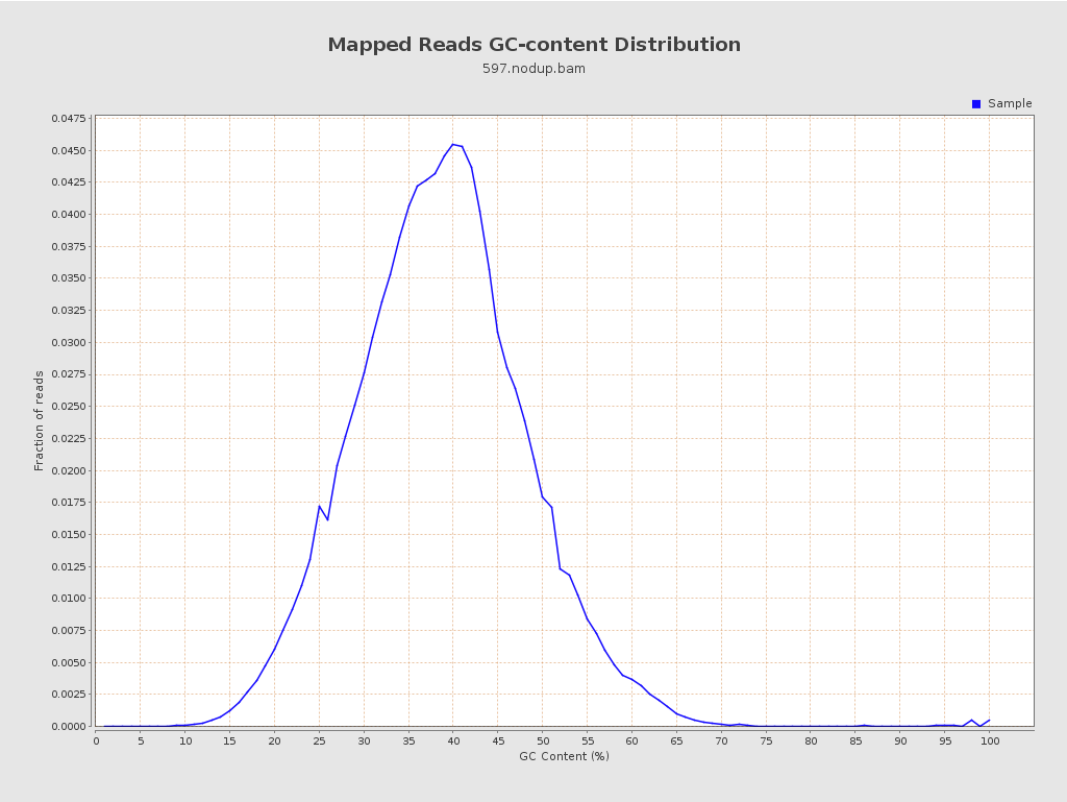
7. Results : Duplication Rate Histogram



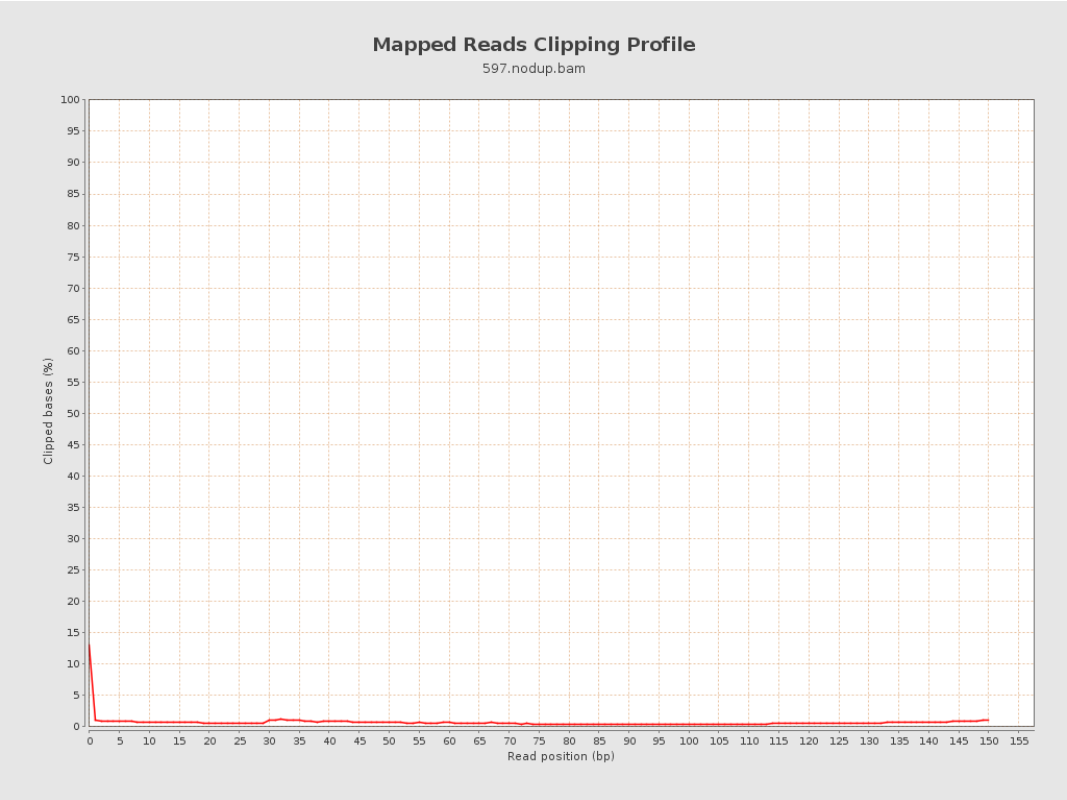
8. Results : Mapped Reads Nucleotide Content



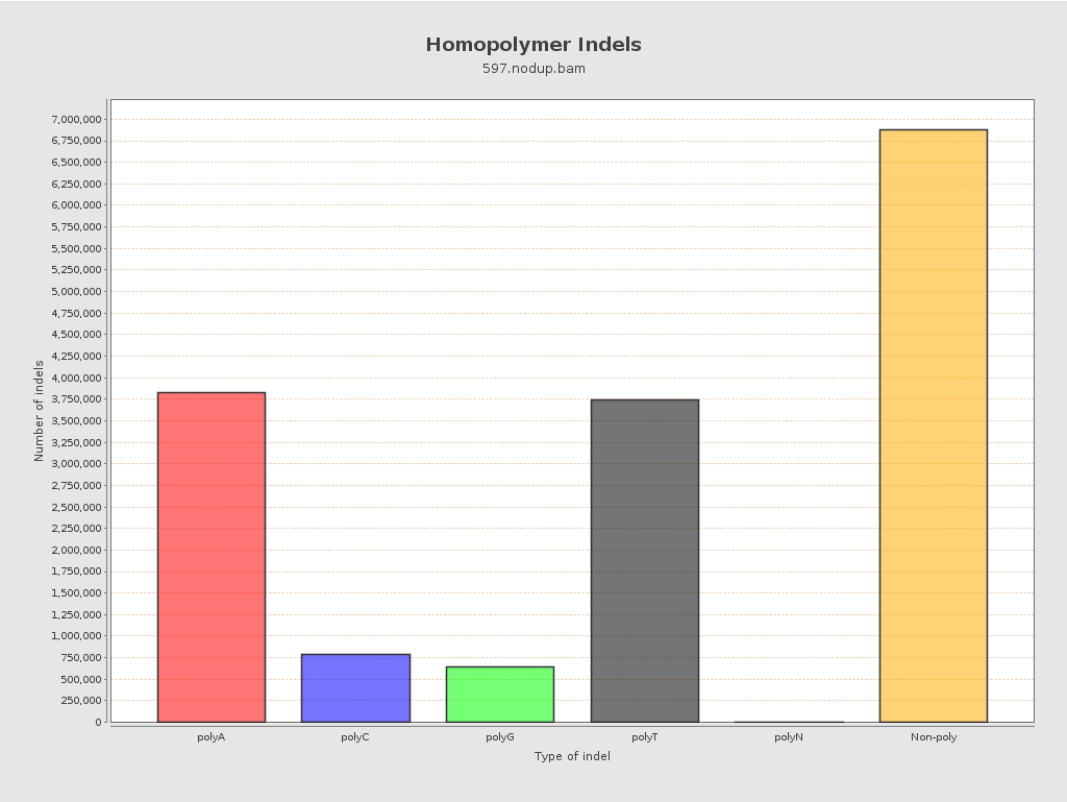
9. Results : Mapped Reads GC-content Distribution



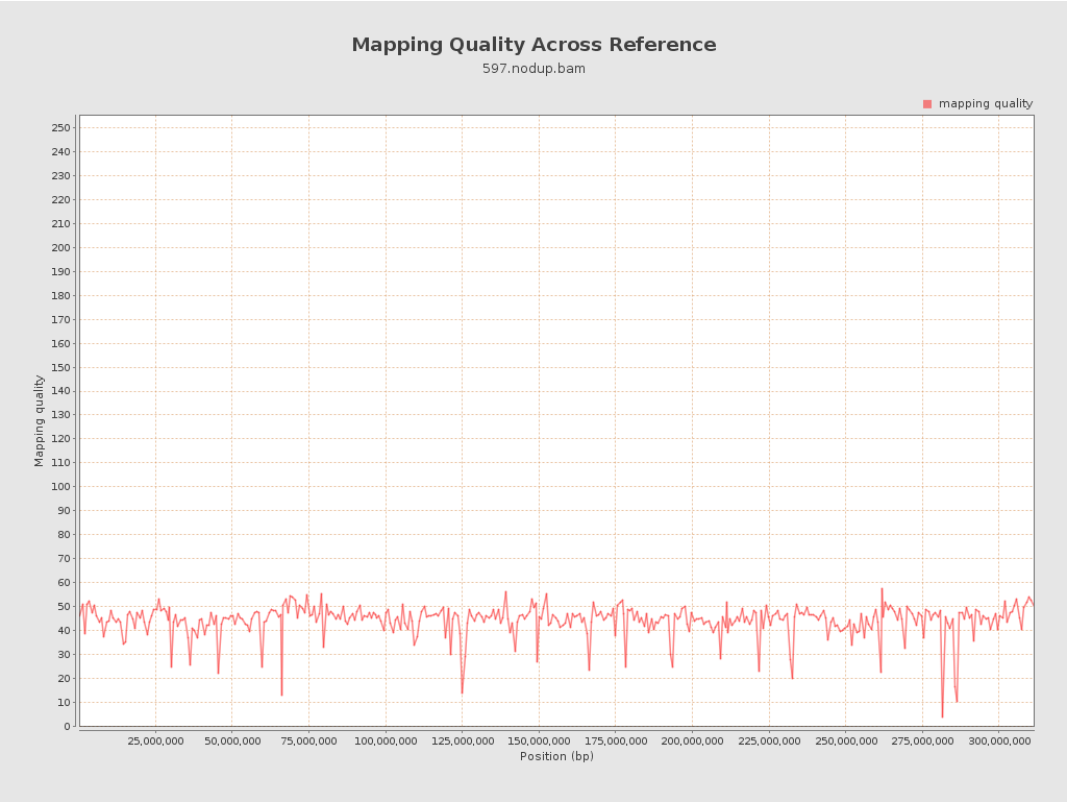
10. Results : Mapped Reads Clipping Profile



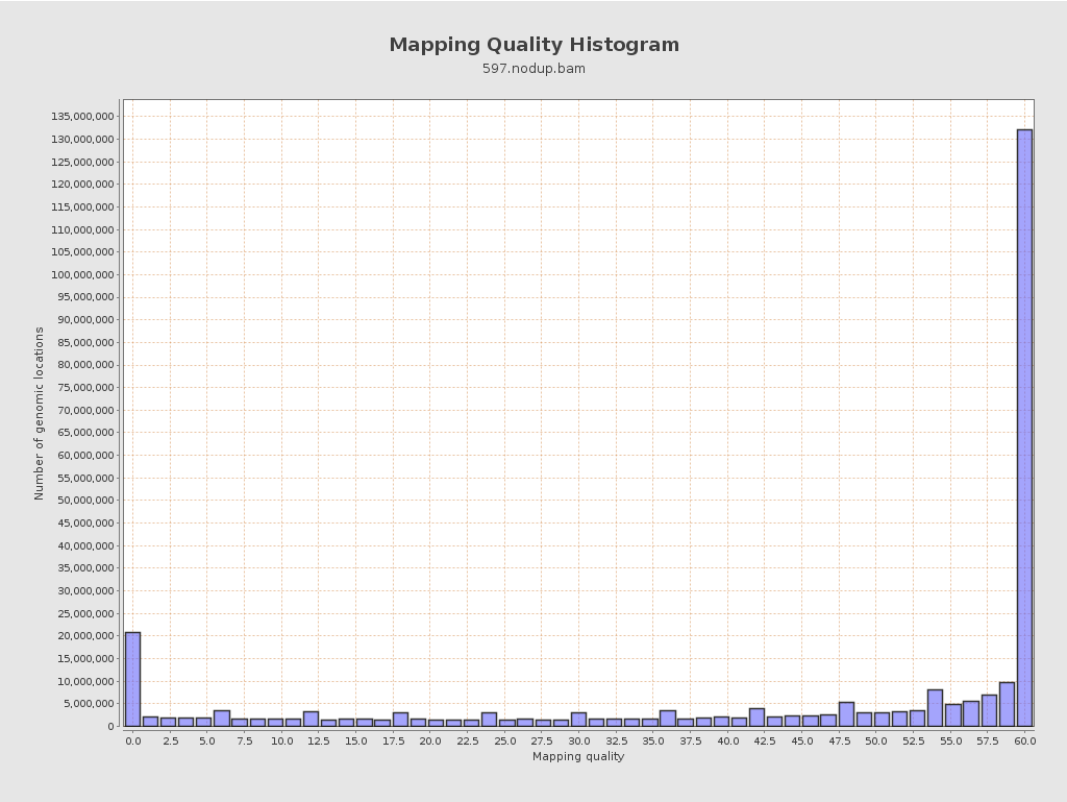
11. Results : Homopolymer Indels



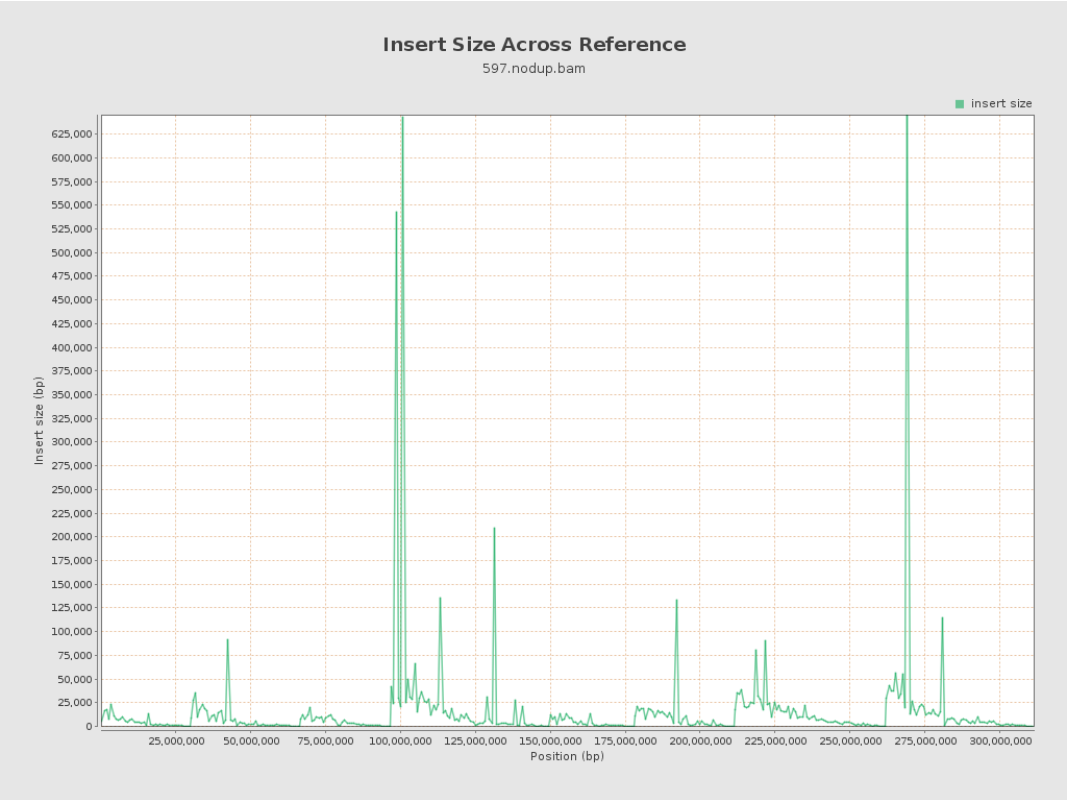
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram