Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397A
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397A .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_593/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_593_S160_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_593/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_593_S160_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:50:03 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	117,250,526
Mapped reads	111,331,770 / 94.95%
Unmapped reads	5,918,756 / 5.05%
Mapped paired reads	111,331,770 / 94.95%
Mapped reads, first in pair	55,810,512 / 47.6%
Mapped reads, second in pair	55,521,258 / 47.35%
Mapped reads, both in pair	109,318,365 / 93.23%
Mapped reads, singletons	2,013,405 / 1.72%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	17,419,454 / 14.86%
Clipped reads	24,908,668 / 21.24%

2.2. ACGT Content

Number/percentage of A's	4,766,866,927 / 30.82%
Number/percentage of C's	2,968,079,016 / 19.19%
Number/percentage of T's	4,767,695,977 / 30.82%
Number/percentage of G's	2,964,441,185 / 19.17%
Number/percentage of N's	75,707 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	49.7587
Standard Deviation	358.3463

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Insert size

Mean	229,065.21
Standard Deviation	2,266,568.27
P25/Median/P75	340 / 448 / 587

2.6. Mismatches and indels

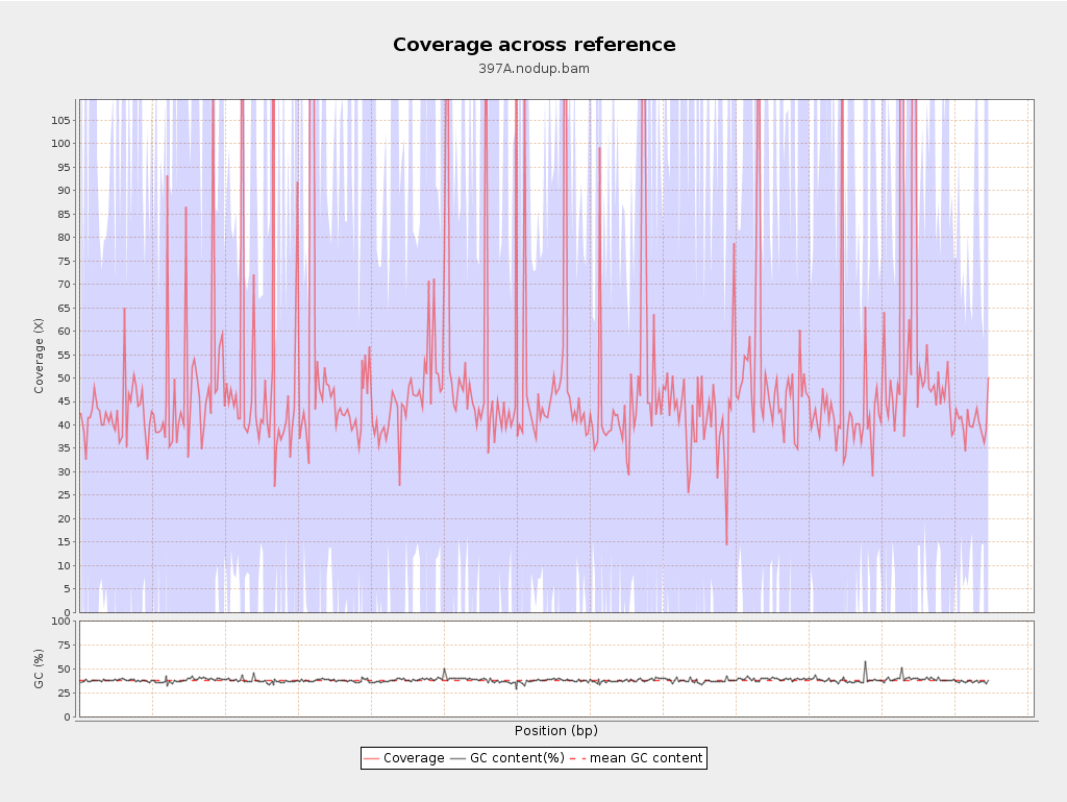
General error rate	2.38%
Mismatches	340,345,139
Insertions	10,067,368
Mapped reads with at least one insertion	8.15%
Deletions	10,506,635
Mapped reads with at least one deletion	8.4%
Homopolymer indels	56.31%

2.7. Chromosome stats

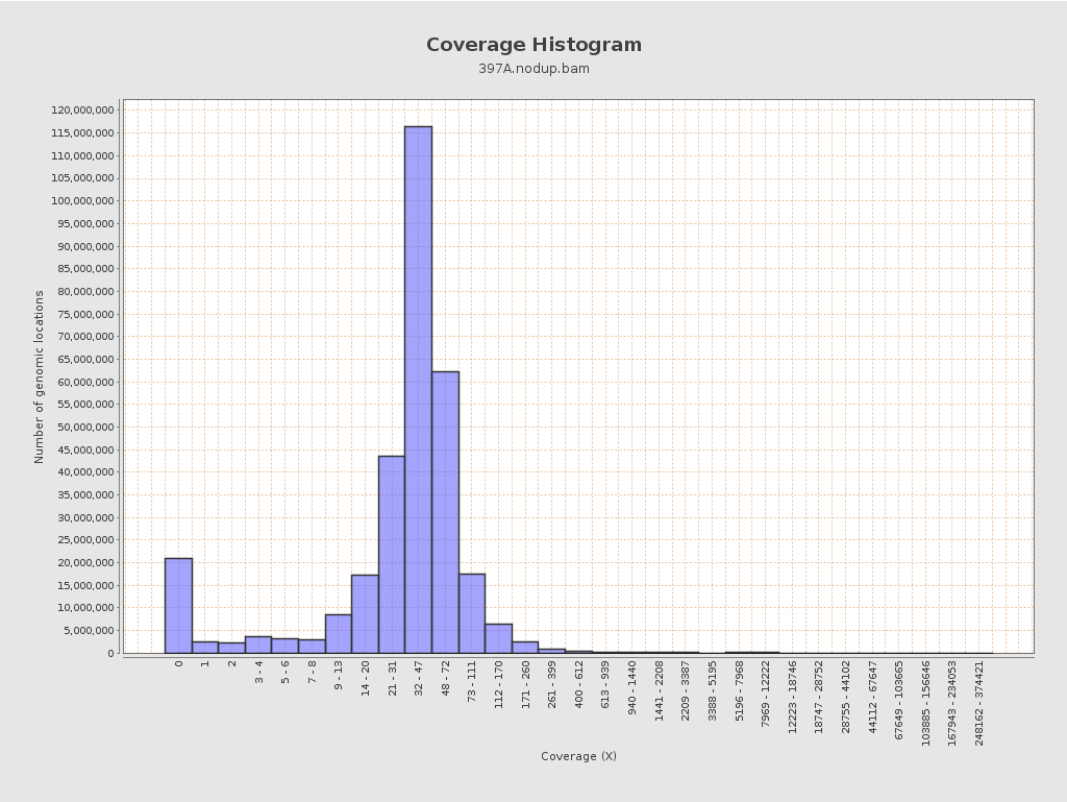
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1249075853	42.022	99.1285

LT669789.1	36598175	1870768702	51.1164	386.359
LT669790.1	30422129	1573685792	51.7283	322.8499
LT669791.1	52758100	2568839146	48.6909	292.3794
LT669792.1	28376109	1397931501	49.2644	414.1329
LT669793.1	33388210	1569405943	47.0048	268.7399
LT669794.1	50579949	2414761894	47.7415	317.1424
LT669795.1	49795044	2862449095	57.4846	534.2304

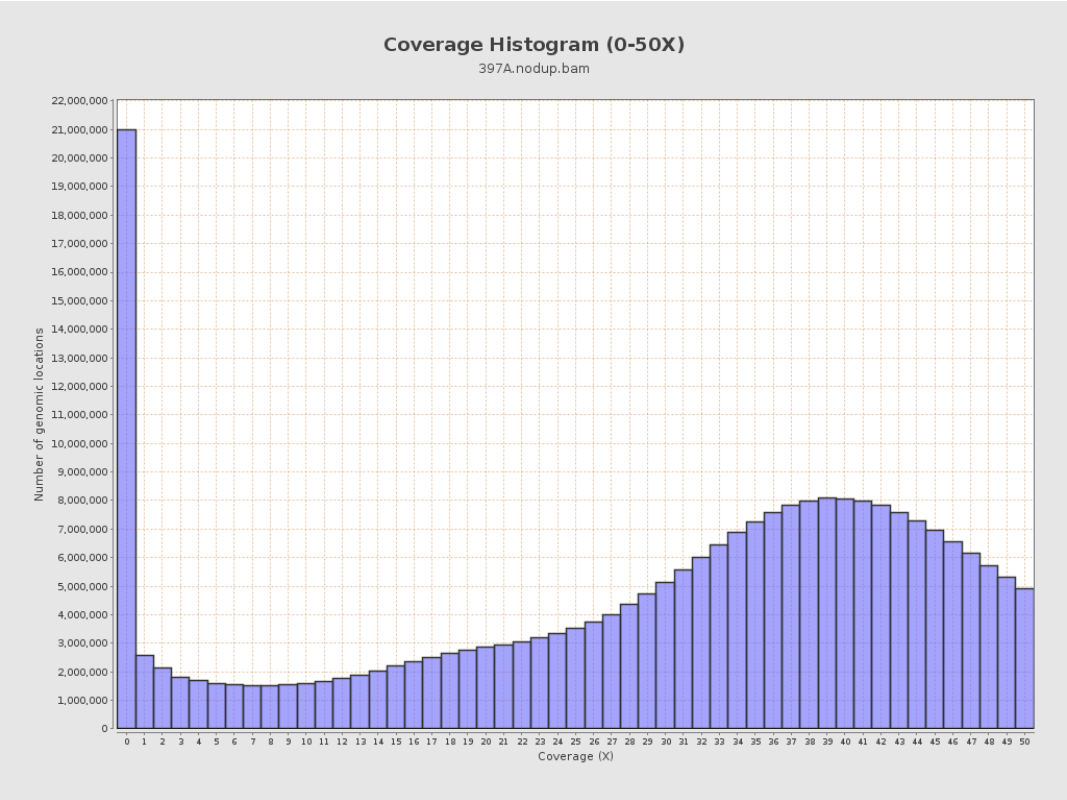
3. Results : Coverage across reference



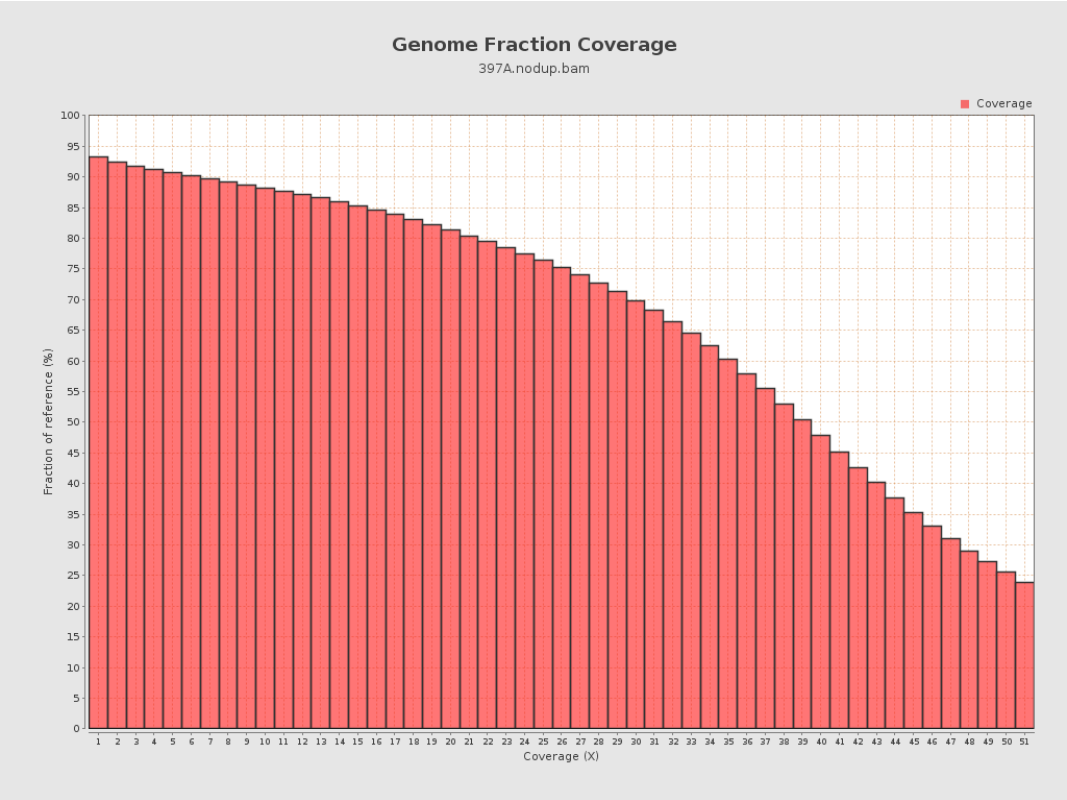
4. Results : Coverage Histogram



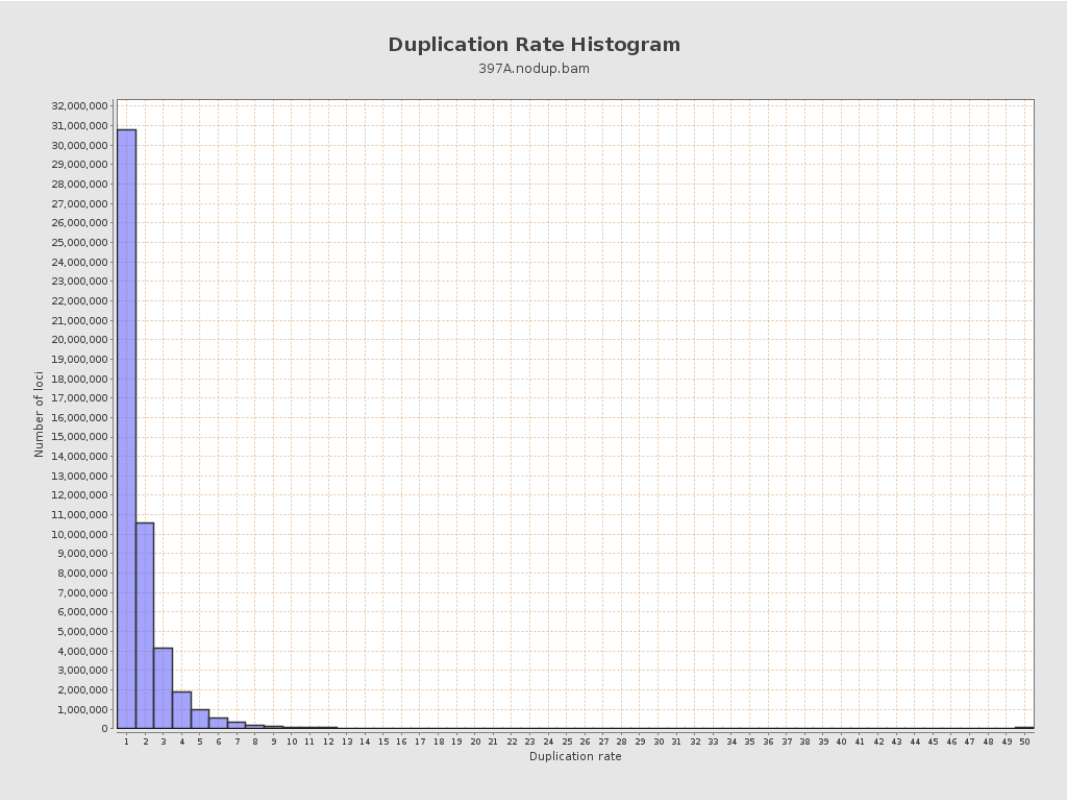
5. Results : Coverage Histogram (0-50X)



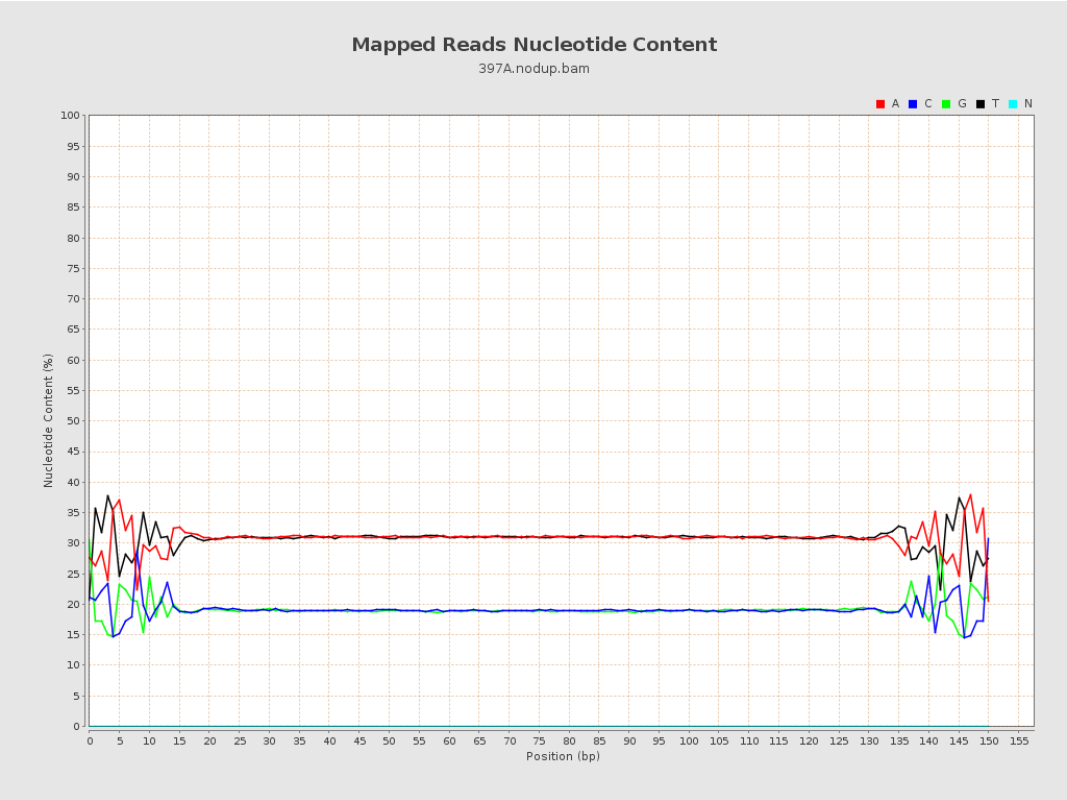
6. Results : Genome Fraction Coverage



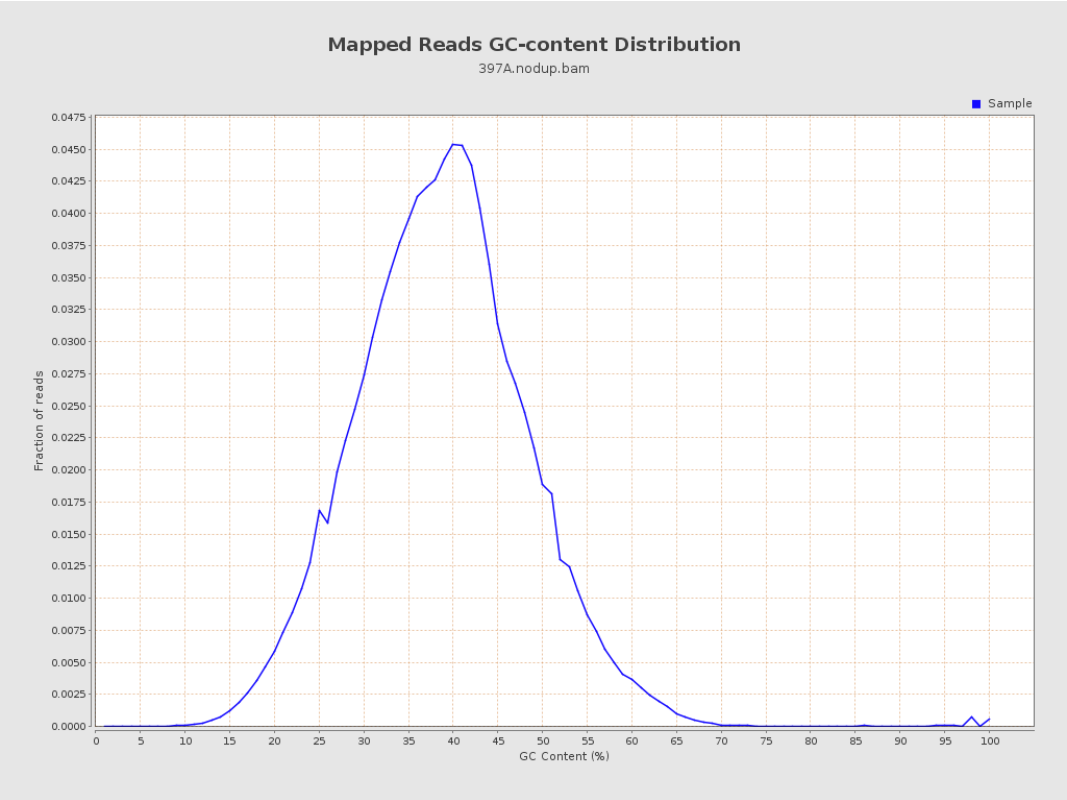
7. Results : Duplication Rate Histogram



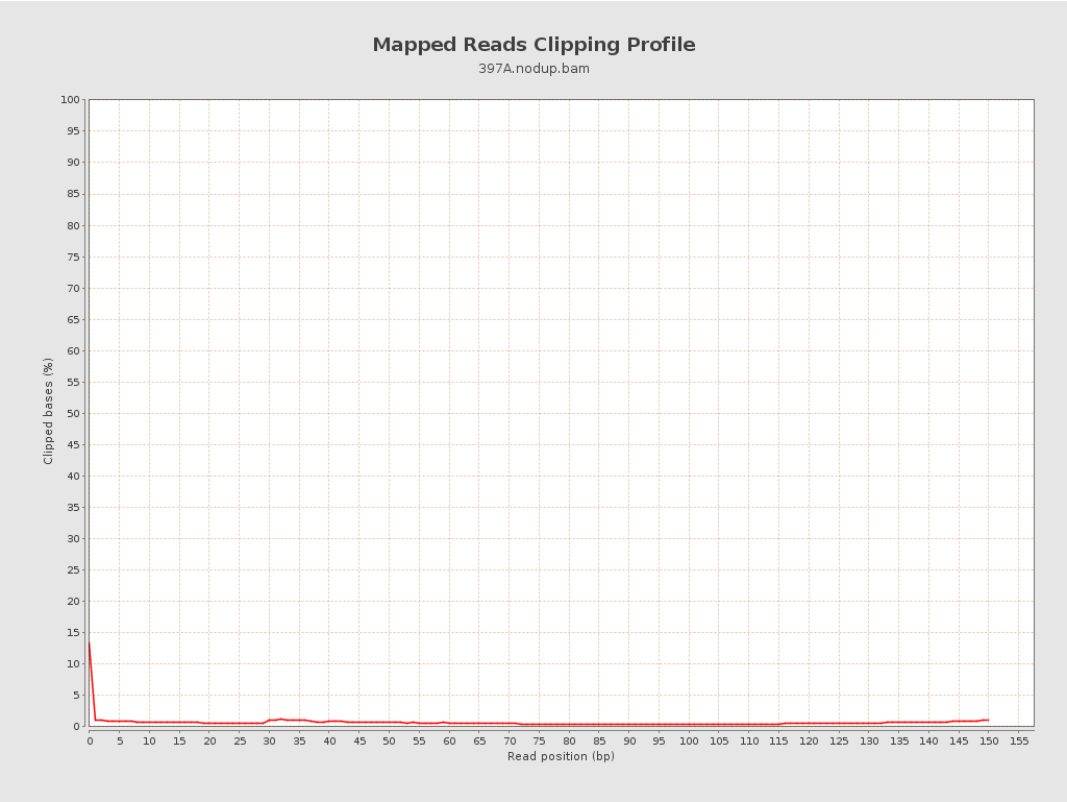
8. Results : Mapped Reads Nucleotide Content



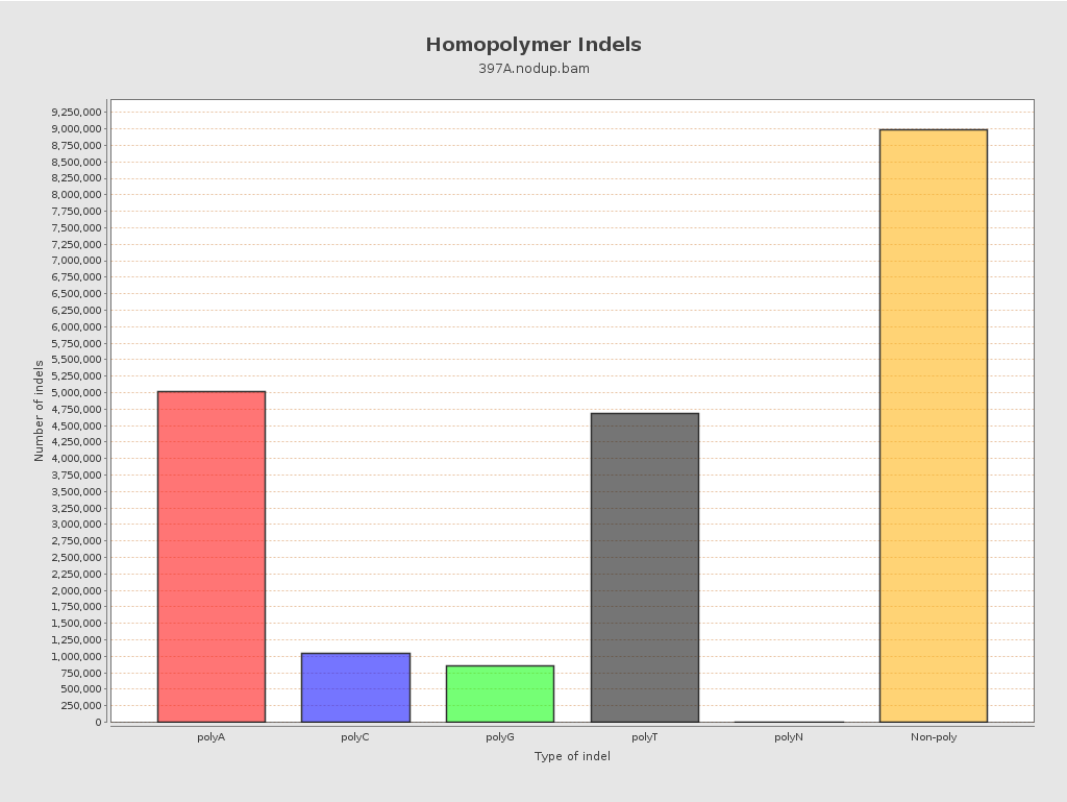
9. Results : Mapped Reads GC-content Distribution



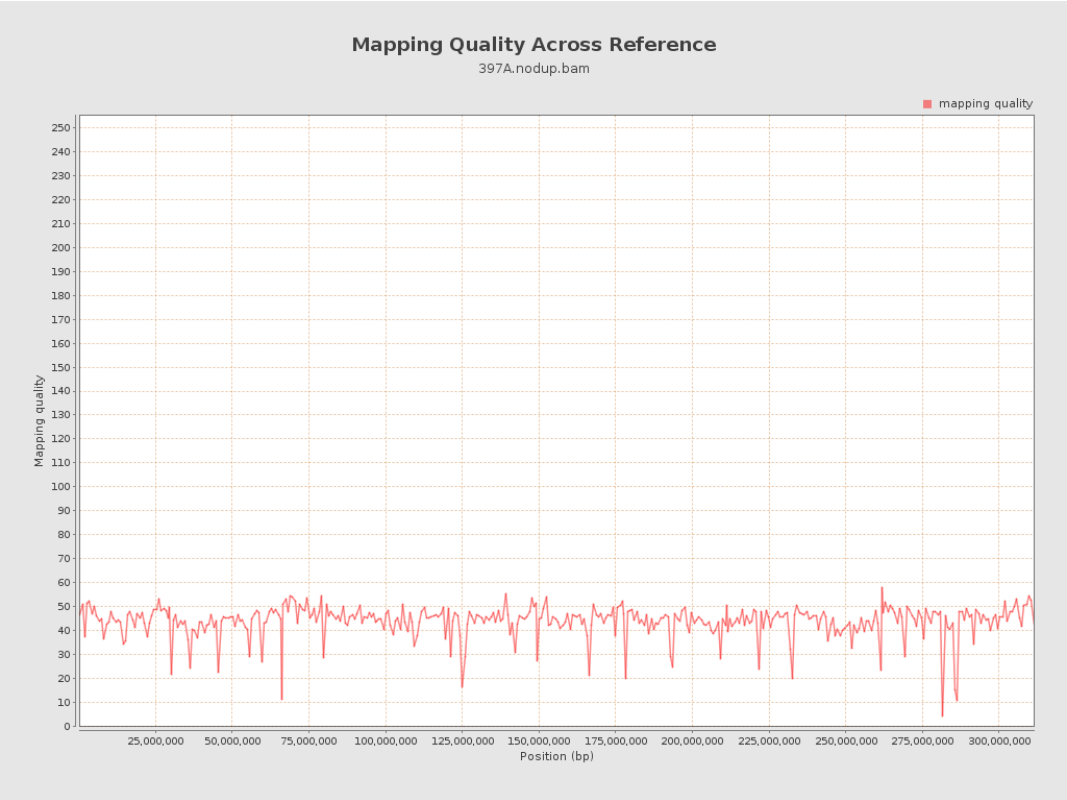
10. Results : Mapped Reads Clipping Profile



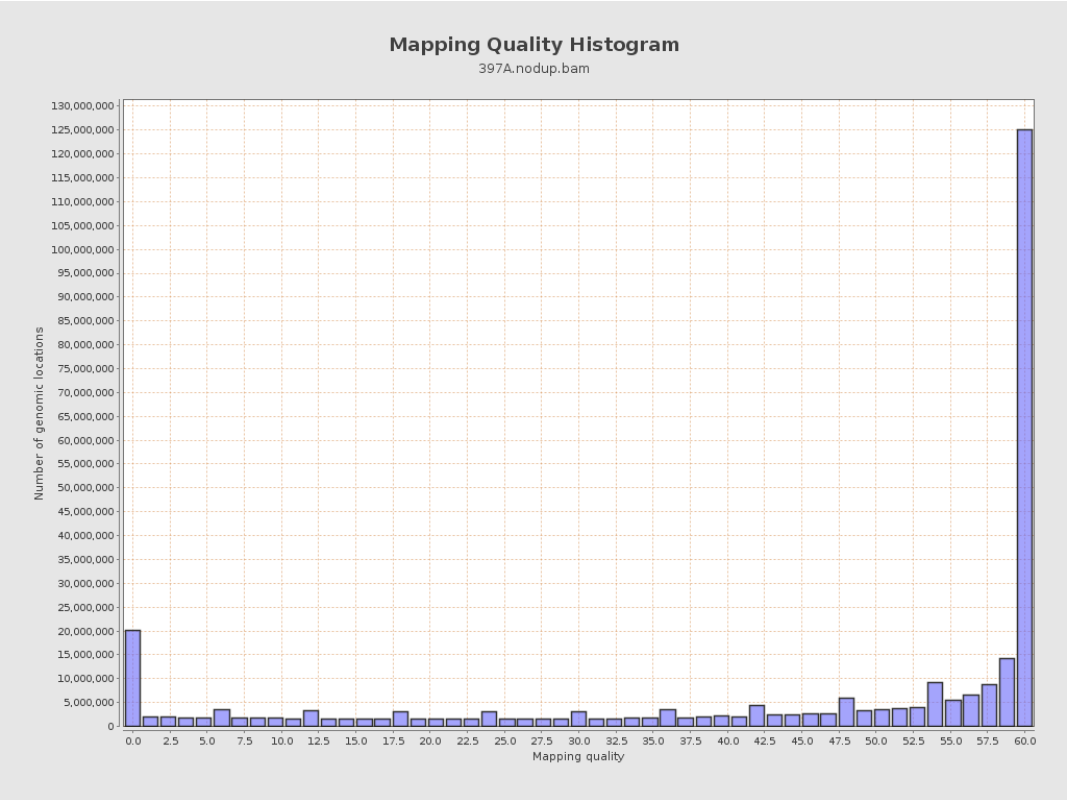
11. Results : Homopolymer Indels



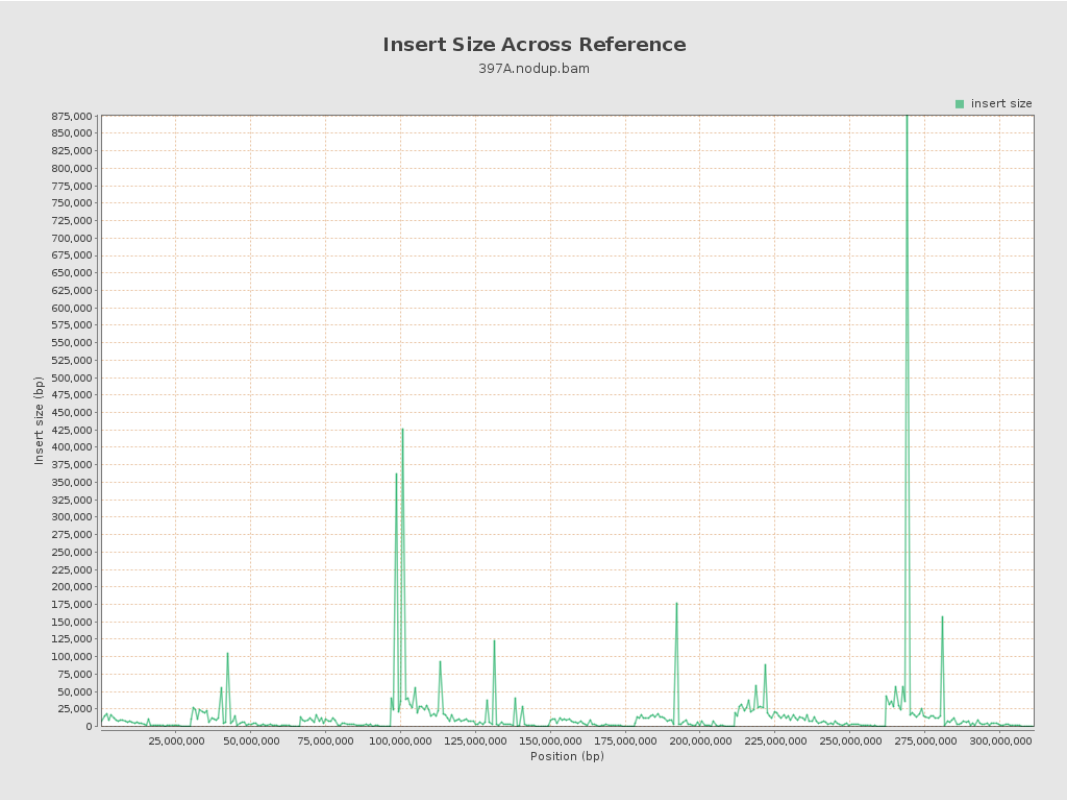
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram