Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/140
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1407 .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_487/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_487_S462_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_487/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_487_S462_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:26 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	57,813,958
Mapped reads	53,963,671 / 93.34%
Unmapped reads	3,850,287 / 6.66%
Mapped paired reads	53,963,671 / 93.34%
Mapped reads, first in pair	27,065,887 / 46.82%
Mapped reads, second in pair	26,897,784 / 46.52%
Mapped reads, both in pair	52,596,586 / 90.98%
Mapped reads, singletons	1,367,085 / 2.36%
Read min/max/mean length	30 / 151 / 148.22
Duplicated reads (flagged)	8,554,398 / 14.8%
Clipped reads	11,797,727 / 20.41%

2.2. ACGT Content

Number/percentage of A's	2,310,046,148 / 30.82%
Number/percentage of C's	1,437,998,636 / 19.19%
Number/percentage of T's	2,313,167,530 / 30.86%
Number/percentage of G's	1,434,042,149 / 19.13%
Number/percentage of N's	25,101 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	24.1116
Standard Deviation	187.4381

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Insert size

Mean	255,668.62
Standard Deviation	2,418,569
P25/Median/P75	382 / 498 / 658

2.6. Mismatches and indels

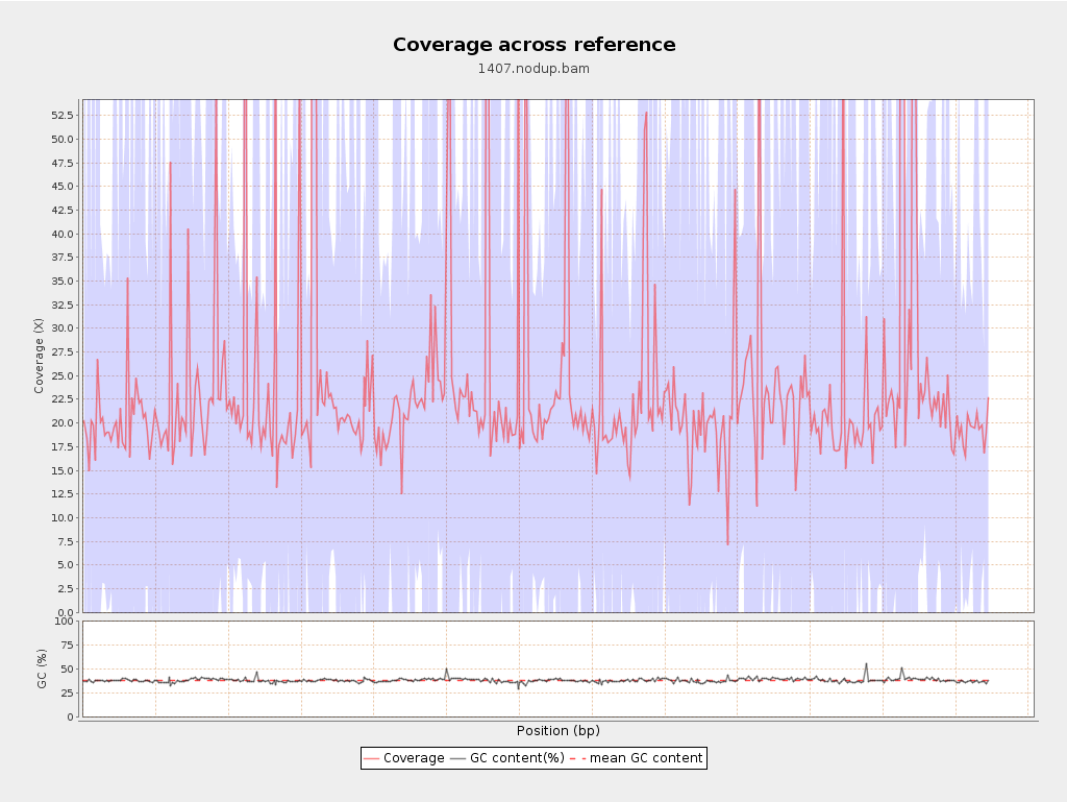
General error rate	2.31%
Mismatches	159,100,766
Insertions	5,042,384
Mapped reads with at least one insertion	8.39%
Deletions	5,009,176
Mapped reads with at least one deletion	8.27%
Homopolymer indels	56.51%

2.7. Chromosome stats

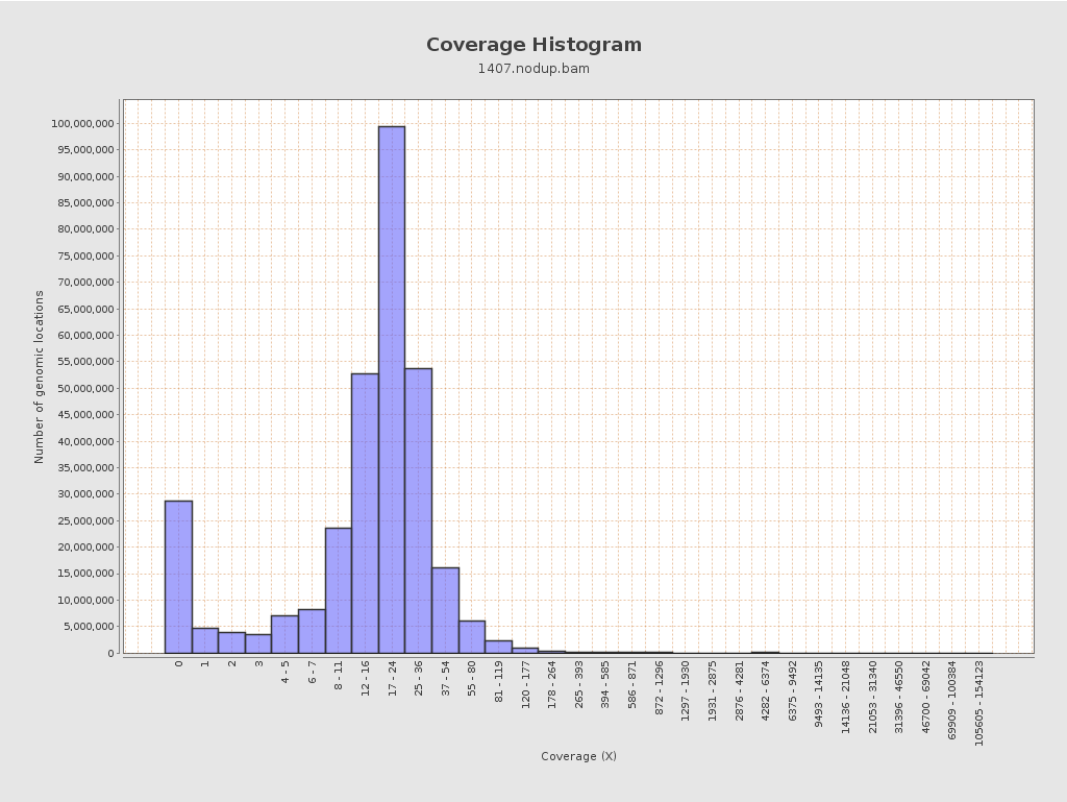
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	594528945	20.0014	58.4764

LT669789.1	36598175	891518360	24.3596	202.5161
LT669790.1	30422129	817038531	26.8567	220.0997
LT669791.1	52758100	1252152066	23.7338	178.2103
LT669792.1	28376109	678610366	23.9148	202.9943
LT669793.1	33388210	736921635	22.0713	127.2712
LT669794.1	50579949	1139617708	22.531	160.1982
LT669795.1	49795044	1403806690	28.1917	252.9869

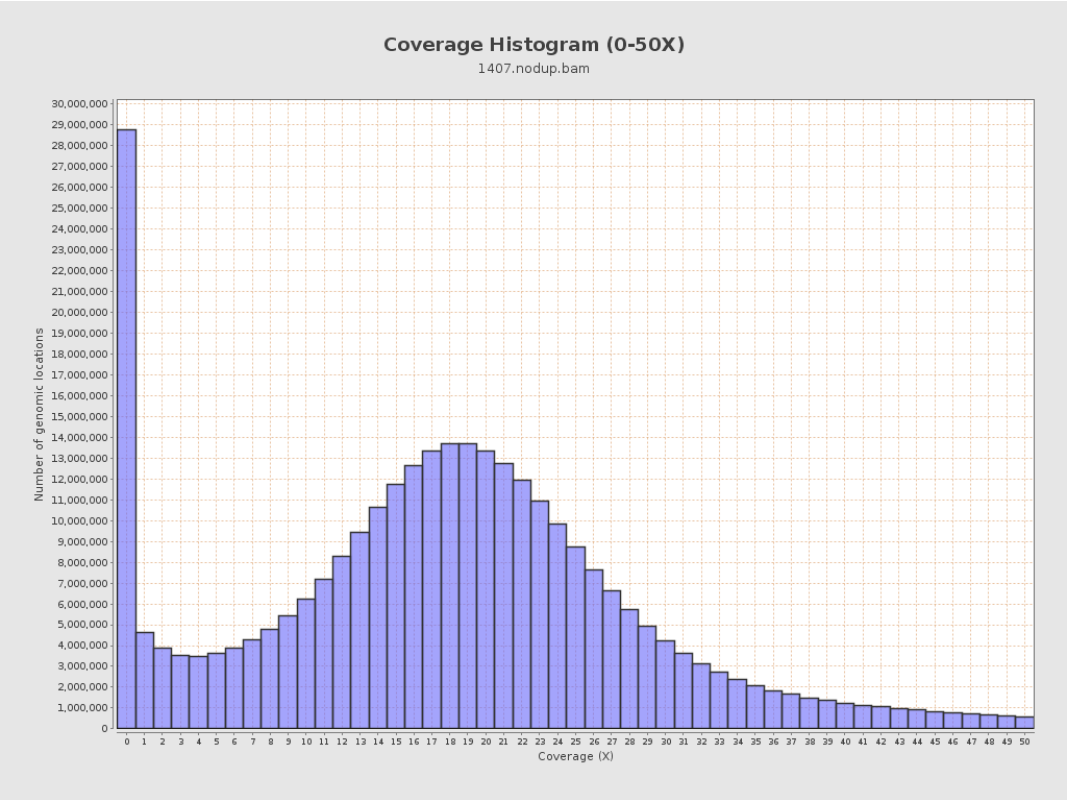
3. Results : Coverage across reference



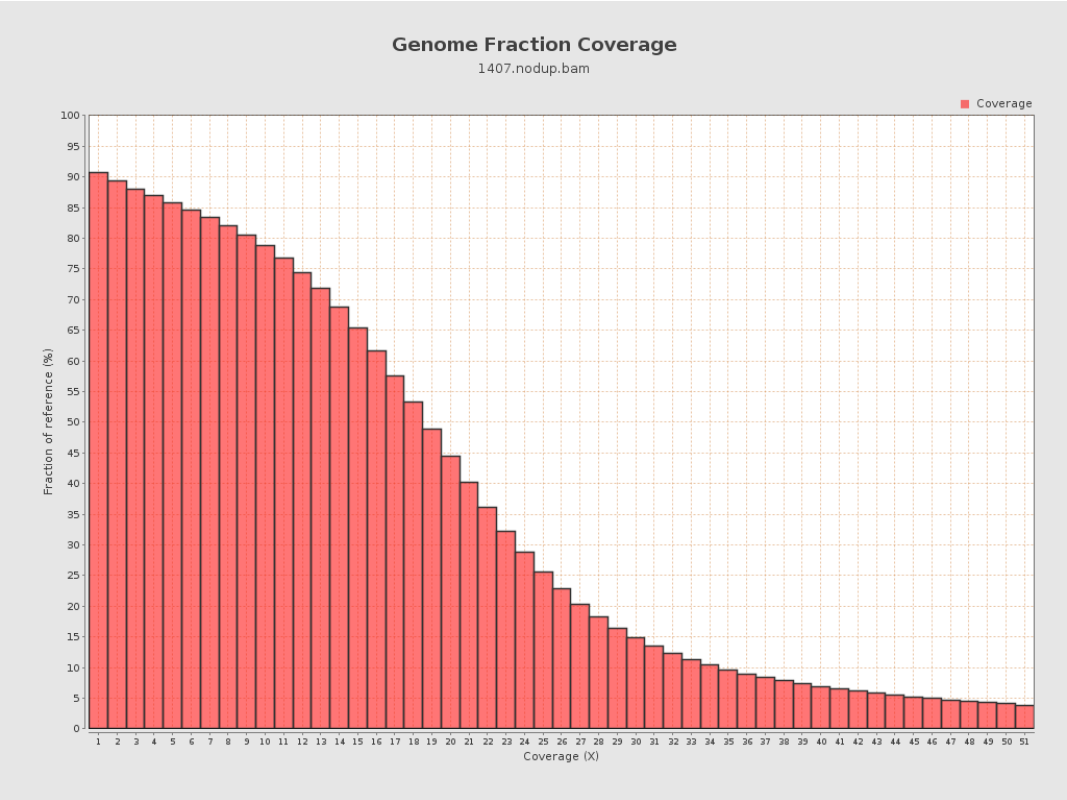
4. Results : Coverage Histogram



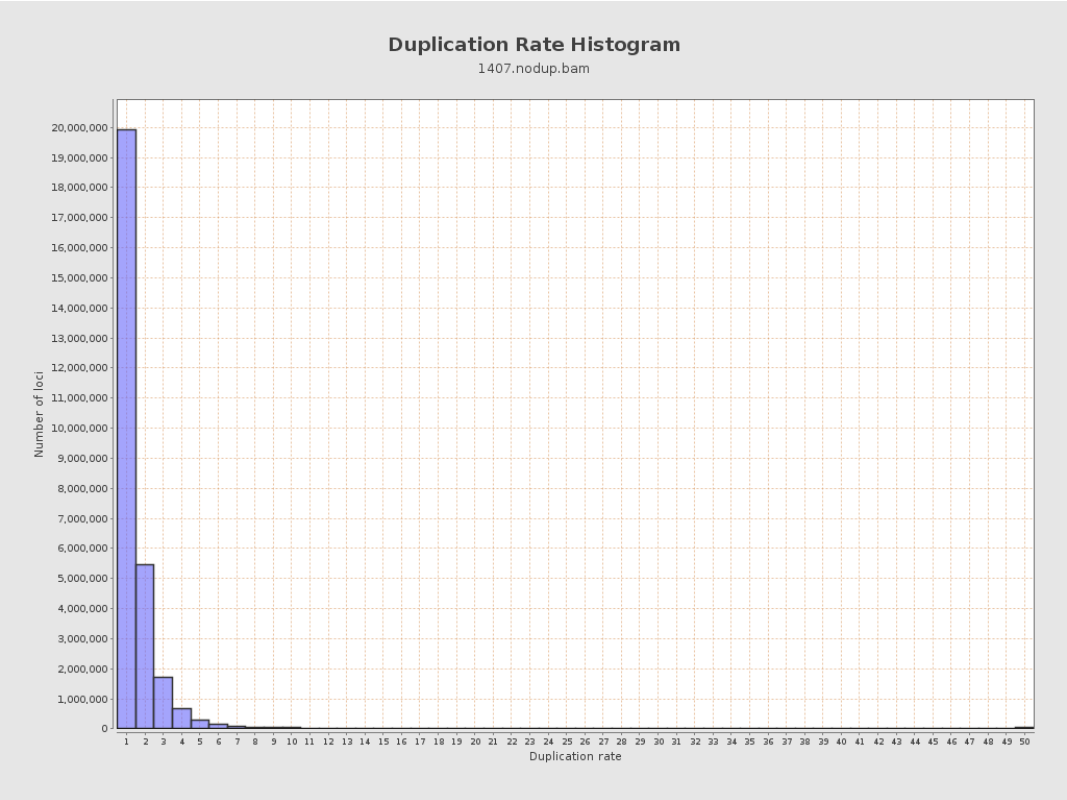
5. Results : Coverage Histogram (0-50X)



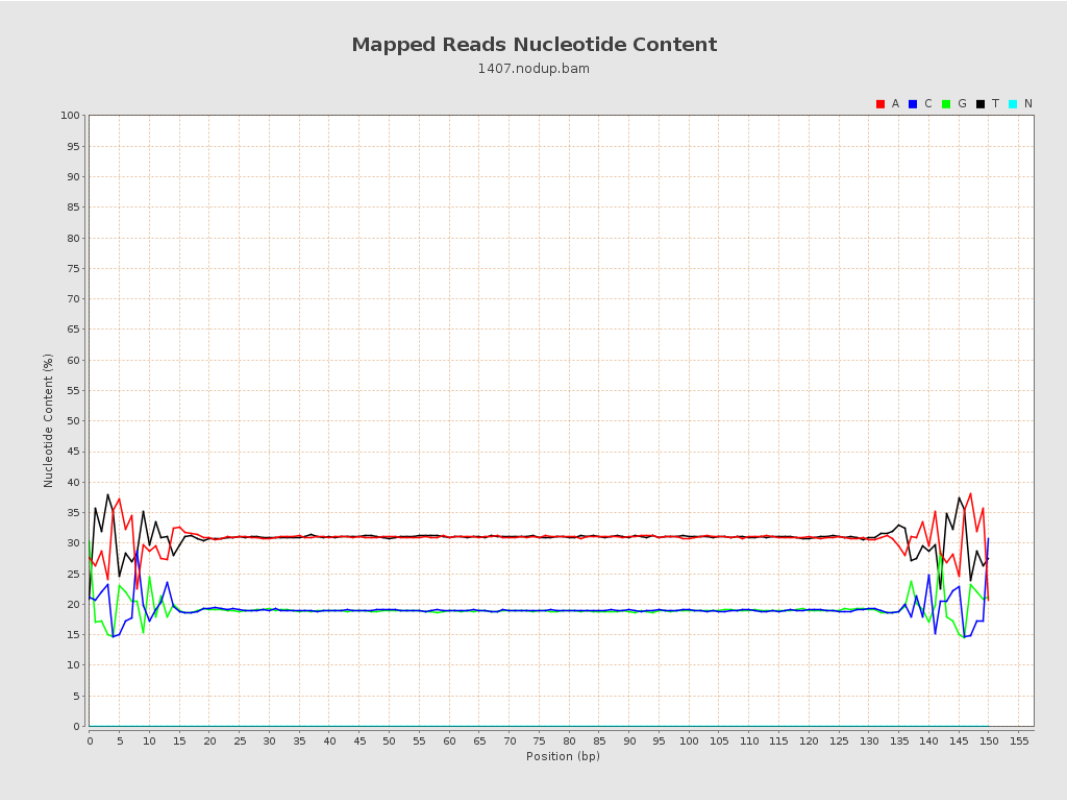
6. Results : Genome Fraction Coverage



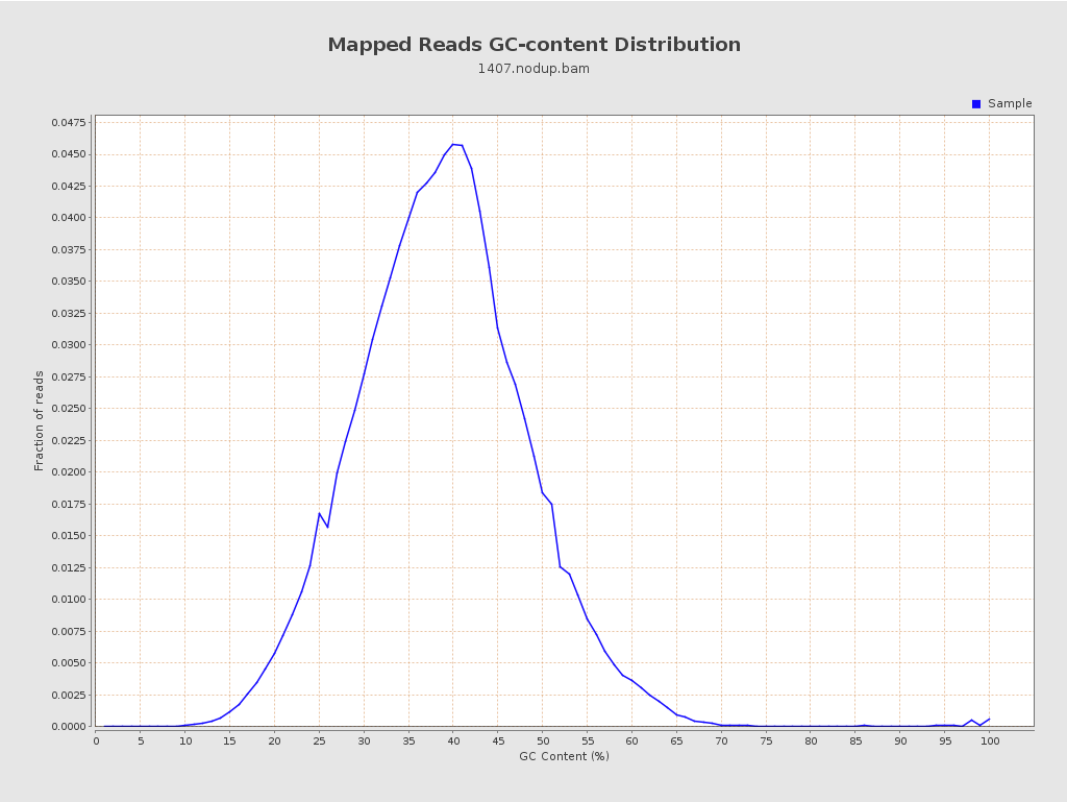
7. Results : Duplication Rate Histogram



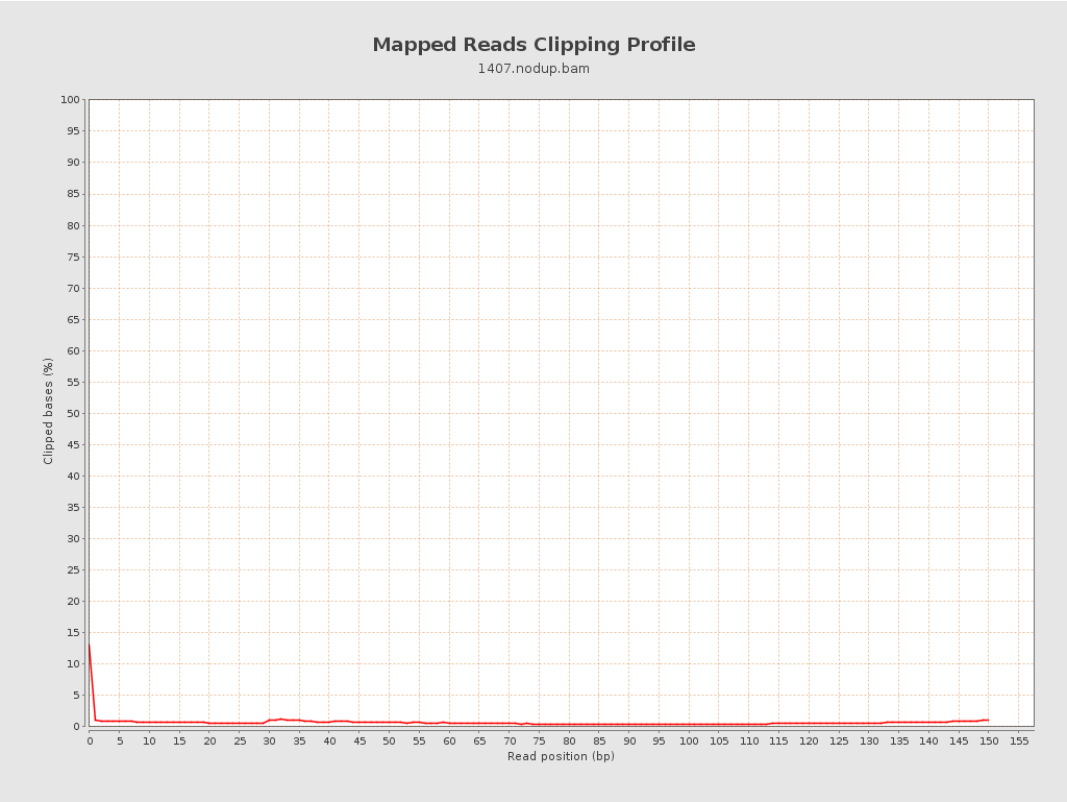
8. Results : Mapped Reads Nucleotide Content



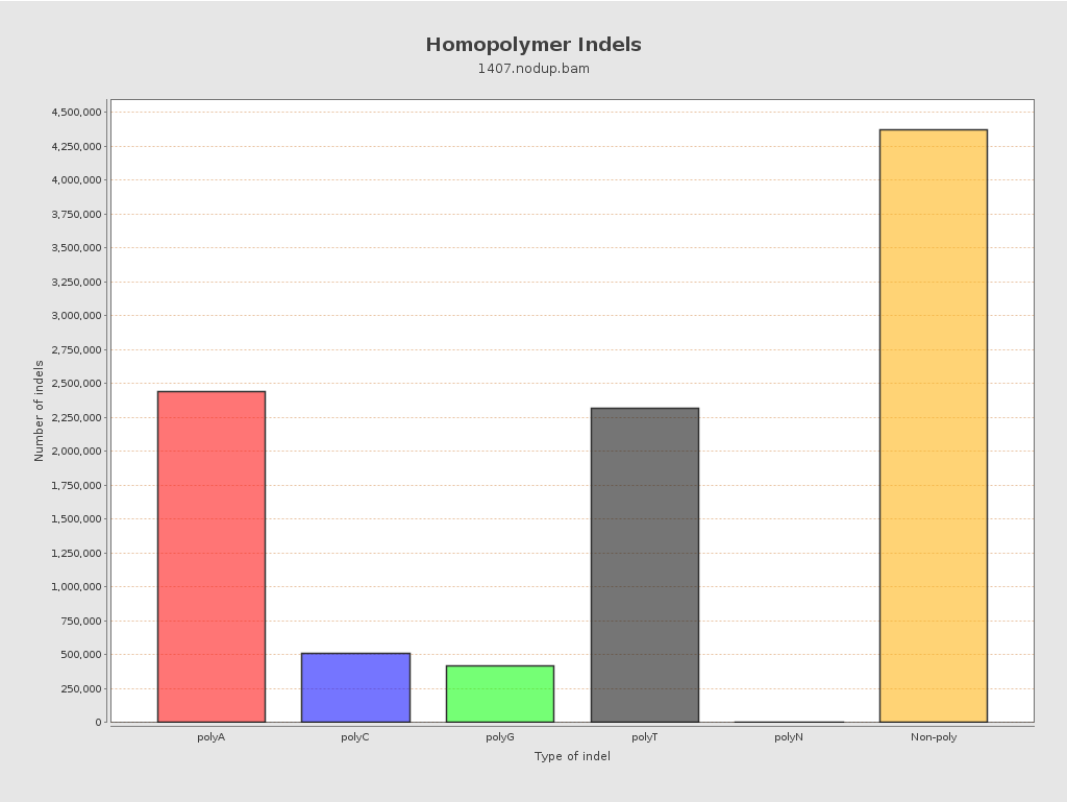
9. Results : Mapped Reads GC-content Distribution



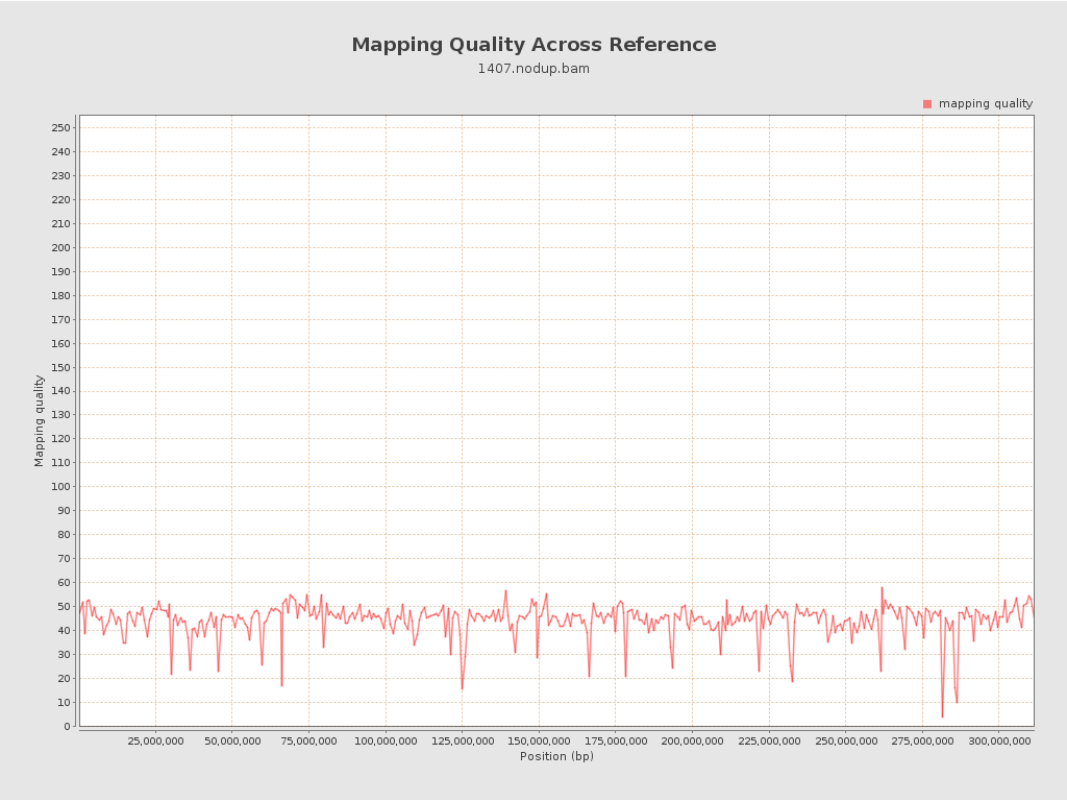
10. Results : Mapped Reads Clipping Profile



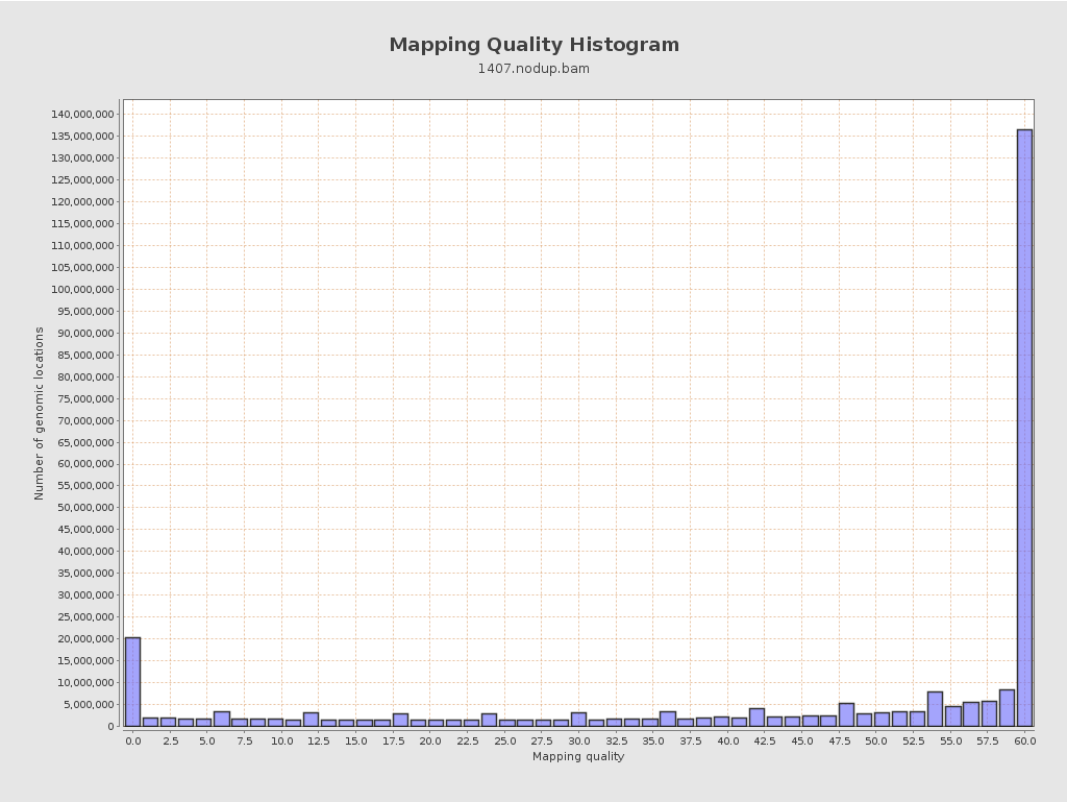
11. Results : Homopolymer Indels



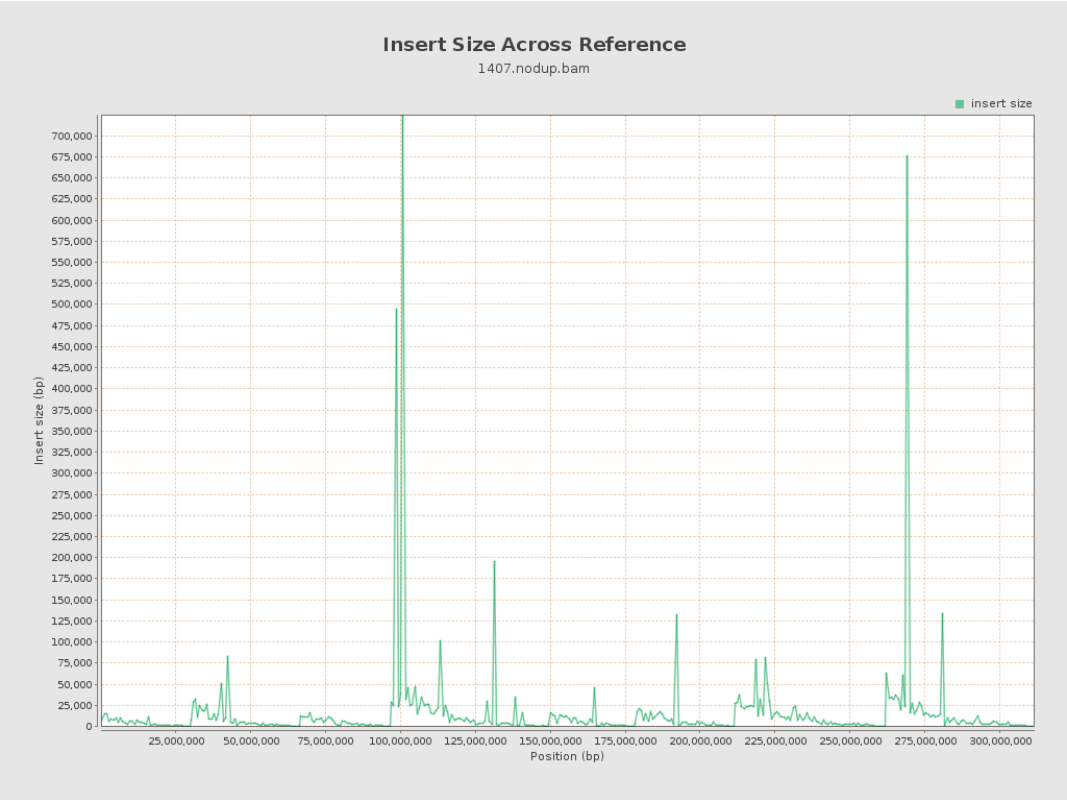
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram