Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1372
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1372 .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_428/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_428_S403_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_428/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_428_S403_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:40:11 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	87,366,986
Mapped reads	82,465,408 / 94.39%
Unmapped reads	4,901,578 / 5.61%
Mapped paired reads	82,465,408 / 94.39%
Mapped reads, first in pair	41,322,108 / 47.3%
Mapped reads, second in pair	41,143,300 / 47.09%
Mapped reads, both in pair	80,791,784 / 92.47%
Mapped reads, singletons	1,673,624 / 1.92%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	14,114,960 / 16.16%
Clipped reads	17,904,863 / 20.49%

2.2. ACGT Content

Number/percentage of A's	3,532,013,447 / 30.82%
Number/percentage of C's	2,198,833,289 / 19.18%
Number/percentage of T's	3,539,737,111 / 30.88%
Number/percentage of G's	2,191,070,483 / 19.12%
Number/percentage of N's	39,285 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	36.8709
Standard Deviation	289.785

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Insert size

Mean	228,324.3
Standard Deviation	2,267,138.86
P25/Median/P75	346 / 452 / 590

2.6. Mismatches and indels

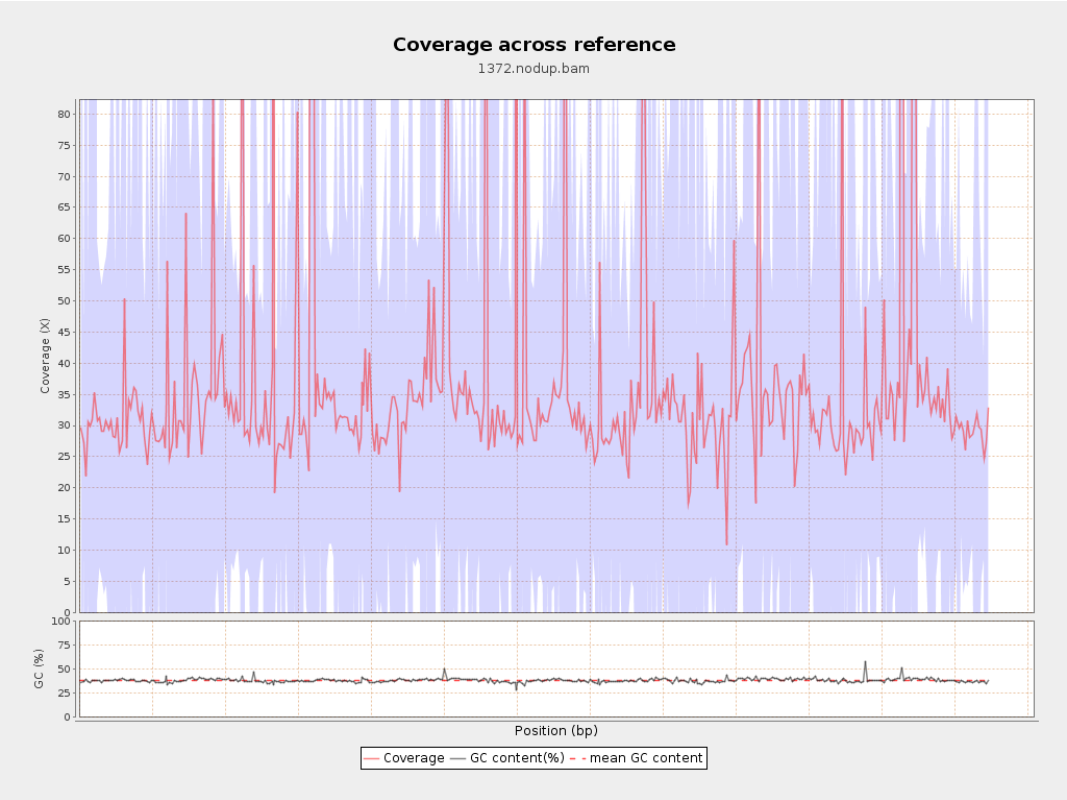
General error rate	2.25%
Mismatches	236,935,868
Insertions	7,554,008
Mapped reads with at least one insertion	8.24%
Deletions	7,622,170
Mapped reads with at least one deletion	8.23%
Homopolymer indels	56.48%

2.7. Chromosome stats

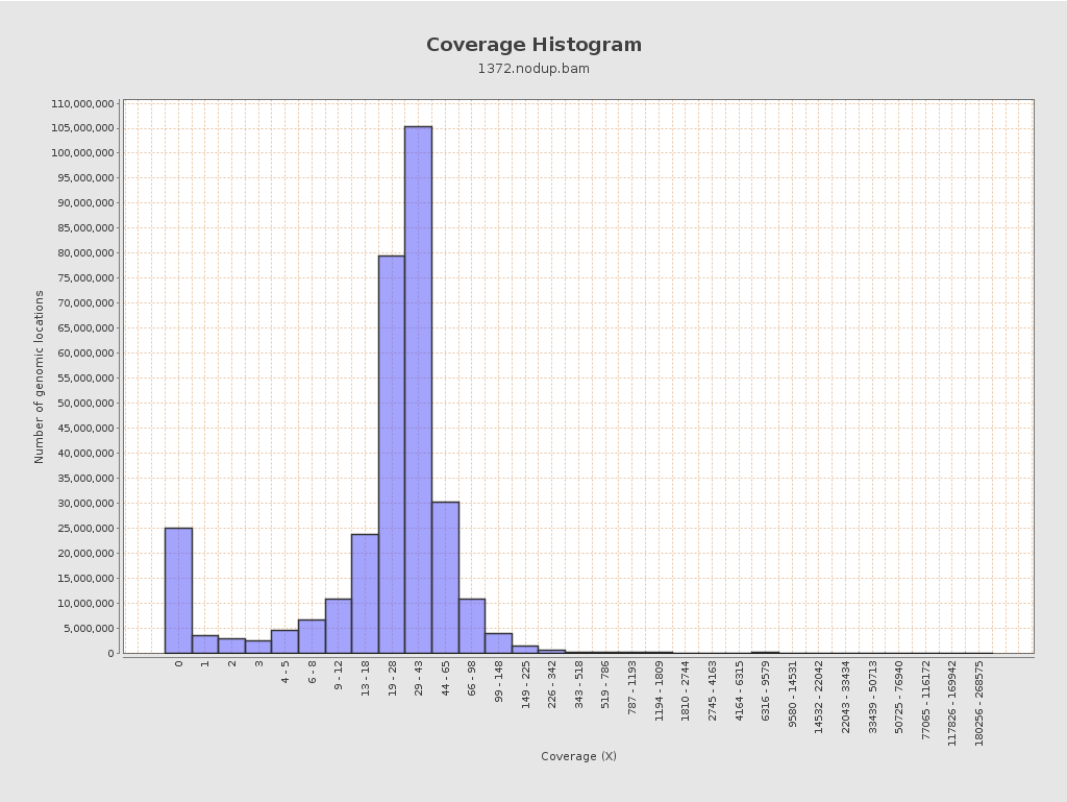
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	899685432	30.2676	86.3775

LT669789.1	36598175	1364382729	37.2801	303.121
LT669790.1	30422129	1188420333	39.0643	281.5765
LT669791.1	52758100	1909784564	36.1989	247.5317
LT669792.1	28376109	1037987601	36.5796	323.2854
LT669793.1	33388210	1138028053	34.0847	197.5918
LT669794.1	50579949	1755344846	34.7044	237.4038
LT669795.1	49795044	2196890631	44.1187	444.0044

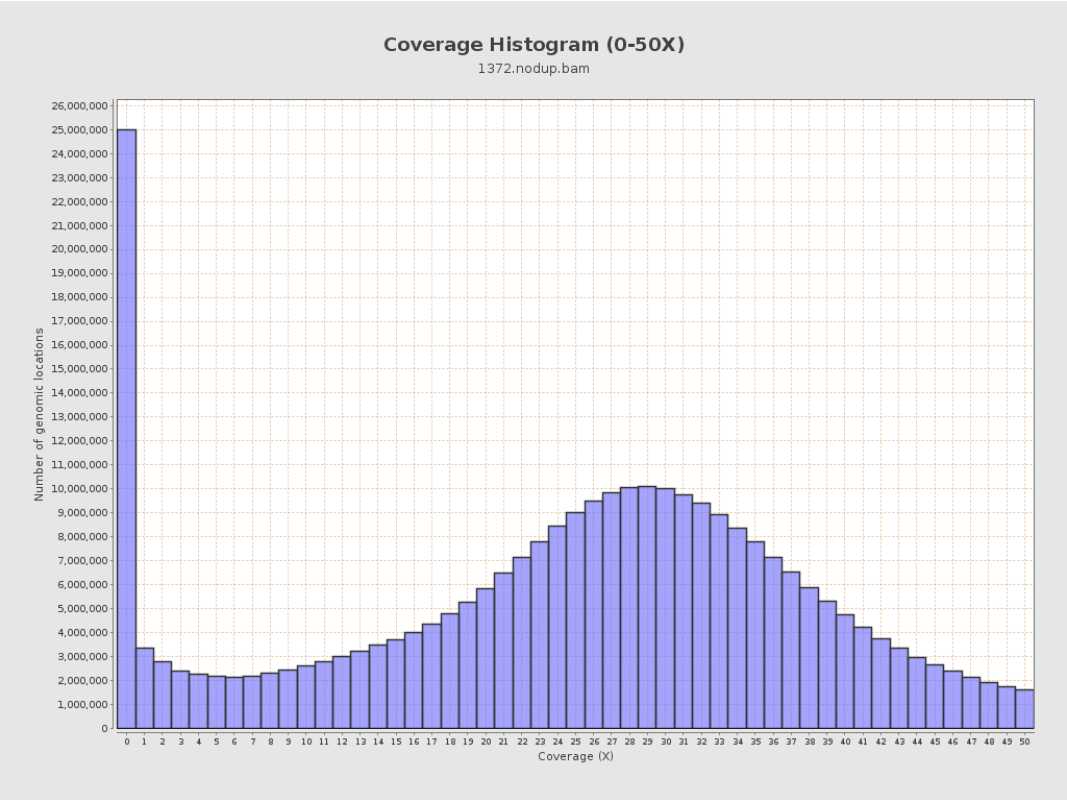
3. Results : Coverage across reference



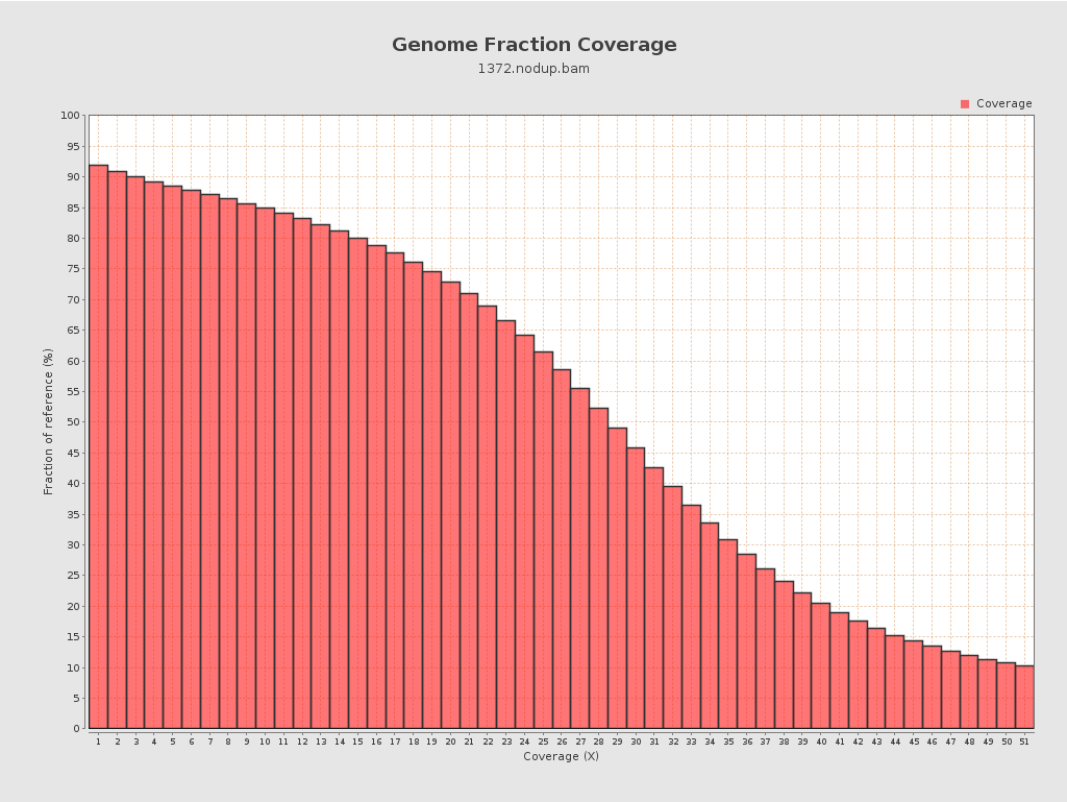
4. Results : Coverage Histogram



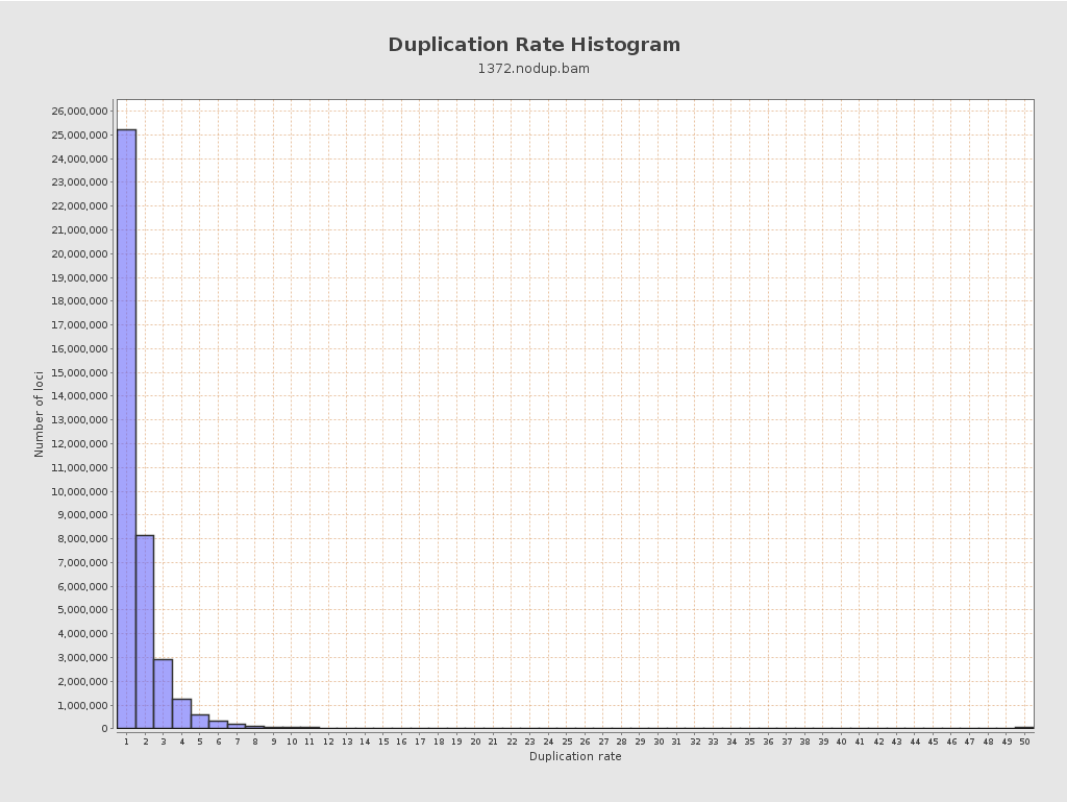
5. Results : Coverage Histogram (0-50X)



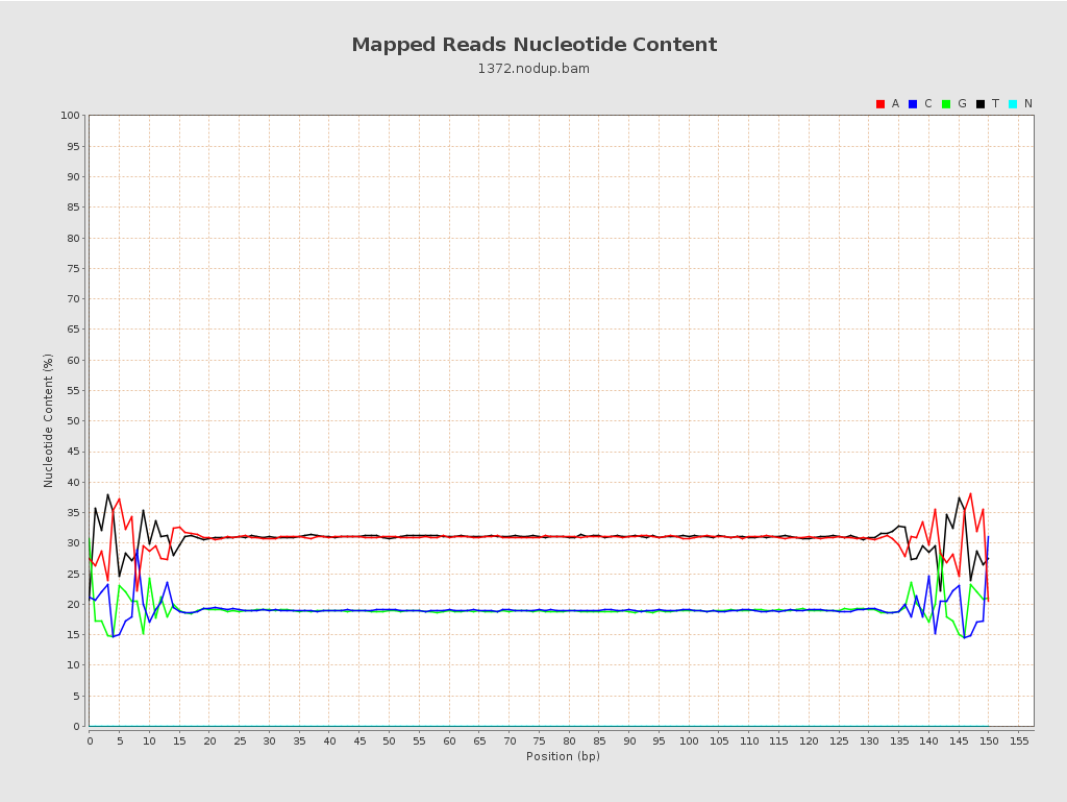
6. Results : Genome Fraction Coverage



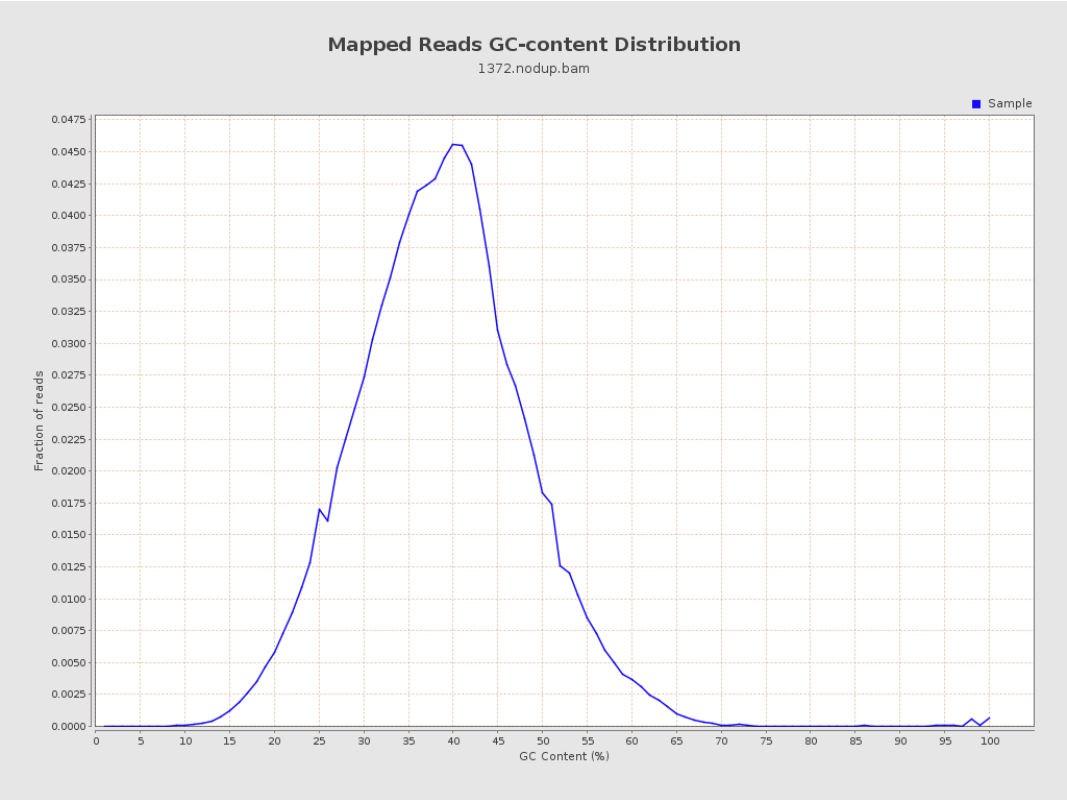
7. Results : Duplication Rate Histogram



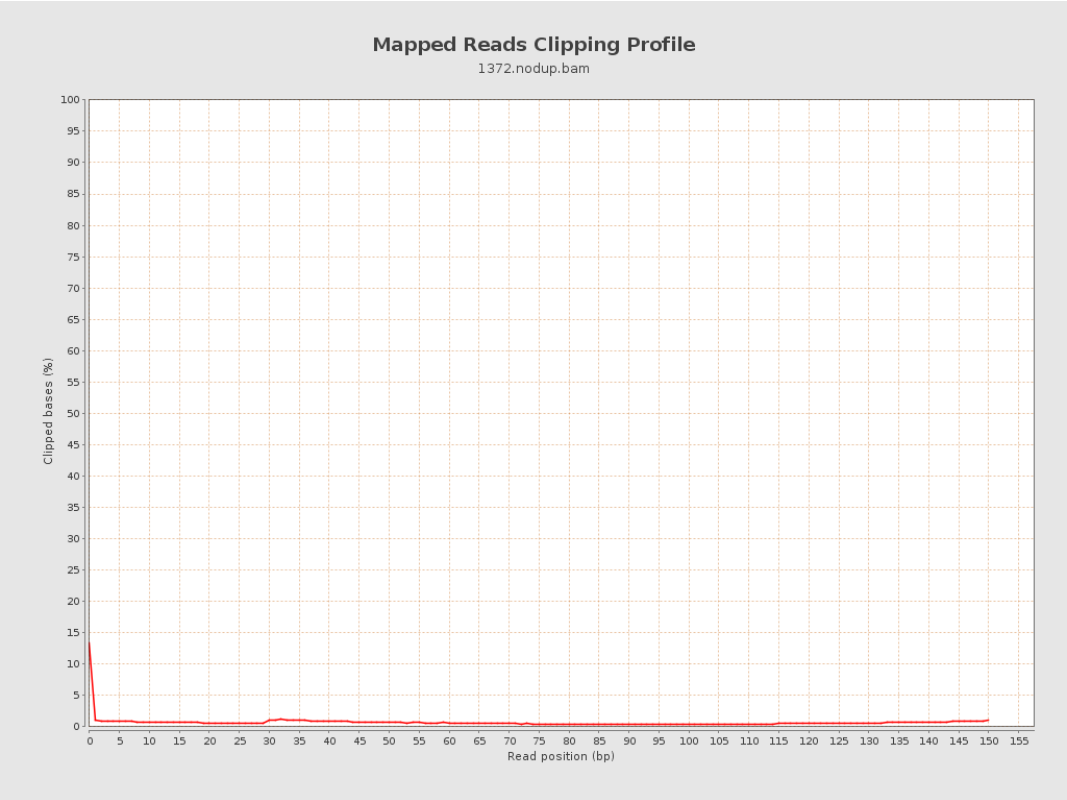
8. Results : Mapped Reads Nucleotide Content



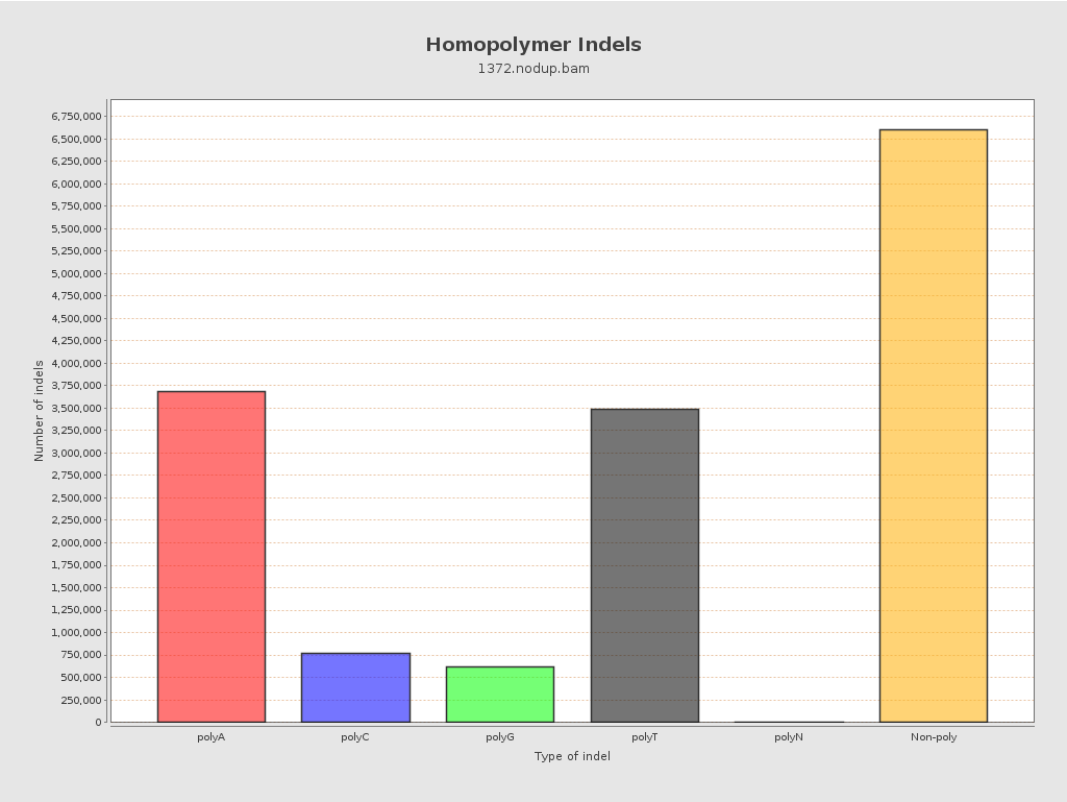
9. Results : Mapped Reads GC-content Distribution



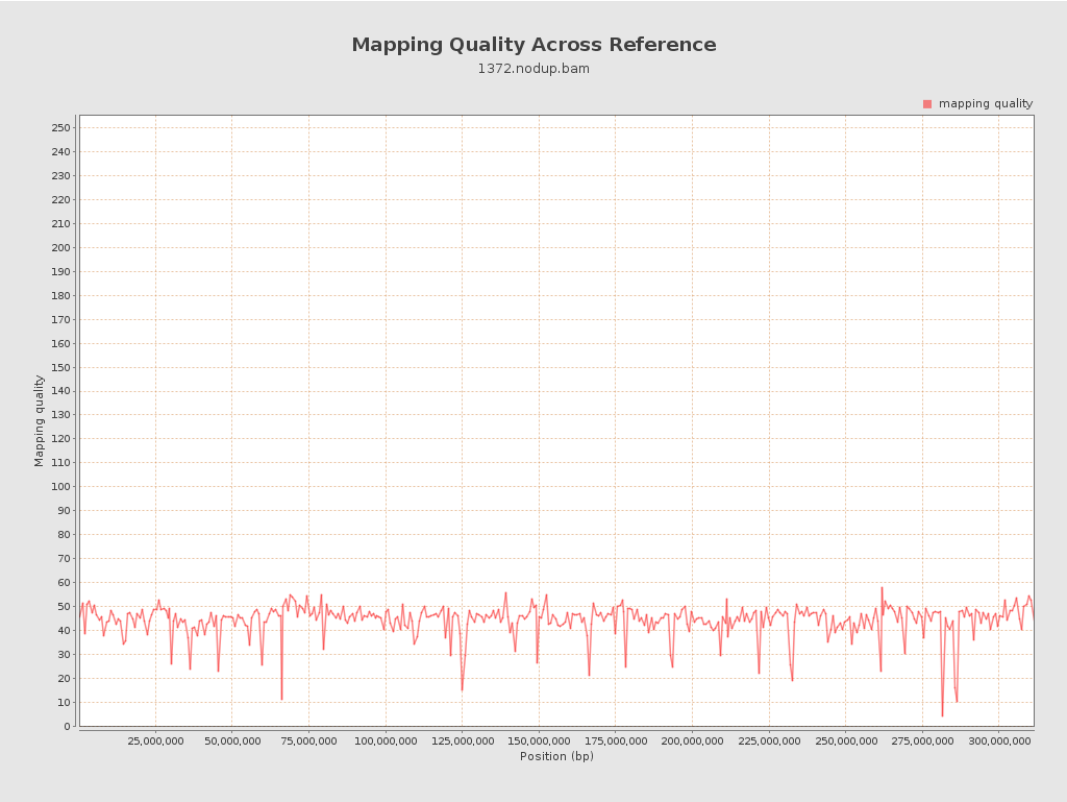
10. Results : Mapped Reads Clipping Profile



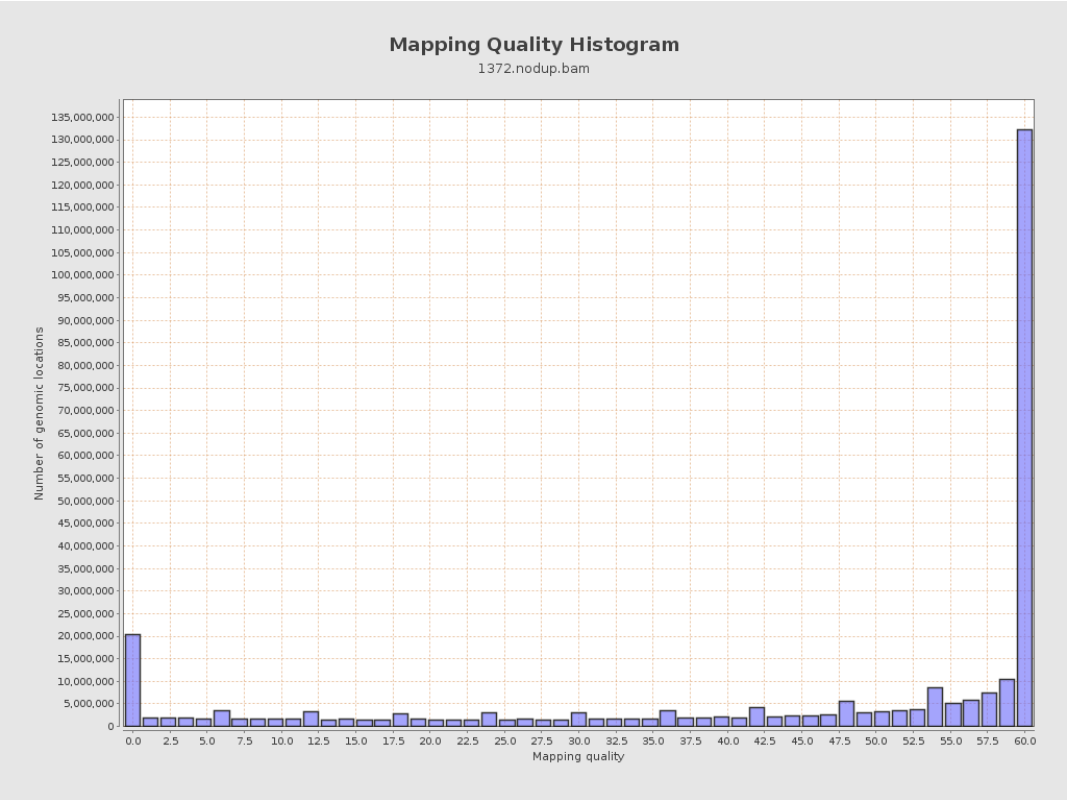
11. Results : Homopolymer Indels



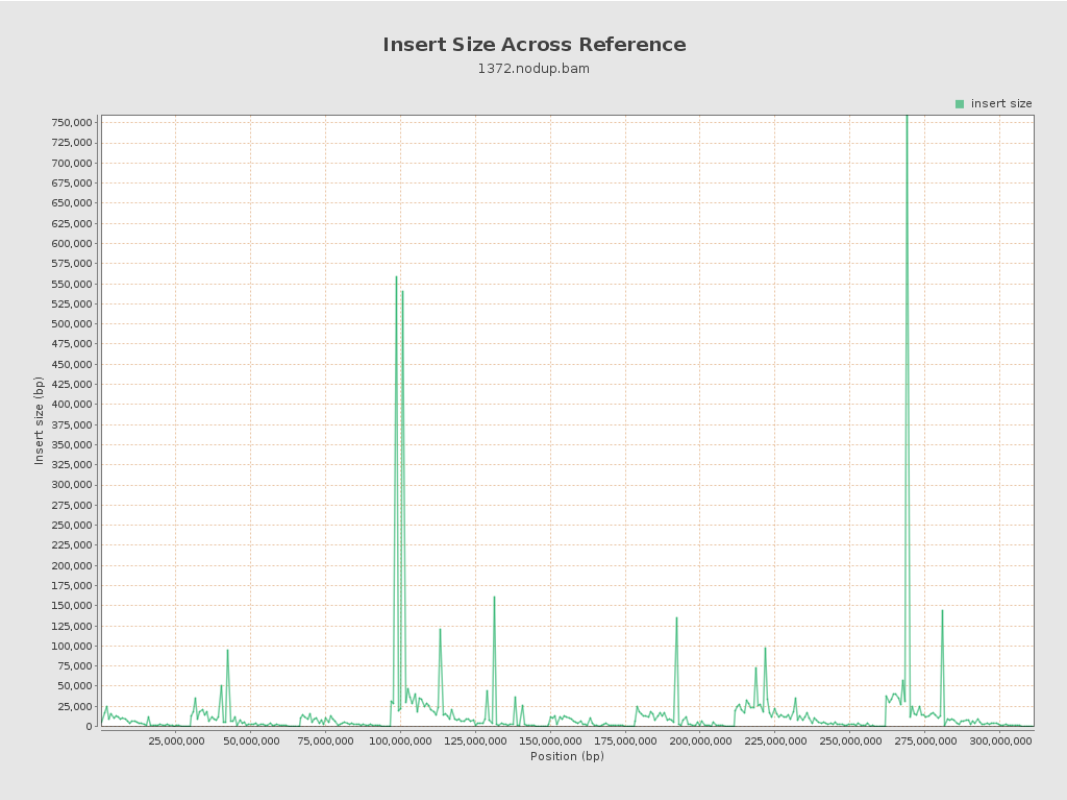
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram