Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1432
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1432 .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_543/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_543_S110_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_543/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_543_S110_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:37:05 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,740,722
Mapped reads	76,416,586 / 94.64%
Unmapped reads	4,324,136 / 5.36%
Mapped paired reads	76,416,586 / 94.64%
Mapped reads, first in pair	38,389,810 / 47.55%
Mapped reads, second in pair	38,026,776 / 47.1%
Mapped reads, both in pair	74,970,792 / 92.85%
Mapped reads, singletons	1,445,794 / 1.79%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	12,709,727 / 15.74%
Clipped reads	19,163,514 / 23.73%

2.2. ACGT Content

Number/percentage of A's	3,238,606,220 / 30.8%
Number/percentage of C's	2,018,304,391 / 19.19%
Number/percentage of T's	3,245,292,095 / 30.86%
Number/percentage of G's	2,014,395,440 / 19.15%
Number/percentage of N's	69,597 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	33.8323
Standard Deviation	265.3661

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Insert size

Mean	208,192.44
Standard Deviation	2,163,712.94
P25/Median/P75	294 / 388 / 500

2.6. Mismatches and indels

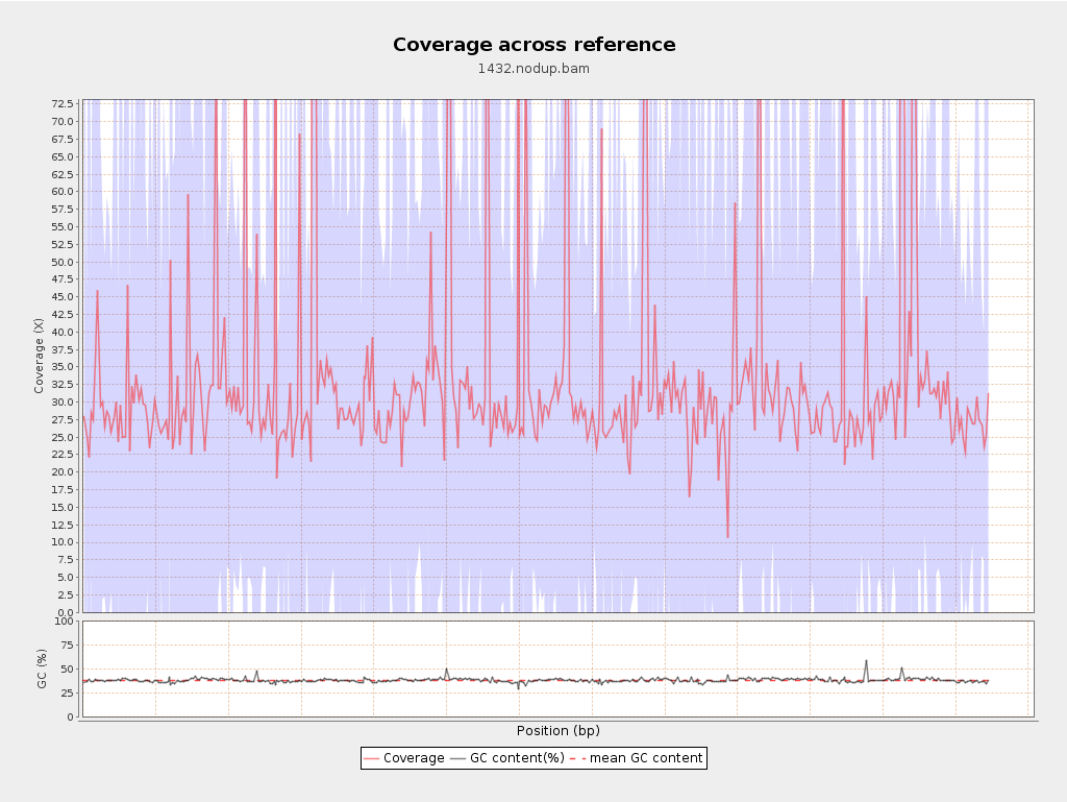
General error rate	2.67%
Mismatches	262,108,524
Insertions	7,029,346
Mapped reads with at least one insertion	8.28%
Deletions	7,191,973
Mapped reads with at least one deletion	8.35%
Homopolymer indels	55.32%

2.7. Chromosome stats

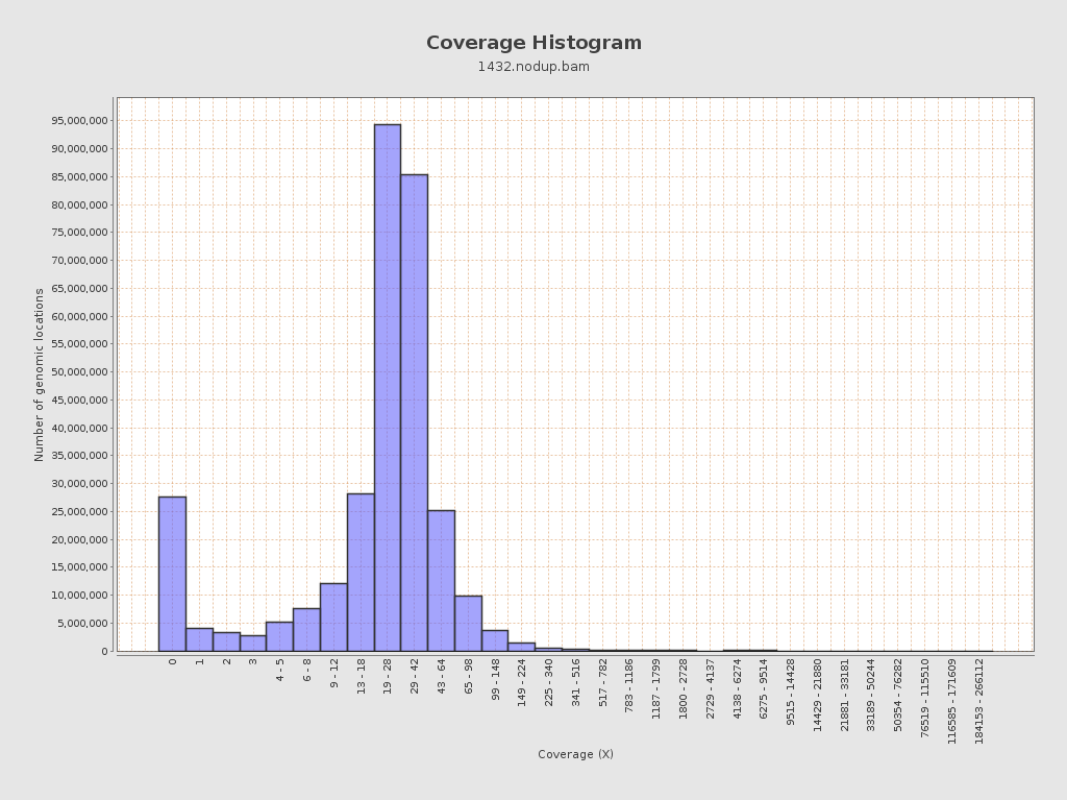
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	858694990	28.8886	95.7797

LT669789.1	36598175	1259758402	34.4213	288.4323
LT669790.1	30422129	1097873960	36.088	245.1856
LT669791.1	52758100	1743052072	33.0386	253.8846
LT669792.1	28376109	949119258	33.4478	288.355
LT669793.1	33388210	1068018040	31.9879	193.024
LT669794.1	50579949	1633570614	32.2968	255.2784
LT669795.1	49795044	1933468535	38.8285	361.2048

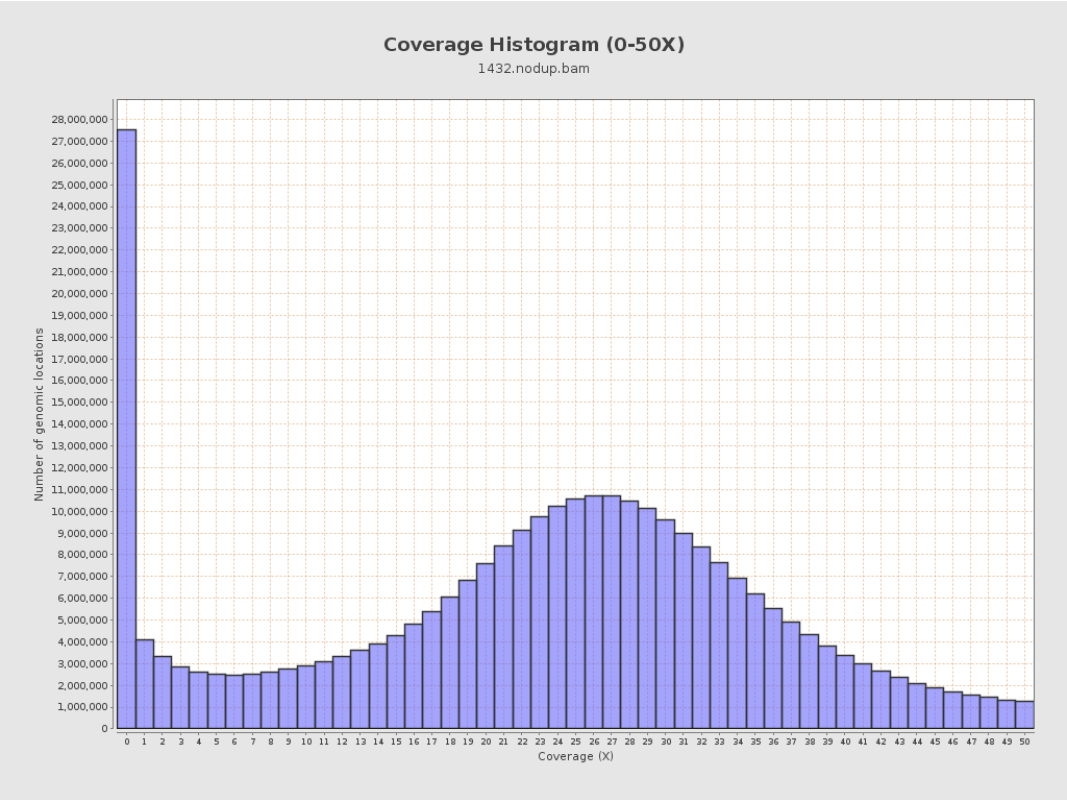
3. Results : Coverage across reference



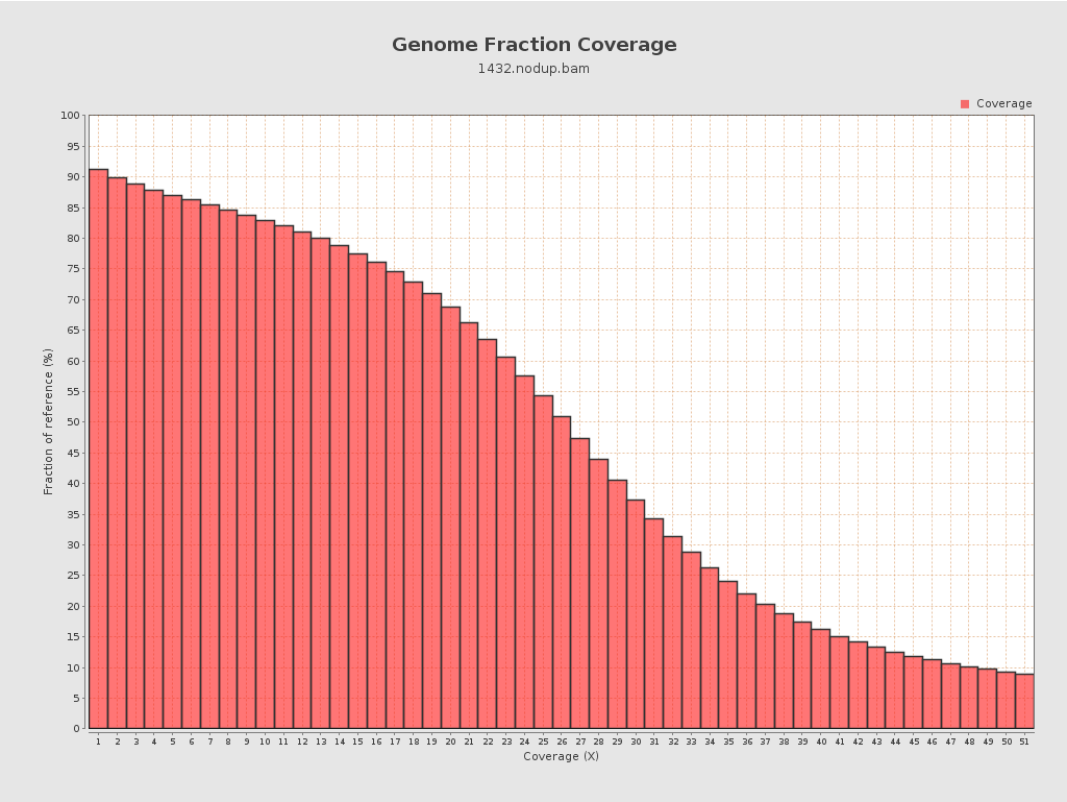
4. Results : Coverage Histogram



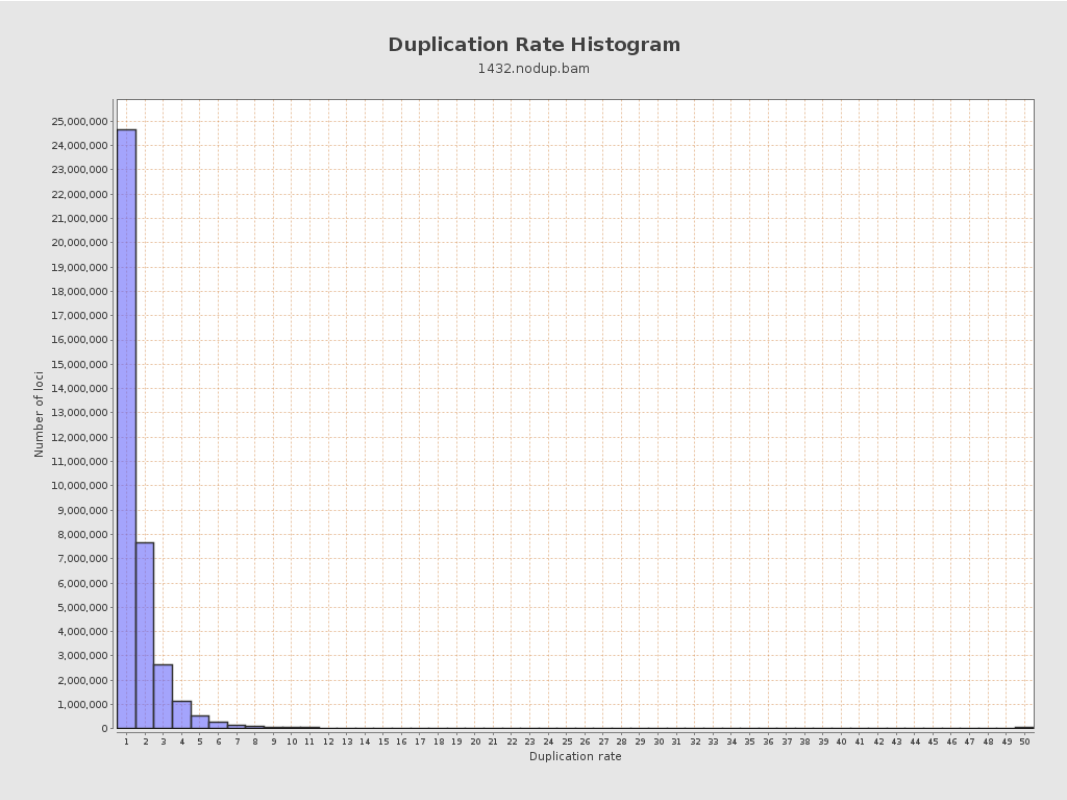
5. Results : Coverage Histogram (0-50X)



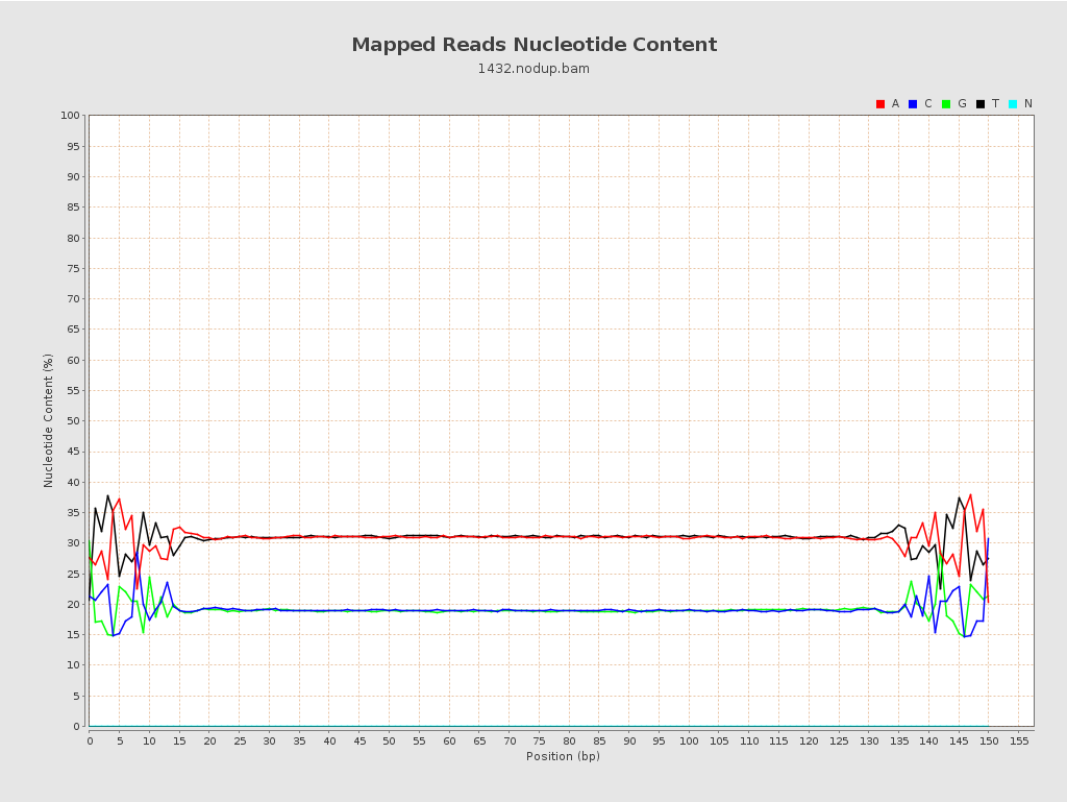
6. Results : Genome Fraction Coverage



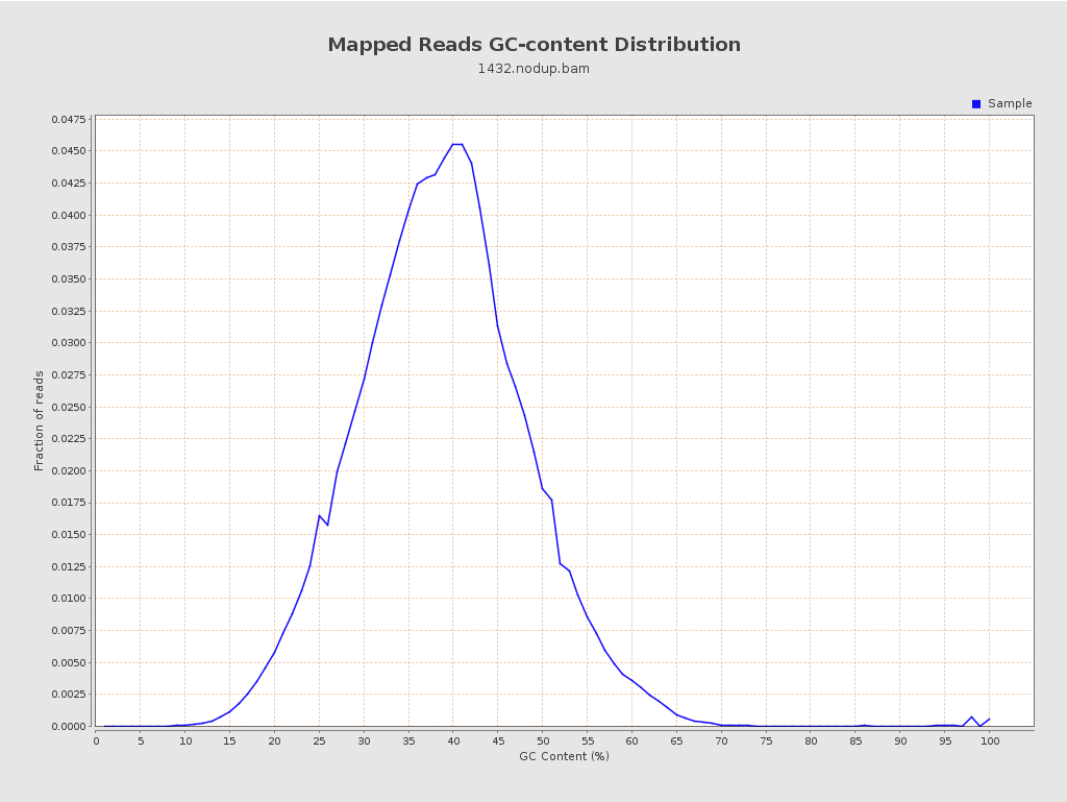
7. Results : Duplication Rate Histogram



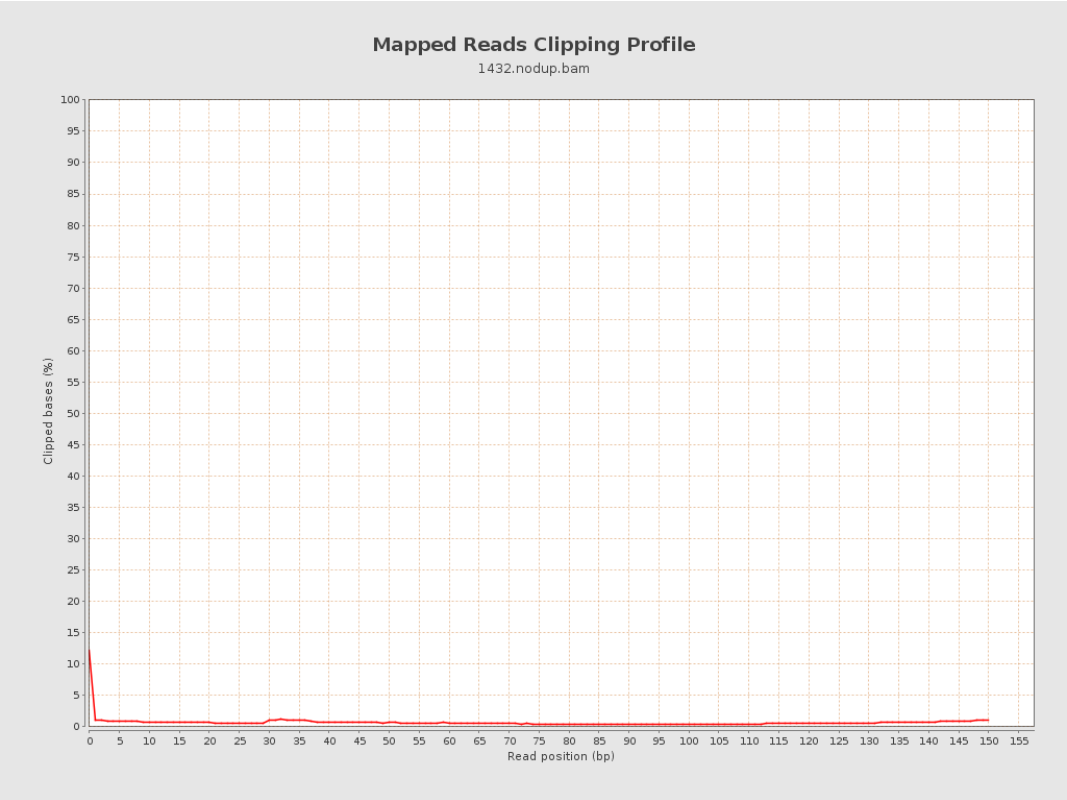
8. Results : Mapped Reads Nucleotide Content



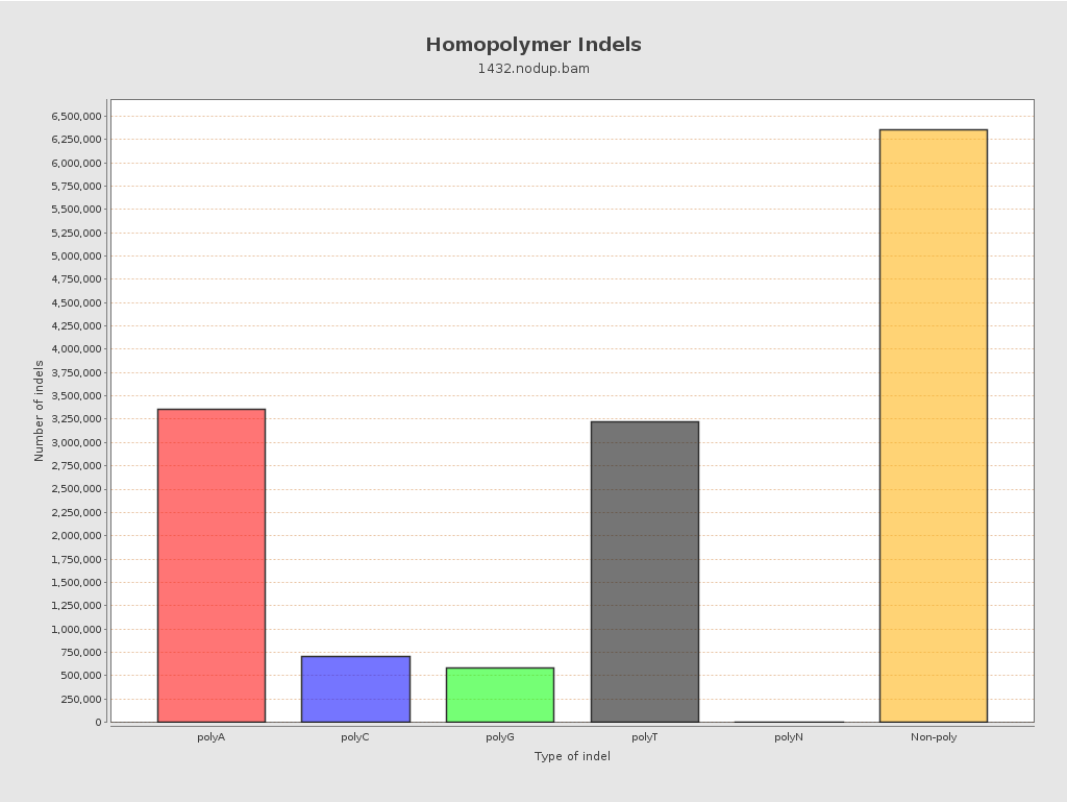
9. Results : Mapped Reads GC-content Distribution



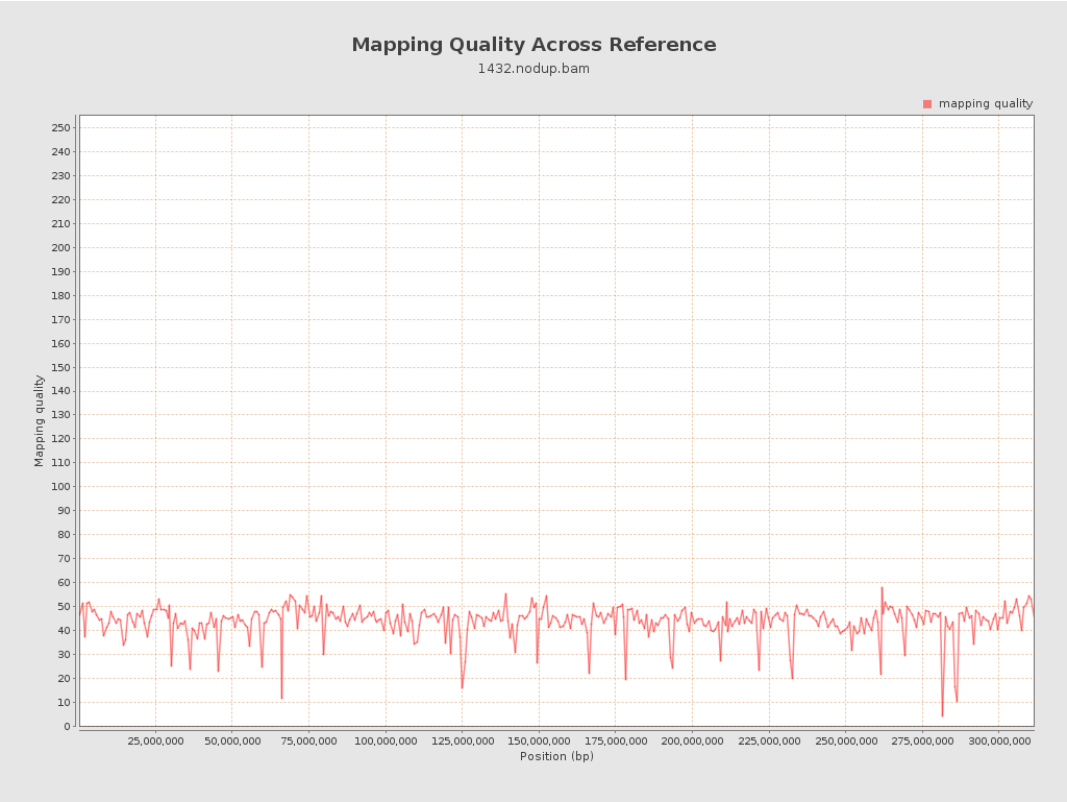
10. Results : Mapped Reads Clipping Profile



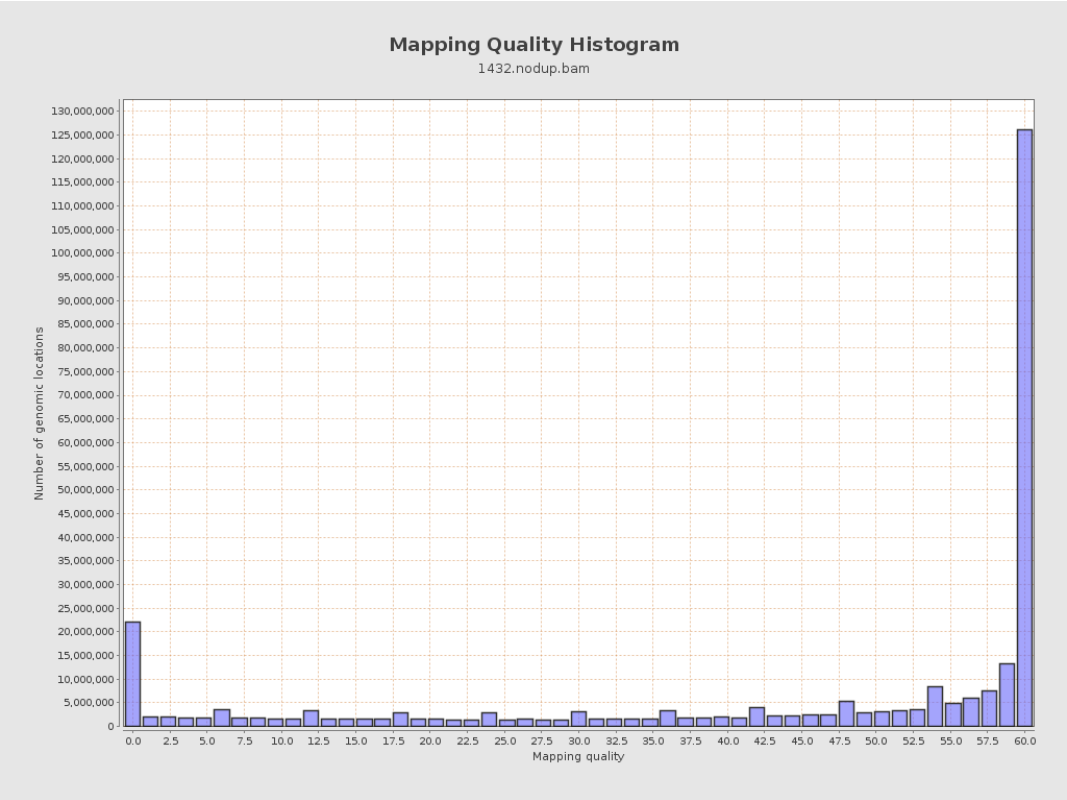
11. Results : Homopolymer Indels



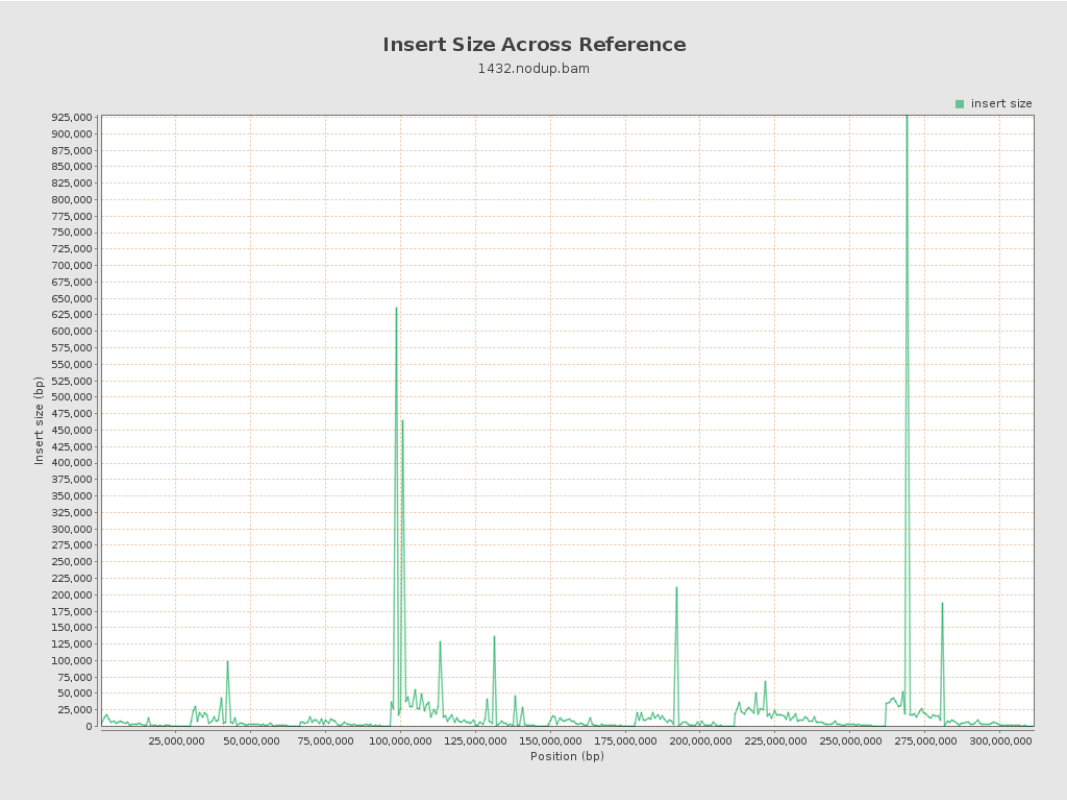
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram