Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/432.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/432.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_151/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_151_S241_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_151/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_151_S241_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:56 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	73,863,506
Mapped reads	66,589,673 / 90.15%
Unmapped reads	7,273,833 / 9.85%
Mapped paired reads	66,589,673 / 90.15%
Mapped reads, first in pair	33,345,957 / 45.15%
Mapped reads, second in pair	33,243,716 / 45.01%
Mapped reads, both in pair	65,112,720 / 88.15%
Mapped reads, singletons	1,476,953 / 2%
Read min/max/mean length	30 / 151 / 148.26
Duplicated reads (flagged)	11,495,429 / 15.56%
Clipped reads	14,964,286 / 20.26%

2.2. ACGT Content

Number/percentage of A's	2,846,085,802 / 30.91%
Number/percentage of C's	1,757,742,214 / 19.09%
Number/percentage of T's	2,849,626,244 / 30.95%
Number/percentage of G's	1,755,109,450 / 19.06%
Number/percentage of N's	38,758 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	29.6251
Standard Deviation	249.5939

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Insert size

Mean	224,363.65
Standard Deviation	2,252,817.73
P25/Median/P75	308 / 407 / 533

2.6. Mismatches and indels

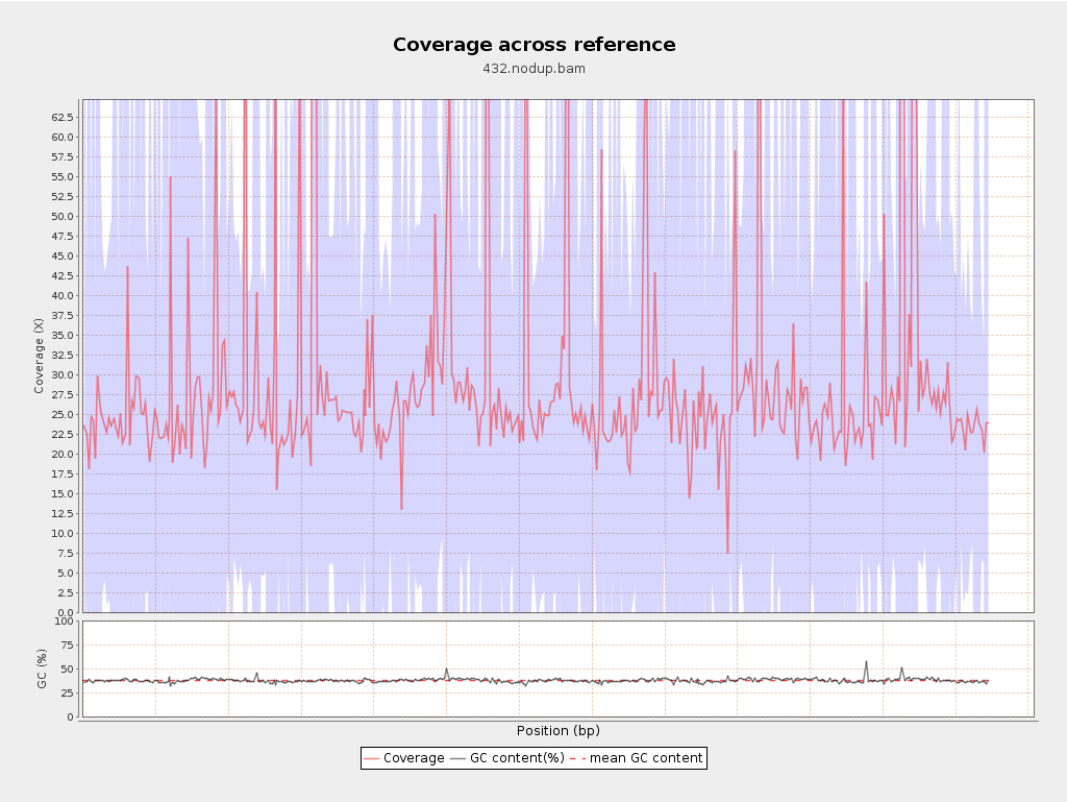
General error rate	2.25%
Mismatches	190,176,141
Insertions	6,211,735
Mapped reads with at least one insertion	8.36%
Deletions	6,282,108
Mapped reads with at least one deletion	8.4%
Homopolymer indels	57.09%

2.7. Chromosome stats

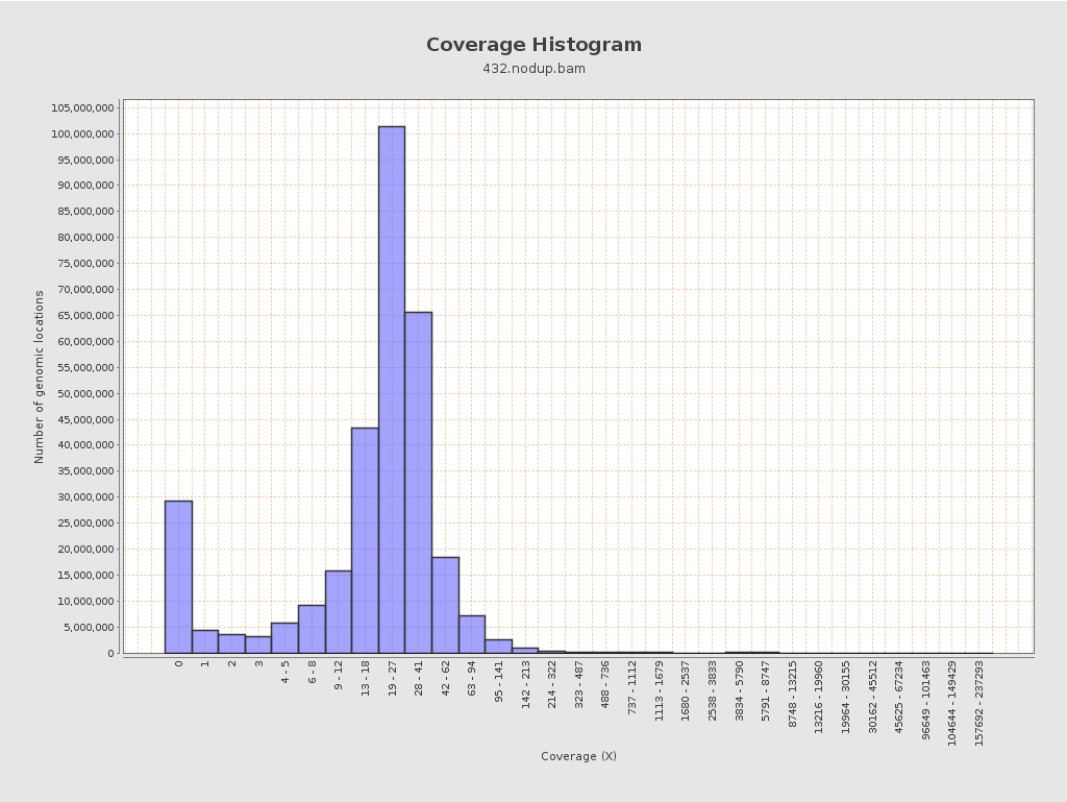
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	723346209	24.3351	76.6377

LT669789.1	36598175	1064825118	29.095	233.1991
LT669790.1	30422129	1009708931	33.1899	291.8303
LT669791.1	52758100	1547465619	29.3313	217.2259
LT669792.1	28376109	830571806	29.2701	260.2526
LT669793.1	33388210	910671705	27.2752	229.5102
LT669794.1	50579949	1400376366	27.6864	202.5239
LT669795.1	49795044	1745465669	35.053	358.8095

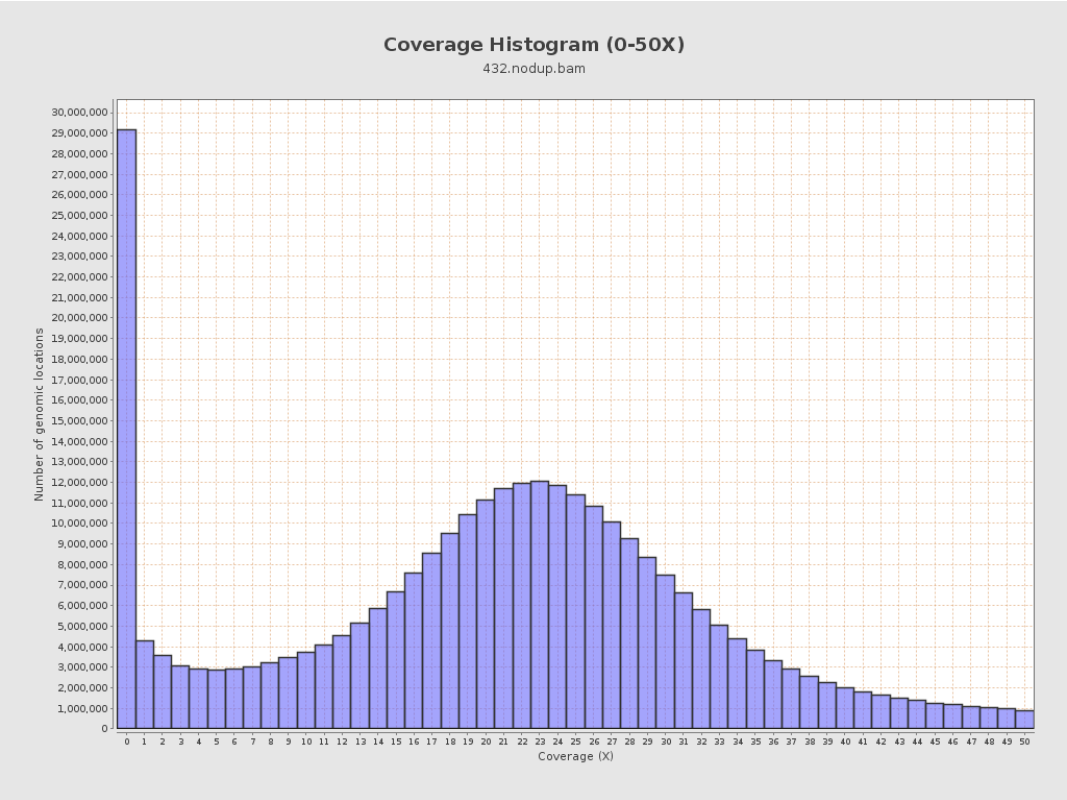
3. Results : Coverage across reference



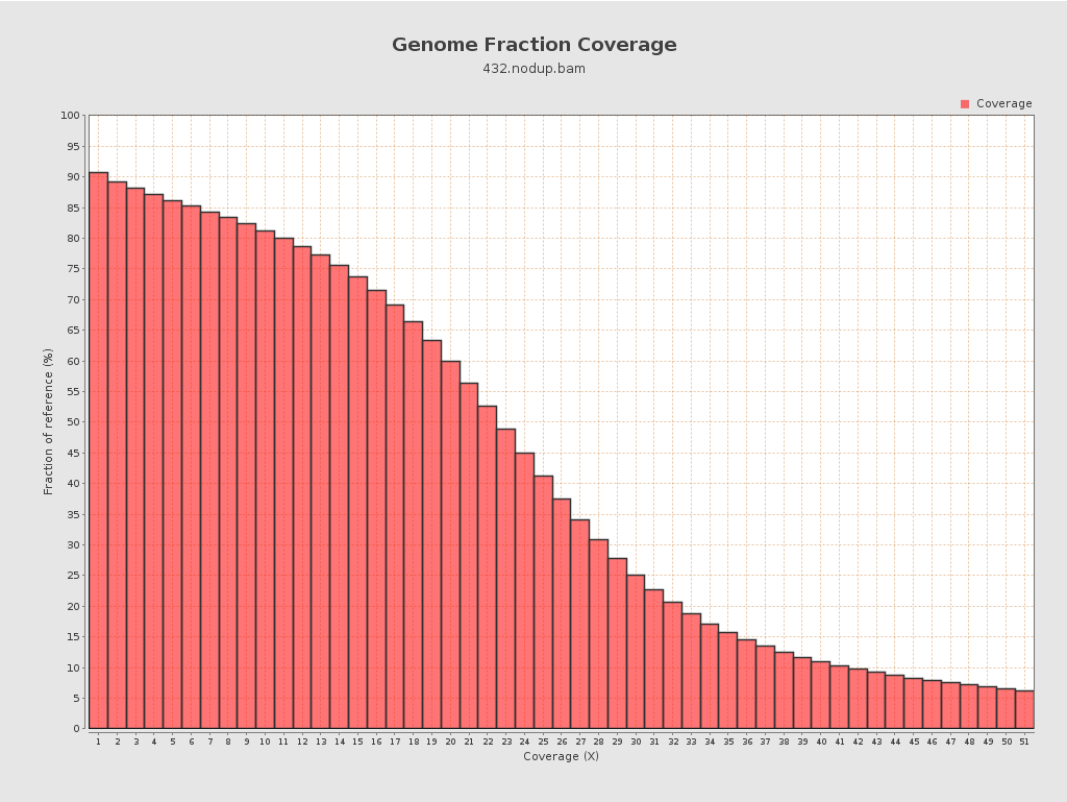
4. Results : Coverage Histogram



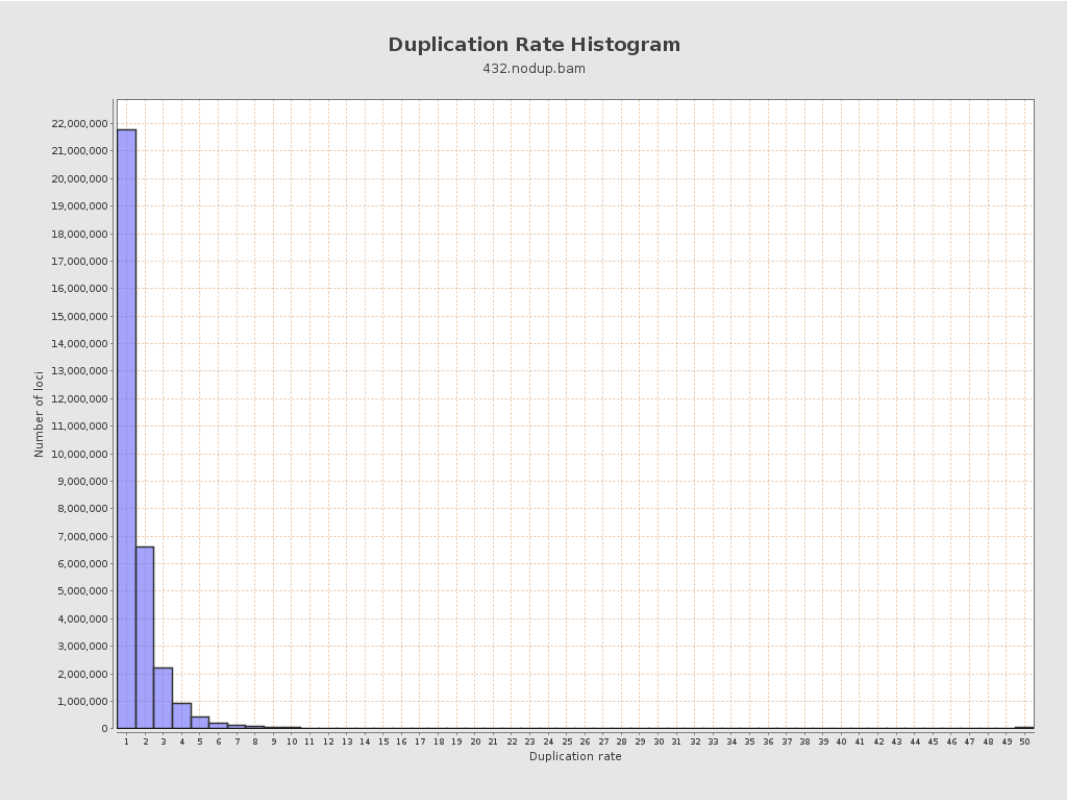
5. Results : Coverage Histogram (0-50X)



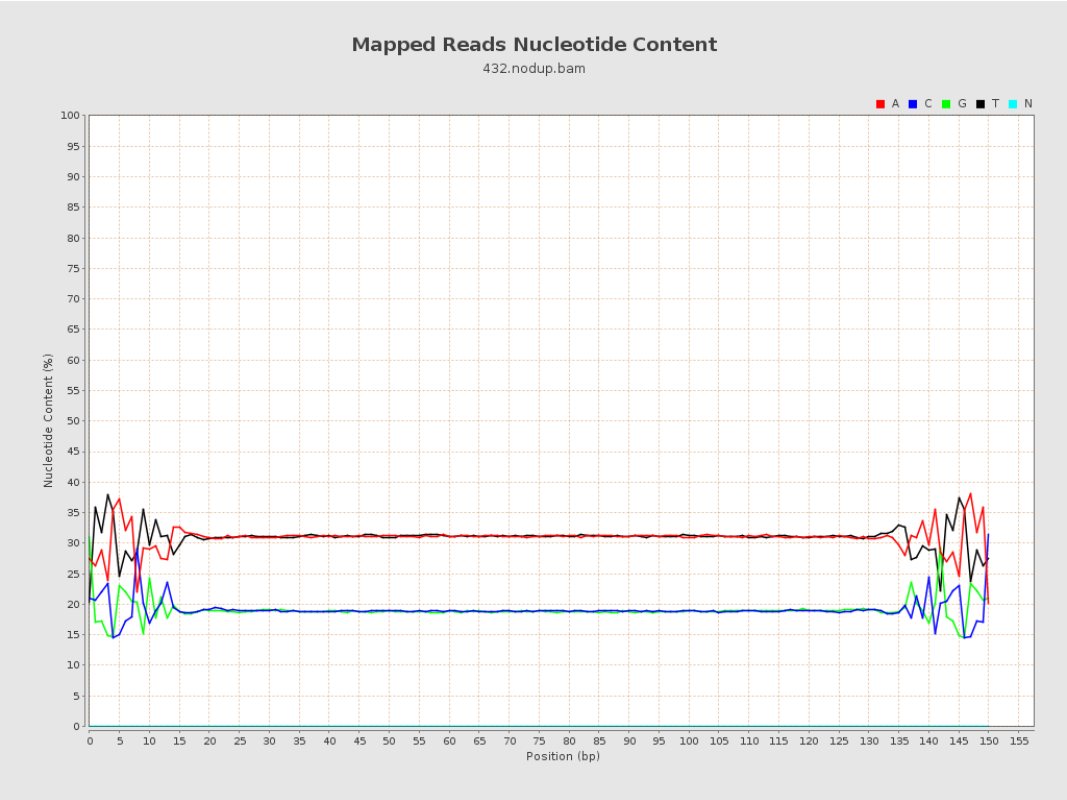
6. Results : Genome Fraction Coverage



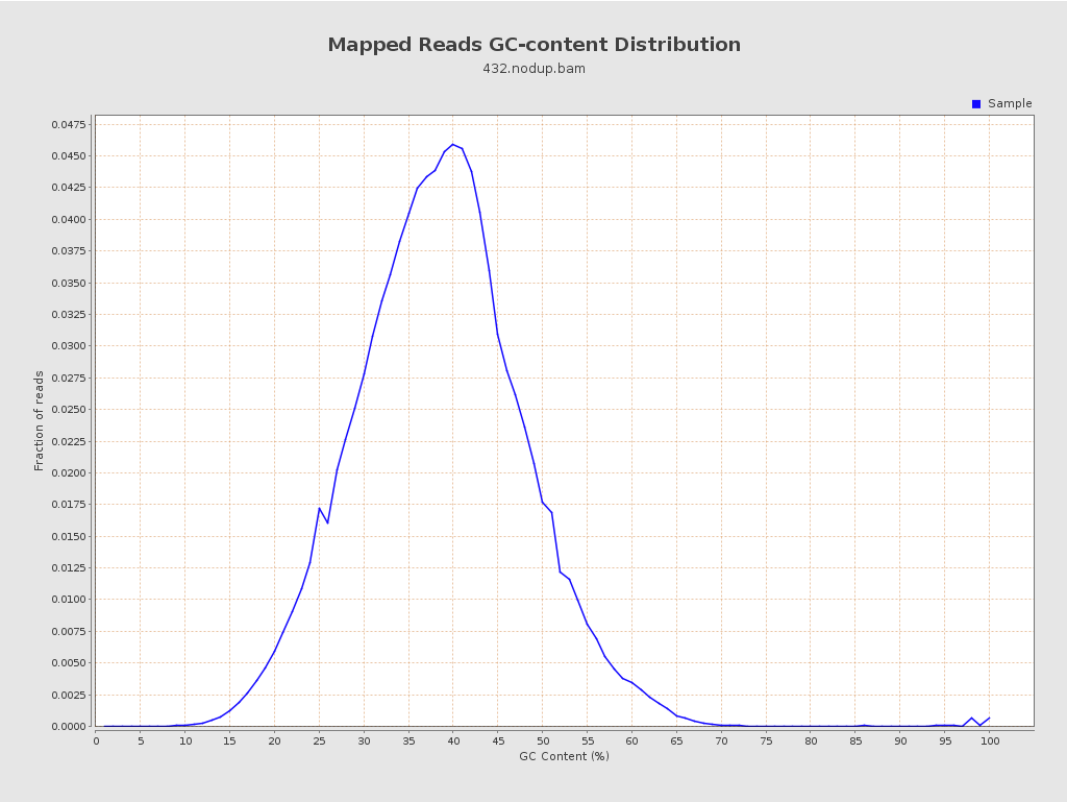
7. Results : Duplication Rate Histogram



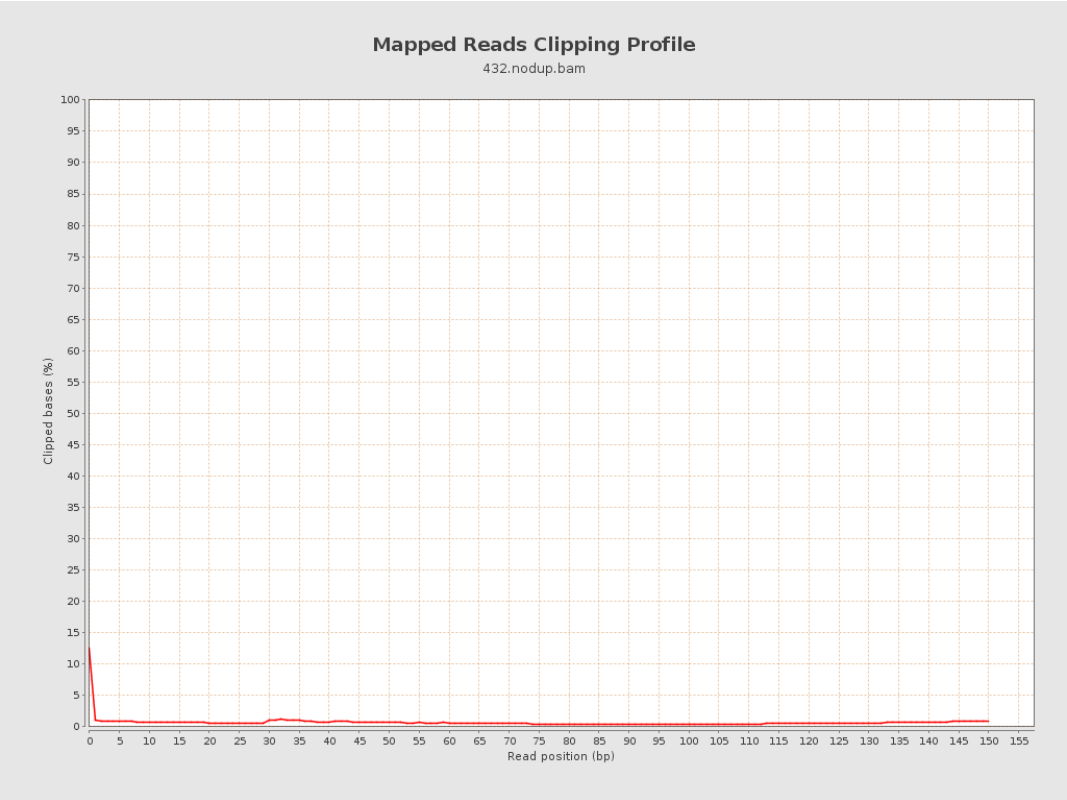
8. Results : Mapped Reads Nucleotide Content



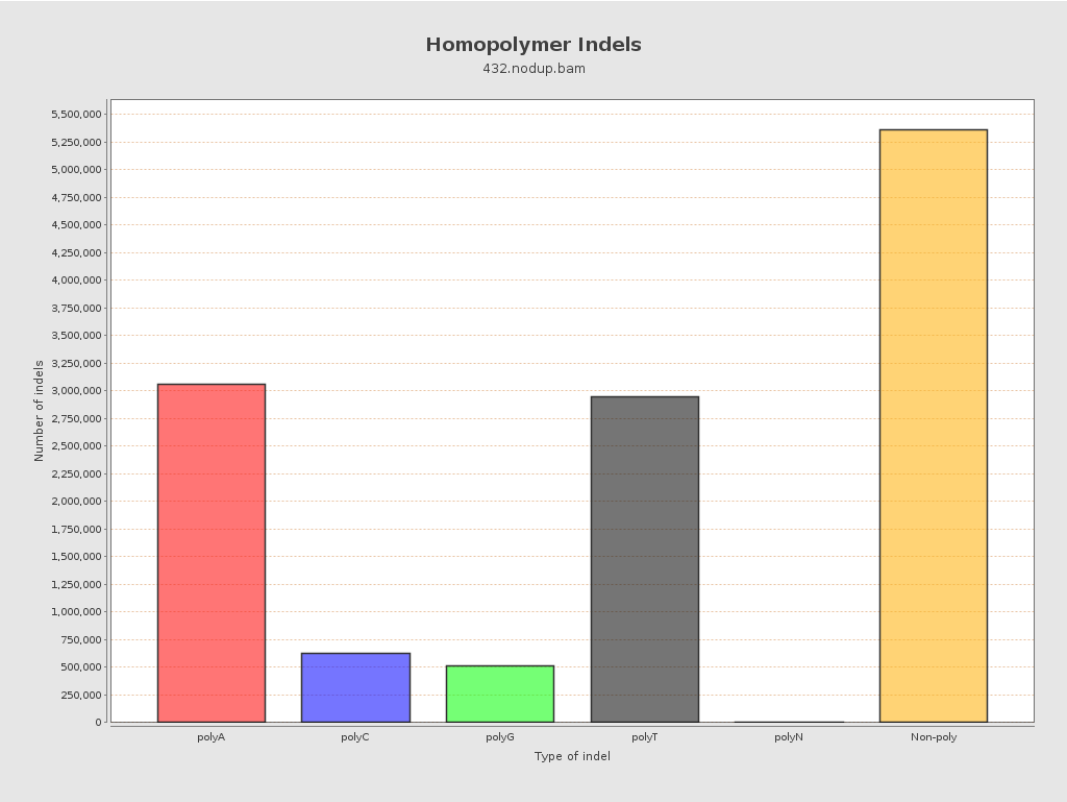
9. Results : Mapped Reads GC-content Distribution



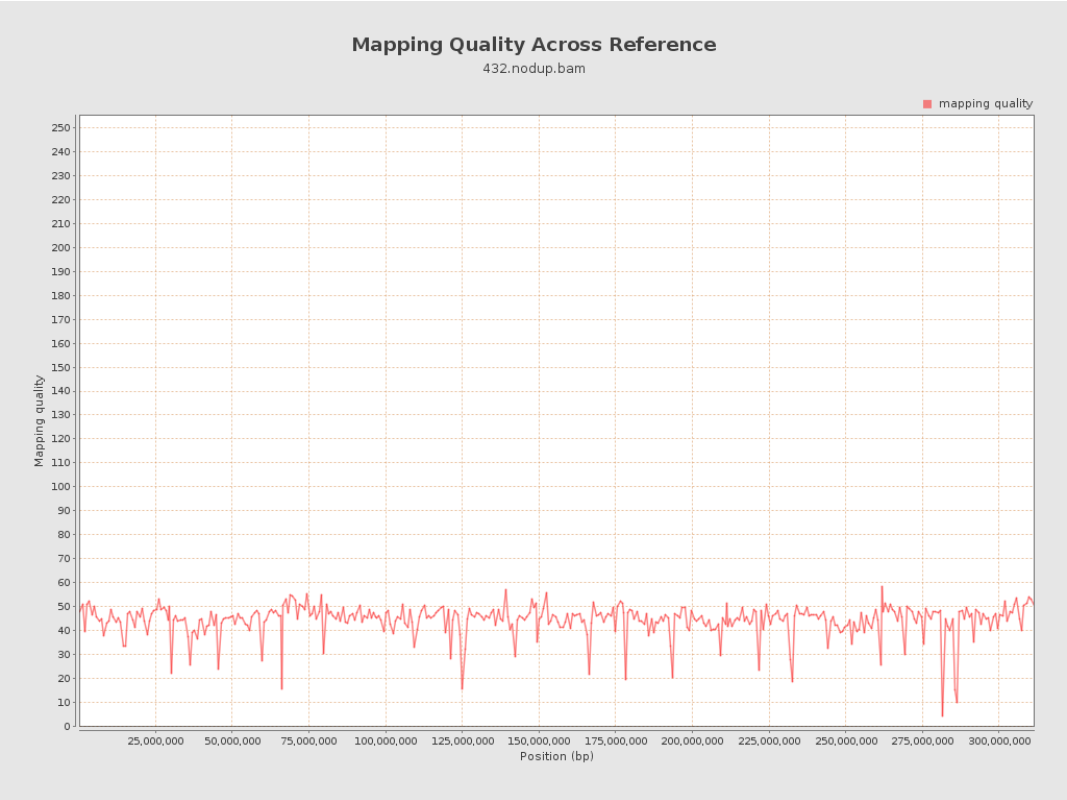
10. Results : Mapped Reads Clipping Profile



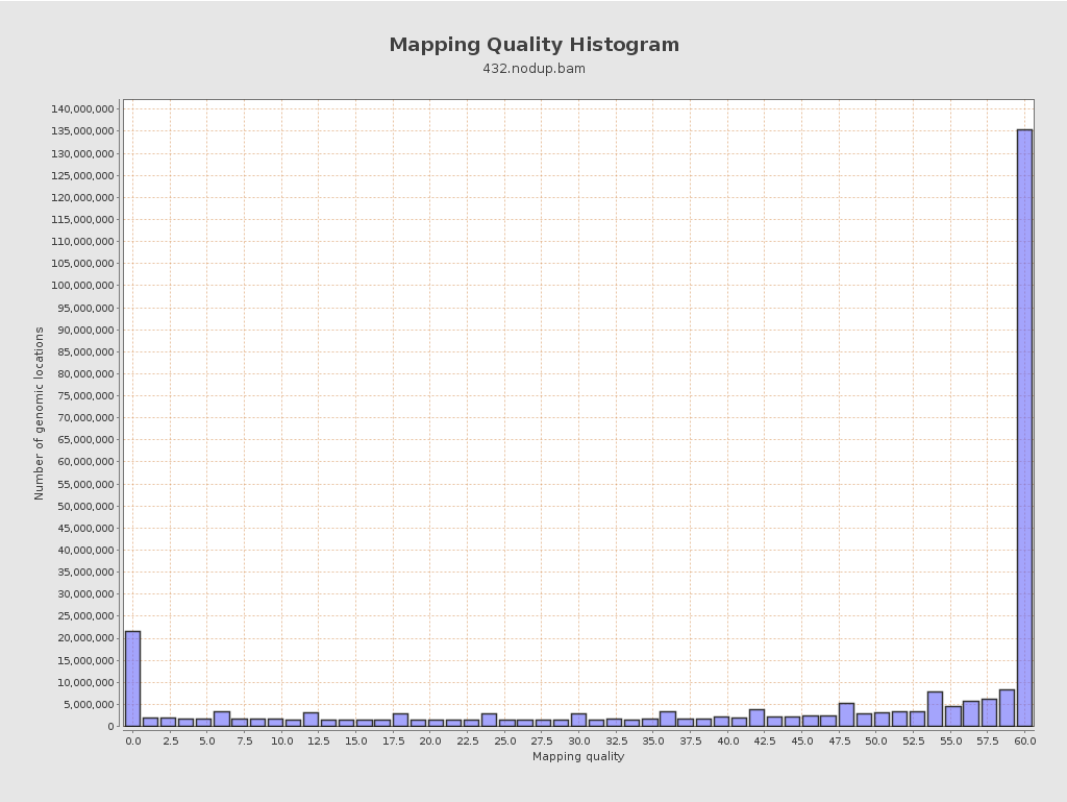
11. Results : Homopolymer Indels



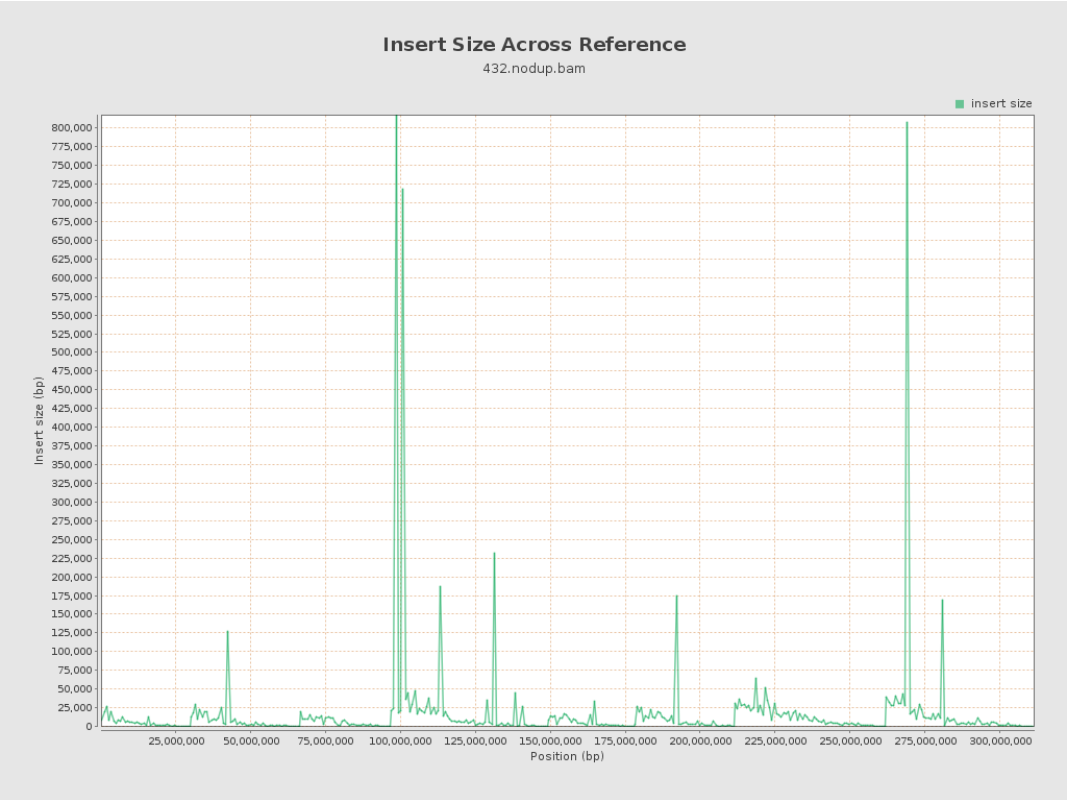
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram