Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/433.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/433.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_537/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_537_S104_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_537/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_537_S104_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,788,713
Mapped reads	61,489,962 / 92.07%
Unmapped reads	5,298,751 / 7.93%
Mapped paired reads	61,489,962 / 92.07%
Mapped reads, first in pair	30,847,580 / 46.19%
Mapped reads, second in pair	30,642,382 / 45.88%
Mapped reads, both in pair	60,177,917 / 90.1%
Mapped reads, singletons	1,312,045 / 1.96%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	9,329,479 / 13.97%
Clipped reads	15,001,285 / 22.46%

2.2. ACGT Content

Number/percentage of A's	2,606,886,349 / 30.84%
Number/percentage of C's	1,618,543,408 / 19.15%
Number/percentage of T's	2,611,407,014 / 30.89%
Number/percentage of G's	1,617,030,291 / 19.13%
Number/percentage of N's	58,792 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	27.198
Standard Deviation	220.2091

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Insert size

Mean	225,405.35
Standard Deviation	2,258,723.43
P25/Median/P75	307 / 405 / 522

2.6. Mismatches and indels

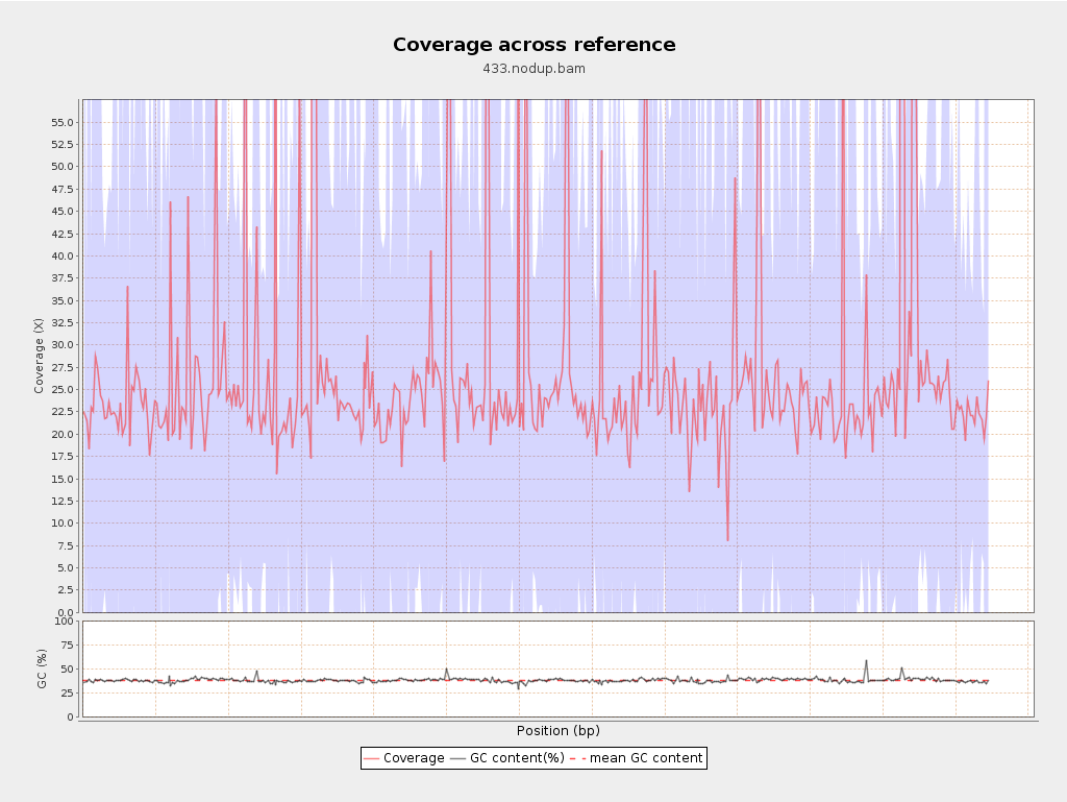
General error rate	2.54%
Mismatches	199,407,837
Insertions	5,712,888
Mapped reads with at least one insertion	8.35%
Deletions	5,876,590
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56%

2.7. Chromosome stats

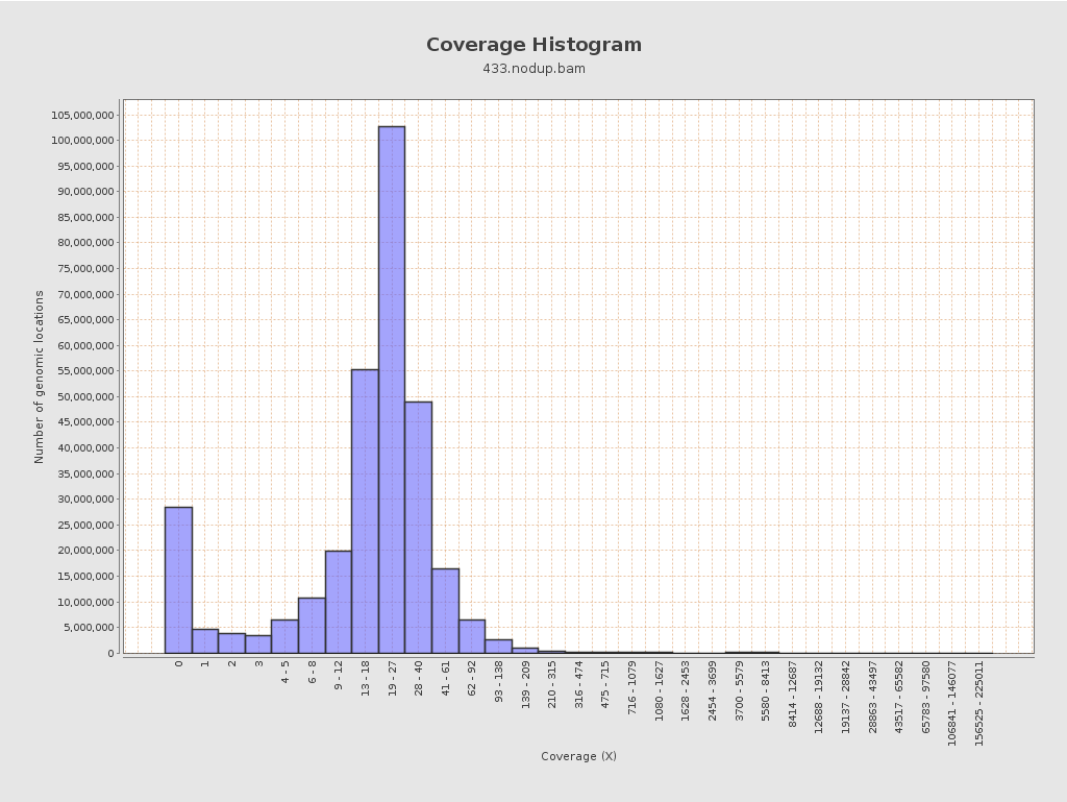
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	684876155	23.0409	81.7454

LT669789.1	36598175	1006849674	27.5109	232.824
LT669790.1	30422129	901288498	29.6261	219.4234
LT669791.1	52758100	1386277465	26.2761	204.217
LT669792.1	28376109	765583477	26.9799	203.1044
LT669793.1	33388210	845612323	25.3267	201.3322
LT669794.1	50579949	1306981947	25.8399	195.7762
LT669795.1	49795044	1578575613	31.7015	310.4804

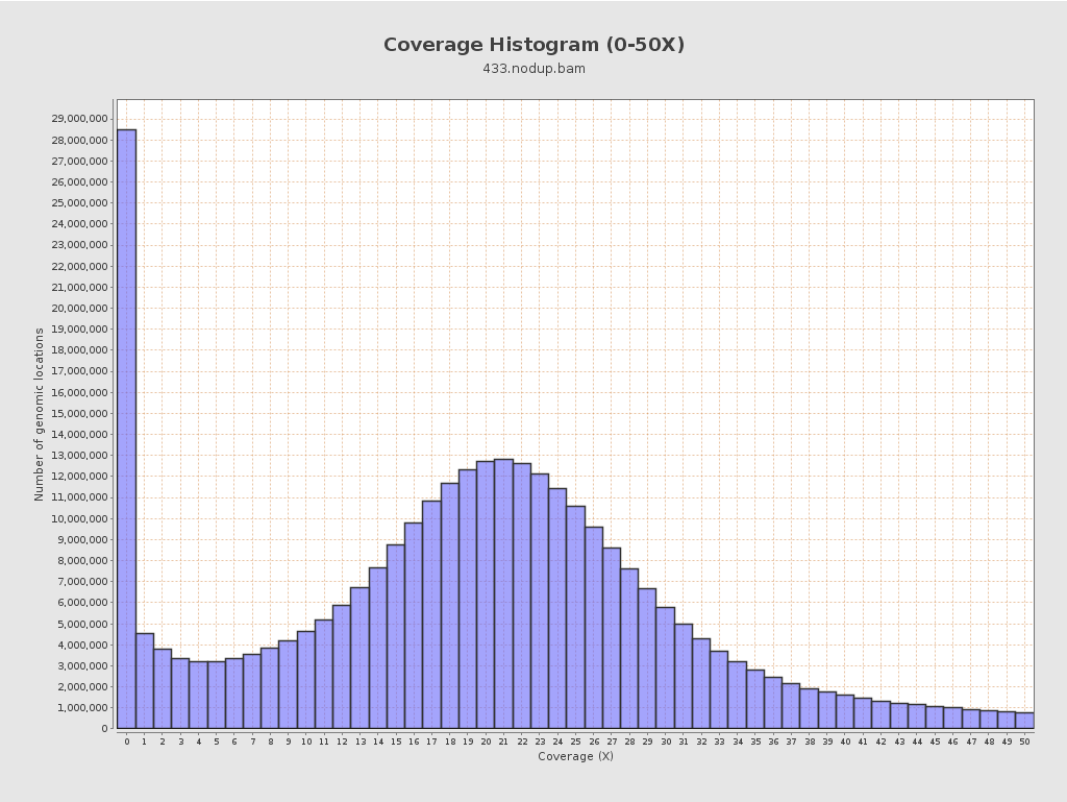
3. Results : Coverage across reference



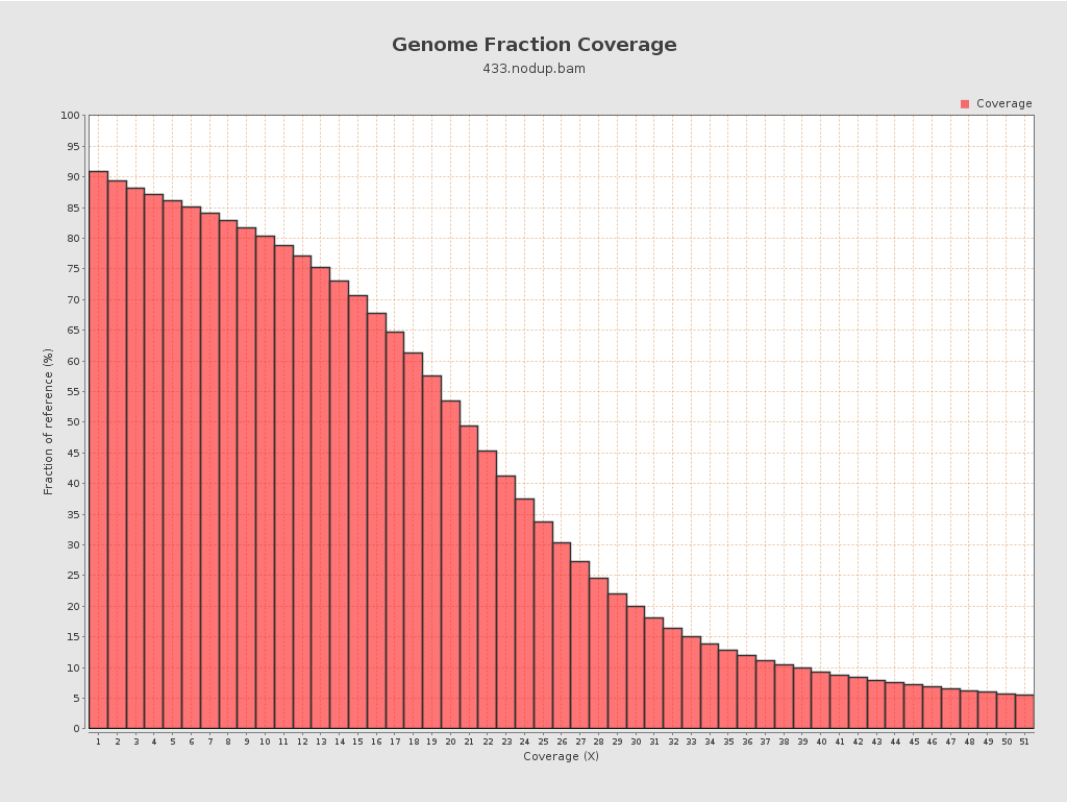
4. Results : Coverage Histogram



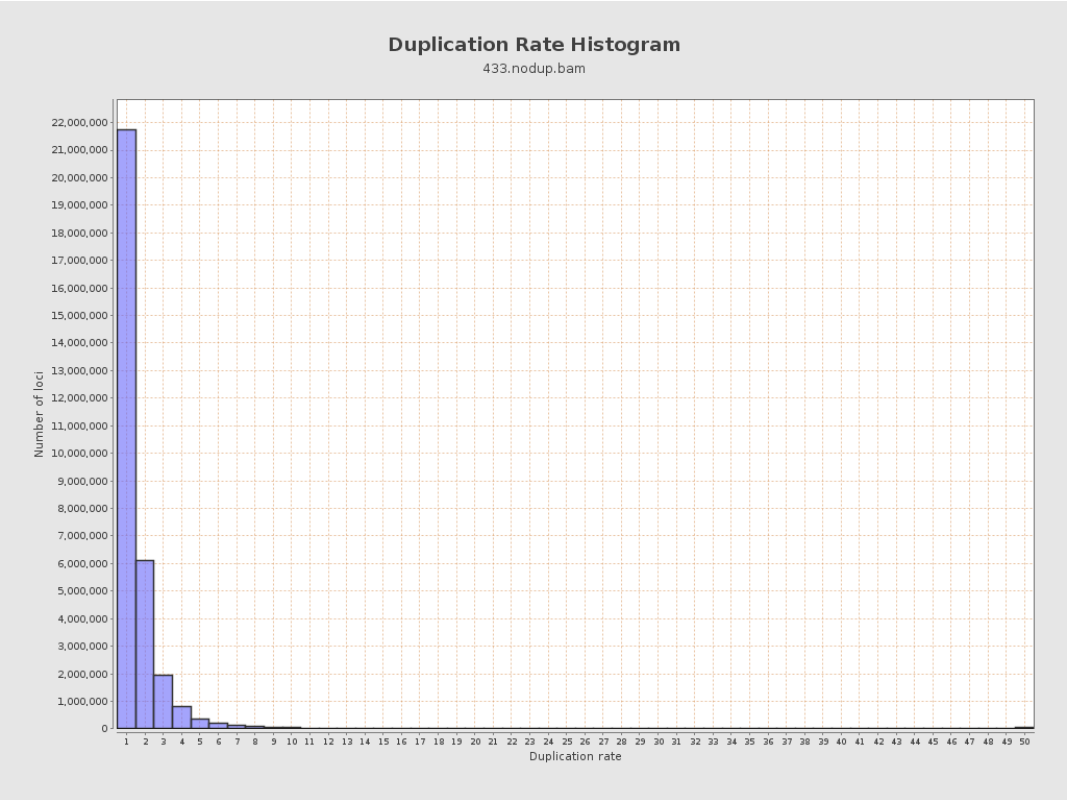
5. Results : Coverage Histogram (0-50X)



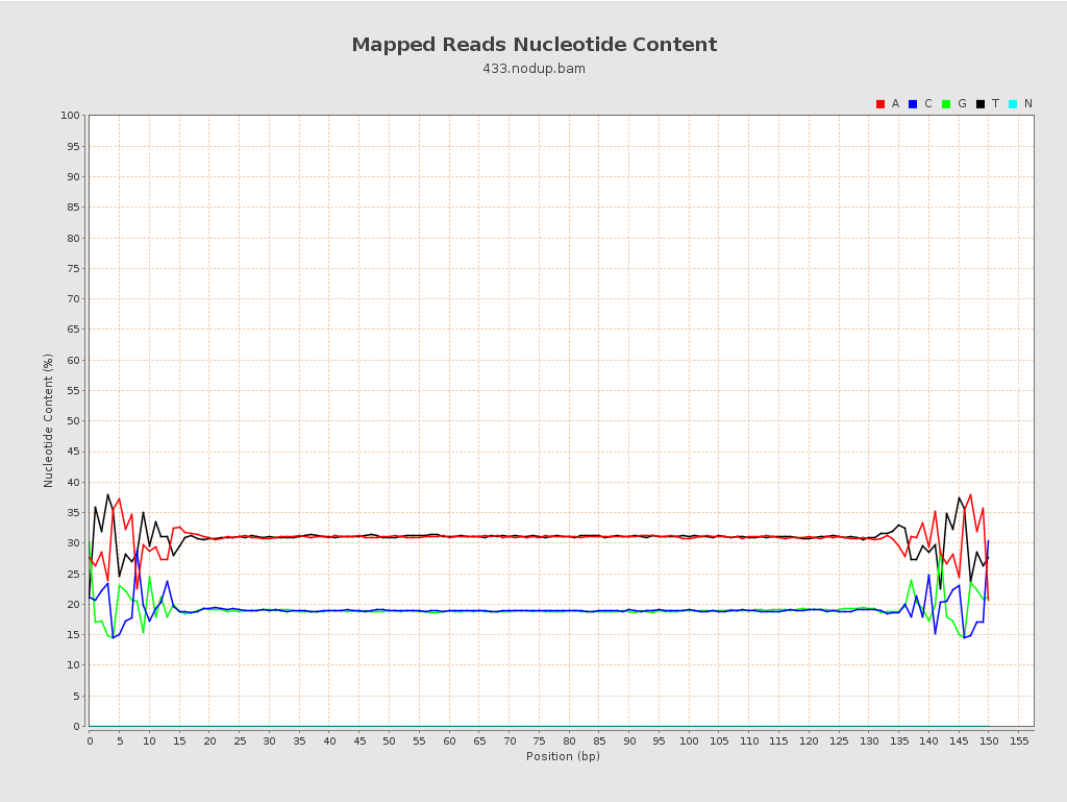
6. Results : Genome Fraction Coverage



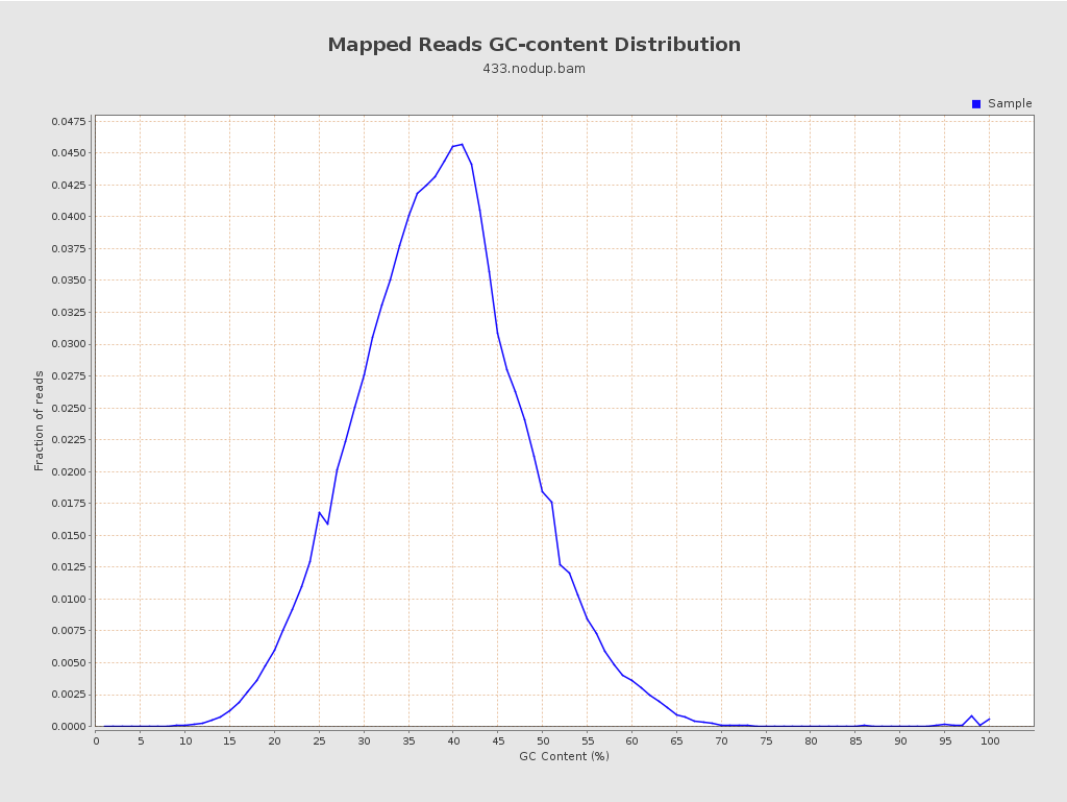
7. Results : Duplication Rate Histogram



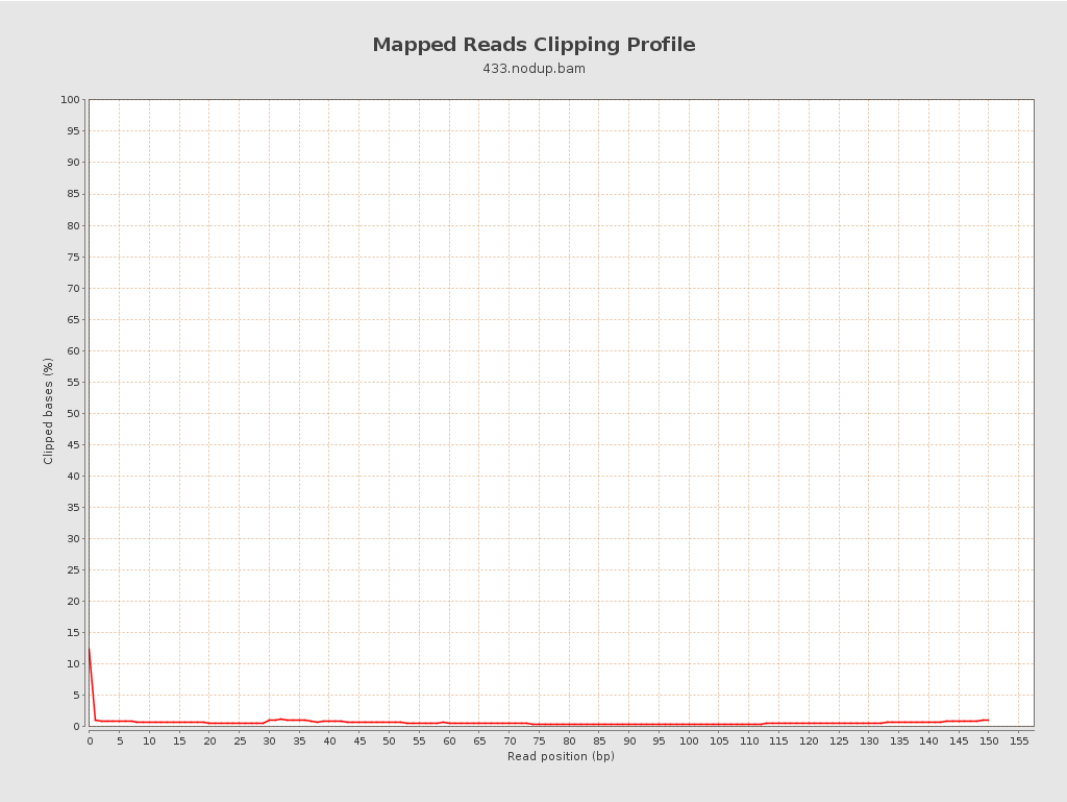
8. Results : Mapped Reads Nucleotide Content



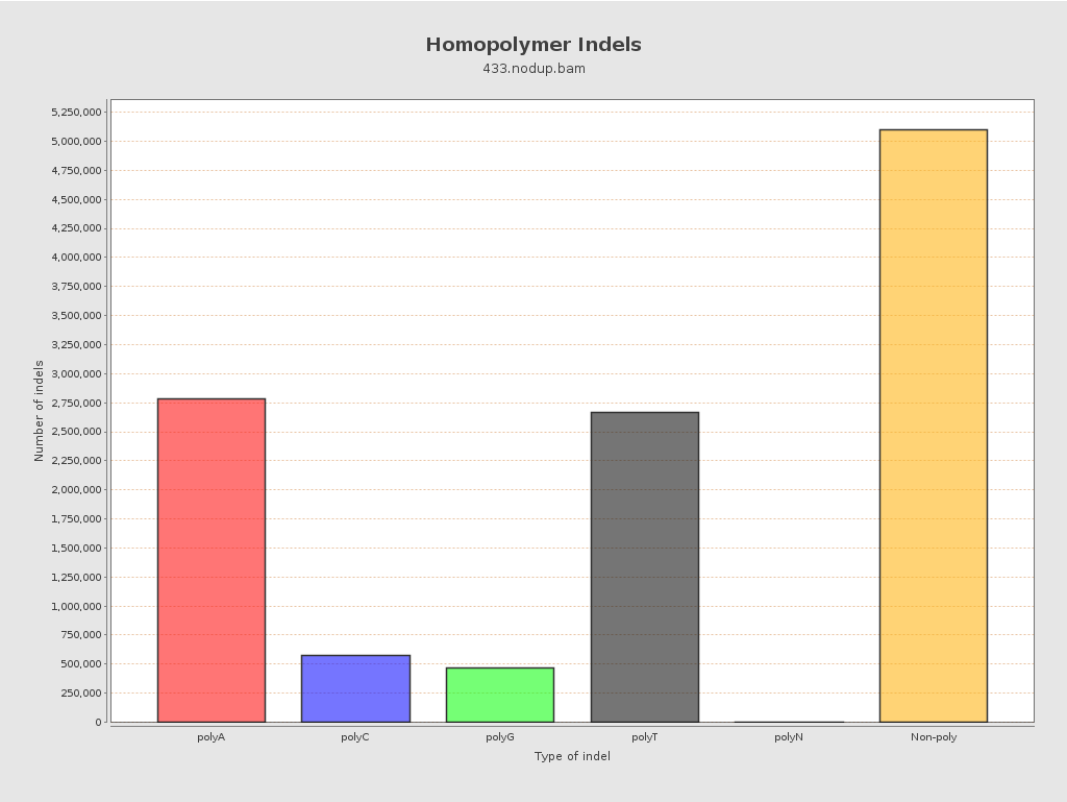
9. Results : Mapped Reads GC-content Distribution



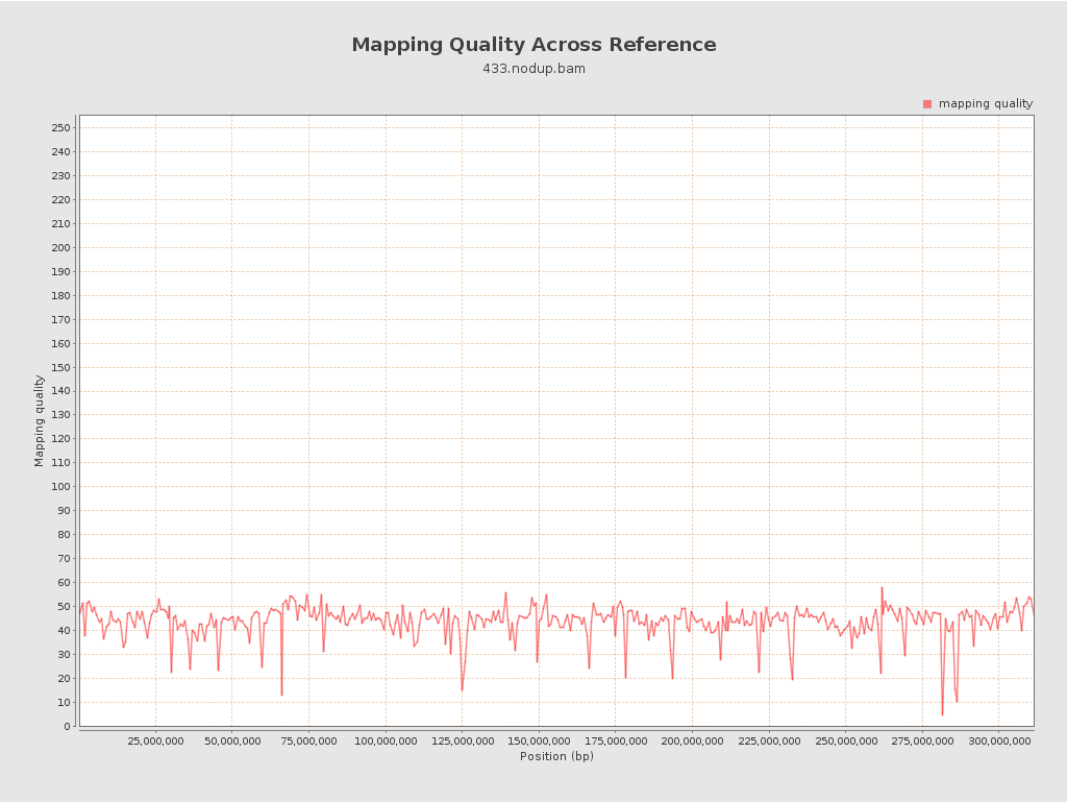
10. Results : Mapped Reads Clipping Profile



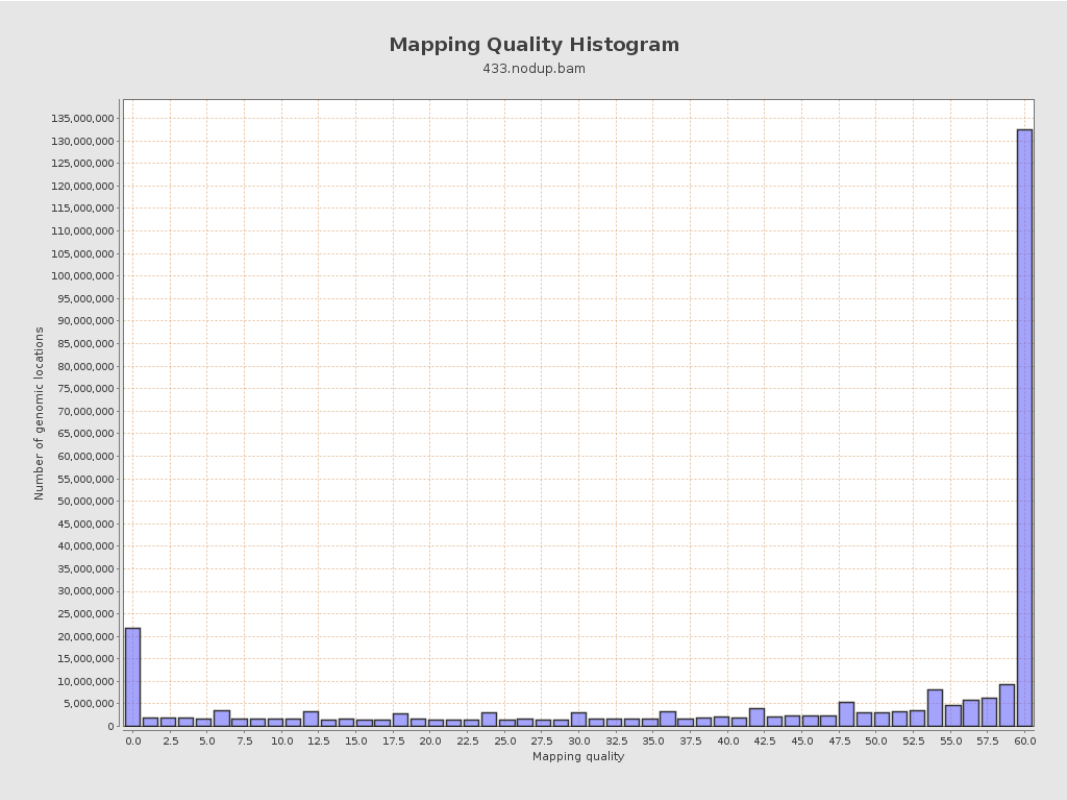
11. Results : Homopolymer Indels



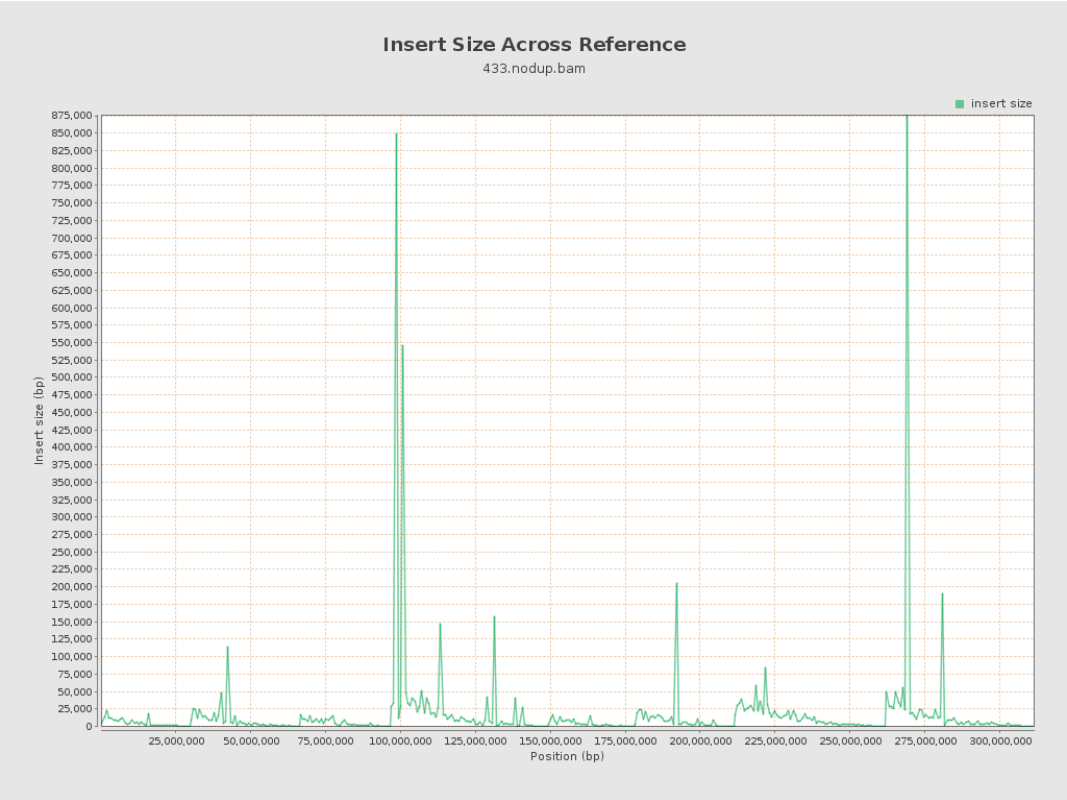
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram