Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/491.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/491.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_413/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_413_S388_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_413/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_413_S388_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,742,790
Mapped reads	59,933,592 / 94.02%
Unmapped reads	3,809,198 / 5.98%
Mapped paired reads	59,933,592 / 94.02%
Mapped reads, first in pair	30,028,381 / 47.11%
Mapped reads, second in pair	29,905,211 / 46.92%
Mapped reads, both in pair	58,632,718 / 91.98%
Mapped reads, singletons	1,300,874 / 2.04%
Read min/max/mean length	30 / 151 / 148.01
Duplicated reads (flagged)	9,137,004 / 14.33%
Clipped reads	13,437,364 / 21.08%

2.2. ACGT Content

Number/percentage of A's	2,549,186,684 / 30.68%
Number/percentage of C's	1,604,179,878 / 19.3%
Number/percentage of T's	2,556,770,730 / 30.77%
Number/percentage of G's	1,599,782,489 / 19.25%
Number/percentage of N's	28,262 / 0%
GC Percentage	38.56%

2.3. Coverage

Mean	26.7358
Standard Deviation	234.5119

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Insert size

Mean	247,414.31
Standard Deviation	2,354,214.04
P25/Median/P75	359 / 470 / 615

2.6. Mismatches and indels

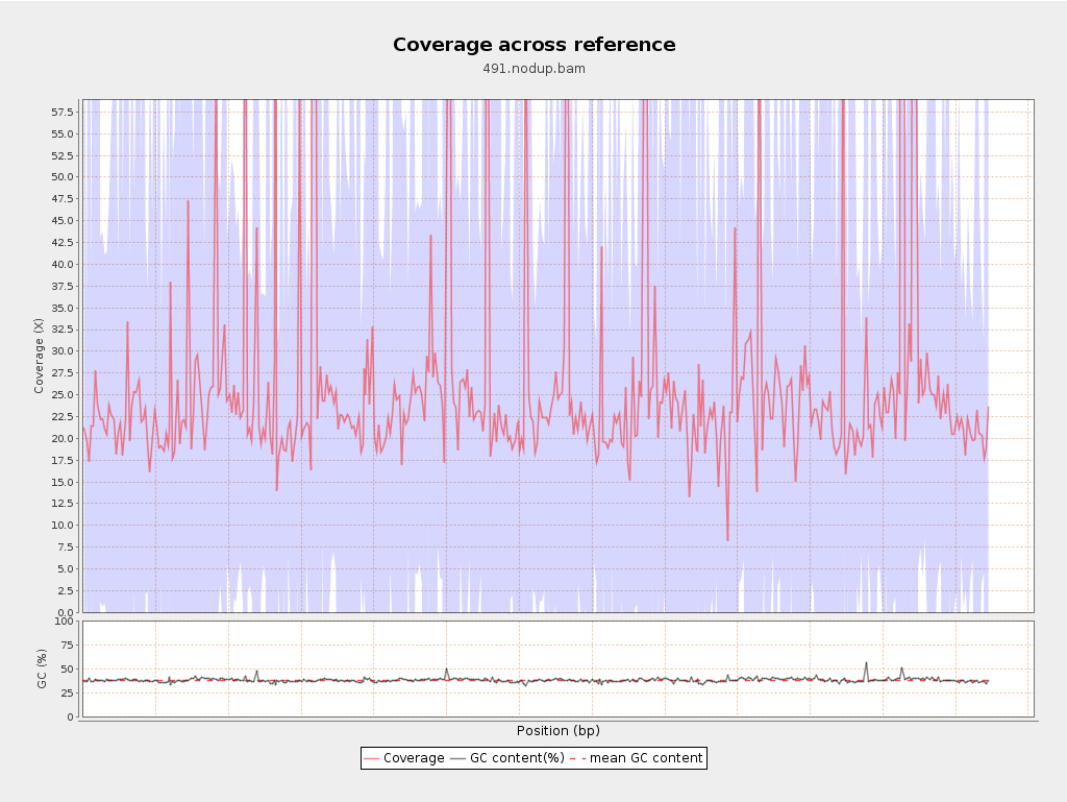
General error rate	2.35%
Mismatches	179,462,838
Insertions	5,637,517
Mapped reads with at least one insertion	8.45%
Deletions	5,767,286
Mapped reads with at least one deletion	8.54%
Homopolymer indels	55.78%

2.7. Chromosome stats

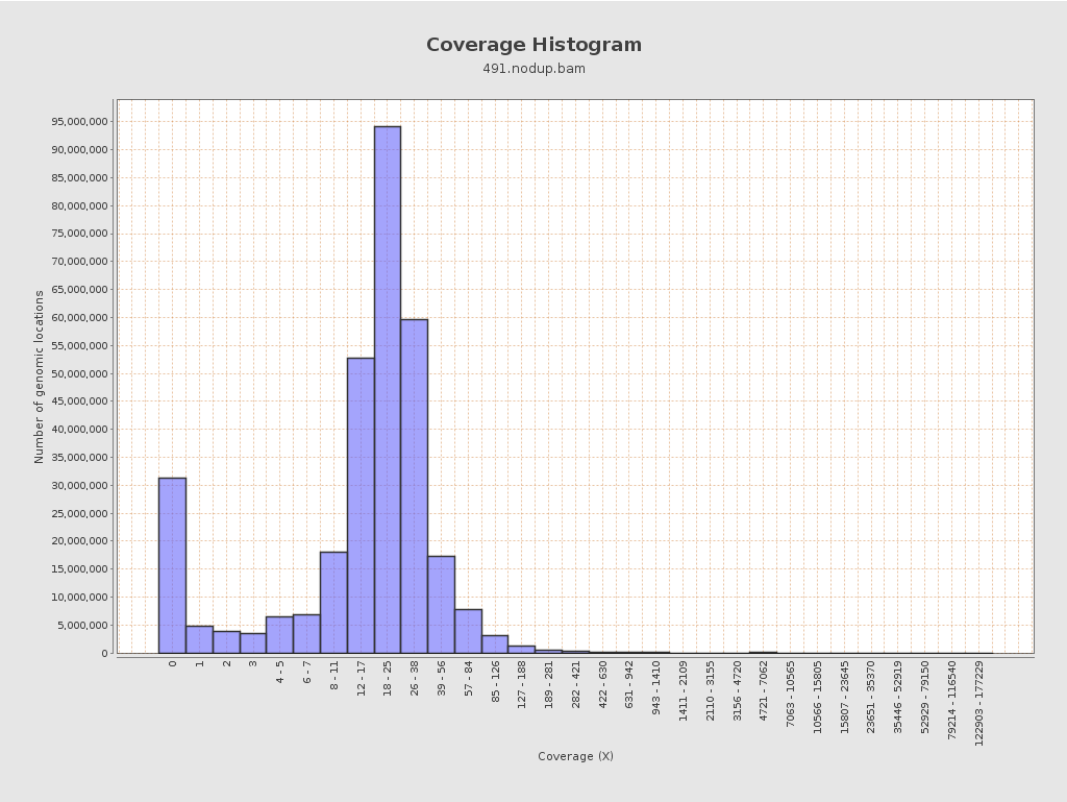
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	646767973	21.7589	82.2381

LT669789.1	36598175	997802108	27.2637	247.3955
LT669790.1	30422129	855238727	28.1124	205.1732
LT669791.1	52758100	1385870870	26.2684	215.292
LT669792.1	28376109	738230328	26.0159	252.0362
LT669793.1	33388210	848363074	25.4091	205.2132
LT669794.1	50579949	1279190998	25.2905	196.7538
LT669795.1	49795044	1580537656	31.7409	341.3798

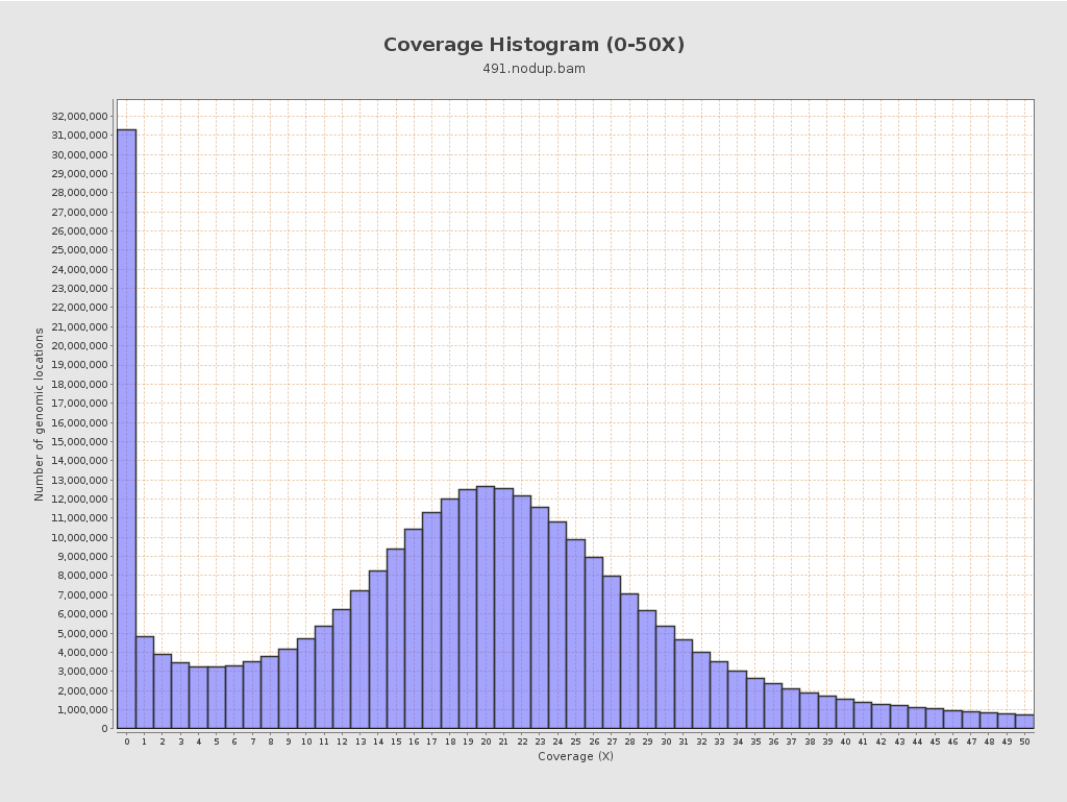
3. Results : Coverage across reference



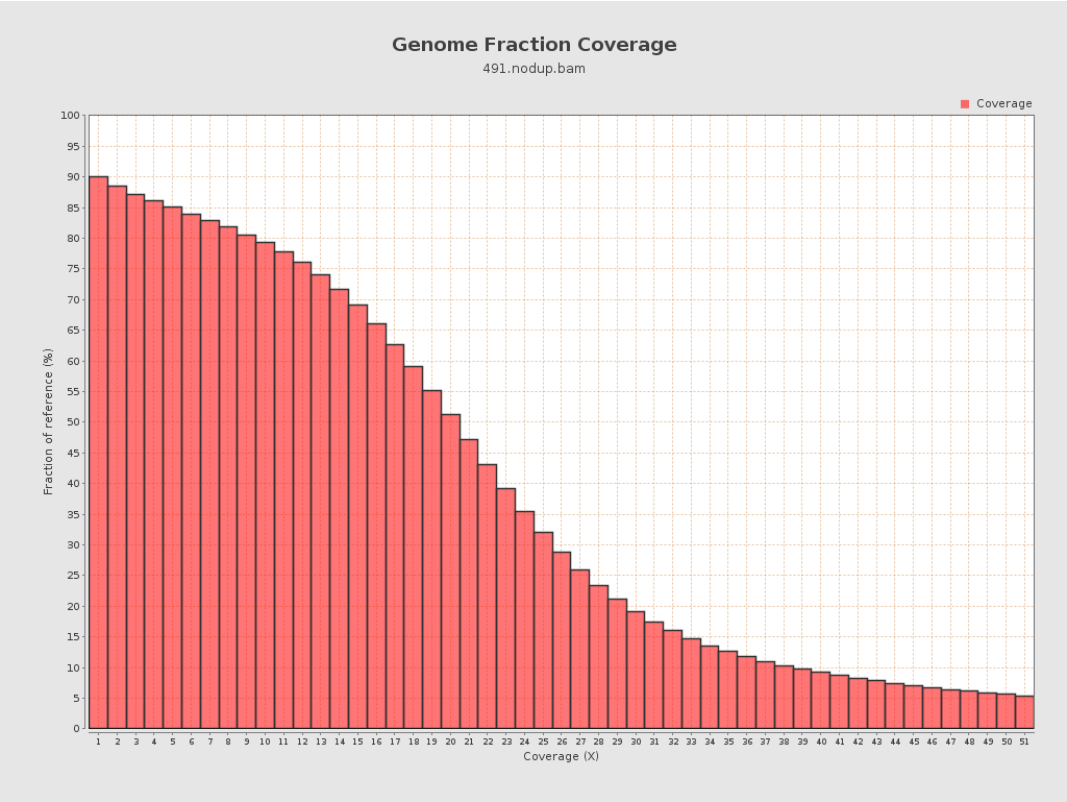
4. Results : Coverage Histogram



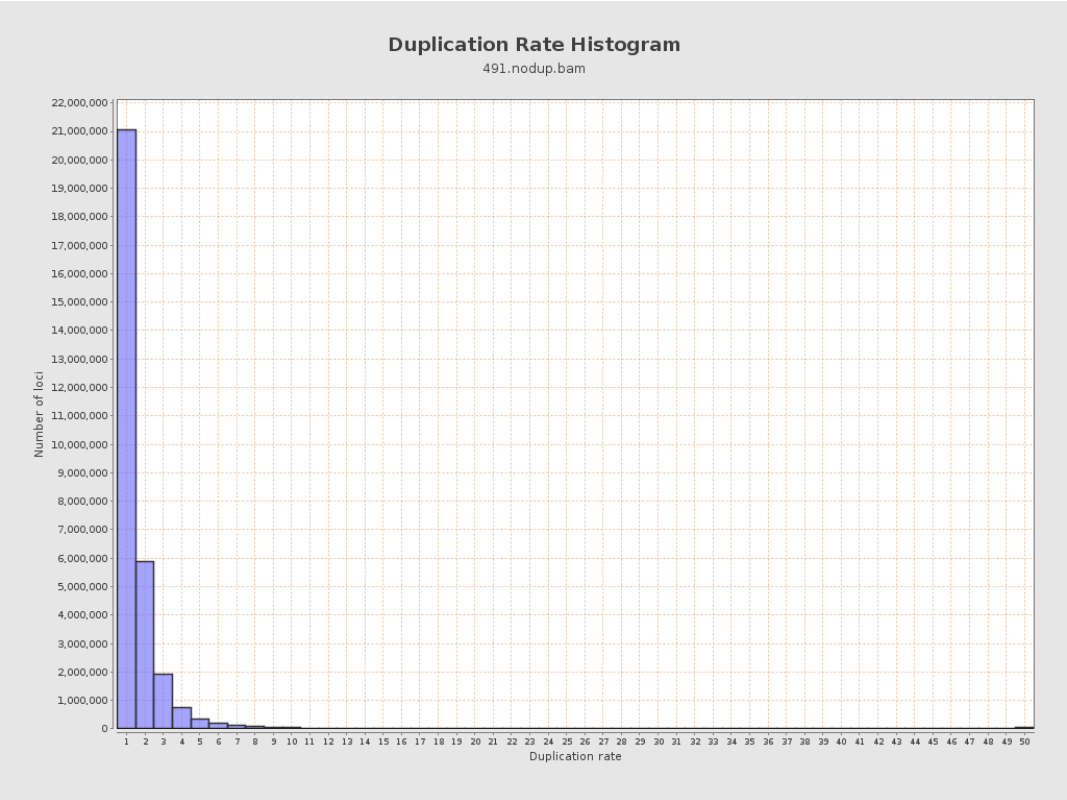
5. Results : Coverage Histogram (0-50X)



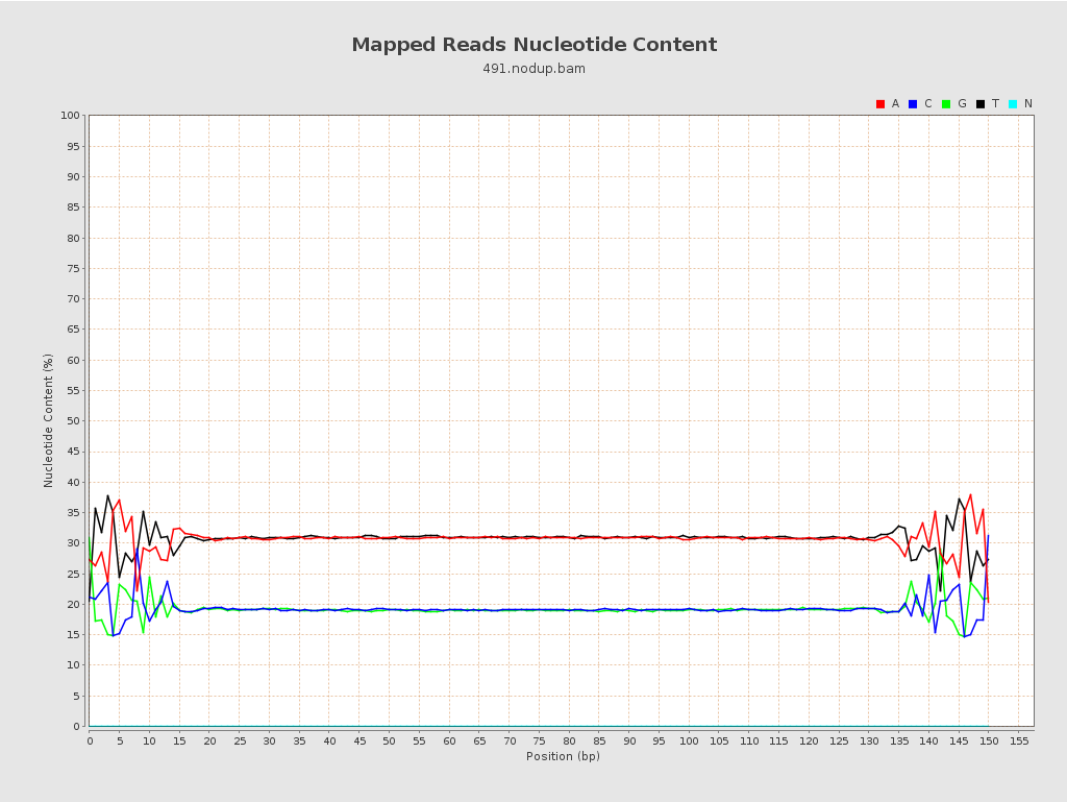
6. Results : Genome Fraction Coverage



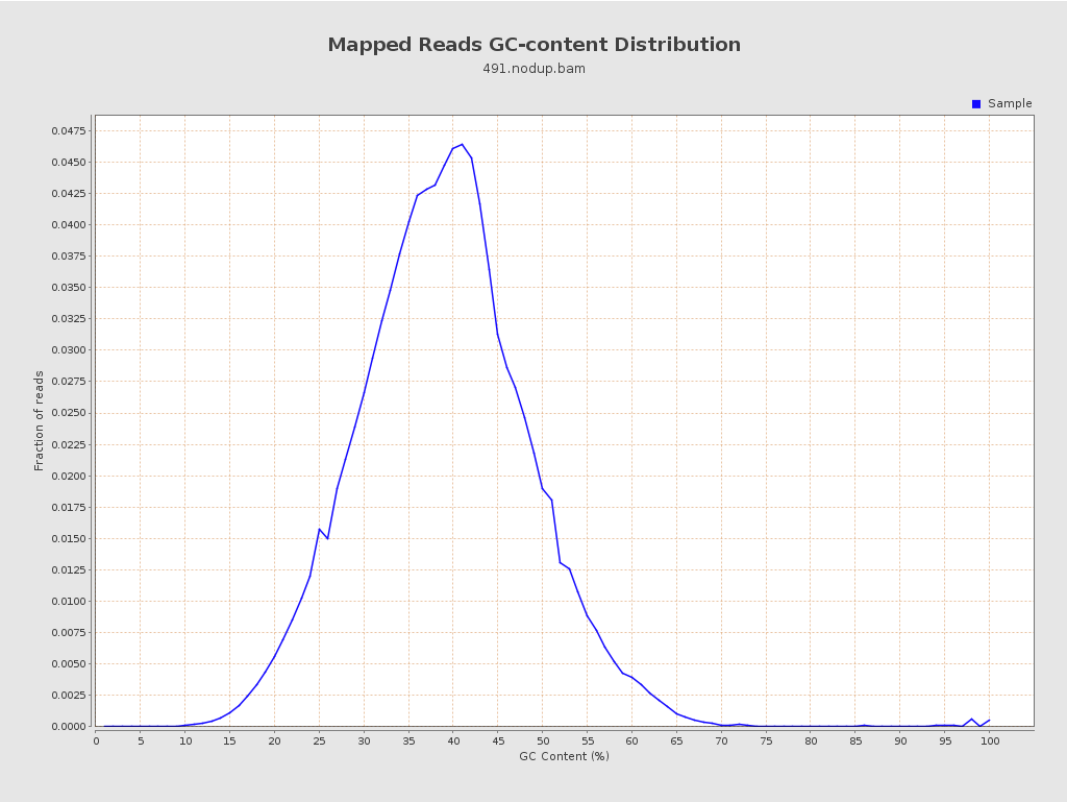
7. Results : Duplication Rate Histogram



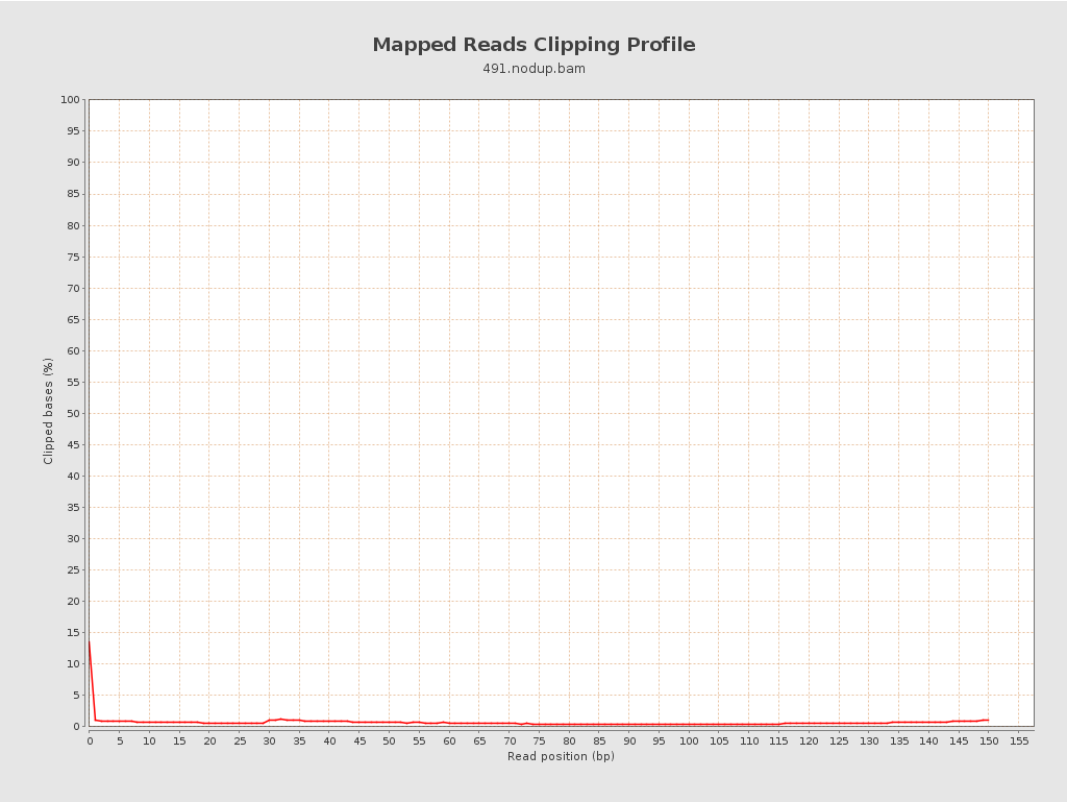
8. Results : Mapped Reads Nucleotide Content



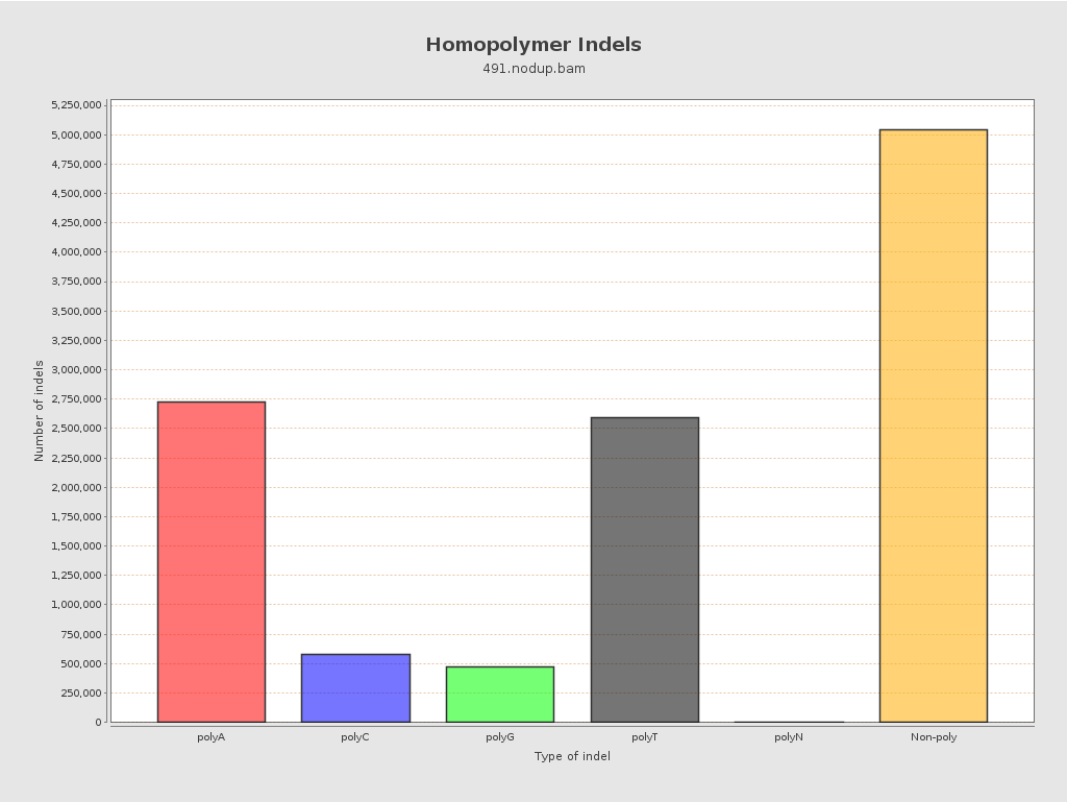
9. Results : Mapped Reads GC-content Distribution



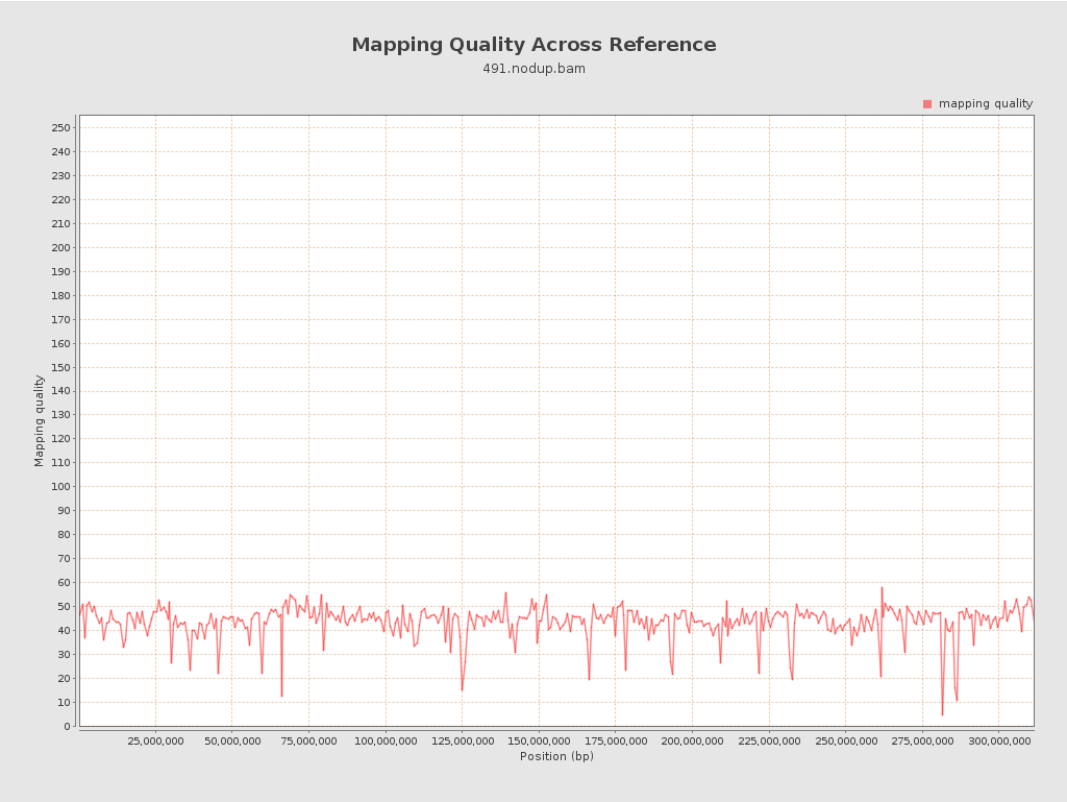
10. Results : Mapped Reads Clipping Profile



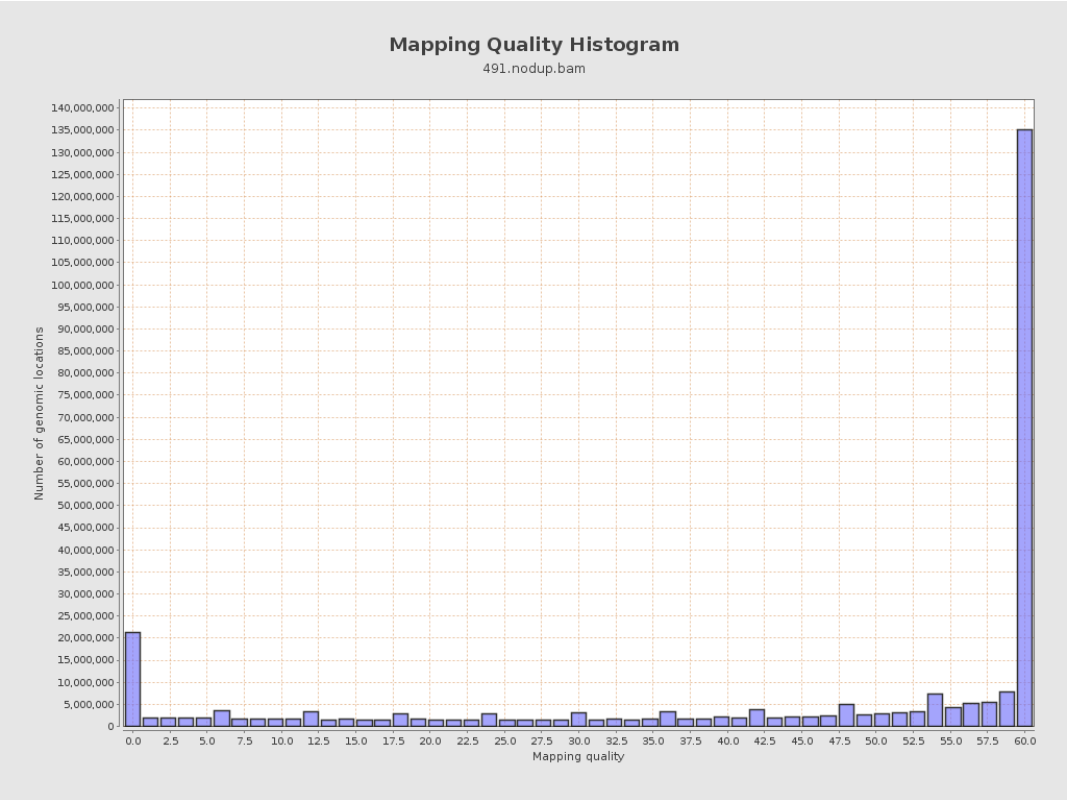
11. Results : Homopolymer Indels



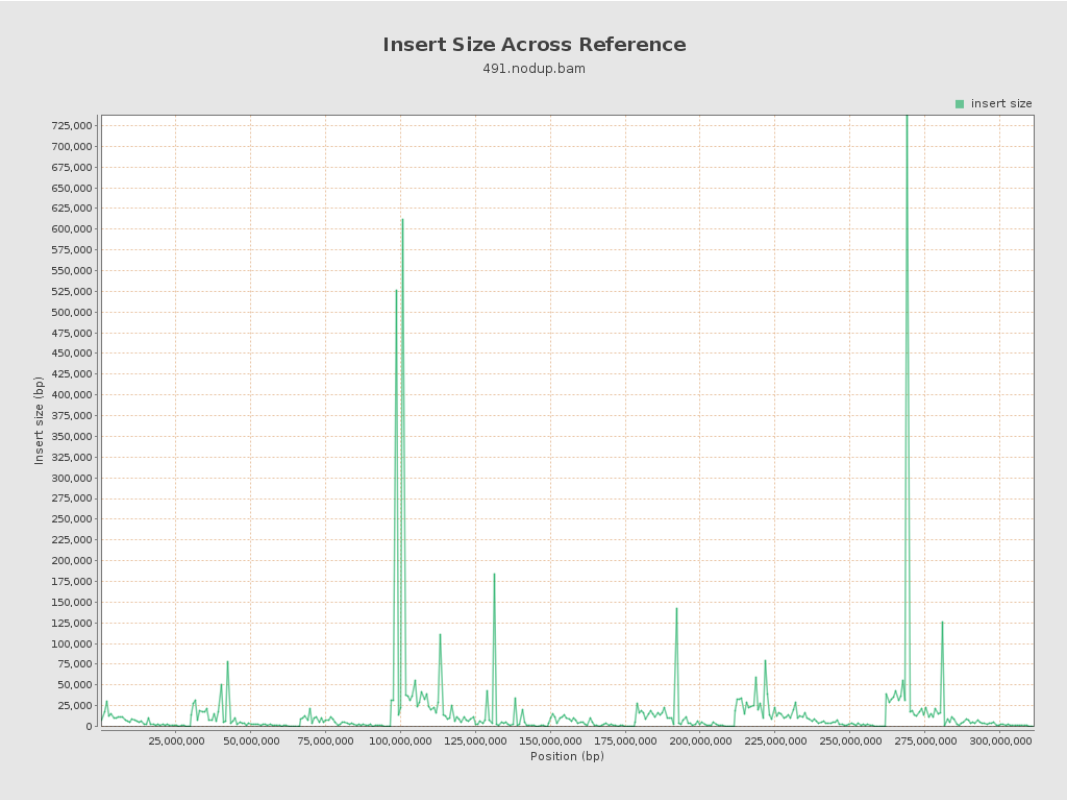
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram