Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1068
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1068 .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_459/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_459_S434_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_459/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_459_S434_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:27:53 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,931,666
Mapped reads	53,469,097 / 90.73%
Unmapped reads	5,462,569 / 9.27%
Mapped paired reads	53,469,097 / 90.73%
Mapped reads, first in pair	26,797,597 / 45.47%
Mapped reads, second in pair	26,671,500 / 45.26%
Mapped reads, both in pair	51,549,678 / 87.47%
Mapped reads, singletons	1,919,419 / 3.26%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	9,697,521 / 16.46%
Clipped reads	13,118,530 / 22.26%

2.2. ACGT Content

Number/percentage of A's	2,256,788,265 / 30.9%
Number/percentage of C's	1,393,783,350 / 19.08%
Number/percentage of T's	2,260,041,181 / 30.95%
Number/percentage of G's	1,392,734,455 / 19.07%
Number/percentage of N's	24,540 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	23.4937
Standard Deviation	256.7749

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Insert size

Mean	283,549.39
Standard Deviation	2,585,393.03
P25/Median/P75	363 / 482 / 632

2.6. Mismatches and indels

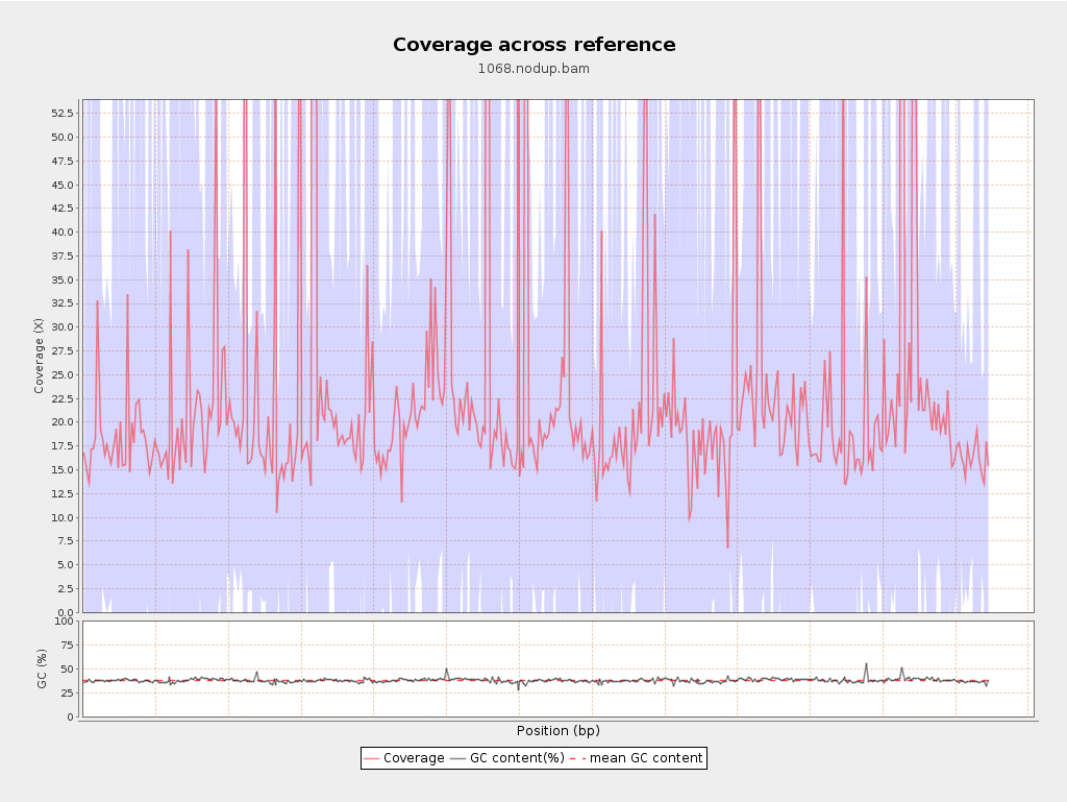
General error rate	2.45%
Mismatches	164,012,742
Insertions	5,442,553
Mapped reads with at least one insertion	9.05%
Deletions	5,007,592
Mapped reads with at least one deletion	8.31%
Homopolymer indels	57.39%

2.7. Chromosome stats

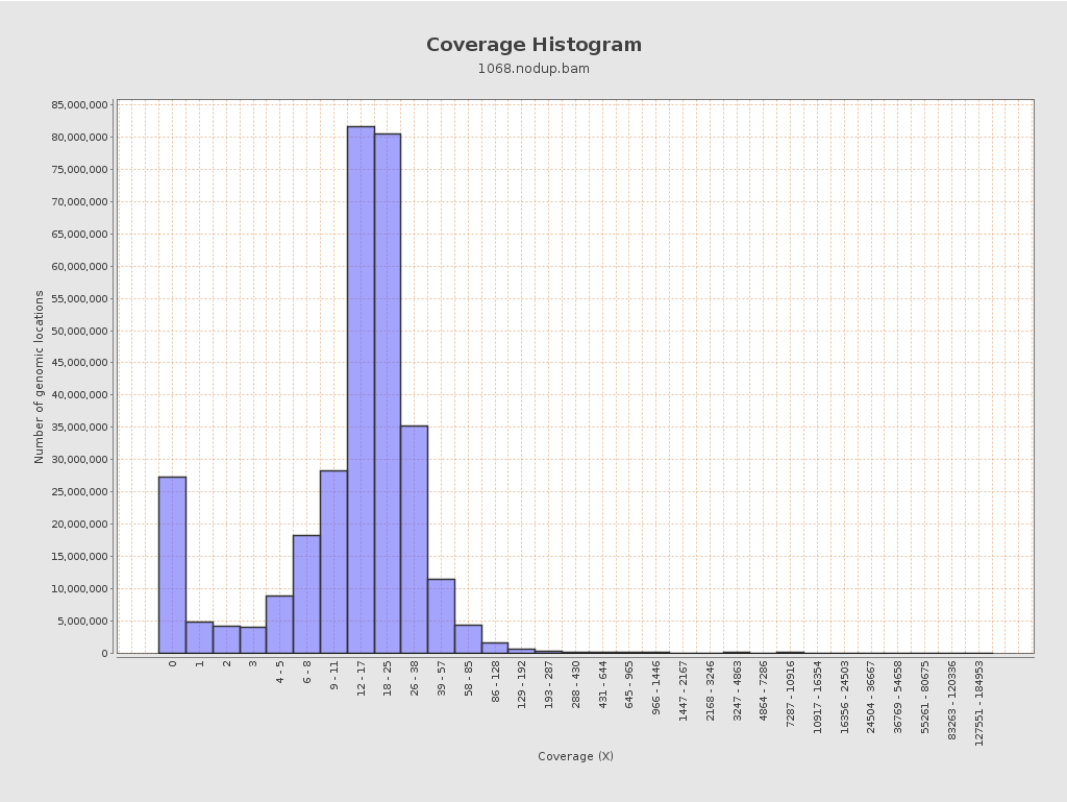
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	537143033	18.0708	100.5561

LT669789.1	36598175	848147782	23.1746	264.2797
LT669790.1	30422129	900352979	29.5953	387.5442
LT669791.1	52758100	1254029372	23.7694	285.0246
LT669792.1	28376109	674139371	23.7573	273.7868
LT669793.1	33388210	702665239	21.0453	161.2492
LT669794.1	50579949	1117003229	22.0839	208.4132
LT669795.1	49795044	1288144319	25.8689	270.4065

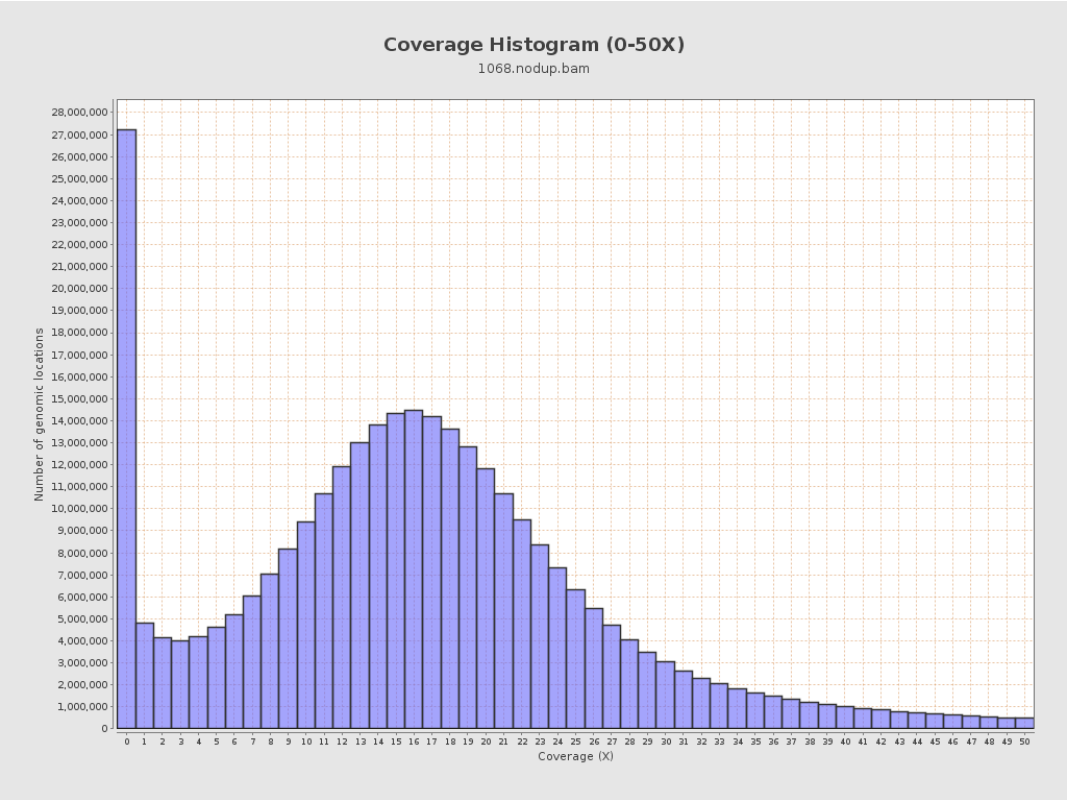
3. Results : Coverage across reference



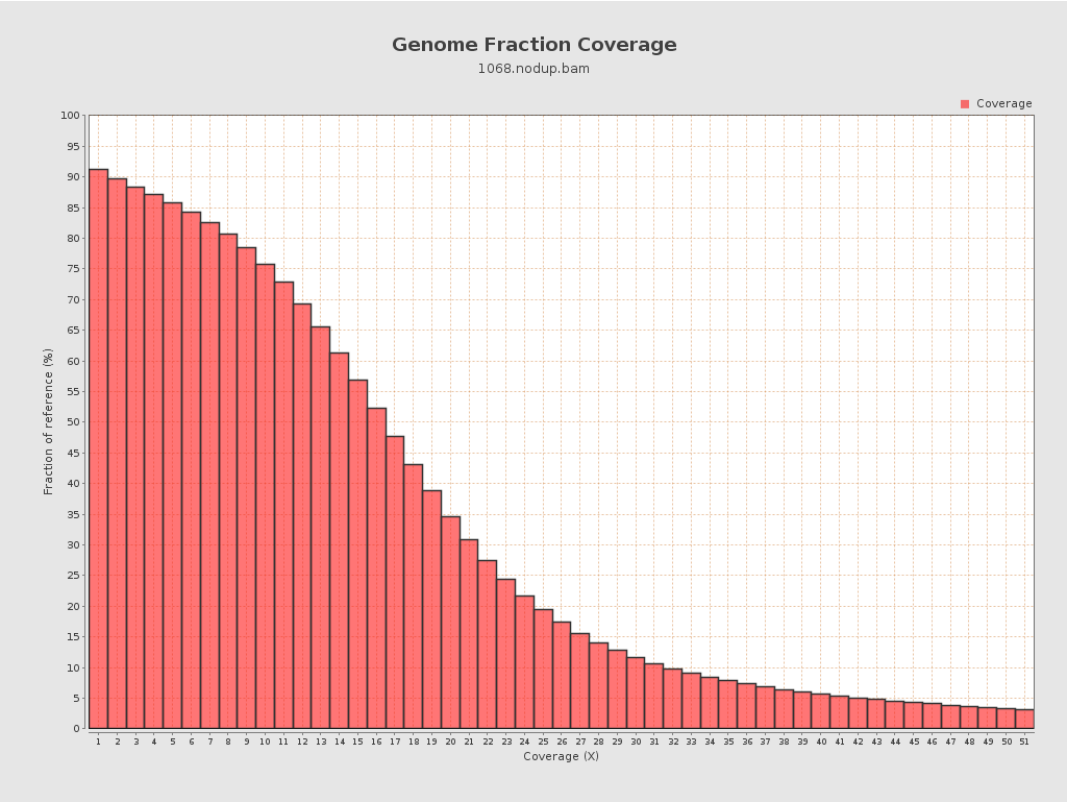
4. Results : Coverage Histogram



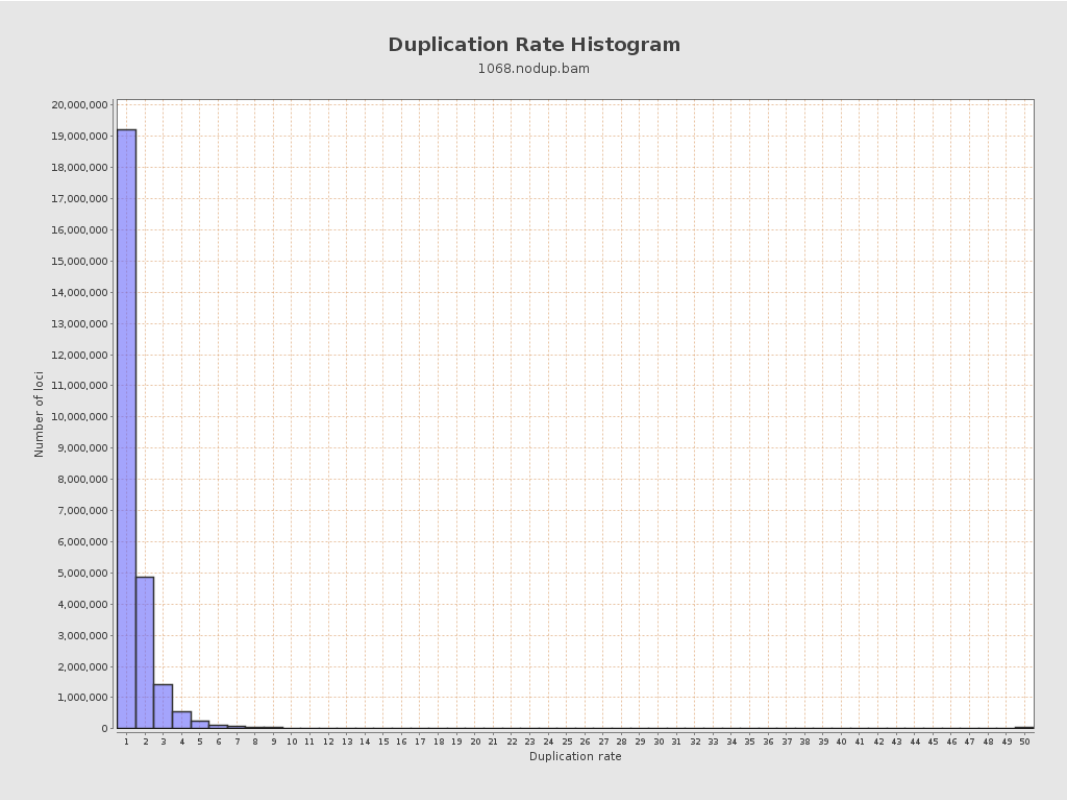
5. Results : Coverage Histogram (0-50X)



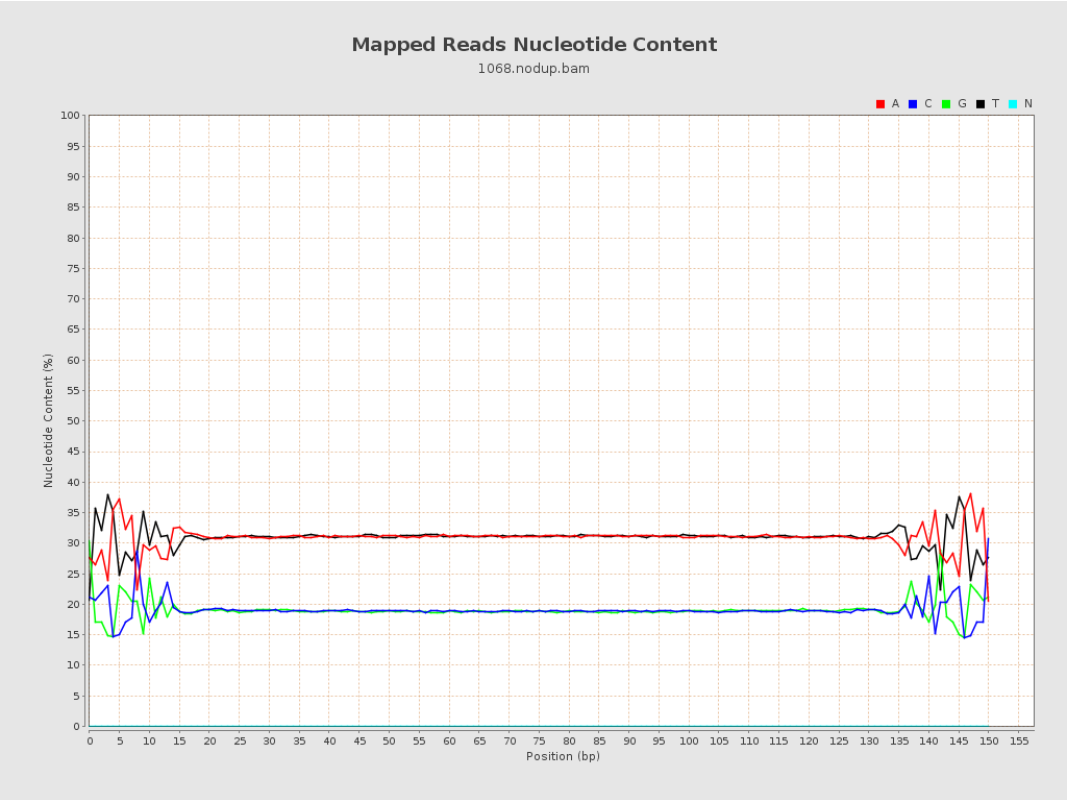
6. Results : Genome Fraction Coverage



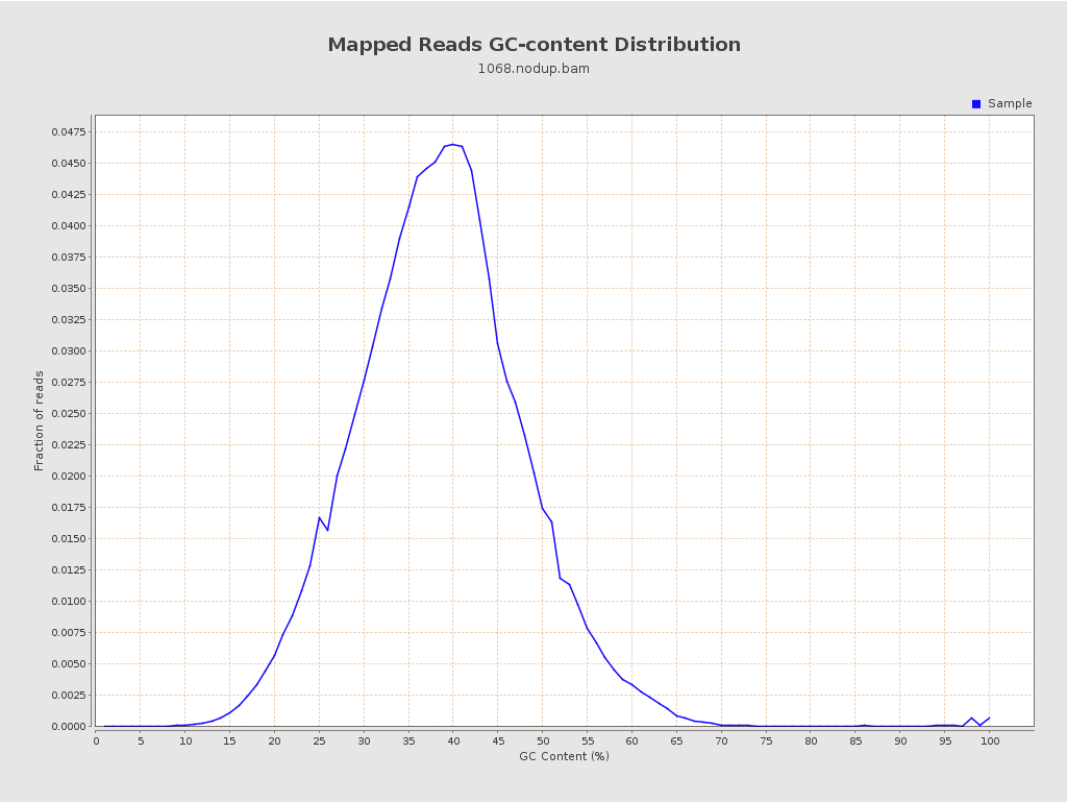
7. Results : Duplication Rate Histogram



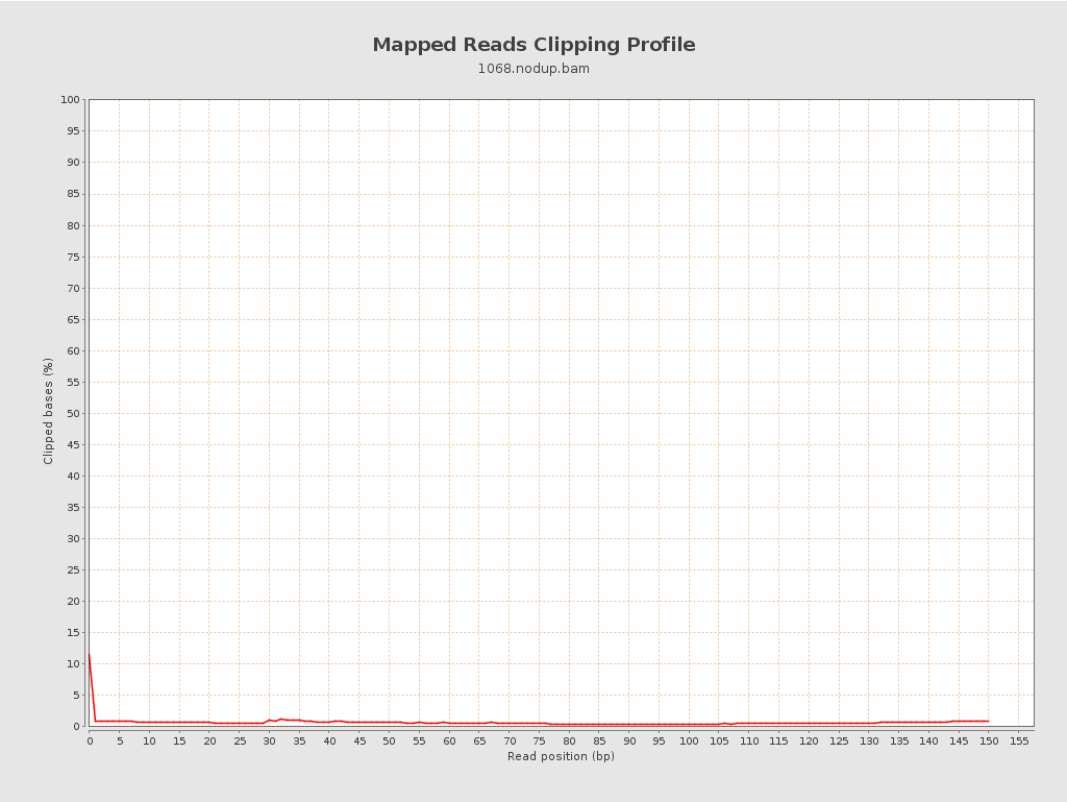
8. Results : Mapped Reads Nucleotide Content



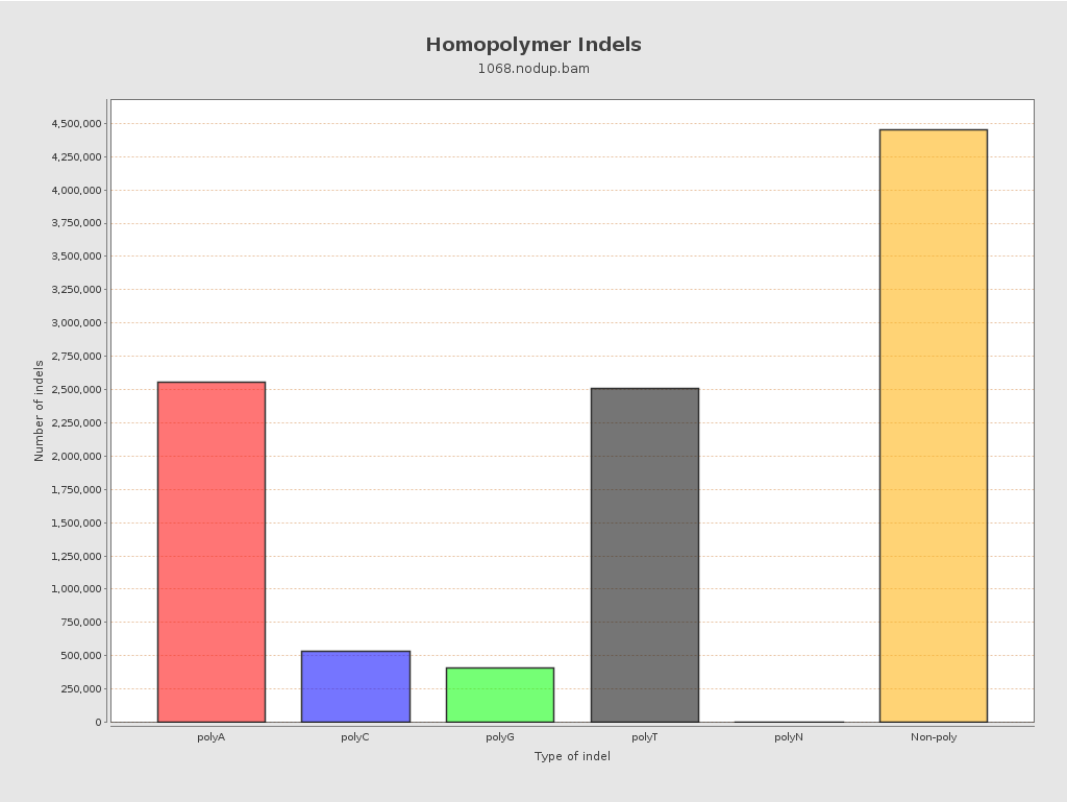
9. Results : Mapped Reads GC-content Distribution



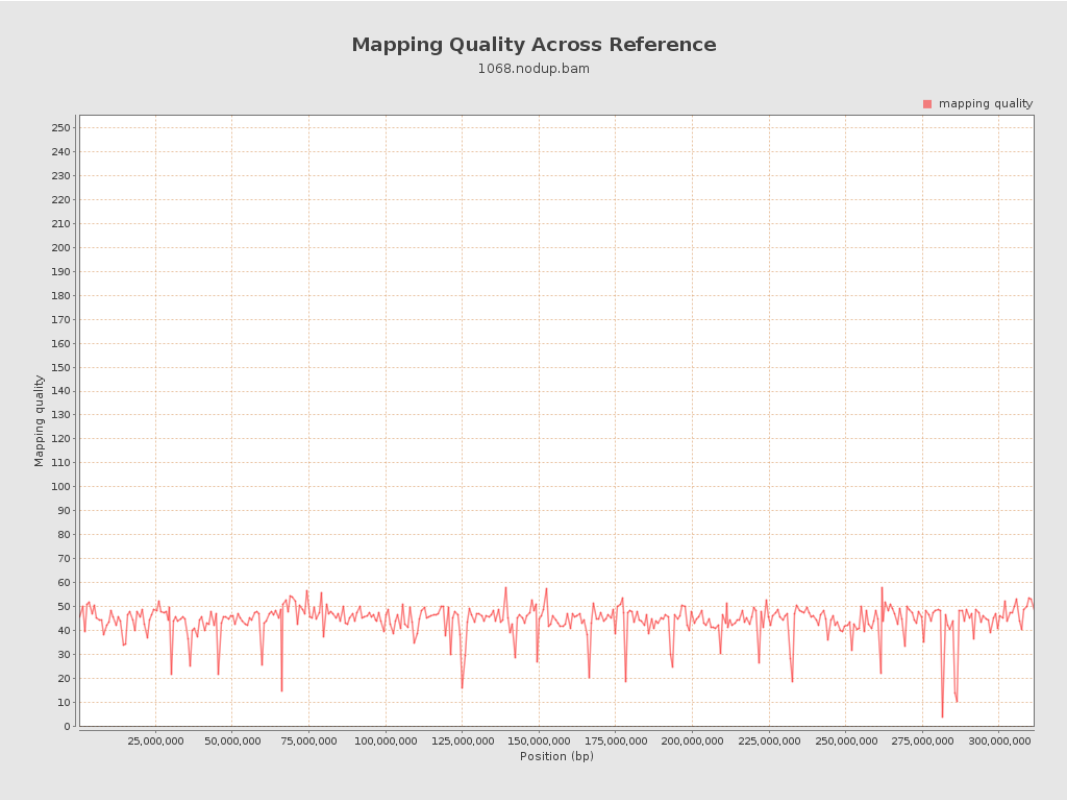
10. Results : Mapped Reads Clipping Profile



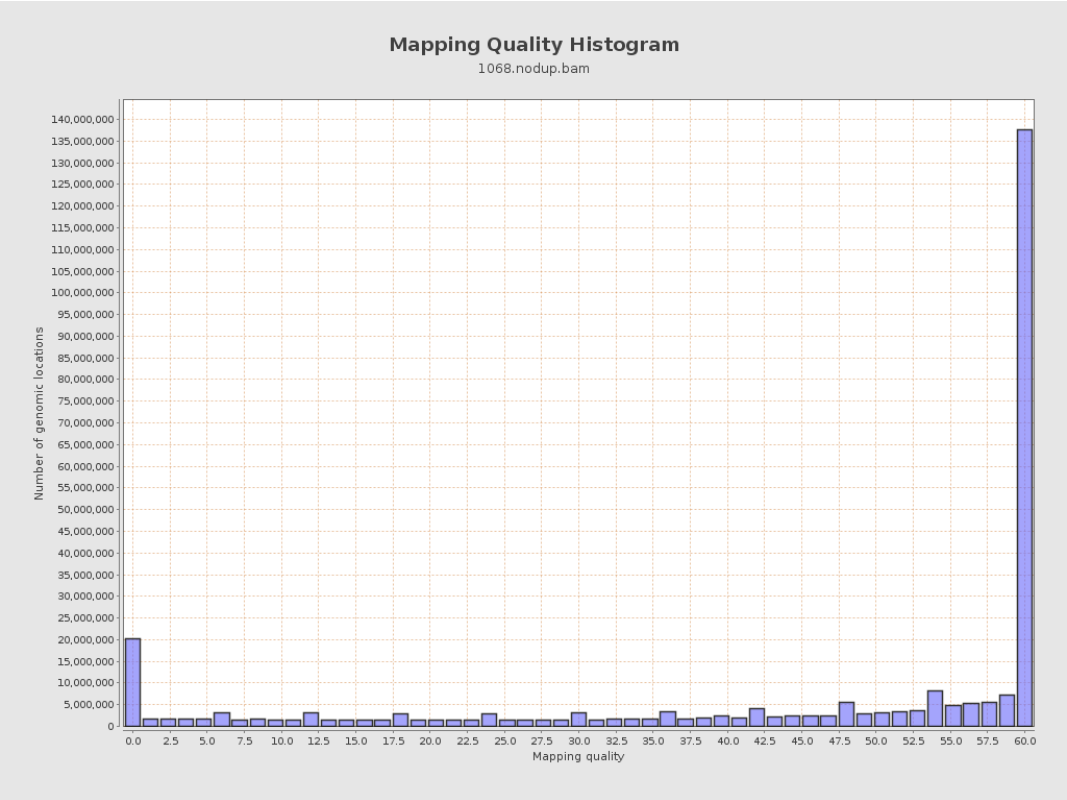
11. Results : Homopolymer Indels



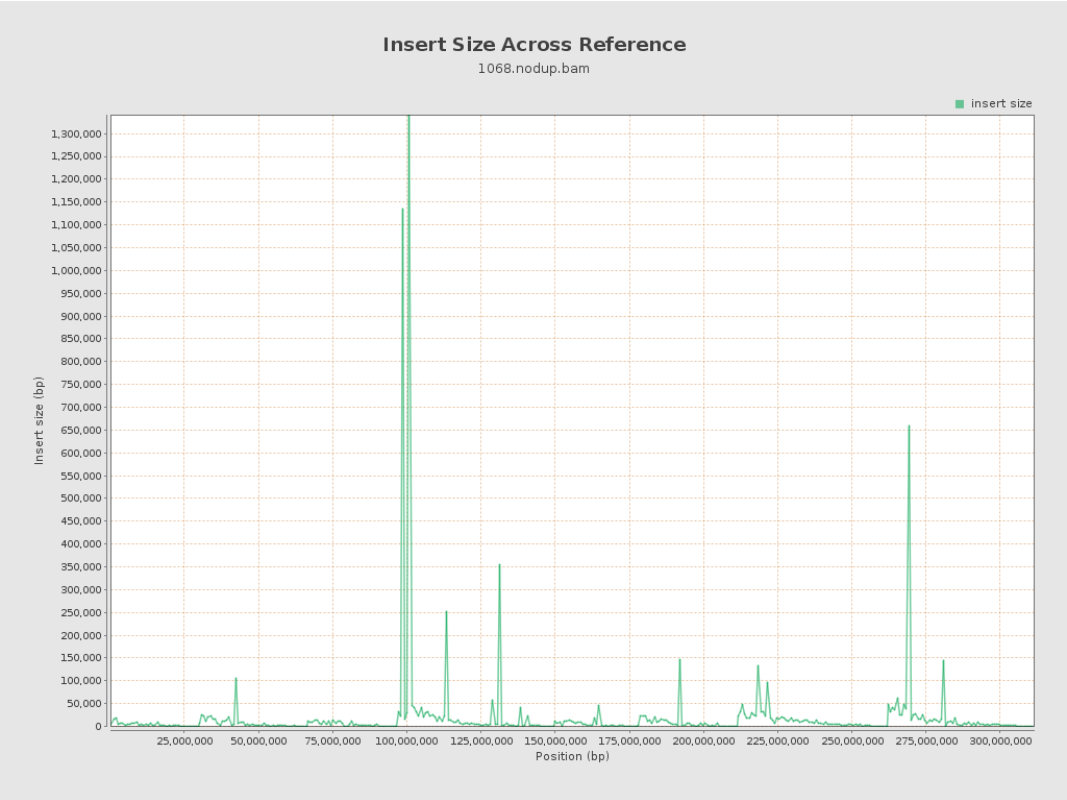
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram