Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:11:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1035
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1035 .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_281/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_281_S362_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_281/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_281_S362_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:11:33 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	956,644
Mapped reads	890,483 / 93.08%
Unmapped reads	66,161 / 6.92%
Mapped paired reads	890,483 / 93.08%
Mapped reads, first in pair	447,764 / 46.81%
Mapped reads, second in pair	442,719 / 46.28%
Mapped reads, both in pair	874,896 / 91.45%
Mapped reads, singletons	15,587 / 1.63%
Read min/max/mean length	30 / 151 / 146.52
Duplicated reads (flagged)	65,039 / 6.8%
Clipped reads	366,810 / 38.34%

2.2. ACGT Content

Number/percentage of A's	33,964,752 / 30.69%
Number/percentage of C's	21,272,793 / 19.22%
Number/percentage of T's	33,953,104 / 30.68%
Number/percentage of G's	21,494,821 / 19.42%
Number/percentage of N's	408 / 0%
GC Percentage	38.64%

2.3. Coverage

Mean	0.3561
Standard Deviation	5.4542

2.4. Mapping Quality

Mean Mapping Quality	43.55

2.5. Insert size

Mean	207,813.05
Standard Deviation	2,201,335.04
P25/Median/P75	140 / 244 / 361

2.6. Mismatches and indels

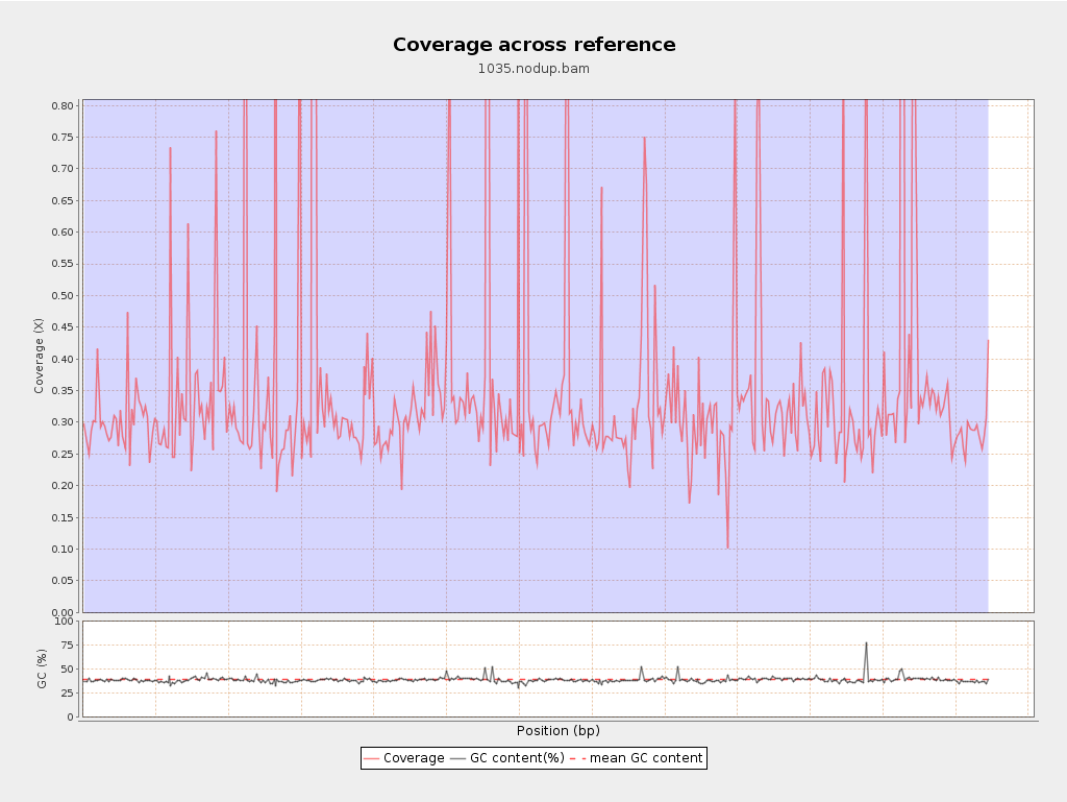
General error rate	2.24%
Mismatches	2,266,527
Insertions	77,229
Mapped reads with at least one insertion	7.79%
Deletions	75,715
Mapped reads with at least one deletion	7.58%
Homopolymer indels	57.93%

2.7. Chromosome stats

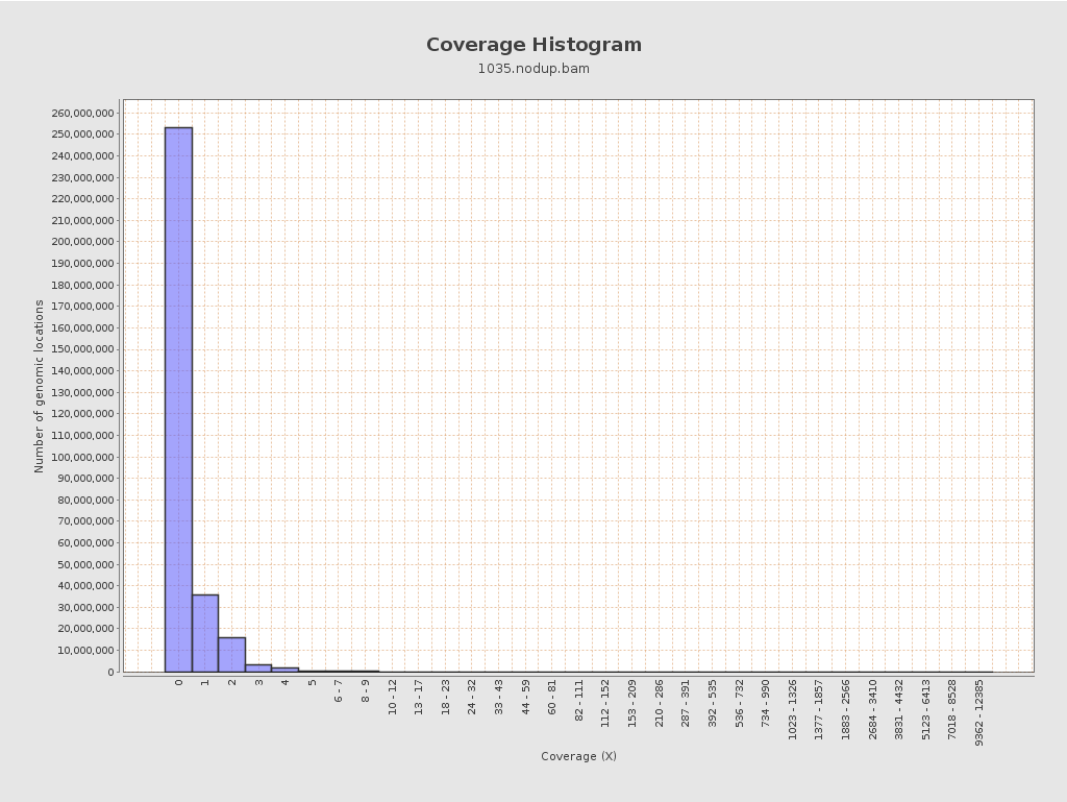
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	8870938	0.2984	1.4407

LT669789.1	36598175	13668844	0.3735	3.7204
LT669790.1	30422129	12713115	0.4179	4.4269
LT669791.1	52758100	18698492	0.3544	4.1439
LT669792.1	28376109	10105714	0.3561	3.4068
LT669793.1	33388210	10822780	0.3241	3.9416
LT669794.1	50579949	17131170	0.3387	2.7435
LT669795.1	49795044	18953873	0.3806	10.9508

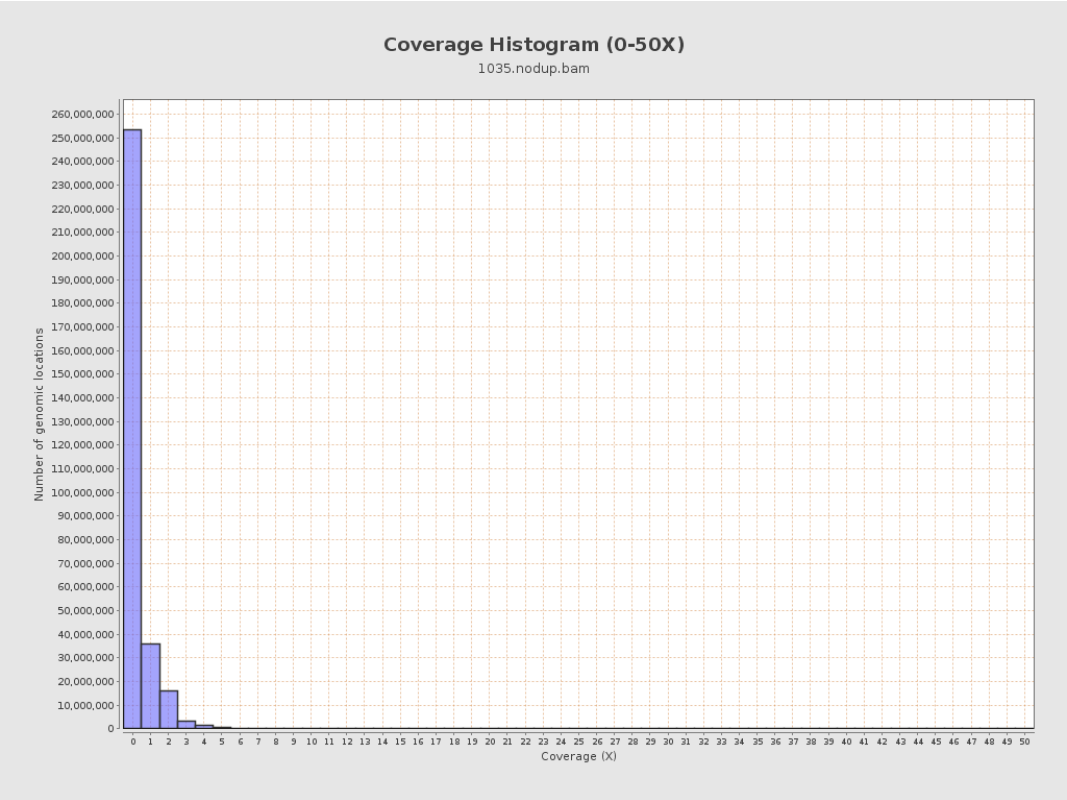
3. Results : Coverage across reference



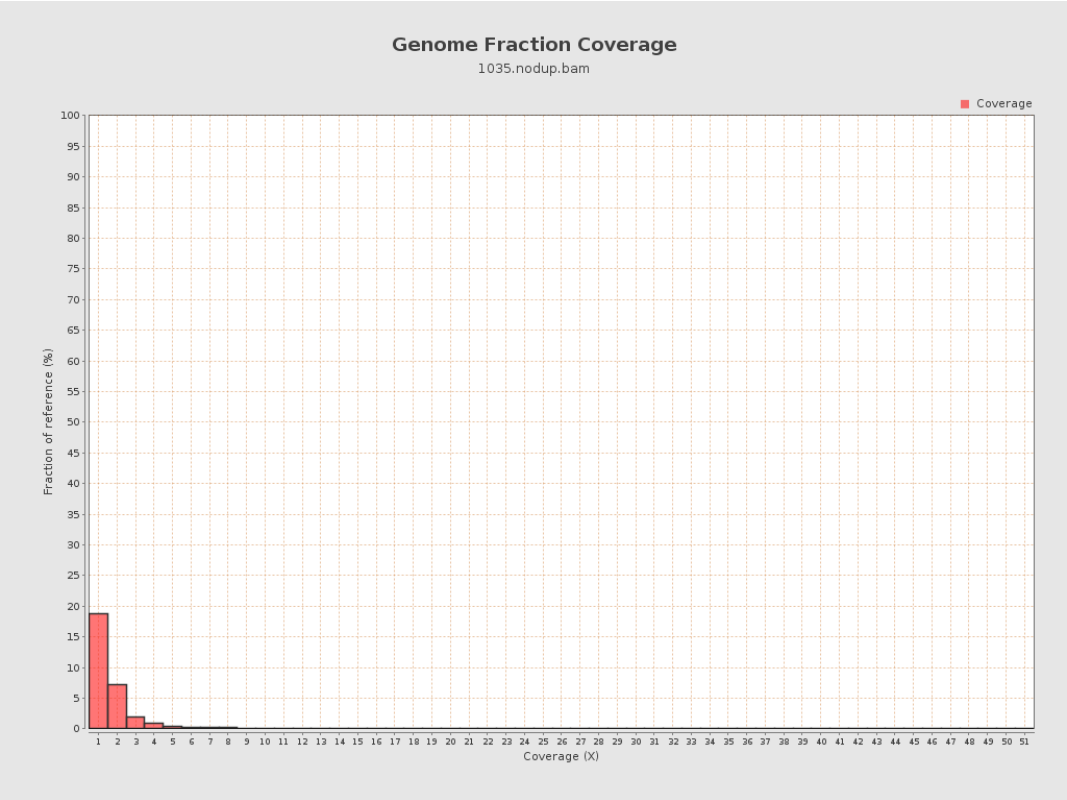
4. Results : Coverage Histogram



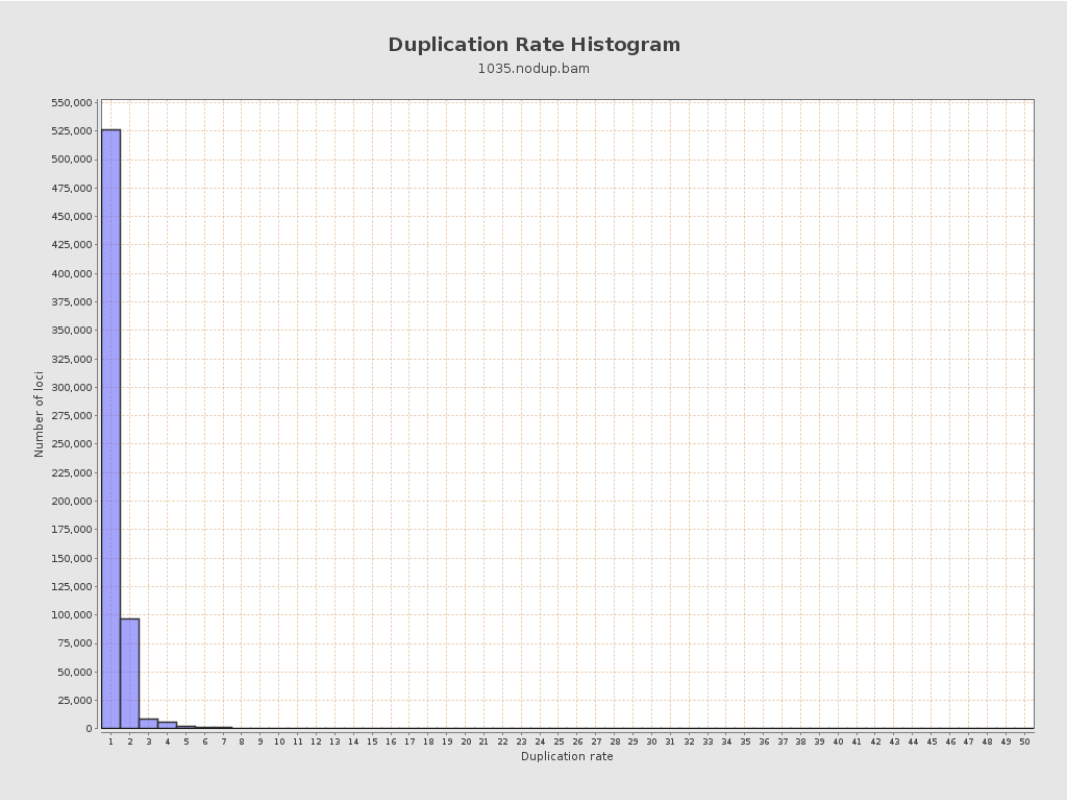
5. Results : Coverage Histogram (0-50X)



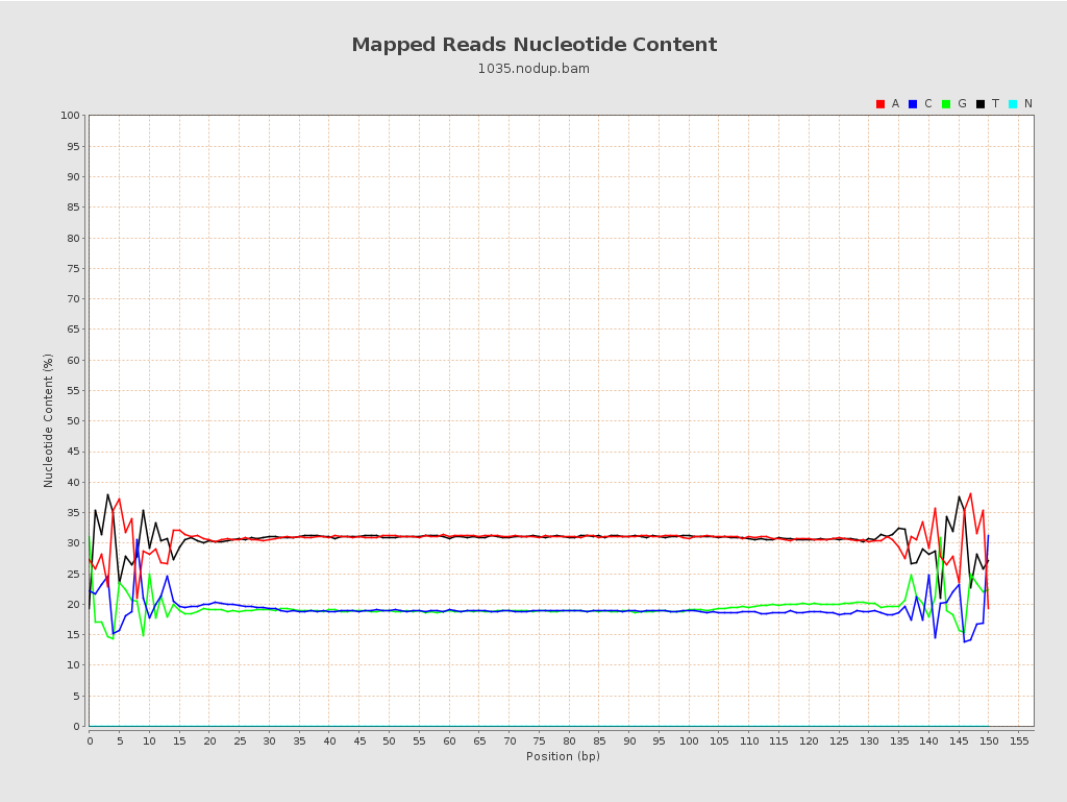
6. Results : Genome Fraction Coverage



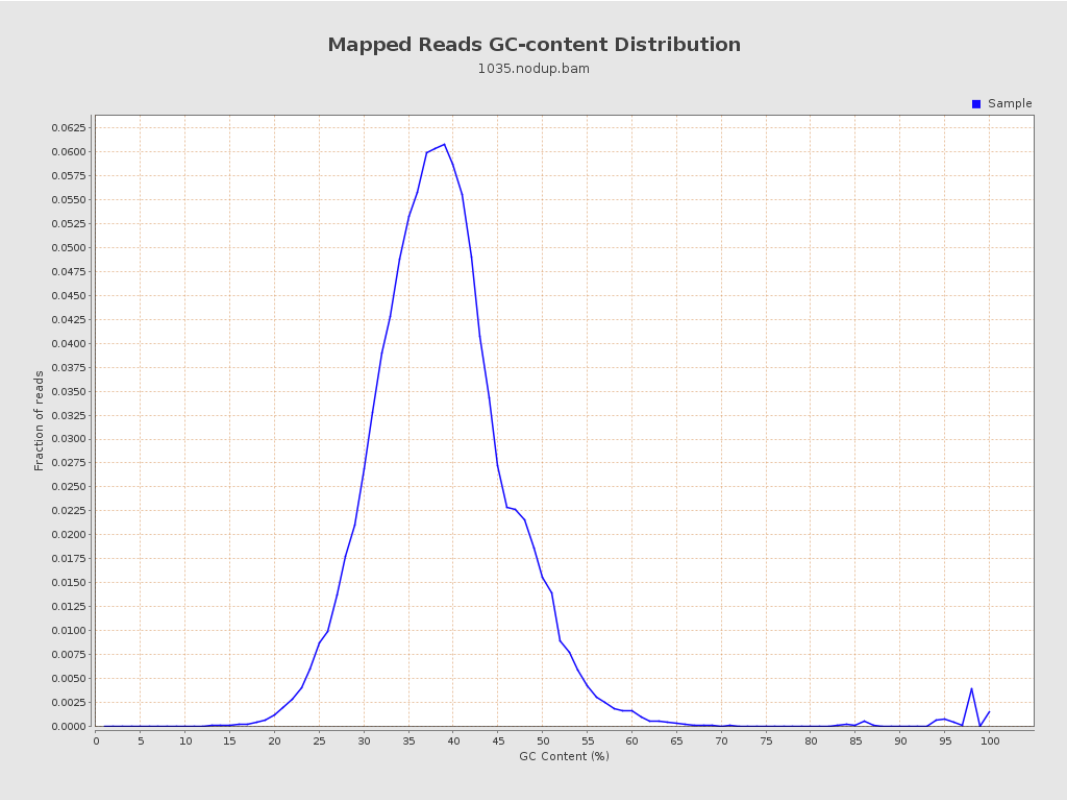
7. Results : Duplication Rate Histogram



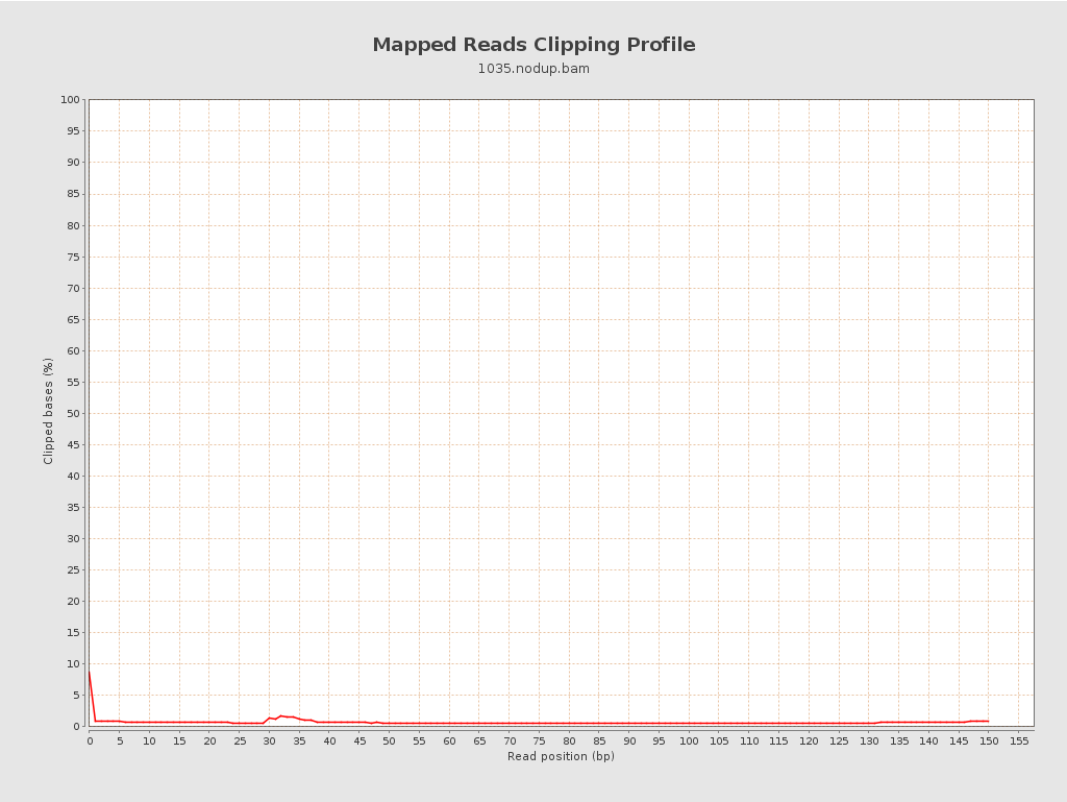
8. Results : Mapped Reads Nucleotide Content



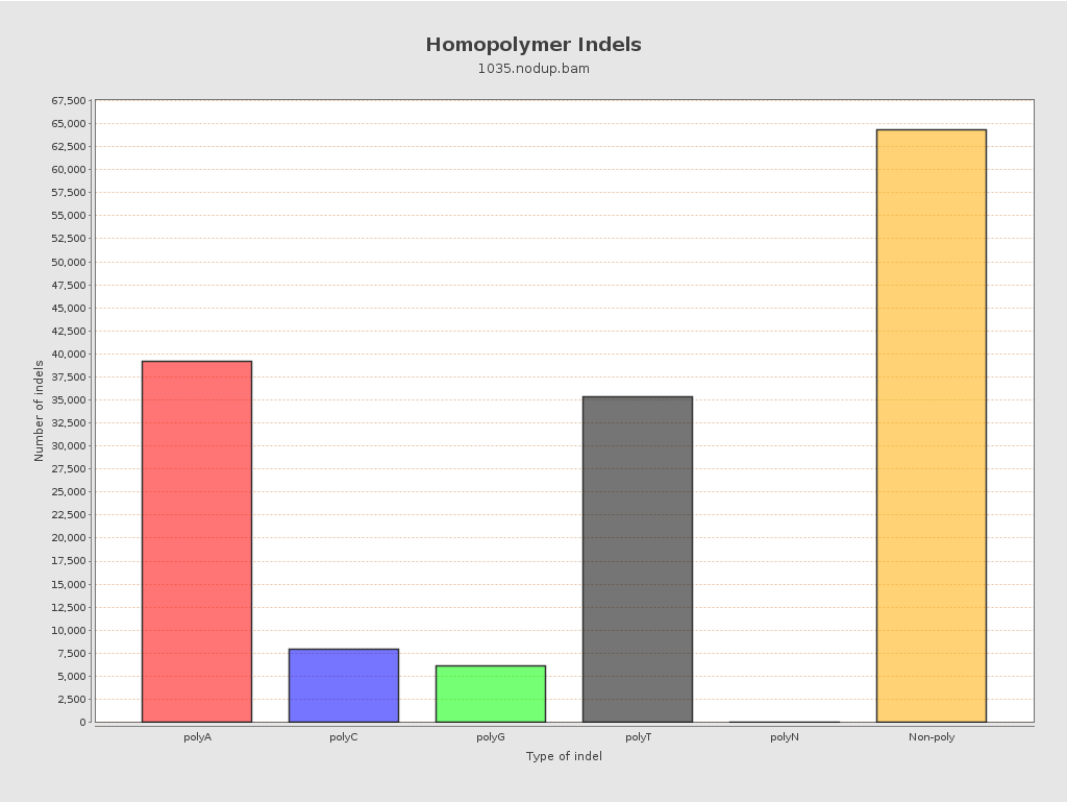
9. Results : Mapped Reads GC-content Distribution



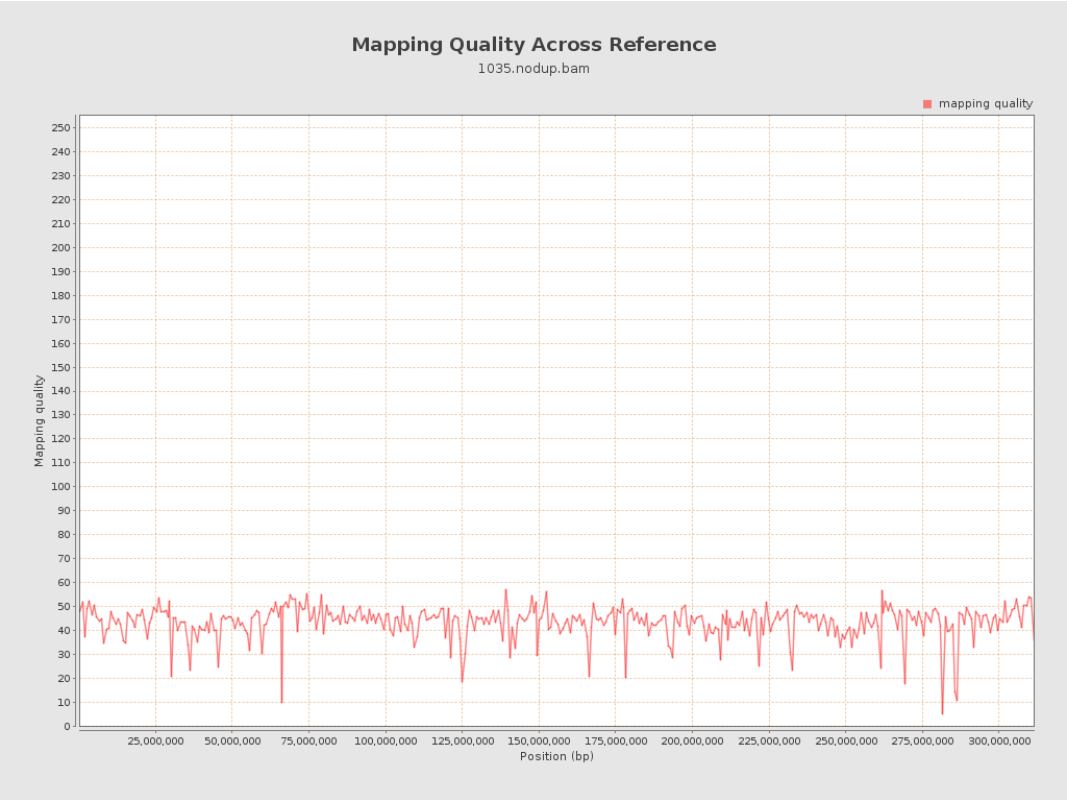
10. Results : Mapped Reads Clipping Profile



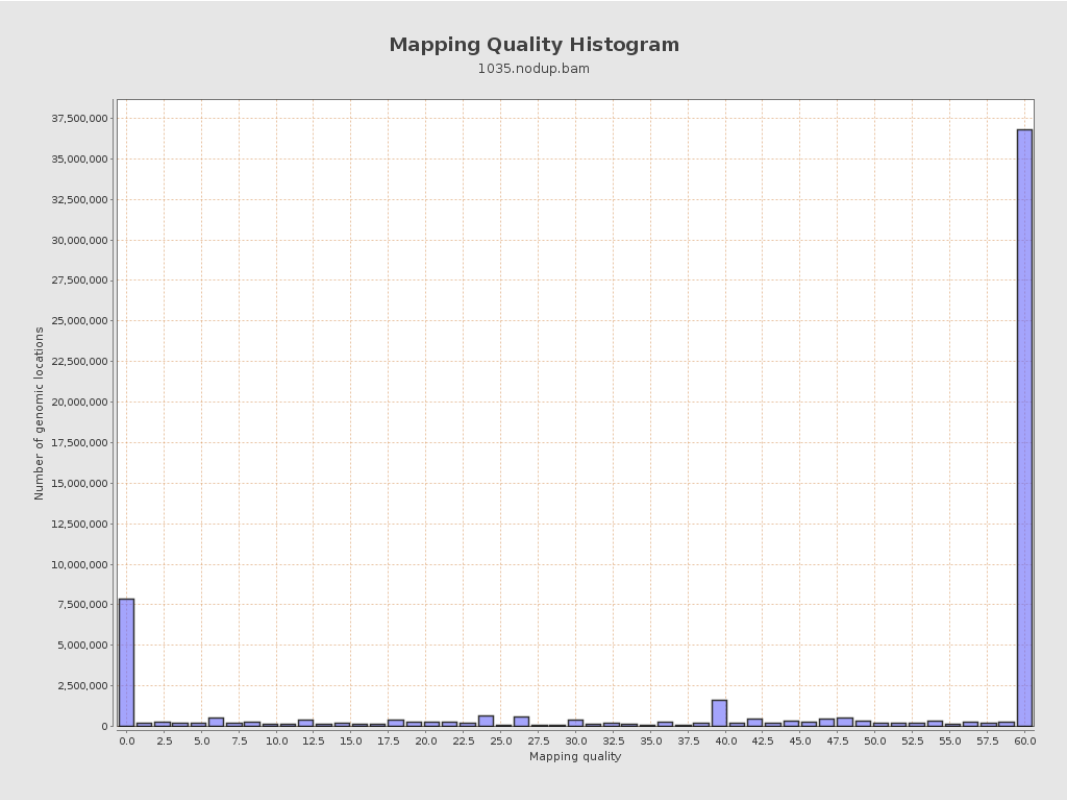
11. Results : Homopolymer Indels



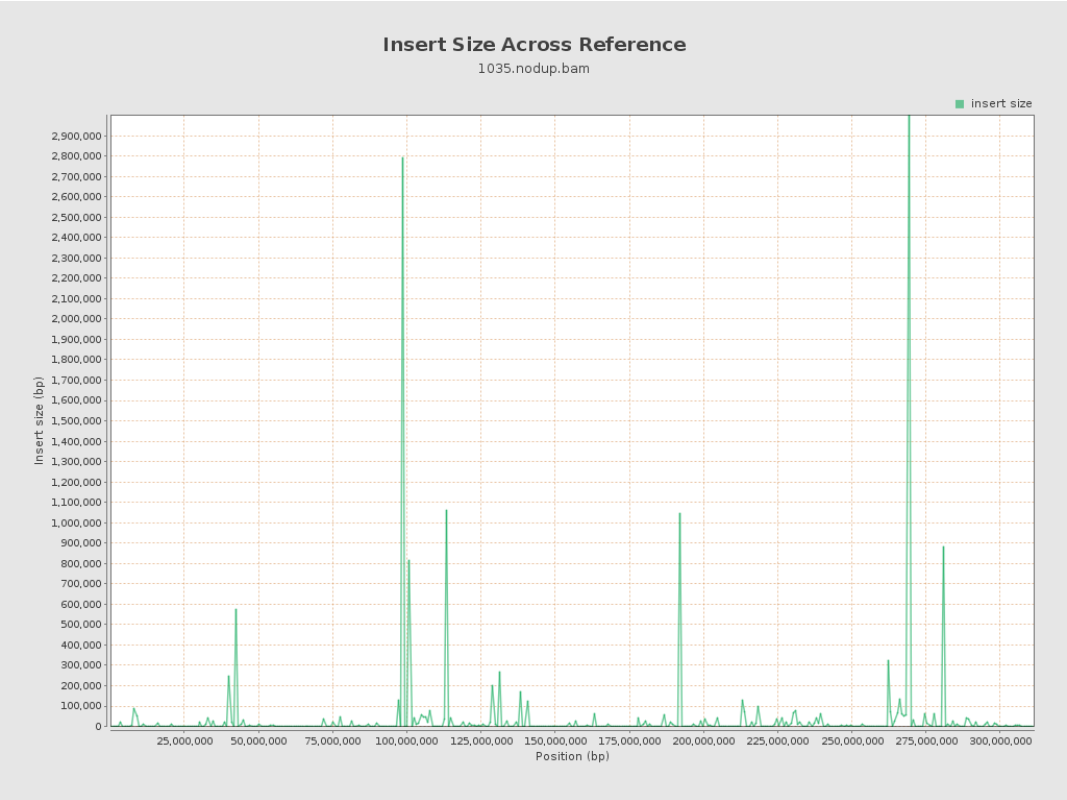
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram