Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1011
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1011 .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_155/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_155_S245_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_155/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_155_S245_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:38:55 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	90,178,698
Mapped reads	83,628,777 / 92.74%
Unmapped reads	6,549,921 / 7.26%
Mapped paired reads	83,628,777 / 92.74%
Mapped reads, first in pair	41,875,122 / 46.44%
Mapped reads, second in pair	41,753,655 / 46.3%
Mapped reads, both in pair	81,748,075 / 90.65%
Mapped reads, singletons	1,880,702 / 2.09%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	15,549,771 / 17.24%
Clipped reads	18,797,036 / 20.84%

2.2. ACGT Content

Number/percentage of A's	3,568,774,602 / 30.84%
Number/percentage of C's	2,215,931,228 / 19.15%
Number/percentage of T's	3,575,077,899 / 30.9%
Number/percentage of G's	2,210,723,031 / 19.11%
Number/percentage of N's	48,268 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	37.225
Standard Deviation	320.6549

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Insert size

Mean	231,306.94
Standard Deviation	2,281,734.53
P25/Median/P75	310 / 407 / 538

2.6. Mismatches and indels

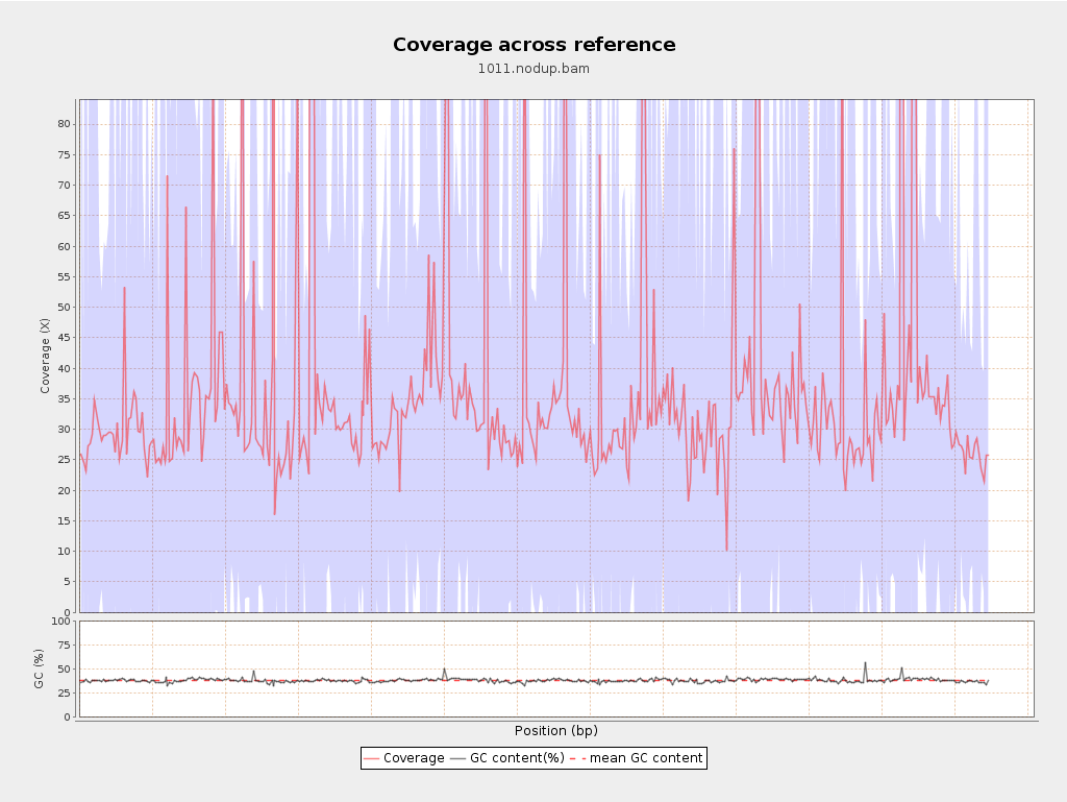
General error rate	2.3%
Mismatches	243,855,123
Insertions	7,952,795
Mapped reads with at least one insertion	8.52%
Deletions	8,029,775
Mapped reads with at least one deletion	8.54%
Homopolymer indels	56.71%

2.7. Chromosome stats

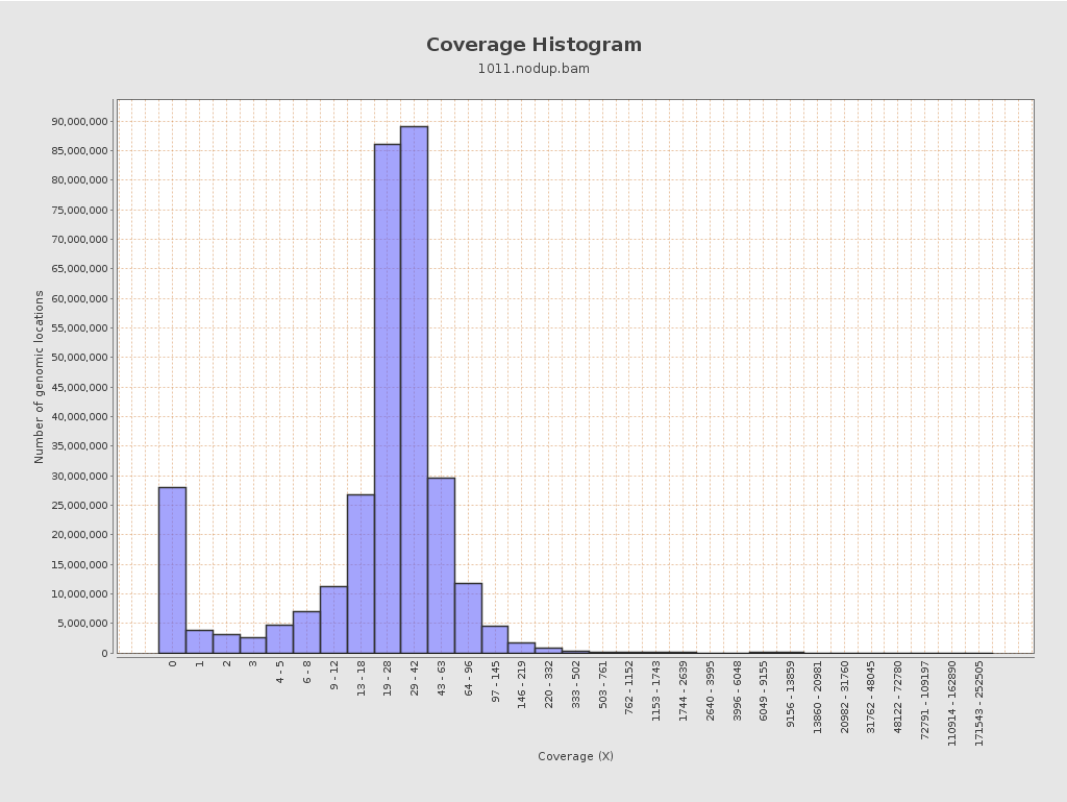
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	863092162	29.0365	99.4331

LT669789.1	36598175	1391511469	38.0213	355.8252
LT669790.1	30422129	1202343240	39.522	341.041
LT669791.1	52758100	1958250706	37.1175	290.3534
LT669792.1	28376109	1020590470	35.9665	354.6635
LT669793.1	33388210	1153944522	34.5614	223.5565
LT669794.1	50579949	1839580009	36.3697	276.9217
LT669795.1	49795044	2171551848	43.6098	448.3091

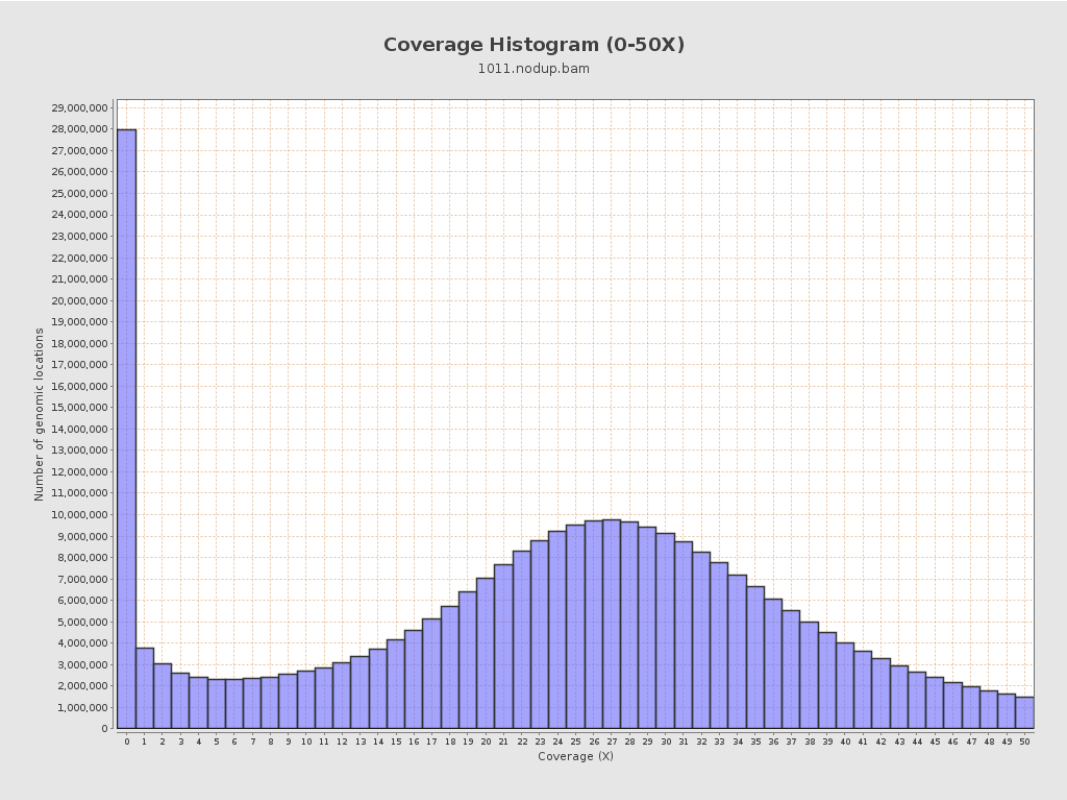
3. Results : Coverage across reference



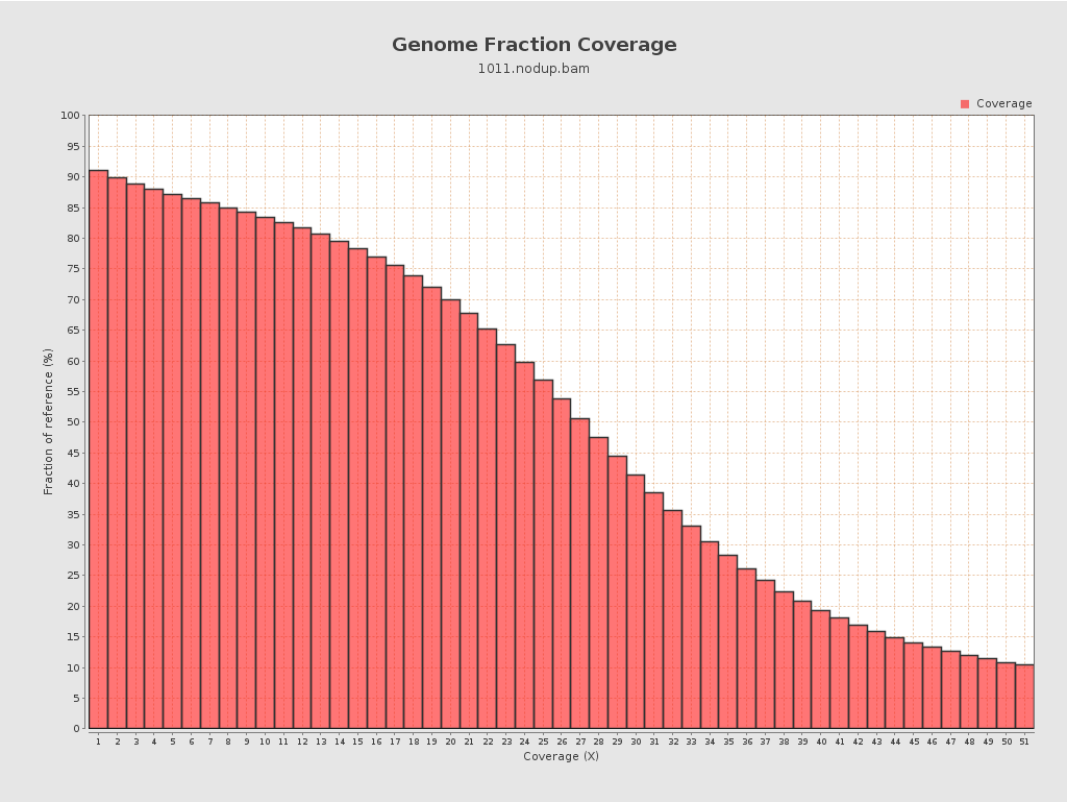
4. Results : Coverage Histogram



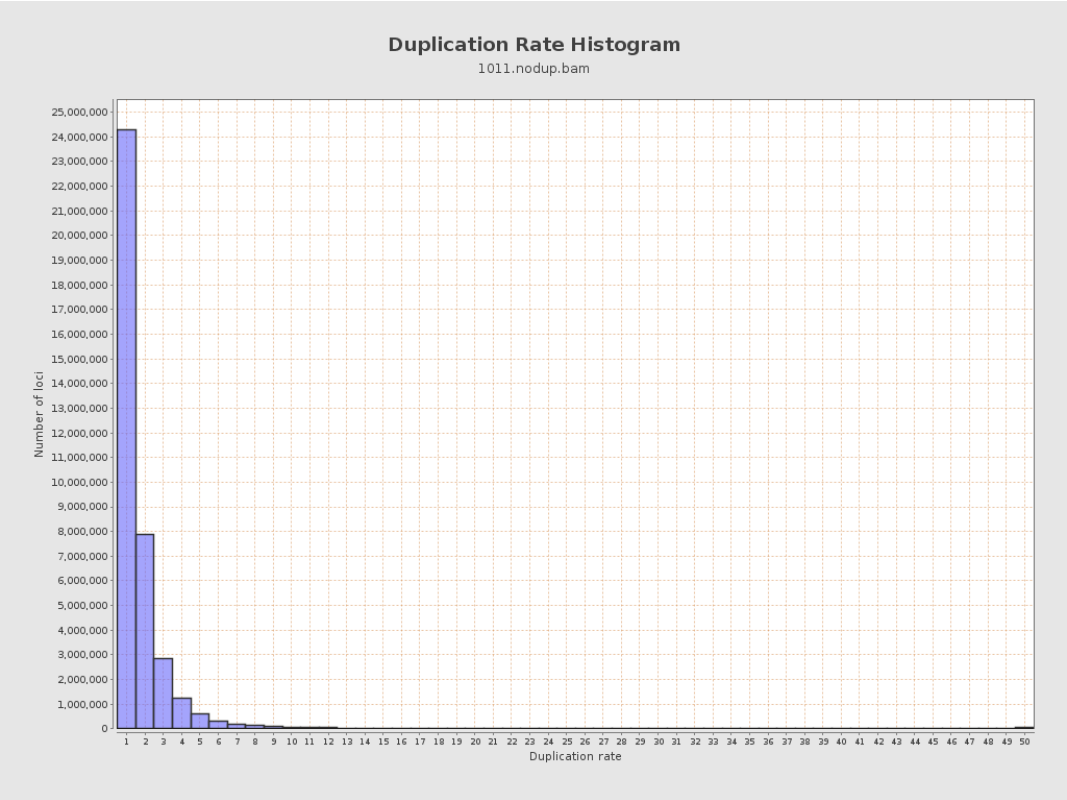
5. Results : Coverage Histogram (0-50X)



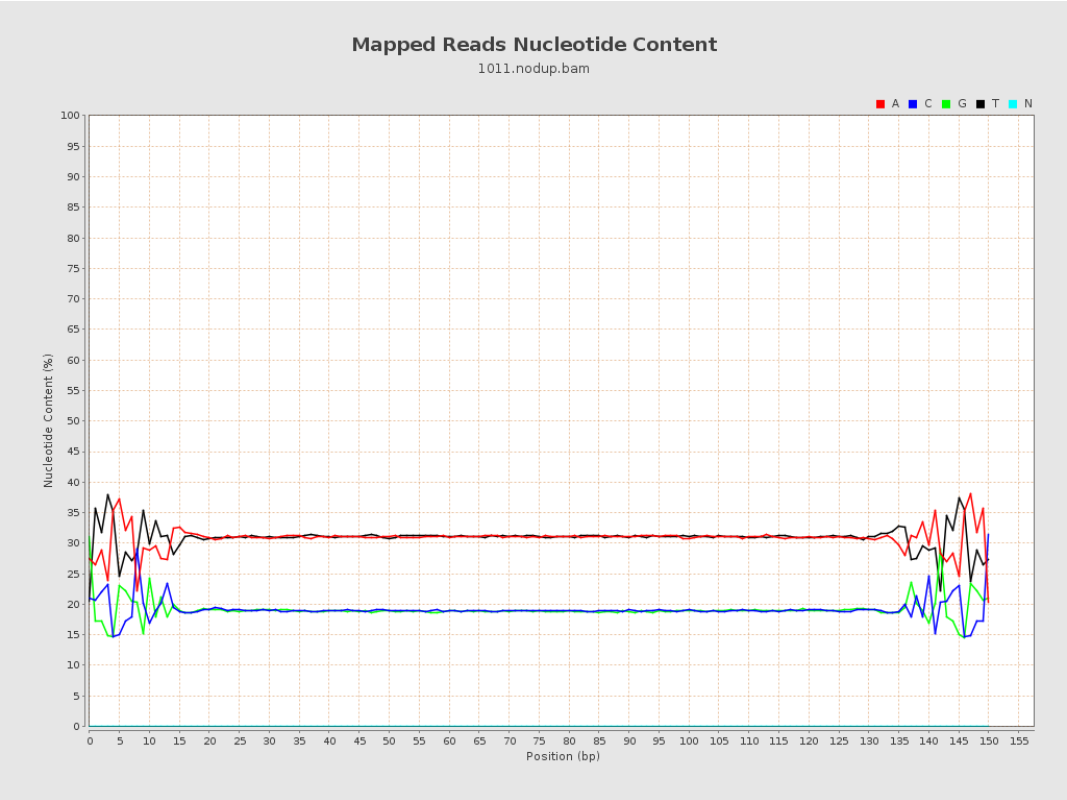
6. Results : Genome Fraction Coverage



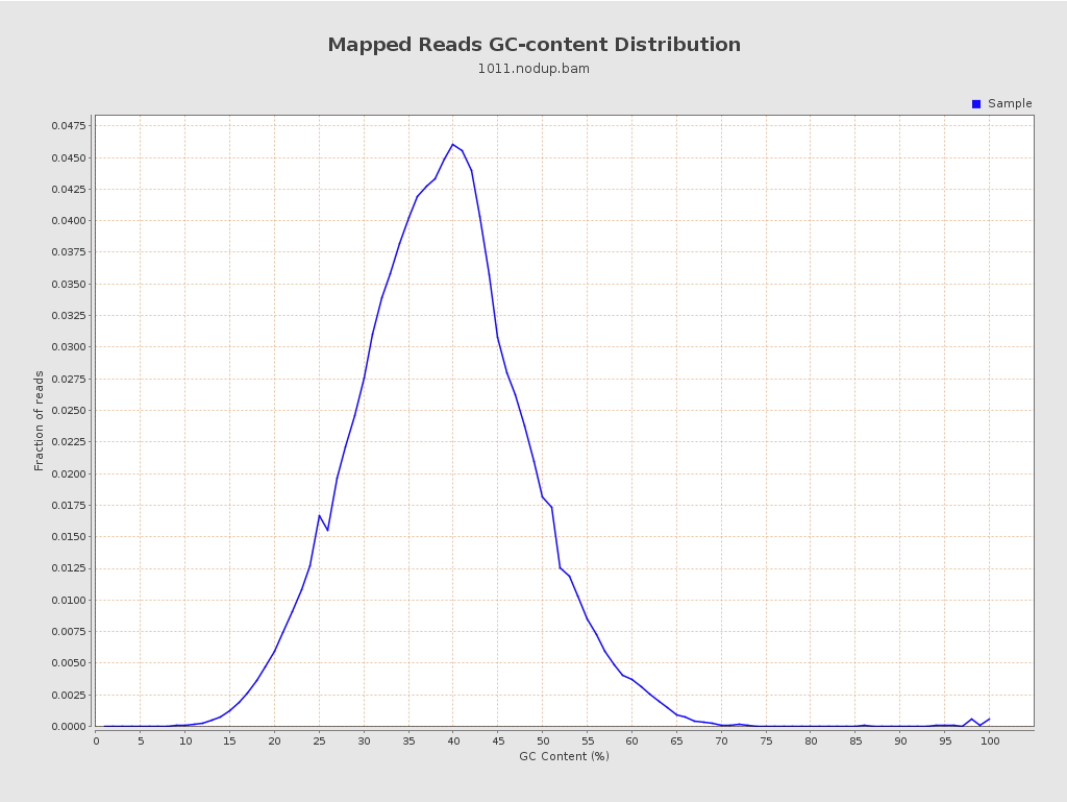
7. Results : Duplication Rate Histogram



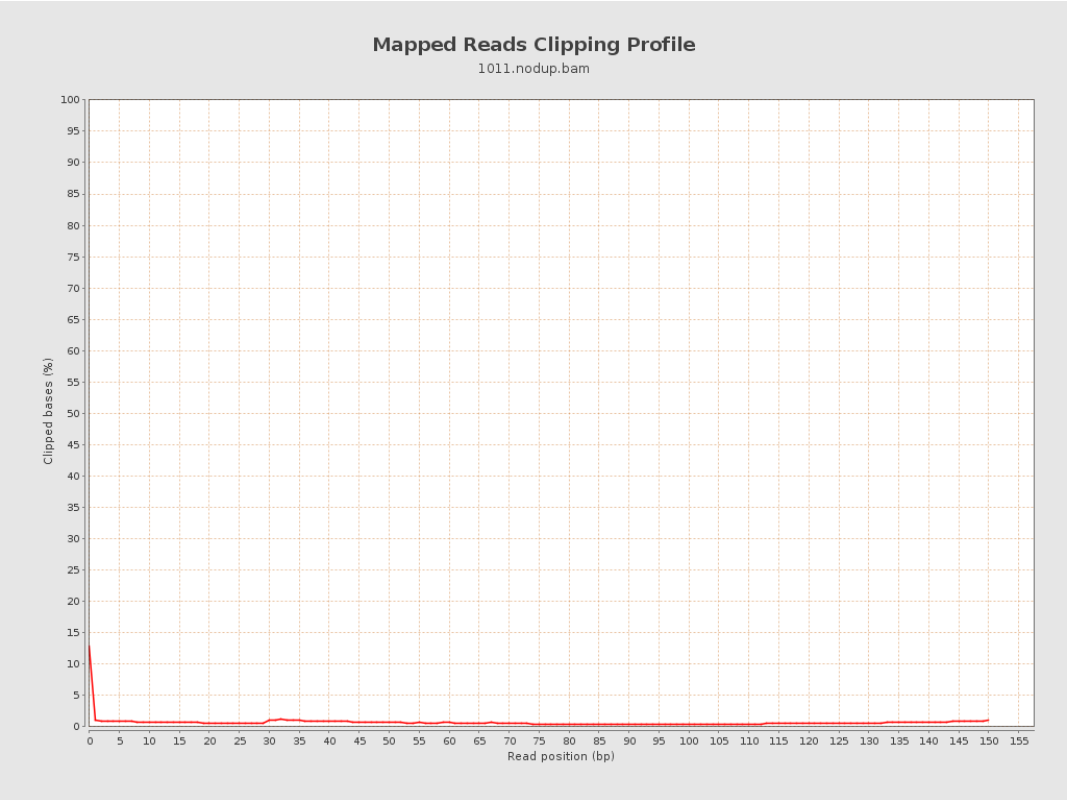
8. Results : Mapped Reads Nucleotide Content



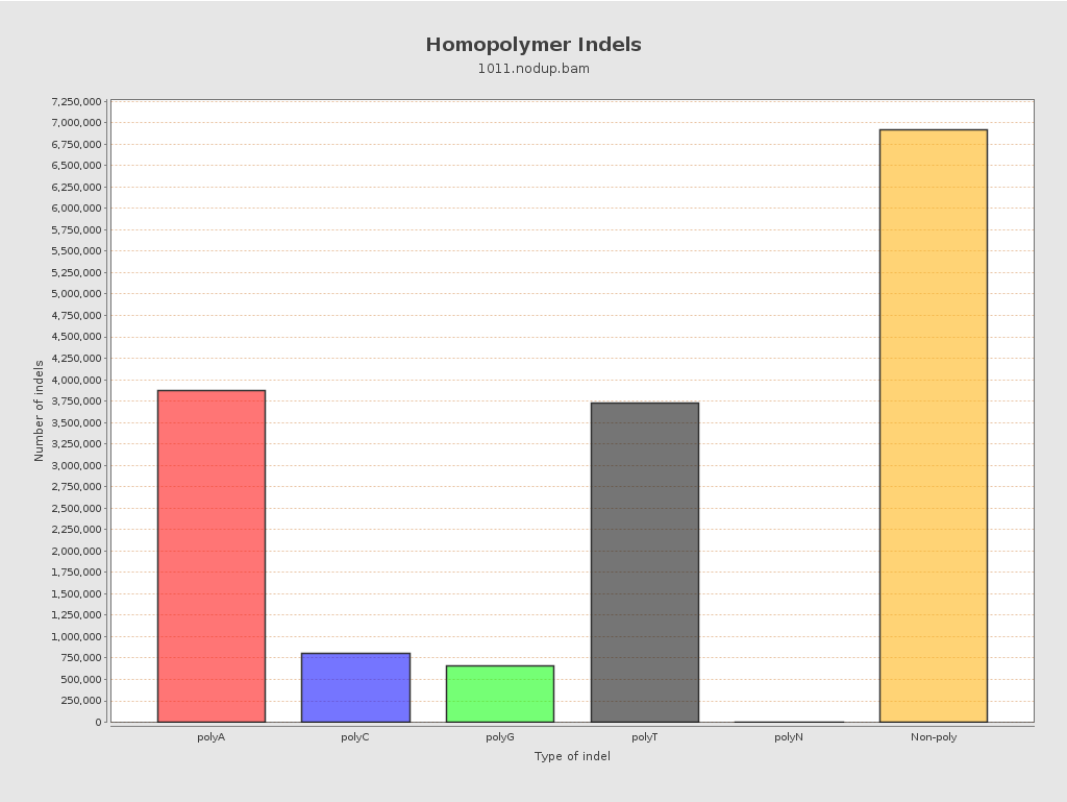
9. Results : Mapped Reads GC-content Distribution



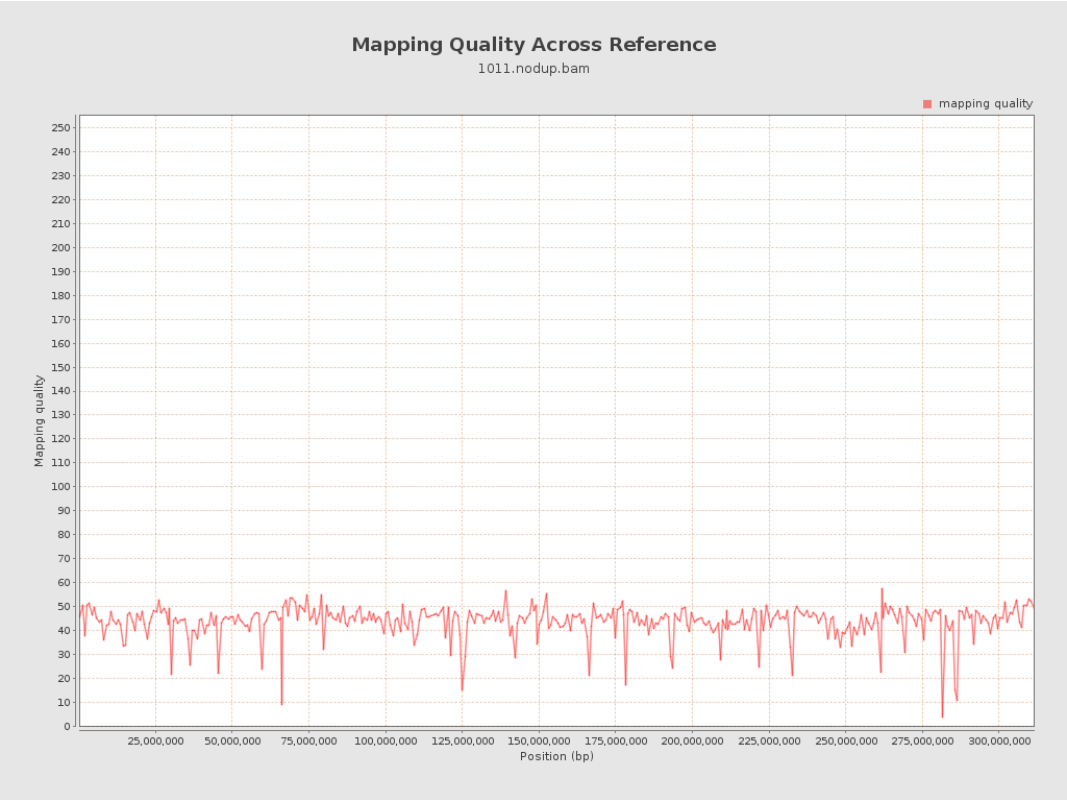
10. Results : Mapped Reads Clipping Profile



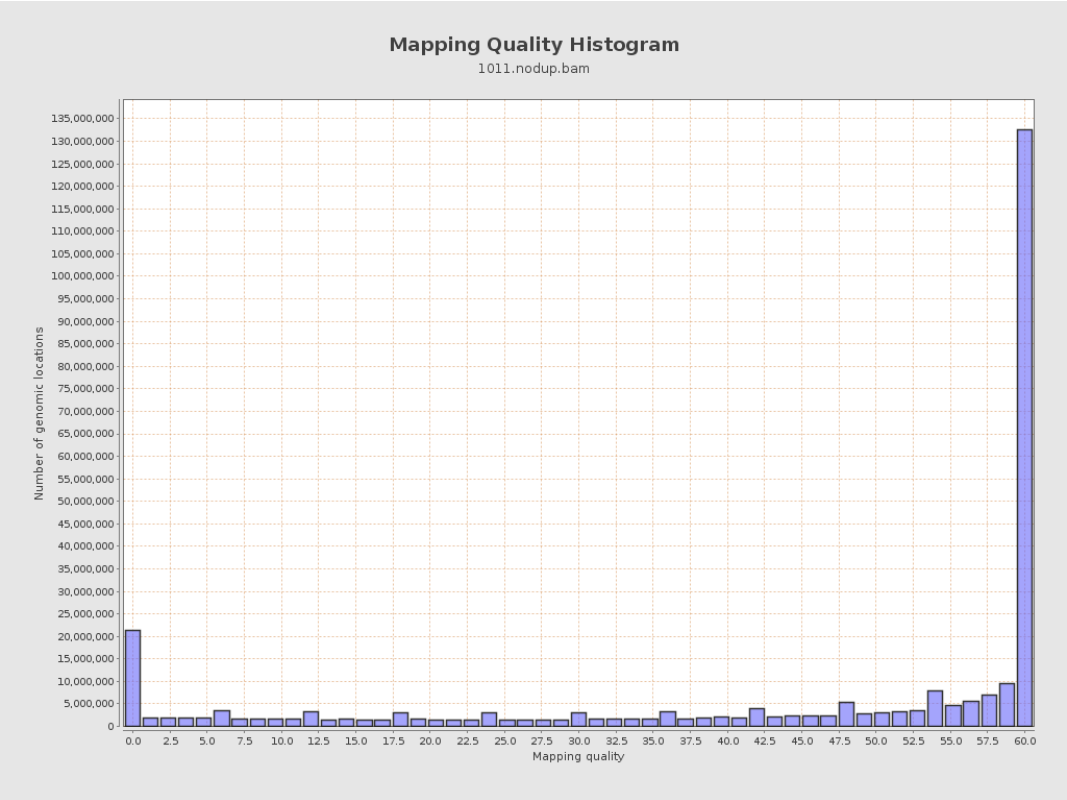
11. Results : Homopolymer Indels



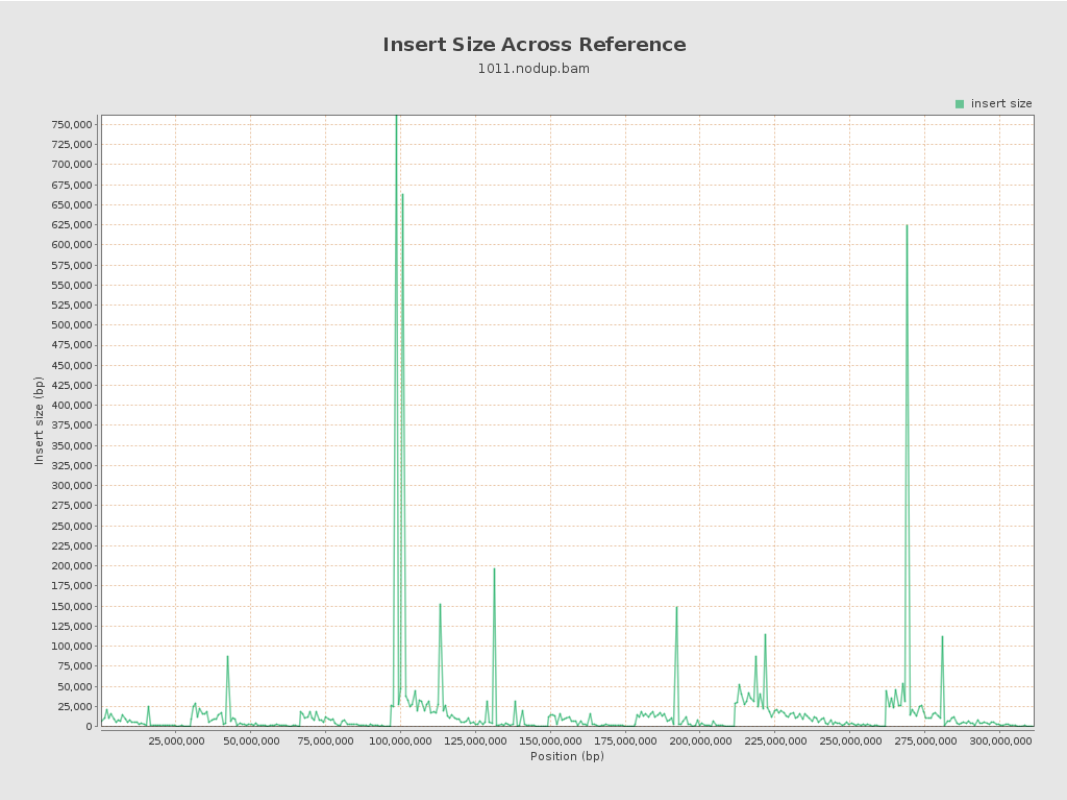
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram