Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1042
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1042 .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_153/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_153_S243_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_153/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_153_S243_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:33:47 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,873,311
Mapped reads	69,981,759 / 92.24%
Unmapped reads	5,891,552 / 7.76%
Mapped paired reads	69,981,759 / 92.24%
Mapped reads, first in pair	35,036,519 / 46.18%
Mapped reads, second in pair	34,945,240 / 46.06%
Mapped reads, both in pair	68,088,525 / 89.74%
Mapped reads, singletons	1,893,234 / 2.5%
Read min/max/mean length	30 / 151 / 147.98
Duplicated reads (flagged)	12,019,363 / 15.84%
Clipped reads	16,547,011 / 21.81%

2.2. ACGT Content

Number/percentage of A's	2,976,067,746 / 30.92%
Number/percentage of C's	1,834,277,402 / 19.06%
Number/percentage of T's	2,978,814,380 / 30.95%
Number/percentage of G's	1,834,379,387 / 19.06%
Number/percentage of N's	39,467 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	30.9644
Standard Deviation	257.9921

2.4. Mapping Quality

Mean Mapping Quality	43.67

2.5. Insert size

Mean	260,096.27
Standard Deviation	2,442,656.73
P25/Median/P75	322 / 424 / 561

2.6. Mismatches and indels

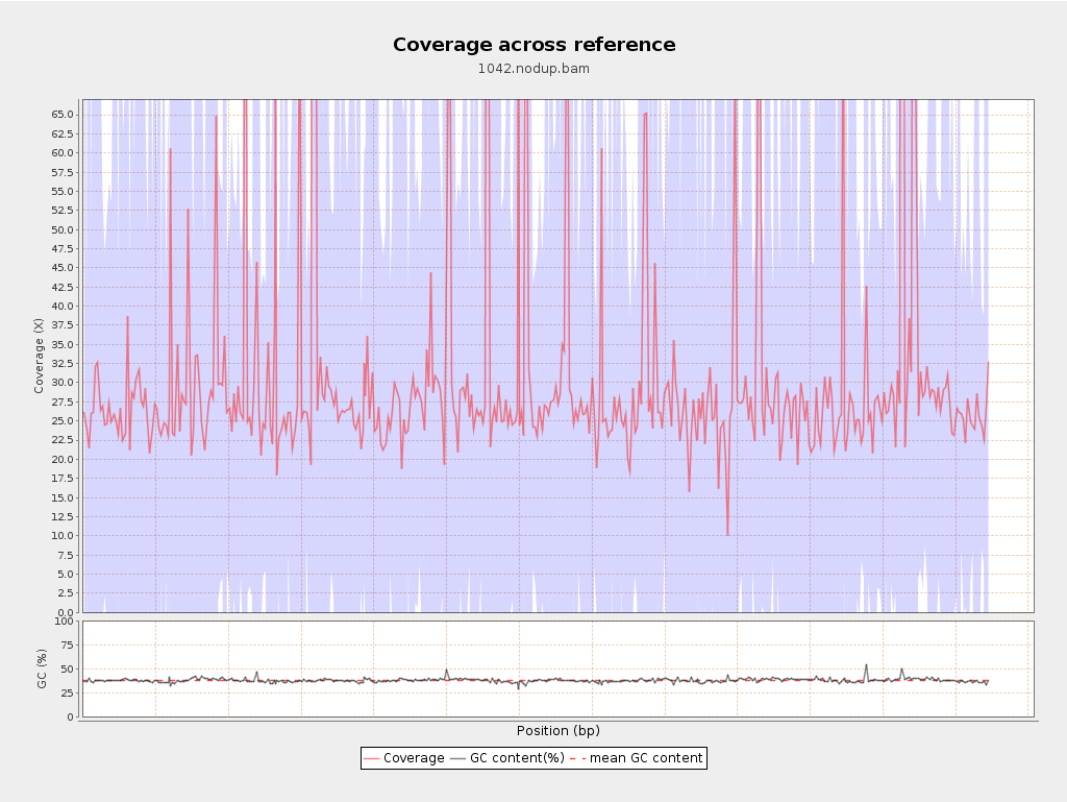
General error rate	2.4%
Mismatches	211,512,745
Insertions	7,037,616
Mapped reads with at least one insertion	8.98%
Deletions	6,955,618
Mapped reads with at least one deletion	8.78%
Homopolymer indels	56.62%

2.7. Chromosome stats

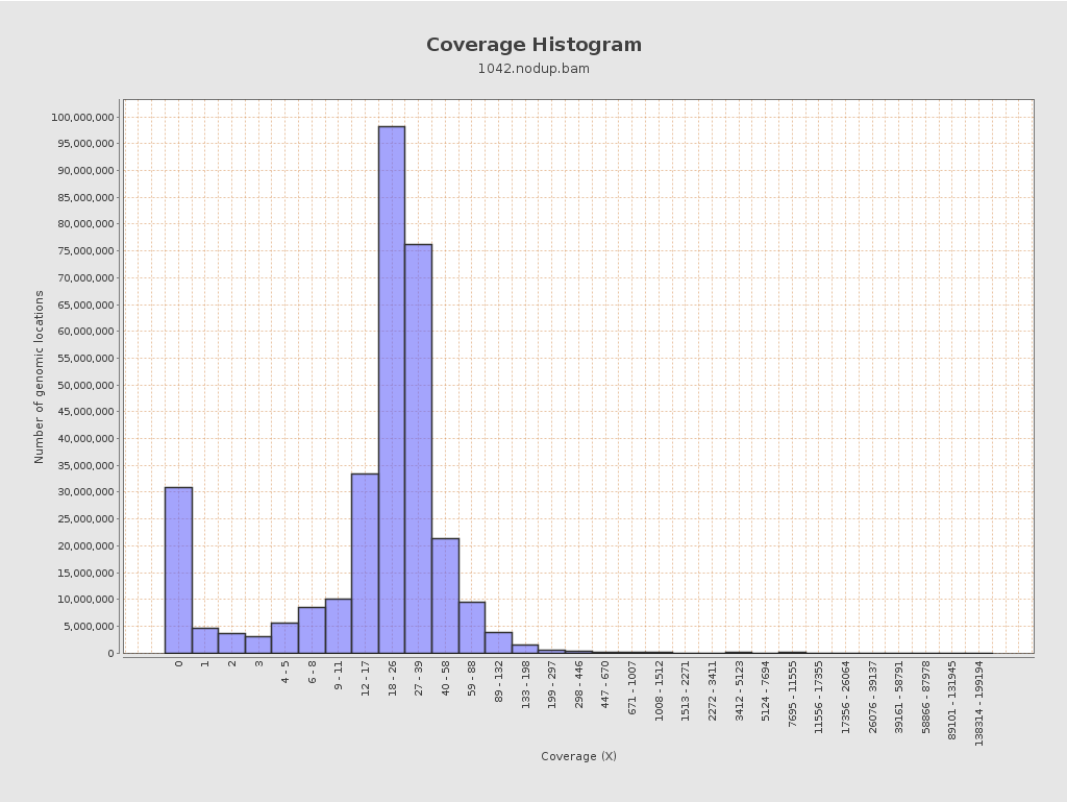
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	778406275	26.1875	105.2716

LT669789.1	36598175	1157531908	31.6281	283.3886
LT669790.1	30422129	1104225360	36.2968	335.5269
LT669791.1	52758100	1584431180	30.032	272.5675
LT669792.1	28376109	889731203	31.3549	261.7278
LT669793.1	33388210	950265848	28.4611	168.1637
LT669794.1	50579949	1467012978	29.0038	230.1048
LT669795.1	49795044	1718198393	34.5054	302.6515

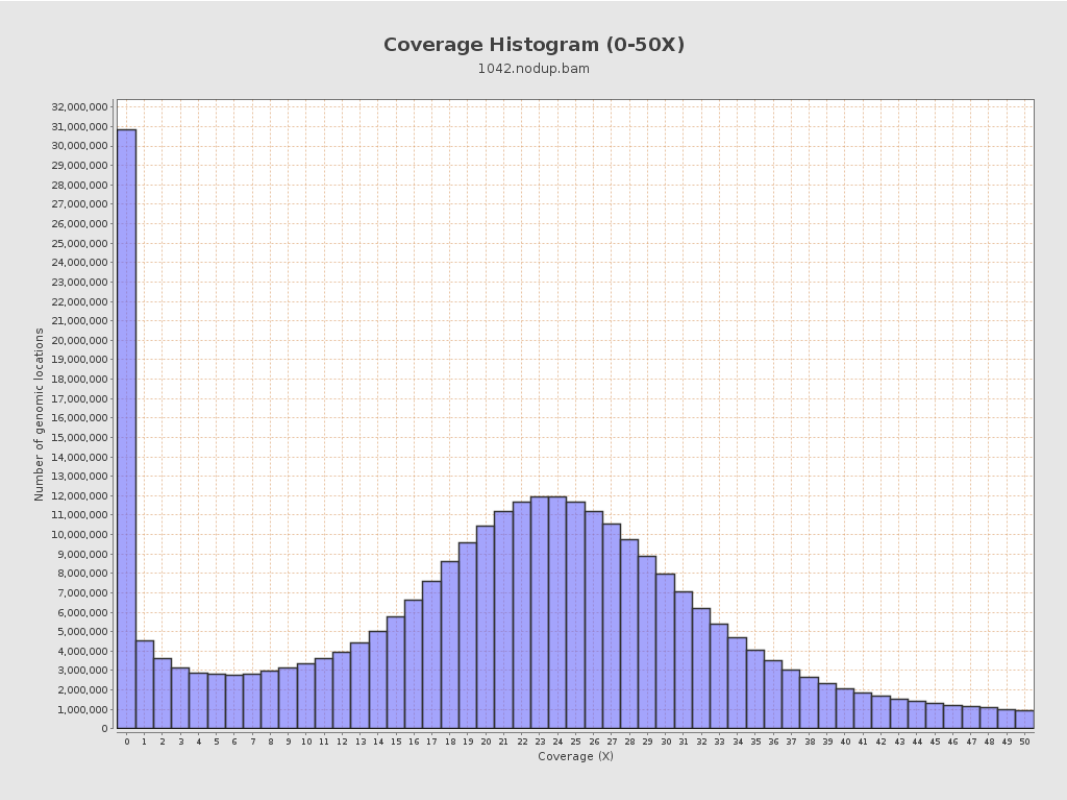
3. Results : Coverage across reference



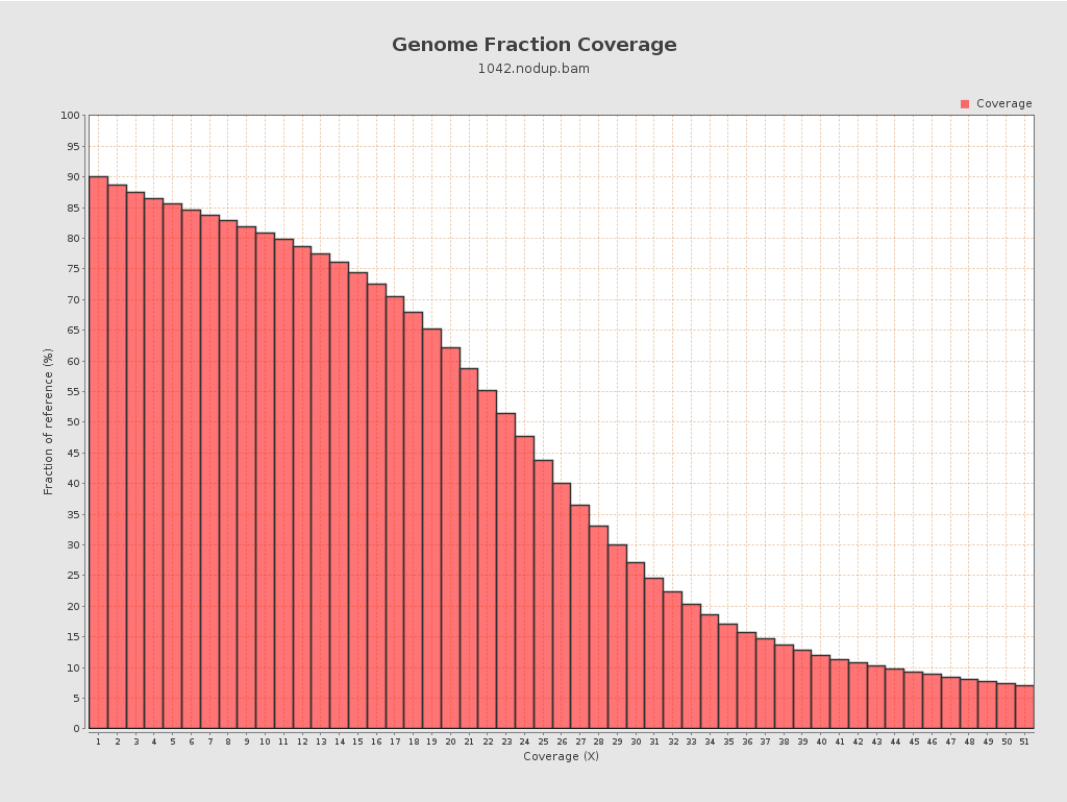
4. Results : Coverage Histogram



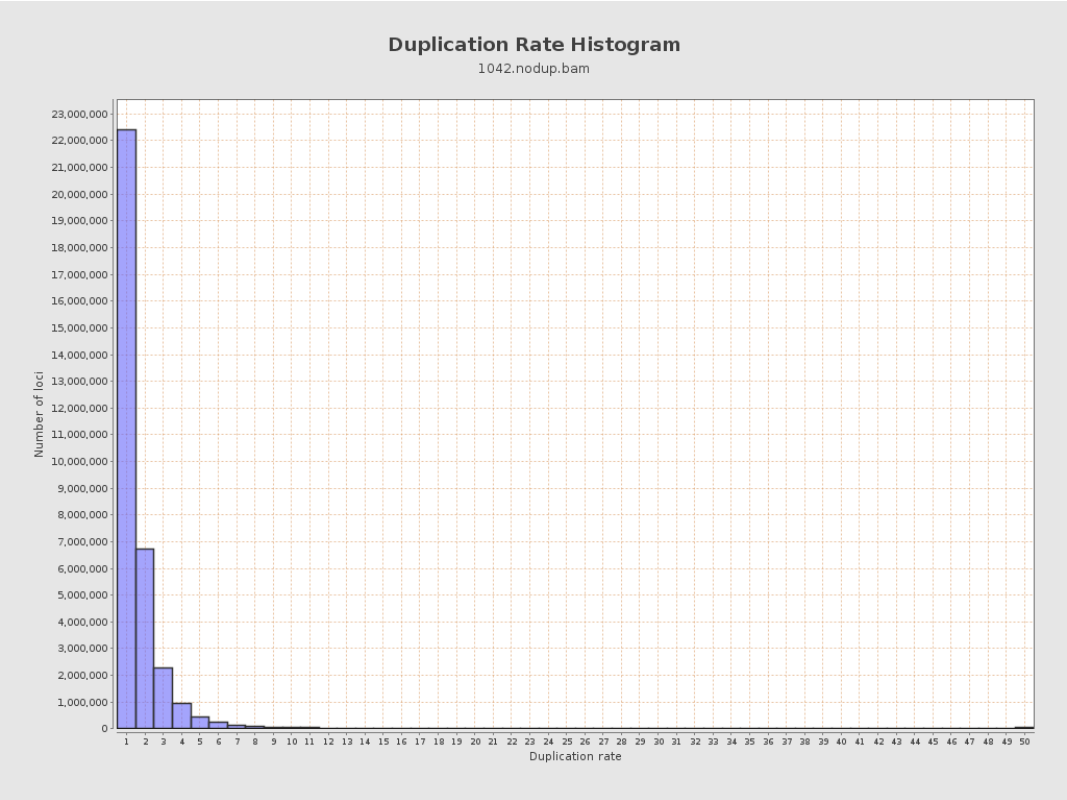
5. Results : Coverage Histogram (0-50X)



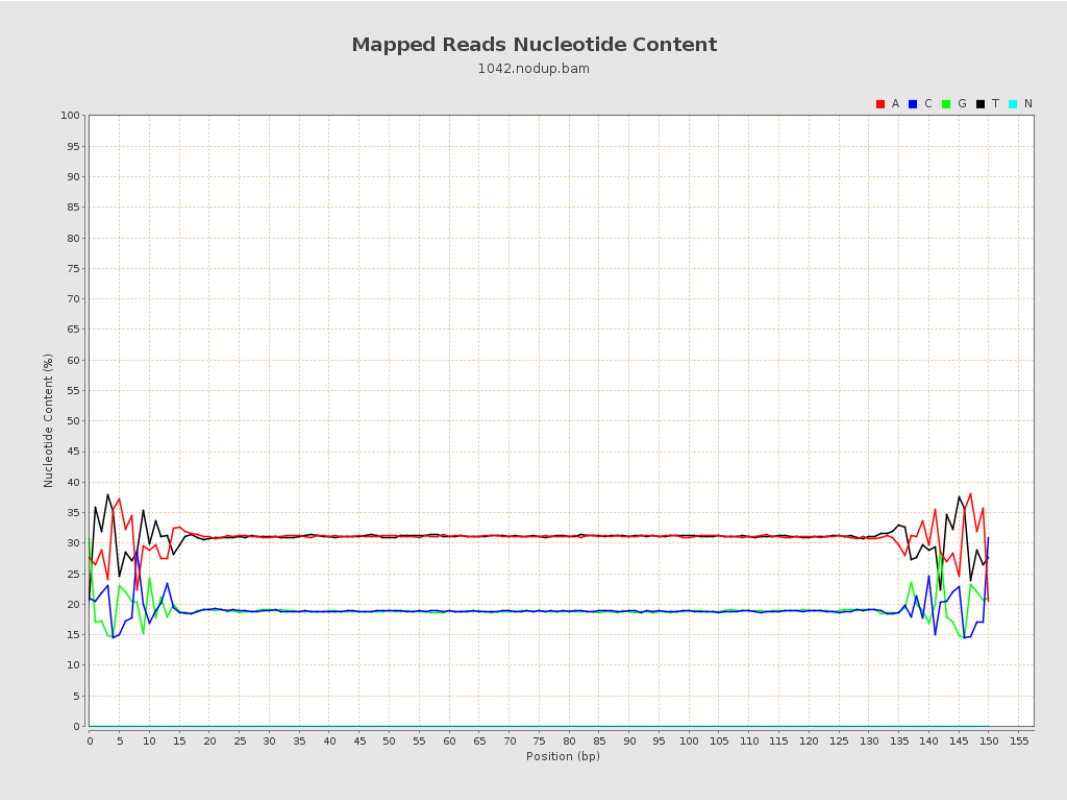
6. Results : Genome Fraction Coverage



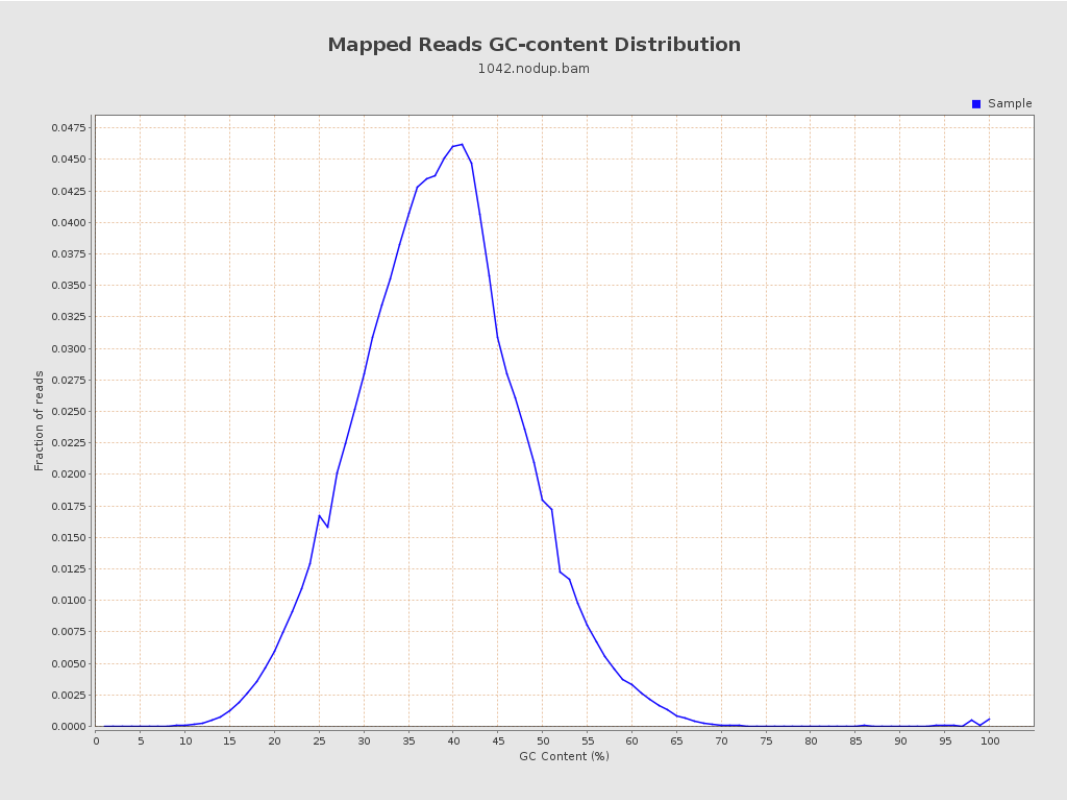
7. Results : Duplication Rate Histogram



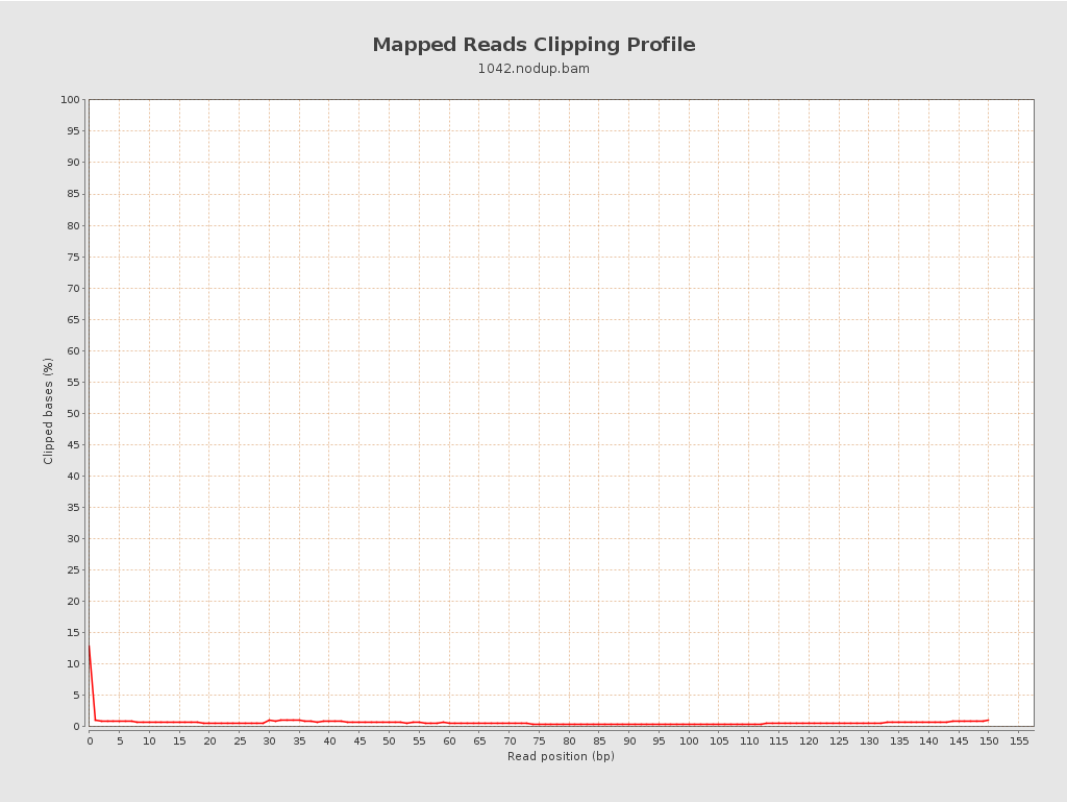
8. Results : Mapped Reads Nucleotide Content



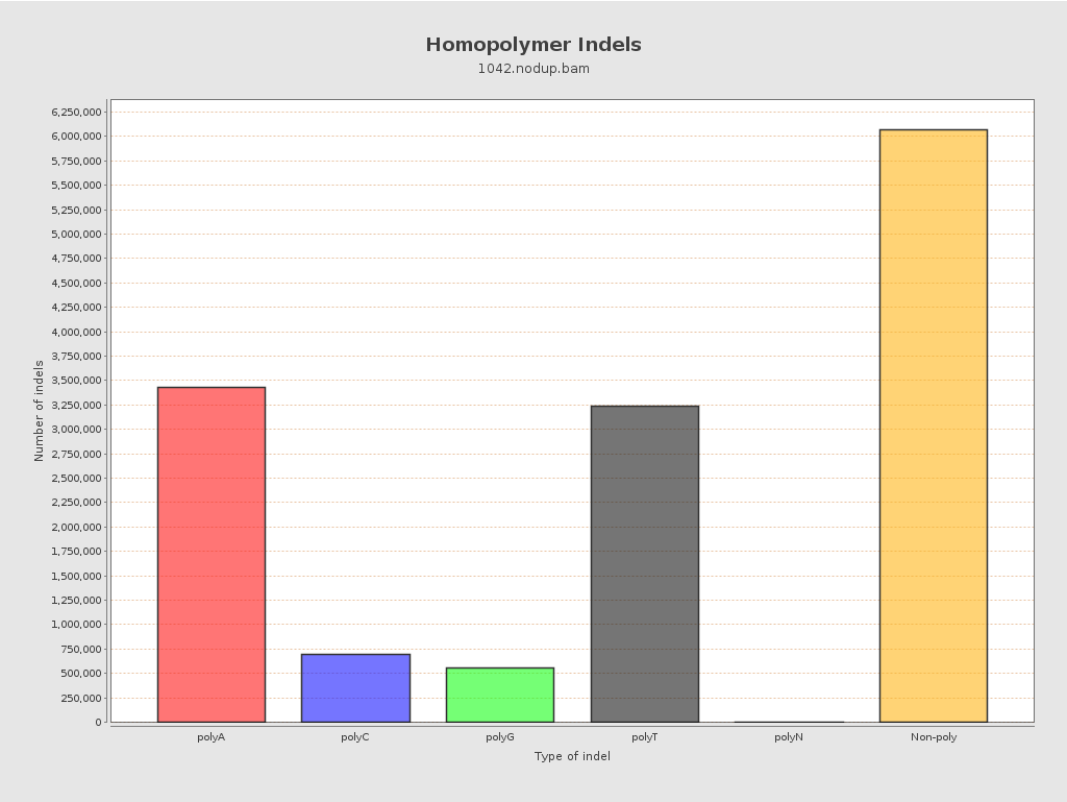
9. Results : Mapped Reads GC-content Distribution



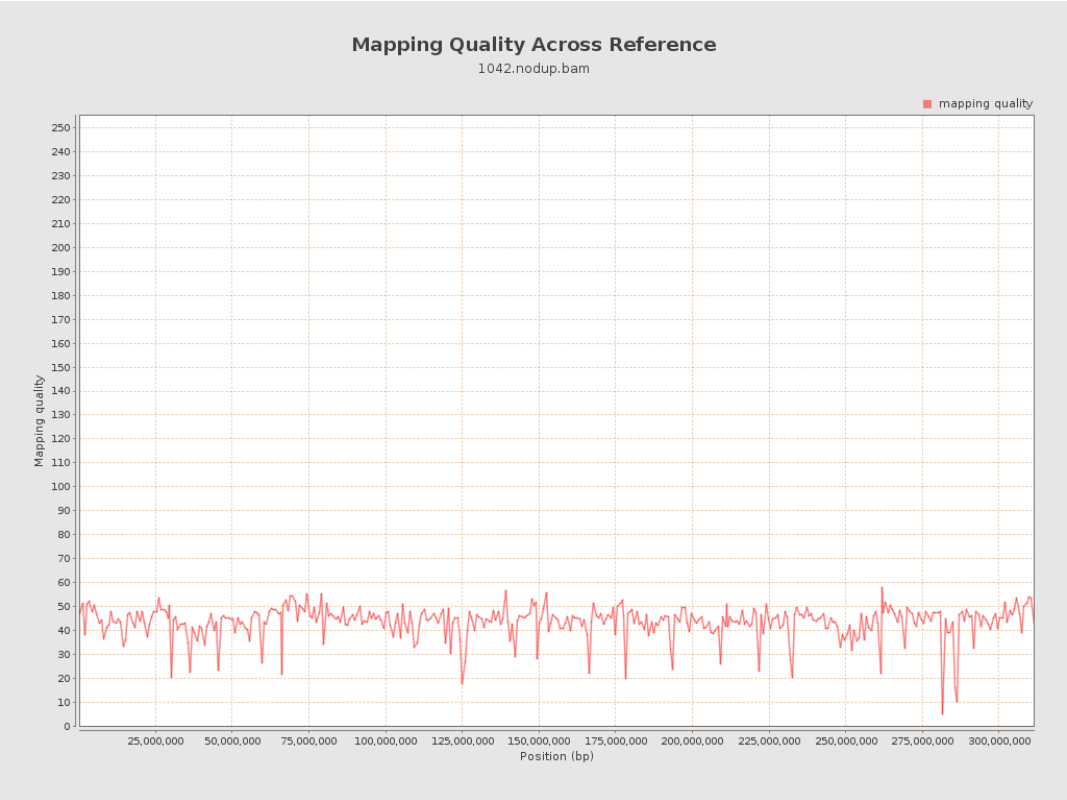
10. Results : Mapped Reads Clipping Profile



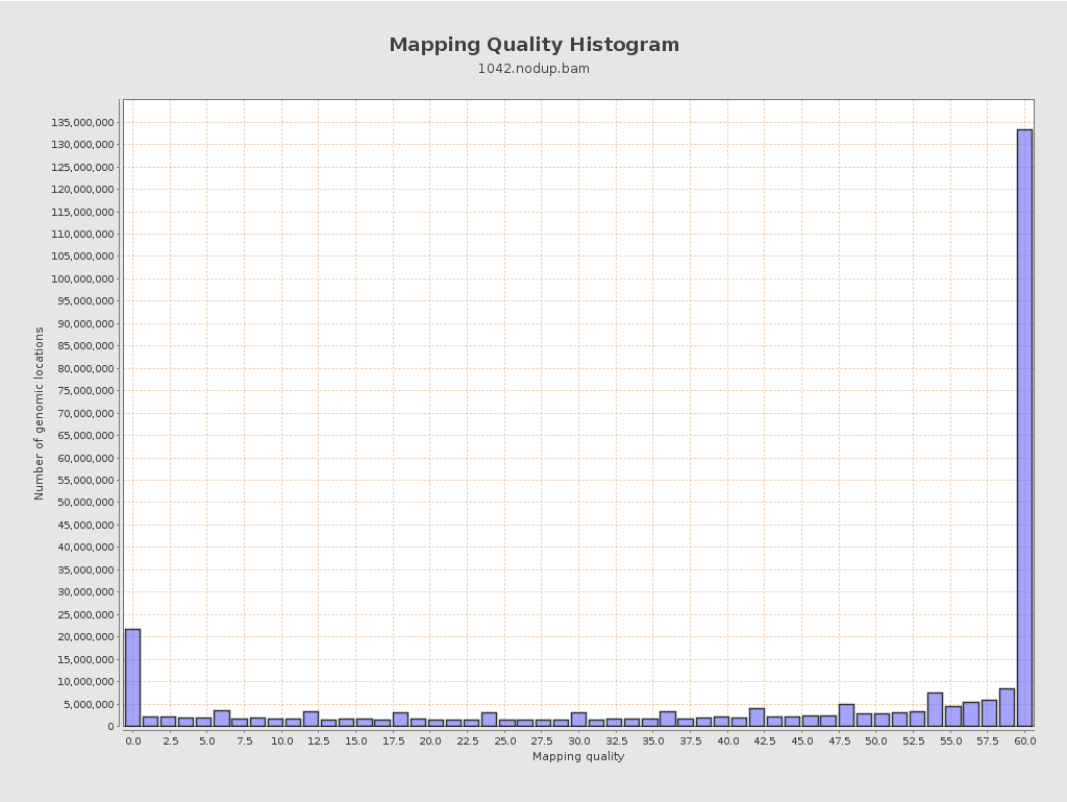
11. Results : Homopolymer Indels



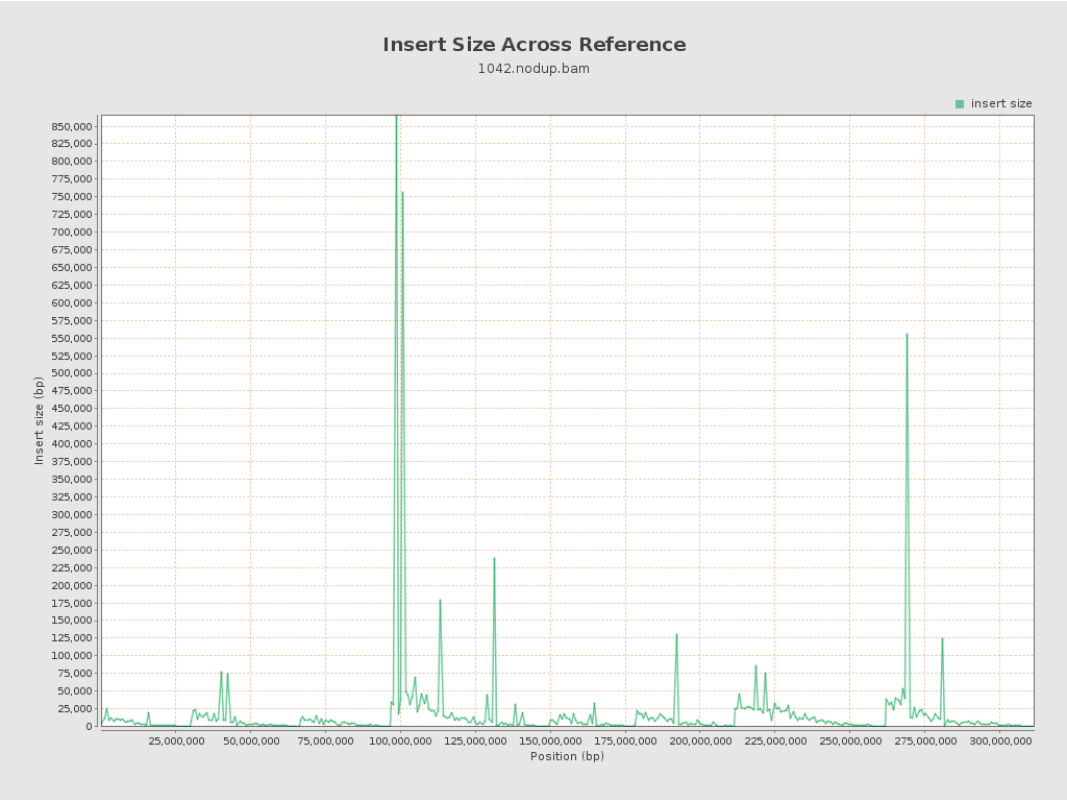
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram