Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1046
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1046 .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_207/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_207_S288_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_207/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_207_S288_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:17 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	62,689,762
Mapped reads	57,443,380 / 91.63%
Unmapped reads	5,246,382 / 8.37%
Mapped paired reads	57,443,380 / 91.63%
Mapped reads, first in pair	28,789,091 / 45.92%
Mapped reads, second in pair	28,654,289 / 45.71%
Mapped reads, both in pair	55,727,224 / 88.89%
Mapped reads, singletons	1,716,156 / 2.74%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	9,210,423 / 14.69%
Clipped reads	13,841,567 / 22.08%

2.2. ACGT Content

Number/percentage of A's	2,431,117,281 / 30.89%
Number/percentage of C's	1,503,712,927 / 19.1%
Number/percentage of T's	2,432,791,424 / 30.91%
Number/percentage of G's	1,503,436,184 / 19.1%
Number/percentage of N's	28,489 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	25.3221
Standard Deviation	227.3602

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Insert size

Mean	258,024.43
Standard Deviation	2,440,501.48
P25/Median/P75	325 / 427 / 559

2.6. Mismatches and indels

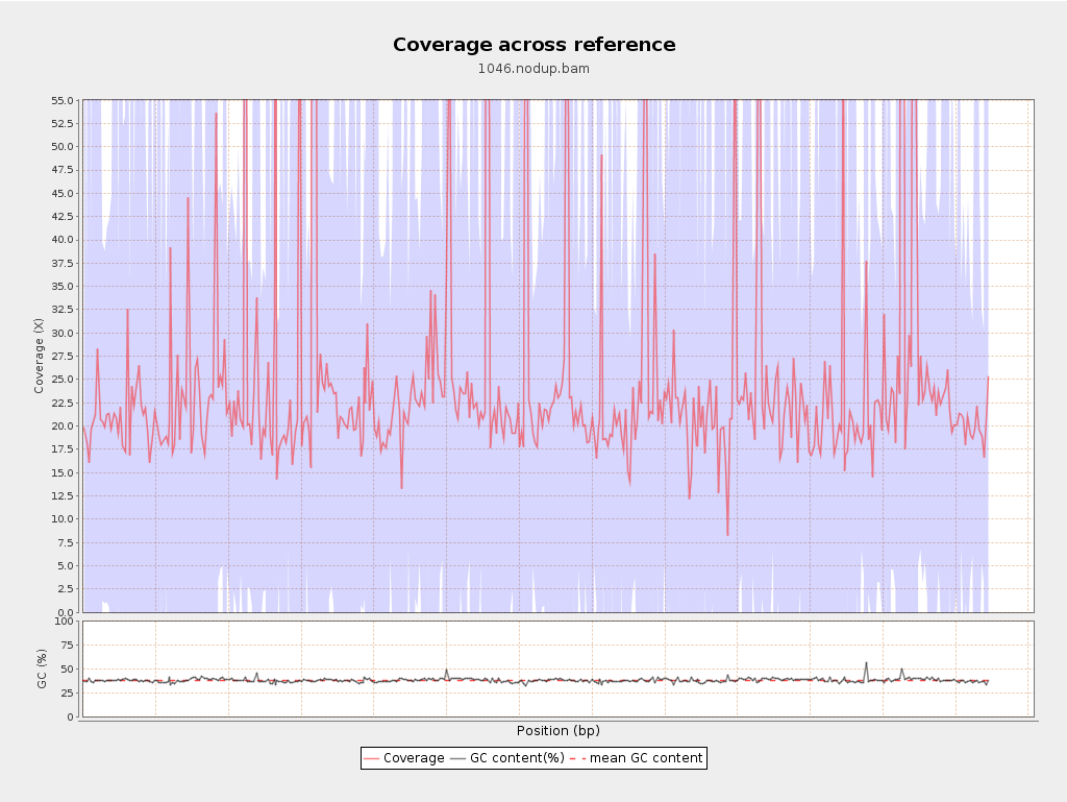
General error rate	2.36%
Mismatches	170,312,511
Insertions	5,648,020
Mapped reads with at least one insertion	8.78%
Deletions	5,457,150
Mapped reads with at least one deletion	8.41%
Homopolymer indels	57.14%

2.7. Chromosome stats

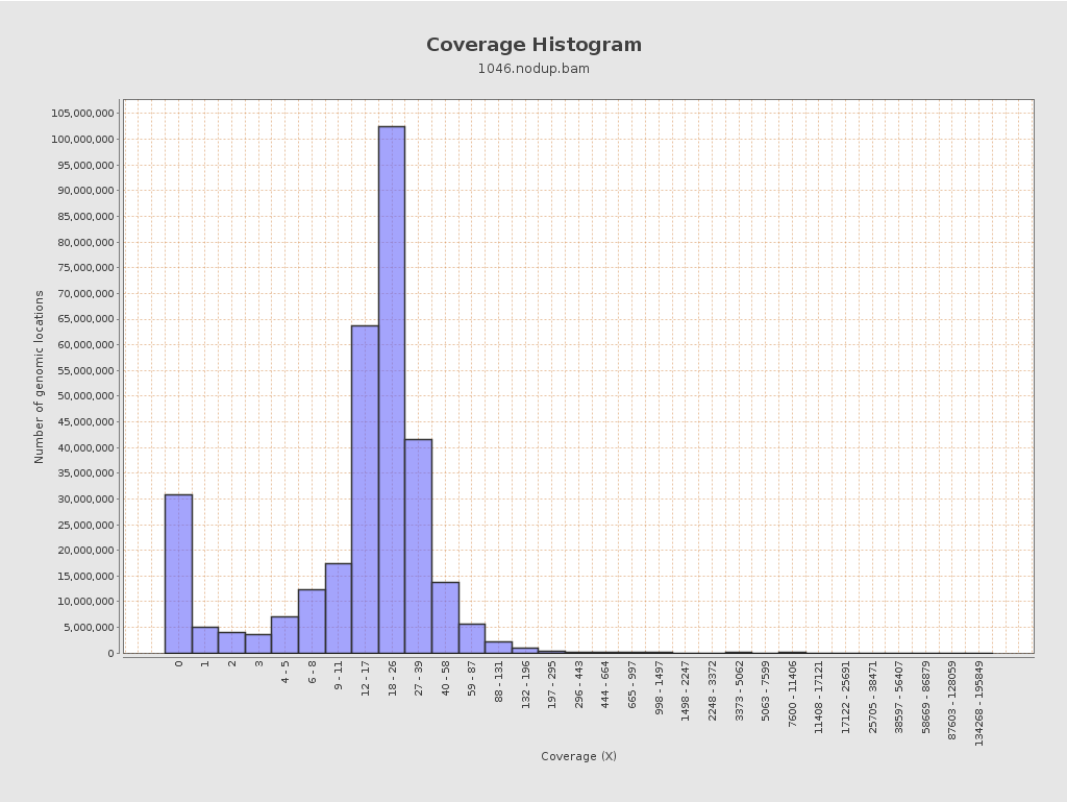
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	615465043	20.7058	85.3441

LT669789.1	36598175	941210285	25.7174	239.3422
LT669790.1	30422129	920494323	30.2574	312.2578
LT669791.1	52758100	1320167611	25.023	236.5075
LT669792.1	28376109	715211731	25.2047	237.2885
LT669793.1	33388210	779306530	23.3408	149.9059
LT669794.1	50579949	1194683935	23.6197	182.6114
LT669795.1	49795044	1404877346	28.2132	277.7856

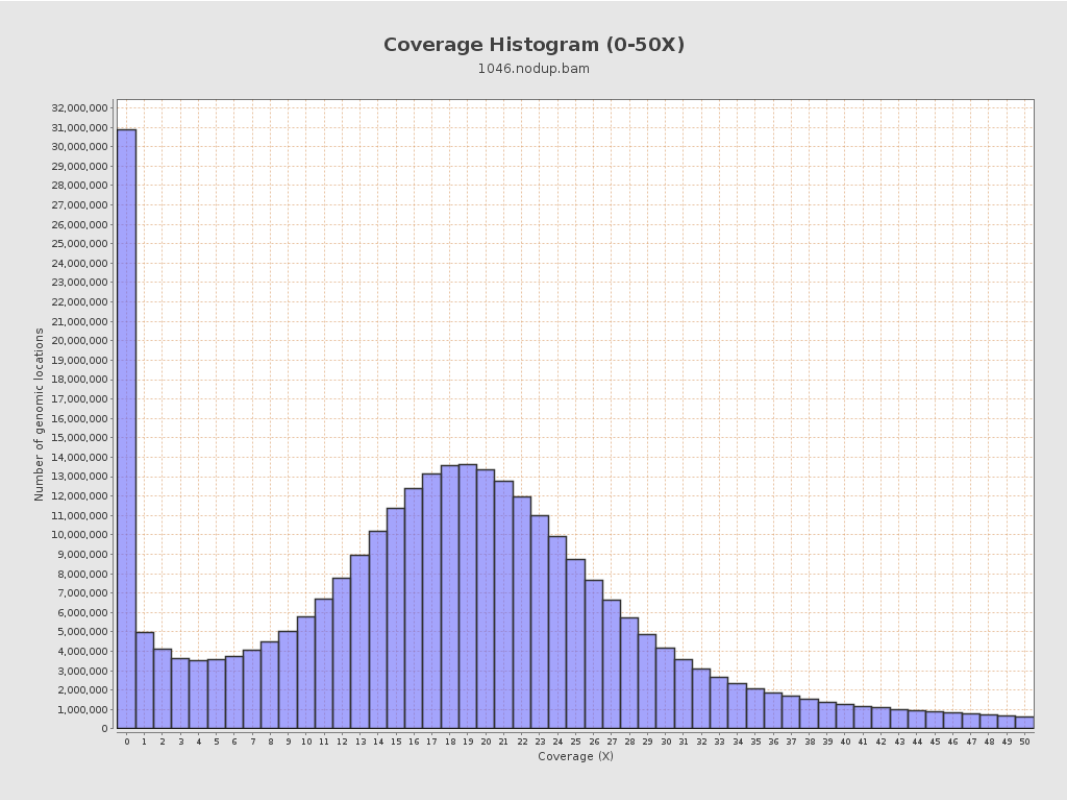
3. Results : Coverage across reference



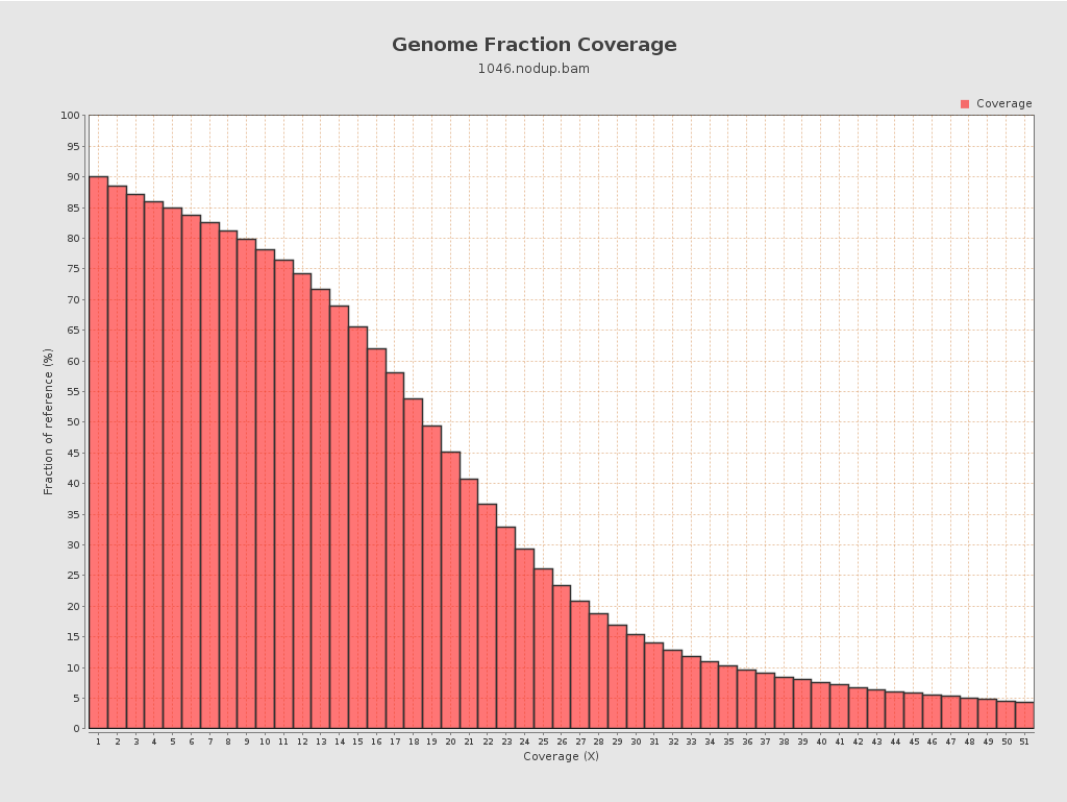
4. Results : Coverage Histogram



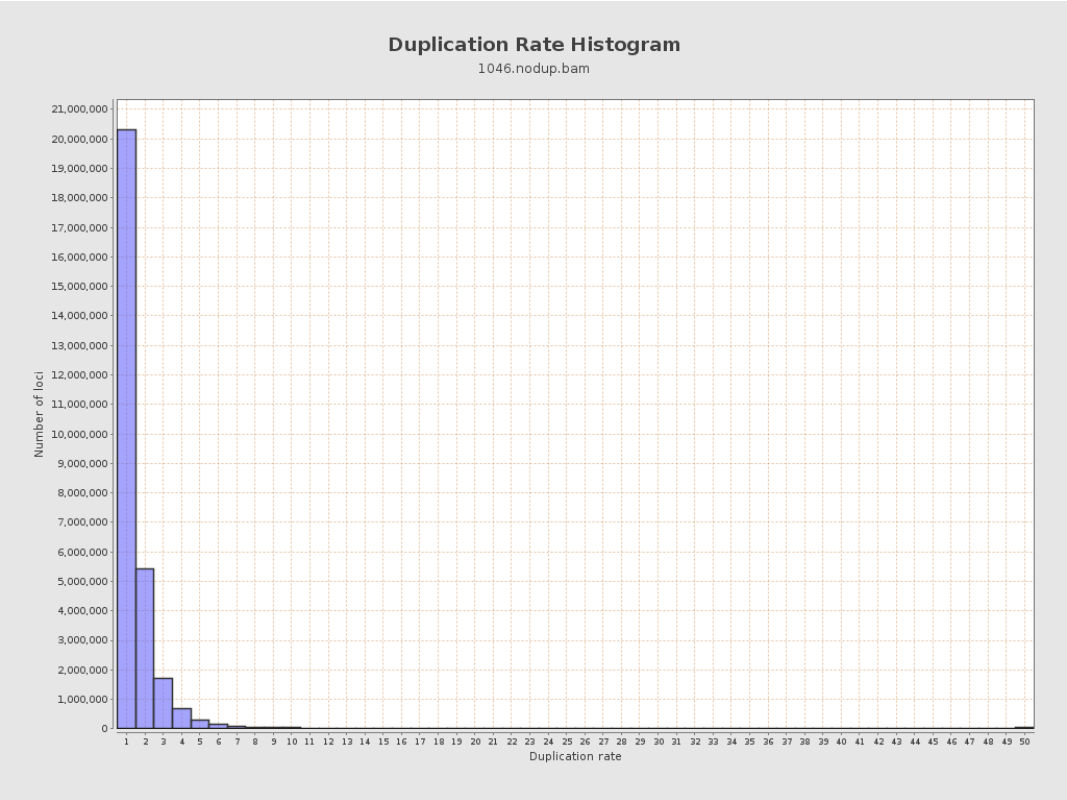
5. Results : Coverage Histogram (0-50X)



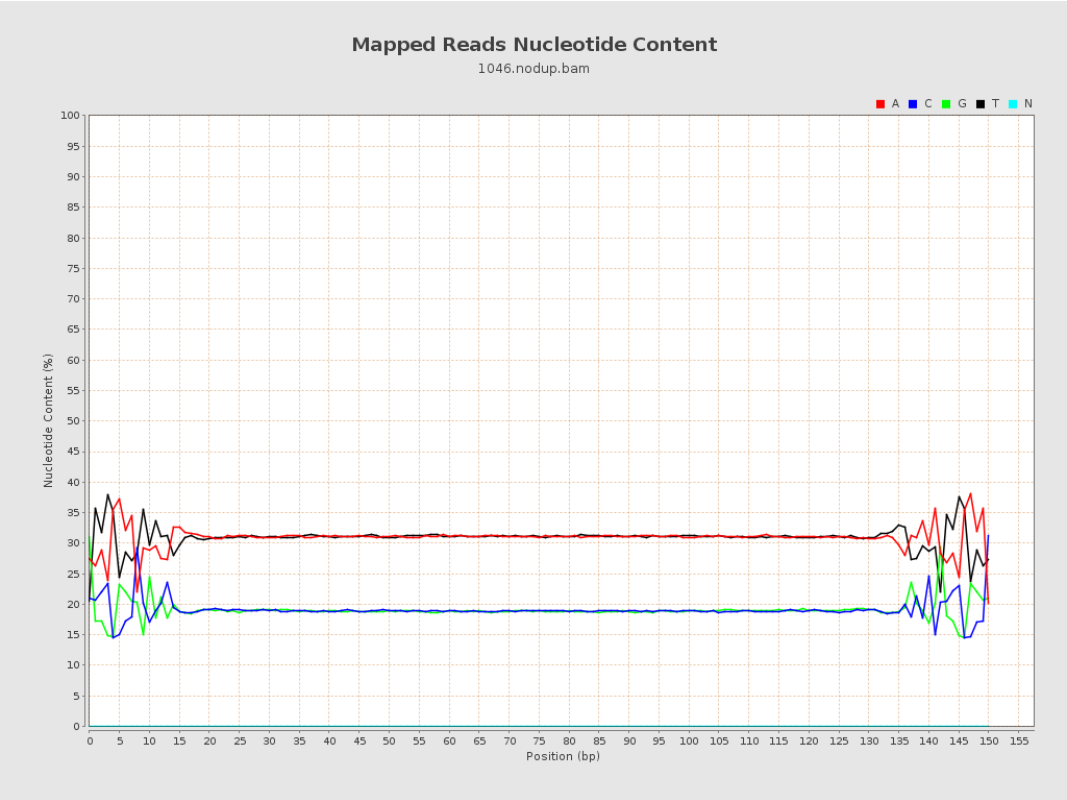
6. Results : Genome Fraction Coverage



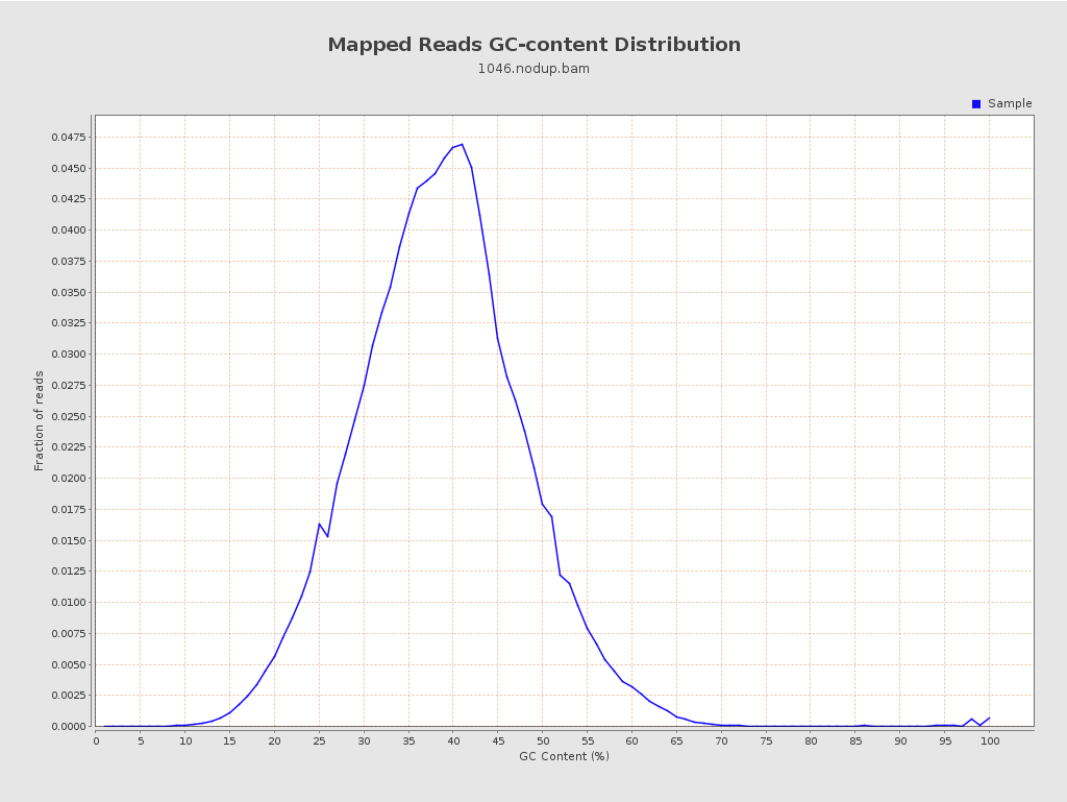
7. Results : Duplication Rate Histogram



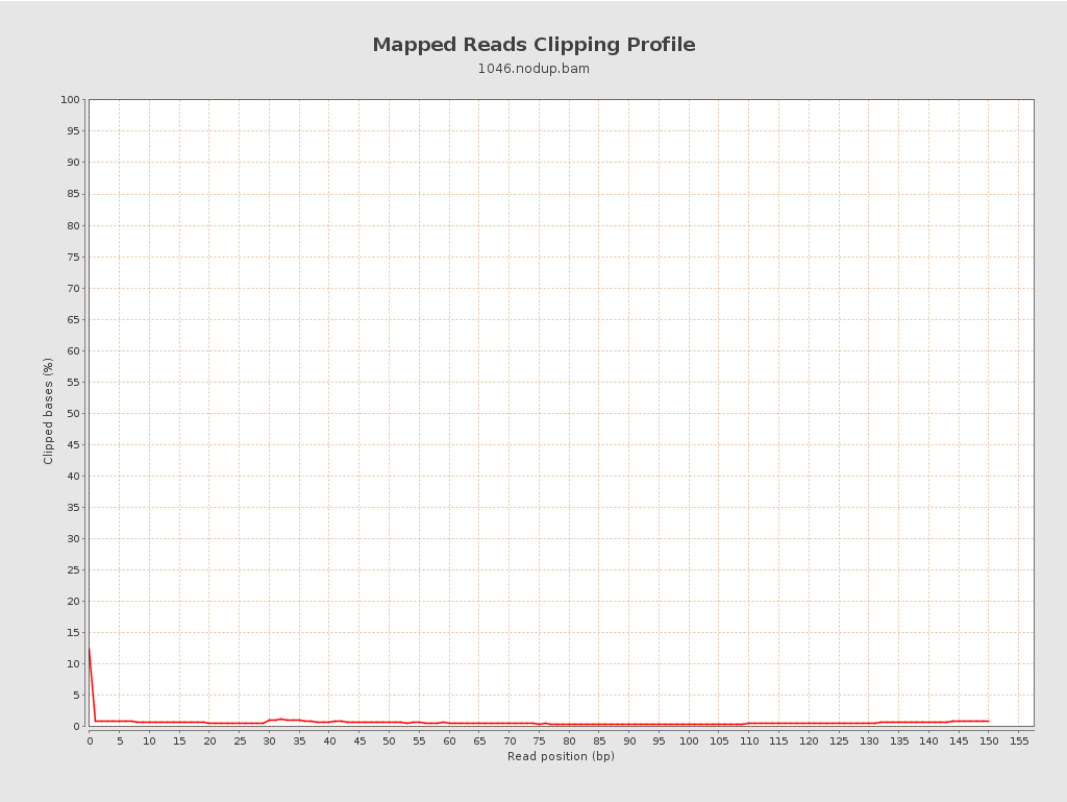
8. Results : Mapped Reads Nucleotide Content



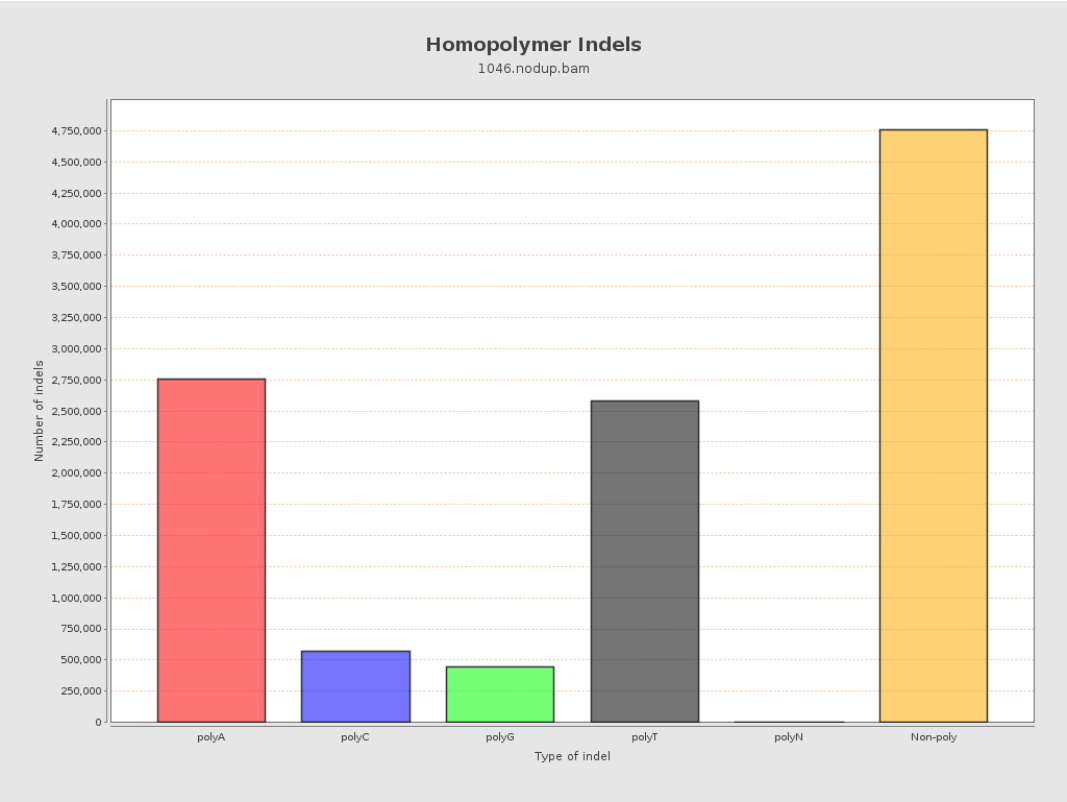
9. Results : Mapped Reads GC-content Distribution



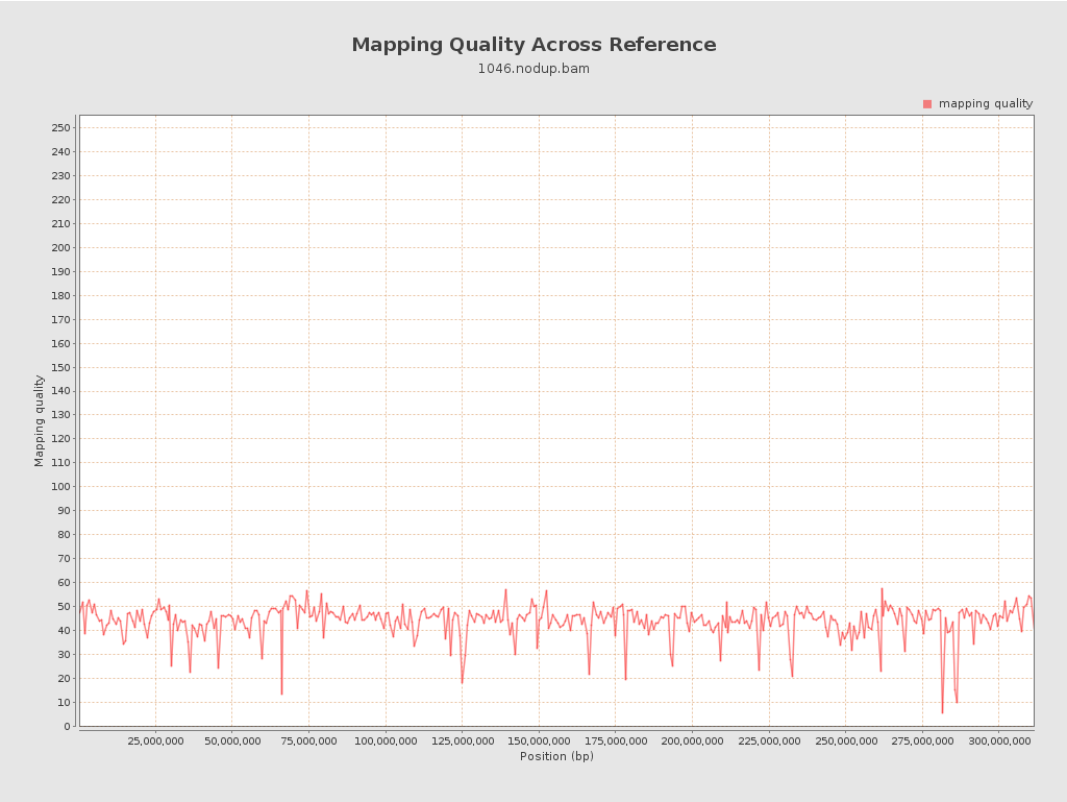
10. Results : Mapped Reads Clipping Profile



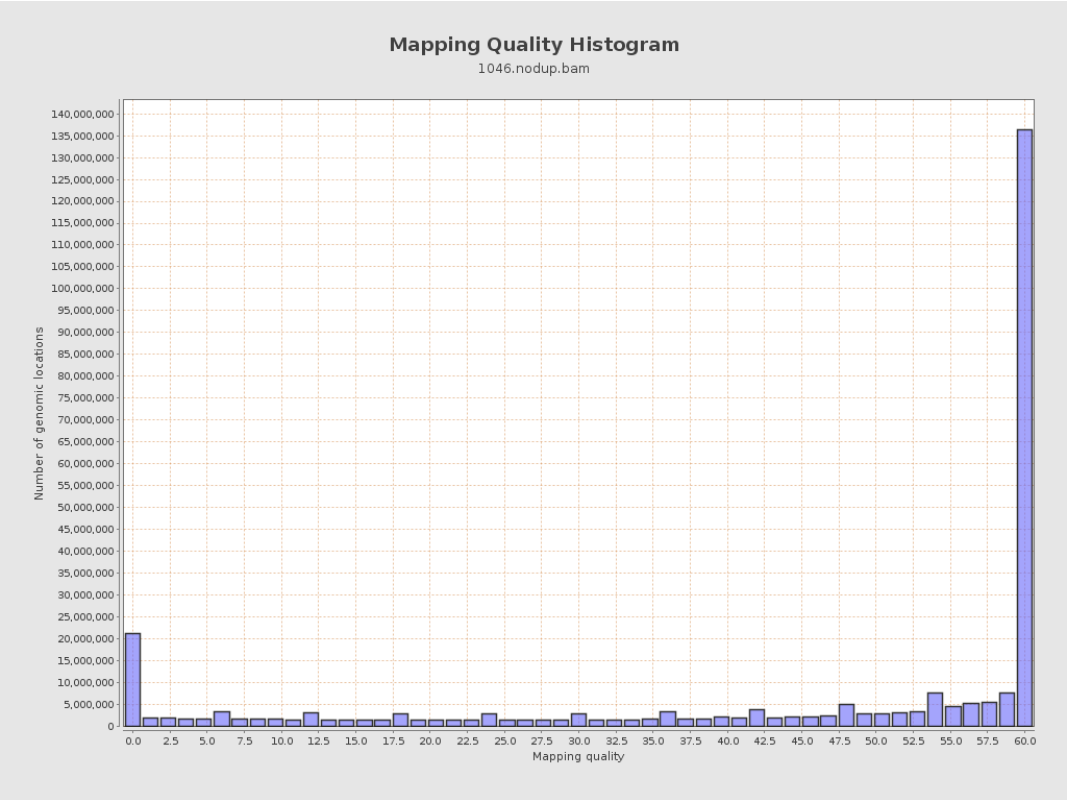
11. Results : Homopolymer Indels



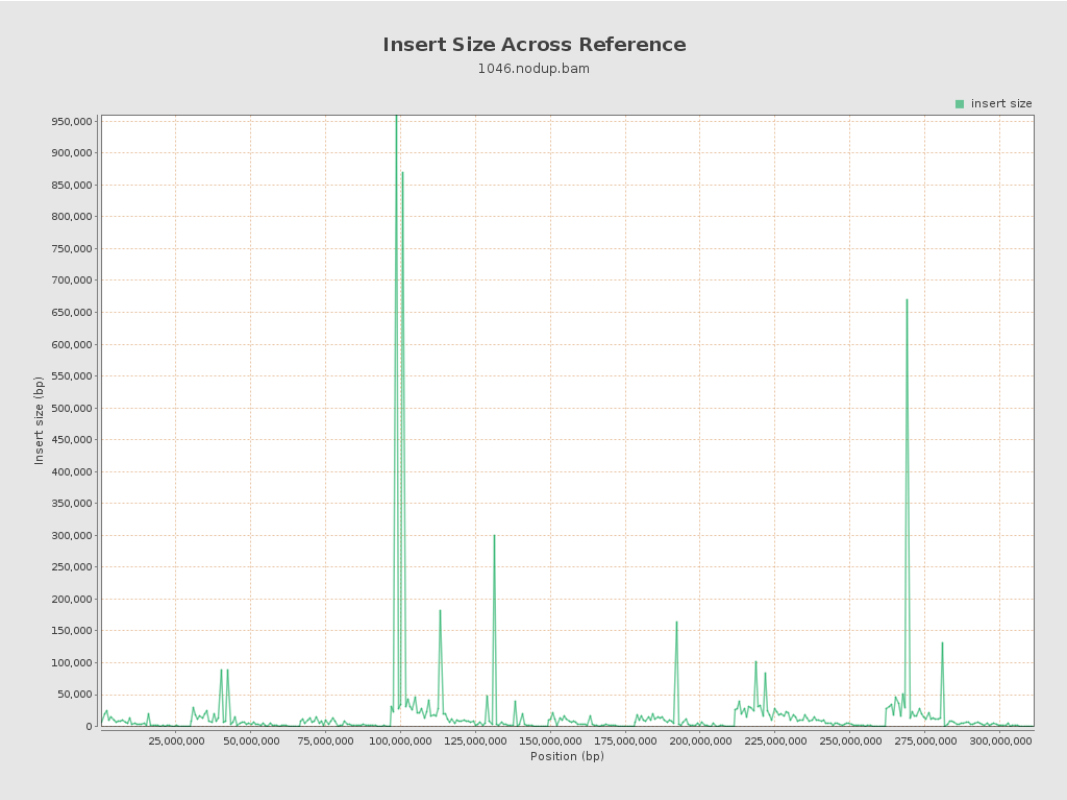
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram