Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1044
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1044 .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_110/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_110_S200_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_110/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_110_S200_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:34:57 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,216,496
Mapped reads	74,472,082 / 92.84%
Unmapped reads	5,744,414 / 7.16%
Mapped paired reads	74,472,082 / 92.84%
Mapped reads, first in pair	37,298,080 / 46.5%
Mapped reads, second in pair	37,174,002 / 46.34%
Mapped reads, both in pair	72,598,935 / 90.5%
Mapped reads, singletons	1,873,147 / 2.34%
Read min/max/mean length	30 / 151 / 148.35
Duplicated reads (flagged)	13,398,965 / 16.7%
Clipped reads	15,764,276 / 19.65%

2.2. ACGT Content

Number/percentage of A's	3,205,244,744 / 30.96%
Number/percentage of C's	1,973,028,847 / 19.06%
Number/percentage of T's	3,207,537,034 / 30.98%
Number/percentage of G's	1,967,396,768 / 19%
Number/percentage of N's	43,852 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	33.3032
Standard Deviation	256.818

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Insert size

Mean	230,262.79
Standard Deviation	2,304,755.5
P25/Median/P75	339 / 441 / 574

2.6. Mismatches and indels

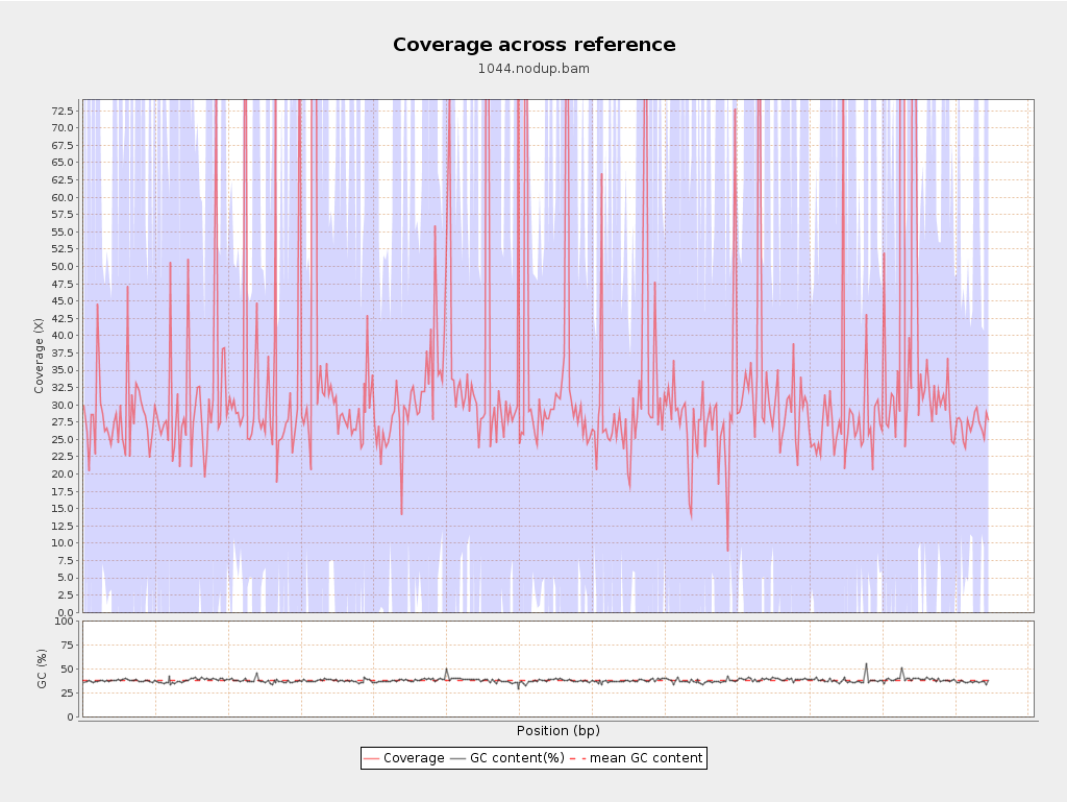
General error rate	2.19%
Mismatches	207,683,181
Insertions	6,889,209
Mapped reads with at least one insertion	8.28%
Deletions	6,768,839
Mapped reads with at least one deletion	8.08%
Homopolymer indels	57.44%

2.7. Chromosome stats

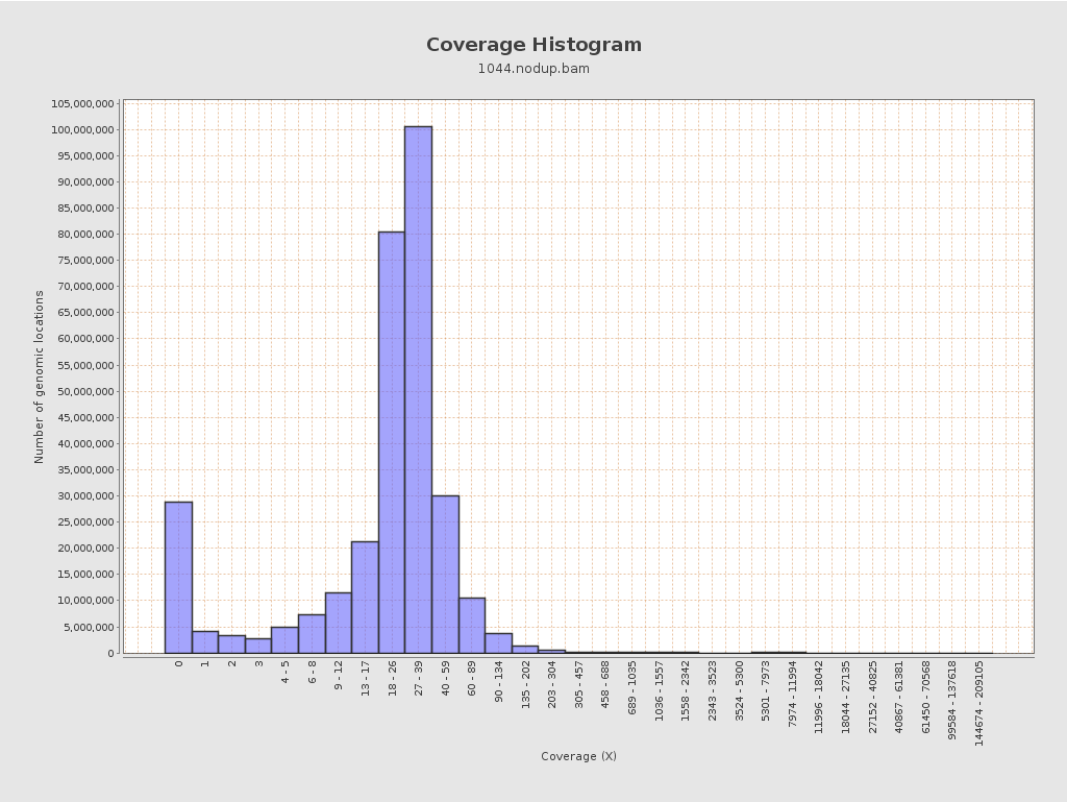
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	837226172	28.1663	88.3368

LT669789.1	36598175	1186390072	32.4166	257.7894
LT669790.1	30422129	1177714170	38.7124	338.1385
LT669791.1	52758100	1741431841	33.0079	248.3845
LT669792.1	28376109	946238107	33.3463	272.1327
LT669793.1	33388210	1017615537	30.4783	181.9642
LT669794.1	50579949	1555374286	30.7508	210.7314
LT669795.1	49795044	1916698176	38.4917	338.3446

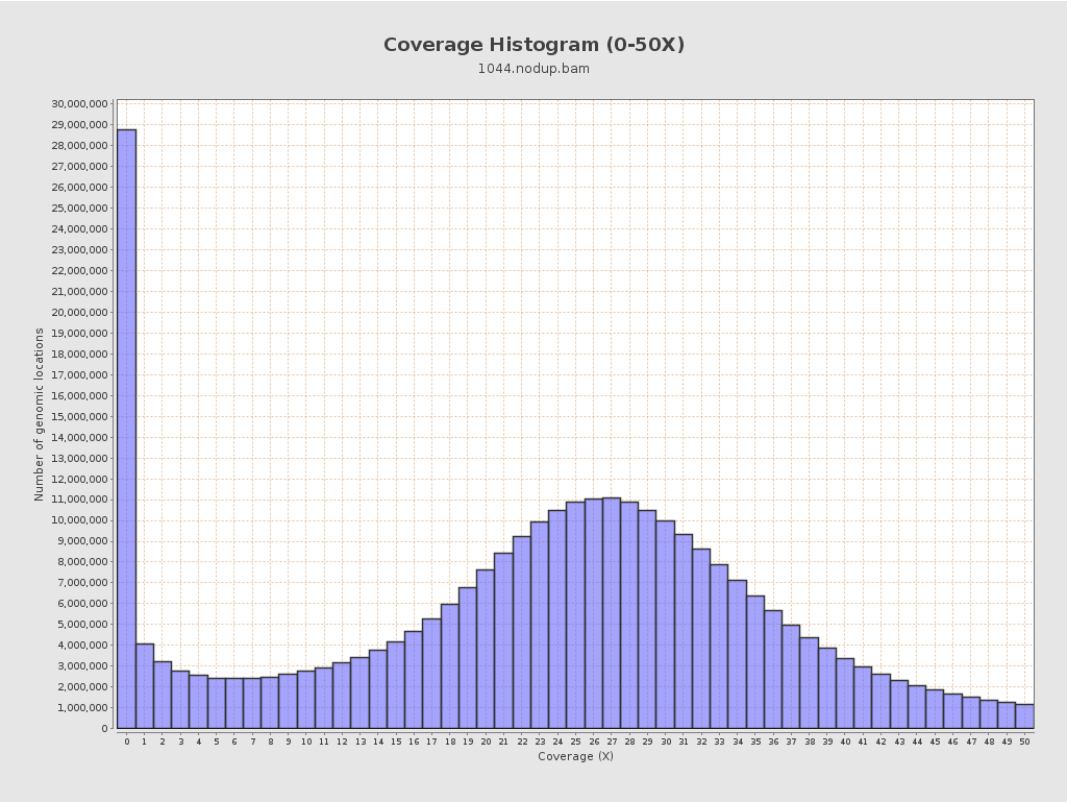
3. Results : Coverage across reference



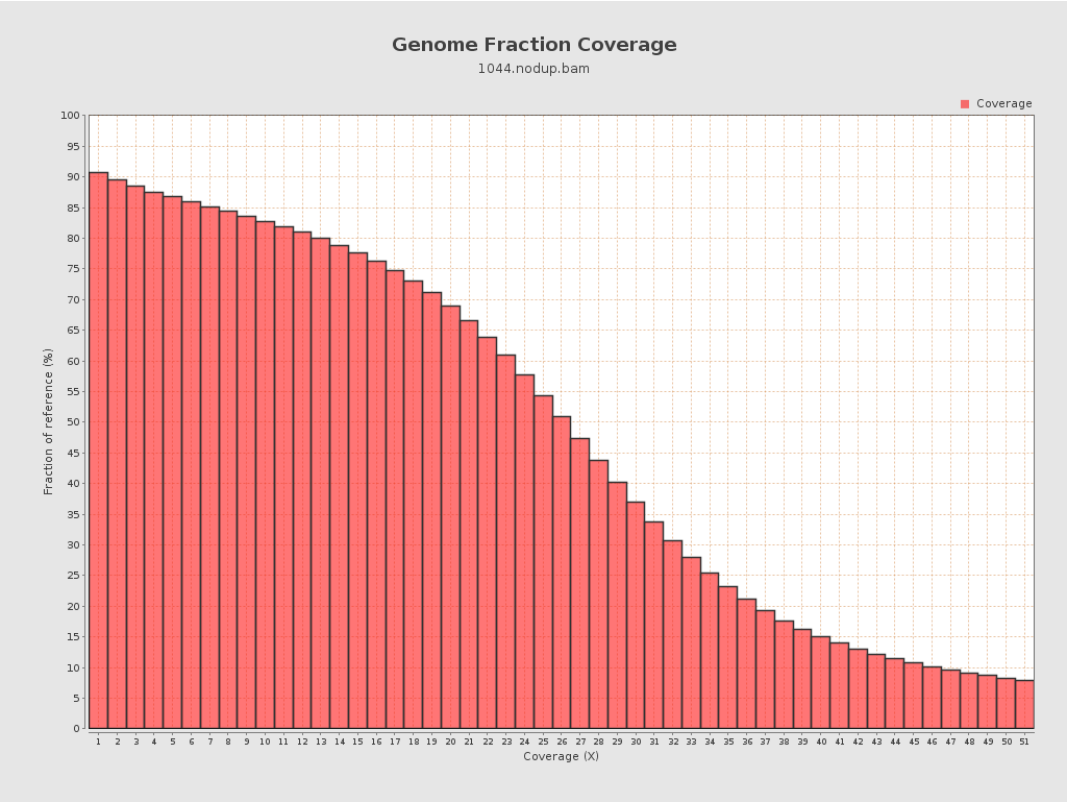
4. Results : Coverage Histogram



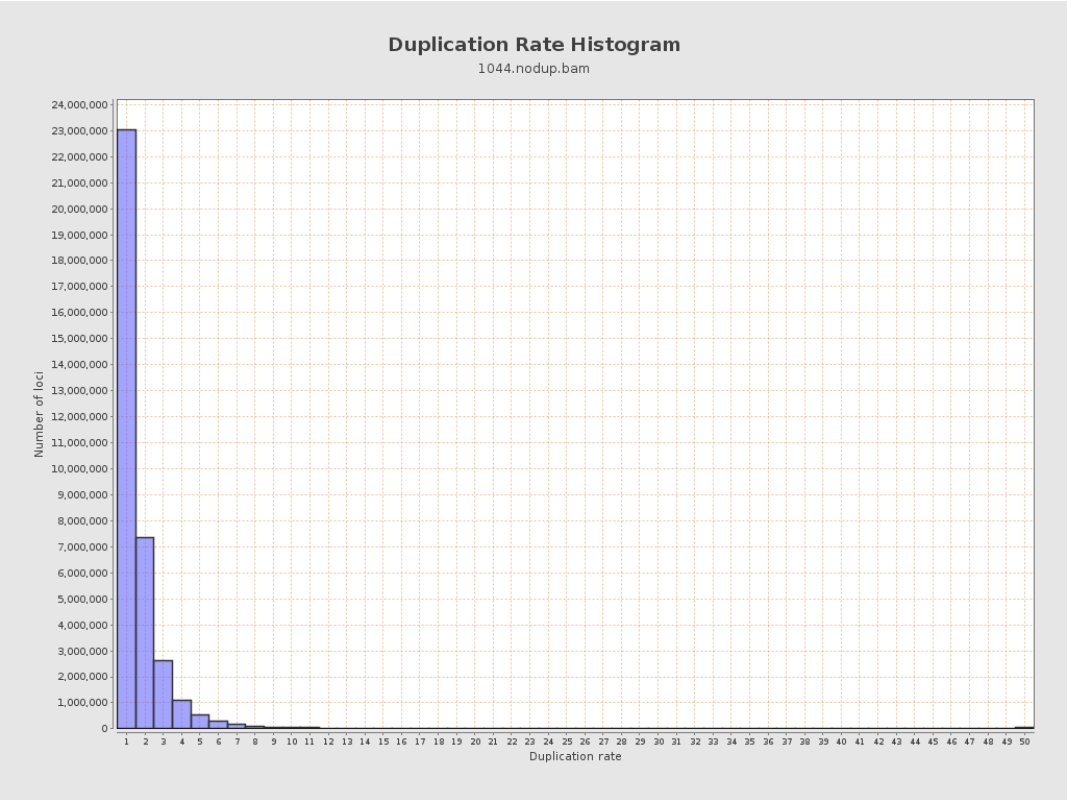
5. Results : Coverage Histogram (0-50X)



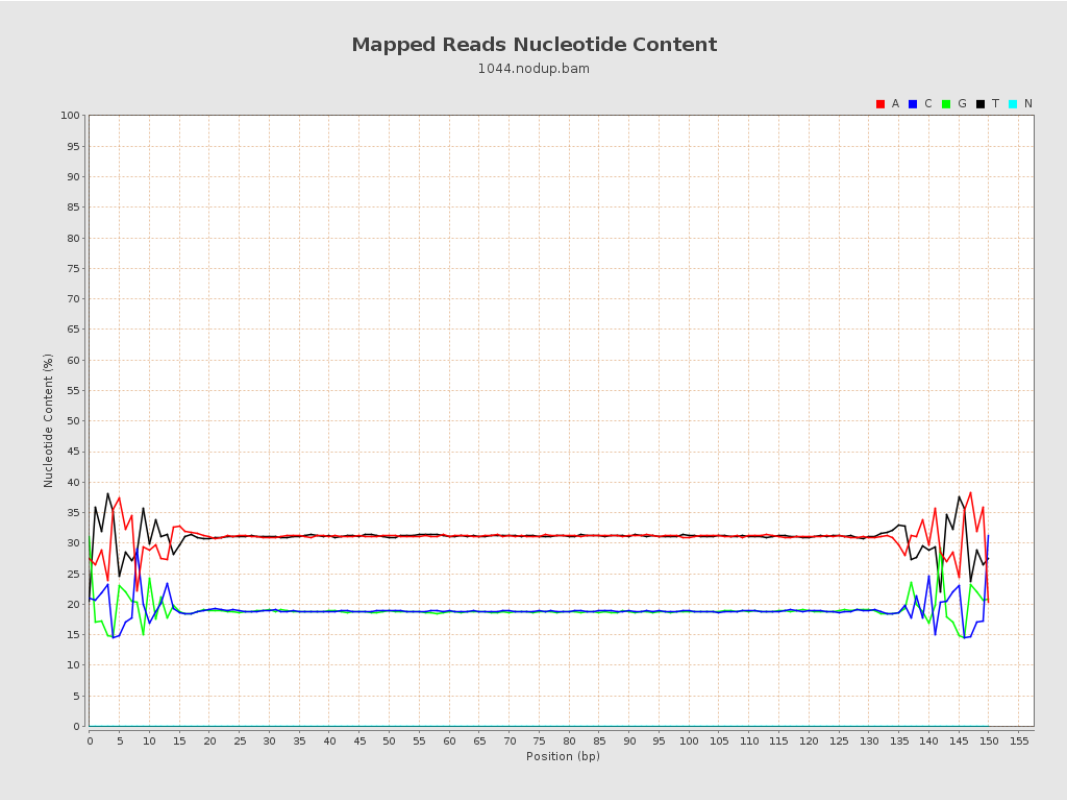
6. Results : Genome Fraction Coverage



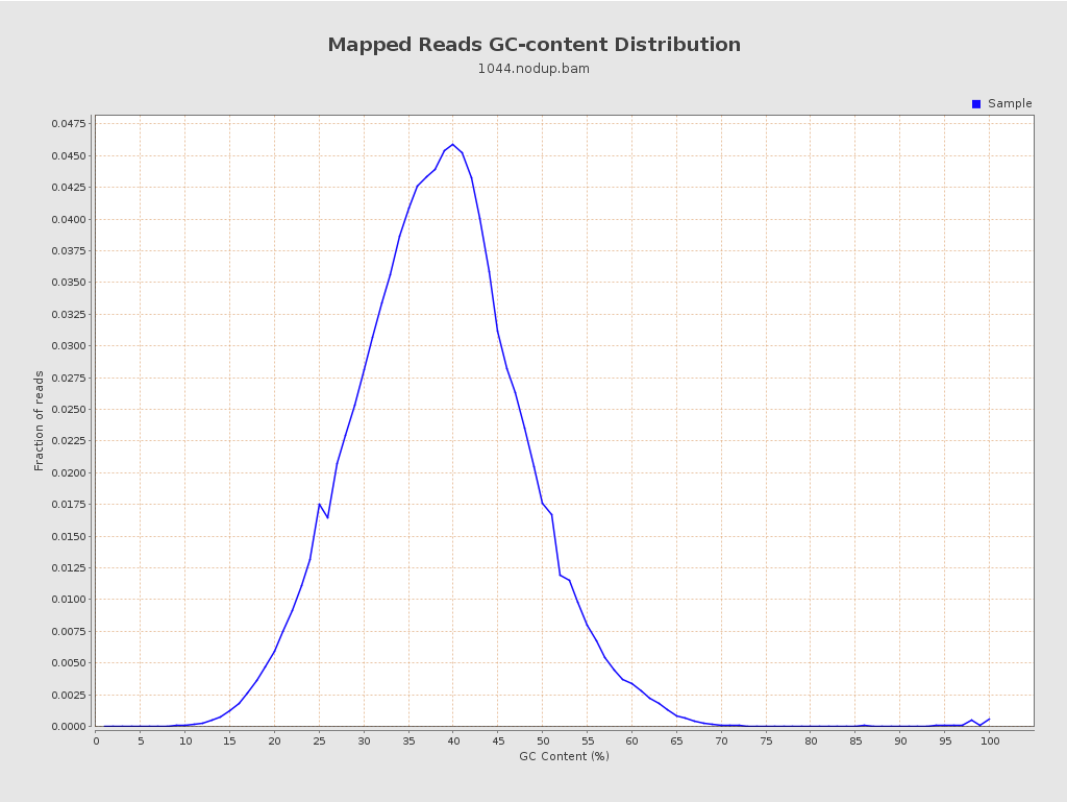
7. Results : Duplication Rate Histogram



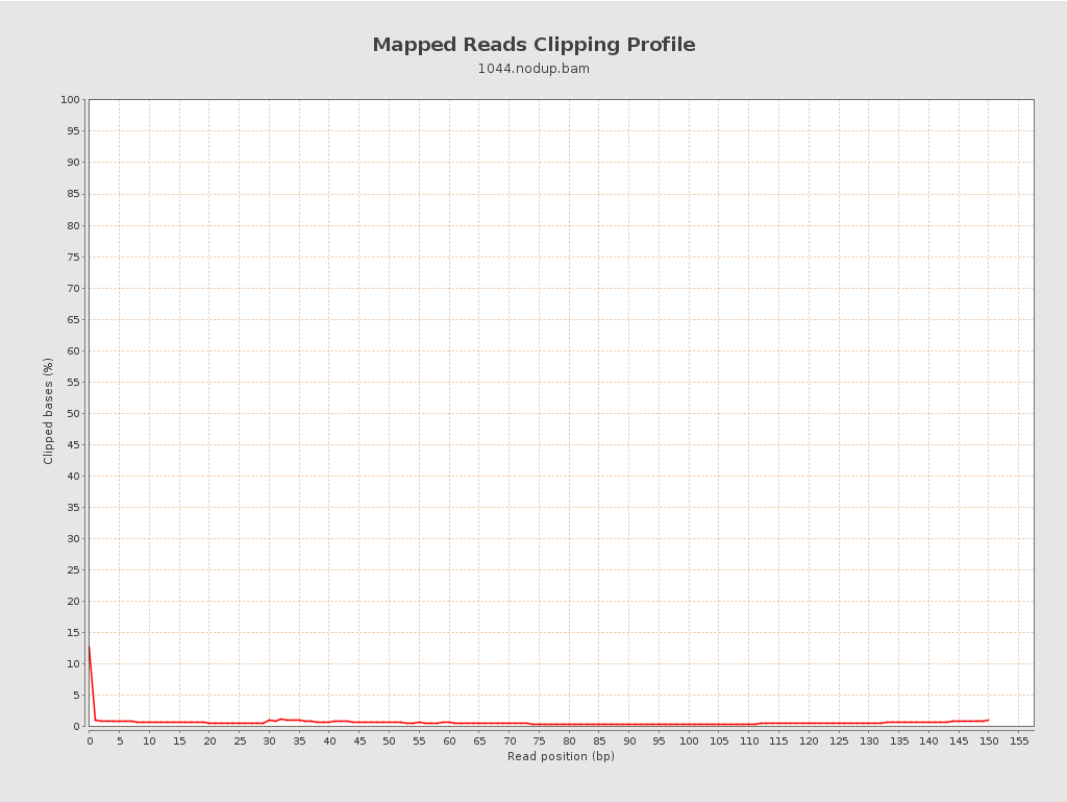
8. Results : Mapped Reads Nucleotide Content



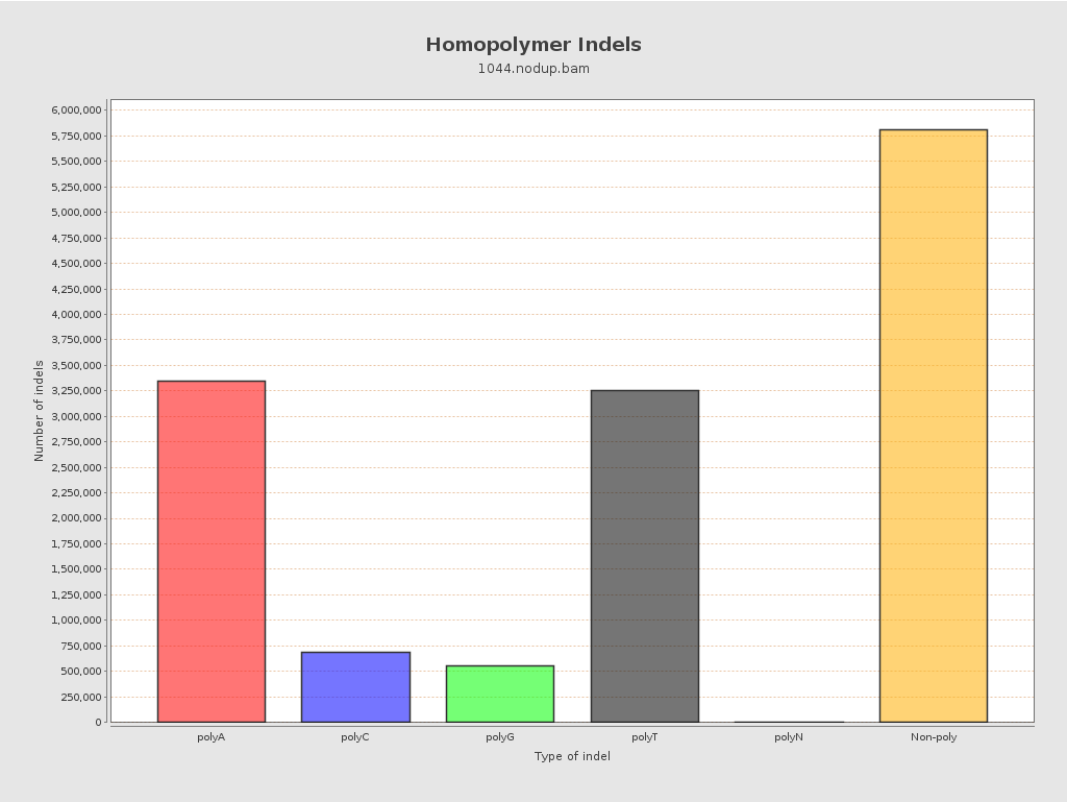
9. Results : Mapped Reads GC-content Distribution



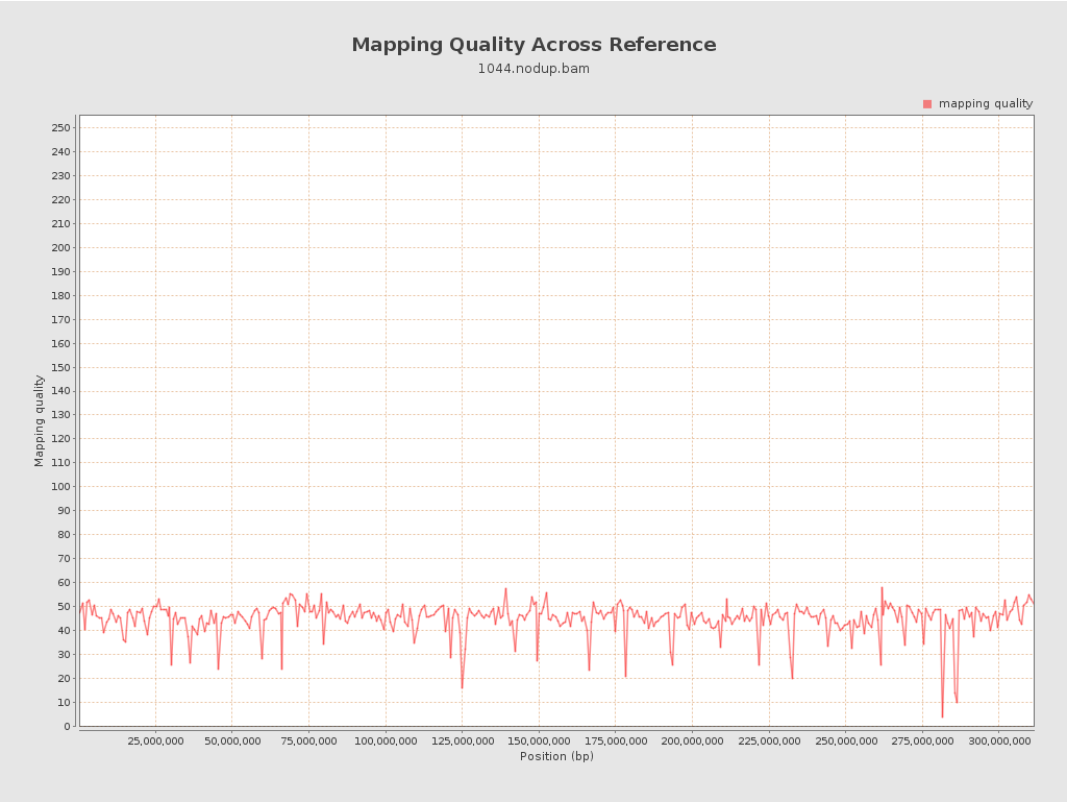
10. Results : Mapped Reads Clipping Profile



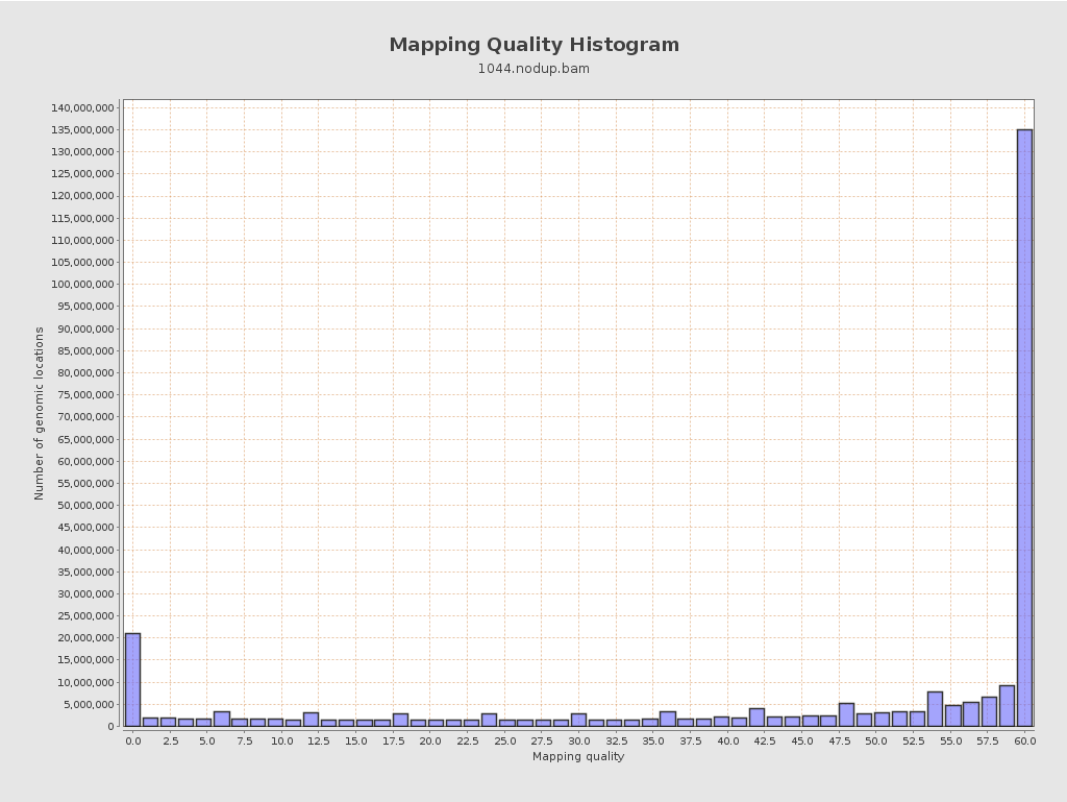
11. Results : Homopolymer Indels



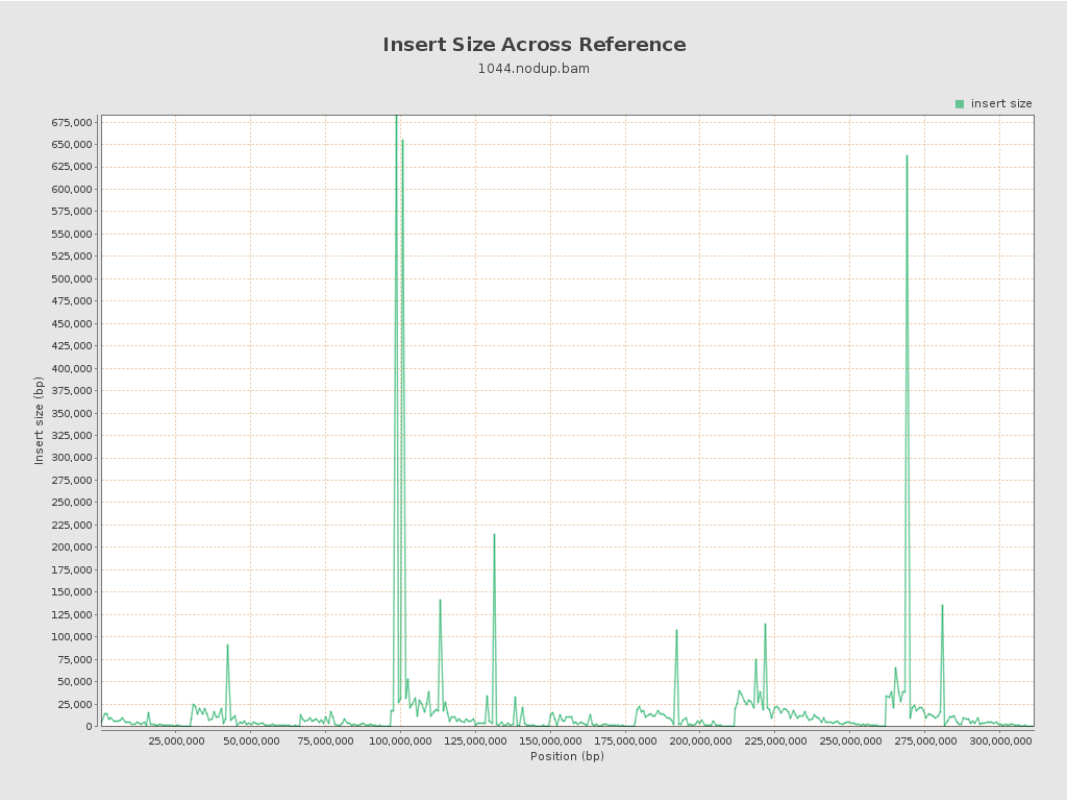
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram