Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:39:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1025
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1025 .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_455/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_455_S430_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_455/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_455_S430_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:39:11 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,541,906
Mapped reads	81,213,904 / 94.94%
Unmapped reads	4,328,002 / 5.06%
Mapped paired reads	81,213,904 / 94.94%
Mapped reads, first in pair	40,654,009 / 47.53%
Mapped reads, second in pair	40,559,895 / 47.42%
Mapped reads, both in pair	79,845,958 / 93.34%
Mapped reads, singletons	1,367,946 / 1.6%
Read min/max/mean length	30 / 151 / 147.9
Duplicated reads (flagged)	13,281,097 / 15.53%
Clipped reads	18,198,425 / 21.27%

2.2. ACGT Content

Number/percentage of A's	3,460,914,417 / 30.74%
Number/percentage of C's	2,170,447,162 / 19.28%
Number/percentage of T's	3,465,766,776 / 30.78%
Number/percentage of G's	2,163,185,935 / 19.21%
Number/percentage of N's	38,107 / 0%
GC Percentage	38.49%

2.3. Coverage

Mean	36.2278
Standard Deviation	313.708

2.4. Mapping Quality

Mean Mapping Quality	43.62

2.5. Insert size

Mean	224,273.74
Standard Deviation	2,227,705.79
P25/Median/P75	313 / 411 / 532

2.6. Mismatches and indels

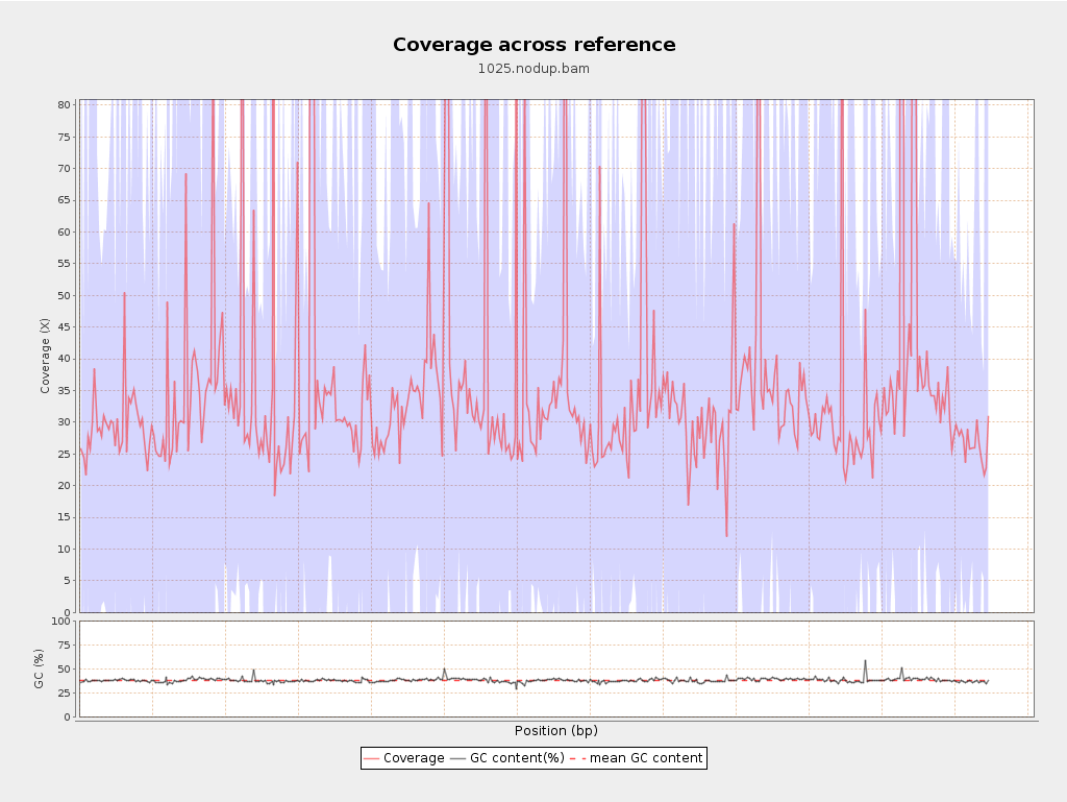
General error rate	2.29%
Mismatches	236,814,346
Insertions	7,577,276
Mapped reads with at least one insertion	8.41%
Deletions	7,894,408
Mapped reads with at least one deletion	8.61%
Homopolymer indels	55.88%

2.7. Chromosome stats

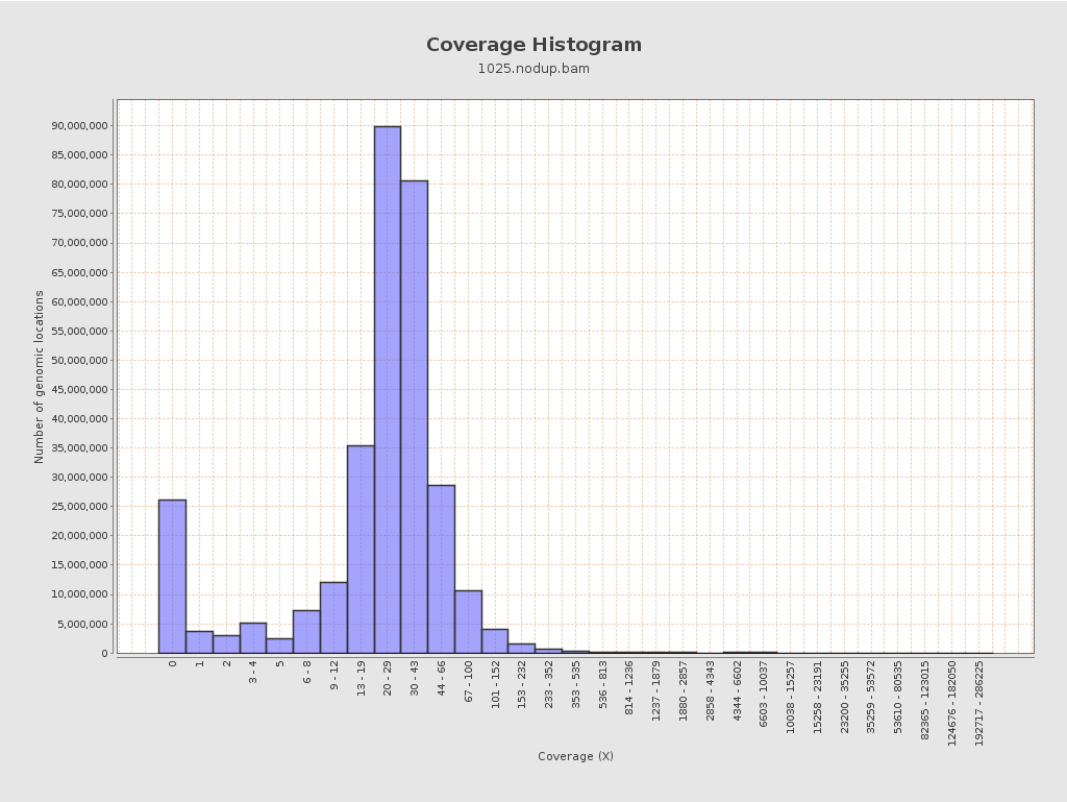
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	859426977	28.9132	80.6642

LT669789.1	36598175	1366891327	37.3486	352.6073
LT669790.1	30422129	1122774455	36.9065	265.5047
LT669791.1	52758100	1887470306	35.7759	288.6745
LT669792.1	28376109	990274420	34.8982	307.1706
LT669793.1	33388210	1143314296	34.2431	220.3433
LT669794.1	50579949	1780746246	35.2066	305.2574
LT669795.1	49795044	2139211852	42.9603	456.3277

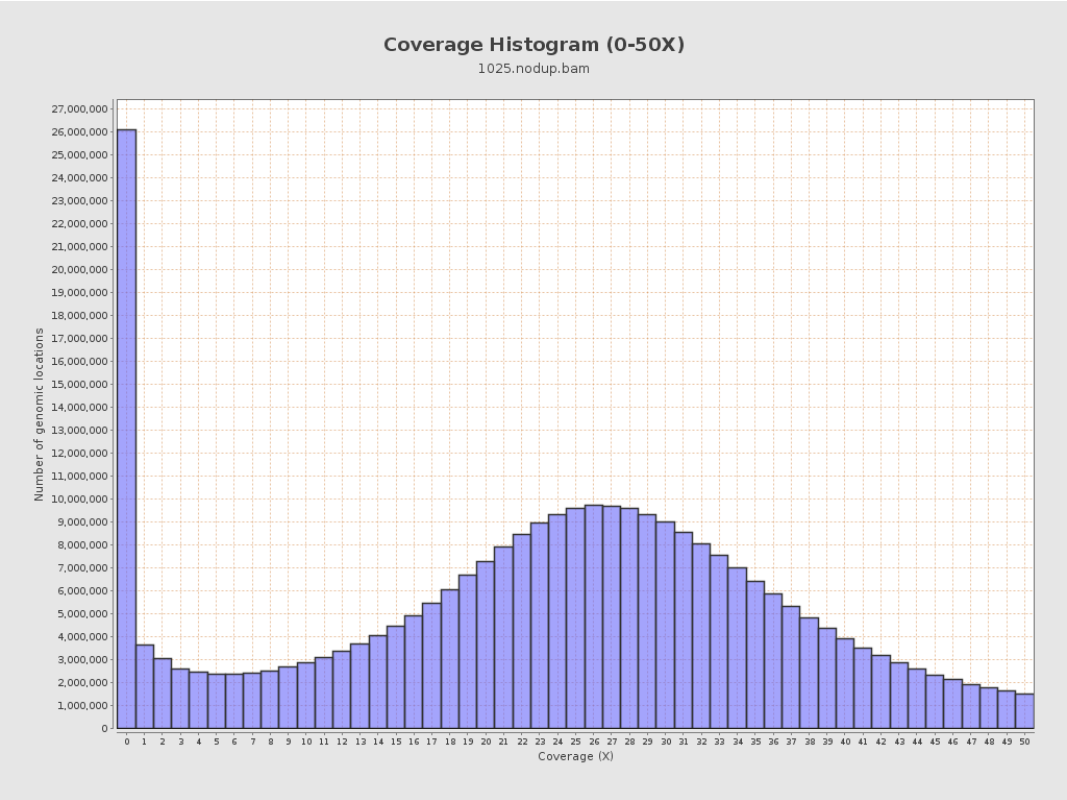
3. Results : Coverage across reference



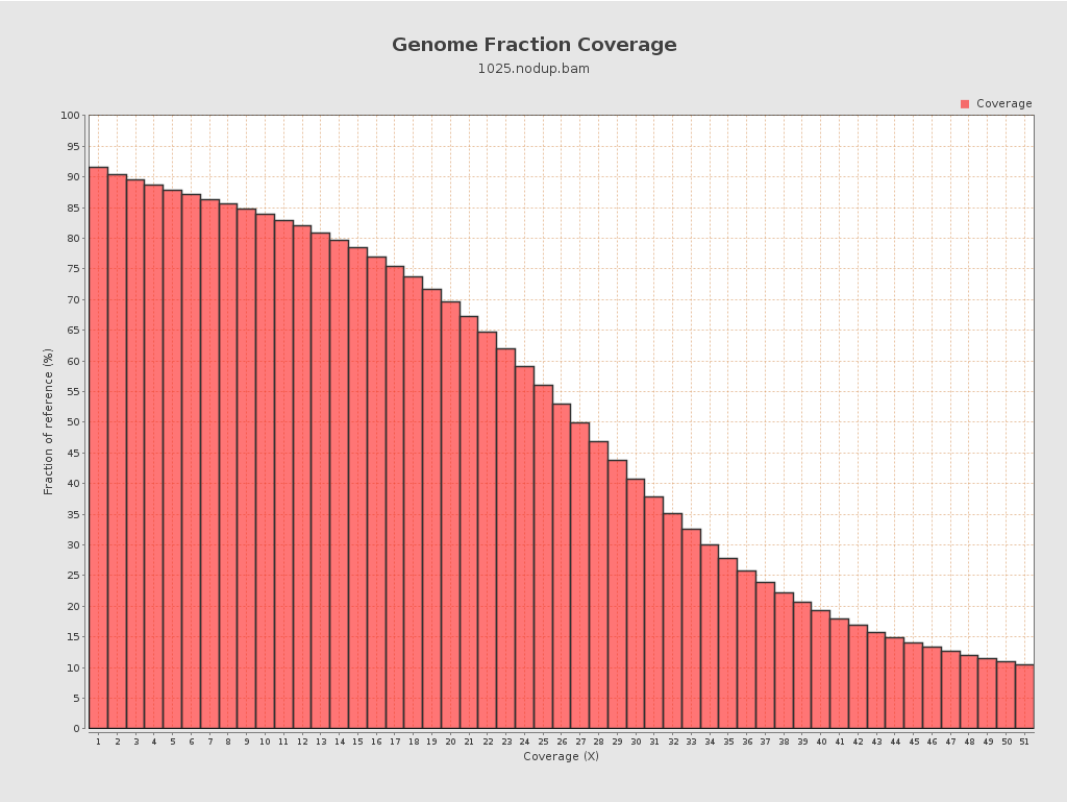
4. Results : Coverage Histogram



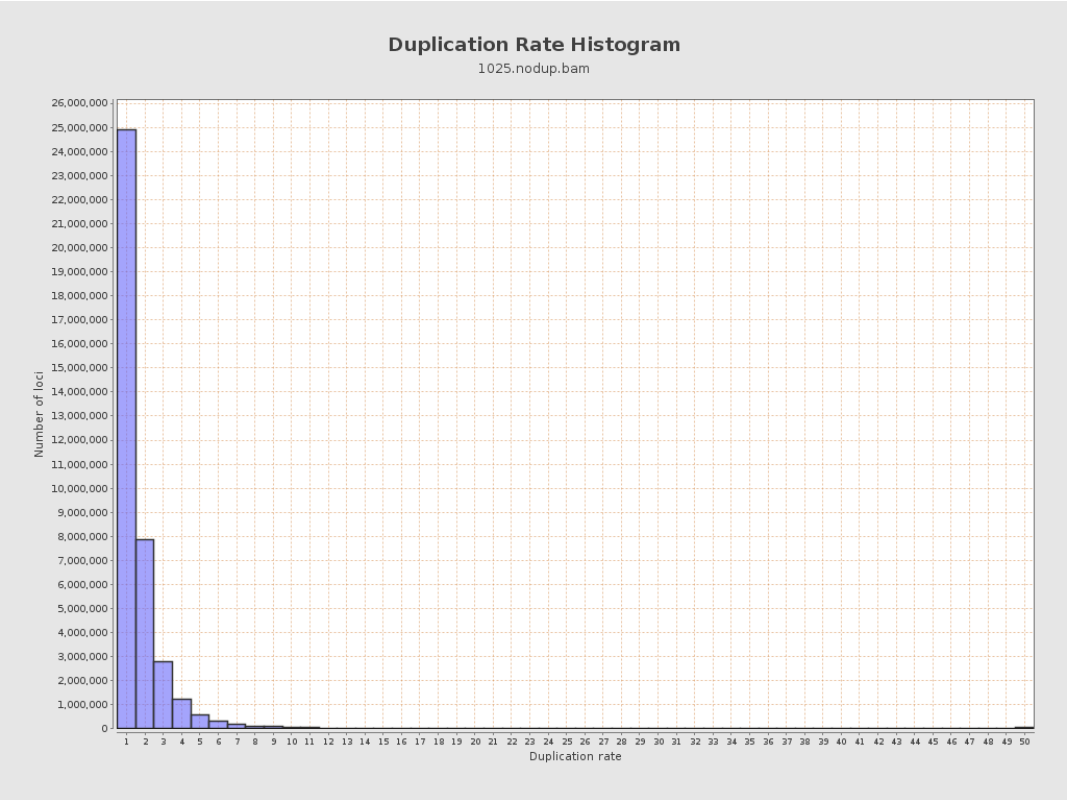
5. Results : Coverage Histogram (0-50X)



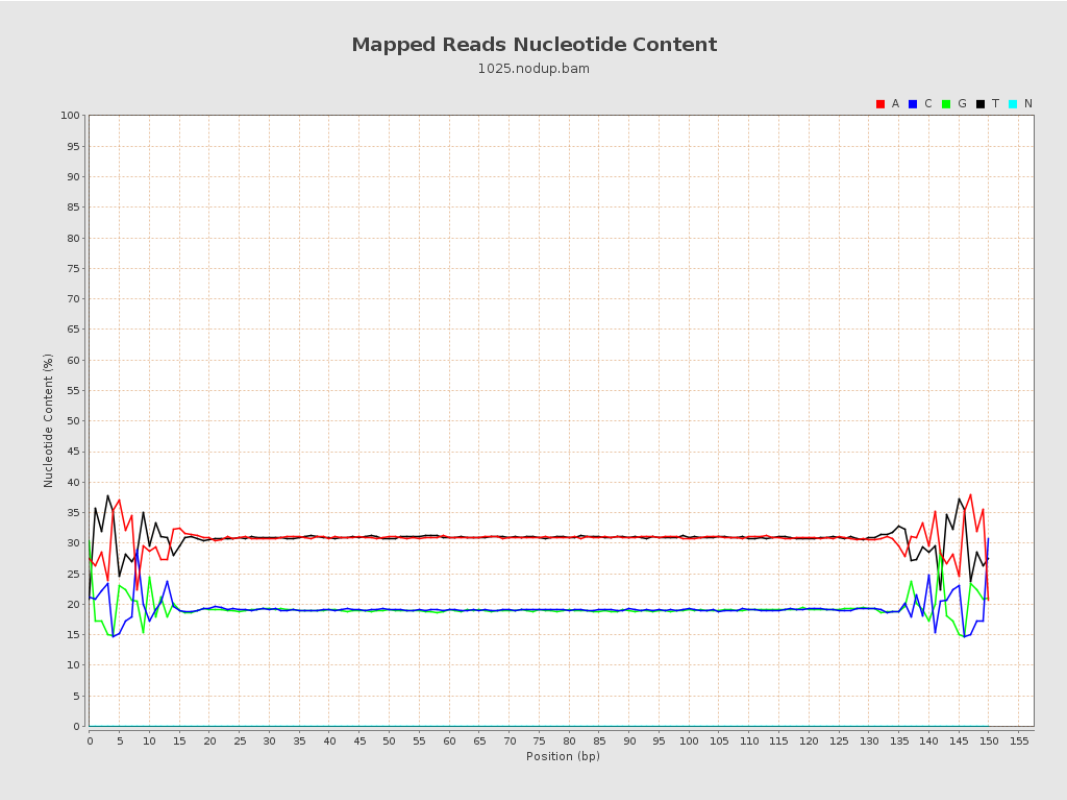
6. Results : Genome Fraction Coverage



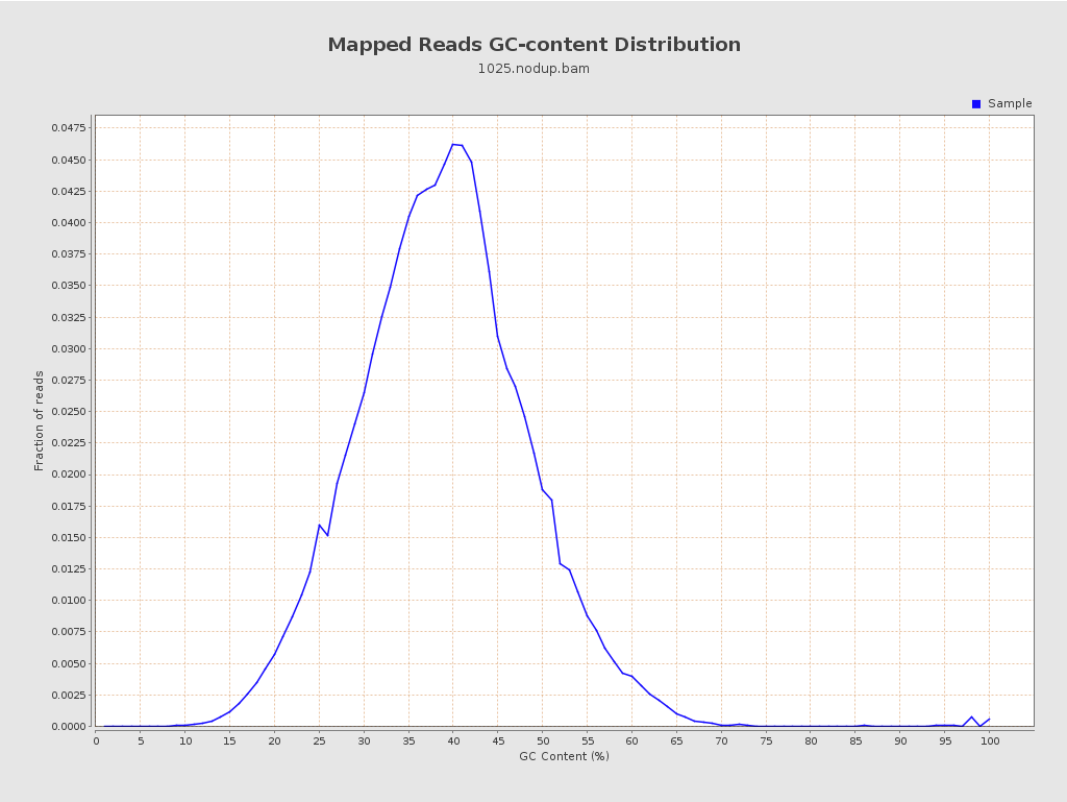
7. Results : Duplication Rate Histogram



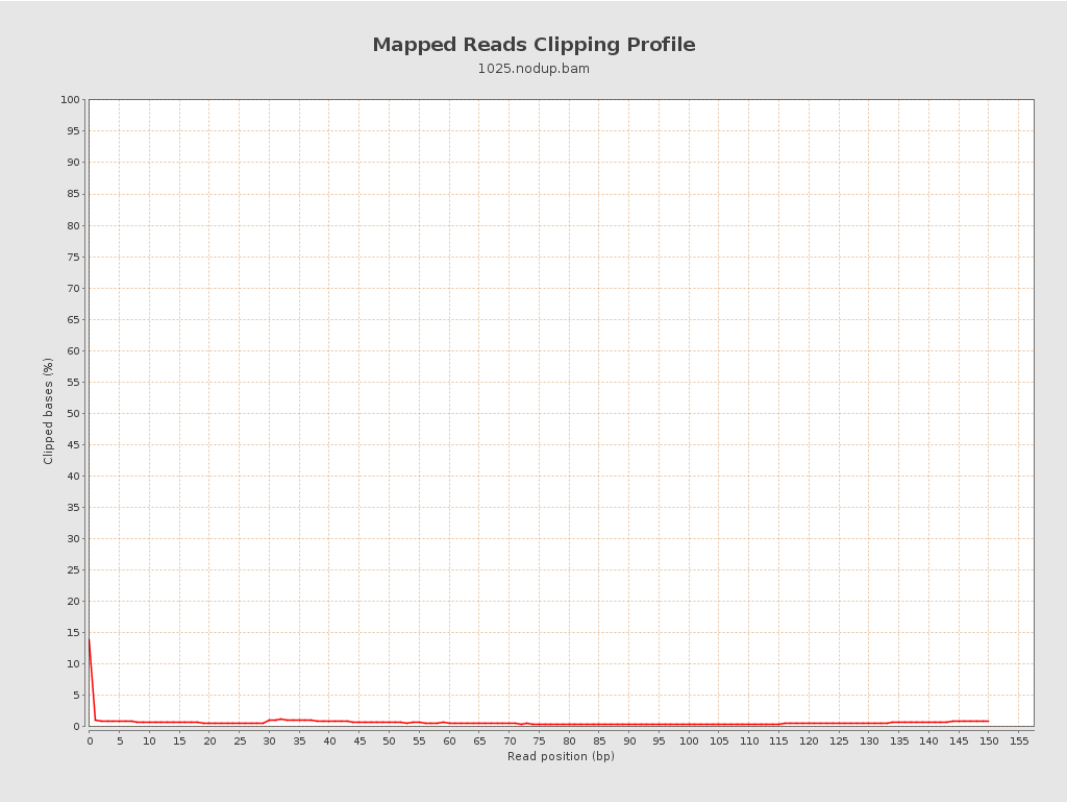
8. Results : Mapped Reads Nucleotide Content



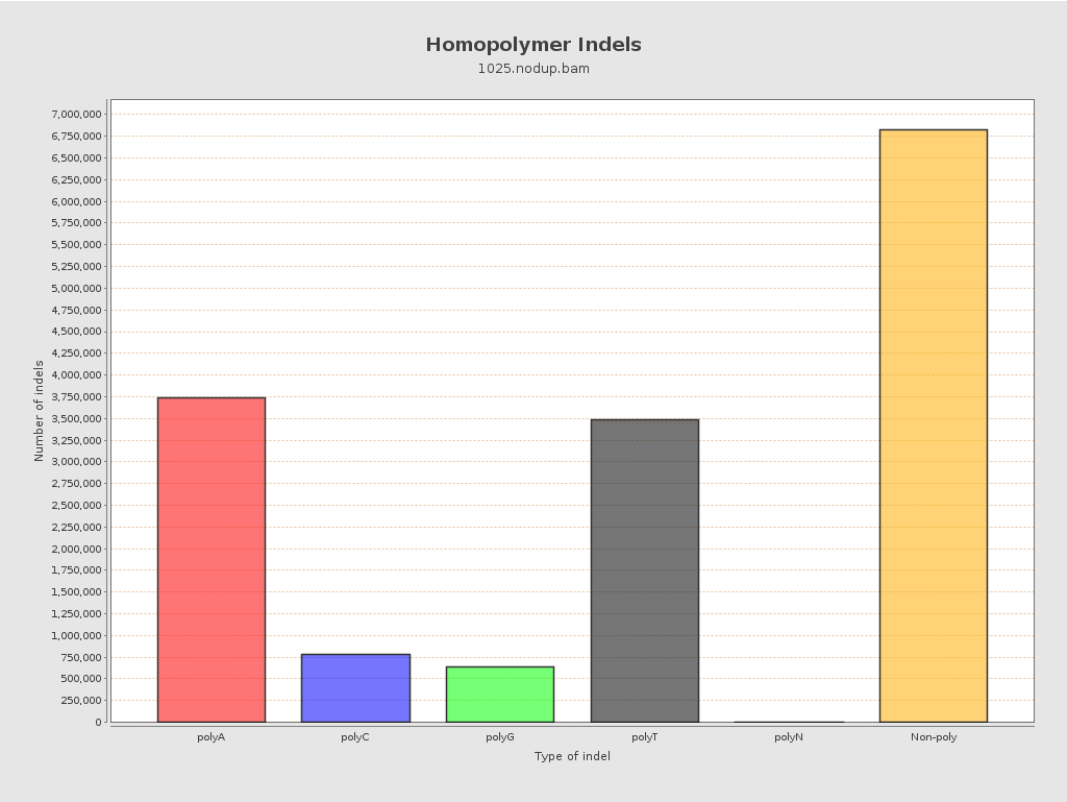
9. Results : Mapped Reads GC-content Distribution



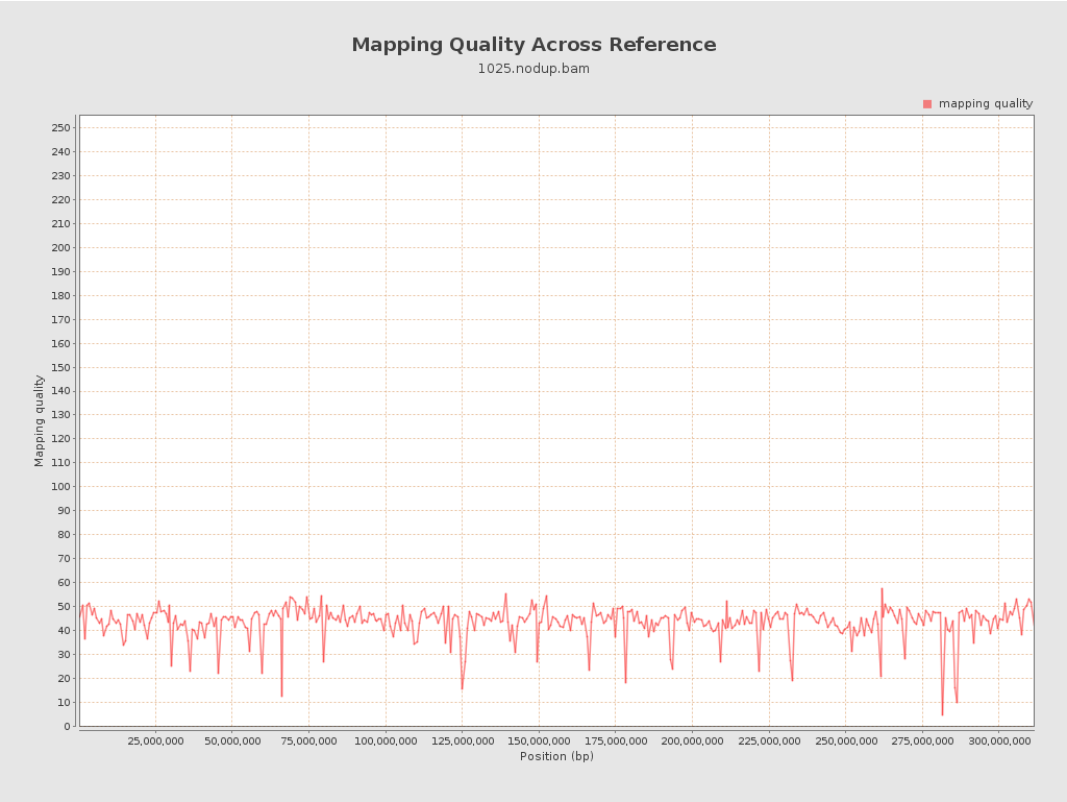
10. Results : Mapped Reads Clipping Profile



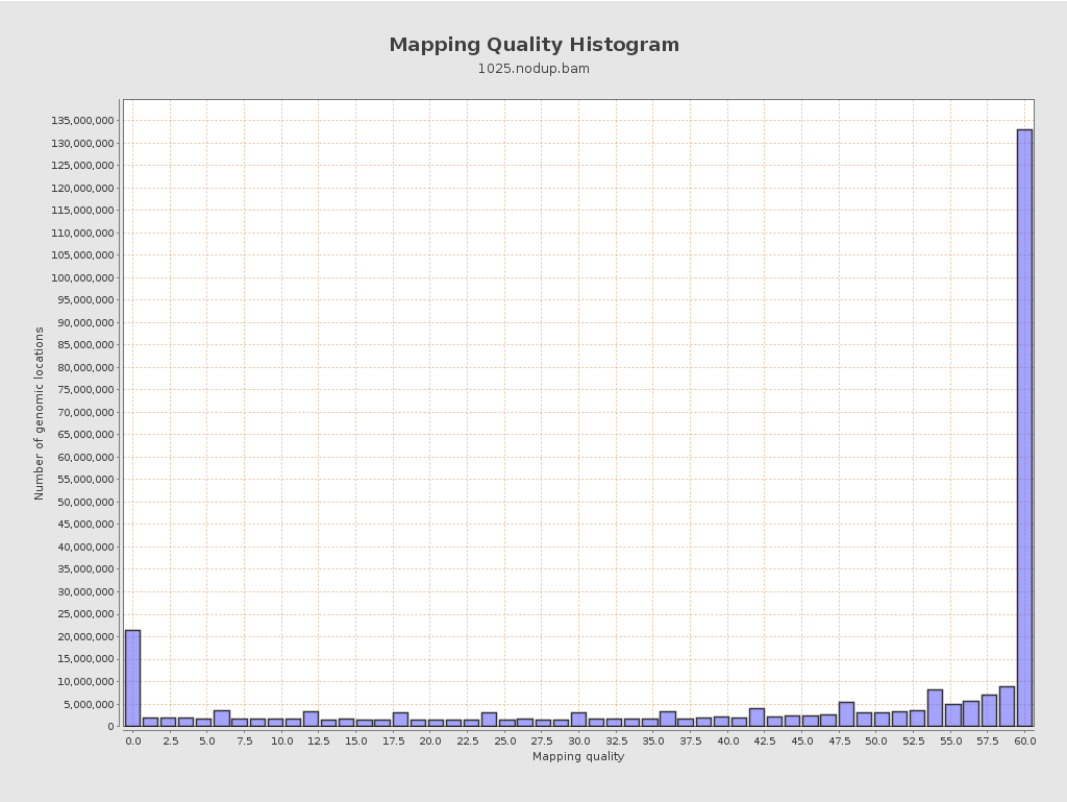
11. Results : Homopolymer Indels



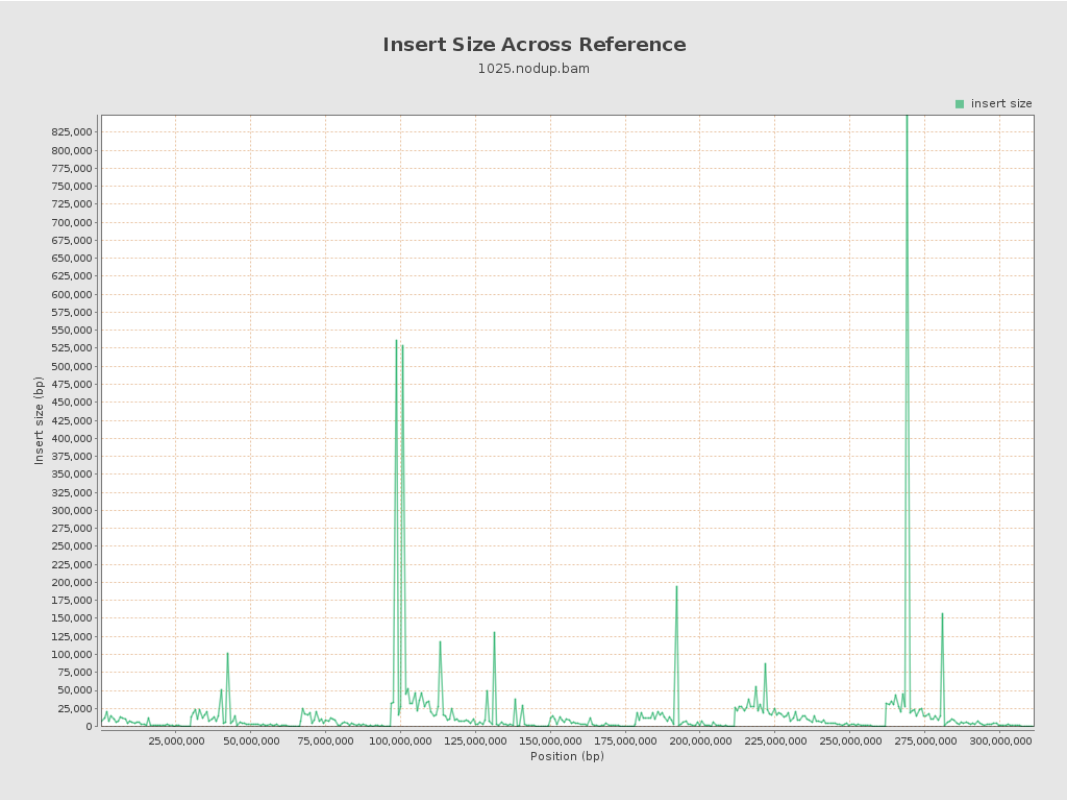
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram