Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1112
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1112 .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_448/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_448_S423_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_448/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_448_S423_L004_R2_001.fastq.gz
Size of a homopolymer:	3

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,631,390
Mapped reads	68,183,338 / 93.88%
Unmapped reads	4,448,052 / 6.12%
Mapped paired reads	68,183,338 / 93.88%
Mapped reads, first in pair	34,181,752 / 47.06%
Mapped reads, second in pair	34,001,586 / 46.81%
Mapped reads, both in pair	66,758,484 / 91.91%
Mapped reads, singletons	1,424,854 / 1.96%
Read min/max/mean length	30 / 151 / 147.9
Duplicated reads (flagged)	11,504,374 / 15.84%
Clipped reads	16,516,897 / 22.74%

2.2. ACGT Content

Number/percentage of A's	2,881,108,249 / 30.81%
Number/percentage of C's	1,796,763,928 / 19.21%
Number/percentage of T's	2,879,293,567 / 30.79%
Number/percentage of G's	1,794,435,575 / 19.19%
Number/percentage of N's	32,194 / 0%
GC Percentage	38.4%

2.3. Coverage

Mean	30.0842
Standard Deviation	277.8598

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Insert size

Mean	229,701.9
Standard Deviation	2,261,329.31
P25/Median/P75	316 / 432 / 574

2.6. Mismatches and indels

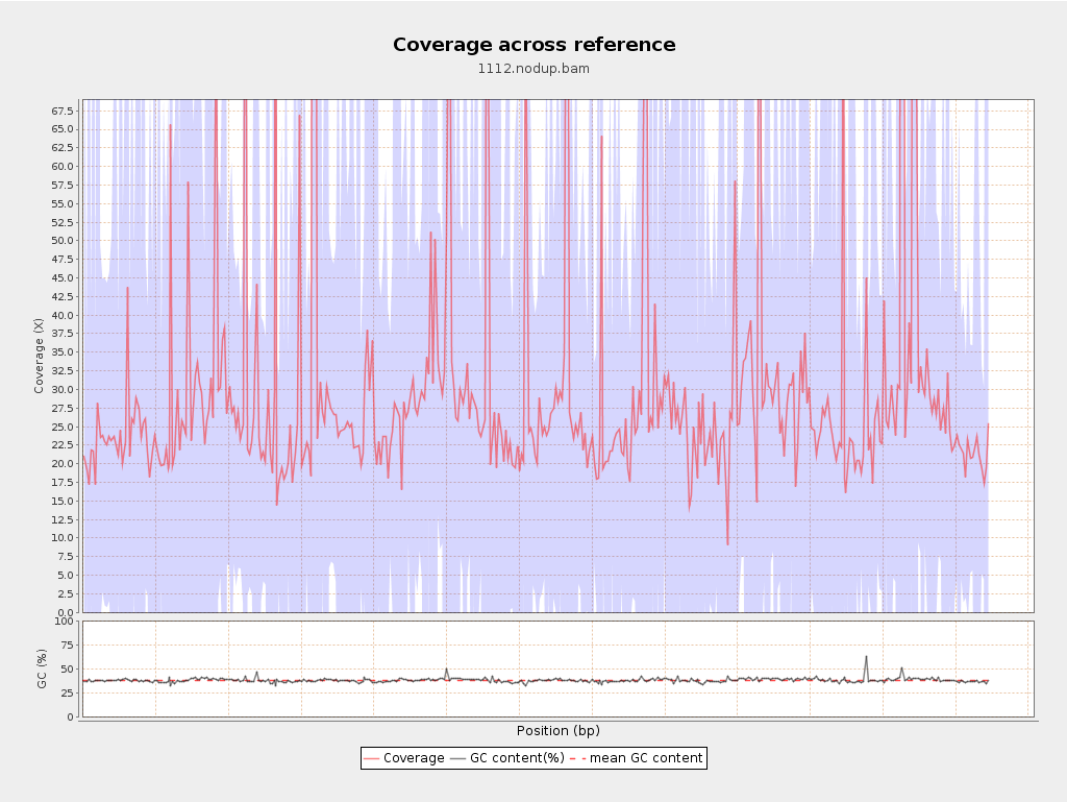
General error rate	2.32%
Mismatches	199,605,534
Insertions	6,249,806
Mapped reads with at least one insertion	8.26%
Deletions	6,443,284
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.73%

2.7. Chromosome stats

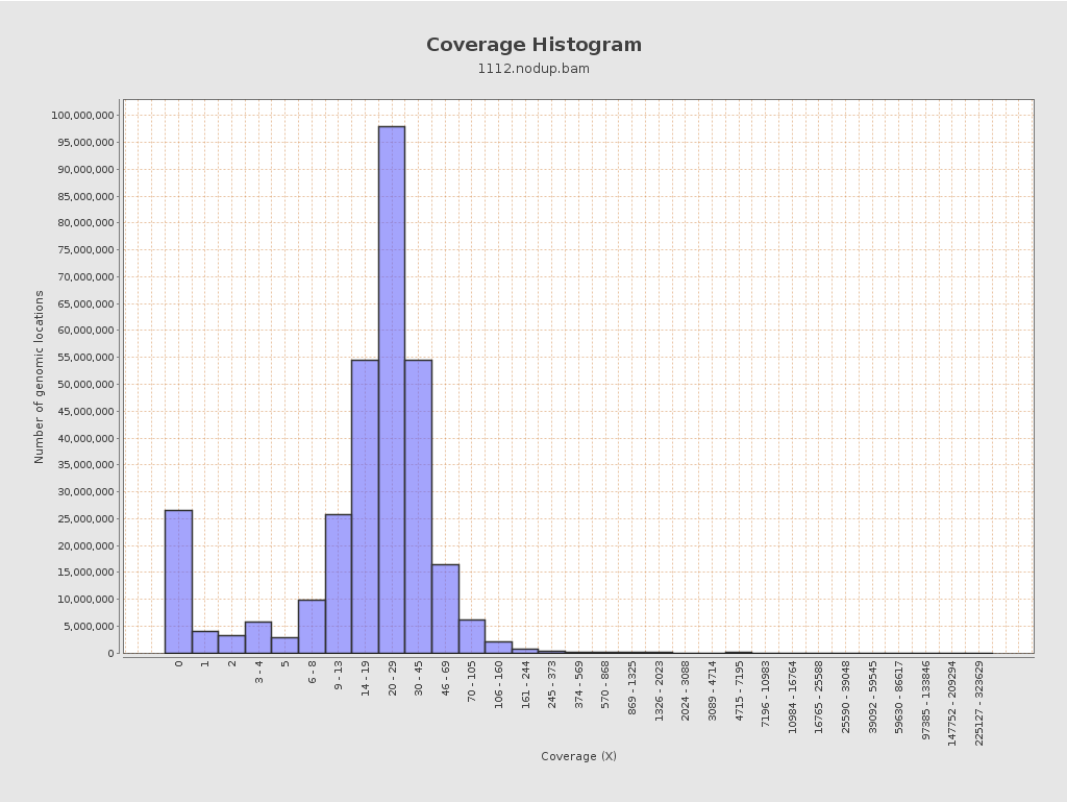
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	686474688	23.0947	66.3281

LT669789.1	36598175	1157082365	31.6158	277.7432
LT669790.1	30422129	967810625	31.8127	287.0326
LT669791.1	52758100	1592040004	30.1762	231.5386
LT669792.1	28376109	820541032	28.9166	302.5532
LT669793.1	33388210	947150135	28.3678	198.3096
LT669794.1	50579949	1482485105	29.3097	265.2664
LT669795.1	49795044	1721920216	34.5802	408.2542

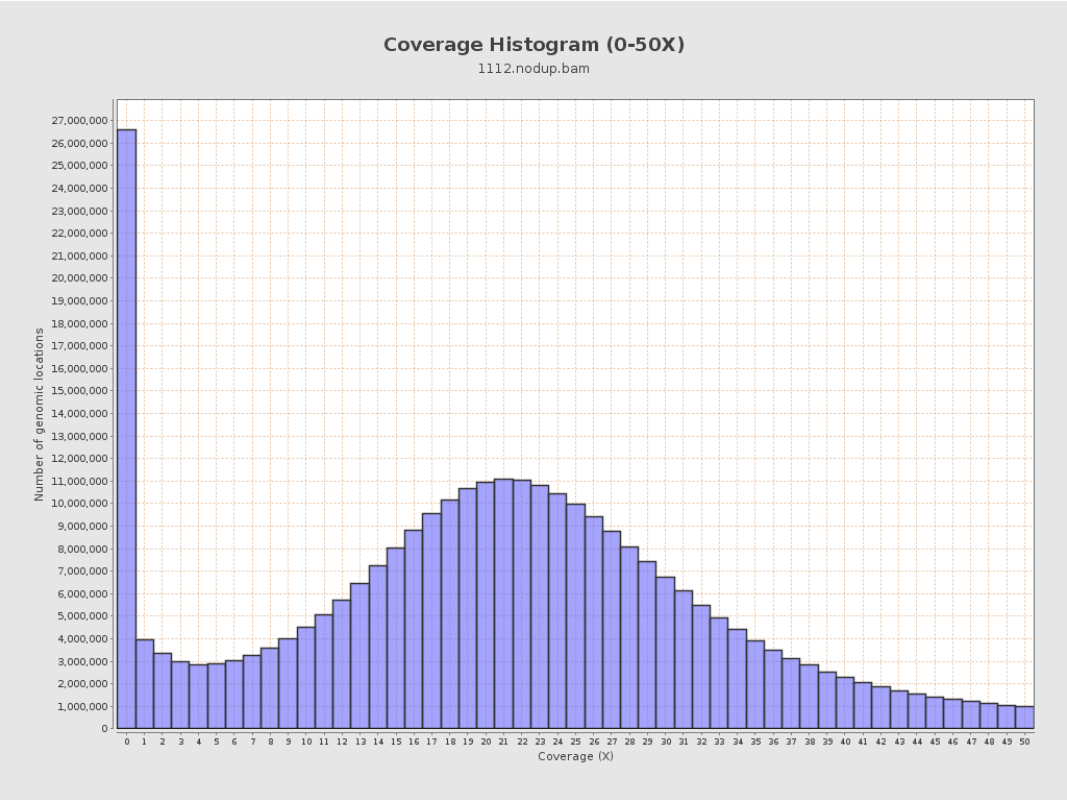
3. Results : Coverage across reference



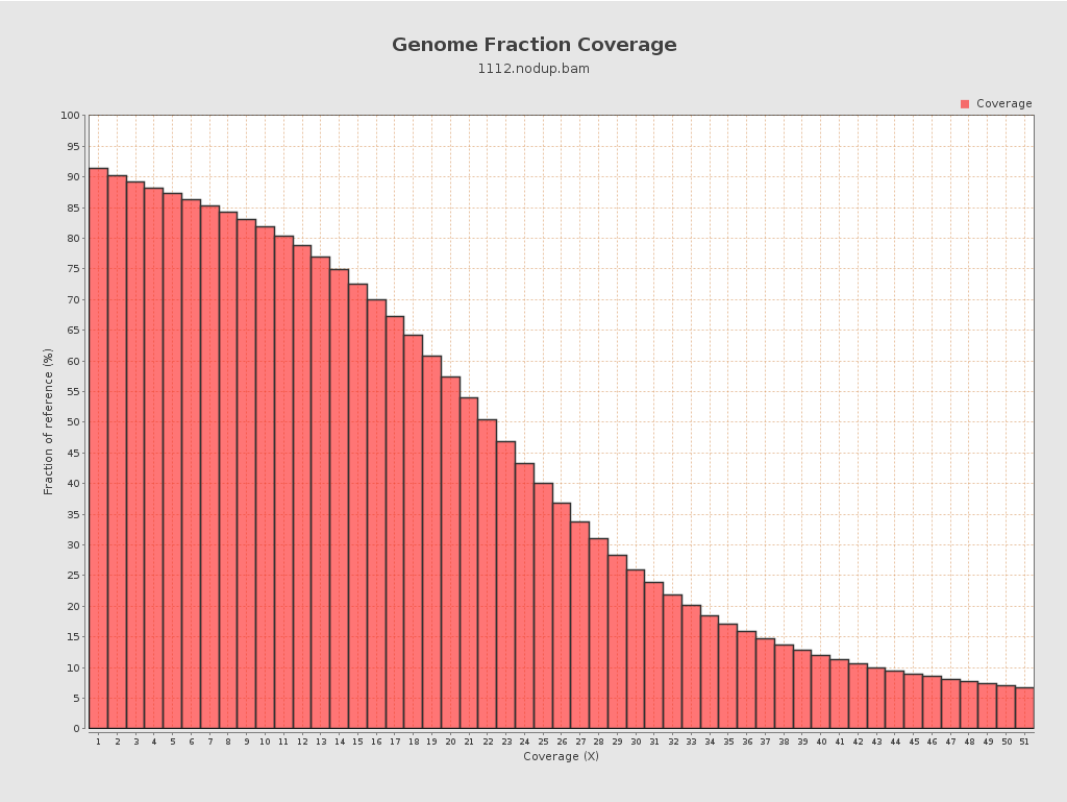
4. Results : Coverage Histogram



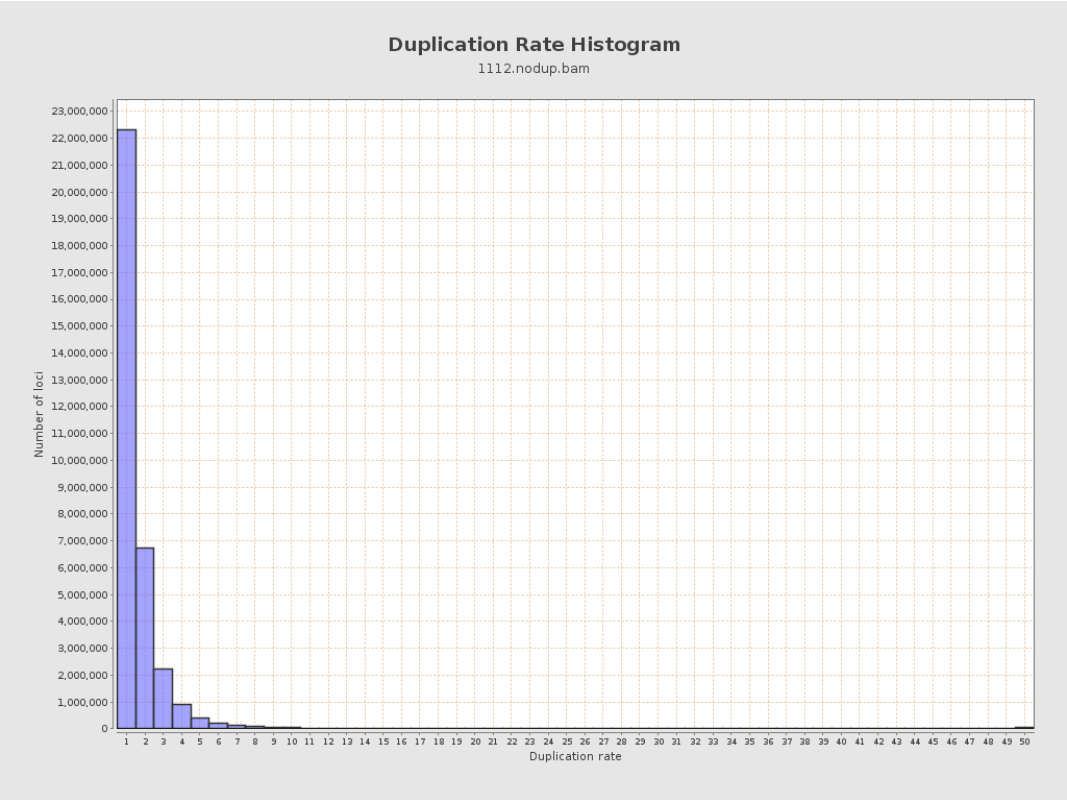
5. Results : Coverage Histogram (0-50X)



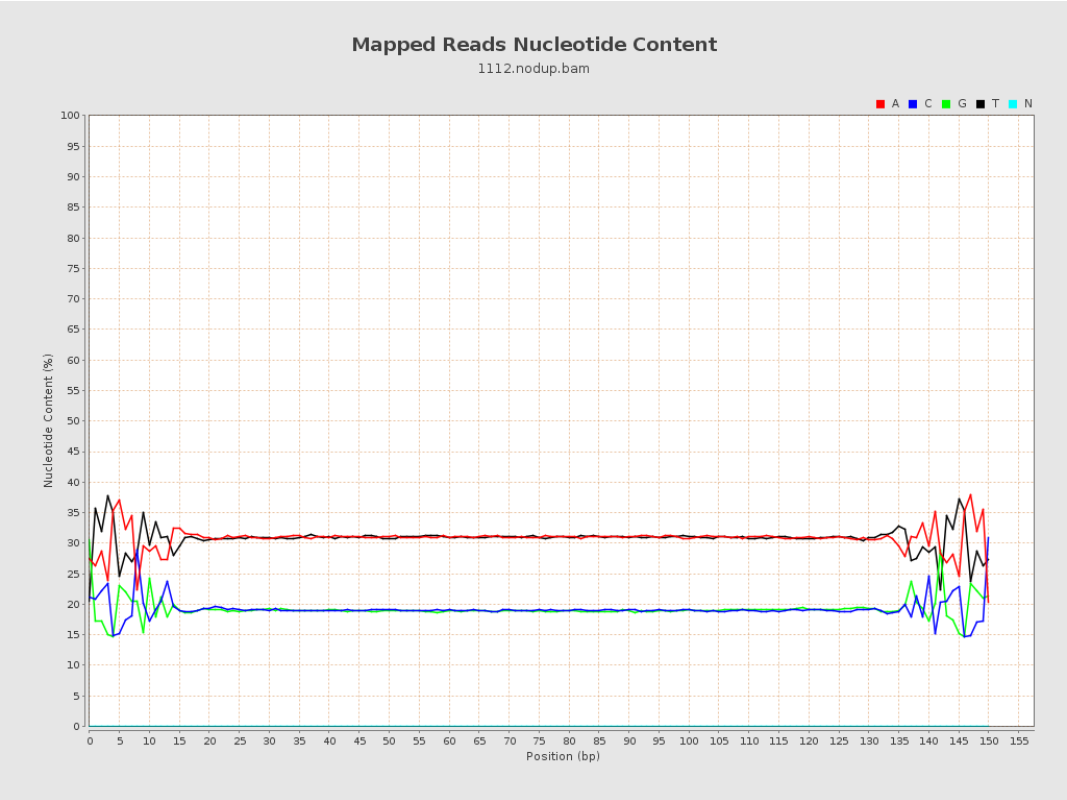
6. Results : Genome Fraction Coverage



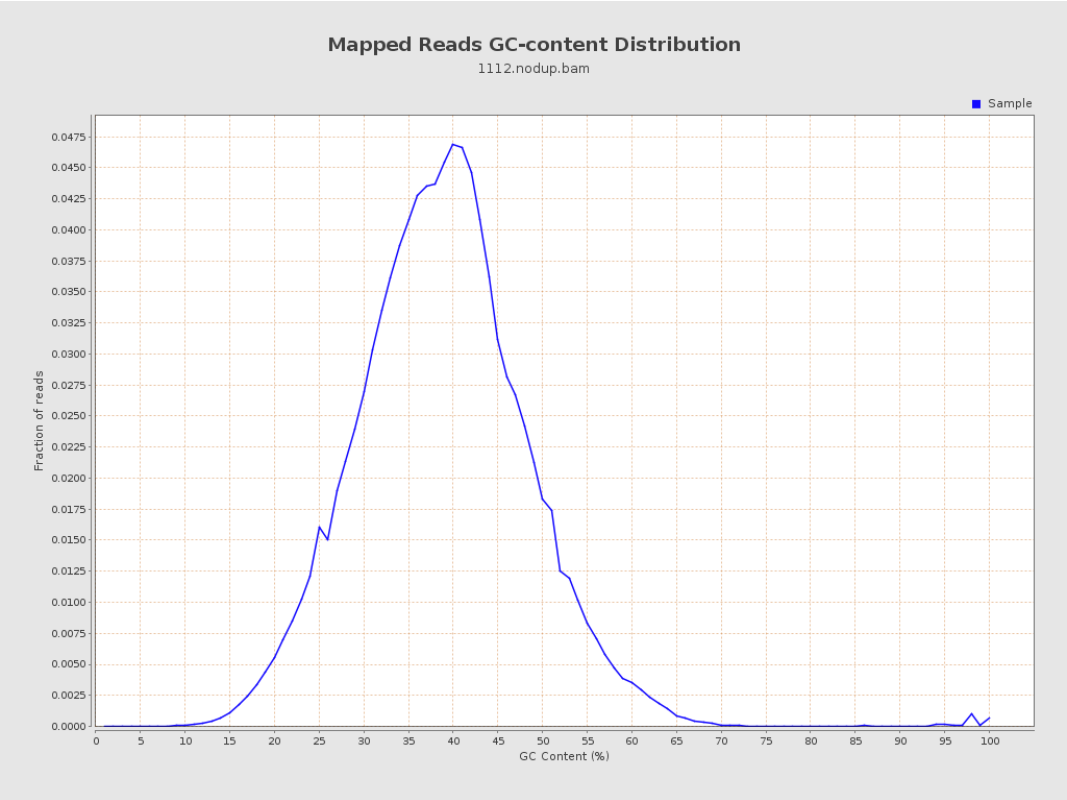
7. Results : Duplication Rate Histogram



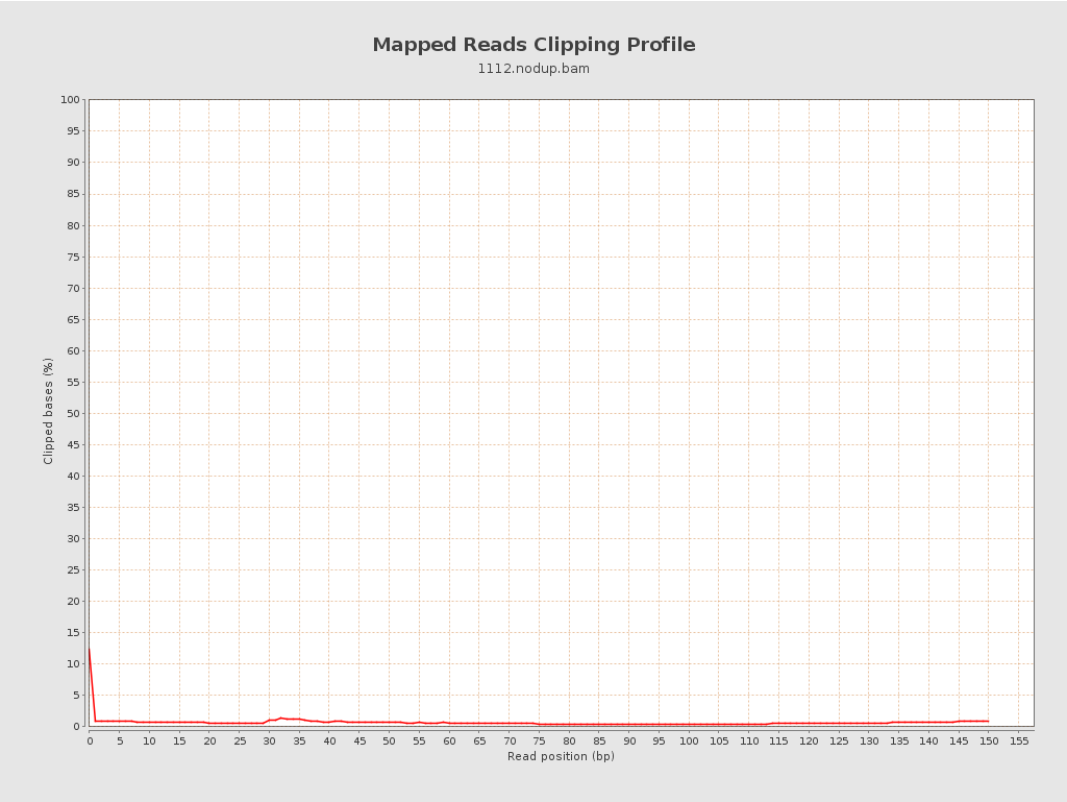
8. Results : Mapped Reads Nucleotide Content



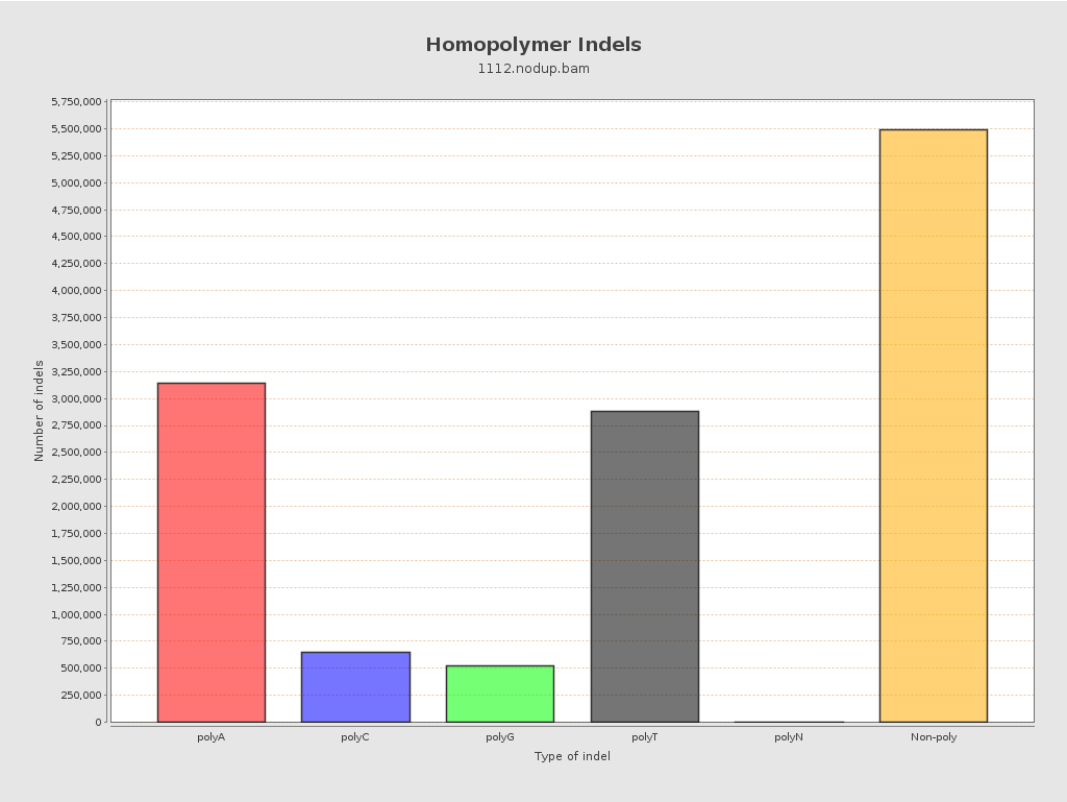
9. Results : Mapped Reads GC-content Distribution



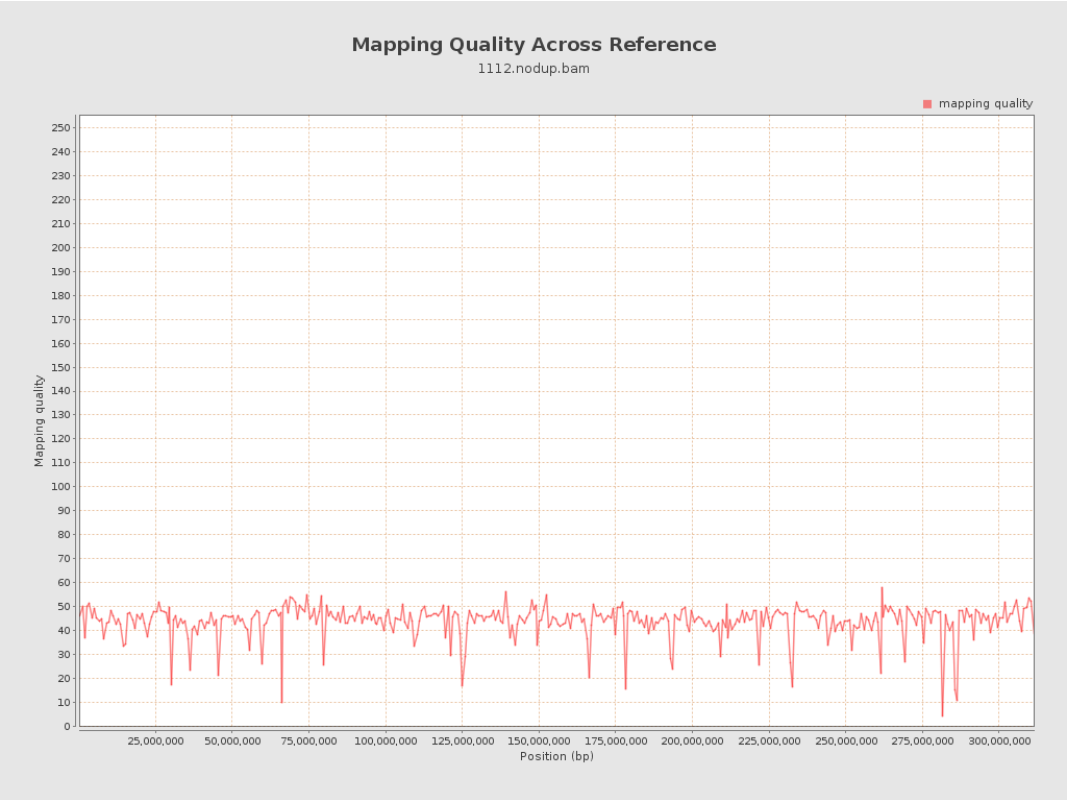
10. Results : Mapped Reads Clipping Profile



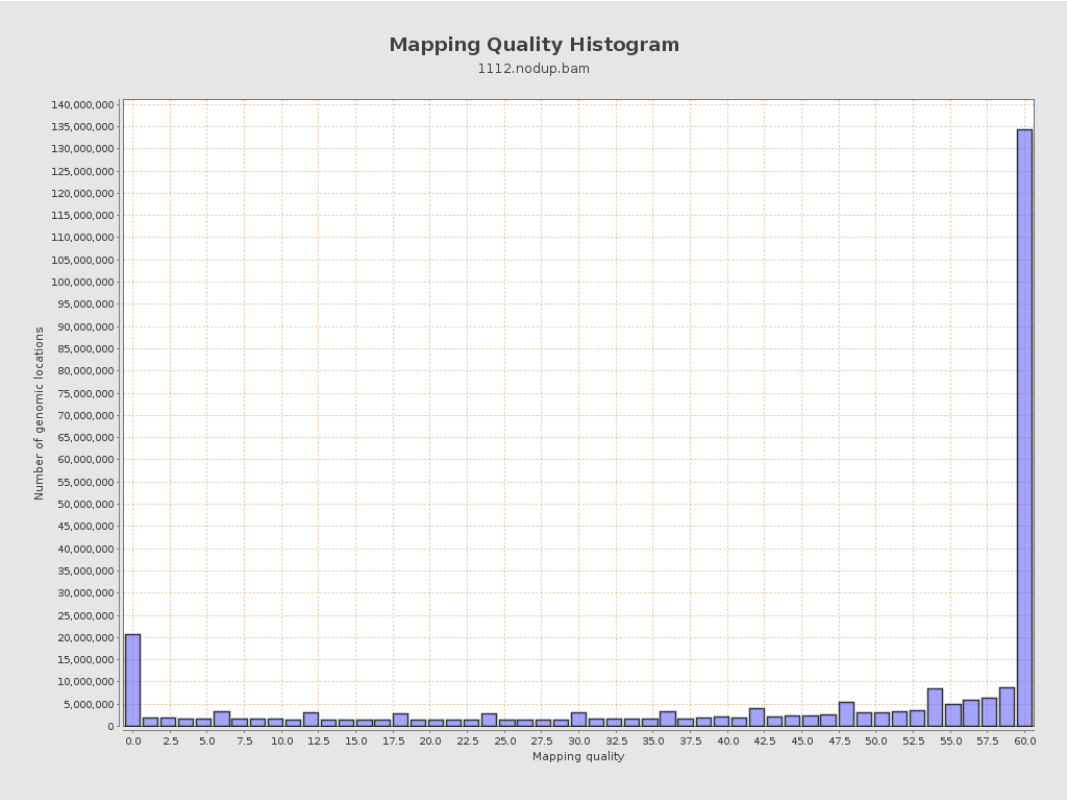
11. Results : Homopolymer Indels



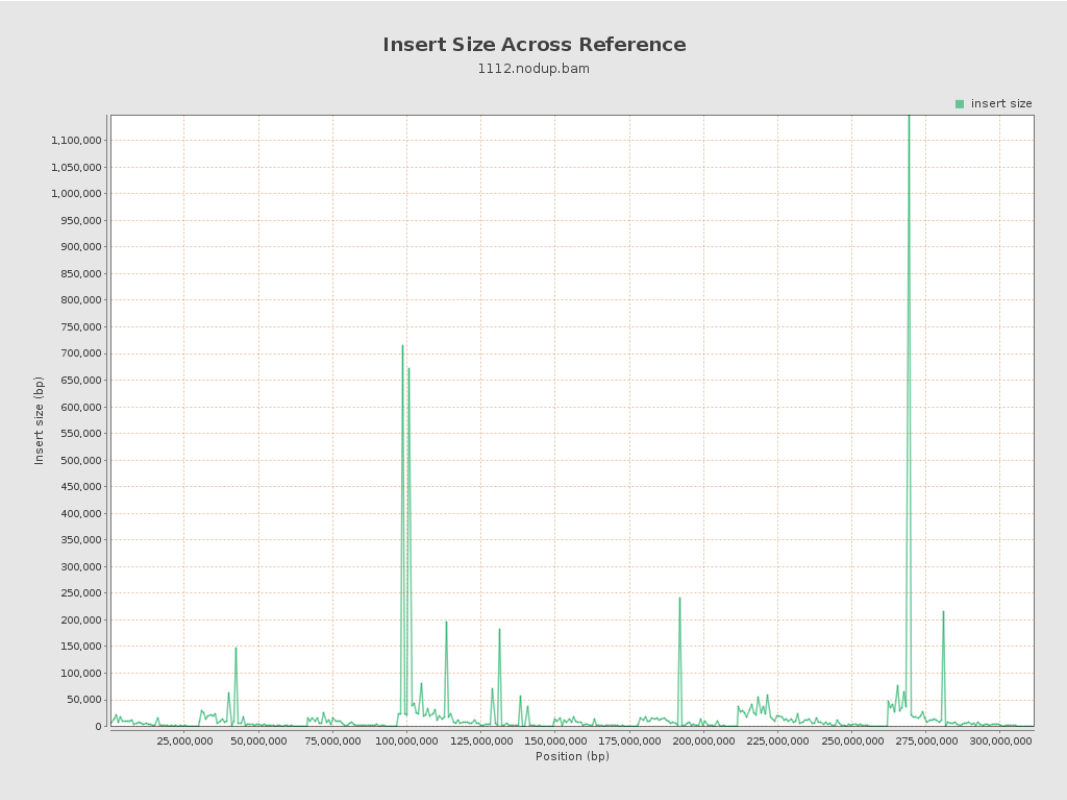
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram