Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1234
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1234 .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_241/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_241_S322_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_241/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_241_S322_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:23 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,317,499
Mapped reads	73,347,080 / 93.65%
Unmapped reads	4,970,419 / 6.35%
Mapped paired reads	73,347,080 / 93.65%
Mapped reads, first in pair	36,743,981 / 46.92%
Mapped reads, second in pair	36,603,099 / 46.74%
Mapped reads, both in pair	71,804,241 / 91.68%
Mapped reads, singletons	1,542,839 / 1.97%
Read min/max/mean length	30 / 151 / 148.04
Duplicated reads (flagged)	11,279,009 / 14.4%
Clipped reads	16,954,862 / 21.65%

2.2. ACGT Content

Number/percentage of A's	3,114,234,527 / 30.79%
Number/percentage of C's	1,942,812,233 / 19.21%
Number/percentage of T's	3,116,857,137 / 30.82%
Number/percentage of G's	1,939,489,566 / 19.18%
Number/percentage of N's	38,061 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	32.5346
Standard Deviation	274.0658

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Insert size

Mean	221,439.79
Standard Deviation	2,231,829.37
P25/Median/P75	306 / 406 / 531

2.6. Mismatches and indels

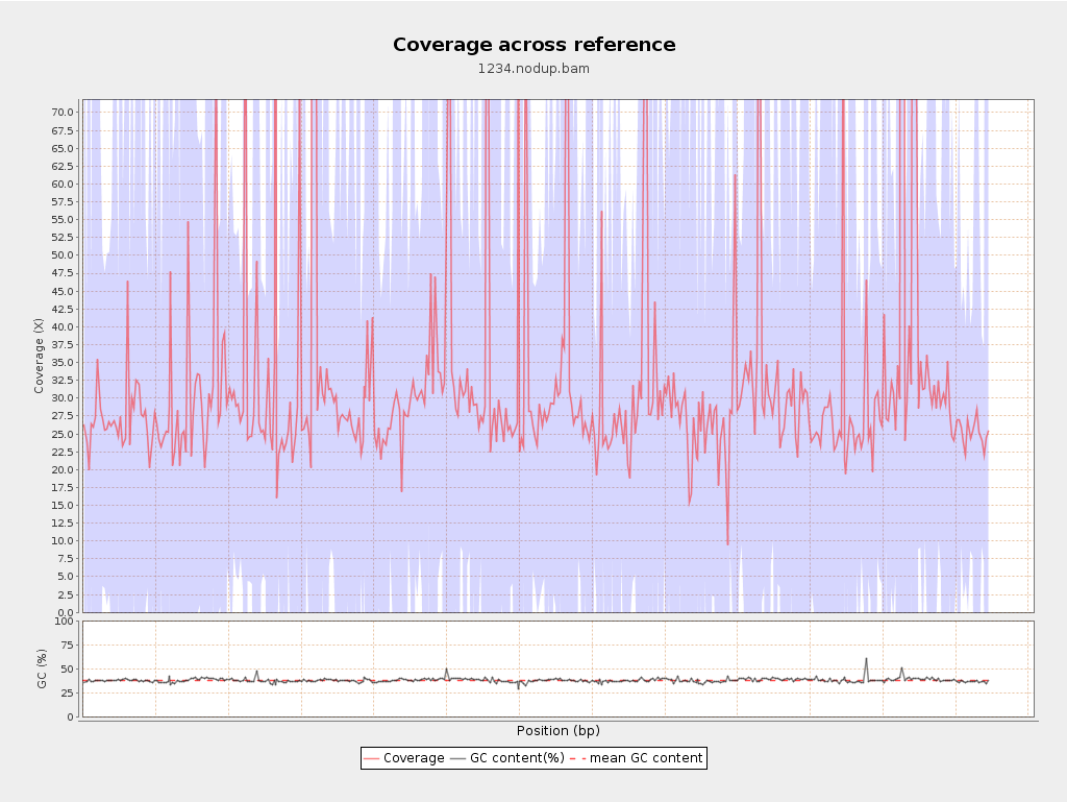
General error rate	2.26%
Mismatches	210,119,481
Insertions	6,707,873
Mapped reads with at least one insertion	8.22%
Deletions	6,815,201
Mapped reads with at least one deletion	8.25%
Homopolymer indels	56.3%

2.7. Chromosome stats

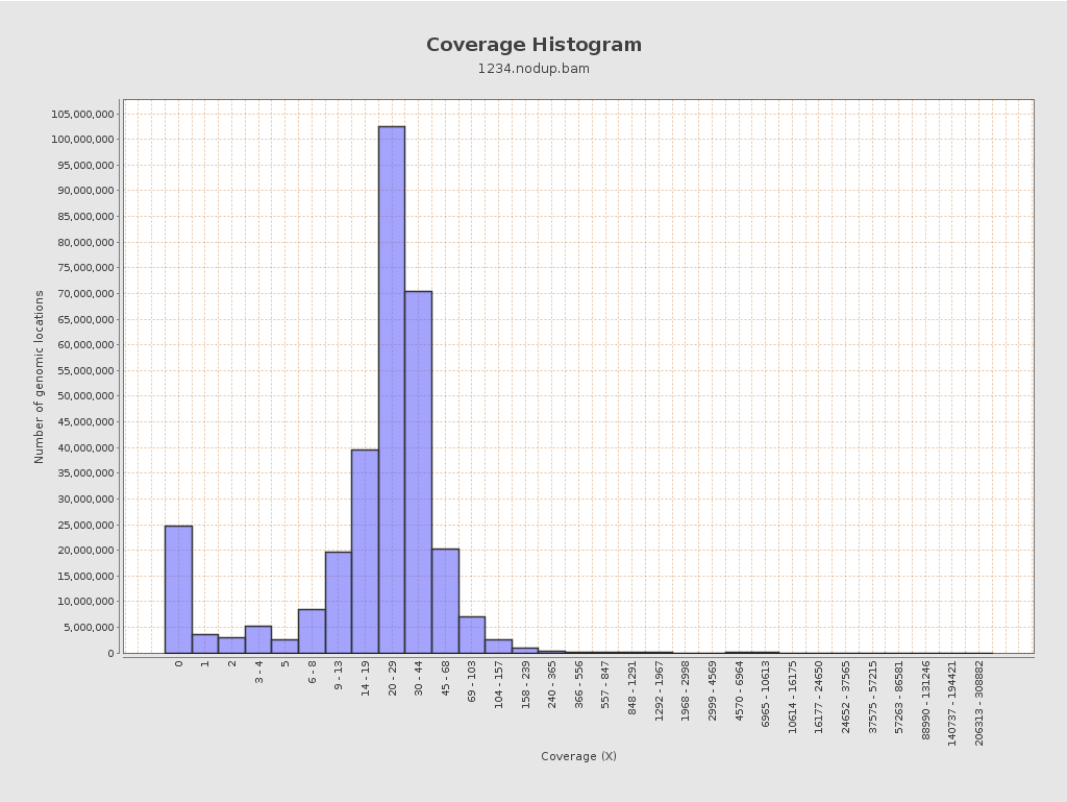
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	798352012	26.8585	81.4395

LT669789.1	36598175	1176552476	32.1478	269.2626
LT669790.1	30422129	1080327979	35.5113	284.3044
LT669791.1	52758100	1697223179	32.1699	237.2476
LT669792.1	28376109	906153128	31.9337	284.4842
LT669793.1	33388210	1008047225	30.1917	185.7491
LT669794.1	50579949	1555098458	30.7454	234.963
LT669795.1	49795044	1917398862	38.5058	422.4037

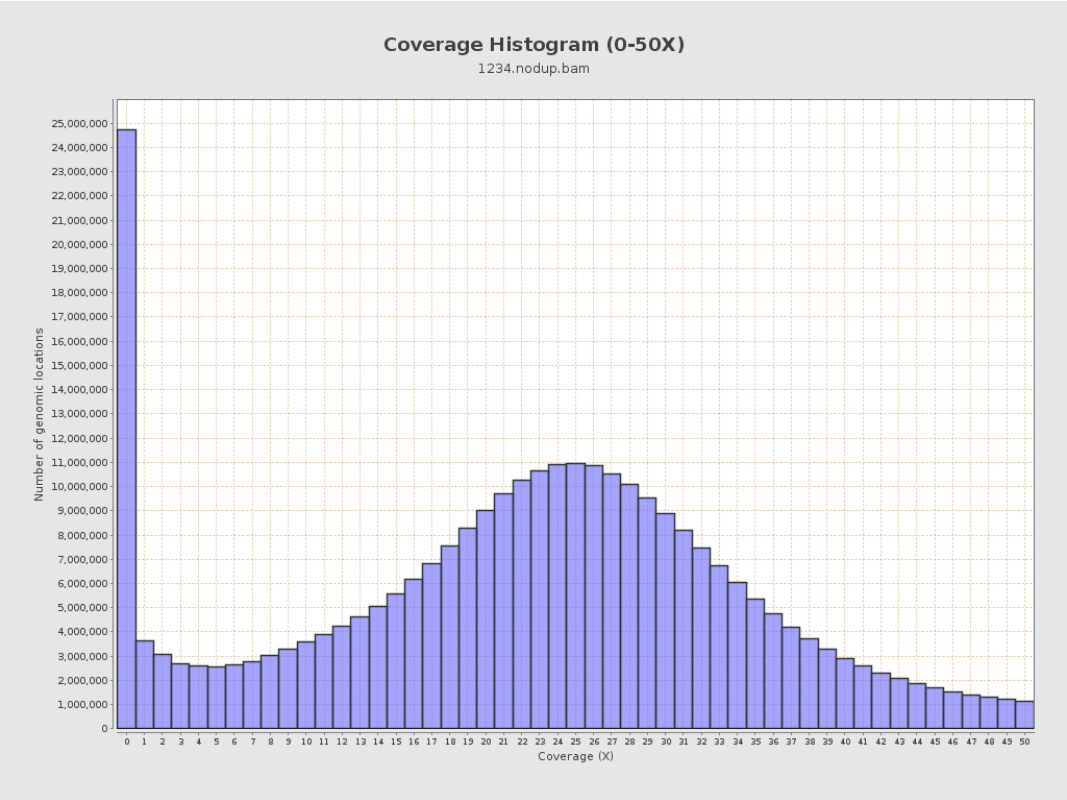
3. Results : Coverage across reference



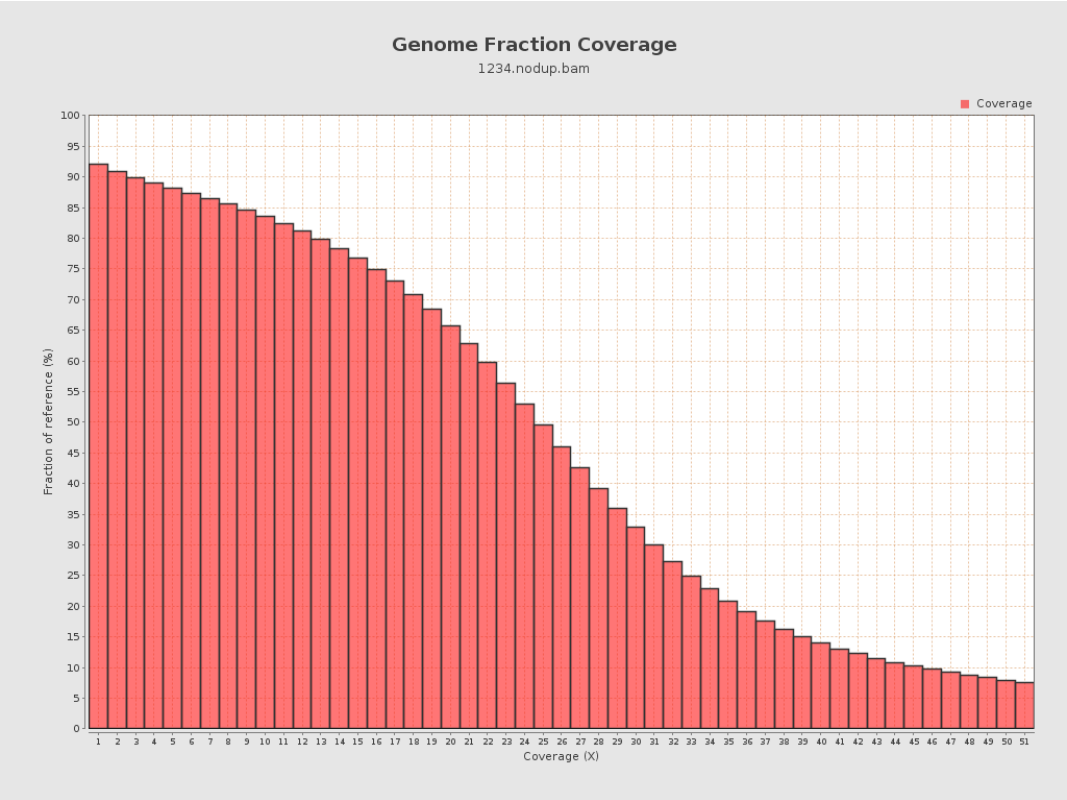
4. Results : Coverage Histogram



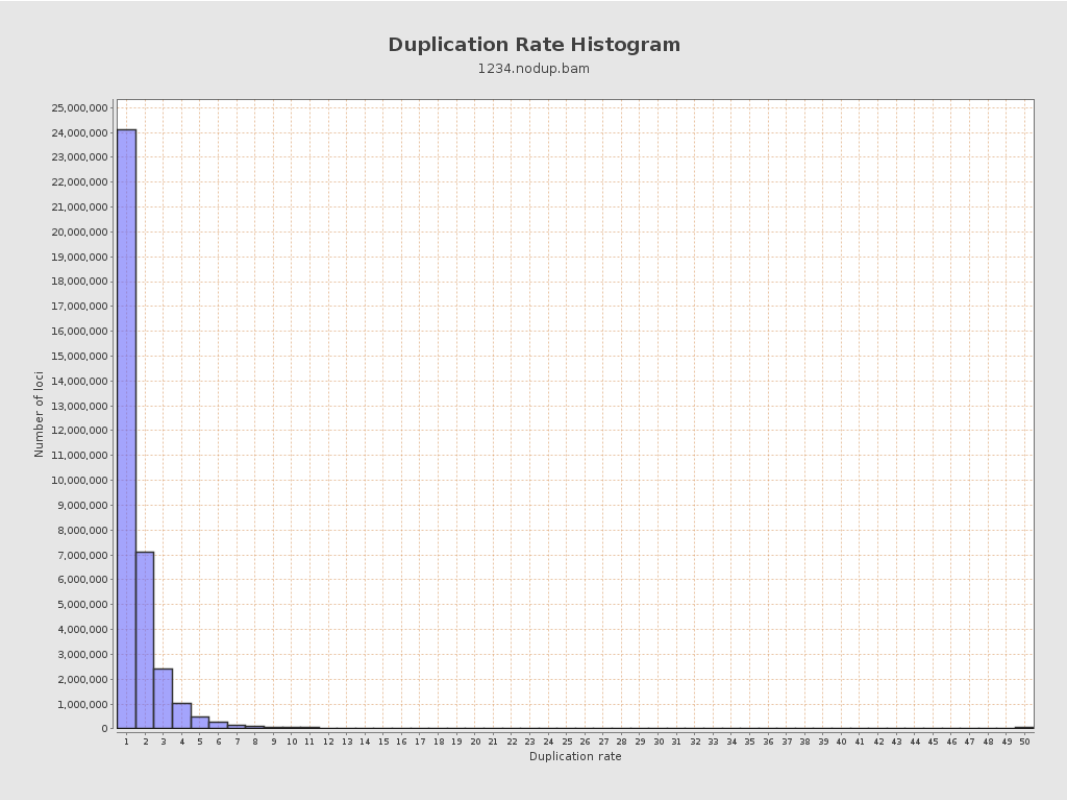
5. Results : Coverage Histogram (0-50X)



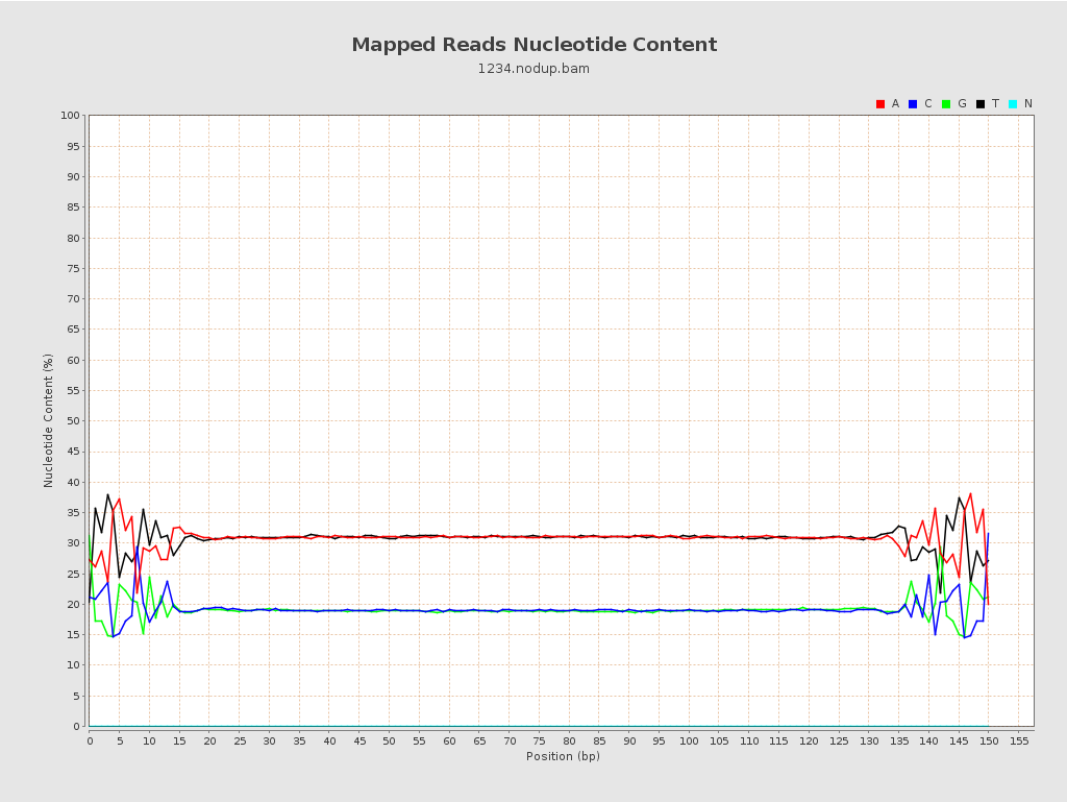
6. Results : Genome Fraction Coverage



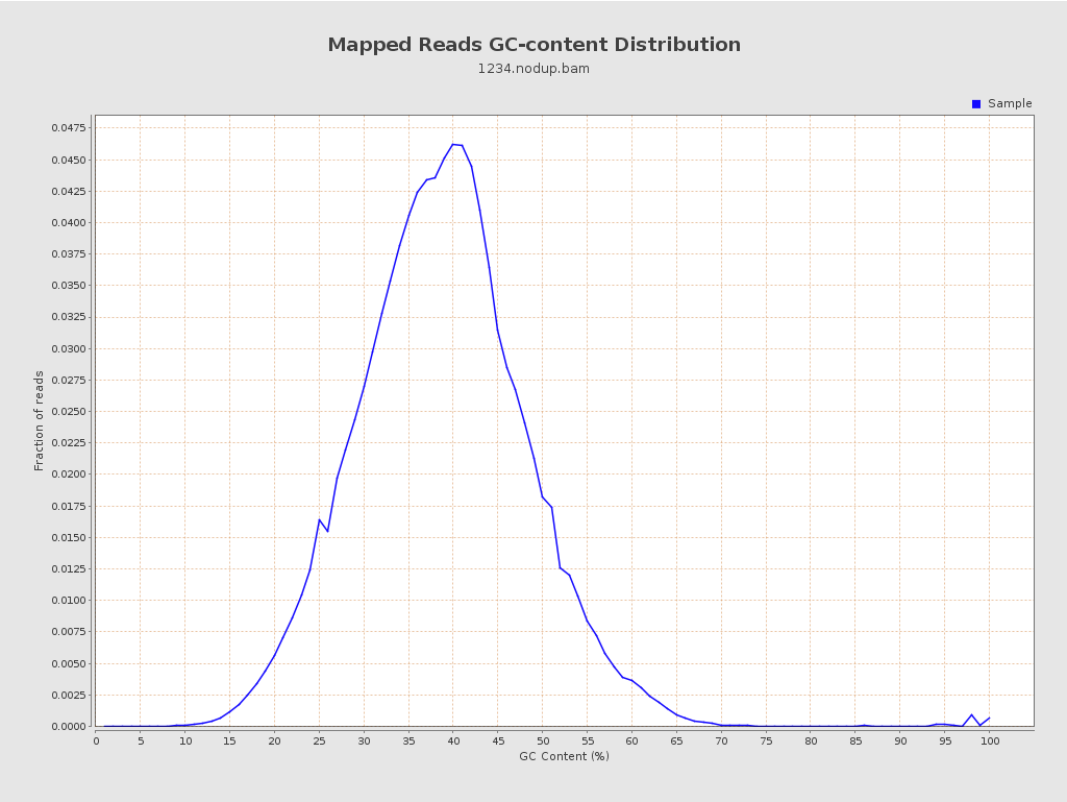
7. Results : Duplication Rate Histogram



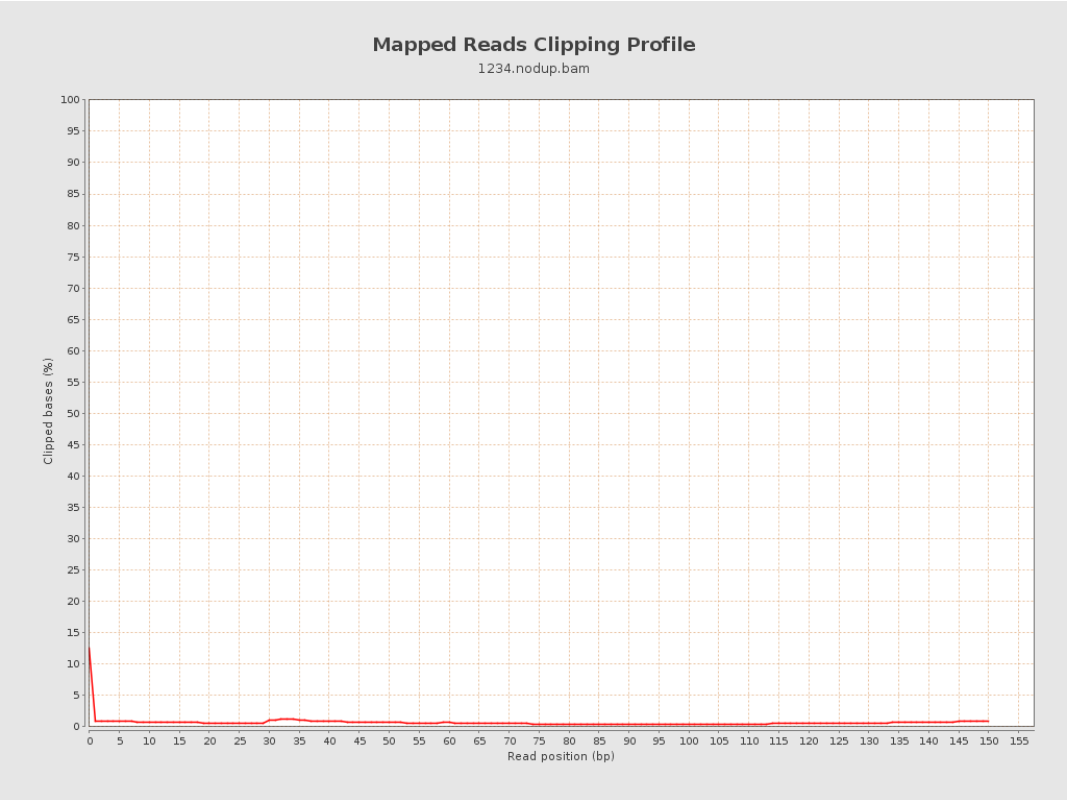
8. Results : Mapped Reads Nucleotide Content



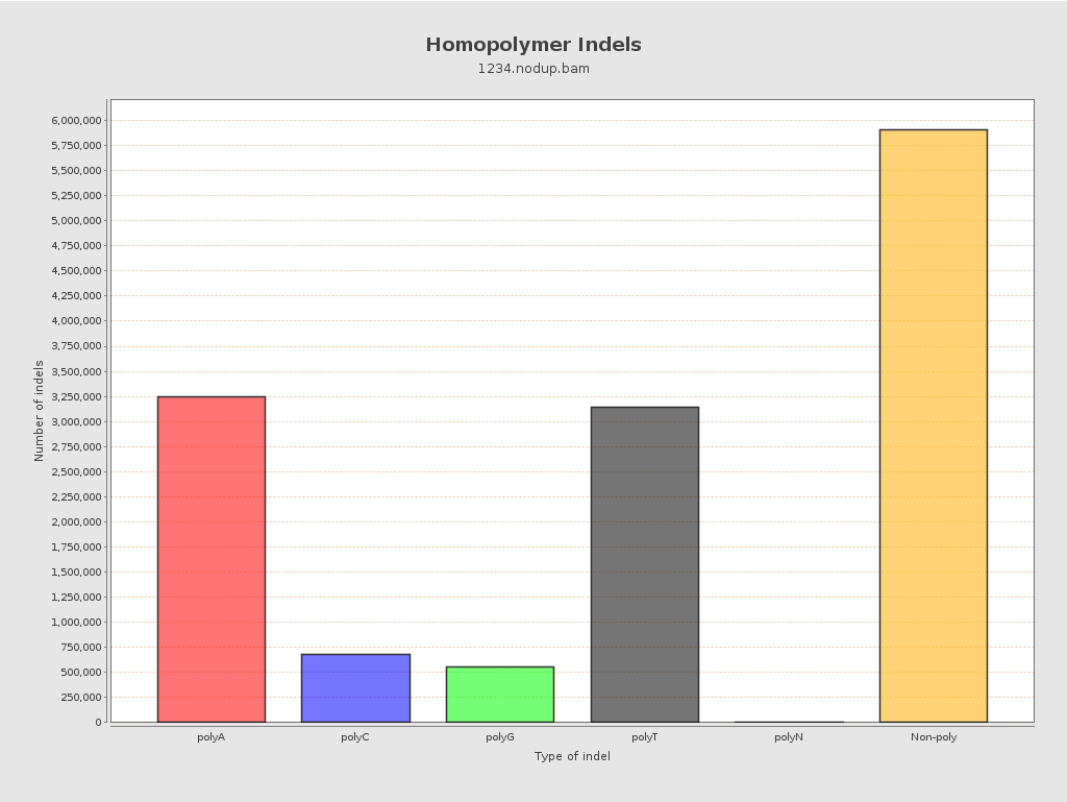
9. Results : Mapped Reads GC-content Distribution



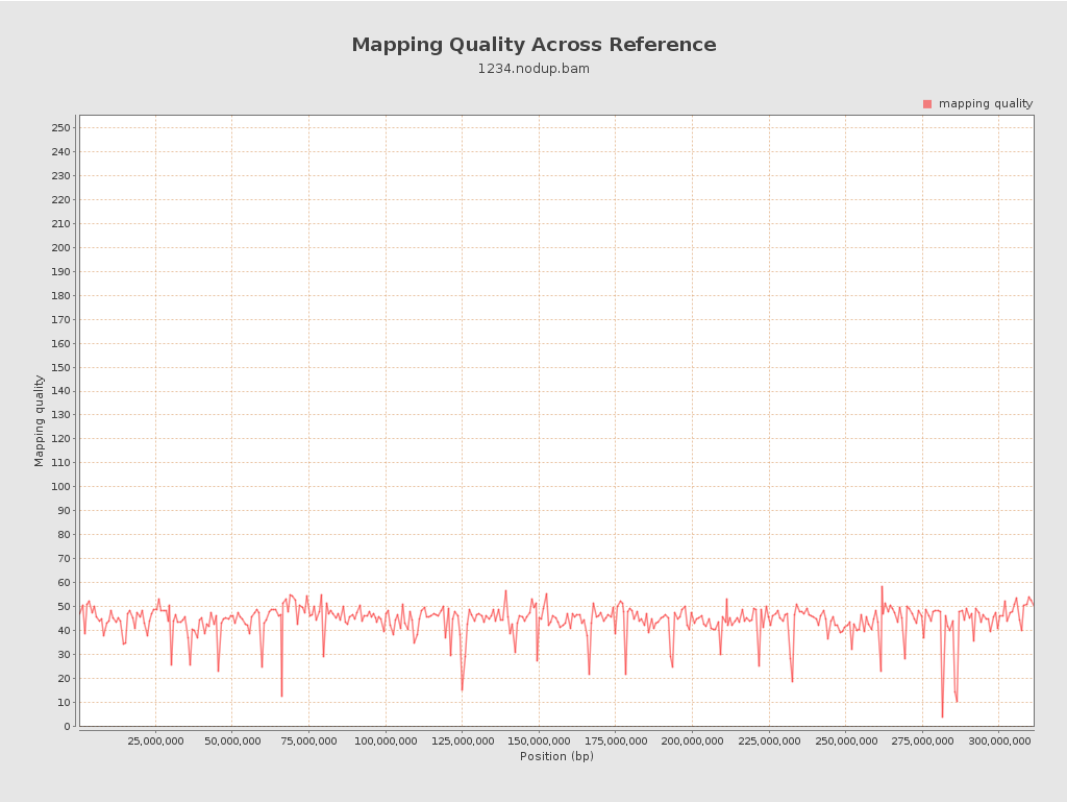
10. Results : Mapped Reads Clipping Profile



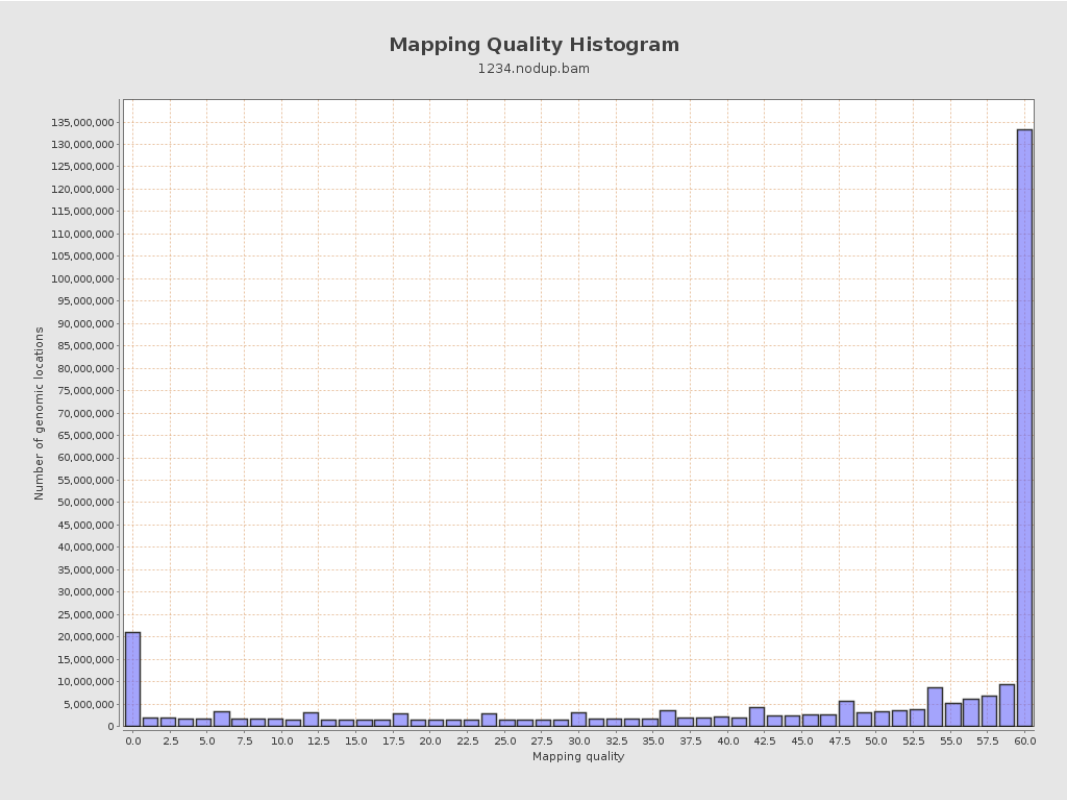
11. Results : Homopolymer Indels



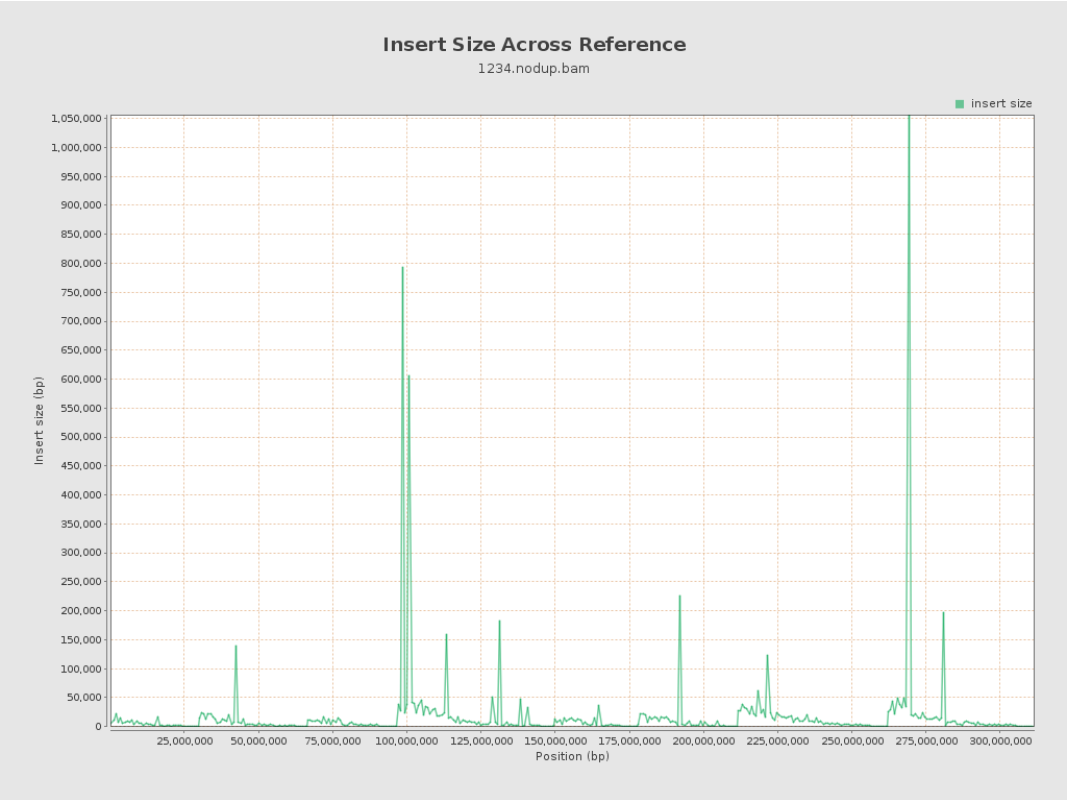
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram