Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1379
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1379 .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_563/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_563_S130_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_563/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_563_S130_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:56 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,735,545
Mapped reads	71,294,471 / 94.14%
Unmapped reads	4,441,074 / 5.86%
Mapped paired reads	71,294,471 / 94.14%
Mapped reads, first in pair	35,847,878 / 47.33%
Mapped reads, second in pair	35,446,593 / 46.8%
Mapped reads, both in pair	69,835,821 / 92.21%
Mapped reads, singletons	1,458,650 / 1.93%
Read min/max/mean length	30 / 151 / 147.84
Duplicated reads (flagged)	10,491,124 / 13.85%
Clipped reads	19,492,590 / 25.74%

2.2. ACGT Content

Number/percentage of A's	2,988,125,172 / 30.88%
Number/percentage of C's	1,846,233,876 / 19.08%
Number/percentage of T's	2,992,388,270 / 30.93%
Number/percentage of G's	1,848,586,244 / 19.11%
Number/percentage of N's	65,227 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	31.1252
Standard Deviation	260.7549

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Insert size

Mean	209,447.59
Standard Deviation	2,171,932.65
P25/Median/P75	280 / 391 / 510

2.6. Mismatches and indels

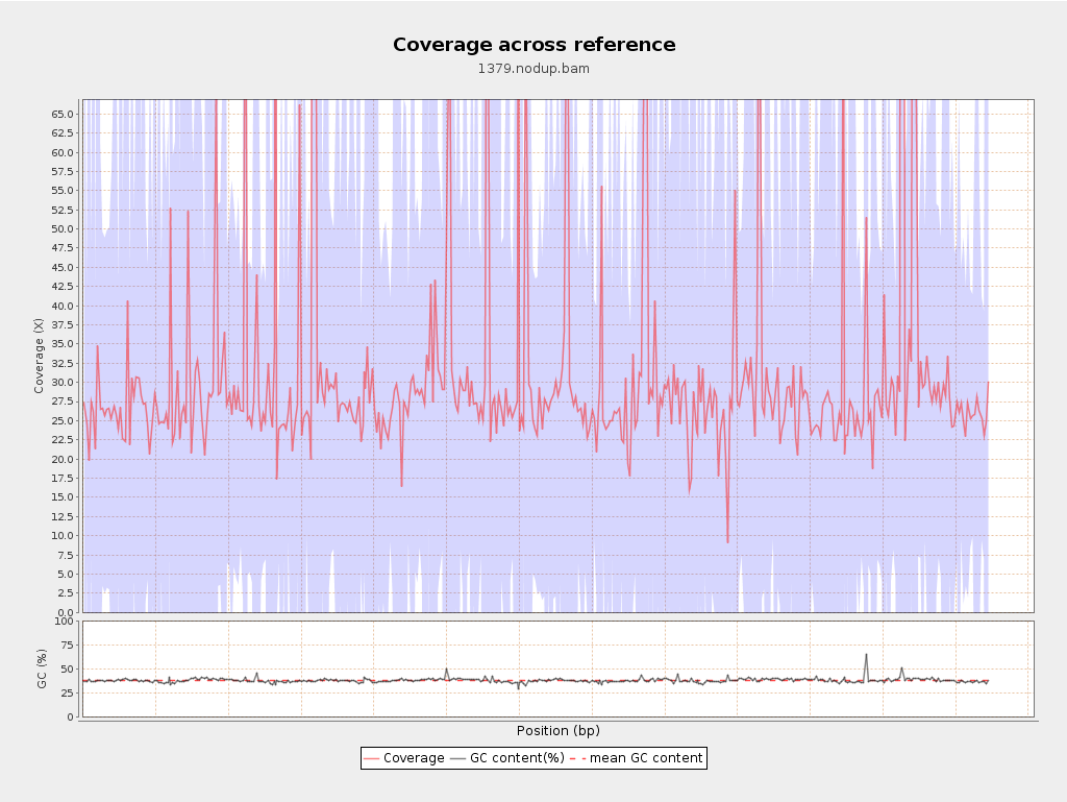
General error rate	2.62%
Mismatches	235,757,266
Insertions	6,333,421
Mapped reads with at least one insertion	8%
Deletions	6,506,729
Mapped reads with at least one deletion	8.13%
Homopolymer indels	56.08%

2.7. Chromosome stats

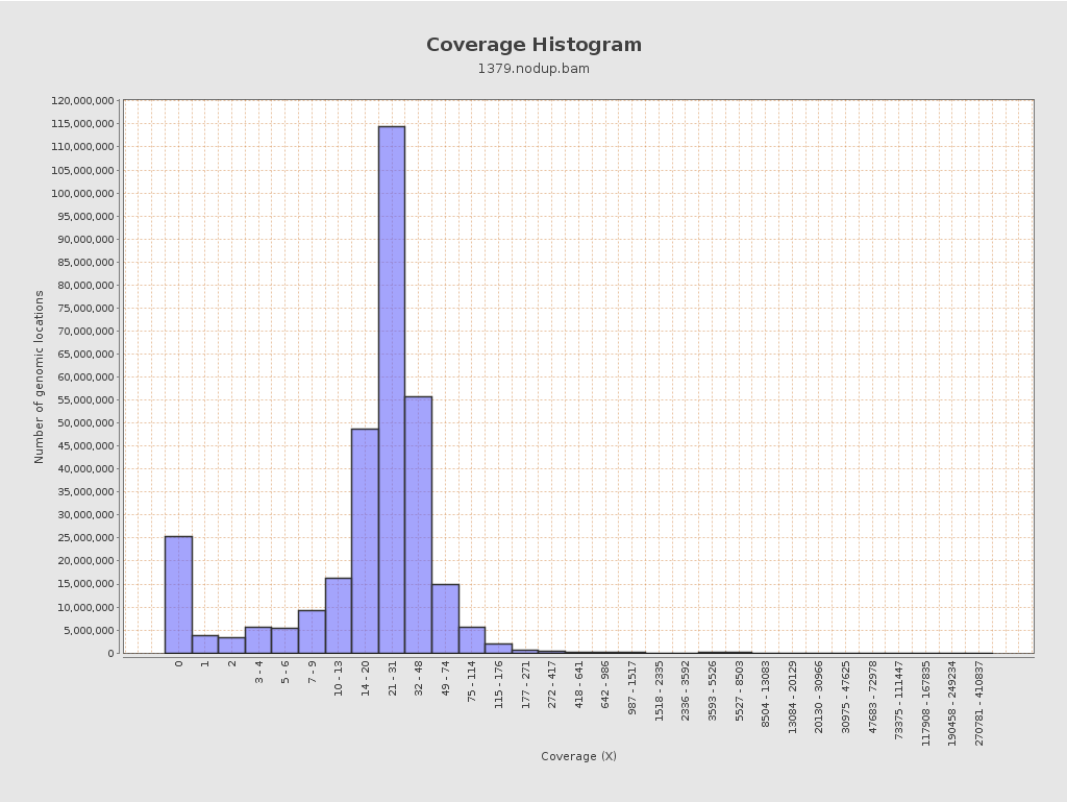
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	783660556	26.3643	60.6452

LT669789.1	36598175	1143402642	31.2421	232.8051
LT669790.1	30422129	1020336383	33.5393	232.3265
LT669791.1	52758100	1602325281	30.3712	199.5614
LT669792.1	28376109	875122353	30.8401	227.9269
LT669793.1	33388210	994358100	29.7817	247.4631
LT669794.1	50579949	1476245406	29.1864	194.8683
LT669795.1	49795044	1804479187	36.2381	446.1475

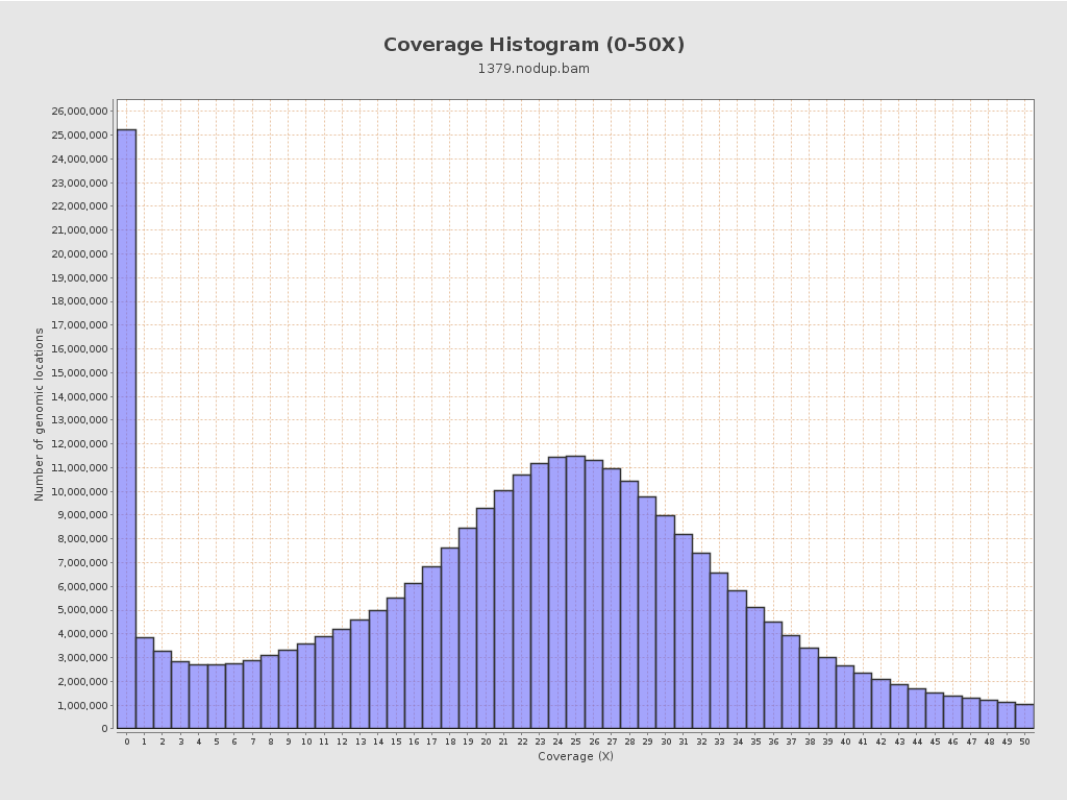
3. Results : Coverage across reference



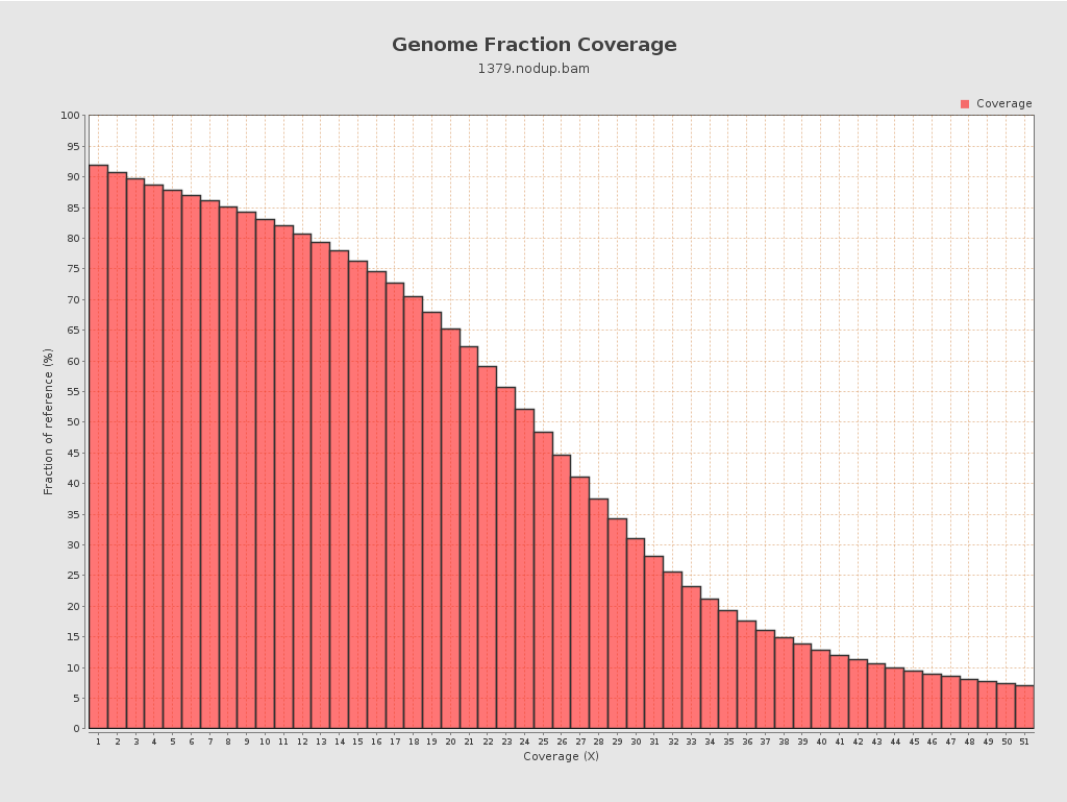
4. Results : Coverage Histogram



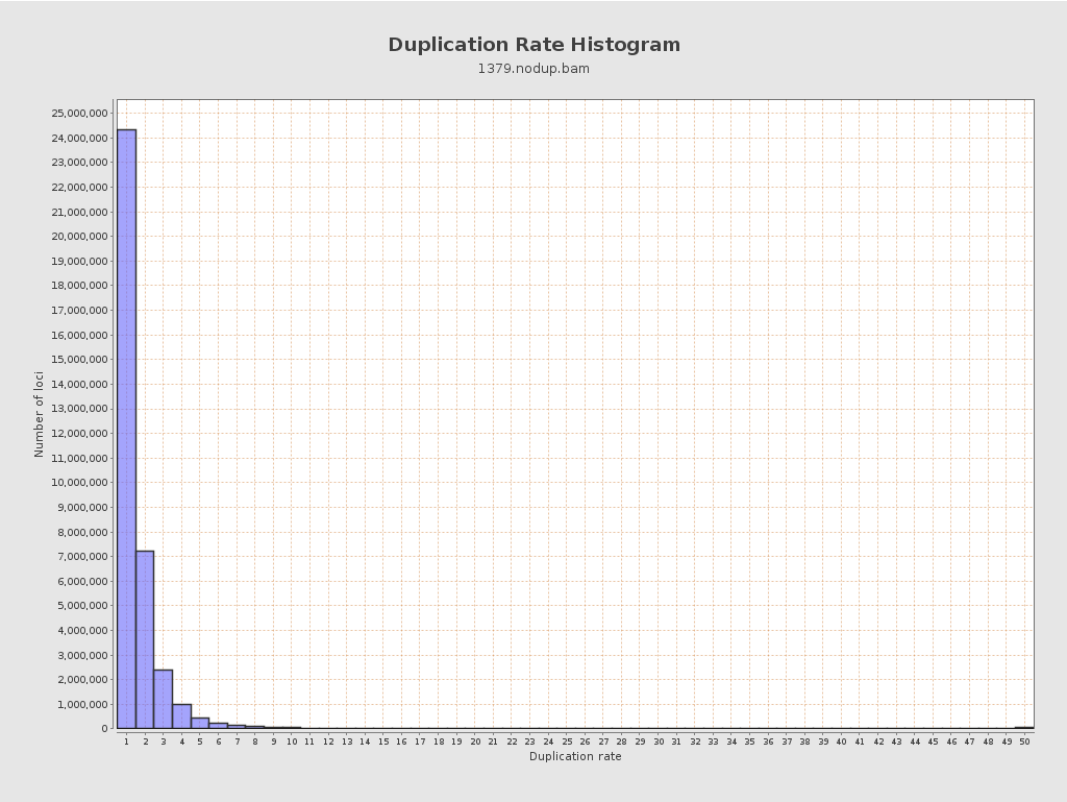
5. Results : Coverage Histogram (0-50X)



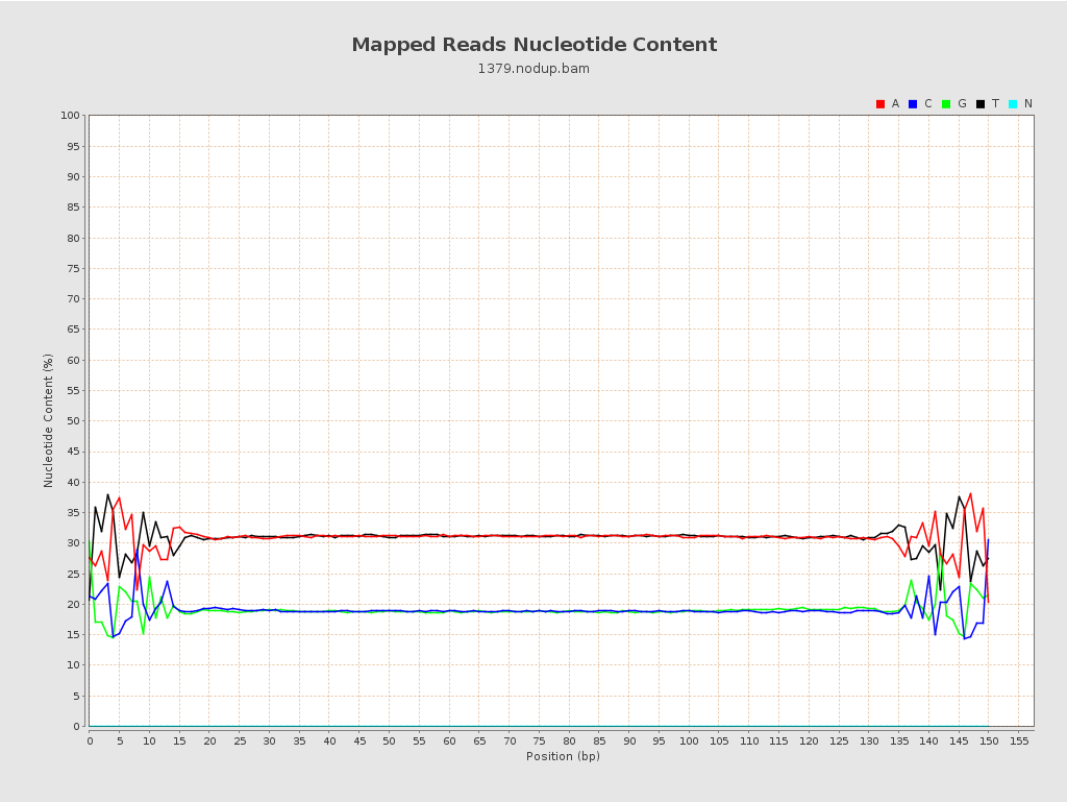
6. Results : Genome Fraction Coverage



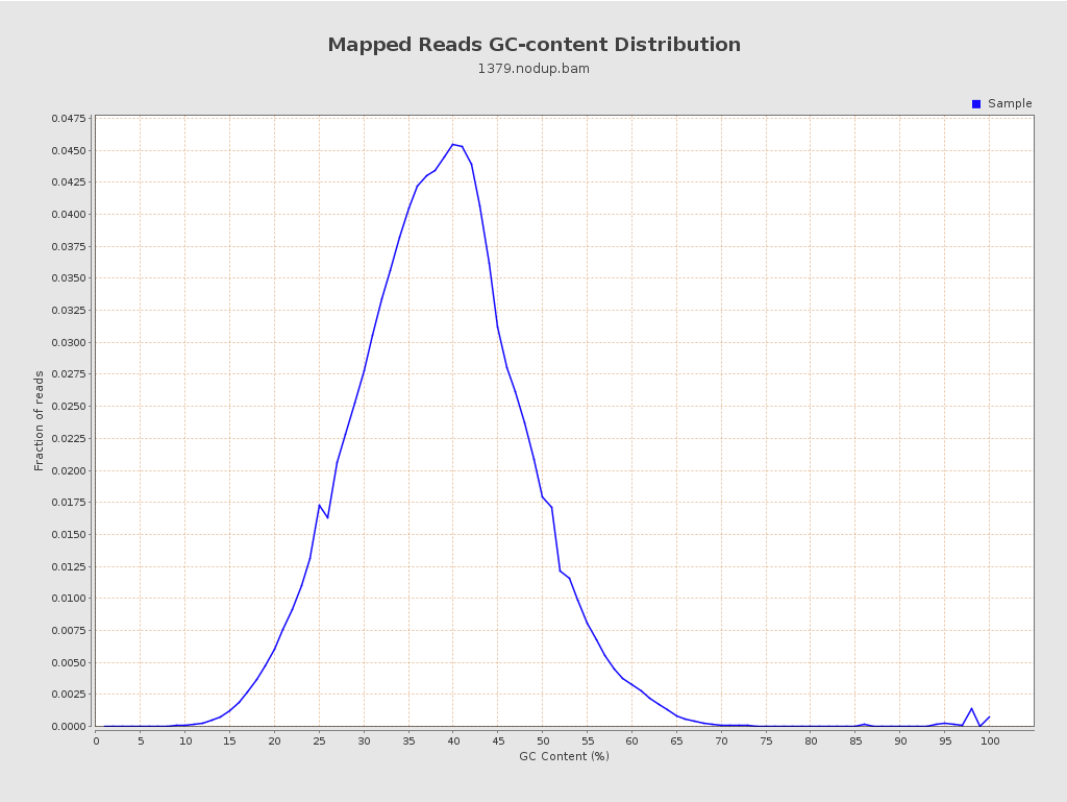
7. Results : Duplication Rate Histogram



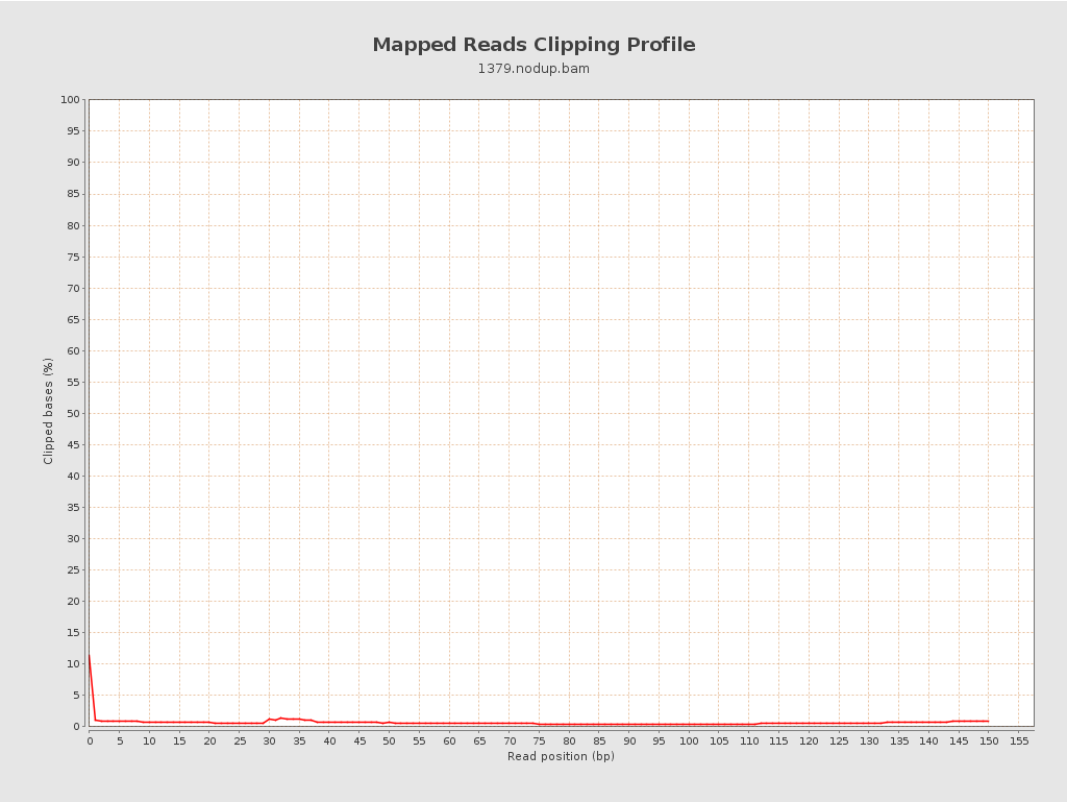
8. Results : Mapped Reads Nucleotide Content



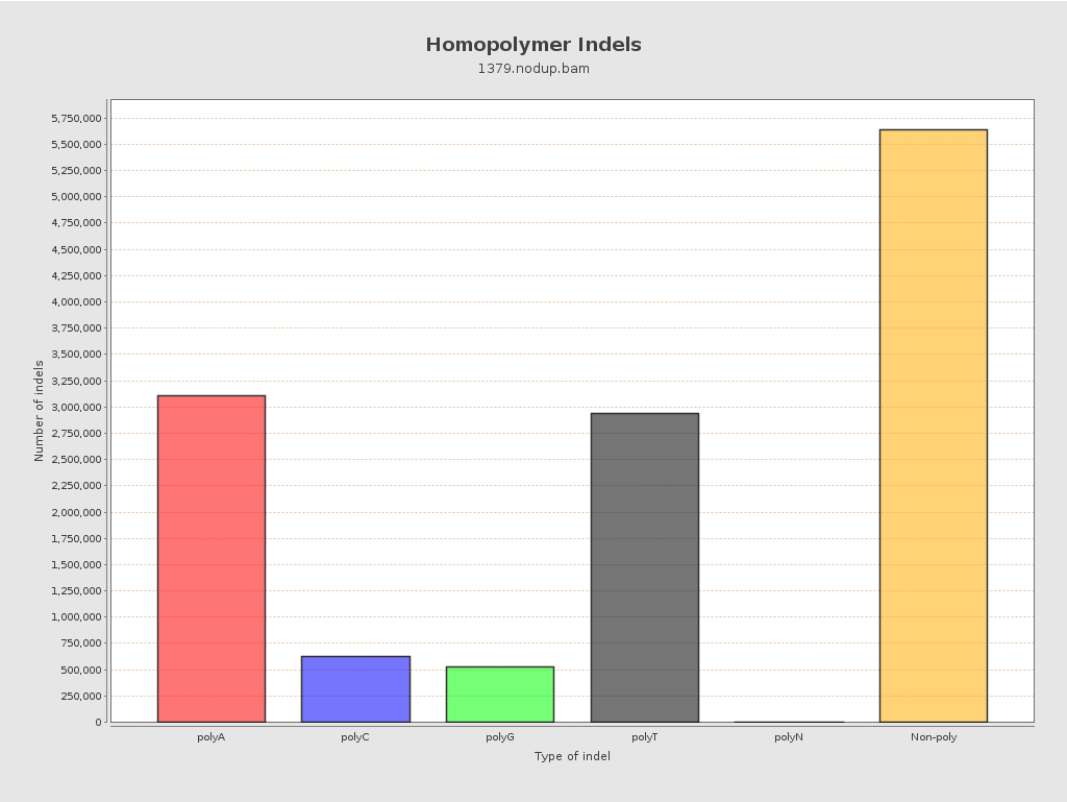
9. Results : Mapped Reads GC-content Distribution



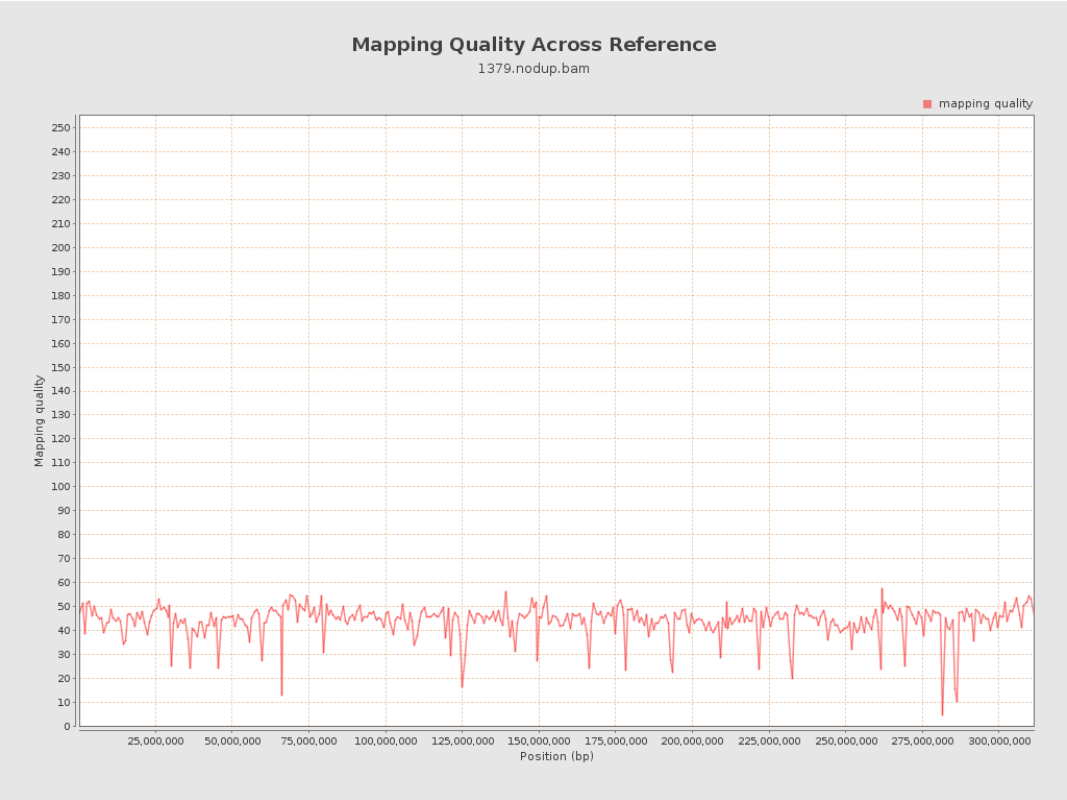
10. Results : Mapped Reads Clipping Profile



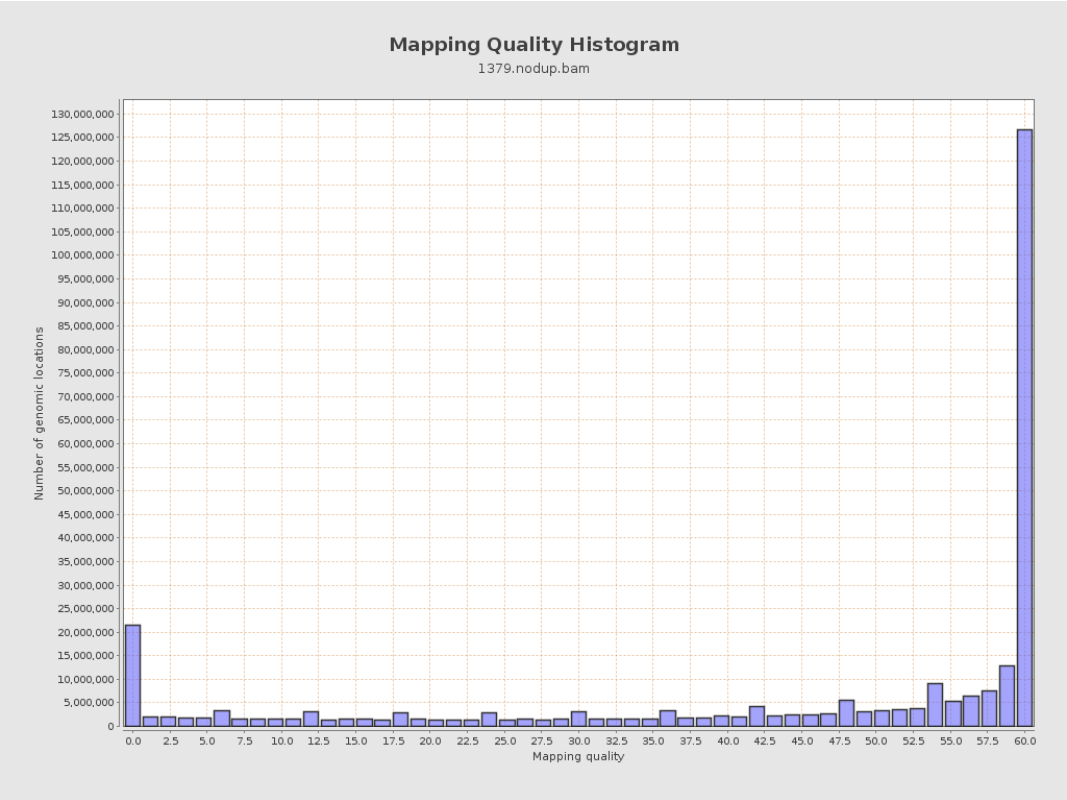
11. Results : Homopolymer Indels



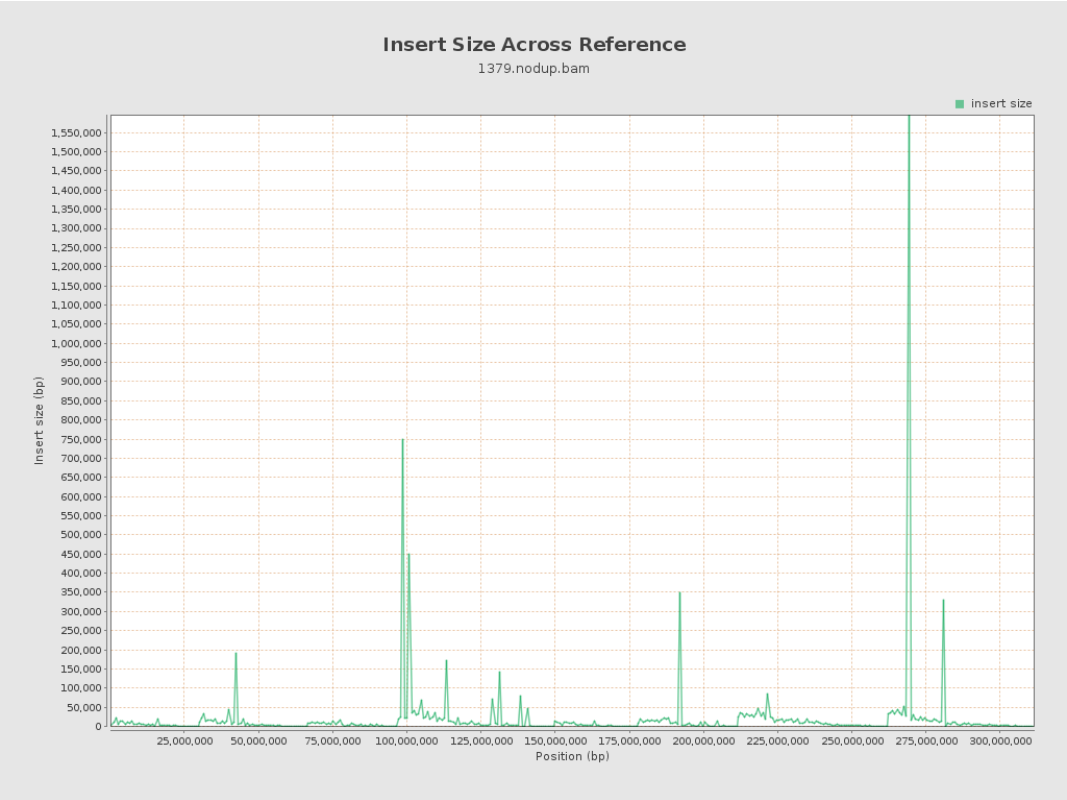
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram