Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1375
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1375 .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_408/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_408_S383_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_408/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_408_S383_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:31:32 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,268,576
Mapped reads	62,849,179 / 94.84%
Unmapped reads	3,419,397 / 5.16%
Mapped paired reads	62,849,179 / 94.84%
Mapped reads, first in pair	31,495,866 / 47.53%
Mapped reads, second in pair	31,353,313 / 47.31%
Mapped reads, both in pair	61,609,784 / 92.97%
Mapped reads, singletons	1,239,395 / 1.87%
Read min/max/mean length	30 / 151 / 147.89
Duplicated reads (flagged)	10,064,582 / 15.19%
Clipped reads	14,416,372 / 21.75%

2.2. ACGT Content

Number/percentage of A's	2,663,853,744 / 30.62%
Number/percentage of C's	1,687,417,352 / 19.4%
Number/percentage of T's	2,669,522,481 / 30.68%
Number/percentage of G's	1,679,462,147 / 19.3%
Number/percentage of N's	29,699 / 0%
GC Percentage	38.7%

2.3. Coverage

Mean	27.9904
Standard Deviation	263.1013

2.4. Mapping Quality

Mean Mapping Quality	42.97

2.5. Insert size

Mean	246,763.07
Standard Deviation	2,338,373.22
P25/Median/P75	341 / 448 / 593

2.6. Mismatches and indels

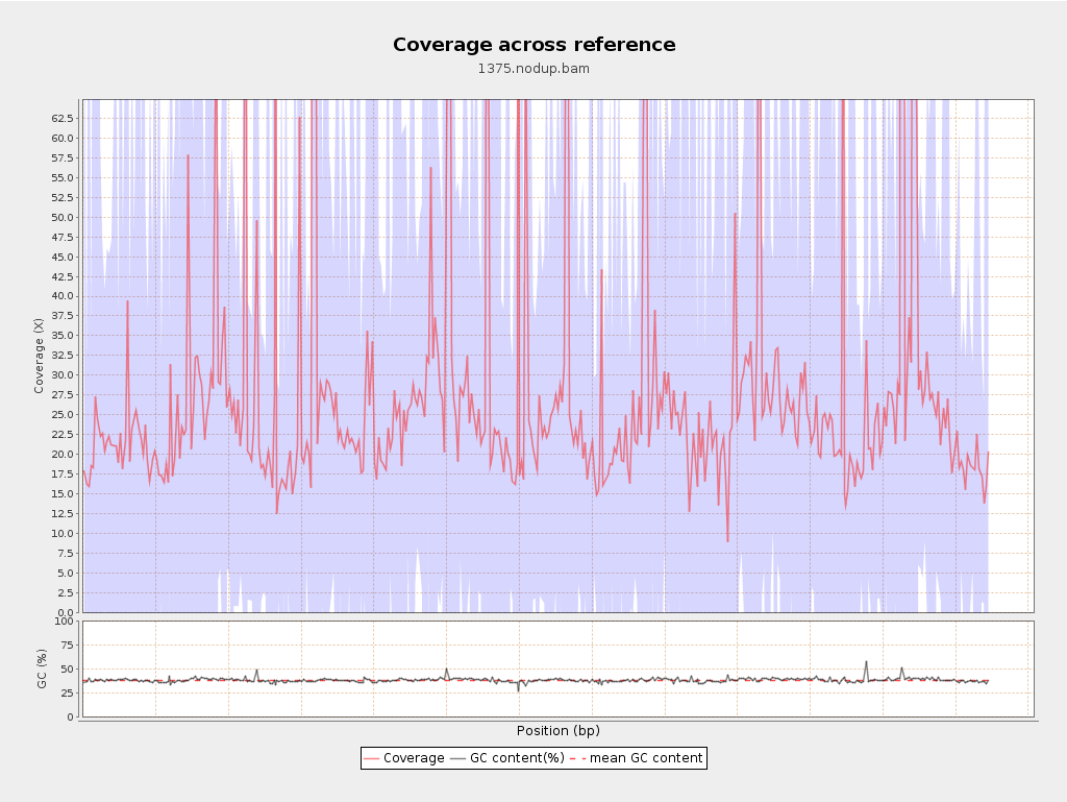
General error rate	2.4%
Mismatches	192,823,321
Insertions	5,960,303
Mapped reads with at least one insertion	8.54%
Deletions	6,060,636
Mapped reads with at least one deletion	8.54%
Homopolymer indels	55.38%

2.7. Chromosome stats

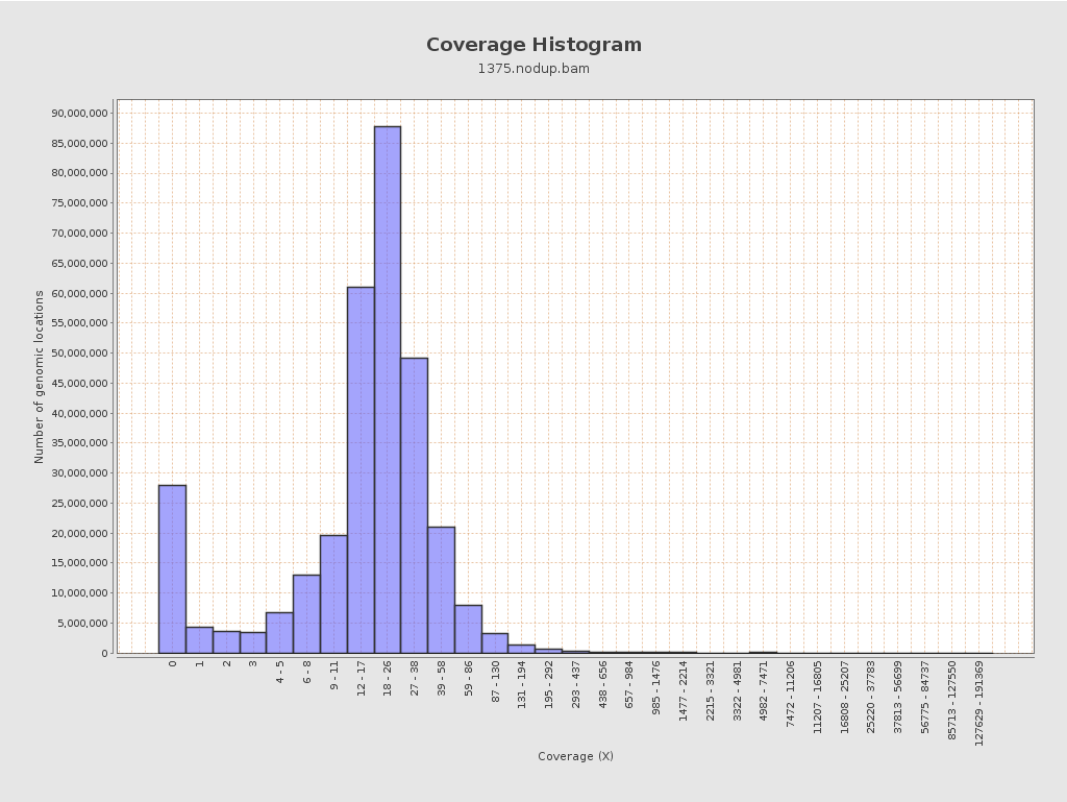
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	621514769	20.9093	91.0283

LT669789.1	36598175	1062968495	29.0443	291.9408
LT669790.1	30422129	870273020	28.6066	230.1439
LT669791.1	52758100	1491803607	28.2763	254.3832
LT669792.1	28376109	766493447	27.0119	298.043
LT669793.1	33388210	870364423	26.068	179.591
LT669794.1	50579949	1391923137	27.5193	250.5408
LT669795.1	49795044	1647640177	33.0884	358.681

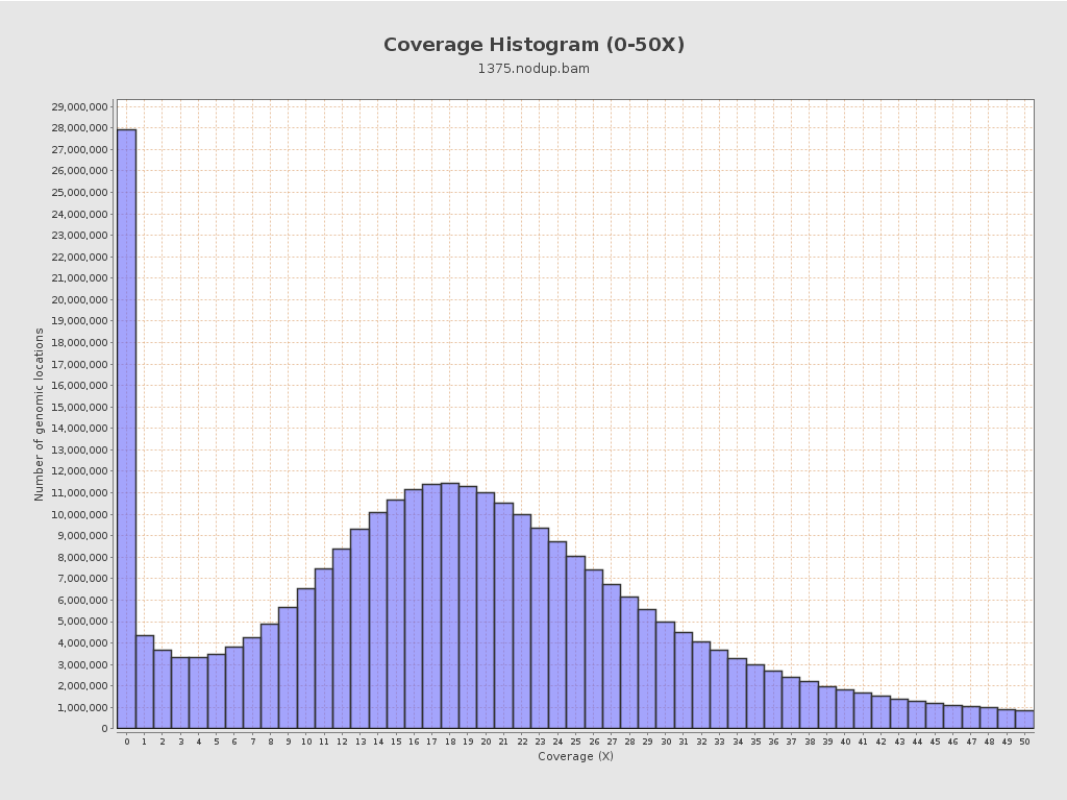
3. Results : Coverage across reference



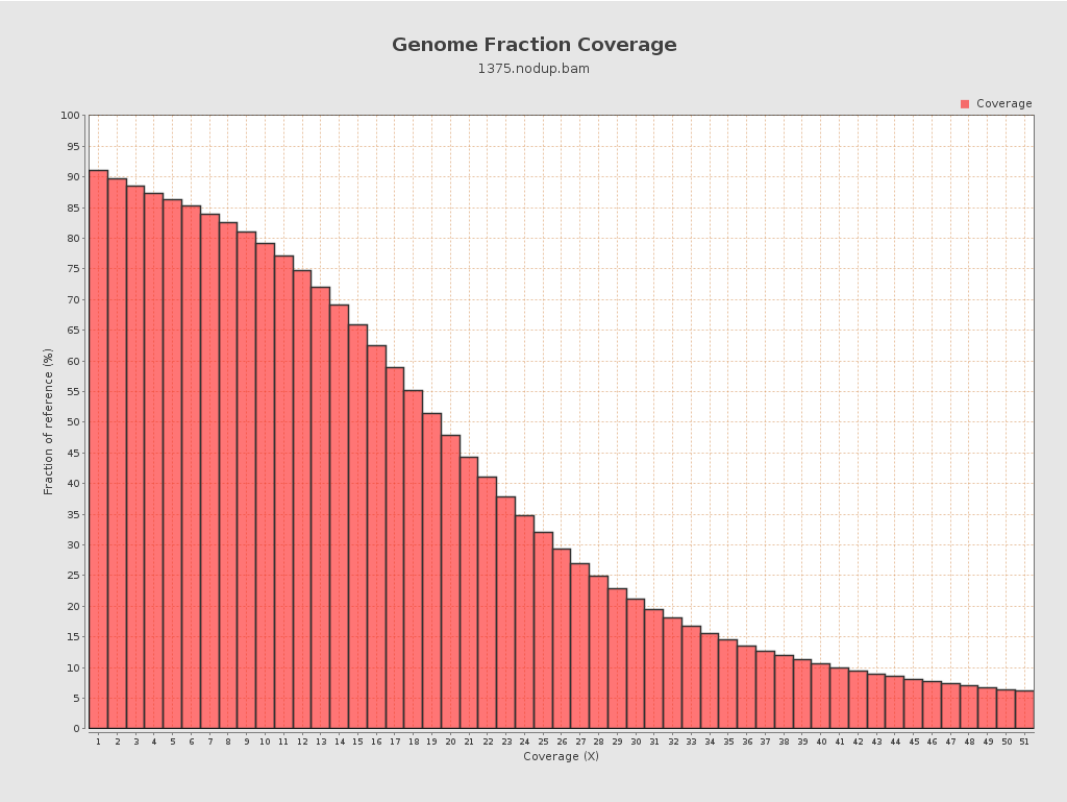
4. Results : Coverage Histogram



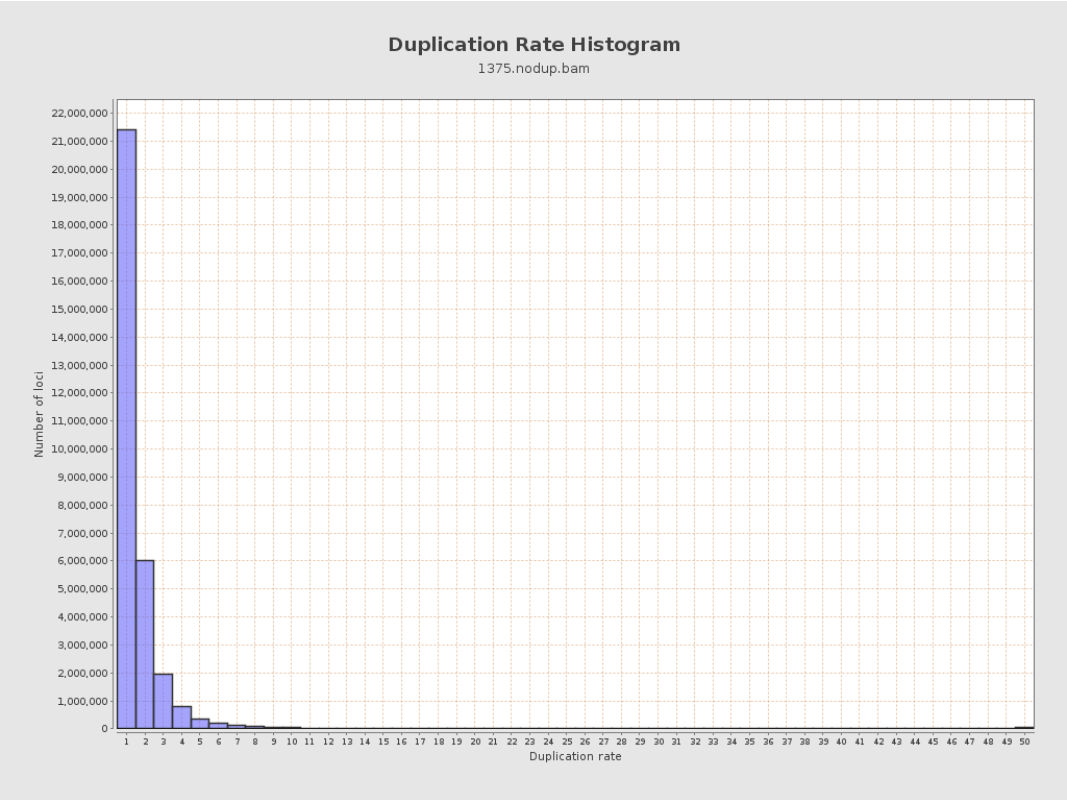
5. Results : Coverage Histogram (0-50X)



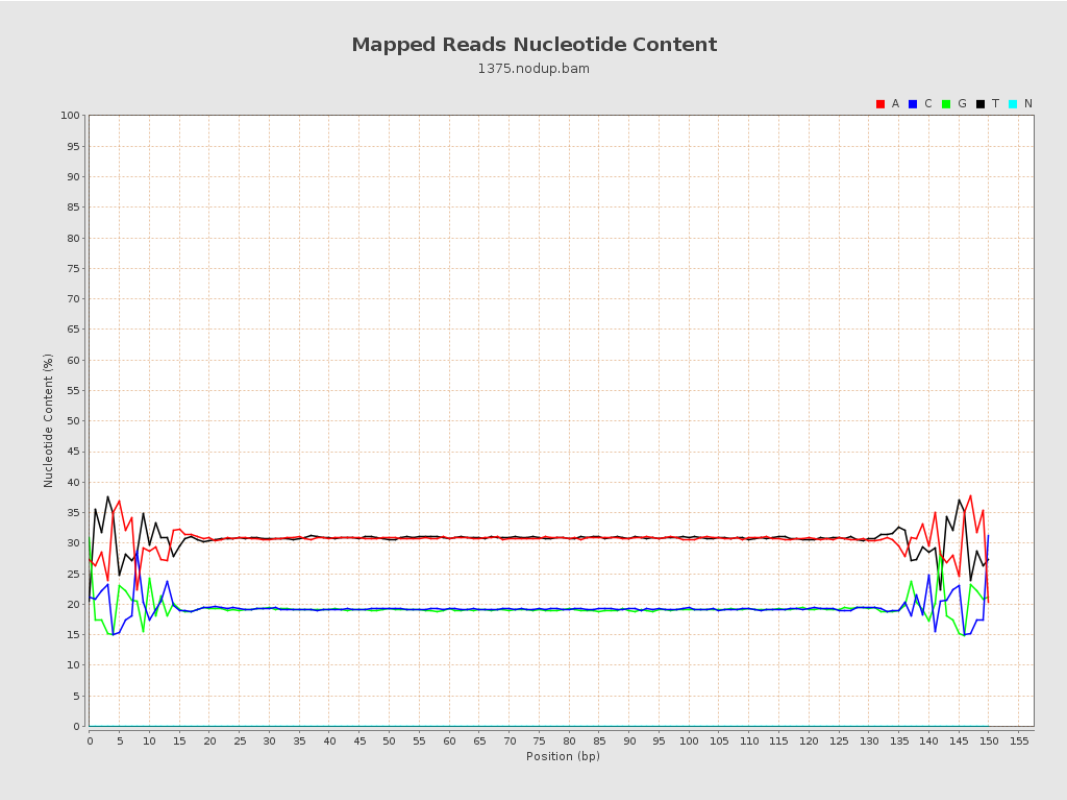
6. Results : Genome Fraction Coverage



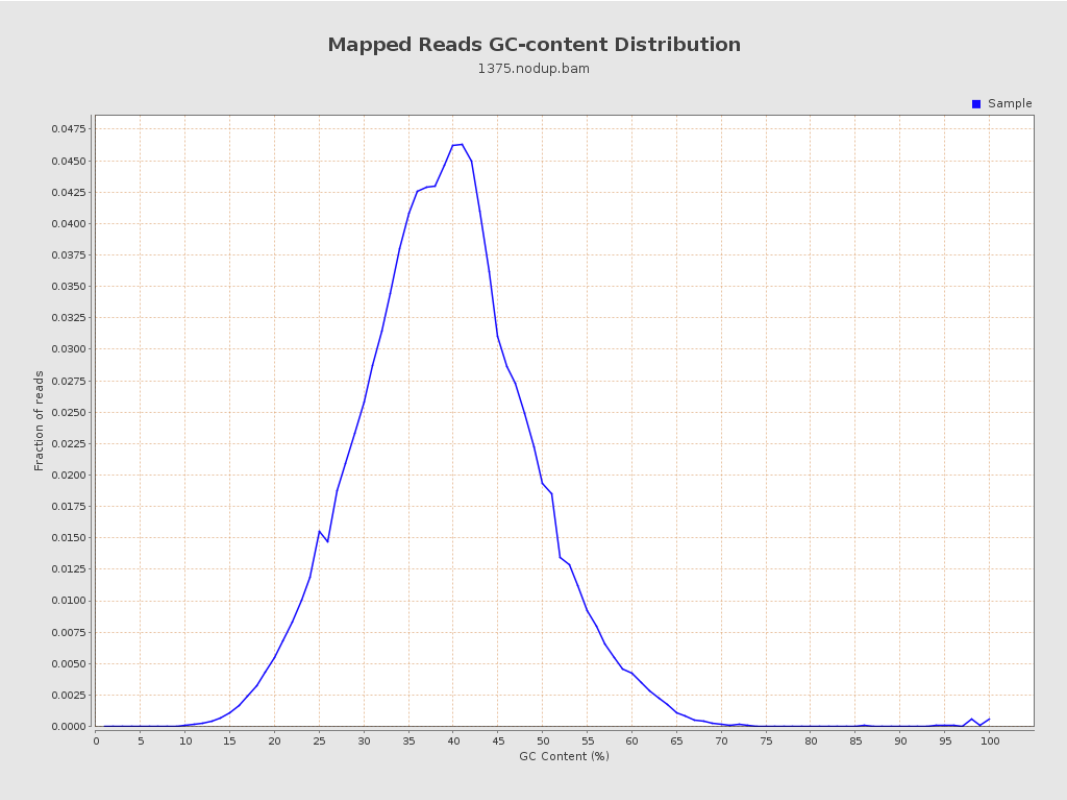
7. Results : Duplication Rate Histogram



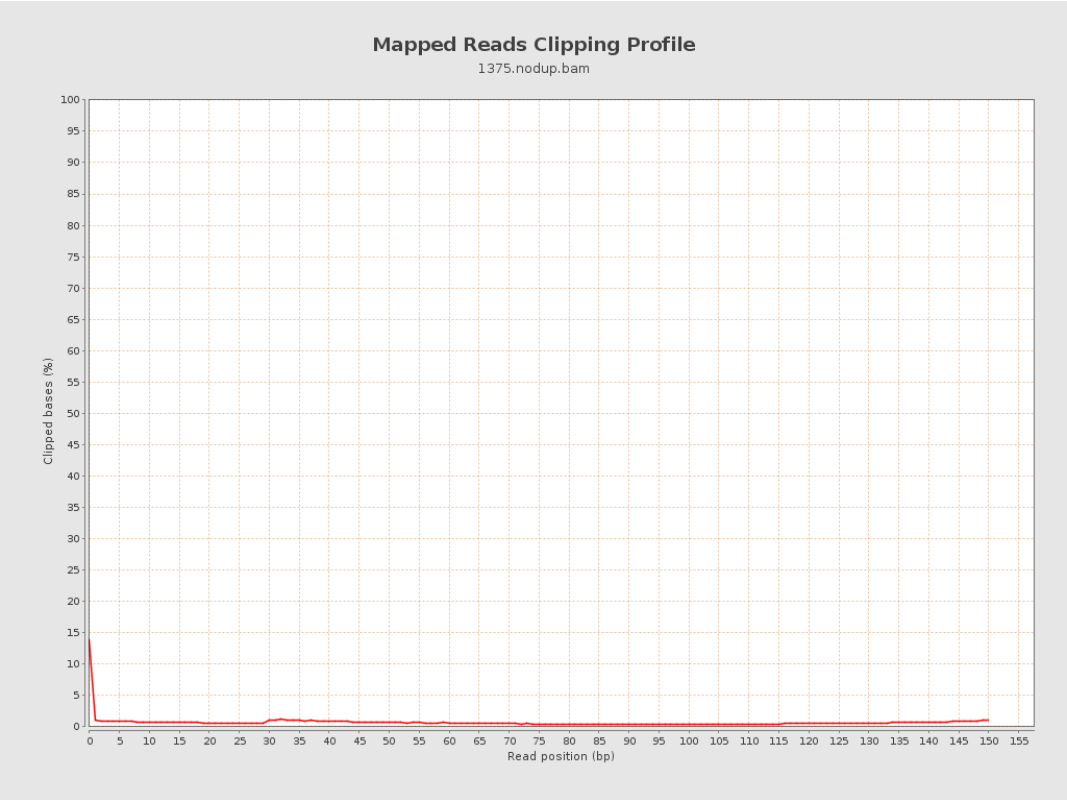
8. Results : Mapped Reads Nucleotide Content



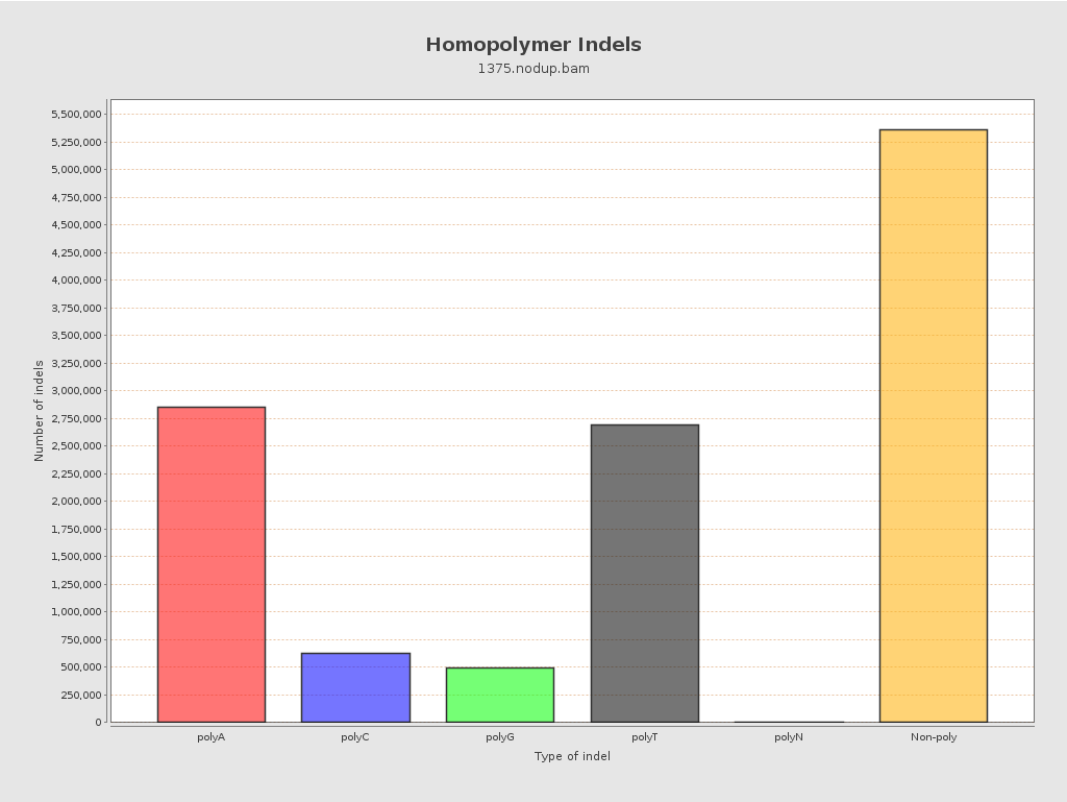
9. Results : Mapped Reads GC-content Distribution



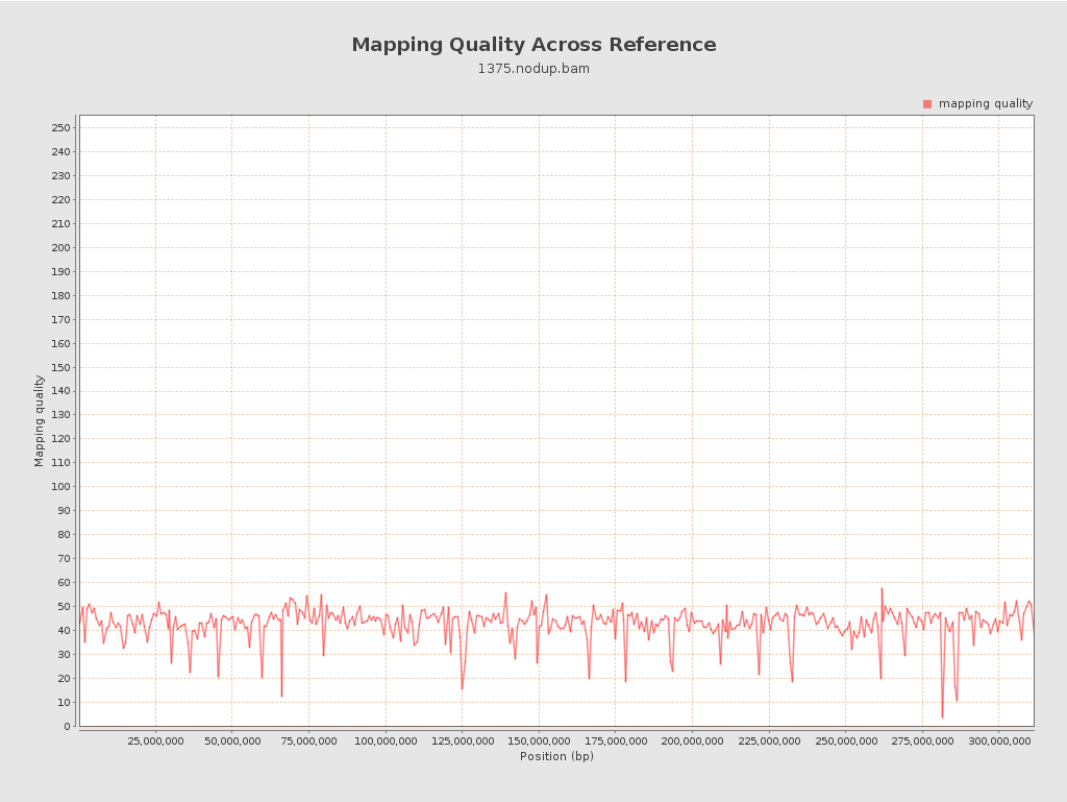
10. Results : Mapped Reads Clipping Profile



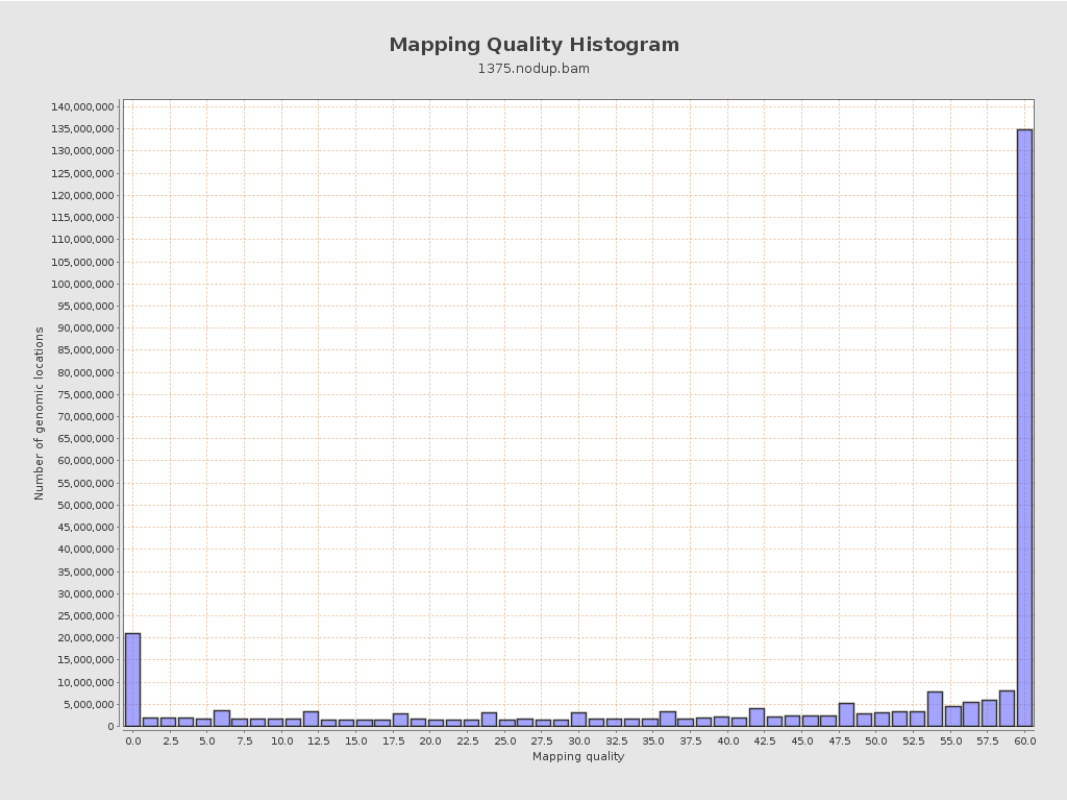
11. Results : Homopolymer Indels



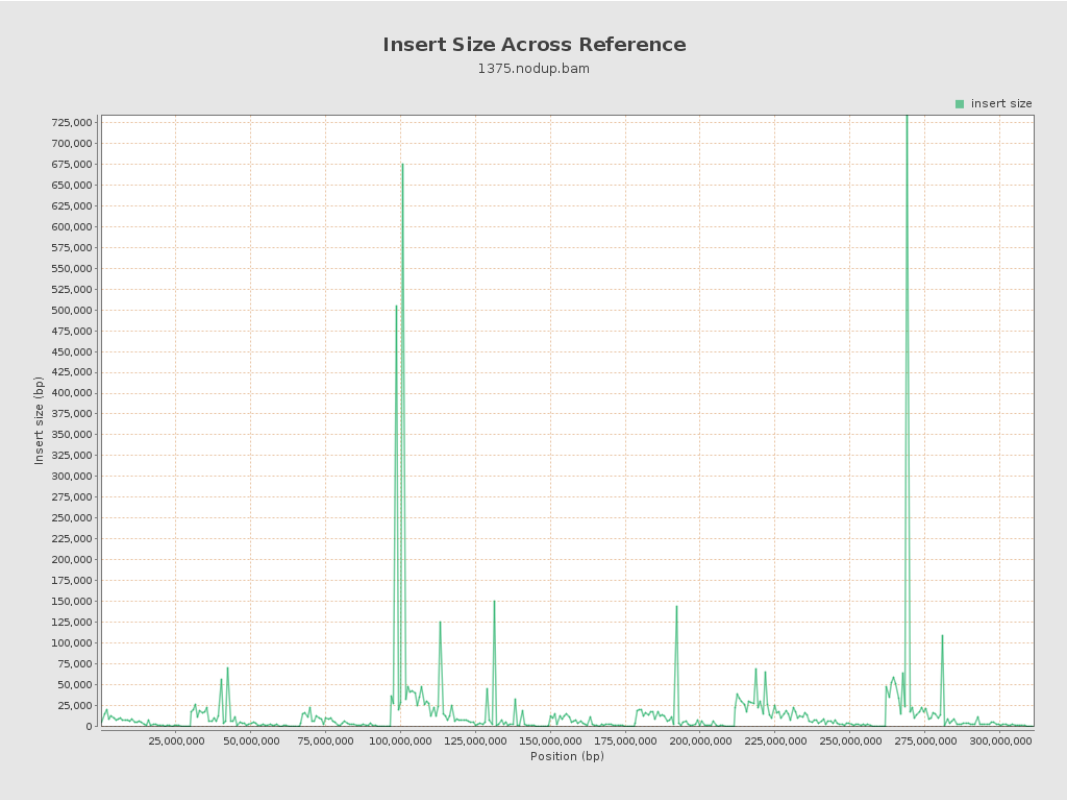
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram