Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1387
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1387 .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_479/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_479_S454_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_479/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_479_S454_L004_R2_001.fastq.gz
Size of a homopolymer:	3

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	40,922,096
Mapped reads	38,809,008 / 94.84%
Unmapped reads	2,113,088 / 5.16%
Mapped paired reads	38,809,008 / 94.84%
Mapped reads, first in pair	19,433,646 / 47.49%
Mapped reads, second in pair	19,375,362 / 47.35%
Mapped reads, both in pair	38,070,830 / 93.03%
Mapped reads, singletons	738,178 / 1.8%
Read min/max/mean length	30 / 151 / 148.28
Duplicated reads (flagged)	5,284,271 / 12.91%
Clipped reads	8,270,220 / 20.21%

2.2. ACGT Content

Number/percentage of A's	1,662,599,520 / 30.66%
Number/percentage of C's	1,051,300,743 / 19.39%
Number/percentage of T's	1,664,802,764 / 30.7%
Number/percentage of G's	1,044,315,465 / 19.26%
Number/percentage of N's	17,582 / 0%
GC Percentage	38.64%

2.3. Coverage

Mean	17.4445
Standard Deviation	157.7351

2.4. Mapping Quality

Mean Mapping Quality	43.81

2.5. Insert size

Mean	229,488.95
Standard Deviation	2,251,751.25
P25/Median/P75	365 / 475 / 623

2.6. Mismatches and indels

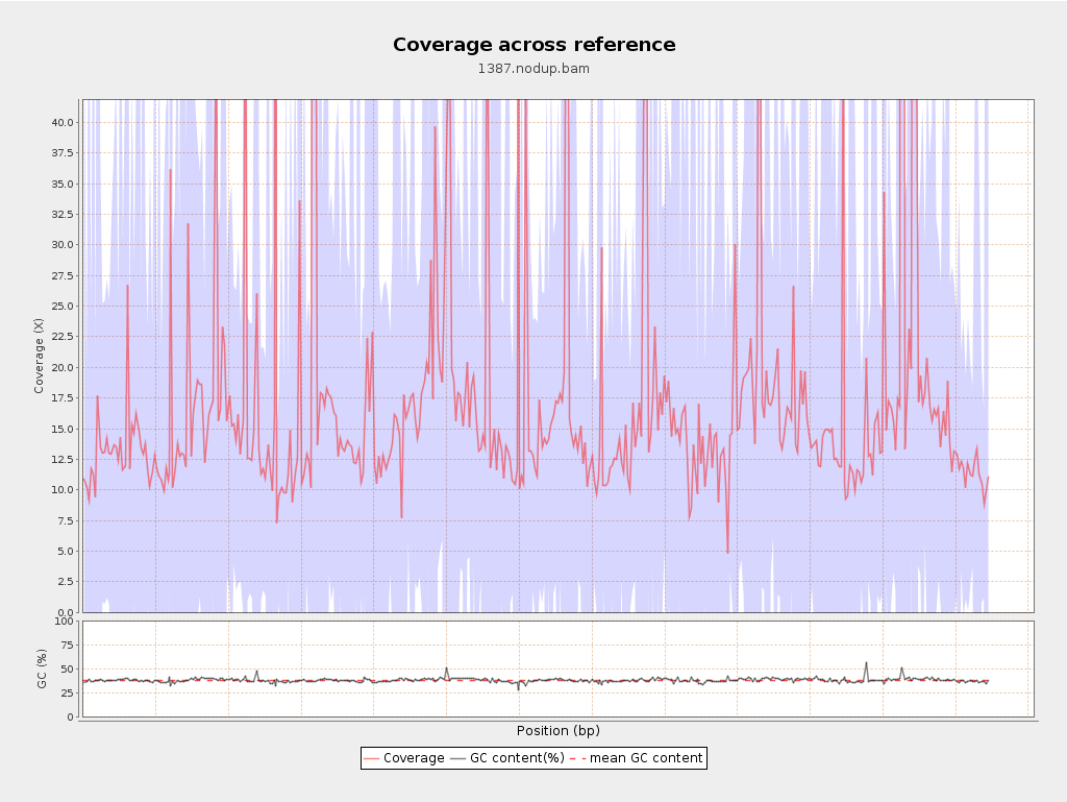
General error rate	2.37%
Mismatches	119,025,798
Insertions	3,485,140
Mapped reads with at least one insertion	8.11%
Deletions	3,567,224
Mapped reads with at least one deletion	8.19%
Homopolymer indels	55.86%

2.7. Chromosome stats

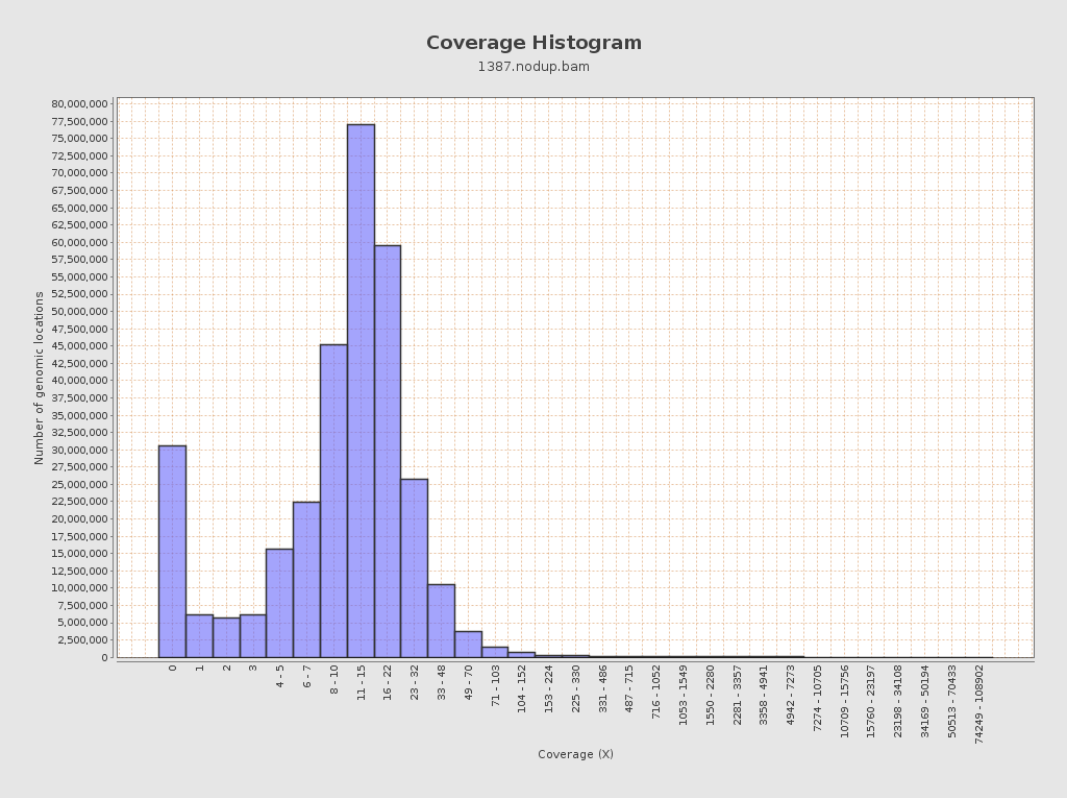
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	383098108	12.8884	34.6472

LT669789.1	36598175	644712645	17.616	161.2439
LT669790.1	30422129	529294837	17.3983	135.1489
LT669791.1	52758100	928555976	17.6003	119.3555
LT669792.1	28376109	471620927	16.6204	191.7944
LT669793.1	33388210	538932168	16.1414	114.2857
LT669794.1	50579949	857543641	16.9542	133.5107
LT669795.1	49795044	1082688604	21.7429	248.5493

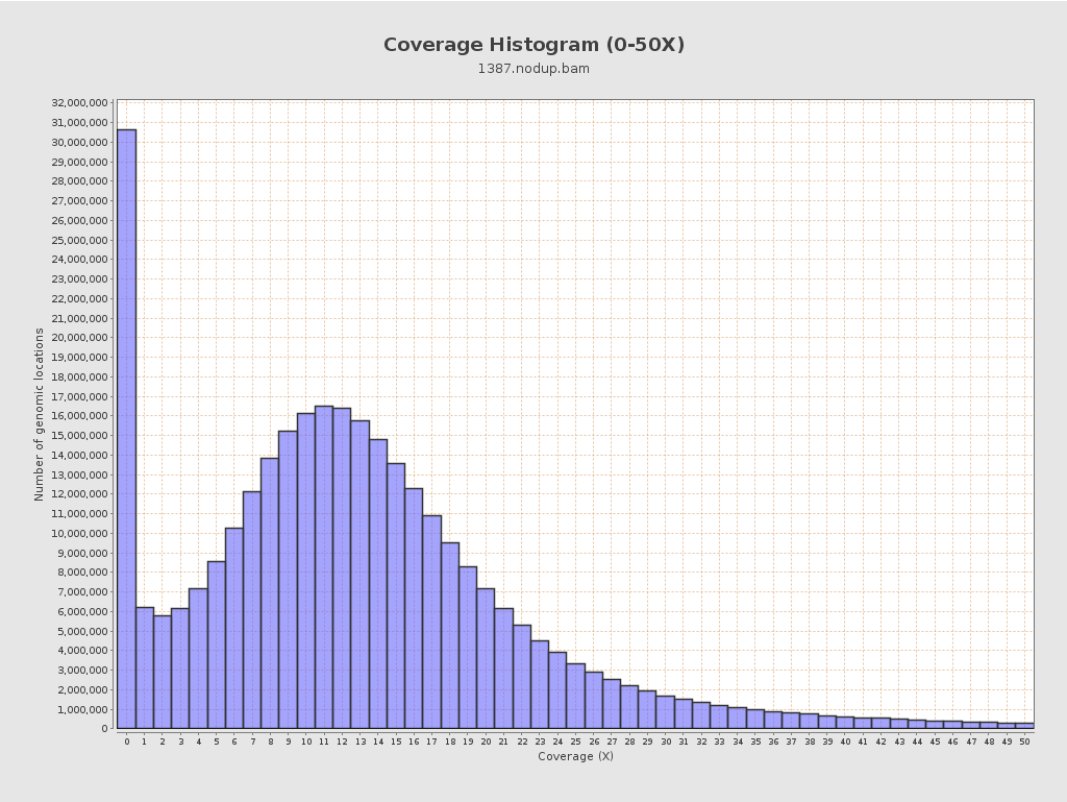
3. Results : Coverage across reference



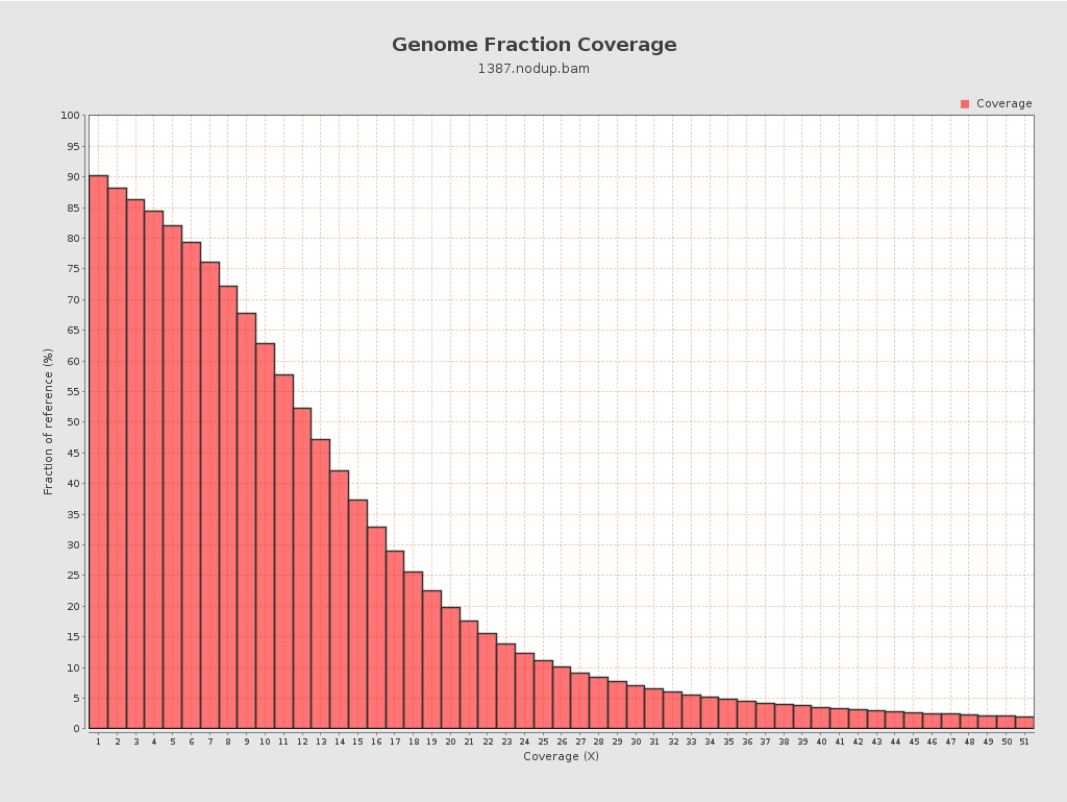
4. Results : Coverage Histogram



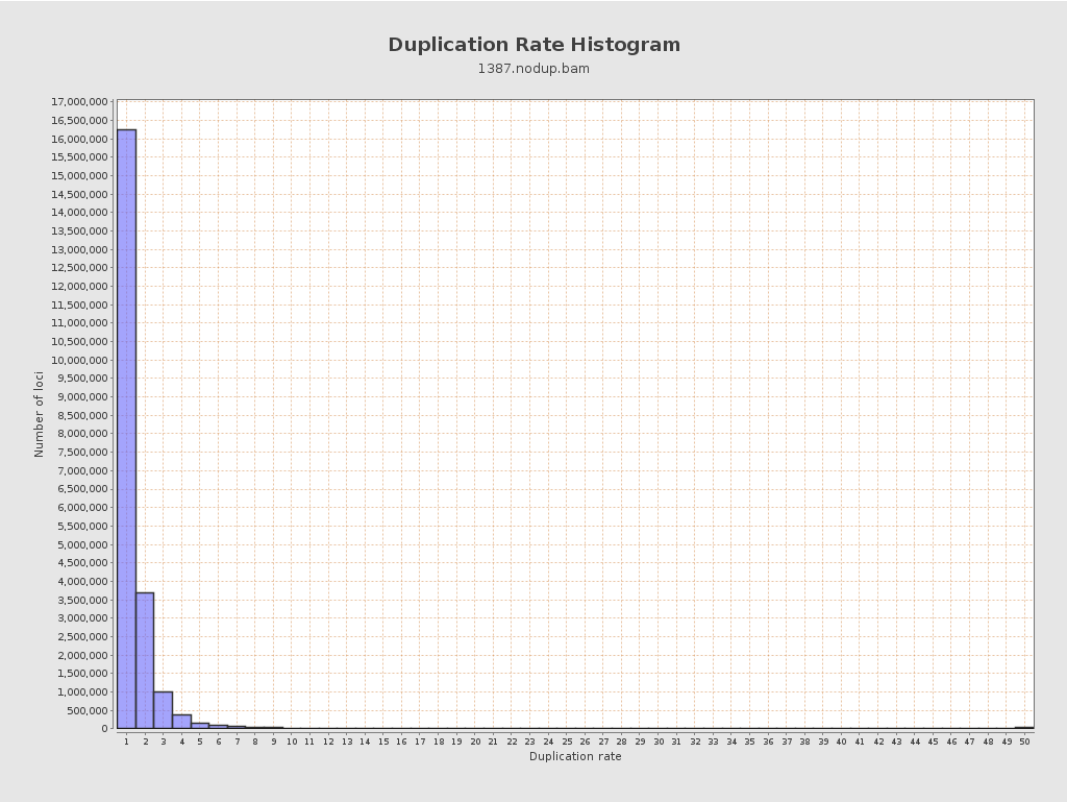
5. Results : Coverage Histogram (0-50X)



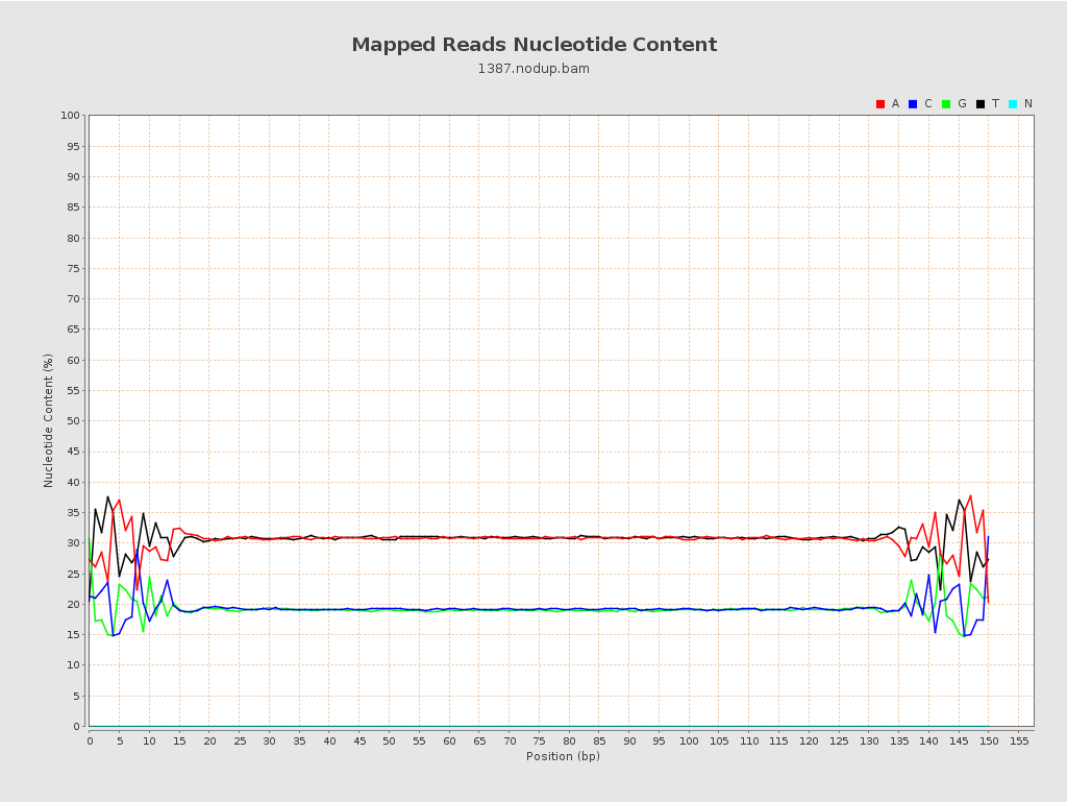
6. Results : Genome Fraction Coverage



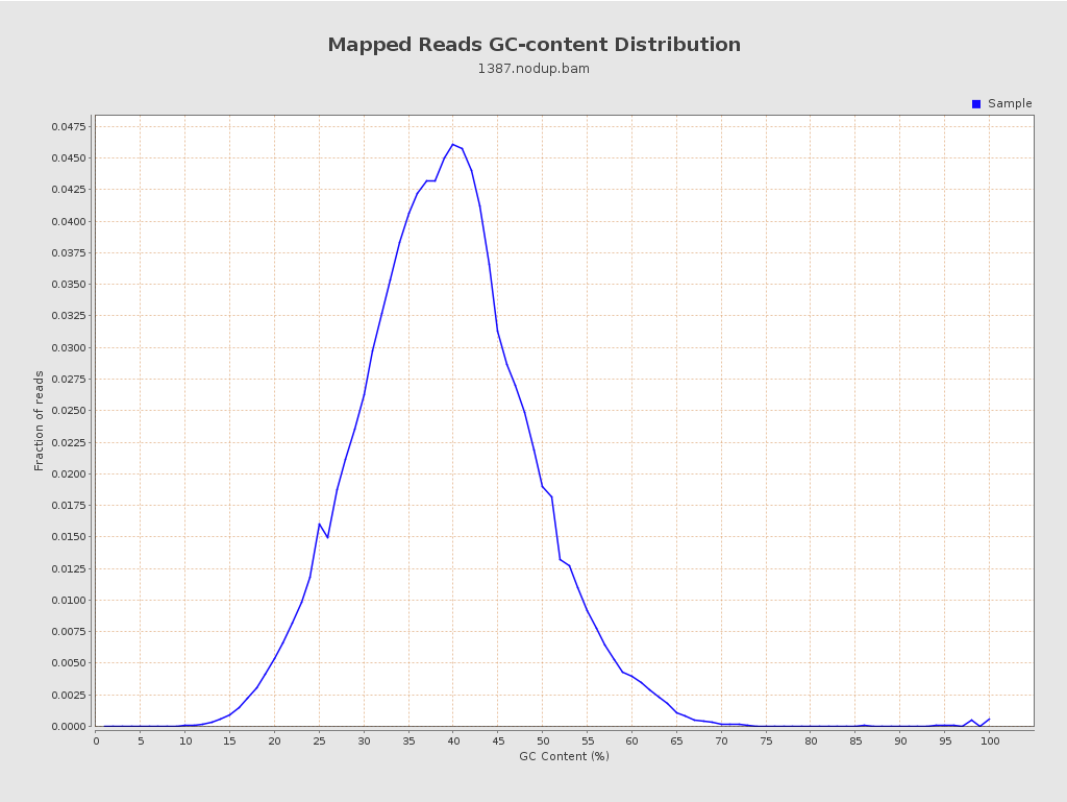
7. Results : Duplication Rate Histogram



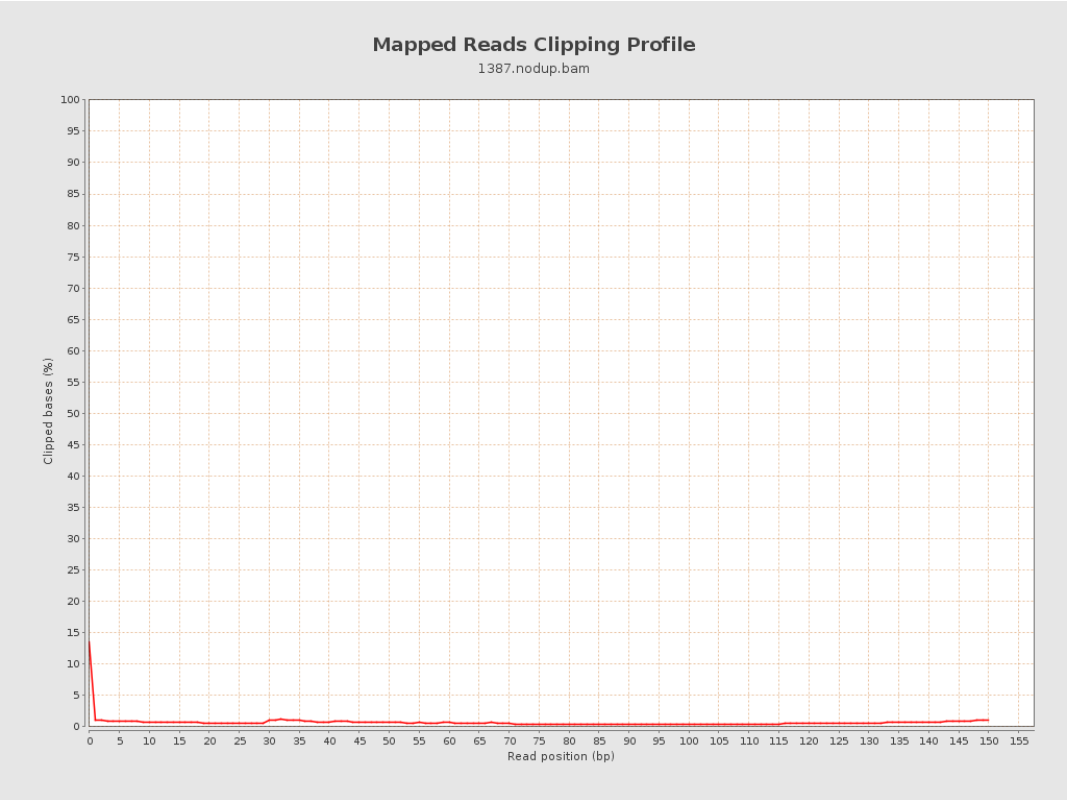
8. Results : Mapped Reads Nucleotide Content



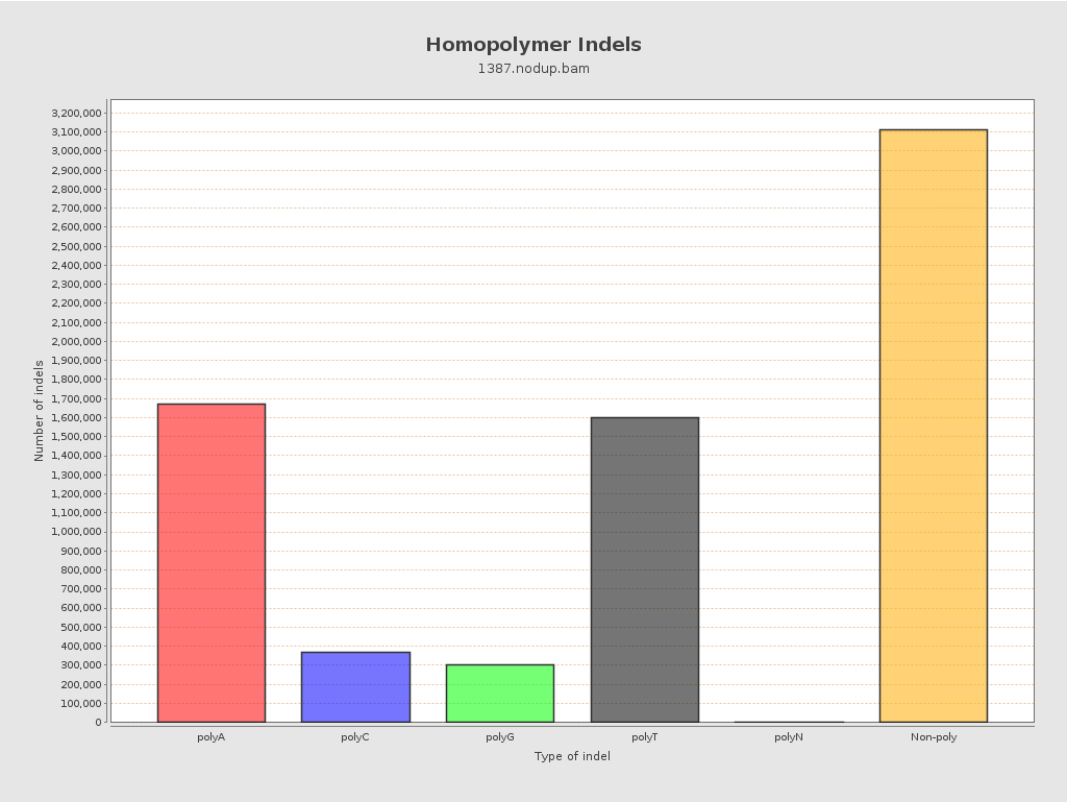
9. Results : Mapped Reads GC-content Distribution



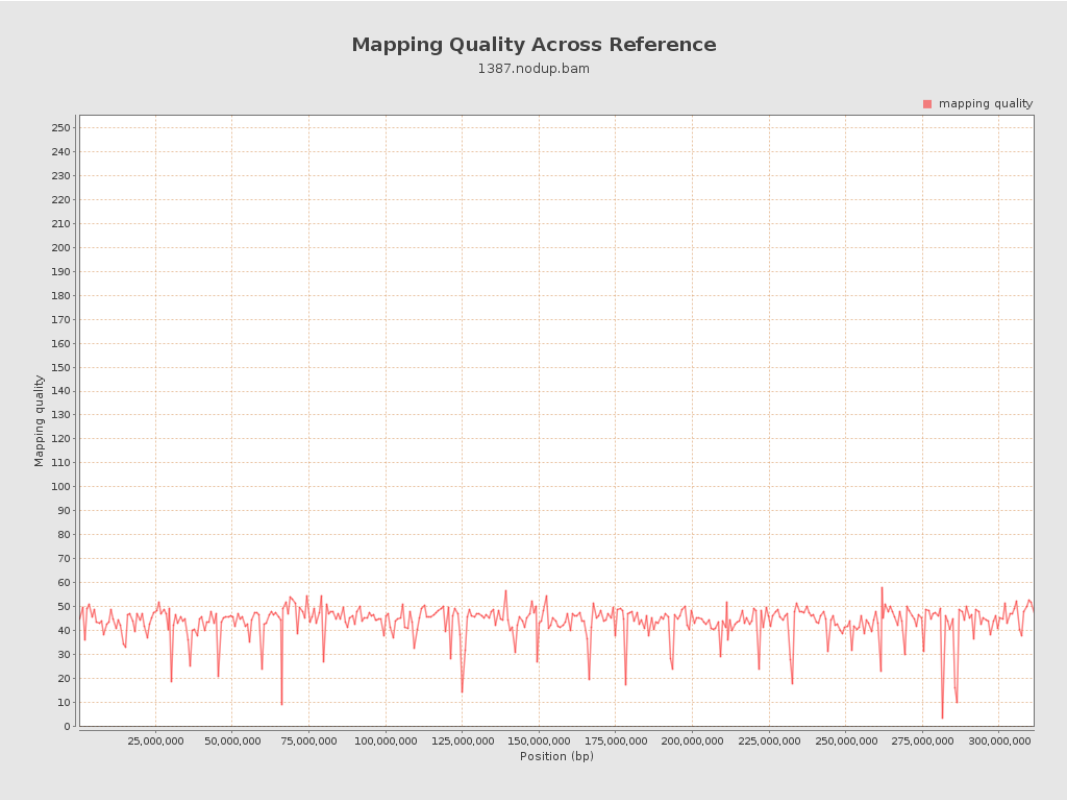
10. Results : Mapped Reads Clipping Profile



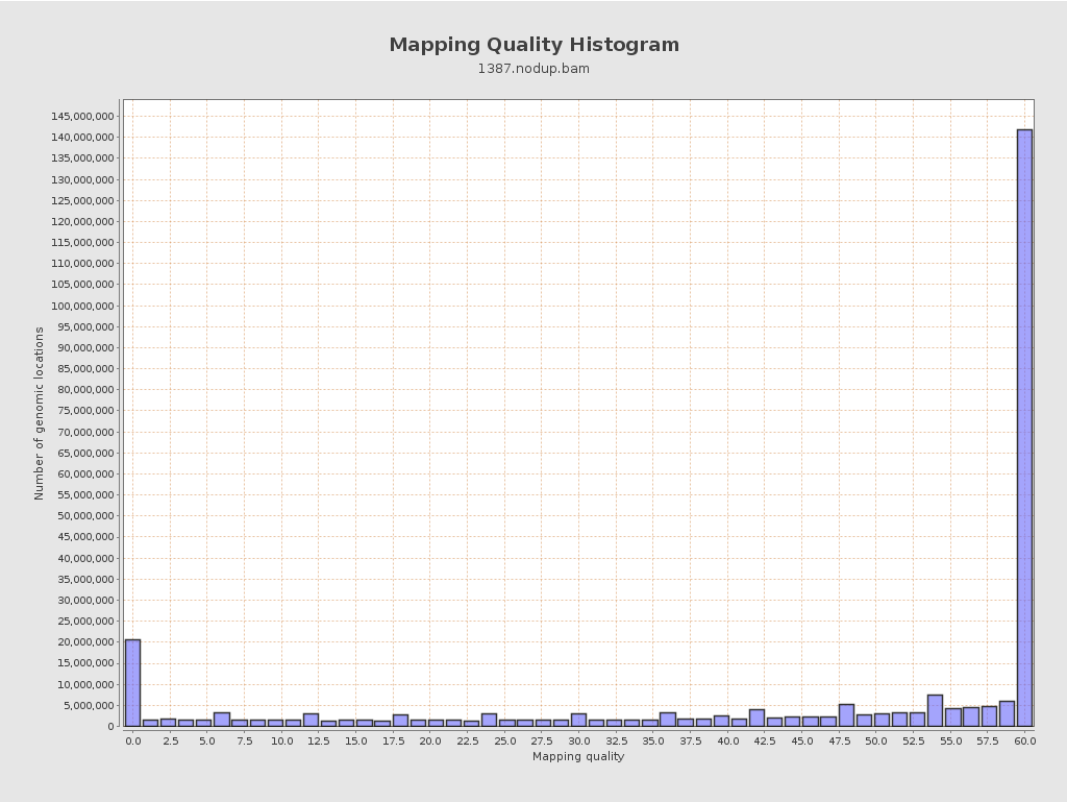
11. Results : Homopolymer Indels



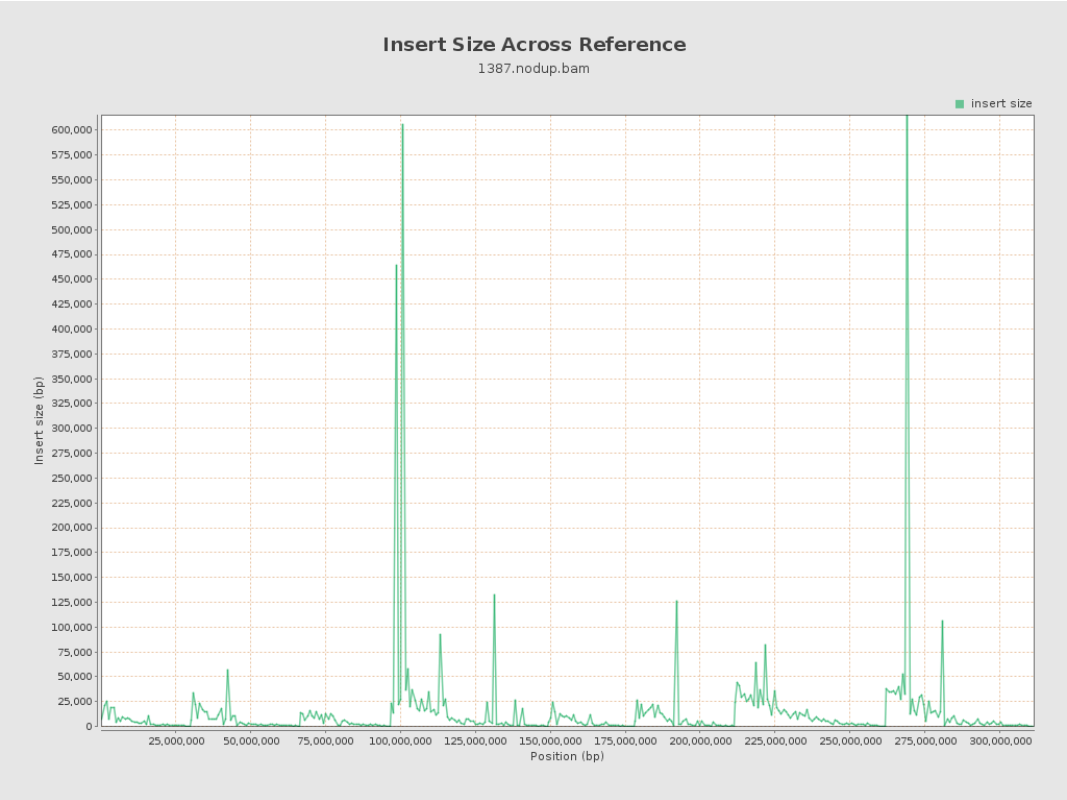
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram