Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1384
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1384 .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_402/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_402_S377_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_402/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_402_S377_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:33:00 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,523,749
Mapped reads	64,594,366 / 94.27%
Unmapped reads	3,929,383 / 5.73%
Mapped paired reads	64,594,366 / 94.27%
Mapped reads, first in pair	32,423,946 / 47.32%
Mapped reads, second in pair	32,170,420 / 46.95%
Mapped reads, both in pair	63,131,949 / 92.13%
Mapped reads, singletons	1,462,417 / 2.13%
Read min/max/mean length	30 / 151 / 148.28
Duplicated reads (flagged)	11,320,865 / 16.52%
Clipped reads	14,256,372 / 20.81%

2.2. ACGT Content

Number/percentage of A's	2,759,265,120 / 30.67%
Number/percentage of C's	1,741,653,208 / 19.36%
Number/percentage of T's	2,762,359,674 / 30.71%
Number/percentage of G's	1,732,222,334 / 19.26%
Number/percentage of N's	30,582 / 0%
GC Percentage	38.62%

2.3. Coverage

Mean	28.9364
Standard Deviation	287.9735

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Insert size

Mean	237,812.82
Standard Deviation	2,290,768.23
P25/Median/P75	373 / 487 / 639

2.6. Mismatches and indels

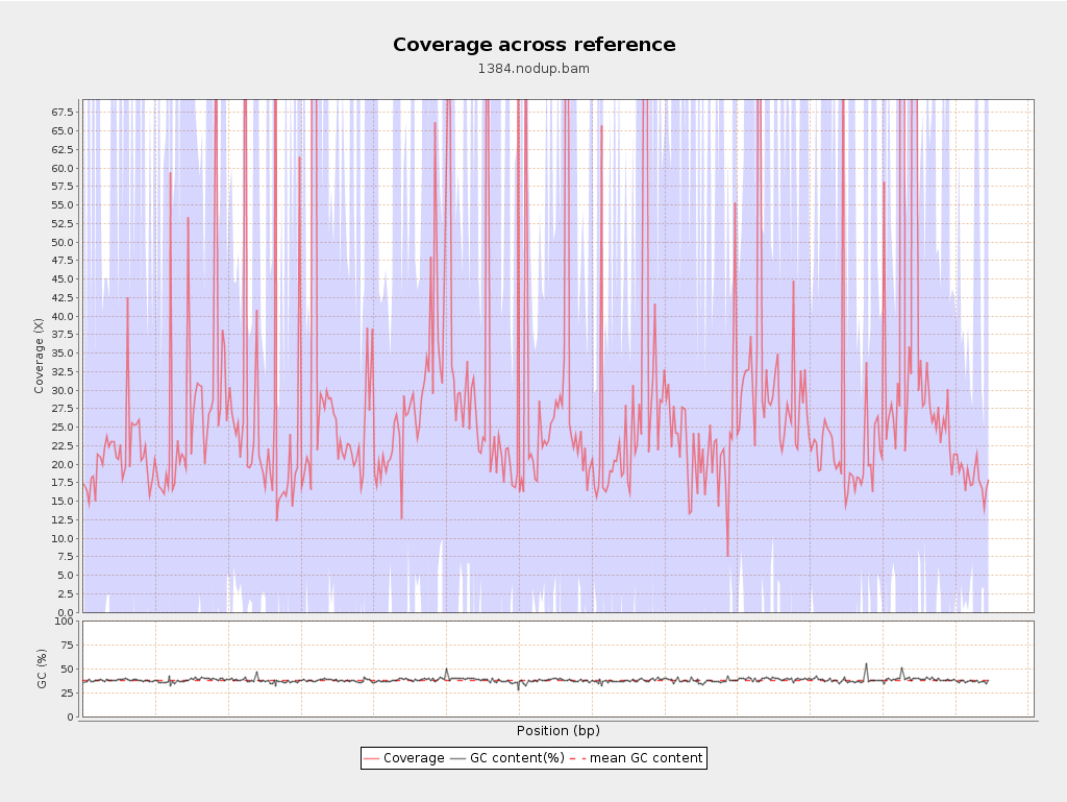
General error rate	2.44%
Mismatches	204,111,442
Insertions	5,838,771
Mapped reads with at least one insertion	8.15%
Deletions	5,958,281
Mapped reads with at least one deletion	8.23%
Homopolymer indels	55.85%

2.7. Chromosome stats

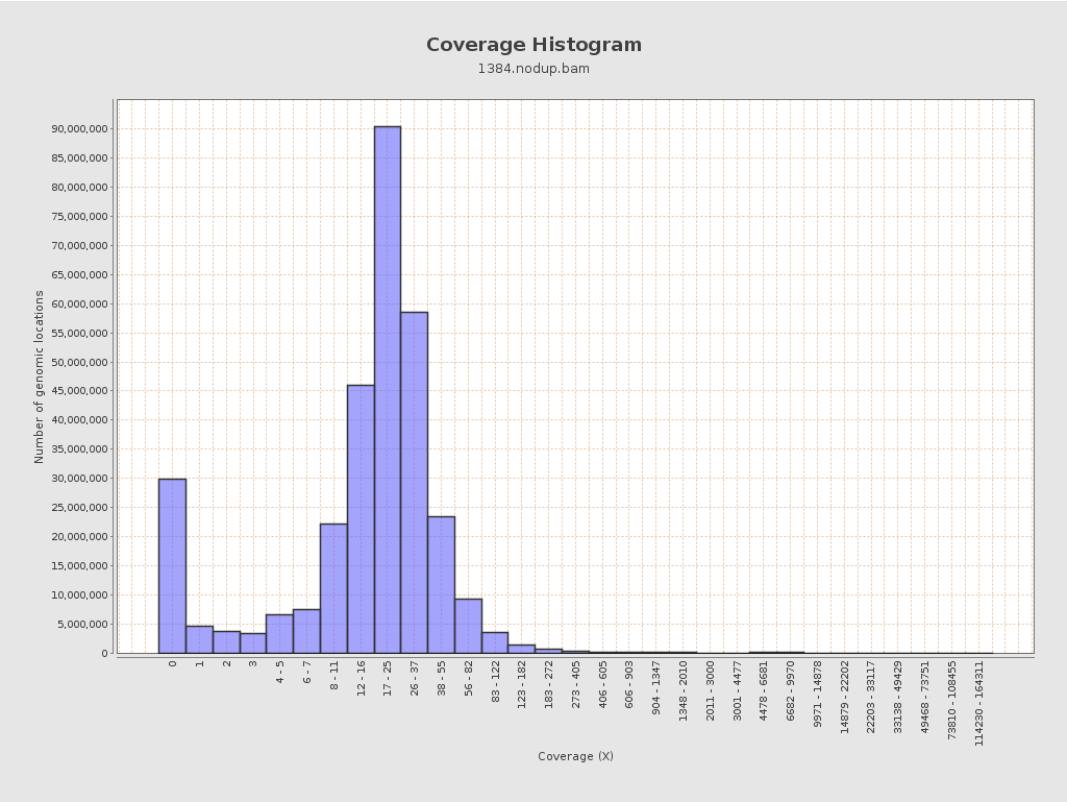
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	614020856	20.6572	65.9184

LT669789.1	36598175	1060875621	28.9871	267.3924
LT669790.1	30422129	895099236	29.4226	253.8431
LT669791.1	52758100	1539723410	29.1846	213.3649
LT669792.1	28376109	776363616	27.3598	329.1559
LT669793.1	33388210	926944825	27.7626	294.2813
LT669794.1	50579949	1414754049	27.9706	230.5335
LT669795.1	49795044	1790026622	35.9479	449.8665

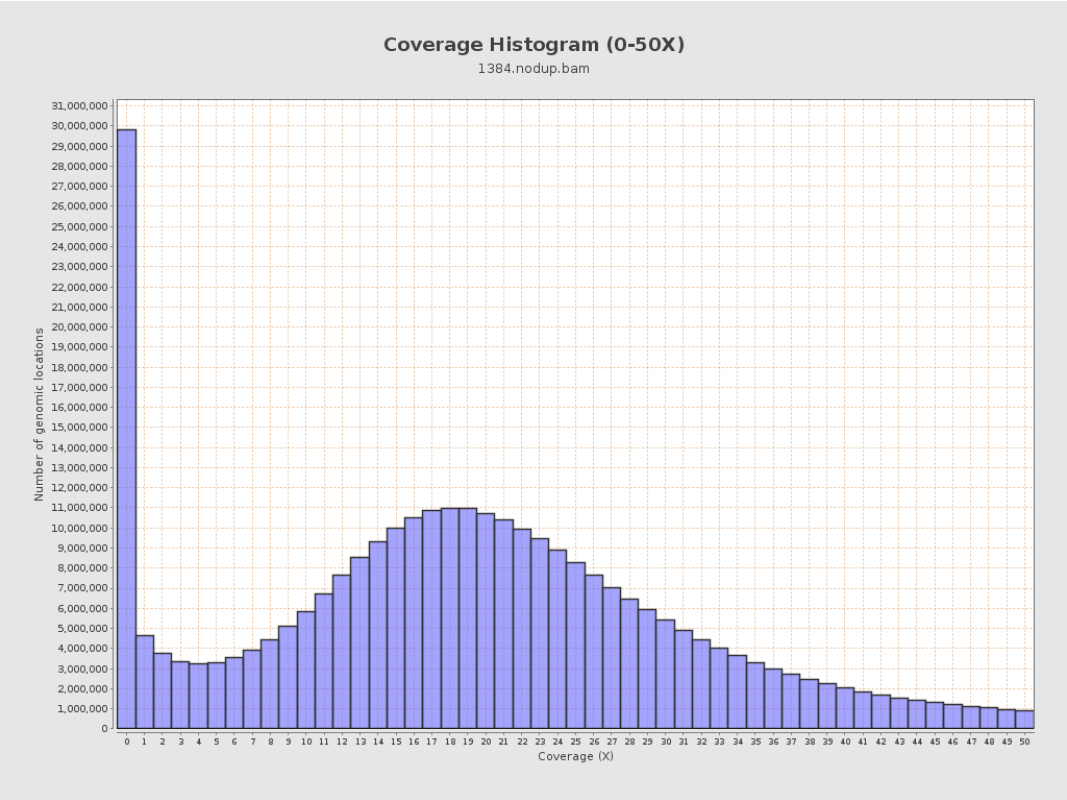
3. Results : Coverage across reference



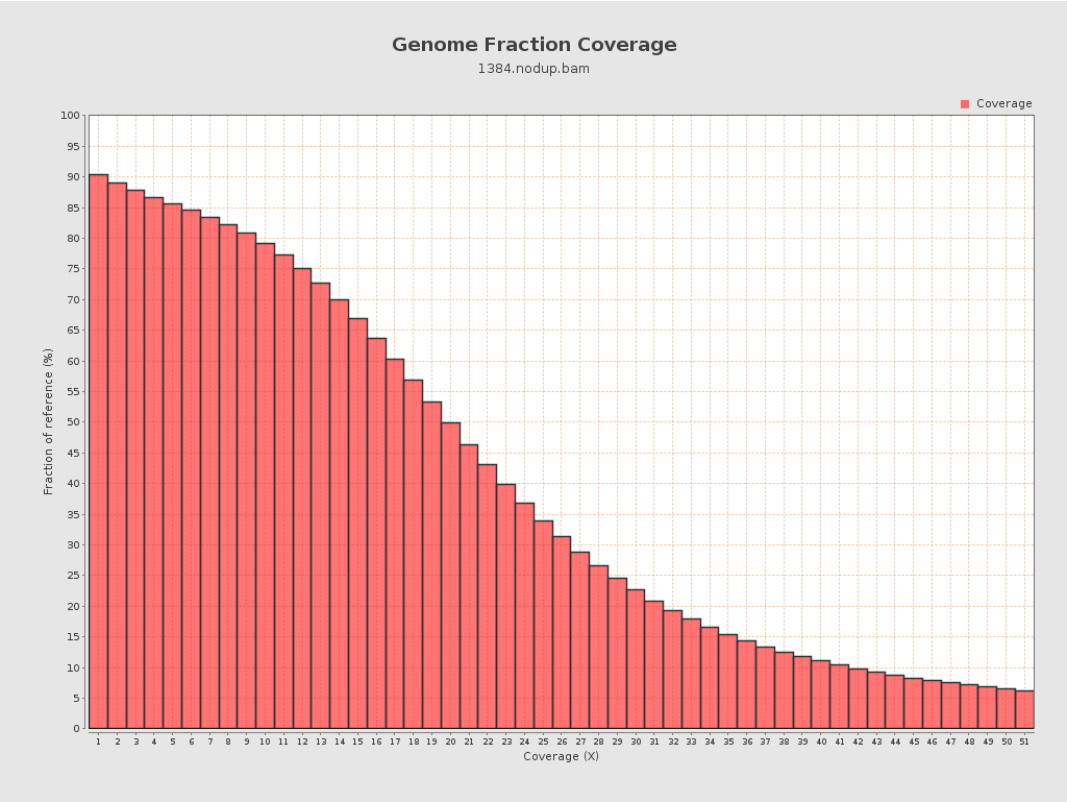
4. Results : Coverage Histogram



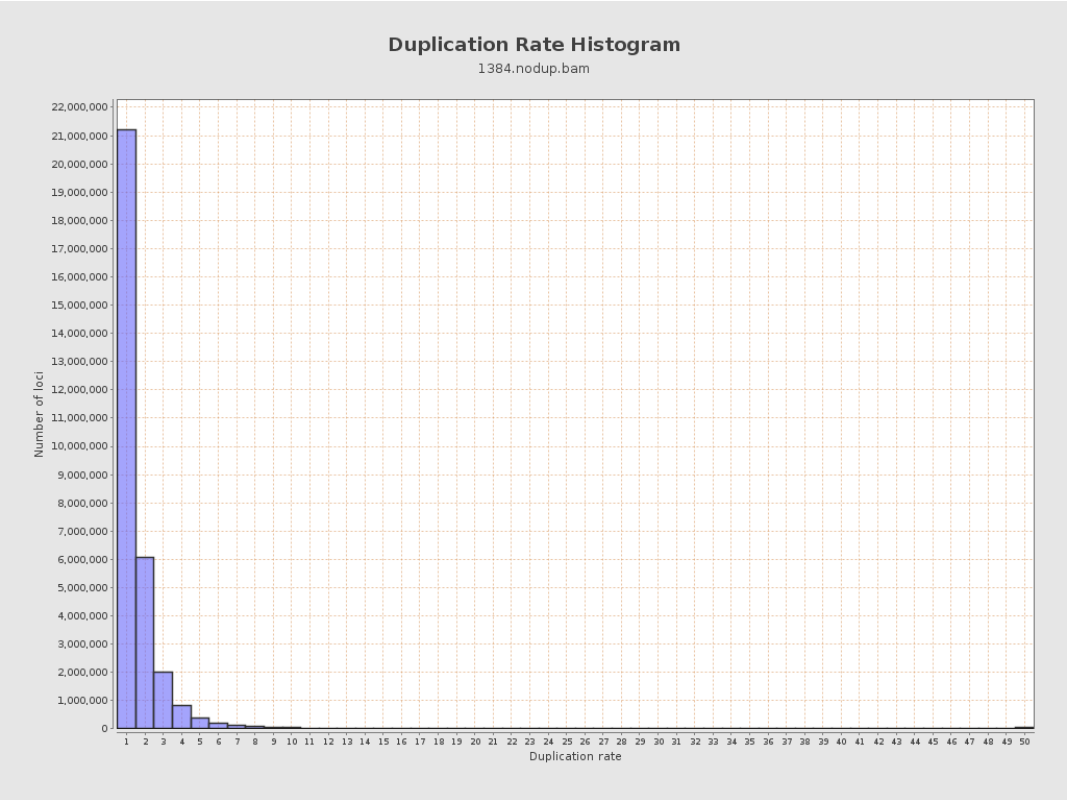
5. Results : Coverage Histogram (0-50X)



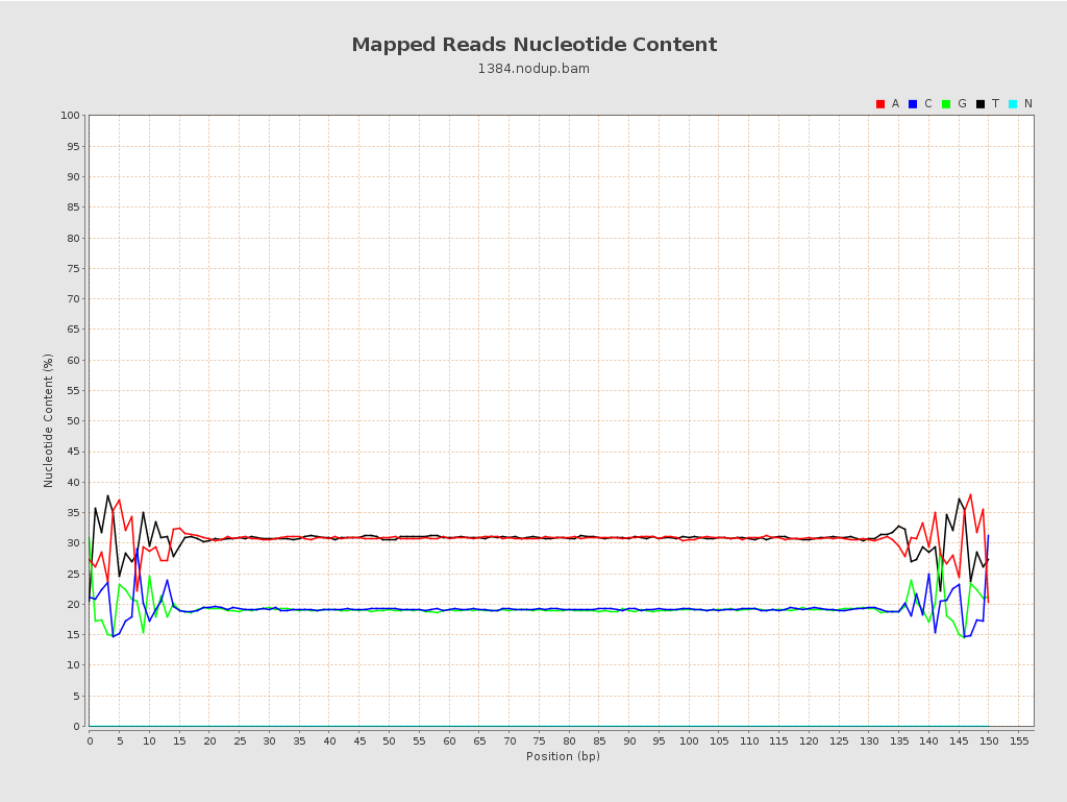
6. Results : Genome Fraction Coverage



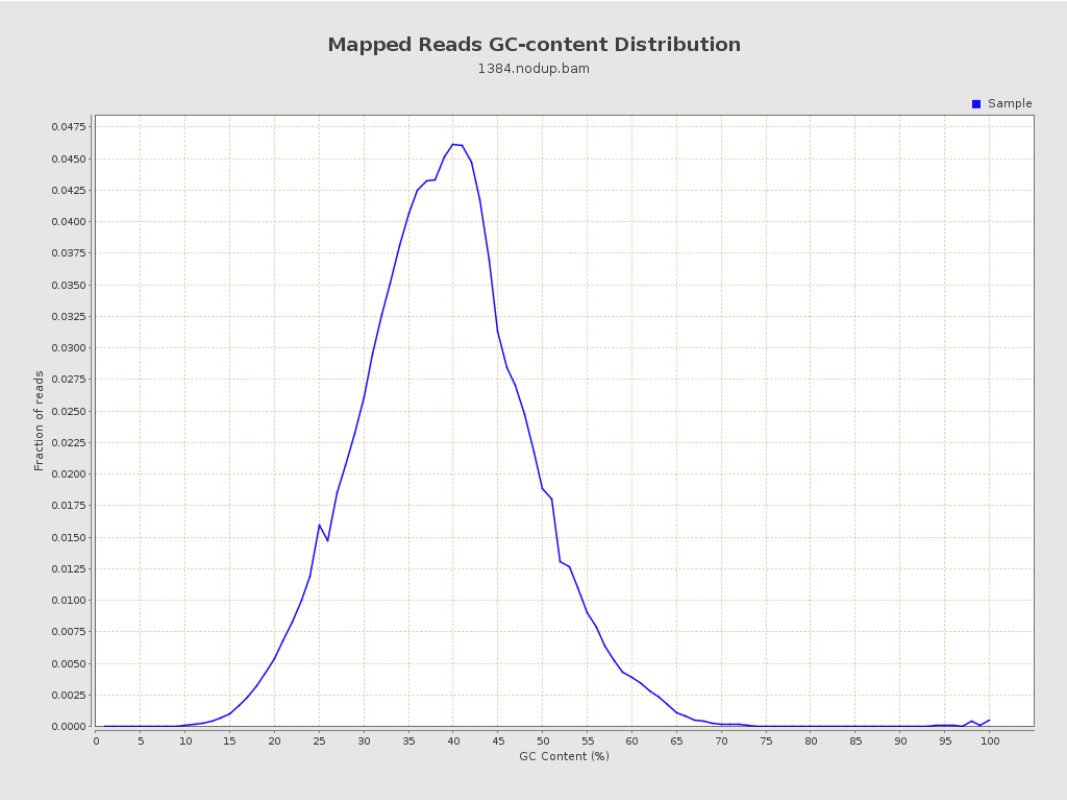
7. Results : Duplication Rate Histogram



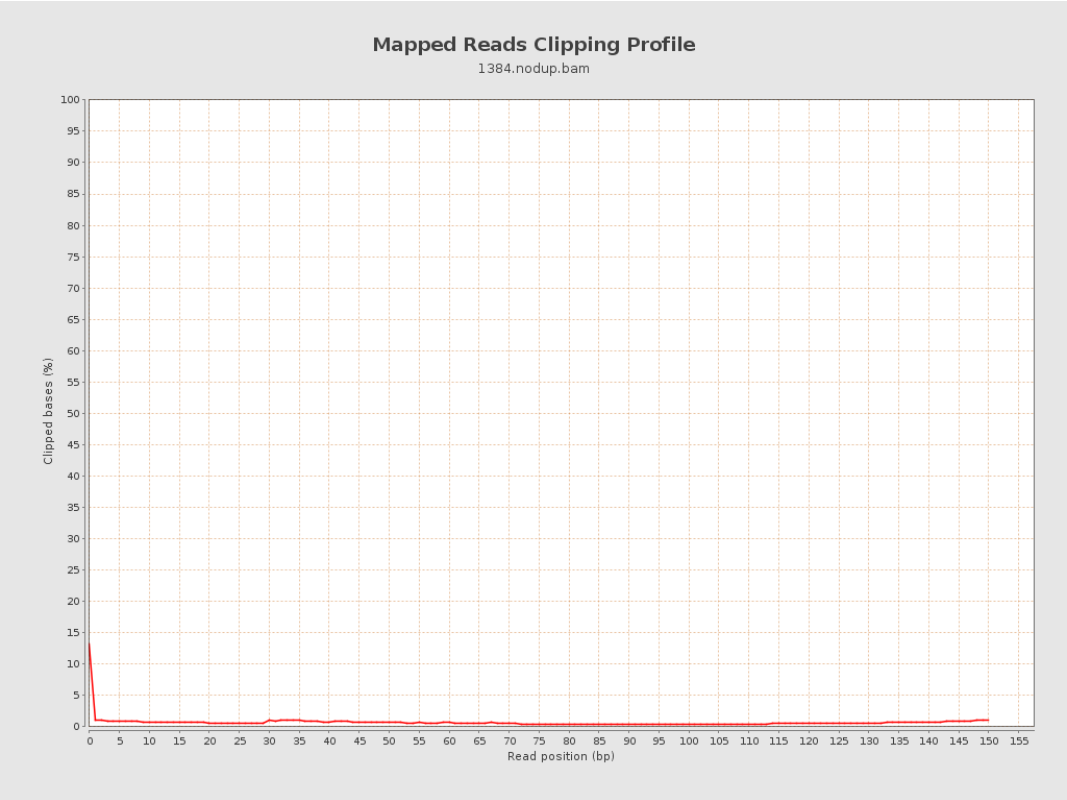
8. Results : Mapped Reads Nucleotide Content



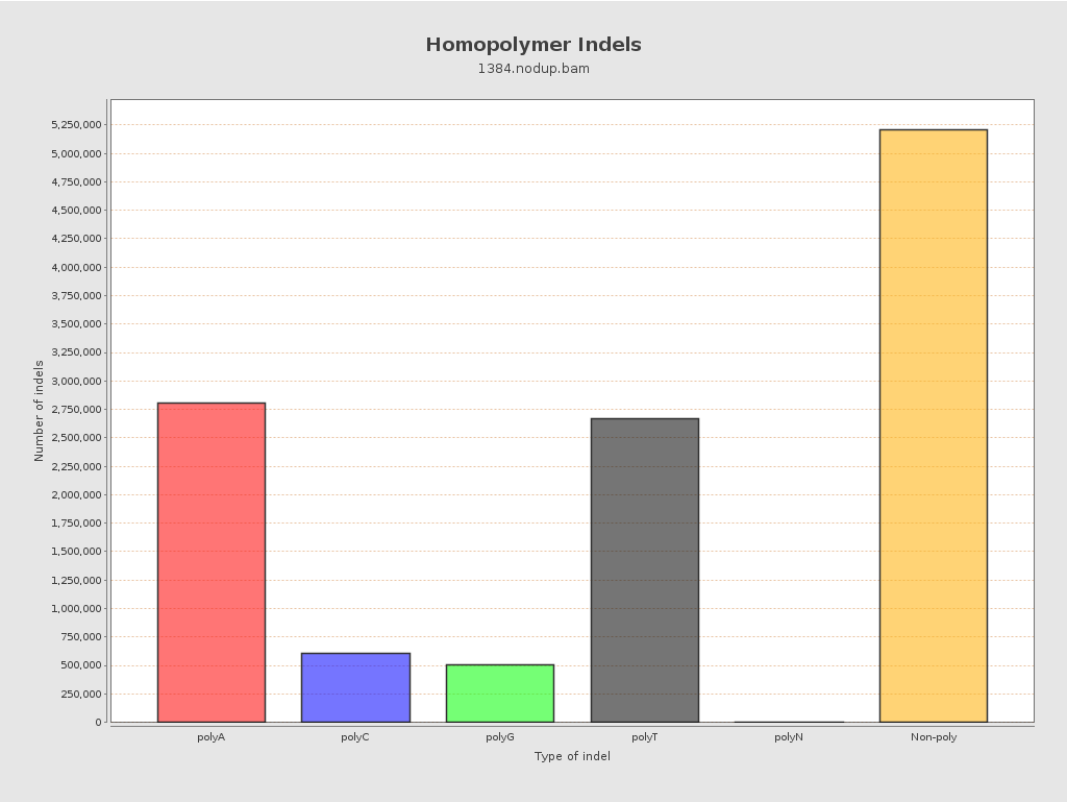
9. Results : Mapped Reads GC-content Distribution



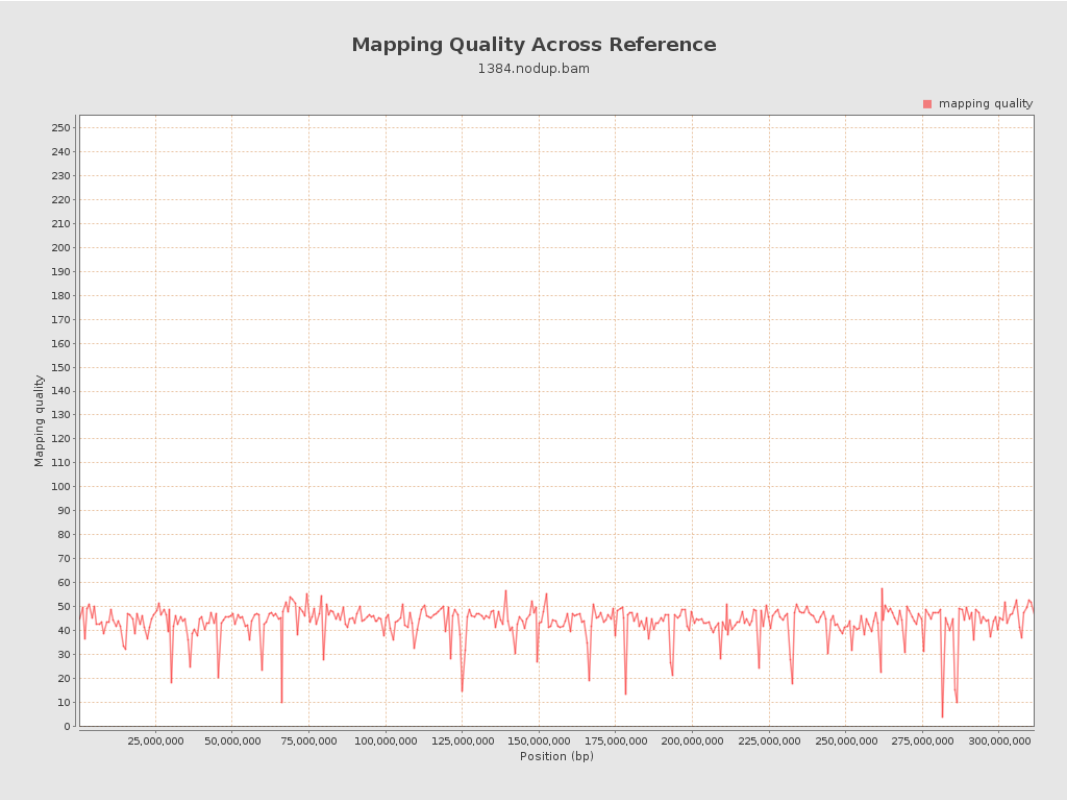
10. Results : Mapped Reads Clipping Profile



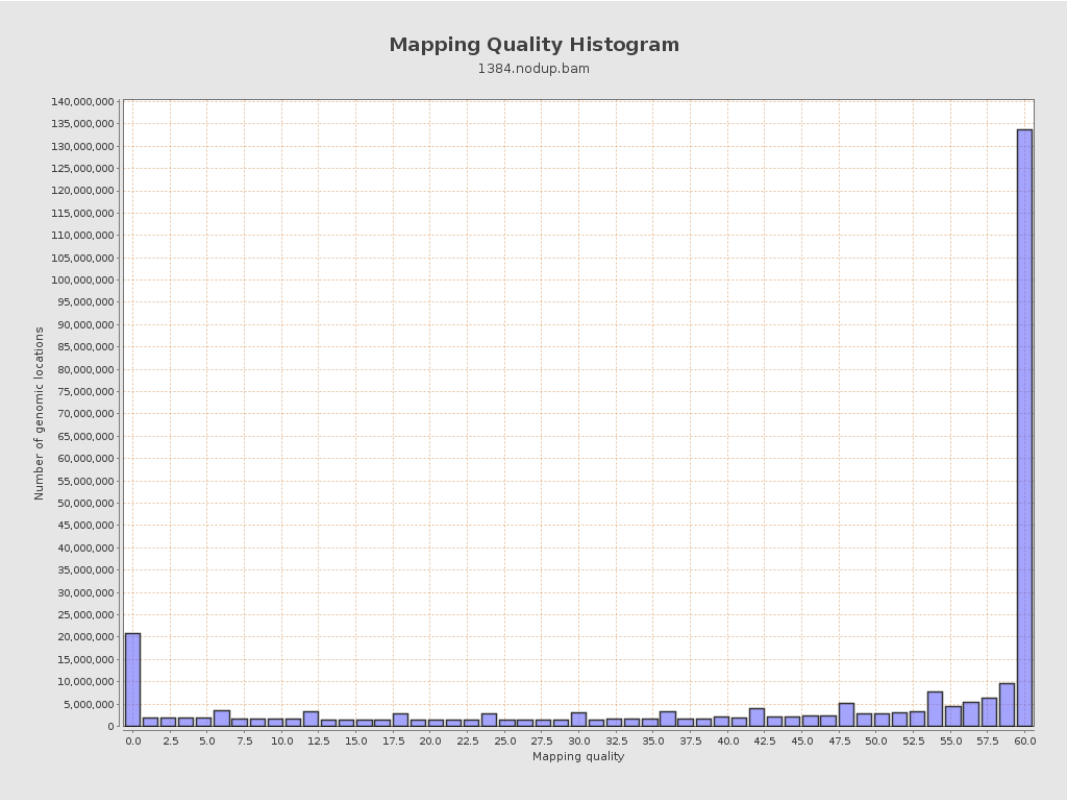
11. Results : Homopolymer Indels



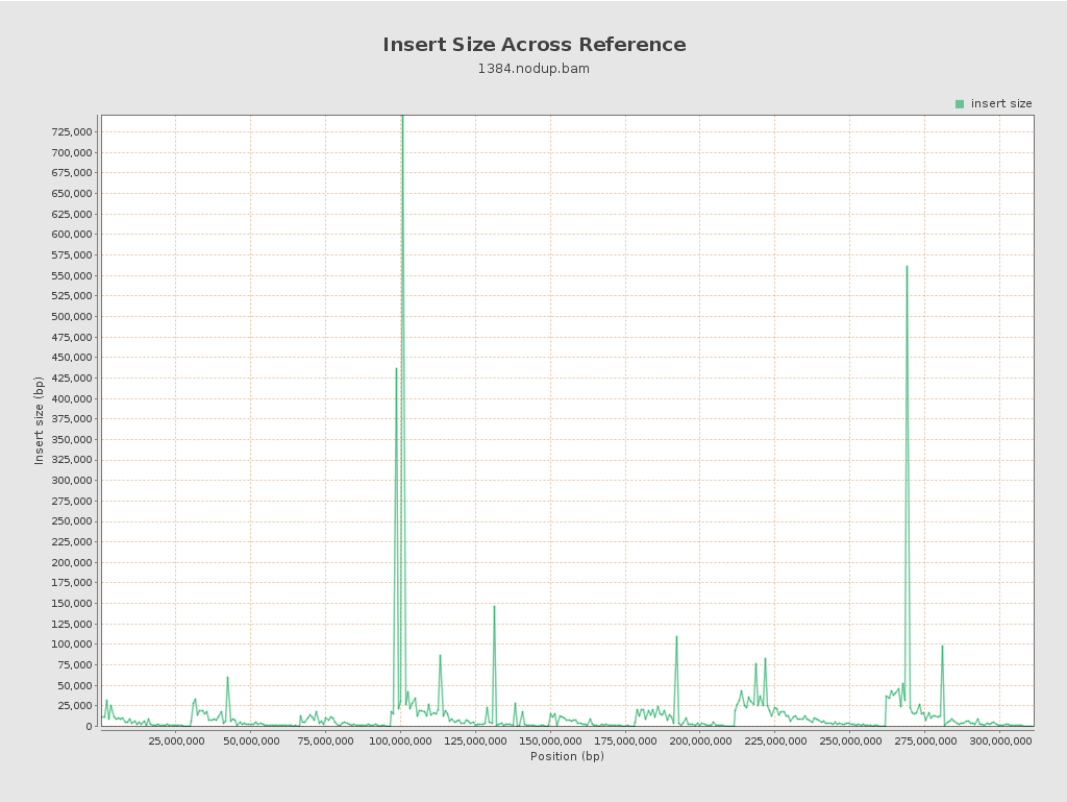
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram