Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1468
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1468 .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_140/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_140_S230_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_140/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_140_S230_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:38:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	84,815,594
Mapped reads	79,019,104 / 93.17%
Unmapped reads	5,796,490 / 6.83%
Mapped paired reads	79,019,104 / 93.17%
Mapped reads, first in pair	39,569,350 / 46.65%
Mapped reads, second in pair	39,449,754 / 46.51%
Mapped reads, both in pair	77,280,867 / 91.12%
Mapped reads, singletons	1,738,237 / 2.05%
Read min/max/mean length	30 / 151 / 148.23
Duplicated reads (flagged)	13,271,523 / 15.65%
Clipped reads	17,057,745 / 20.11%

2.2. ACGT Content

Number/percentage of A's	3,397,357,645 / 30.94%
Number/percentage of C's	2,093,866,519 / 19.07%
Number/percentage of T's	3,399,071,465 / 30.96%
Number/percentage of G's	2,089,459,715 / 19.03%
Number/percentage of N's	47,247 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	35.3243
Standard Deviation	264.5401

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Insert size

Mean	226,014.33
Standard Deviation	2,267,195.86
P25/Median/P75	312 / 409 / 541

2.6. Mismatches and indels

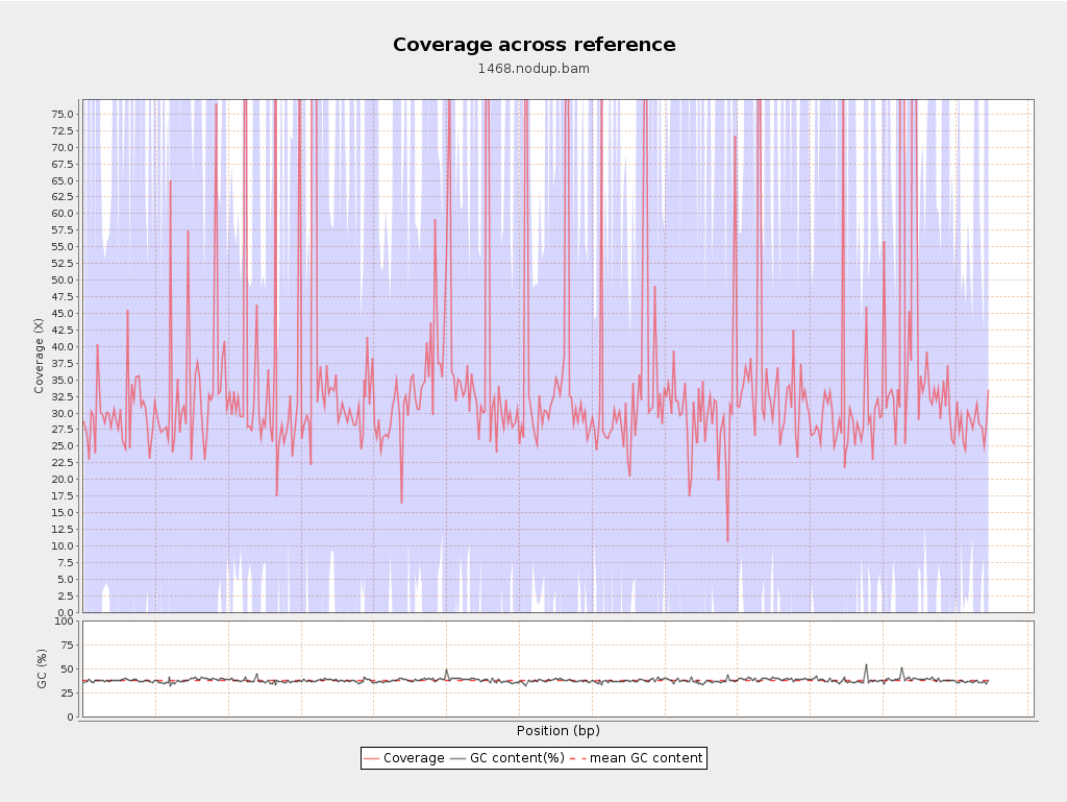
General error rate	2.24%
Mismatches	225,067,031
Insertions	7,466,631
Mapped reads with at least one insertion	8.47%
Deletions	7,515,236
Mapped reads with at least one deletion	8.45%
Homopolymer indels	57.19%

2.7. Chromosome stats

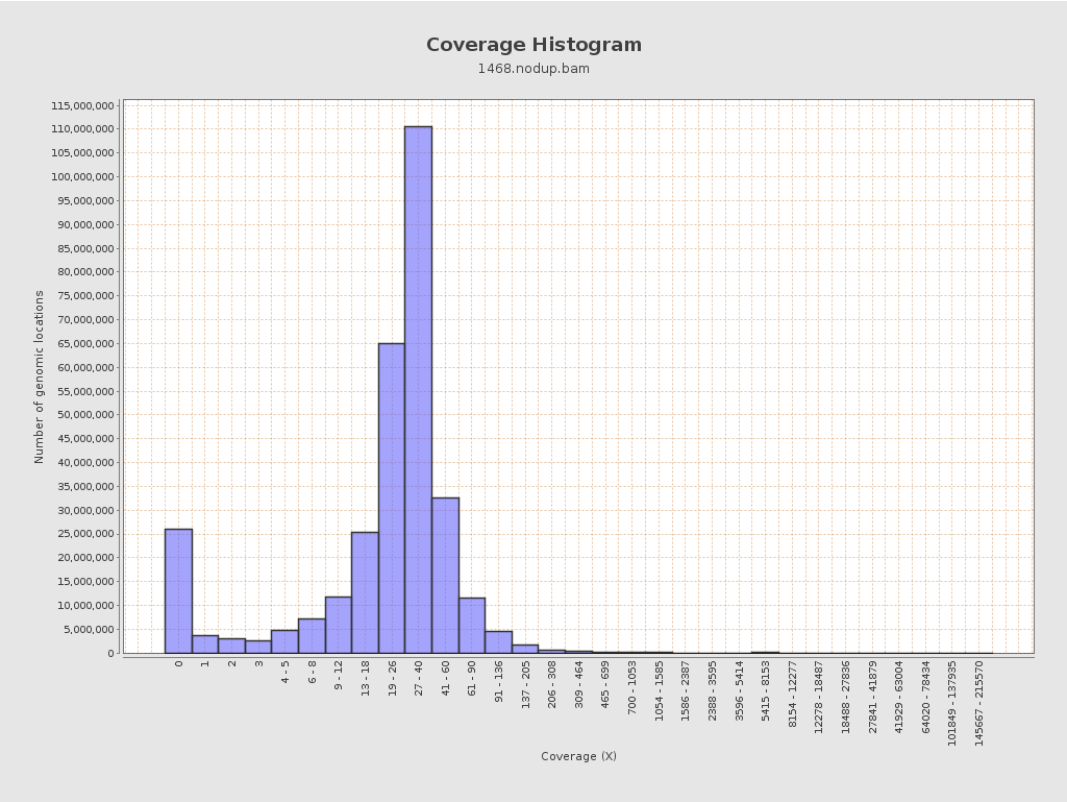
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	880324861	29.6163	82.7606

LT669789.1	36598175	1299606345	35.5101	269.0011
LT669790.1	30422129	1201220652	39.4851	320.4058
LT669791.1	52758100	1844349627	34.9586	241.4864
LT669792.1	28376109	993453947	35.0102	300.1263
LT669793.1	33388210	1101678452	32.996	190.2723
LT669794.1	50579949	1671846830	33.0535	215.7365
LT669795.1	49795044	2016058980	40.4871	365.0393

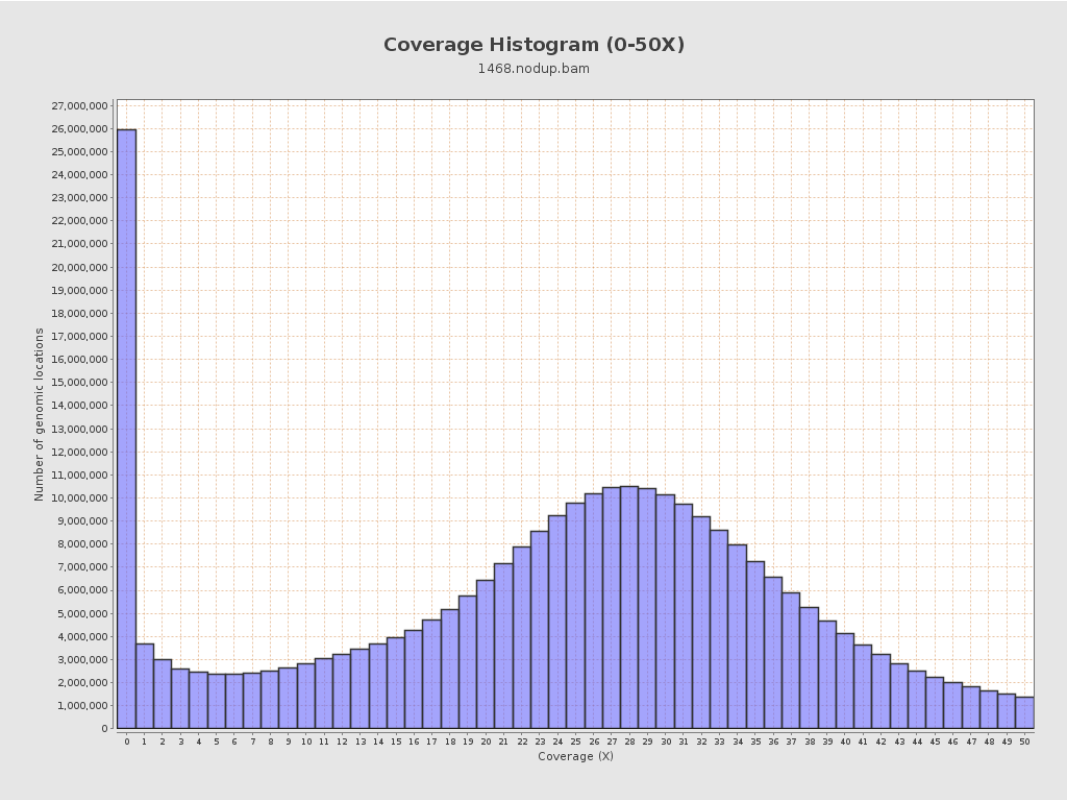
3. Results : Coverage across reference



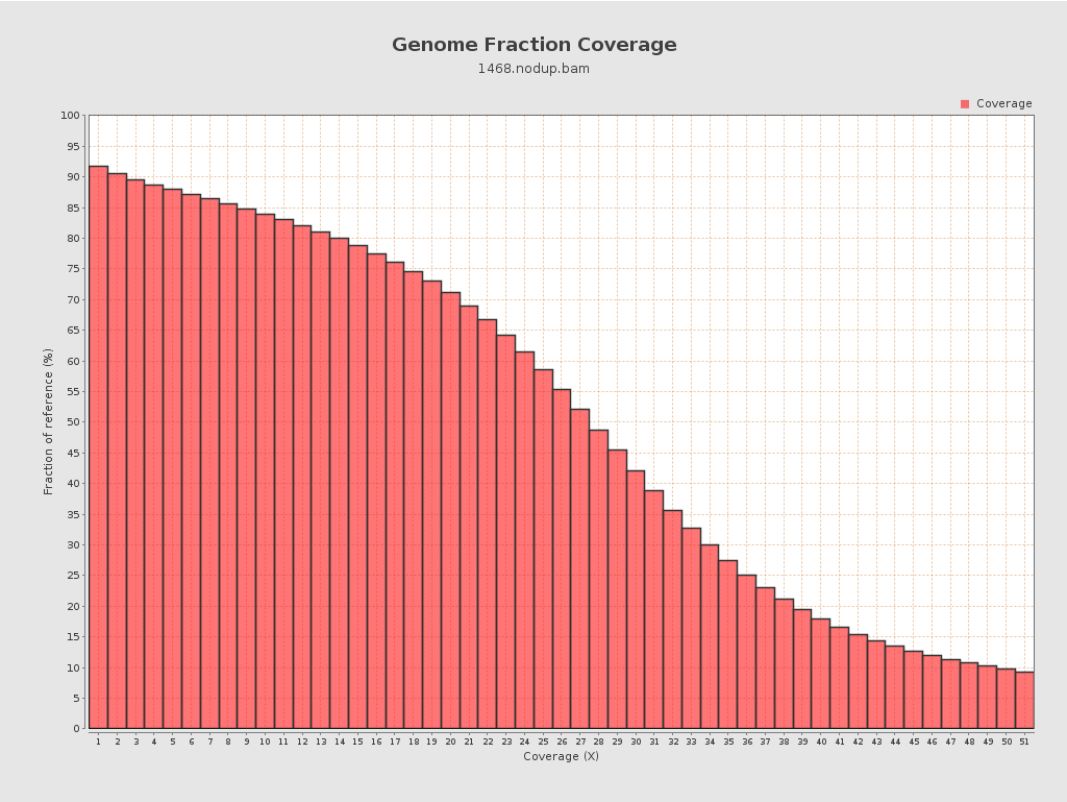
4. Results : Coverage Histogram



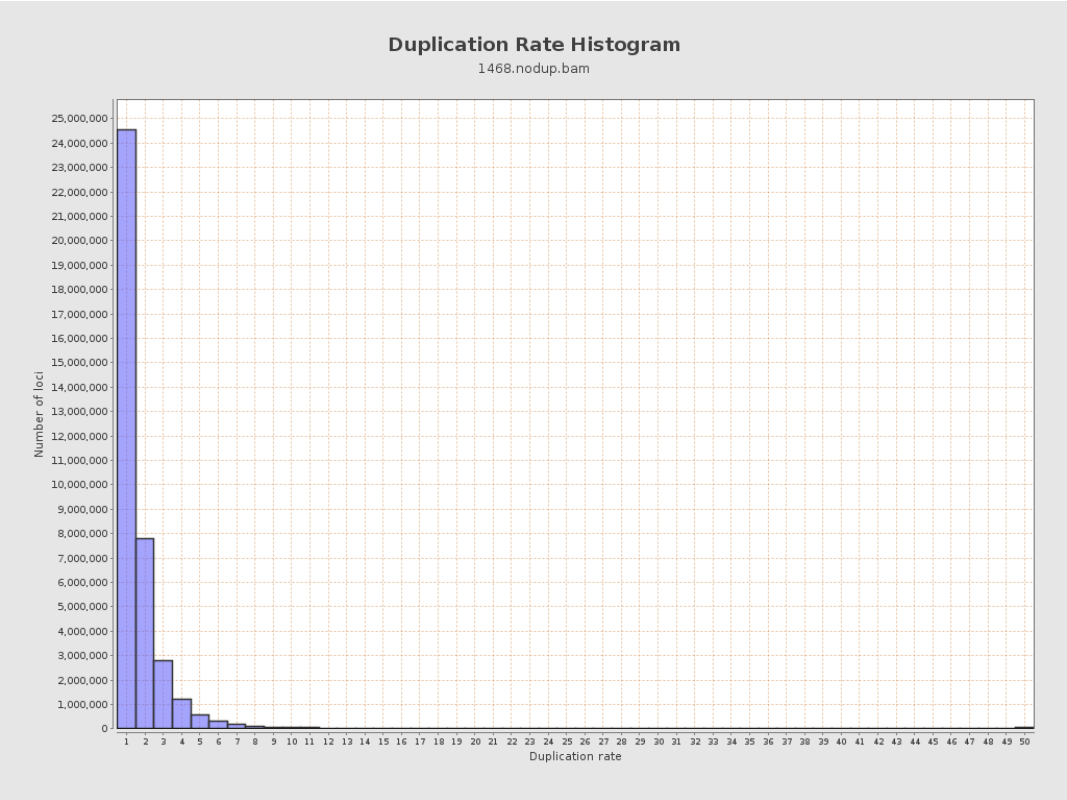
5. Results : Coverage Histogram (0-50X)



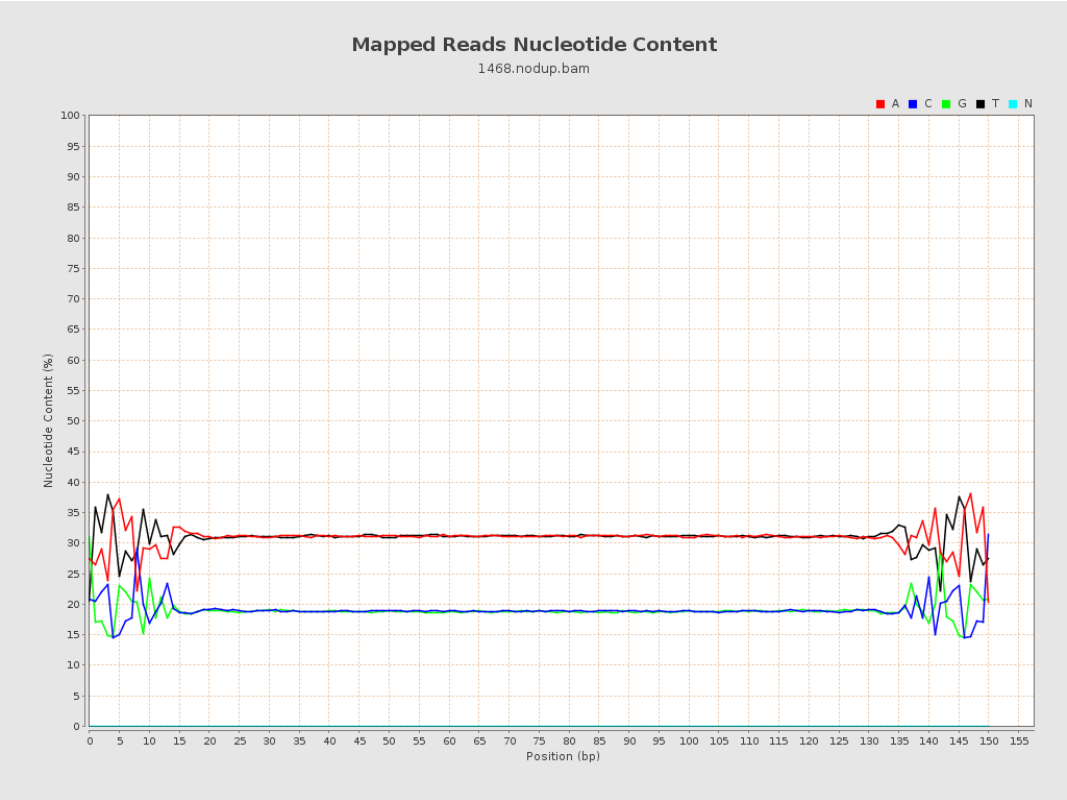
6. Results : Genome Fraction Coverage



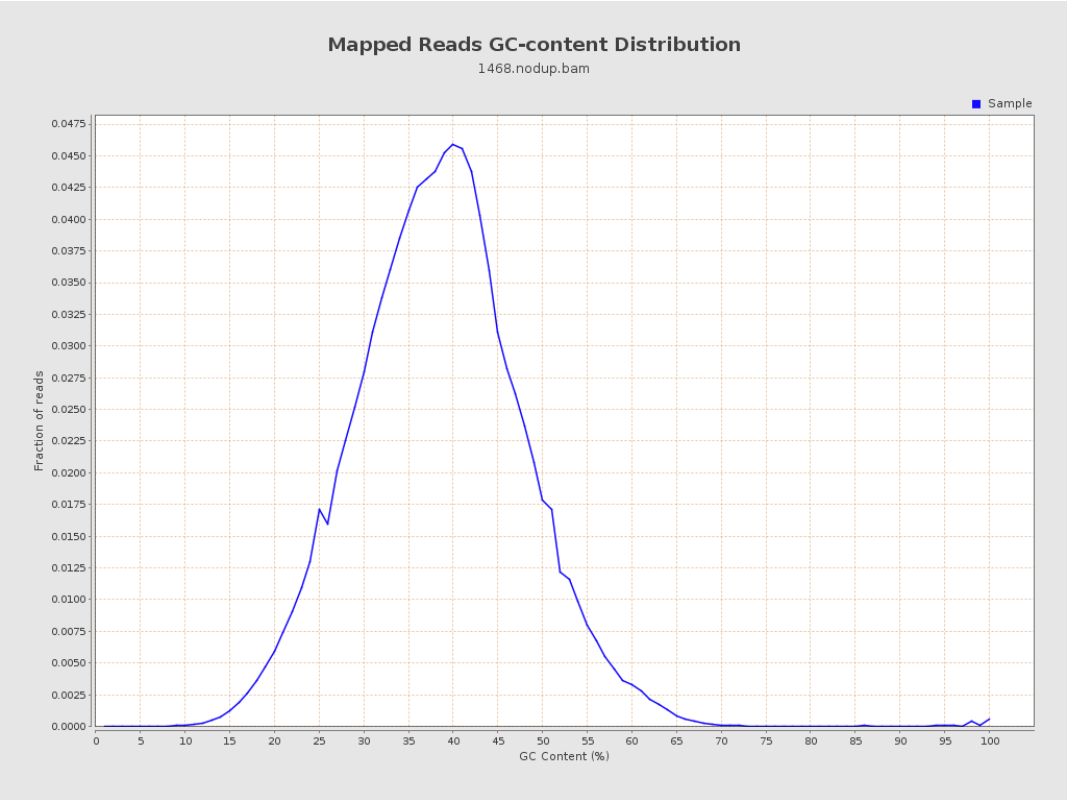
7. Results : Duplication Rate Histogram



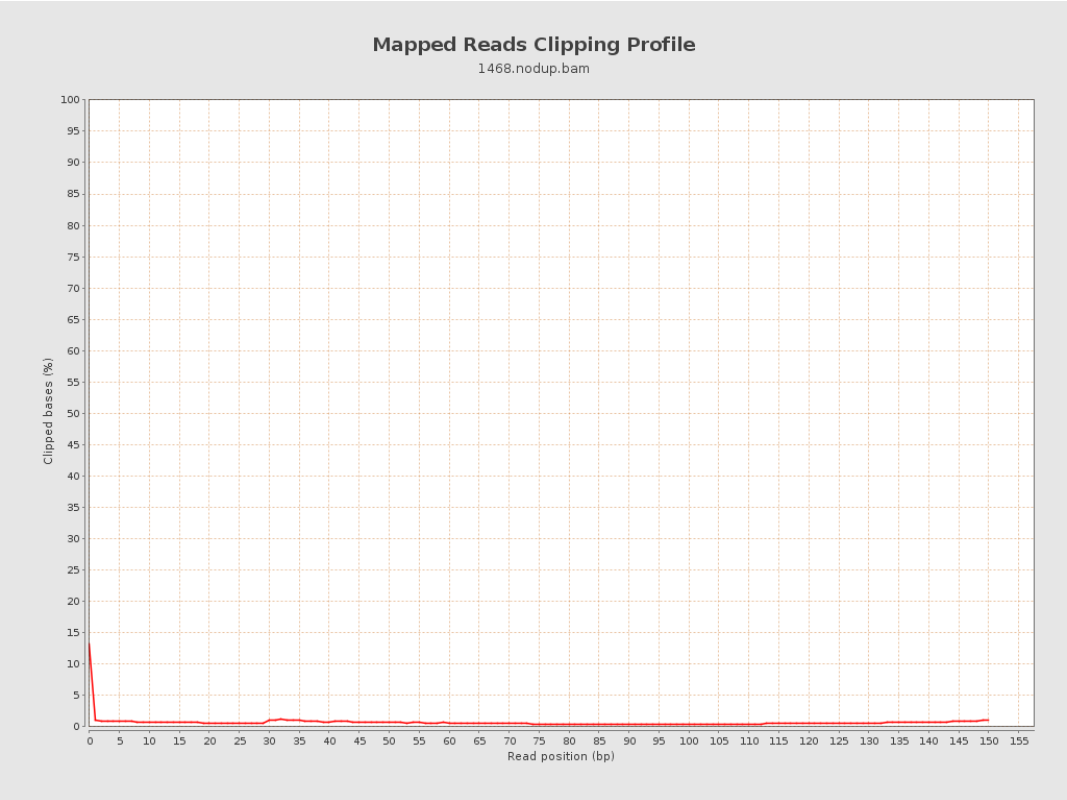
8. Results : Mapped Reads Nucleotide Content



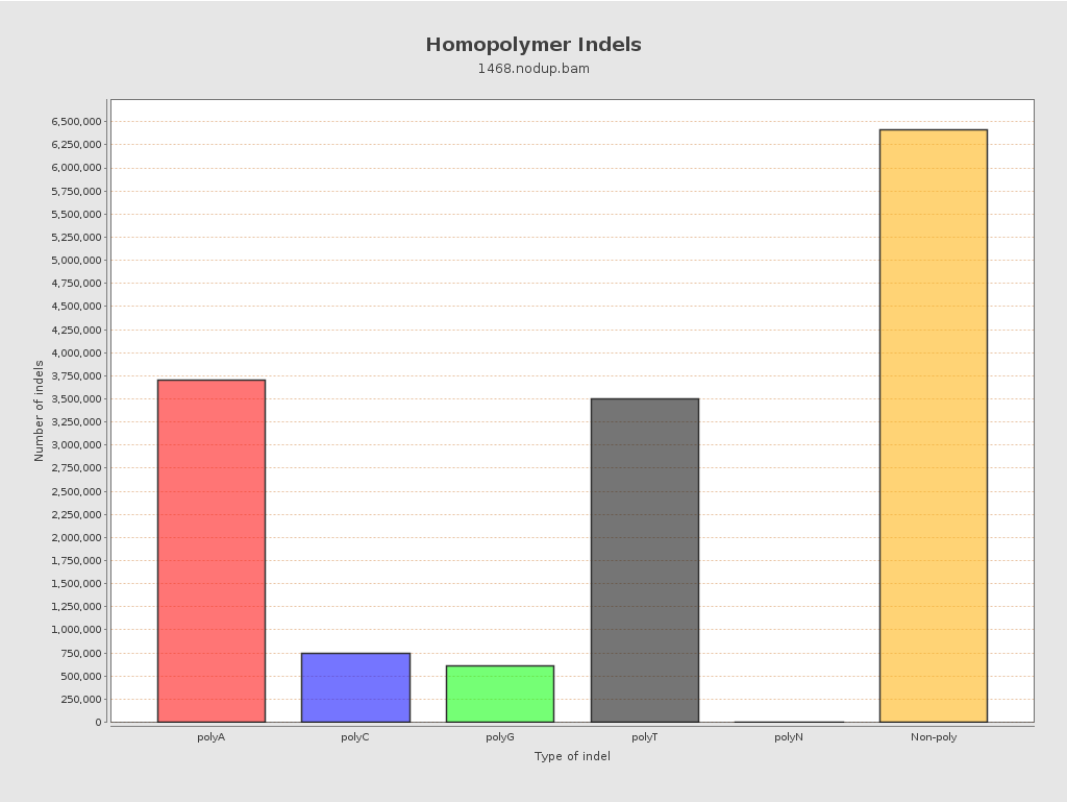
9. Results : Mapped Reads GC-content Distribution



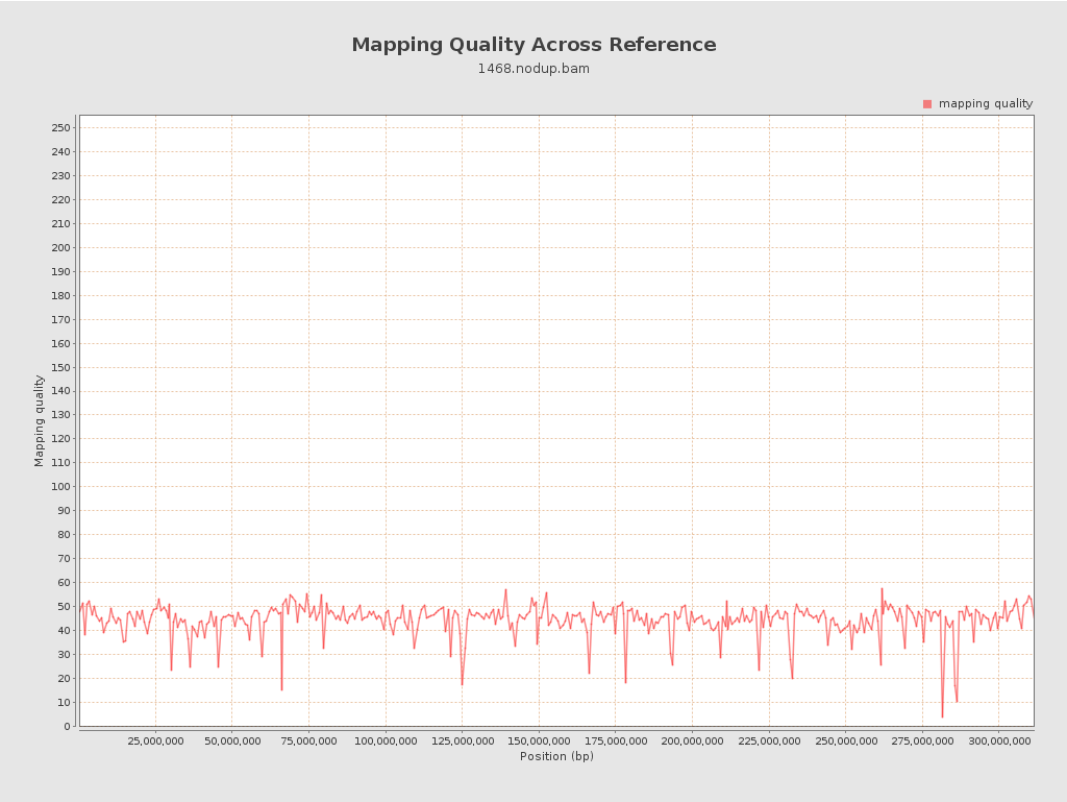
10. Results : Mapped Reads Clipping Profile



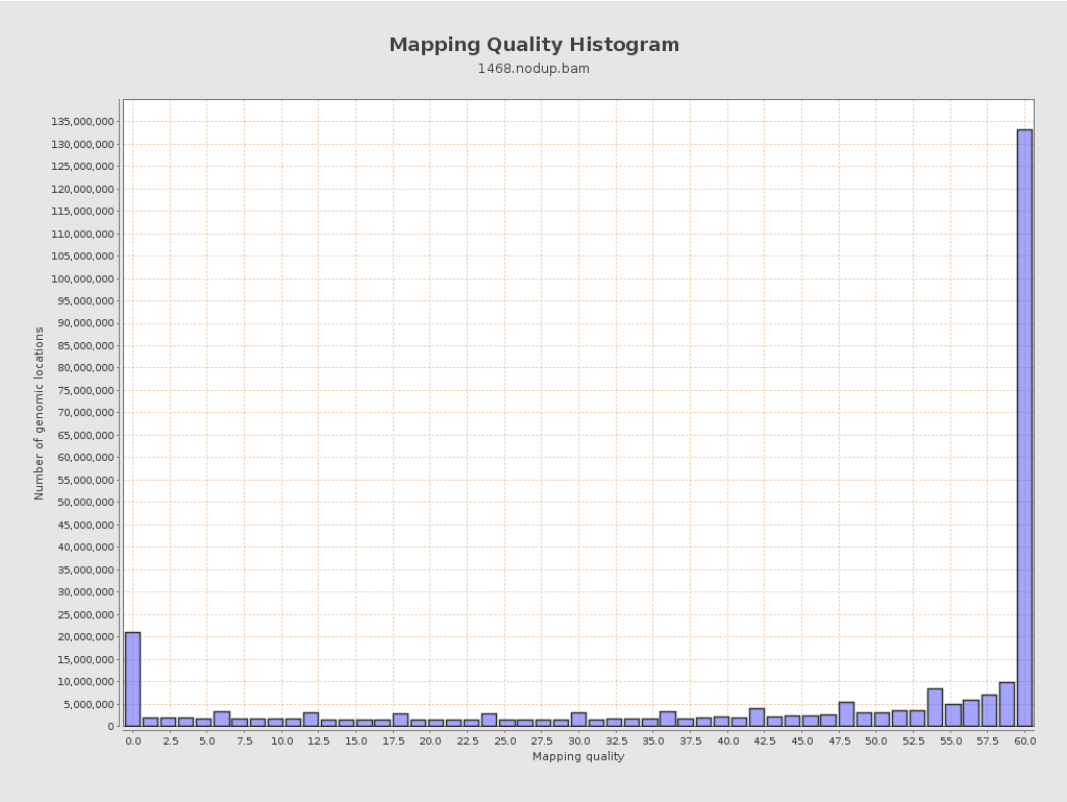
11. Results : Homopolymer Indels



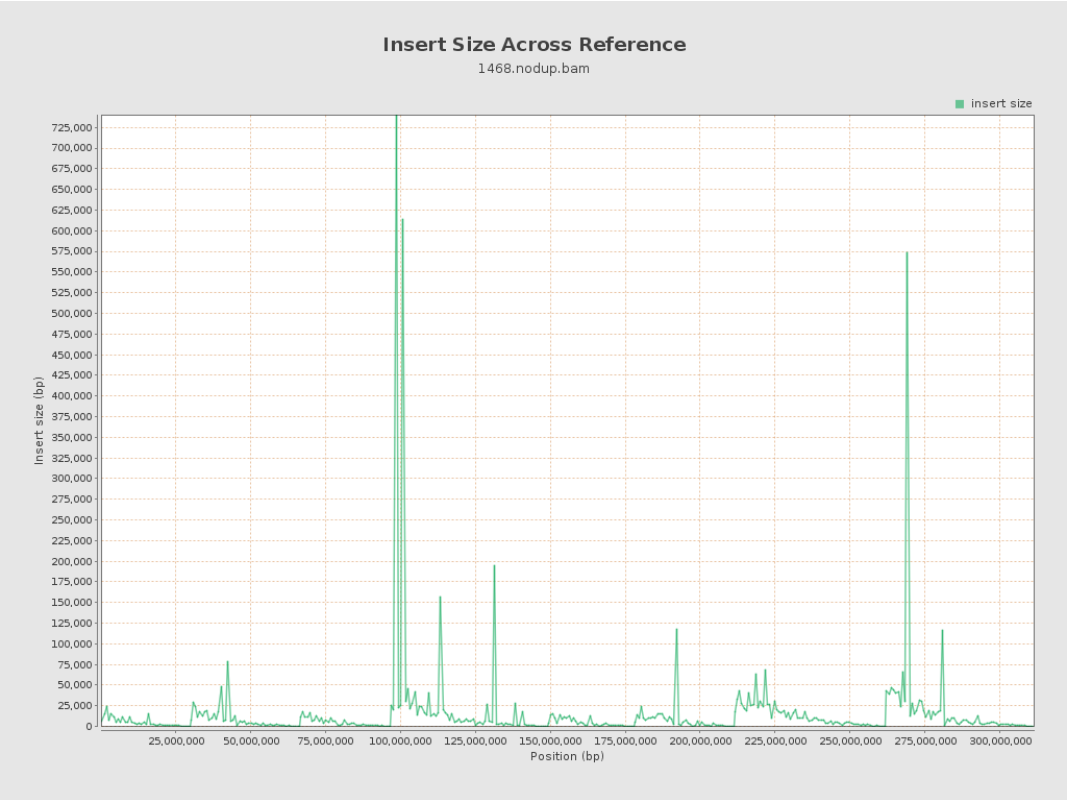
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram