Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/448.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/448.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_135/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_135_S225_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_135/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_135_S225_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:38:12 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	84,358,657
Mapped reads	79,811,416 / 94.61%
Unmapped reads	4,547,241 / 5.39%
Mapped paired reads	79,811,416 / 94.61%
Mapped reads, first in pair	39,978,772 / 47.39%
Mapped reads, second in pair	39,832,644 / 47.22%
Mapped reads, both in pair	78,335,388 / 92.86%
Mapped reads, singletons	1,476,028 / 1.75%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	12,974,159 / 15.38%
Clipped reads	16,973,107 / 20.12%

2.2. ACGT Content

Number/percentage of A's	3,446,371,454 / 30.96%
Number/percentage of C's	2,120,364,704 / 19.05%
Number/percentage of T's	3,446,099,065 / 30.96%
Number/percentage of G's	2,117,084,464 / 19.02%
Number/percentage of N's	47,001 / 0%
GC Percentage	38.07%

2.3. Coverage

Mean	35.8059
Standard Deviation	257.8442

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Insert size

Mean	225,903.82
Standard Deviation	2,246,460.47
P25/Median/P75	338 / 442 / 579

2.6. Mismatches and indels

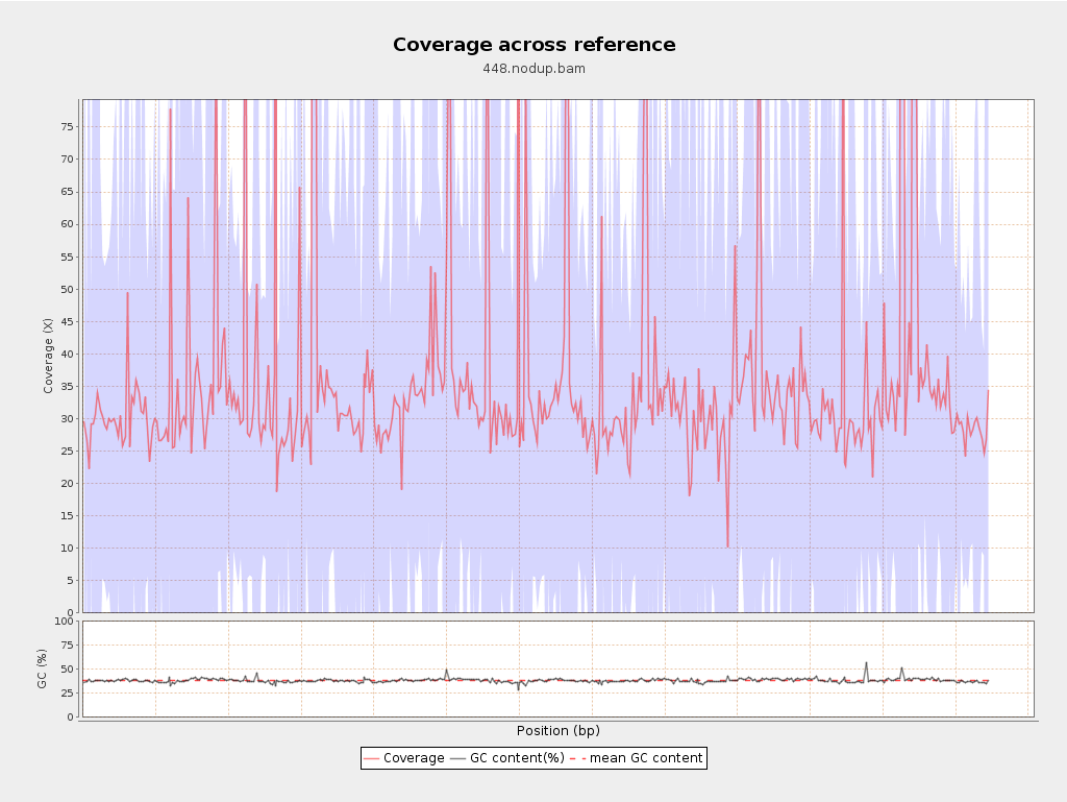
General error rate	2.24%
Mismatches	229,498,993
Insertions	7,287,846
Mapped reads with at least one insertion	8.22%
Deletions	7,609,123
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56.6%

2.7. Chromosome stats

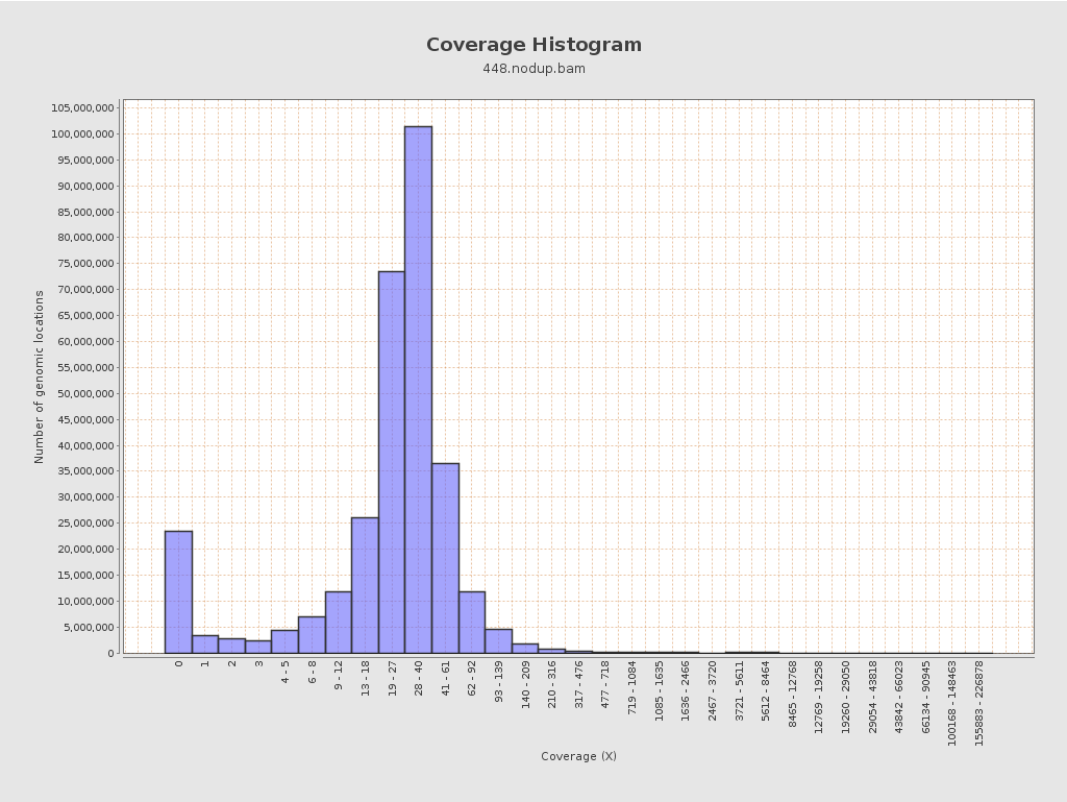
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	883535554	29.7243	72.5402

LT669789.1	36598175	1359990125	37.1601	286.6062
LT669790.1	30422129	1120114159	36.8191	234.5635
LT669791.1	52758100	1852716566	35.1172	212.3622
LT669792.1	28376109	1005418807	35.4319	288.1077
LT669793.1	33388210	1124978873	33.6939	193.6828
LT669794.1	50579949	1747914899	34.5575	240.9913
LT669795.1	49795044	2063969552	41.4493	373.7242

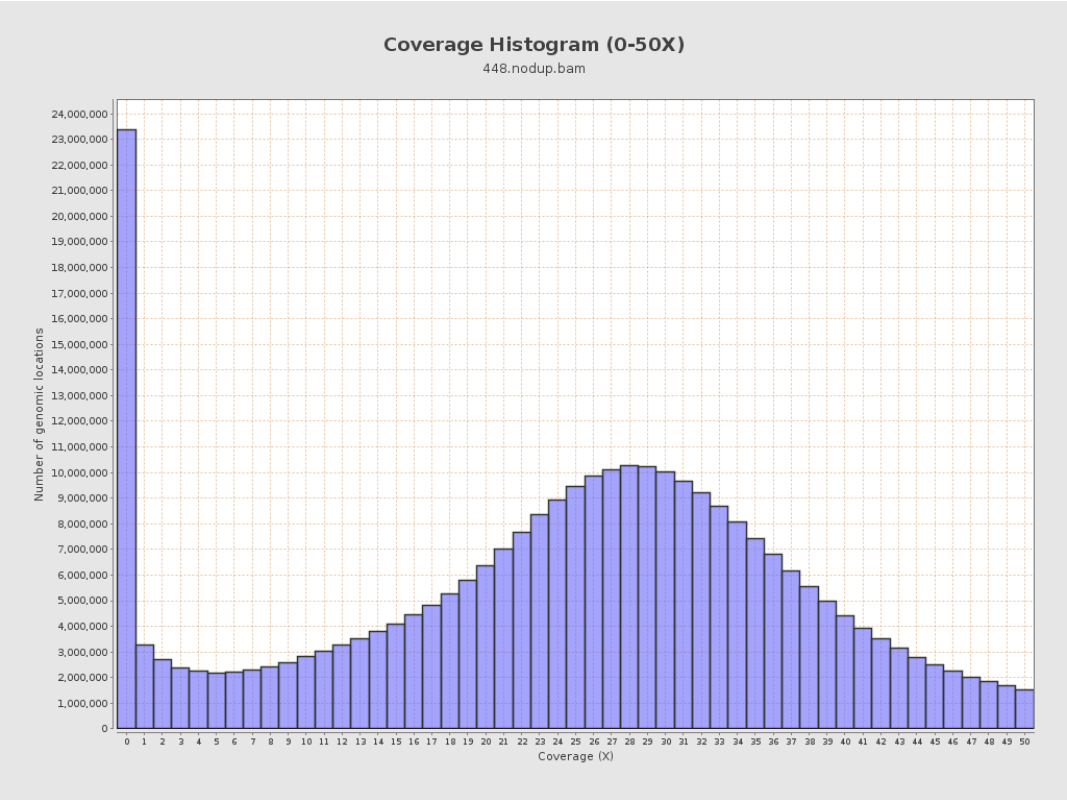
3. Results : Coverage across reference



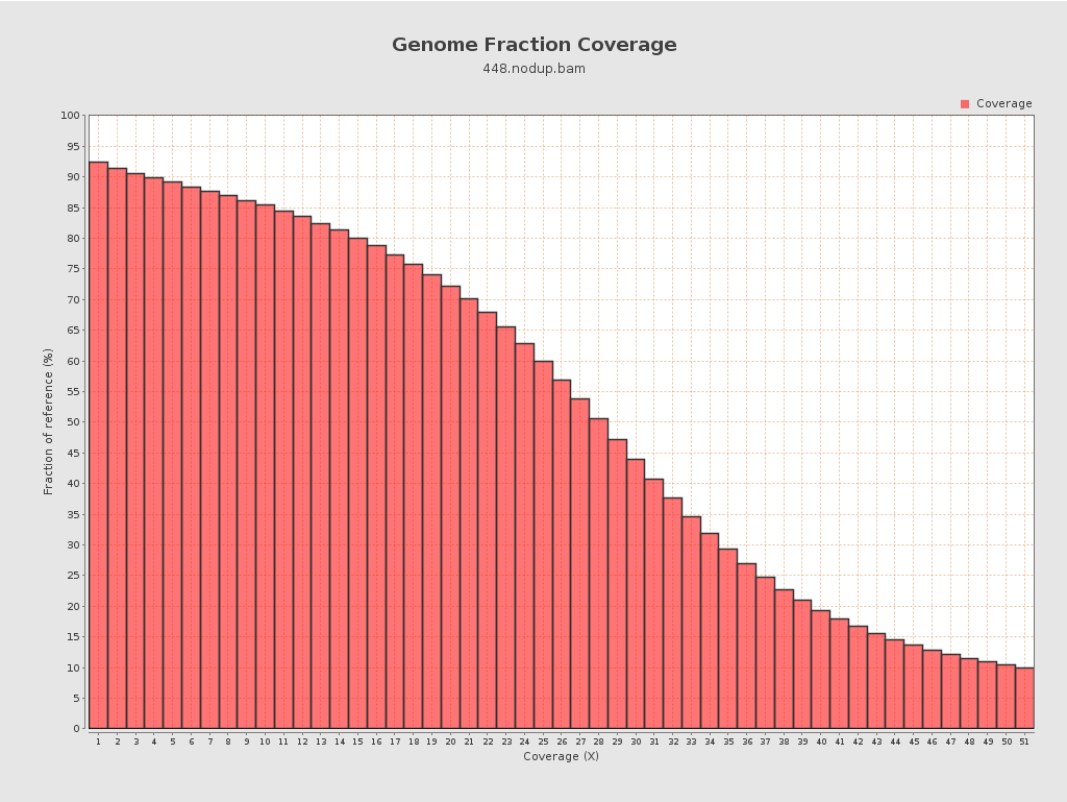
4. Results : Coverage Histogram



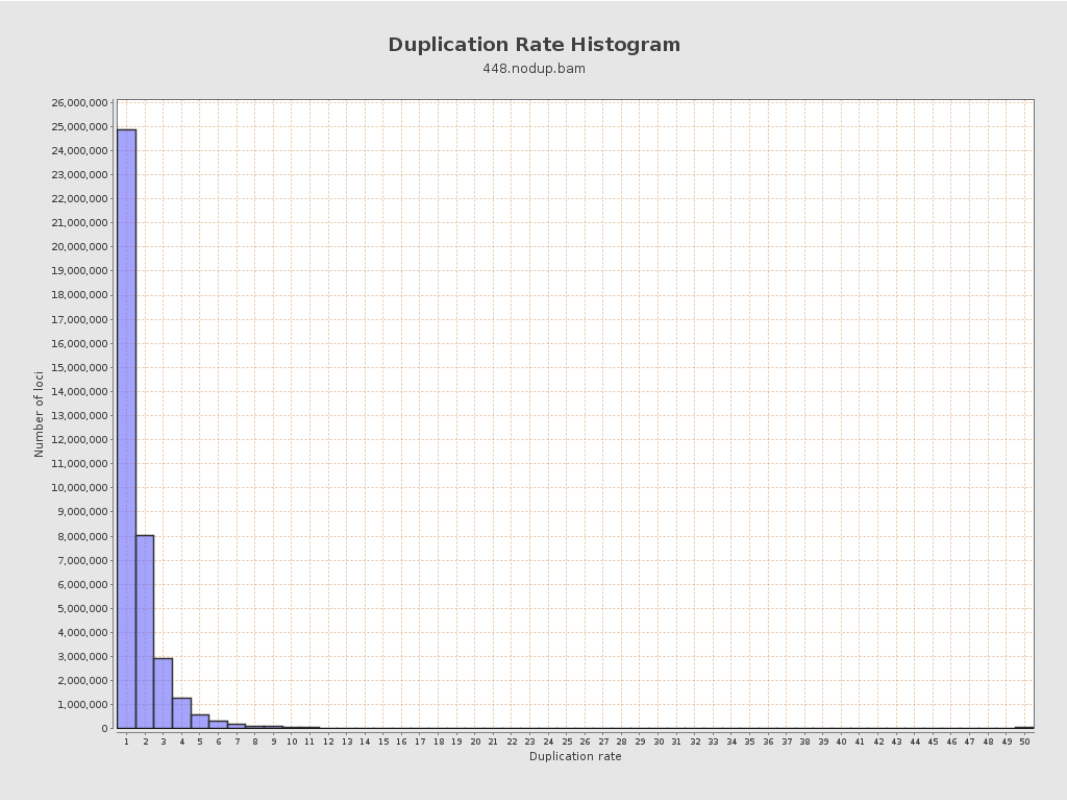
5. Results : Coverage Histogram (0-50X)



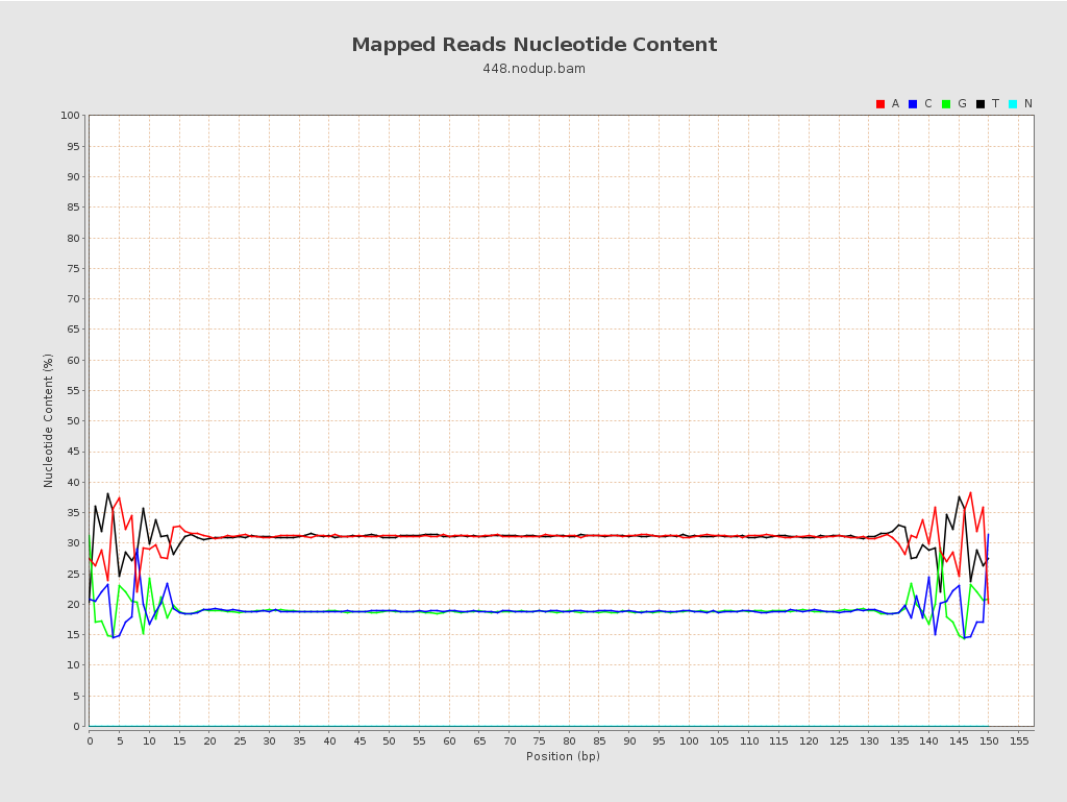
6. Results : Genome Fraction Coverage



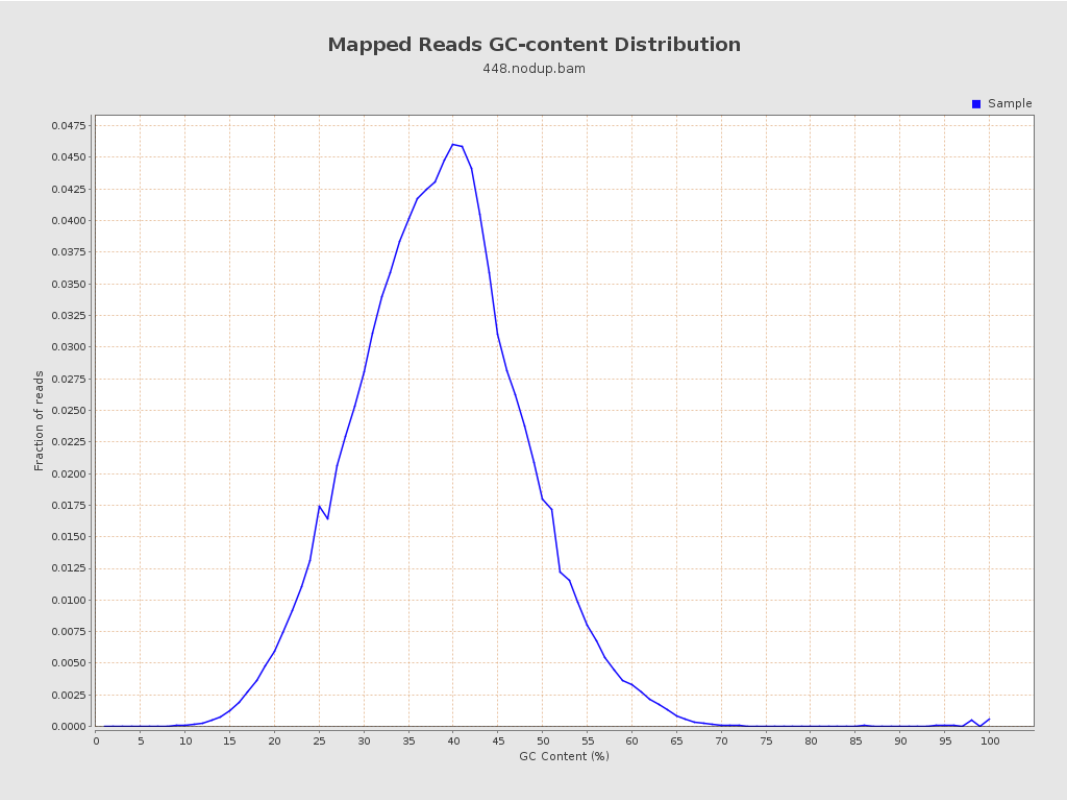
7. Results : Duplication Rate Histogram



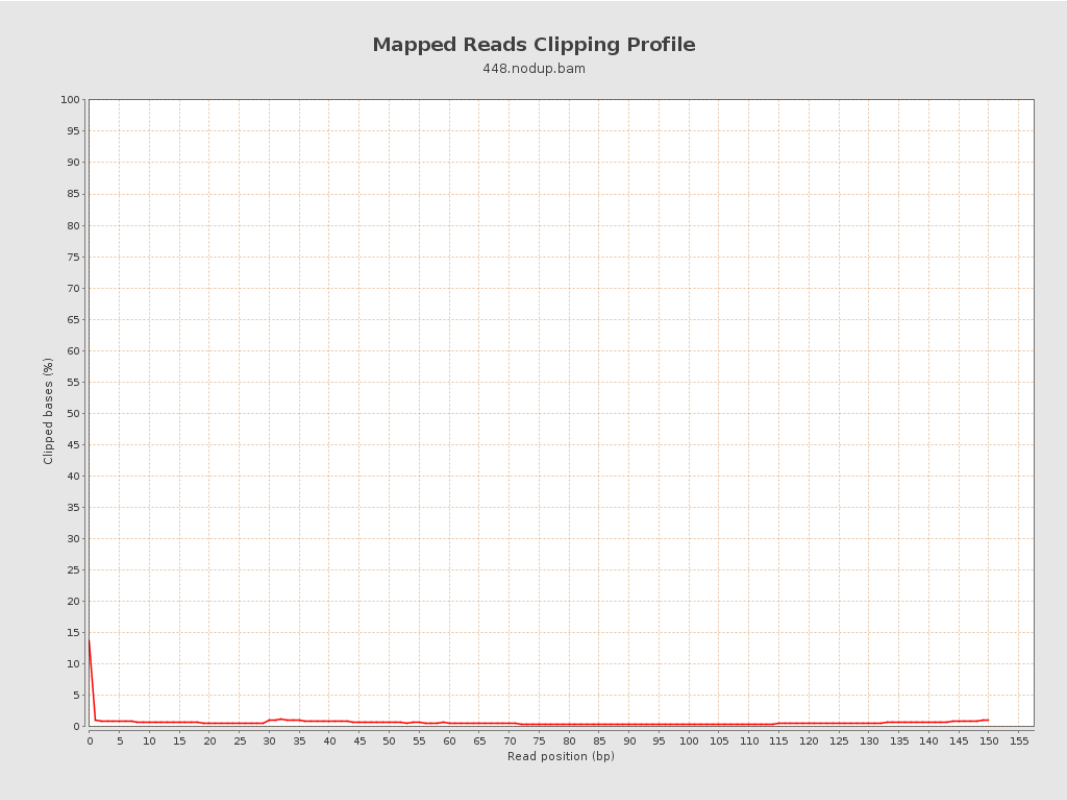
8. Results : Mapped Reads Nucleotide Content



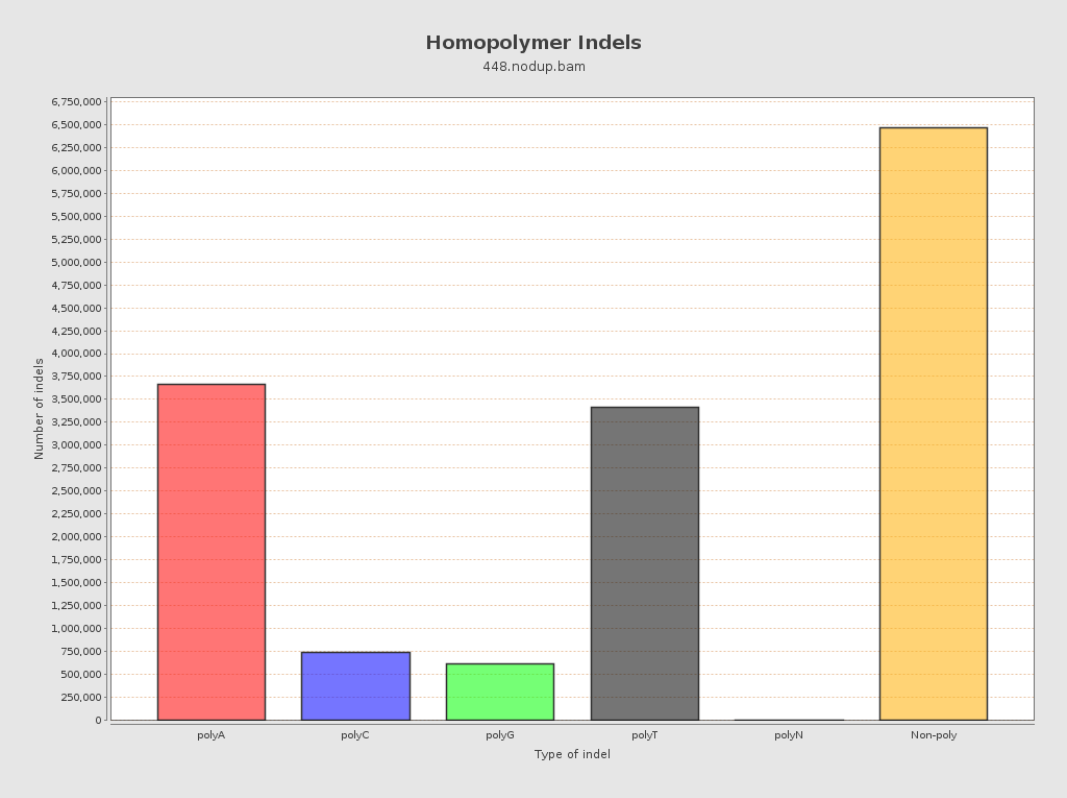
9. Results : Mapped Reads GC-content Distribution



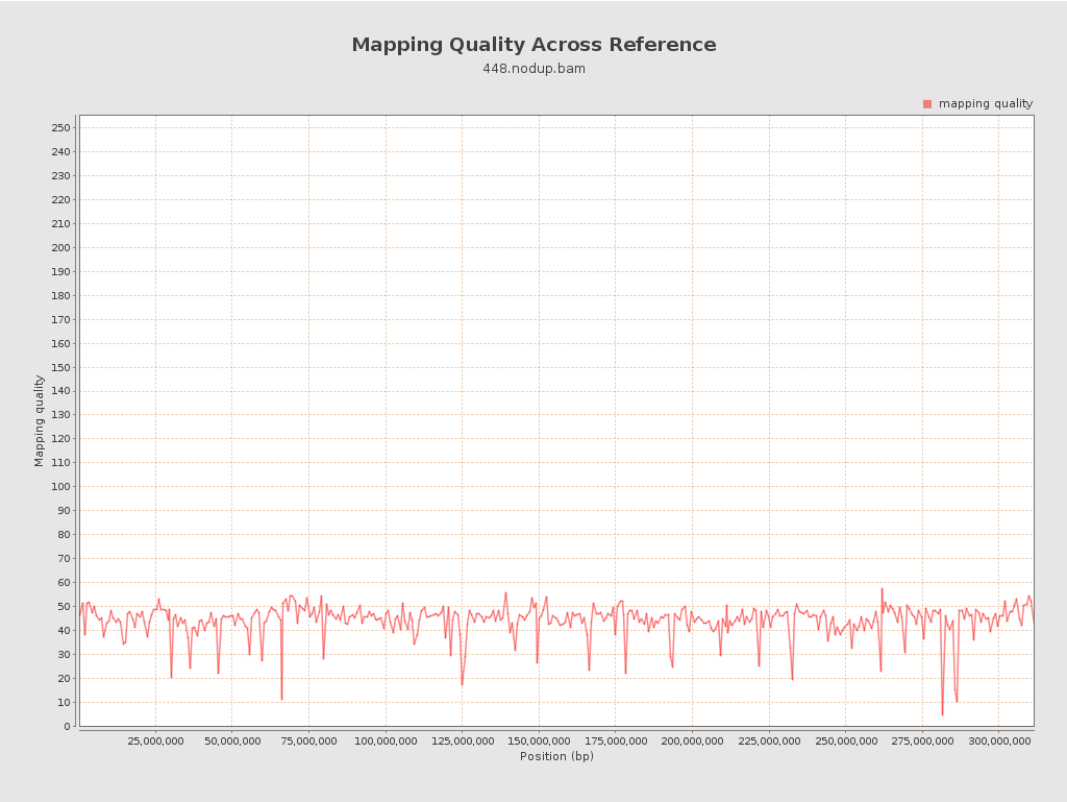
10. Results : Mapped Reads Clipping Profile



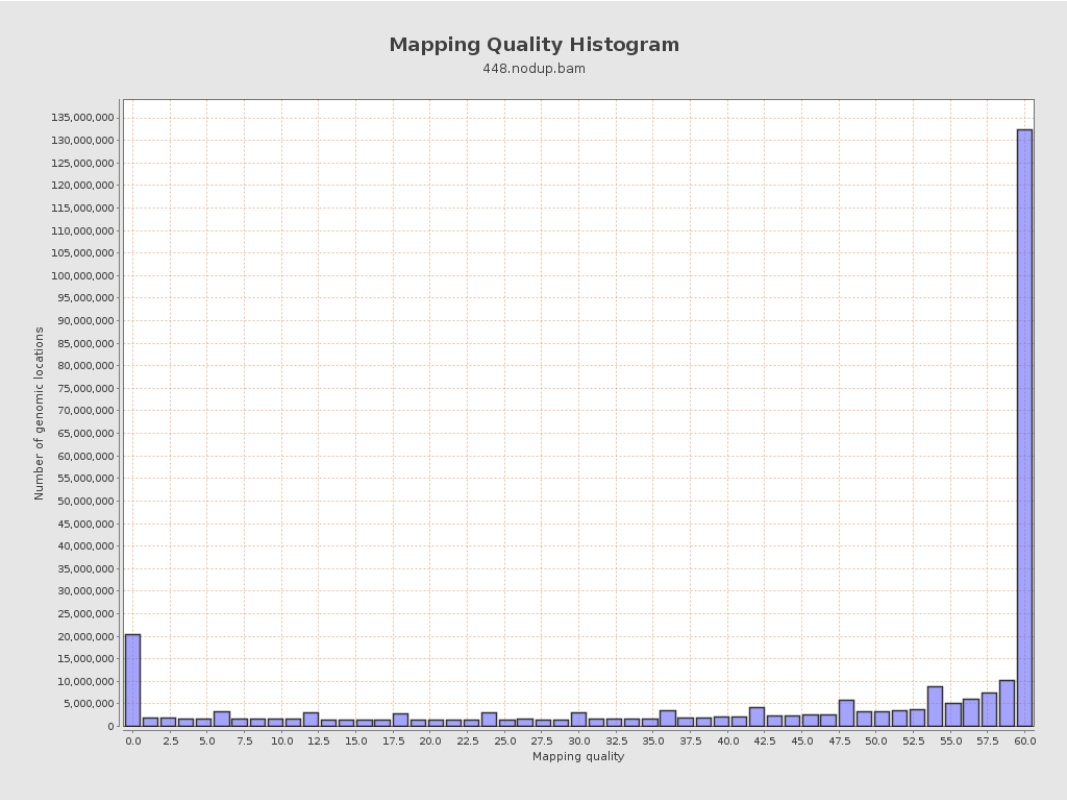
11. Results : Homopolymer Indels



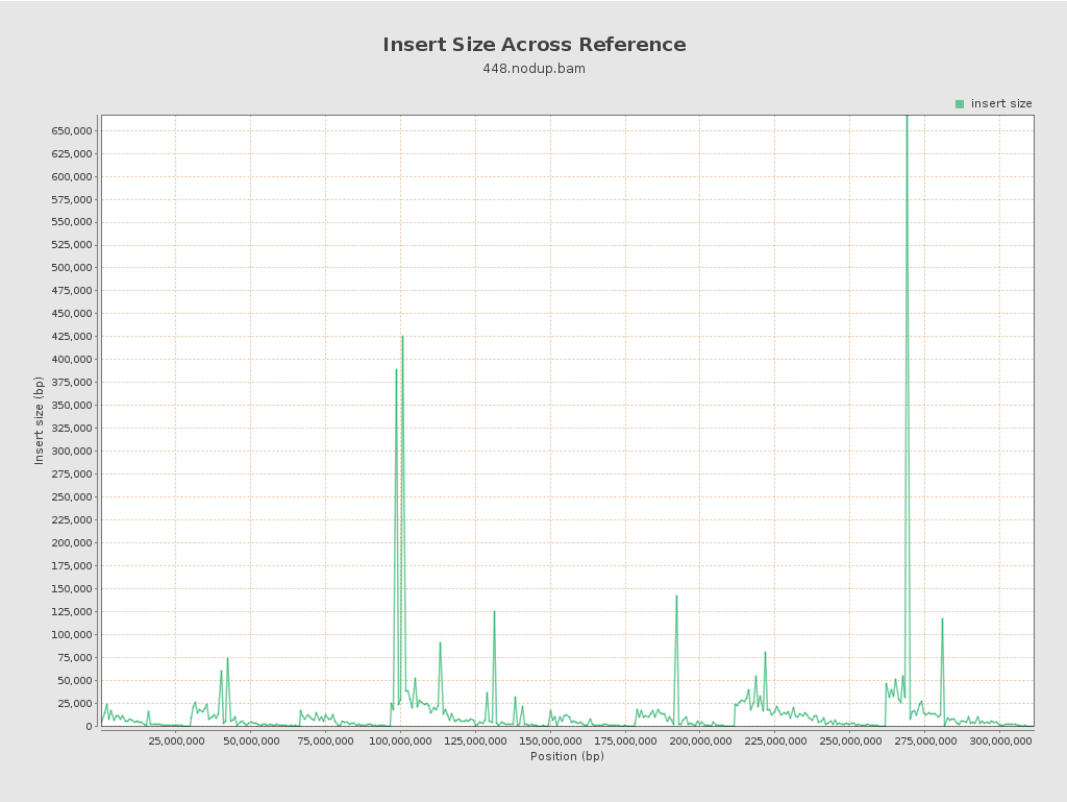
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram