Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/447.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/447.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_180/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_180_S270_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_180/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_180_S270_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:29:28 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,046,383
Mapped reads	56,348,621 / 89.38%
Unmapped reads	6,697,762 / 10.62%
Mapped paired reads	56,348,621 / 89.38%
Mapped reads, first in pair	28,258,197 / 44.82%
Mapped reads, second in pair	28,090,424 / 44.56%
Mapped reads, both in pair	54,865,784 / 87.02%
Mapped reads, singletons	1,482,837 / 2.35%
Read min/max/mean length	30 / 151 / 148.34
Duplicated reads (flagged)	9,271,720 / 14.71%
Clipped reads	12,754,862 / 20.23%

2.2. ACGT Content

Number/percentage of A's	2,409,208,041 / 30.93%
Number/percentage of C's	1,487,684,750 / 19.1%
Number/percentage of T's	2,408,975,397 / 30.92%
Number/percentage of G's	1,484,606,213 / 19.06%
Number/percentage of N's	32,481 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	25.0609
Standard Deviation	205.7557

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Insert size

Mean	230,281.59
Standard Deviation	2,298,380.96
P25/Median/P75	329 / 432 / 568

2.6. Mismatches and indels

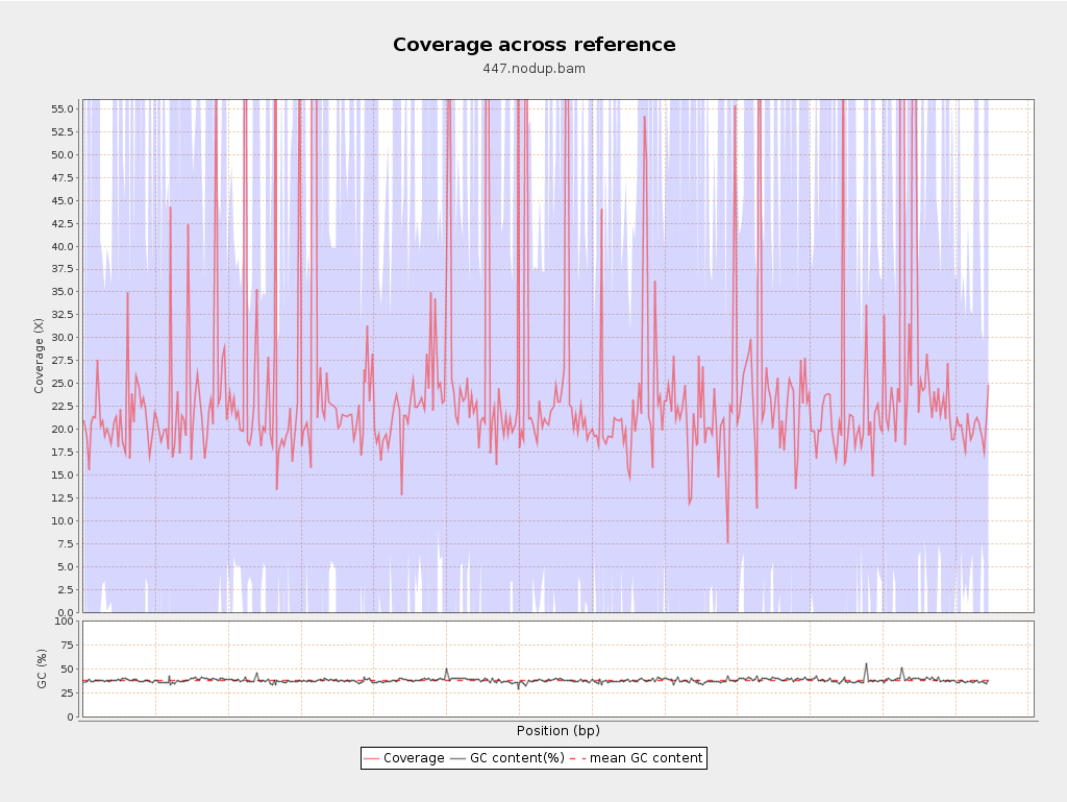
General error rate	2.35%
Mismatches	168,009,975
Insertions	5,339,648
Mapped reads with at least one insertion	8.5%
Deletions	5,297,944
Mapped reads with at least one deletion	8.36%
Homopolymer indels	57.15%

2.7. Chromosome stats

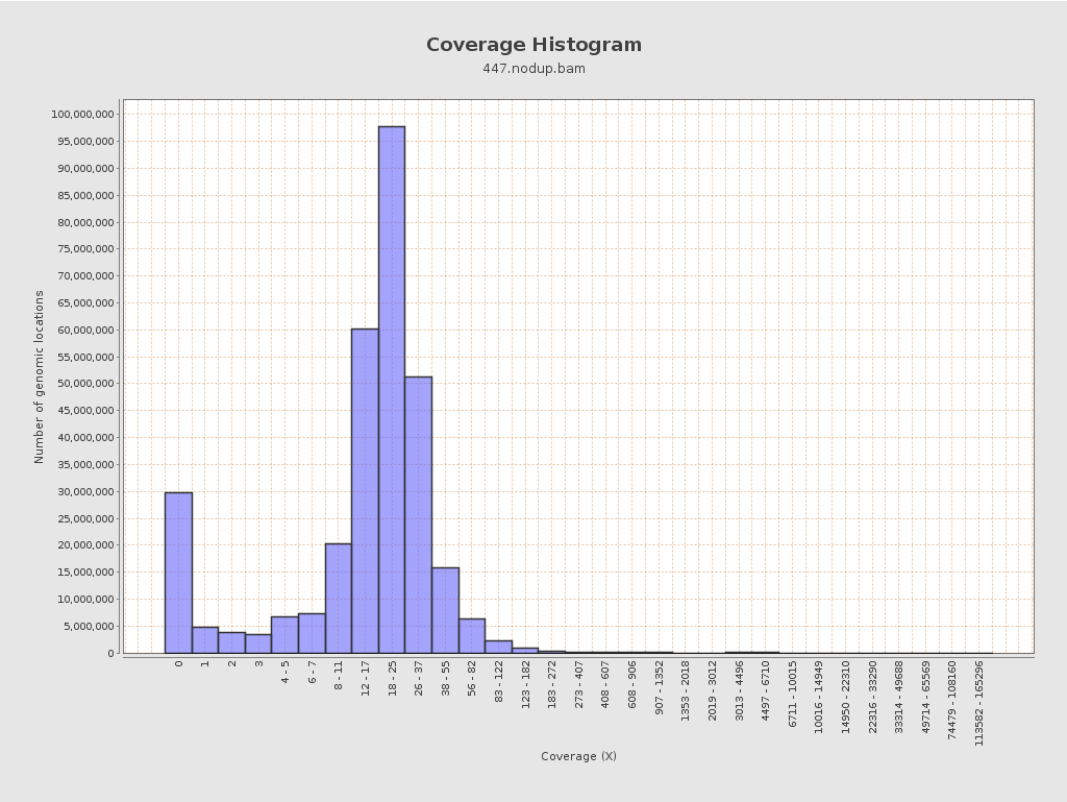
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	621461770	20.9075	72.4513

LT669789.1	36598175	929844273	25.4068	219.0484
LT669790.1	30422129	876851397	28.8228	270.0537
LT669791.1	52758100	1299600431	24.6332	203.1261
LT669792.1	28376109	715540246	25.2163	232.7159
LT669793.1	33388210	758820309	22.7272	108.188
LT669794.1	50579949	1202532446	23.7749	198.7751
LT669795.1	49795044	1405385695	28.2234	243.7356

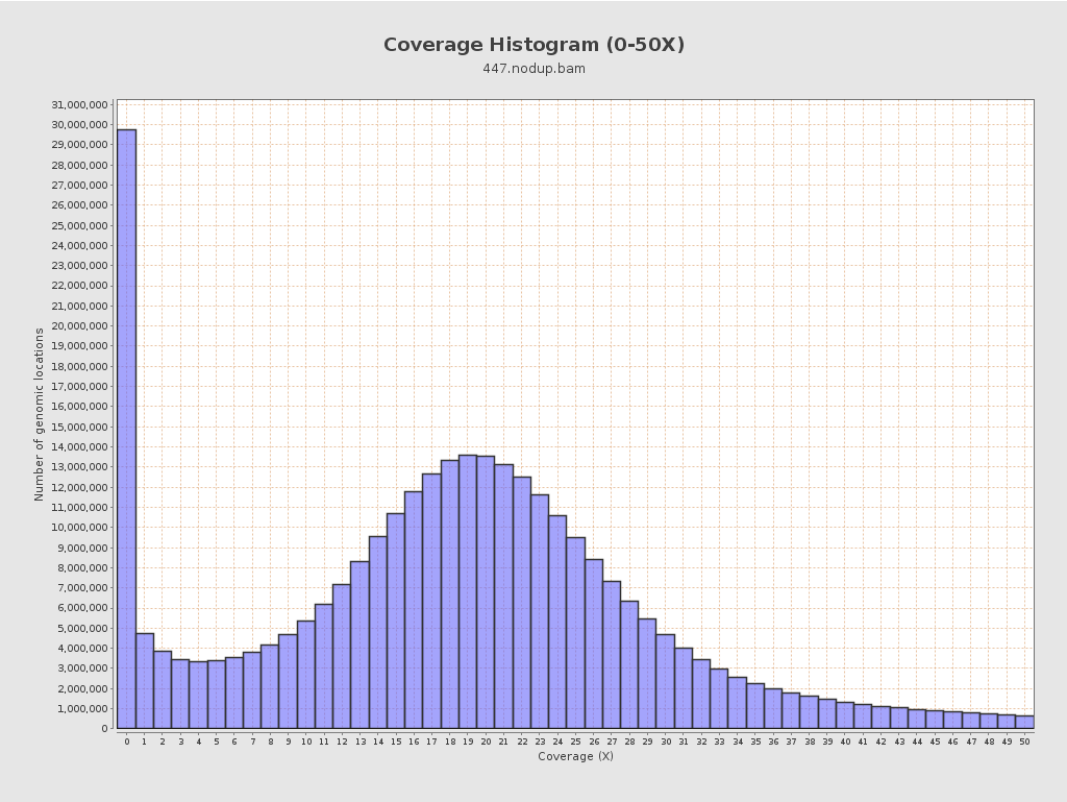
3. Results : Coverage across reference



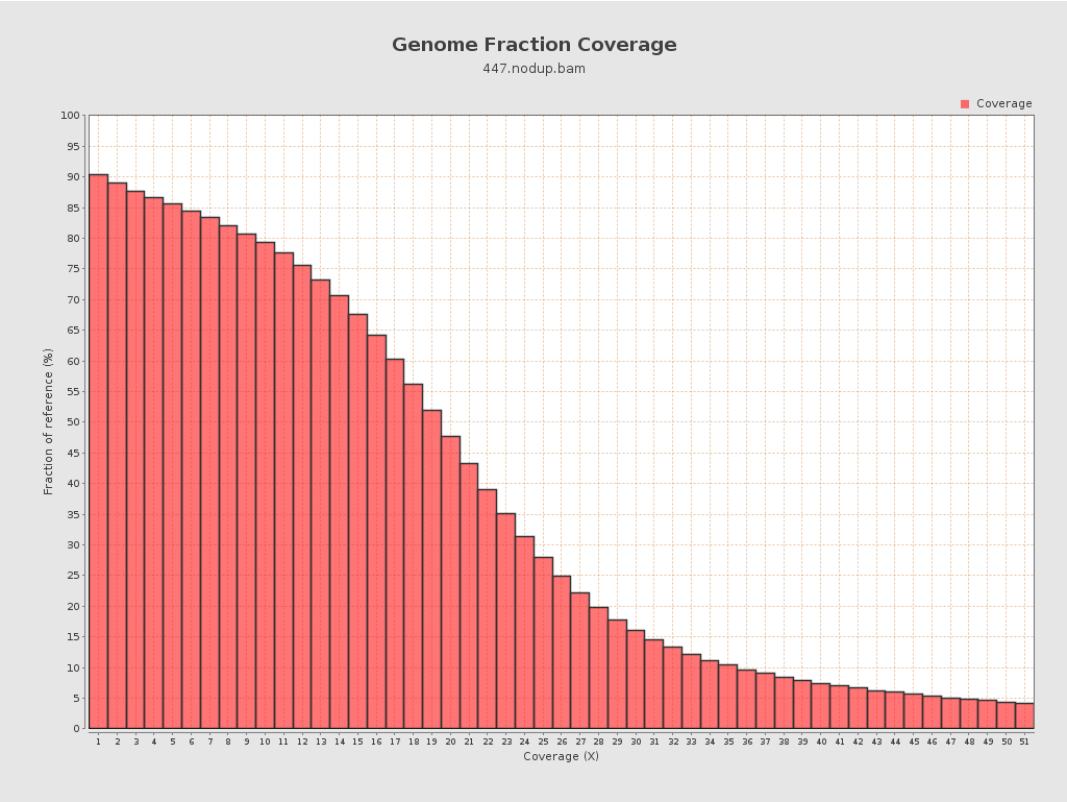
4. Results : Coverage Histogram



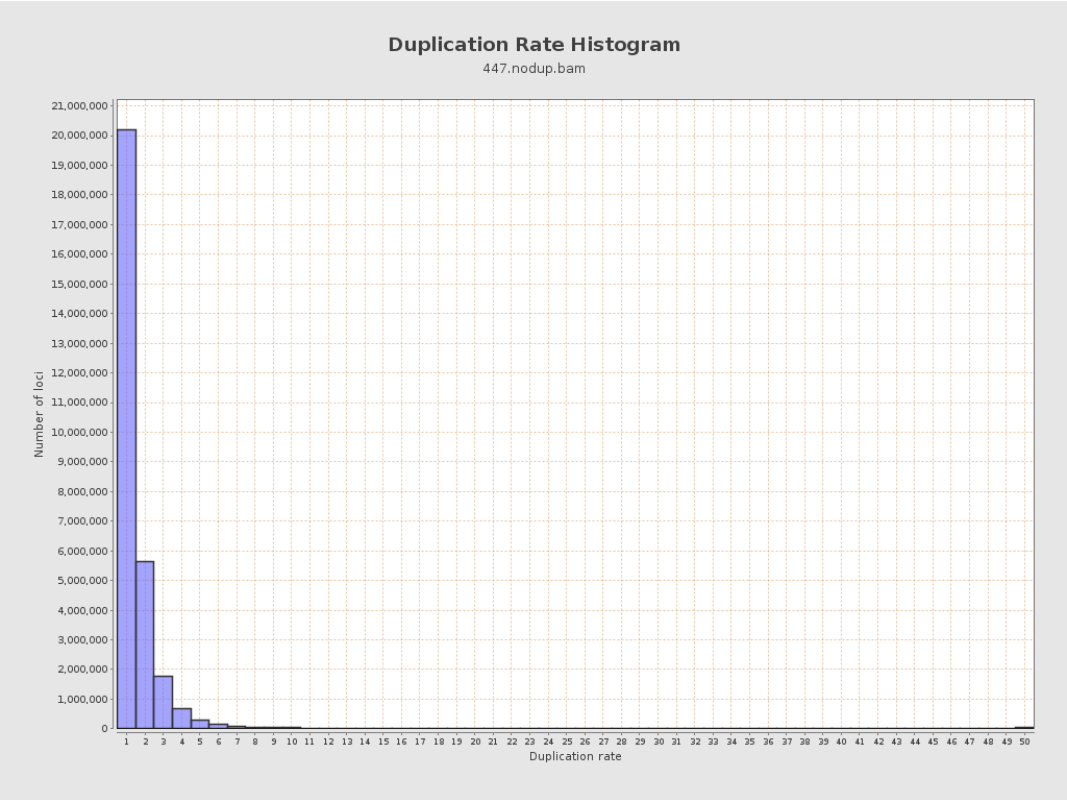
5. Results : Coverage Histogram (0-50X)



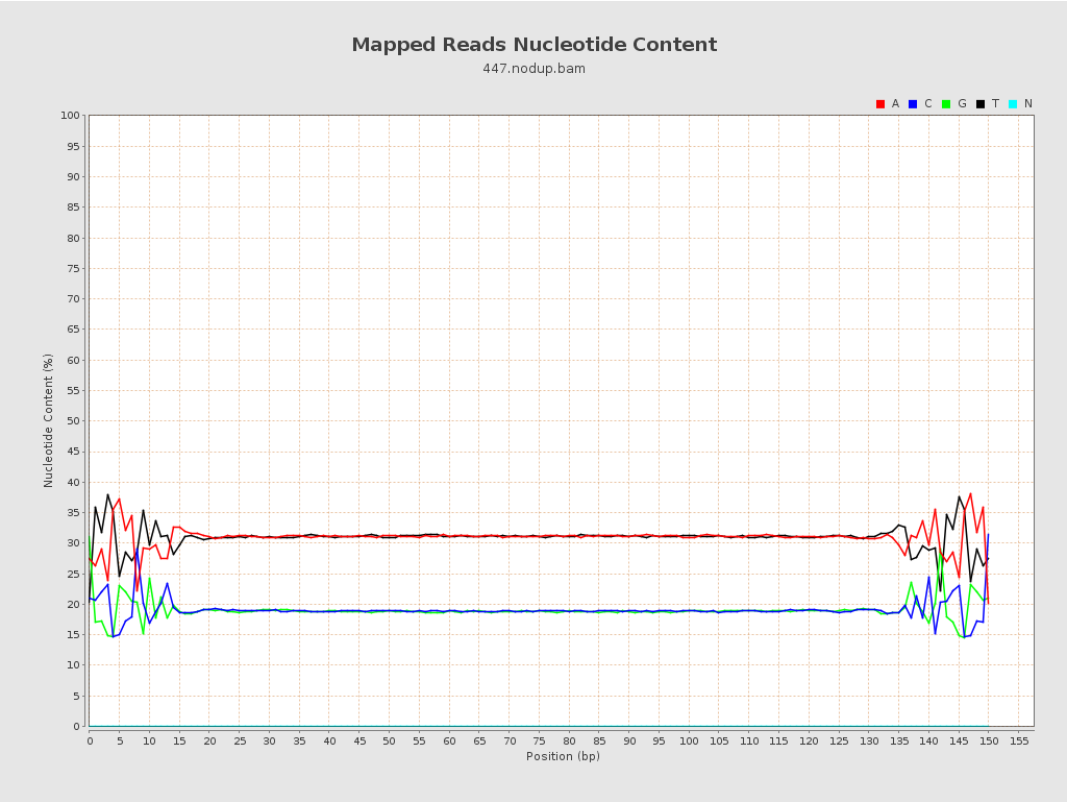
6. Results : Genome Fraction Coverage



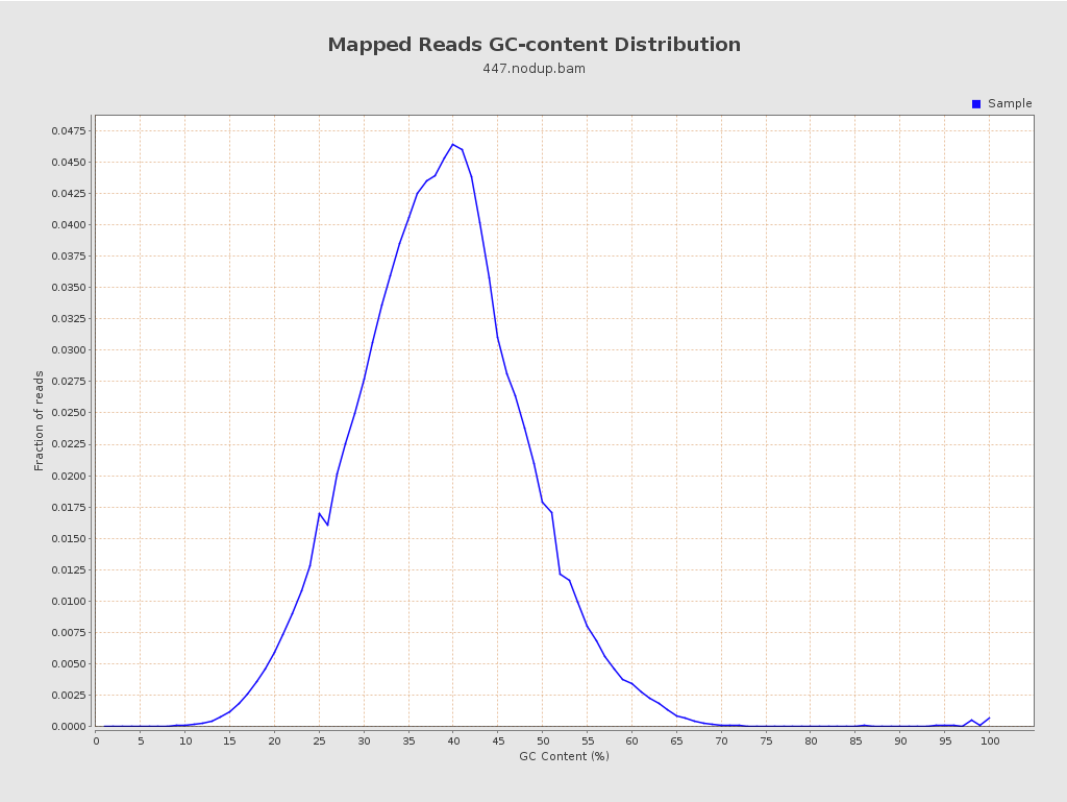
7. Results : Duplication Rate Histogram



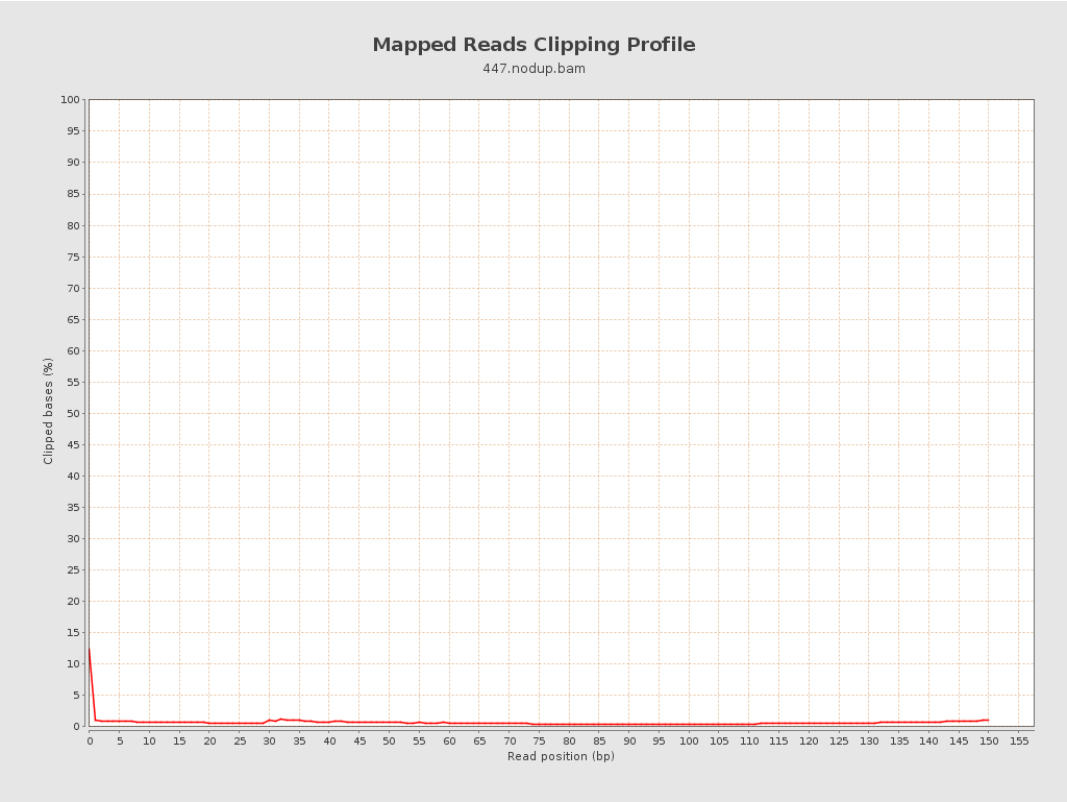
8. Results : Mapped Reads Nucleotide Content



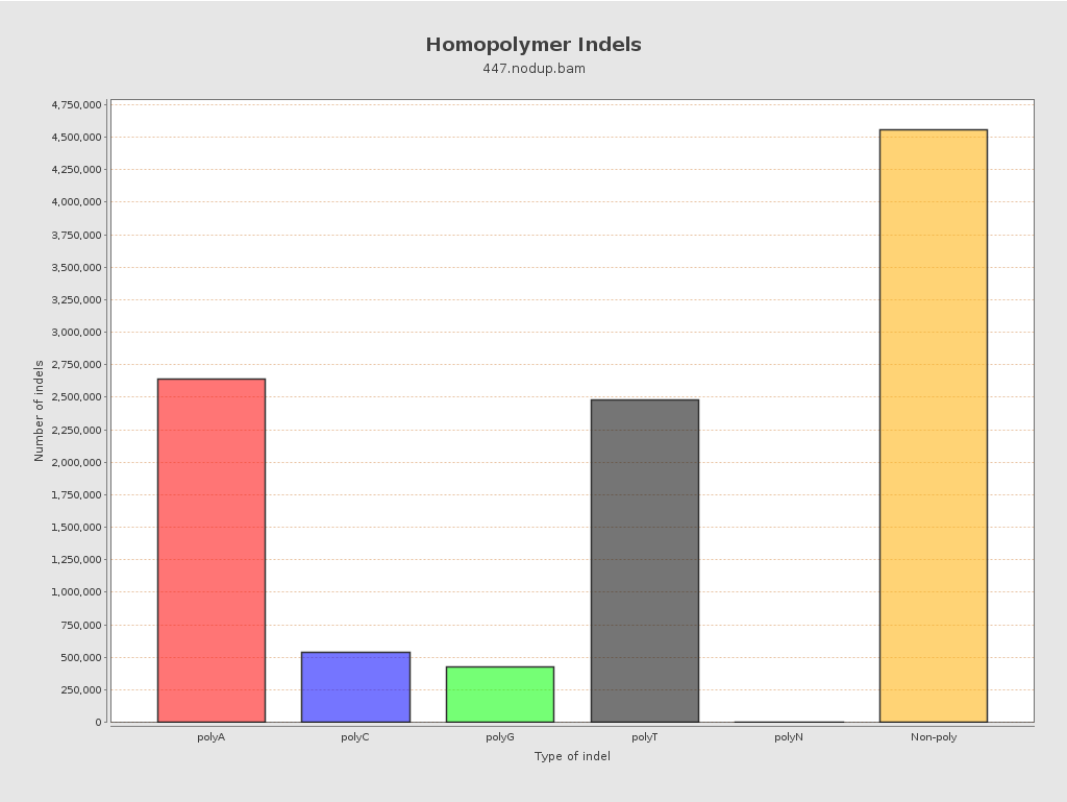
9. Results : Mapped Reads GC-content Distribution



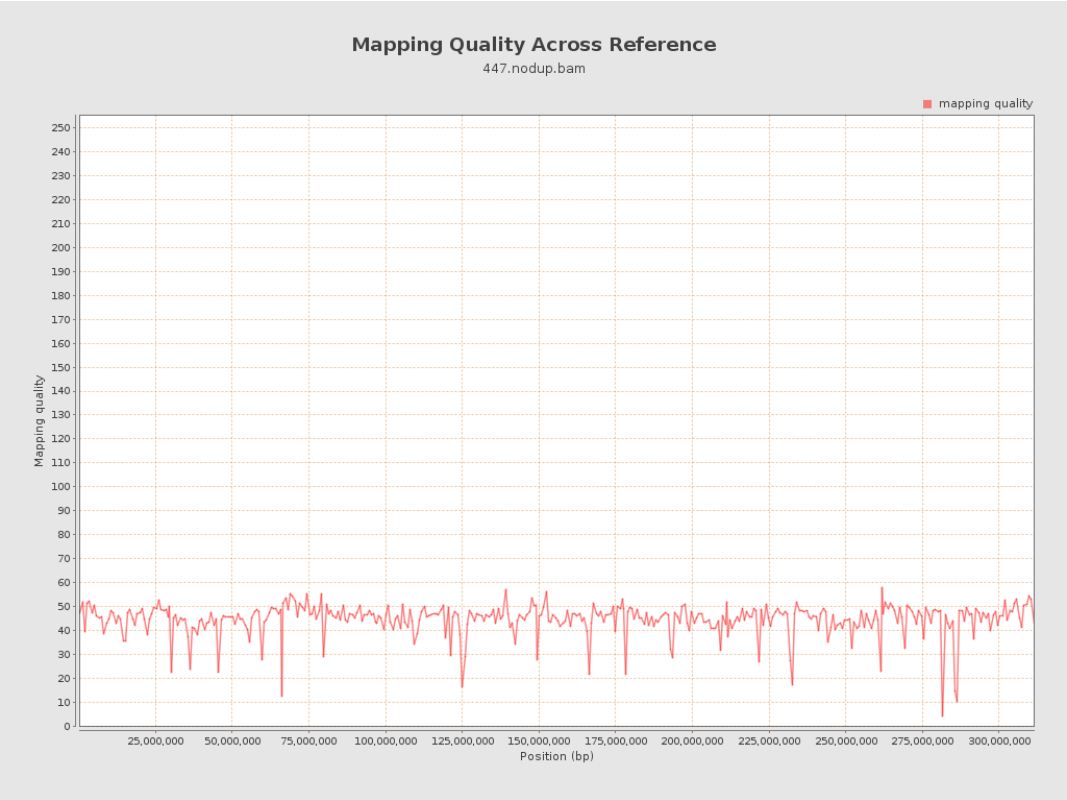
10. Results : Mapped Reads Clipping Profile



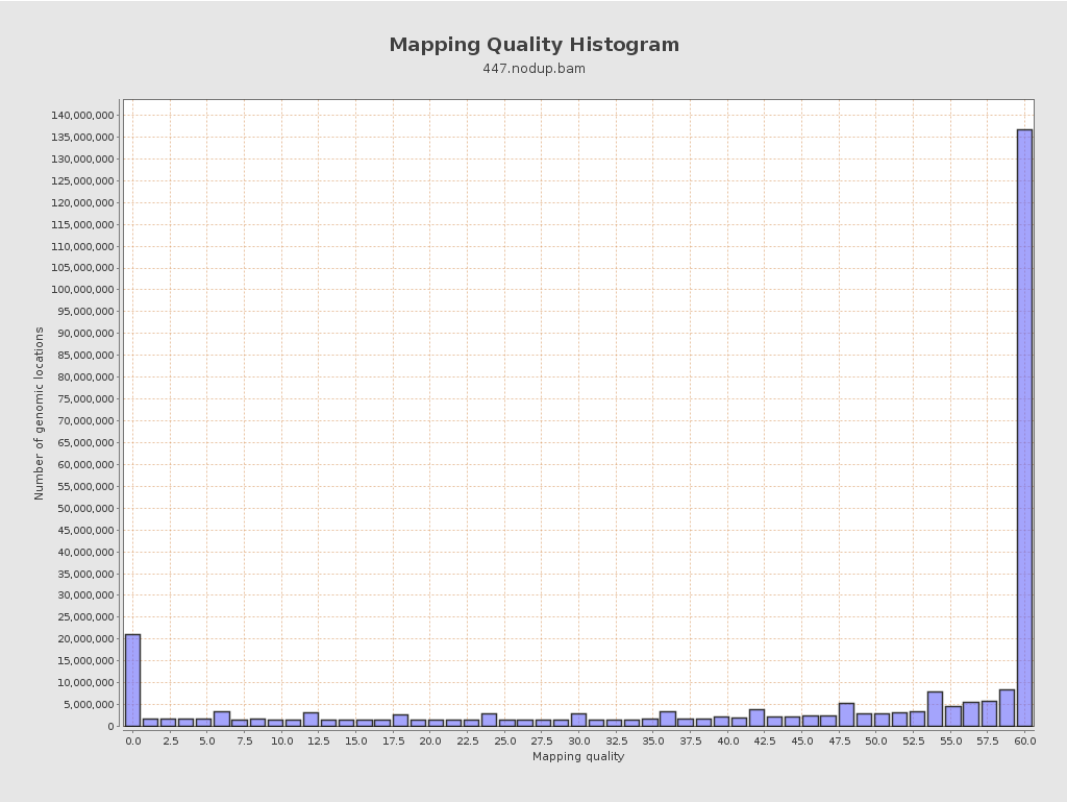
11. Results : Homopolymer Indels



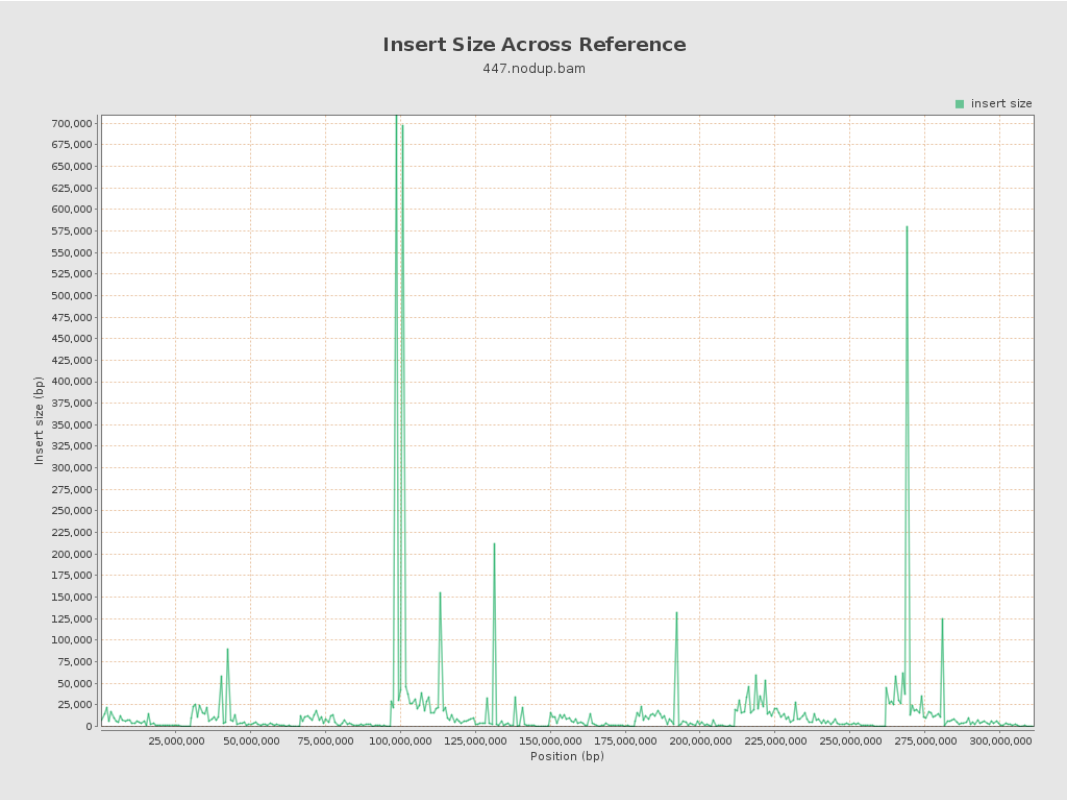
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram