Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/449.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/449.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_216/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_216_S297_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_216/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_216_S297_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:20 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	67,293,403
Mapped reads	62,327,733 / 92.62%
Unmapped reads	4,965,670 / 7.38%
Mapped paired reads	62,327,733 / 92.62%
Mapped reads, first in pair	31,216,168 / 46.39%
Mapped reads, second in pair	31,111,565 / 46.23%
Mapped reads, both in pair	60,818,251 / 90.38%
Mapped reads, singletons	1,509,482 / 2.24%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	9,319,705 / 13.85%
Clipped reads	14,162,050 / 21.05%

2.2. ACGT Content

Number/percentage of A's	2,661,646,493 / 30.93%
Number/percentage of C's	1,642,192,429 / 19.08%
Number/percentage of T's	2,661,567,372 / 30.92%
Number/percentage of G's	1,641,249,279 / 19.07%
Number/percentage of N's	31,738 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	27.6869
Standard Deviation	225.9178

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Insert size

Mean	230,066.03
Standard Deviation	2,292,340.97
P25/Median/P75	317 / 416 / 541

2.6. Mismatches and indels

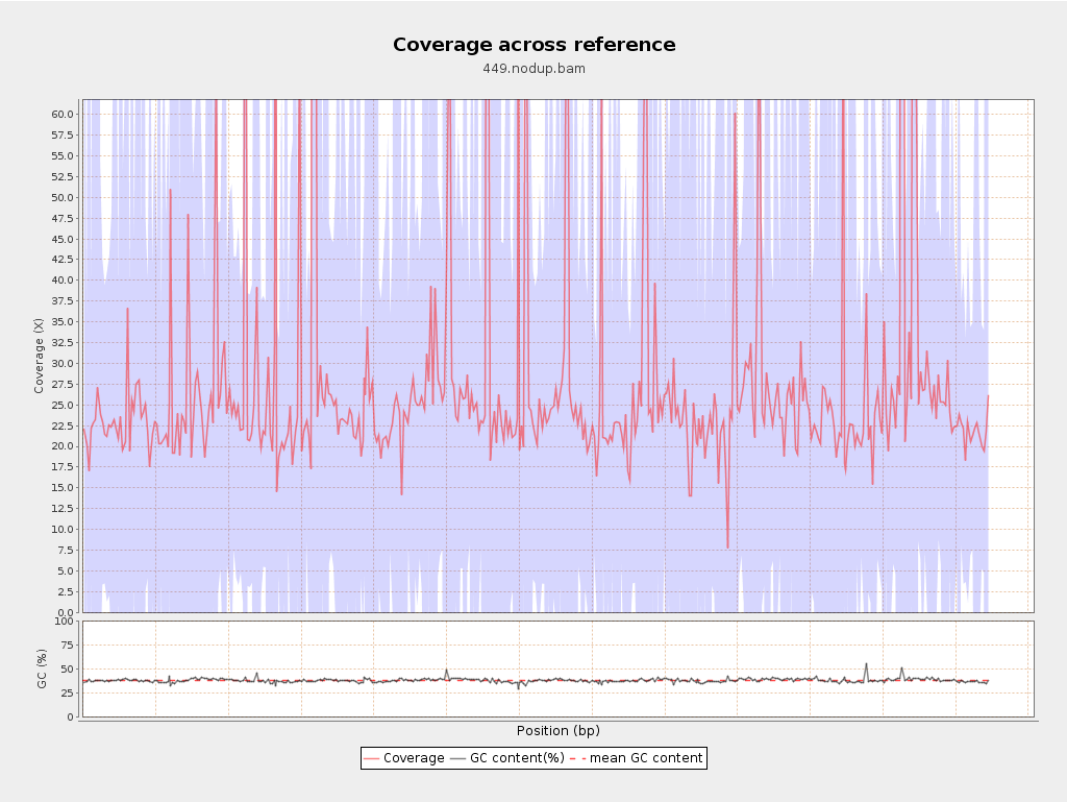
General error rate	2.27%
Mismatches	179,216,823
Insertions	5,857,262
Mapped reads with at least one insertion	8.42%
Deletions	5,835,075
Mapped reads with at least one deletion	8.32%
Homopolymer indels	57.18%

2.7. Chromosome stats

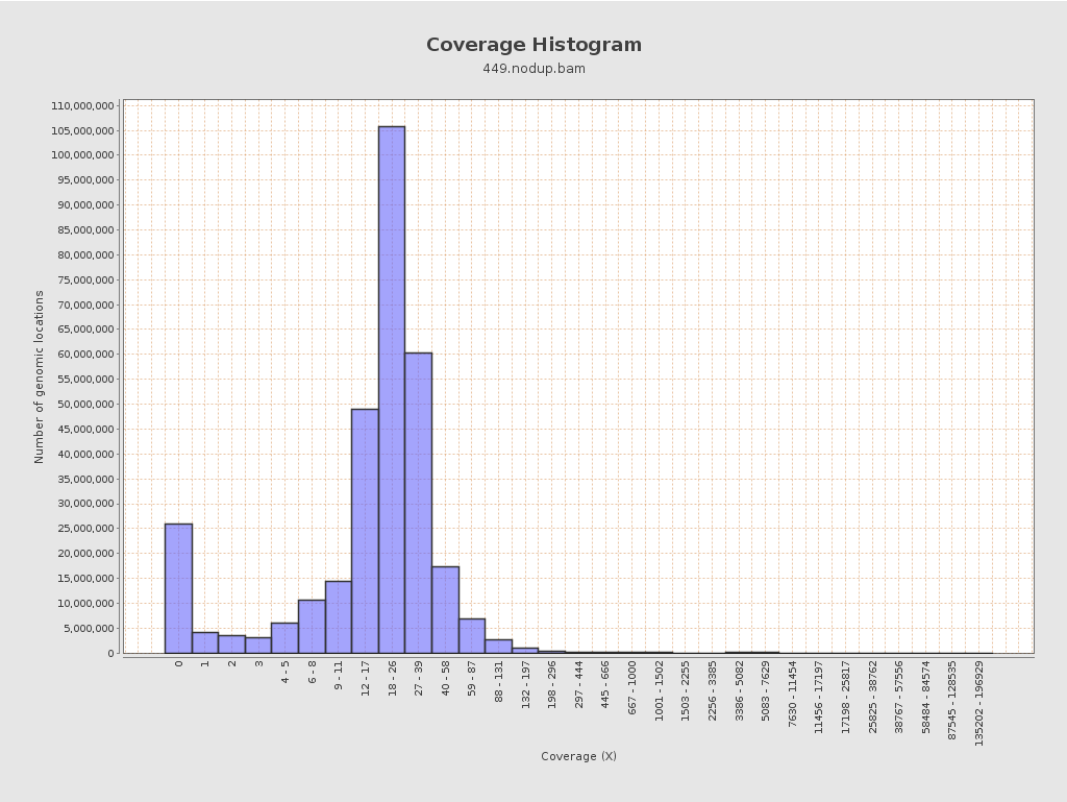
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	675154732	22.7139	77.679

LT669789.1	36598175	1029771746	28.1372	242.4357
LT669790.1	30422129	945023714	31.0637	272.7393
LT669791.1	52758100	1437875241	27.2541	218.9647
LT669792.1	28376109	781943689	27.5564	237.1595
LT669793.1	33388210	867184272	25.9728	165.8187
LT669794.1	50579949	1327296120	26.2415	195.2026
LT669795.1	49795044	1564166612	31.4121	295.2098

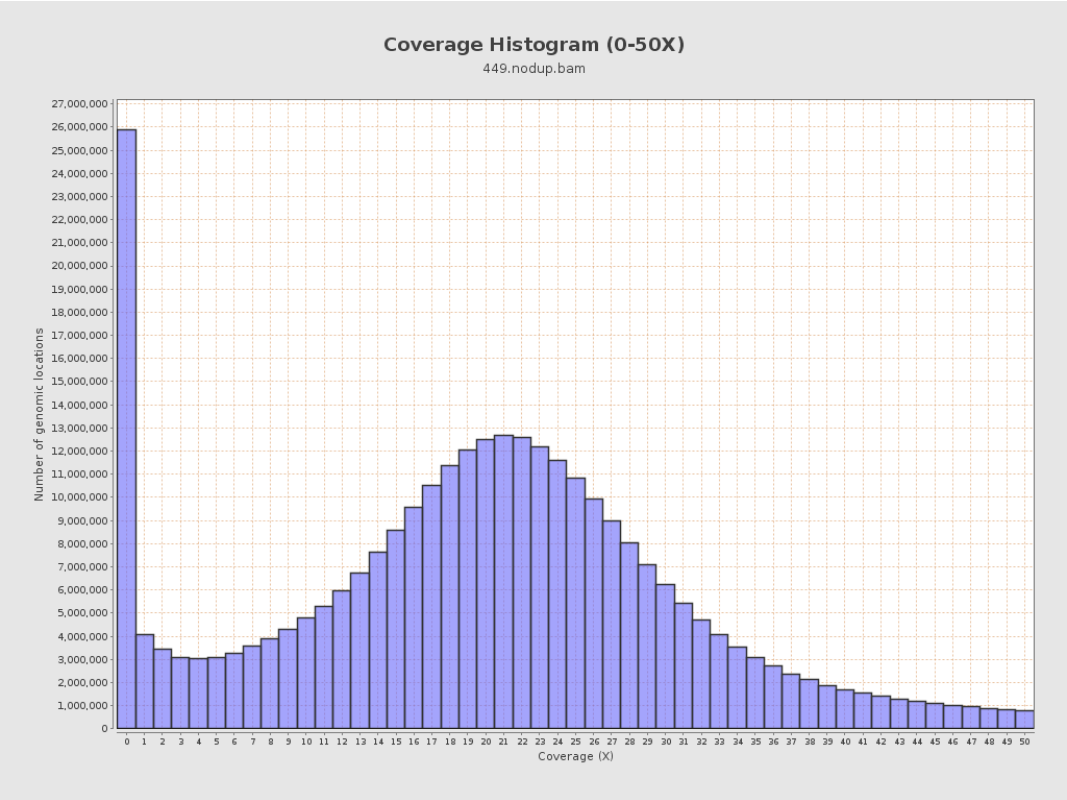
3. Results : Coverage across reference



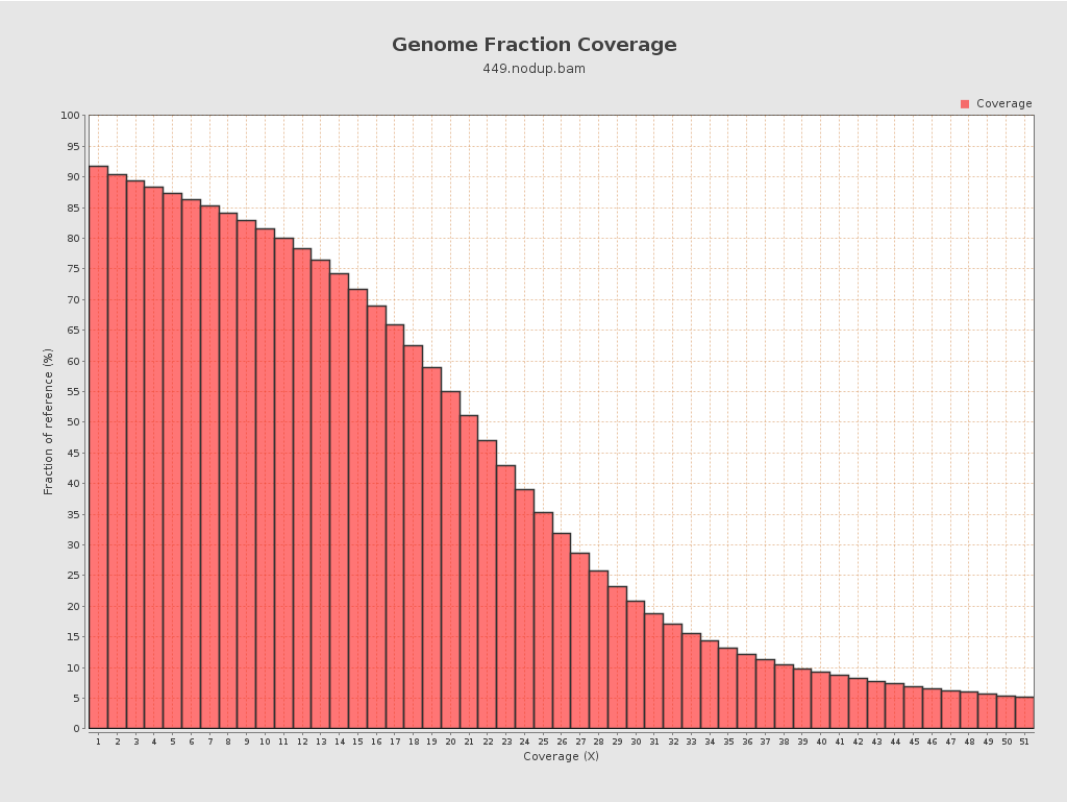
4. Results : Coverage Histogram



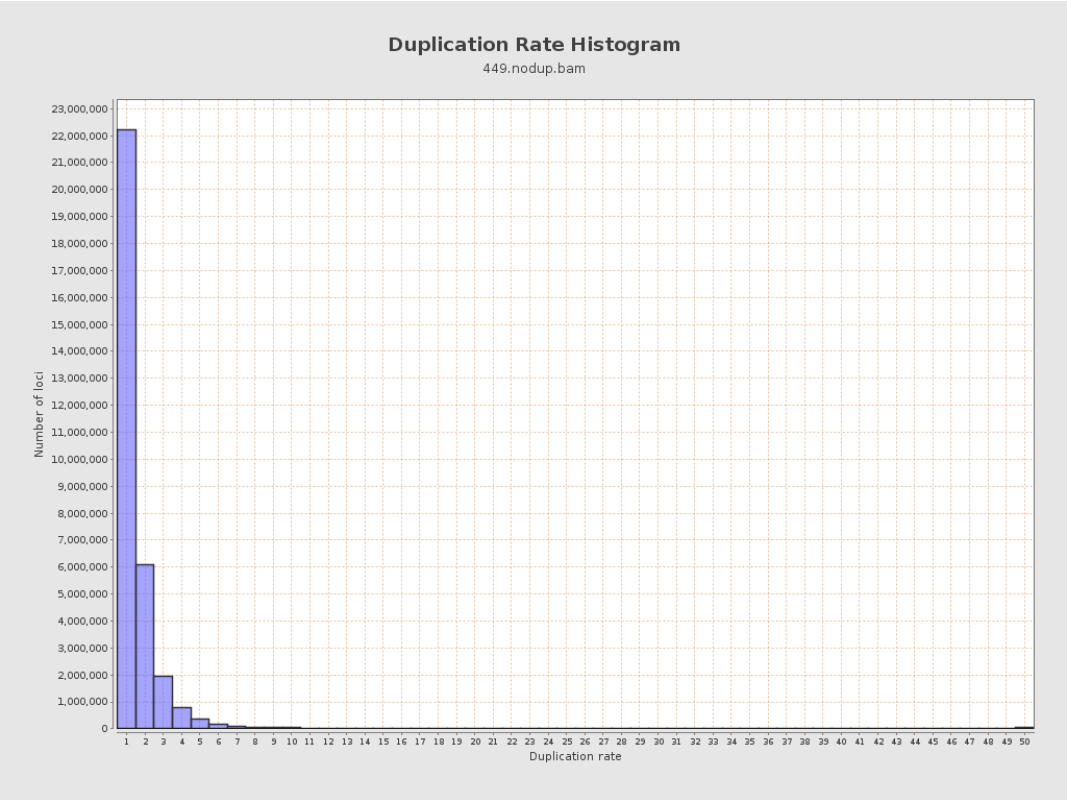
5. Results : Coverage Histogram (0-50X)



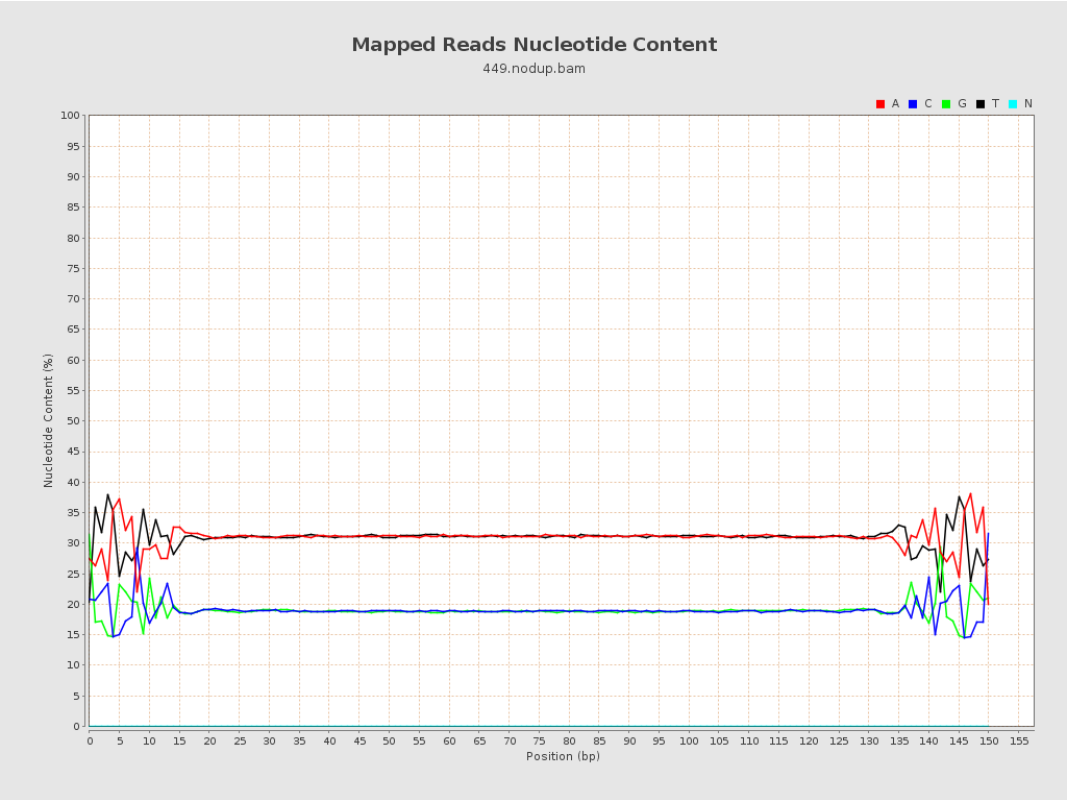
6. Results : Genome Fraction Coverage



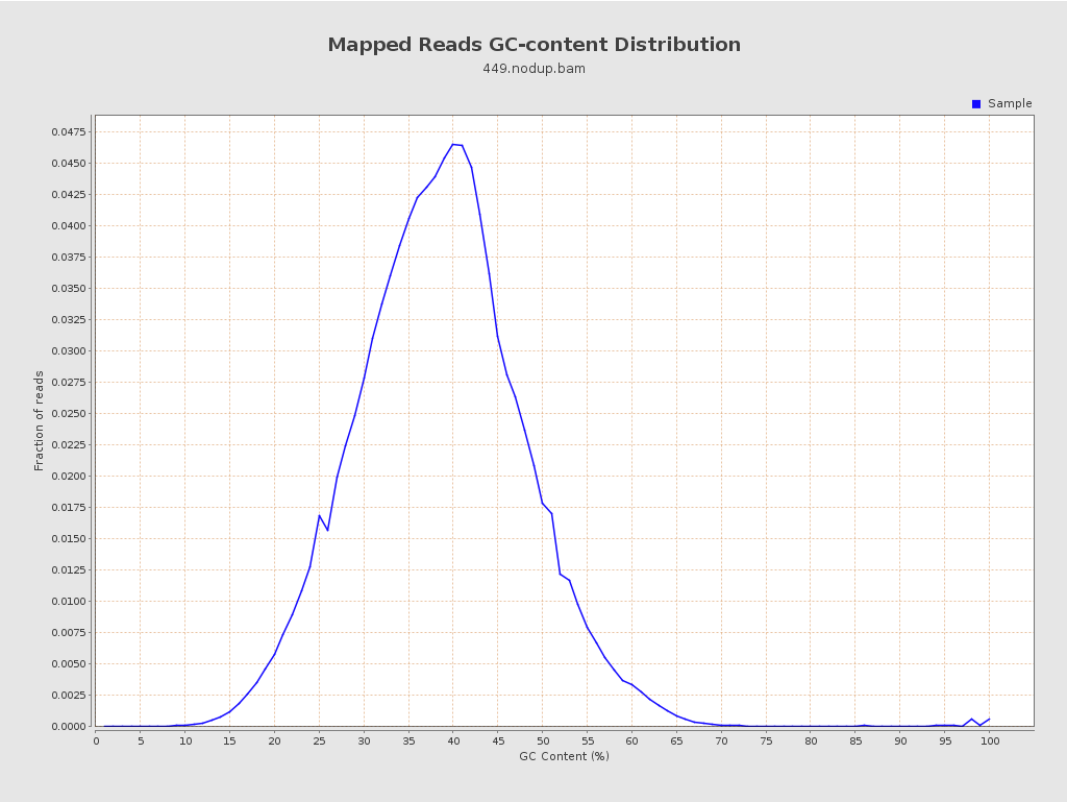
7. Results : Duplication Rate Histogram



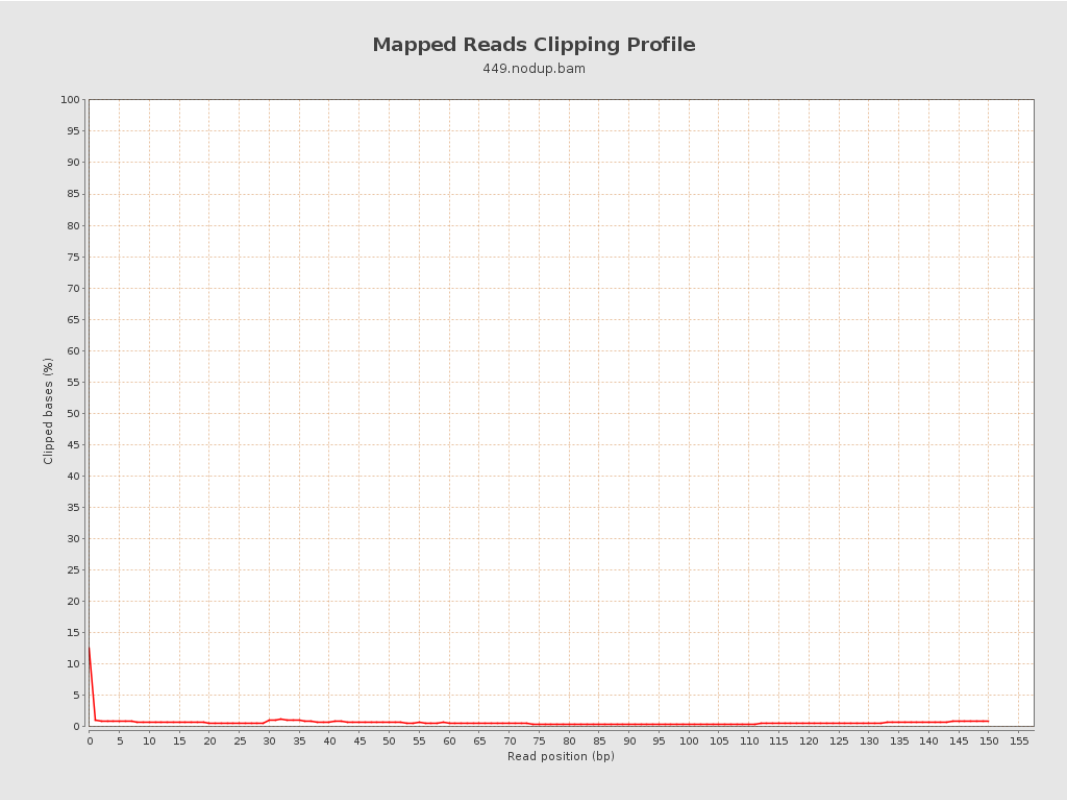
8. Results : Mapped Reads Nucleotide Content



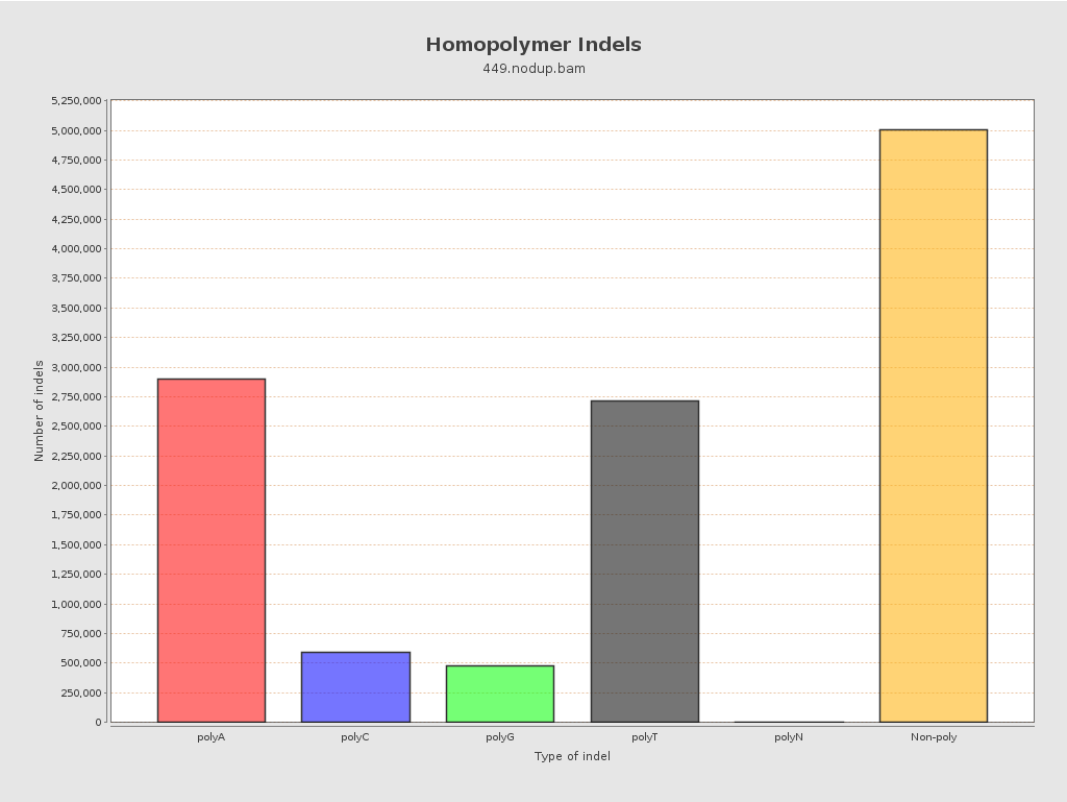
9. Results : Mapped Reads GC-content Distribution



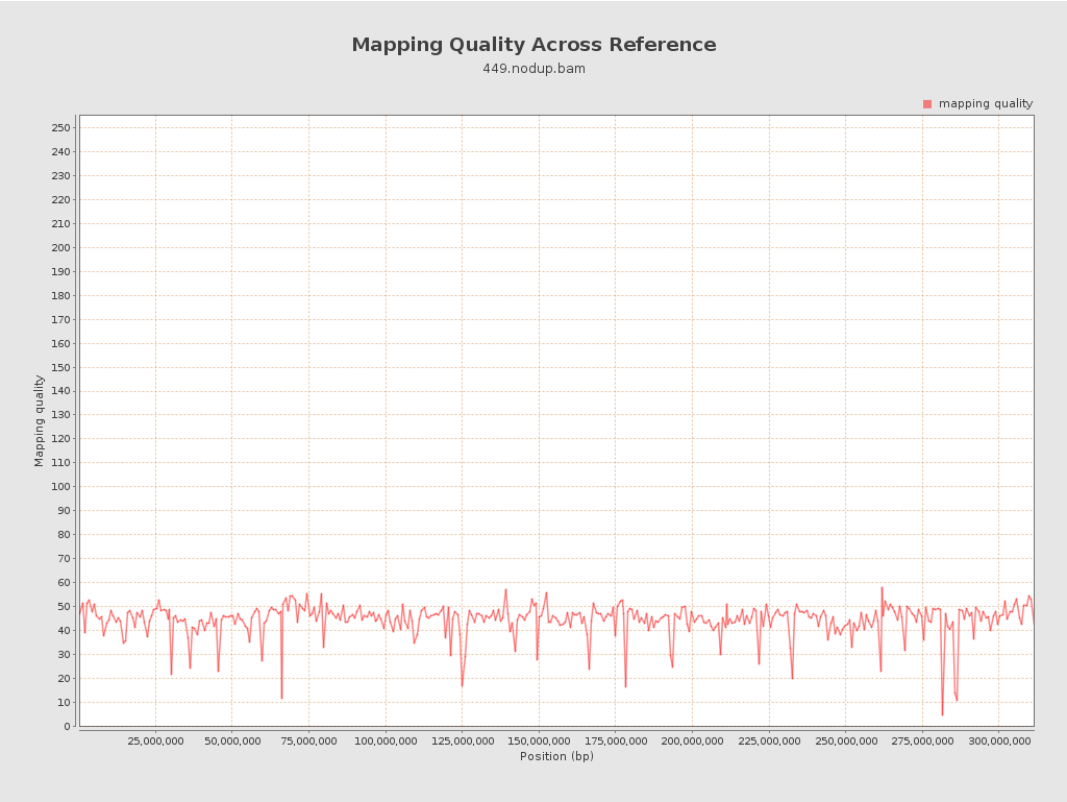
10. Results : Mapped Reads Clipping Profile



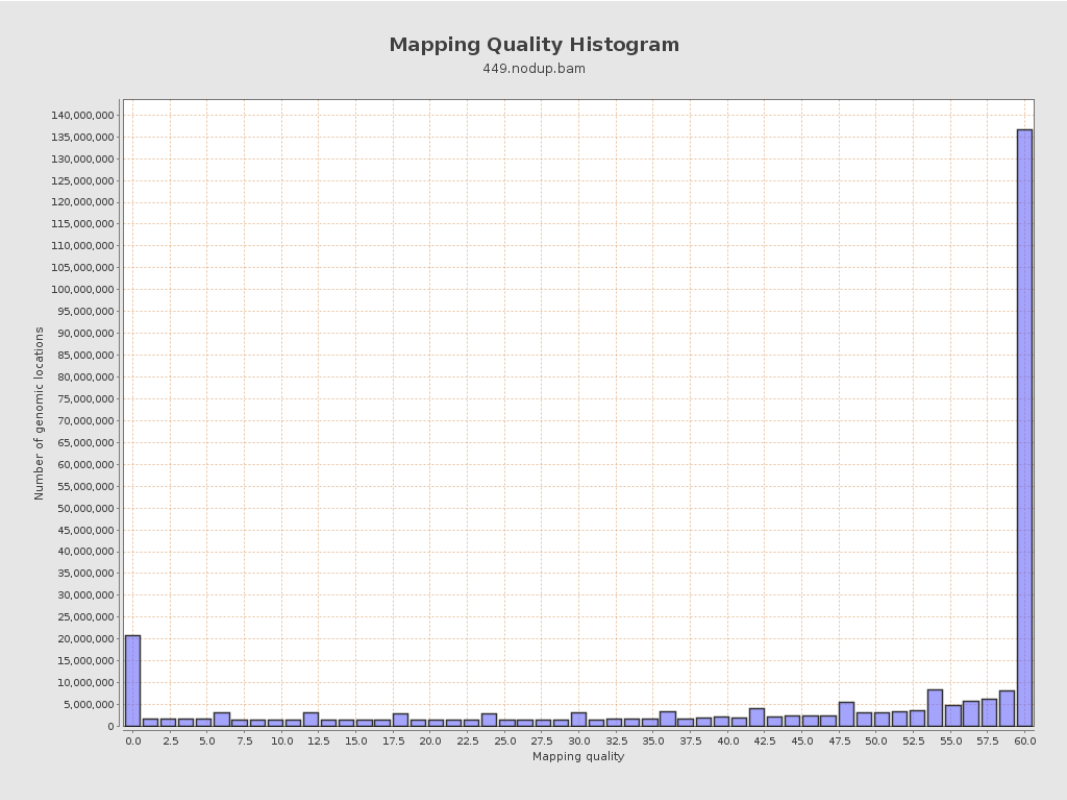
11. Results : Homopolymer Indels



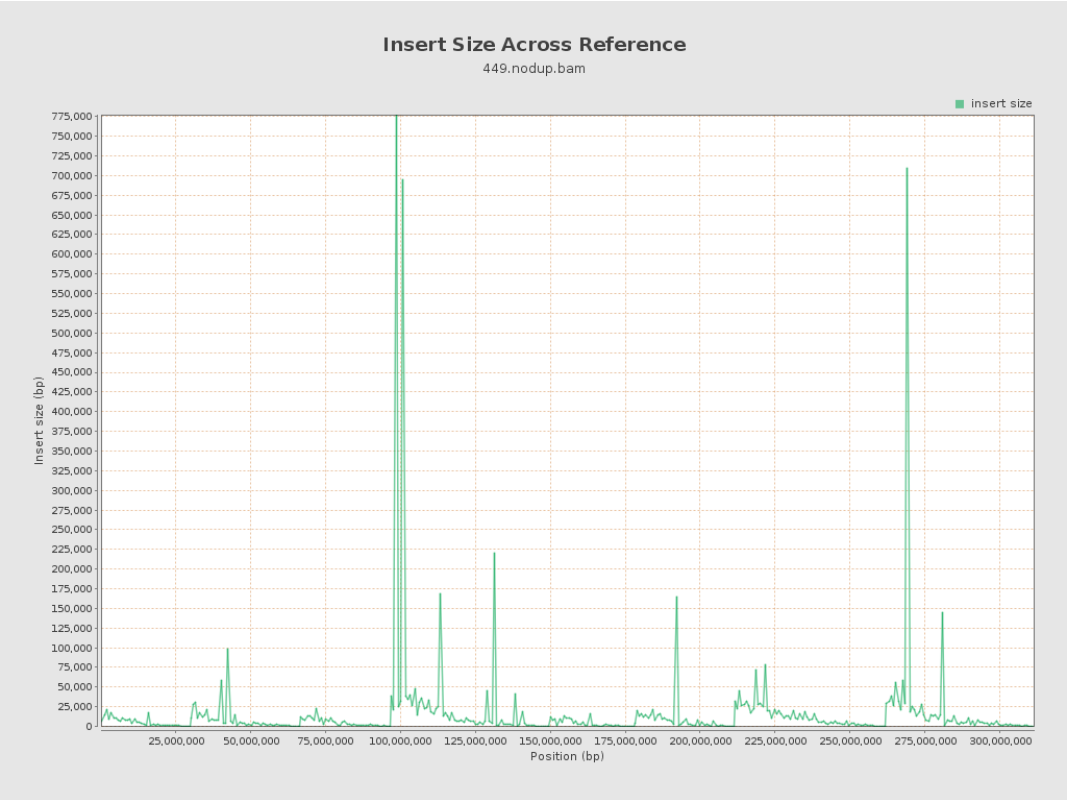
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram