Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/407.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/407.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_230/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_230_S311_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_230/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_230_S311_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:13 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	57,597,855
Mapped reads	52,951,915 / 91.93%
Unmapped reads	4,645,940 / 8.07%
Mapped paired reads	52,951,915 / 91.93%
Mapped reads, first in pair	26,563,272 / 46.12%
Mapped reads, second in pair	26,388,643 / 45.82%
Mapped reads, both in pair	51,456,880 / 89.34%
Mapped reads, singletons	1,495,035 / 2.6%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	7,589,445 / 13.18%
Clipped reads	12,565,702 / 21.82%

2.2. ACGT Content

Number/percentage of A's	2,239,858,544 / 30.8%
Number/percentage of C's	1,394,740,399 / 19.18%
Number/percentage of T's	2,245,357,584 / 30.88%
Number/percentage of G's	1,391,226,577 / 19.13%
Number/percentage of N's	26,693 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	23.3908
Standard Deviation	204.5136

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Insert size

Mean	240,056.27
Standard Deviation	2,353,496.48
P25/Median/P75	330 / 437 / 575

2.6. Mismatches and indels

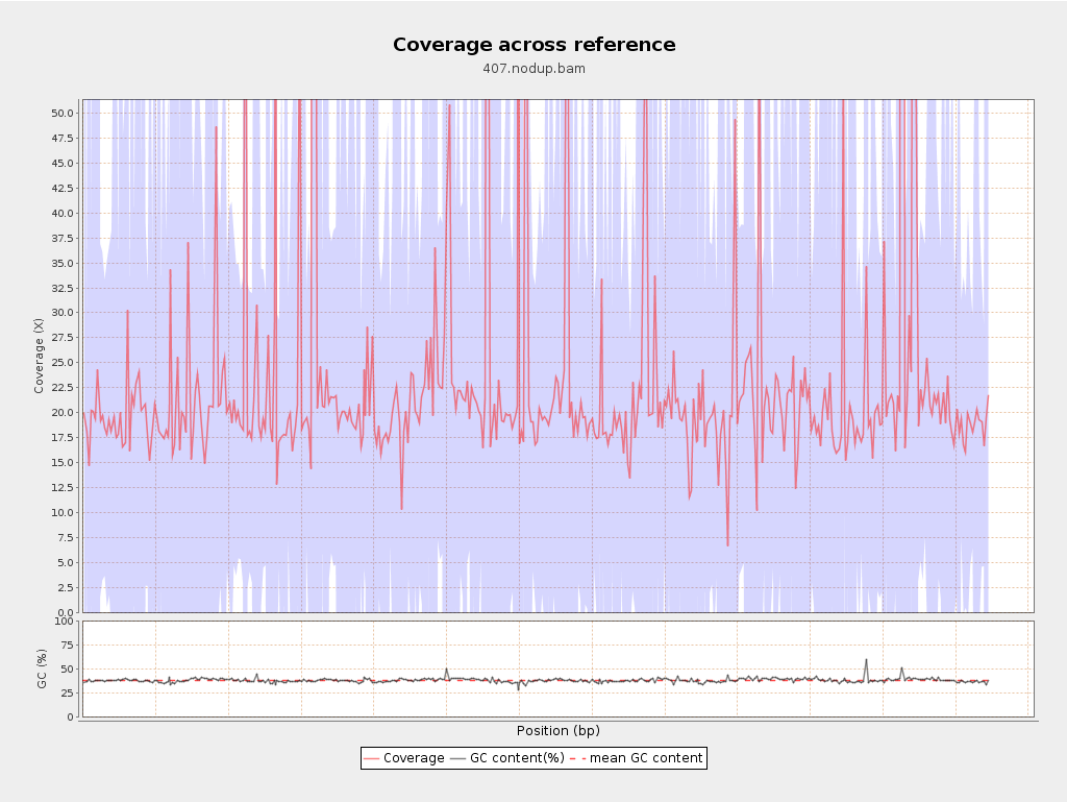
General error rate	2.31%
Mismatches	153,810,078
Insertions	4,972,155
Mapped reads with at least one insertion	8.4%
Deletions	4,827,235
Mapped reads with at least one deletion	8.12%
Homopolymer indels	57.08%

2.7. Chromosome stats

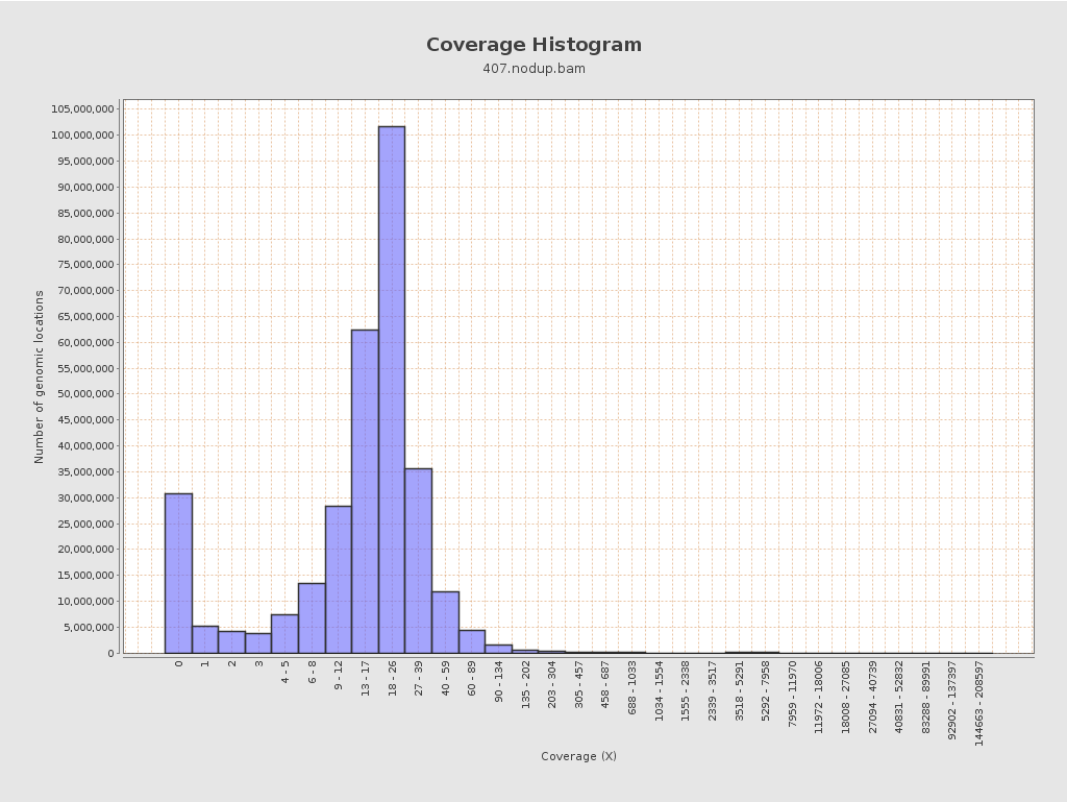
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	576571378	19.3973	72.5248

LT669789.1	36598175	841706429	22.9986	190.3917
LT669790.1	30422129	822155475	27.0249	250.4809
LT669791.1	52758100	1218902385	23.1036	197.7858
LT669792.1	28376109	666958353	23.5042	221.45
LT669793.1	33388210	708145163	21.2094	127.7249
LT669794.1	50579949	1077200561	21.297	143.5808
LT669795.1	49795044	1377925476	27.6719	303.8718

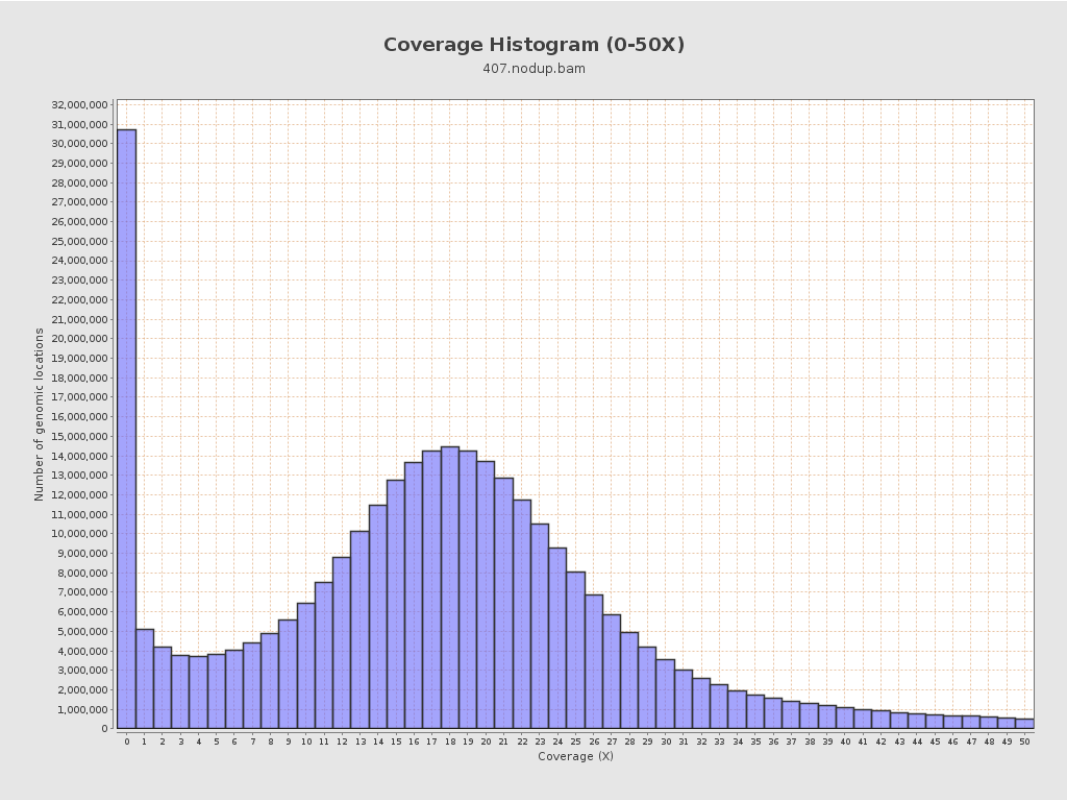
3. Results : Coverage across reference



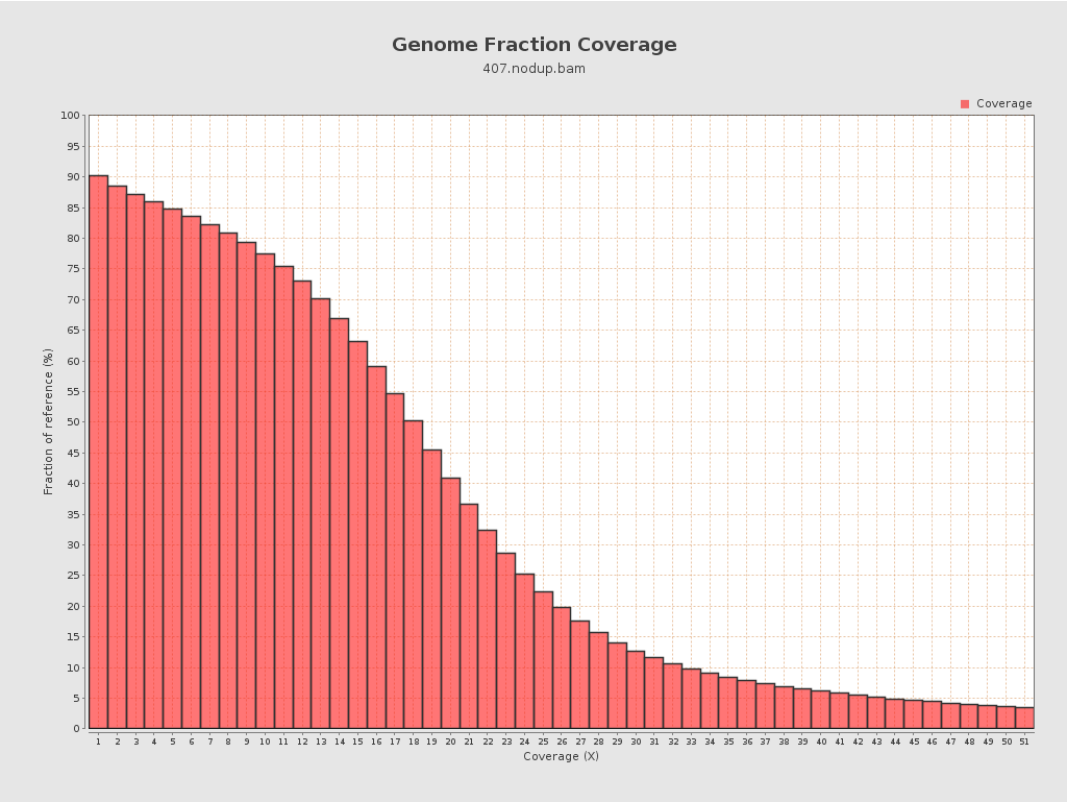
4. Results : Coverage Histogram



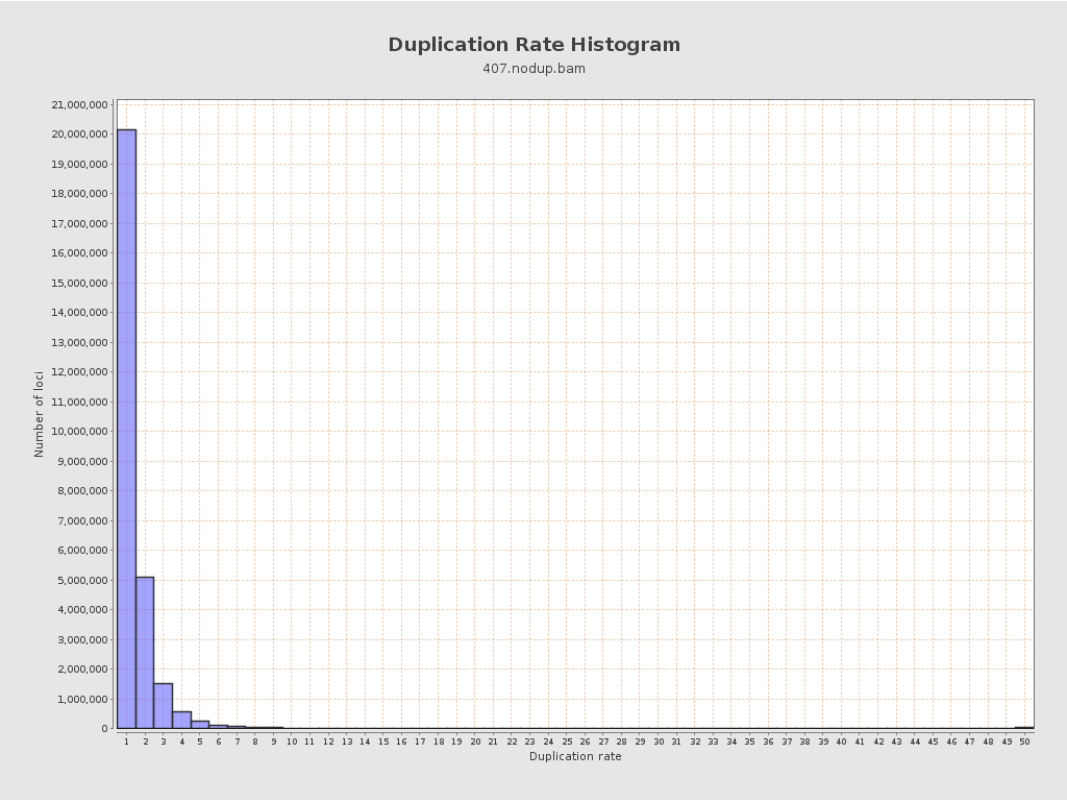
5. Results : Coverage Histogram (0-50X)



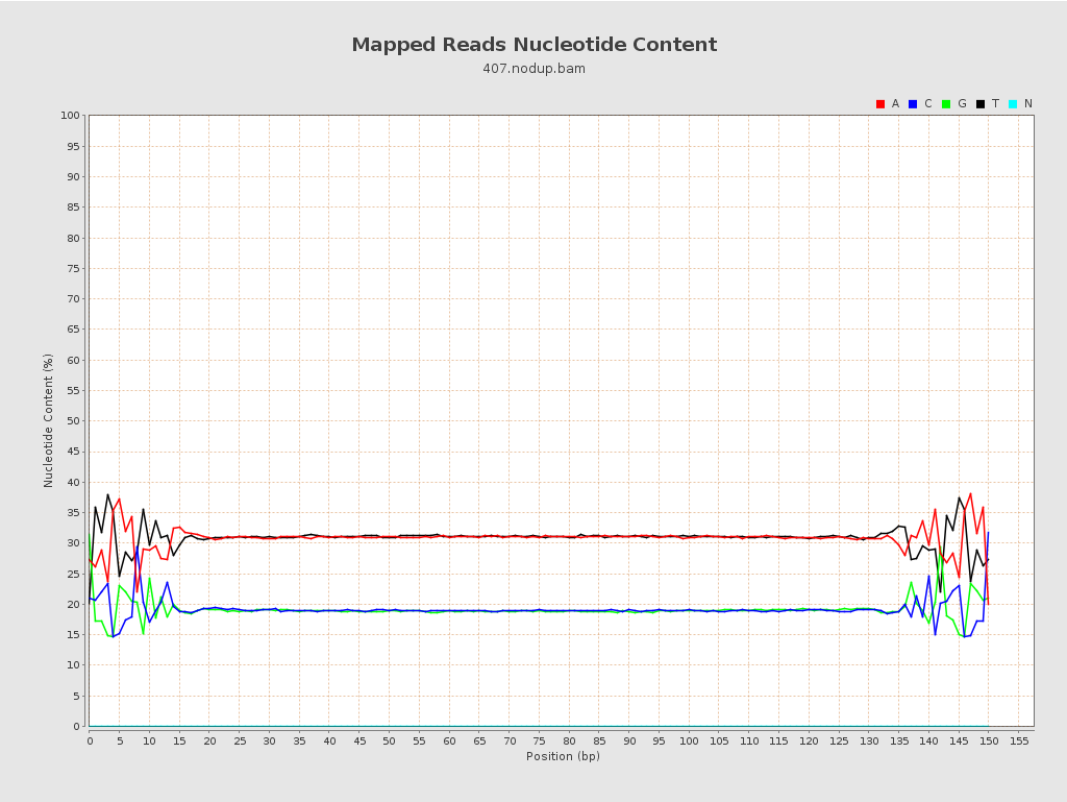
6. Results : Genome Fraction Coverage



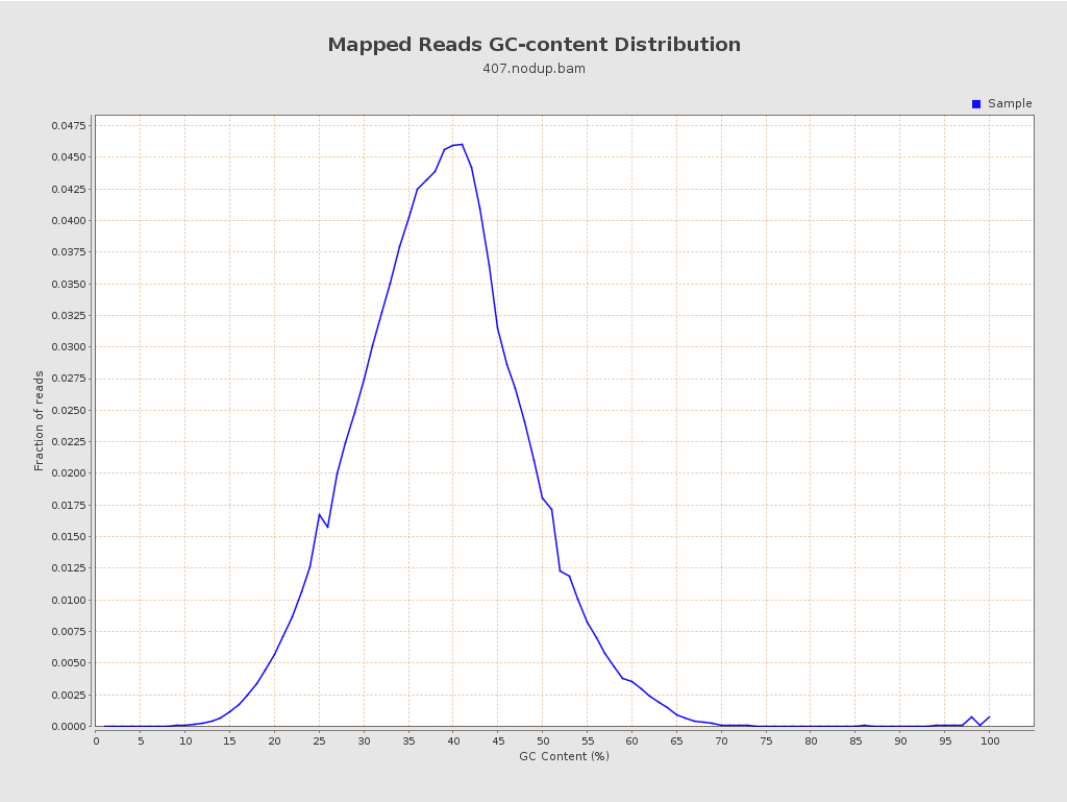
7. Results : Duplication Rate Histogram



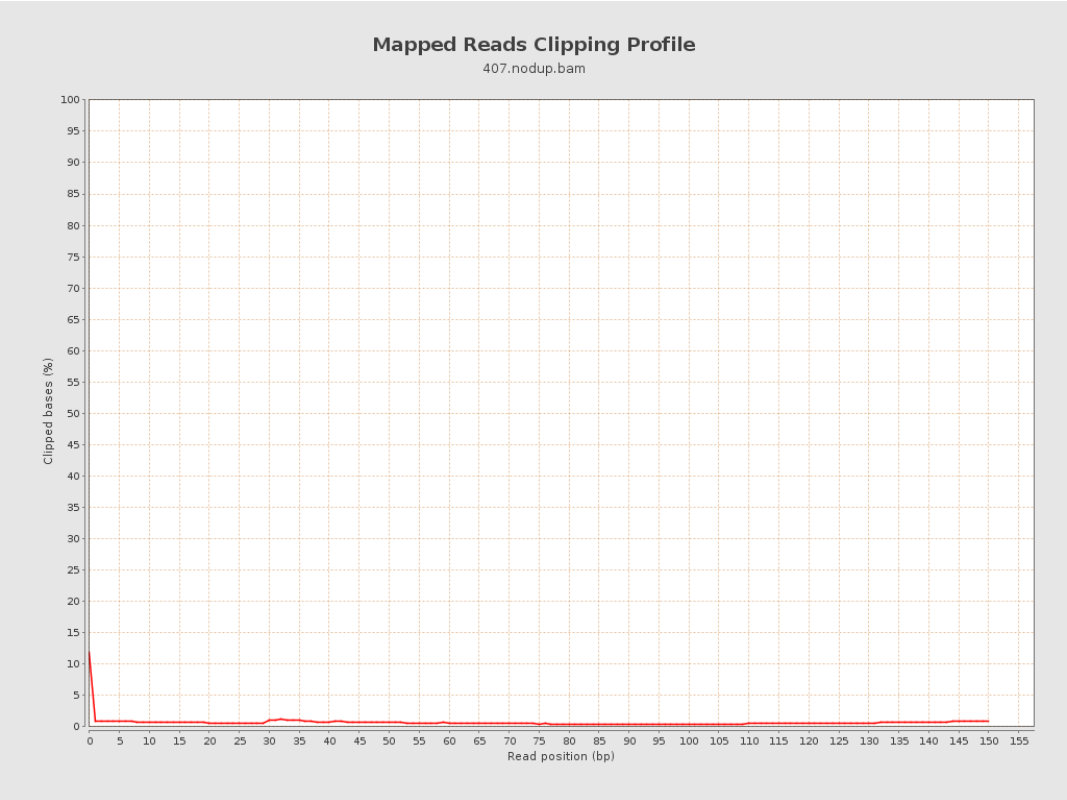
8. Results : Mapped Reads Nucleotide Content



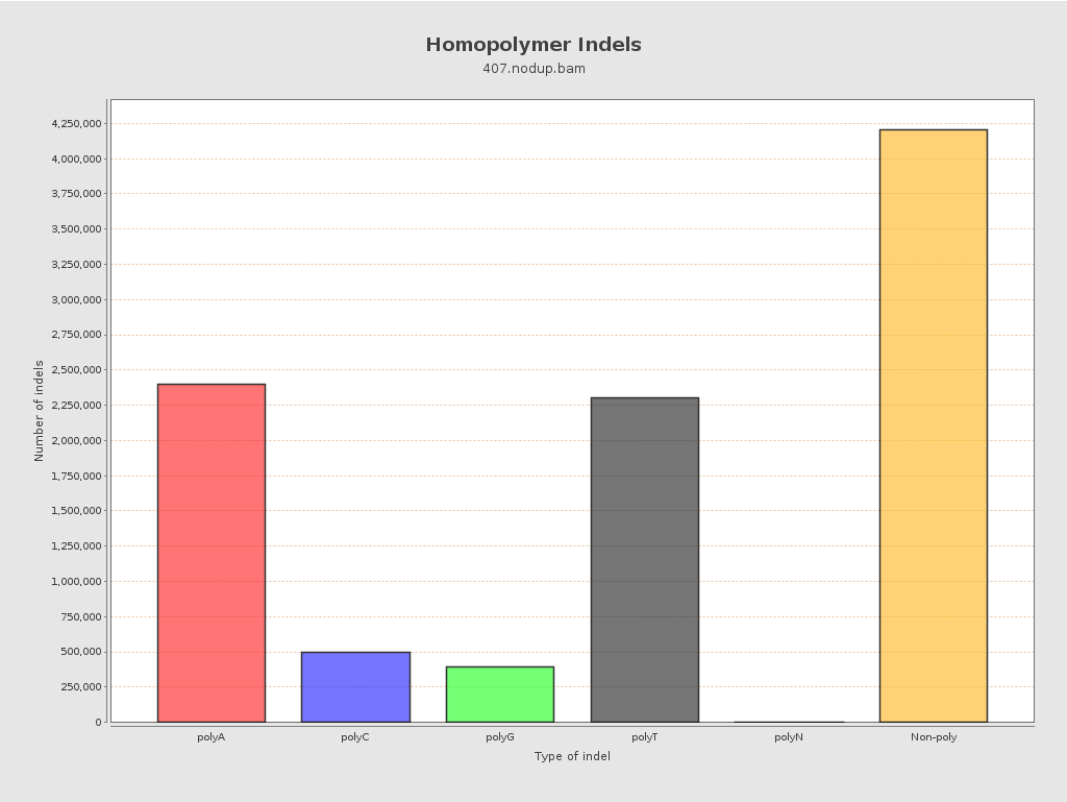
9. Results : Mapped Reads GC-content Distribution



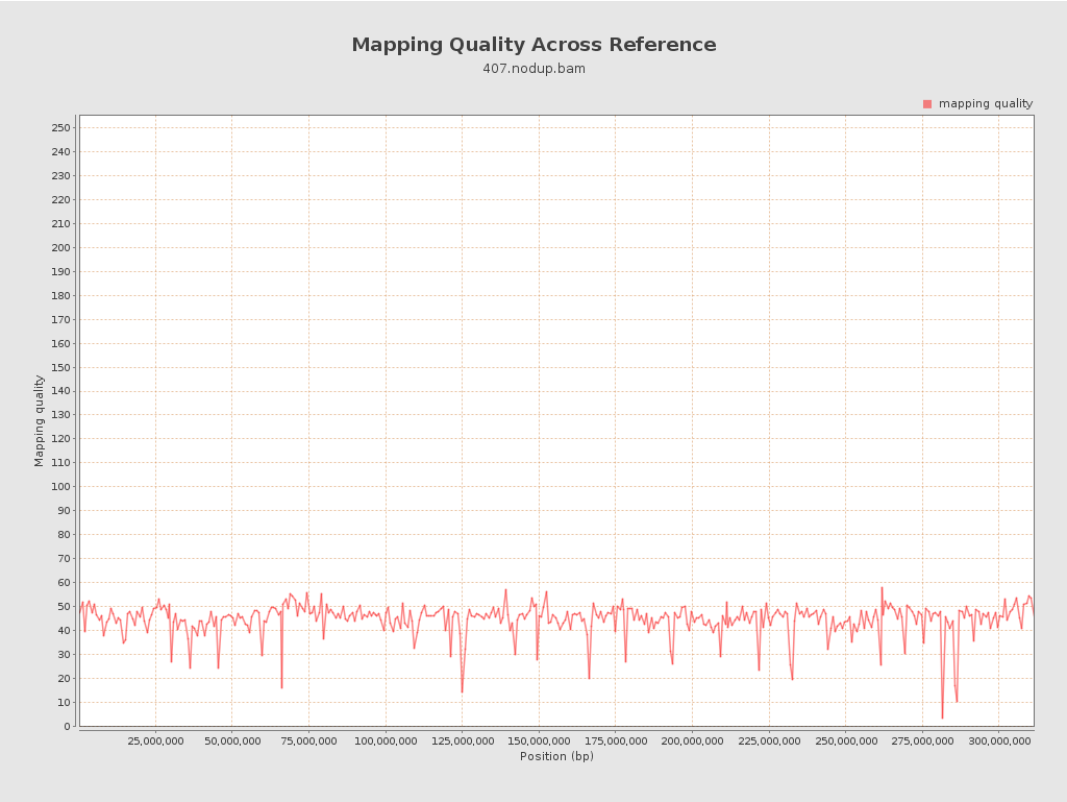
10. Results : Mapped Reads Clipping Profile



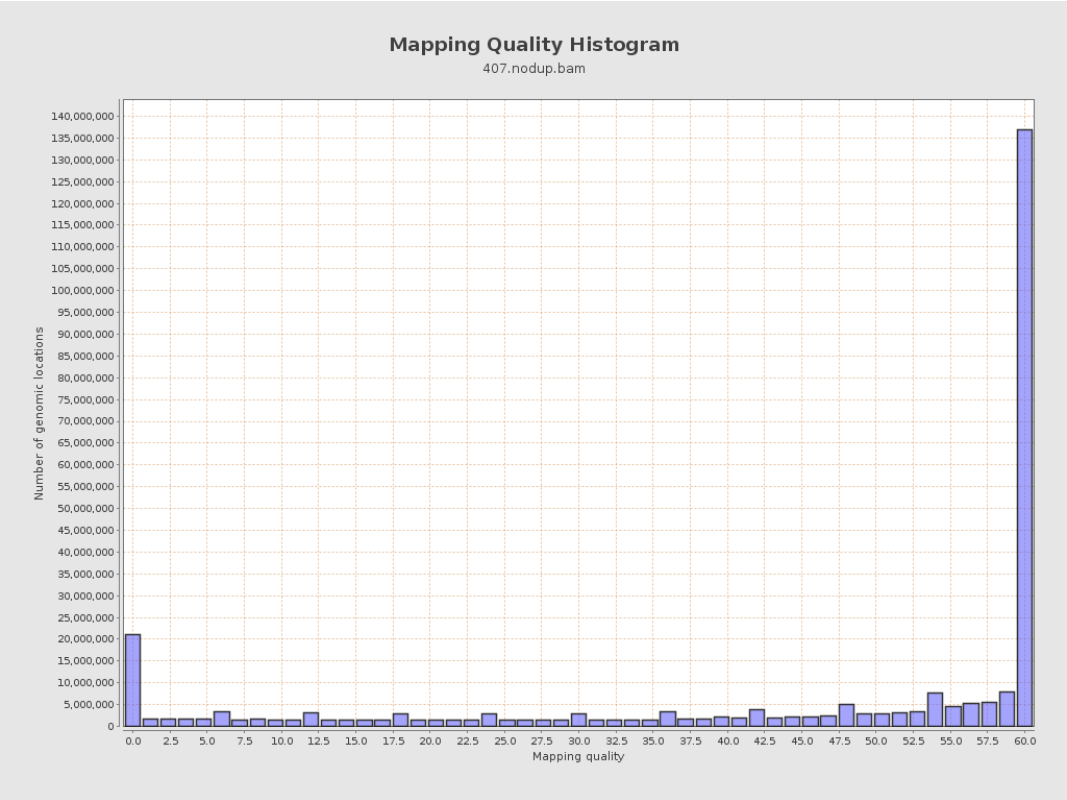
11. Results : Homopolymer Indels



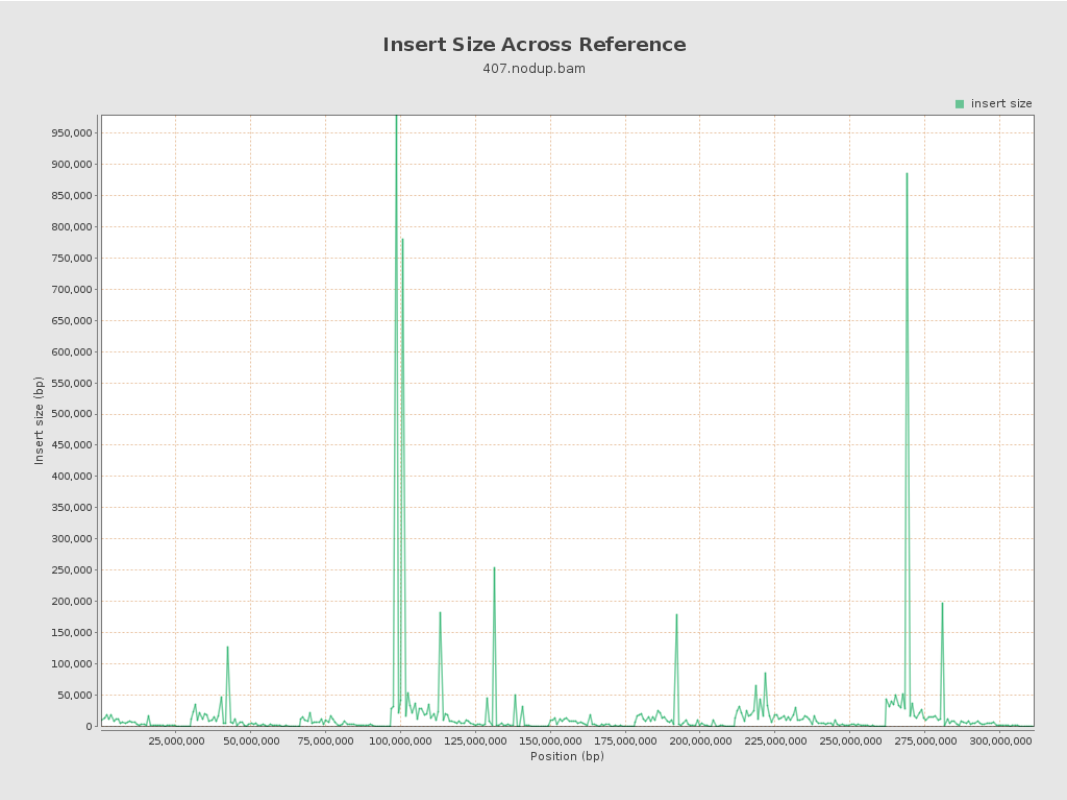
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram