Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/410.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/410.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_141/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_141_S231_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_141/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_141_S231_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:51 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	77,092,771
Mapped reads	71,327,246 / 92.52%
Unmapped reads	5,765,525 / 7.48%
Mapped paired reads	71,327,246 / 92.52%
Mapped reads, first in pair	35,740,361 / 46.36%
Mapped reads, second in pair	35,586,885 / 46.16%
Mapped reads, both in pair	69,425,321 / 90.05%
Mapped reads, singletons	1,901,925 / 2.47%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	13,579,227 / 17.61%
Clipped reads	16,042,464 / 20.81%

2.2. ACGT Content

Number/percentage of A's	3,043,003,221 / 30.87%
Number/percentage of C's	1,884,276,239 / 19.12%
Number/percentage of T's	3,049,809,891 / 30.94%
Number/percentage of G's	1,878,801,754 / 19.06%
Number/percentage of N's	42,115 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	31.7067
Standard Deviation	257.2086

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Insert size

Mean	247,864.86
Standard Deviation	2,397,826.81
P25/Median/P75	343 / 447 / 582

2.6. Mismatches and indels

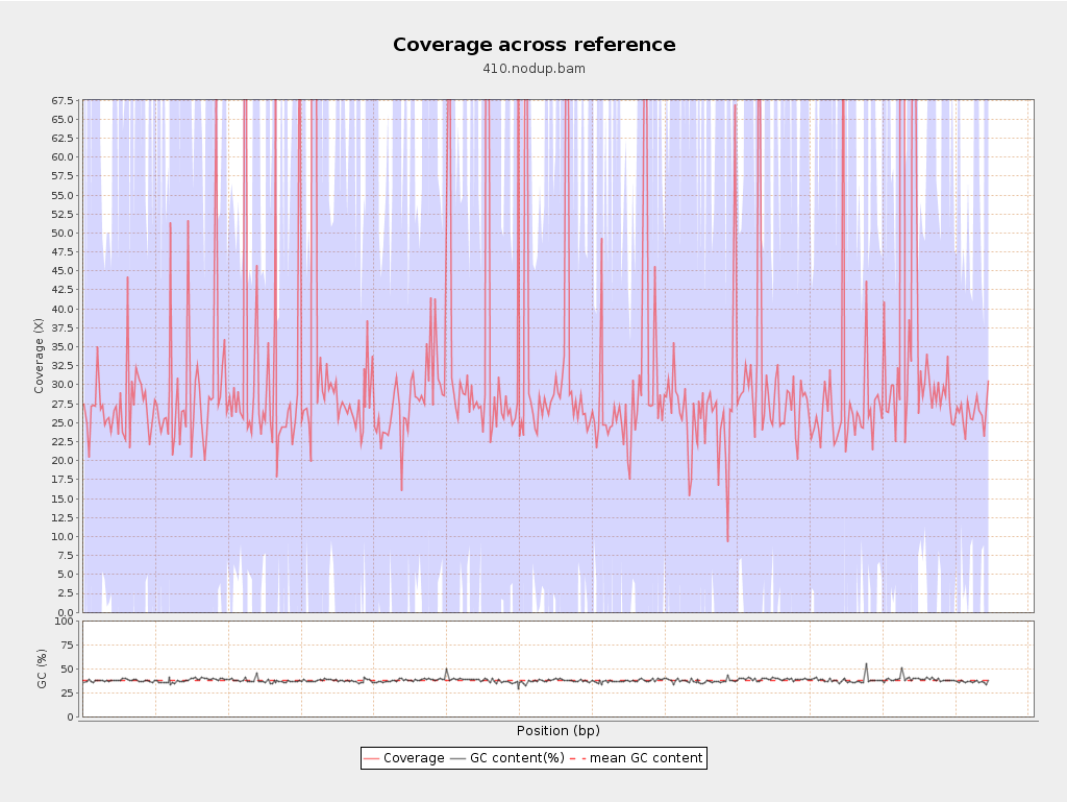
General error rate	2.28%
Mismatches	205,584,476
Insertions	6,797,467
Mapped reads with at least one insertion	8.53%
Deletions	6,679,621
Mapped reads with at least one deletion	8.3%
Homopolymer indels	56.9%

2.7. Chromosome stats

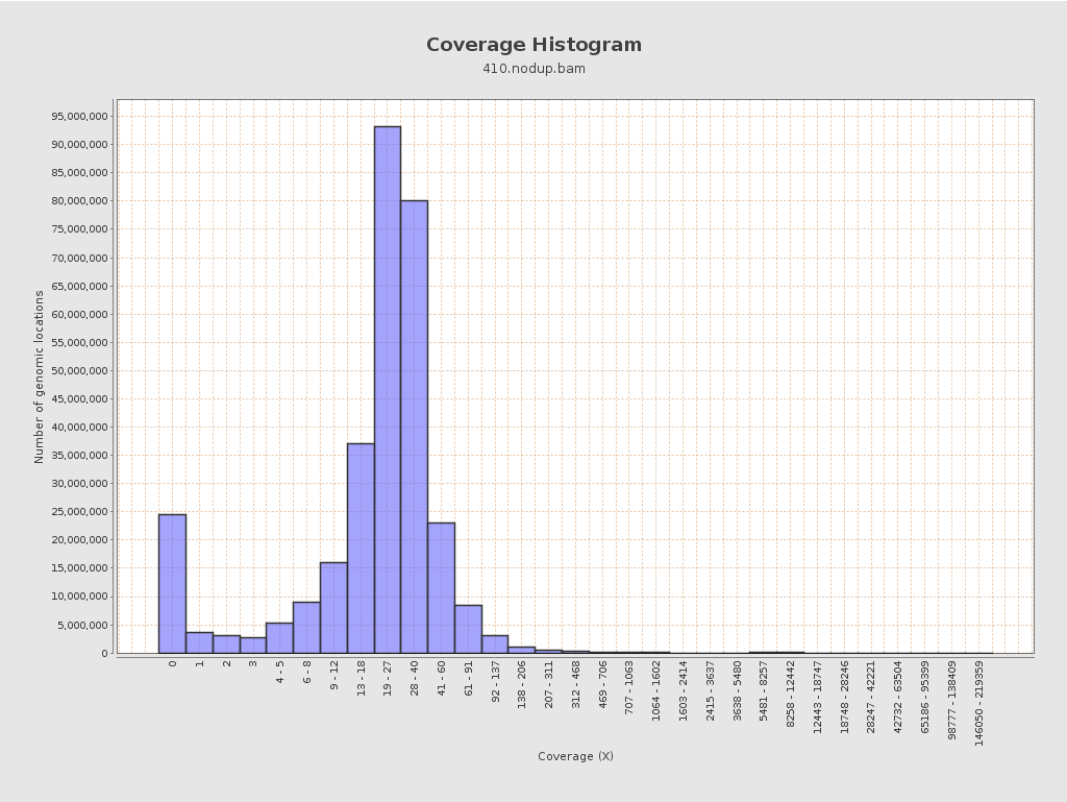
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	800011206	26.9143	94.3102

LT669789.1	36598175	1144764780	31.2793	268.2646
LT669790.1	30422129	1111016404	36.52	323.5143
LT669791.1	52758100	1636447933	31.0179	260.2134
LT669792.1	28376109	901998647	31.7873	273.0912
LT669793.1	33388210	968453728	29.0059	168.7794
LT669794.1	50579949	1472680515	29.1159	206.6265
LT669795.1	49795044	1845753360	37.067	339.2895

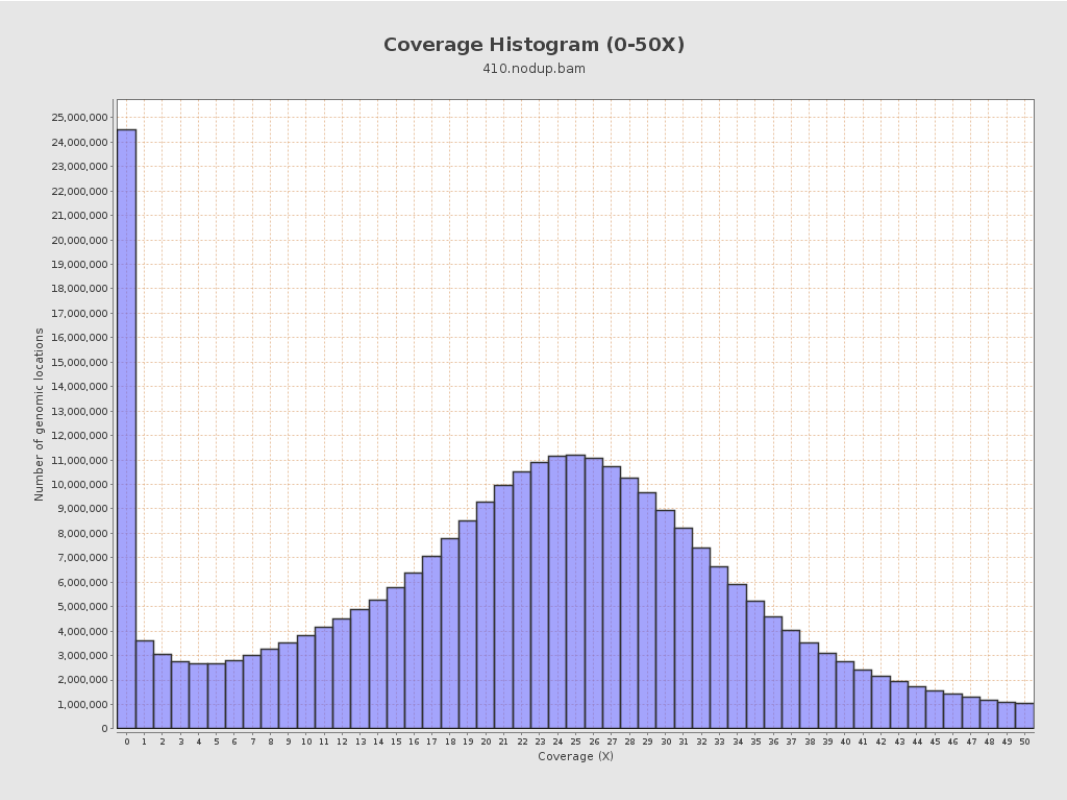
3. Results : Coverage across reference



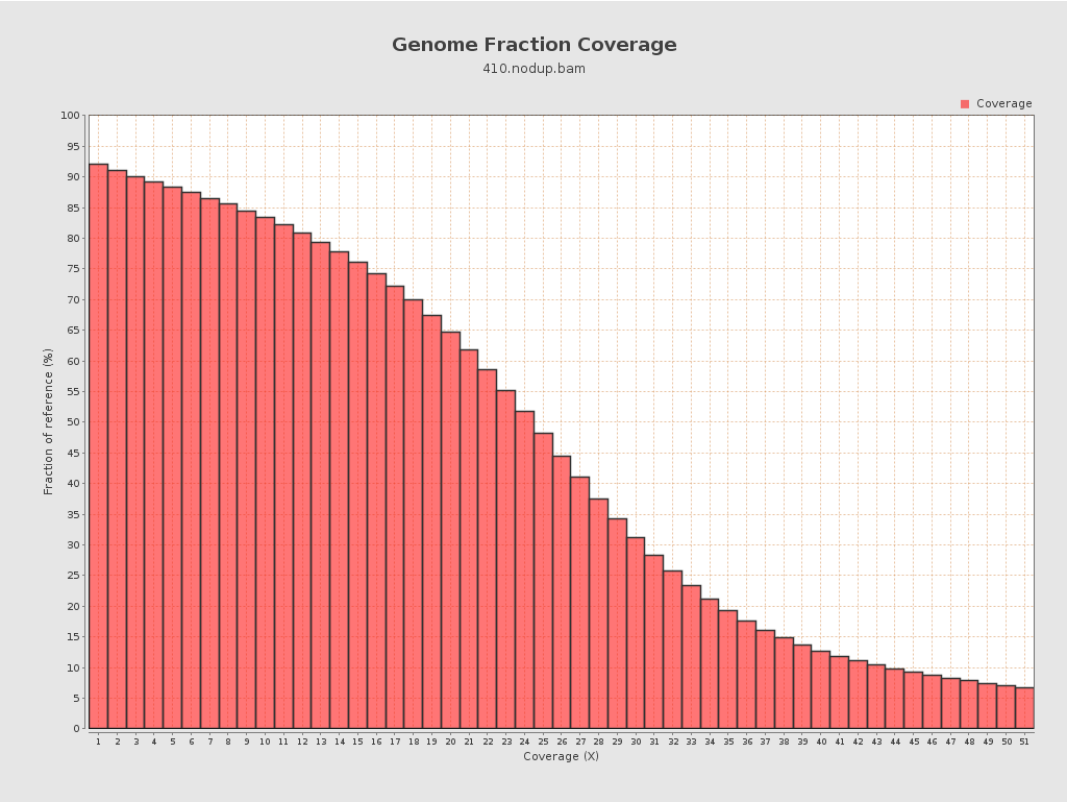
4. Results : Coverage Histogram



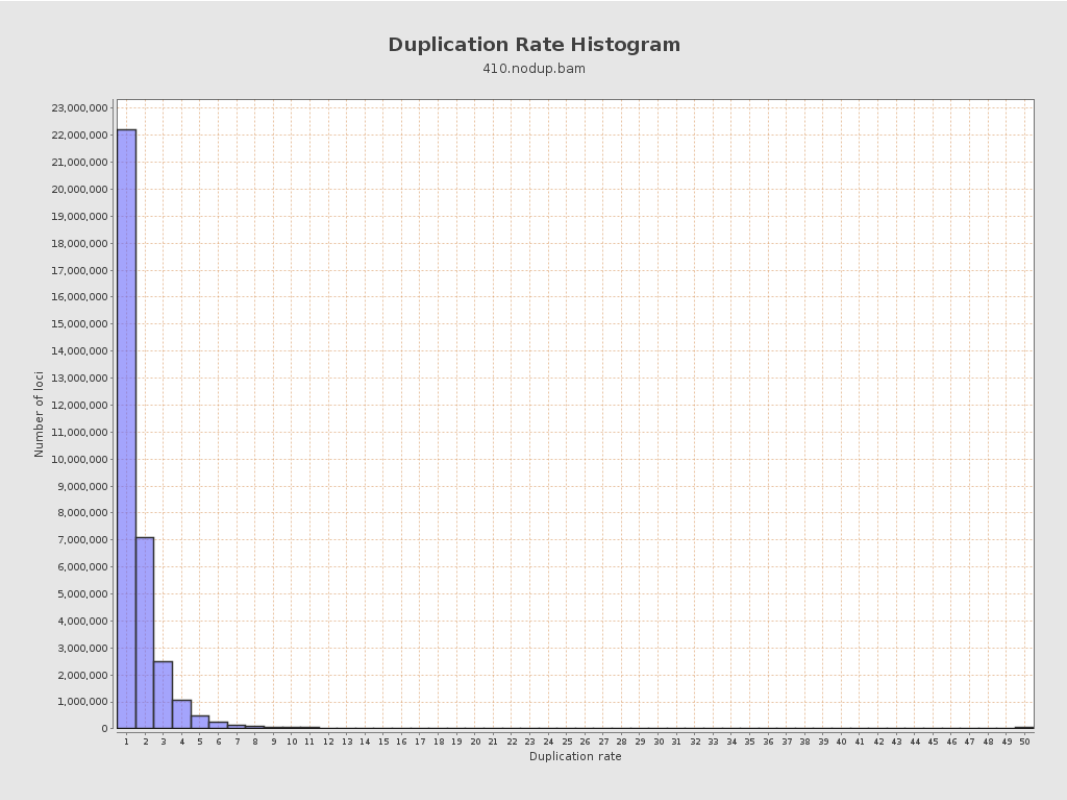
5. Results : Coverage Histogram (0-50X)



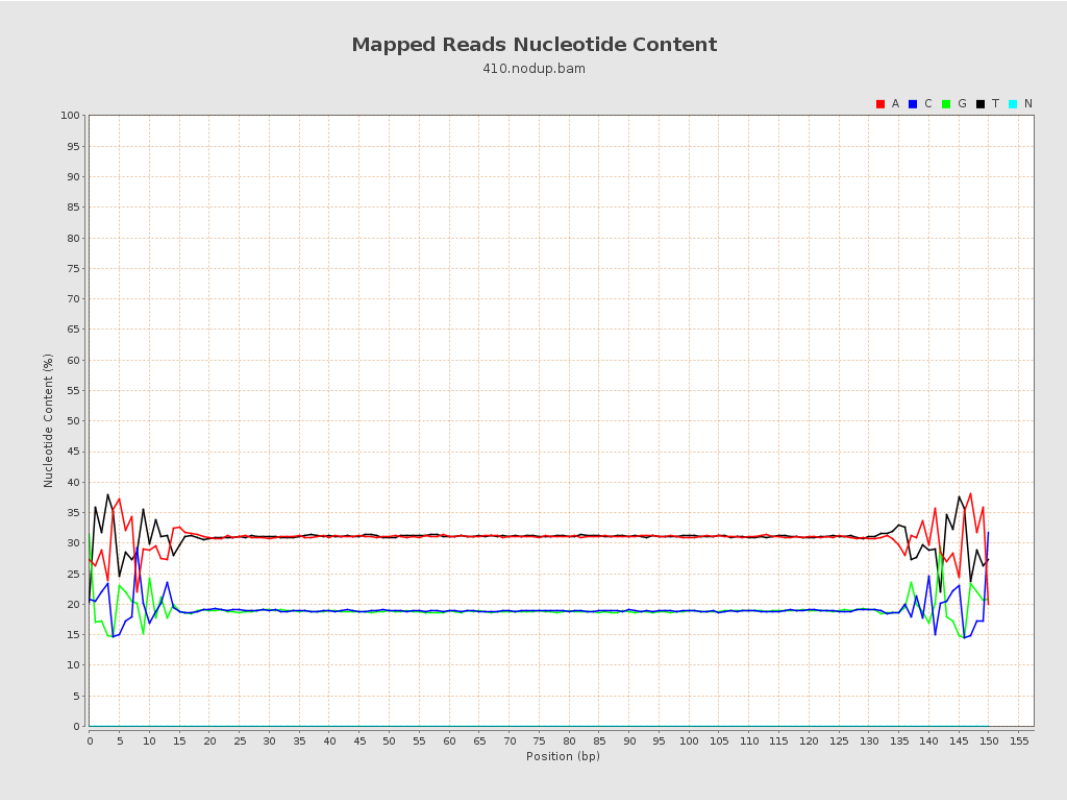
6. Results : Genome Fraction Coverage



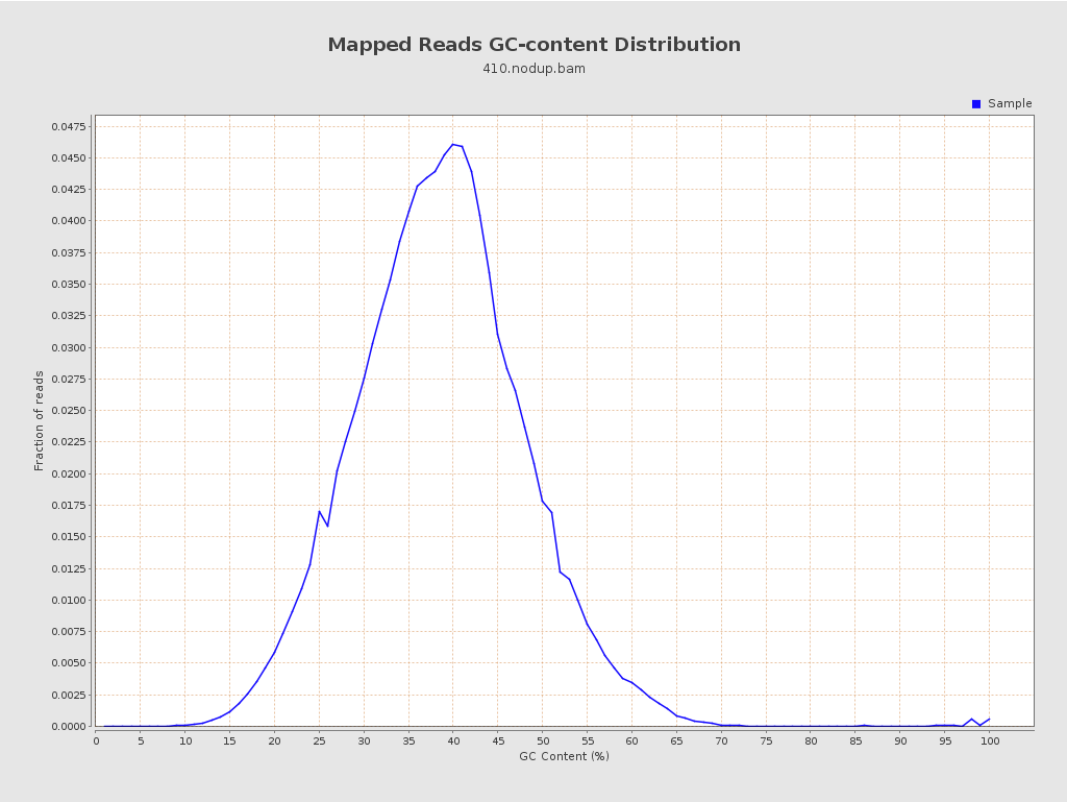
7. Results : Duplication Rate Histogram



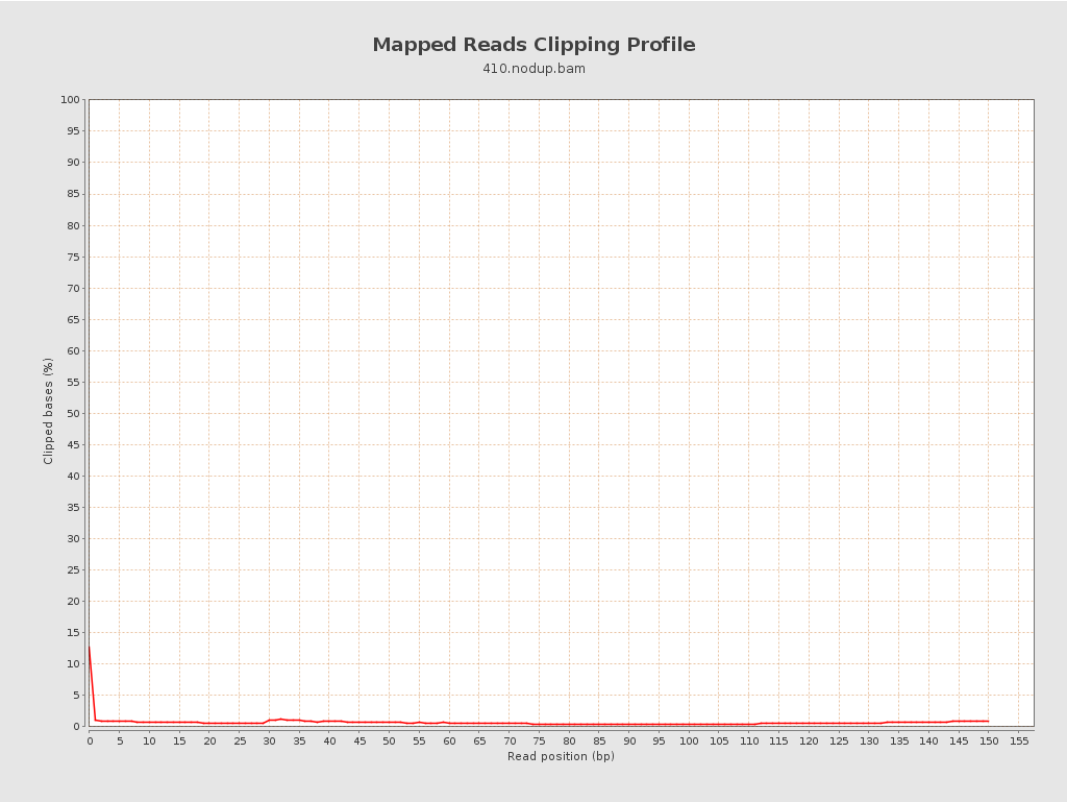
8. Results : Mapped Reads Nucleotide Content



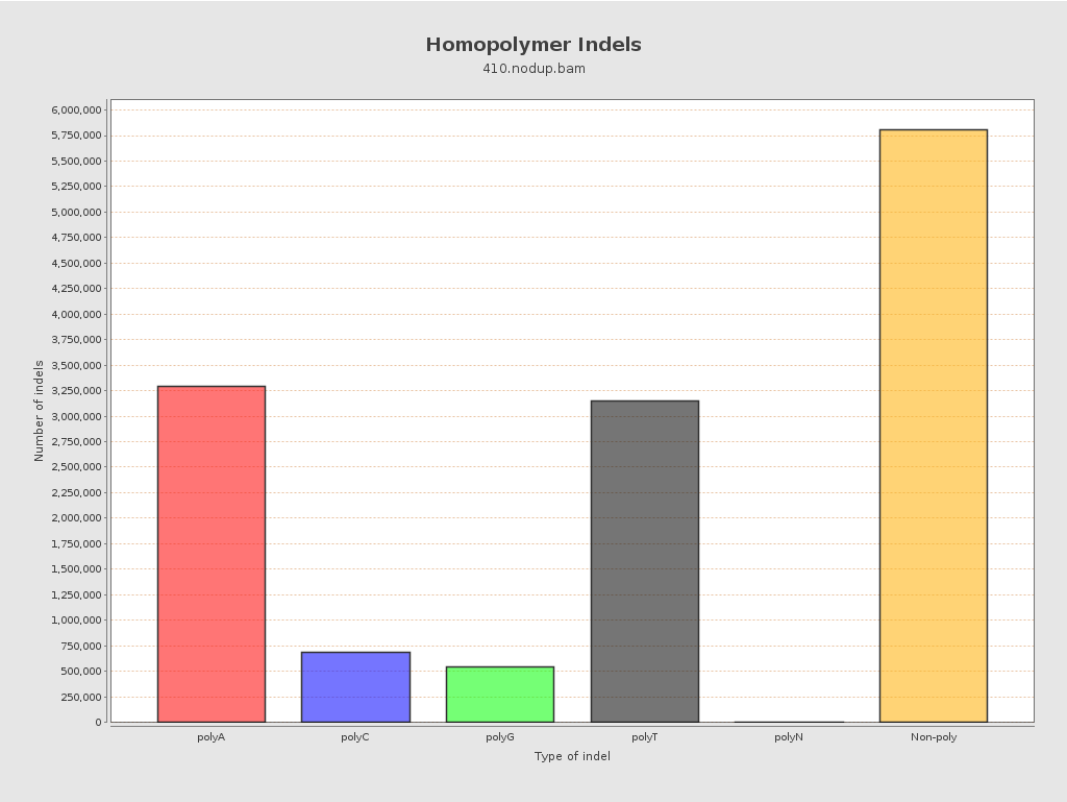
9. Results : Mapped Reads GC-content Distribution



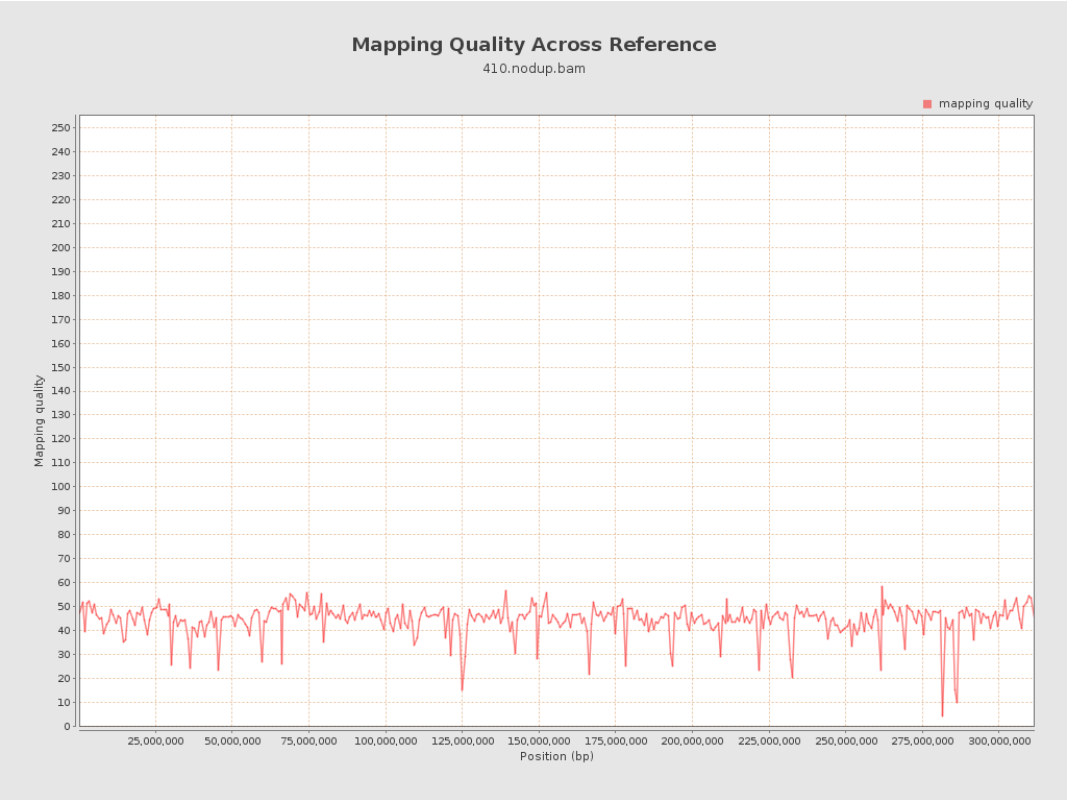
10. Results : Mapped Reads Clipping Profile



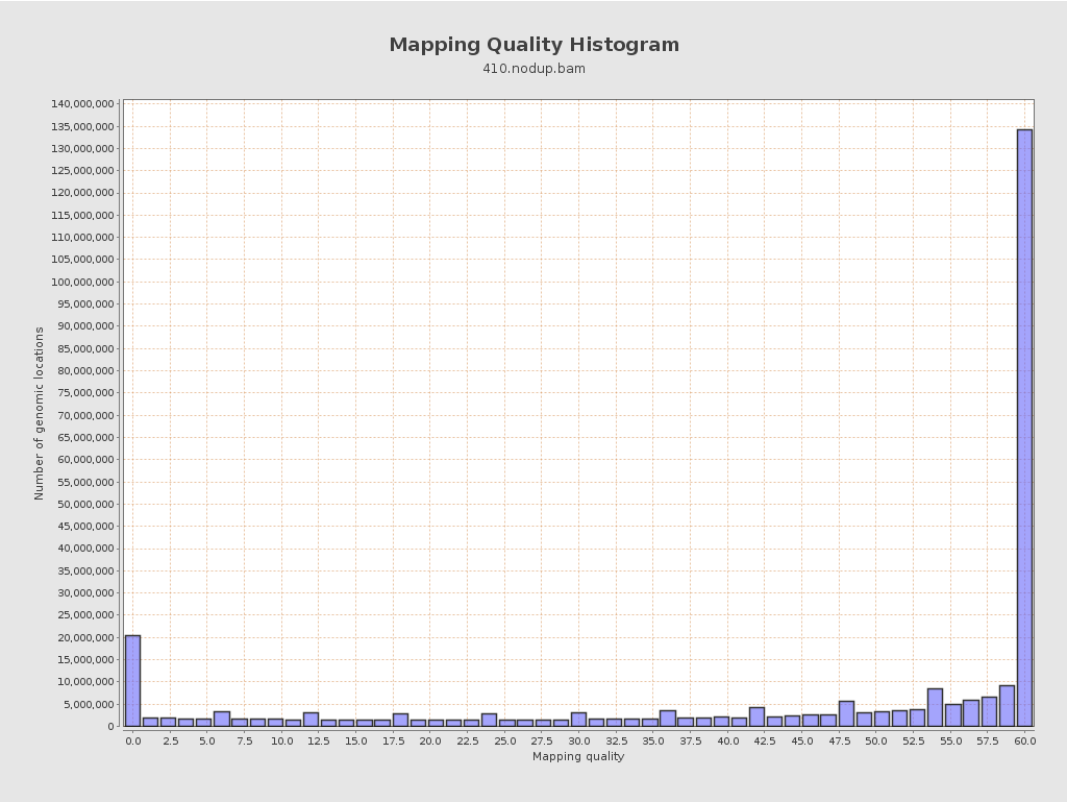
11. Results : Homopolymer Indels



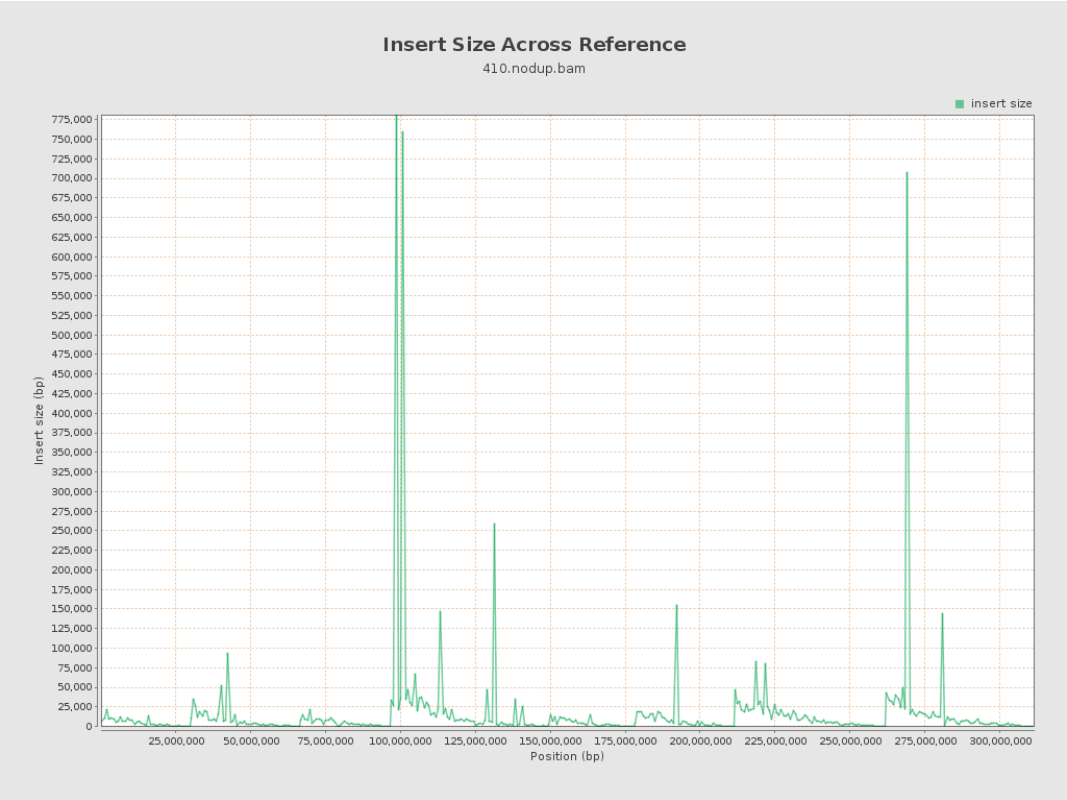
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram