Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/140
6
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1406 .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_548/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_548_S115_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_548/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_548_S115_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,120,181
Mapped reads	53,631,701 / 82.36%
Unmapped reads	11,488,480 / 17.64%
Mapped paired reads	53,631,701 / 82.36%
Mapped reads, first in pair	26,915,900 / 41.33%
Mapped reads, second in pair	26,715,801 / 41.03%
Mapped reads, both in pair	52,370,708 / 80.42%
Mapped reads, singletons	1,260,993 / 1.94%
Read min/max/mean length	30 / 151 / 148.42
Duplicated reads (flagged)	8,079,700 / 12.41%
Clipped reads	13,851,825 / 21.27%

2.2. ACGT Content

Number/percentage of A's	2,242,568,627 / 30.83%
Number/percentage of C's	1,393,264,147 / 19.15%
Number/percentage of T's	2,246,146,033 / 30.88%
Number/percentage of G's	1,392,115,433 / 19.14%
Number/percentage of N's	51,721 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	23.4021
Standard Deviation	205.3182

2.4. Mapping Quality

Mean Mapping Quality	43.47

2.5. Insert size

Mean	226,213.75
Standard Deviation	2,251,352.29
P25/Median/P75	303 / 404 / 526

2.6. Mismatches and indels

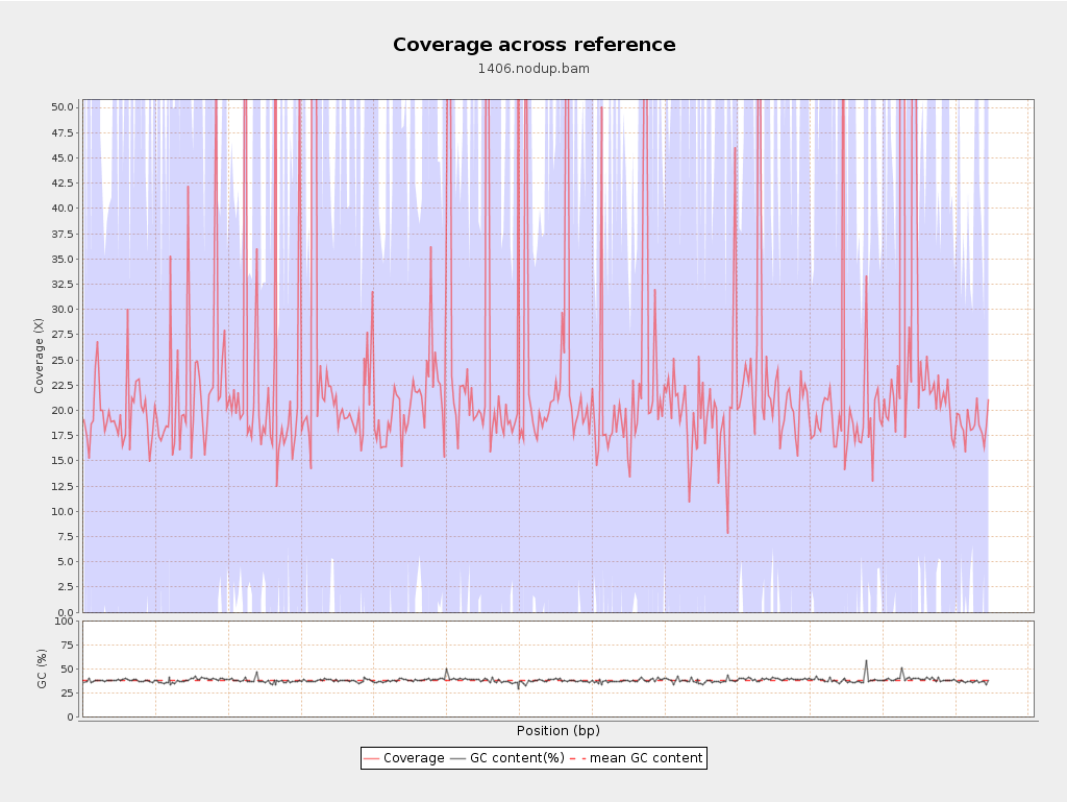
General error rate	2.6%
Mismatches	175,349,371
Insertions	5,039,094
Mapped reads with at least one insertion	8.44%
Deletions	5,082,026
Mapped reads with at least one deletion	8.4%
Homopolymer indels	55.63%

2.7. Chromosome stats

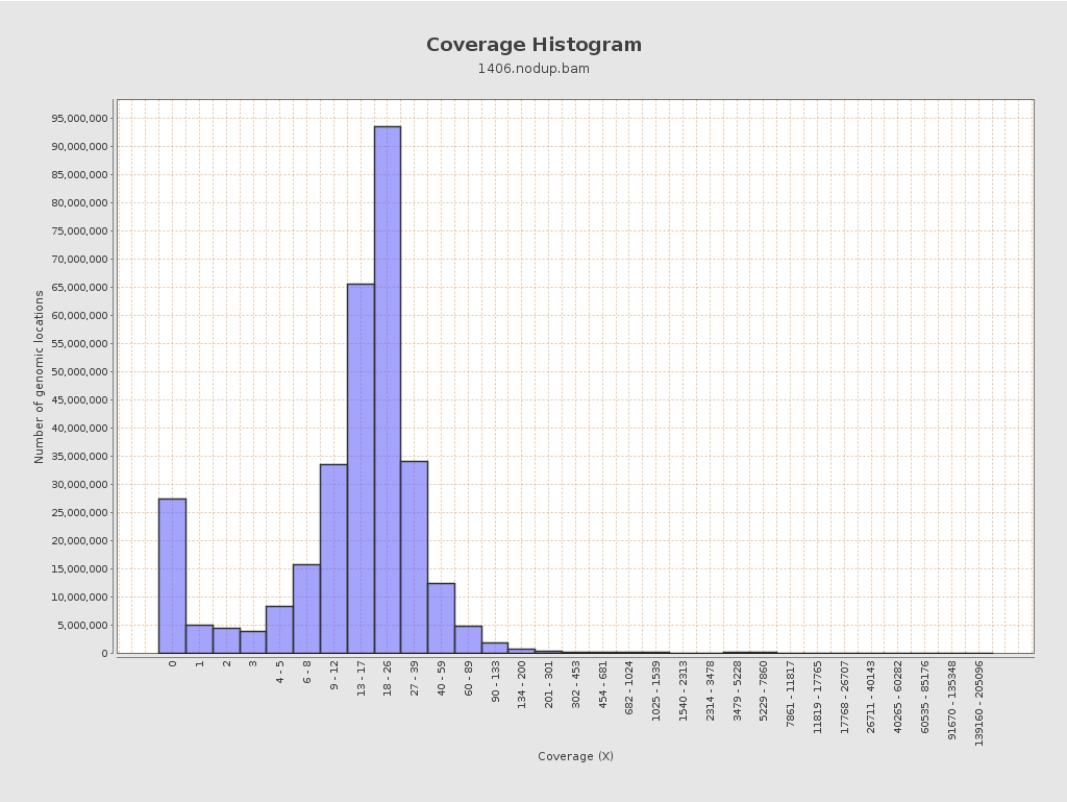
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	579341196	19.4905	72.2039

LT669789.1	36598175	862676988	23.5716	201.3459
LT669790.1	30422129	785666492	25.8255	214.541
LT669791.1	52758100	1207240007	22.8826	200.325
LT669792.1	28376109	656034177	23.1192	224.6039
LT669793.1	33388210	731038771	21.8951	139.9327
LT669794.1	50579949	1120569768	22.1544	184.8997
LT669795.1	49795044	1350514306	27.1215	289.2231

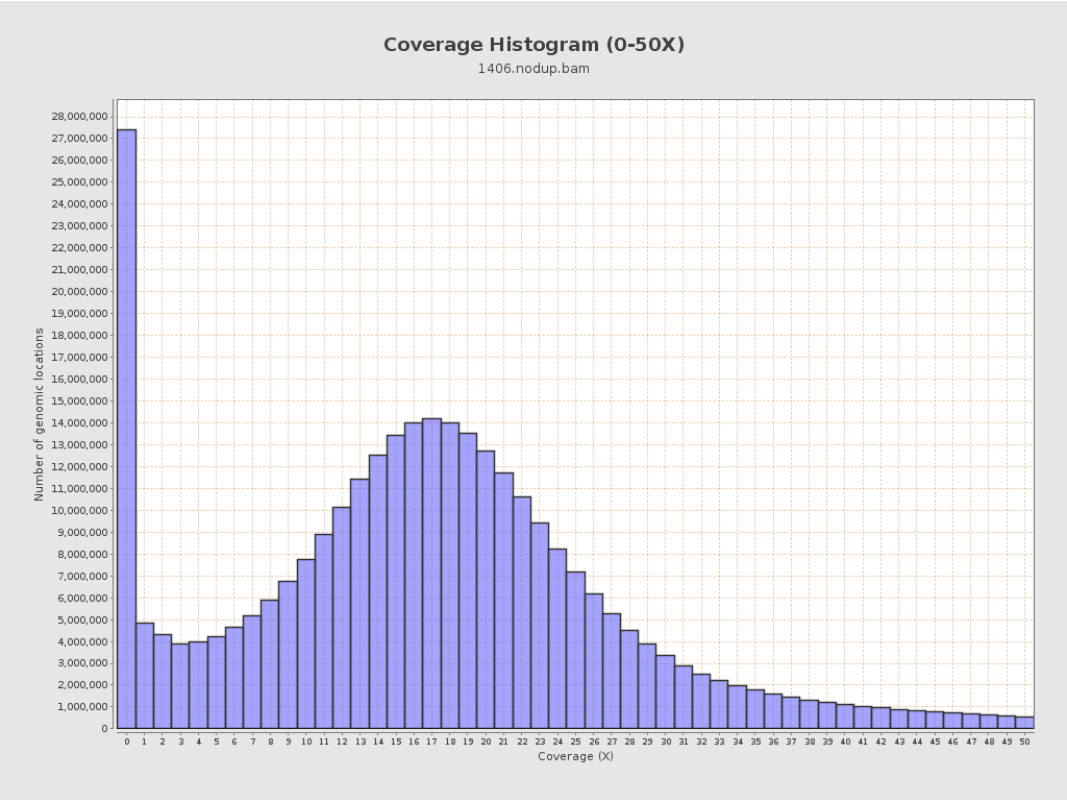
3. Results : Coverage across reference



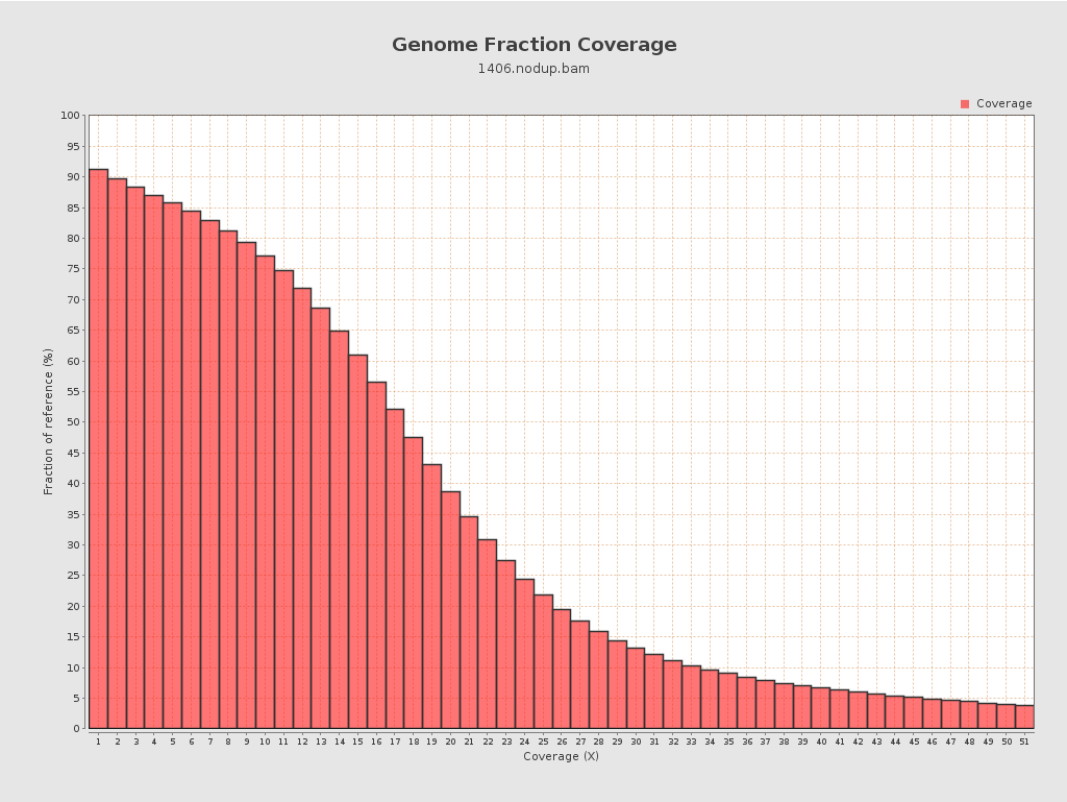
4. Results : Coverage Histogram



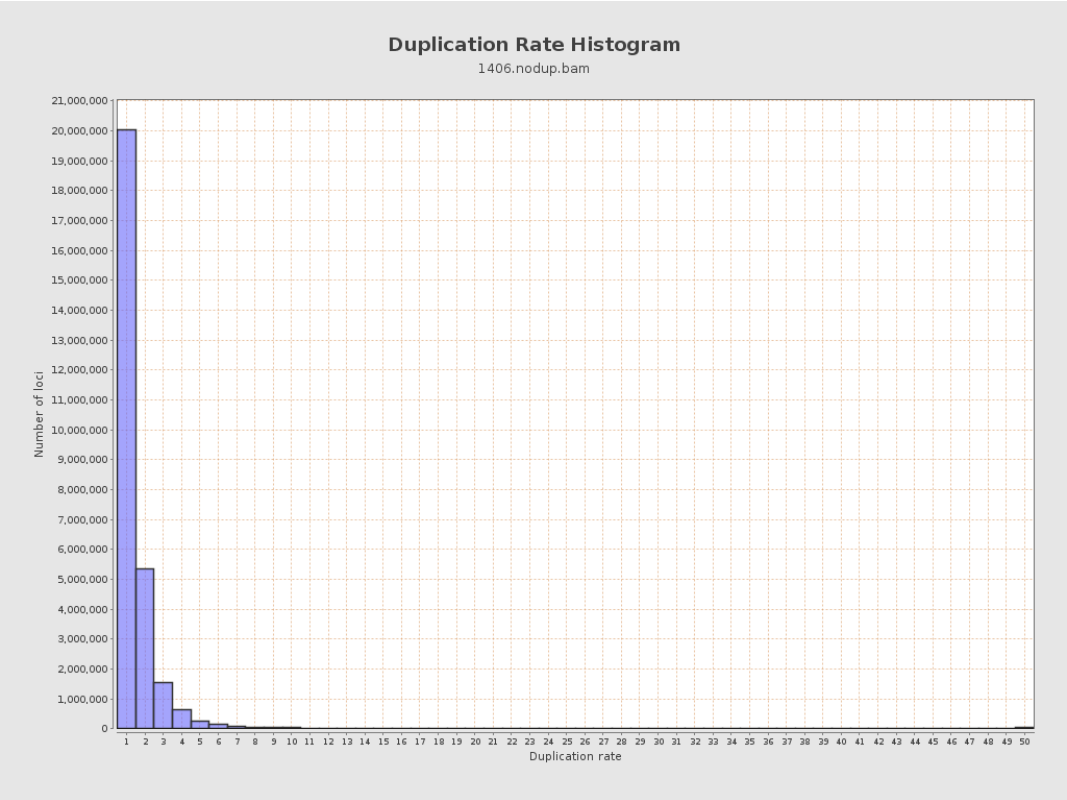
5. Results : Coverage Histogram (0-50X)



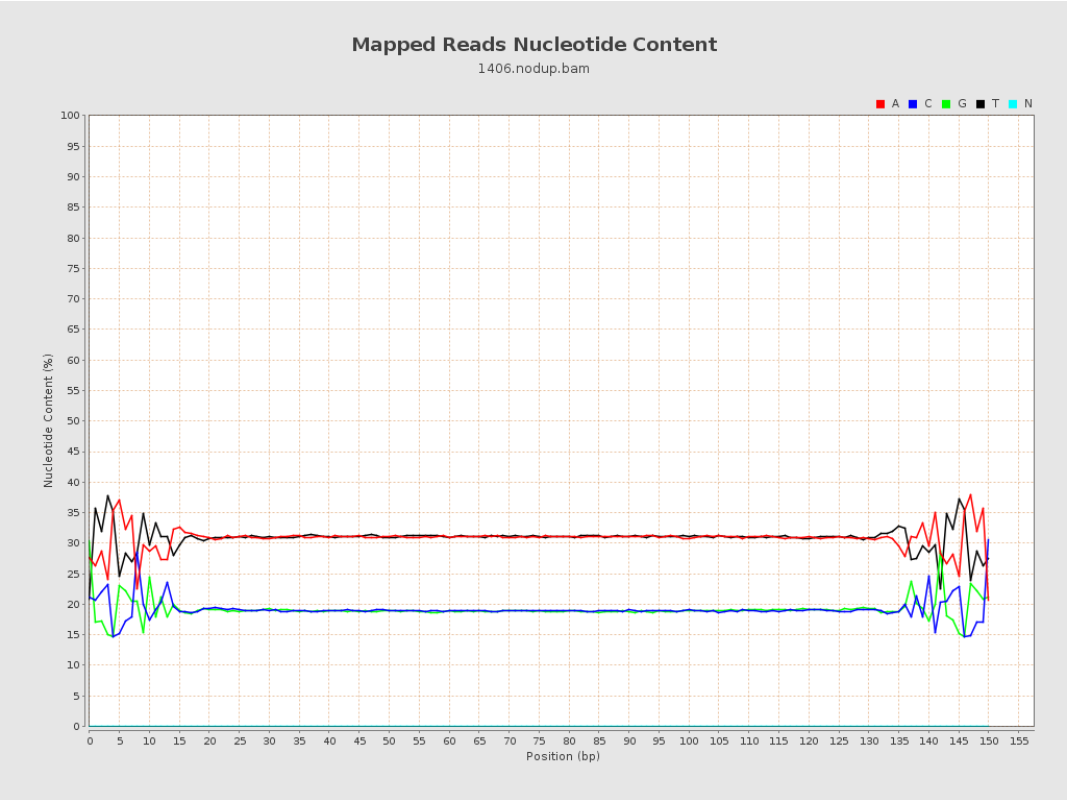
6. Results : Genome Fraction Coverage



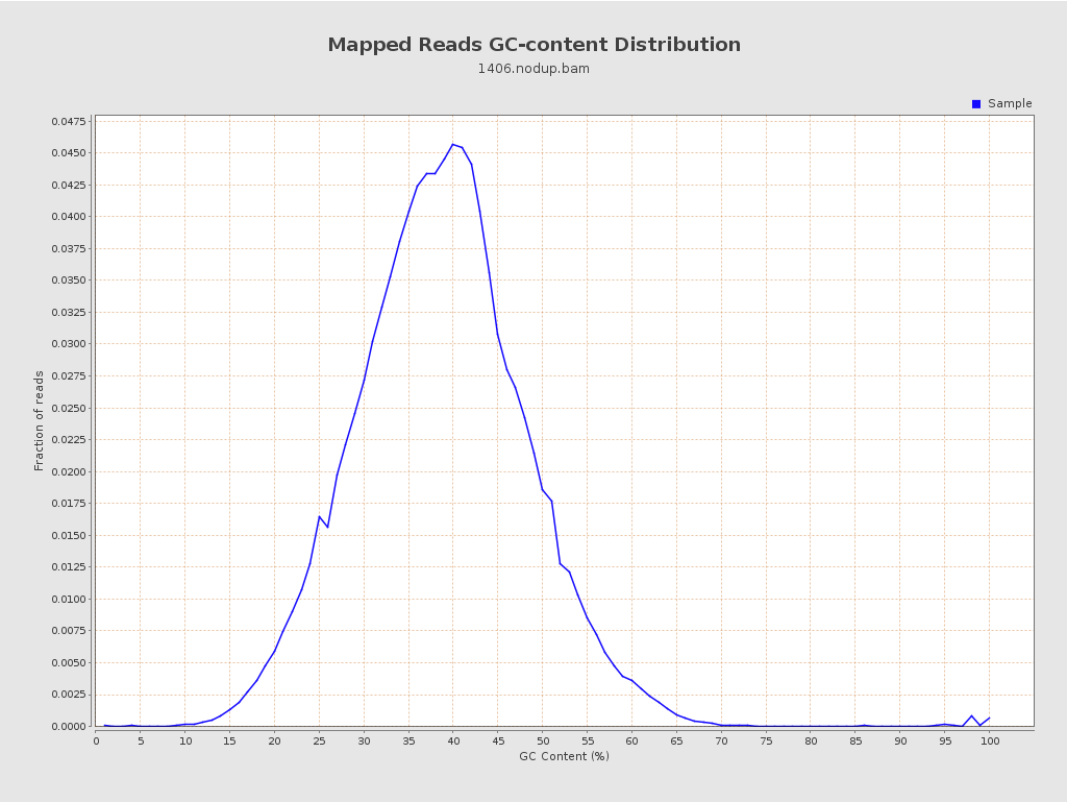
7. Results : Duplication Rate Histogram



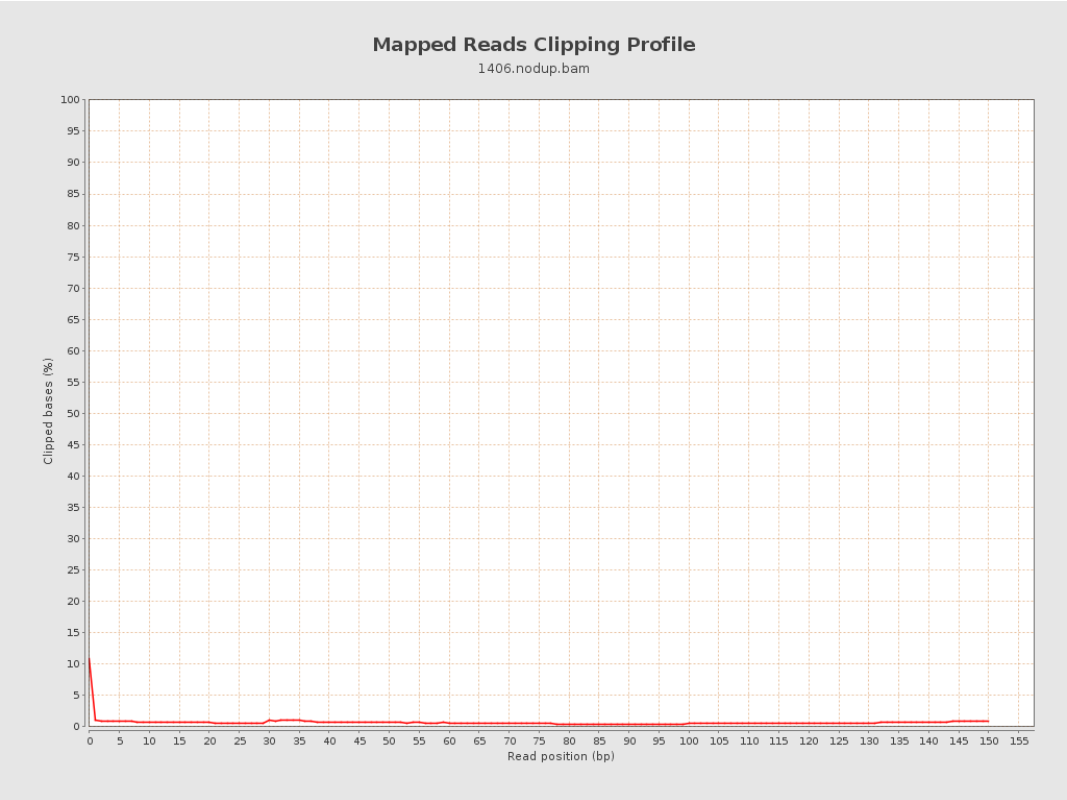
8. Results : Mapped Reads Nucleotide Content



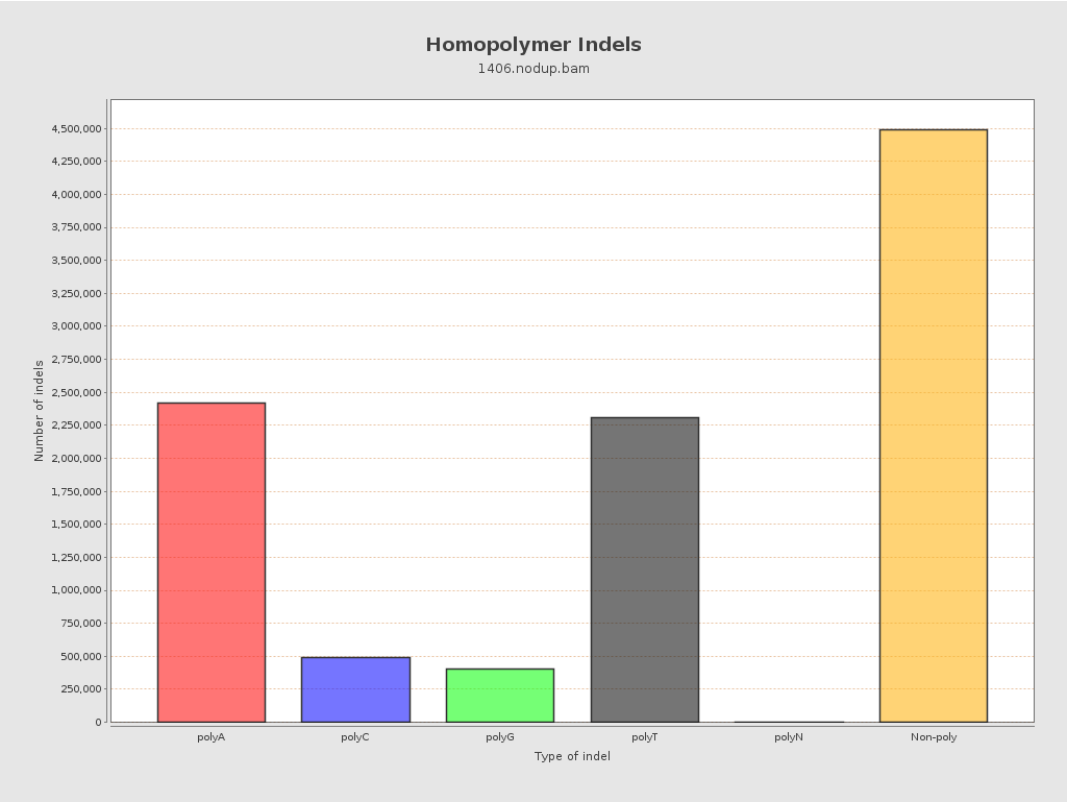
9. Results : Mapped Reads GC-content Distribution



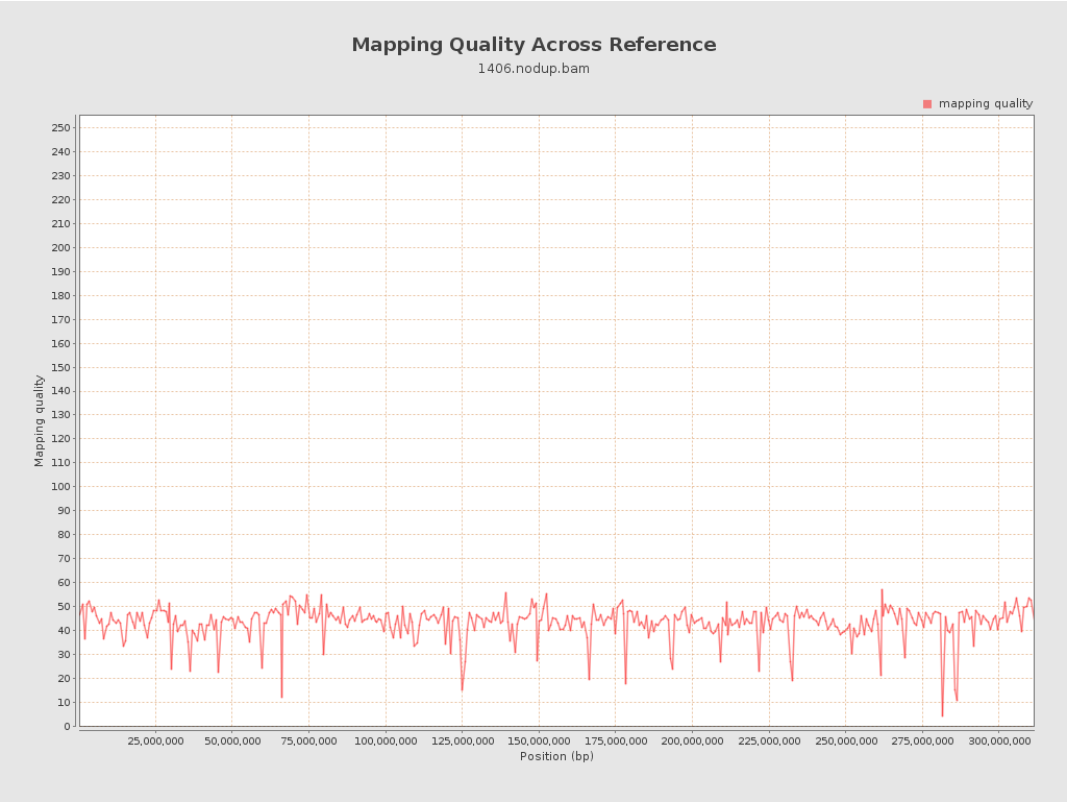
10. Results : Mapped Reads Clipping Profile



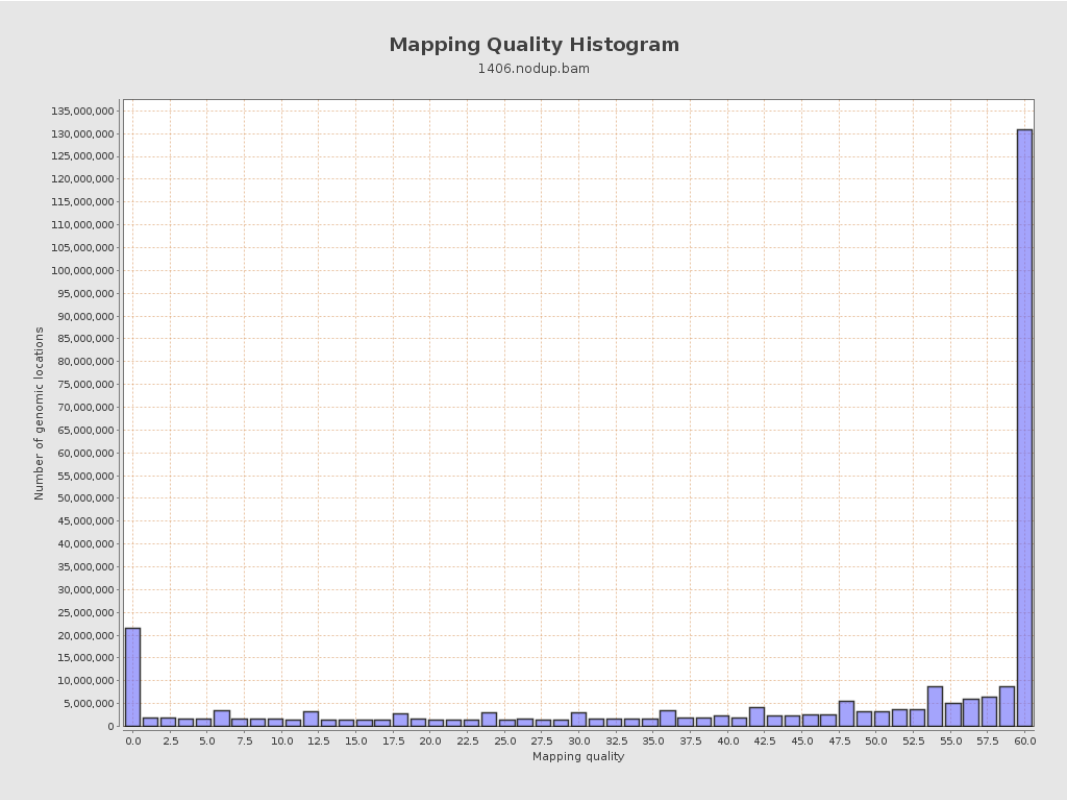
11. Results : Homopolymer Indels



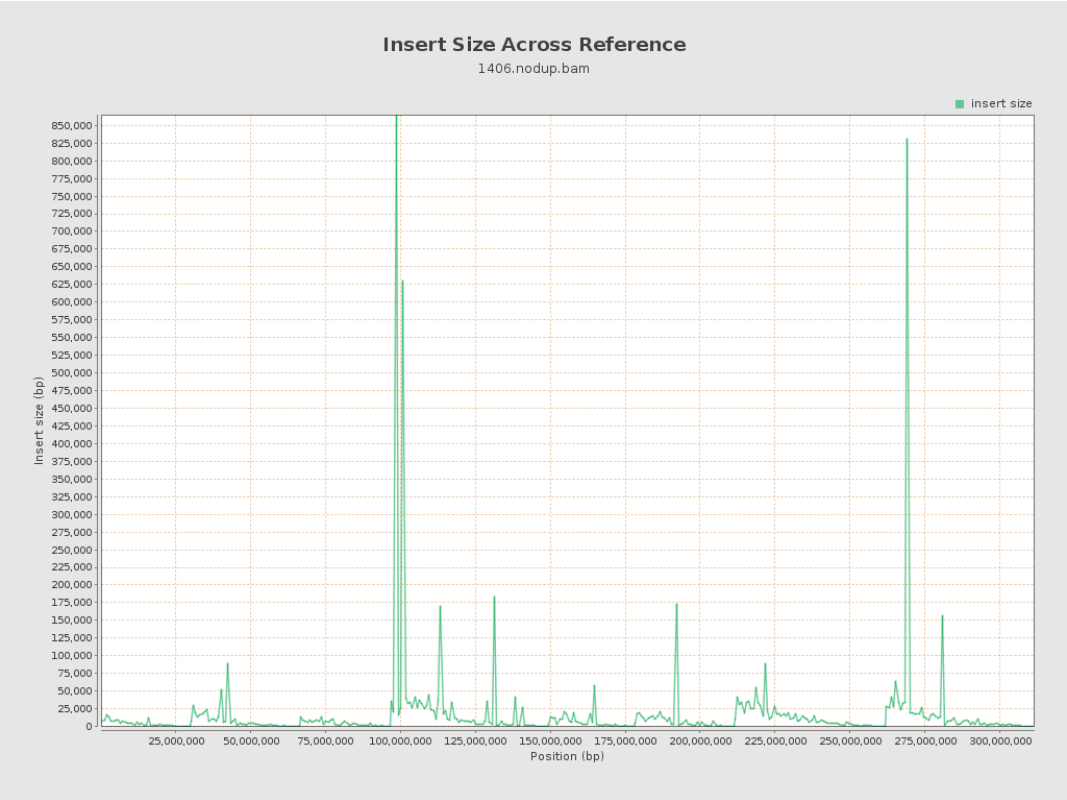
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram