Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/404.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/404.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_403/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_403_S378_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_403/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_403_S378_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:00 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,330,071
Mapped reads	76,218,773 / 94.88%
Unmapped reads	4,111,298 / 5.12%
Mapped paired reads	76,218,773 / 94.88%
Mapped reads, first in pair	38,148,853 / 47.49%
Mapped reads, second in pair	38,069,920 / 47.39%
Mapped reads, both in pair	74,873,855 / 93.21%
Mapped reads, singletons	1,344,918 / 1.67%
Read min/max/mean length	30 / 151 / 148.32
Duplicated reads (flagged)	12,251,489 / 15.25%
Clipped reads	15,352,323 / 19.11%

2.2. ACGT Content

Number/percentage of A's	3,297,315,218 / 30.85%
Number/percentage of C's	2,047,551,088 / 19.16%
Number/percentage of T's	3,304,793,161 / 30.92%
Number/percentage of G's	2,038,200,740 / 19.07%
Number/percentage of N's	36,275 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	34.3825
Standard Deviation	251.2407

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Insert size

Mean	216,221.69
Standard Deviation	2,209,412.27
P25/Median/P75	346 / 448 / 585

2.6. Mismatches and indels

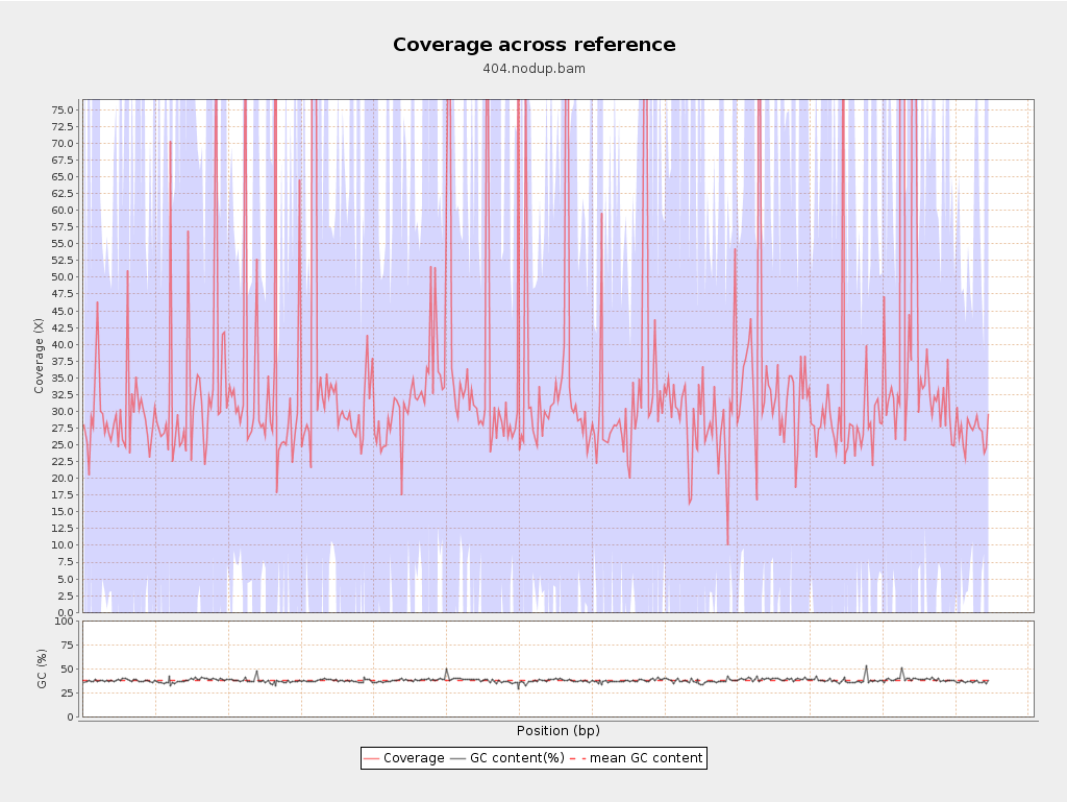
General error rate	2.2%
Mismatches	216,391,625
Insertions	6,907,383
Mapped reads with at least one insertion	8.16%
Deletions	7,135,979
Mapped reads with at least one deletion	8.32%
Homopolymer indels	56.17%

2.7. Chromosome stats

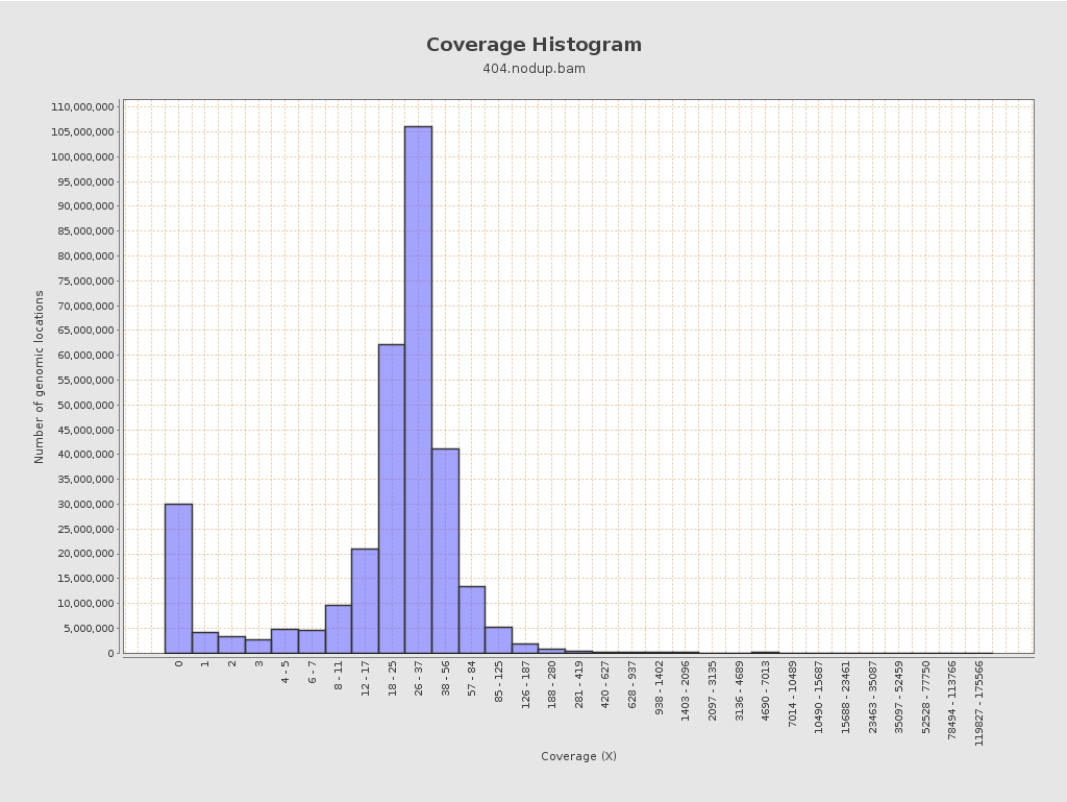
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	866144809	29.1392	98.8822

LT669789.1	36598175	1267166597	34.6238	285.0759
LT669790.1	30422129	1081546187	35.5513	235.7585
LT669791.1	52758100	1784376933	33.8219	209.1953
LT669792.1	28376109	952181038	33.5557	270.5814
LT669793.1	33388210	1074597192	32.1849	186.3921
LT669794.1	50579949	1652882081	32.6786	238.4284
LT669795.1	49795044	2036129771	40.8902	355.4284

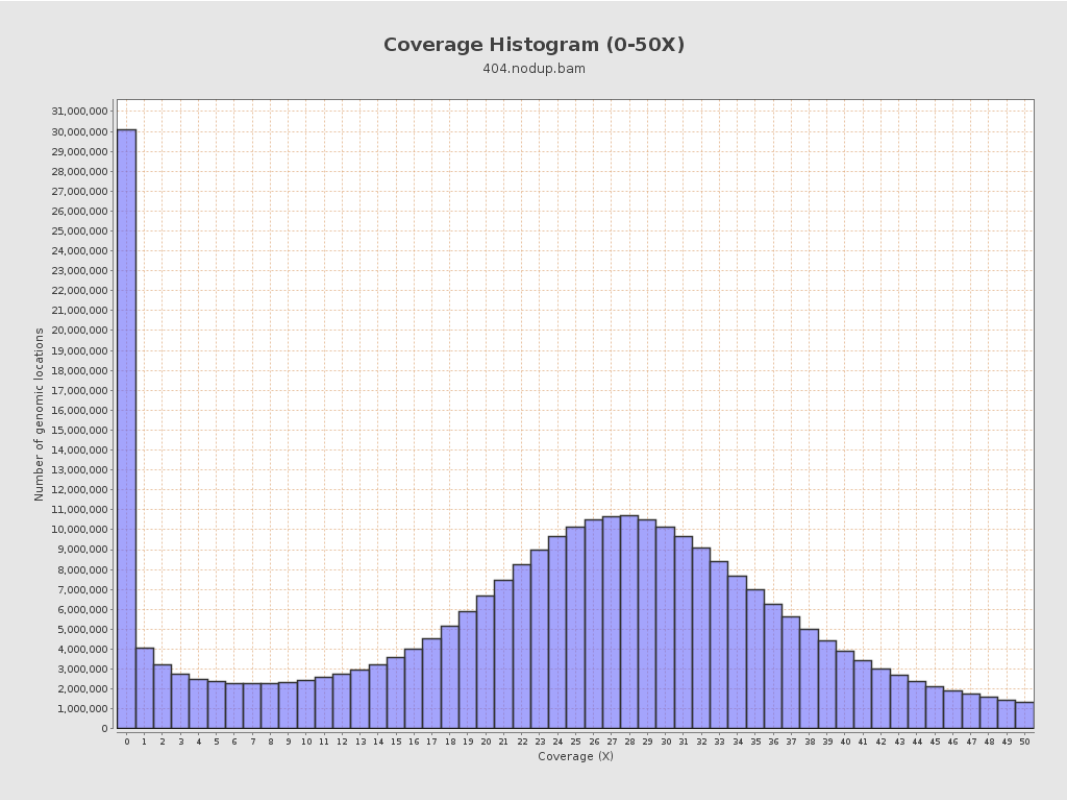
3. Results : Coverage across reference



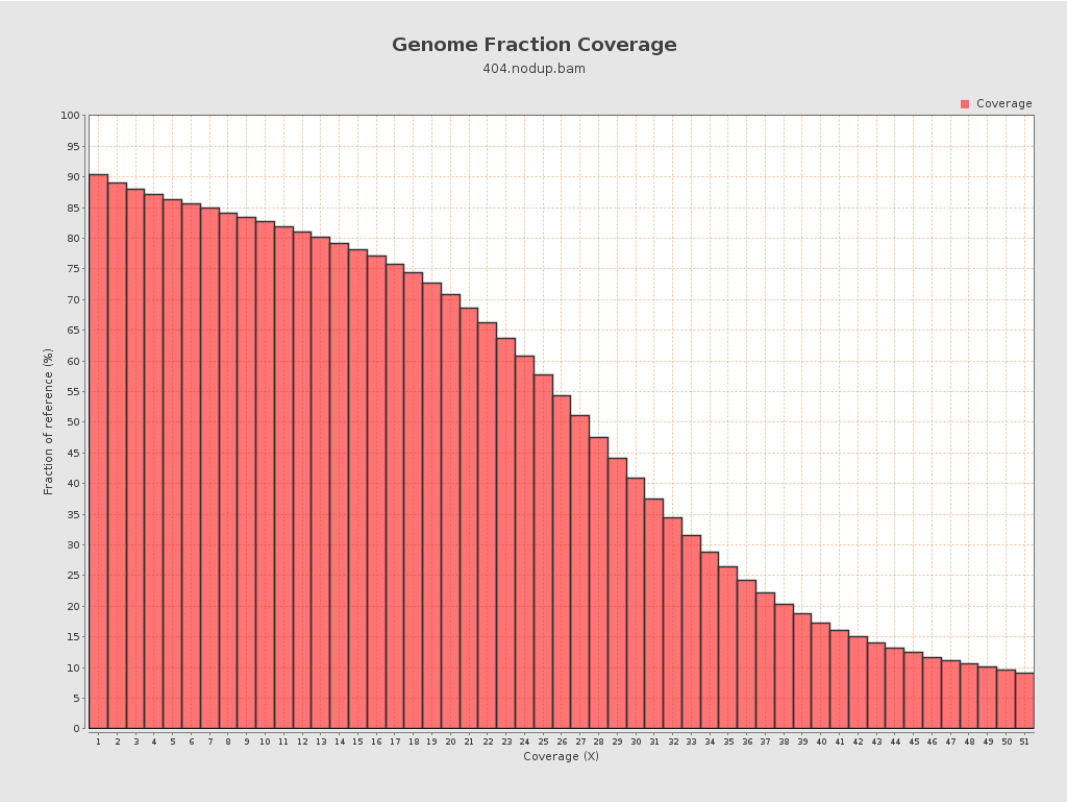
4. Results : Coverage Histogram



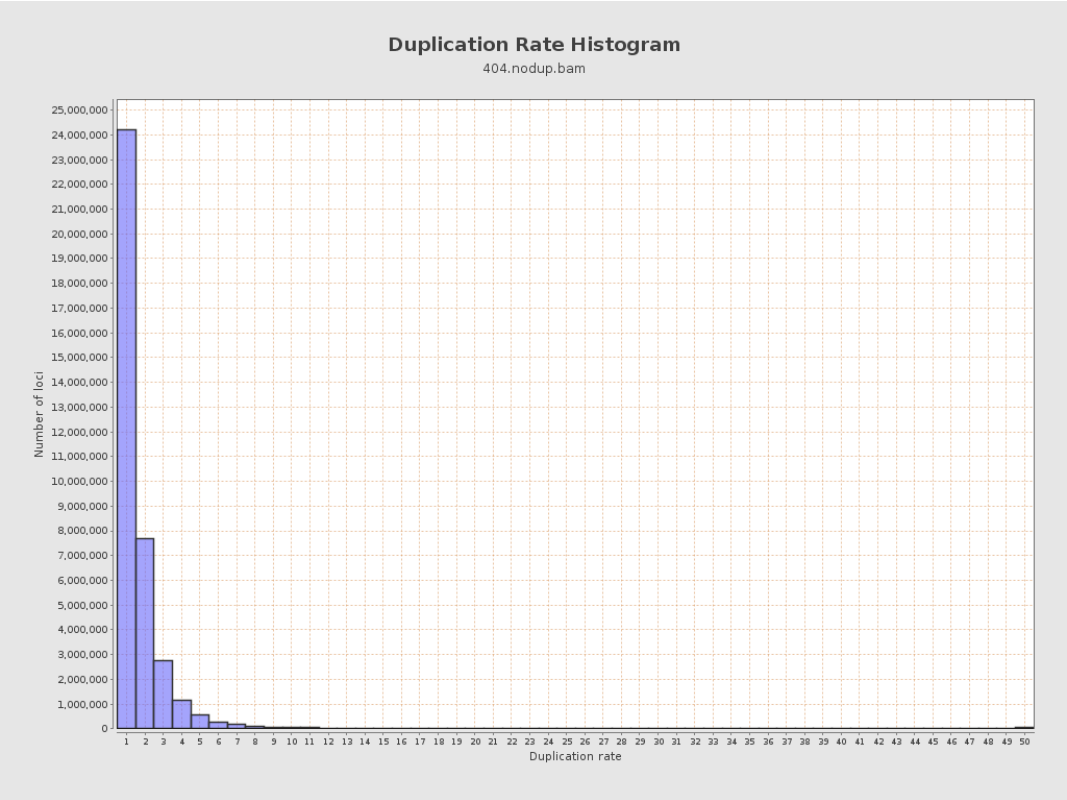
5. Results : Coverage Histogram (0-50X)



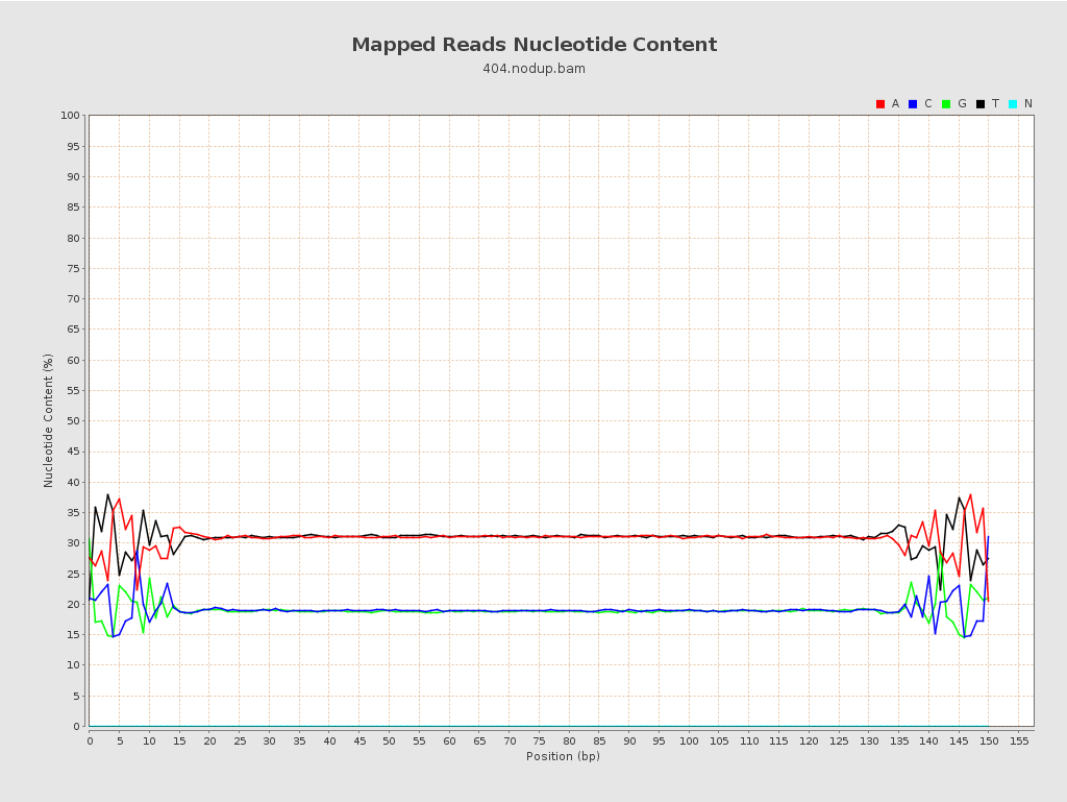
6. Results : Genome Fraction Coverage



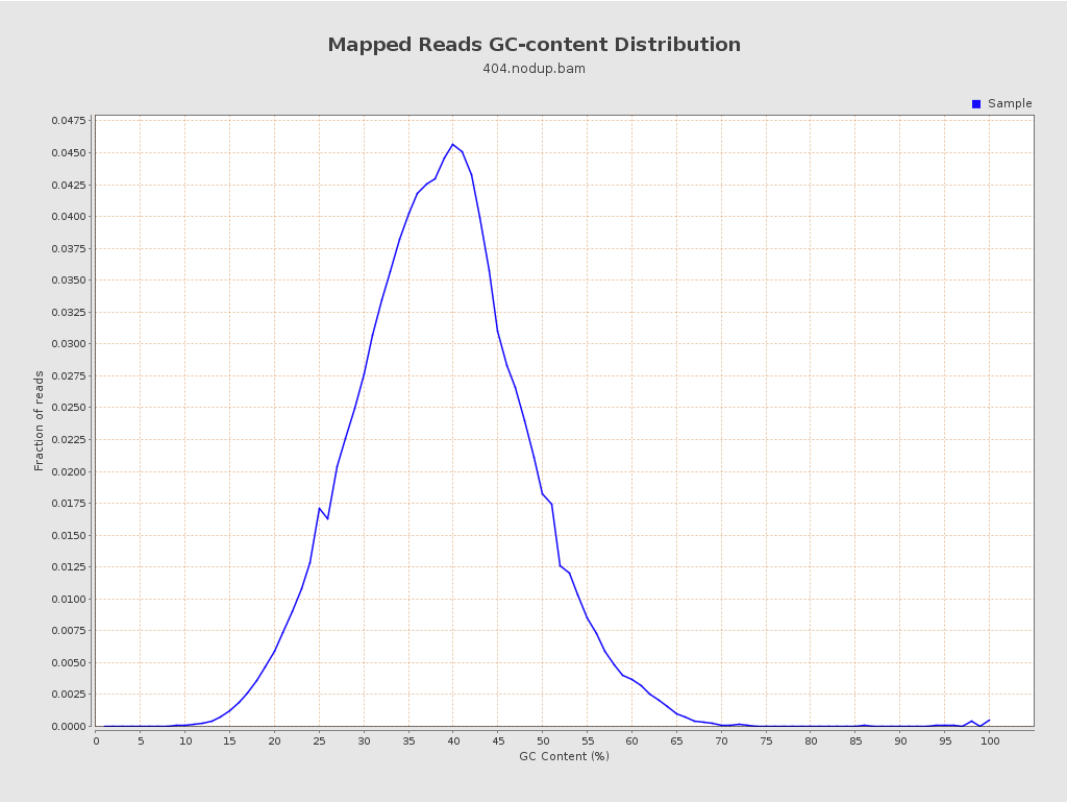
7. Results : Duplication Rate Histogram



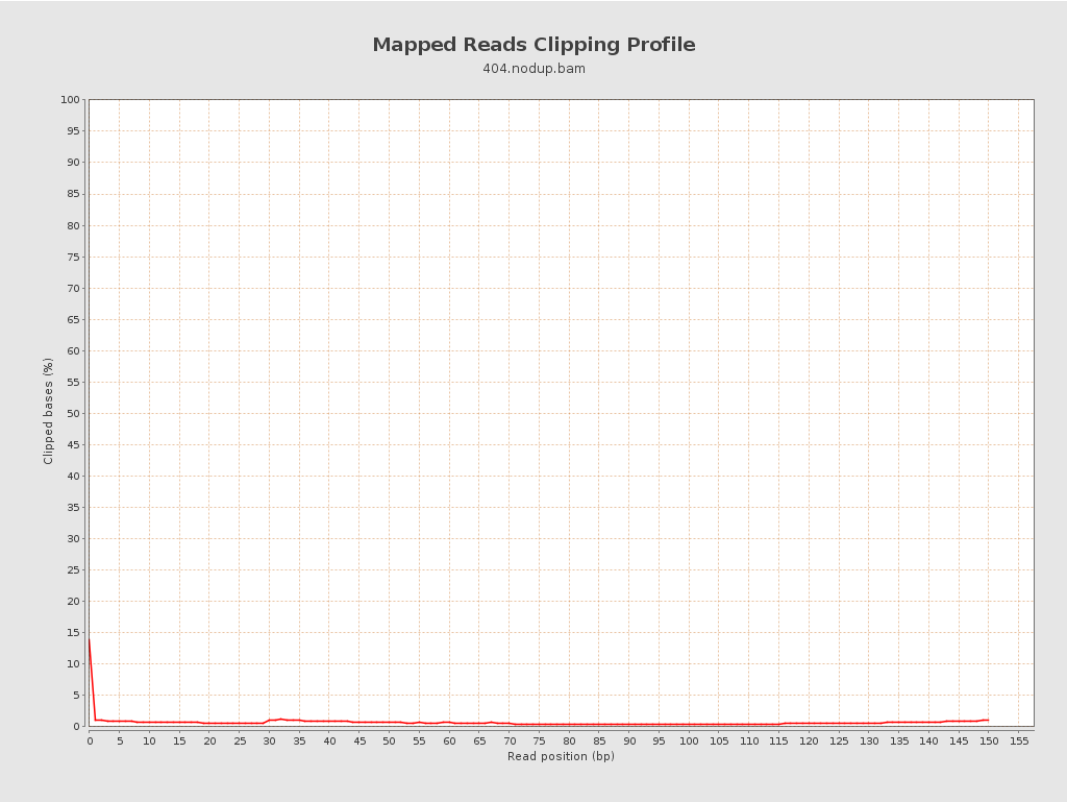
8. Results : Mapped Reads Nucleotide Content



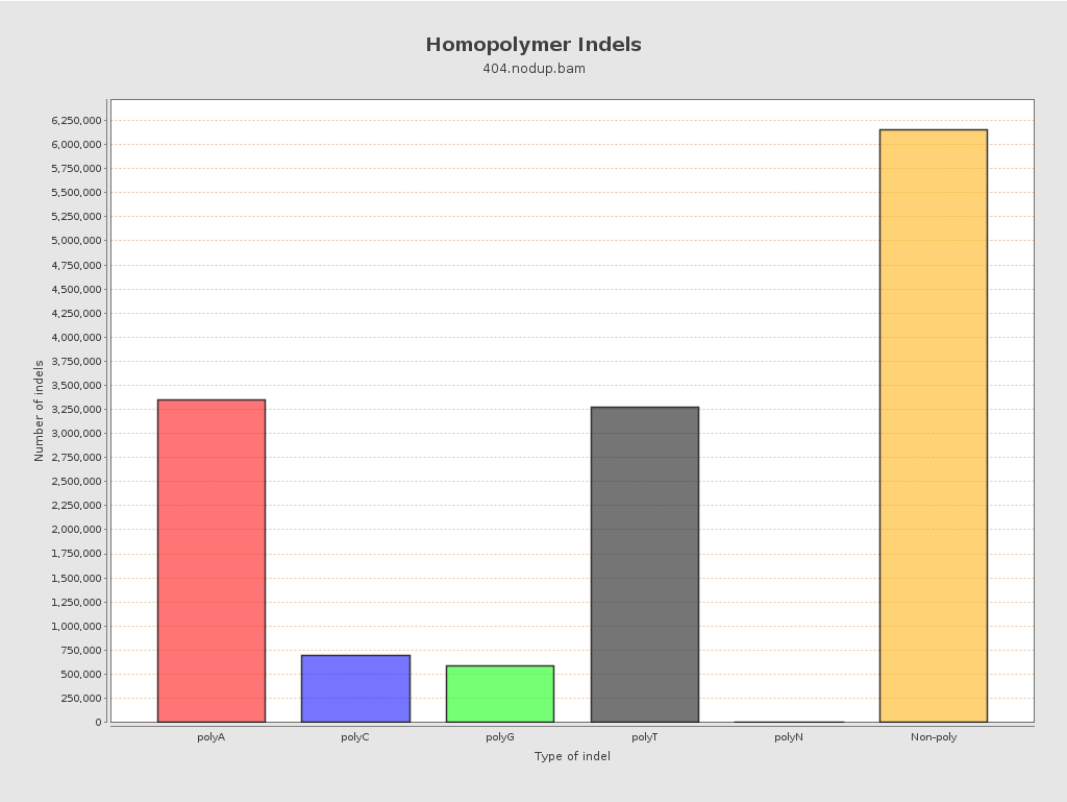
9. Results : Mapped Reads GC-content Distribution



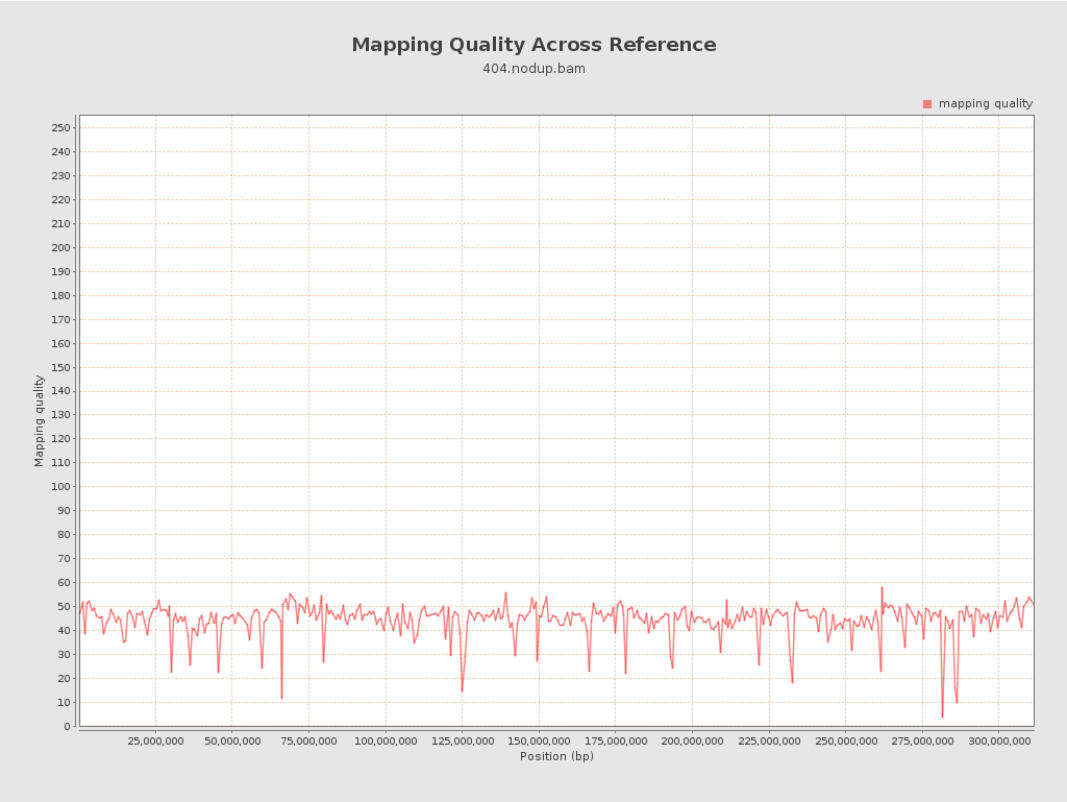
10. Results : Mapped Reads Clipping Profile



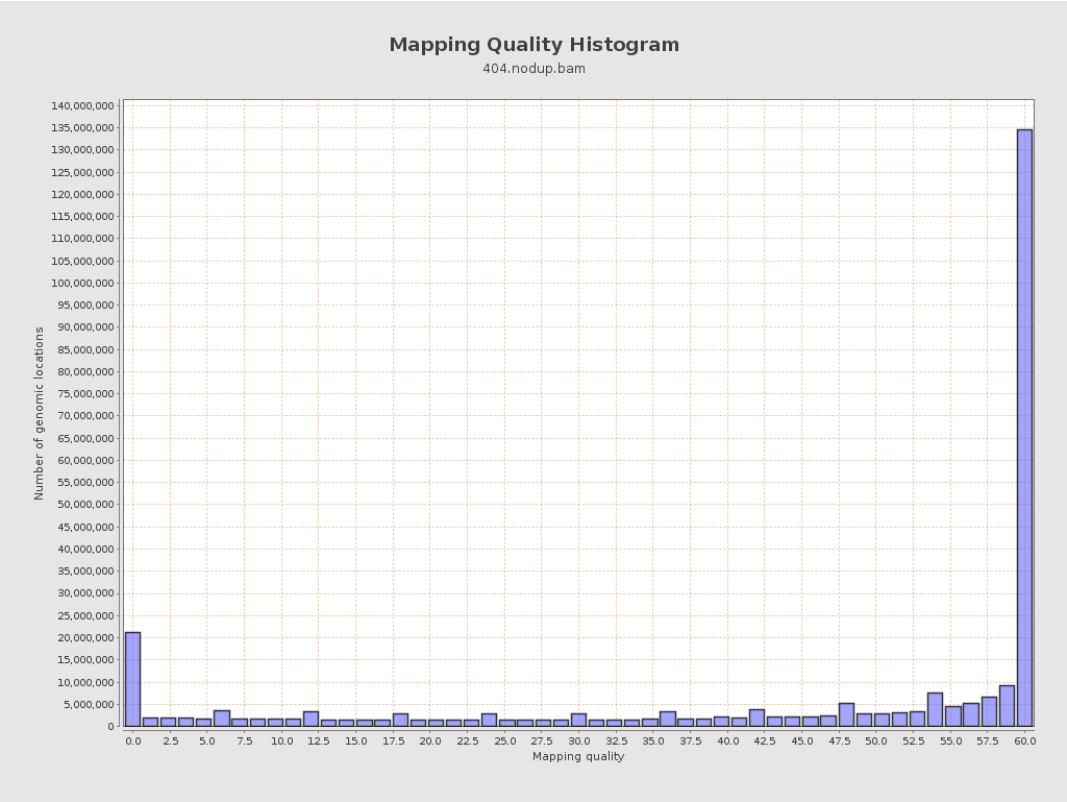
11. Results : Homopolymer Indels



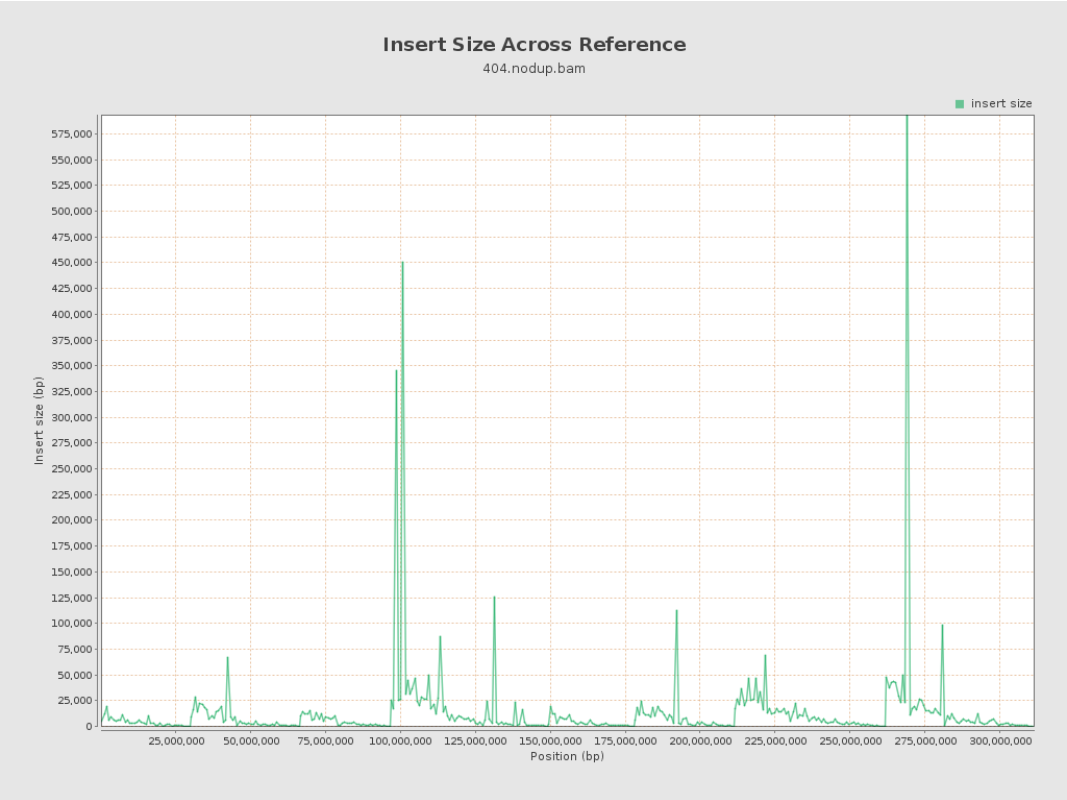
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram