Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/402.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/402.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_270/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_270_S351_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_270/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_270_S351_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:00 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	54,282,911
Mapped reads	50,146,641 / 92.38%
Unmapped reads	4,136,270 / 7.62%
Mapped paired reads	50,146,641 / 92.38%
Mapped reads, first in pair	25,137,031 / 46.31%
Mapped reads, second in pair	25,009,610 / 46.07%
Mapped reads, both in pair	48,996,876 / 90.26%
Mapped reads, singletons	1,149,765 / 2.12%
Read min/max/mean length	30 / 151 / 148.23
Duplicated reads (flagged)	7,222,915 / 13.31%
Clipped reads	11,243,194 / 20.71%

2.2. ACGT Content

Number/percentage of A's	2,142,992,072 / 30.85%
Number/percentage of C's	1,330,193,189 / 19.15%
Number/percentage of T's	2,146,376,930 / 30.9%
Number/percentage of G's	1,327,096,146 / 19.1%
Number/percentage of N's	25,447 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	22.3453
Standard Deviation	178.1987

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Insert size

Mean	227,367.58
Standard Deviation	2,272,105.39
P25/Median/P75	347 / 452 / 580

2.6. Mismatches and indels

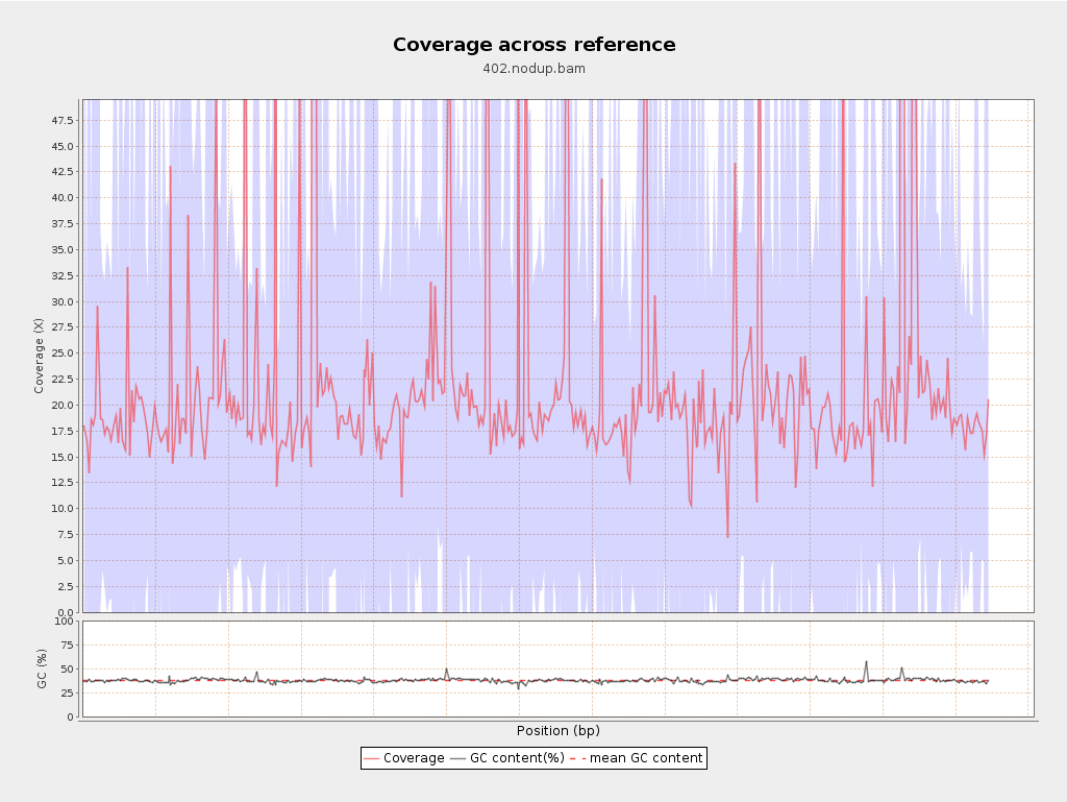
General error rate	2.28%
Mismatches	145,410,795
Insertions	4,592,790
Mapped reads with at least one insertion	8.24%
Deletions	4,578,854
Mapped reads with at least one deletion	8.12%
Homopolymer indels	56.57%

2.7. Chromosome stats

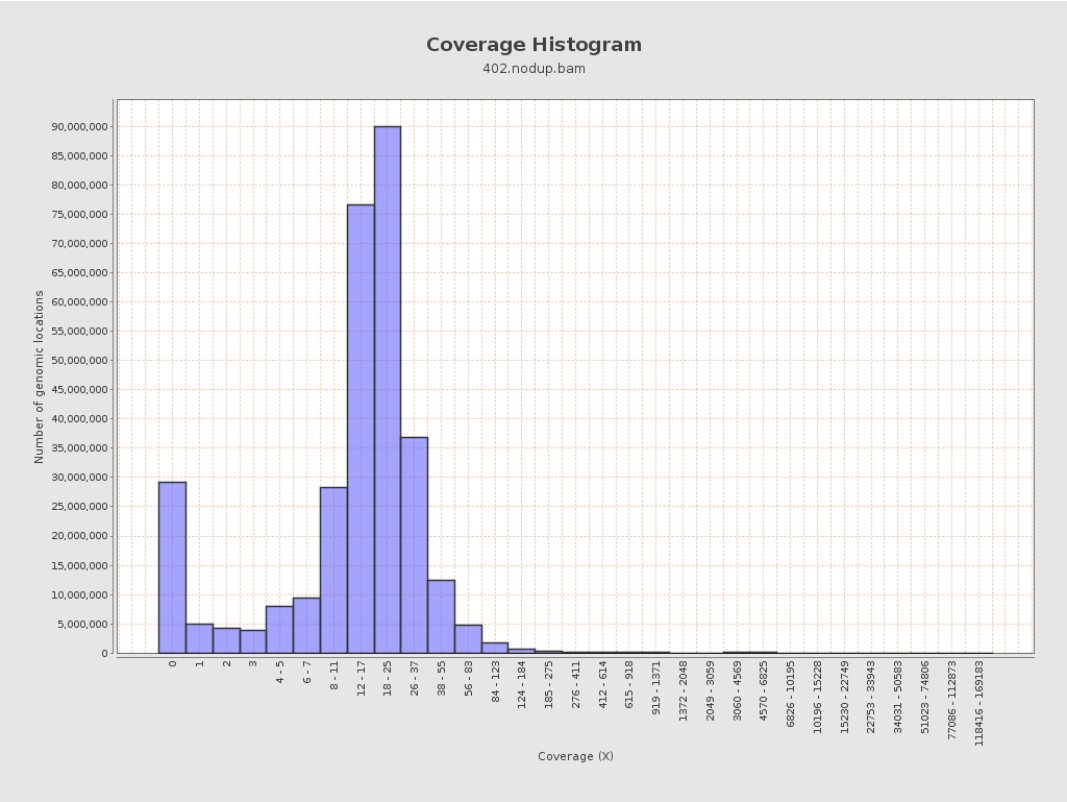
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	553909901	18.6349	56.5655

LT669789.1	36598175	827526102	22.6111	191.4672
LT669790.1	30422129	739763286	24.3166	190.674
LT669791.1	52758100	1156322008	21.9174	159.6021
LT669792.1	28376109	624780928	22.0179	198.3857
LT669793.1	33388210	691941305	20.7241	125.3938
LT669794.1	50579949	1062983115	21.0159	155.7858
LT669795.1	49795044	1306500683	26.2376	251.0587

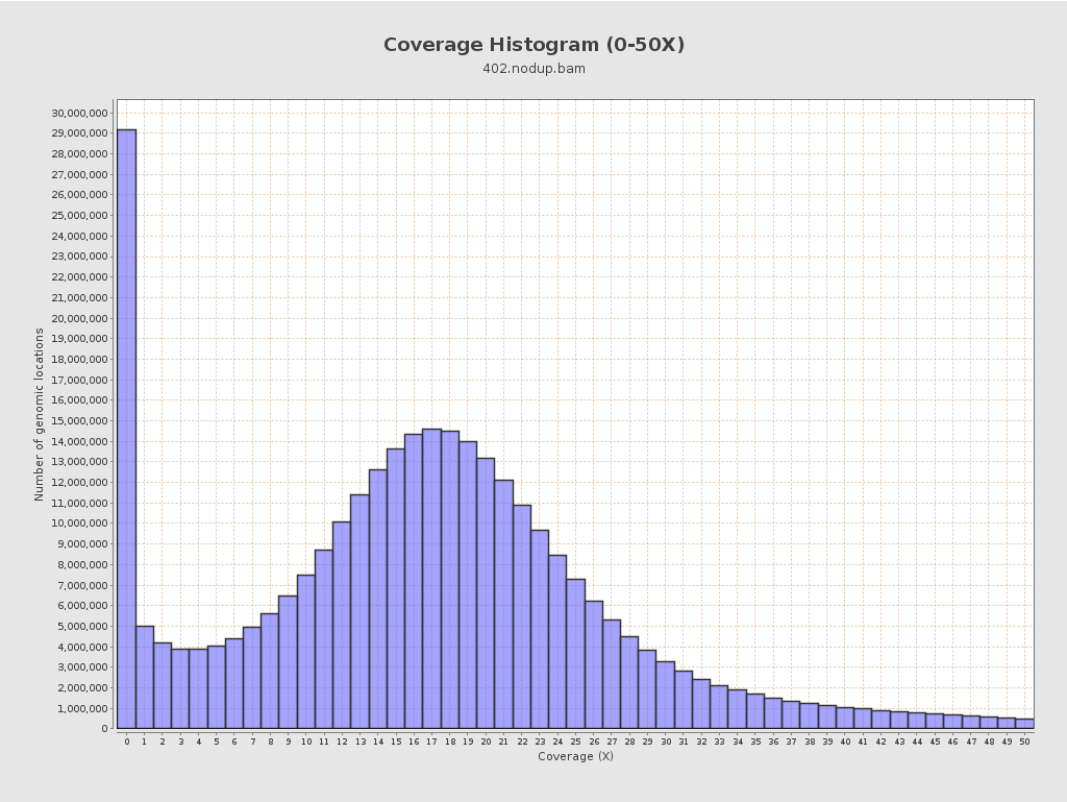
3. Results : Coverage across reference



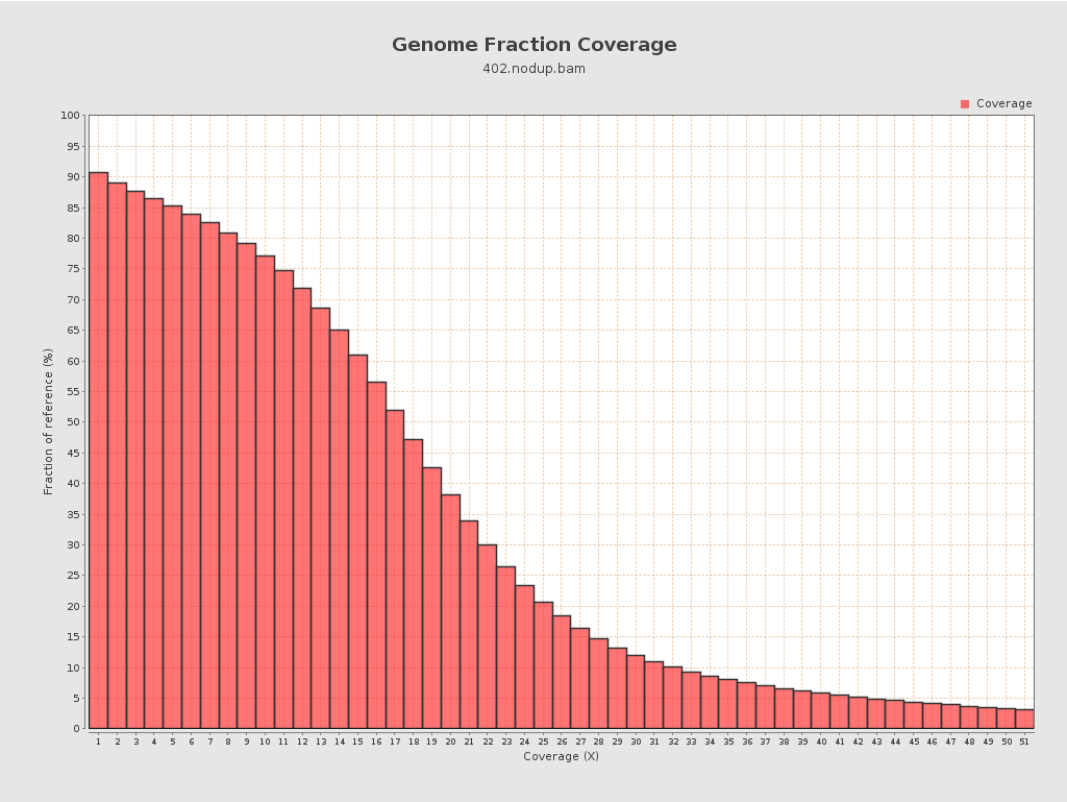
4. Results : Coverage Histogram



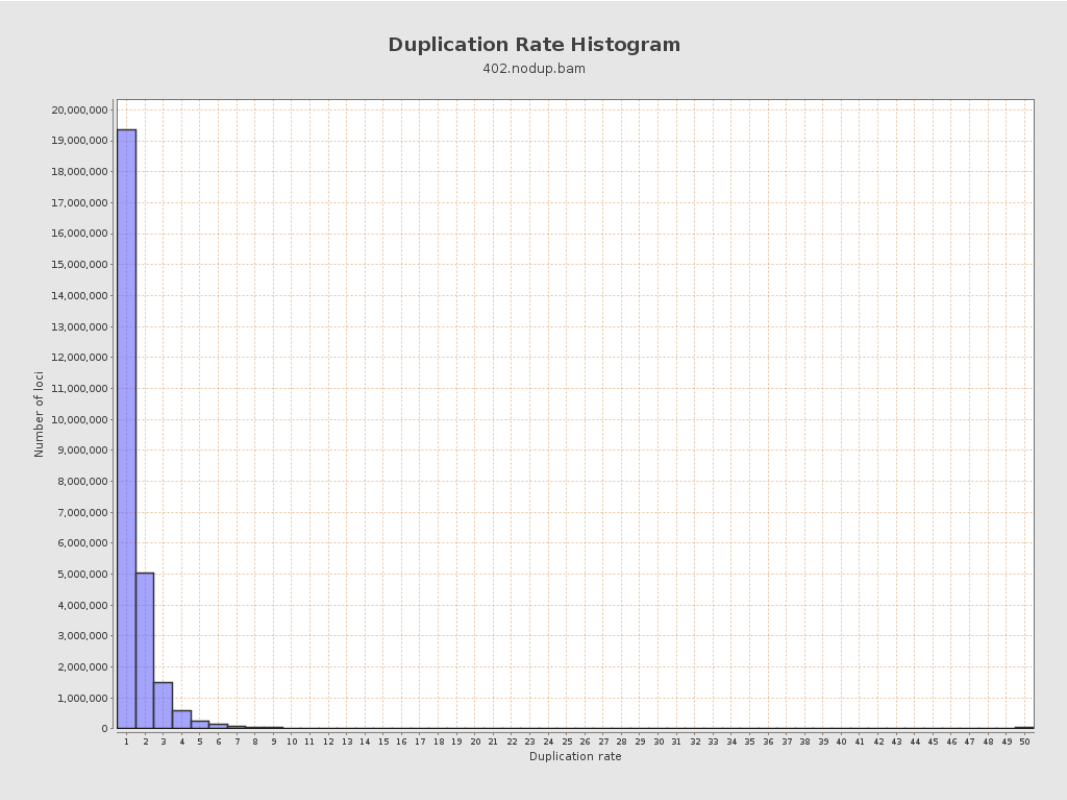
5. Results : Coverage Histogram (0-50X)



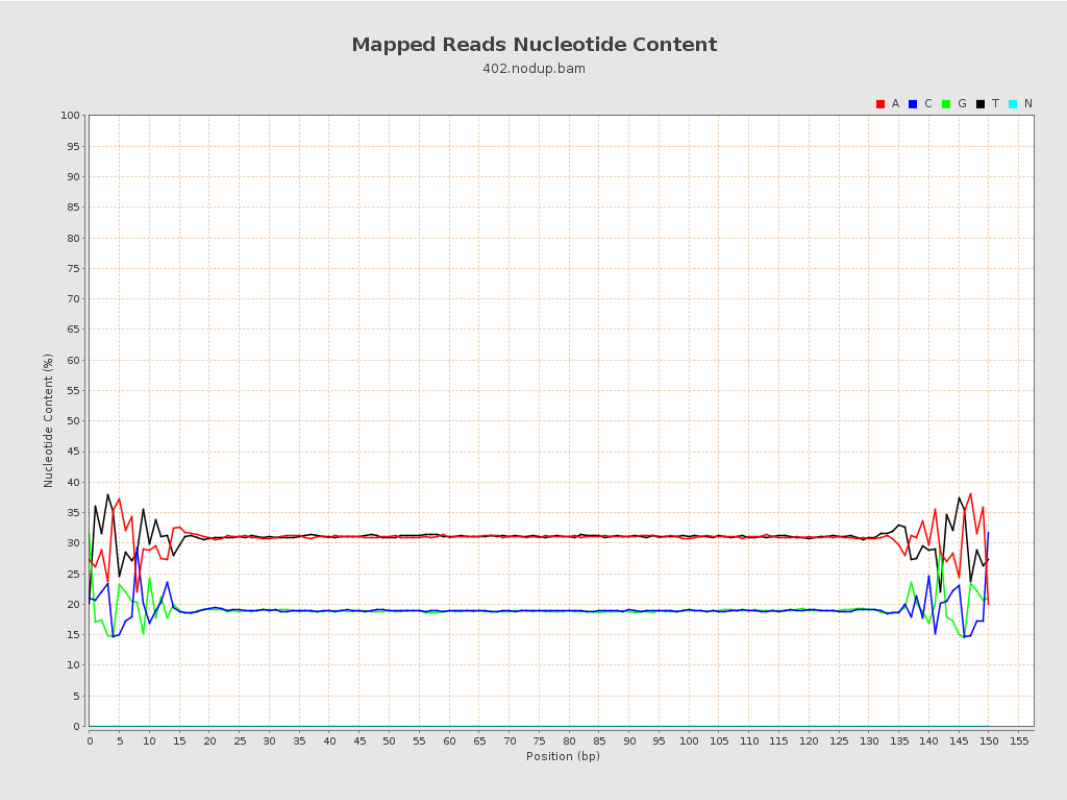
6. Results : Genome Fraction Coverage



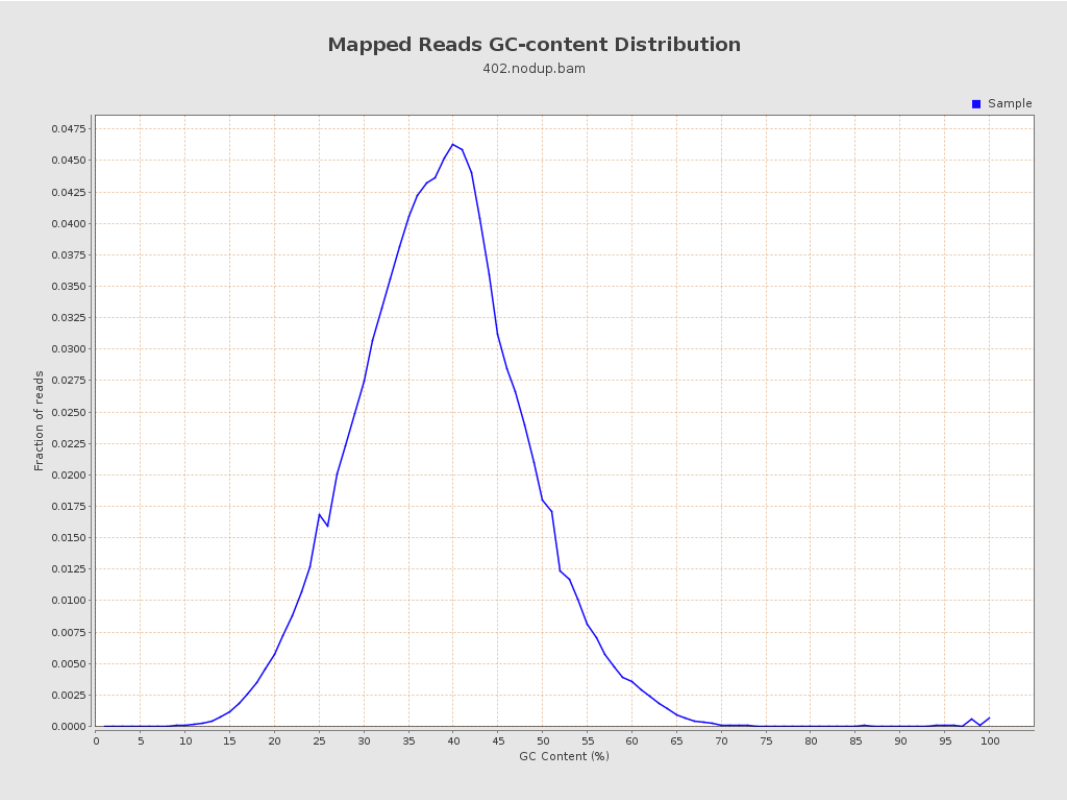
7. Results : Duplication Rate Histogram



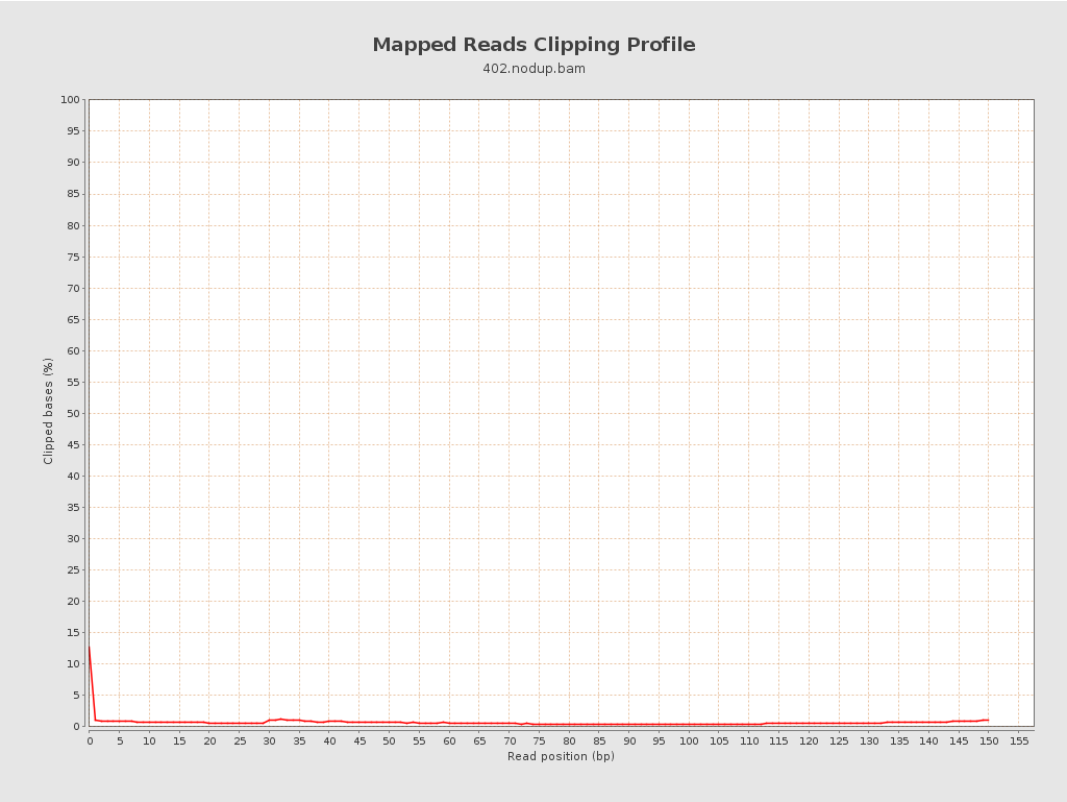
8. Results : Mapped Reads Nucleotide Content



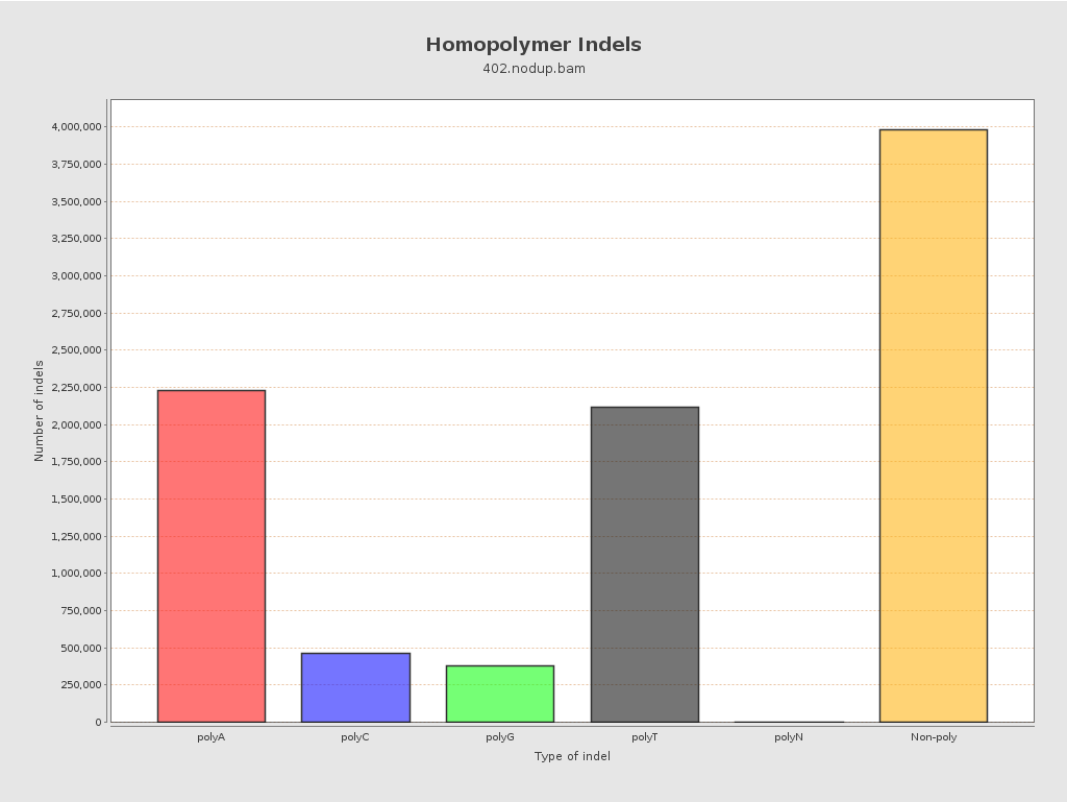
9. Results : Mapped Reads GC-content Distribution



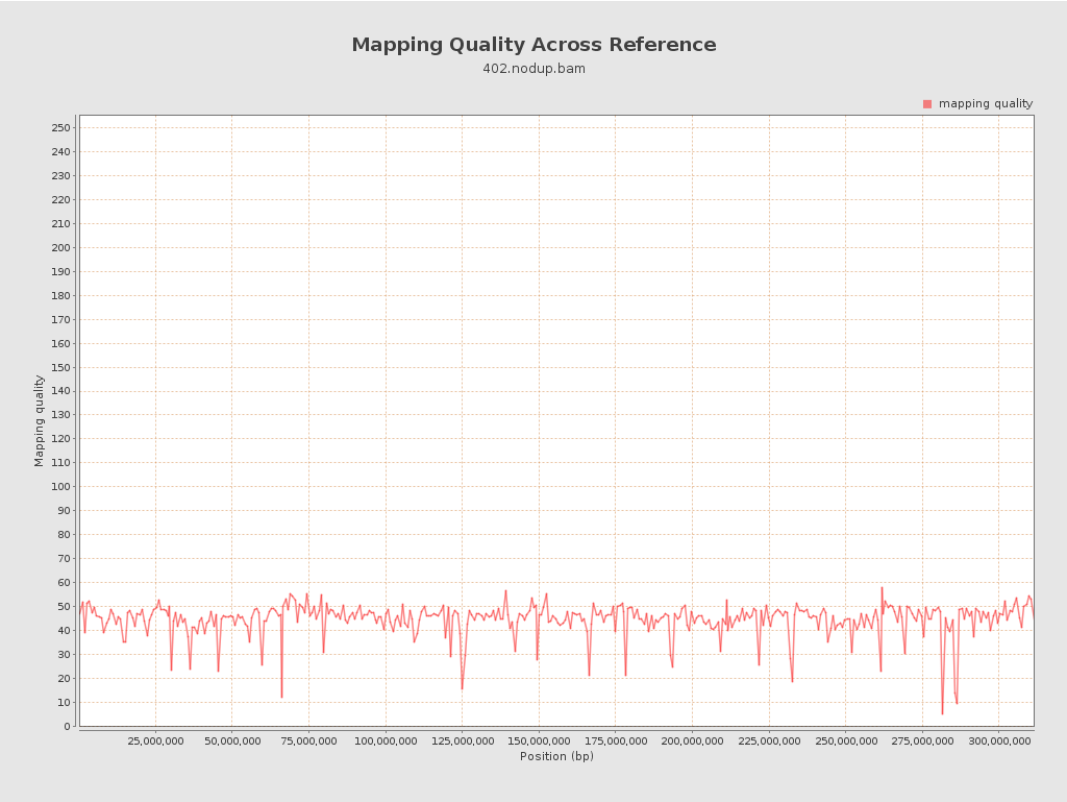
10. Results : Mapped Reads Clipping Profile



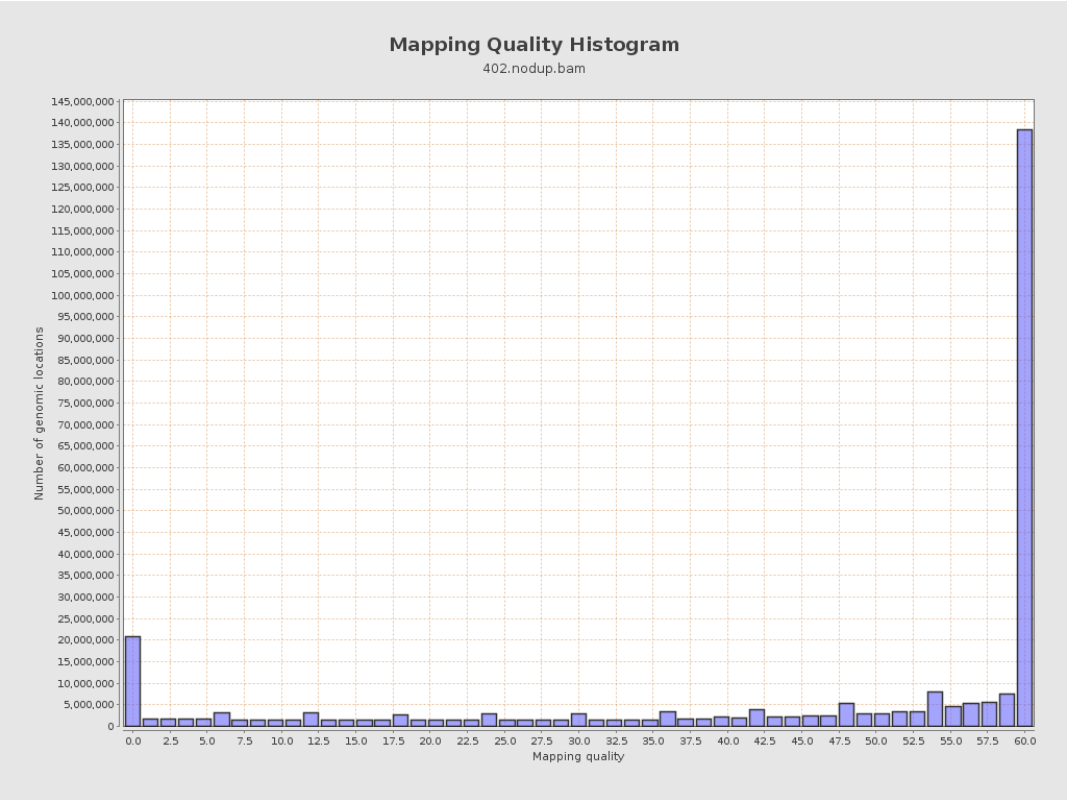
11. Results : Homopolymer Indels



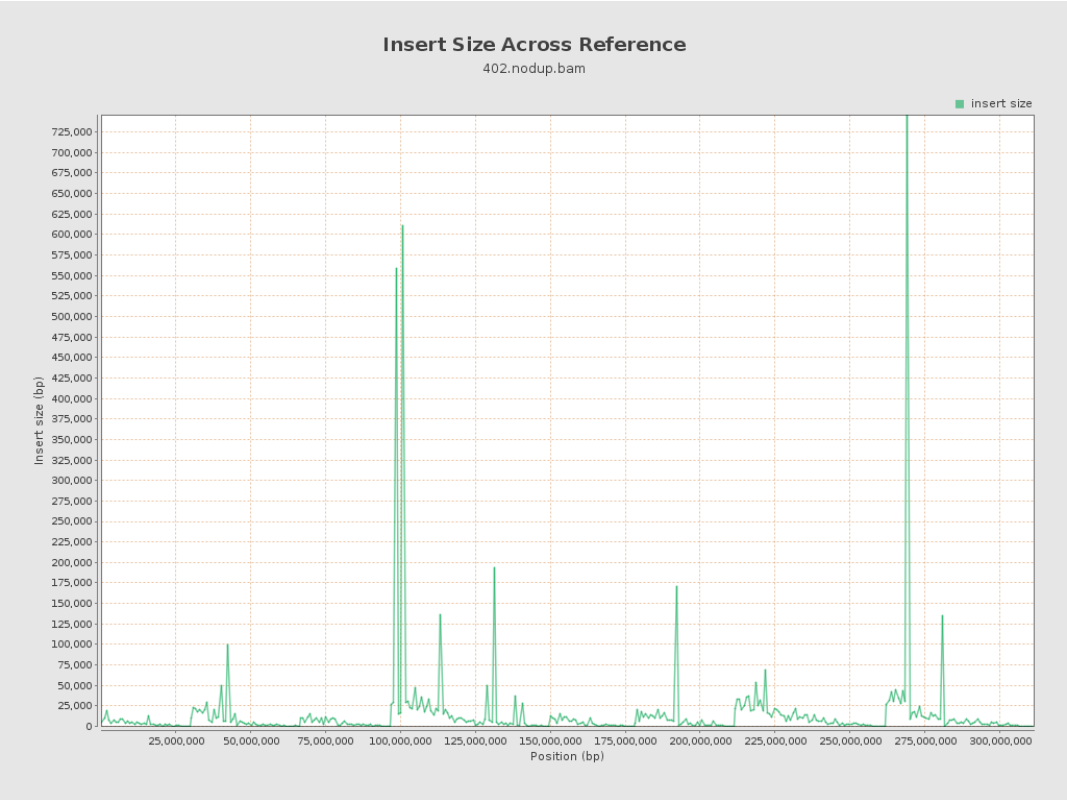
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram