Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/409.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/409.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_222/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_222_S303_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_222/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_222_S303_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,529,403
Mapped reads	54,834,456 / 93.69%
Unmapped reads	3,694,947 / 6.31%
Mapped paired reads	54,834,456 / 93.69%
Mapped reads, first in pair	27,468,706 / 46.93%
Mapped reads, second in pair	27,365,750 / 46.76%
Mapped reads, both in pair	53,643,617 / 91.65%
Mapped reads, singletons	1,190,839 / 2.03%
Read min/max/mean length	30 / 151 / 147.98
Duplicated reads (flagged)	7,491,039 / 12.8%
Clipped reads	12,717,512 / 21.73%

2.2. ACGT Content

Number/percentage of A's	2,329,879,483 / 30.8%
Number/percentage of C's	1,452,367,233 / 19.2%
Number/percentage of T's	2,333,184,063 / 30.84%
Number/percentage of G's	1,448,830,962 / 19.15%
Number/percentage of N's	28,071 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	24.3358
Standard Deviation	196.3

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Insert size

Mean	234,254.83
Standard Deviation	2,303,915.48
P25/Median/P75	314 / 414 / 543

2.6. Mismatches and indels

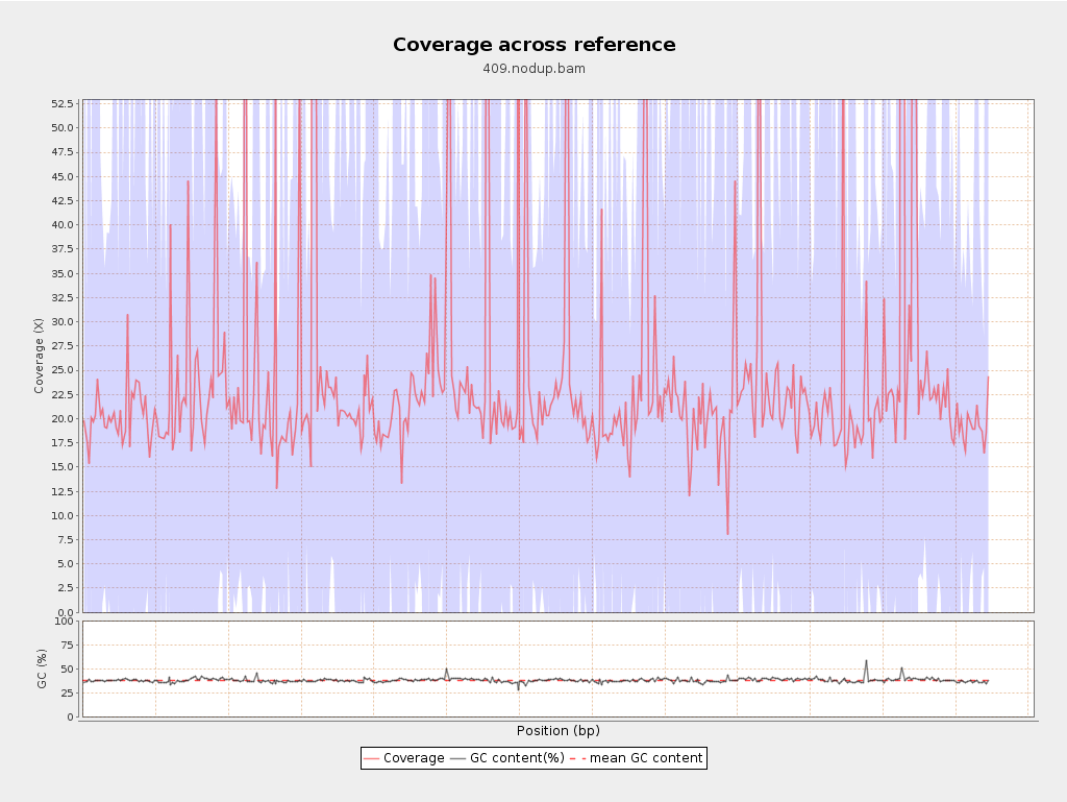
General error rate	2.29%
Mismatches	158,628,919
Insertions	5,158,239
Mapped reads with at least one insertion	8.45%
Deletions	5,204,004
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.57%

2.7. Chromosome stats

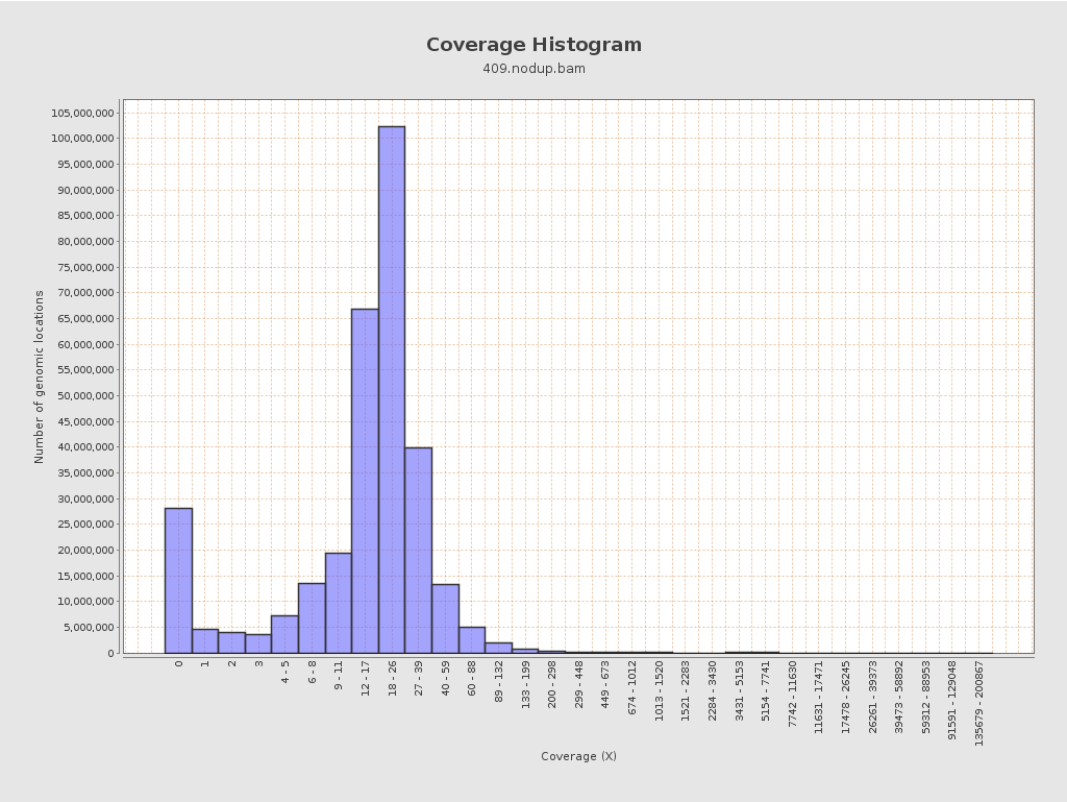
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	596632858	20.0722	61.1727

LT669789.1	36598175	906124644	24.7587	208.8138
LT669790.1	30422129	808400142	26.5728	206.3791
LT669791.1	52758100	1257609493	23.8373	174.3046
LT669792.1	28376109	686468819	24.1918	198.8741
LT669793.1	33388210	756407784	22.6549	137.0051
LT669794.1	50579949	1153755761	22.8105	161.6546
LT669795.1	49795044	1418666977	28.4901	294.9003

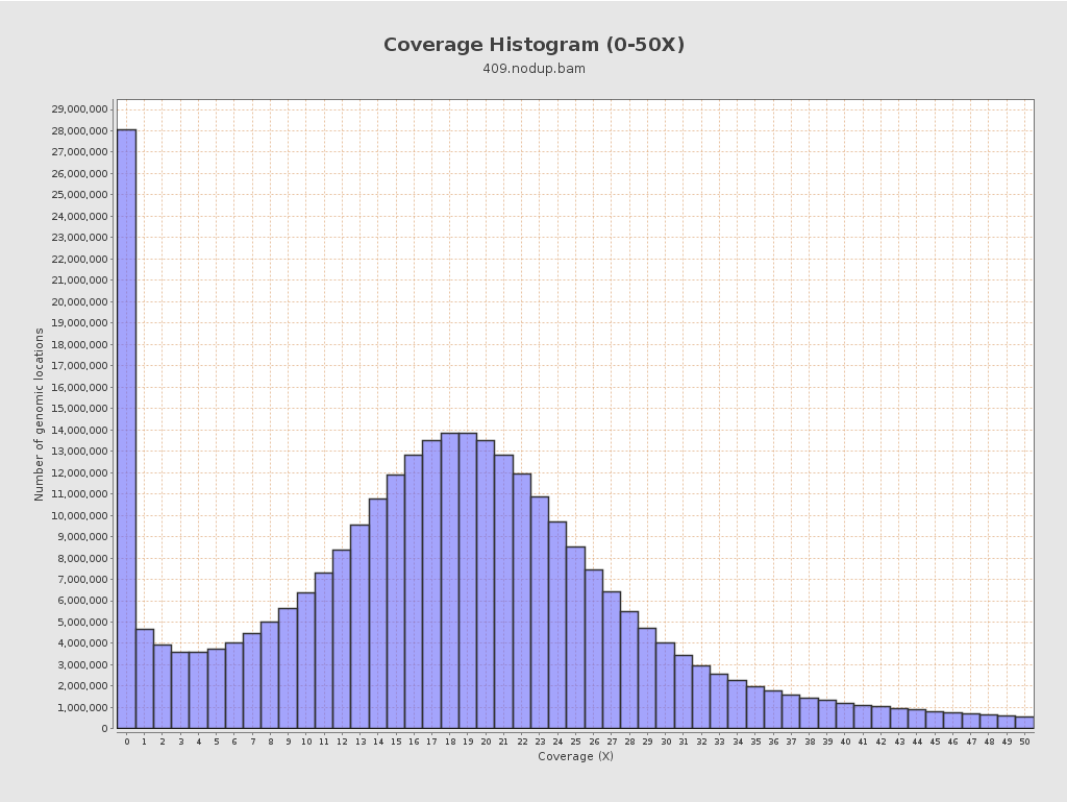
3. Results : Coverage across reference



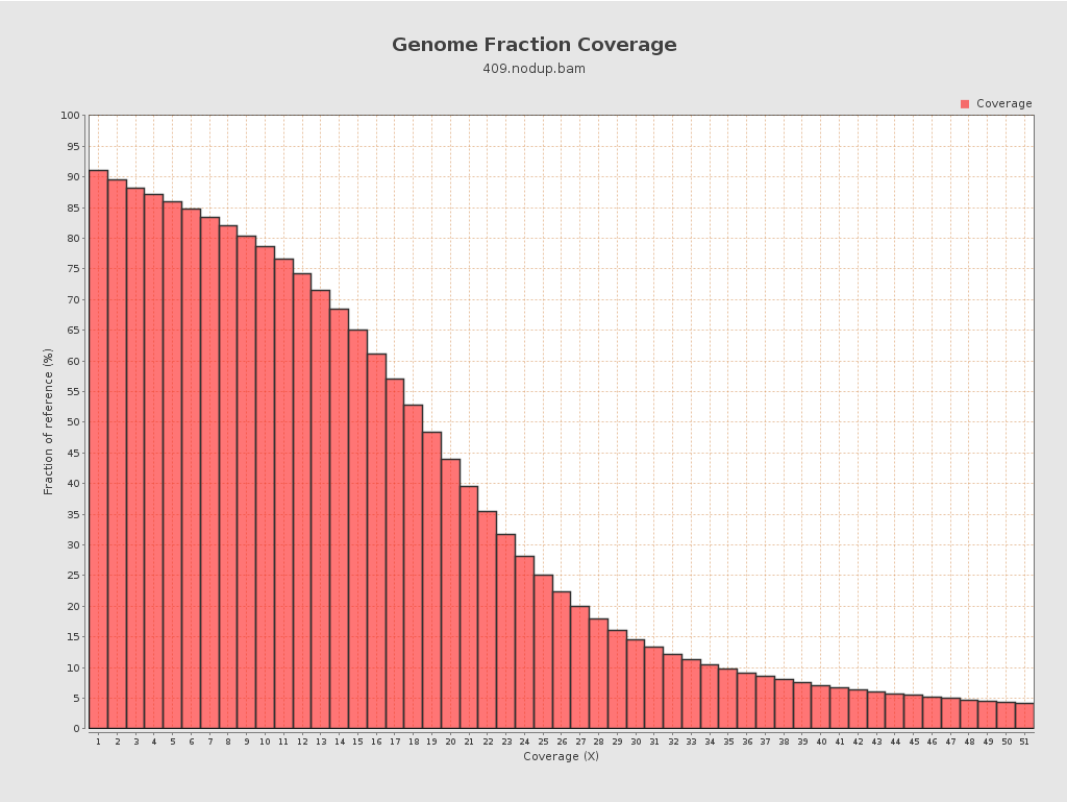
4. Results : Coverage Histogram



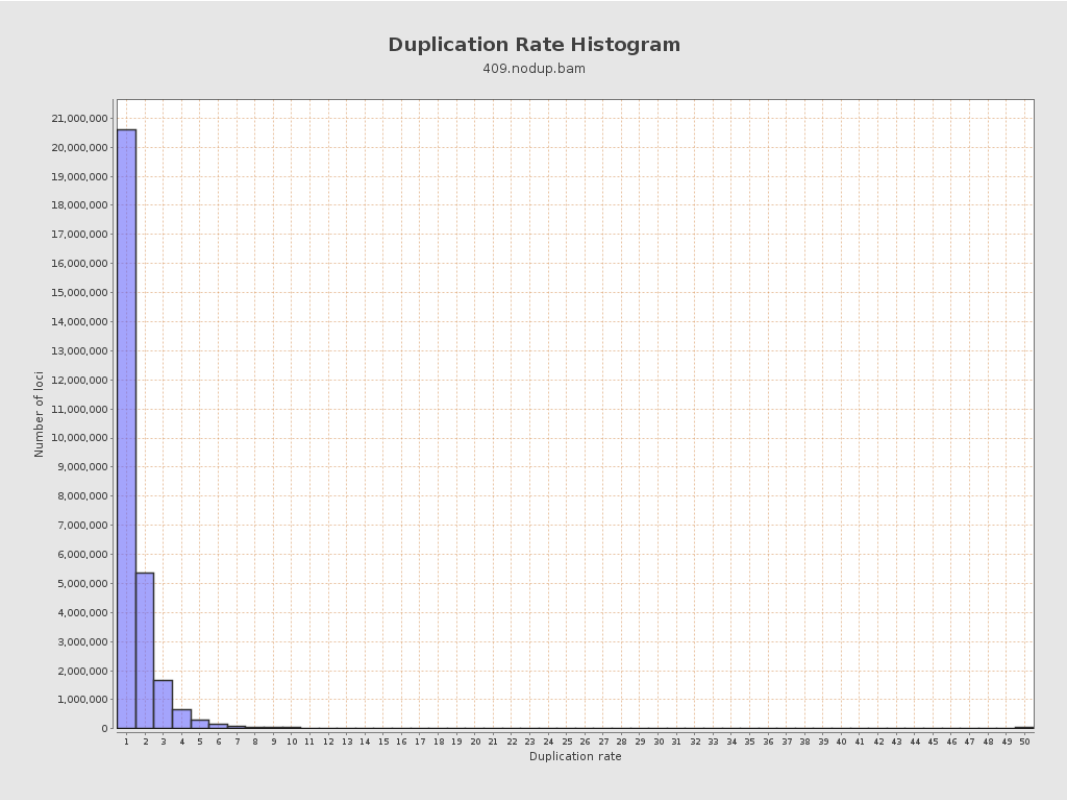
5. Results : Coverage Histogram (0-50X)



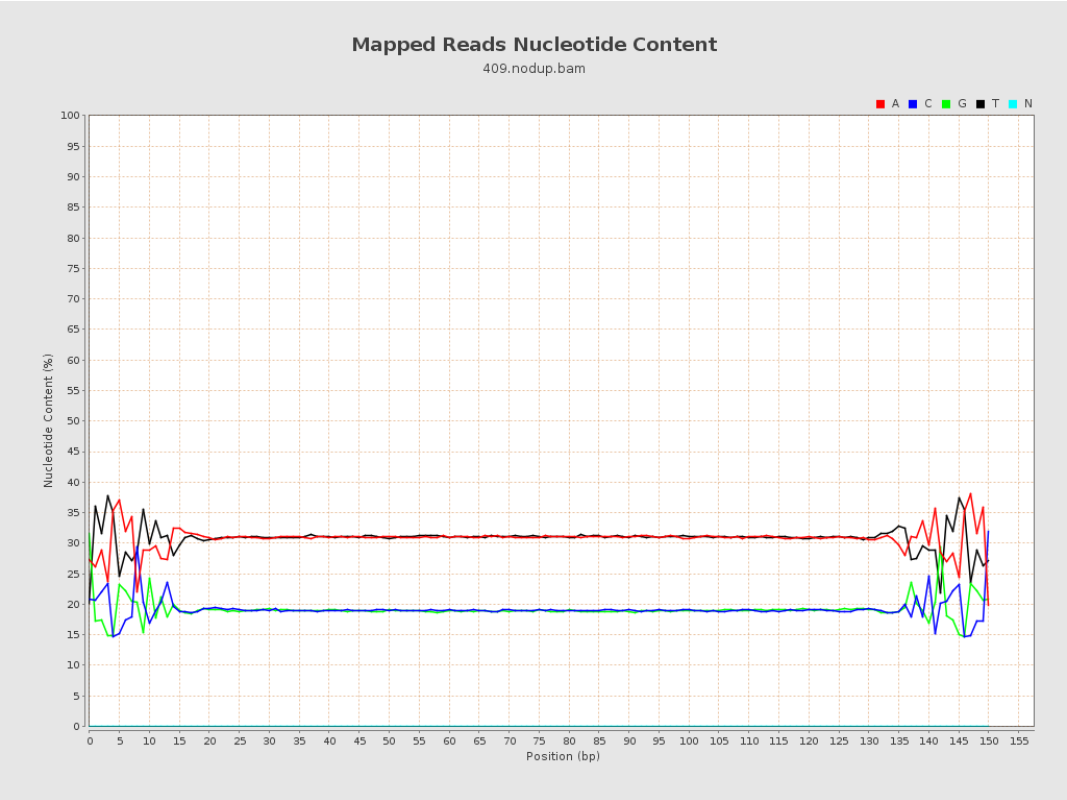
6. Results : Genome Fraction Coverage



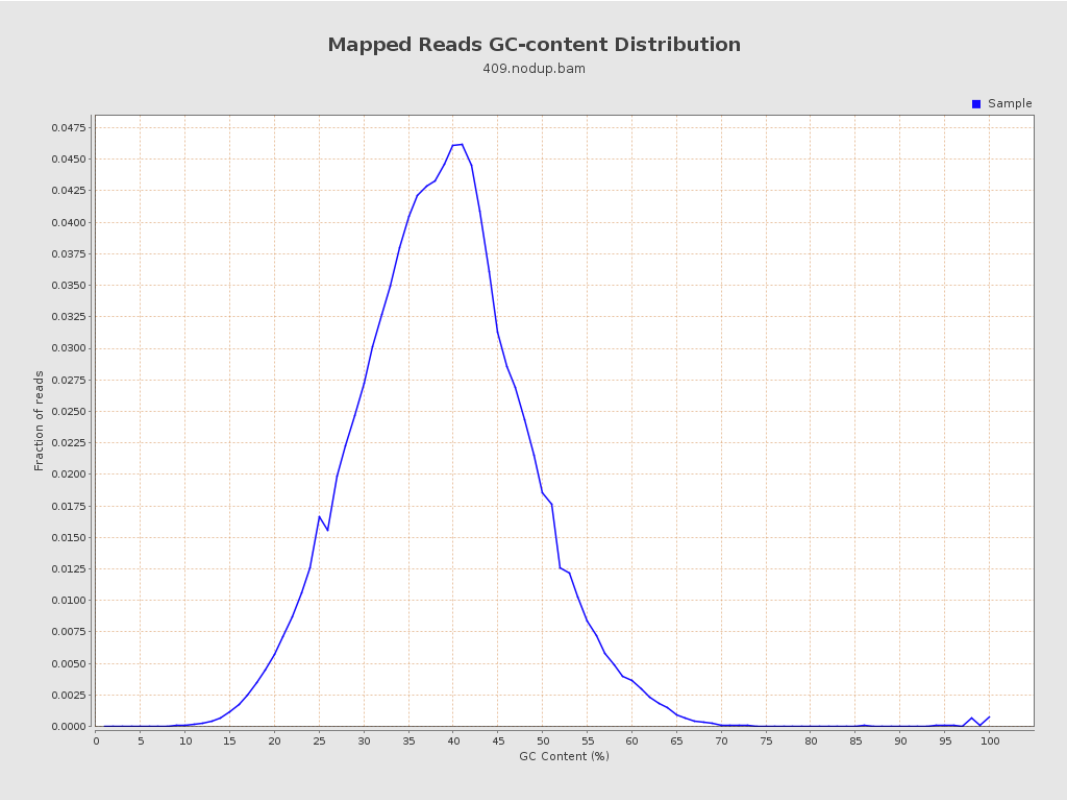
7. Results : Duplication Rate Histogram



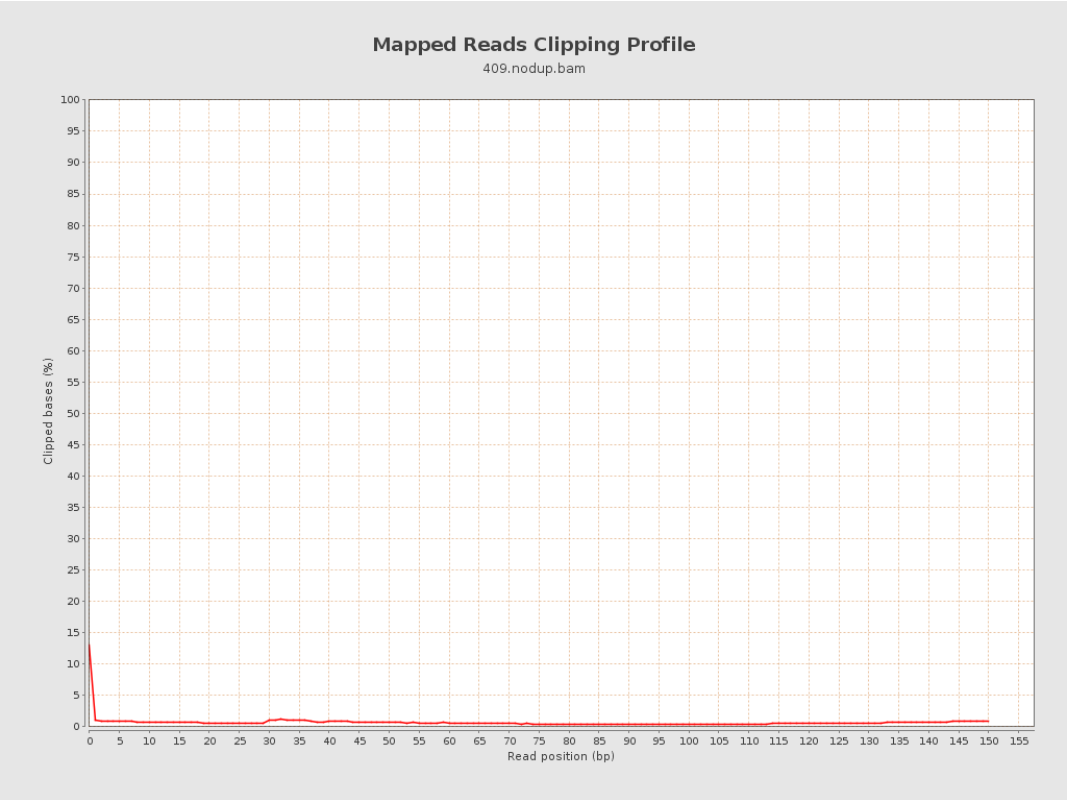
8. Results : Mapped Reads Nucleotide Content



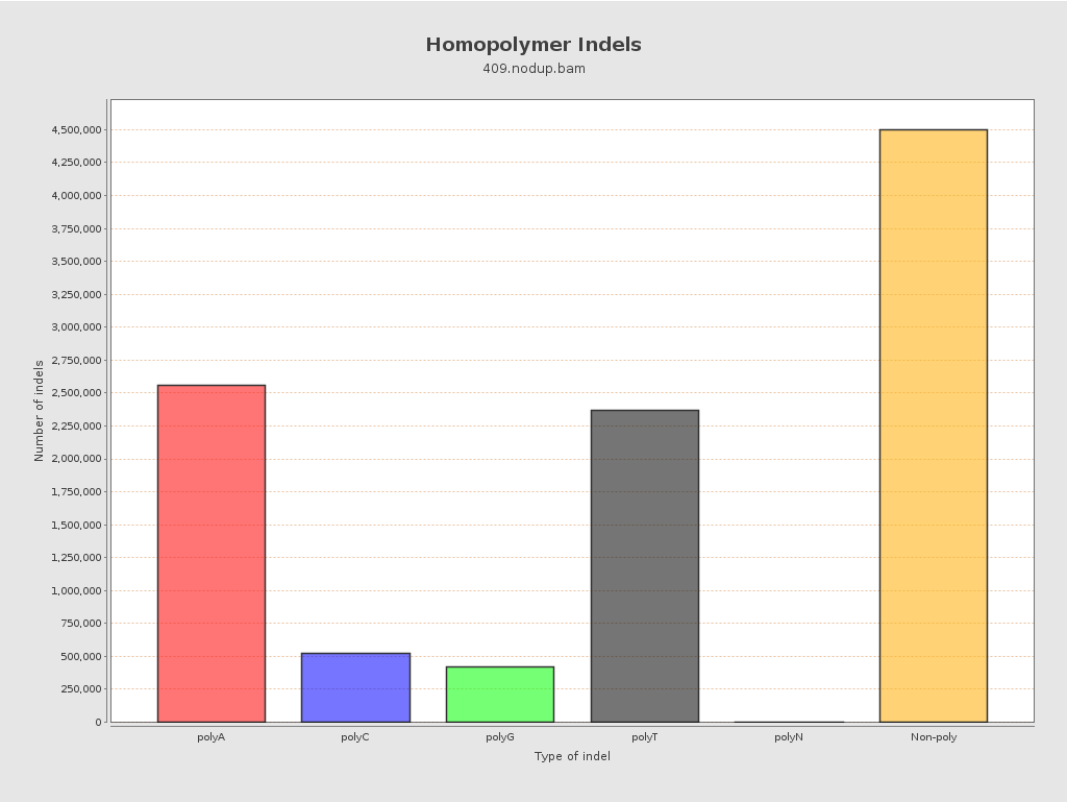
9. Results : Mapped Reads GC-content Distribution



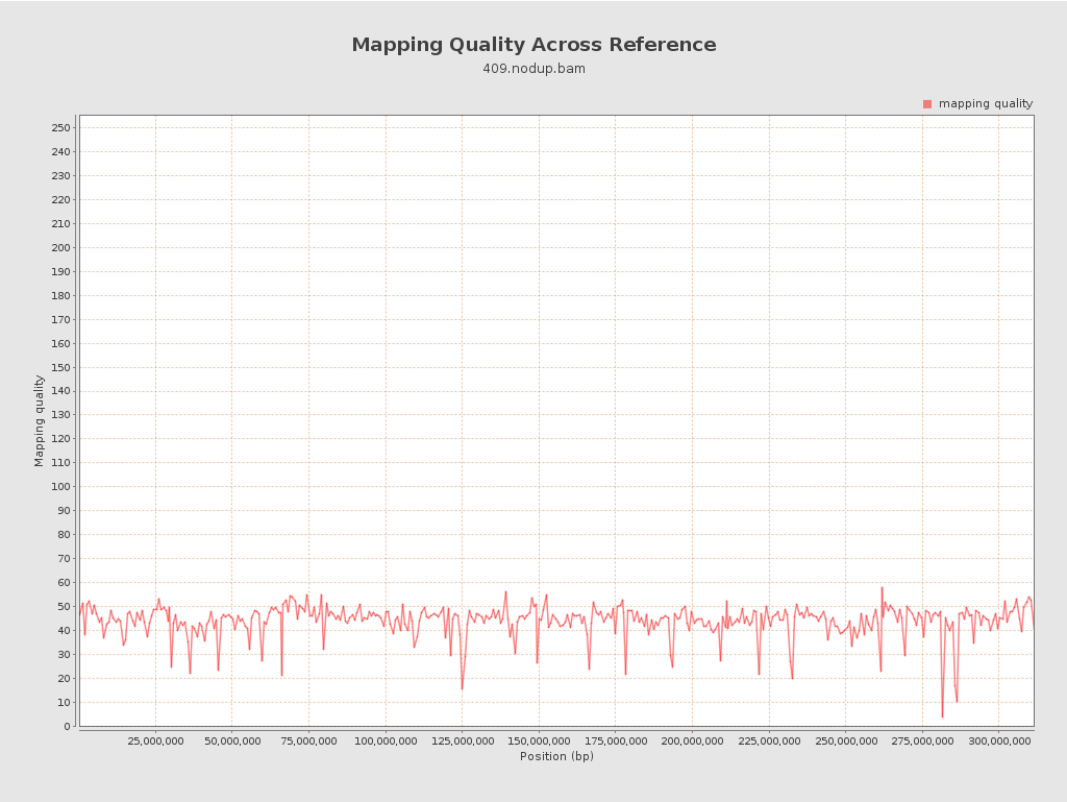
10. Results : Mapped Reads Clipping Profile



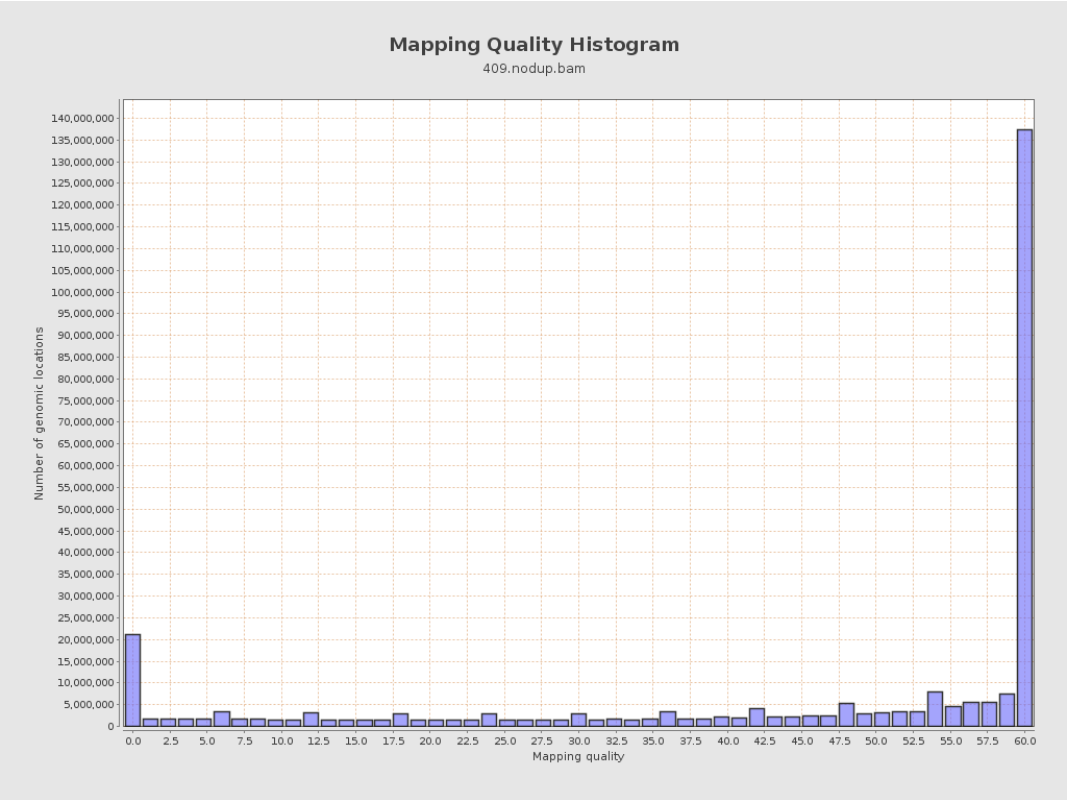
11. Results : Homopolymer Indels



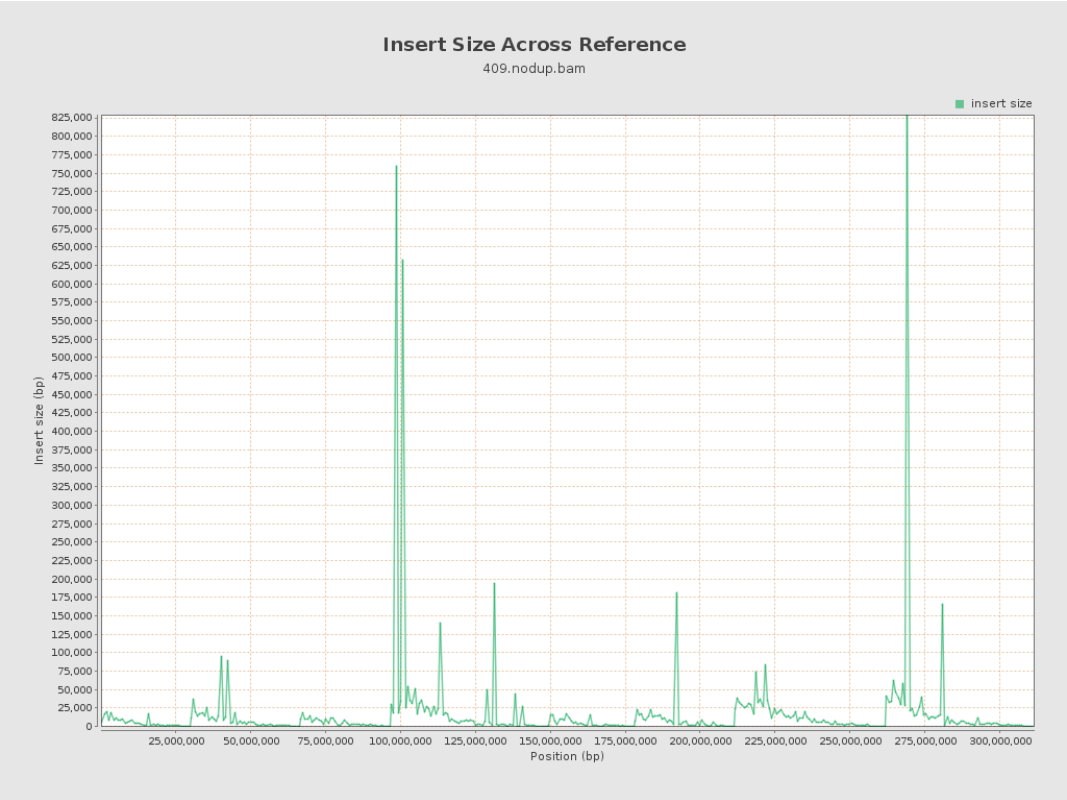
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram