Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:50:39

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397N .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397N .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_590/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_590_S157_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_590/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_590_S157_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:50:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	115,595,637
Mapped reads	107,802,558 / 93.26%
Unmapped reads	7,793,079 / 6.74%
Mapped paired reads	107,802,558 / 93.26%
Mapped reads, first in pair	54,070,031 / 46.78%
Mapped reads, second in pair	53,732,527 / 46.48%
Mapped reads, both in pair	105,157,392 / 90.97%
Mapped reads, singletons	2,645,166 / 2.29%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	18,184,318 / 15.73%
Clipped reads	25,532,476 / 22.09%

2.2. ACGT Content

Number/percentage of A's	4,583,039,737 / 30.88%
Number/percentage of C's	2,838,182,644 / 19.12%
Number/percentage of T's	4,587,250,080 / 30.91%
Number/percentage of G's	2,833,846,574 / 19.09%
Number/percentage of N's	69,678 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	47.7488
Standard Deviation	396.4957

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Insert size

Mean	235,973.7
Standard Deviation	2,317,896.61
P25/Median/P75	317 / 421 / 553

2.6. Mismatches and indels

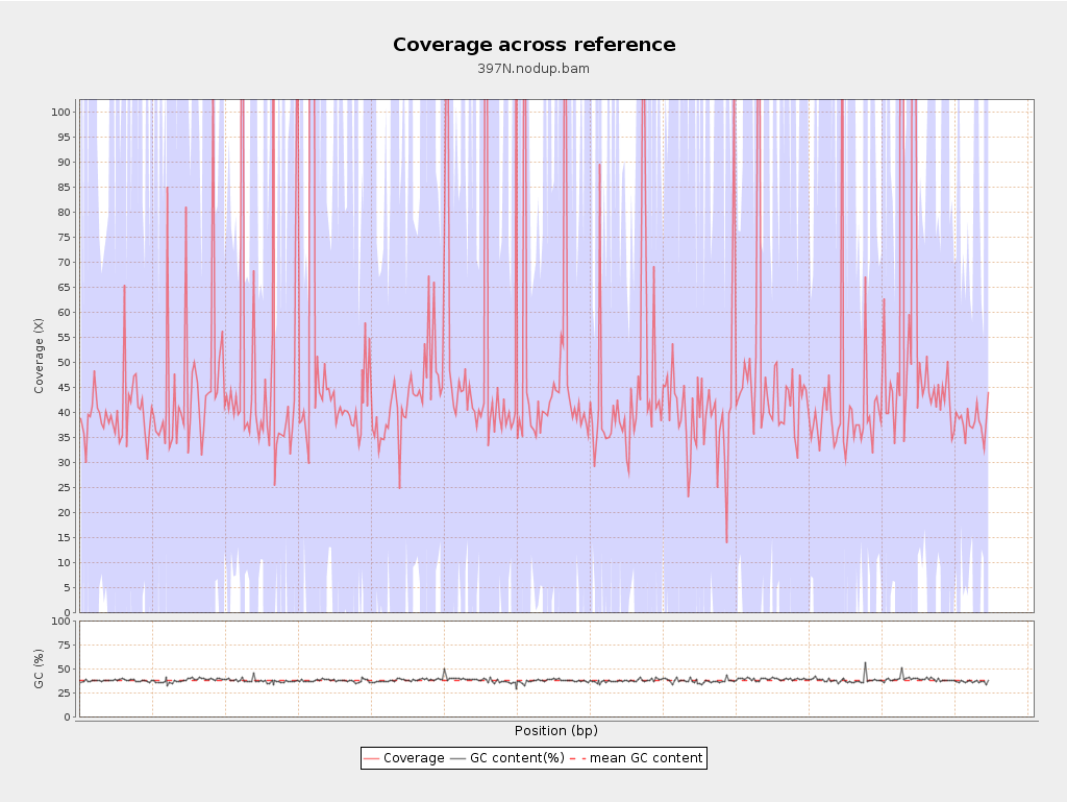
General error rate	2.41%
Mismatches	329,172,490
Insertions	10,272,402
Mapped reads with at least one insertion	8.53%
Deletions	10,191,693
Mapped reads with at least one deletion	8.4%
Homopolymer indels	56.63%

2.7. Chromosome stats

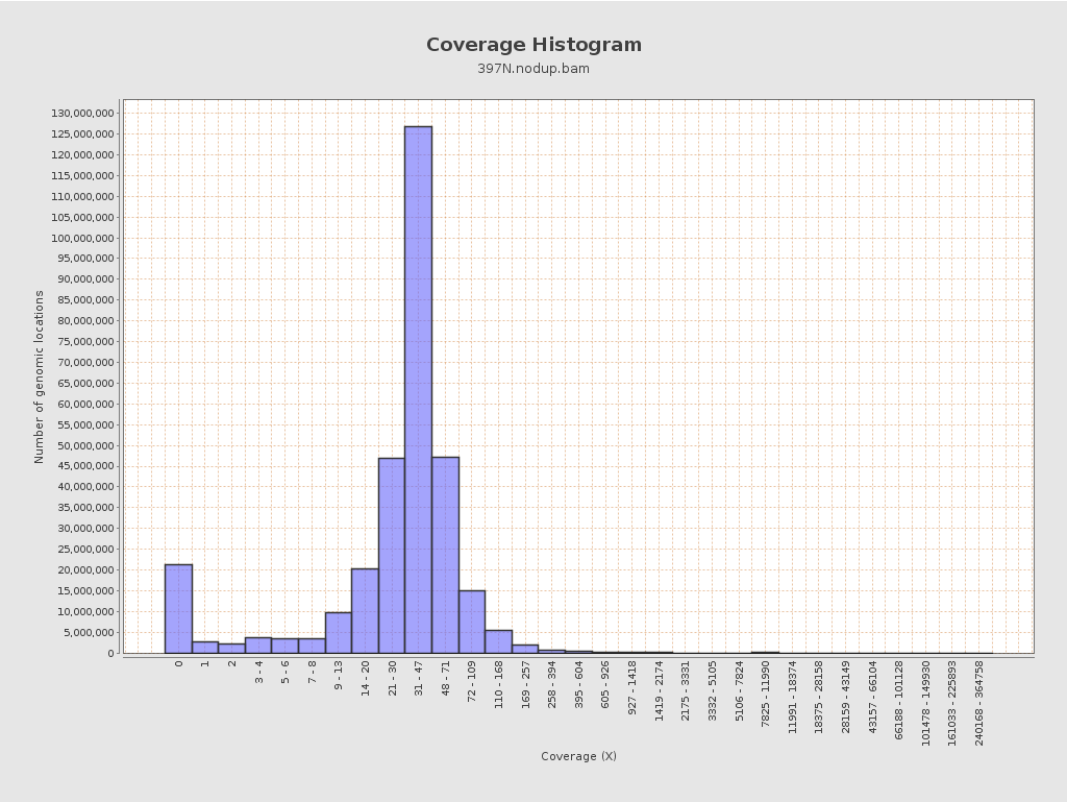
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1171423394	39.4096	134.8621

LT669789.1	36598175	1757937196	48.0335	408.6389
LT669790.1	30422129	1654840881	54.396	487.5364
LT669791.1	52758100	2479177325	46.9914	383.2184
LT669792.1	28376109	1356407426	47.801	428.2188
LT669793.1	33388210	1457218639	43.6447	268.3397
LT669794.1	50579949	2265968876	44.7997	336.0305
LT669795.1	49795044	2737550051	54.9764	530.9213

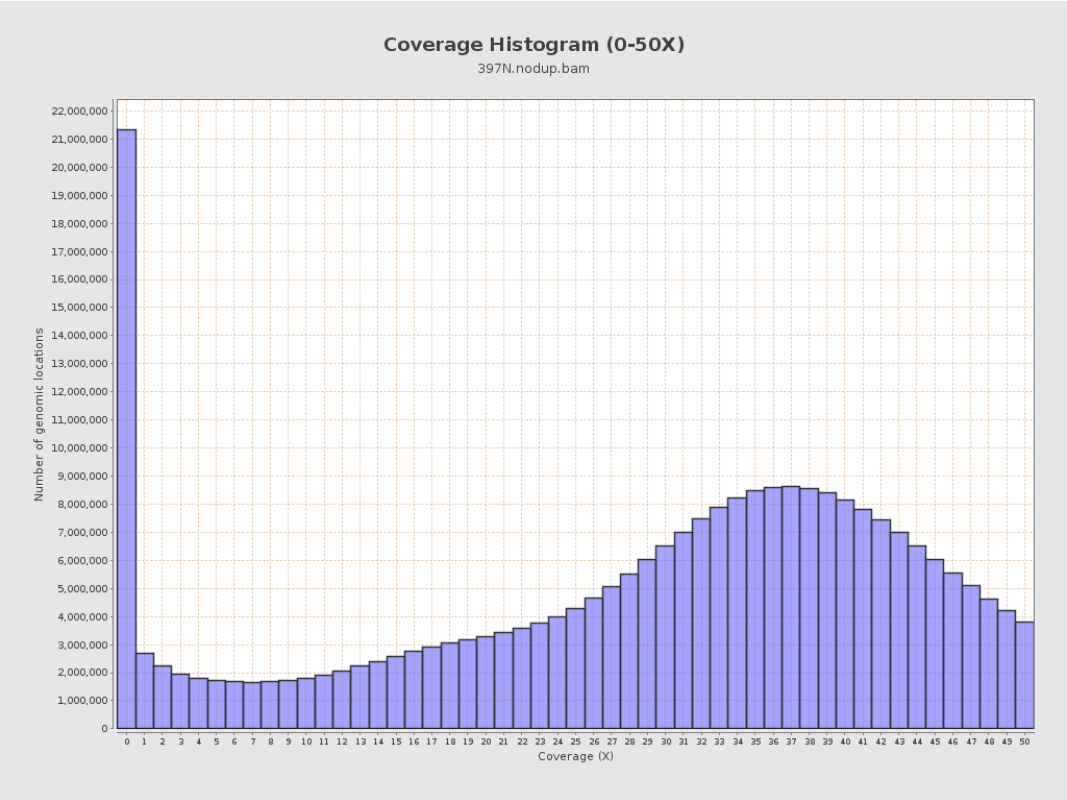
3. Results : Coverage across reference



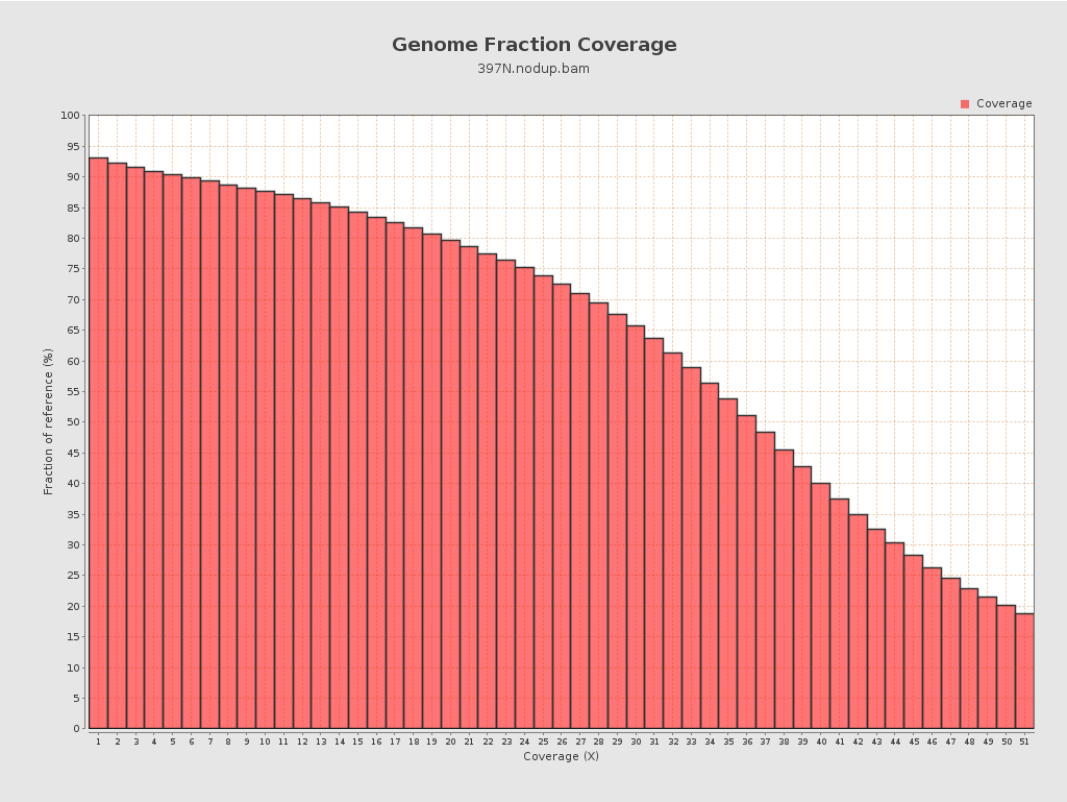
4. Results : Coverage Histogram



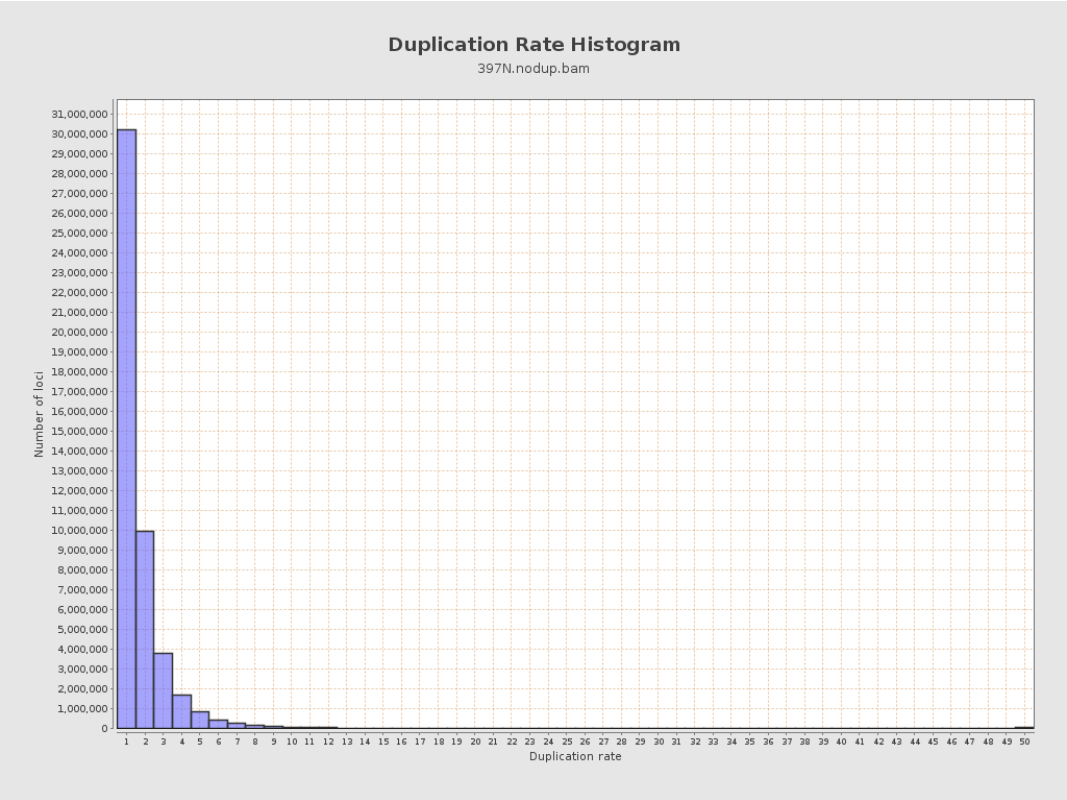
5. Results : Coverage Histogram (0-50X)



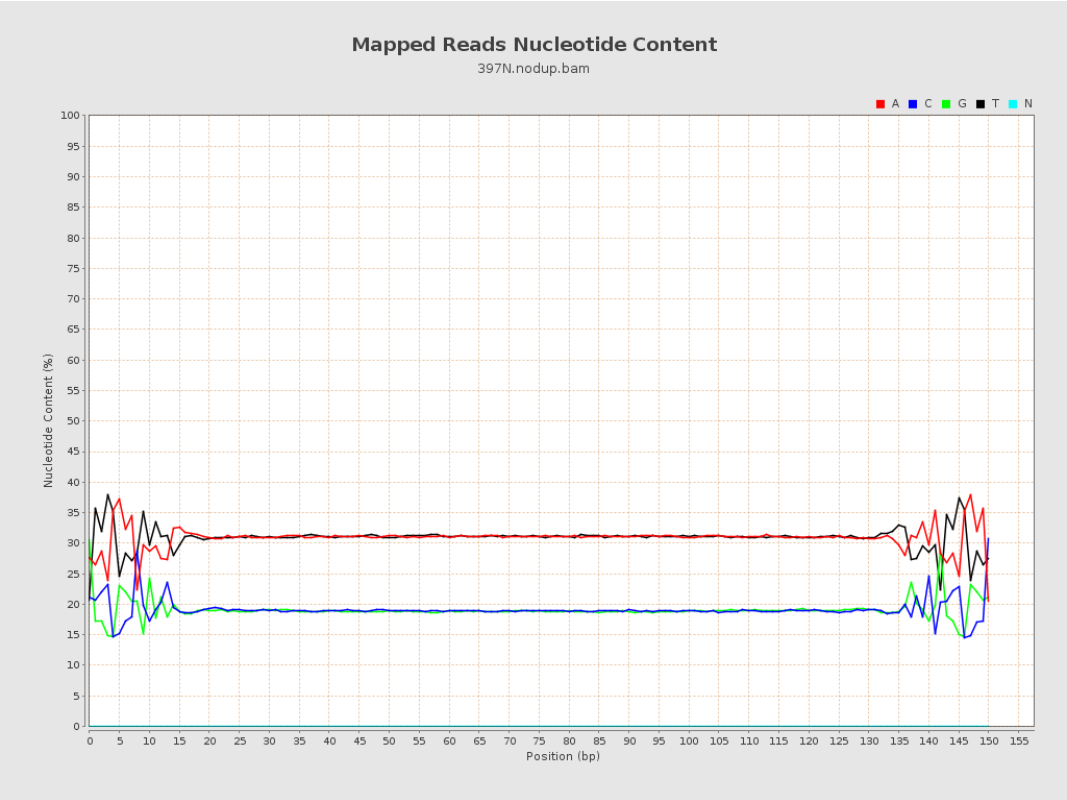
6. Results : Genome Fraction Coverage



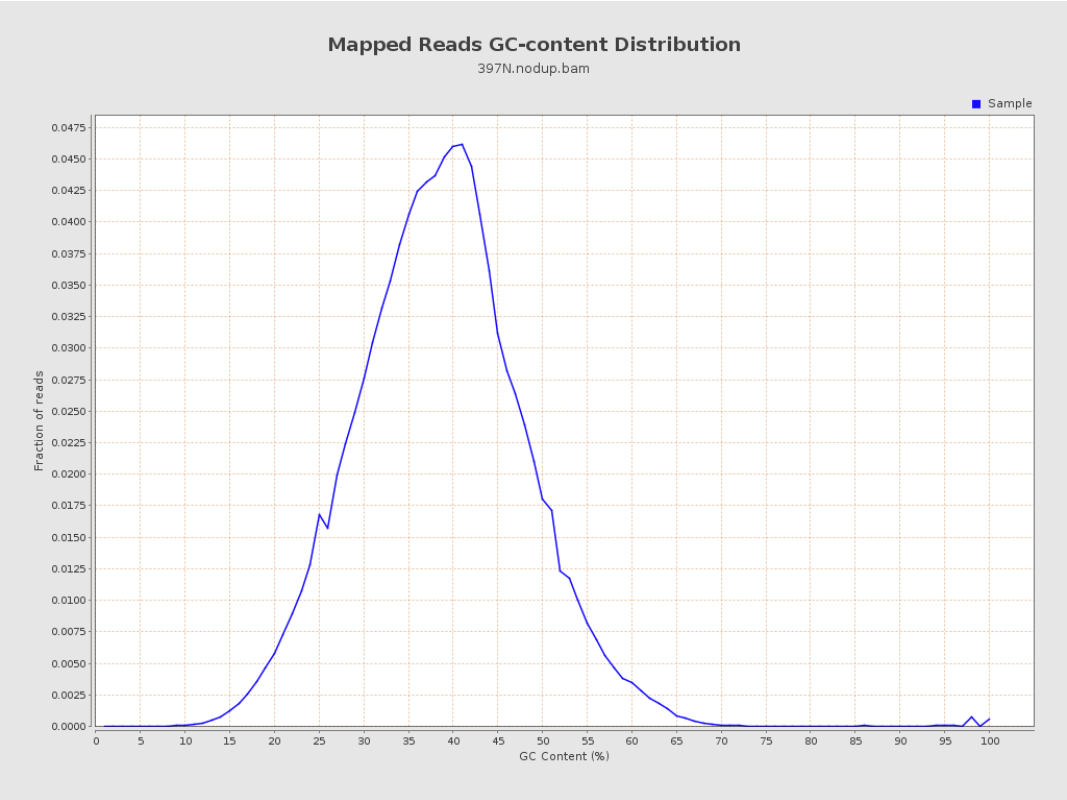
7. Results : Duplication Rate Histogram



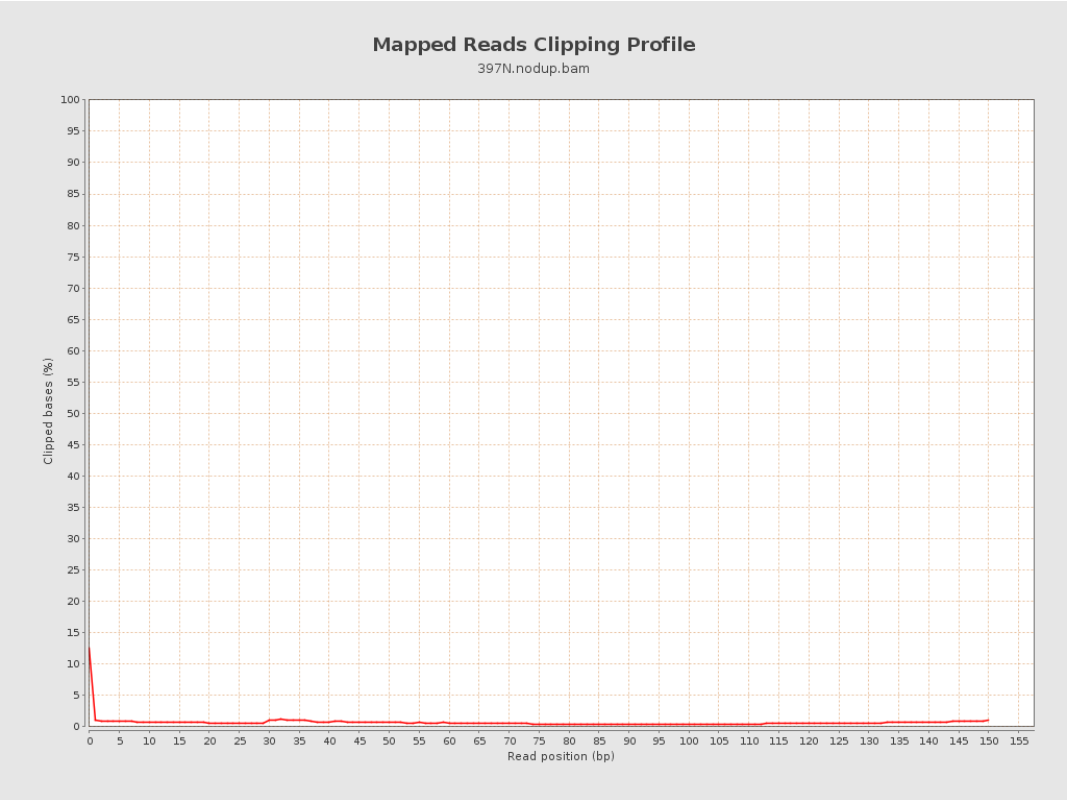
8. Results : Mapped Reads Nucleotide Content



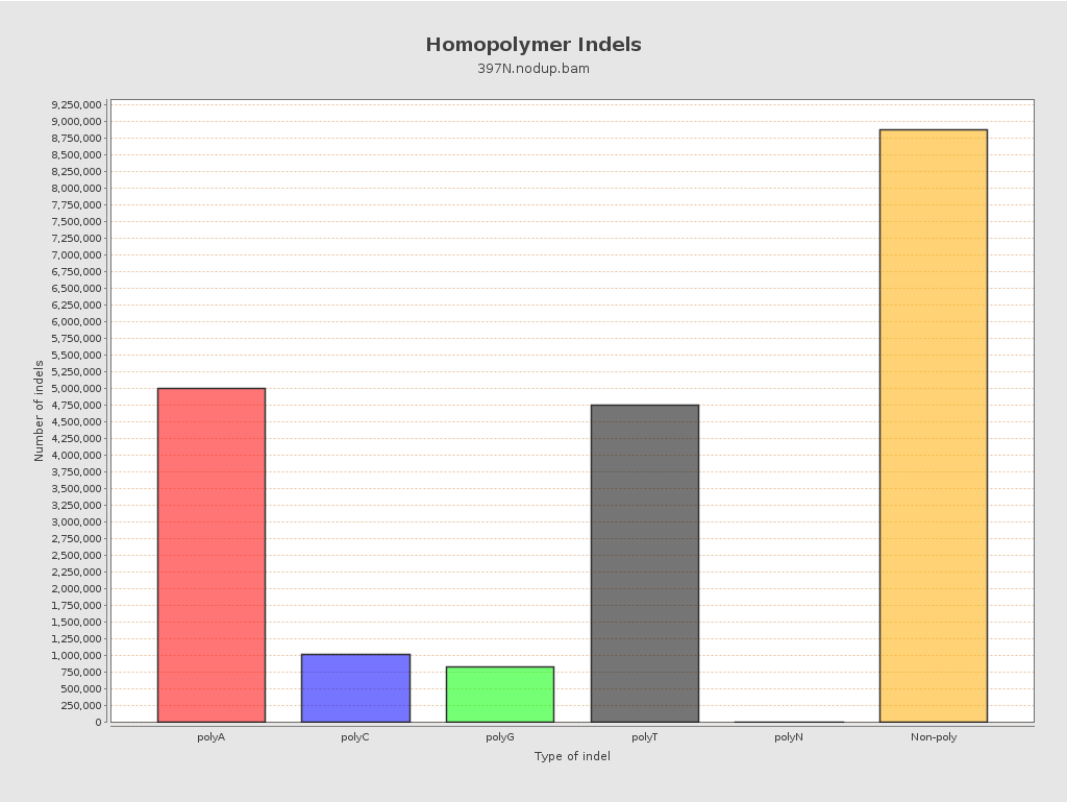
9. Results : Mapped Reads GC-content Distribution



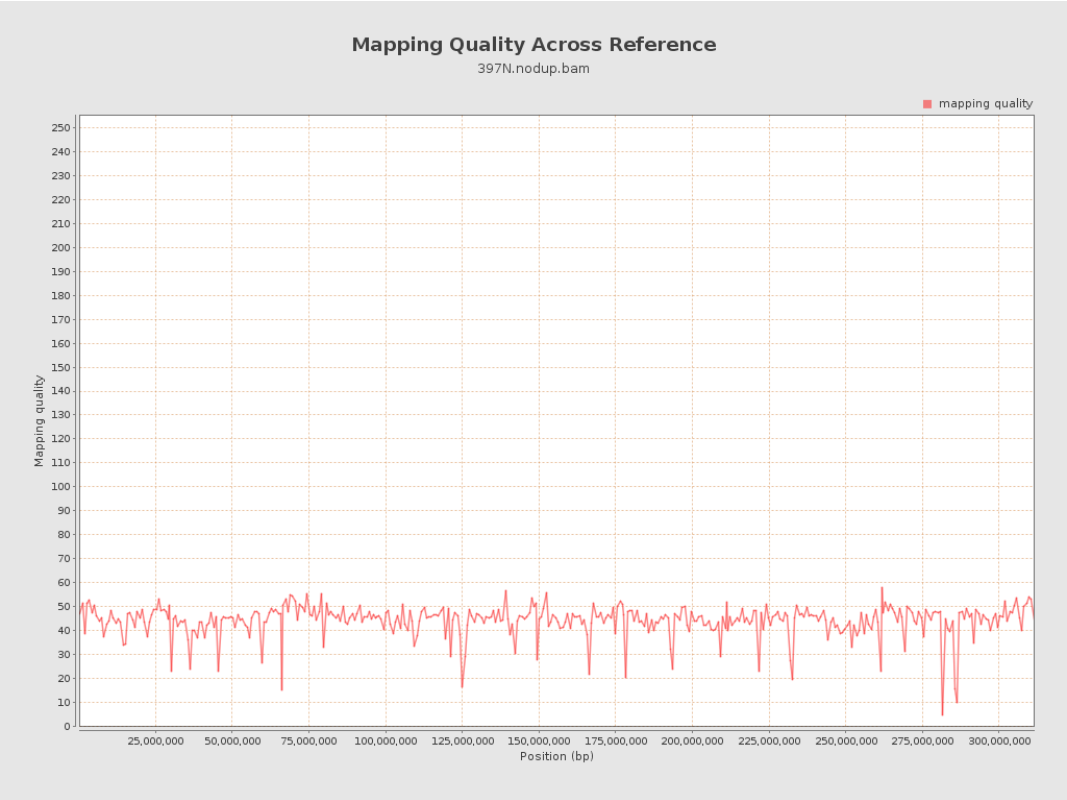
10. Results : Mapped Reads Clipping Profile



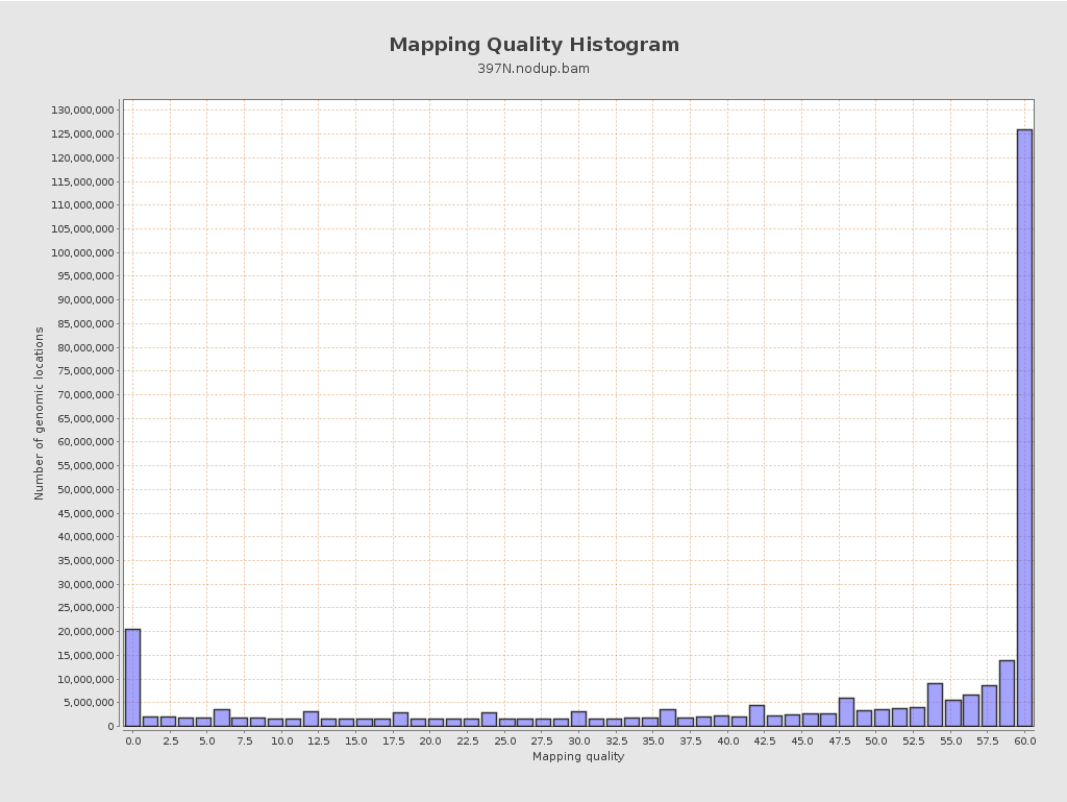
11. Results : Homopolymer Indels



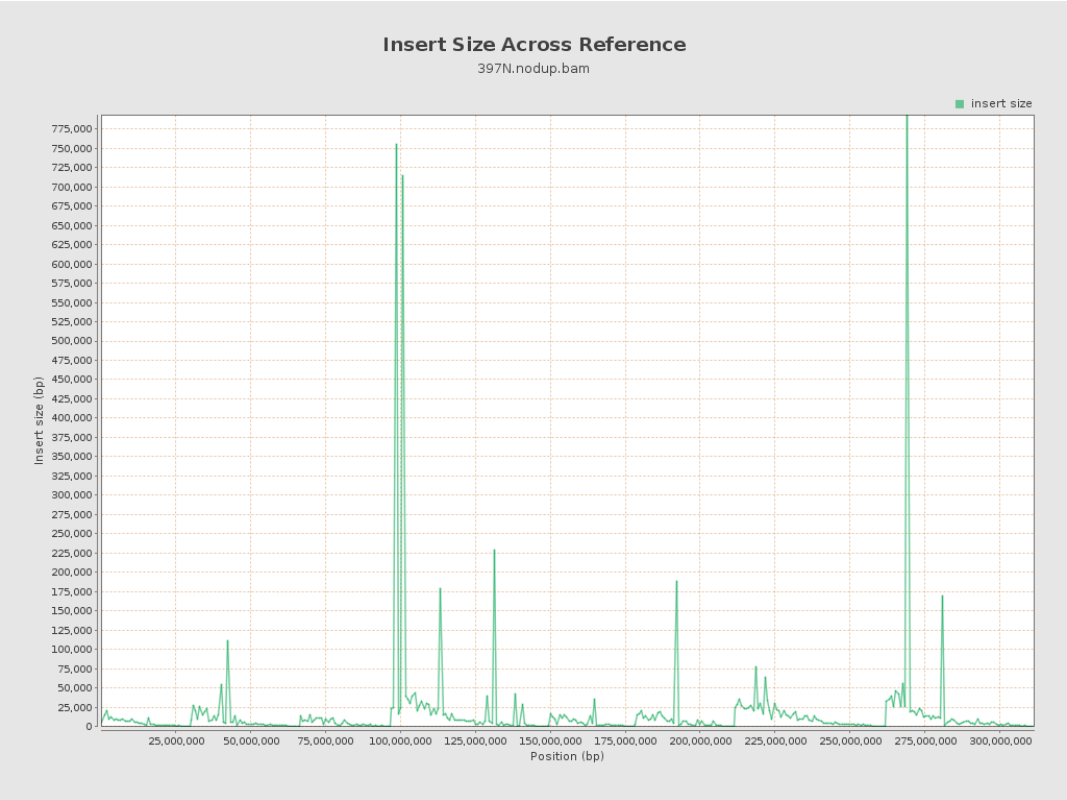
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram