Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:19

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1231 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1231 .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_175/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_175_S265_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_175/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_175_S265_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:18 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,945,833
Mapped reads	54,639,672 / 92.69%
Unmapped reads	4,306,161 / 7.31%
Mapped paired reads	54,639,672 / 92.69%
Mapped reads, first in pair	27,384,479 / 46.46%
Mapped reads, second in pair	27,255,193 / 46.24%
Mapped reads, both in pair	53,210,633 / 90.27%
Mapped reads, singletons	1,429,039 / 2.42%
Read min/max/mean length	30 / 151 / 147.96
Duplicated reads (flagged)	8,935,230 / 15.16%
Clipped reads	12,991,844 / 22.04%

2.2. ACGT Content

Number/percentage of A's	2,313,449,698 / 30.81%
Number/percentage of C's	1,440,584,693 / 19.19%
Number/percentage of T's	2,315,056,026 / 30.83%
Number/percentage of G's	1,439,775,847 / 19.17%
Number/percentage of N's	31,923 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	24.1582
Standard Deviation	202.5727

2.4. Mapping Quality

Mean Mapping Quality	43.71

2.5. Insert size

Mean	255,875.41
Standard Deviation	2,412,167.16
P25/Median/P75	325 / 429 / 561

2.6. Mismatches and indels

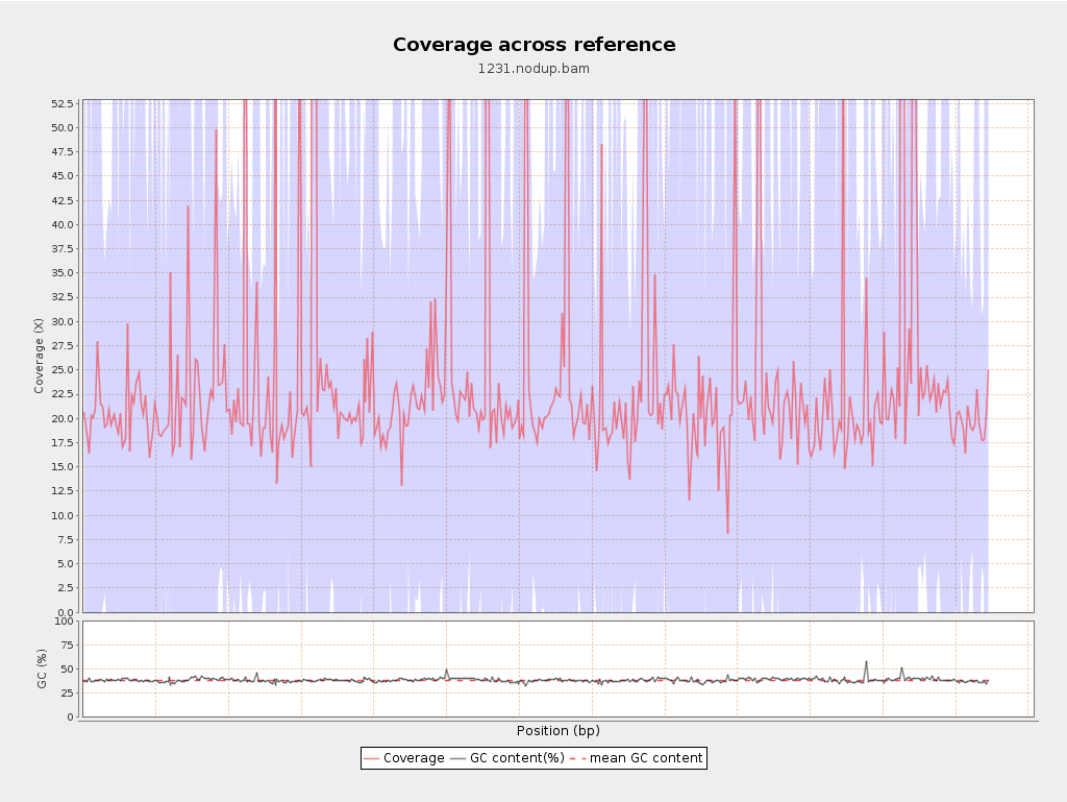
General error rate	2.39%
Mismatches	164,349,192
Insertions	5,364,755
Mapped reads with at least one insertion	8.78%
Deletions	5,253,903
Mapped reads with at least one deletion	8.51%
Homopolymer indels	56.47%

2.7. Chromosome stats

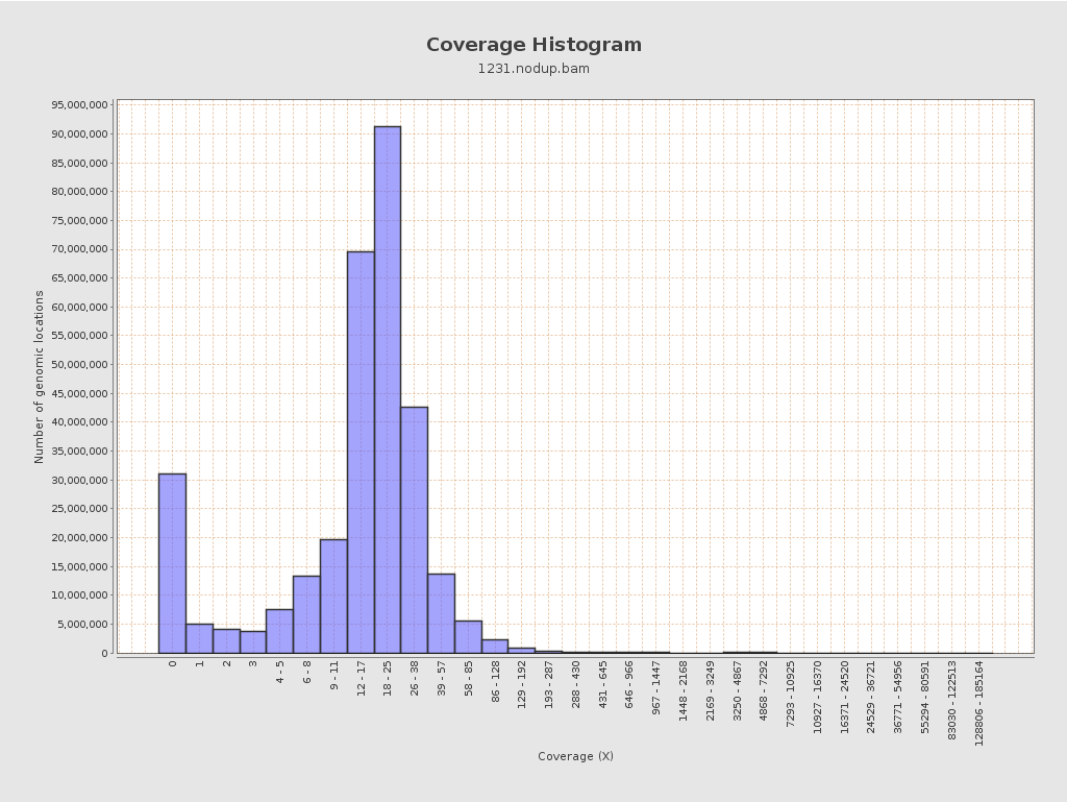
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	604148321	20.325	72.7492

LT669789.1	36598175	892959536	24.399	215.4676
LT669790.1	30422129	863209864	28.3744	259.7339
LT669791.1	52758100	1249123182	23.6764	202.0255
LT669792.1	28376109	682776807	24.0617	228.6169
LT669793.1	33388210	750377645	22.4743	136.8321
LT669794.1	50579949	1143065292	22.5992	162.7792
LT669795.1	49795044	1343040322	26.9714	256.5091

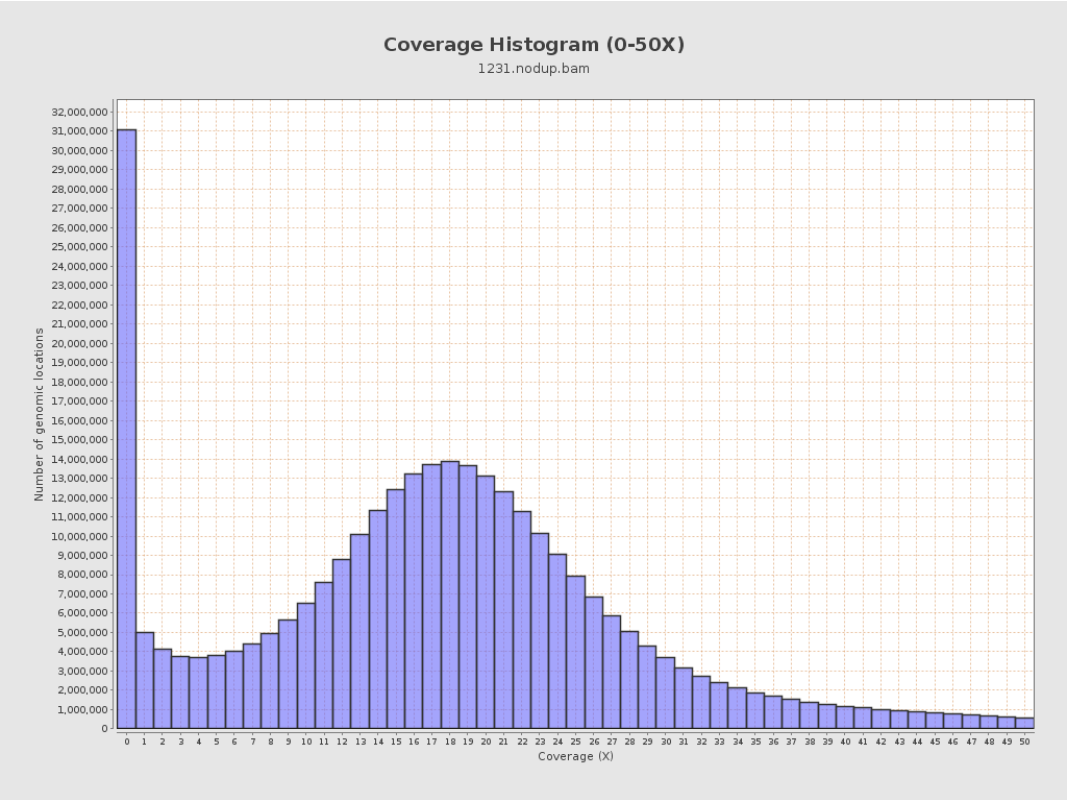
3. Results : Coverage across reference



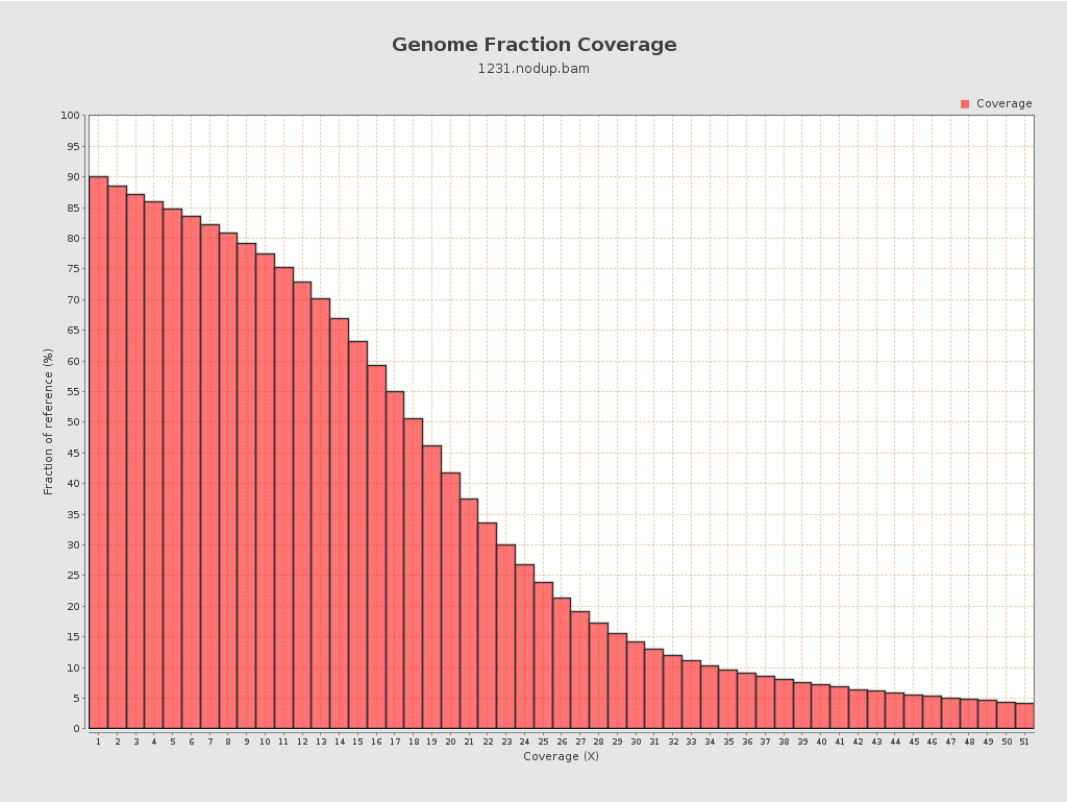
4. Results : Coverage Histogram



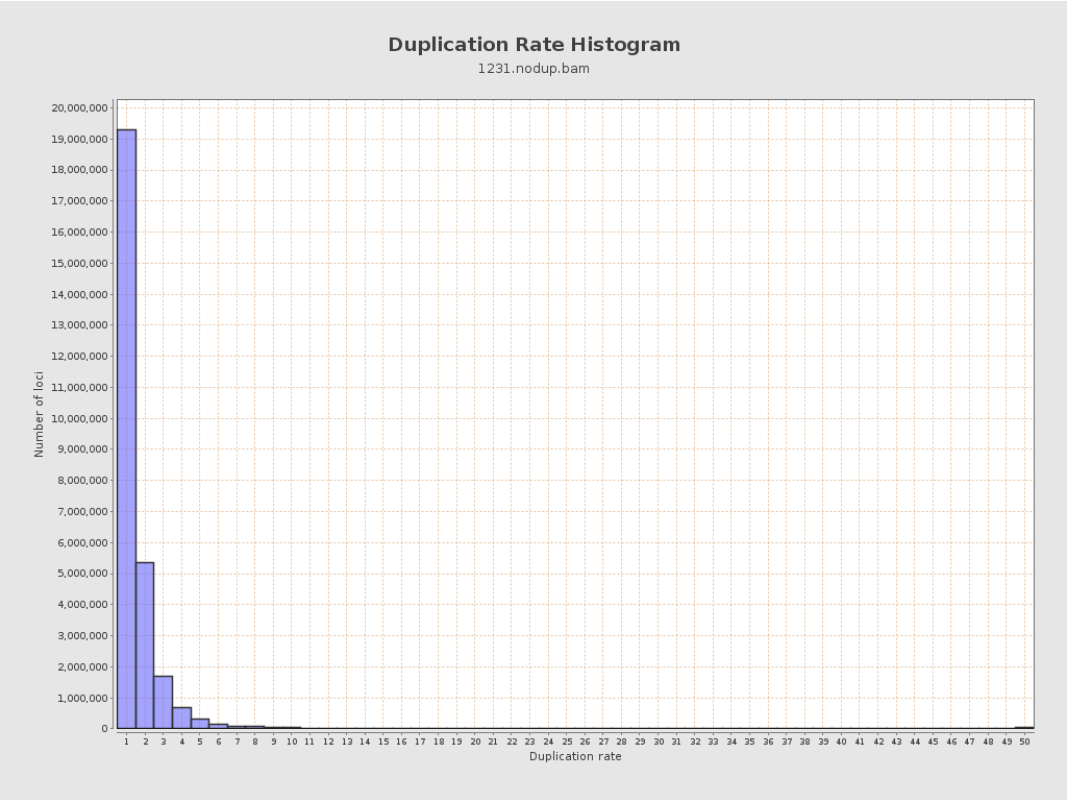
5. Results : Coverage Histogram (0-50X)



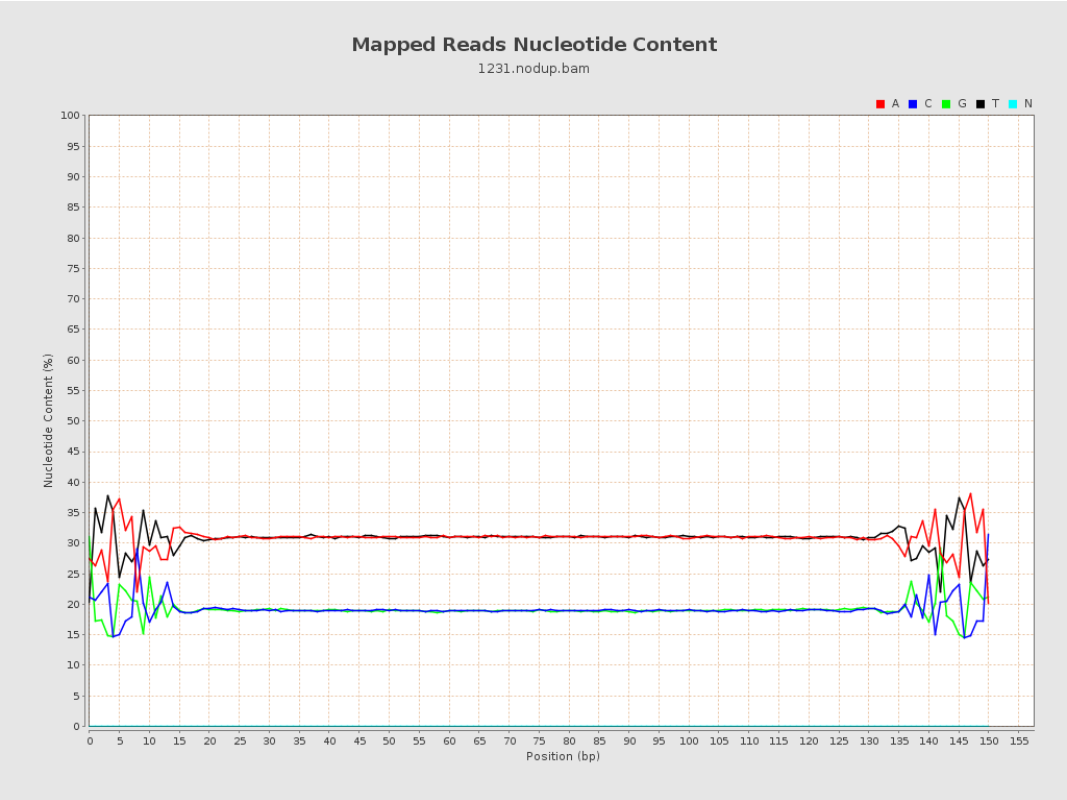
6. Results : Genome Fraction Coverage



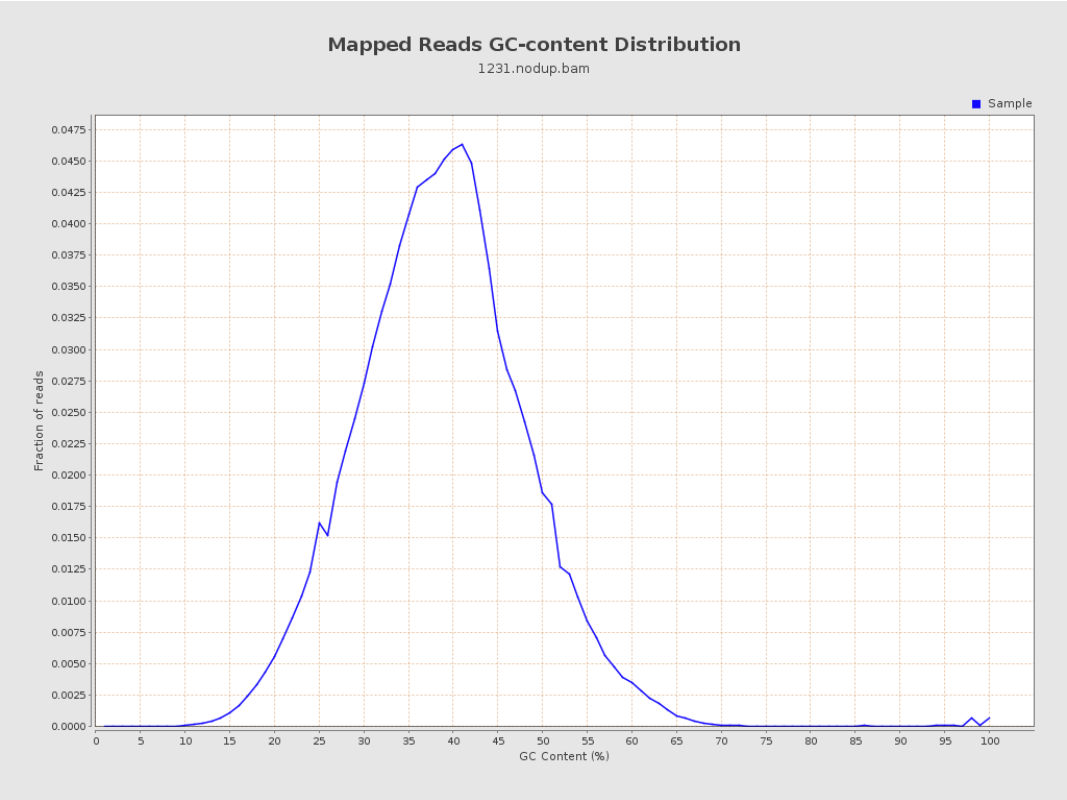
7. Results : Duplication Rate Histogram



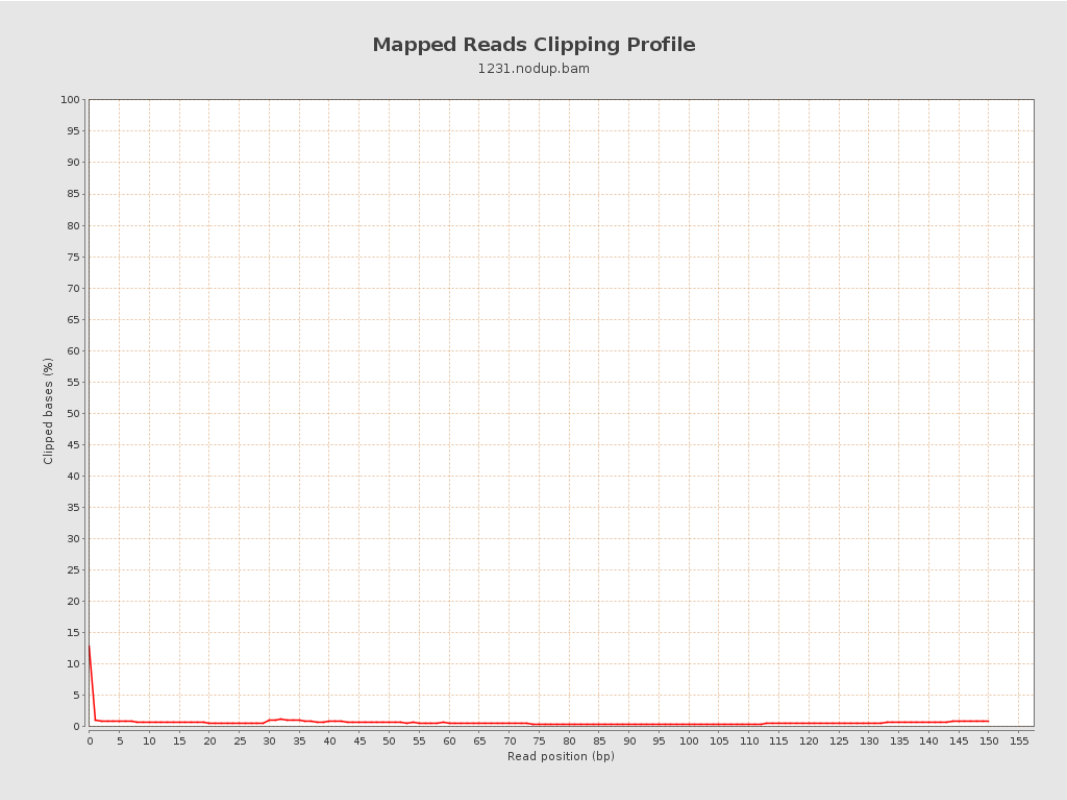
8. Results : Mapped Reads Nucleotide Content



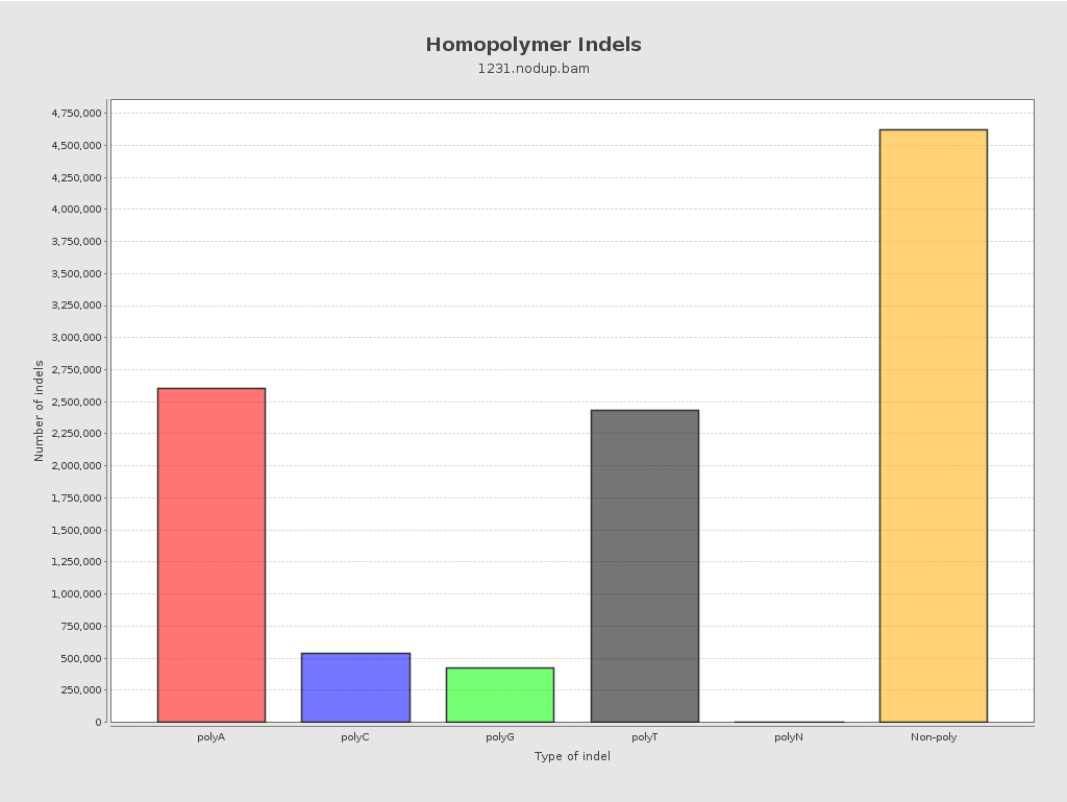
9. Results : Mapped Reads GC-content Distribution



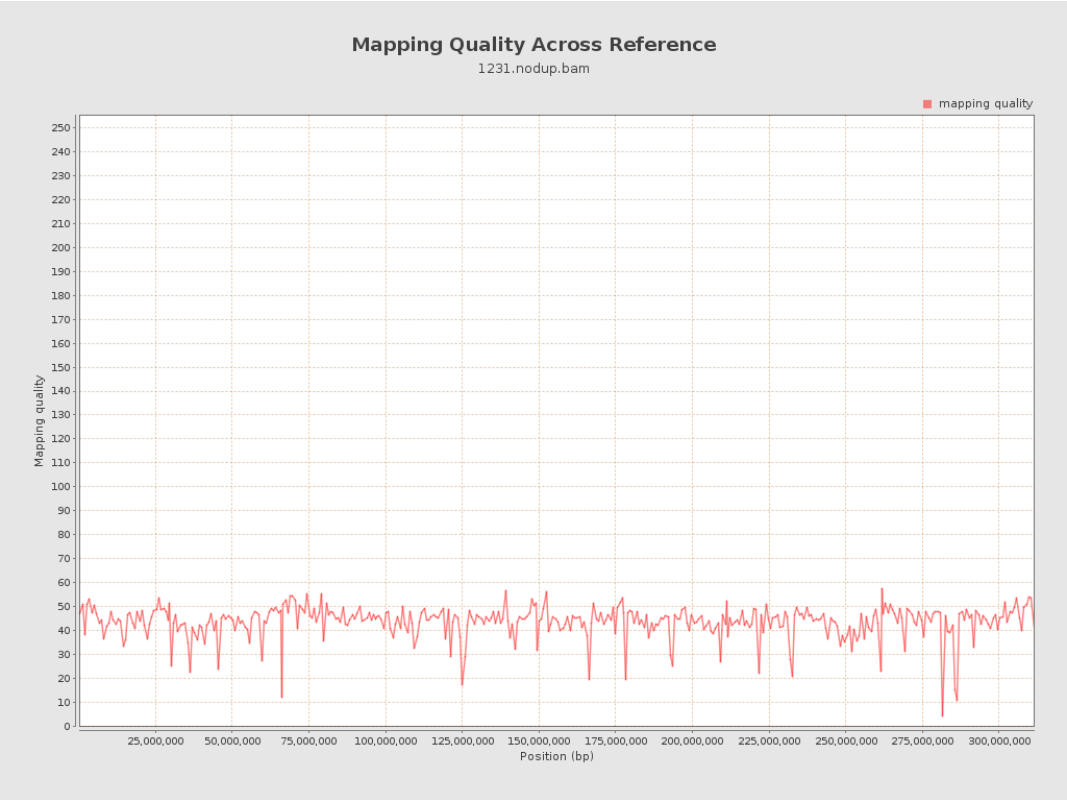
10. Results : Mapped Reads Clipping Profile



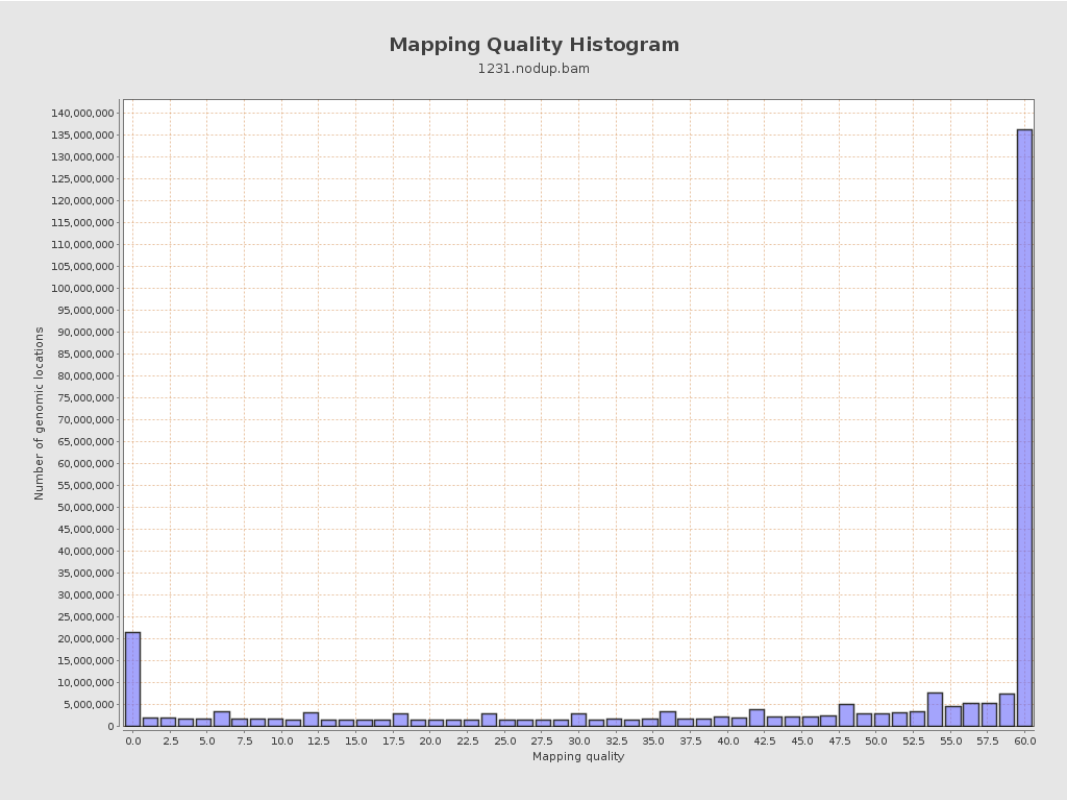
11. Results : Homopolymer Indels



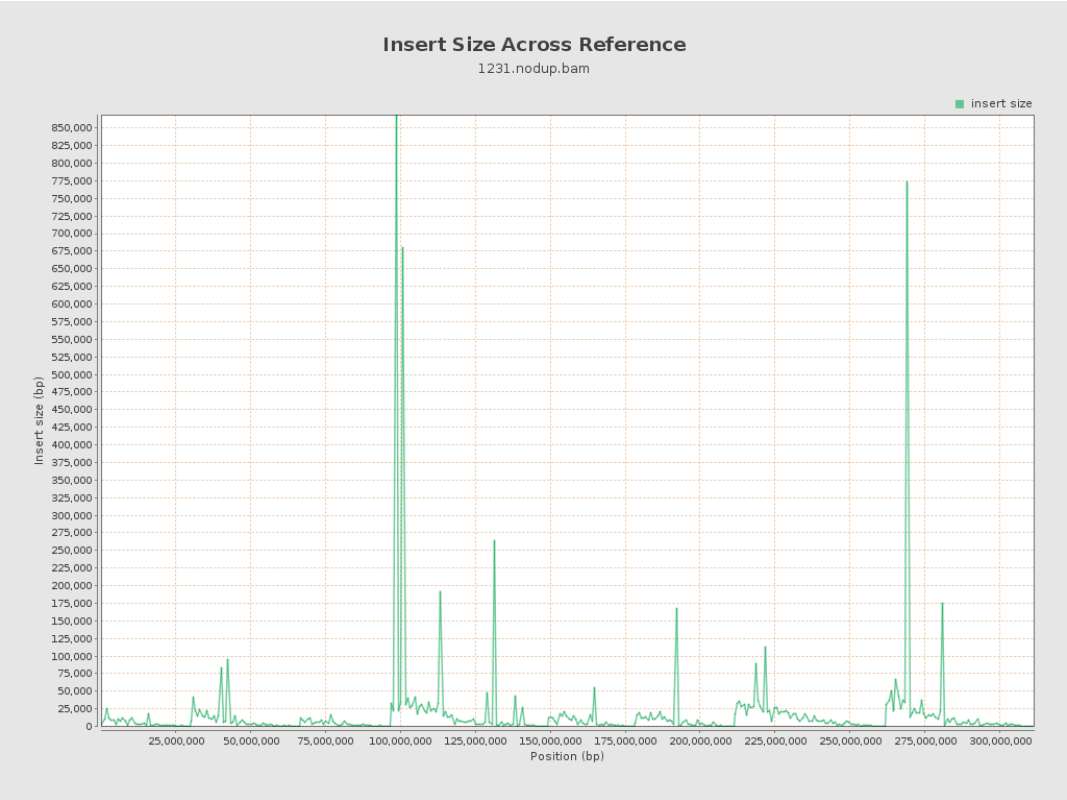
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram