Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:21

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1034 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1034 .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_239/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_239_S320_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_239/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_239_S320_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:36:20 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	84,738,991
Mapped reads	75,495,564 / 89.09%
Unmapped reads	9,243,427 / 10.91%
Mapped paired reads	75,495,564 / 89.09%
Mapped reads, first in pair	37,845,700 / 44.66%
Mapped reads, second in pair	37,649,864 / 44.43%
Mapped reads, both in pair	72,659,882 / 85.75%
Mapped reads, singletons	2,835,682 / 3.35%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	15,652,115 / 18.47%
Clipped reads	18,895,373 / 22.3%

2.2. ACGT Content

Number/percentage of A's	3,178,444,542 / 31.03%
Number/percentage of C's	1,942,402,425 / 18.96%
Number/percentage of T's	3,181,320,197 / 31.05%
Number/percentage of G's	1,941,995,287 / 18.96%
Number/percentage of N's	39,575 / 0%
GC Percentage	37.92%

2.3. Coverage

Mean	32.9541
Standard Deviation	381.3833

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Insert size

Mean	253,161.09
Standard Deviation	2,463,567.29
P25/Median/P75	296 / 390 / 509

2.6. Mismatches and indels

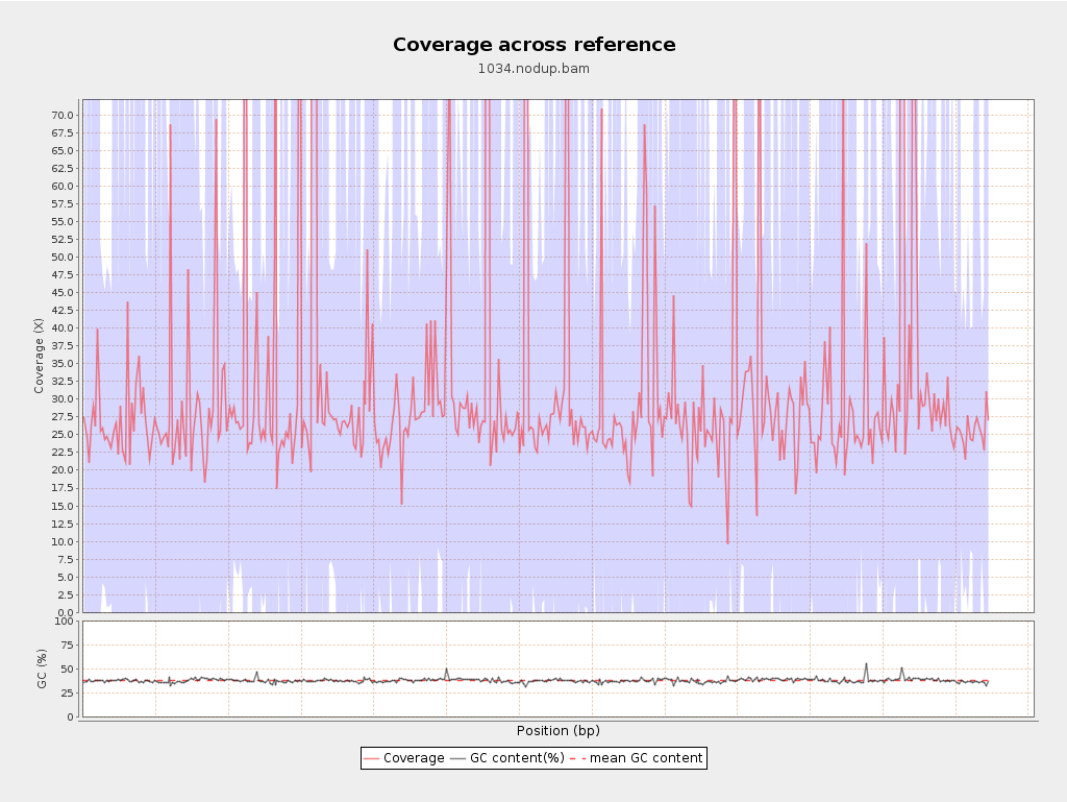
General error rate	2.36%
Mismatches	220,265,134
Insertions	7,795,273
Mapped reads with at least one insertion	9.16%
Deletions	7,054,334
Mapped reads with at least one deletion	8.29%
Homopolymer indels	58.27%

2.7. Chromosome stats

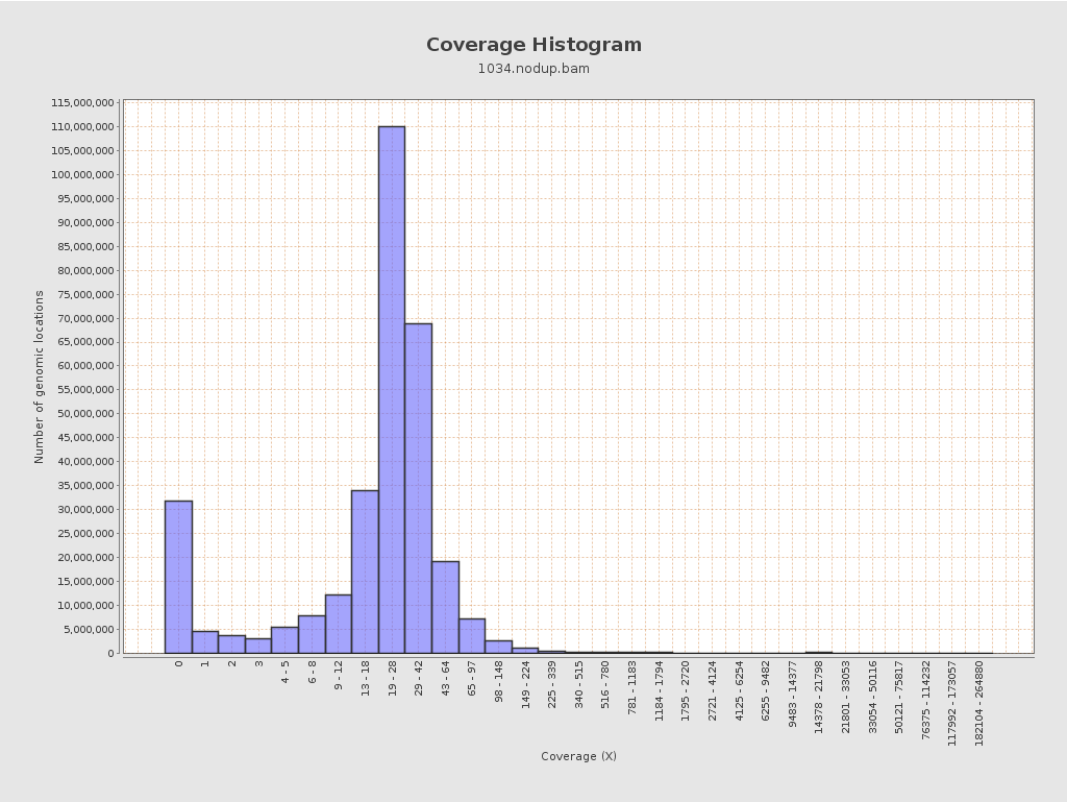
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	791663540	26.6335	164.0699

LT669789.1	36598175	1183671984	32.3424	393.4254
LT669790.1	30422129	1346776723	44.2696	612.9275
LT669791.1	52758100	1730343363	32.7977	445.75
LT669792.1	28376109	946800375	33.3661	389.0192
LT669793.1	33388210	965965857	28.9313	207.8011
LT669794.1	50579949	1526522056	30.1804	301.9418
LT669795.1	49795044	1778151735	35.7094	364.037

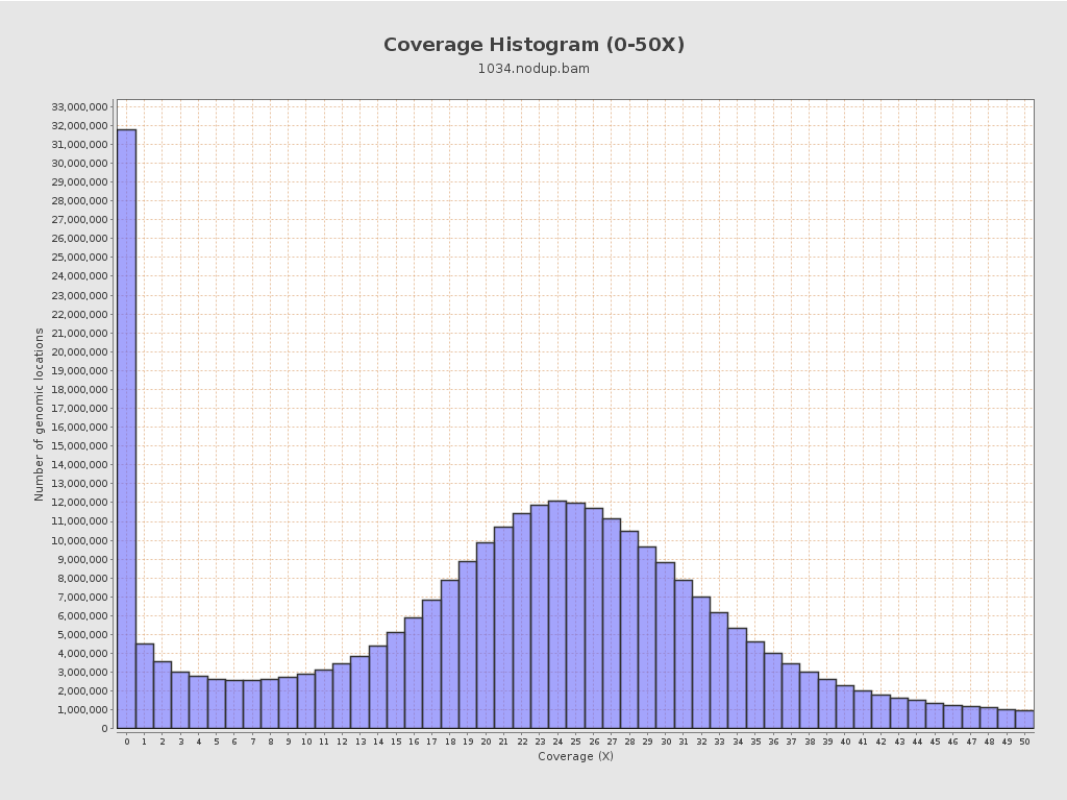
3. Results : Coverage across reference



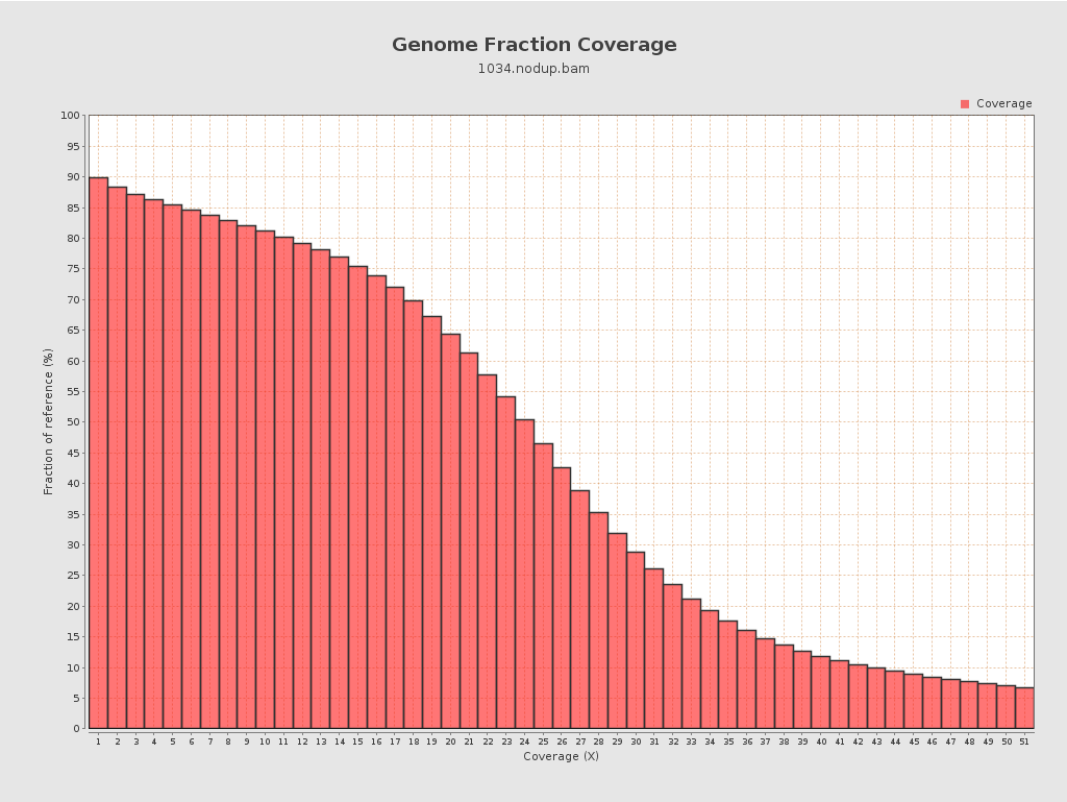
4. Results : Coverage Histogram



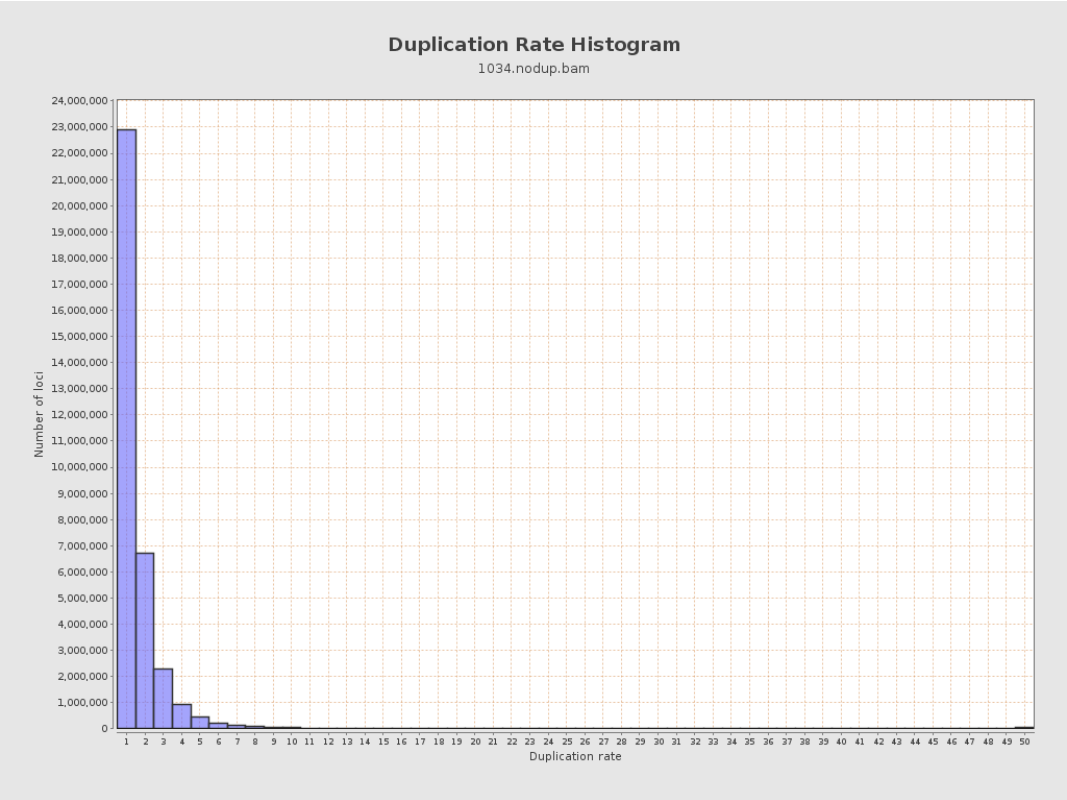
5. Results : Coverage Histogram (0-50X)



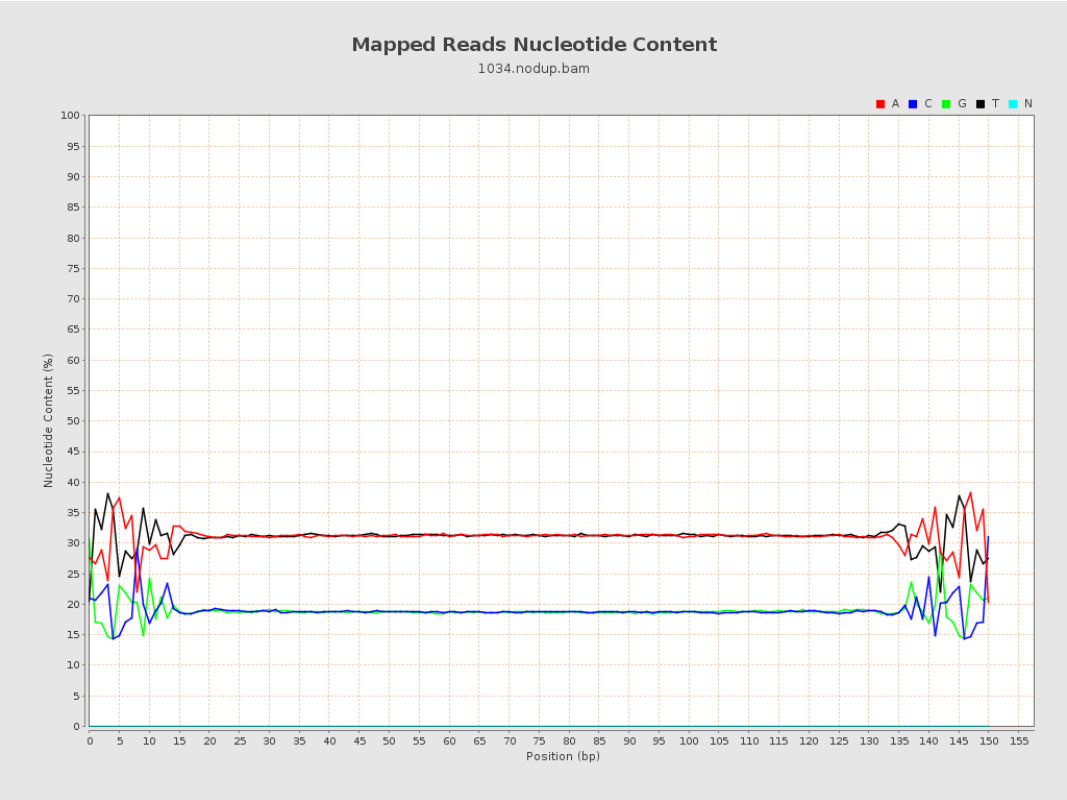
6. Results : Genome Fraction Coverage



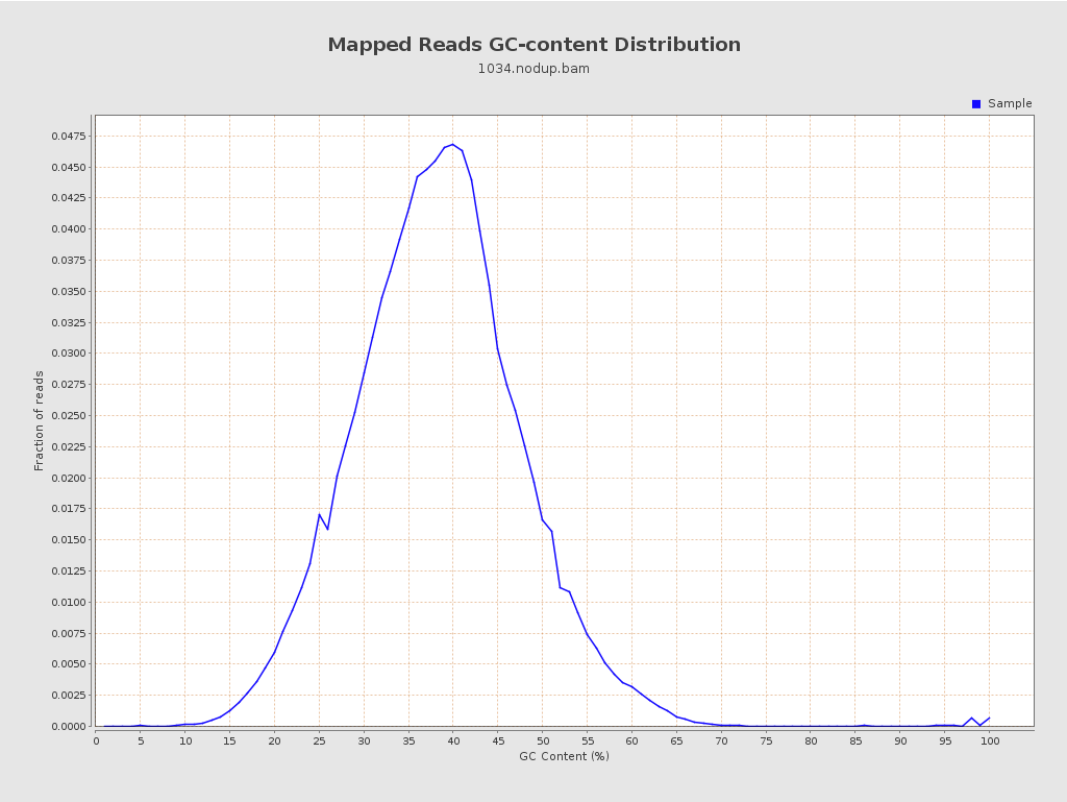
7. Results : Duplication Rate Histogram



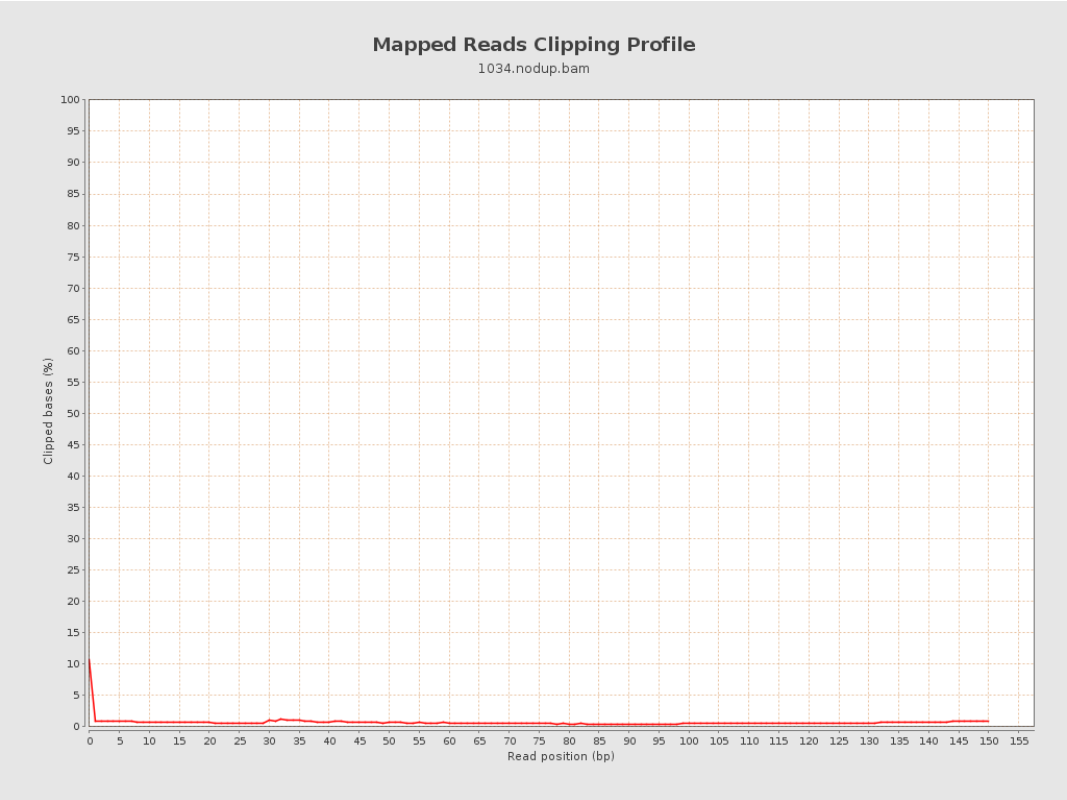
8. Results : Mapped Reads Nucleotide Content



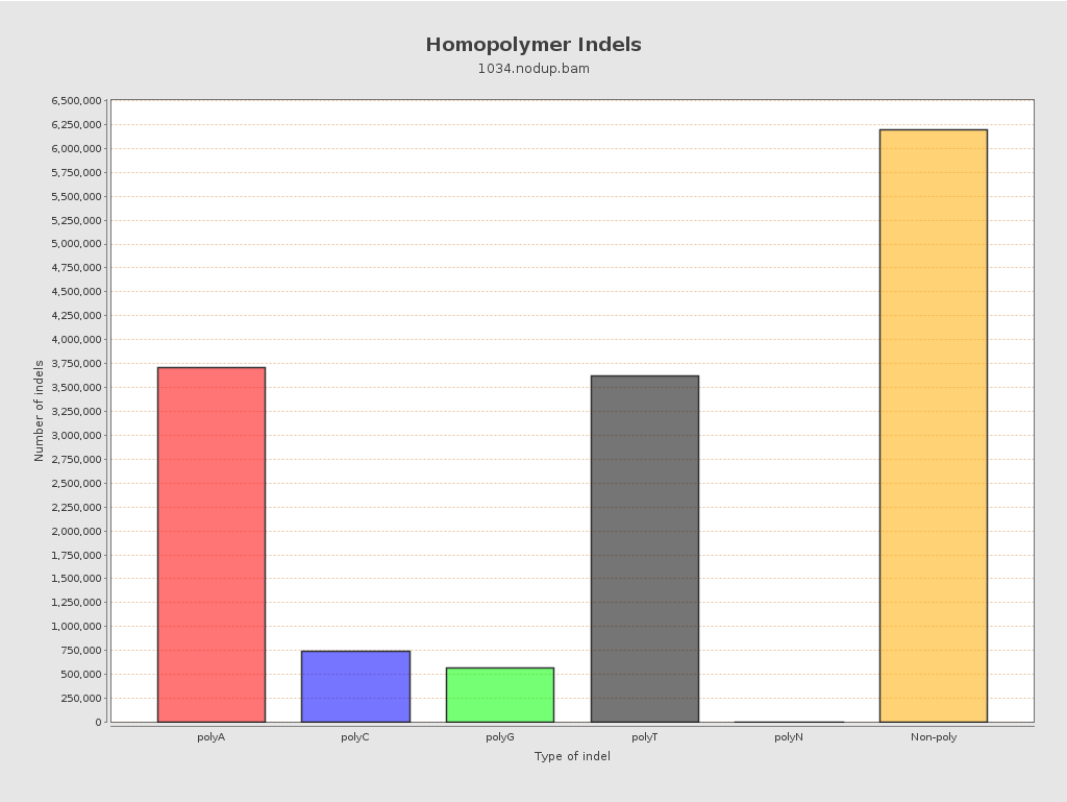
9. Results : Mapped Reads GC-content Distribution



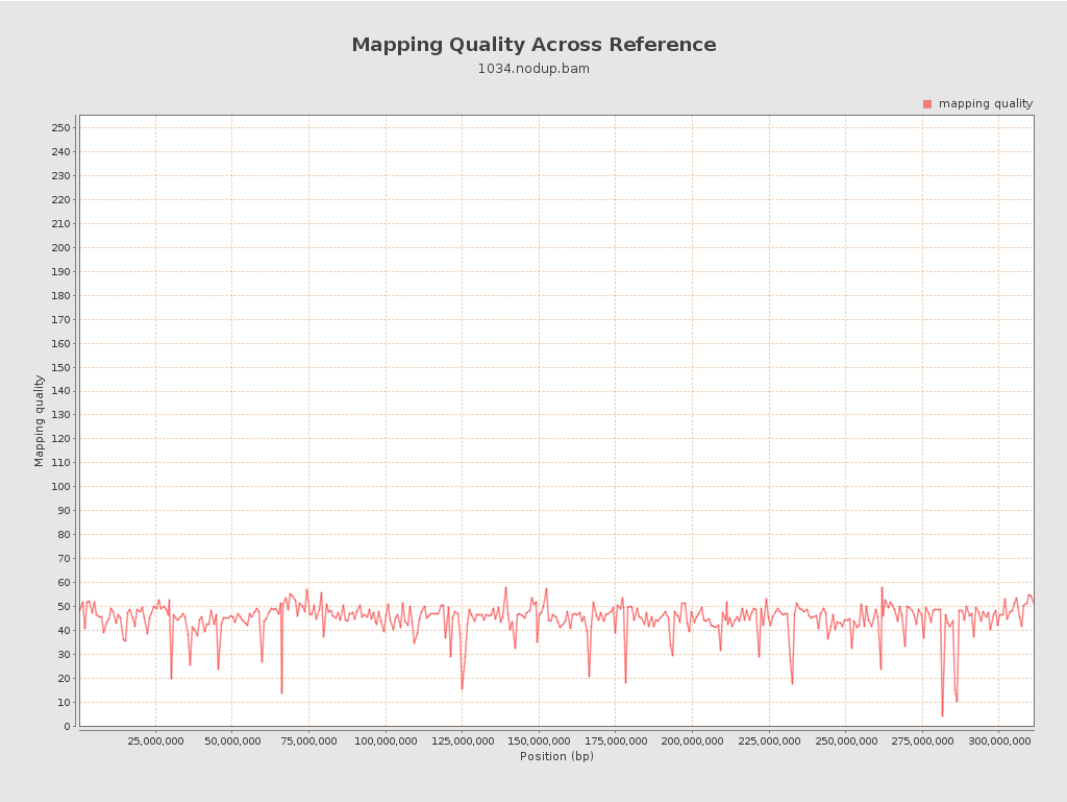
10. Results : Mapped Reads Clipping Profile



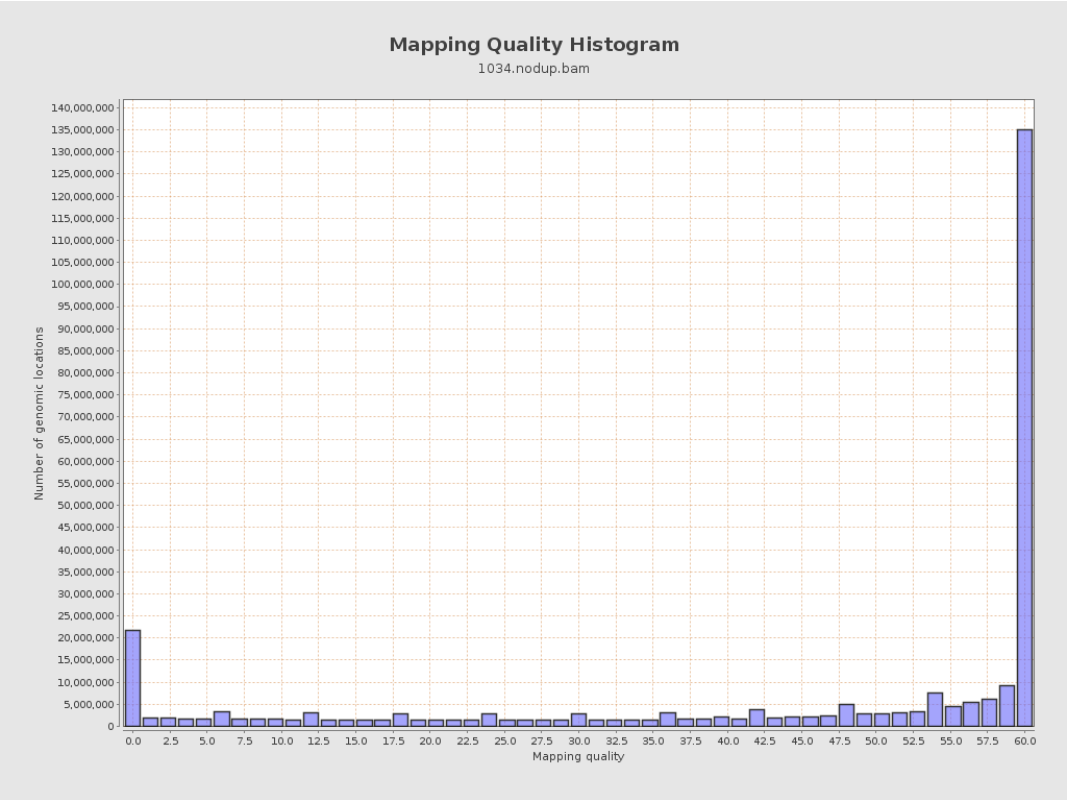
11. Results : Homopolymer Indels



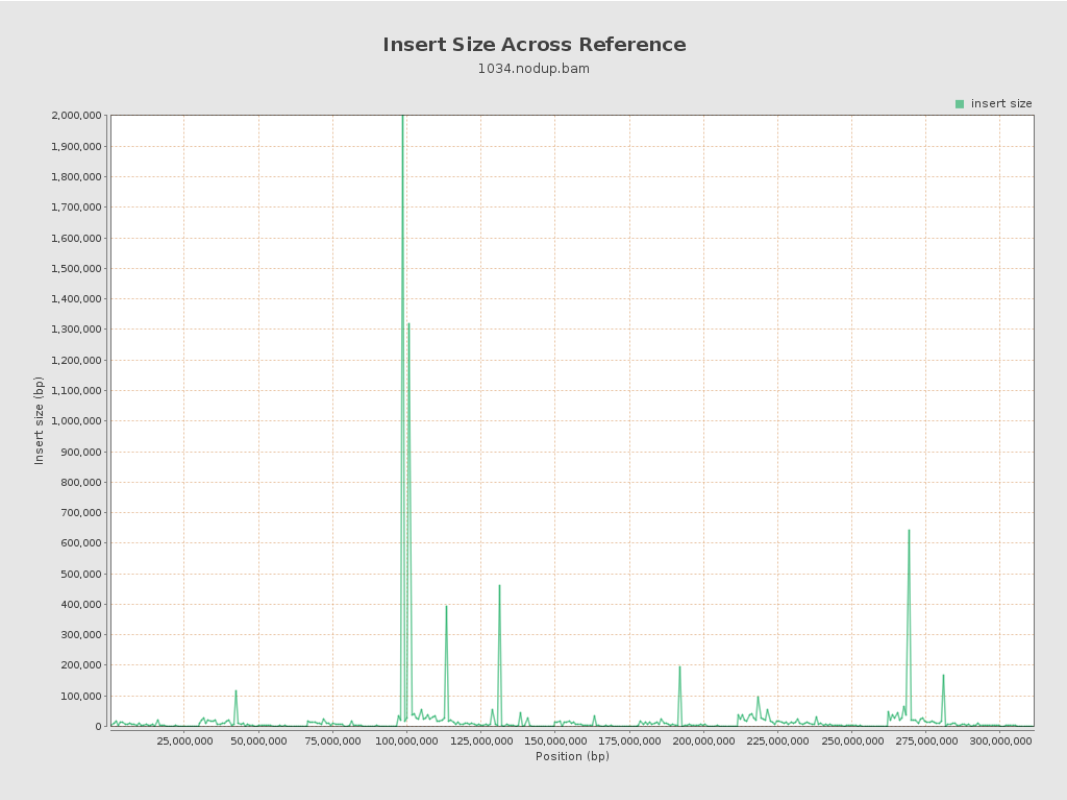
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram