Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:22:17

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1017 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1017 .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_572/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_572_S139_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_572/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_572_S139_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:22:16 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	40,186,139
Mapped reads	37,051,233 / 92.2%
Unmapped reads	3,134,906 / 7.8%
Mapped paired reads	37,051,233 / 92.2%
Mapped reads, first in pair	18,610,134 / 46.31%
Mapped reads, second in pair	18,441,099 / 45.89%
Mapped reads, both in pair	36,033,819 / 89.67%
Mapped reads, singletons	1,017,414 / 2.53%
Read min/max/mean length	30 / 151 / 148.35
Duplicated reads (flagged)	5,202,993 / 12.95%
Clipped reads	8,648,697 / 21.52%

2.2. ACGT Content

Number/percentage of A's	1,584,336,021 / 30.93%
Number/percentage of C's	977,048,137 / 19.07%
Number/percentage of T's	1,585,703,064 / 30.95%
Number/percentage of G's	975,995,957 / 19.05%
Number/percentage of N's	34,805 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	16.4808
Standard Deviation	130.4931

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Insert size

Mean	242,290.82
Standard Deviation	2,362,857.01
P25/Median/P75	350 / 451 / 571

2.6. Mismatches and indels

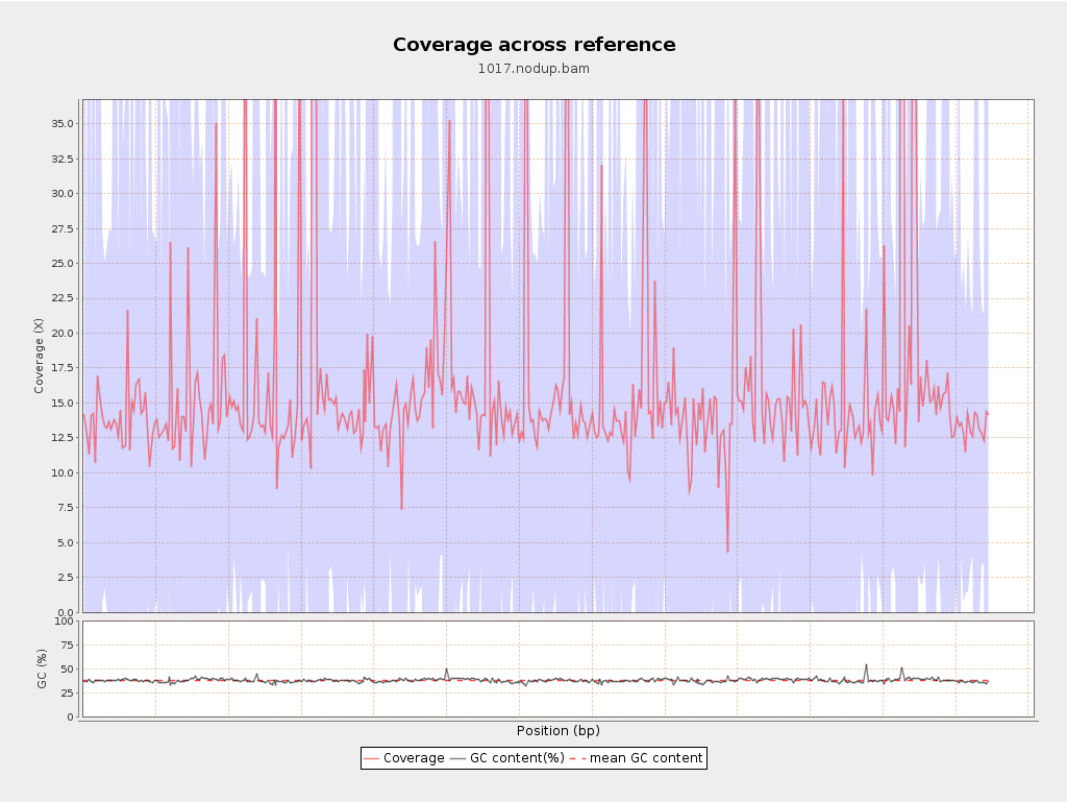
General error rate	2.58%
Mismatches	122,774,137
Insertions	3,475,999
Mapped reads with at least one insertion	8.39%
Deletions	3,427,666
Mapped reads with at least one deletion	8.24%
Homopolymer indels	56.8%

2.7. Chromosome stats

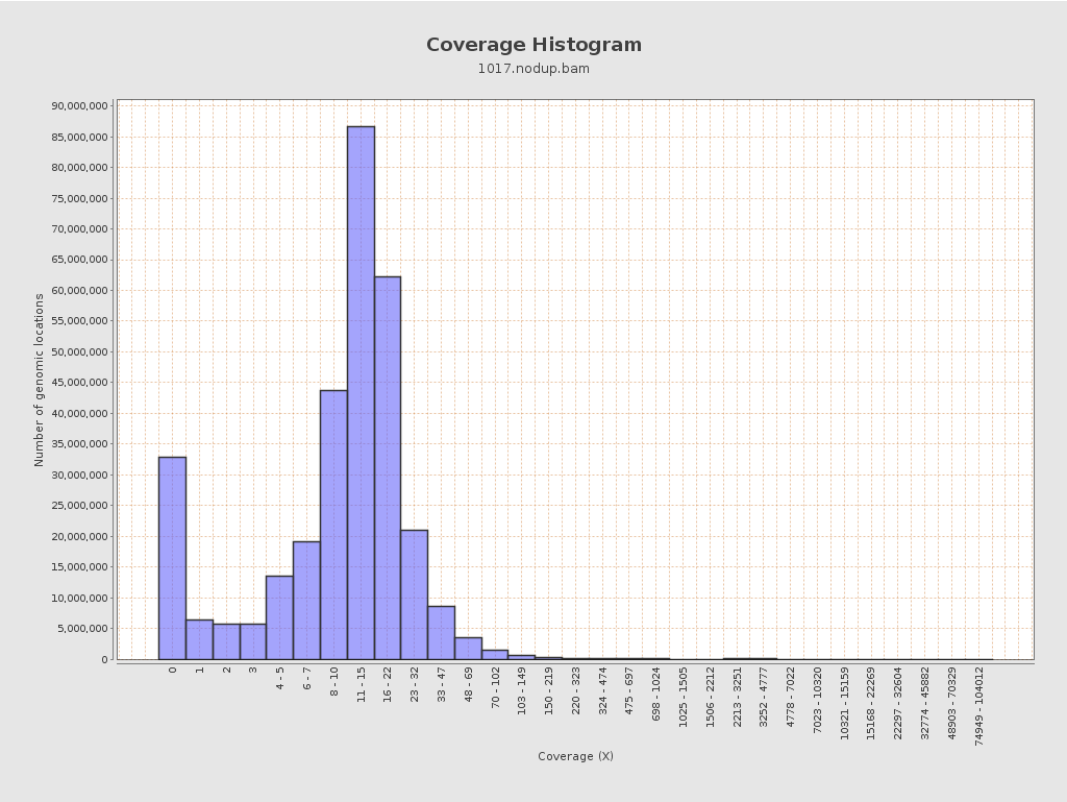
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	408935217	13.7576	45.2904

LT669789.1	36598175	592993779	16.2028	127.603
LT669790.1	30422129	571677051	18.7915	166.9813
LT669791.1	52758100	857223771	16.2482	128.5985
LT669792.1	28376109	467364499	16.4704	152.7425
LT669793.1	33388210	507821989	15.2096	90.6732
LT669794.1	50579949	785127286	15.5225	98.8672
LT669795.1	49795044	944955773	18.9769	173.4121

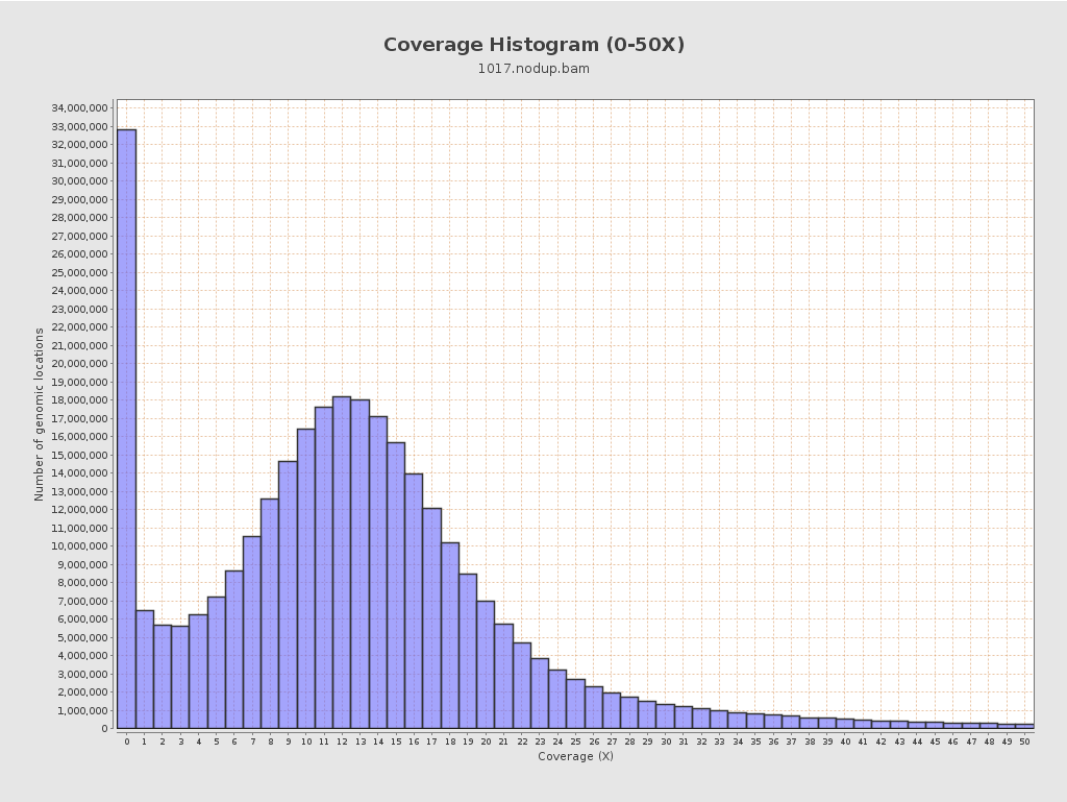
3. Results : Coverage across reference



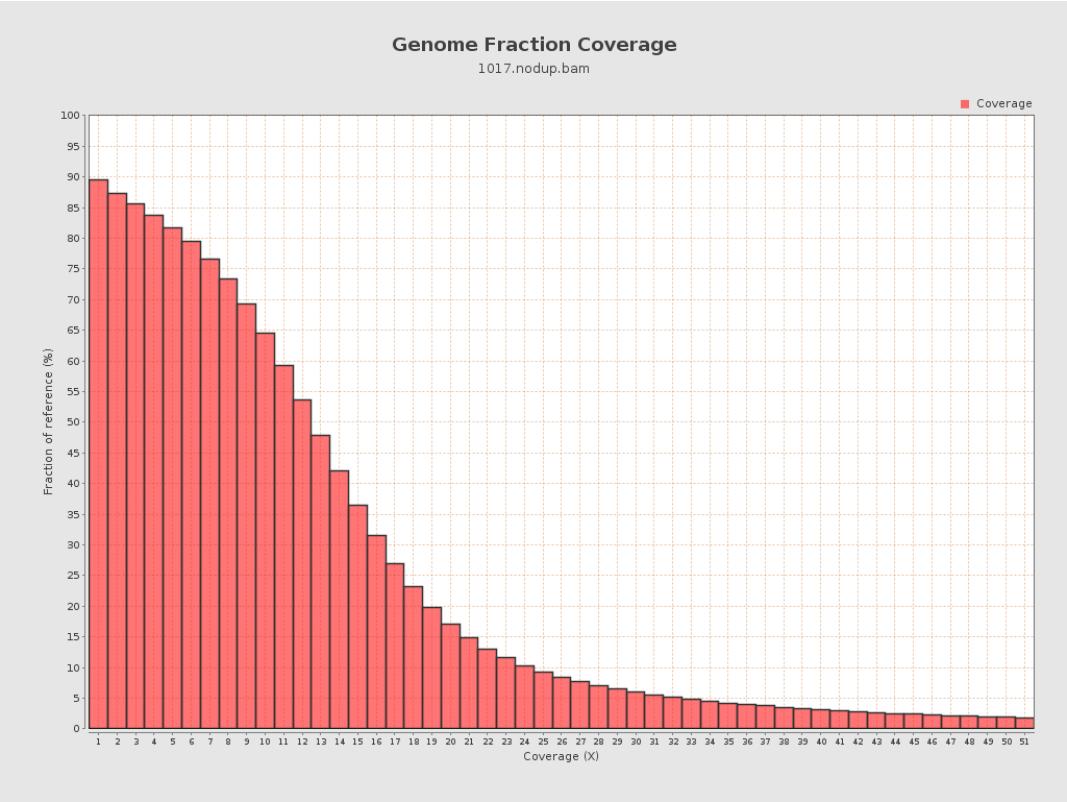
4. Results : Coverage Histogram



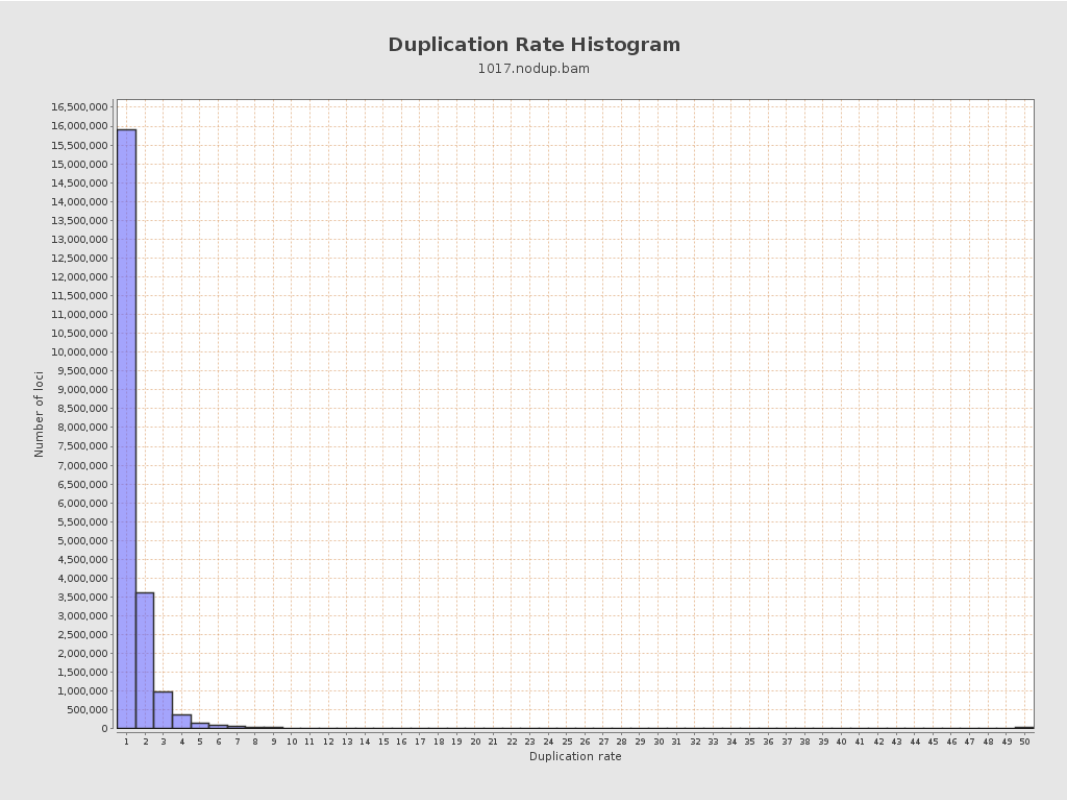
5. Results : Coverage Histogram (0-50X)



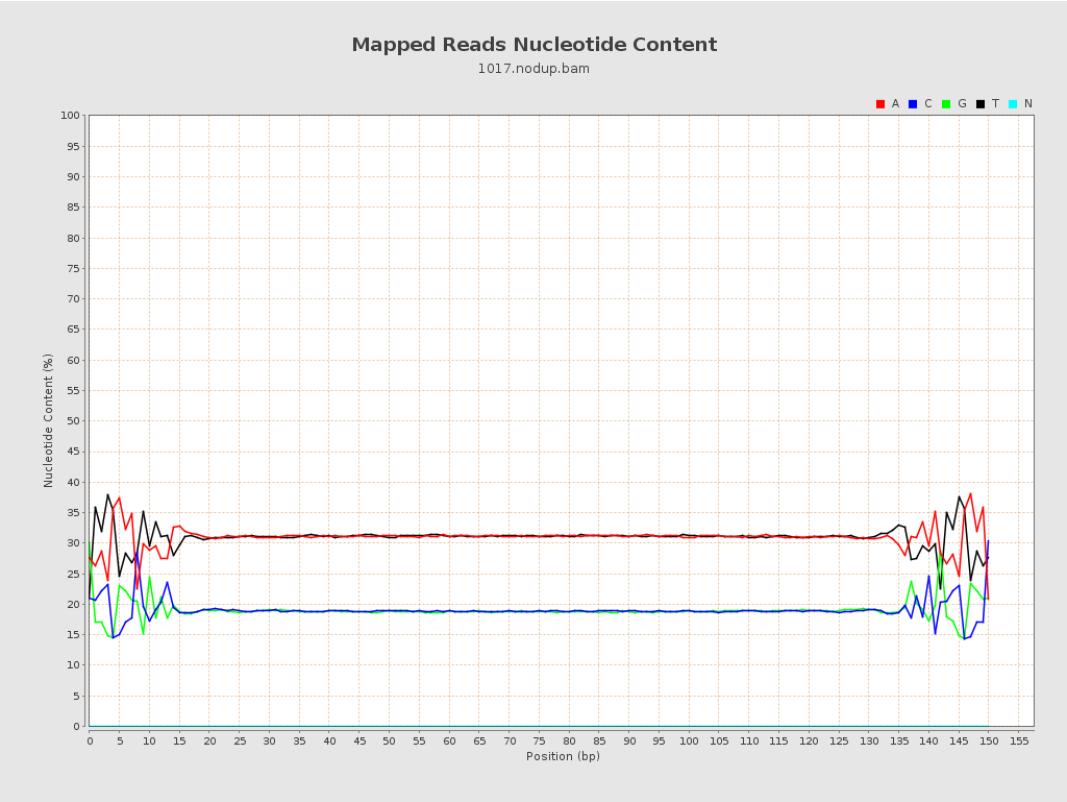
6. Results : Genome Fraction Coverage



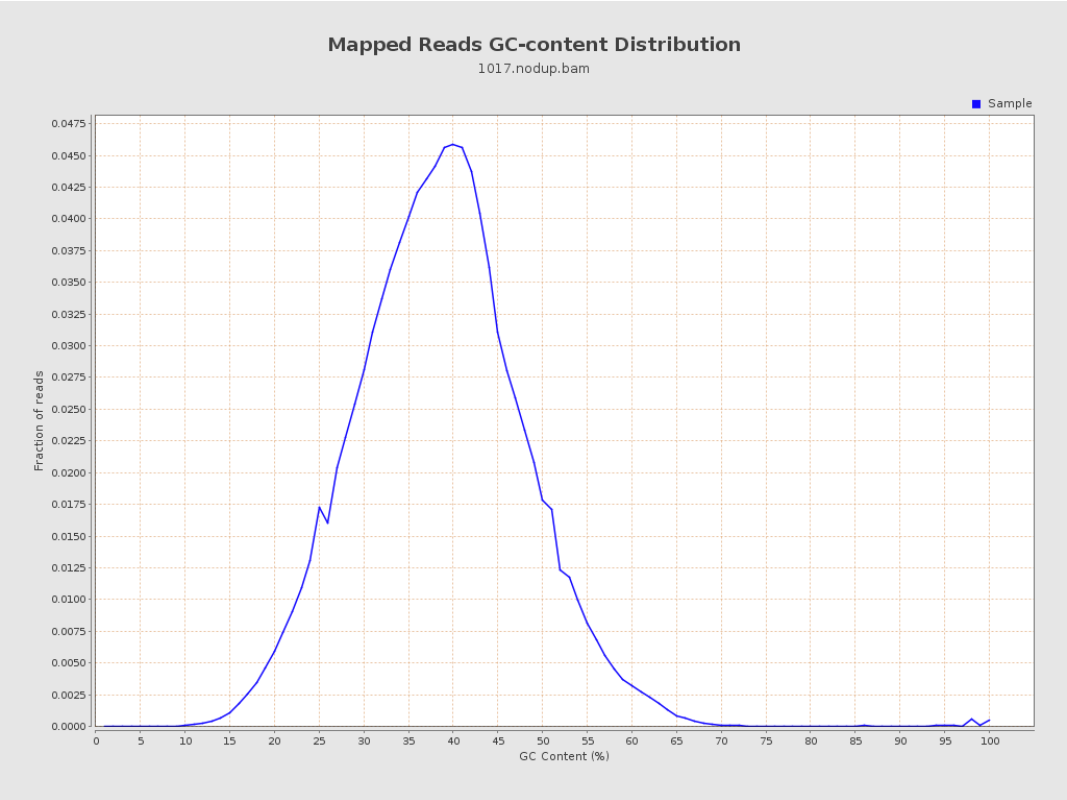
7. Results : Duplication Rate Histogram



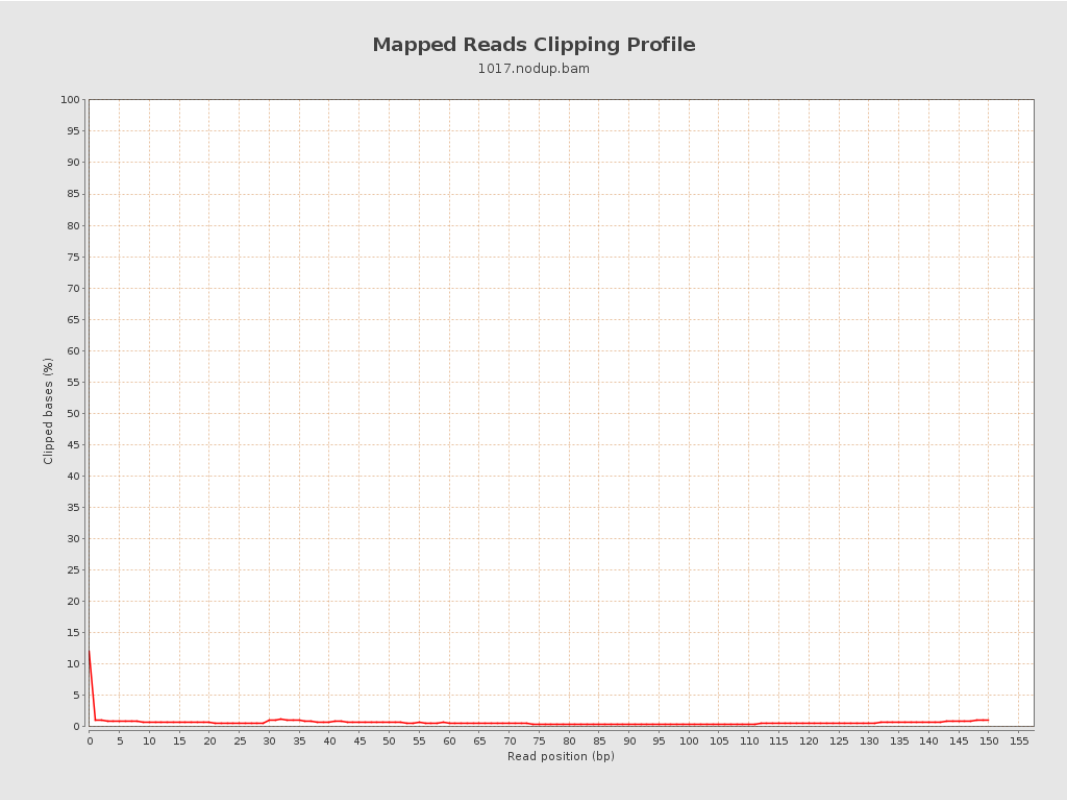
8. Results : Mapped Reads Nucleotide Content



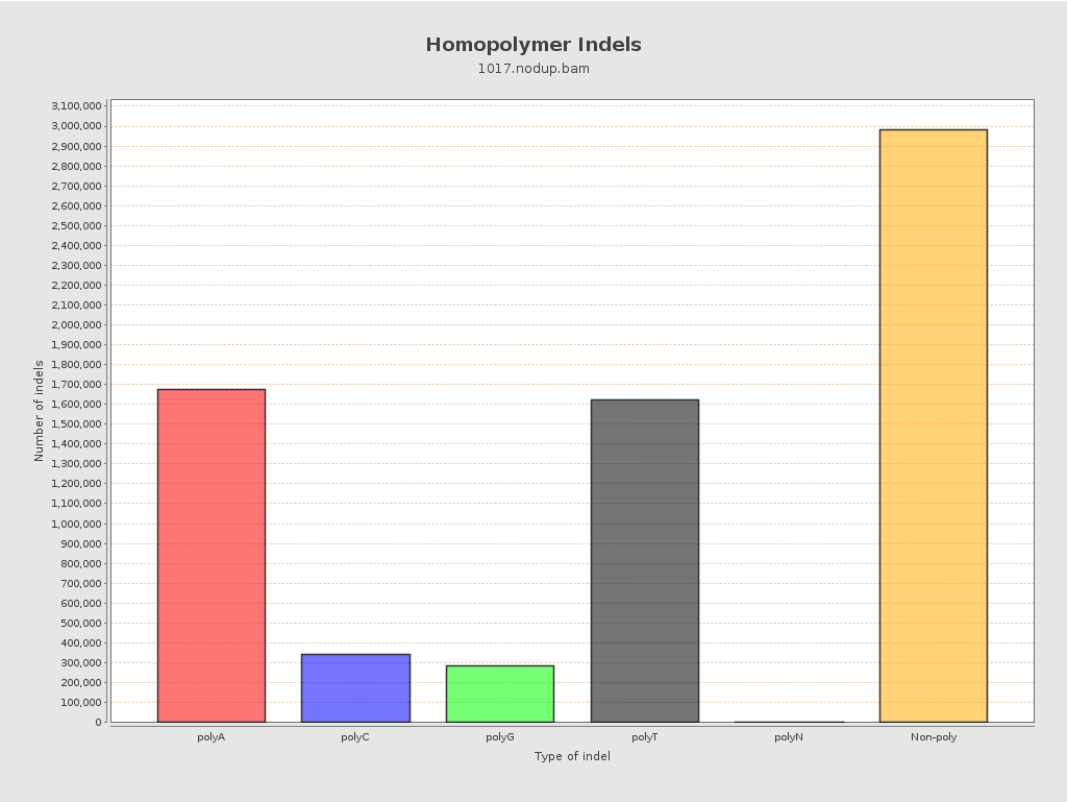
9. Results : Mapped Reads GC-content Distribution



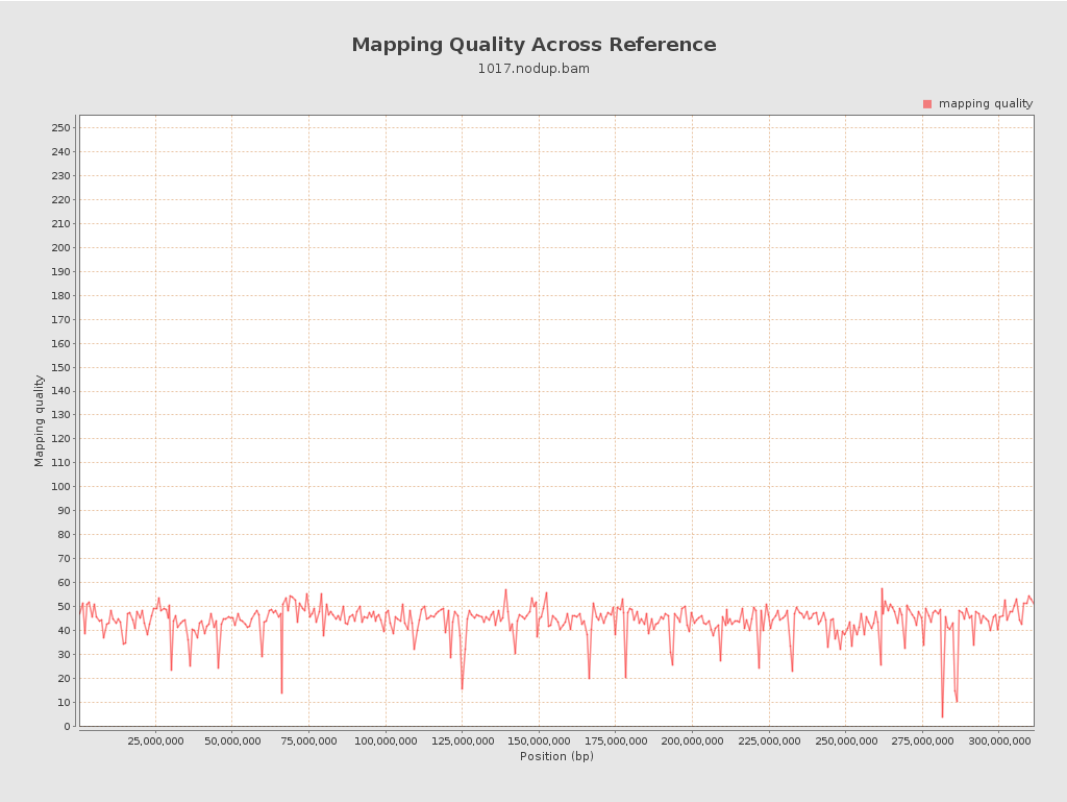
10. Results : Mapped Reads Clipping Profile



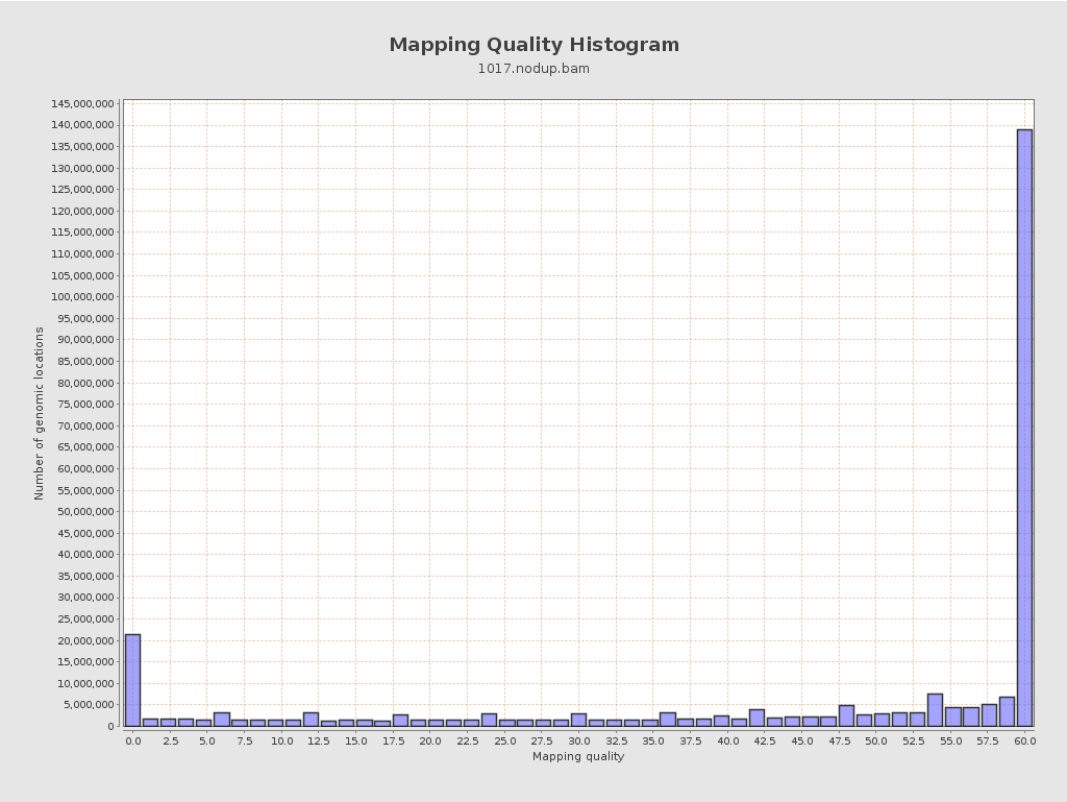
11. Results : Homopolymer Indels



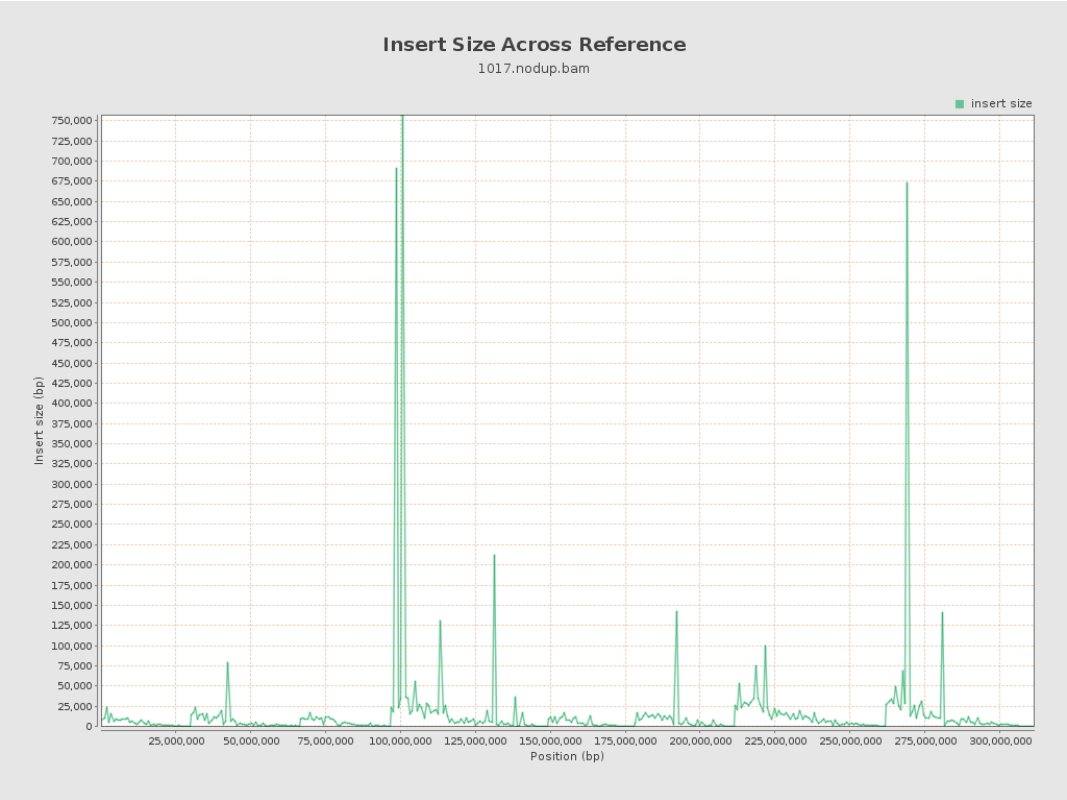
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram