Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:21

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1037 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1037 .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_565/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_565_S132_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_565/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_565_S132_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:23:20 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	42,386,506
Mapped reads	37,921,120 / 89.47%
Unmapped reads	4,465,386 / 10.53%
Mapped paired reads	37,921,120 / 89.47%
Mapped reads, first in pair	19,010,261 / 44.85%
Mapped reads, second in pair	18,910,859 / 44.62%
Mapped reads, both in pair	37,136,802 / 87.61%
Mapped reads, singletons	784,318 / 1.85%
Read min/max/mean length	30 / 151 / 148.33
Duplicated reads (flagged)	5,083,710 / 11.99%
Clipped reads	8,722,748 / 20.58%

2.2. ACGT Content

Number/percentage of A's	1,617,918,251 / 30.82%
Number/percentage of C's	1,006,036,377 / 19.17%
Number/percentage of T's	1,620,063,065 / 30.87%
Number/percentage of G's	1,004,728,640 / 19.14%
Number/percentage of N's	38,273 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	16.8853
Standard Deviation	135.2814

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Insert size

Mean	215,950.32
Standard Deviation	2,217,592.67
P25/Median/P75	304 / 397 / 514

2.6. Mismatches and indels

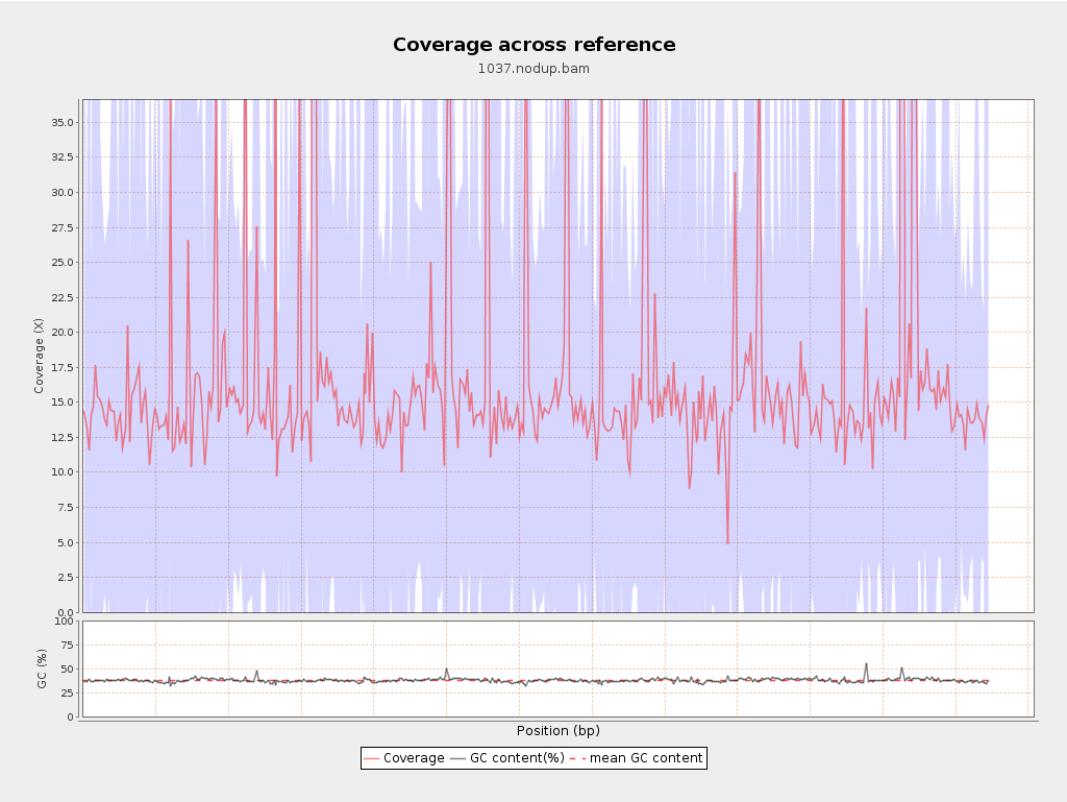
General error rate	2.47%
Mismatches	119,862,565
Insertions	3,480,374
Mapped reads with at least one insertion	8.24%
Deletions	3,551,333
Mapped reads with at least one deletion	8.31%
Homopolymer indels	56.02%

2.7. Chromosome stats

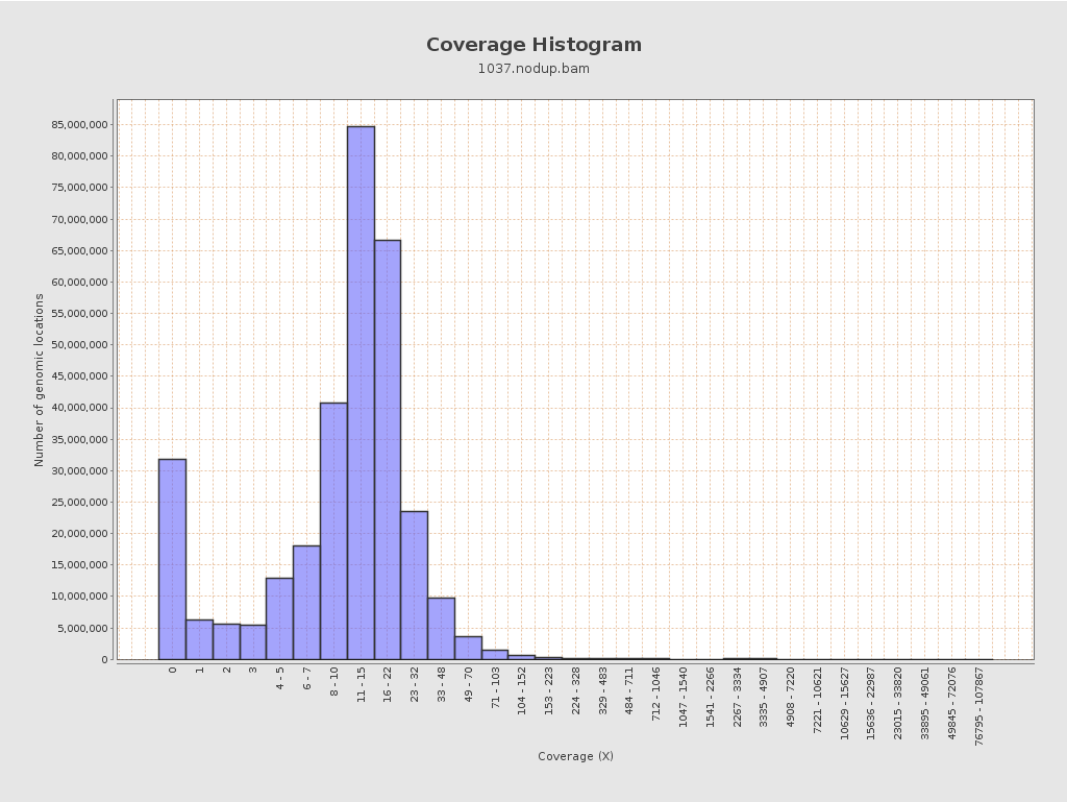
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	423331085	14.2419	50.2207

LT669789.1	36598175	616395643	16.8423	147.8985
LT669790.1	30422129	558880851	18.3709	132.5219
LT669791.1	52758100	862583748	16.3498	128.8128
LT669792.1	28376109	470618886	16.585	137.3396
LT669793.1	33388210	529325664	15.8537	92.1296
LT669794.1	50579949	807427399	15.9634	112.865
LT669795.1	49795044	993619406	19.9542	198.1137

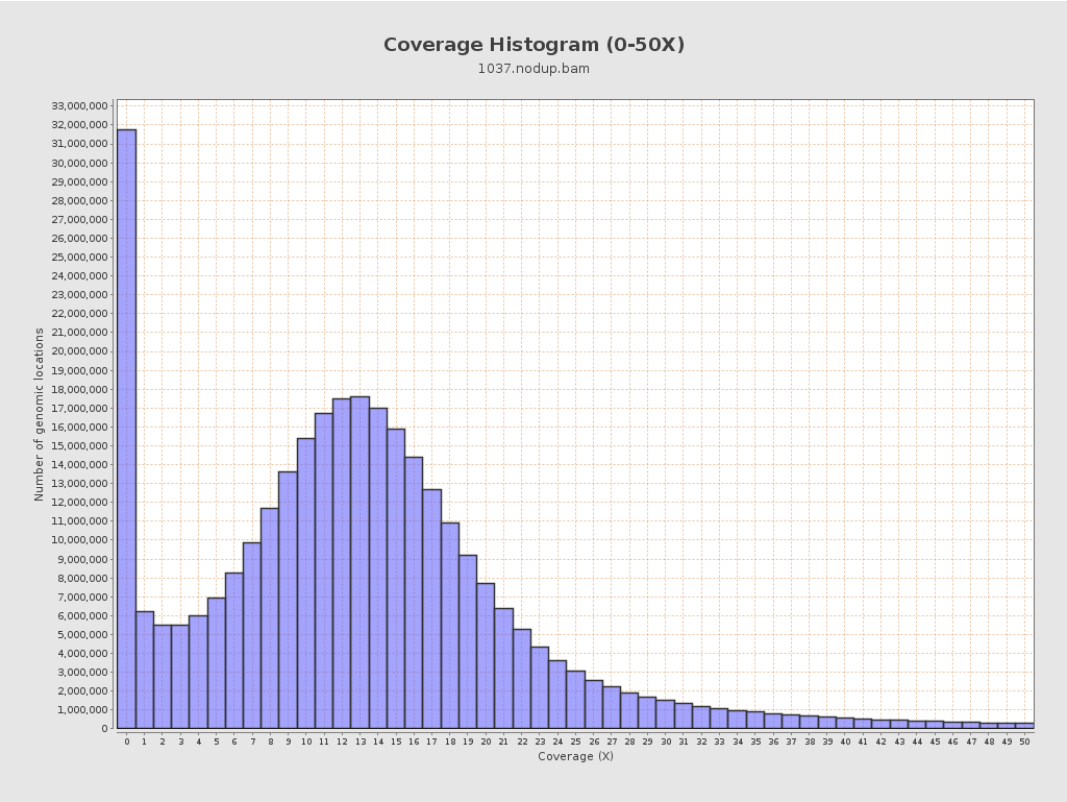
3. Results : Coverage across reference



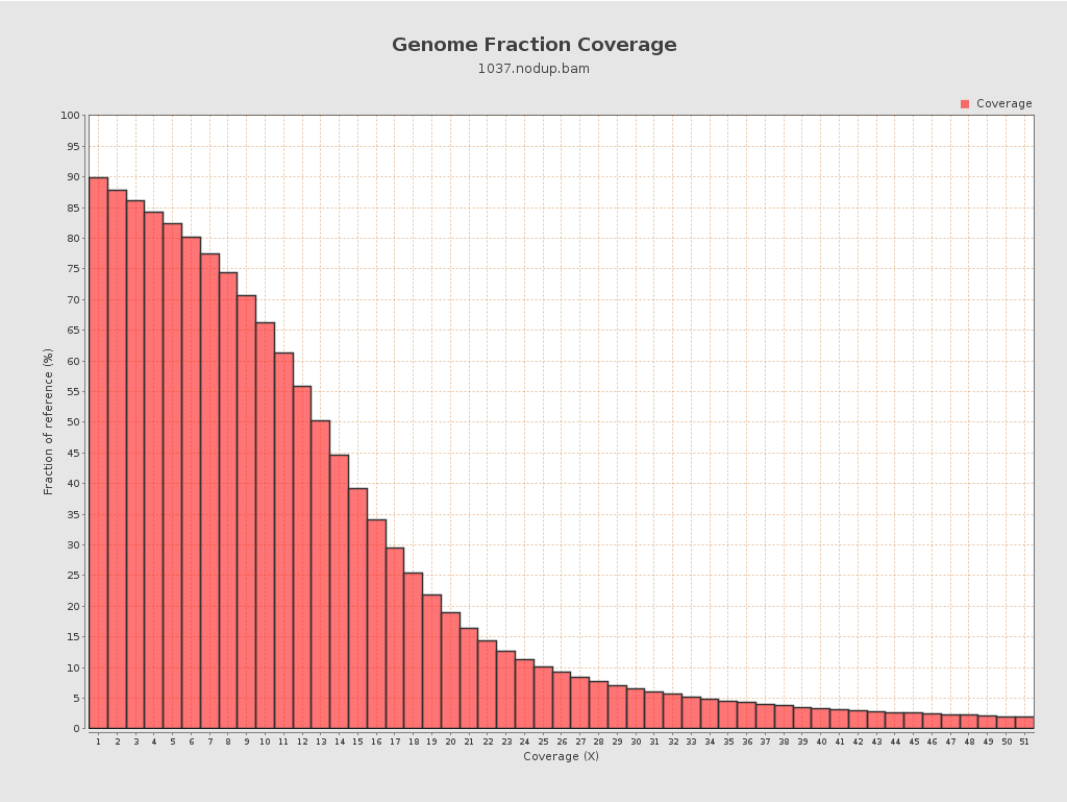
4. Results : Coverage Histogram



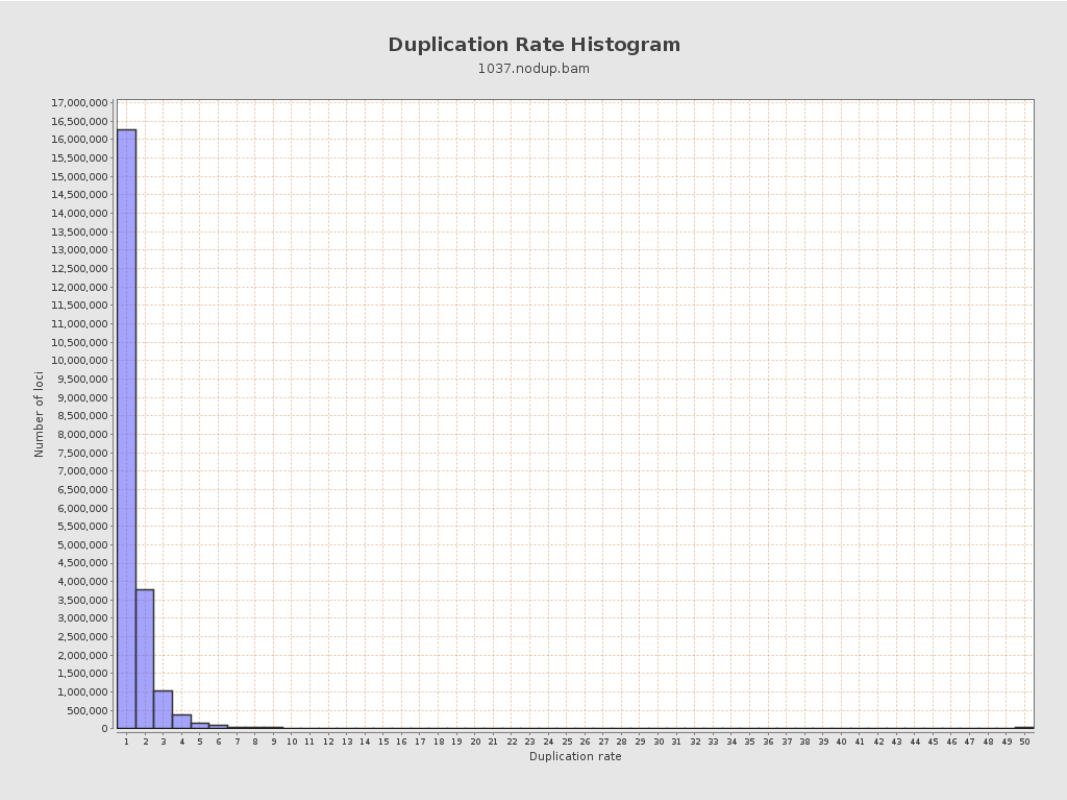
5. Results : Coverage Histogram (0-50X)



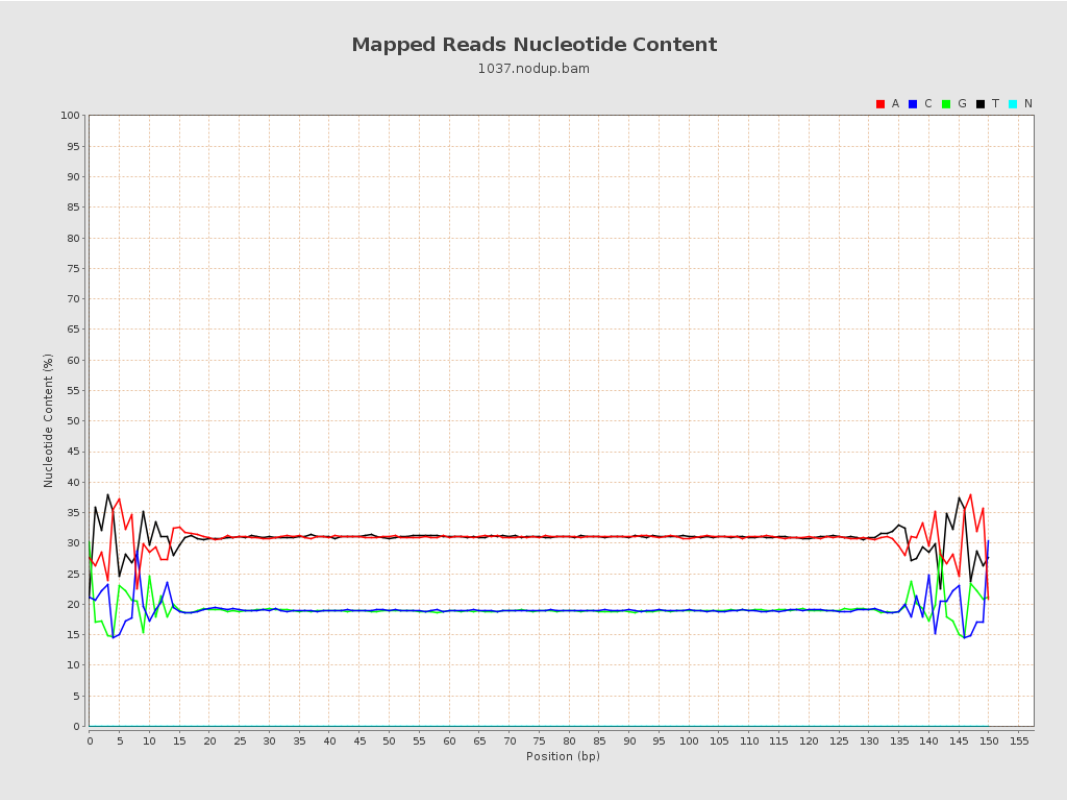
6. Results : Genome Fraction Coverage



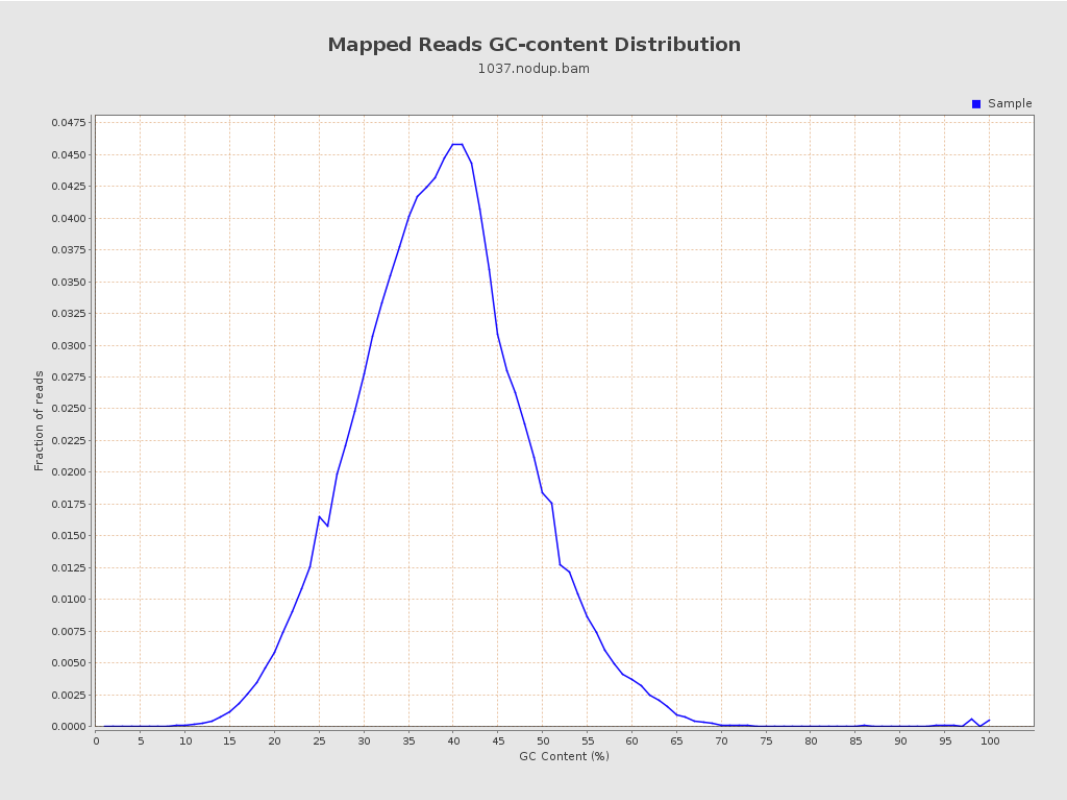
7. Results : Duplication Rate Histogram



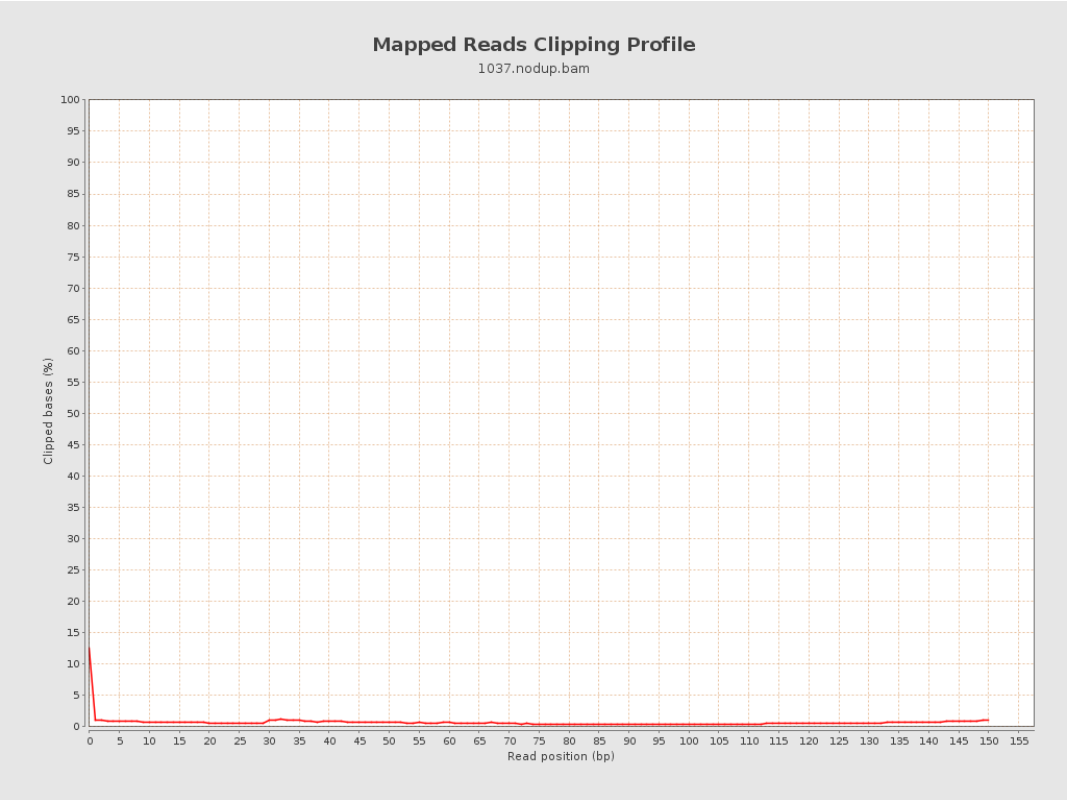
8. Results : Mapped Reads Nucleotide Content



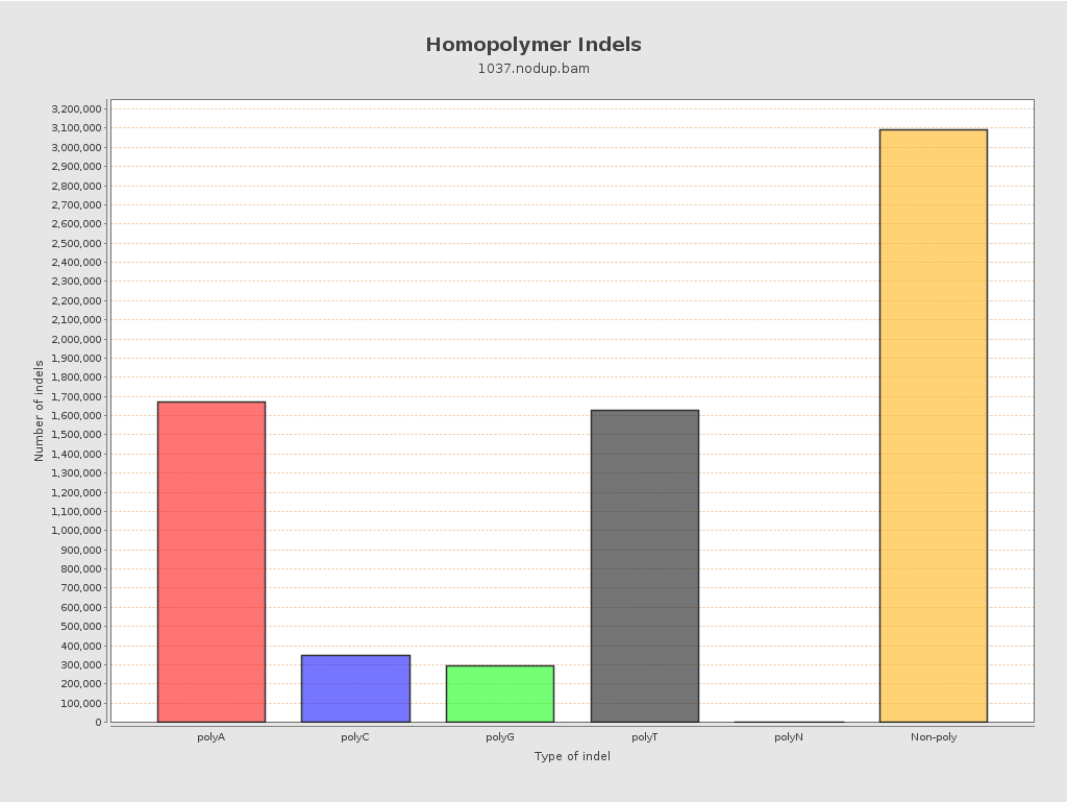
9. Results : Mapped Reads GC-content Distribution



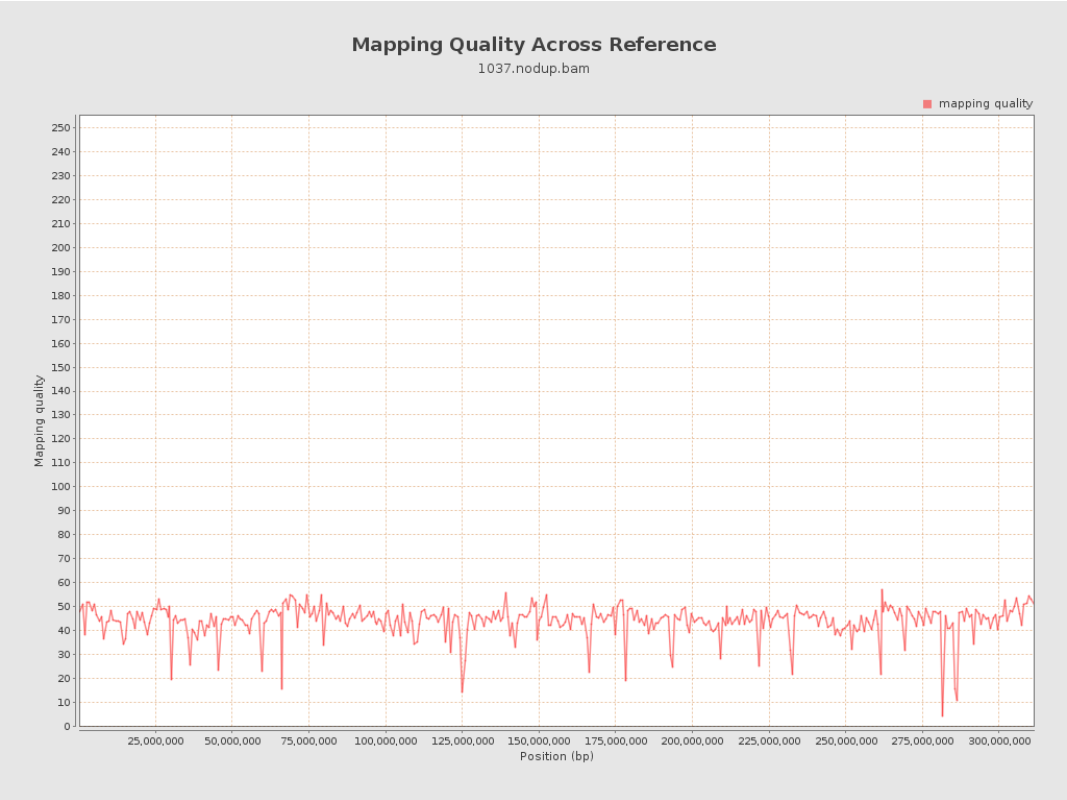
10. Results : Mapped Reads Clipping Profile



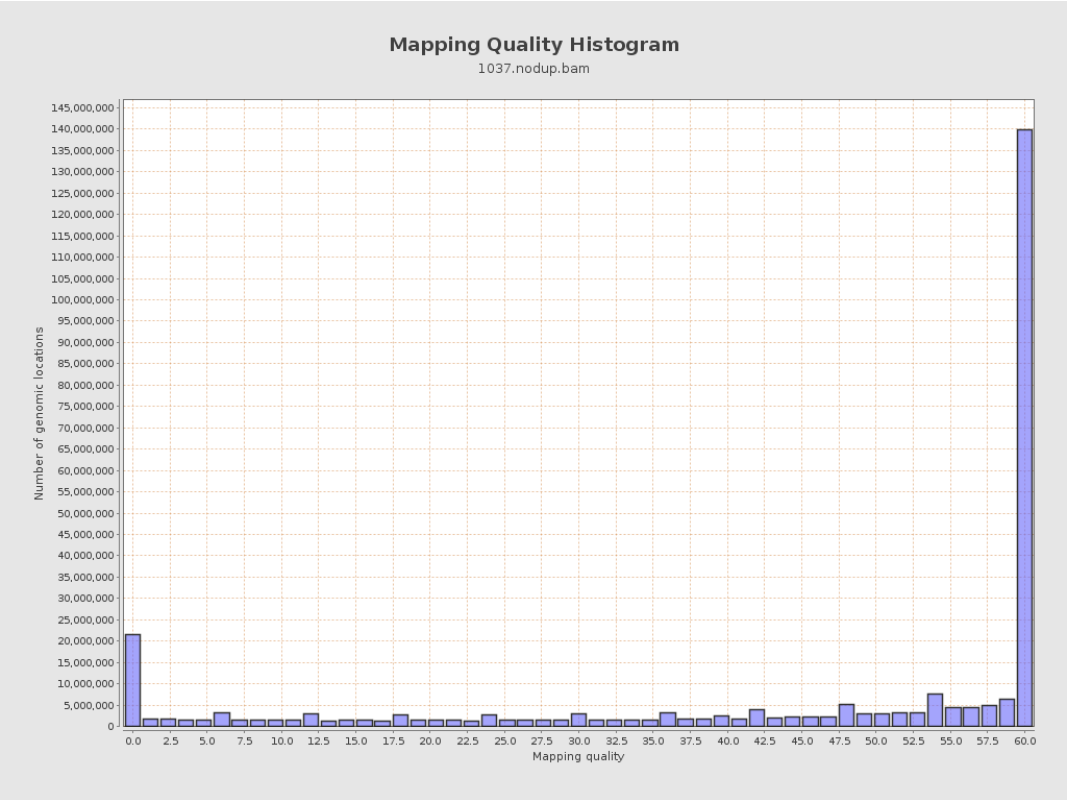
11. Results : Homopolymer Indels



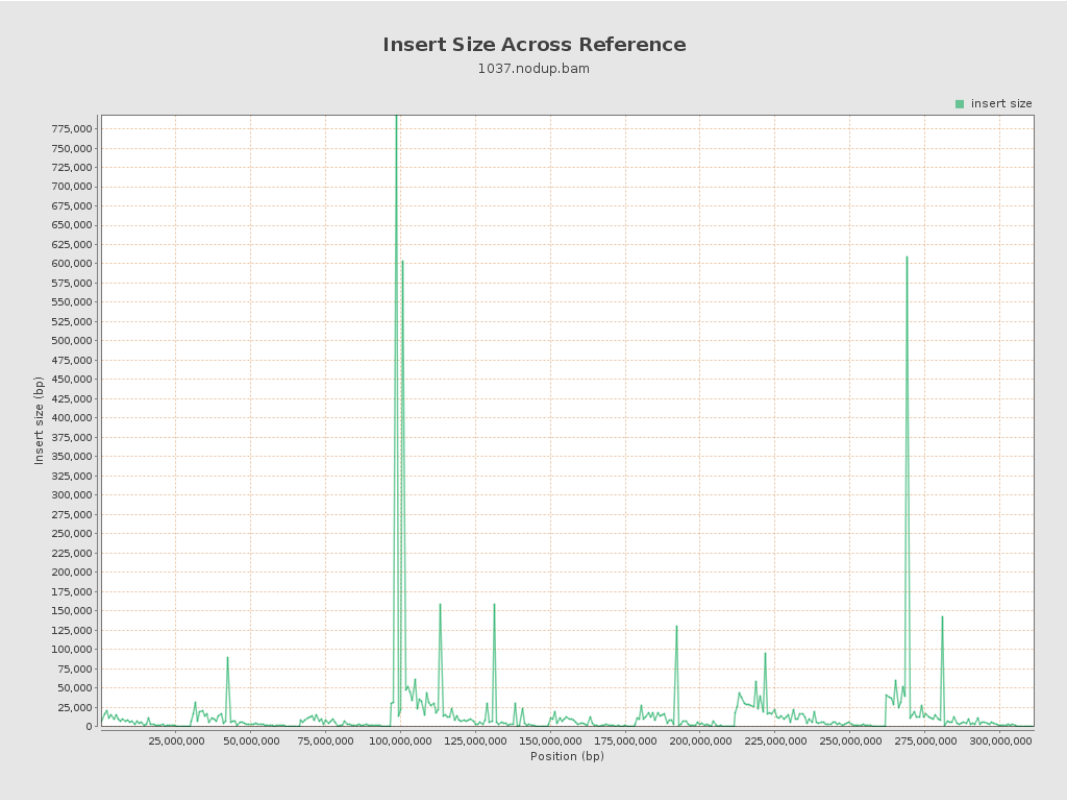
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram