Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:28

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1478 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1478 .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_447/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_447_S422_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_447/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_447_S422_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:27:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	54,031,559
Mapped reads	49,195,886 / 91.05%
Unmapped reads	4,835,673 / 8.95%
Mapped paired reads	49,195,886 / 91.05%
Mapped reads, first in pair	24,668,589 / 45.66%
Mapped reads, second in pair	24,527,297 / 45.39%
Mapped reads, both in pair	47,592,483 / 88.08%
Mapped reads, singletons	1,603,403 / 2.97%
Read min/max/mean length	30 / 151 / 147.98
Duplicated reads (flagged)	8,169,431 / 15.12%
Clipped reads	12,023,538 / 22.25%

2.2. ACGT Content

Number/percentage of A's	2,078,098,211 / 30.89%
Number/percentage of C's	1,282,247,538 / 19.06%
Number/percentage of T's	2,084,067,804 / 30.98%
Number/percentage of G's	1,283,391,273 / 19.08%
Number/percentage of N's	22,201 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	21.6446
Standard Deviation	210.6805

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Insert size

Mean	297,766.24
Standard Deviation	2,655,156.92
P25/Median/P75	405 / 536 / 690

2.6. Mismatches and indels

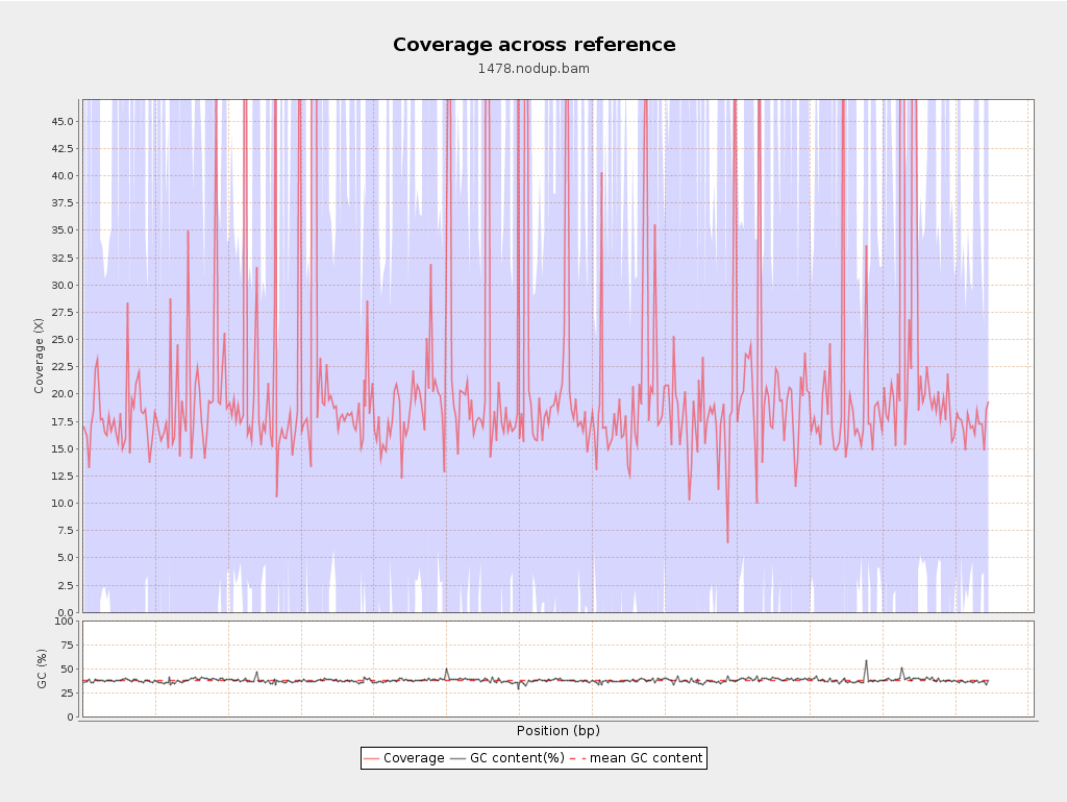
General error rate	2.4%
Mismatches	148,051,222
Insertions	4,898,029
Mapped reads with at least one insertion	8.87%
Deletions	4,698,444
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56.93%

2.7. Chromosome stats

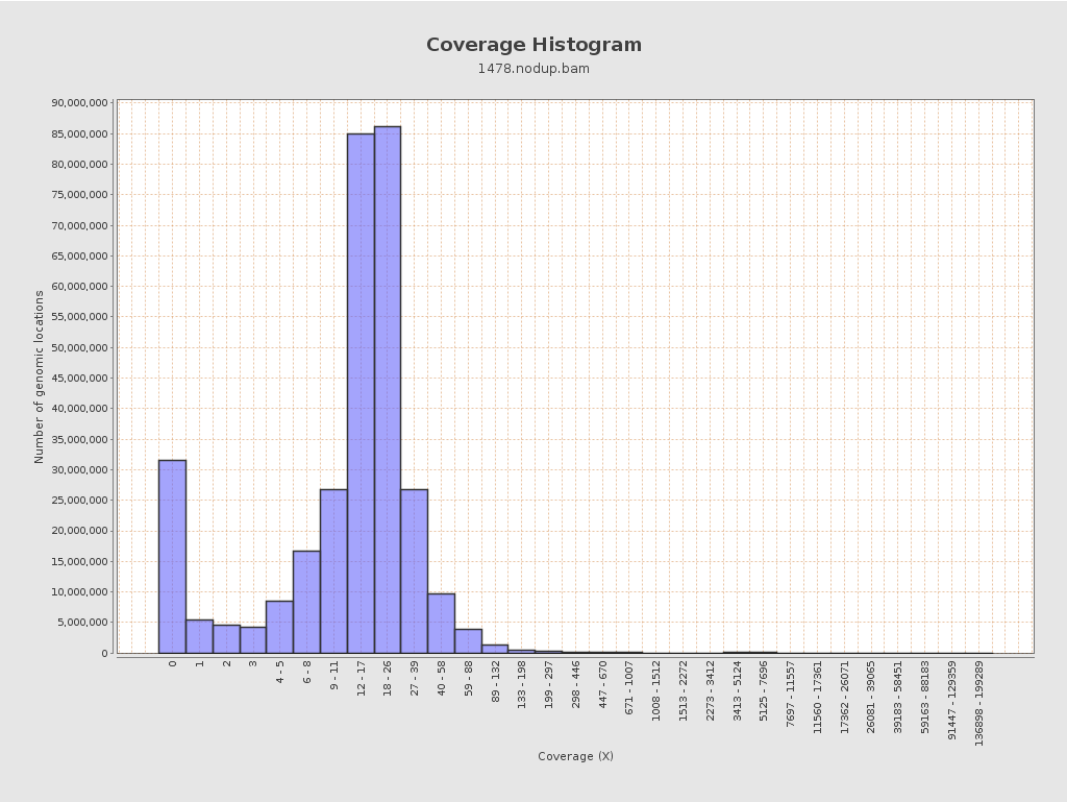
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	525495051	17.6789	86.3112

LT669789.1	36598175	790099753	21.5885	210.3145
LT669790.1	30422129	794943548	26.1304	282.0877
LT669791.1	52758100	1118091192	21.1928	222.3638
LT669792.1	28376109	617071647	21.7462	193.5455
LT669793.1	33388210	659252413	19.7451	170.0216
LT669794.1	50579949	1023396171	20.2332	177.373
LT669795.1	49795044	1217030658	24.4408	259.0577

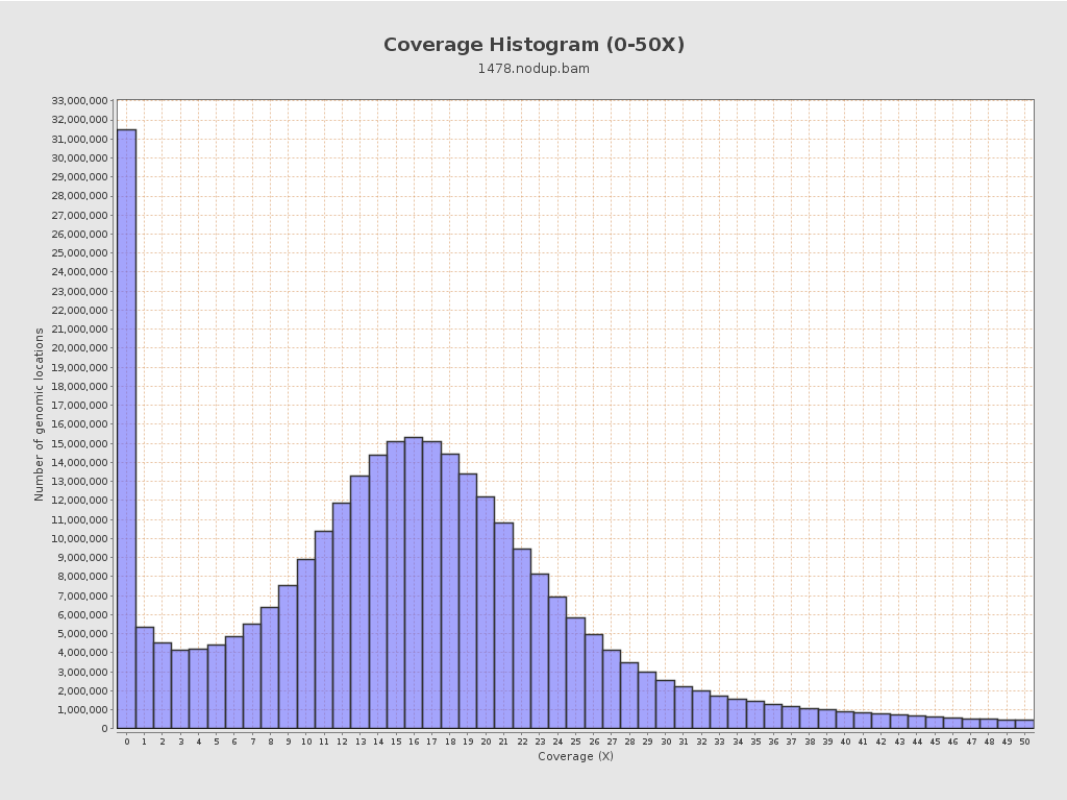
3. Results : Coverage across reference



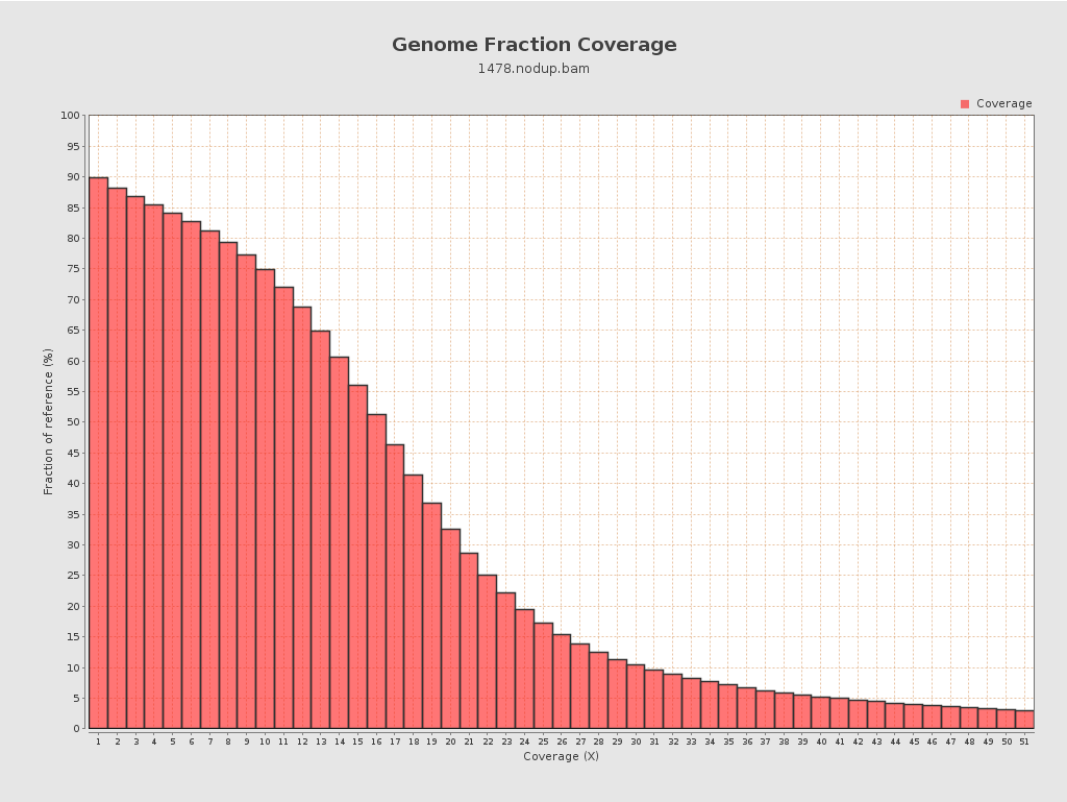
4. Results : Coverage Histogram



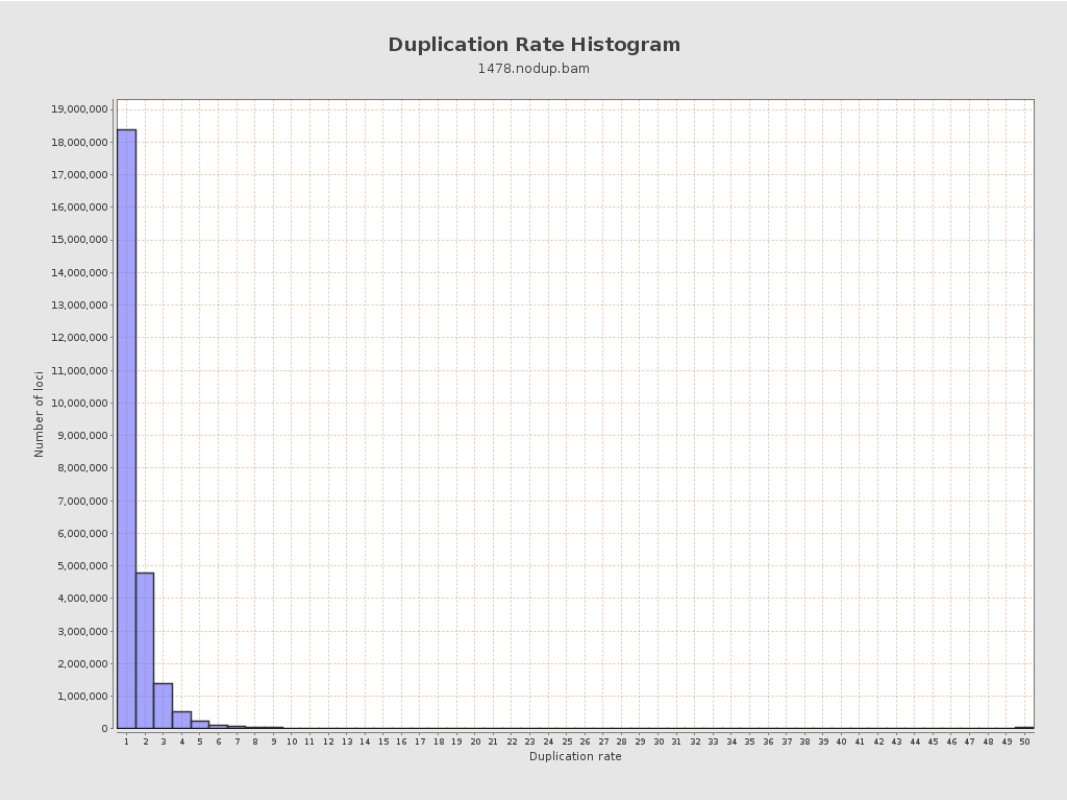
5. Results : Coverage Histogram (0-50X)



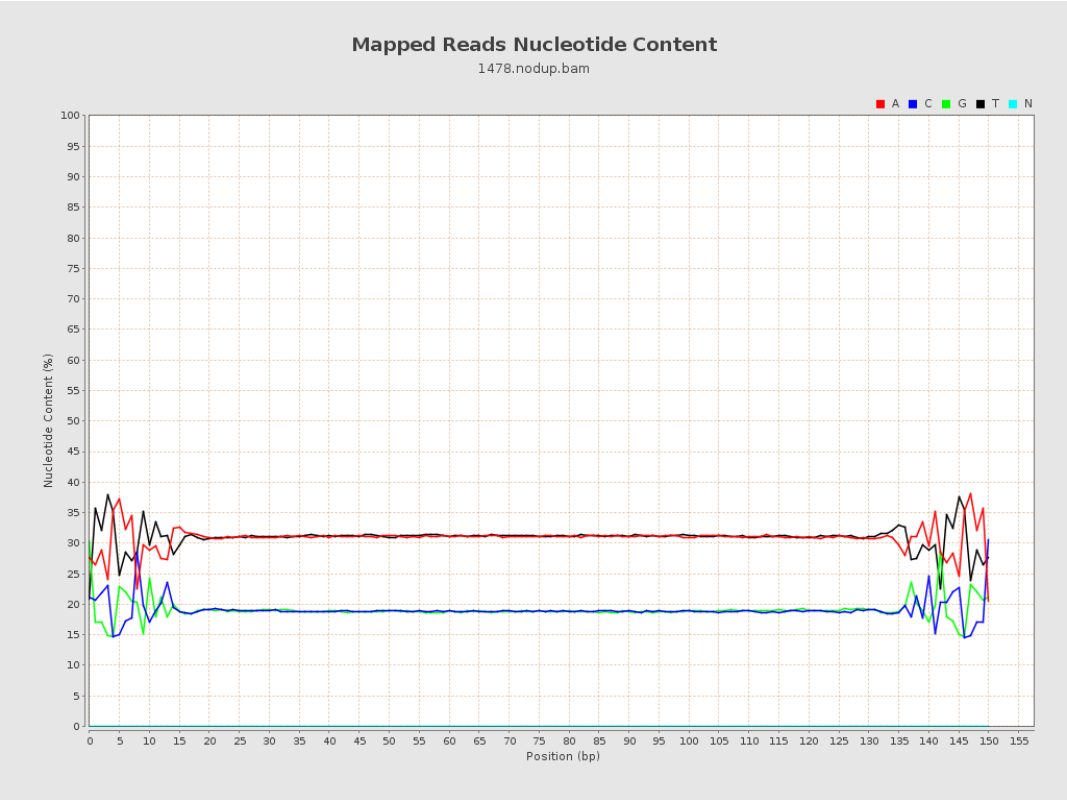
6. Results : Genome Fraction Coverage



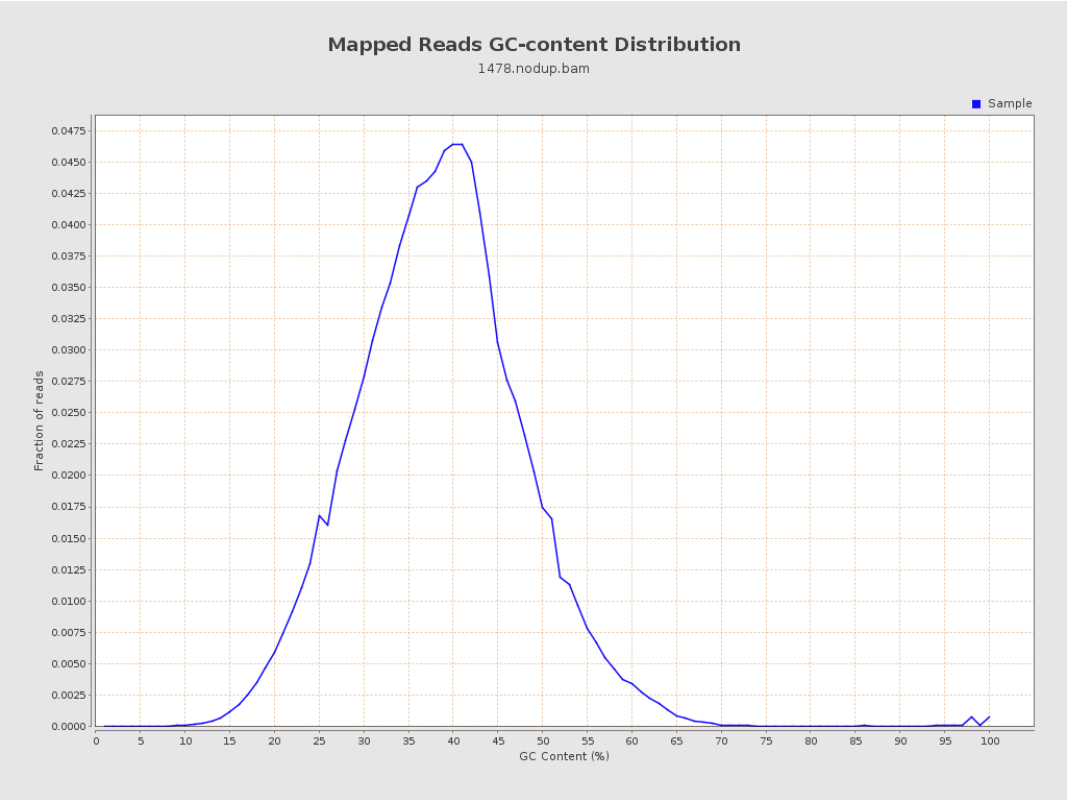
7. Results : Duplication Rate Histogram



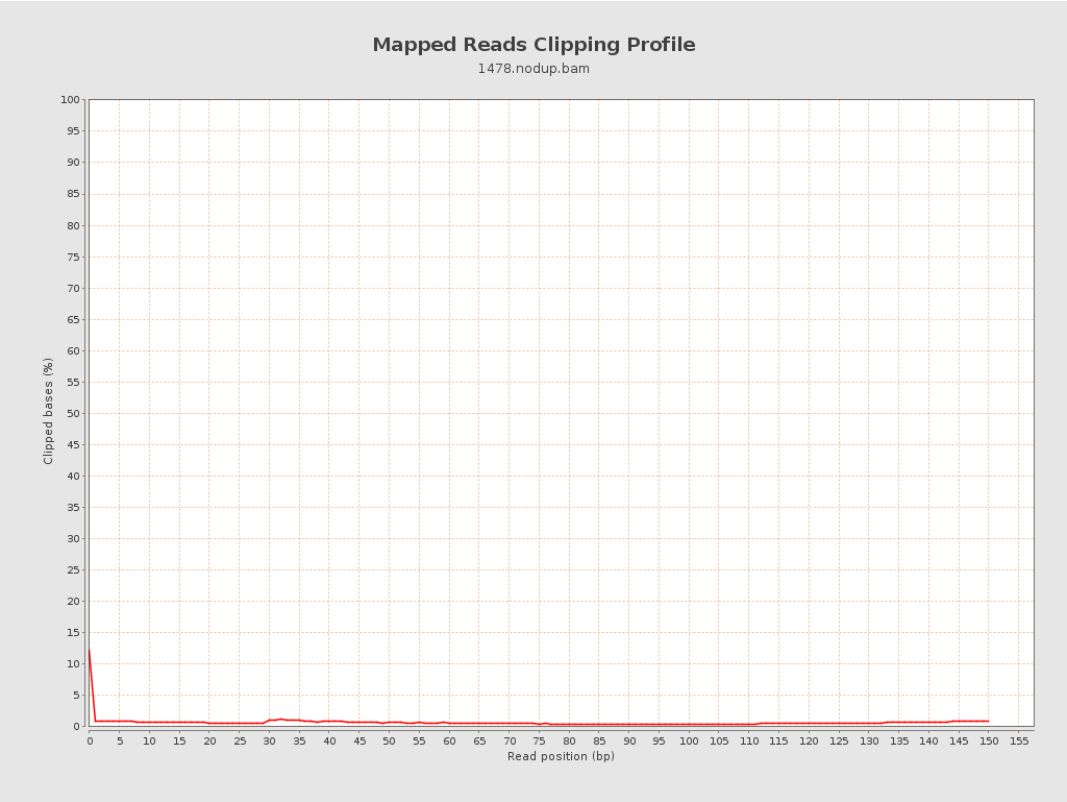
8. Results : Mapped Reads Nucleotide Content



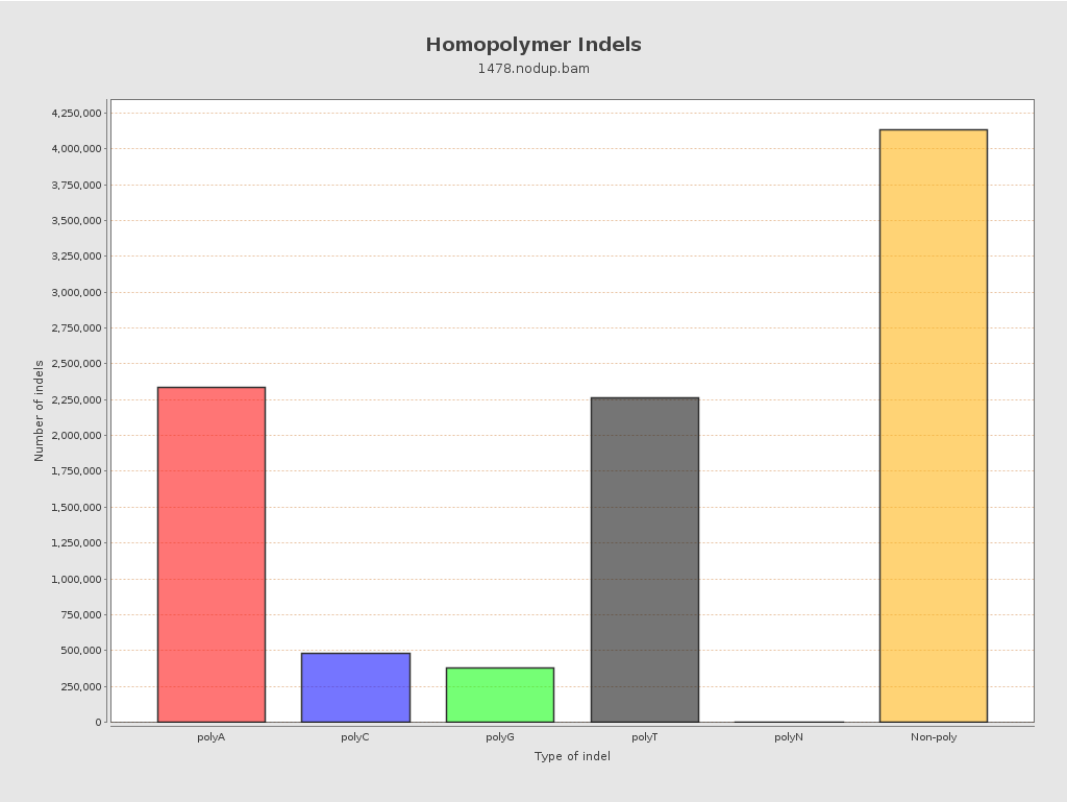
9. Results : Mapped Reads GC-content Distribution



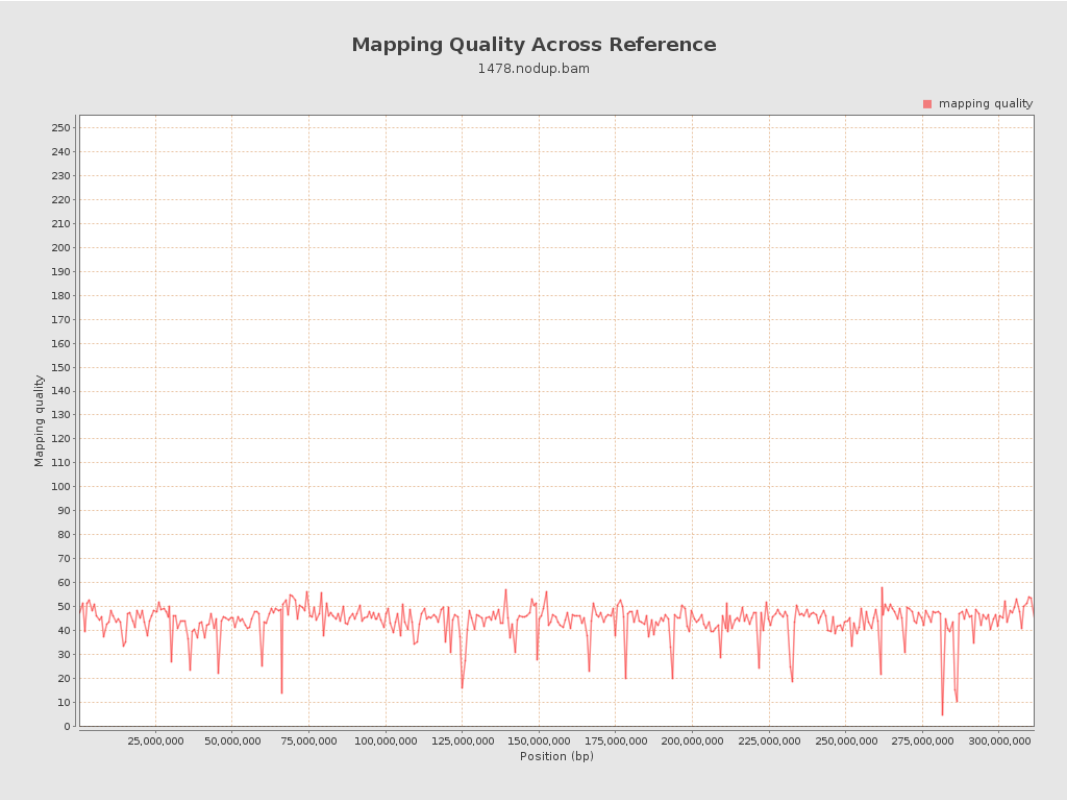
10. Results : Mapped Reads Clipping Profile



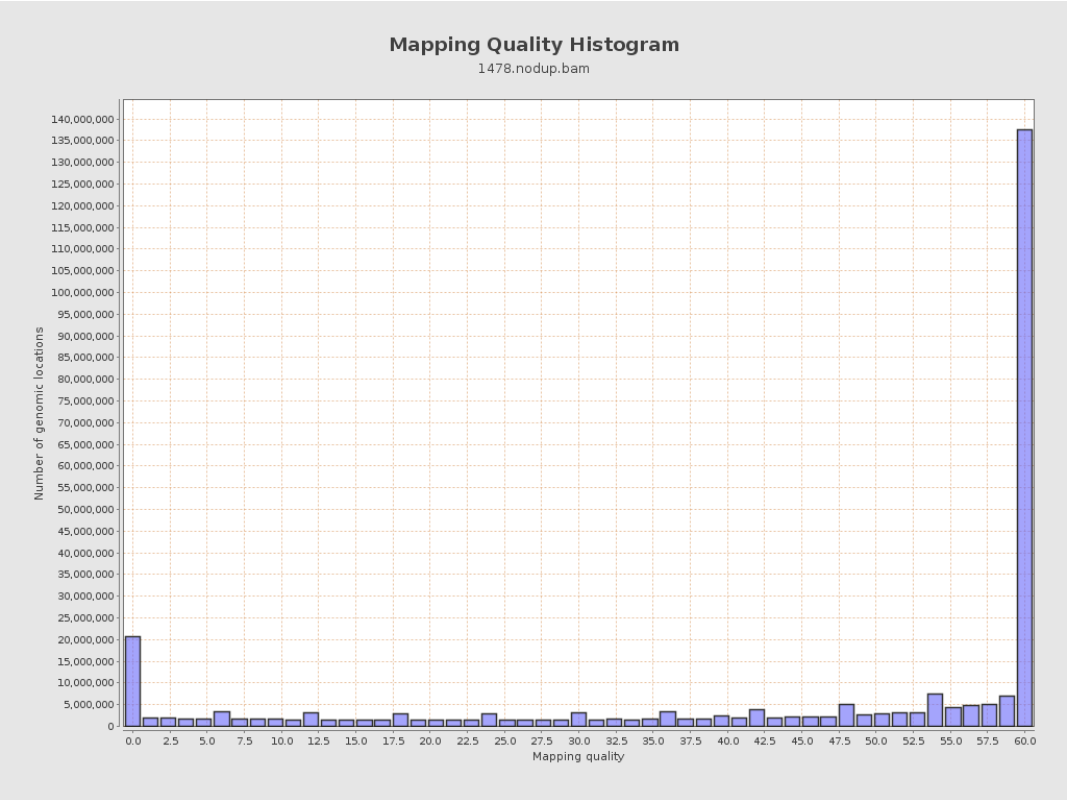
11. Results : Homopolymer Indels



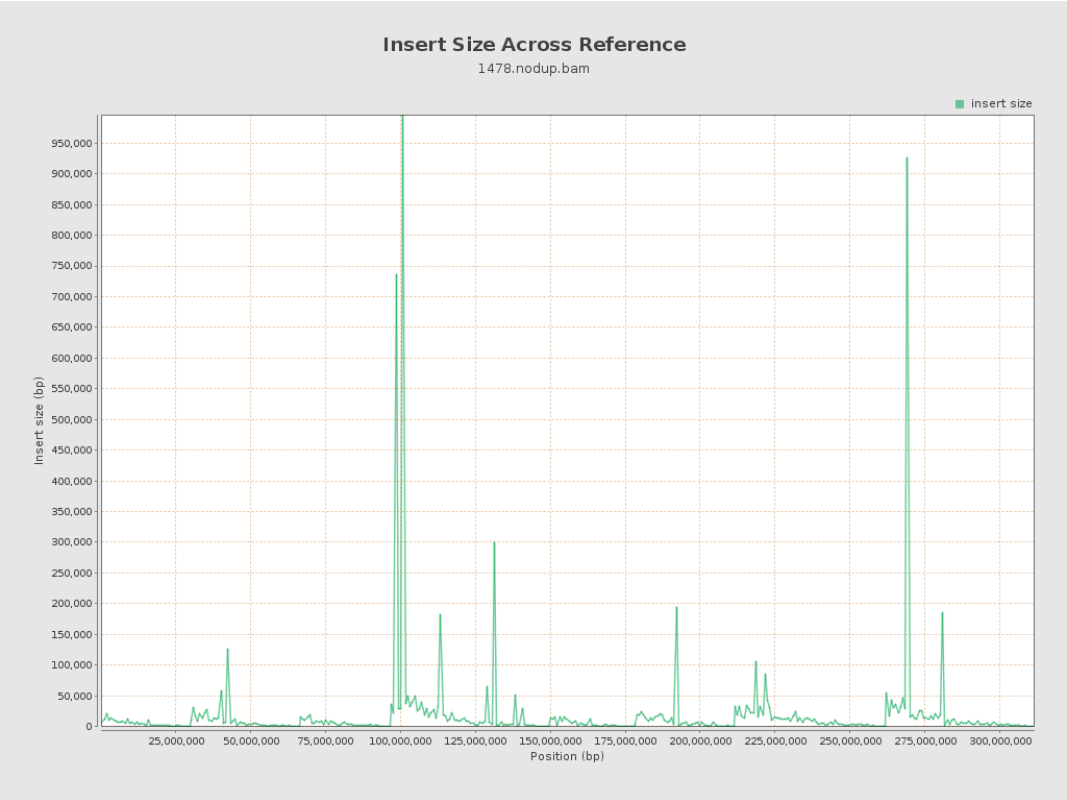
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram