Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:41:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1456
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1456 .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_426/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_426_S401_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_426/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_426_S401_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:41:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	93,346,359
Mapped reads	88,242,001 / 94.53%
Unmapped reads	5,104,358 / 5.47%
Mapped paired reads	88,242,001 / 94.53%
Mapped reads, first in pair	44,209,672 / 47.36%
Mapped reads, second in pair	44,032,329 / 47.17%
Mapped reads, both in pair	86,516,416 / 92.68%
Mapped reads, singletons	1,725,585 / 1.85%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	14,625,881 / 15.67%
Clipped reads	19,163,071 / 20.53%

2.2. ACGT Content

Number/percentage of A's	3,782,738,944 / 30.81%
Number/percentage of C's	2,356,044,195 / 19.19%
Number/percentage of T's	3,791,640,133 / 30.88%
Number/percentage of G's	2,347,440,566 / 19.12%
Number/percentage of N's	41,763 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	39.4993
Standard Deviation	297.3557

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Insert size

Mean	228,402.79
Standard Deviation	2,267,708.15
P25/Median/P75	334 / 442 / 589

2.6. Mismatches and indels

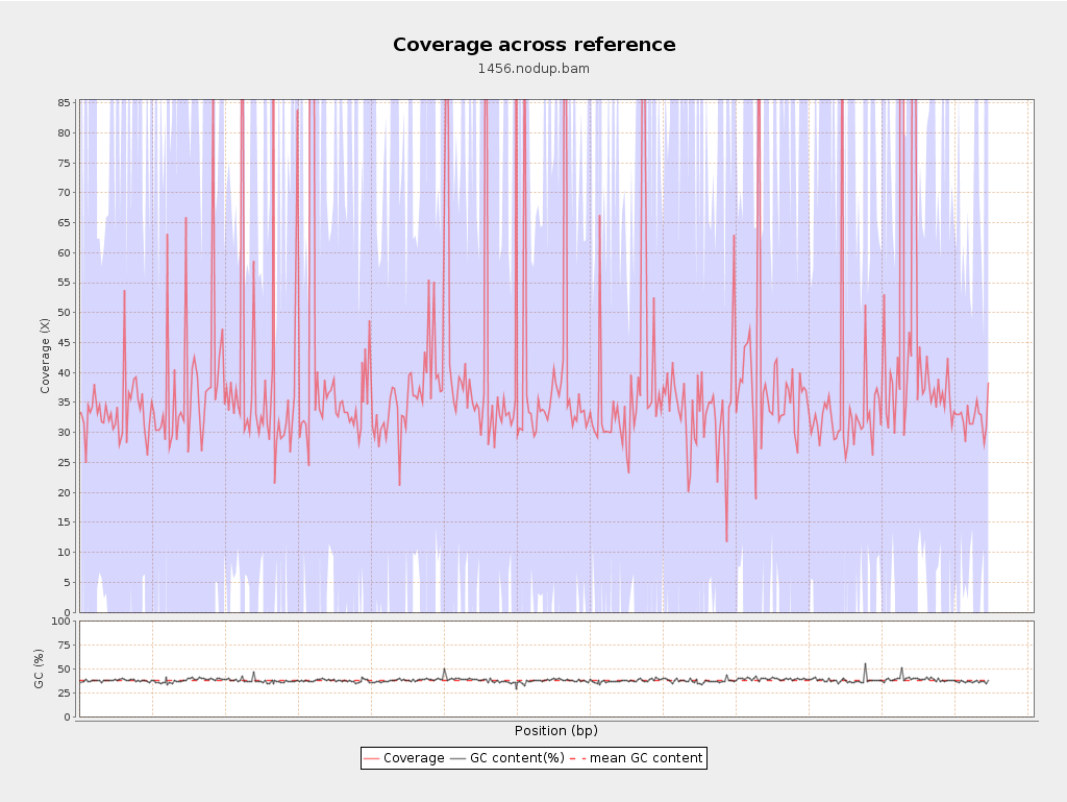
General error rate	2.28%
Mismatches	257,195,264
Insertions	8,180,355
Mapped reads with at least one insertion	8.33%
Deletions	8,333,459
Mapped reads with at least one deletion	8.4%
Homopolymer indels	56.43%

2.7. Chromosome stats

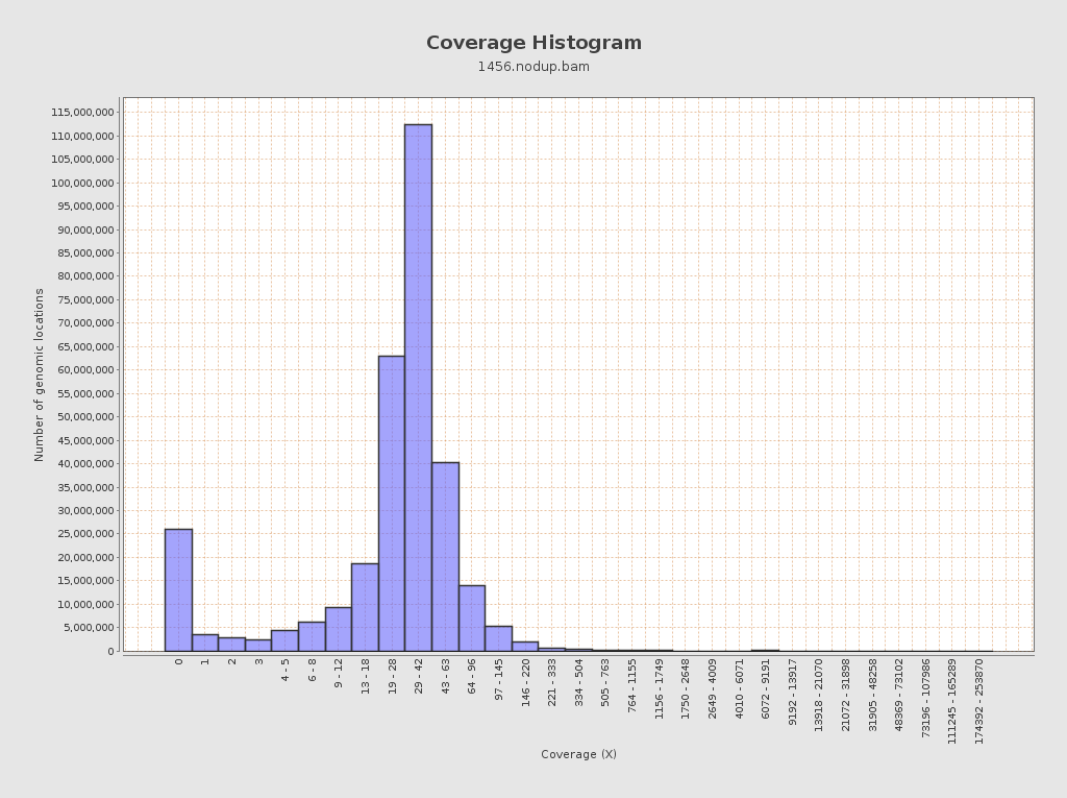
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	988407376	33.2525	89.6721

LT669789.1	36598175	1449324769	39.601	303.567
LT669790.1	30422129	1269587344	41.7324	293.3822
LT669791.1	52758100	2044817316	38.7584	256.0487
LT669792.1	28376109	1116036456	39.3301	354.8318
LT669793.1	33388210	1231382579	36.8808	203.6211
LT669794.1	50579949	1858301296	36.7399	242.3788
LT669795.1	49795044	2351798020	47.2296	446.6306

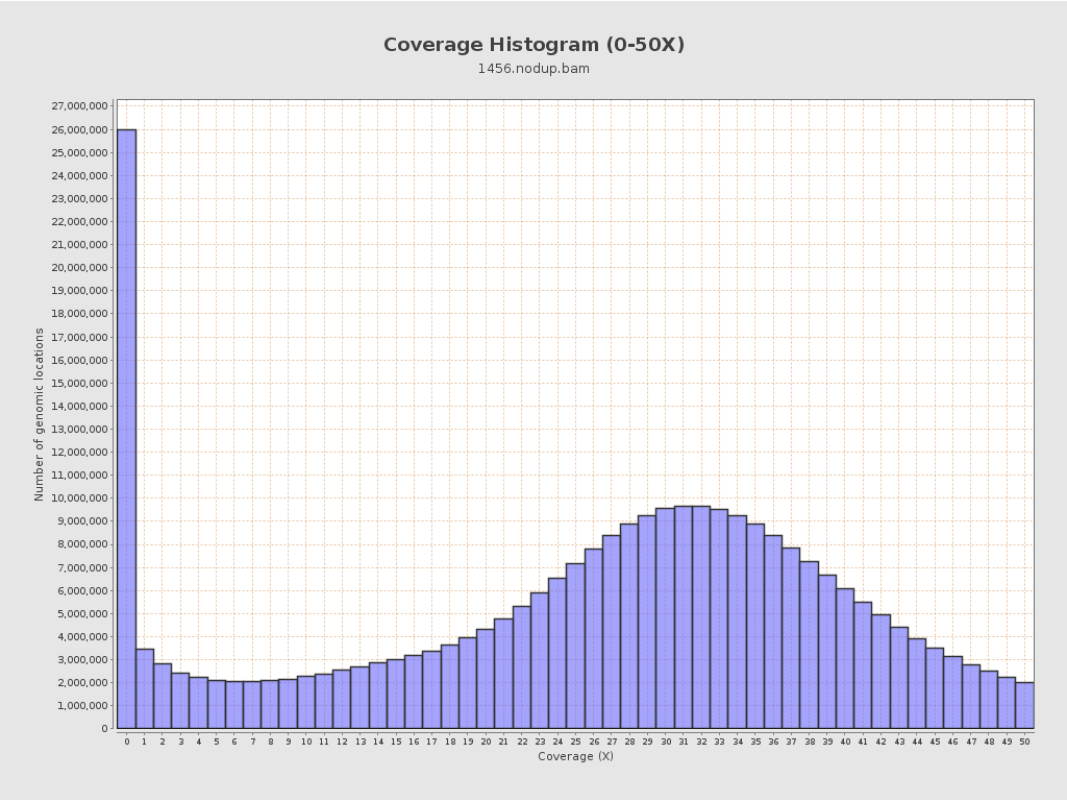
3. Results : Coverage across reference



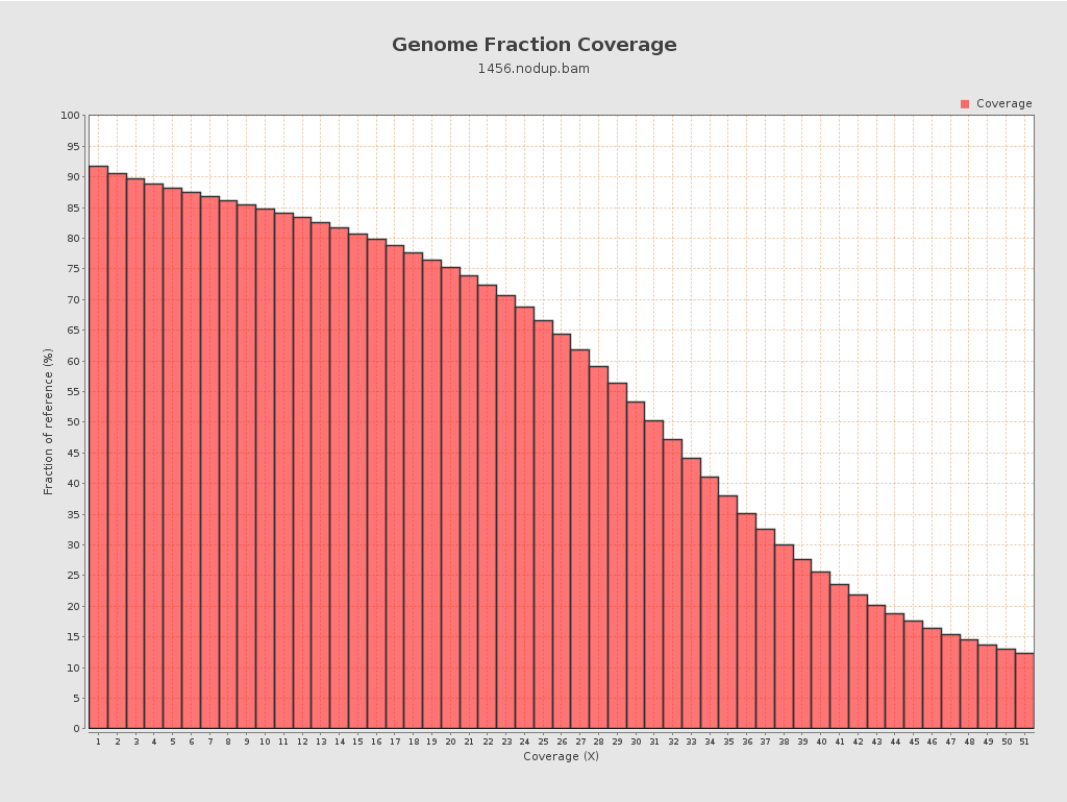
4. Results : Coverage Histogram



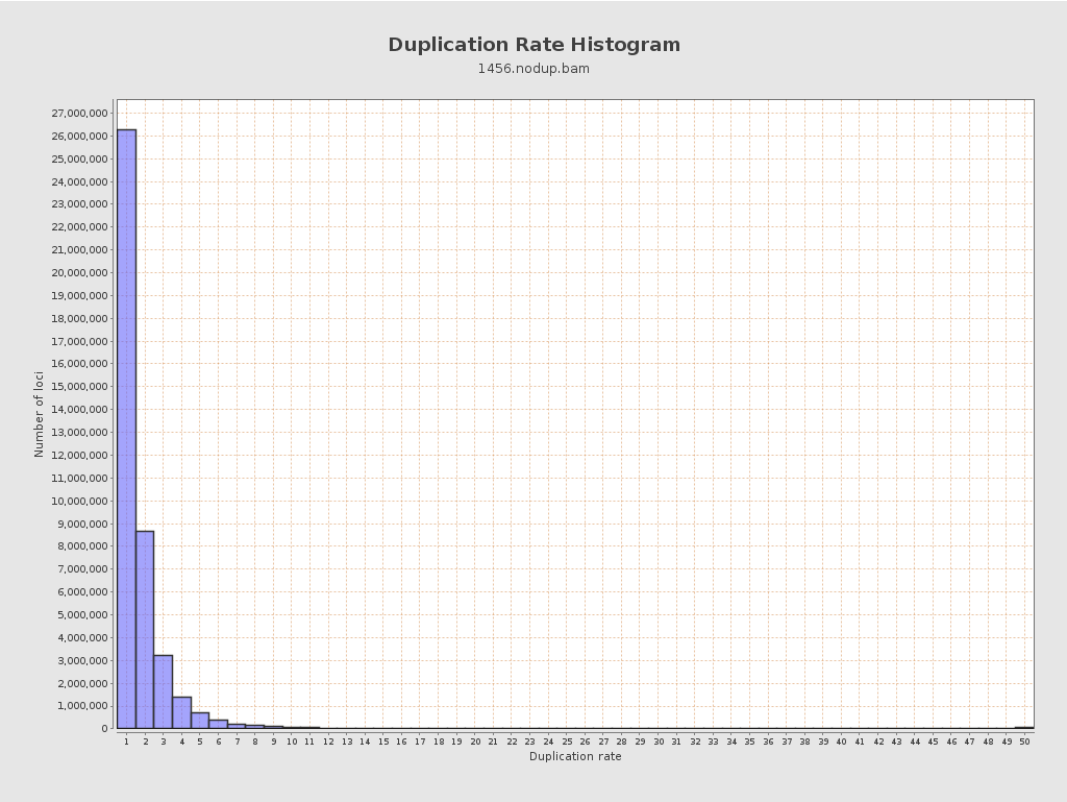
5. Results : Coverage Histogram (0-50X)



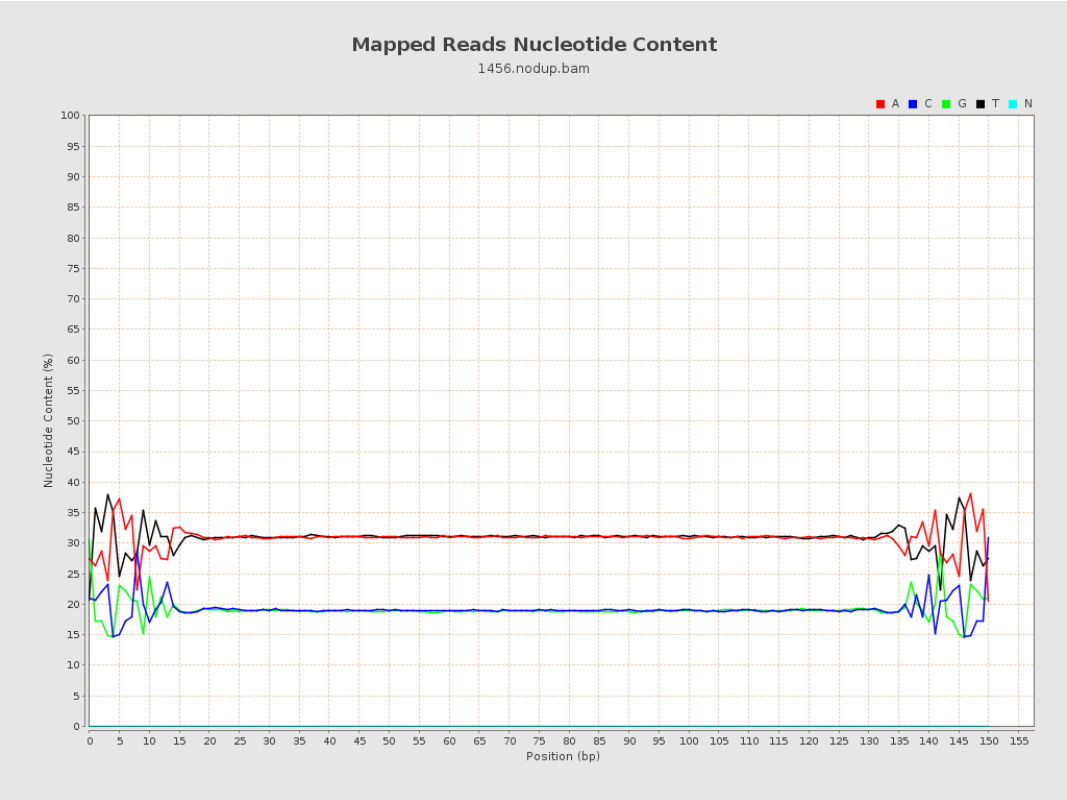
6. Results : Genome Fraction Coverage



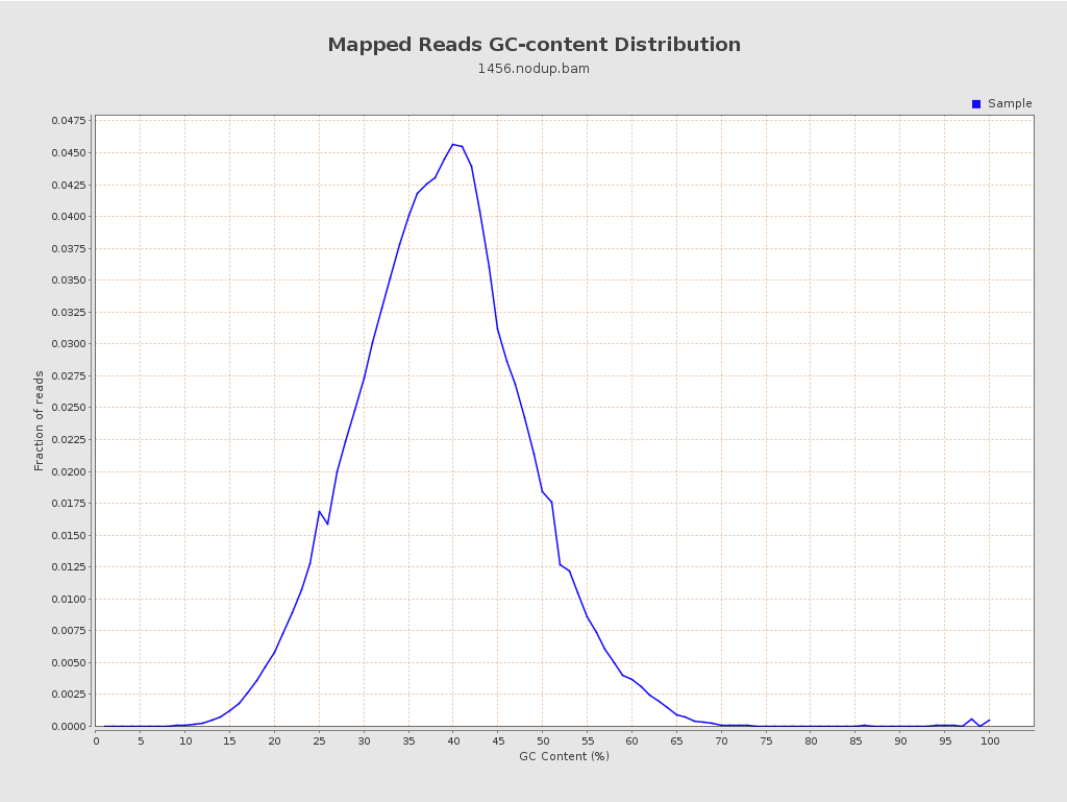
7. Results : Duplication Rate Histogram



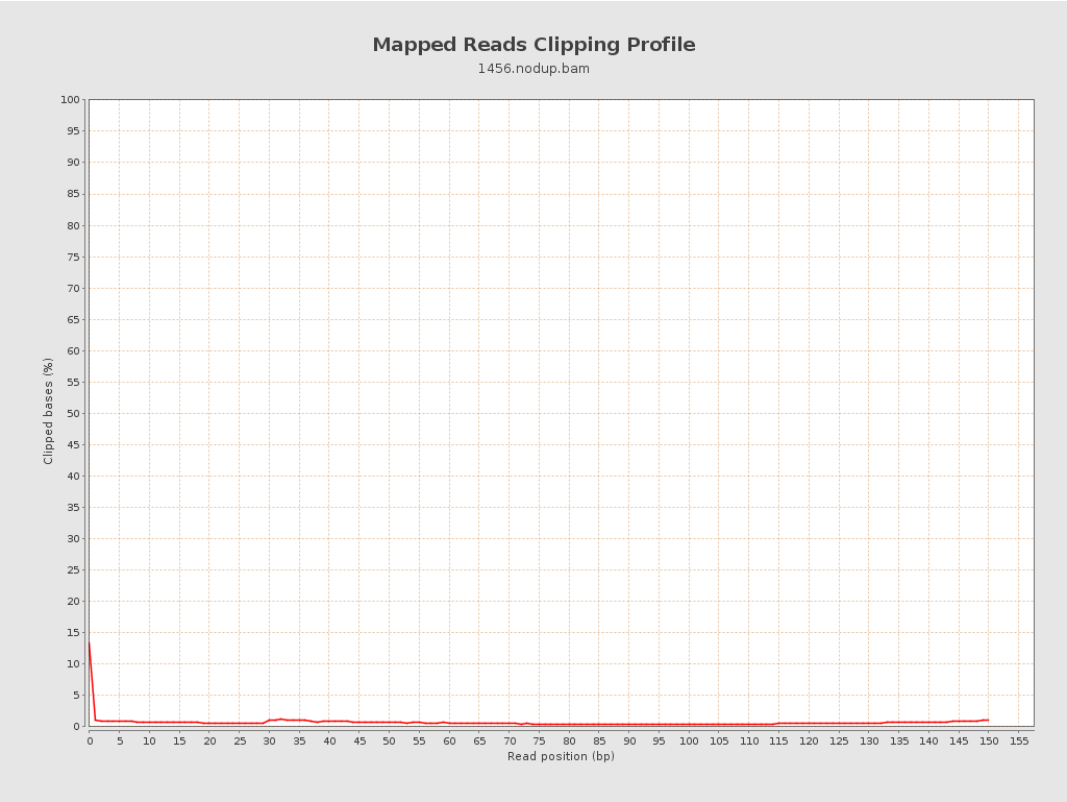
8. Results : Mapped Reads Nucleotide Content



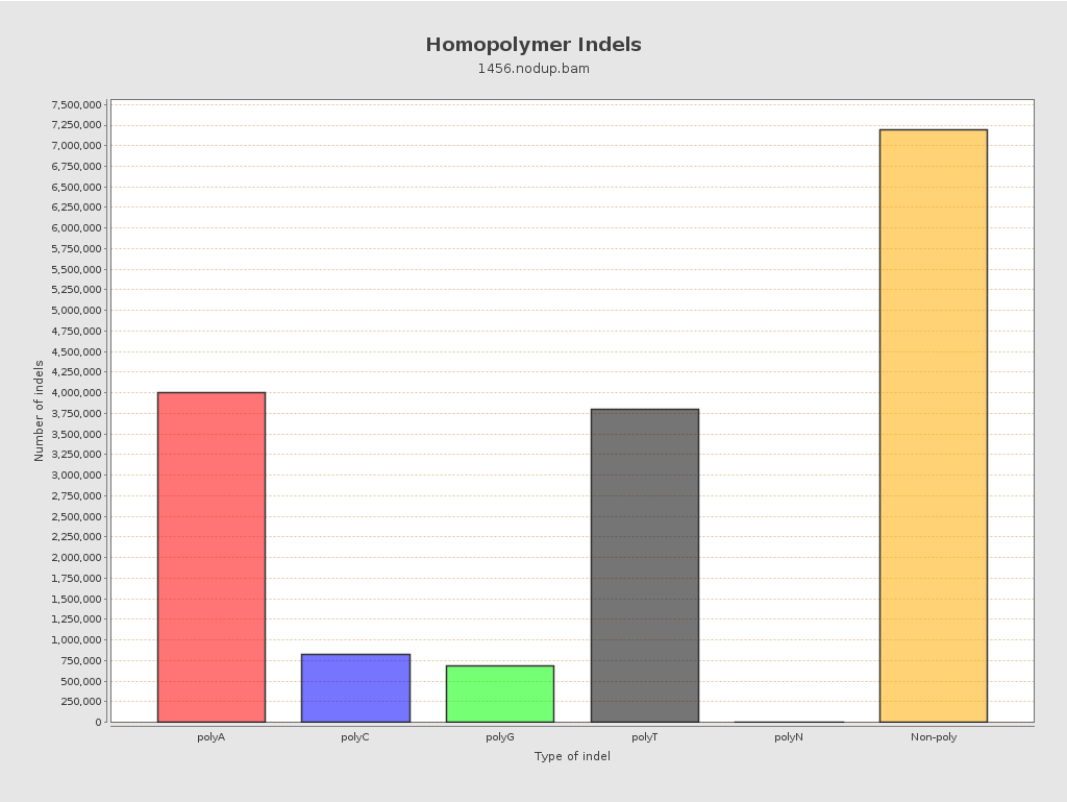
9. Results : Mapped Reads GC-content Distribution



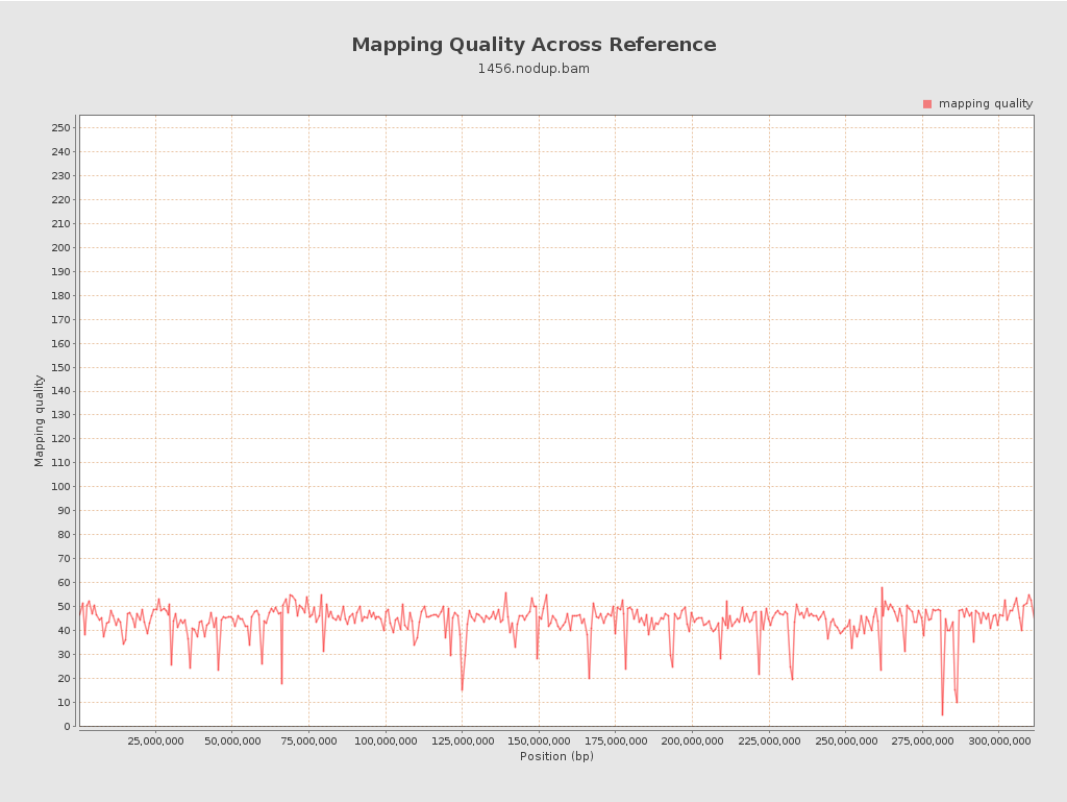
10. Results : Mapped Reads Clipping Profile



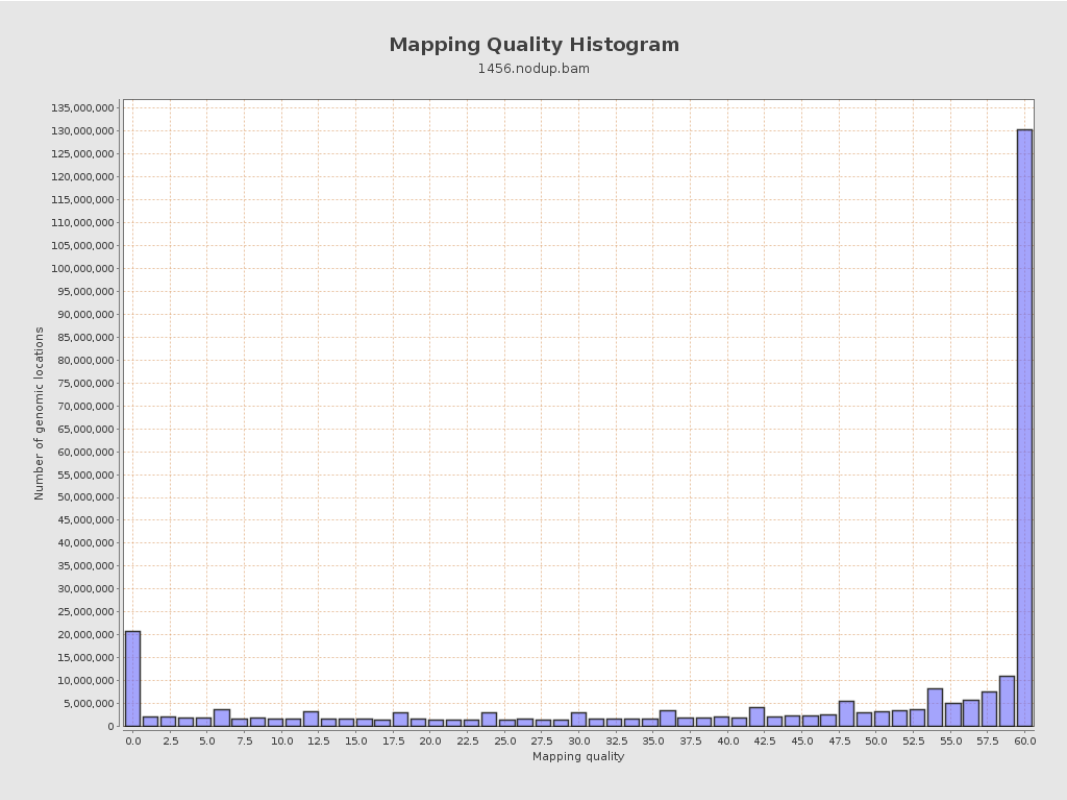
11. Results : Homopolymer Indels



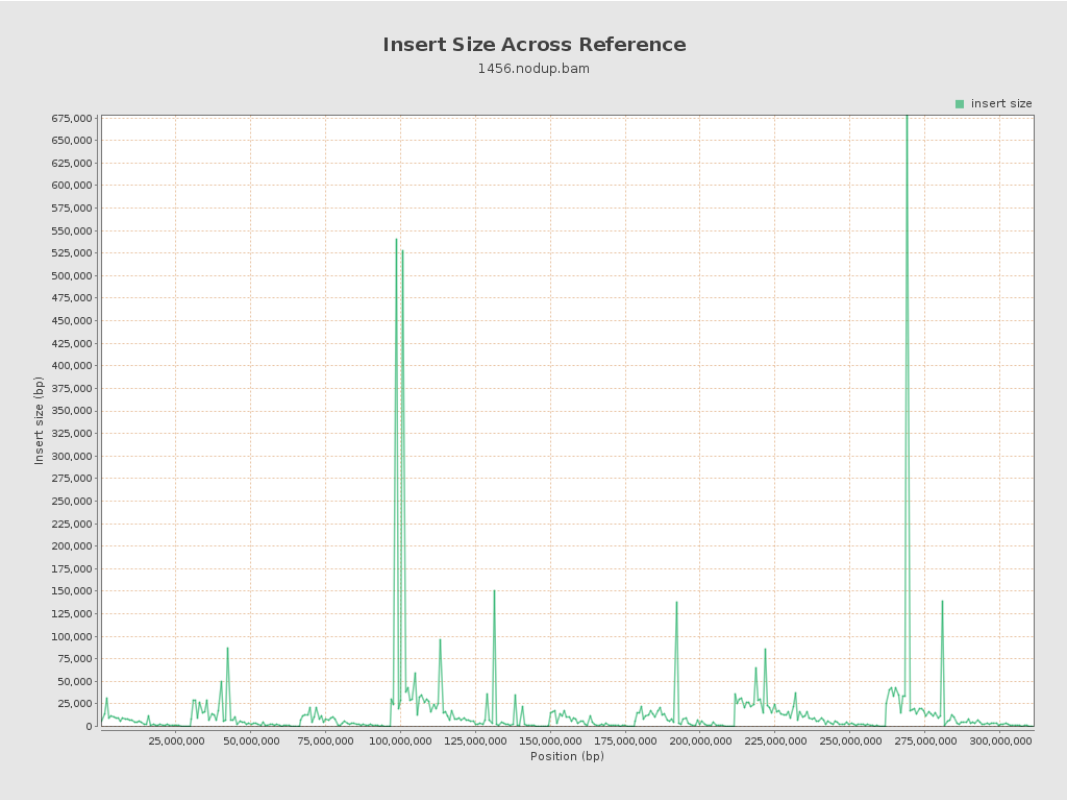
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram