Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:42:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/641.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/641.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_163/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_163_S253_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_163/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_163_S253_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:42:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	97,072,786
Mapped reads	90,295,135 / 93.02%
Unmapped reads	6,777,651 / 6.98%
Mapped paired reads	90,295,135 / 93.02%
Mapped reads, first in pair	45,161,067 / 46.52%
Mapped reads, second in pair	45,134,068 / 46.5%
Mapped reads, both in pair	88,066,387 / 90.72%
Mapped reads, singletons	2,228,748 / 2.3%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	17,947,375 / 18.49%
Clipped reads	20,400,238 / 21.02%

2.2. ACGT Content

Number/percentage of A's	3,866,489,522 / 30.94%
Number/percentage of C's	2,382,626,940 / 19.07%
Number/percentage of T's	3,869,012,025 / 30.96%
Number/percentage of G's	2,378,314,323 / 19.03%
Number/percentage of N's	48,696 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	40.2049
Standard Deviation	363.9128

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Insert size

Mean	237,985.89
Standard Deviation	2,319,723.24
P25/Median/P75	318 / 415 / 541

2.6. Mismatches and indels

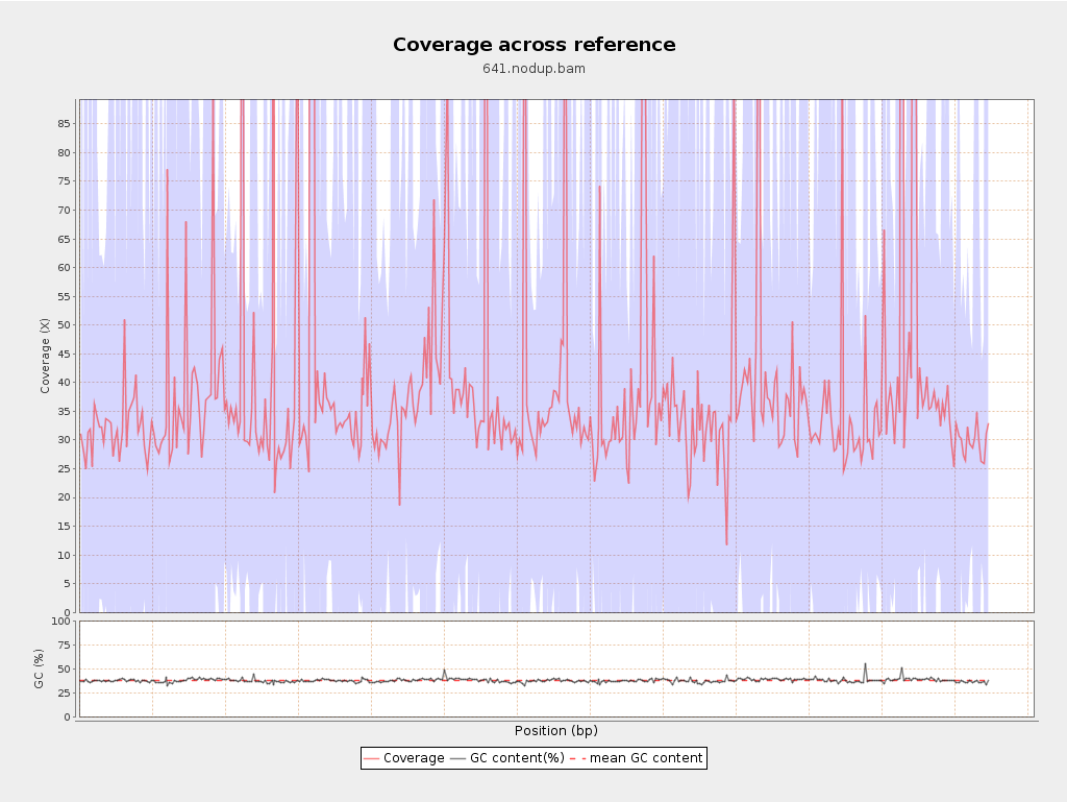
General error rate	2.39%
Mismatches	273,666,970
Insertions	8,845,409
Mapped reads with at least one insertion	8.76%
Deletions	8,744,978
Mapped reads with at least one deletion	8.61%
Homopolymer indels	57.15%

2.7. Chromosome stats

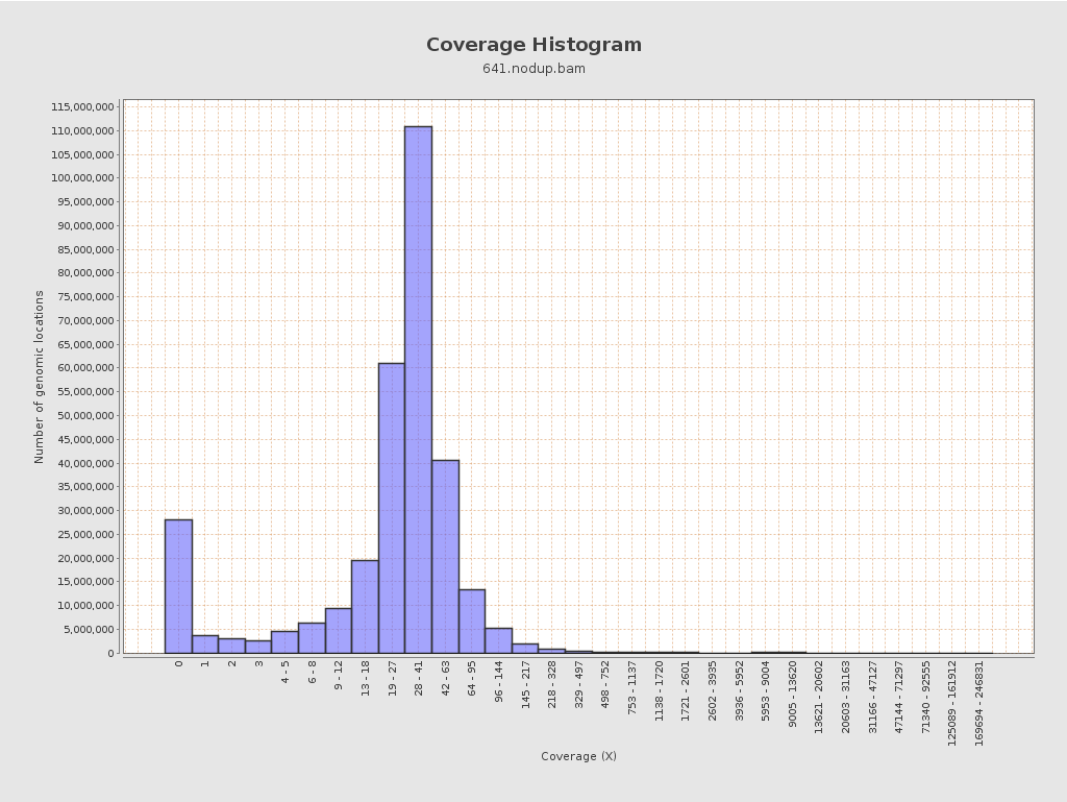
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	943416588	31.7389	114.7523

LT669789.1	36598175	1482353254	40.5035	356.6396
LT669790.1	30422129	1404584224	46.1698	455.4591
LT669791.1	52758100	2112649347	40.0441	334.0443
LT669792.1	28376109	1123105995	39.5793	388.3157
LT669793.1	33388210	1266513185	37.9329	323.0552
LT669794.1	50579949	1911820902	37.798	287.5297
LT669795.1	49795044	2285106524	45.8902	492.4773

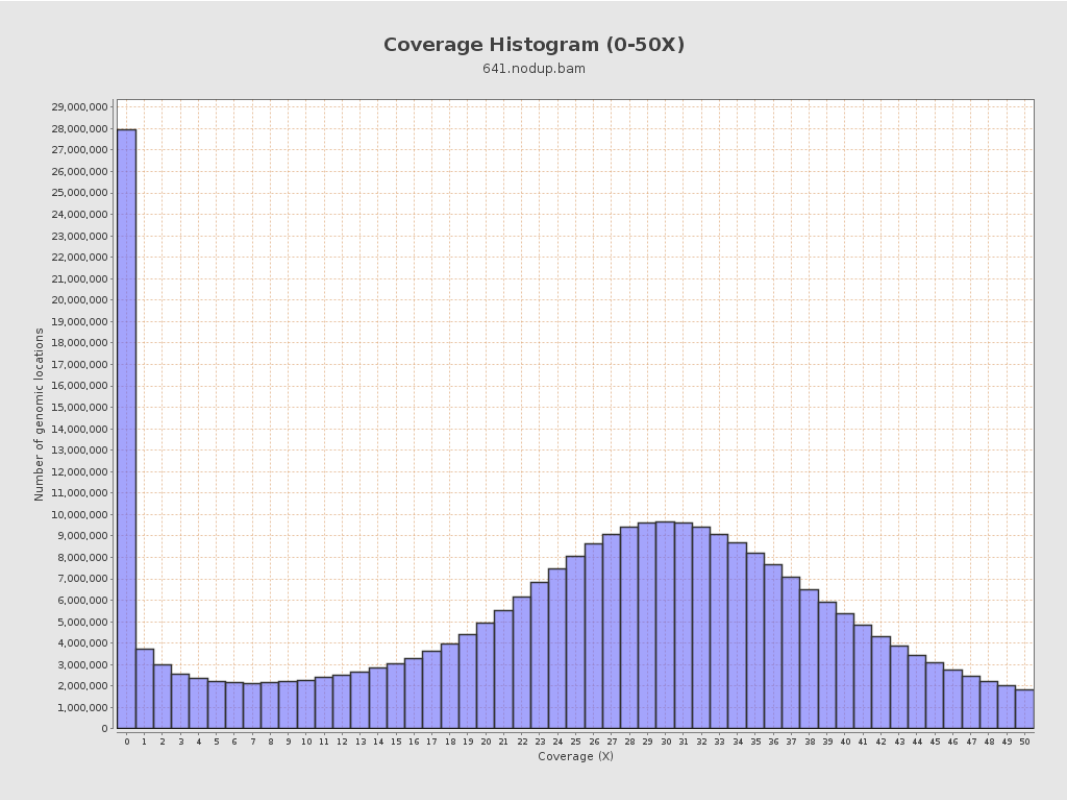
3. Results : Coverage across reference



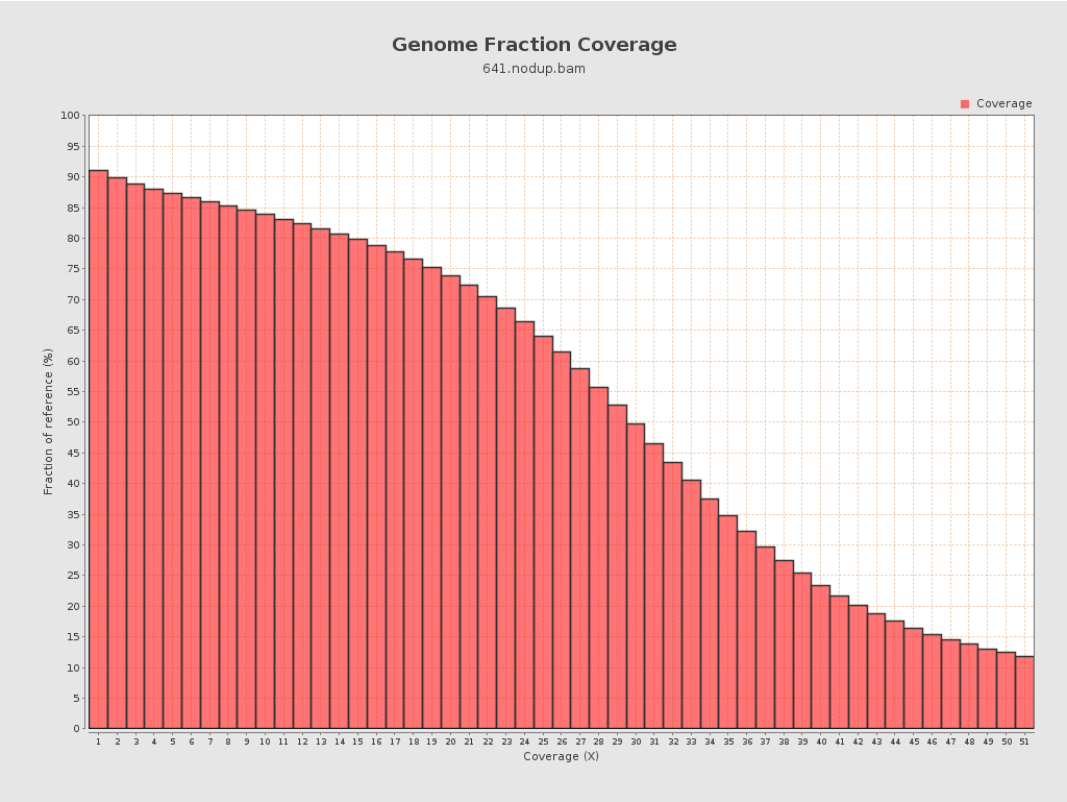
4. Results : Coverage Histogram



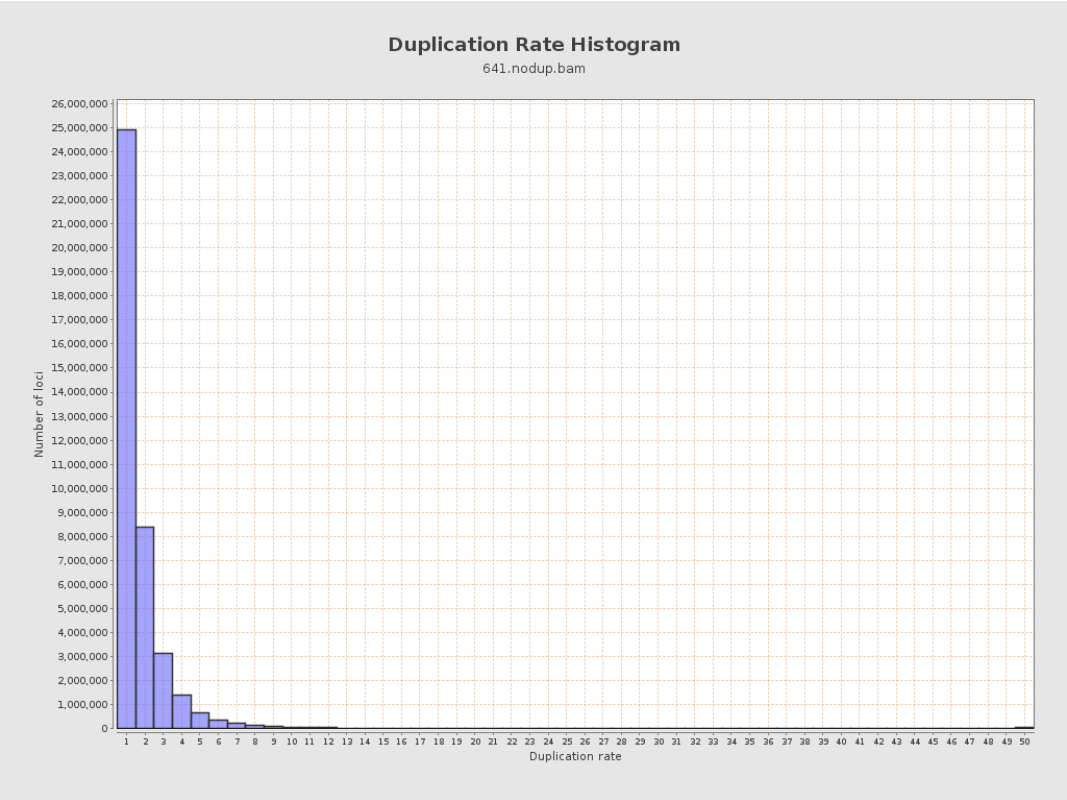
5. Results : Coverage Histogram (0-50X)



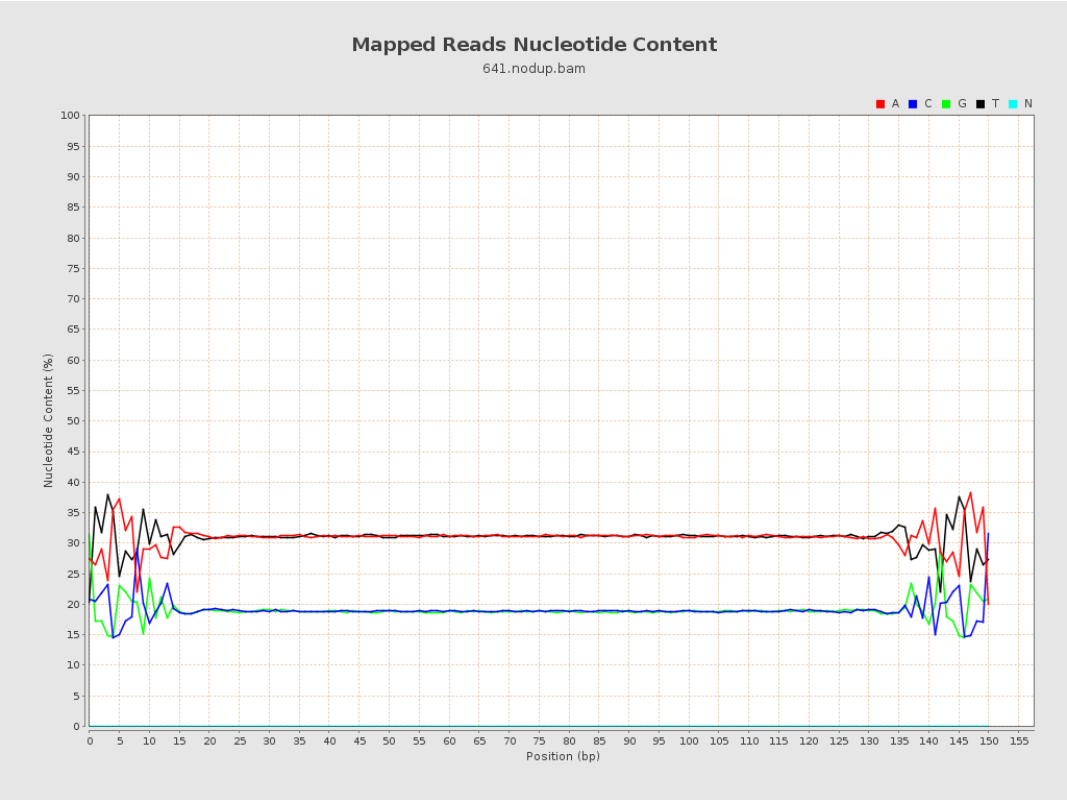
6. Results : Genome Fraction Coverage



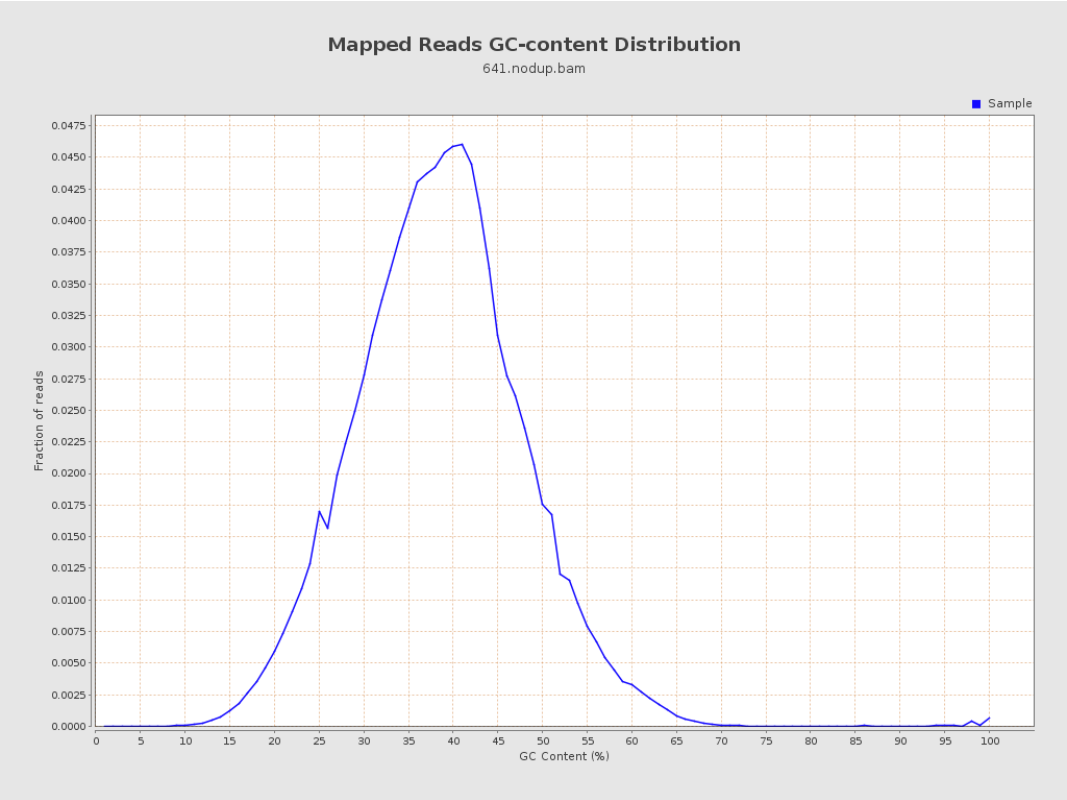
7. Results : Duplication Rate Histogram



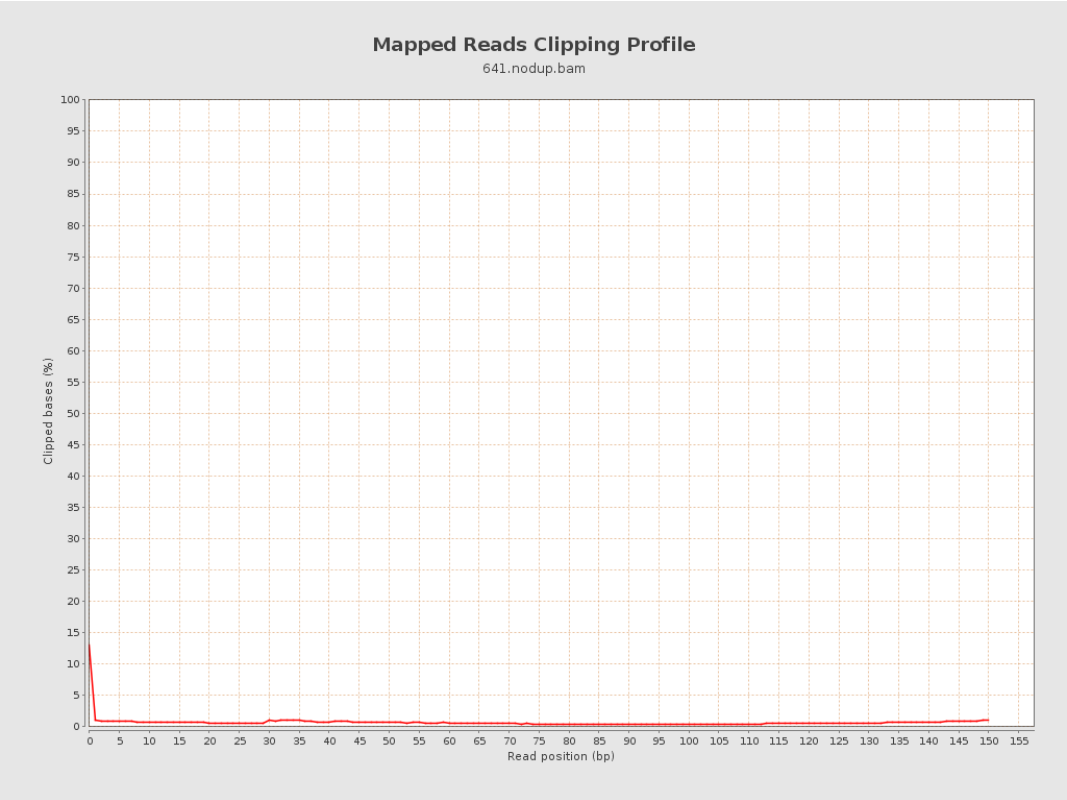
8. Results : Mapped Reads Nucleotide Content



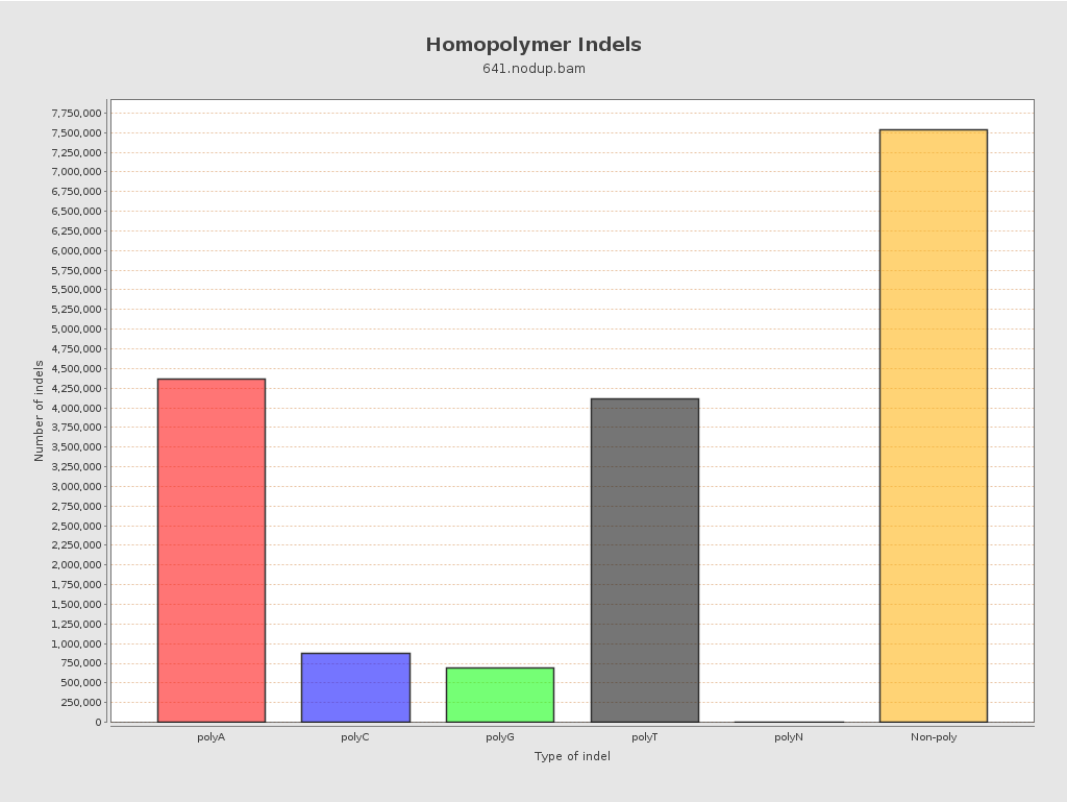
9. Results : Mapped Reads GC-content Distribution



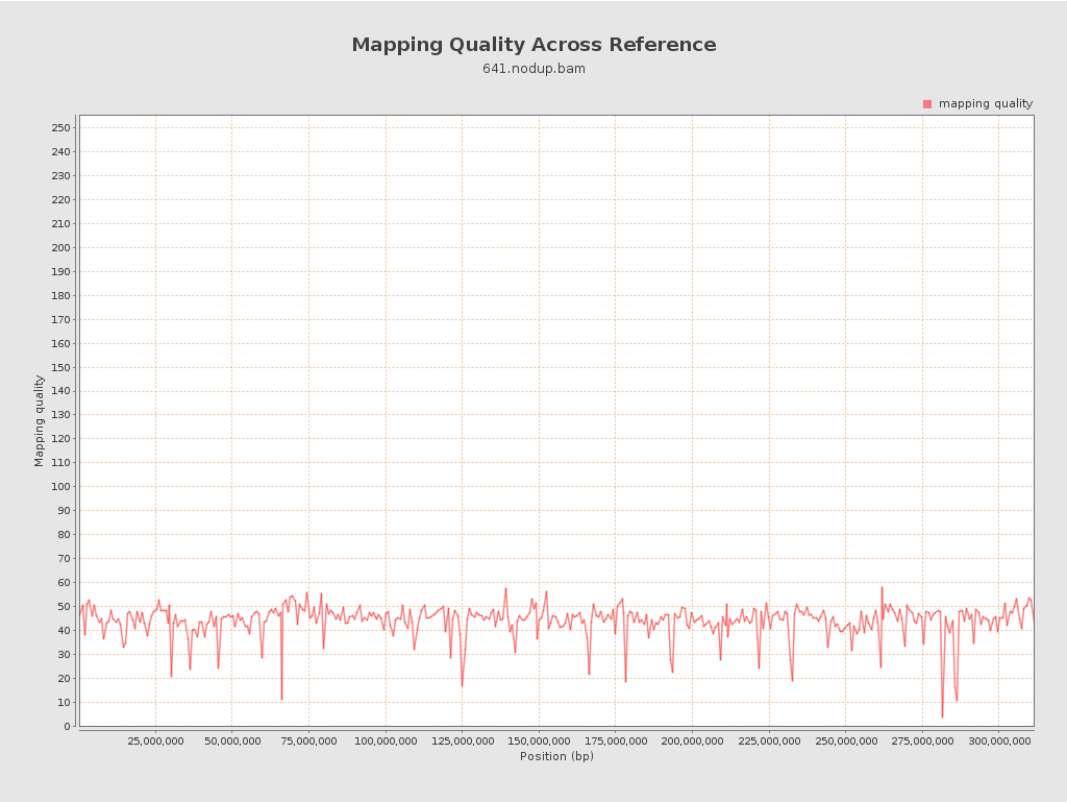
10. Results : Mapped Reads Clipping Profile



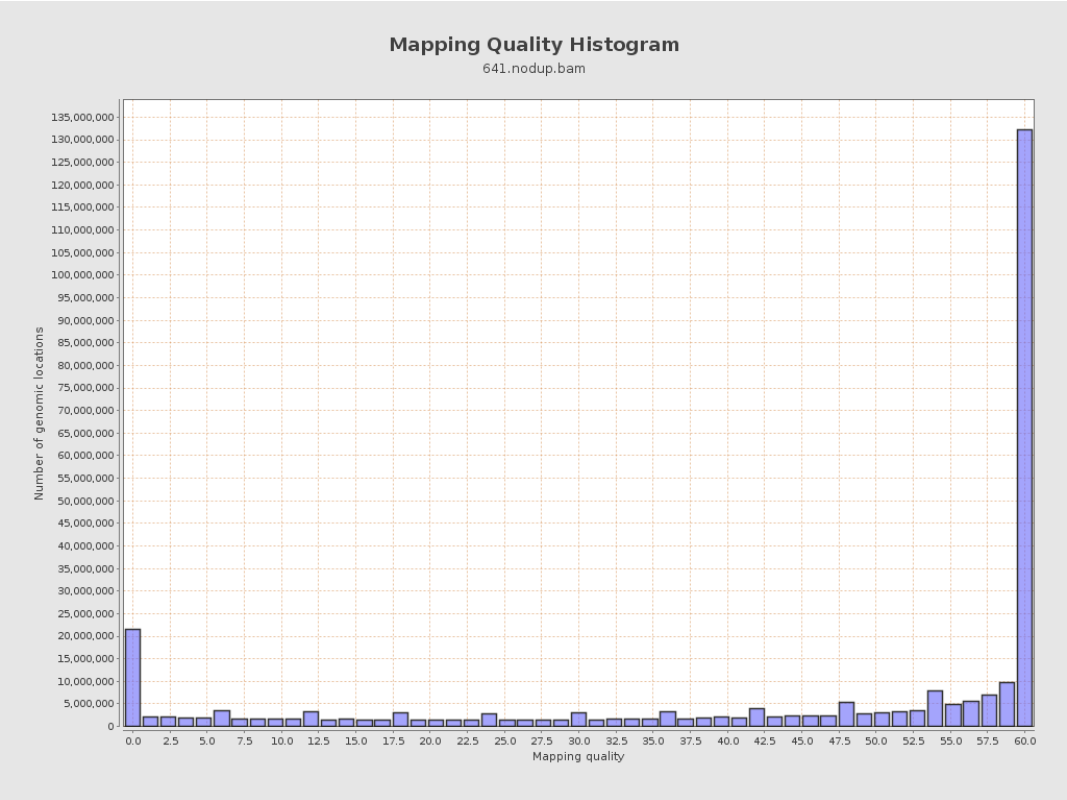
11. Results : Homopolymer Indels



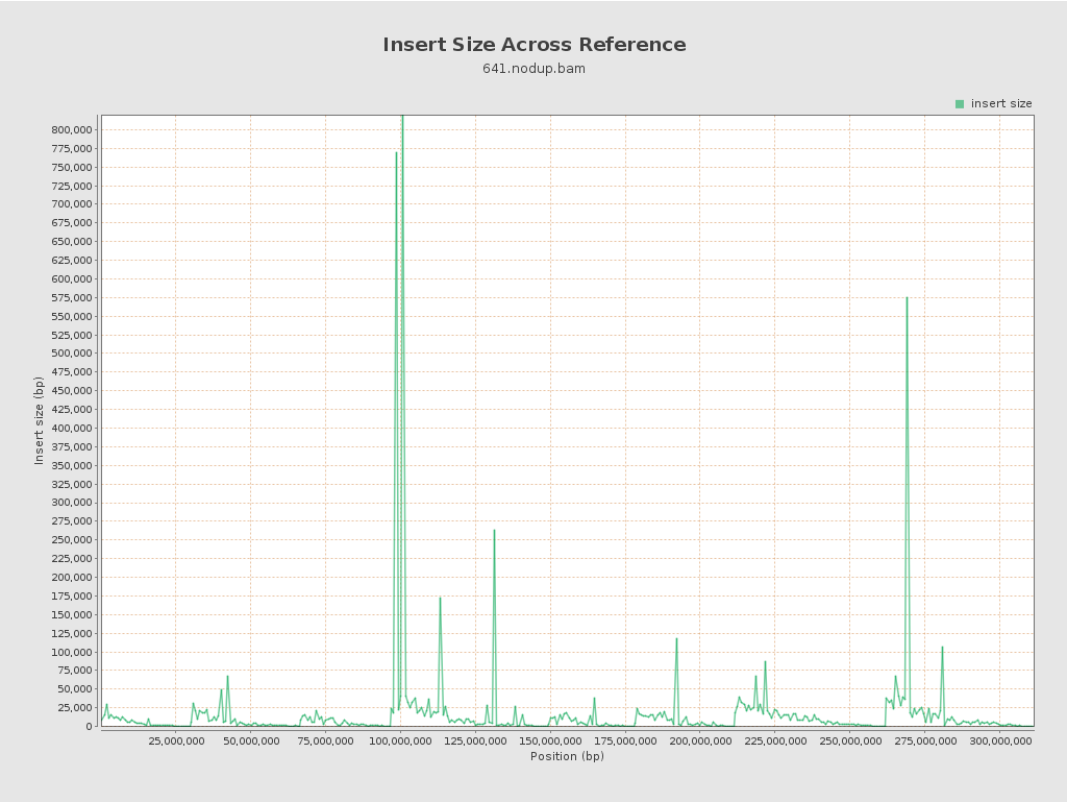
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram