Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/461.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/461.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_217/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_217_S298_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_217/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_217_S298_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:06 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,062,802
Mapped reads	64,500,519 / 94.77%
Unmapped reads	3,562,283 / 5.23%
Mapped paired reads	64,500,519 / 94.77%
Mapped reads, first in pair	32,324,313 / 47.49%
Mapped reads, second in pair	32,176,206 / 47.27%
Mapped reads, both in pair	63,312,508 / 93.02%
Mapped reads, singletons	1,188,011 / 1.75%
Read min/max/mean length	30 / 151 / 147.99
Duplicated reads (flagged)	8,850,987 / 13%
Clipped reads	14,650,403 / 21.52%

2.2. ACGT Content

Number/percentage of A's	2,748,320,681 / 30.76%
Number/percentage of C's	1,720,906,662 / 19.26%
Number/percentage of T's	2,751,935,141 / 30.8%
Number/percentage of G's	1,714,849,409 / 19.19%
Number/percentage of N's	33,631 / 0%
GC Percentage	38.45%

2.3. Coverage

Mean	28.7489
Standard Deviation	238.4652

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Insert size

Mean	225,879.39
Standard Deviation	2,250,832.45
P25/Median/P75	318 / 418 / 546

2.6. Mismatches and indels

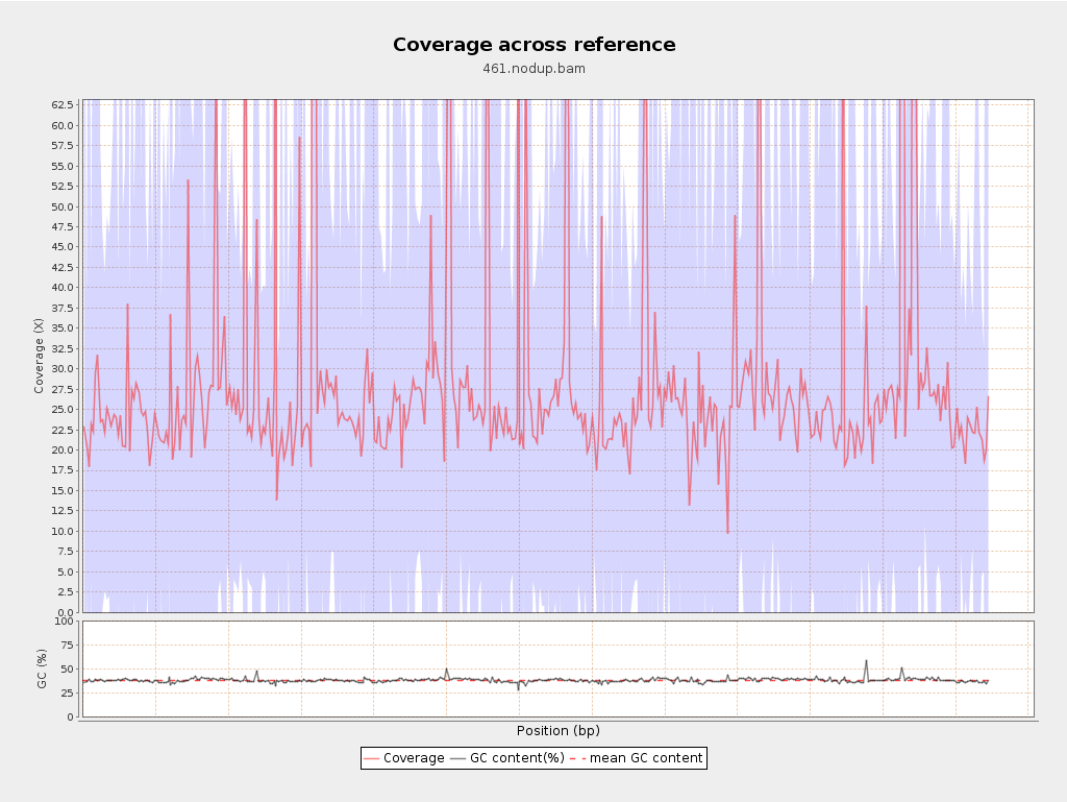
General error rate	2.32%
Mismatches	190,826,863
Insertions	6,041,972
Mapped reads with at least one insertion	8.43%
Deletions	6,187,784
Mapped reads with at least one deletion	8.49%
Homopolymer indels	55.74%

2.7. Chromosome stats

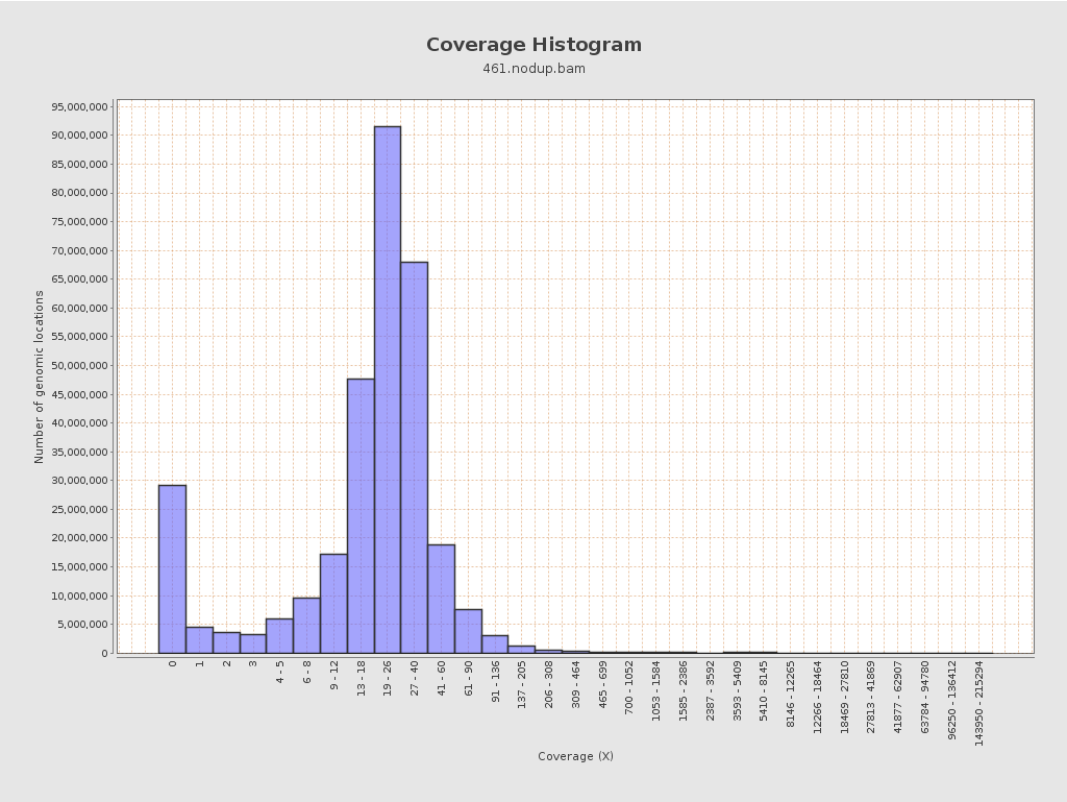
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	705637887	23.7394	82.6802

LT669789.1	36598175	1074932365	29.3712	270.5321
LT669790.1	30422129	917296318	30.1523	215.5887
LT669791.1	52758100	1488645156	28.2164	224.1678
LT669792.1	28376109	806697886	28.4288	244.9903
LT669793.1	33388210	880497887	26.3715	120.3073
LT669794.1	50579949	1401731304	27.7132	234.2104
LT669795.1	49795044	1683923243	33.8171	341.6283

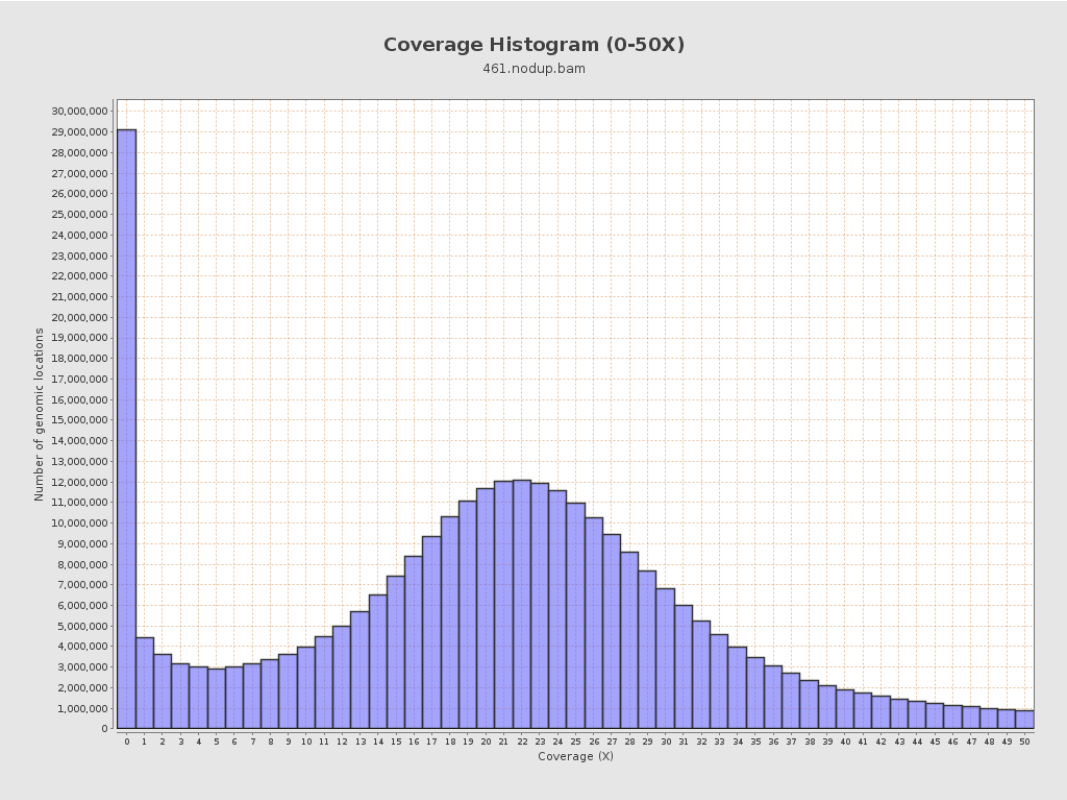
3. Results : Coverage across reference



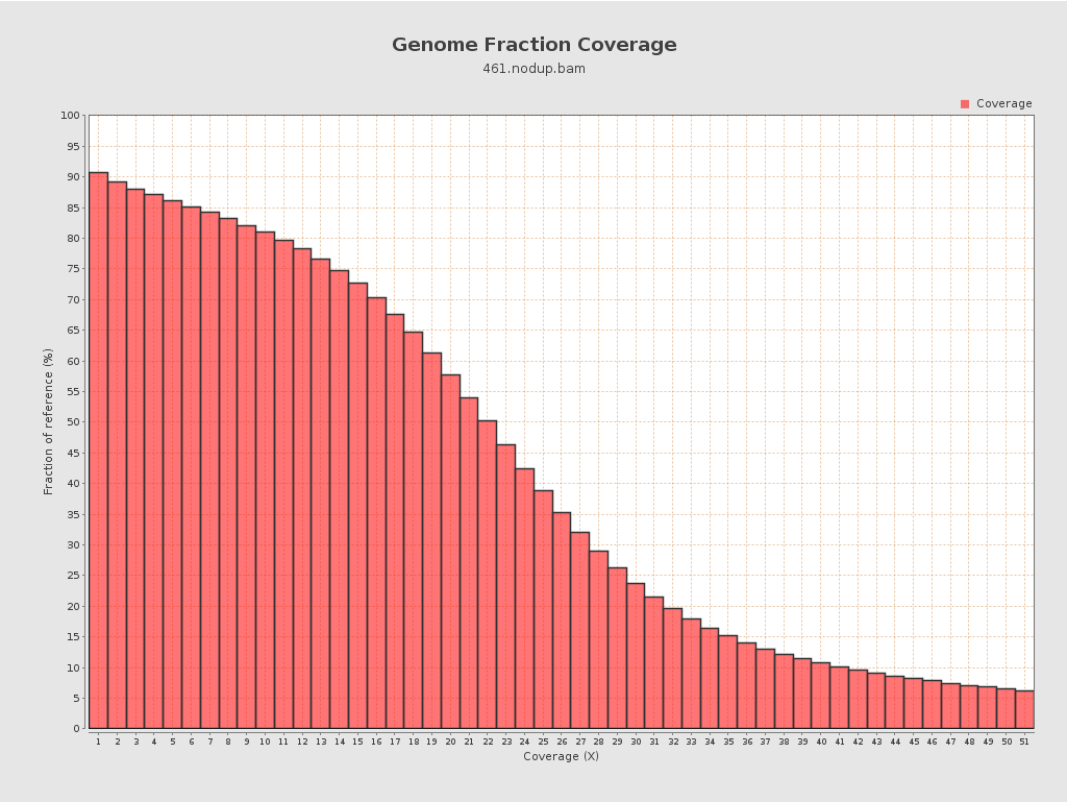
4. Results : Coverage Histogram



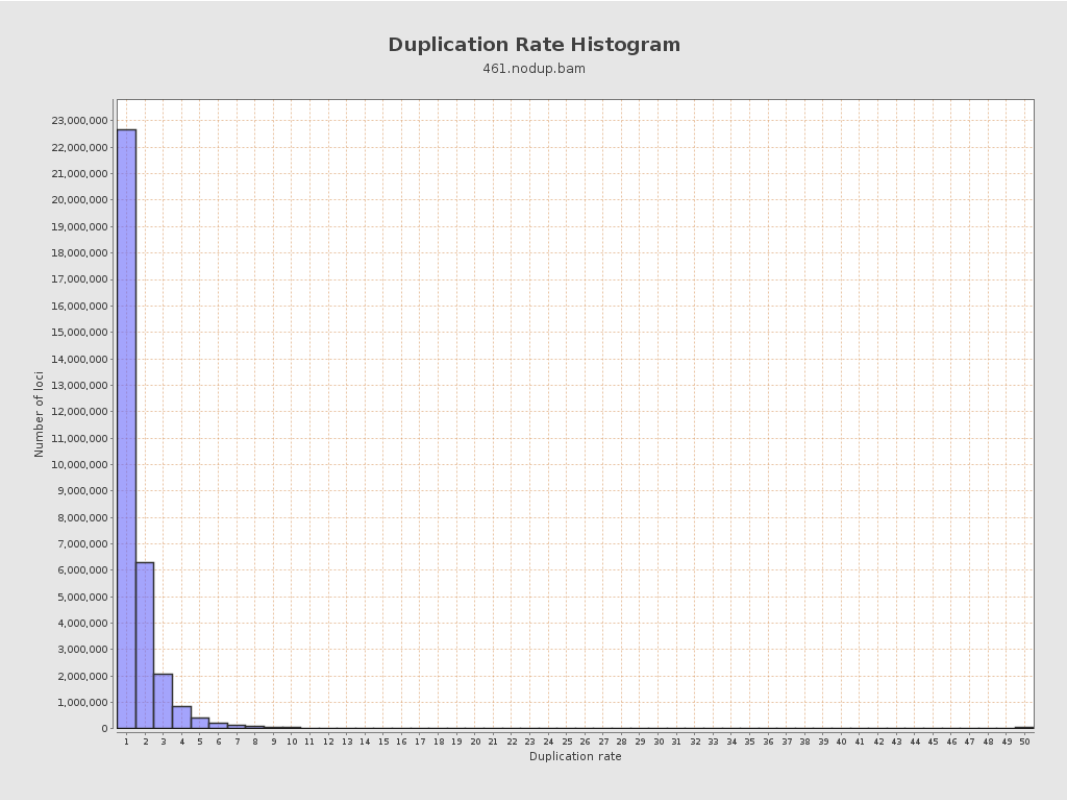
5. Results : Coverage Histogram (0-50X)



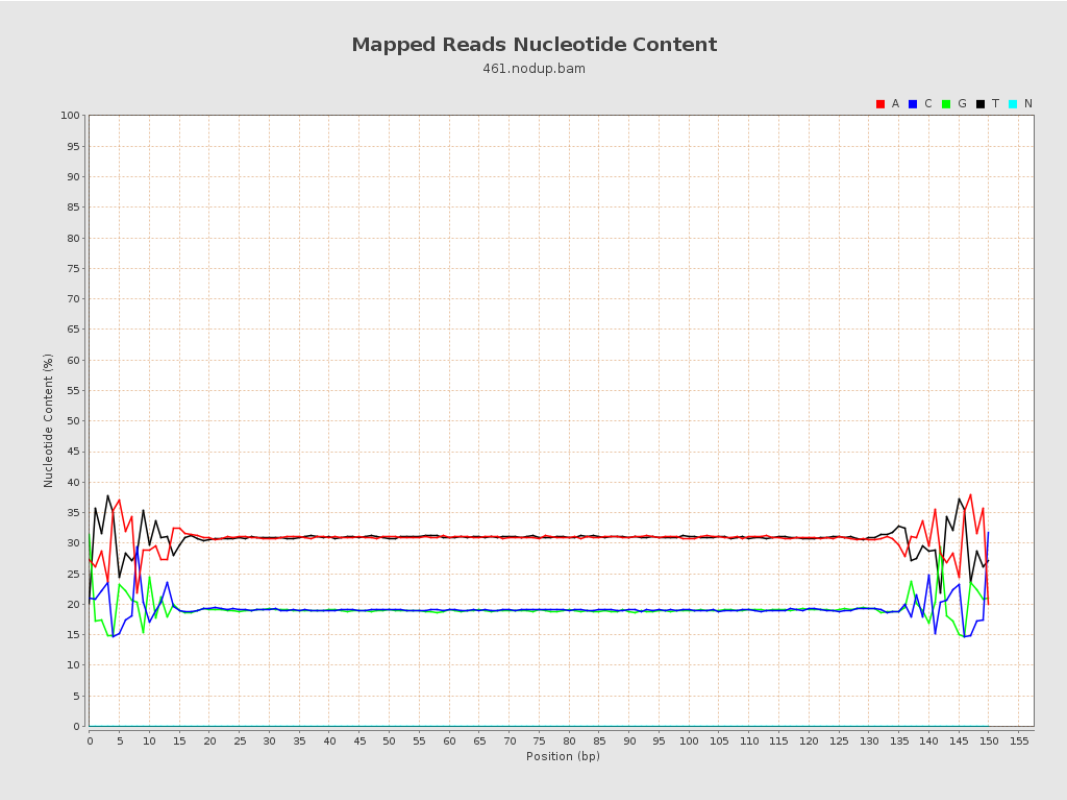
6. Results : Genome Fraction Coverage



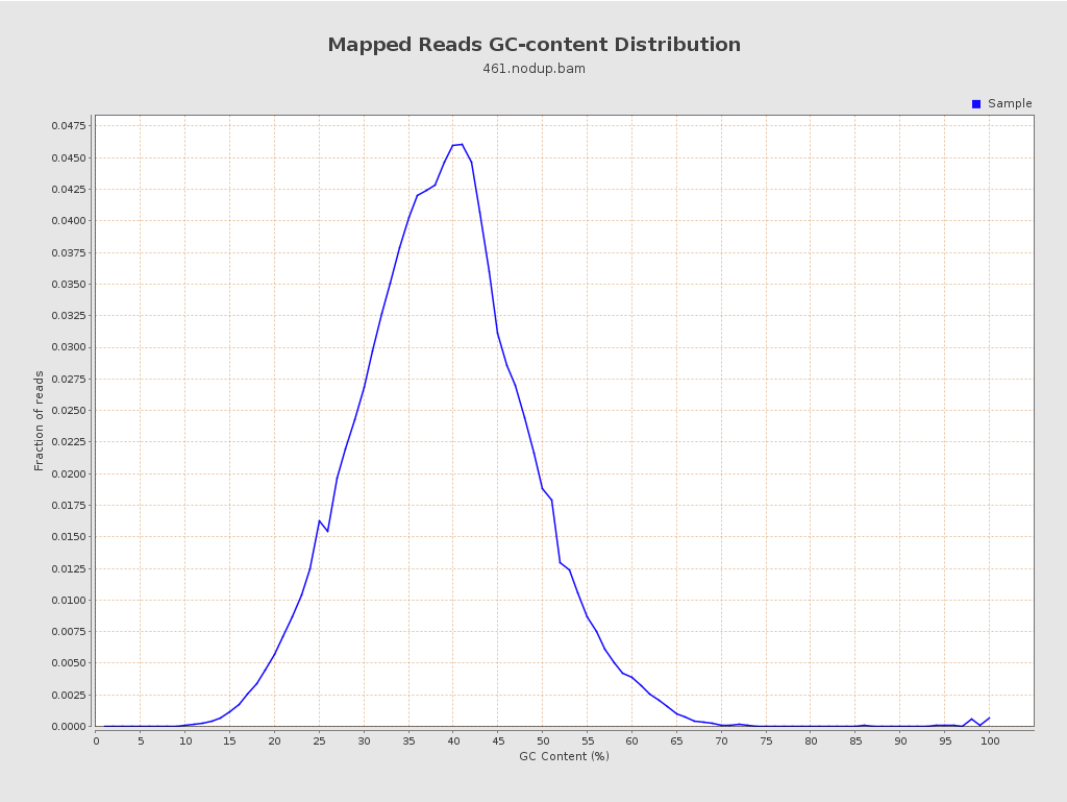
7. Results : Duplication Rate Histogram



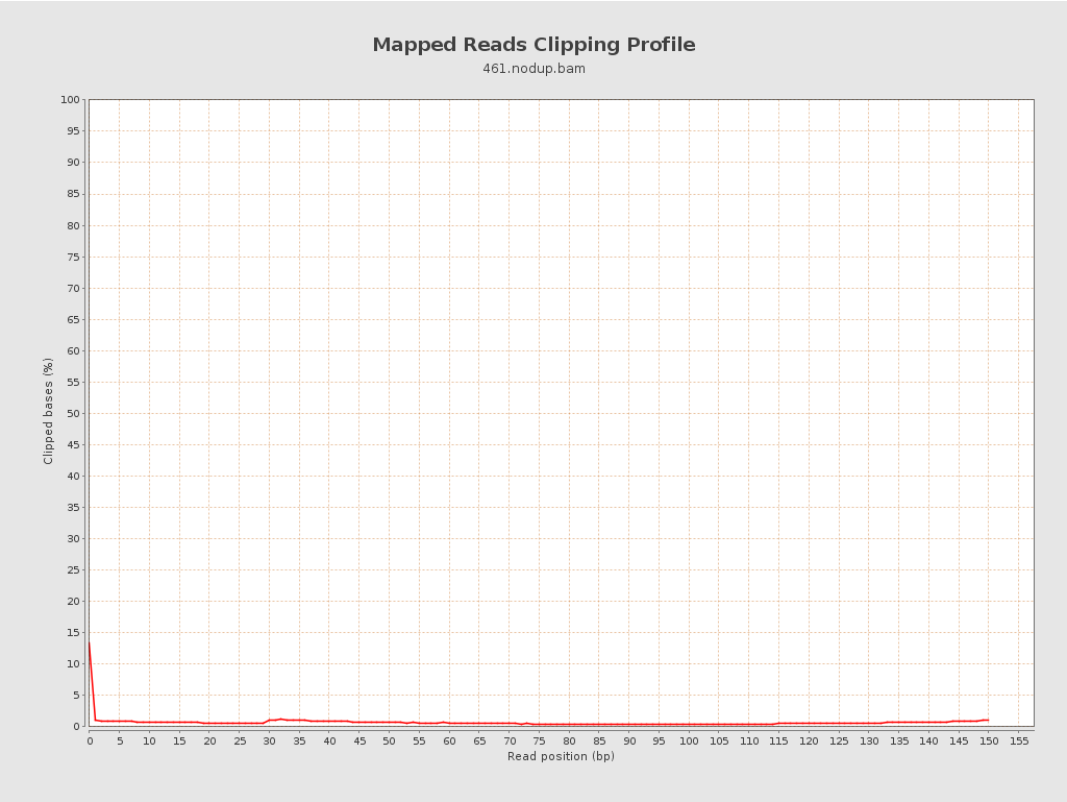
8. Results : Mapped Reads Nucleotide Content



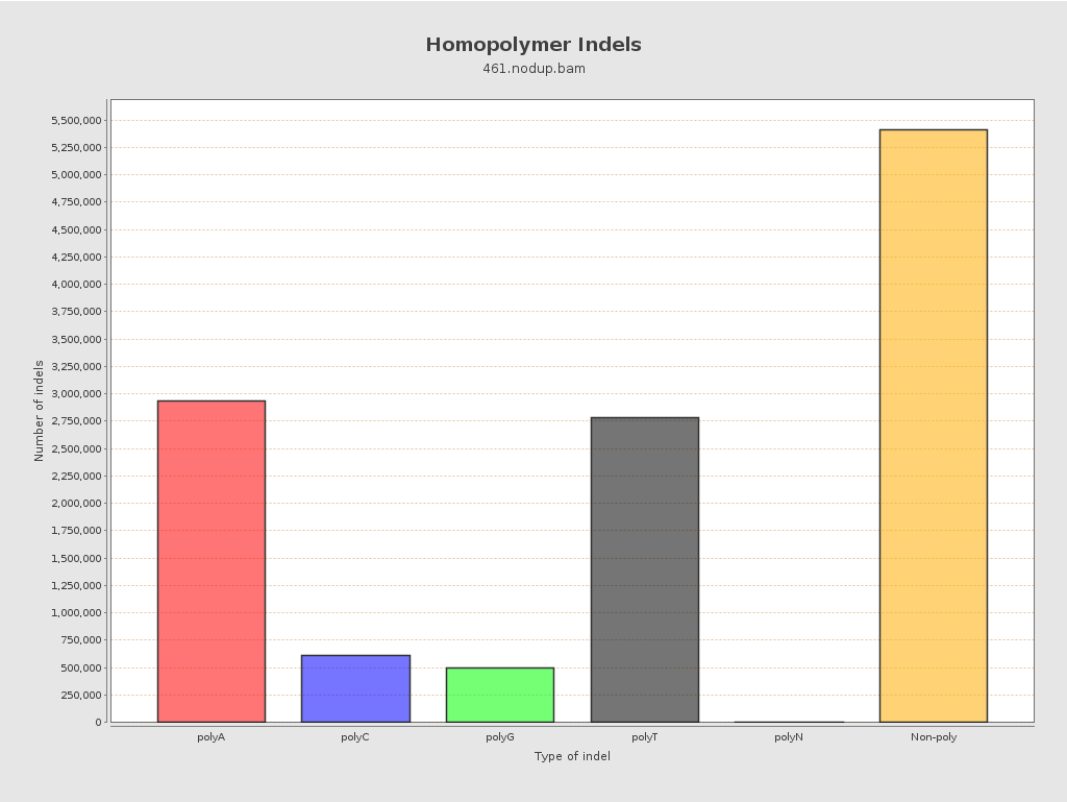
9. Results : Mapped Reads GC-content Distribution



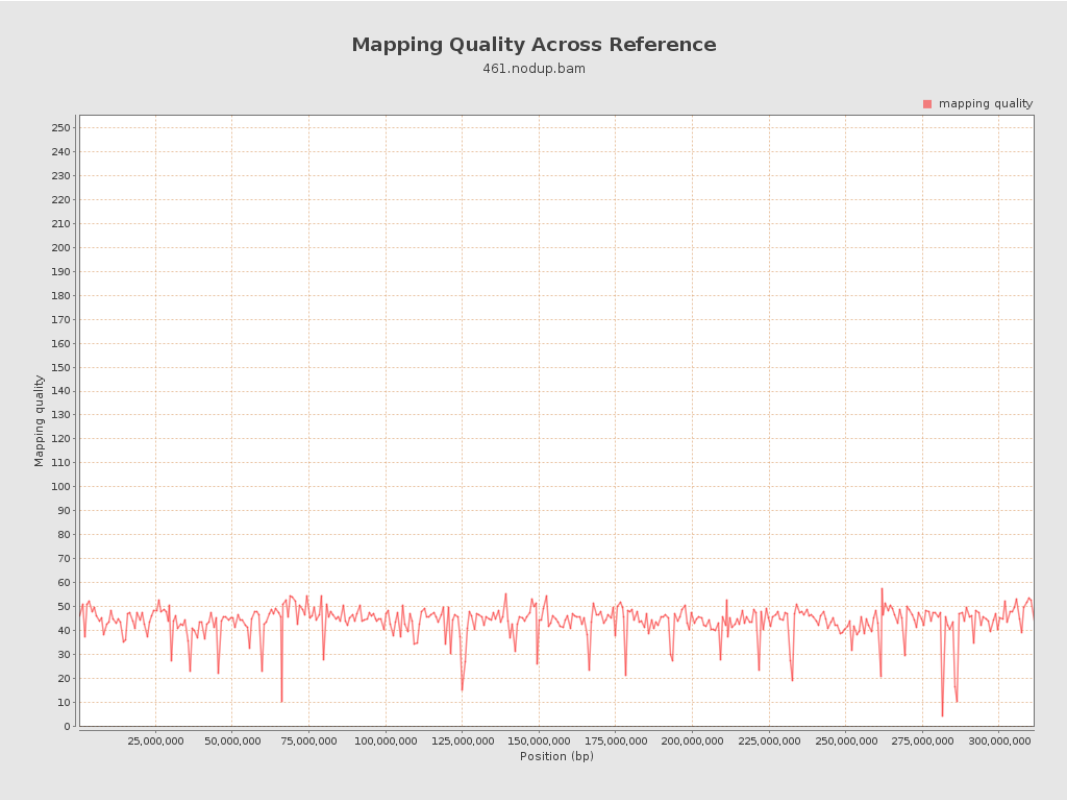
10. Results : Mapped Reads Clipping Profile



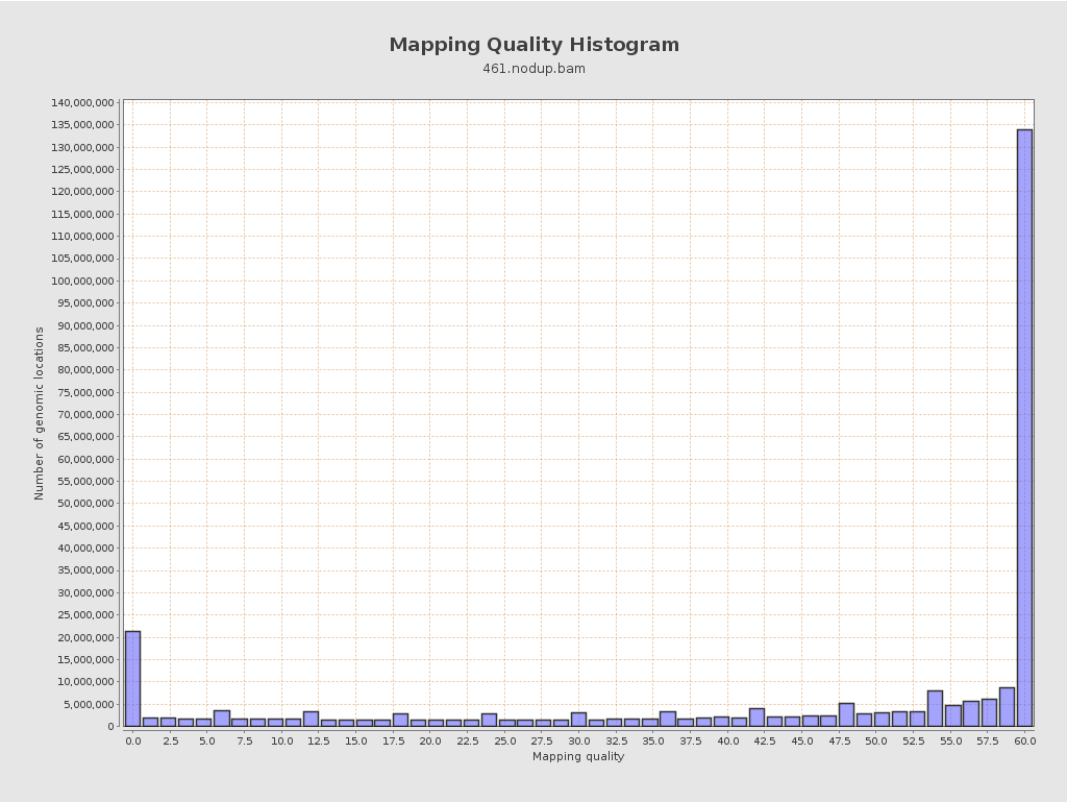
11. Results : Homopolymer Indels



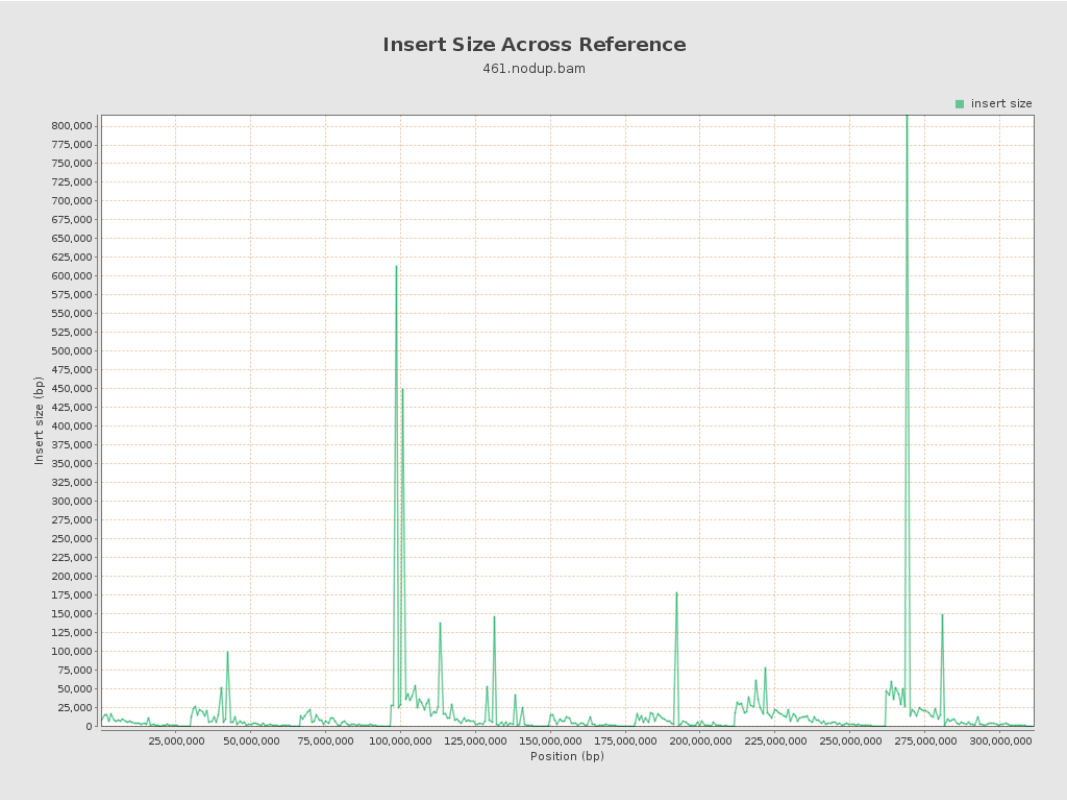
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram