Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/620.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/620.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_243/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_243_S324_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_243/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_243_S324_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	86,930,668
Mapped reads	79,765,328 / 91.76%
Unmapped reads	7,165,340 / 8.24%
Mapped paired reads	79,765,328 / 91.76%
Mapped reads, first in pair	39,982,543 / 45.99%
Mapped reads, second in pair	39,782,785 / 45.76%
Mapped reads, both in pair	77,390,178 / 89.03%
Mapped reads, singletons	2,375,150 / 2.73%
Read min/max/mean length	30 / 151 / 148.01
Duplicated reads (flagged)	15,020,760 / 17.28%
Clipped reads	19,880,313 / 22.87%

2.2. ACGT Content

Number/percentage of A's	3,371,805,420 / 30.97%
Number/percentage of C's	2,070,909,659 / 19.02%
Number/percentage of T's	3,373,419,811 / 30.99%
Number/percentage of G's	2,070,853,791 / 19.02%
Number/percentage of N's	39,360 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	35.0256
Standard Deviation	353.4344

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Insert size

Mean	258,068.7
Standard Deviation	2,447,786.12
P25/Median/P75	314 / 416 / 546

2.6. Mismatches and indels

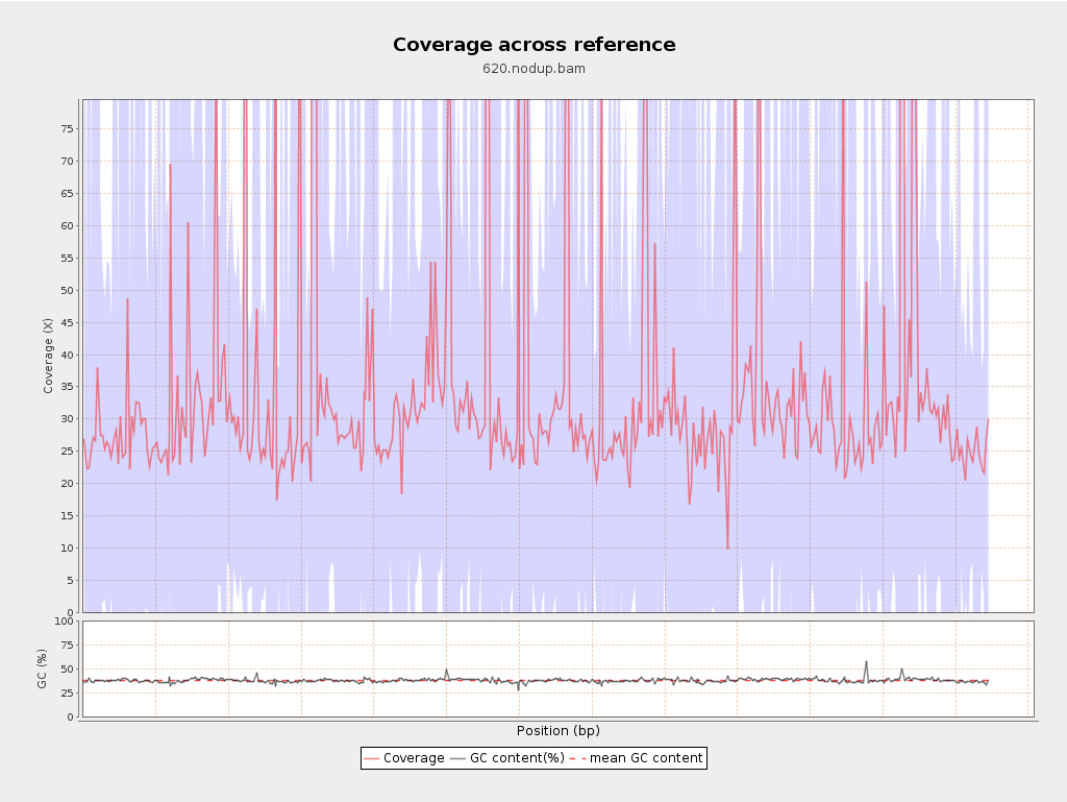
General error rate	2.43%
Mismatches	242,972,982
Insertions	8,042,388
Mapped reads with at least one insertion	9%
Deletions	7,711,586
Mapped reads with at least one deletion	8.58%
Homopolymer indels	57.27%

2.7. Chromosome stats

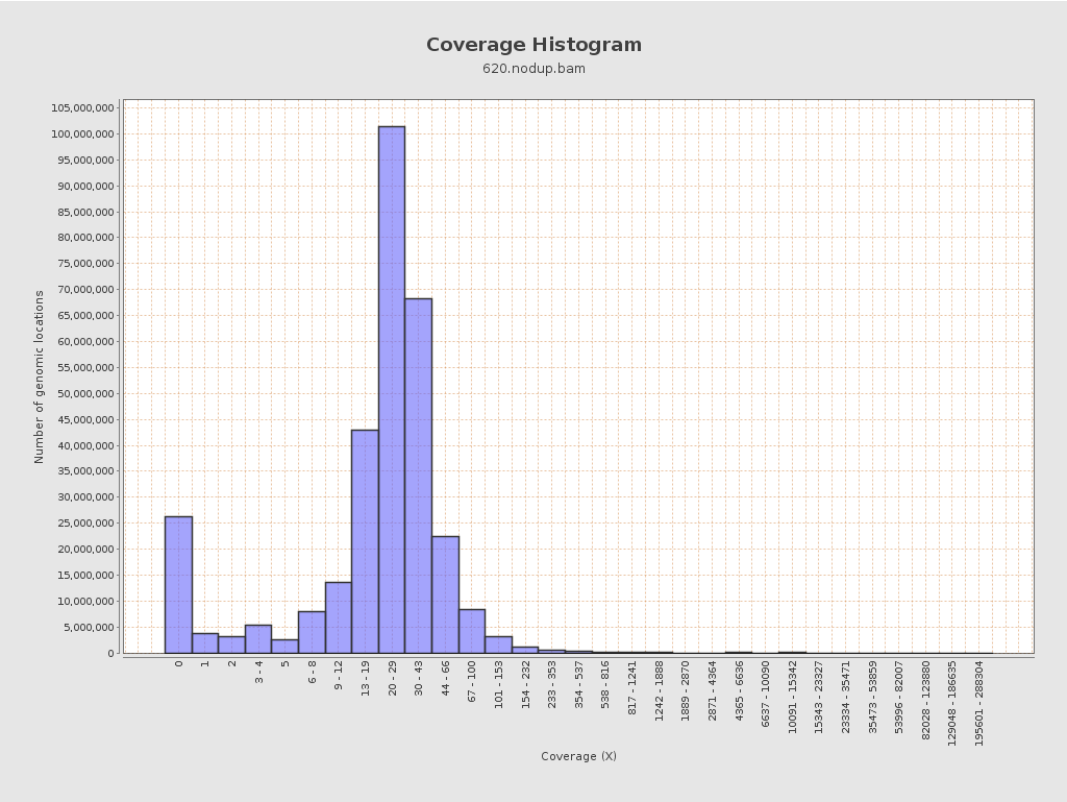
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	806312013	27.1263	129.5565

LT669789.1	36598175	1316971155	35.9846	366.639
LT669790.1	30422129	1264226479	41.5561	476.9606
LT669791.1	52758100	1864163375	35.3342	379.0397
LT669792.1	28376109	1004423560	35.3968	429.7525
LT669793.1	33388210	1084548199	32.483	252.0315
LT669794.1	50579949	1686173232	33.3368	295.5498
LT669795.1	49795044	1888627237	37.928	380.9459

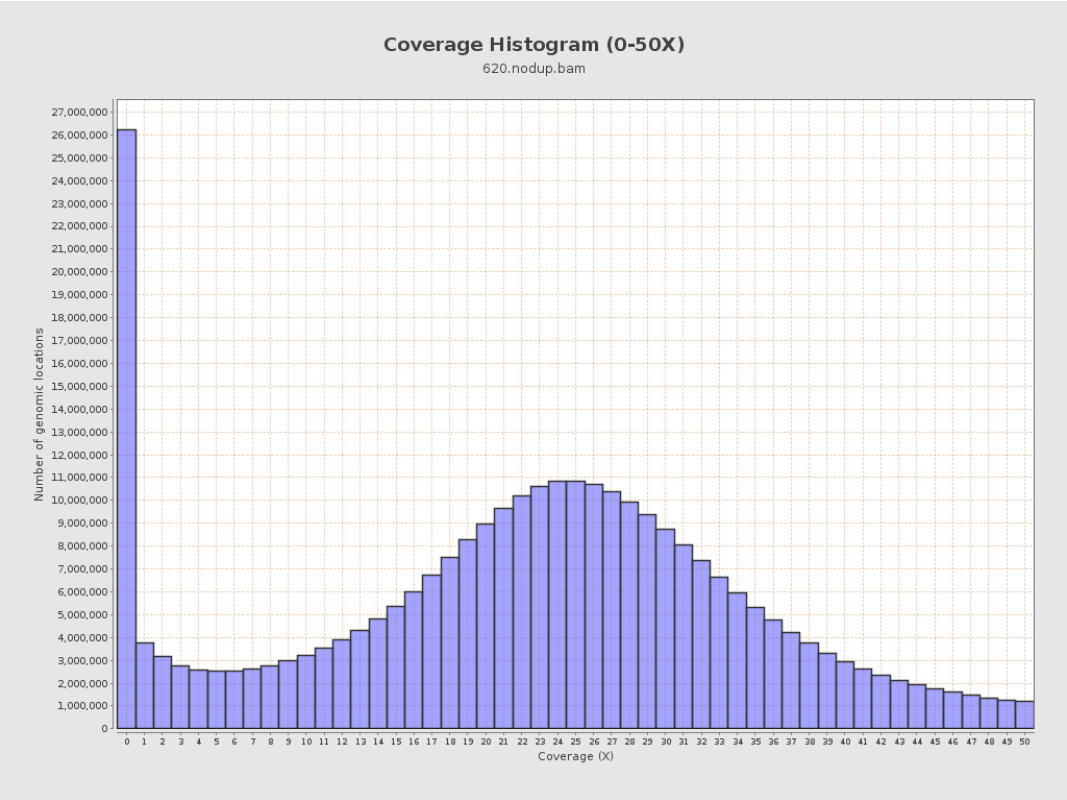
3. Results : Coverage across reference



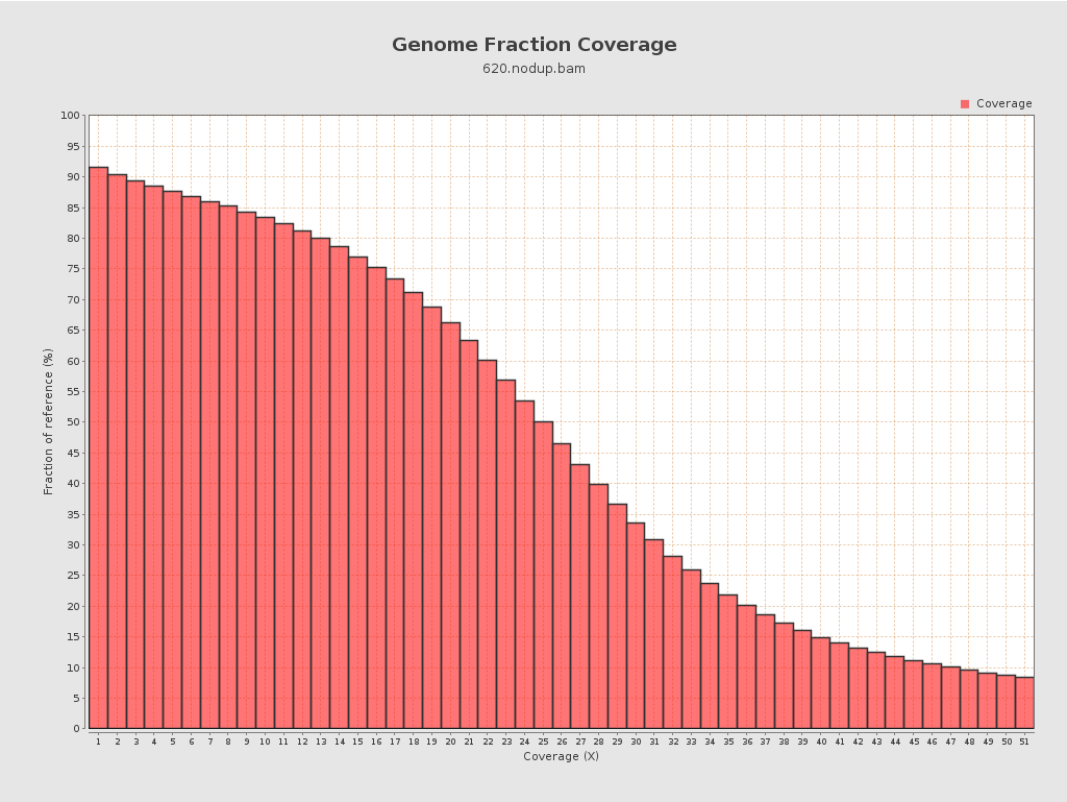
4. Results : Coverage Histogram



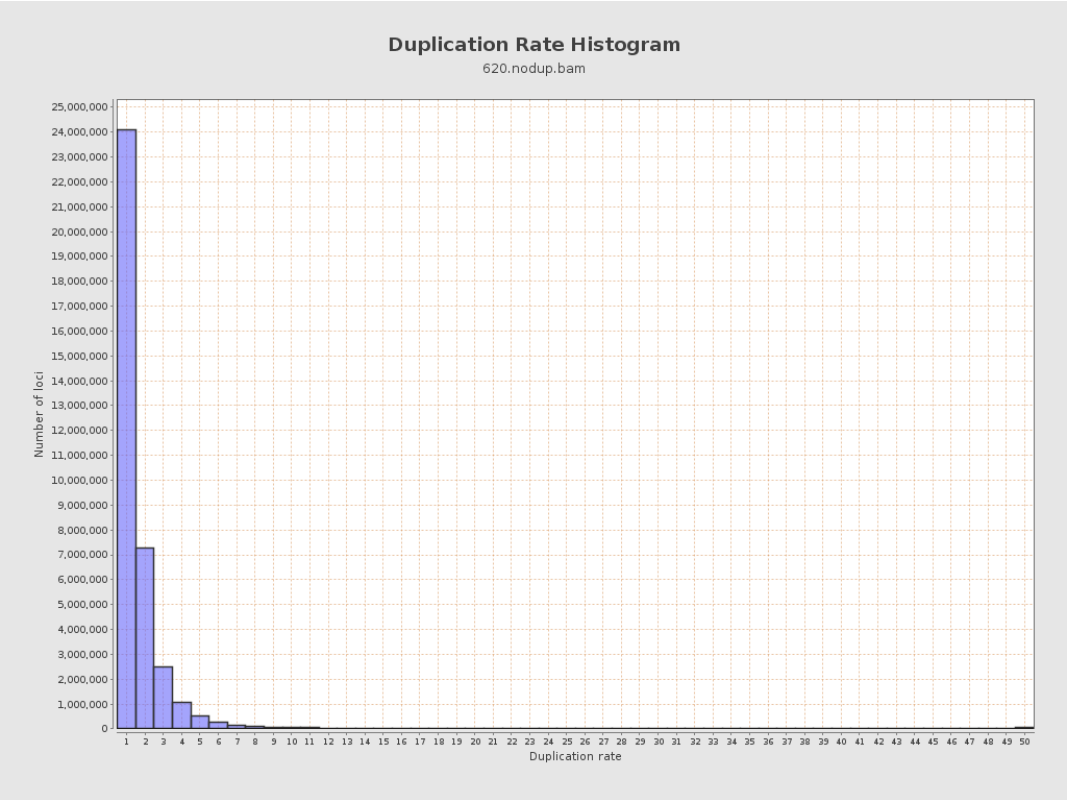
5. Results : Coverage Histogram (0-50X)



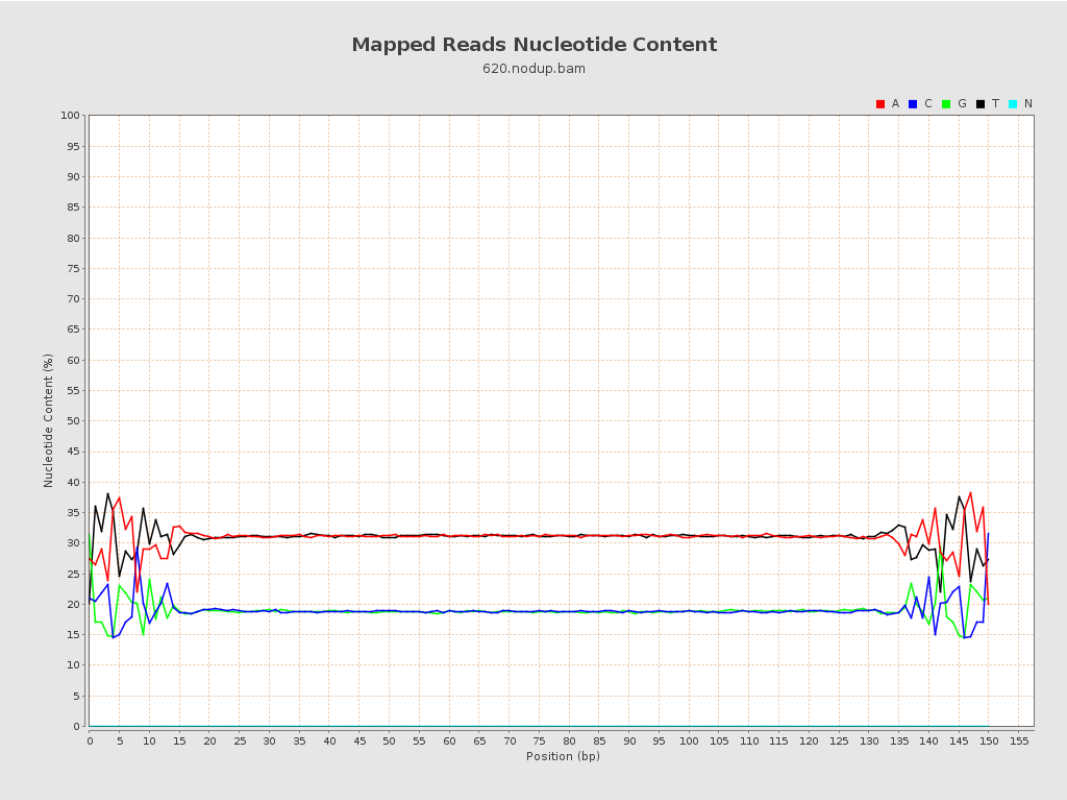
6. Results : Genome Fraction Coverage



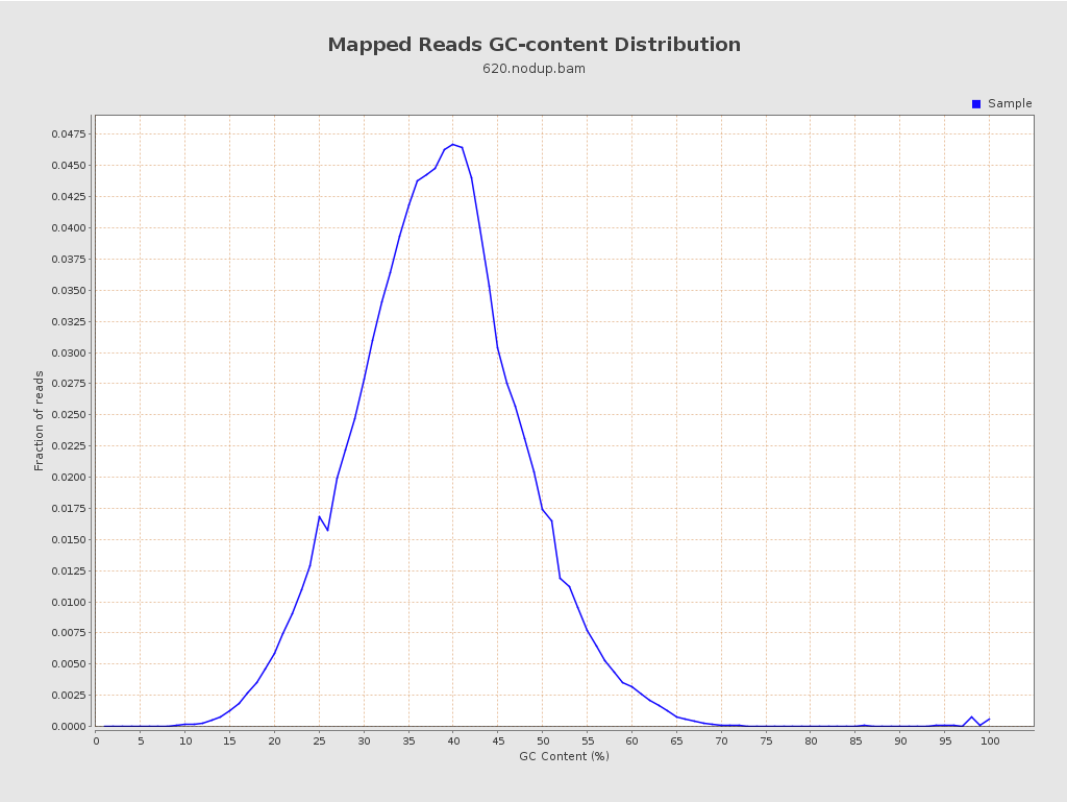
7. Results : Duplication Rate Histogram



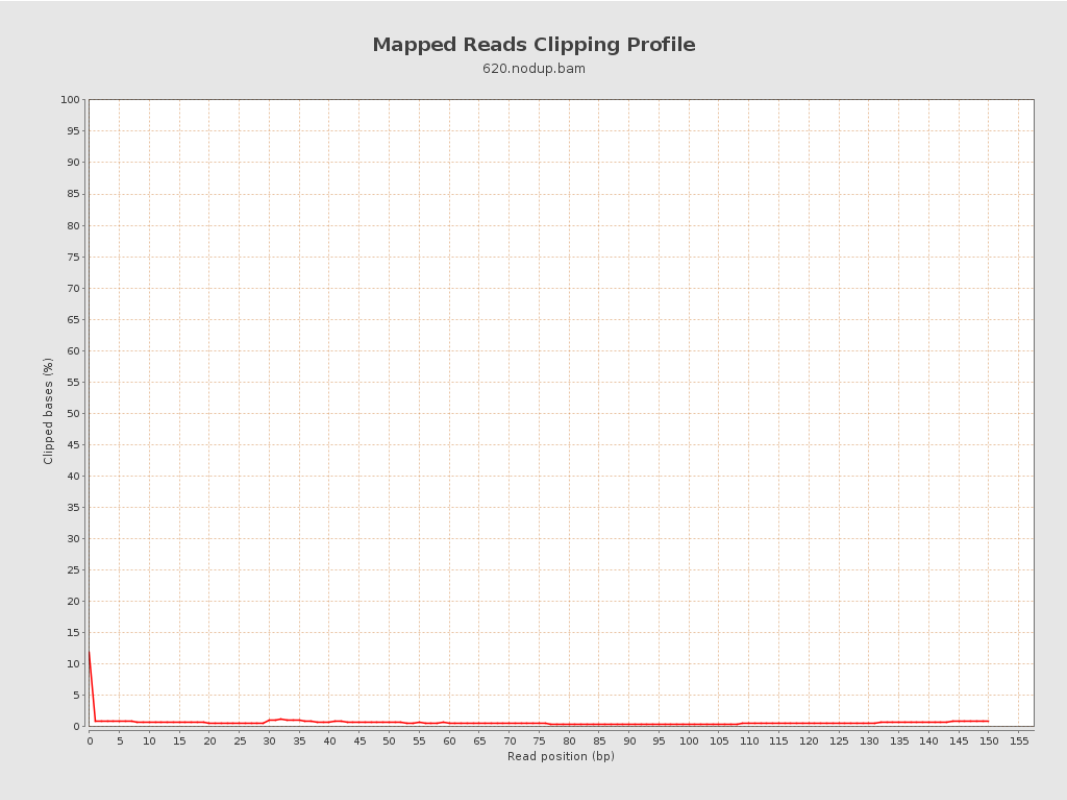
8. Results : Mapped Reads Nucleotide Content



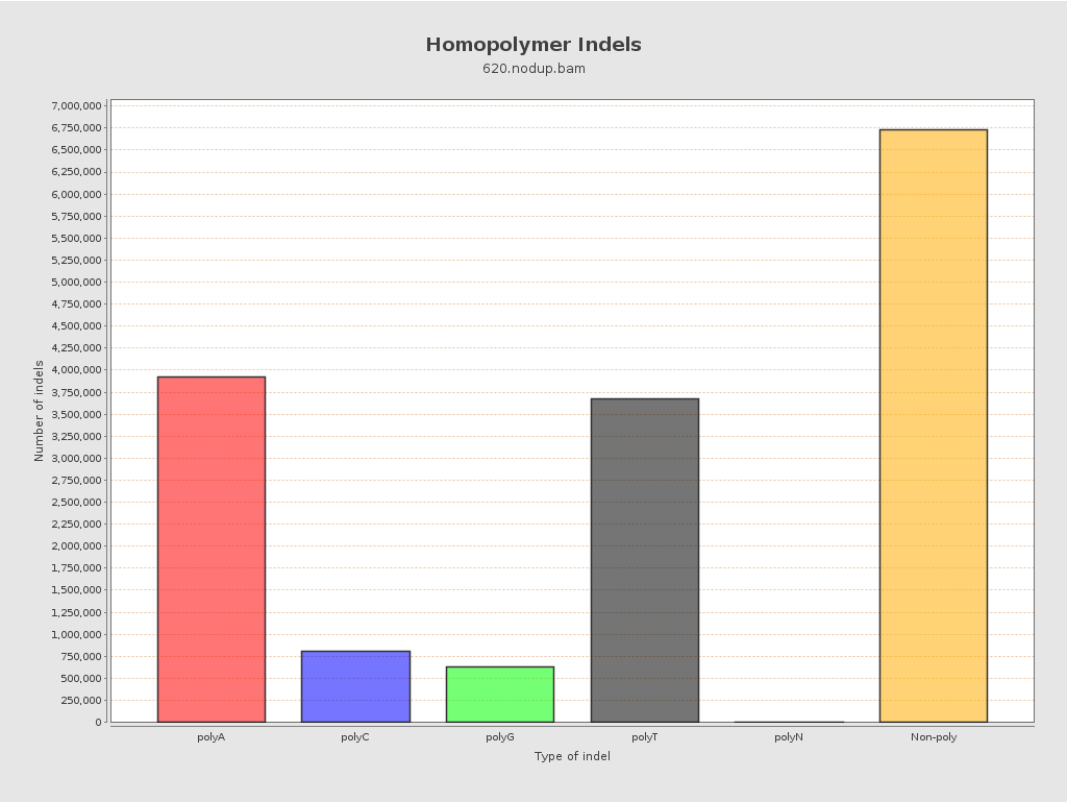
9. Results : Mapped Reads GC-content Distribution



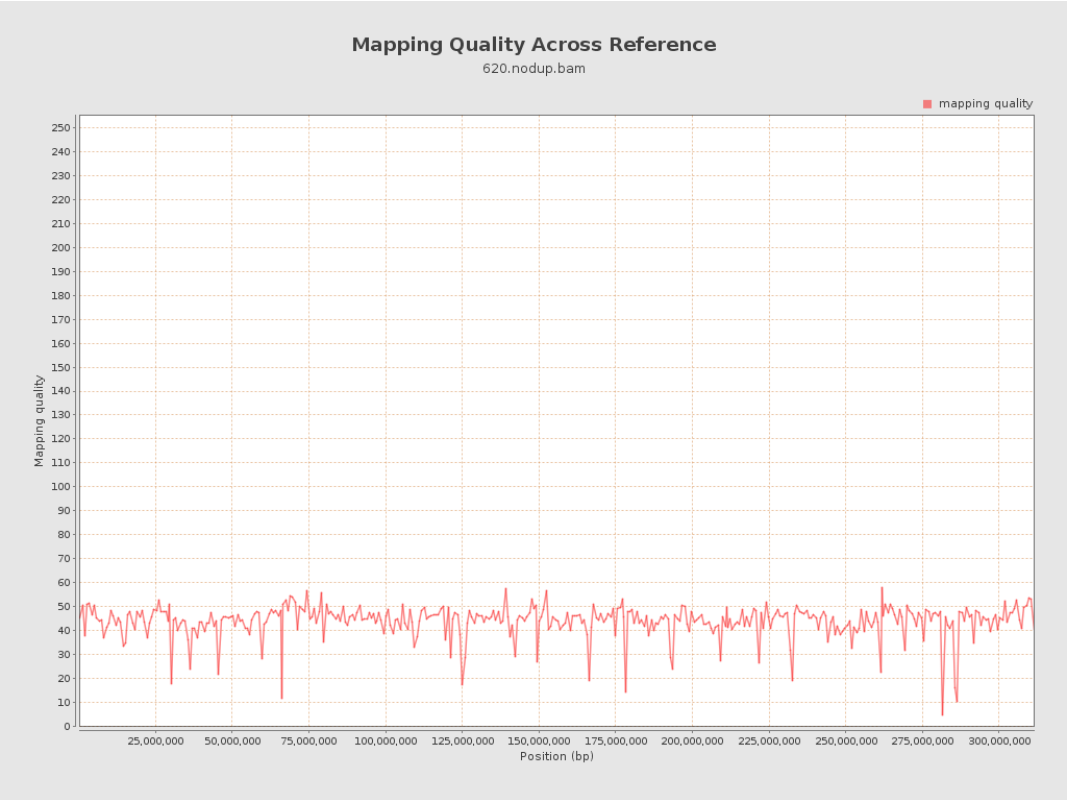
10. Results : Mapped Reads Clipping Profile



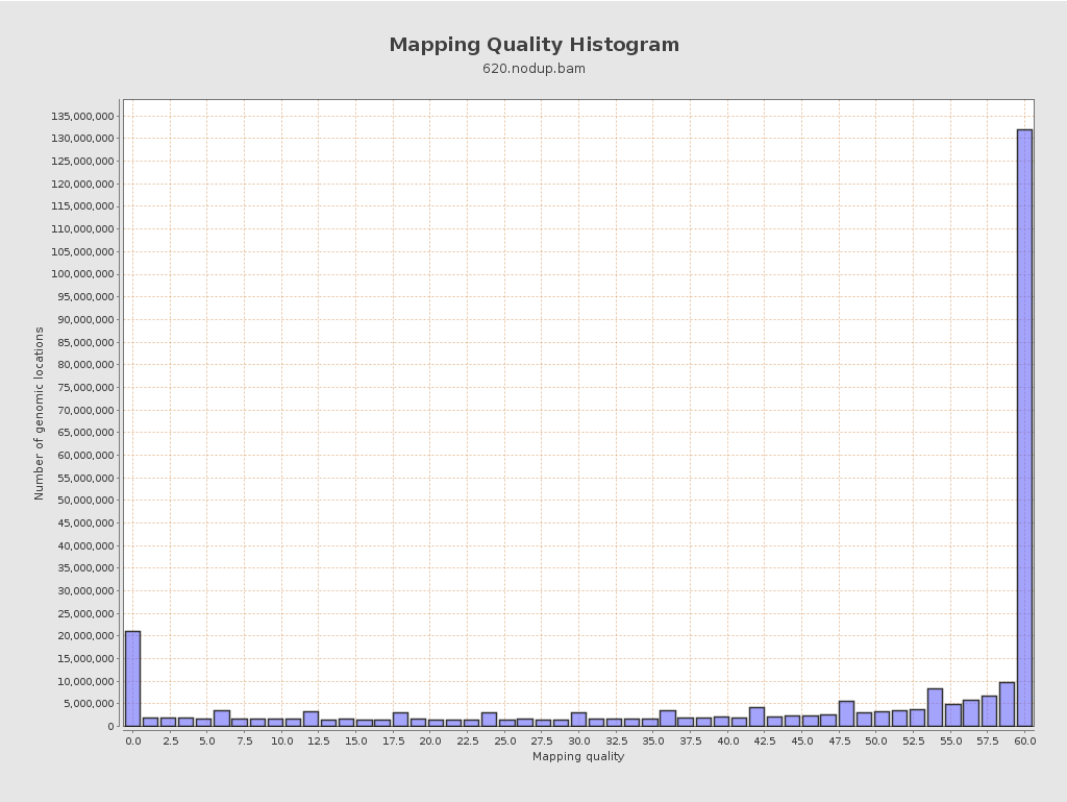
11. Results : Homopolymer Indels



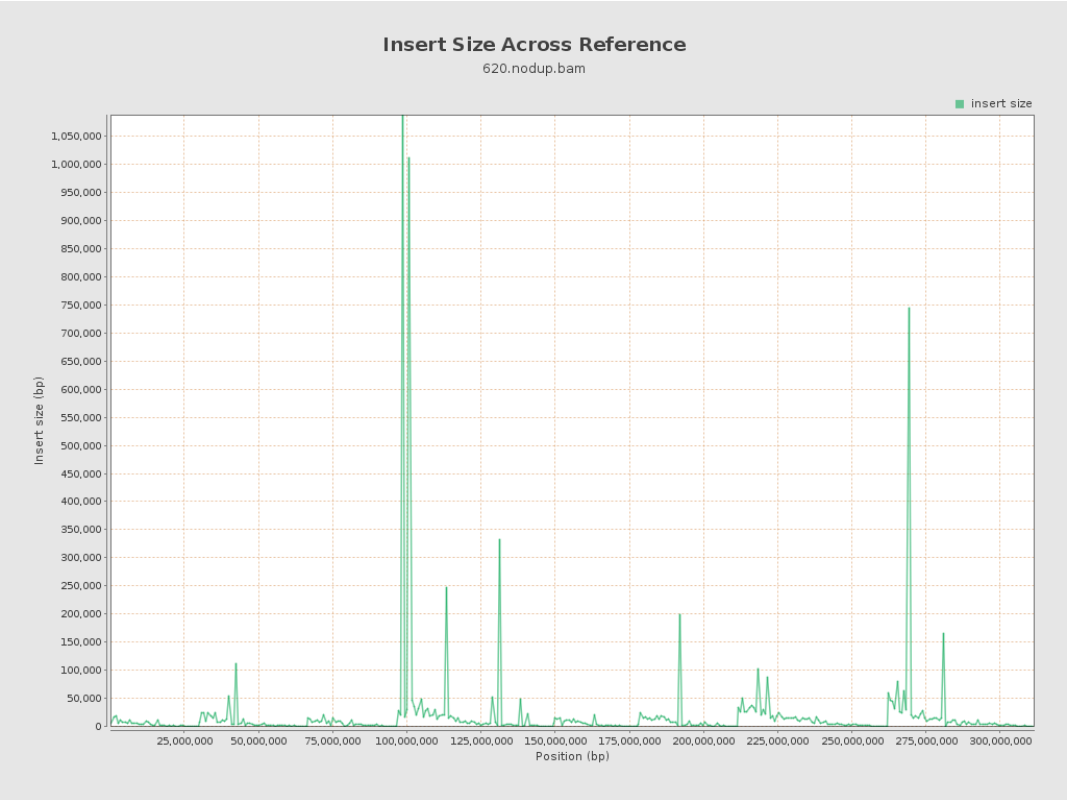
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram