Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/607.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/607.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_261/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_261_S342_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_261/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_261_S342_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	69,274,602
Mapped reads	65,971,924 / 95.23%
Unmapped reads	3,302,678 / 4.77%
Mapped paired reads	65,971,924 / 95.23%
Mapped reads, first in pair	33,035,031 / 47.69%
Mapped reads, second in pair	32,936,893 / 47.55%
Mapped reads, both in pair	64,852,327 / 93.62%
Mapped reads, singletons	1,119,597 / 1.62%
Read min/max/mean length	30 / 151 / 147.94
Duplicated reads (flagged)	8,708,705 / 12.57%
Clipped reads	15,151,336 / 21.87%

2.2. ACGT Content

Number/percentage of A's	2,814,790,643 / 30.78%
Number/percentage of C's	1,757,173,493 / 19.22%
Number/percentage of T's	2,819,064,635 / 30.83%
Number/percentage of G's	1,753,616,825 / 19.18%
Number/percentage of N's	33,843 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	29.4238
Standard Deviation	253.6776

2.4. Mapping Quality

Mean Mapping Quality	43.43

2.5. Insert size

Mean	227,733.99
Standard Deviation	2,242,338.91
P25/Median/P75	316 / 415 / 540

2.6. Mismatches and indels

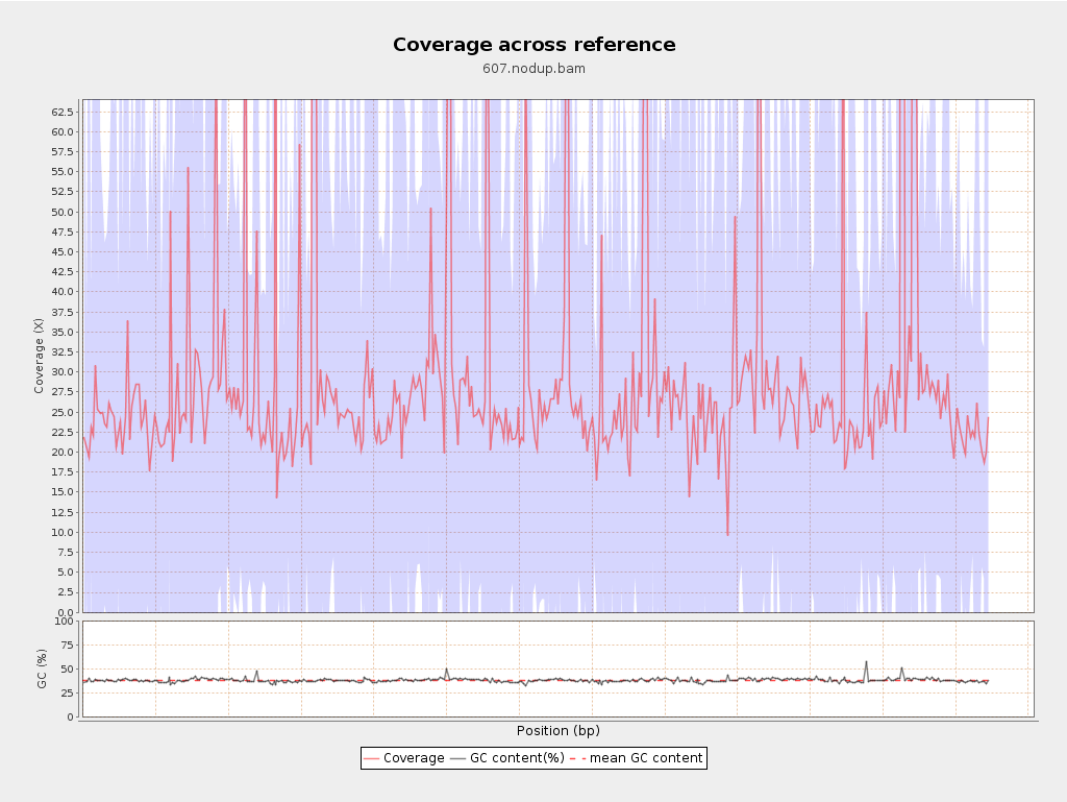
General error rate	2.39%
Mismatches	201,485,093
Insertions	6,208,381
Mapped reads with at least one insertion	8.46%
Deletions	6,571,379
Mapped reads with at least one deletion	8.83%
Homopolymer indels	55.87%

2.7. Chromosome stats

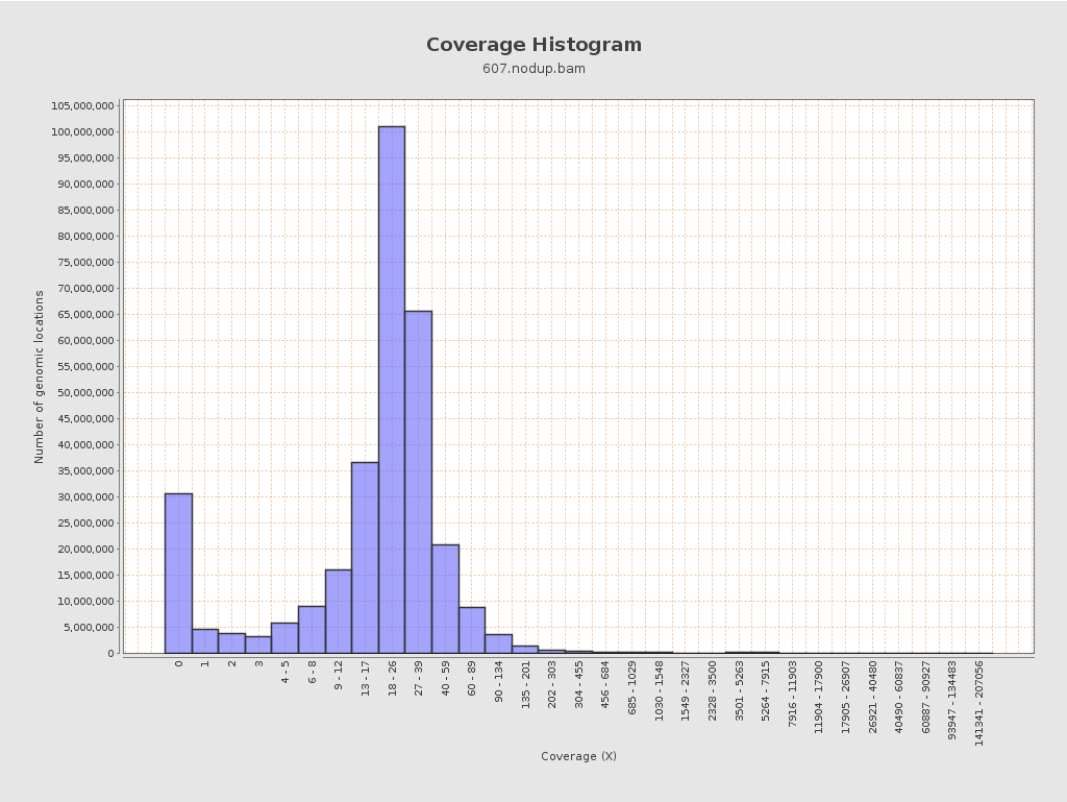
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	709457870	23.8679	83.4057

LT669789.1	36598175	1108461364	30.2873	258.3514
LT669790.1	30422129	924496800	30.389	227.6532
LT669791.1	52758100	1522751992	28.8629	219.4091
LT669792.1	28376109	806524729	28.4227	241.5618
LT669793.1	33388210	950678329	28.4735	239.2505
LT669794.1	50579949	1446030782	28.589	248.7358
LT669795.1	49795044	1701283262	34.1657	363.7991

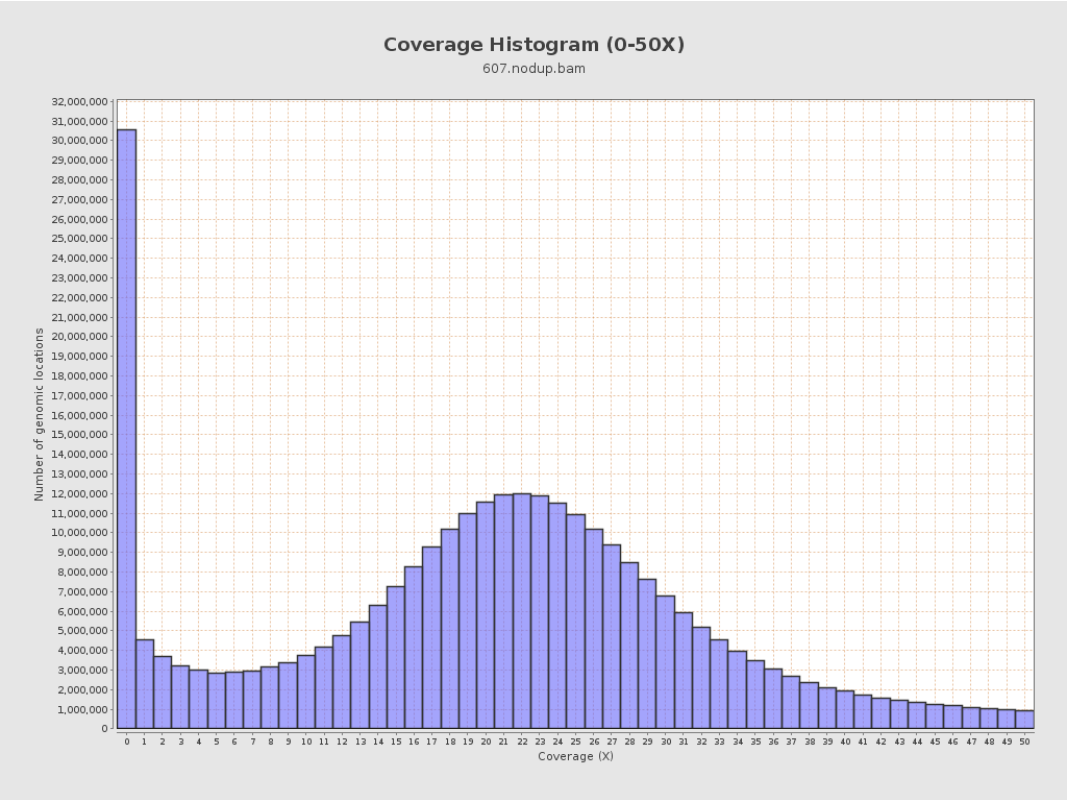
3. Results : Coverage across reference



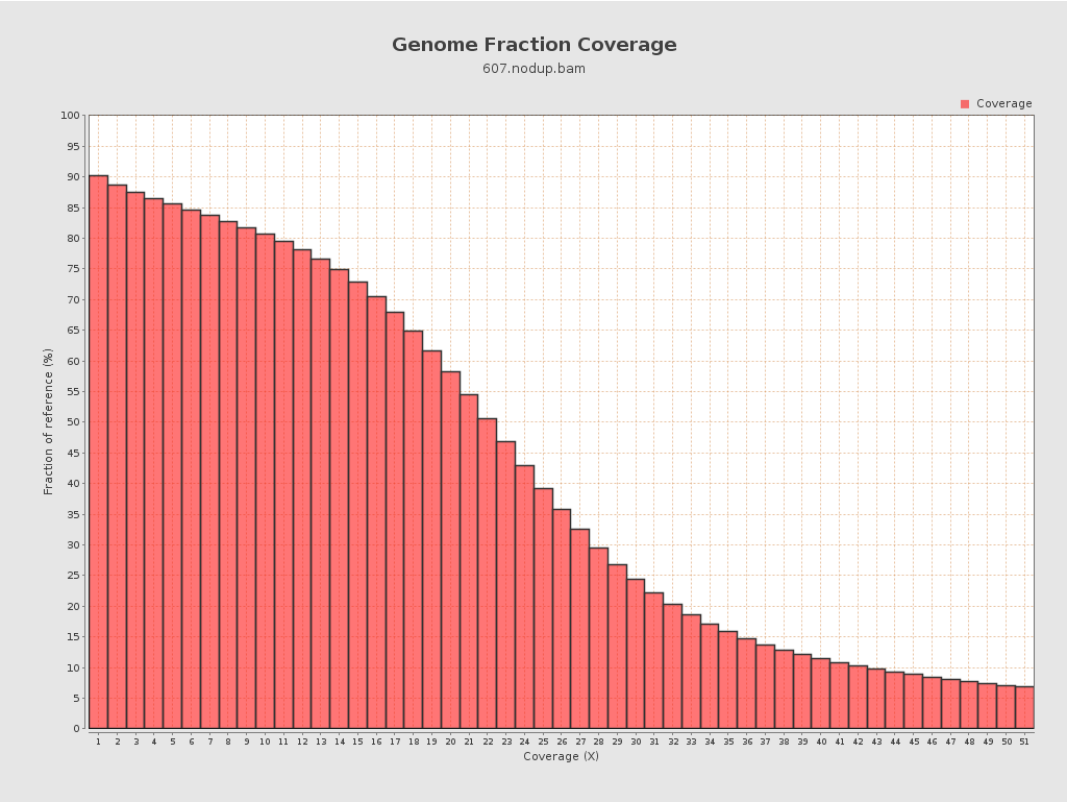
4. Results : Coverage Histogram



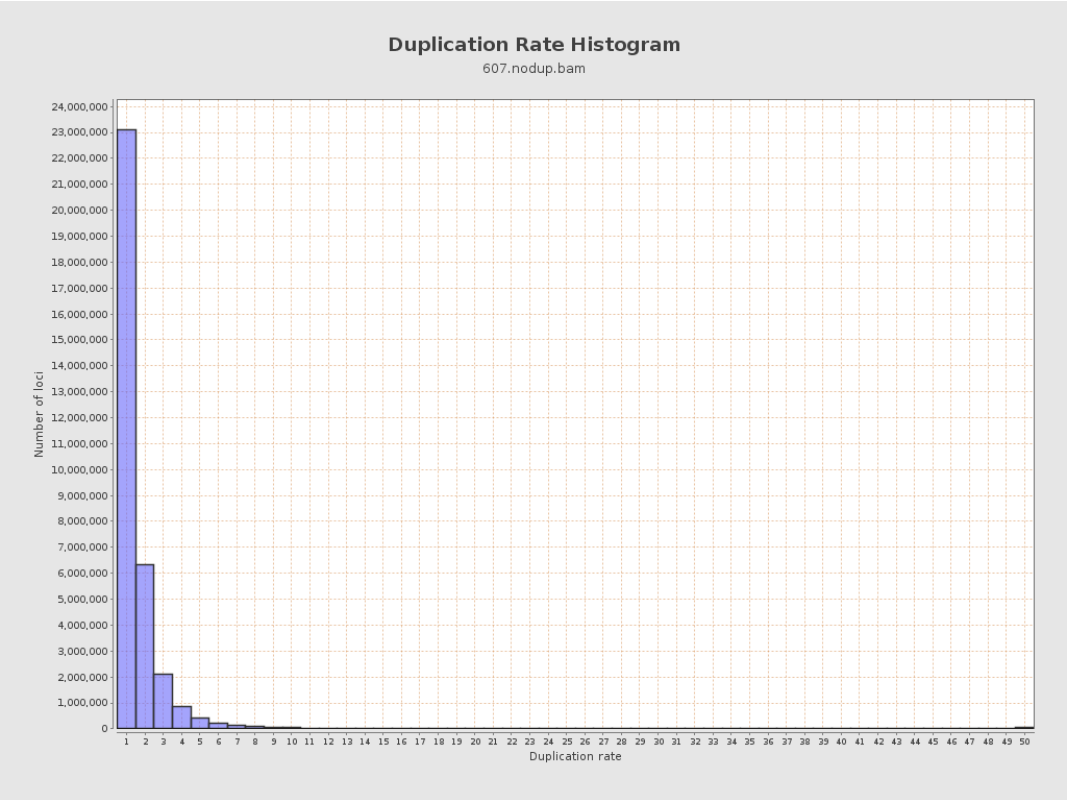
5. Results : Coverage Histogram (0-50X)



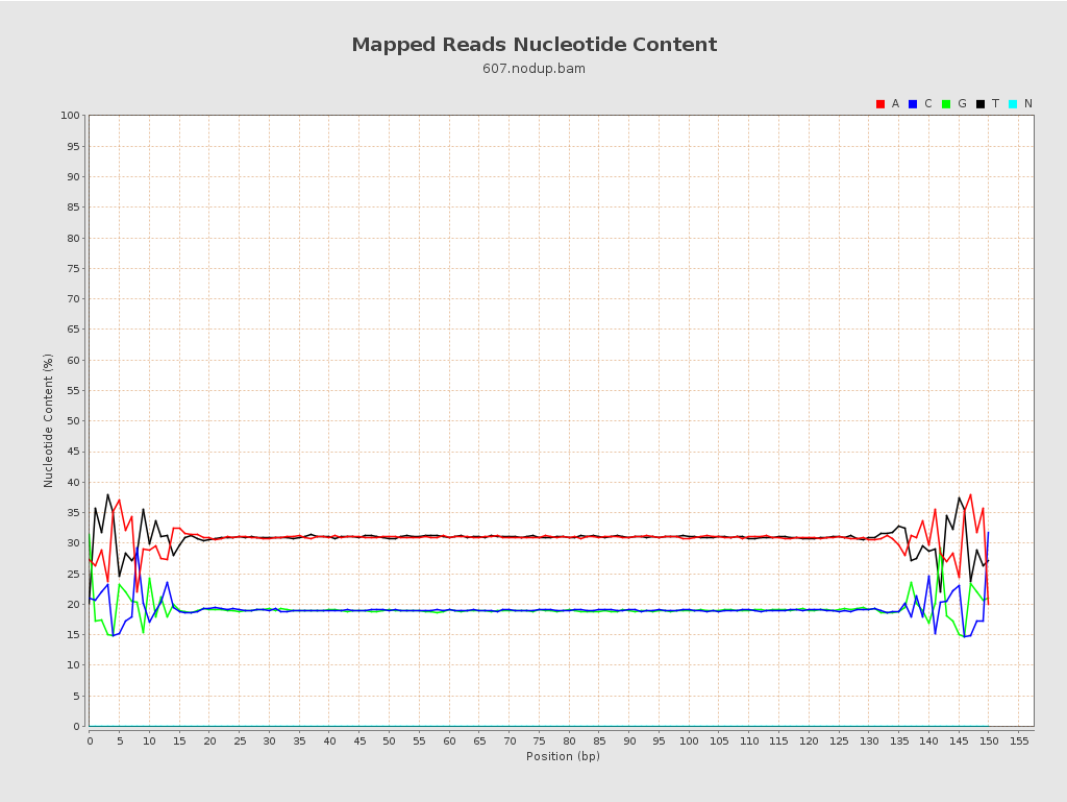
6. Results : Genome Fraction Coverage



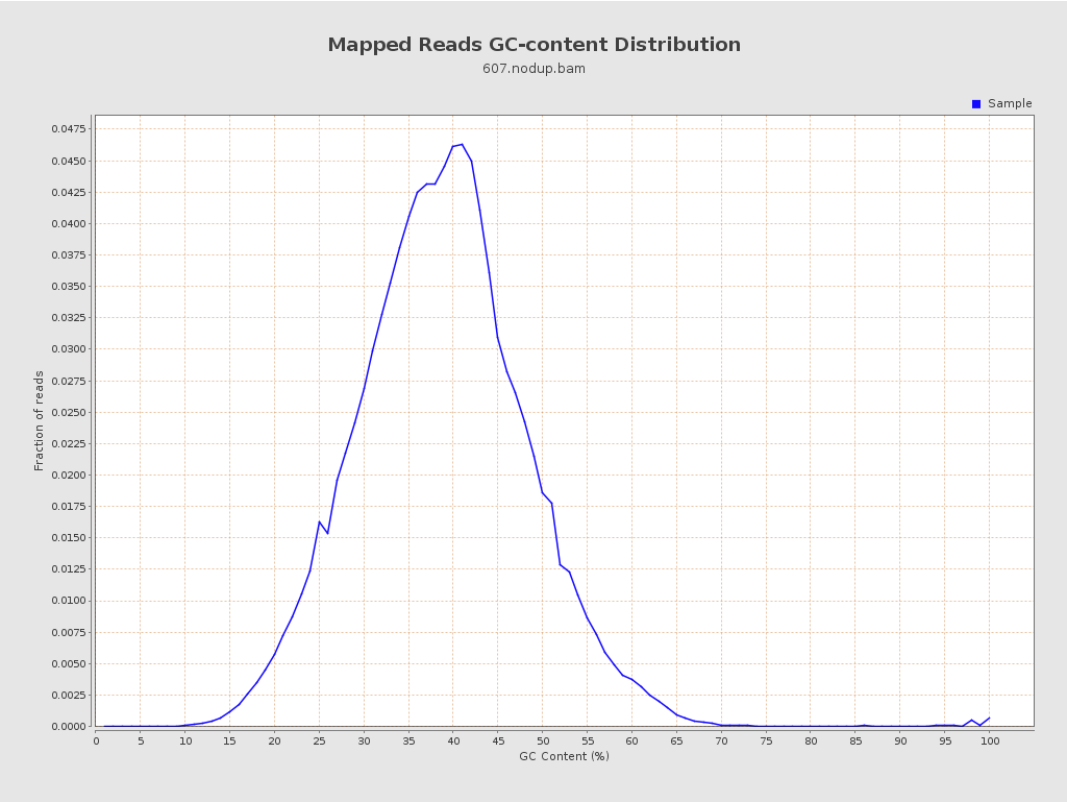
7. Results : Duplication Rate Histogram



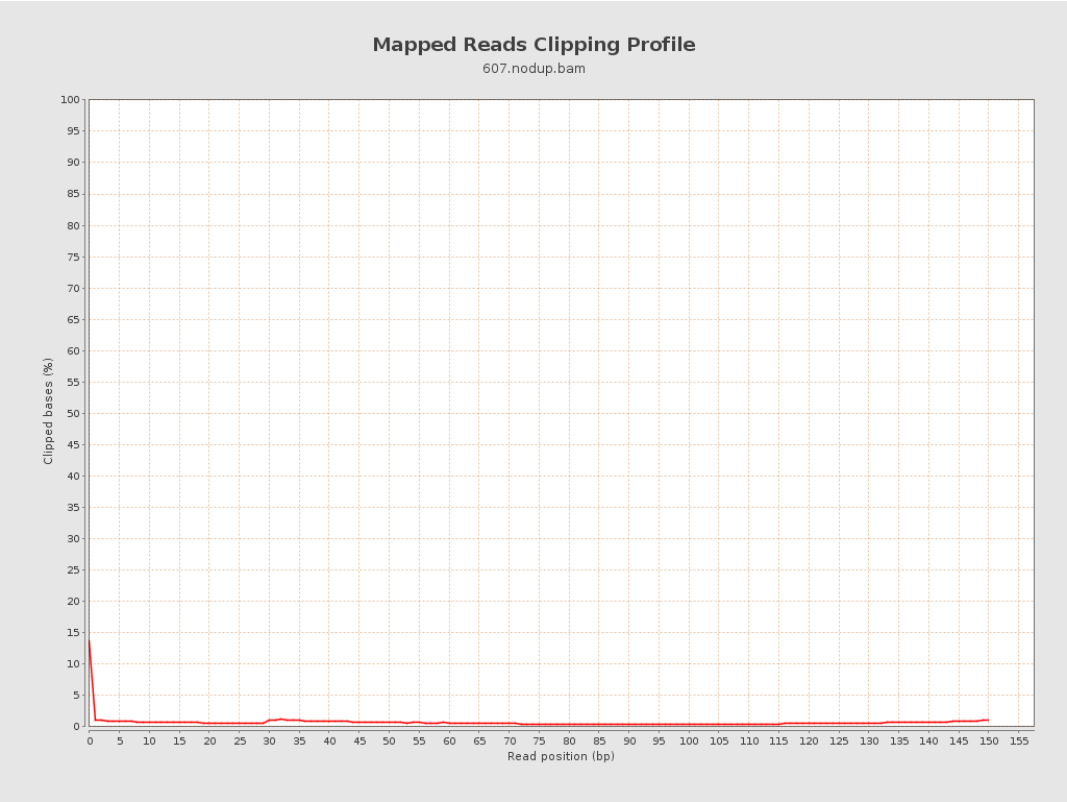
8. Results : Mapped Reads Nucleotide Content



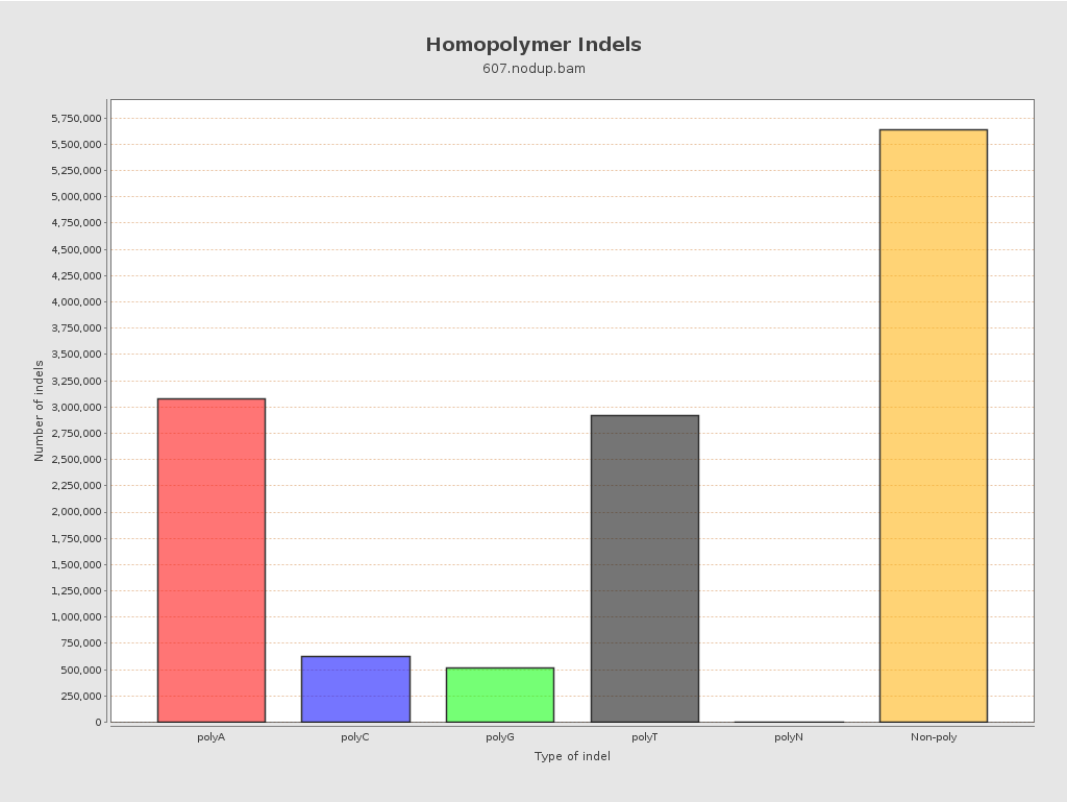
9. Results : Mapped Reads GC-content Distribution



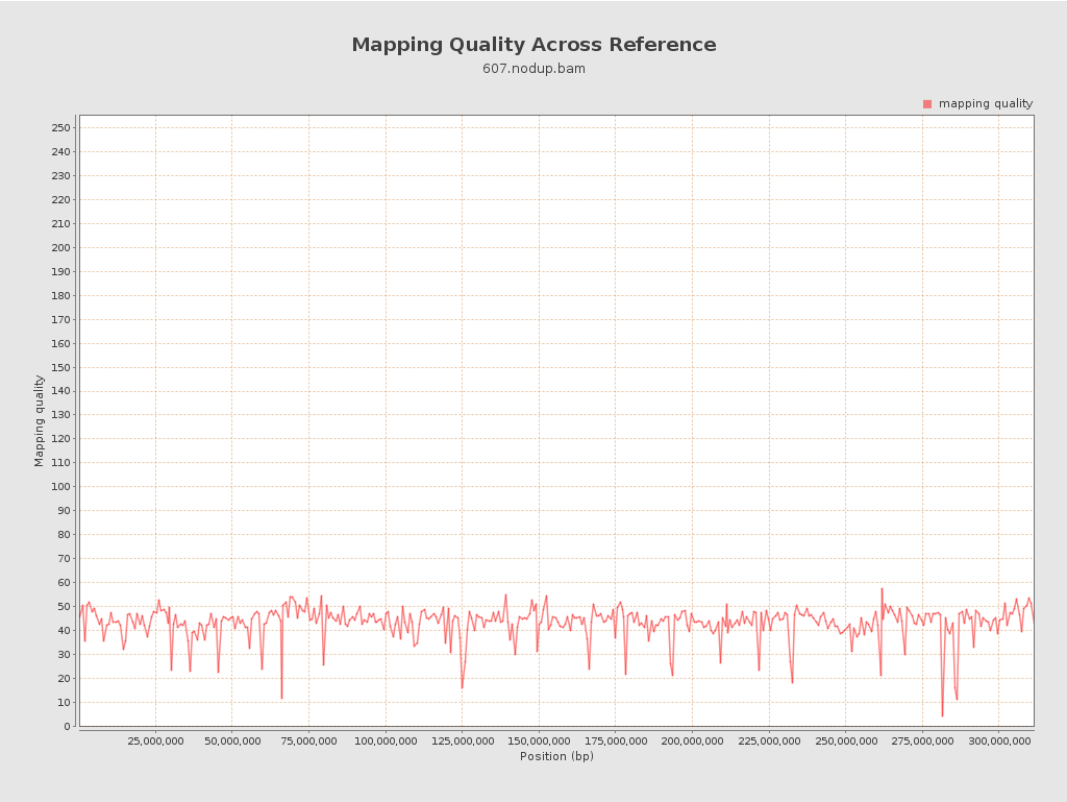
10. Results : Mapped Reads Clipping Profile



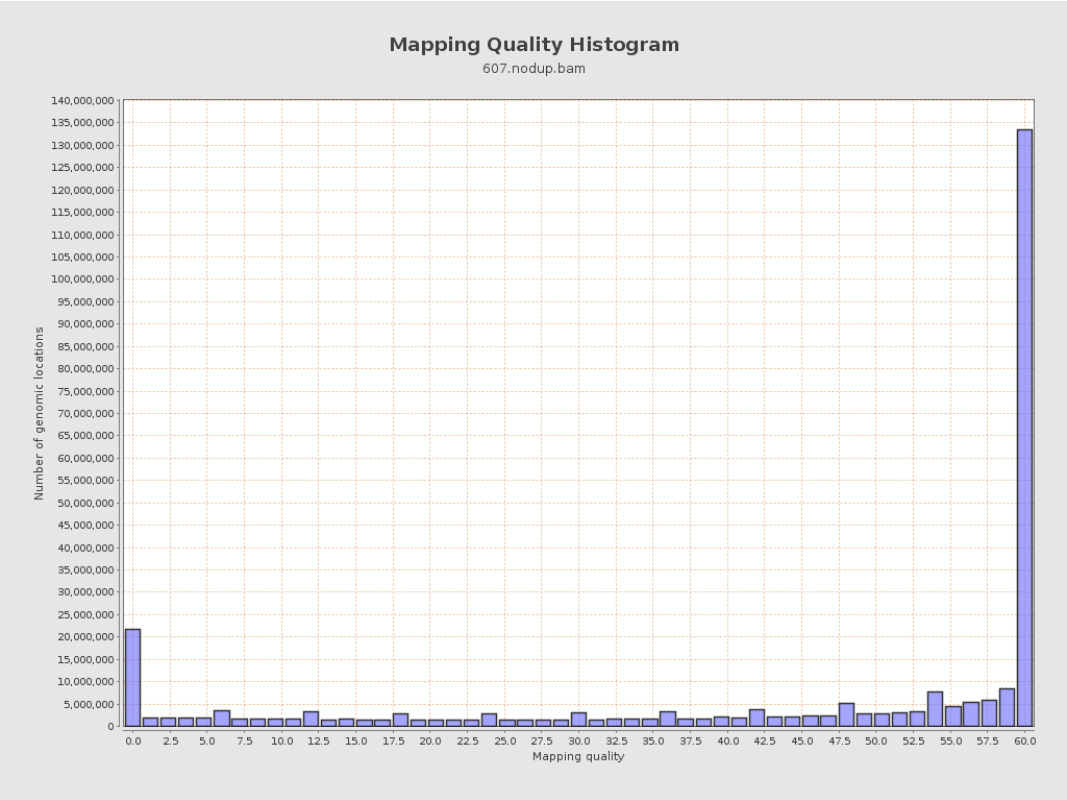
11. Results : Homopolymer Indels



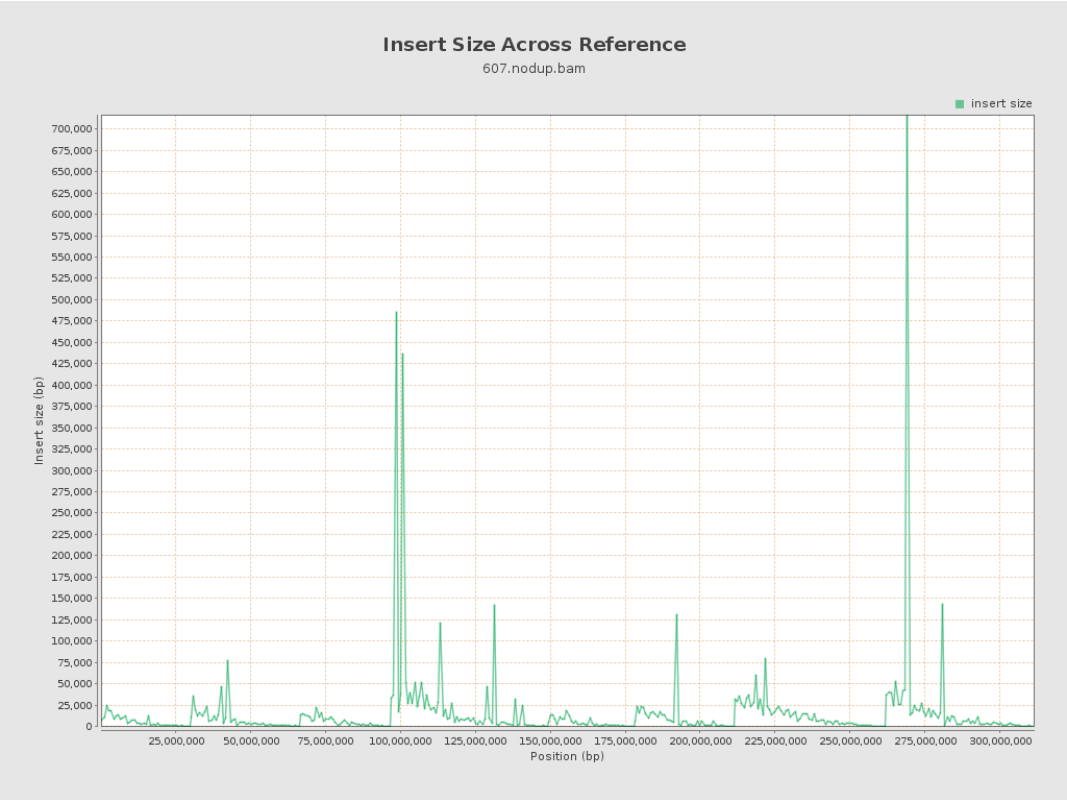
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram