Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/593.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/593.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_430/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_430_S405_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_430/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_430_S405_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:37 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,904,039
Mapped reads	66,401,974 / 92.35%
Unmapped reads	5,502,065 / 7.65%
Mapped paired reads	66,401,974 / 92.35%
Mapped reads, first in pair	33,270,622 / 46.27%
Mapped reads, second in pair	33,131,352 / 46.08%
Mapped reads, both in pair	64,577,122 / 89.81%
Mapped reads, singletons	1,824,852 / 2.54%
Read min/max/mean length	30 / 151 / 148.24
Duplicated reads (flagged)	11,604,096 / 16.14%
Clipped reads	14,775,420 / 20.55%

2.2. ACGT Content

Number/percentage of A's	2,841,349,317 / 30.96%
Number/percentage of C's	1,747,961,866 / 19.05%
Number/percentage of T's	2,844,410,889 / 30.99%
Number/percentage of G's	1,744,222,957 / 19%
Number/percentage of N's	32,096 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	29.5234
Standard Deviation	259.3892

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Insert size

Mean	243,382.71
Standard Deviation	2,368,766.83
P25/Median/P75	354 / 462 / 597

2.6. Mismatches and indels

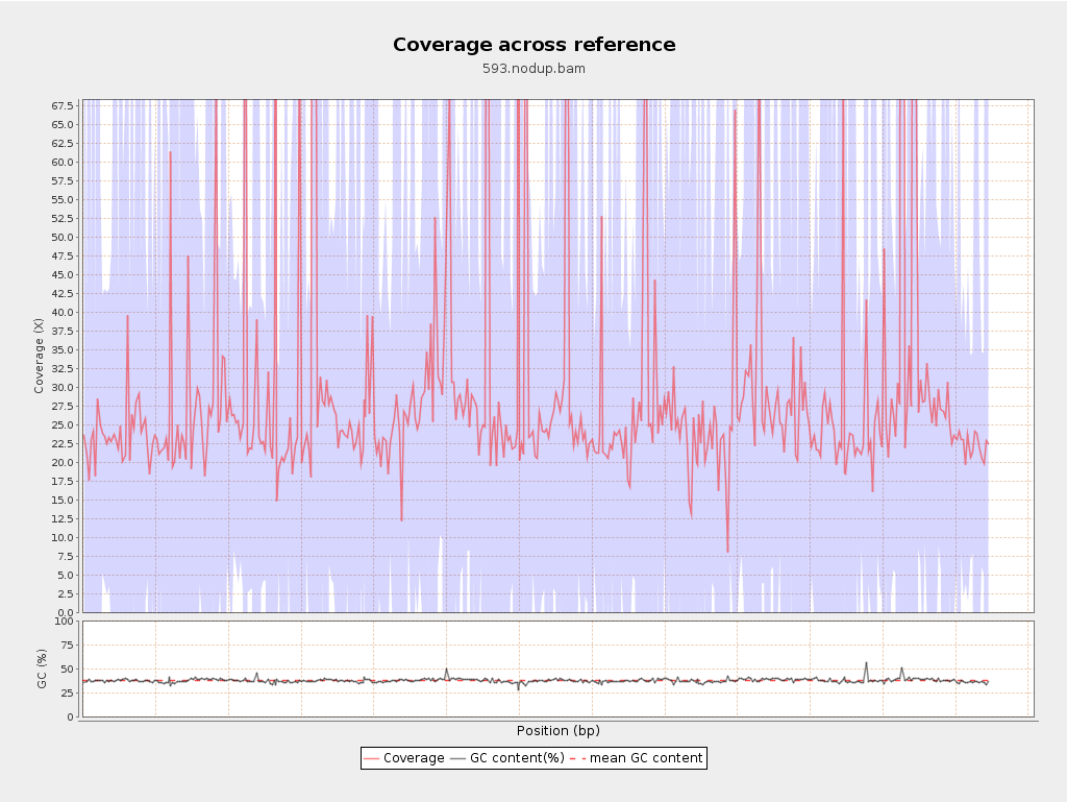
General error rate	2.25%
Mismatches	189,042,630
Insertions	6,289,939
Mapped reads with at least one insertion	8.47%
Deletions	6,090,315
Mapped reads with at least one deletion	8.16%
Homopolymer indels	57.29%

2.7. Chromosome stats

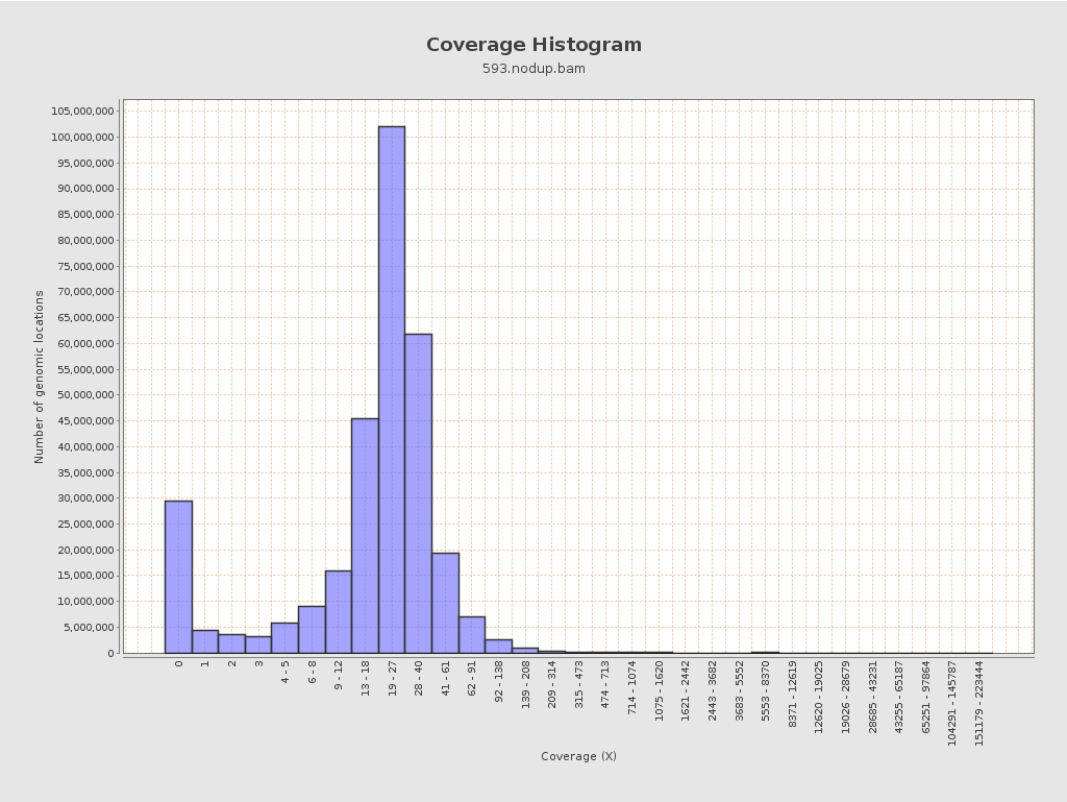
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	697830977	23.4767	83.2163

LT669789.1	36598175	1070817556	29.2588	258.5646
LT669790.1	30422129	1013486908	33.3141	313.8406
LT669791.1	52758100	1553885987	29.453	248.4555
LT669792.1	28376109	844006548	29.7436	309.1539
LT669793.1	33388210	898884128	26.9222	177.2317
LT669794.1	50579949	1404216635	27.7623	191.2535
LT669795.1	49795044	1717605348	34.4935	359.8539

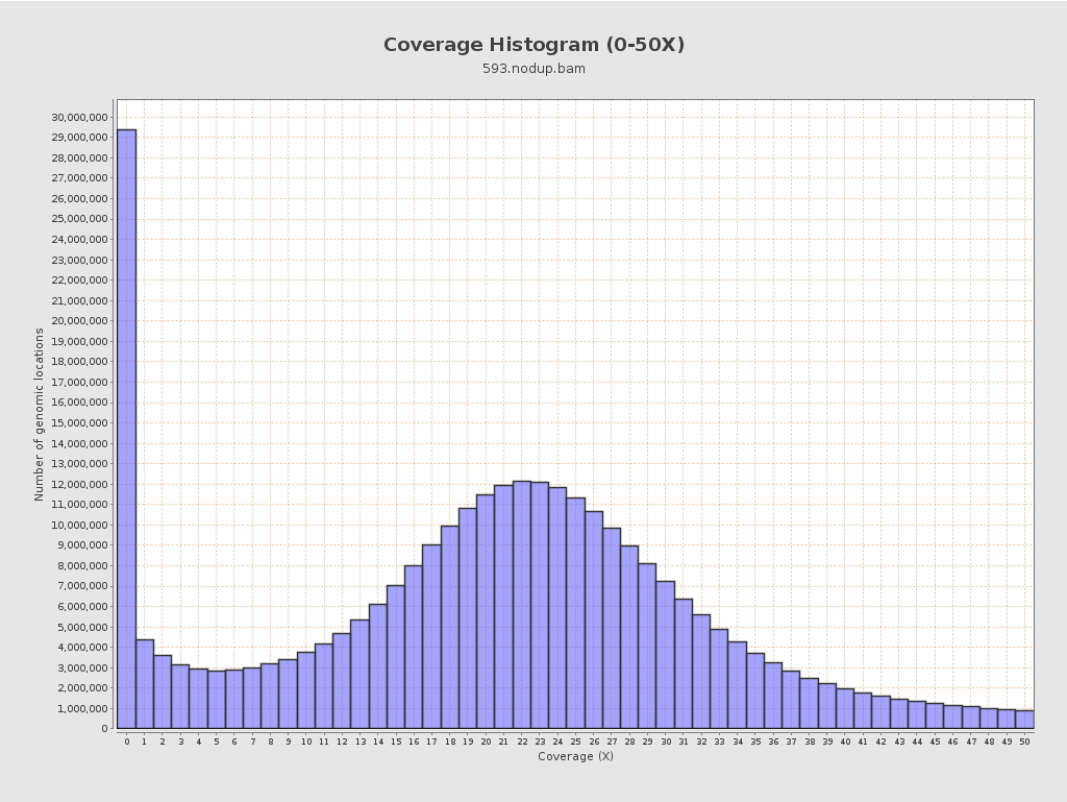
3. Results : Coverage across reference



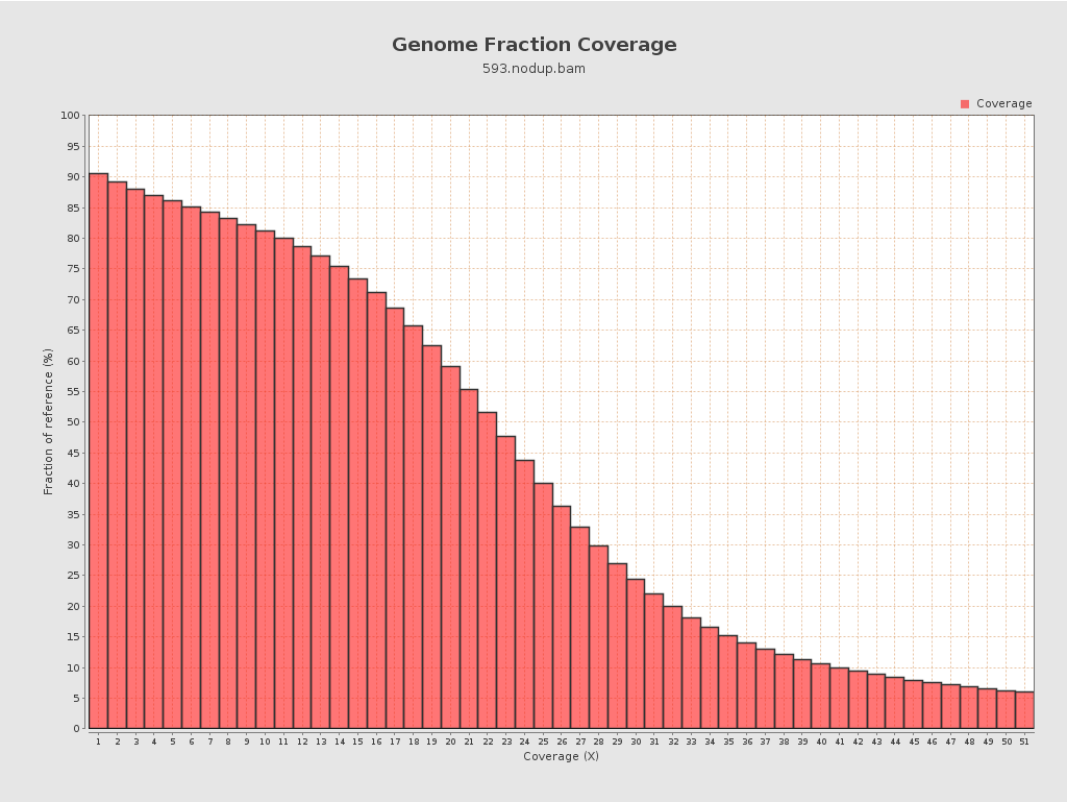
4. Results : Coverage Histogram



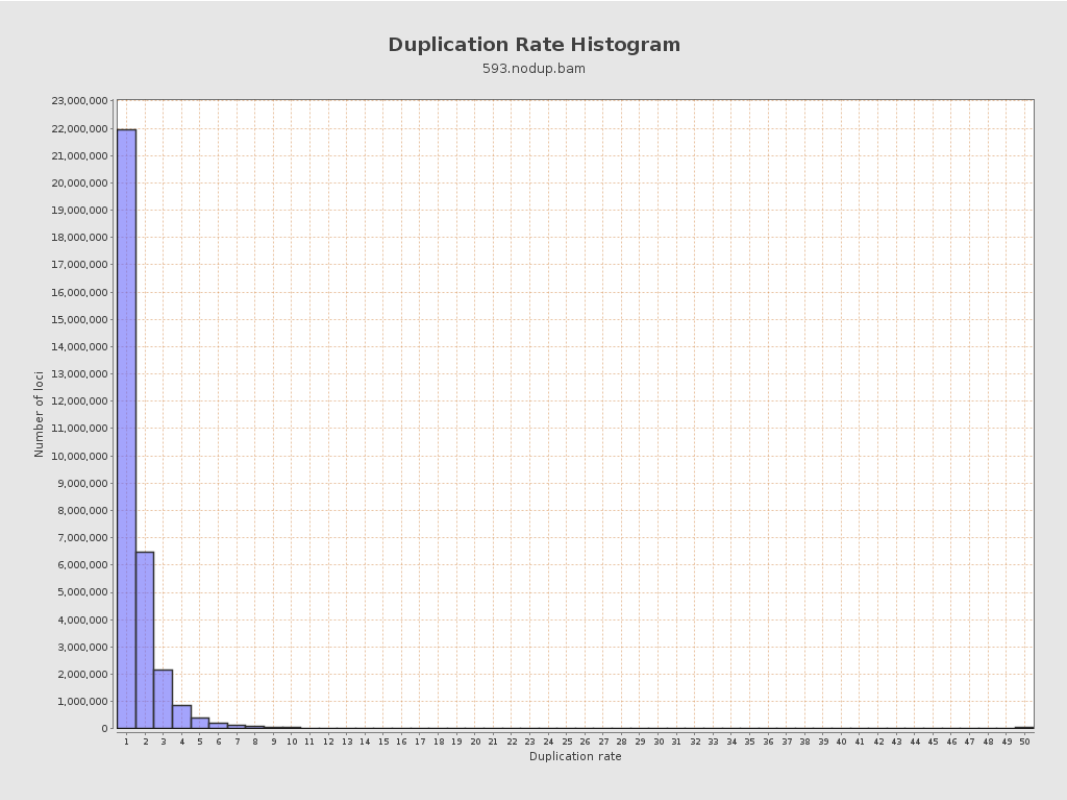
5. Results : Coverage Histogram (0-50X)



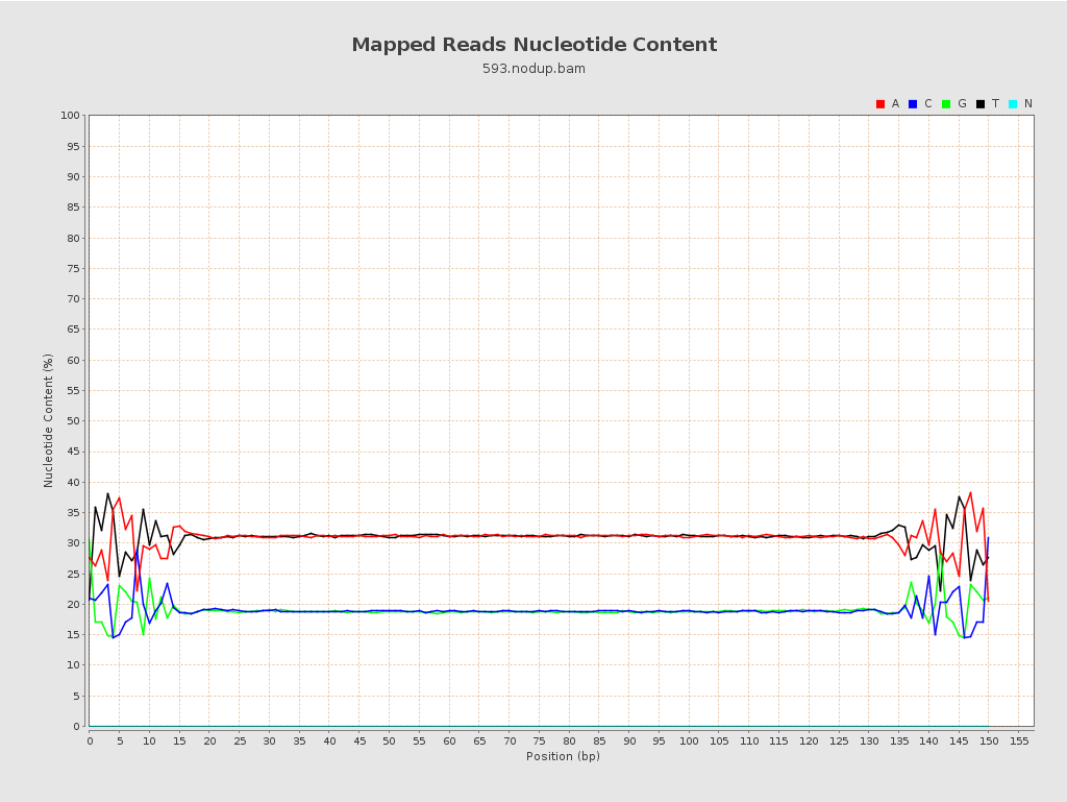
6. Results : Genome Fraction Coverage



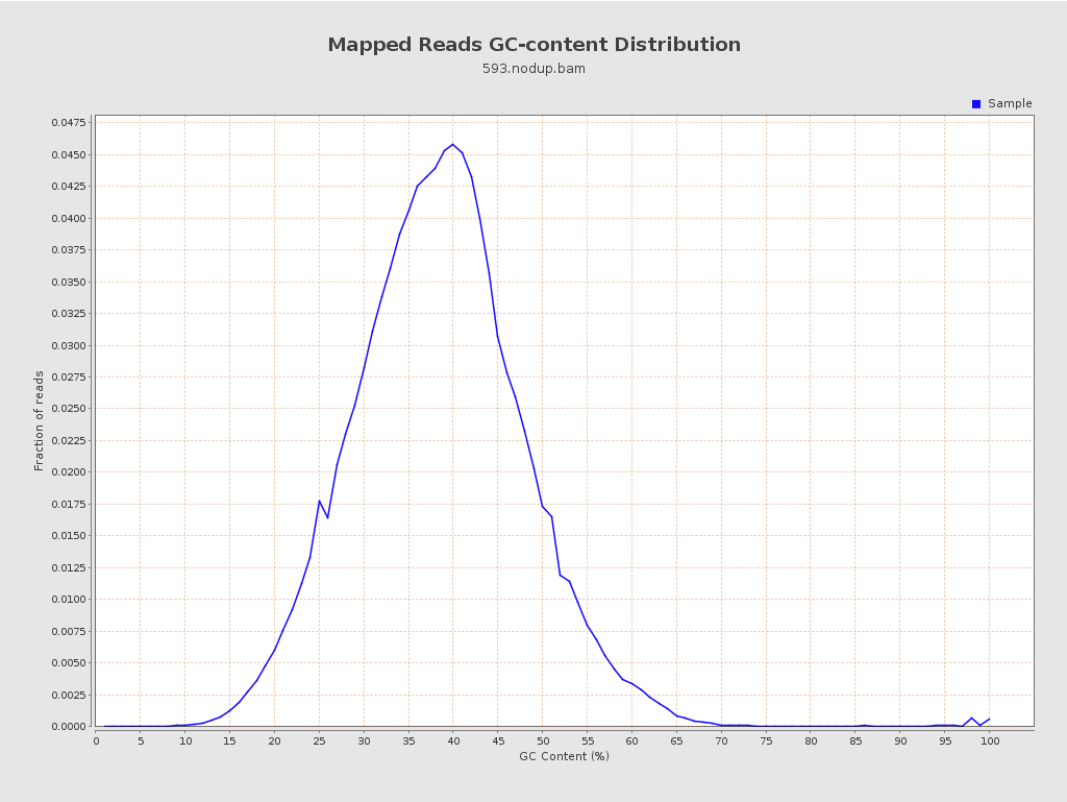
7. Results : Duplication Rate Histogram



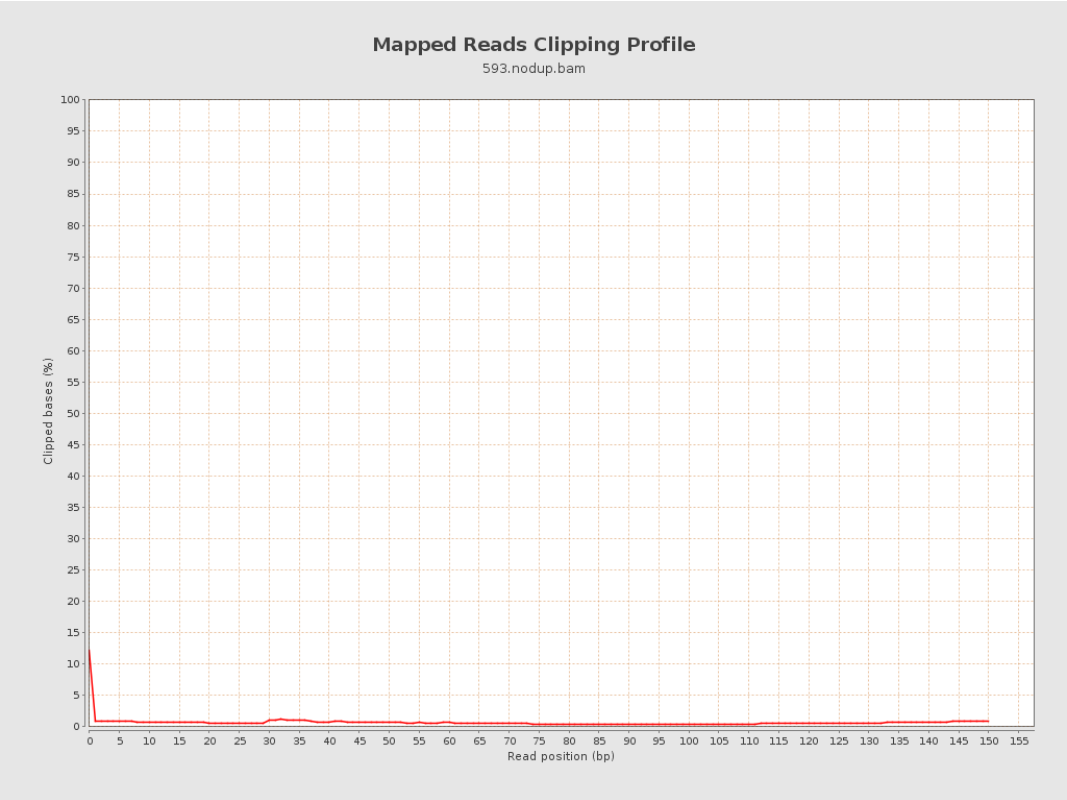
8. Results : Mapped Reads Nucleotide Content



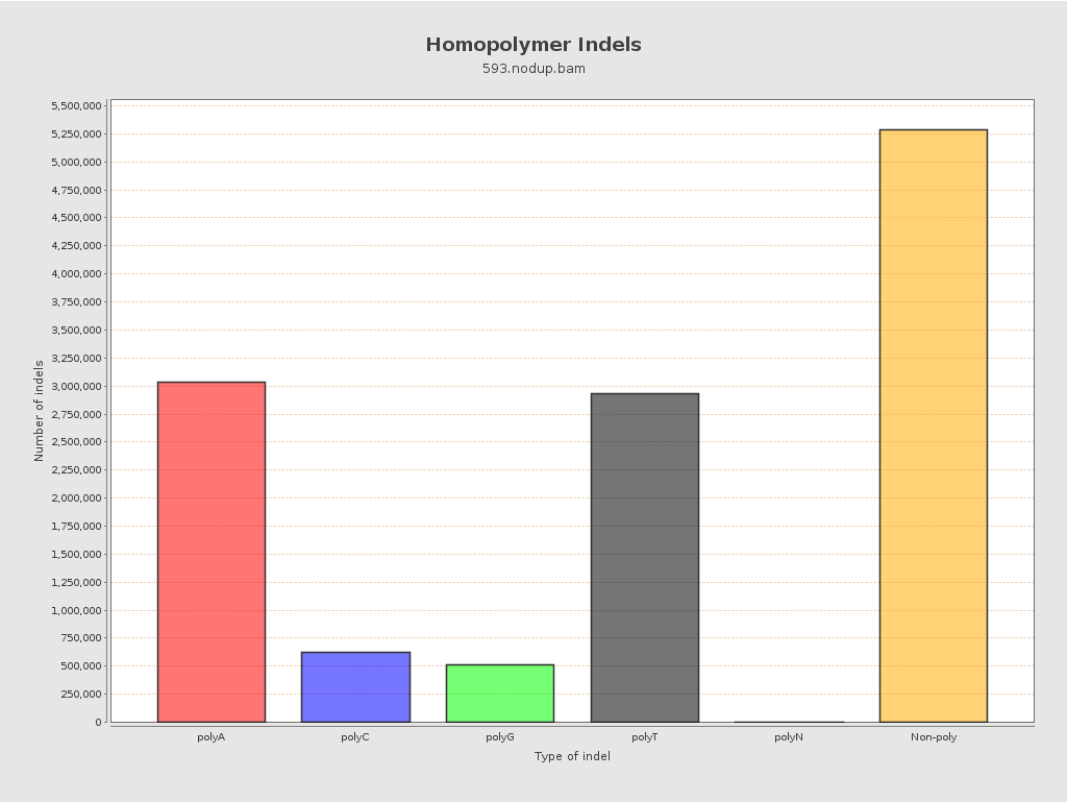
9. Results : Mapped Reads GC-content Distribution



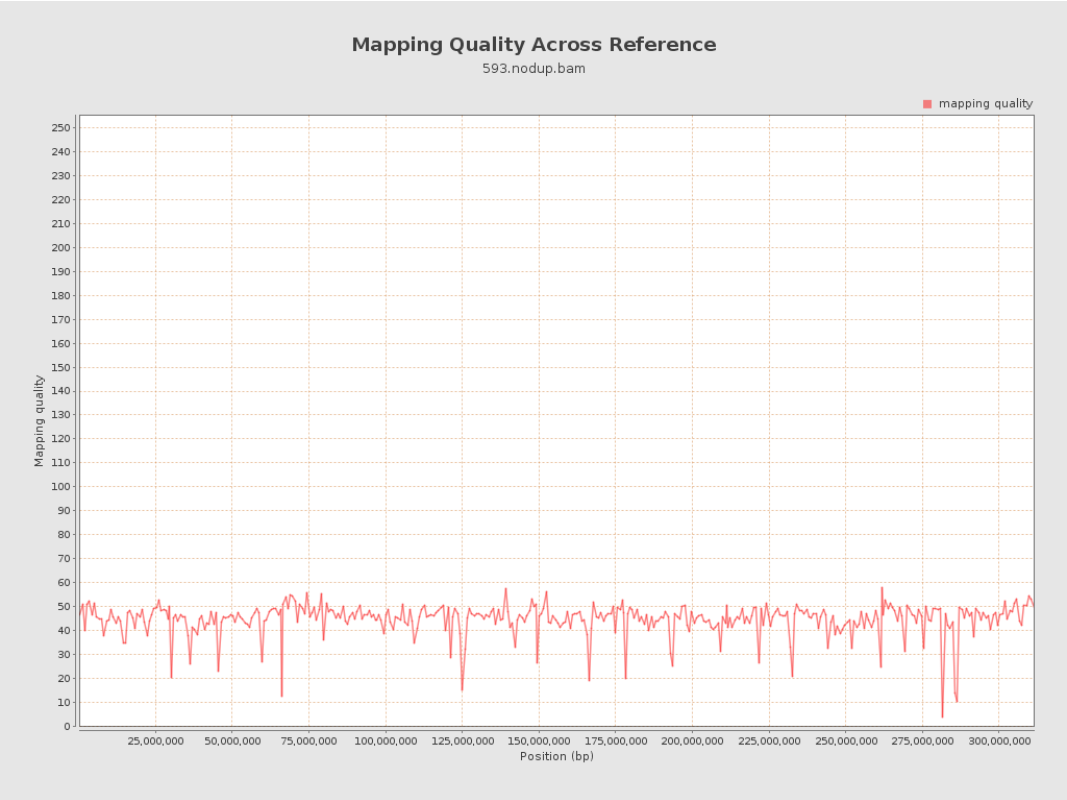
10. Results : Mapped Reads Clipping Profile



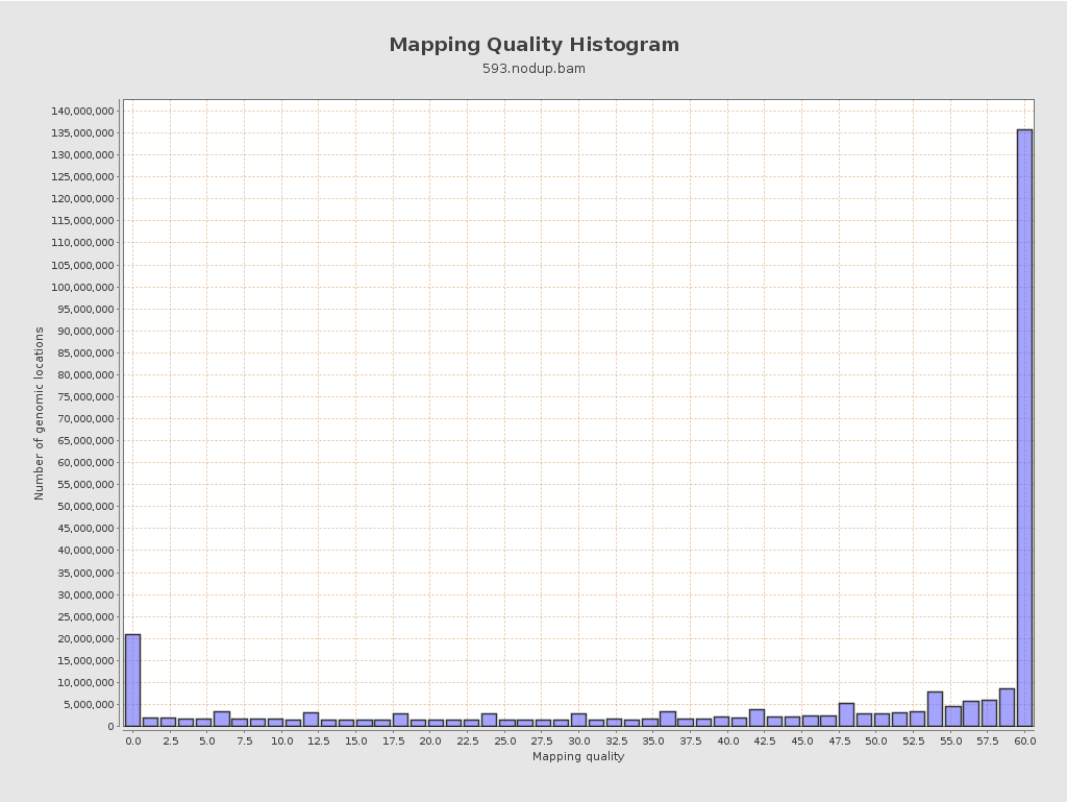
11. Results : Homopolymer Indels



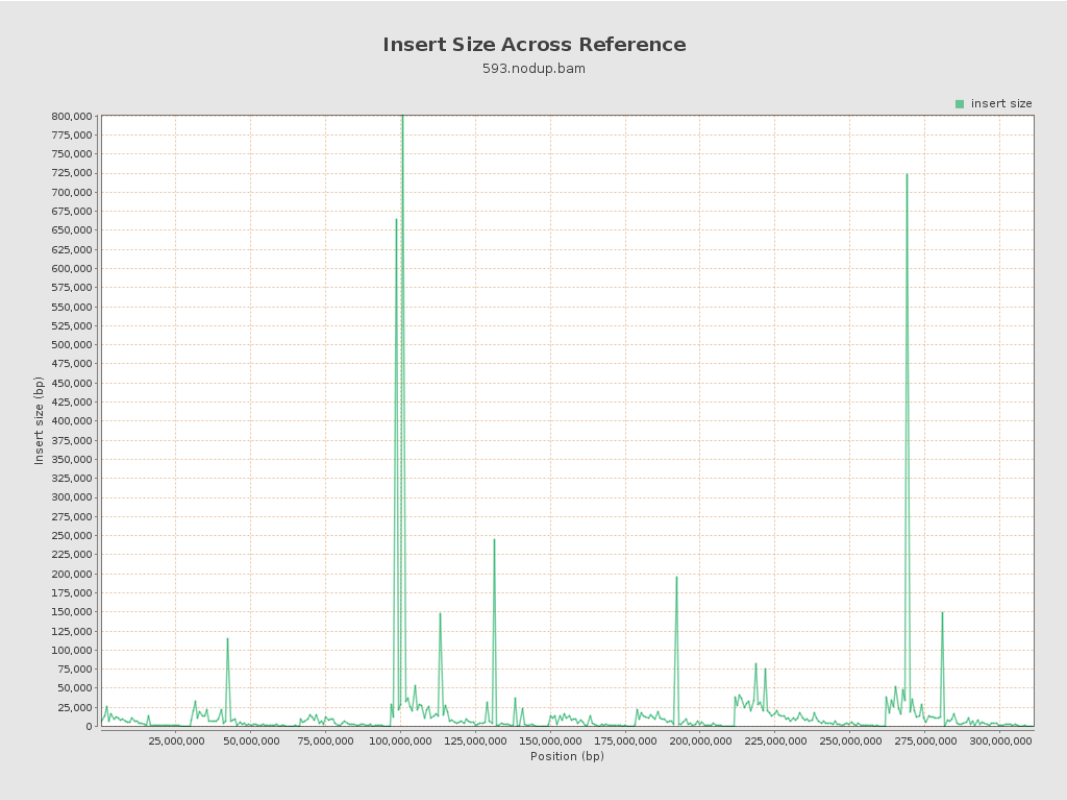
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram