Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/959.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/959.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_446/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_446_S421_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_446/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_446_S421_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:14 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,821,957
Mapped reads	71,473,905 / 94.27%
Unmapped reads	4,348,052 / 5.73%
Mapped paired reads	71,473,905 / 94.27%
Mapped reads, first in pair	35,823,419 / 47.25%
Mapped reads, second in pair	35,650,486 / 47.02%
Mapped reads, both in pair	69,970,837 / 92.28%
Mapped reads, singletons	1,503,068 / 1.98%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	11,808,470 / 15.57%
Clipped reads	15,893,439 / 20.96%

2.2. ACGT Content

Number/percentage of A's	3,054,120,448 / 30.78%
Number/percentage of C's	1,908,957,564 / 19.24%
Number/percentage of T's	3,059,050,211 / 30.83%
Number/percentage of G's	1,901,438,734 / 19.16%
Number/percentage of N's	33,508 / 0%
GC Percentage	38.4%

2.3. Coverage

Mean	31.9257
Standard Deviation	269.5005

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Insert size

Mean	245,210.12
Standard Deviation	2,337,670.49
P25/Median/P75	361 / 472 / 617

2.6. Mismatches and indels

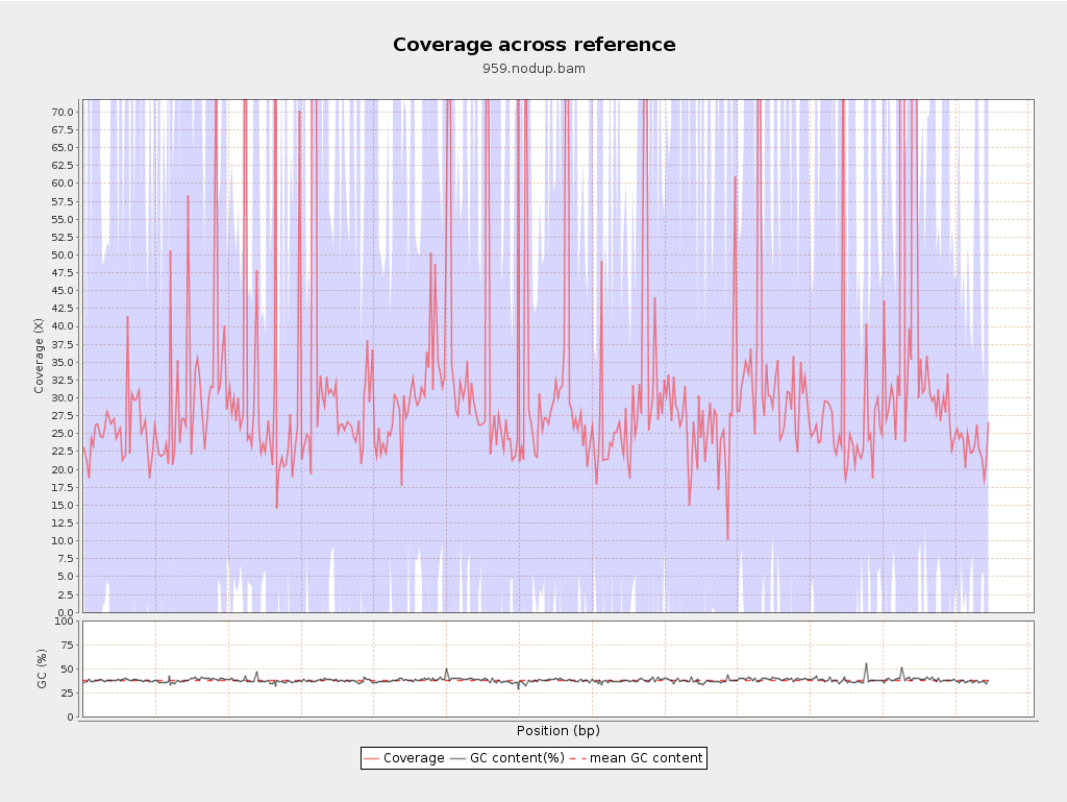
General error rate	2.35%
Mismatches	214,774,201
Insertions	6,685,022
Mapped reads with at least one insertion	8.41%
Deletions	6,841,389
Mapped reads with at least one deletion	8.5%
Homopolymer indels	56.2%

2.7. Chromosome stats

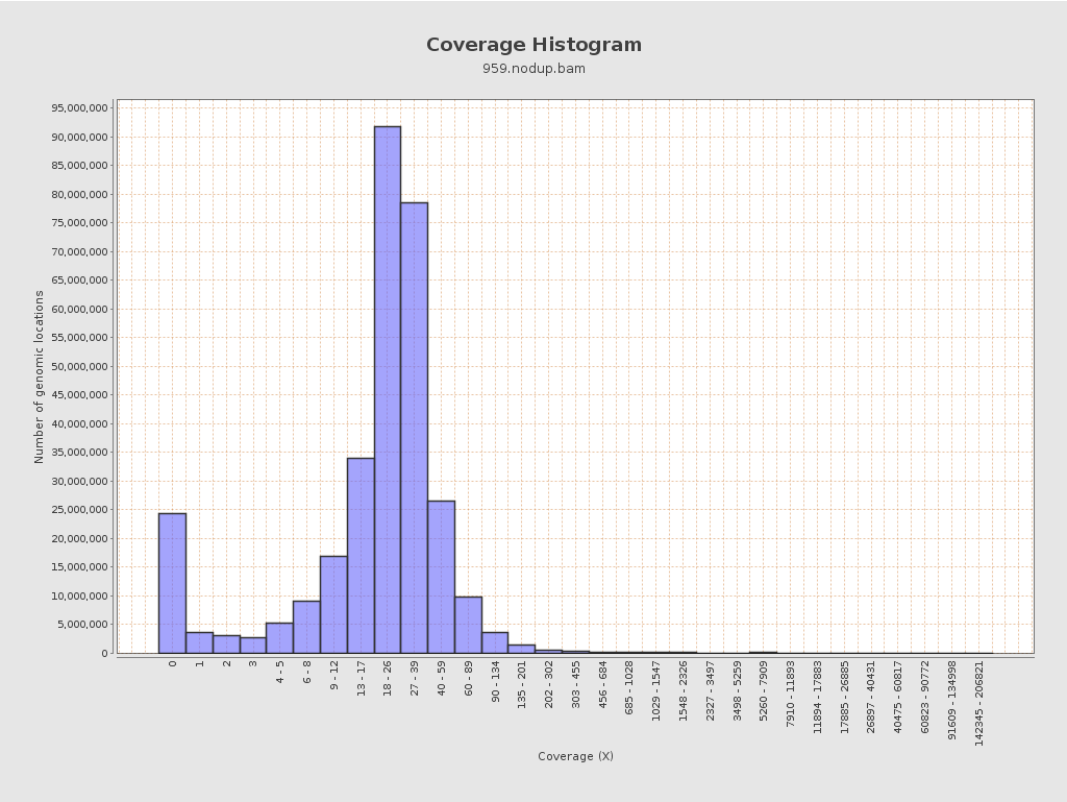
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	745003645	25.0638	75.8818

LT669789.1	36598175	1199917780	32.7863	279.0813
LT669790.1	30422129	1018374313	33.4748	261.0858
LT669791.1	52758100	1674455292	31.7384	224.496
LT669792.1	28376109	885083332	31.1911	304.7557
LT669793.1	33388210	990193145	29.657	184.7213
LT669794.1	50579949	1554438838	30.7323	232.6704
LT669795.1	49795044	1881917603	37.7933	409.8403

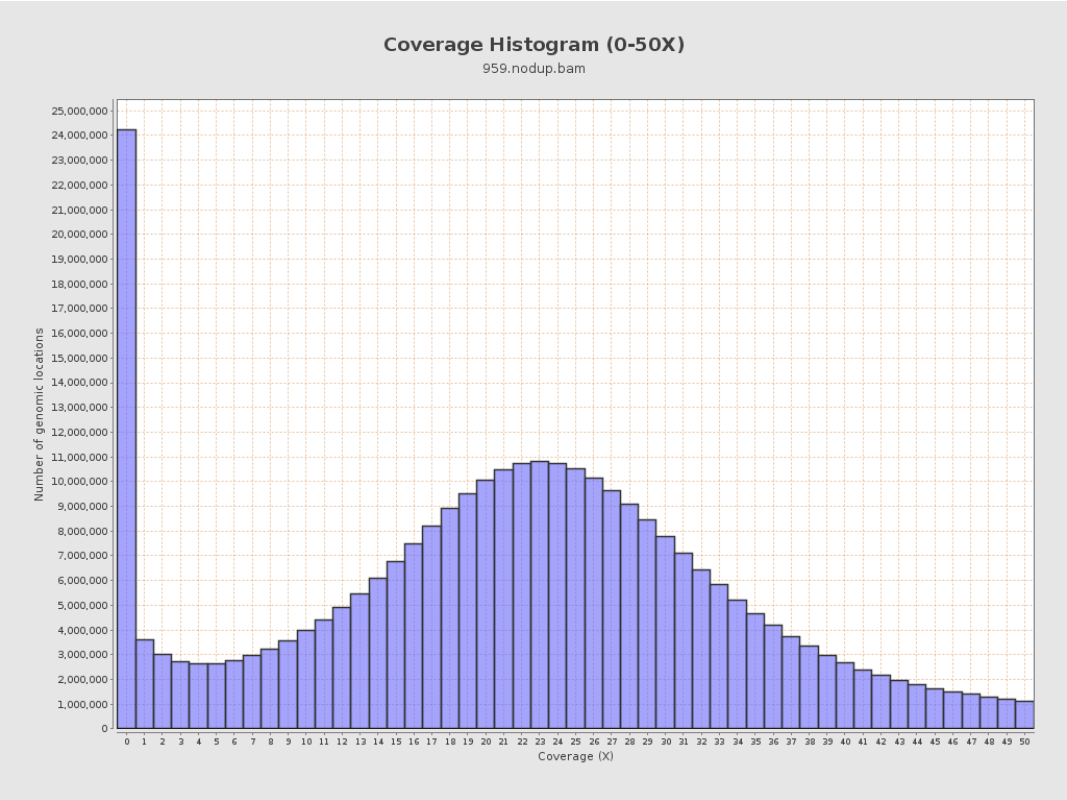
3. Results : Coverage across reference



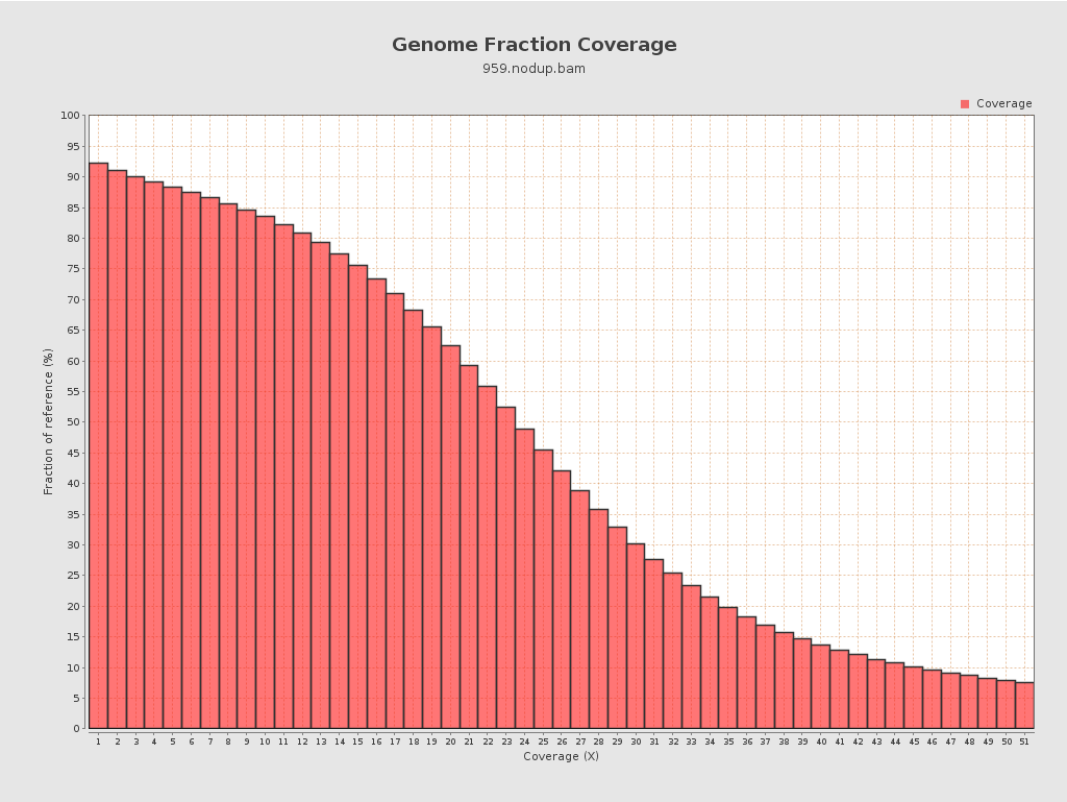
4. Results : Coverage Histogram



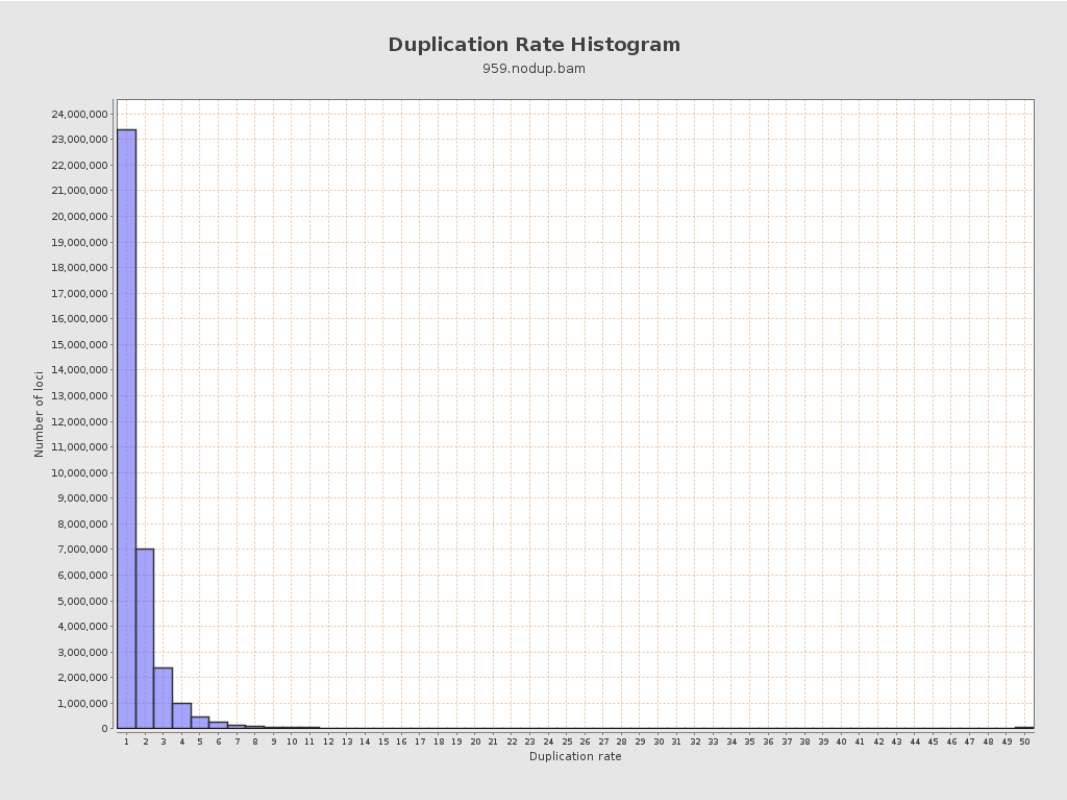
5. Results : Coverage Histogram (0-50X)



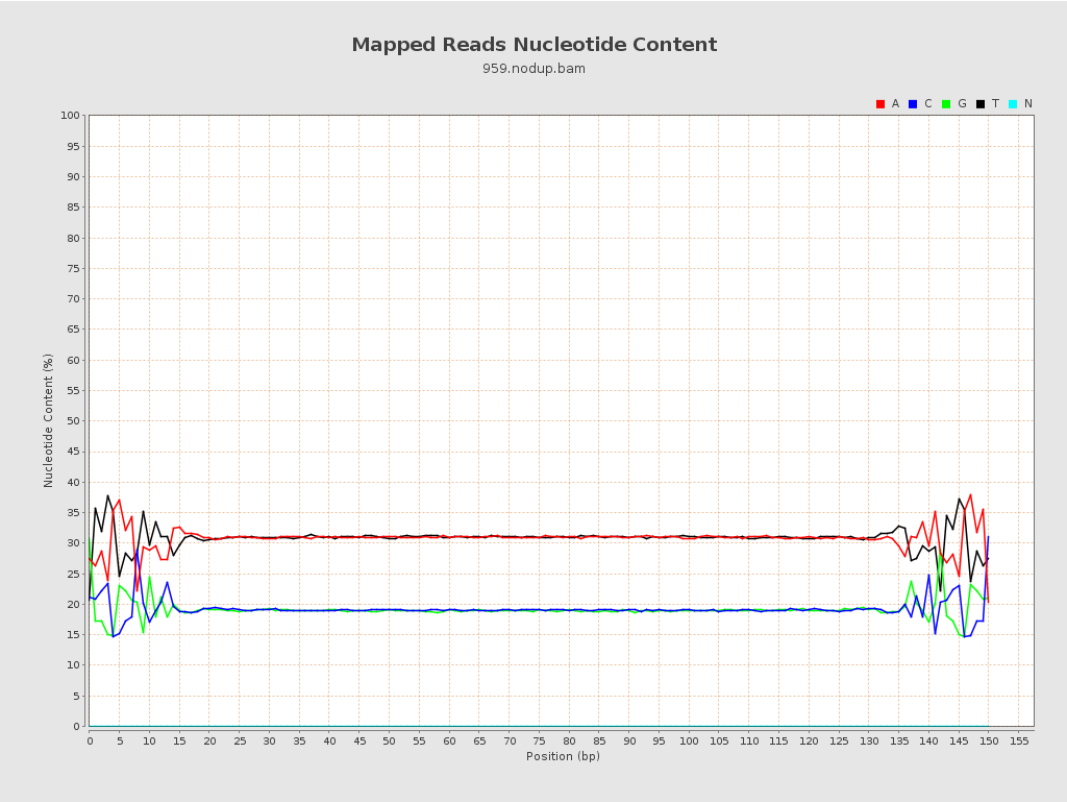
6. Results : Genome Fraction Coverage



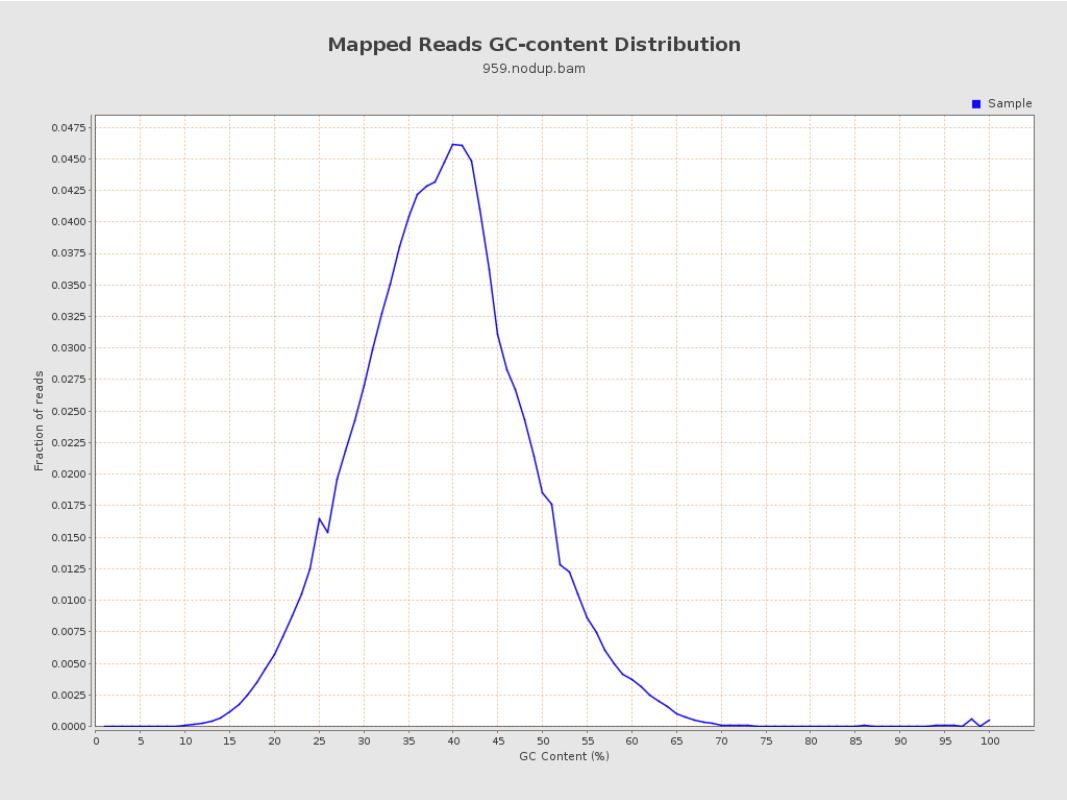
7. Results : Duplication Rate Histogram



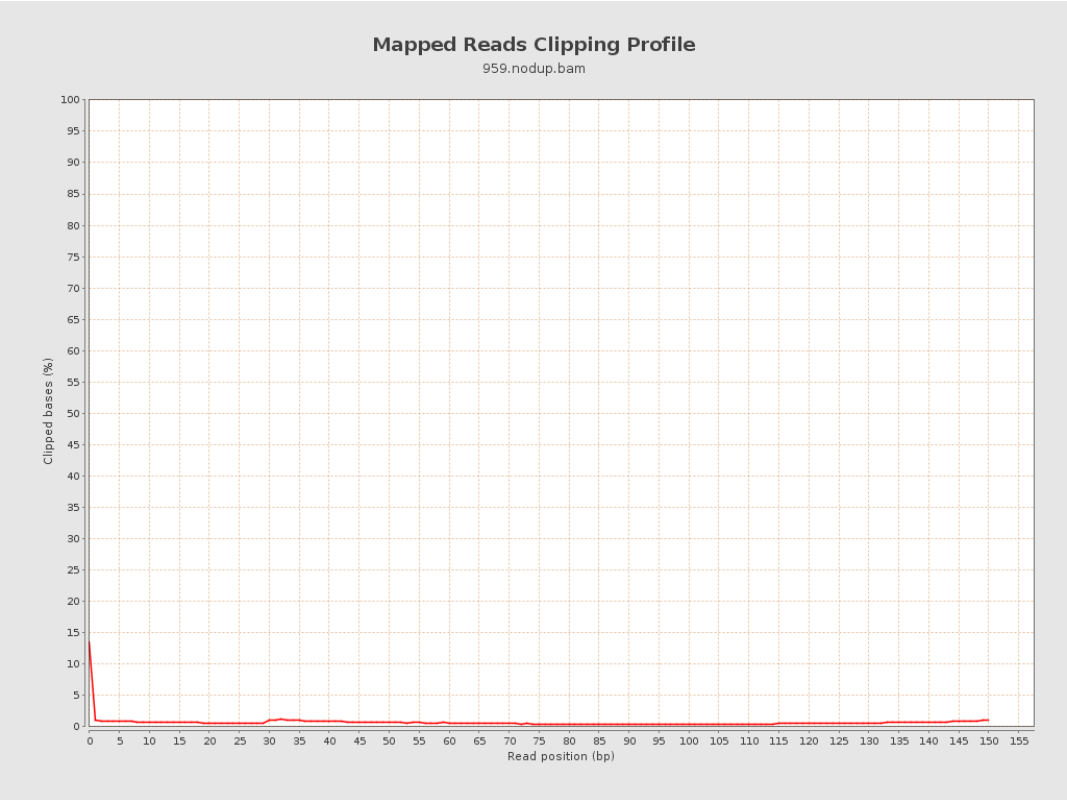
8. Results : Mapped Reads Nucleotide Content



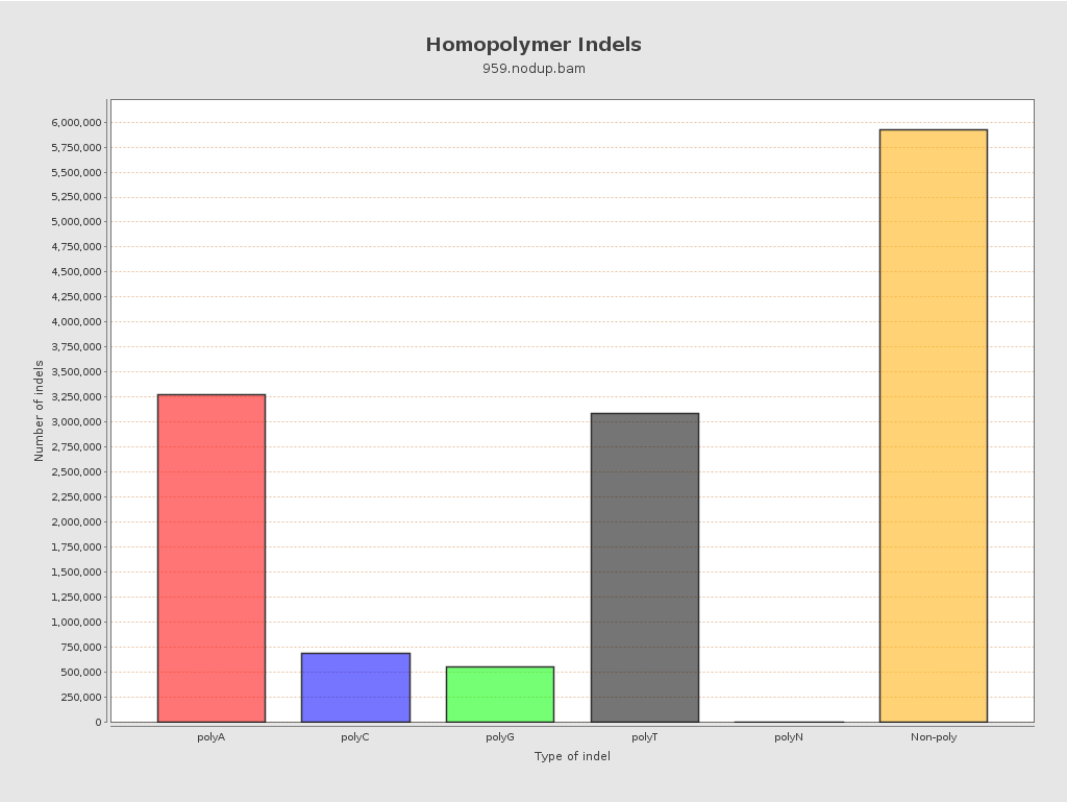
9. Results : Mapped Reads GC-content Distribution



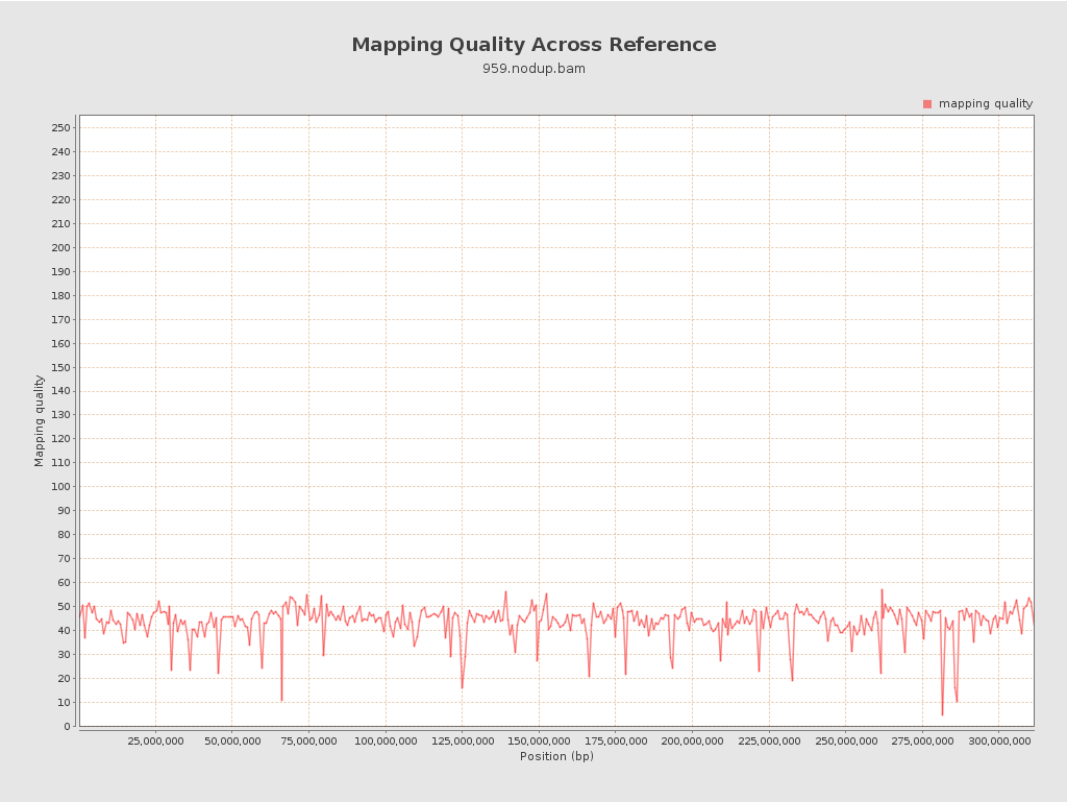
10. Results : Mapped Reads Clipping Profile



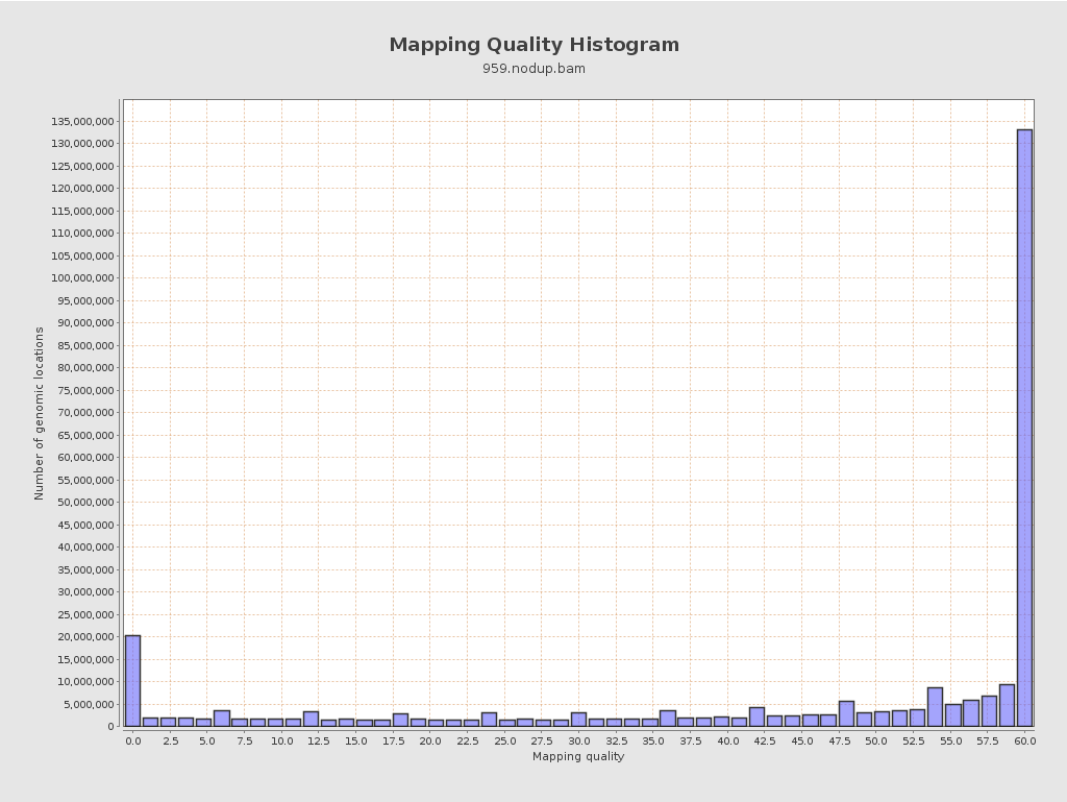
11. Results : Homopolymer Indels



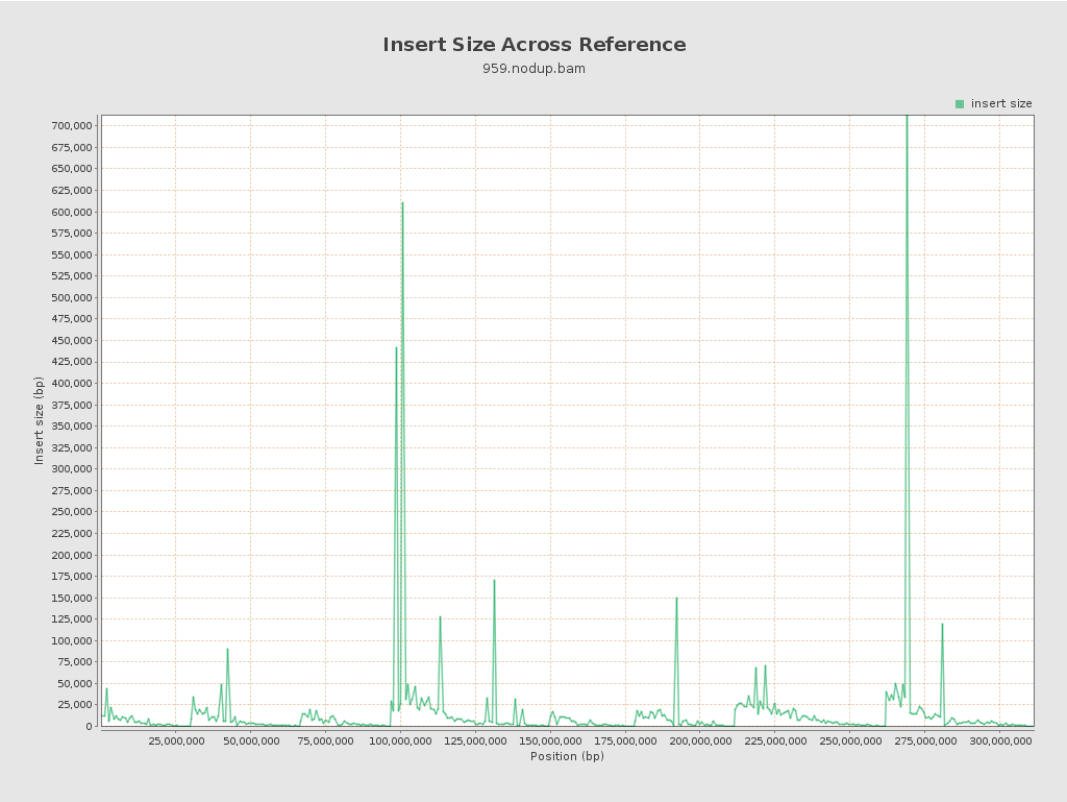
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram