Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/950.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/950.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_137/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_137_S227_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_137/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_137_S227_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:46 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,156,319
Mapped reads	56,197,363 / 91.89%
Unmapped reads	4,958,956 / 8.11%
Mapped paired reads	56,197,363 / 91.89%
Mapped reads, first in pair	28,125,239 / 45.99%
Mapped reads, second in pair	28,072,124 / 45.9%
Mapped reads, both in pair	54,929,047 / 89.82%
Mapped reads, singletons	1,268,316 / 2.07%
Read min/max/mean length	30 / 151 / 148.25
Duplicated reads (flagged)	9,311,133 / 15.23%
Clipped reads	12,270,706 / 20.06%

2.2. ACGT Content

Number/percentage of A's	2,400,544,012 / 30.79%
Number/percentage of C's	1,500,390,893 / 19.24%
Number/percentage of T's	2,400,832,133 / 30.79%
Number/percentage of G's	1,494,966,885 / 19.17%
Number/percentage of N's	32,723 / 0%
GC Percentage	38.42%

2.3. Coverage

Mean	25.0794
Standard Deviation	230.028

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Insert size

Mean	222,139.05
Standard Deviation	2,239,812.64
P25/Median/P75	334 / 437 / 574

2.6. Mismatches and indels

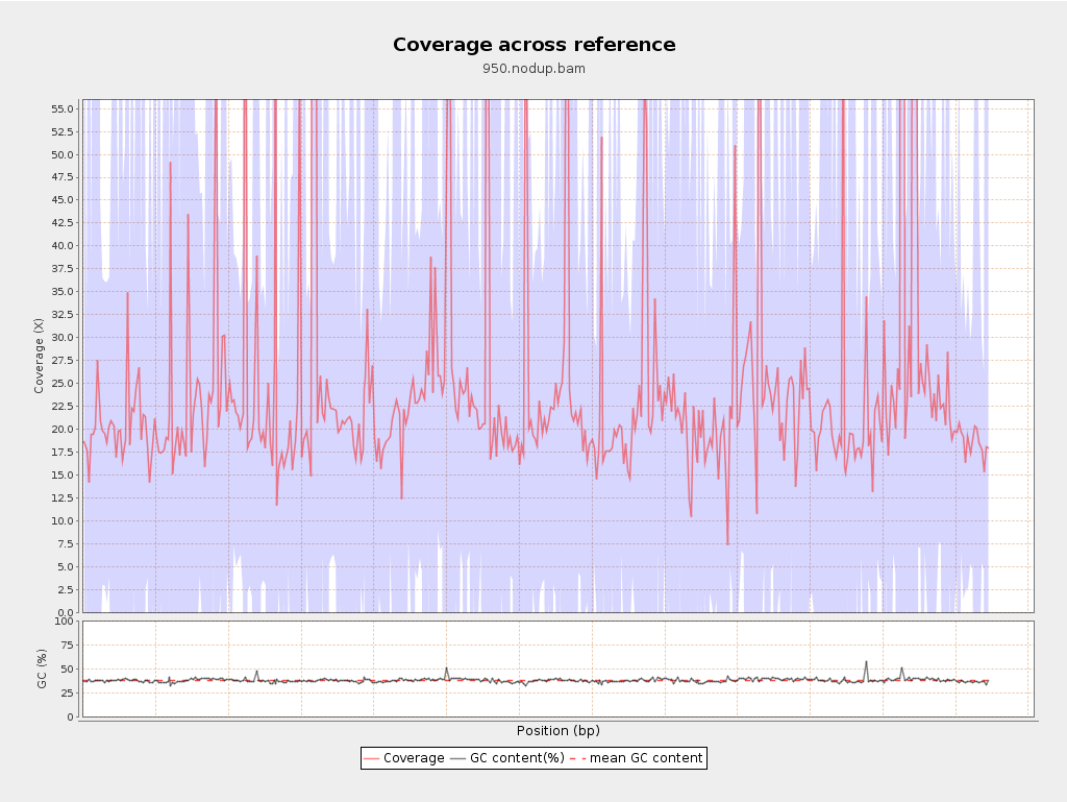
General error rate	2.25%
Mismatches	160,911,432
Insertions	5,135,010
Mapped reads with at least one insertion	8.21%
Deletions	5,166,729
Mapped reads with at least one deletion	8.18%
Homopolymer indels	56.95%

2.7. Chromosome stats

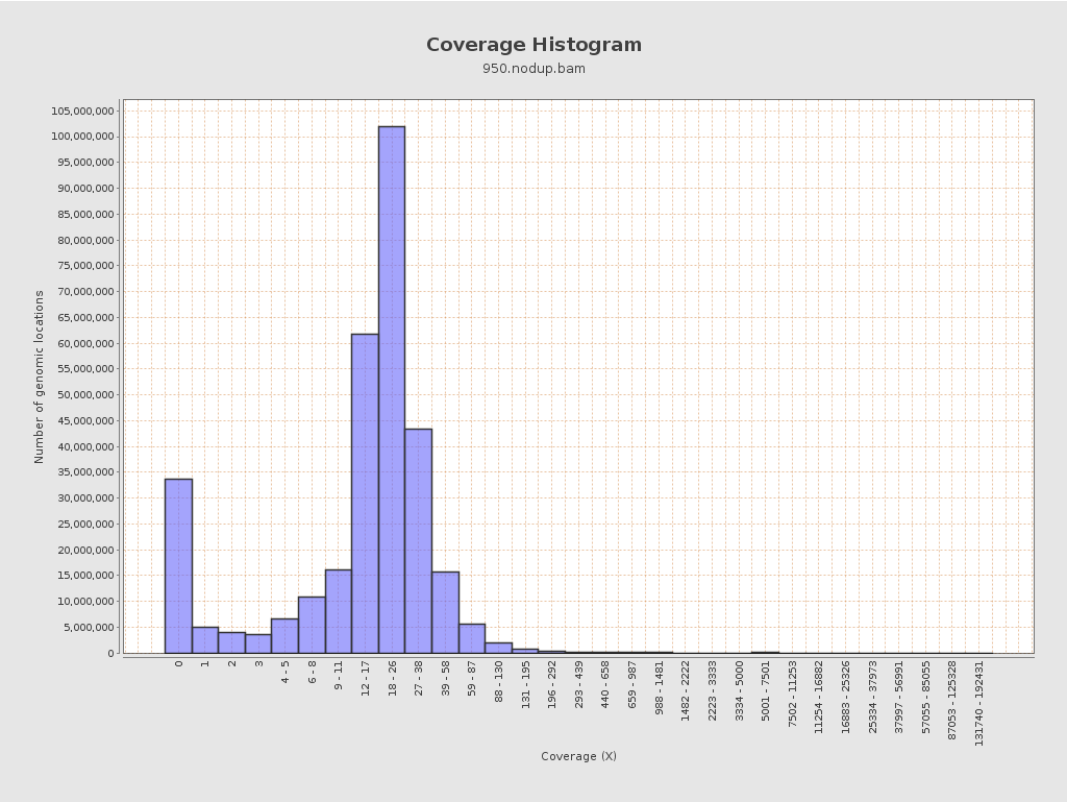
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	595718955	20.0415	68.5344

LT669789.1	36598175	916270726	25.036	231.7575
LT669790.1	30422129	832208661	27.3554	255.9576
LT669791.1	52758100	1310571560	24.8411	197.9608
LT669792.1	28376109	684797812	24.1329	221.5283
LT669793.1	33388210	753192582	22.5586	111.618
LT669794.1	50579949	1200908418	23.7428	210.6943
LT669795.1	49795044	1522136978	30.568	354.7706

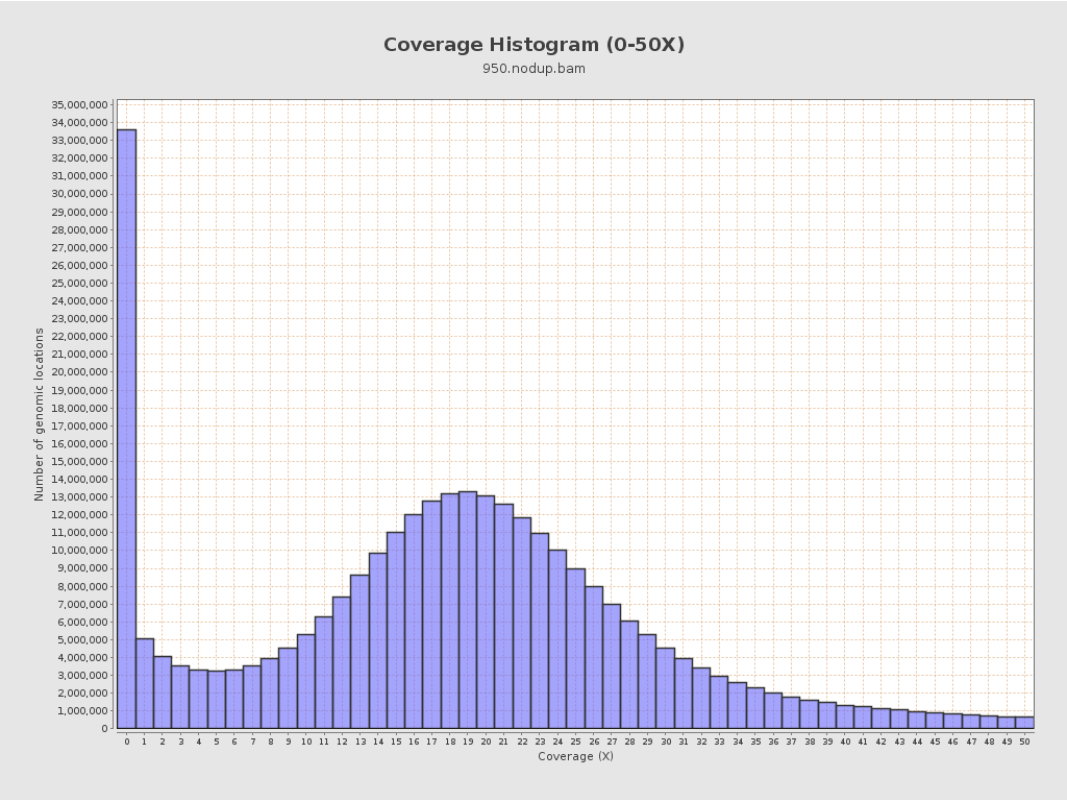
3. Results : Coverage across reference



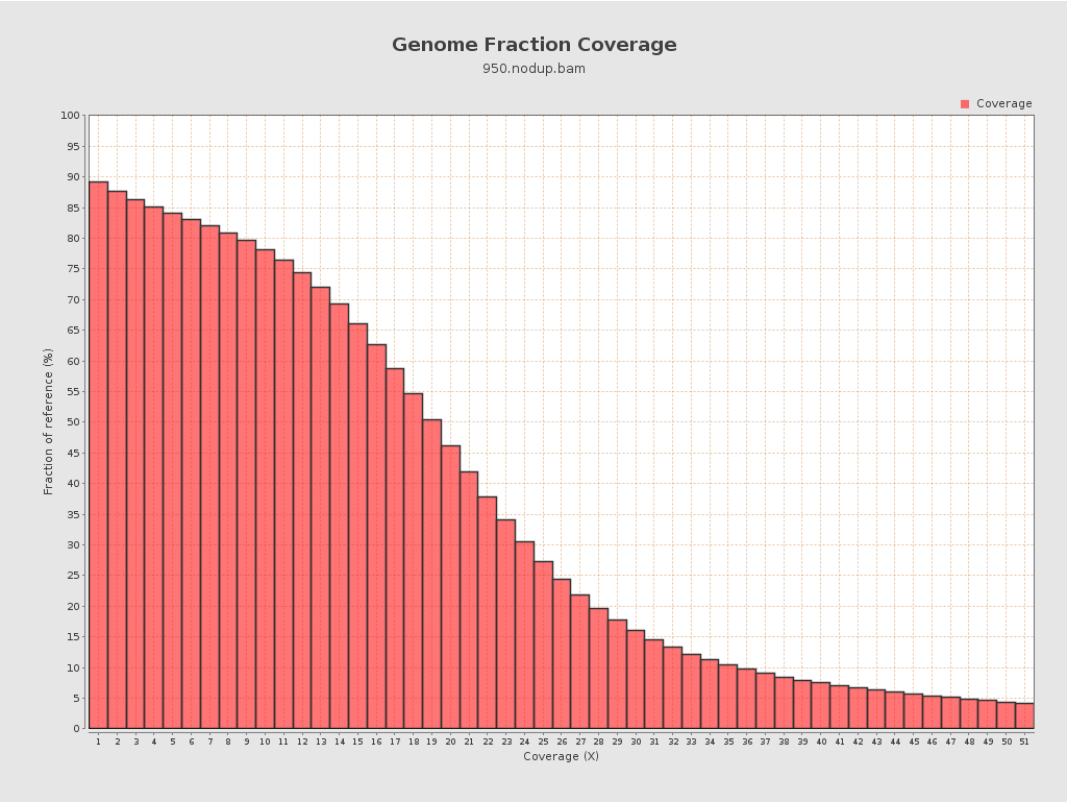
4. Results : Coverage Histogram



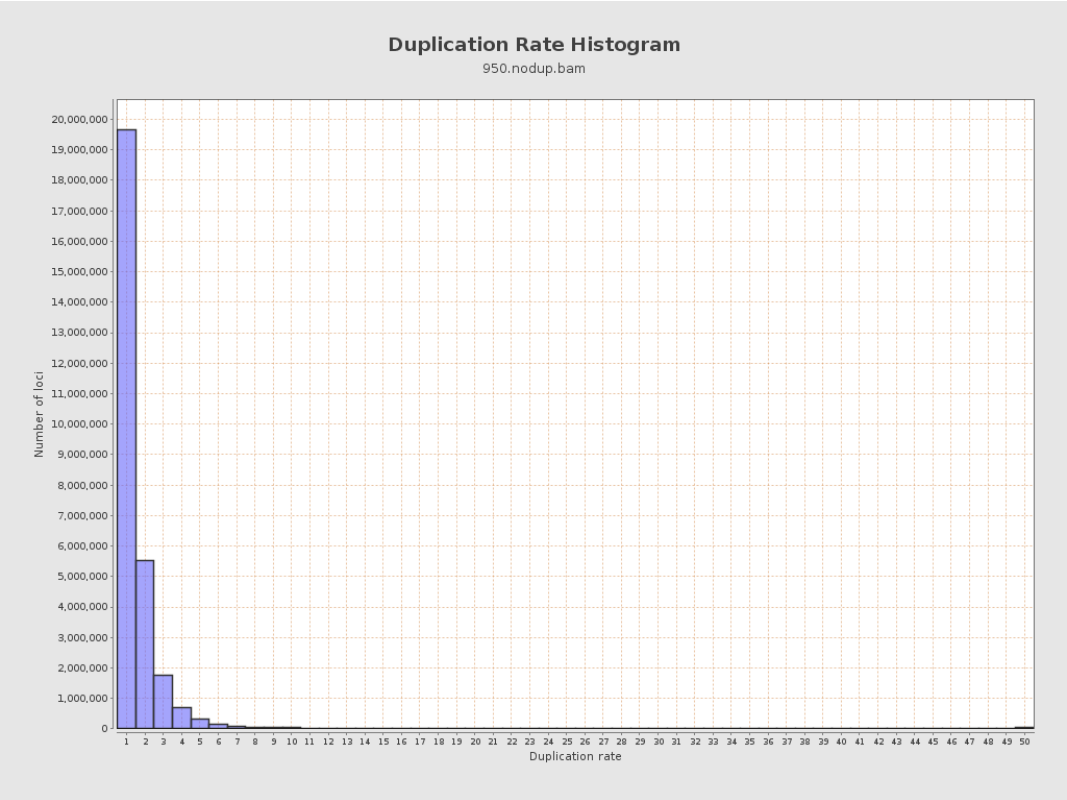
5. Results : Coverage Histogram (0-50X)



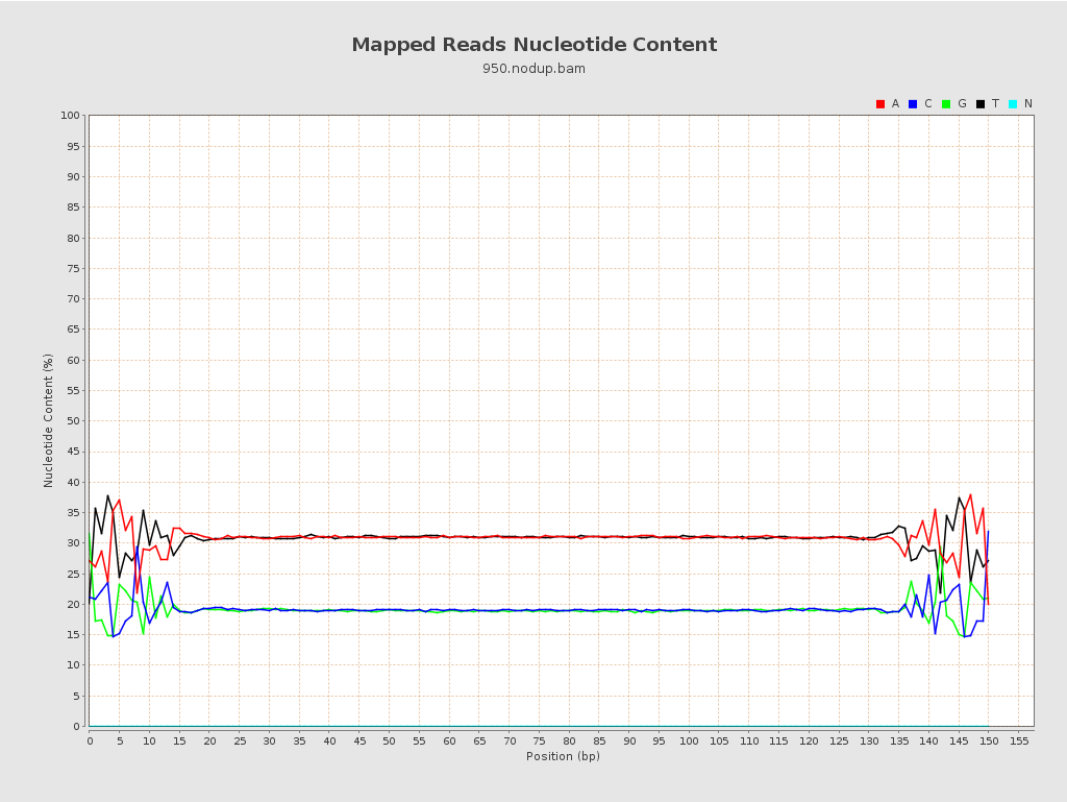
6. Results : Genome Fraction Coverage



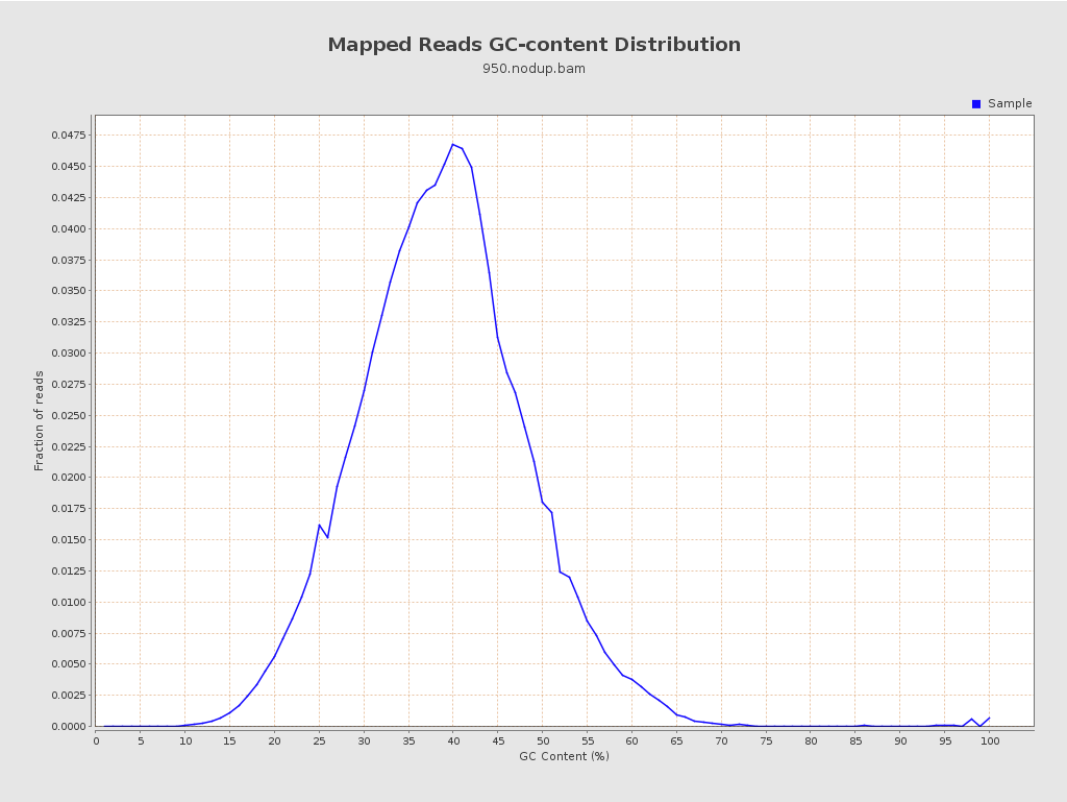
7. Results : Duplication Rate Histogram



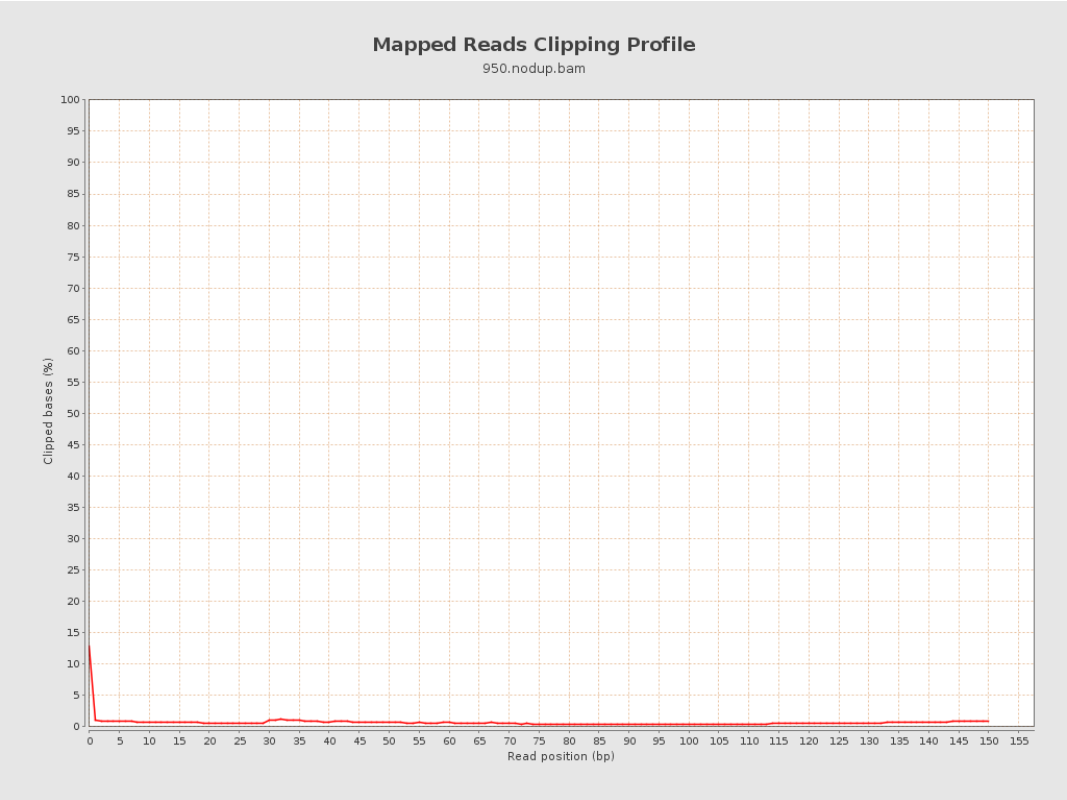
8. Results : Mapped Reads Nucleotide Content



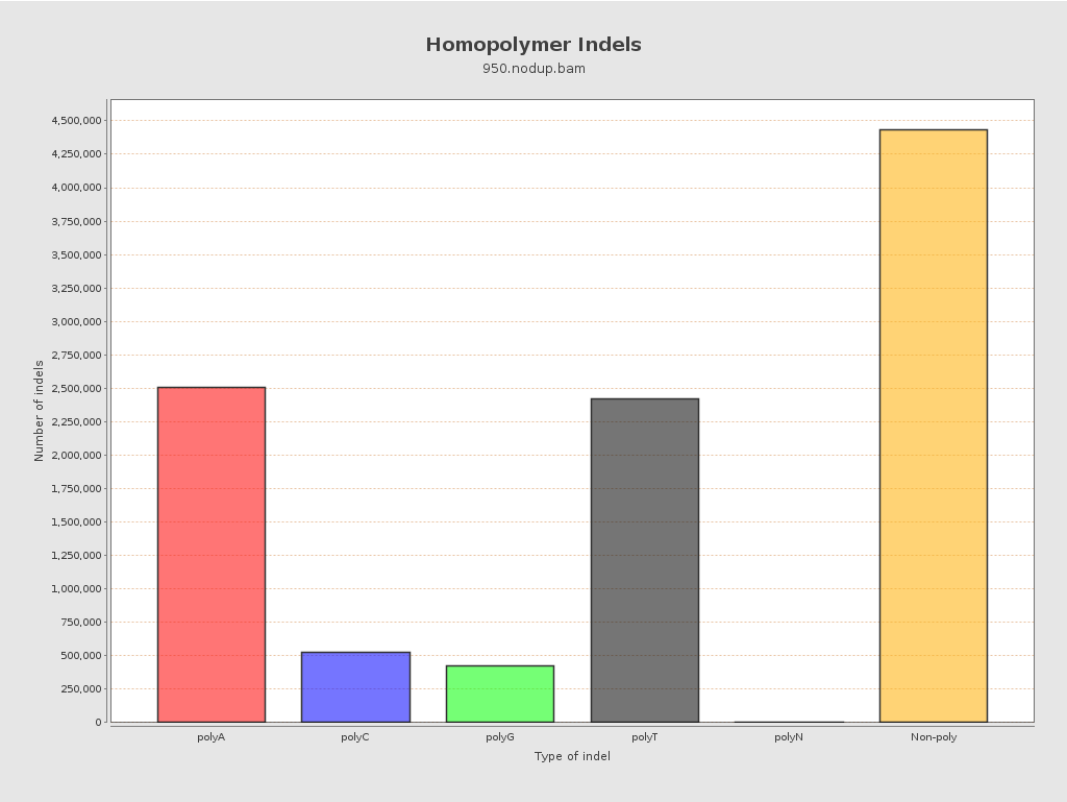
9. Results : Mapped Reads GC-content Distribution



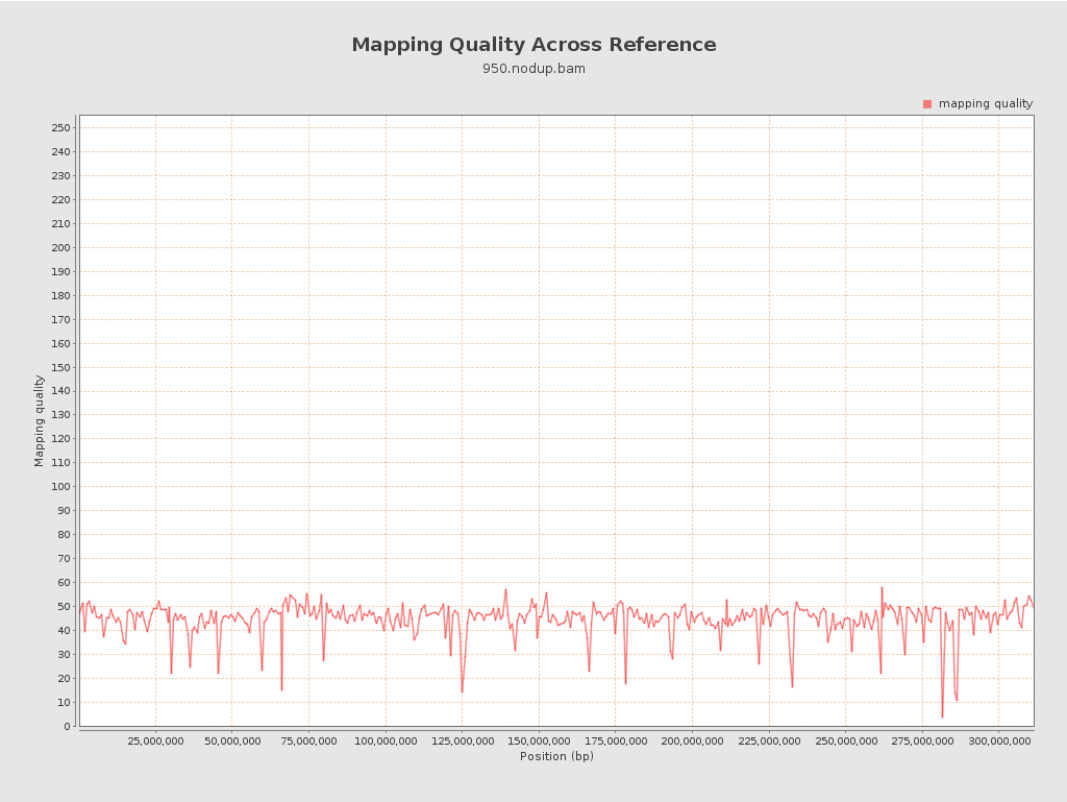
10. Results : Mapped Reads Clipping Profile



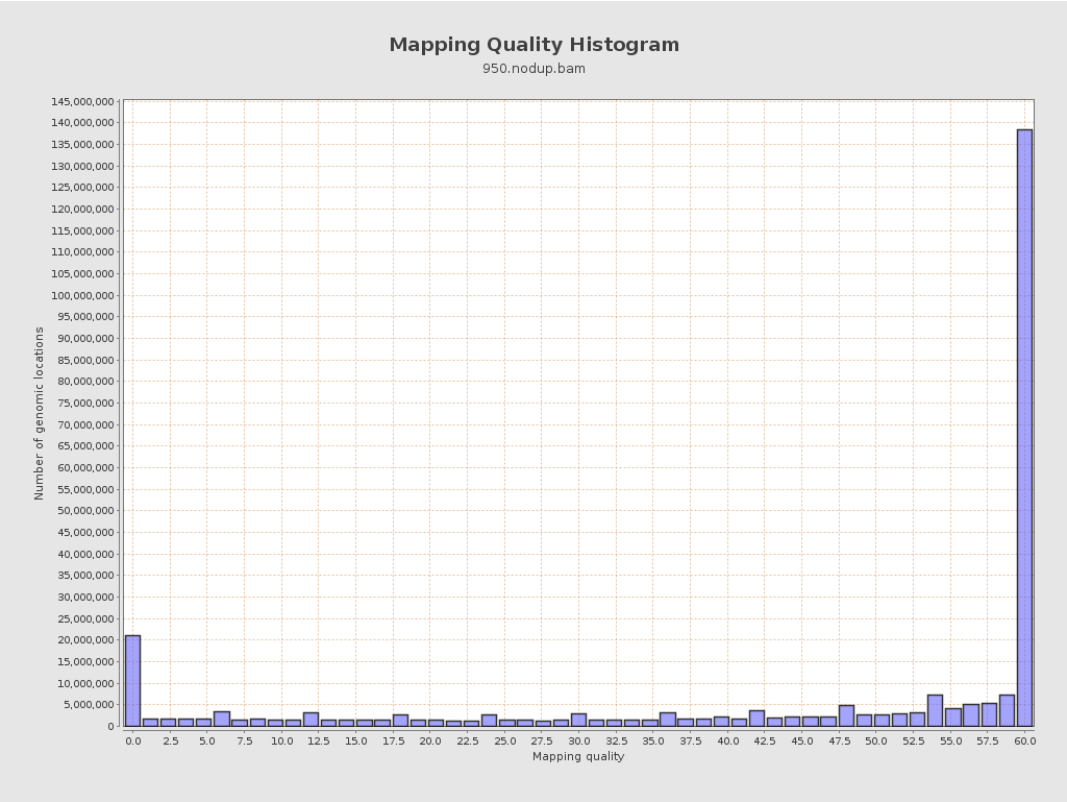
11. Results : Homopolymer Indels



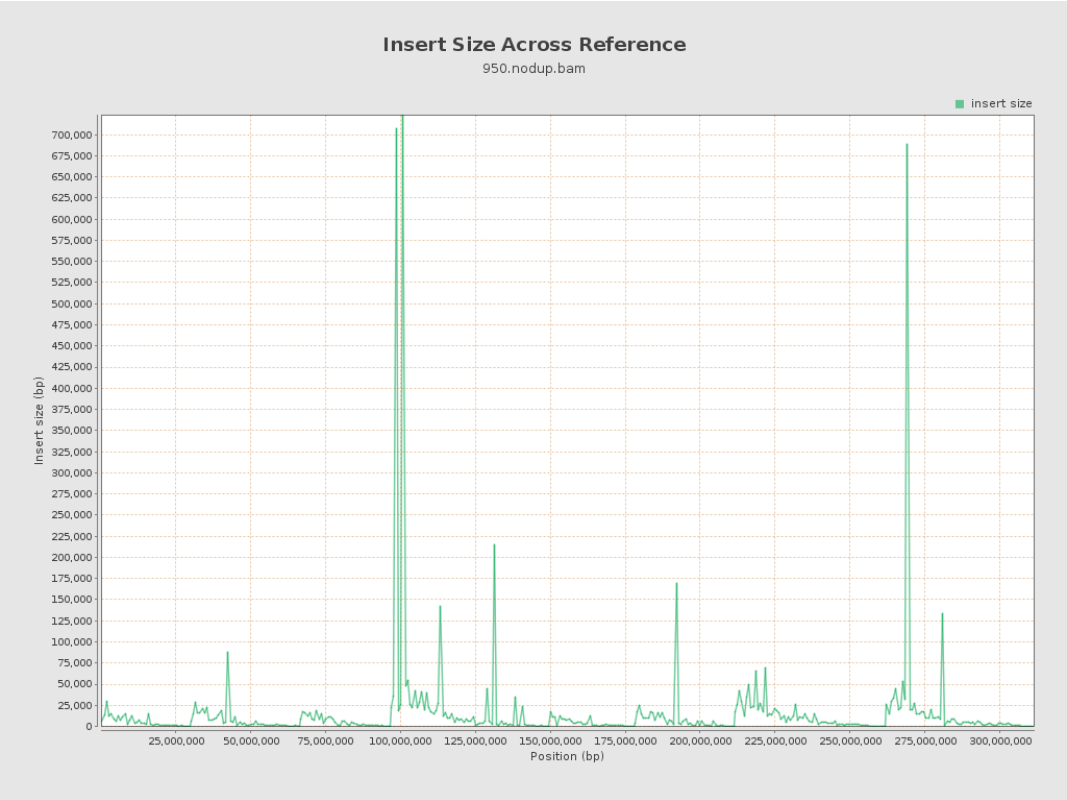
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram