Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/953.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/953.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_434/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_434_S409_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_434/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_434_S409_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	53,436,605
Mapped reads	50,867,631 / 95.19%
Unmapped reads	2,568,974 / 4.81%
Mapped paired reads	50,867,631 / 95.19%
Mapped reads, first in pair	25,512,045 / 47.74%
Mapped reads, second in pair	25,355,586 / 47.45%
Mapped reads, both in pair	49,997,089 / 93.56%
Mapped reads, singletons	870,542 / 1.63%
Read min/max/mean length	30 / 151 / 147.67
Duplicated reads (flagged)	6,965,430 / 13.03%
Clipped reads	12,542,908 / 23.47%

2.2. ACGT Content

Number/percentage of A's	2,146,643,777 / 30.73%
Number/percentage of C's	1,346,208,677 / 19.27%
Number/percentage of T's	2,149,514,840 / 30.77%
Number/percentage of G's	1,343,223,576 / 19.23%
Number/percentage of N's	24,141 / 0%
GC Percentage	38.5%

2.3. Coverage

Mean	22.4768
Standard Deviation	190.2162

2.4. Mapping Quality

Mean Mapping Quality	43.01

2.5. Insert size

Mean	245,284.26
Standard Deviation	2,329,403.63
P25/Median/P75	323 / 444 / 586

2.6. Mismatches and indels

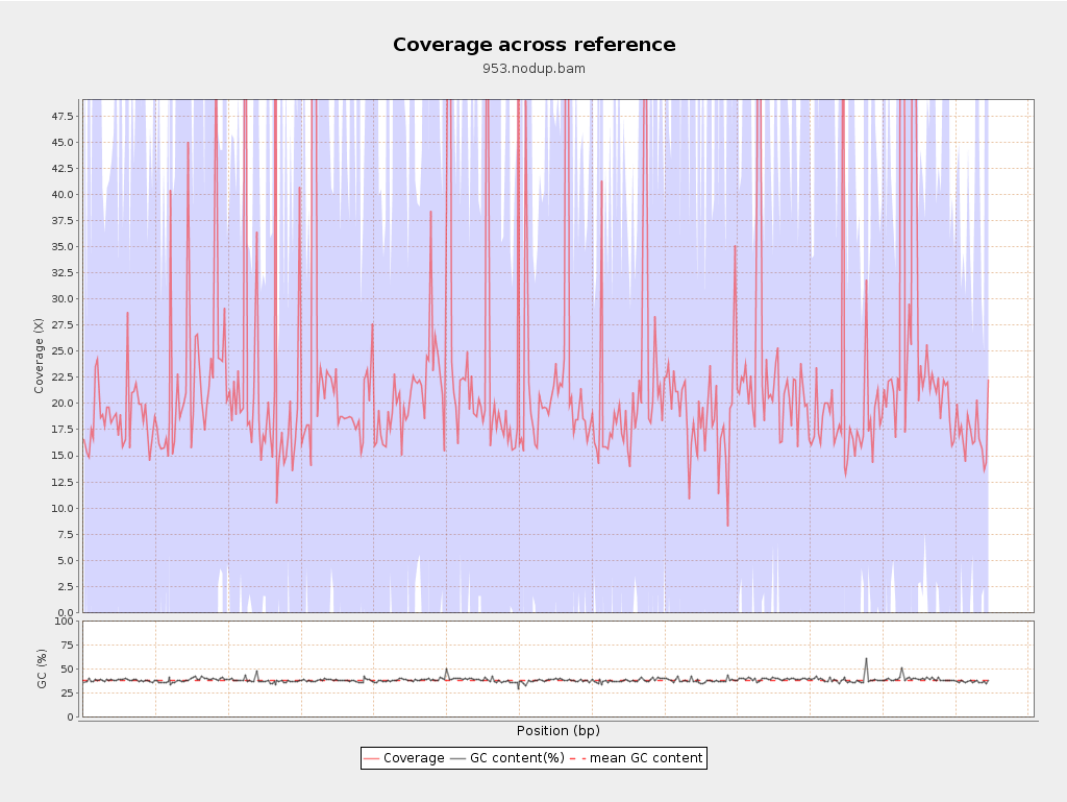
General error rate	2.39%
Mismatches	154,063,669
Insertions	4,819,296
Mapped reads with at least one insertion	8.53%
Deletions	5,024,400
Mapped reads with at least one deletion	8.72%
Homopolymer indels	55.42%

2.7. Chromosome stats

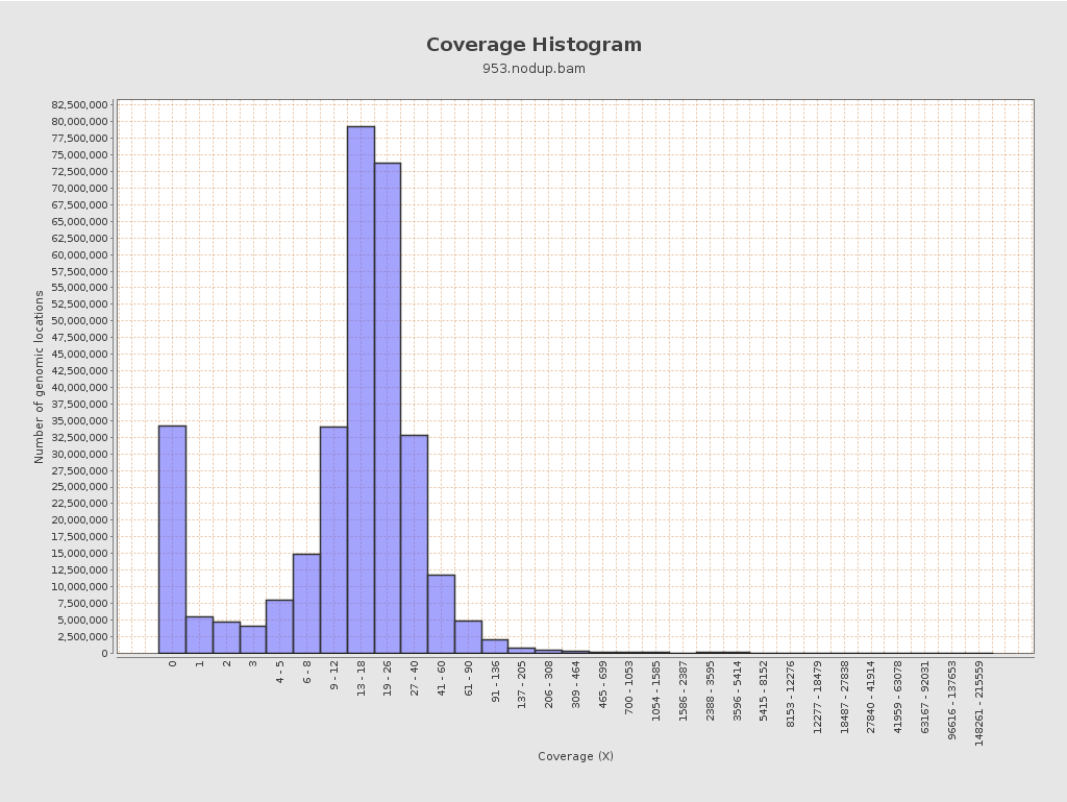
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	546986840	18.402	62.6106

LT669789.1	36598175	868191360	23.7223	210.9346
LT669790.1	30422129	691126019	22.7179	142.4558
LT669791.1	52758100	1169767156	22.1723	172.066
LT669792.1	28376109	629299717	22.1771	221.2312
LT669793.1	33388210	697506000	20.8908	98.5055
LT669794.1	50579949	1108764626	21.921	181.0095
LT669795.1	49795044	1293060586	25.9677	282.7269

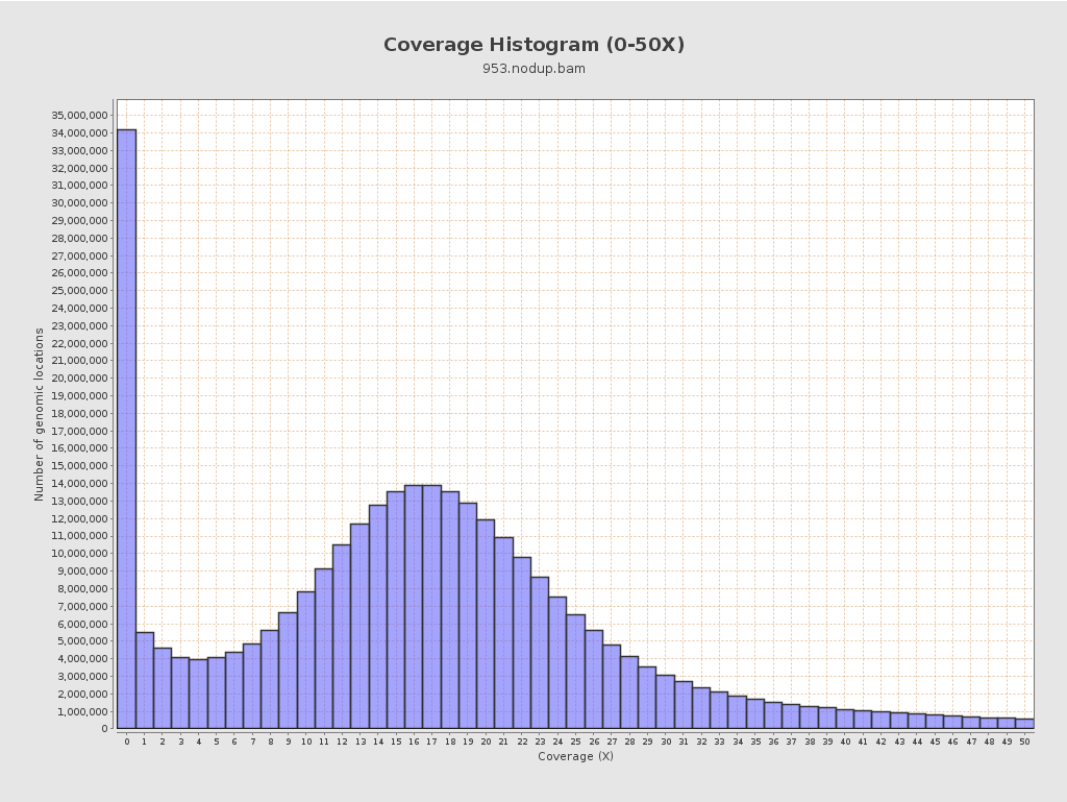
3. Results : Coverage across reference



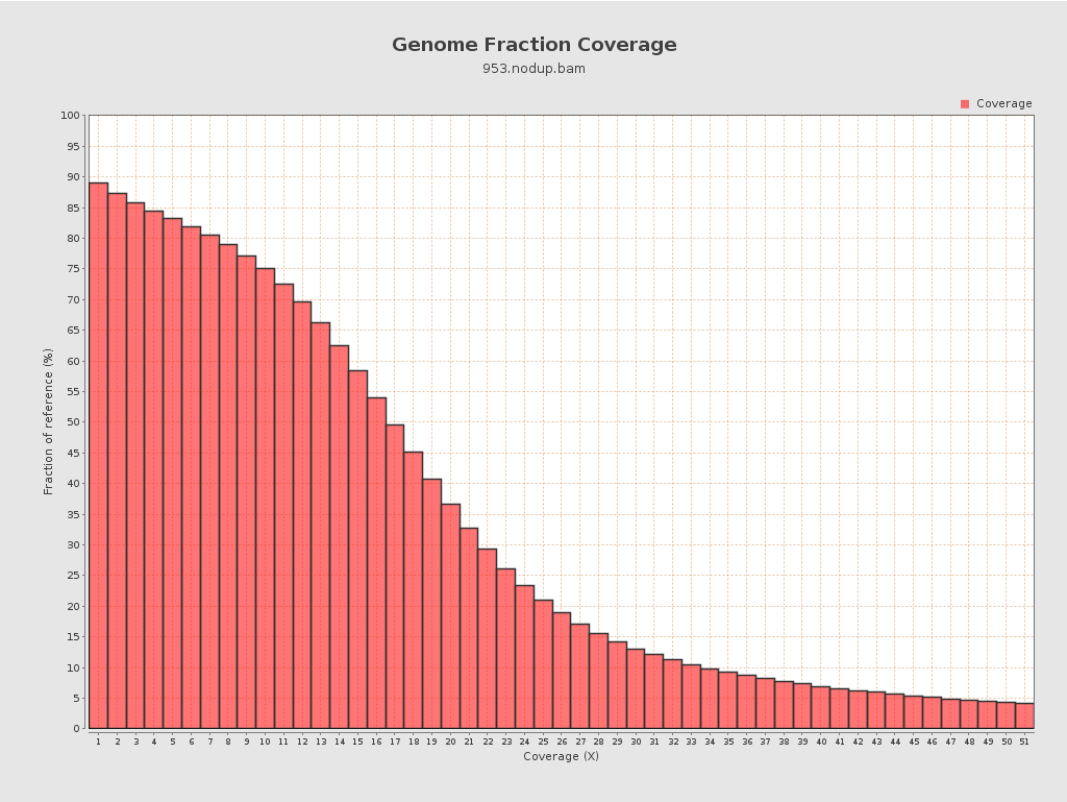
4. Results : Coverage Histogram



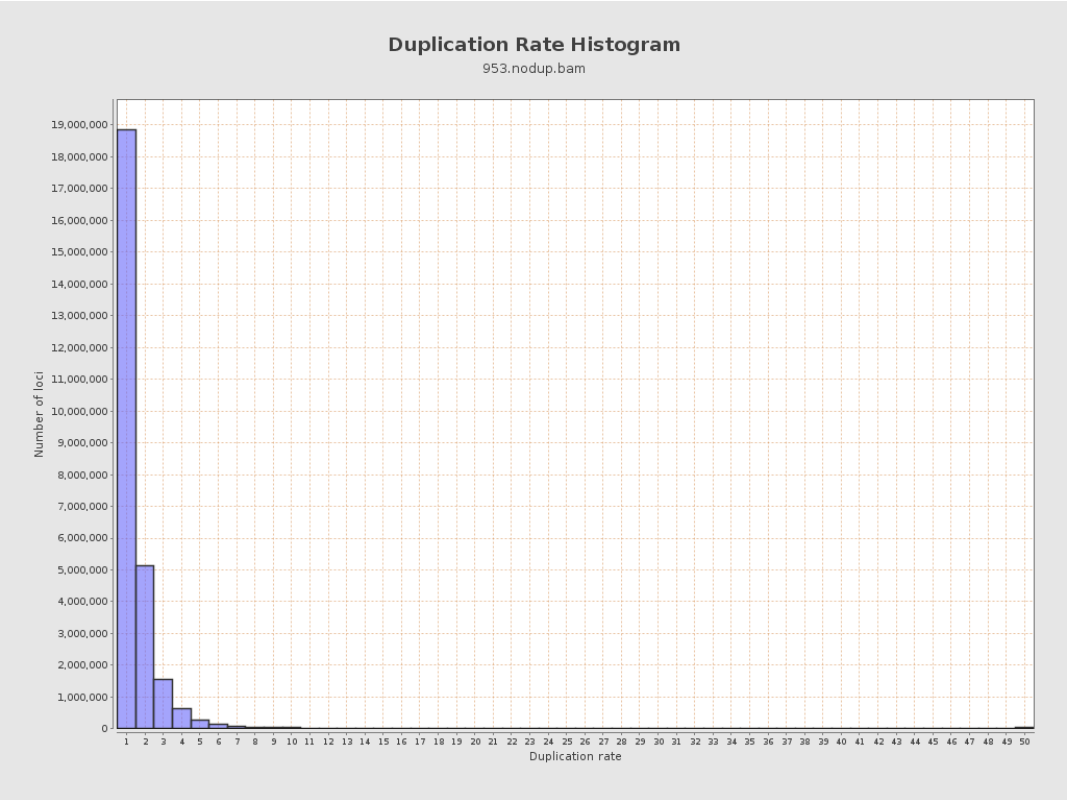
5. Results : Coverage Histogram (0-50X)



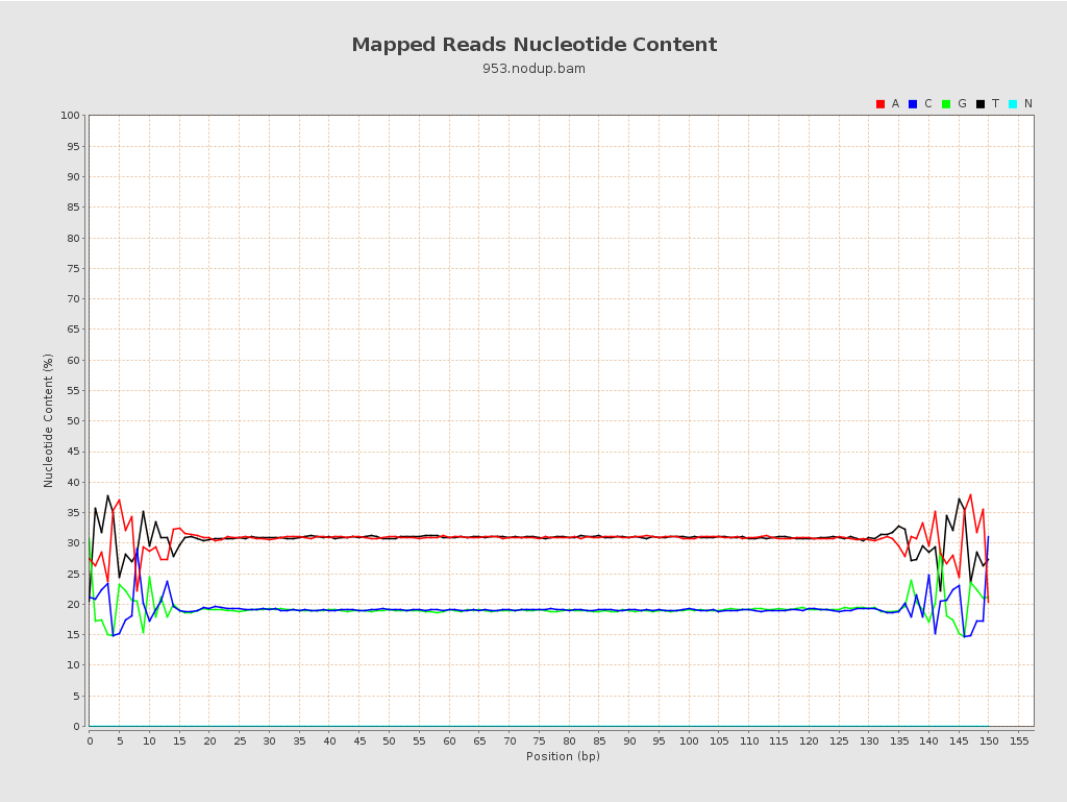
6. Results : Genome Fraction Coverage



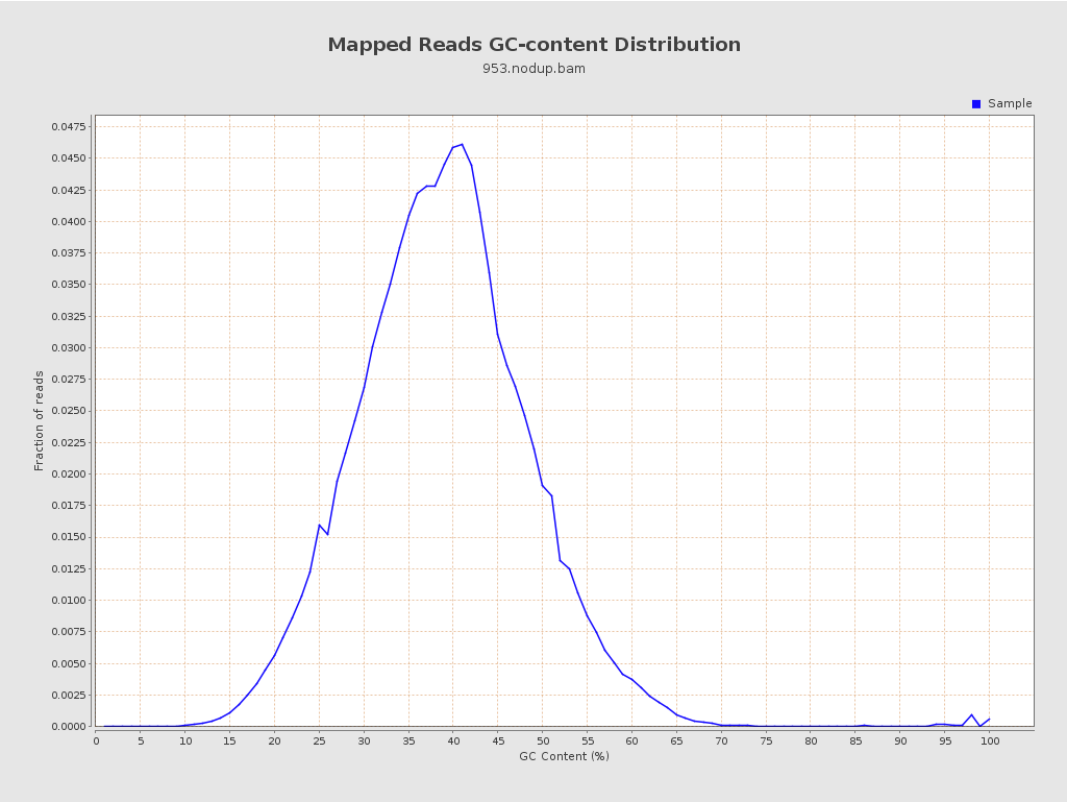
7. Results : Duplication Rate Histogram



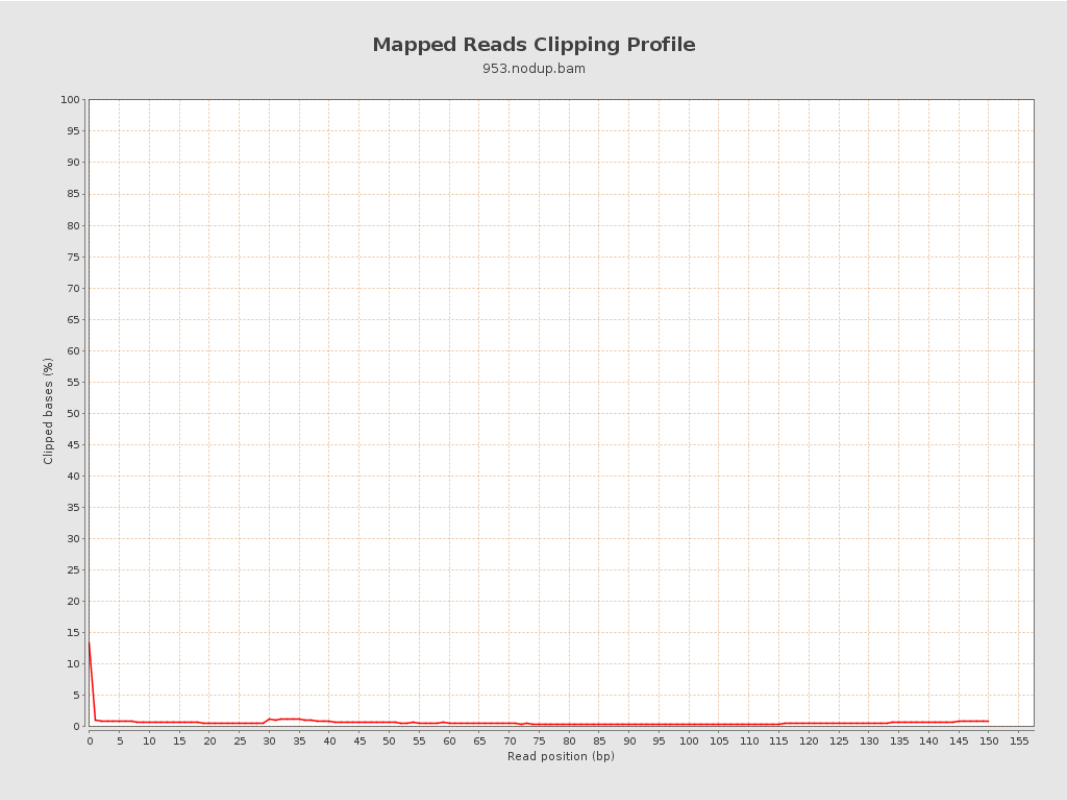
8. Results : Mapped Reads Nucleotide Content



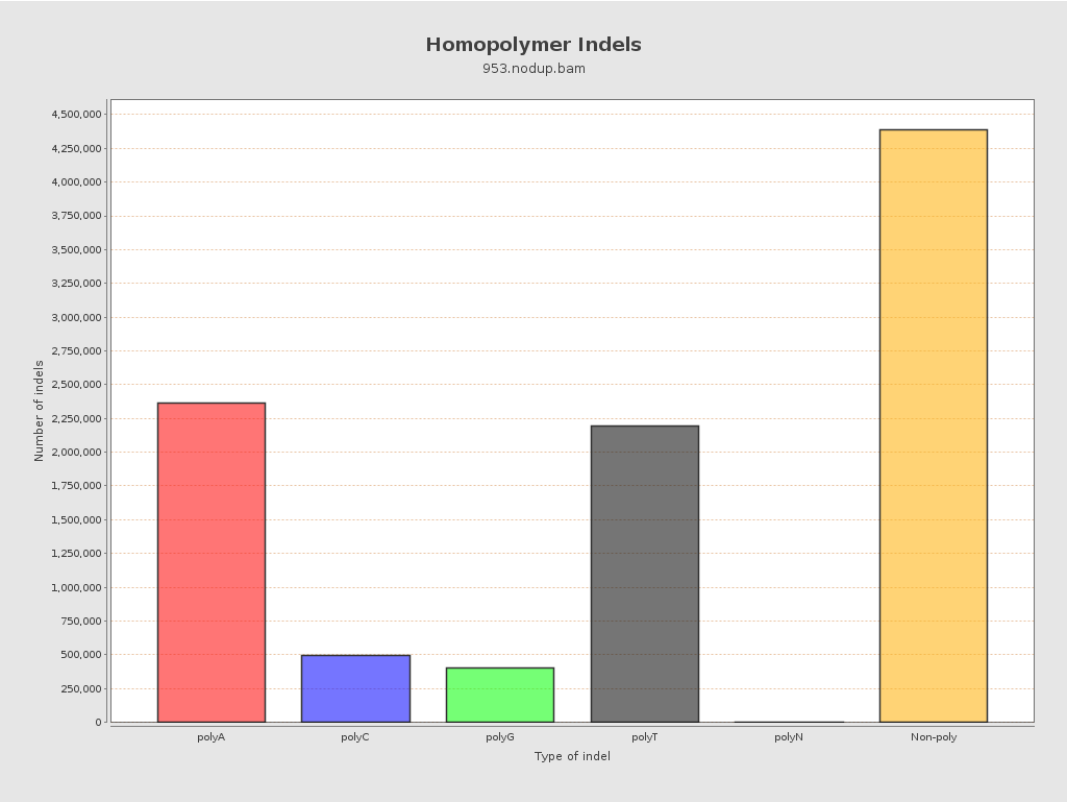
9. Results : Mapped Reads GC-content Distribution



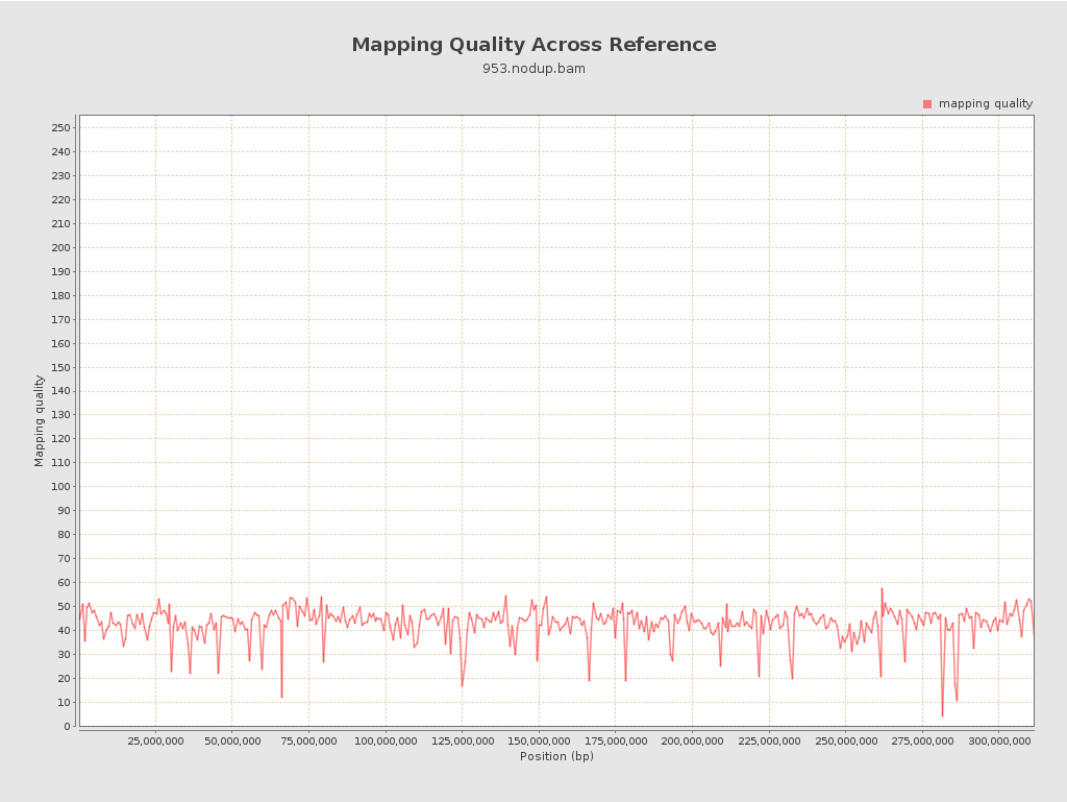
10. Results : Mapped Reads Clipping Profile



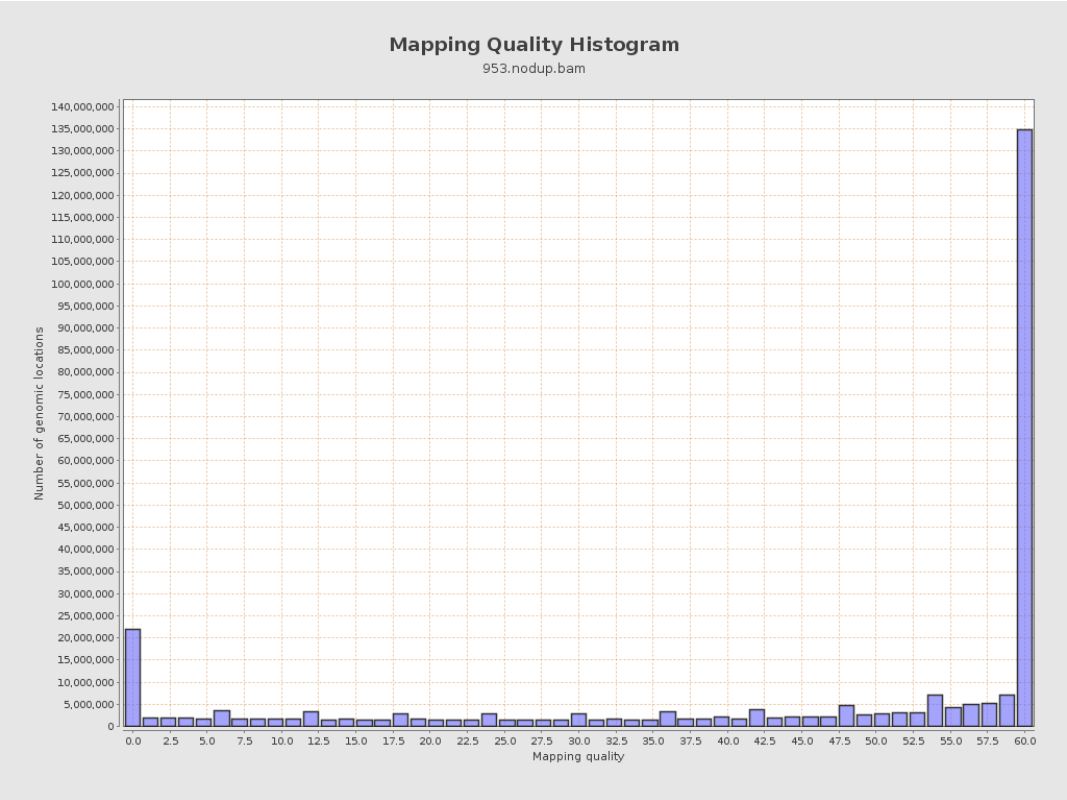
11. Results : Homopolymer Indels



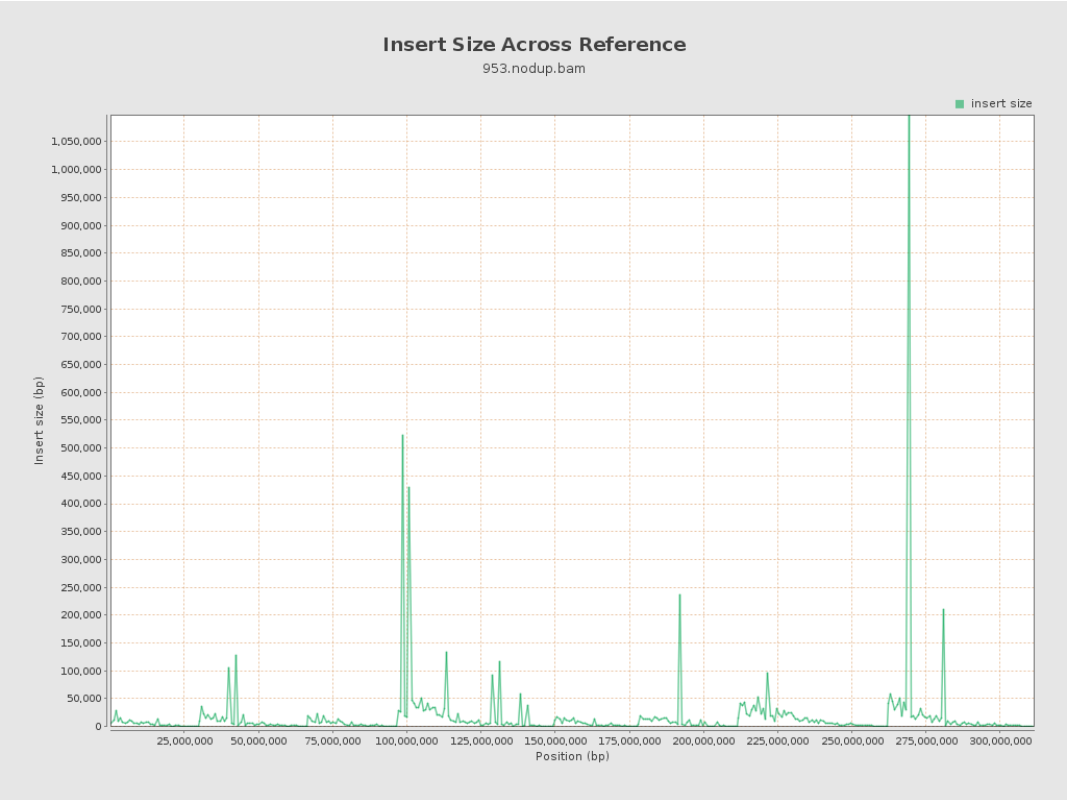
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram