Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/957.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/957.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_144/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_144_S234_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_144/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_144_S234_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:12 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,460,692
Mapped reads	68,970,074 / 95.18%
Unmapped reads	3,490,618 / 4.82%
Mapped paired reads	68,970,074 / 95.18%
Mapped reads, first in pair	34,482,729 / 47.59%
Mapped reads, second in pair	34,487,345 / 47.59%
Mapped reads, both in pair	67,830,003 / 93.61%
Mapped reads, singletons	1,140,071 / 1.57%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	10,623,007 / 14.66%
Clipped reads	14,965,796 / 20.65%

2.2. ACGT Content

Number/percentage of A's	2,971,399,528 / 30.92%
Number/percentage of C's	1,835,520,909 / 19.1%
Number/percentage of T's	2,974,406,812 / 30.95%
Number/percentage of G's	1,829,493,327 / 19.04%
Number/percentage of N's	36,137 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	30.9187
Standard Deviation	227.3362

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Insert size

Mean	221,464.62
Standard Deviation	2,223,686.43
P25/Median/P75	334 / 434 / 560

2.6. Mismatches and indels

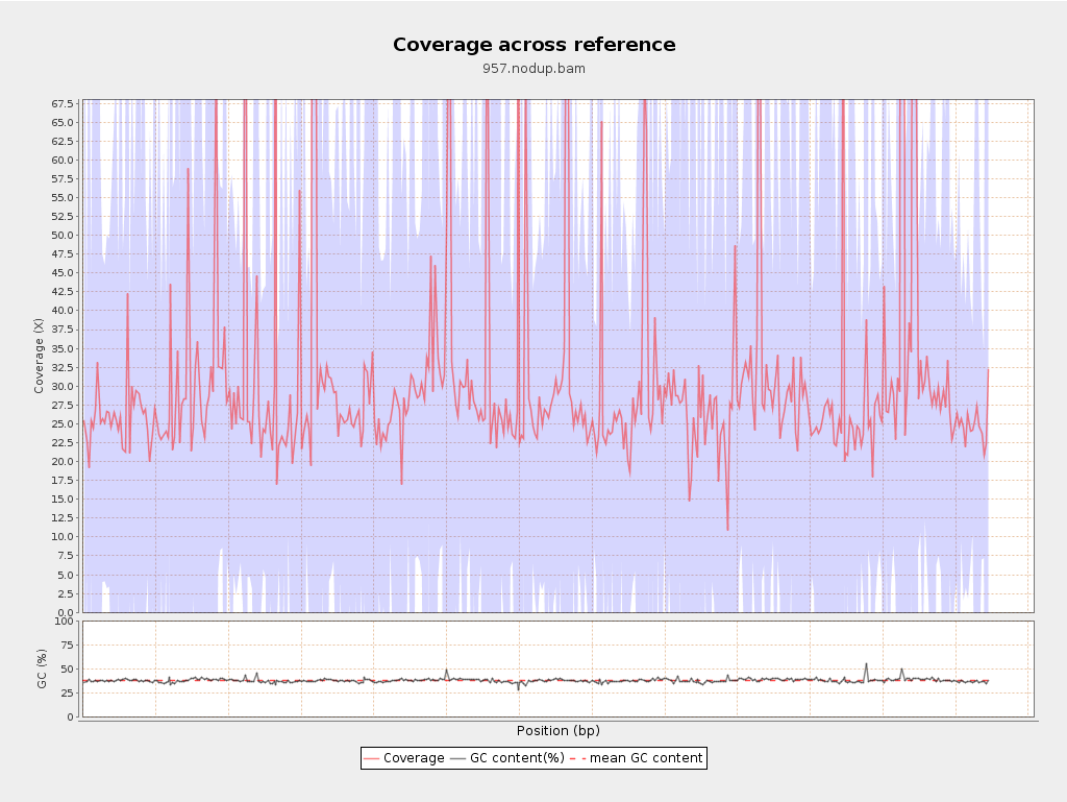
General error rate	2.32%
Mismatches	204,913,223
Insertions	6,419,614
Mapped reads with at least one insertion	8.39%
Deletions	6,595,501
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56.22%

2.7. Chromosome stats

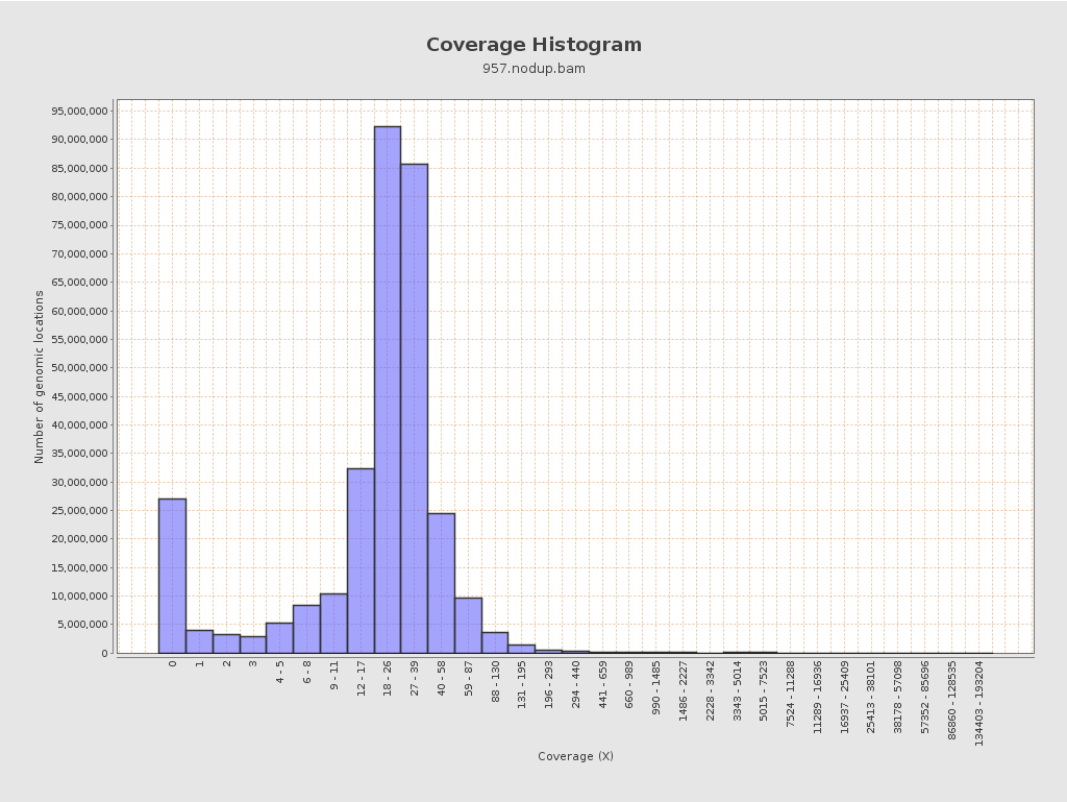
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	761569301	25.6211	62.412

LT669789.1	36598175	1161996964	31.7501	252.5329
LT669790.1	30422129	976821833	32.1089	204.8449
LT669791.1	52758100	1605681183	30.4348	185.2023
LT669792.1	28376109	865186865	30.49	274.34
LT669793.1	33388210	955510761	28.6182	125.8736
LT669794.1	50579949	1504907872	29.7531	210.0102
LT669795.1	49795044	1803895523	36.2264	337.5095

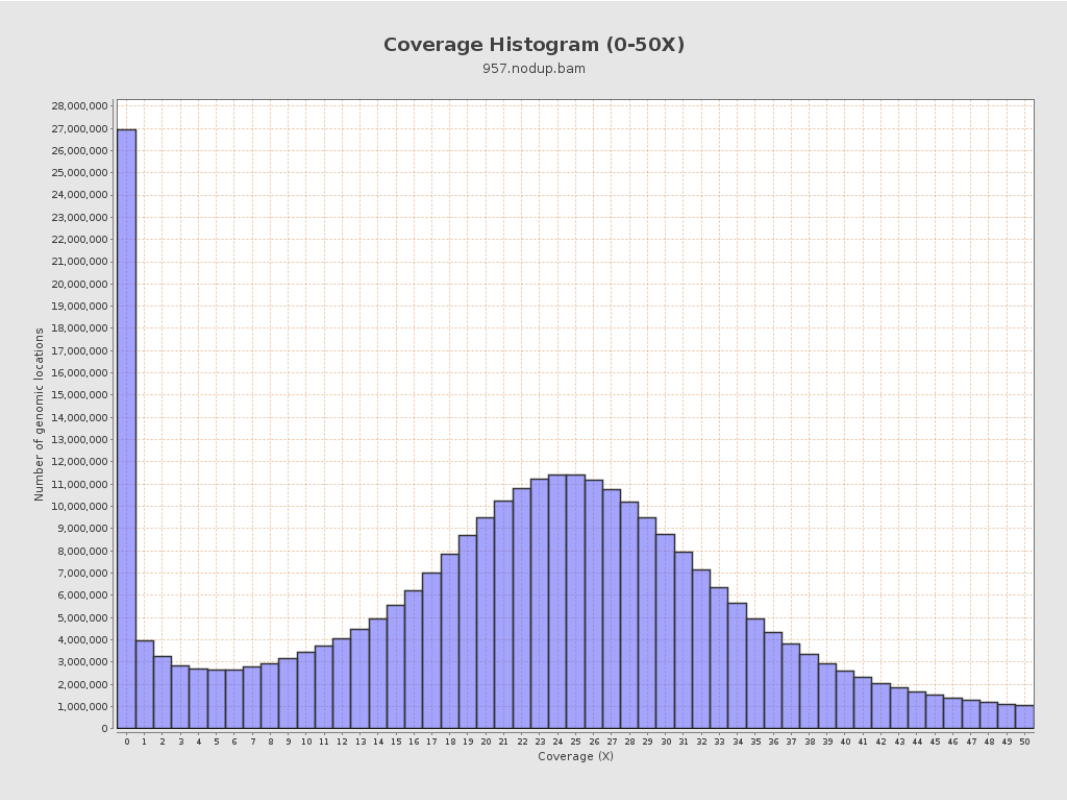
3. Results : Coverage across reference



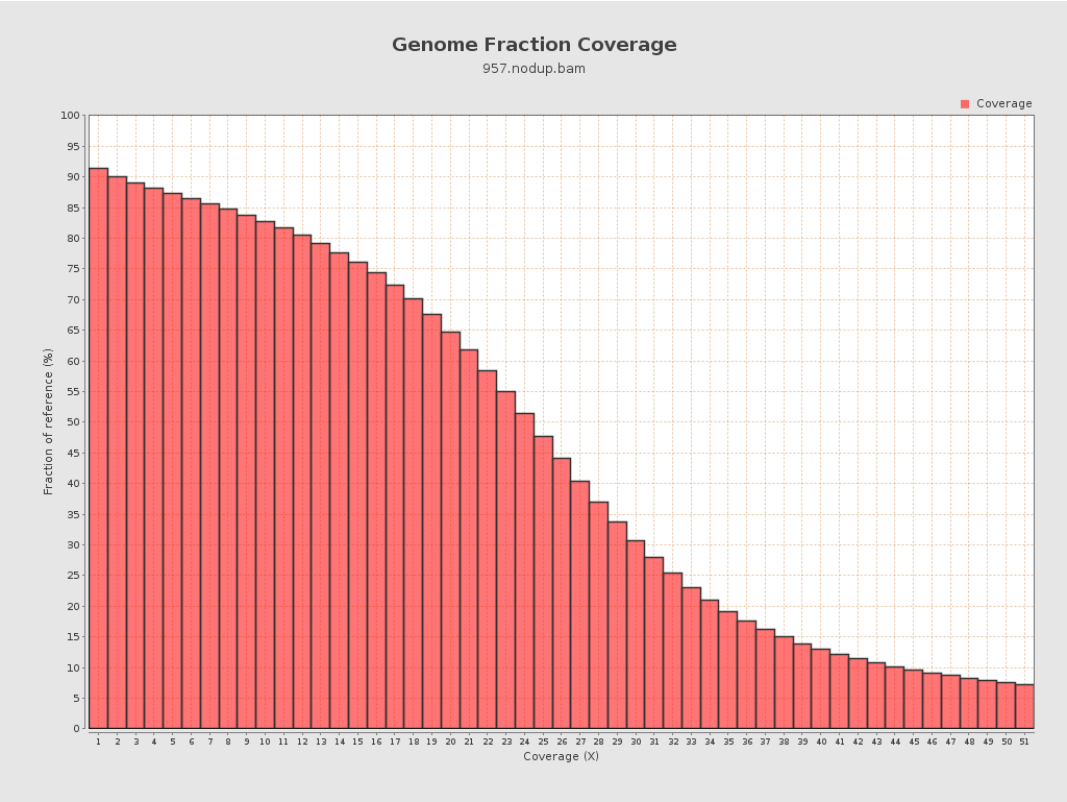
4. Results : Coverage Histogram



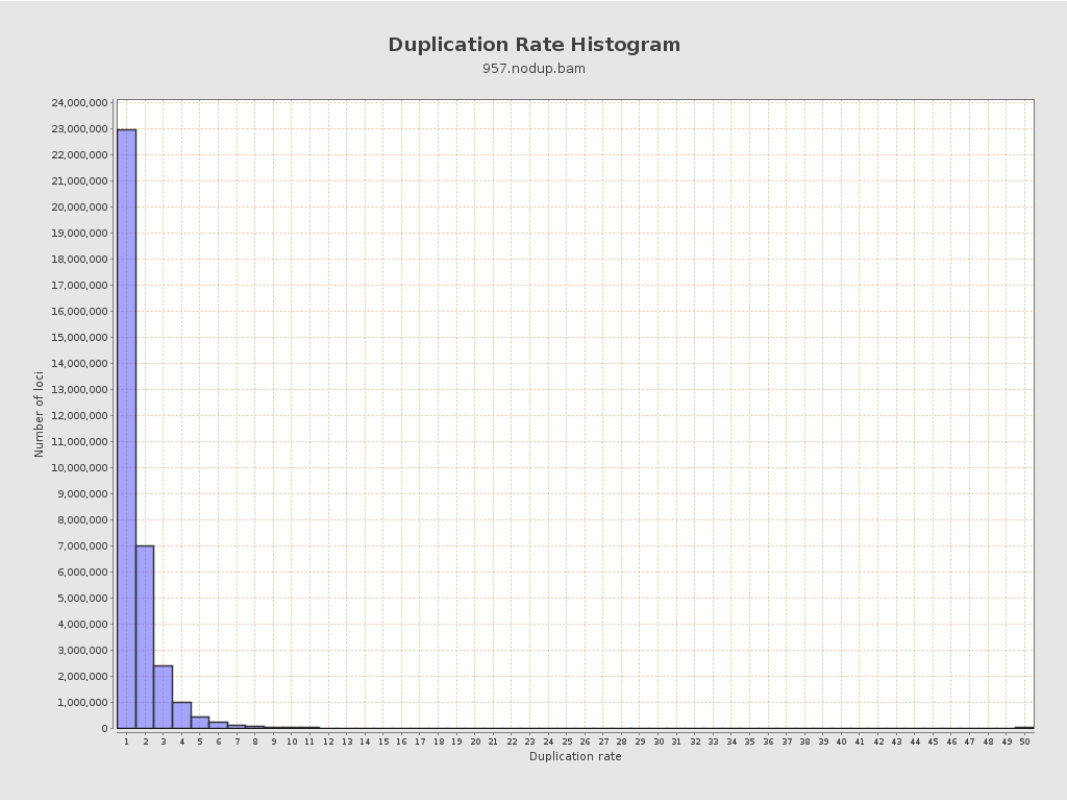
5. Results : Coverage Histogram (0-50X)



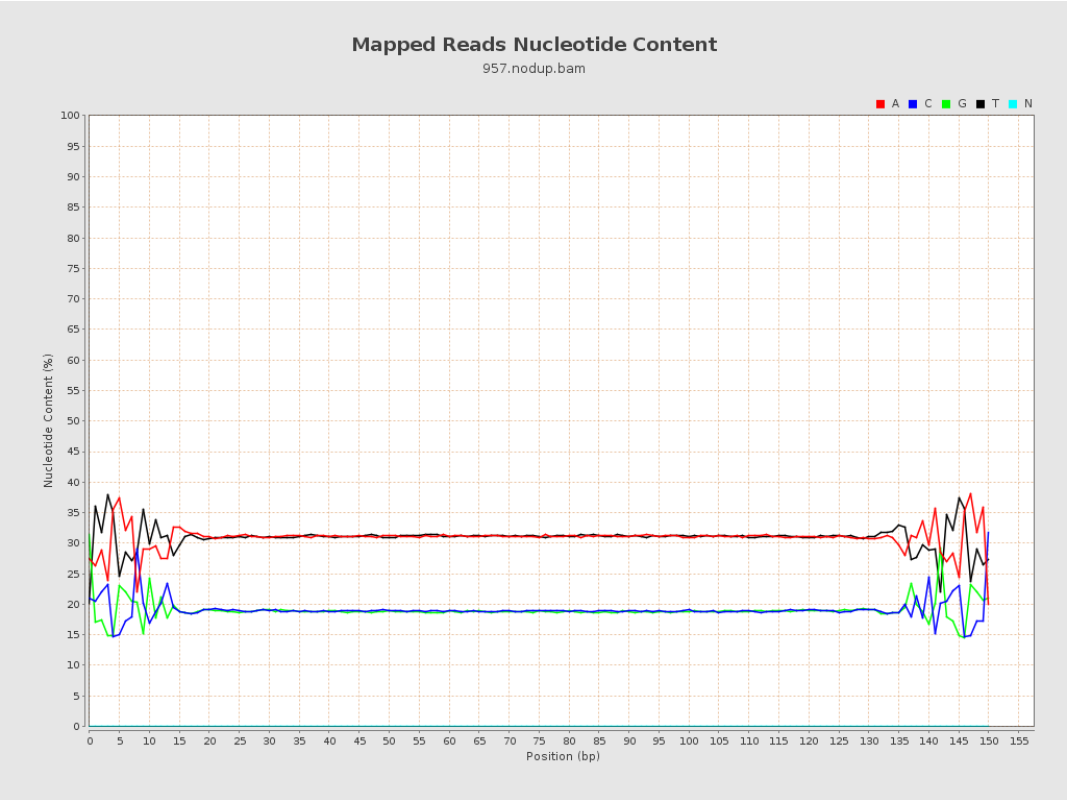
6. Results : Genome Fraction Coverage



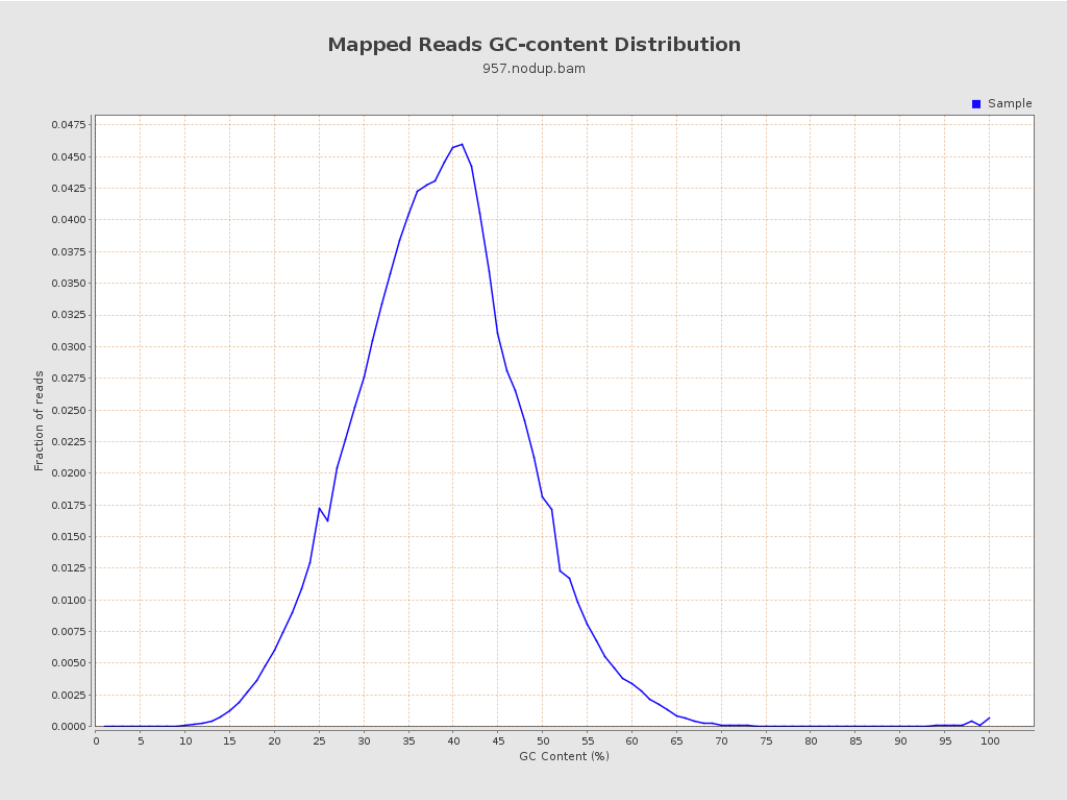
7. Results : Duplication Rate Histogram



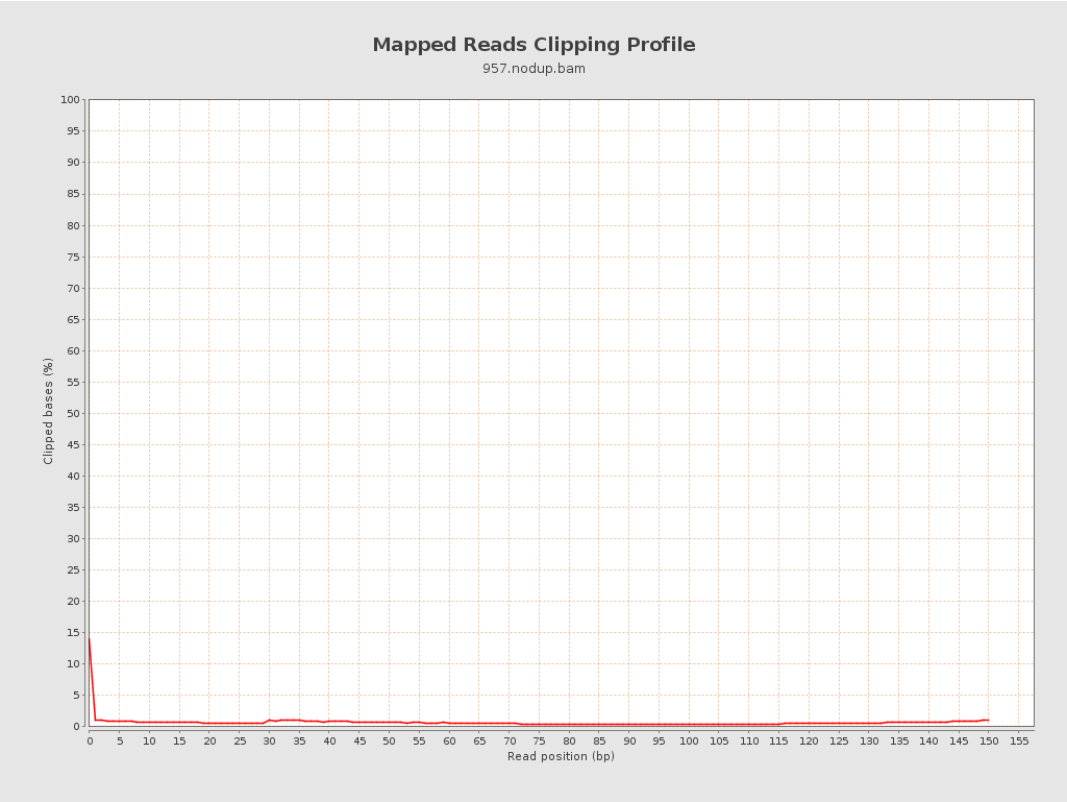
8. Results : Mapped Reads Nucleotide Content



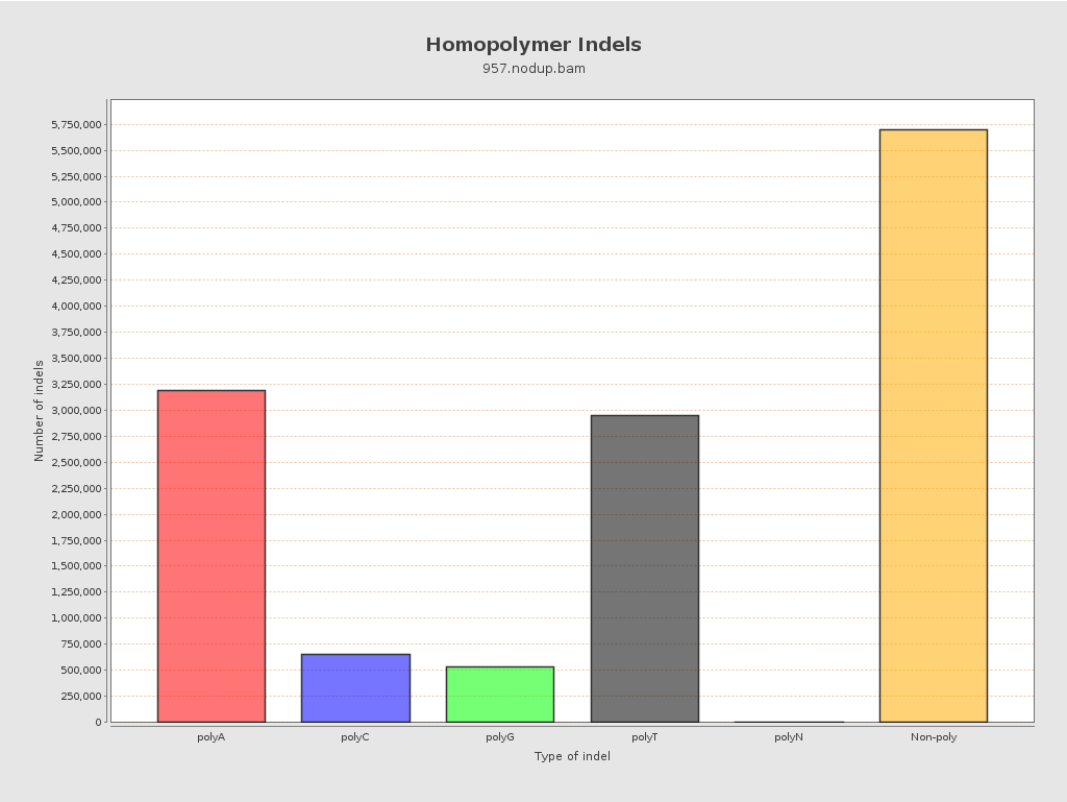
9. Results : Mapped Reads GC-content Distribution



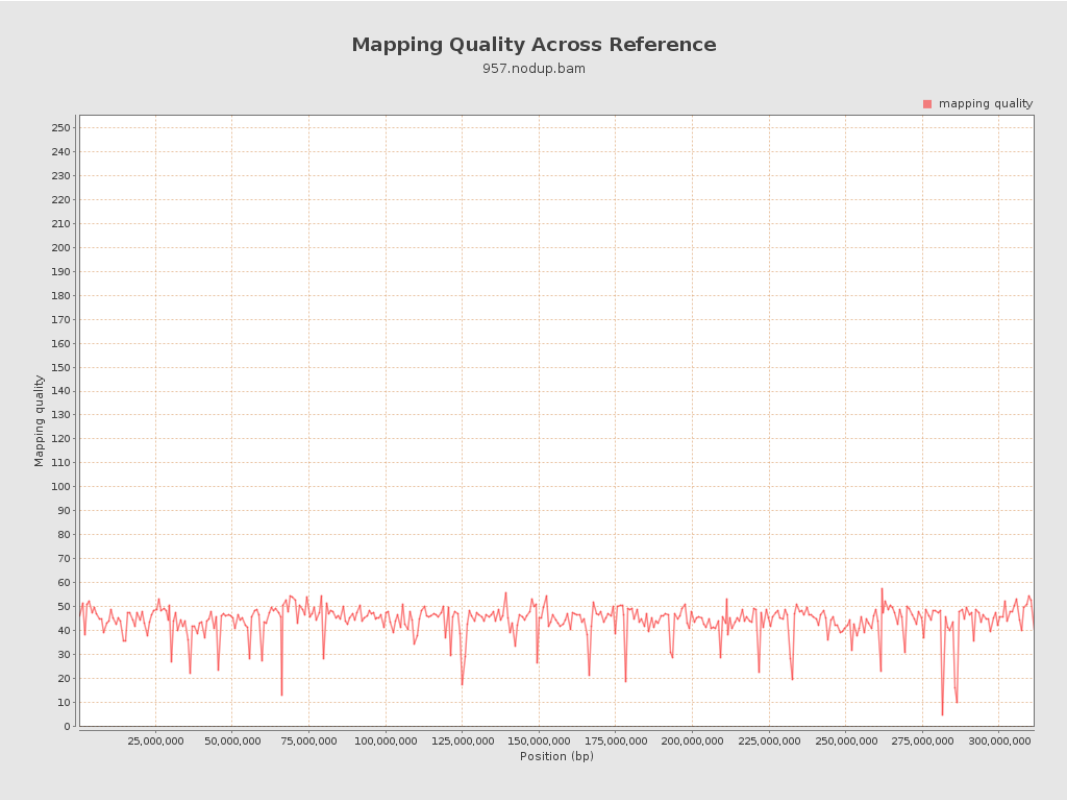
10. Results : Mapped Reads Clipping Profile



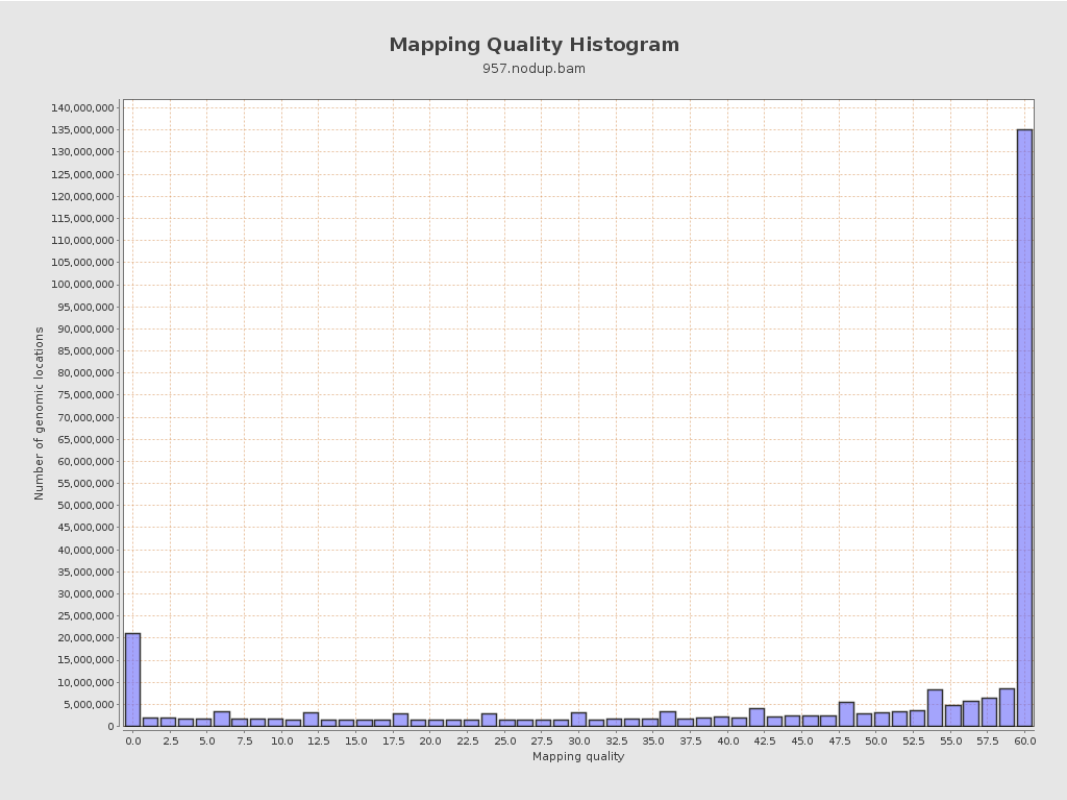
11. Results : Homopolymer Indels



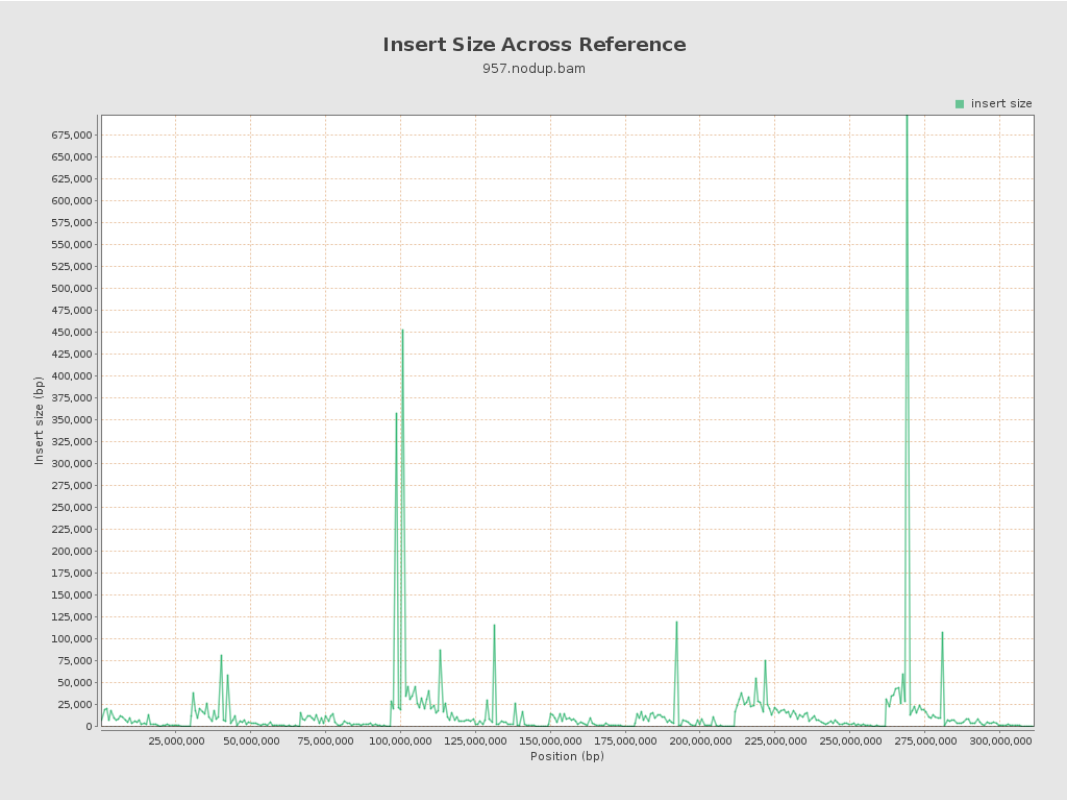
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram