Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/945.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/945.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_586/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_586_S153_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_586/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_586_S153_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:45 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,678,861
Mapped reads	55,568,717 / 93.11%
Unmapped reads	4,110,144 / 6.89%
Mapped paired reads	55,568,717 / 93.11%
Mapped reads, first in pair	27,906,290 / 46.76%
Mapped reads, second in pair	27,662,427 / 46.35%
Mapped reads, both in pair	54,477,688 / 91.28%
Mapped reads, singletons	1,091,029 / 1.83%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	8,256,758 / 13.84%
Clipped reads	13,465,307 / 22.56%

2.2. ACGT Content

Number/percentage of A's	2,363,109,402 / 30.82%
Number/percentage of C's	1,471,158,842 / 19.19%
Number/percentage of T's	2,365,194,377 / 30.84%
Number/percentage of G's	1,468,589,803 / 19.15%
Number/percentage of N's	51,150 / 0%
GC Percentage	38.34%

2.3. Coverage

Mean	24.6688
Standard Deviation	194.9585

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Insert size

Mean	213,762.36
Standard Deviation	2,178,751.24
P25/Median/P75	308 / 405 / 523

2.6. Mismatches and indels

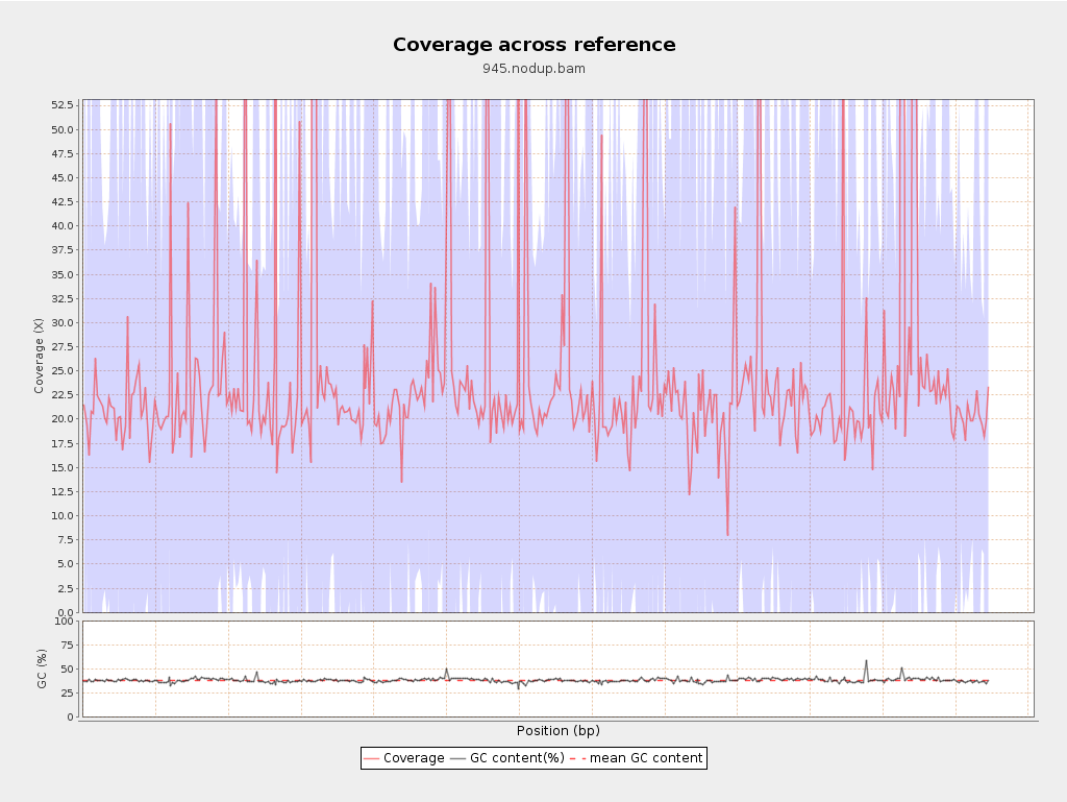
General error rate	2.61%
Mismatches	185,974,297
Insertions	5,115,004
Mapped reads with at least one insertion	8.28%
Deletions	5,255,266
Mapped reads with at least one deletion	8.4%
Homopolymer indels	55.63%

2.7. Chromosome stats

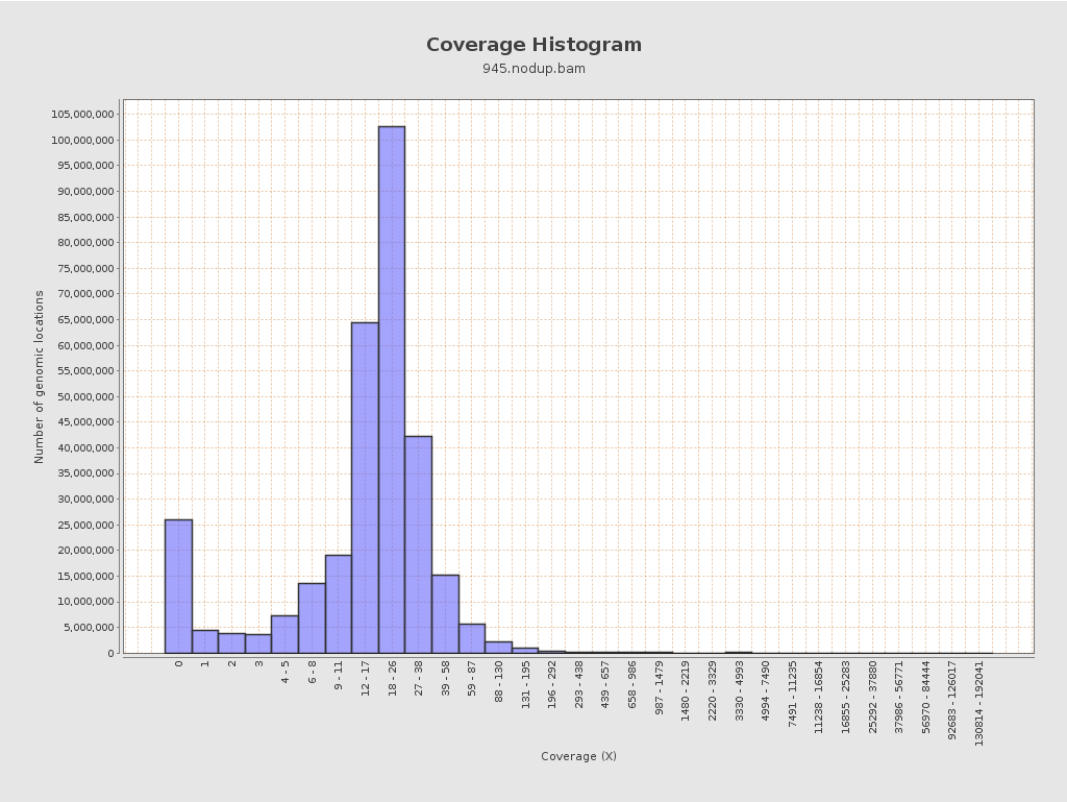
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	620561545	20.8772	69.6775

LT669789.1	36598175	911576508	24.9077	197.3169
LT669790.1	30422129	801976529	26.3616	183.2214
LT669791.1	52758100	1268602585	24.0456	161.956
LT669792.1	28376109	694628057	24.4793	223.4038
LT669793.1	33388210	772195120	23.1278	134.878
LT669794.1	50579949	1173752703	23.2059	162.668
LT669795.1	49795044	1444558162	29.0101	300.8551

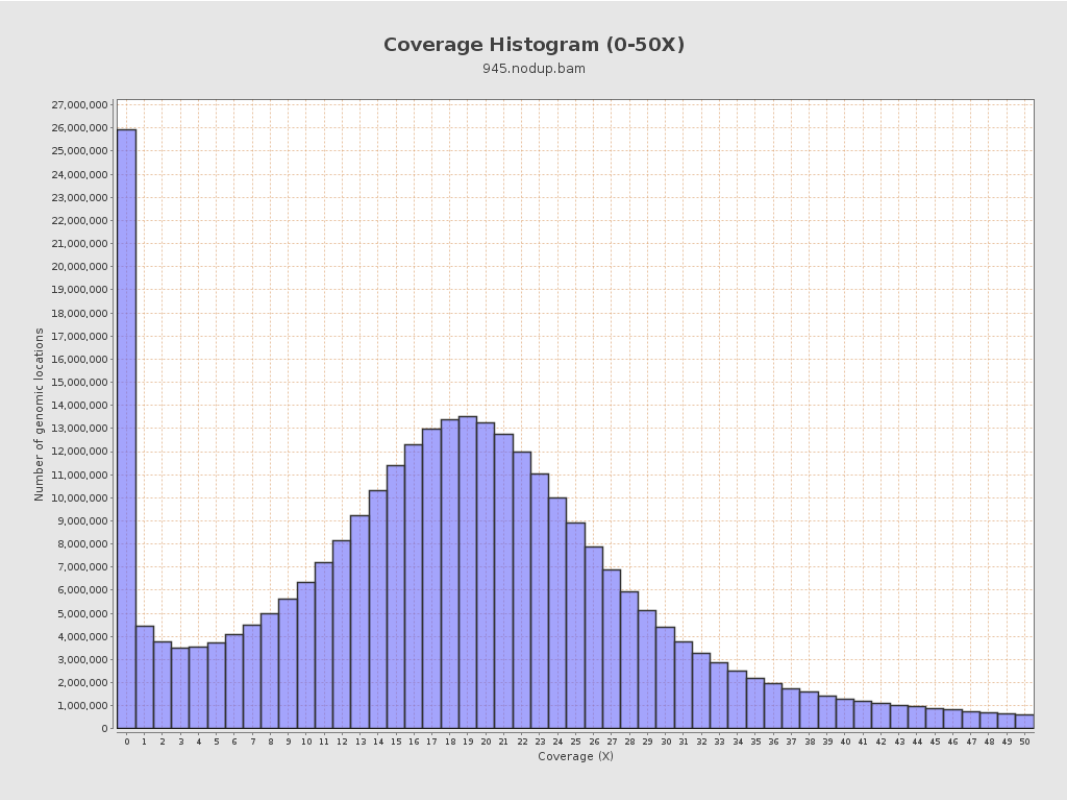
3. Results : Coverage across reference



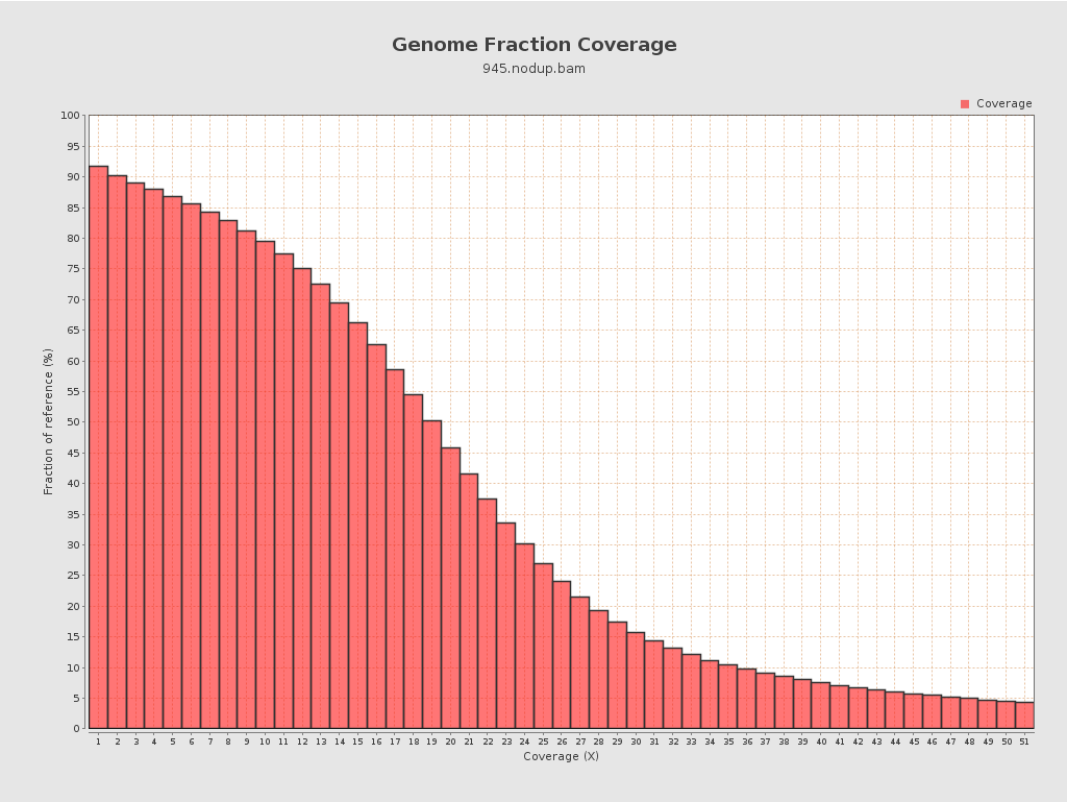
4. Results : Coverage Histogram



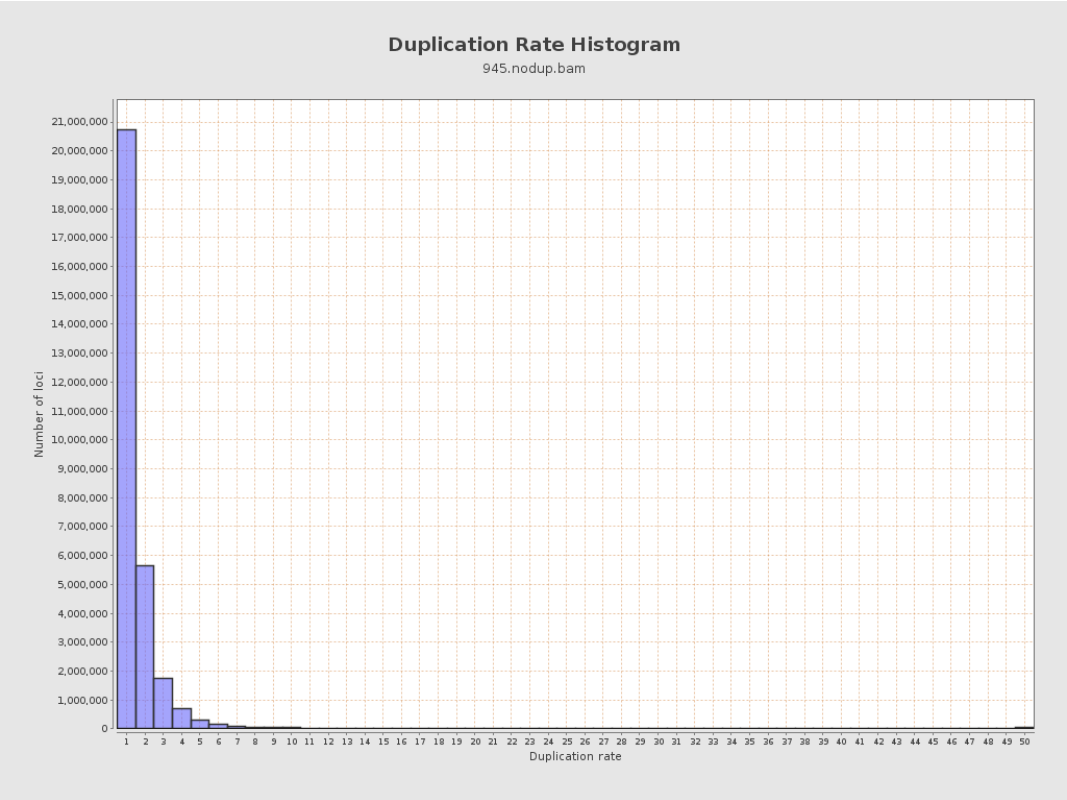
5. Results : Coverage Histogram (0-50X)



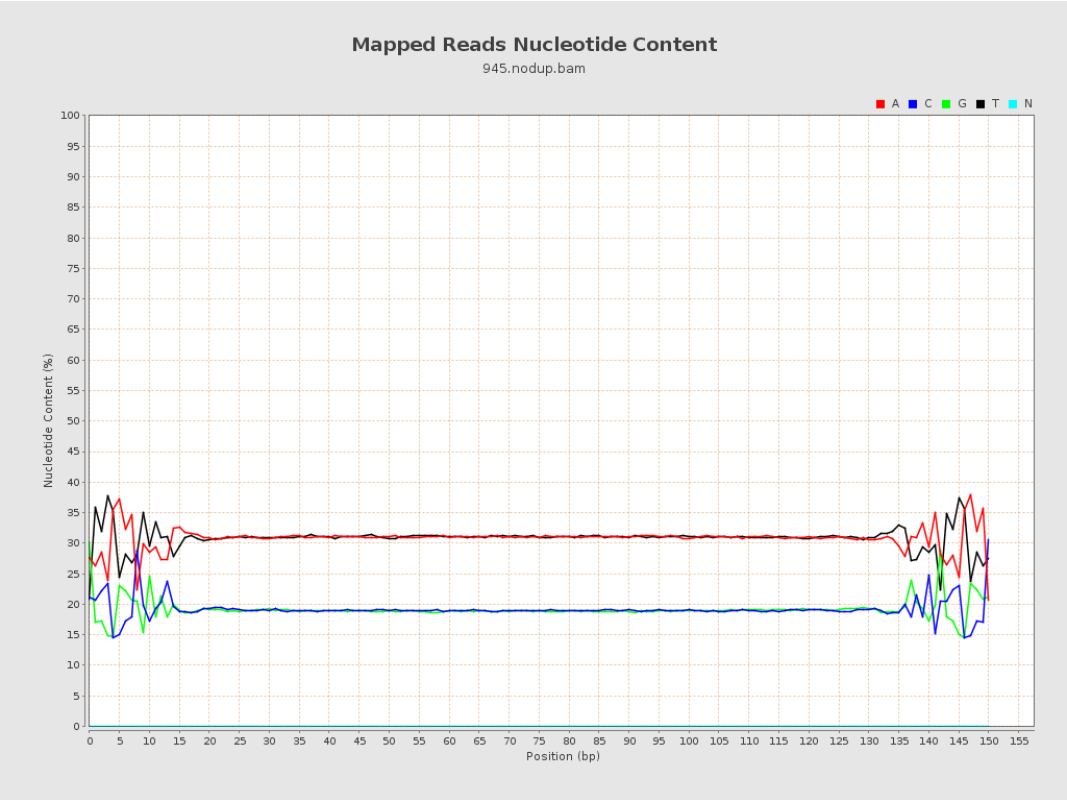
6. Results : Genome Fraction Coverage



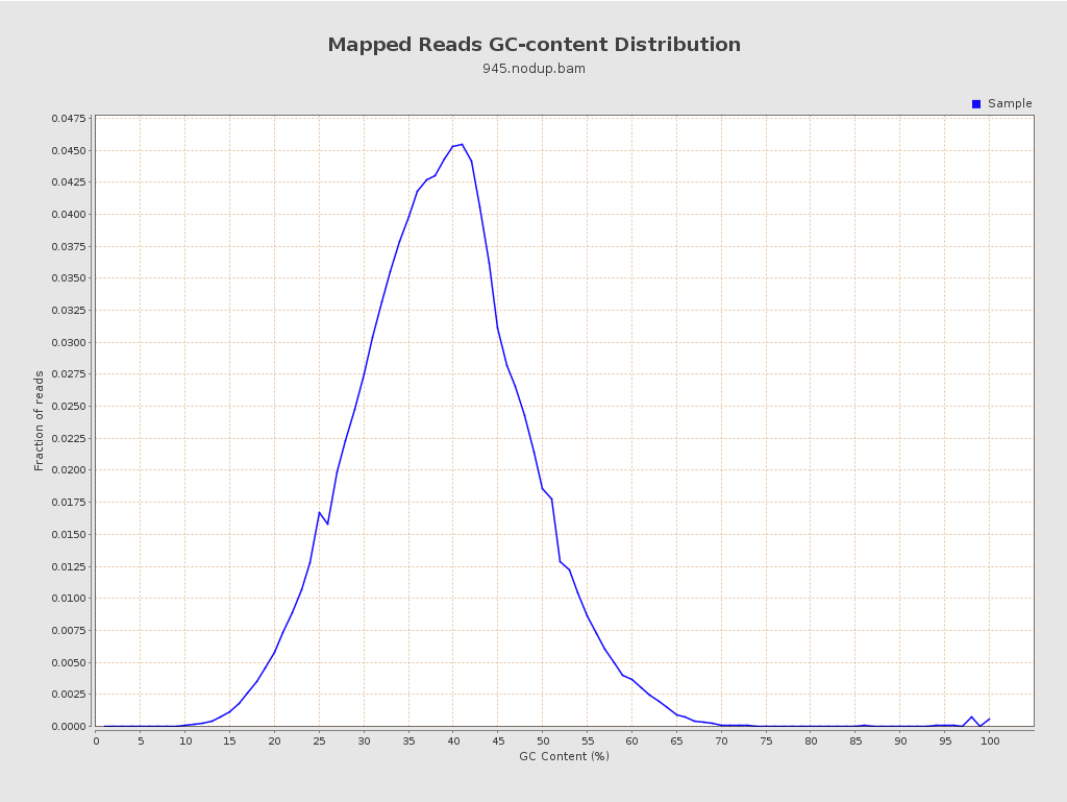
7. Results : Duplication Rate Histogram



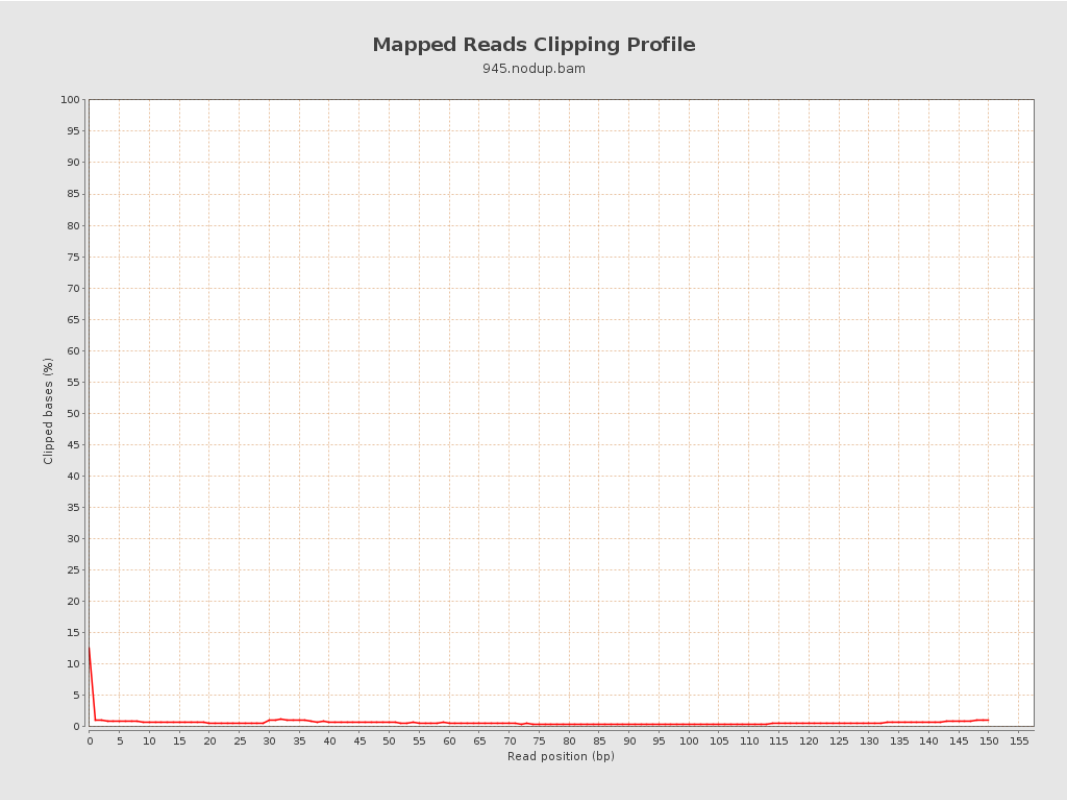
8. Results : Mapped Reads Nucleotide Content



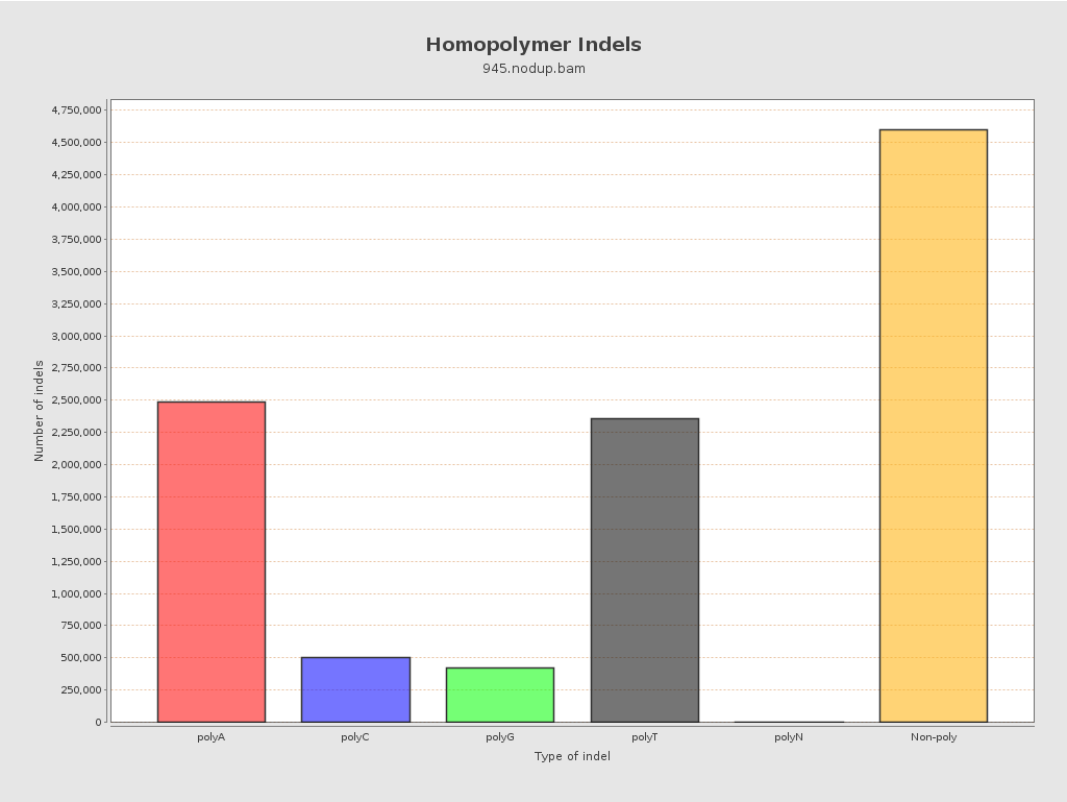
9. Results : Mapped Reads GC-content Distribution



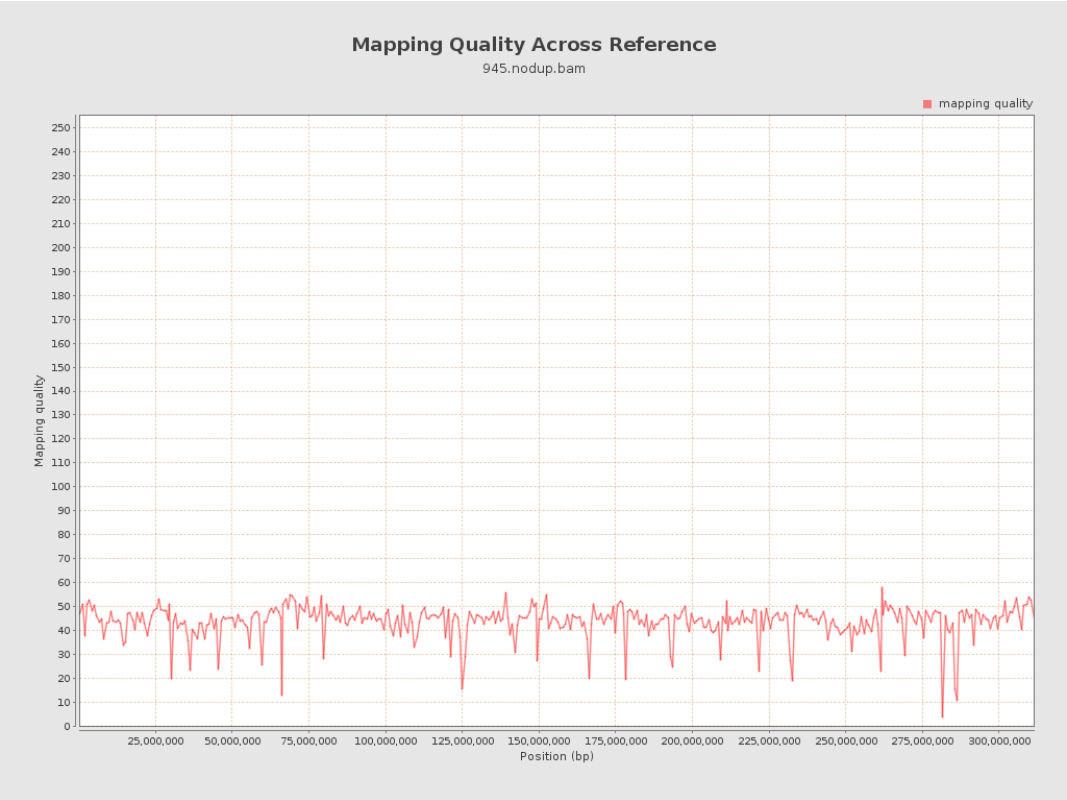
10. Results : Mapped Reads Clipping Profile



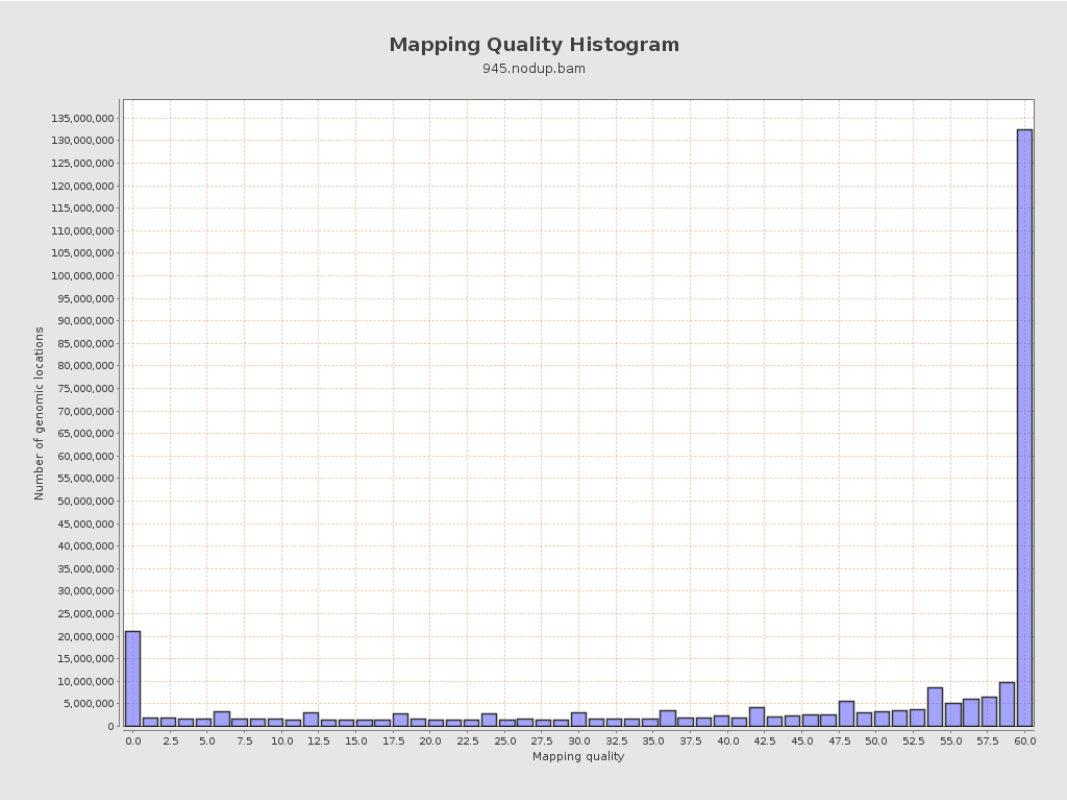
11. Results : Homopolymer Indels



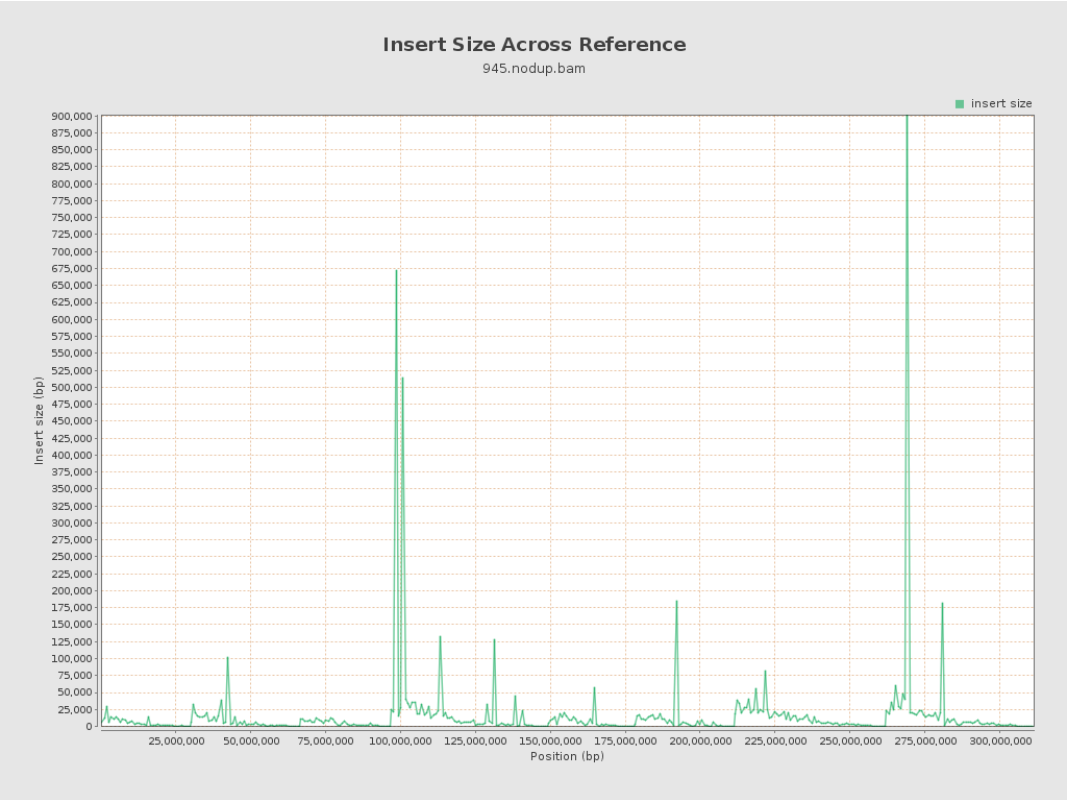
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram