Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:25:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/943.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/943.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_189/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_189_S279_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_189/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_189_S279_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:25:57 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	52,802,857
Mapped reads	48,785,998 / 92.39%
Unmapped reads	4,016,859 / 7.61%
Mapped paired reads	48,785,998 / 92.39%
Mapped reads, first in pair	24,458,587 / 46.32%
Mapped reads, second in pair	24,327,411 / 46.07%
Mapped reads, both in pair	47,428,907 / 89.82%
Mapped reads, singletons	1,357,091 / 2.57%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	7,936,979 / 15.03%
Clipped reads	11,123,235 / 21.07%

2.2. ACGT Content

Number/percentage of A's	2,085,275,261 / 30.92%
Number/percentage of C's	1,286,737,679 / 19.08%
Number/percentage of T's	2,087,431,405 / 30.95%
Number/percentage of G's	1,284,604,350 / 19.05%
Number/percentage of N's	28,341 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	21.6986
Standard Deviation	177.9231

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Insert size

Mean	261,506.36
Standard Deviation	2,443,333.54
P25/Median/P75	364 / 472 / 608

2.6. Mismatches and indels

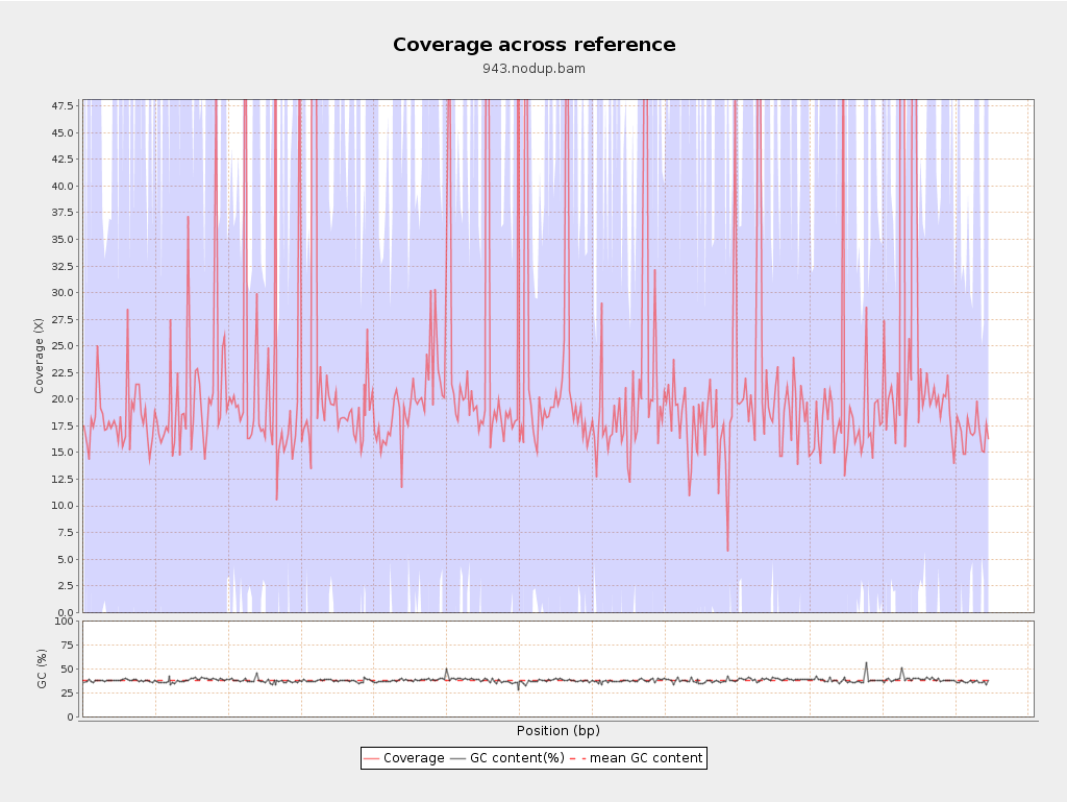
General error rate	2.39%
Mismatches	148,295,856
Insertions	4,711,334
Mapped reads with at least one insertion	8.64%
Deletions	4,743,850
Mapped reads with at least one deletion	8.62%
Homopolymer indels	56.67%

2.7. Chromosome stats

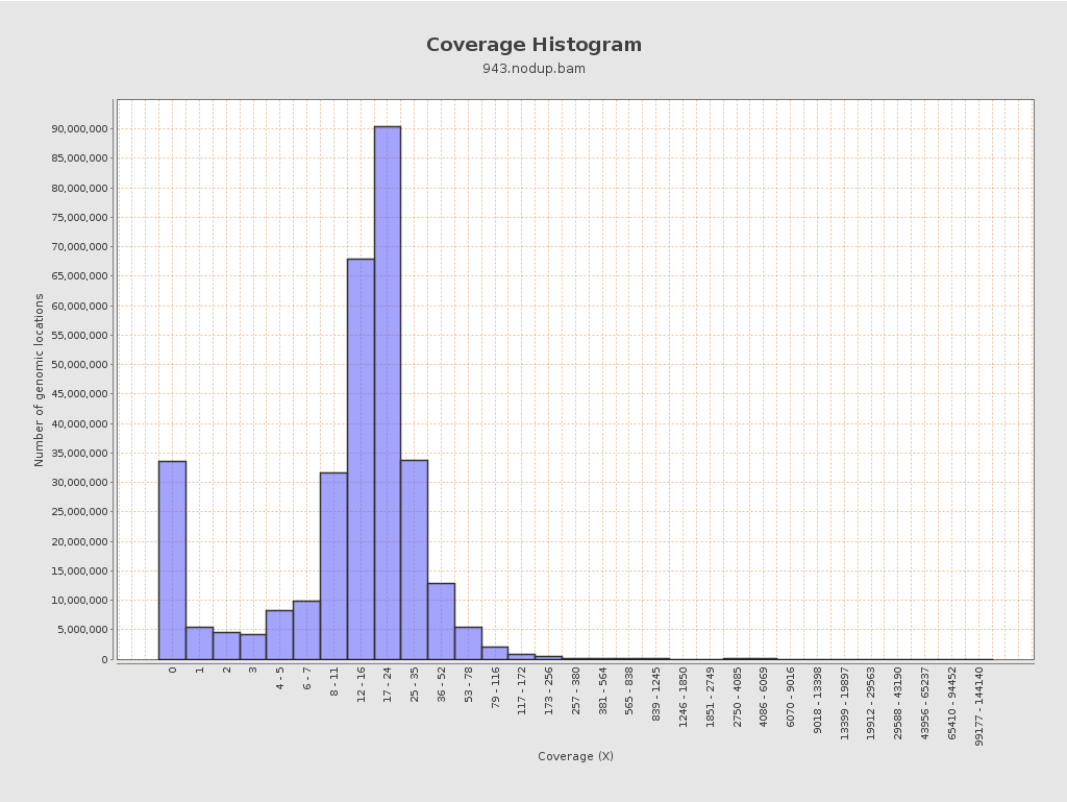
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	535327179	18.0097	60.8862

LT669789.1	36598175	791221969	21.6192	174.1487
LT669790.1	30422129	750355481	24.6648	224.2299
LT669791.1	52758100	1126909664	21.3599	166.2989
LT669792.1	28376109	620067311	21.8517	179.8334
LT669793.1	33388210	681901066	20.4234	161.4083
LT669794.1	50579949	1034180441	20.4465	157.7106
LT669795.1	49795044	1222228730	24.5452	228.9415

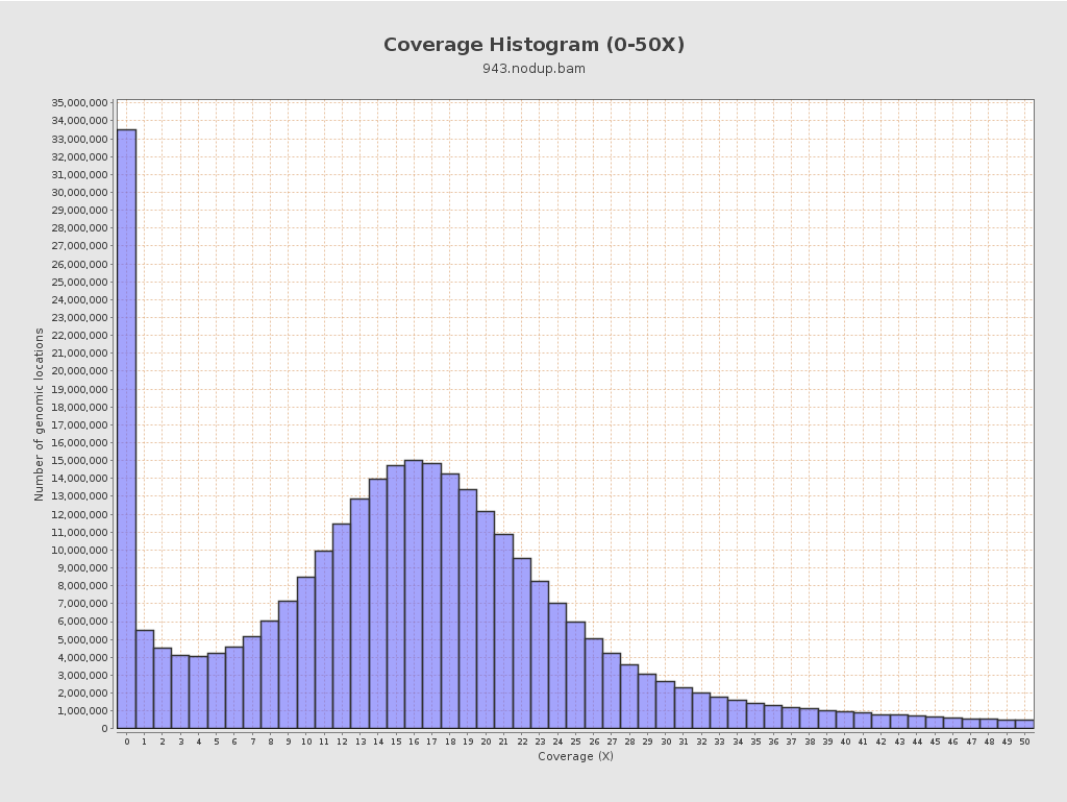
3. Results : Coverage across reference



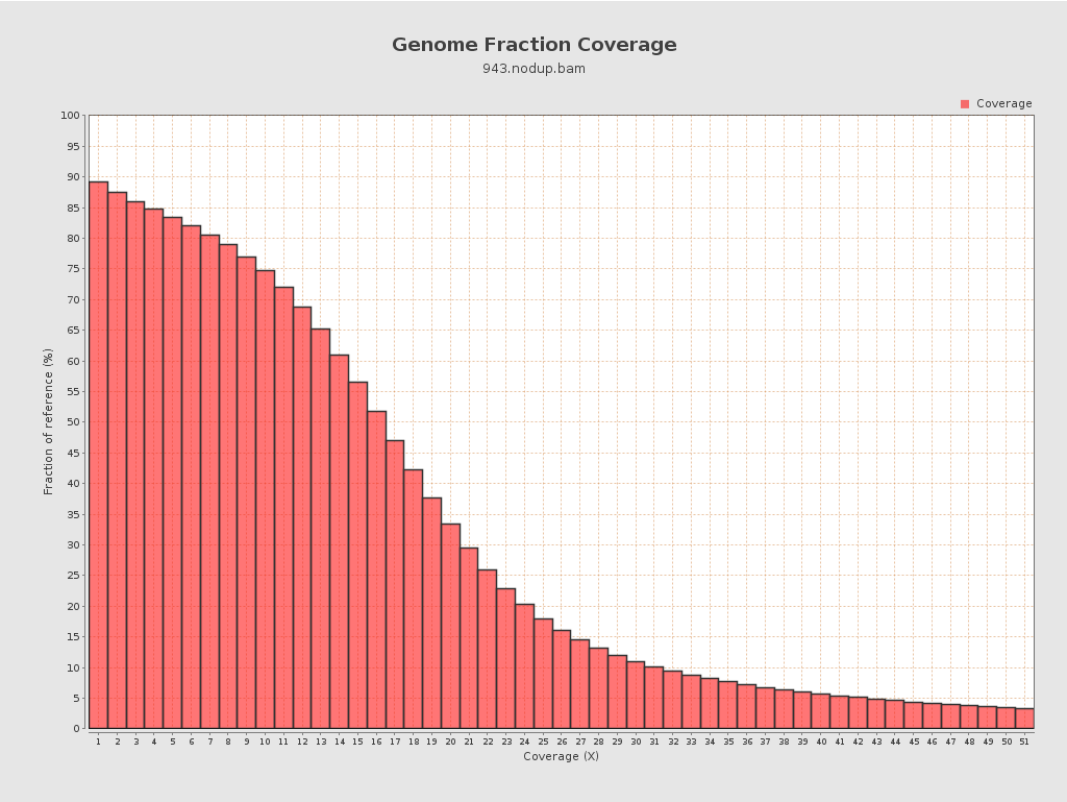
4. Results : Coverage Histogram



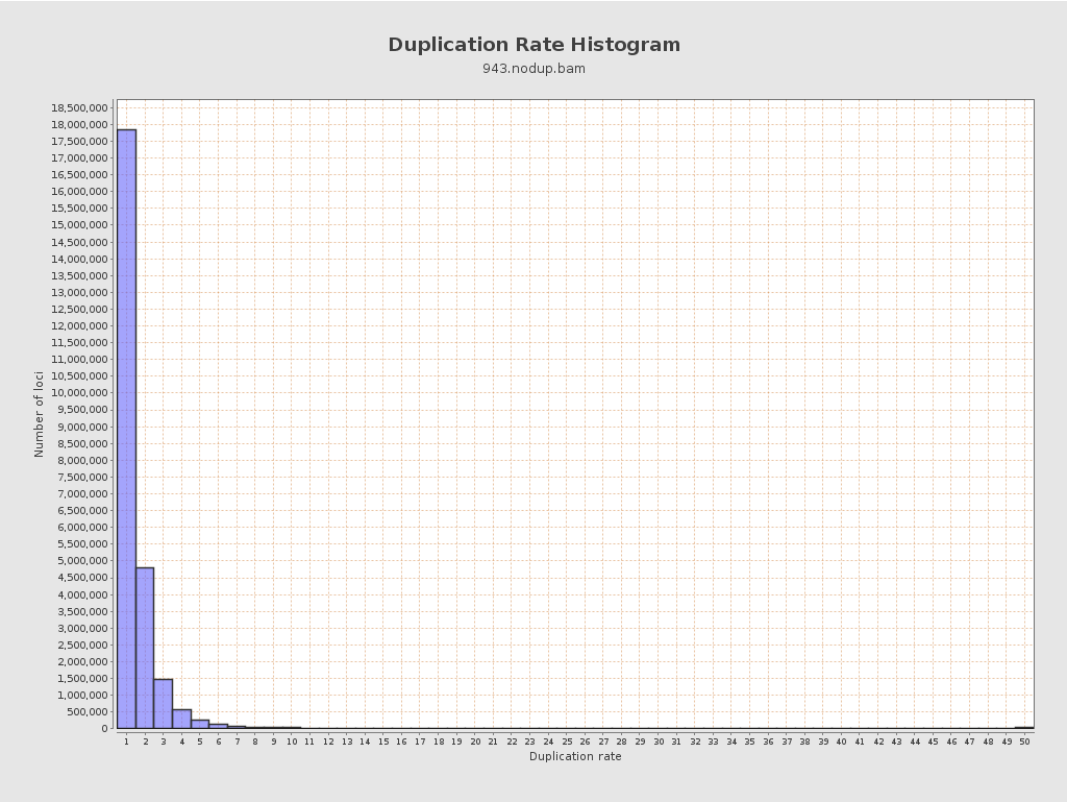
5. Results : Coverage Histogram (0-50X)



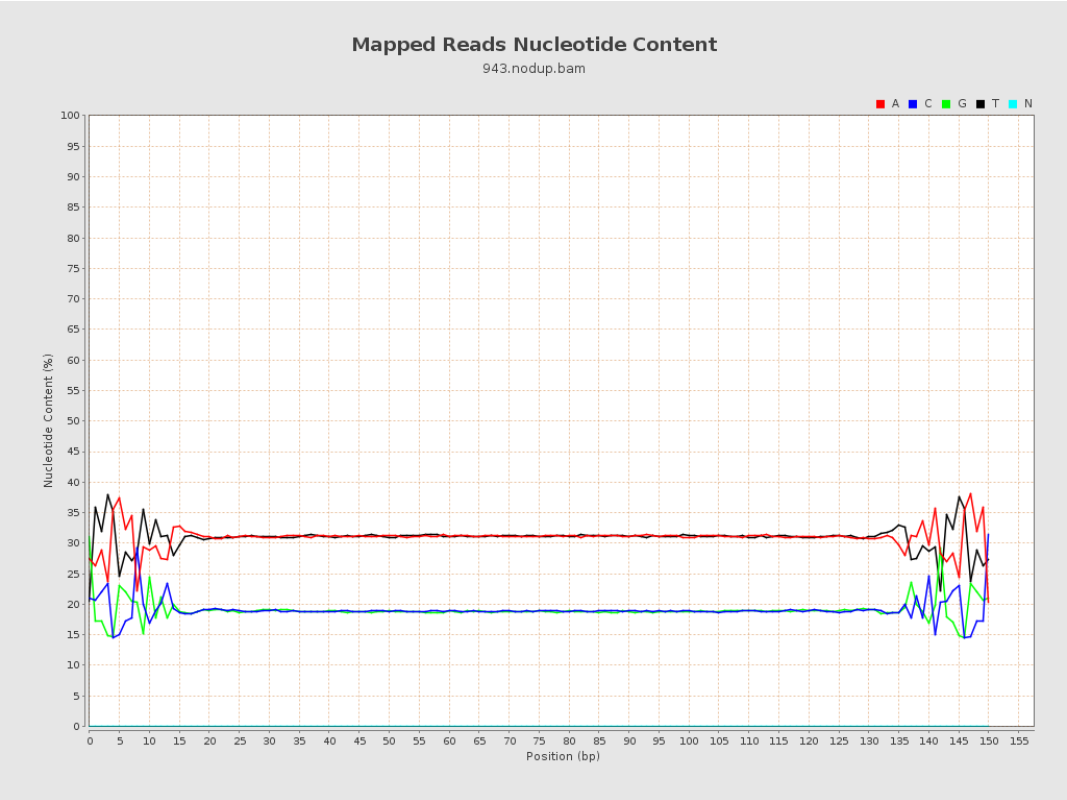
6. Results : Genome Fraction Coverage



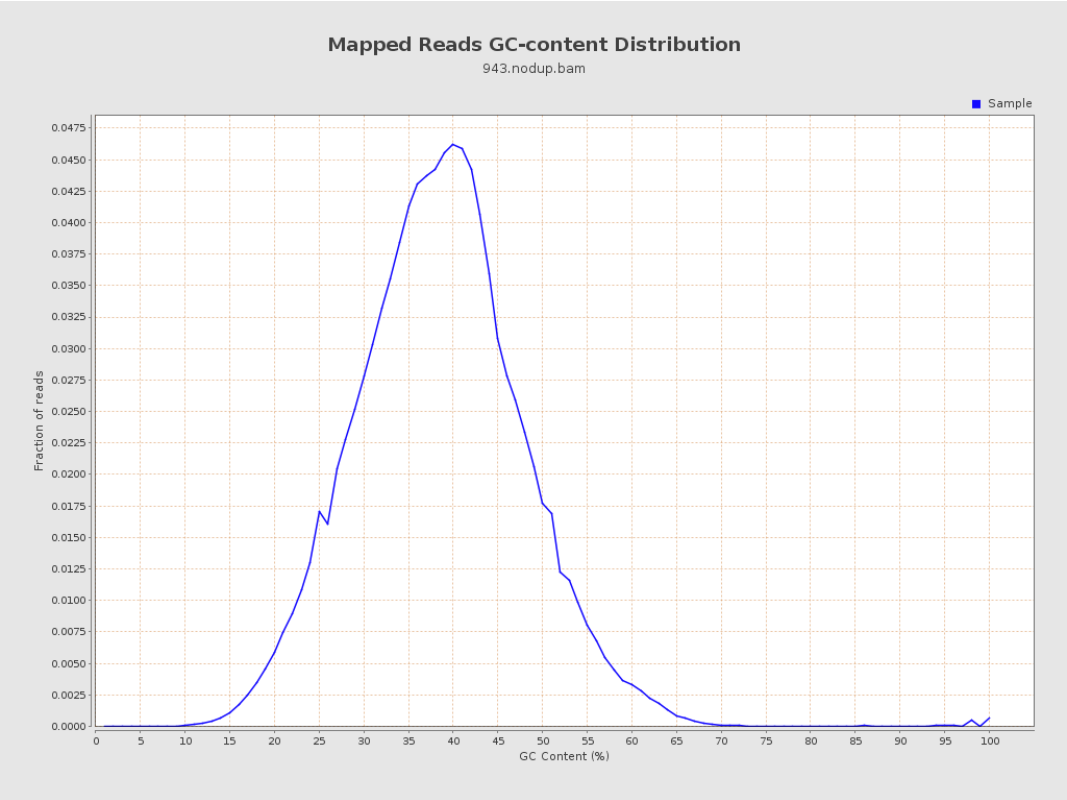
7. Results : Duplication Rate Histogram



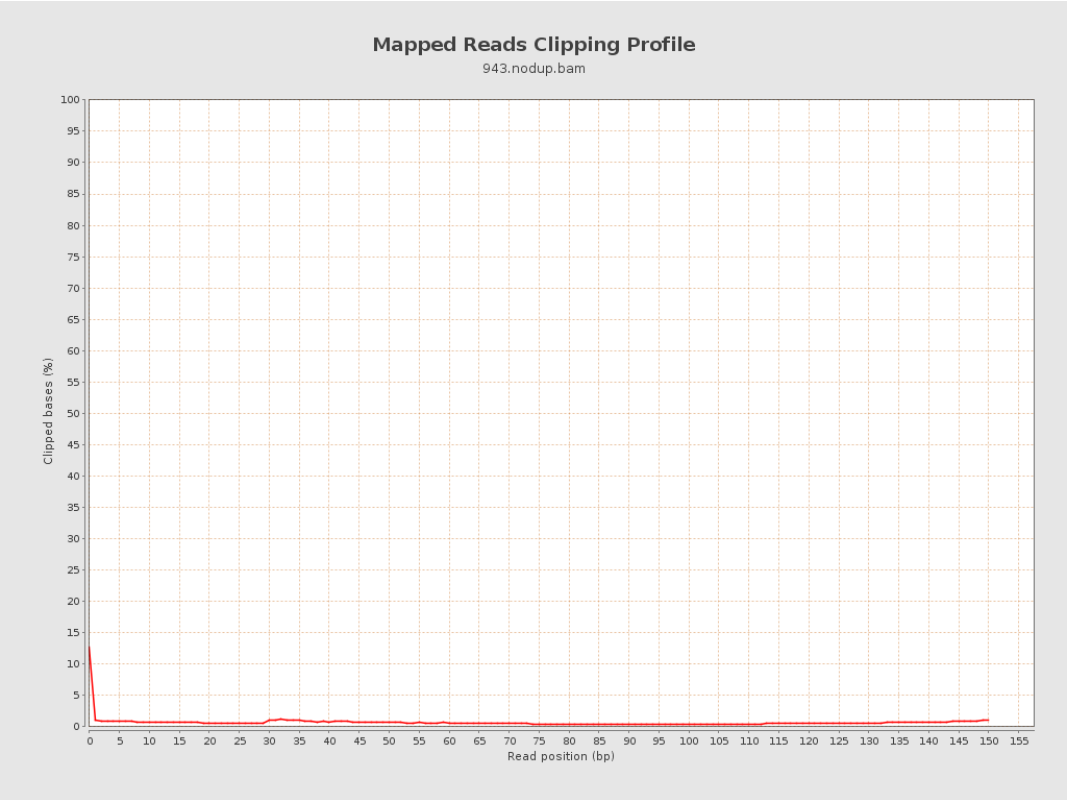
8. Results : Mapped Reads Nucleotide Content



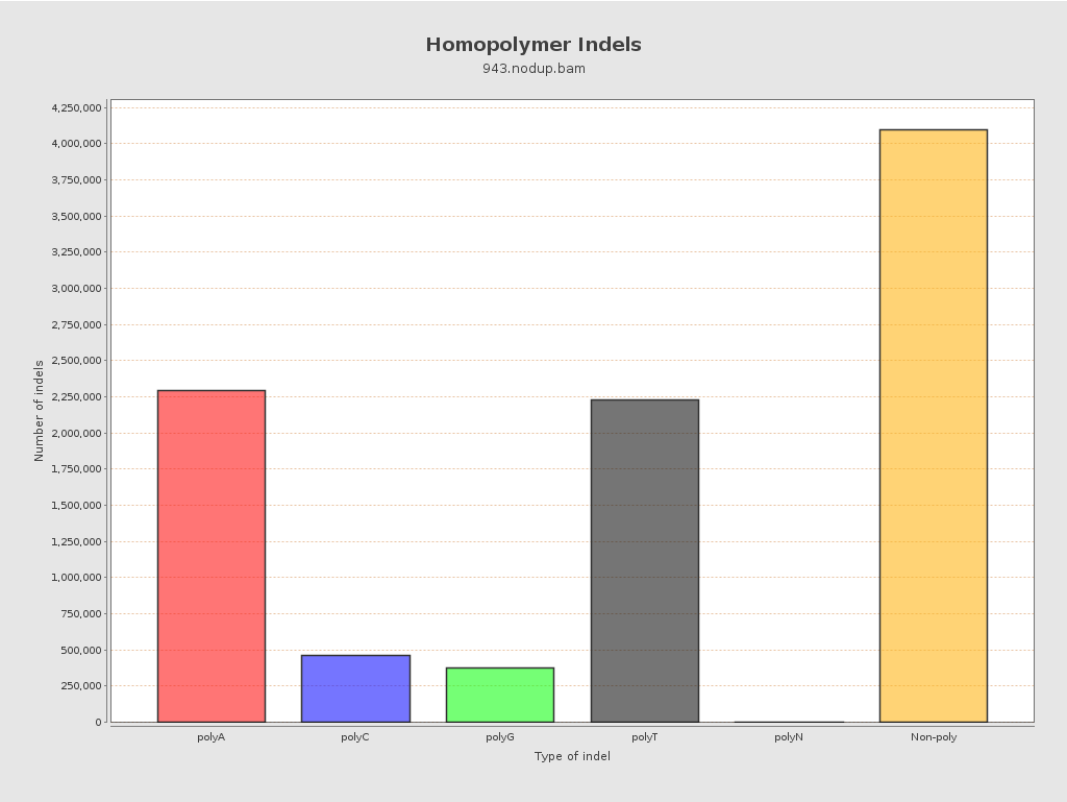
9. Results : Mapped Reads GC-content Distribution



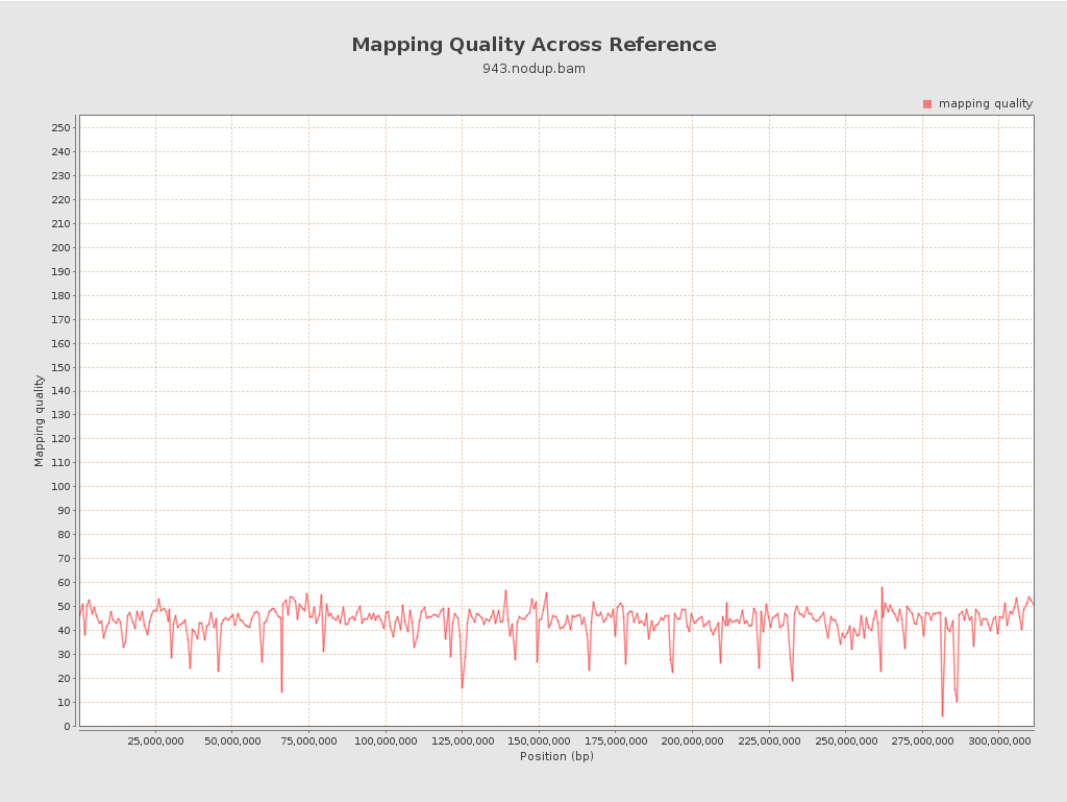
10. Results : Mapped Reads Clipping Profile



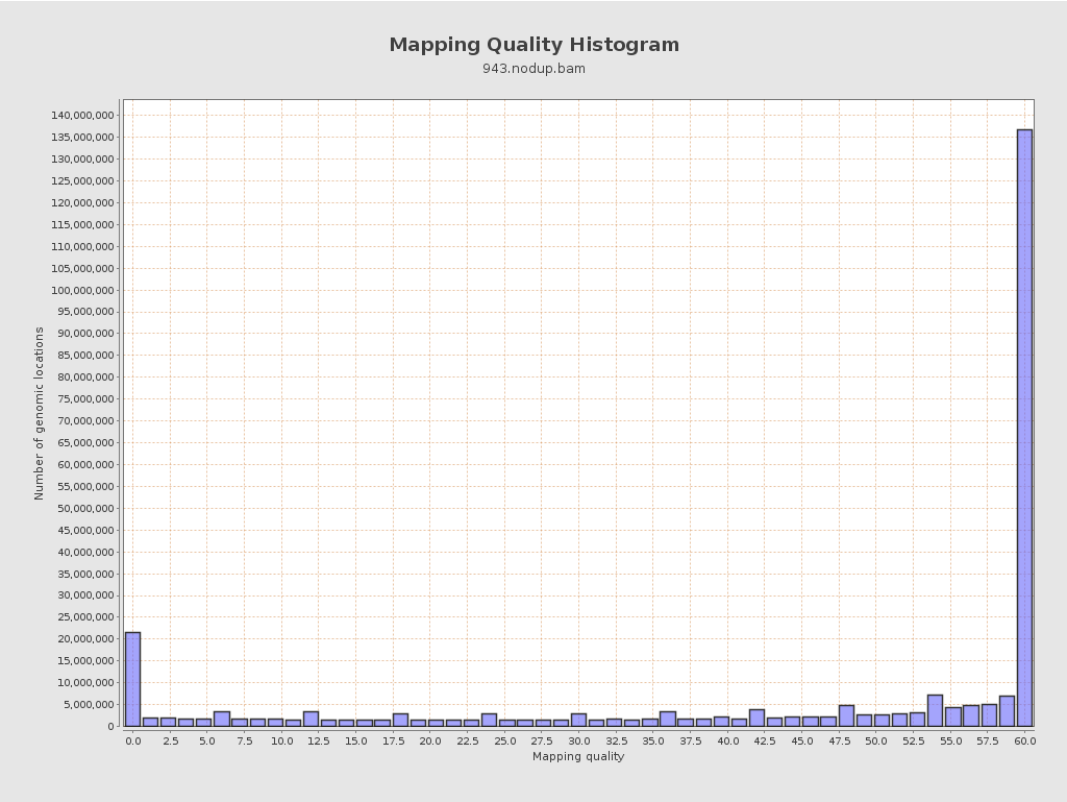
11. Results : Homopolymer Indels



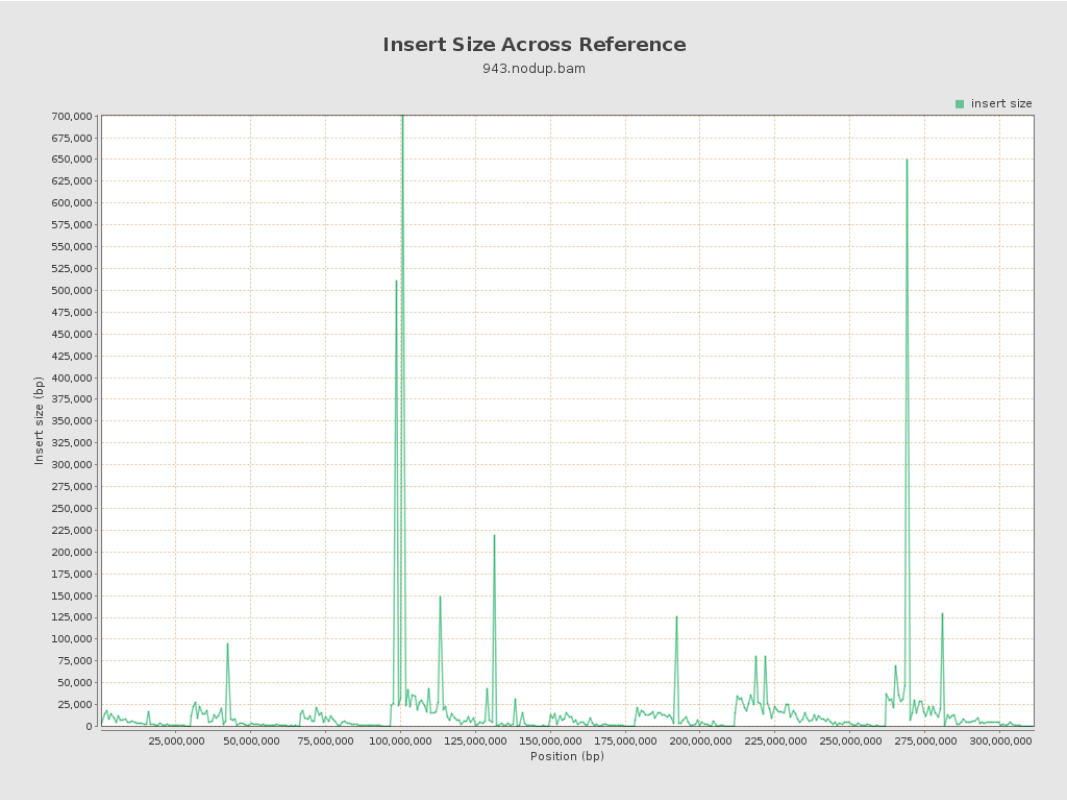
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram