Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/543.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/543.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_463/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_463_S438_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_463/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_463_S438_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:44 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	81,007,737
Mapped reads	74,157,517 / 91.54%
Unmapped reads	6,850,220 / 8.46%
Mapped paired reads	74,157,517 / 91.54%
Mapped reads, first in pair	37,143,585 / 45.85%
Mapped reads, second in pair	37,013,932 / 45.69%
Mapped reads, both in pair	71,906,762 / 88.77%
Mapped reads, singletons	2,250,755 / 2.78%
Read min/max/mean length	30 / 151 / 147.96
Duplicated reads (flagged)	13,522,886 / 16.69%
Clipped reads	17,844,412 / 22.03%

2.2. ACGT Content

Number/percentage of A's	3,128,119,266 / 30.81%
Number/percentage of C's	1,948,138,917 / 19.19%
Number/percentage of T's	3,128,795,187 / 30.82%
Number/percentage of G's	1,946,885,702 / 19.18%
Number/percentage of N's	35,794 / 0%
GC Percentage	38.37%

2.3. Coverage

Mean	32.6606
Standard Deviation	310.9796

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Insert size

Mean	262,171.64
Standard Deviation	2,467,863.67
P25/Median/P75	313 / 414 / 542

2.6. Mismatches and indels

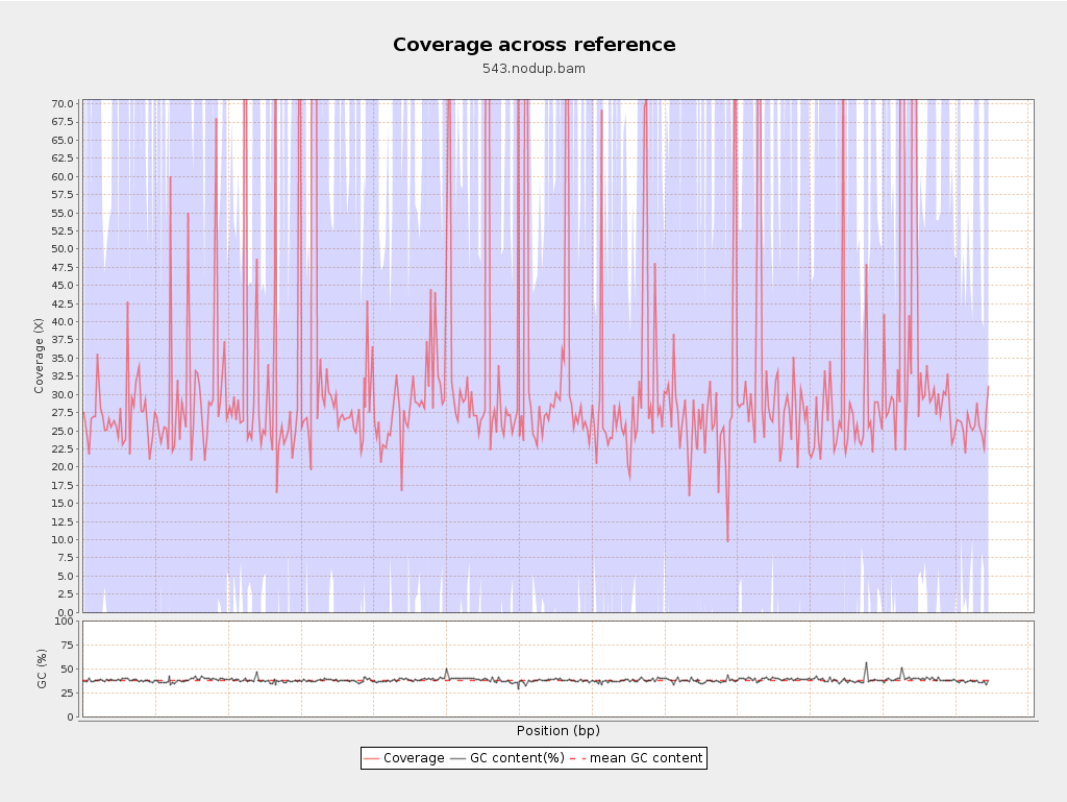
General error rate	2.33%
Mismatches	215,926,738
Insertions	7,349,985
Mapped reads with at least one insertion	8.84%
Deletions	7,063,775
Mapped reads with at least one deletion	8.43%
Homopolymer indels	57.14%

2.7. Chromosome stats

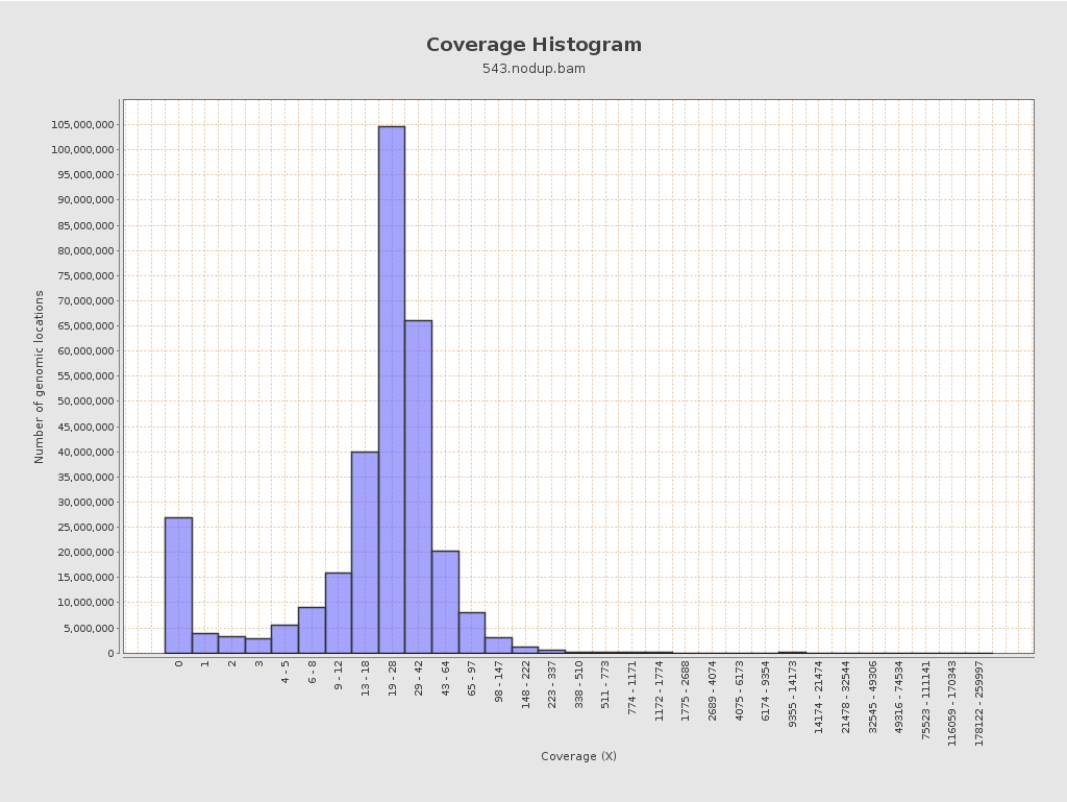
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	796346854	26.7911	124.7803

LT669789.1	36598175	1191695694	32.5616	323.623
LT669790.1	30422129	1216082861	39.9736	444.1748
LT669791.1	52758100	1701679972	32.2544	333.6939
LT669792.1	28376109	928890633	32.735	309.6969
LT669793.1	33388210	982494857	29.4264	198.5298
LT669794.1	50579949	1526440851	30.1788	248.7757
LT669795.1	49795044	1834788071	36.8468	369.3699

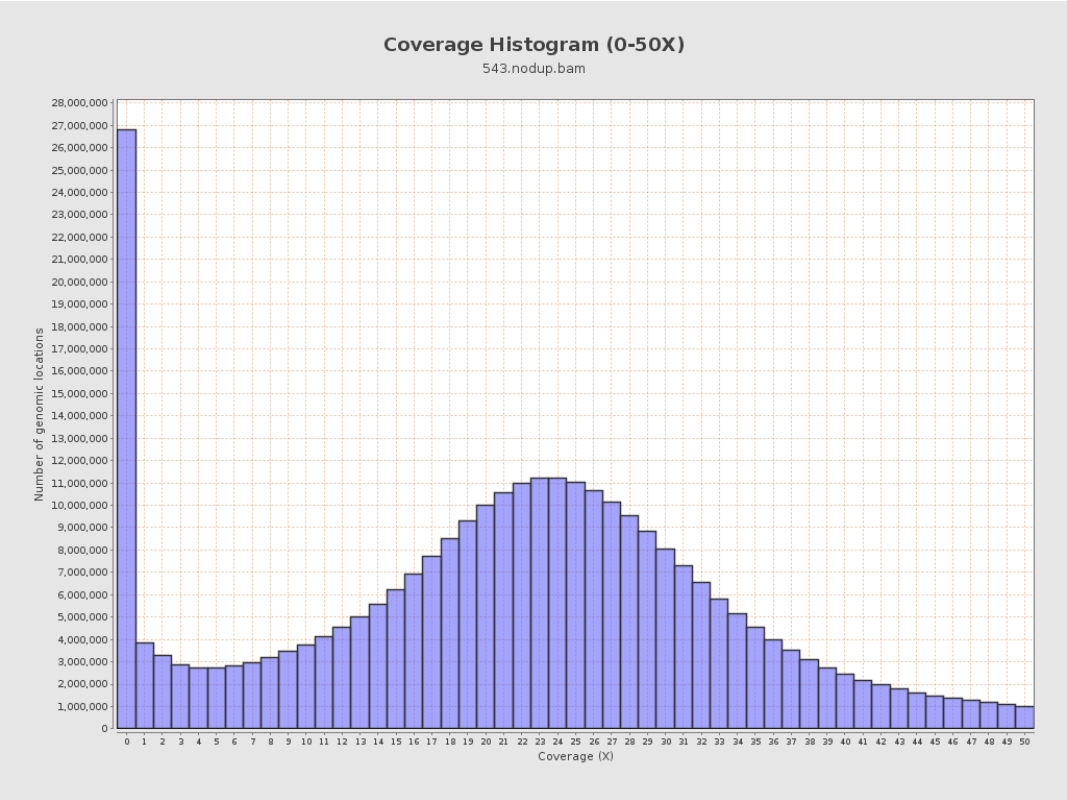
3. Results : Coverage across reference



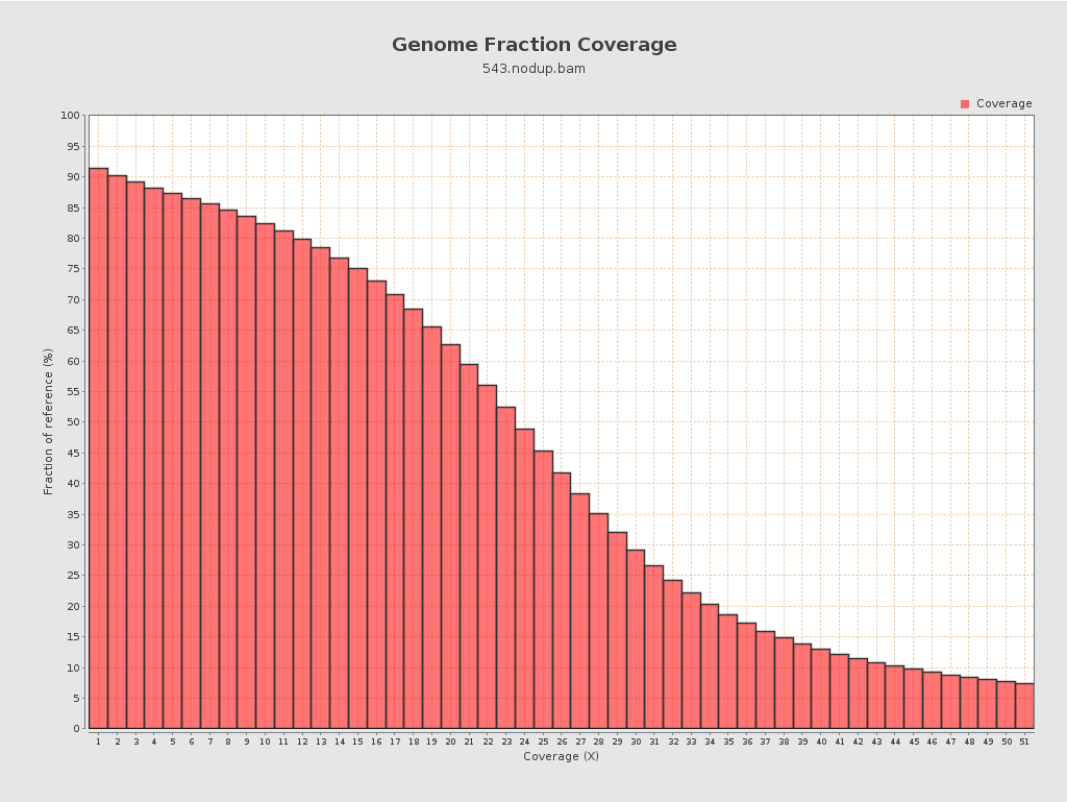
4. Results : Coverage Histogram



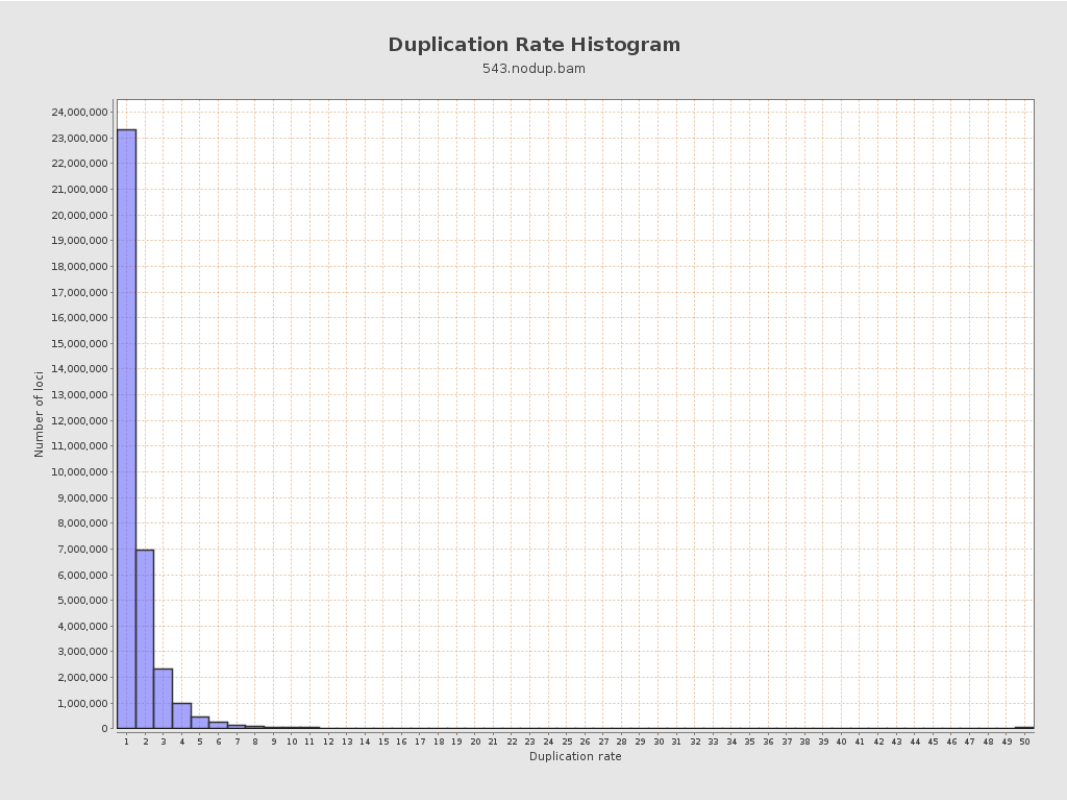
5. Results : Coverage Histogram (0-50X)



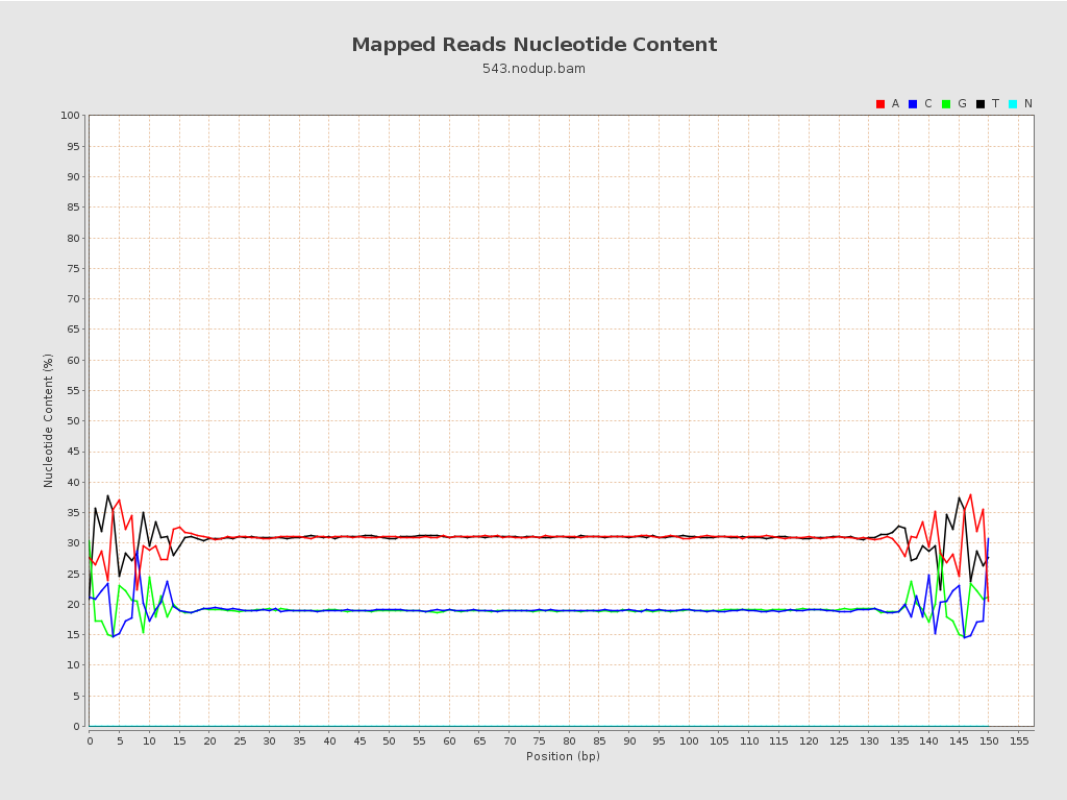
6. Results : Genome Fraction Coverage



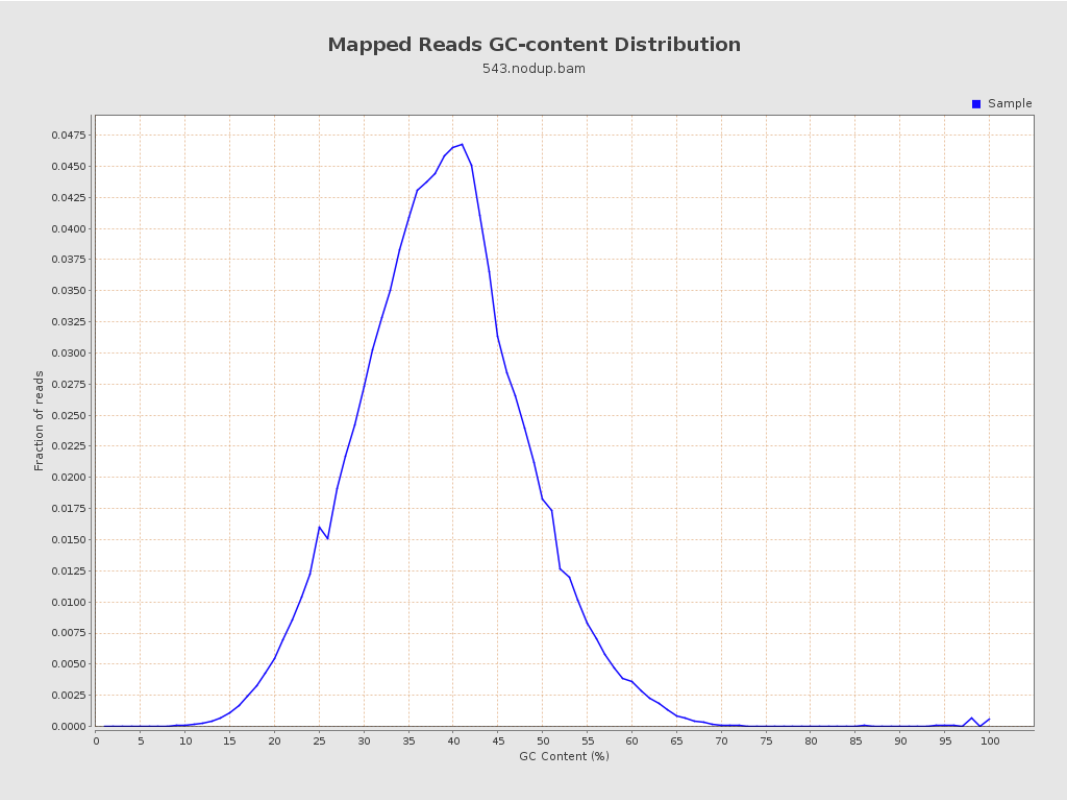
7. Results : Duplication Rate Histogram



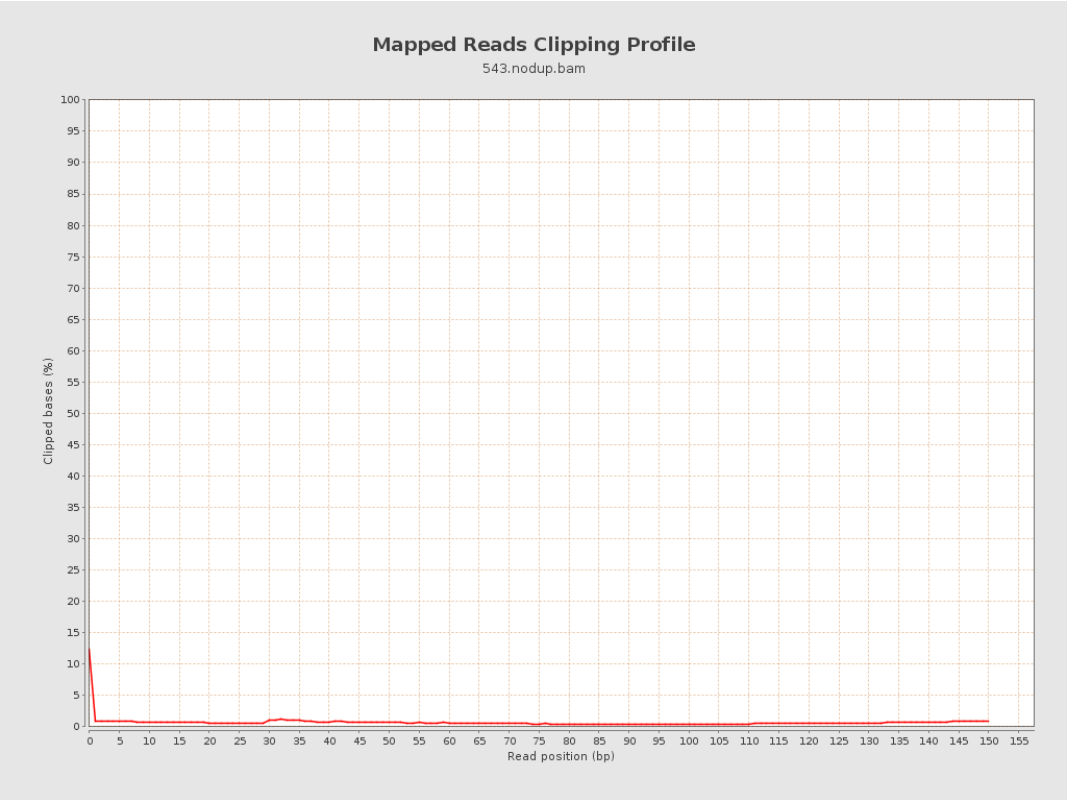
8. Results : Mapped Reads Nucleotide Content



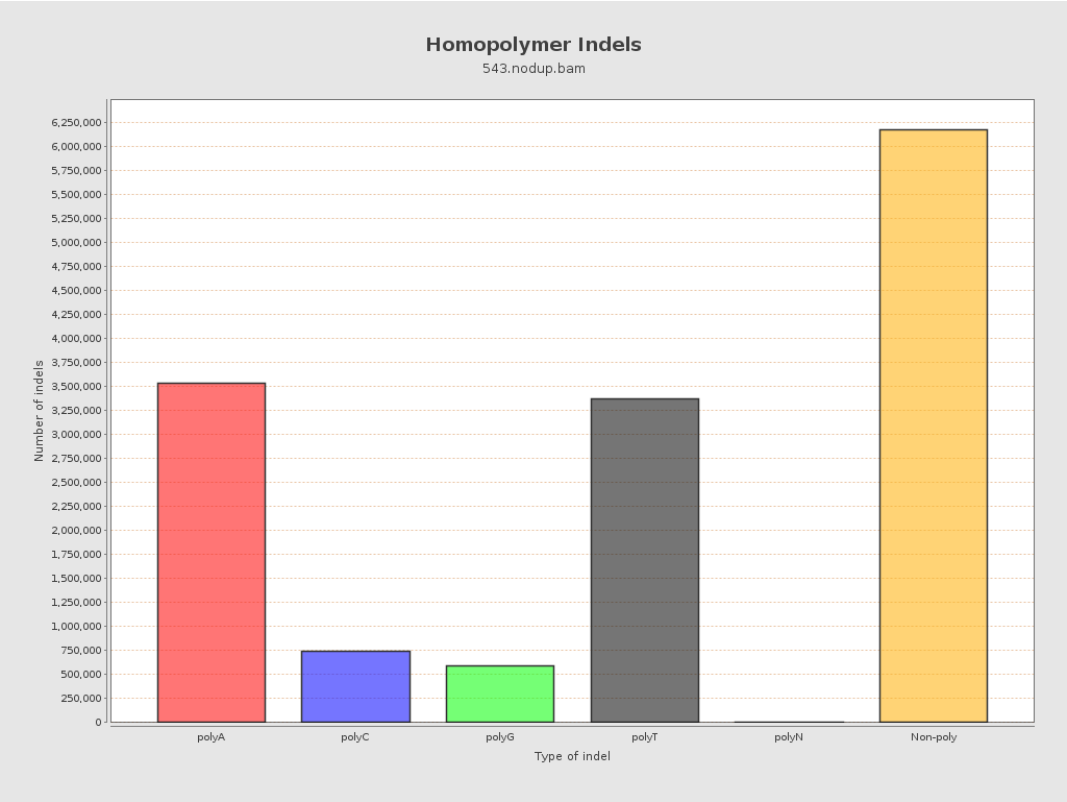
9. Results : Mapped Reads GC-content Distribution



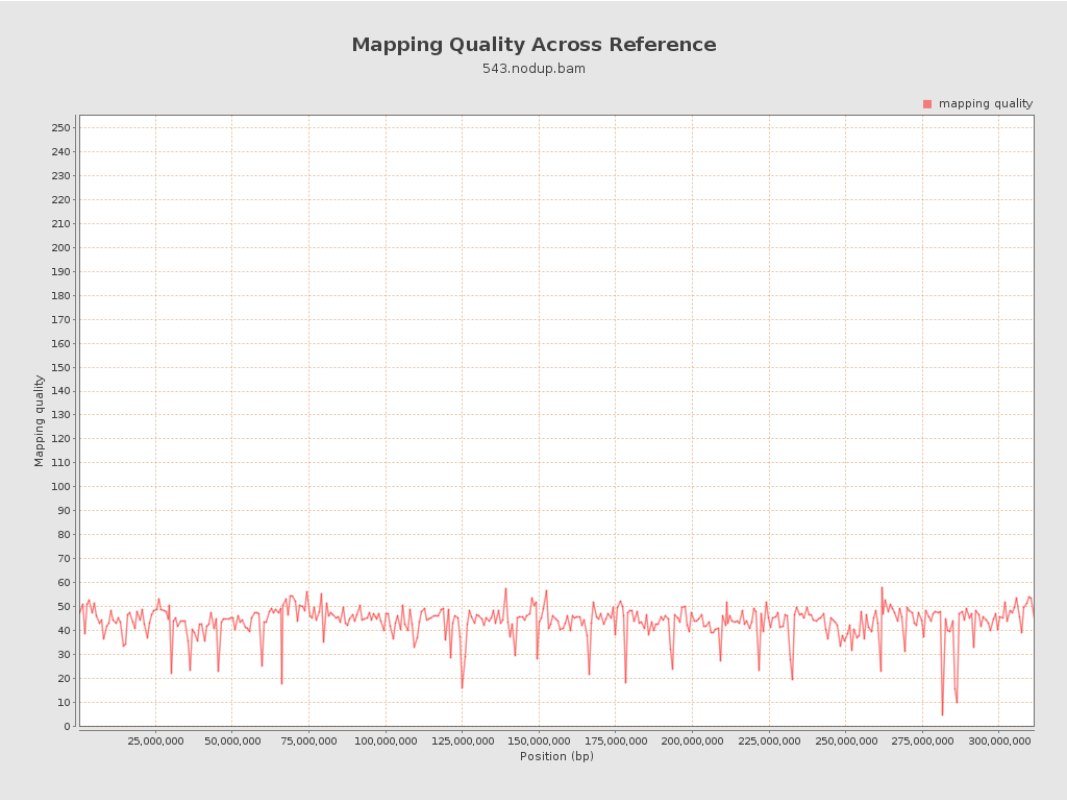
10. Results : Mapped Reads Clipping Profile



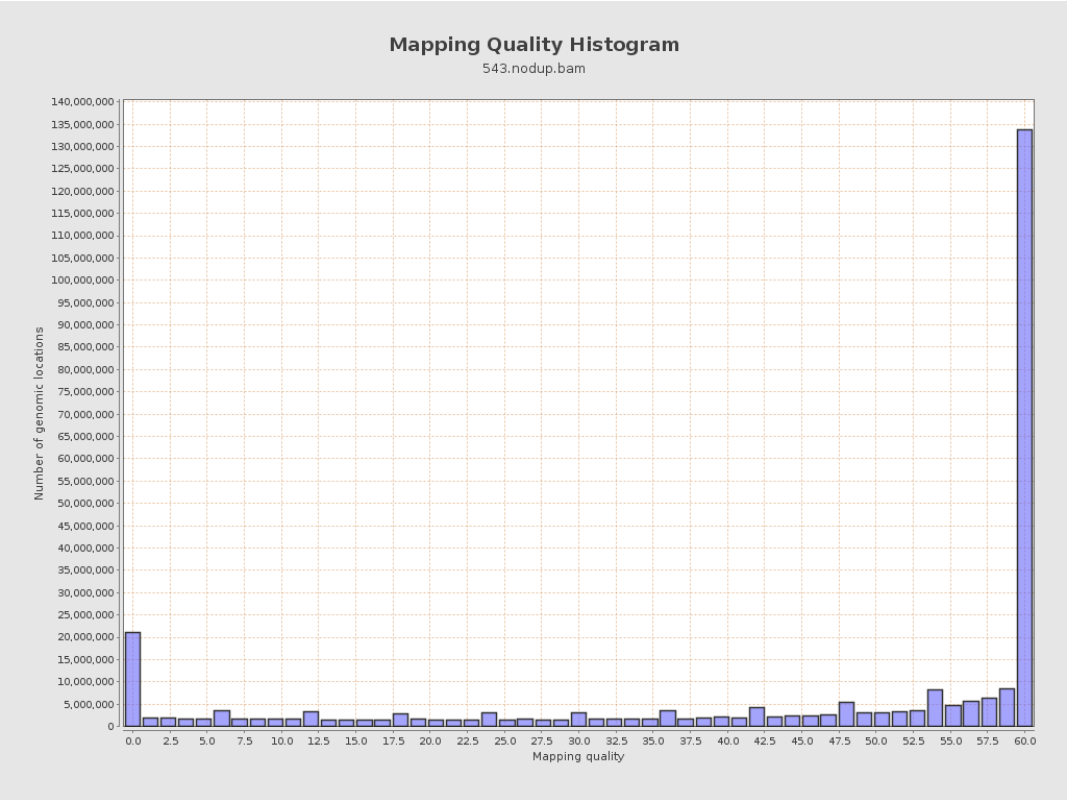
11. Results : Homopolymer Indels



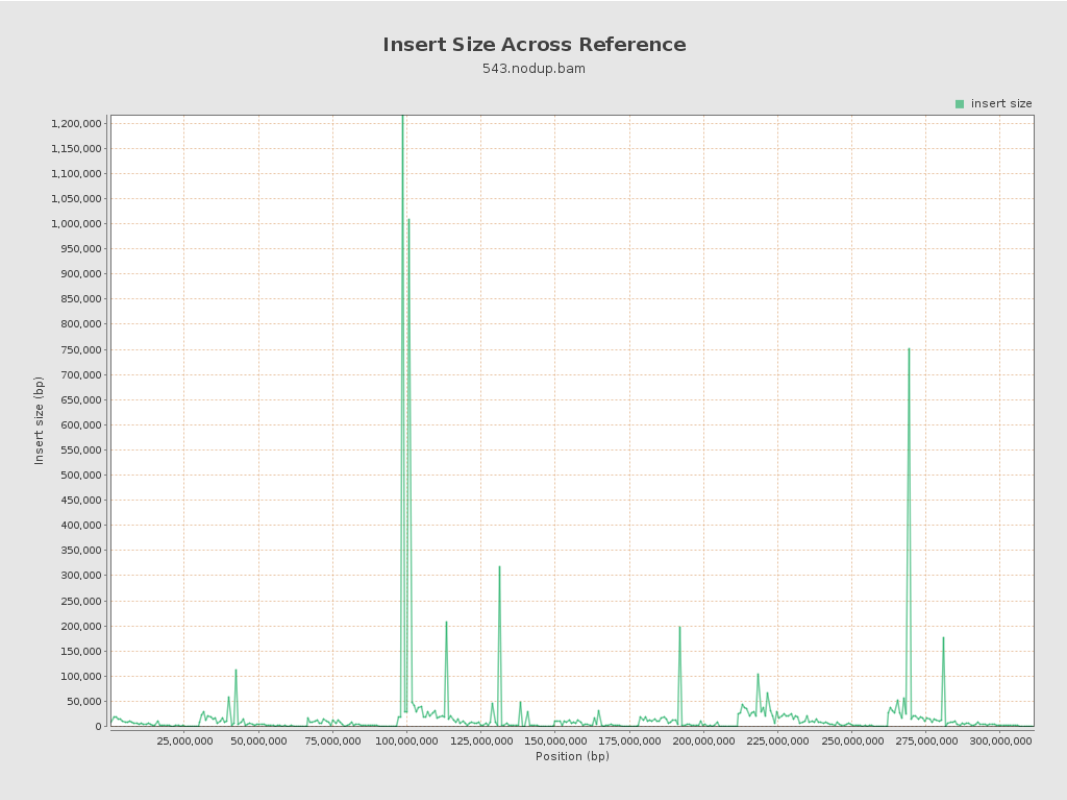
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram