Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/542.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/542.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_233/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_233_S314_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_233/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_233_S314_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,837,322
Mapped reads	59,886,034 / 93.81%
Unmapped reads	3,951,288 / 6.19%
Mapped paired reads	59,886,034 / 93.81%
Mapped reads, first in pair	30,010,295 / 47.01%
Mapped reads, second in pair	29,875,739 / 46.8%
Mapped reads, both in pair	58,589,159 / 91.78%
Mapped reads, singletons	1,296,875 / 2.03%
Read min/max/mean length	30 / 151 / 147.97
Duplicated reads (flagged)	8,762,031 / 13.73%
Clipped reads	14,108,816 / 22.1%

2.2. ACGT Content

Number/percentage of A's	2,547,602,161 / 30.86%
Number/percentage of C's	1,578,941,684 / 19.13%
Number/percentage of T's	2,549,522,313 / 30.88%
Number/percentage of G's	1,578,942,173 / 19.13%
Number/percentage of N's	30,376 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	26.5585
Standard Deviation	223.1098

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Insert size

Mean	238,147.59
Standard Deviation	2,318,127.3
P25/Median/P75	313 / 415 / 541

2.6. Mismatches and indels

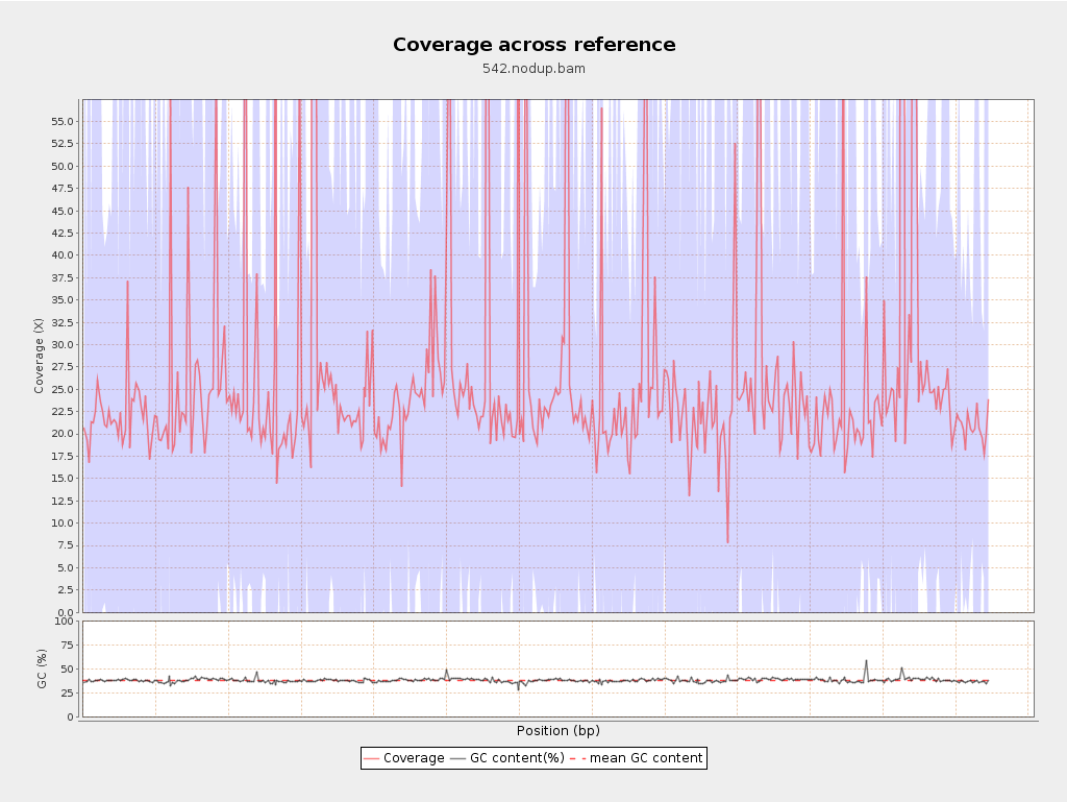
General error rate	2.35%
Mismatches	178,701,429
Insertions	5,678,687
Mapped reads with at least one insertion	8.51%
Deletions	5,755,197
Mapped reads with at least one deletion	8.51%
Homopolymer indels	56.27%

2.7. Chromosome stats

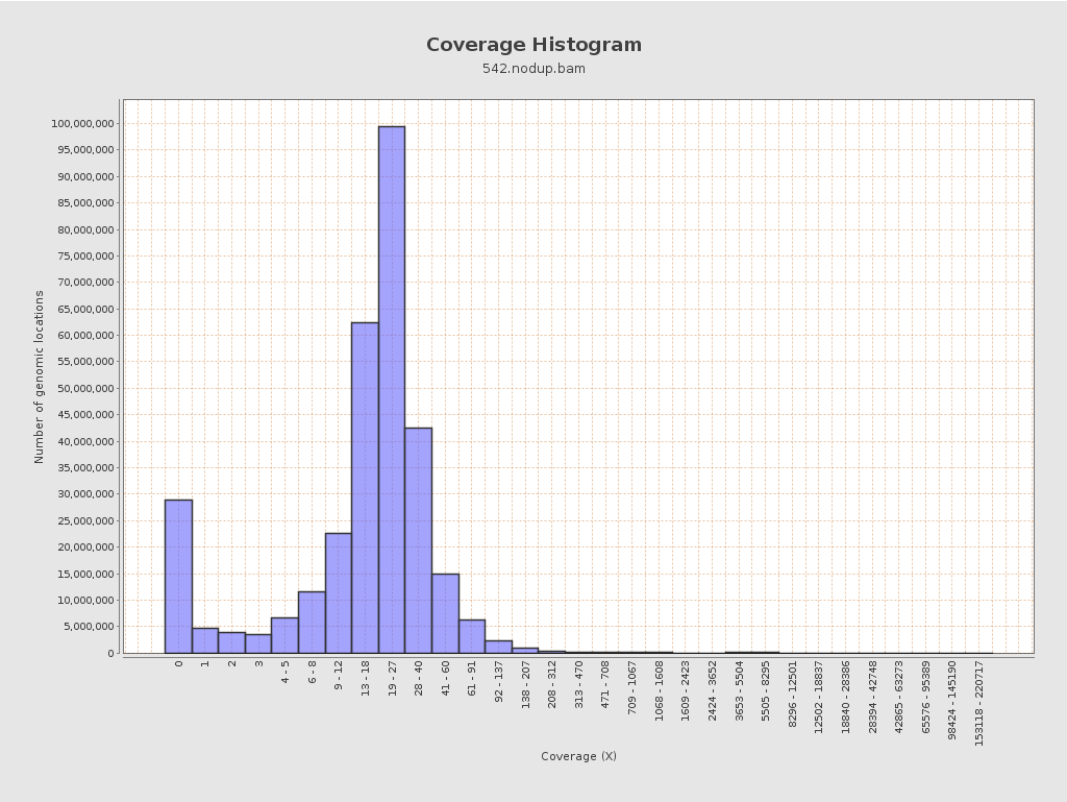
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	646490795	21.7495	70.1553

LT669789.1	36598175	988356019	27.0056	228.442
LT669790.1	30422129	890866403	29.2835	234.7238
LT669791.1	52758100	1373656051	26.0369	197.1959
LT669792.1	28376109	751430087	26.4811	240.1617
LT669793.1	33388210	821962070	24.6183	212.6469
LT669794.1	50579949	1266924528	25.048	183.4535
LT669795.1	49795044	1537054763	30.8676	312.995

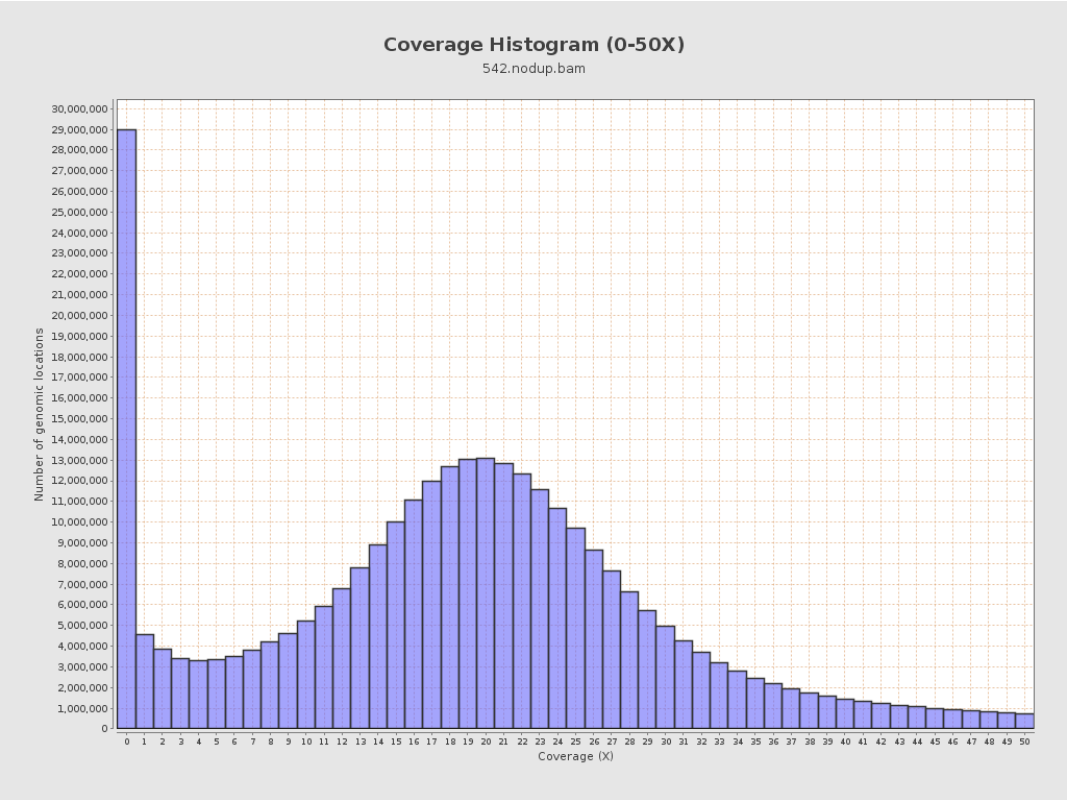
3. Results : Coverage across reference



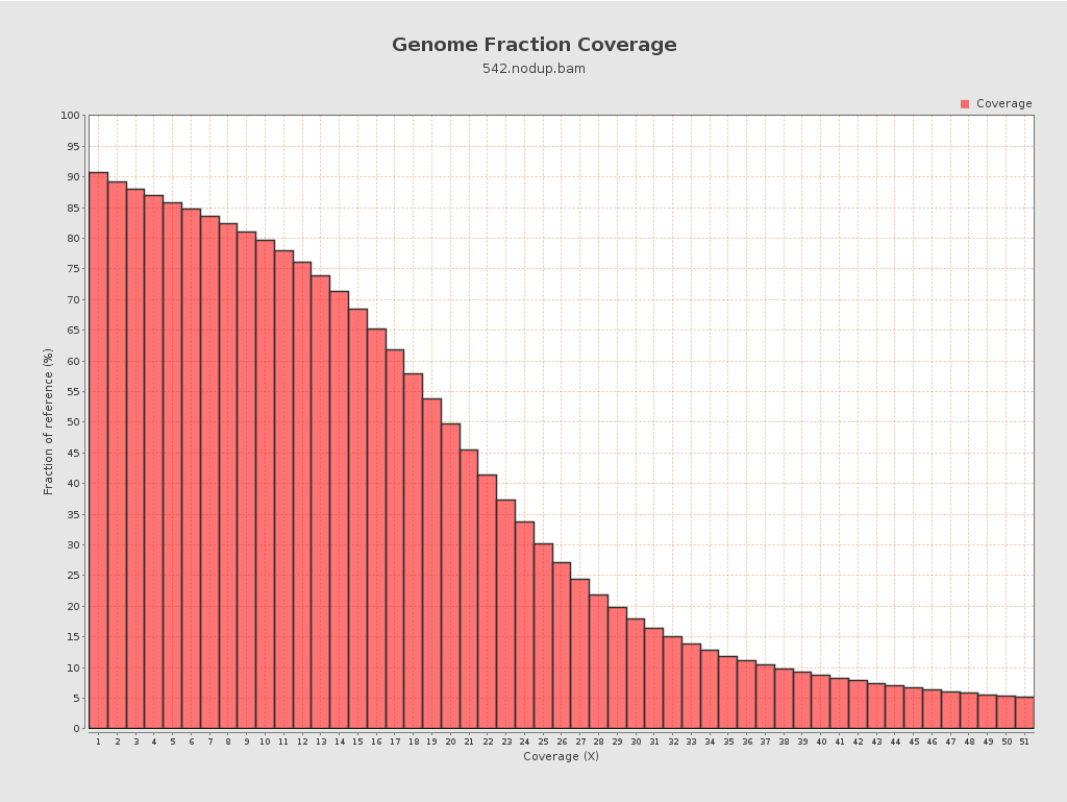
4. Results : Coverage Histogram



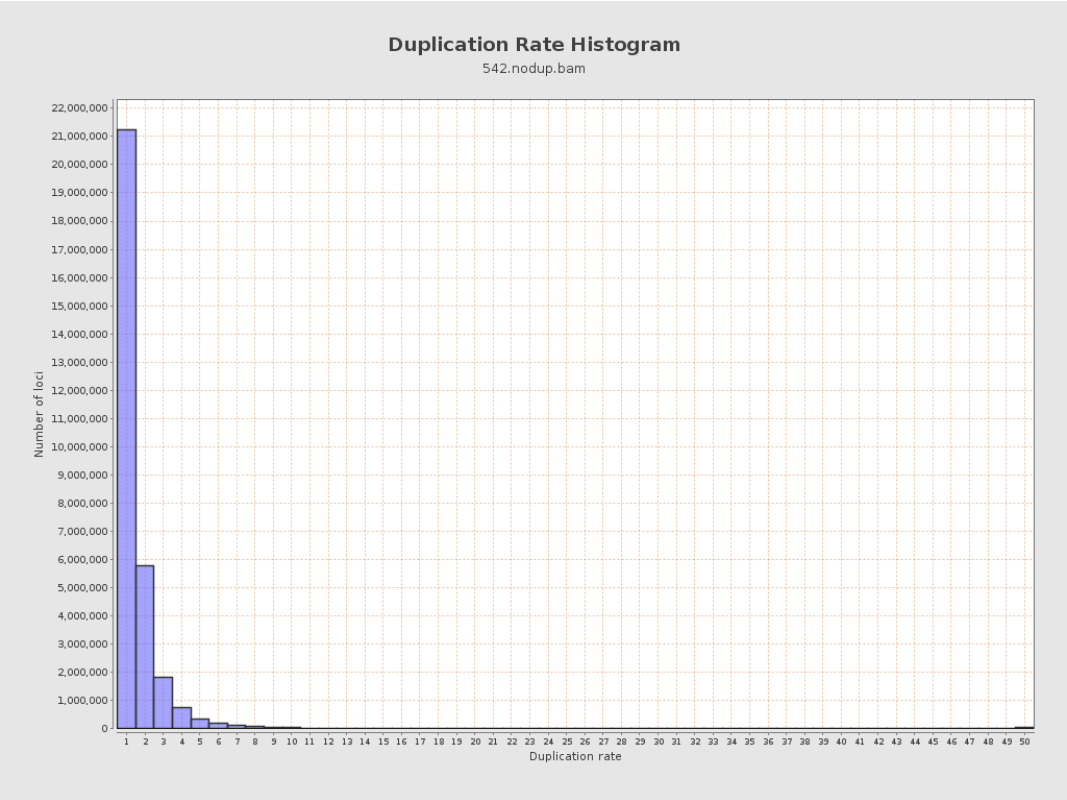
5. Results : Coverage Histogram (0-50X)



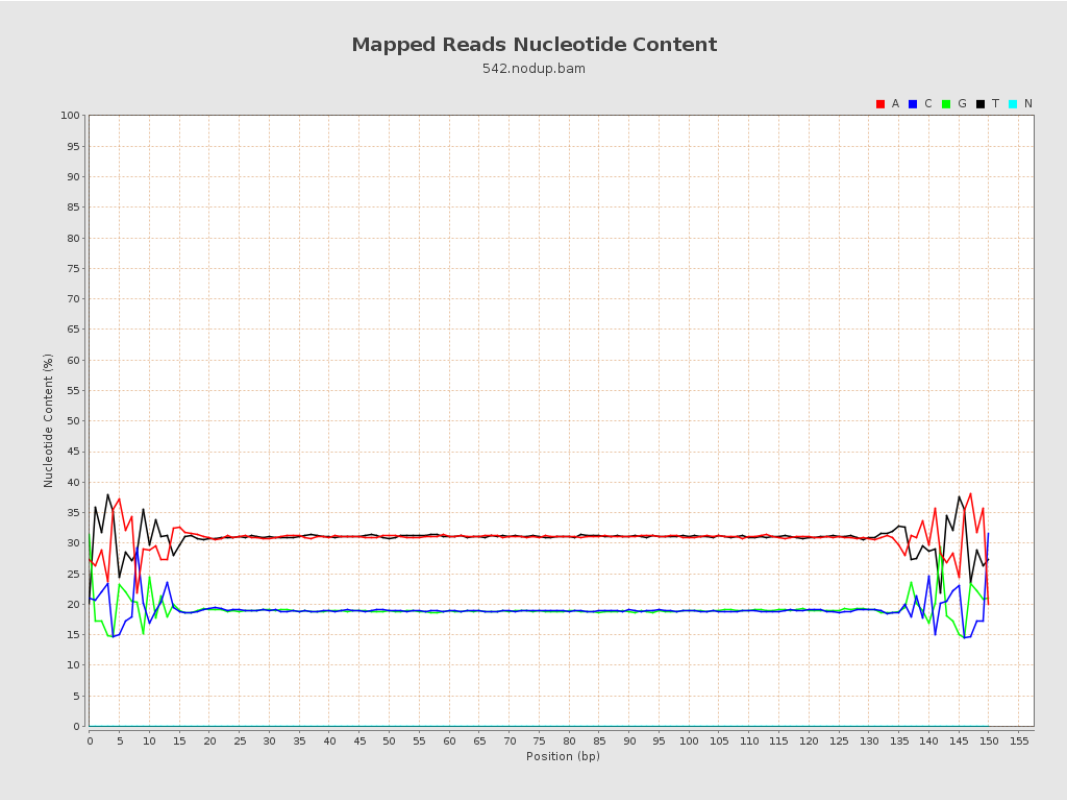
6. Results : Genome Fraction Coverage



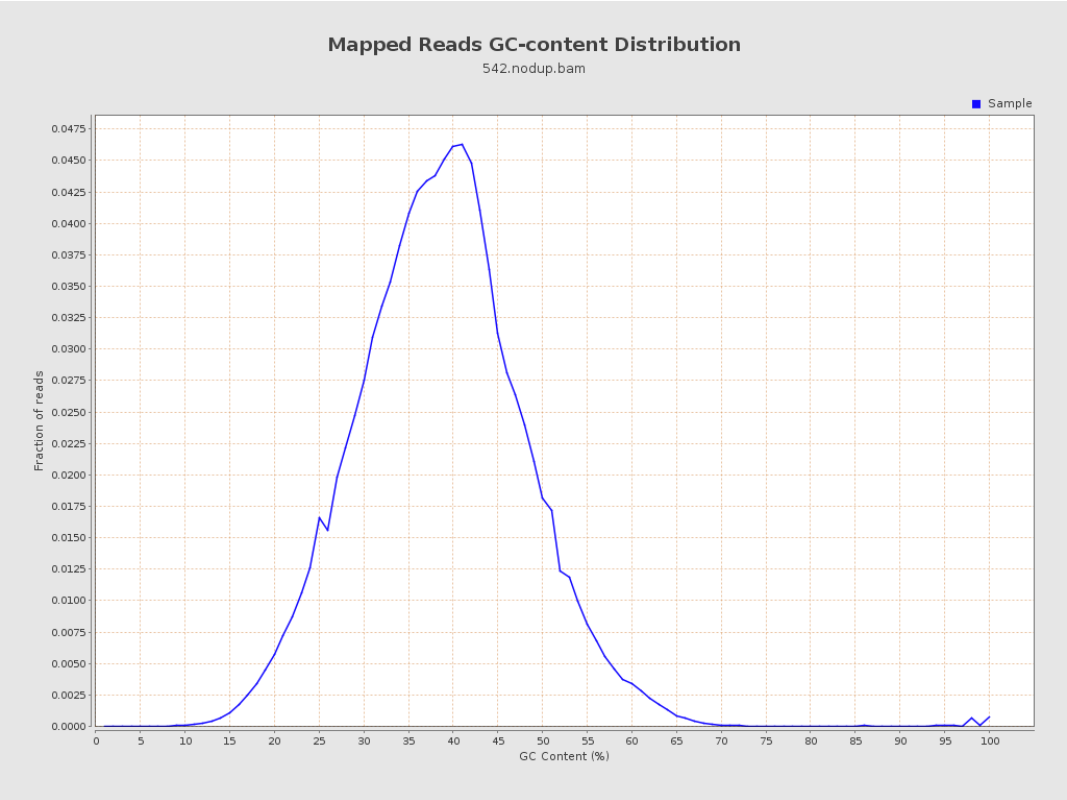
7. Results : Duplication Rate Histogram



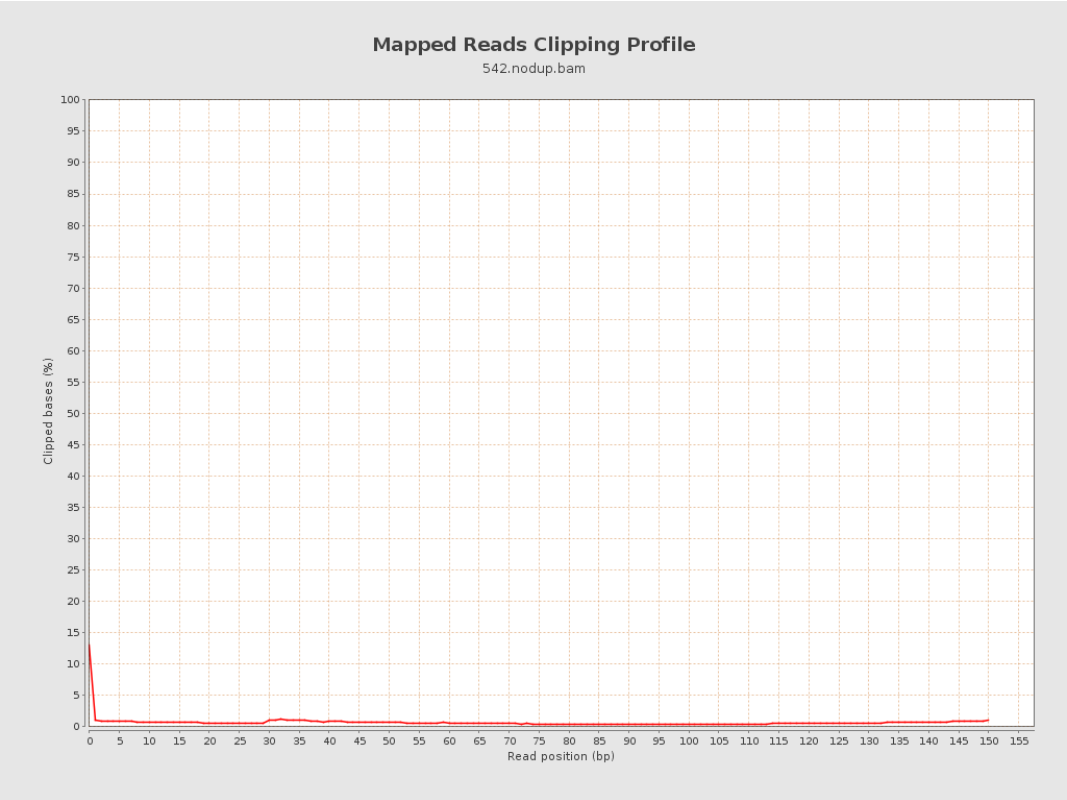
8. Results : Mapped Reads Nucleotide Content



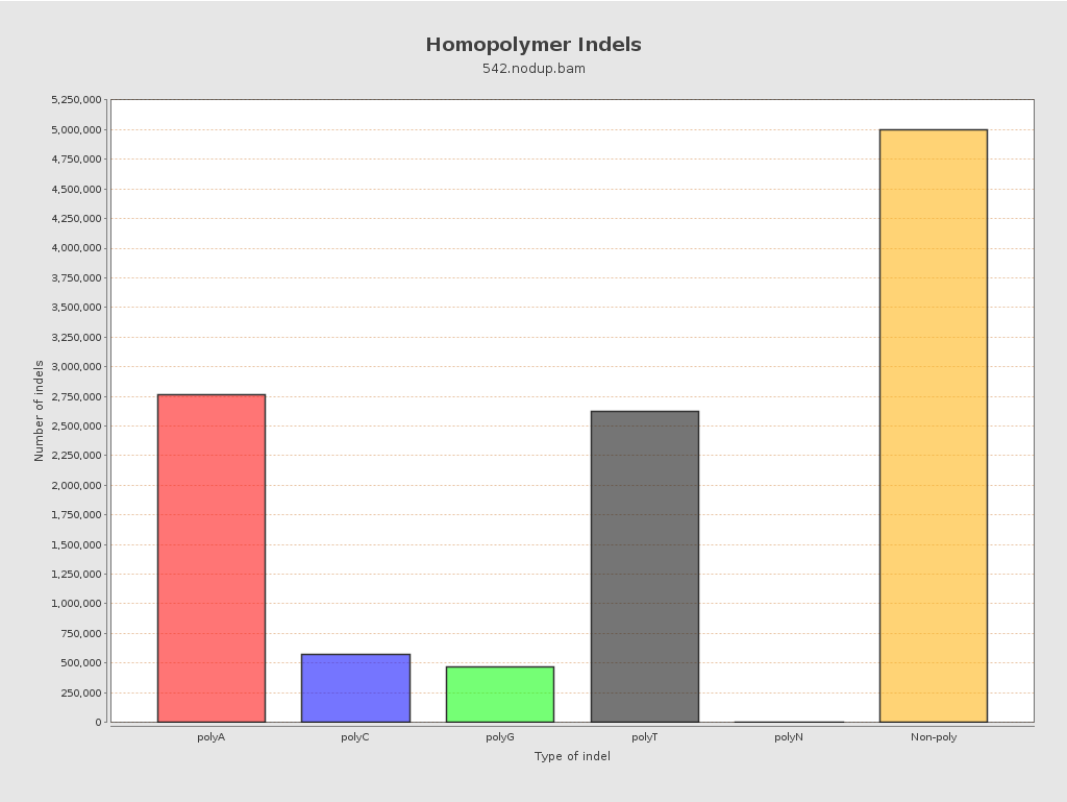
9. Results : Mapped Reads GC-content Distribution



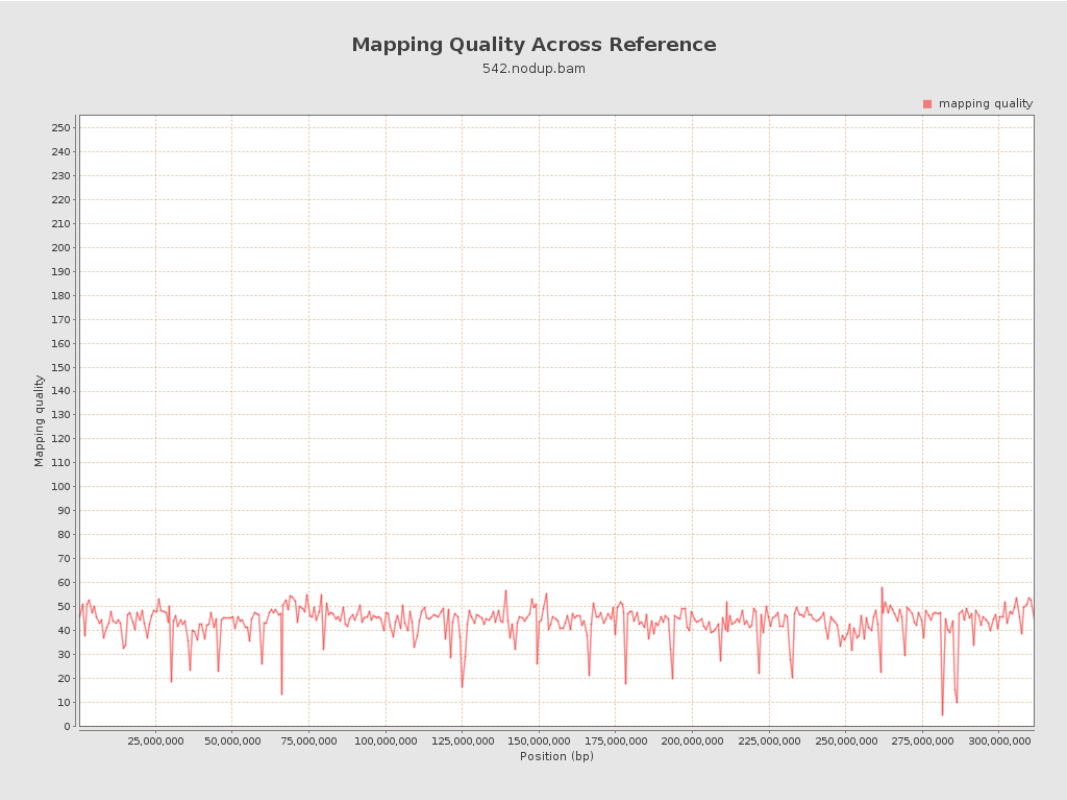
10. Results : Mapped Reads Clipping Profile



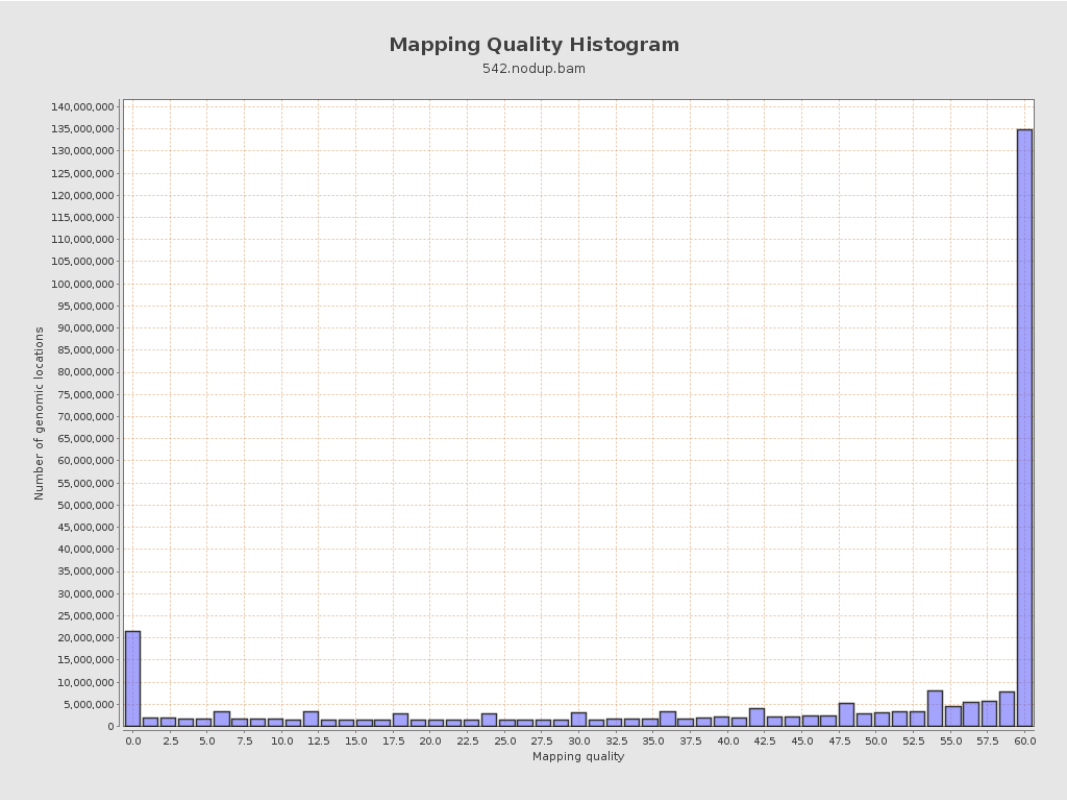
11. Results : Homopolymer Indels



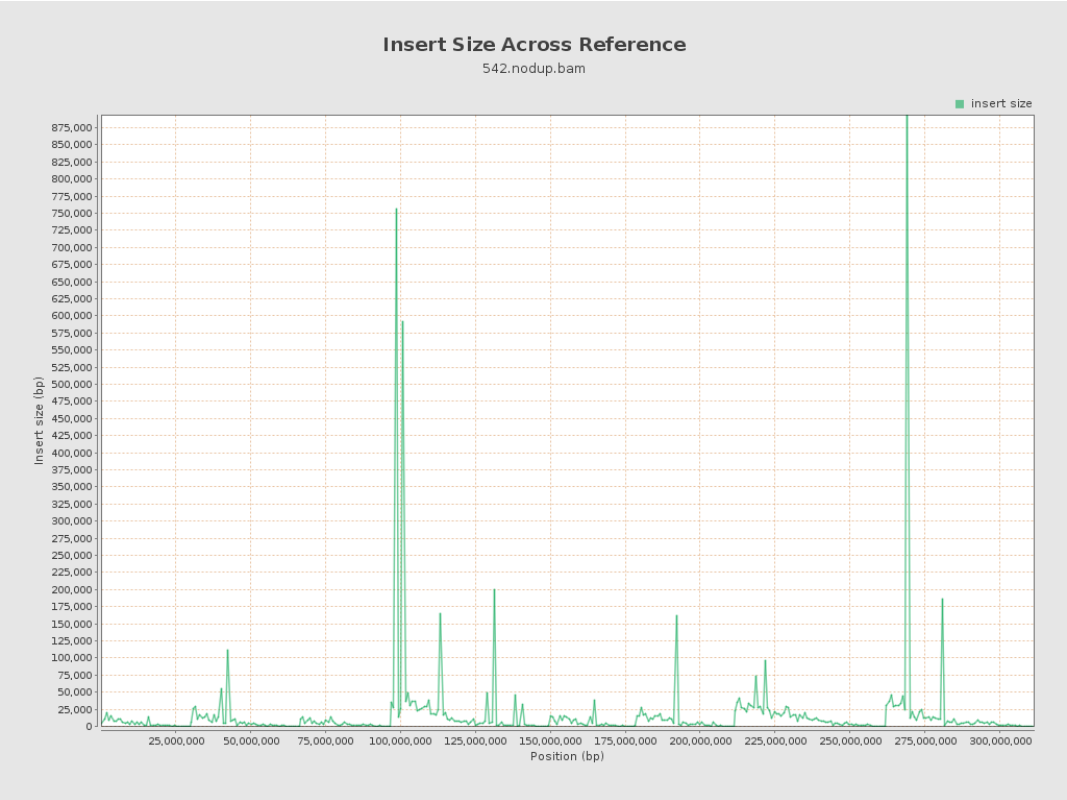
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram