Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/545.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/545.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_265/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_265_S346_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_265/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_265_S346_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	53,832,463
Mapped reads	51,089,676 / 94.9%
Unmapped reads	2,742,787 / 5.1%
Mapped paired reads	51,089,676 / 94.9%
Mapped reads, first in pair	25,577,276 / 47.51%
Mapped reads, second in pair	25,512,400 / 47.39%
Mapped reads, both in pair	50,150,094 / 93.16%
Mapped reads, singletons	939,582 / 1.75%
Read min/max/mean length	30 / 151 / 147.93
Duplicated reads (flagged)	6,775,761 / 12.59%
Clipped reads	12,125,891 / 22.53%

2.2. ACGT Content

Number/percentage of A's	2,173,960,609 / 30.81%
Number/percentage of C's	1,353,976,385 / 19.19%
Number/percentage of T's	2,176,487,092 / 30.84%
Number/percentage of G's	1,351,911,544 / 19.16%
Number/percentage of N's	24,947 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	22.7025
Standard Deviation	195.2794

2.4. Mapping Quality

Mean Mapping Quality	43.5

2.5. Insert size

Mean	236,254.27
Standard Deviation	2,293,692.33
P25/Median/P75	332 / 437 / 566

2.6. Mismatches and indels

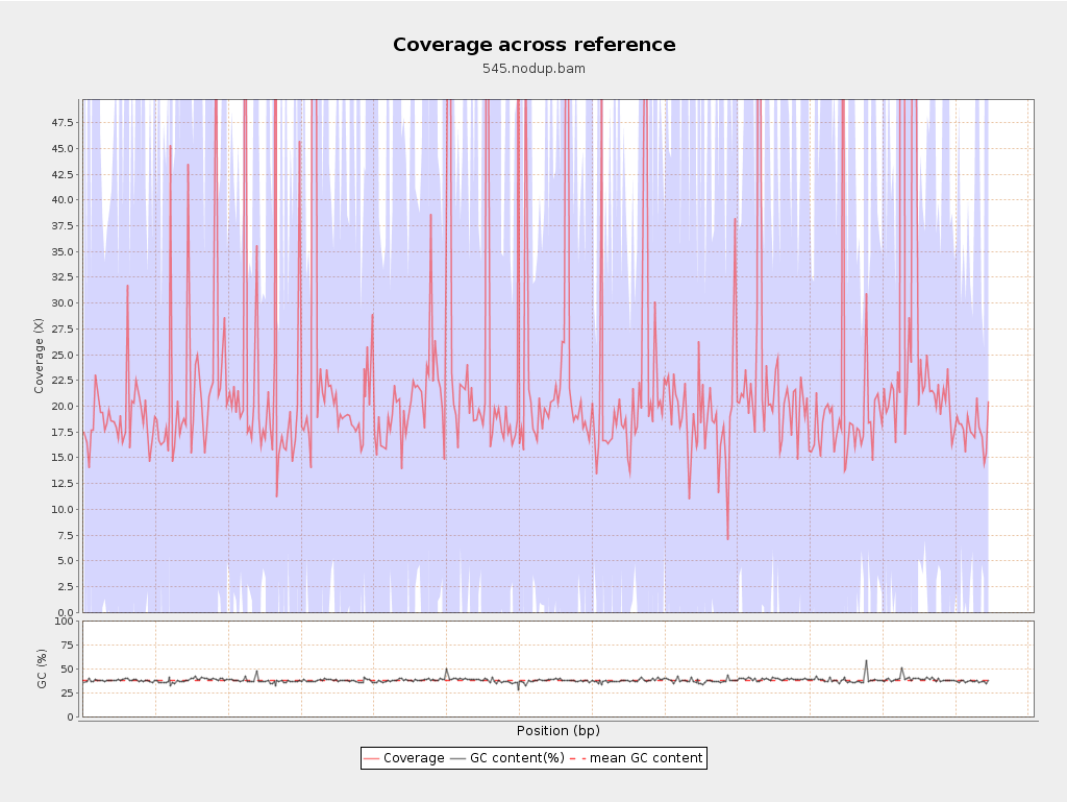
General error rate	2.43%
Mismatches	158,565,442
Insertions	4,823,436
Mapped reads with at least one insertion	8.5%
Deletions	5,002,648
Mapped reads with at least one deletion	8.66%
Homopolymer indels	55.53%

2.7. Chromosome stats

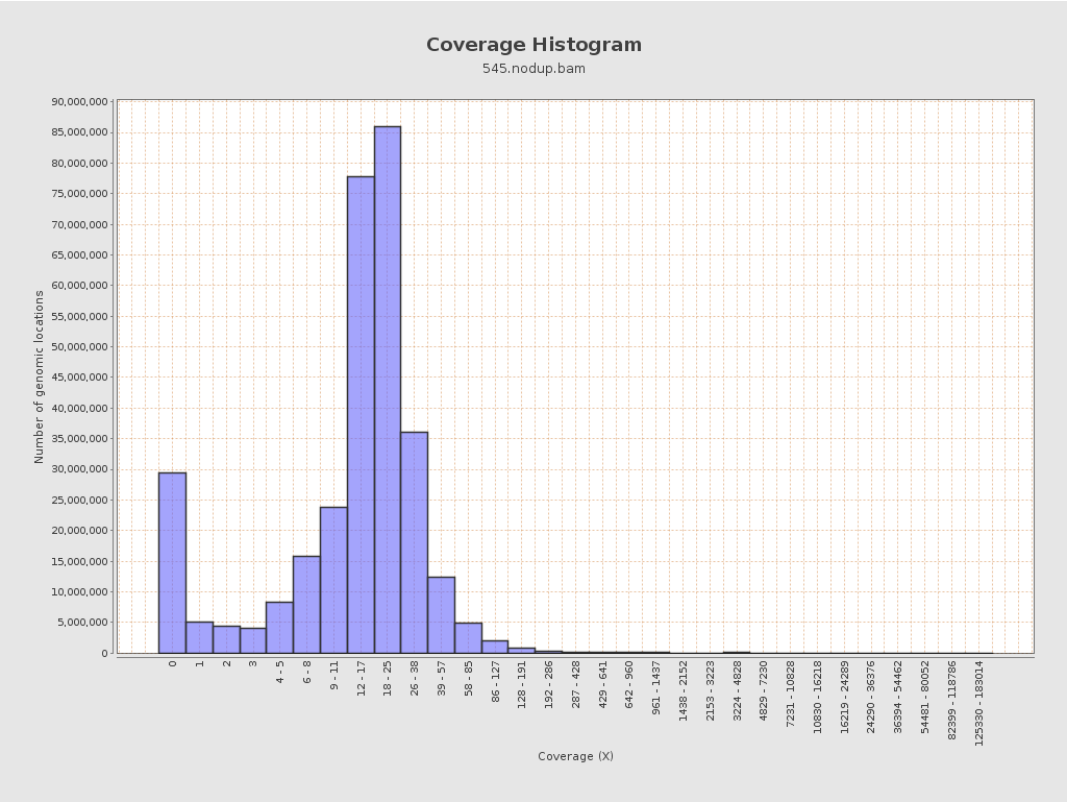
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	553862171	18.6333	61.8702

LT669789.1	36598175	857736797	23.4366	205.6103
LT669790.1	30422129	720381974	23.6795	168.3075
LT669791.1	52758100	1170047140	22.1776	183.8272
LT669792.1	28376109	637757361	22.4752	217.1827
LT669793.1	33388210	709684053	21.2555	139.7136
LT669794.1	50579949	1094039492	21.6299	195.2377
LT669795.1	49795044	1331551642	26.7406	271.0703

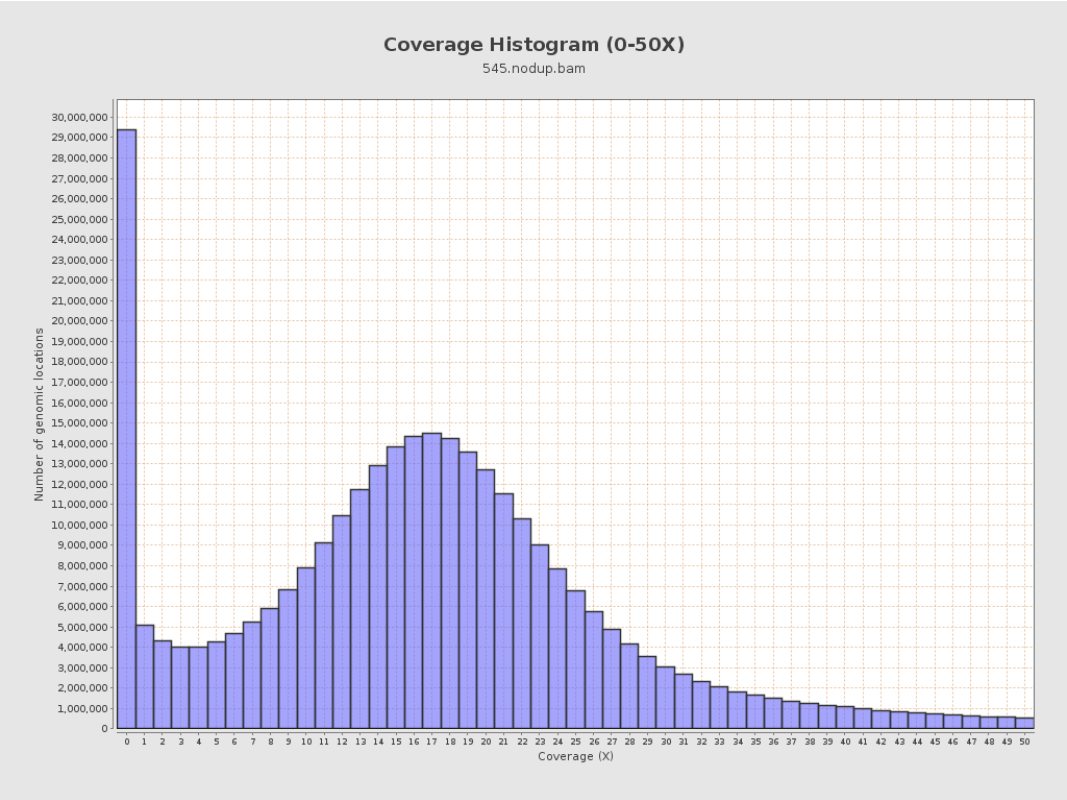
3. Results : Coverage across reference



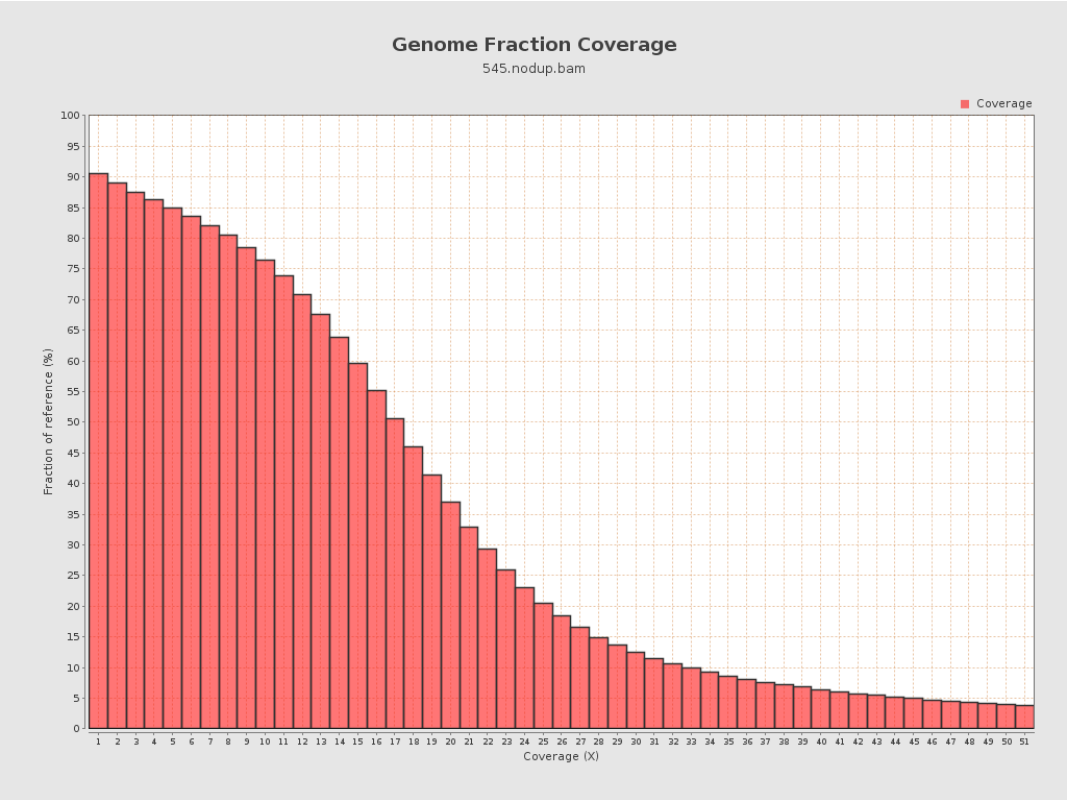
4. Results : Coverage Histogram



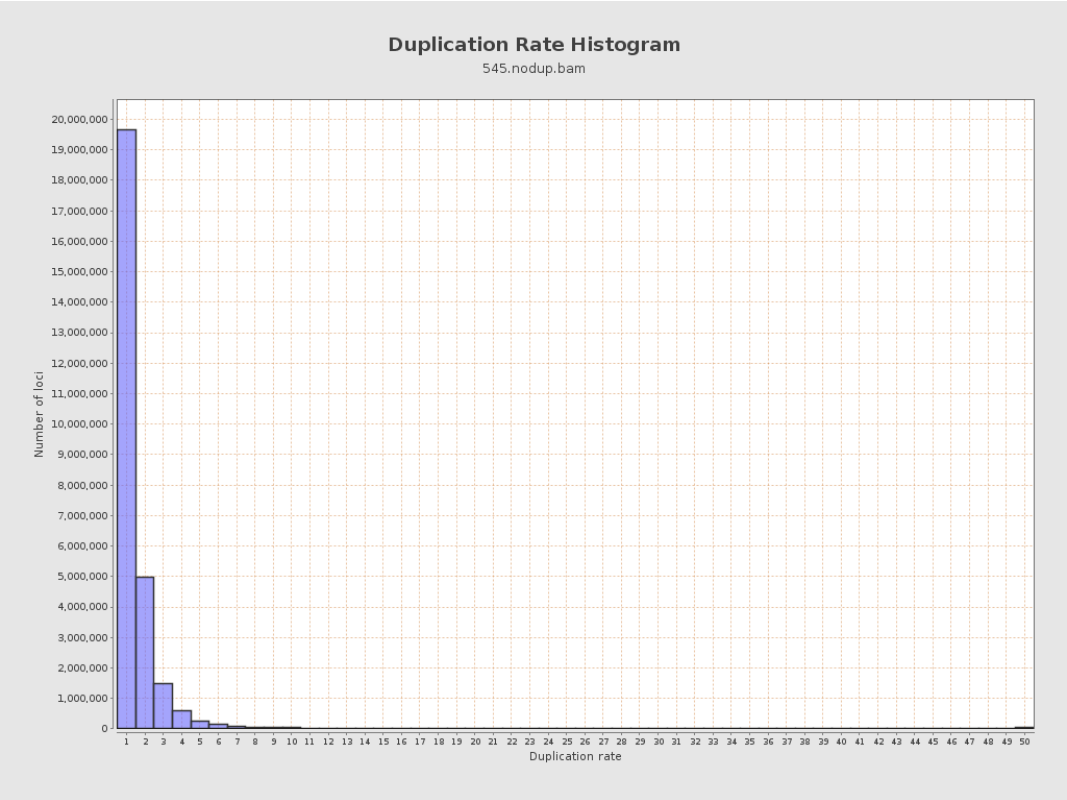
5. Results : Coverage Histogram (0-50X)



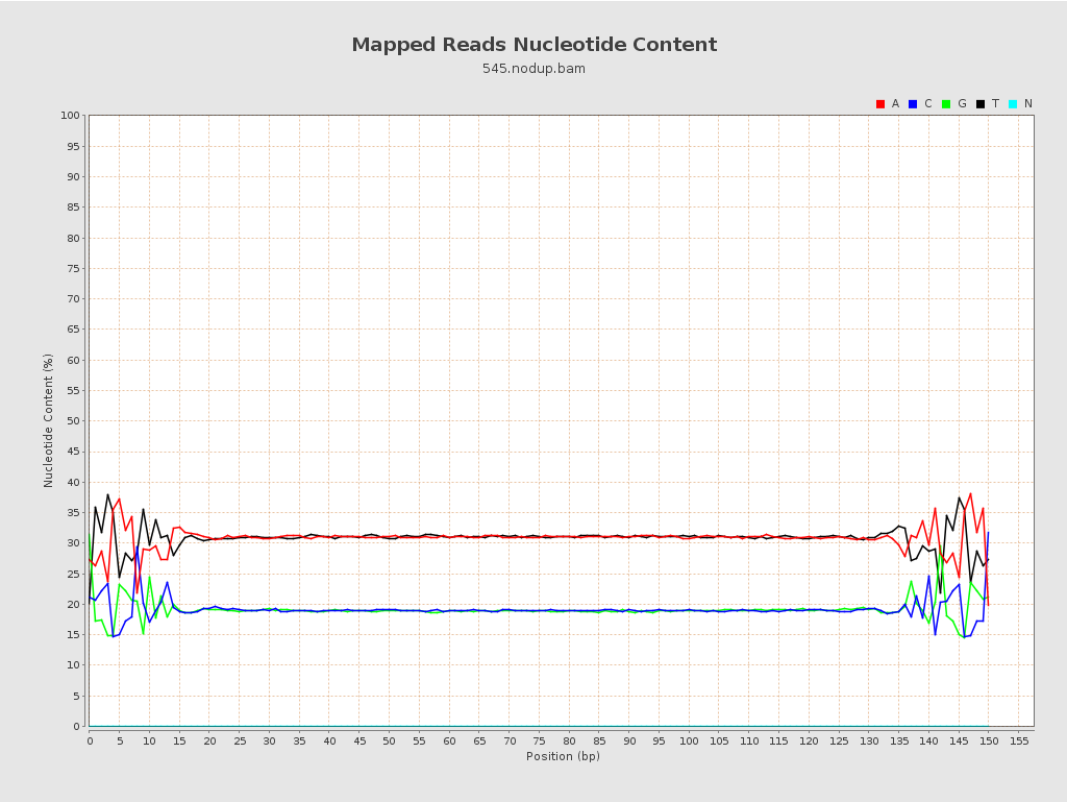
6. Results : Genome Fraction Coverage



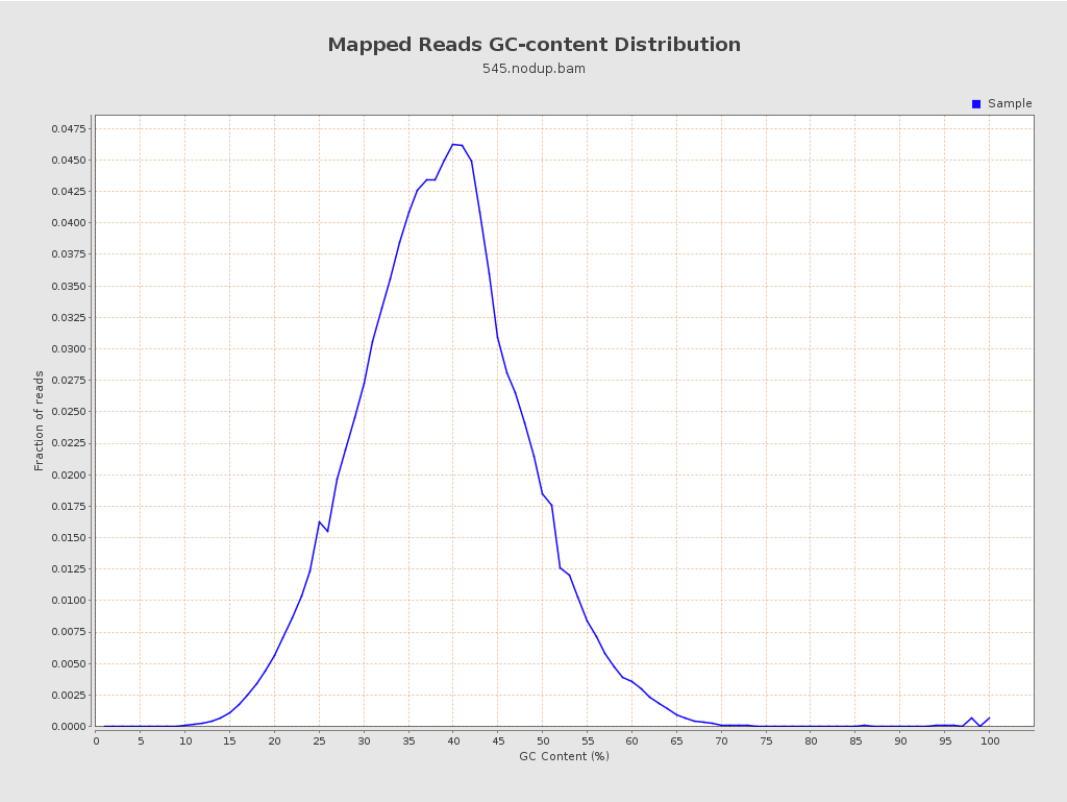
7. Results : Duplication Rate Histogram



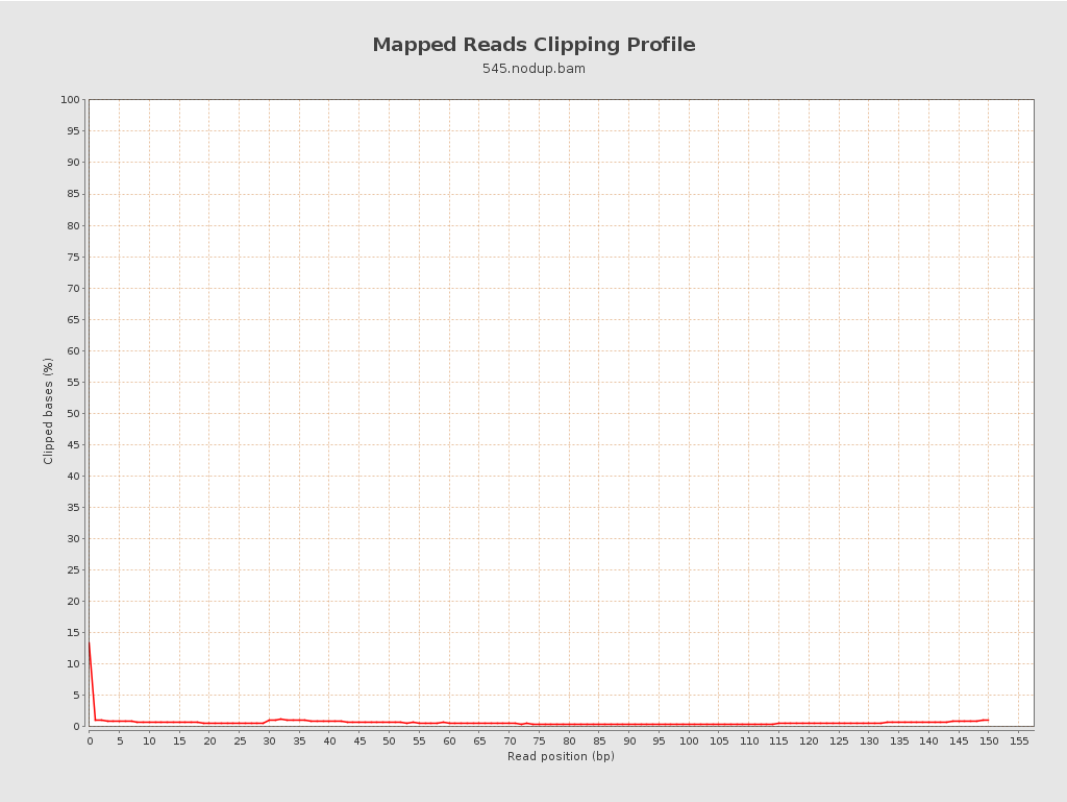
8. Results : Mapped Reads Nucleotide Content



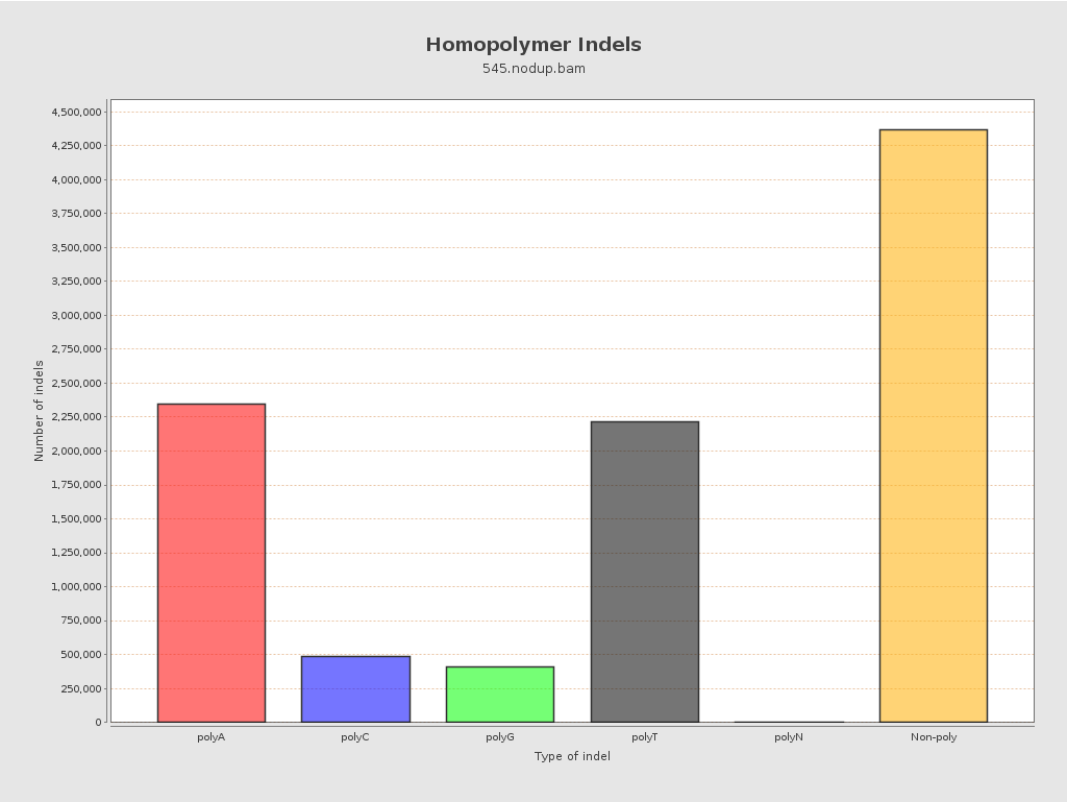
9. Results : Mapped Reads GC-content Distribution



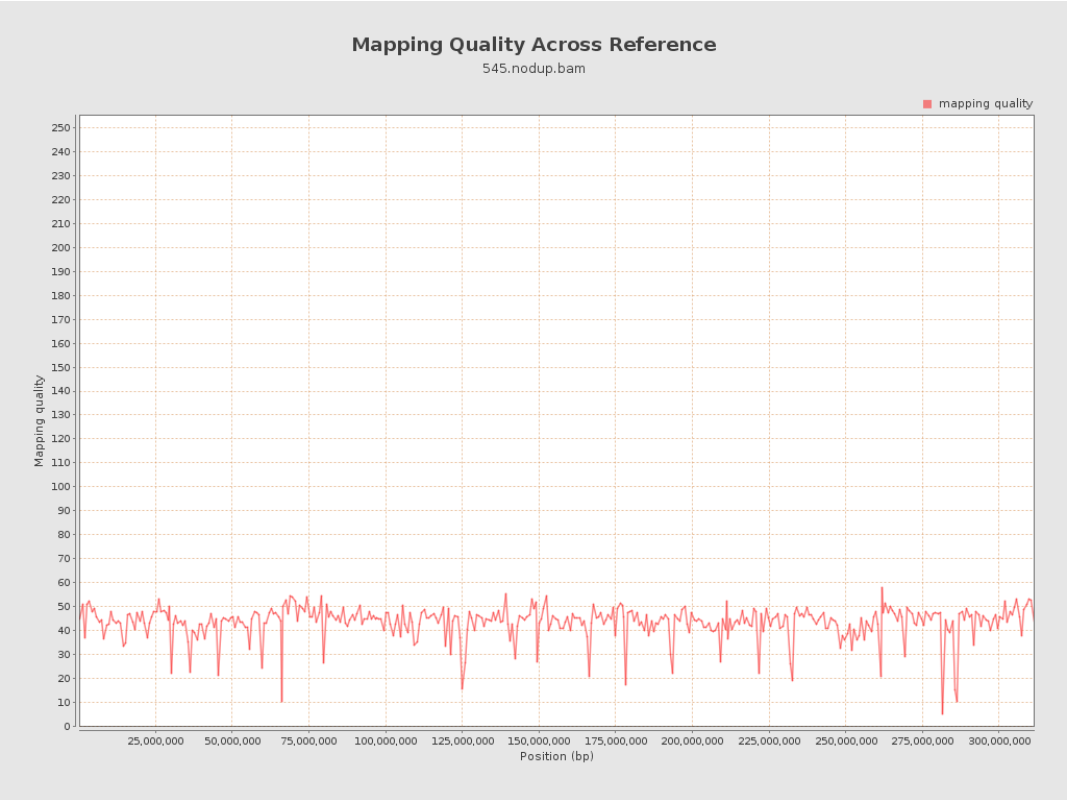
10. Results : Mapped Reads Clipping Profile



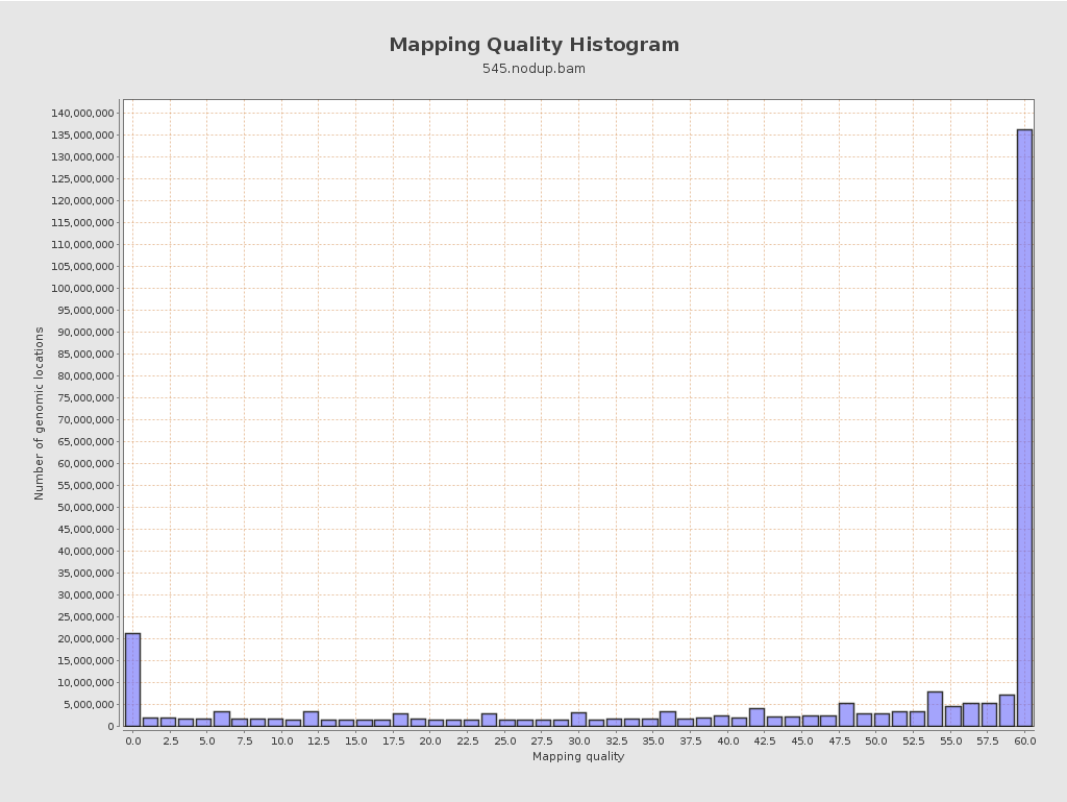
11. Results : Homopolymer Indels



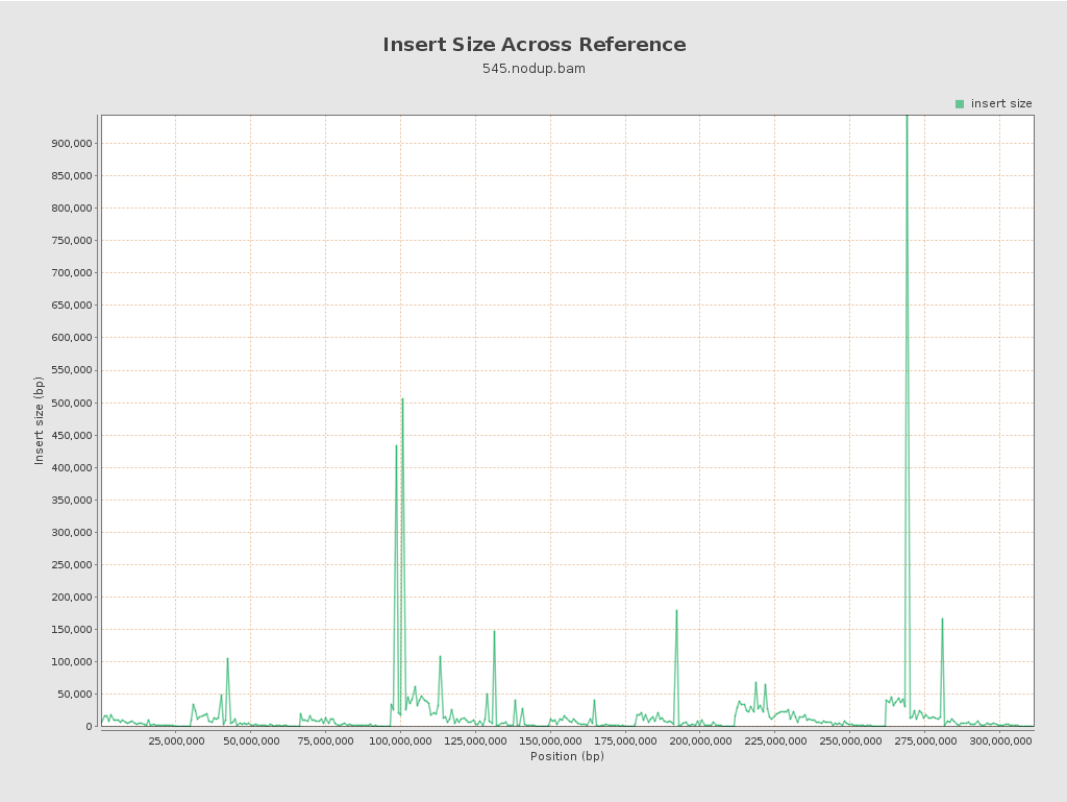
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram