Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/509.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/509.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_146/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_146_S236_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_146/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_146_S236_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,315,474
Mapped reads	57,459,329 / 90.75%
Unmapped reads	5,856,145 / 9.25%
Mapped paired reads	57,459,329 / 90.75%
Mapped reads, first in pair	28,796,303 / 45.48%
Mapped reads, second in pair	28,663,026 / 45.27%
Mapped reads, both in pair	55,510,211 / 87.67%
Mapped reads, singletons	1,949,118 / 3.08%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	10,706,690 / 16.91%
Clipped reads	13,814,742 / 21.82%

2.2. ACGT Content

Number/percentage of A's	2,425,579,828 / 30.87%
Number/percentage of C's	1,499,390,880 / 19.08%
Number/percentage of T's	2,434,292,732 / 30.98%
Number/percentage of G's	1,497,669,629 / 19.06%
Number/percentage of N's	33,121 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	25.2797
Standard Deviation	237.9243

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Insert size

Mean	271,013.54
Standard Deviation	2,528,046.4
P25/Median/P75	328 / 428 / 555

2.6. Mismatches and indels

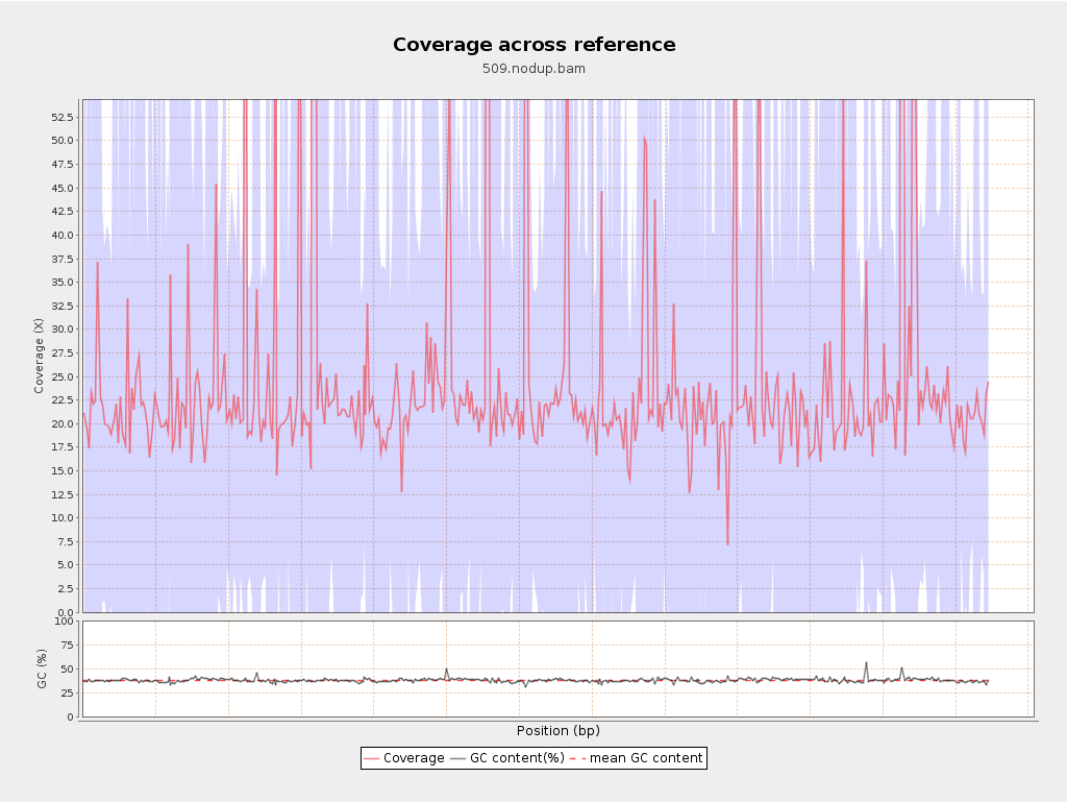
General error rate	2.34%
Mismatches	167,192,560
Insertions	5,926,765
Mapped reads with at least one insertion	9.14%
Deletions	5,592,023
Mapped reads with at least one deletion	8.59%
Homopolymer indels	57.92%

2.7. Chromosome stats

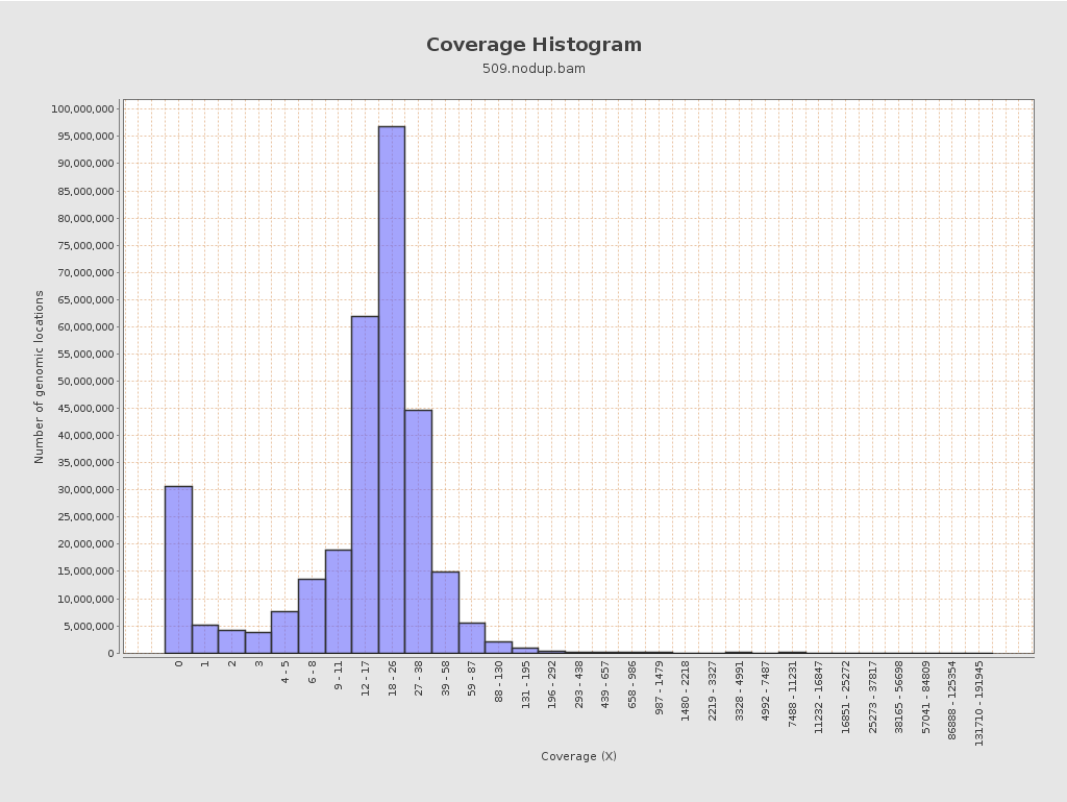
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	641544020	21.5831	107.415

LT669789.1	36598175	916331705	25.0376	259.1698
LT669790.1	30422129	959621964	31.5436	362.0214
LT669791.1	52758100	1306319224	24.7605	264.4866
LT669792.1	28376109	711853329	25.0864	204.7631
LT669793.1	33388210	763794198	22.8762	147.5574
LT669794.1	50579949	1161290906	22.9595	176.8112
LT669795.1	49795044	1417449606	28.4657	271.1843

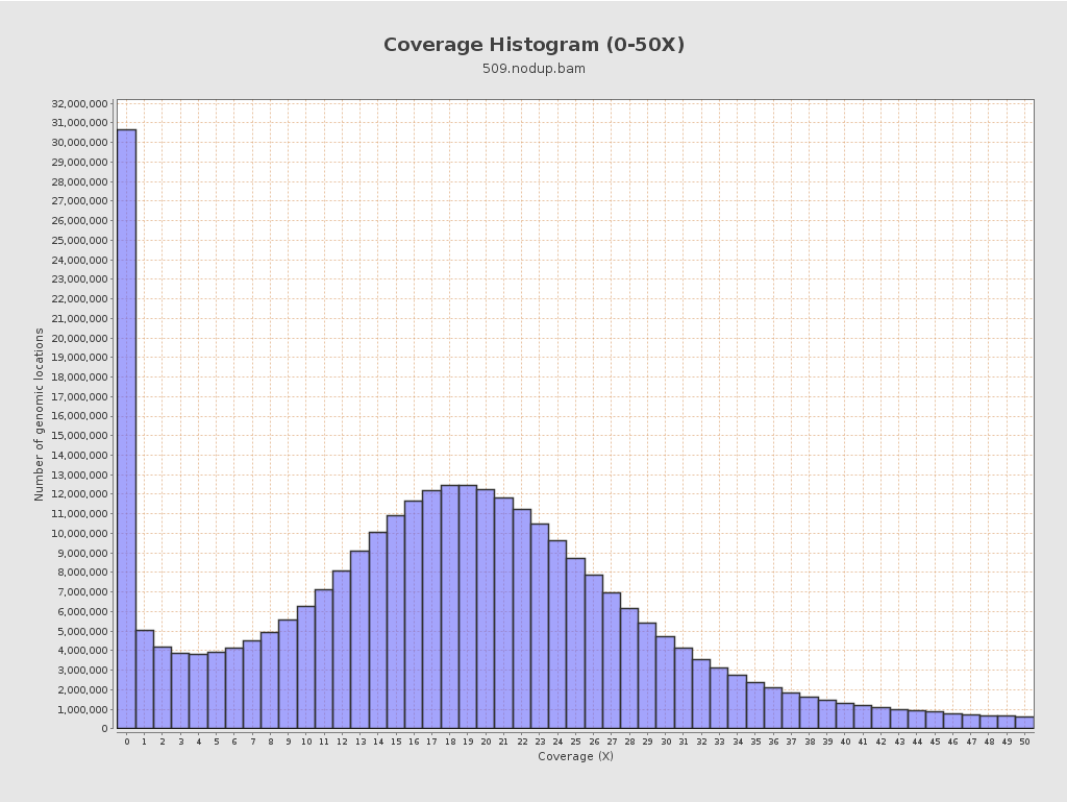
3. Results : Coverage across reference



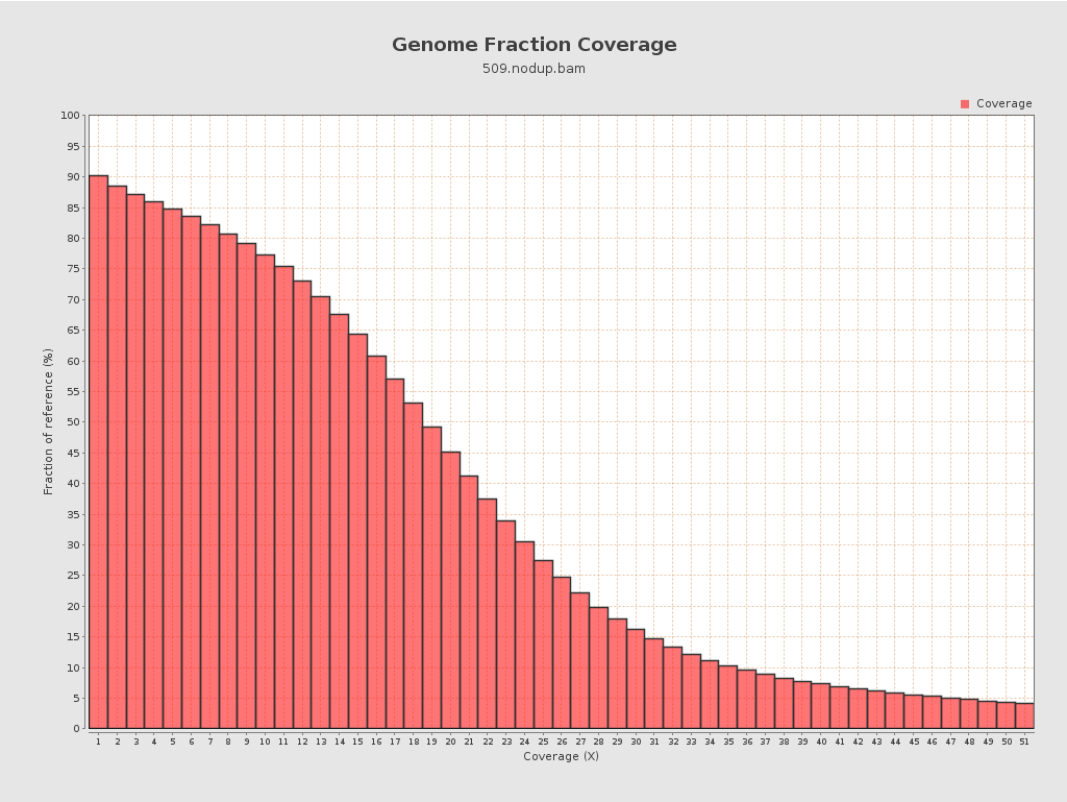
4. Results : Coverage Histogram



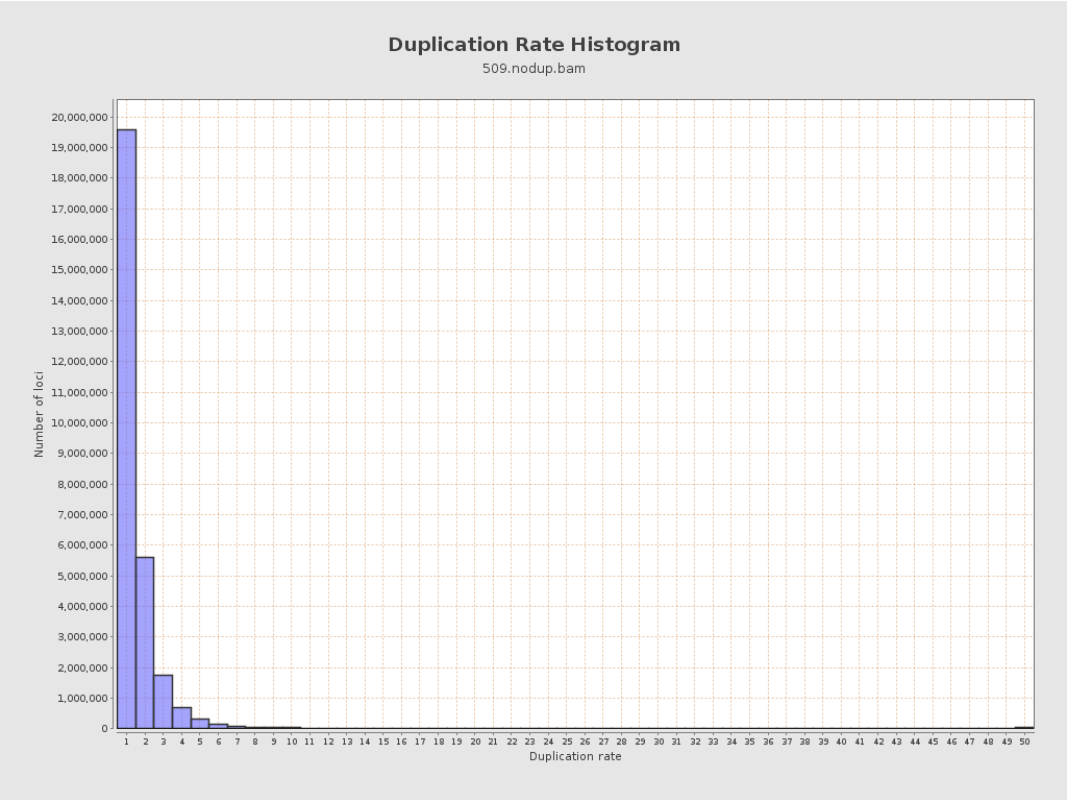
5. Results : Coverage Histogram (0-50X)



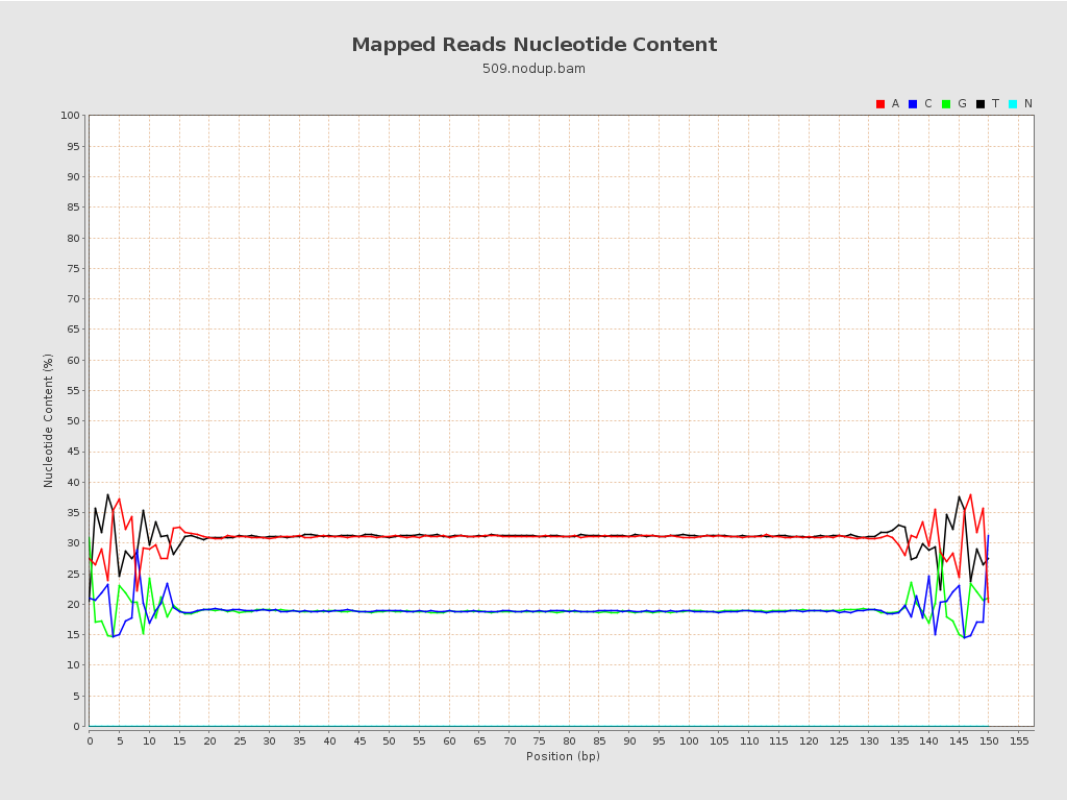
6. Results : Genome Fraction Coverage



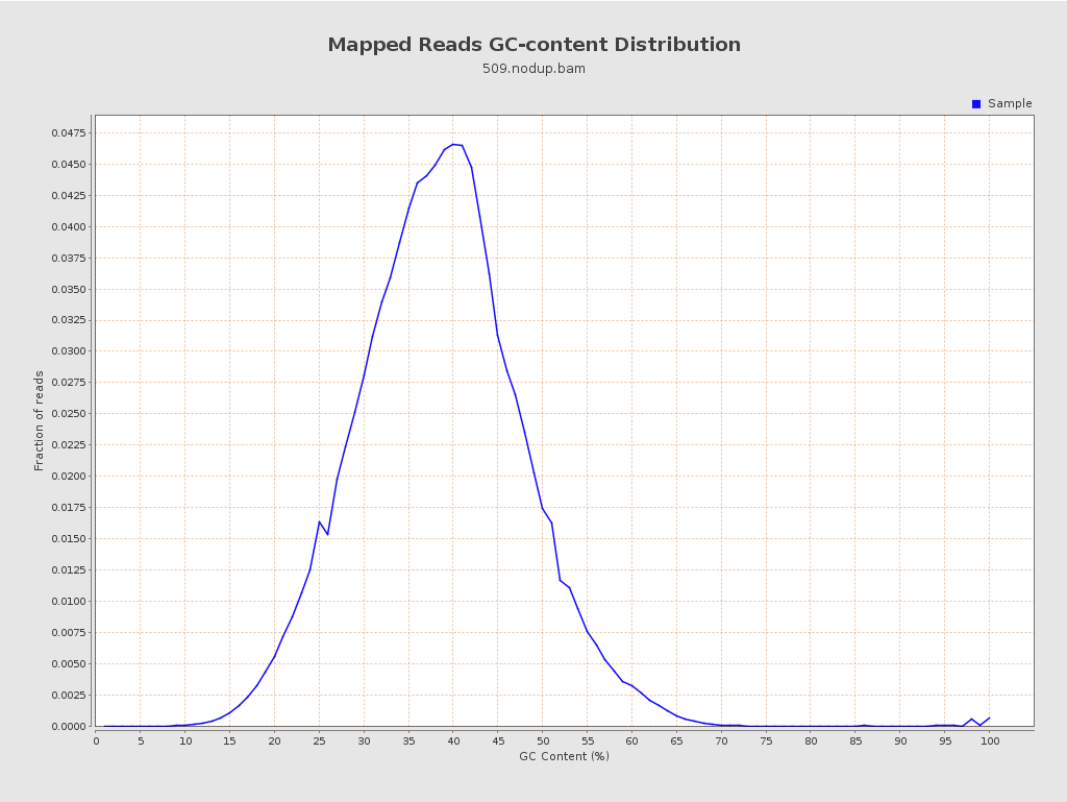
7. Results : Duplication Rate Histogram



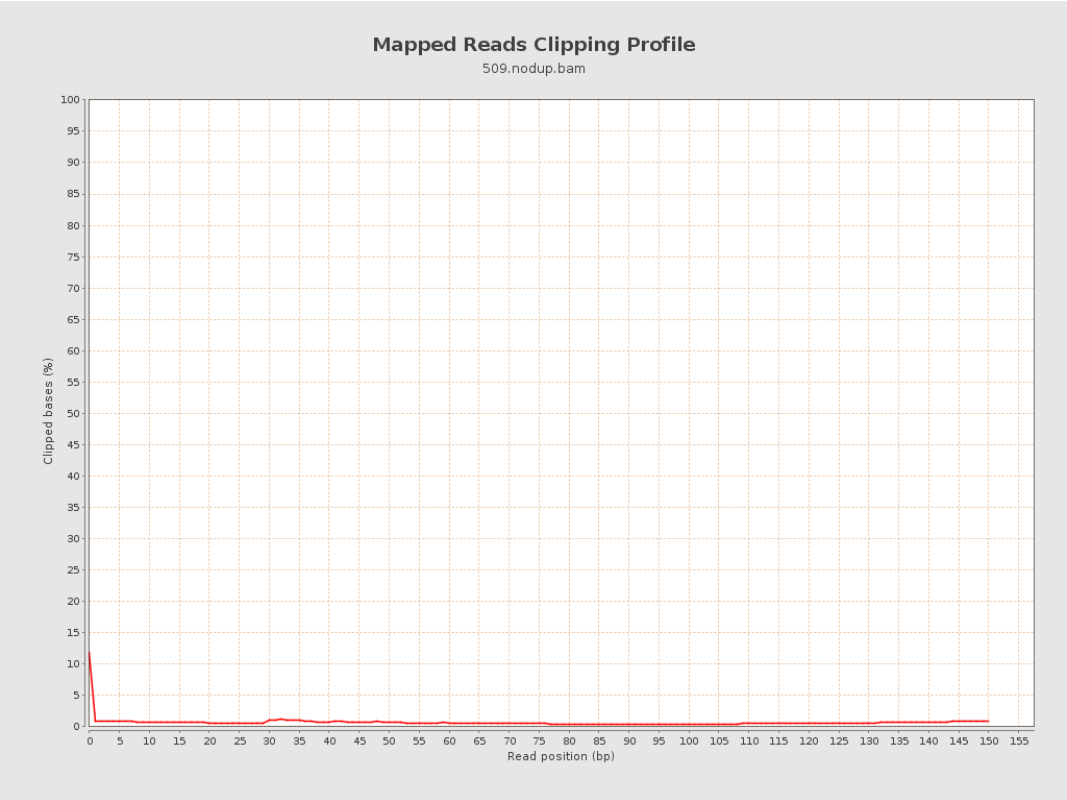
8. Results : Mapped Reads Nucleotide Content



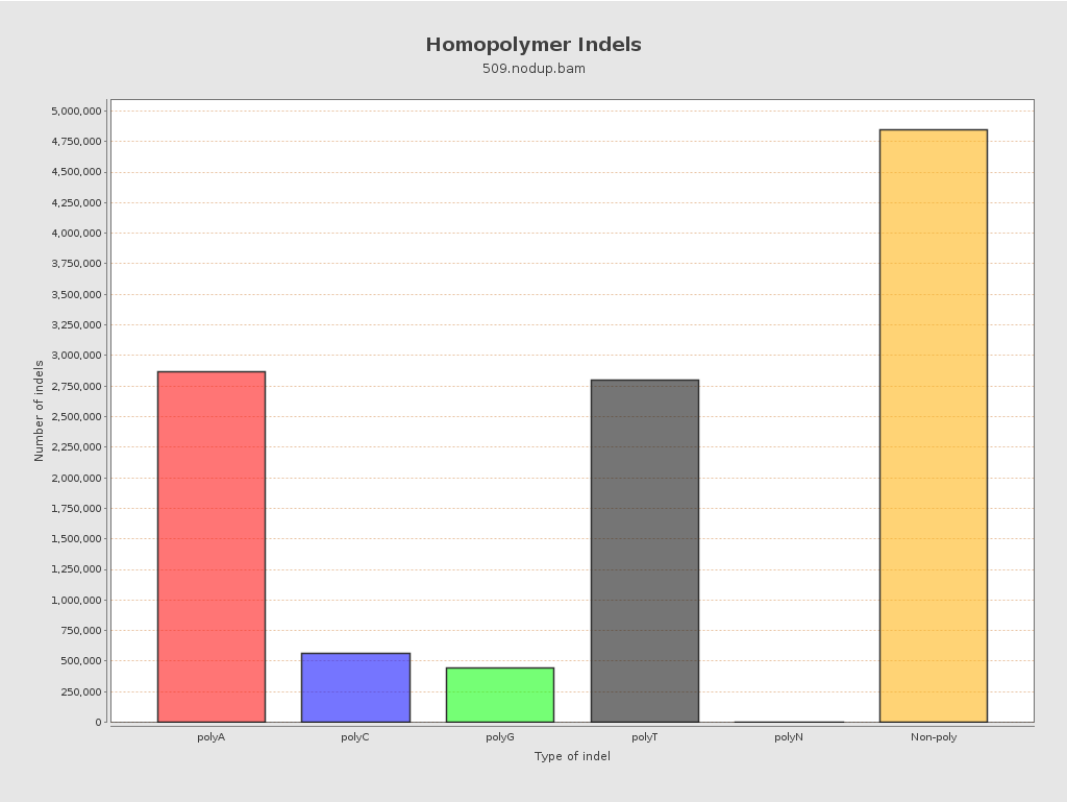
9. Results : Mapped Reads GC-content Distribution



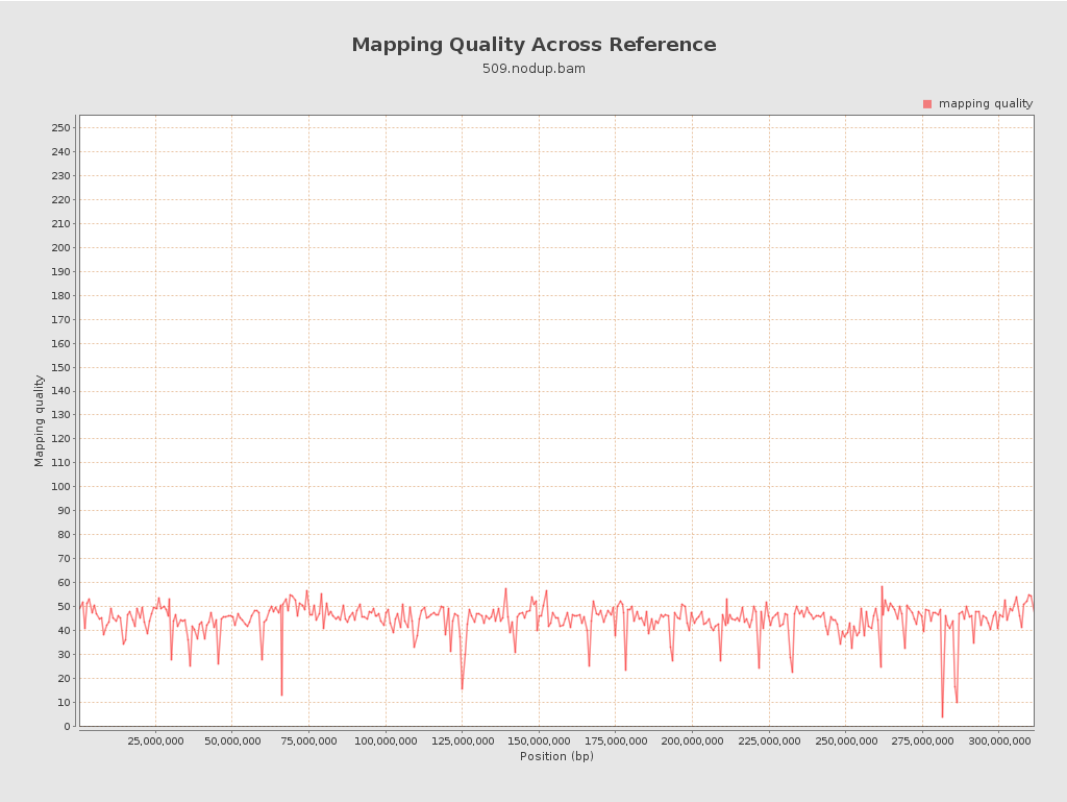
10. Results : Mapped Reads Clipping Profile



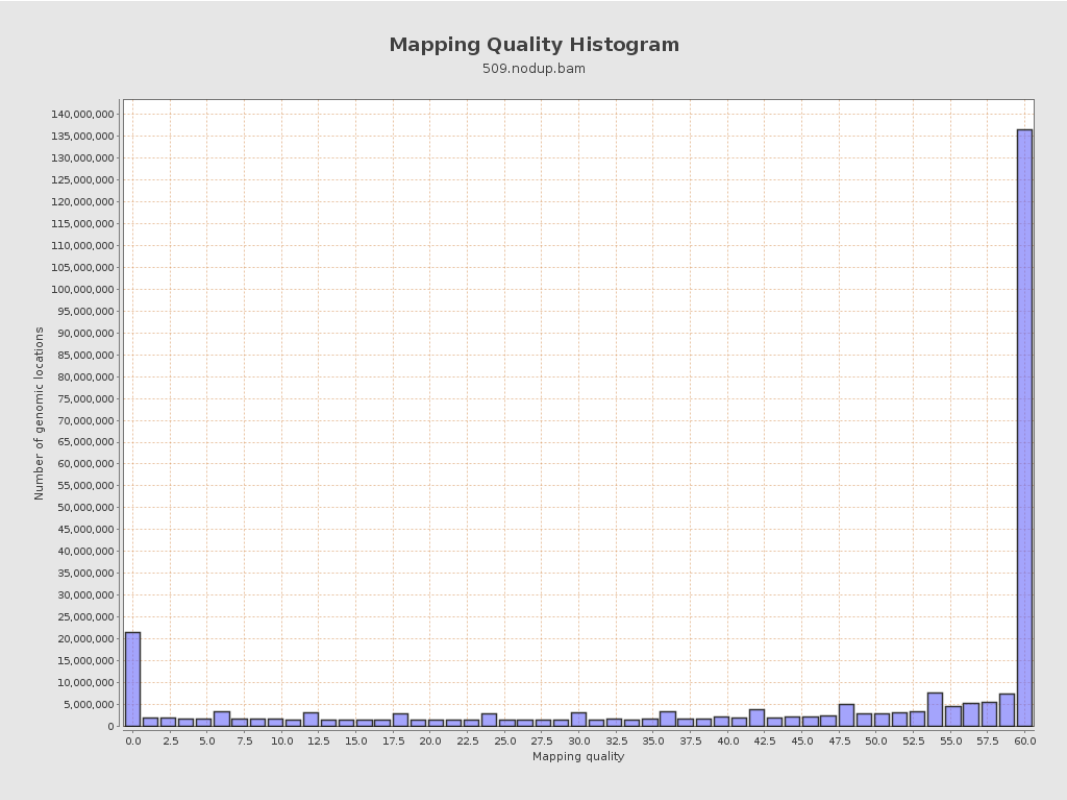
11. Results : Homopolymer Indels



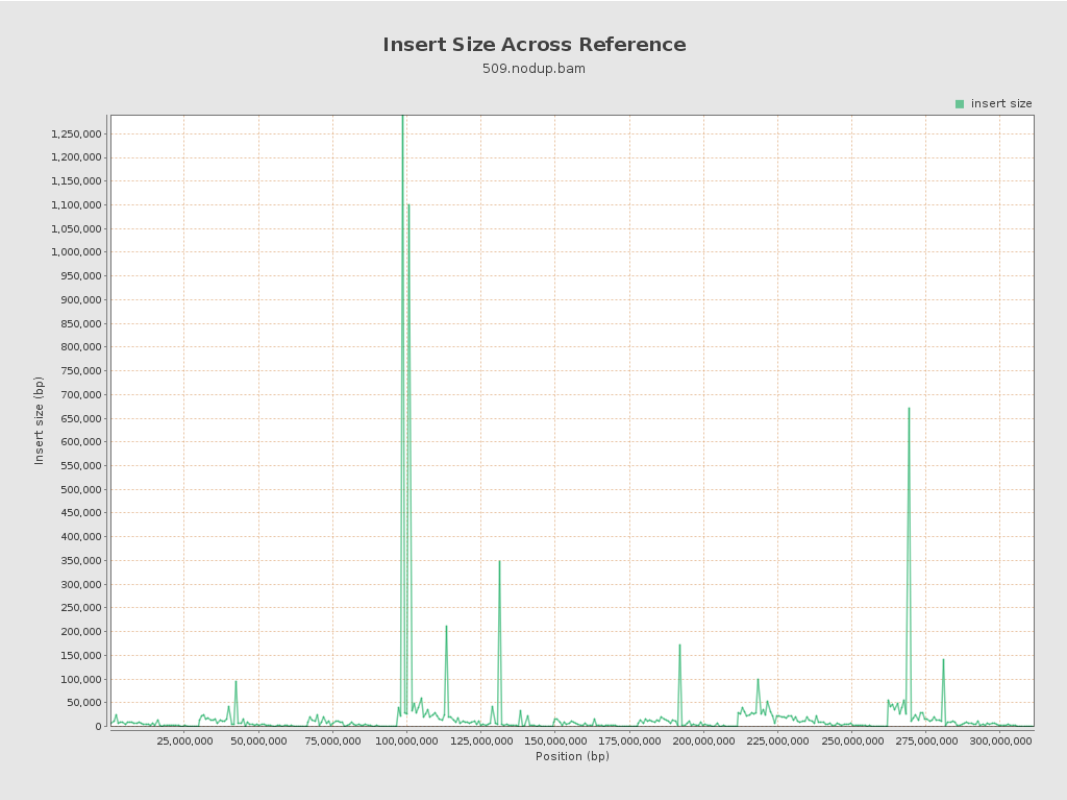
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram