Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/523.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/523.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_247/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_247_S328_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_247/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_247_S328_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:23 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,406,143
Mapped reads	79,308,539 / 92.86%
Unmapped reads	6,097,604 / 7.14%
Mapped paired reads	79,308,539 / 92.86%
Mapped reads, first in pair	39,774,705 / 46.57%
Mapped reads, second in pair	39,533,834 / 46.29%
Mapped reads, both in pair	77,256,795 / 90.46%
Mapped reads, singletons	2,051,744 / 2.4%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	12,493,048 / 14.63%
Clipped reads	18,854,168 / 22.08%

2.2. ACGT Content

Number/percentage of A's	3,376,581,223 / 30.97%
Number/percentage of C's	2,073,422,161 / 19.02%
Number/percentage of T's	3,381,762,828 / 31.02%
Number/percentage of G's	2,071,006,876 / 19%
Number/percentage of N's	41,963 / 0%
GC Percentage	38.01%

2.3. Coverage

Mean	35.0751
Standard Deviation	291.8645

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Insert size

Mean	242,516.87
Standard Deviation	2,362,284.33
P25/Median/P75	316 / 418 / 548

2.6. Mismatches and indels

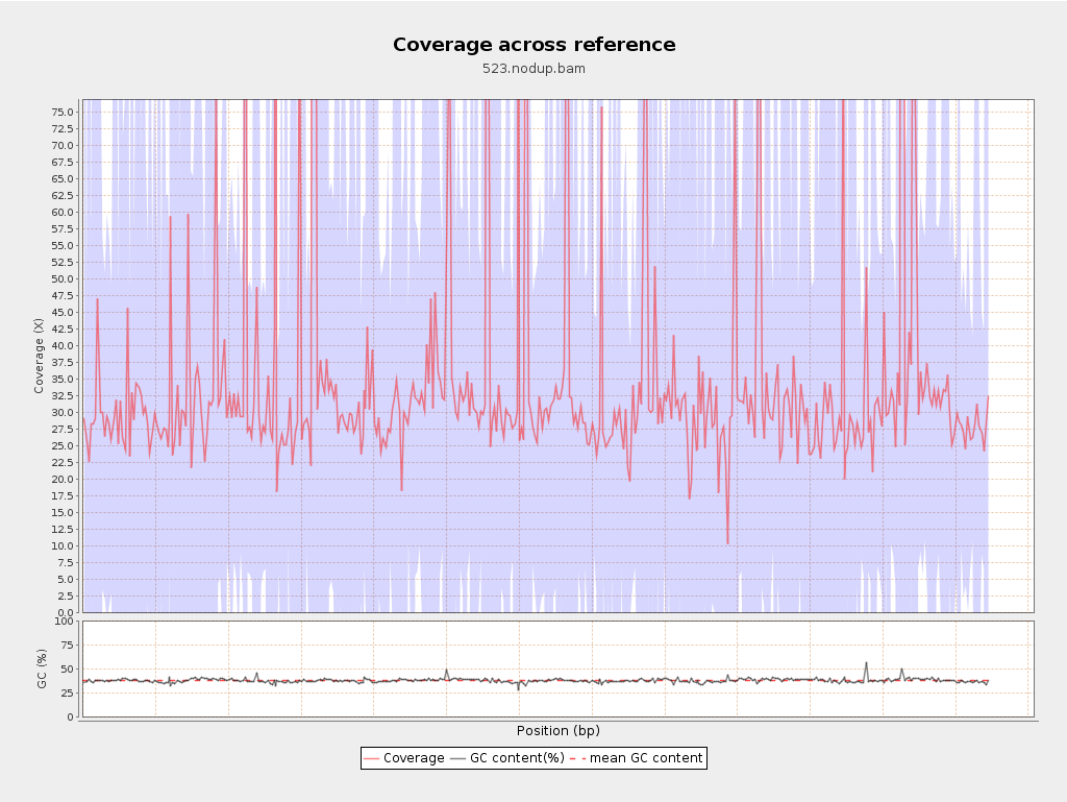
General error rate	2.35%
Mismatches	235,499,951
Insertions	7,681,732
Mapped reads with at least one insertion	8.67%
Deletions	7,530,330
Mapped reads with at least one deletion	8.41%
Homopolymer indels	57.04%

2.7. Chromosome stats

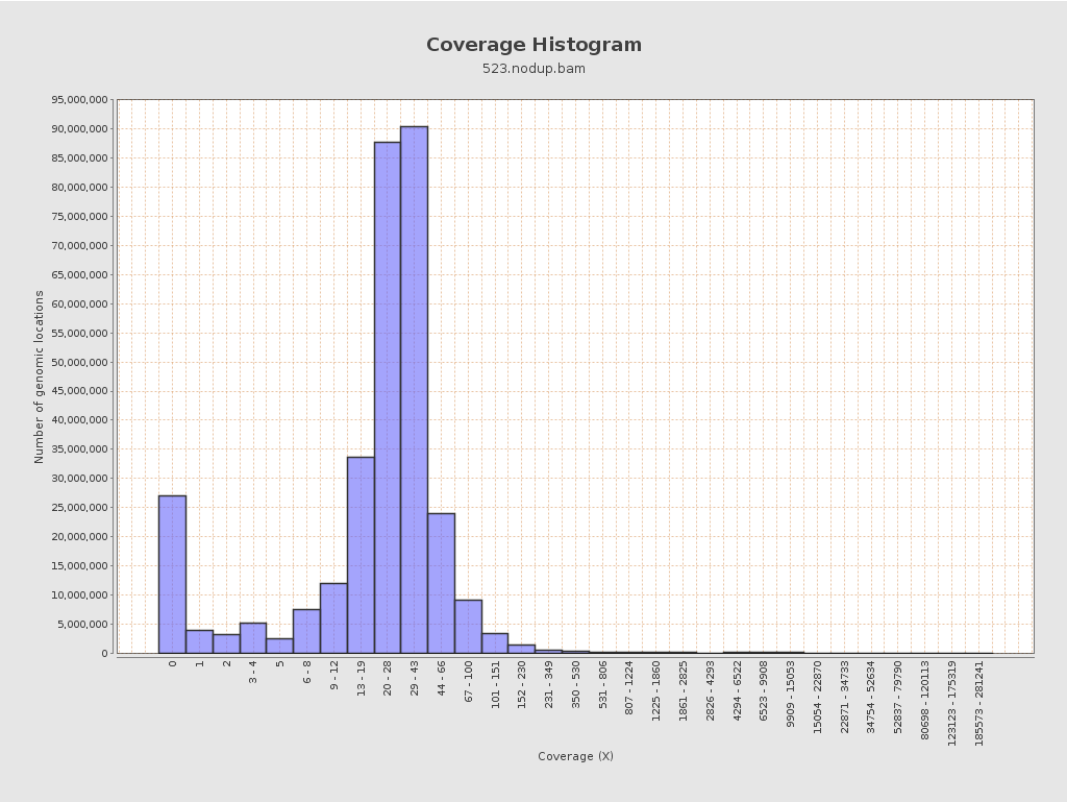
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	868815804	29.2291	104.4183

LT669789.1	36598175	1294491680	35.3704	307.6098
LT669790.1	30422129	1238114839	40.6978	378.6523
LT669791.1	52758100	1823377431	34.5611	284.1104
LT669792.1	28376109	999528304	35.2243	322.9815
LT669793.1	33388210	1088456058	32.6	207.2007
LT669794.1	50579949	1663175514	32.8821	240.8698
LT669795.1	49795044	1954910231	39.2591	369.7636

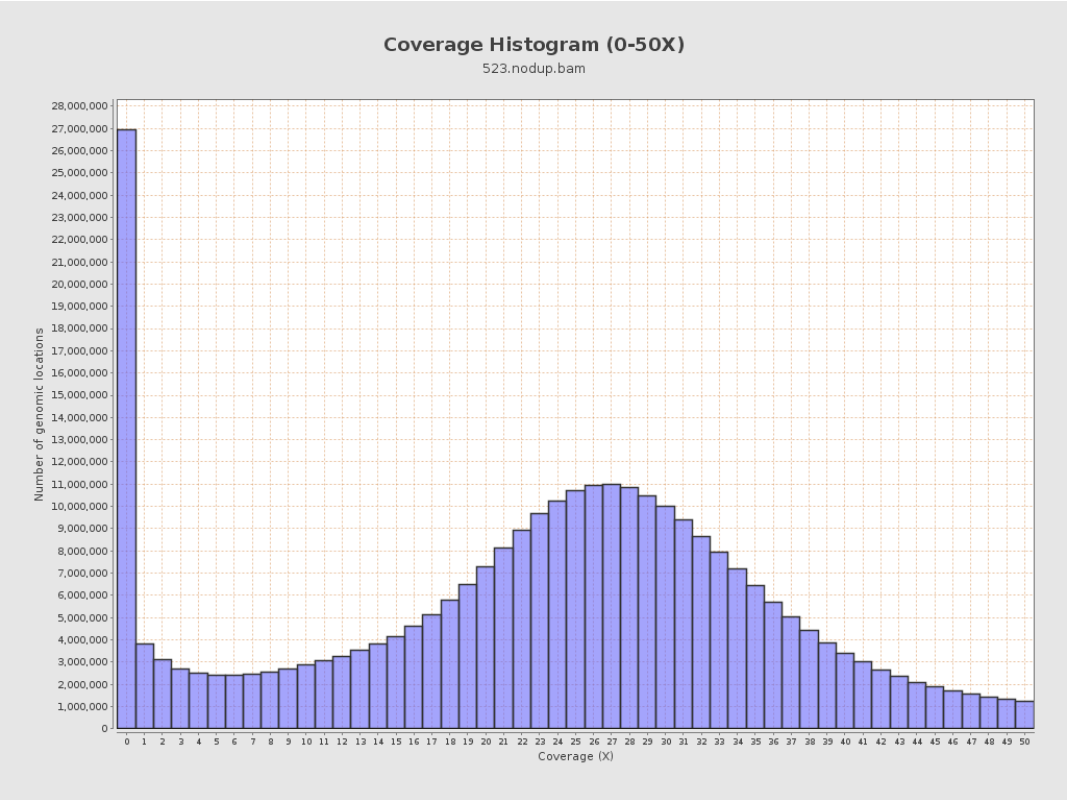
3. Results : Coverage across reference



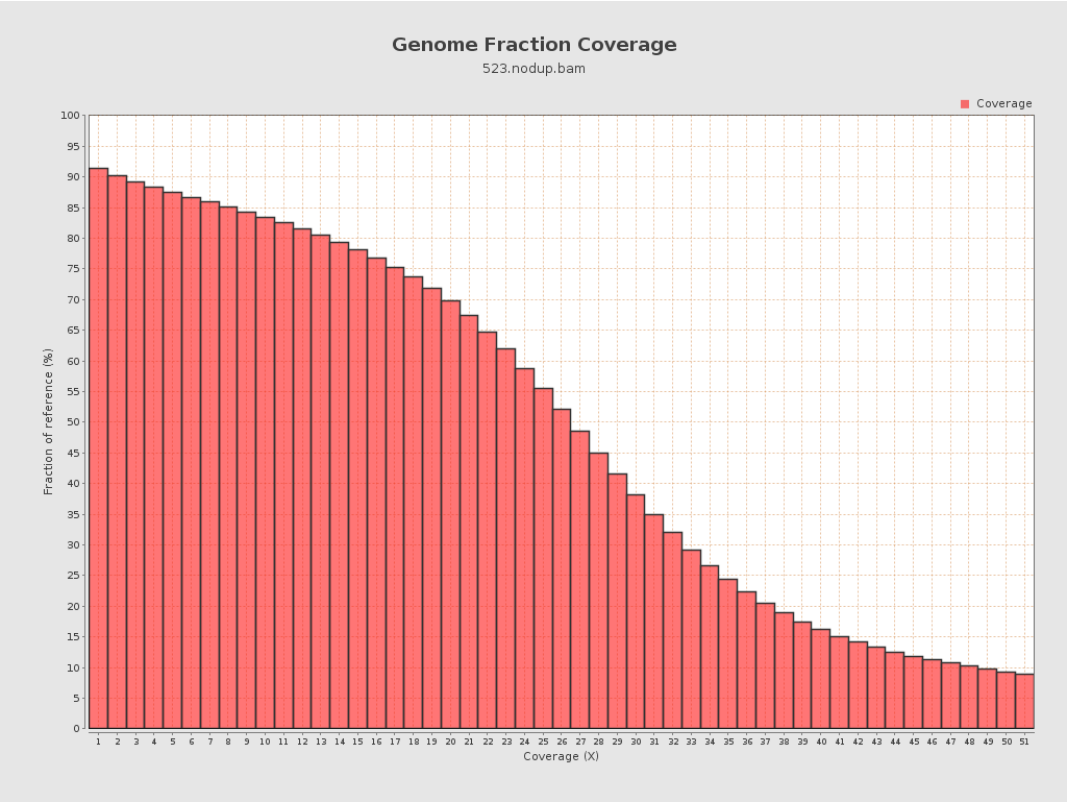
4. Results : Coverage Histogram



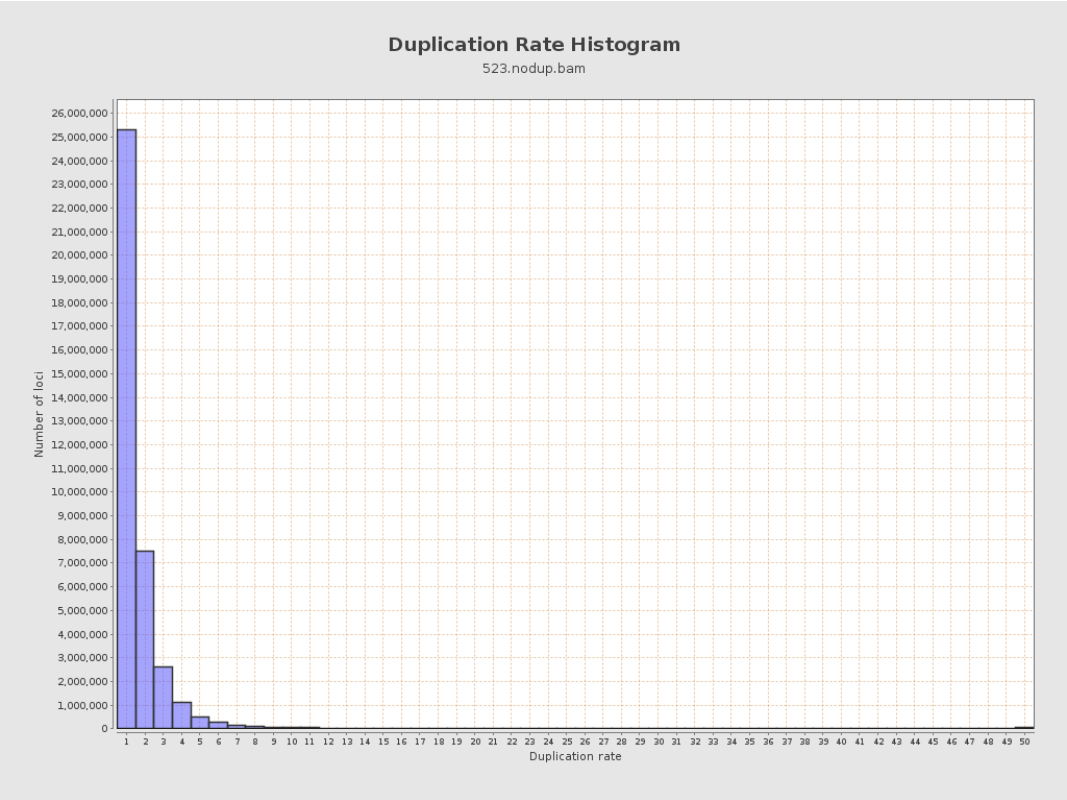
5. Results : Coverage Histogram (0-50X)



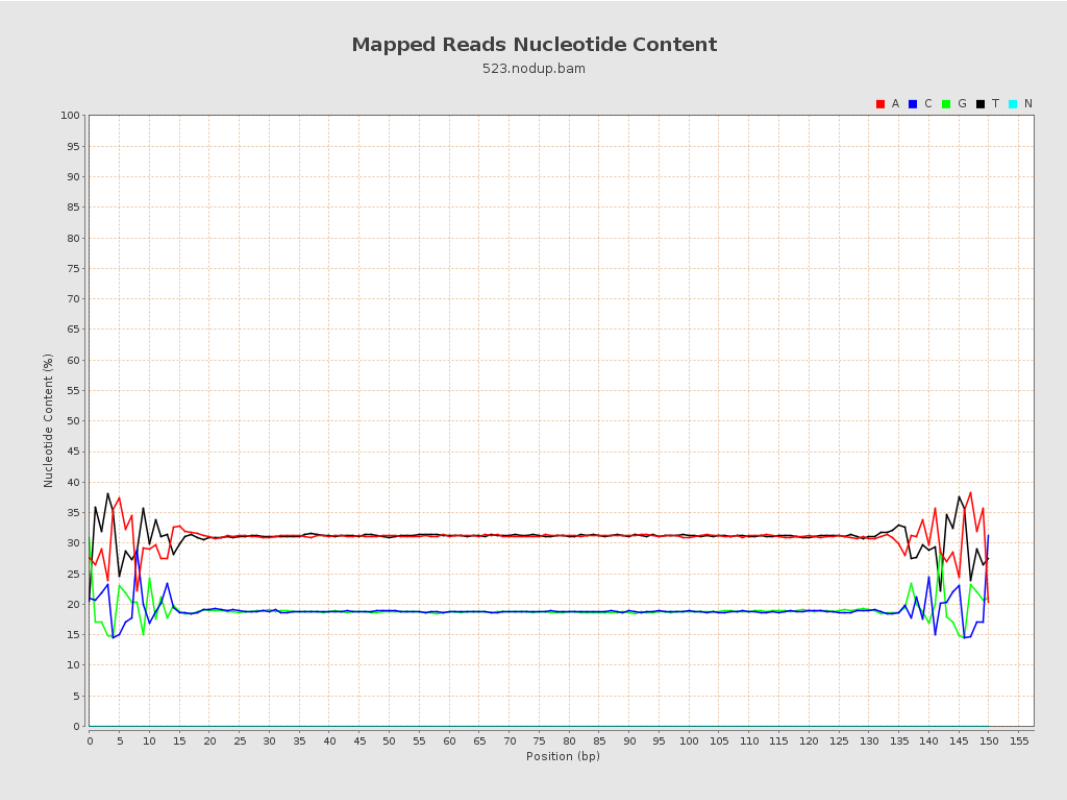
6. Results : Genome Fraction Coverage



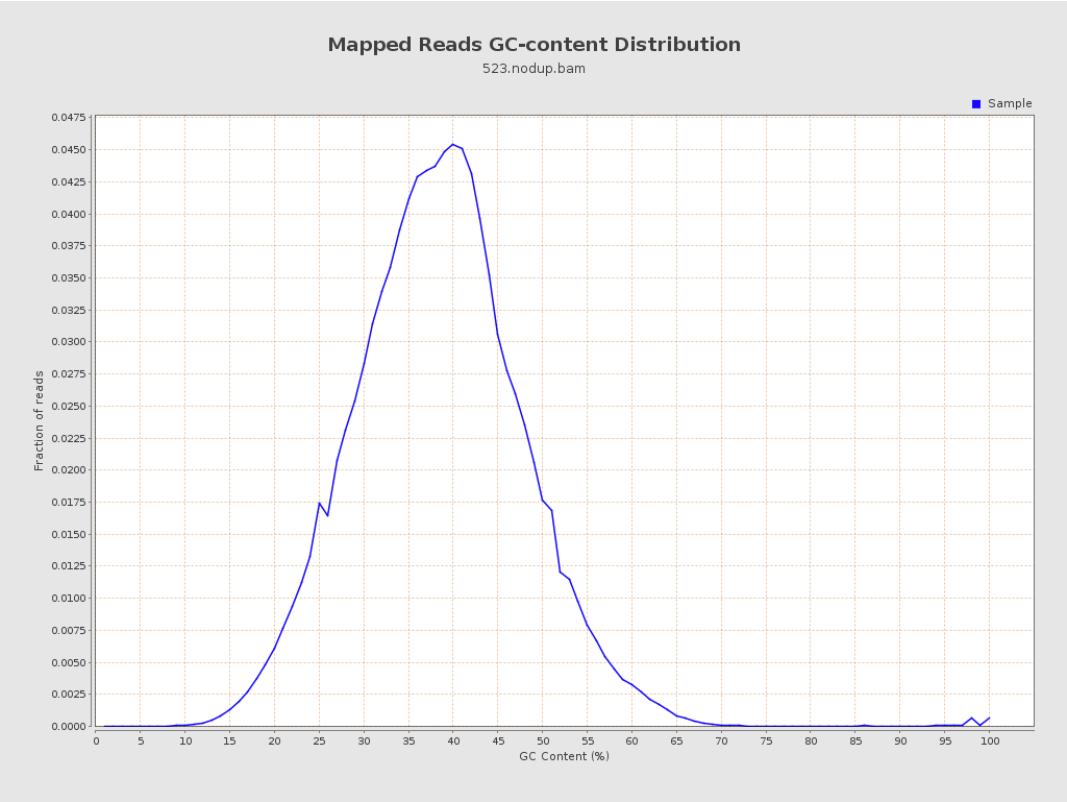
7. Results : Duplication Rate Histogram



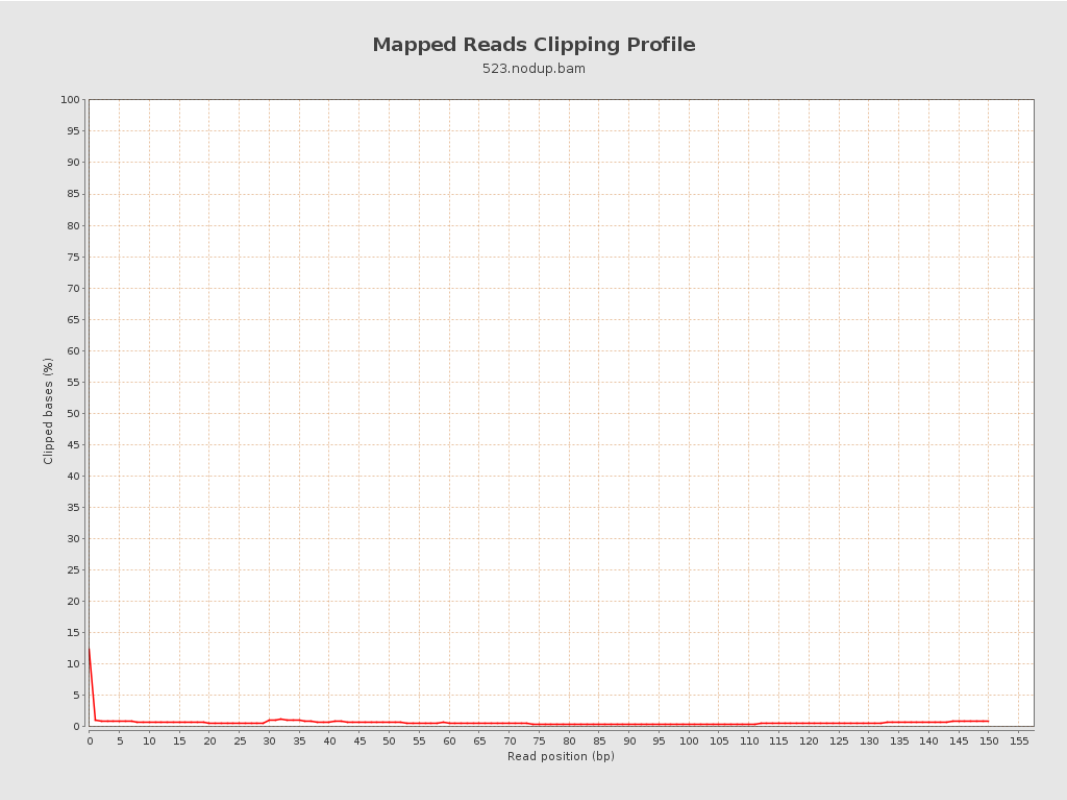
8. Results : Mapped Reads Nucleotide Content



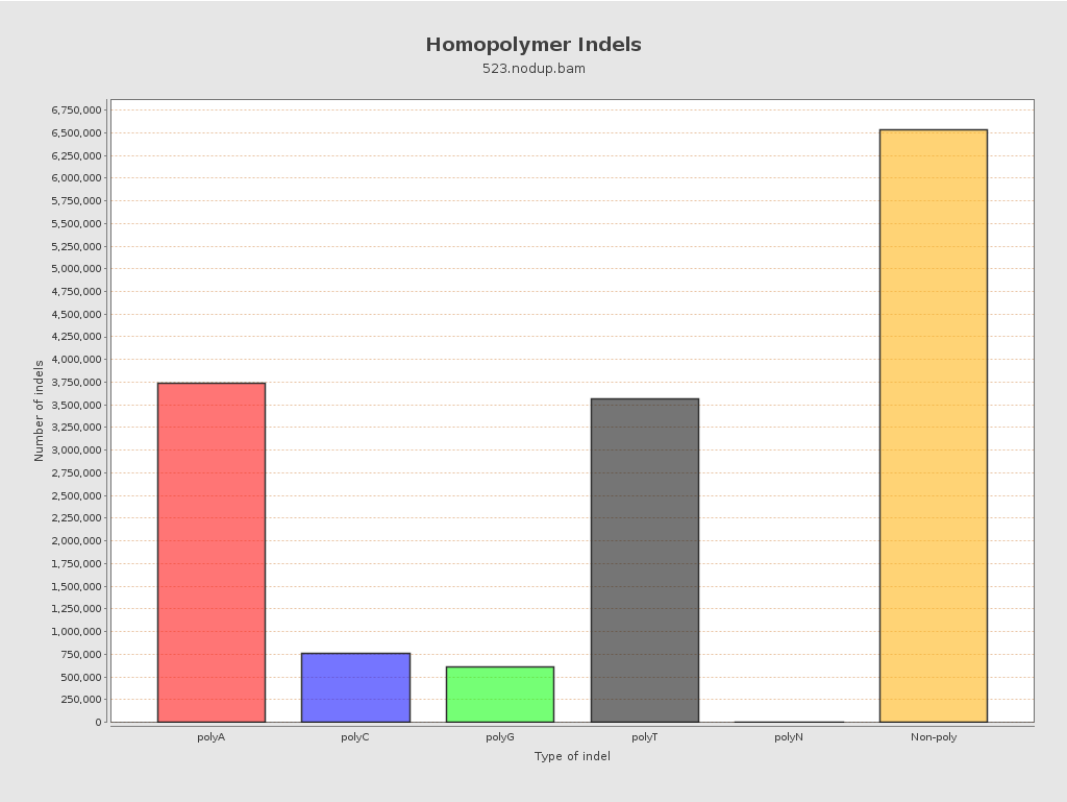
9. Results : Mapped Reads GC-content Distribution



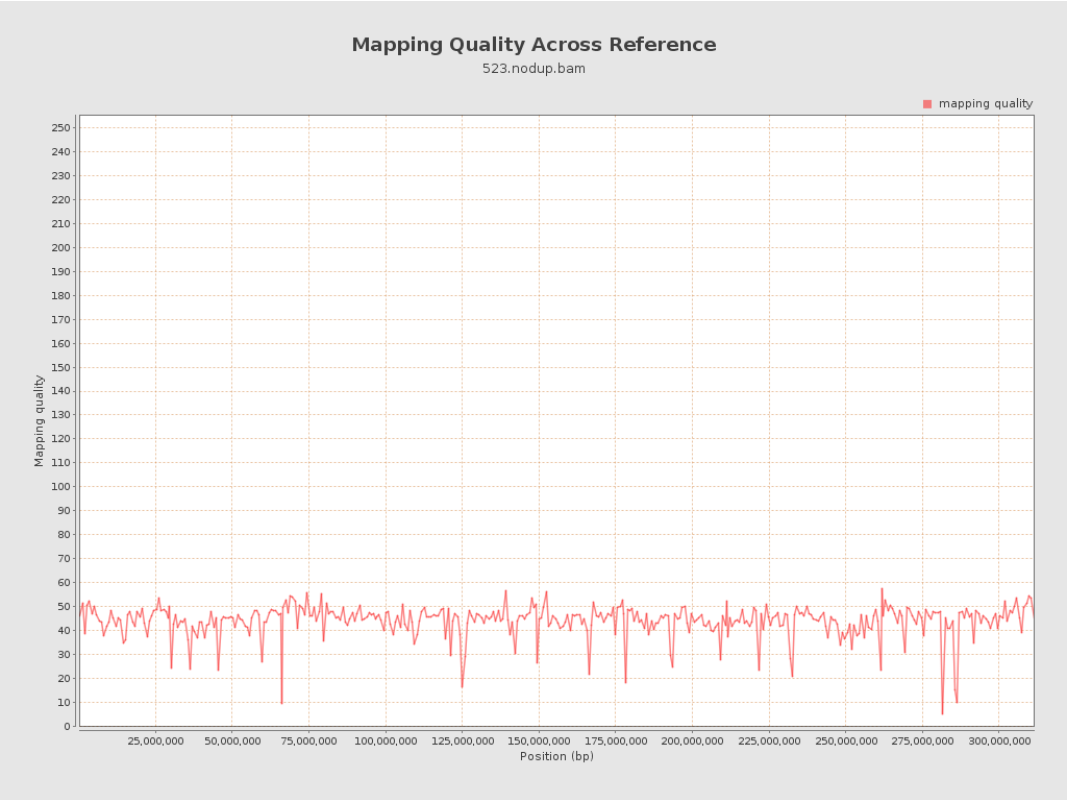
10. Results : Mapped Reads Clipping Profile



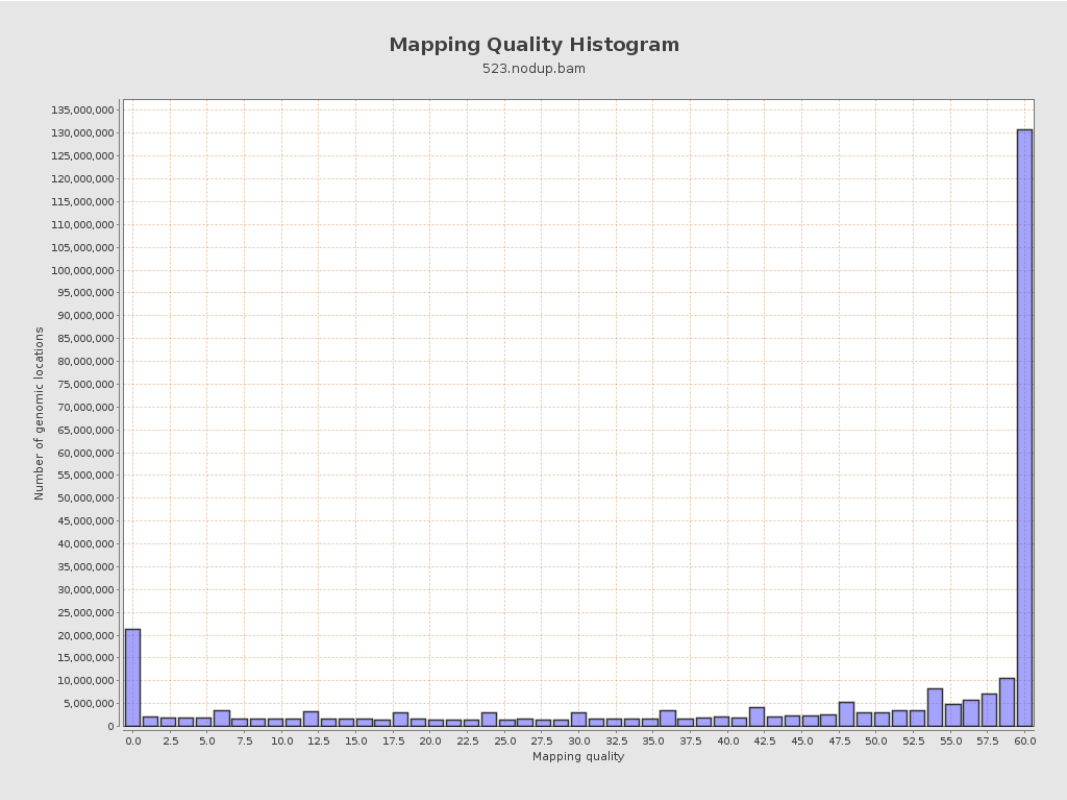
11. Results : Homopolymer Indels



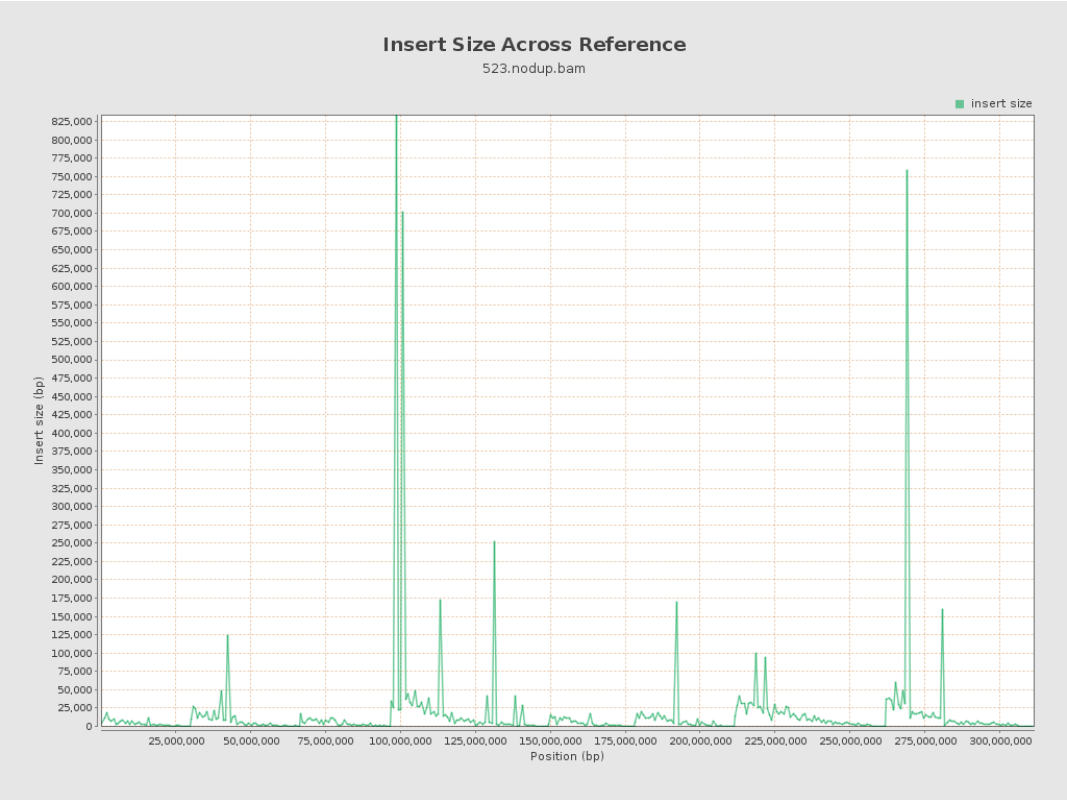
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram