Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/511.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/511.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_422/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_422_S397_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_422/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_422_S397_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:47 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	81,216,483
Mapped reads	75,942,334 / 93.51%
Unmapped reads	5,274,149 / 6.49%
Mapped paired reads	75,942,334 / 93.51%
Mapped reads, first in pair	38,059,395 / 46.86%
Mapped reads, second in pair	37,882,939 / 46.64%
Mapped reads, both in pair	74,079,405 / 91.21%
Mapped reads, singletons	1,862,929 / 2.29%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	13,621,197 / 16.77%
Clipped reads	16,470,557 / 20.28%

2.2. ACGT Content

Number/percentage of A's	3,265,249,739 / 30.94%
Number/percentage of C's	2,014,026,663 / 19.08%
Number/percentage of T's	3,267,774,471 / 30.96%
Number/percentage of G's	2,007,869,101 / 19.02%
Number/percentage of N's	36,011 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	33.9571
Standard Deviation	269.7643

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Insert size

Mean	252,080.57
Standard Deviation	2,400,307.71
P25/Median/P75	368 / 478 / 623

2.6. Mismatches and indels

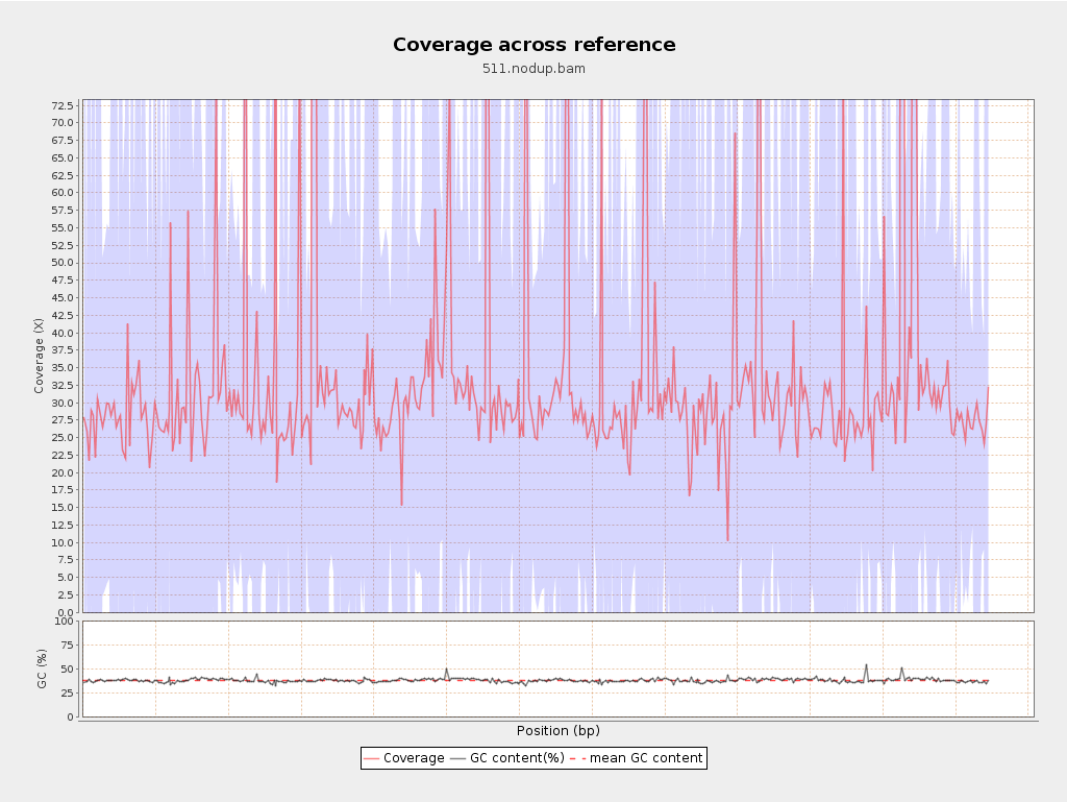
General error rate	2.3%
Mismatches	222,251,836
Insertions	7,212,413
Mapped reads with at least one insertion	8.51%
Deletions	7,227,392
Mapped reads with at least one deletion	8.45%
Homopolymer indels	57.07%

2.7. Chromosome stats

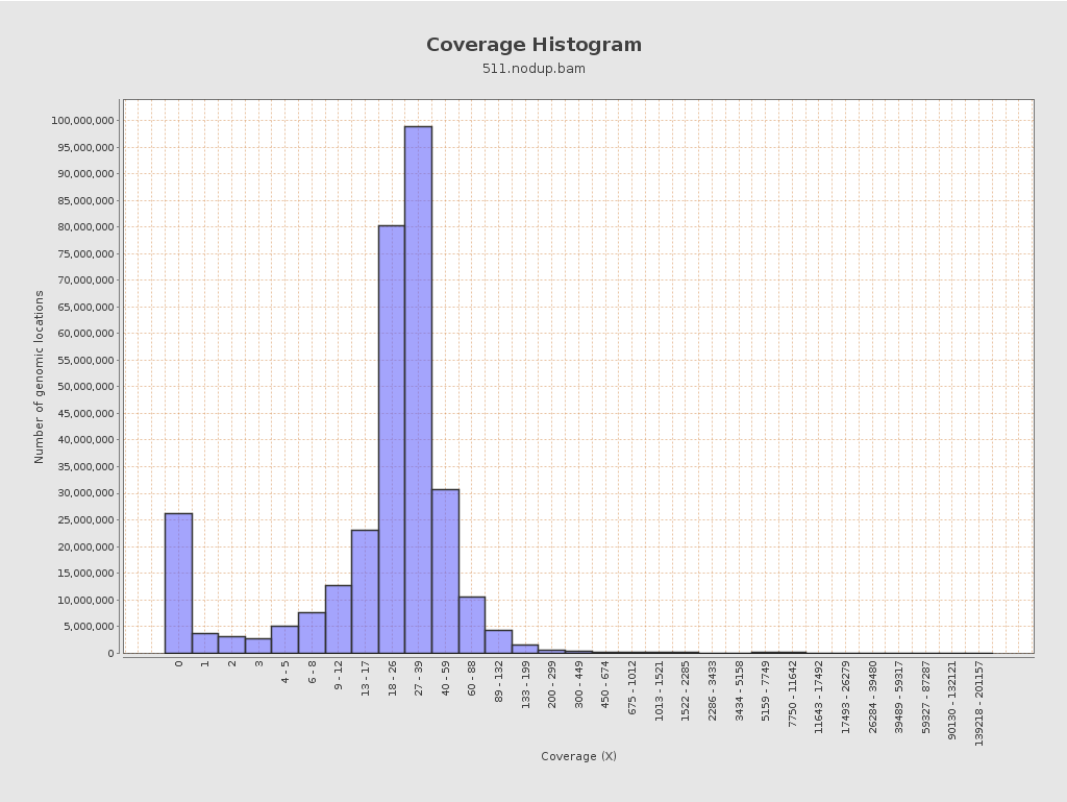
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	828486417	27.8723	85.6376

LT669789.1	36598175	1239586068	33.8702	263.5359
LT669790.1	30422129	1161404235	38.1763	320.4827
LT669791.1	52758100	1769439350	33.5387	240.933
LT669792.1	28376109	952939781	33.5825	299.4419
LT669793.1	33388210	1052246889	31.5155	193.3005
LT669794.1	50579949	1615324562	31.9361	220.7473
LT669795.1	49795044	1963027549	39.4221	387.3676

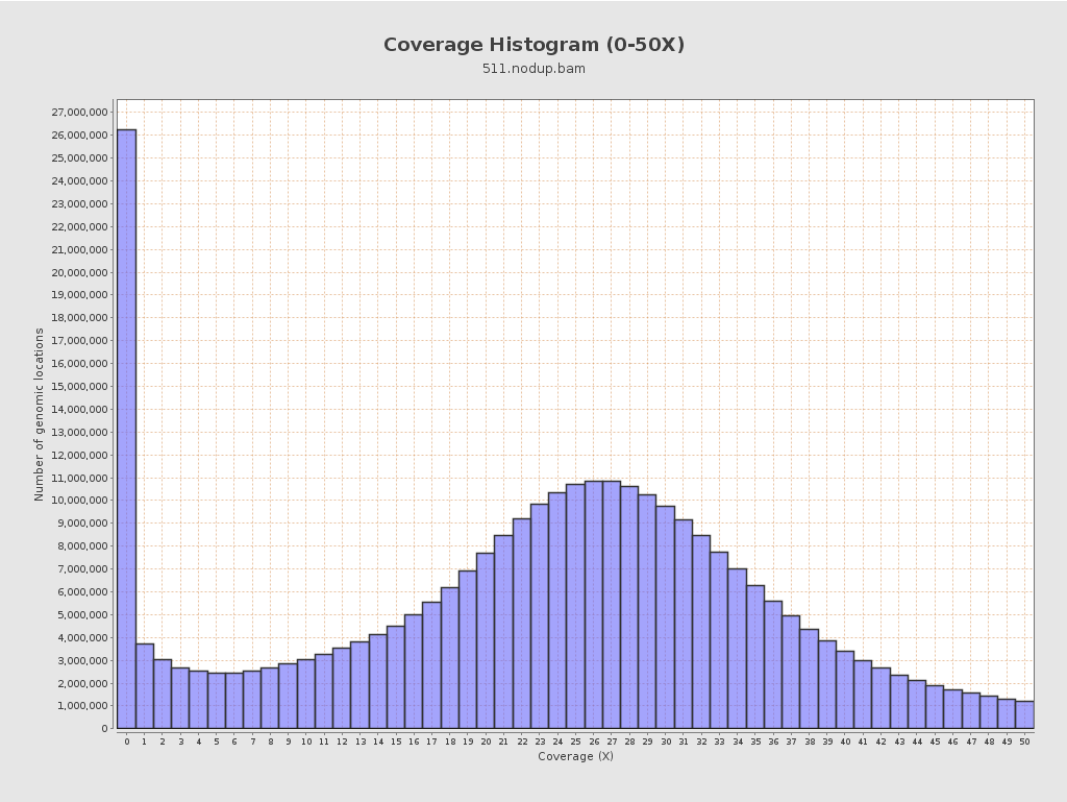
3. Results : Coverage across reference



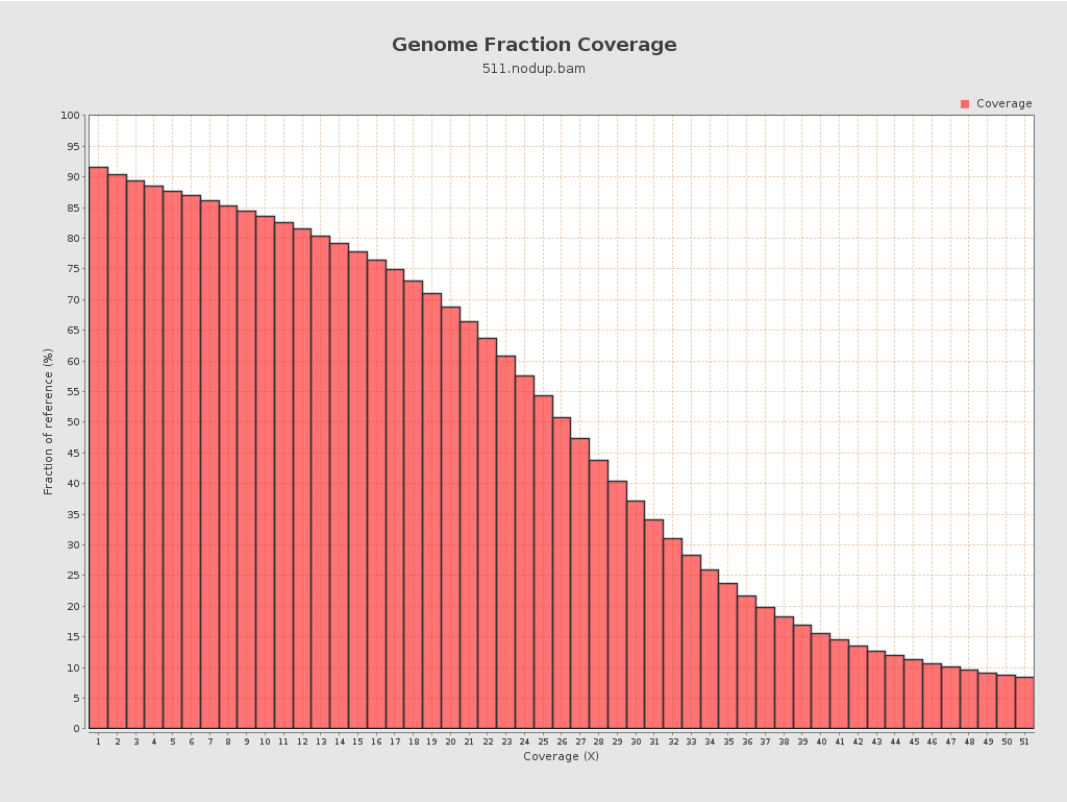
4. Results : Coverage Histogram



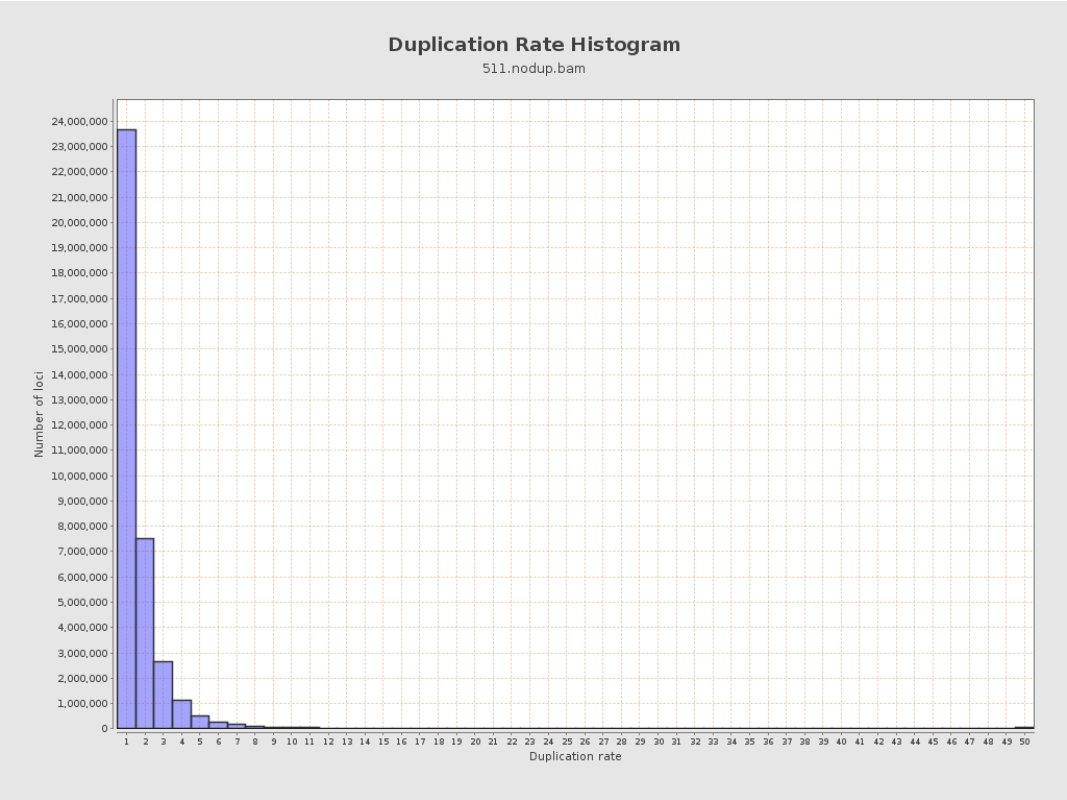
5. Results : Coverage Histogram (0-50X)



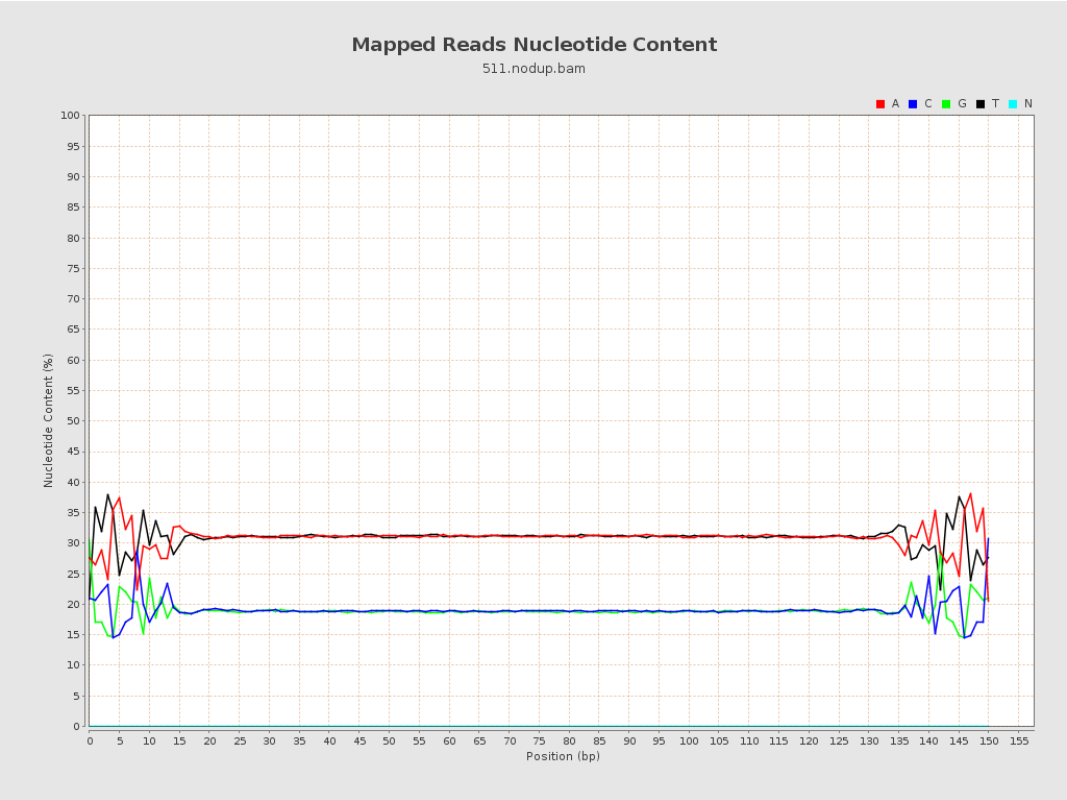
6. Results : Genome Fraction Coverage



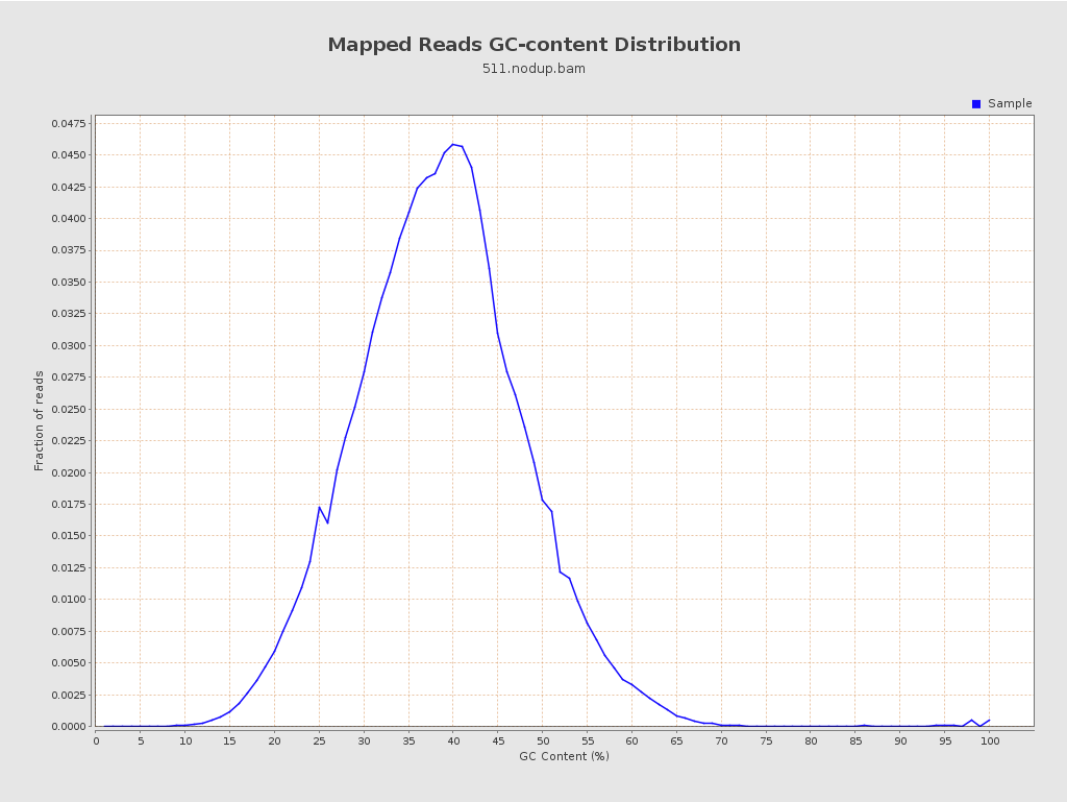
7. Results : Duplication Rate Histogram



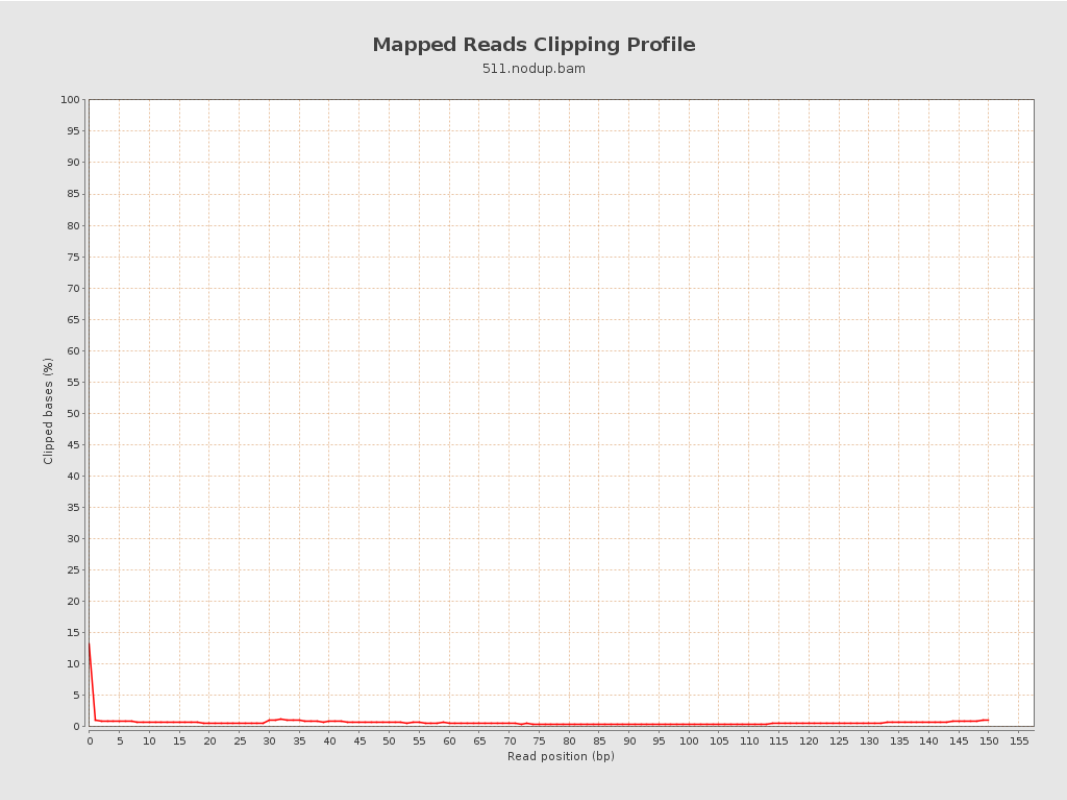
8. Results : Mapped Reads Nucleotide Content



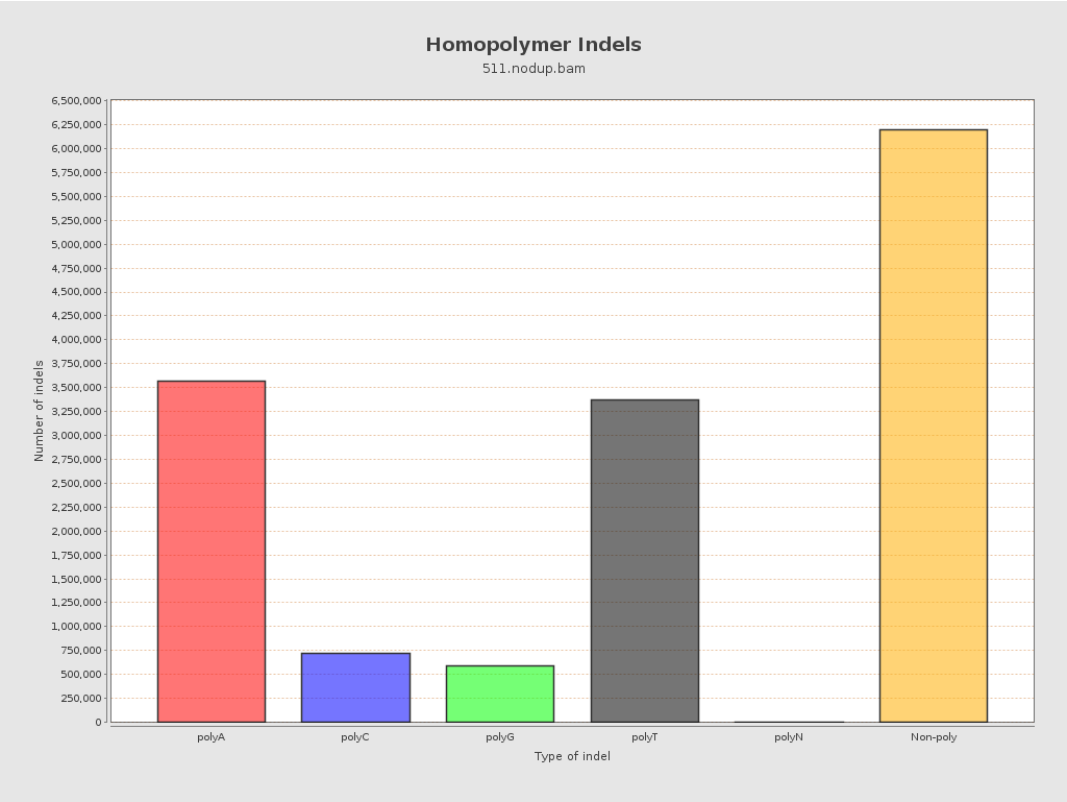
9. Results : Mapped Reads GC-content Distribution



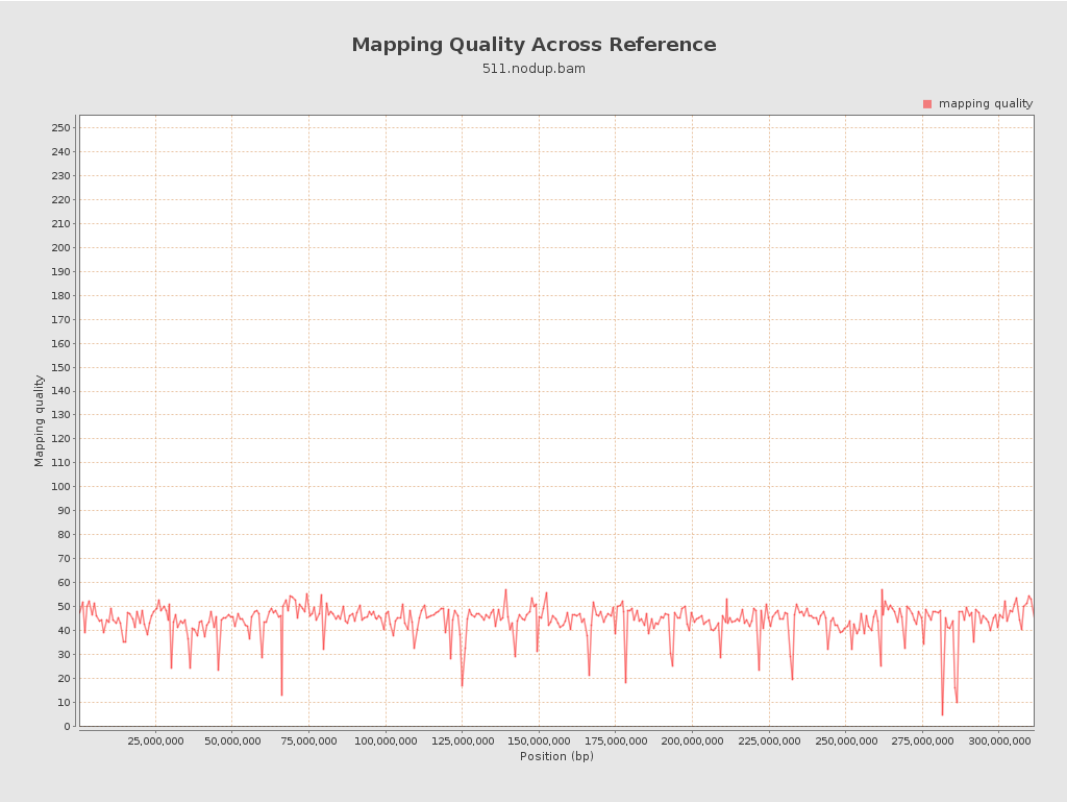
10. Results : Mapped Reads Clipping Profile



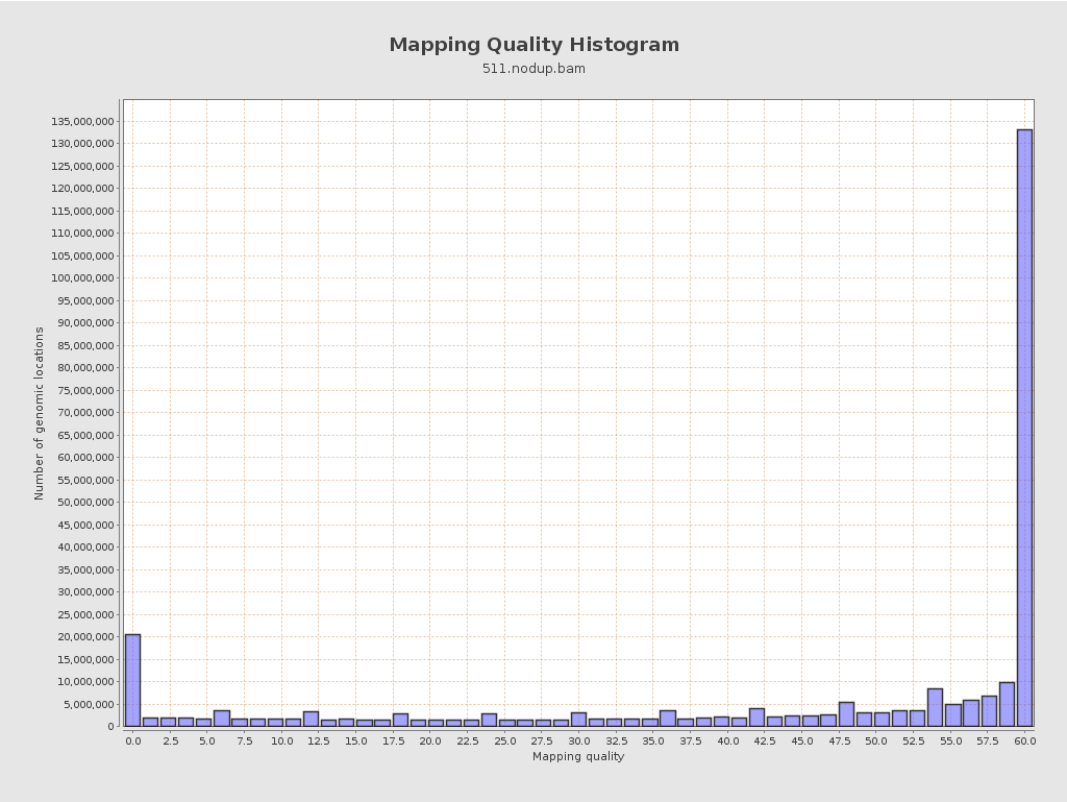
11. Results : Homopolymer Indels



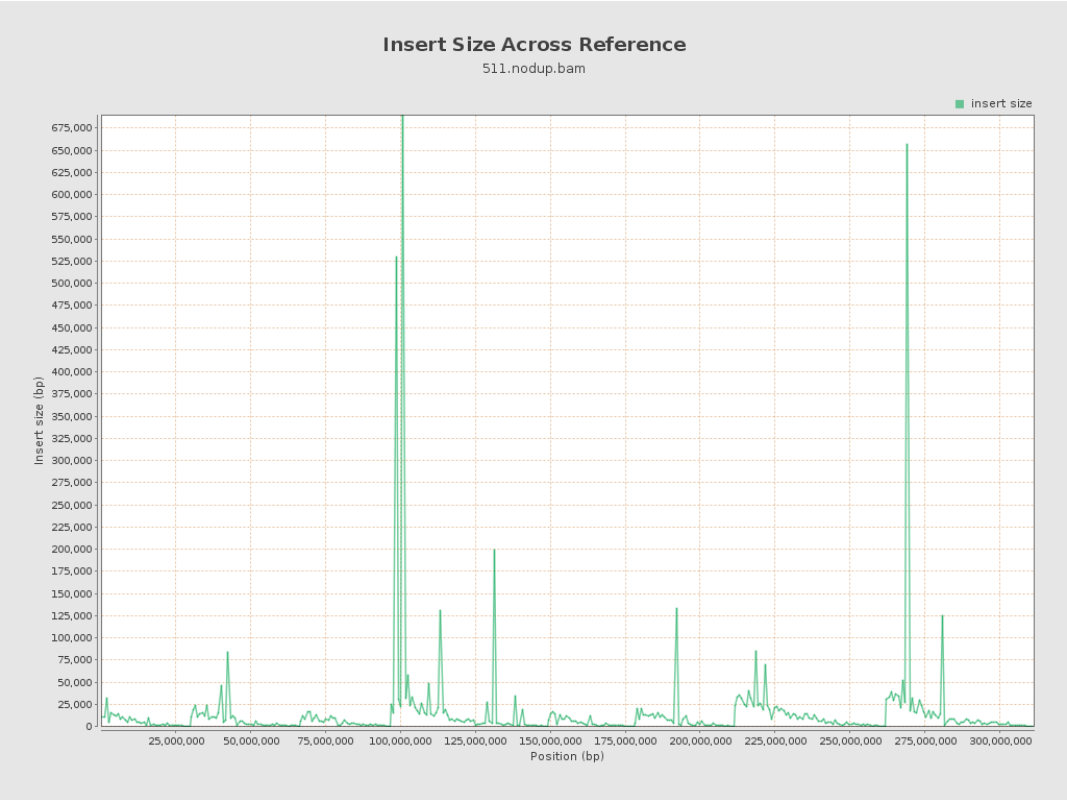
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram