Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/515.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/515.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_419/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_419_S394_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_419/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_419_S394_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:22 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	74,148,208
Mapped reads	68,427,708 / 92.29%
Unmapped reads	5,720,500 / 7.71%
Mapped paired reads	68,427,708 / 92.29%
Mapped reads, first in pair	34,248,501 / 46.19%
Mapped reads, second in pair	34,179,207 / 46.1%
Mapped reads, both in pair	66,558,830 / 89.76%
Mapped reads, singletons	1,868,878 / 2.52%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	11,600,268 / 15.64%
Clipped reads	15,953,115 / 21.52%

2.2. ACGT Content

Number/percentage of A's	2,908,407,436 / 30.85%
Number/percentage of C's	1,806,310,080 / 19.16%
Number/percentage of T's	2,912,985,380 / 30.89%
Number/percentage of G's	1,800,982,027 / 19.1%
Number/percentage of N's	31,915 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	30.3353
Standard Deviation	260.9897

2.4. Mapping Quality

Mean Mapping Quality	43.66

2.5. Insert size

Mean	266,619.19
Standard Deviation	2,471,574.47
P25/Median/P75	358 / 470 / 615

2.6. Mismatches and indels

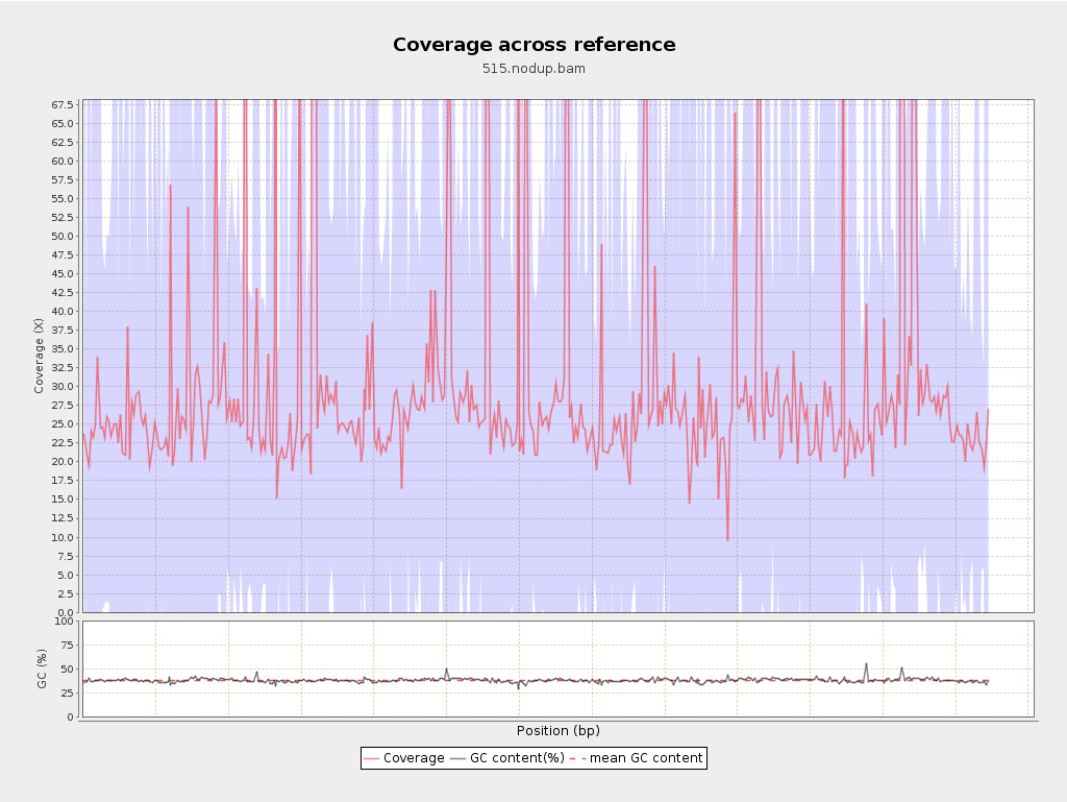
General error rate	2.39%
Mismatches	206,881,287
Insertions	6,732,098
Mapped reads with at least one insertion	8.8%
Deletions	6,668,654
Mapped reads with at least one deletion	8.62%
Homopolymer indels	56.62%

2.7. Chromosome stats

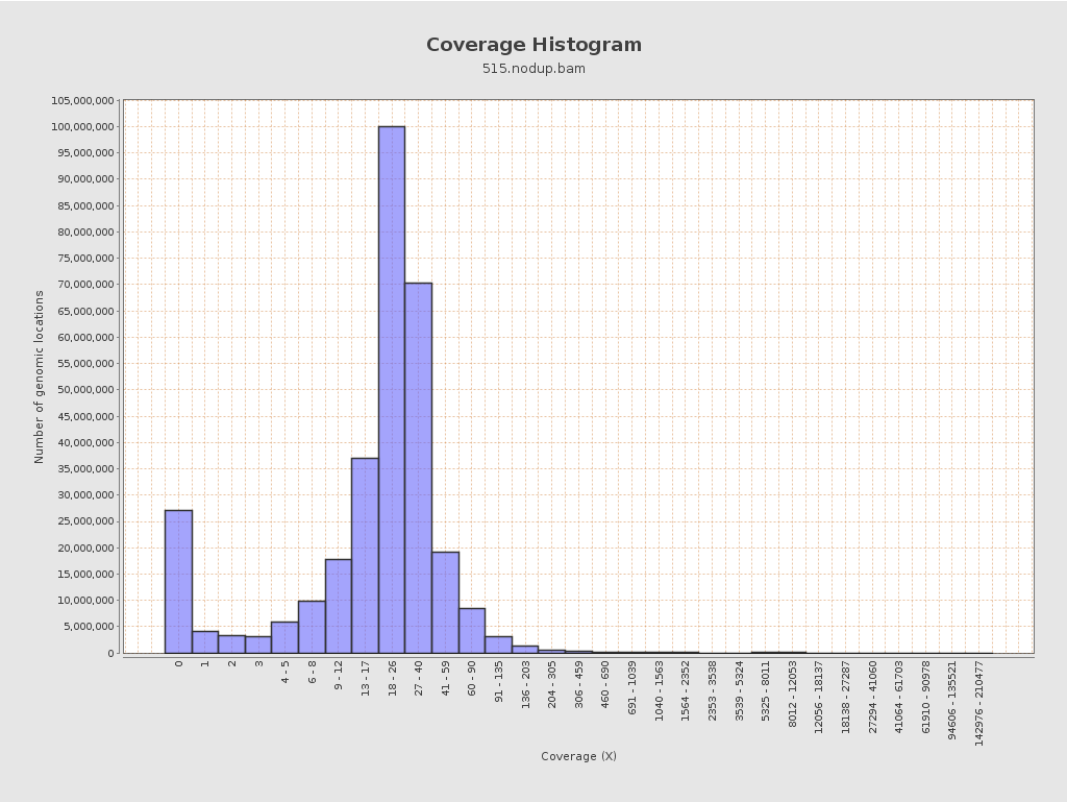
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	726286084	24.434	88.3906

LT669789.1	36598175	1143311077	31.2396	284.7643
LT669790.1	30422129	1035184163	34.0273	311.655
LT669791.1	52758100	1586891567	30.0786	251.3965
LT669792.1	28376109	855714240	30.1562	307.8311
LT669793.1	33388210	930884946	27.8806	177.916
LT669794.1	50579949	1456282282	28.7917	219.9637
LT669795.1	49795044	1719215138	34.5258	333.634

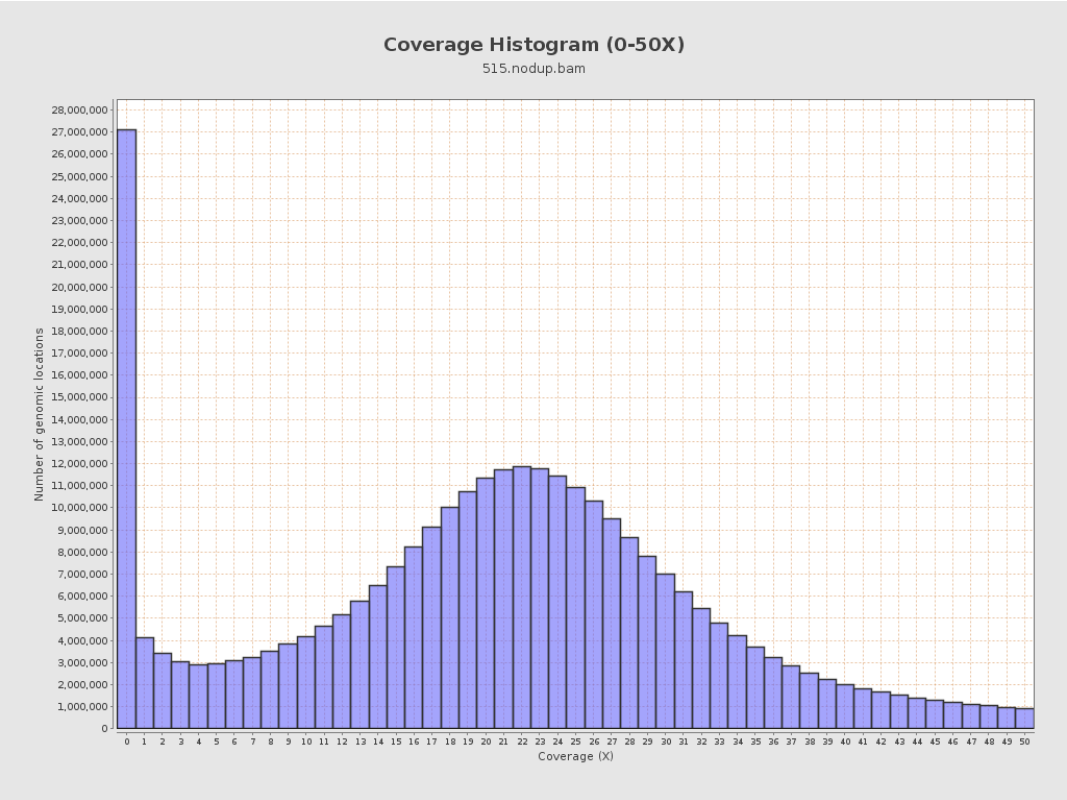
3. Results : Coverage across reference



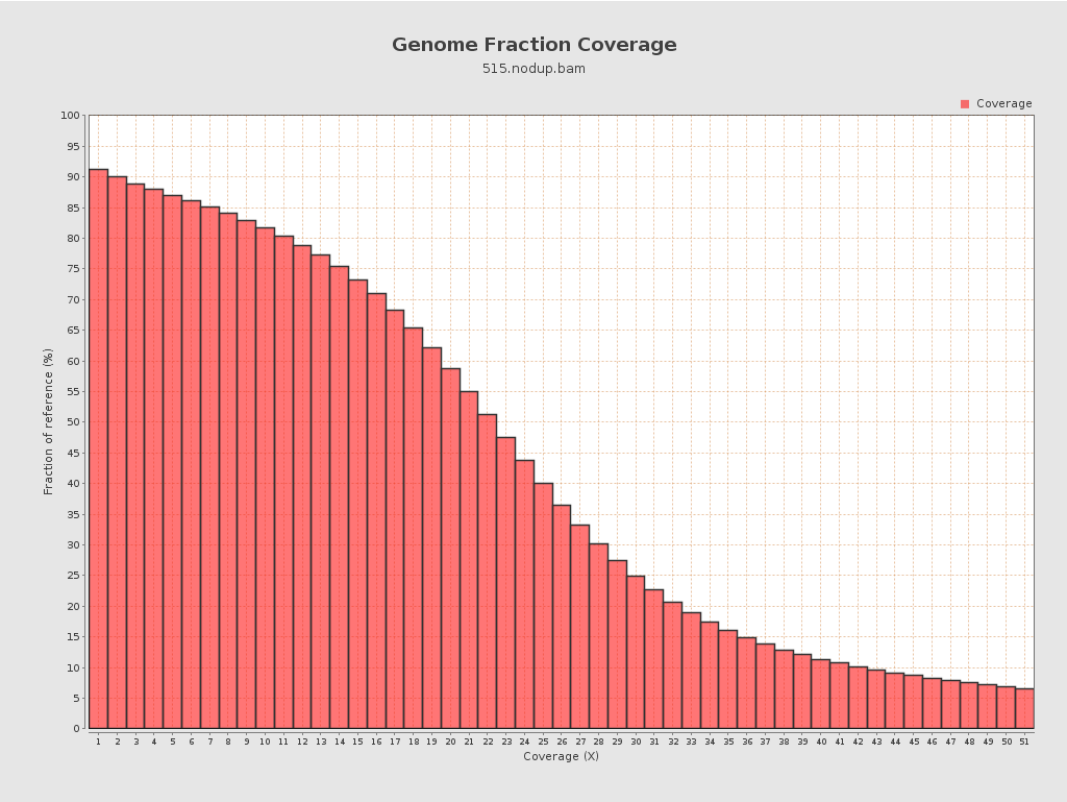
4. Results : Coverage Histogram



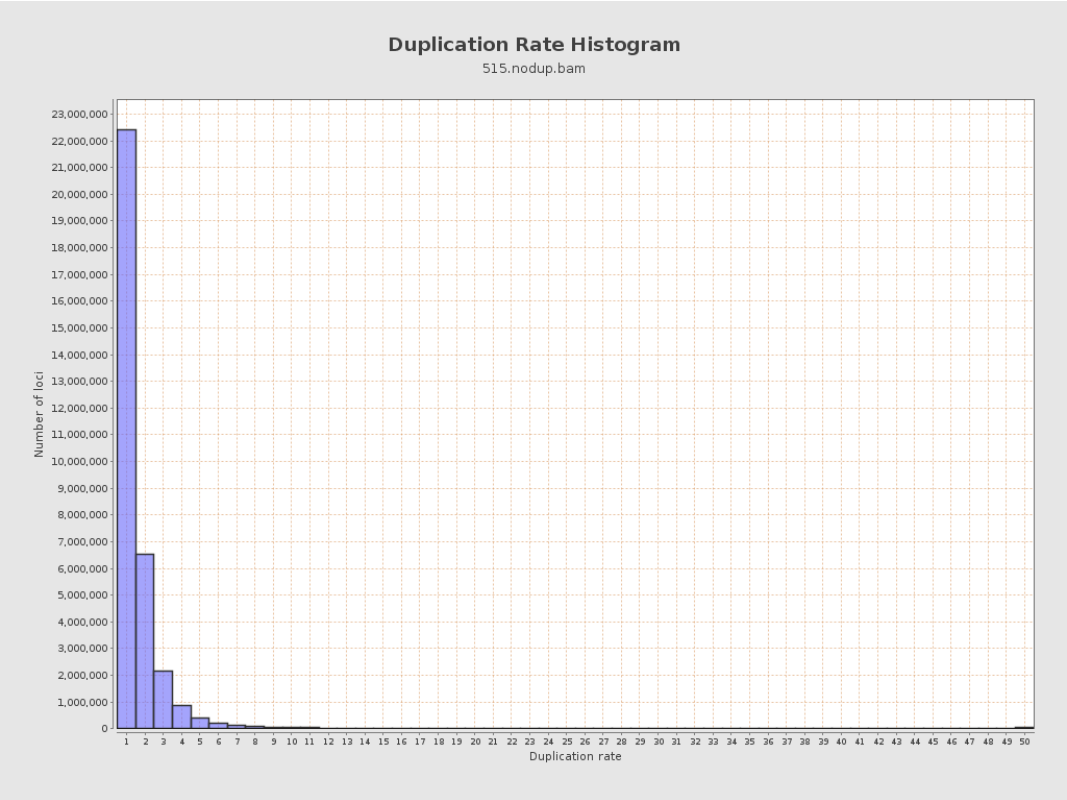
5. Results : Coverage Histogram (0-50X)



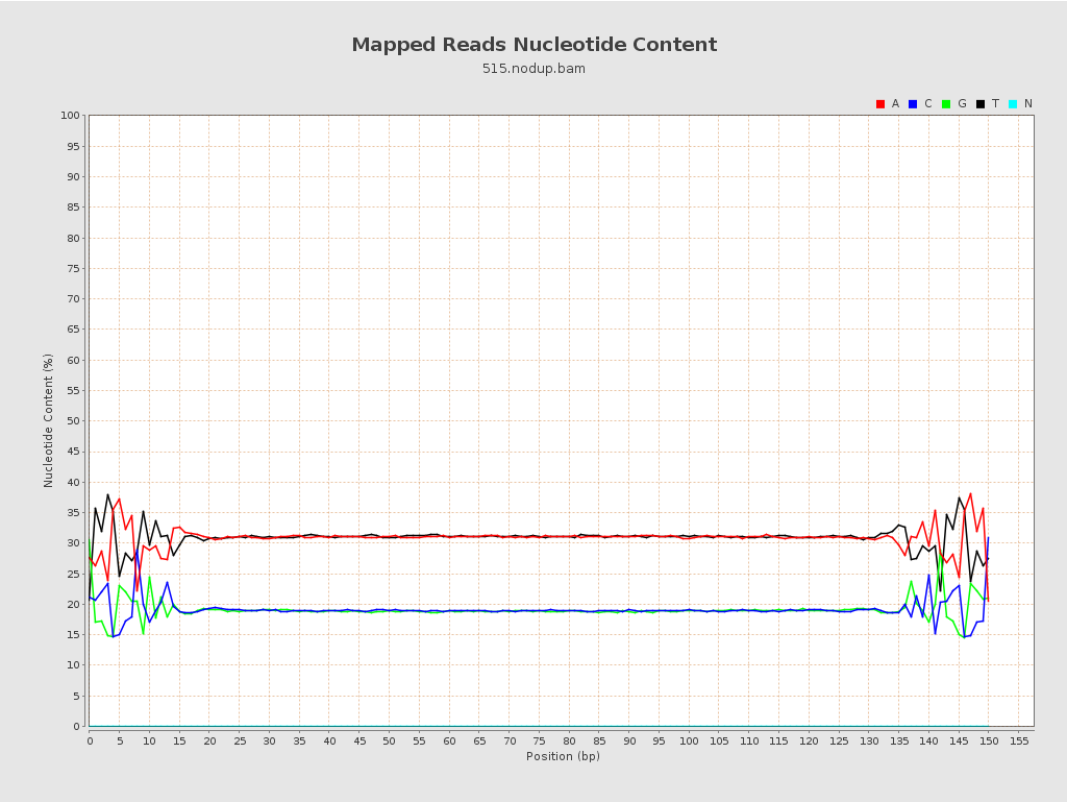
6. Results : Genome Fraction Coverage



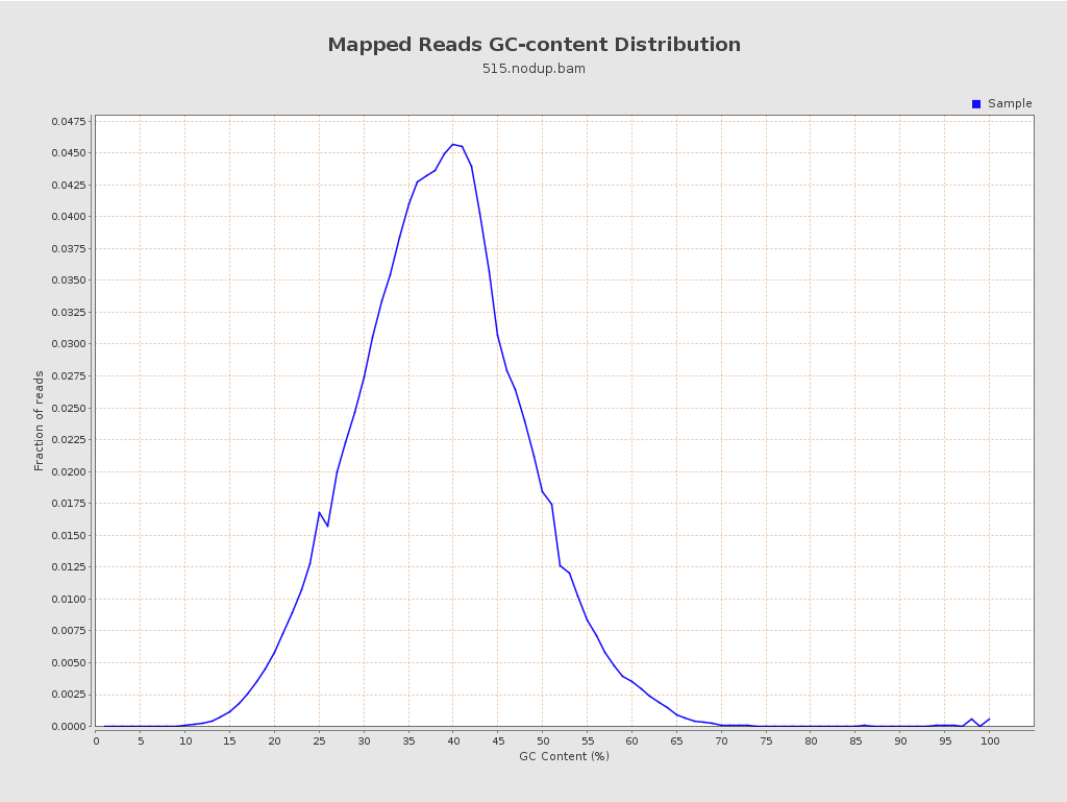
7. Results : Duplication Rate Histogram



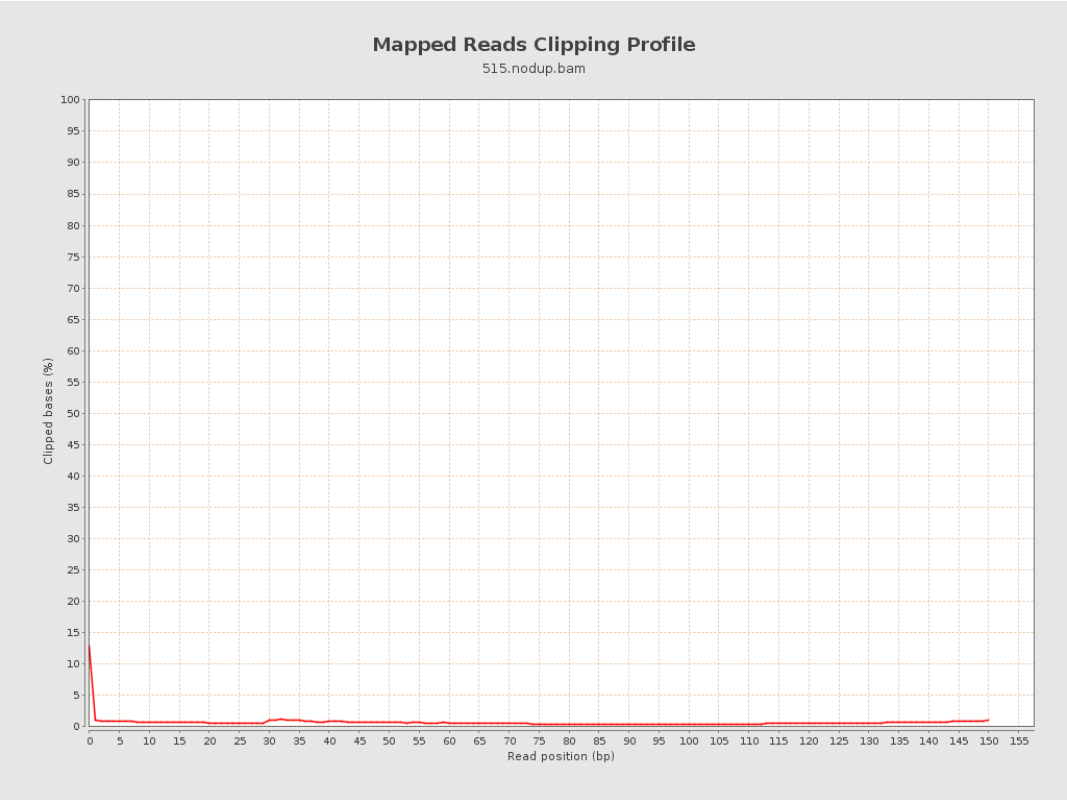
8. Results : Mapped Reads Nucleotide Content



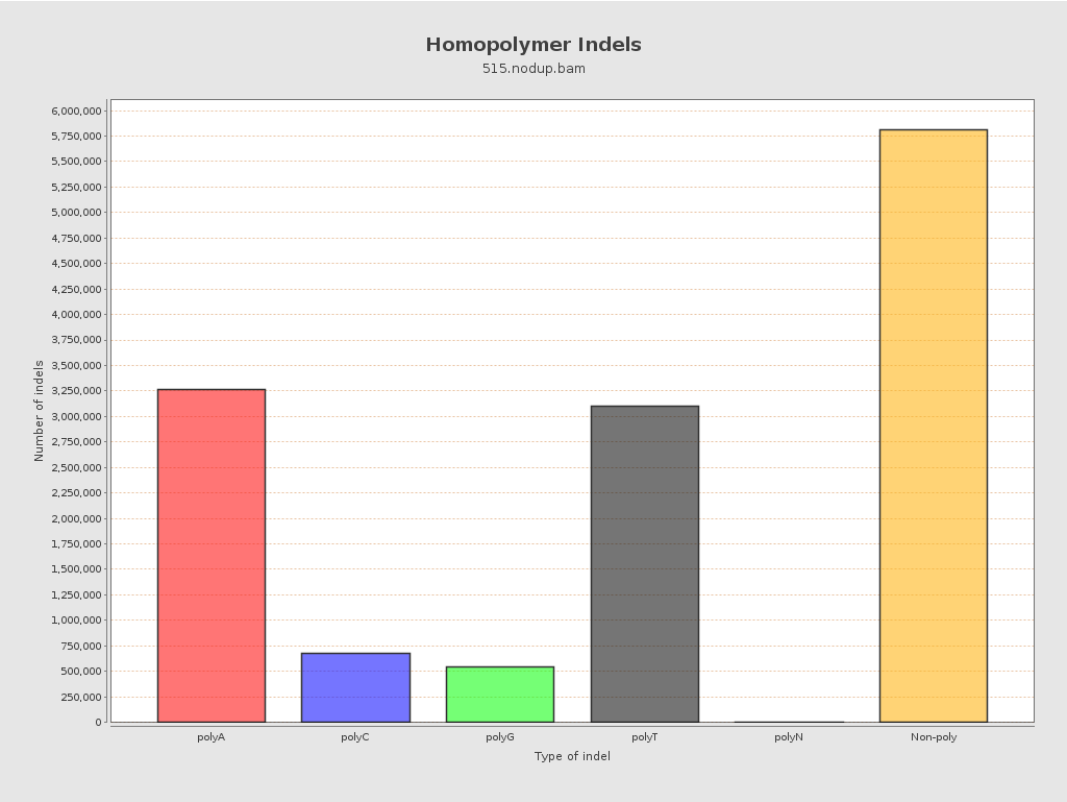
9. Results : Mapped Reads GC-content Distribution



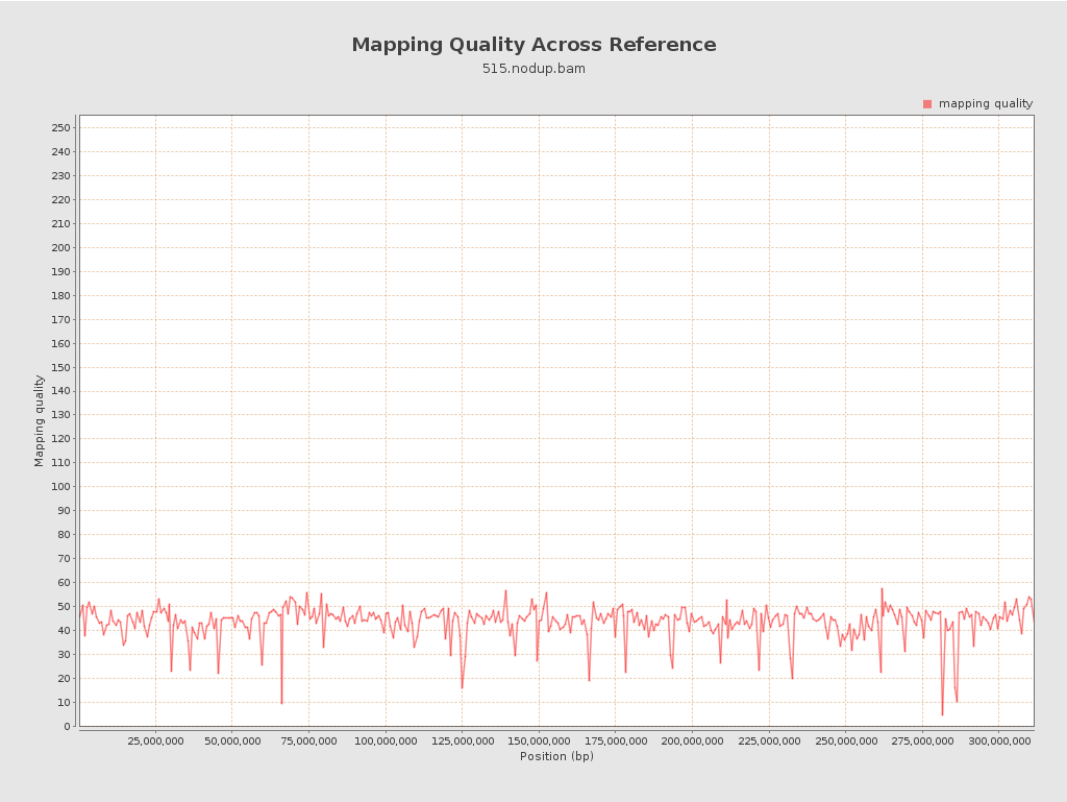
10. Results : Mapped Reads Clipping Profile



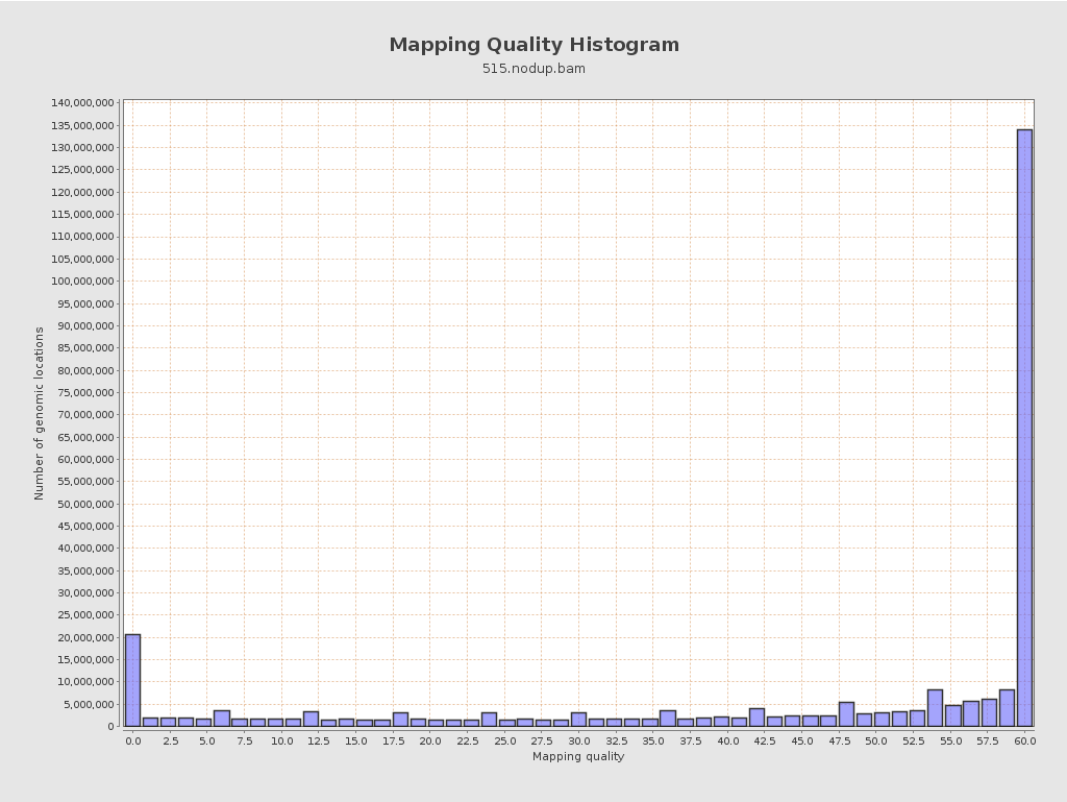
11. Results : Homopolymer Indels



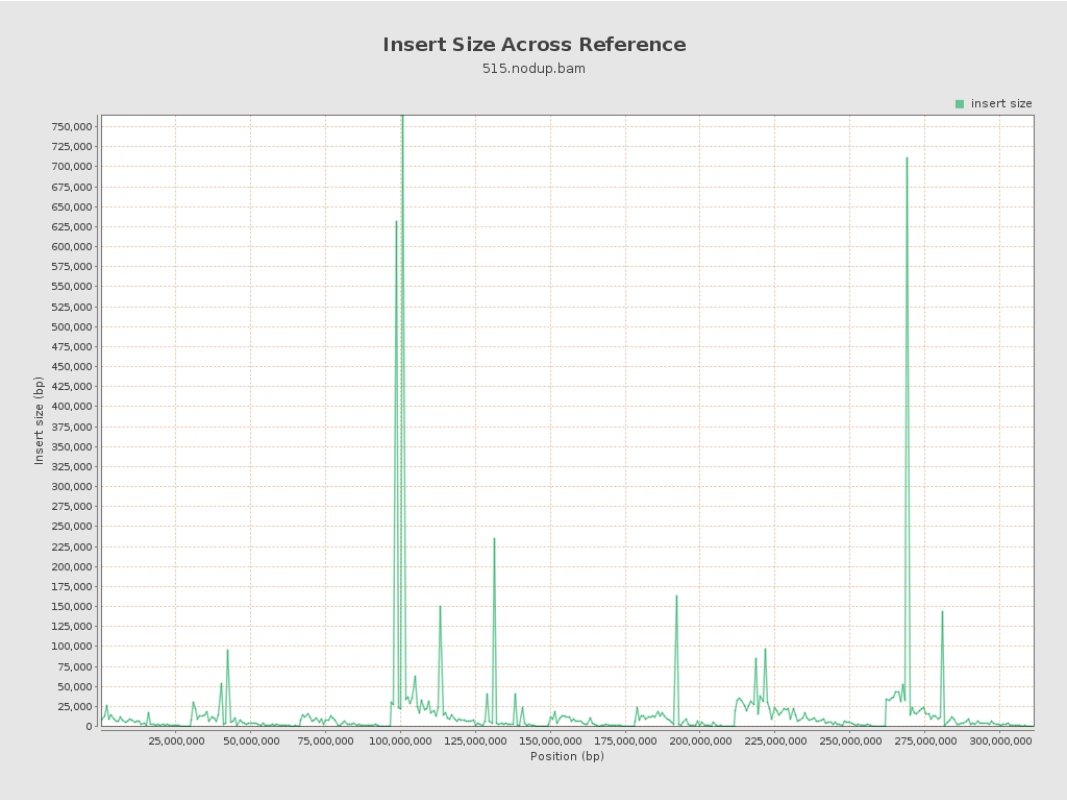
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram