Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/512.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/512.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_224/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_224_S305_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_224/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_224_S305_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	70,801,365
Mapped reads	65,002,656 / 91.81%
Unmapped reads	5,798,709 / 8.19%
Mapped paired reads	65,002,656 / 91.81%
Mapped reads, first in pair	32,569,535 / 46%
Mapped reads, second in pair	32,433,121 / 45.81%
Mapped reads, both in pair	63,117,430 / 89.15%
Mapped reads, singletons	1,885,226 / 2.66%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	10,420,647 / 14.72%
Clipped reads	15,328,095 / 21.65%

2.2. ACGT Content

Number/percentage of A's	2,760,164,795 / 30.91%
Number/percentage of C's	1,704,100,919 / 19.08%
Number/percentage of T's	2,765,706,275 / 30.97%
Number/percentage of G's	1,699,877,915 / 19.04%
Number/percentage of N's	33,120 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	28.7266
Standard Deviation	262.4623

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Insert size

Mean	241,227.52
Standard Deviation	2,369,503.1
P25/Median/P75	316 / 418 / 549

2.6. Mismatches and indels

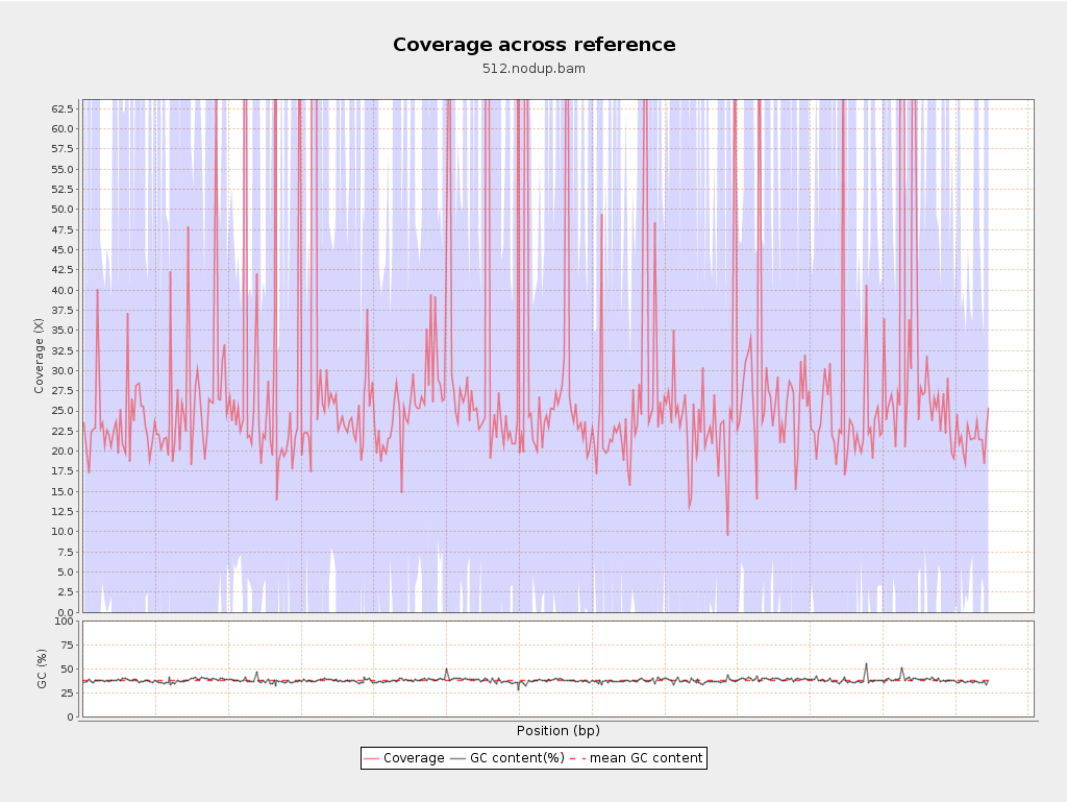
General error rate	2.34%
Mismatches	190,774,008
Insertions	6,421,910
Mapped reads with at least one insertion	8.82%
Deletions	6,100,614
Mapped reads with at least one deletion	8.34%
Homopolymer indels	57.52%

2.7. Chromosome stats

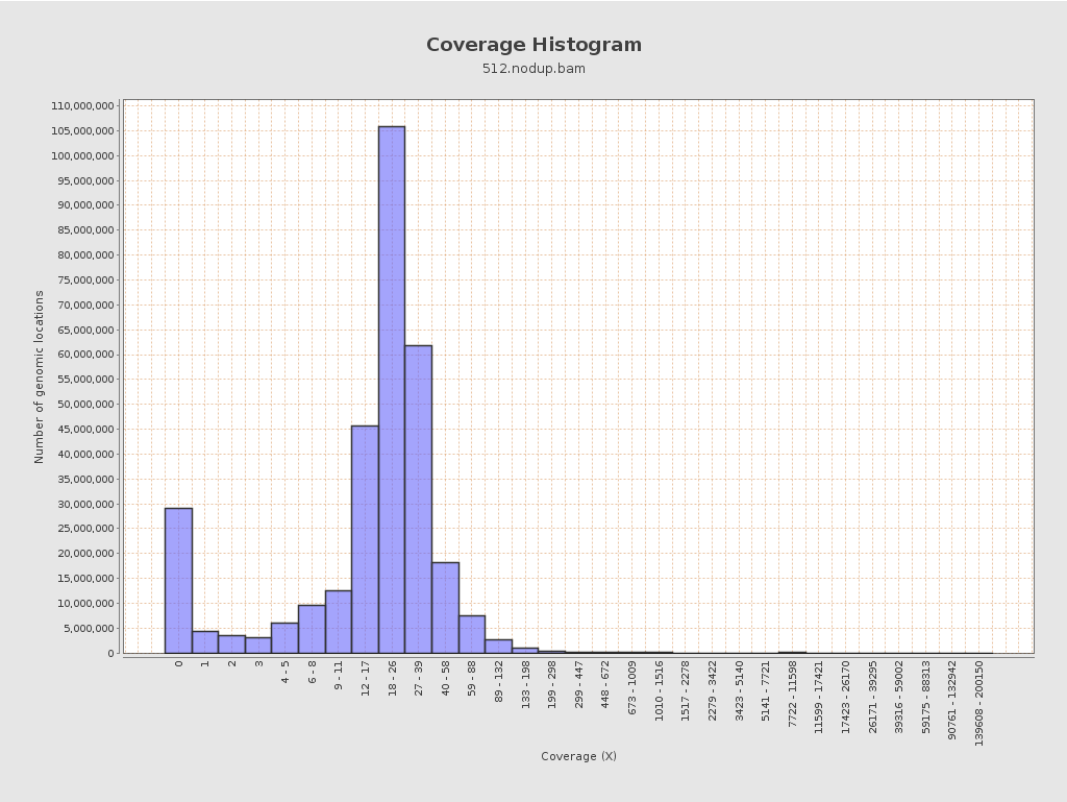
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	690270528	23.2224	101.309

LT669789.1	36598175	1062341899	29.0272	284.1847
LT669790.1	30422129	1050096840	34.5175	379.2561
LT669791.1	52758100	1501411302	28.4584	267.4796
LT669792.1	28376109	821291619	28.9431	273.309
LT669793.1	33388210	873925519	26.1747	177.3583
LT669794.1	50579949	1362416986	26.9359	219.412
LT669795.1	49795044	1590675227	31.9444	298.9107

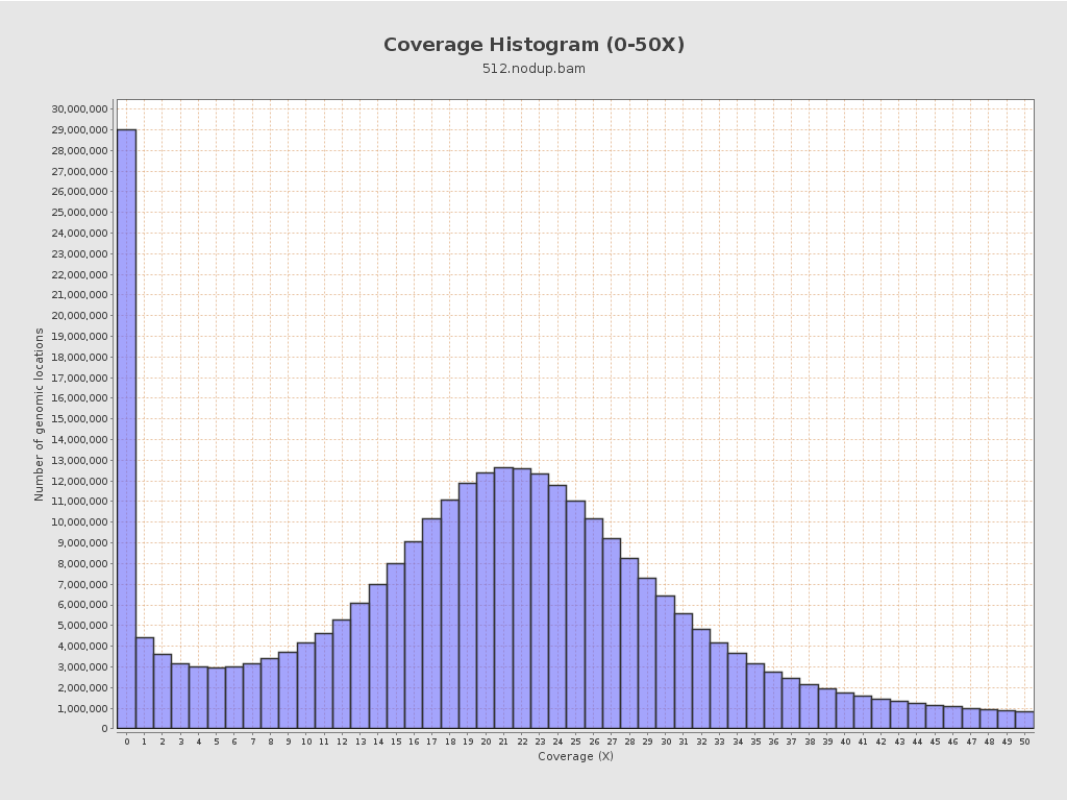
3. Results : Coverage across reference



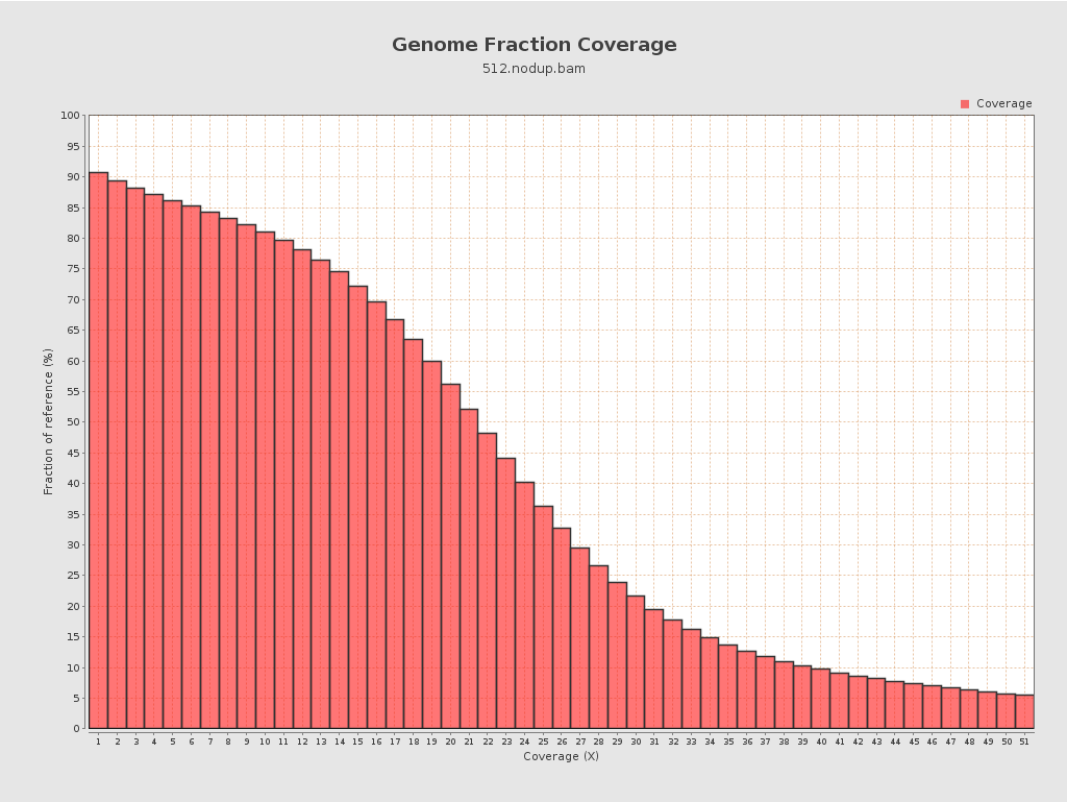
4. Results : Coverage Histogram



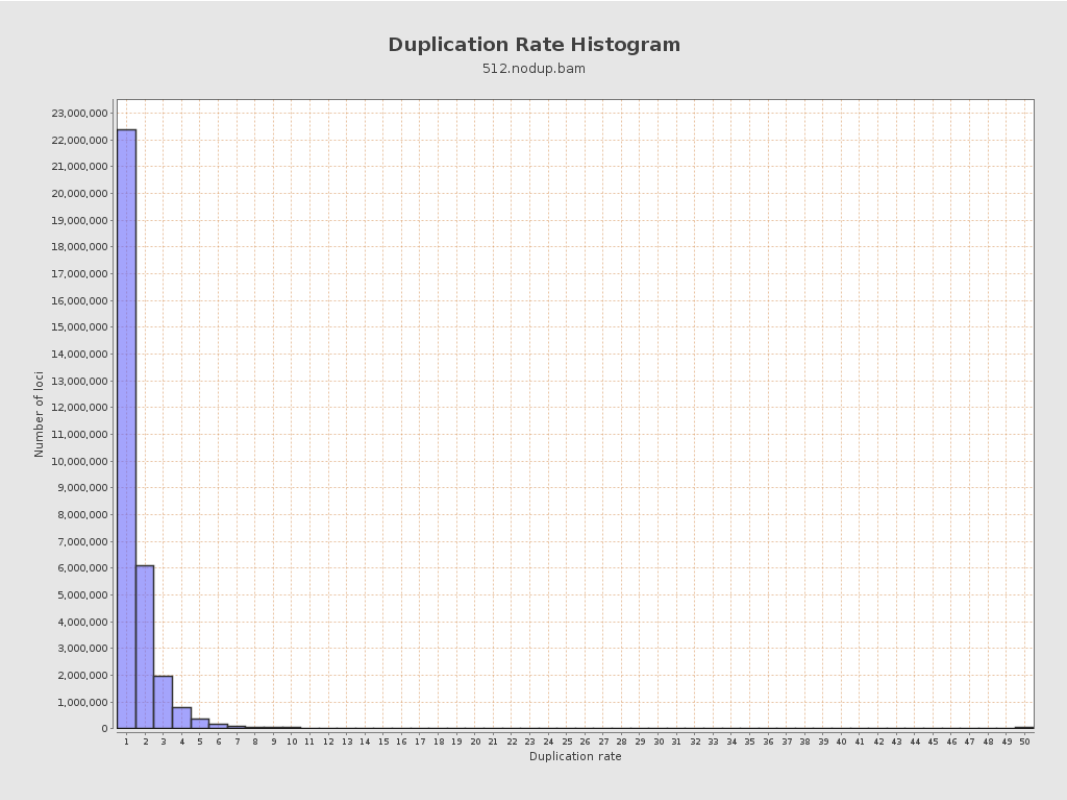
5. Results : Coverage Histogram (0-50X)



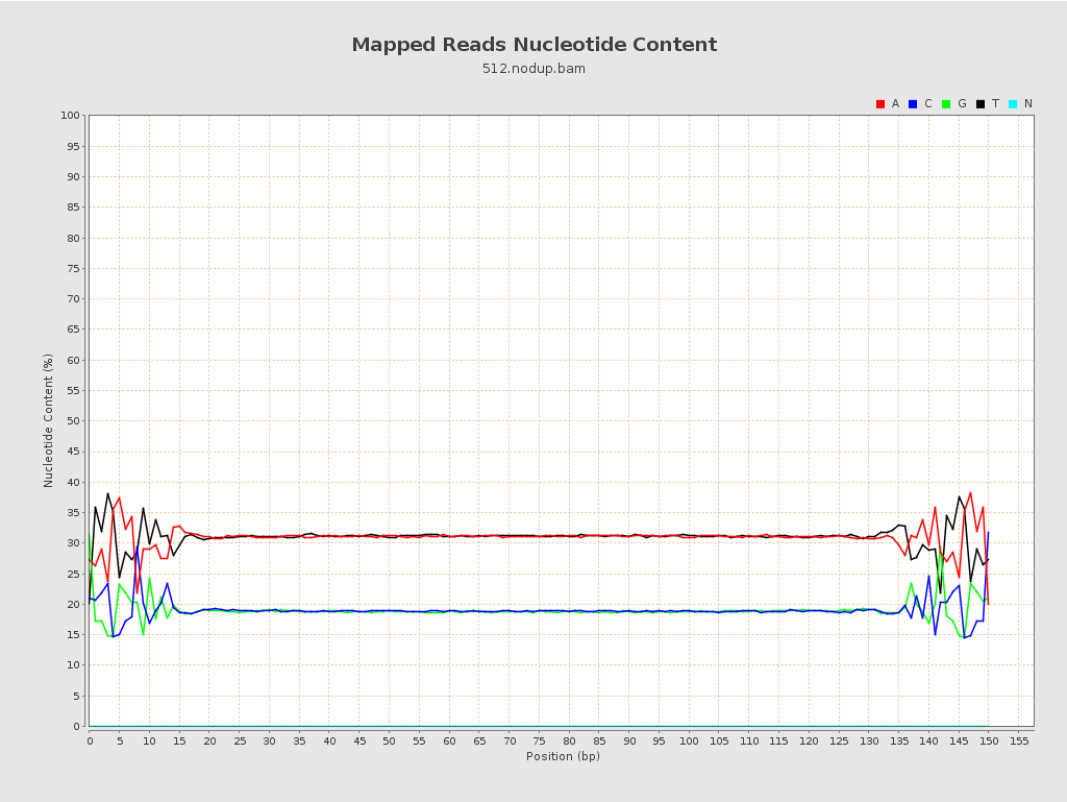
6. Results : Genome Fraction Coverage



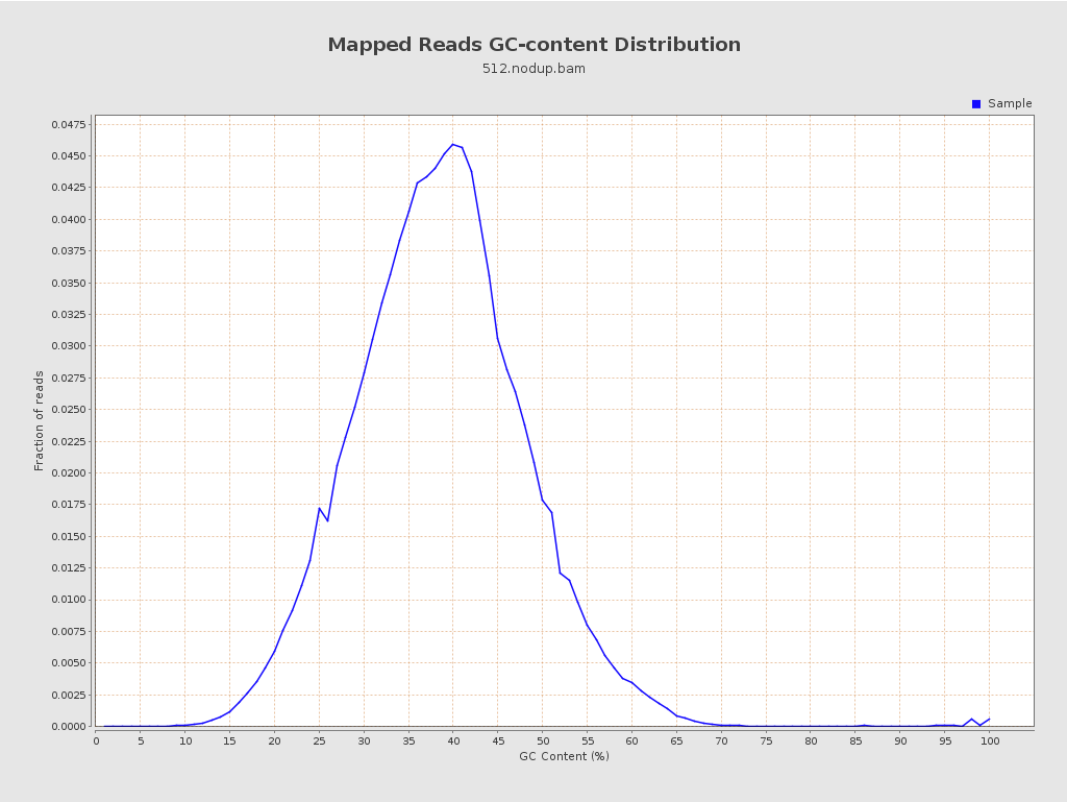
7. Results : Duplication Rate Histogram



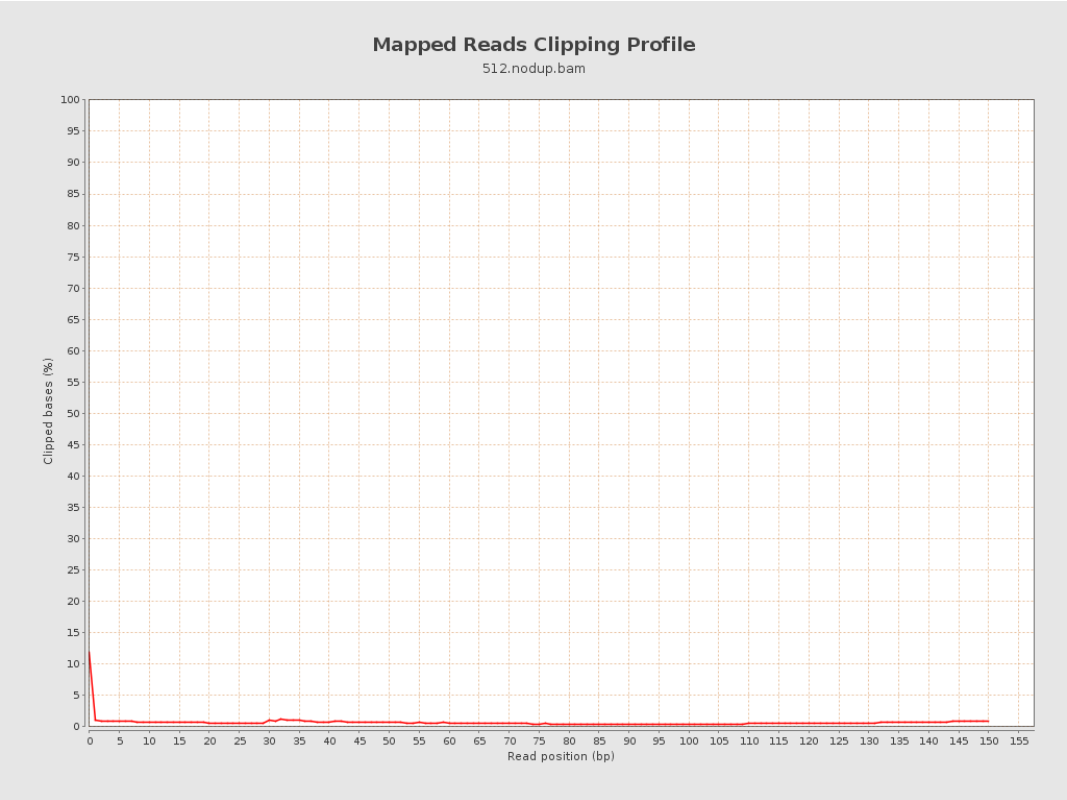
8. Results : Mapped Reads Nucleotide Content



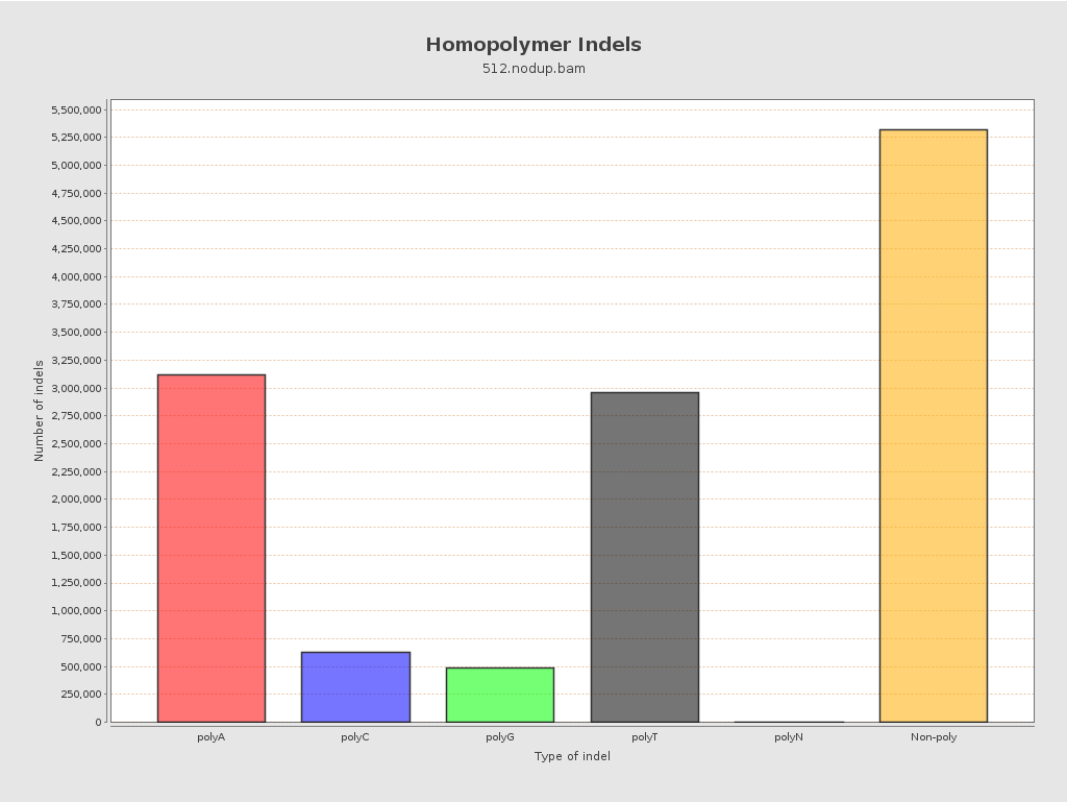
9. Results : Mapped Reads GC-content Distribution



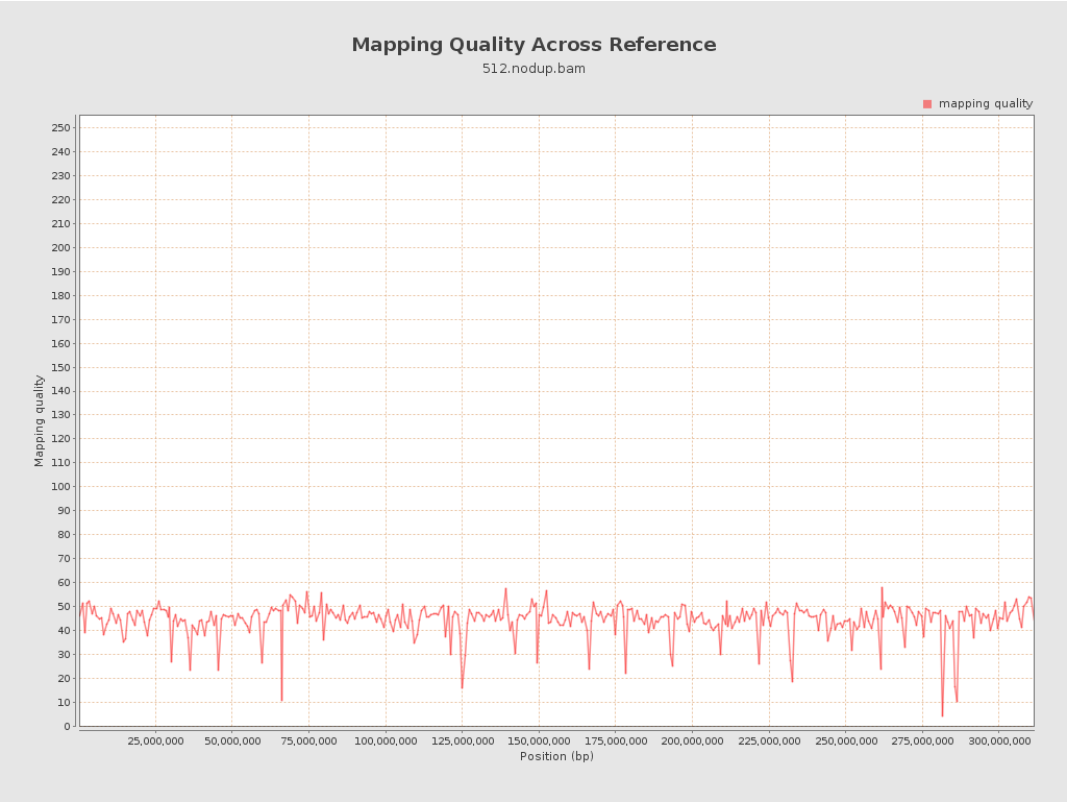
10. Results : Mapped Reads Clipping Profile



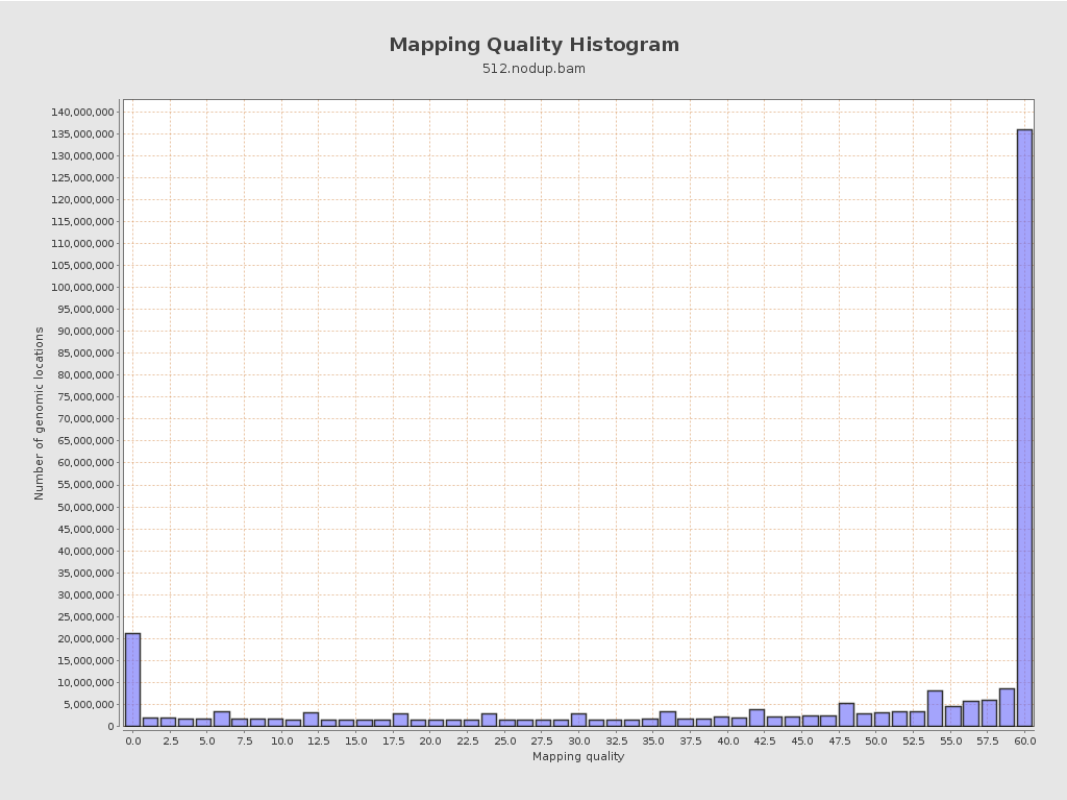
11. Results : Homopolymer Indels



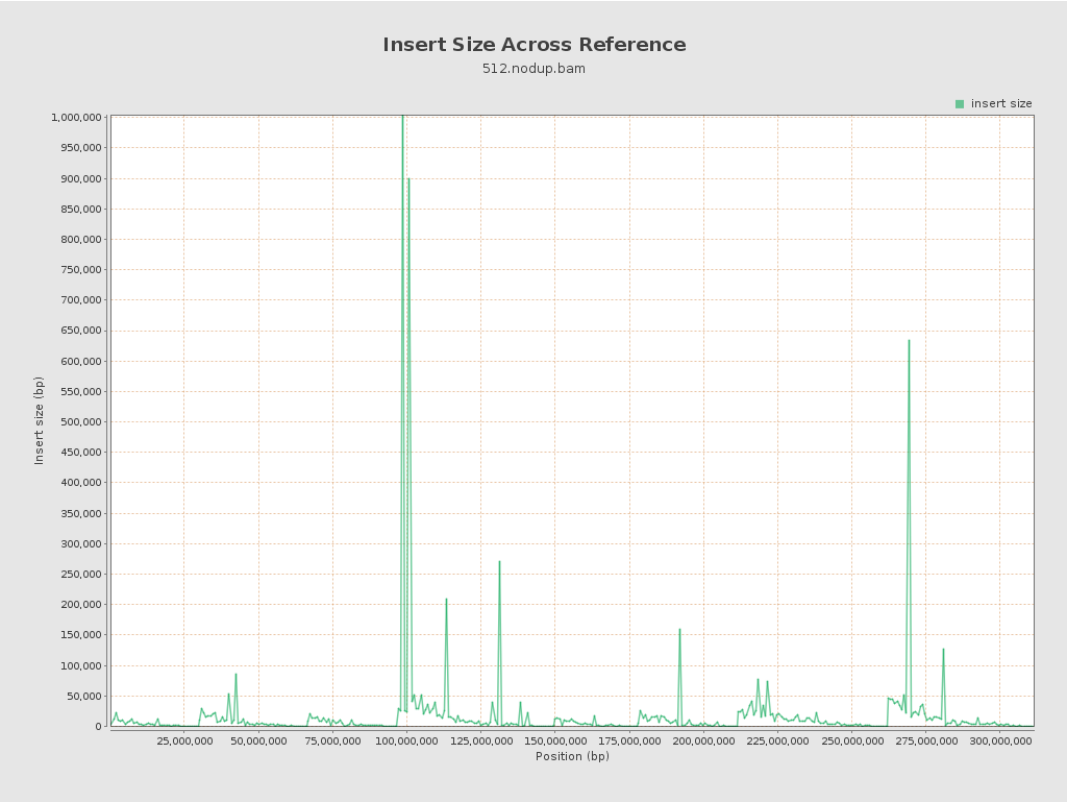
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram