Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:25:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/504.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/504.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_476/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_476_S451_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_476/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_476_S451_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:25:10 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	47,181,772
Mapped reads	44,966,330 / 95.3%
Unmapped reads	2,215,442 / 4.7%
Mapped paired reads	44,966,330 / 95.3%
Mapped reads, first in pair	22,543,108 / 47.78%
Mapped reads, second in pair	22,423,222 / 47.53%
Mapped reads, both in pair	44,187,642 / 93.65%
Mapped reads, singletons	778,688 / 1.65%
Read min/max/mean length	30 / 151 / 148.28
Duplicated reads (flagged)	6,614,959 / 14.02%
Clipped reads	9,441,167 / 20.01%

2.2. ACGT Content

Number/percentage of A's	1,941,736,722 / 30.88%
Number/percentage of C's	1,205,386,061 / 19.17%
Number/percentage of T's	1,941,055,622 / 30.86%
Number/percentage of G's	1,200,757,570 / 19.09%
Number/percentage of N's	20,981 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	20.2292
Standard Deviation	161.5436

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Insert size

Mean	219,465.64
Standard Deviation	2,200,179.3
P25/Median/P75	363 / 477 / 631

2.6. Mismatches and indels

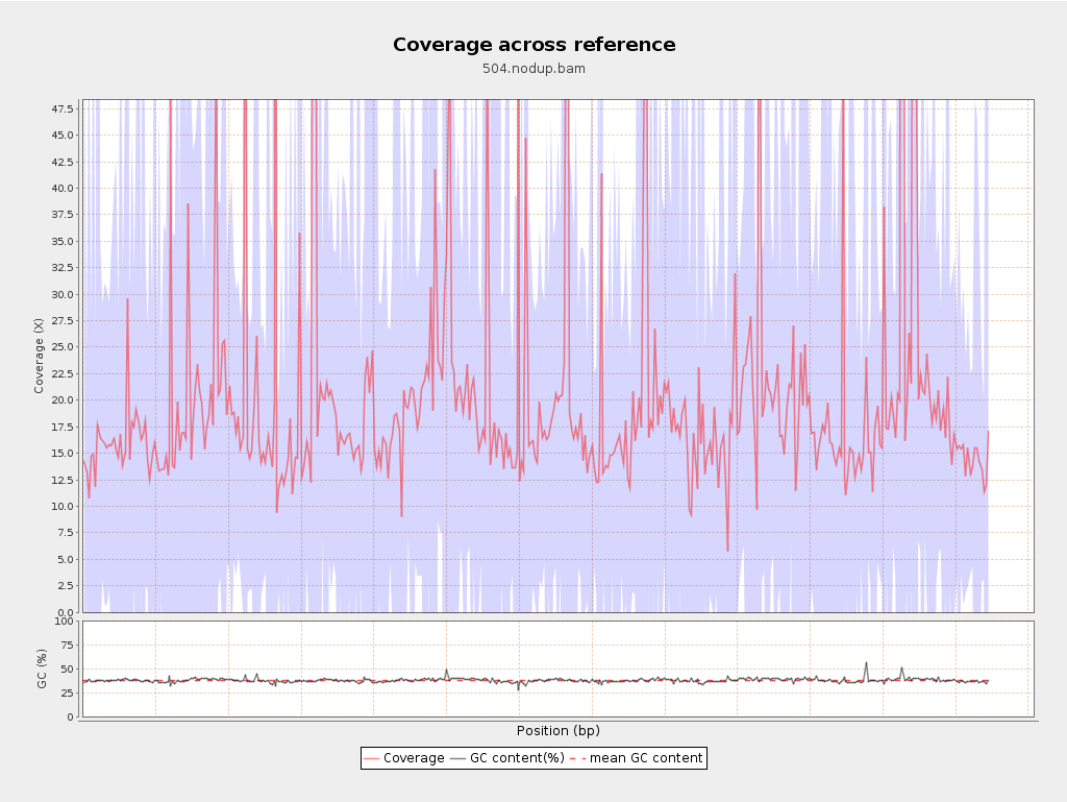
General error rate	2.26%
Mismatches	131,194,986
Insertions	3,949,798
Mapped reads with at least one insertion	7.94%
Deletions	4,112,184
Mapped reads with at least one deletion	8.16%
Homopolymer indels	56.64%

2.7. Chromosome stats

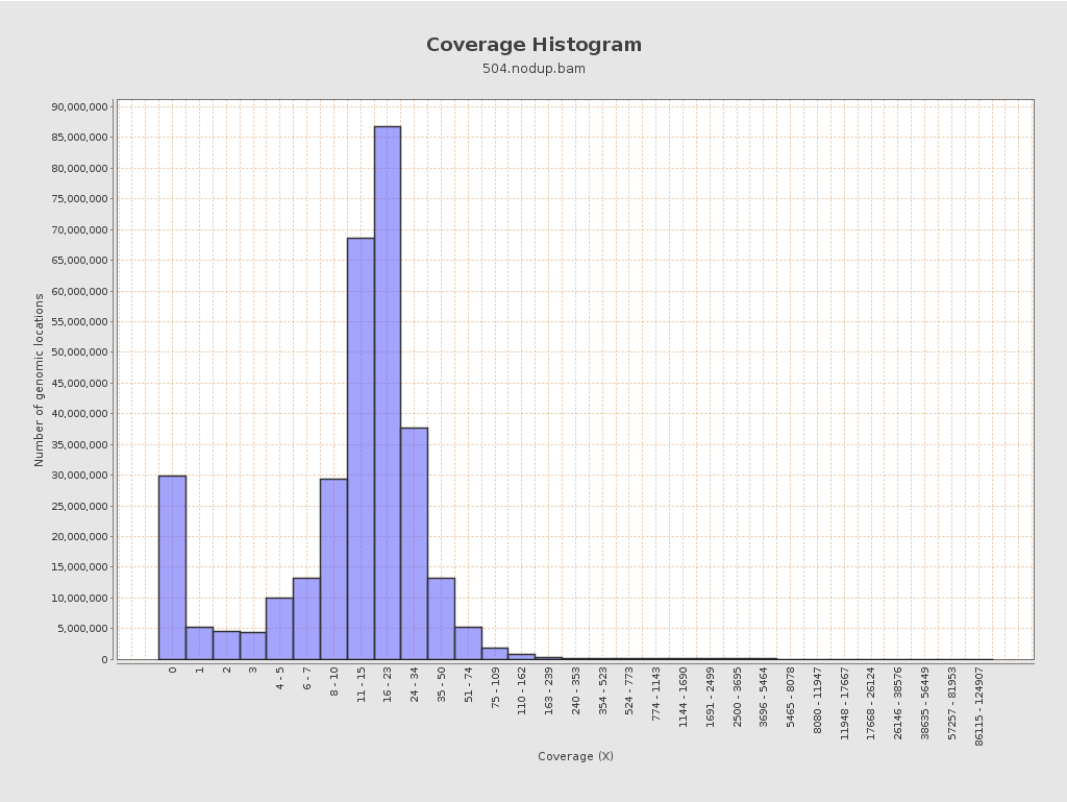
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	463997781	15.61	34.834

LT669789.1	36598175	782663647	21.3853	177.6021
LT669790.1	30422129	614246253	20.1908	141.2526
LT669791.1	52758100	1074792356	20.3721	119.2773
LT669792.1	28376109	555685722	19.5829	203.5696
LT669793.1	33388210	636562879	19.0655	125.9711
LT669794.1	50579949	996185868	19.6953	149.0145
LT669795.1	49795044	1180124425	23.6996	235.1917

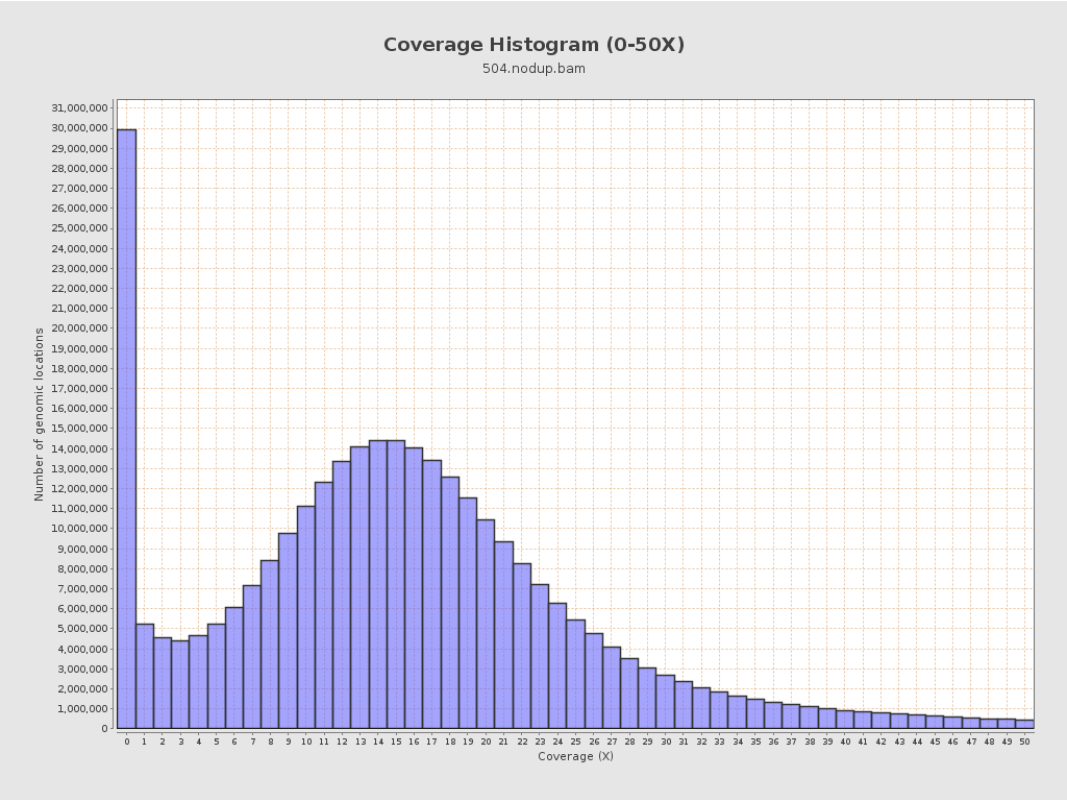
3. Results : Coverage across reference



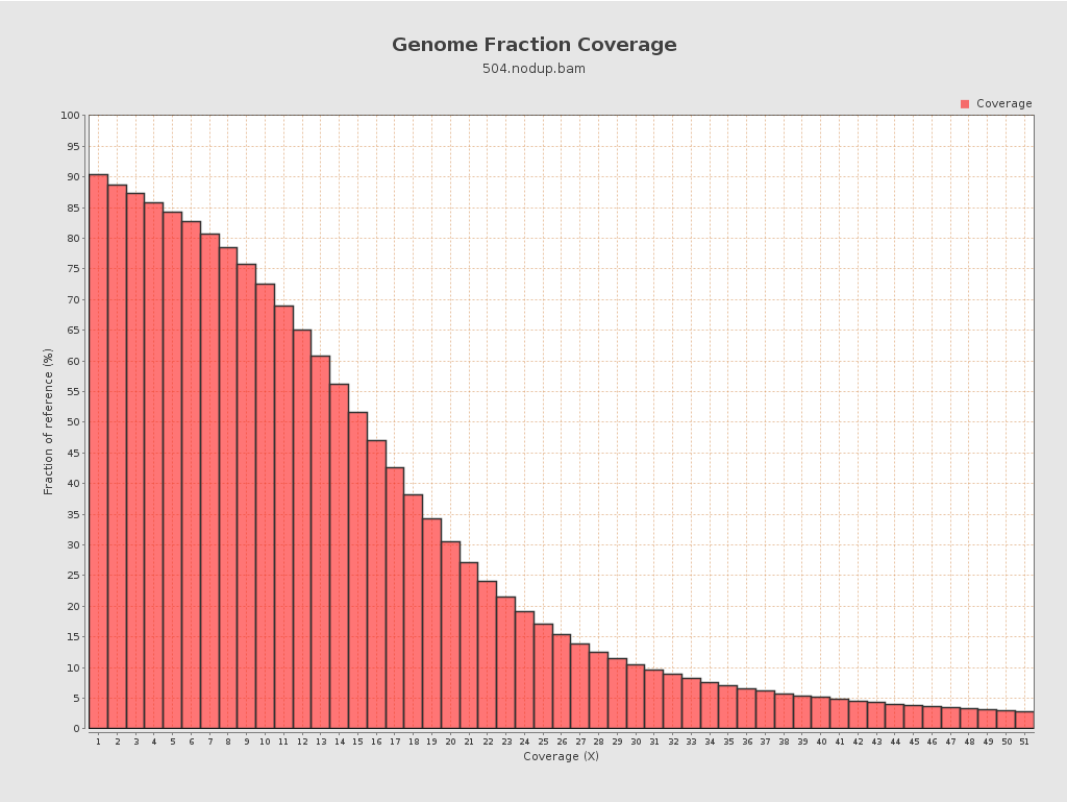
4. Results : Coverage Histogram



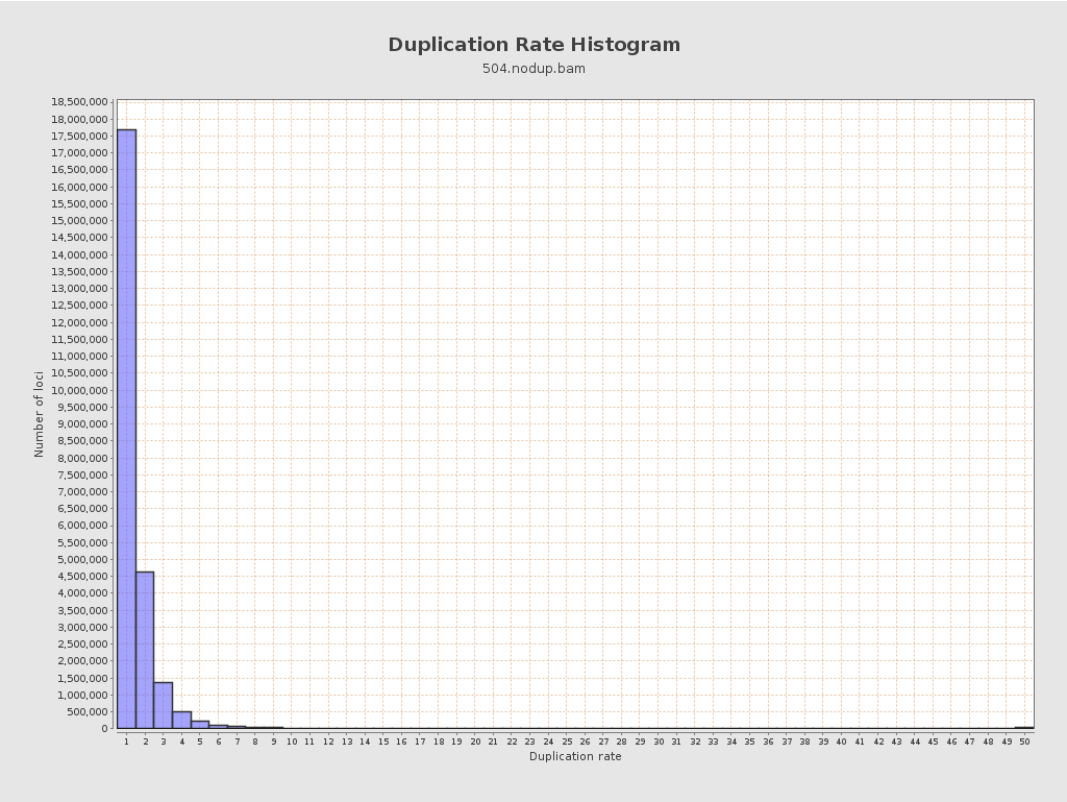
5. Results : Coverage Histogram (0-50X)



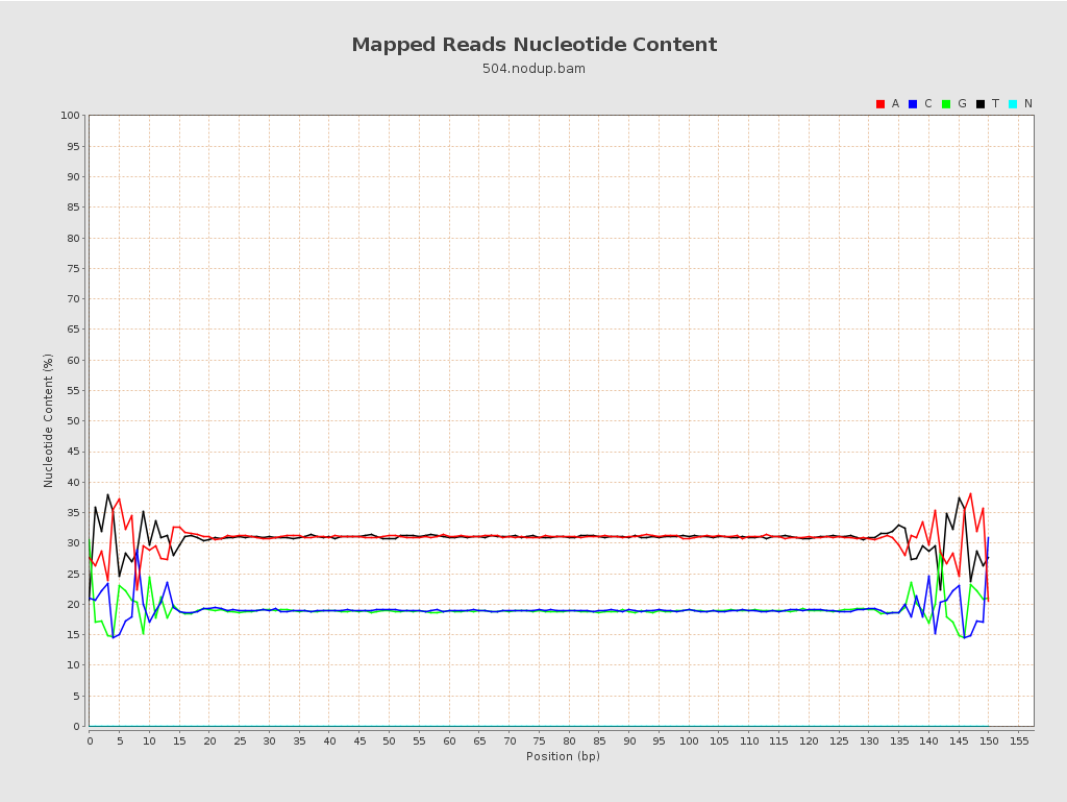
6. Results : Genome Fraction Coverage



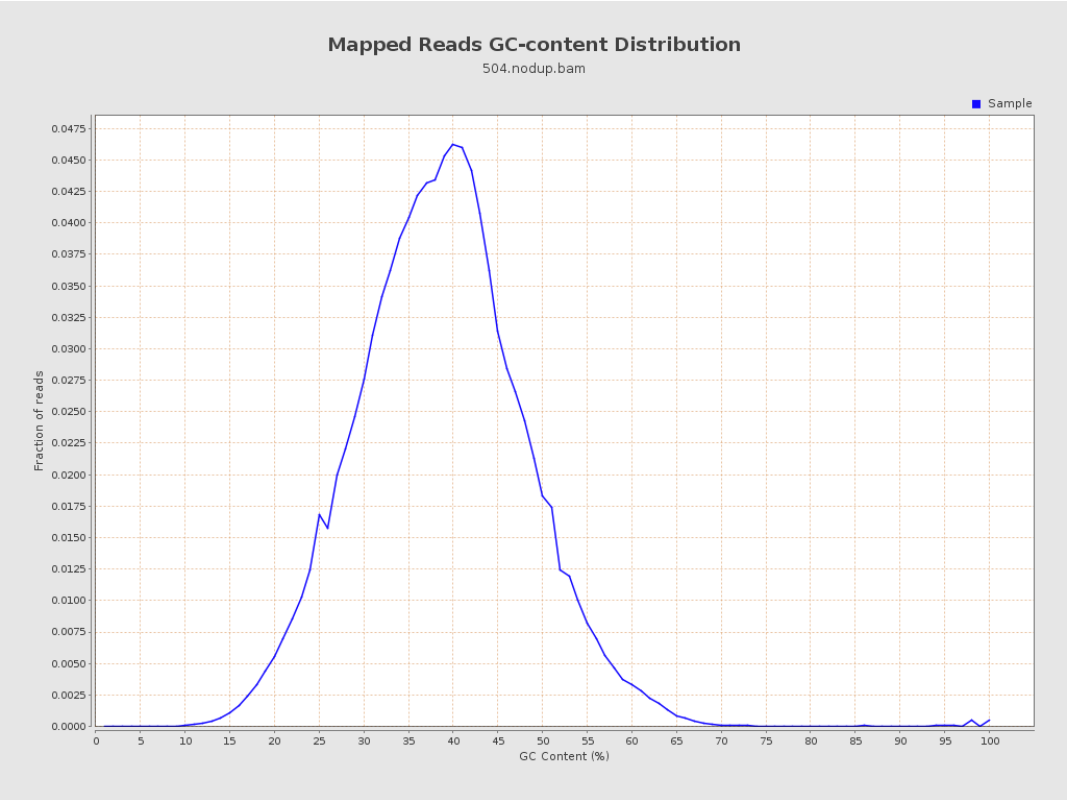
7. Results : Duplication Rate Histogram



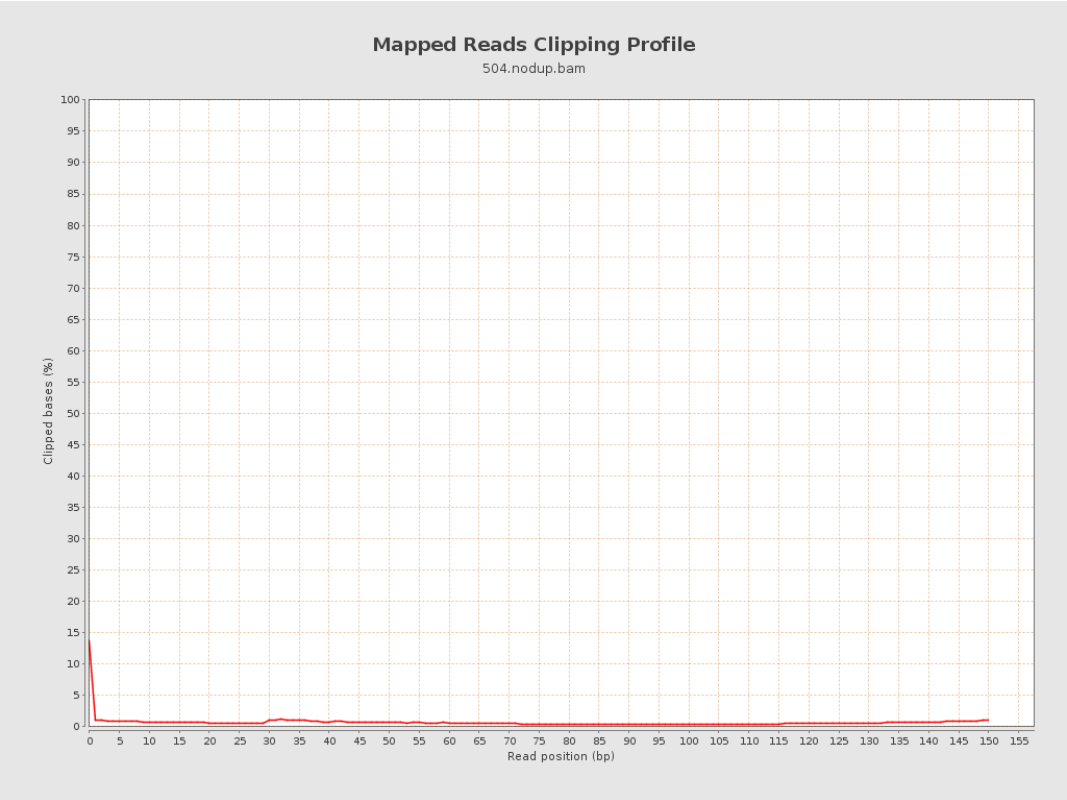
8. Results : Mapped Reads Nucleotide Content



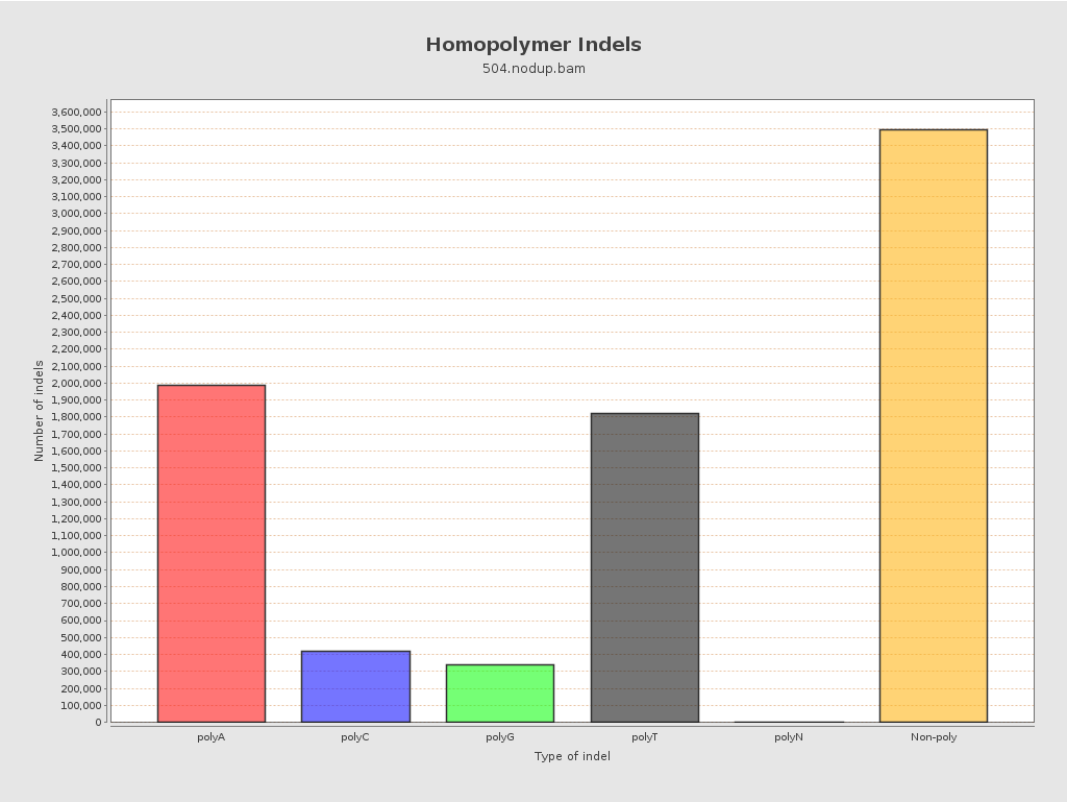
9. Results : Mapped Reads GC-content Distribution



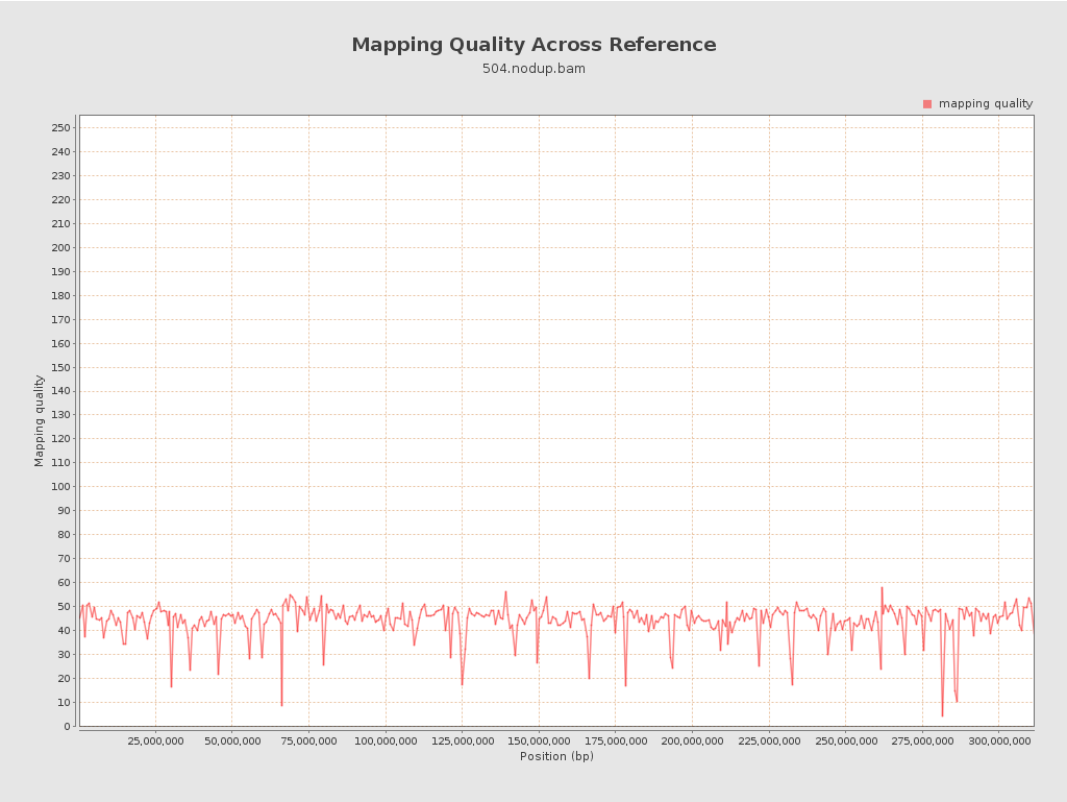
10. Results : Mapped Reads Clipping Profile



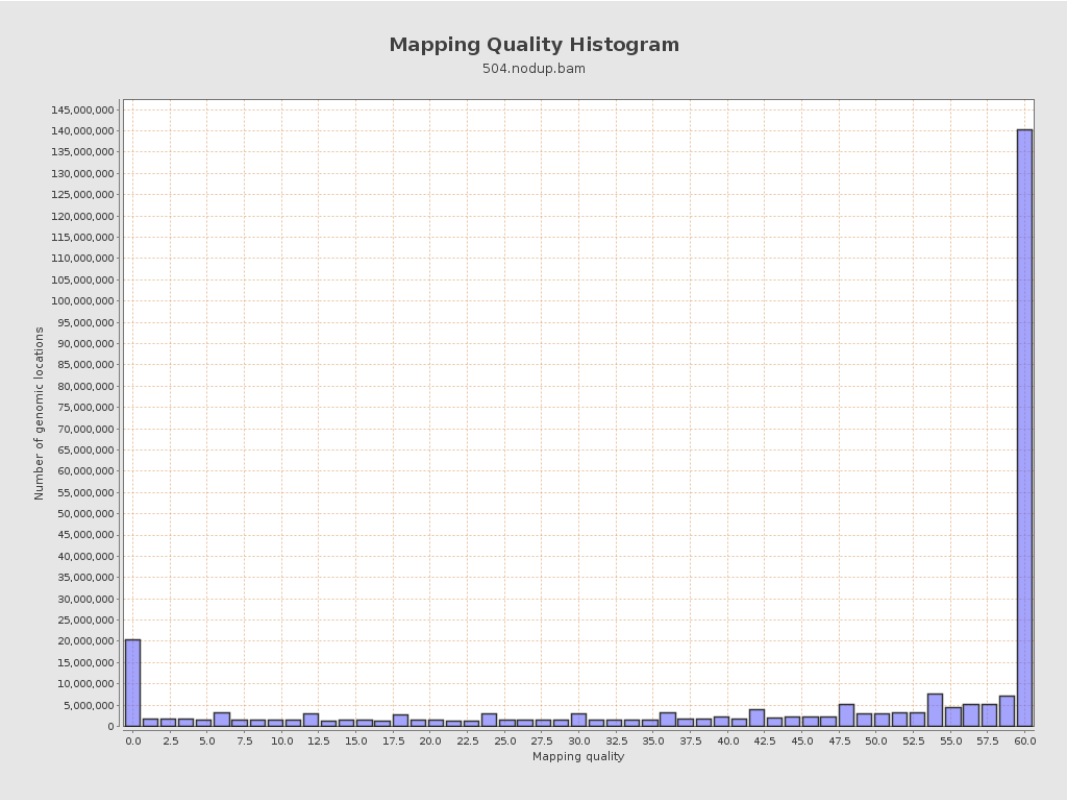
11. Results : Homopolymer Indels



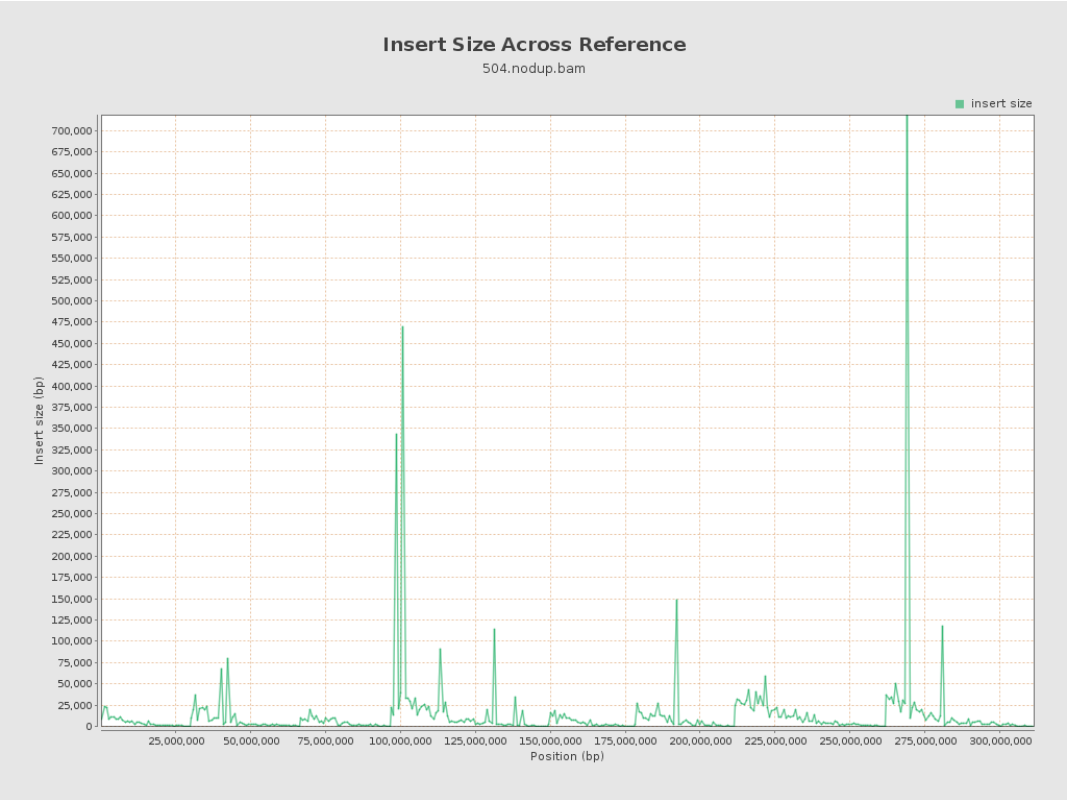
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram