Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/414.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/414.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_124/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_124_S214_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_124/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_124_S214_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:34 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,549,457
Mapped reads	74,240,531 / 92.17%
Unmapped reads	6,308,926 / 7.83%
Mapped paired reads	74,240,531 / 92.17%
Mapped reads, first in pair	37,178,628 / 46.16%
Mapped reads, second in pair	37,061,903 / 46.01%
Mapped reads, both in pair	72,324,484 / 89.79%
Mapped reads, singletons	1,916,047 / 2.38%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	13,609,129 / 16.9%
Clipped reads	16,637,037 / 20.65%

2.2. ACGT Content

Number/percentage of A's	3,169,720,509 / 30.88%
Number/percentage of C's	1,962,874,660 / 19.12%
Number/percentage of T's	3,170,954,657 / 30.89%
Number/percentage of G's	1,960,752,181 / 19.1%
Number/percentage of N's	43,430 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	33.0215
Standard Deviation	267.7851

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Insert size

Mean	236,231.06
Standard Deviation	2,316,350.76
P25/Median/P75	320 / 417 / 547

2.6. Mismatches and indels

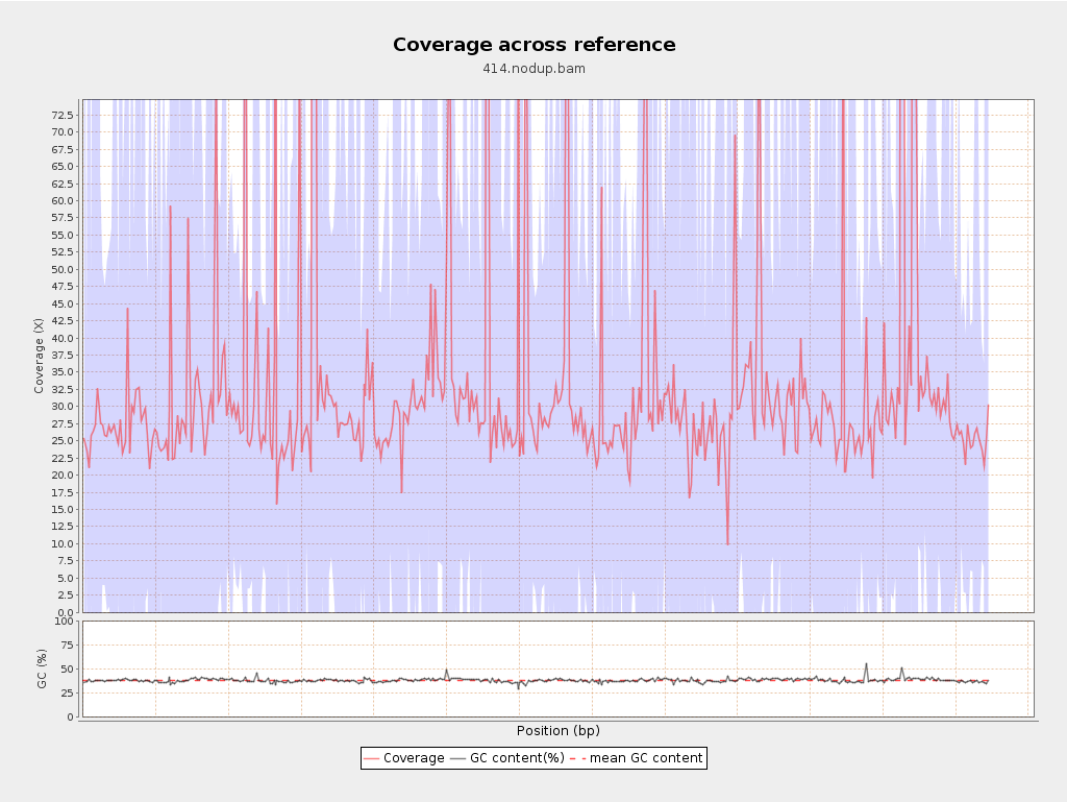
General error rate	2.28%
Mismatches	214,969,156
Insertions	7,062,740
Mapped reads with at least one insertion	8.52%
Deletions	7,062,220
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.92%

2.7. Chromosome stats

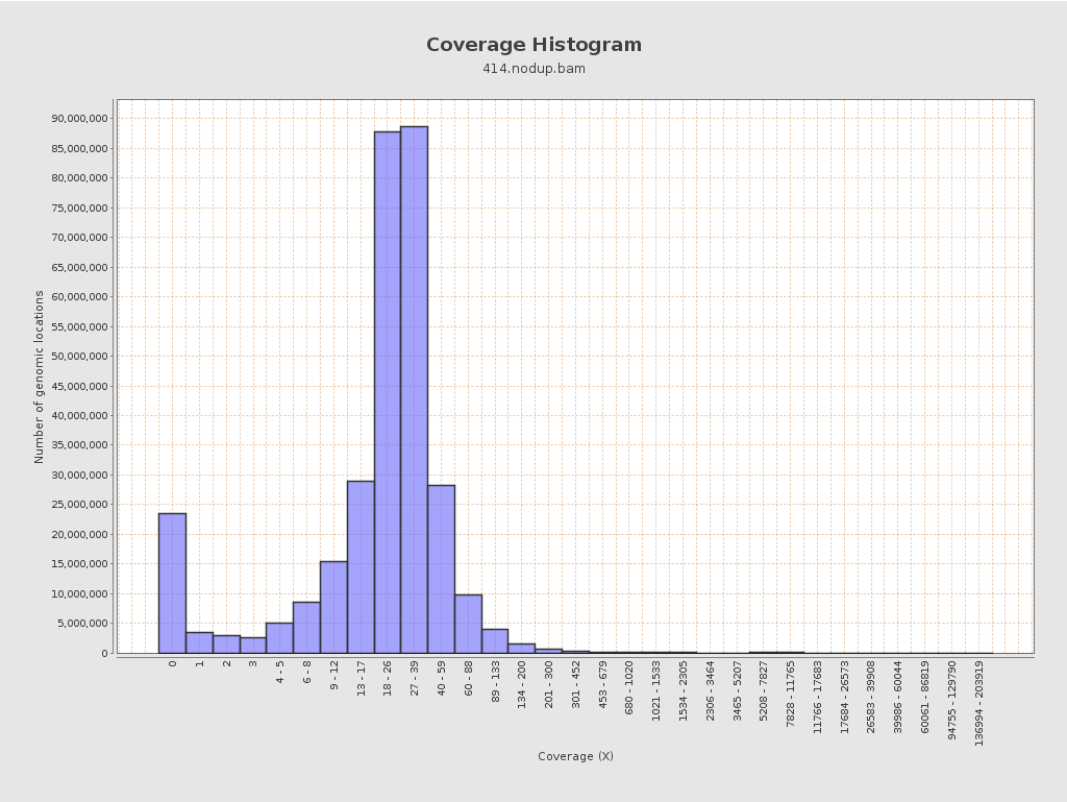
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	796806868	26.8065	91.1689

LT669789.1	36598175	1236771090	33.7932	286.7003
LT669790.1	30422129	1112157639	36.5575	316.2687
LT669791.1	52758100	1729768788	32.7868	263.071
LT669792.1	28376109	928138290	32.7084	302.7155
LT669793.1	33388210	1026089176	30.7321	186.9202
LT669794.1	50579949	1594702518	31.5284	231.0504
LT669795.1	49795044	1866449215	37.4826	345.0369

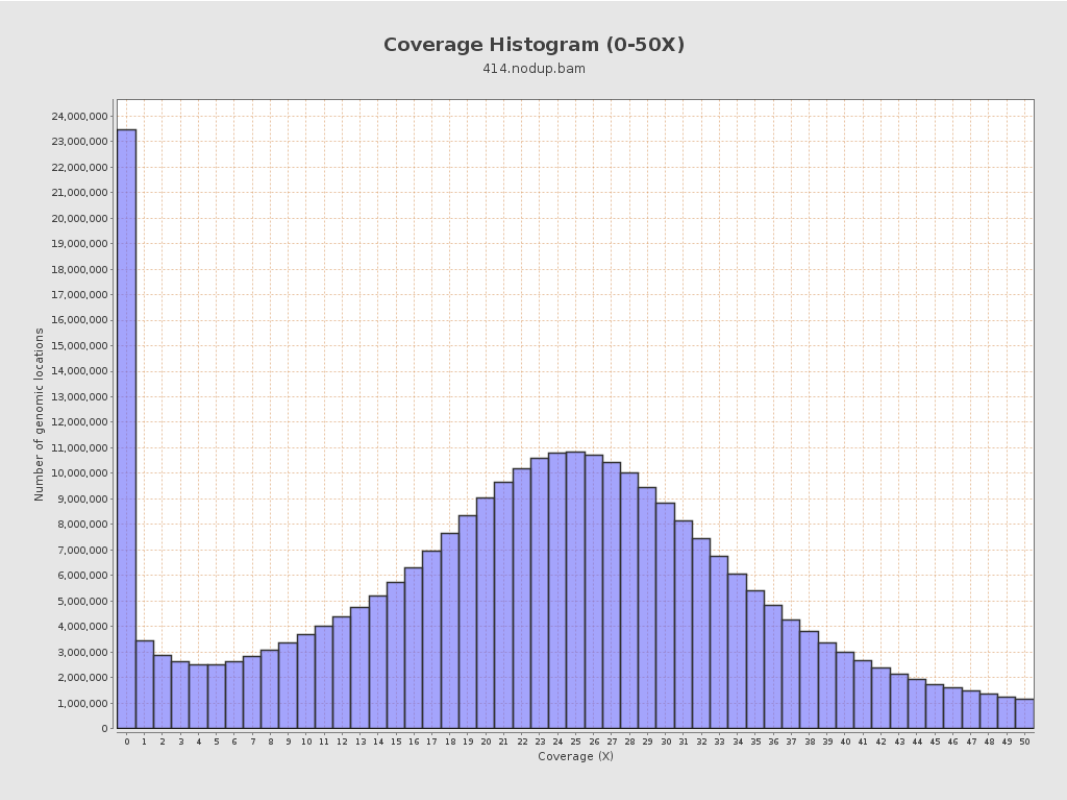
3. Results : Coverage across reference



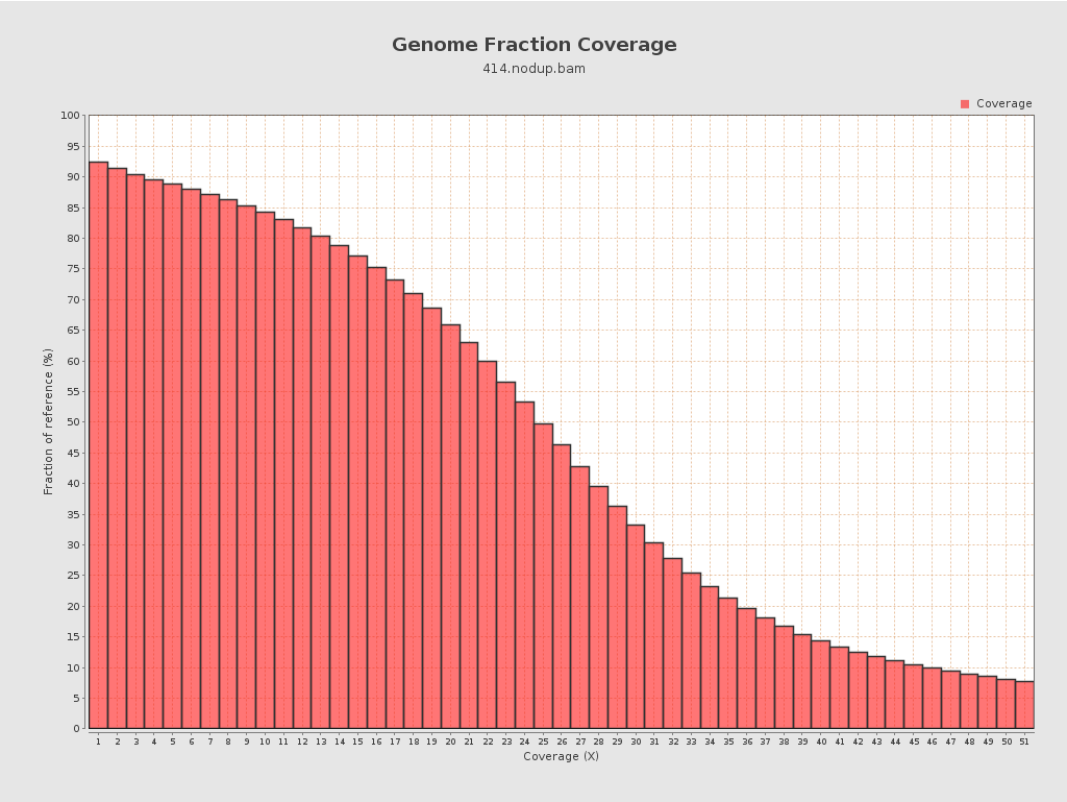
4. Results : Coverage Histogram



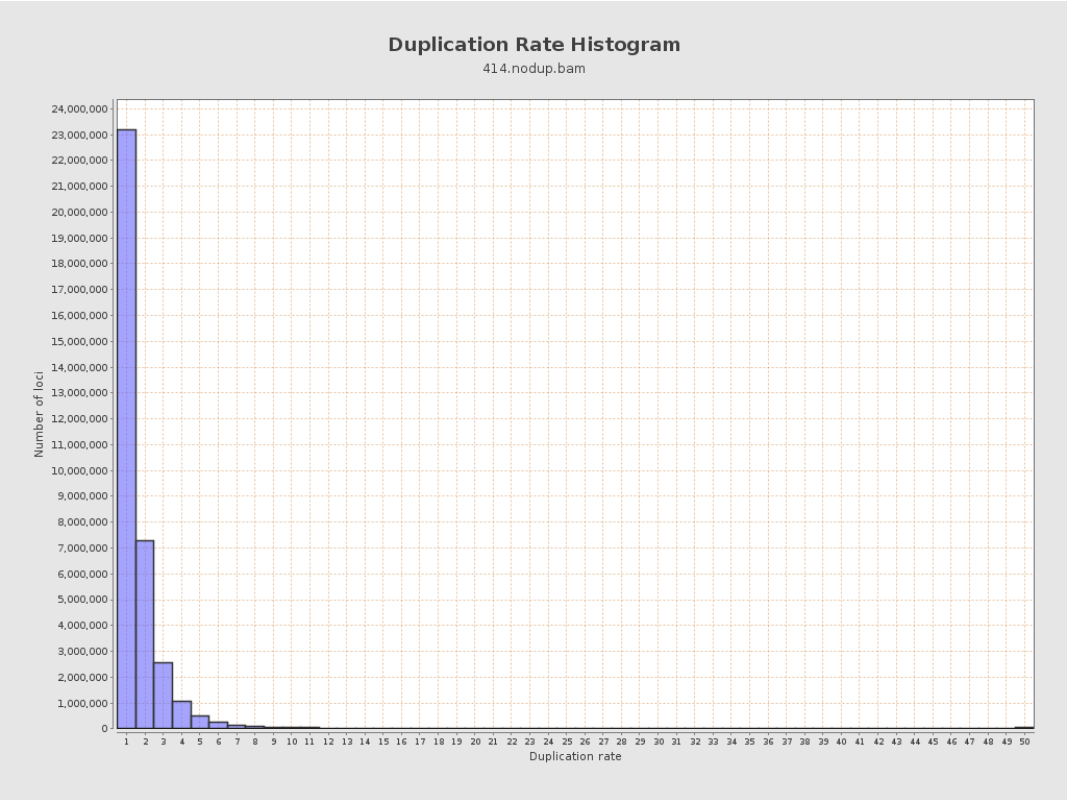
5. Results : Coverage Histogram (0-50X)



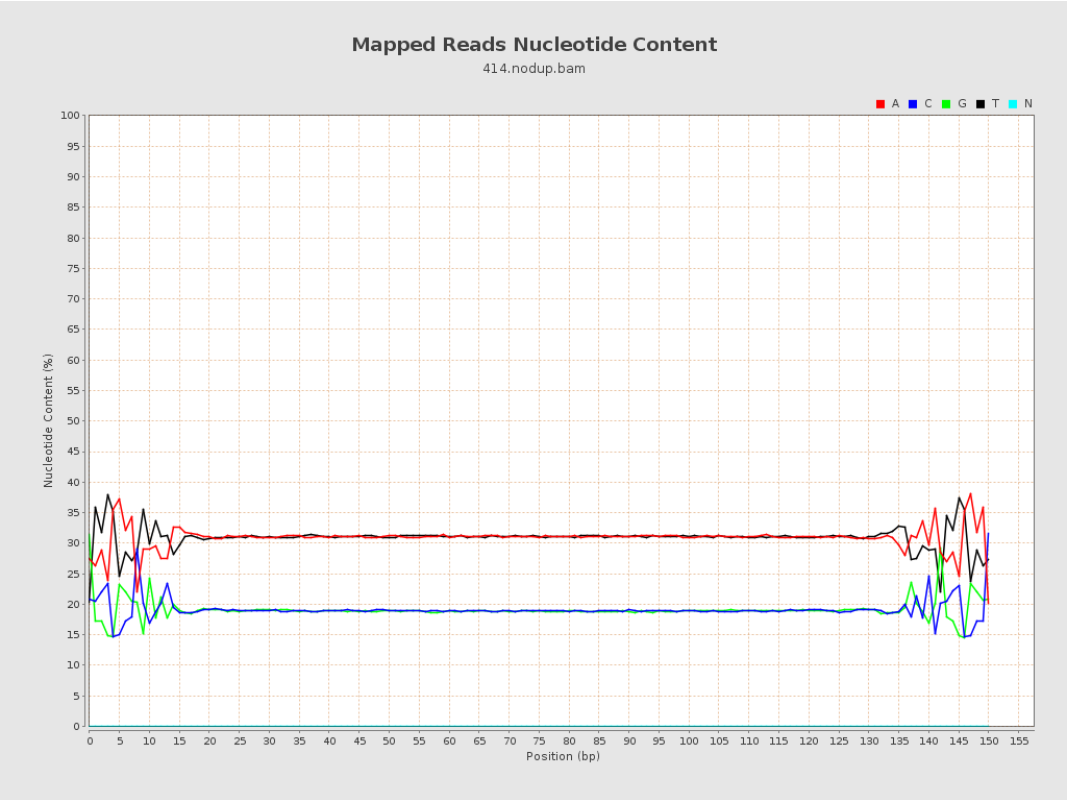
6. Results : Genome Fraction Coverage



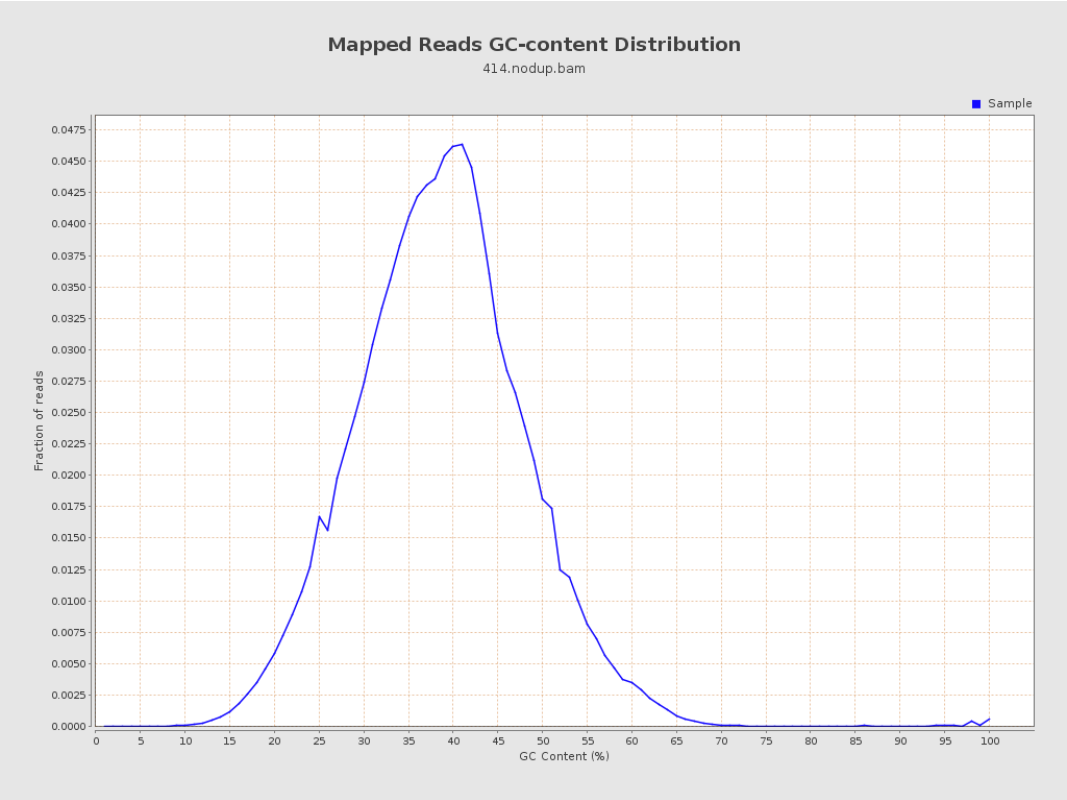
7. Results : Duplication Rate Histogram



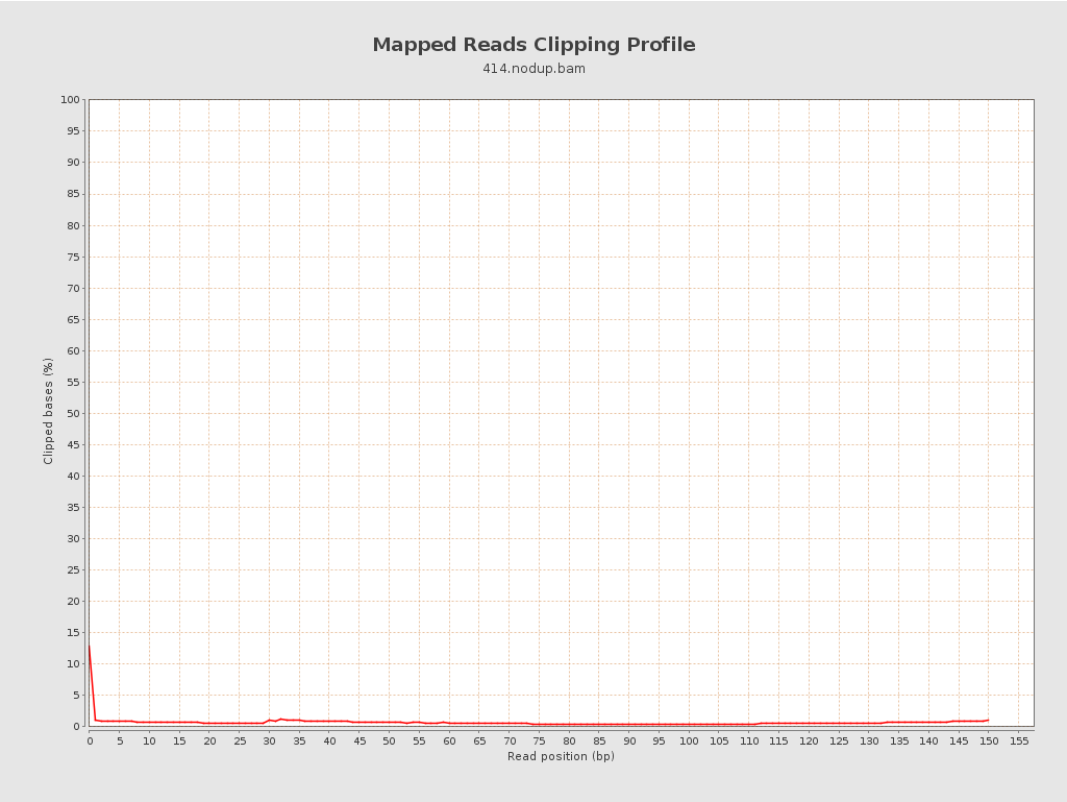
8. Results : Mapped Reads Nucleotide Content



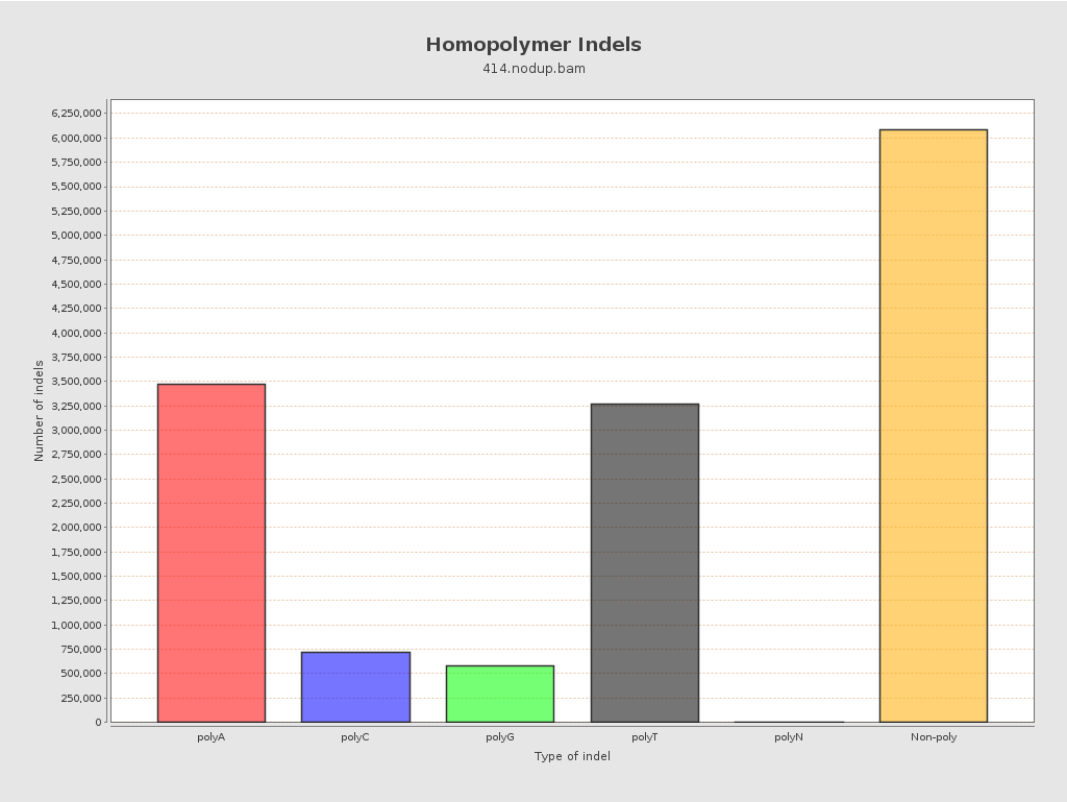
9. Results : Mapped Reads GC-content Distribution



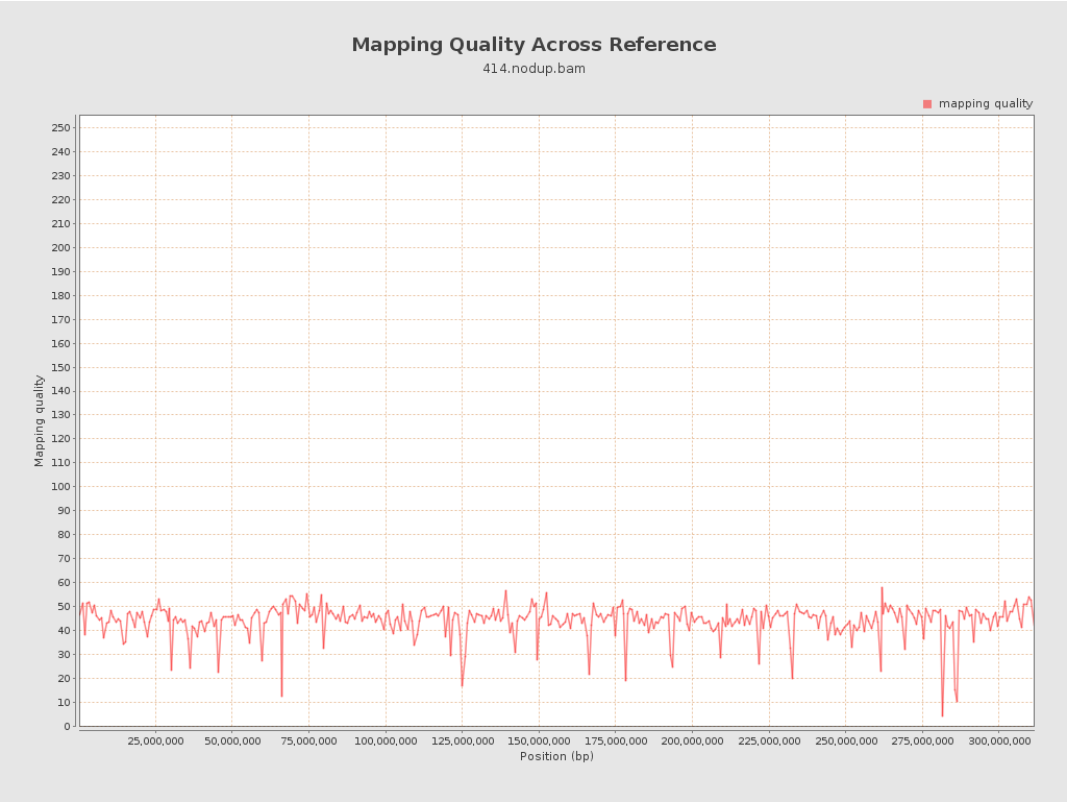
10. Results : Mapped Reads Clipping Profile



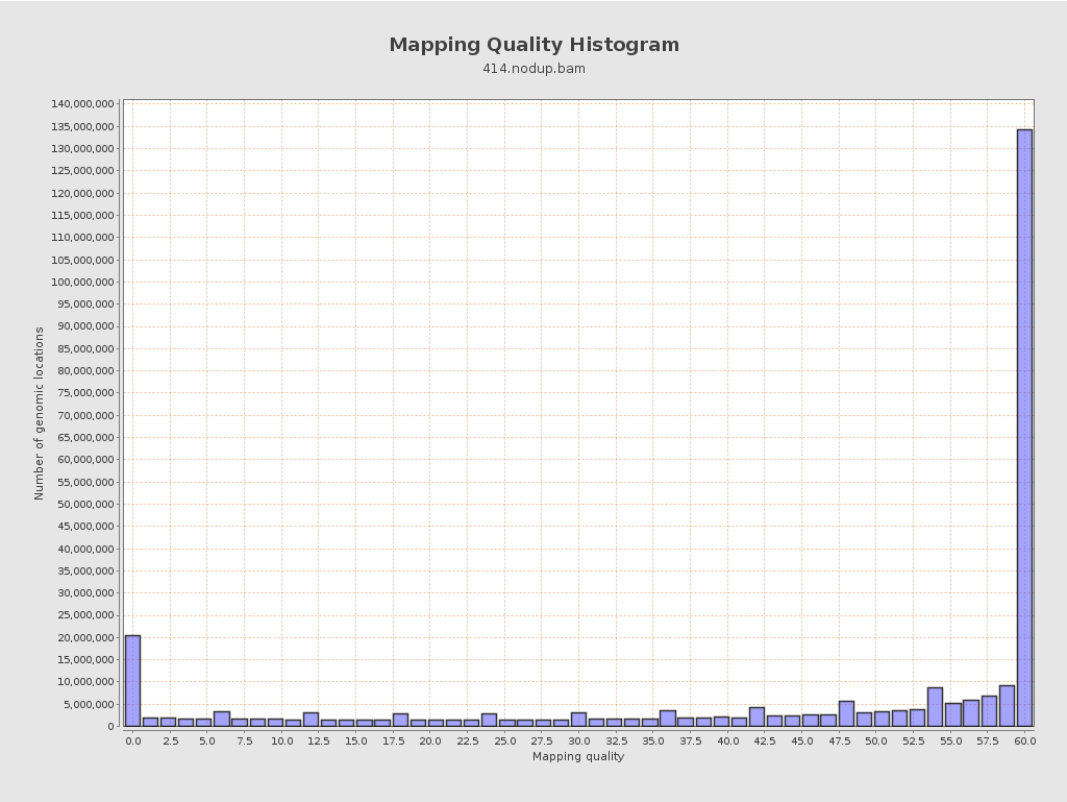
11. Results : Homopolymer Indels



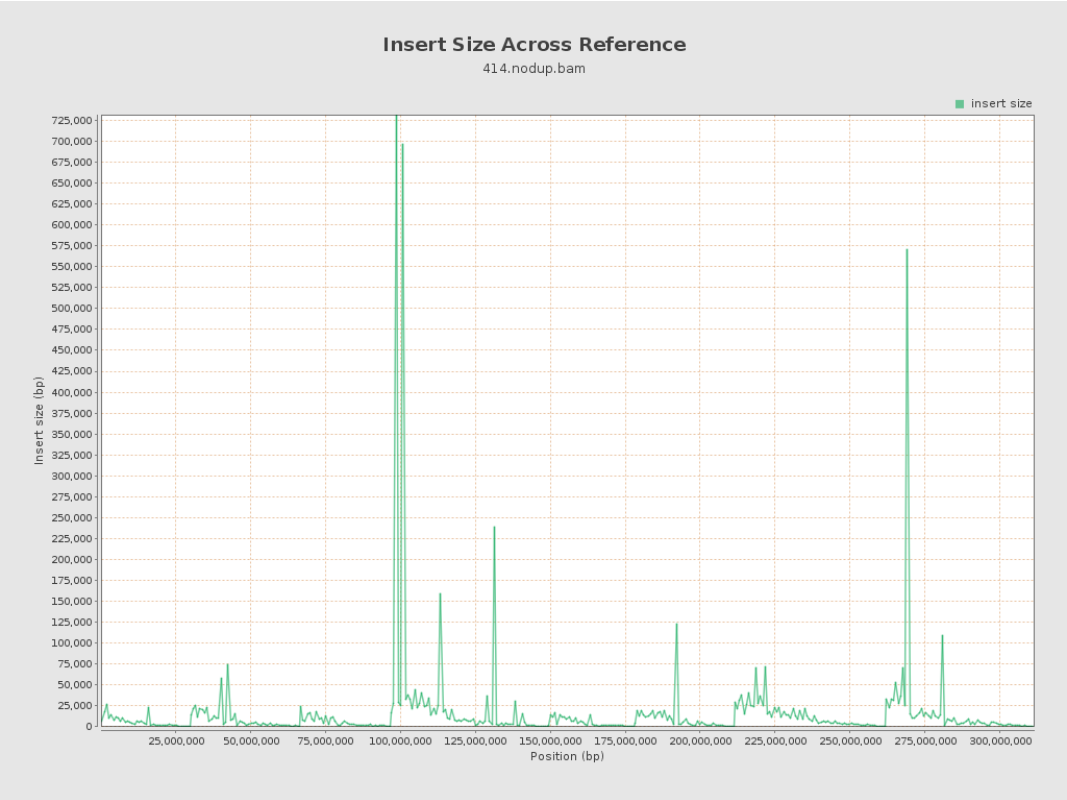
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram