Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1422
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1422 .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_147/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_147_S237_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_147/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_147_S237_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:36:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	81,859,176
Mapped reads	75,797,331 / 92.59%
Unmapped reads	6,061,845 / 7.41%
Mapped paired reads	75,797,331 / 92.59%
Mapped reads, first in pair	37,979,637 / 46.4%
Mapped reads, second in pair	37,817,694 / 46.2%
Mapped reads, both in pair	73,853,796 / 90.22%
Mapped reads, singletons	1,943,535 / 2.37%
Read min/max/mean length	30 / 151 / 148.29
Duplicated reads (flagged)	13,624,762 / 16.64%
Clipped reads	16,567,476 / 20.24%

2.2. ACGT Content

Number/percentage of A's	3,258,197,669 / 31%
Number/percentage of C's	1,997,729,291 / 19.01%
Number/percentage of T's	3,260,658,788 / 31.03%
Number/percentage of G's	1,992,723,143 / 18.96%
Number/percentage of N's	43,930 / 0%
GC Percentage	37.97%

2.3. Coverage

Mean	33.8067
Standard Deviation	270.1638

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Insert size

Mean	237,278.47
Standard Deviation	2,338,060.04
P25/Median/P75	335 / 438 / 573

2.6. Mismatches and indels

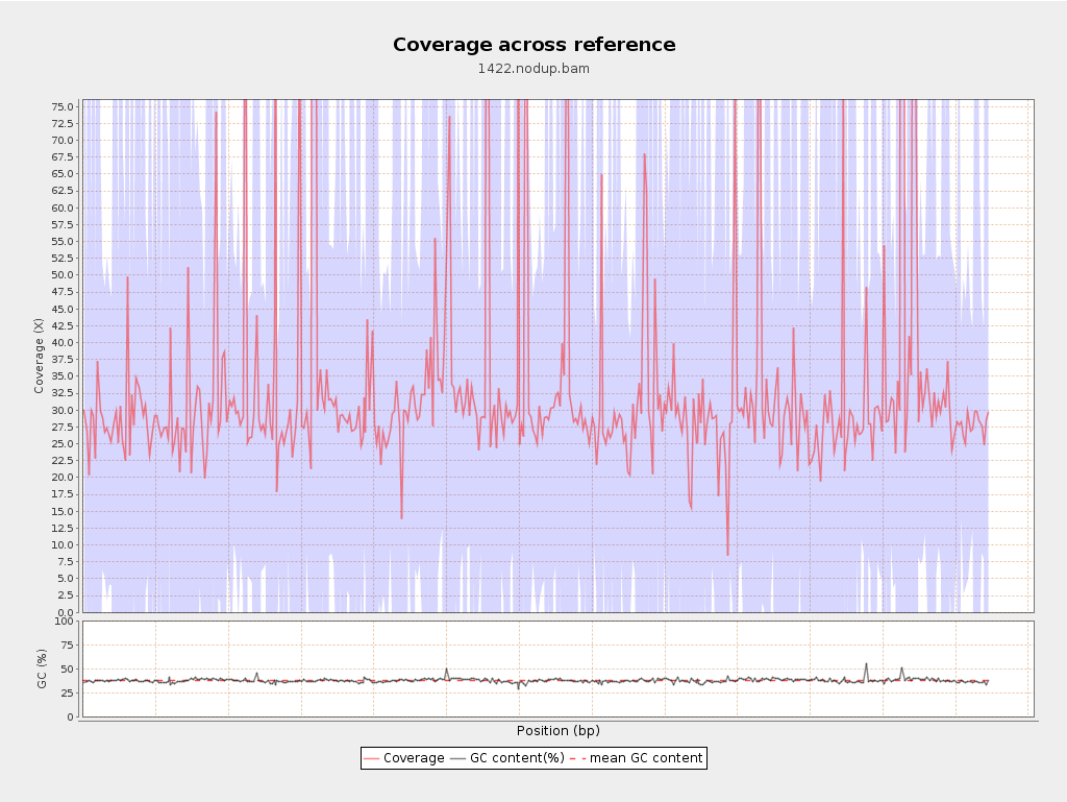
General error rate	2.26%
Mismatches	216,939,201
Insertions	7,189,006
Mapped reads with at least one insertion	8.49%
Deletions	7,014,907
Mapped reads with at least one deletion	8.22%
Homopolymer indels	57.32%

2.7. Chromosome stats

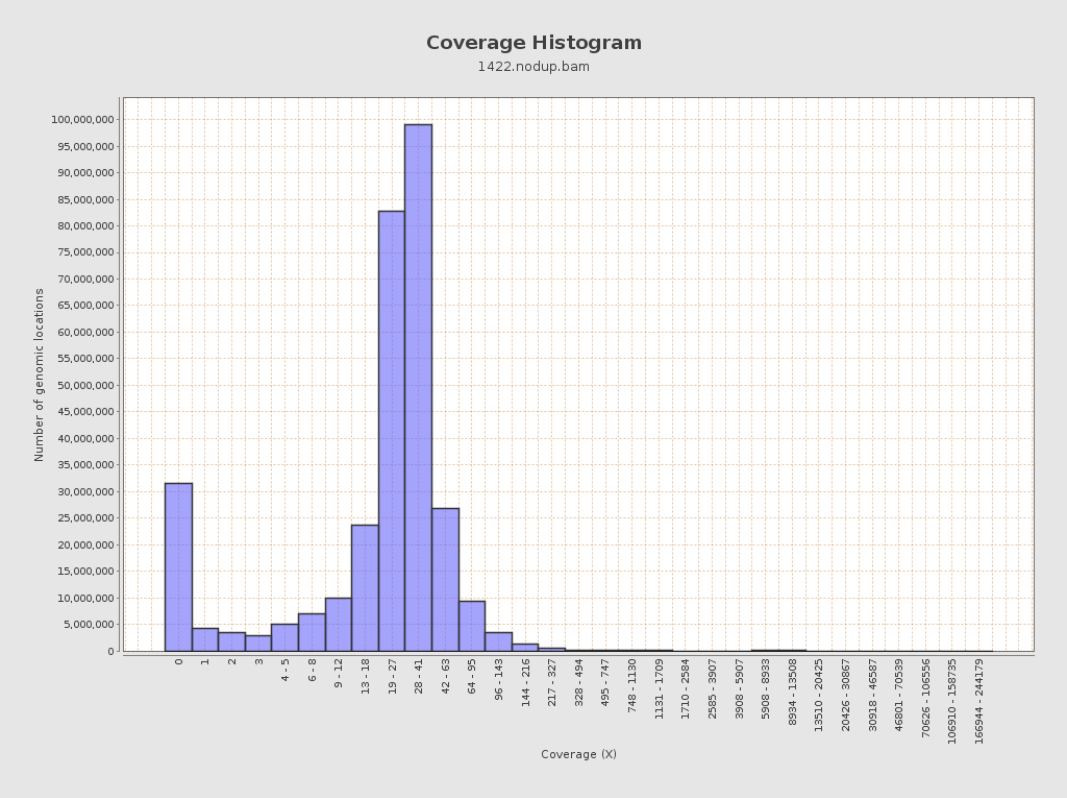
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	848757669	28.5543	94.7734

LT669789.1	36598175	1195996957	32.6791	265.1576
LT669790.1	30422129	1204500497	39.5929	361.8607
LT669791.1	52758100	1769972572	33.5488	267.132
LT669792.1	28376109	970508608	34.2016	297.2328
LT669793.1	33388210	1023118058	30.6431	147.3476
LT669794.1	50579949	1568033679	31.0011	219.665
LT669795.1	49795044	1954713210	39.2552	360.7736

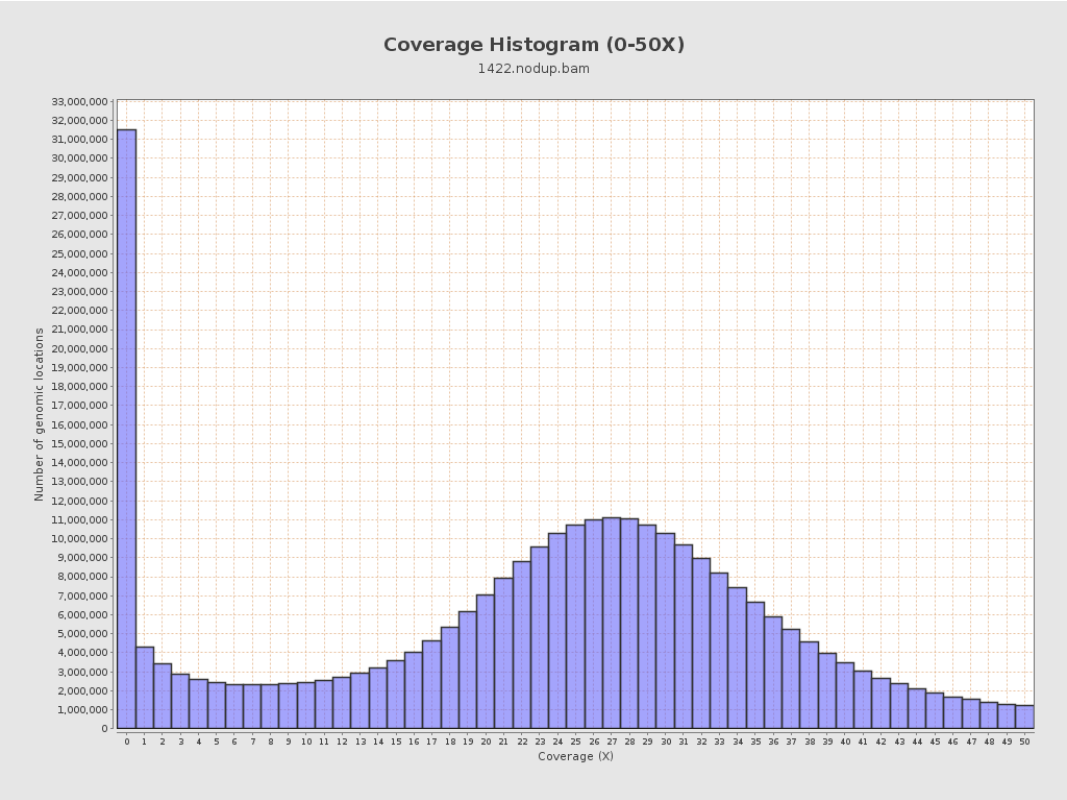
3. Results : Coverage across reference



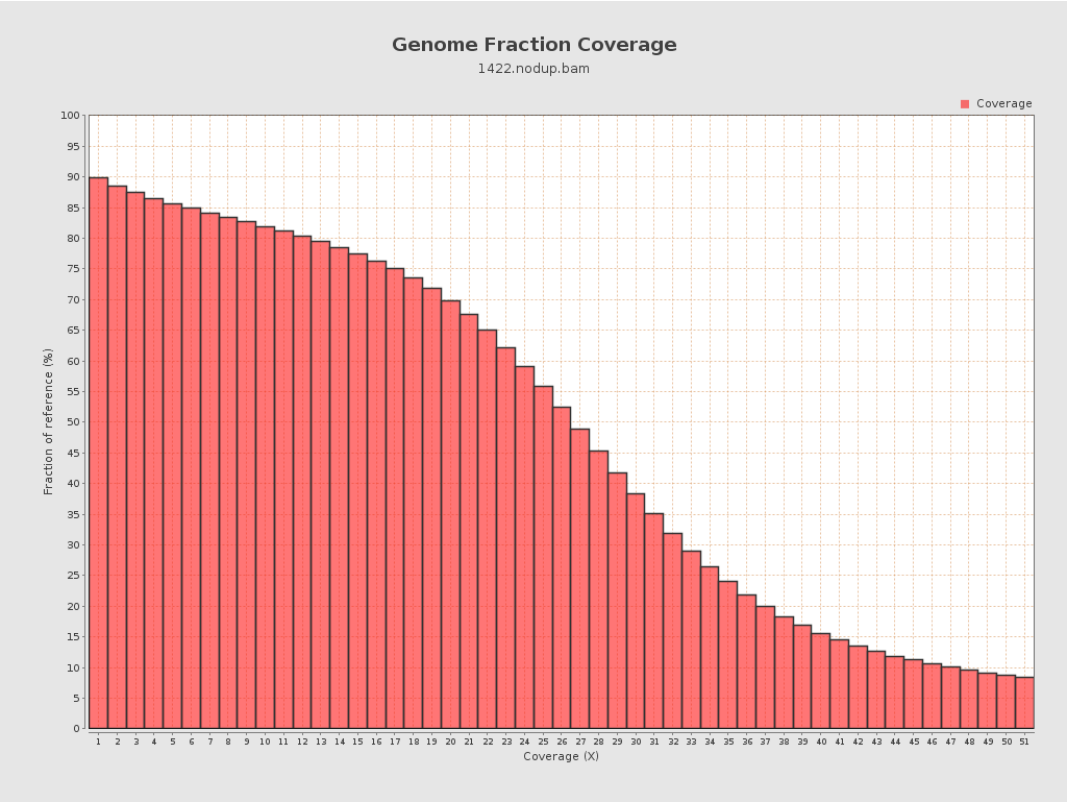
4. Results : Coverage Histogram



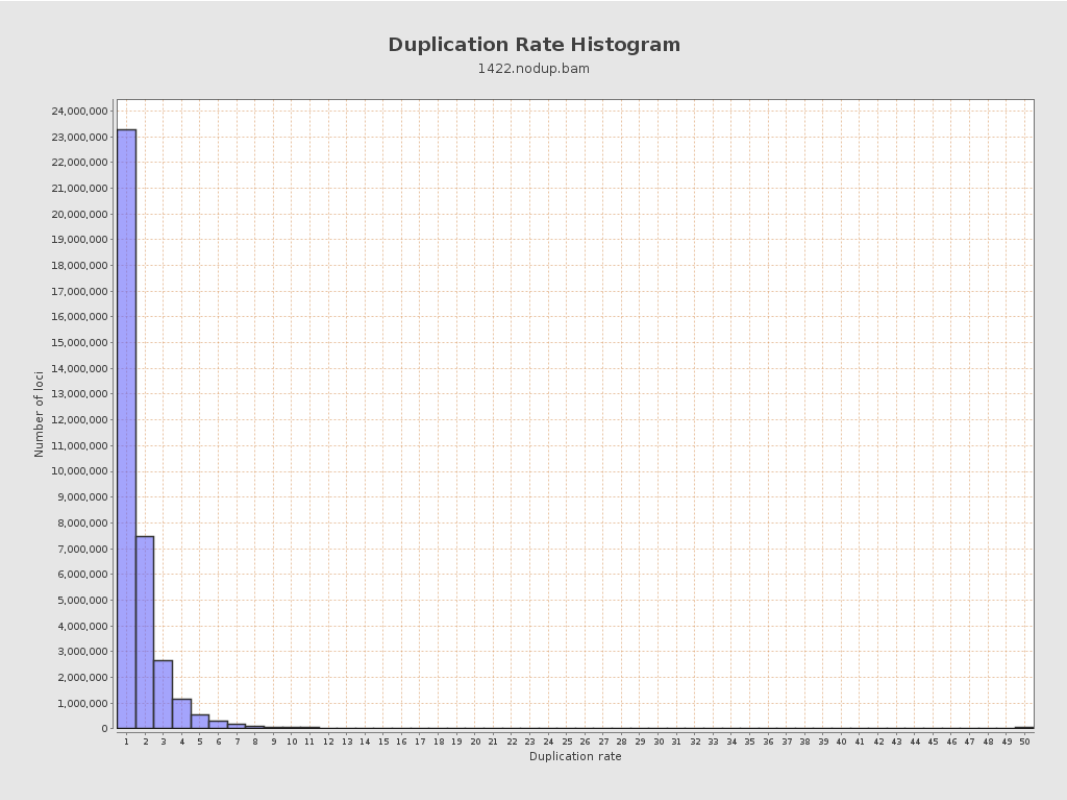
5. Results : Coverage Histogram (0-50X)



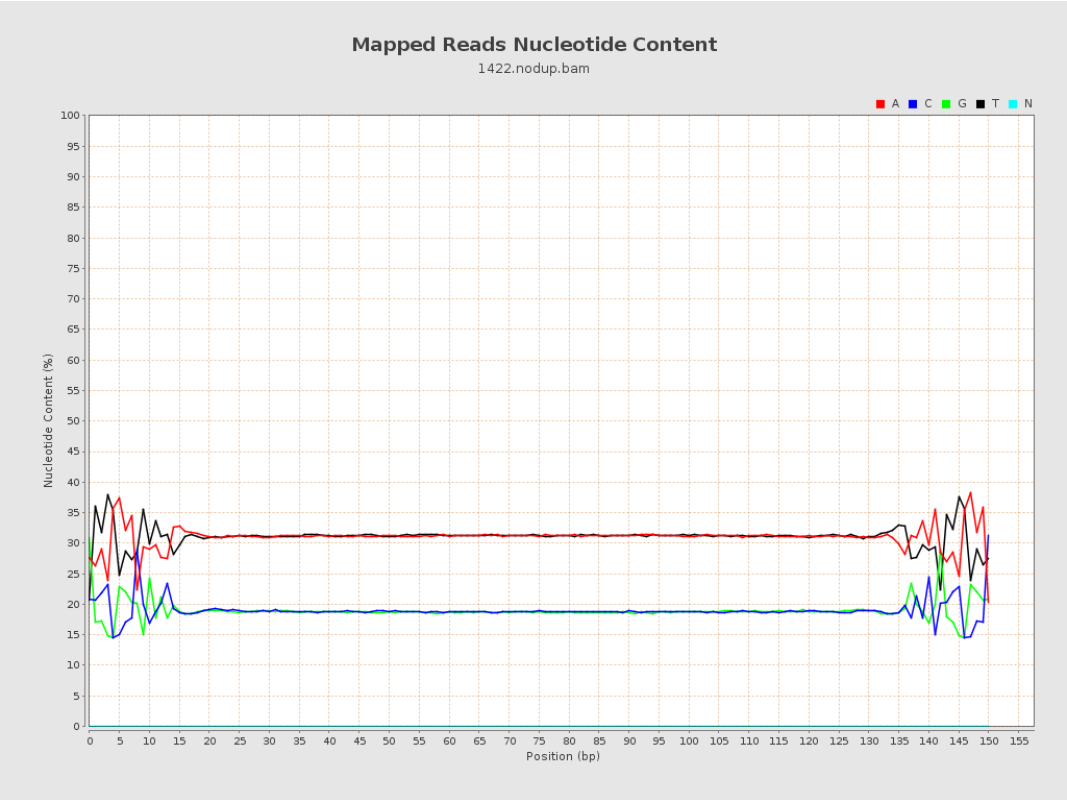
6. Results : Genome Fraction Coverage



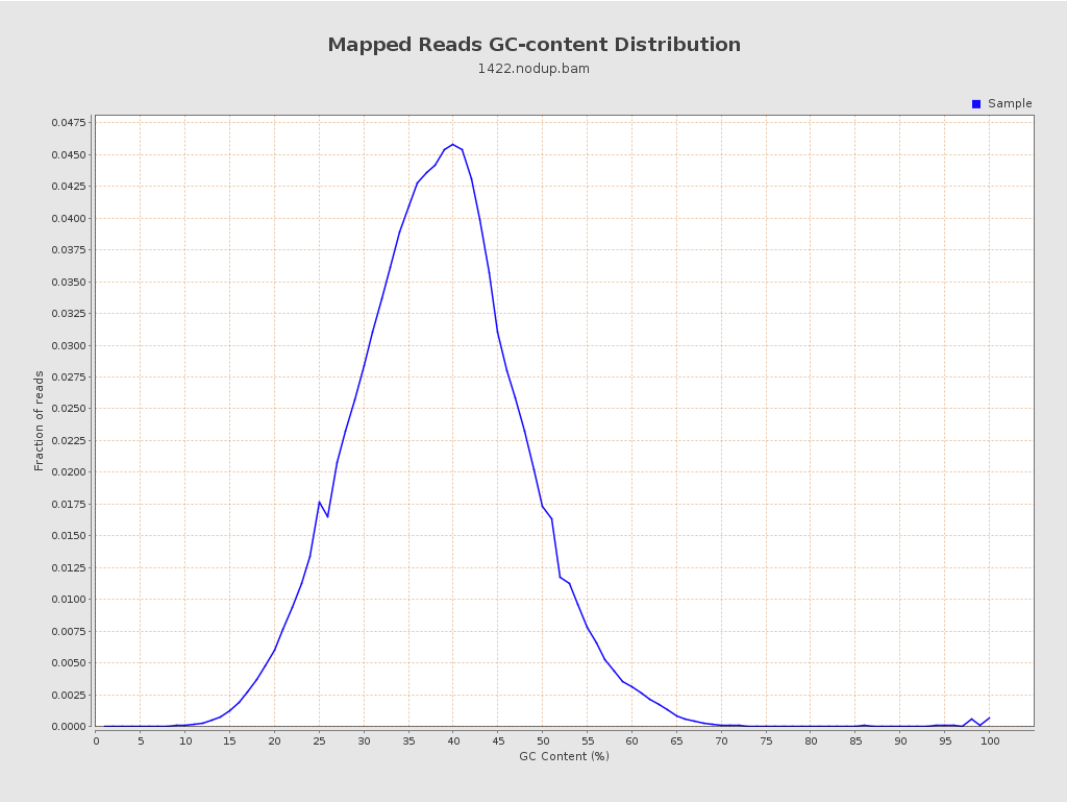
7. Results : Duplication Rate Histogram



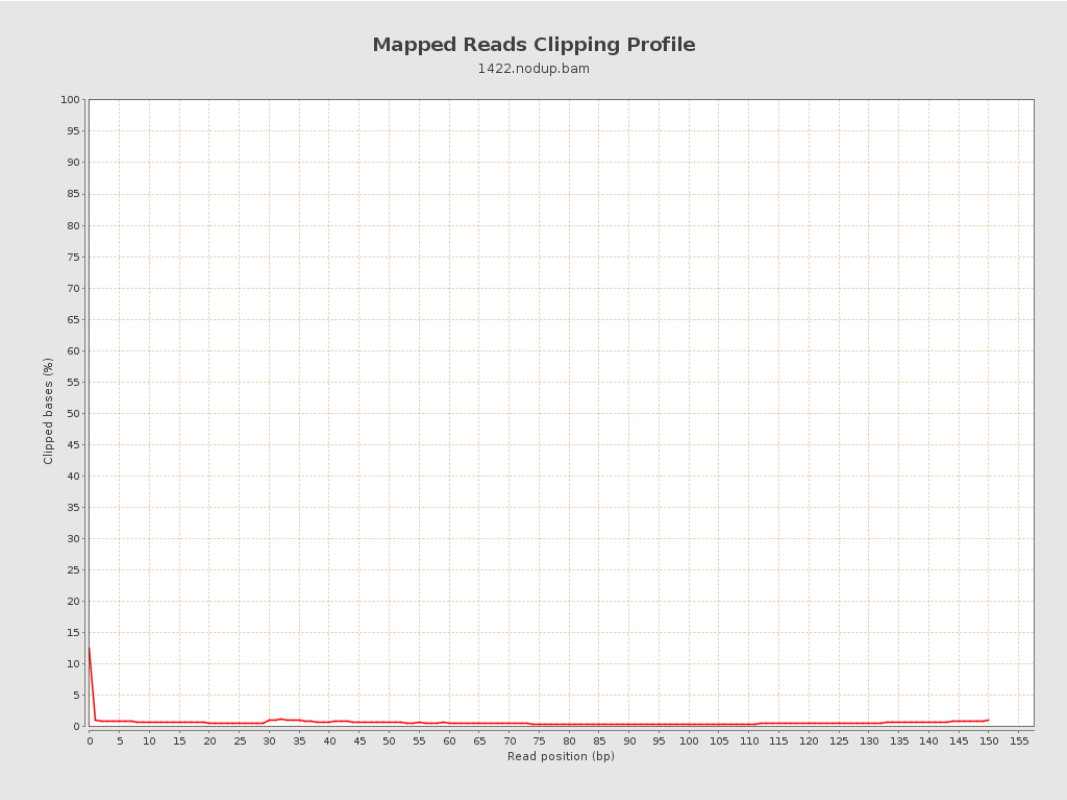
8. Results : Mapped Reads Nucleotide Content



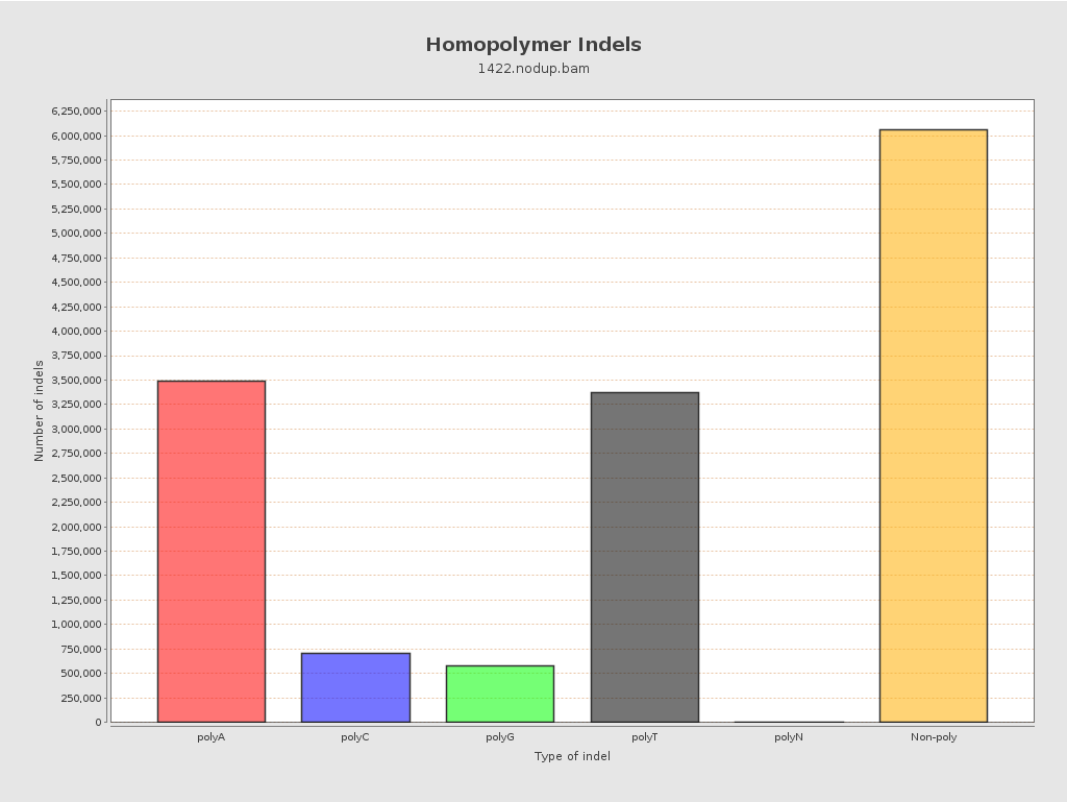
9. Results : Mapped Reads GC-content Distribution



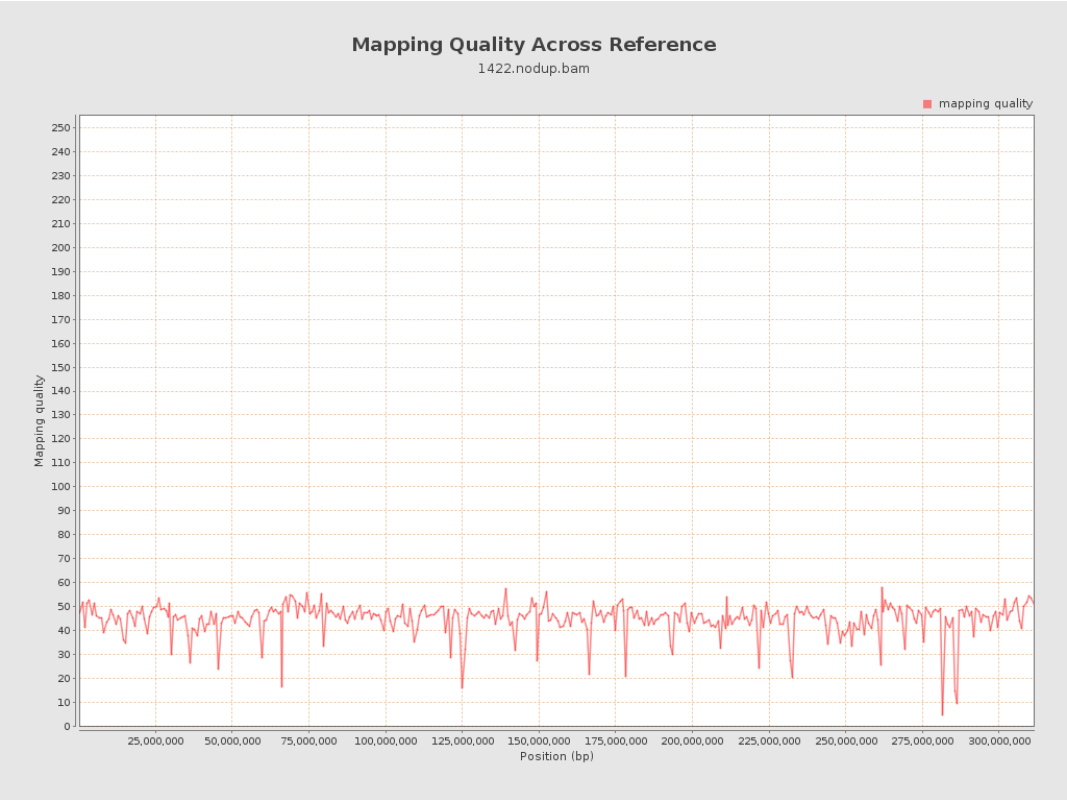
10. Results : Mapped Reads Clipping Profile



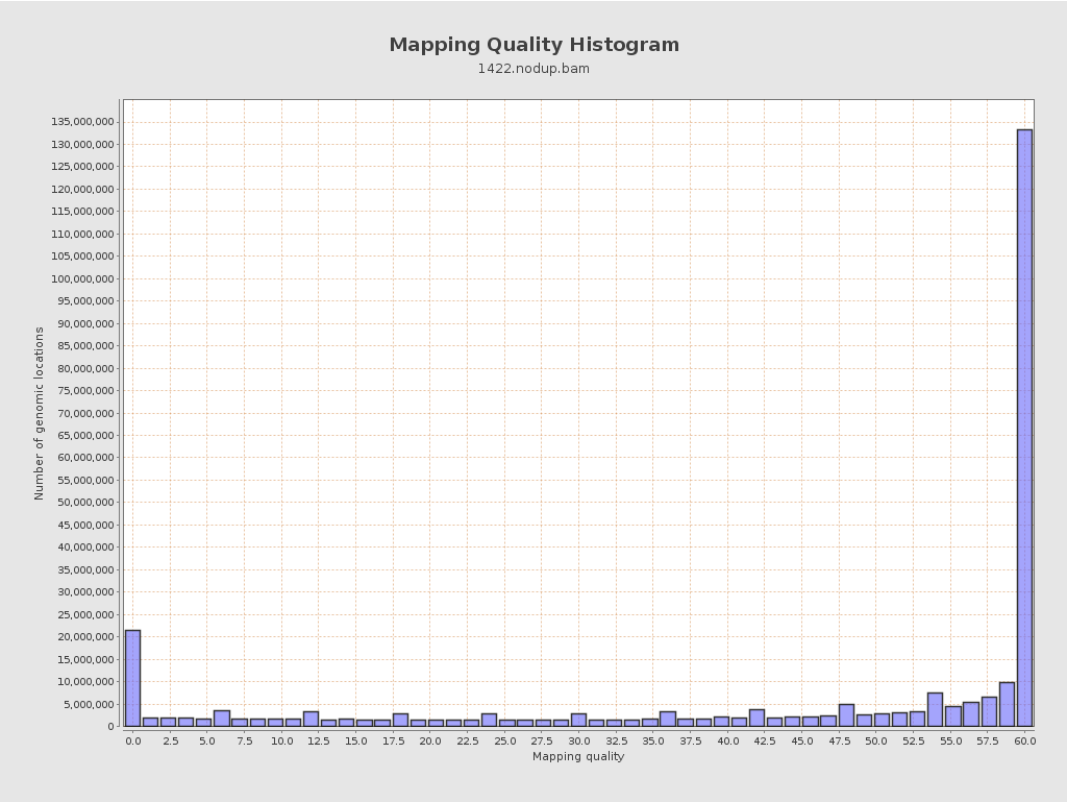
11. Results : Homopolymer Indels



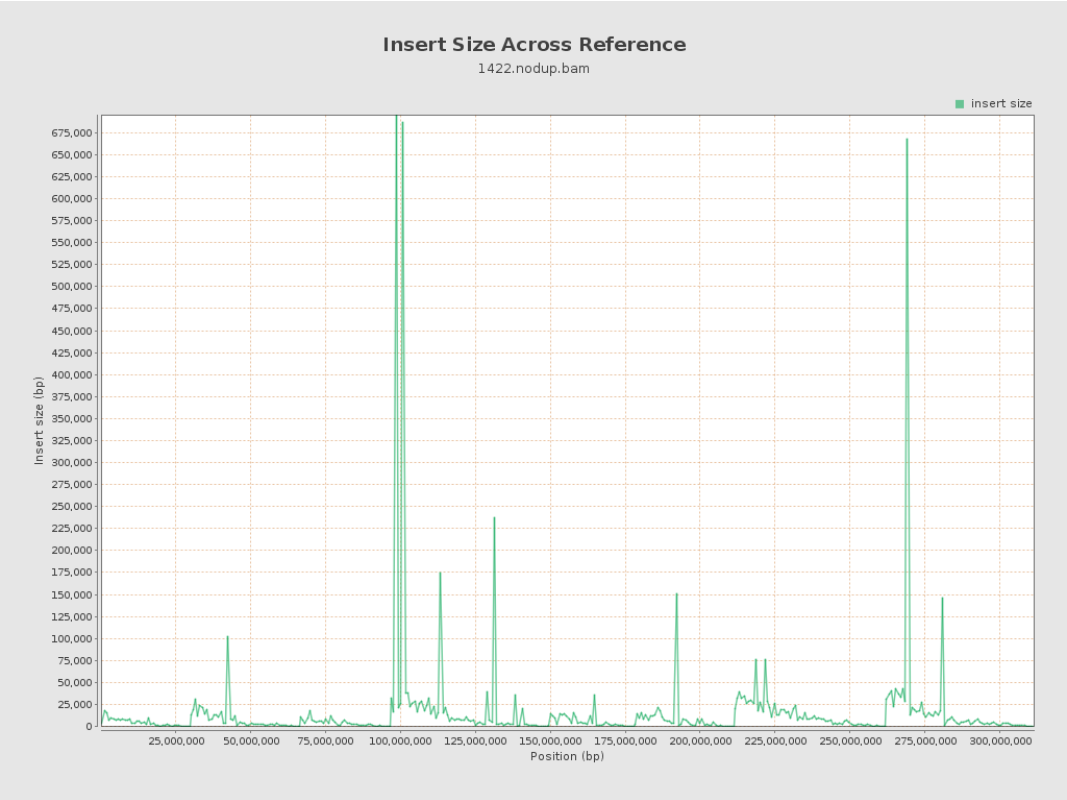
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram