

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/422
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/422.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/awdata/P26207/P26207_188/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_188_S278_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_188/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_188_S278_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:58 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,595,776
Mapped reads	53,771,955 / 90.23%
Unmapped reads	5,823,821 / 9.77%
Mapped paired reads	53,771,955 / 90.23%
Mapped reads, first in pair	26,932,828 / 45.19%
Mapped reads, second in pair	26,839,127 / 45.04%
Mapped reads, both in pair	51,883,944 / 87.06%
Mapped reads, singletons	1,888,011 / 3.17%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	10,469,654 / 17.57%
Clipped reads	12,952,891 / 21.73%

2.2. ACGT Content

Number/percentage of A's	2,282,316,109 / 30.96%
Number/percentage of C's	1,403,791,369 / 19.05%
Number/percentage of T's	2,282,997,592 / 30.97%
Number/percentage of G's	1,401,741,970 / 19.02%
Number/percentage of N's	30,415 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	23.7132
Standard Deviation	234.8222

2.4. Mapping Quality

Mean Mapping Quality	44.16
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2.5. Insert size

Mean	272,470.74
Standard Deviation	2,522,581.8
P25/Median/P75	345 / 446 / 572

2.6. Mismatches and indels

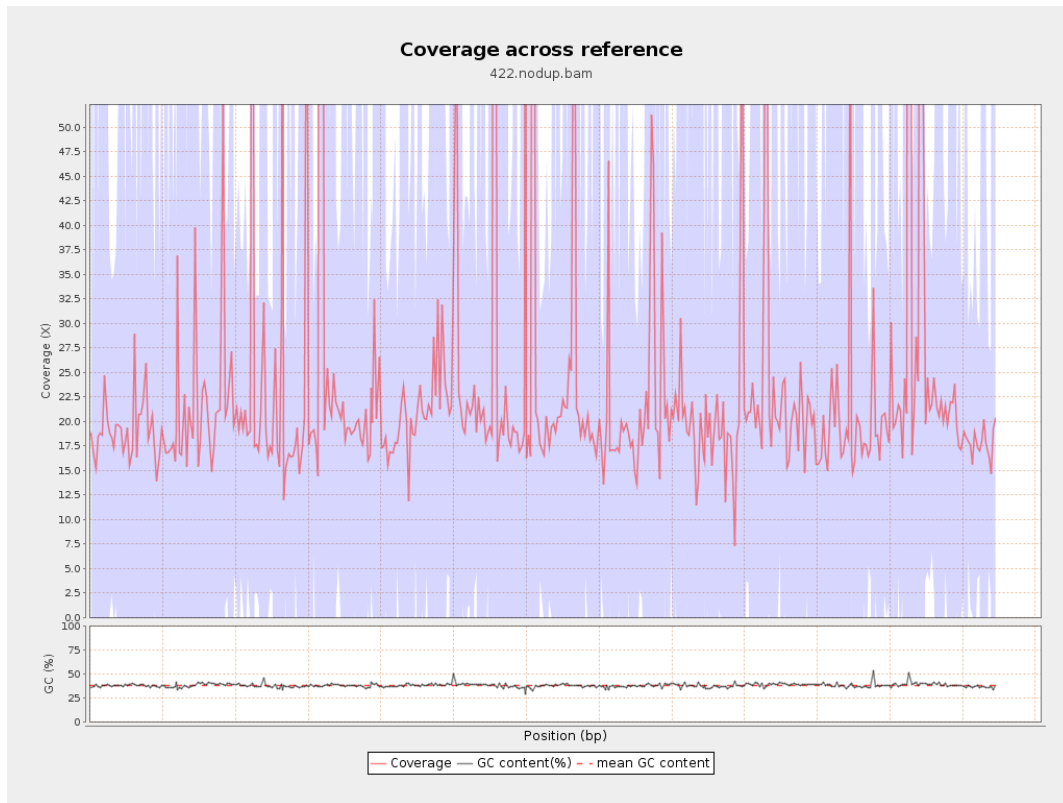
General error rate	2.49%
Mismatches	168,321,730
Insertions	5,514,151
Mapped reads with at least one insertion	9.13%
Deletions	5,203,409
Mapped reads with at least one deletion	8.57%
Homopolymer indels	57.19%

2.7. Chromosome stats

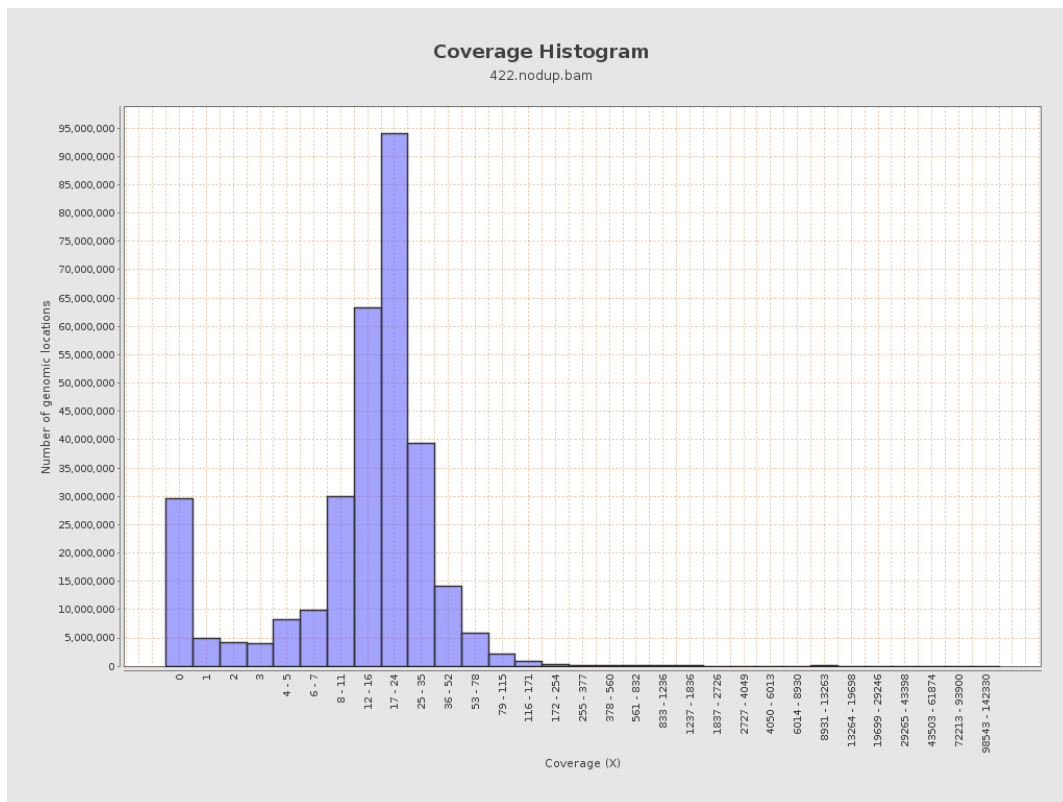
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	557771068	18.7648	92.2868

LT669789.1	36598175	865345812	23.6445	240.5655
LT669790.1	30422129	897634206	29.506	346.3857
LT669791.1	52758100	1236930484	23.4453	252.5152
LT669792.1	28376109	683560823	24.0893	255.6303
LT669793.1	33388210	707295992	21.184	126.6842
LT669794.1	50579949	1121769065	22.1781	193.8058
LT669795.1	49795044	1319723368	26.5031	265.3698

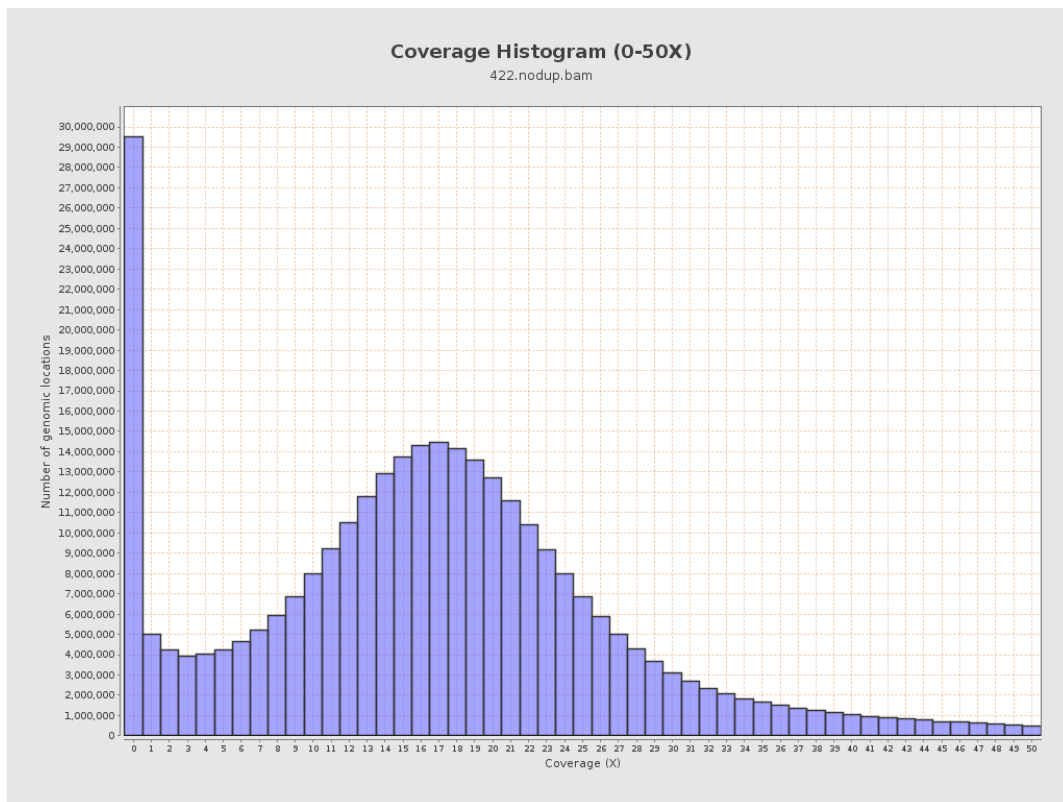
3. Results : Coverage across reference



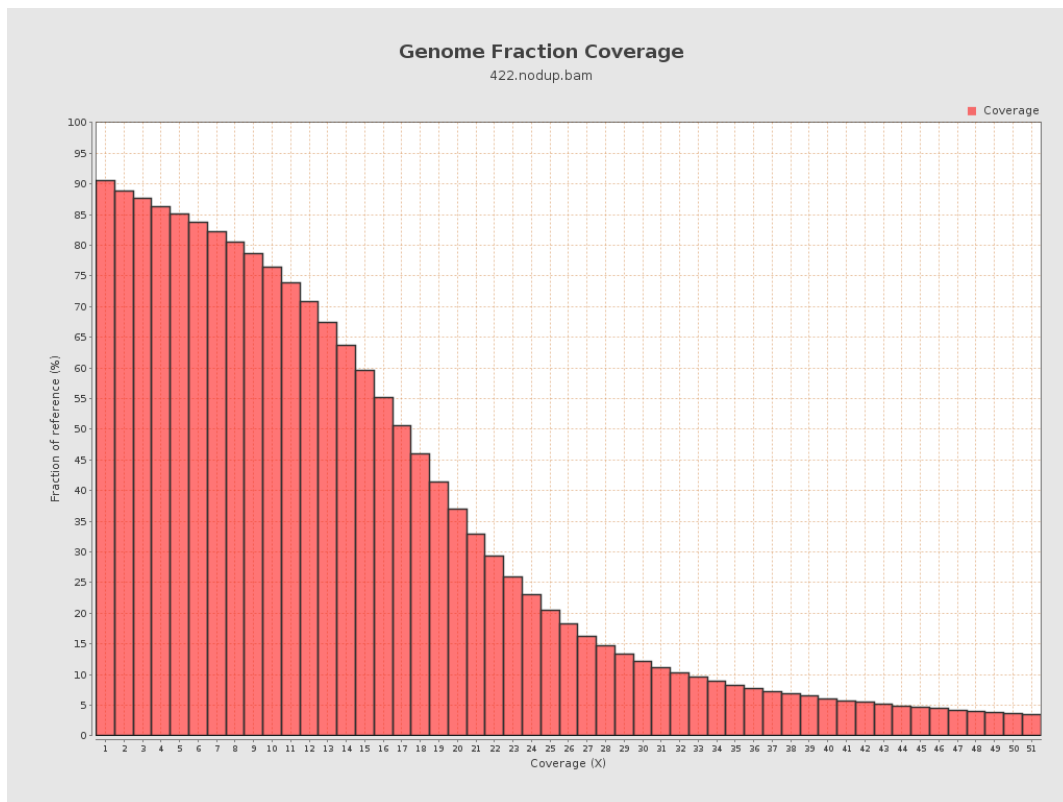
4. Results : Coverage Histogram



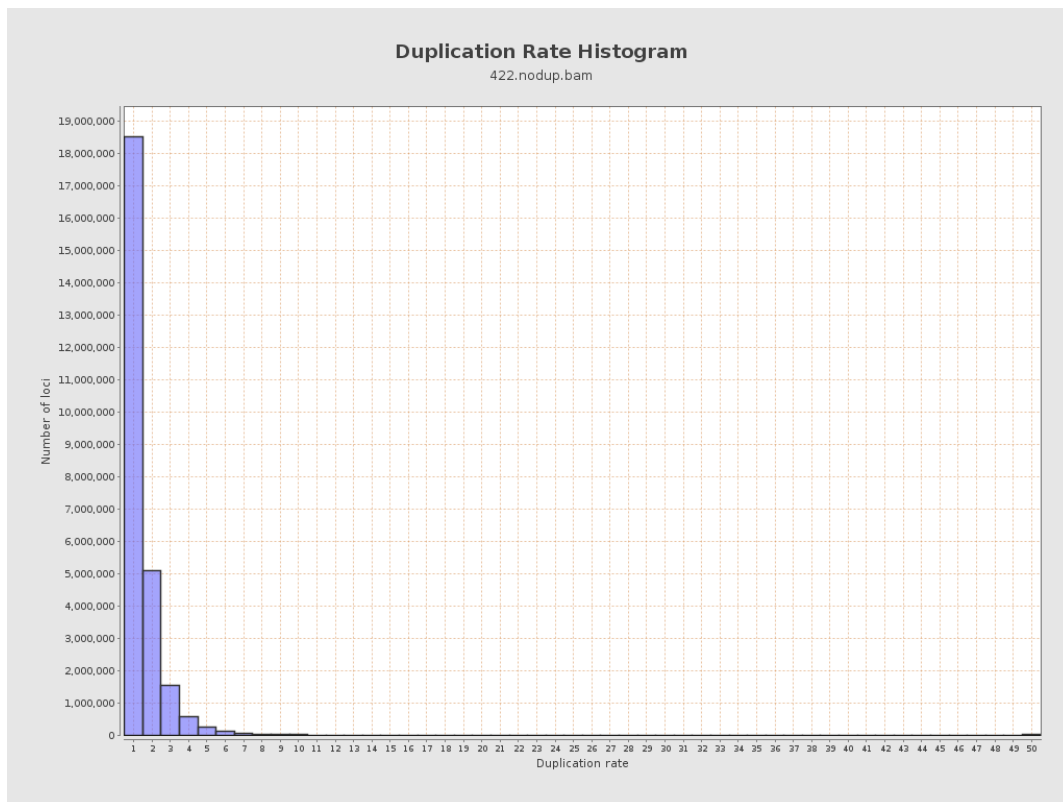
5. Results : Coverage Histogram (0-50X)



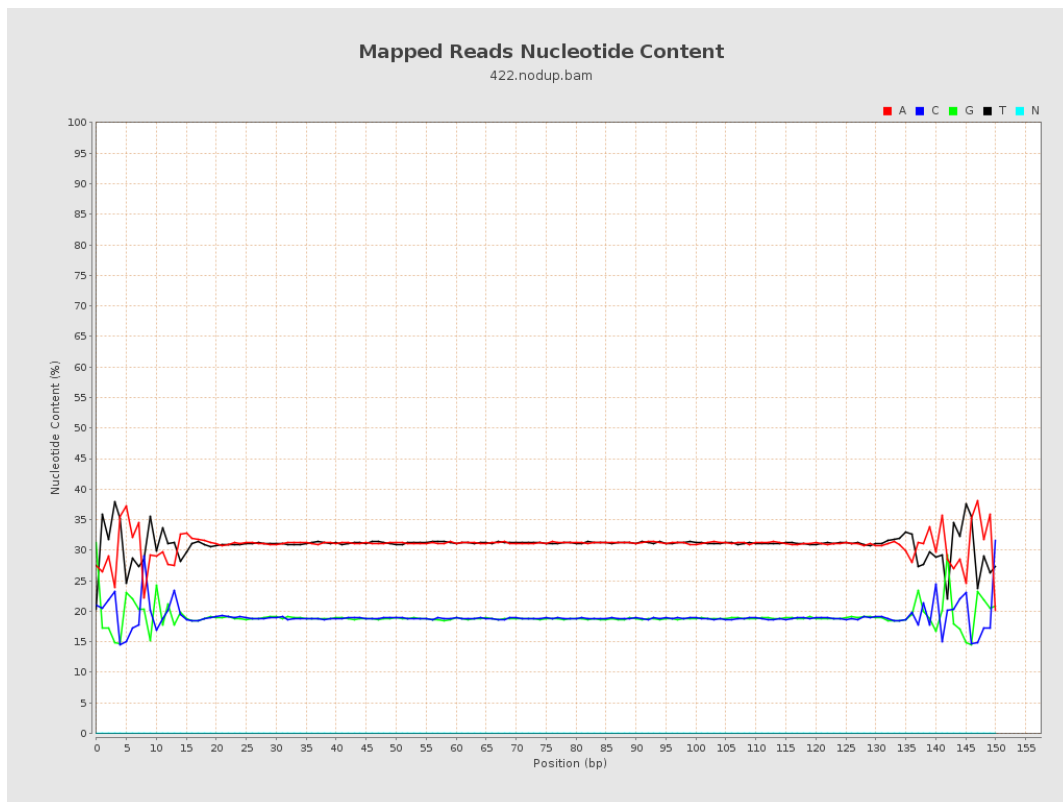
6. Results : Genome Fraction Coverage



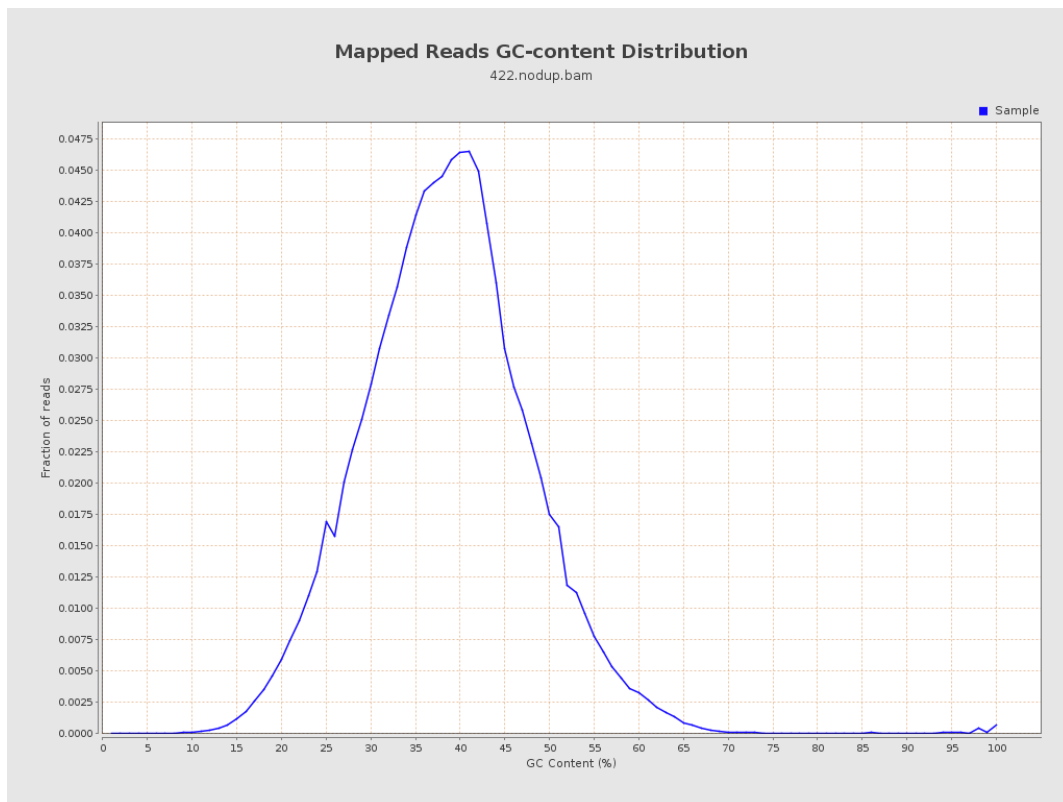
7. Results : Duplication Rate Histogram



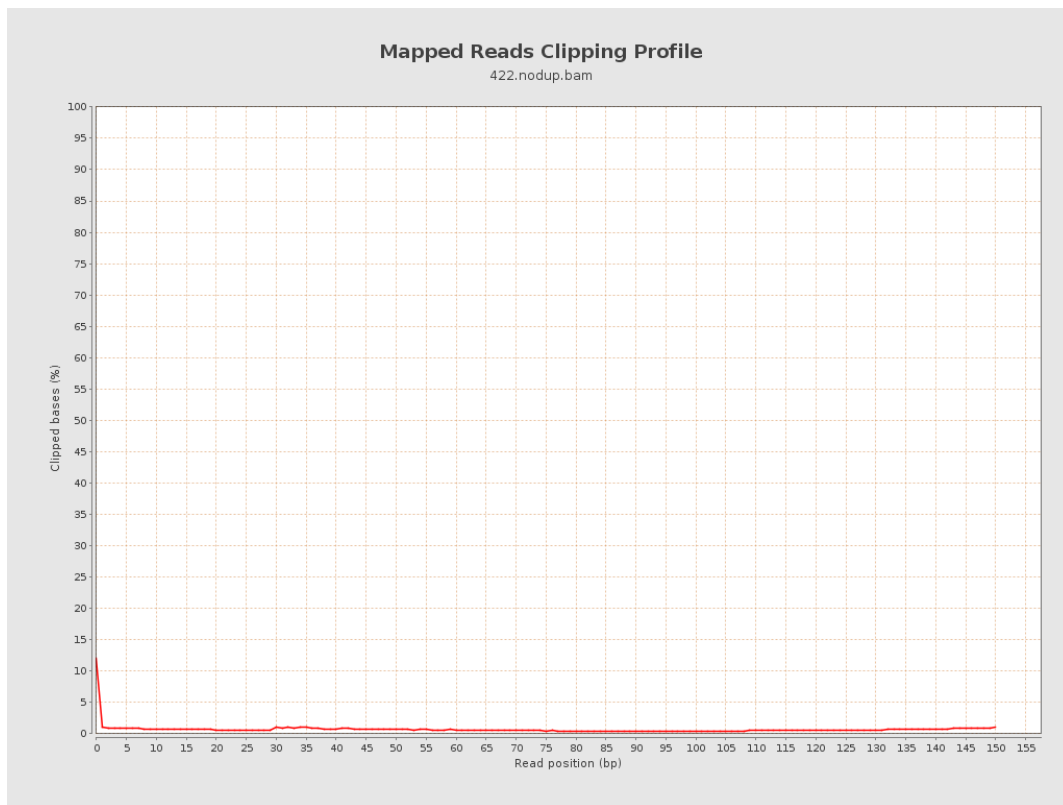
8. Results : Mapped Reads Nucleotide Content



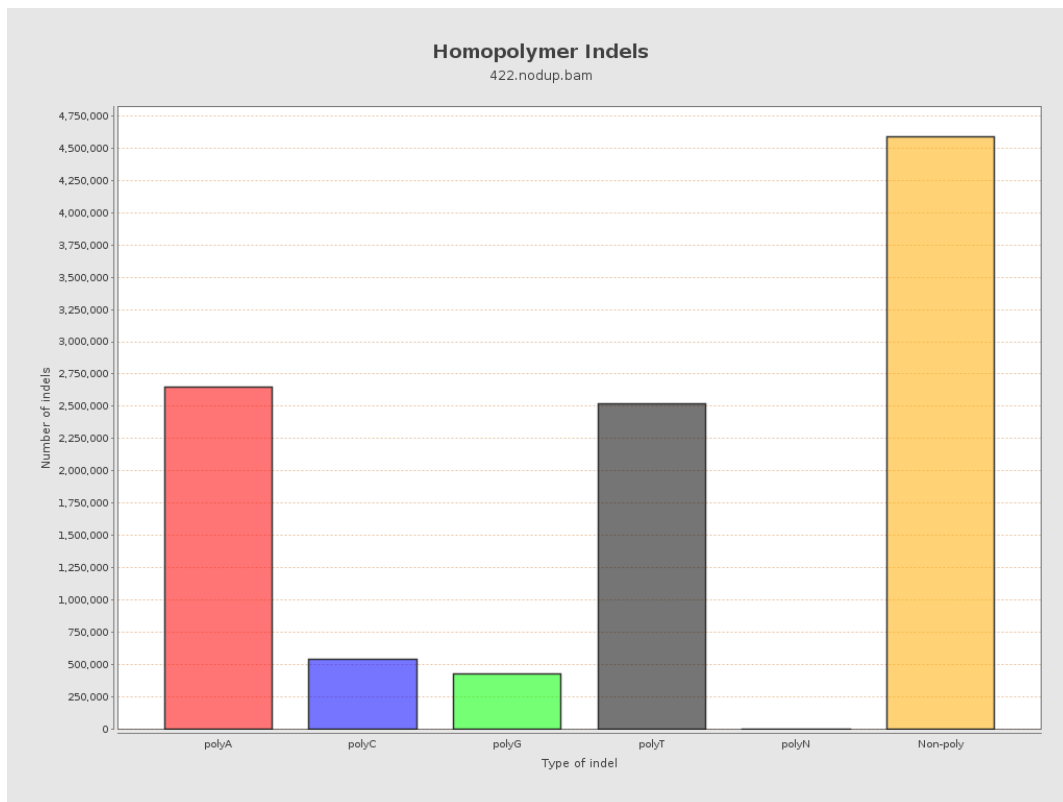
9. Results : Mapped Reads GC-content Distribution



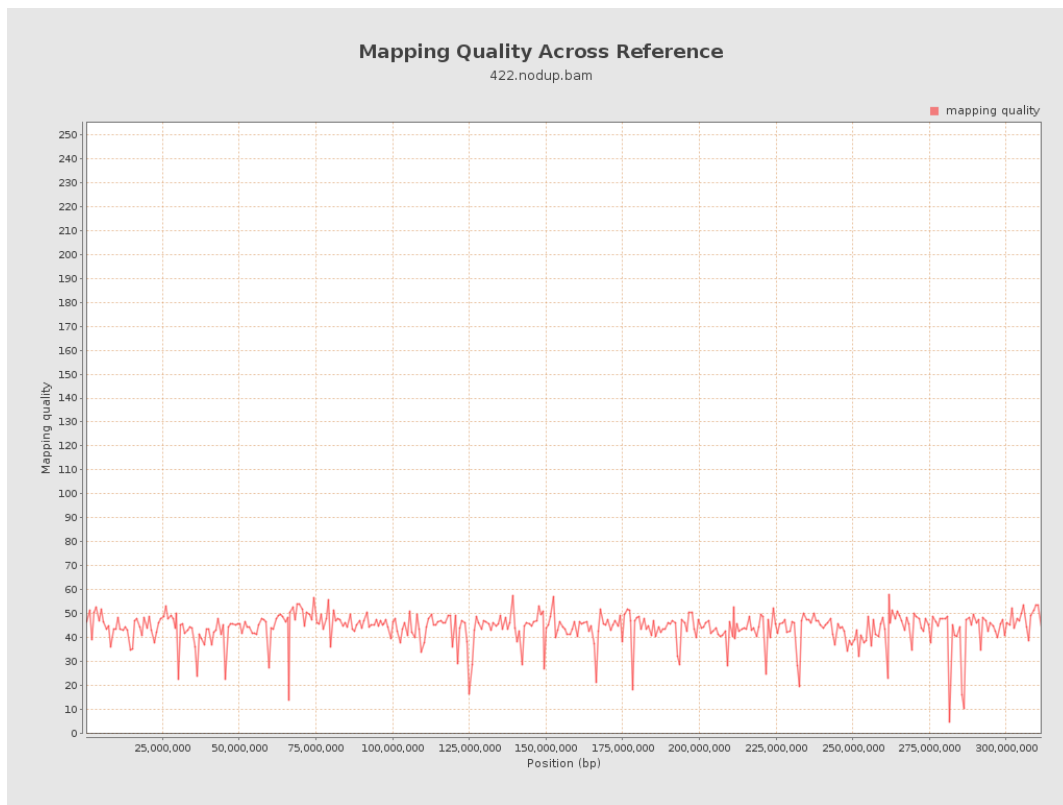
10. Results : Mapped Reads Clipping Profile



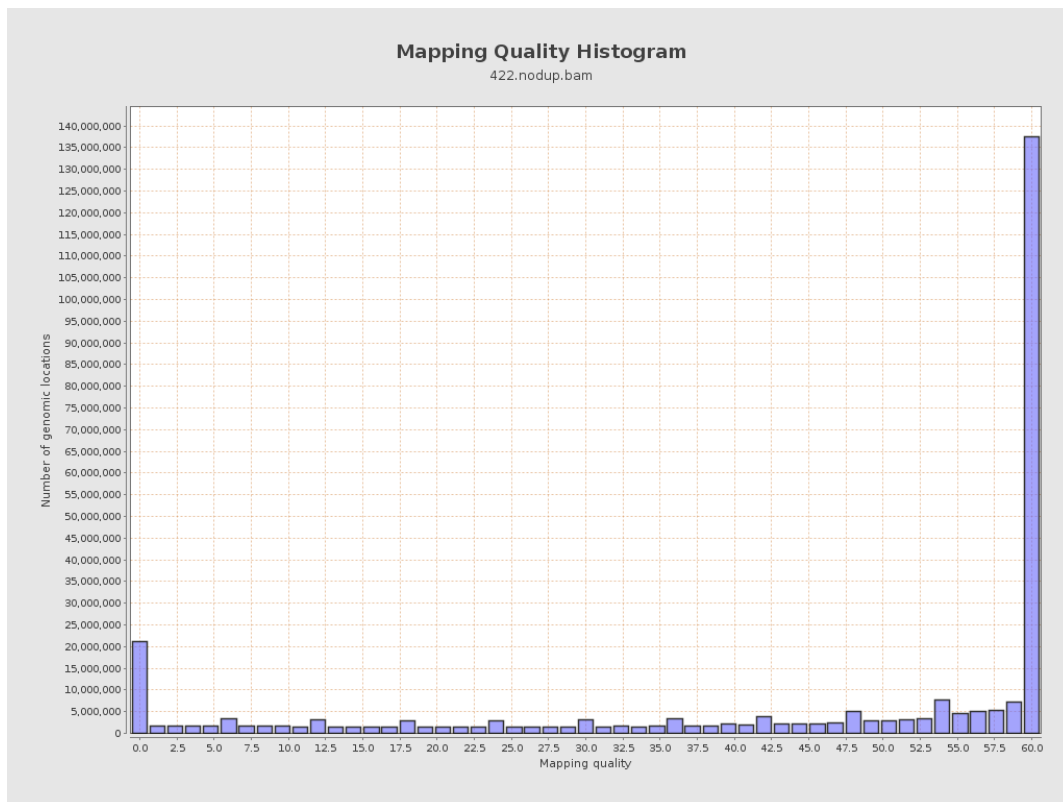
11. Results : Homopolymer Indels



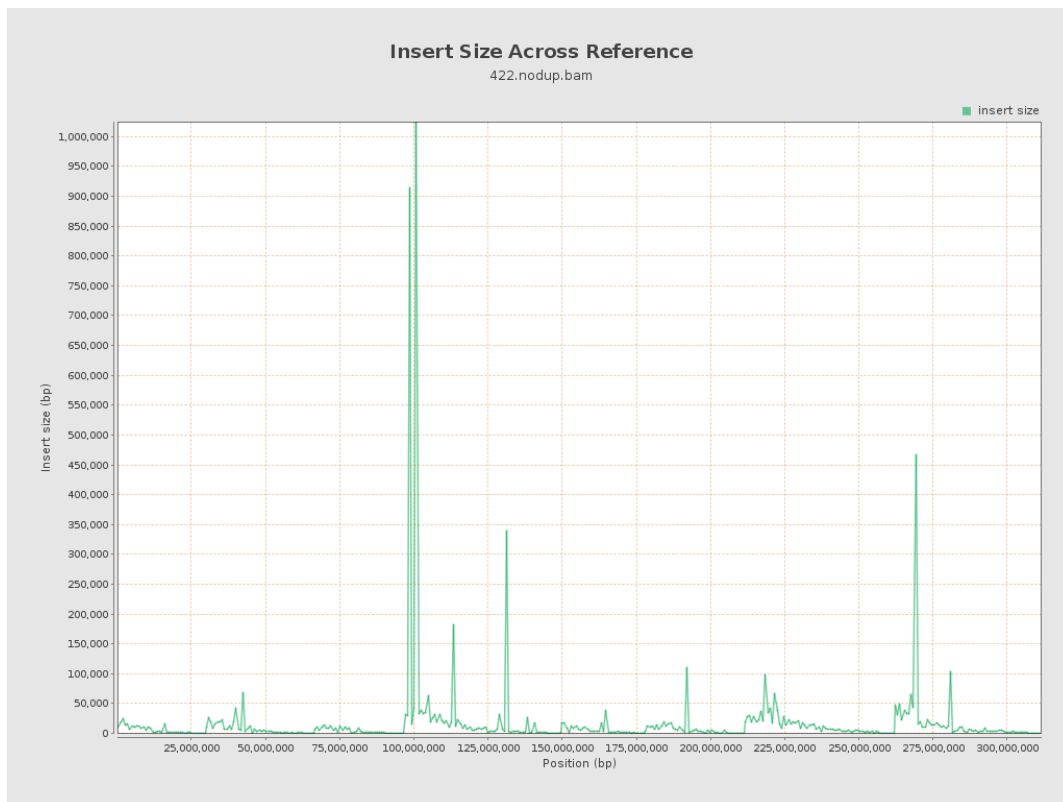
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

