Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/428.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/428.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_271/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_271_S352_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_271/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_271_S352_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,697,824
Mapped reads	61,741,231 / 92.57%
Unmapped reads	4,956,593 / 7.43%
Mapped paired reads	61,741,231 / 92.57%
Mapped reads, first in pair	30,910,200 / 46.34%
Mapped reads, second in pair	30,831,031 / 46.22%
Mapped reads, both in pair	60,176,194 / 90.22%
Mapped reads, singletons	1,565,037 / 2.35%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	9,472,645 / 14.2%
Clipped reads	14,094,770 / 21.13%

2.2. ACGT Content

Number/percentage of A's	2,632,672,196 / 30.88%
Number/percentage of C's	1,631,351,127 / 19.14%
Number/percentage of T's	2,633,879,809 / 30.9%
Number/percentage of G's	1,626,474,459 / 19.08%
Number/percentage of N's	31,481 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	27.4202
Standard Deviation	225.301

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Insert size

Mean	232,062.7
Standard Deviation	2,304,221.4
P25/Median/P75	322 / 421 / 547

2.6. Mismatches and indels

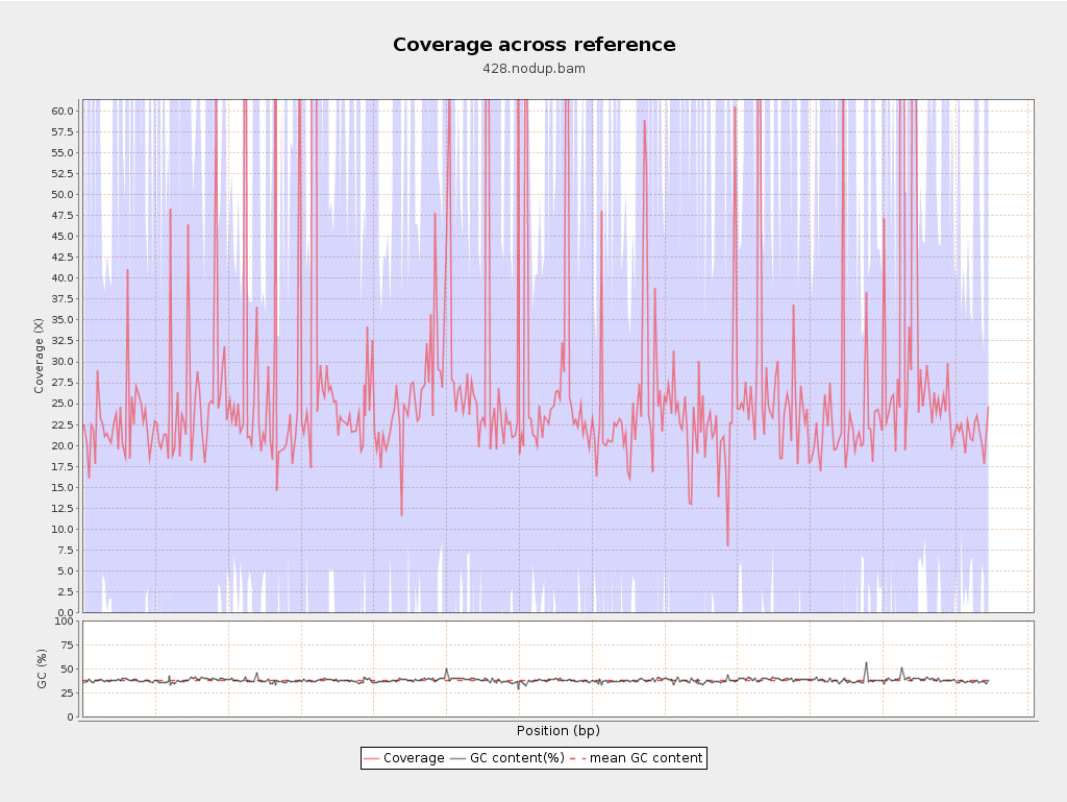
General error rate	2.3%
Mismatches	179,877,691
Insertions	5,769,970
Mapped reads with at least one insertion	8.38%
Deletions	5,623,414
Mapped reads with at least one deletion	8.09%
Homopolymer indels	57%

2.7. Chromosome stats

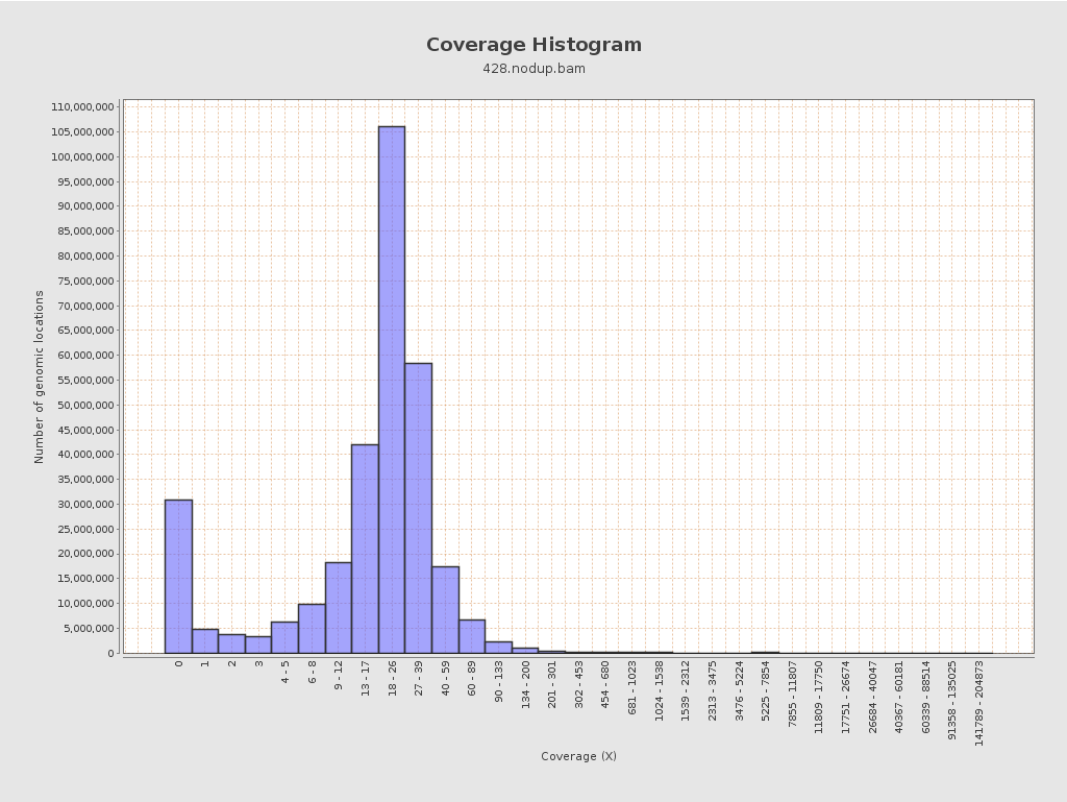
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	665243686	22.3804	77.3353

LT669789.1	36598175	1005297379	27.4685	234.3831
LT669790.1	30422129	963669333	31.6766	285.7444
LT669791.1	52758100	1441600135	27.3247	220.9729
LT669792.1	28376109	776592648	27.3678	254.6543
LT669793.1	33388210	822868767	24.6455	119.3018
LT669794.1	50579949	1282841455	25.3626	181.4712
LT669795.1	49795044	1587172722	31.8741	303.5057

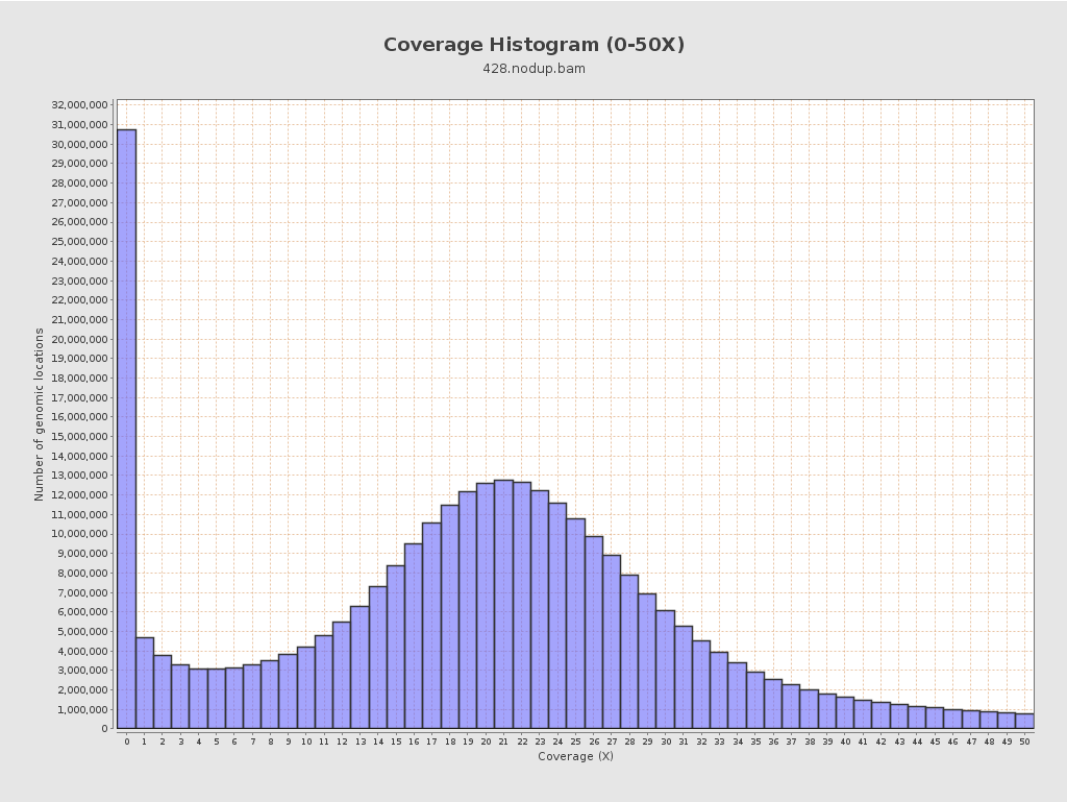
3. Results : Coverage across reference



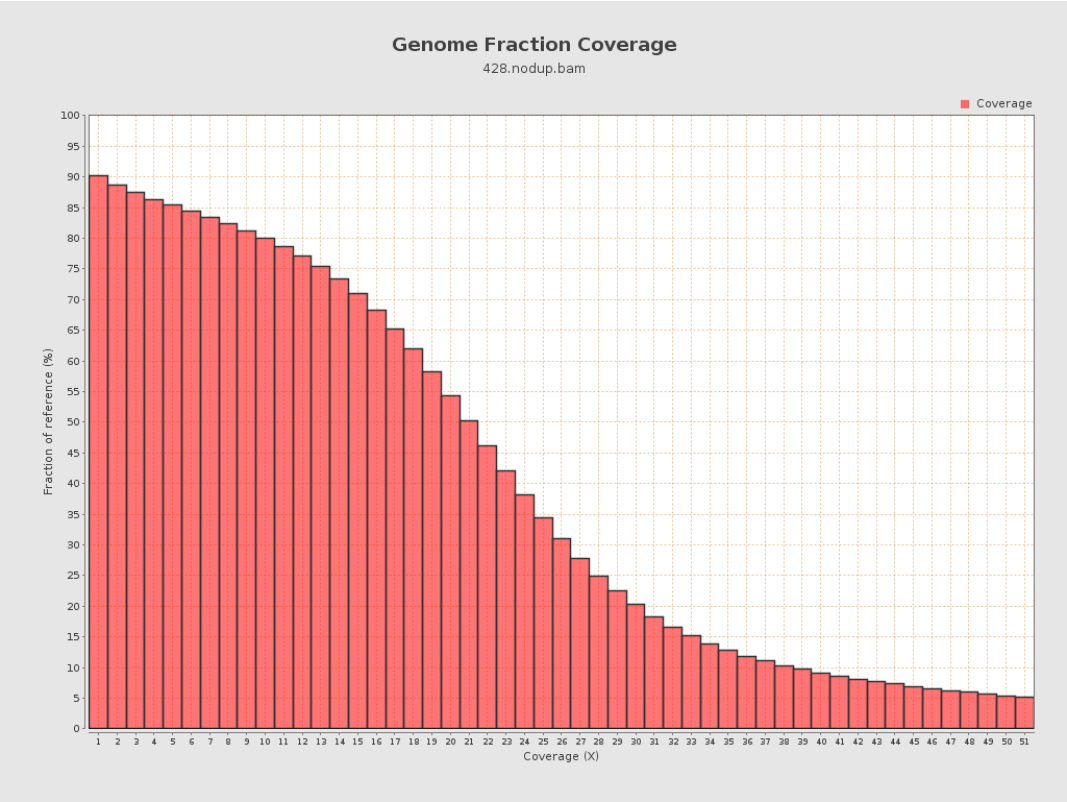
4. Results : Coverage Histogram



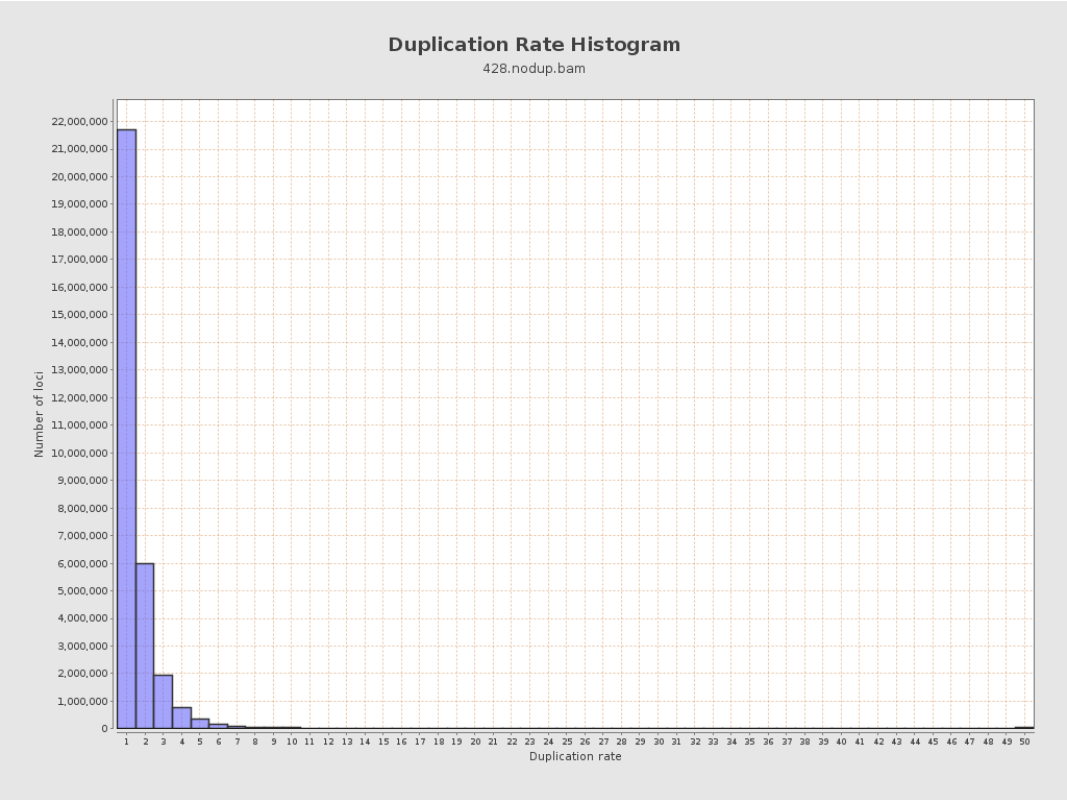
5. Results : Coverage Histogram (0-50X)



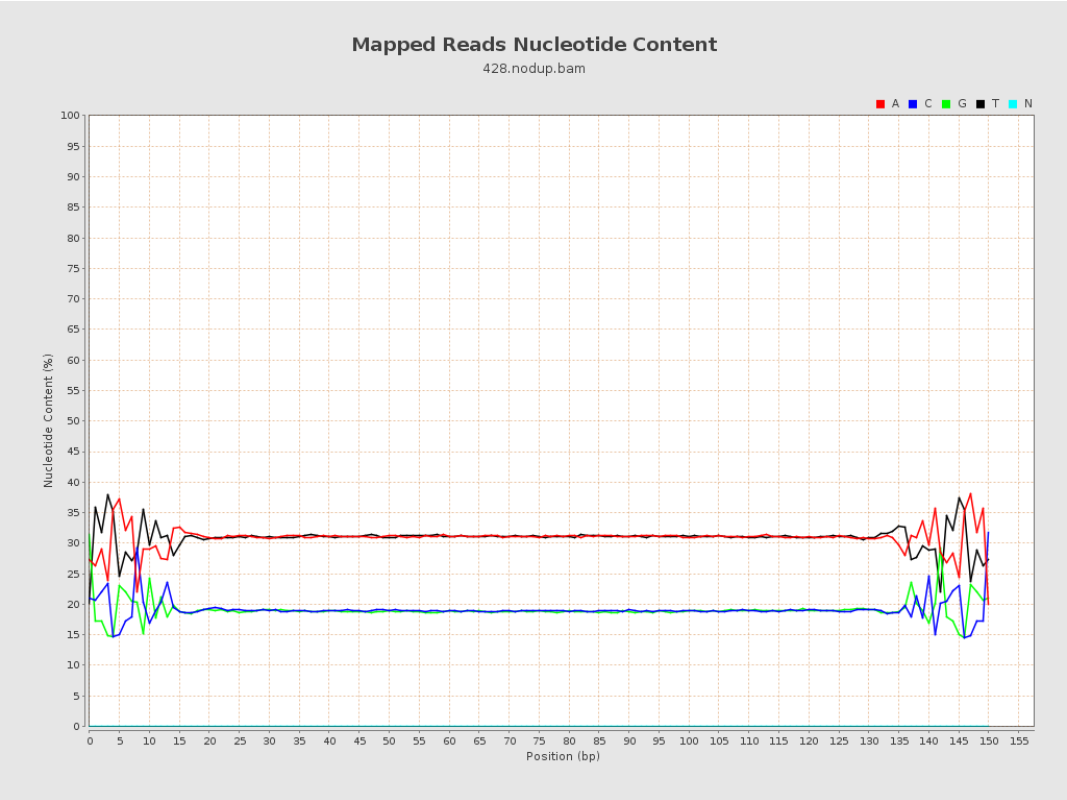
6. Results : Genome Fraction Coverage



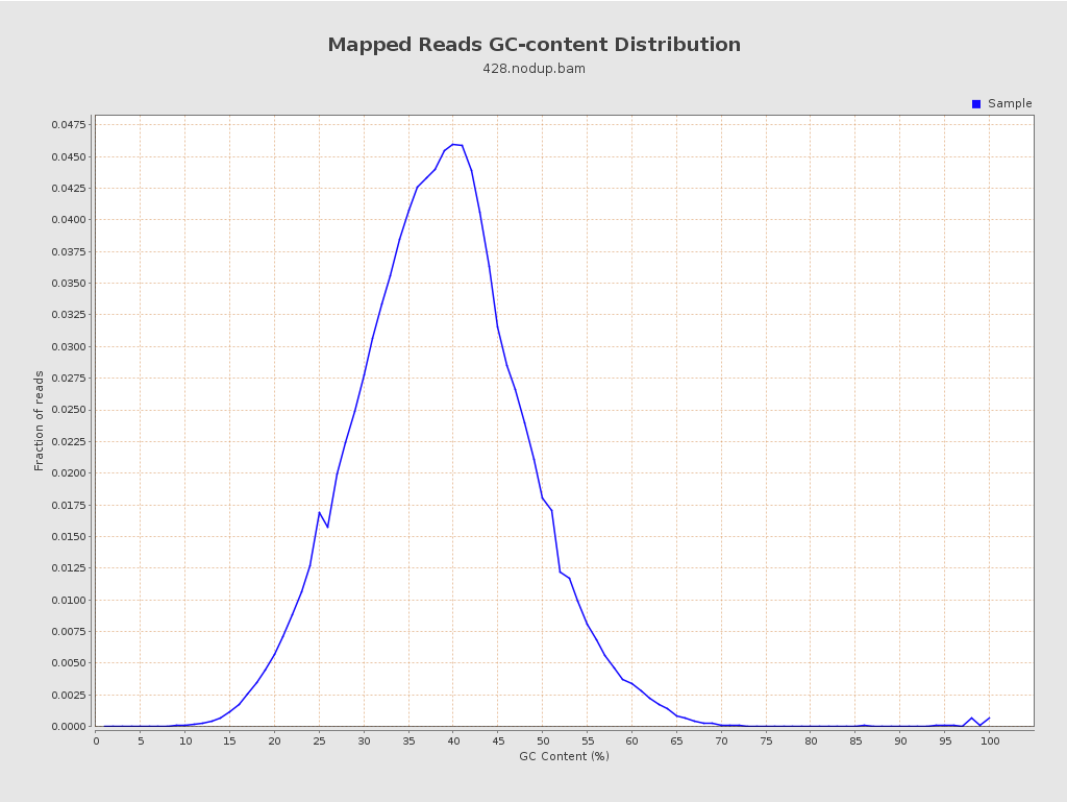
7. Results : Duplication Rate Histogram



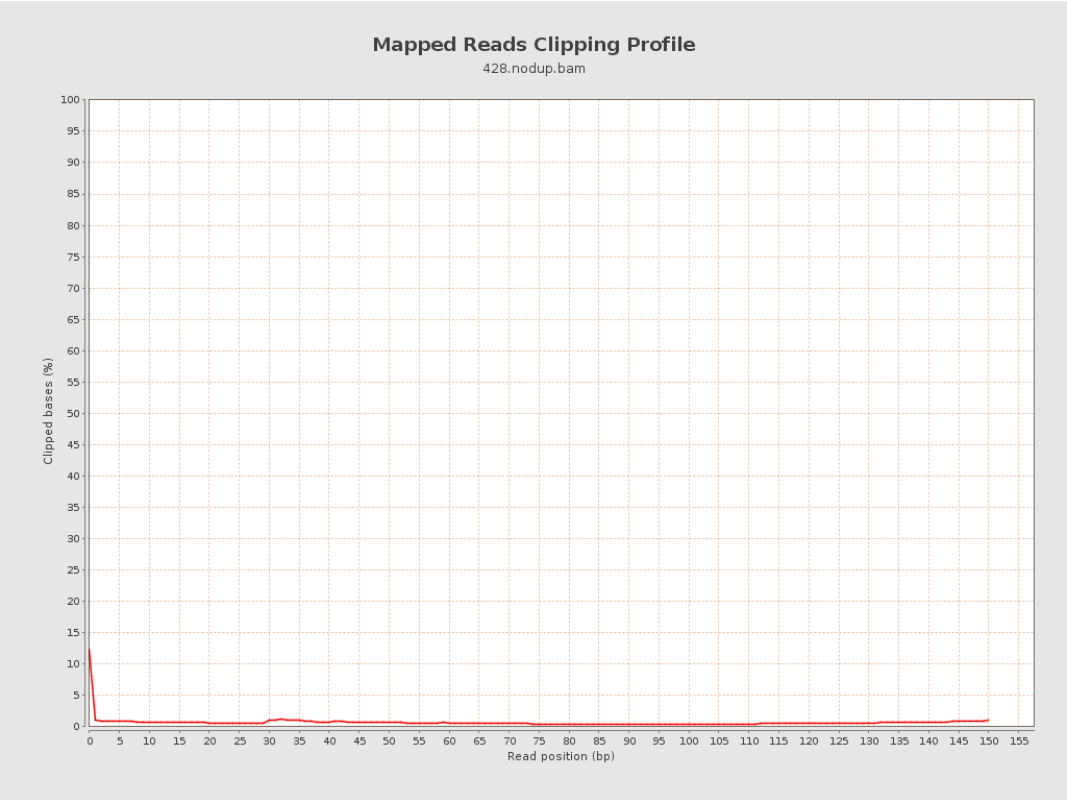
8. Results : Mapped Reads Nucleotide Content



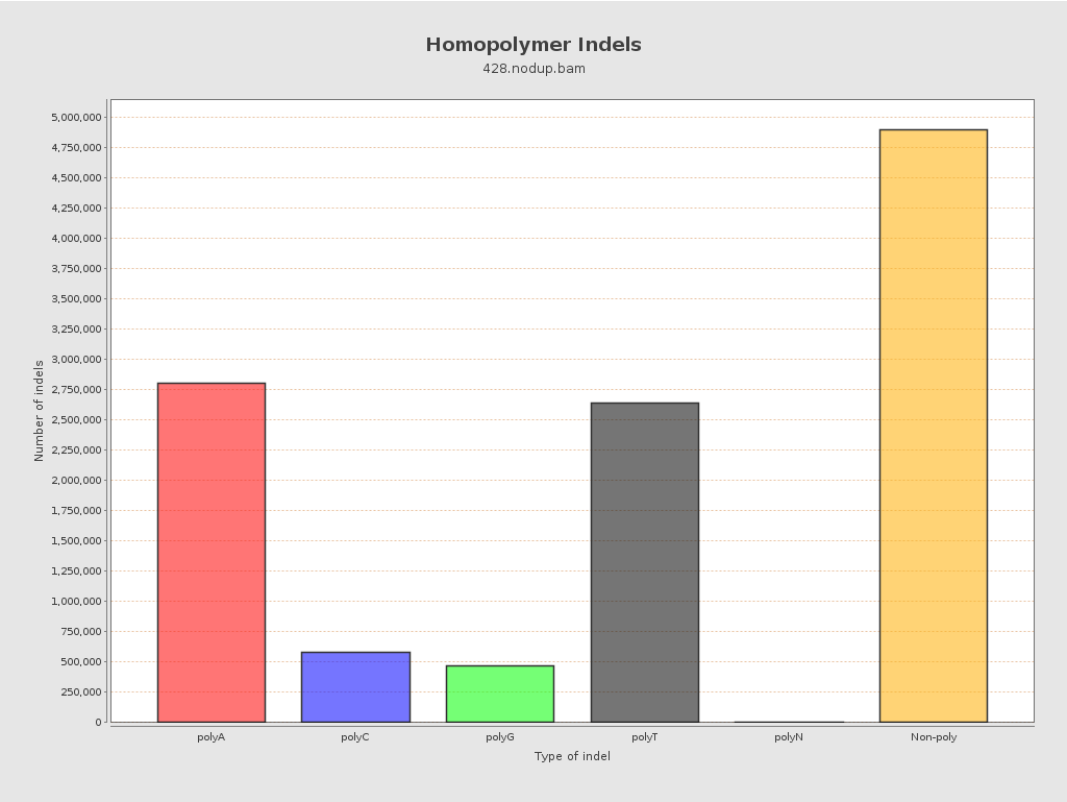
9. Results : Mapped Reads GC-content Distribution



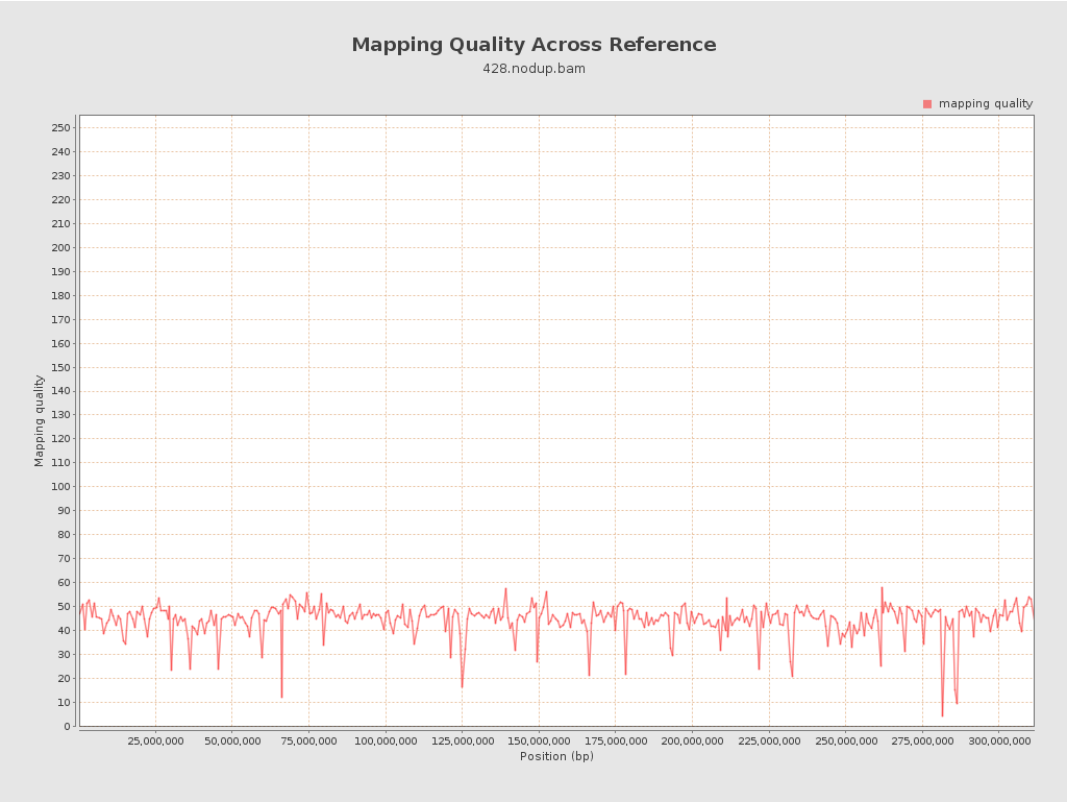
10. Results : Mapped Reads Clipping Profile



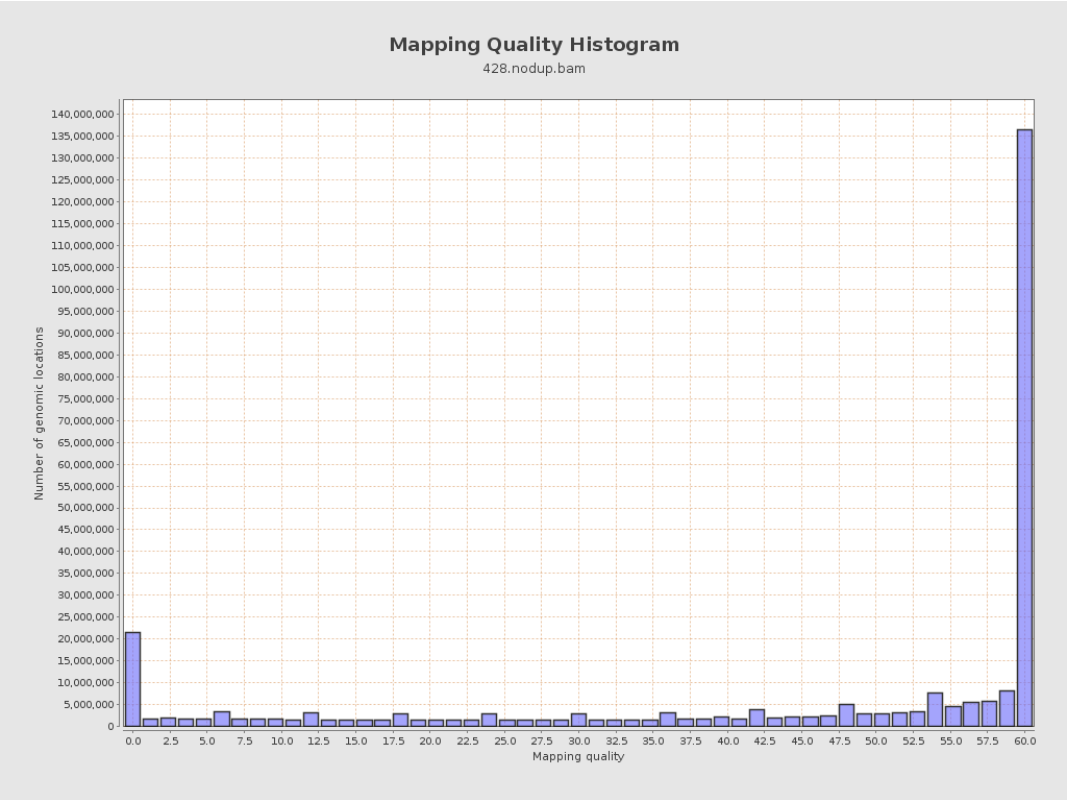
11. Results : Homopolymer Indels



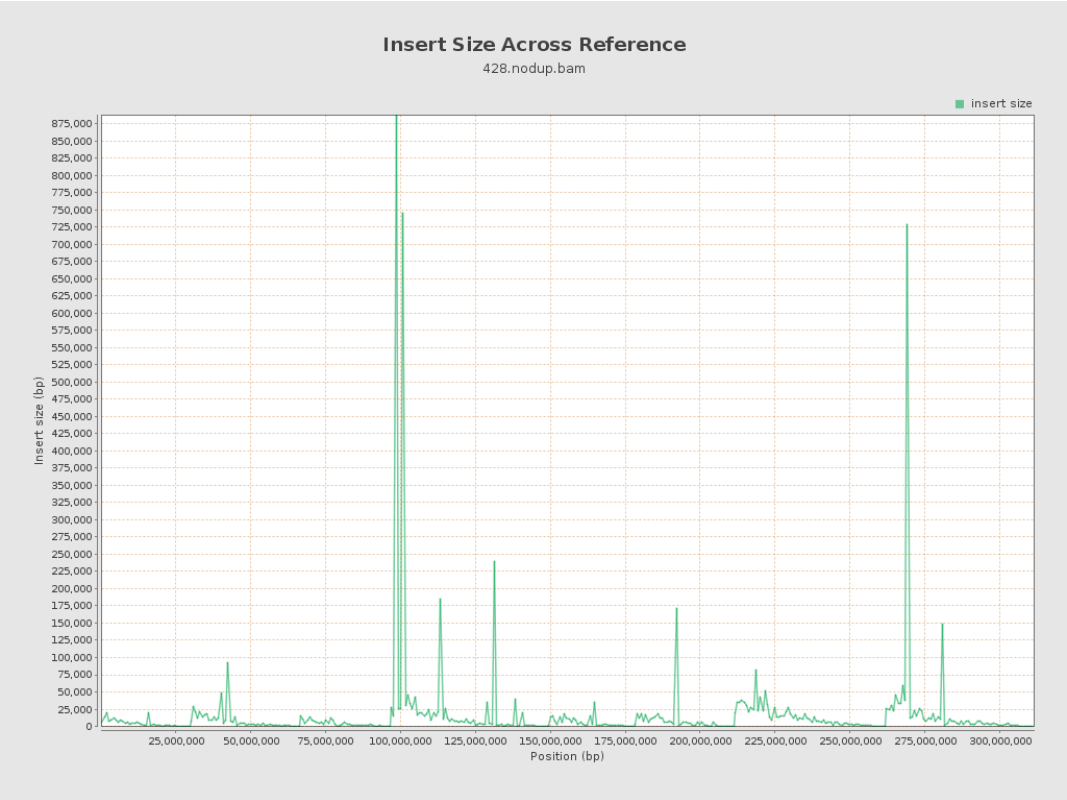
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram