Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1106
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1106 .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_441/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_441_S416_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_441/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_441_S416_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,214,994
Mapped reads	58,711,226 / 92.88%
Unmapped reads	4,503,768 / 7.12%
Mapped paired reads	58,711,226 / 92.88%
Mapped reads, first in pair	29,424,133 / 46.55%
Mapped reads, second in pair	29,287,093 / 46.33%
Mapped reads, both in pair	57,148,118 / 90.4%
Mapped reads, singletons	1,563,108 / 2.47%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	9,782,948 / 15.48%
Clipped reads	13,517,032 / 21.38%

2.2. ACGT Content

Number/percentage of A's	2,494,218,217 / 30.79%
Number/percentage of C's	1,556,692,414 / 19.21%
Number/percentage of T's	2,498,102,349 / 30.83%
Number/percentage of G's	1,552,795,062 / 19.17%
Number/percentage of N's	27,511 / 0%
GC Percentage	38.38%

2.3. Coverage

Mean	26.0627
Standard Deviation	251.2258

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Insert size

Mean	255,393.31
Standard Deviation	2,409,204.04
P25/Median/P75	358 / 471 / 618

2.6. Mismatches and indels

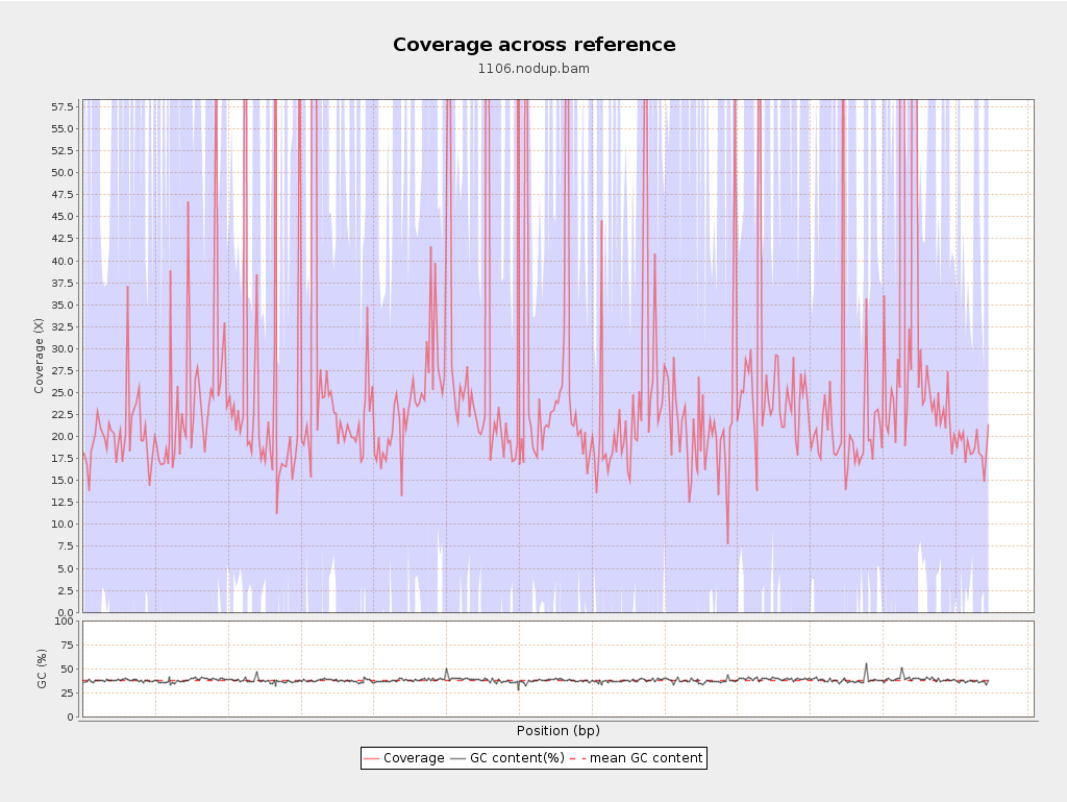
General error rate	2.38%
Mismatches	177,024,506
Insertions	5,621,608
Mapped reads with at least one insertion	8.58%
Deletions	5,507,884
Mapped reads with at least one deletion	8.34%
Homopolymer indels	56.76%

2.7. Chromosome stats

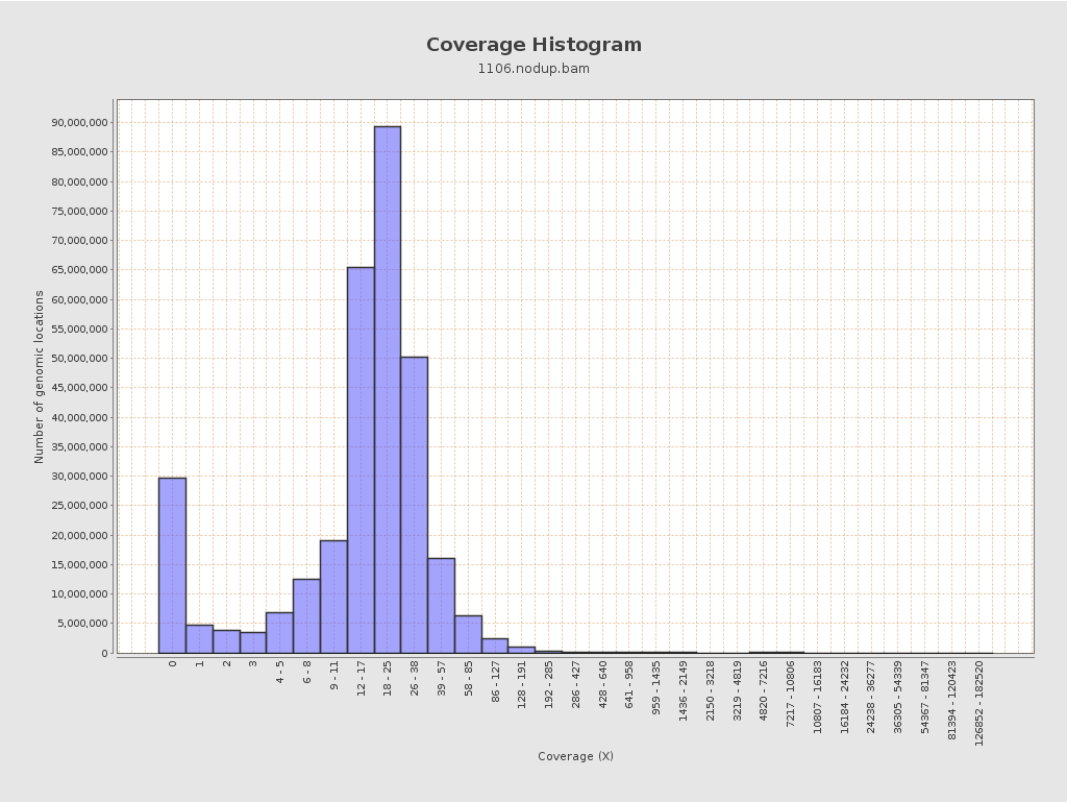
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	589028262	19.8164	81.7731

LT669789.1	36598175	968770881	26.4705	255.998
LT669790.1	30422129	897991089	29.5177	298.2132
LT669791.1	52758100	1369291464	25.9541	232.8986
LT669792.1	28376109	722376547	25.4572	251.4181
LT669793.1	33388210	791925962	23.7187	223.1986
LT669794.1	50579949	1241065099	24.5367	198.3976
LT669795.1	49795044	1541791930	30.9628	348.674

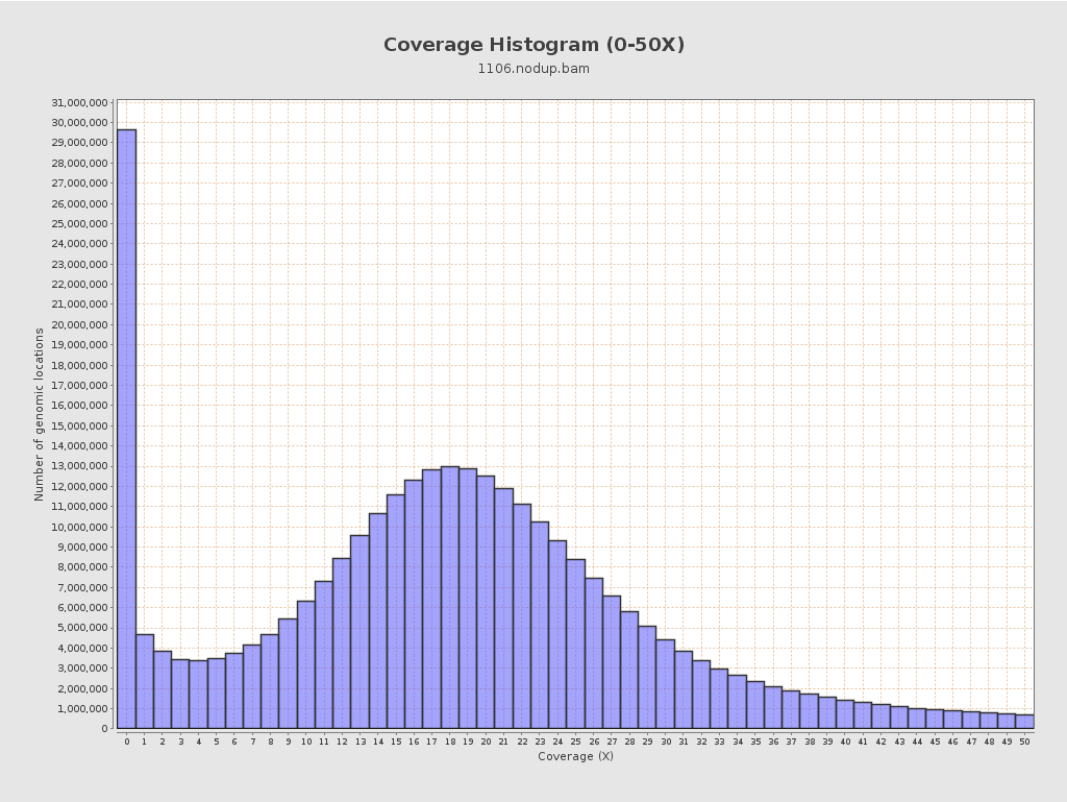
3. Results : Coverage across reference



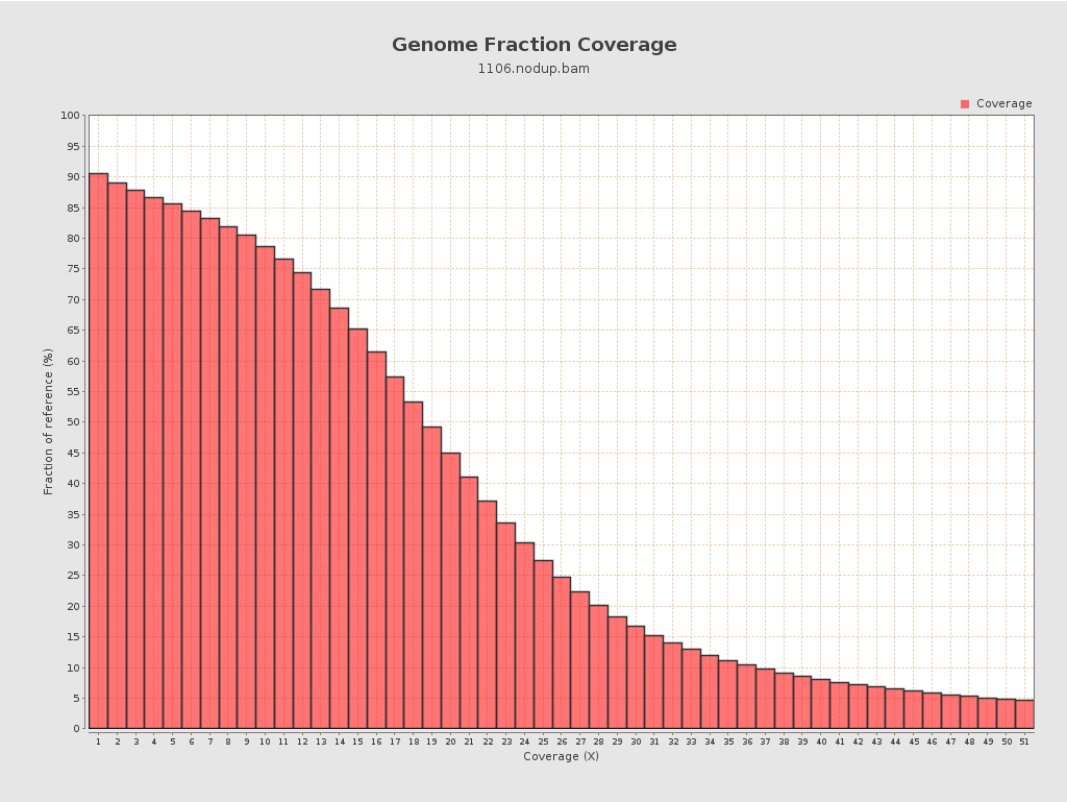
4. Results : Coverage Histogram



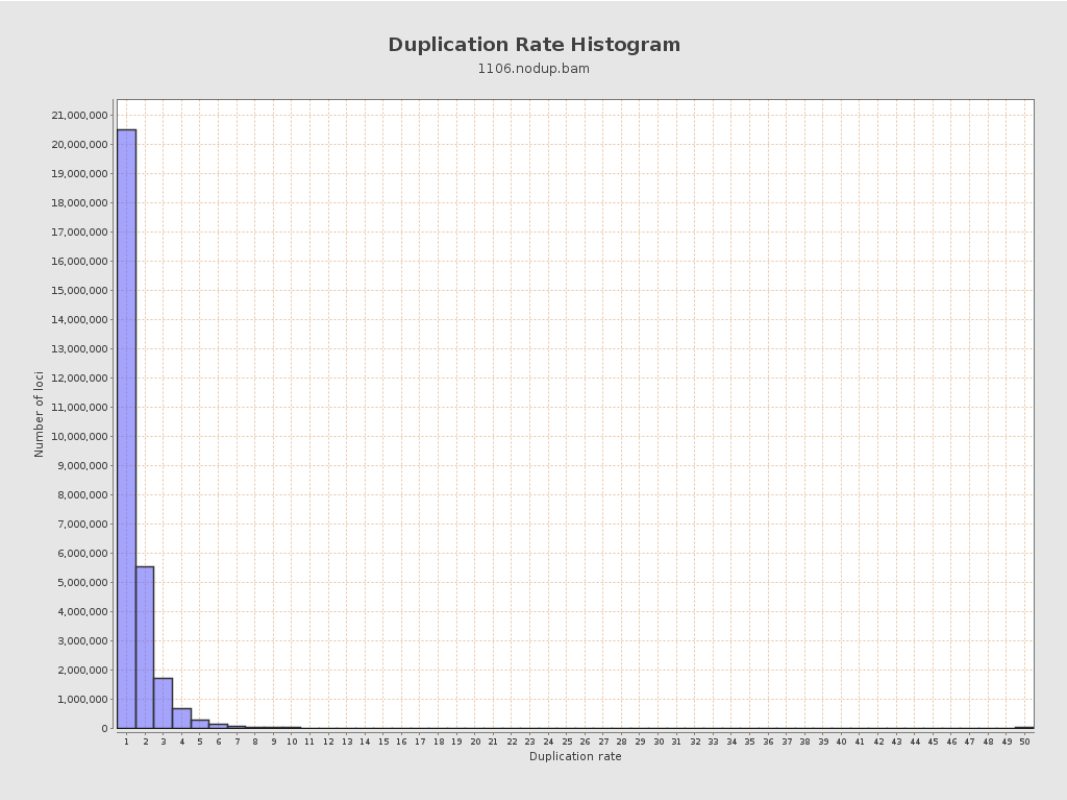
5. Results : Coverage Histogram (0-50X)



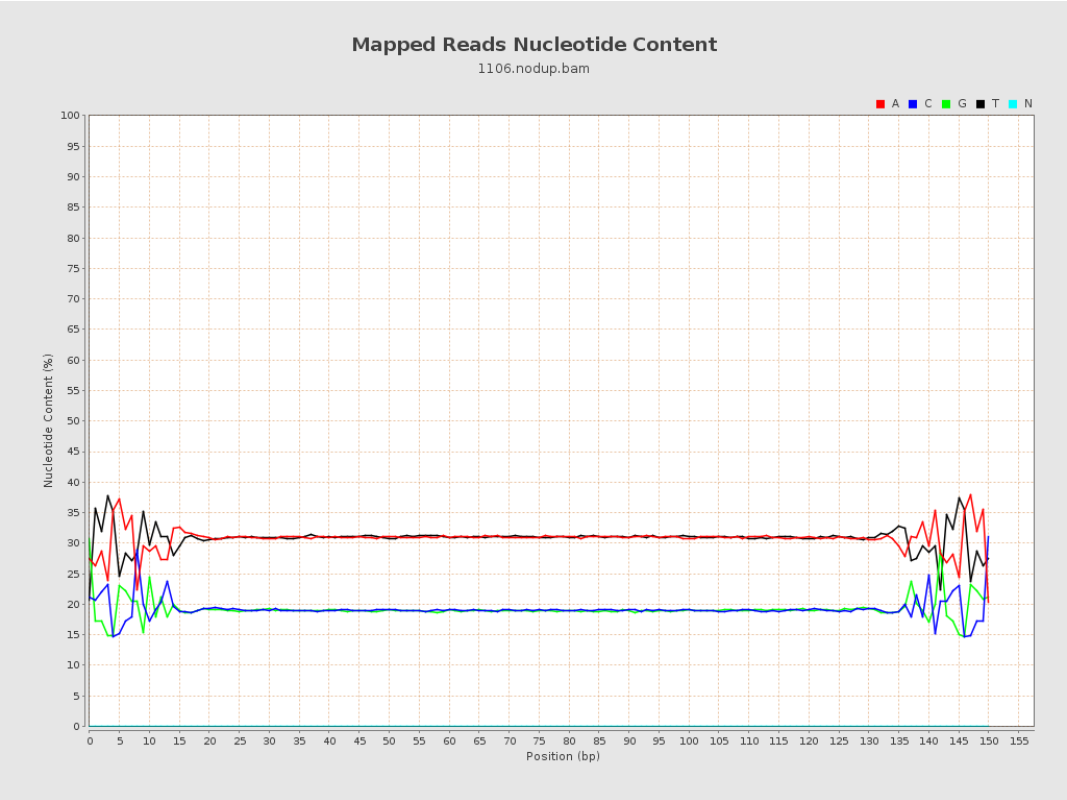
6. Results : Genome Fraction Coverage



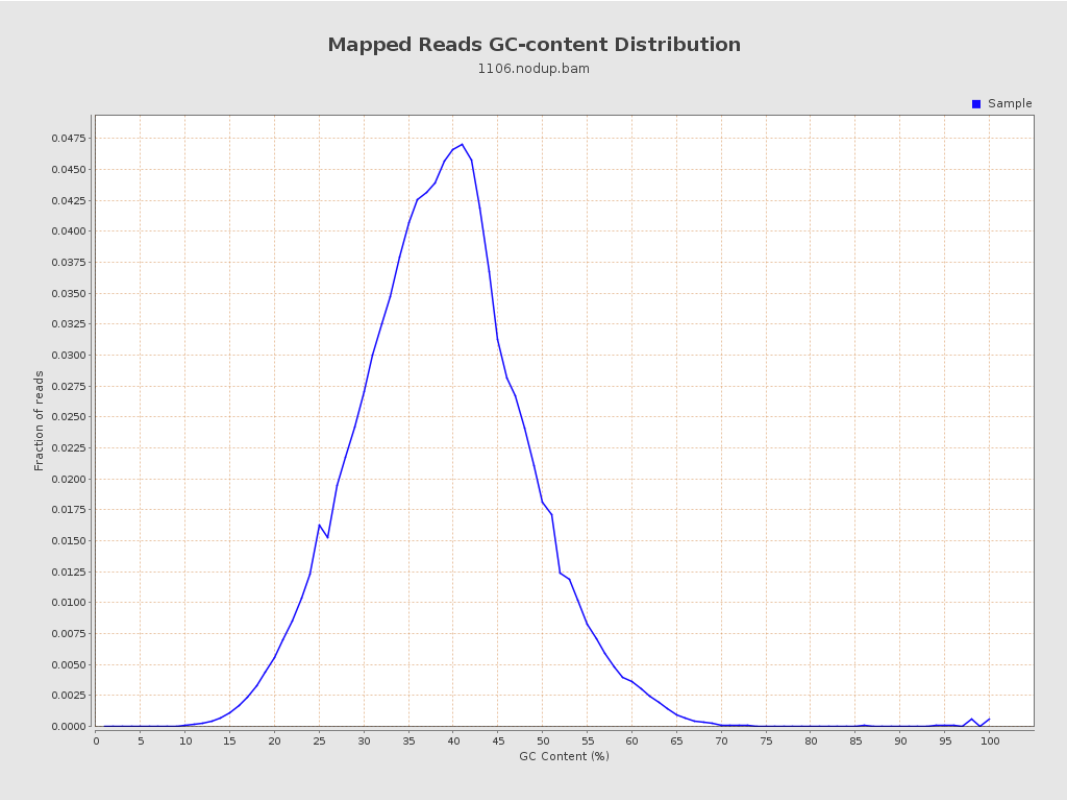
7. Results : Duplication Rate Histogram



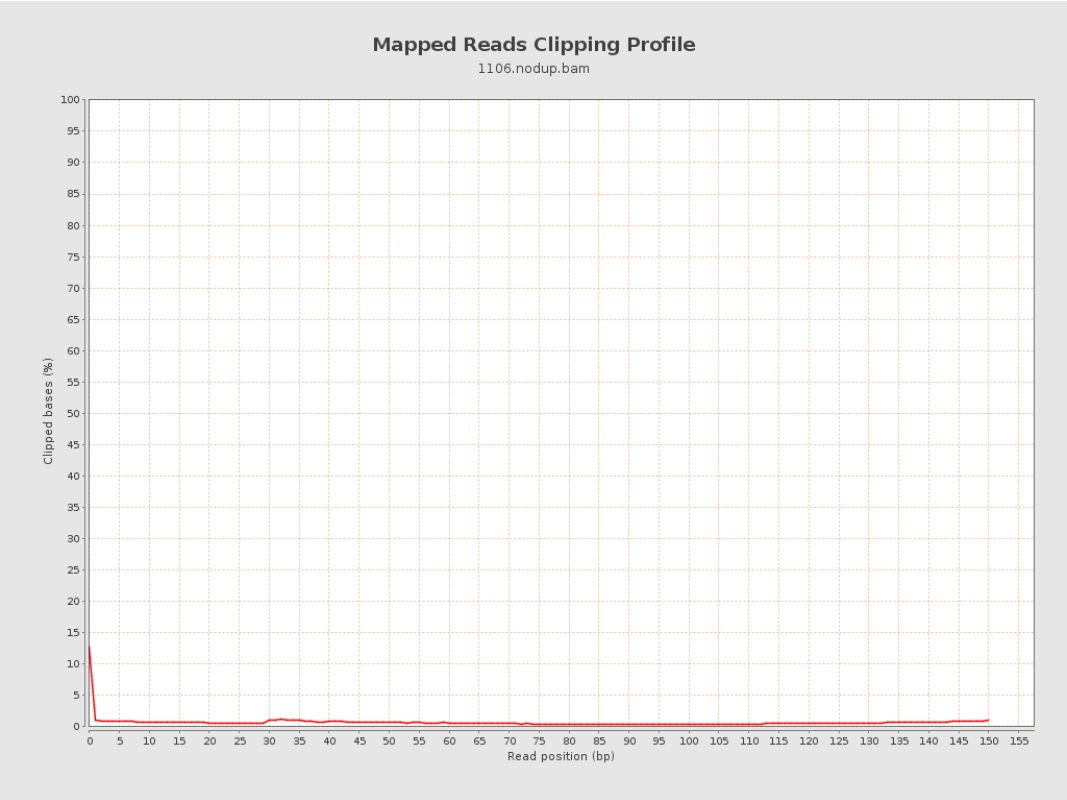
8. Results : Mapped Reads Nucleotide Content



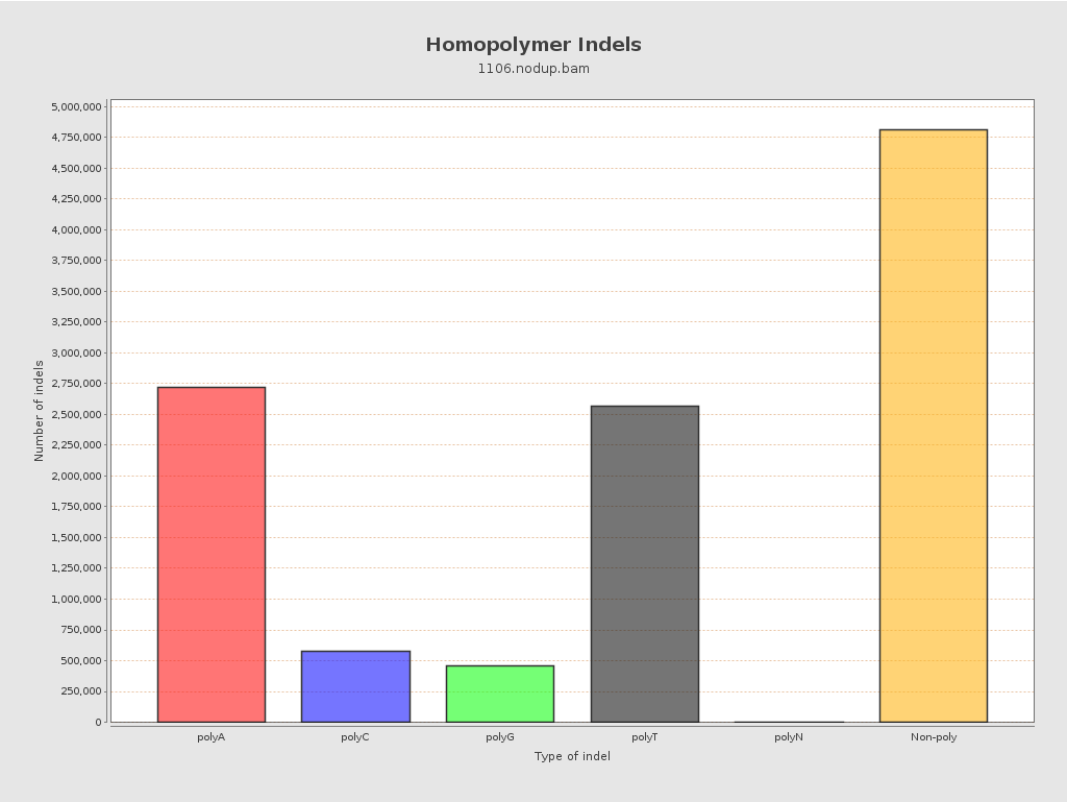
9. Results : Mapped Reads GC-content Distribution



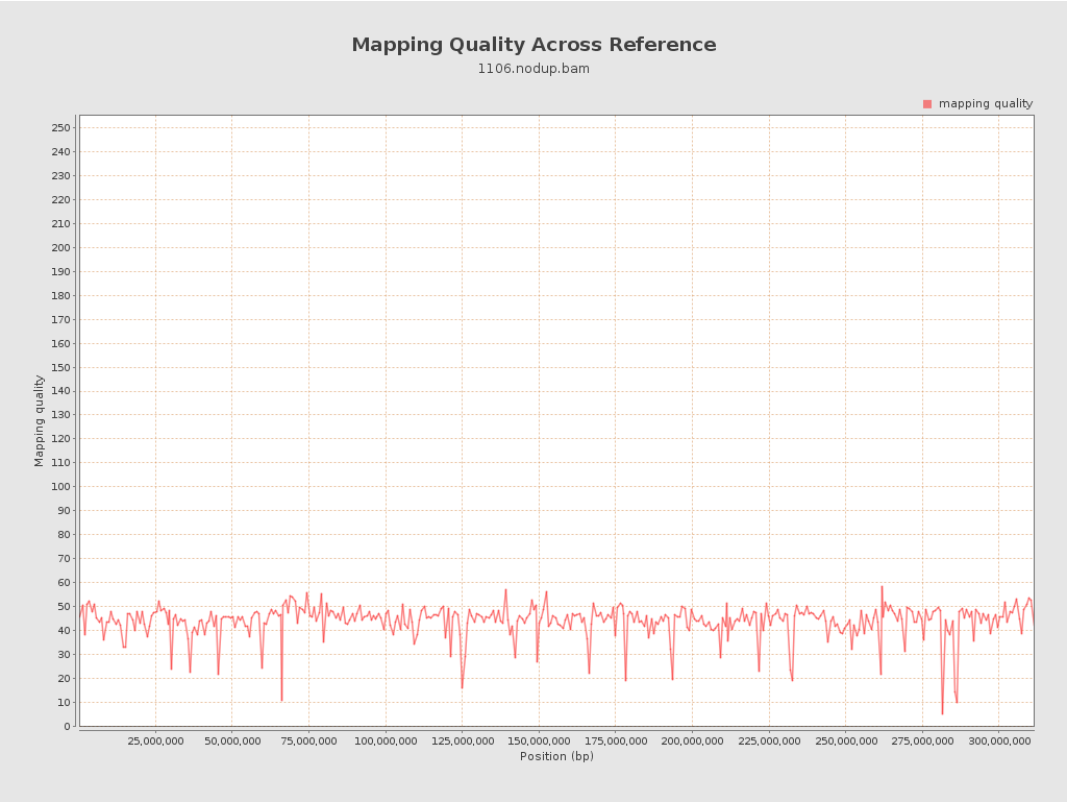
10. Results : Mapped Reads Clipping Profile



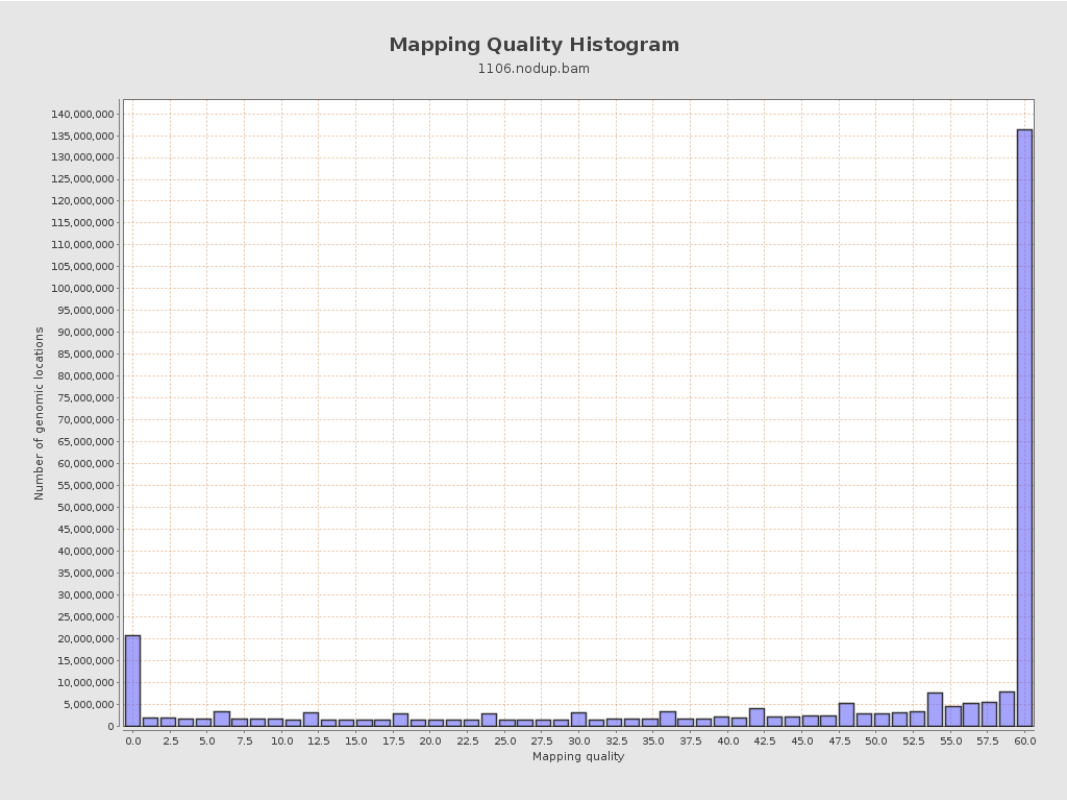
11. Results : Homopolymer Indels



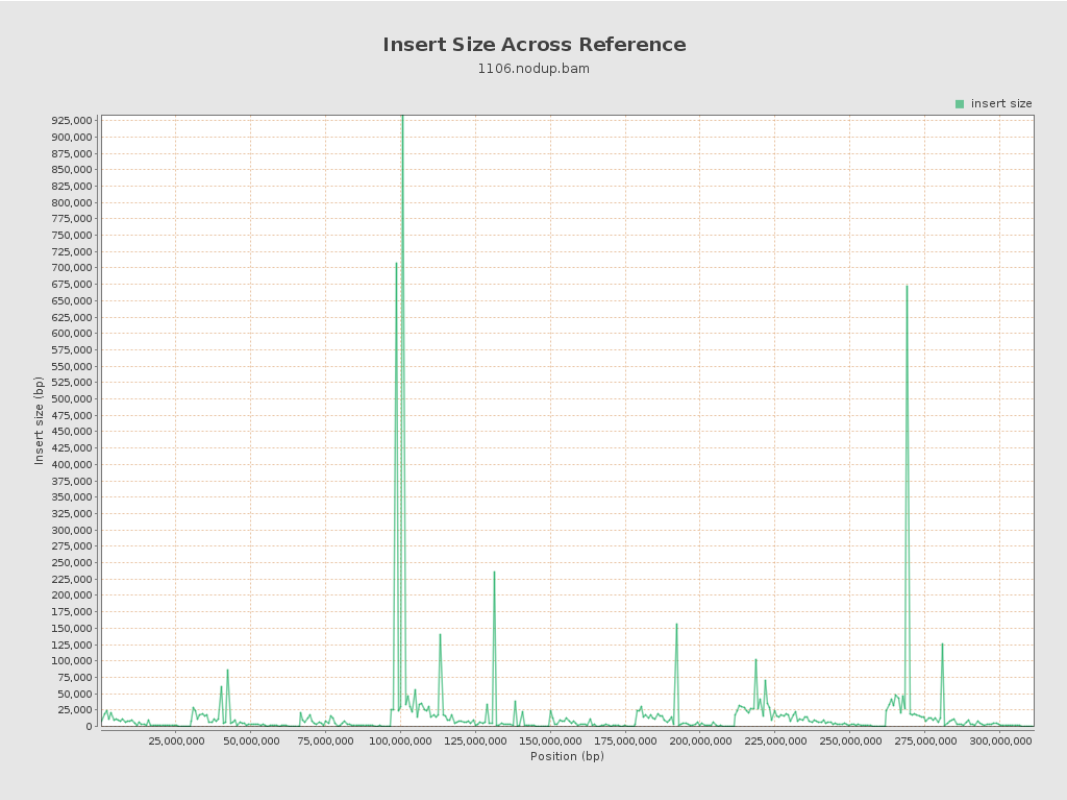
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram