Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1348
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1348 .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_111/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_111_S201_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_111/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_111_S201_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:31:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,101,366
Mapped reads	60,842,344 / 93.46%
Unmapped reads	4,259,022 / 6.54%
Mapped paired reads	60,842,344 / 93.46%
Mapped reads, first in pair	30,437,471 / 46.75%
Mapped reads, second in pair	30,404,873 / 46.7%
Mapped reads, both in pair	59,522,812 / 91.43%
Mapped reads, singletons	1,319,532 / 2.03%
Read min/max/mean length	30 / 151 / 148.25
Duplicated reads (flagged)	9,619,738 / 14.78%
Clipped reads	12,965,568 / 19.92%

2.2. ACGT Content

Number/percentage of A's	2,624,015,529 / 30.98%
Number/percentage of C's	1,612,915,765 / 19.04%
Number/percentage of T's	2,624,898,625 / 30.99%
Number/percentage of G's	1,609,462,024 / 19%
Number/percentage of N's	34,397 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	27.2539
Standard Deviation	199.6865

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Insert size

Mean	230,031.3
Standard Deviation	2,285,346.76
P25/Median/P75	323 / 419 / 546

2.6. Mismatches and indels

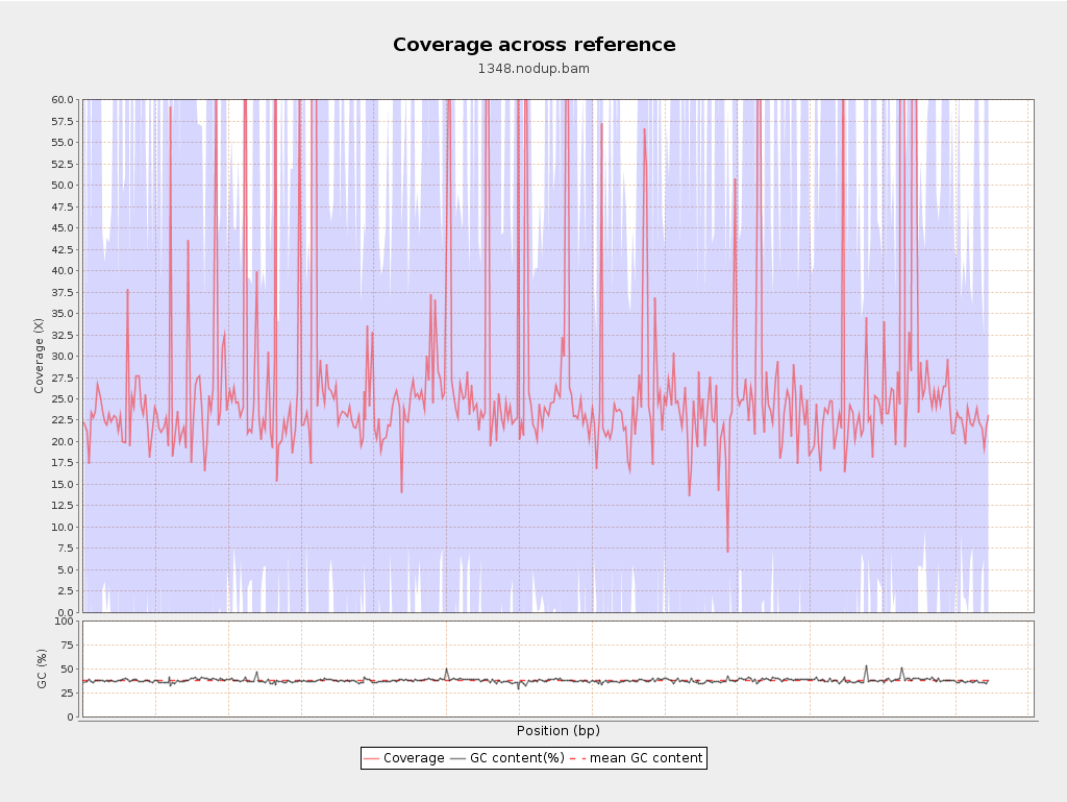
General error rate	2.26%
Mismatches	175,313,804
Insertions	5,762,135
Mapped reads with at least one insertion	8.49%
Deletions	5,844,852
Mapped reads with at least one deletion	8.51%
Homopolymer indels	56.64%

2.7. Chromosome stats

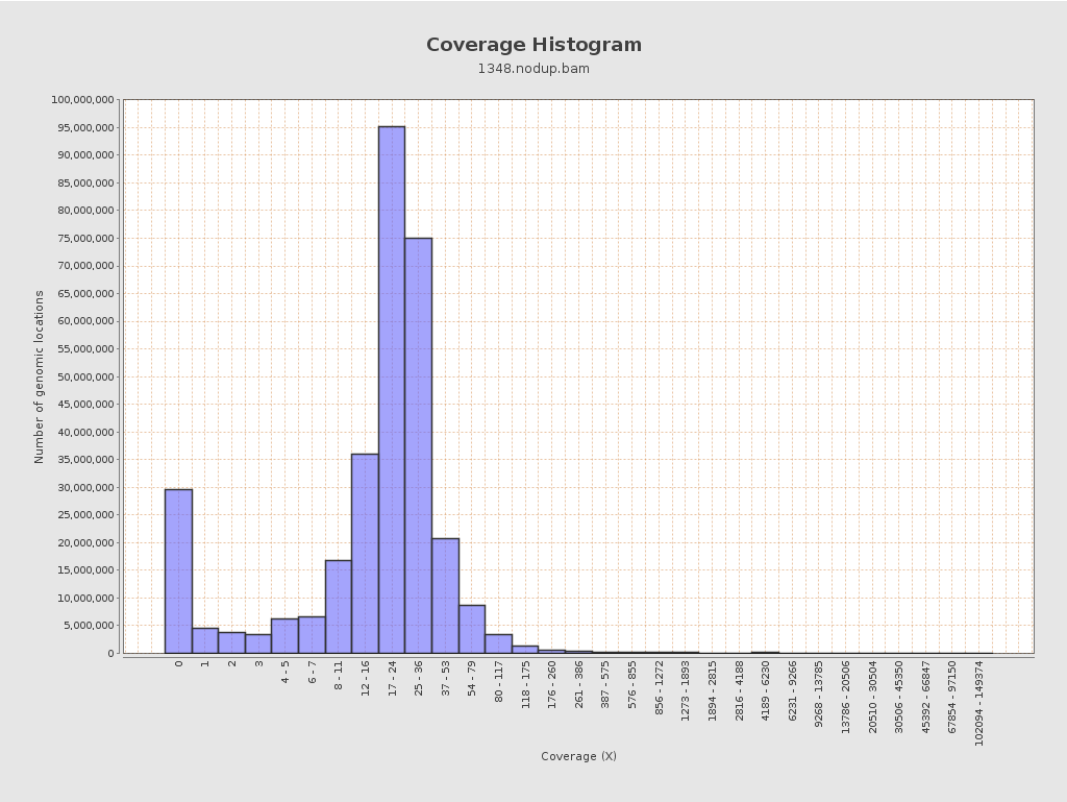
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	685660776	23.0673	66.034

LT669789.1	36598175	995875147	27.2111	218.3181
LT669790.1	30422129	915758151	30.1017	226.9347
LT669791.1	52758100	1410680374	26.7387	184.8634
LT669792.1	28376109	772431834	27.2212	220.7261
LT669793.1	33388210	835511055	25.0241	106.2148
LT669794.1	50579949	1291078417	25.5255	178.5199
LT669795.1	49795044	1586465313	31.8599	276.6

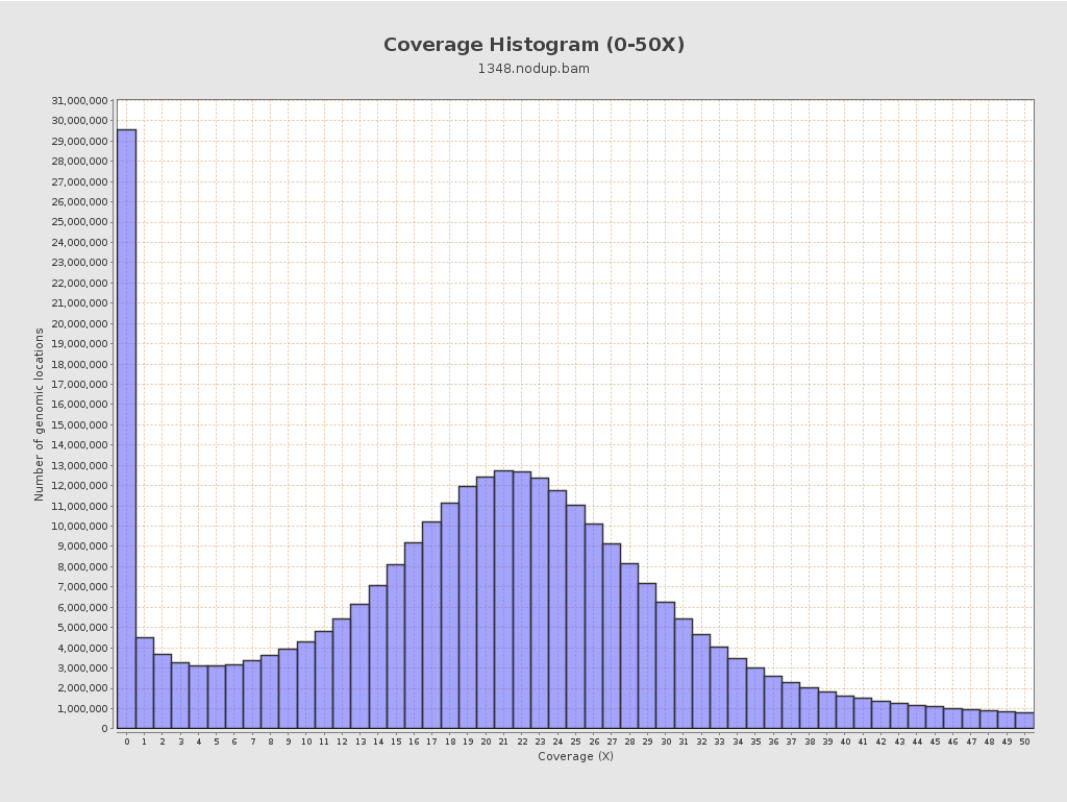
3. Results : Coverage across reference



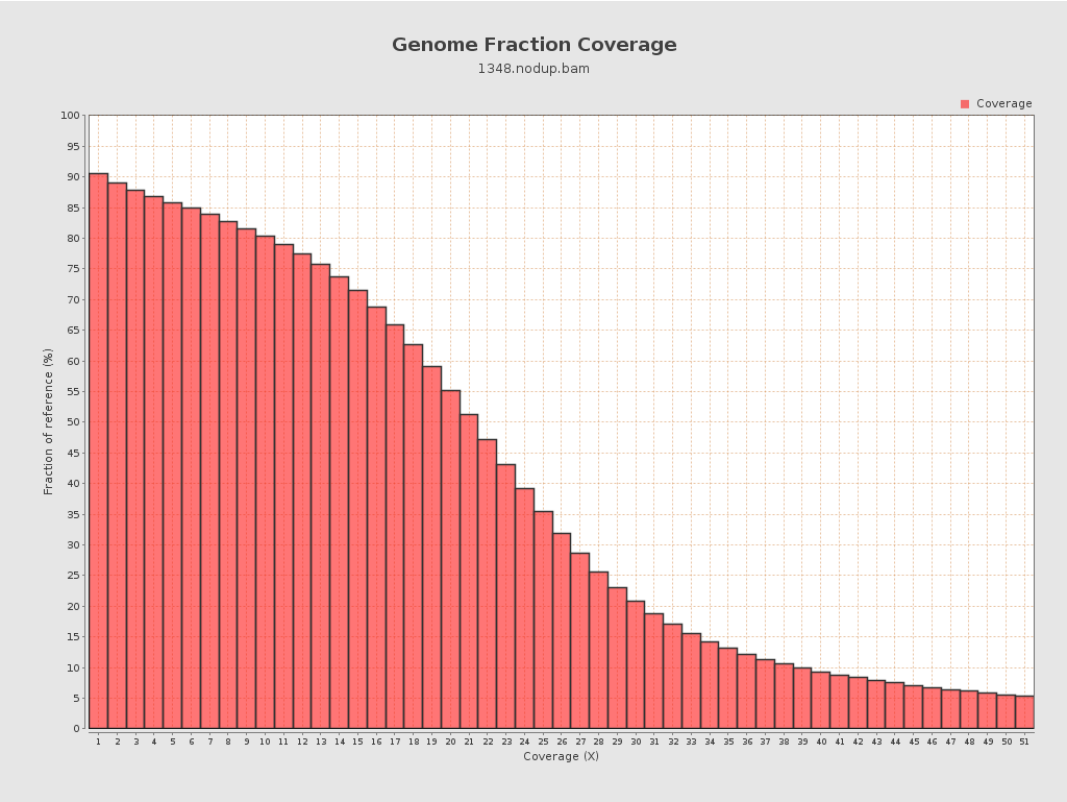
4. Results : Coverage Histogram



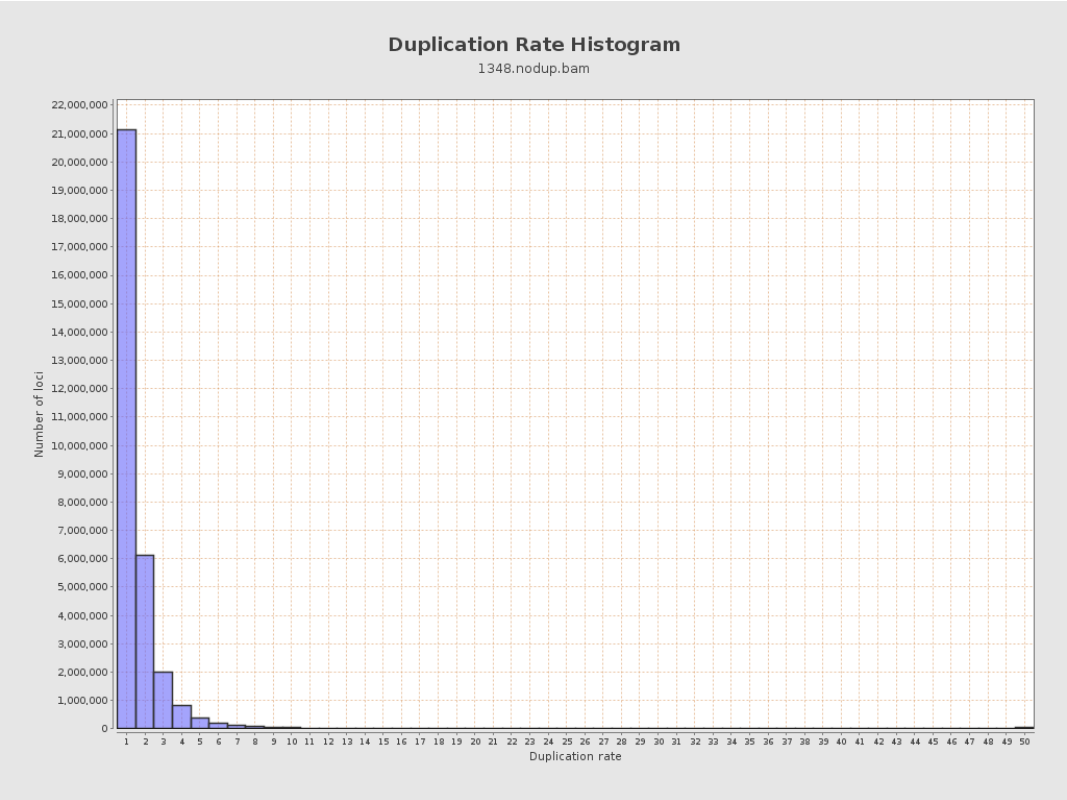
5. Results : Coverage Histogram (0-50X)



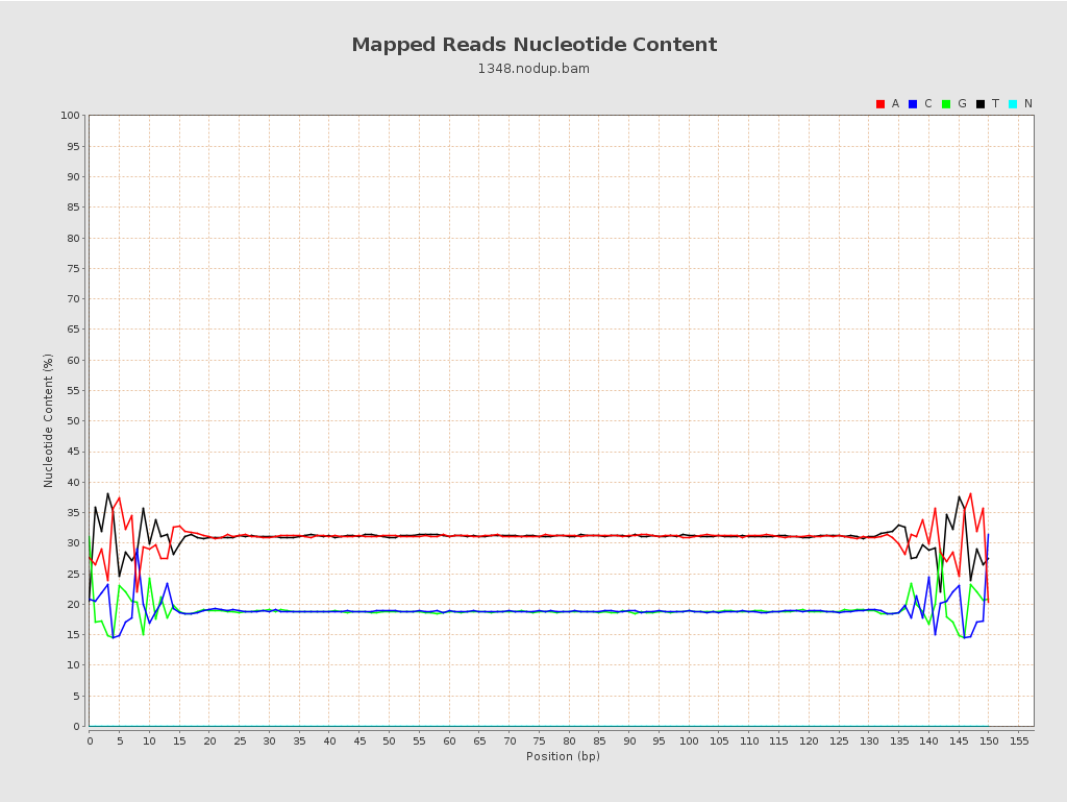
6. Results : Genome Fraction Coverage



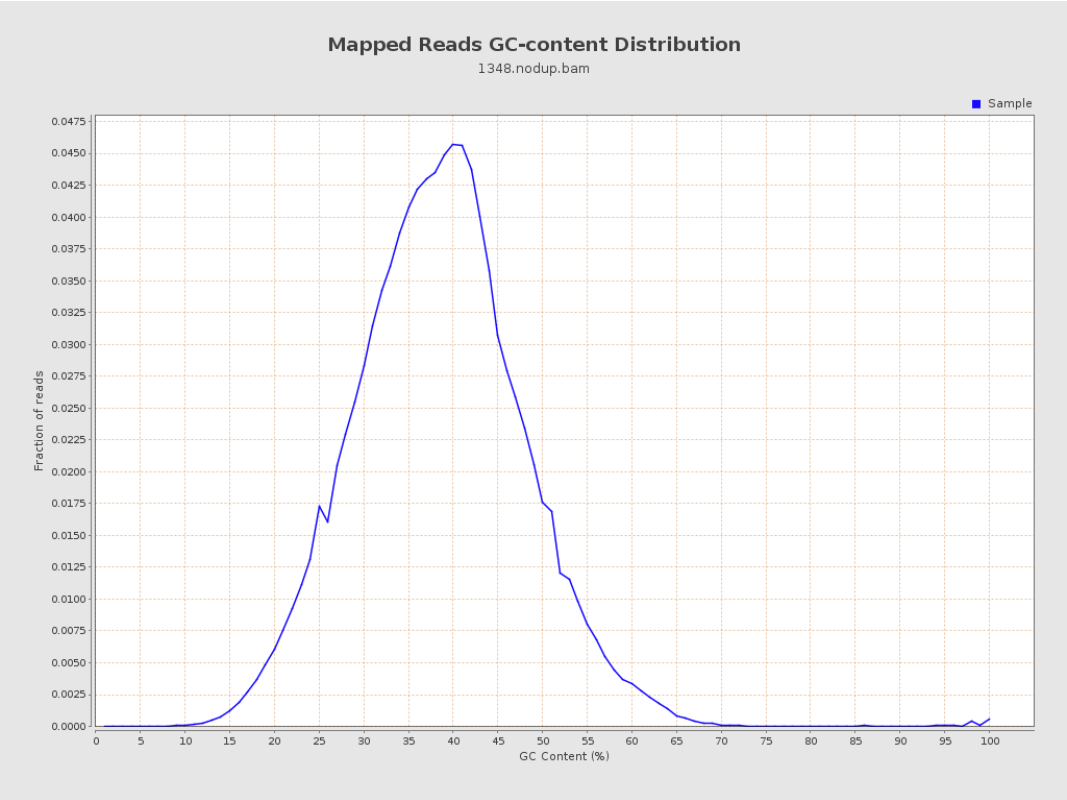
7. Results : Duplication Rate Histogram



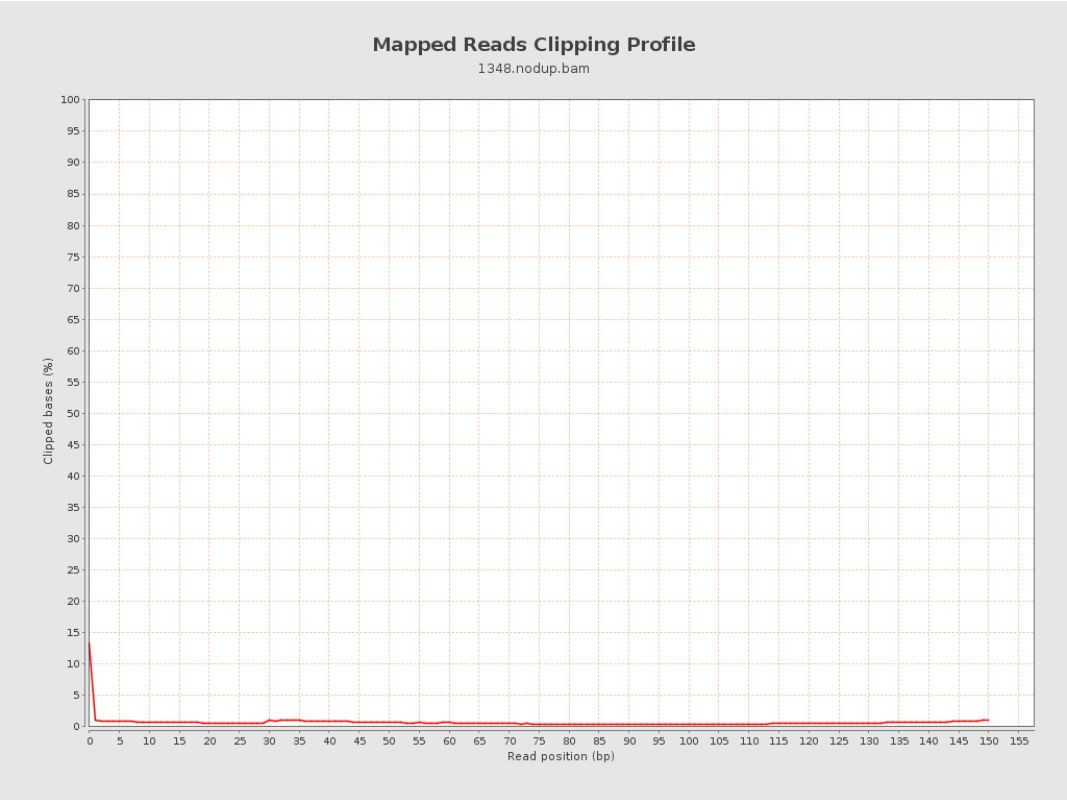
8. Results : Mapped Reads Nucleotide Content



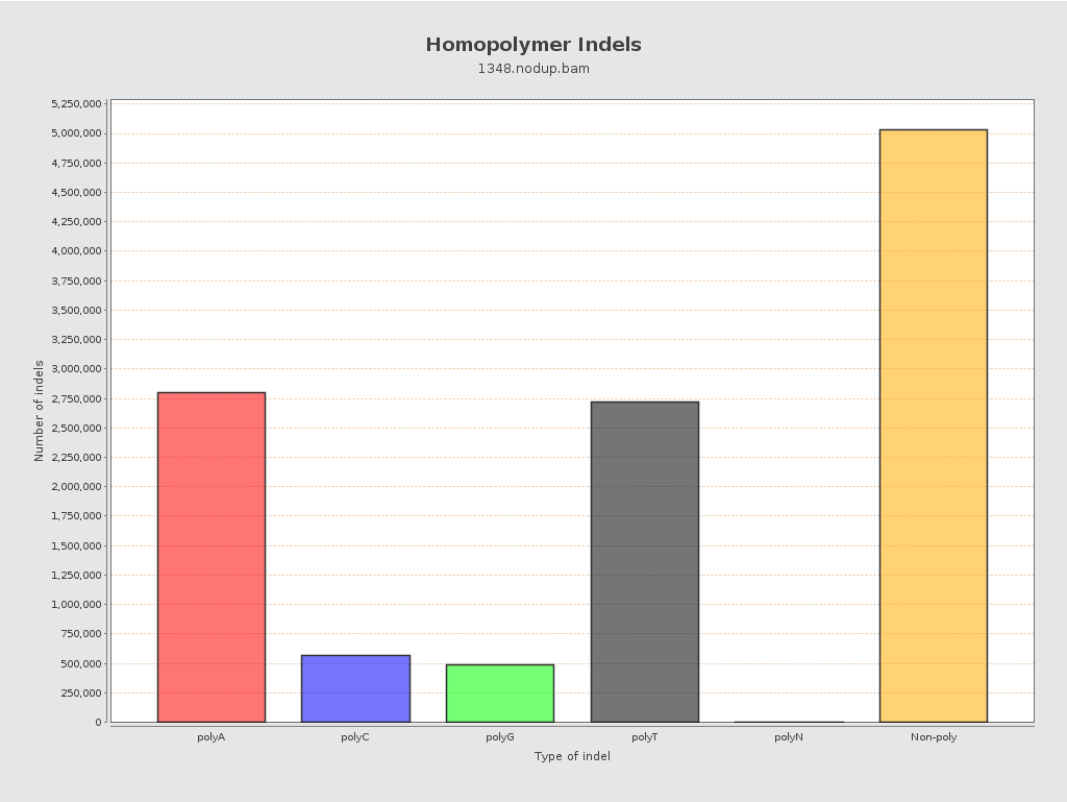
9. Results : Mapped Reads GC-content Distribution



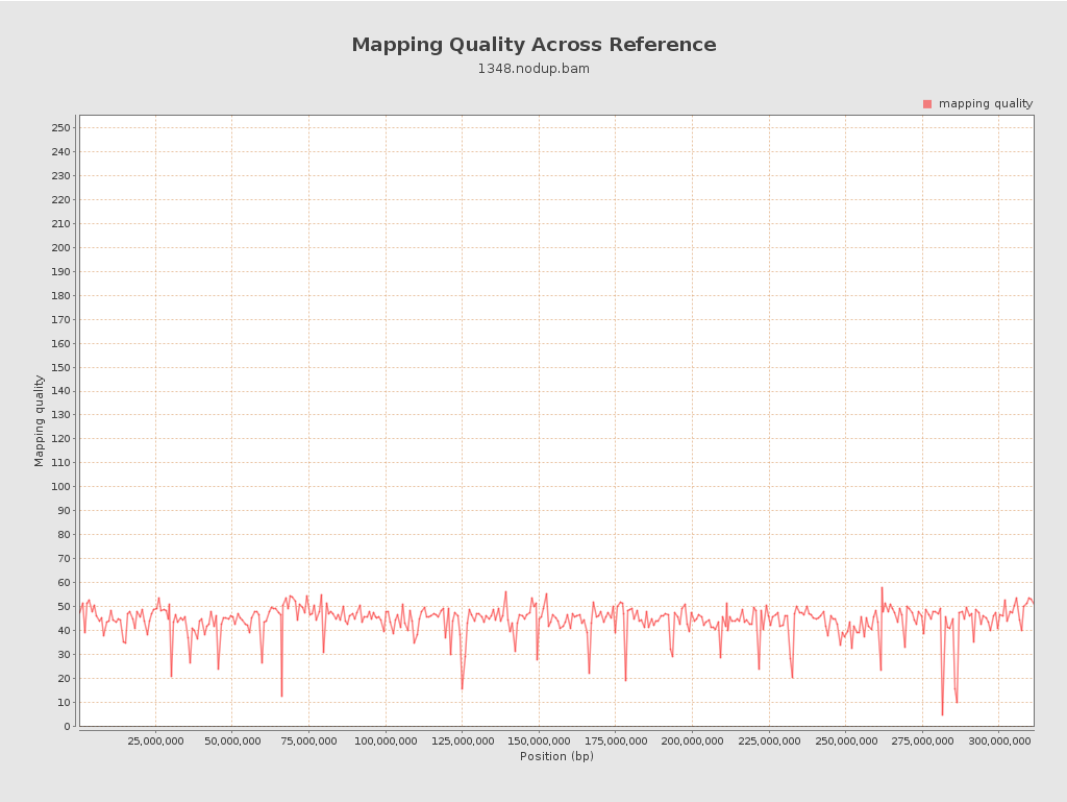
10. Results : Mapped Reads Clipping Profile



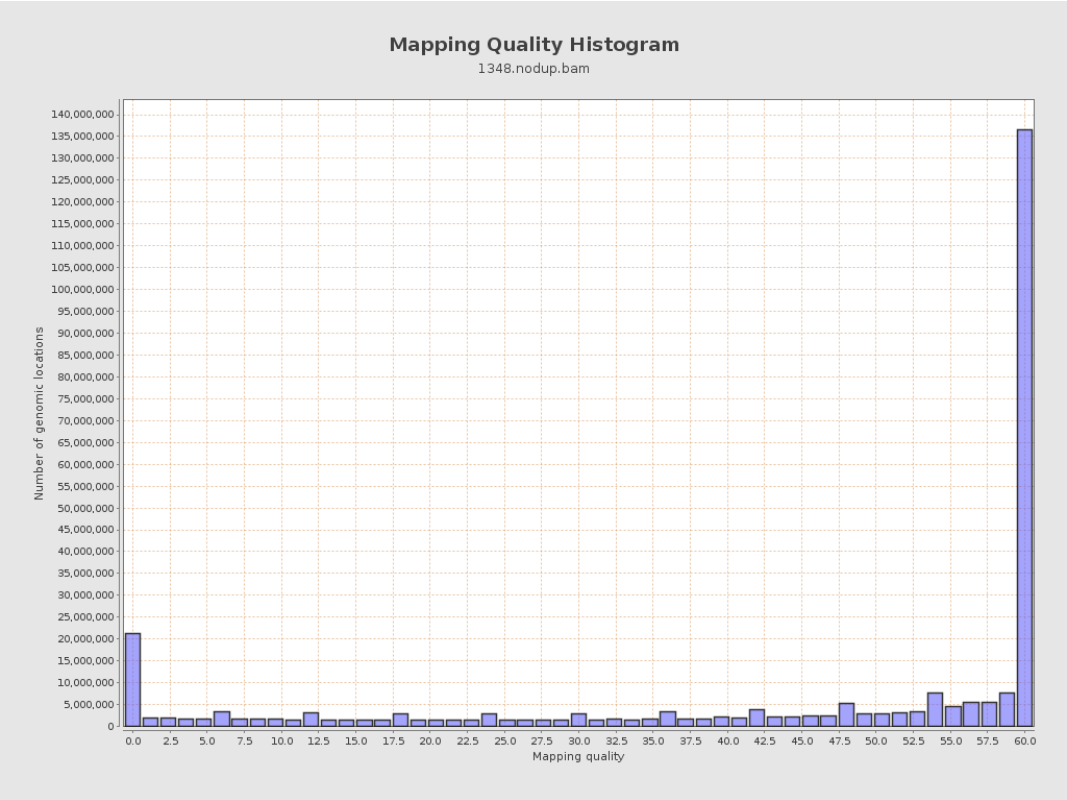
11. Results : Homopolymer Indels



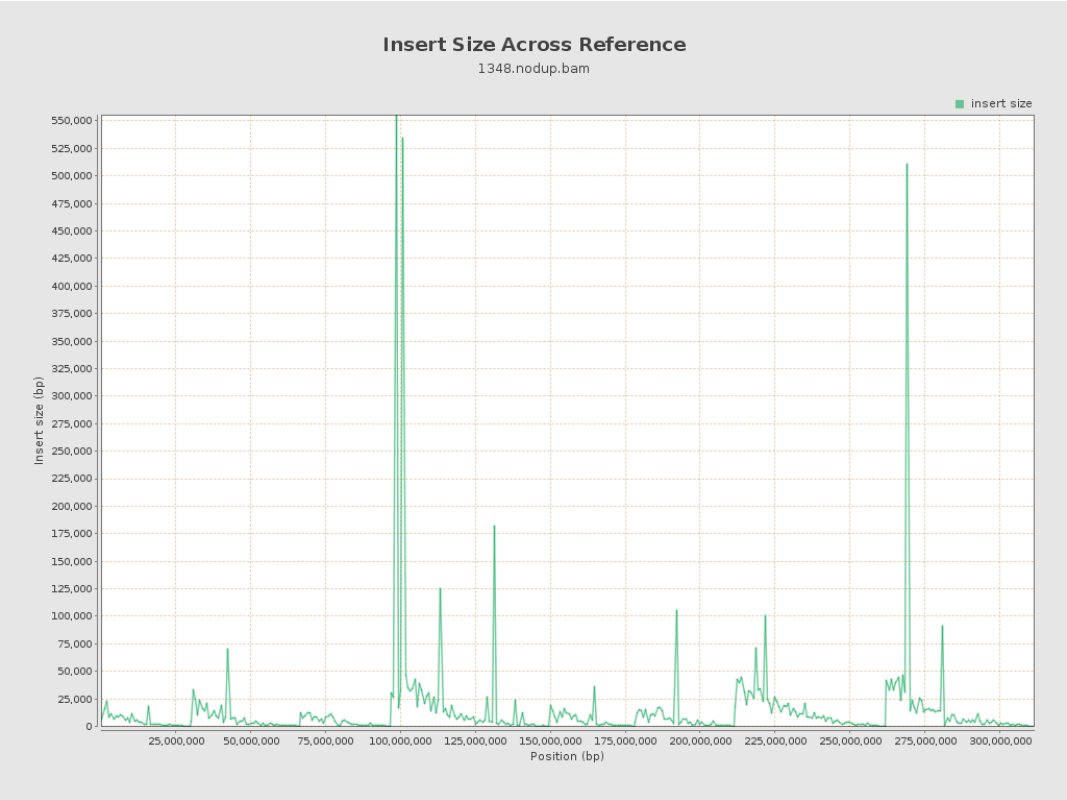
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram