Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1347
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1347 .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_456/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_456_S431_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_456/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_456_S431_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:23:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	41,526,371
Mapped reads	39,284,240 / 94.6%
Unmapped reads	2,242,131 / 5.4%
Mapped paired reads	39,284,240 / 94.6%
Mapped reads, first in pair	19,693,463 / 47.42%
Mapped reads, second in pair	19,590,777 / 47.18%
Mapped reads, both in pair	38,467,455 / 92.63%
Mapped reads, singletons	816,785 / 1.97%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	5,351,857 / 12.89%
Clipped reads	8,456,808 / 20.36%

2.2. ACGT Content

Number/percentage of A's	1,692,587,362 / 30.89%
Number/percentage of C's	1,047,315,552 / 19.11%
Number/percentage of T's	1,693,990,642 / 30.92%
Number/percentage of G's	1,045,389,202 / 19.08%
Number/percentage of N's	18,485 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	17.6279
Standard Deviation	137.4726

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Insert size

Mean	258,464.29
Standard Deviation	2,408,027.36
P25/Median/P75	425 / 542 / 675

2.6. Mismatches and indels

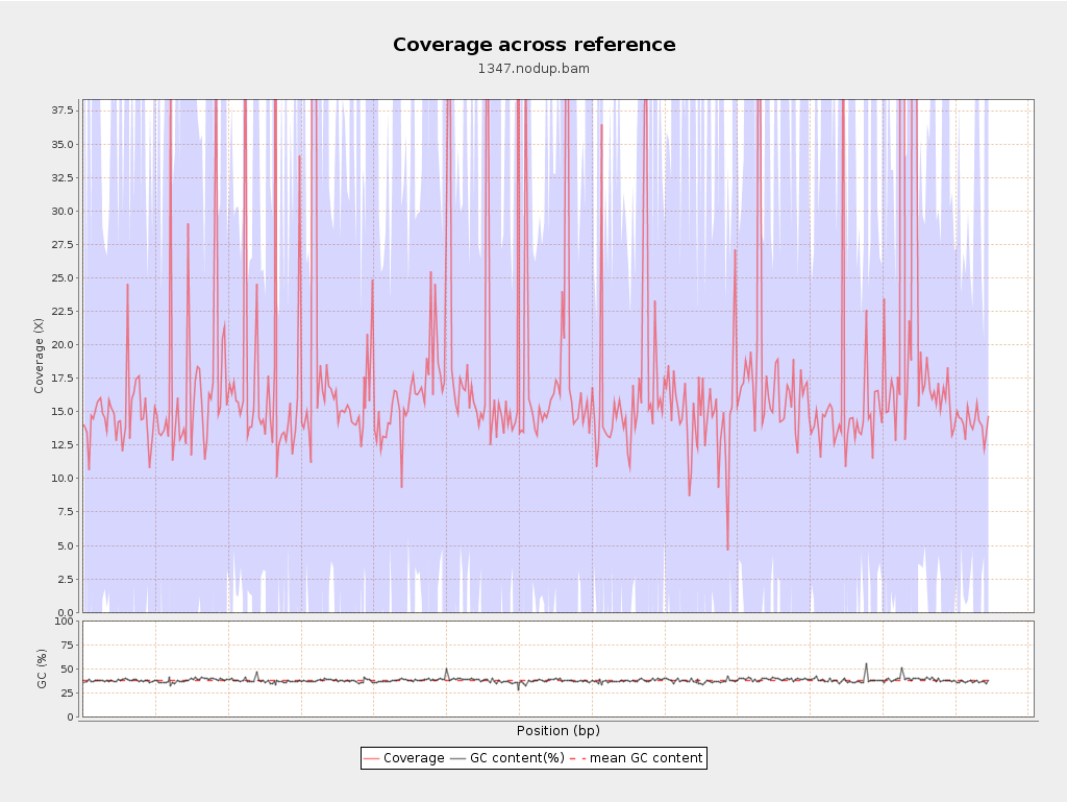
General error rate	2.34%
Mismatches	118,119,610
Insertions	3,631,600
Mapped reads with at least one insertion	8.31%
Deletions	3,758,309
Mapped reads with at least one deletion	8.5%
Homopolymer indels	55.76%

2.7. Chromosome stats

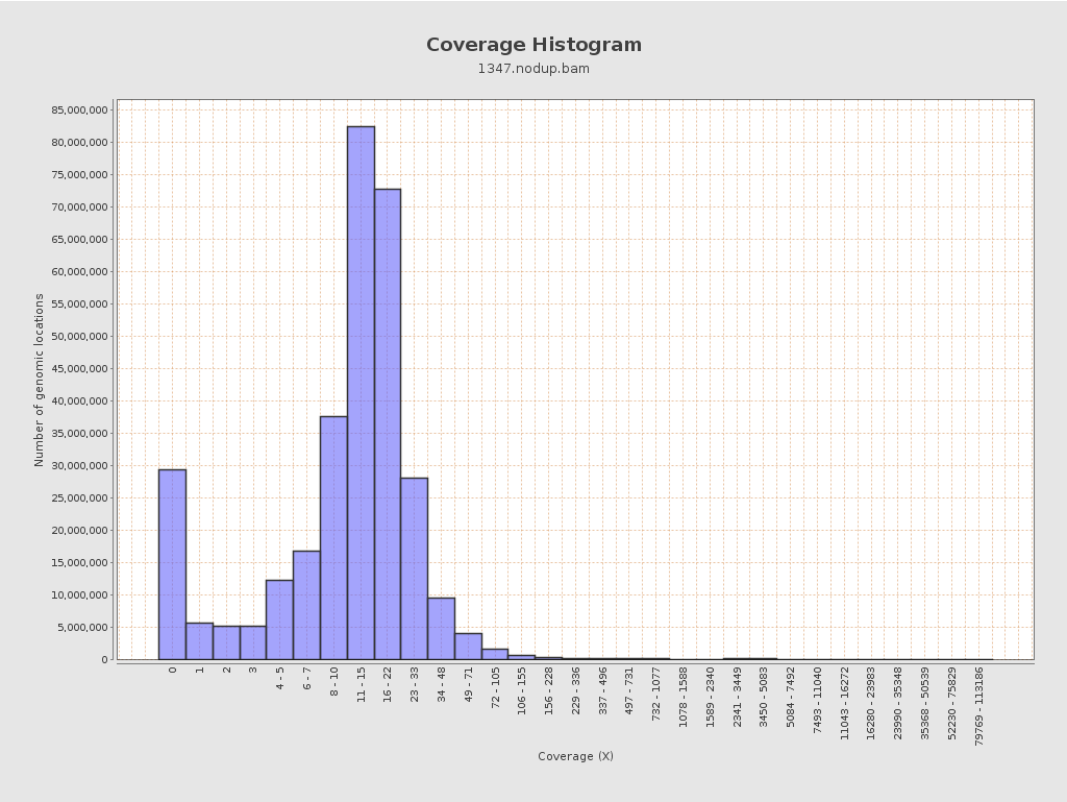
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	434843120	14.6292	38.0114

LT669789.1	36598175	646027371	17.6519	136.425
LT669790.1	30422129	562096742	18.4766	120.5858
LT669791.1	52758100	909247604	17.2343	112.3013
LT669792.1	28376109	500625675	17.6425	167.6384
LT669793.1	33388210	545915338	16.3505	94.7403
LT669794.1	50579949	841823516	16.6434	118.9447
LT669795.1	49795044	1053015506	21.147	212.2872

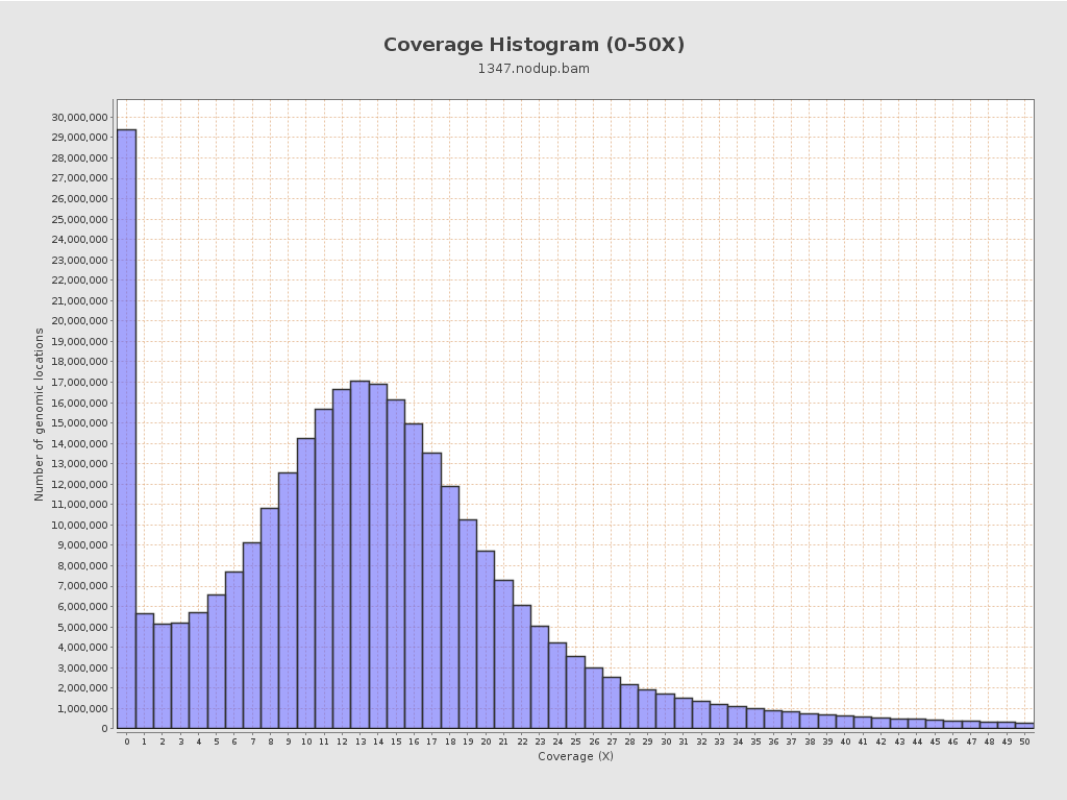
3. Results : Coverage across reference



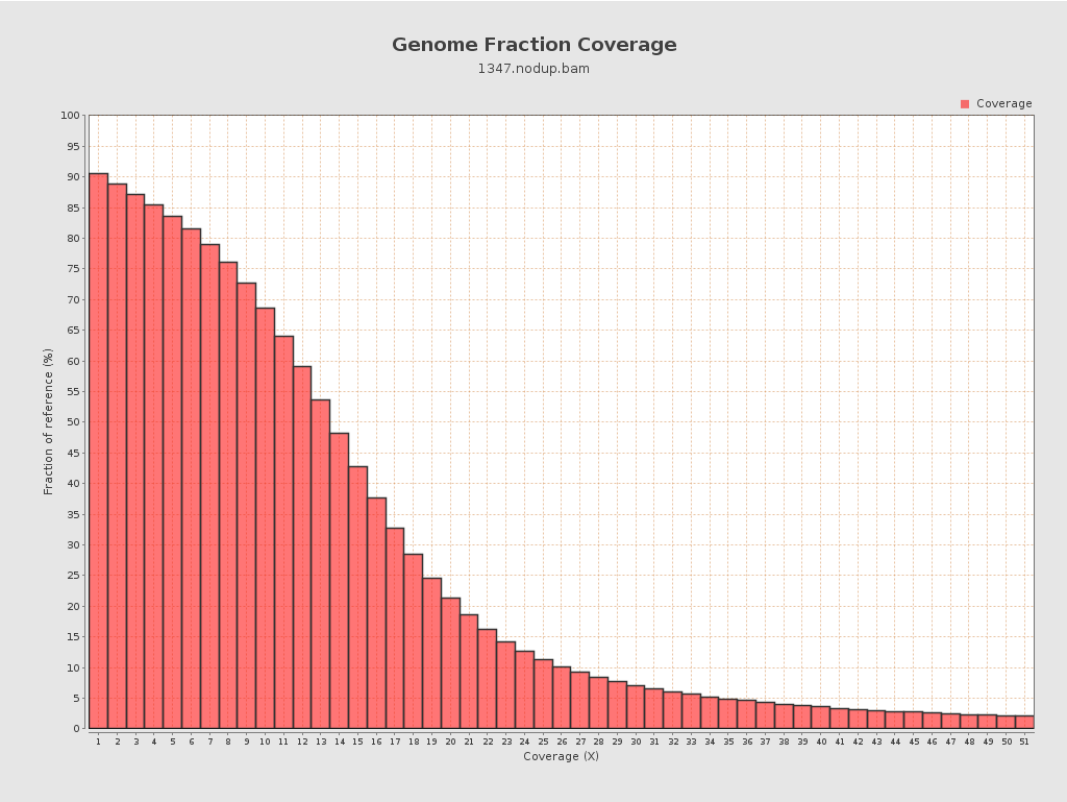
4. Results : Coverage Histogram



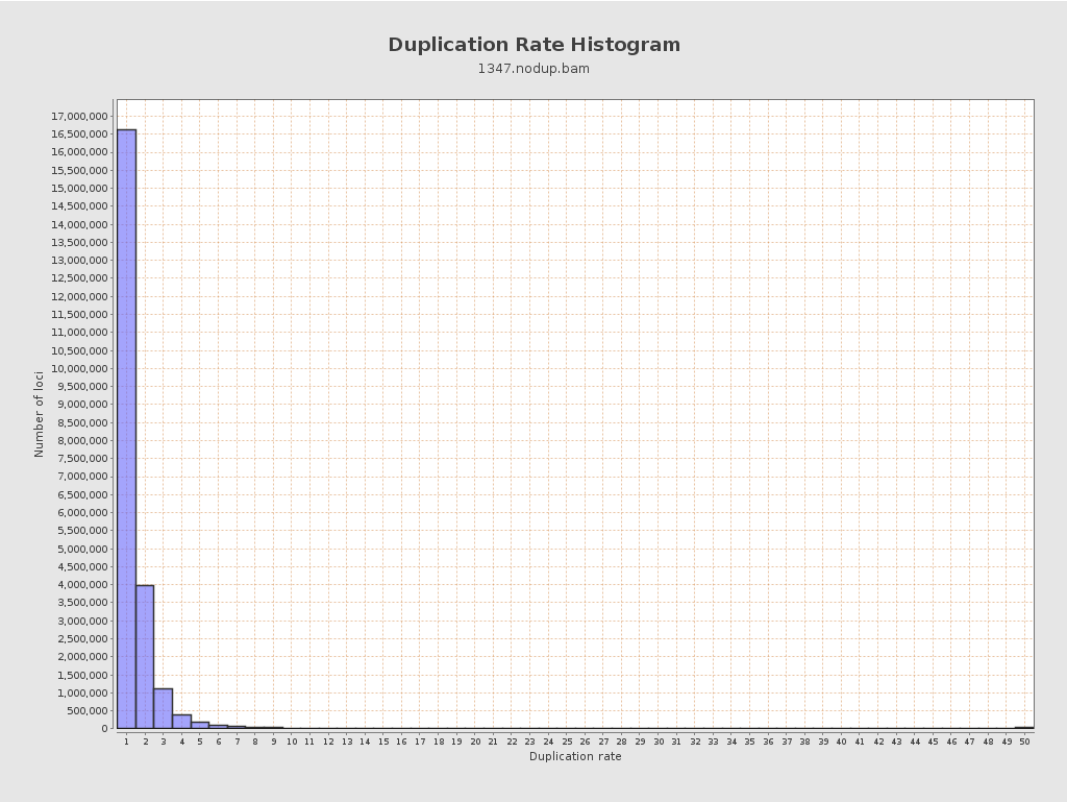
5. Results : Coverage Histogram (0-50X)



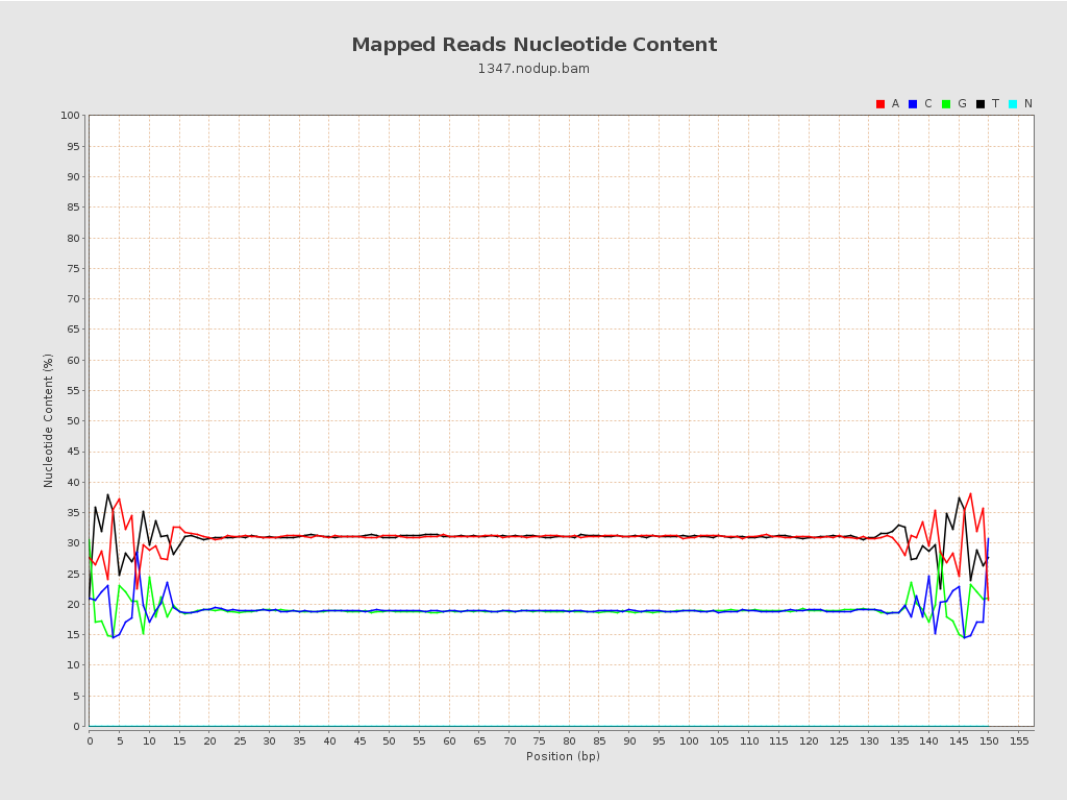
6. Results : Genome Fraction Coverage



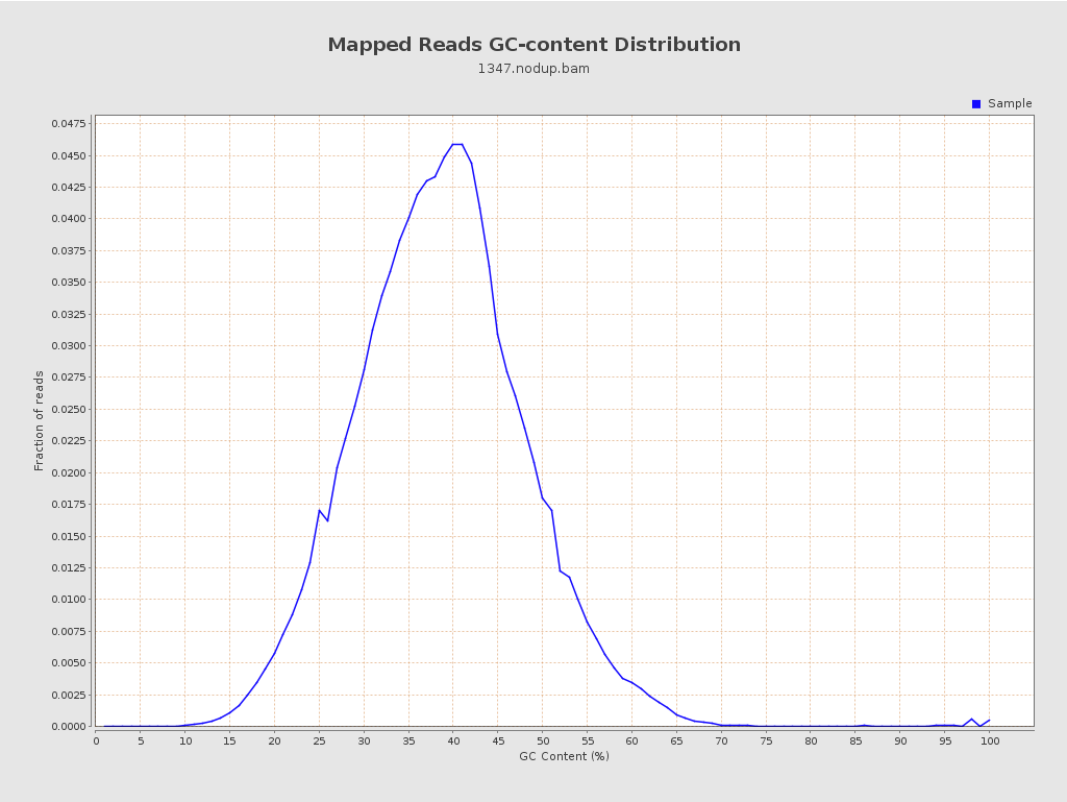
7. Results : Duplication Rate Histogram



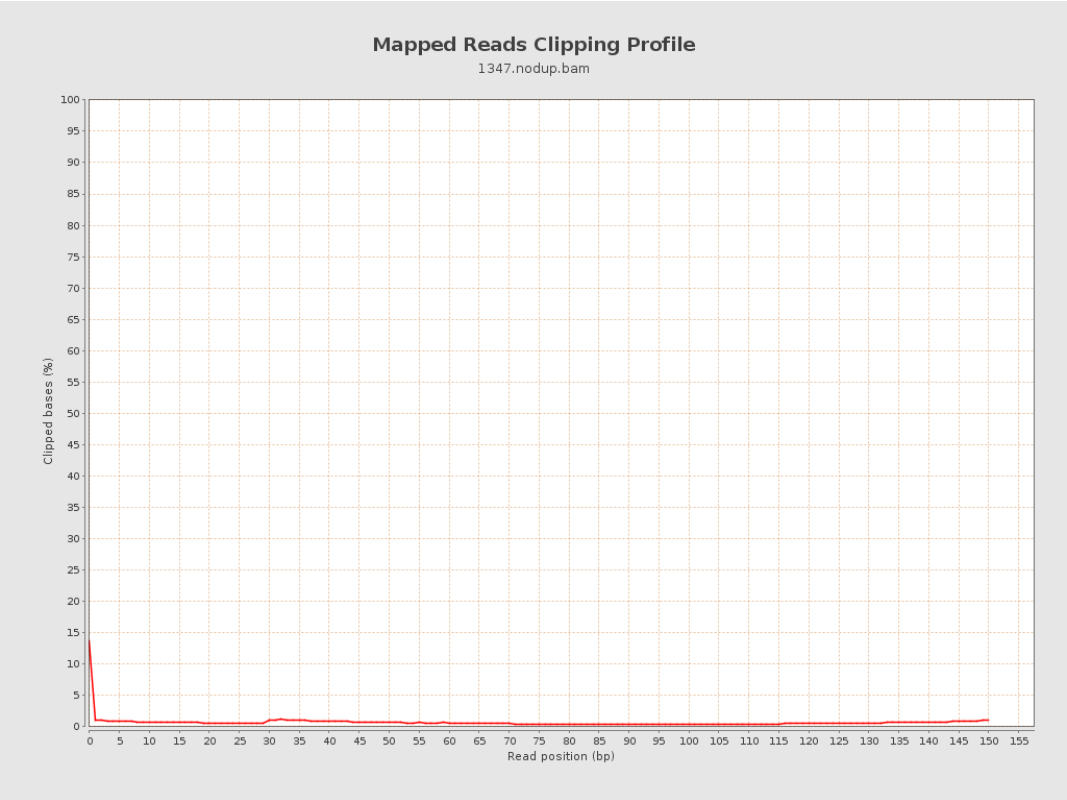
8. Results : Mapped Reads Nucleotide Content



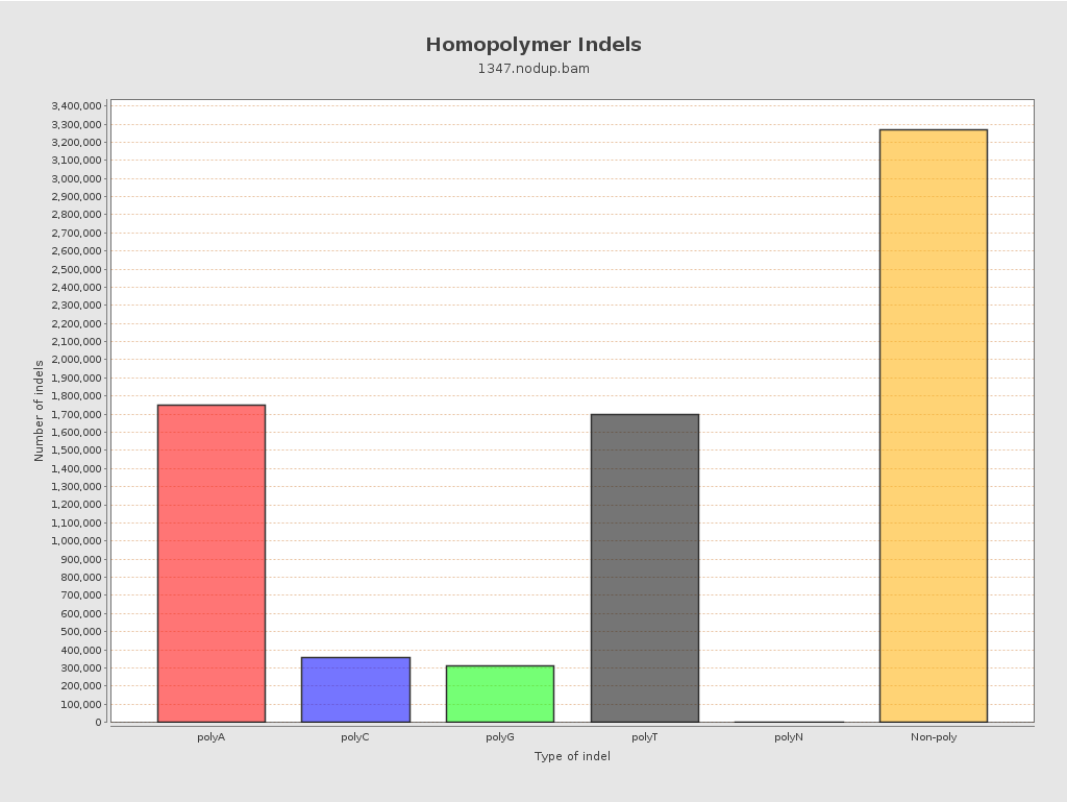
9. Results : Mapped Reads GC-content Distribution



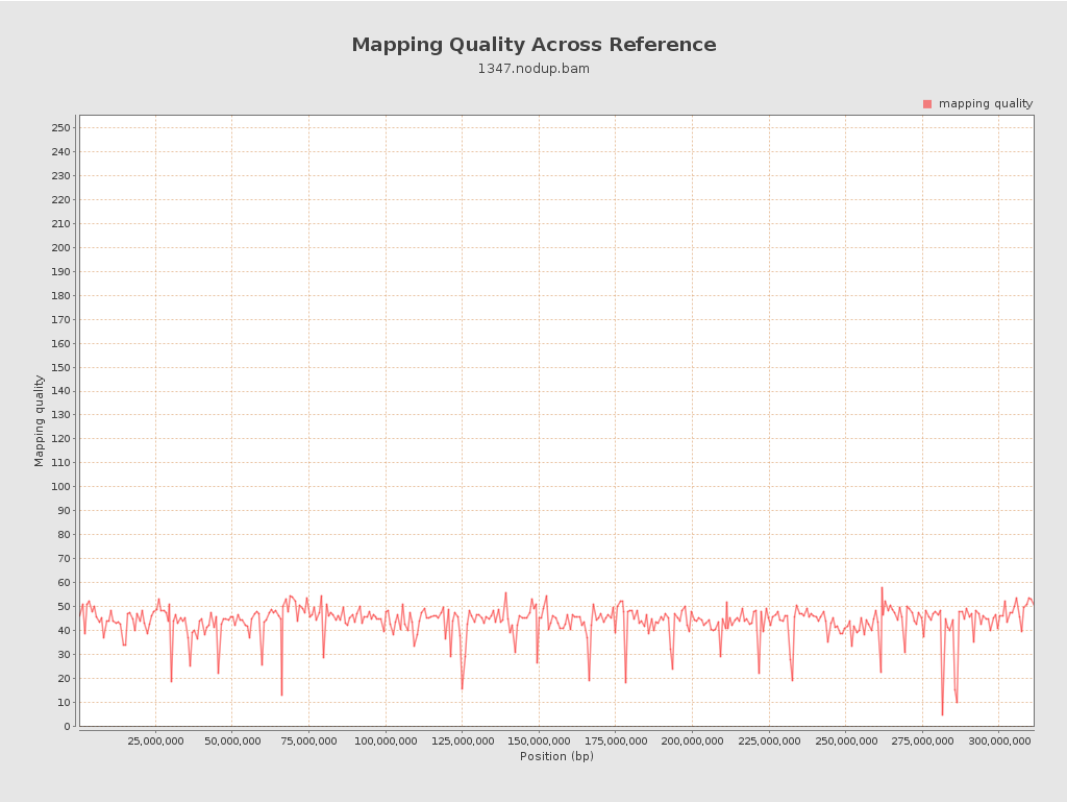
10. Results : Mapped Reads Clipping Profile



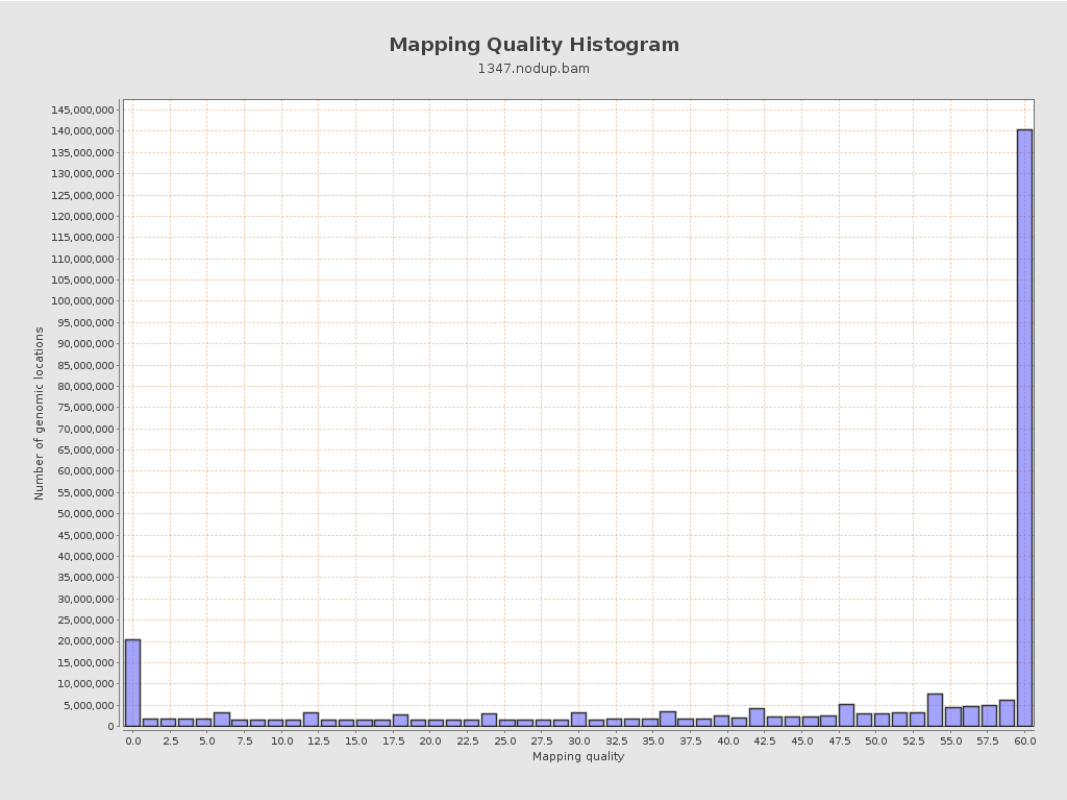
11. Results : Homopolymer Indels



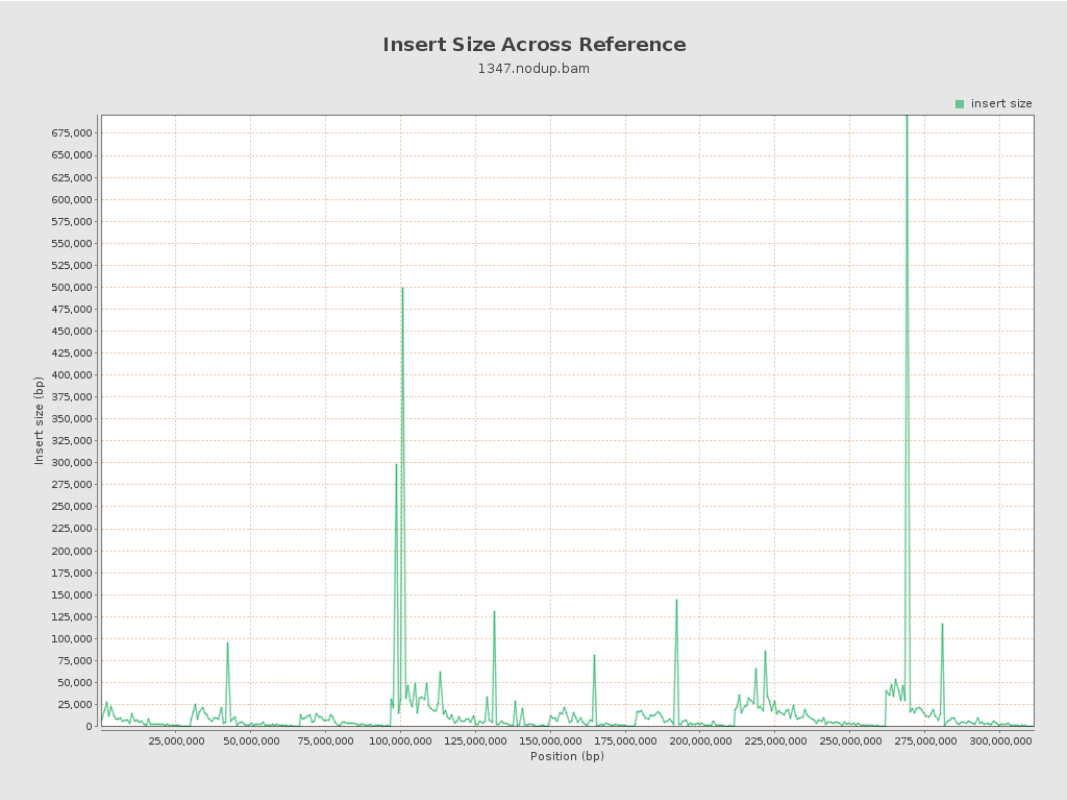
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram