Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1350
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1350 .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_255/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_255_S336_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_255/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_255_S336_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:40:09 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	88,525,127
Mapped reads	81,612,474 / 92.19%
Unmapped reads	6,912,653 / 7.81%
Mapped paired reads	81,612,474 / 92.19%
Mapped reads, first in pair	40,884,841 / 46.18%
Mapped reads, second in pair	40,727,633 / 46.01%
Mapped reads, both in pair	79,414,972 / 89.71%
Mapped reads, singletons	2,197,502 / 2.48%
Read min/max/mean length	30 / 151 / 147.91
Duplicated reads (flagged)	13,005,712 / 14.69%
Clipped reads	19,987,916 / 22.58%

2.2. ACGT Content

Number/percentage of A's	3,460,159,341 / 30.98%
Number/percentage of C's	2,123,149,126 / 19.01%
Number/percentage of T's	3,459,121,281 / 30.97%
Number/percentage of G's	2,127,357,968 / 19.05%
Number/percentage of N's	41,052 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	35.9375
Standard Deviation	320.4147

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Insert size

Mean	256,673.29
Standard Deviation	2,433,950.2
P25/Median/P75	317 / 419 / 547

2.6. Mismatches and indels

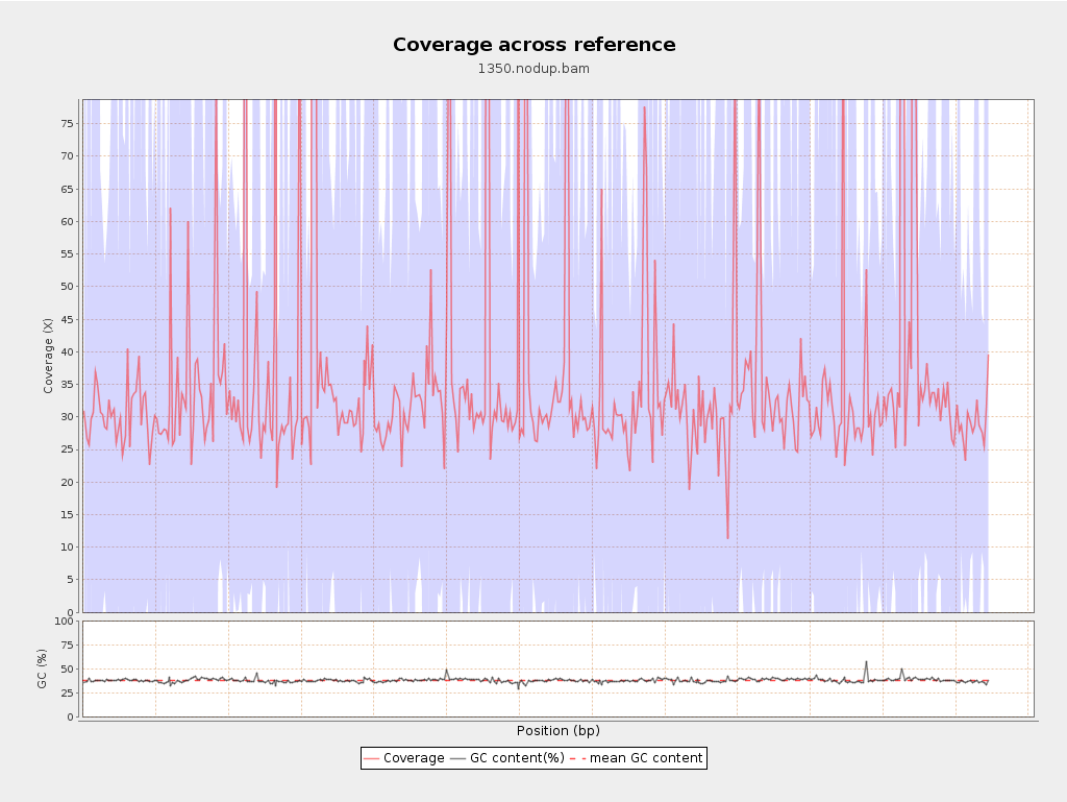
General error rate	2.4%
Mismatches	245,525,062
Insertions	8,129,515
Mapped reads with at least one insertion	8.89%
Deletions	7,980,052
Mapped reads with at least one deletion	8.66%
Homopolymer indels	57.09%

2.7. Chromosome stats

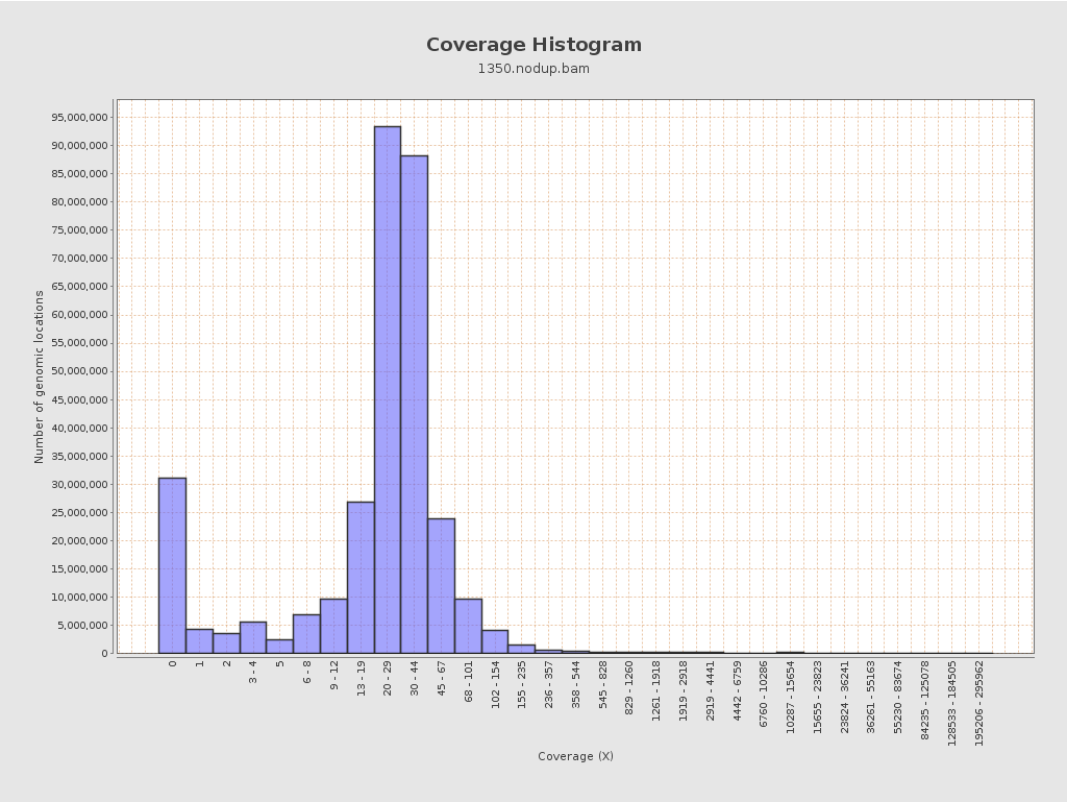
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	891492603	29.992	130.6252

LT669789.1	36598175	1365838941	37.3199	341.0744
LT669790.1	30422129	1295544591	42.5856	409.4712
LT669791.1	52758100	1867819806	35.4035	342.1463
LT669792.1	28376109	1031837371	36.3629	352.6212
LT669793.1	33388210	1100818976	32.9703	168.4515
LT669794.1	50579949	1728351044	34.1707	265.412
LT669795.1	49795044	1917944276	38.5168	398.5942

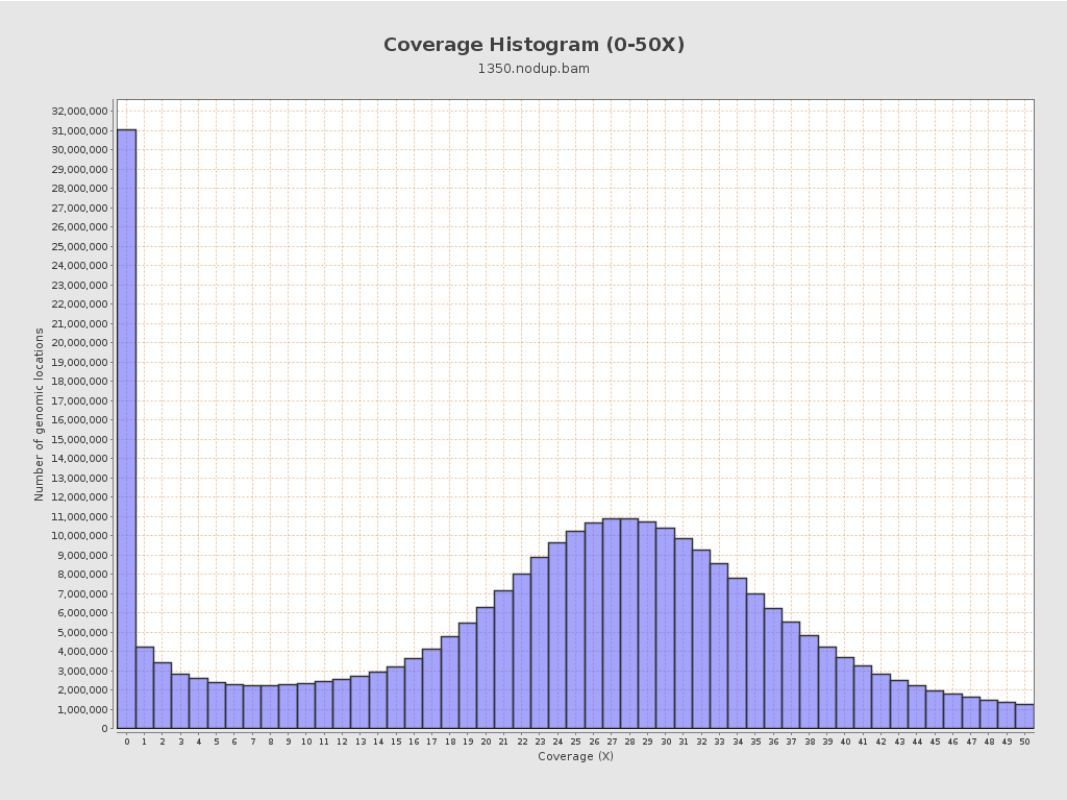
3. Results : Coverage across reference



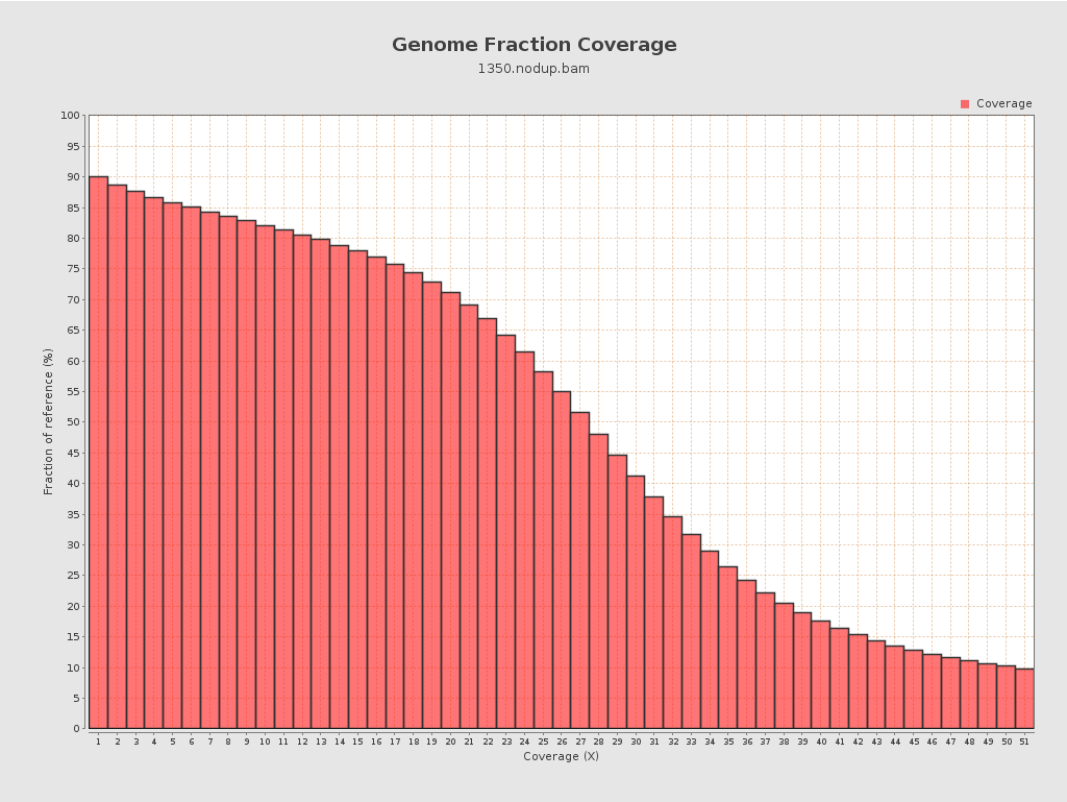
4. Results : Coverage Histogram



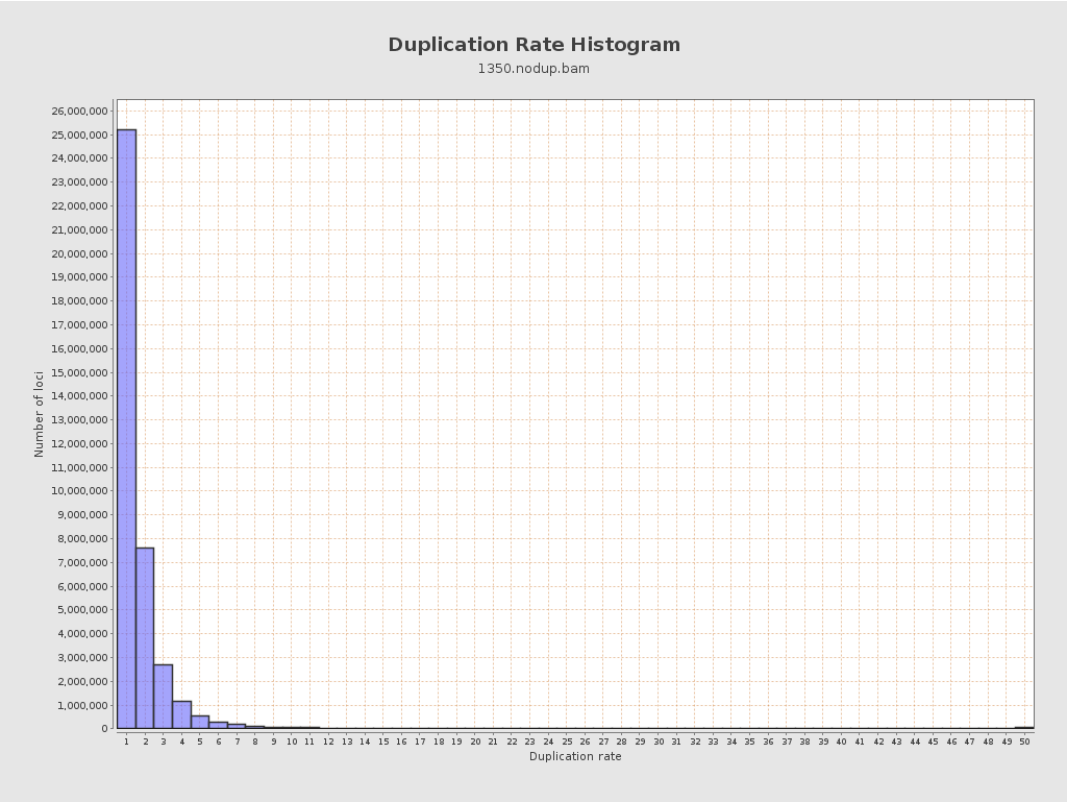
5. Results : Coverage Histogram (0-50X)



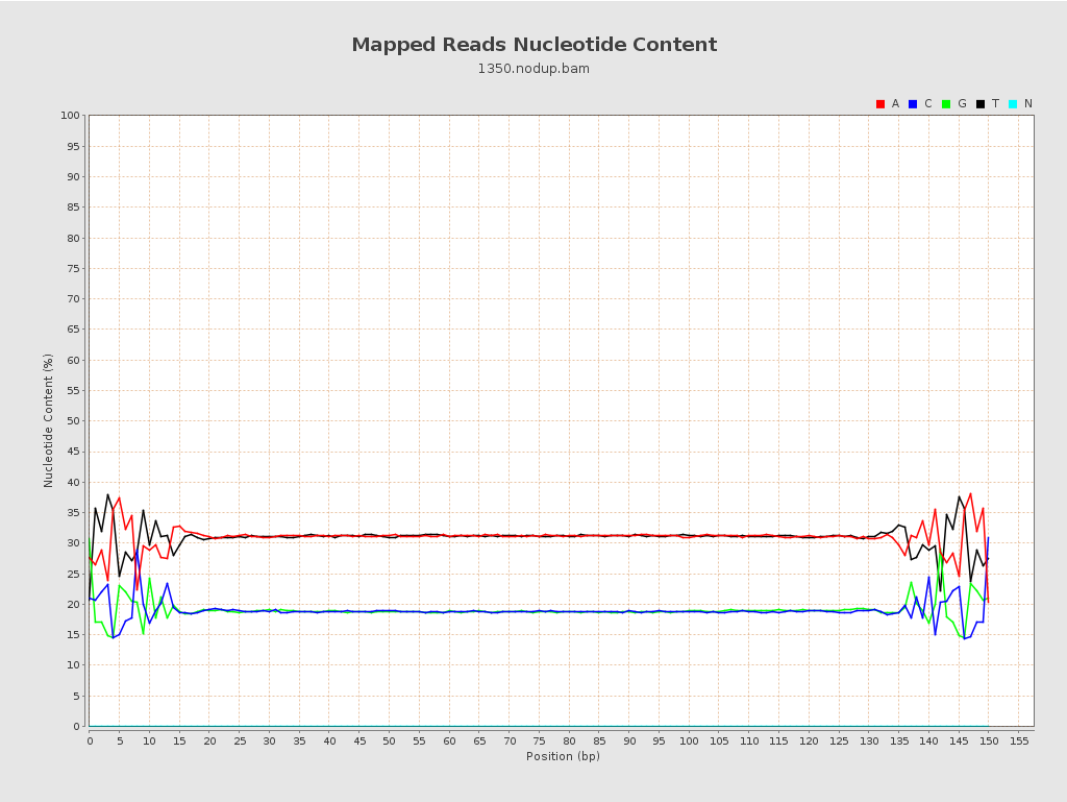
6. Results : Genome Fraction Coverage



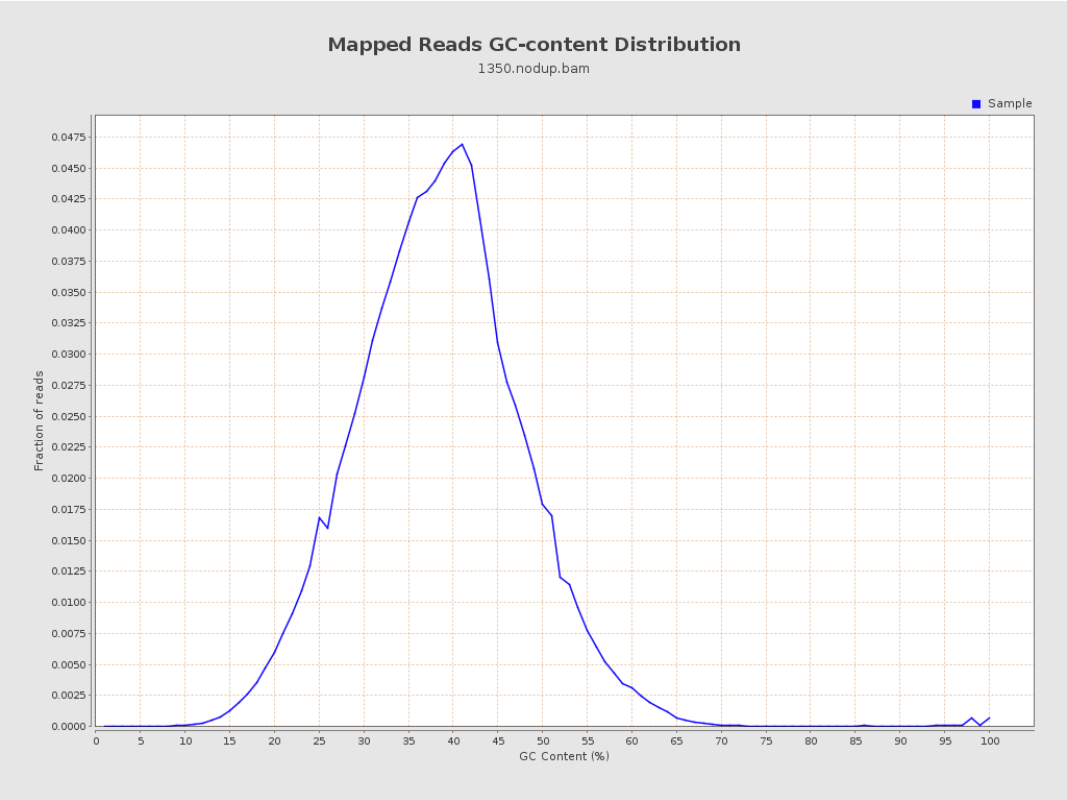
7. Results : Duplication Rate Histogram



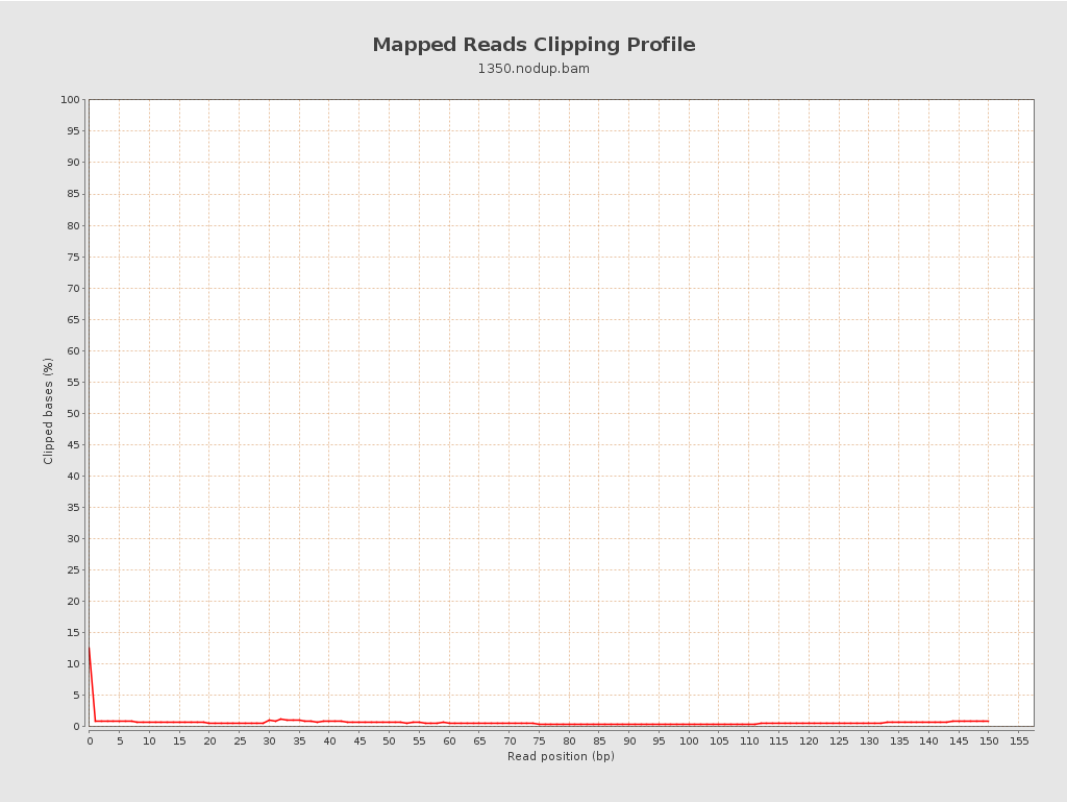
8. Results : Mapped Reads Nucleotide Content



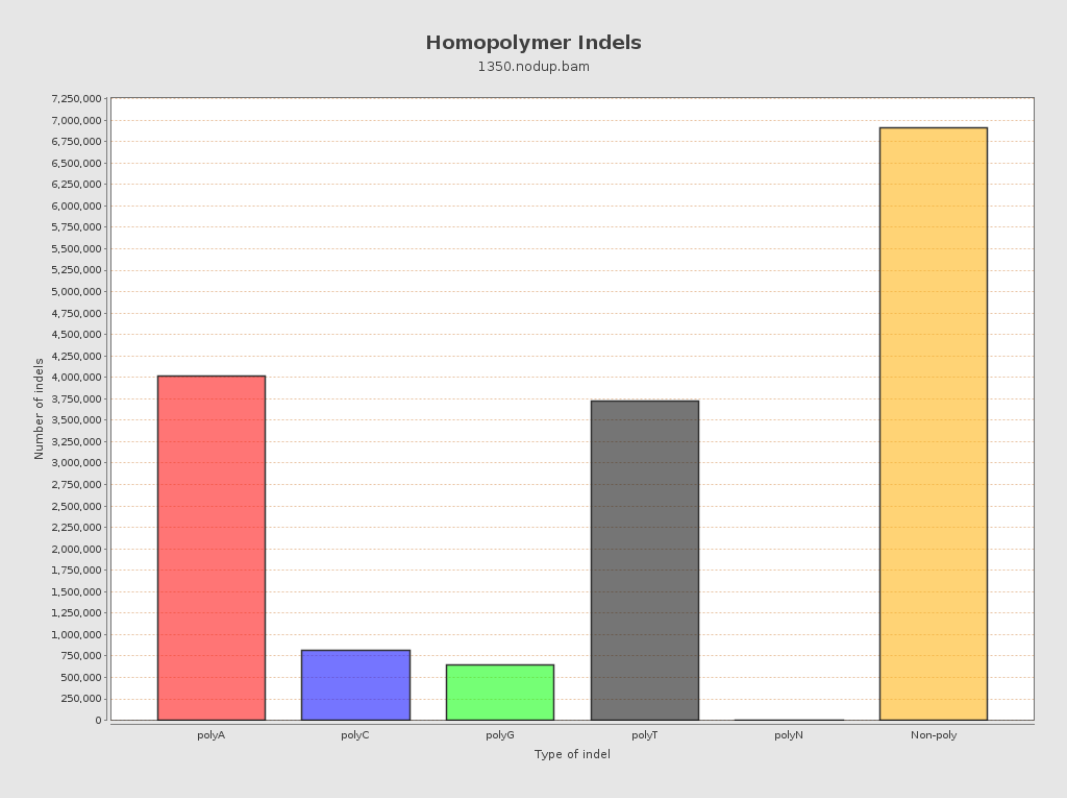
9. Results : Mapped Reads GC-content Distribution



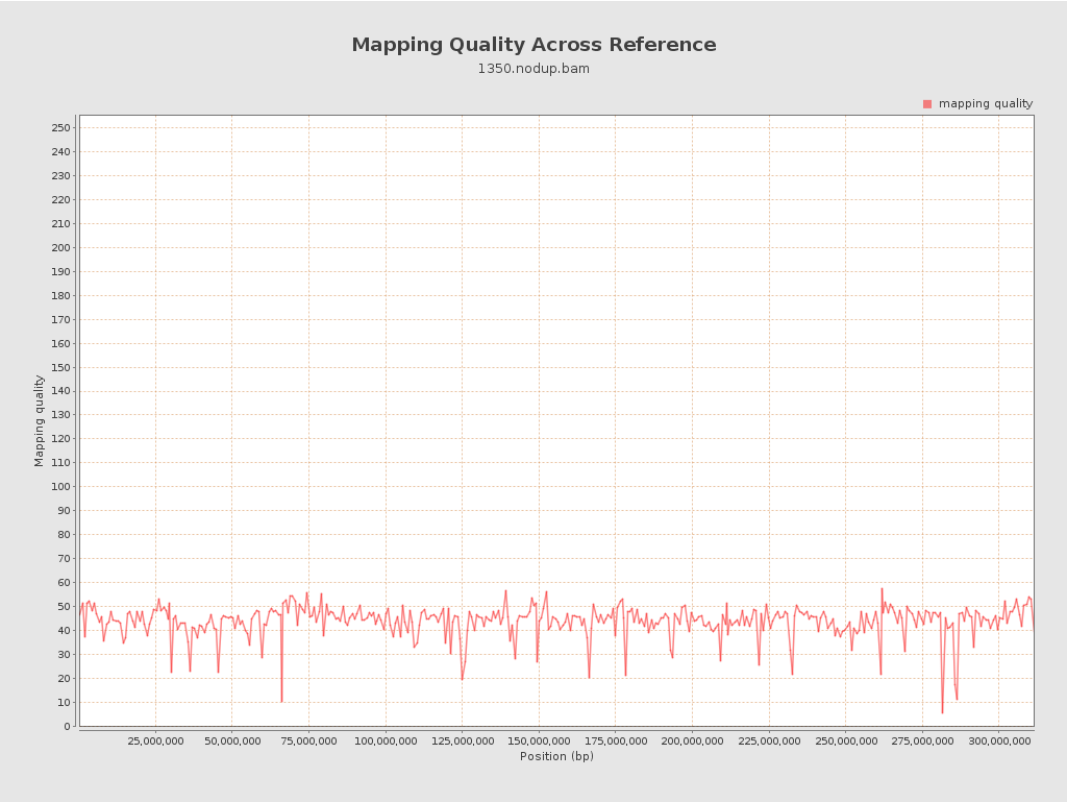
10. Results : Mapped Reads Clipping Profile



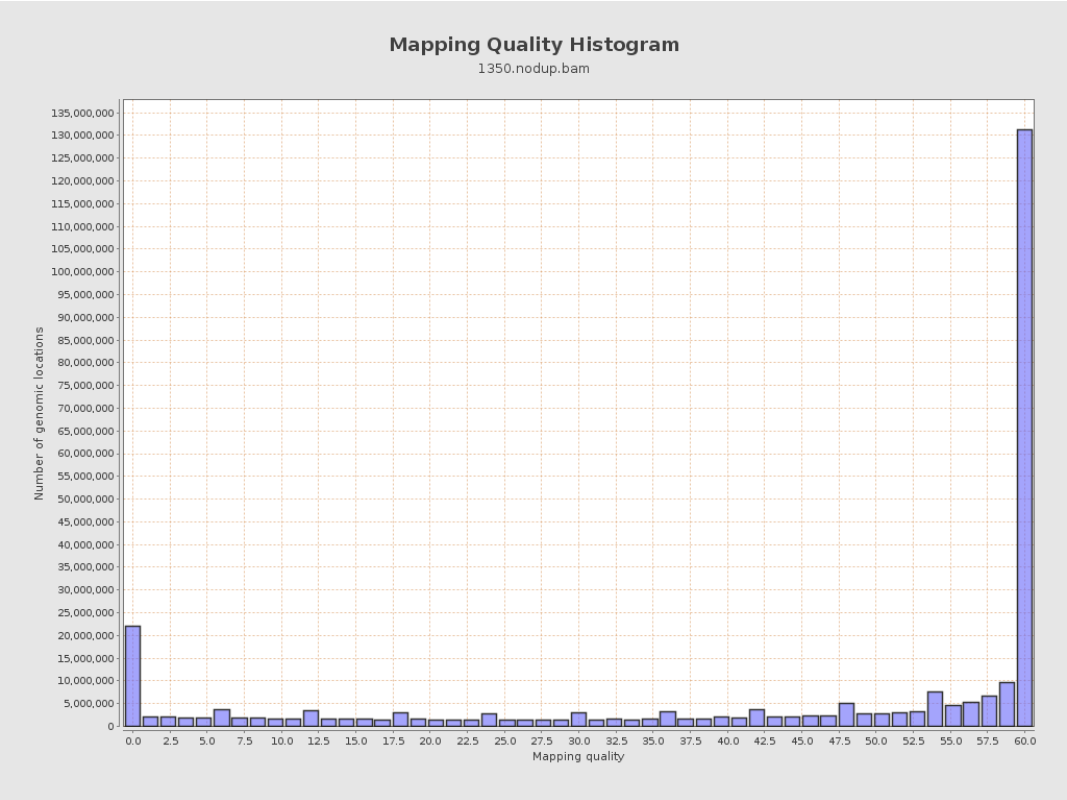
11. Results : Homopolymer Indels



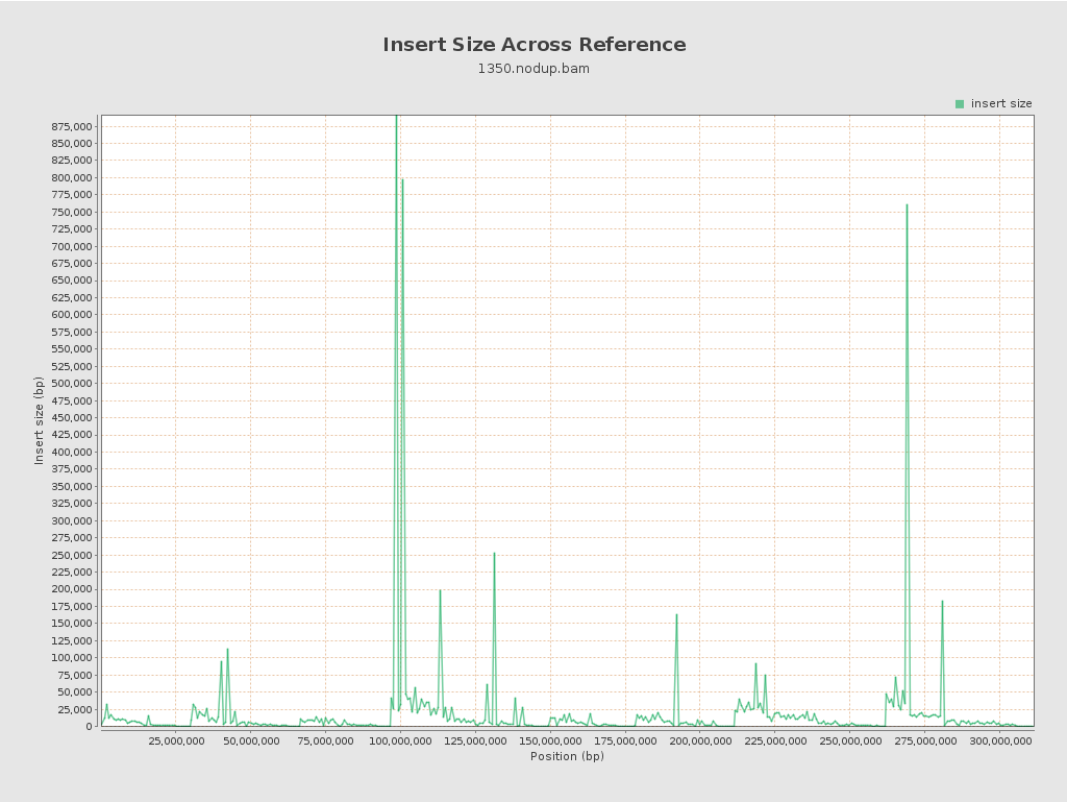
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram