

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/115
0
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1150 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_582/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_582_S149_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_582/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_582_S149_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:23:53 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	44,527,987
Mapped reads	41,560,682 / 93.34%
Unmapped reads	2,967,305 / 6.66%
Mapped paired reads	41,560,682 / 93.34%
Mapped reads, first in pair	20,924,593 / 46.99%
Mapped reads, second in pair	20,636,089 / 46.34%
Mapped reads, both in pair	40,487,168 / 90.93%
Mapped reads, singletons	1,073,514 / 2.41%
Read min/max/mean length	30 / 151 / 148.28
Duplicated reads (flagged)	6,313,757 / 14.18%
Clipped reads	10,149,418 / 22.79%

2.2. ACGT Content

Number/percentage of A's	1,773,763,494 / 30.95%
Number/percentage of C's	1,092,683,922 / 19.07%
Number/percentage of T's	1,774,730,321 / 30.97%
Number/percentage of G's	1,088,969,971 / 19%
Number/percentage of N's	37,941 / 0%
GC Percentage	38.07%

2.3. Coverage

Mean	18.432
Standard Deviation	150.3866

2.4. Mapping Quality

Mean Mapping Quality	44.14
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2.5. Insert size

Mean	224,922.03
Standard Deviation	2,244,417.72
P25/Median/P75	339 / 440 / 561

2.6. Mismatches and indels

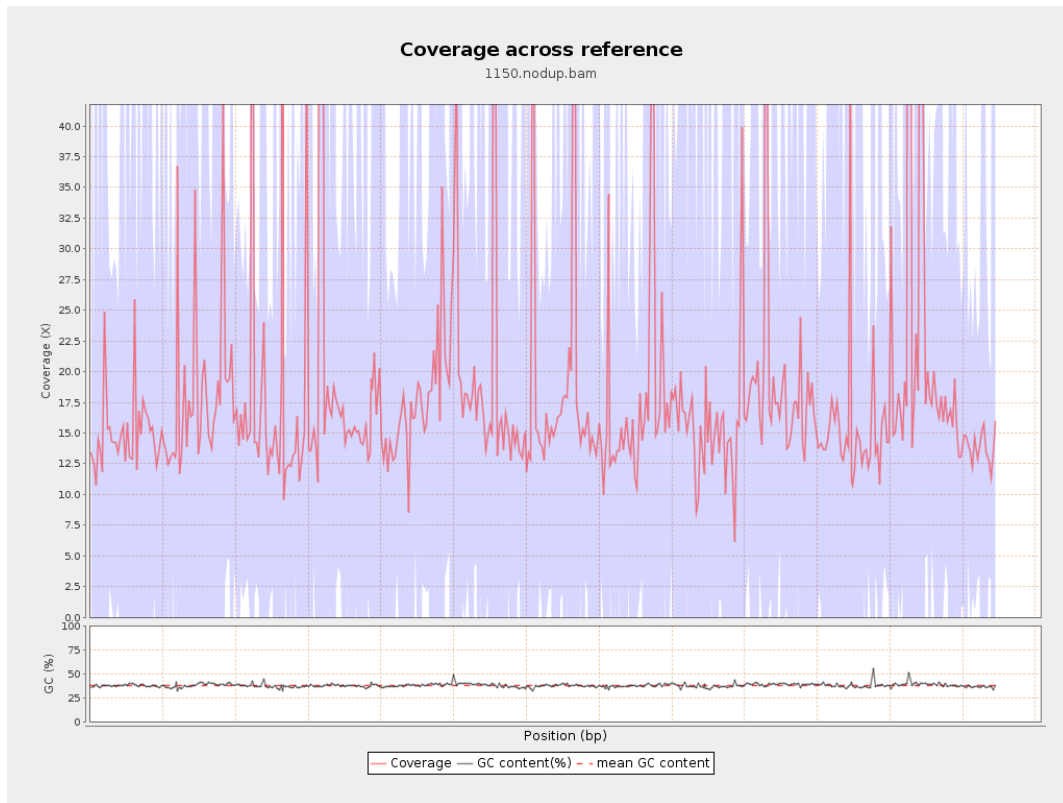
General error rate	2.72%
Mismatches	145,620,226
Insertions	3,866,889
Mapped reads with at least one insertion	8.37%
Deletions	3,824,728
Mapped reads with at least one deletion	8.21%
Homopolymer indels	56.59%

2.7. Chromosome stats

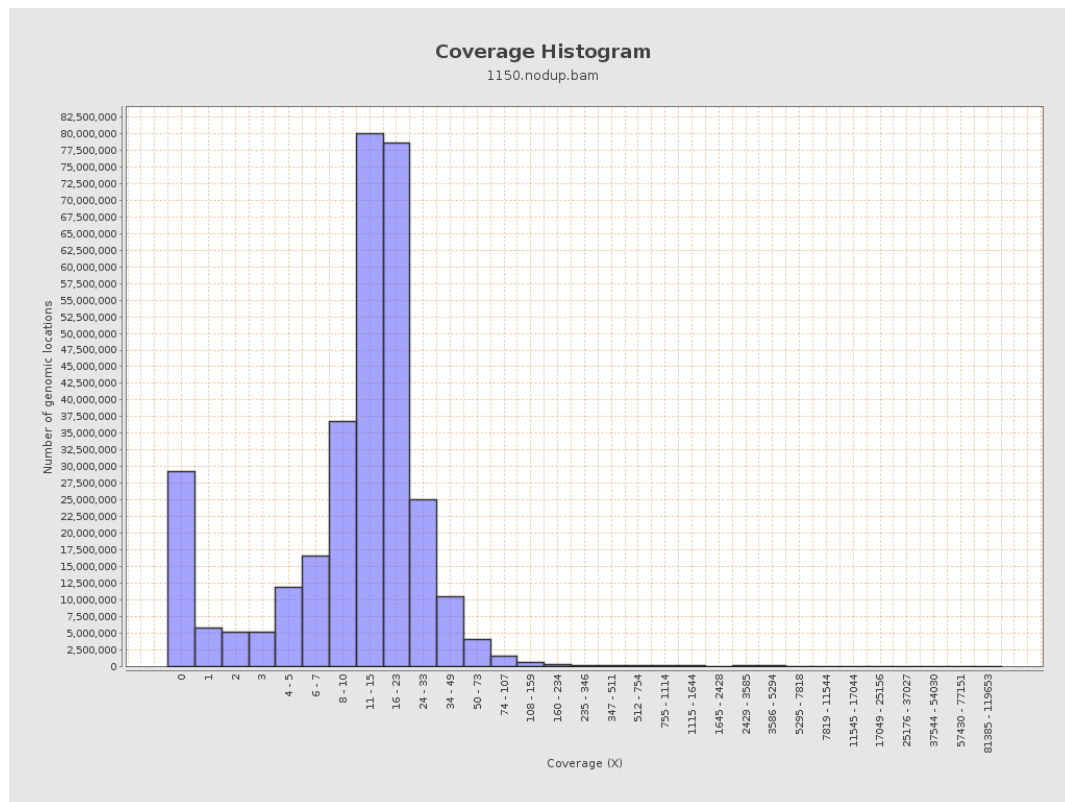
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	437836970	14.7299	44.6811

LT669789.1	36598175	698257977	19.079	162.0877
LT669790.1	30422129	624983550	20.5437	186.4005
LT669791.1	52758100	973185821	18.4462	137.9061
LT669792.1	28376109	512329734	18.055	175.0547
LT669793.1	33388210	572035901	17.1329	109.9628
LT669794.1	50579949	892478512	17.6449	132.8741
LT669795.1	49795044	1033078941	20.7466	190.11

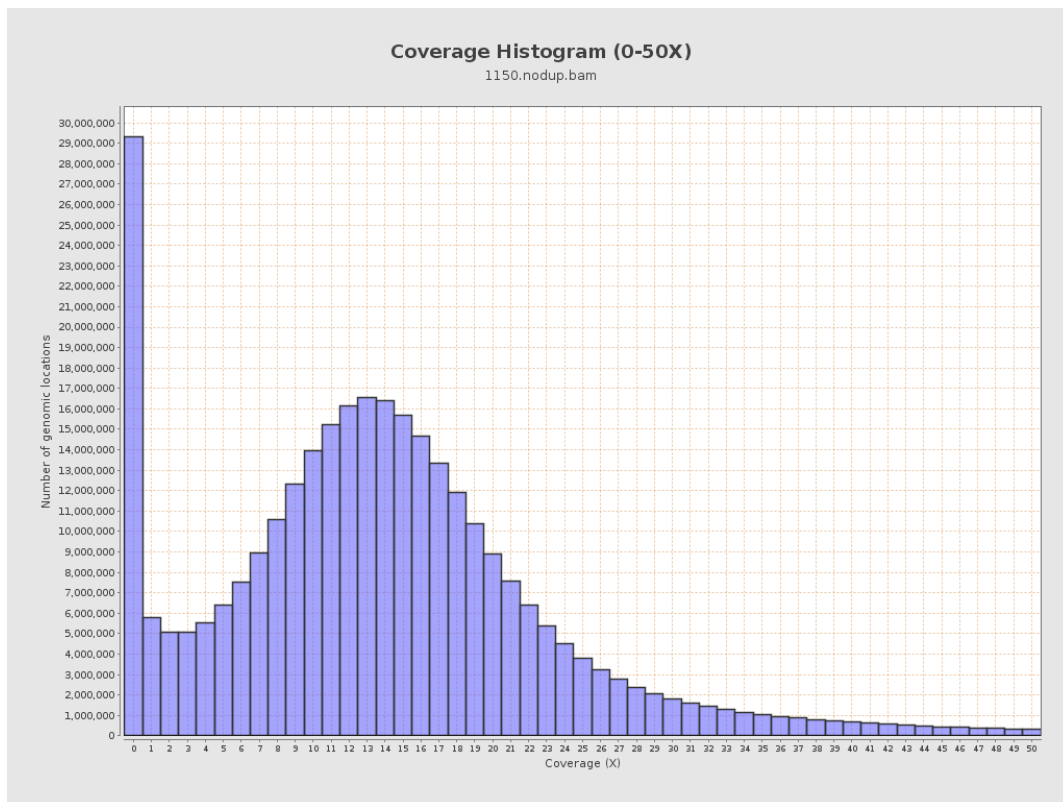
3. Results : Coverage across reference



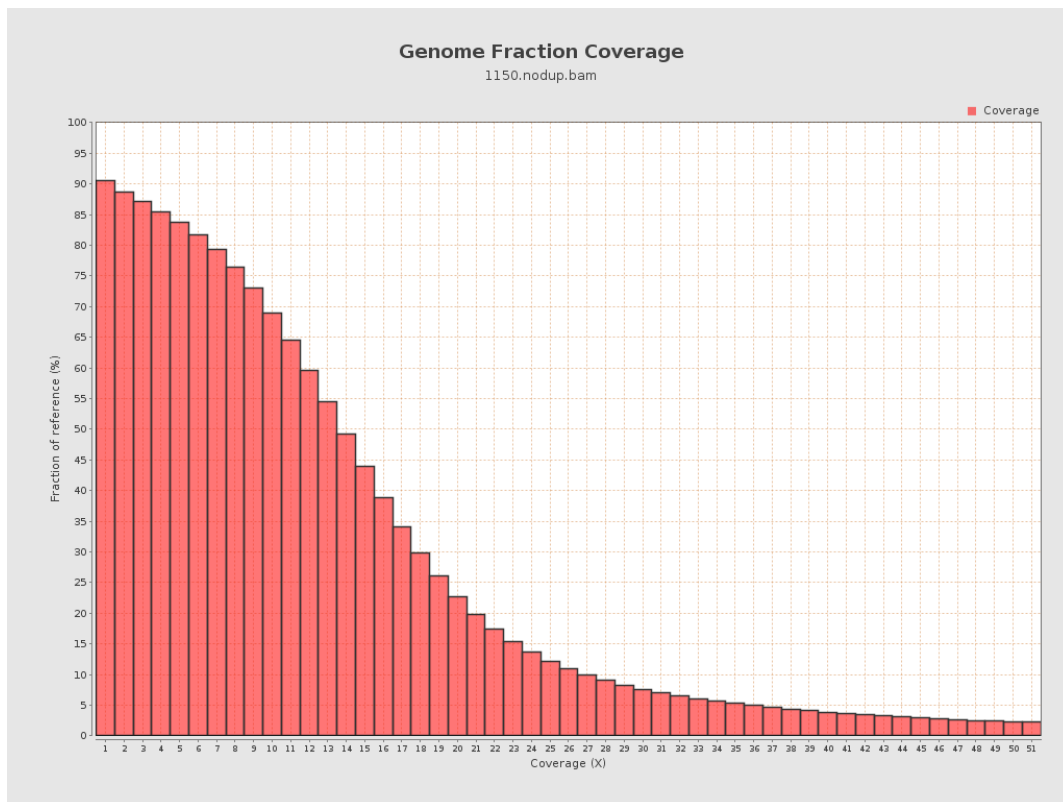
4. Results : Coverage Histogram



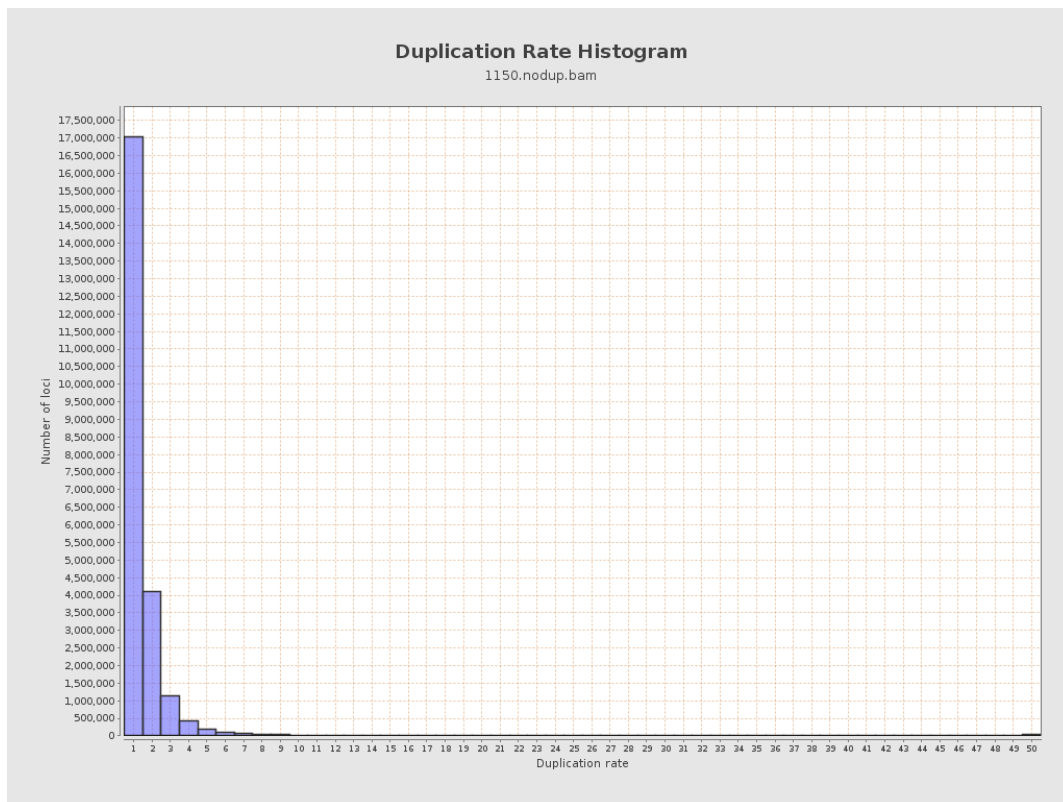
5. Results : Coverage Histogram (0-50X)



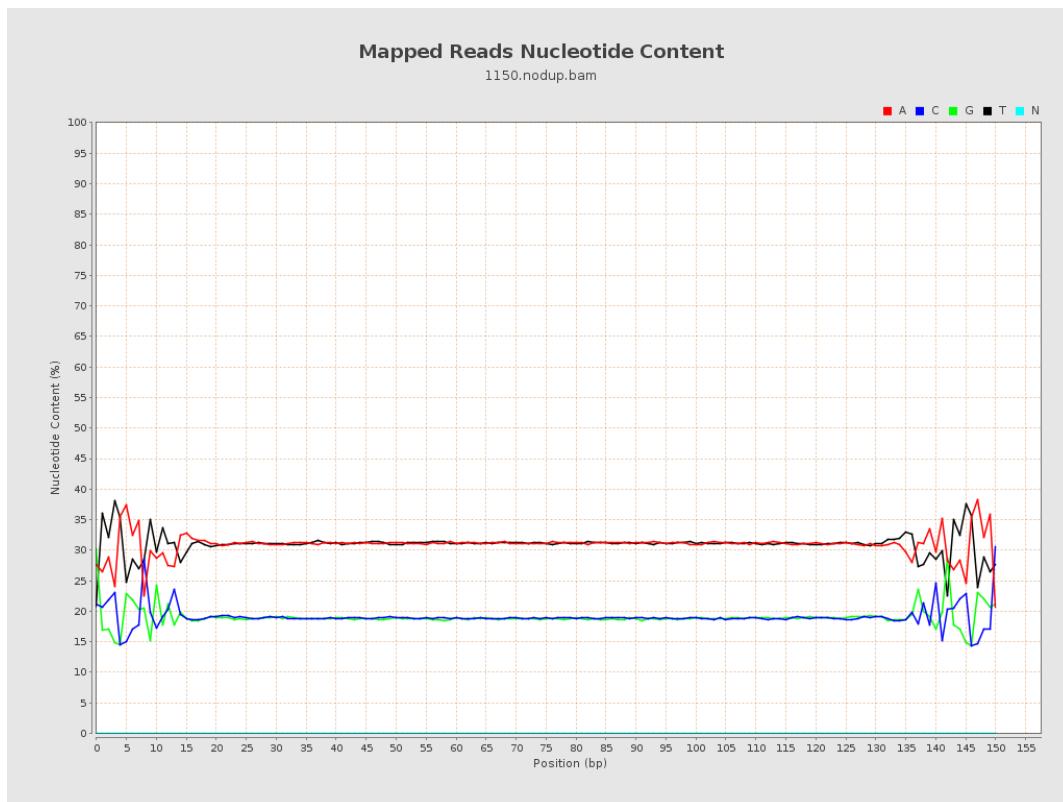
6. Results : Genome Fraction Coverage



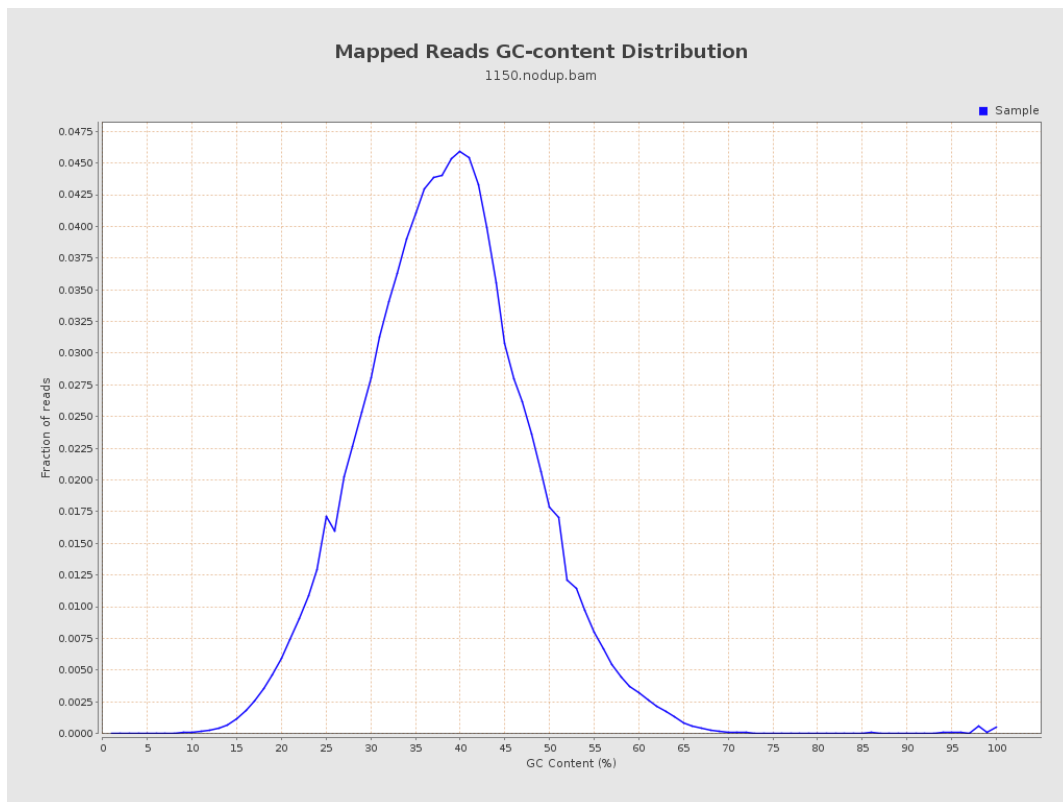
7. Results : Duplication Rate Histogram



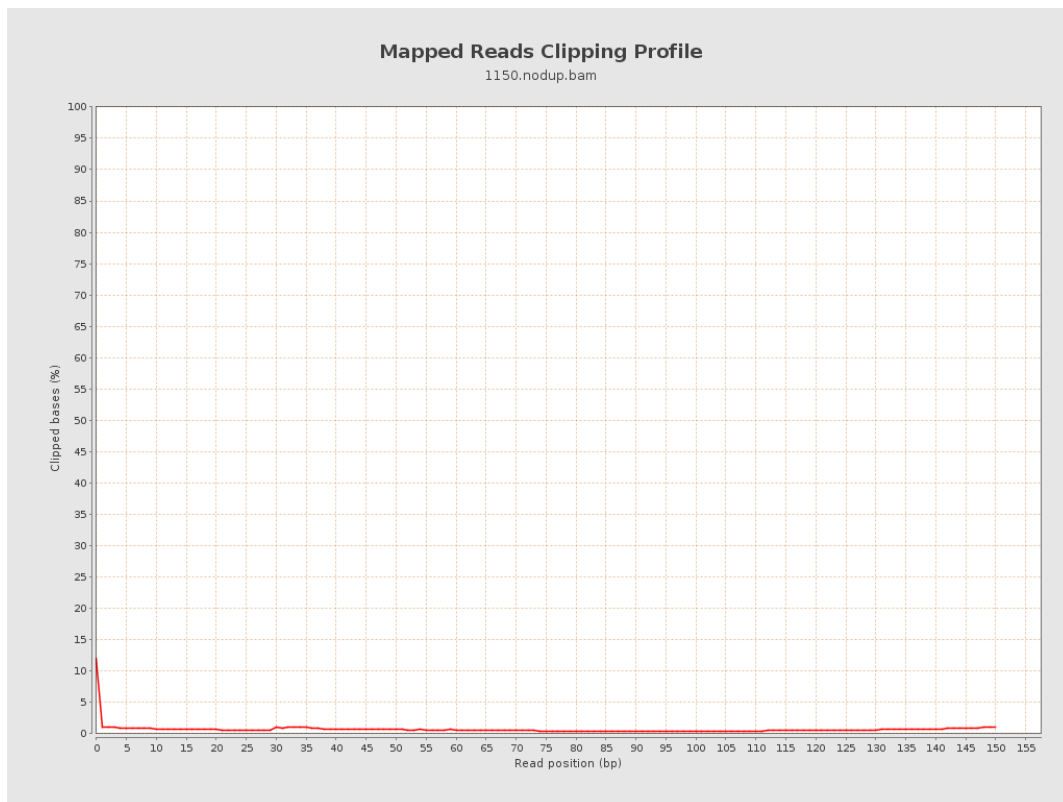
8. Results : Mapped Reads Nucleotide Content



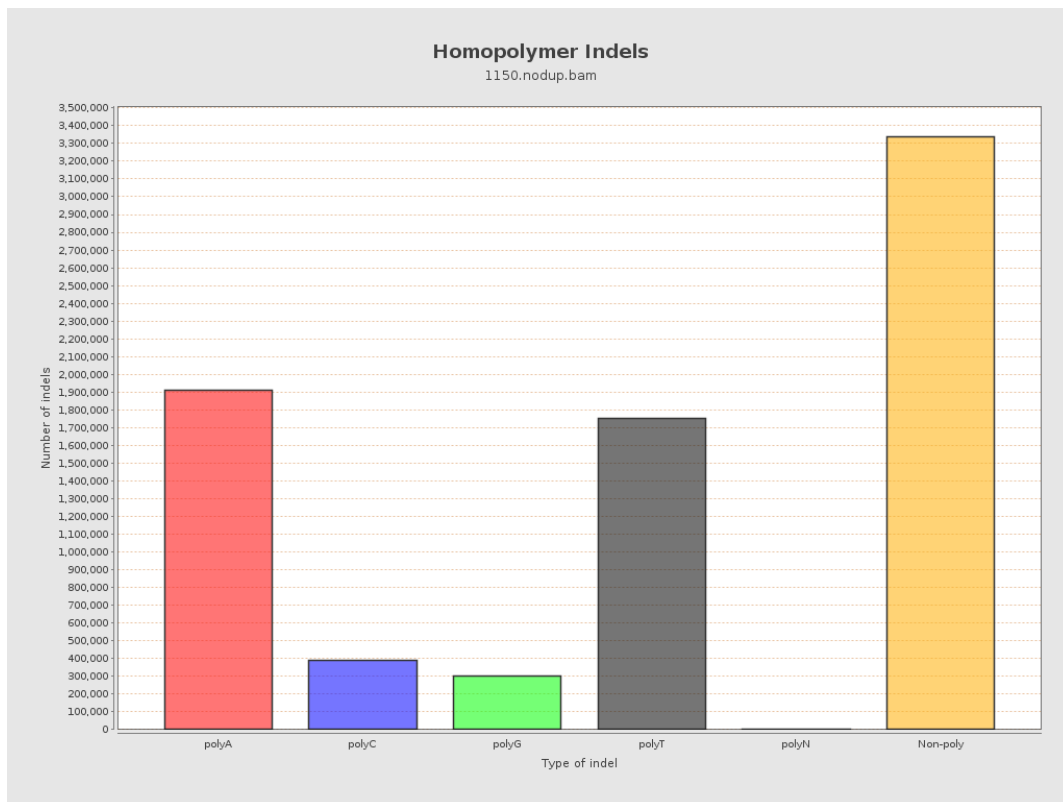
9. Results : Mapped Reads GC-content Distribution



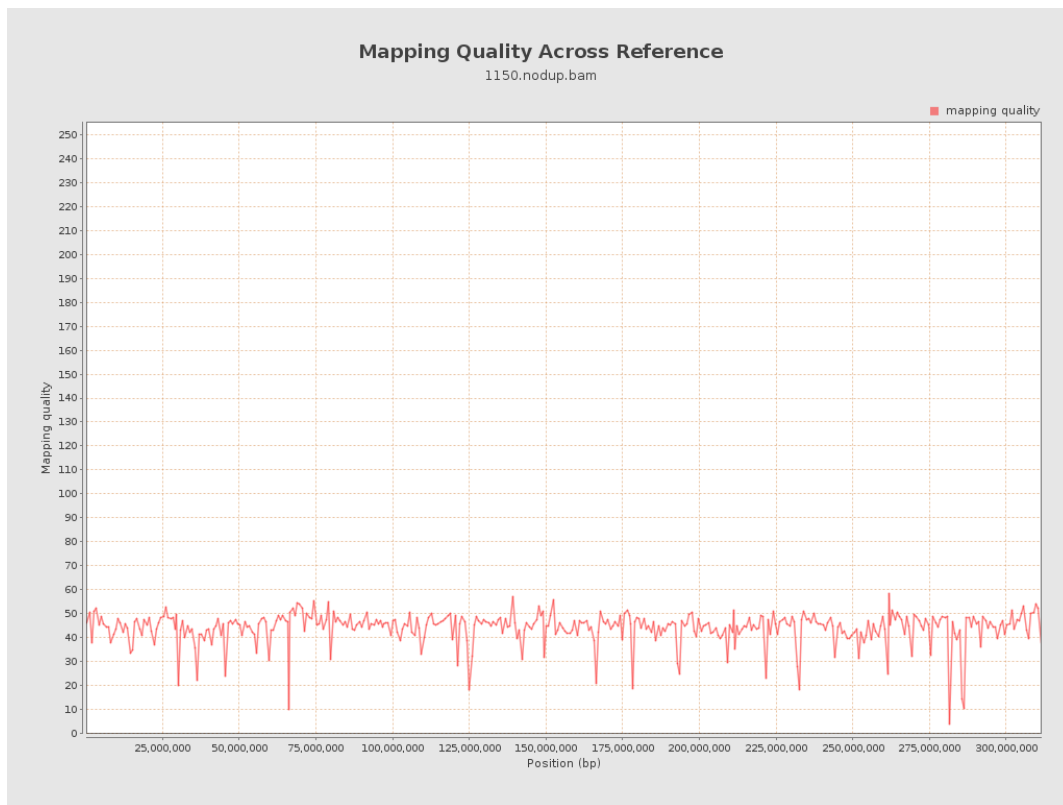
10. Results : Mapped Reads Clipping Profile



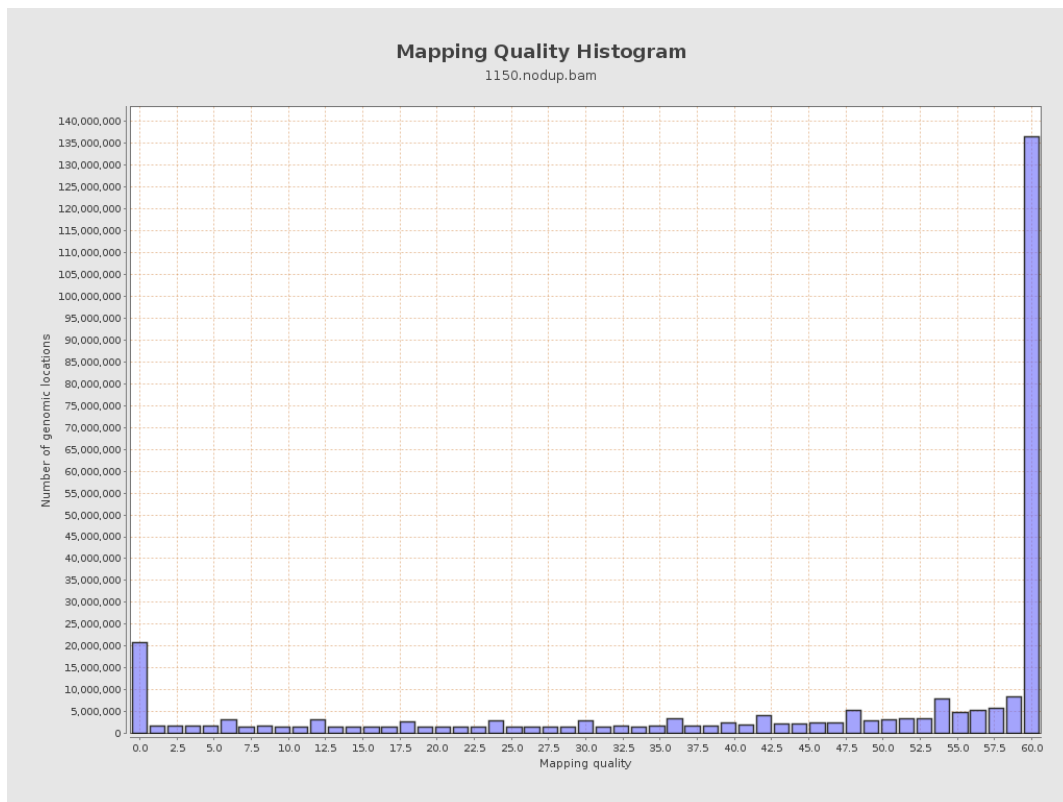
11. Results : Homopolymer Indels



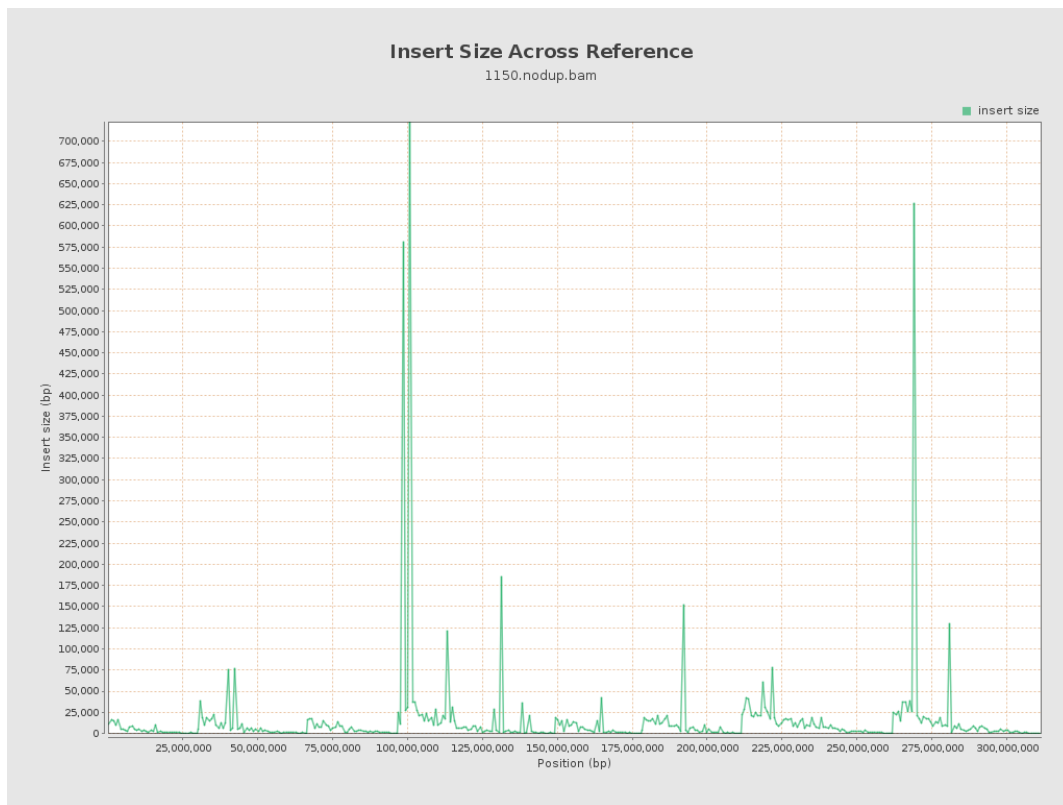
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

