Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:25:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1170
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1170 .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_587/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_587_S154_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_587/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_587_S154_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:25:09 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	44,938,673
Mapped reads	42,606,489 / 94.81%
Unmapped reads	2,332,184 / 5.19%
Mapped paired reads	42,606,489 / 94.81%
Mapped reads, first in pair	21,376,117 / 47.57%
Mapped reads, second in pair	21,230,372 / 47.24%
Mapped reads, both in pair	41,799,342 / 93.01%
Mapped reads, singletons	807,147 / 1.8%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	5,578,714 / 12.41%
Clipped reads	9,650,938 / 21.48%

2.2. ACGT Content

Number/percentage of A's	1,832,333,299 / 30.92%
Number/percentage of C's	1,131,426,023 / 19.09%
Number/percentage of T's	1,834,448,947 / 30.96%
Number/percentage of G's	1,127,744,822 / 19.03%
Number/percentage of N's	42,233 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	19.0648
Standard Deviation	132.2014

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Insert size

Mean	217,532.11
Standard Deviation	2,209,628.87
P25/Median/P75	325 / 422 / 546

2.6. Mismatches and indels

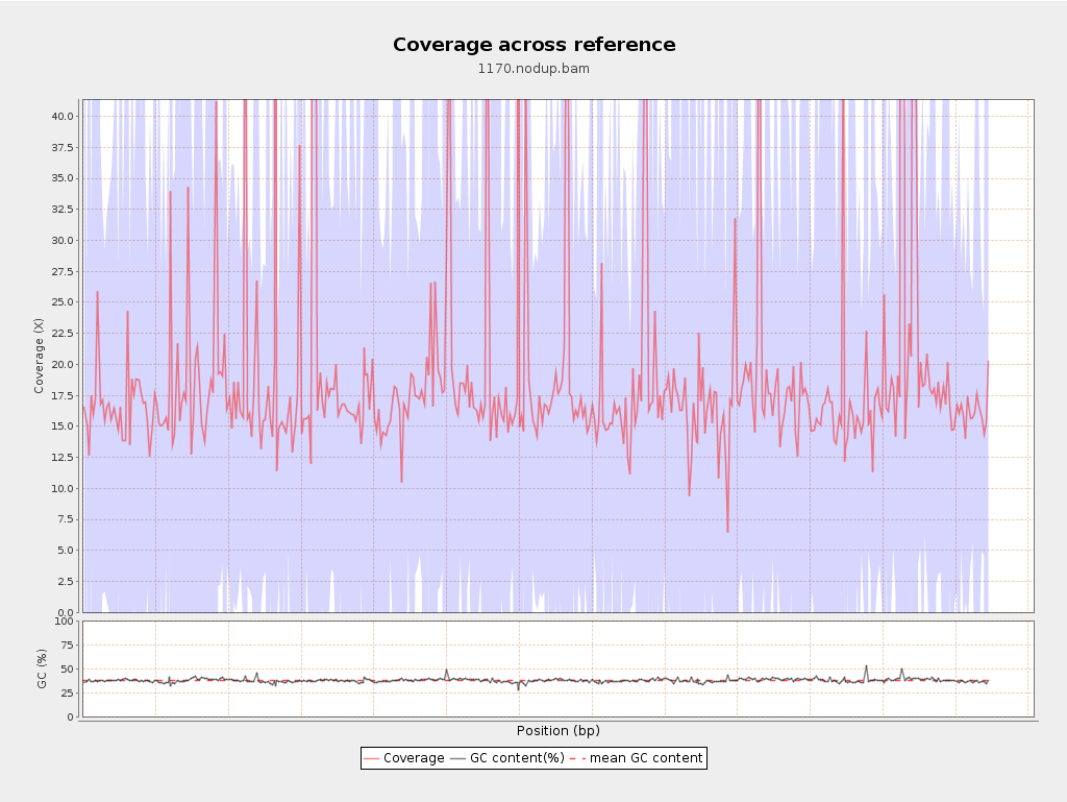
General error rate	2.53%
Mismatches	139,464,712
Insertions	3,919,739
Mapped reads with at least one insertion	8.28%
Deletions	4,057,954
Mapped reads with at least one deletion	8.46%
Homopolymer indels	56.06%

2.7. Chromosome stats

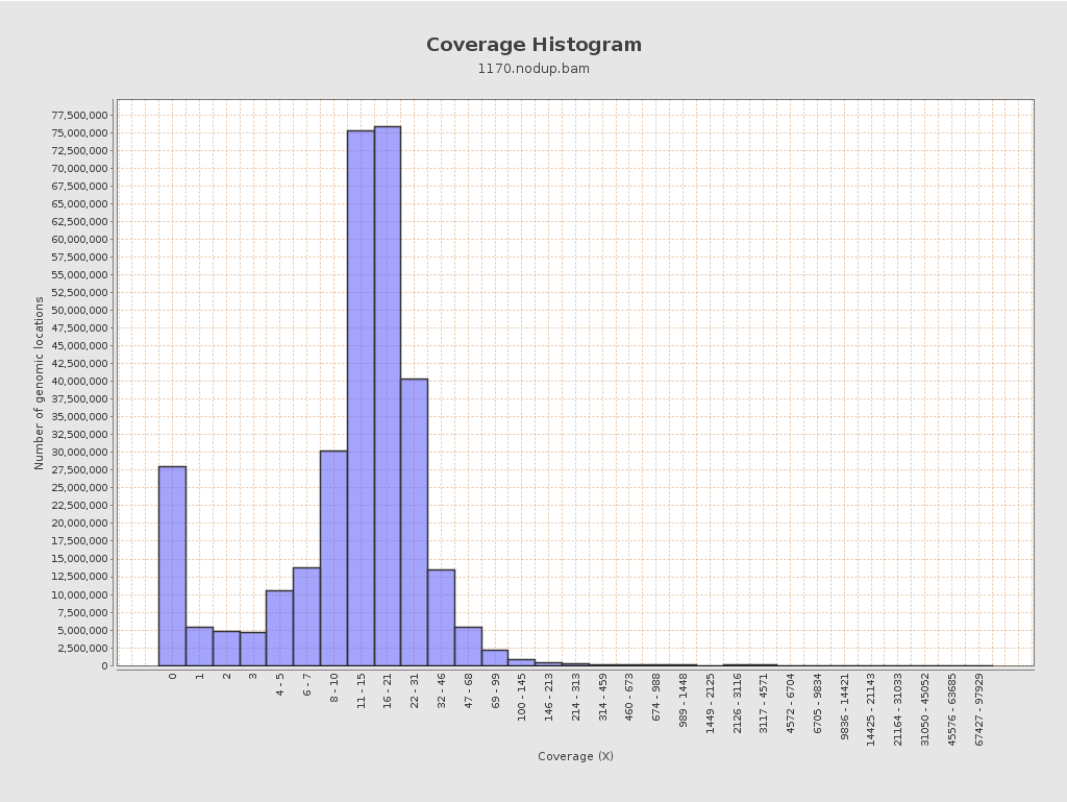
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	490730261	16.5094	39.5755

LT669789.1	36598175	717041097	19.5923	151.9656
LT669790.1	30422129	608379227	19.9979	128.9837
LT669791.1	52758100	976415118	18.5074	111.2765
LT669792.1	28376109	540724670	19.0556	154.7679
LT669793.1	33388210	595540632	17.8369	94.7797
LT669794.1	50579949	914536477	18.081	119.0524
LT669795.1	49795044	1098010756	22.0506	184.6711

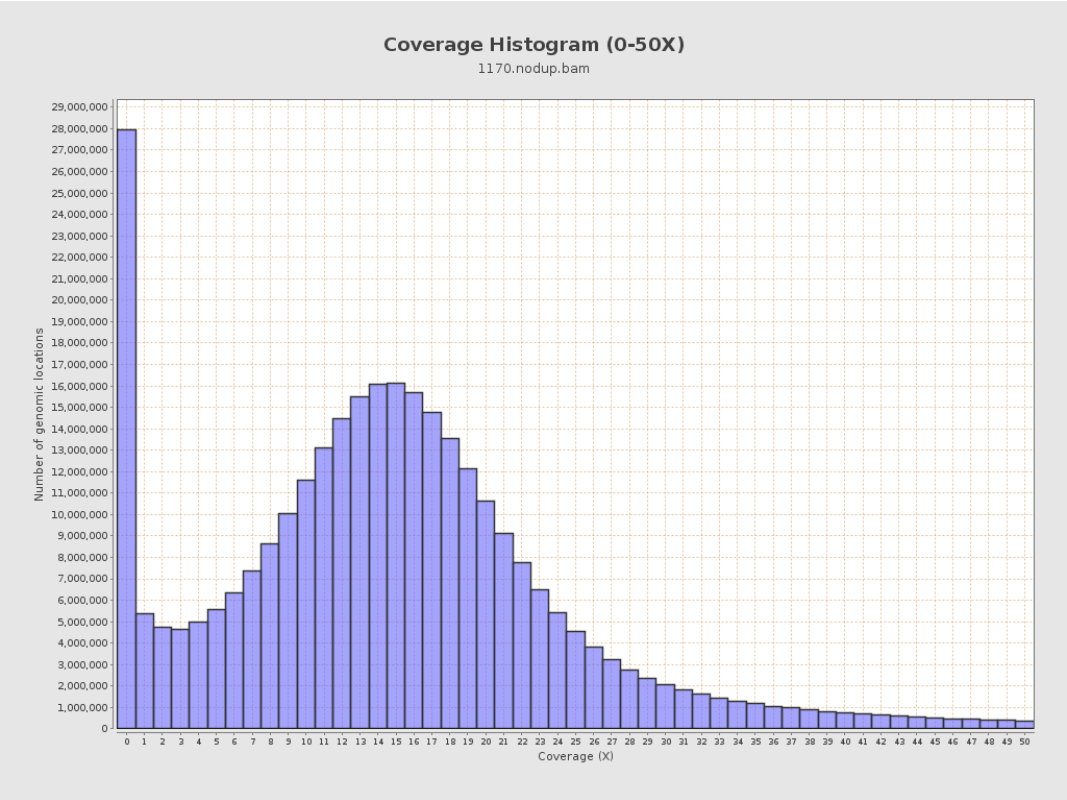
3. Results : Coverage across reference



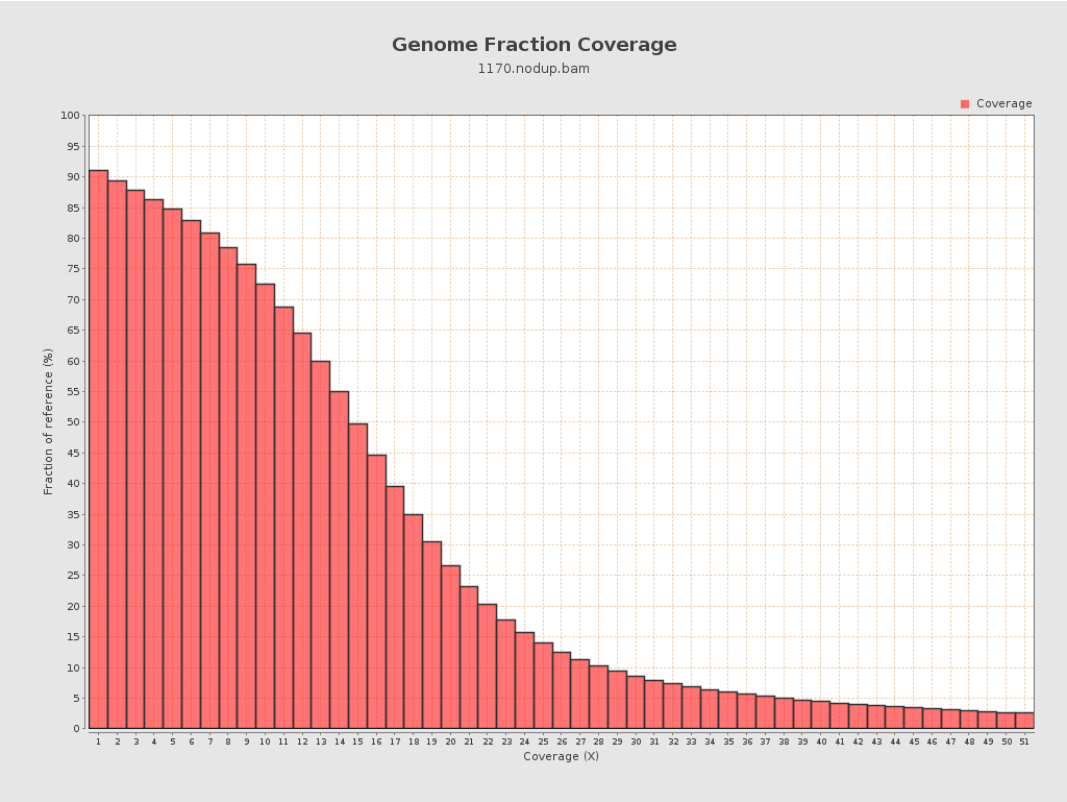
4. Results : Coverage Histogram



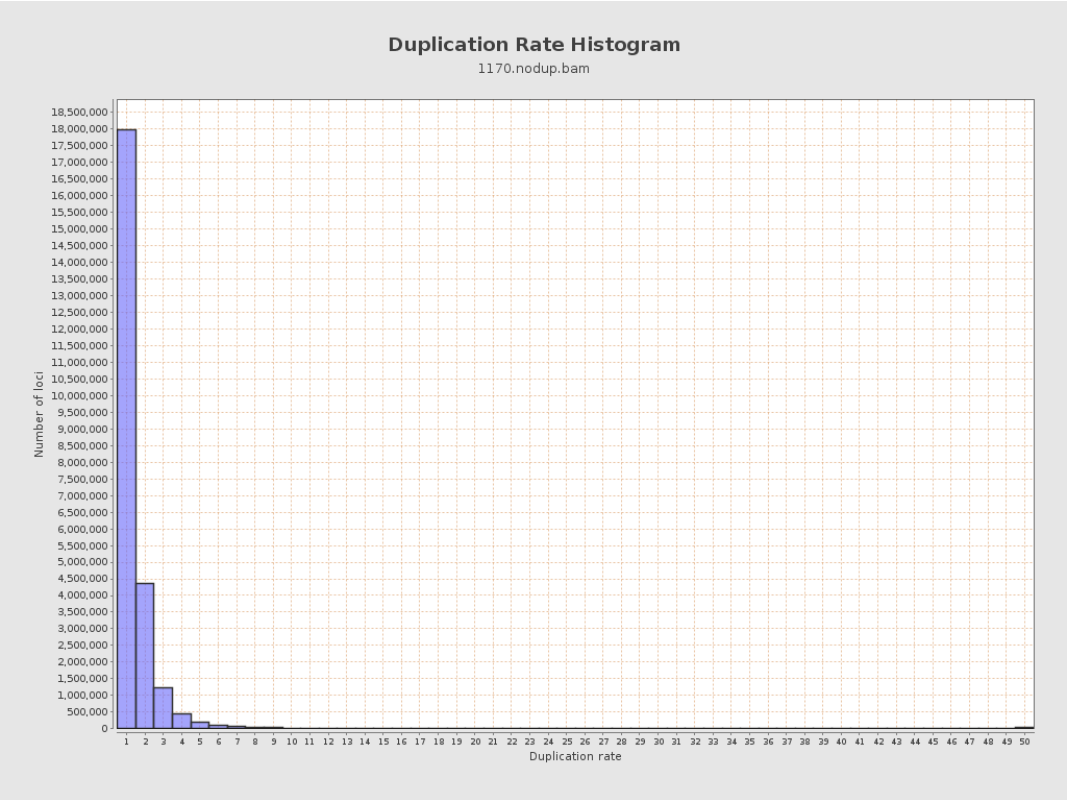
5. Results : Coverage Histogram (0-50X)



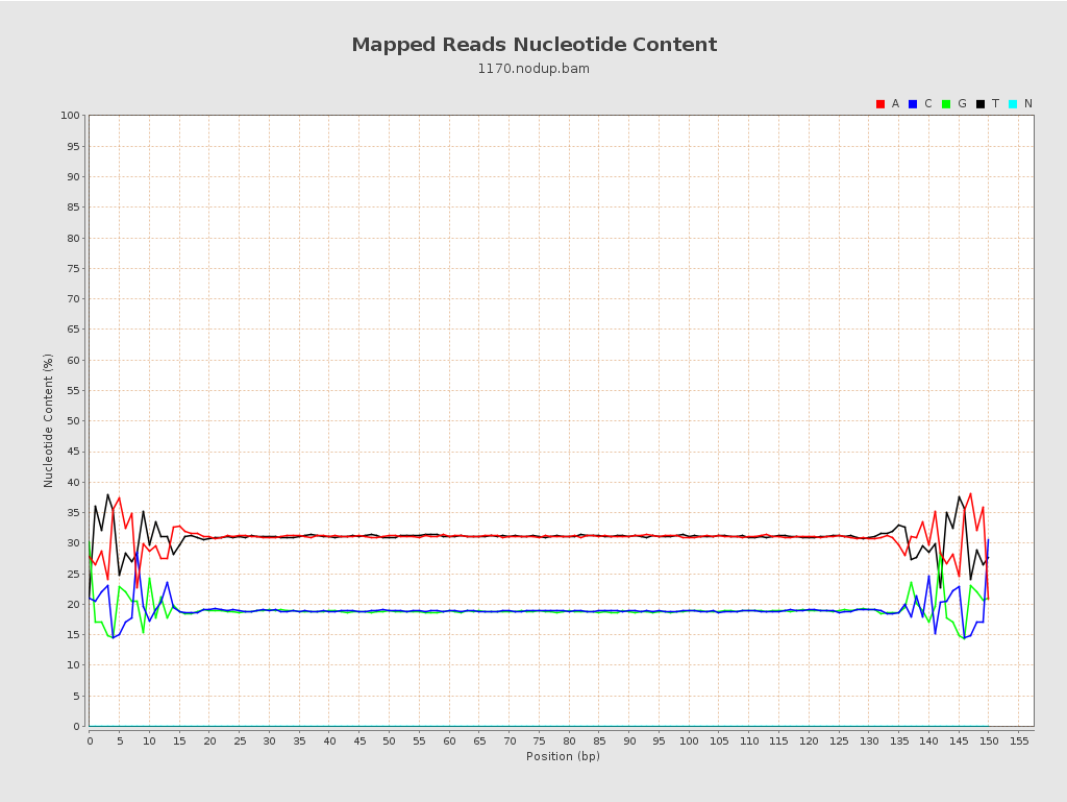
6. Results : Genome Fraction Coverage



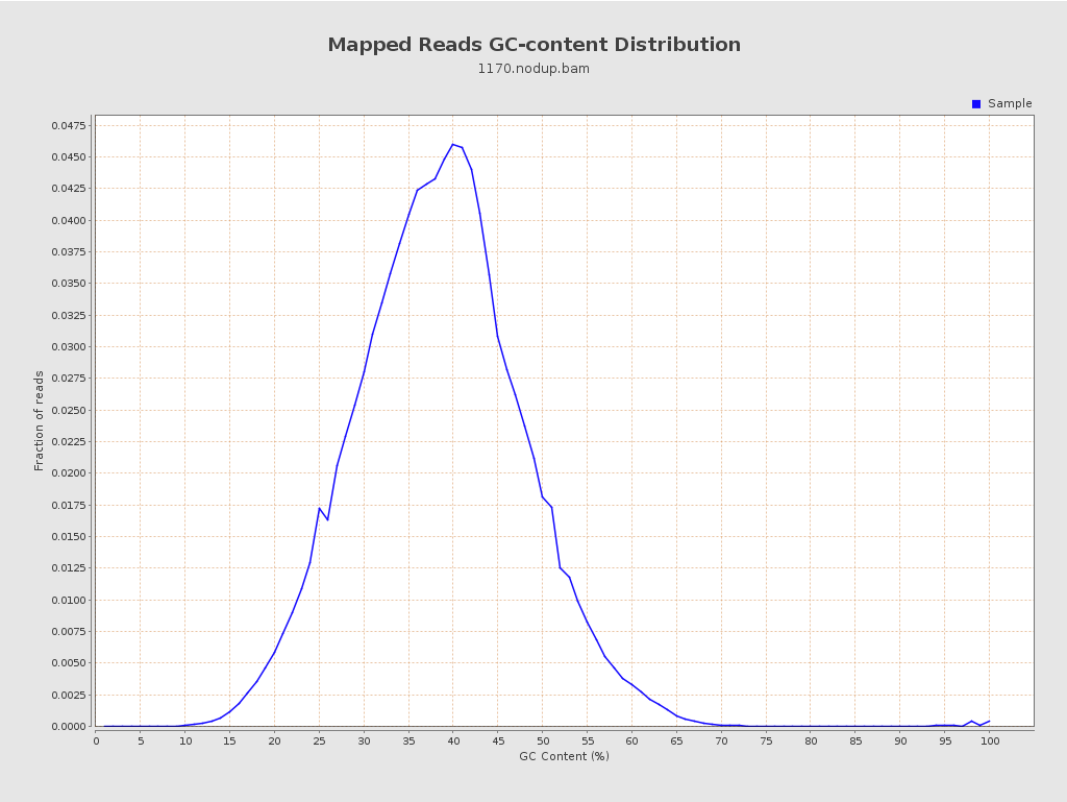
7. Results : Duplication Rate Histogram



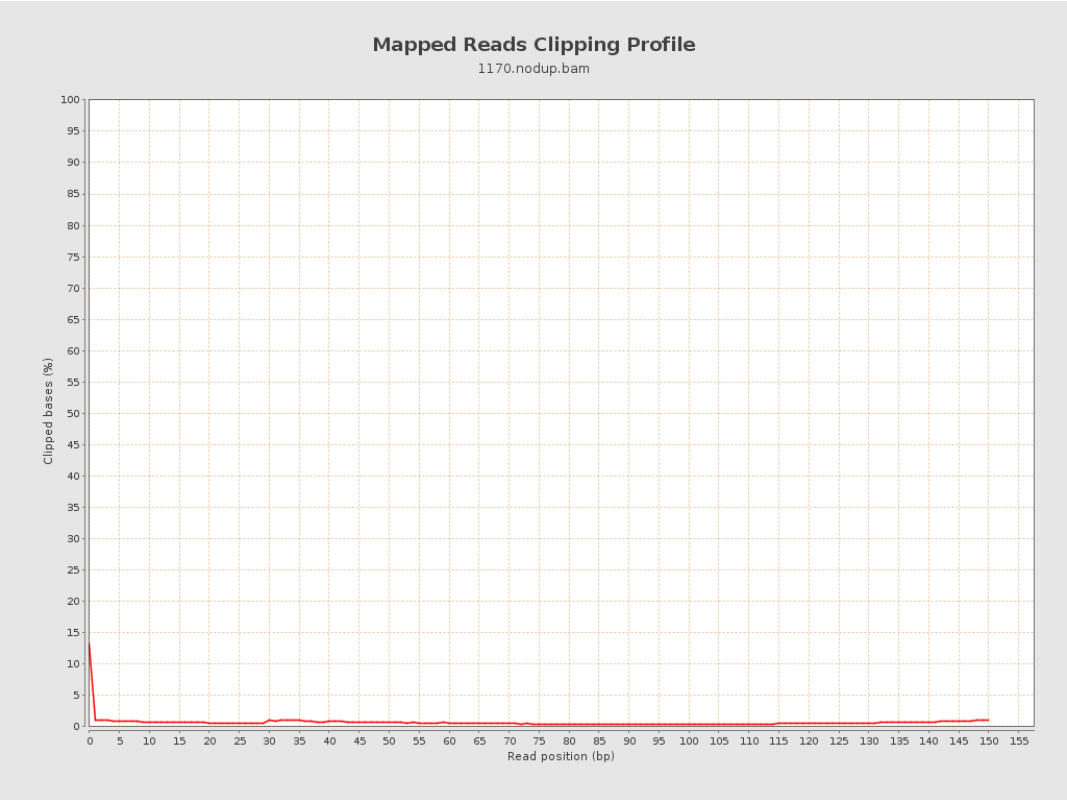
8. Results : Mapped Reads Nucleotide Content



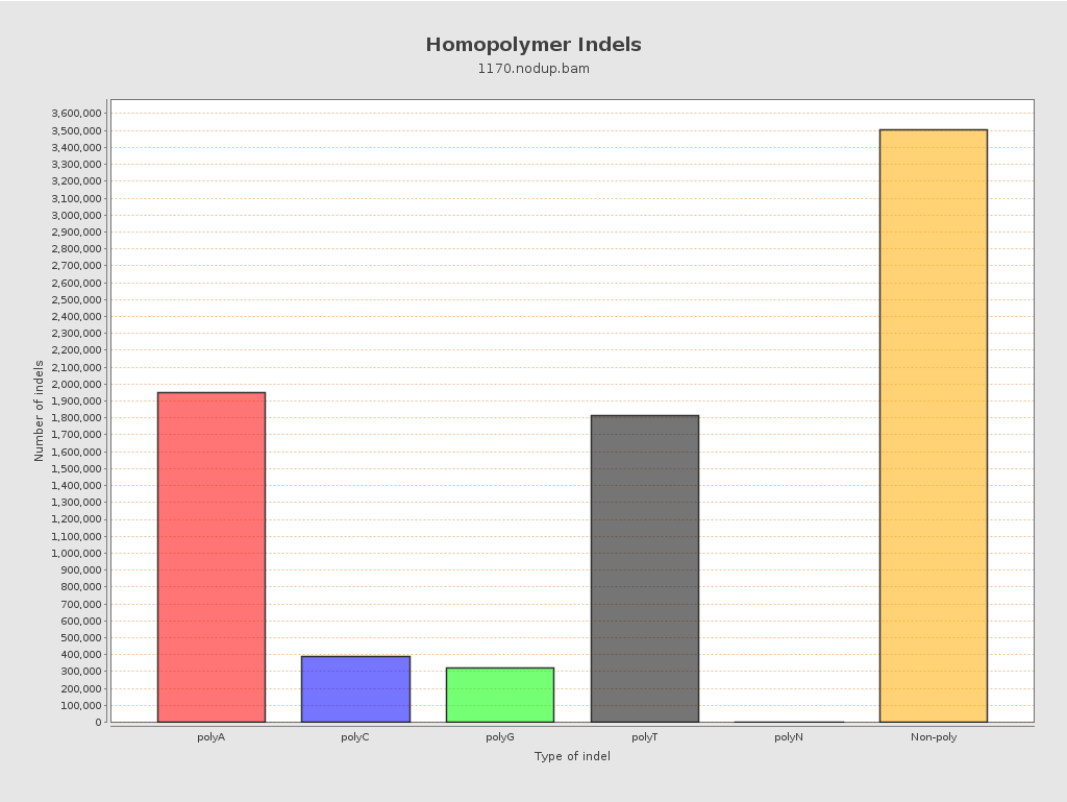
9. Results : Mapped Reads GC-content Distribution



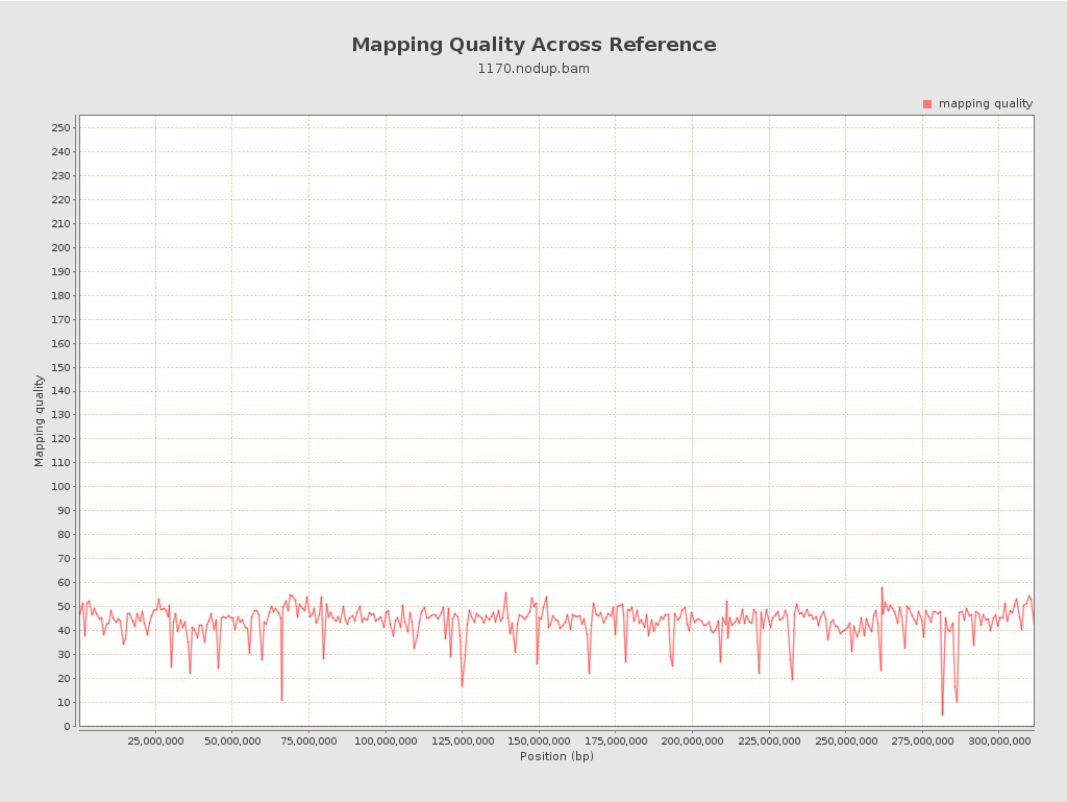
10. Results : Mapped Reads Clipping Profile



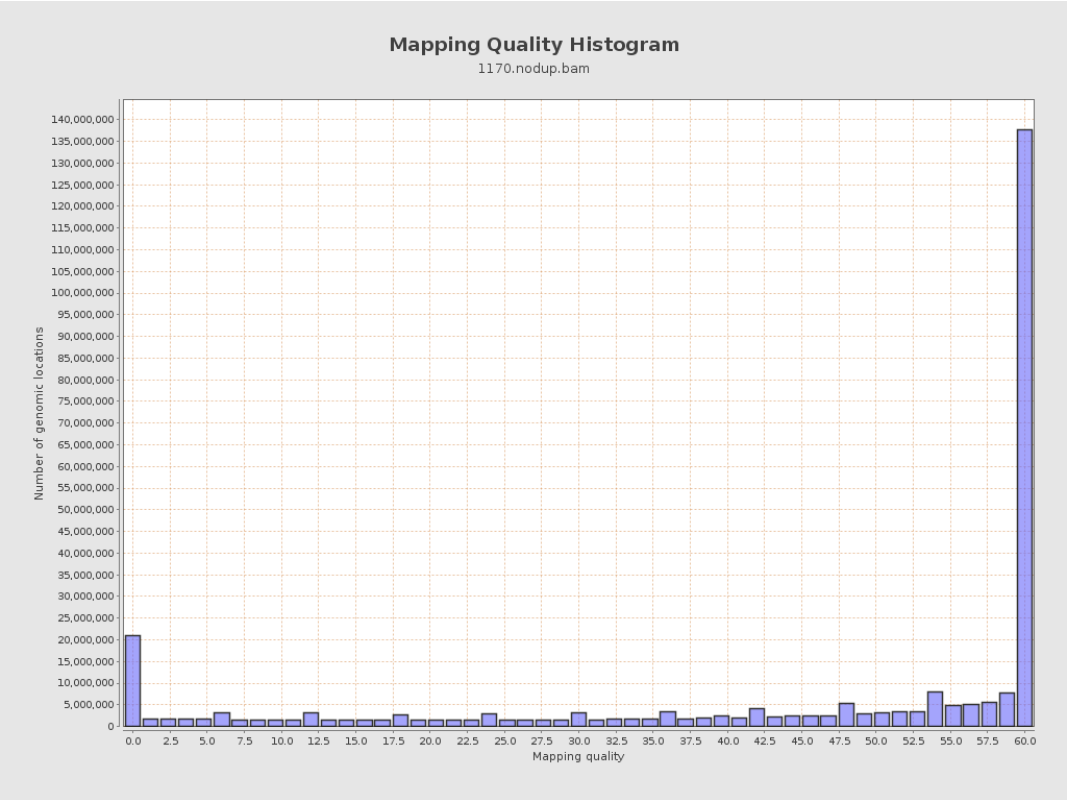
11. Results : Homopolymer Indels



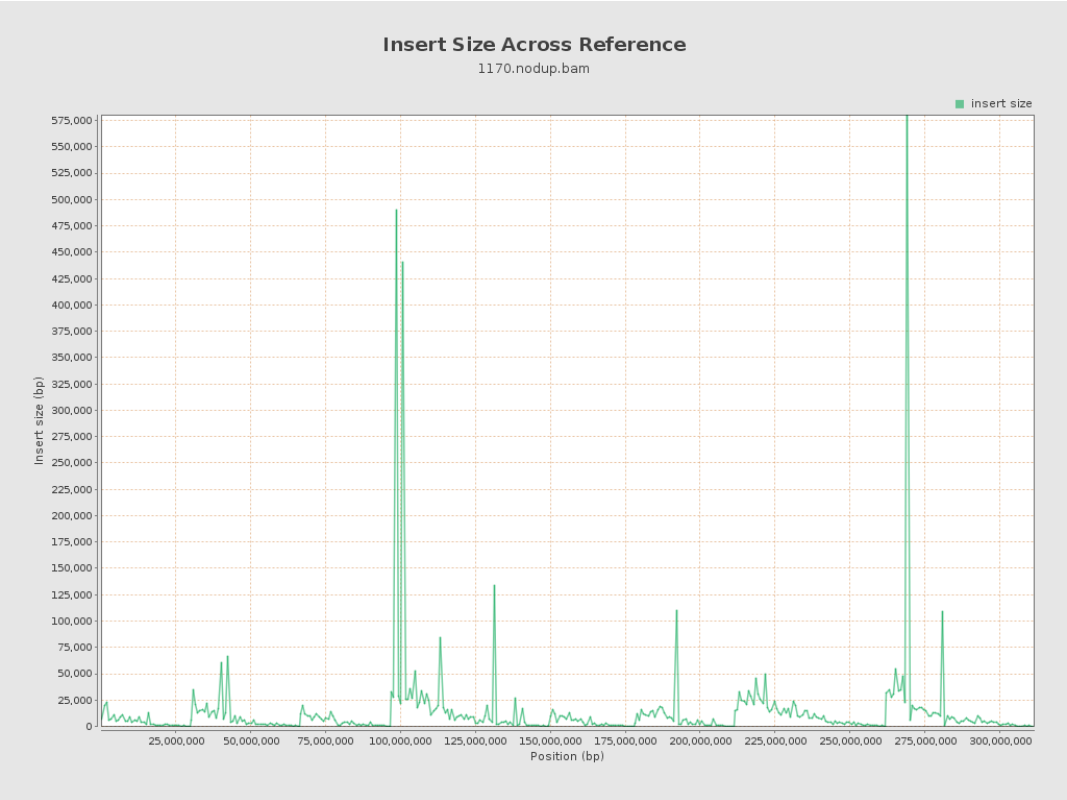
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram