Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1270
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1270 .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_252/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_252_S333_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_252/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_252_S333_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:37:55 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	90,229,818
Mapped reads	81,618,580 / 90.46%
Unmapped reads	8,611,238 / 9.54%
Mapped paired reads	81,618,580 / 90.46%
Mapped reads, first in pair	40,857,771 / 45.28%
Mapped reads, second in pair	40,760,809 / 45.17%
Mapped reads, both in pair	78,931,067 / 87.48%
Mapped reads, singletons	2,687,513 / 2.98%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	14,428,972 / 15.99%
Clipped reads	20,372,986 / 22.58%

2.2. ACGT Content

Number/percentage of A's	3,446,709,371 / 31.03%
Number/percentage of C's	2,104,875,854 / 18.95%
Number/percentage of T's	3,450,702,523 / 31.06%
Number/percentage of G's	2,106,171,836 / 18.96%
Number/percentage of N's	39,405 / 0%
GC Percentage	37.91%

2.3. Coverage

Mean	35.7368
Standard Deviation	359.8932

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Insert size

Mean	253,915.03
Standard Deviation	2,439,896.02
P25/Median/P75	303 / 402 / 523

2.6. Mismatches and indels

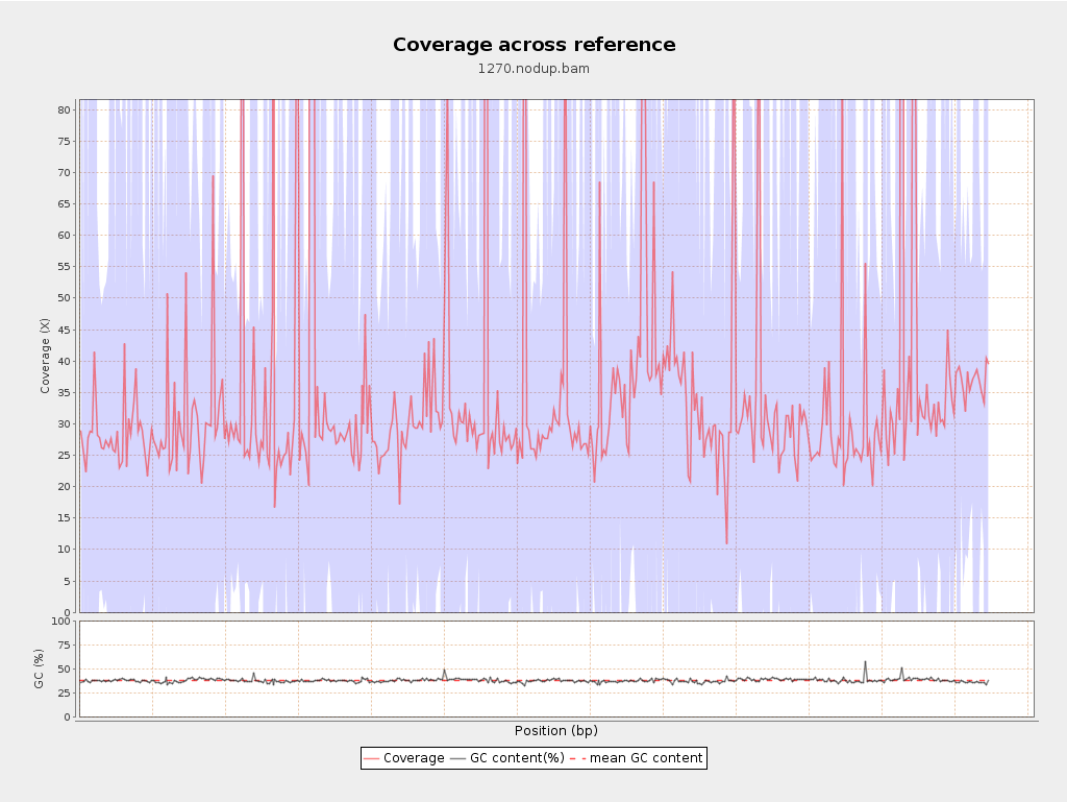
General error rate	2.37%
Mismatches	240,068,134
Insertions	8,283,391
Mapped reads with at least one insertion	9.02%
Deletions	7,753,297
Mapped reads with at least one deletion	8.43%
Homopolymer indels	57.84%

2.7. Chromosome stats

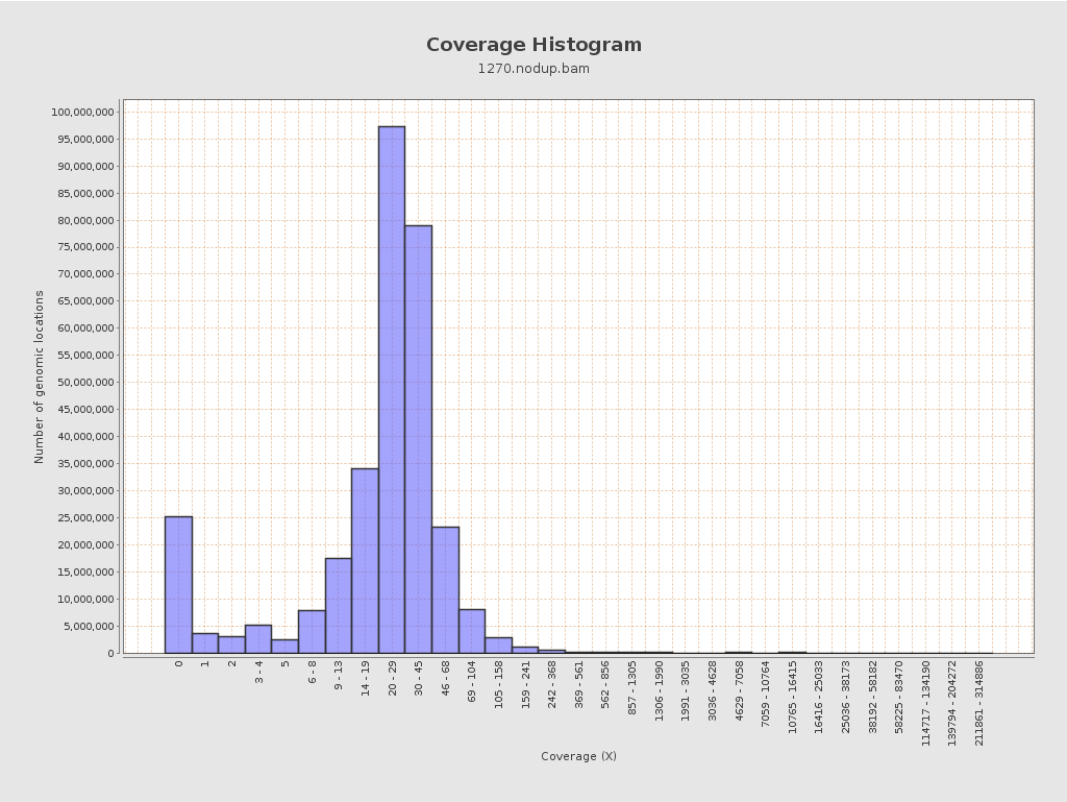
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	833889548	28.0541	147.0402

LT669789.1	36598175	1238195315	33.8322	354.9906
LT669790.1	30422129	1343877338	44.1743	560.215
LT669791.1	52758100	1788169256	33.8937	392.2094
LT669792.1	28376109	981092219	34.5746	349.8712
LT669793.1	33388210	1336196126	40.02	241.7309
LT669794.1	50579949	1607690525	31.7851	282.2803
LT669795.1	49795044	2007991350	40.3251	400.4521

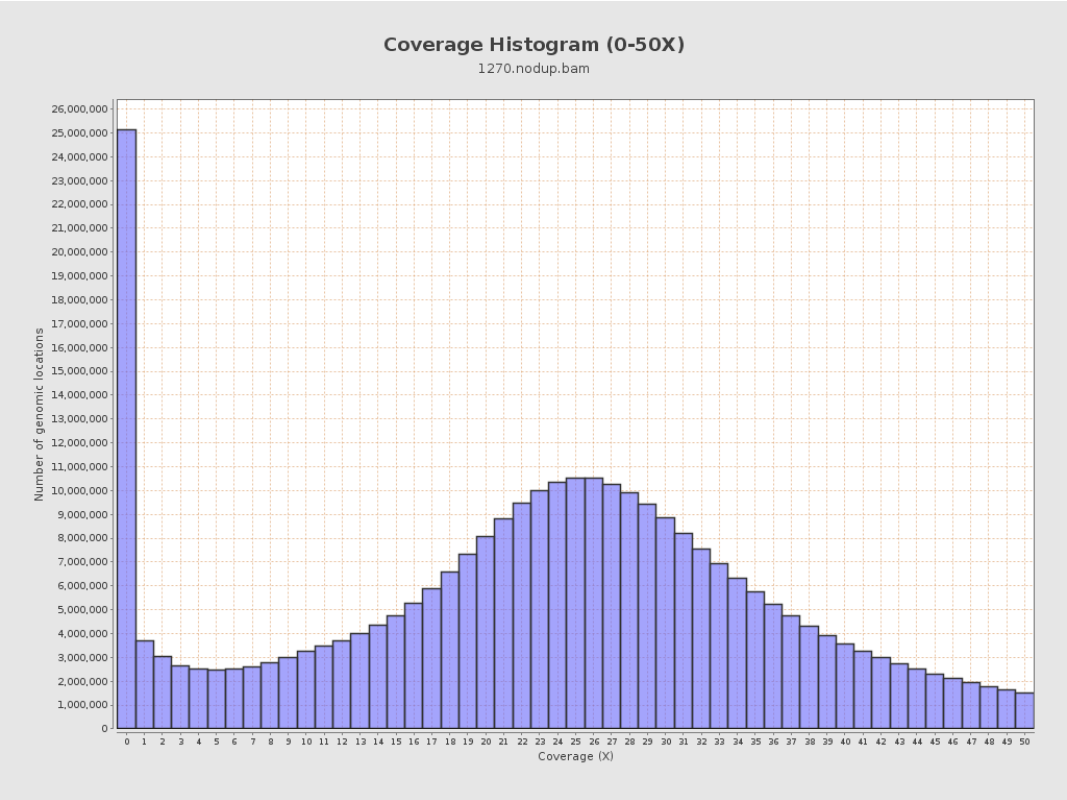
3. Results : Coverage across reference



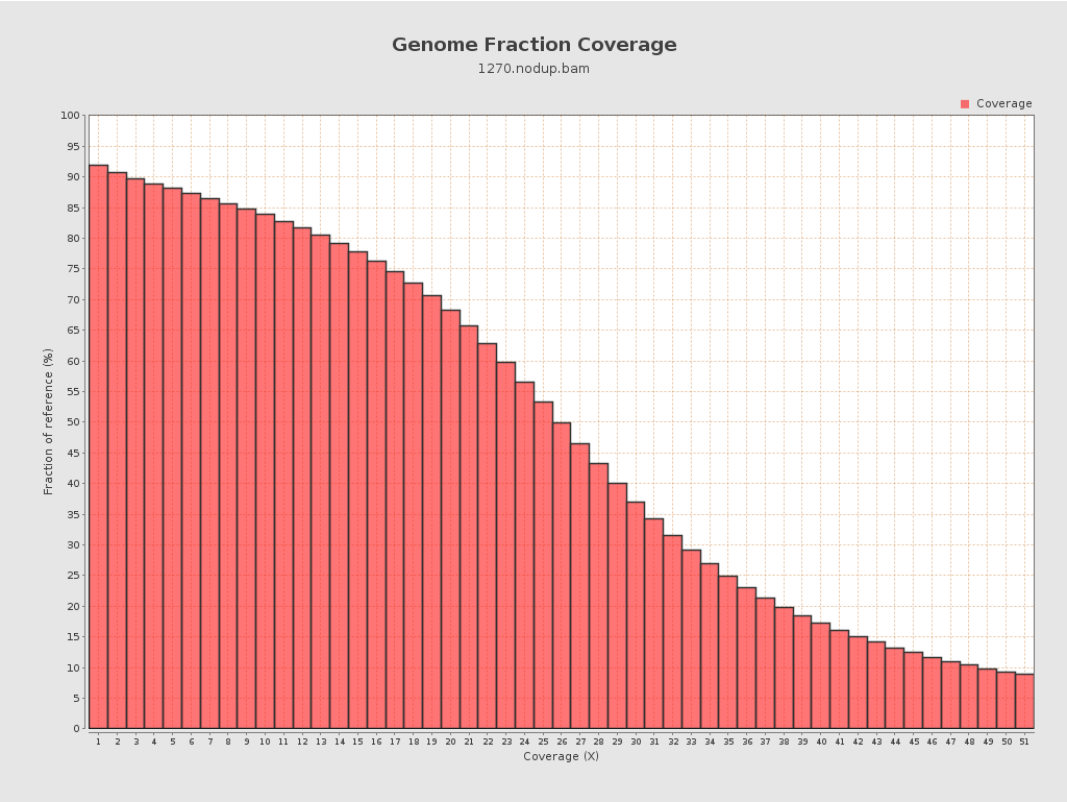
4. Results : Coverage Histogram



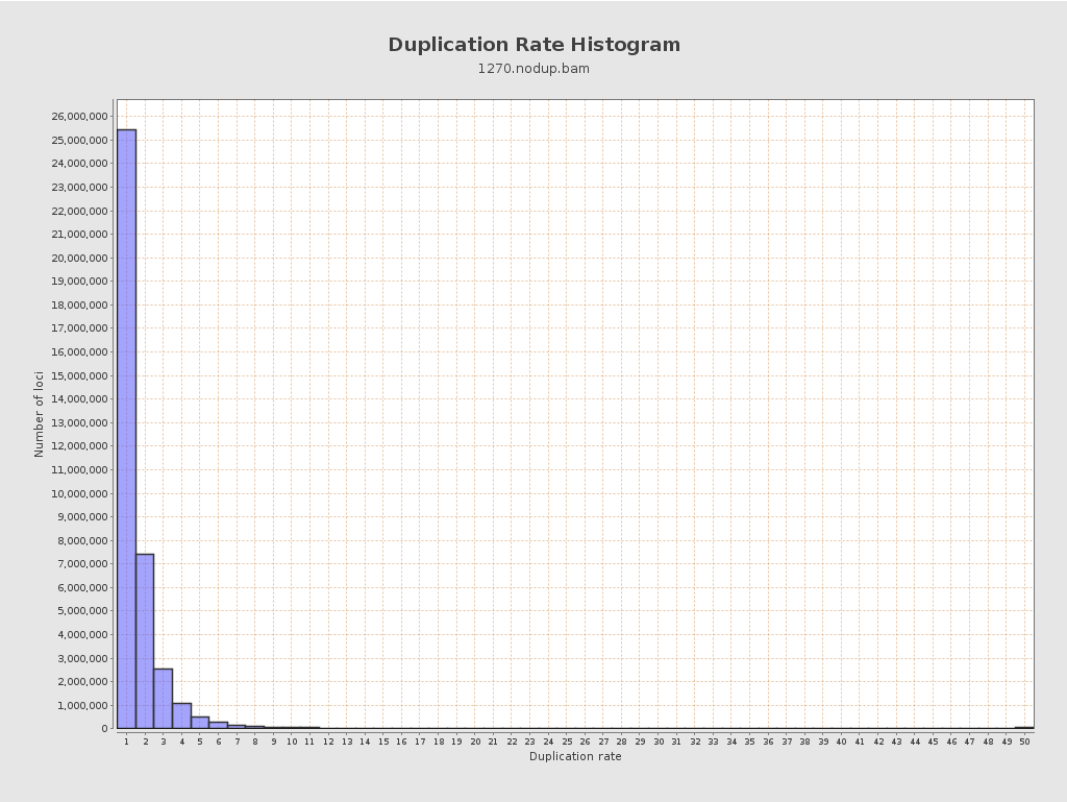
5. Results : Coverage Histogram (0-50X)



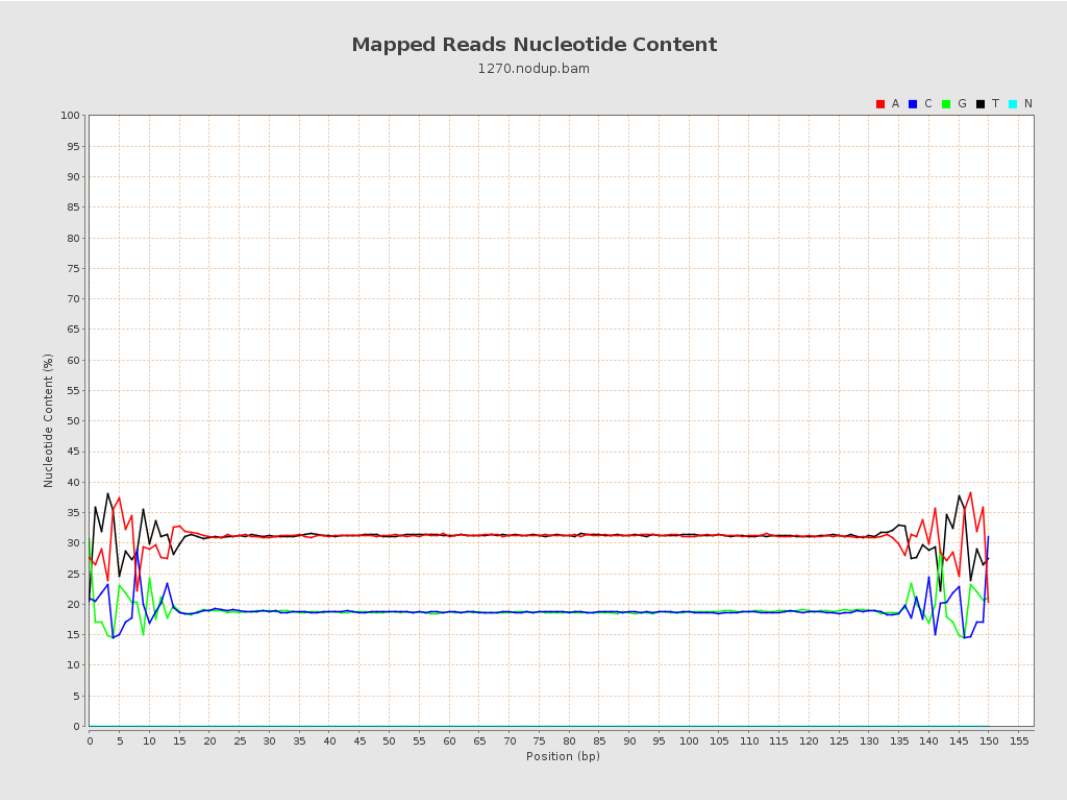
6. Results : Genome Fraction Coverage



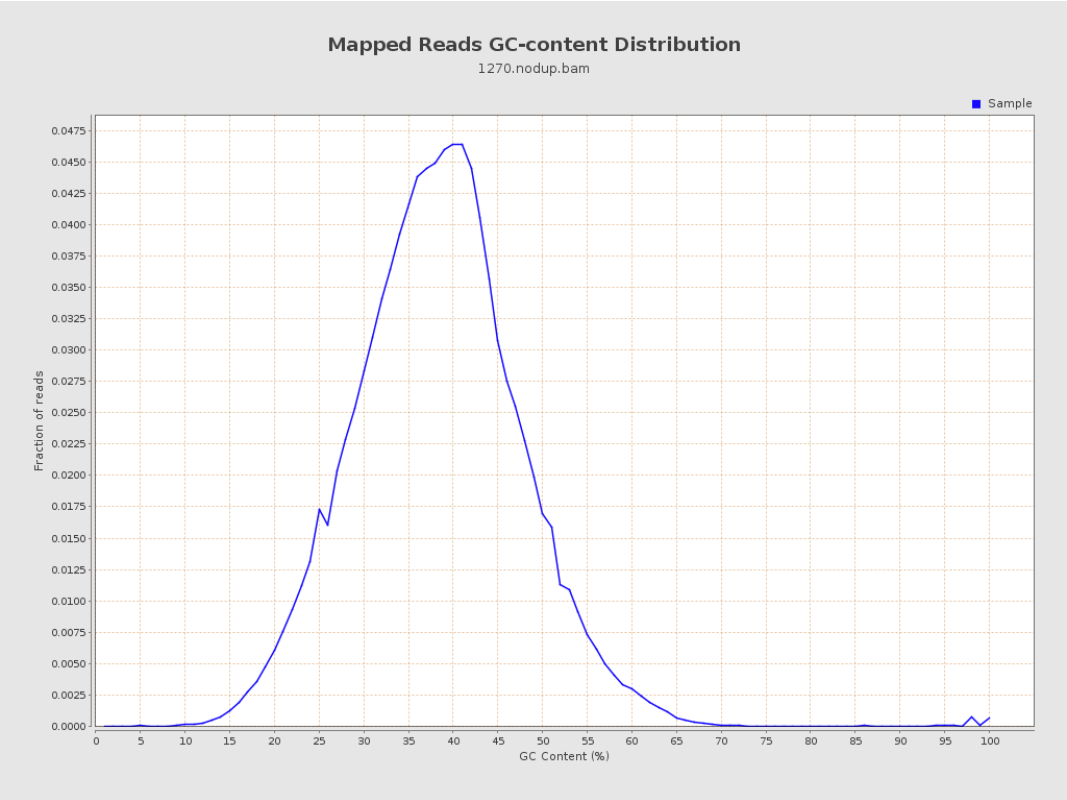
7. Results : Duplication Rate Histogram



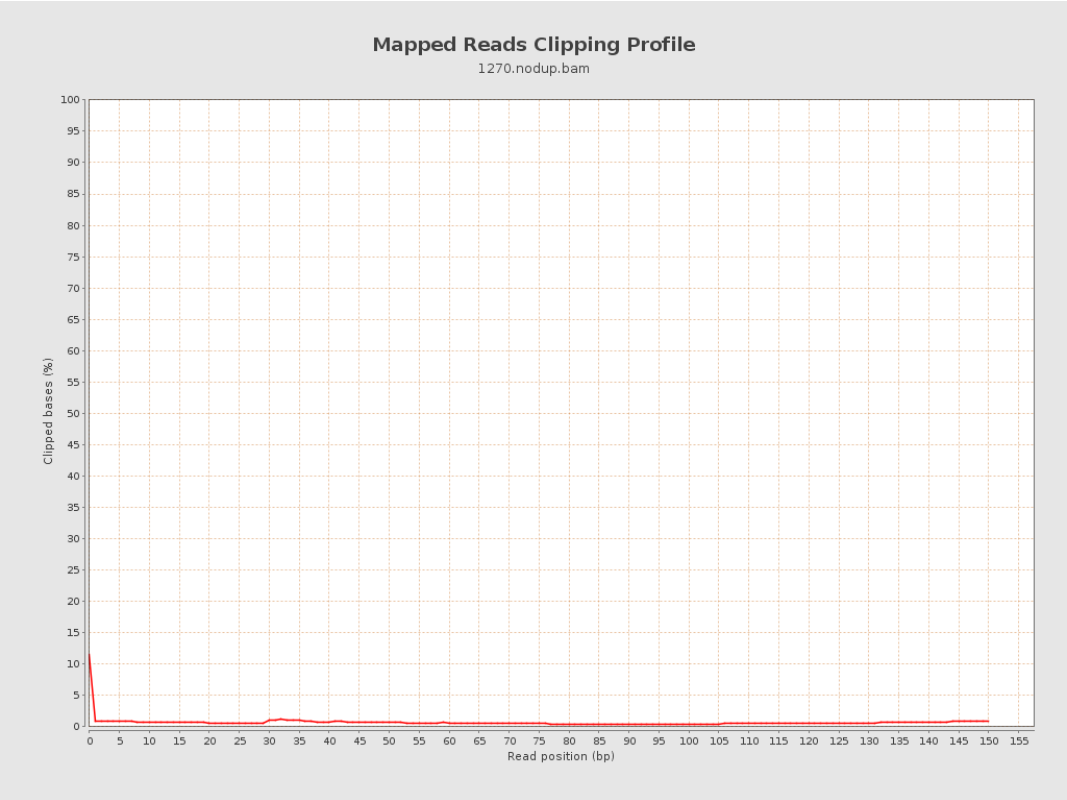
8. Results : Mapped Reads Nucleotide Content



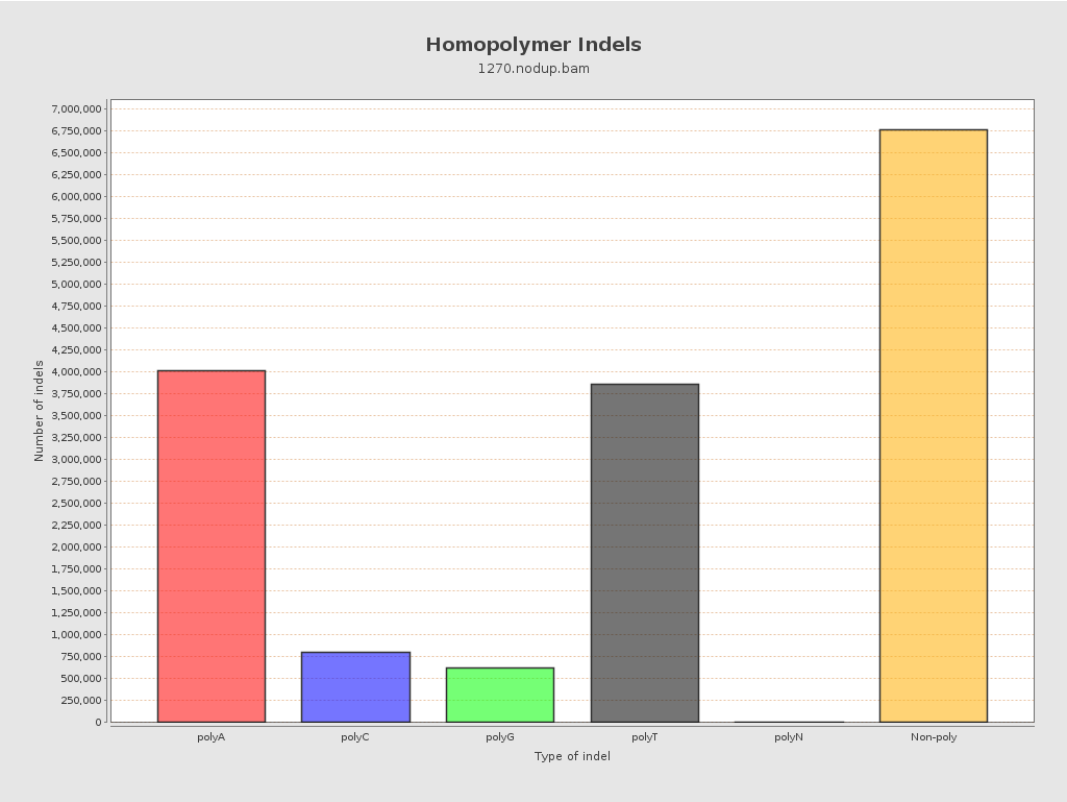
9. Results : Mapped Reads GC-content Distribution



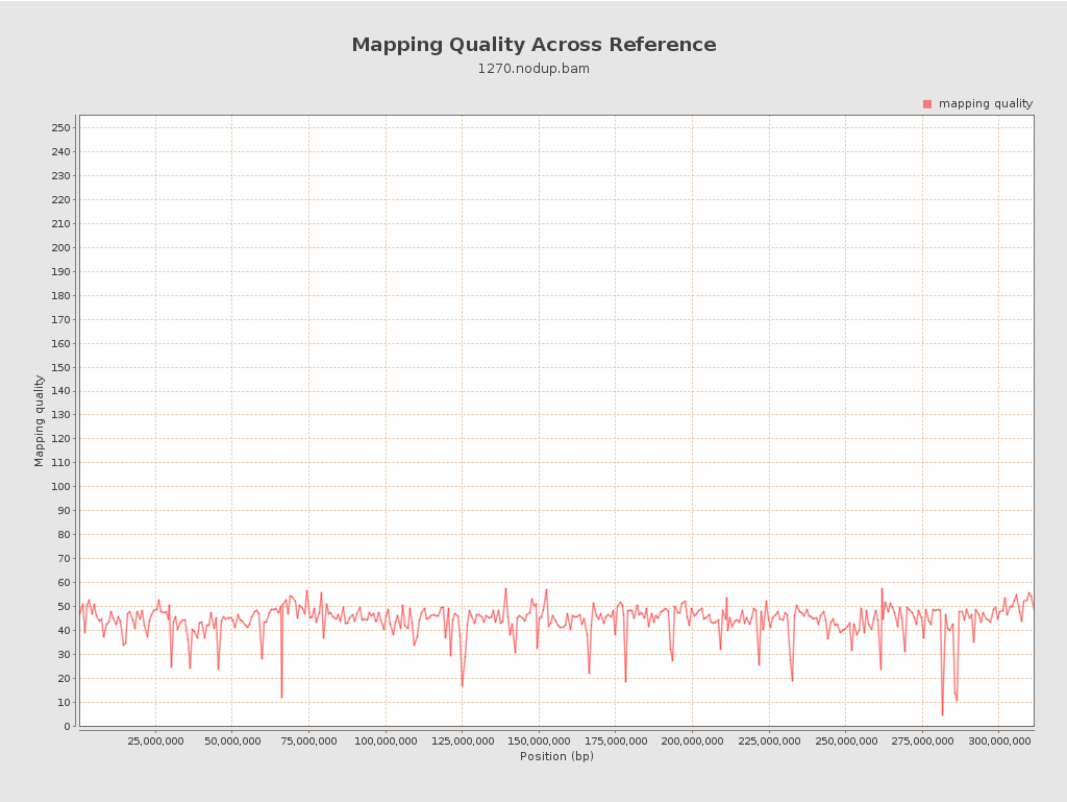
10. Results : Mapped Reads Clipping Profile



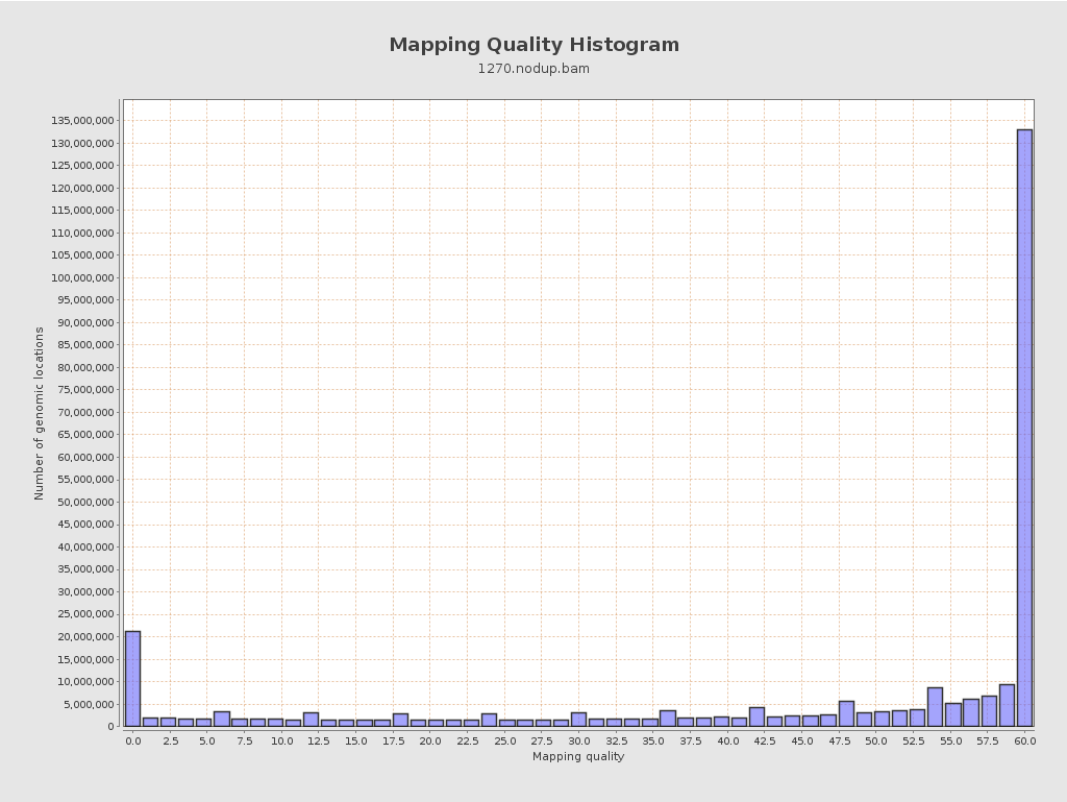
11. Results : Homopolymer Indels



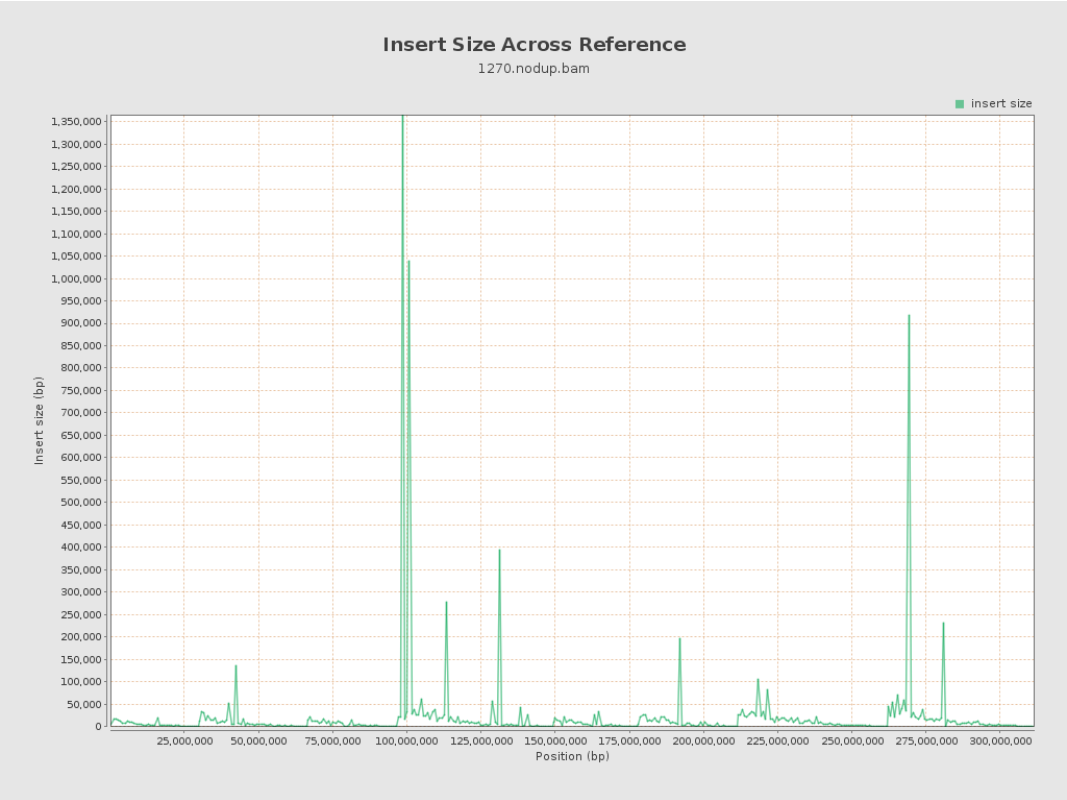
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram