Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1470
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1470 .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_101/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_101_S191_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_101/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_101_S191_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:26:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	57,921,505
Mapped reads	52,793,995 / 91.15%
Unmapped reads	5,127,510 / 8.85%
Mapped paired reads	52,793,995 / 91.15%
Mapped reads, first in pair	26,457,460 / 45.68%
Mapped reads, second in pair	26,336,535 / 45.47%
Mapped reads, both in pair	51,242,858 / 88.47%
Mapped reads, singletons	1,551,137 / 2.68%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	9,242,090 / 15.96%
Clipped reads	12,036,067 / 20.78%

2.2. ACGT Content

Number/percentage of A's	2,258,624,056 / 31.02%
Number/percentage of C's	1,380,989,896 / 18.97%
Number/percentage of T's	2,263,122,087 / 31.08%
Number/percentage of G's	1,378,802,456 / 18.94%
Number/percentage of N's	32,049 / 0%
GC Percentage	37.9%

2.3. Coverage

Mean	23.4268
Standard Deviation	200.677

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Insert size

Mean	252,660.47
Standard Deviation	2,417,216.53
P25/Median/P75	332 / 431 / 561

2.6. Mismatches and indels

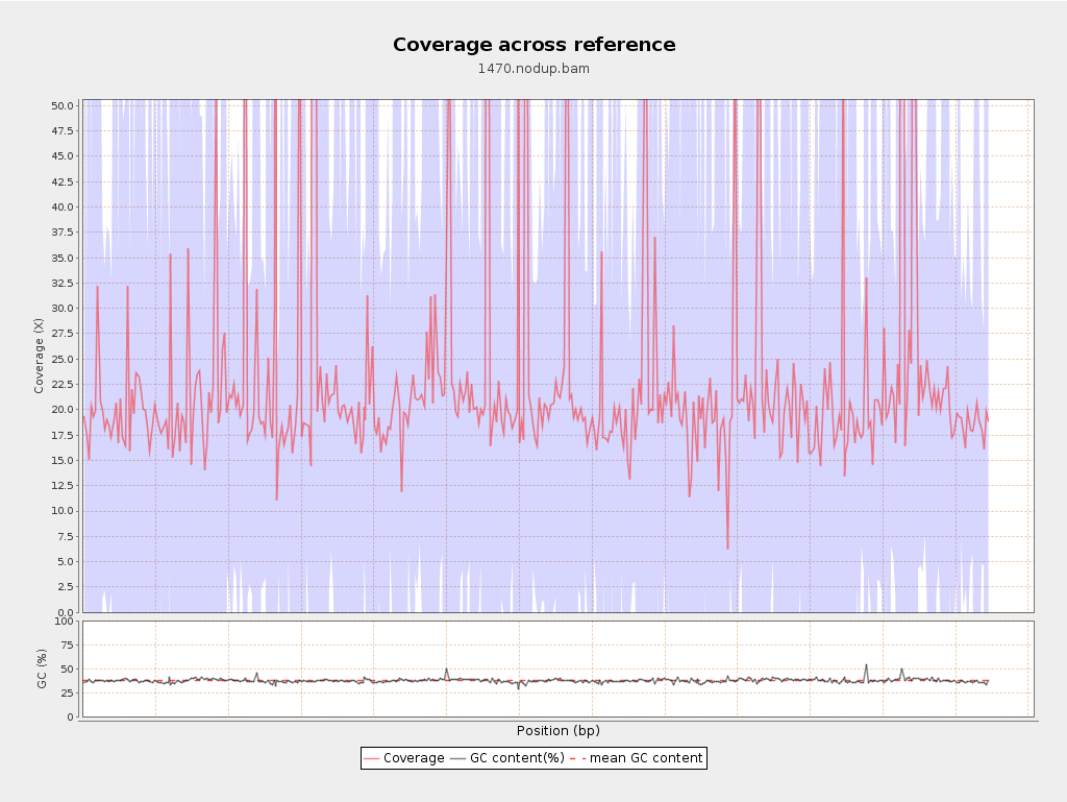
General error rate	2.35%
Mismatches	156,305,759
Insertions	5,245,770
Mapped reads with at least one insertion	8.85%
Deletions	5,104,213
Mapped reads with at least one deletion	8.56%
Homopolymer indels	57.23%

2.7. Chromosome stats

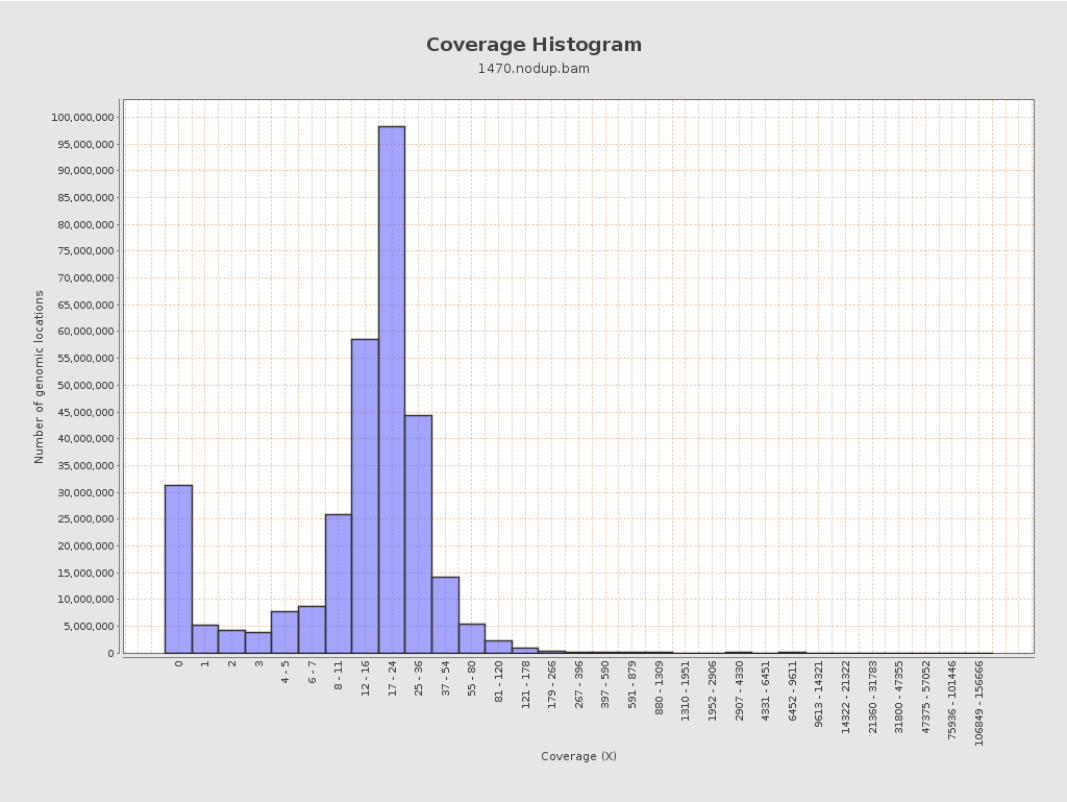
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	585769512	19.7067	77.7254

LT669789.1	36598175	851537909	23.2672	211.4275
LT669790.1	30422129	838552594	27.5639	278.5322
LT669791.1	52758100	1227220508	23.2613	211.4268
LT669792.1	28376109	671746826	23.673	215.4522
LT669793.1	33388210	711470036	21.309	129.6534
LT669794.1	50579949	1102122089	21.7897	164.0124
LT669795.1	49795044	1312358069	26.3552	236.0872

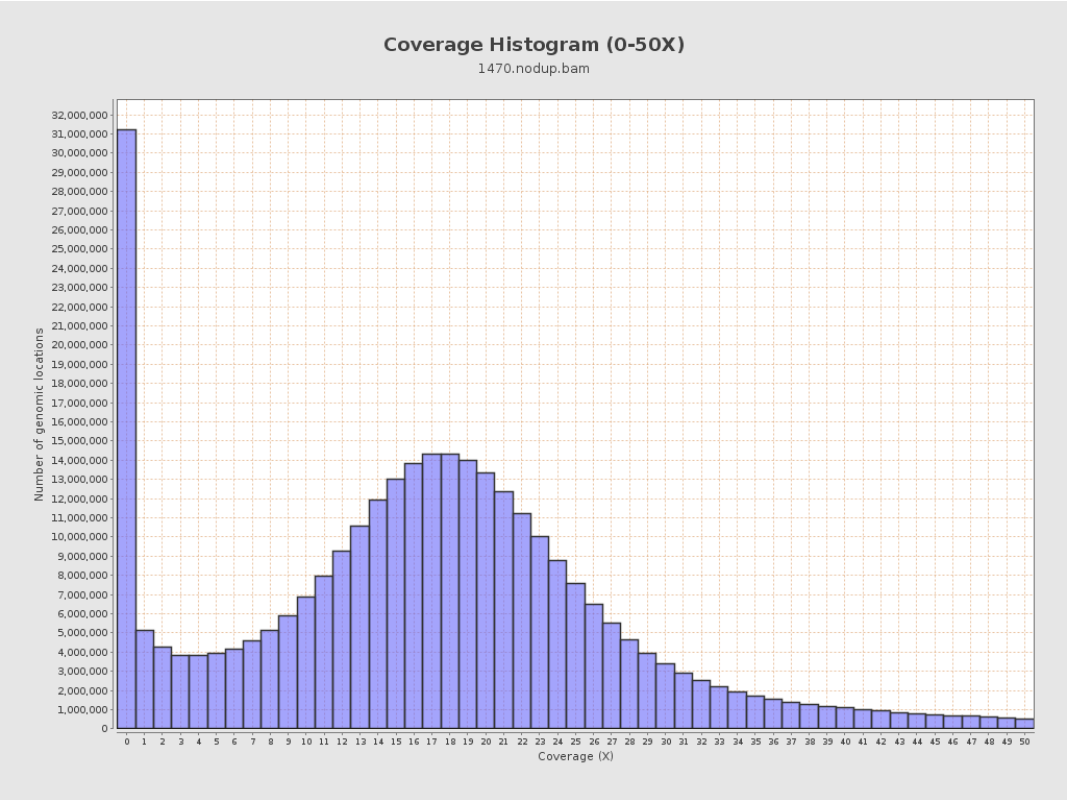
3. Results : Coverage across reference



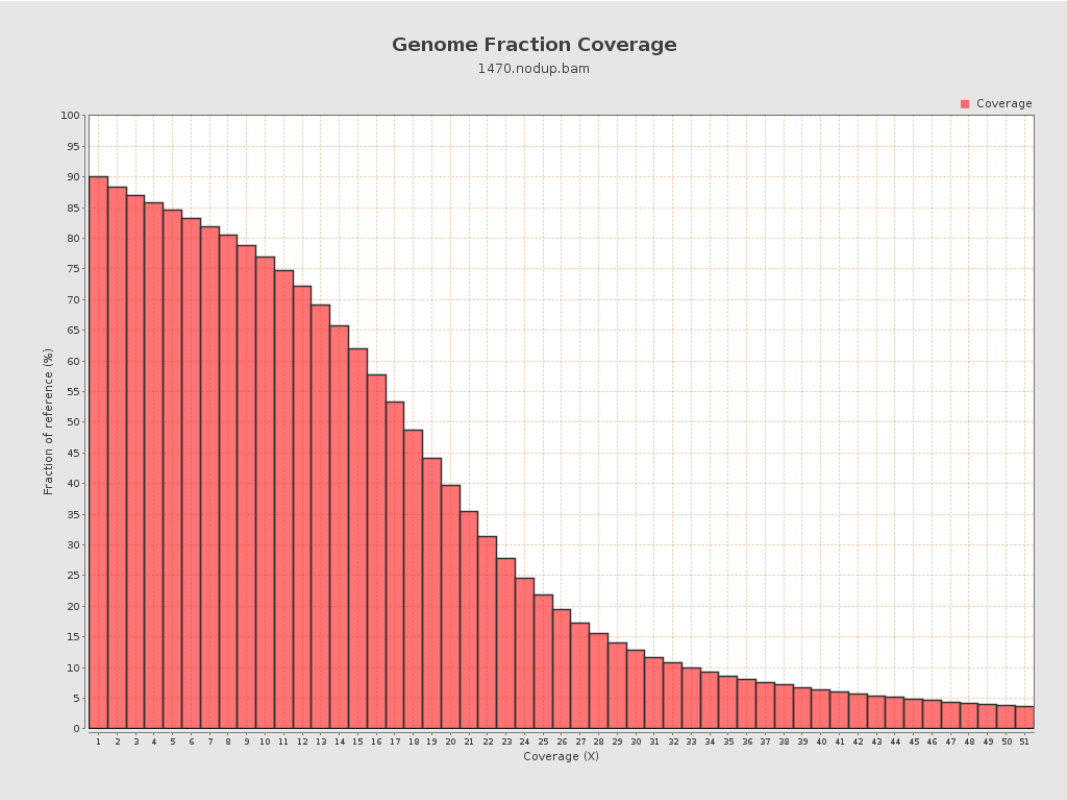
4. Results : Coverage Histogram



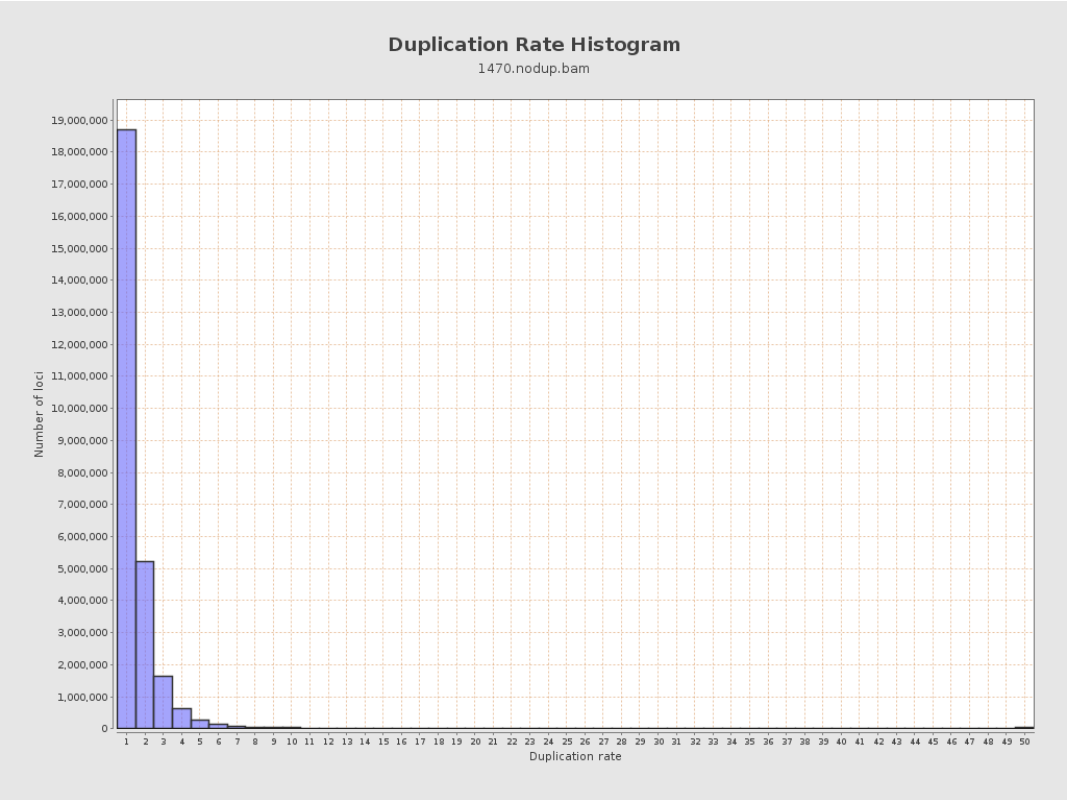
5. Results : Coverage Histogram (0-50X)



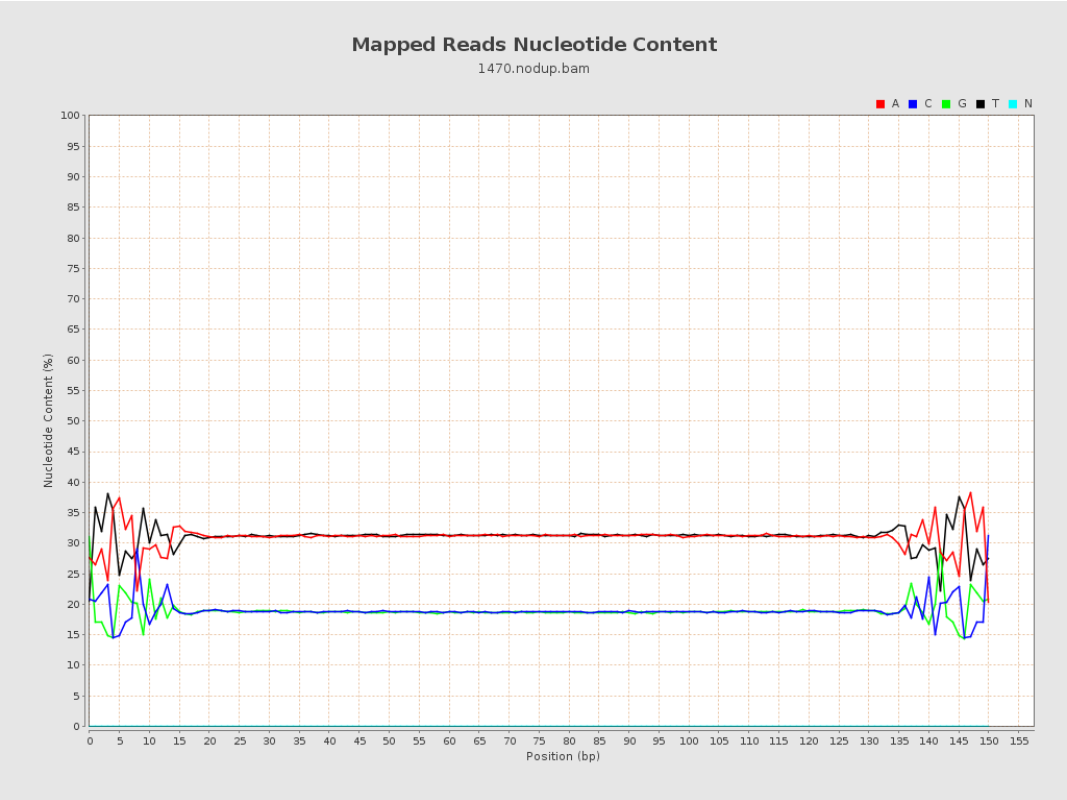
6. Results : Genome Fraction Coverage



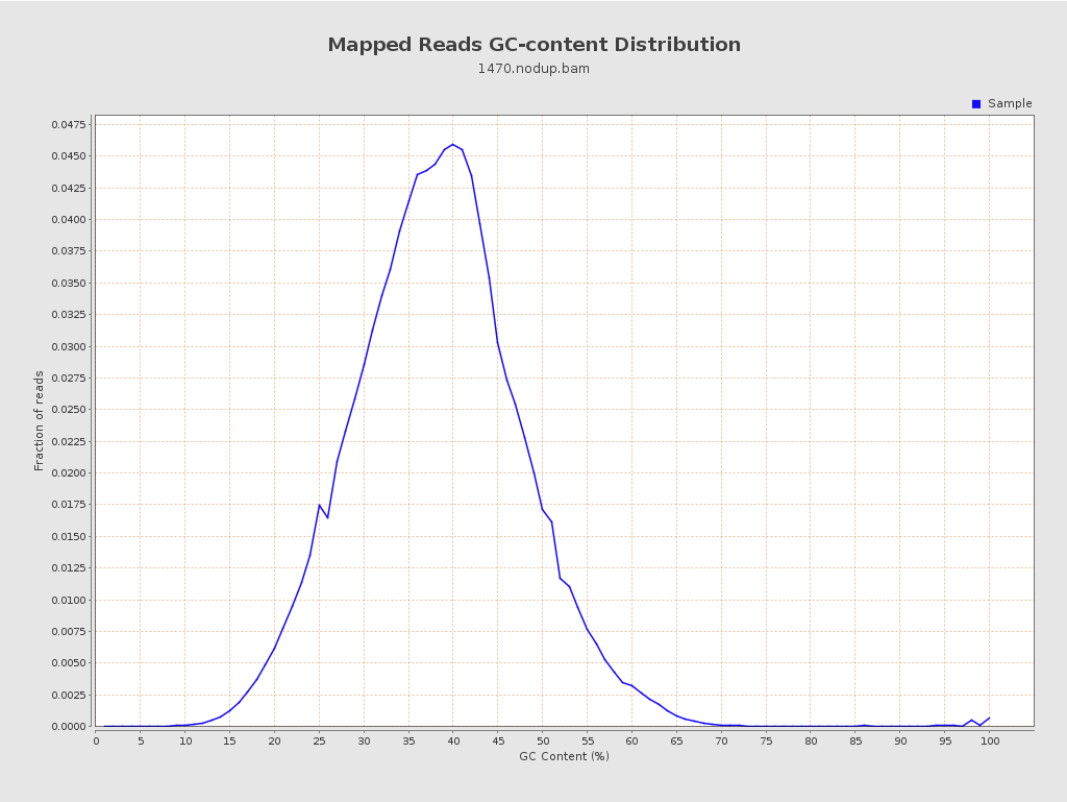
7. Results : Duplication Rate Histogram



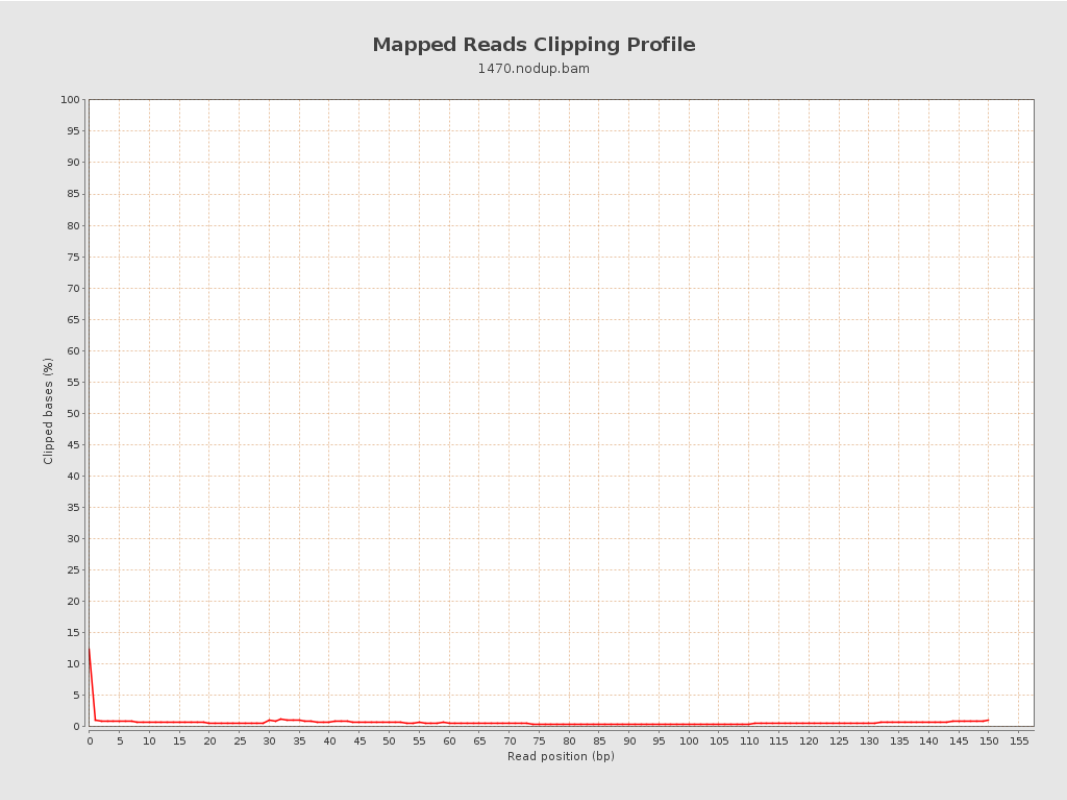
8. Results : Mapped Reads Nucleotide Content



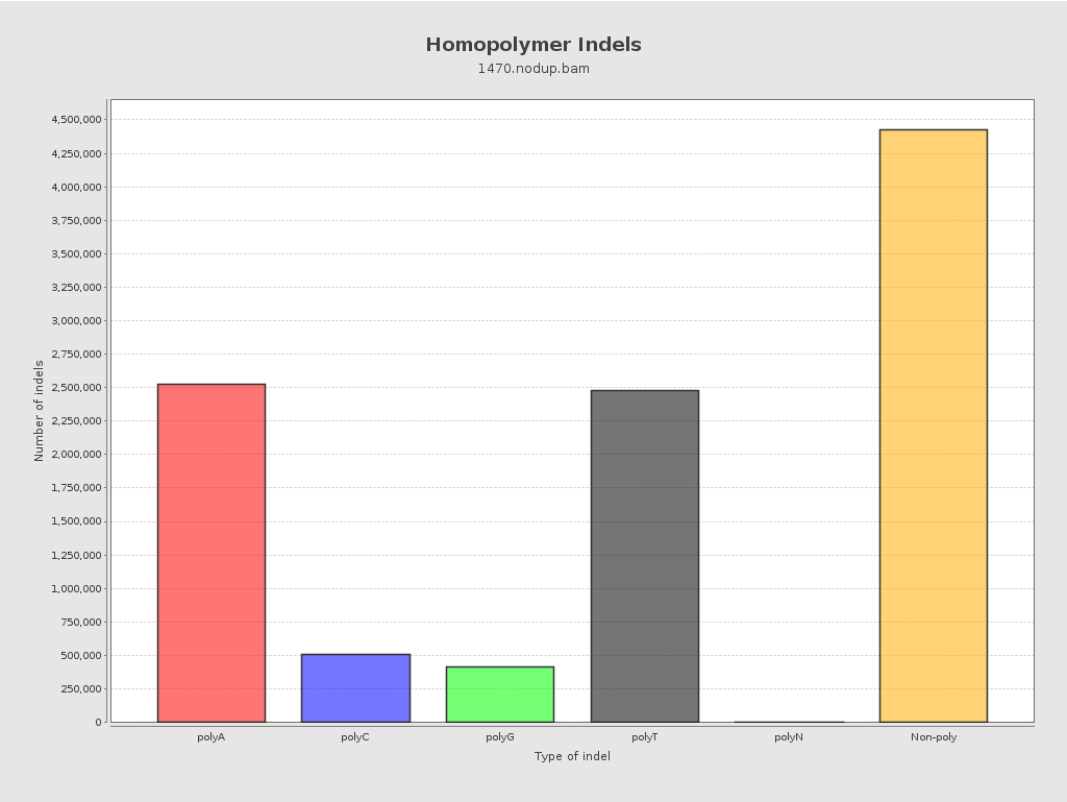
9. Results : Mapped Reads GC-content Distribution



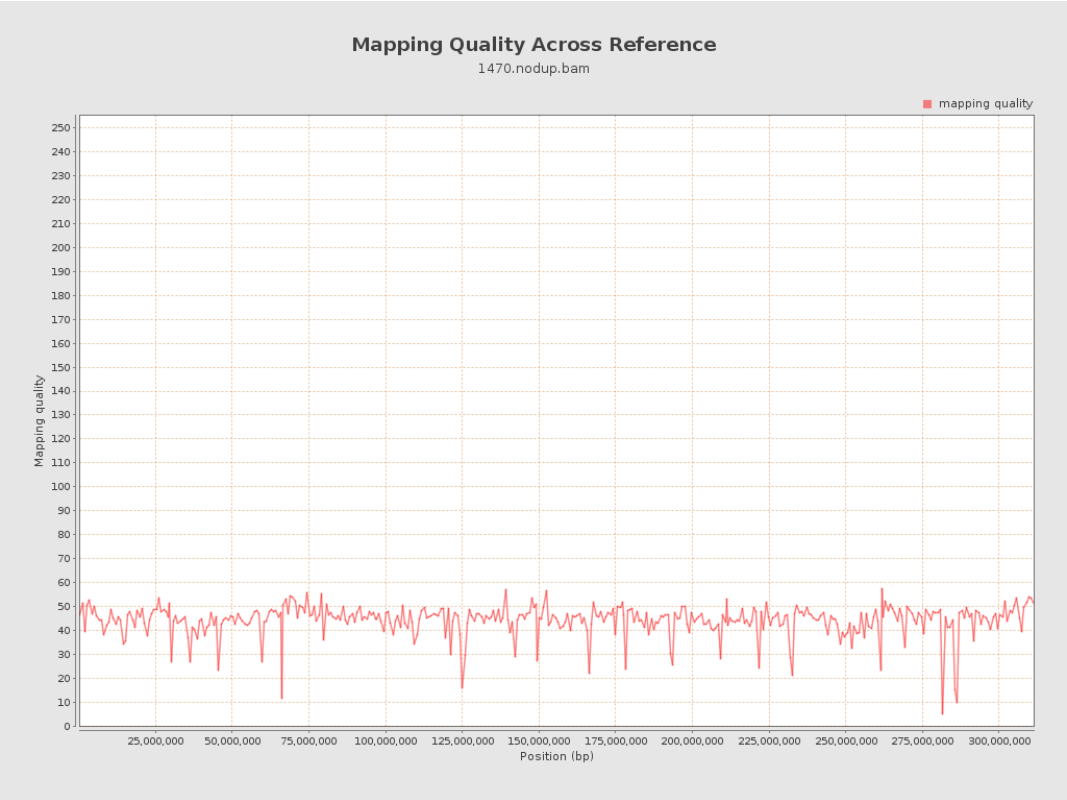
10. Results : Mapped Reads Clipping Profile



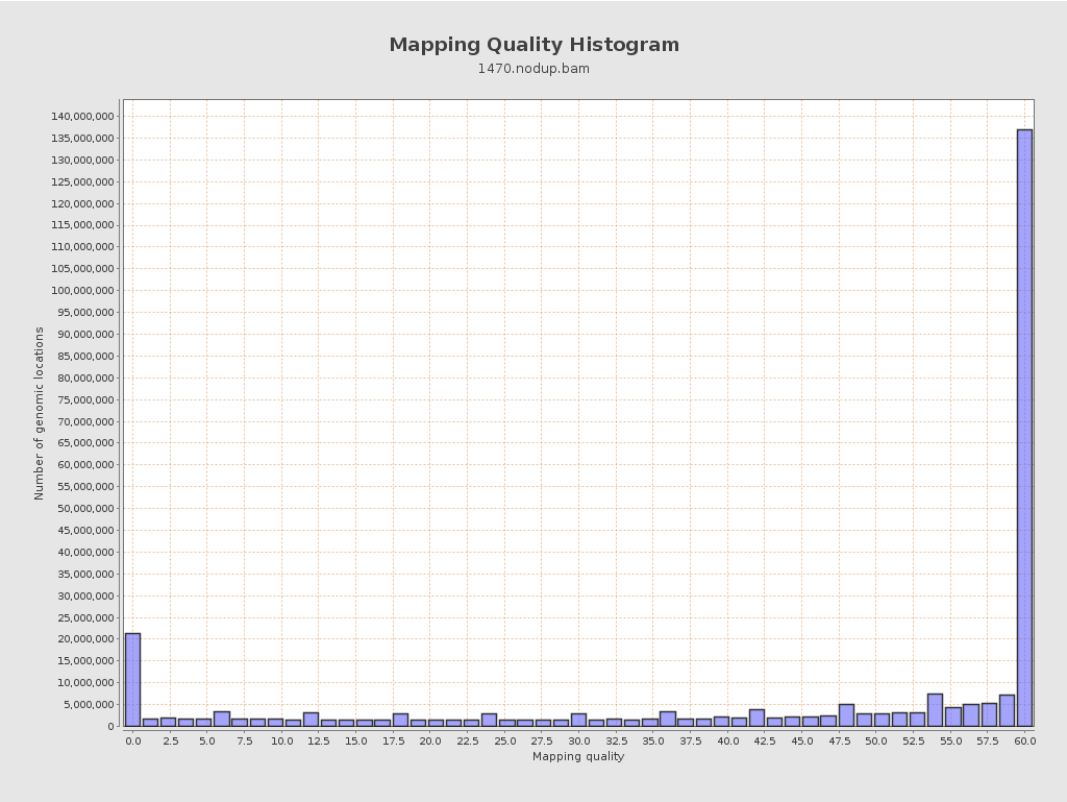
11. Results : Homopolymer Indels



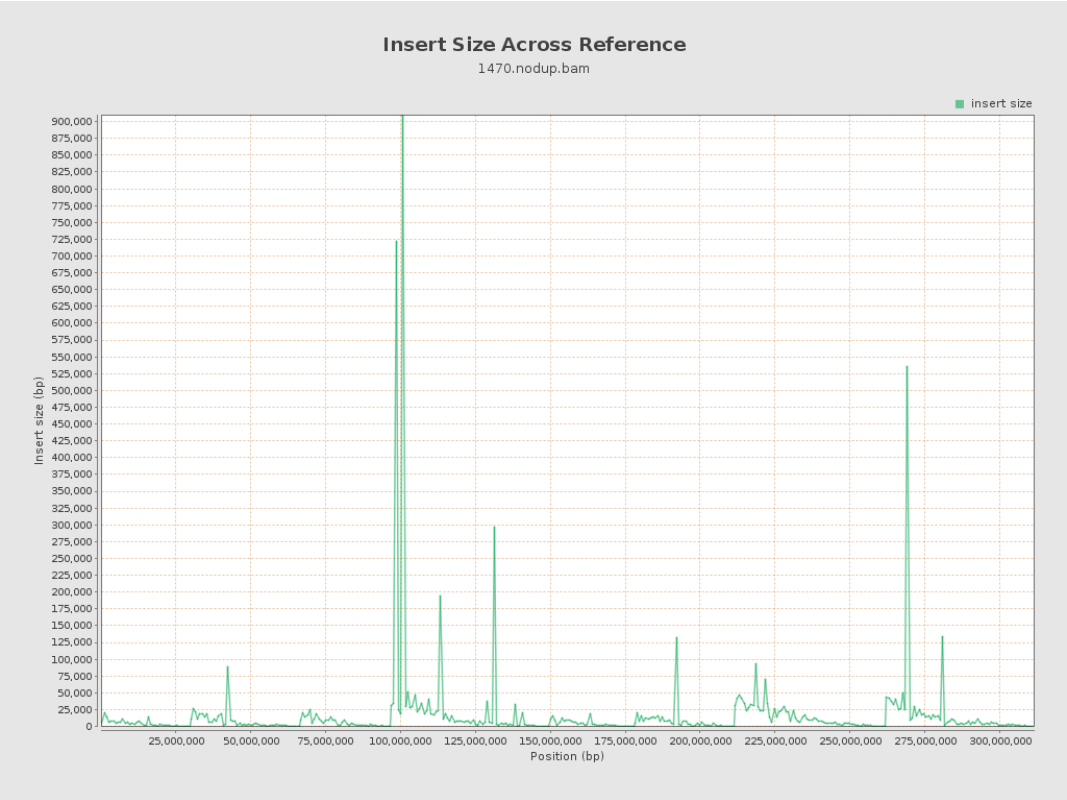
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram