Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/127
1
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1271 .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_425/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_425_S400_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_425/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_425_S400_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:37 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,952,868
Mapped reads	73,273,023 / 92.81%
Unmapped reads	5,679,845 / 7.19%
Mapped paired reads	73,273,023 / 92.81%
Mapped reads, first in pair	36,684,728 / 46.46%
Mapped reads, second in pair	36,588,295 / 46.34%
Mapped reads, both in pair	71,858,485 / 91.01%
Mapped reads, singletons	1,414,538 / 1.79%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	11,082,649 / 14.04%
Clipped reads	15,923,911 / 20.17%

2.2. ACGT Content

Number/percentage of A's	3,150,164,549 / 30.9%
Number/percentage of C's	1,947,117,300 / 19.1%
Number/percentage of T's	3,153,409,978 / 30.94%
Number/percentage of G's	1,942,796,678 / 19.06%
Number/percentage of N's	34,757 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	32.7953
Standard Deviation	232.642

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Insert size

Mean	243,718.72
Standard Deviation	2,335,459.33
P25/Median/P75	358 / 467 / 611

2.6. Mismatches and indels

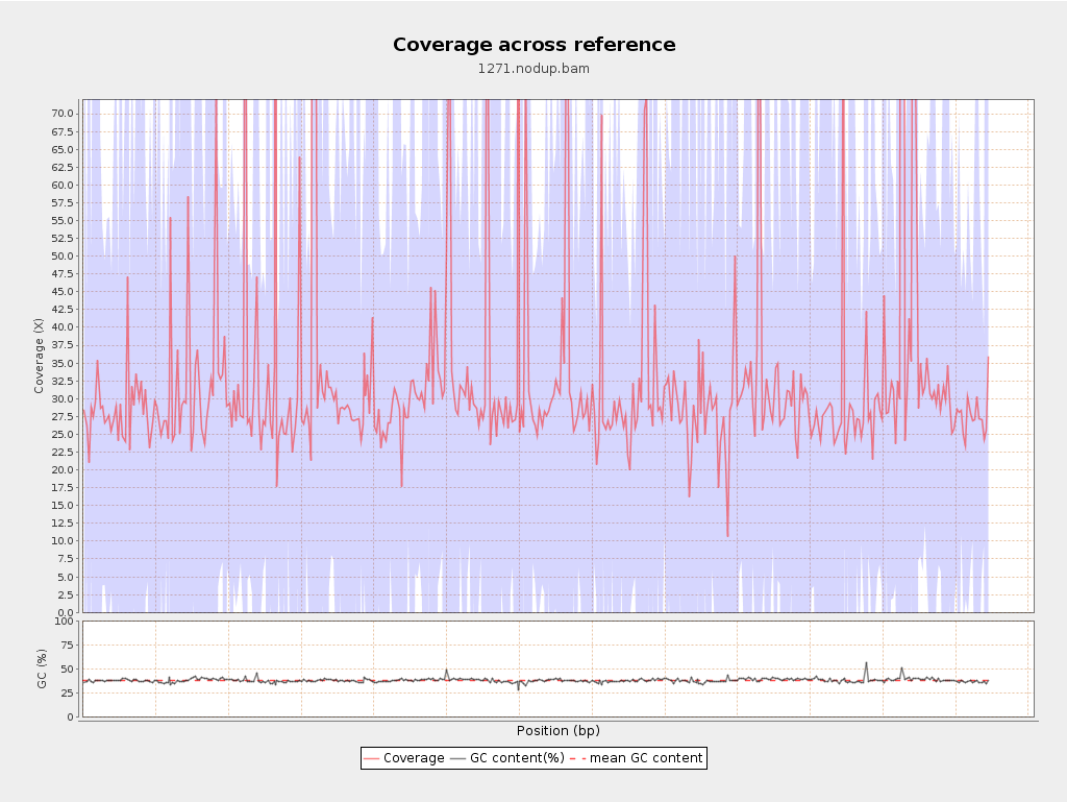
General error rate	2.29%
Mismatches	214,276,063
Insertions	6,904,751
Mapped reads with at least one insertion	8.48%
Deletions	7,063,158
Mapped reads with at least one deletion	8.56%
Homopolymer indels	55.99%

2.7. Chromosome stats

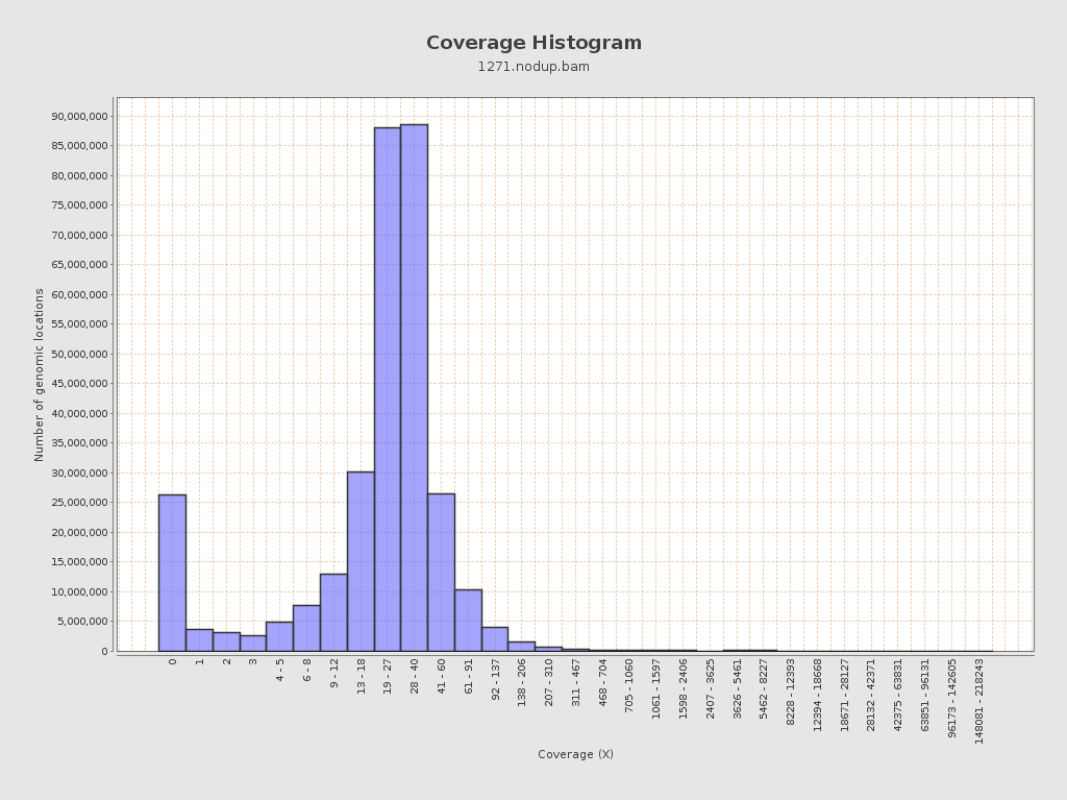
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	837195651	28.1653	68.5392

LT669789.1	36598175	1231401430	33.6465	258.1344
LT669790.1	30422129	1054435781	34.6602	218.4653
LT669791.1	52758100	1684342498	31.9258	203.1974
LT669792.1	28376109	936505545	33.0033	297.5228
LT669793.1	33388210	1026216849	30.7359	171.1275
LT669794.1	50579949	1569964906	31.0393	207.8544
LT669795.1	49795044	1880345548	37.7617	316.2761

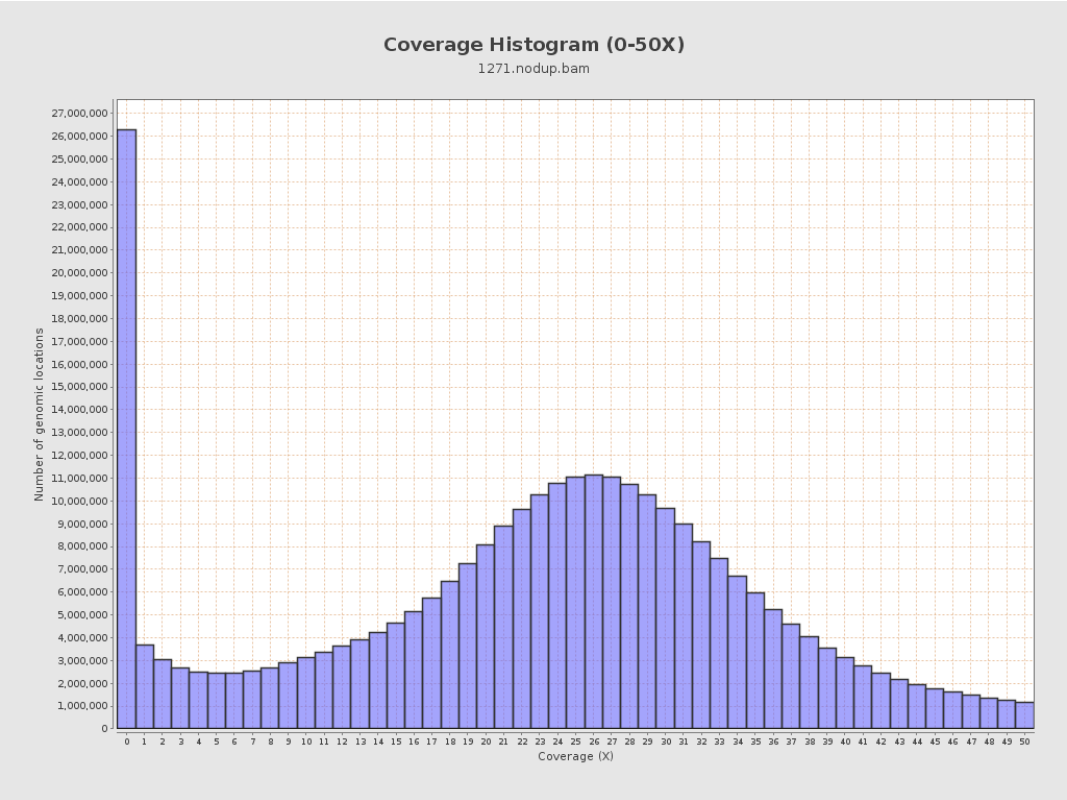
3. Results : Coverage across reference



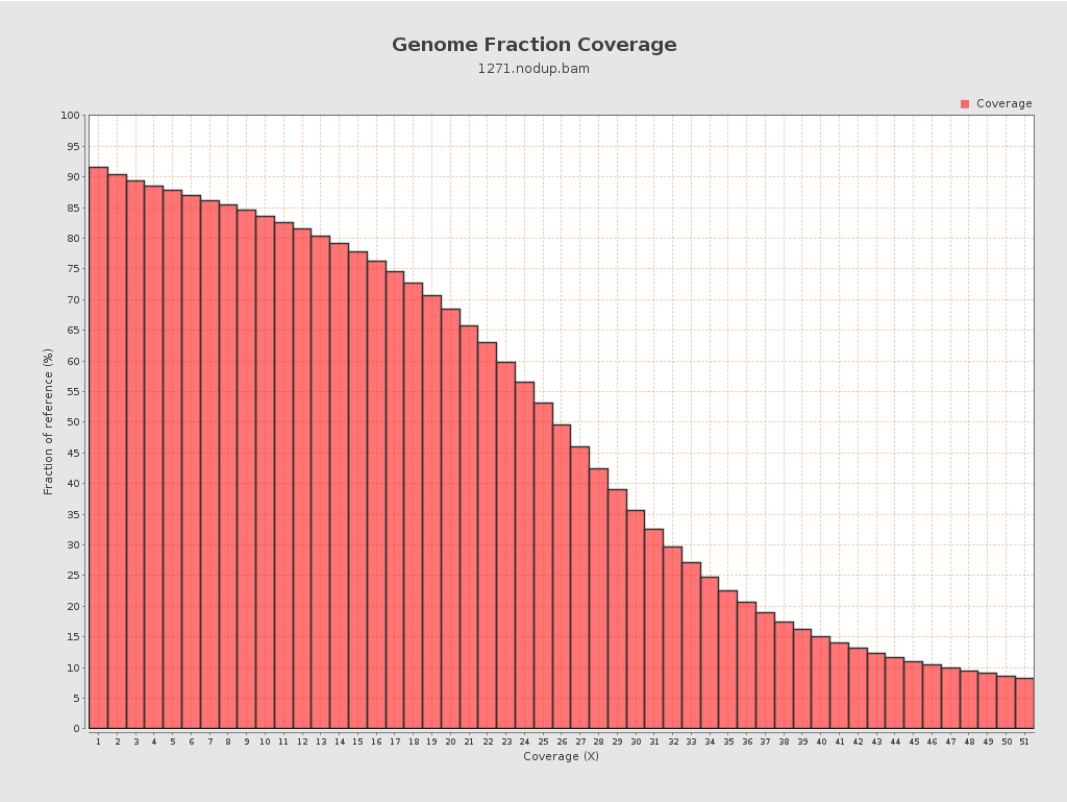
4. Results : Coverage Histogram



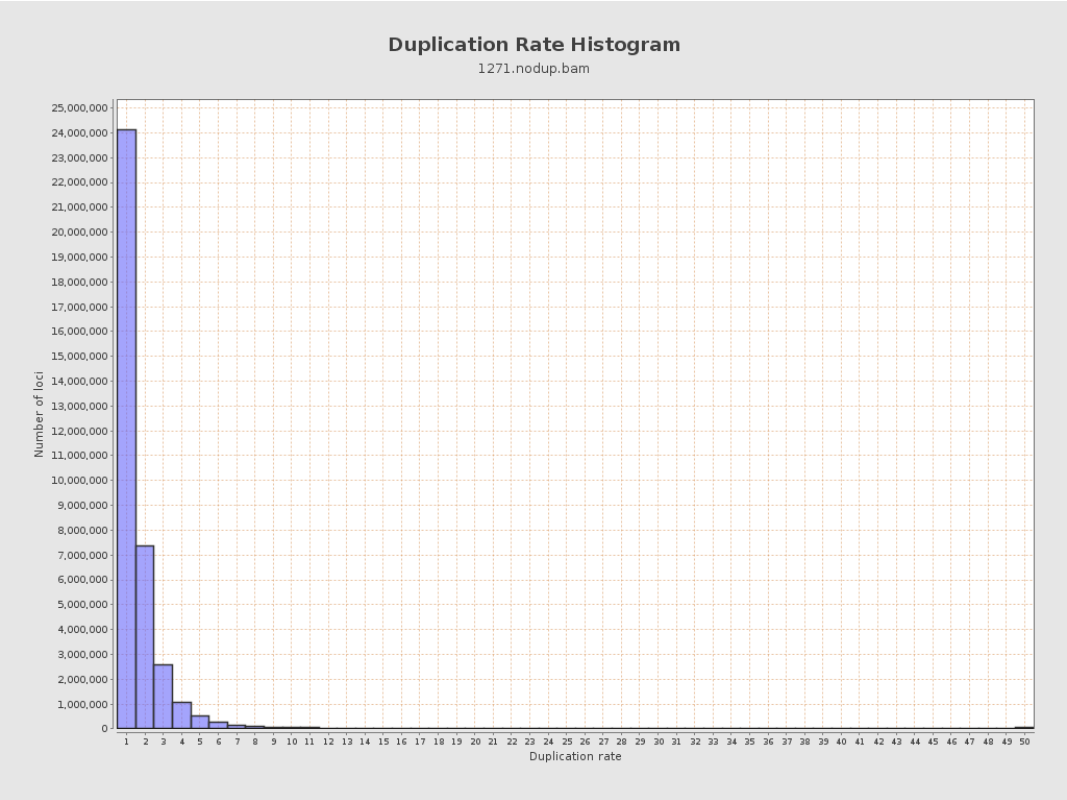
5. Results : Coverage Histogram (0-50X)



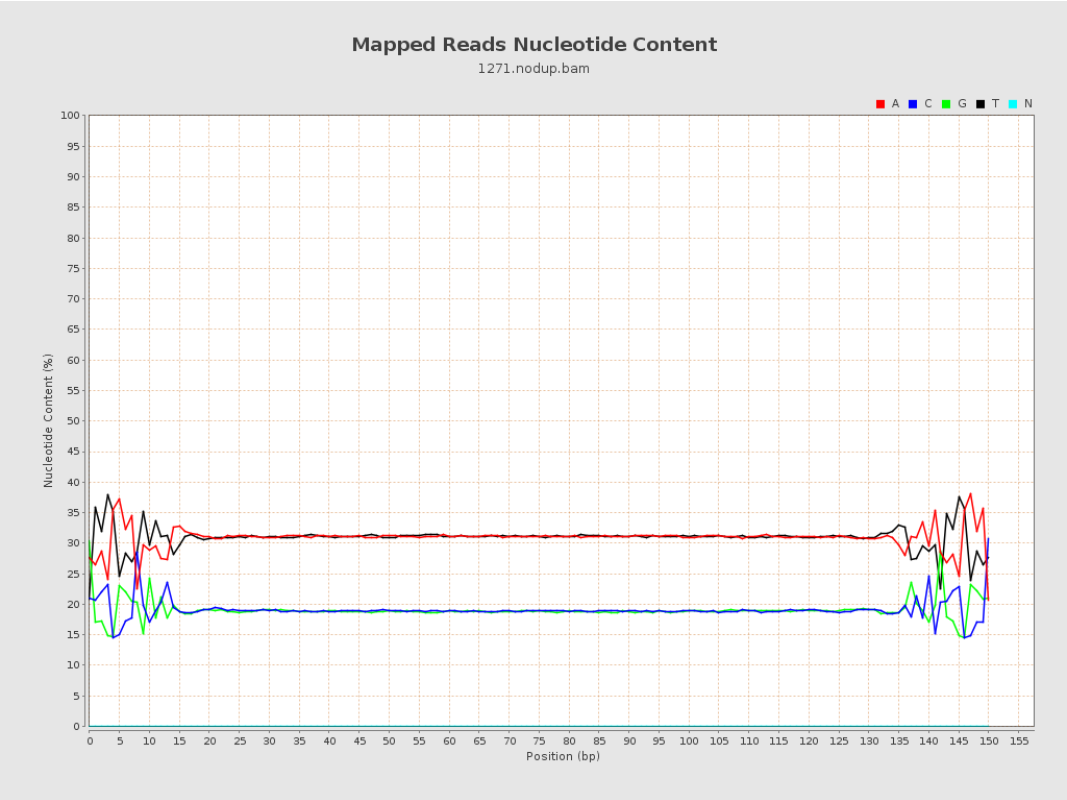
6. Results : Genome Fraction Coverage



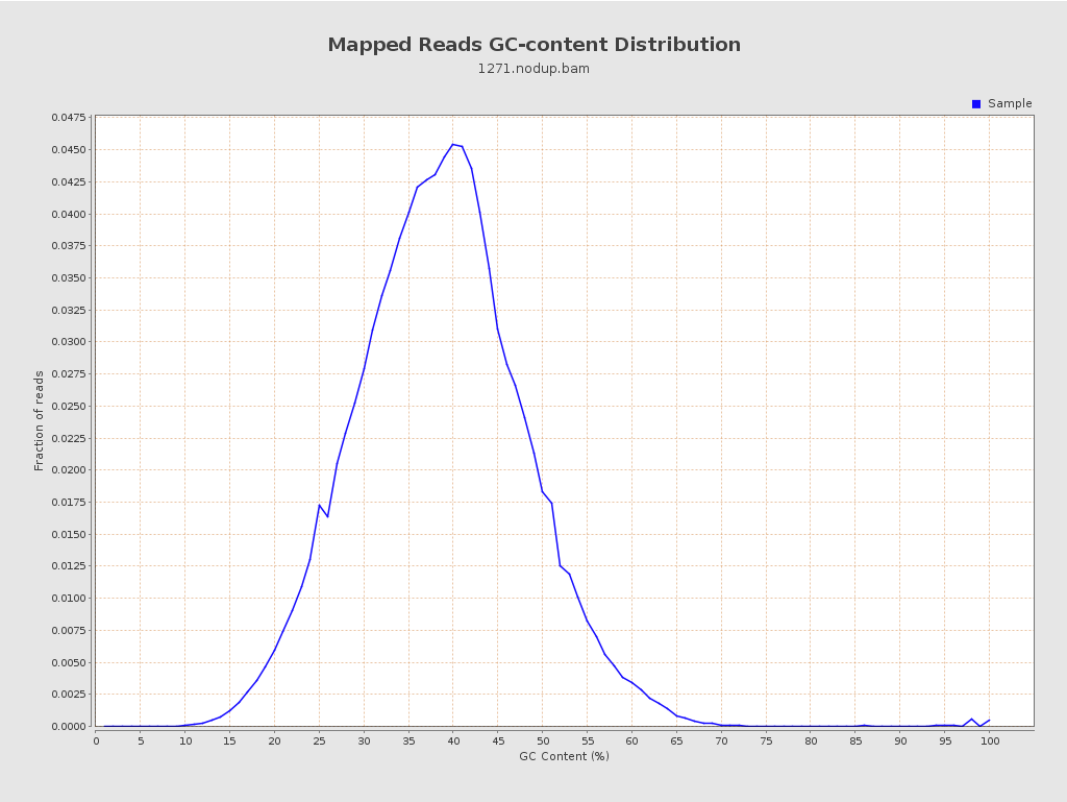
7. Results : Duplication Rate Histogram



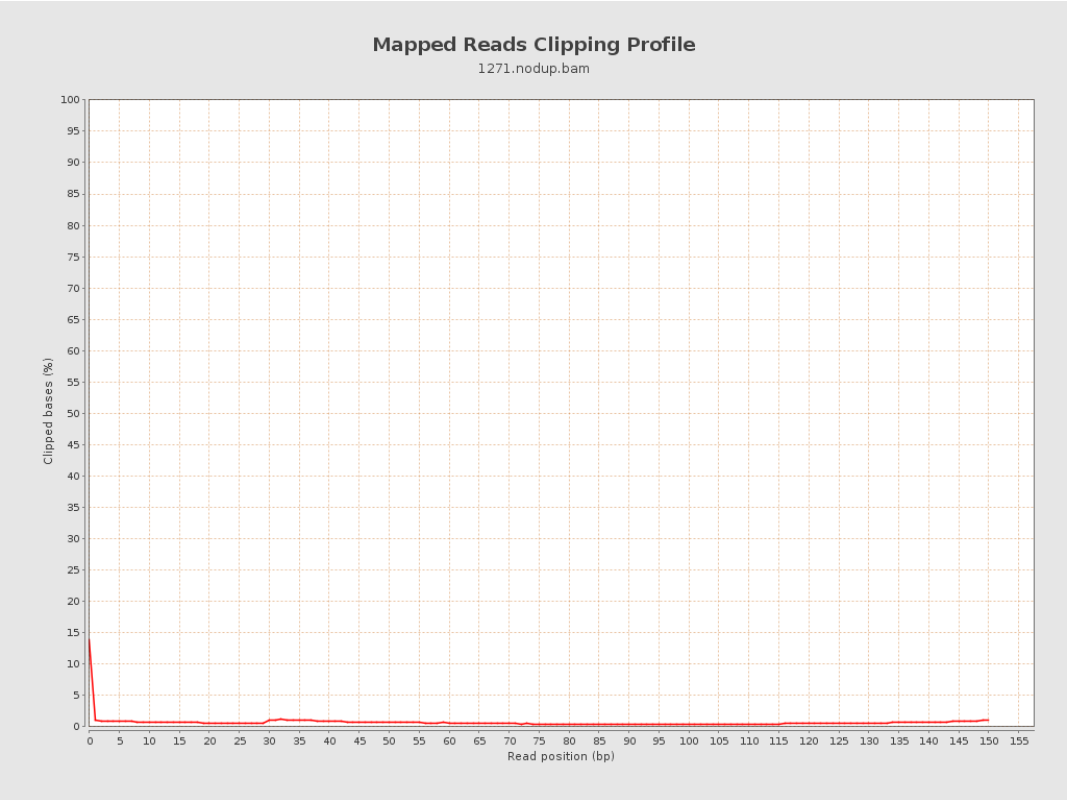
8. Results : Mapped Reads Nucleotide Content



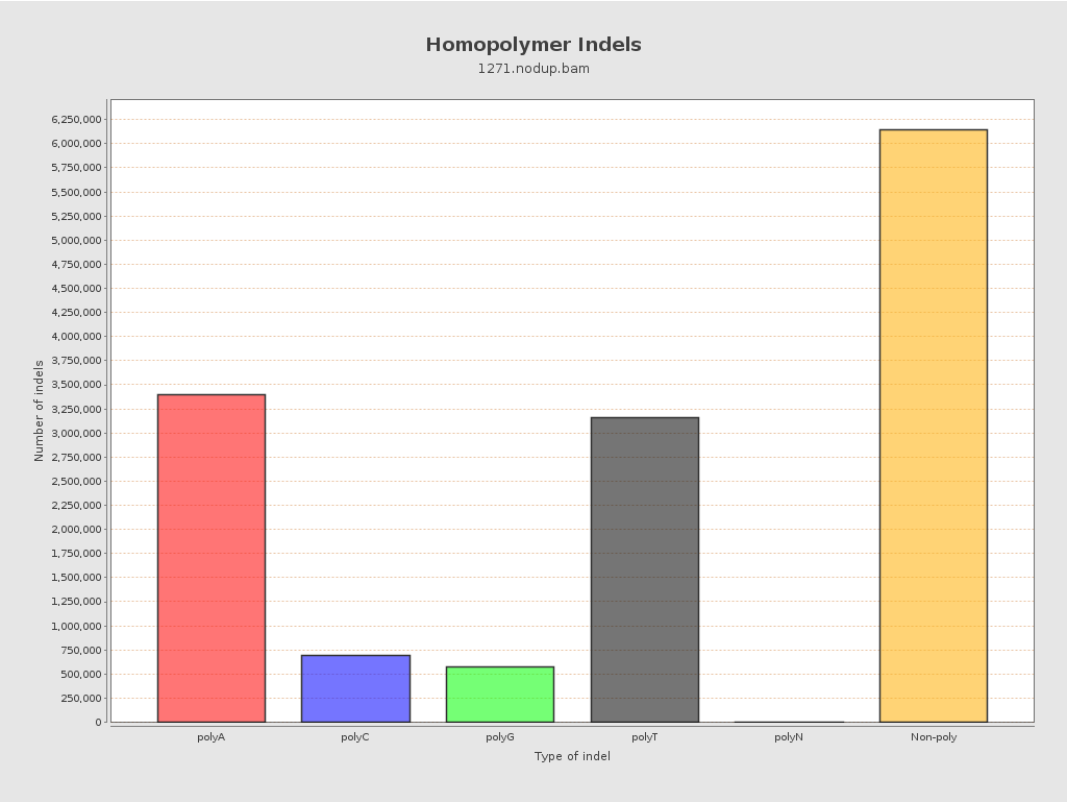
9. Results : Mapped Reads GC-content Distribution



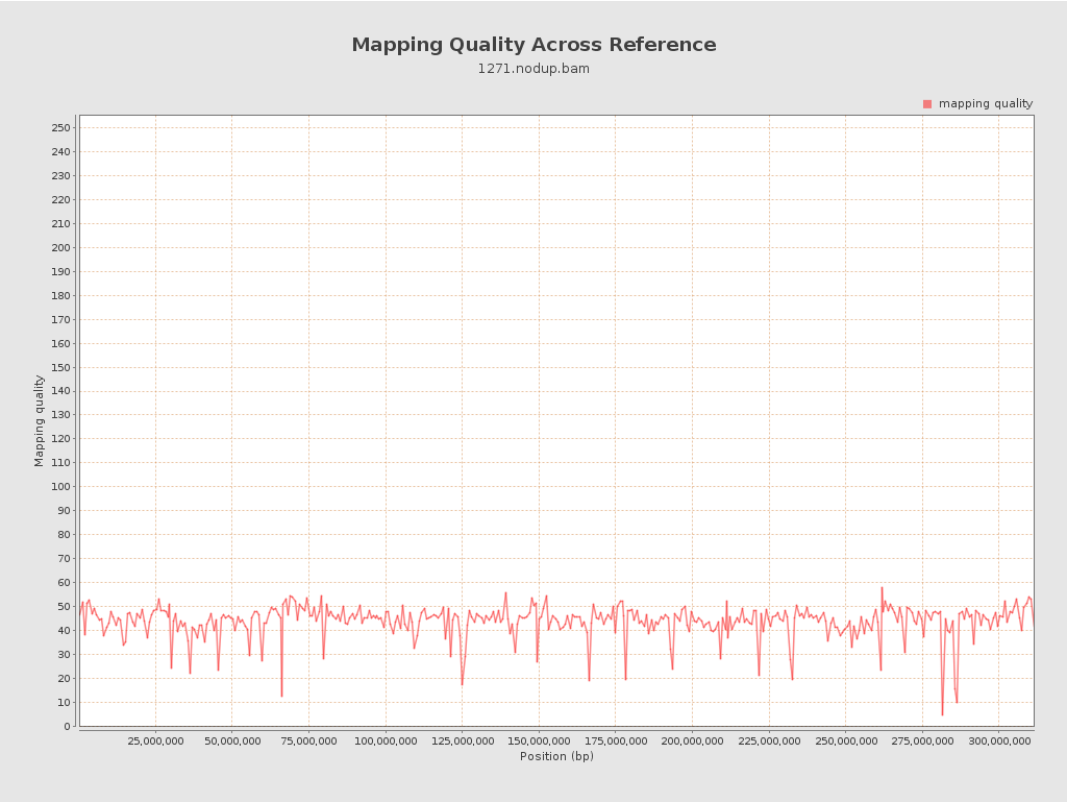
10. Results : Mapped Reads Clipping Profile



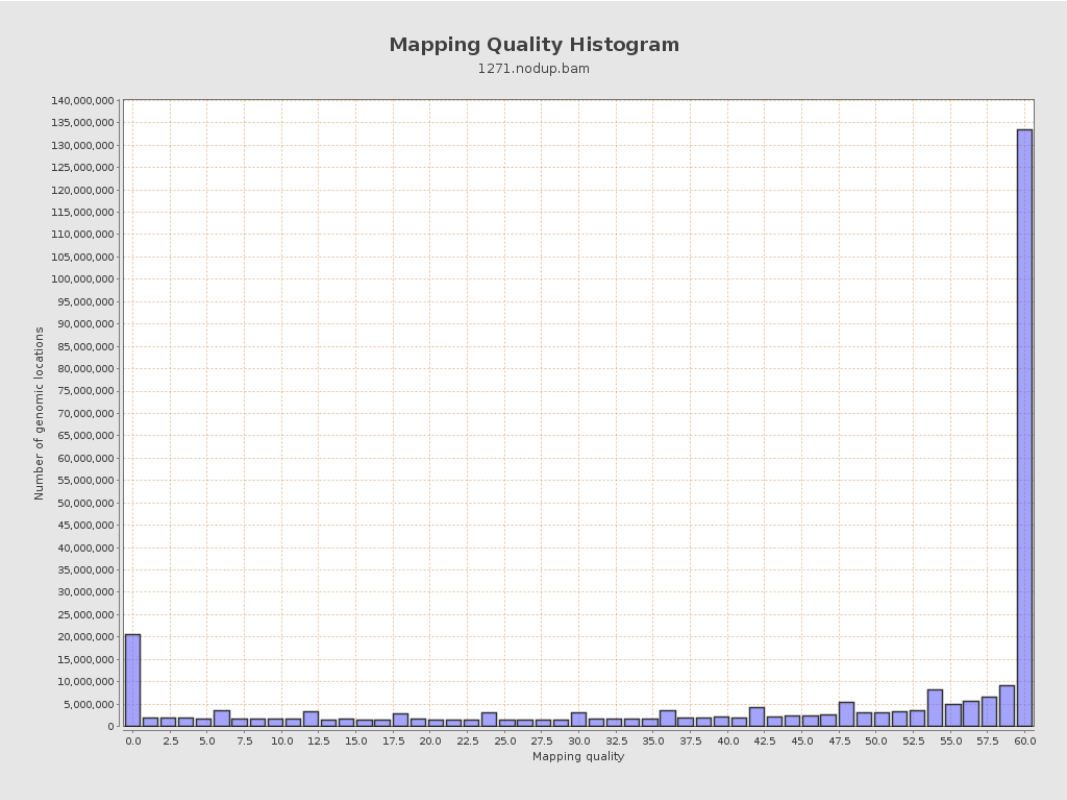
11. Results : Homopolymer Indels



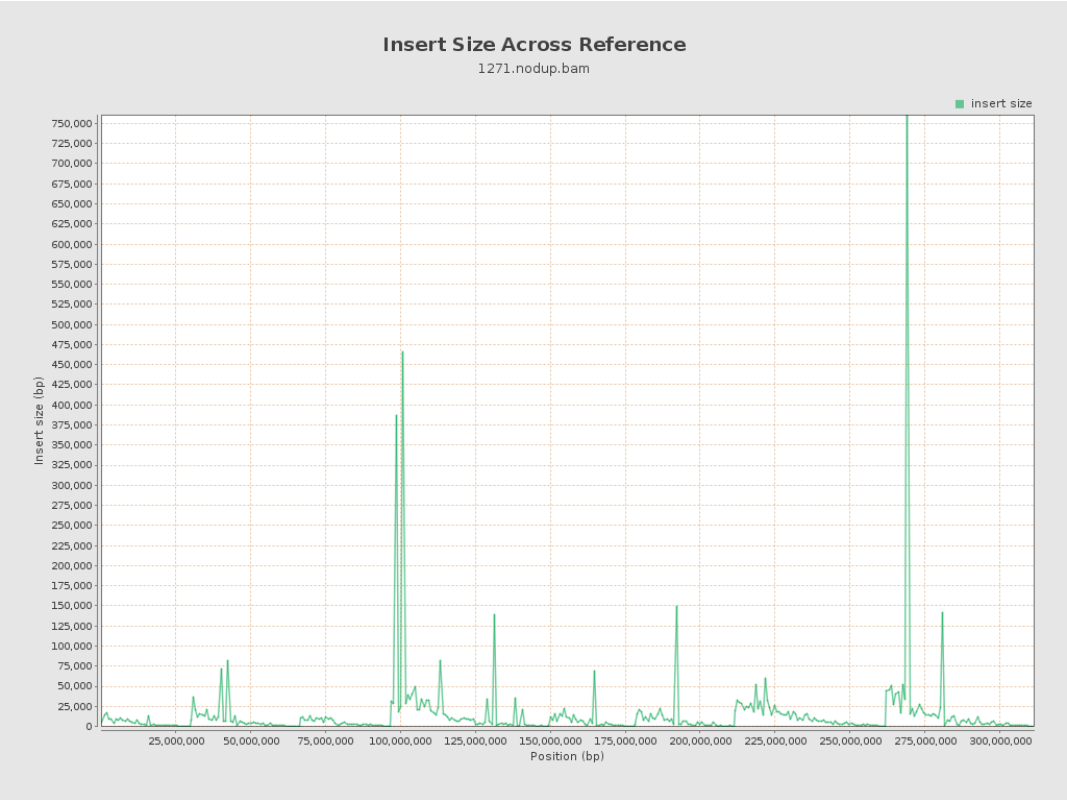
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram