Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1275
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1275 .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_470/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_470_S445_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_470/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_470_S445_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:14 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	69,709,415
Mapped reads	65,122,527 / 93.42%
Unmapped reads	4,586,888 / 6.58%
Mapped paired reads	65,122,527 / 93.42%
Mapped reads, first in pair	32,640,366 / 46.82%
Mapped reads, second in pair	32,482,161 / 46.6%
Mapped reads, both in pair	63,591,373 / 91.22%
Mapped reads, singletons	1,531,154 / 2.2%
Read min/max/mean length	30 / 151 / 148.31
Duplicated reads (flagged)	10,552,519 / 15.14%
Clipped reads	13,698,184 / 19.65%

2.2. ACGT Content

Number/percentage of A's	2,815,161,863 / 31.02%
Number/percentage of C's	1,723,381,082 / 18.99%
Number/percentage of T's	2,815,857,417 / 31.03%
Number/percentage of G's	1,720,826,495 / 18.96%
Number/percentage of N's	31,756 / 0%
GC Percentage	37.95%

2.3. Coverage

Mean	29.1933
Standard Deviation	210.6262

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Insert size

Mean	235,196.05
Standard Deviation	2,319,408.63
P25/Median/P75	357 / 462 / 599

2.6. Mismatches and indels

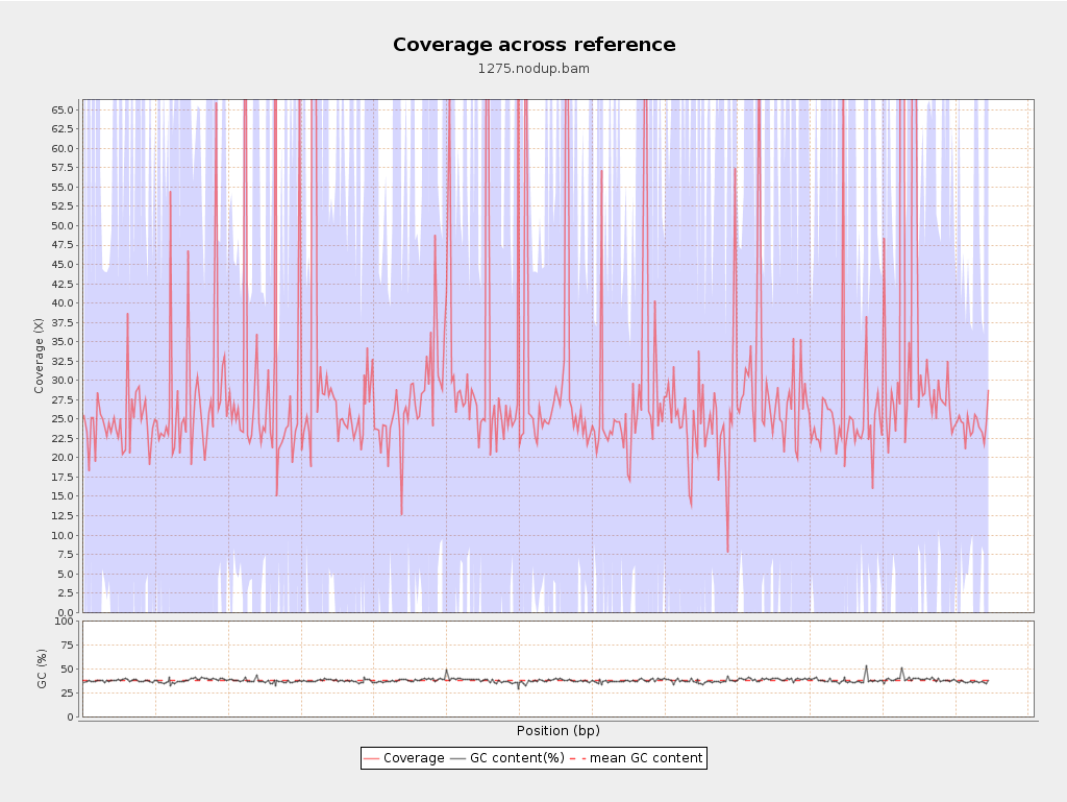
General error rate	2.24%
Mismatches	186,534,690
Insertions	5,977,669
Mapped reads with at least one insertion	8.23%
Deletions	6,005,823
Mapped reads with at least one deletion	8.21%
Homopolymer indels	57.31%

2.7. Chromosome stats

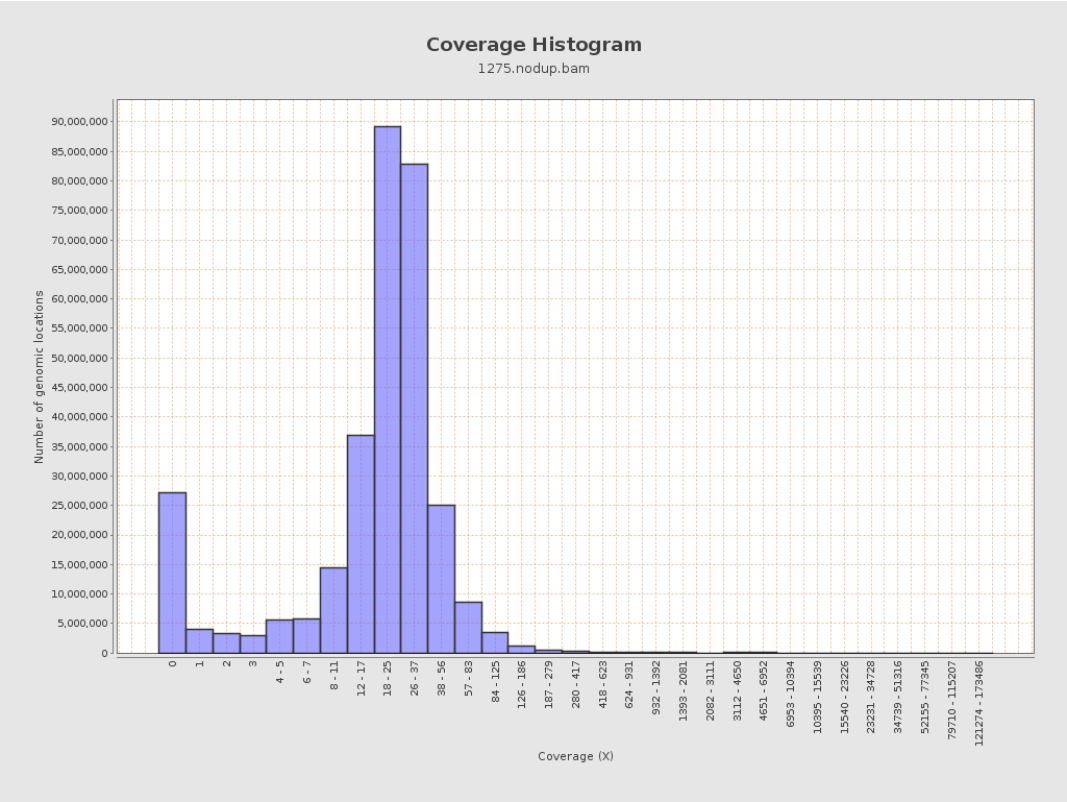
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	726494744	24.4411	64.7475

LT669789.1	36598175	1077358066	29.4375	223.8115
LT669790.1	30422129	975115681	32.0528	240.9828
LT669791.1	52758100	1521711747	28.8432	191.5329
LT669792.1	28376109	828303087	29.1902	246.6185
LT669793.1	33388210	908129692	27.1991	155.3717
LT669794.1	50579949	1396744826	27.6146	167.8129
LT669795.1	49795044	1664010982	33.4172	290.6717

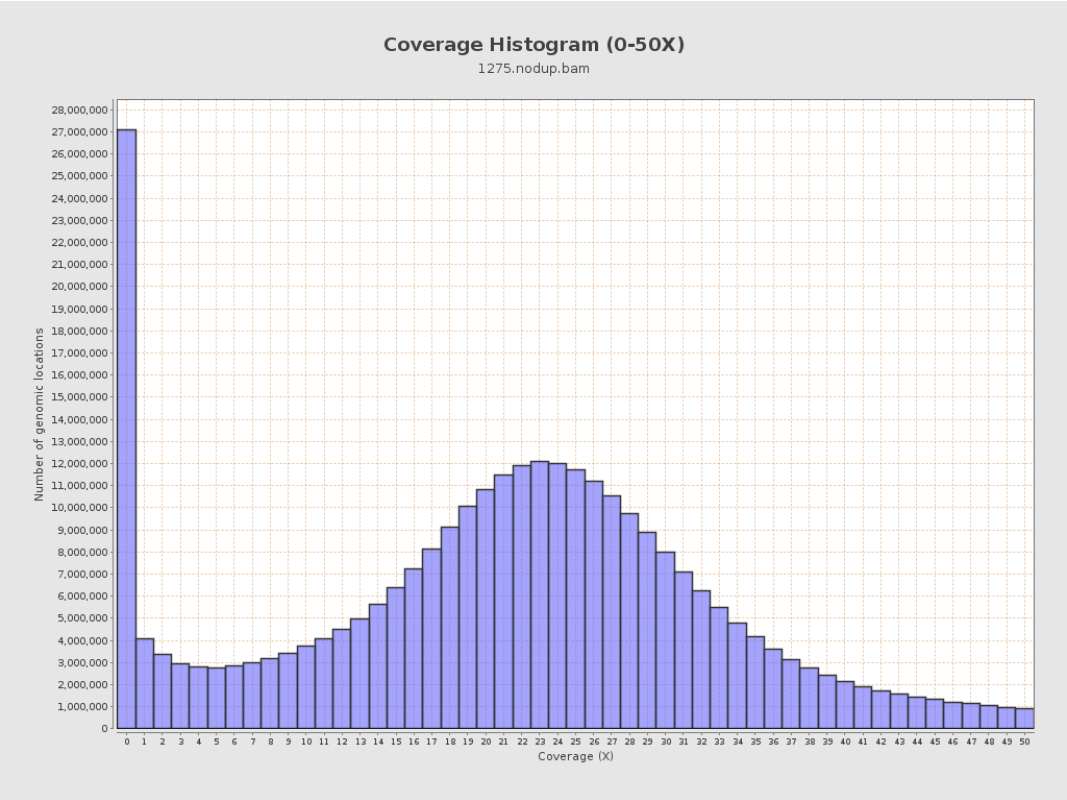
3. Results : Coverage across reference



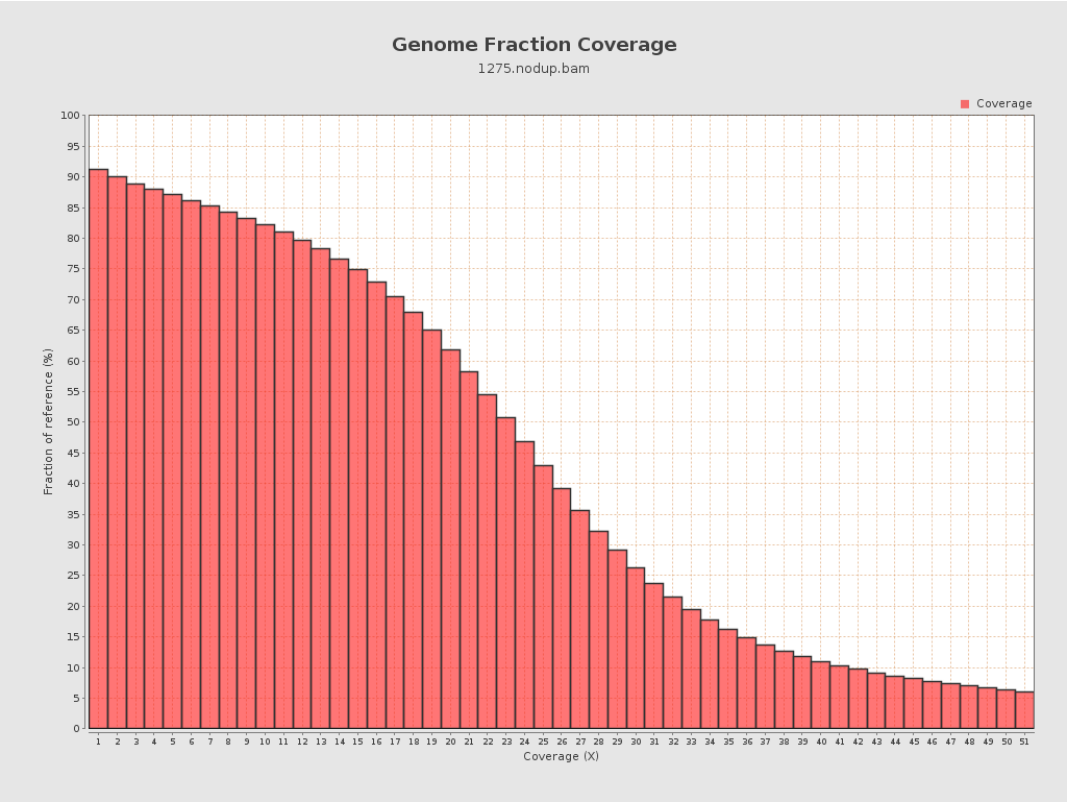
4. Results : Coverage Histogram



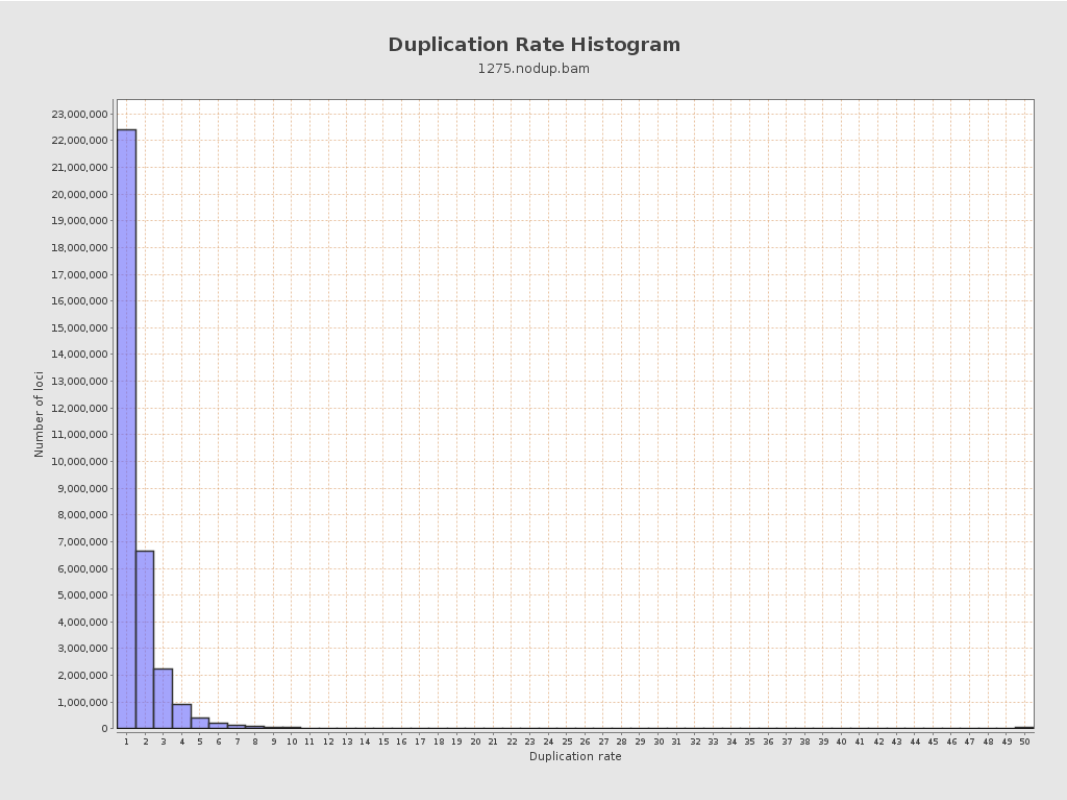
5. Results : Coverage Histogram (0-50X)



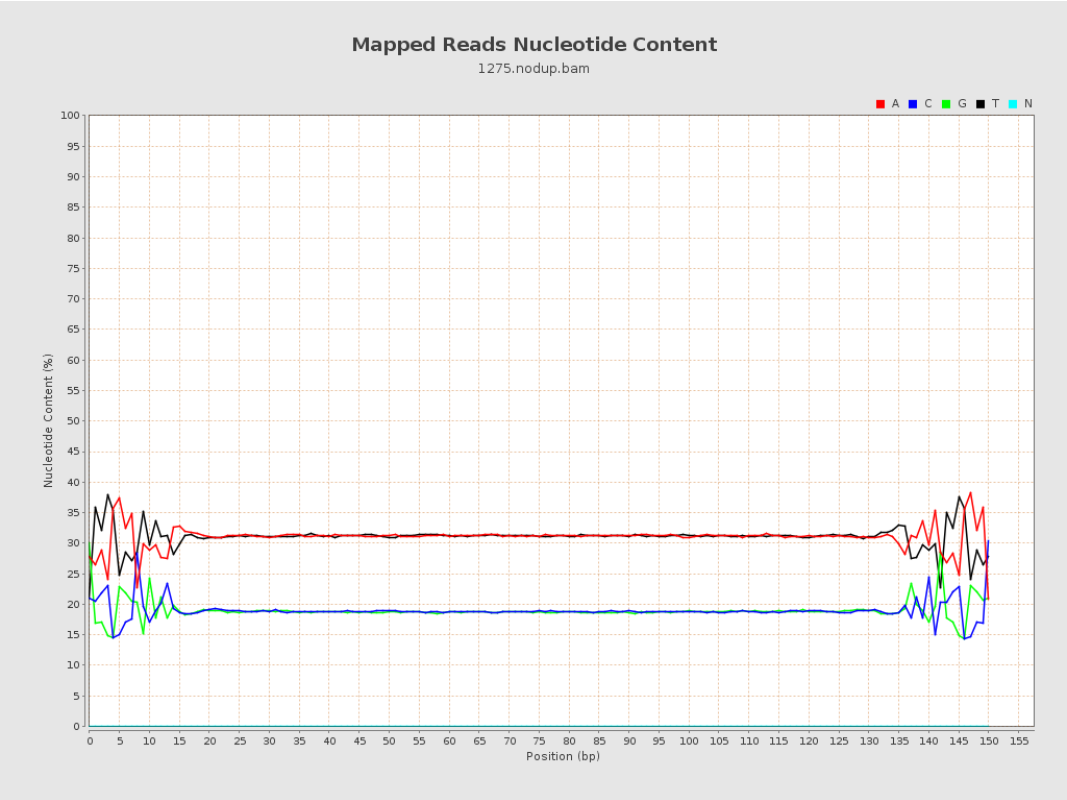
6. Results : Genome Fraction Coverage



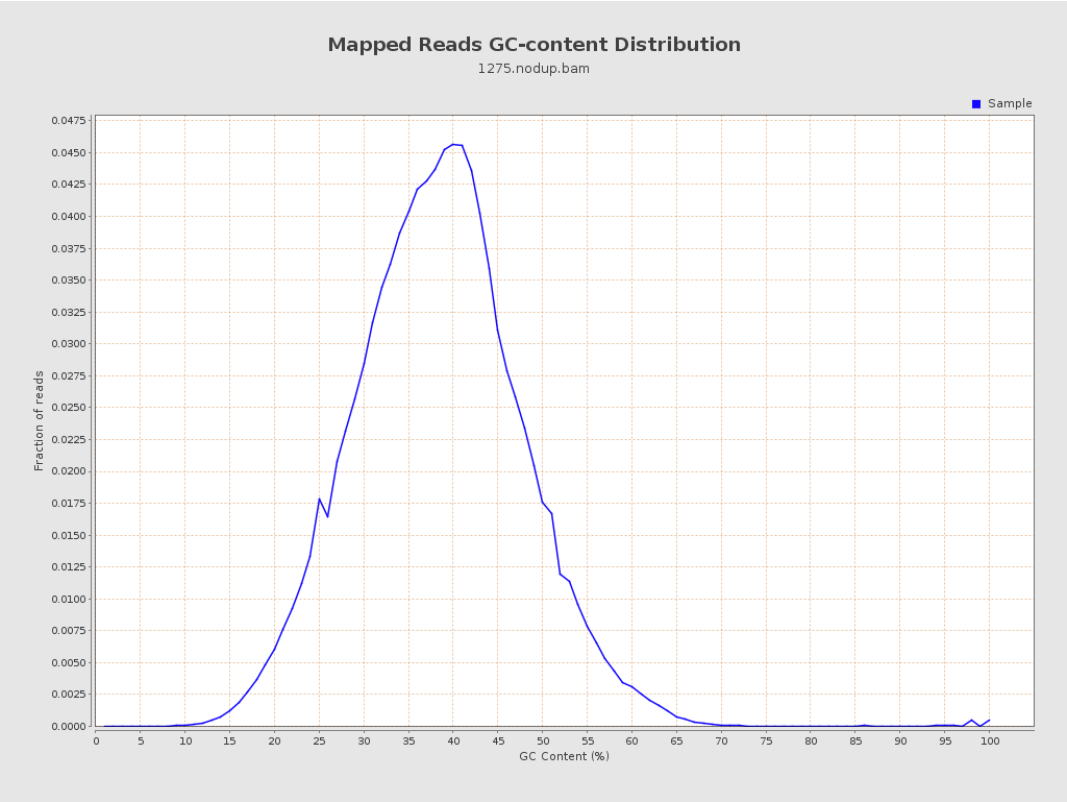
7. Results : Duplication Rate Histogram



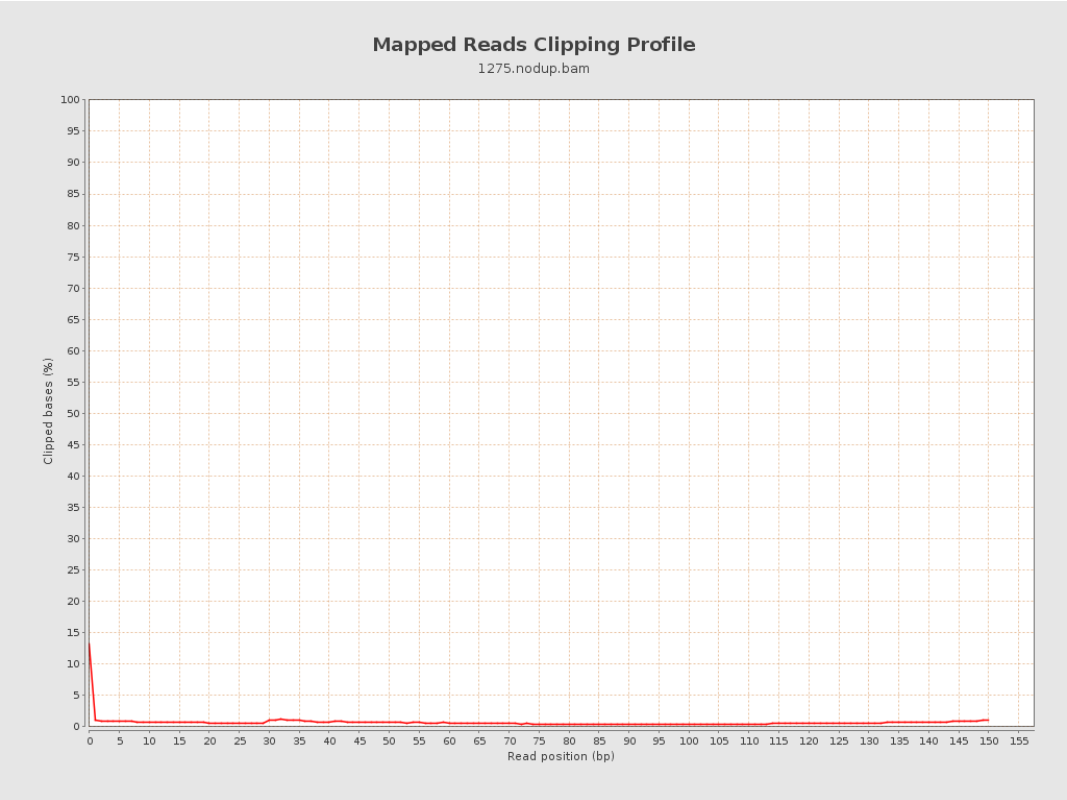
8. Results : Mapped Reads Nucleotide Content



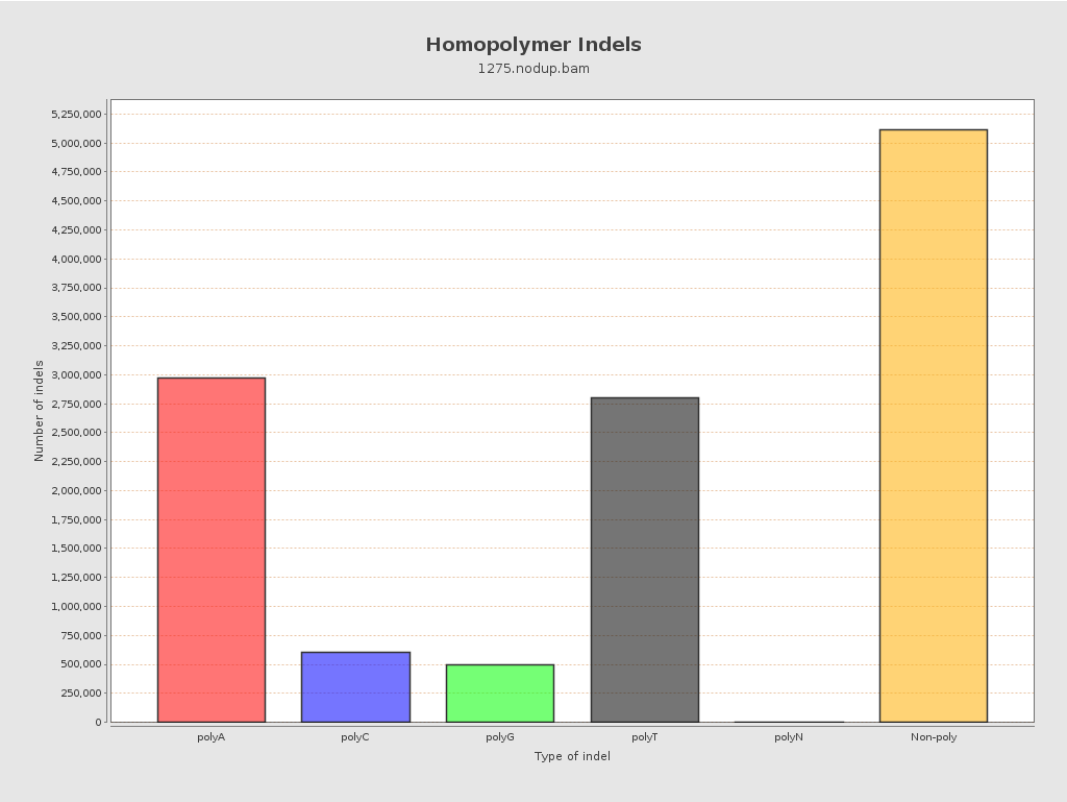
9. Results : Mapped Reads GC-content Distribution



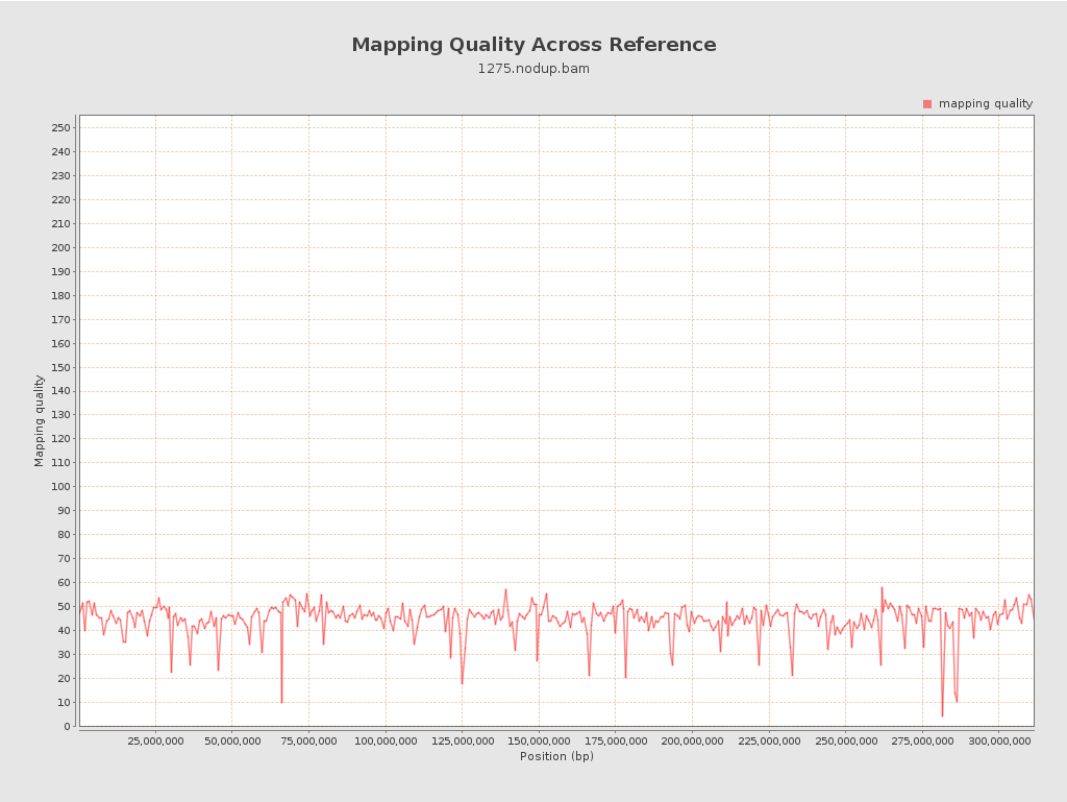
10. Results : Mapped Reads Clipping Profile



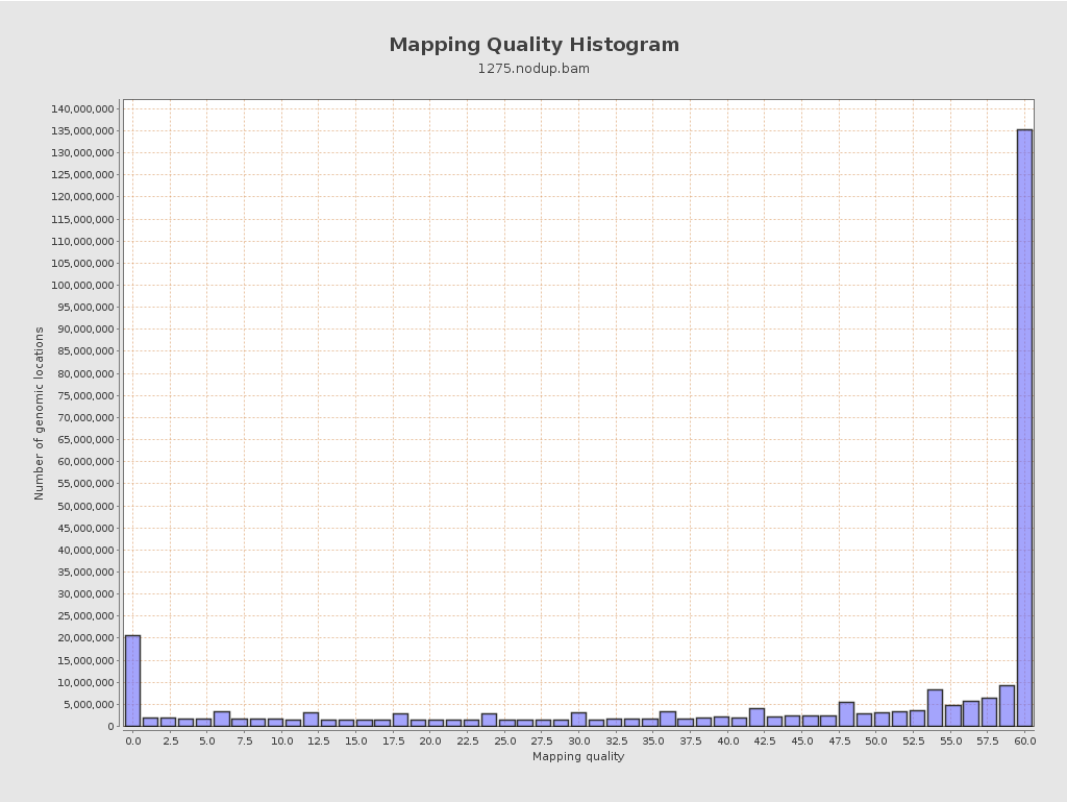
11. Results : Homopolymer Indels



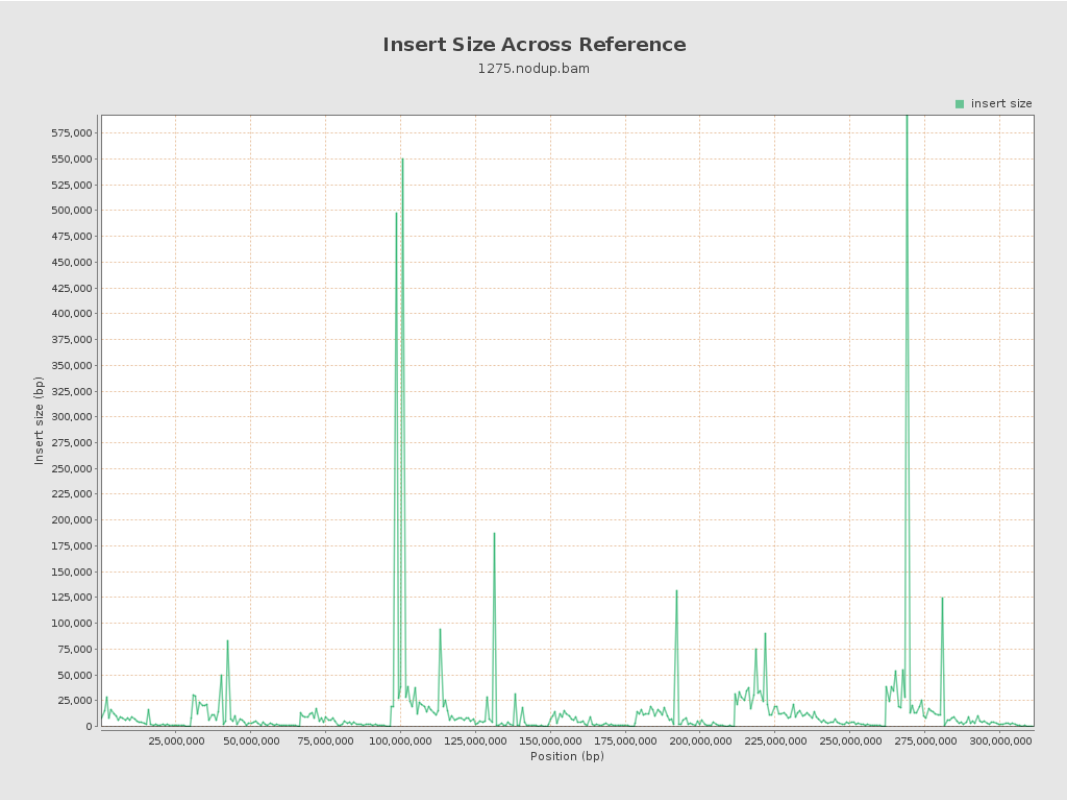
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram