Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1278
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1278 .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_132/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_132_S222_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_132/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_132_S222_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,736,428
Mapped reads	72,904,649 / 91.43%
Unmapped reads	6,831,779 / 8.57%
Mapped paired reads	72,904,649 / 91.43%
Mapped reads, first in pair	36,527,250 / 45.81%
Mapped reads, second in pair	36,377,399 / 45.62%
Mapped reads, both in pair	70,649,395 / 88.6%
Mapped reads, singletons	2,255,254 / 2.83%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	13,224,807 / 16.59%
Clipped reads	17,329,804 / 21.73%

2.2. ACGT Content

Number/percentage of A's	3,102,656,809 / 31.02%
Number/percentage of C's	1,897,030,318 / 18.97%
Number/percentage of T's	3,102,140,722 / 31.02%
Number/percentage of G's	1,899,804,563 / 18.99%
Number/percentage of N's	41,966 / 0%
GC Percentage	37.96%

2.3. Coverage

Mean	32.1796
Standard Deviation	290.1166

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Insert size

Mean	271,735.24
Standard Deviation	2,514,764.56
P25/Median/P75	325 / 426 / 558

2.6. Mismatches and indels

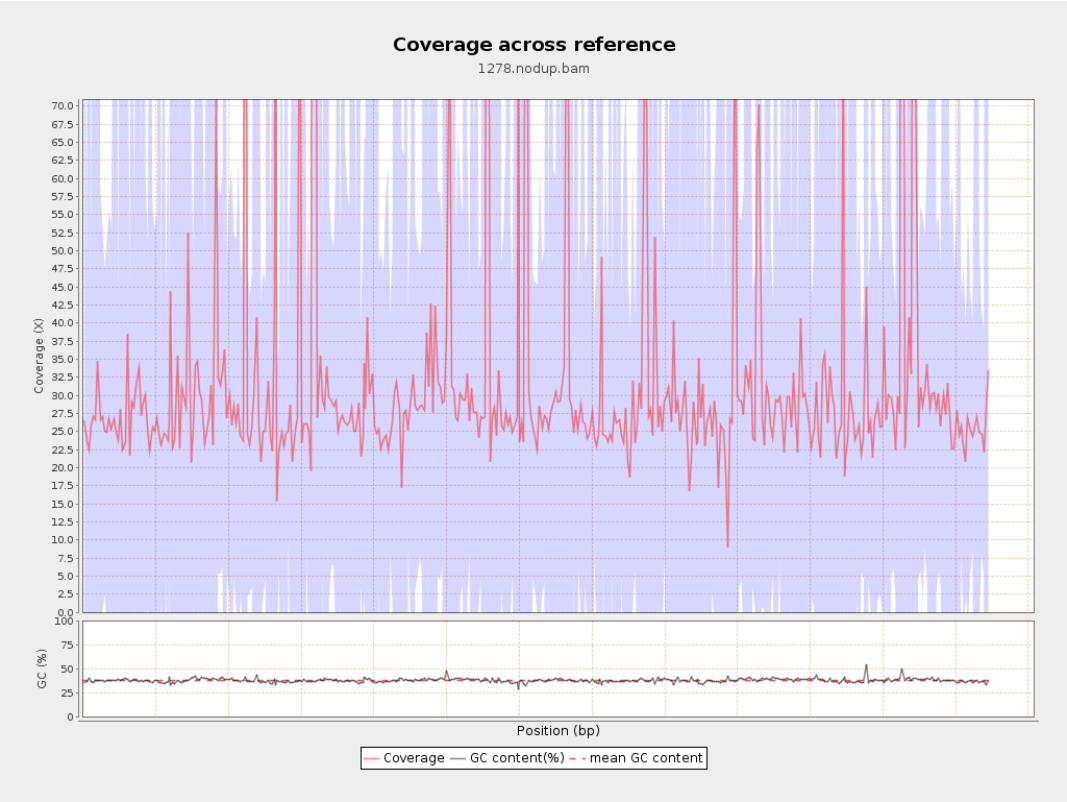
General error rate	2.4%
Mismatches	219,149,514
Insertions	7,421,250
Mapped reads with at least one insertion	9.05%
Deletions	7,174,957
Mapped reads with at least one deletion	8.73%
Homopolymer indels	57.79%

2.7. Chromosome stats

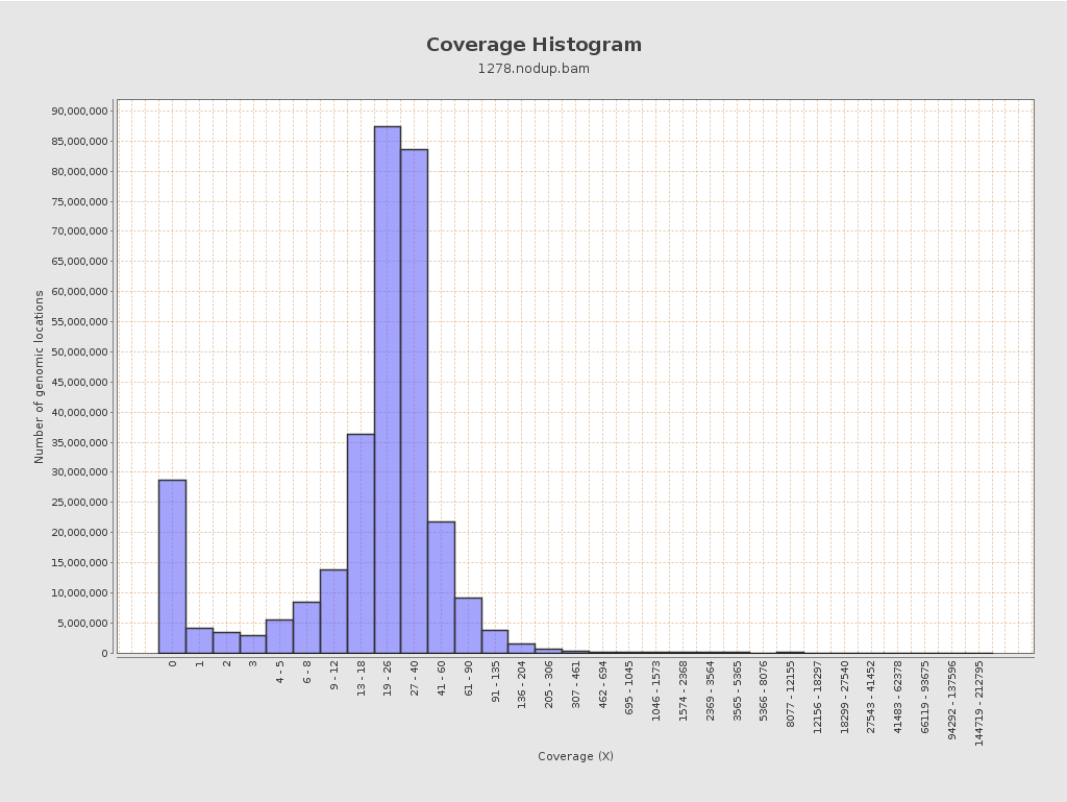
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	788289950	26.52	119.334

LT669789.1	36598175	1208698834	33.0262	313.3467
LT669790.1	30422129	1187598478	39.0373	427.2838
LT669791.1	52758100	1688351889	32.0018	324.0878
LT669792.1	28376109	932093531	32.8478	312.2292
LT669793.1	33388210	988495294	29.6061	189.2584
LT669794.1	50579949	1544486727	30.5356	228.9326
LT669795.1	49795044	1690502288	33.9492	300.6786

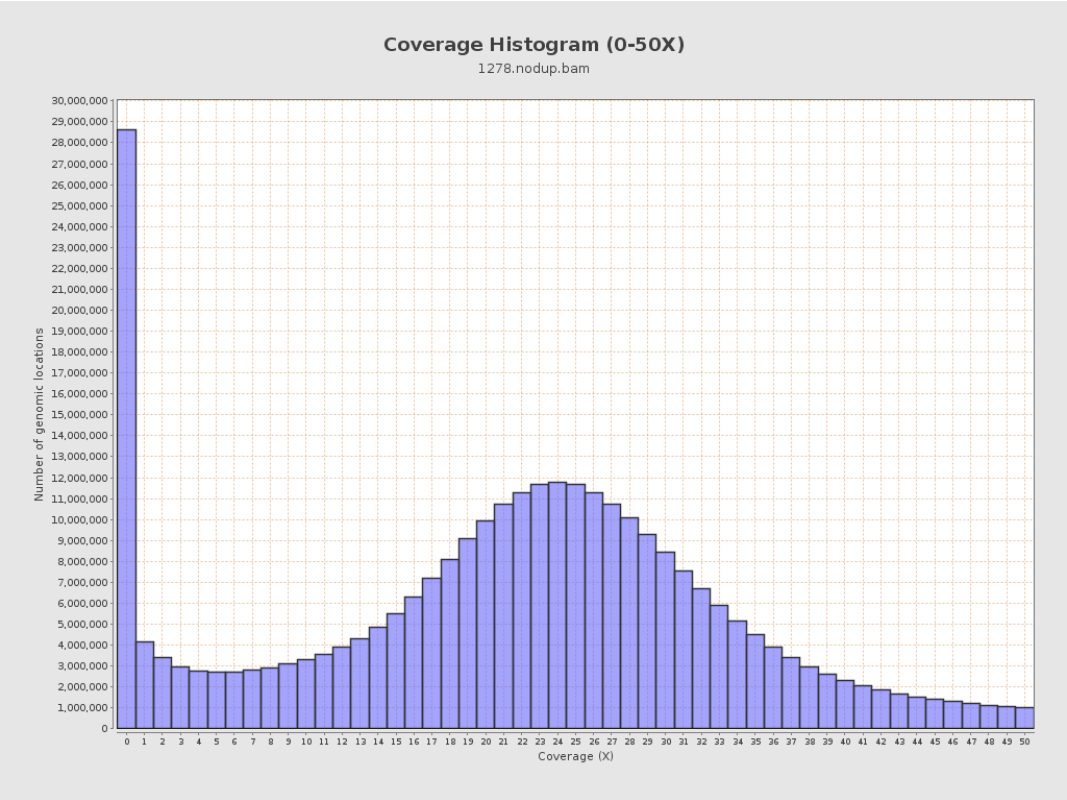
3. Results : Coverage across reference



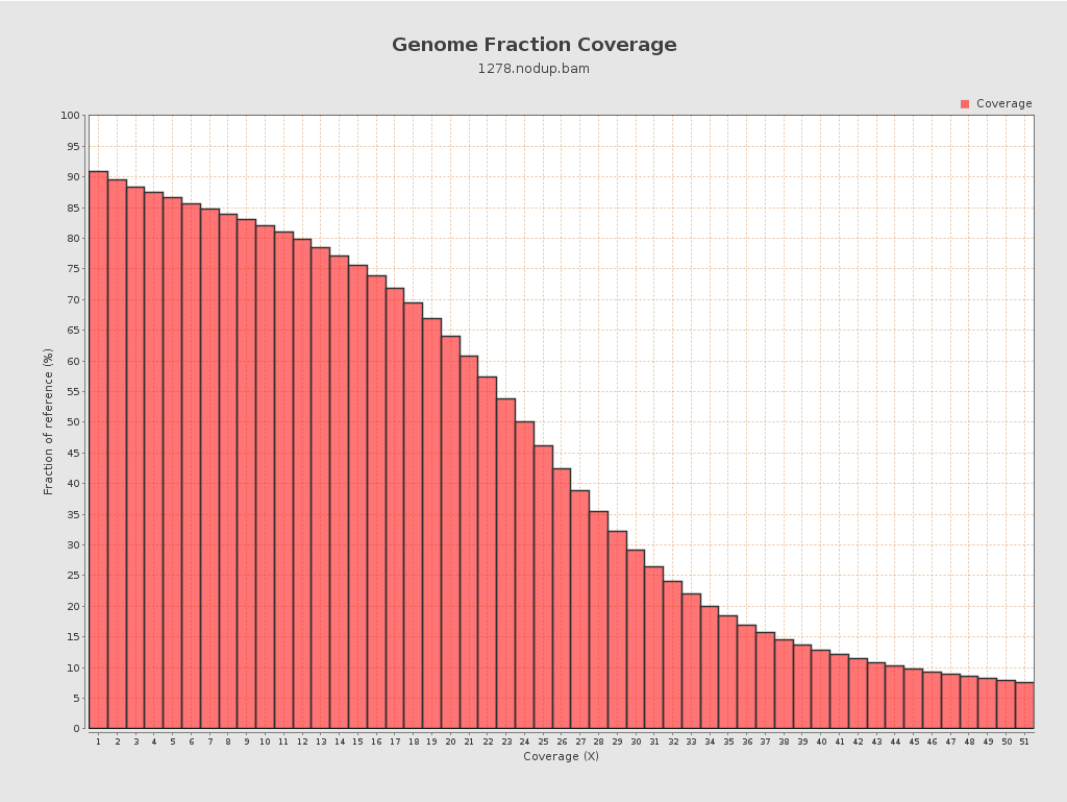
4. Results : Coverage Histogram



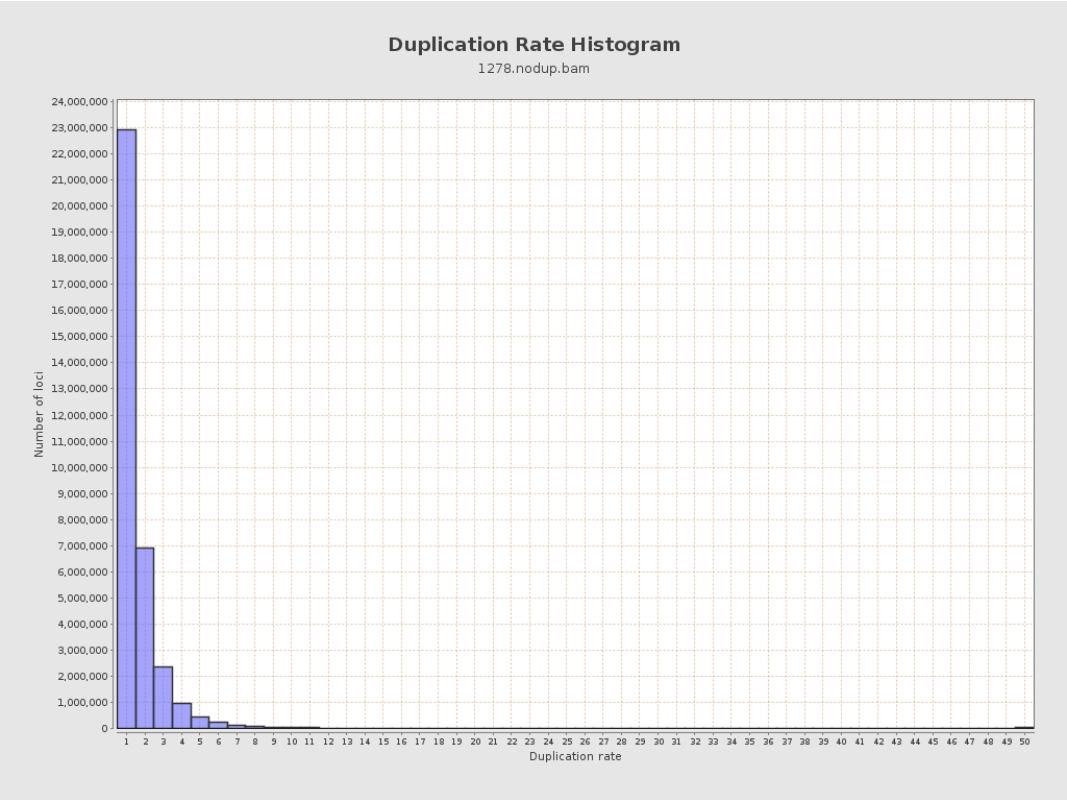
5. Results : Coverage Histogram (0-50X)



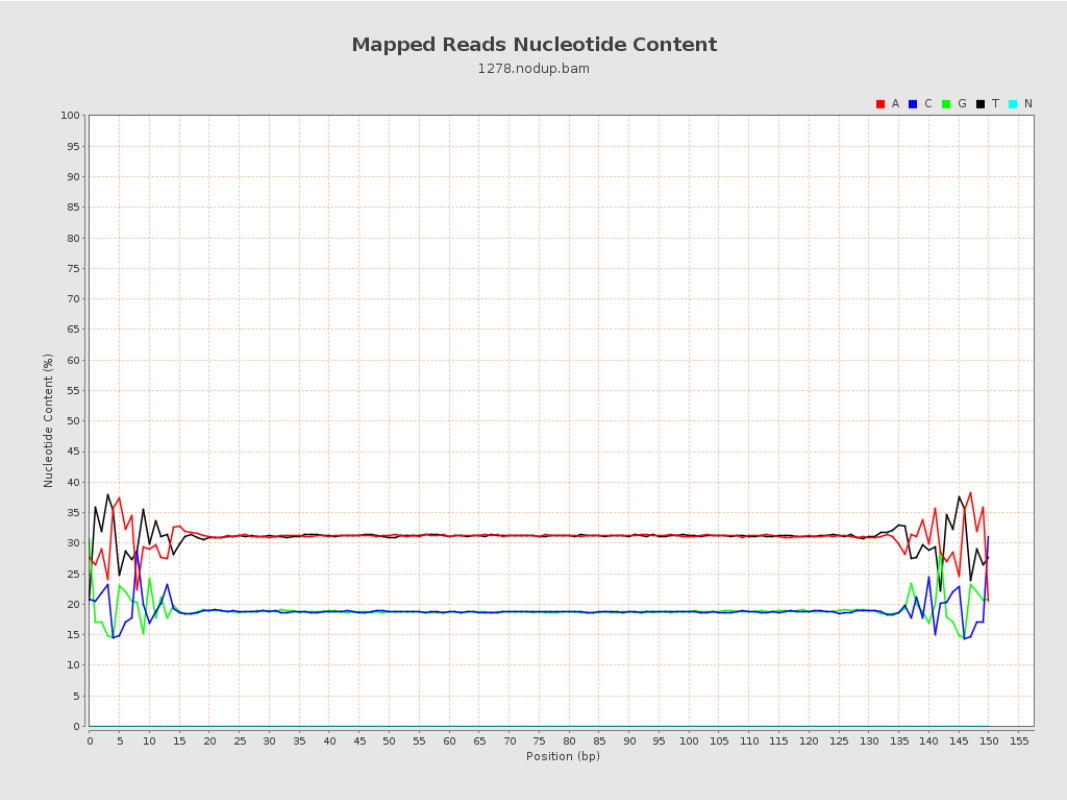
6. Results : Genome Fraction Coverage



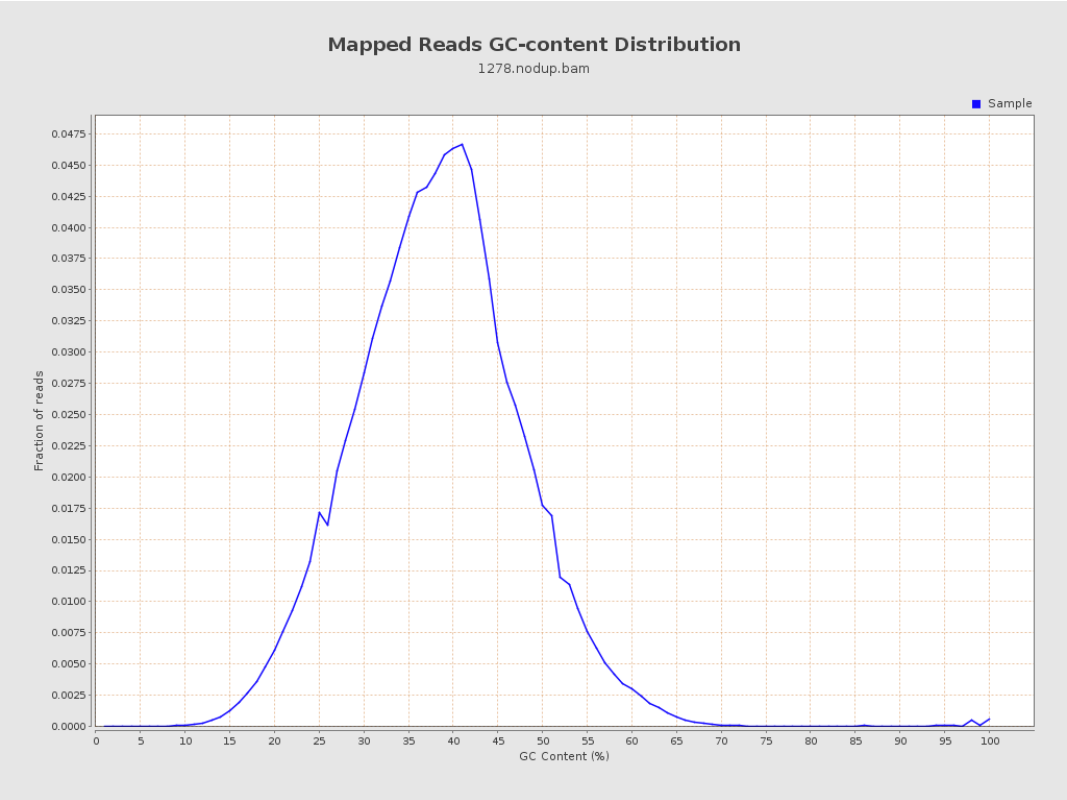
7. Results : Duplication Rate Histogram



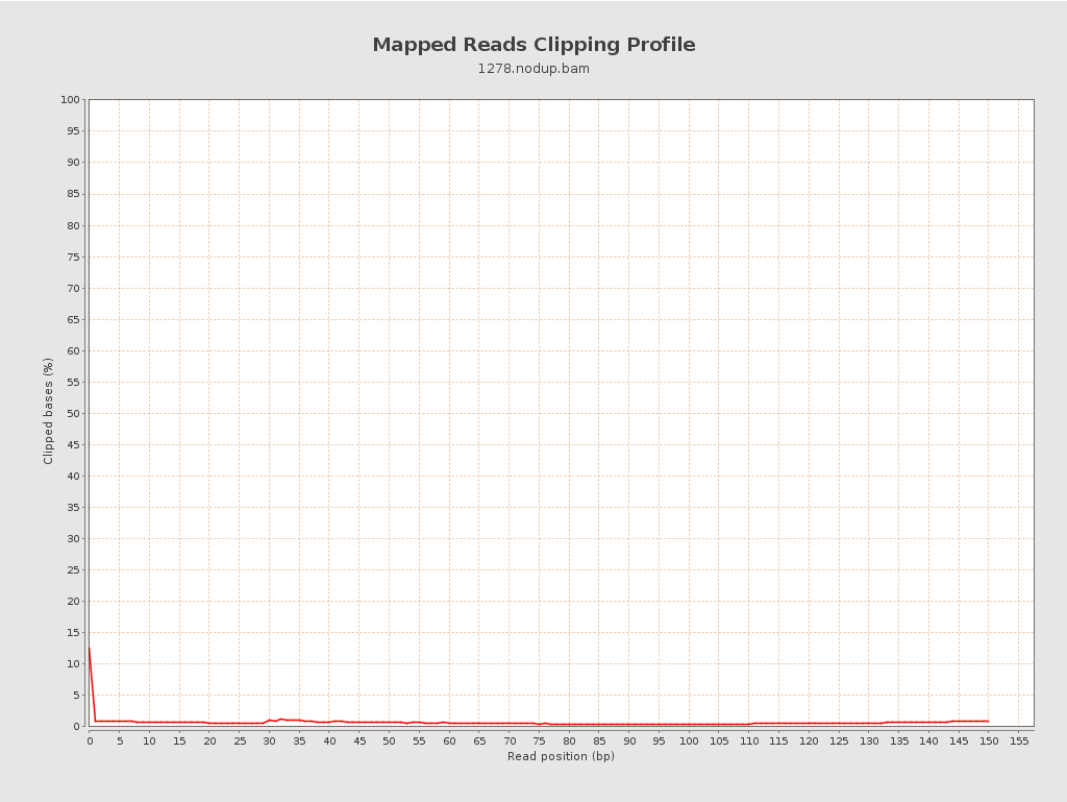
8. Results : Mapped Reads Nucleotide Content



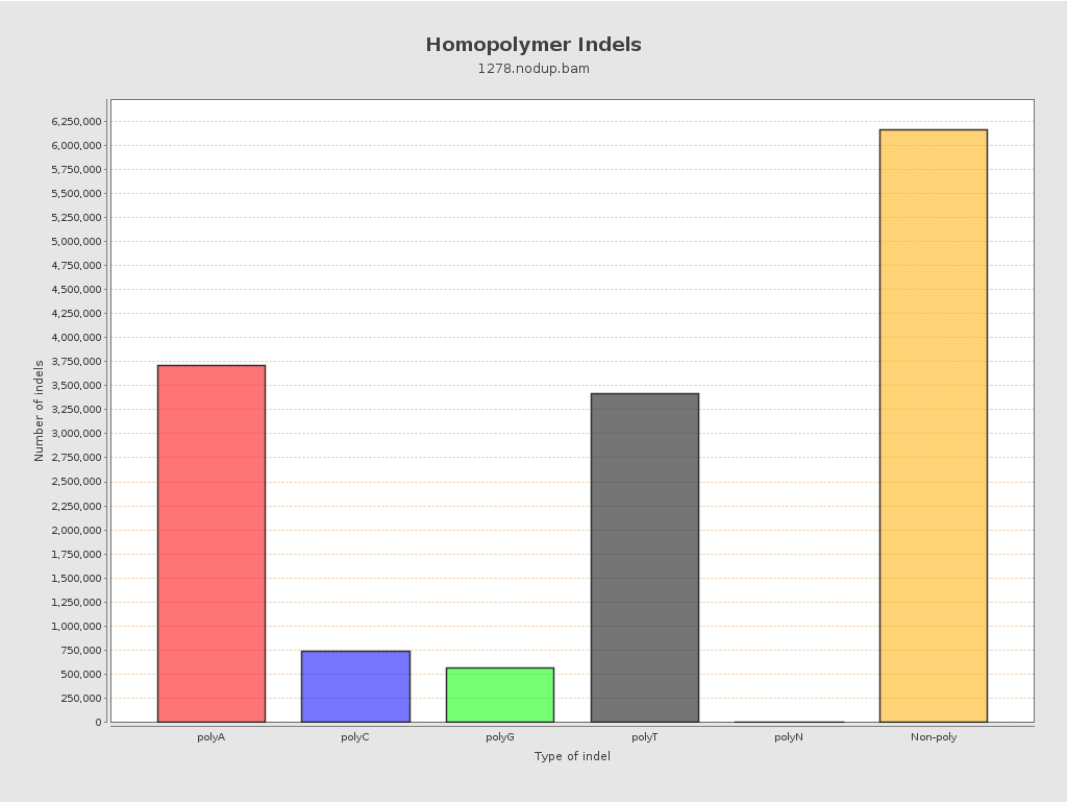
9. Results : Mapped Reads GC-content Distribution



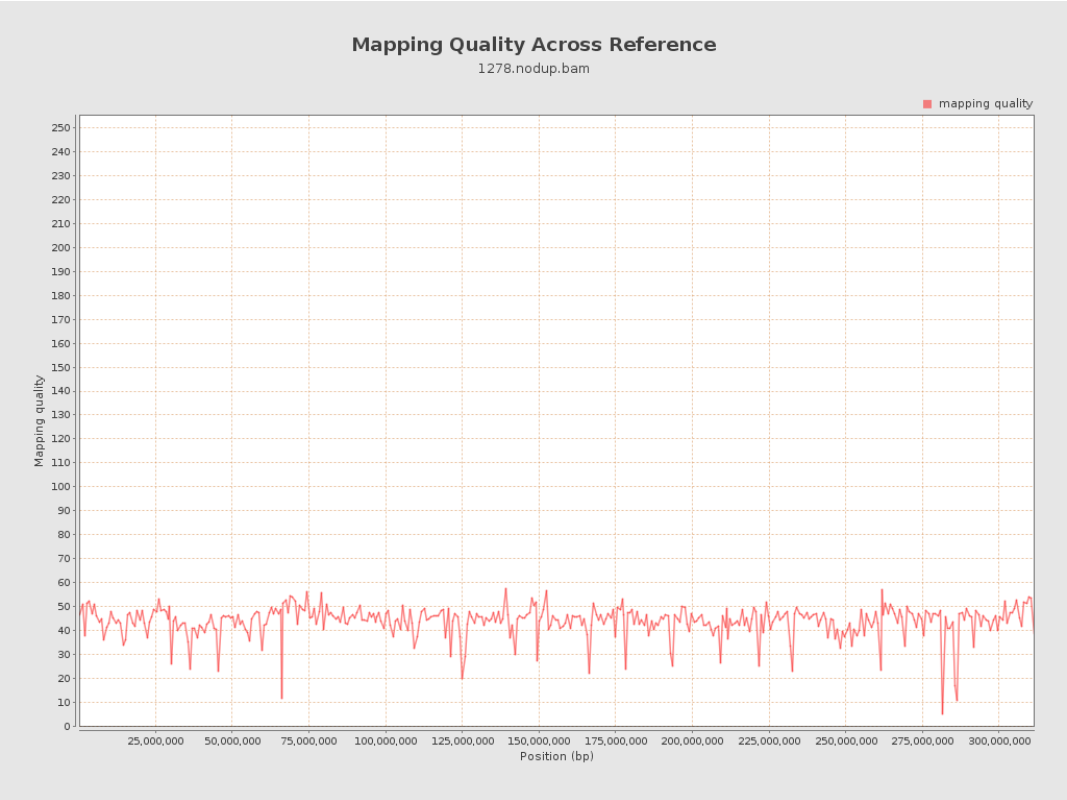
10. Results : Mapped Reads Clipping Profile



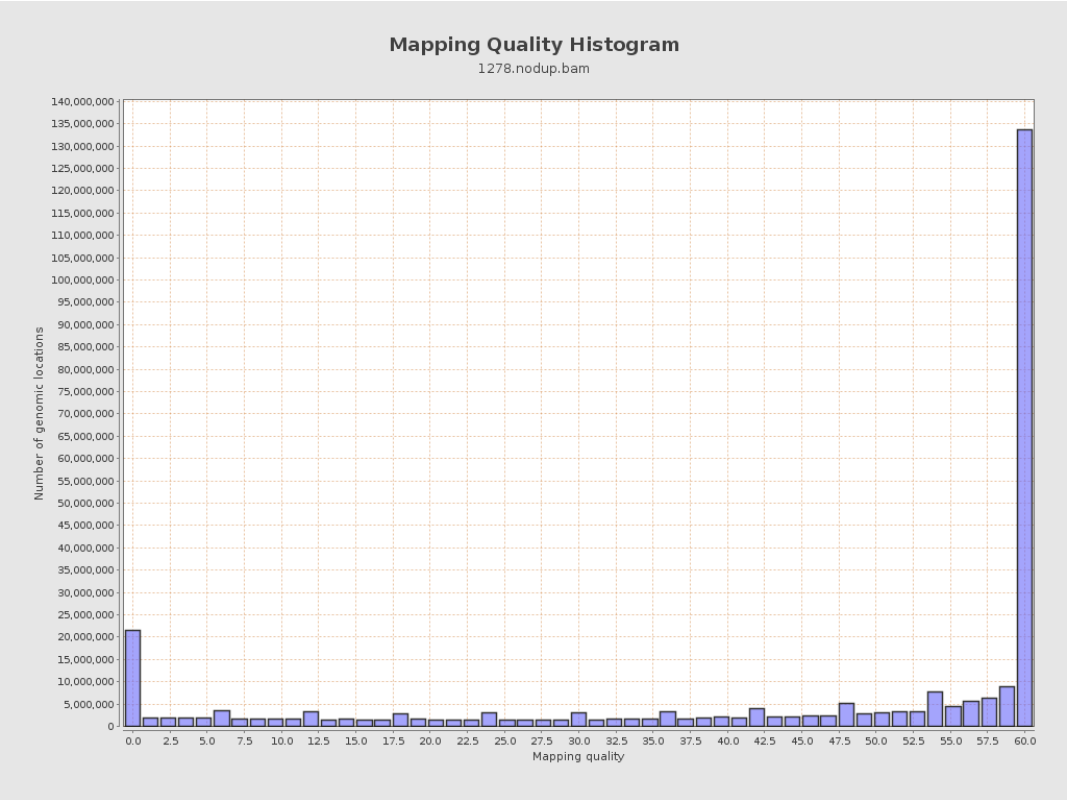
11. Results : Homopolymer Indels



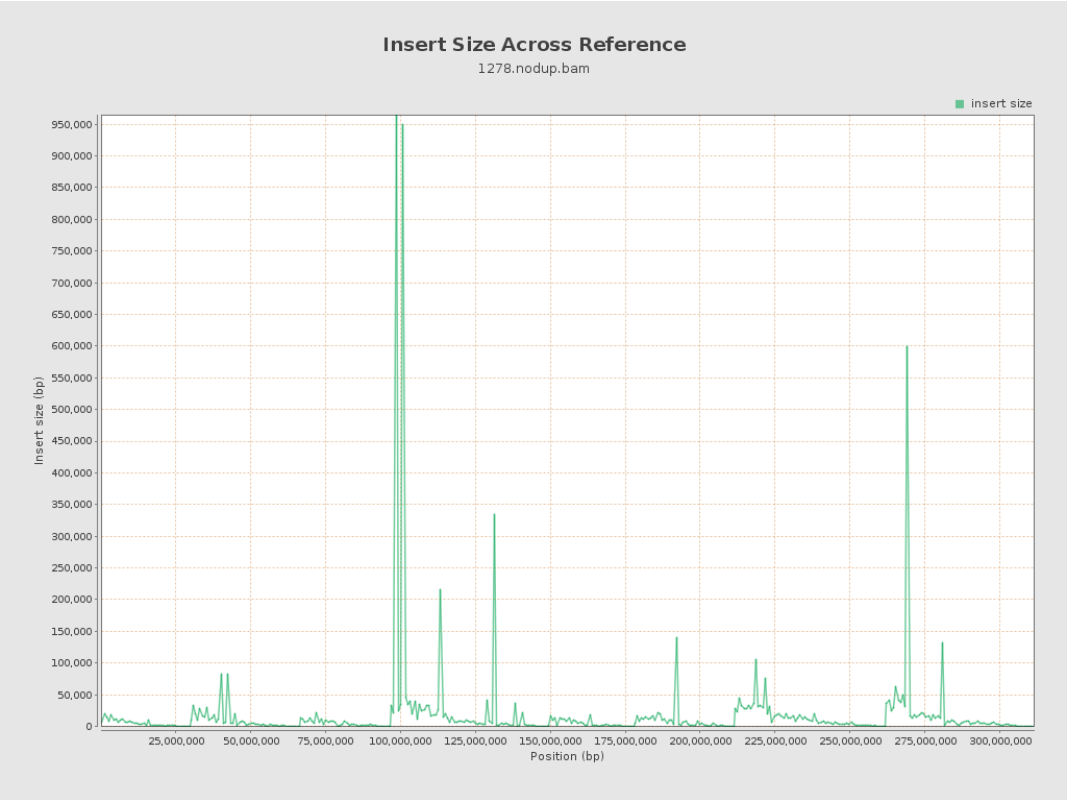
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram