Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:19:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1429
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1429 .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_482/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_482_S457_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_482/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_482_S457_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:19:25 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	29,868,421
Mapped reads	28,363,495 / 94.96%
Unmapped reads	1,504,926 / 5.04%
Mapped paired reads	28,363,495 / 94.96%
Mapped reads, first in pair	14,229,329 / 47.64%
Mapped reads, second in pair	14,134,166 / 47.32%
Mapped reads, both in pair	27,796,149 / 93.06%
Mapped reads, singletons	567,346 / 1.9%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	3,362,905 / 11.26%
Clipped reads	6,268,215 / 20.99%

2.2. ACGT Content

Number/percentage of A's	1,216,443,325 / 30.86%
Number/percentage of C's	754,327,692 / 19.13%
Number/percentage of T's	1,218,640,335 / 30.91%
Number/percentage of G's	752,884,150 / 19.1%
Number/percentage of N's	13,357 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	12.6827
Standard Deviation	96.0096

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Insert size

Mean	253,657.65
Standard Deviation	2,391,060.44
P25/Median/P75	408 / 532 / 679

2.6. Mismatches and indels

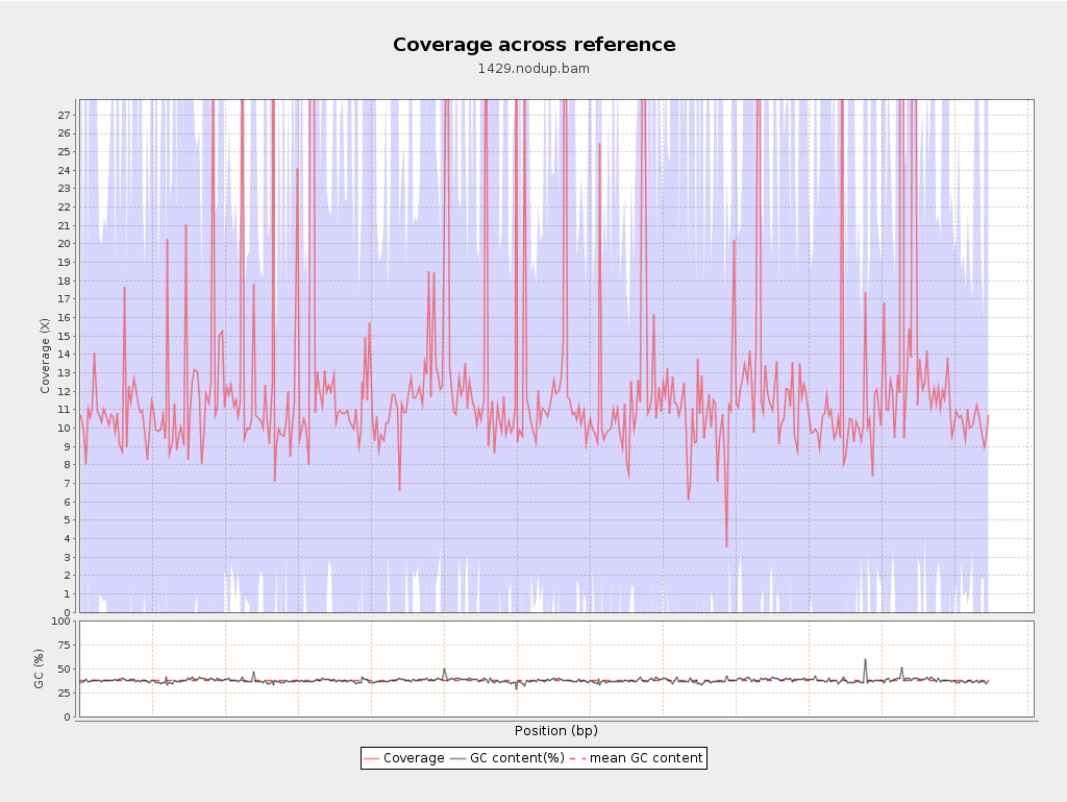
General error rate	2.31%
Mismatches	84,079,163
Insertions	2,567,470
Mapped reads with at least one insertion	8.15%
Deletions	2,670,352
Mapped reads with at least one deletion	8.36%
Homopolymer indels	56.06%

2.7. Chromosome stats

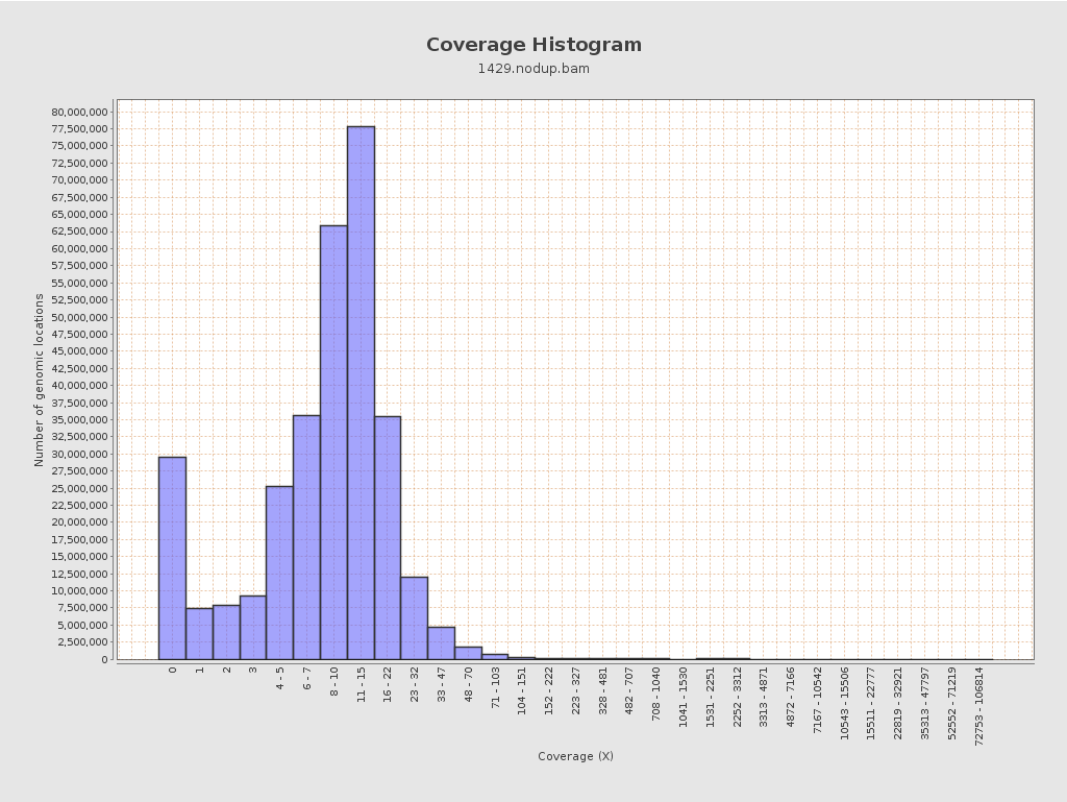
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	318890013	10.7282	26.1899

LT669789.1	36598175	458340916	12.5236	92.1679
LT669790.1	30422129	401787793	13.2071	83.1069
LT669791.1	52758100	654897389	12.4132	76.1545
LT669792.1	28376109	354300312	12.4859	104.9509
LT669793.1	33388210	399199515	11.9563	70.3452
LT669794.1	50579949	609644244	12.0531	84.6568
LT669795.1	49795044	755417717	15.1705	154.2352

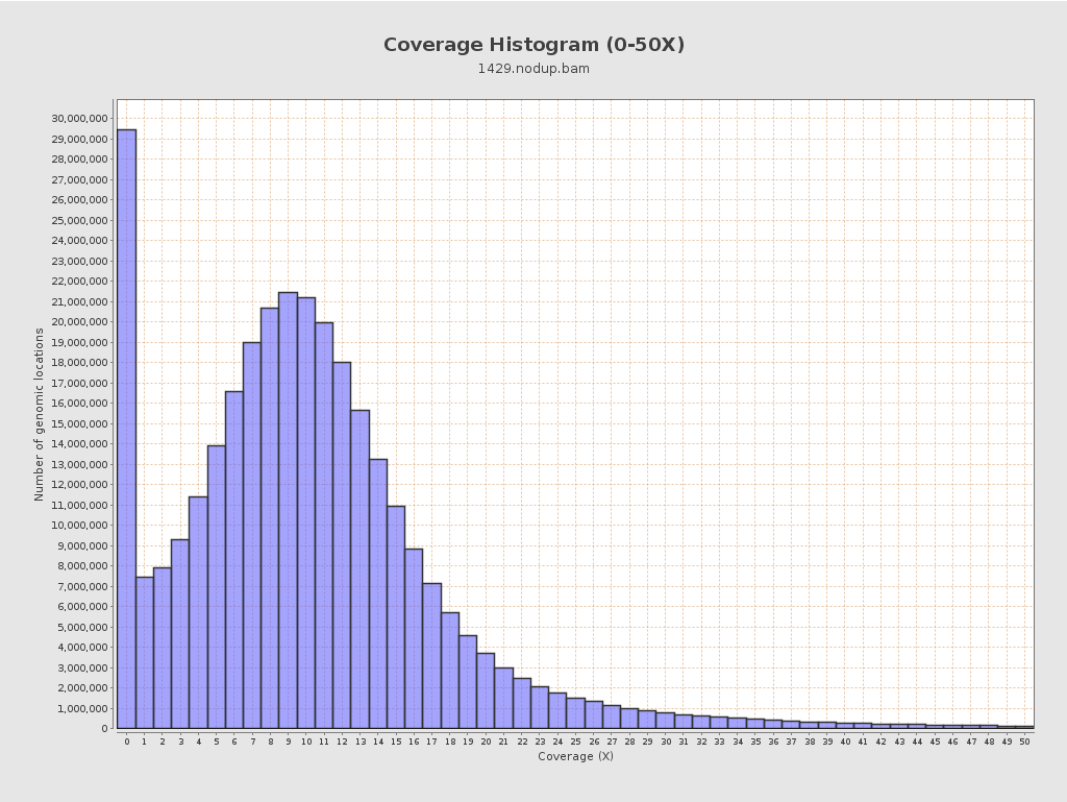
3. Results : Coverage across reference



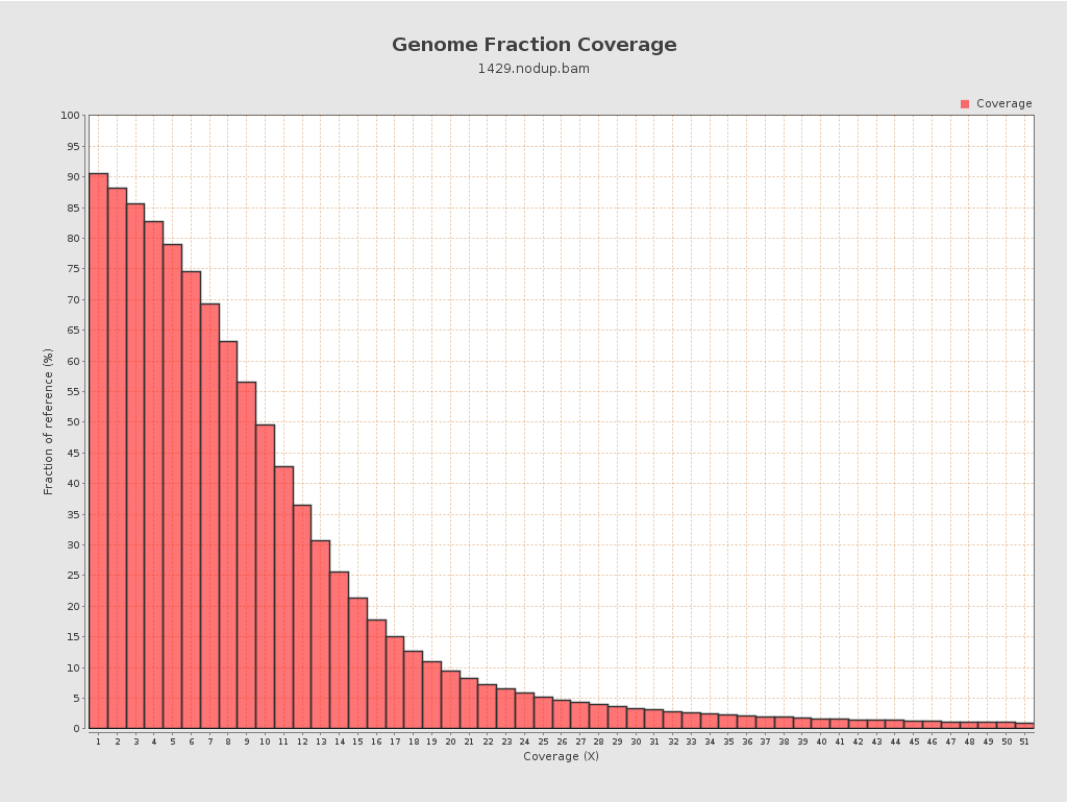
4. Results : Coverage Histogram



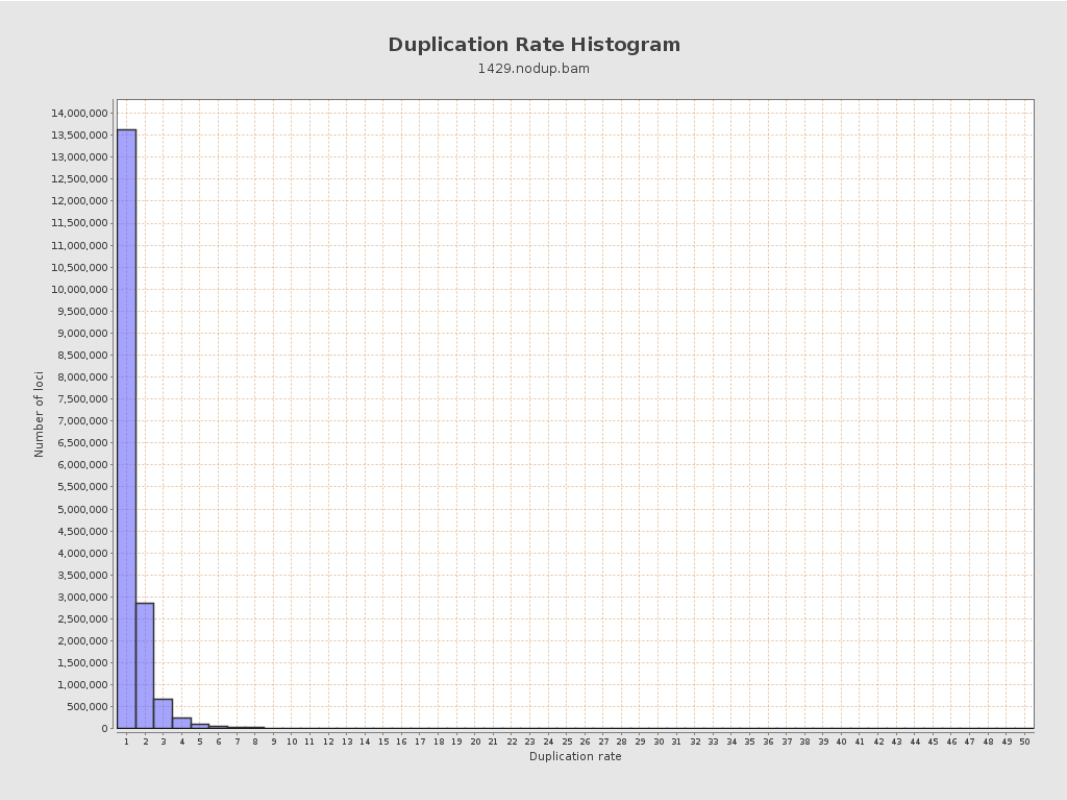
5. Results : Coverage Histogram (0-50X)



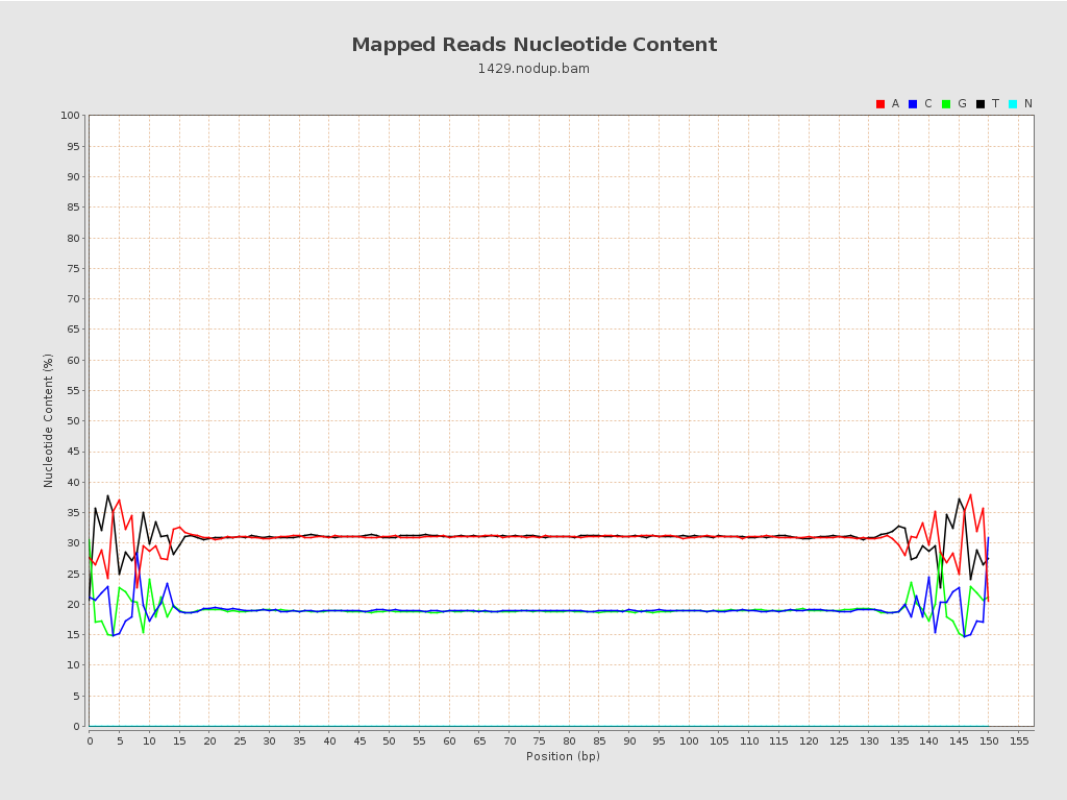
6. Results : Genome Fraction Coverage



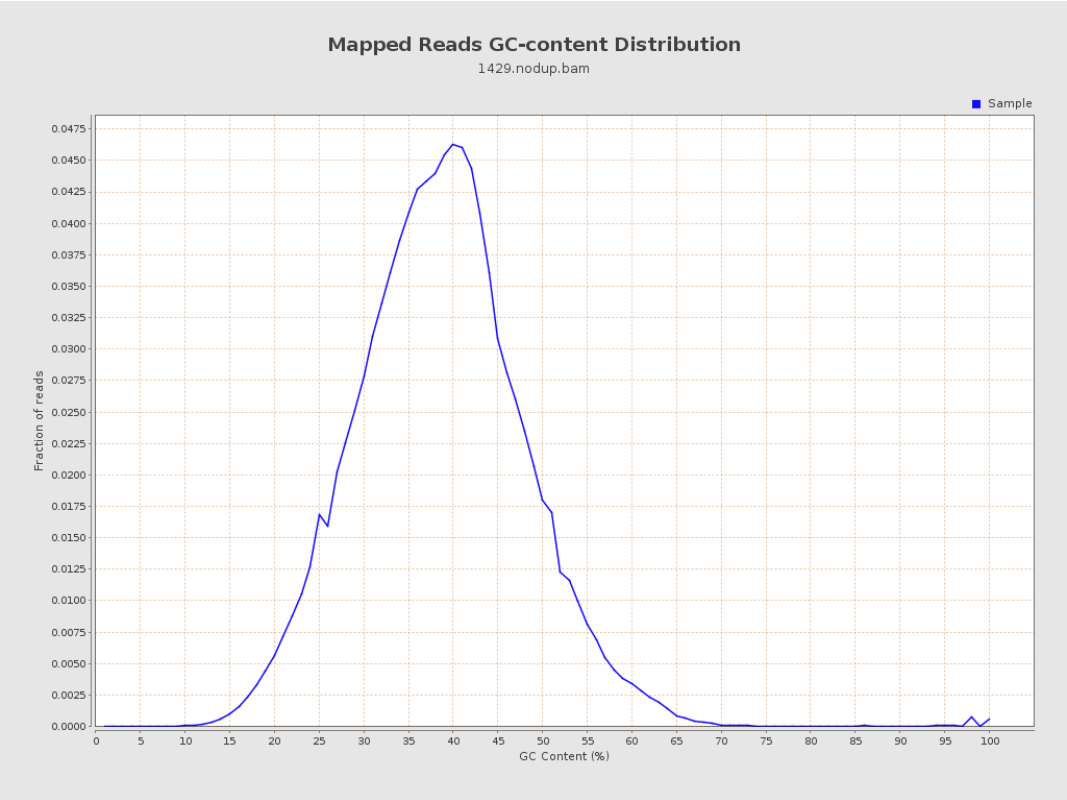
7. Results : Duplication Rate Histogram



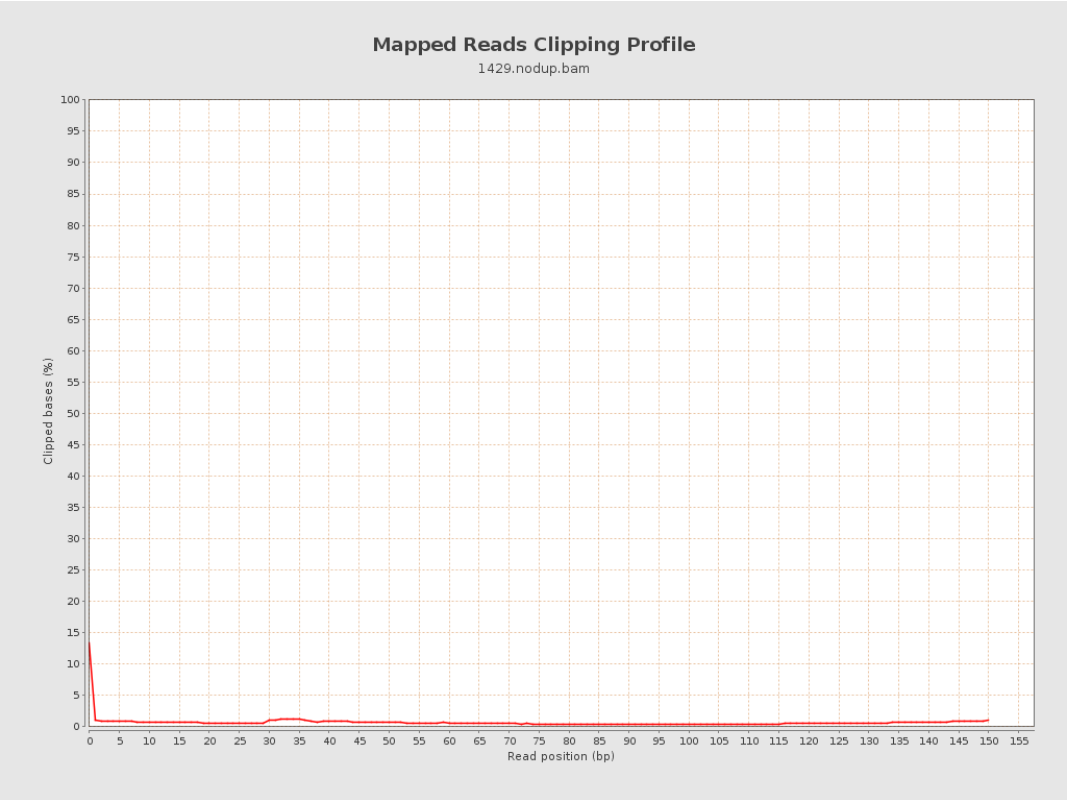
8. Results : Mapped Reads Nucleotide Content



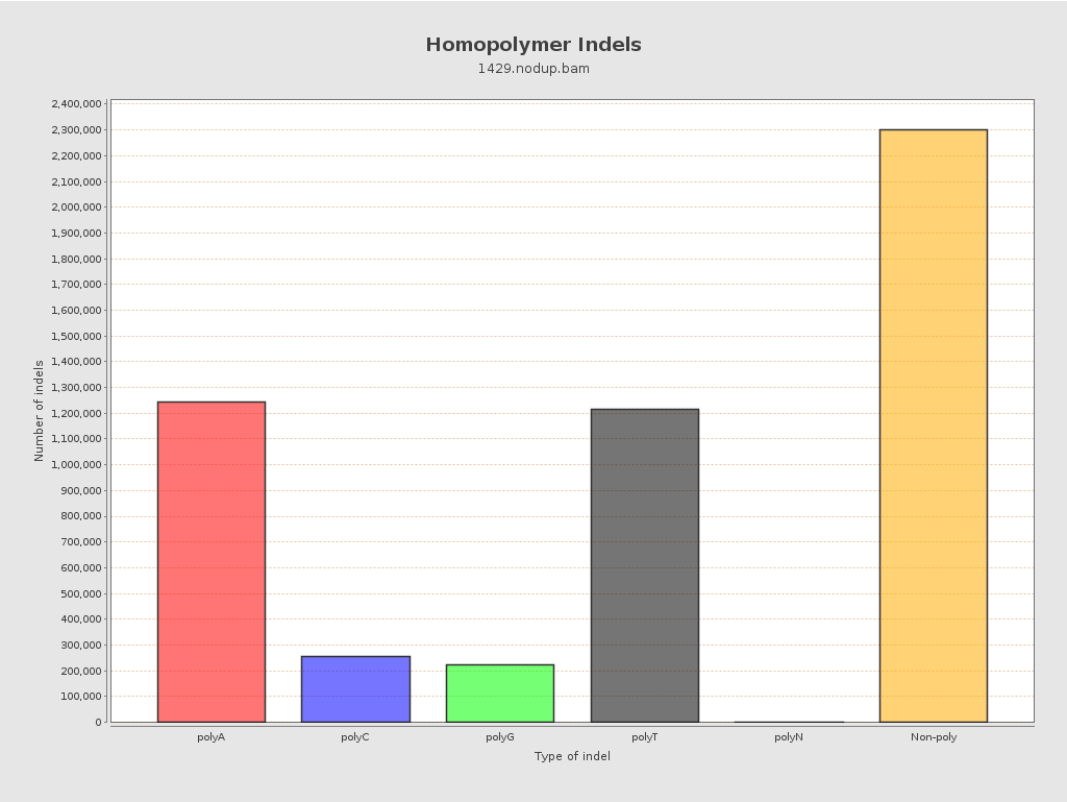
9. Results : Mapped Reads GC-content Distribution



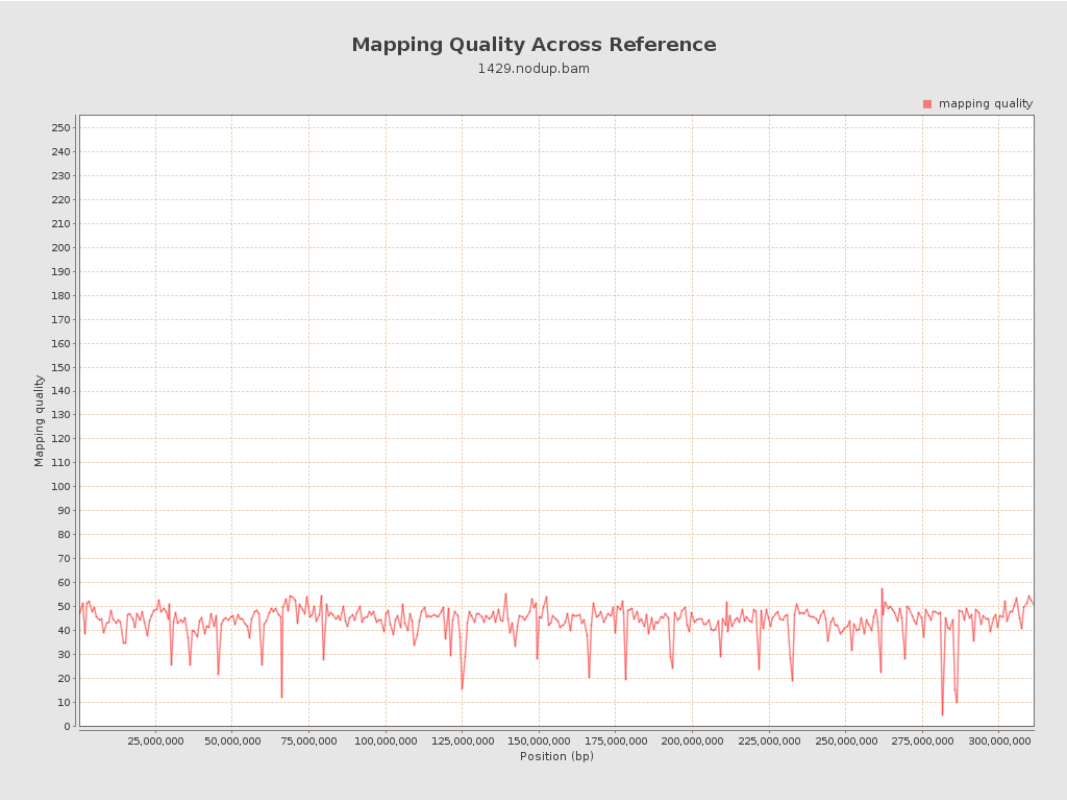
10. Results : Mapped Reads Clipping Profile



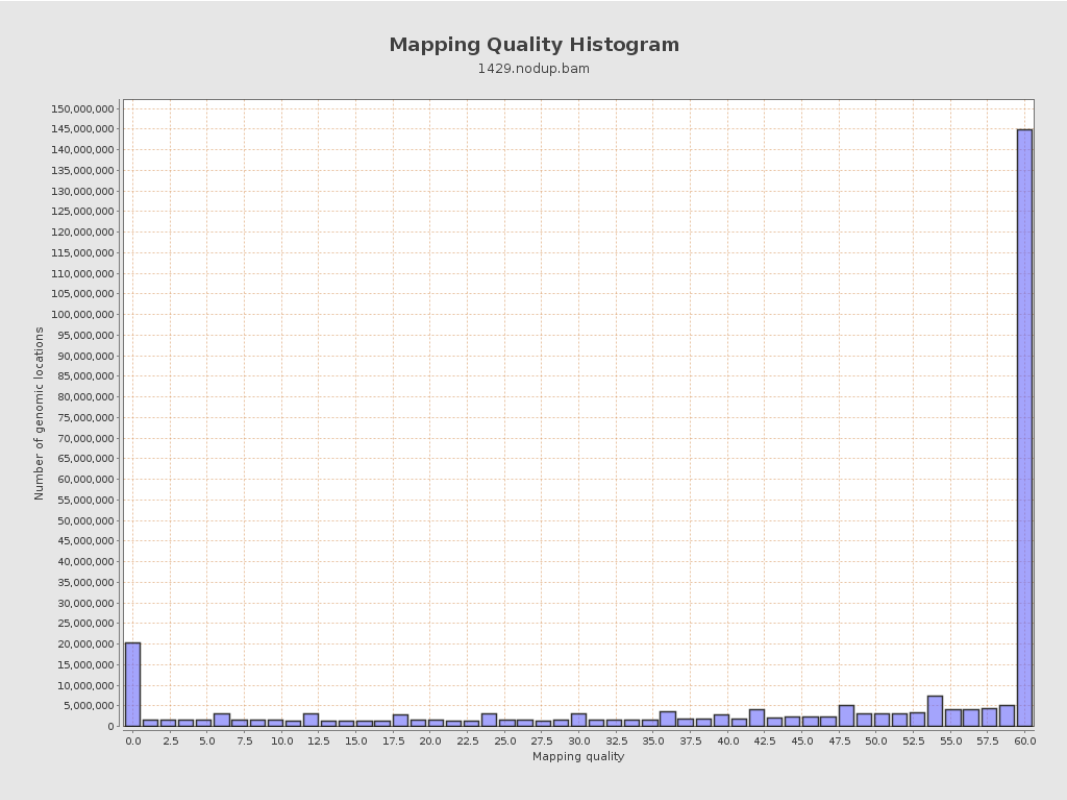
11. Results : Homopolymer Indels



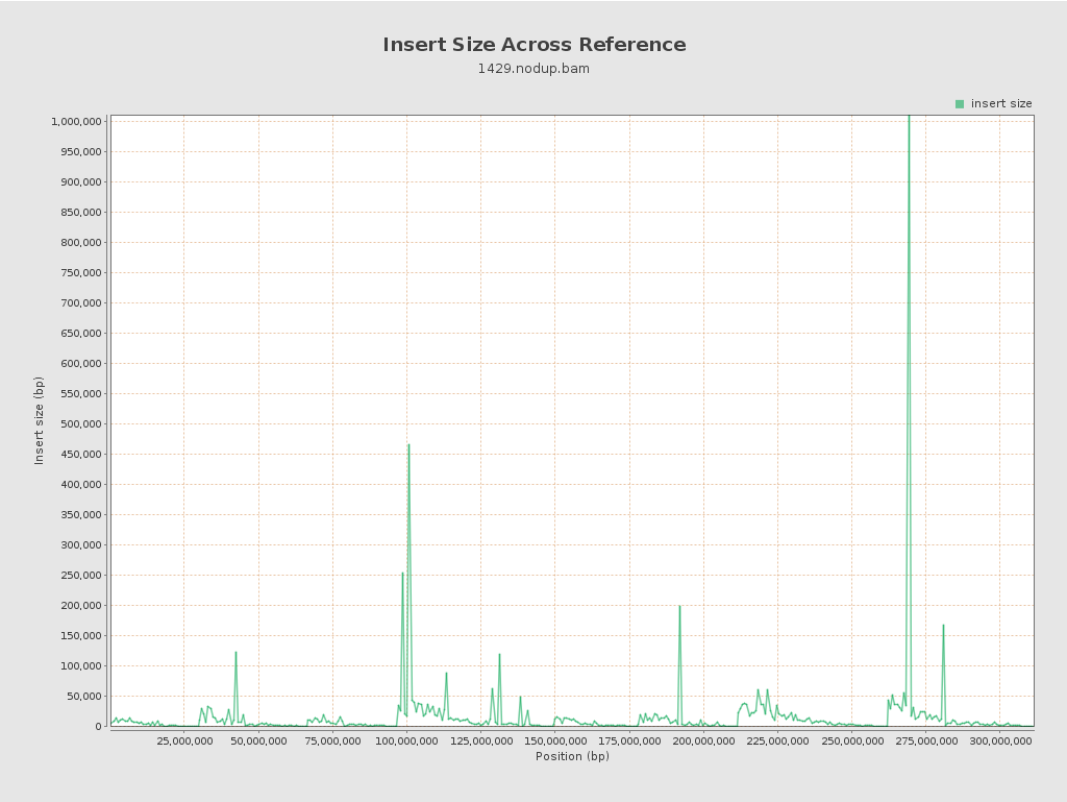
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram