Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1469
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1469 .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_492/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_492_S467_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_492/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_492_S467_L004_R2_001.fastq.gz
Size of a homopolymer:	3

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	60,577,339
Mapped reads	56,417,013 / 93.13%
Unmapped reads	4,160,326 / 6.87%
Mapped paired reads	56,417,013 / 93.13%
Mapped reads, first in pair	28,272,164 / 46.67%
Mapped reads, second in pair	28,144,849 / 46.46%
Mapped reads, both in pair	54,969,969 / 90.74%
Mapped reads, singletons	1,447,044 / 2.39%
Read min/max/mean length	30 / 151 / 148.29
Duplicated reads (flagged)	8,718,037 / 14.39%
Clipped reads	12,007,493 / 19.82%

2.2. ACGT Content

Number/percentage of A's	2,423,953,157 / 30.86%
Number/percentage of C's	1,502,907,720 / 19.14%
Number/percentage of T's	2,428,584,542 / 30.92%
Number/percentage of G's	1,498,456,040 / 19.08%
Number/percentage of N's	26,836 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	25.266
Standard Deviation	204.996

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Insert size

Mean	245,888.89
Standard Deviation	2,379,649.34
P25/Median/P75	351 / 456 / 599

2.6. Mismatches and indels

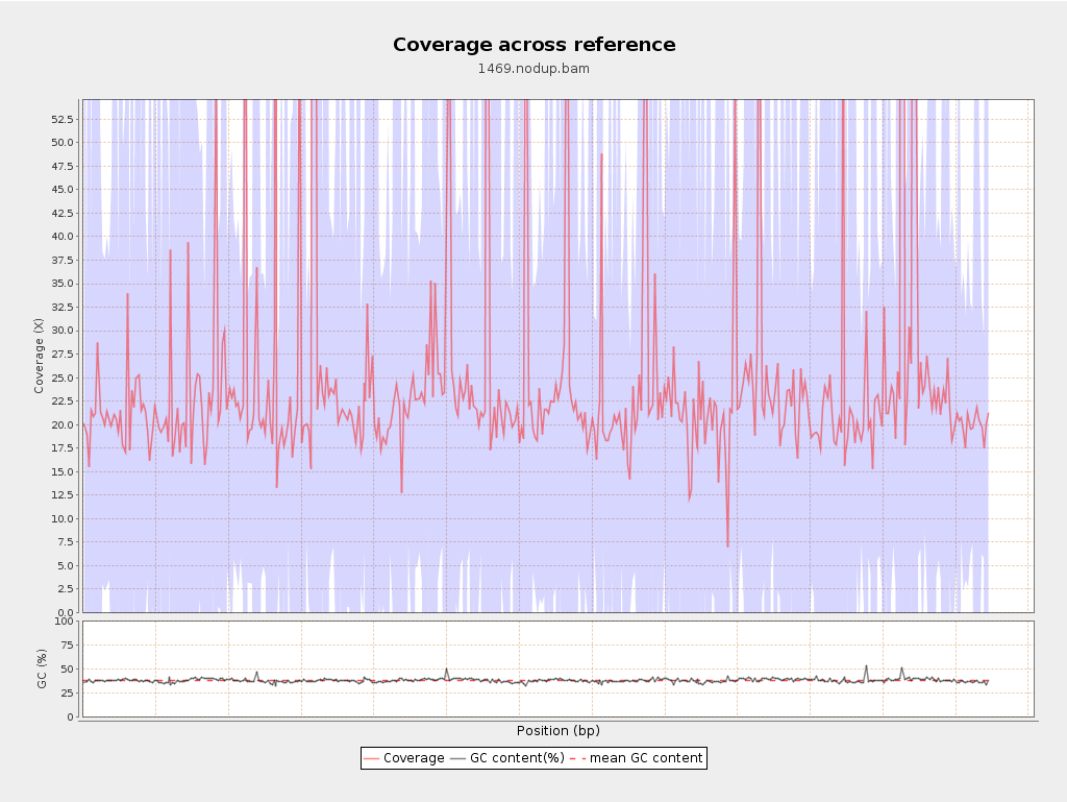
General error rate	2.3%
Mismatches	165,491,047
Insertions	5,368,309
Mapped reads with at least one insertion	8.52%
Deletions	5,313,714
Mapped reads with at least one deletion	8.35%
Homopolymer indels	56.87%

2.7. Chromosome stats

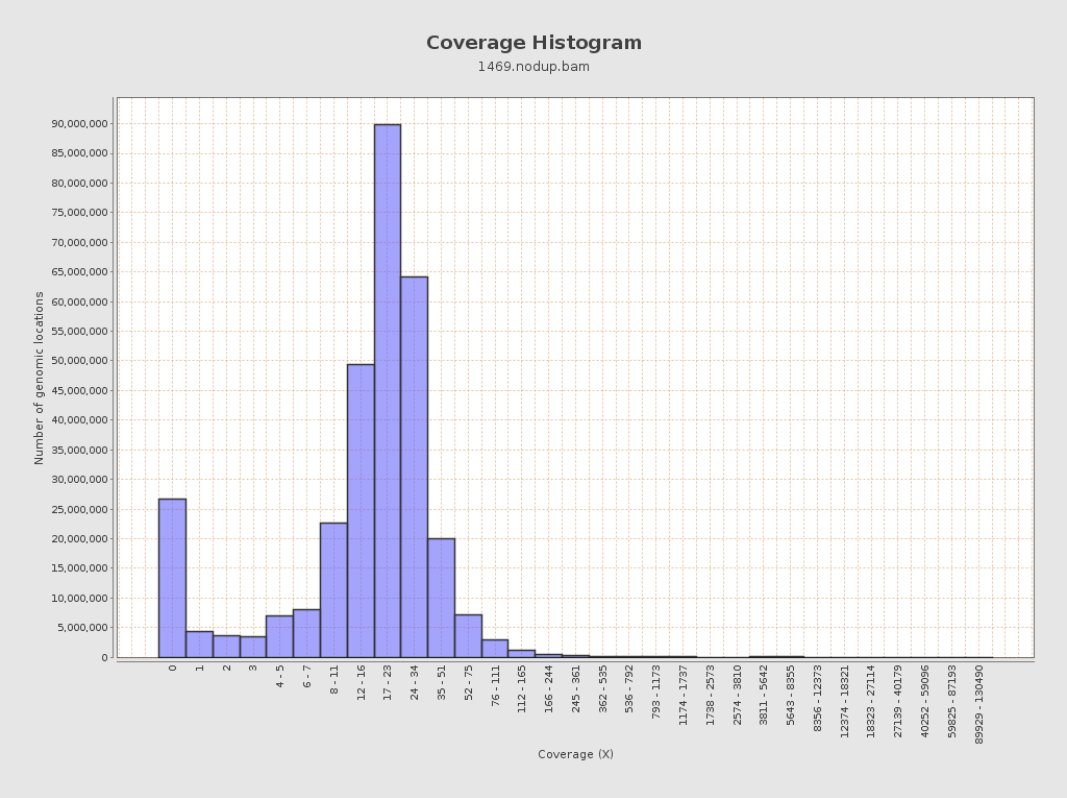
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	622137566	20.9302	73.1791

LT669789.1	36598175	914553441	24.989	222.5965
LT669790.1	30422129	874649007	28.7504	261.269
LT669791.1	52758100	1315317425	24.9311	200.3235
LT669792.1	28376109	703000329	24.7744	205.2781
LT669793.1	33388210	775371380	23.2229	139.1685
LT669794.1	50579949	1199741162	23.7197	172.3829
LT669795.1	49795044	1469182351	29.5046	268.2186

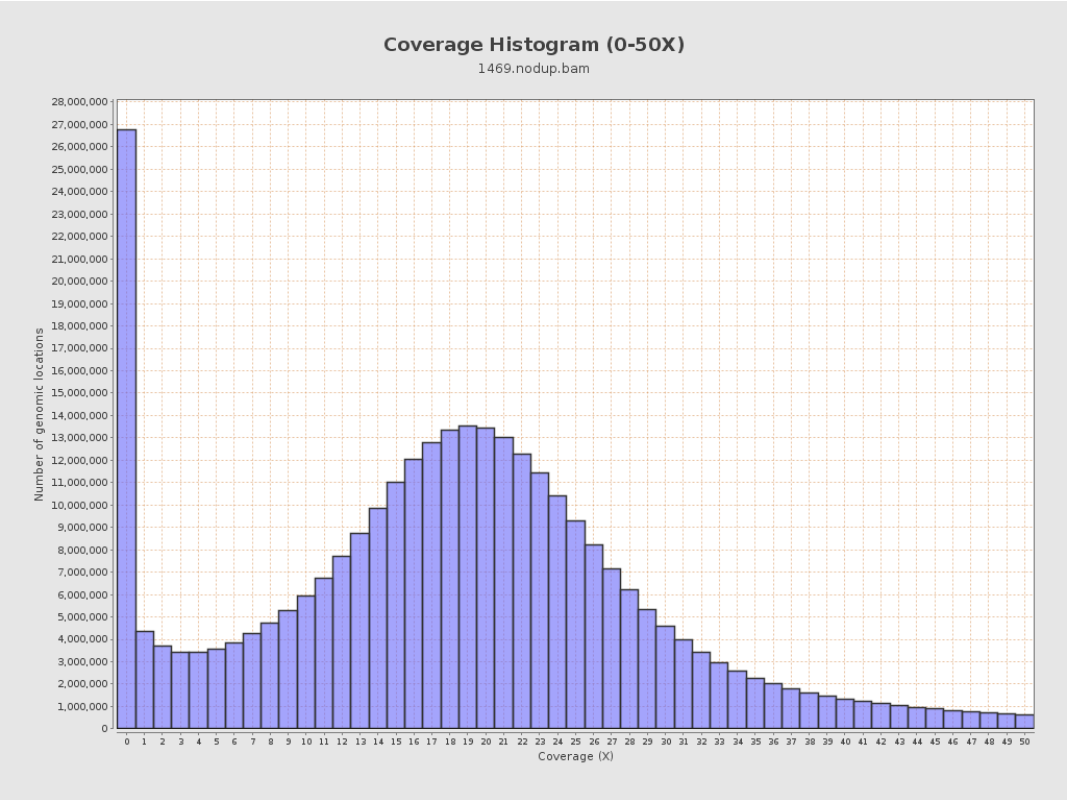
3. Results : Coverage across reference



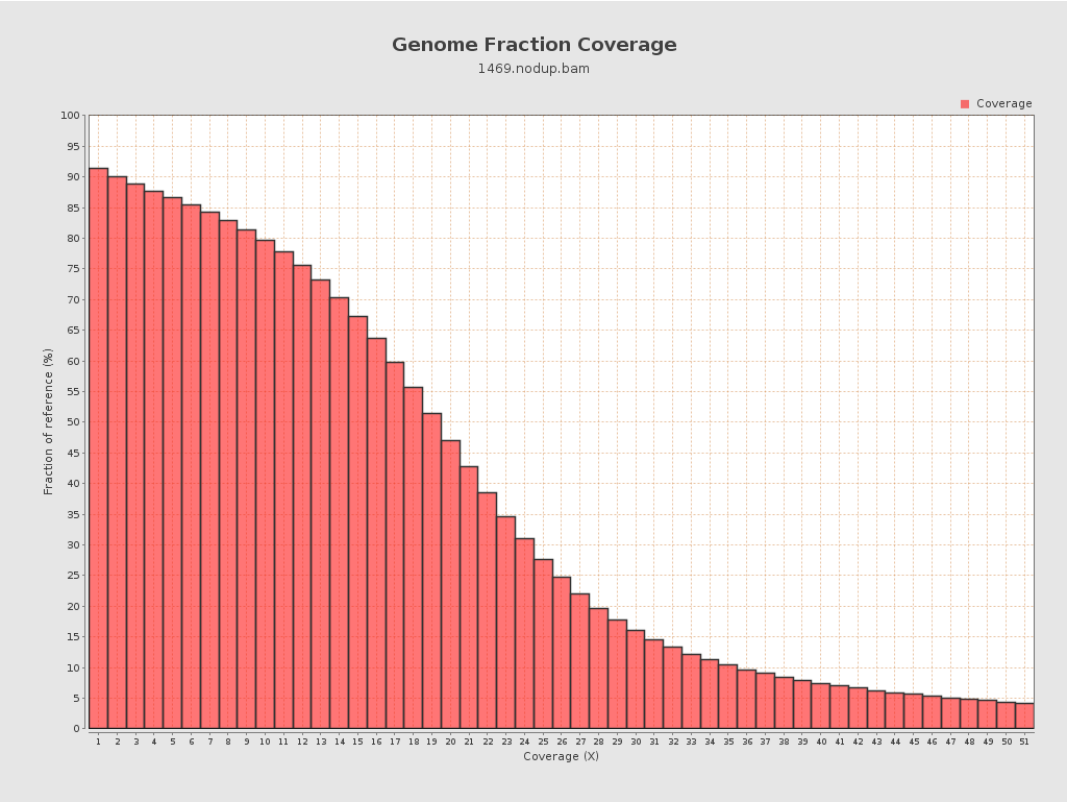
4. Results : Coverage Histogram



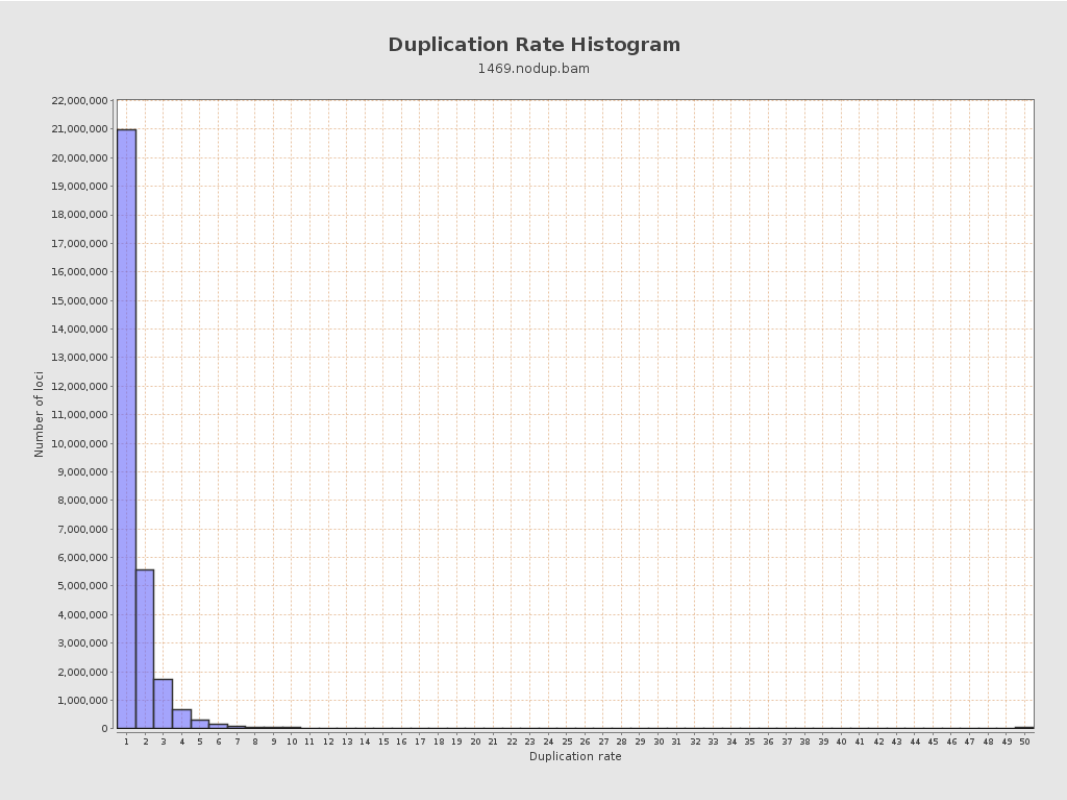
5. Results : Coverage Histogram (0-50X)



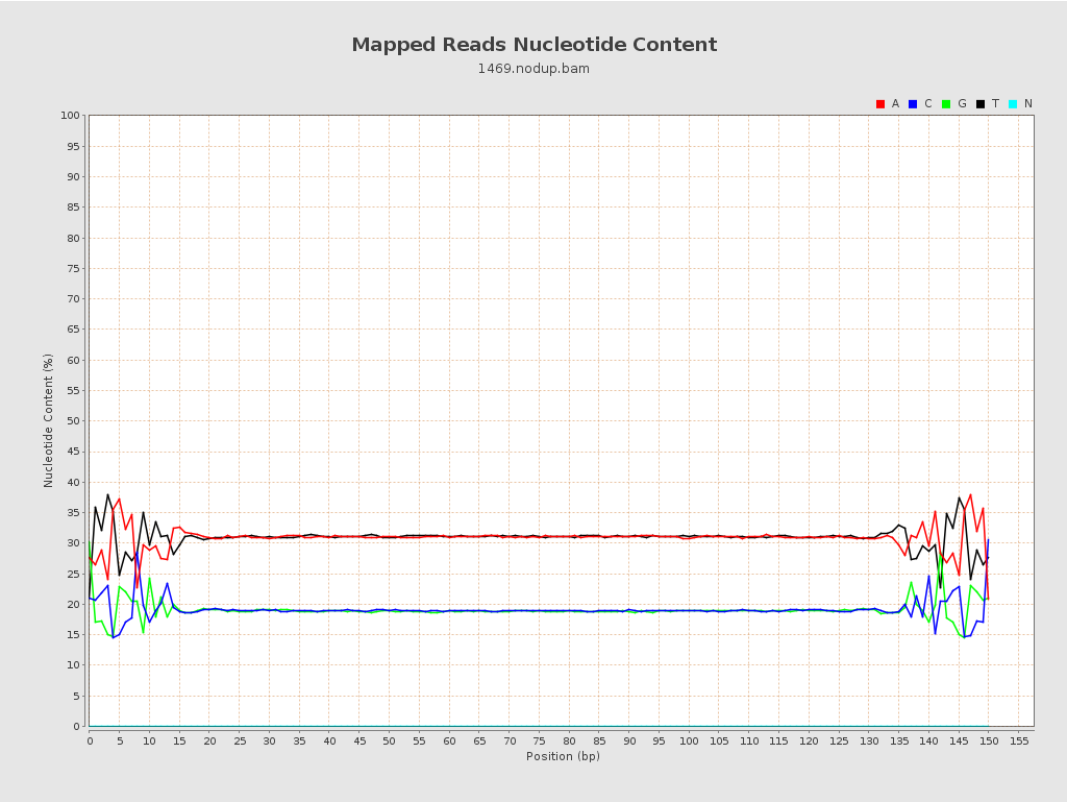
6. Results : Genome Fraction Coverage



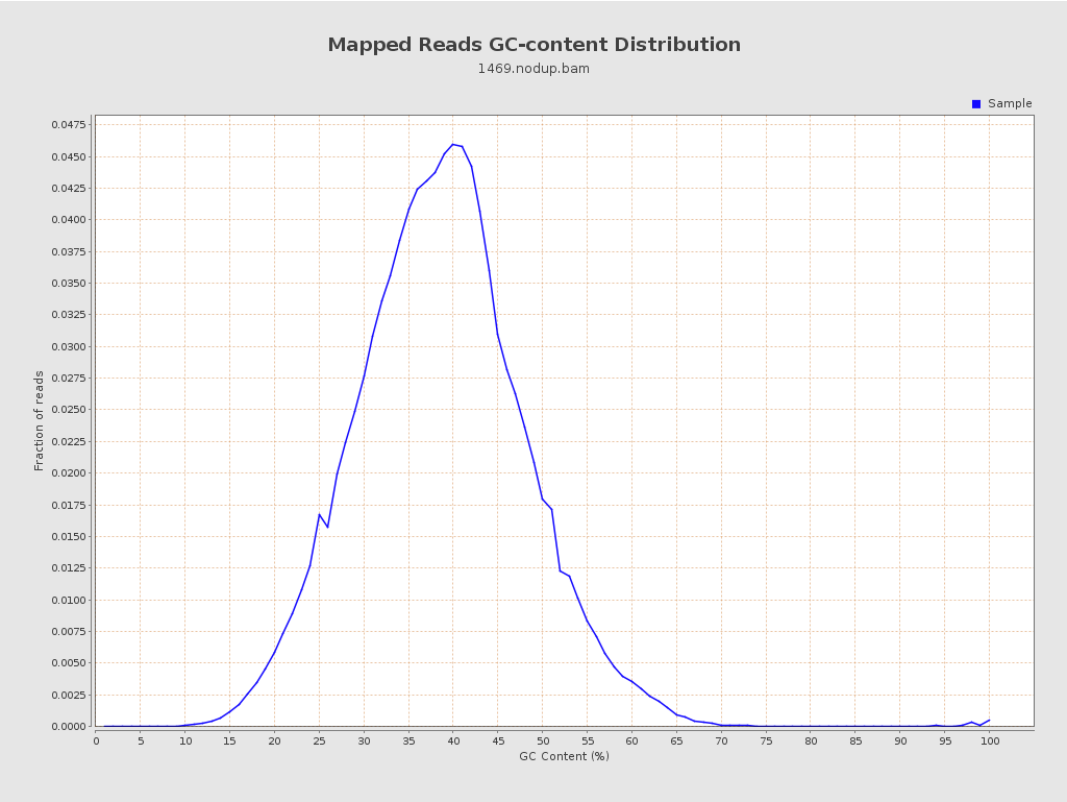
7. Results : Duplication Rate Histogram



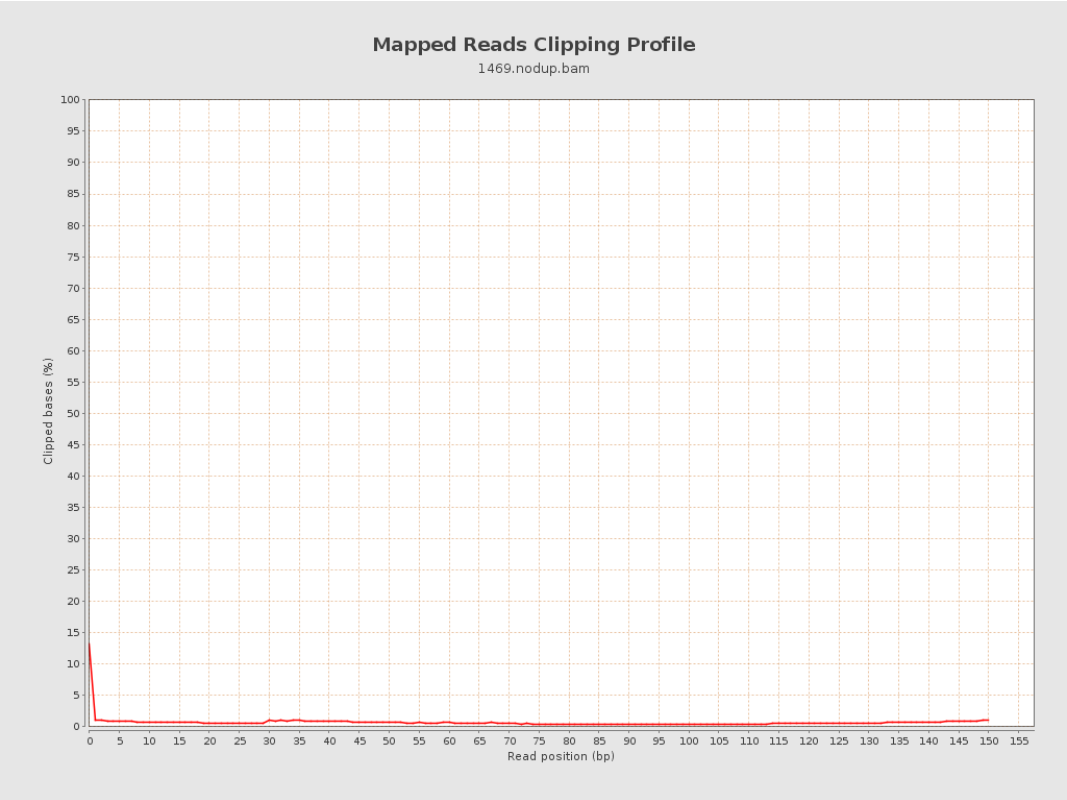
8. Results : Mapped Reads Nucleotide Content



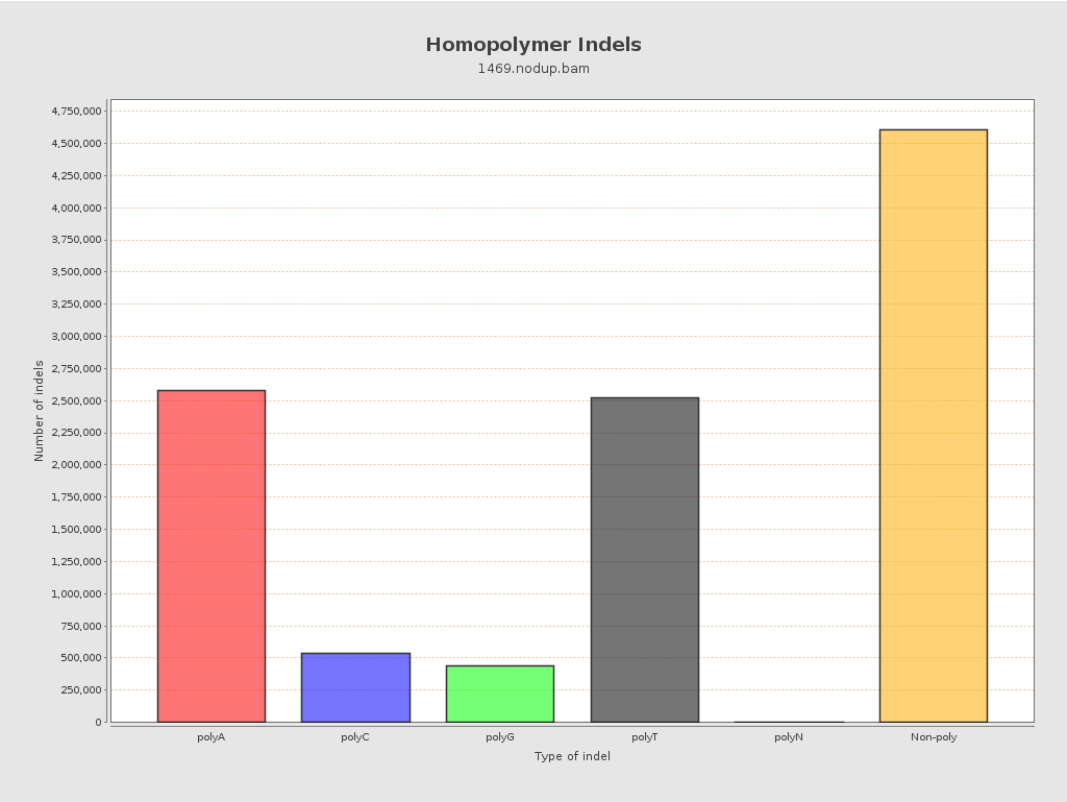
9. Results : Mapped Reads GC-content Distribution



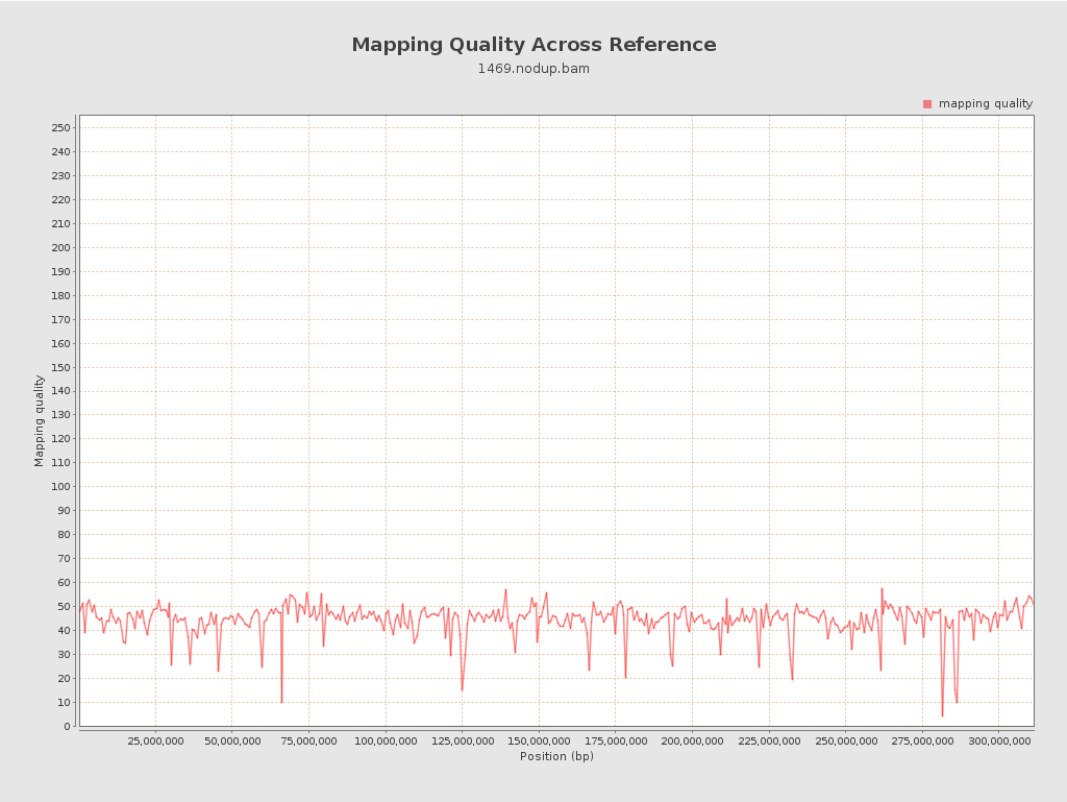
10. Results : Mapped Reads Clipping Profile



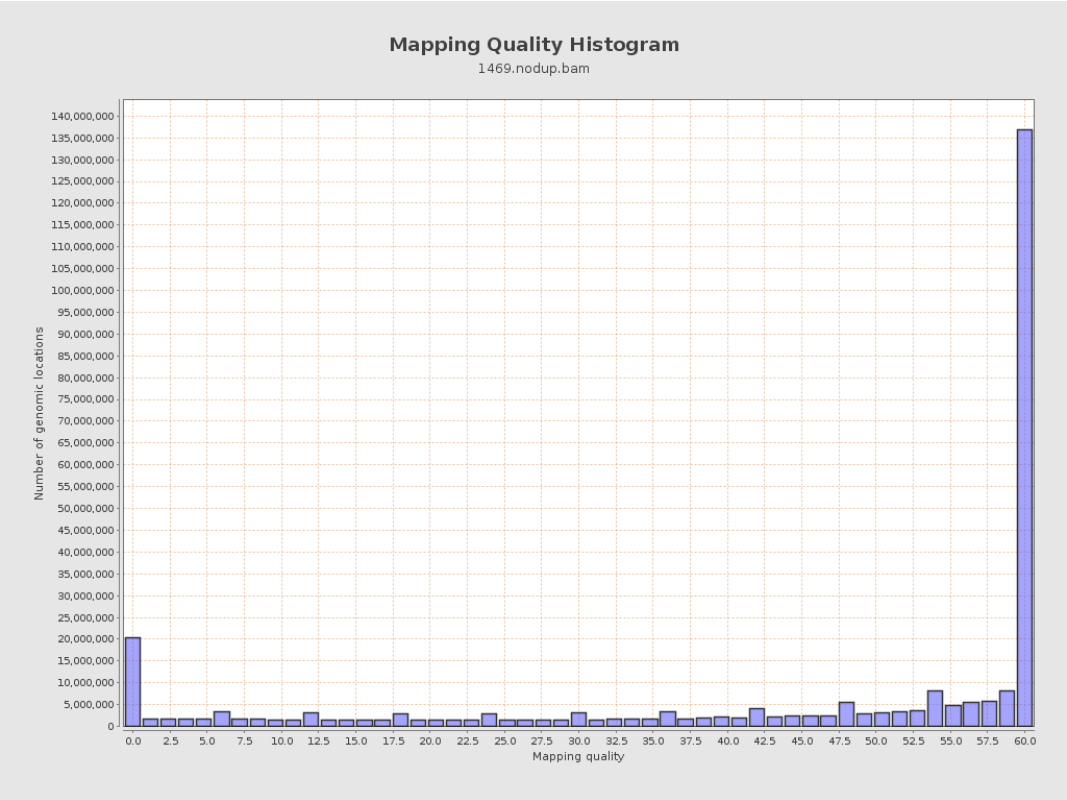
11. Results : Homopolymer Indels



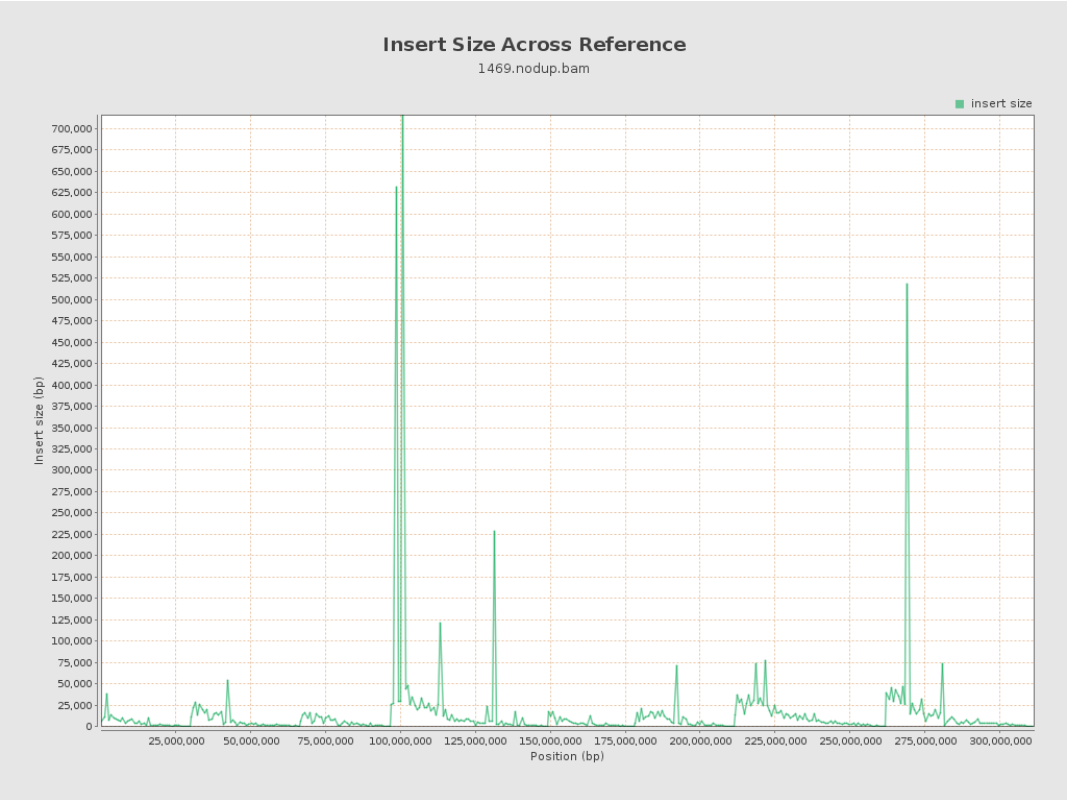
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram