Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1174
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1174 .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_578/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_578_S145_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_578/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_578_S145_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:23:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	44,293,879
Mapped reads	40,664,393 / 91.81%
Unmapped reads	3,629,486 / 8.19%
Mapped paired reads	40,664,393 / 91.81%
Mapped reads, first in pair	20,408,156 / 46.07%
Mapped reads, second in pair	20,256,237 / 45.73%
Mapped reads, both in pair	39,475,568 / 89.12%
Mapped reads, singletons	1,188,825 / 2.68%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	6,729,796 / 15.19%
Clipped reads	10,076,058 / 22.75%

2.2. ACGT Content

Number/percentage of A's	1,720,321,651 / 30.89%
Number/percentage of C's	1,064,096,063 / 19.11%
Number/percentage of T's	1,722,741,031 / 30.94%
Number/percentage of G's	1,061,555,511 / 19.06%
Number/percentage of N's	41,329 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	17.9132
Standard Deviation	170.1168

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Insert size

Mean	237,485.42
Standard Deviation	2,337,134.37
P25/Median/P75	332 / 435 / 558

2.6. Mismatches and indels

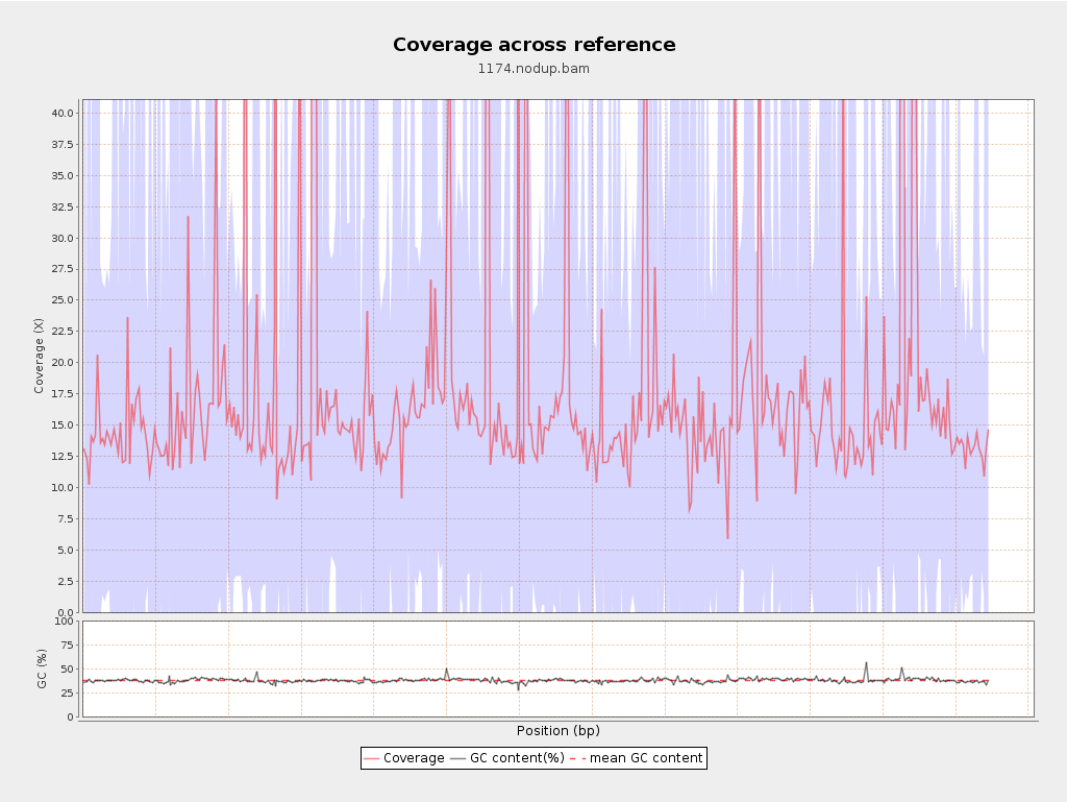
General error rate	2.58%
Mismatches	133,080,561
Insertions	3,907,653
Mapped reads with at least one insertion	8.6%
Deletions	3,748,059
Mapped reads with at least one deletion	8.21%
Homopolymer indels	56.94%

2.7. Chromosome stats

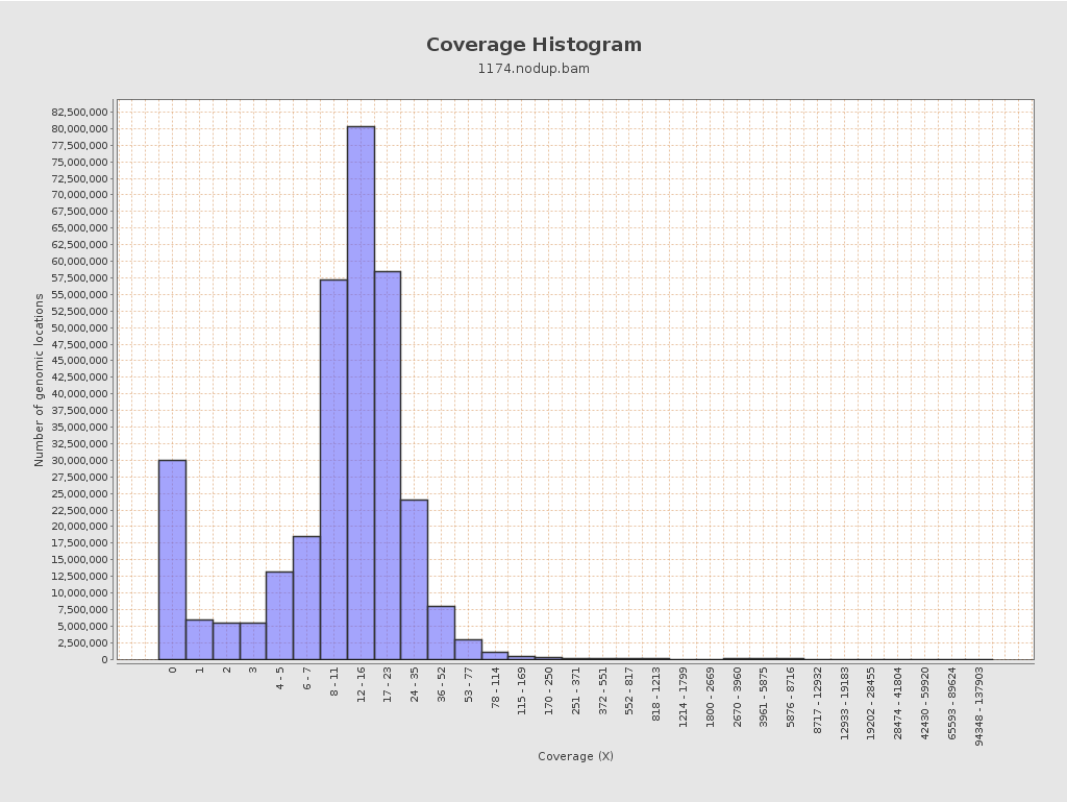
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	420305486	14.1401	61.2499

LT669789.1	36598175	665099067	18.173	181.0085
LT669790.1	30422129	638909623	21.0015	229.6879
LT669791.1	52758100	940096079	17.819	173.2477
LT669792.1	28376109	505589041	17.8174	170.8542
LT669793.1	33388210	543455574	16.2769	112.5158
LT669794.1	50579949	857632163	16.956	143.4086
LT669795.1	49795044	1011431331	20.3119	211.4953

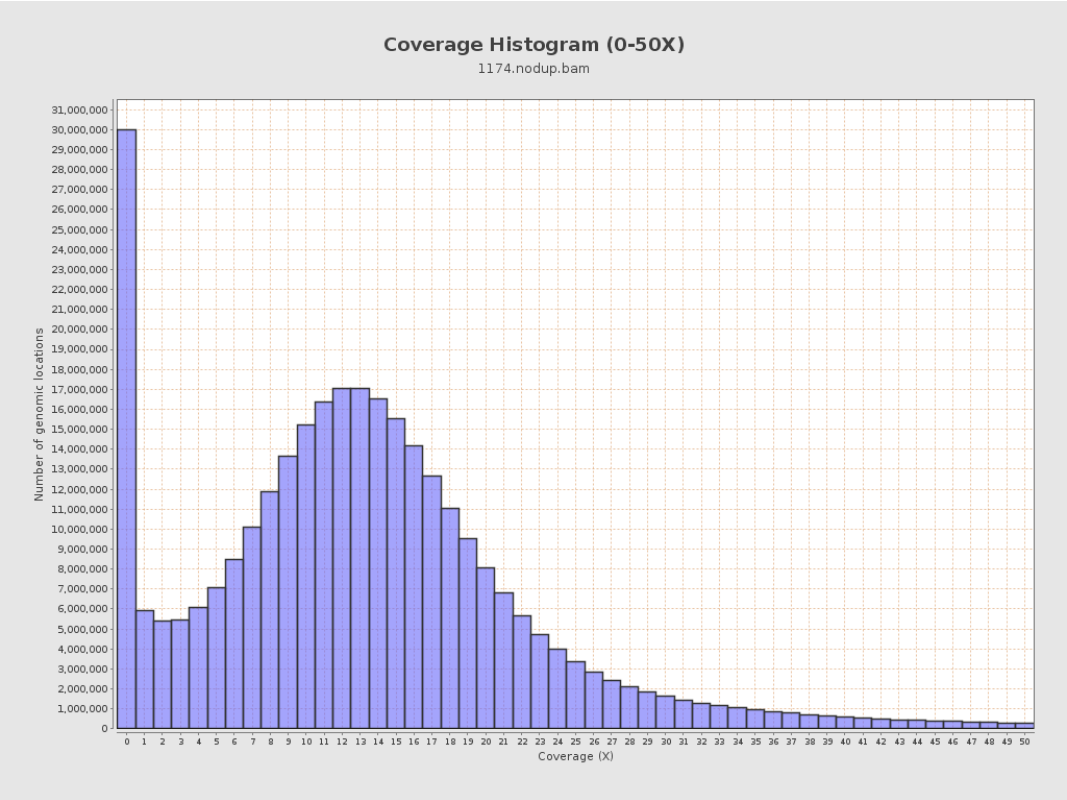
3. Results : Coverage across reference



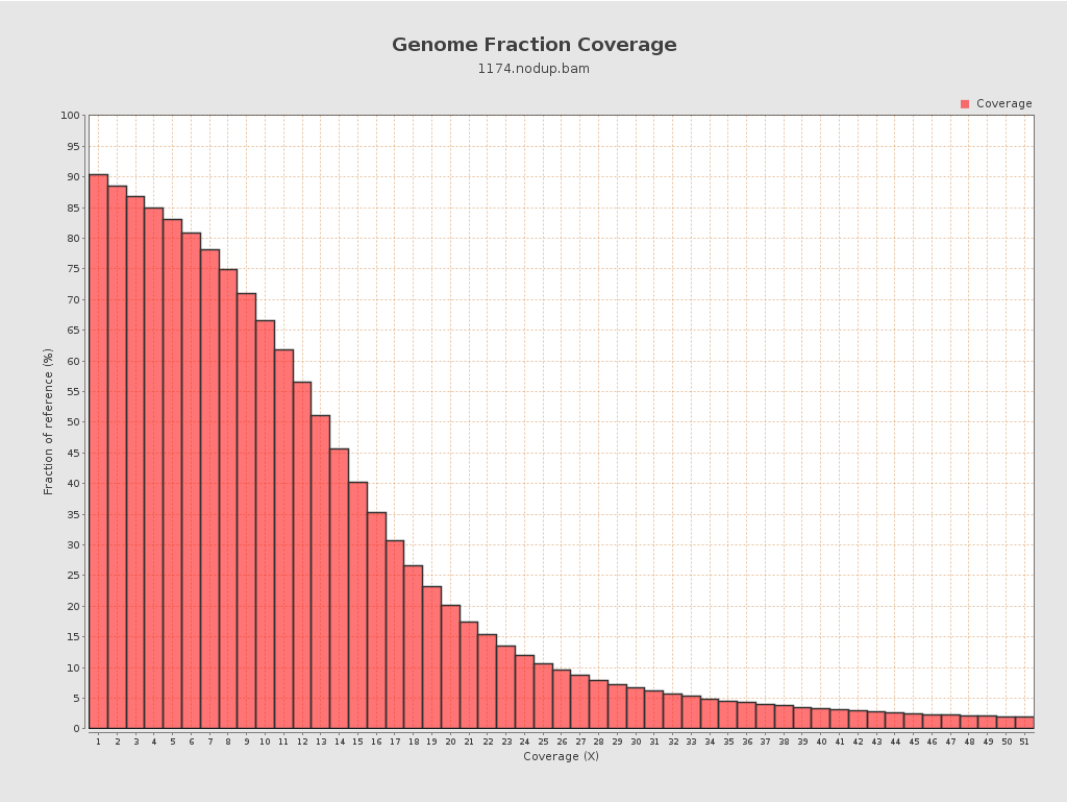
4. Results : Coverage Histogram



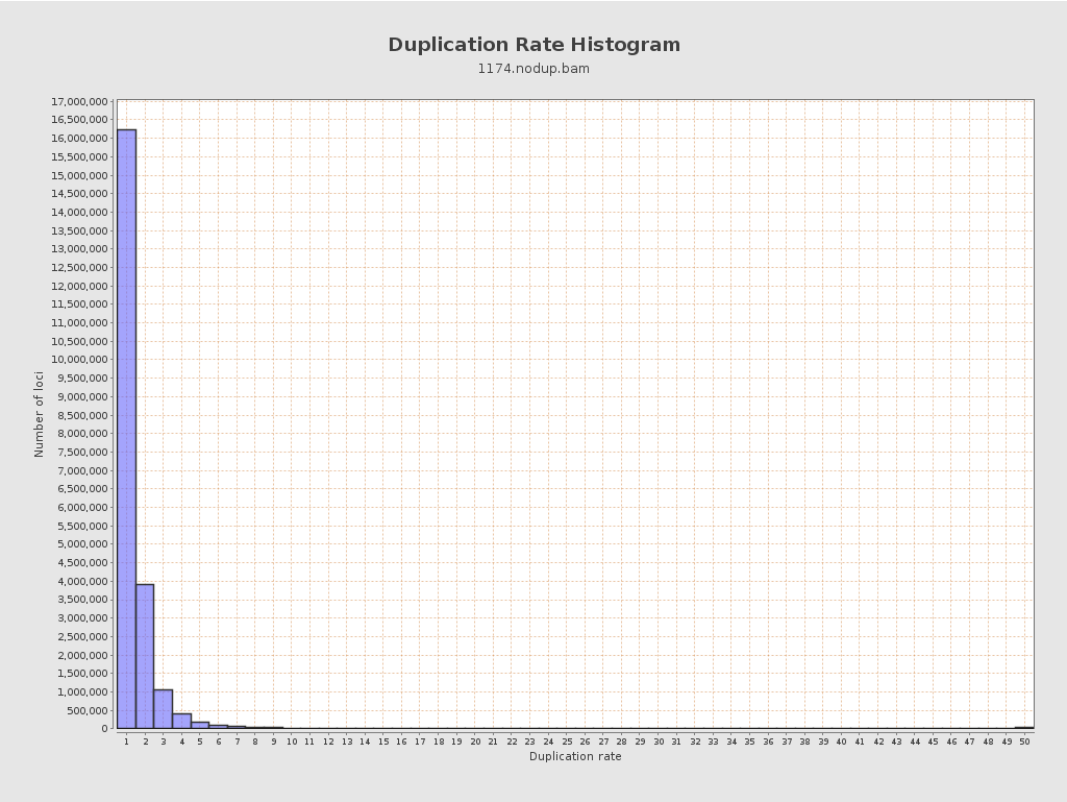
5. Results : Coverage Histogram (0-50X)



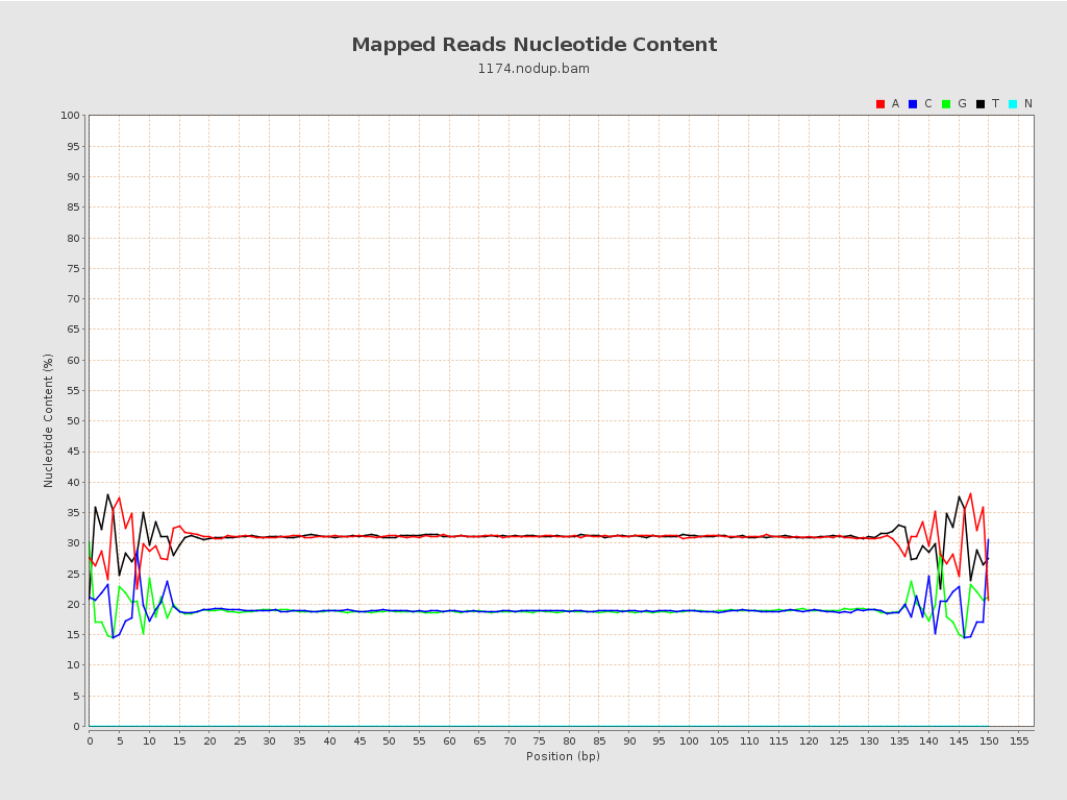
6. Results : Genome Fraction Coverage



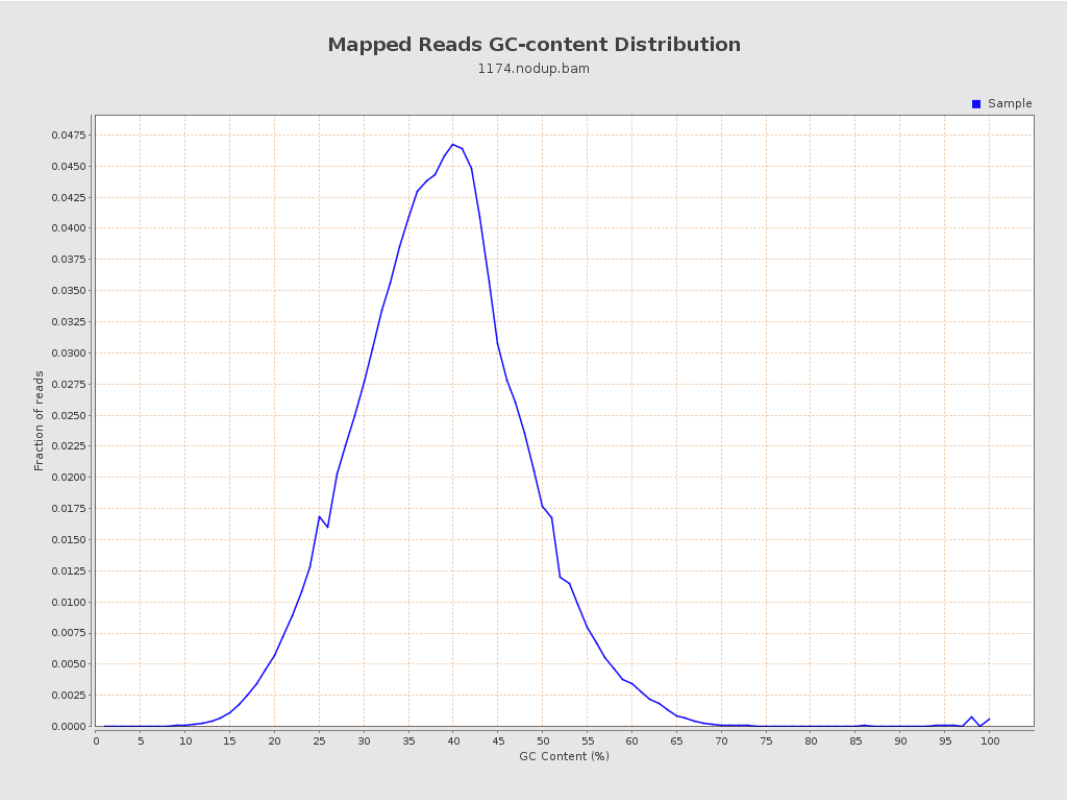
7. Results : Duplication Rate Histogram



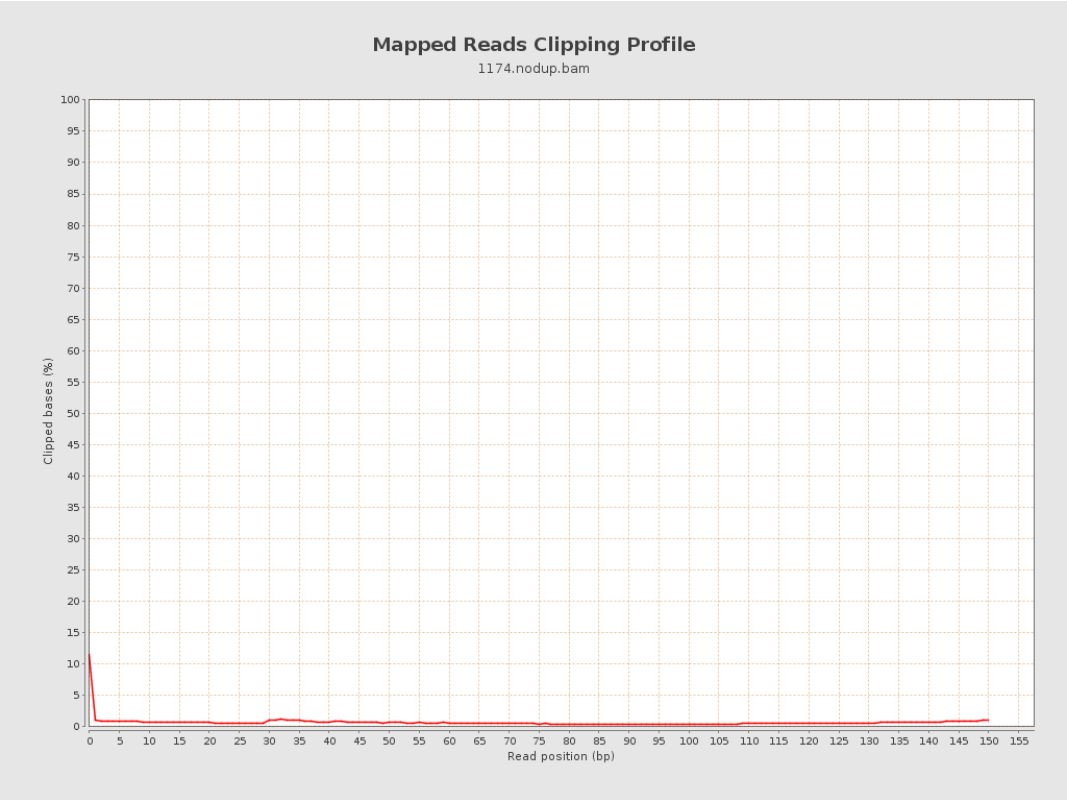
8. Results : Mapped Reads Nucleotide Content



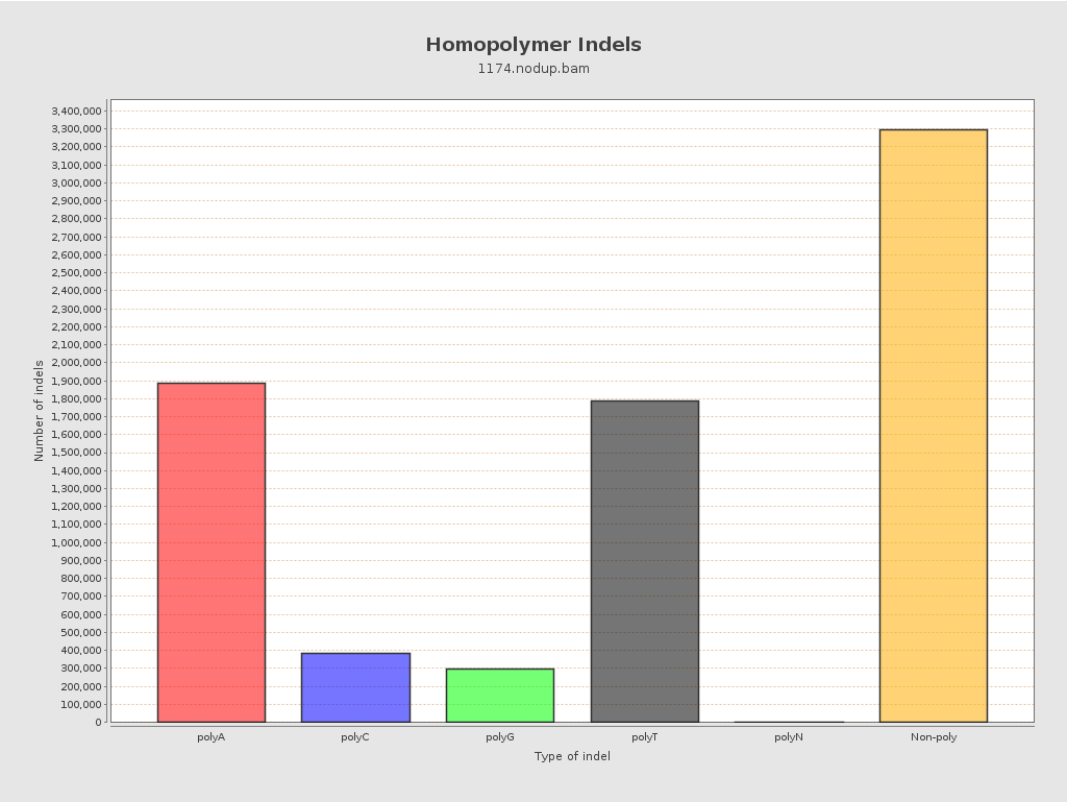
9. Results : Mapped Reads GC-content Distribution



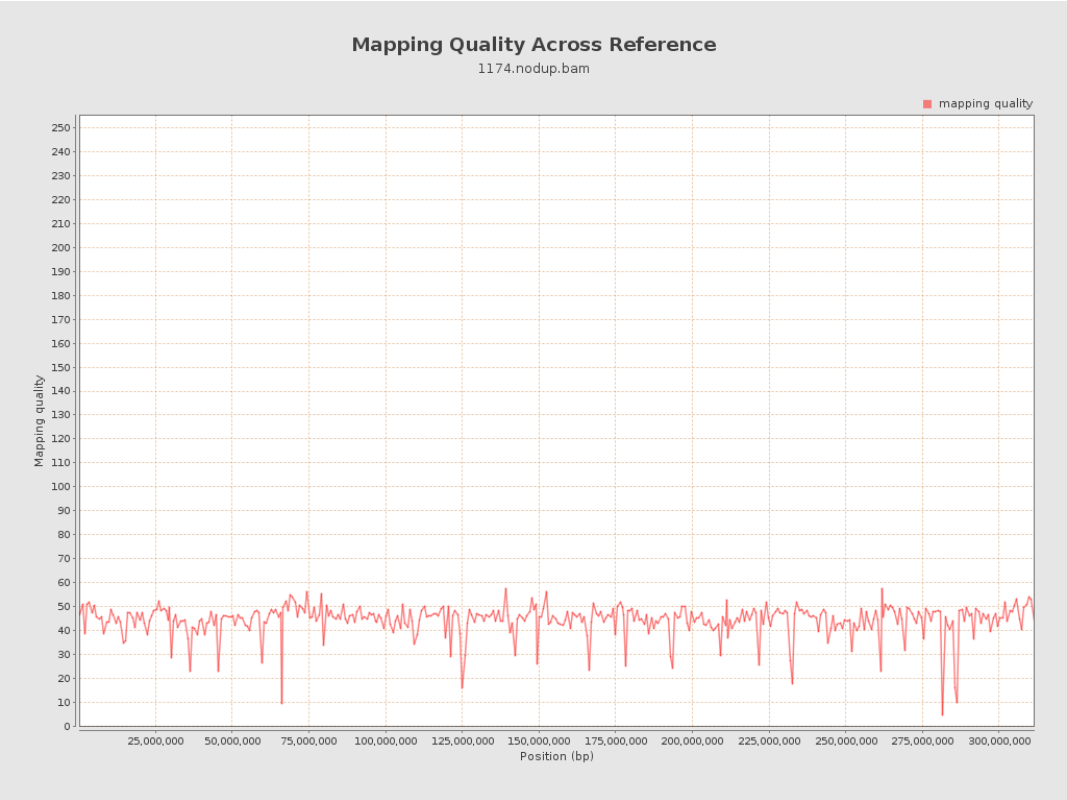
10. Results : Mapped Reads Clipping Profile



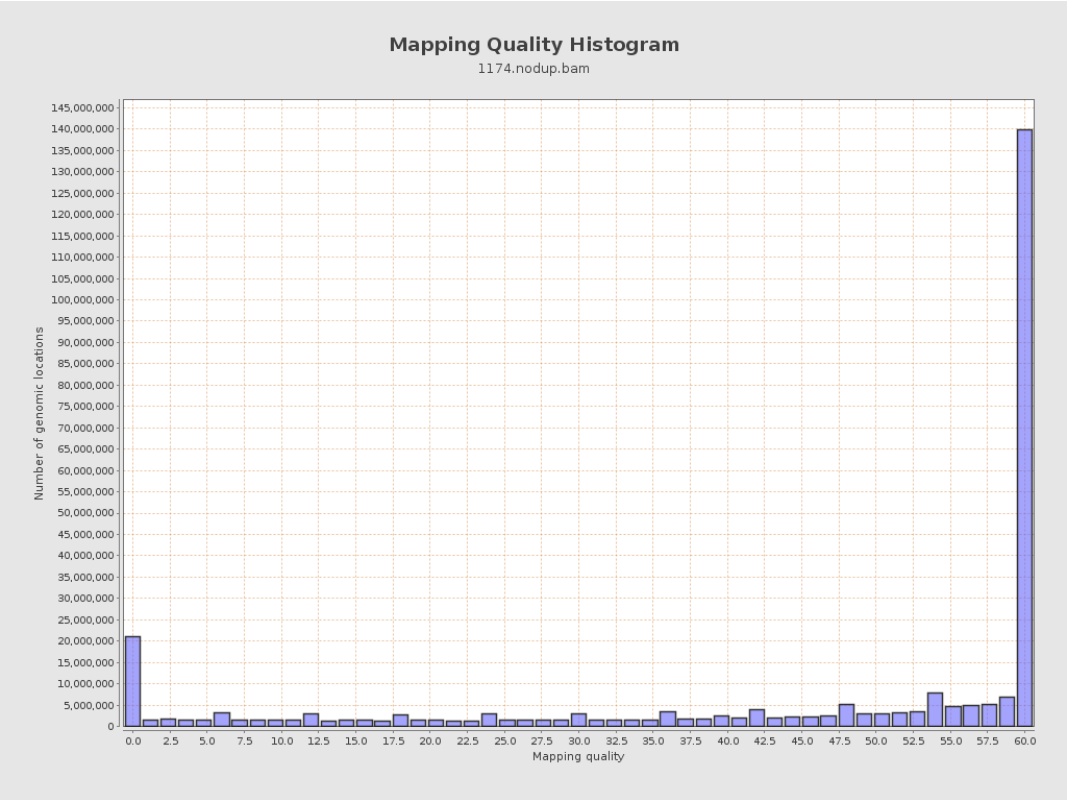
11. Results : Homopolymer Indels



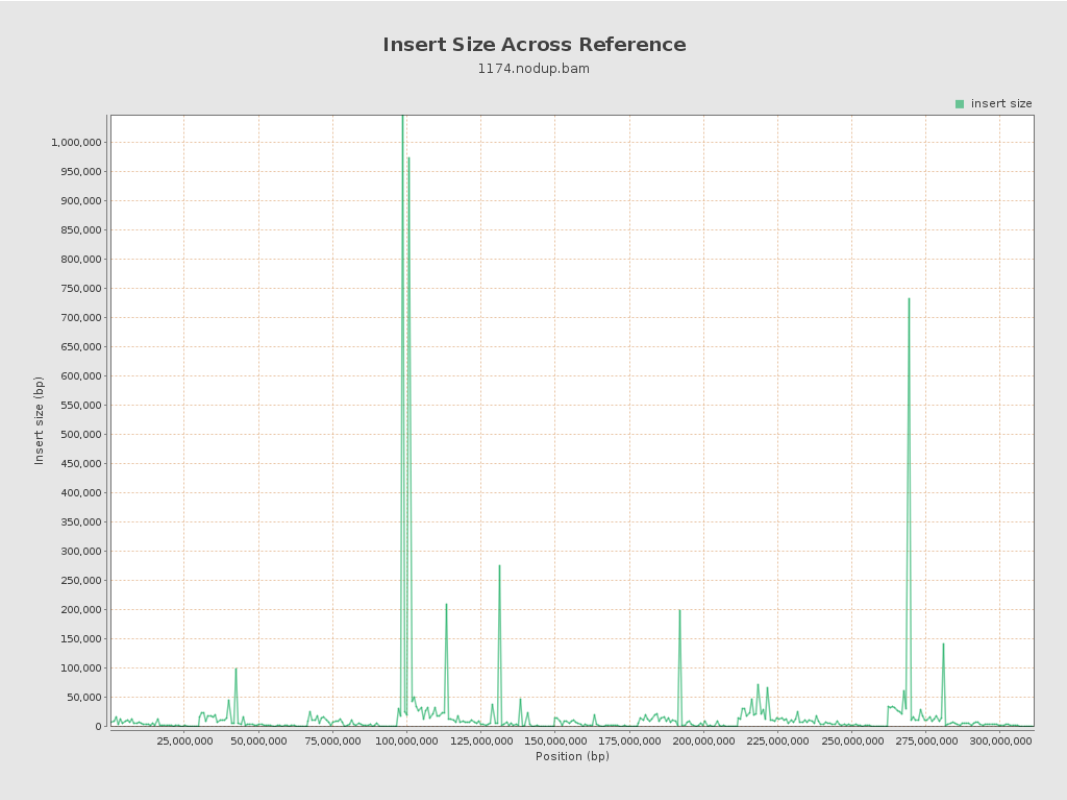
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram