Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1380
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1380 .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_576/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_576_S143_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_576/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_576_S143_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:27:53 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	57,337,023
Mapped reads	53,637,415 / 93.55%
Unmapped reads	3,699,608 / 6.45%
Mapped paired reads	53,637,415 / 93.55%
Mapped reads, first in pair	26,900,895 / 46.92%
Mapped reads, second in pair	26,736,520 / 46.63%
Mapped reads, both in pair	52,539,643 / 91.63%
Mapped reads, singletons	1,097,772 / 1.91%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	7,868,131 / 13.72%
Clipped reads	12,809,281 / 22.34%

2.2. ACGT Content

Number/percentage of A's	2,286,956,091 / 30.89%
Number/percentage of C's	1,414,456,642 / 19.11%
Number/percentage of T's	2,290,269,348 / 30.94%
Number/percentage of G's	1,411,319,666 / 19.06%
Number/percentage of N's	54,485 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	23.8181
Standard Deviation	184.4593

2.4. Mapping Quality

Mean Mapping Quality	43.71

2.5. Insert size

Mean	228,554.4
Standard Deviation	2,269,824.82
P25/Median/P75	315 / 414 / 535

2.6. Mismatches and indels

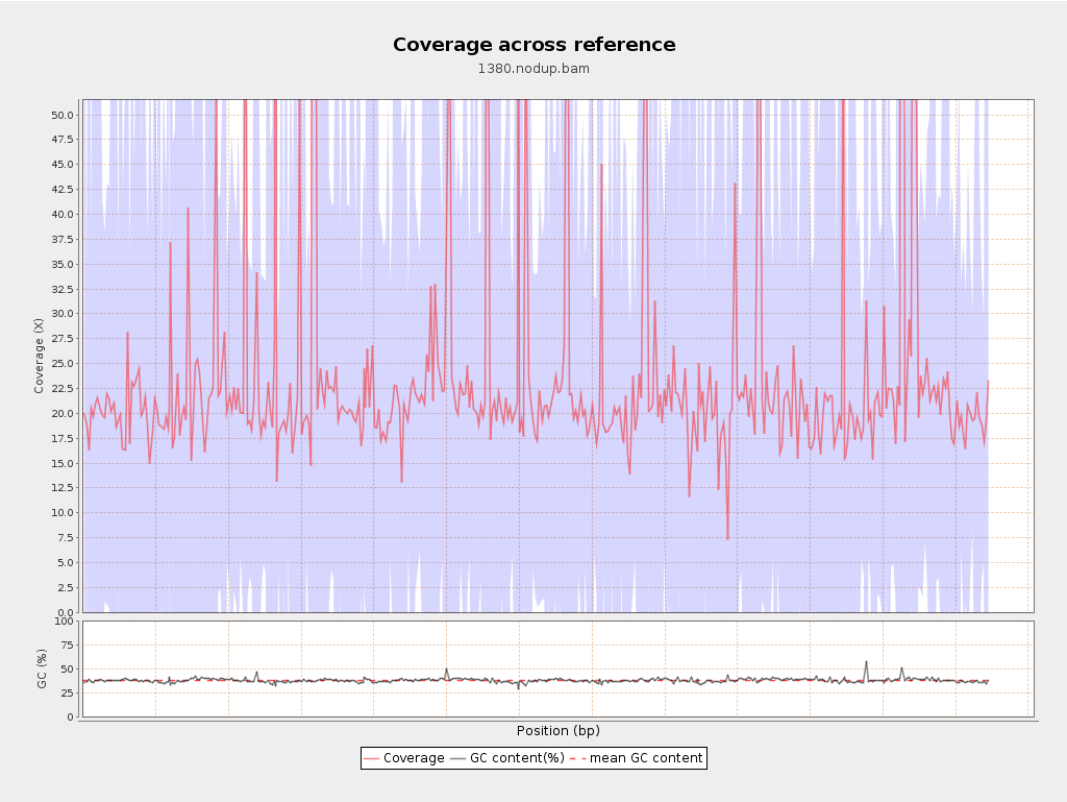
General error rate	2.52%
Mismatches	173,155,375
Insertions	5,023,191
Mapped reads with at least one insertion	8.41%
Deletions	5,166,805
Mapped reads with at least one deletion	8.54%
Homopolymer indels	56.04%

2.7. Chromosome stats

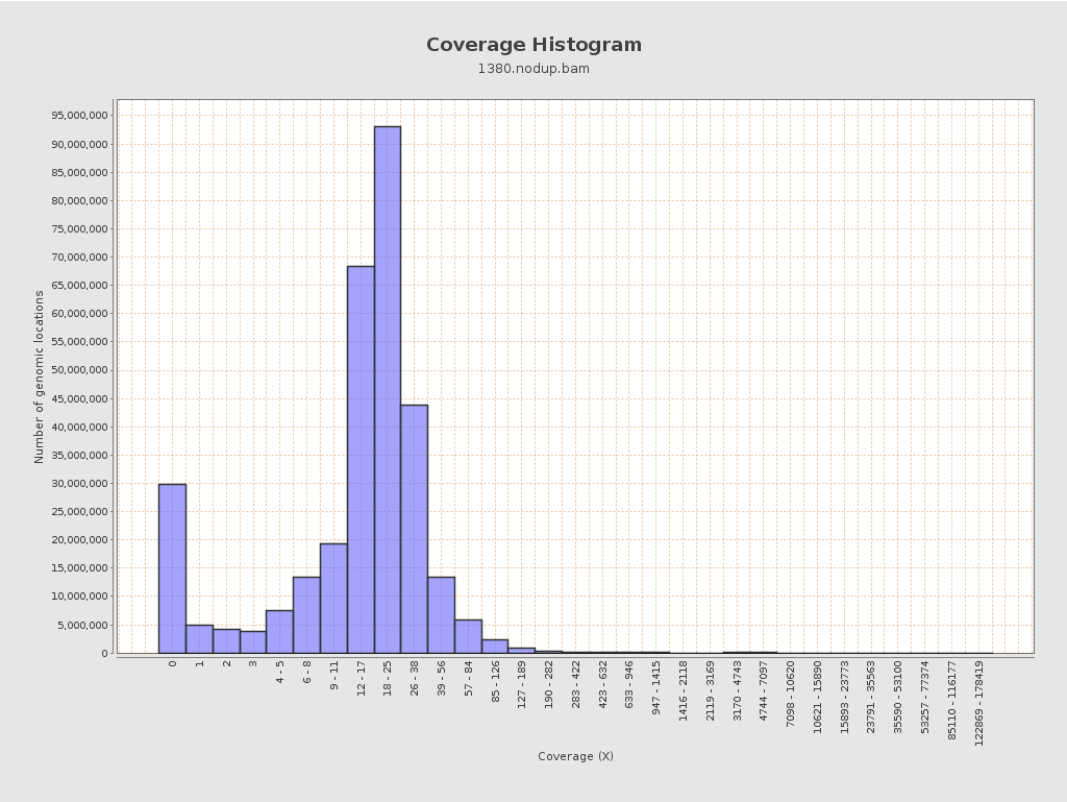
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	595448212	20.0323	55.577

LT669789.1	36598175	883824576	24.1494	195.0989
LT669790.1	30422129	786126250	25.8406	183.2199
LT669791.1	52758100	1227357736	23.2639	154.4993
LT669792.1	28376109	671566440	23.6666	196.1304
LT669793.1	33388210	747545393	22.3895	129.7287
LT669794.1	50579949	1131104200	22.3627	151.5403
LT669795.1	49795044	1379742583	27.7084	284.1932

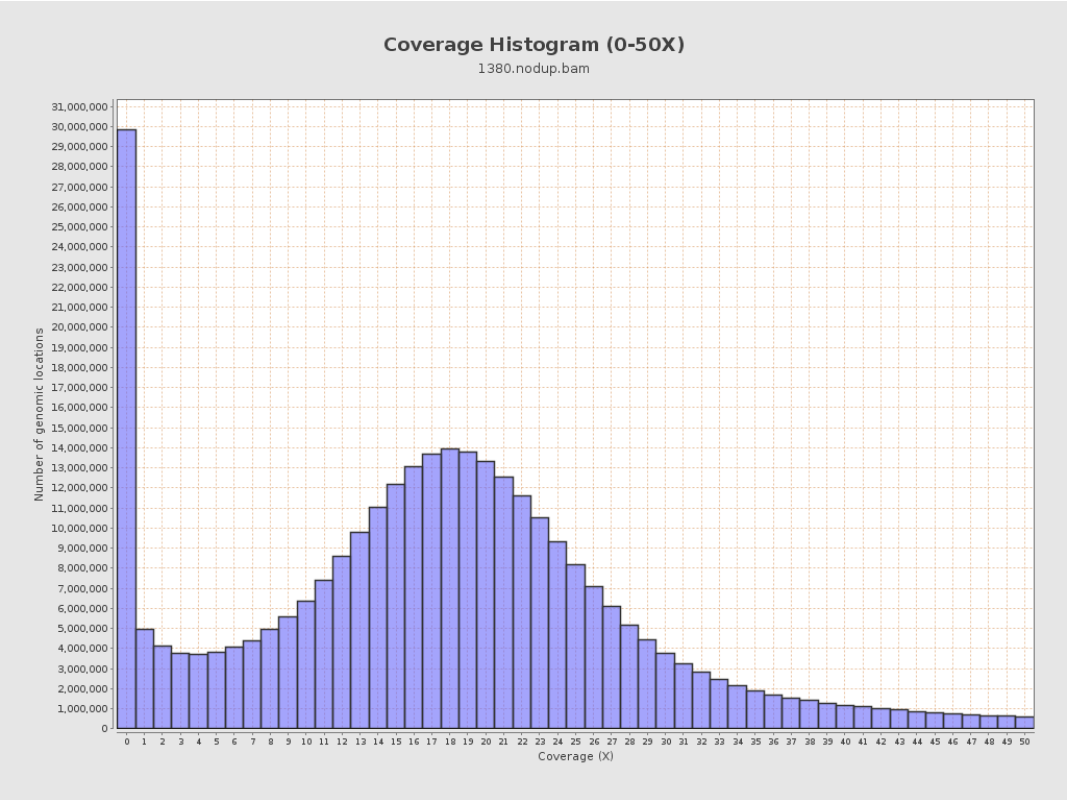
3. Results : Coverage across reference



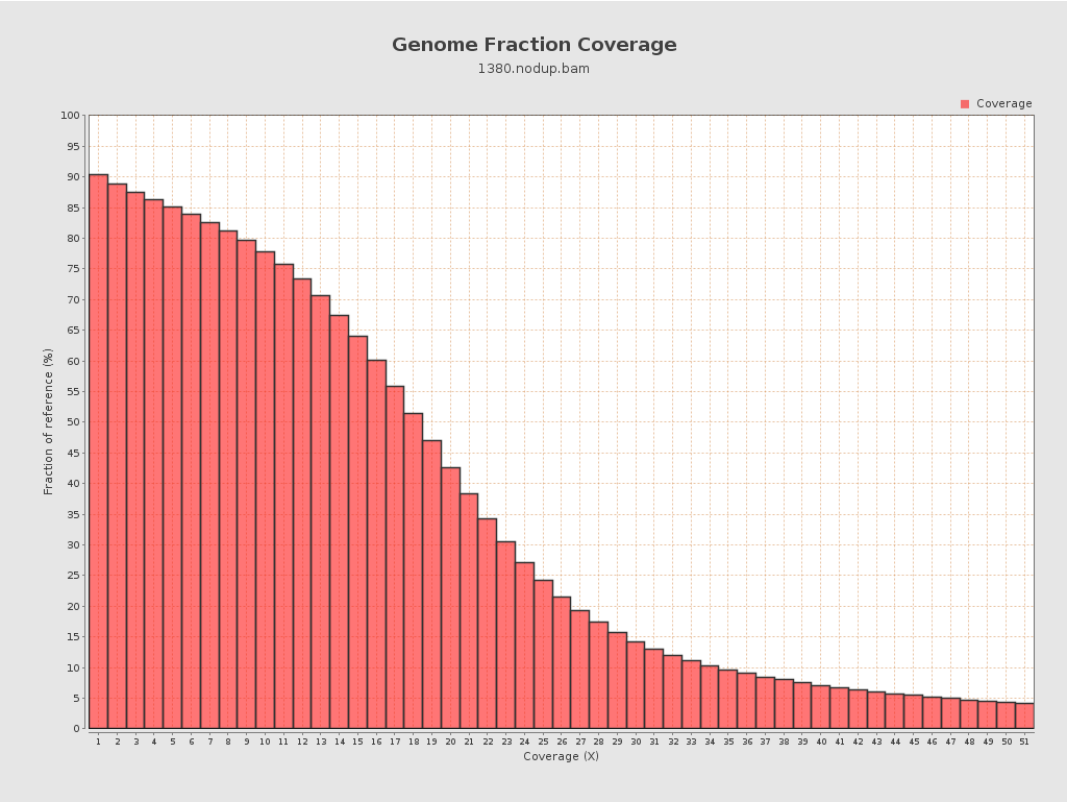
4. Results : Coverage Histogram



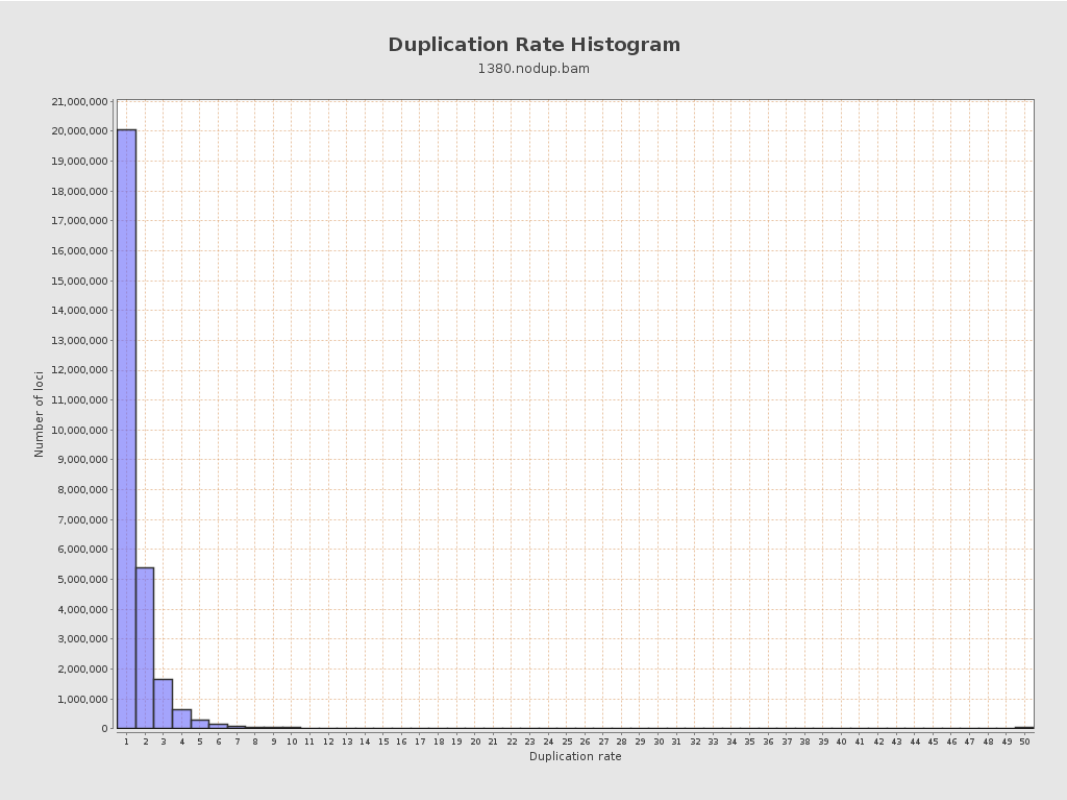
5. Results : Coverage Histogram (0-50X)



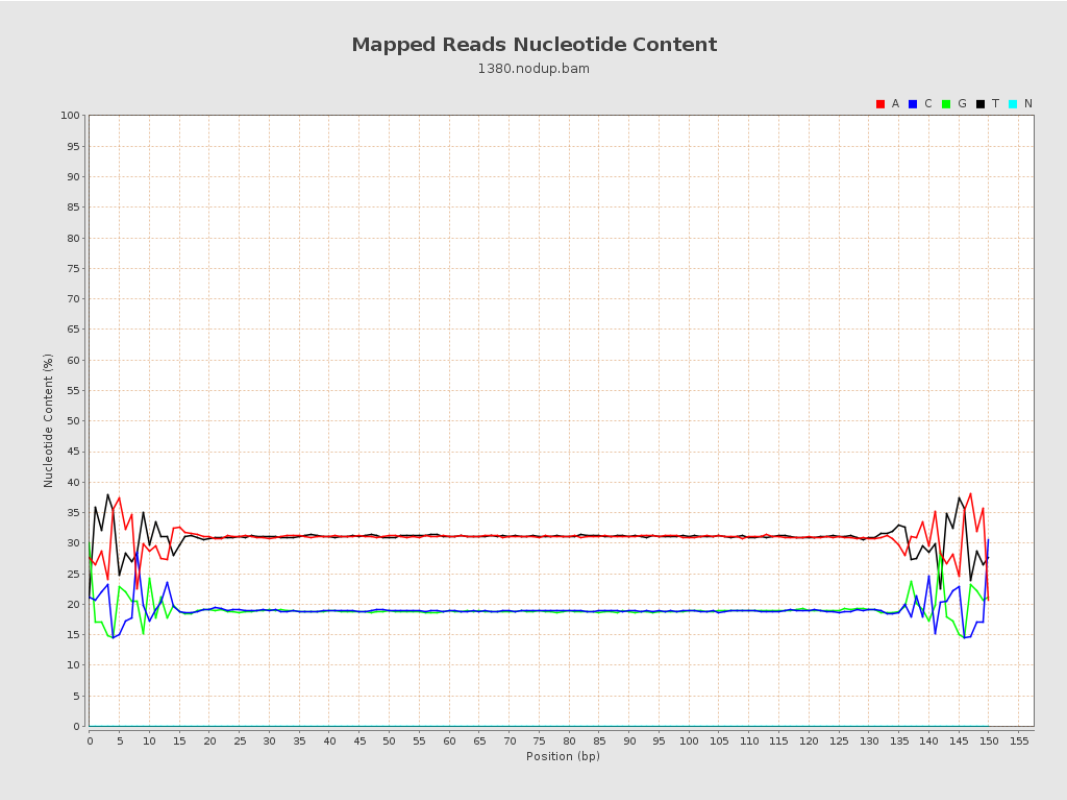
6. Results : Genome Fraction Coverage



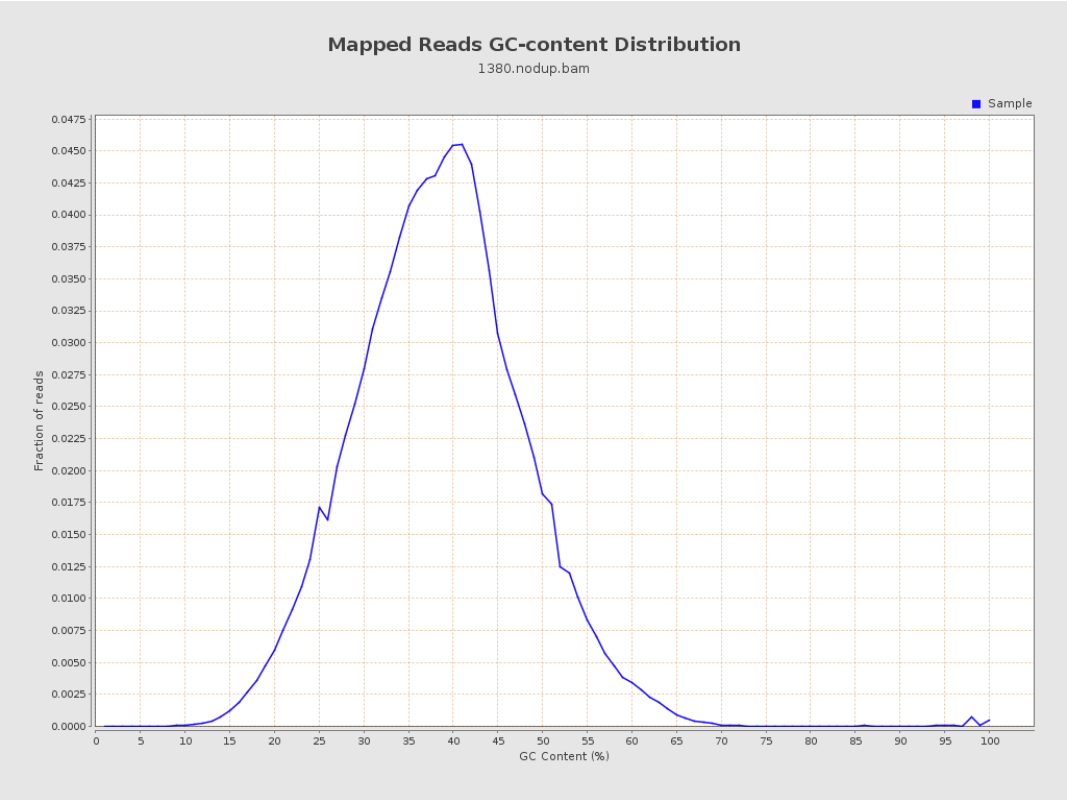
7. Results : Duplication Rate Histogram



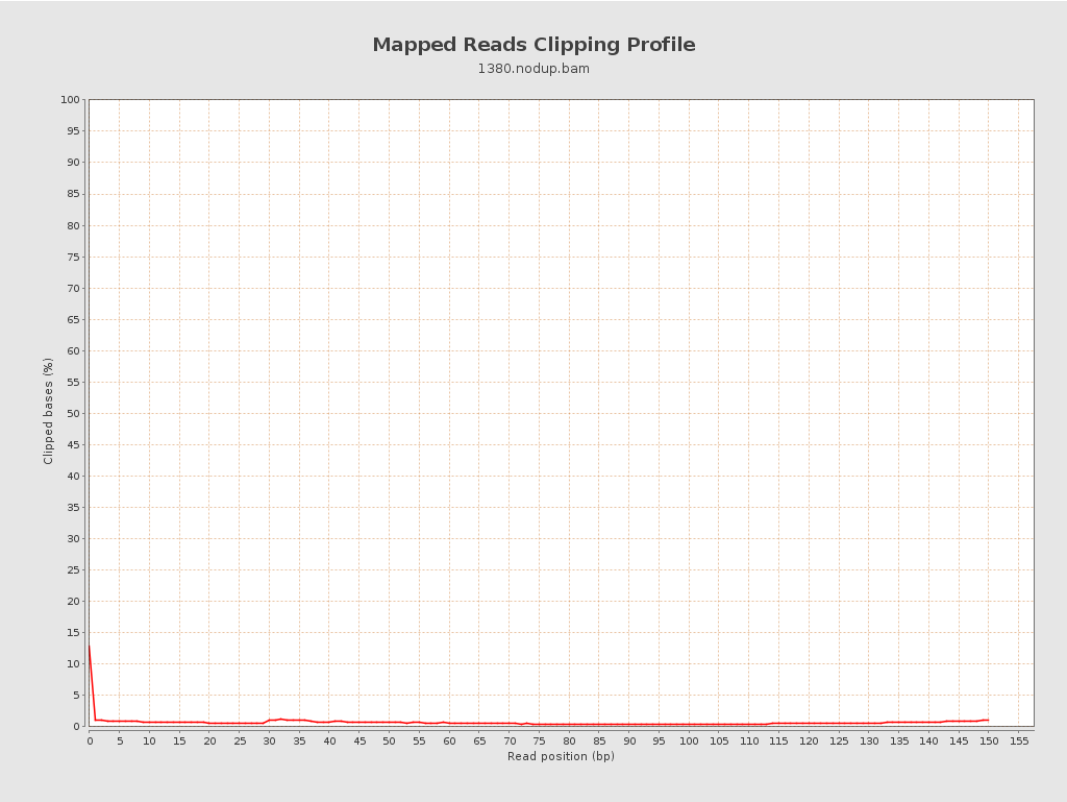
8. Results : Mapped Reads Nucleotide Content



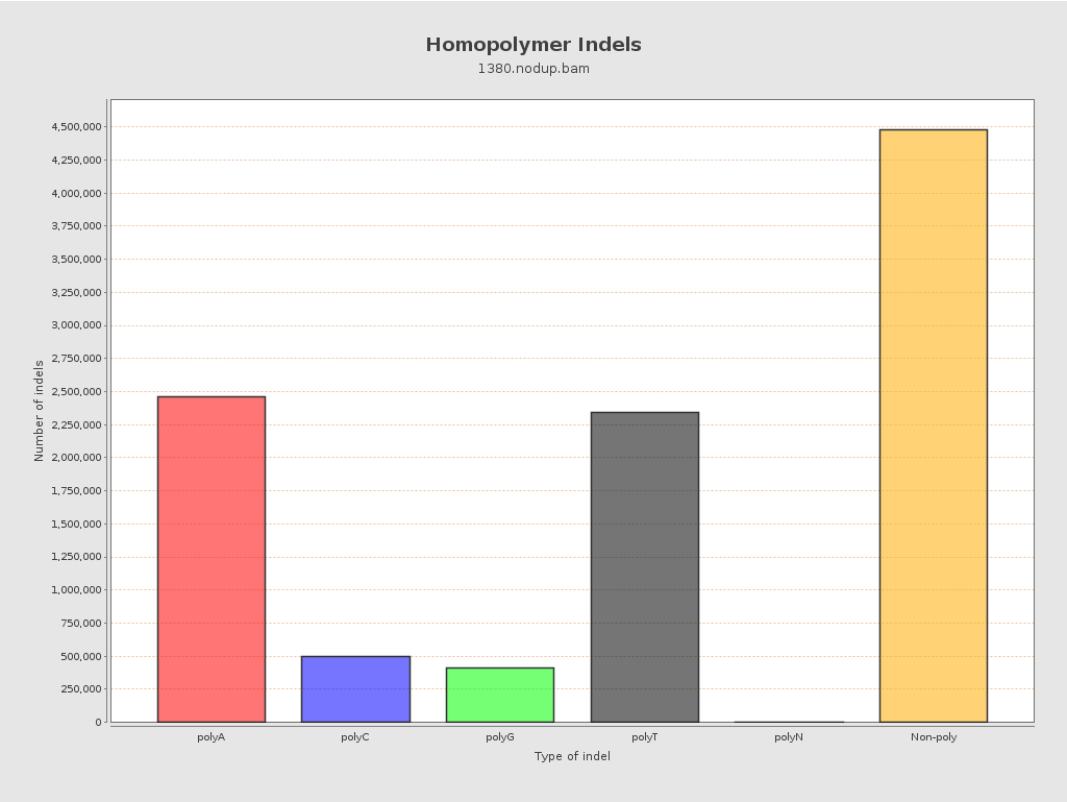
9. Results : Mapped Reads GC-content Distribution



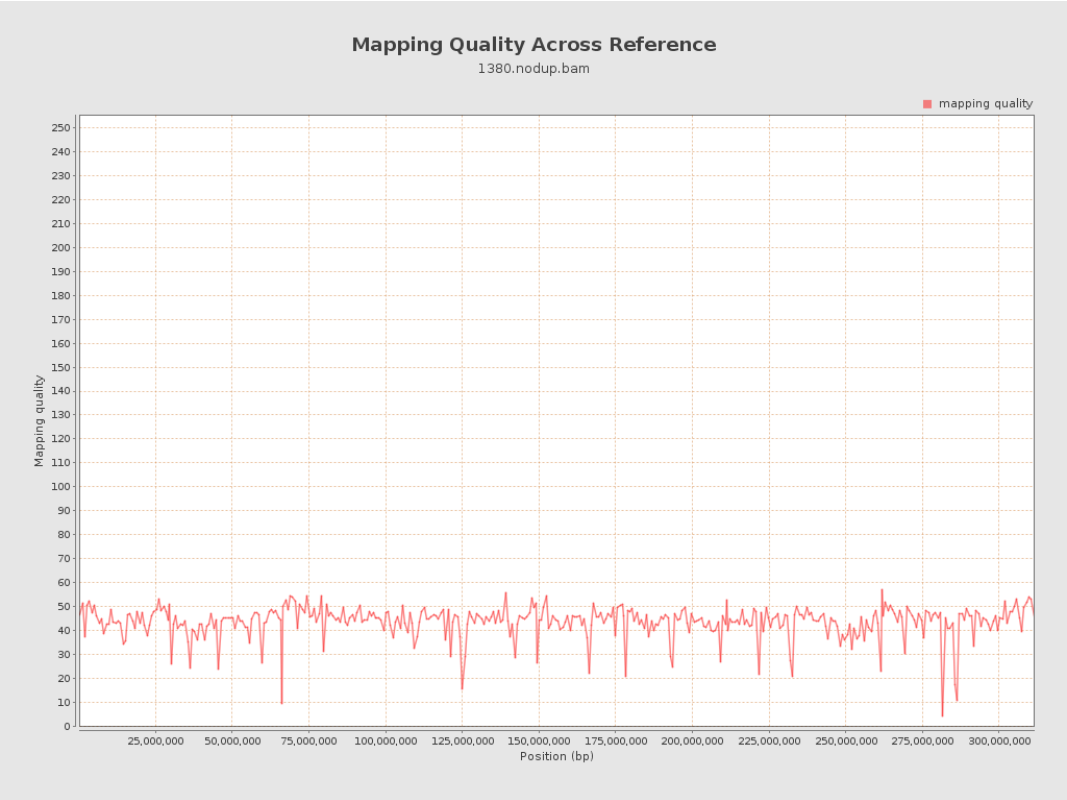
10. Results : Mapped Reads Clipping Profile



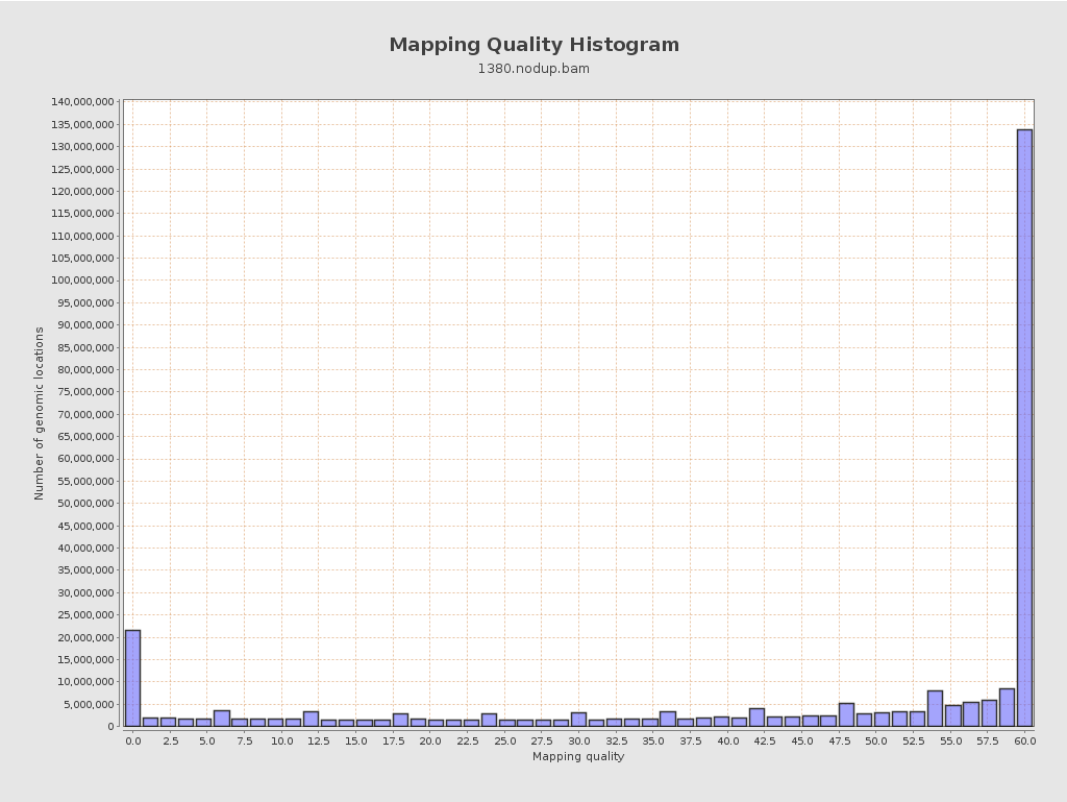
11. Results : Homopolymer Indels



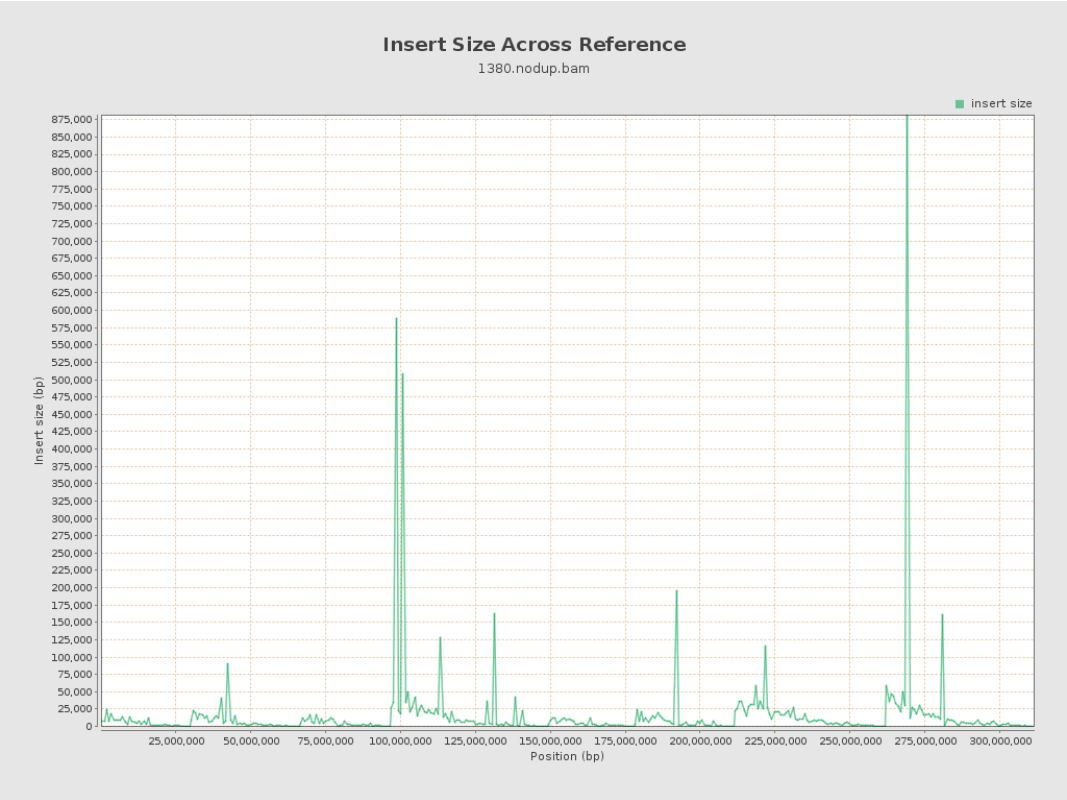
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram