Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1116
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1116 .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_449/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_449_S424_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_449/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_449_S424_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,389,158
Mapped reads	58,022,857 / 94.52%
Unmapped reads	3,366,301 / 5.48%
Mapped paired reads	58,022,857 / 94.52%
Mapped reads, first in pair	29,075,953 / 47.36%
Mapped reads, second in pair	28,946,904 / 47.15%
Mapped reads, both in pair	56,861,673 / 92.62%
Mapped reads, singletons	1,161,184 / 1.89%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	8,795,398 / 14.33%
Clipped reads	12,819,317 / 20.88%

2.2. ACGT Content

Number/percentage of A's	2,489,711,854 / 30.9%
Number/percentage of C's	1,539,995,419 / 19.11%
Number/percentage of T's	2,491,044,993 / 30.91%
Number/percentage of G's	1,537,189,726 / 19.08%
Number/percentage of N's	27,667 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	25.9223
Standard Deviation	211.6863

2.4. Mapping Quality

Mean Mapping Quality	44.01

2.5. Insert size

Mean	249,675.56
Standard Deviation	2,362,507.4
P25/Median/P75	386 / 506 / 657

2.6. Mismatches and indels

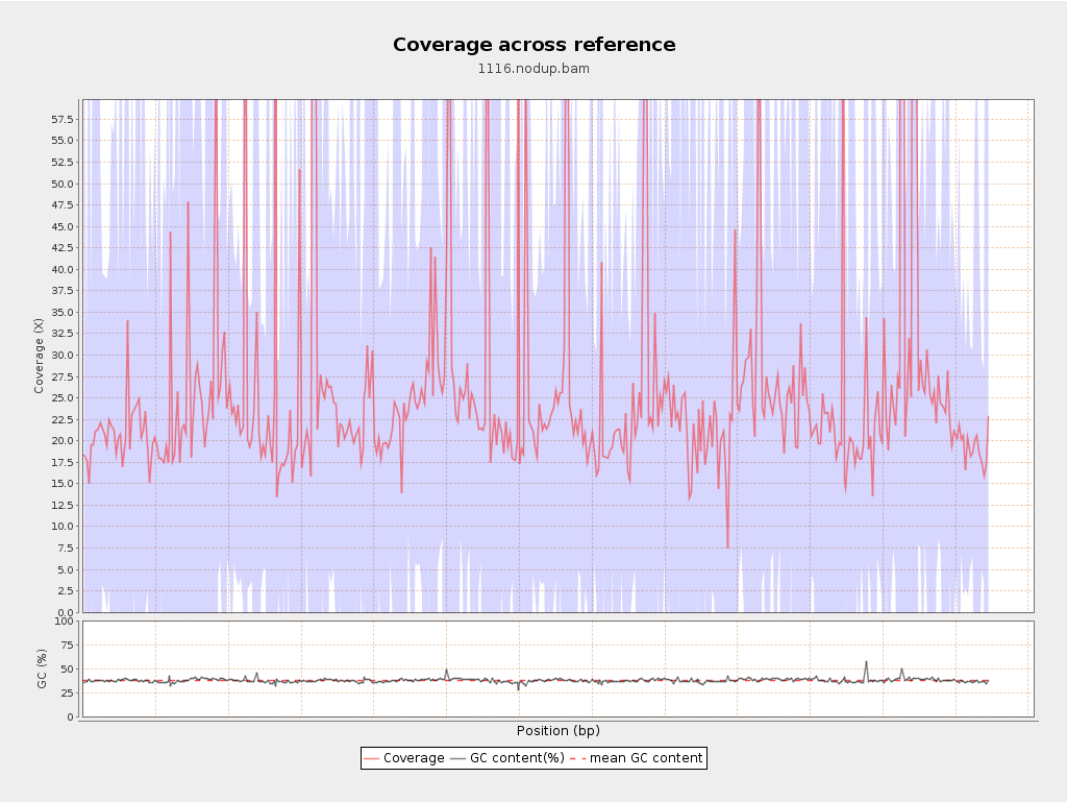
General error rate	2.3%
Mismatches	170,815,640
Insertions	5,316,915
Mapped reads with at least one insertion	8.24%
Deletions	5,487,125
Mapped reads with at least one deletion	8.41%
Homopolymer indels	56.37%

2.7. Chromosome stats

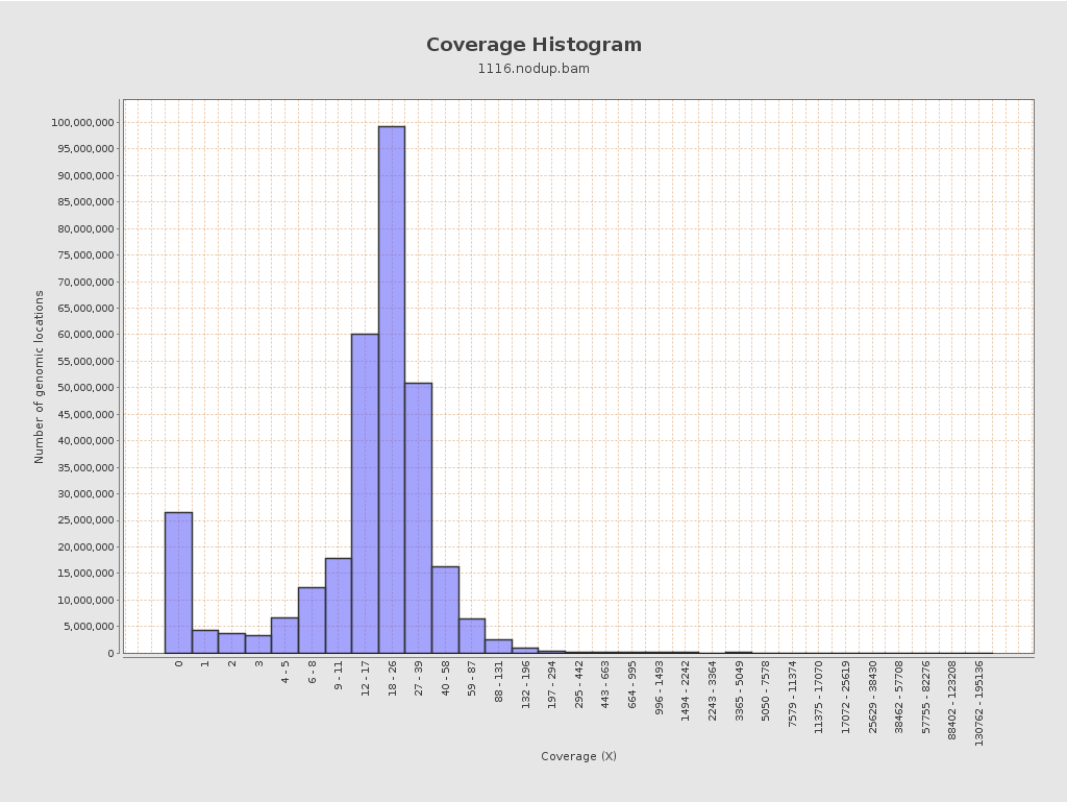
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	607633402	20.4423	56.2052

LT669789.1	36598175	981155287	26.8089	217.4656
LT669790.1	30422129	806955763	26.5253	181.5211
LT669791.1	52758100	1363682907	25.8478	173.7567
LT669792.1	28376109	721029481	25.4097	250.2638
LT669793.1	33388210	813211399	24.3562	151.111
LT669794.1	50579949	1282084446	25.3477	181.425
LT669795.1	49795044	1502738895	30.1785	327.4336

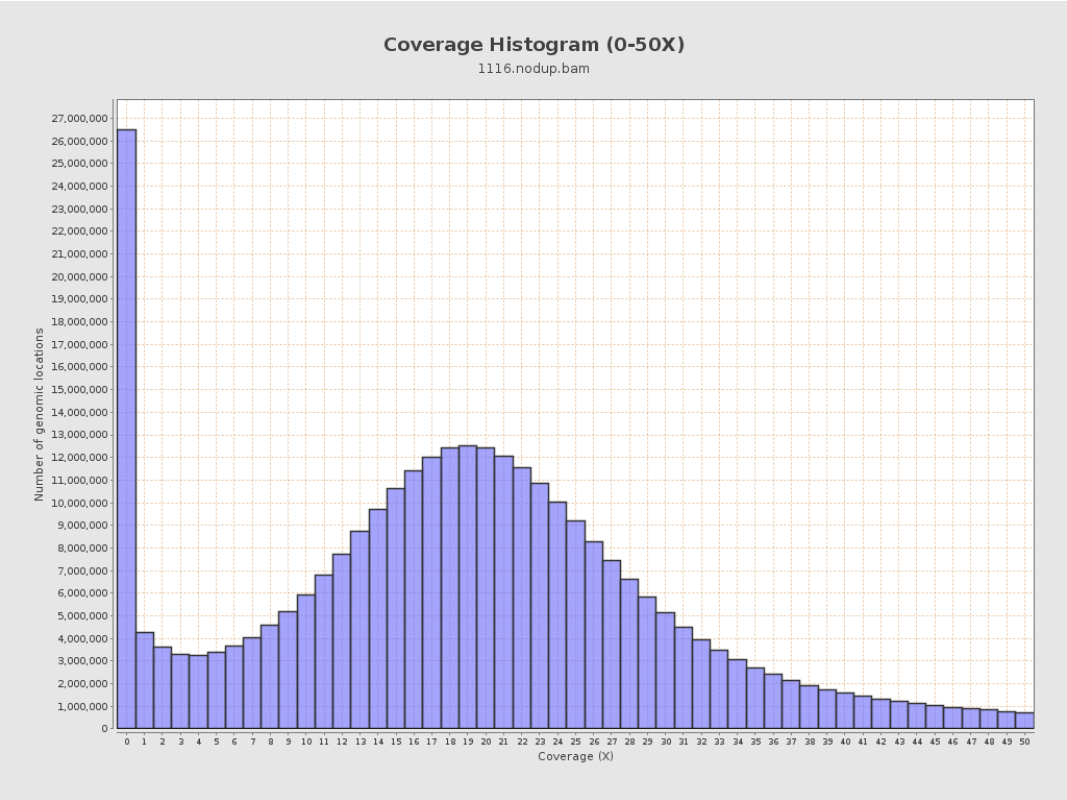
3. Results : Coverage across reference



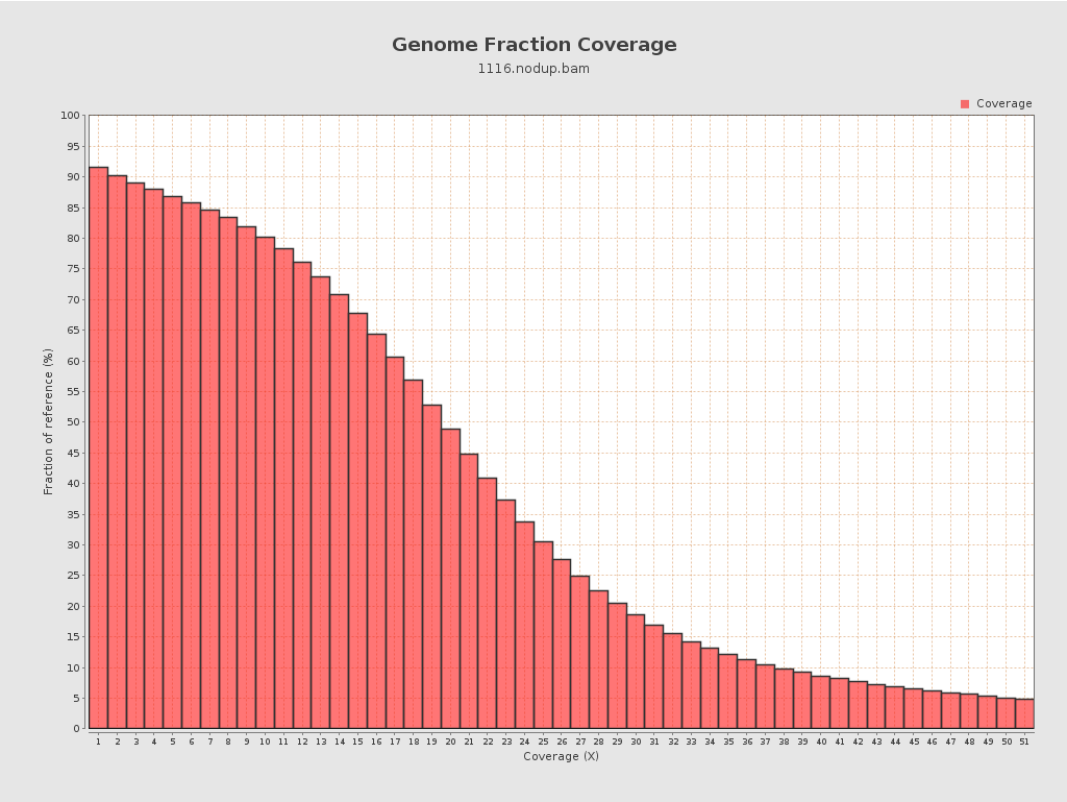
4. Results : Coverage Histogram



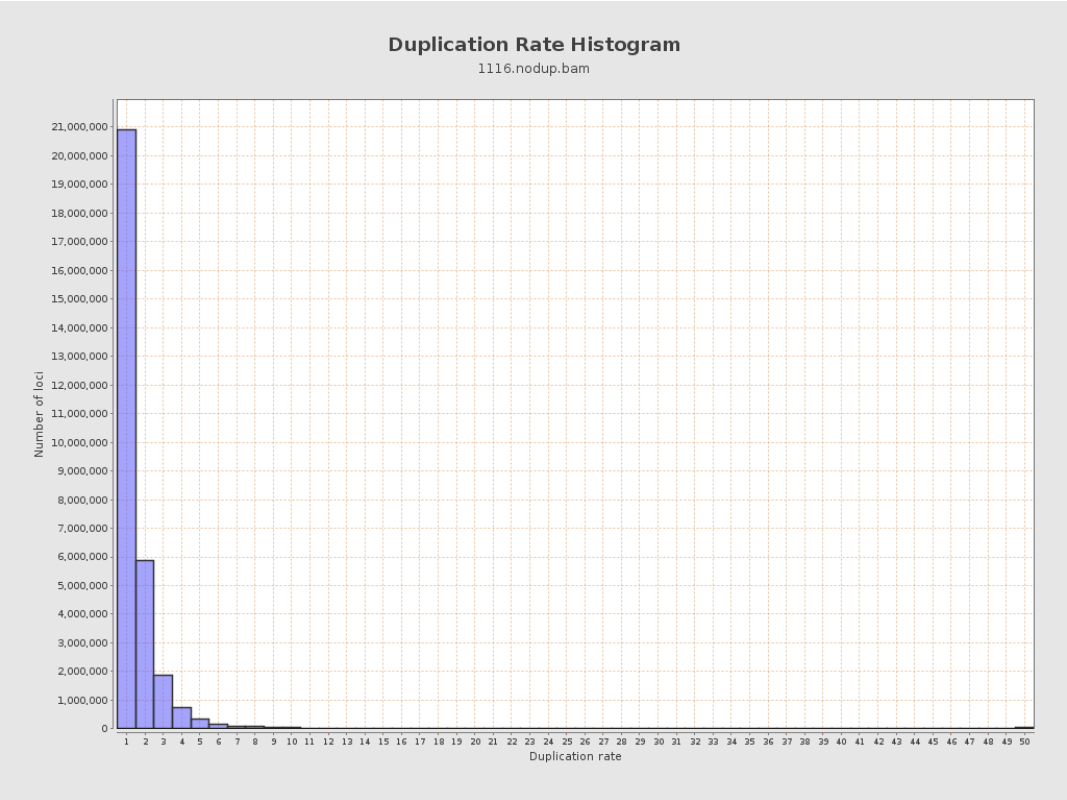
5. Results : Coverage Histogram (0-50X)



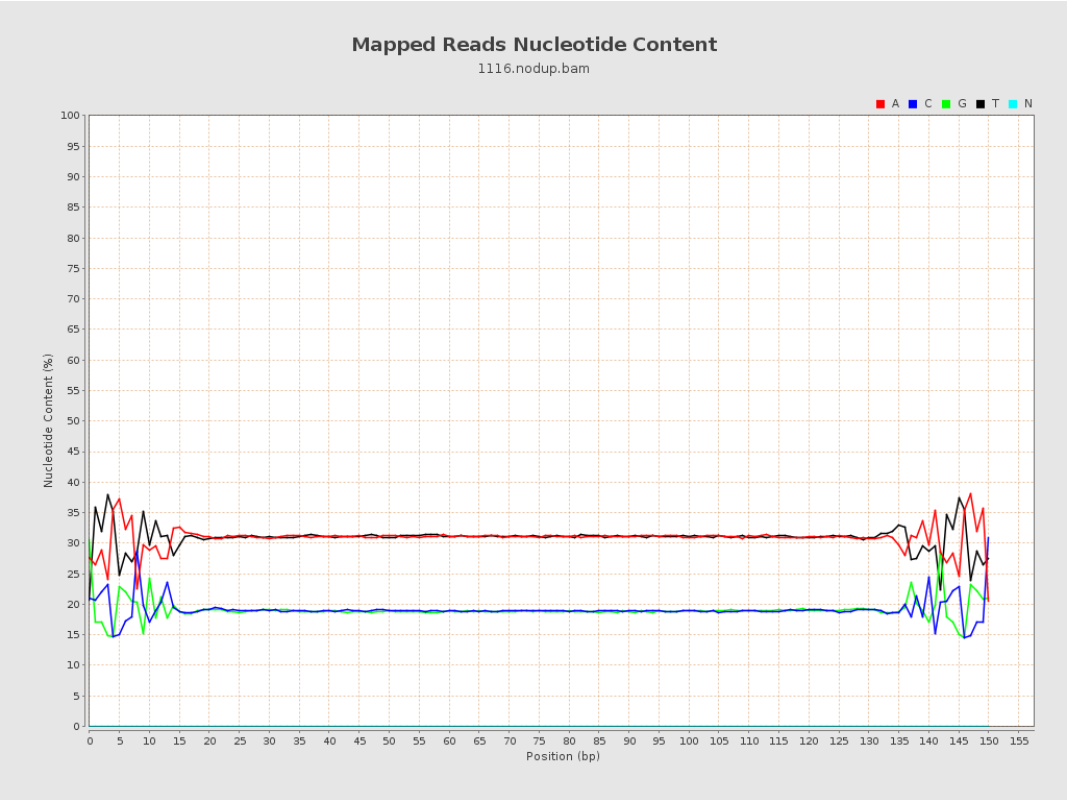
6. Results : Genome Fraction Coverage



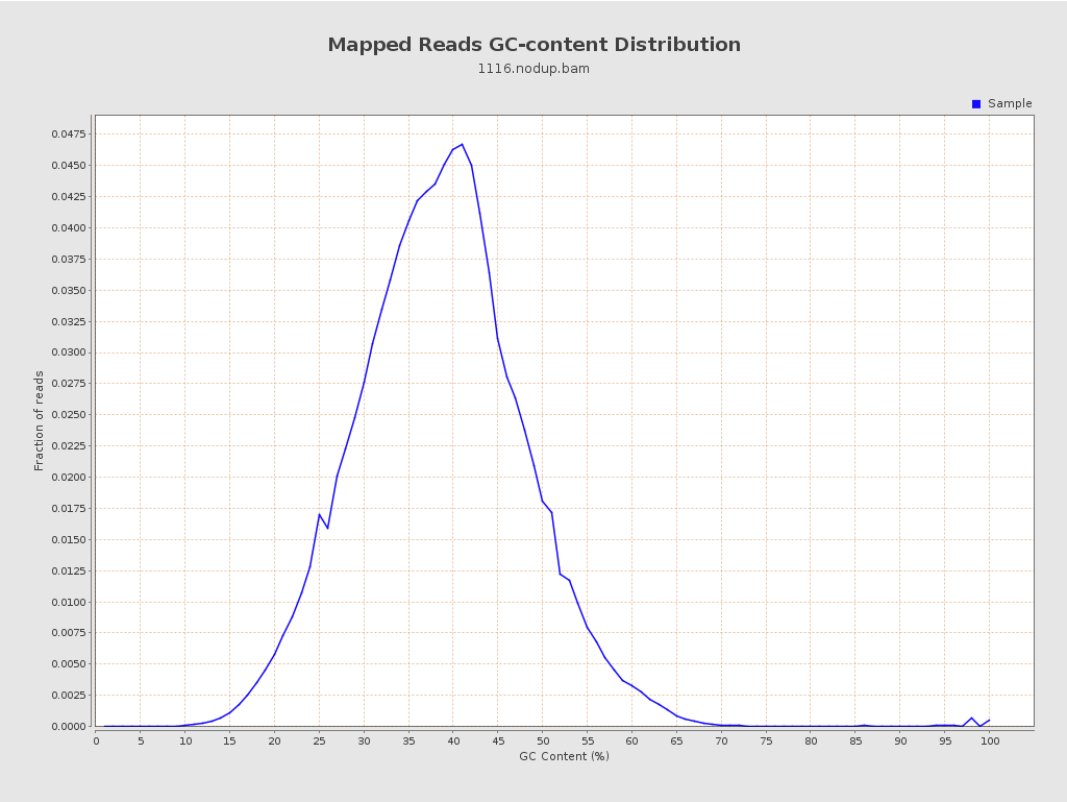
7. Results : Duplication Rate Histogram



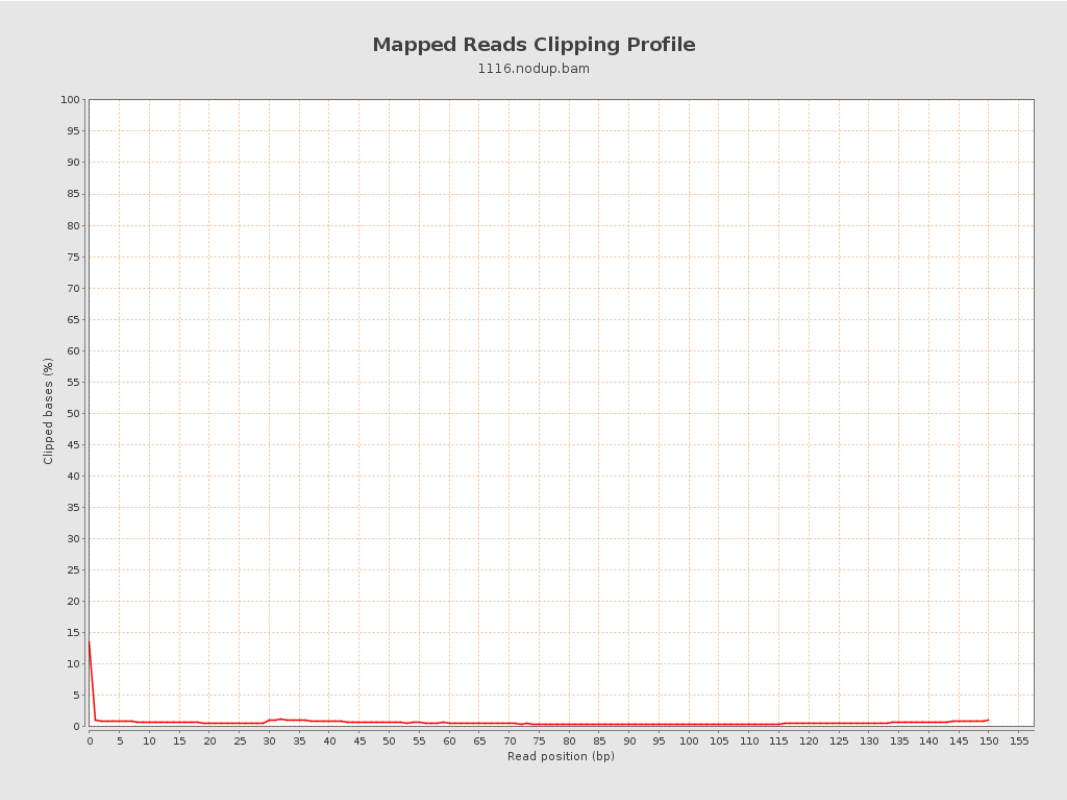
8. Results : Mapped Reads Nucleotide Content



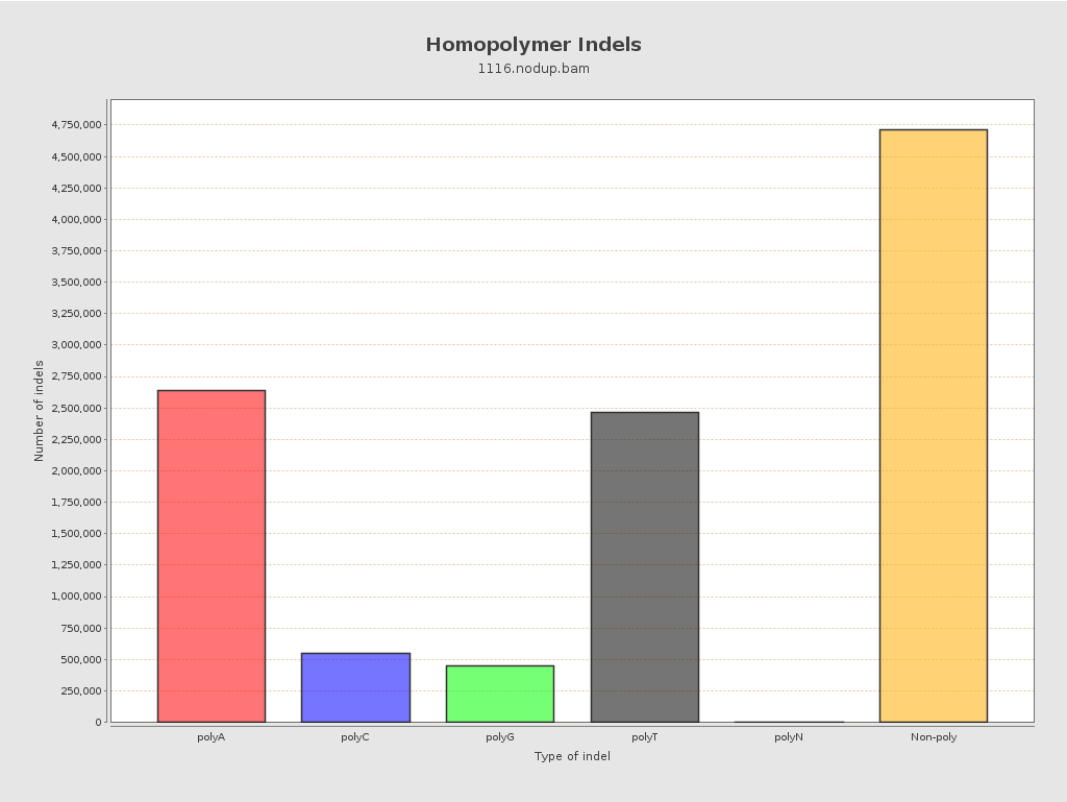
9. Results : Mapped Reads GC-content Distribution



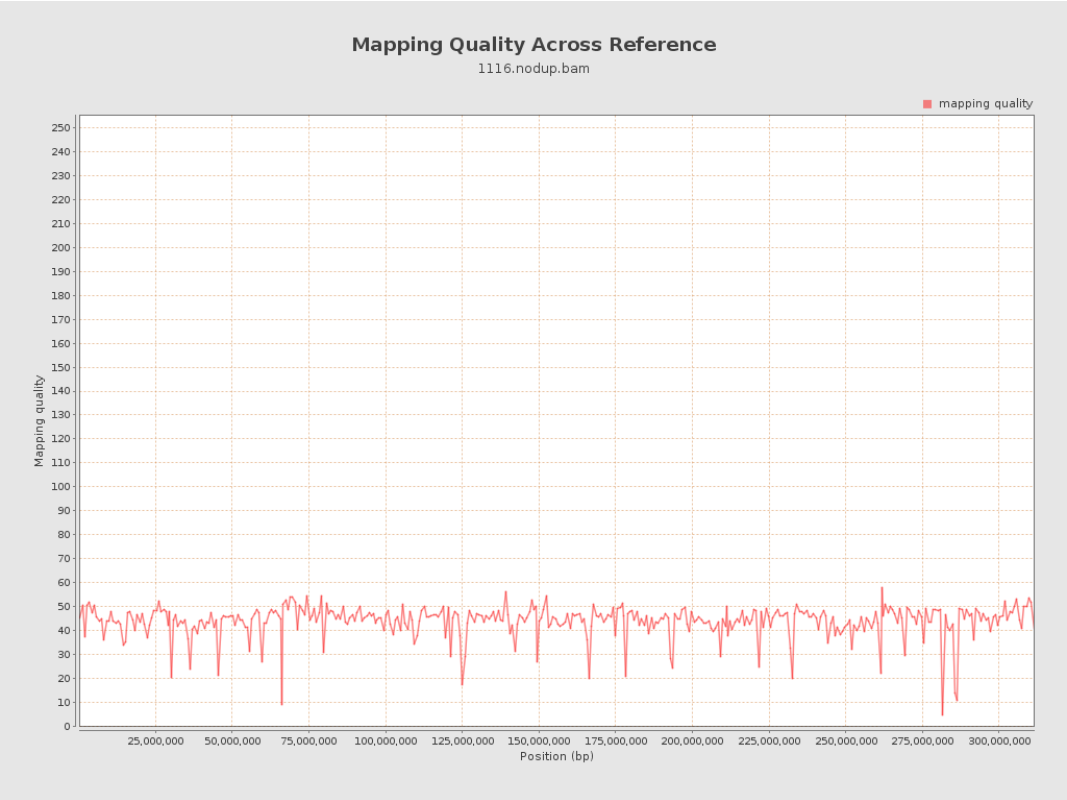
10. Results : Mapped Reads Clipping Profile



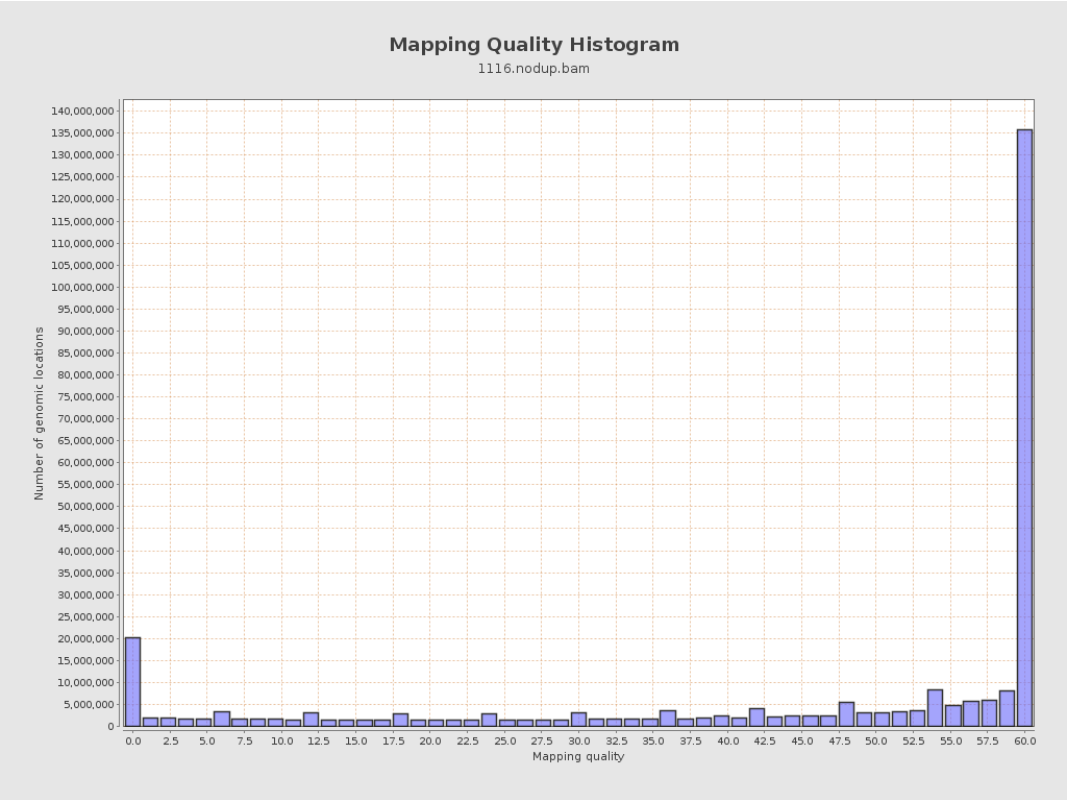
11. Results : Homopolymer Indels



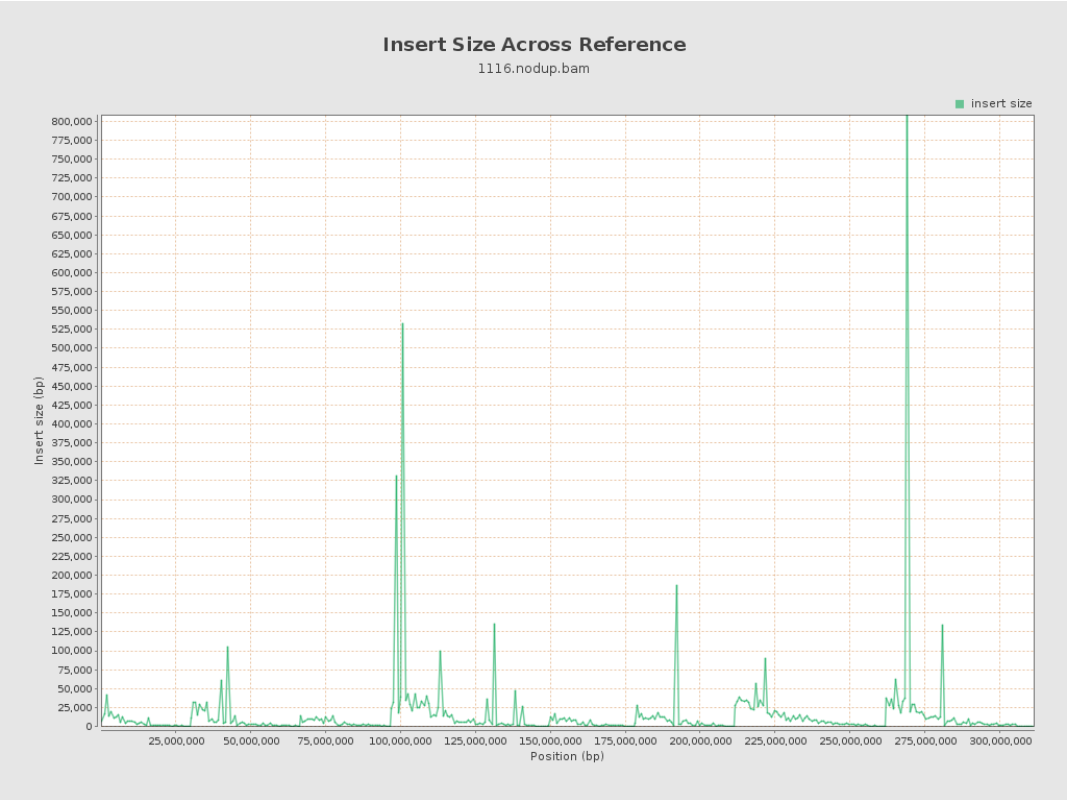
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram