Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/648.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/648.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_142/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_142_S232_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_142/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_142_S232_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:24 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	82,302,602
Mapped reads	75,336,670 / 91.54%
Unmapped reads	6,965,932 / 8.46%
Mapped paired reads	75,336,670 / 91.54%
Mapped reads, first in pair	37,770,797 / 45.89%
Mapped reads, second in pair	37,565,873 / 45.64%
Mapped reads, both in pair	72,980,327 / 88.67%
Mapped reads, singletons	2,356,343 / 2.86%
Read min/max/mean length	30 / 151 / 147.97
Duplicated reads (flagged)	14,317,227 / 17.4%
Clipped reads	18,363,157 / 22.31%

2.2. ACGT Content

Number/percentage of A's	3,191,815,506 / 30.99%
Number/percentage of C's	1,956,634,307 / 19%
Number/percentage of T's	3,195,911,530 / 31.03%
Number/percentage of G's	1,955,909,726 / 18.99%
Number/percentage of N's	43,932 / 0%
GC Percentage	37.98%

2.3. Coverage

Mean	33.1378
Standard Deviation	318.8817

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Insert size

Mean	264,420.46
Standard Deviation	2,471,889.43
P25/Median/P75	327 / 433 / 574

2.6. Mismatches and indels

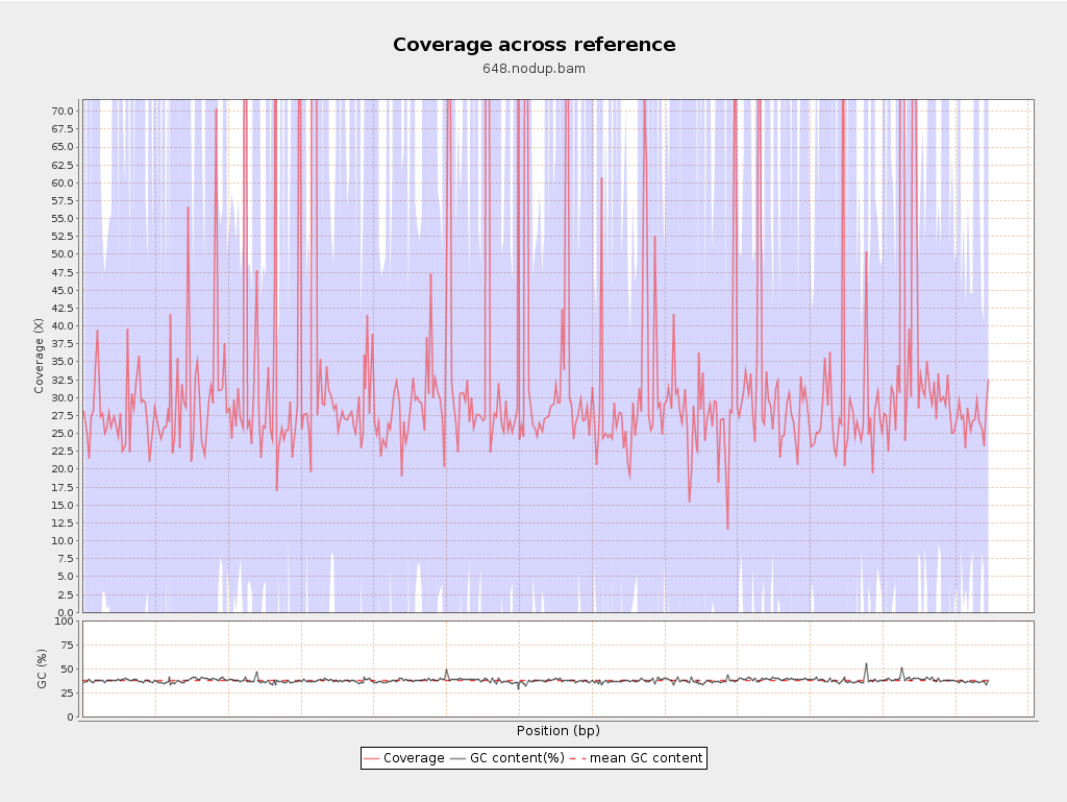
General error rate	2.39%
Mismatches	224,729,373
Insertions	7,702,151
Mapped reads with at least one insertion	9.11%
Deletions	7,291,630
Mapped reads with at least one deletion	8.56%
Homopolymer indels	57.03%

2.7. Chromosome stats

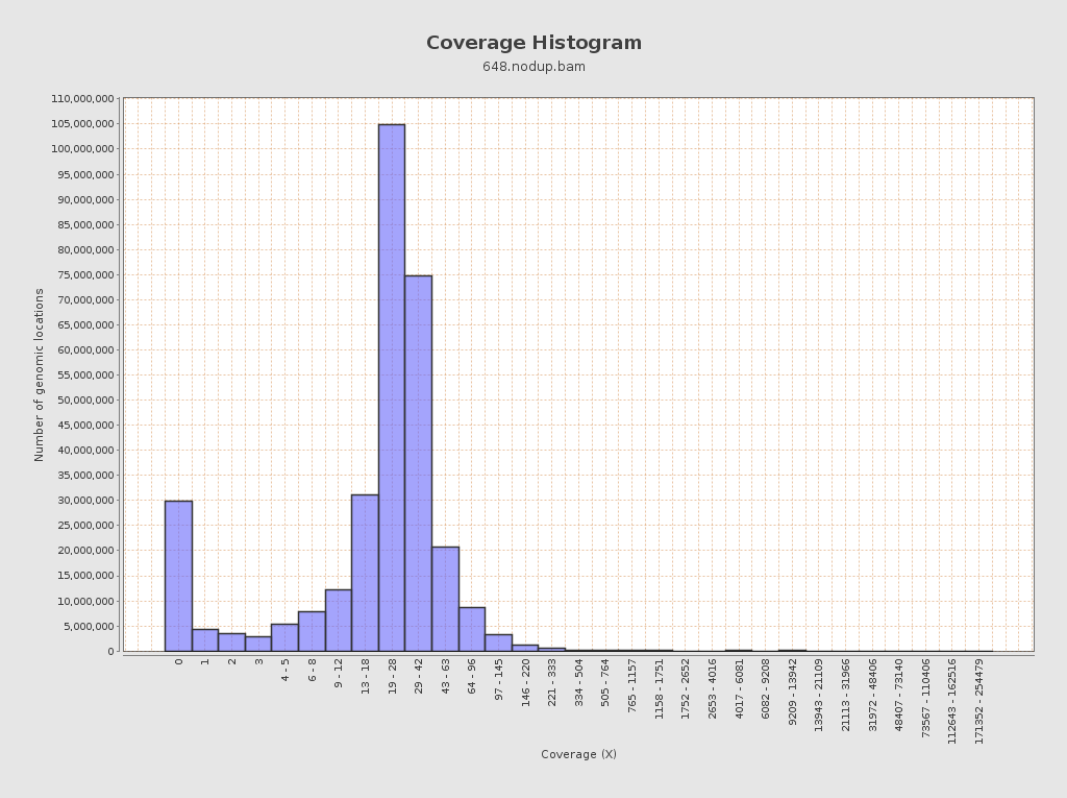
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	821422657	27.6347	132.3047

LT669789.1	36598175	1227959719	33.5525	338.0246
LT669790.1	30422129	1238796589	40.7202	450.268
LT669791.1	52758100	1711201721	32.4349	352.2082
LT669792.1	28376109	960693112	33.8557	345.1914
LT669793.1	33388210	994188819	29.7766	167.9717
LT669794.1	50579949	1564656957	30.9343	271.8434
LT669795.1	49795044	1808220643	36.3133	353.1479

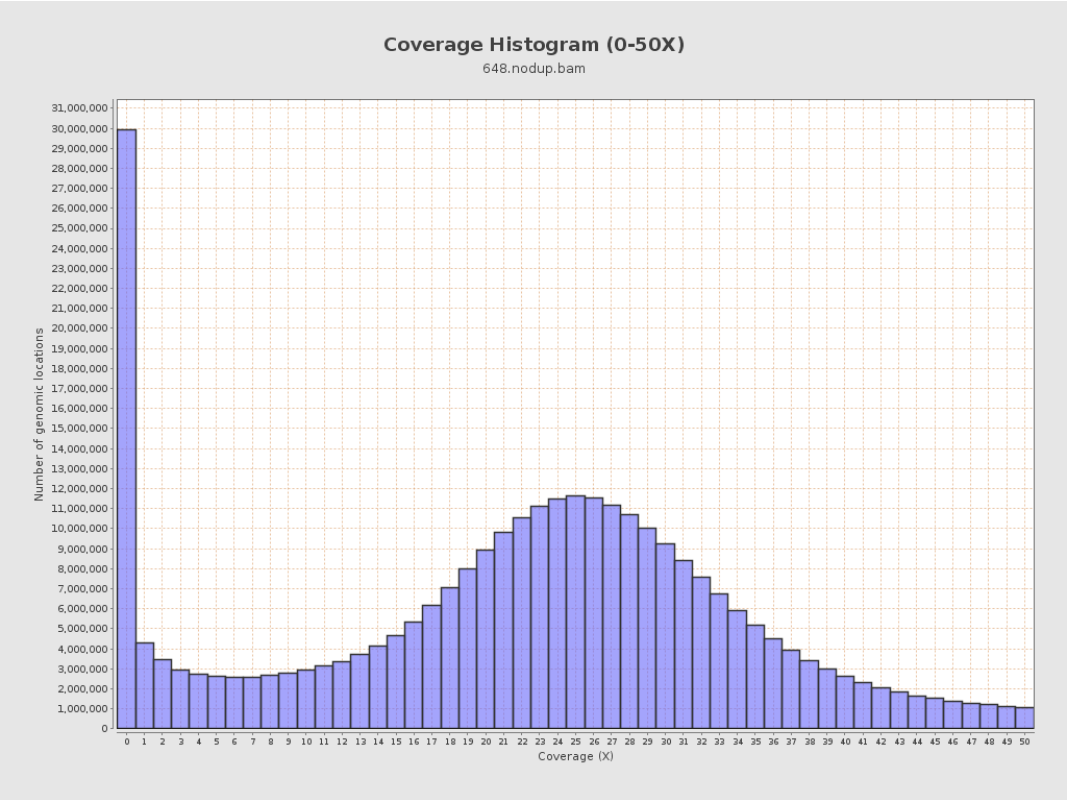
3. Results : Coverage across reference



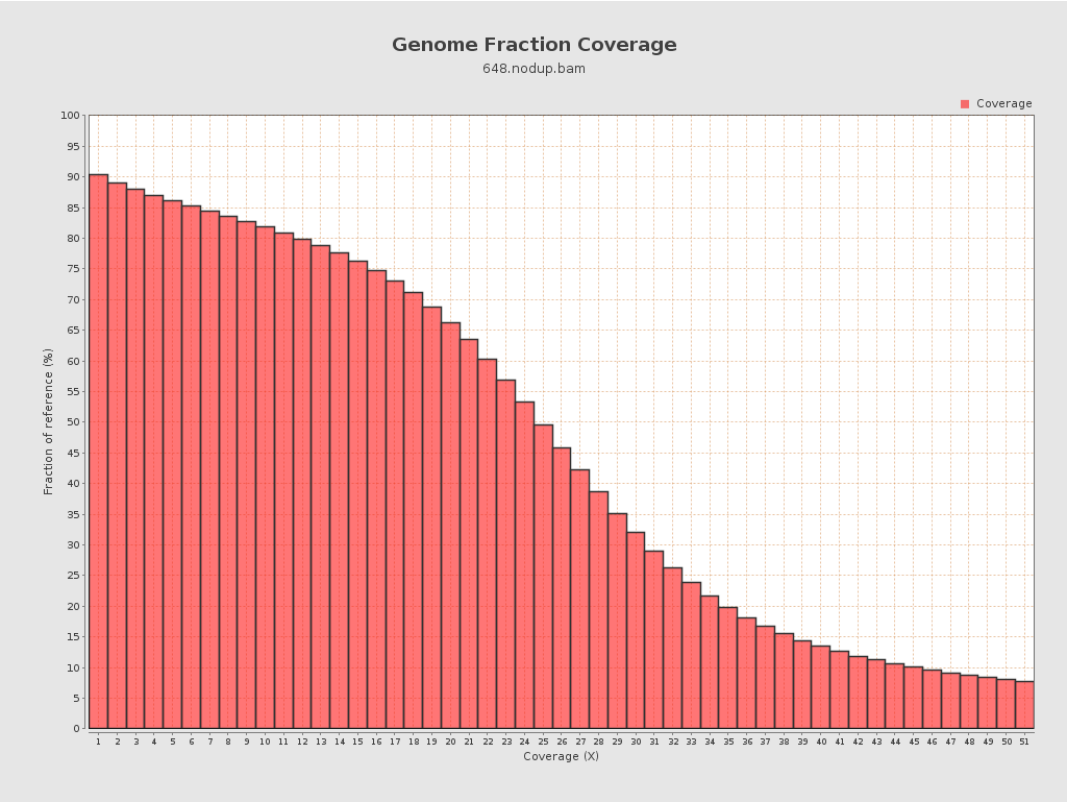
4. Results : Coverage Histogram



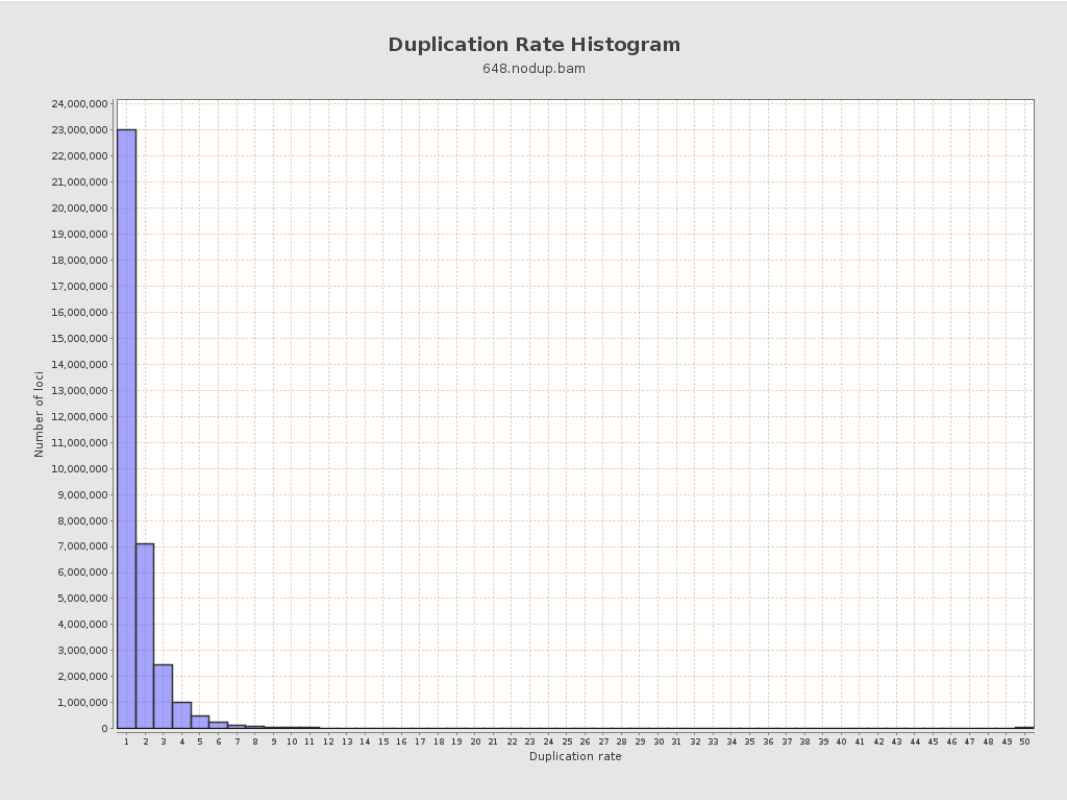
5. Results : Coverage Histogram (0-50X)



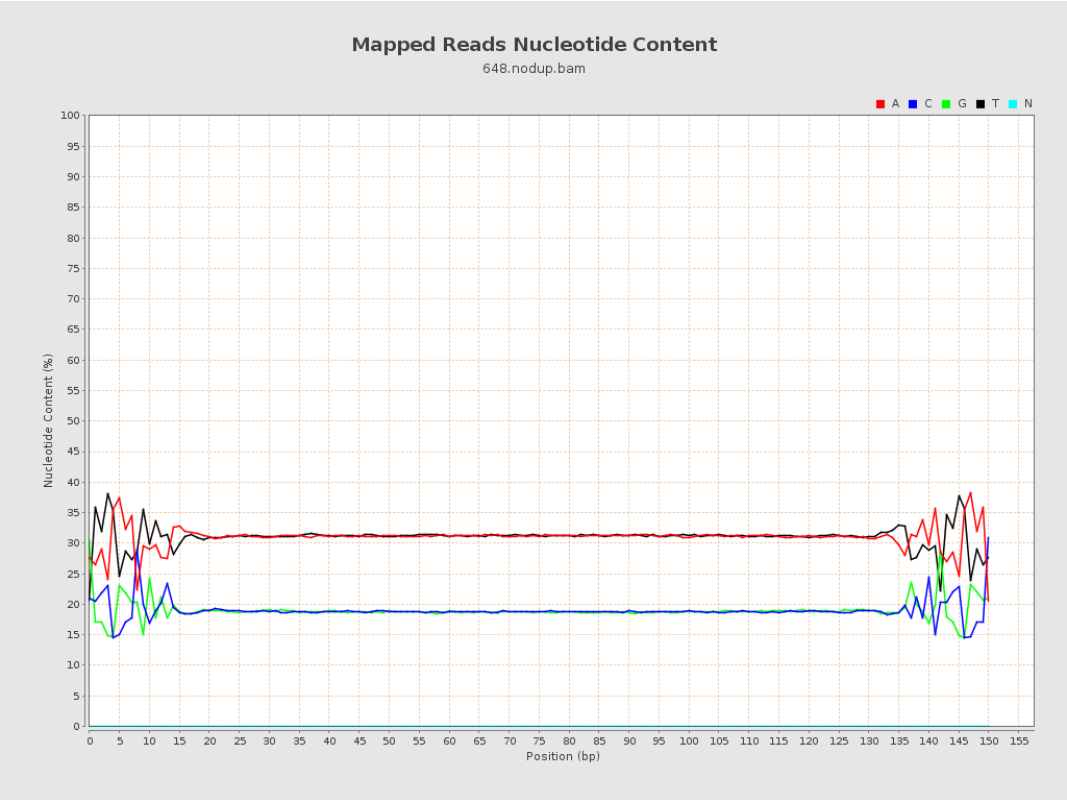
6. Results : Genome Fraction Coverage



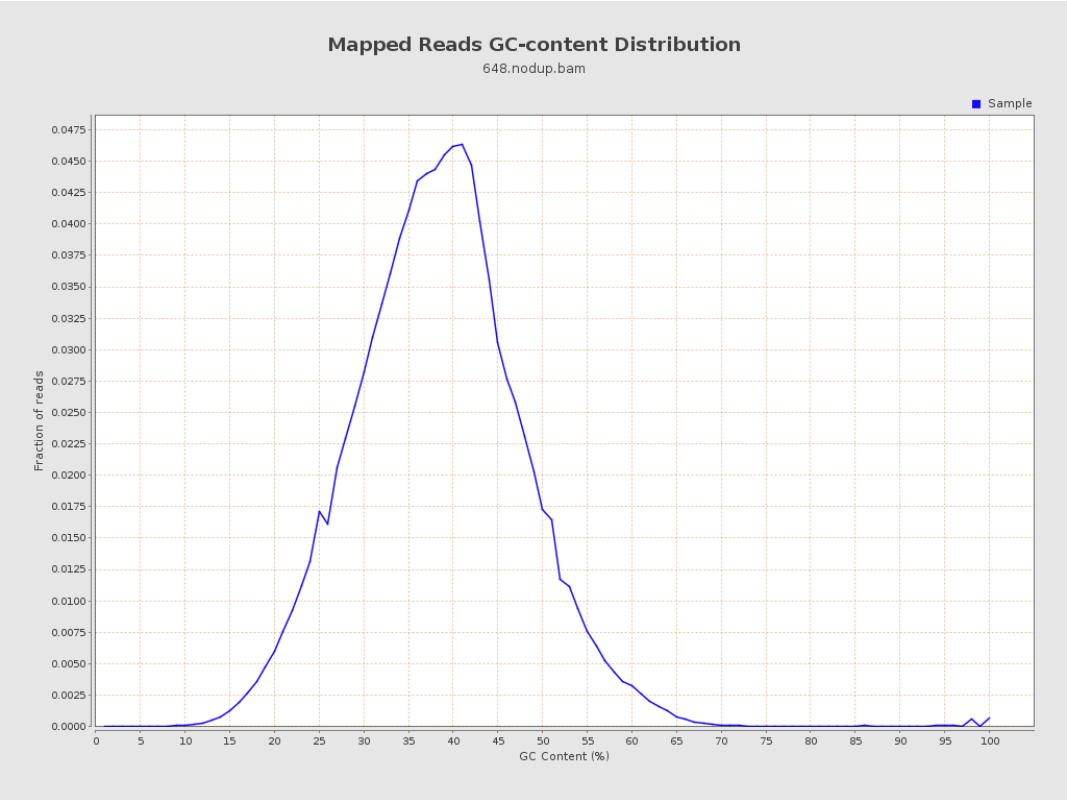
7. Results : Duplication Rate Histogram



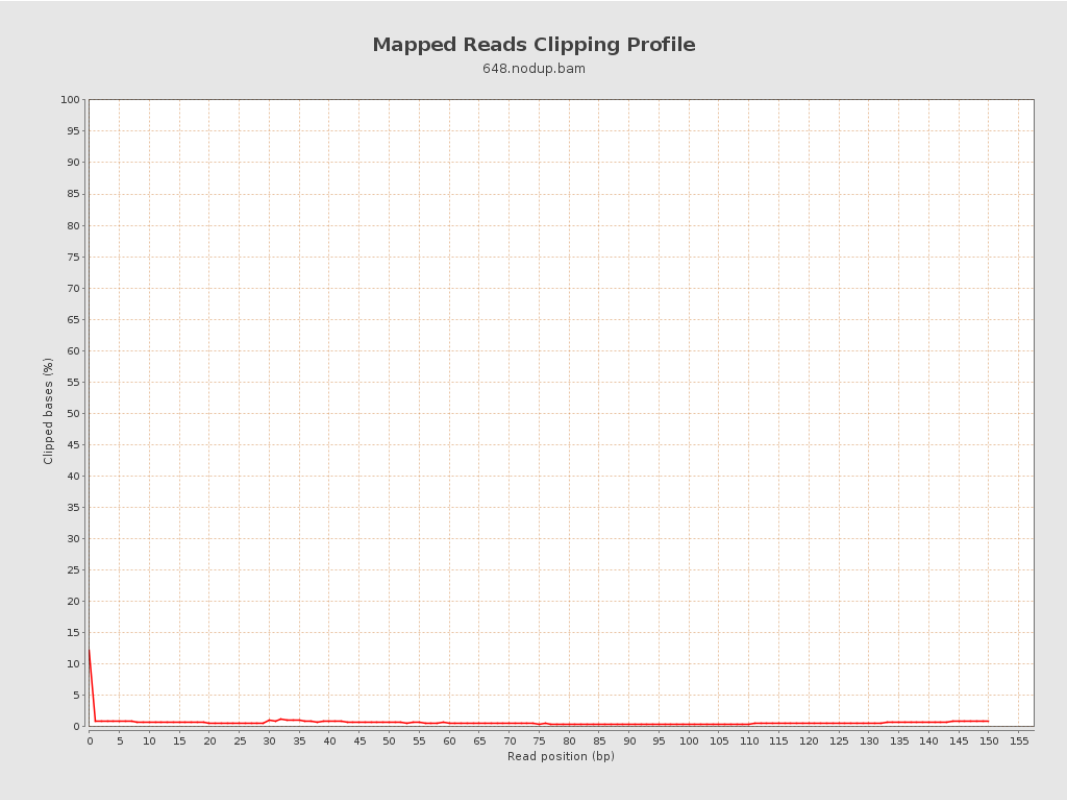
8. Results : Mapped Reads Nucleotide Content



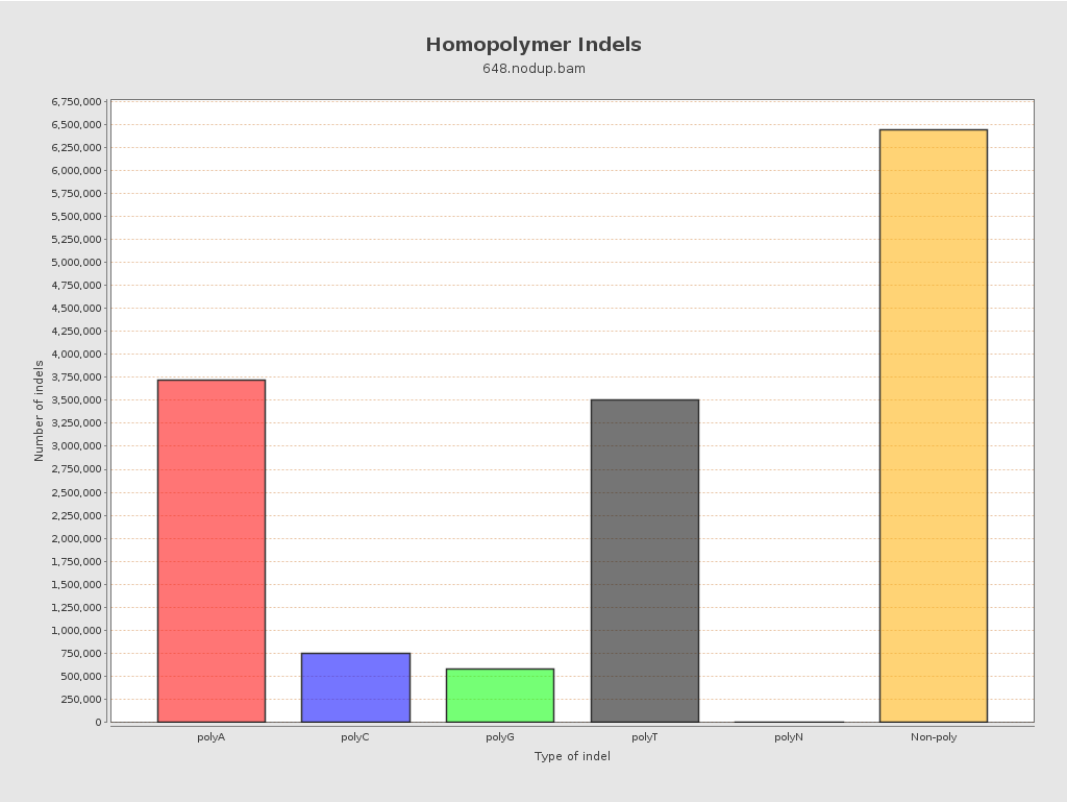
9. Results : Mapped Reads GC-content Distribution



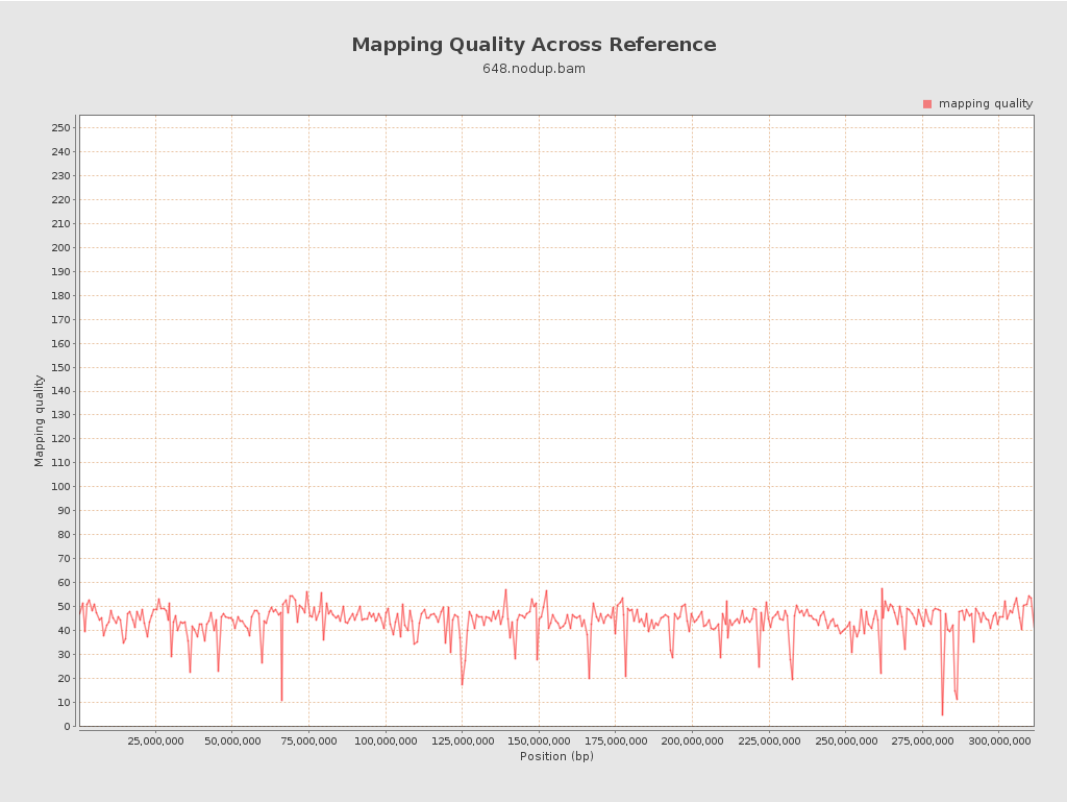
10. Results : Mapped Reads Clipping Profile



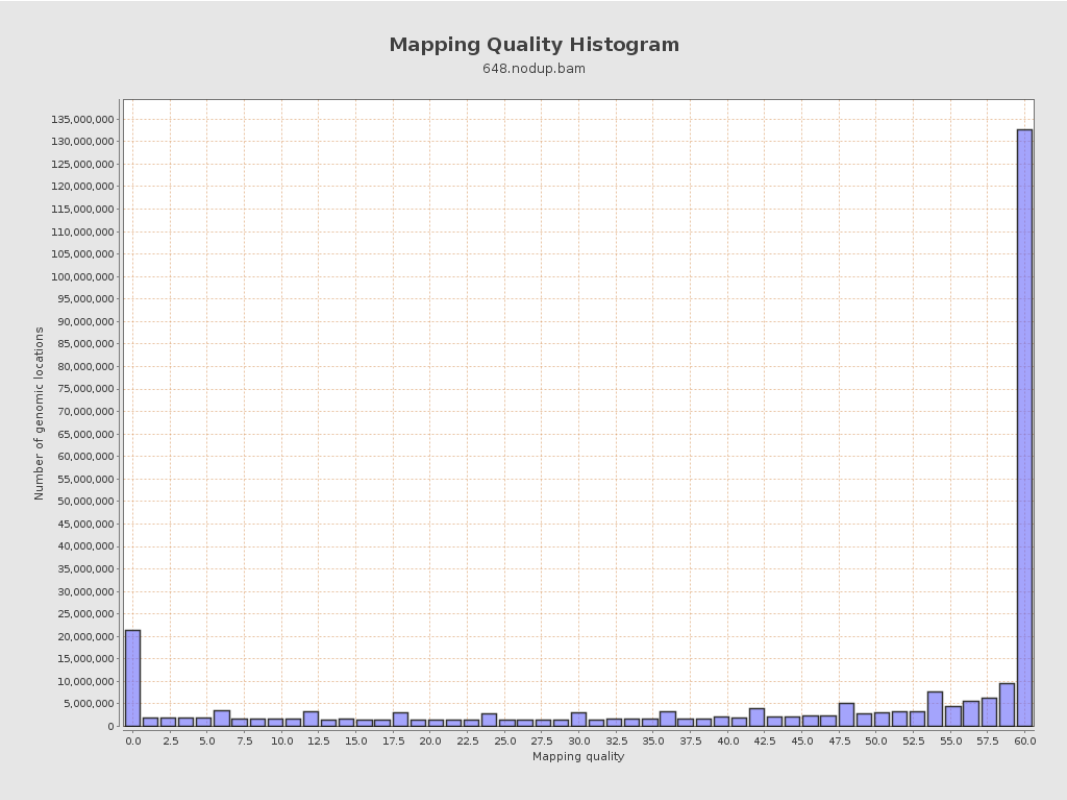
11. Results : Homopolymer Indels



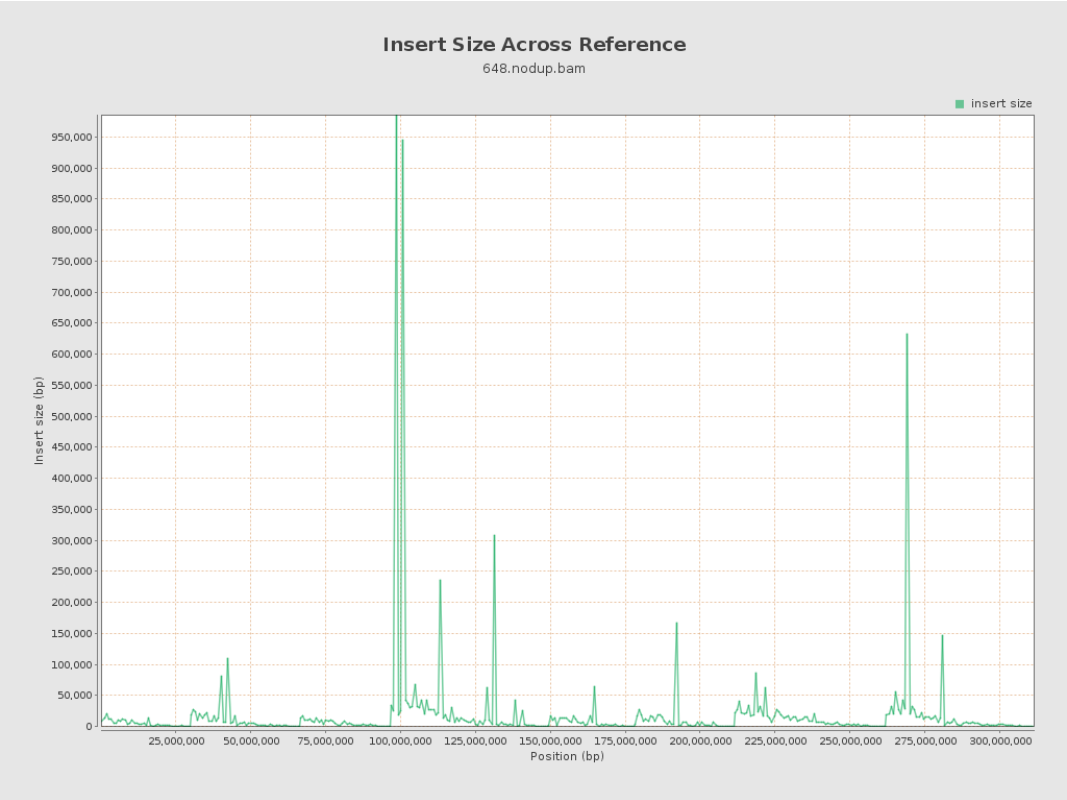
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram