Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1448
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1448 .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_103/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_103_S193_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_103/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_103_S193_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:26:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	55,269,618
Mapped reads	50,728,448 / 91.78%
Unmapped reads	4,541,170 / 8.22%
Mapped paired reads	50,728,448 / 91.78%
Mapped reads, first in pair	25,408,273 / 45.97%
Mapped reads, second in pair	25,320,175 / 45.81%
Mapped reads, both in pair	49,422,994 / 89.42%
Mapped reads, singletons	1,305,454 / 2.36%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	8,895,678 / 16.1%
Clipped reads	11,213,740 / 20.29%

2.2. ACGT Content

Number/percentage of A's	2,174,969,894 / 30.95%
Number/percentage of C's	1,339,236,439 / 19.06%
Number/percentage of T's	2,178,147,237 / 31%
Number/percentage of G's	1,334,731,844 / 18.99%
Number/percentage of N's	29,303 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	22.6076
Standard Deviation	179.1286

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Insert size

Mean	253,068.32
Standard Deviation	2,412,246.96
P25/Median/P75	349 / 450 / 576

2.6. Mismatches and indels

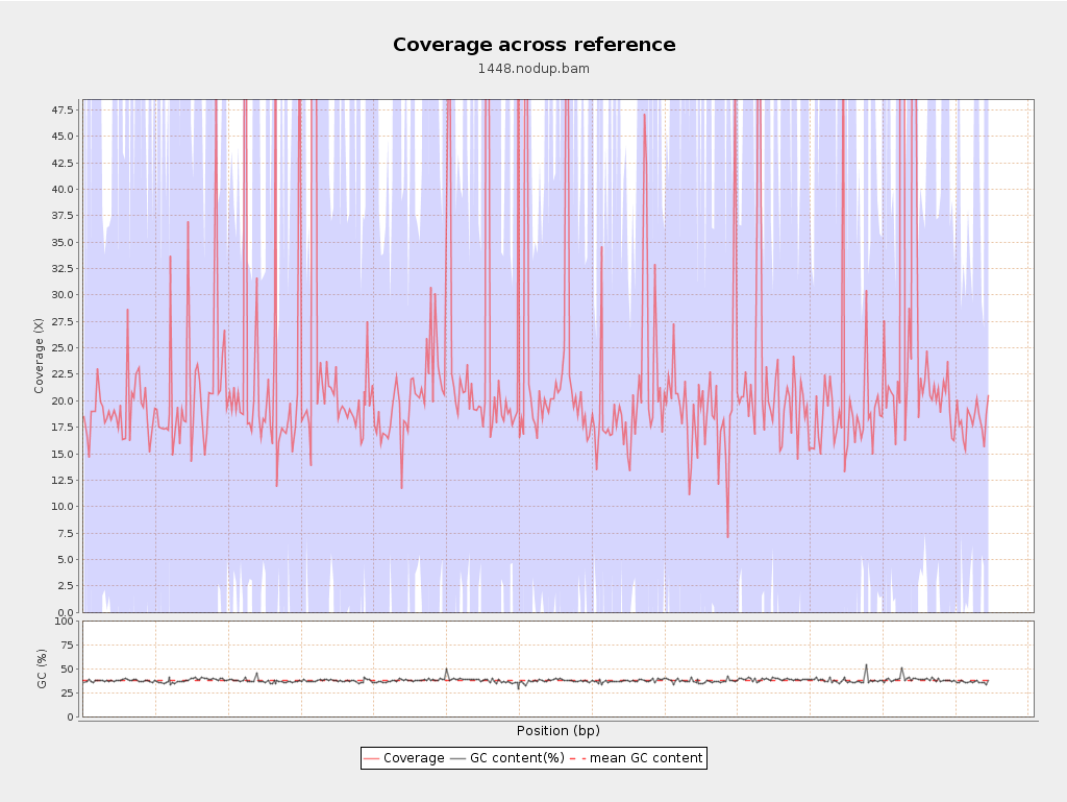
General error rate	2.29%
Mismatches	146,901,171
Insertions	4,931,151
Mapped reads with at least one insertion	8.69%
Deletions	4,874,985
Mapped reads with at least one deletion	8.51%
Homopolymer indels	57.21%

2.7. Chromosome stats

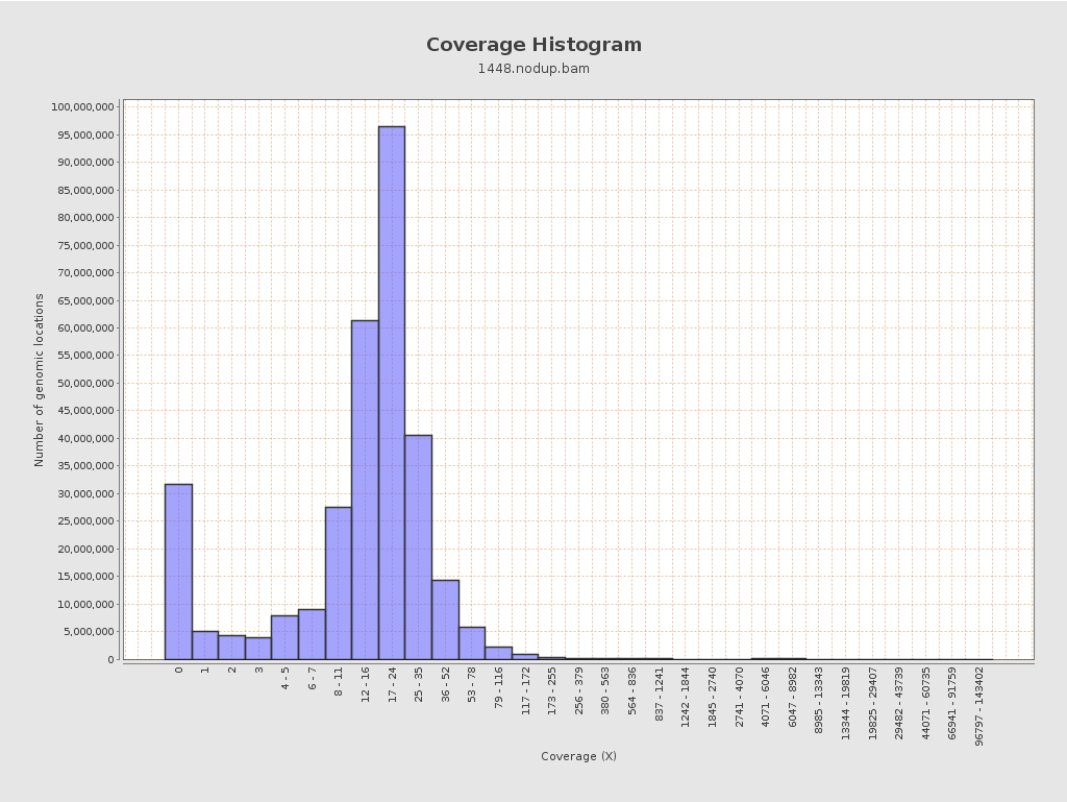
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	562136299	18.9116	64.9998

LT669789.1	36598175	820133254	22.4091	185.841
LT669790.1	30422129	790590609	25.9874	230.3932
LT669791.1	52758100	1174535620	22.2627	176.9604
LT669792.1	28376109	643625918	22.682	182.798
LT669793.1	33388210	679712334	20.3579	93.049
LT669794.1	50579949	1067473999	21.1047	150.2199
LT669795.1	49795044	1307281937	26.2533	243.9258

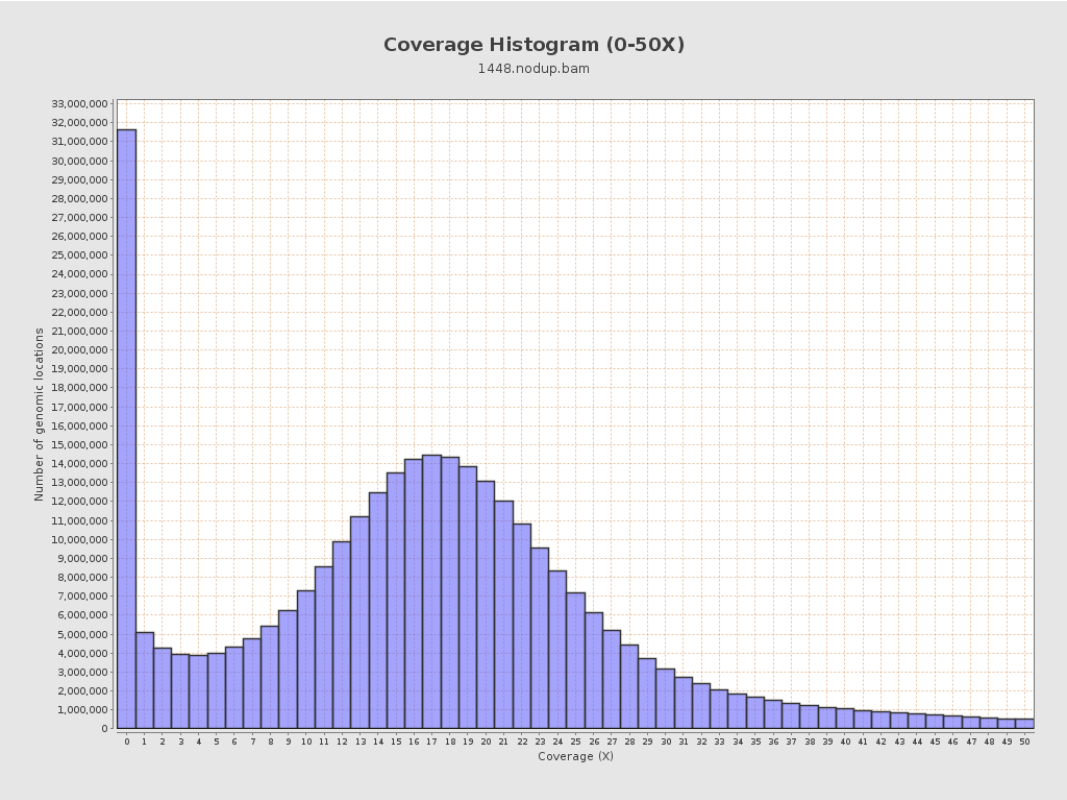
3. Results : Coverage across reference



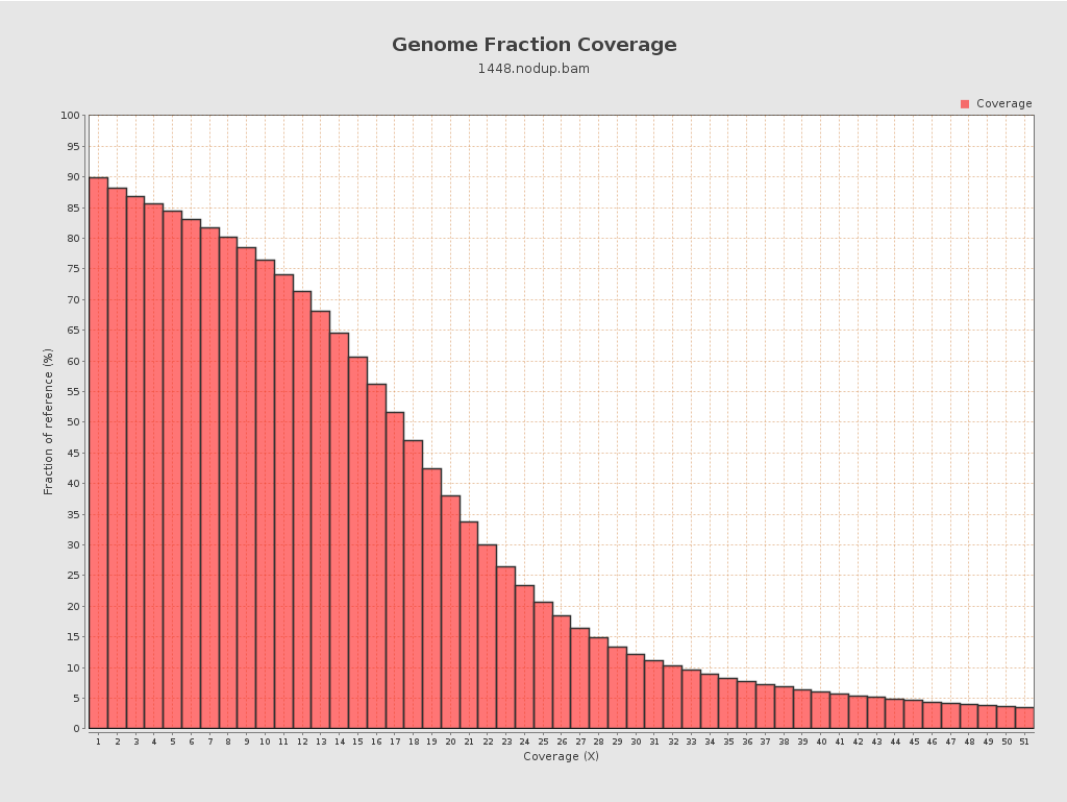
4. Results : Coverage Histogram



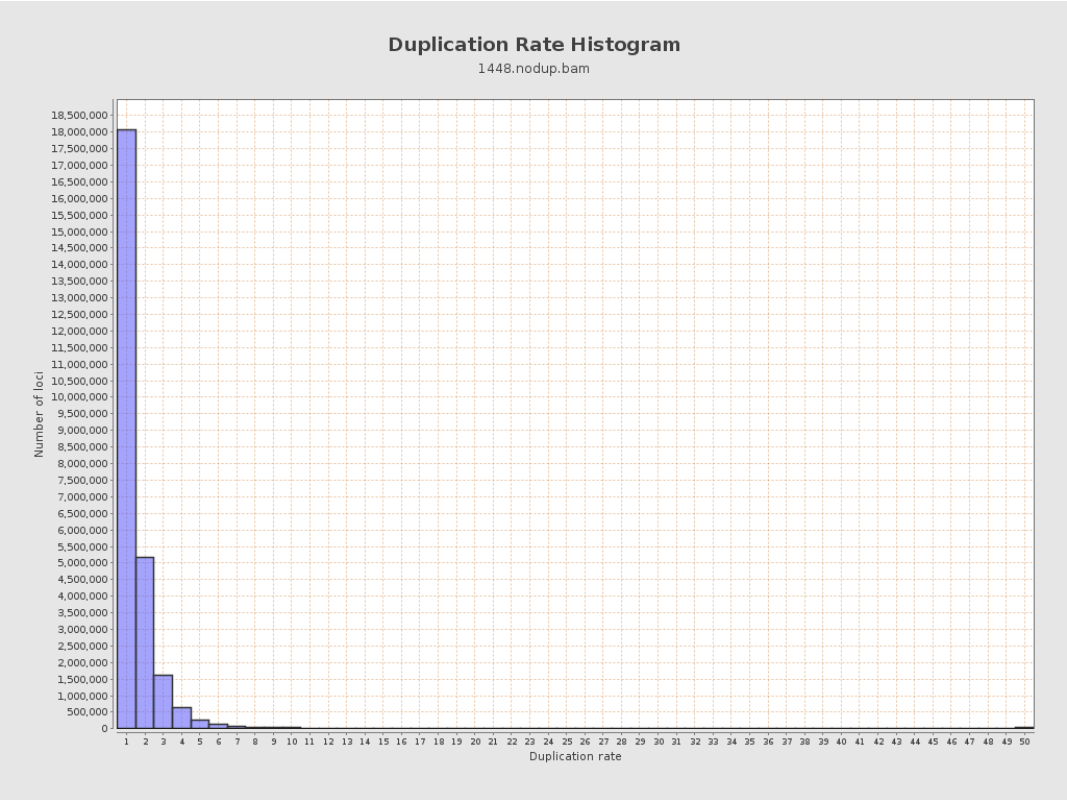
5. Results : Coverage Histogram (0-50X)



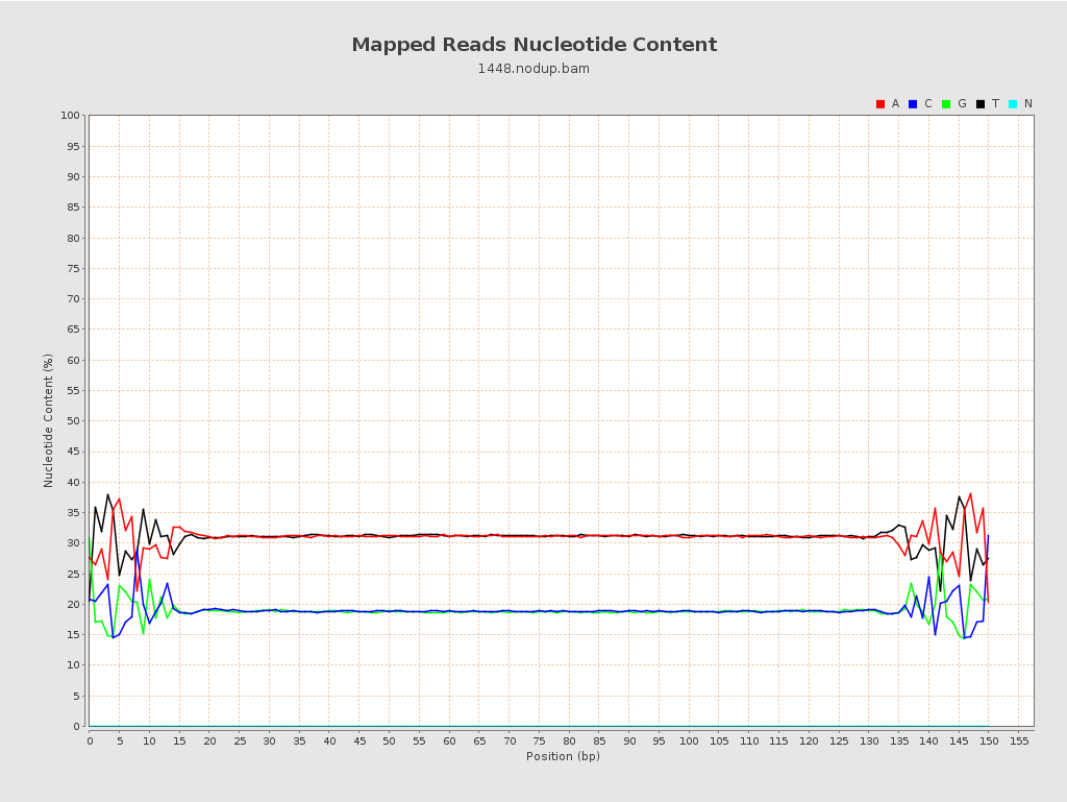
6. Results : Genome Fraction Coverage



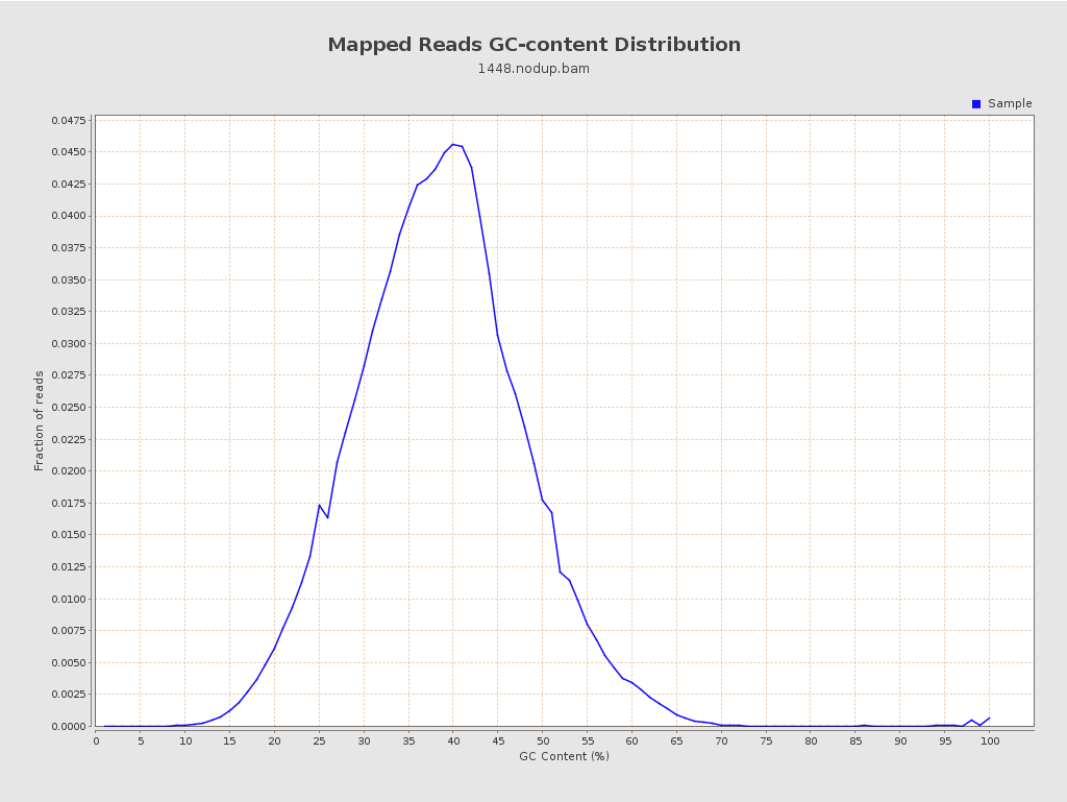
7. Results : Duplication Rate Histogram



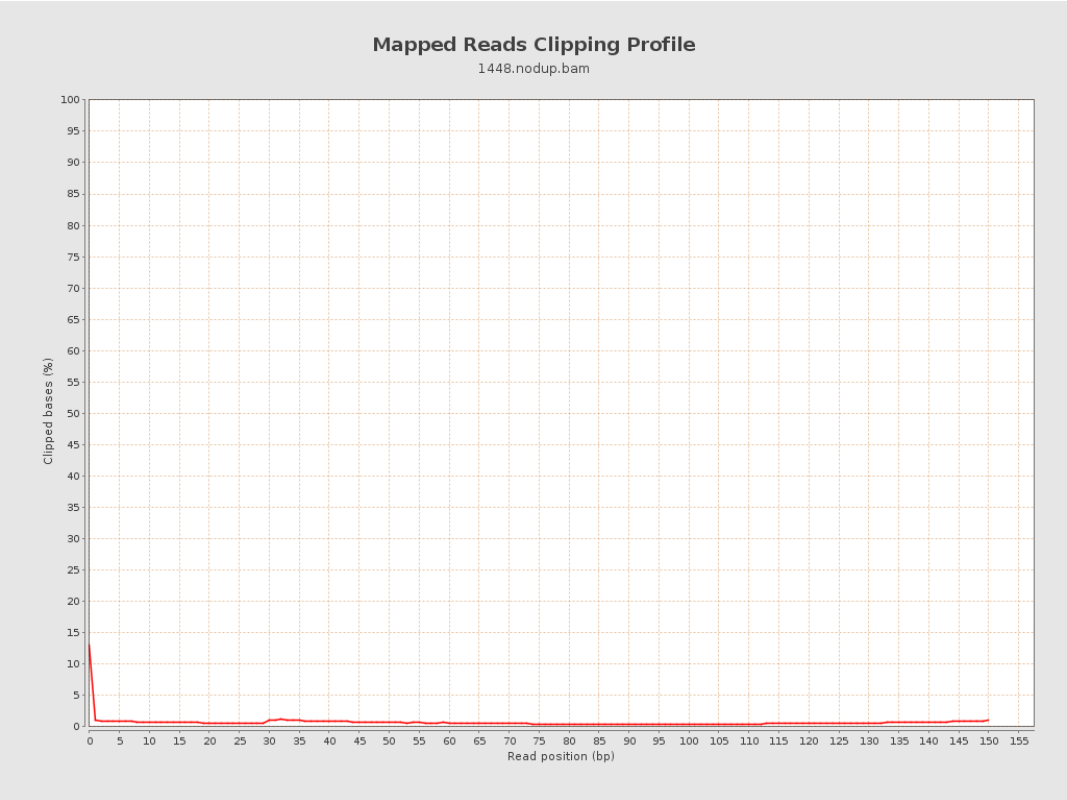
8. Results : Mapped Reads Nucleotide Content



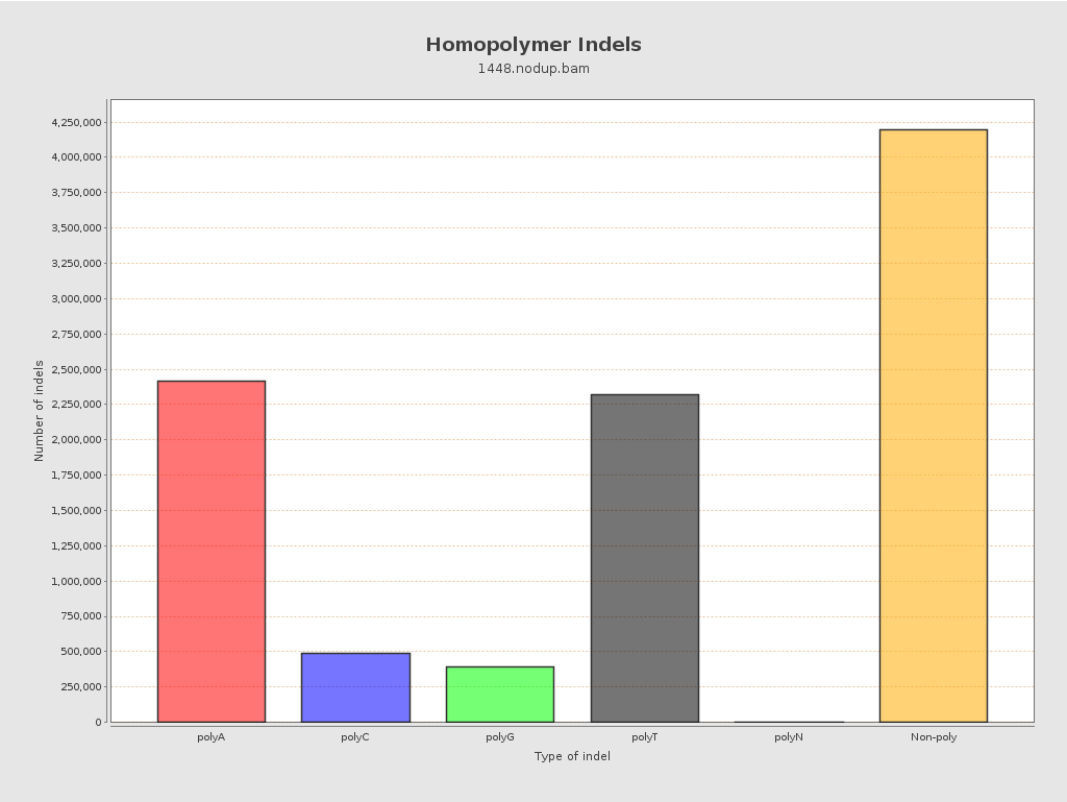
9. Results : Mapped Reads GC-content Distribution



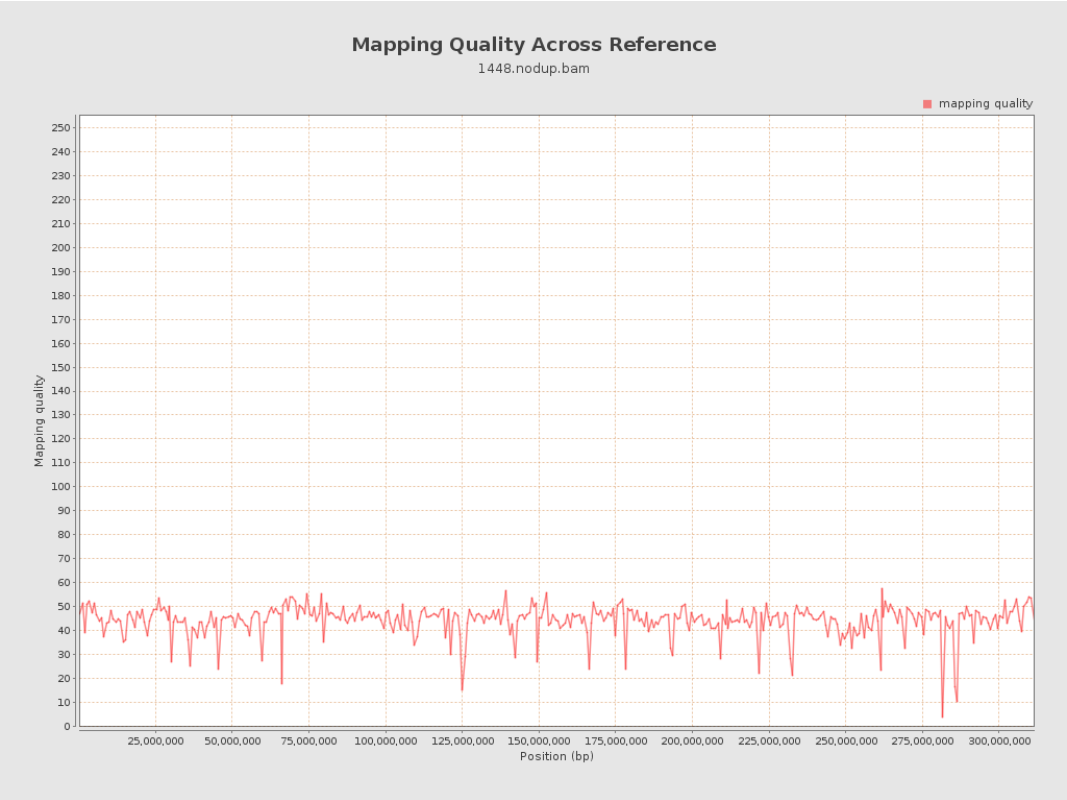
10. Results : Mapped Reads Clipping Profile



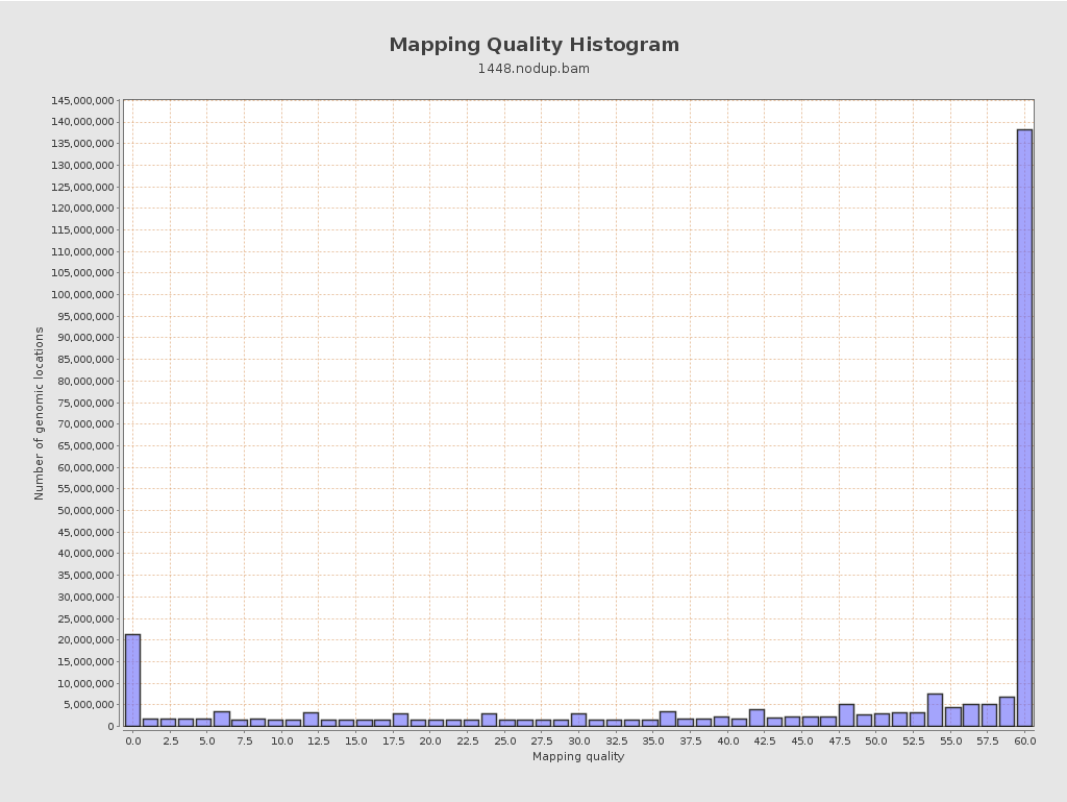
11. Results : Homopolymer Indels



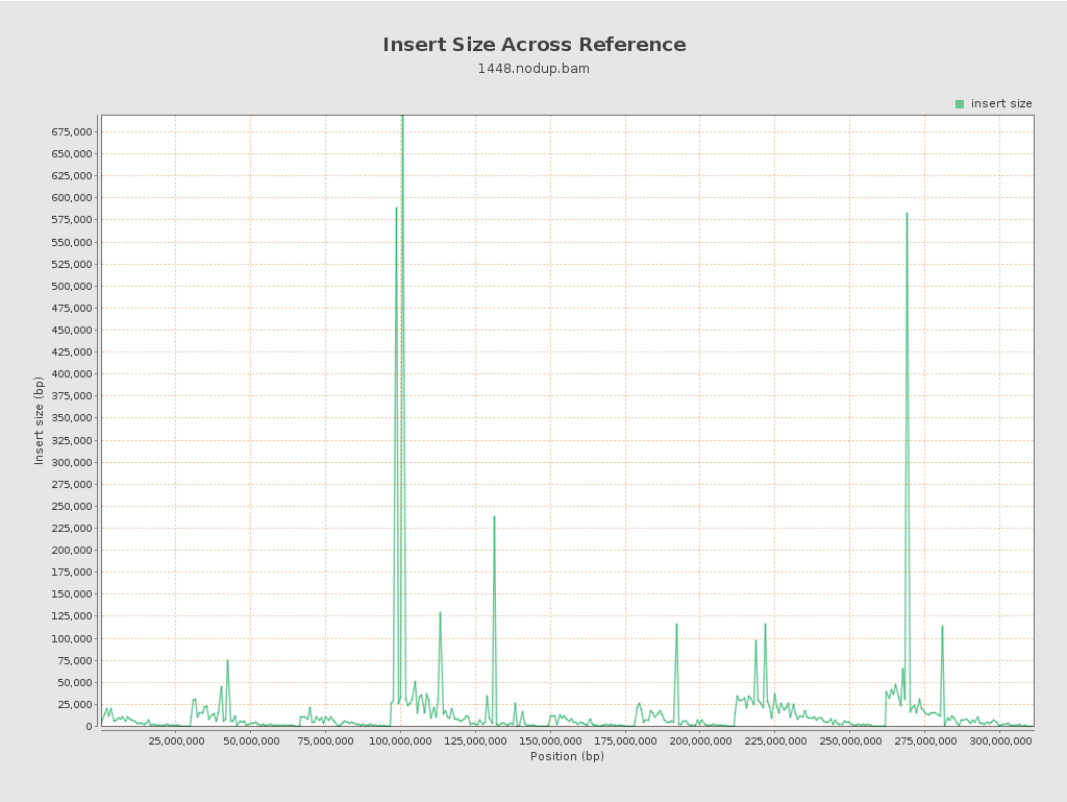
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram