Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/880.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/880.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_113/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_113_S203_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_113/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_113_S203_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	81,871,988
Mapped reads	72,955,910 / 89.11%
Unmapped reads	8,916,078 / 10.89%
Mapped paired reads	72,955,910 / 89.11%
Mapped reads, first in pair	36,513,542 / 44.6%
Mapped reads, second in pair	36,442,368 / 44.51%
Mapped reads, both in pair	70,157,665 / 85.69%
Mapped reads, singletons	2,798,245 / 3.42%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	16,831,517 / 20.56%
Clipped reads	17,724,161 / 21.65%

2.2. ACGT Content

Number/percentage of A's	3,083,894,491 / 31.04%
Number/percentage of C's	1,883,133,957 / 18.95%
Number/percentage of T's	3,086,497,050 / 31.07%
Number/percentage of G's	1,881,493,617 / 18.94%
Number/percentage of N's	41,347 / 0%
GC Percentage	37.89%

2.3. Coverage

Mean	31.9605
Standard Deviation	381.2389

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Insert size

Mean	267,164.92
Standard Deviation	2,530,045.07
P25/Median/P75	299 / 392 / 513

2.6. Mismatches and indels

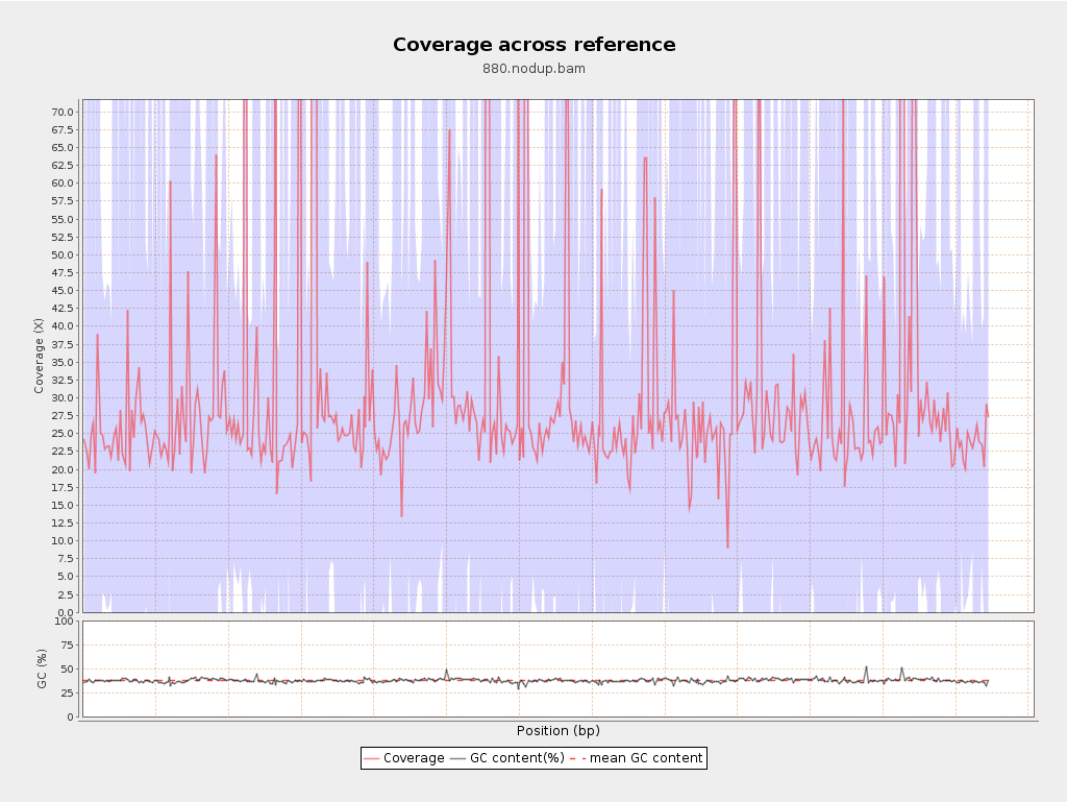
General error rate	2.36%
Mismatches	213,139,691
Insertions	7,717,424
Mapped reads with at least one insertion	9.36%
Deletions	6,871,253
Mapped reads with at least one deletion	8.36%
Homopolymer indels	58.6%

2.7. Chromosome stats

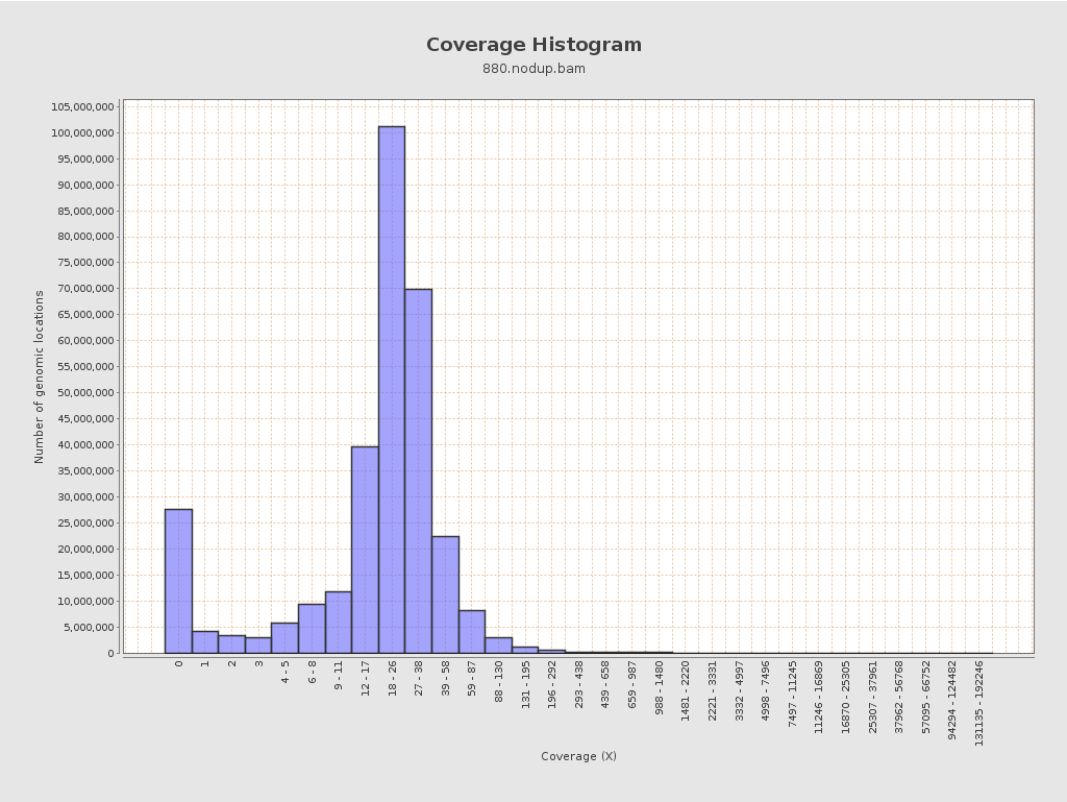
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	743570658	25.0155	170.1522

LT669789.1	36598175	1158884655	31.6651	403.7993
LT669790.1	30422129	1330531740	43.7357	636.1532
LT669791.1	52758100	1710900354	32.4292	464.7666
LT669792.1	28376109	916569227	32.3007	367.0931
LT669793.1	33388210	929835496	27.8492	227.183
LT669794.1	50579949	1470100755	29.0649	282.0868
LT669795.1	49795044	1699843729	34.1368	322.546

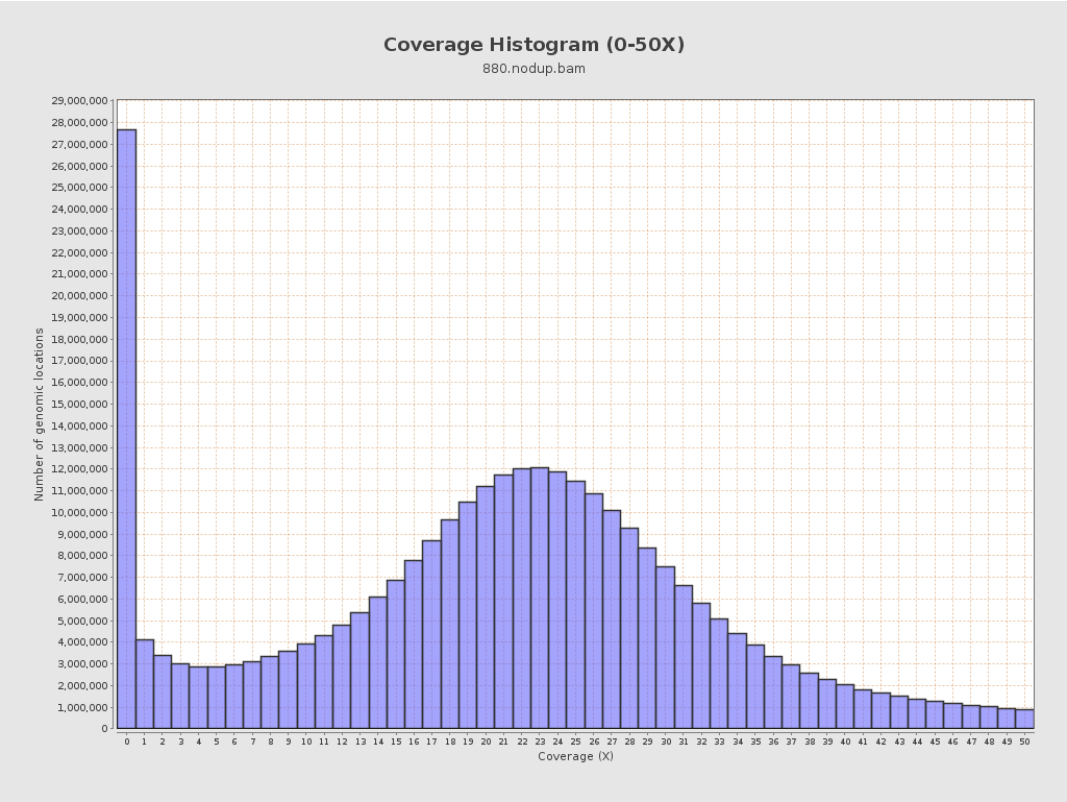
3. Results : Coverage across reference



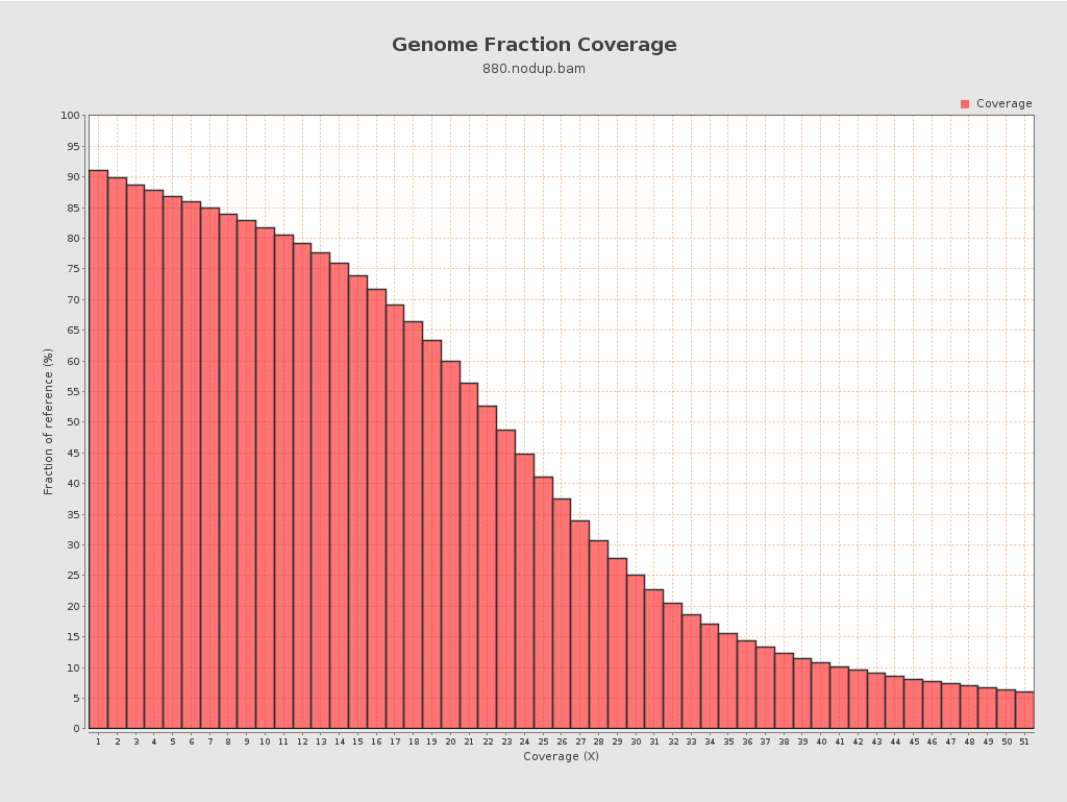
4. Results : Coverage Histogram



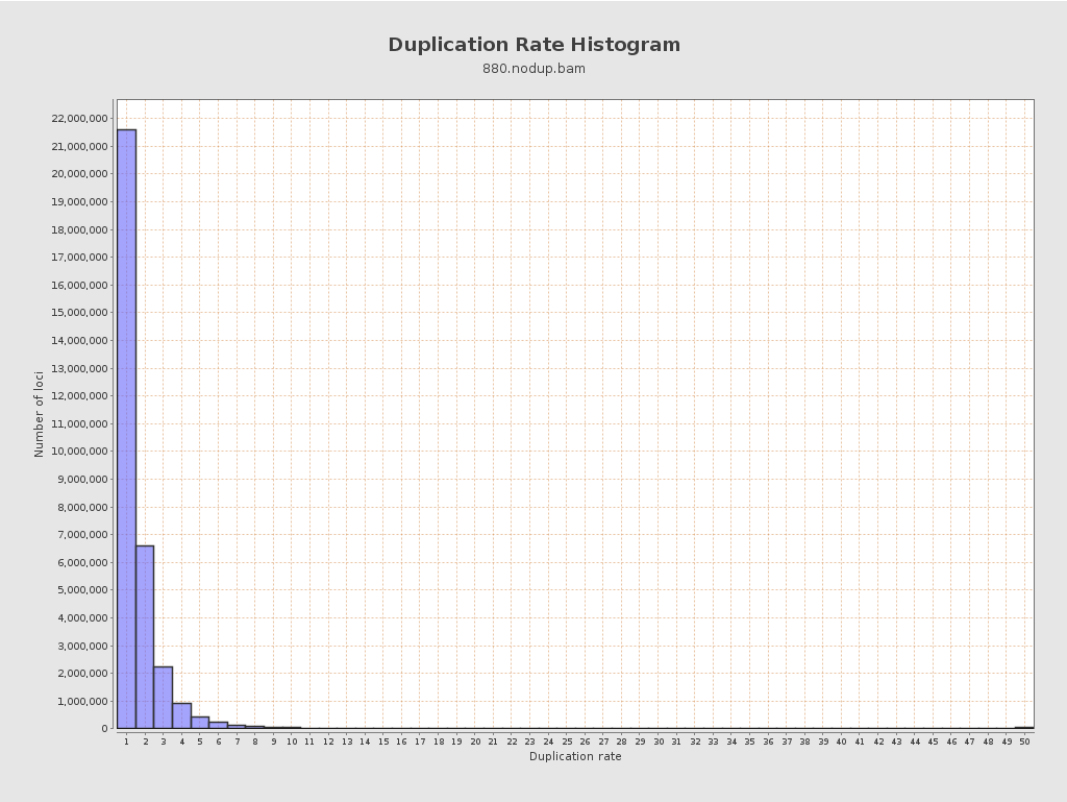
5. Results : Coverage Histogram (0-50X)



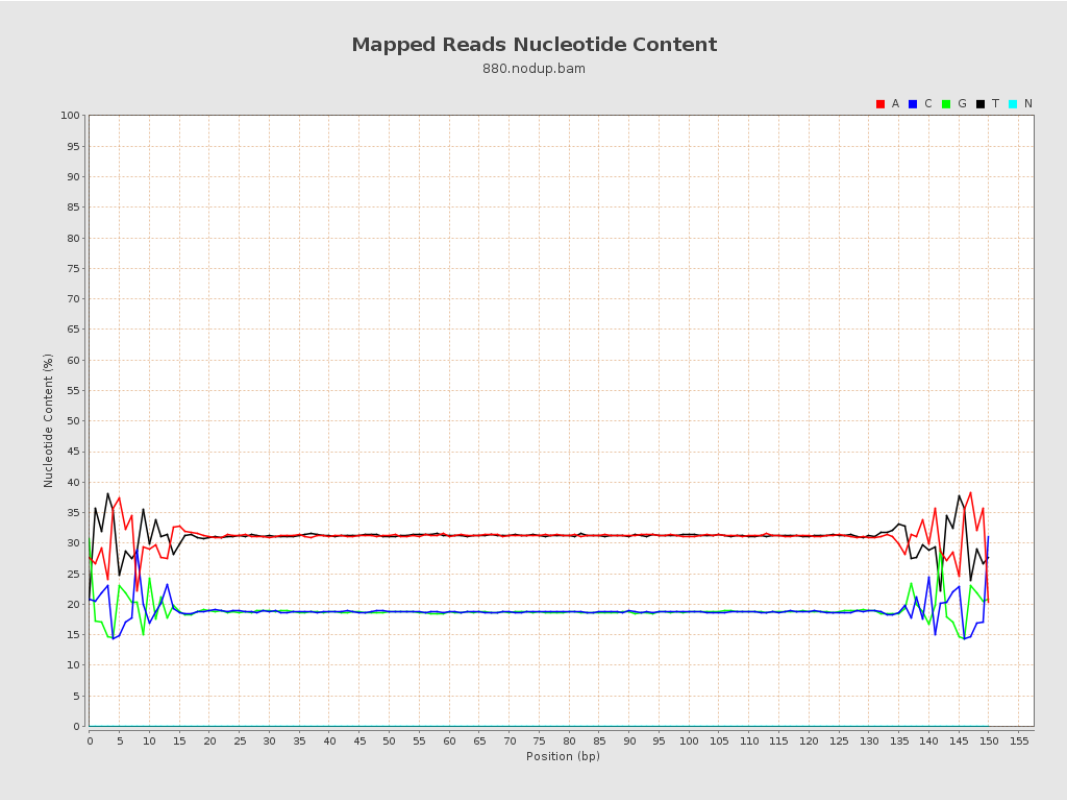
6. Results : Genome Fraction Coverage



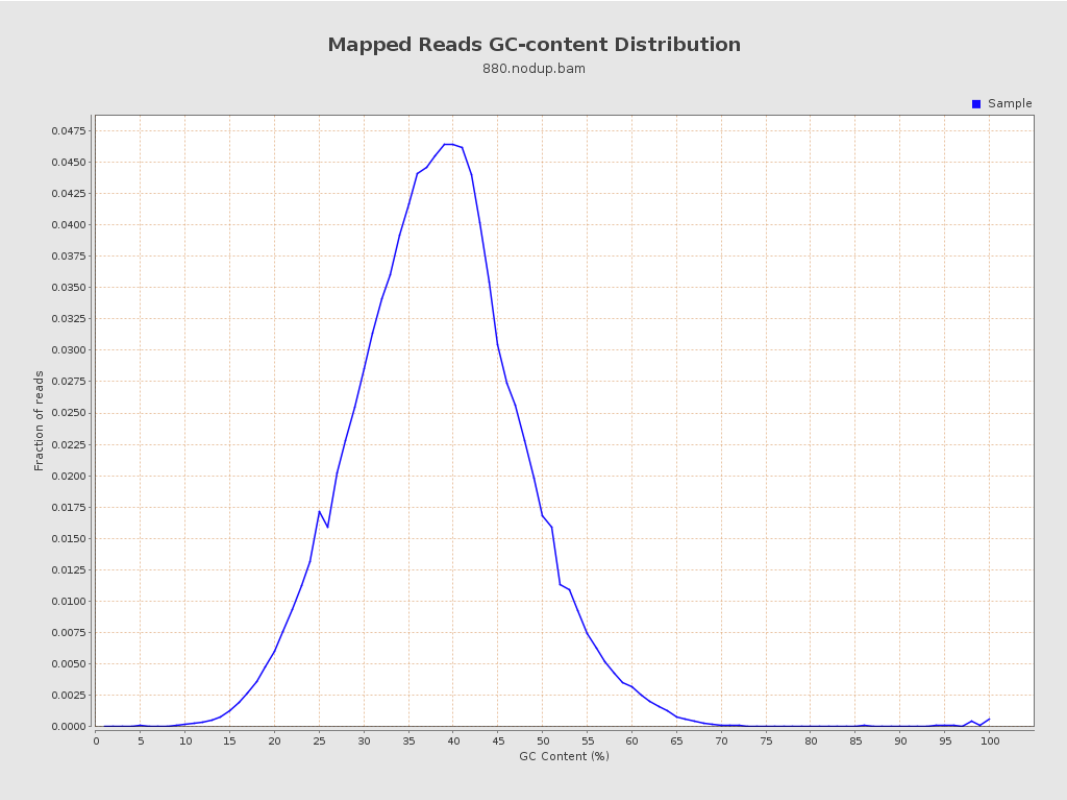
7. Results : Duplication Rate Histogram



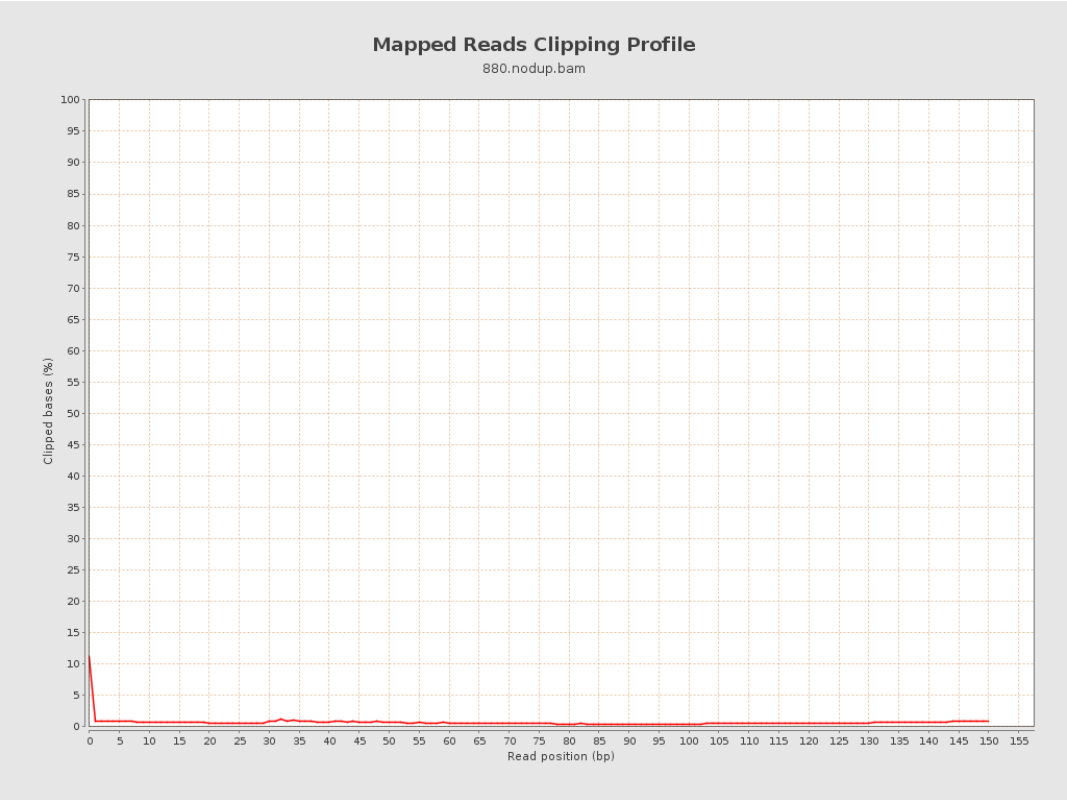
8. Results : Mapped Reads Nucleotide Content



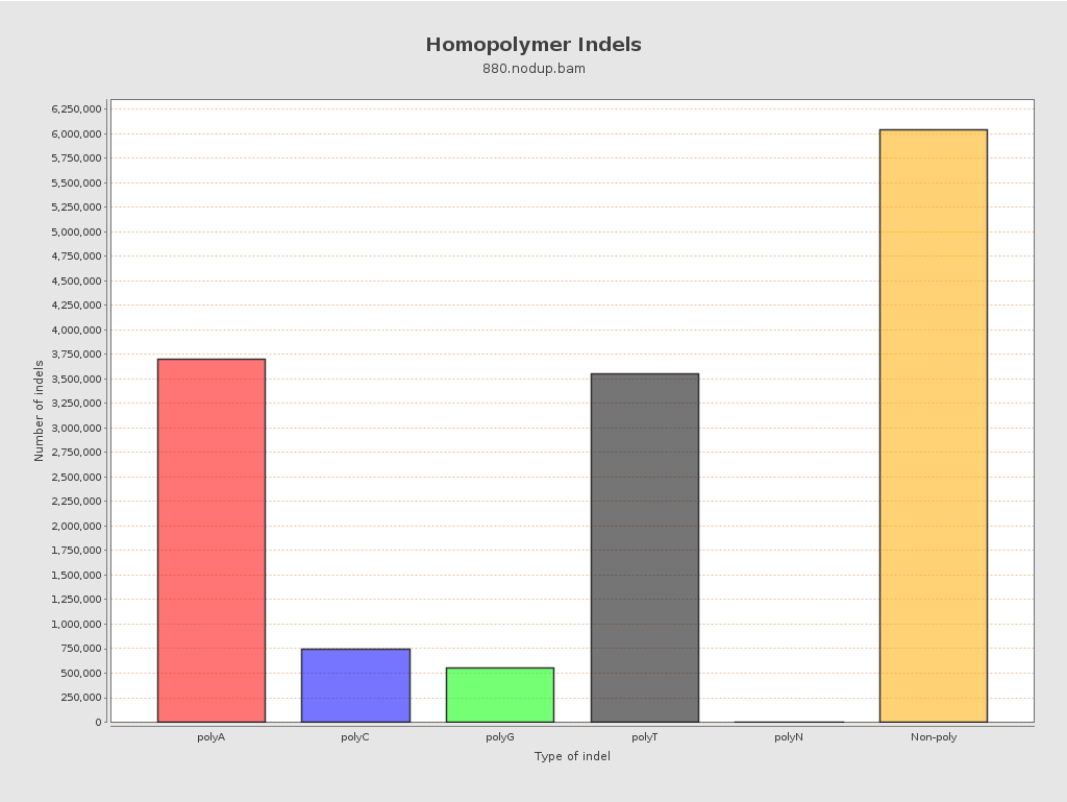
9. Results : Mapped Reads GC-content Distribution



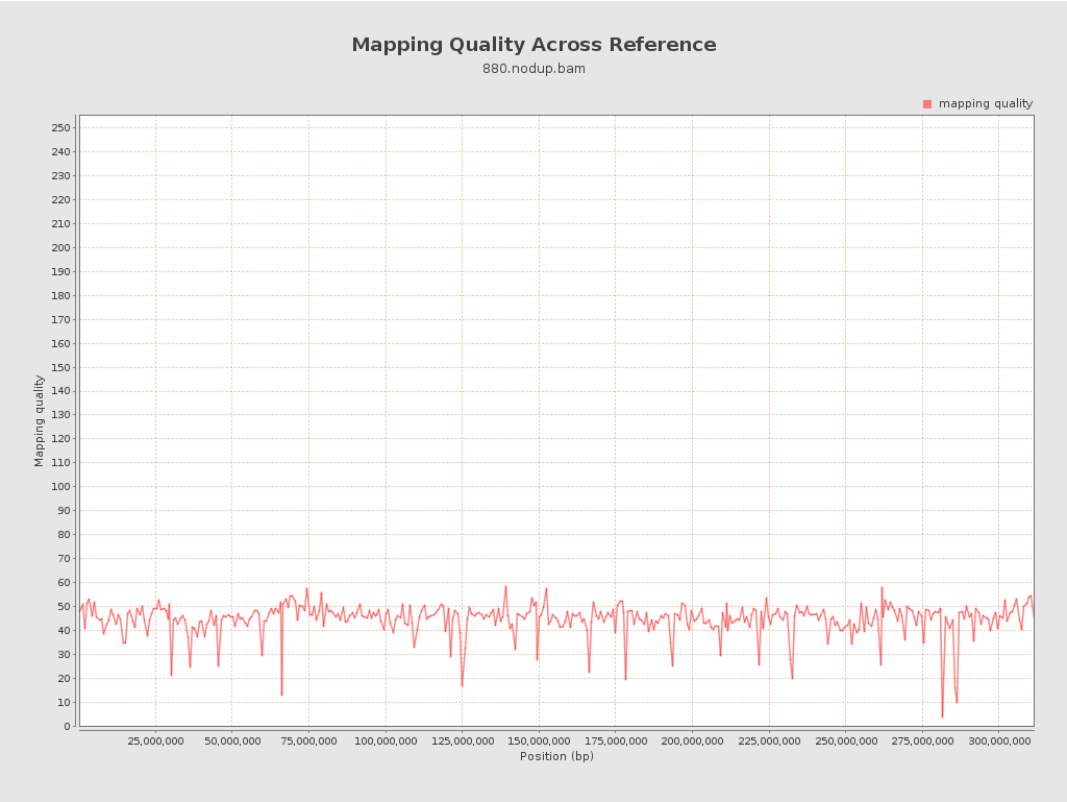
10. Results : Mapped Reads Clipping Profile



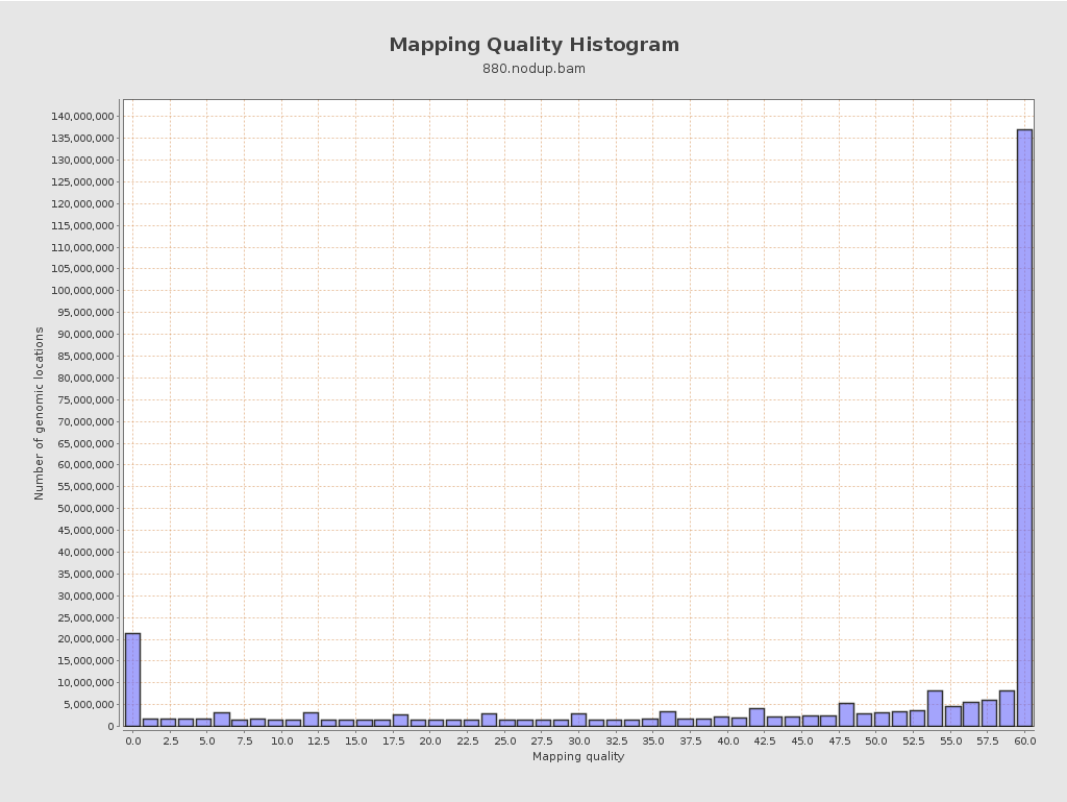
11. Results : Homopolymer Indels



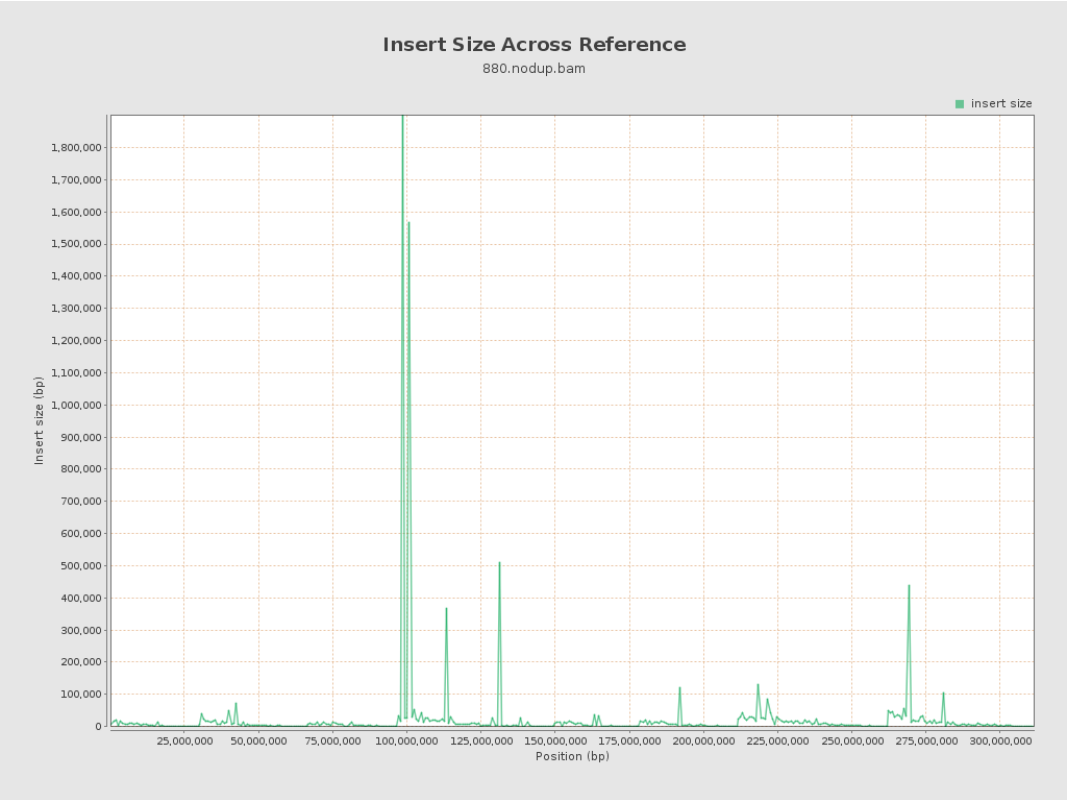
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram