Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/530.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/530.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_123/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_123_S213_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_123/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_123_S213_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:50 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	83,432,631
Mapped reads	76,129,382 / 91.25%
Unmapped reads	7,303,249 / 8.75%
Mapped paired reads	76,129,382 / 91.25%
Mapped reads, first in pair	38,138,772 / 45.71%
Mapped reads, second in pair	37,990,610 / 45.53%
Mapped reads, both in pair	73,753,759 / 88.4%
Mapped reads, singletons	2,375,623 / 2.85%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	15,521,178 / 18.6%
Clipped reads	18,013,456 / 21.59%

2.2. ACGT Content

Number/percentage of A's	3,235,250,416 / 30.91%
Number/percentage of C's	1,997,666,806 / 19.09%
Number/percentage of T's	3,238,087,811 / 30.94%
Number/percentage of G's	1,995,851,113 / 19.07%
Number/percentage of N's	44,639 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	33.6767
Standard Deviation	321.2226

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Insert size

Mean	269,618.58
Standard Deviation	2,491,477.3
P25/Median/P75	337 / 439 / 574

2.6. Mismatches and indels

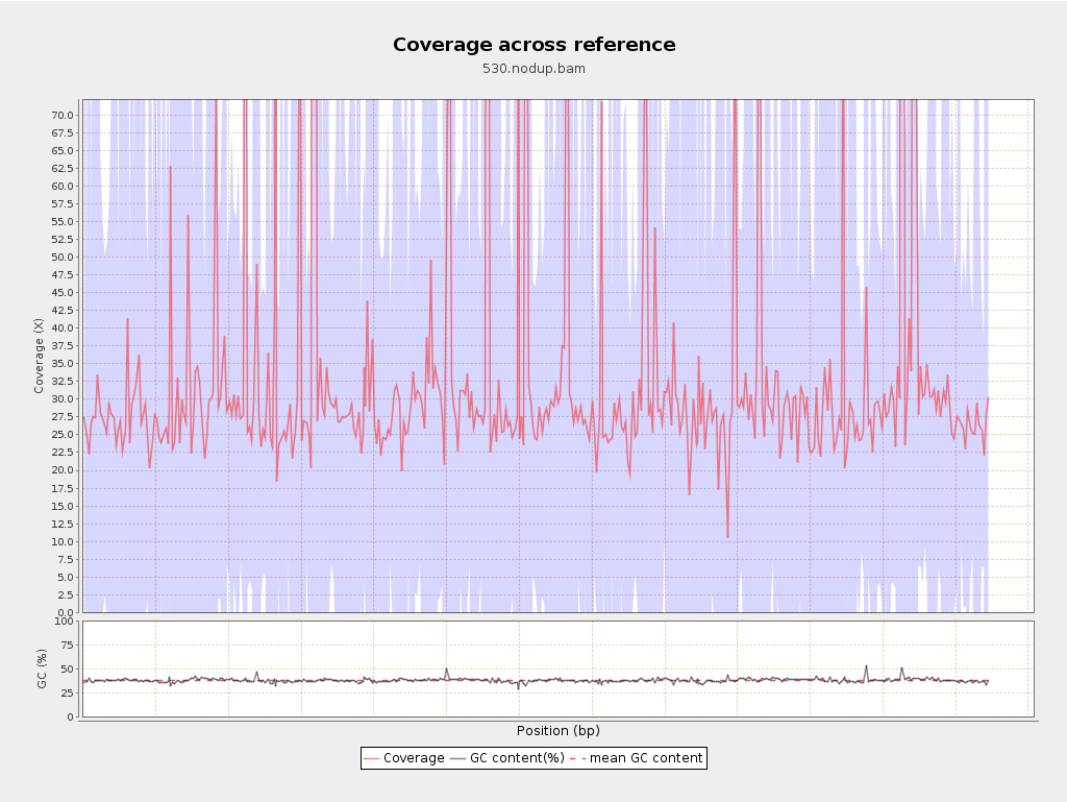
General error rate	2.44%
Mismatches	233,643,994
Insertions	7,765,924
Mapped reads with at least one insertion	9.09%
Deletions	7,560,926
Mapped reads with at least one deletion	8.79%
Homopolymer indels	56.94%

2.7. Chromosome stats

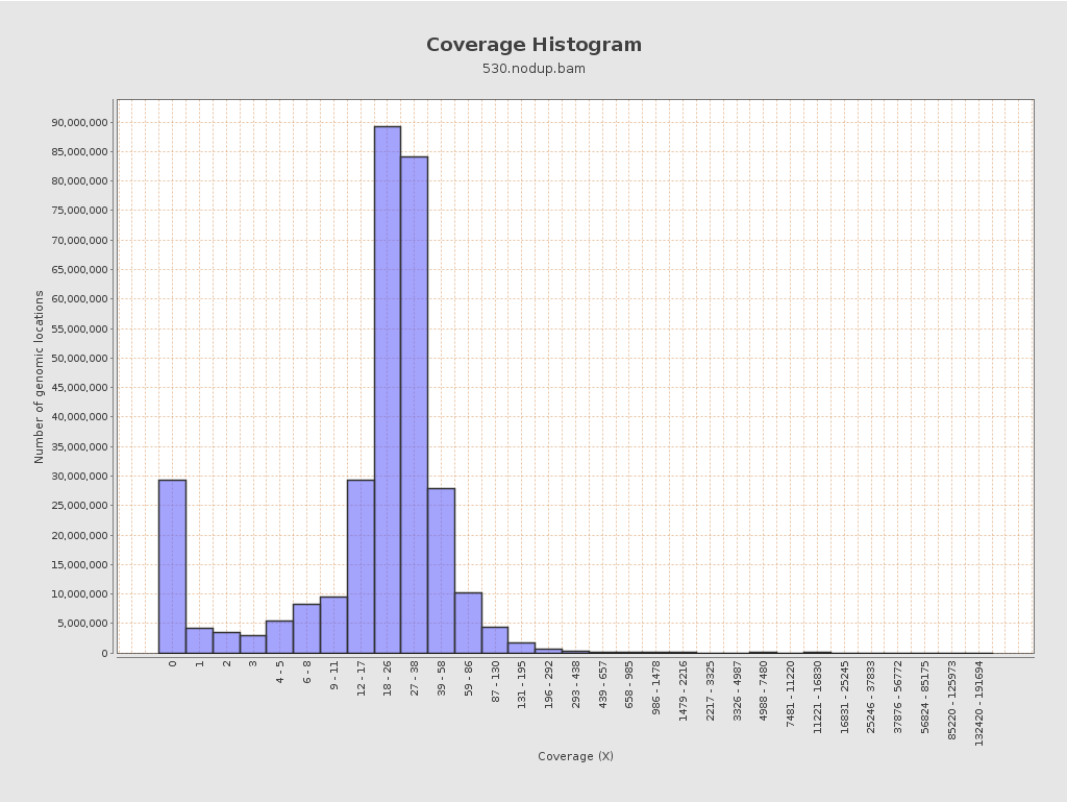
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	806781415	27.1421	118.5275

LT669789.1	36598175	1246631948	34.0627	337.4484
LT669790.1	30422129	1233013626	40.5302	440.0792
LT669791.1	52758100	1737805608	32.9391	347.9062
LT669792.1	28376109	962674825	33.9255	325.9642
LT669793.1	33388210	1025177950	30.7048	202.5364
LT669794.1	50579949	1586771053	31.3715	282.9751
LT669795.1	49795044	1896205988	38.0802	371.0226

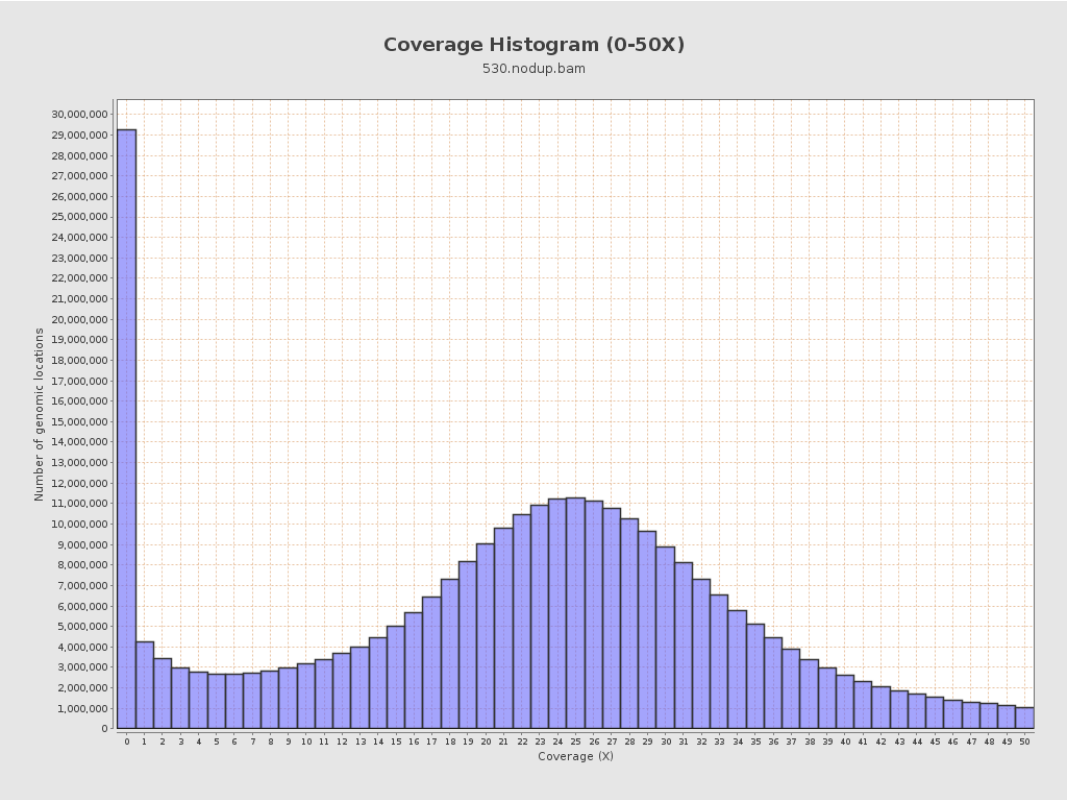
3. Results : Coverage across reference



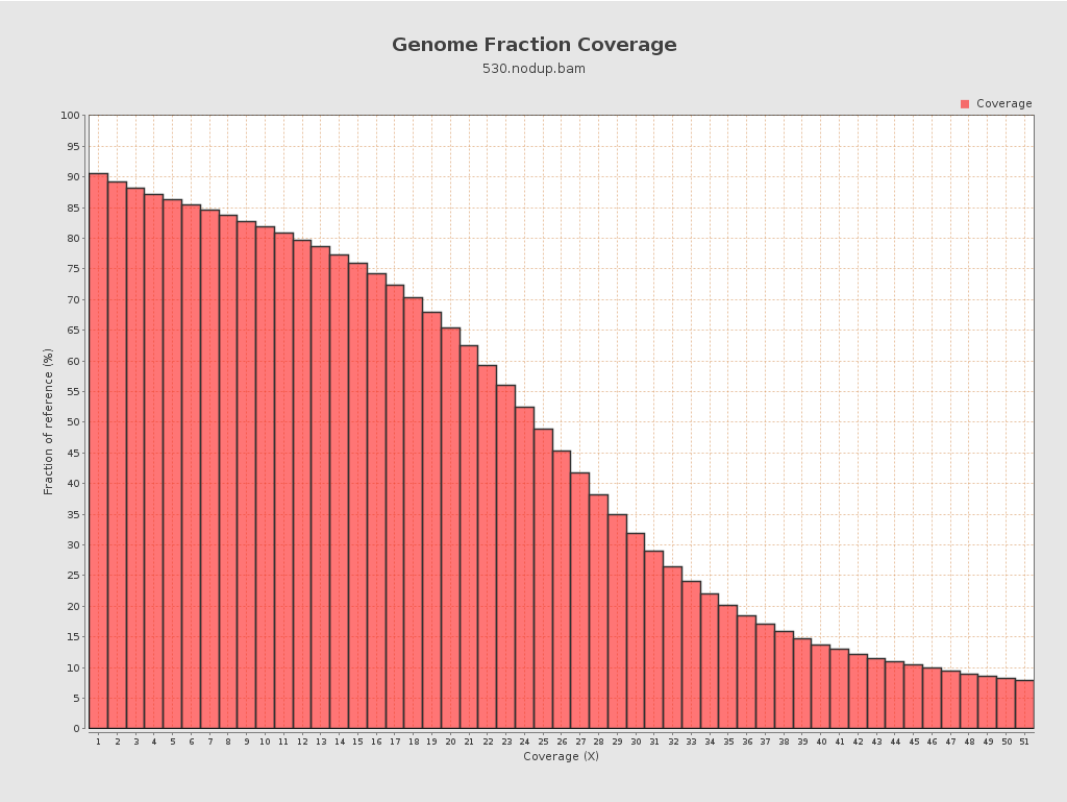
4. Results : Coverage Histogram



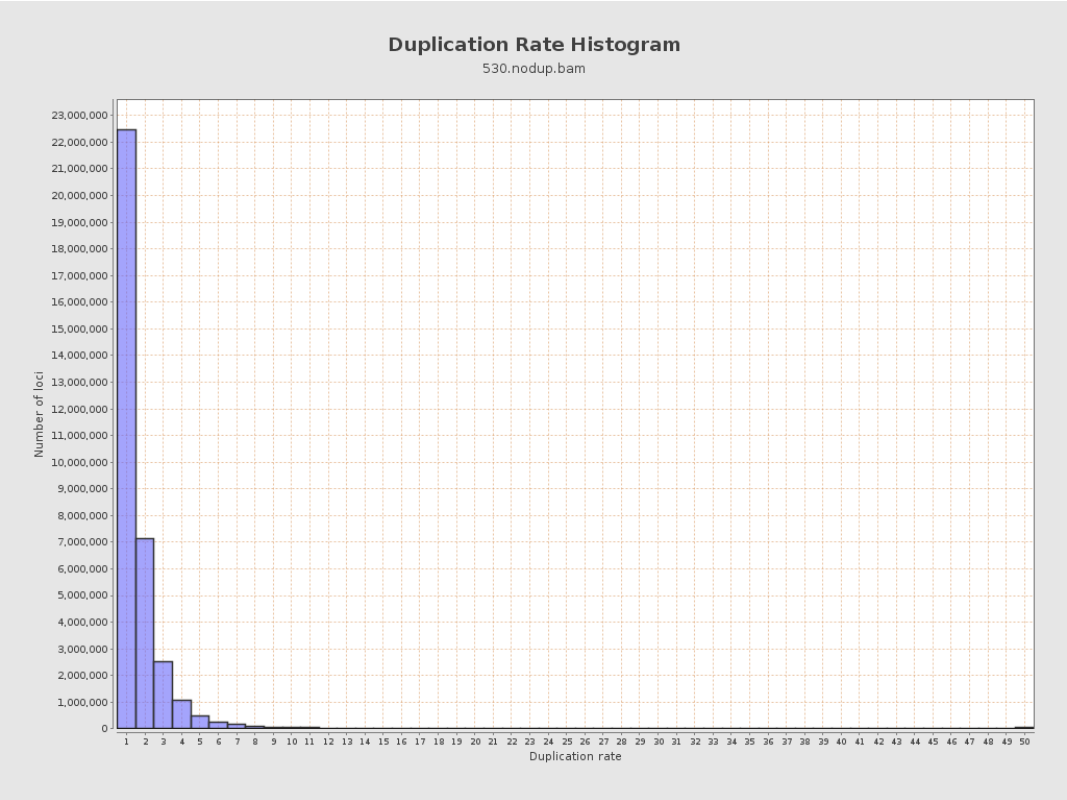
5. Results : Coverage Histogram (0-50X)



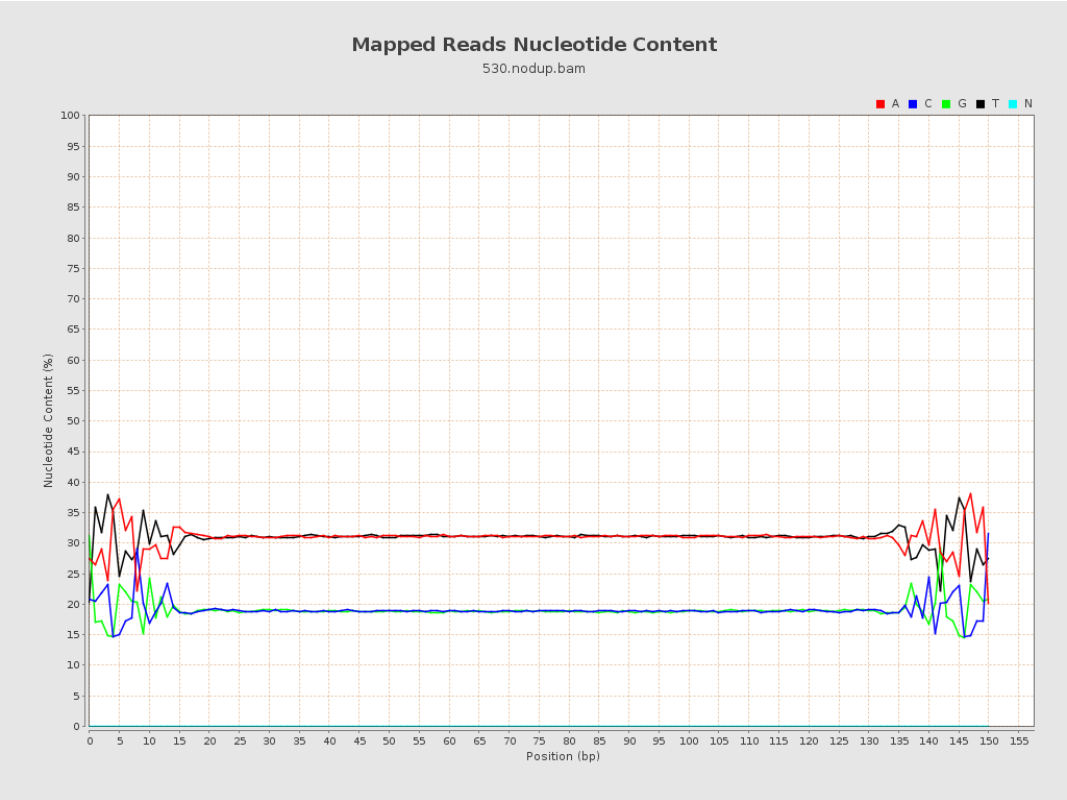
6. Results : Genome Fraction Coverage



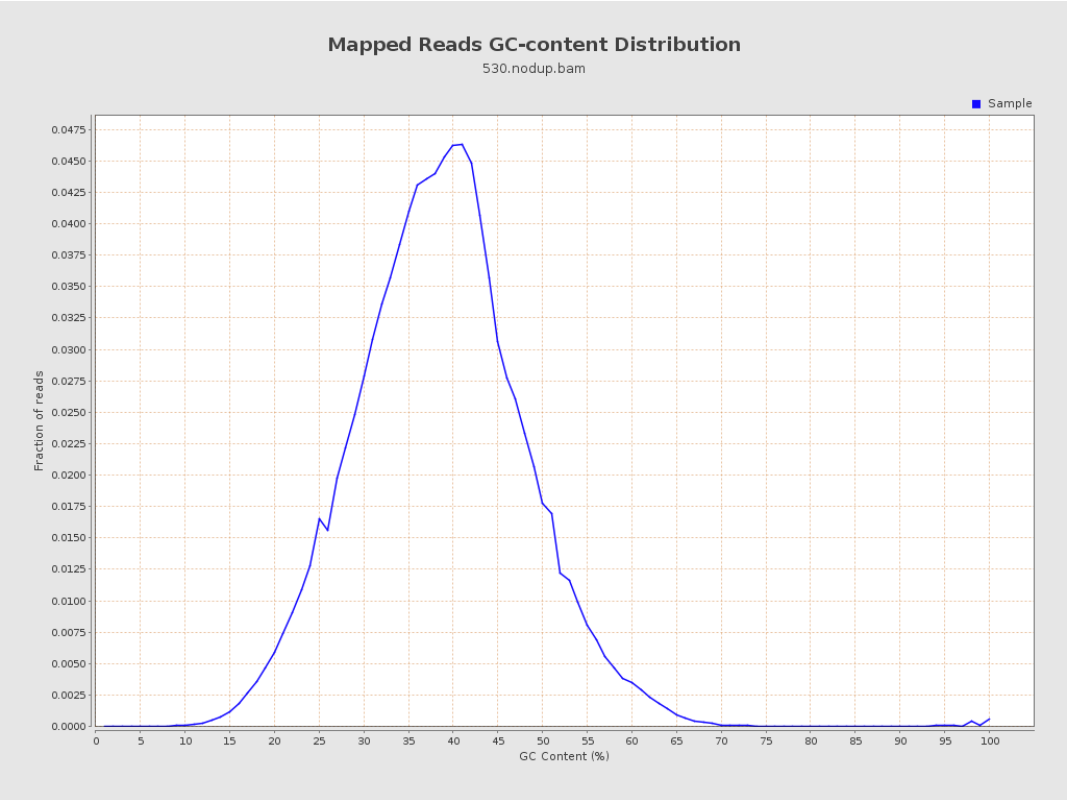
7. Results : Duplication Rate Histogram



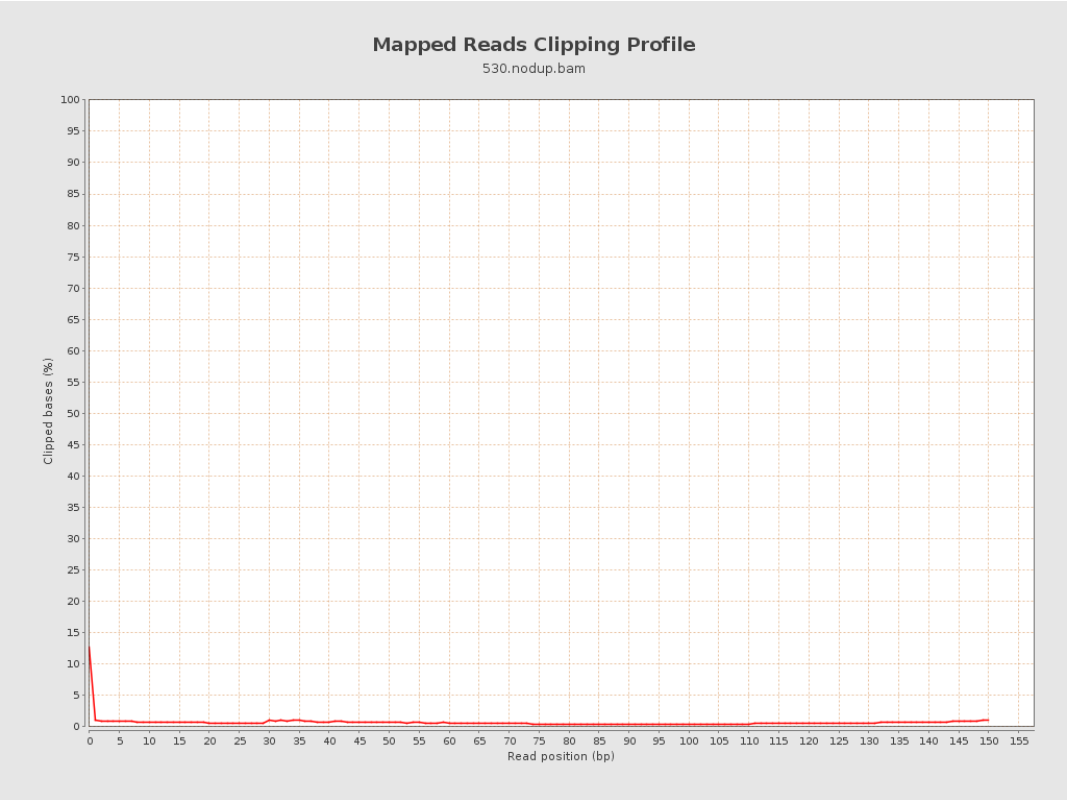
8. Results : Mapped Reads Nucleotide Content



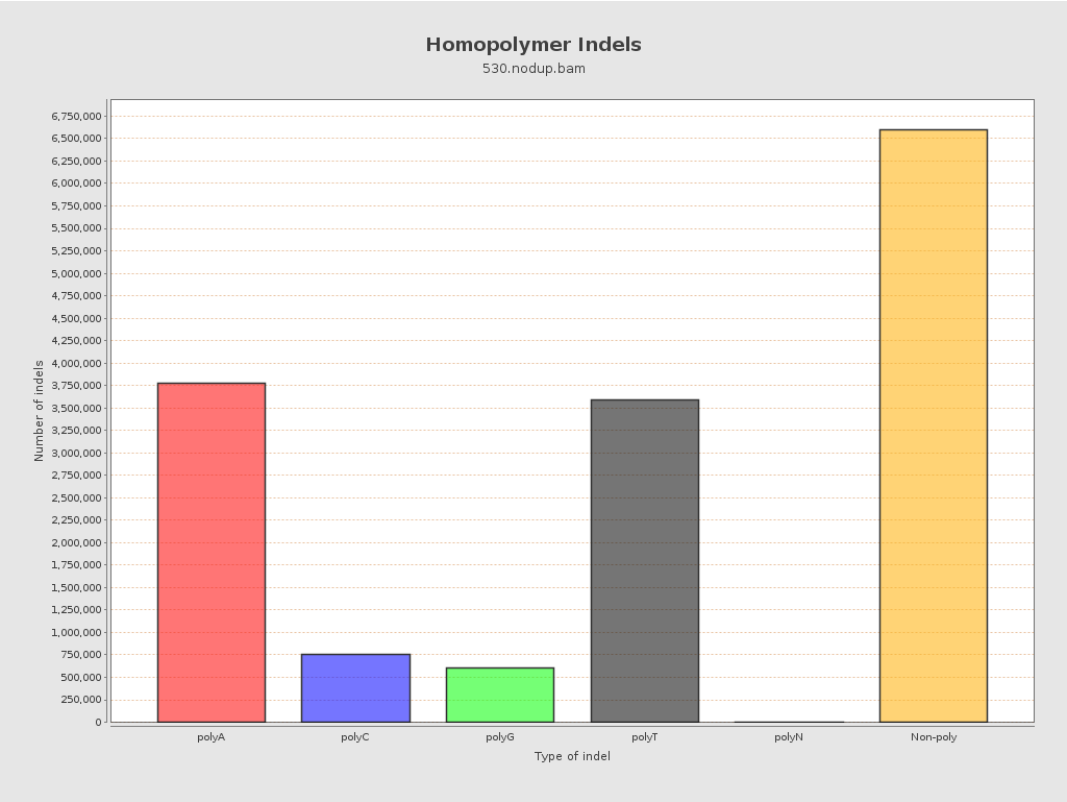
9. Results : Mapped Reads GC-content Distribution



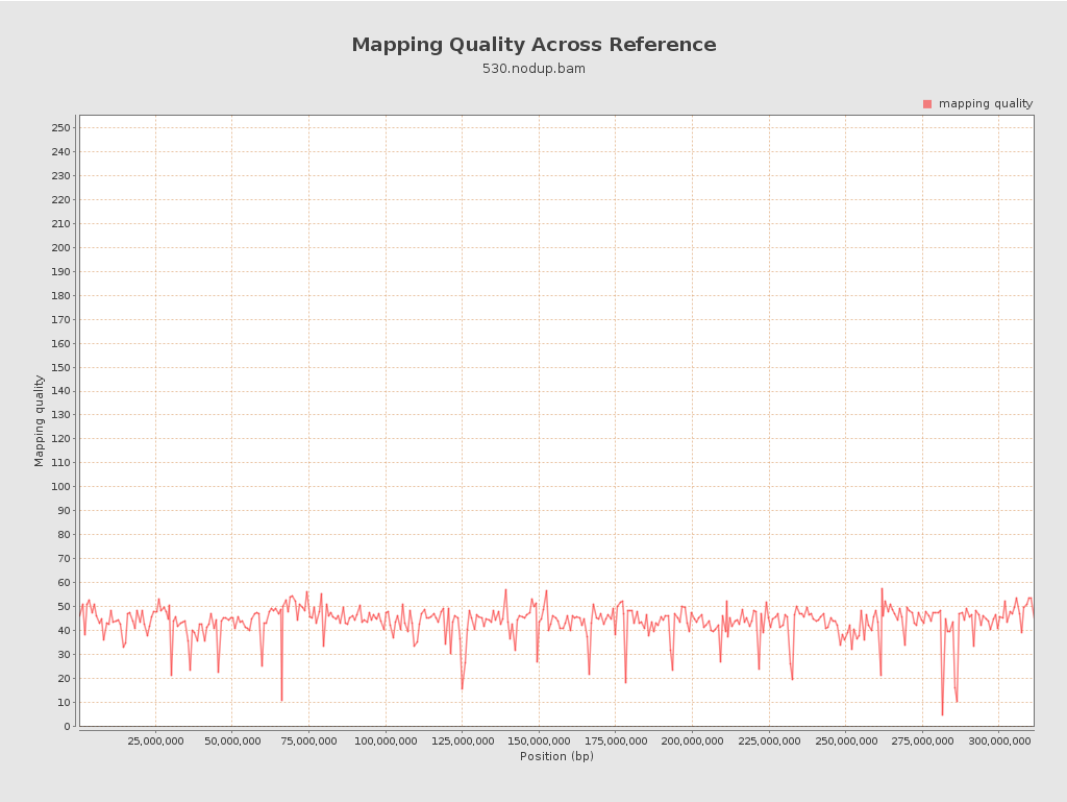
10. Results : Mapped Reads Clipping Profile



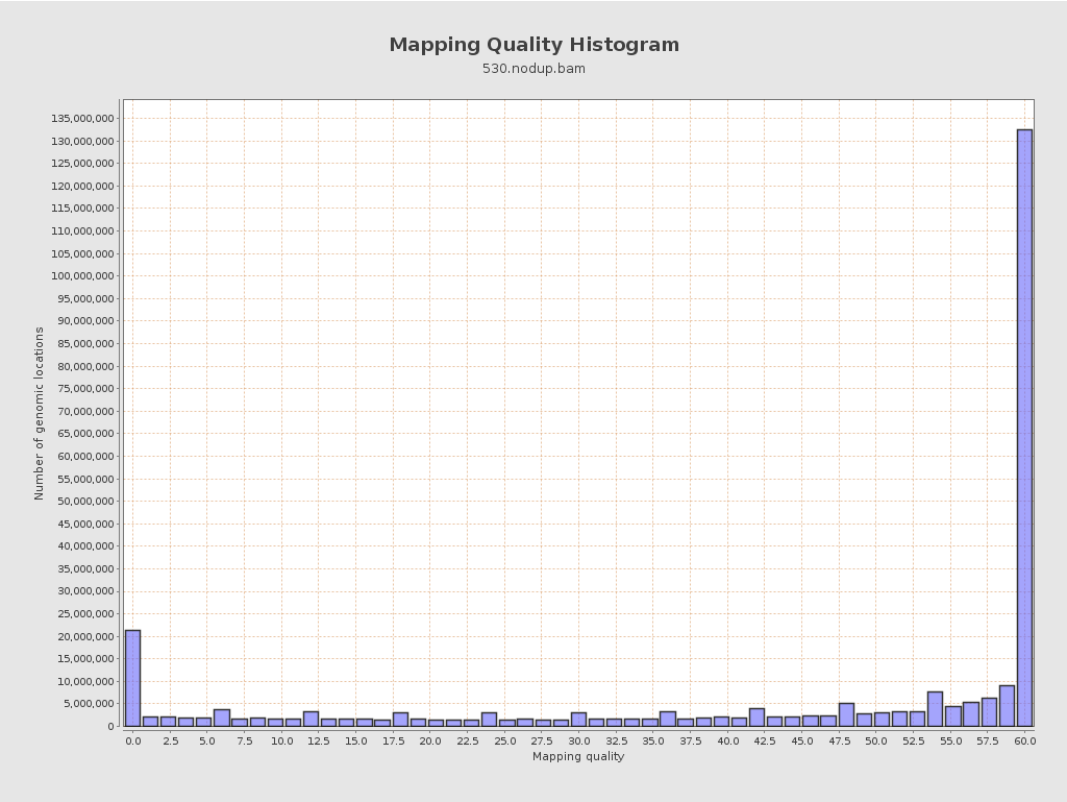
11. Results : Homopolymer Indels



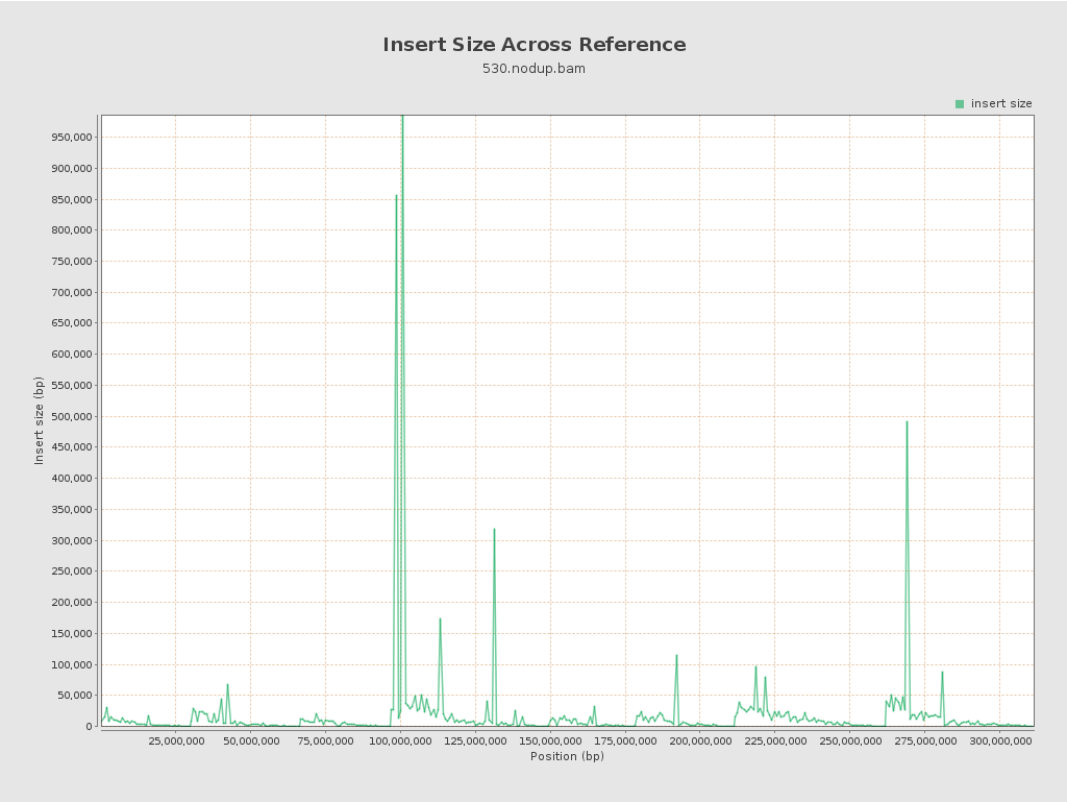
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram