

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/460
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/460.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_274/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_274_S355_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_274/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_274_S355_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,587,501
Mapped reads	60,334,696 / 94.88%
Unmapped reads	3,252,805 / 5.12%
Mapped paired reads	60,334,696 / 94.88%
Mapped reads, first in pair	30,222,333 / 47.53%
Mapped reads, second in pair	30,112,363 / 47.36%
Mapped reads, both in pair	59,270,613 / 93.21%
Mapped reads, singletons	1,064,083 / 1.67%
Read min/max/mean length	30 / 151 / 148.04
Duplicated reads (flagged)	8,059,705 / 12.67%
Clipped reads	13,604,099 / 21.39%

2.2. ACGT Content

Number/percentage of A's	2,583,838,963 / 30.89%
Number/percentage of C's	1,600,263,143 / 19.13%
Number/percentage of T's	2,585,287,661 / 30.9%
Number/percentage of G's	1,596,602,913 / 19.08%
Number/percentage of N's	30,979 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	26.9141
Standard Deviation	206.6463

2.4. Mapping Quality

Mean Mapping Quality	44.36
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2.5. Insert size

Mean	219,098.04
Standard Deviation	2,215,238.15
P25/Median/P75	320 / 420 / 547

2.6. Mismatches and indels

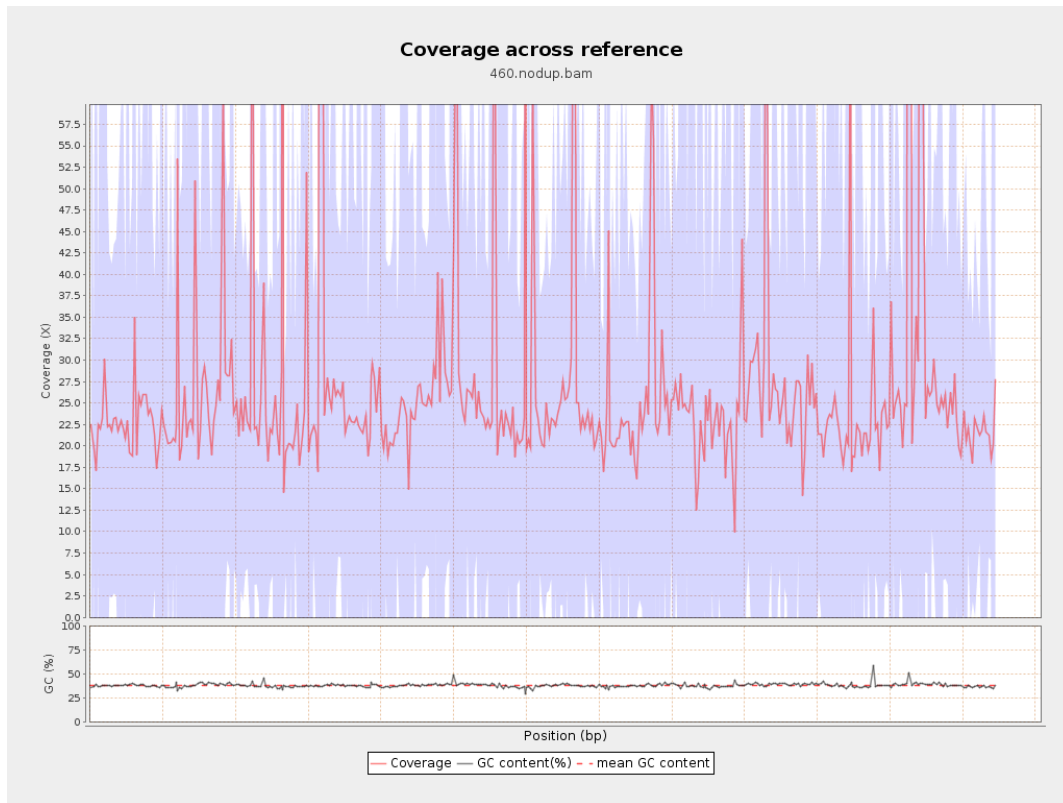
General error rate	2.29%
Mismatches	176,283,519
Insertions	5,571,605
Mapped reads with at least one insertion	8.32%
Deletions	5,710,345
Mapped reads with at least one deletion	8.41%
Homopolymer indels	56.33%

2.7. Chromosome stats

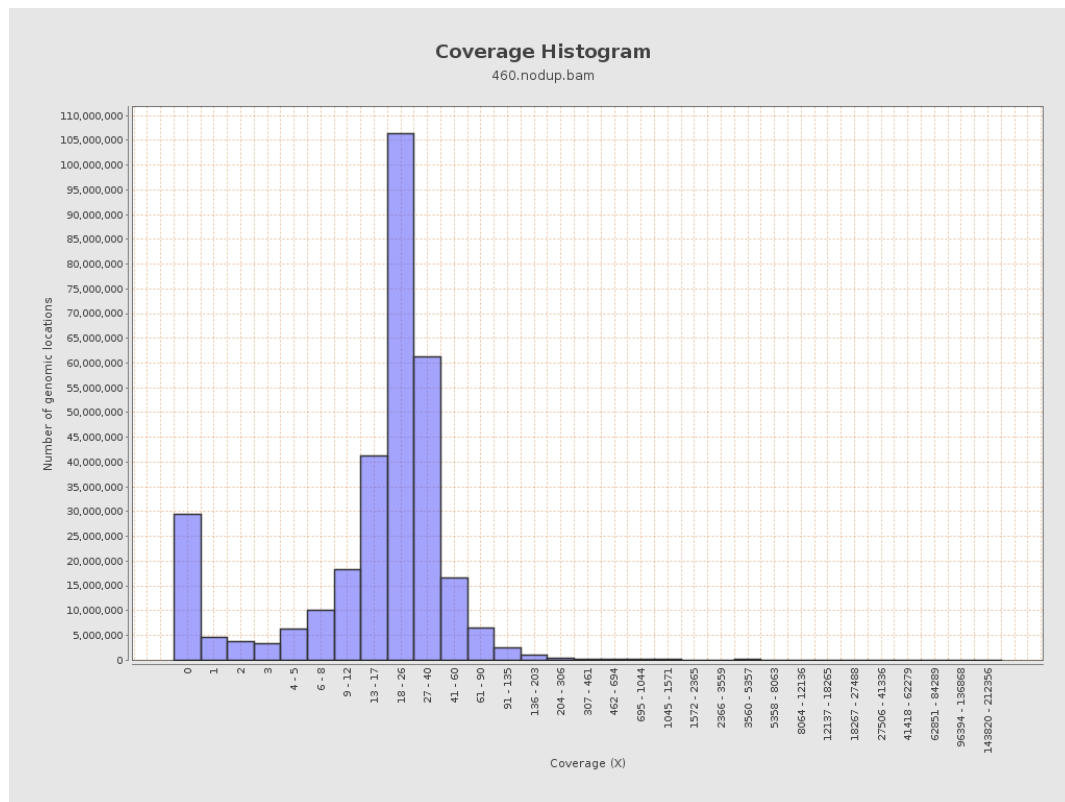
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	669403438	22.5204	56.4694

LT669789.1	36598175	1019239898	27.8495	229.8862
LT669790.1	30422129	865226658	28.4407	196.5681
LT669791.1	52758100	1393687190	26.4166	168.4102
LT669792.1	28376109	754207746	26.579	240.8396
LT669793.1	33388210	826962176	24.7681	105.3361
LT669794.1	50579949	1309285614	25.8855	191.3204
LT669795.1	49795044	1549552828	31.1186	308.4533

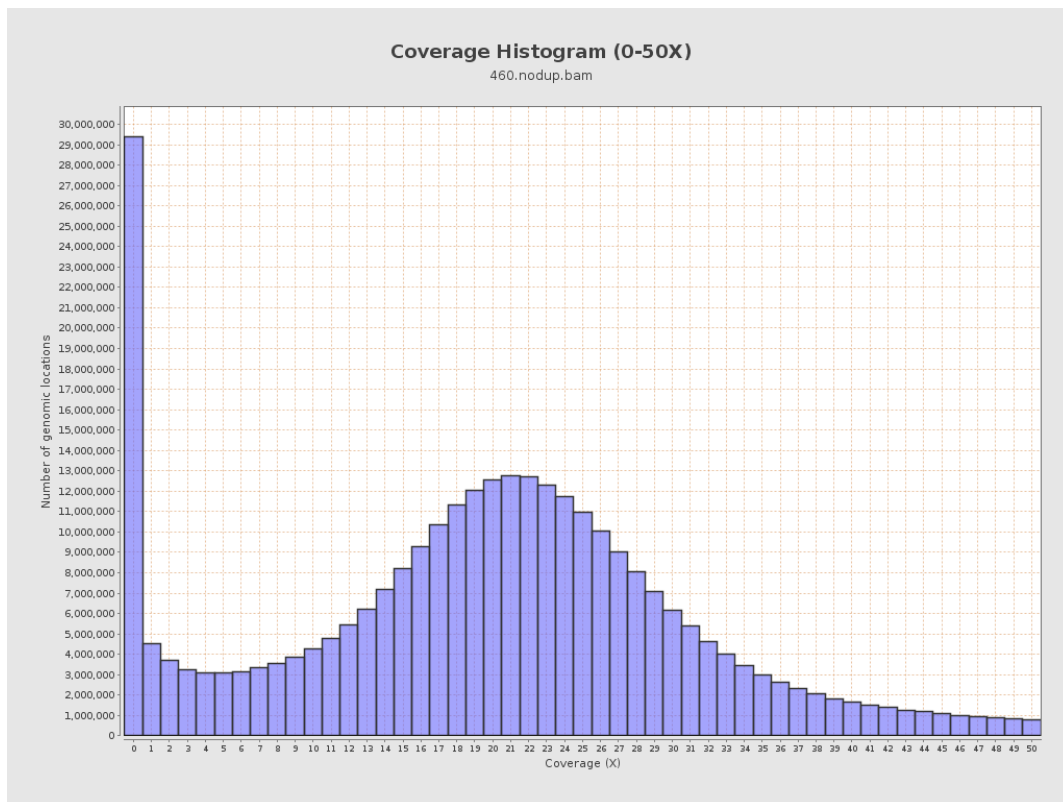
3. Results : Coverage across reference



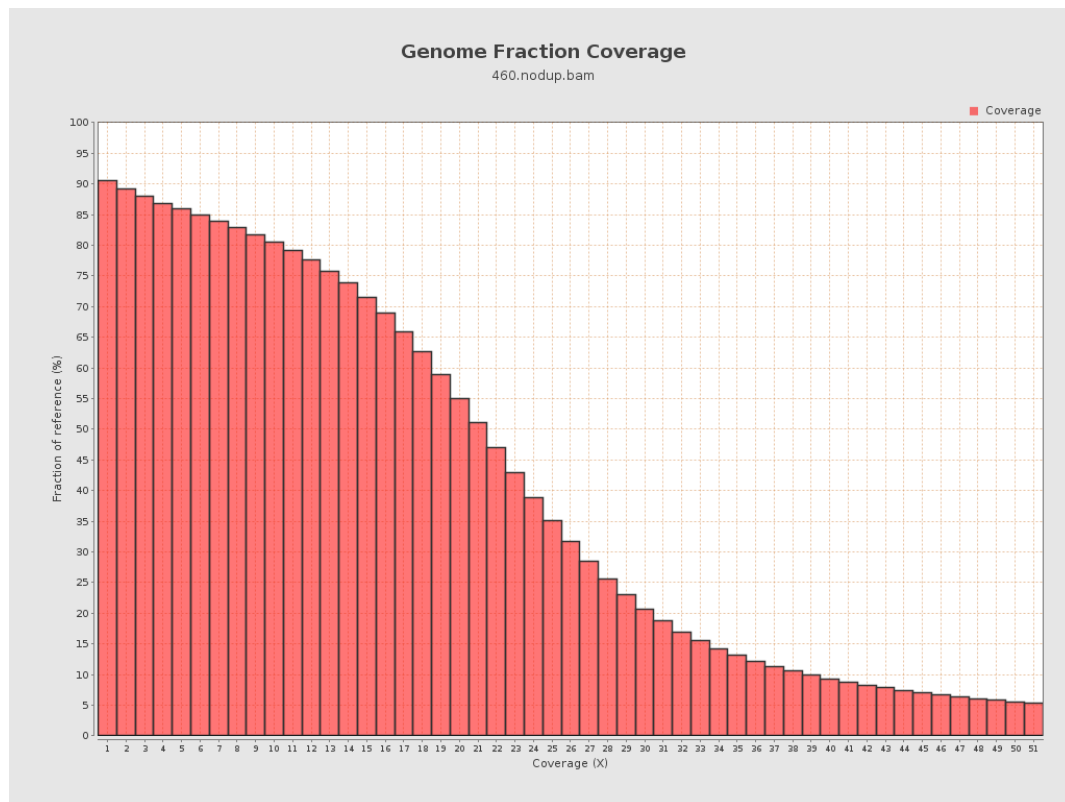
4. Results : Coverage Histogram



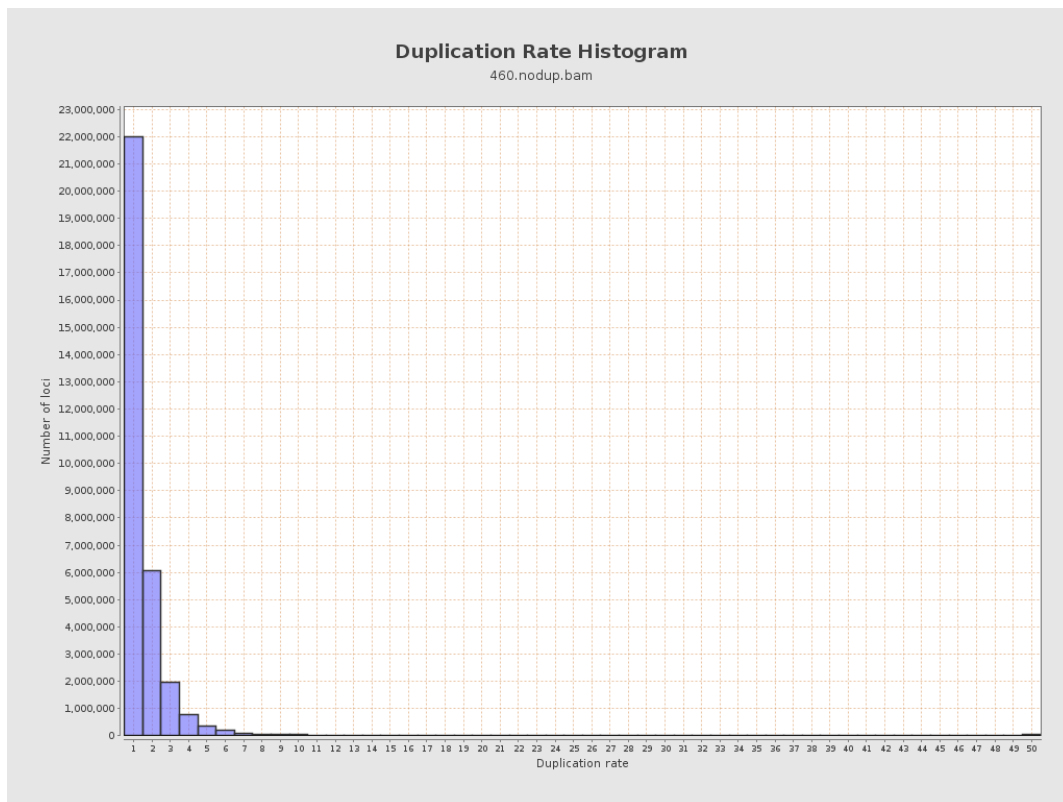
5. Results : Coverage Histogram (0-50X)



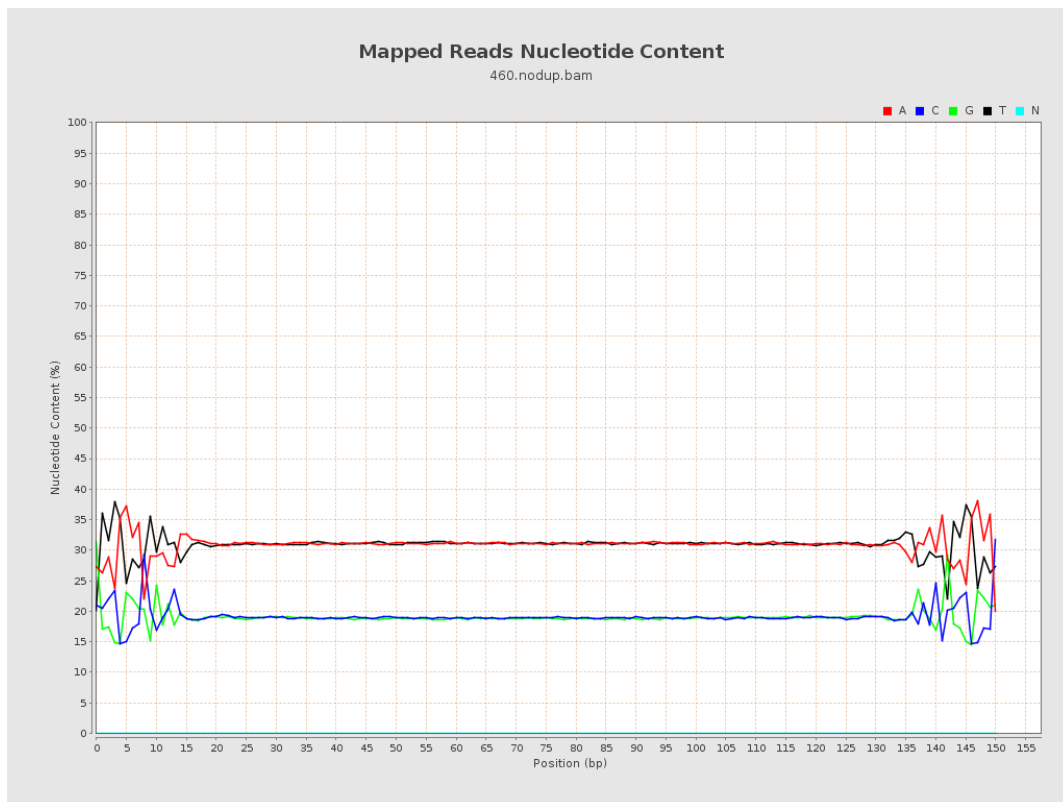
6. Results : Genome Fraction Coverage



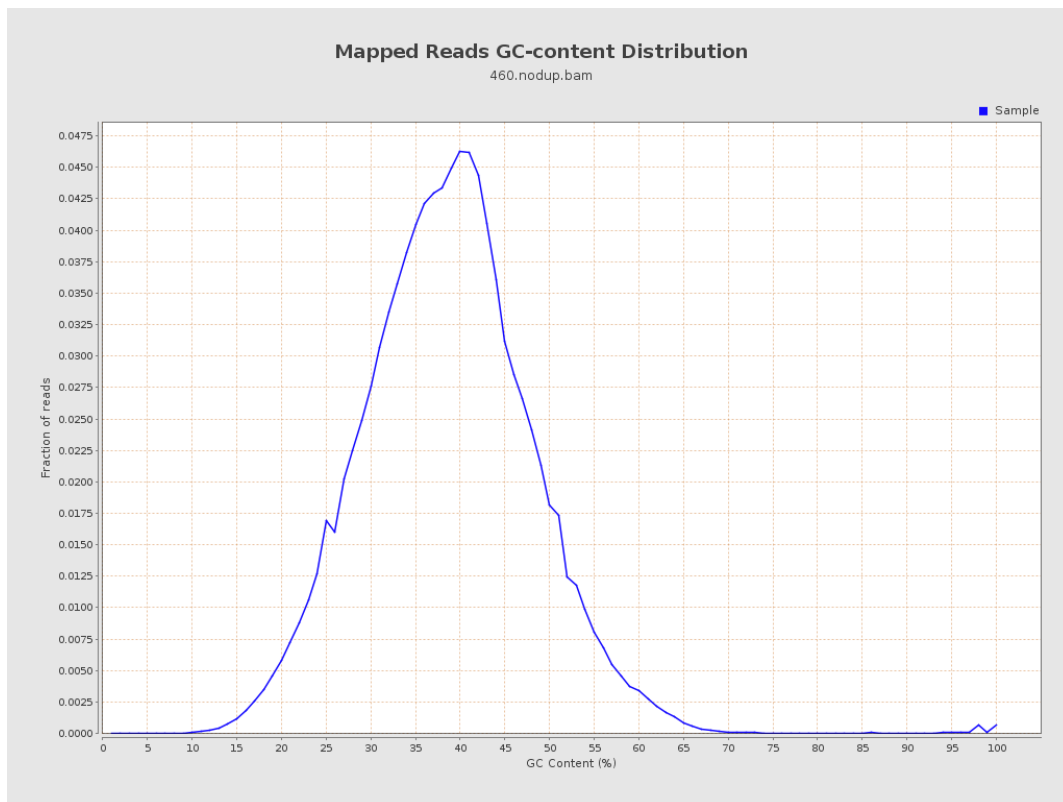
7. Results : Duplication Rate Histogram



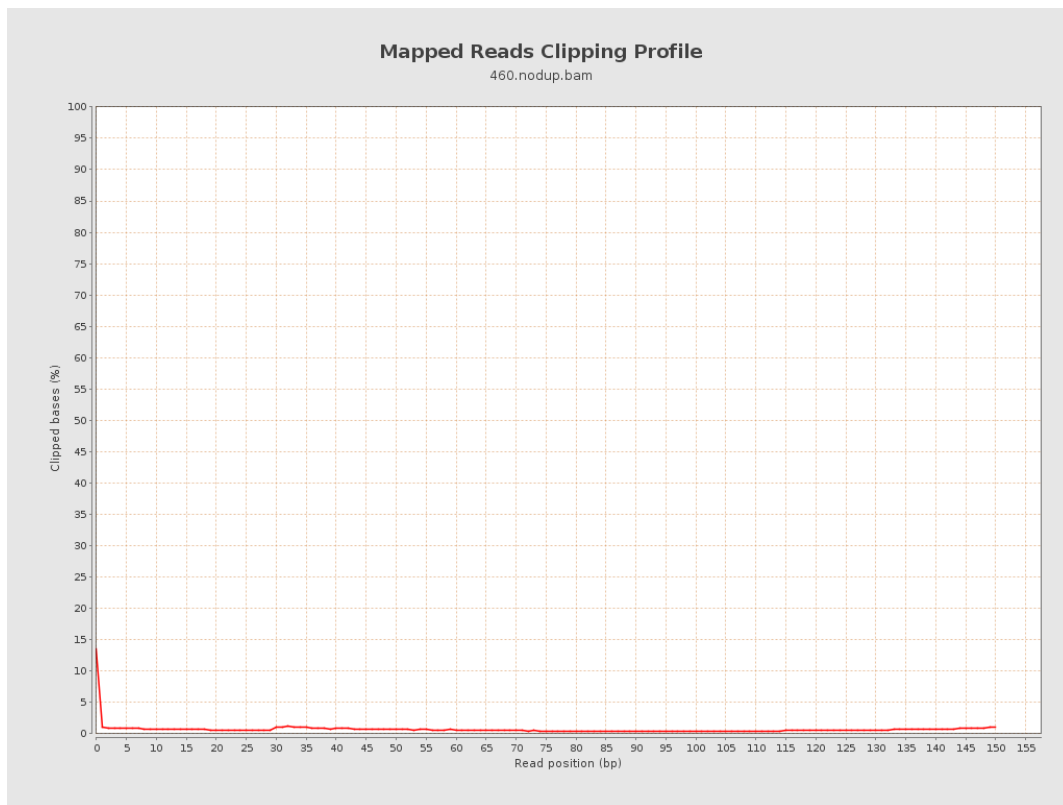
8. Results : Mapped Reads Nucleotide Content



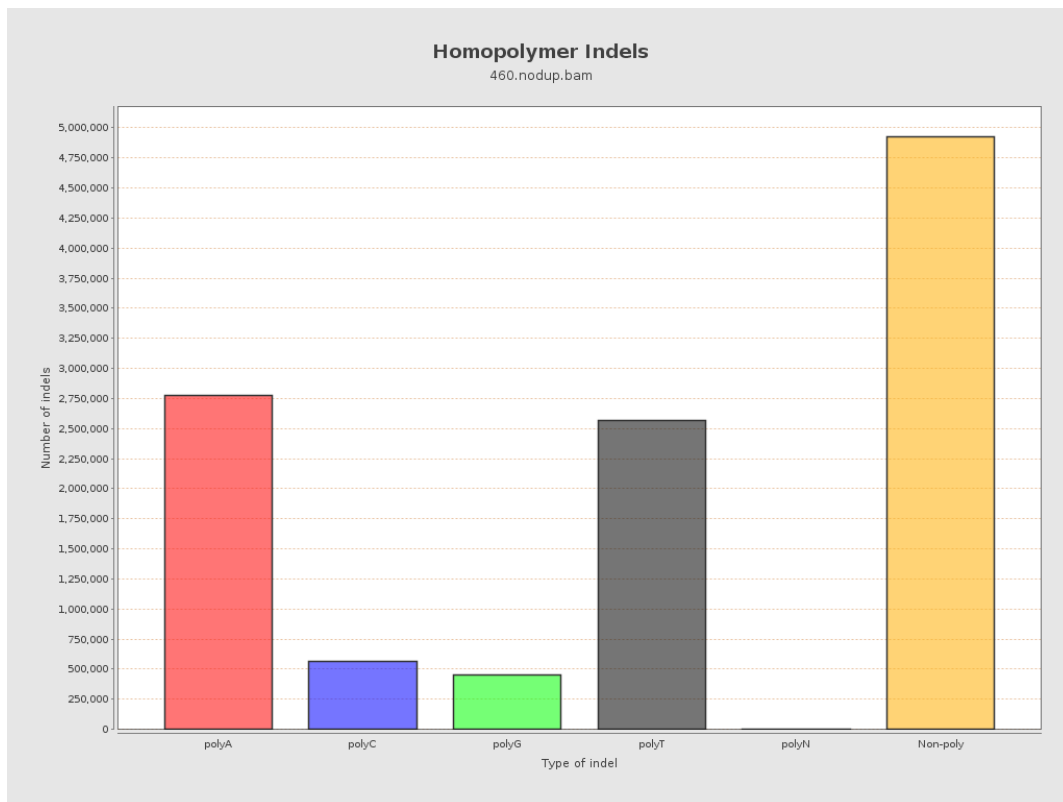
9. Results : Mapped Reads GC-content Distribution



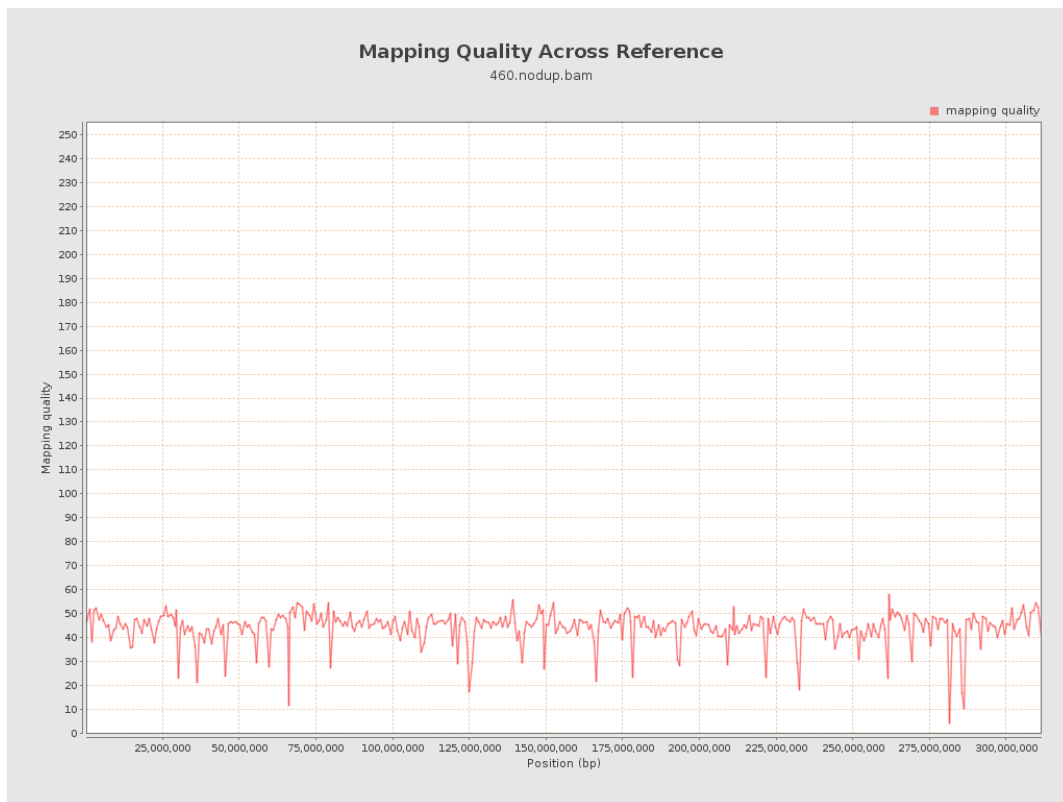
10. Results : Mapped Reads Clipping Profile



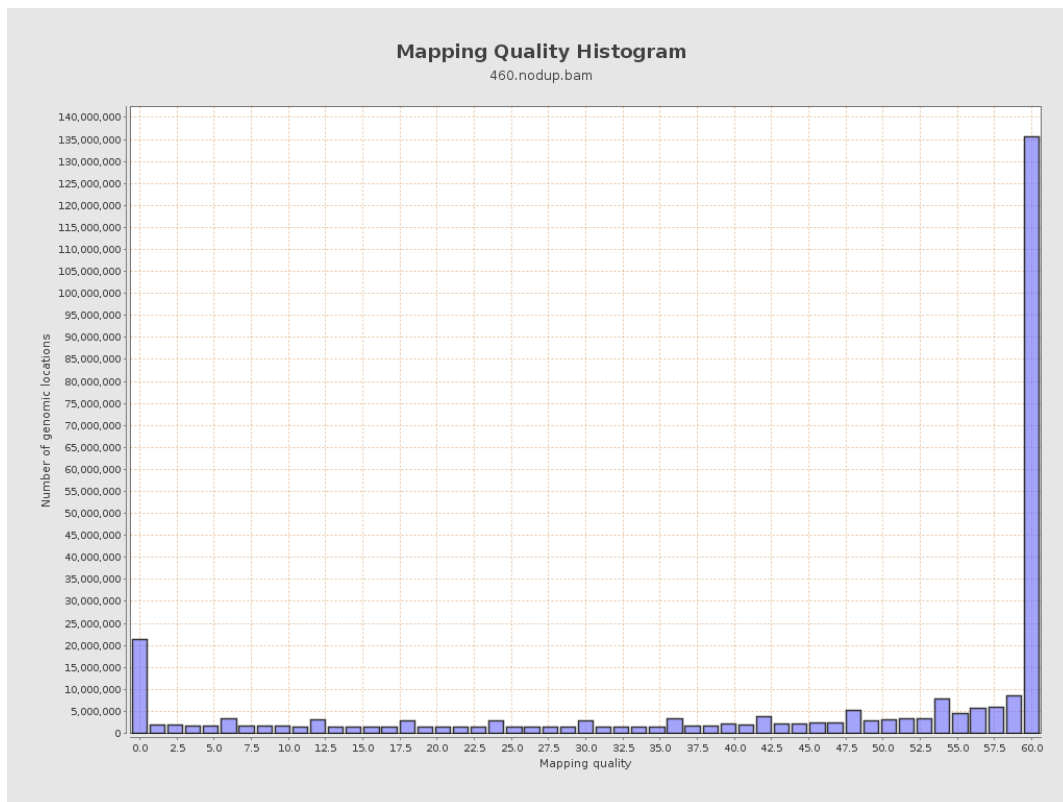
11. Results : Homopolymer Indels



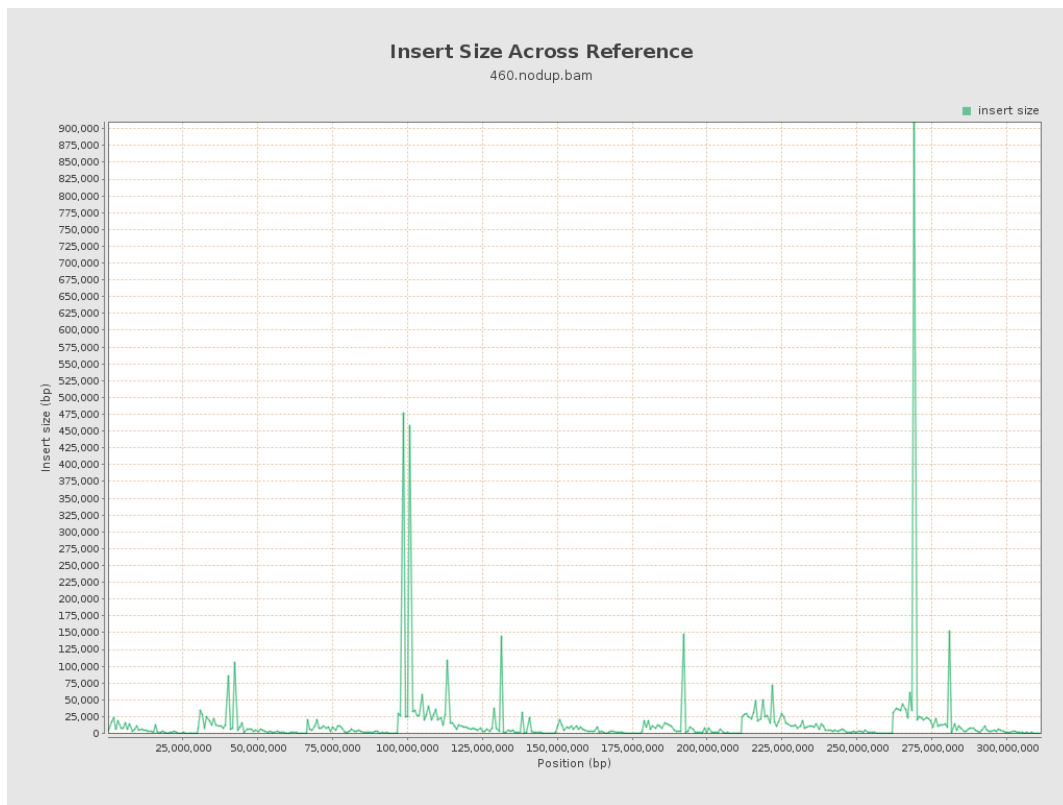
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

