Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/759.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/759.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_414/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_414_S389_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_414/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_414_S389_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	56,512,592
Mapped reads	53,314,982 / 94.34%
Unmapped reads	3,197,610 / 5.66%
Mapped paired reads	53,314,982 / 94.34%
Mapped reads, first in pair	26,724,586 / 47.29%
Mapped reads, second in pair	26,590,396 / 47.05%
Mapped reads, both in pair	52,228,050 / 92.42%
Mapped reads, singletons	1,086,932 / 1.92%
Read min/max/mean length	30 / 151 / 147.84
Duplicated reads (flagged)	7,872,739 / 13.93%
Clipped reads	12,490,017 / 22.1%

2.2. ACGT Content

Number/percentage of A's	2,269,945,272 / 30.89%
Number/percentage of C's	1,404,082,602 / 19.1%
Number/percentage of T's	2,269,491,958 / 30.88%
Number/percentage of G's	1,405,966,874 / 19.13%
Number/percentage of N's	25,770 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	23.6453
Standard Deviation	197.1726

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Insert size

Mean	257,697.06
Standard Deviation	2,405,275.45
P25/Median/P75	372 / 491 / 636

2.6. Mismatches and indels

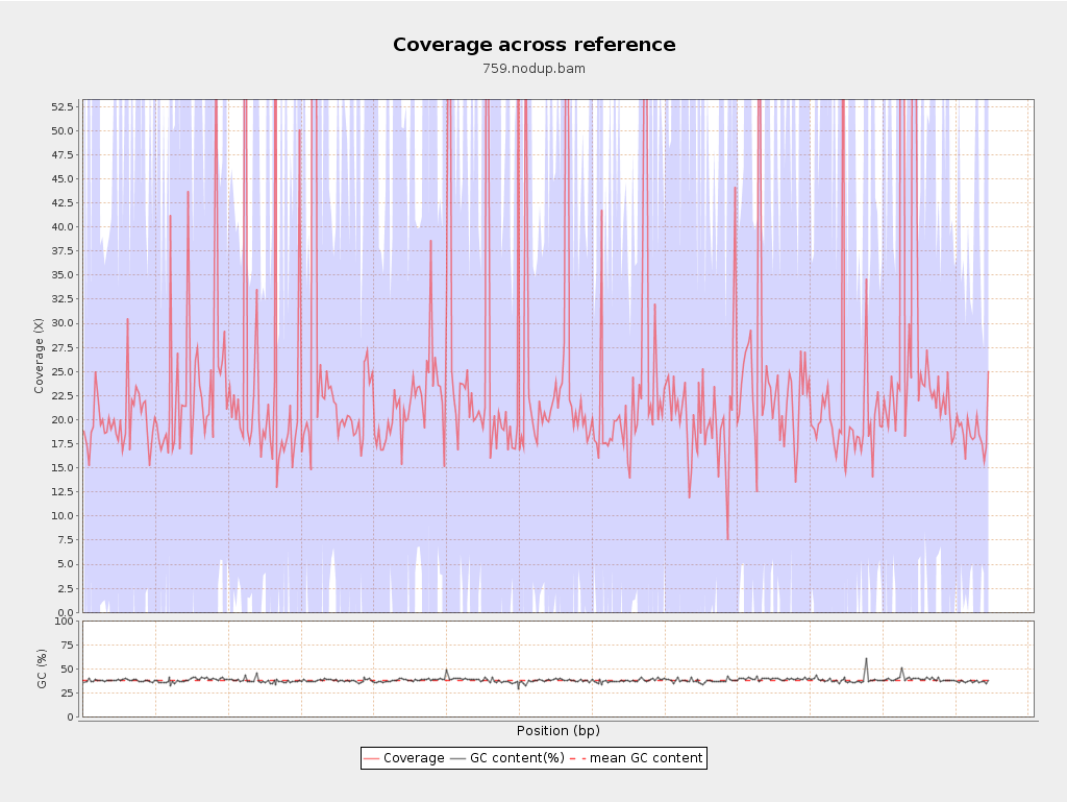
General error rate	2.34%
Mismatches	158,188,078
Insertions	4,996,340
Mapped reads with at least one insertion	8.42%
Deletions	5,179,165
Mapped reads with at least one deletion	8.62%
Homopolymer indels	56.42%

2.7. Chromosome stats

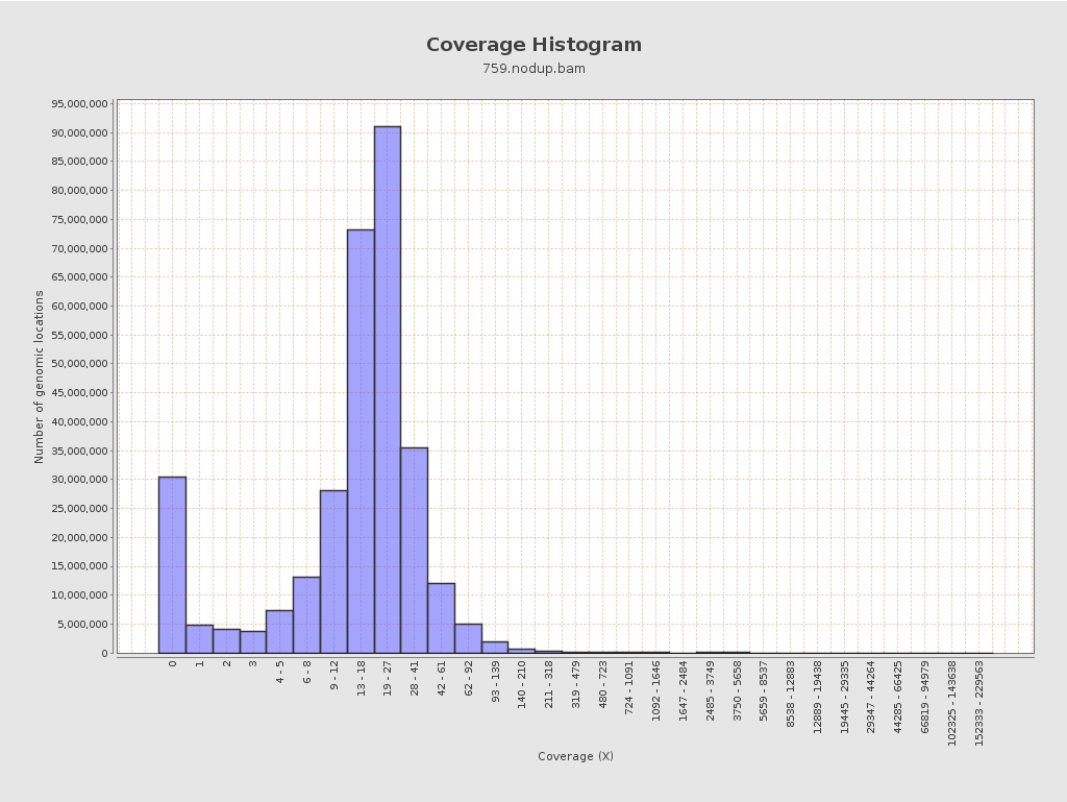
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	583500395	19.6304	69.8242

LT669789.1	36598175	909583602	24.8533	202.3376
LT669790.1	30422129	772414051	25.3899	192.8623
LT669791.1	52758100	1228192124	23.2797	184.0796
LT669792.1	28376109	670421813	23.6263	207.6882
LT669793.1	33388210	748585923	22.4207	136.7028
LT669794.1	50579949	1161112675	22.956	198.2214
LT669795.1	49795044	1295062265	26.0079	273.2089

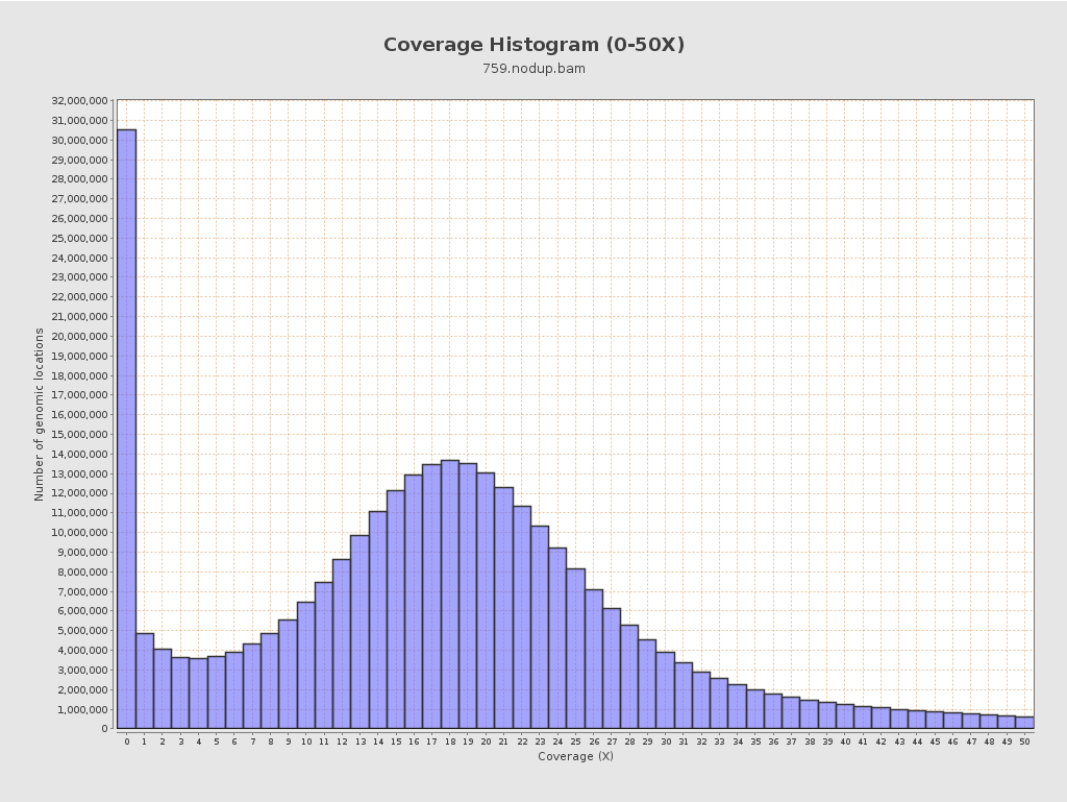
3. Results : Coverage across reference



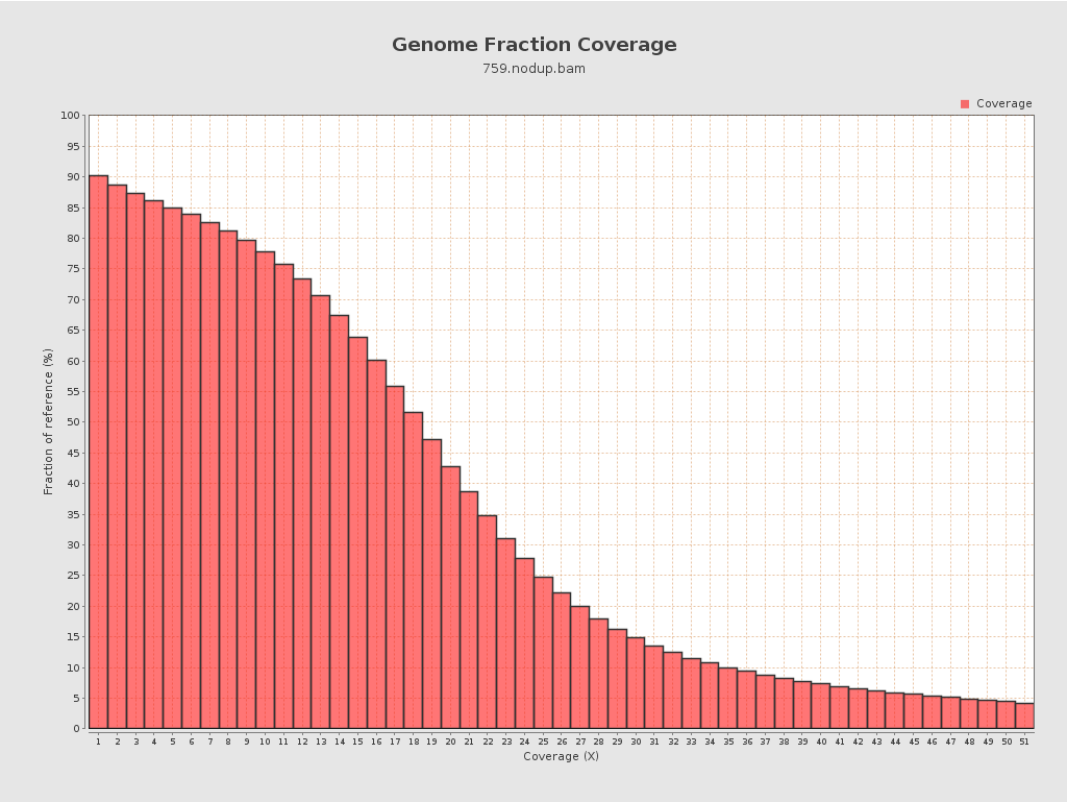
4. Results : Coverage Histogram



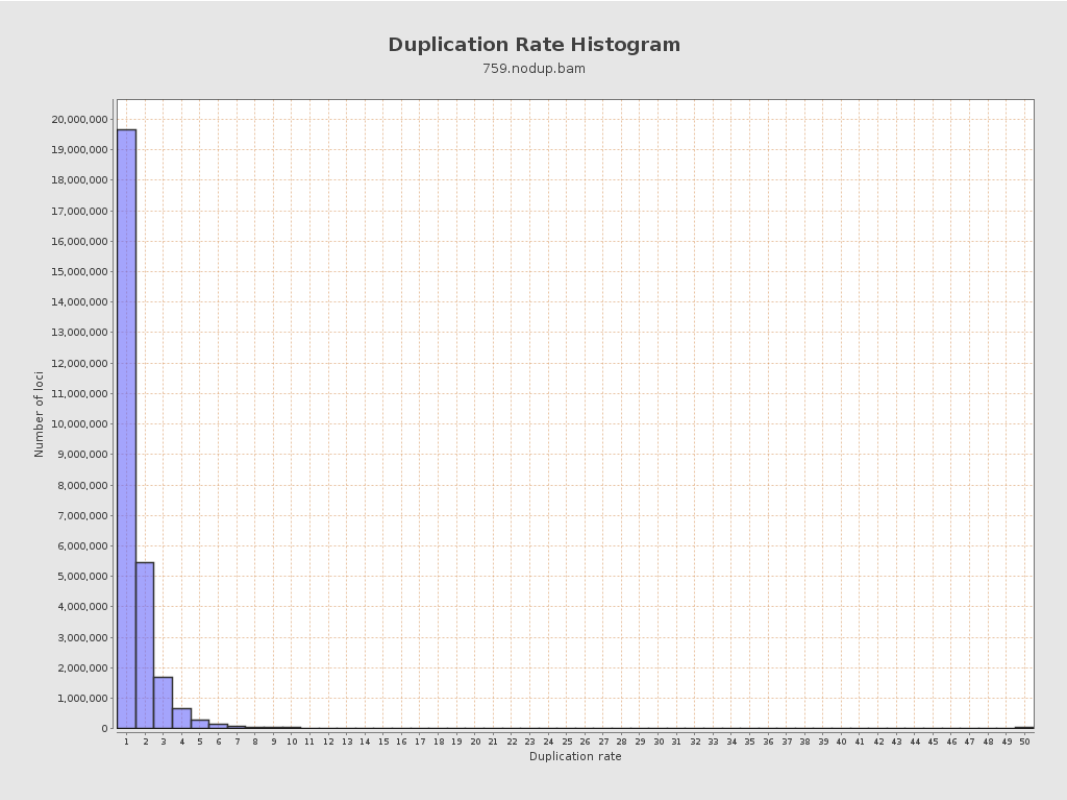
5. Results : Coverage Histogram (0-50X)



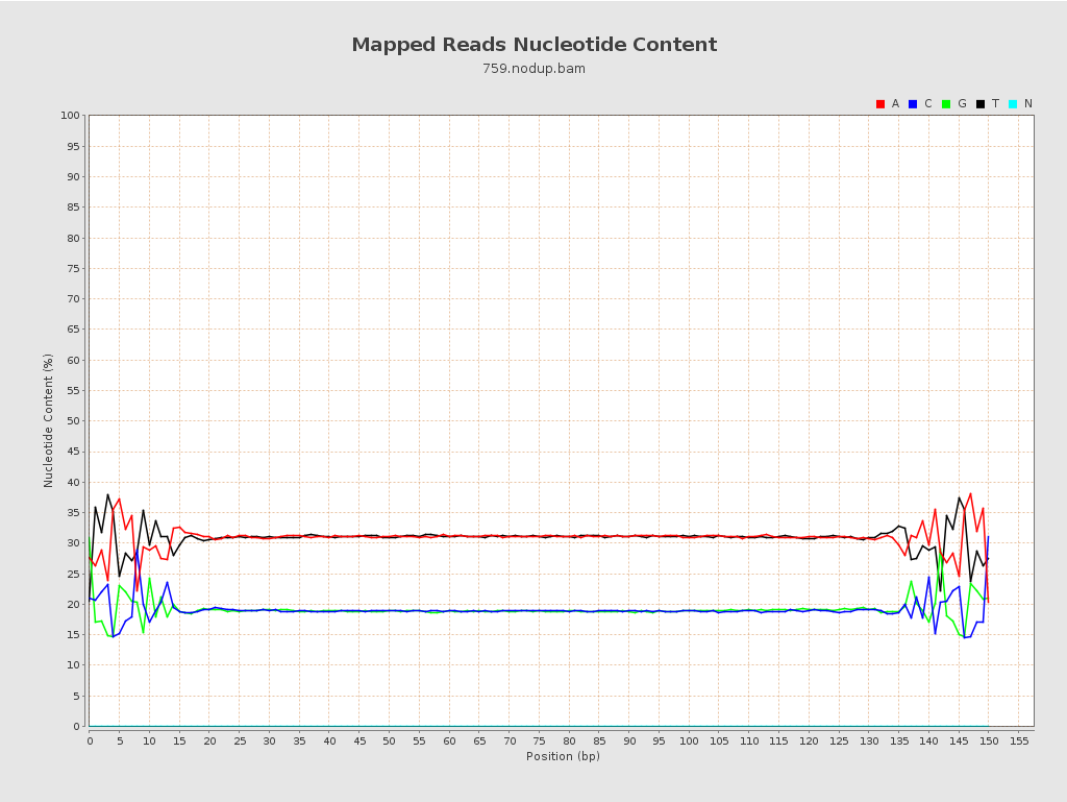
6. Results : Genome Fraction Coverage



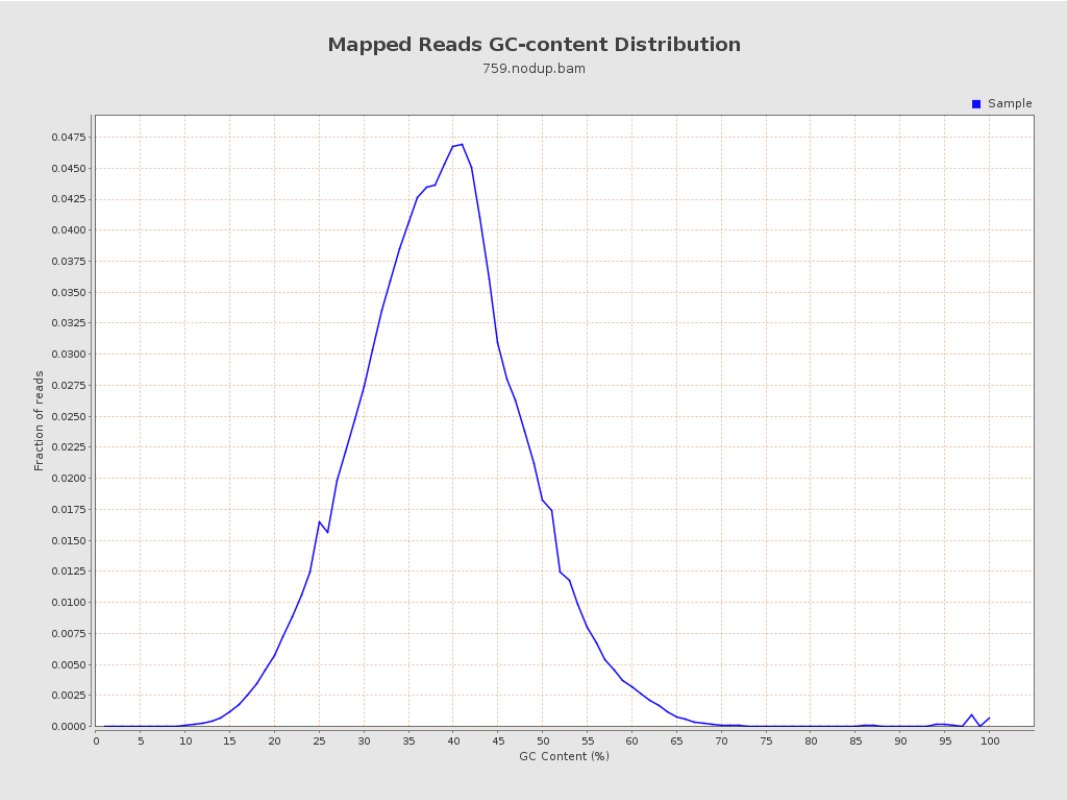
7. Results : Duplication Rate Histogram



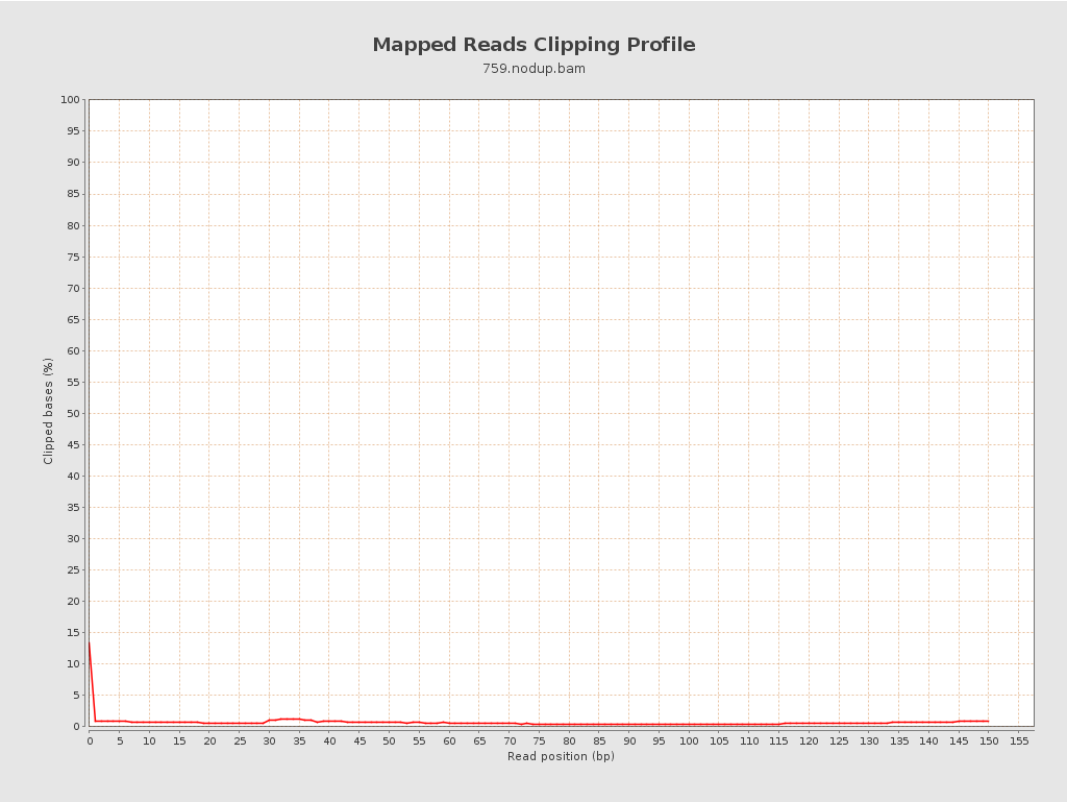
8. Results : Mapped Reads Nucleotide Content



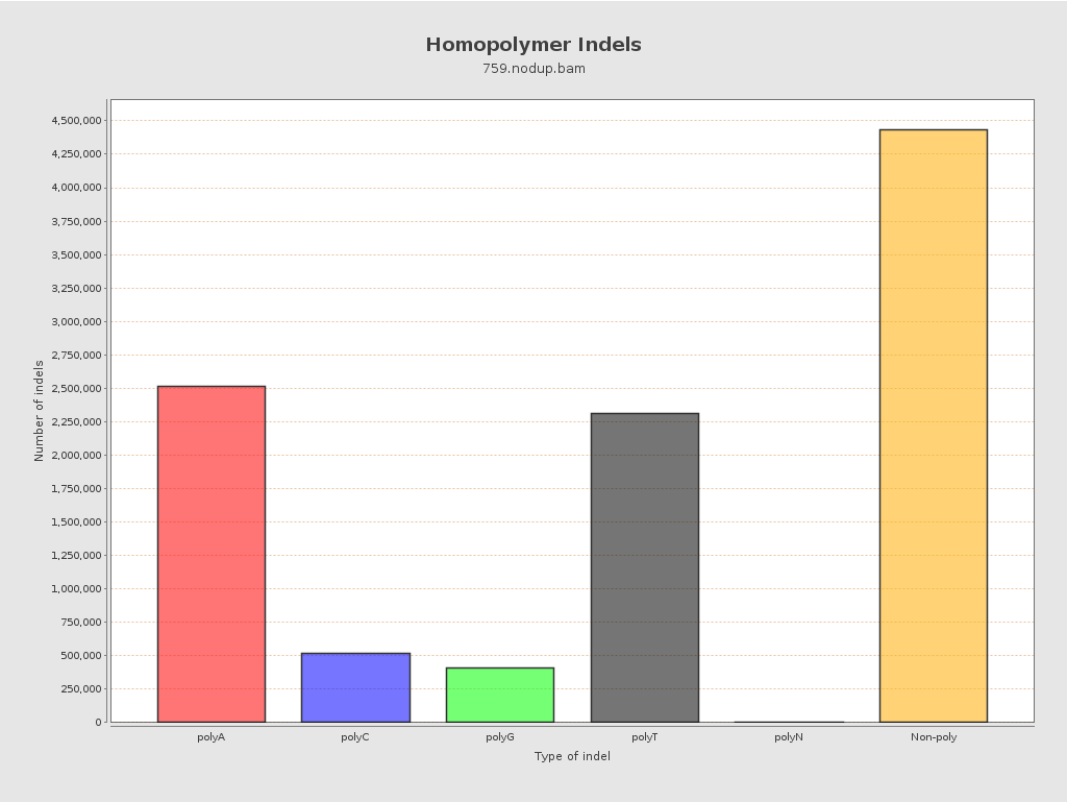
9. Results : Mapped Reads GC-content Distribution



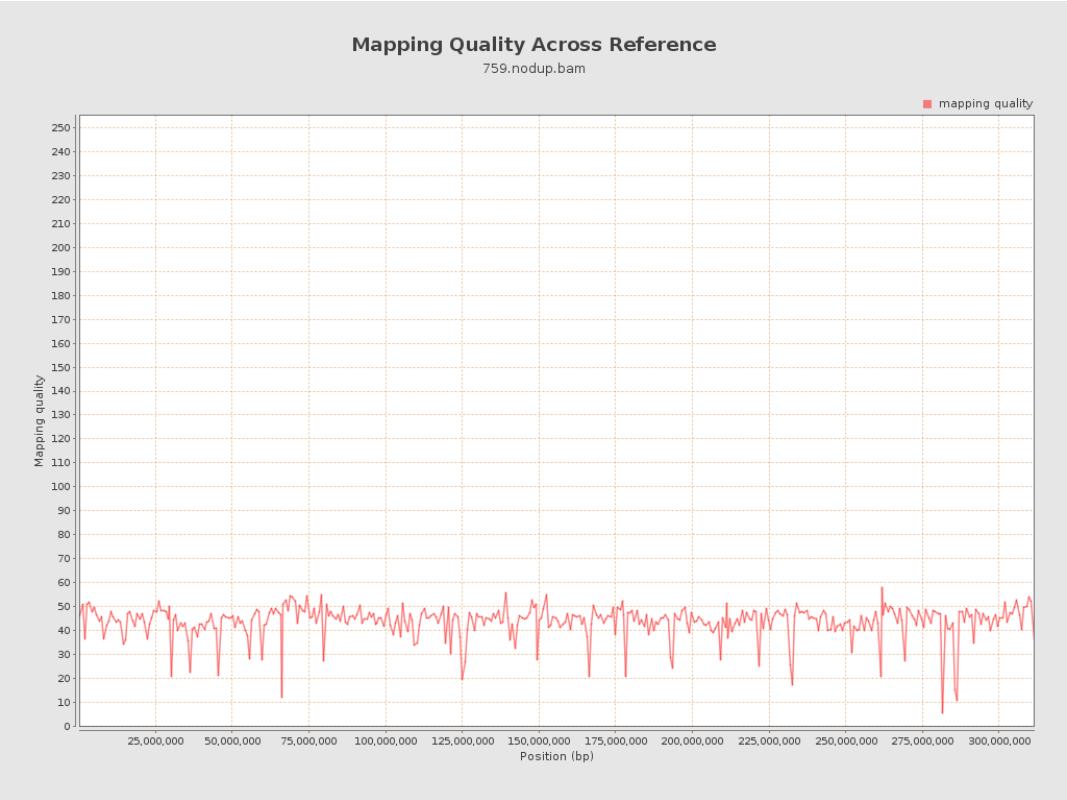
10. Results : Mapped Reads Clipping Profile



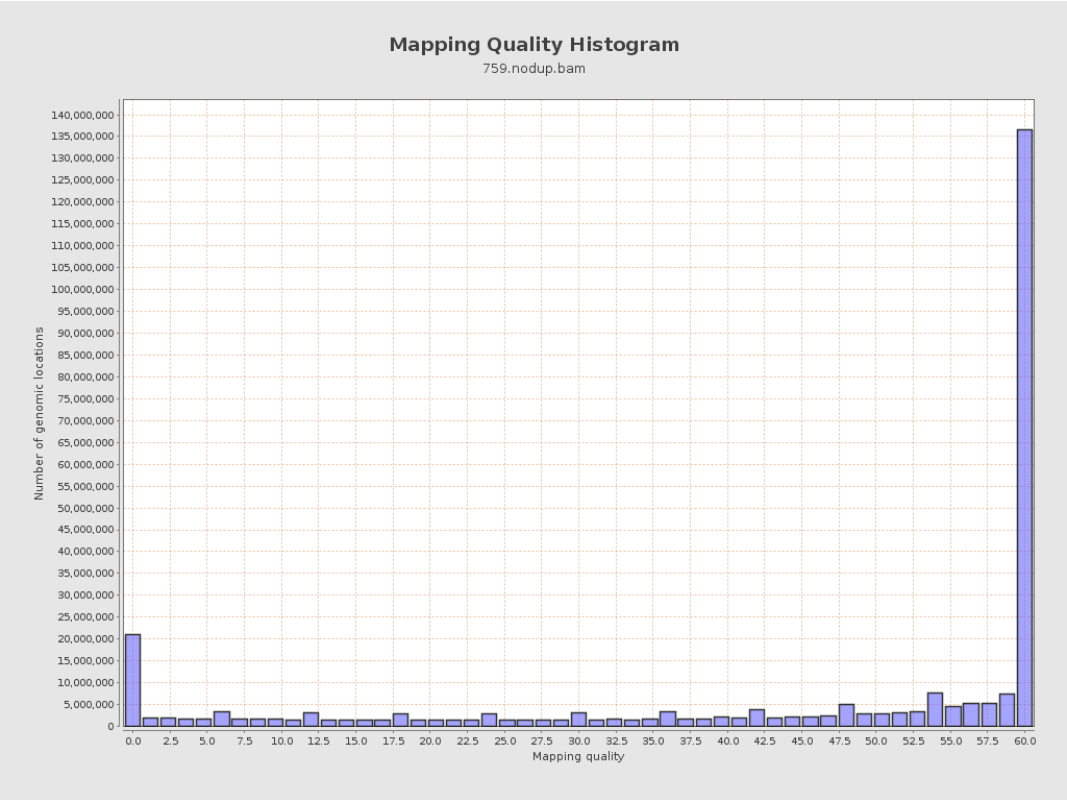
11. Results : Homopolymer Indels



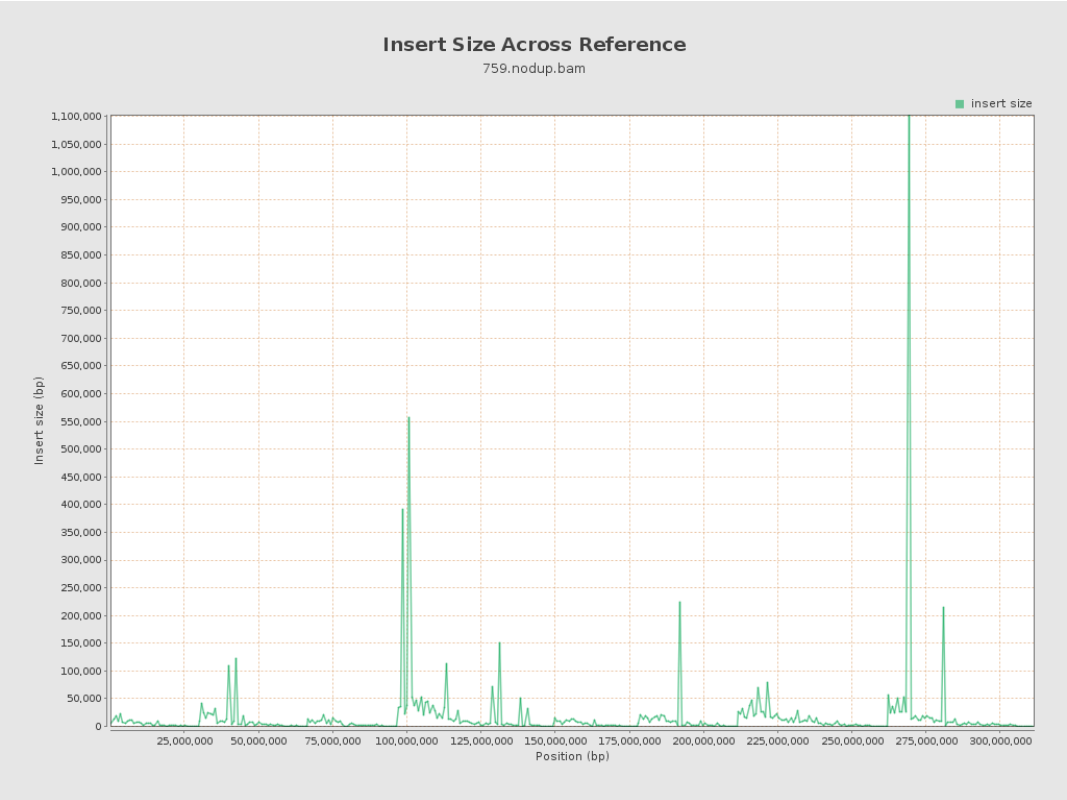
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram