Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/592.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/592.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_115/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_115_S205_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_115/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_115_S205_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	64,440,140
Mapped reads	60,750,636 / 94.27%
Unmapped reads	3,689,504 / 5.73%
Mapped paired reads	60,750,636 / 94.27%
Mapped reads, first in pair	30,415,087 / 47.2%
Mapped reads, second in pair	30,335,549 / 47.08%
Mapped reads, both in pair	59,586,019 / 92.47%
Mapped reads, singletons	1,164,617 / 1.81%
Read min/max/mean length	30 / 151 / 148.35
Duplicated reads (flagged)	9,110,693 / 14.14%
Clipped reads	12,478,303 / 19.36%

2.2. ACGT Content

Number/percentage of A's	2,633,390,732 / 30.99%
Number/percentage of C's	1,617,455,558 / 19.03%
Number/percentage of T's	2,633,655,935 / 30.99%
Number/percentage of G's	1,613,114,108 / 18.98%
Number/percentage of N's	35,346 / 0%
GC Percentage	38.02%

2.3. Coverage

Mean	27.3345
Standard Deviation	194.5692

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Insert size

Mean	215,601.98
Standard Deviation	2,204,643.48
P25/Median/P75	334 / 434 / 567

2.6. Mismatches and indels

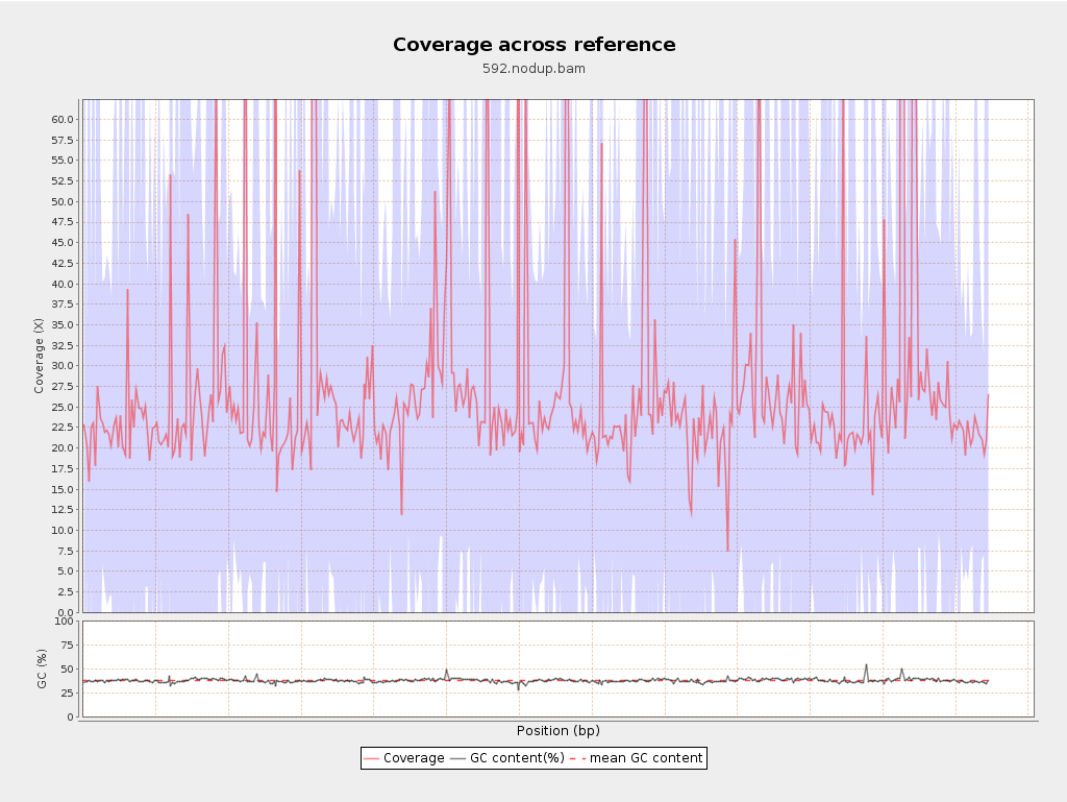
General error rate	2.2%
Mismatches	171,789,704
Insertions	5,491,953
Mapped reads with at least one insertion	8.14%
Deletions	5,592,835
Mapped reads with at least one deletion	8.2%
Homopolymer indels	56.98%

2.7. Chromosome stats

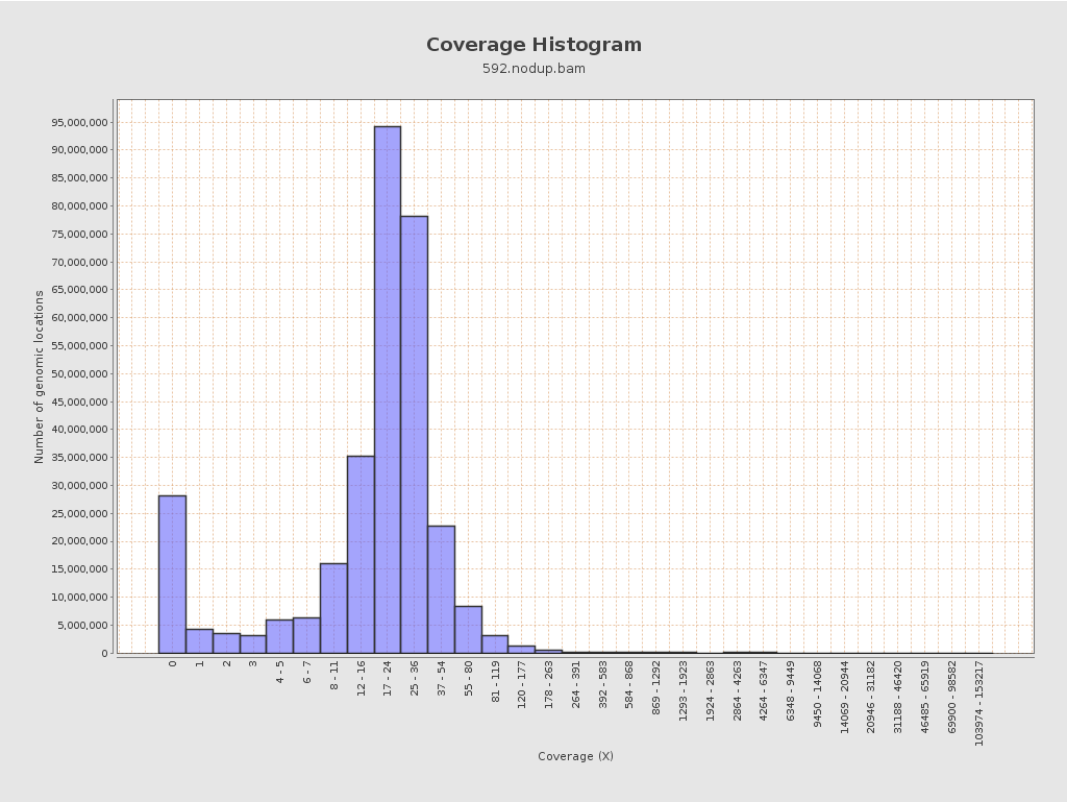
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	671042702	22.5755	51.0012

LT669789.1	36598175	1018166254	27.8201	208.2438
LT669790.1	30422129	874097024	28.7323	190.844
LT669791.1	52758100	1430708023	27.1183	162.2036
LT669792.1	28376109	774163821	27.2822	256.8903
LT669793.1	33388210	856212468	25.6442	156.5804
LT669794.1	50579949	1318165331	26.061	164.6538
LT669795.1	49795044	1576009736	31.6499	267.8724

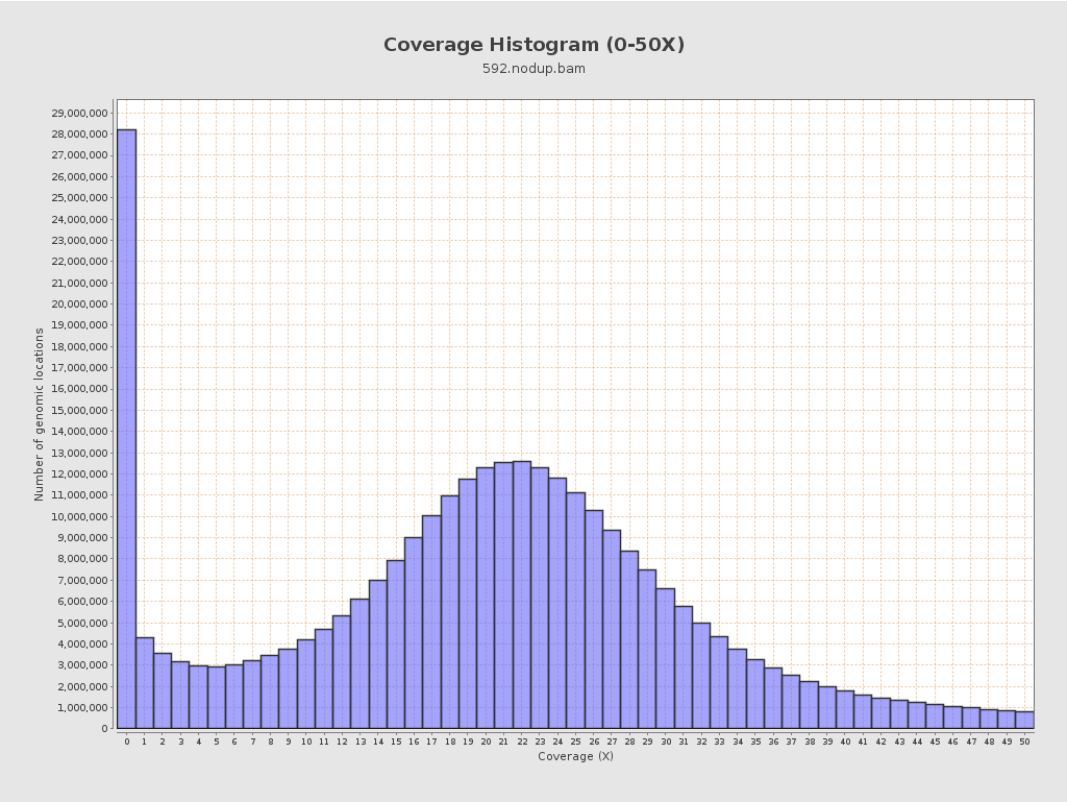
3. Results : Coverage across reference



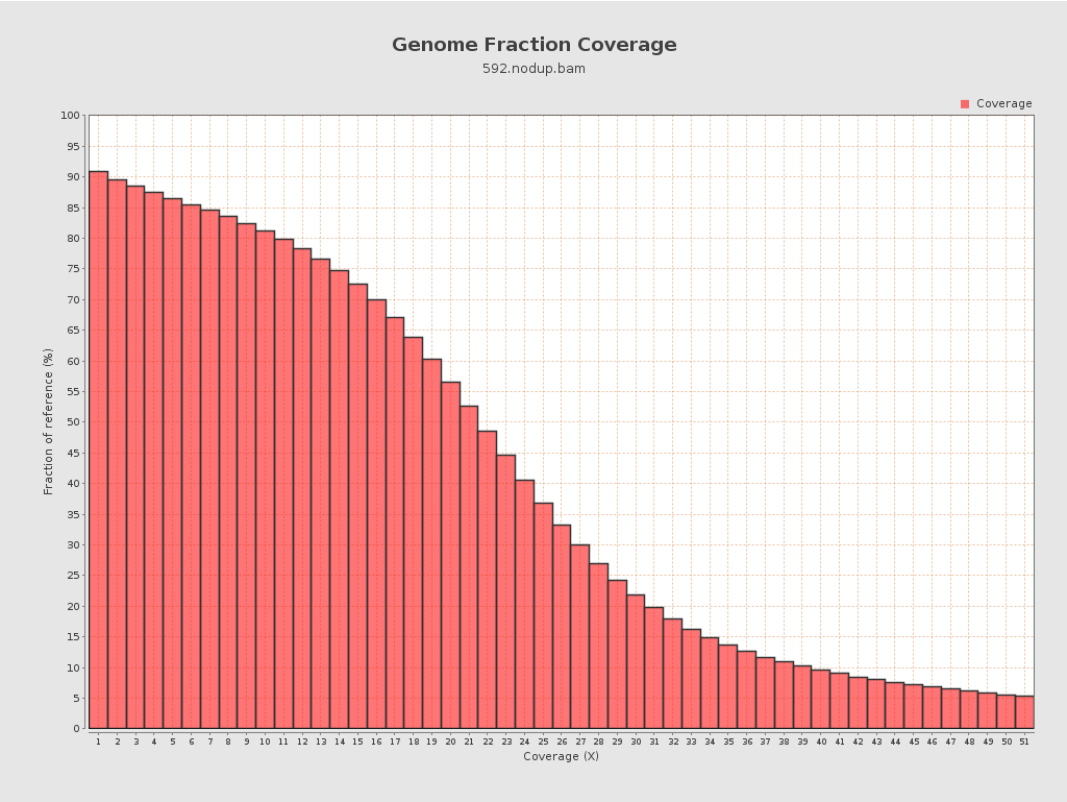
4. Results : Coverage Histogram



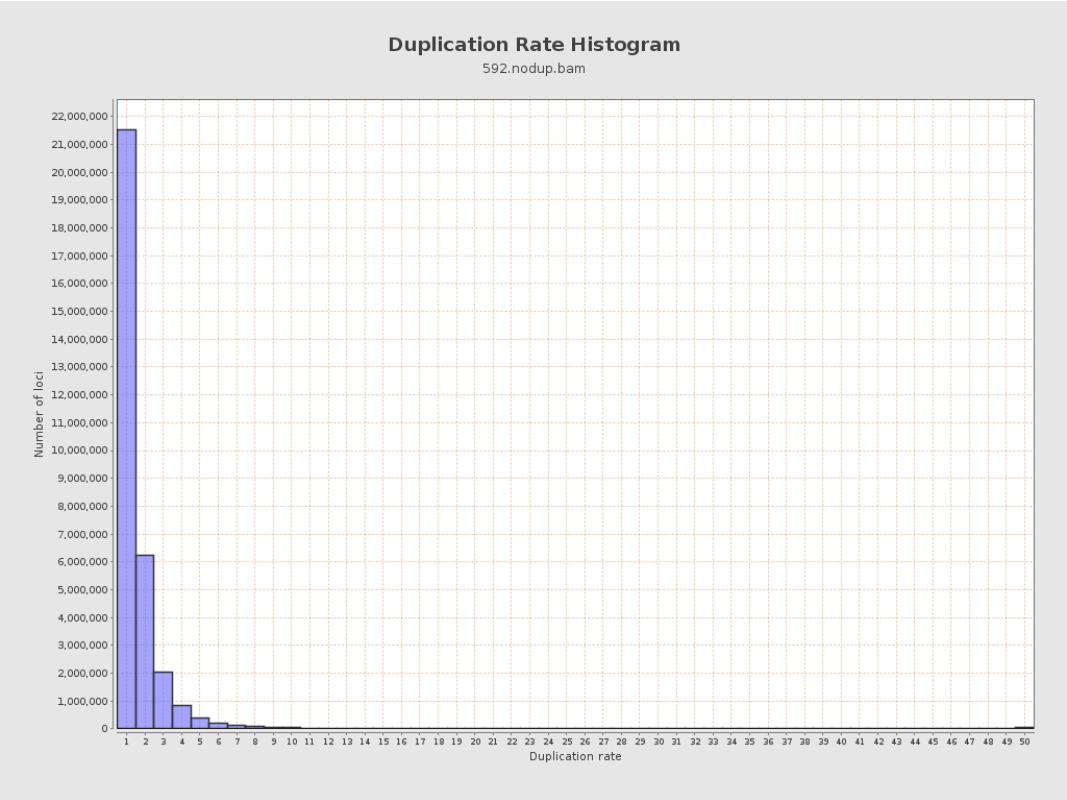
5. Results : Coverage Histogram (0-50X)



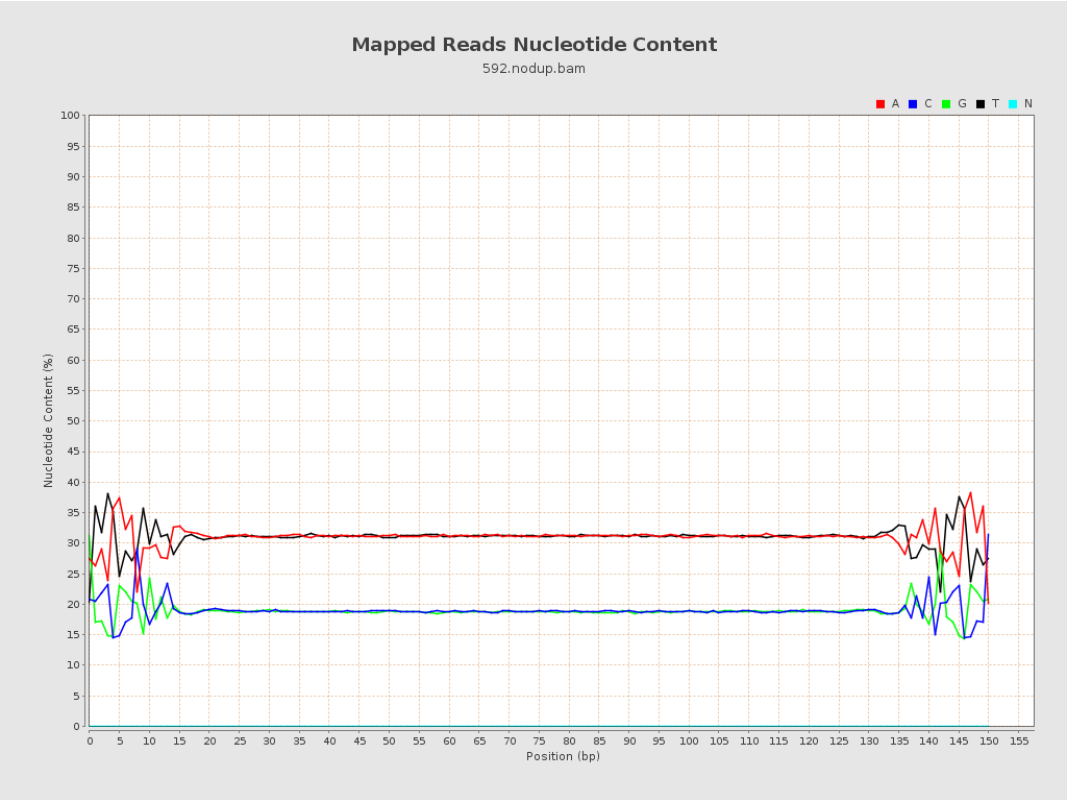
6. Results : Genome Fraction Coverage



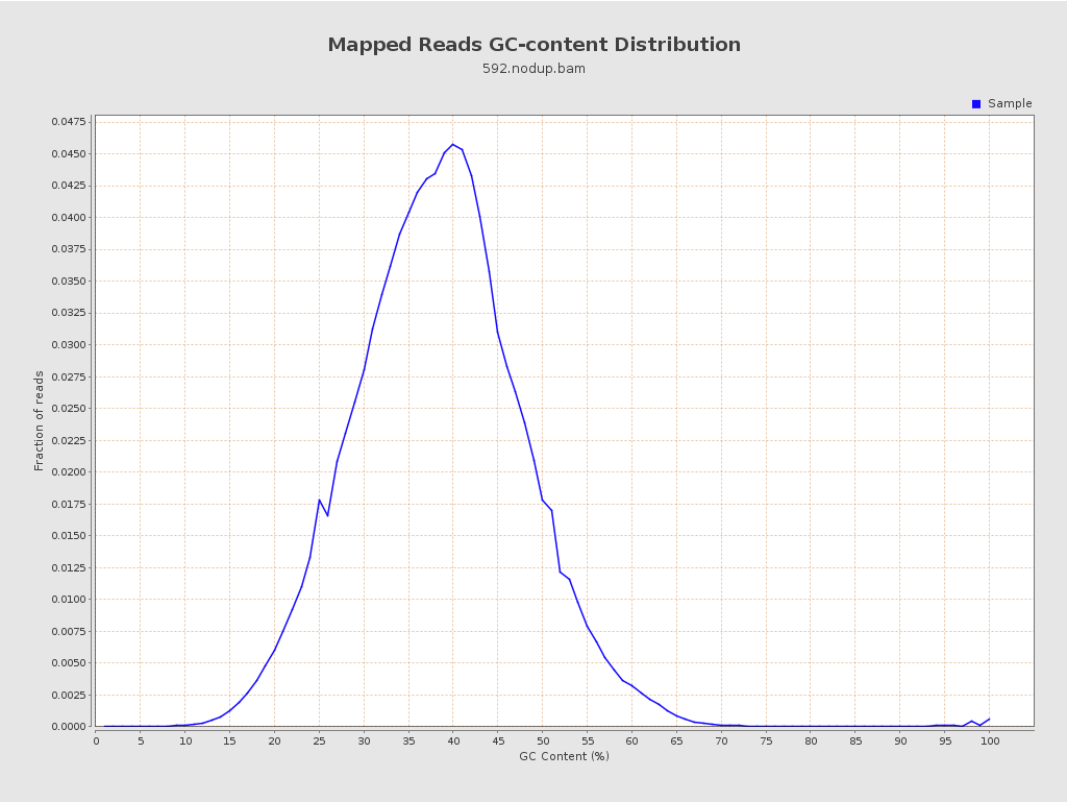
7. Results : Duplication Rate Histogram



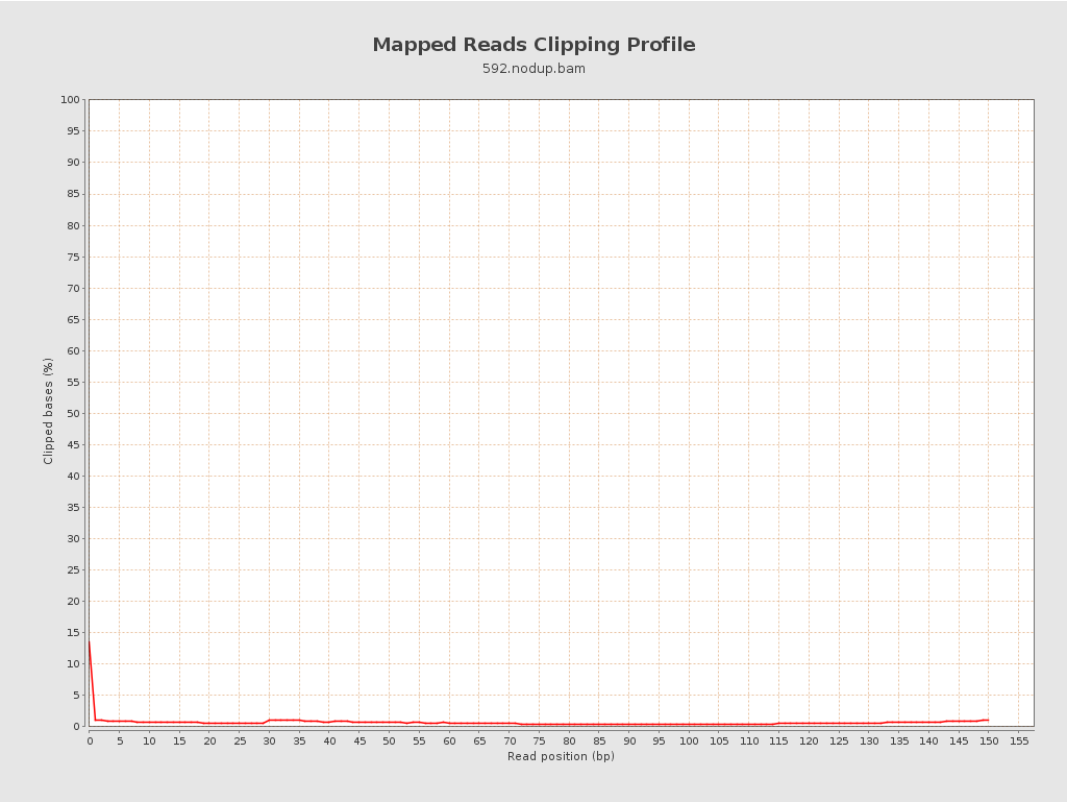
8. Results : Mapped Reads Nucleotide Content



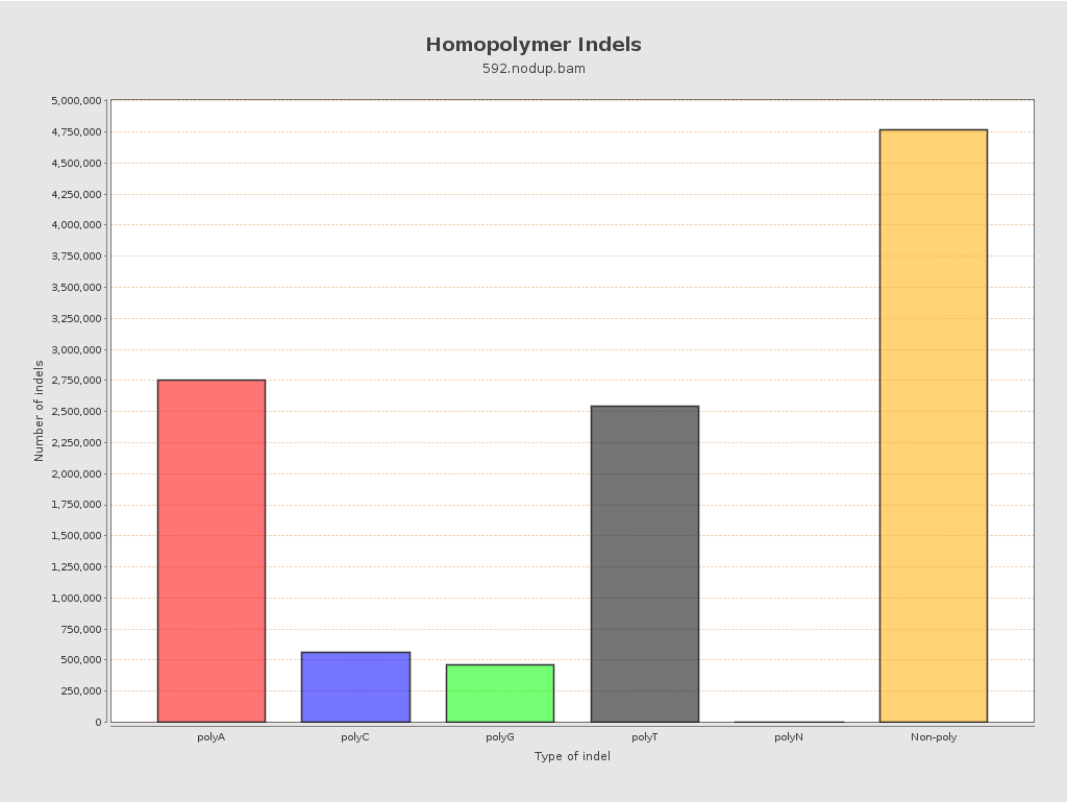
9. Results : Mapped Reads GC-content Distribution



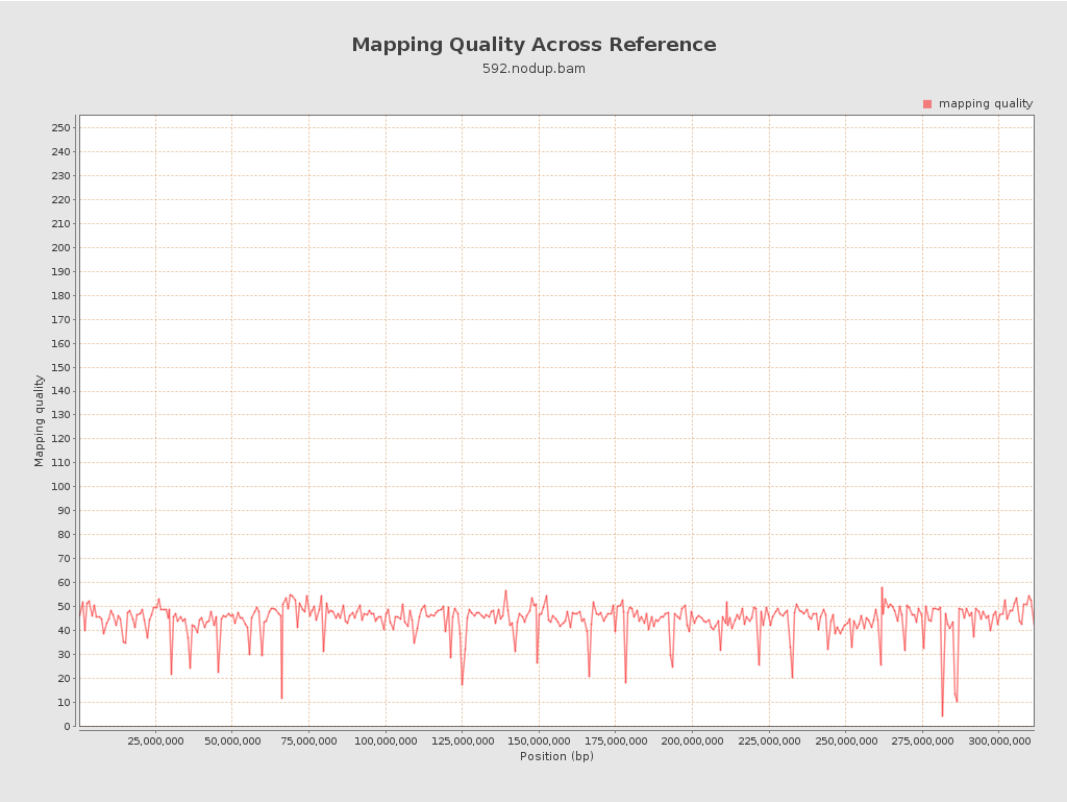
10. Results : Mapped Reads Clipping Profile



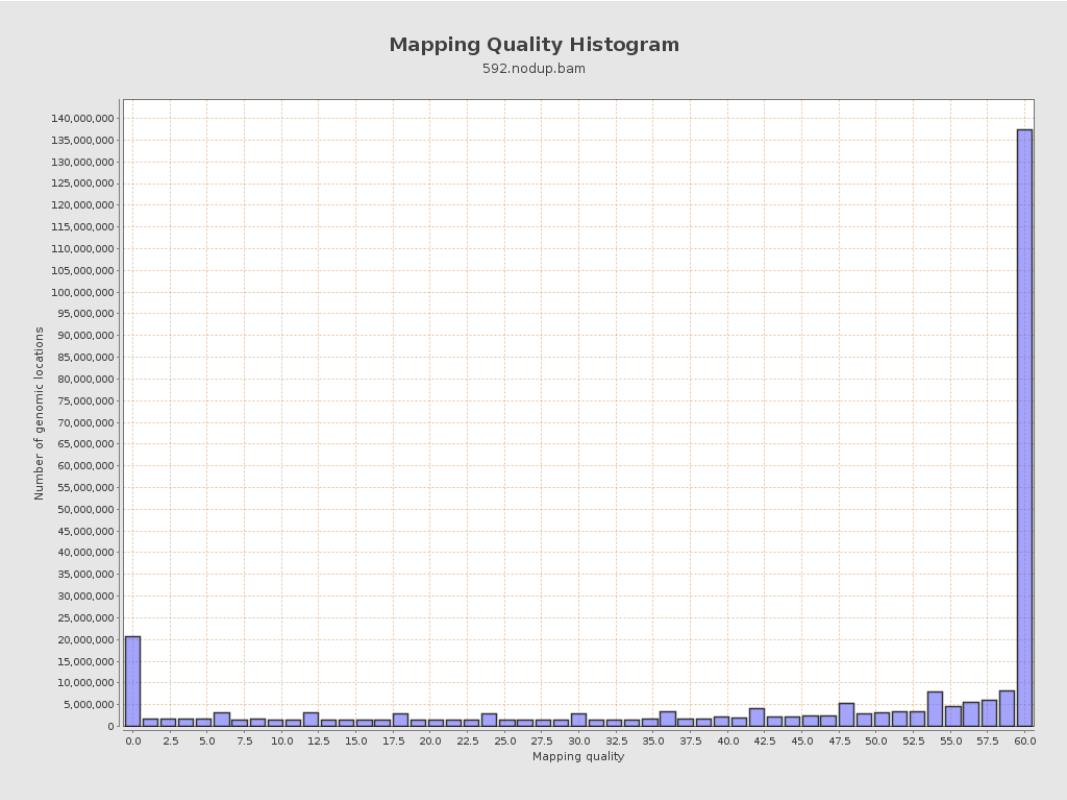
11. Results : Homopolymer Indels



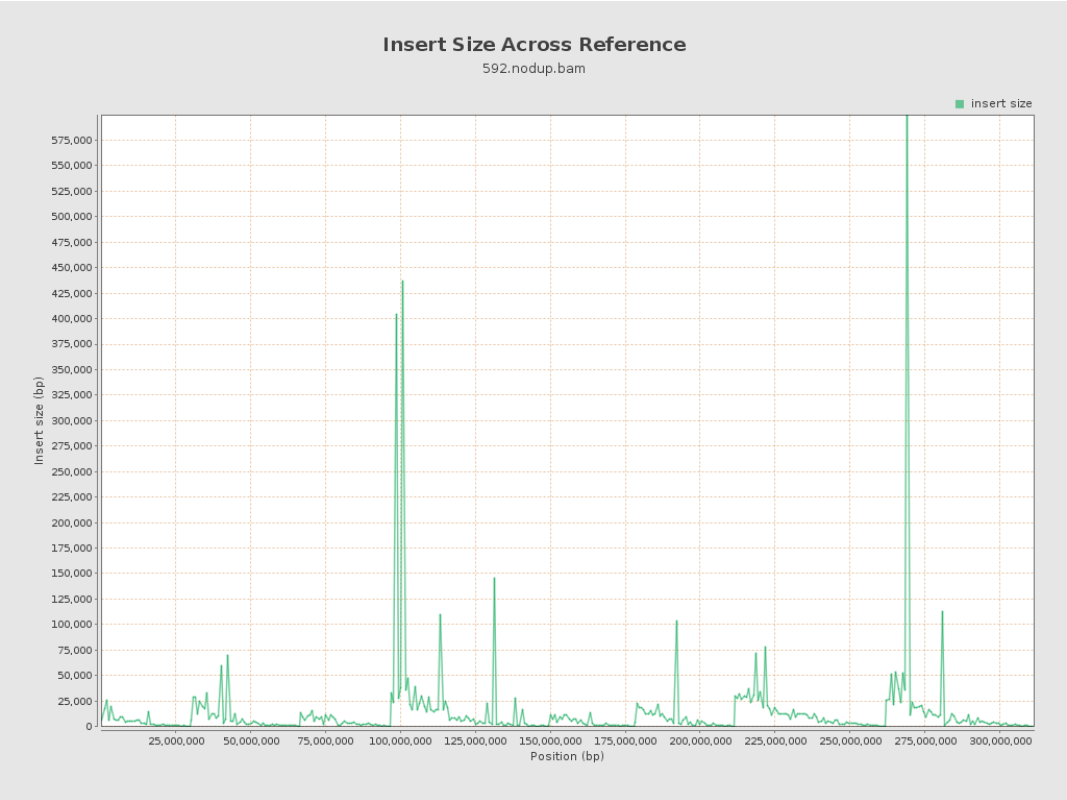
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram