Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/962.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/962.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_293/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_293_S374_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_293/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_293_S374_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:00 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,064,221
Mapped reads	55,122,986 / 93.33%
Unmapped reads	3,941,235 / 6.67%
Mapped paired reads	55,122,986 / 93.33%
Mapped reads, first in pair	27,679,934 / 46.86%
Mapped reads, second in pair	27,443,052 / 46.46%
Mapped reads, both in pair	53,841,676 / 91.16%
Mapped reads, singletons	1,281,310 / 2.17%
Read min/max/mean length	30 / 151 / 148.25
Duplicated reads (flagged)	7,777,809 / 13.17%
Clipped reads	13,285,032 / 22.49%

2.2. ACGT Content

Number/percentage of A's	2,330,364,802 / 30.63%
Number/percentage of C's	1,473,021,168 / 19.36%
Number/percentage of T's	2,335,809,845 / 30.71%
Number/percentage of G's	1,468,033,302 / 19.3%
Number/percentage of N's	26,567 / 0%
GC Percentage	38.66%

2.3. Coverage

Mean	24.4696
Standard Deviation	206.3032

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Insert size

Mean	216,498.01
Standard Deviation	2,214,055.57
P25/Median/P75	323 / 422 / 544

2.6. Mismatches and indels

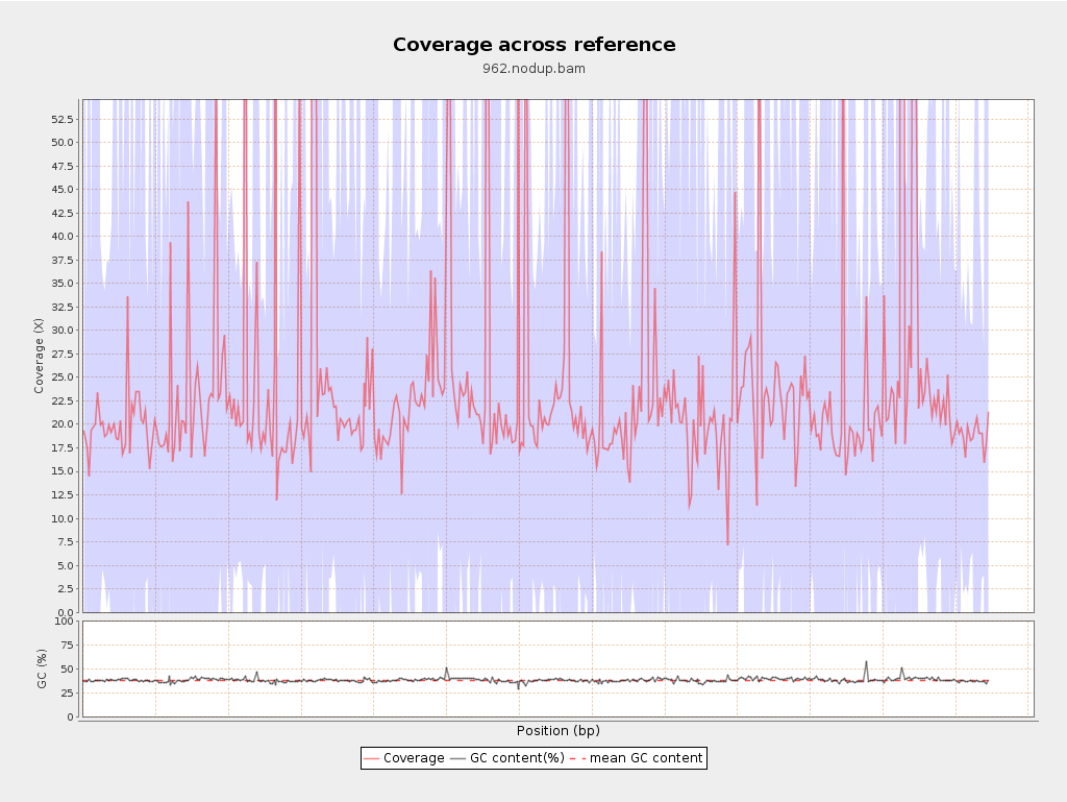
General error rate	2.52%
Mismatches	177,955,928
Insertions	5,026,033
Mapped reads with at least one insertion	8.2%
Deletions	4,974,044
Mapped reads with at least one deletion	8.05%
Homopolymer indels	56.02%

2.7. Chromosome stats

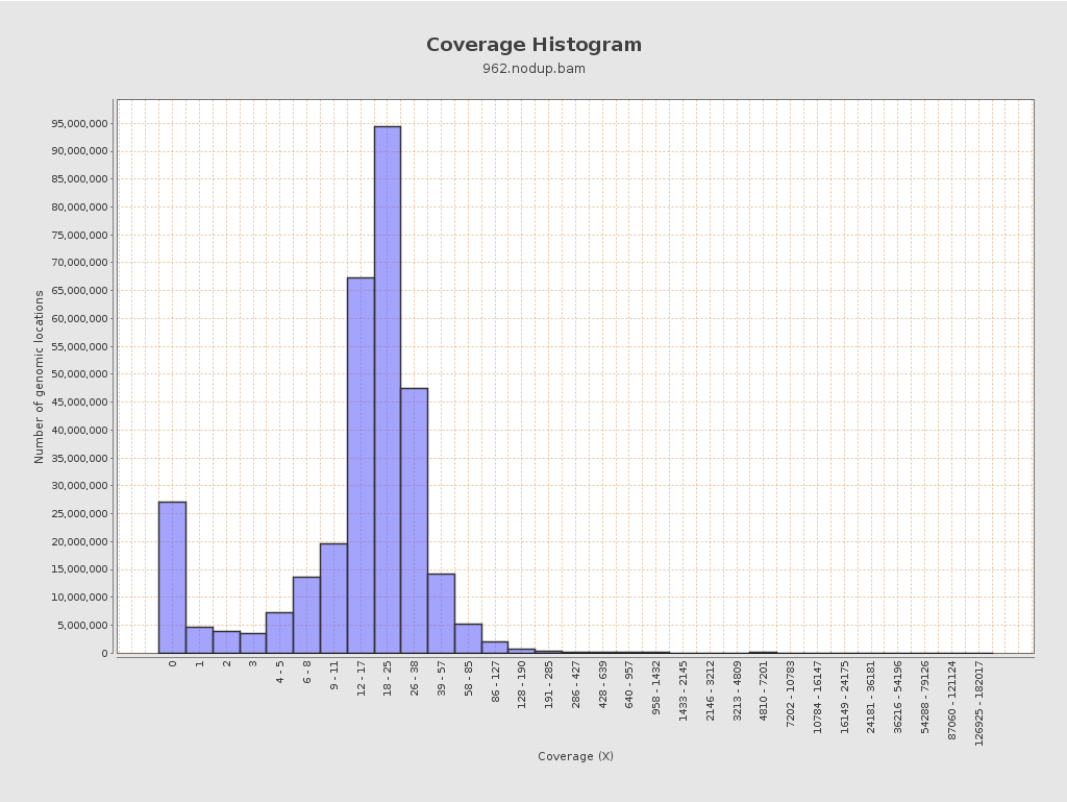
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
LT669788.1	29724344	584884446	19.677	62.1544

LT669789.1	36598175	904077717	24.7028	214.968
LT669790.1	30422129	809856725	26.6206	215.5528
LT669791.1	52758100	1271155182	24.094	182.6158
LT669792.1	28376109	685566150	24.16	232.5907
LT669793.1	33388210	749734075	22.4551	141.097
LT669794.1	50579949	1161096127	22.9557	168.5317
LT669795.1	49795044	1459394424	29.308	305.459

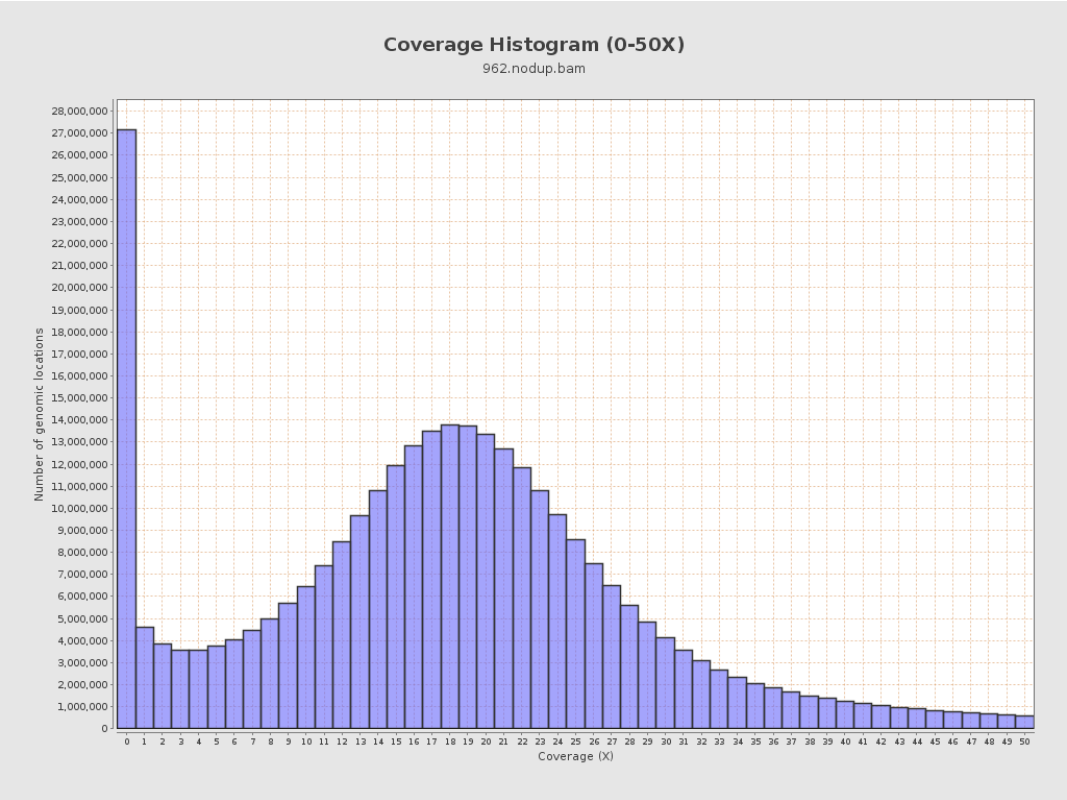
3. Results : Coverage across reference



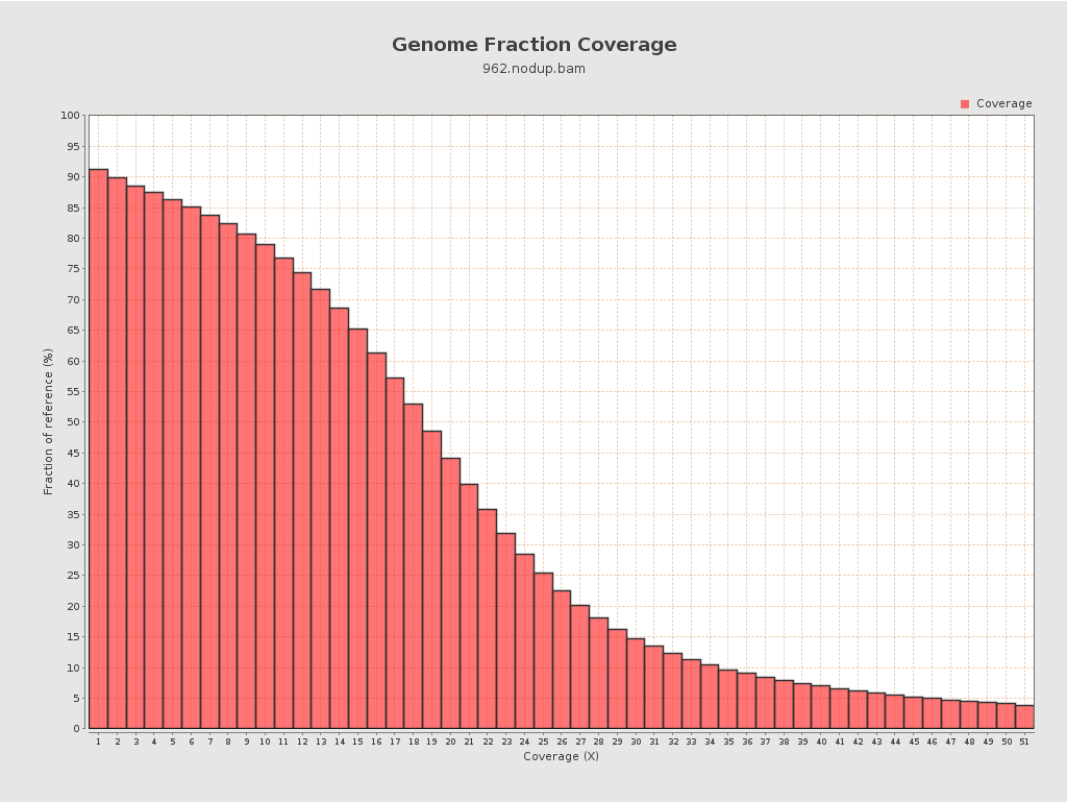
4. Results : Coverage Histogram



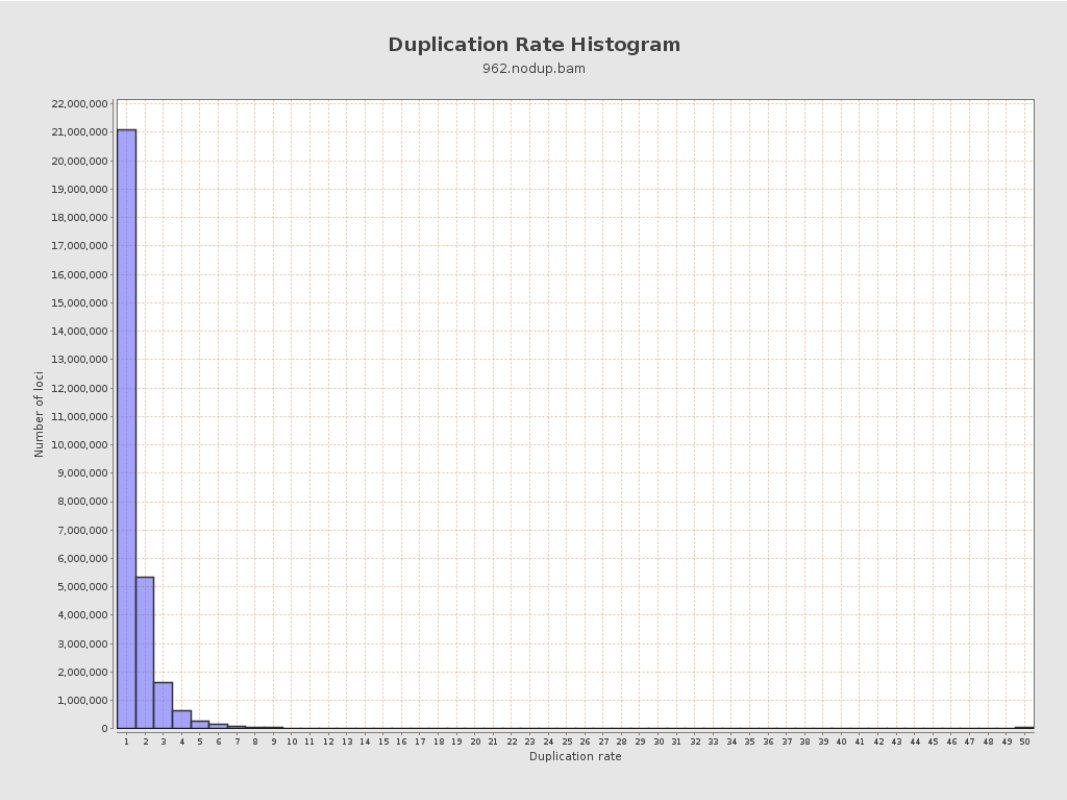
5. Results : Coverage Histogram (0-50X)



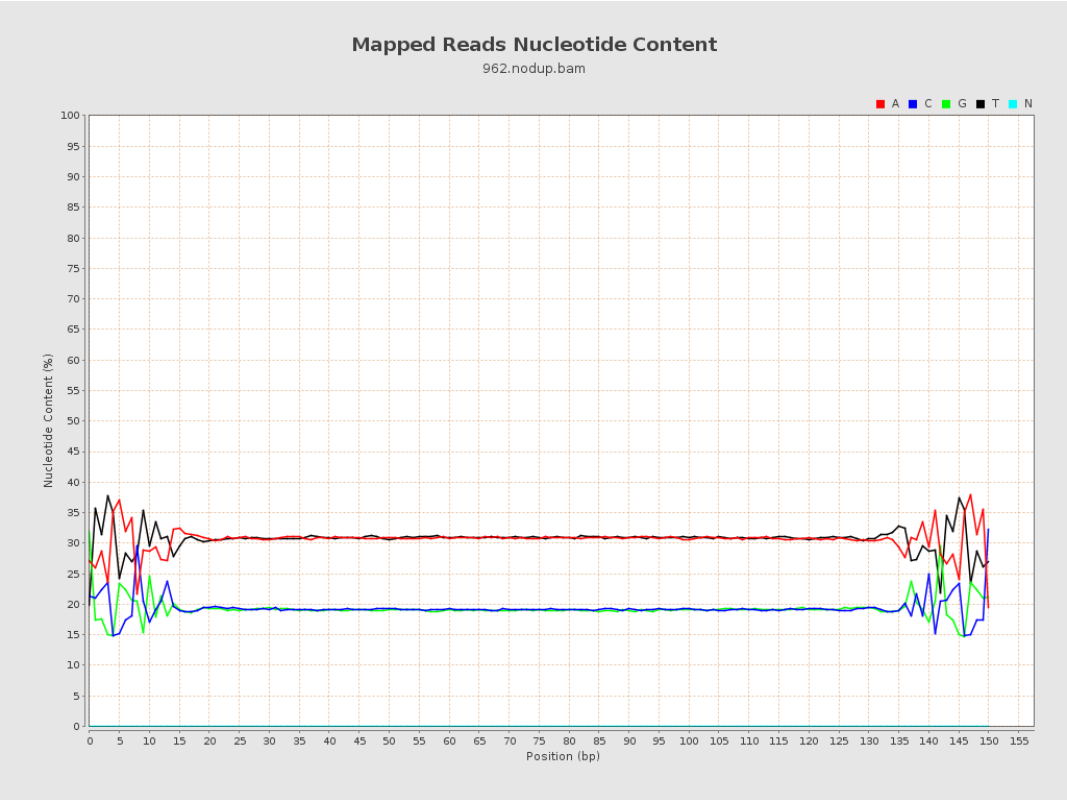
6. Results : Genome Fraction Coverage



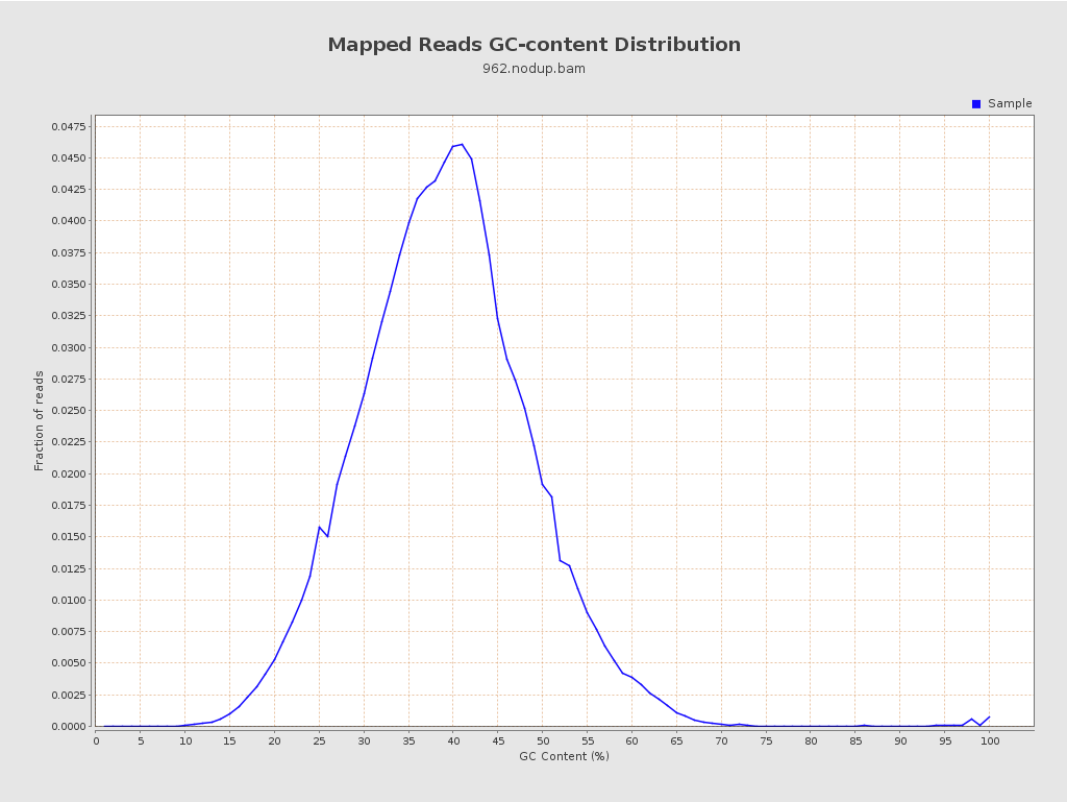
7. Results : Duplication Rate Histogram



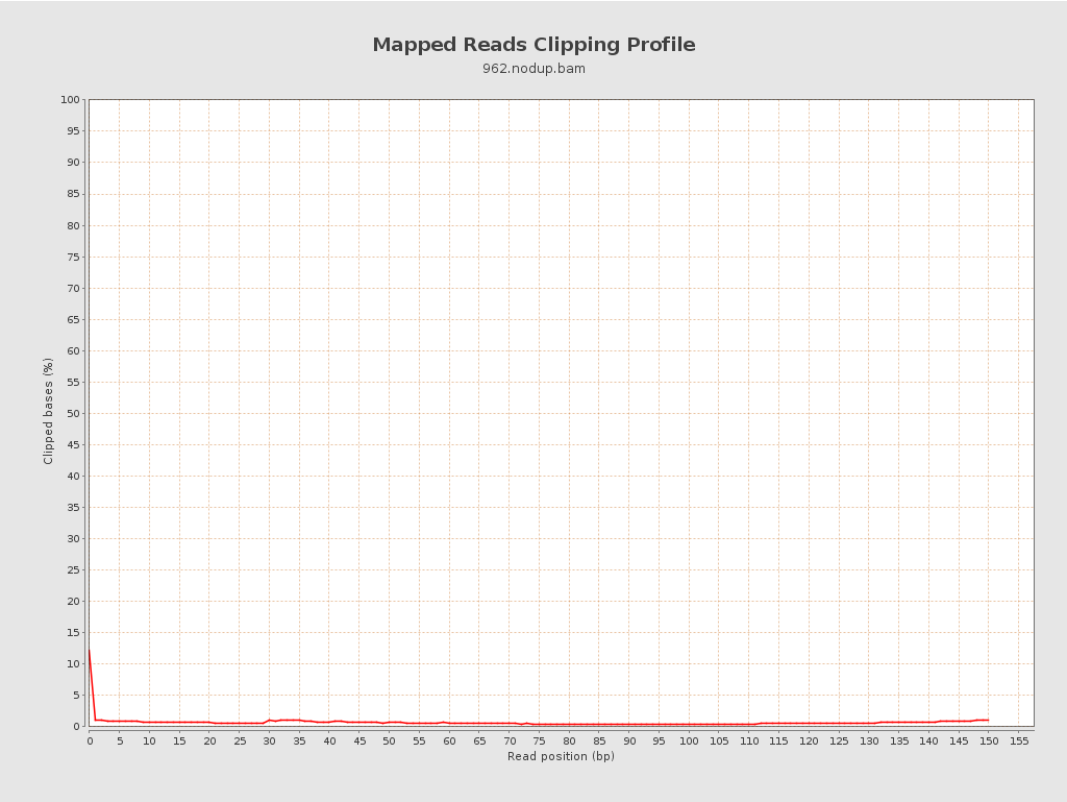
8. Results : Mapped Reads Nucleotide Content



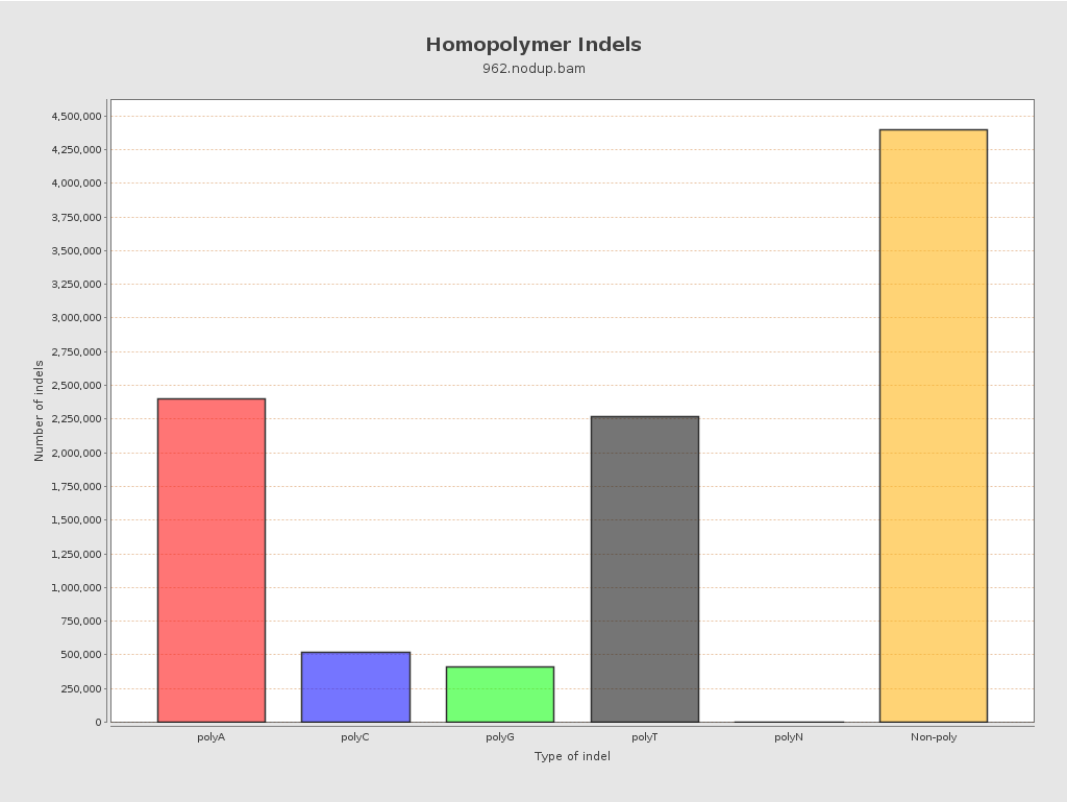
9. Results : Mapped Reads GC-content Distribution



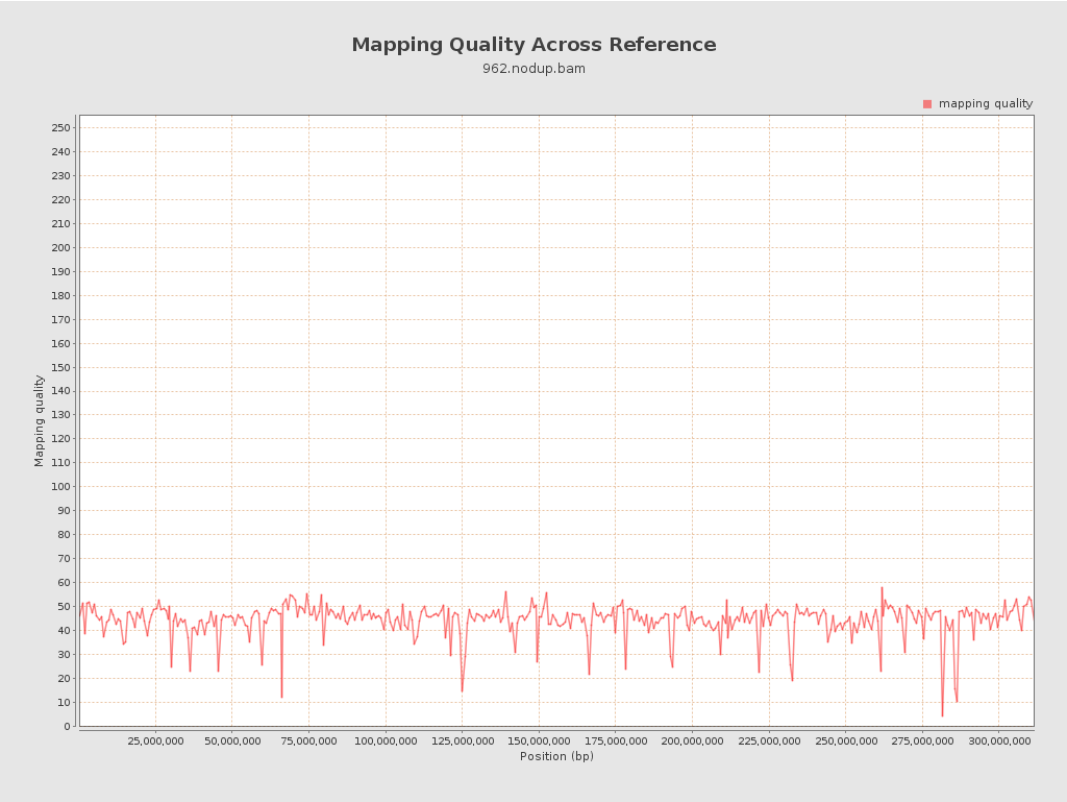
10. Results : Mapped Reads Clipping Profile



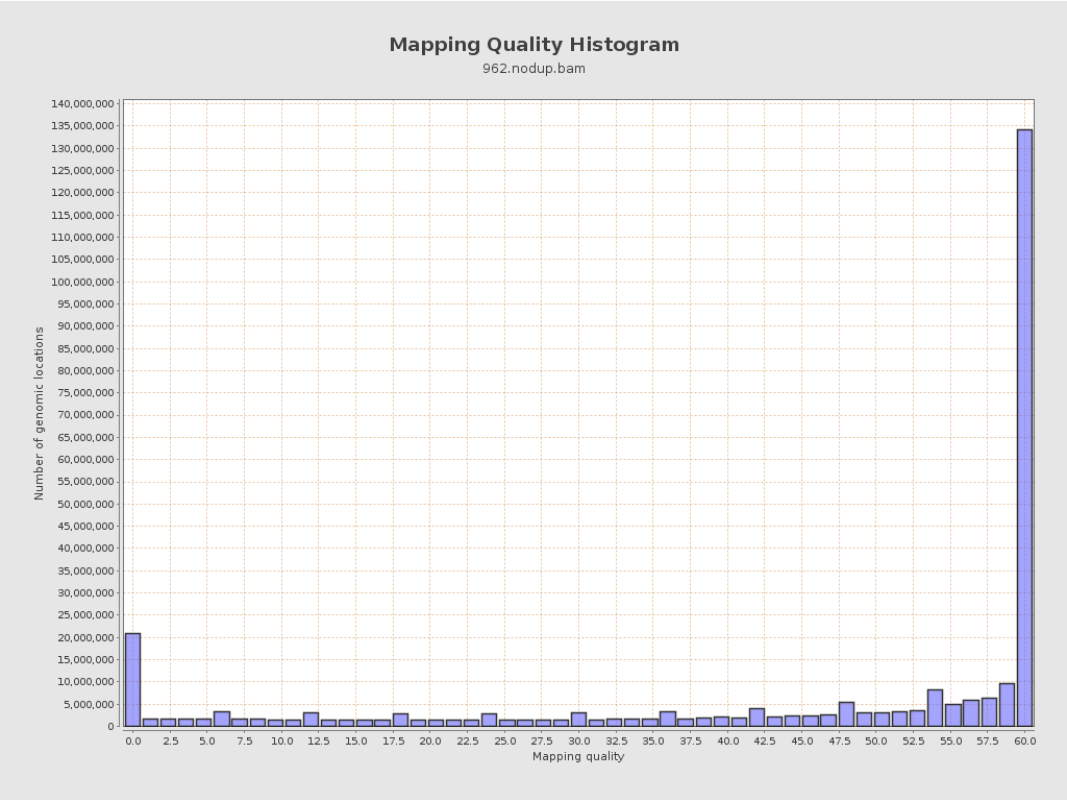
11. Results : Homopolymer Indels



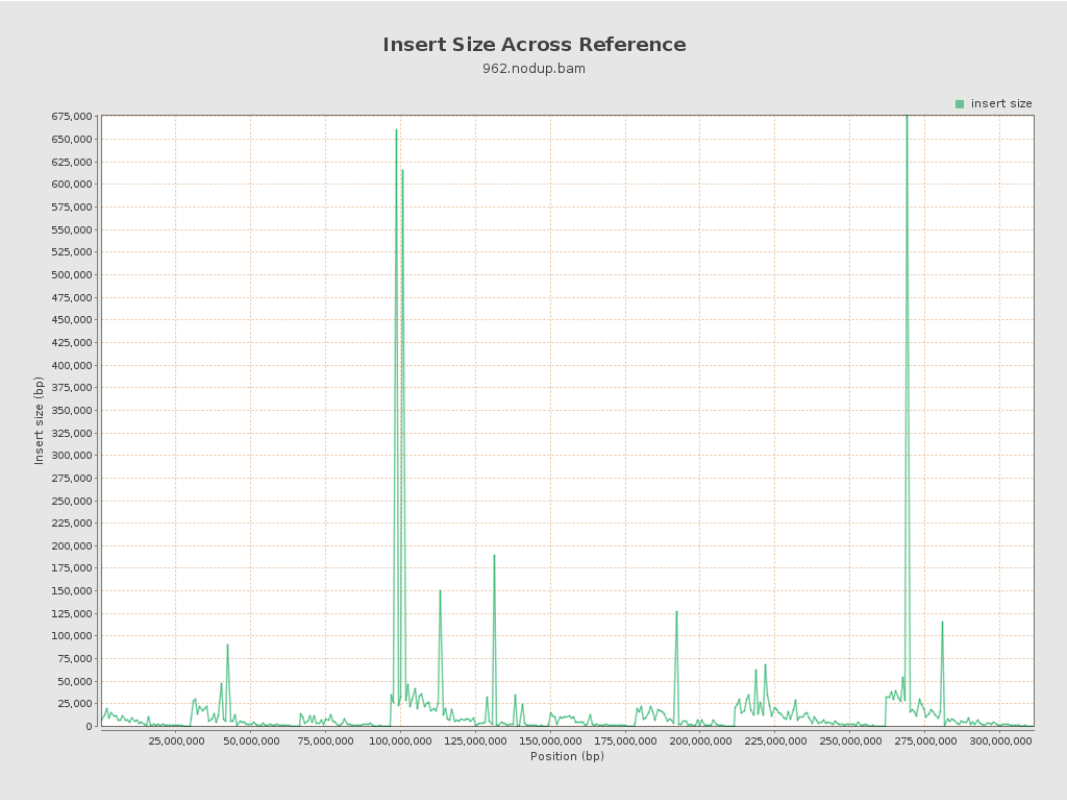
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram