Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:31:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094158.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094158 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094158_1.fastq.gz ERR2094158_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:31:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,440
Mapped reads	756 / 2.66%
Unmapped reads	27,684 / 97.34%
Mapped paired reads	756 / 2.66%
Mapped reads, first in pair	282 / 0.99%
Mapped reads, second in pair	474 / 1.67%
Mapped reads, both in pair	514 / 1.81%
Mapped reads, singletons	242 / 0.85%
Secondary alignments	0
Supplementary alignments	24 / 0.08%
Read min/max/mean length	30 / 151 / 54.73
Duplicated reads (estimated)	484 / 1.7%
Duplication rate	21.62%
Clipped reads	584 / 2.05%

2.2. ACGT Content

Number/percentage of A's	11,268 / 19.2%
Number/percentage of C's	8,608 / 14.67%
Number/percentage of T's	9,677 / 16.49%
Number/percentage of G's	29,133 / 49.64%
Number/percentage of N's	0 / 0%

GC Percentage	64.31%

2.3. Coverage

Mean	0
Standard Deviation	0.0274

2.4. Mapping Quality

Mean Mapping Quality	8.16

2.5. Insert size

Mean	221.24
Standard Deviation	1,832.25
P25/Median/P75	30 / 36 / 175

2.6. Mismatches and indels

General error rate	2.93%
Mismatches	1,394
Insertions	67
Mapped reads with at least one insertion	6.08%
Deletions	65
Mapped reads with at least one deletion	8.6%
Homopolymer indels	46.97%

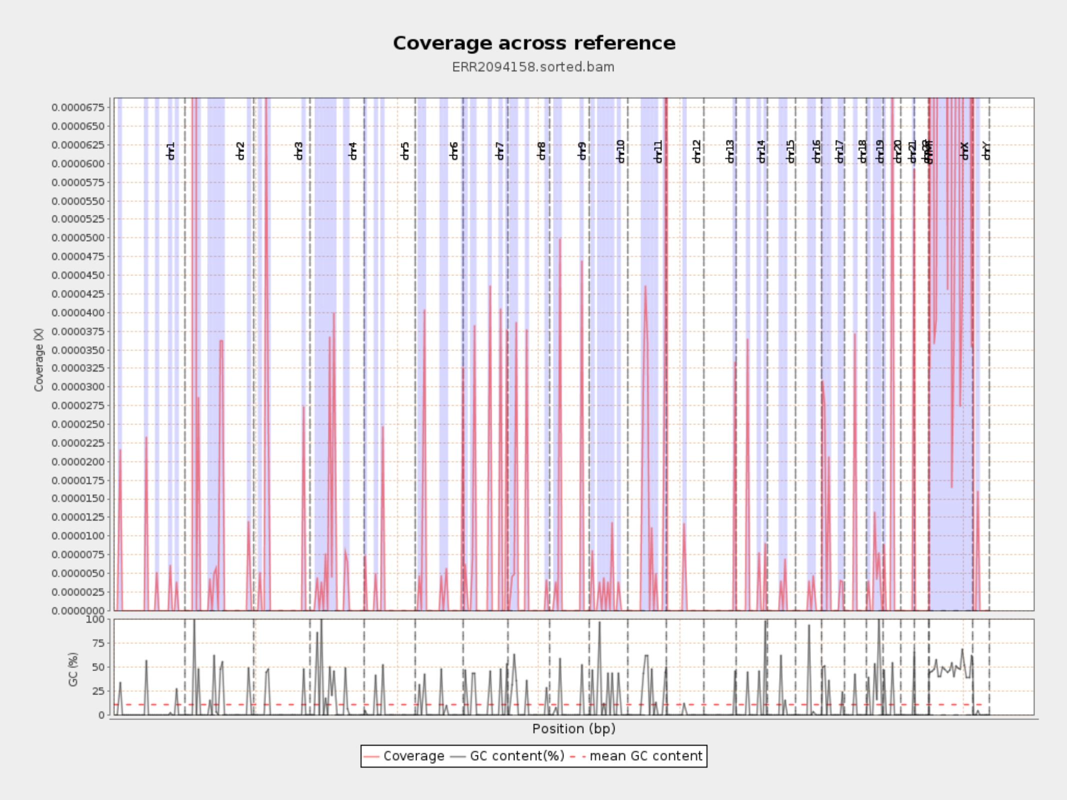
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

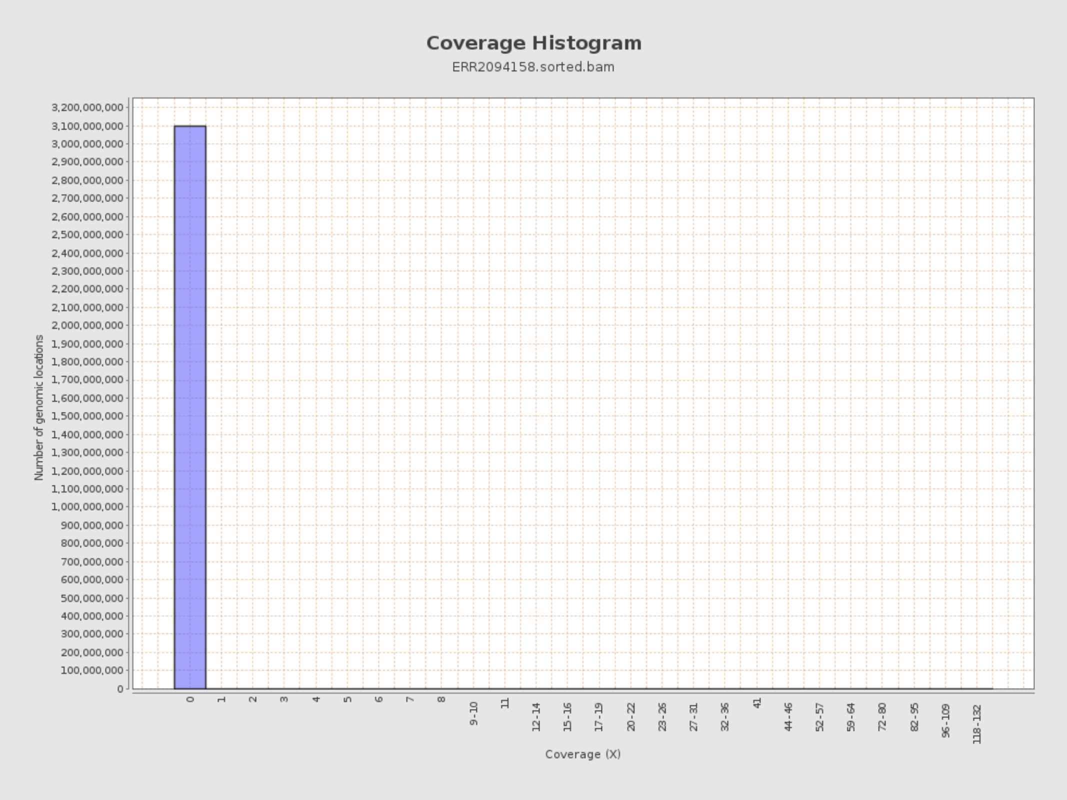
		bases	coverage	deviation
chr1	249250621	466	0	0.0015
chr2	243199373	21661	0.0001	0.0852
chr3	198022430	985	0	0.0028
chr4	191154276	861	0	0.0022
chr5	180915260	287	0	0.0013
chr6	171115067	531	0	0.002
chr7	159138663	1331	0	0.0038
chr8	146364022	697	0	0.0028
chr9	141213431	780	0	0.0026
chr10	135534747	278	0	0.0018
chr11	135006516	1589	0	0.0045
chr12	133851895	91	0	0.0008
chr13	115169878	258	0	0.0021
chr14	107349540	412	0	0.0022
chr15	102531392	85	0	0.0009
chr16	90354753	68	0	0.0009
chr17	81195210	662	0	0.0037
chr18	78077248	288	0	0.0027
chr19	59128983	226	0	0.0022
chr20	63025520	638	0	0.0038
chr21	48129895	291	0	0.0029
chr22	51304566	0	0	0
chrMT	16571	5553	0.3351	1.6458
chrX	155270560	20912	0.0001	0.0563

chrY	59373566	124	0	0.002

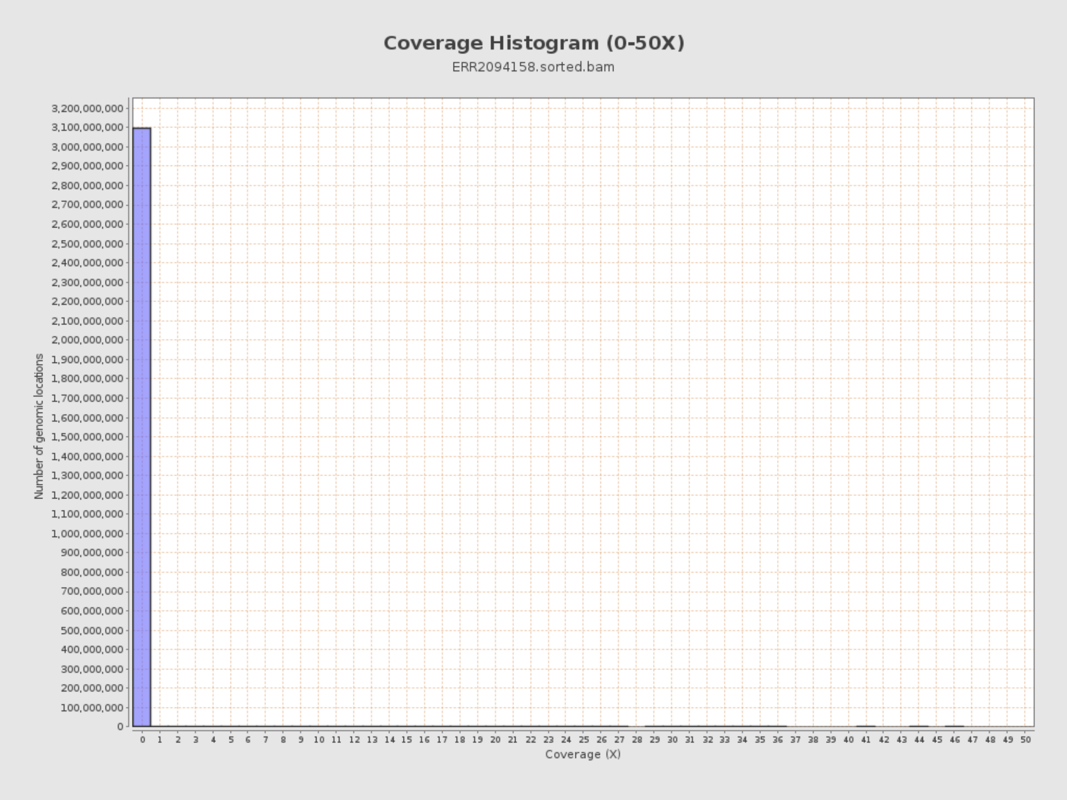
3. Results : Coverage across reference



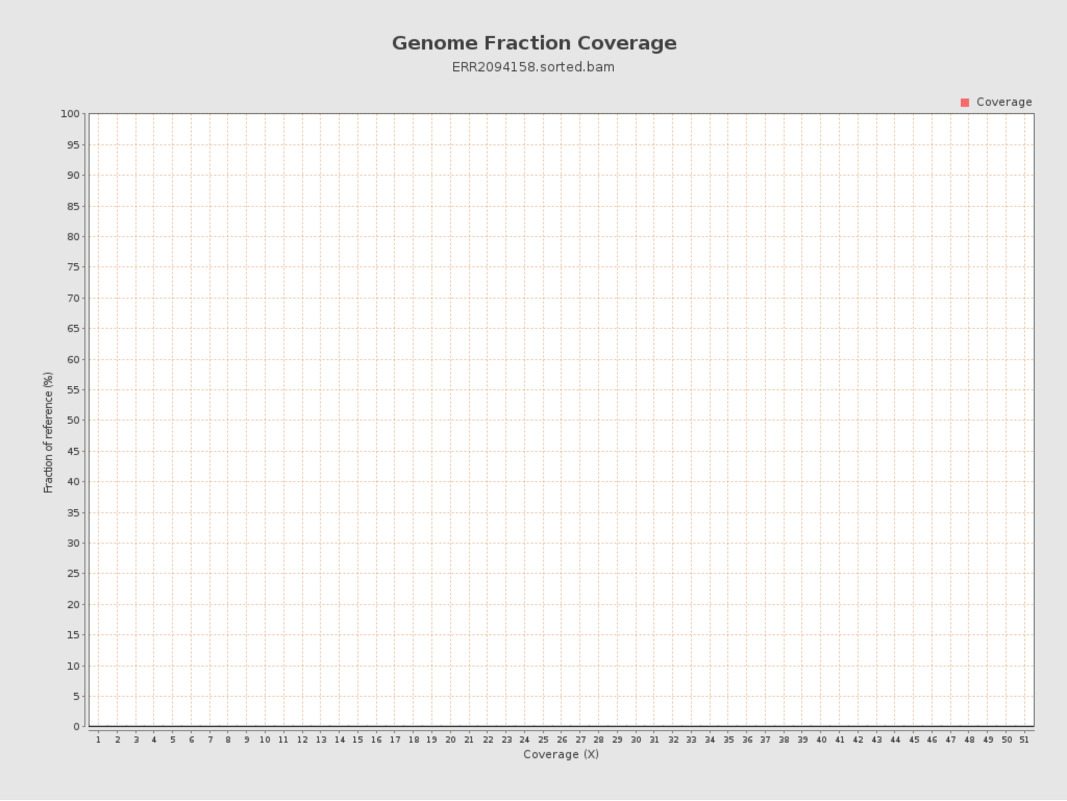
4. Results : Coverage Histogram



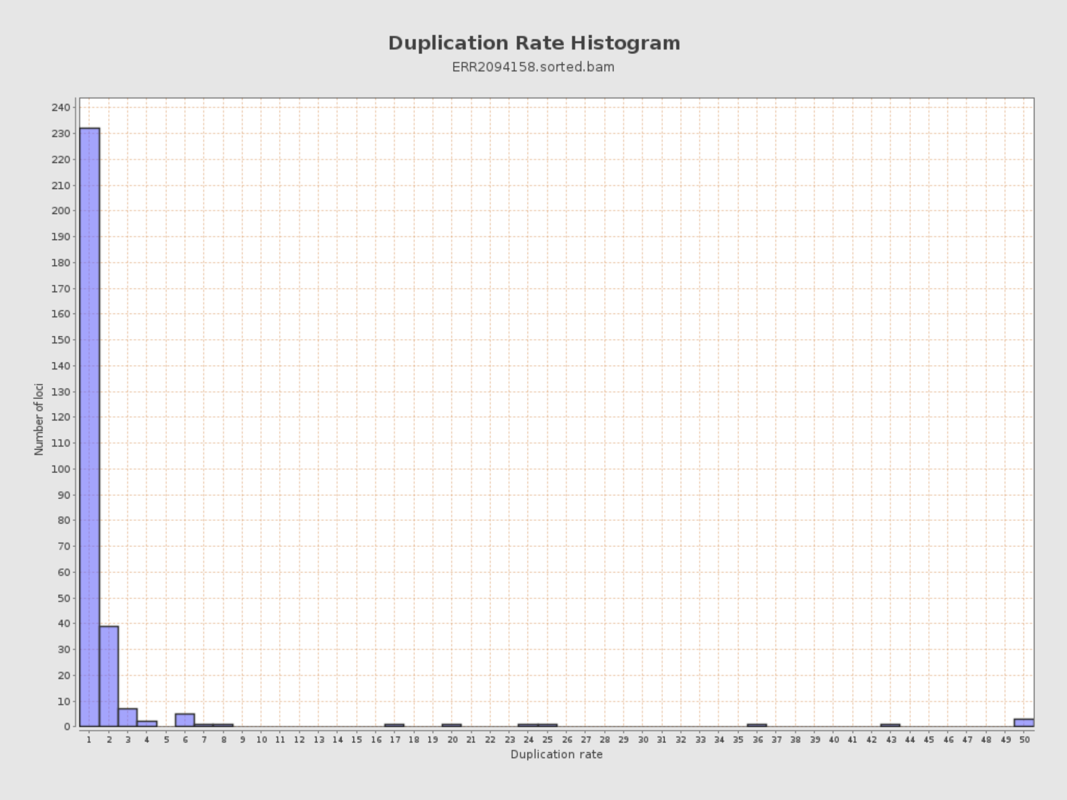
5. Results : Coverage Histogram (0-50X)



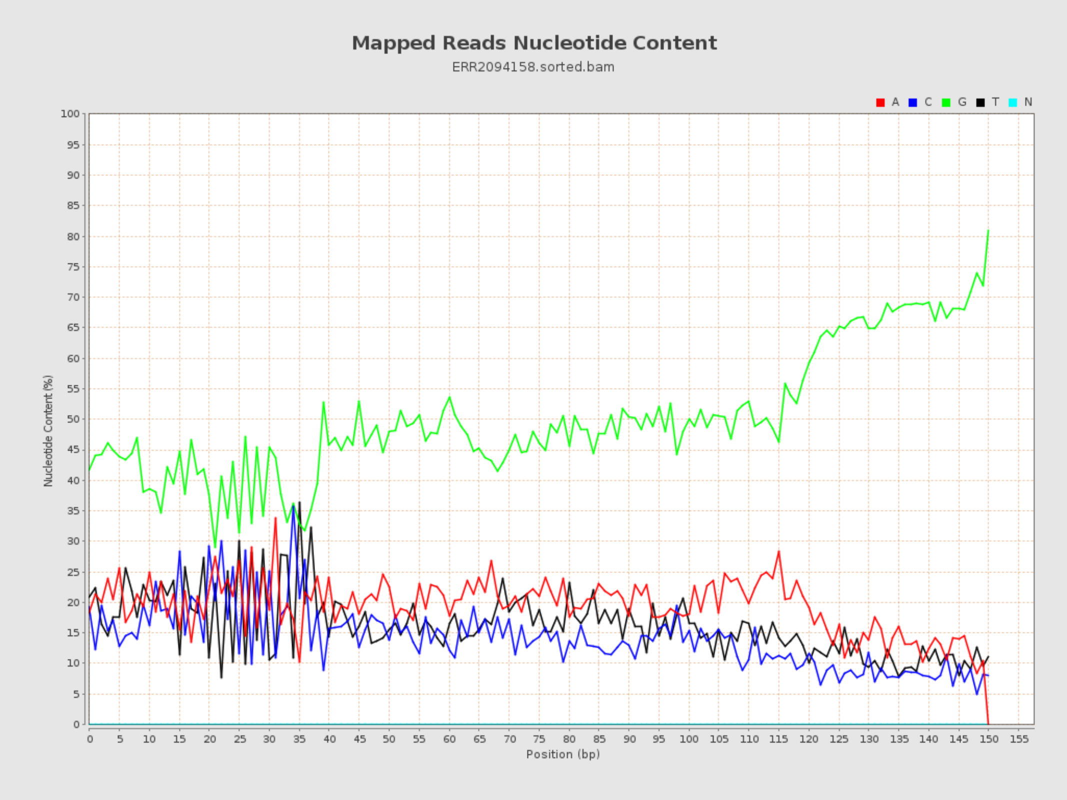
6. Results : Genome Fraction Coverage



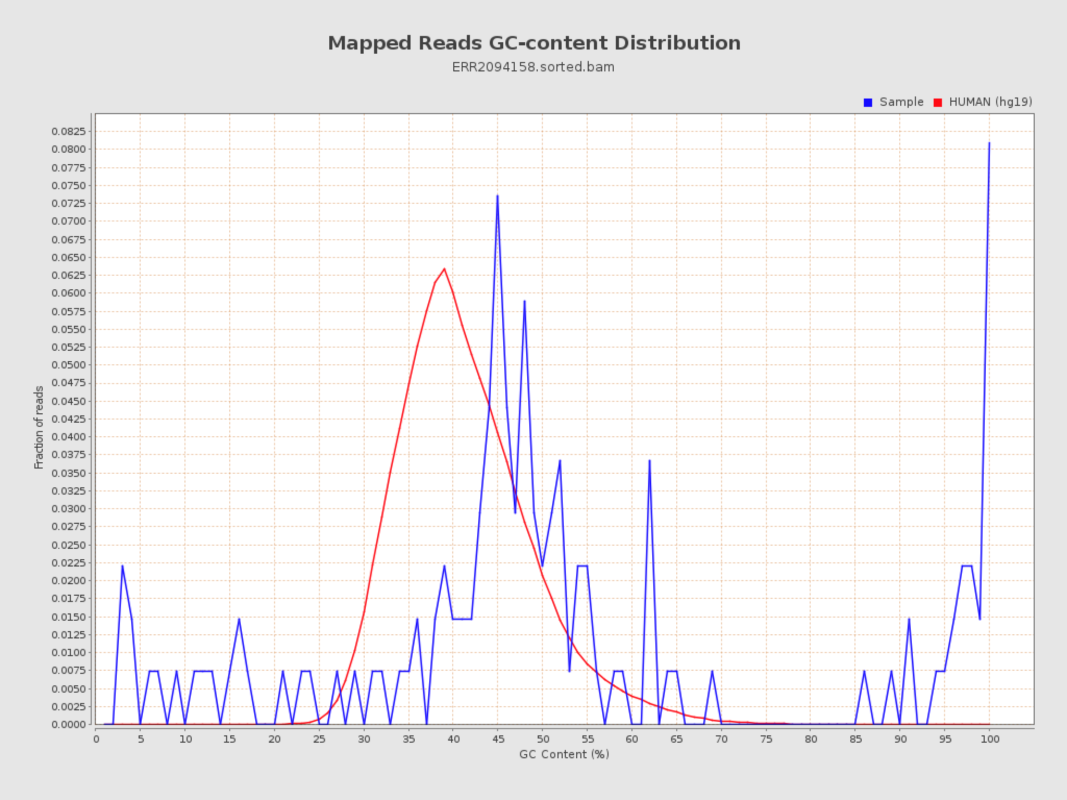
7. Results : Duplication Rate Histogram



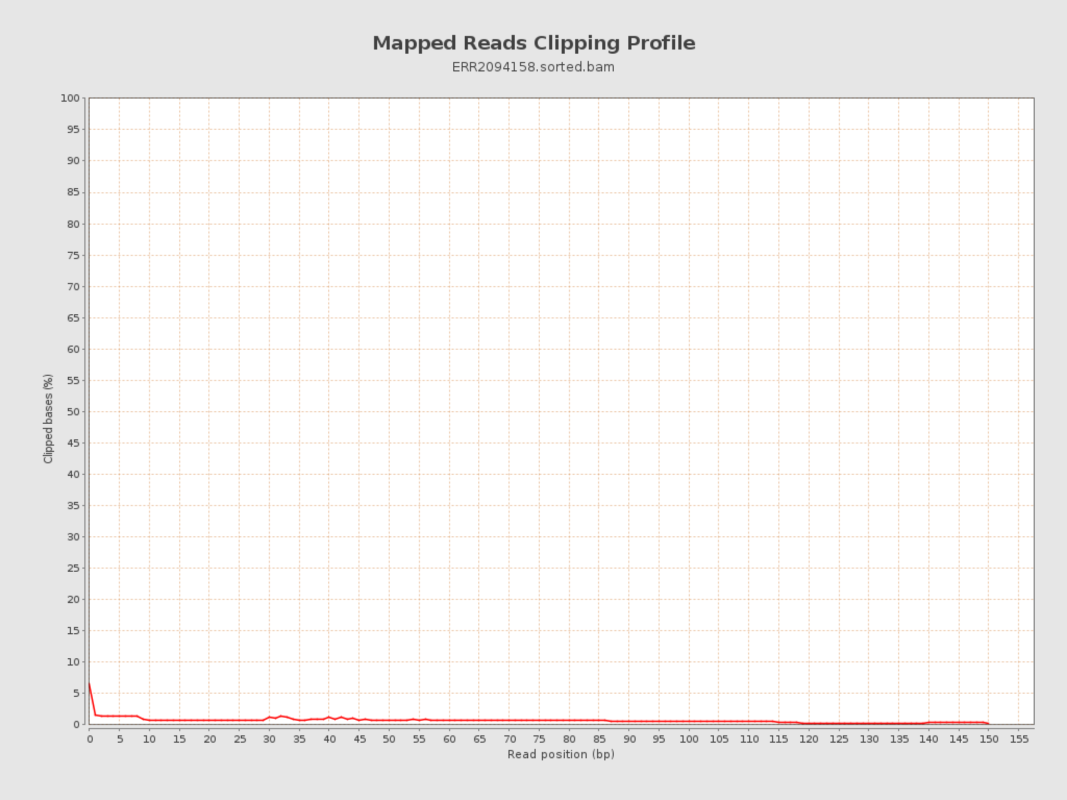
8. Results : Mapped Reads Nucleotide Content



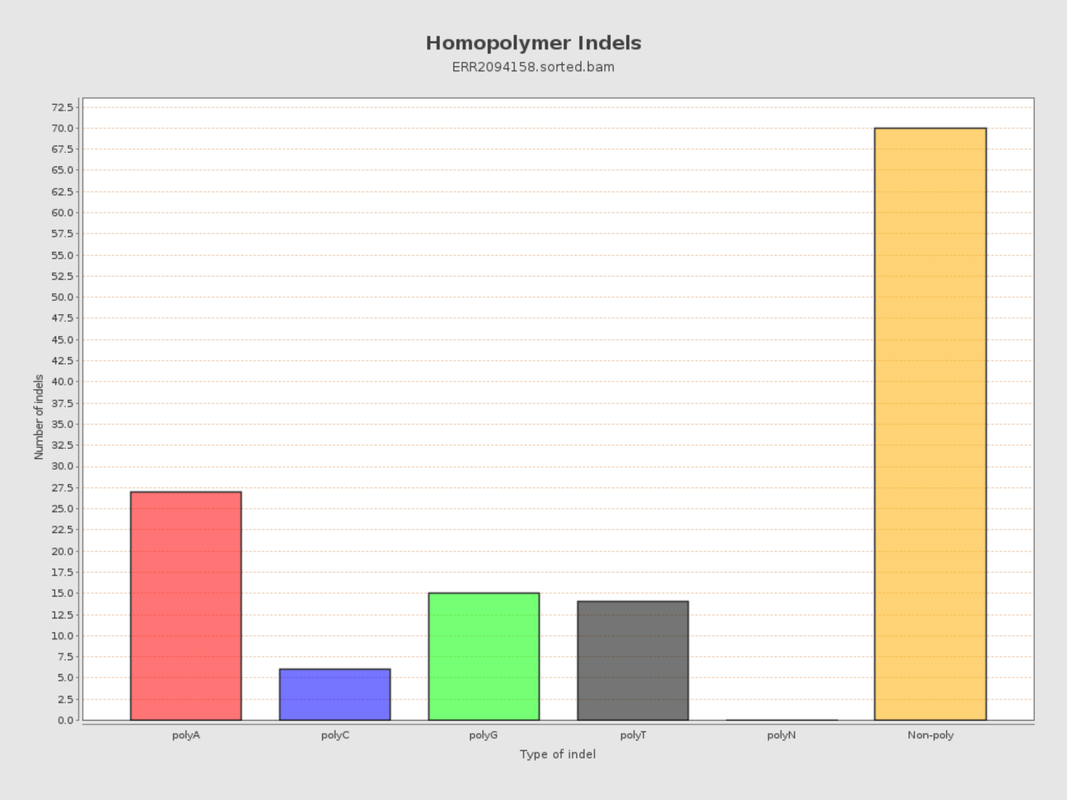
9. Results : Mapped Reads GC-content Distribution



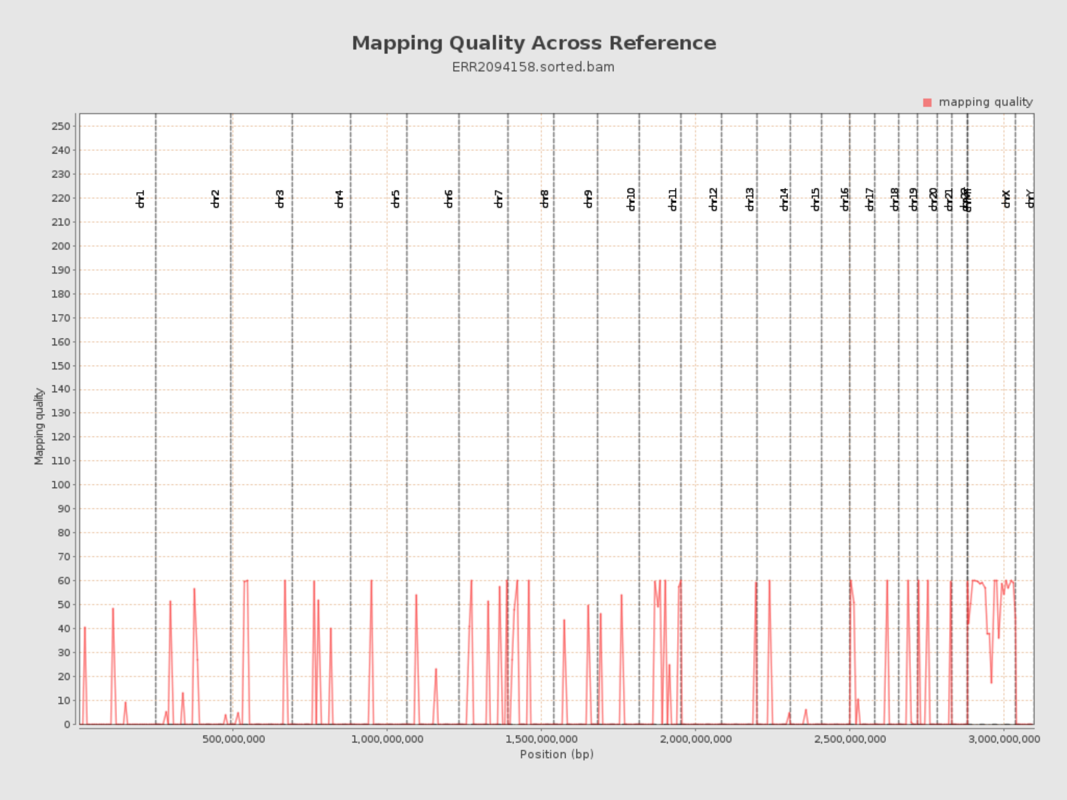
10. Results : Mapped Reads Clipping Profile



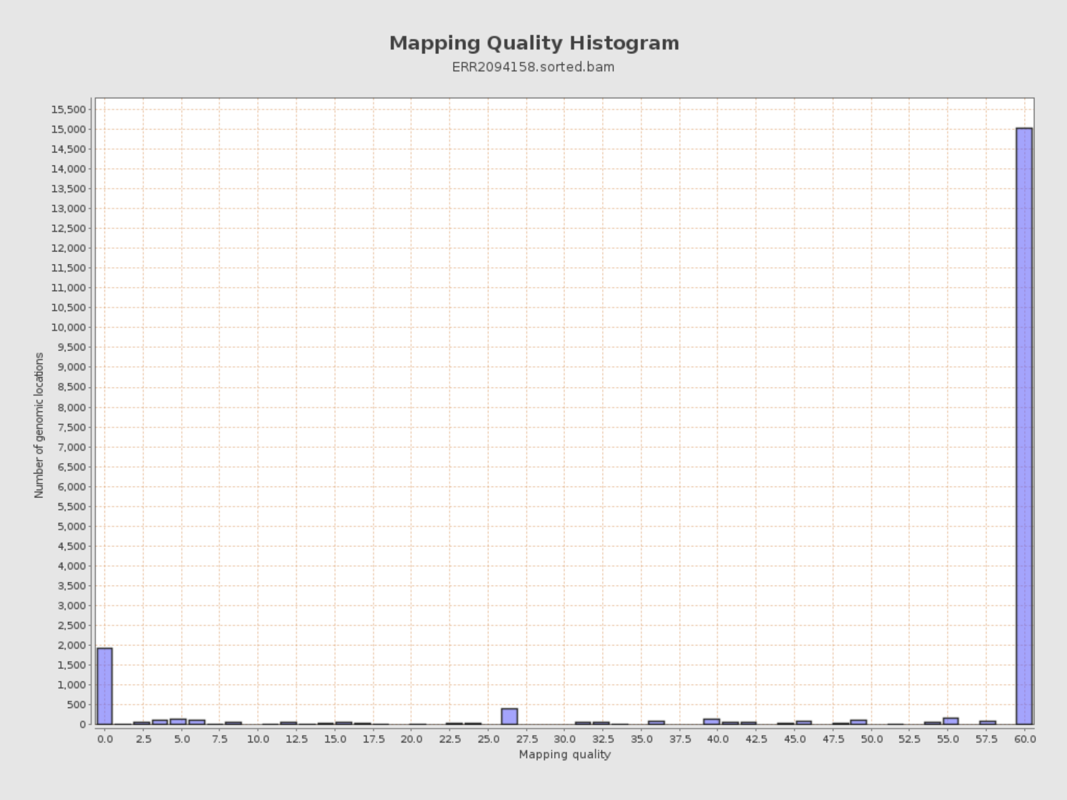
11. Results : Homopolymer Indels



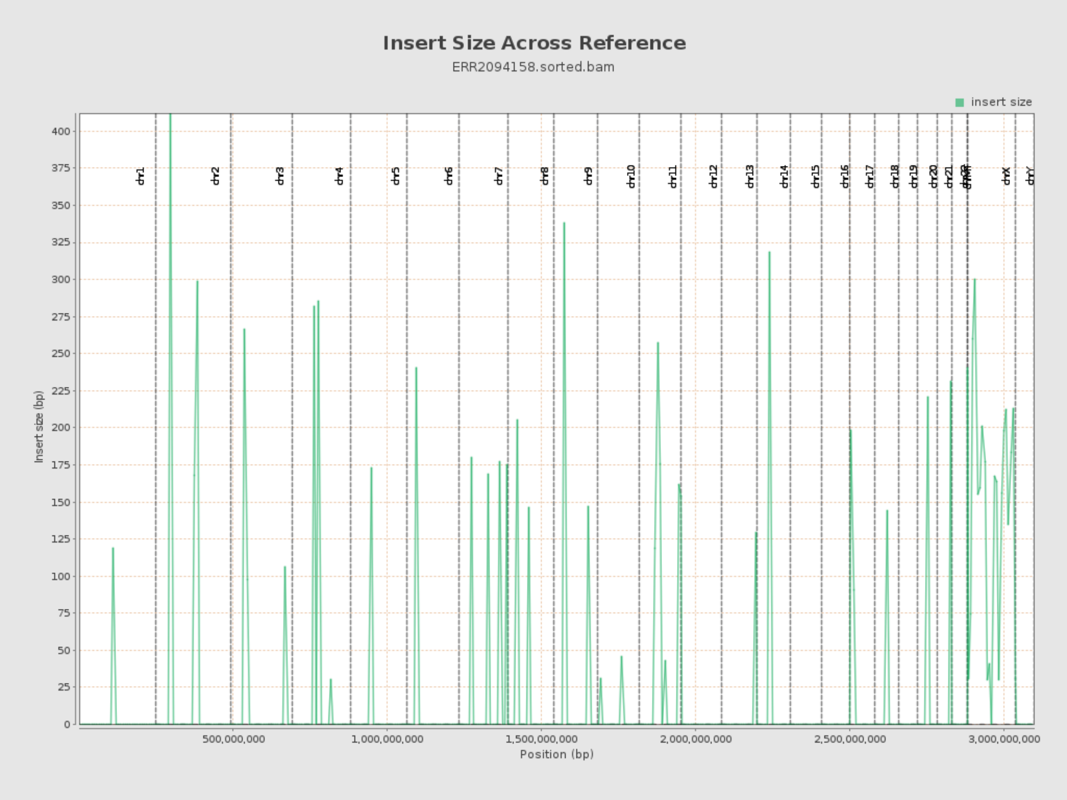
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram