Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:02:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094156.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_ERR2094156 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094156_1.fastq.gz ERR2094156_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:01:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,492
Mapped reads	931 / 3.16%
Unmapped reads	28,561 / 96.84%
Mapped paired reads	931 / 3.16%
Mapped reads, first in pair	333 / 1.13%
Mapped reads, second in pair	598 / 2.03%
Mapped reads, both in pair	538 / 1.82%
Mapped reads, singletons	393 / 1.33%
Secondary alignments	0
Supplementary alignments	26 / 0.09%
Read min/max/mean length	30 / 151 / 65.56
Duplicated reads (estimated)	657 / 2.23%
Duplication rate	26.33%
Clipped reads	740 / 2.51%

2.2. ACGT Content

Number/percentage of A's	8,580 / 13.38%
Number/percentage of C's	6,355 / 9.91%
Number/percentage of T's	7,049 / 10.99%
Number/percentage of G's	42,163 / 65.73%
Number/percentage of N's	0 / 0%

GC Percentage	75.64%

2.3. Coverage

Mean	0
Standard Deviation	0.0471

2.4. Mapping Quality

Mean Mapping Quality	5.63

2.5. Insert size

Mean	60.87
Standard Deviation	49.77
P25/Median/P75	30 / 32 / 65

2.6. Mismatches and indels

General error rate	2.89%
Mismatches	1,496
Insertions	61
Mapped reads with at least one insertion	5.05%
Deletions	56
Mapped reads with at least one deletion	5.91%
Homopolymer indels	45.3%

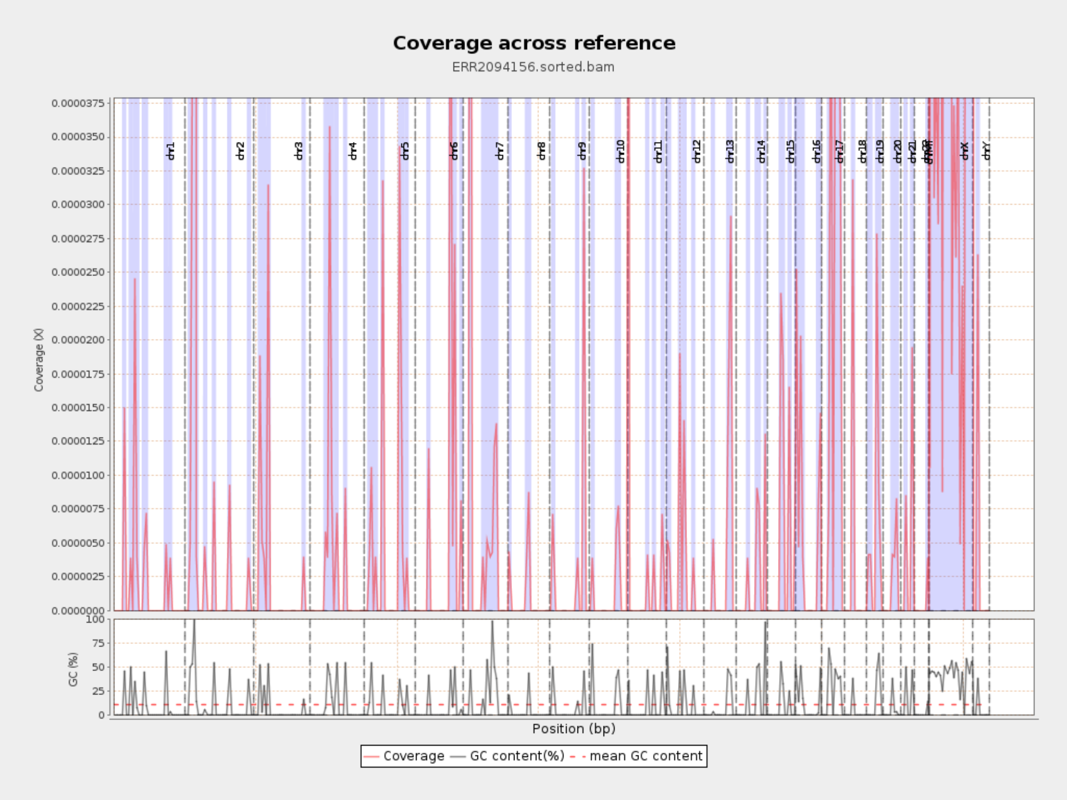
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

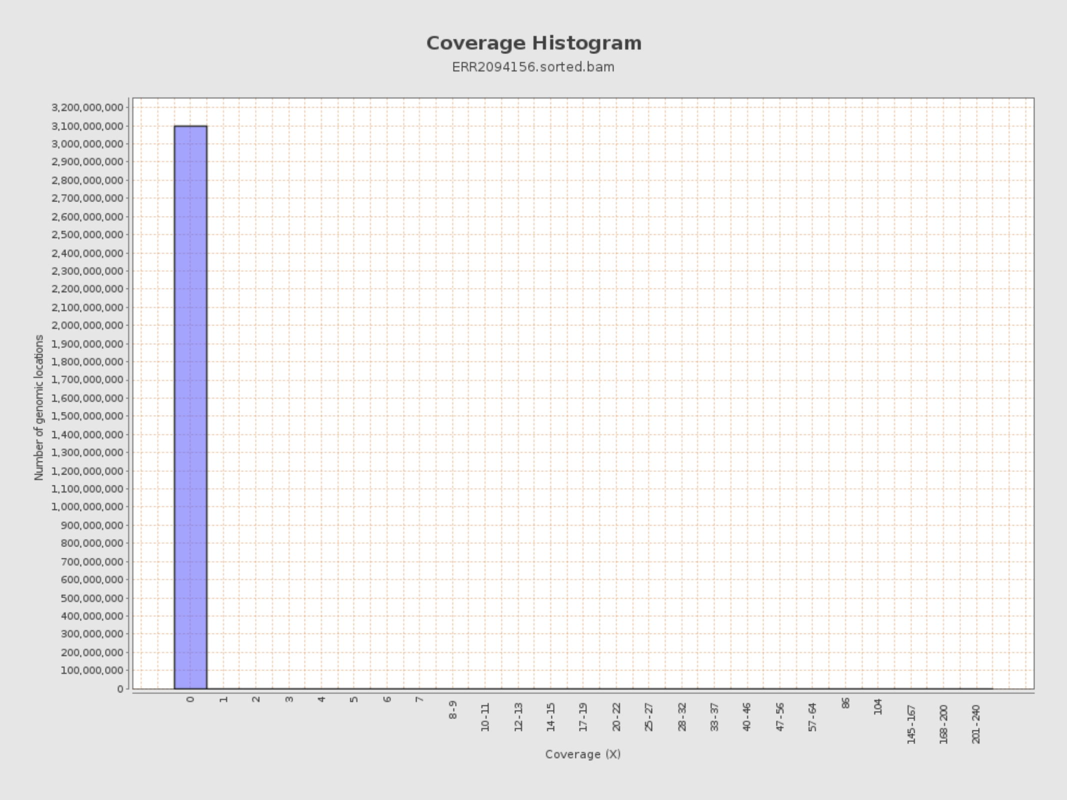
		bases	coverage	deviation
chr1	249250621	526	0	0.0018
chr2	243199373	37073	0.0002	0.1575
chr3	198022430	491	0	0.0021
chr4	191154276	544	0	0.0021
chr5	180915260	718	0	0.0027
chr6	171115067	896	0	0.0036
chr7	159138663	1084	0	0.008
chr8	146364022	133	0	0.0012
chr9	141213431	338	0	0.002
chr10	135534747	137	0	0.0012
chr11	135006516	311	0	0.0016
chr12	133851895	356	0	0.0018
chr13	115169878	361	0	0.0022
chr14	107349540	261	0	0.0023
chr15	102531392	485	0	0.003
chr16	90354753	522	0	0.0029
chr17	81195210	1484	0	0.0069
chr18	78077248	247	0	0.0025
chr19	59128983	346	0	0.0031
chr20	63025520	127	0	0.0014
chr21	48129895	217	0	0.0024
chr22	51304566	30	0	0.0008
chrMT	16571	298	0.018	0.1434
chrX	155270560	17310	0.0001	0.0725

chrY	59373566	204	0	0.0021

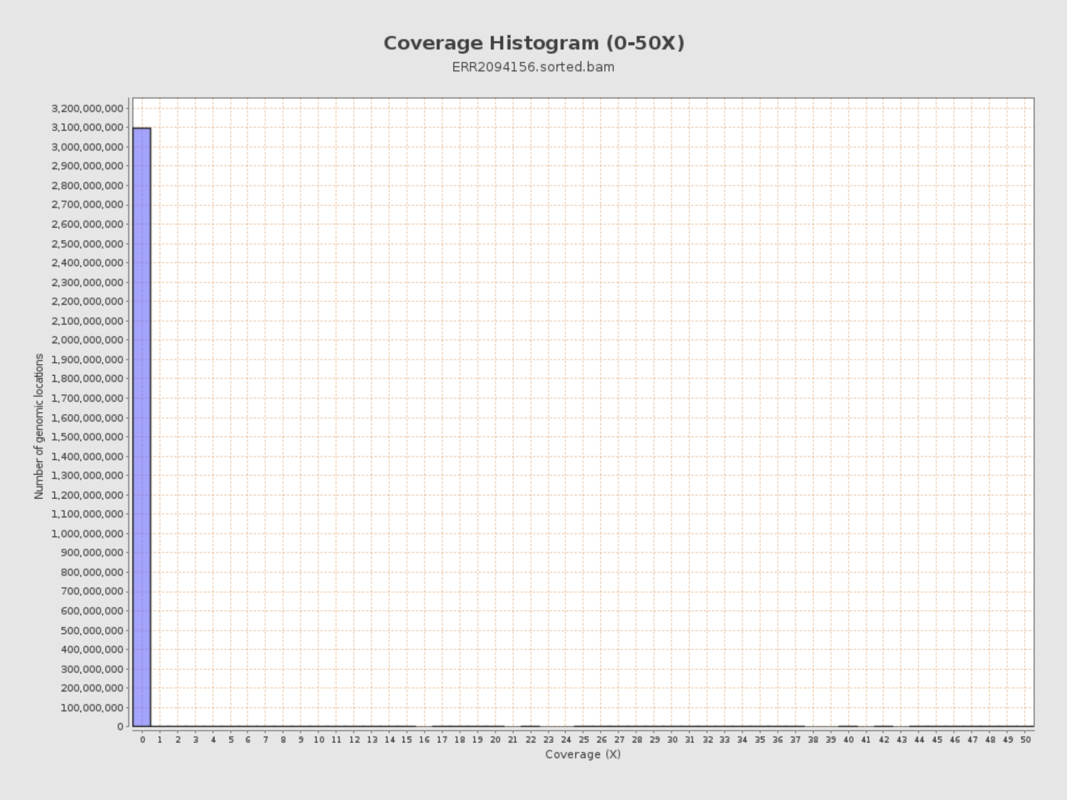
3. Results : Coverage across reference



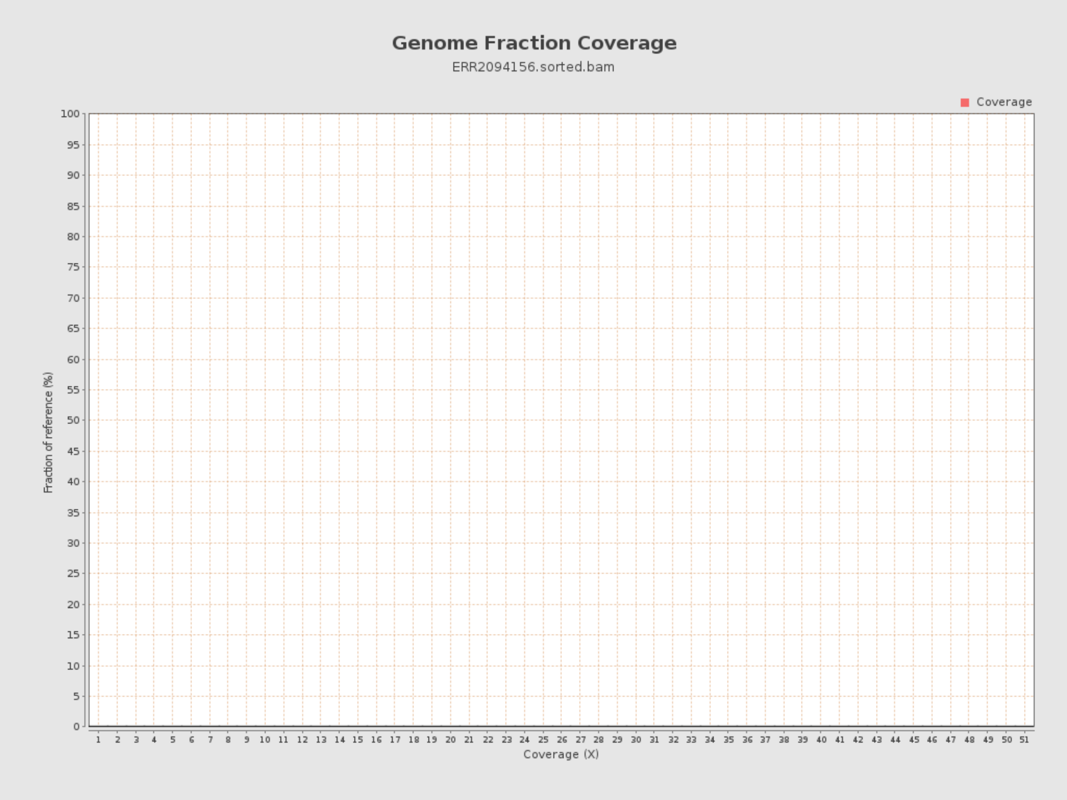
4. Results : Coverage Histogram



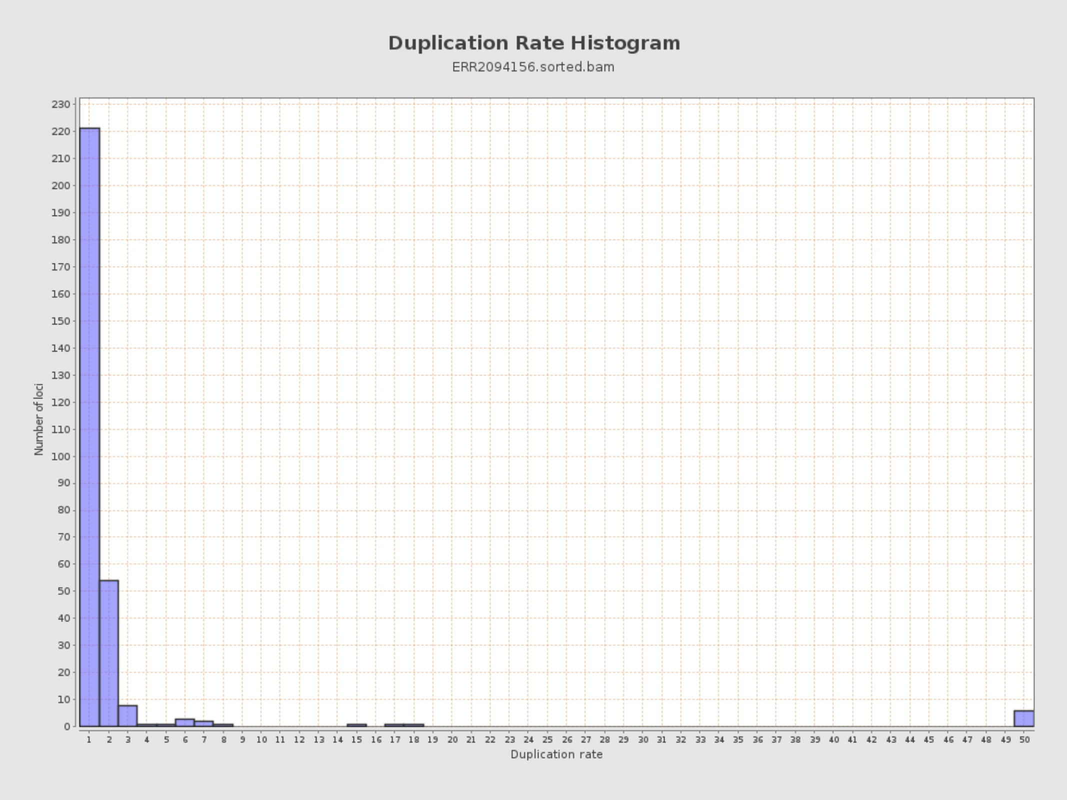
5. Results : Coverage Histogram (0-50X)



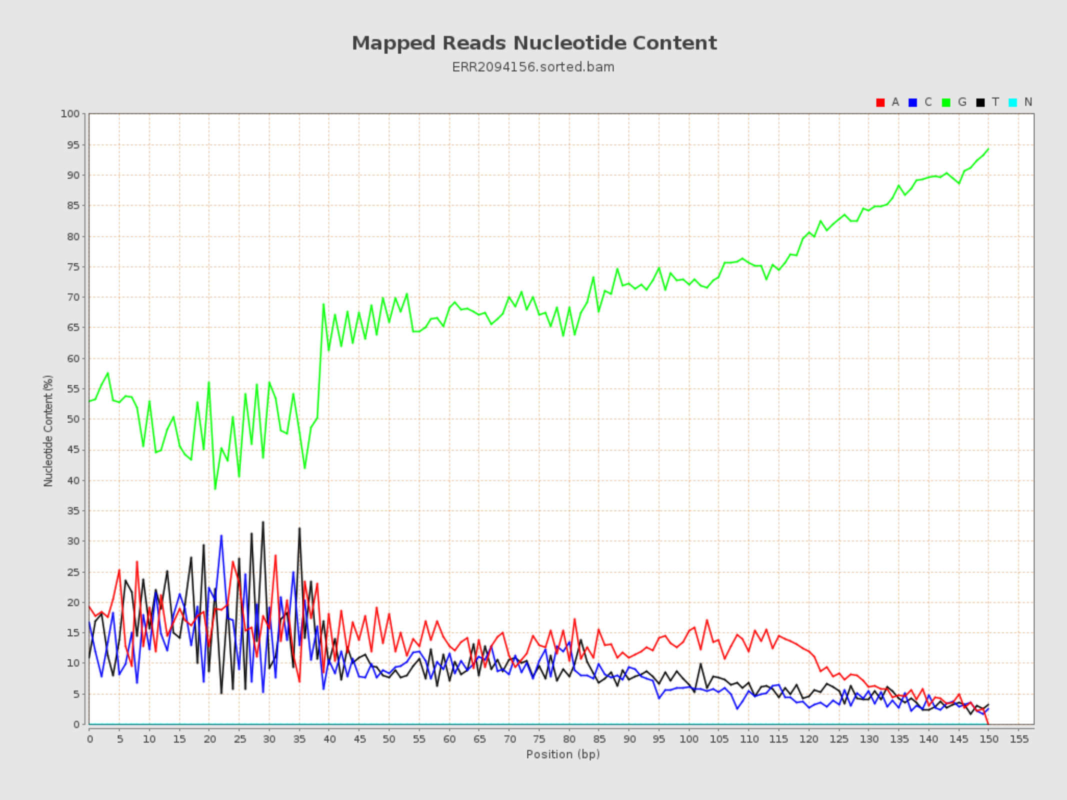
6. Results : Genome Fraction Coverage



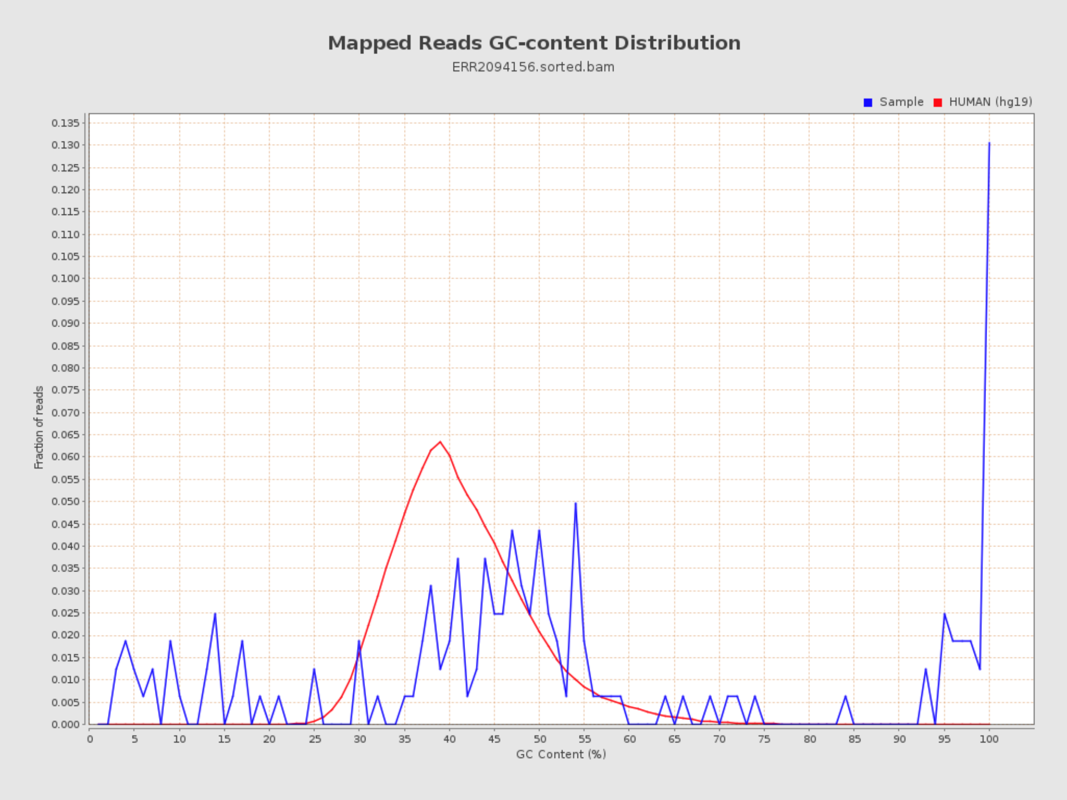
7. Results : Duplication Rate Histogram



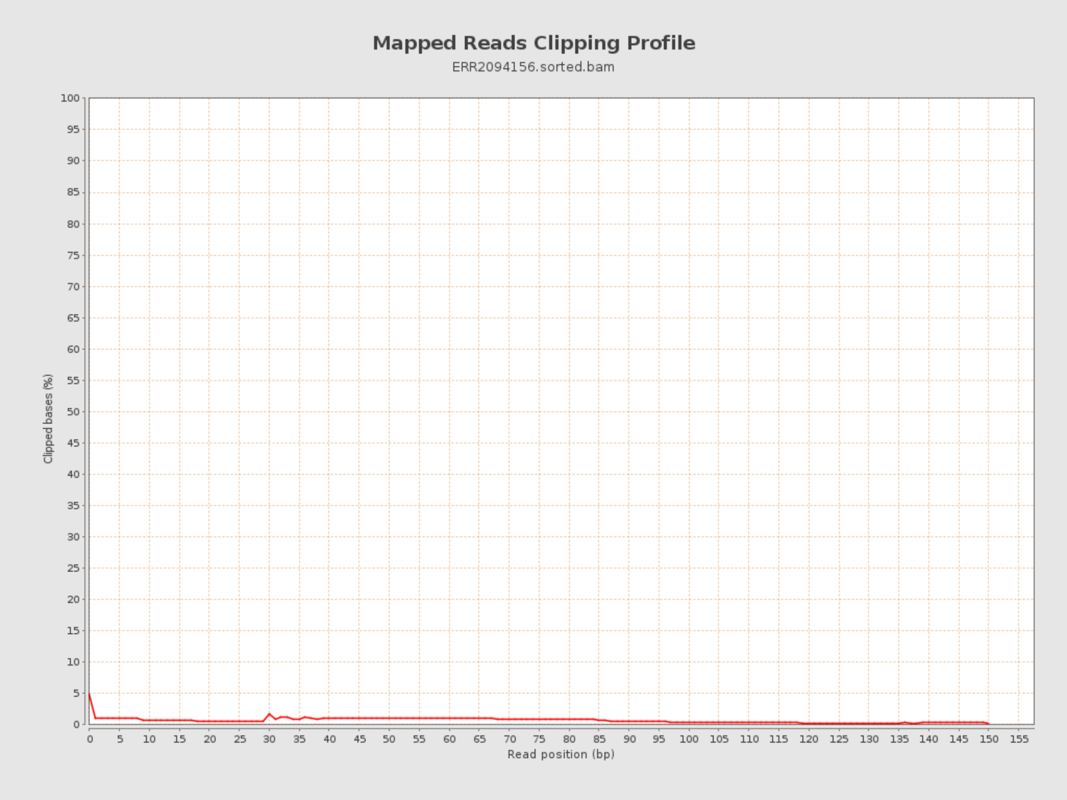
8. Results : Mapped Reads Nucleotide Content



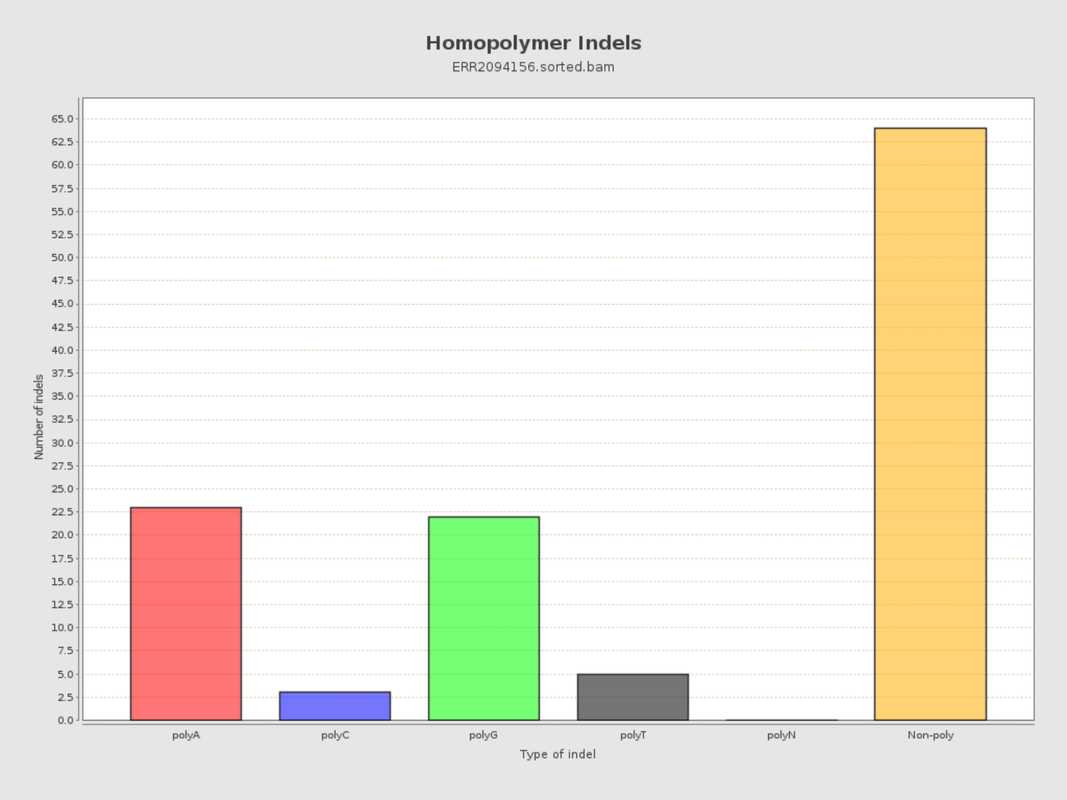
9. Results : Mapped Reads GC-content Distribution



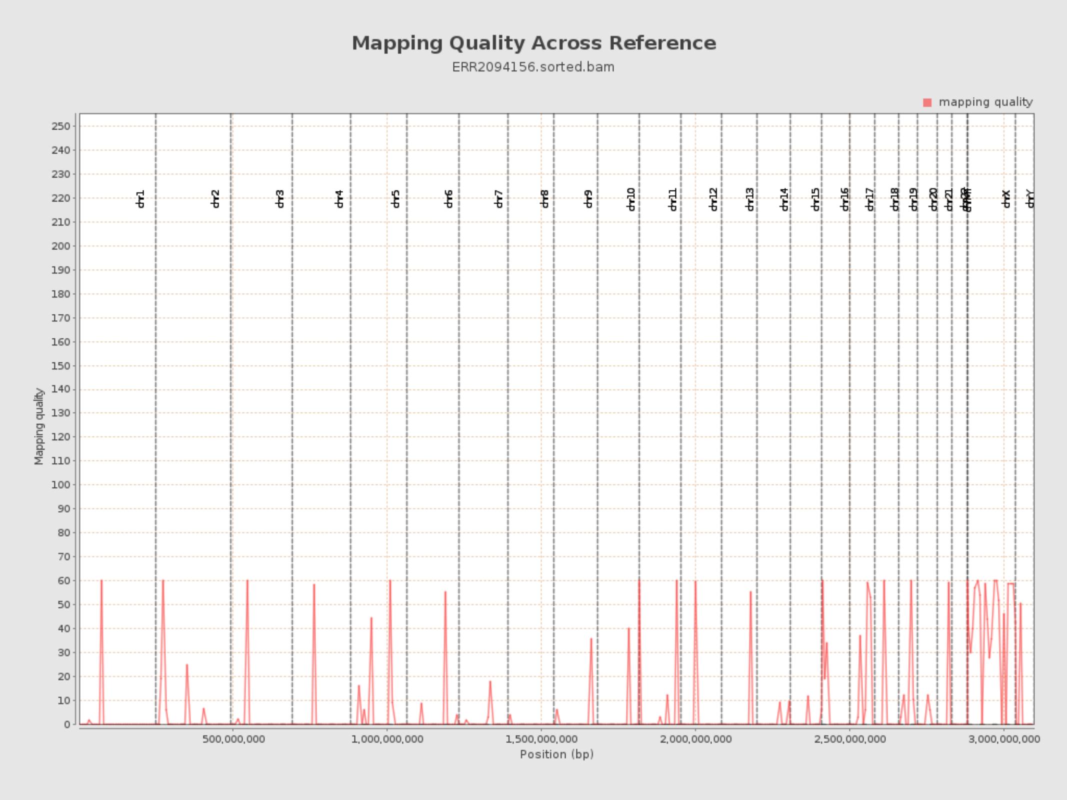
10. Results : Mapped Reads Clipping Profile



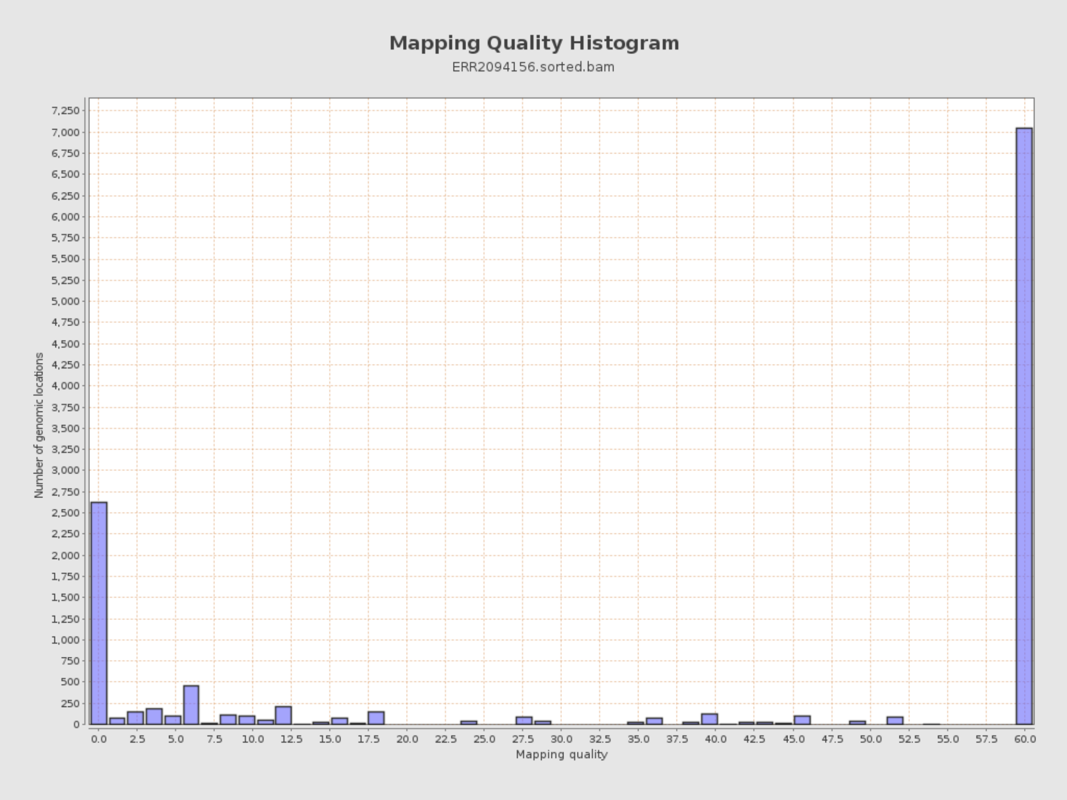
11. Results : Homopolymer Indels



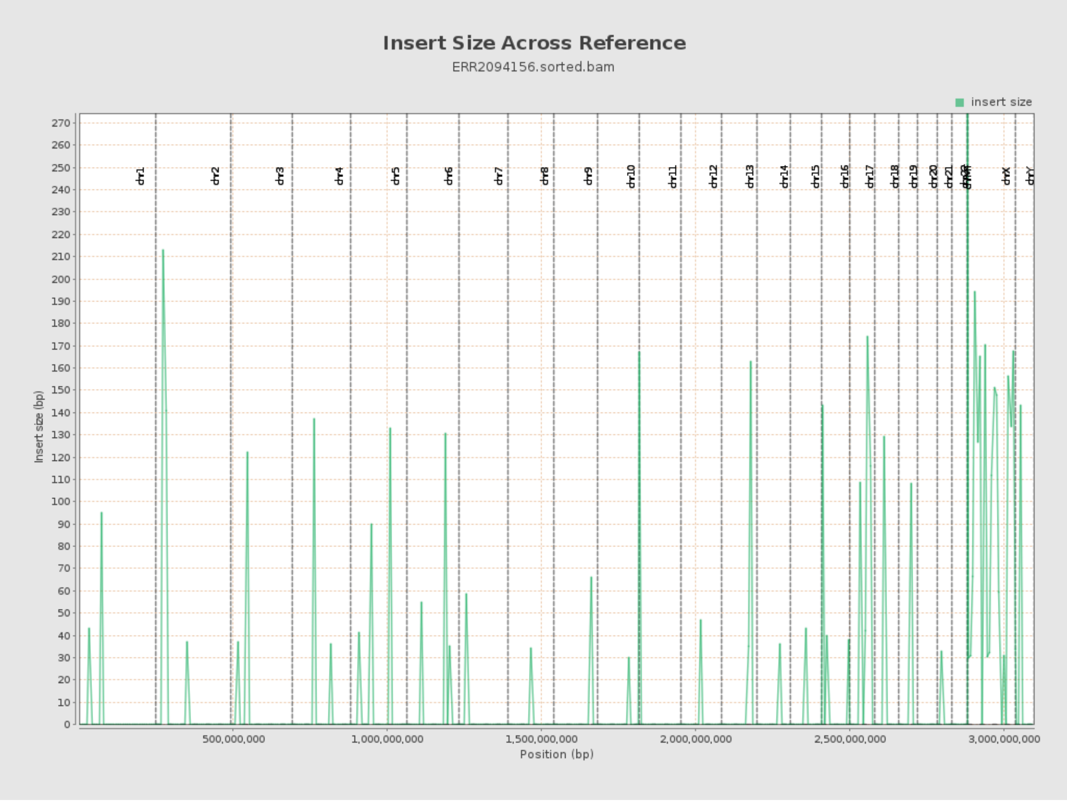
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram