Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:24:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094000.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_ERR2094000 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094000_1.fastq.gz ERR2094000_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:24:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	381,092
Mapped reads	362,395 / 95.09%
Unmapped reads	18,697 / 4.91%
Mapped paired reads	362,395 / 95.09%
Mapped reads, first in pair	182,375 / 47.86%
Mapped reads, second in pair	180,020 / 47.24%
Mapped reads, both in pair	358,768 / 94.14%
Mapped reads, singletons	3,627 / 0.95%
Secondary alignments	0
Supplementary alignments	22,250 / 5.84%
Read min/max/mean length	30 / 151 / 141.35
Duplicated reads (estimated)	344,708 / 90.45%
Duplication rate	51.37%
Clipped reads	171,215 / 44.93%

2.2. ACGT Content

Number/percentage of A's	11,768,905 / 25.6%
Number/percentage of C's	11,187,155 / 24.33%
Number/percentage of T's	11,118,075 / 24.18%
Number/percentage of G's	11,898,057 / 25.88%
Number/percentage of N's	417 / 0%

GC Percentage	50.22%

2.3. Coverage

Mean	0.0151
Standard Deviation	3.2812

2.4. Mapping Quality

Mean Mapping Quality	41.04

2.5. Insert size

Mean	1,044,940.89
Standard Deviation	9,300,268.85
P25/Median/P75	127 / 164 / 201

2.6. Mismatches and indels

General error rate	3.34%
Mismatches	1,489,029
Insertions	23,114
Mapped reads with at least one insertion	6.26%
Deletions	119,378
Mapped reads with at least one deletion	31.63%
Homopolymer indels	30.24%

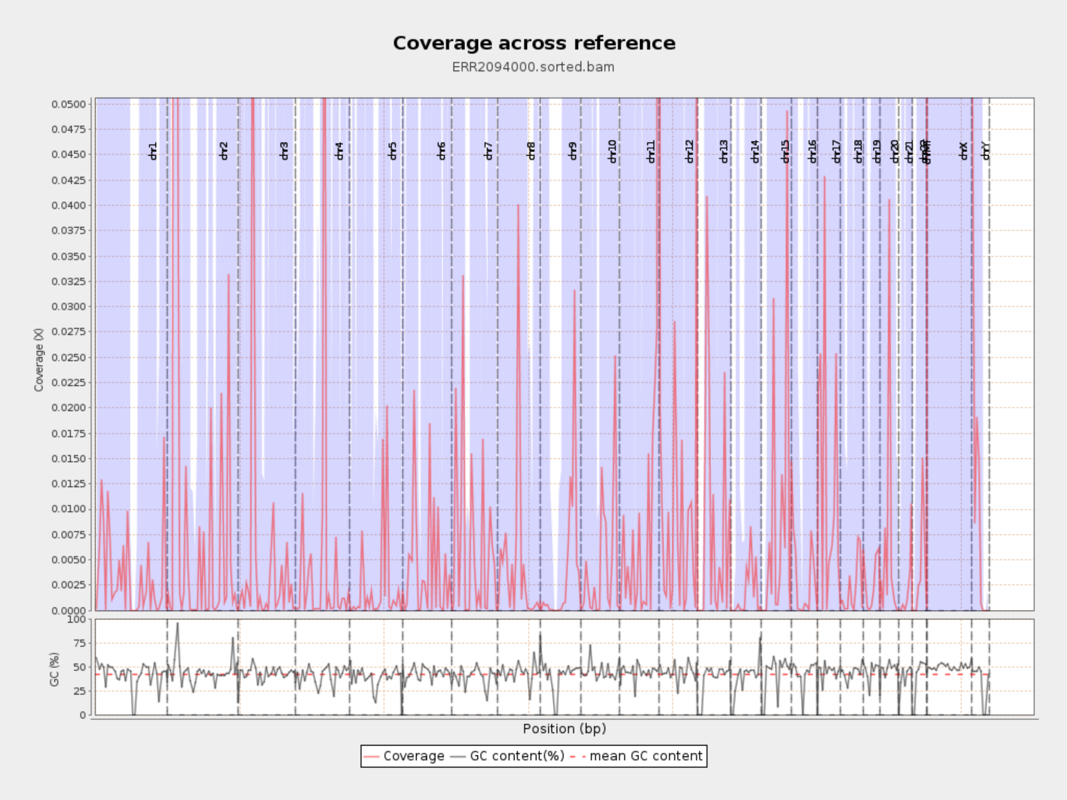
2.7. Chromosome stats

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

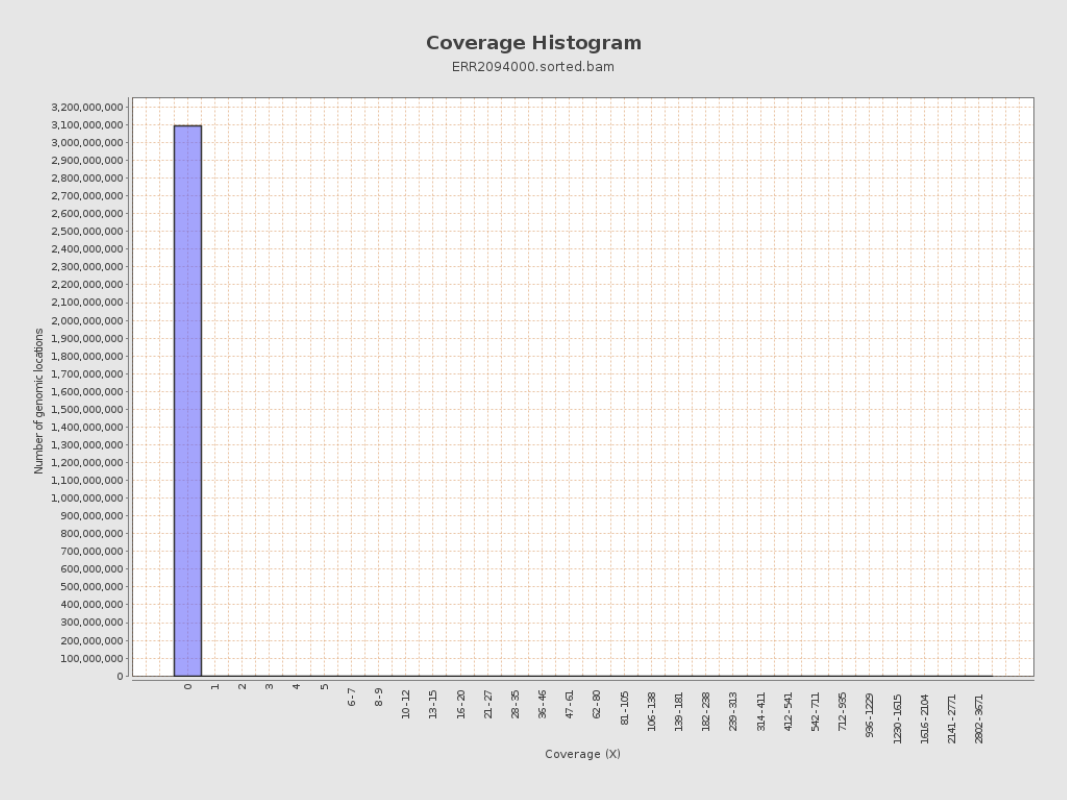
		bases	**coverage**	**deviation**
chr1	249250621	875964	0.0035	1.1115
chr2	243199373	3015615	0.0124	4.1581
chr3	198022430	925872	0.0047	1.8252
chr4	191154276	1015146	0.0053	1.7721
chr5	180915260	443399	0.0025	1.3191
chr6	171115067	771684	0.0045	1.3768
chr7	159138663	978354	0.0061	1.7062
chr8	146364022	650208	0.0044	1.6726
chr9	141213431	574267	0.0041	1.2058
chr10	135534747	590697	0.0044	1.4342
chr11	135006516	1209474	0.009	2.5734
chr12	133851895	1105202	0.0083	2.1205
chr13	115169878	921524	0.008	2.64
chr14	107349540	182709	0.0017	0.6298
chr15	102531392	891934	0.0087	2.3999
chr16	90354753	305551	0.0034	0.9767
chr17	81195210	1083120	0.0133	3.2872
chr18	78077248	176618	0.0023	0.6173
chr19	59128983	152294	0.0026	0.6556
chr20	63025520	440894	0.007	2.6234
chr21	48129895	96481	0.002	0.4084
chr22	51304566	180895	0.0035	1.1286
chrMT	16571	1333373	80.4642	377.3602
chrX	155270560	28247245	0.1819	10.9037

chrY	59373566	590892	0.01	1.6933

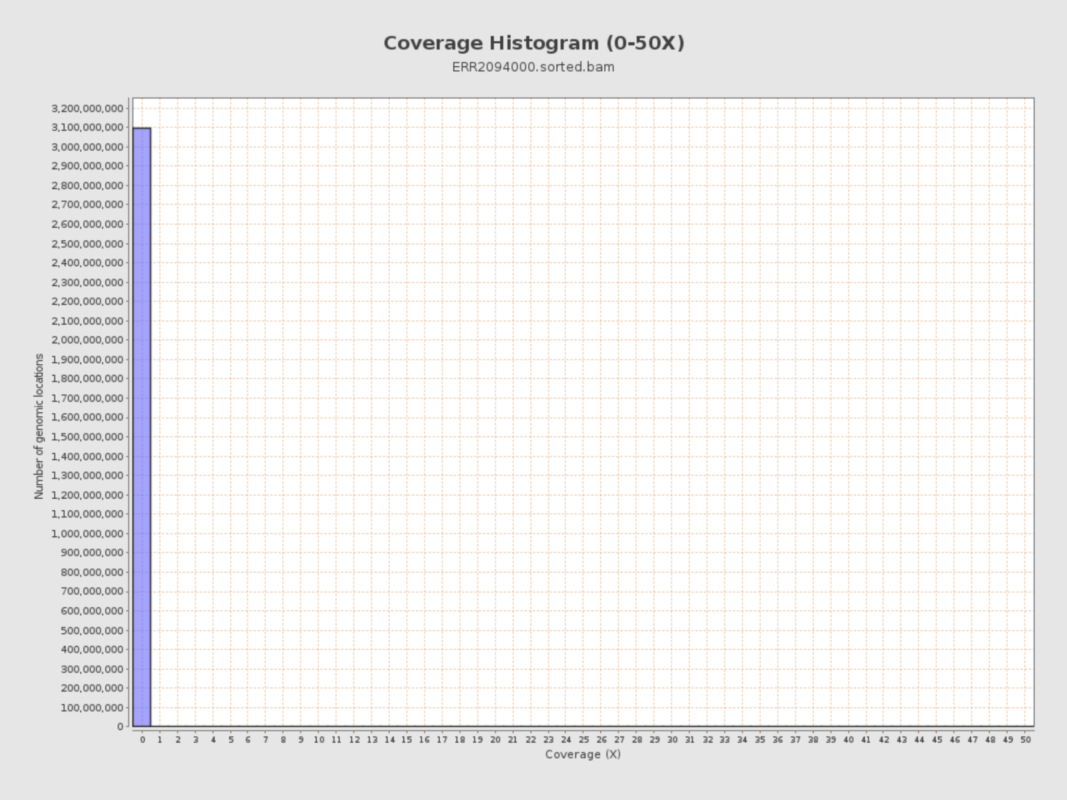
3. Results : Coverage across reference



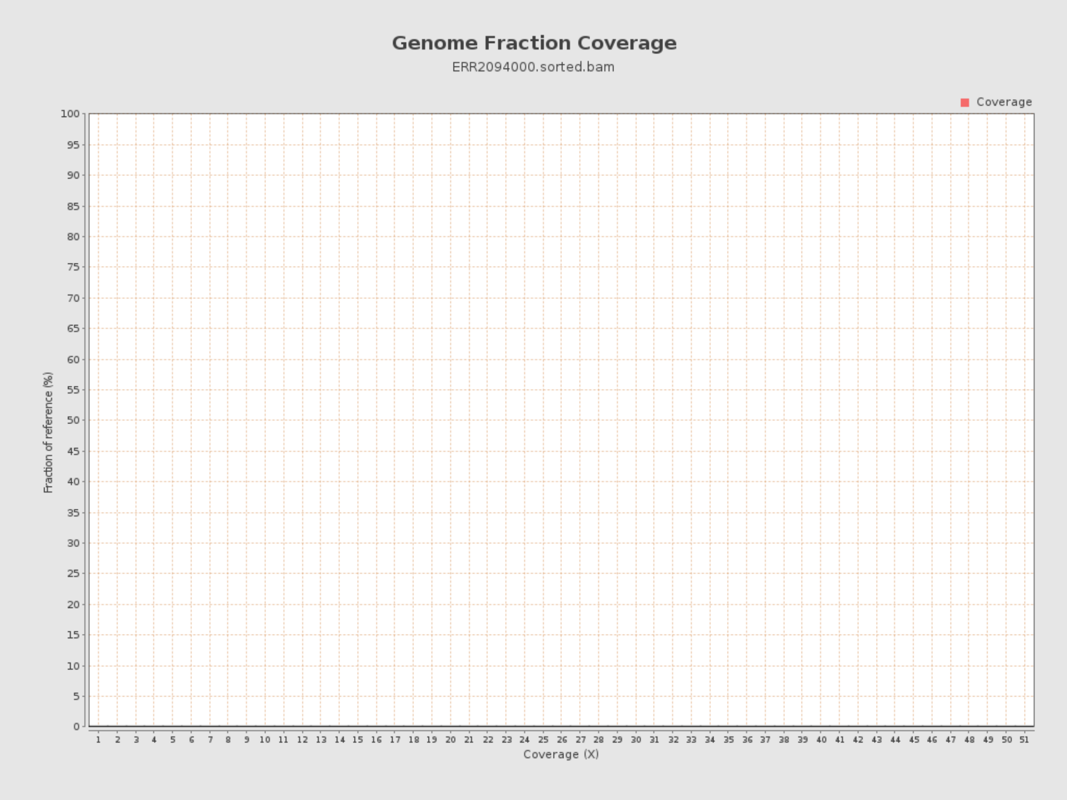
4. Results : Coverage Histogram



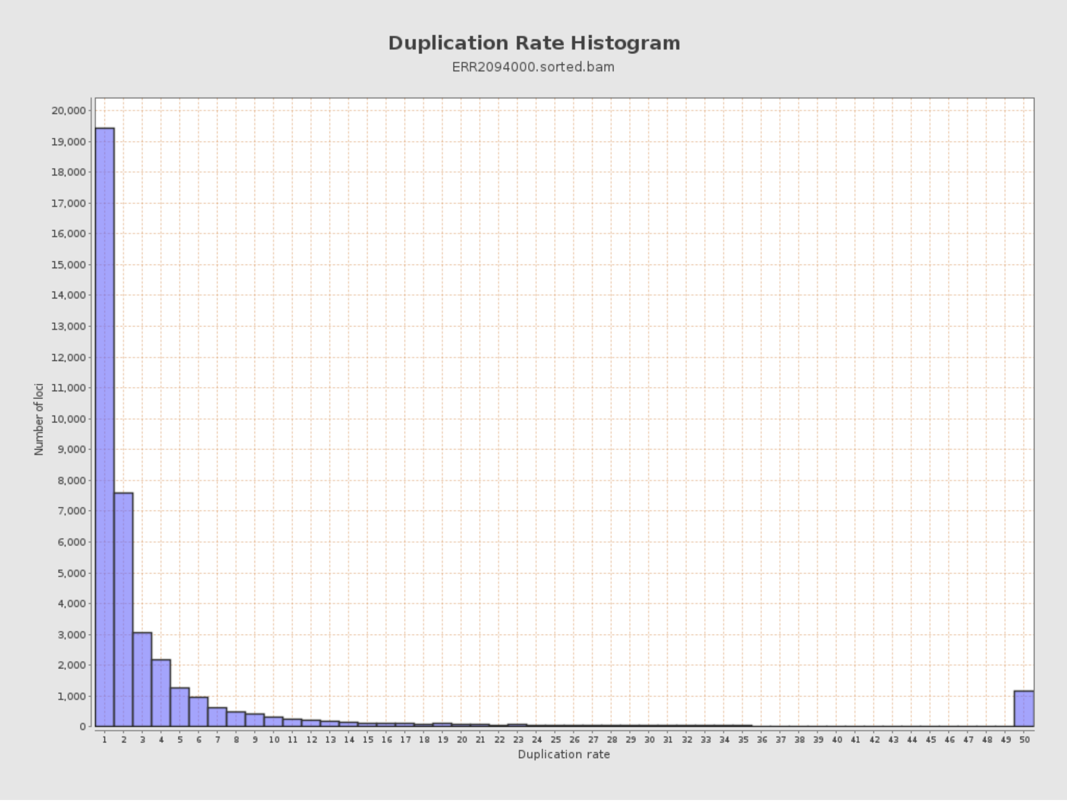
5. Results : Coverage Histogram (0-50X)



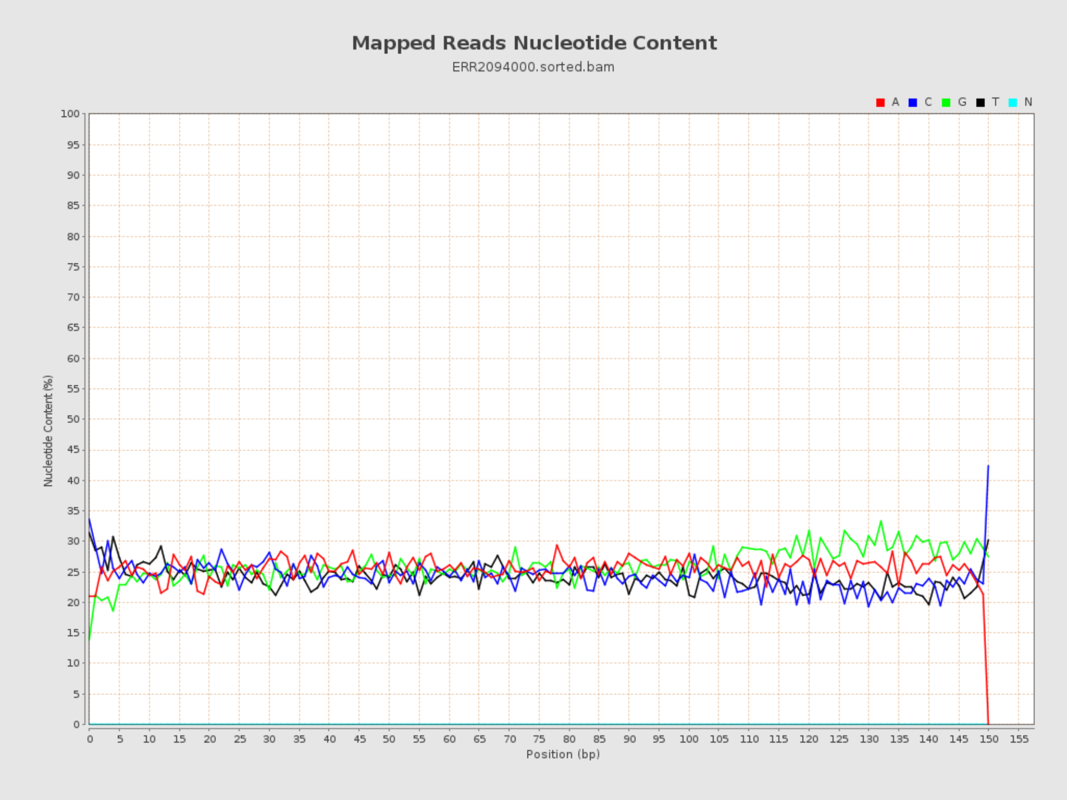
6. Results : Genome Fraction Coverage



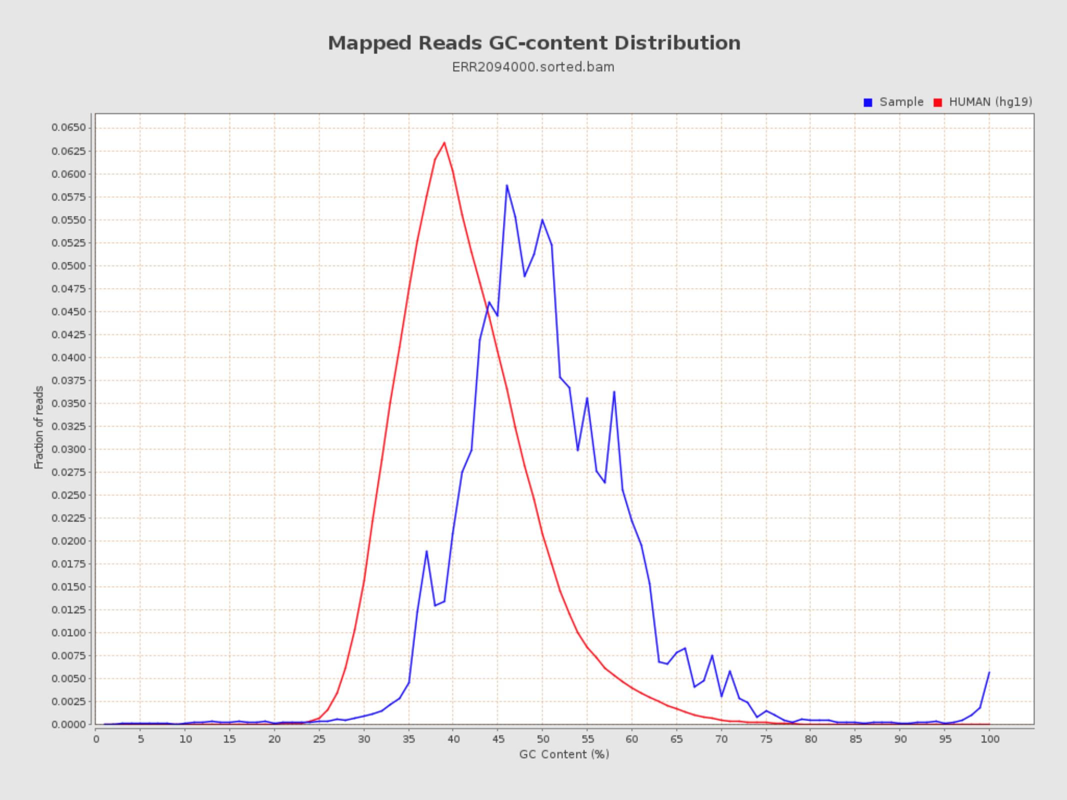
7. Results : Duplication Rate Histogram



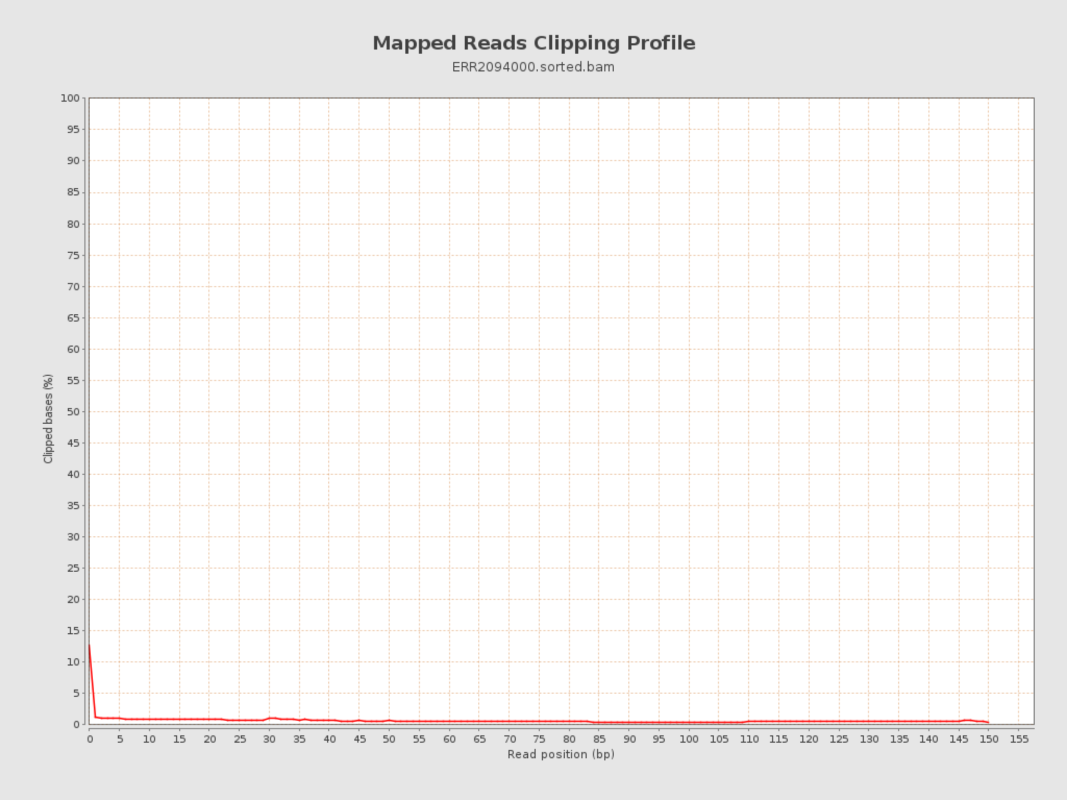
8. Results : Mapped Reads Nucleotide Content



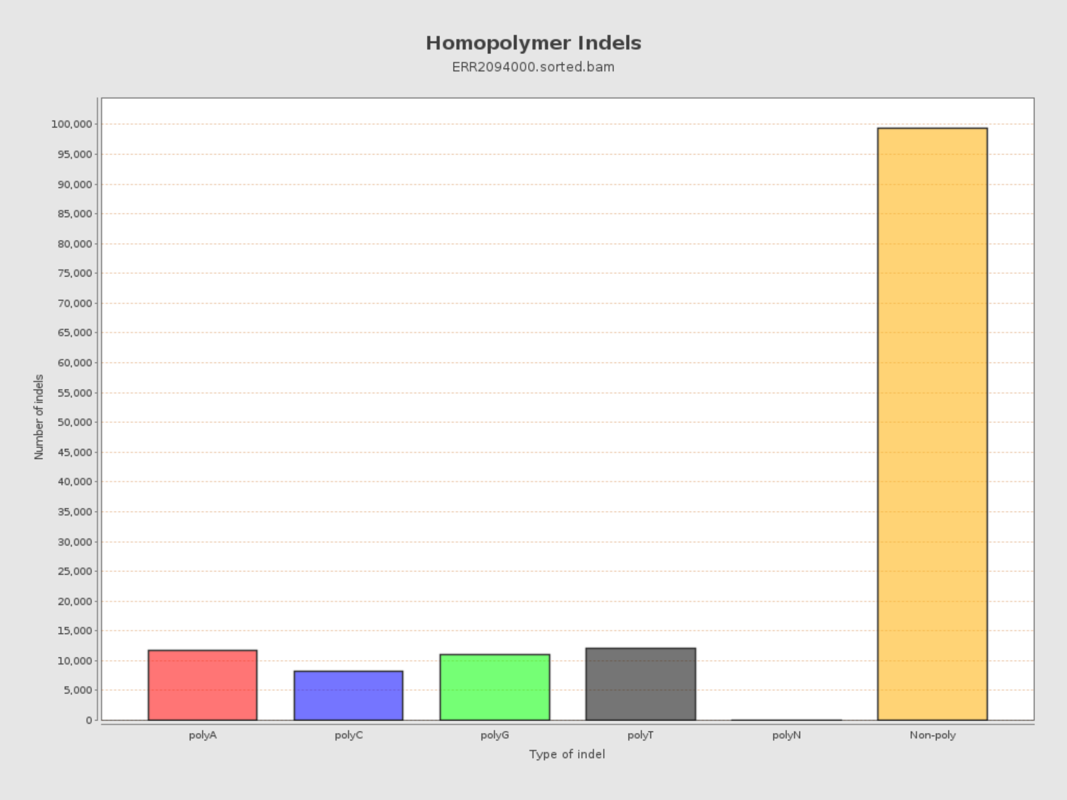
9. Results : Mapped Reads GC-content Distribution



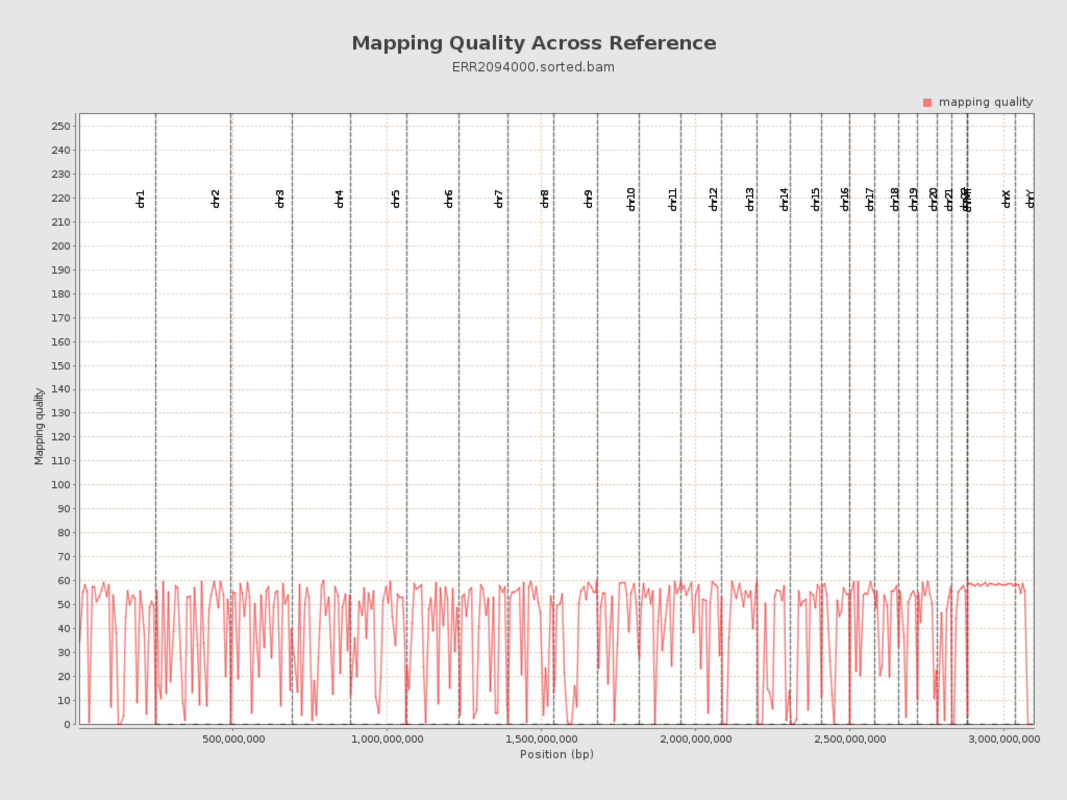
10. Results : Mapped Reads Clipping Profile



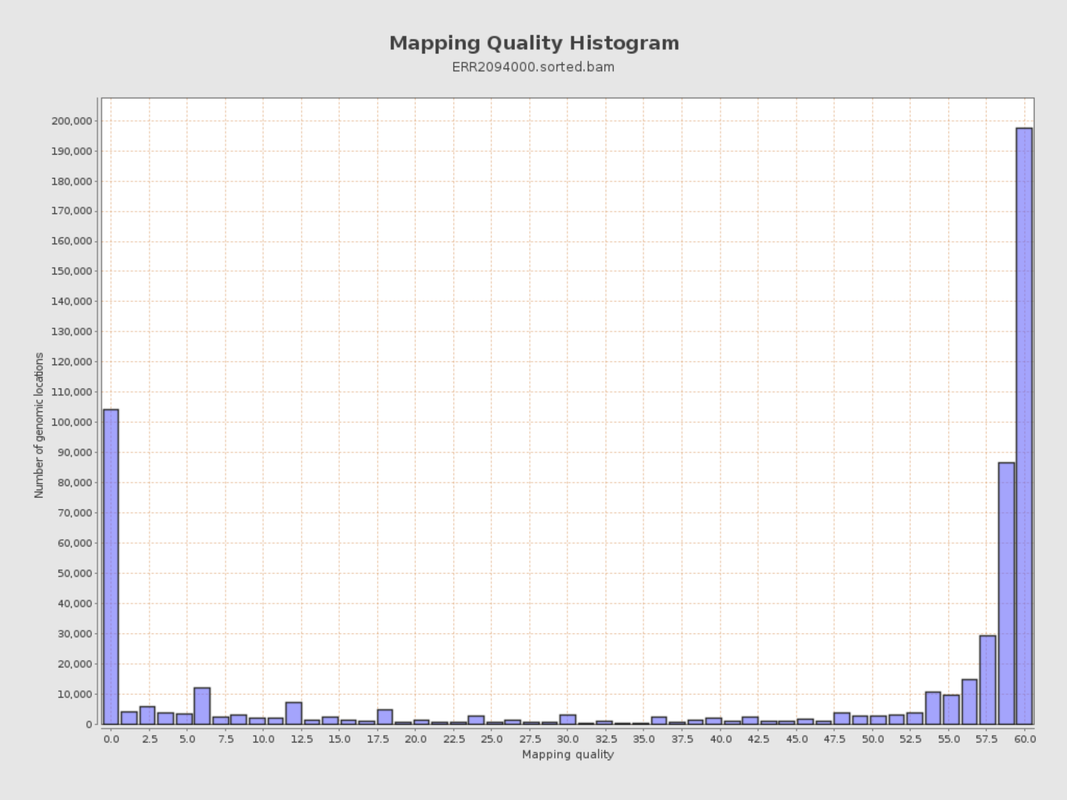
11. Results : Homopolymer Indels



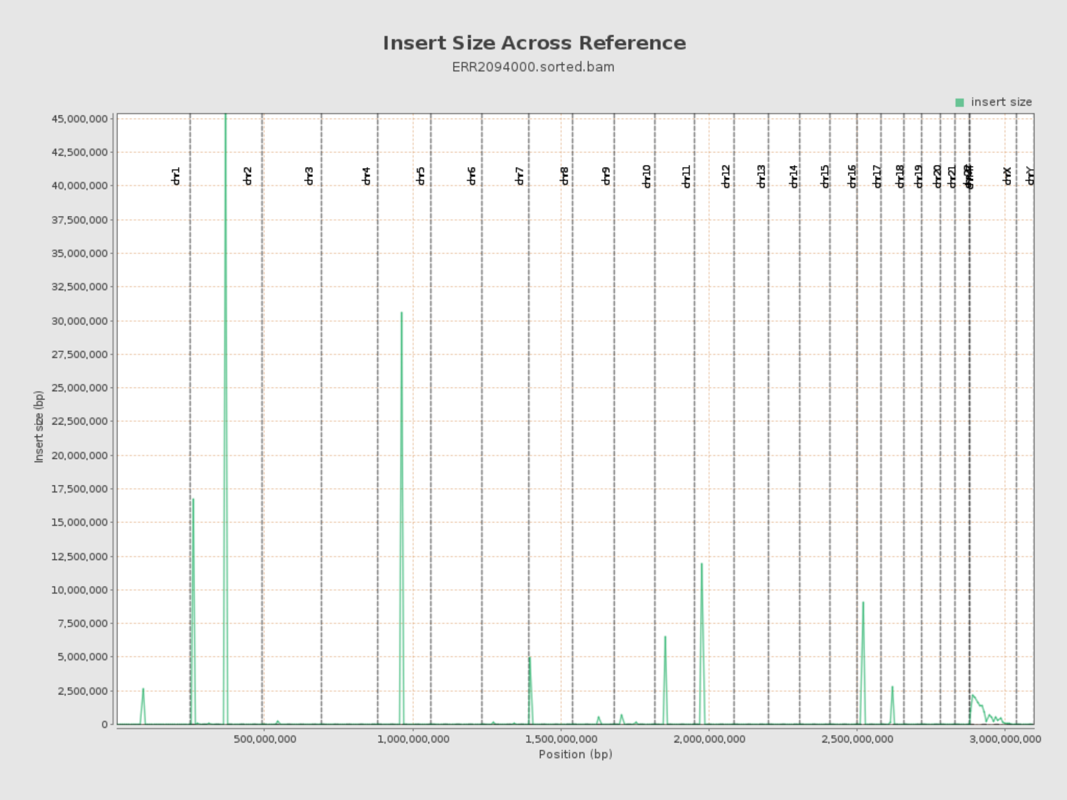
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram