Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:30:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094110.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_ERR2094110 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094110_1.fastq.gz ERR2094110_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:30:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	407,496
Mapped reads	390,342 / 95.79%
Unmapped reads	17,154 / 4.21%
Mapped paired reads	390,342 / 95.79%
Mapped reads, first in pair	196,154 / 48.14%
Mapped reads, second in pair	194,188 / 47.65%
Mapped reads, both in pair	387,314 / 95.05%
Mapped reads, singletons	3,028 / 0.74%
Secondary alignments	0
Supplementary alignments	31,874 / 7.82%
Read min/max/mean length	30 / 151 / 140.61
Duplicated reads (estimated)	378,003 / 92.76%
Duplication rate	52.81%
Clipped reads	217,051 / 53.26%

2.2. ACGT Content

Number/percentage of A's	13,935,673 / 29.07%
Number/percentage of C's	10,237,019 / 21.35%
Number/percentage of T's	12,950,637 / 27.01%
Number/percentage of G's	10,818,160 / 22.57%
Number/percentage of N's	693 / 0%

GC Percentage	43.92%

2.3. Coverage

Mean	0.0158
Standard Deviation	3.3458

2.4. Mapping Quality

Mean Mapping Quality	40.42

2.5. Insert size

Mean	1,840,455.48
Standard Deviation	11,841,008.45
P25/Median/P75	116 / 149 / 176

2.6. Mismatches and indels

General error rate	3.49%
Mismatches	1,602,207
Insertions	32,073
Mapped reads with at least one insertion	8.09%
Deletions	124,465
Mapped reads with at least one deletion	31.02%
Homopolymer indels	29.21%

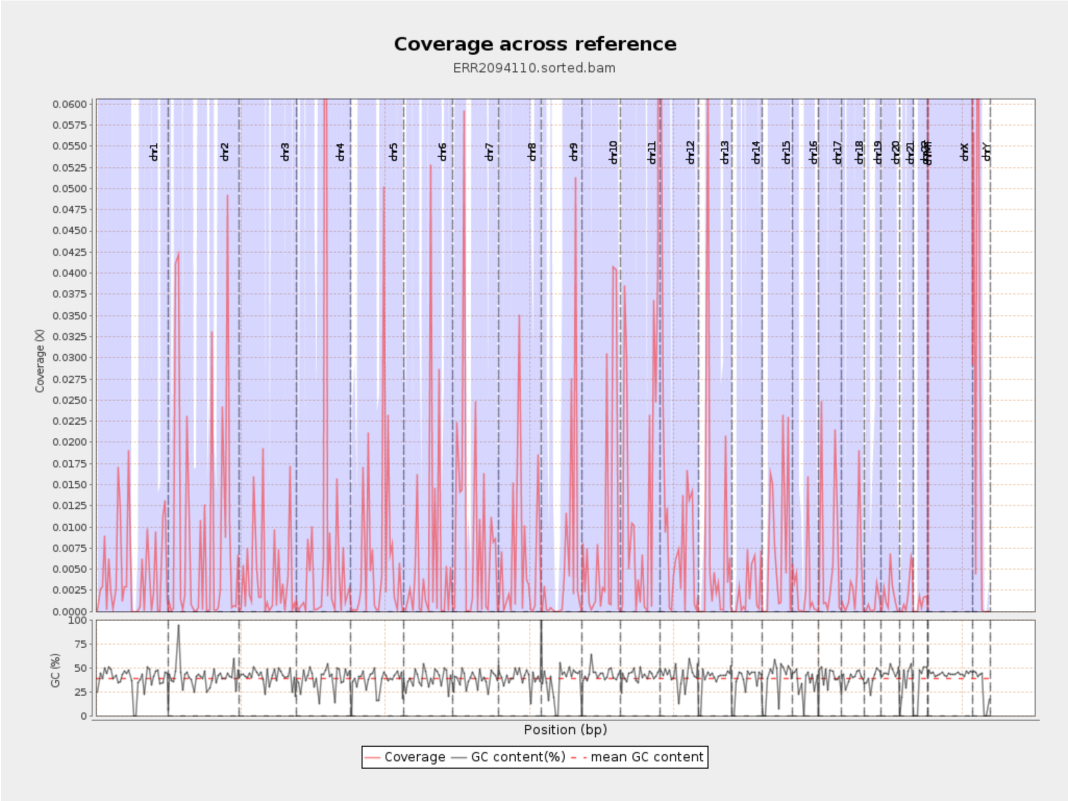
2.7. Chromosome stats

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

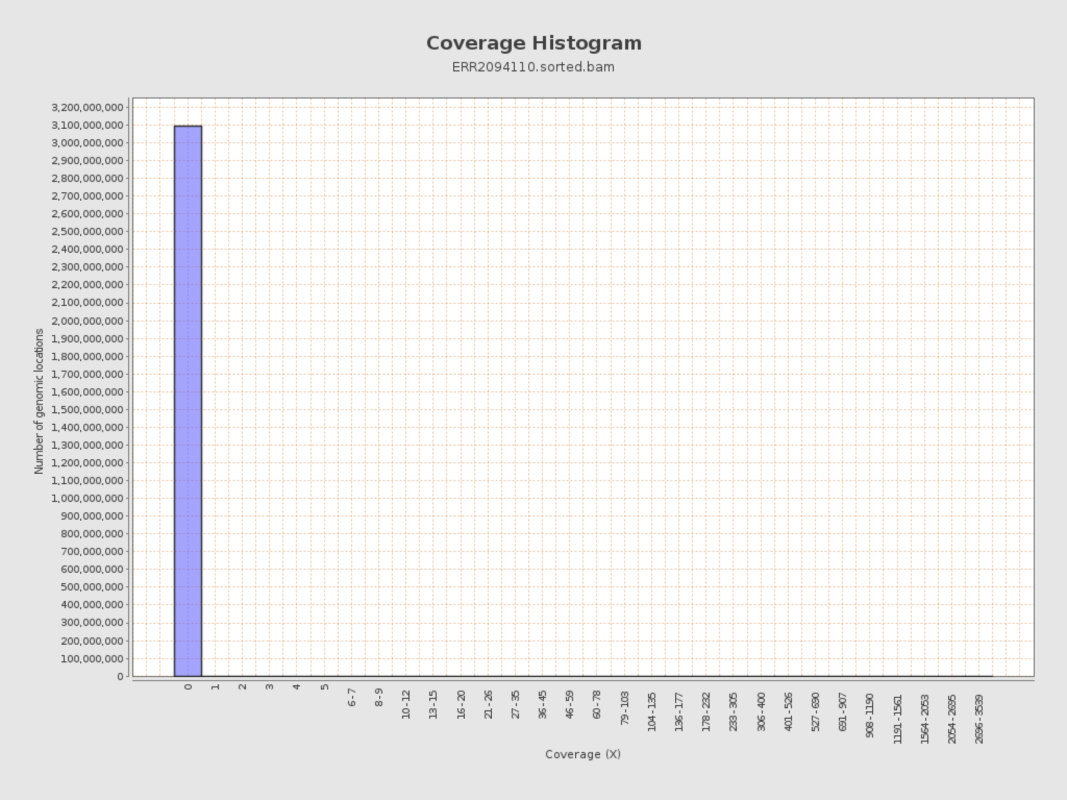
		bases	coverage	deviation
chr1	249250621	1093795	0.0044	1.5097
chr2	243199373	2199131	0.009	2.7276
chr3	198022430	832531	0.0042	1.2698
chr4	191154276	1631096	0.0085	2.5161
chr5	180915260	1228692	0.0068	2.9503
chr6	171115067	1081484	0.0063	2.137
chr7	159138663	1498311	0.0094	2.5329
chr8	146364022	952238	0.0065	1.6691
chr9	141213431	839249	0.0059	2.206
chr10	135534747	1140537	0.0084	2.8206
chr11	135006516	2018197	0.0149	3.738
chr12	133851895	1445699	0.0108	3.0387
chr13	115169878	863660	0.0075	2.0328
chr14	107349540	255761	0.0024	0.8031
chr15	102531392	748481	0.0073	1.9345
chr16	90354753	249535	0.0028	1.0375
chr17	81195210	557873	0.0069	1.9236
chr18	78077248	305688	0.0039	1.3751
chr19	59128983	48412	0.0008	0.2028
chr20	63025520	121352	0.0019	0.5504
chr21	48129895	102226	0.0021	0.4863
chr22	51304566	44254	0.0009	0.2279
chrMT	16571	172246	10.3944	61.3243
chrX	155270560	28151904	0.1813	11.2042

chrY	59373566	1249968	0.0211	4.115

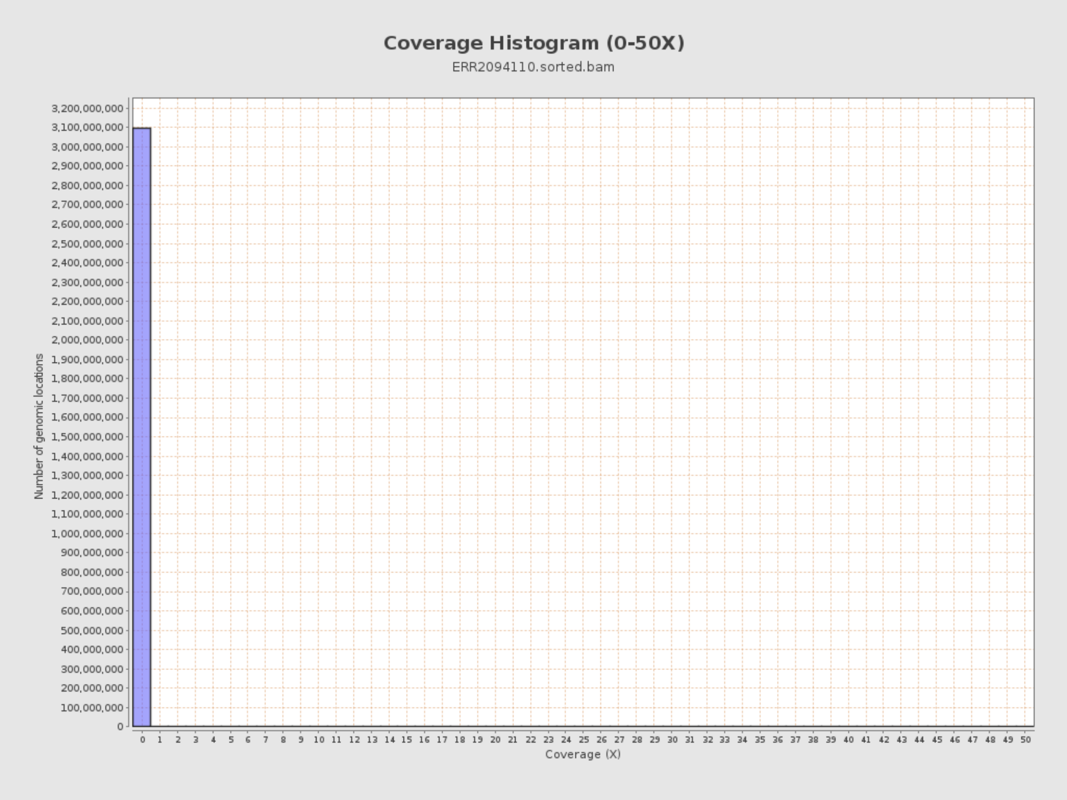
3. Results : Coverage across reference



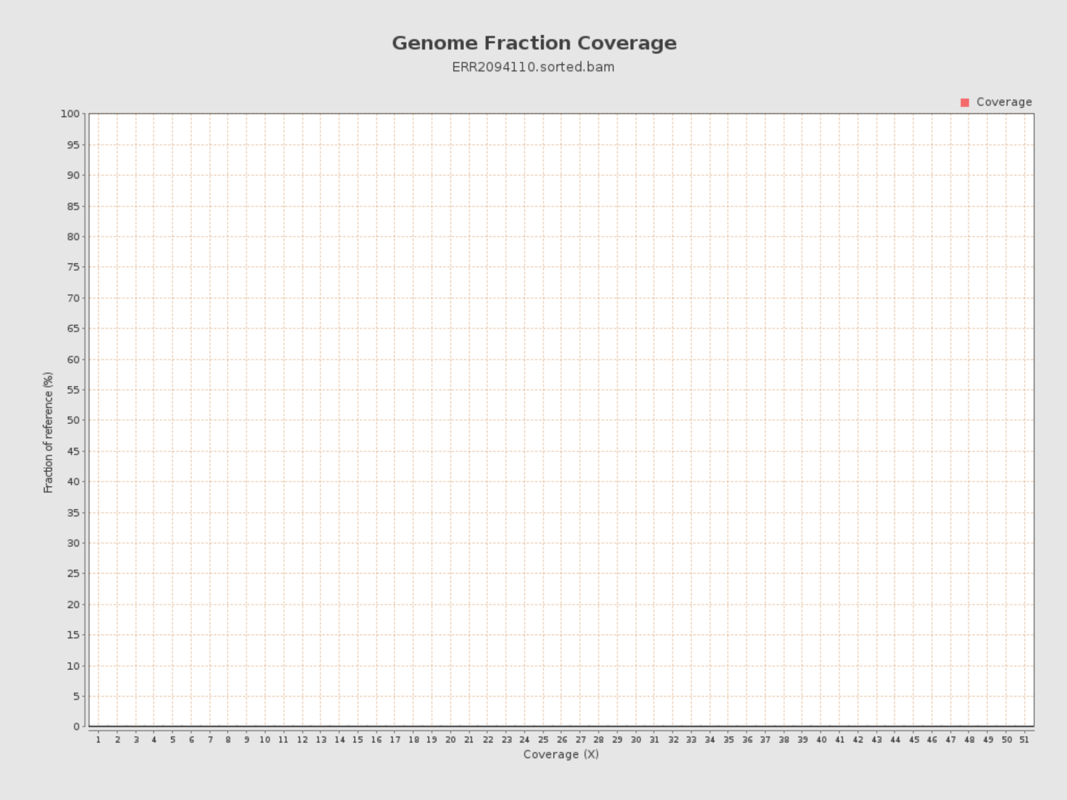
4. Results : Coverage Histogram



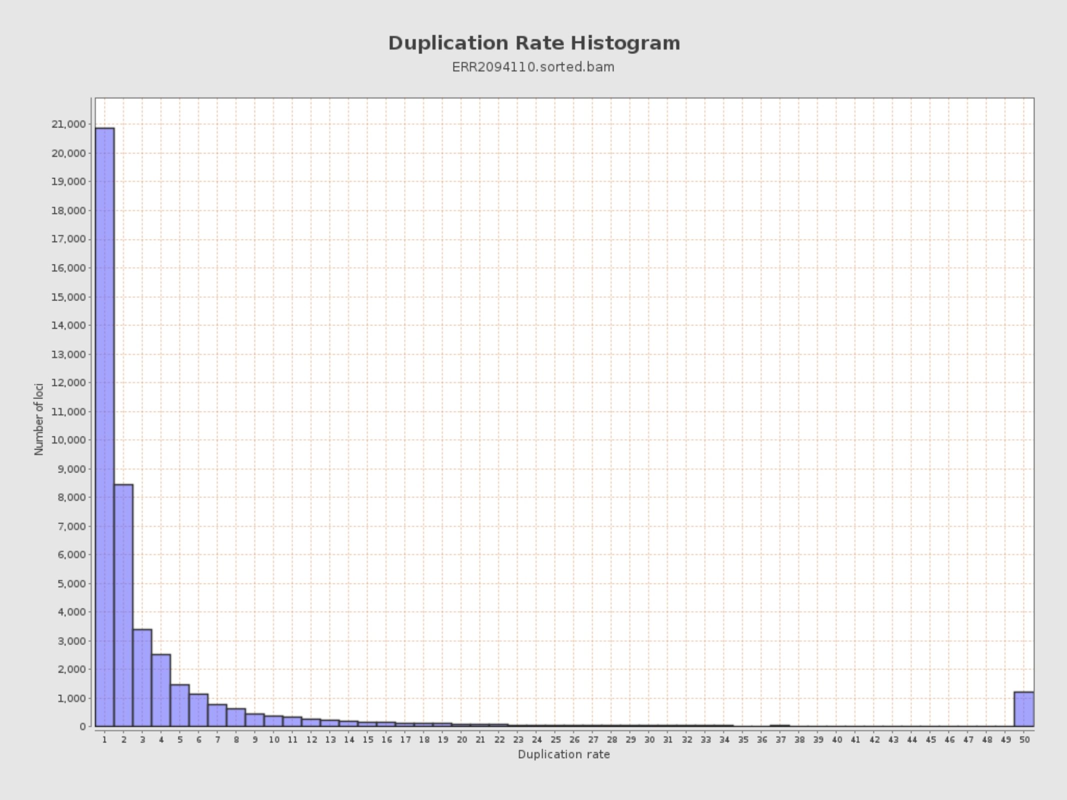
5. Results : Coverage Histogram (0-50X)



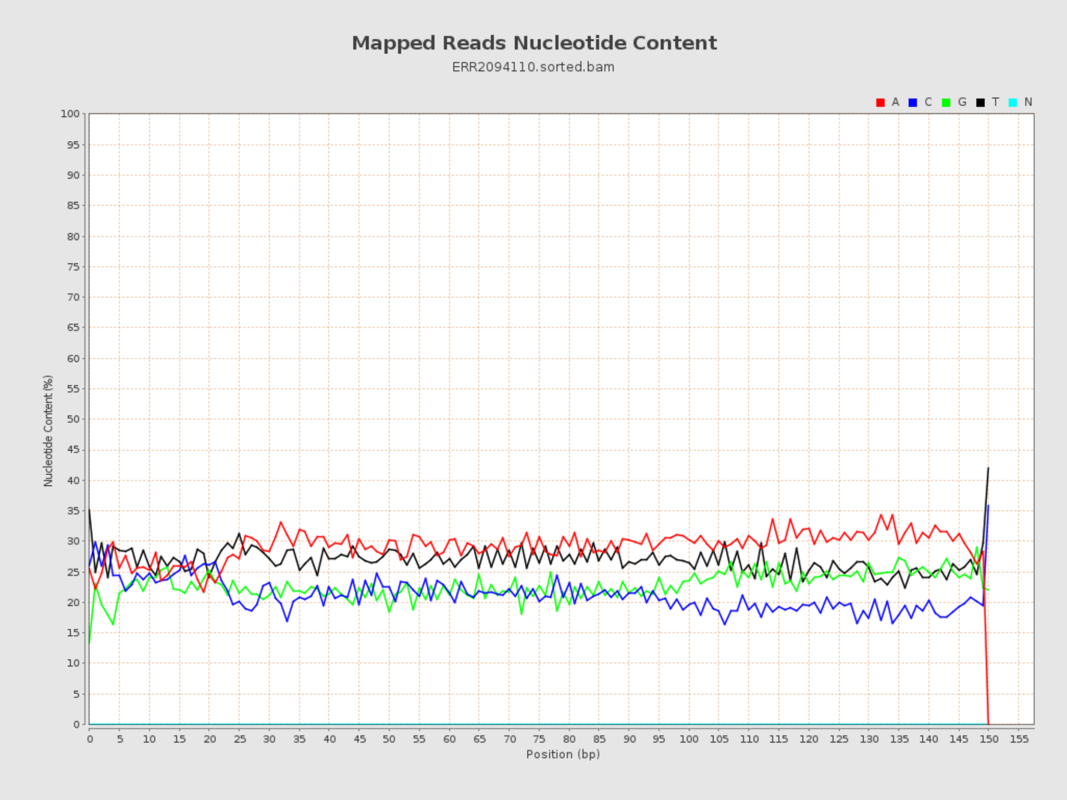
6. Results : Genome Fraction Coverage



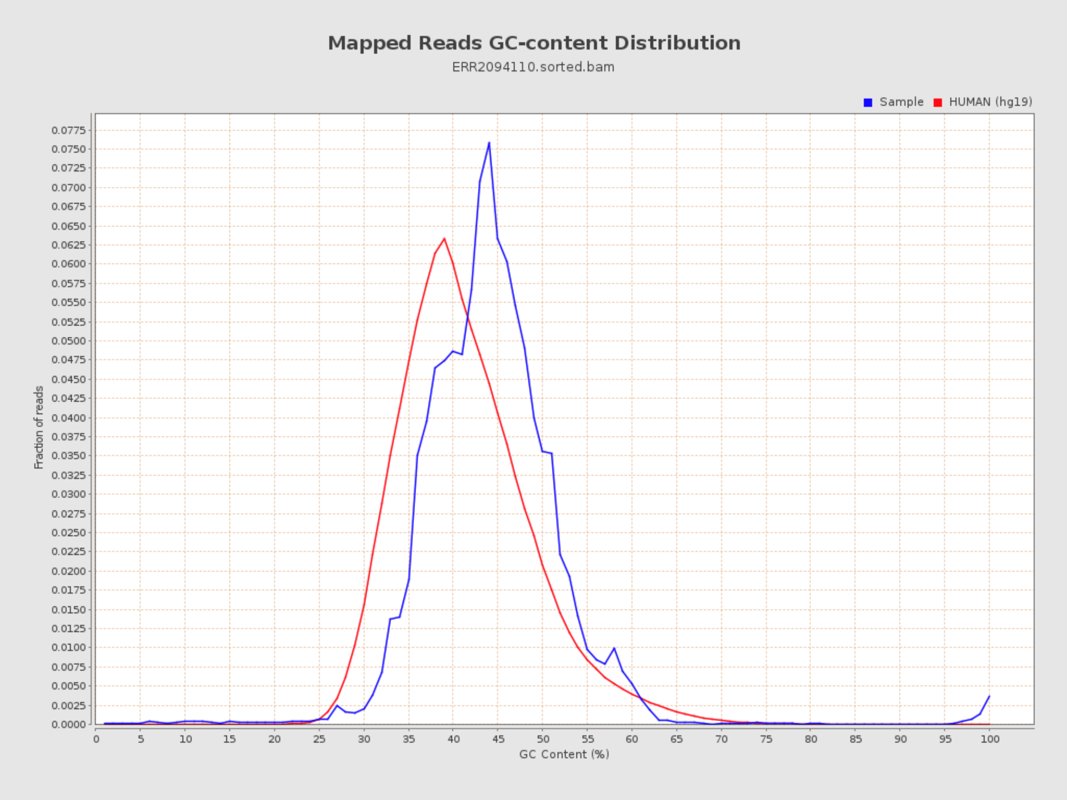
7. Results : Duplication Rate Histogram



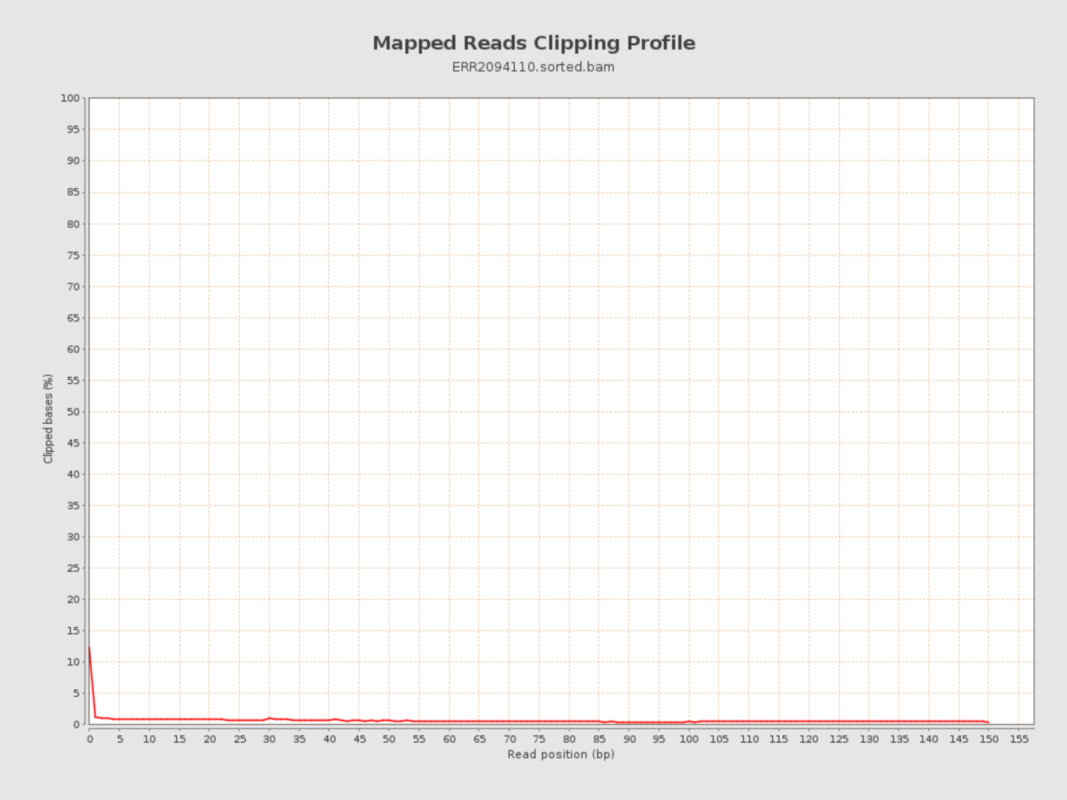
8. Results : Mapped Reads Nucleotide Content



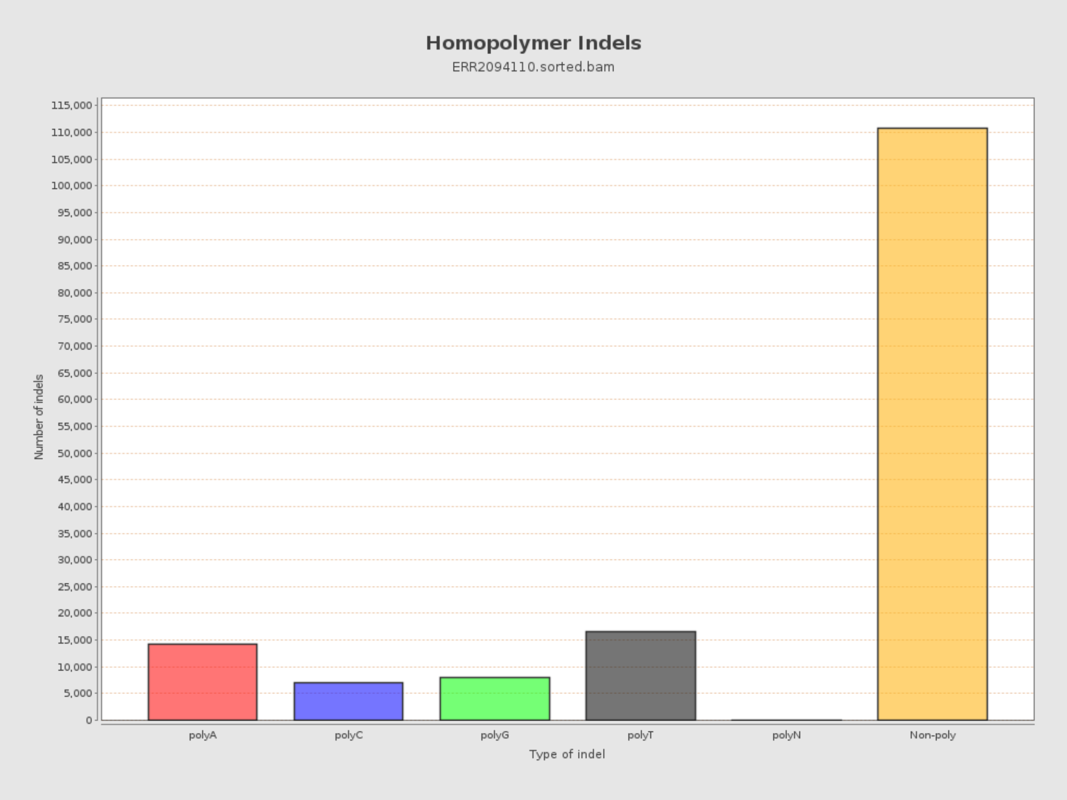
9. Results : Mapped Reads GC-content Distribution



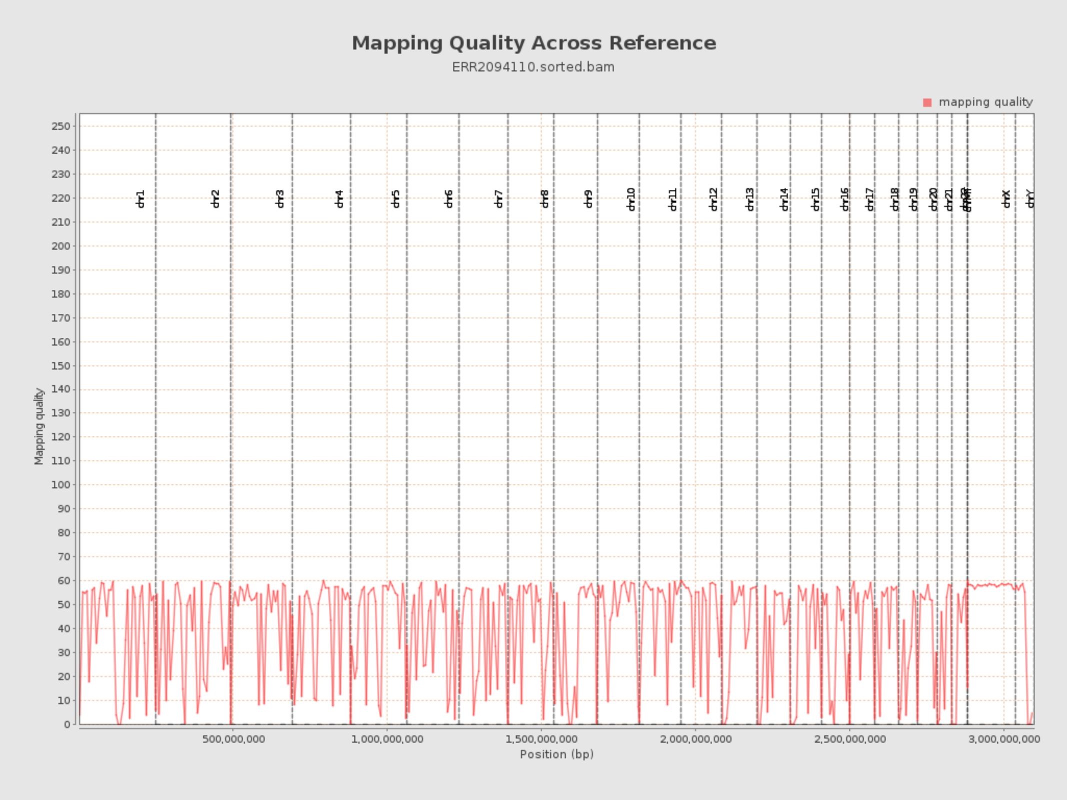
10. Results : Mapped Reads Clipping Profile



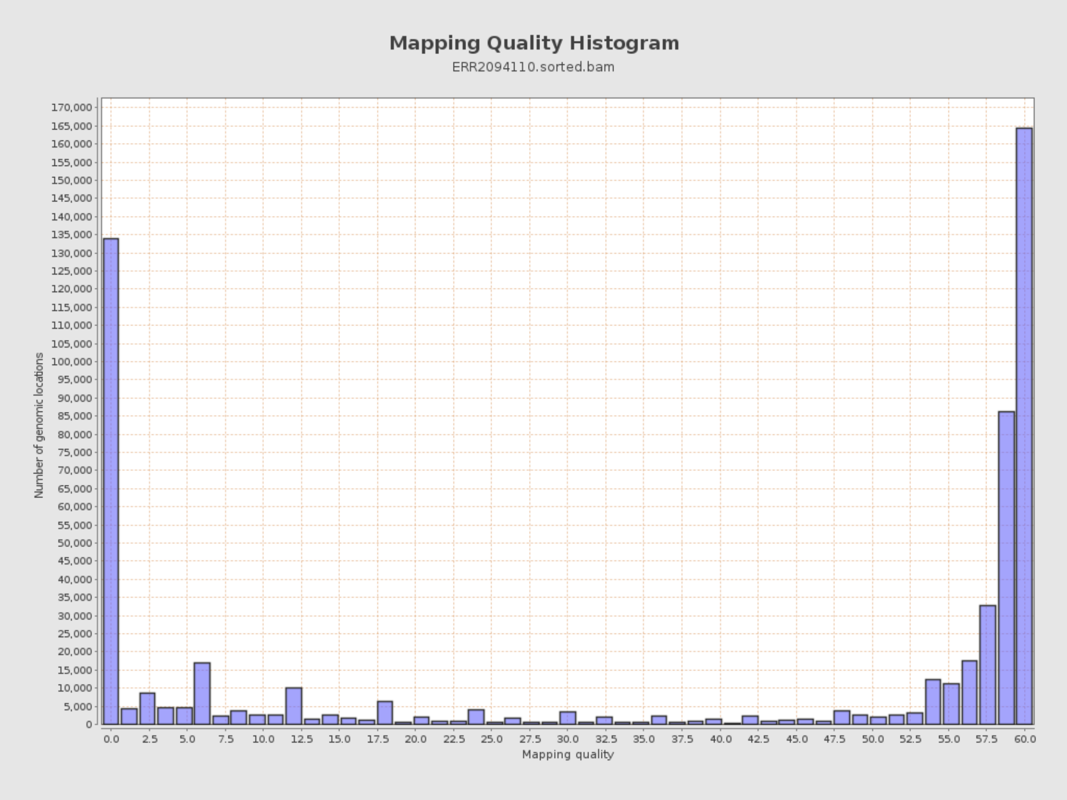
11. Results : Homopolymer Indels



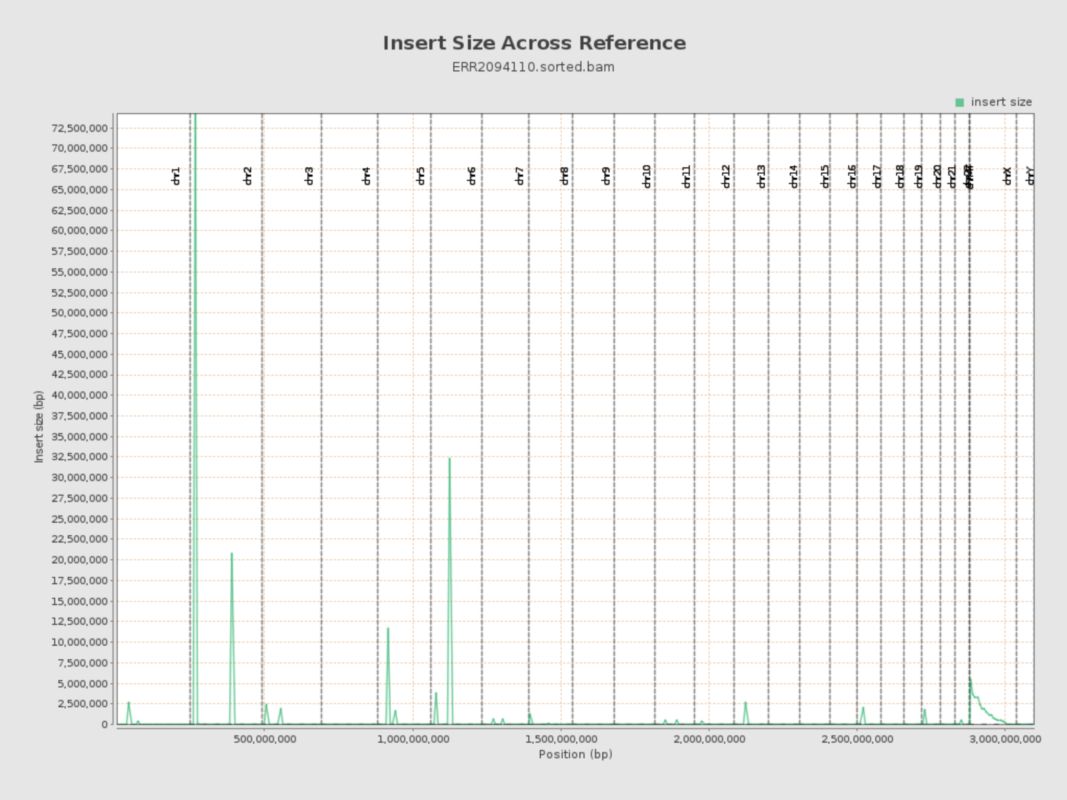
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram