Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:07:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094122.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_ERR2094122 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094122_1.fastq.gz ERR2094122_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:07:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	484,064
Mapped reads	457,703 / 94.55%
Unmapped reads	26,361 / 5.45%
Mapped paired reads	457,703 / 94.55%
Mapped reads, first in pair	229,494 / 47.41%
Mapped reads, second in pair	228,209 / 47.14%
Mapped reads, both in pair	455,788 / 94.16%
Mapped reads, singletons	1,915 / 0.4%
Secondary alignments	0
Supplementary alignments	1,156 / 0.24%
Read min/max/mean length	30 / 151 / 145.74
Duplicated reads (estimated)	456,280 / 94.26%
Duplication rate	46.53%
Clipped reads	41,686 / 8.61%

2.2. ACGT Content

Number/percentage of A's	18,865,115 / 27.76%
Number/percentage of C's	14,643,394 / 21.55%
Number/percentage of T's	19,388,138 / 28.53%
Number/percentage of G's	15,054,573 / 22.15%
Number/percentage of N's	862 / 0%

GC Percentage	43.7%

2.3. Coverage

Mean	0.022
Standard Deviation	39.7308

2.4. Mapping Quality

Mean Mapping Quality	12.83

2.5. Insert size

Mean	5,980.35
Standard Deviation	893,051.46
P25/Median/P75	217 / 237 / 266

2.6. Mismatches and indels

General error rate	1.61%
Mismatches	1,068,827
Insertions	18,175
Mapped reads with at least one insertion	3.93%
Deletions	48,387
Mapped reads with at least one deletion	10.35%
Homopolymer indels	68.06%

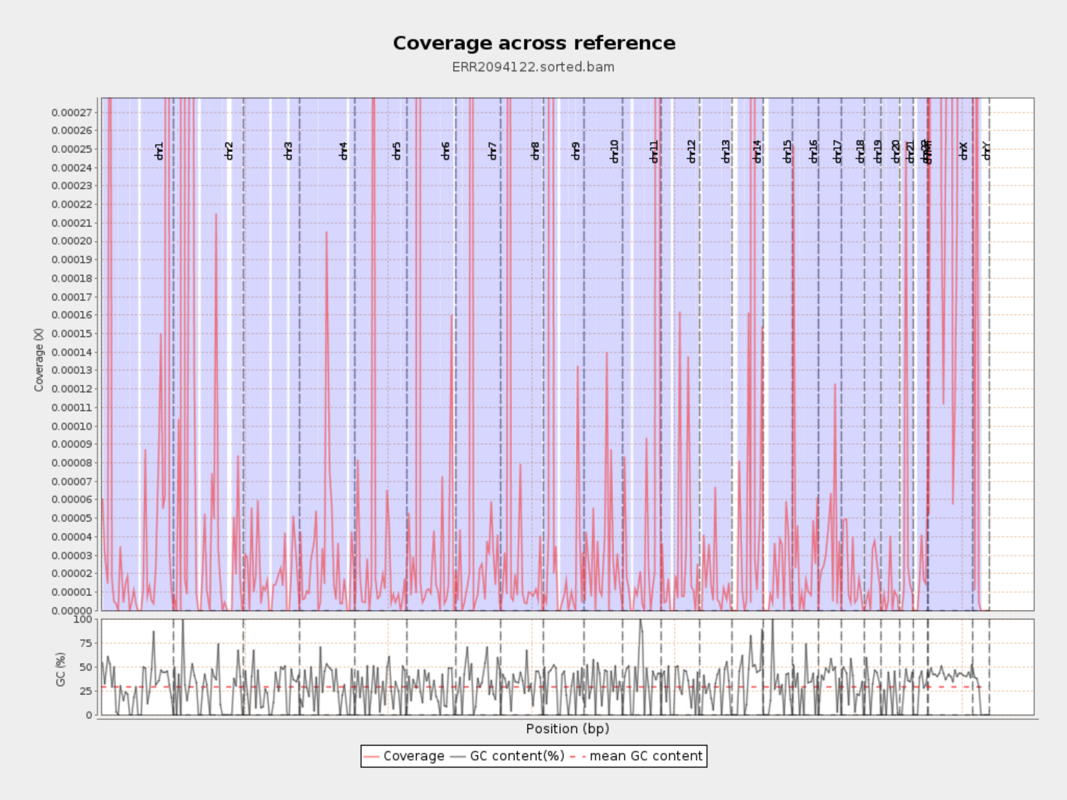
2.7. Chromosome stats

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

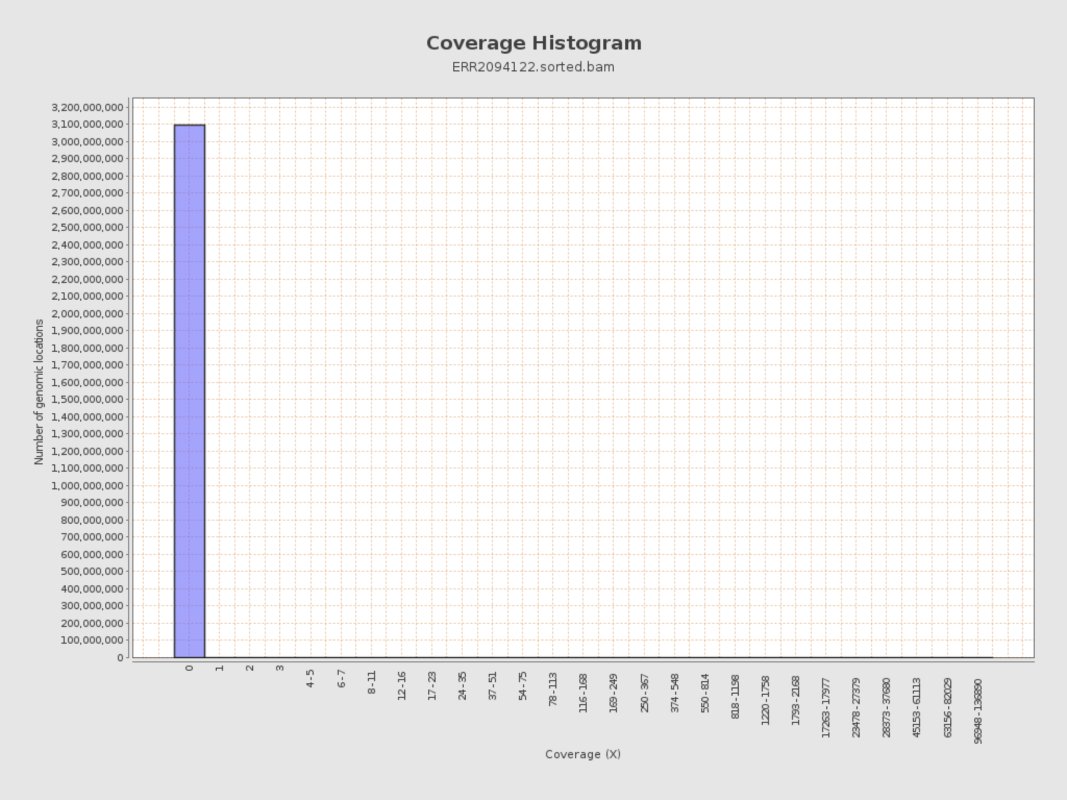
		bases	coverage	deviation
chr1	249250621	30180	0.0001	0.1228
chr2	243199373	164413	0.0007	0.6305
chr3	198022430	3718	0	0.006
chr4	191154276	5578	0	0.0121
chr5	180915260	6667	0	0.0222
chr6	171115067	38567	0.0002	0.2266
chr7	159138663	10030	0.0001	0.0427
chr8	146364022	8490	0.0001	0.0369
chr9	141213431	20360	0.0001	0.1391
chr10	135534747	4226	0	0.0138
chr11	135006516	17317	0.0001	0.0959
chr12	133851895	3721	0	0.0112
chr13	115169878	1698	0	0.0047
chr14	107349540	55277	0.0005	0.2991
chr15	102531392	1871	0	0.0067
chr16	90354753	3146	0	0.0124
chr17	81195210	2863	0	0.0099
chr18	78077248	1554	0	0.0048
chr19	59128983	980	0	0.0053
chr20	63025520	562	0	0.0048
chr21	48129895	2389	0	0.0201
chr22	51304566	847	0	0.0046
chrMT	16571	67042078	4,045.7473	16,688.5664
chrX	155270560	585572	0.0038	1.9055

chrY	59373566	4627	0.0001	0.0278

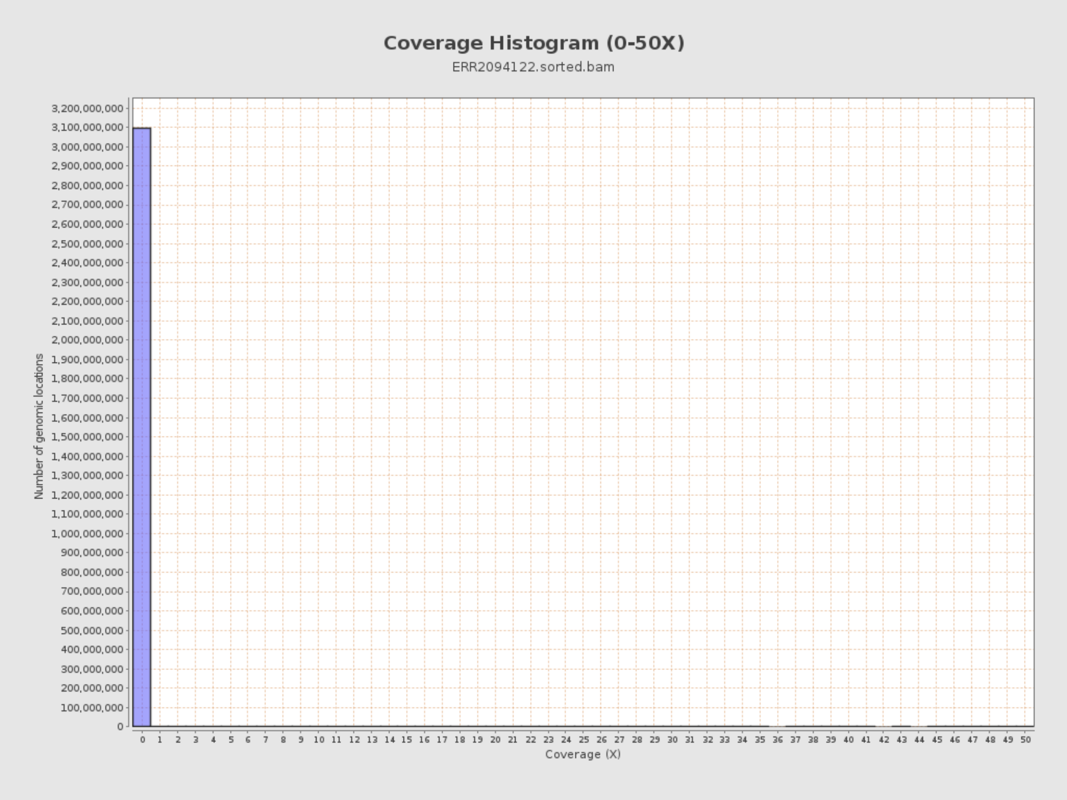
3. Results : Coverage across reference



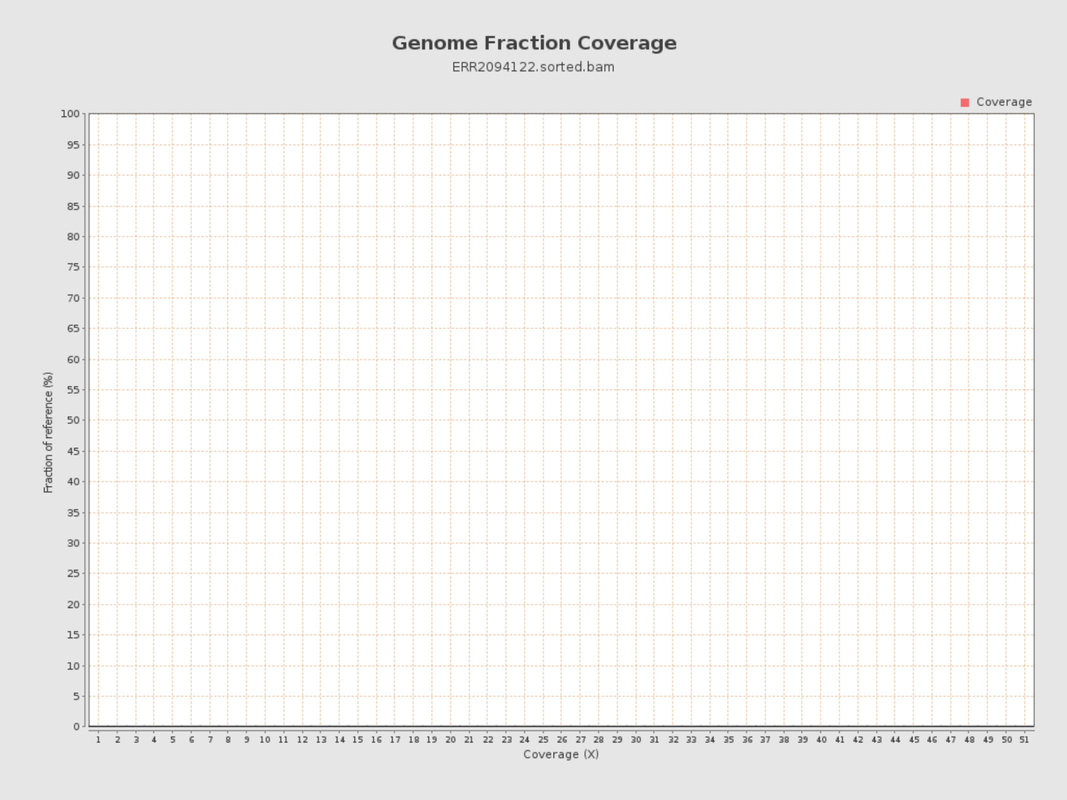
4. Results : Coverage Histogram



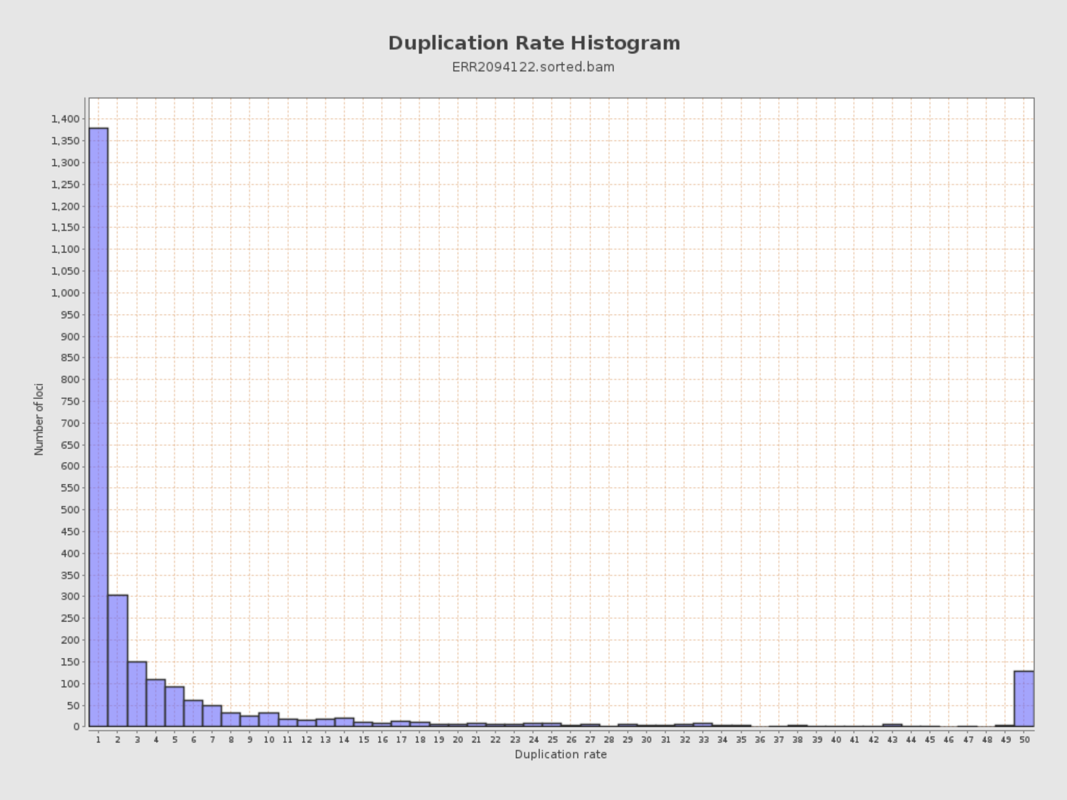
5. Results : Coverage Histogram (0-50X)



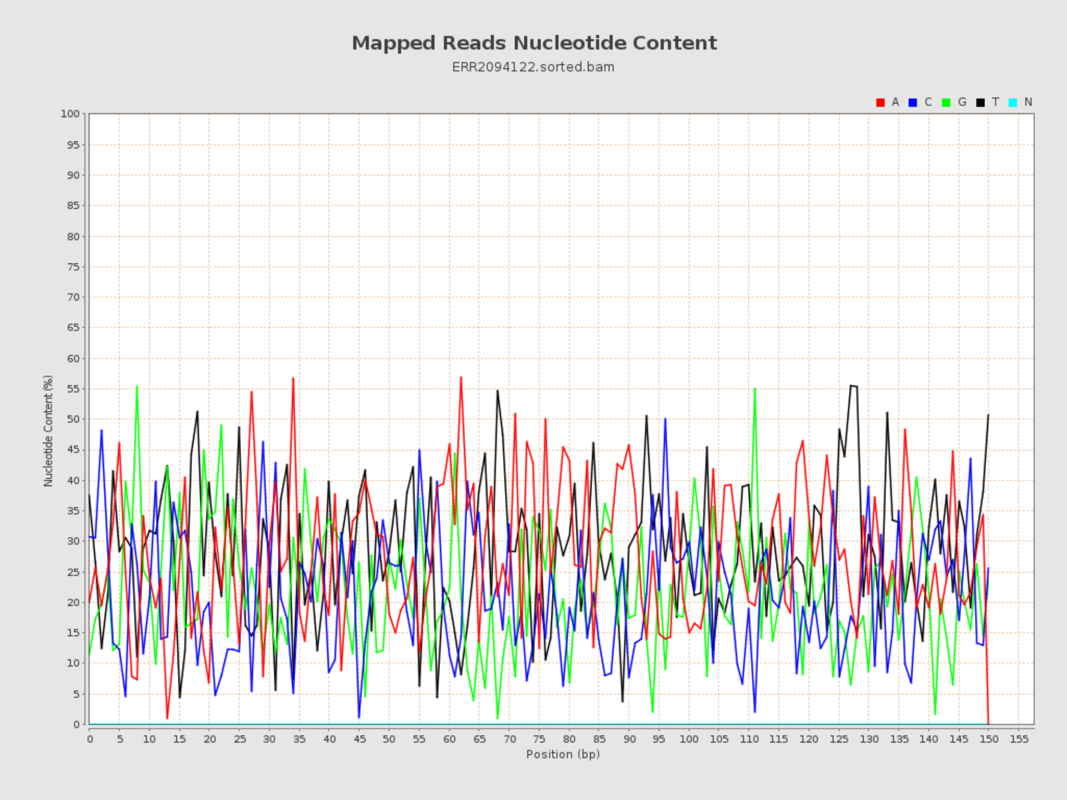
6. Results : Genome Fraction Coverage



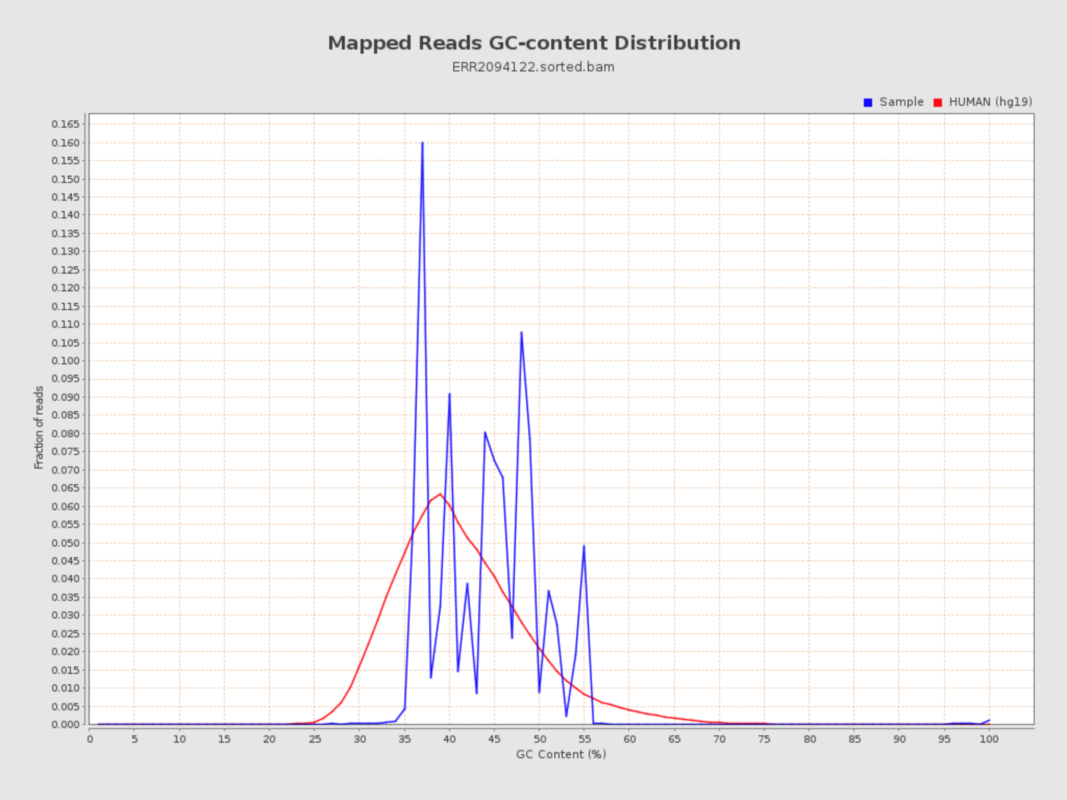
7. Results : Duplication Rate Histogram



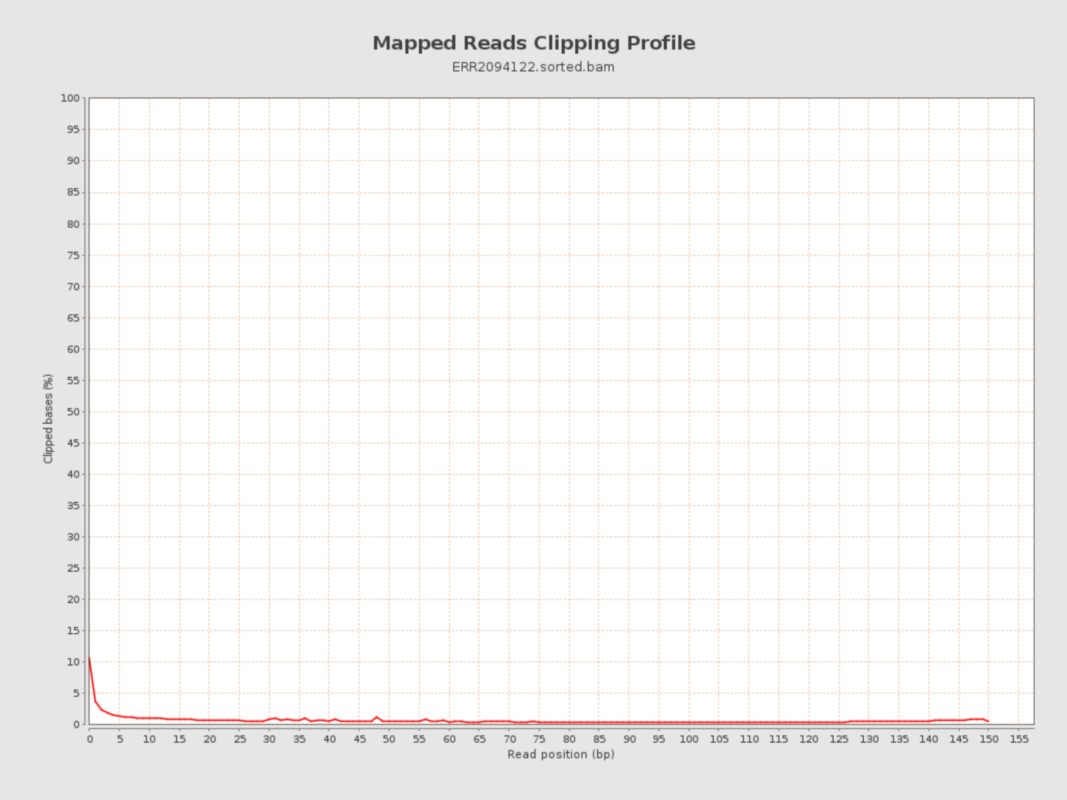
8. Results : Mapped Reads Nucleotide Content



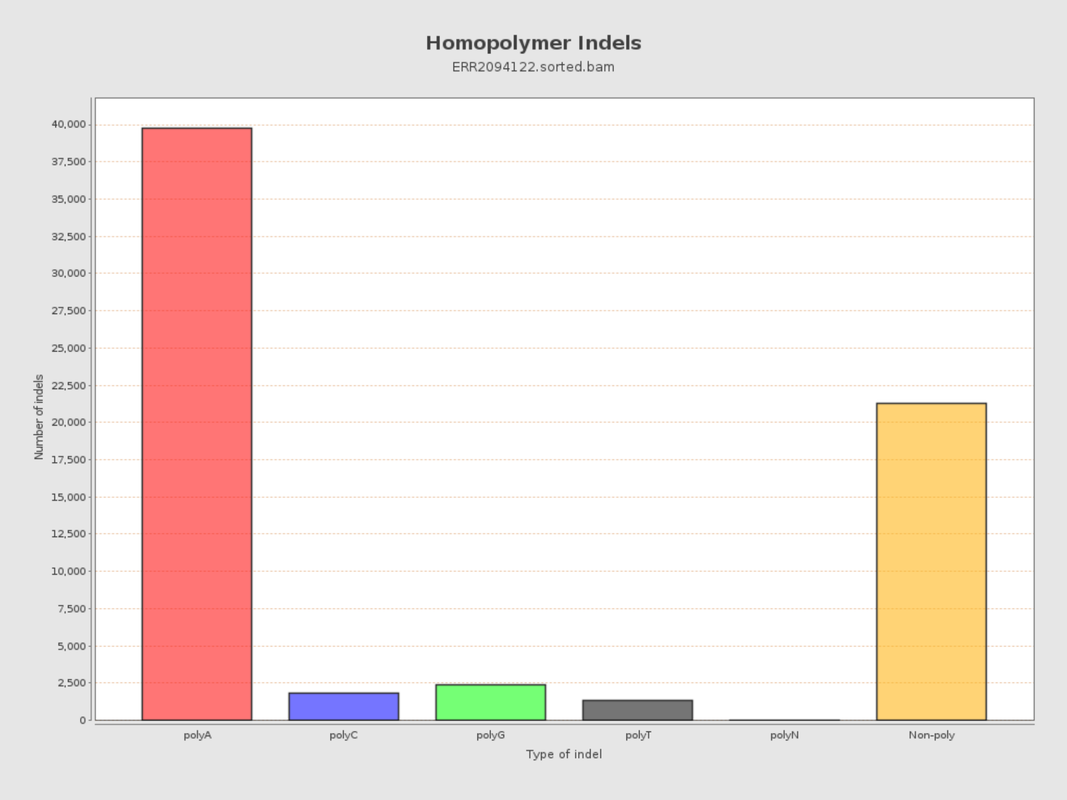
9. Results : Mapped Reads GC-content Distribution



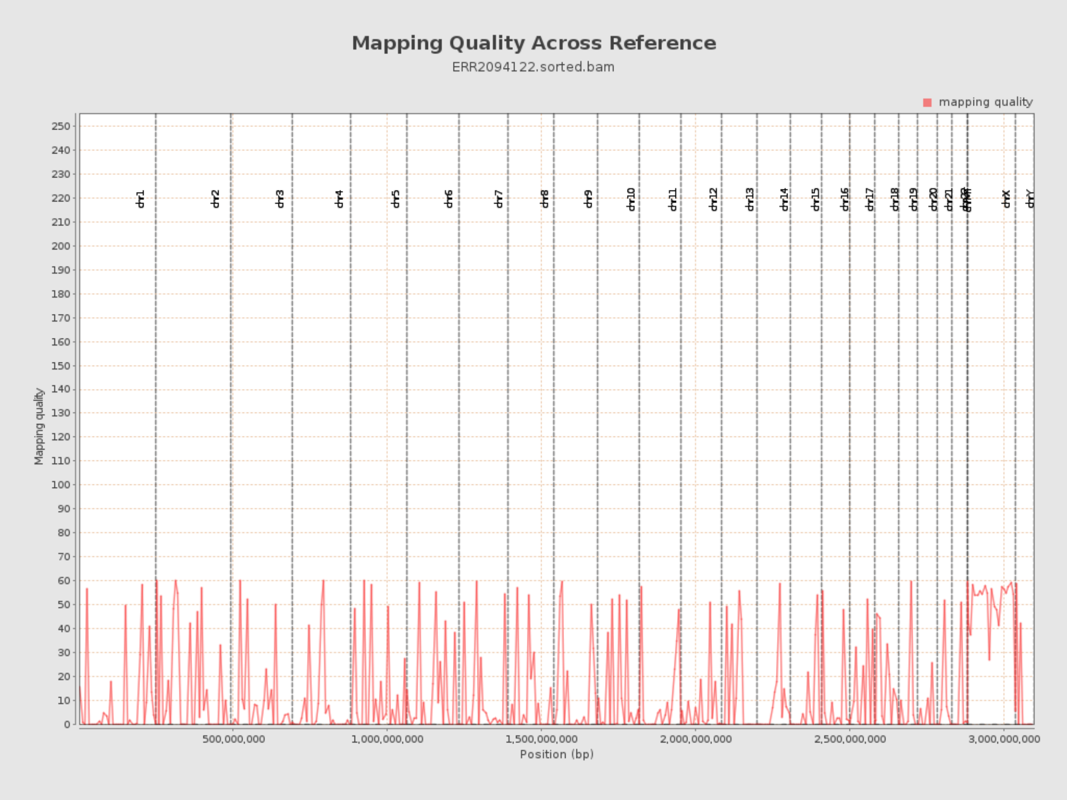
10. Results : Mapped Reads Clipping Profile



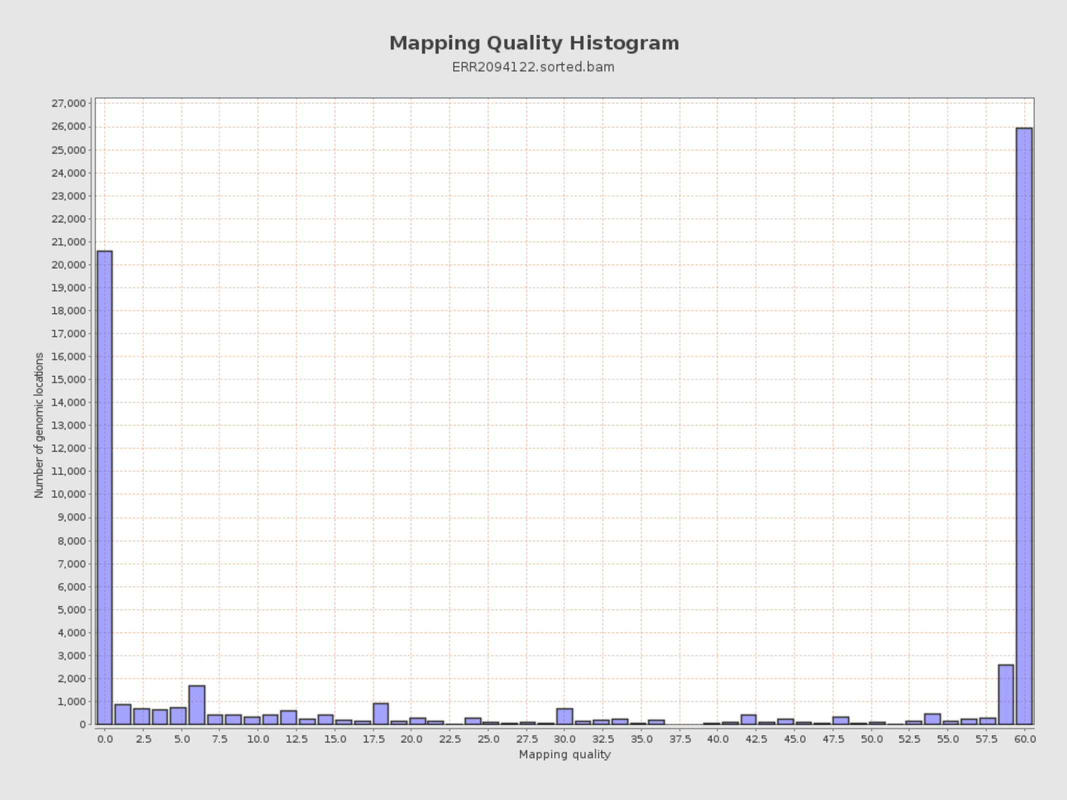
11. Results : Homopolymer Indels



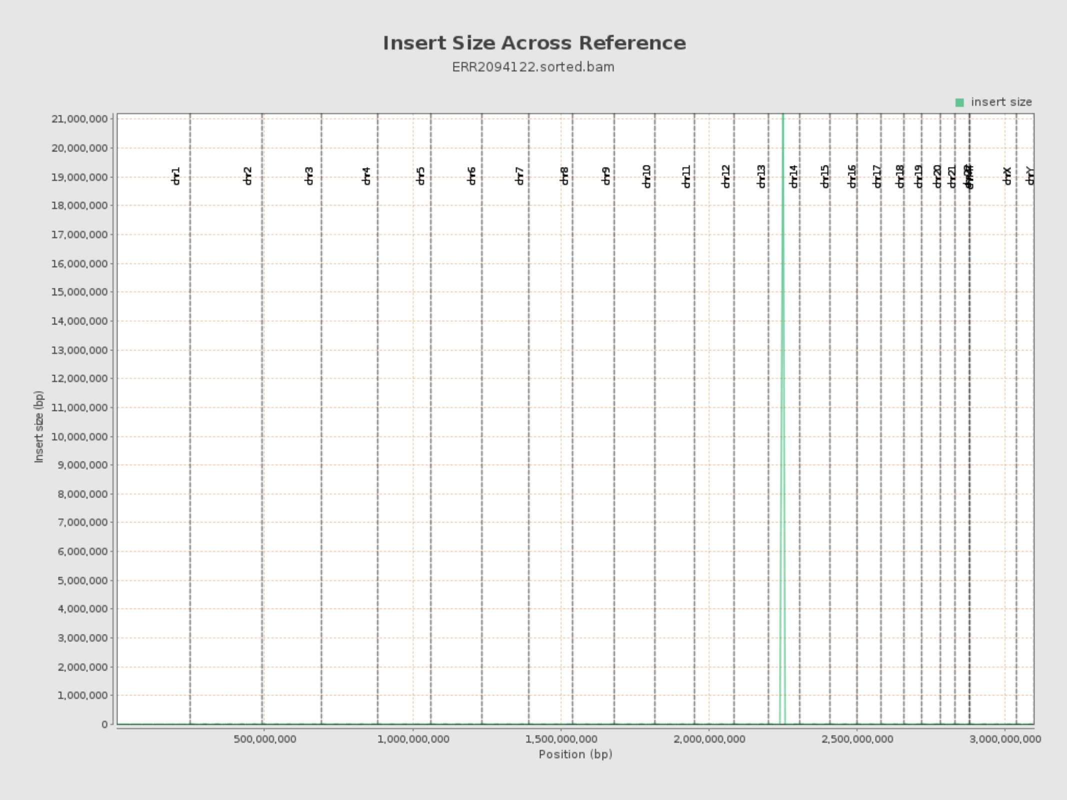
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram