Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:29:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094139.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_ERR2094139 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094139_1.fastq.gz ERR2094139_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:29:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	508,872
Mapped reads	485,095 / 95.33%
Unmapped reads	23,777 / 4.67%
Mapped paired reads	485,095 / 95.33%
Mapped reads, first in pair	243,411 / 47.83%
Mapped reads, second in pair	241,684 / 47.49%
Mapped reads, both in pair	482,520 / 94.82%
Mapped reads, singletons	2,575 / 0.51%
Secondary alignments	0
Supplementary alignments	7,617 / 1.5%
Read min/max/mean length	30 / 151 / 145.51
Duplicated reads (estimated)	483,597 / 95.03%
Duplication rate	44.57%
Clipped reads	114,193 / 22.44%

2.2. ACGT Content

Number/percentage of A's	19,183,961 / 27.78%
Number/percentage of C's	14,976,663 / 21.68%
Number/percentage of T's	19,407,057 / 28.1%
Number/percentage of G's	15,497,104 / 22.44%
Number/percentage of N's	803 / 0%

GC Percentage	44.12%

2.3. Coverage

Mean	0.0225
Standard Deviation	28.6451

2.4. Mapping Quality

Mean Mapping Quality	20.4

2.5. Insert size

Mean	98,119.25
Standard Deviation	3,680,838.08
P25/Median/P75	187 / 217 / 256

2.6. Mismatches and indels

General error rate	2.45%
Mismatches	1,656,991
Insertions	24,677
Mapped reads with at least one insertion	5.03%
Deletions	90,139
Mapped reads with at least one deletion	18.08%
Homopolymer indels	40.91%

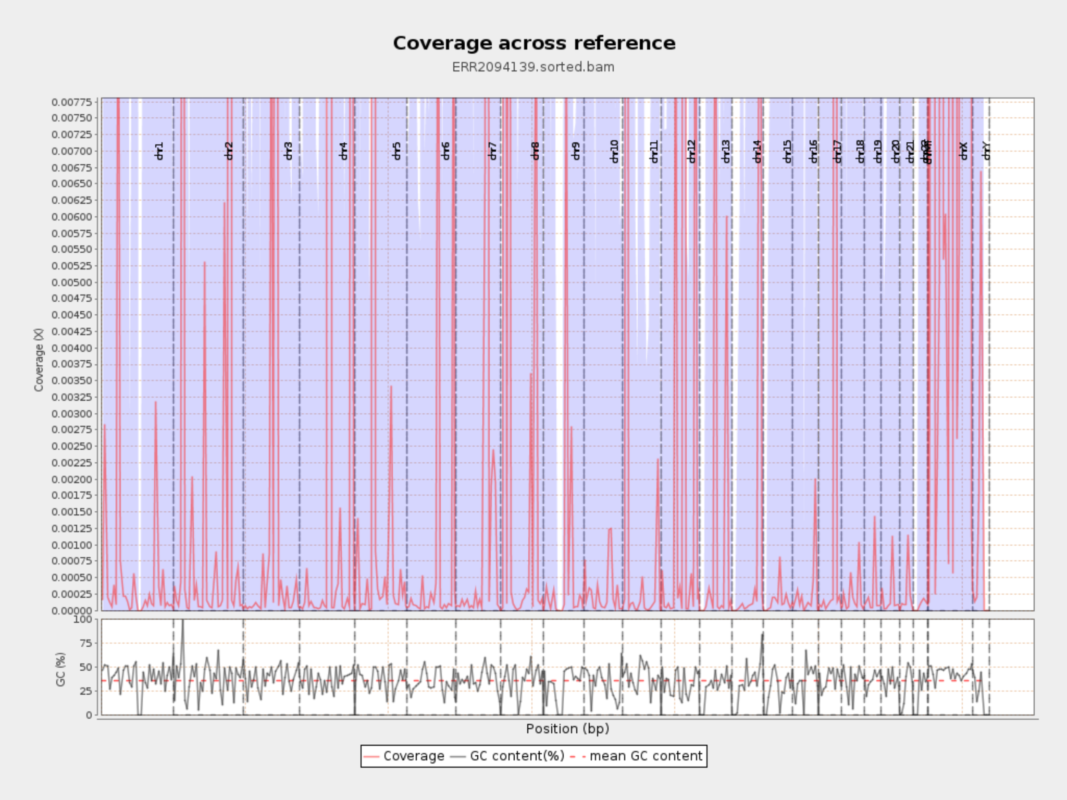
2.7. Chromosome stats

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

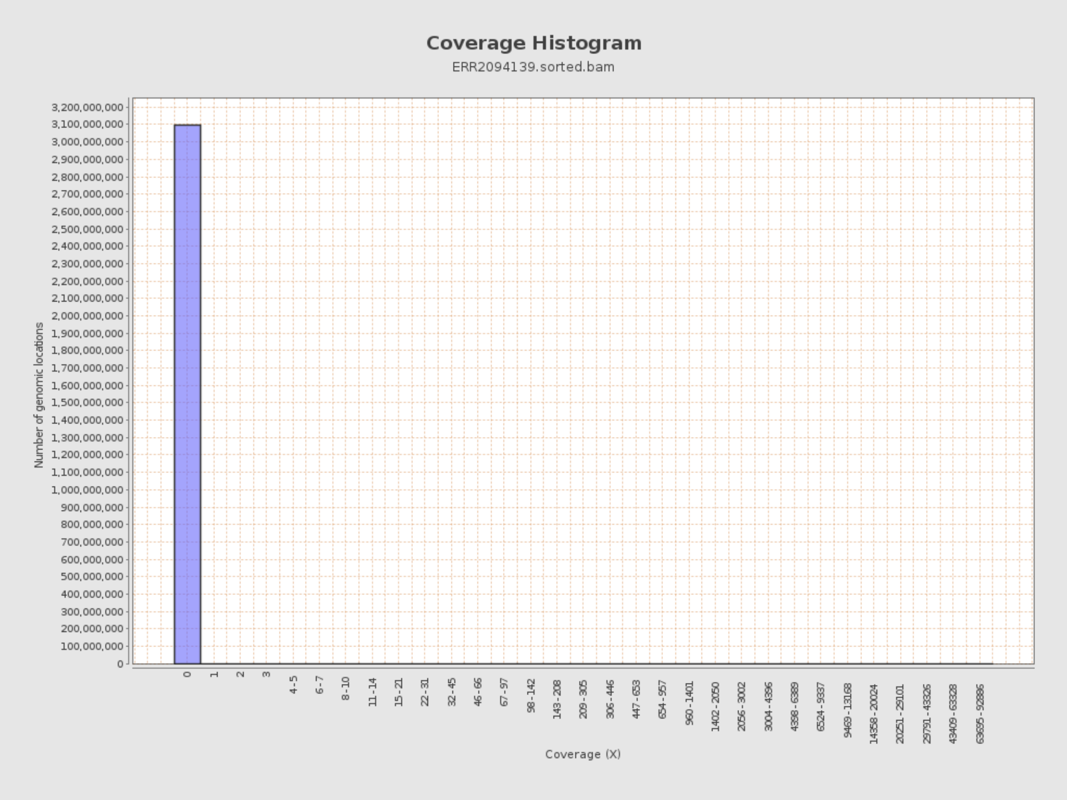
		bases	coverage	deviation
chr1	249250621	179158	0.0007	0.5394
chr2	243199373	1859175	0.0076	7.6176
chr3	198022430	342413	0.0017	0.92
chr4	191154276	2431838	0.0127	7.9863
chr5	180915260	4645329	0.0257	24.1731
chr6	171115067	209464	0.0012	0.8574
chr7	159138663	422433	0.0027	2.3412
chr8	146364022	603681	0.0041	2.8883
chr9	141213431	107618	0.0008	0.5125
chr10	135534747	42054	0.0003	0.1231
chr11	135006516	241771	0.0018	1.2356
chr12	133851895	584045	0.0044	2.6494
chr13	115169878	157911	0.0014	0.7615
chr14	107349540	126134	0.0012	0.4166
chr15	102531392	15965	0.0002	0.0903
chr16	90354753	27663	0.0003	0.1052
chr17	81195210	391753	0.0048	3.2214
chr18	78077248	19016	0.0002	0.0703
chr19	59128983	15991	0.0003	0.1277
chr20	63025520	14068	0.0002	0.078
chr21	48129895	13230	0.0003	0.1029
chr22	51304566	4288	0.0001	0.0172
chrMT	16571	46602932	2,812.3186	11,539.7383
chrX	155270560	10623346	0.0684	20.6142

chrY	59373566	69630	0.0012	0.5555

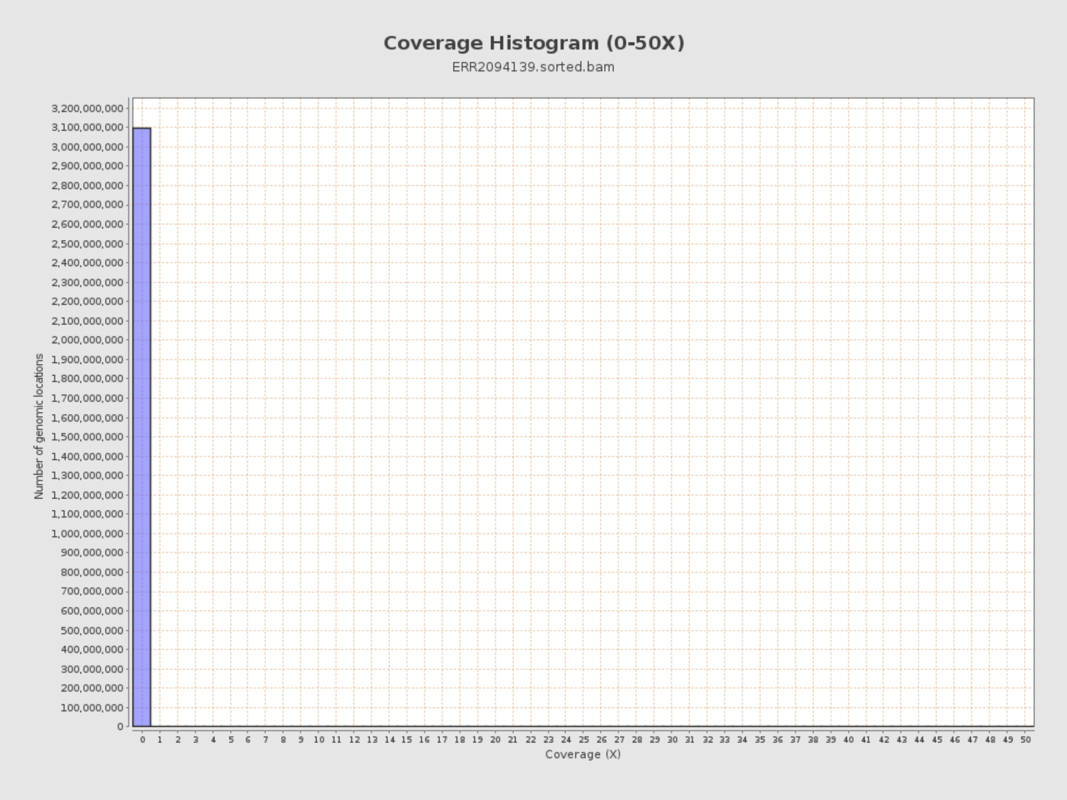
3. Results : Coverage across reference



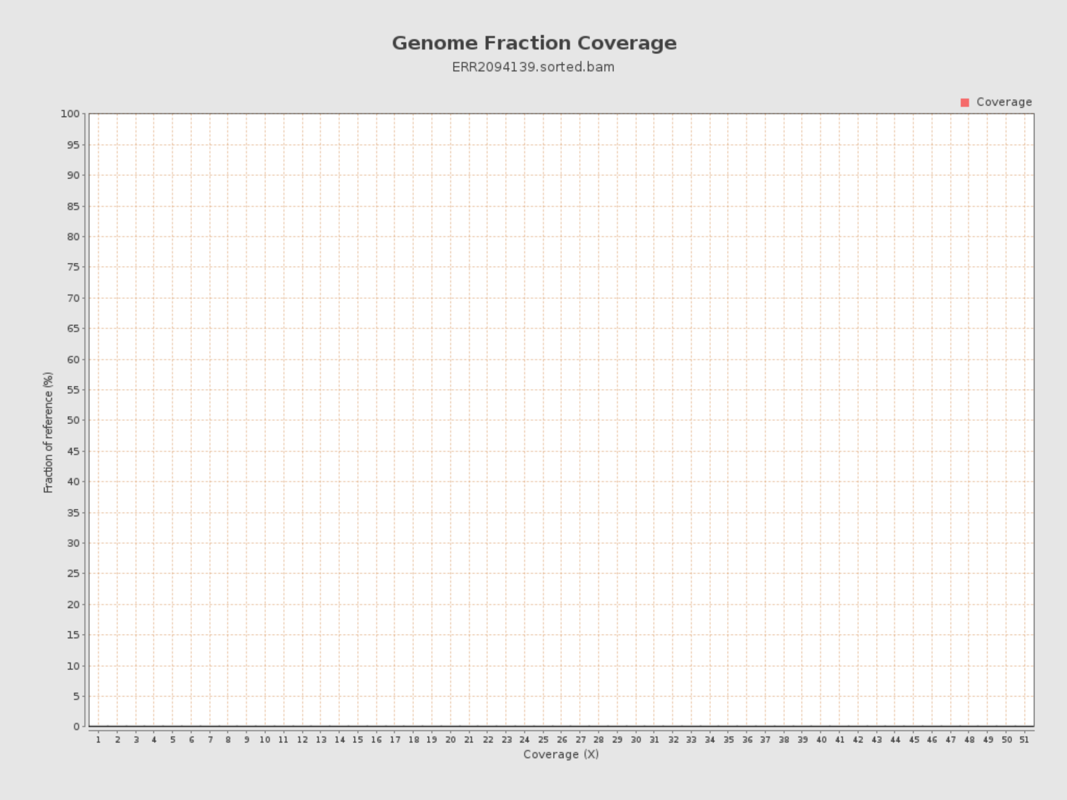
4. Results : Coverage Histogram



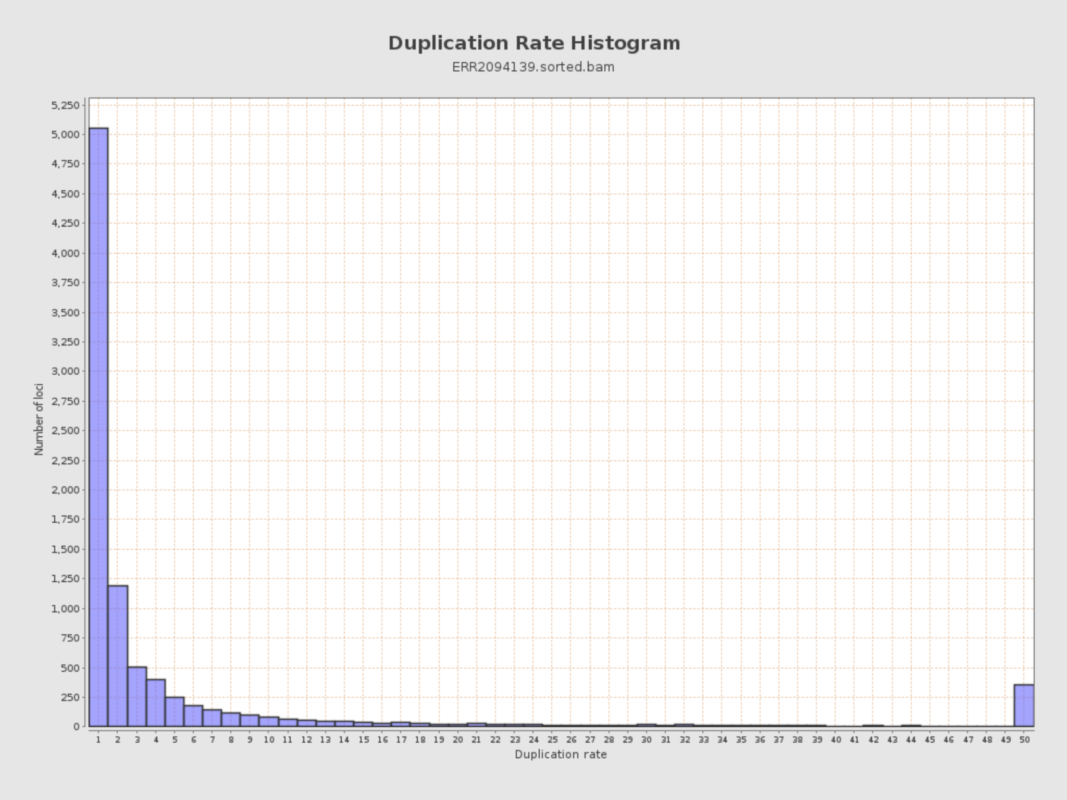
5. Results : Coverage Histogram (0-50X)



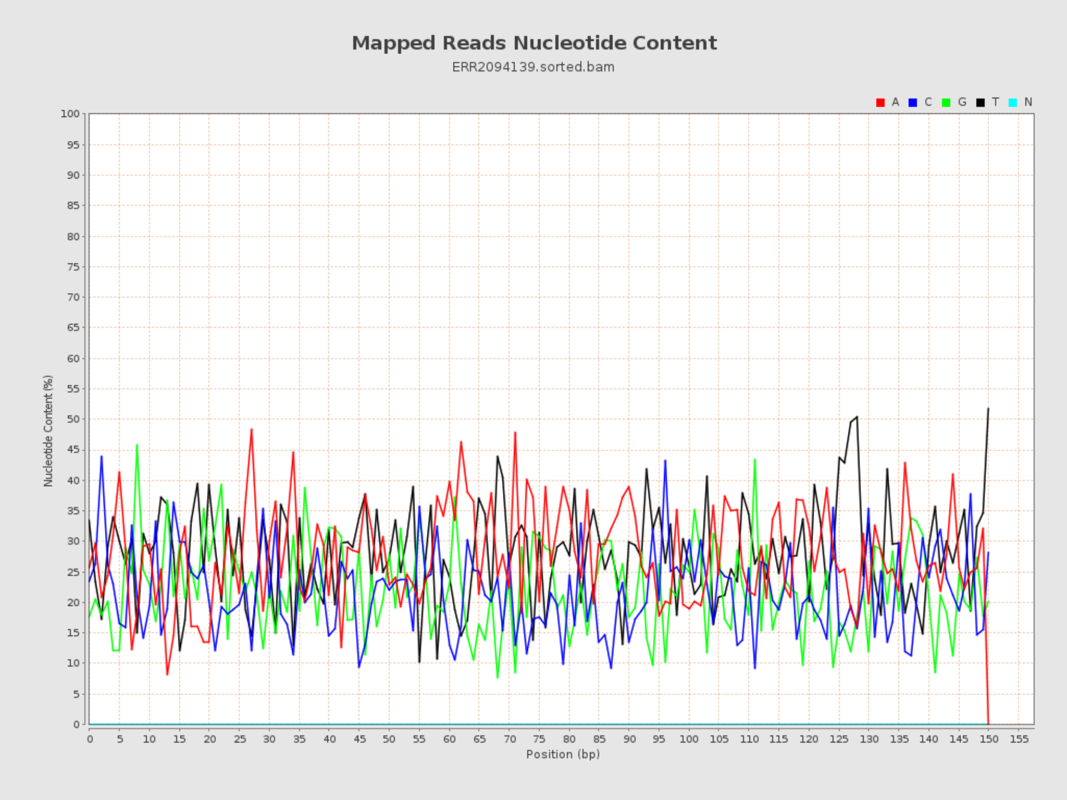
6. Results : Genome Fraction Coverage



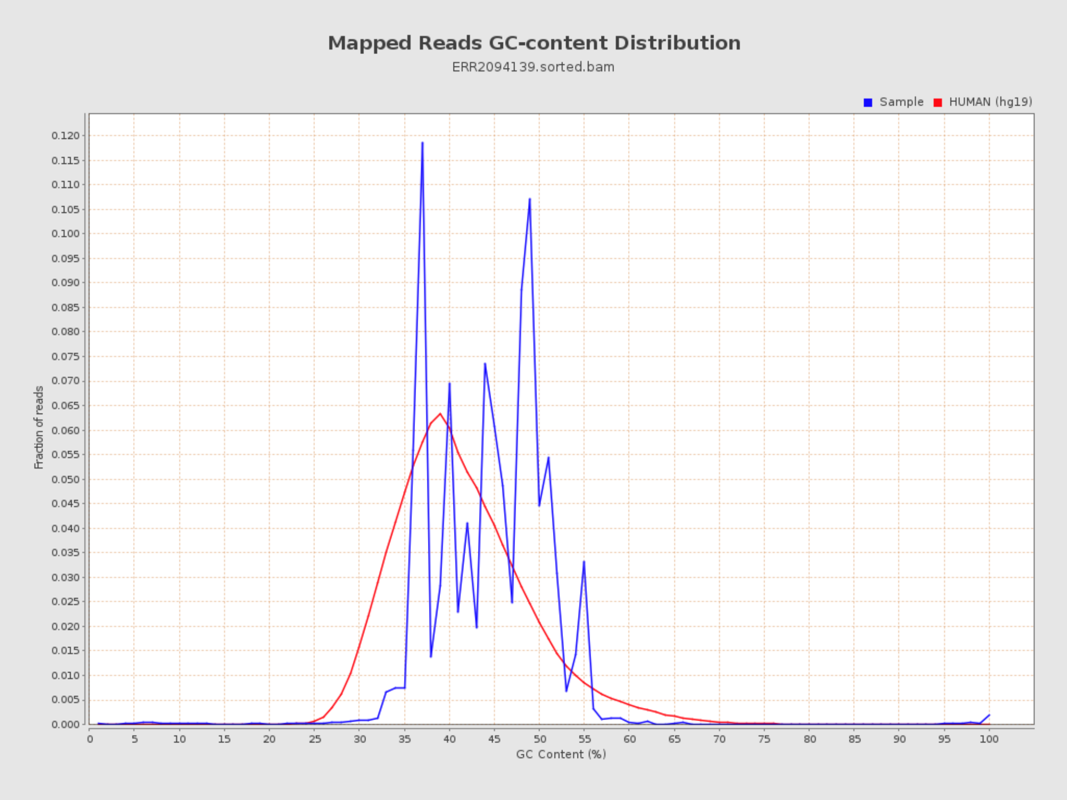
7. Results : Duplication Rate Histogram



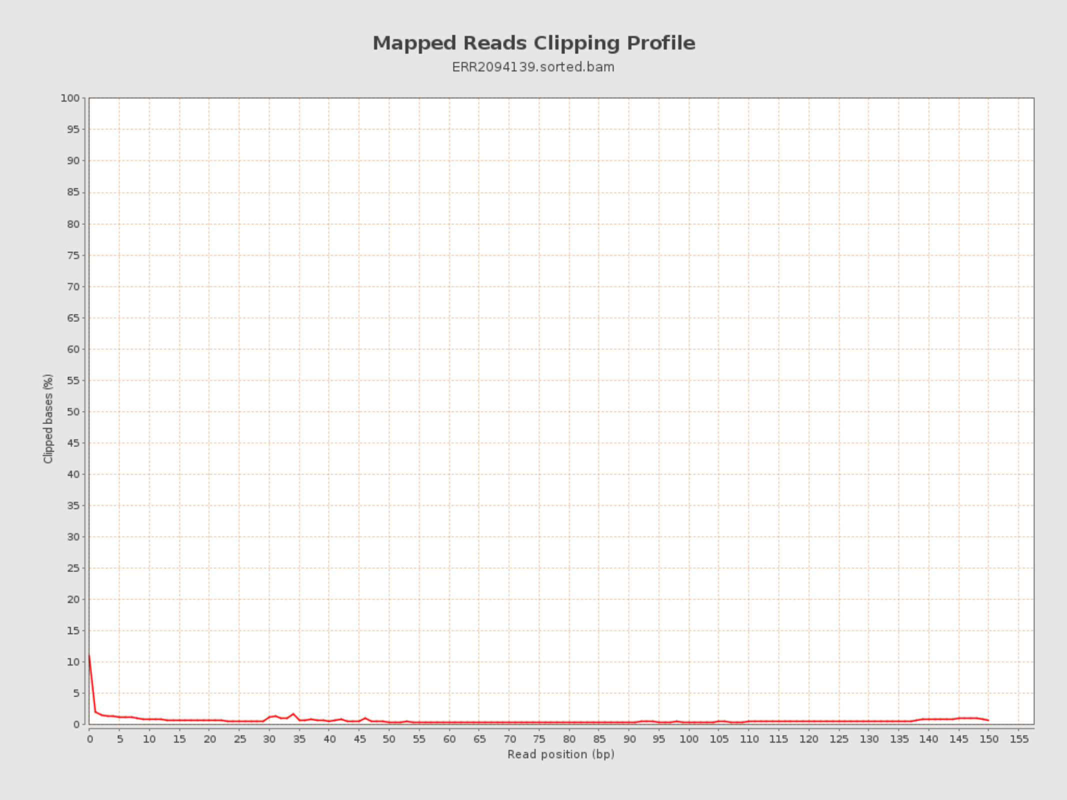
8. Results : Mapped Reads Nucleotide Content



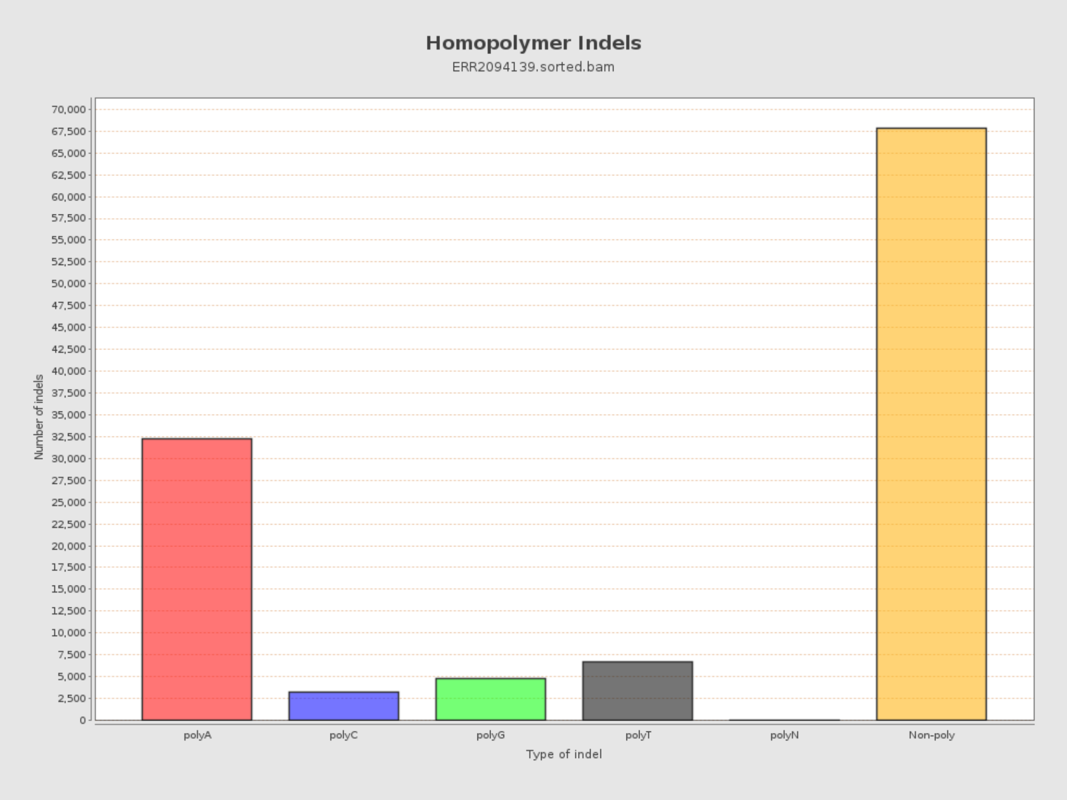
9. Results : Mapped Reads GC-content Distribution



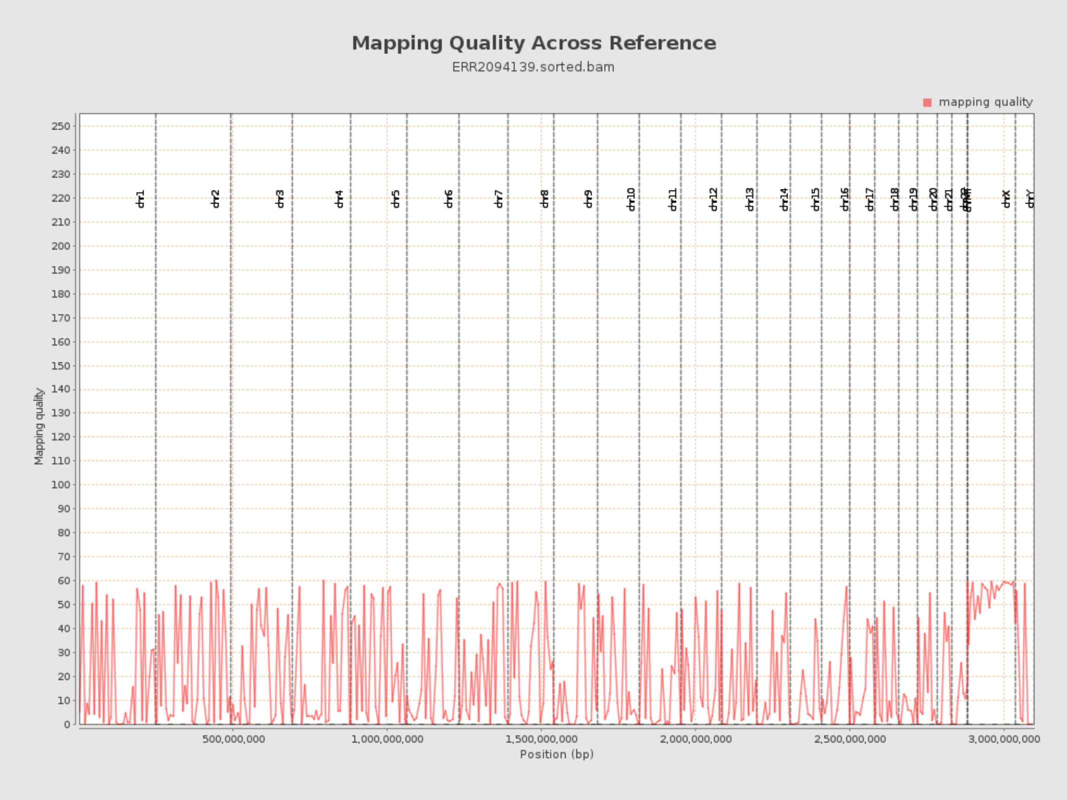
10. Results : Mapped Reads Clipping Profile



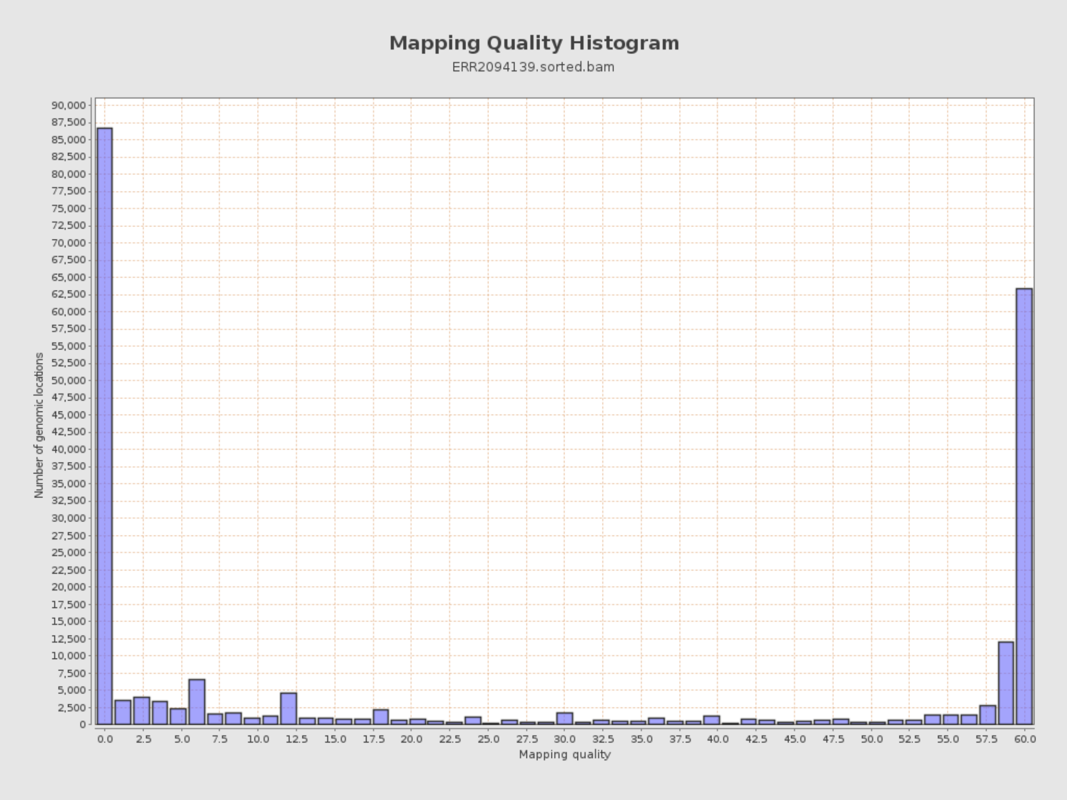
11. Results : Homopolymer Indels



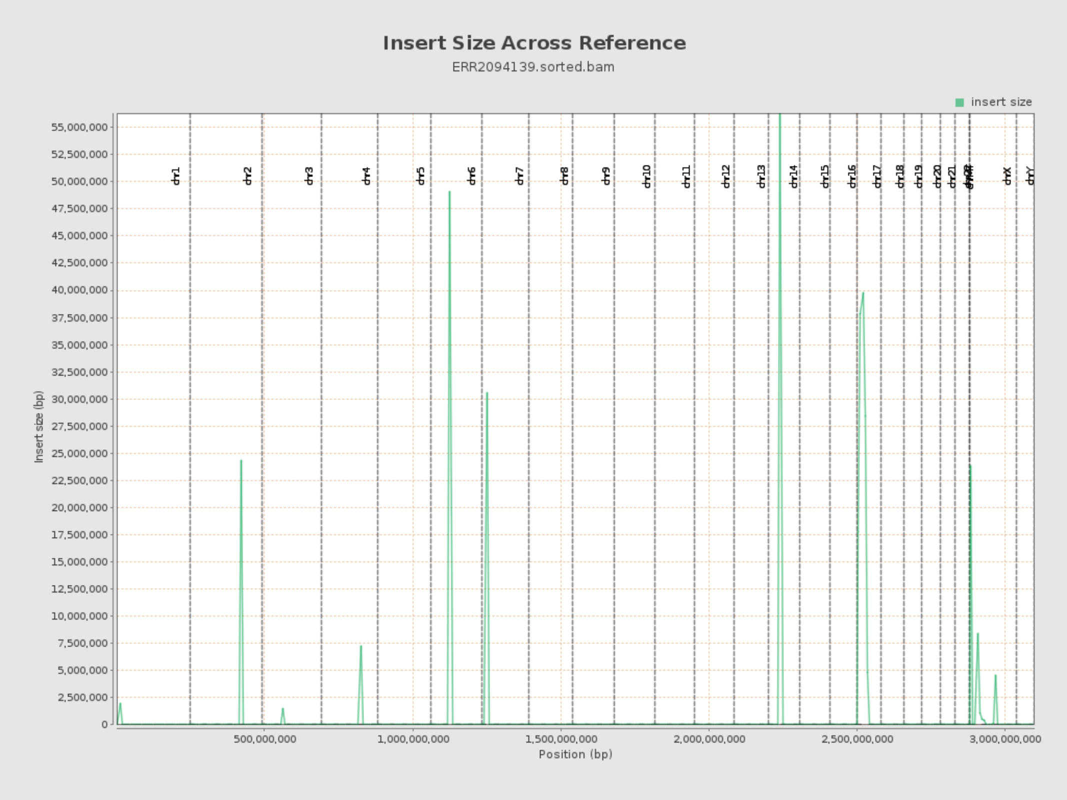
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram