Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:04:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094044.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_ERR2094044 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094044_1.fastq.gz ERR2094044_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:04:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	438,438
Mapped reads	418,101 / 95.36%
Unmapped reads	20,337 / 4.64%
Mapped paired reads	418,101 / 95.36%
Mapped reads, first in pair	210,034 / 47.91%
Mapped reads, second in pair	208,067 / 47.46%
Mapped reads, both in pair	415,118 / 94.68%
Mapped reads, singletons	2,983 / 0.68%
Secondary alignments	0
Supplementary alignments	14,352 / 3.27%
Read min/max/mean length	30 / 151 / 142.33
Duplicated reads (estimated)	398,751 / 90.95%
Duplication rate	49.46%
Clipped reads	166,260 / 37.92%

2.2. ACGT Content

Number/percentage of A's	15,287,512 / 27.87%
Number/percentage of C's	12,121,373 / 22.09%
Number/percentage of T's	14,660,670 / 26.72%
Number/percentage of G's	12,790,363 / 23.31%
Number/percentage of N's	414 / 0%

GC Percentage	45.41%

2.3. Coverage

Mean	0.0181
Standard Deviation	5.2103

2.4. Mapping Quality

Mean Mapping Quality	38.12

2.5. Insert size

Mean	374,641.92
Standard Deviation	5,568,858.31
P25/Median/P75	148 / 173 / 206

2.6. Mismatches and indels

General error rate	4.34%
Mismatches	2,299,031
Insertions	41,497
Mapped reads with at least one insertion	9.59%
Deletions	182,727
Mapped reads with at least one deletion	40.48%
Homopolymer indels	29.99%

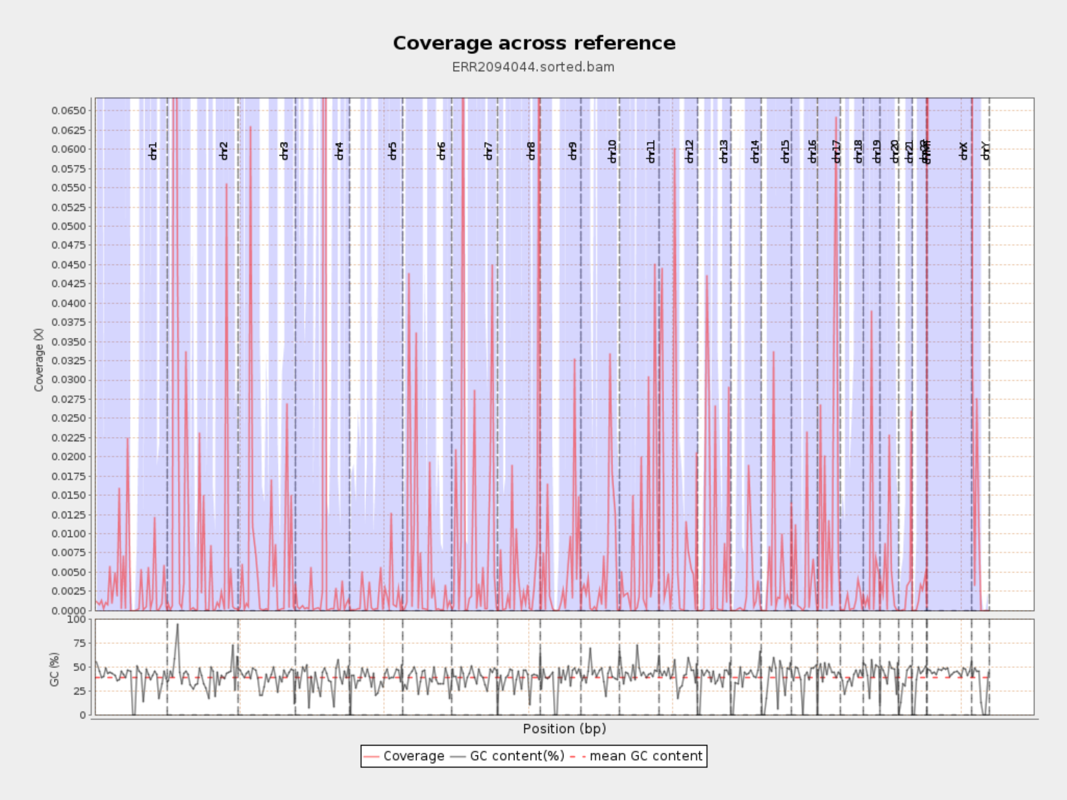
2.7. Chromosome stats

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

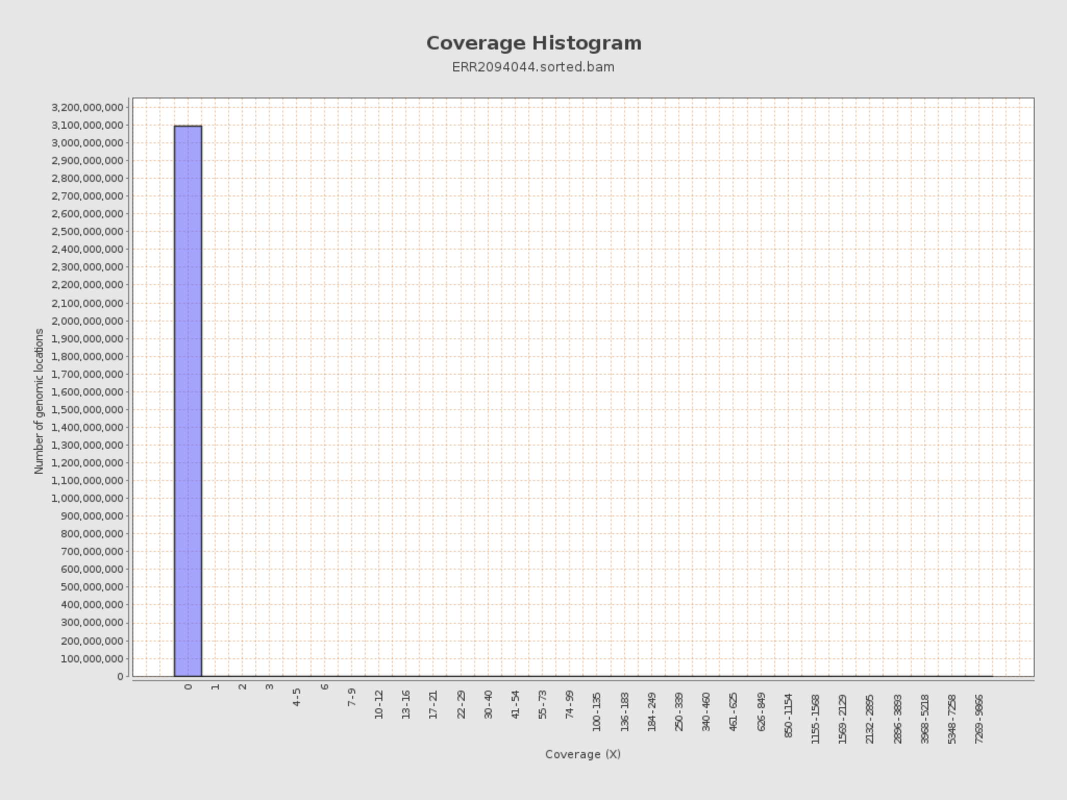
		bases	coverage	deviation
chr1	249250621	762169	0.0031	1.084
chr2	243199373	2713501	0.0112	3.8048
chr3	198022430	1289880	0.0065	2.7213
chr4	191154276	1563836	0.0082	3.2423
chr5	180915260	301072	0.0017	0.613
chr6	171115067	1013954	0.0059	2.7325
chr7	159138663	1730561	0.0109	3.7006
chr8	146364022	1084606	0.0074	3.6468
chr9	141213431	772697	0.0055	1.9001
chr10	135534747	737264	0.0054	1.6489
chr11	135006516	1149645	0.0085	2.4155
chr12	133851895	1485580	0.0111	3.8376
chr13	115169878	1079409	0.0094	2.6417
chr14	107349540	311543	0.0029	1.3655
chr15	102531392	469527	0.0046	1.754
chr16	90354753	444614	0.0049	1.908
chr17	81195210	1317084	0.0162	4.4857
chr18	78077248	84278	0.0011	0.2495
chr19	59128983	417134	0.0071	2.7401
chr20	63025520	329126	0.0052	1.1152
chr21	48129895	184005	0.0038	1.0649
chr22	51304566	95573	0.0019	0.4217
chrMT	16571	4755557	286.9807	1,192.1595
chrX	155270560	31605669	0.2036	15.735

chrY	59373566	481865	0.0081	2.6163

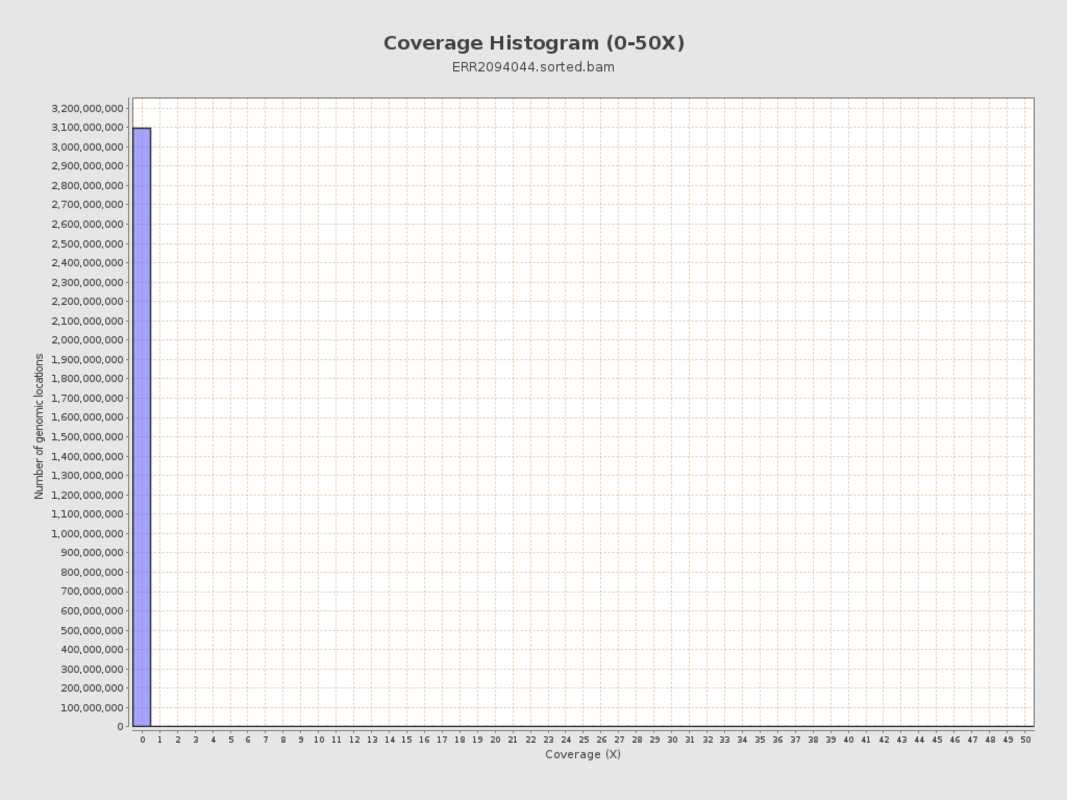
3. Results : Coverage across reference



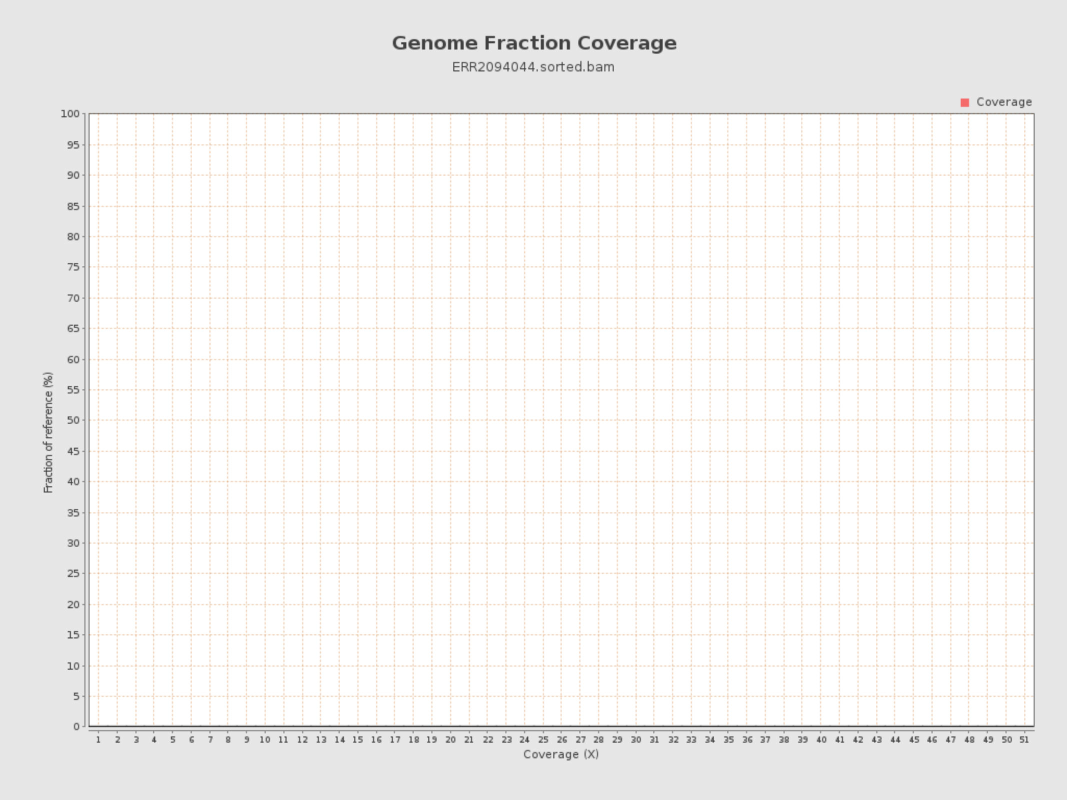
4. Results : Coverage Histogram



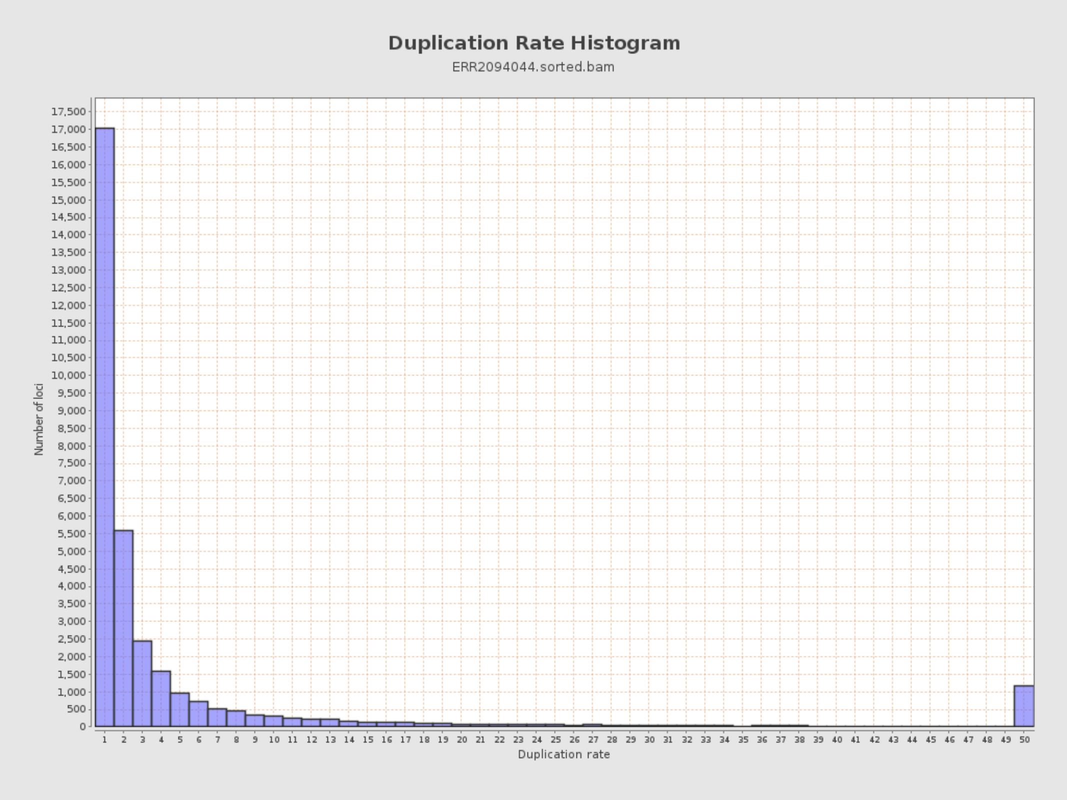
5. Results : Coverage Histogram (0-50X)



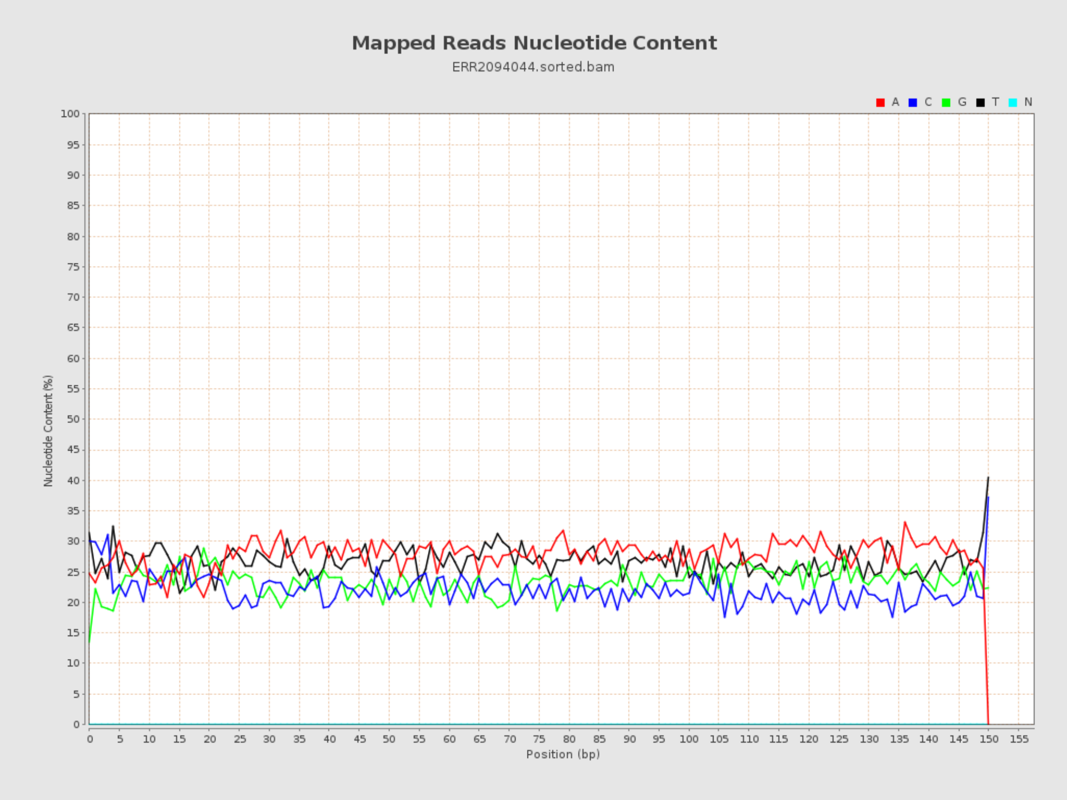
6. Results : Genome Fraction Coverage



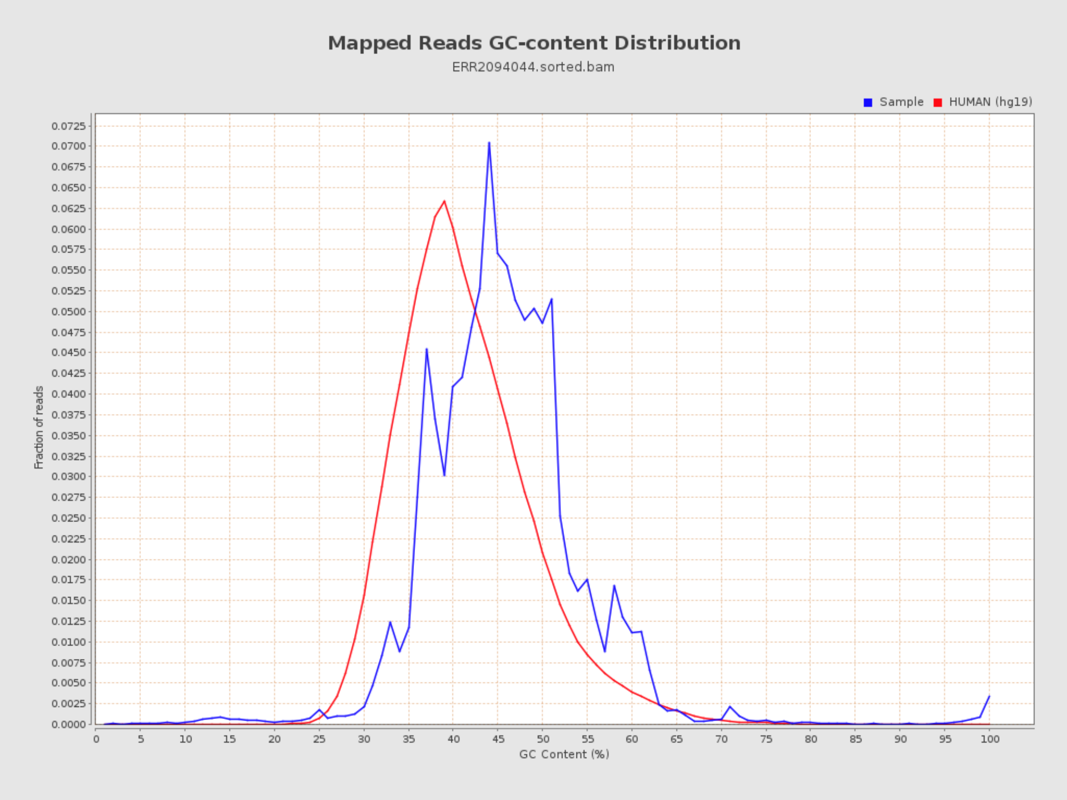
7. Results : Duplication Rate Histogram



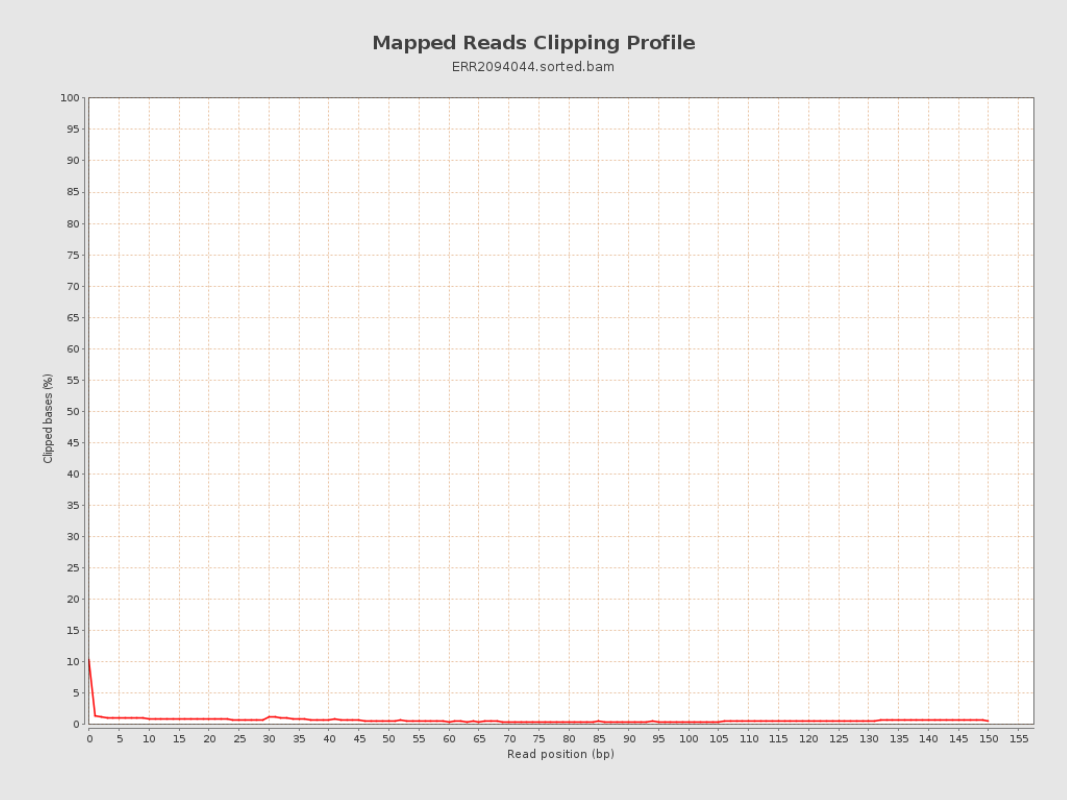
8. Results : Mapped Reads Nucleotide Content



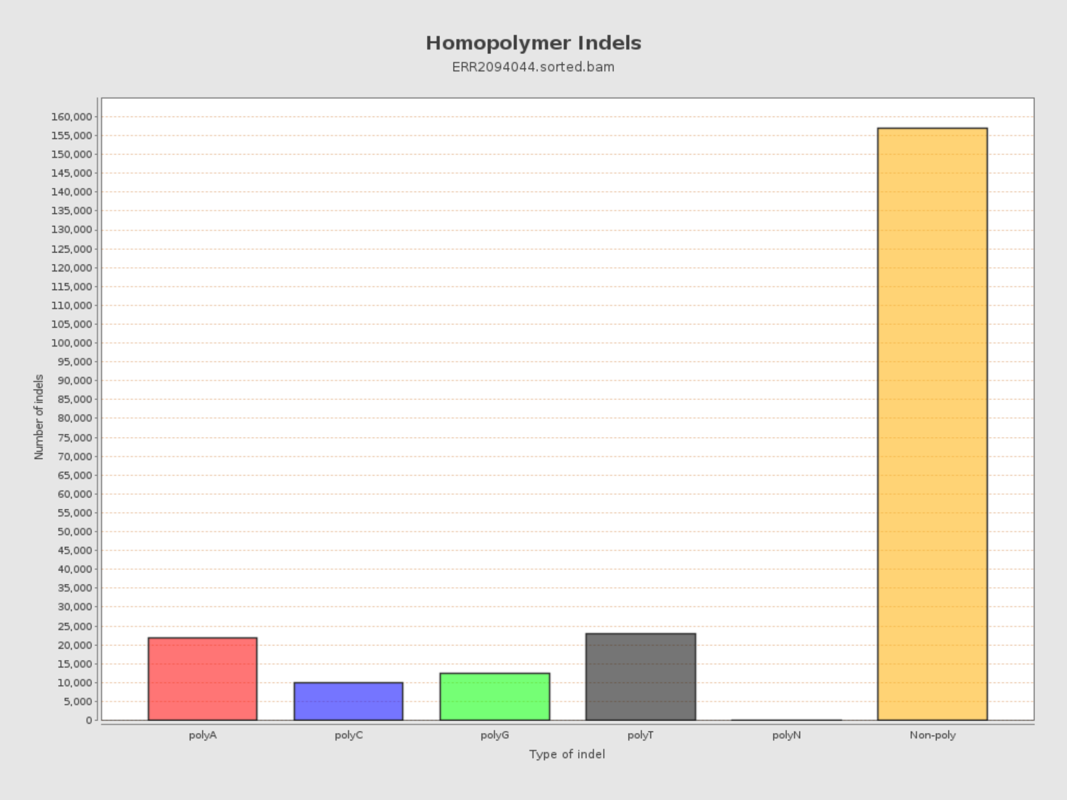
9. Results : Mapped Reads GC-content Distribution



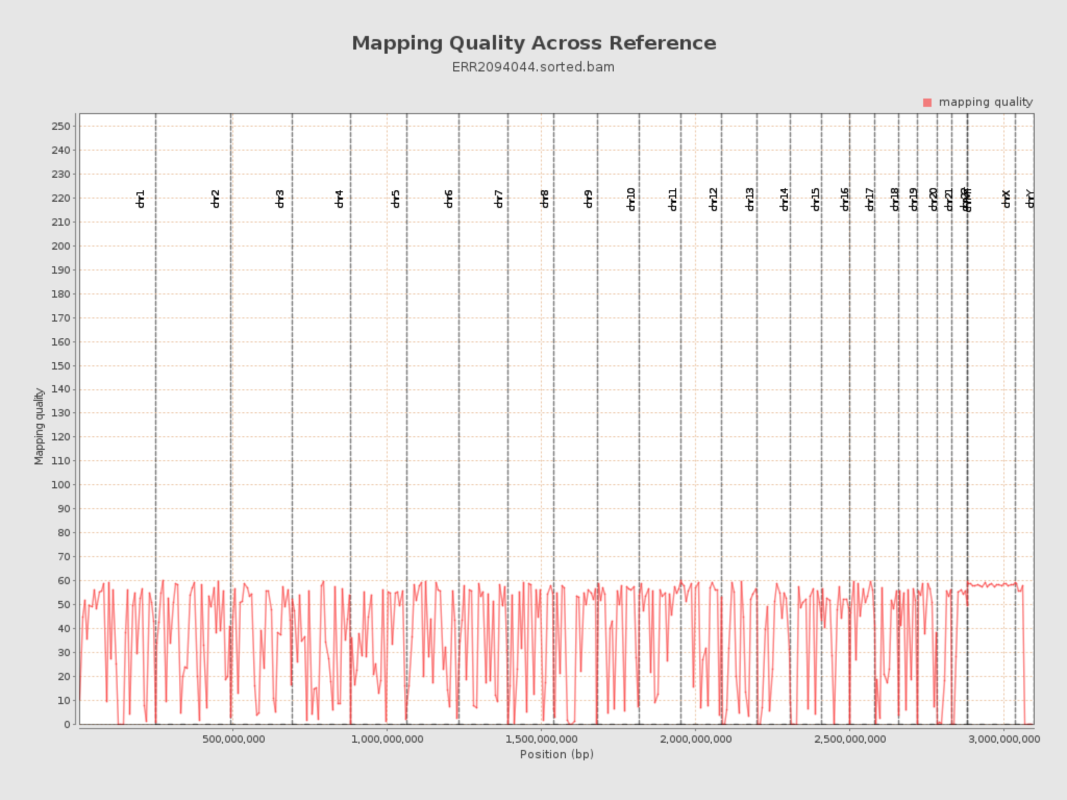
10. Results : Mapped Reads Clipping Profile



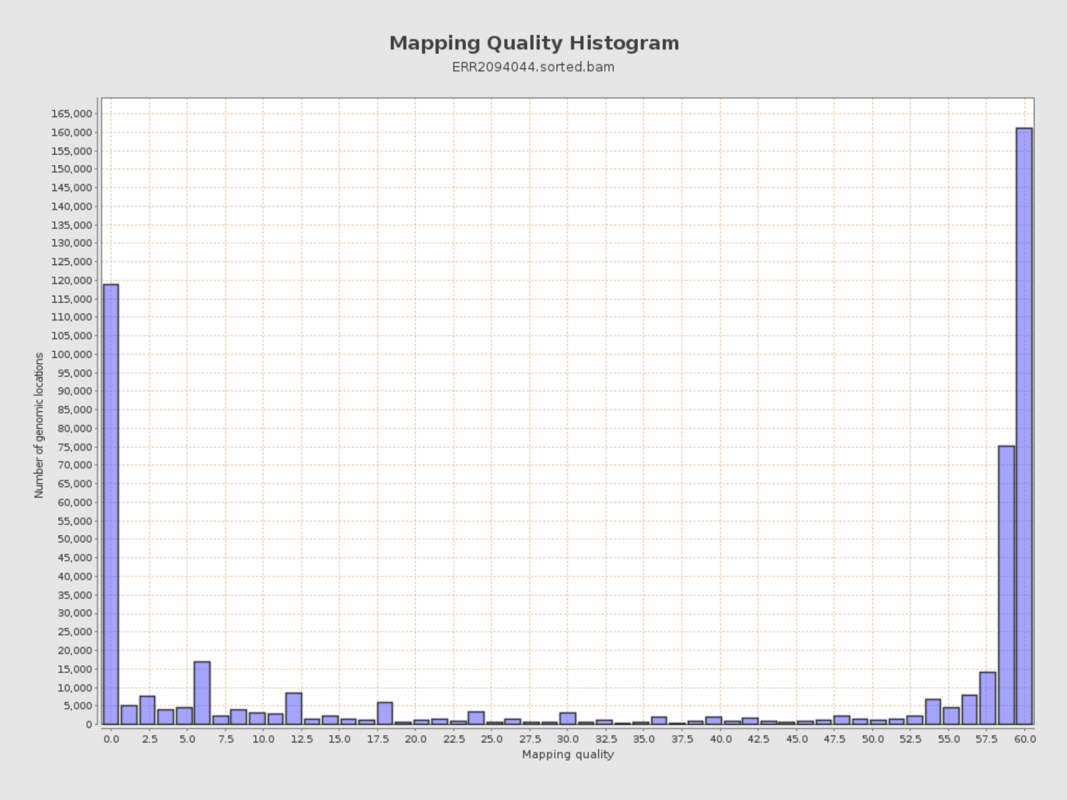
11. Results : Homopolymer Indels



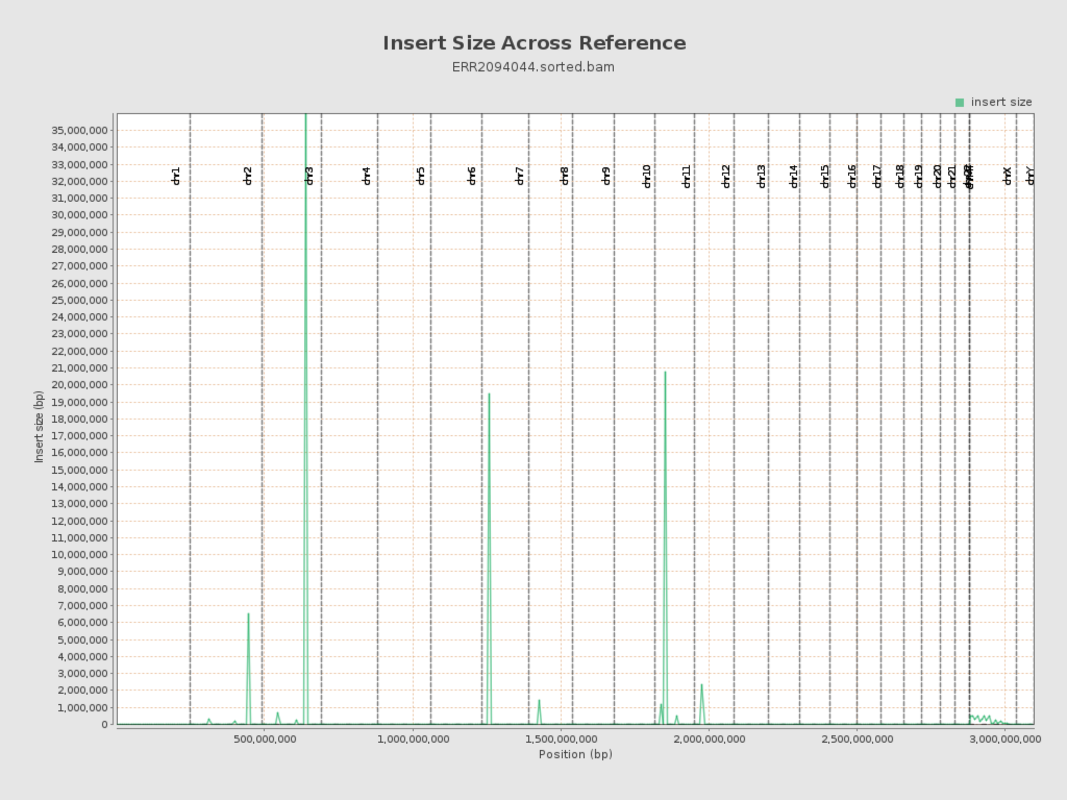
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram