Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:34:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094066.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_ERR2094066 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094066_1.fastq.gz ERR2094066_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:34:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	439,272
Mapped reads	424,682 / 96.68%
Unmapped reads	14,590 / 3.32%
Mapped paired reads	424,682 / 96.68%
Mapped reads, first in pair	213,309 / 48.56%
Mapped reads, second in pair	211,373 / 48.12%
Mapped reads, both in pair	421,870 / 96.04%
Mapped reads, singletons	2,812 / 0.64%
Secondary alignments	0
Supplementary alignments	14,876 / 3.39%
Read min/max/mean length	30 / 151 / 142.09
Duplicated reads (estimated)	409,204 / 93.16%
Duplication rate	50.25%
Clipped reads	160,062 / 36.44%

2.2. ACGT Content

Number/percentage of A's	14,578,421 / 26.33%
Number/percentage of C's	13,152,287 / 23.75%
Number/percentage of T's	13,901,823 / 25.1%
Number/percentage of G's	13,742,079 / 24.82%
Number/percentage of N's	656 / 0%

GC Percentage	48.57%

2.3. Coverage

Mean	0.0183
Standard Deviation	5.4633

2.4. Mapping Quality

Mean Mapping Quality	36.74

2.5. Insert size

Mean	347,564.6
Standard Deviation	5,311,352.52
P25/Median/P75	138 / 168 / 198

2.6. Mismatches and indels

General error rate	3.8%
Mismatches	2,029,648
Insertions	31,660
Mapped reads with at least one insertion	7.36%
Deletions	165,510
Mapped reads with at least one deletion	37.28%
Homopolymer indels	29.6%

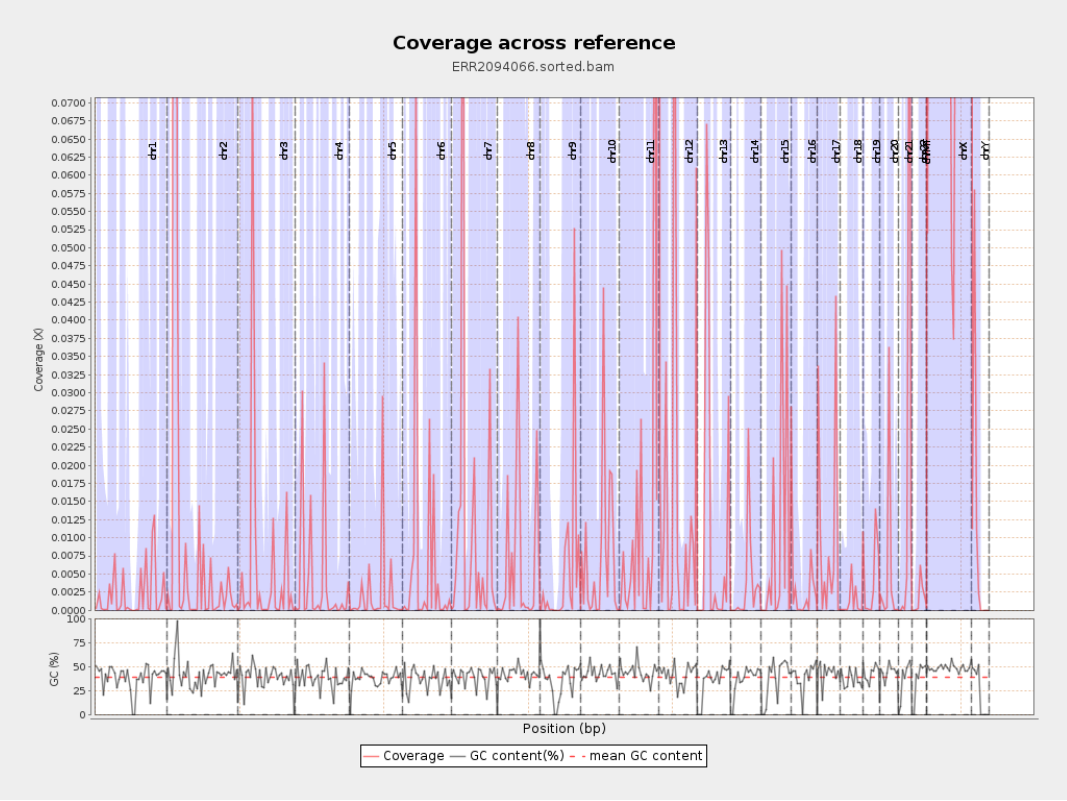
2.7. Chromosome stats

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

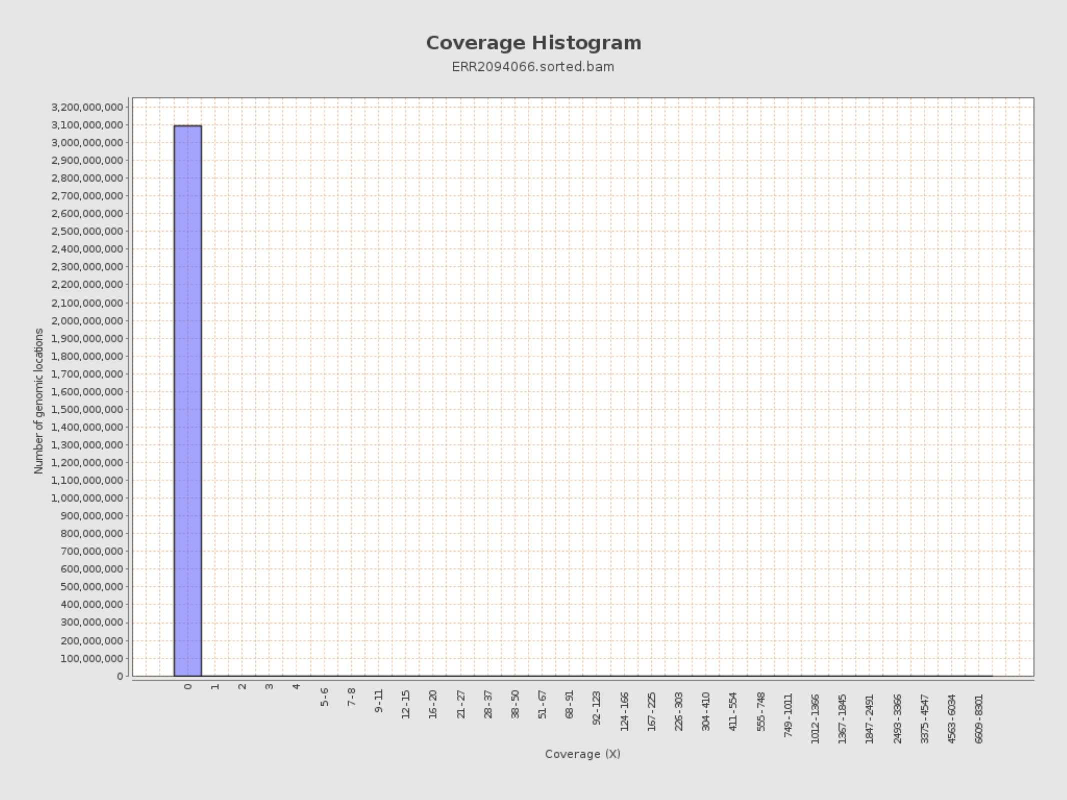
		bases	**coverage**	**deviation**
chr1	249250621	535302	0.0021	0.8142
chr2	243199373	3023524	0.0124	5.6614
chr3	198022430	1050025	0.0053	2.6648
chr4	191154276	762442	0.004	1.8301
chr5	180915260	406991	0.0022	1.4958
chr6	171115067	1098198	0.0064	3.7537
chr7	159138663	1819218	0.0114	4.8315
chr8	146364022	942327	0.0064	2.4317
chr9	141213431	726486	0.0051	2.4549
chr10	135534747	1016171	0.0075	2.649
chr11	135006516	2014818	0.0149	4.4515
chr12	133851895	1816877	0.0136	5.3477
chr13	115169878	1209573	0.0105	3.3897
chr14	107349540	381418	0.0036	1.5384
chr15	102531392	974378	0.0095	3.3357
chr16	90354753	297379	0.0033	1.4484
chr17	81195210	819521	0.0101	3.5883
chr18	78077248	90940	0.0012	0.511
chr19	59128983	227340	0.0038	1.082
chr20	63025520	327606	0.0052	1.8511
chr21	48129895	945081	0.0196	8.4936
chr22	51304566	87981	0.0017	0.4333
chrMT	16571	2133396	128.7427	606.3182
chrX	155270560	33186078	0.2137	18.2849

chrY	59373566	615862	0.0104	3.3486

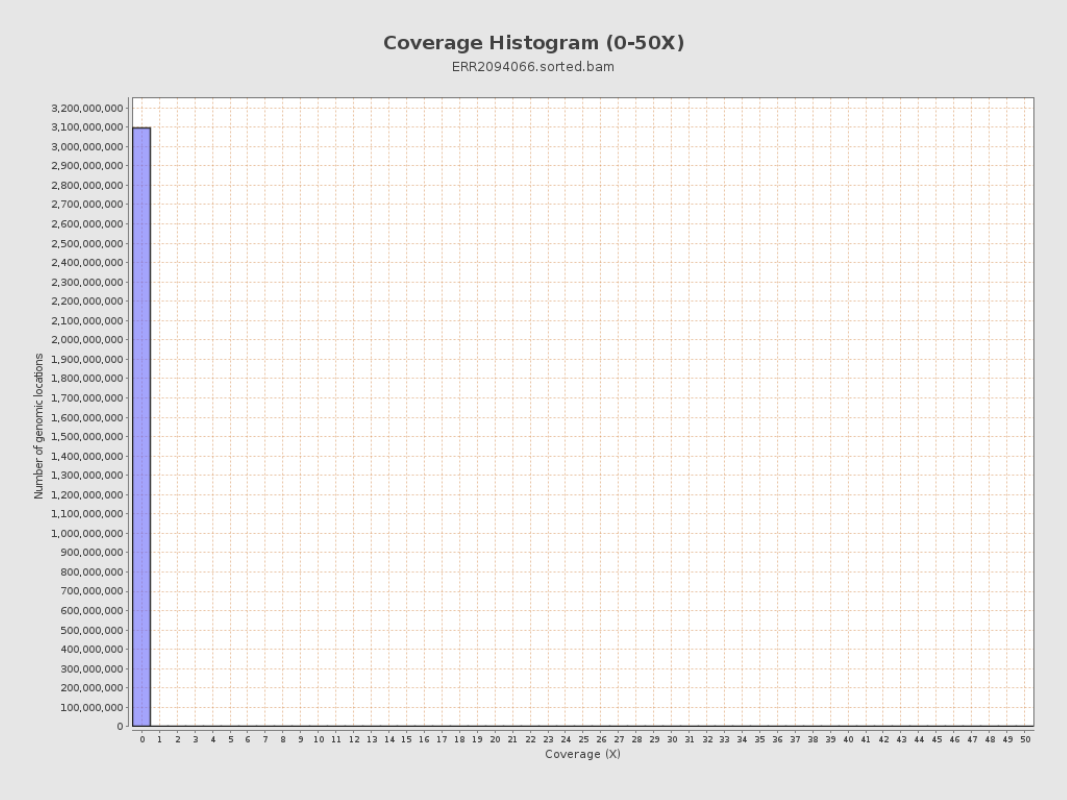
3. Results : Coverage across reference



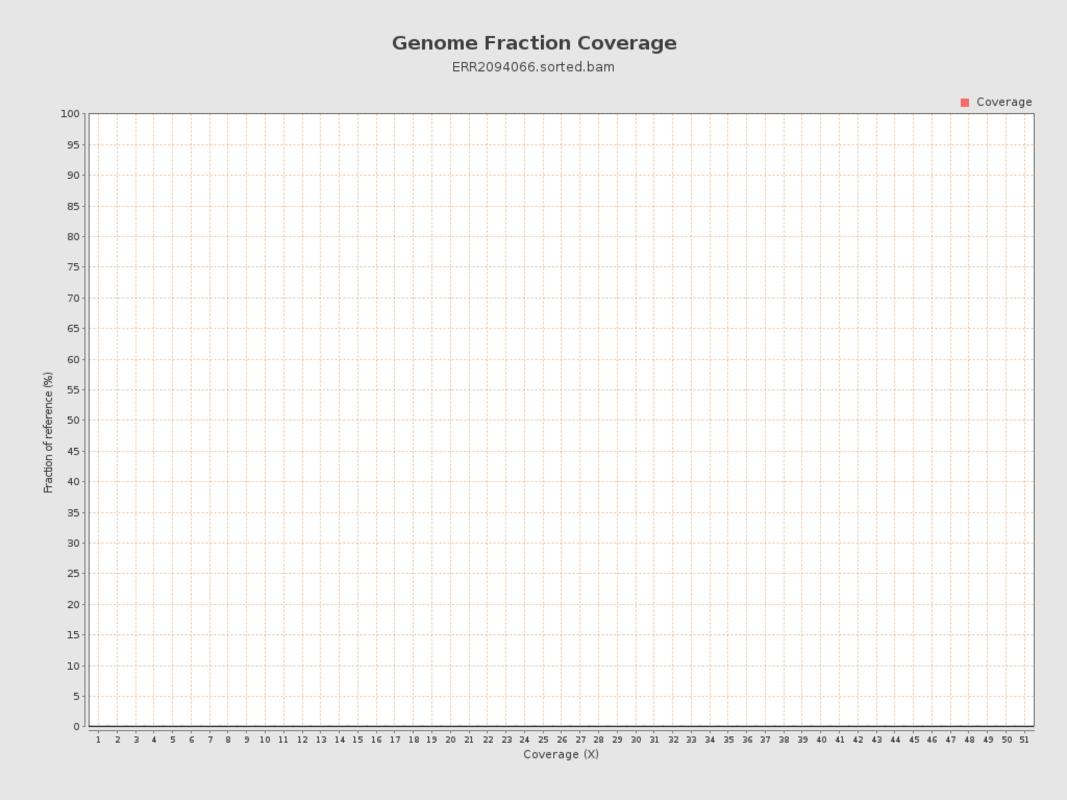
4. Results : Coverage Histogram



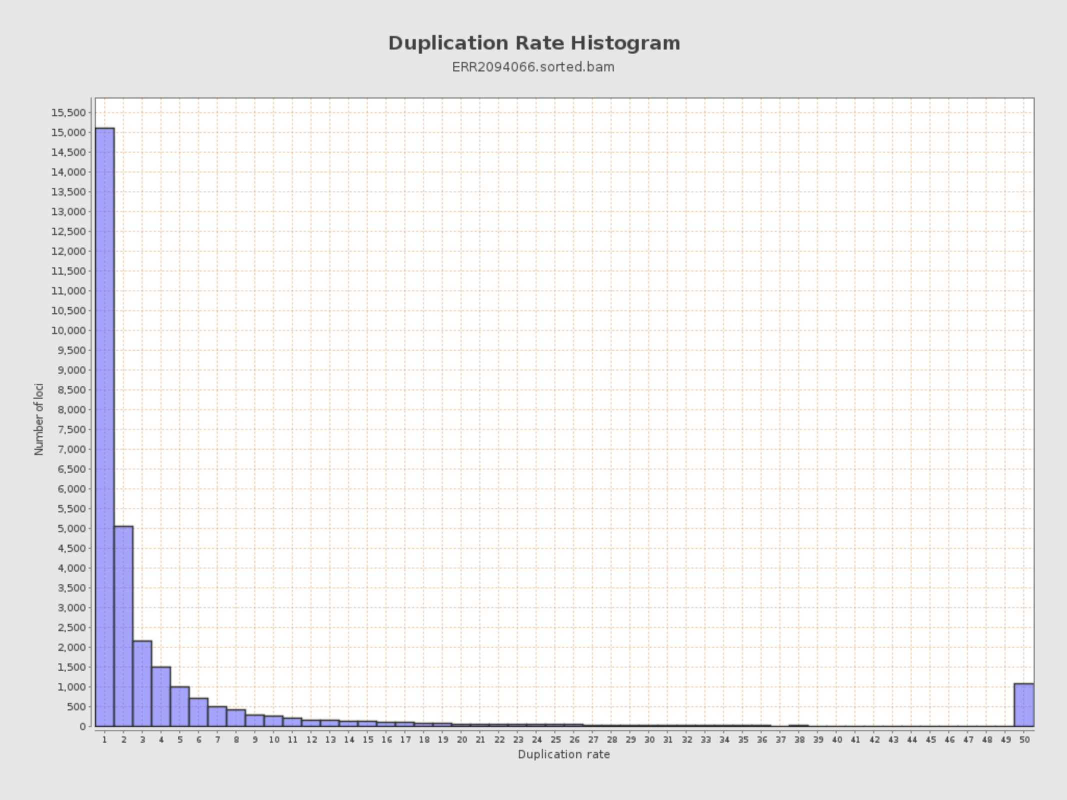
5. Results : Coverage Histogram (0-50X)



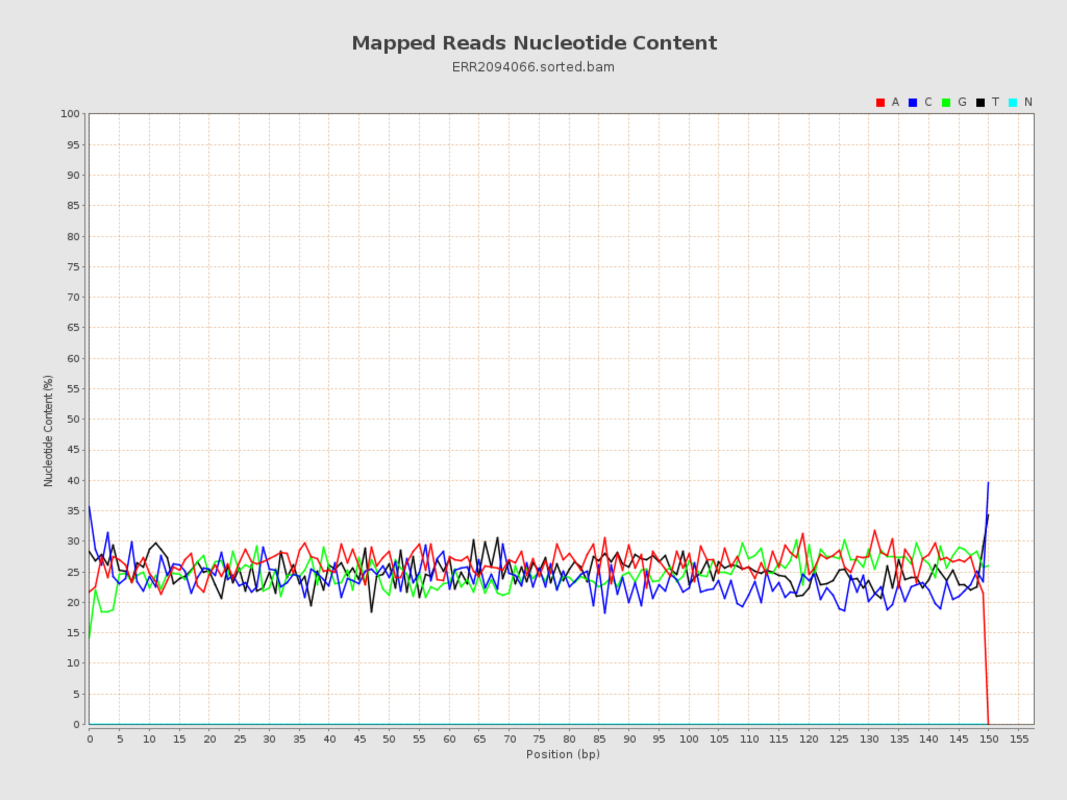
6. Results : Genome Fraction Coverage



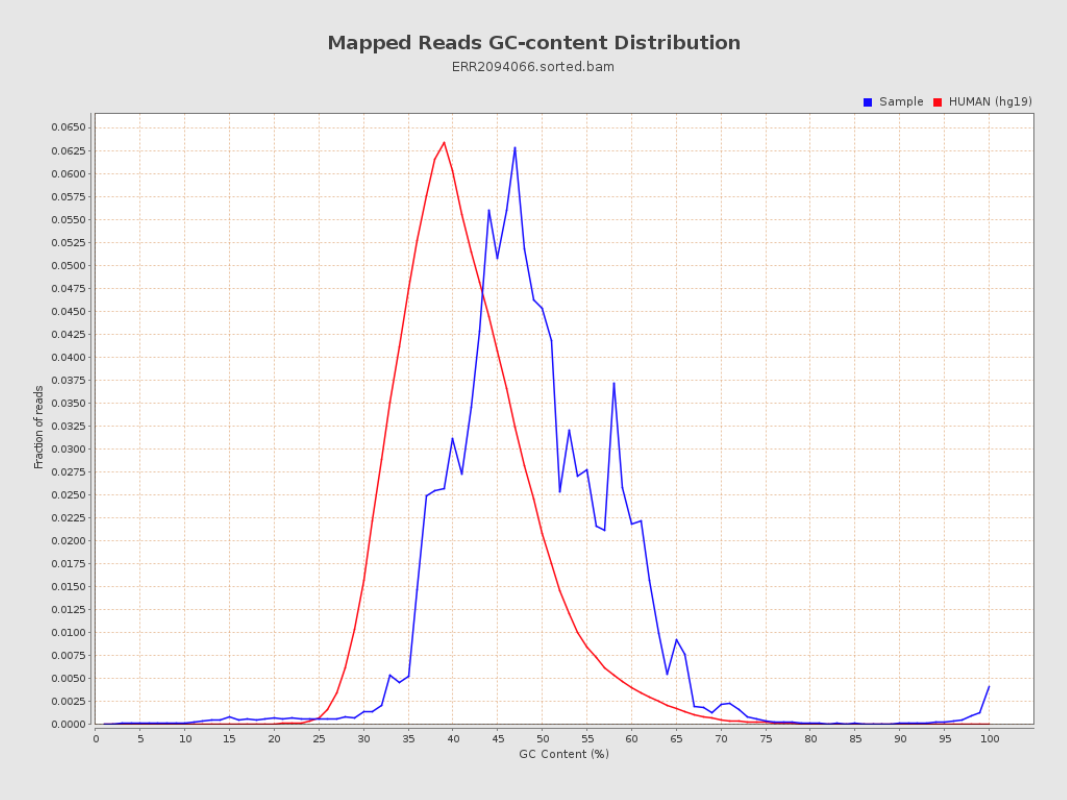
7. Results : Duplication Rate Histogram



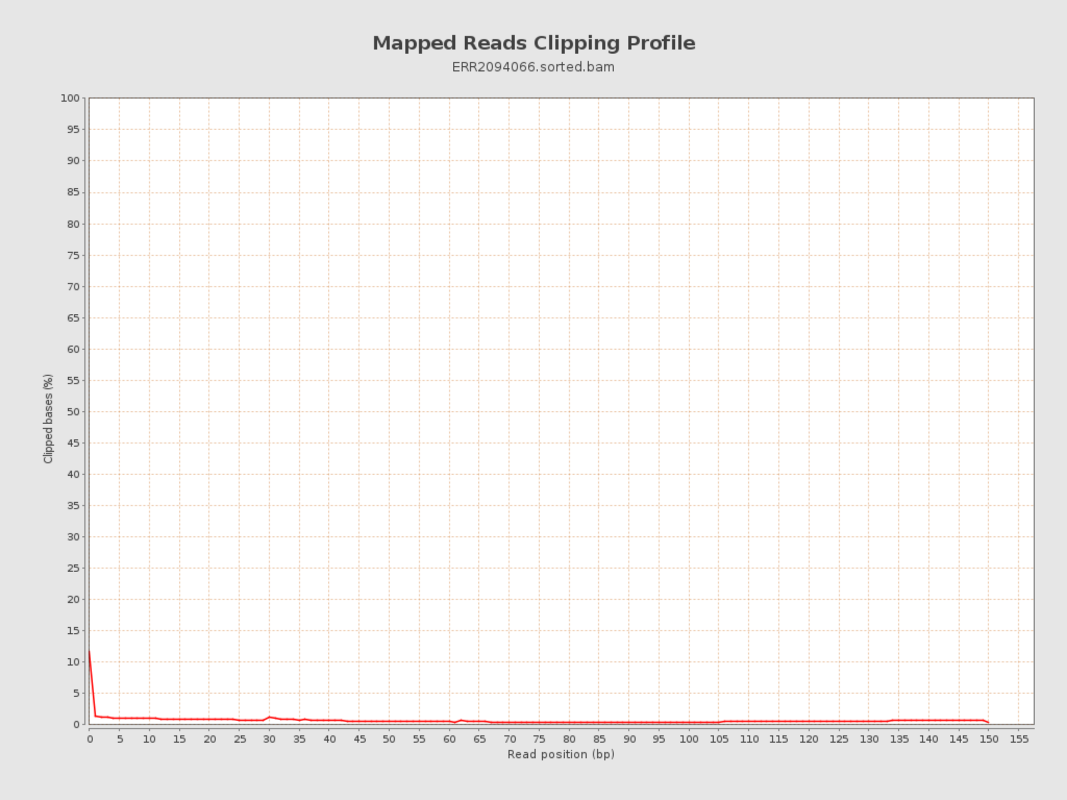
8. Results : Mapped Reads Nucleotide Content



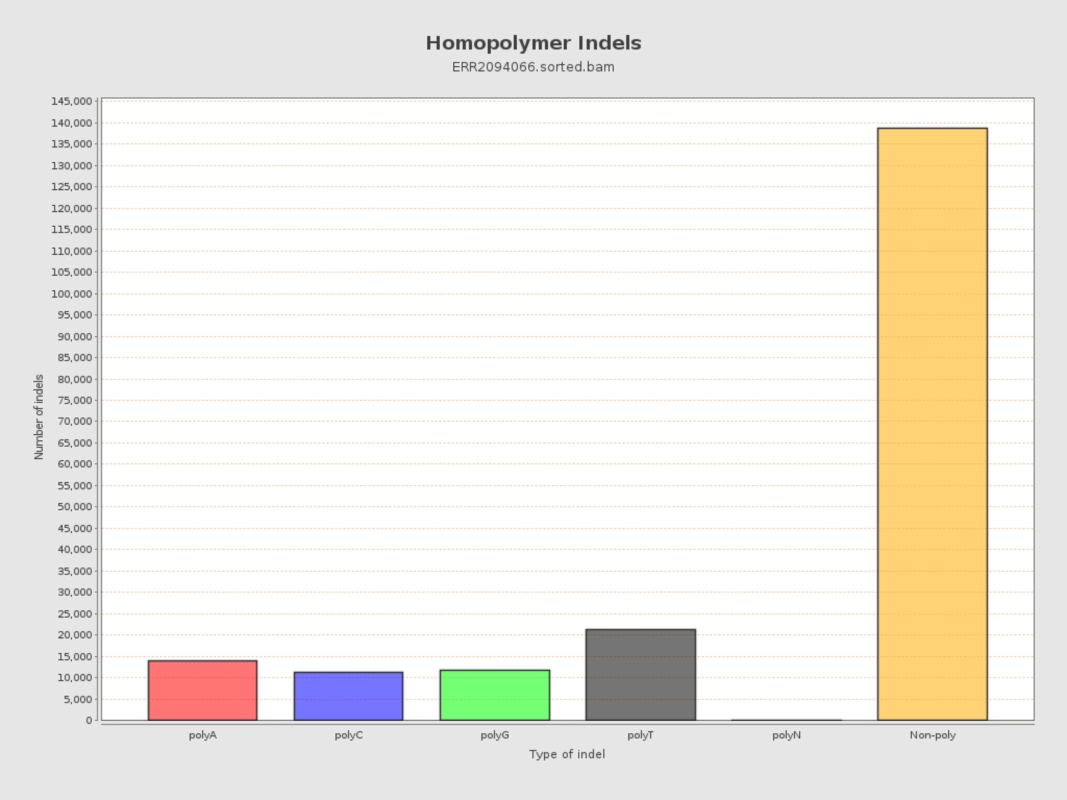
9. Results : Mapped Reads GC-content Distribution



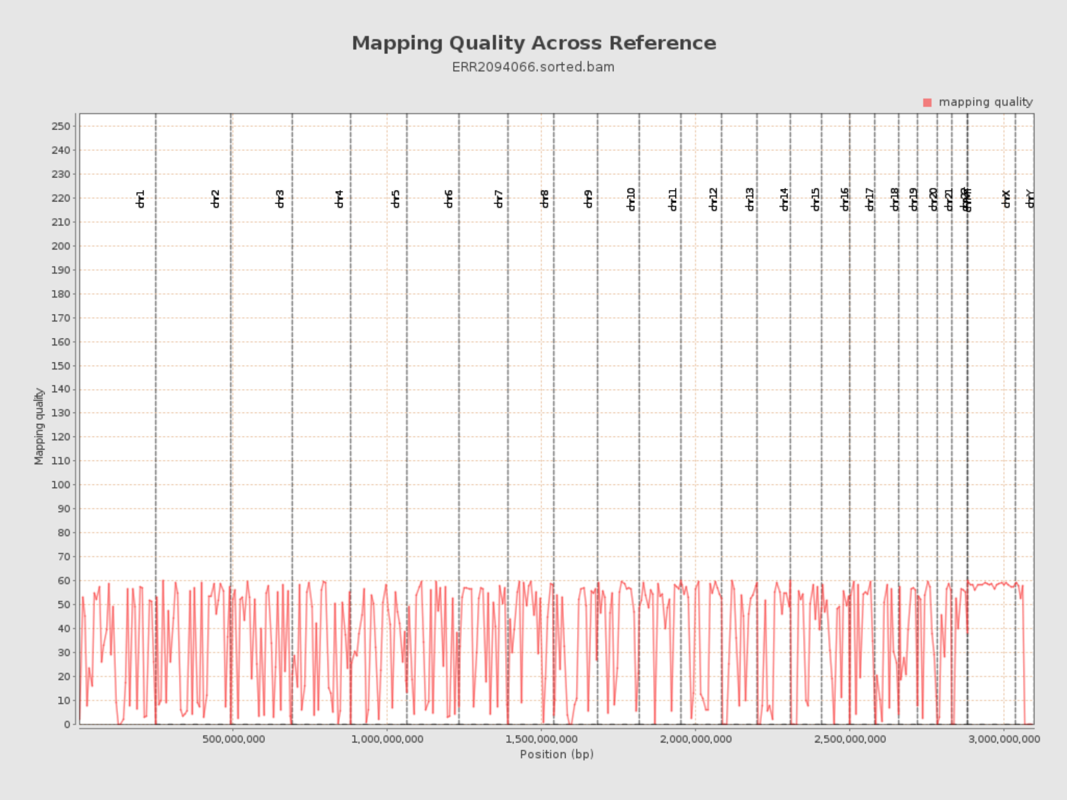
10. Results : Mapped Reads Clipping Profile



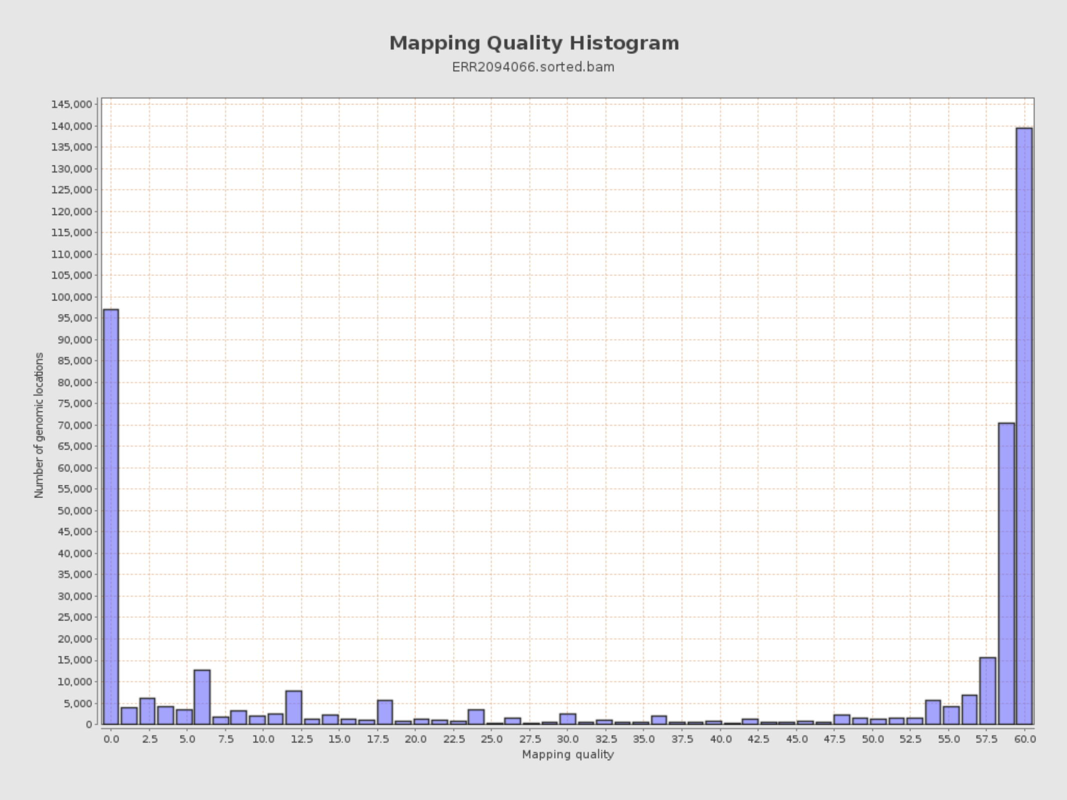
11. Results : Homopolymer Indels



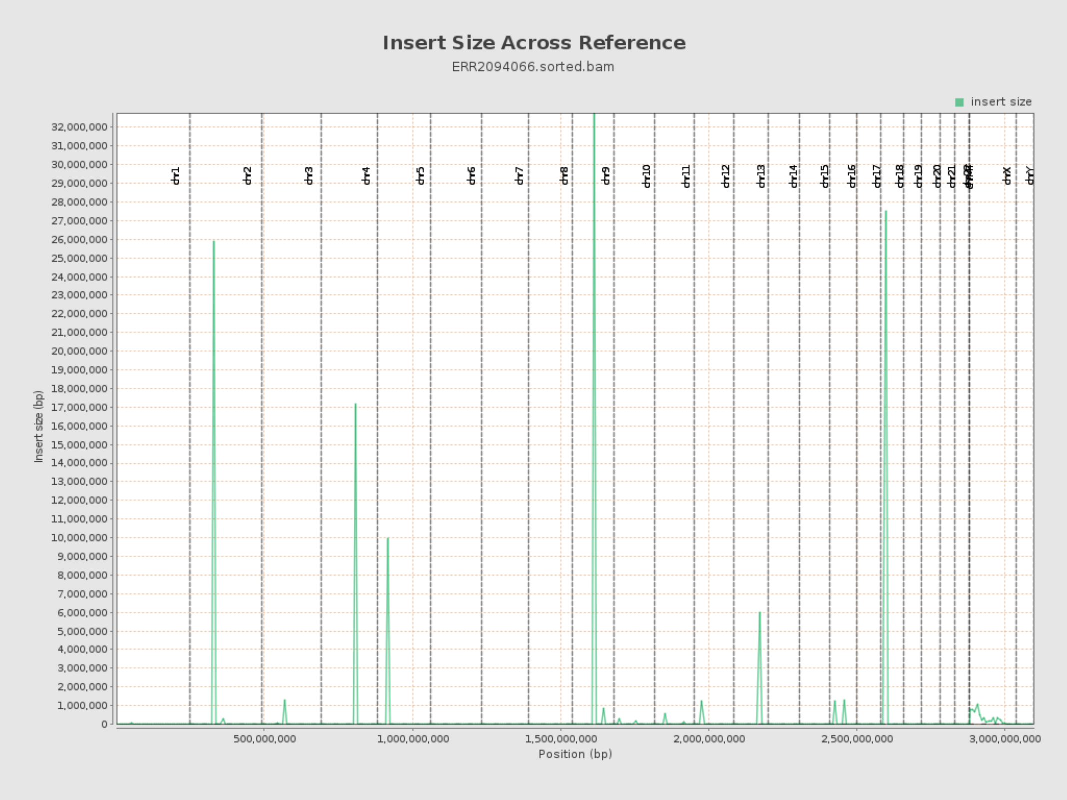
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram