Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:25:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093978.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_ERR2093978 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093978_1.fastq.gz ERR2093978_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:24:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	368,736
Mapped reads	353,467 / 95.86%
Unmapped reads	15,269 / 4.14%
Mapped paired reads	353,467 / 95.86%
Mapped reads, first in pair	177,656 / 48.18%
Mapped reads, second in pair	175,811 / 47.68%
Mapped reads, both in pair	350,602 / 95.08%
Mapped reads, singletons	2,865 / 0.78%
Secondary alignments	0
Supplementary alignments	21,620 / 5.86%
Read min/max/mean length	30 / 151 / 141.77
Duplicated reads (estimated)	333,362 / 90.41%
Duplication rate	50.28%
Clipped reads	175,399 / 47.57%

2.2. ACGT Content

Number/percentage of A's	11,746,637 / 26.32%
Number/percentage of C's	10,491,799 / 23.51%
Number/percentage of T's	11,108,779 / 24.9%
Number/percentage of G's	11,274,654 / 25.27%
Number/percentage of N's	406 / 0%

GC Percentage	48.78%

2.3. Coverage

Mean	0.0147
Standard Deviation	2.8248

2.4. Mapping Quality

Mean Mapping Quality	40.44

2.5. Insert size

Mean	1,017,563.8
Standard Deviation	9,174,504.23
P25/Median/P75	129 / 165 / 201

2.6. Mismatches and indels

General error rate	3.54%
Mismatches	1,532,065
Insertions	23,843
Mapped reads with at least one insertion	6.6%
Deletions	122,677
Mapped reads with at least one deletion	33.36%
Homopolymer indels	29.2%

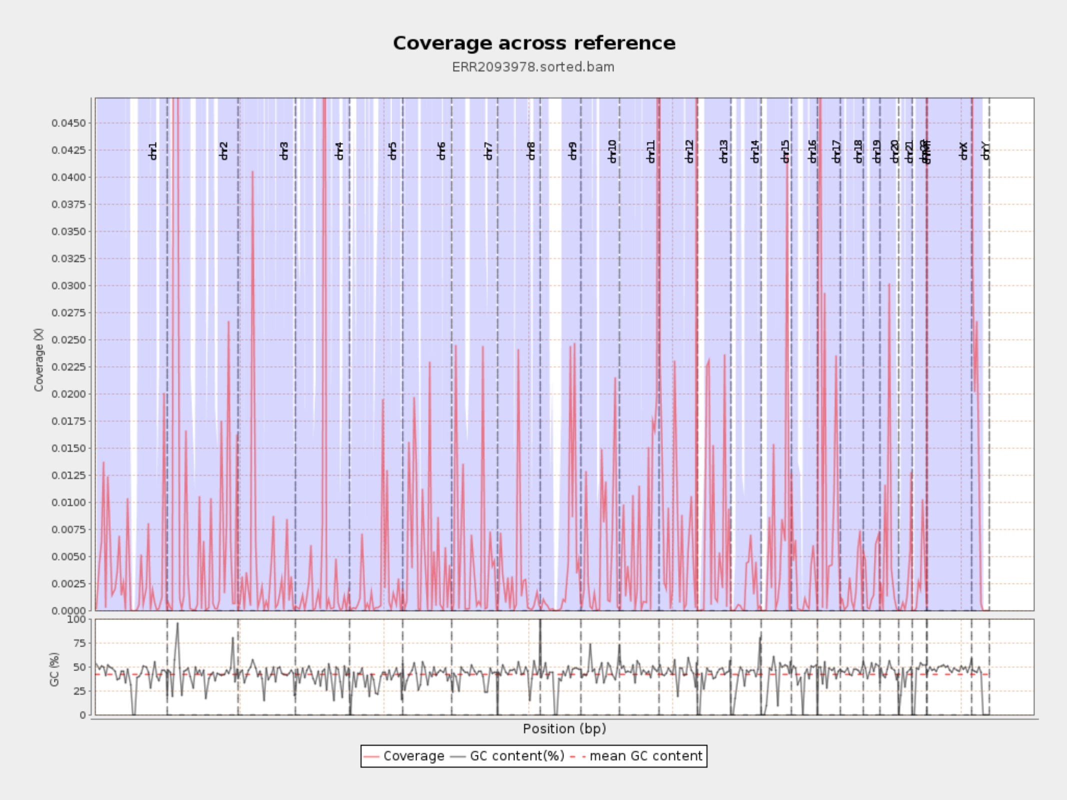
2.7. Chromosome stats

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

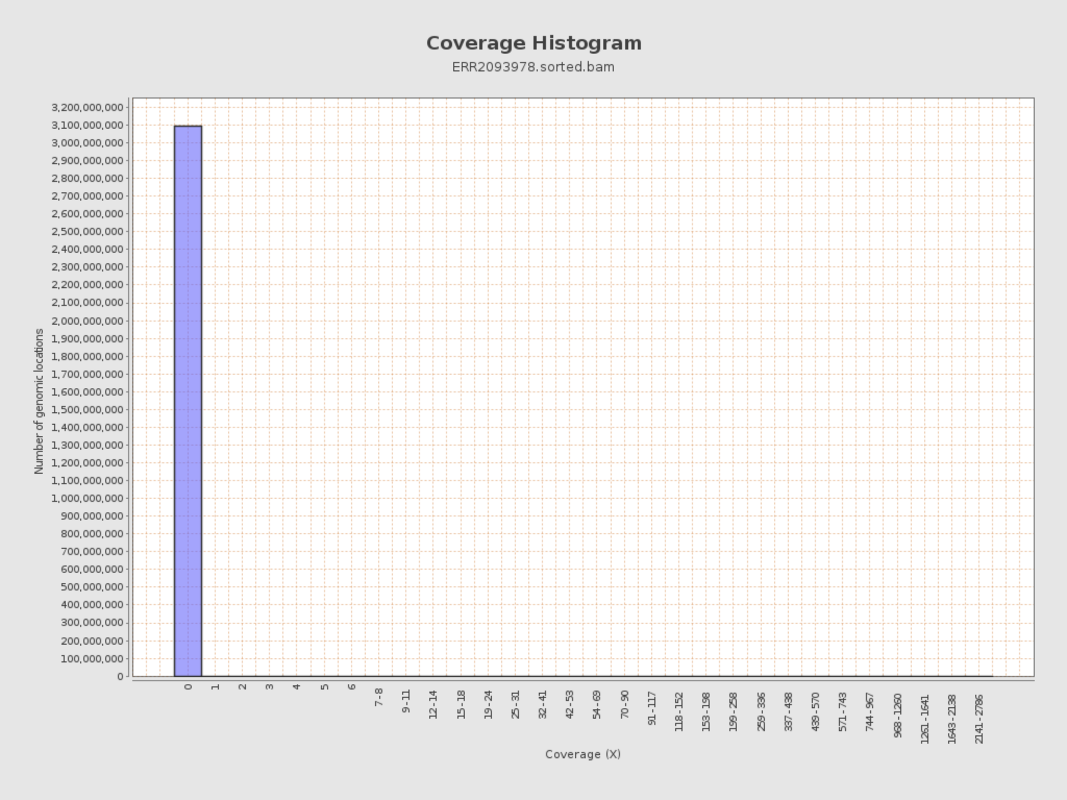
		bases	**coverage**	**deviation**
chr1	249250621	885765	0.0036	1.1486
chr2	243199373	2431788	0.01	3.0301
chr3	198022430	716252	0.0036	1.0806
chr4	191154276	863282	0.0045	1.43
chr5	180915260	414564	0.0023	1.169
chr6	171115067	936137	0.0055	1.5529
chr7	159138663	766983	0.0048	1.5316
chr8	146364022	414569	0.0028	1.0142
chr9	141213431	579201	0.0041	1.1796
chr10	135534747	655899	0.0048	1.4733
chr11	135006516	1002094	0.0074	1.7677
chr12	133851895	1048699	0.0078	1.9286
chr13	115169878	819537	0.0071	1.911
chr14	107349540	182564	0.0017	0.5764
chr15	102531392	677606	0.0066	1.7414
chr16	90354753	253743	0.0028	0.7906
chr17	81195210	1246699	0.0154	3.4137
chr18	78077248	161875	0.0021	0.5285
chr19	59128983	176524	0.003	0.7914
chr20	63025520	388058	0.0062	2.0604
chr21	48129895	121834	0.0025	0.4893
chr22	51304566	134473	0.0026	0.6243
chrMT	16571	1242523	74.9818	314.5207
chrX	155270560	28680180	0.1847	9.7968

chrY	59373566	640918	0.0108	1.6263

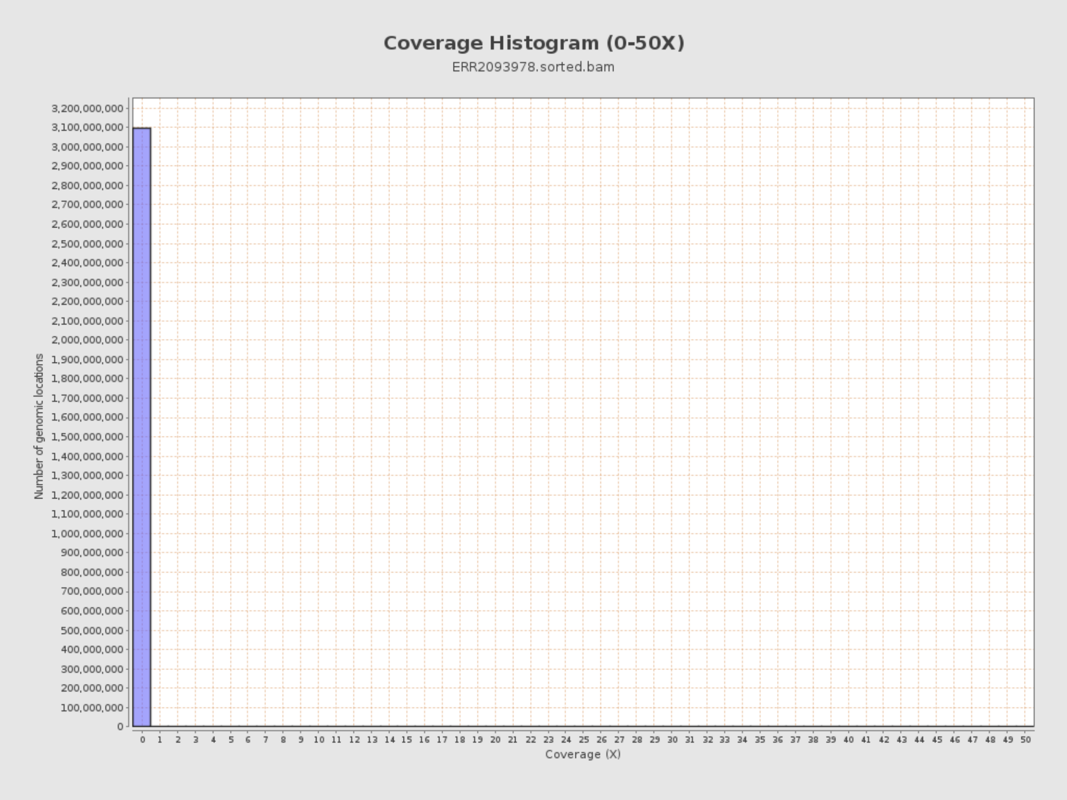
3. Results : Coverage across reference



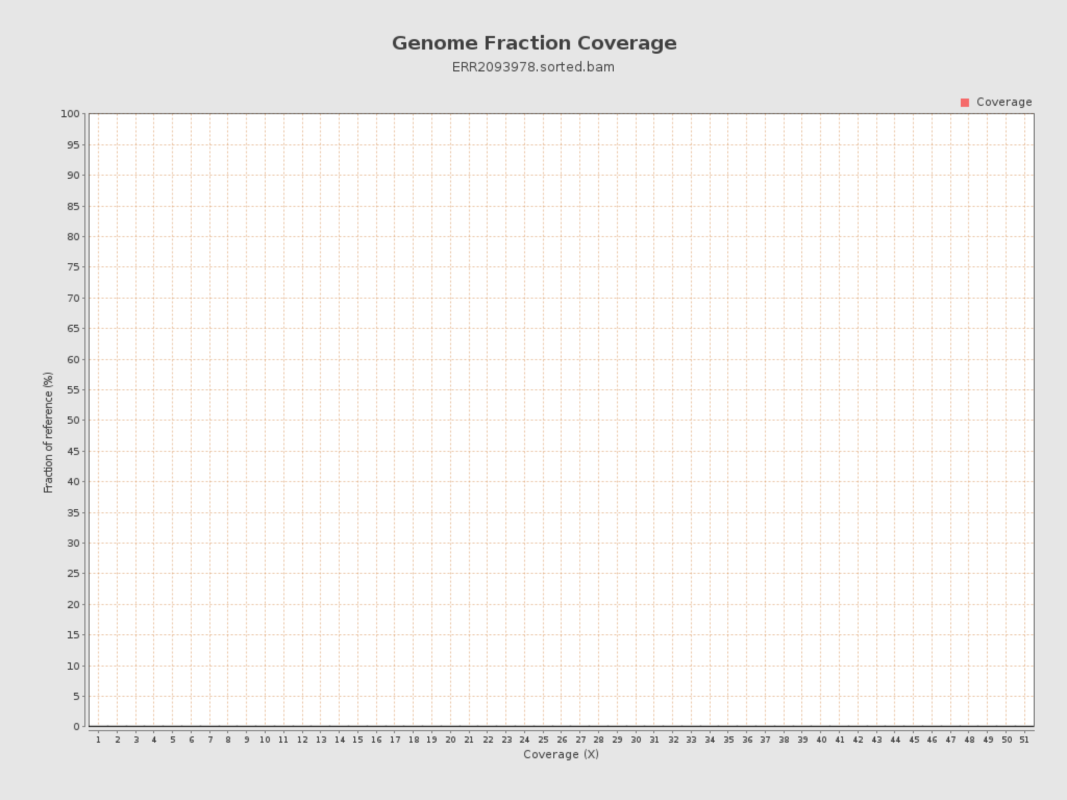
4. Results : Coverage Histogram



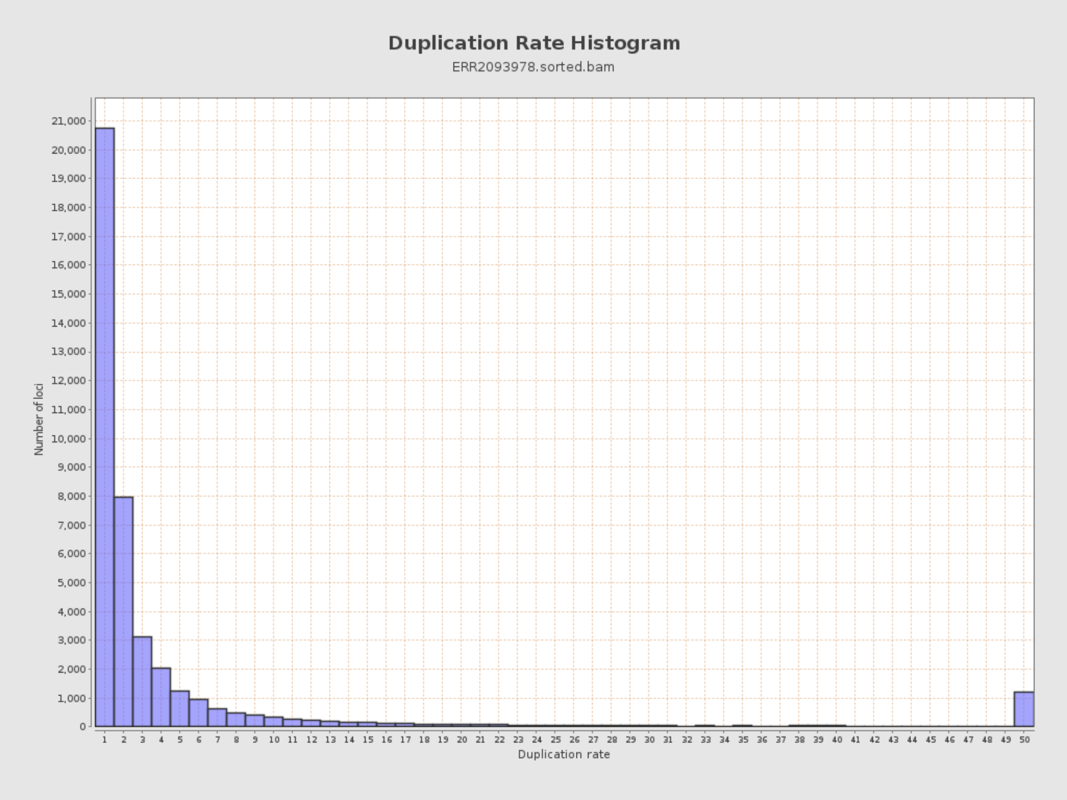
5. Results : Coverage Histogram (0-50X)



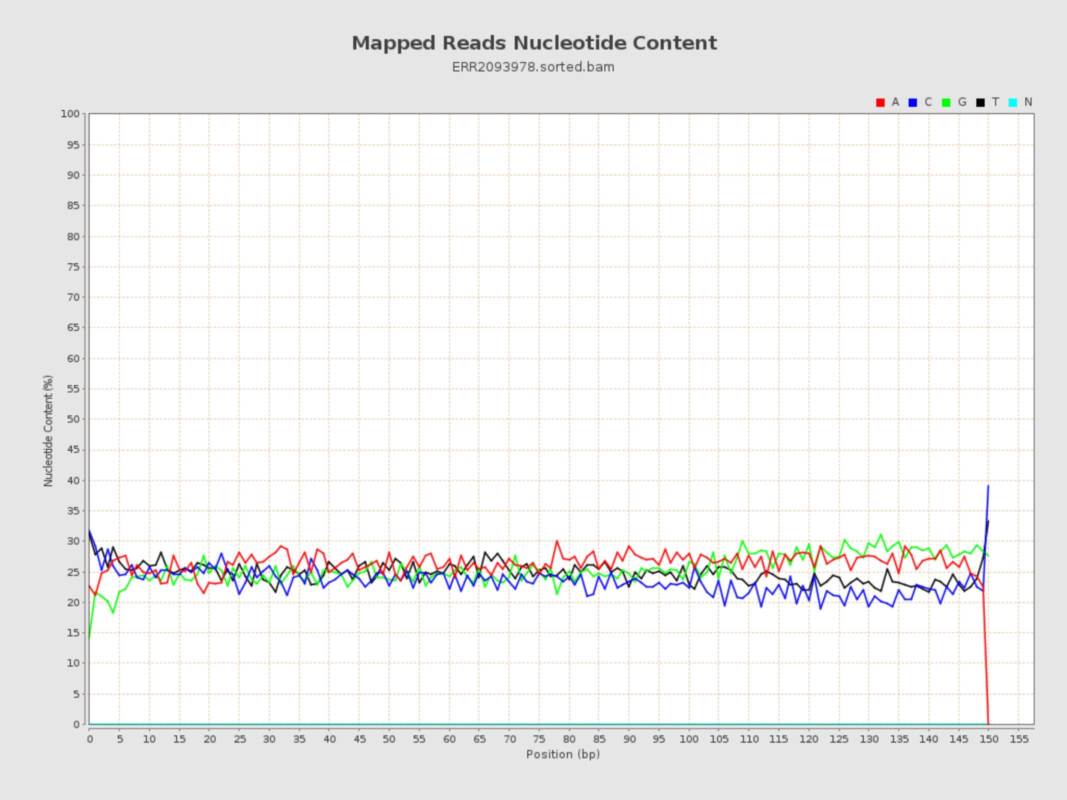
6. Results : Genome Fraction Coverage



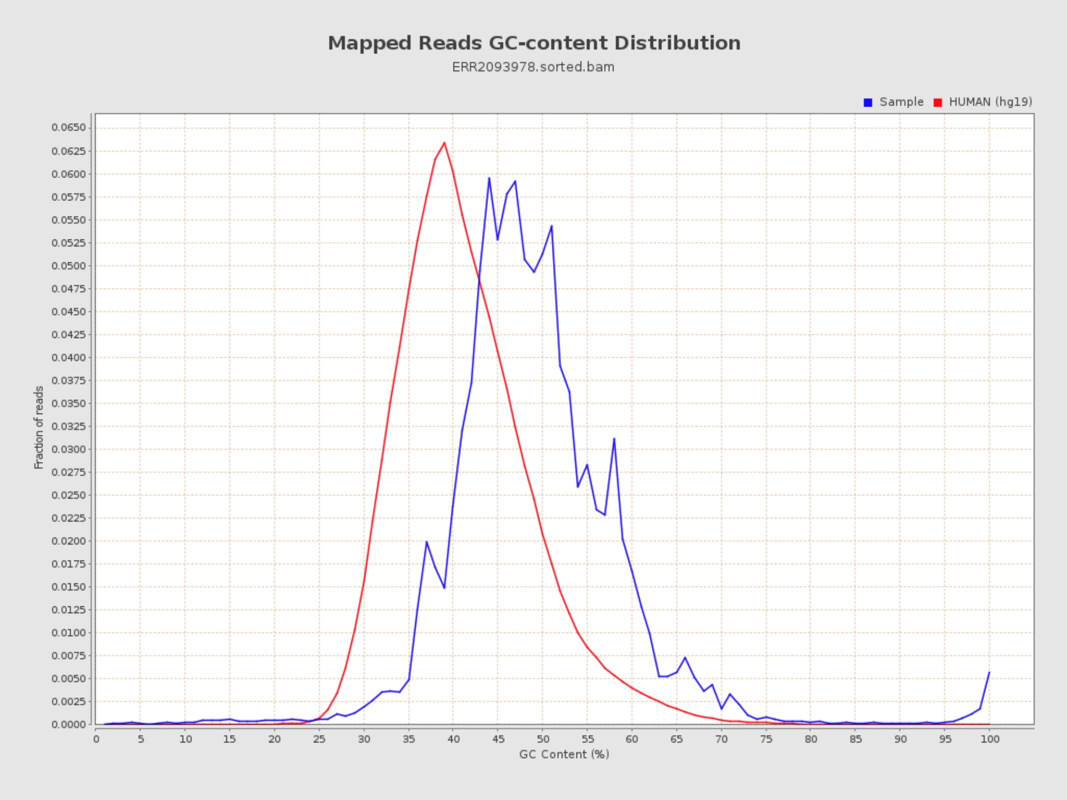
7. Results : Duplication Rate Histogram



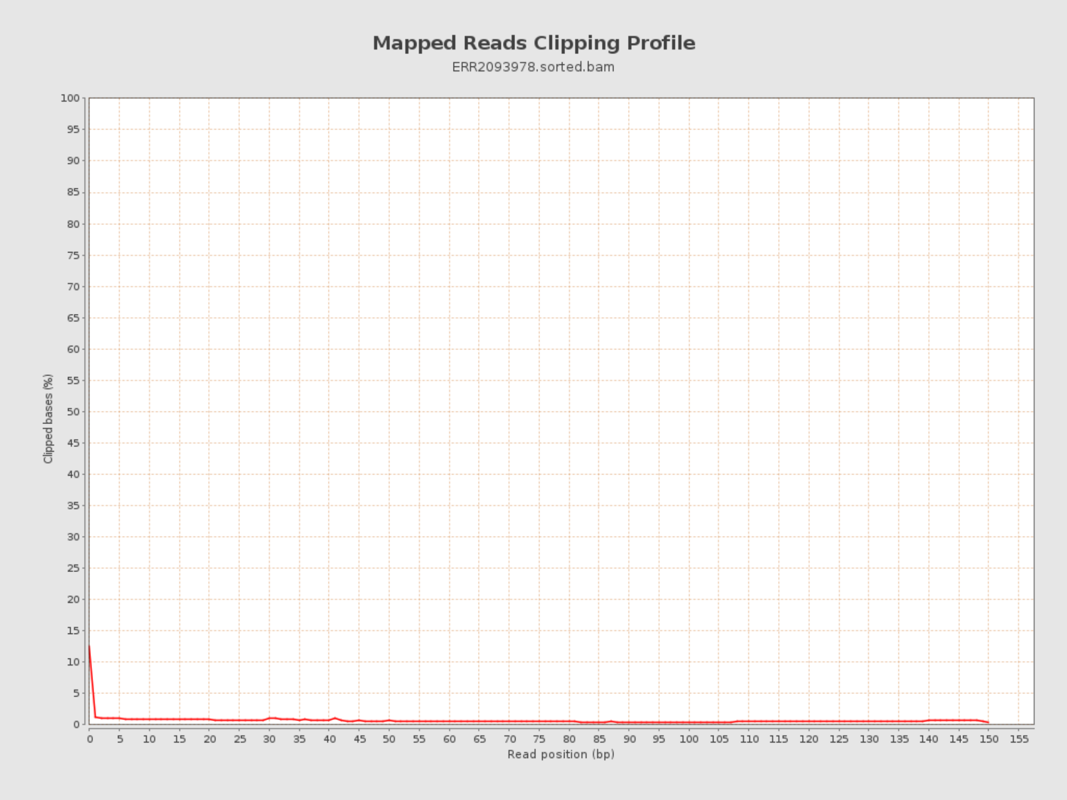
8. Results : Mapped Reads Nucleotide Content



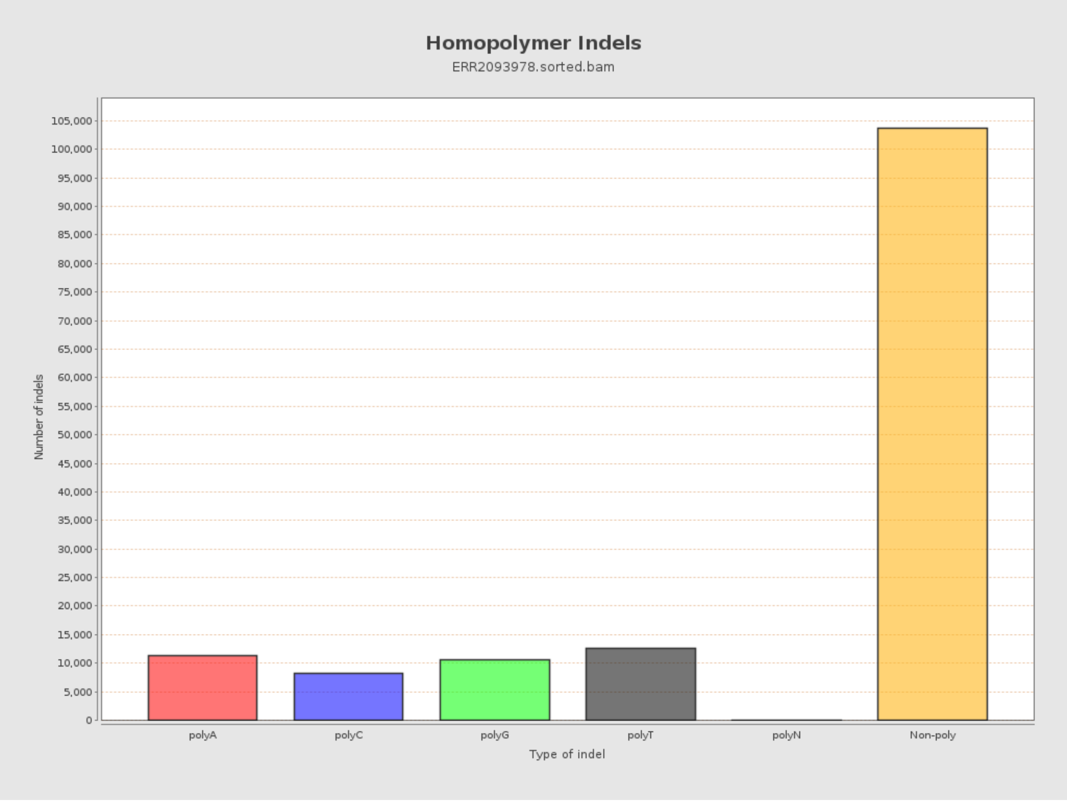
9. Results : Mapped Reads GC-content Distribution



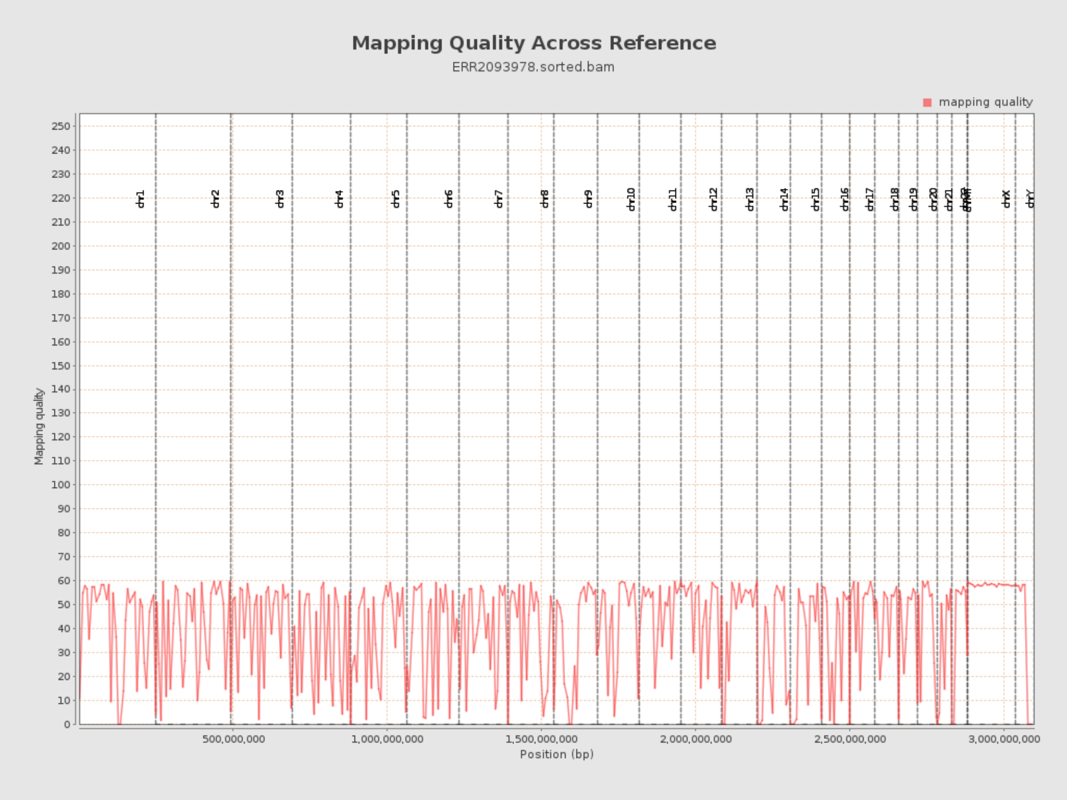
10. Results : Mapped Reads Clipping Profile



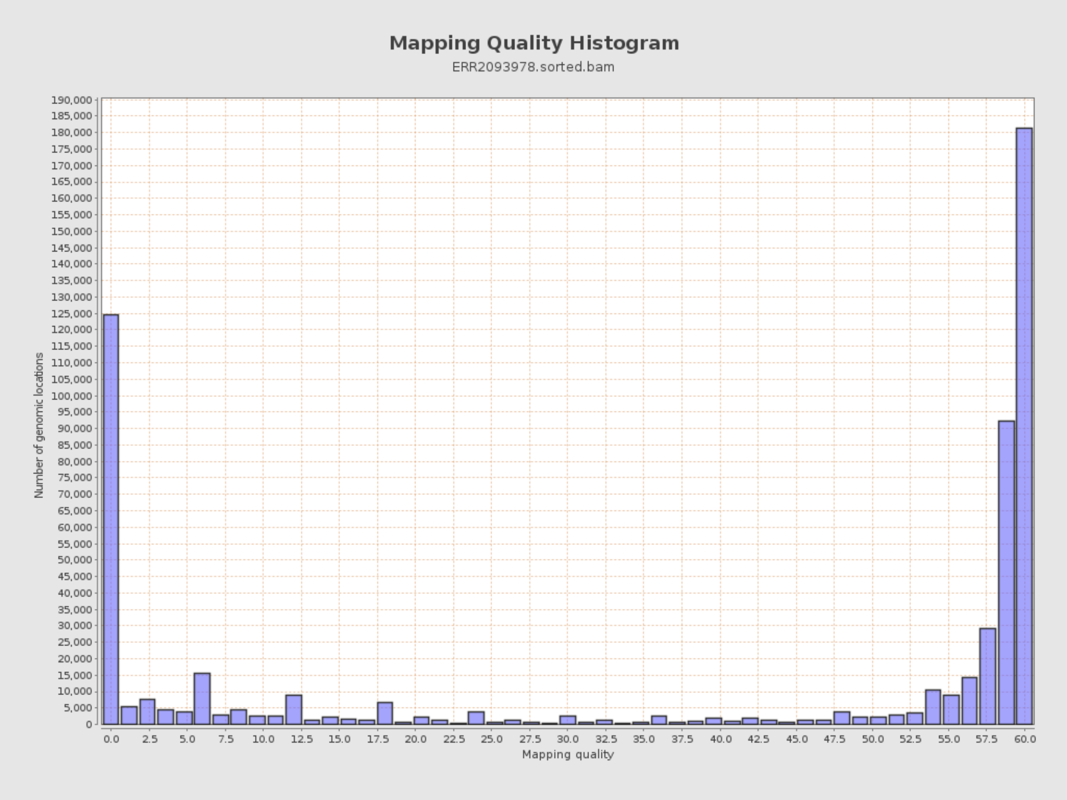
11. Results : Homopolymer Indels



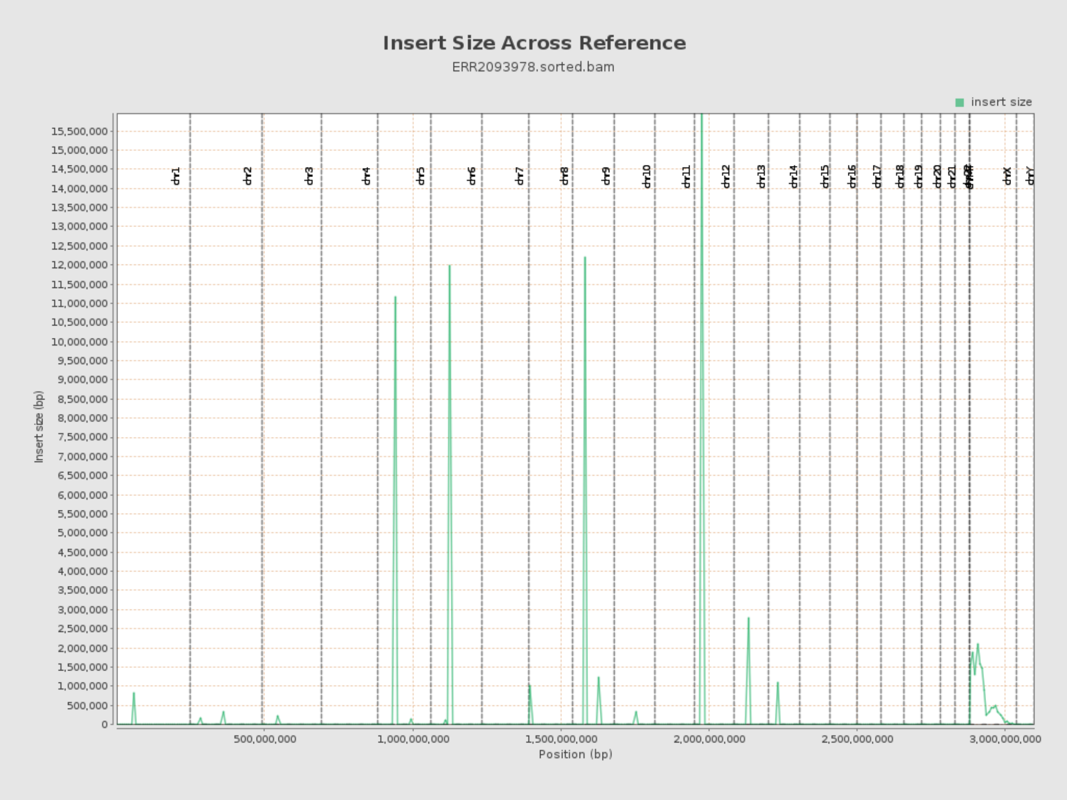
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram