Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/08/26 19:10:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093974.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_ERR2093974 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093974_1.fastq.gz ERR2093974_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:10:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	480,768
Mapped reads	188,447 / 39.2%
Unmapped reads	292,321 / 60.8%
Mapped paired reads	188,447 / 39.2%
Mapped reads, first in pair	93,299 / 19.41%
Mapped reads, second in pair	95,148 / 19.79%
Mapped reads, both in pair	184,468 / 38.37%
Mapped reads, singletons	3,979 / 0.83%
Secondary alignments	0
Supplementary alignments	6,573 / 1.37%
Read min/max/mean length	30 / 151 / 88.95
Duplicated reads (estimated)	188,359 / 39.18%
Duplication rate	36.72%
Clipped reads	94,894 / 19.74%

2.2. ACGT Content

Number/percentage of A's	6,361,332 / 25.76%
Number/percentage of C's	5,176,405 / 20.96%
Number/percentage of T's	6,930,832 / 28.06%
Number/percentage of G's	6,228,335 / 25.22%
Number/percentage of N's	337 / 0%

GC Percentage	46.18%

2.3. Coverage

Mean	0.008
Standard Deviation	16.4362

2.4. Mapping Quality

Mean Mapping Quality	22.69

2.5. Insert size

Mean	120,761.13
Standard Deviation	3,645,639.08
P25/Median/P75	177 / 208 / 237

2.6. Mismatches and indels

General error rate	2.25%
Mismatches	545,915
Insertions	3,687
Mapped reads with at least one insertion	1.81%
Deletions	12,865
Mapped reads with at least one deletion	6.68%
Homopolymer indels	35.23%

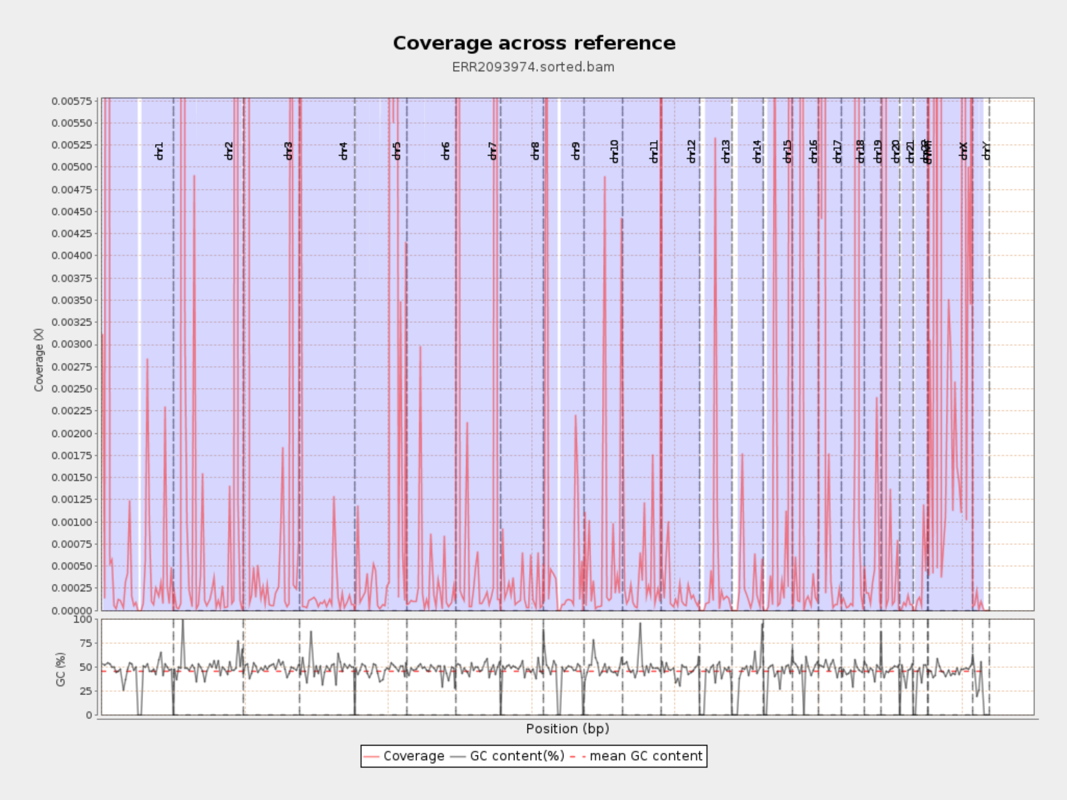
2.7. Chromosome stats

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

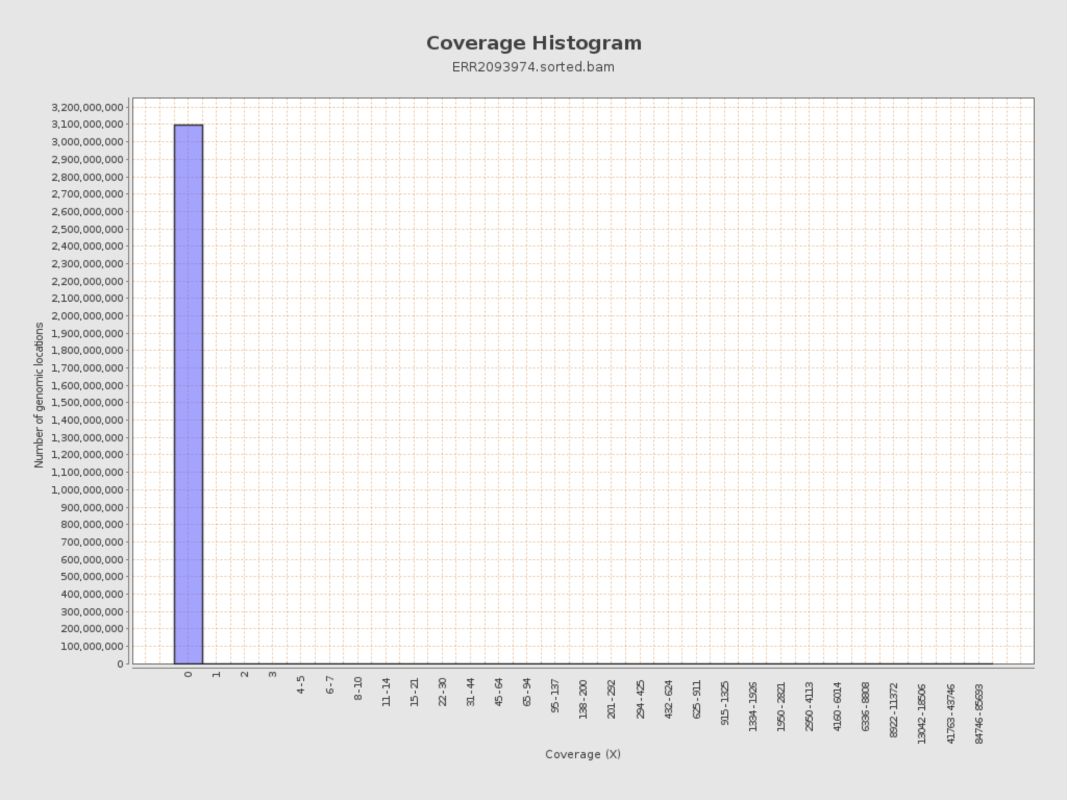
		bases	**coverage**	**deviation**
chr1	249250621	357575	0.0014	1.5311
chr2	243199373	775178	0.0032	2.0179
chr3	198022430	586478	0.003	1.9398
chr4	191154276	77802	0.0004	0.3135
chr5	180915260	796278	0.0044	3.1677
chr6	171115067	55032	0.0003	0.1425
chr7	159138663	396264	0.0025	1.541
chr8	146364022	37081	0.0003	0.0767
chr9	141213431	116536	0.0008	0.4846
chr10	135534747	97069	0.0007	0.3418
chr11	135006516	64287	0.0005	0.2016
chr12	133851895	29869	0.0002	0.0645
chr13	115169878	60504	0.0005	0.2938
chr14	107349540	31849	0.0003	0.1339
chr15	102531392	295463	0.0029	2.5717
chr16	90354753	181850	0.002	1.051
chr17	81195210	986128	0.0121	6.3378
chr18	78077248	2010456	0.0257	13.378
chr19	59128983	30546	0.0005	0.1713
chr20	63025520	1248888	0.0198	11.9599
chr21	48129895	3441	0.0001	0.0161
chr22	51304566	17540	0.0003	0.0778
chrMT	16571	12972009	782.8139	6,814.7197
chrX	155270560	3503462	0.0226	12.676

chrY	59373566	3184	0.0001	0.0238

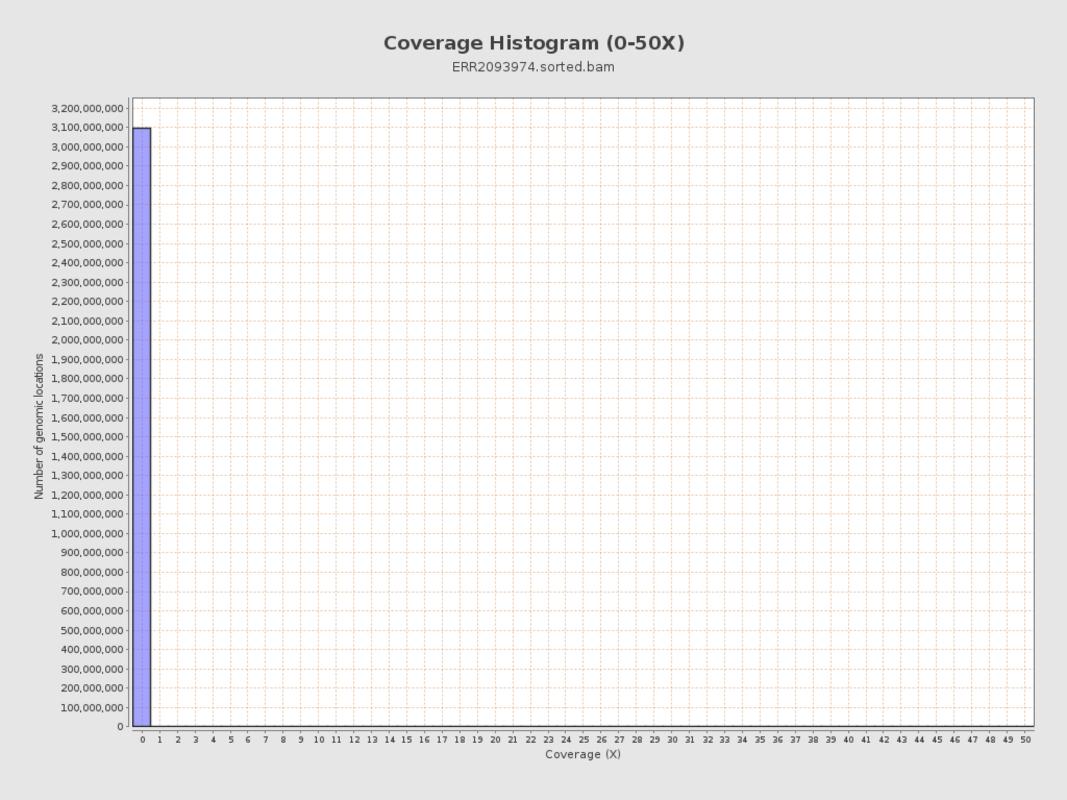
3. Results : Coverage across reference



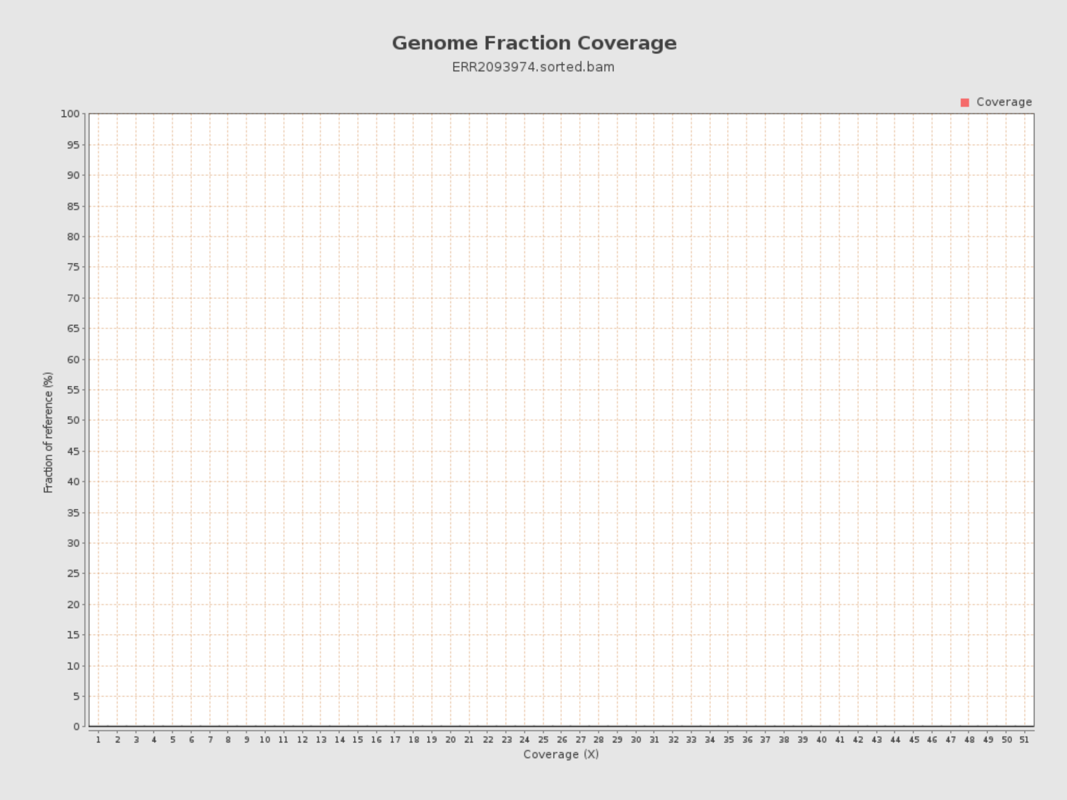
4. Results : Coverage Histogram



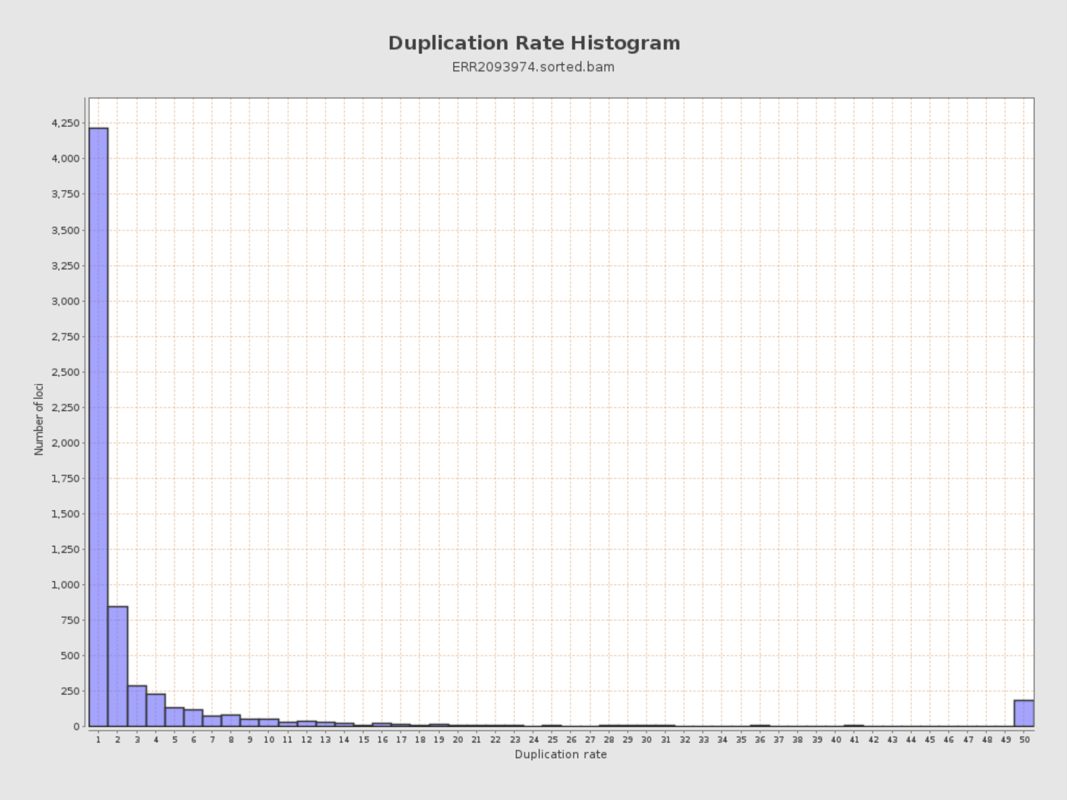
5. Results : Coverage Histogram (0-50X)



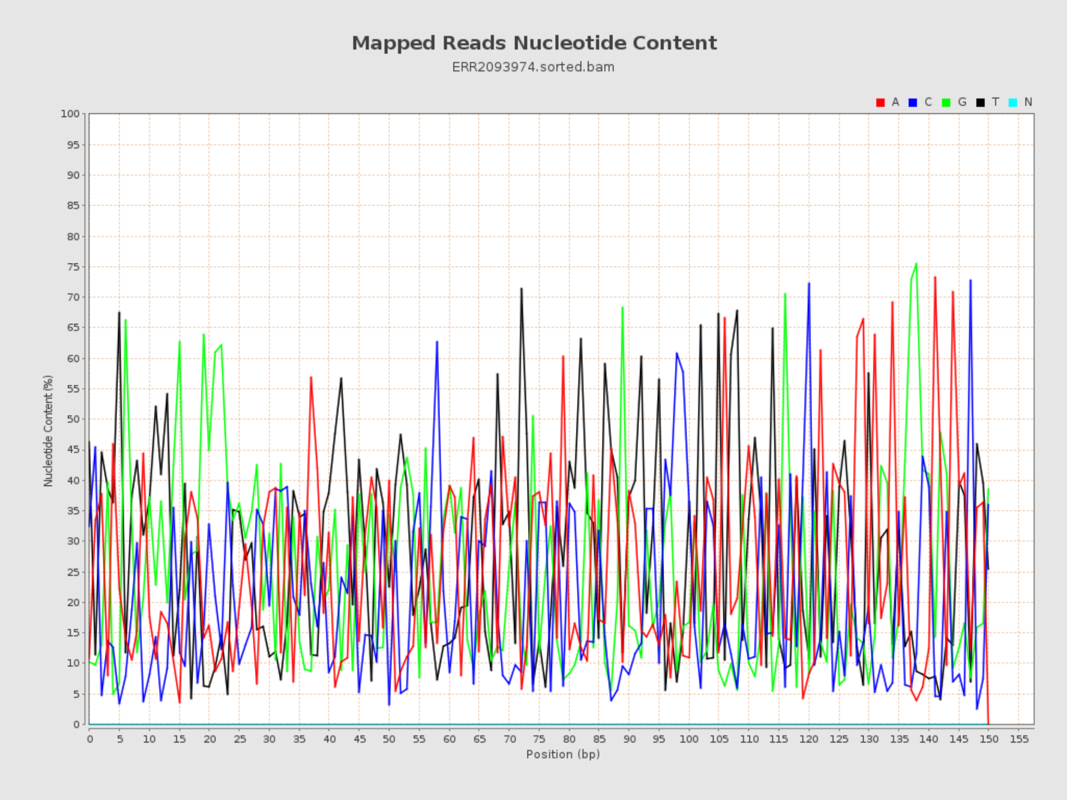
6. Results : Genome Fraction Coverage



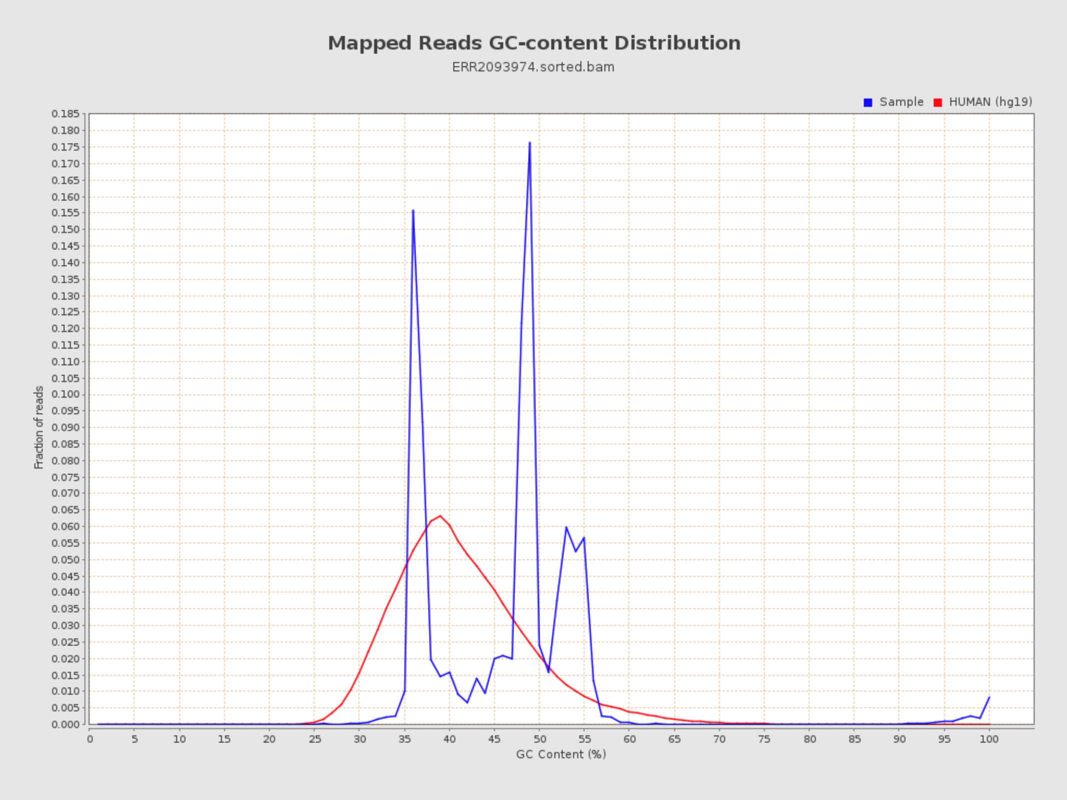
7. Results : Duplication Rate Histogram



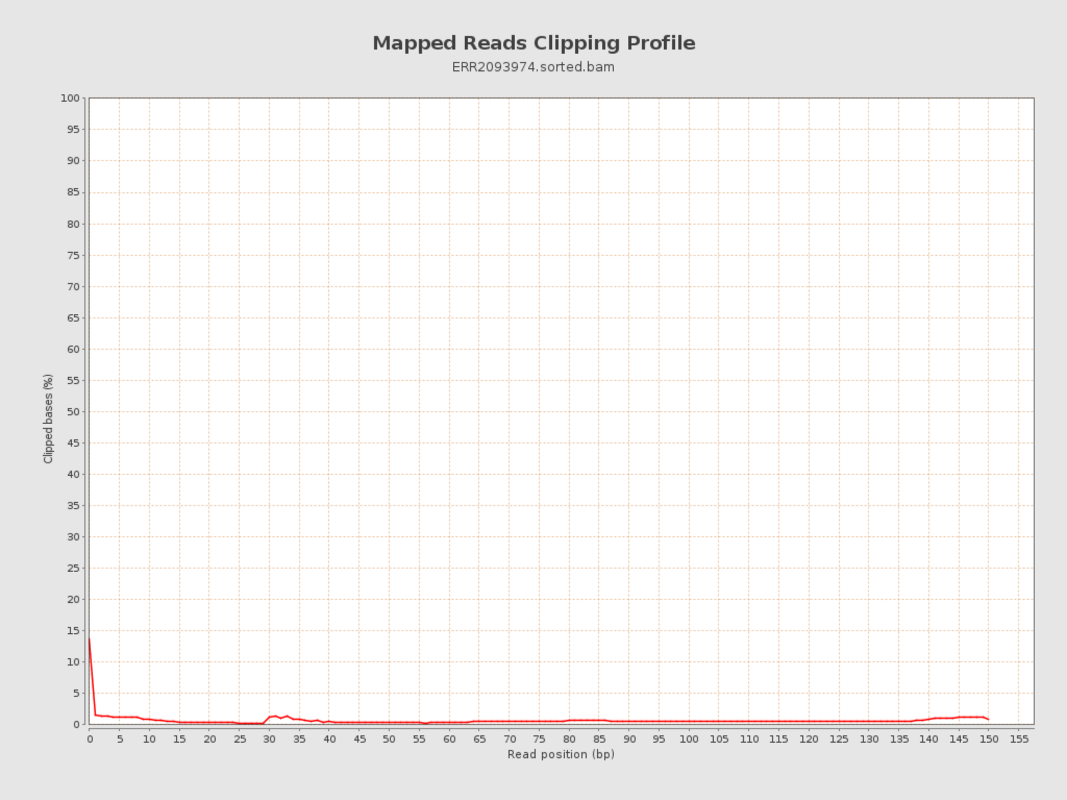
8. Results : Mapped Reads Nucleotide Content



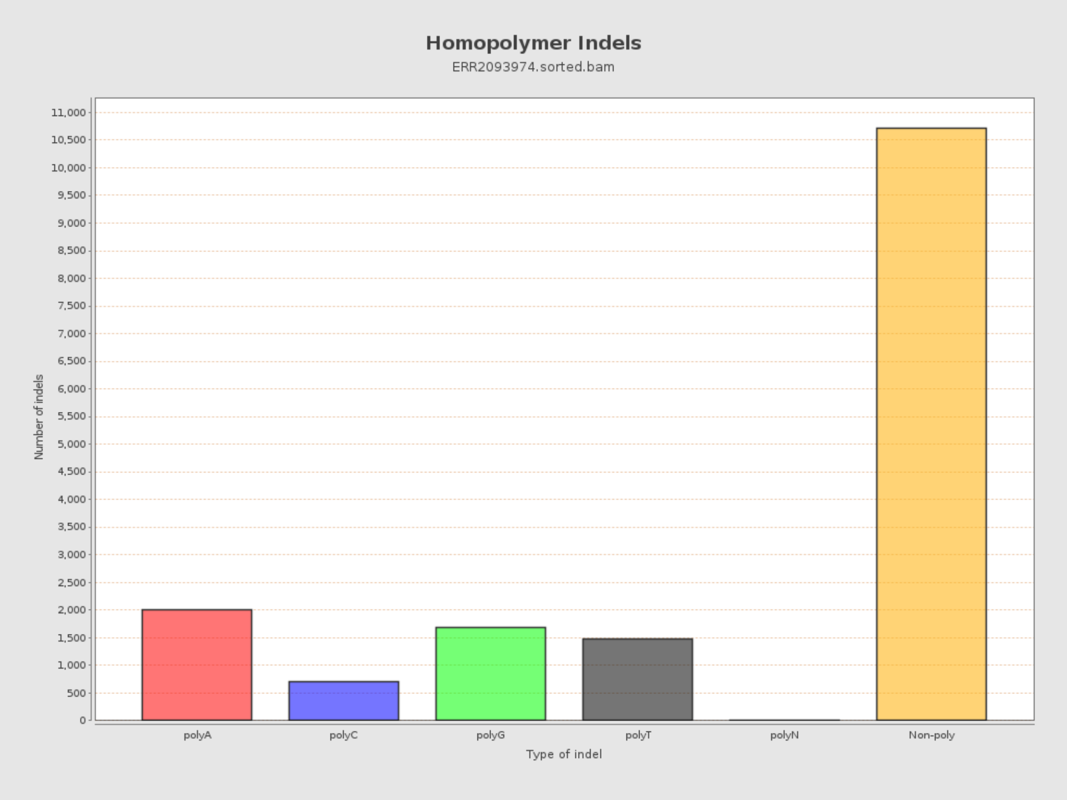
9. Results : Mapped Reads GC-content Distribution



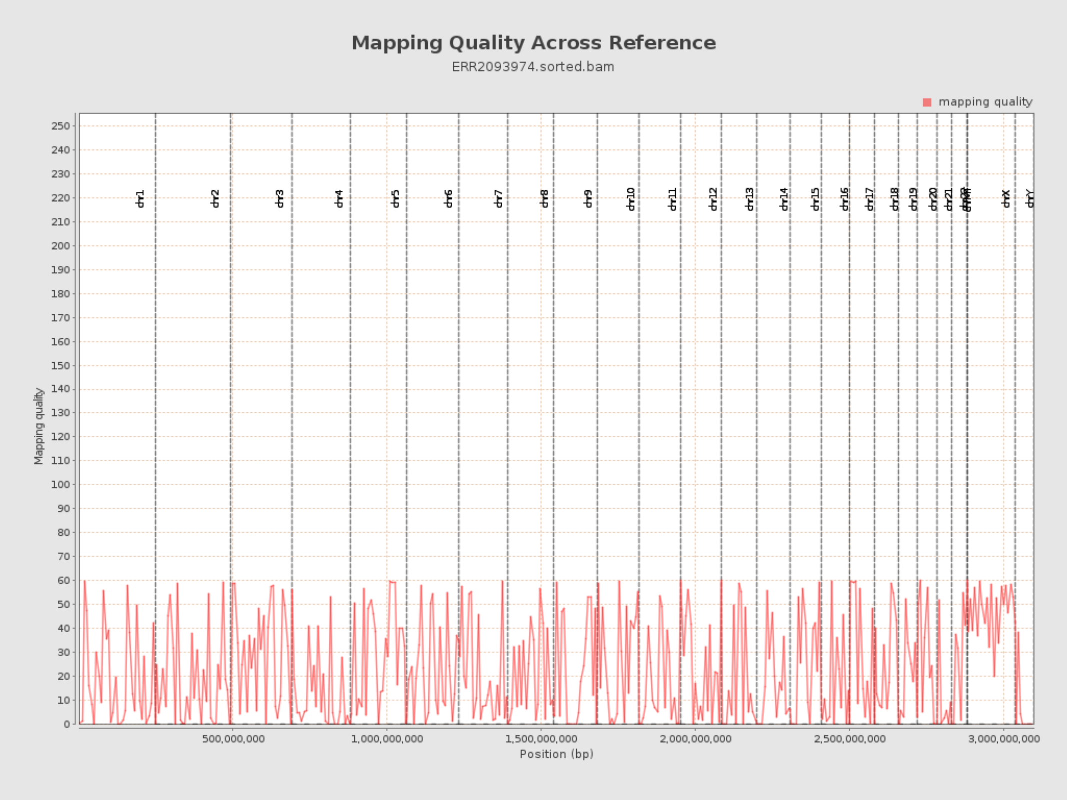
10. Results : Mapped Reads Clipping Profile



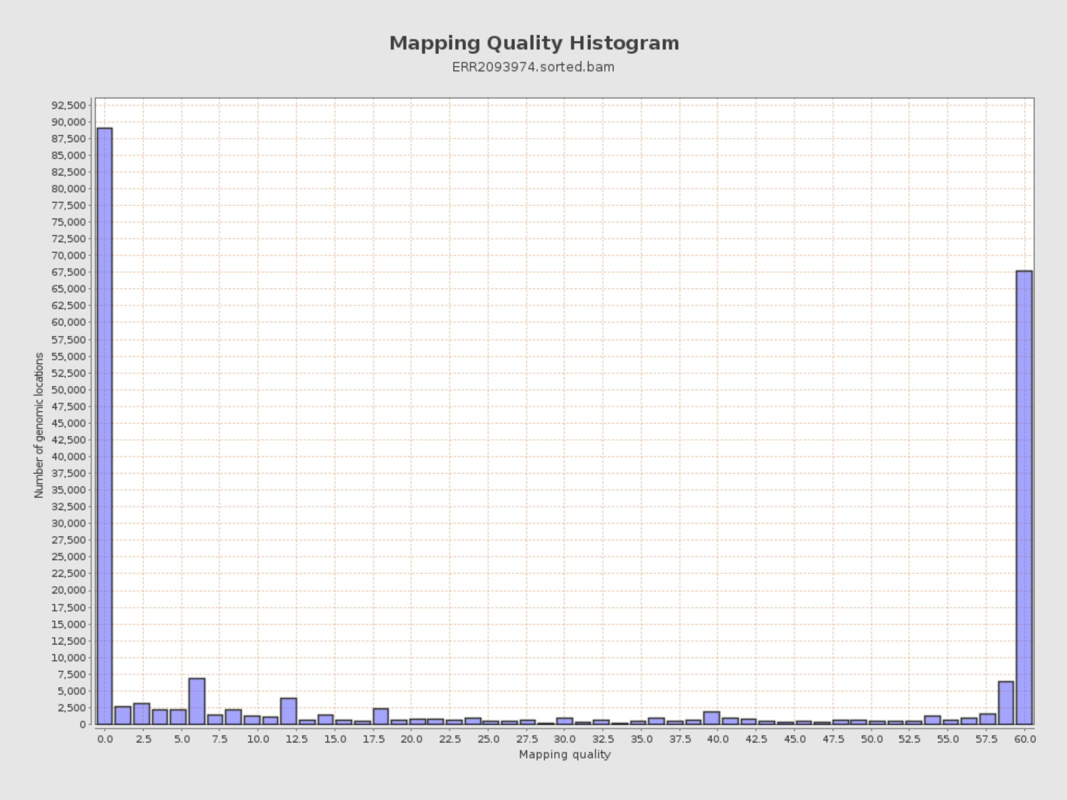
11. Results : Homopolymer Indels



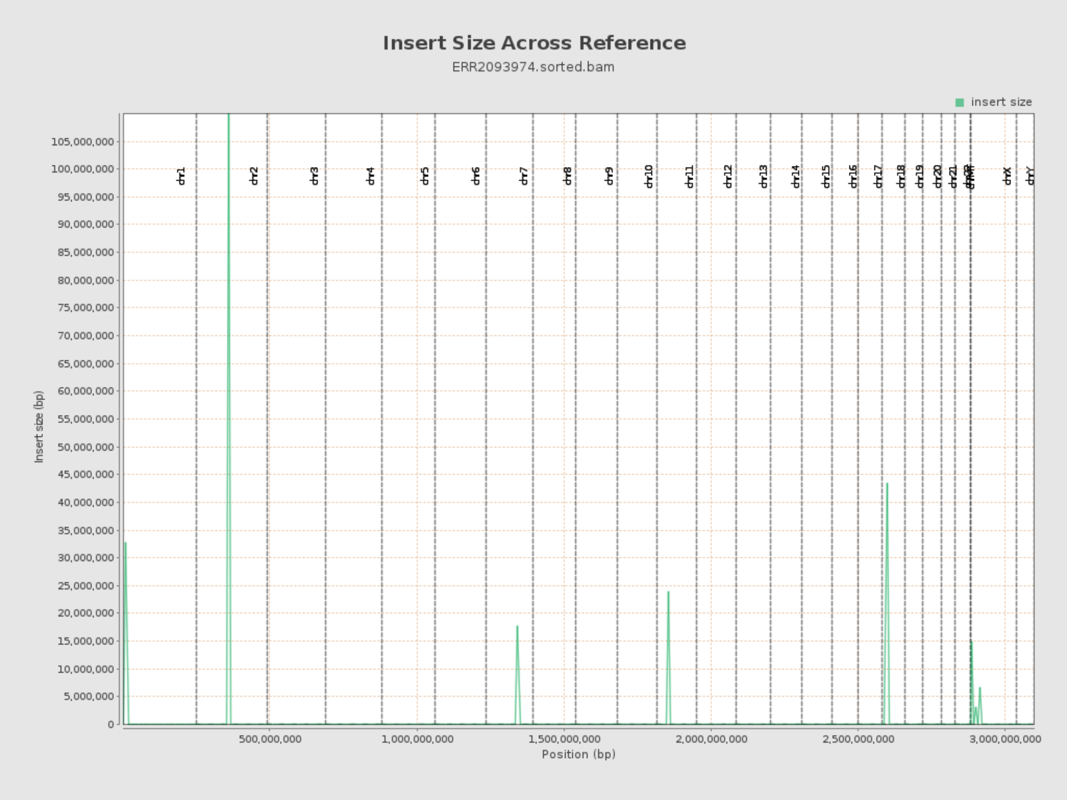
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram