Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:12:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094023.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_ERR2094023 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094023_1.fastq.gz ERR2094023_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:12:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	499,408
Mapped reads	458,442 / 91.8%
Unmapped reads	40,966 / 8.2%
Mapped paired reads	458,442 / 91.8%
Mapped reads, first in pair	230,433 / 46.14%
Mapped reads, second in pair	228,009 / 45.66%
Mapped reads, both in pair	451,978 / 90.5%
Mapped reads, singletons	6,464 / 1.29%
Secondary alignments	0
Supplementary alignments	27,594 / 5.53%
Read min/max/mean length	30 / 151 / 143.96
Duplicated reads (estimated)	443,800 / 88.87%
Duplication rate	45.05%
Clipped reads	231,482 / 46.35%

2.2. ACGT Content

Number/percentage of A's	17,029,932 / 28.8%
Number/percentage of C's	12,643,479 / 21.38%
Number/percentage of T's	16,060,439 / 27.16%
Number/percentage of G's	13,392,644 / 22.65%
Number/percentage of N's	550 / 0%

GC Percentage	44.03%

2.3. Coverage

Mean	0.0194
Standard Deviation	9.1925

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Insert size

Mean	328,097.2
Standard Deviation	5,385,387.68
P25/Median/P75	146 / 179 / 217

2.6. Mismatches and indels

General error rate	3.19%
Mismatches	1,794,214
Insertions	32,467
Mapped reads with at least one insertion	6.84%
Deletions	130,322
Mapped reads with at least one deletion	27.32%
Homopolymer indels	34.98%

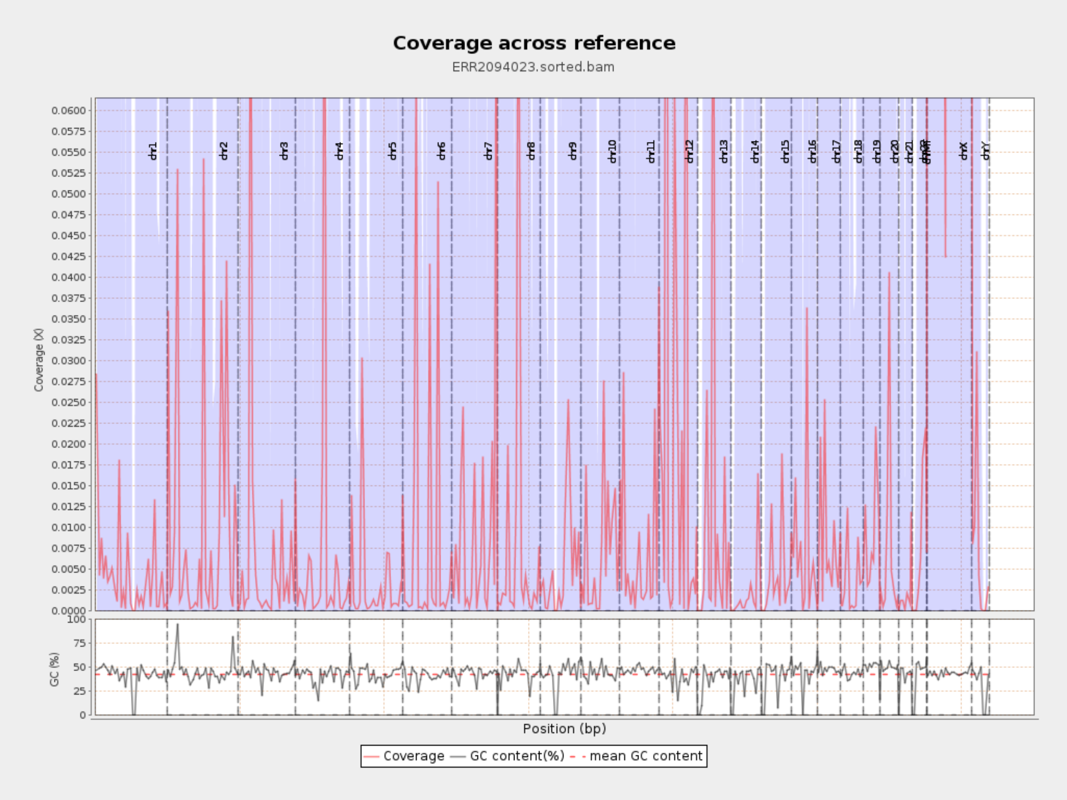
2.7. Chromosome stats

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

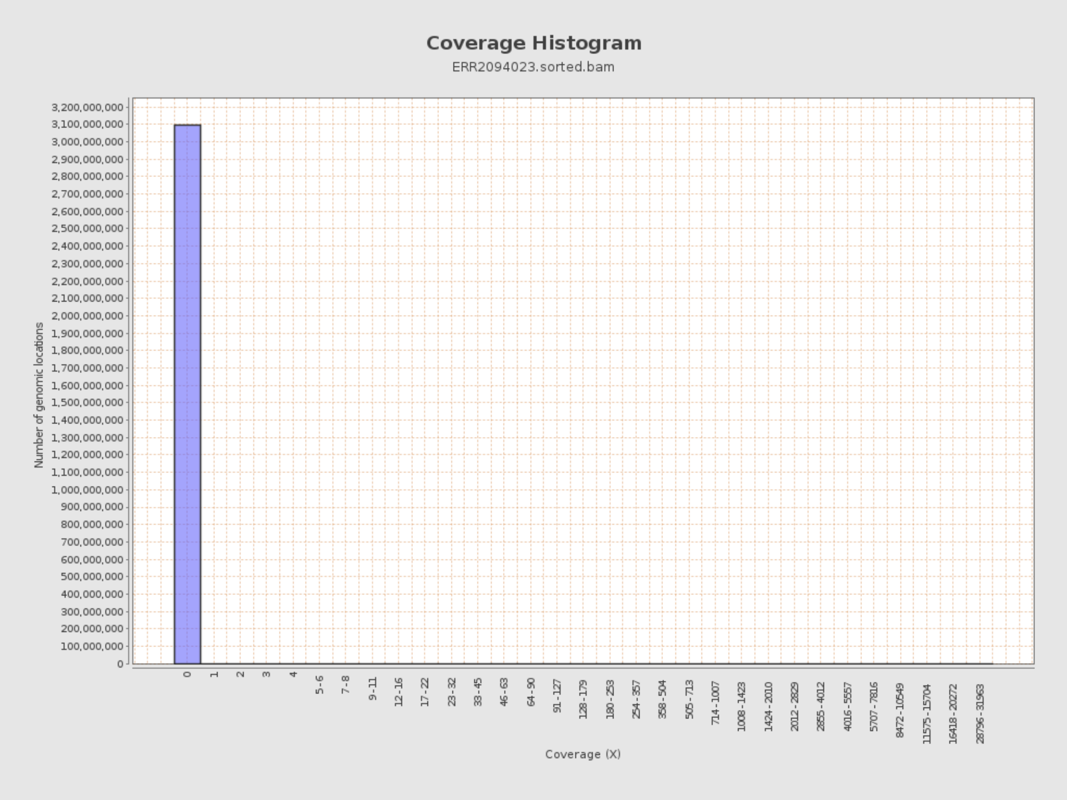
		bases	coverage	deviation
chr1	249250621	1080639	0.0043	1.1342
chr2	243199373	2519836	0.0104	2.847
chr3	198022430	1360744	0.0069	3.5061
chr4	191154276	1322706	0.0069	2.5353
chr5	180915260	589610	0.0033	1.278
chr6	171115067	1559670	0.0091	4.2396
chr7	159138663	1749616	0.011	2.0125
chr8	146364022	1176789	0.008	4.3308
chr9	141213431	749066	0.0053	1.285
chr10	135534747	958559	0.0071	1.9521
chr11	135006516	855728	0.0063	1.356
chr12	133851895	3421122	0.0256	9.5759
chr13	115169878	1377565	0.012	4.9714
chr14	107349540	248431	0.0023	0.3379
chr15	102531392	412976	0.004	0.9752
chr16	90354753	691461	0.0077	1.8175
chr17	81195210	669816	0.0082	1.6162
chr18	78077248	243127	0.0031	0.8125
chr19	59128983	518287	0.0088	1.3682
chr20	63025520	495653	0.0079	2.3452
chr21	48129895	101094	0.0021	0.3921
chr22	51304566	393043	0.0077	1.0591
chrMT	16571	12951299	781.5641	3,415.6269
chrX	155270560	24148432	0.1555	13.4061

chrY	59373566	417851	0.007	1.9293

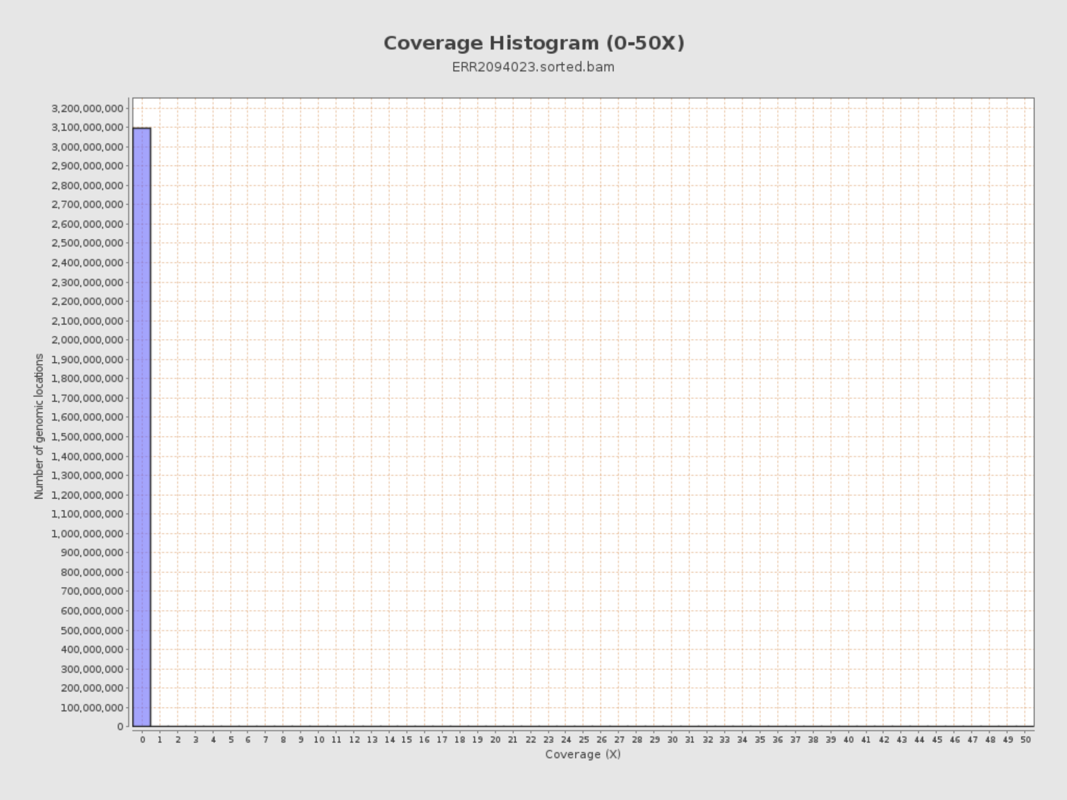
3. Results : Coverage across reference



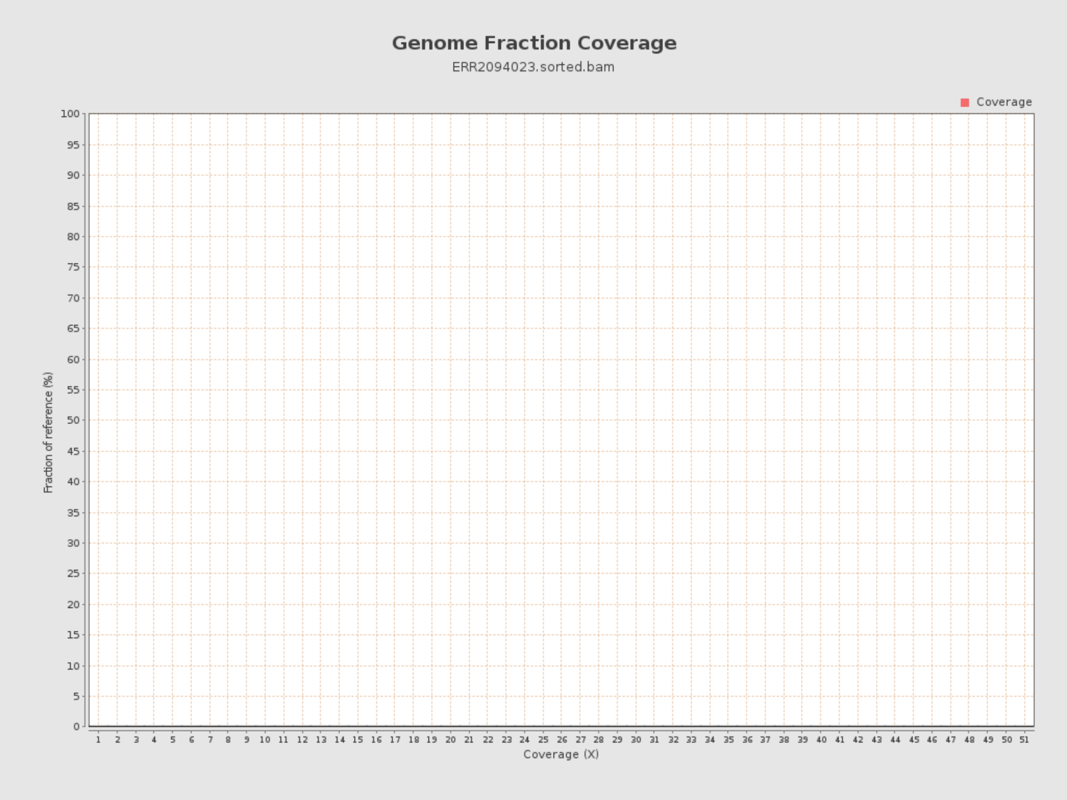
4. Results : Coverage Histogram



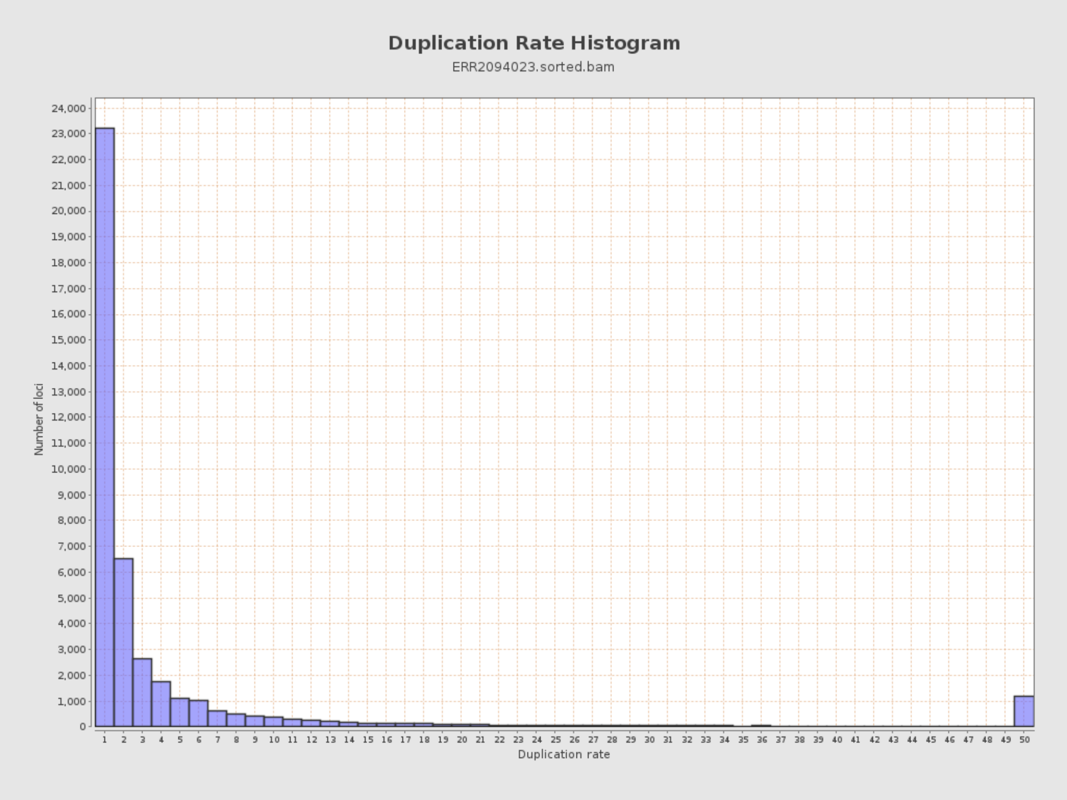
5. Results : Coverage Histogram (0-50X)



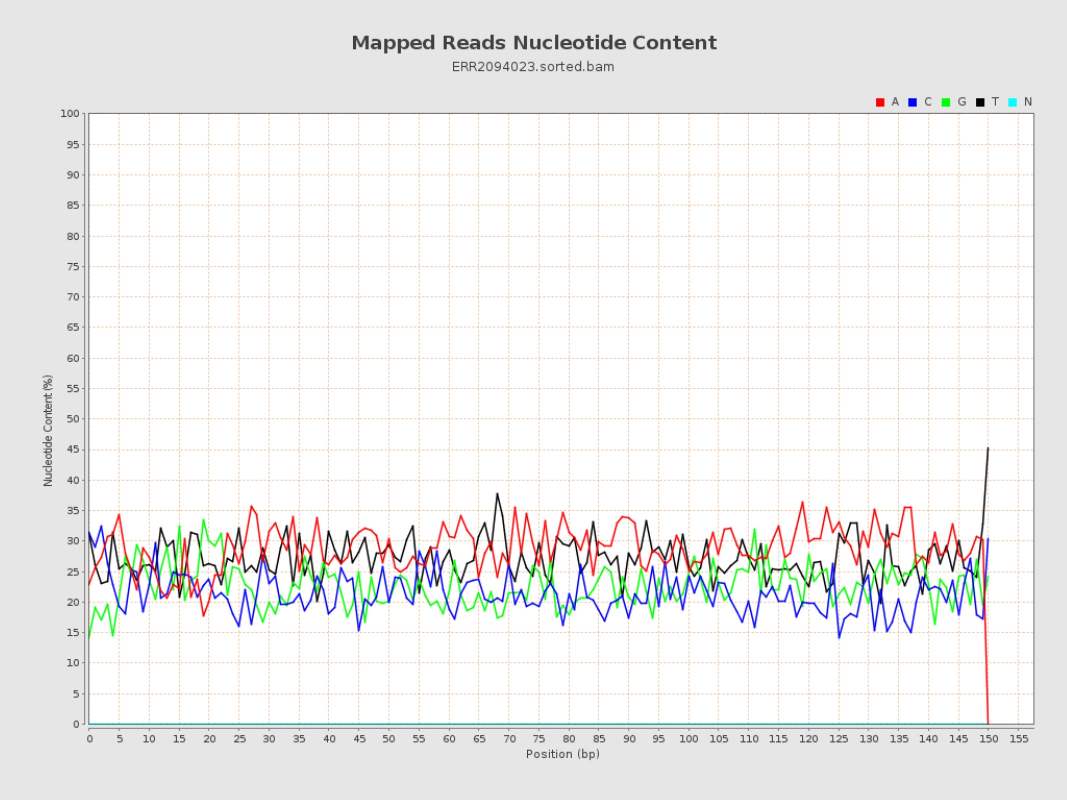
6. Results : Genome Fraction Coverage



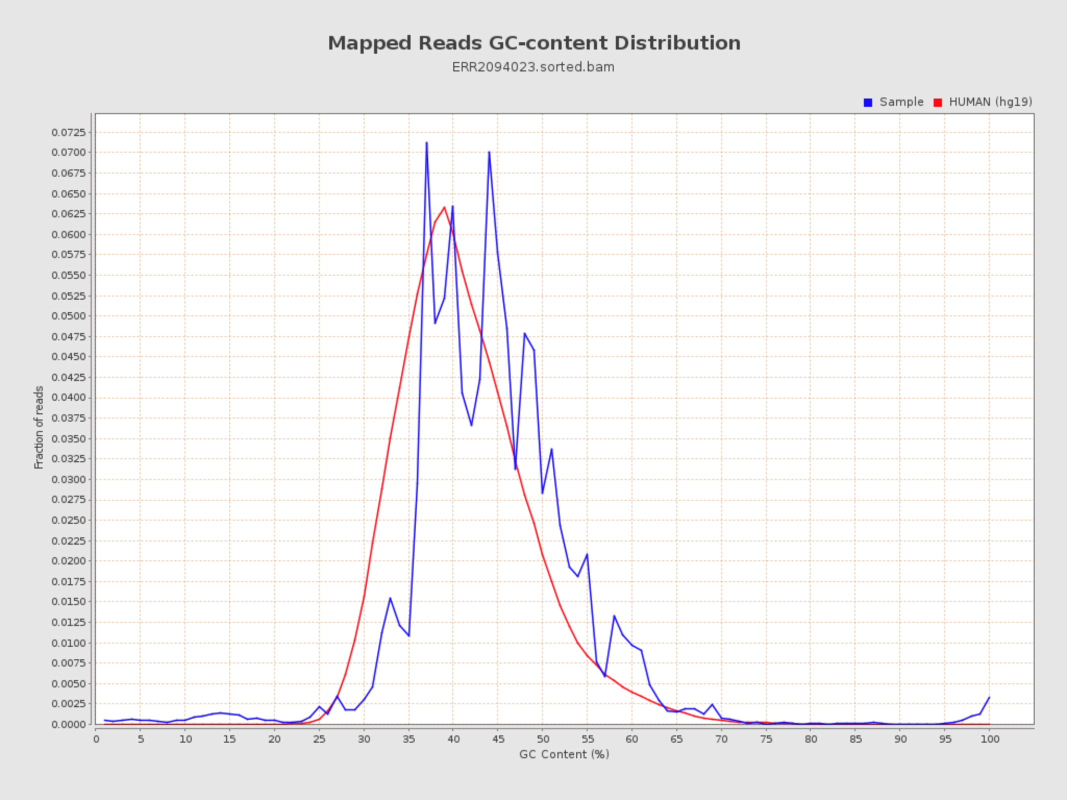
7. Results : Duplication Rate Histogram



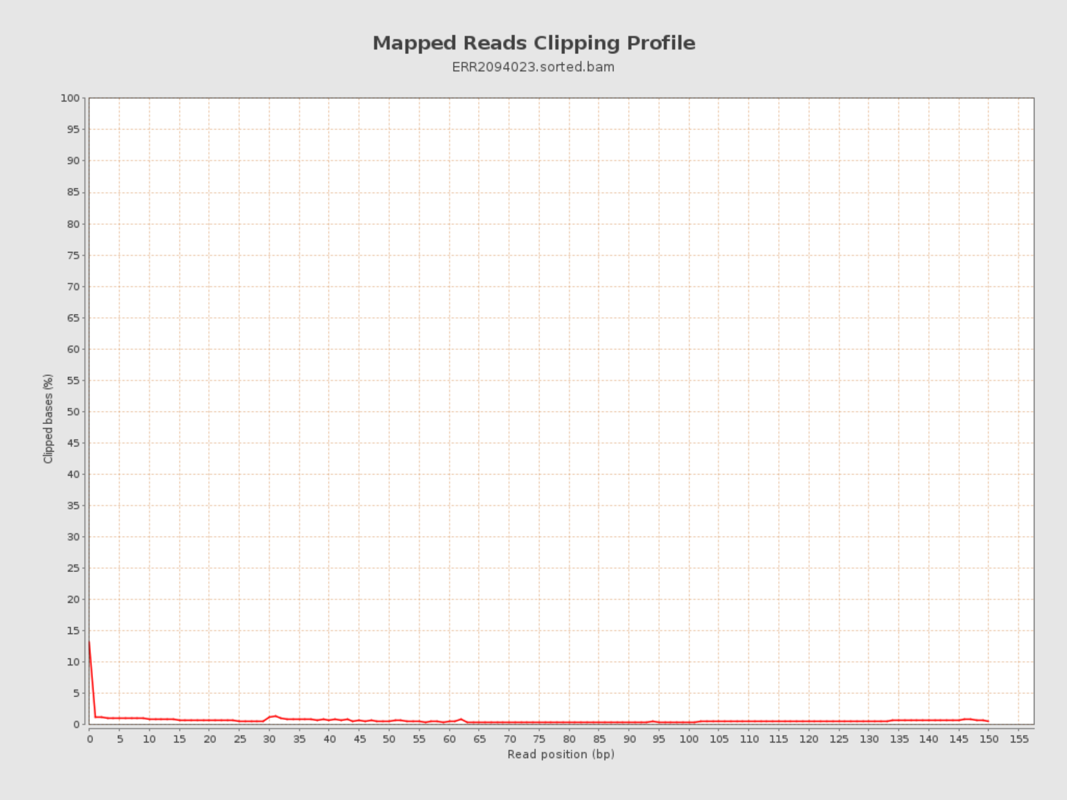
8. Results : Mapped Reads Nucleotide Content



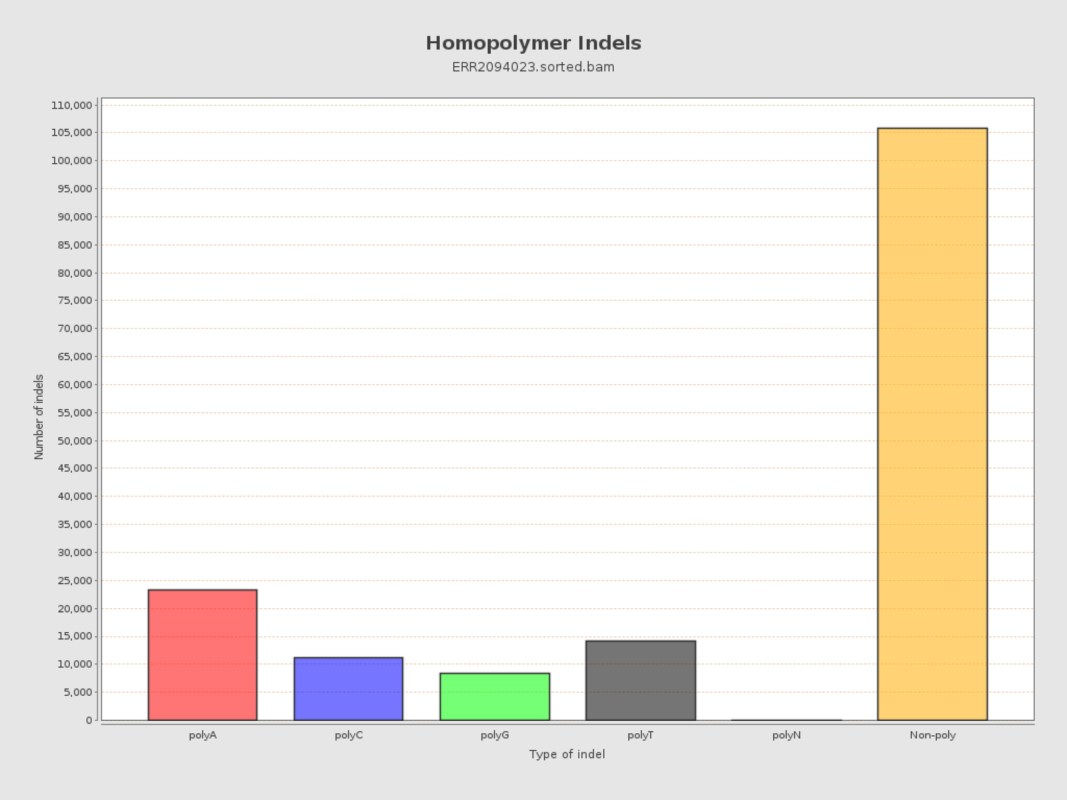
9. Results : Mapped Reads GC-content Distribution



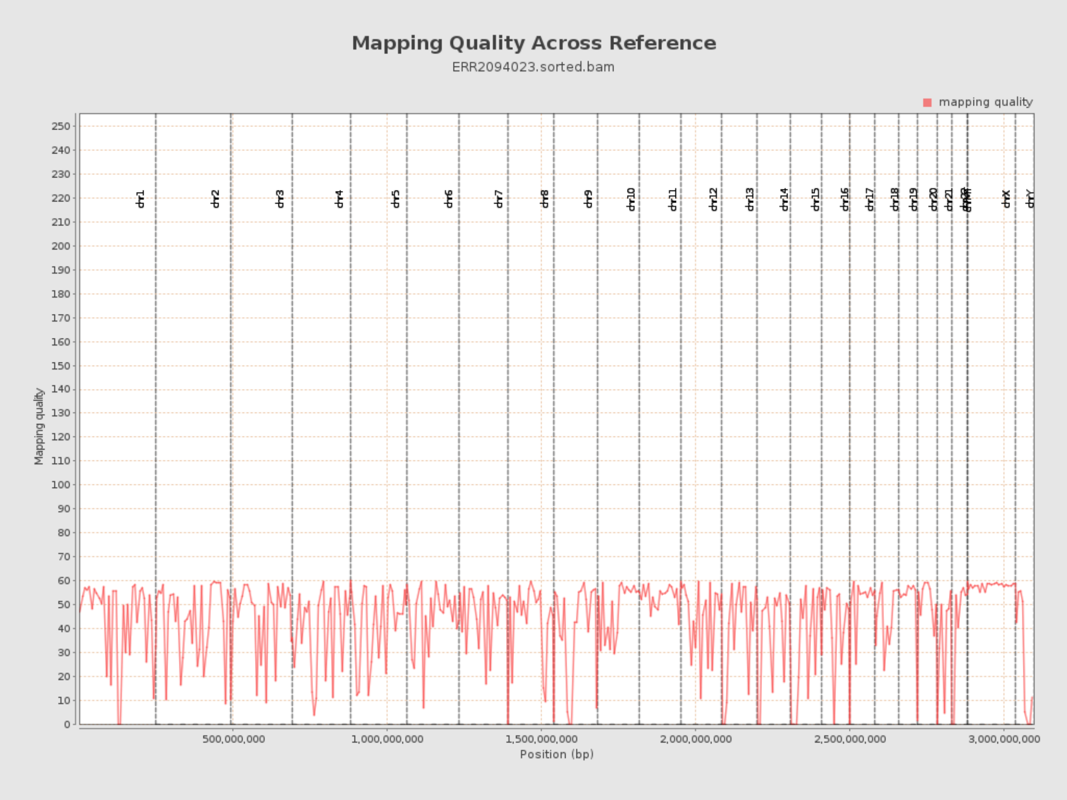
10. Results : Mapped Reads Clipping Profile



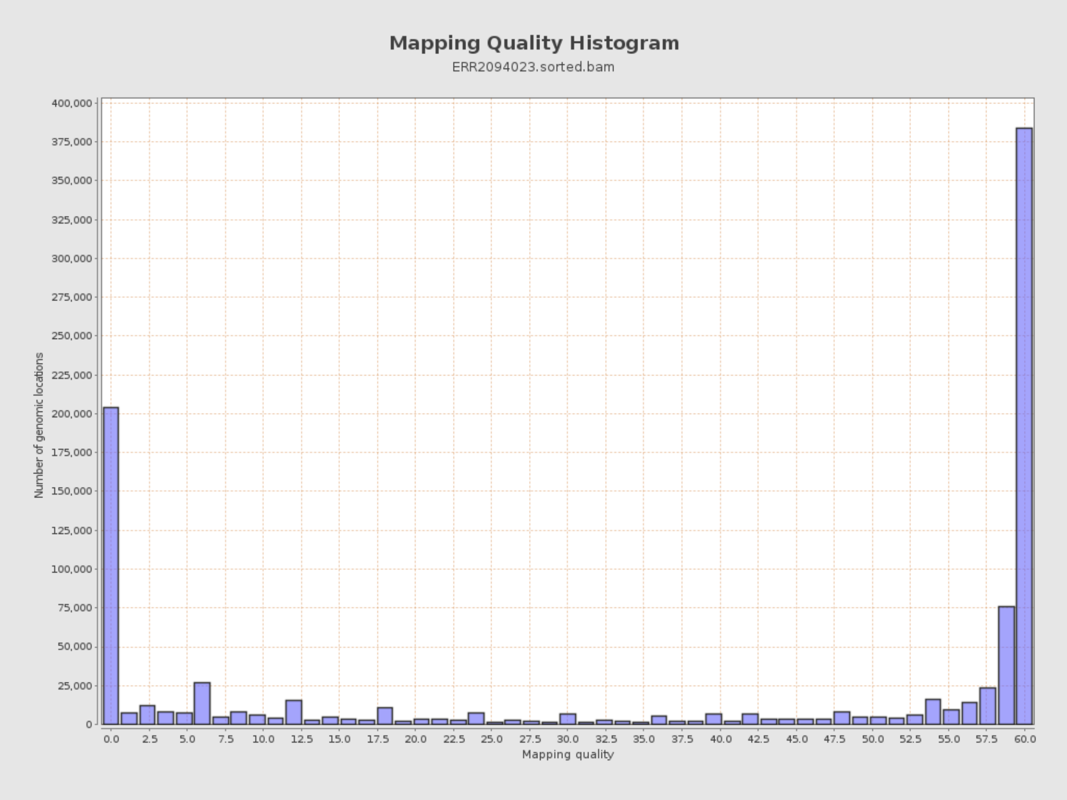
11. Results : Homopolymer Indels



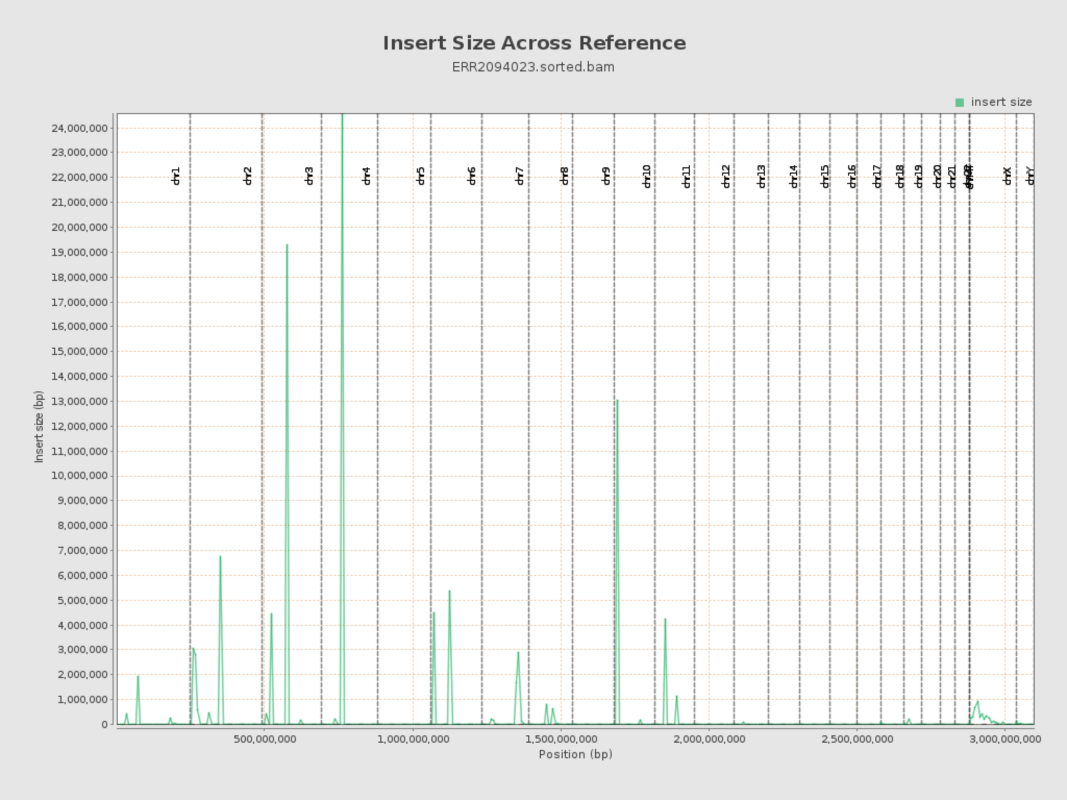
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram