Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:14:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094059.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_ERR2094059 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094059_1.fastq.gz ERR2094059_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:14:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	399,850
Mapped reads	379,148 / 94.82%
Unmapped reads	20,702 / 5.18%
Mapped paired reads	379,148 / 94.82%
Mapped reads, first in pair	190,418 / 47.62%
Mapped reads, second in pair	188,730 / 47.2%
Mapped reads, both in pair	376,668 / 94.2%
Mapped reads, singletons	2,480 / 0.62%
Secondary alignments	0
Supplementary alignments	8,169 / 2.04%
Read min/max/mean length	30 / 151 / 140.37
Duplicated reads (estimated)	362,225 / 90.59%
Duplication rate	50.57%
Clipped reads	131,932 / 33%

2.2. ACGT Content

Number/percentage of A's	13,675,026 / 27.3%
Number/percentage of C's	11,312,282 / 22.58%
Number/percentage of T's	13,389,387 / 26.73%
Number/percentage of G's	11,712,008 / 23.38%
Number/percentage of N's	540 / 0%

GC Percentage	45.97%

2.3. Coverage

Mean	0.0166
Standard Deviation	6.4567

2.4. Mapping Quality

Mean Mapping Quality	41.7

2.5. Insert size

Mean	295,490.45
Standard Deviation	4,994,525.75
P25/Median/P75	143 / 173 / 206

2.6. Mismatches and indels

General error rate	4.38%
Mismatches	2,098,762
Insertions	43,781
Mapped reads with at least one insertion	11.27%
Deletions	167,004
Mapped reads with at least one deletion	41.23%
Homopolymer indels	33.13%

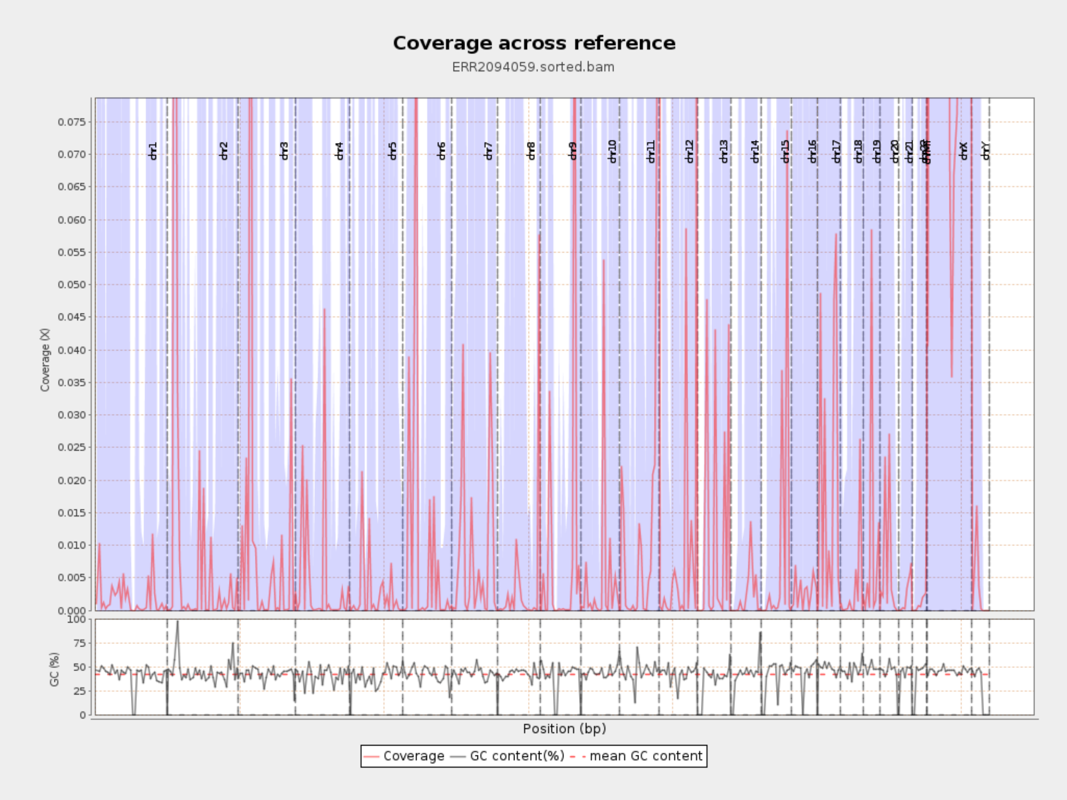
2.7. Chromosome stats

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

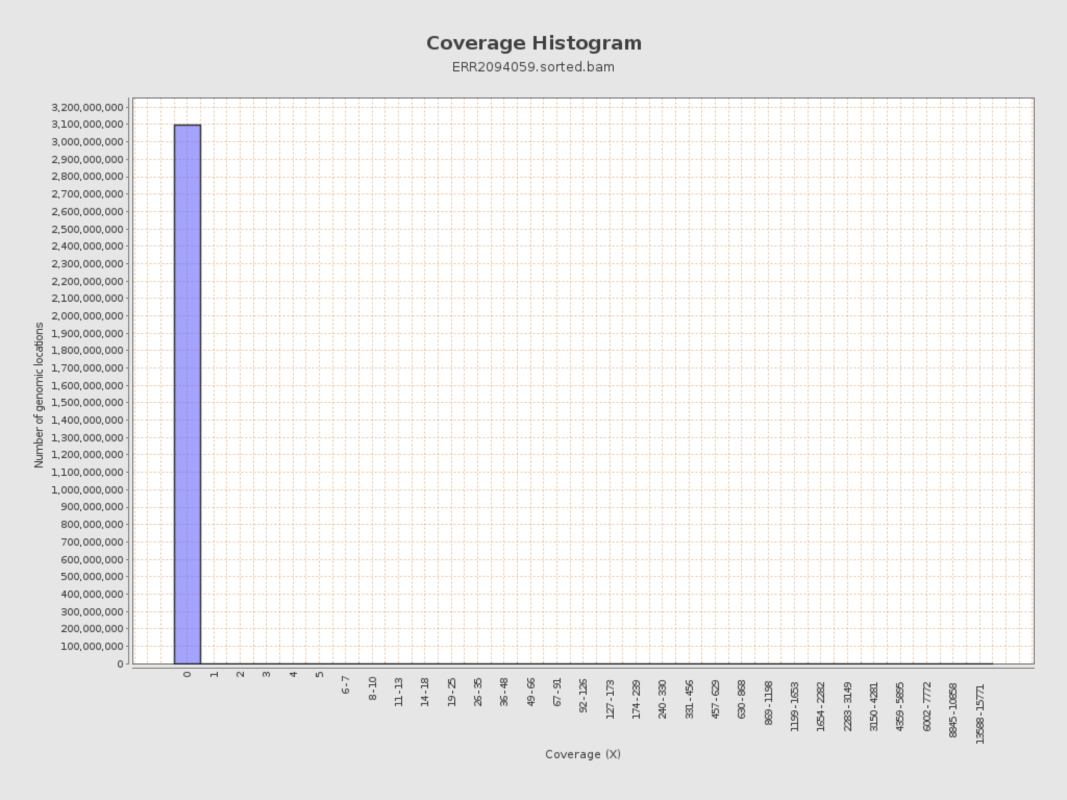
		bases	coverage	deviation
chr1	249250621	491977	0.002	0.7864
chr2	243199373	2244402	0.0092	3.7725
chr3	198022430	2206226	0.0111	6.389
chr4	191154276	881355	0.0046	2.1542
chr5	180915260	466523	0.0026	1.1195
chr6	171115067	1794612	0.0105	5.5457
chr7	159138663	1306245	0.0082	2.7979
chr8	146364022	597394	0.0041	2.436
chr9	141213431	1357229	0.0096	5.689
chr10	135534747	668809	0.0049	2.8499
chr11	135006516	1998708	0.0148	4.8148
chr12	133851895	1016759	0.0076	3.524
chr13	115169878	1307392	0.0114	4.1073
chr14	107349540	242100	0.0023	0.9259
chr15	102531392	916227	0.0089	3.4505
chr16	90354753	254972	0.0028	0.6497
chr17	81195210	1580150	0.0195	5.0736
chr18	78077248	283536	0.0036	1.3515
chr19	59128983	619683	0.0105	4.1225
chr20	63025520	464236	0.0074	2.1029
chr21	48129895	115024	0.0024	0.4629
chr22	51304566	84866	0.0017	0.4644
chrMT	16571	7445856	449.3305	1,885.9819
chrX	155270560	22749916	0.1465	13.7029

chrY	59373566	210856	0.0036	1.4998

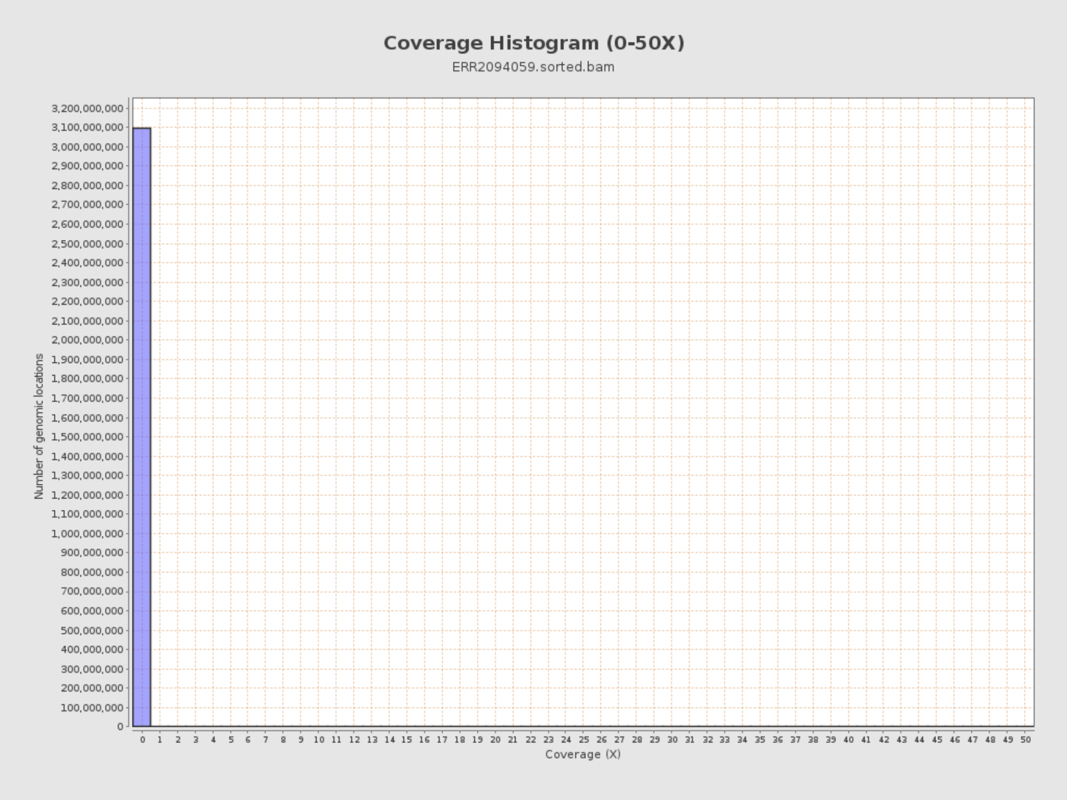
3. Results : Coverage across reference



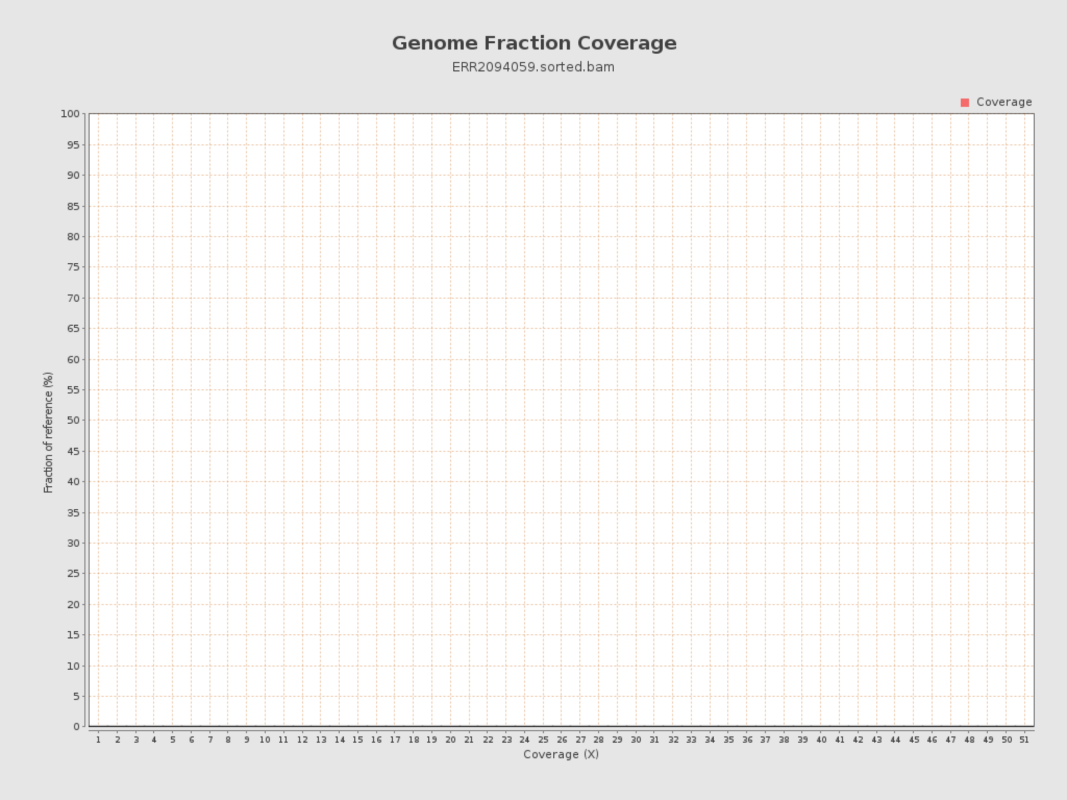
4. Results : Coverage Histogram



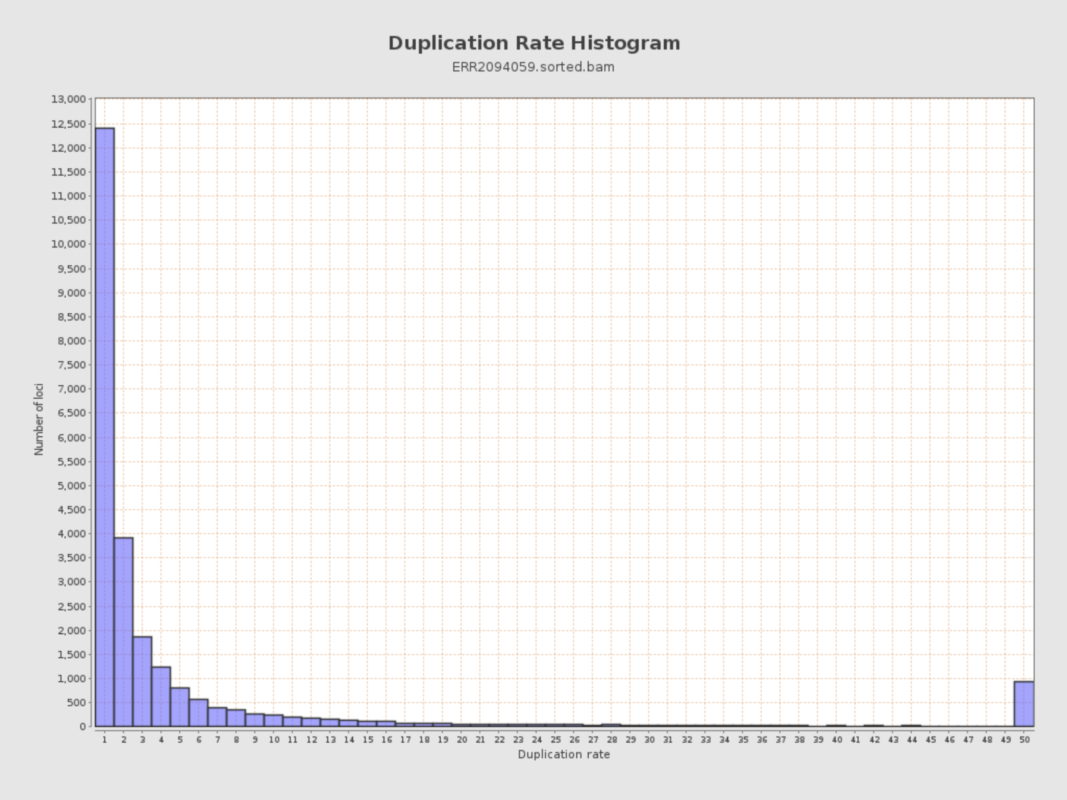
5. Results : Coverage Histogram (0-50X)



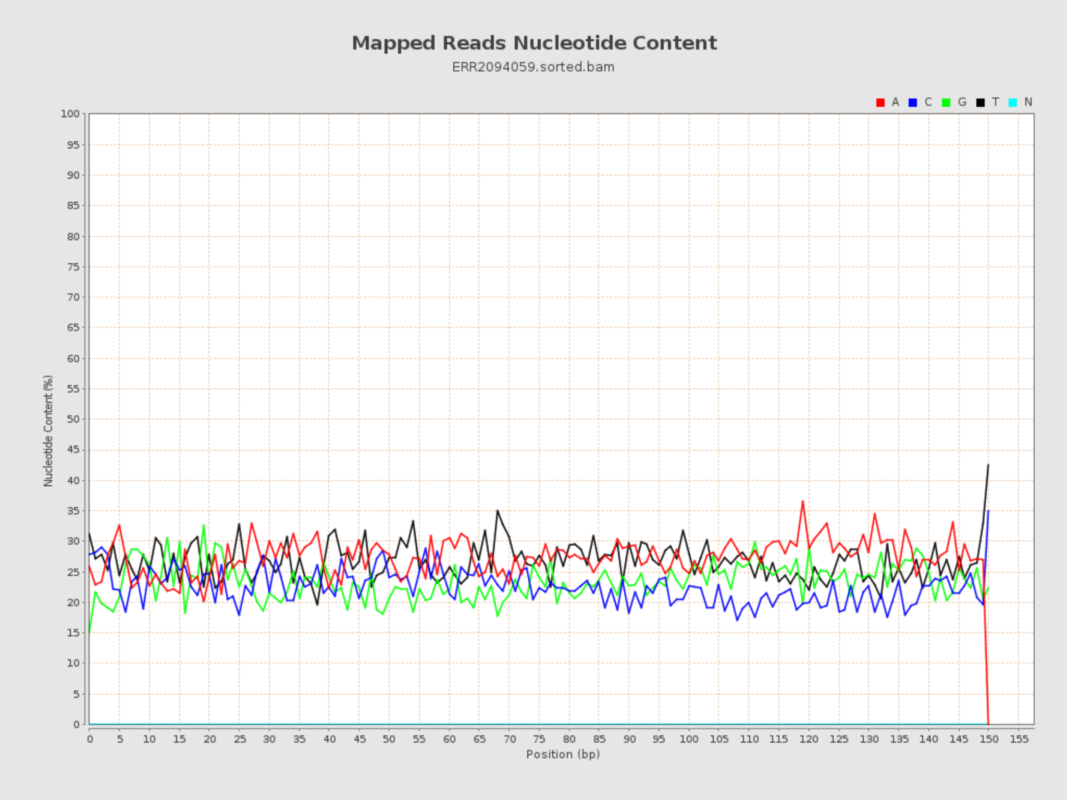
6. Results : Genome Fraction Coverage



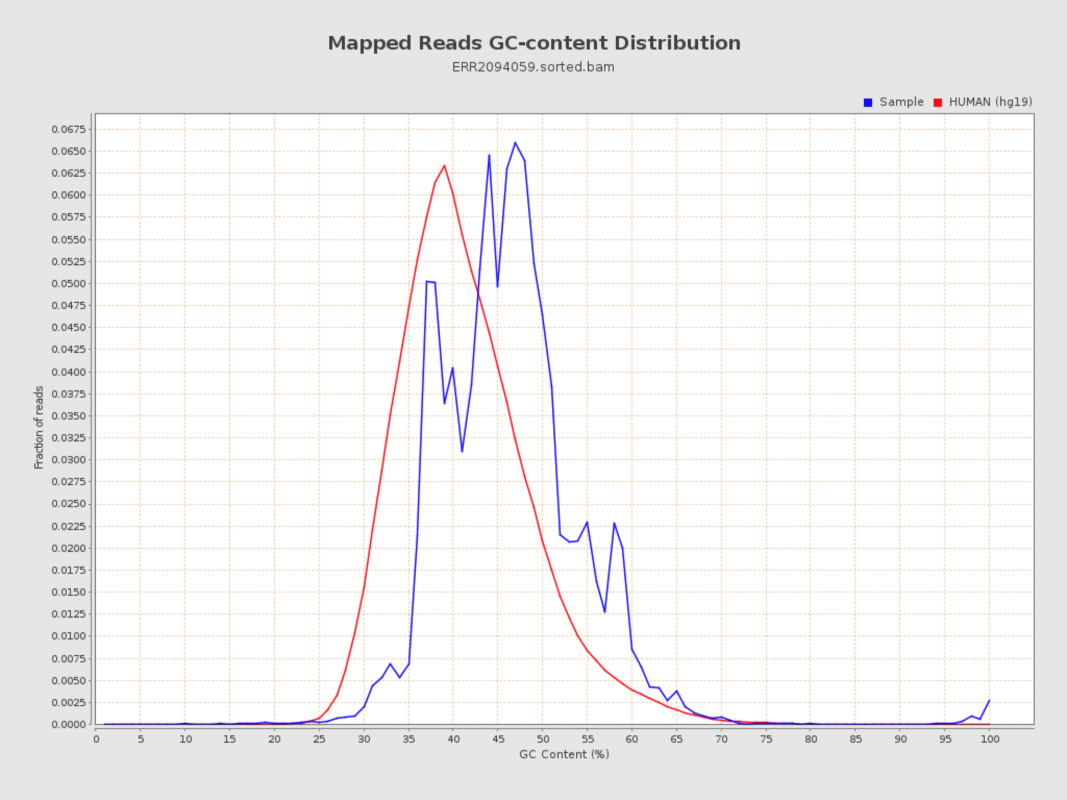
7. Results : Duplication Rate Histogram



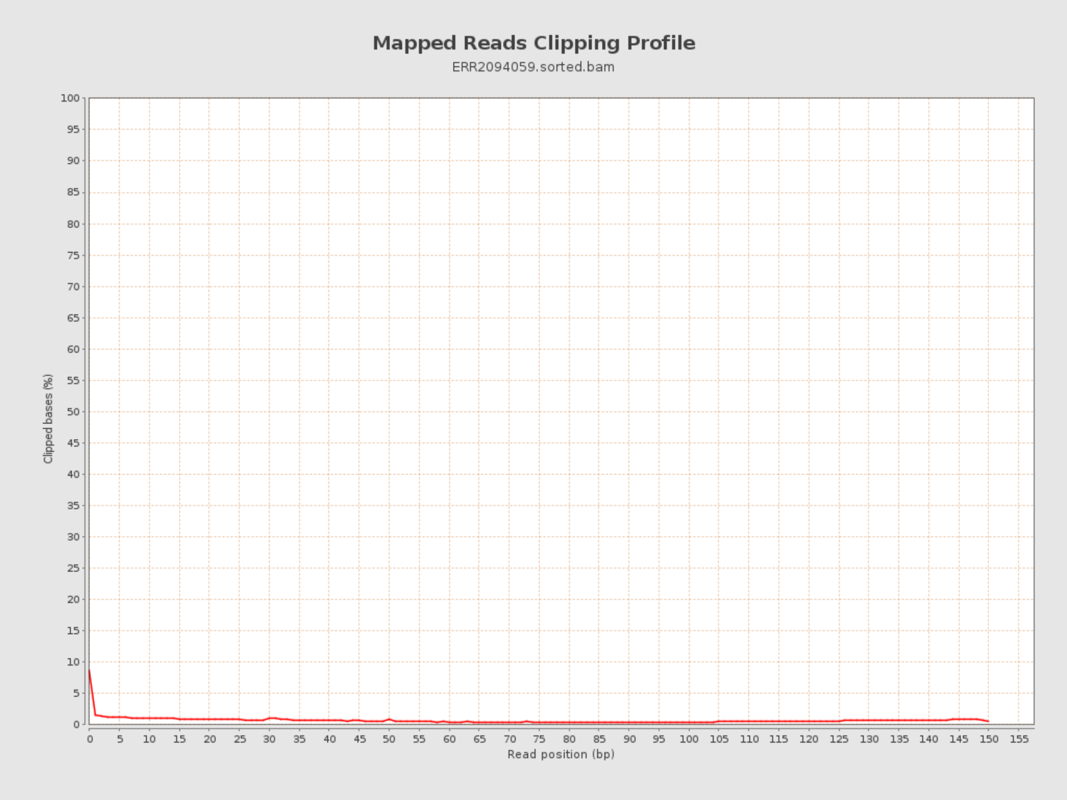
8. Results : Mapped Reads Nucleotide Content



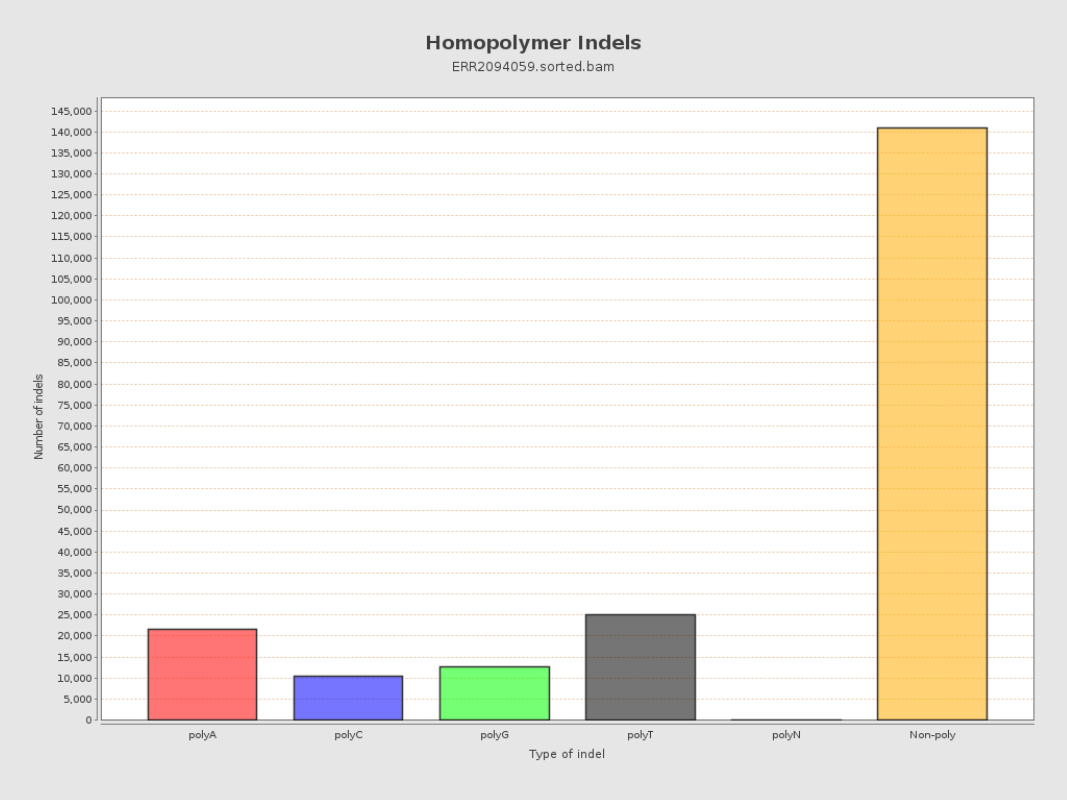
9. Results : Mapped Reads GC-content Distribution



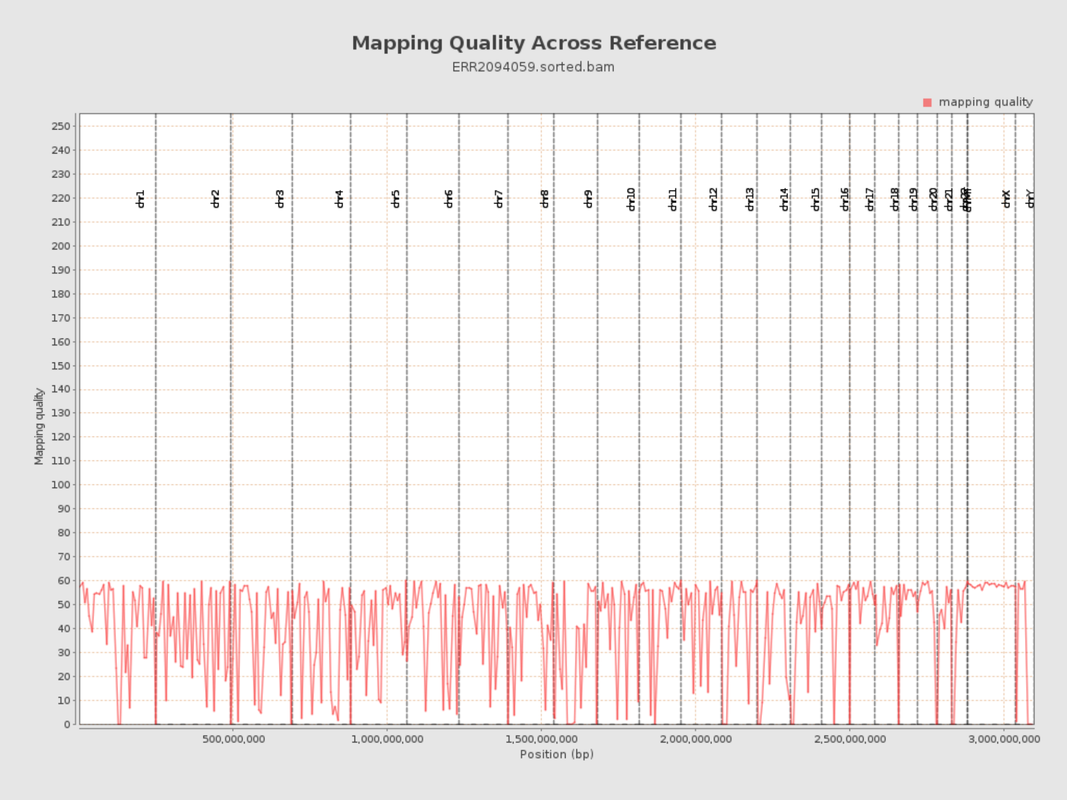
10. Results : Mapped Reads Clipping Profile



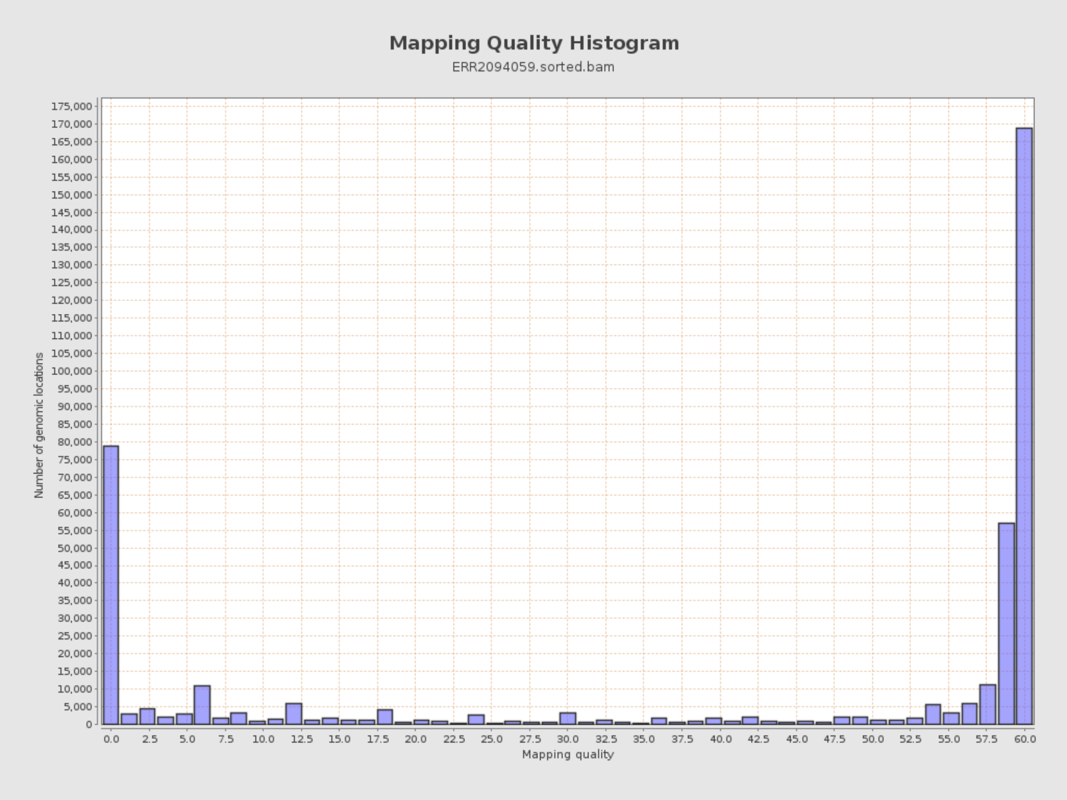
11. Results : Homopolymer Indels



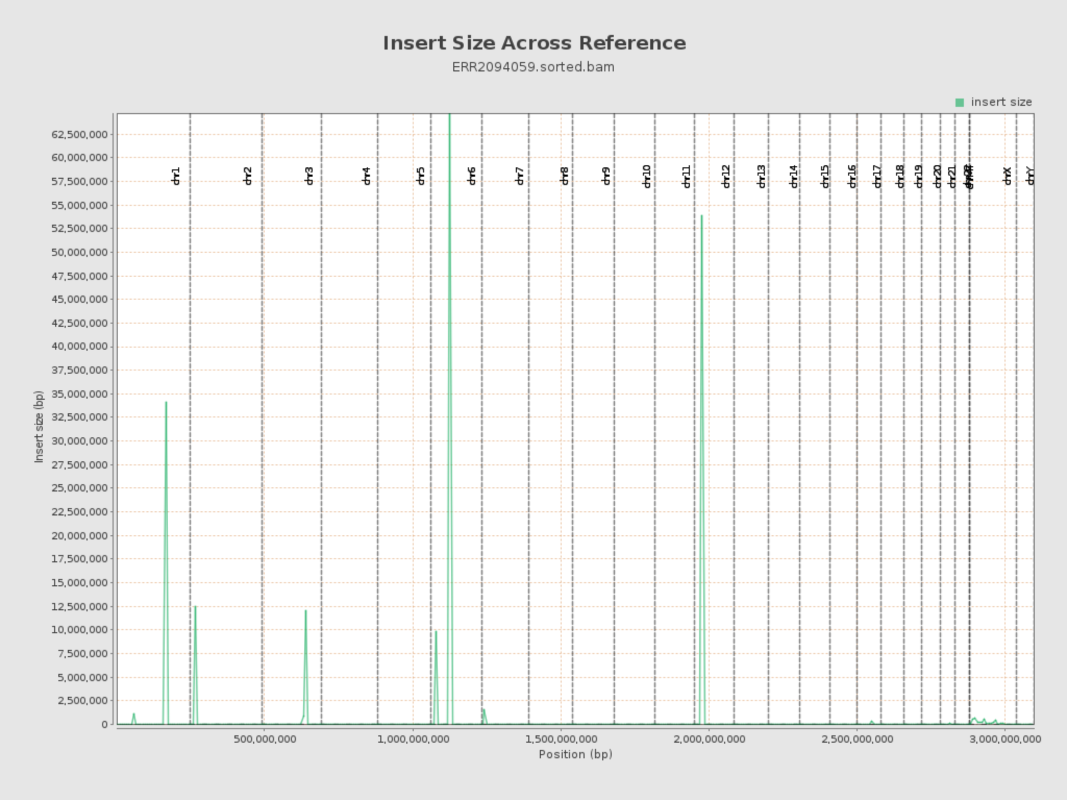
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram