Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:05:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094057.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_ERR2094057 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094057_1.fastq.gz ERR2094057_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:05:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	424,800
Mapped reads	406,058 / 95.59%
Unmapped reads	18,742 / 4.41%
Mapped paired reads	406,058 / 95.59%
Mapped reads, first in pair	203,957 / 48.01%
Mapped reads, second in pair	202,101 / 47.58%
Mapped reads, both in pair	403,004 / 94.87%
Mapped reads, singletons	3,054 / 0.72%
Secondary alignments	0
Supplementary alignments	17,338 / 4.08%
Read min/max/mean length	30 / 151 / 140.74
Duplicated reads (estimated)	381,430 / 89.79%
Duplication rate	50.05%
Clipped reads	174,329 / 41.04%

2.2. ACGT Content

Number/percentage of A's	14,588,115 / 27.97%
Number/percentage of C's	11,627,913 / 22.29%
Number/percentage of T's	13,895,505 / 26.64%
Number/percentage of G's	12,048,622 / 23.1%
Number/percentage of N's	598 / 0%

GC Percentage	45.39%

2.3. Coverage

Mean	0.0173
Standard Deviation	3.786

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Insert size

Mean	649,875.09
Standard Deviation	7,174,792.39
P25/Median/P75	132 / 166 / 194

2.6. Mismatches and indels

General error rate	4.57%
Mismatches	2,304,511
Insertions	39,132
Mapped reads with at least one insertion	9.45%
Deletions	185,126
Mapped reads with at least one deletion	42.37%
Homopolymer indels	27.95%

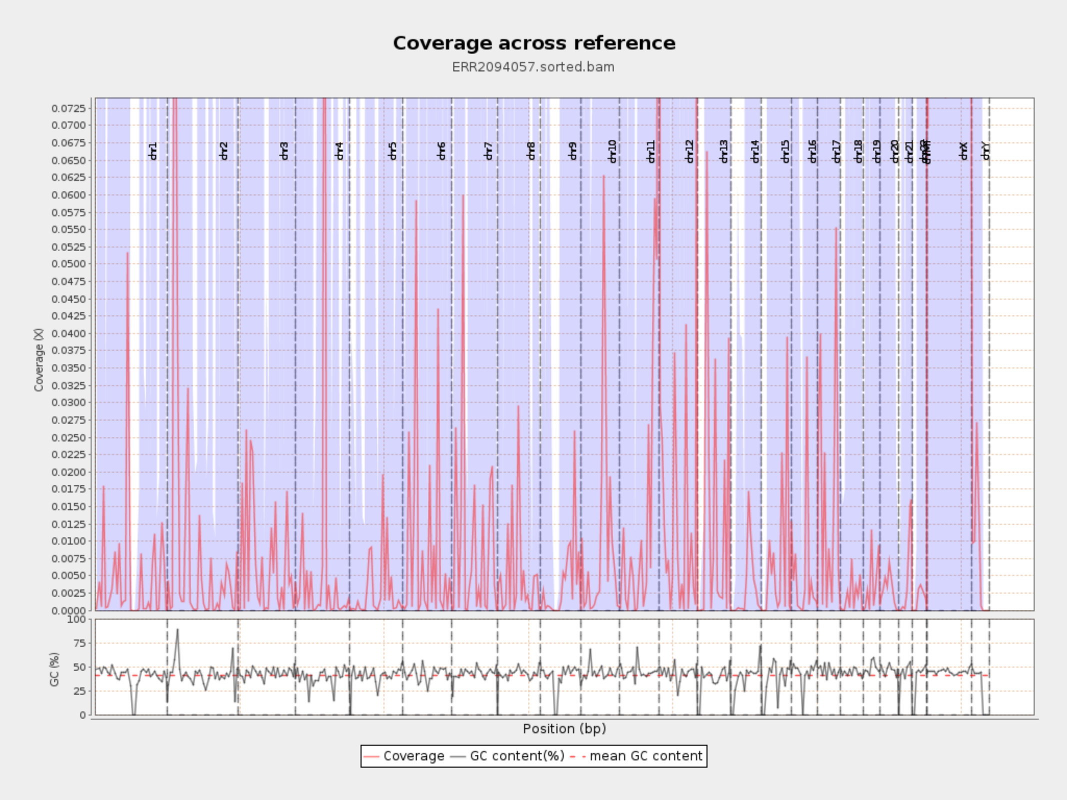
2.7. Chromosome stats

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

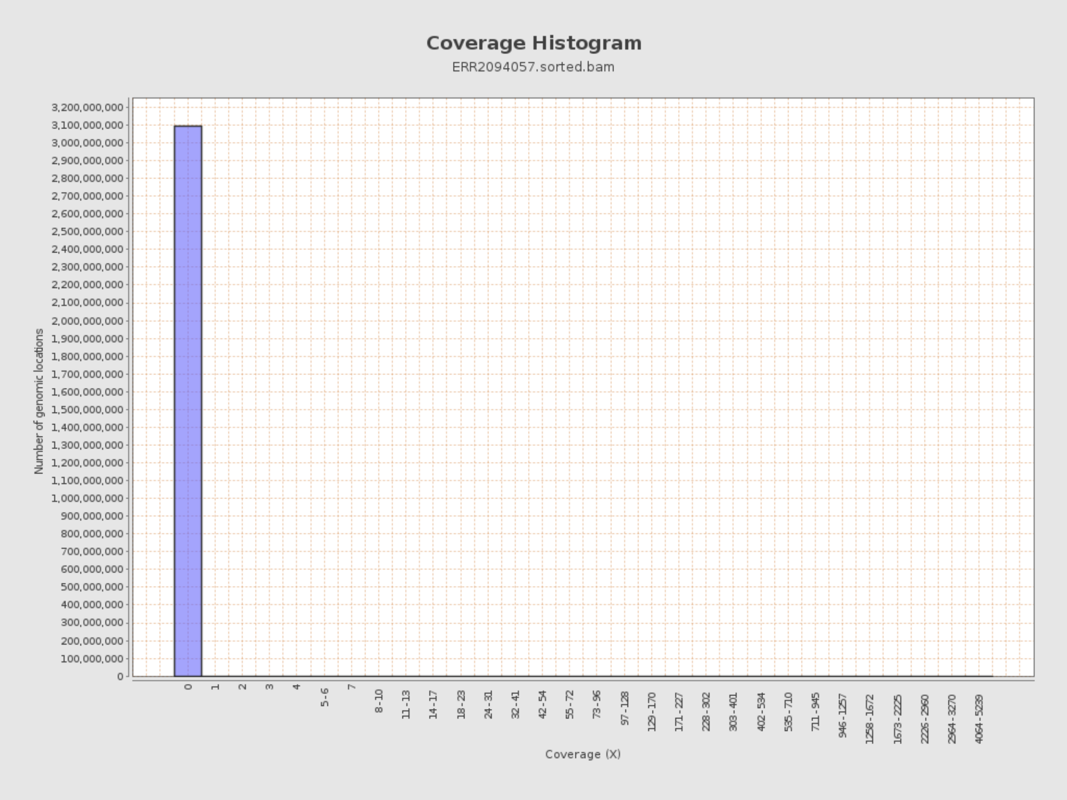
		bases	coverage	deviation
chr1	249250621	1186910	0.0048	1.8428
chr2	243199373	2202045	0.0091	2.689
chr3	198022430	1370468	0.0069	1.8387
chr4	191154276	1467708	0.0077	2.6865
chr5	180915260	549342	0.003	1.2611
chr6	171115067	1567109	0.0092	3.7996
chr7	159138663	1494052	0.0094	2.5484
chr8	146364022	730061	0.005	1.356
chr9	141213431	581845	0.0041	1.2609
chr10	135534747	1365765	0.0101	3.1816
chr11	135006516	2039531	0.0151	3.7509
chr12	133851895	1698369	0.0127	3.2499
chr13	115169878	1537806	0.0134	3.3092
chr14	107349540	334732	0.0031	1.2358
chr15	102531392	712077	0.0069	2.022
chr16	90354753	537438	0.0059	2.2457
chr17	81195210	1388410	0.0171	4.2696
chr18	78077248	170881	0.0022	0.6327
chr19	59128983	224586	0.0038	0.9463
chr20	63025520	196319	0.0031	0.7203
chr21	48129895	223495	0.0046	1.1233
chr22	51304566	90234	0.0018	0.3605
chrMT	16571	2547941	153.759	639.8162
chrX	155270560	28876182	0.186	11.1723

chrY	59373566	458218	0.0077	1.9421

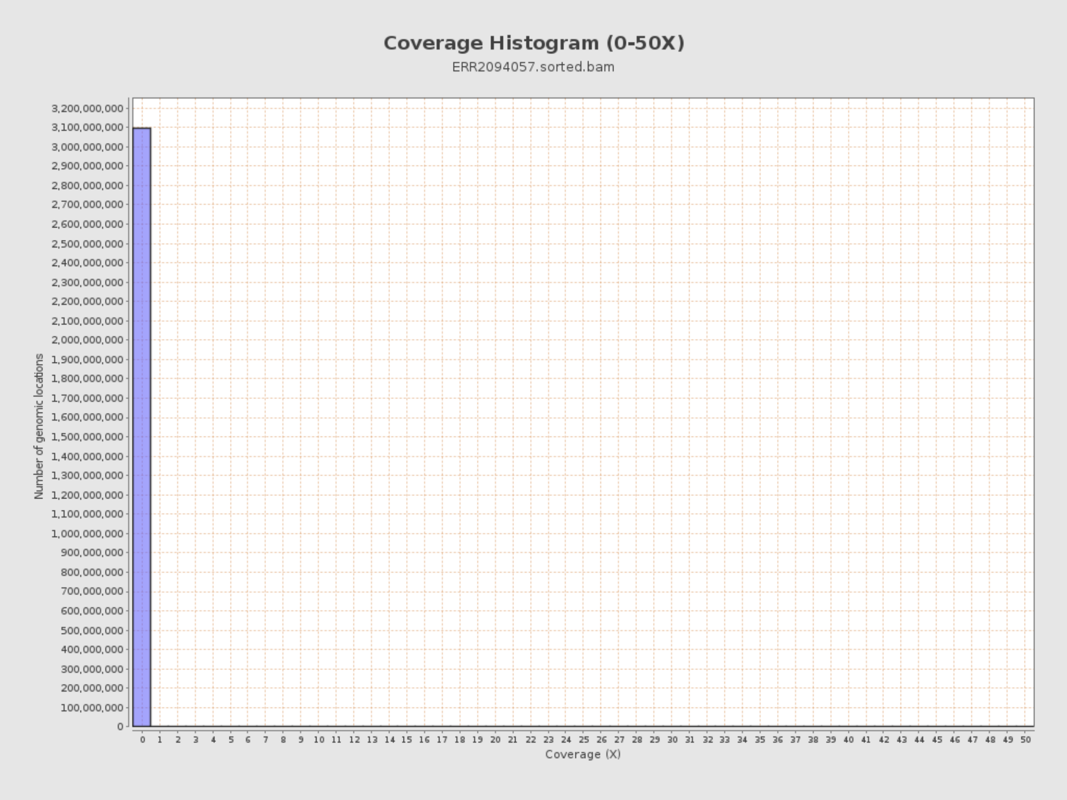
3. Results : Coverage across reference



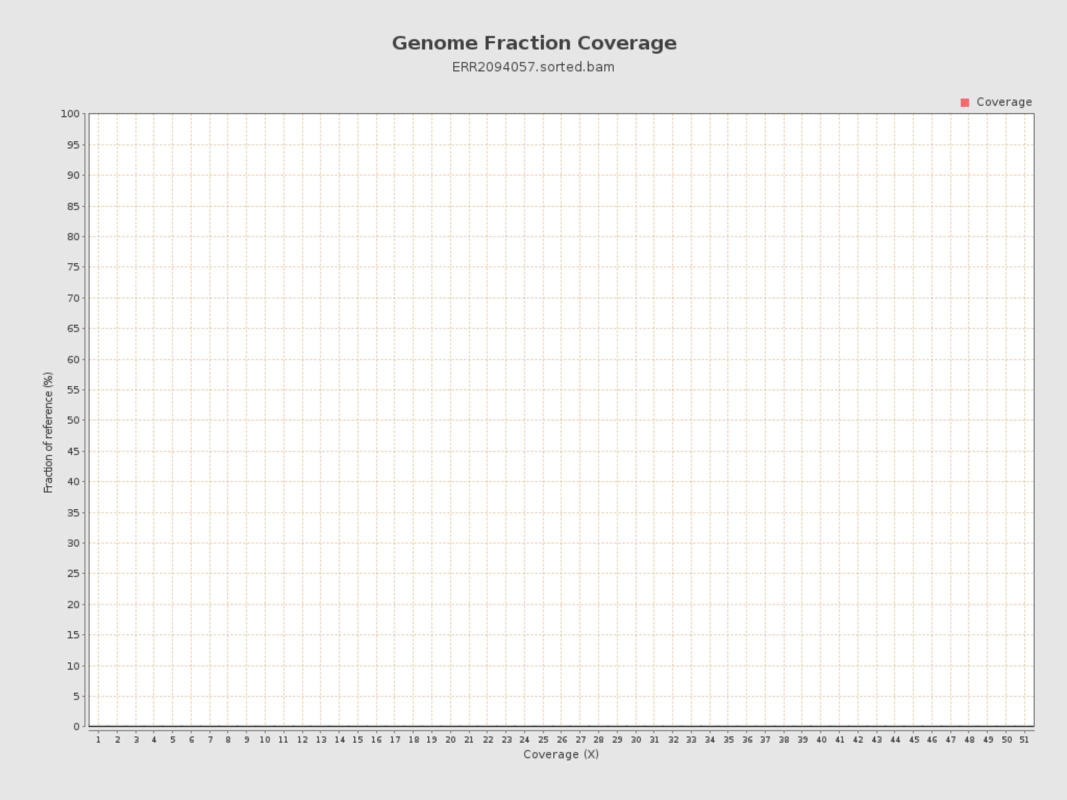
4. Results : Coverage Histogram



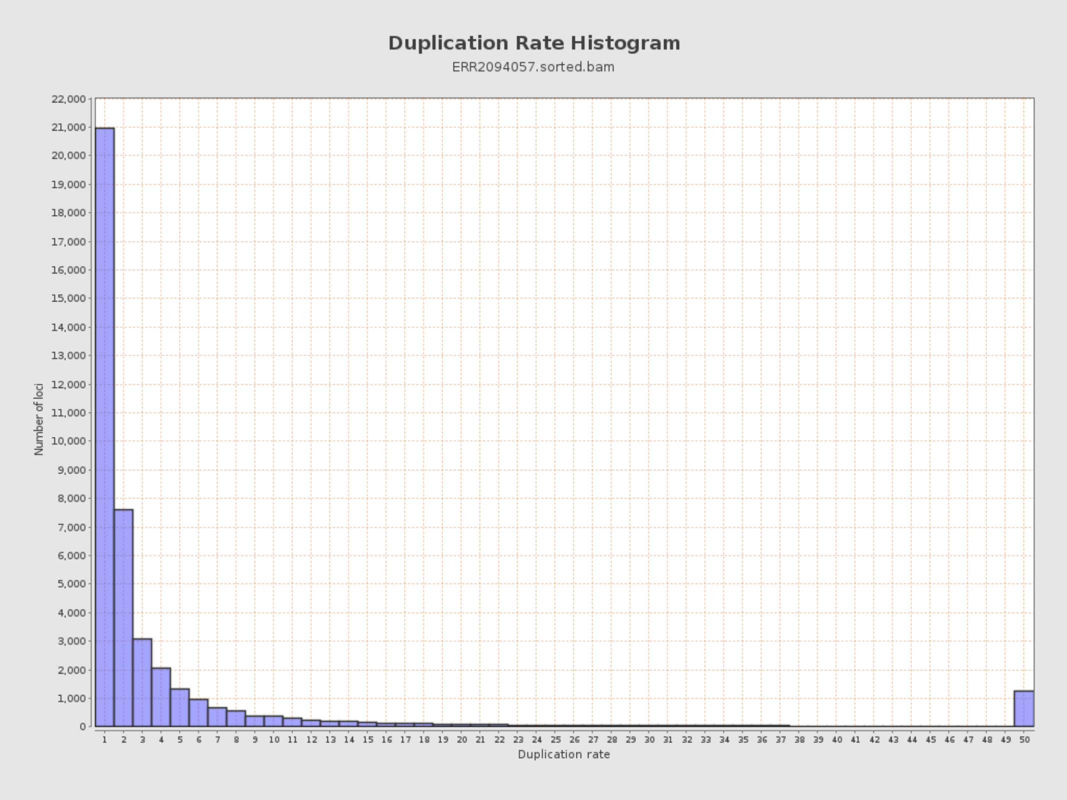
5. Results : Coverage Histogram (0-50X)



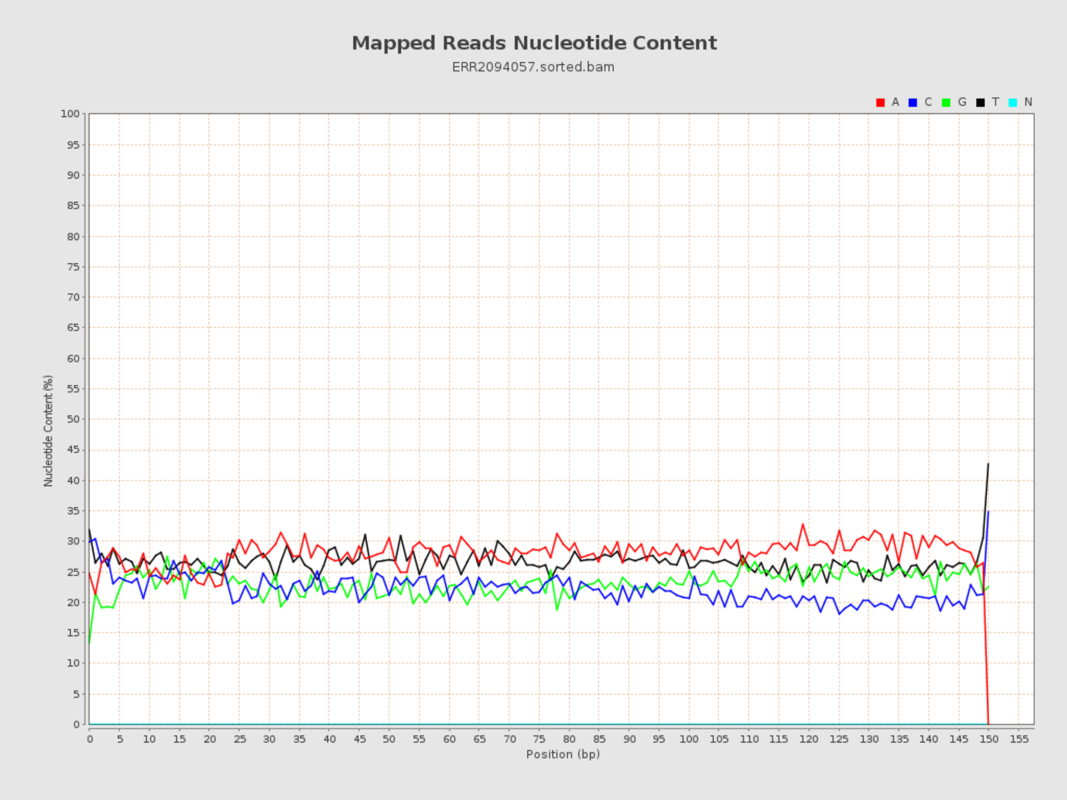
6. Results : Genome Fraction Coverage



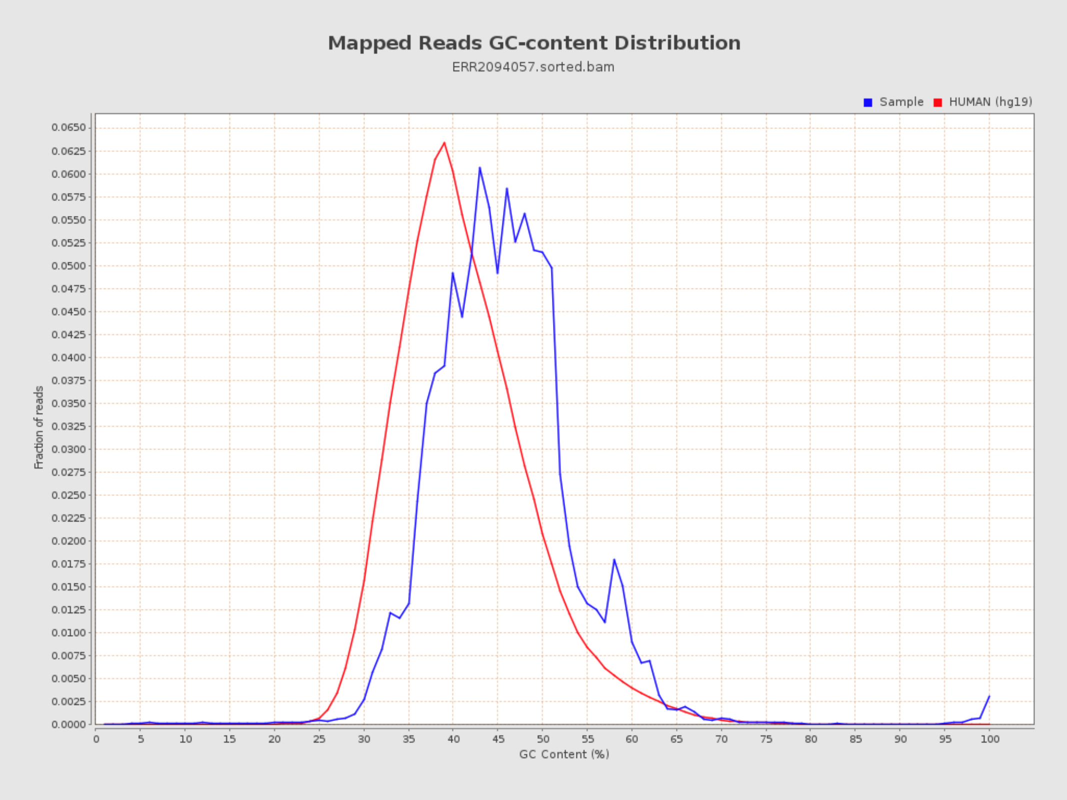
7. Results : Duplication Rate Histogram



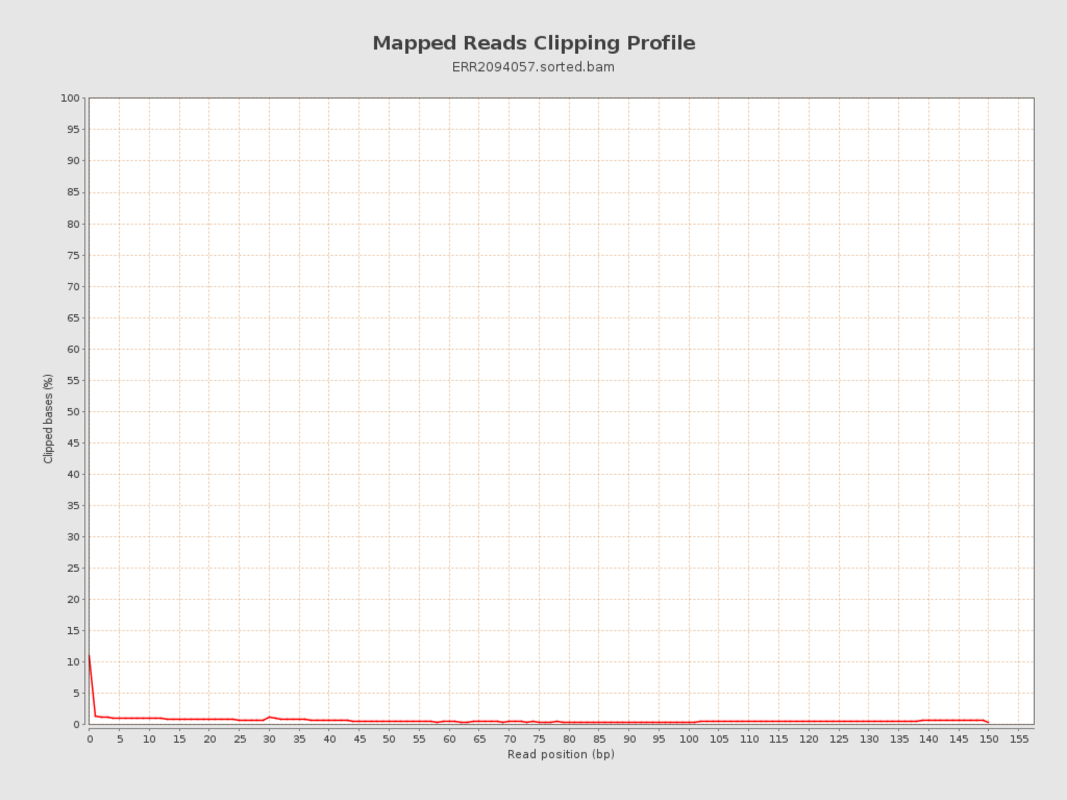
8. Results : Mapped Reads Nucleotide Content



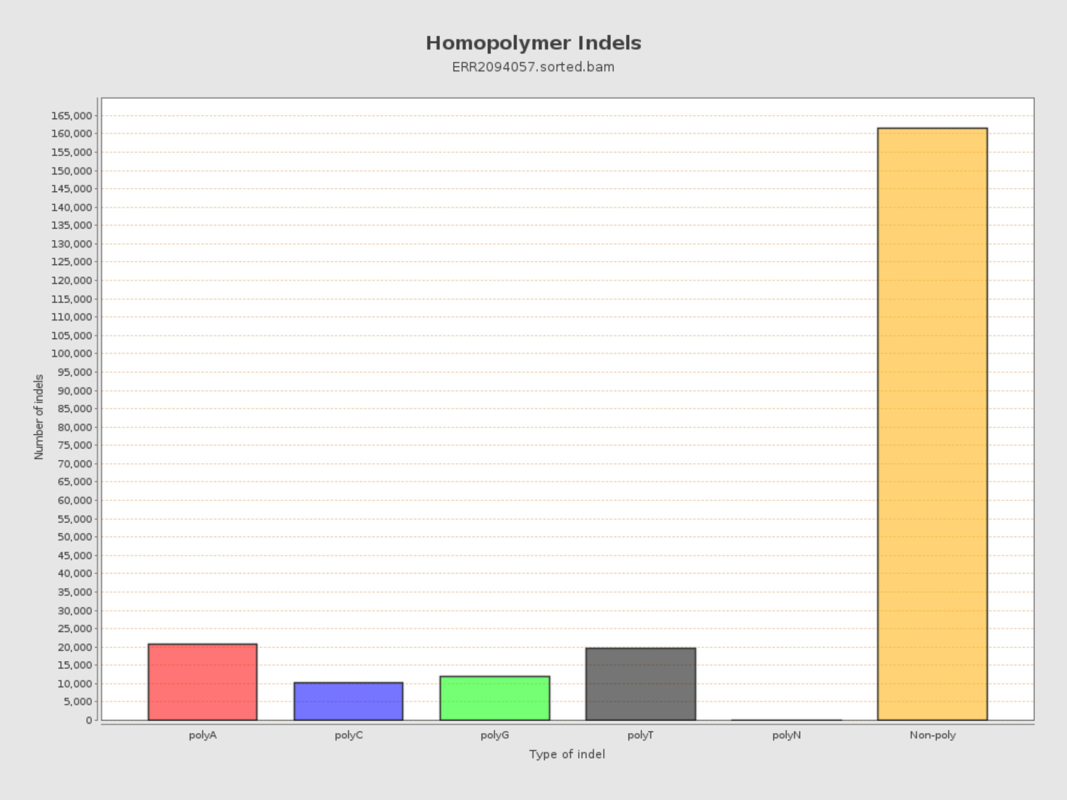
9. Results : Mapped Reads GC-content Distribution



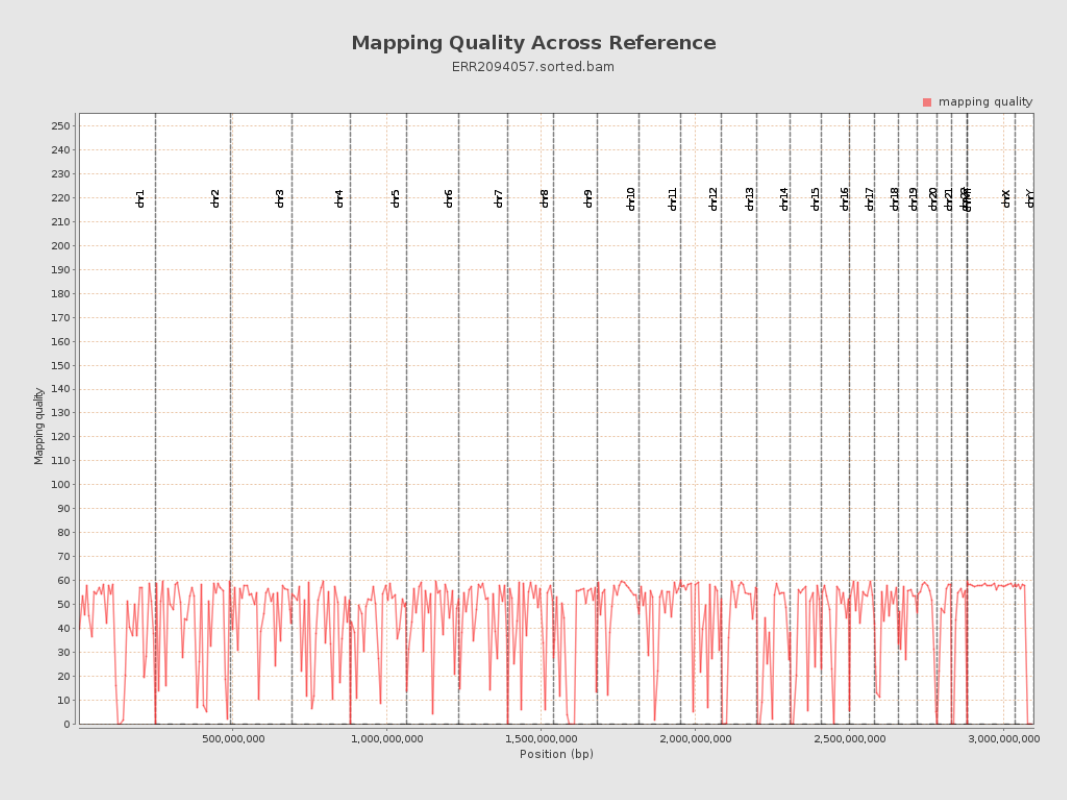
10. Results : Mapped Reads Clipping Profile



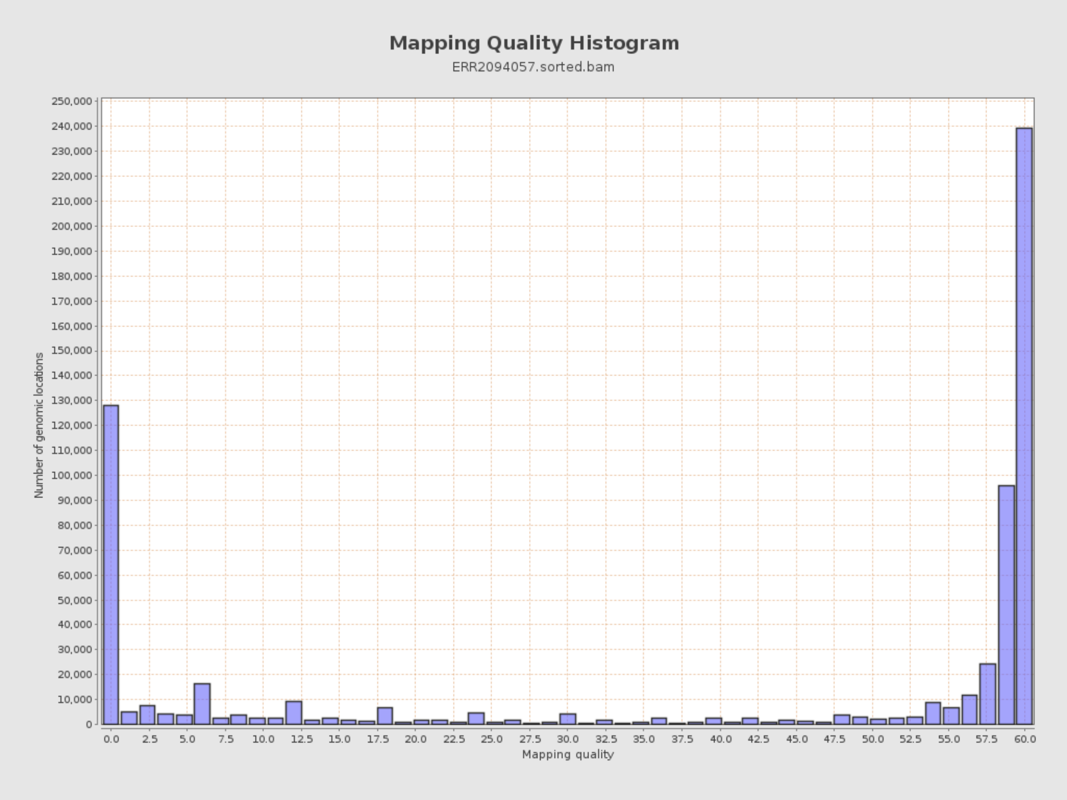
11. Results : Homopolymer Indels



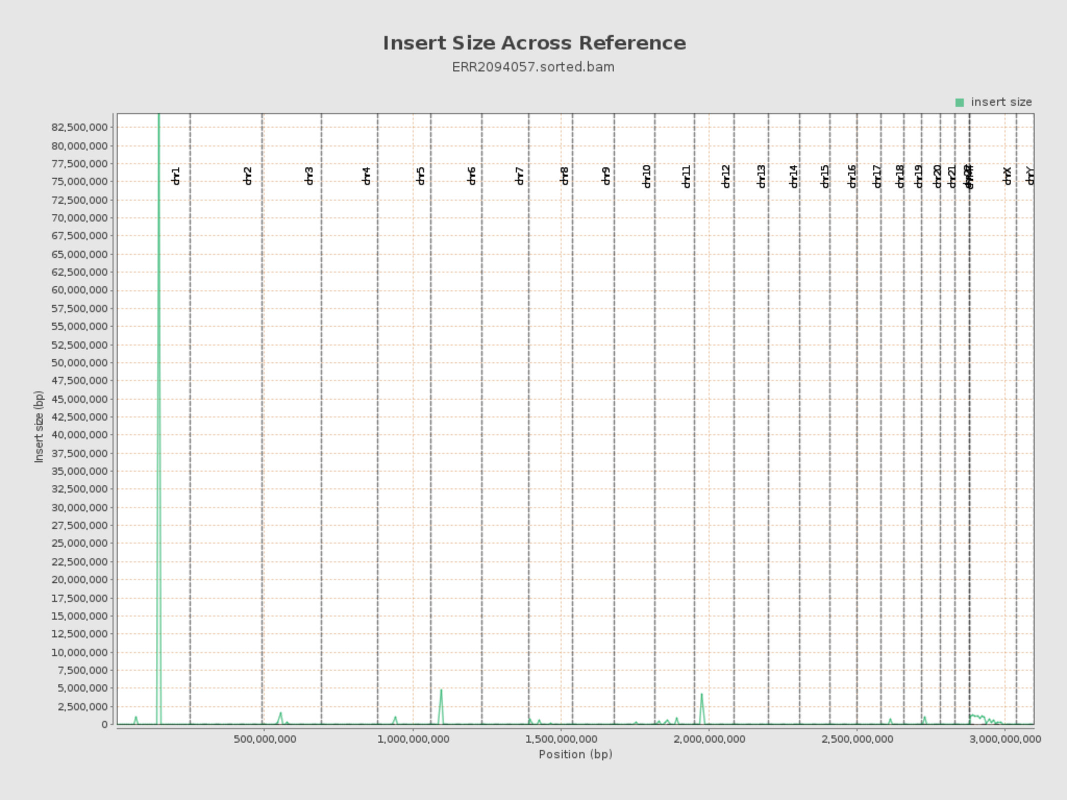
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram