Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:51:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094055.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_ERR2094055 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094055_1.fastq.gz ERR2094055_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:51:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	453,752
Mapped reads	431,281 / 95.05%
Unmapped reads	22,471 / 4.95%
Mapped paired reads	431,281 / 95.05%
Mapped reads, first in pair	216,587 / 47.73%
Mapped reads, second in pair	214,694 / 47.32%
Mapped reads, both in pair	428,518 / 94.44%
Mapped reads, singletons	2,763 / 0.61%
Secondary alignments	0
Supplementary alignments	18,961 / 4.18%
Read min/max/mean length	30 / 151 / 141.09
Duplicated reads (estimated)	412,127 / 90.83%
Duplication rate	50.23%
Clipped reads	181,596 / 40.02%

2.2. ACGT Content

Number/percentage of A's	15,598,048 / 27.77%
Number/percentage of C's	12,554,095 / 22.35%
Number/percentage of T's	14,947,811 / 26.61%
Number/percentage of G's	13,077,093 / 23.28%
Number/percentage of N's	674 / 0%

GC Percentage	45.63%

2.3. Coverage

Mean	0.0186
Standard Deviation	4.8833

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Insert size

Mean	537,202.63
Standard Deviation	6,620,356.29
P25/Median/P75	139 / 170 / 202

2.6. Mismatches and indels

General error rate	4.31%
Mismatches	2,348,202
Insertions	40,356
Mapped reads with at least one insertion	9.19%
Deletions	186,231
Mapped reads with at least one deletion	40.18%
Homopolymer indels	28.6%

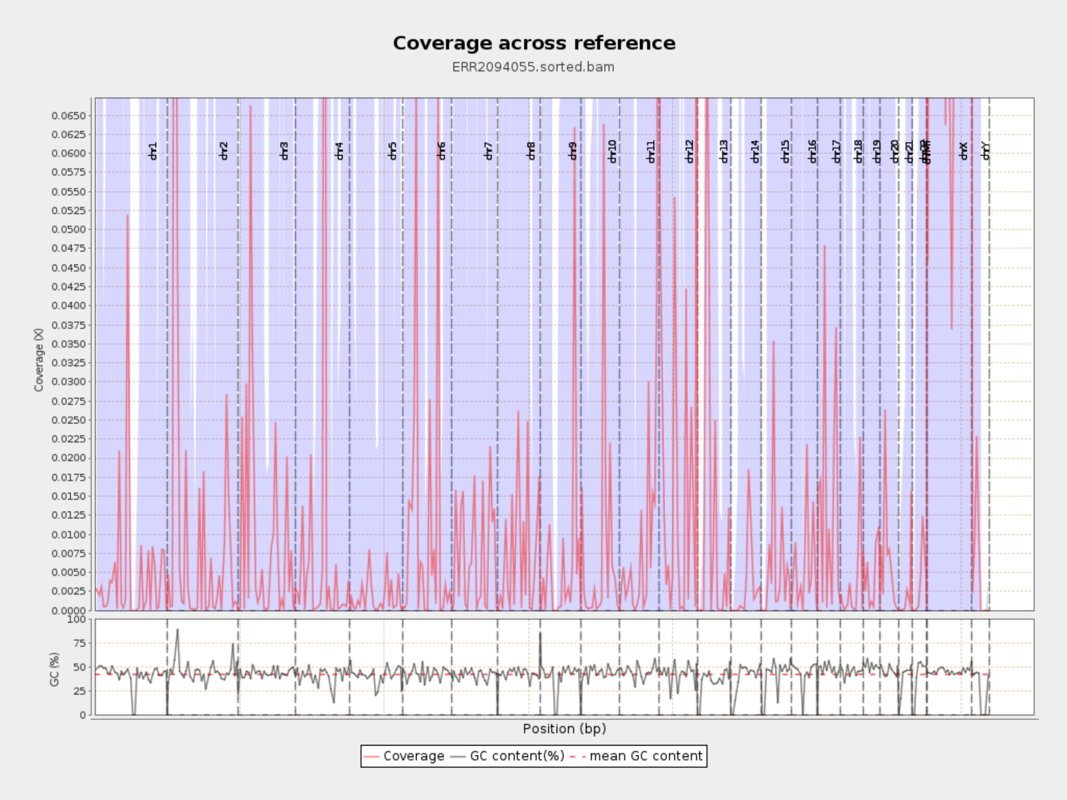
2.7. Chromosome stats

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

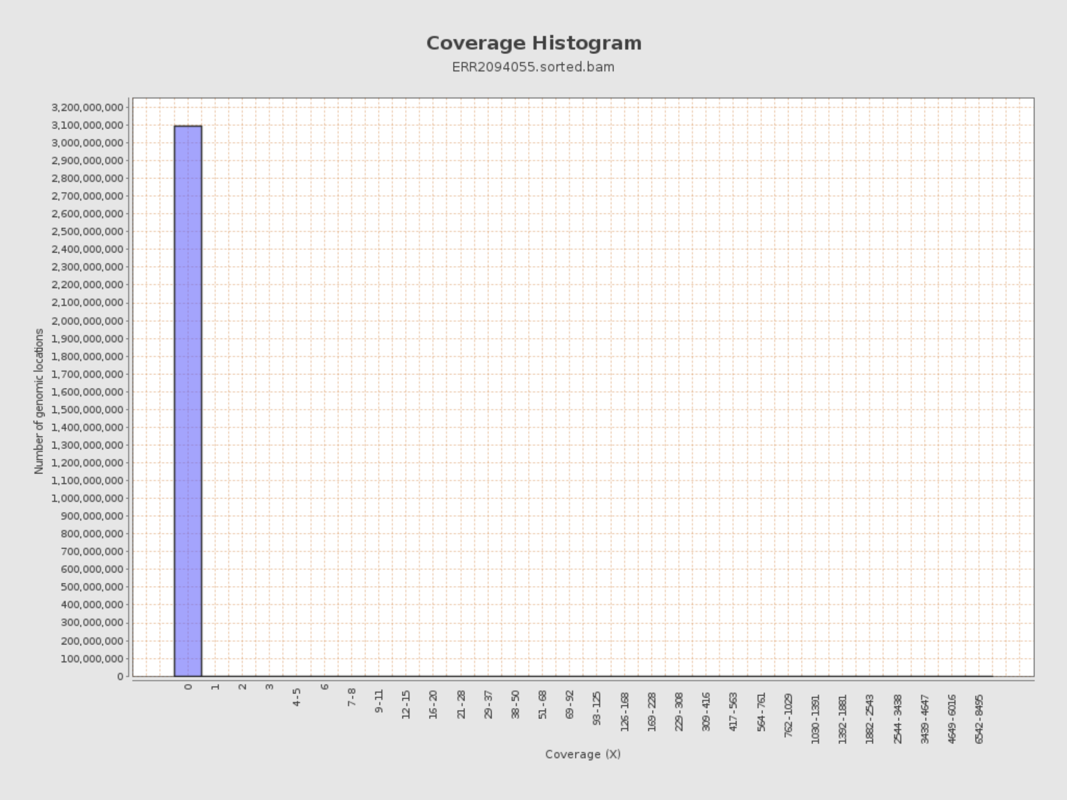
		bases	**coverage**	**deviation**
chr1	249250621	1161478	0.0047	2.0187
chr2	243199373	2595182	0.0107	3.5662
chr3	198022430	1952405	0.0099	3.0954
chr4	191154276	1827003	0.0096	3.0692
chr5	180915260	358418	0.002	0.5757
chr6	171115067	1955335	0.0114	4.9077
chr7	159138663	1141522	0.0072	1.85
chr8	146364022	1107759	0.0076	2.0803
chr9	141213431	950819	0.0067	2.7567
chr10	135534747	1045742	0.0077	2.9625
chr11	135006516	1298368	0.0096	2.5958
chr12	133851895	2438531	0.0182	4.9715
chr13	115169878	1402438	0.0122	3.6388
chr14	107349540	360225	0.0034	1.351
chr15	102531392	605684	0.0059	1.612
chr16	90354753	538269	0.006	1.7758
chr17	81195210	1216724	0.015	3.6457
chr18	78077248	288201	0.0037	1.0914
chr19	59128983	262380	0.0044	0.892
chr20	63025520	439254	0.007	2.0651
chr21	48129895	106516	0.0022	0.572
chr22	51304566	175880	0.0034	0.8031
chrMT	16571	4474482	270.0188	1,090.8322
chrX	155270560	29540278	0.1903	13.7394

chrY	59373566	336410	0.0057	1.4572

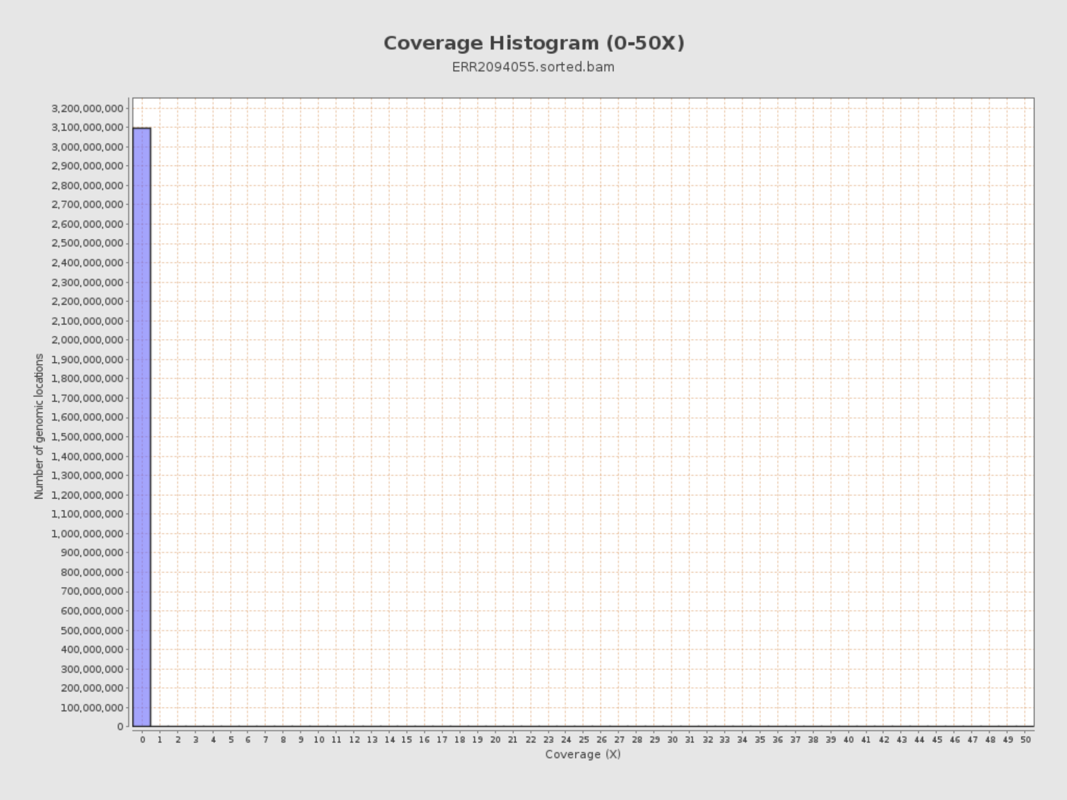
3. Results : Coverage across reference



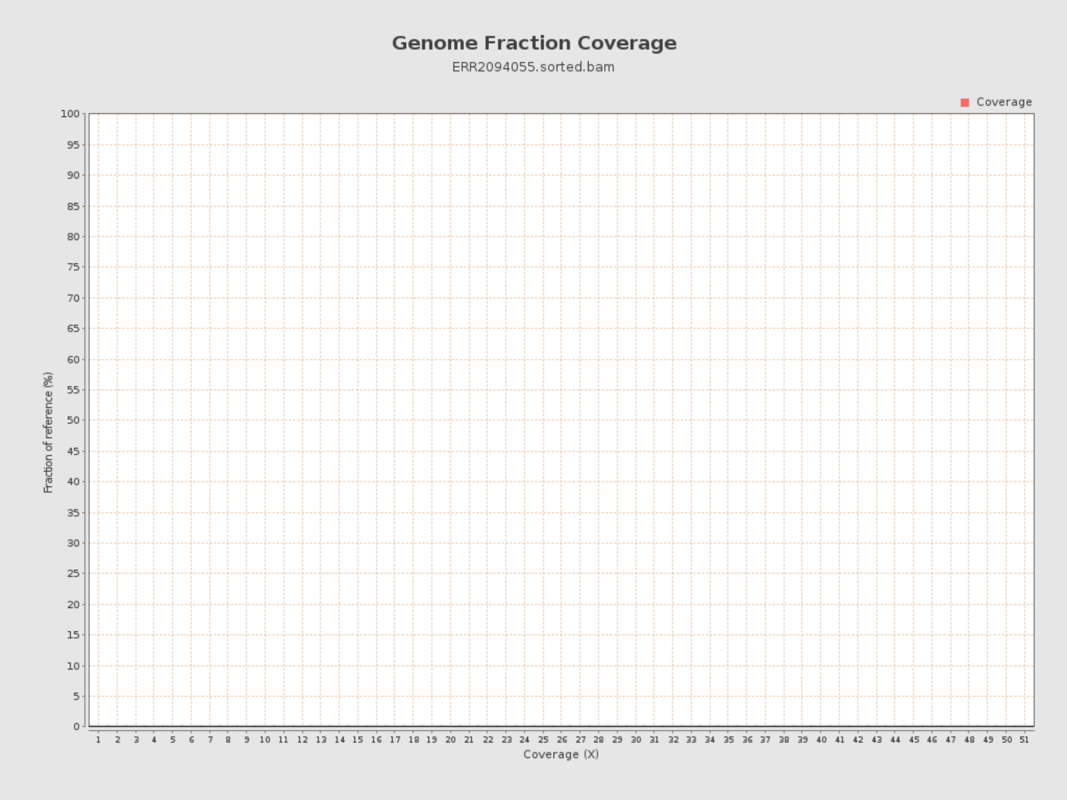
4. Results : Coverage Histogram



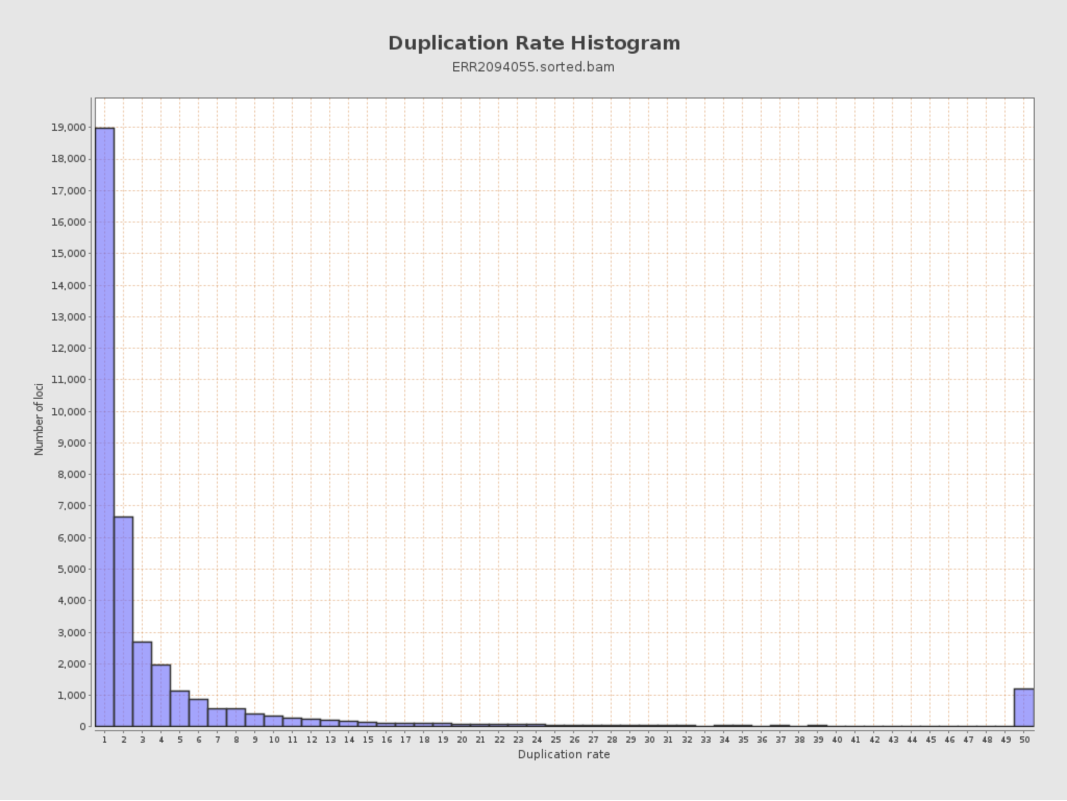
5. Results : Coverage Histogram (0-50X)



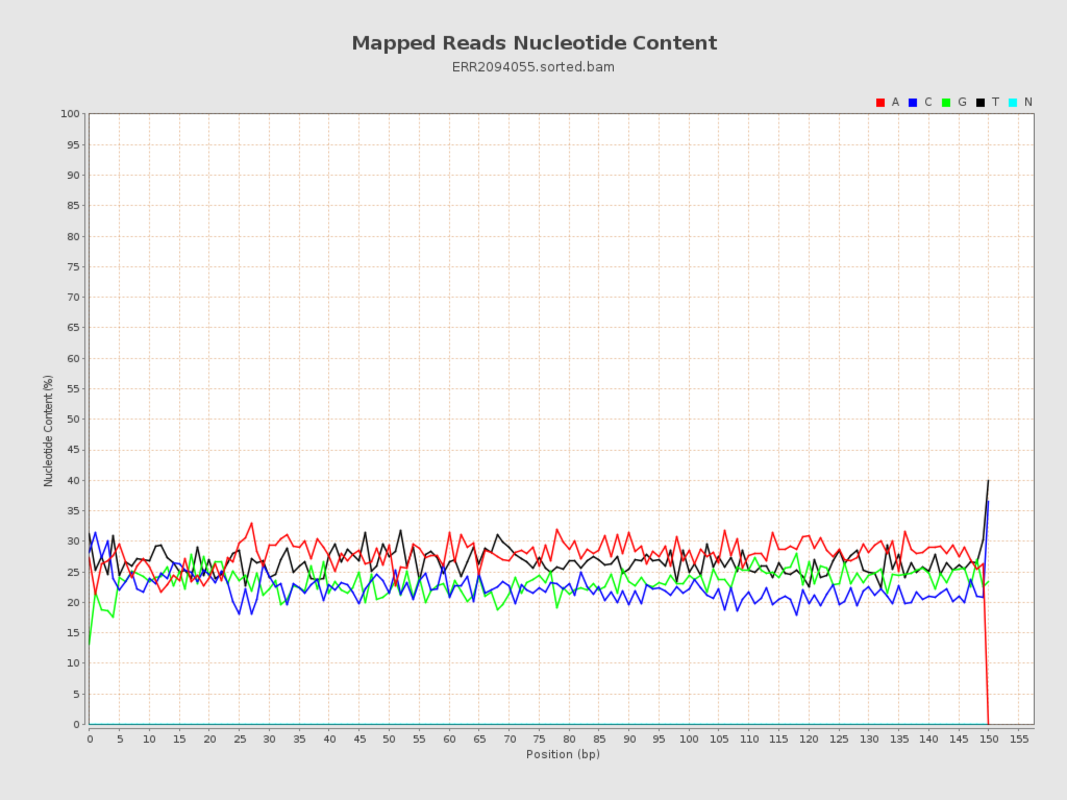
6. Results : Genome Fraction Coverage



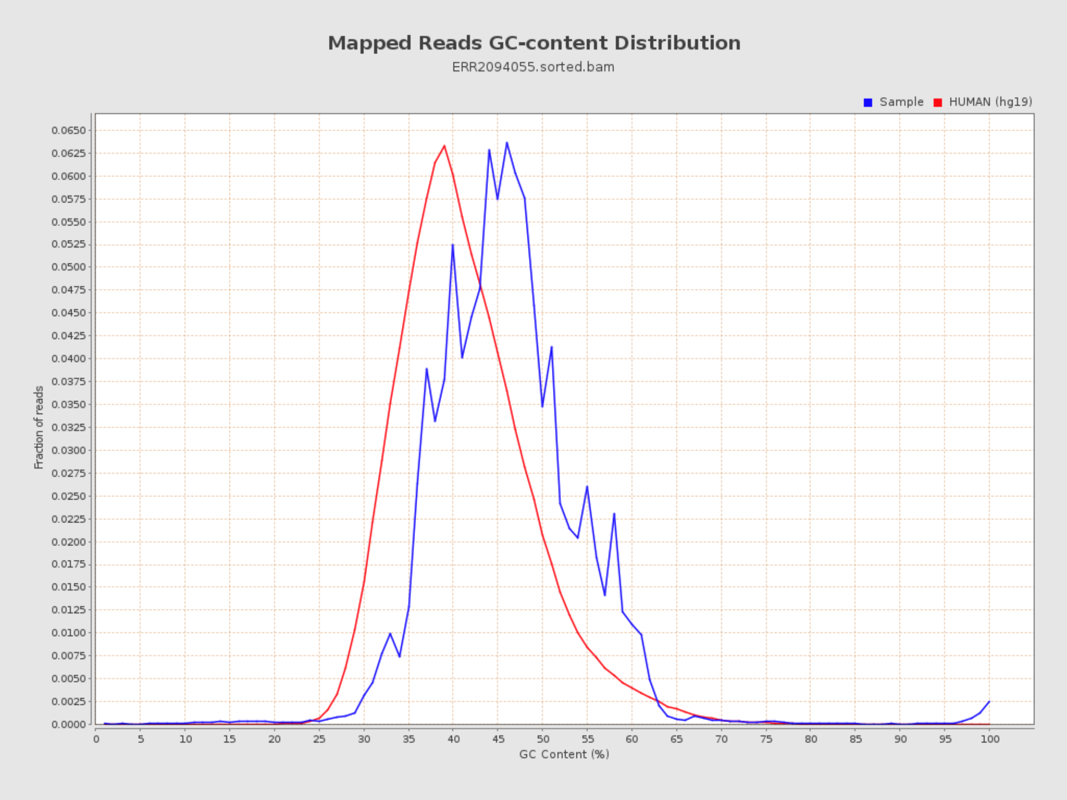
7. Results : Duplication Rate Histogram



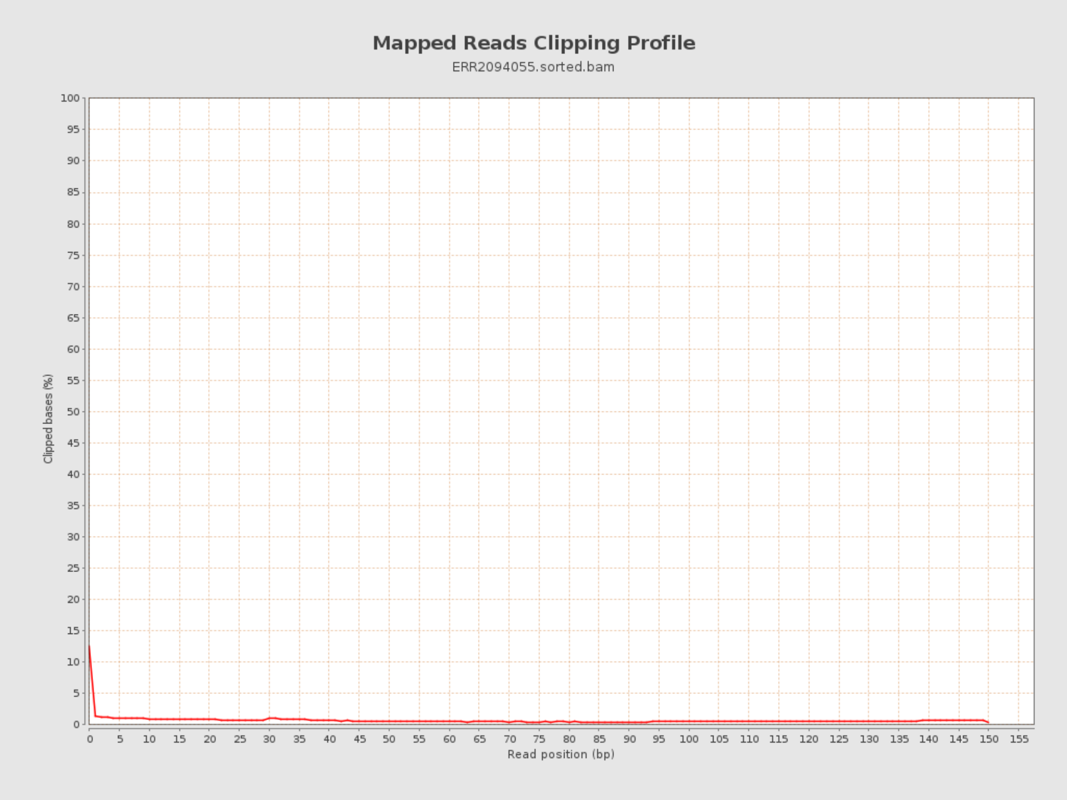
8. Results : Mapped Reads Nucleotide Content



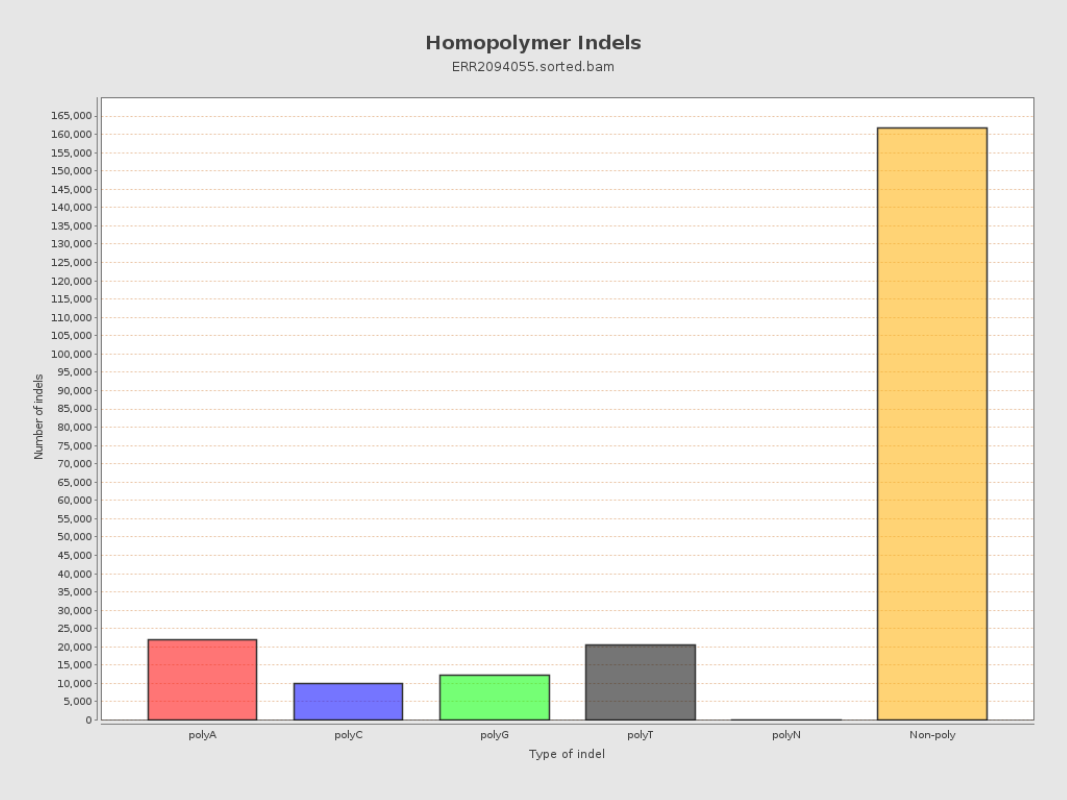
9. Results : Mapped Reads GC-content Distribution



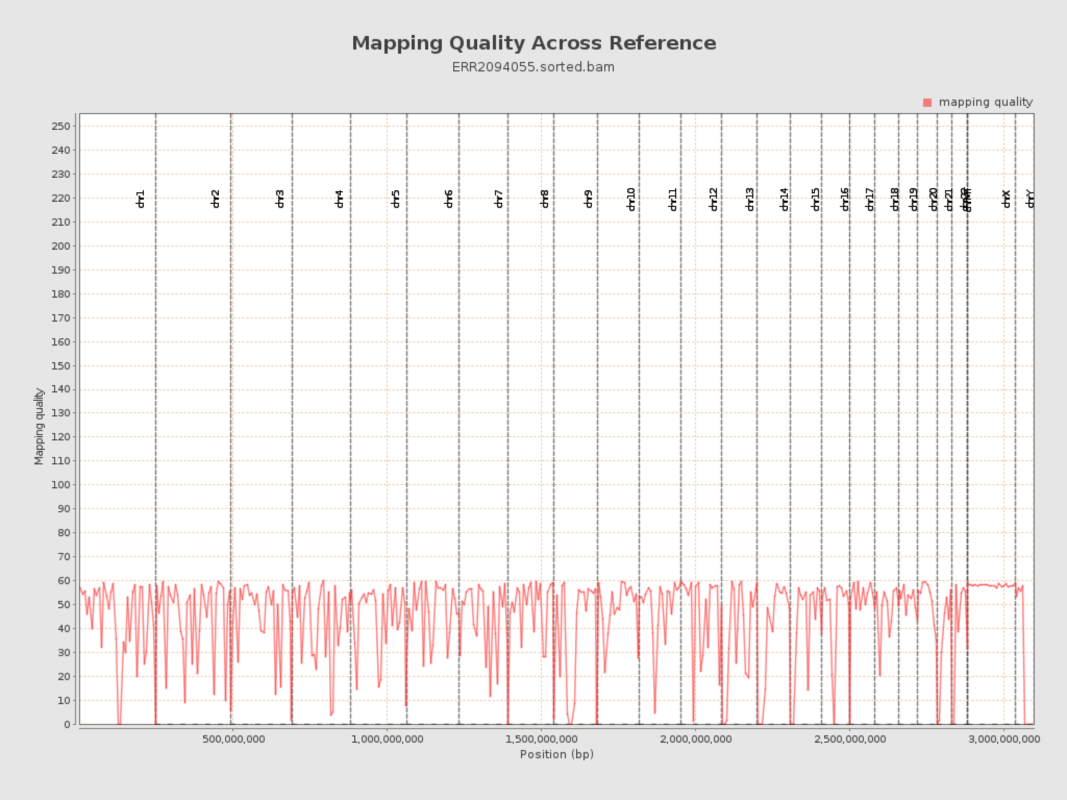
10. Results : Mapped Reads Clipping Profile



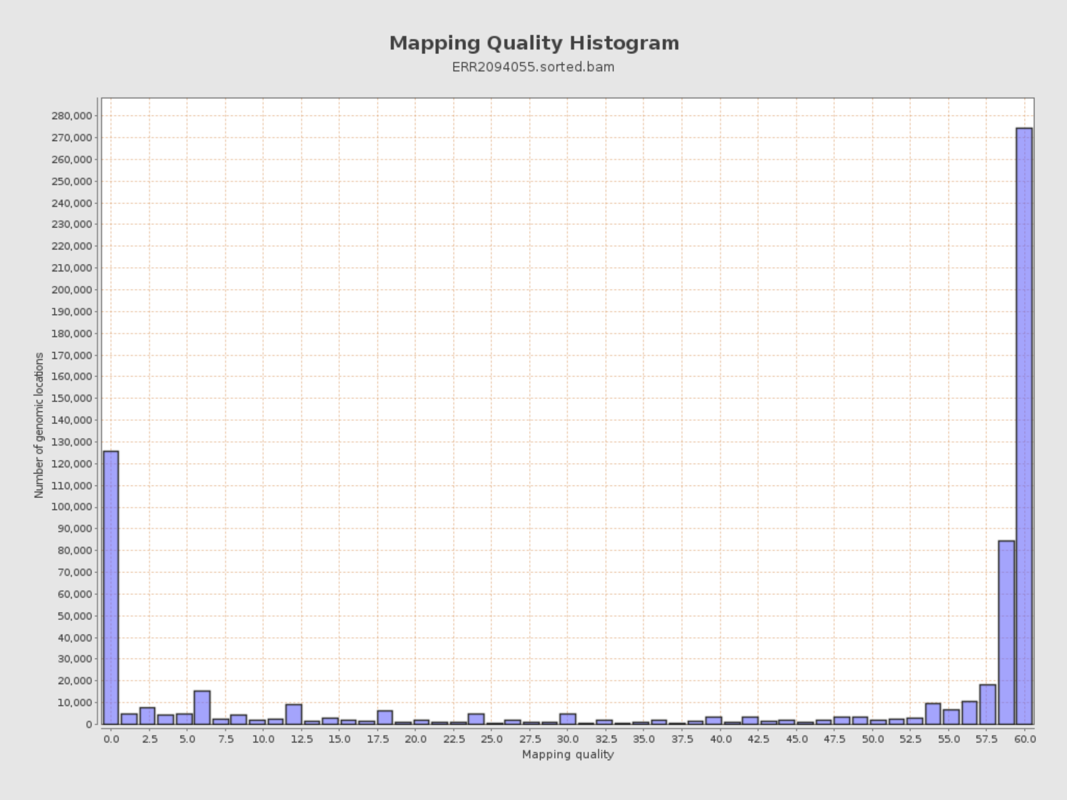
11. Results : Homopolymer Indels



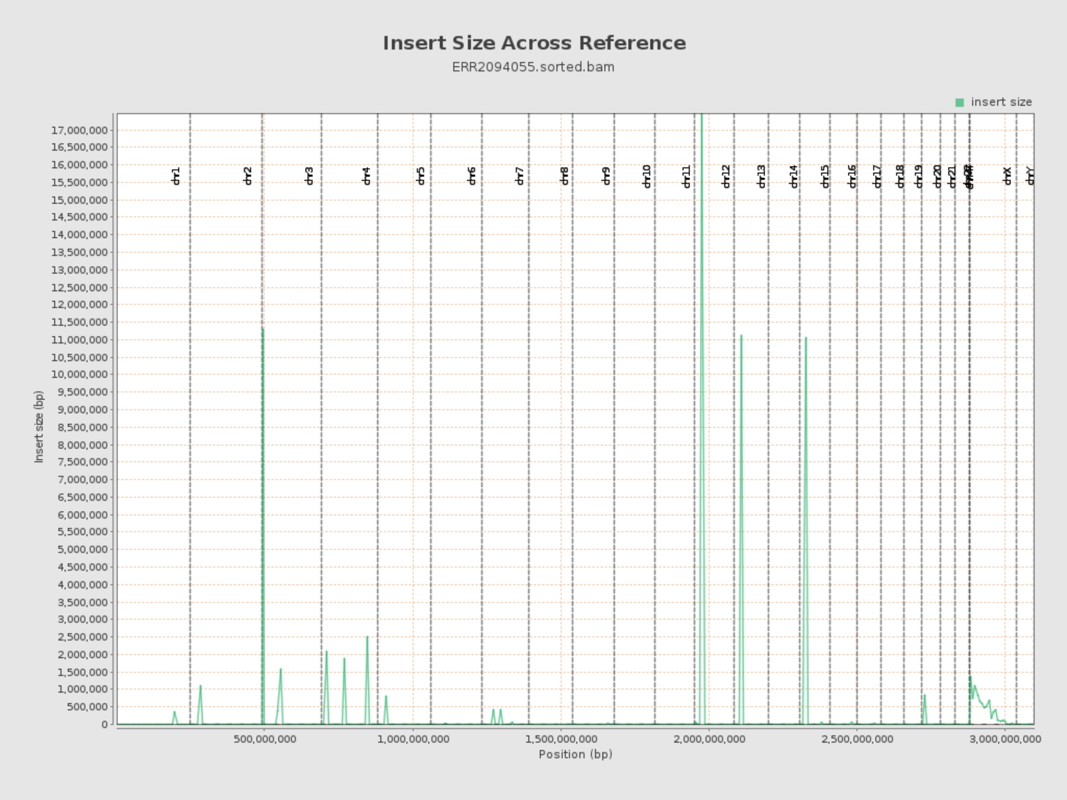
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram