Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:10:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094058.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_ERR2094058 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094058_1.fastq.gz ERR2094058_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:10:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	432,402
Mapped reads	409,130 / 94.62%
Unmapped reads	23,272 / 5.38%
Mapped paired reads	409,130 / 94.62%
Mapped reads, first in pair	205,444 / 47.51%
Mapped reads, second in pair	203,686 / 47.11%
Mapped reads, both in pair	406,216 / 93.94%
Mapped reads, singletons	2,914 / 0.67%
Secondary alignments	0
Supplementary alignments	11,924 / 2.76%
Read min/max/mean length	30 / 151 / 139.21
Duplicated reads (estimated)	392,056 / 90.67%
Duplication rate	50.34%
Clipped reads	155,040 / 35.86%

2.2. ACGT Content

Number/percentage of A's	14,569,731 / 27.52%
Number/percentage of C's	11,989,029 / 22.64%
Number/percentage of T's	14,095,487 / 26.62%
Number/percentage of G's	12,296,073 / 23.22%
Number/percentage of N's	573 / 0%

GC Percentage	45.86%

2.3. Coverage

Mean	0.0175
Standard Deviation	5.8863

2.4. Mapping Quality

Mean Mapping Quality	41.91

2.5. Insert size

Mean	278,044.94
Standard Deviation	4,823,025.51
P25/Median/P75	134 / 168 / 195

2.6. Mismatches and indels

General error rate	4.3%
Mismatches	2,196,214
Insertions	44,728
Mapped reads with at least one insertion	10.71%
Deletions	179,760
Mapped reads with at least one deletion	40.34%
Homopolymer indels	31.11%

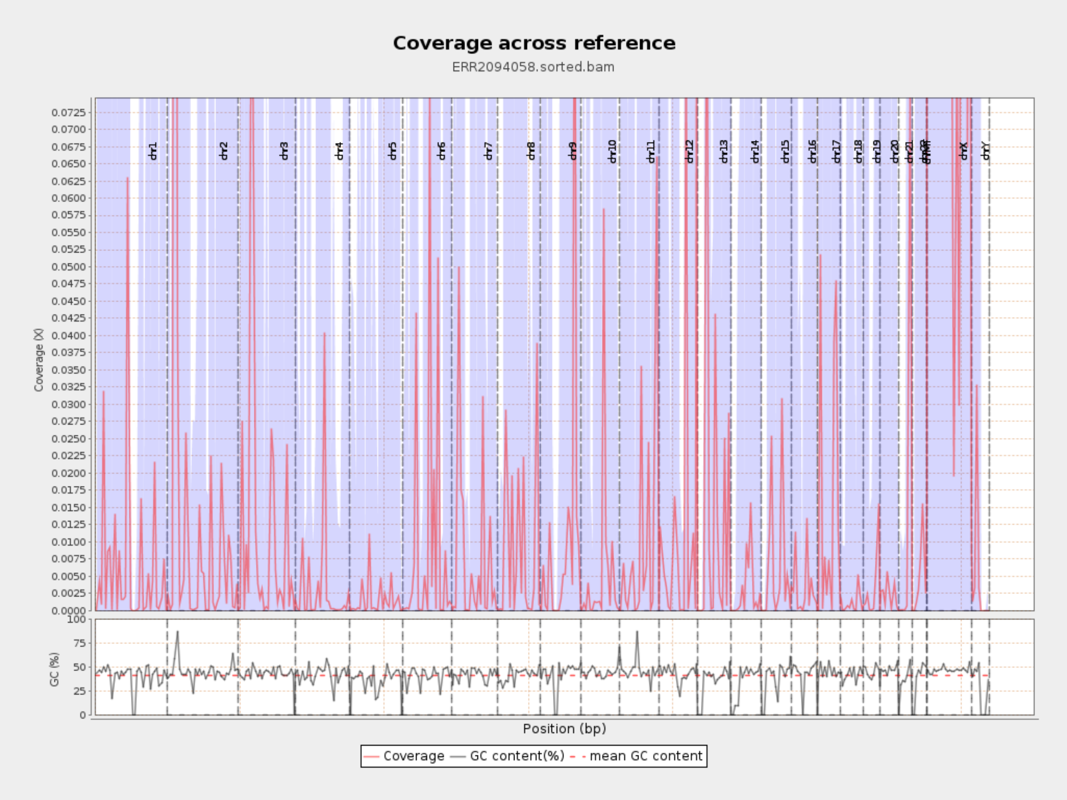
2.7. Chromosome stats

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

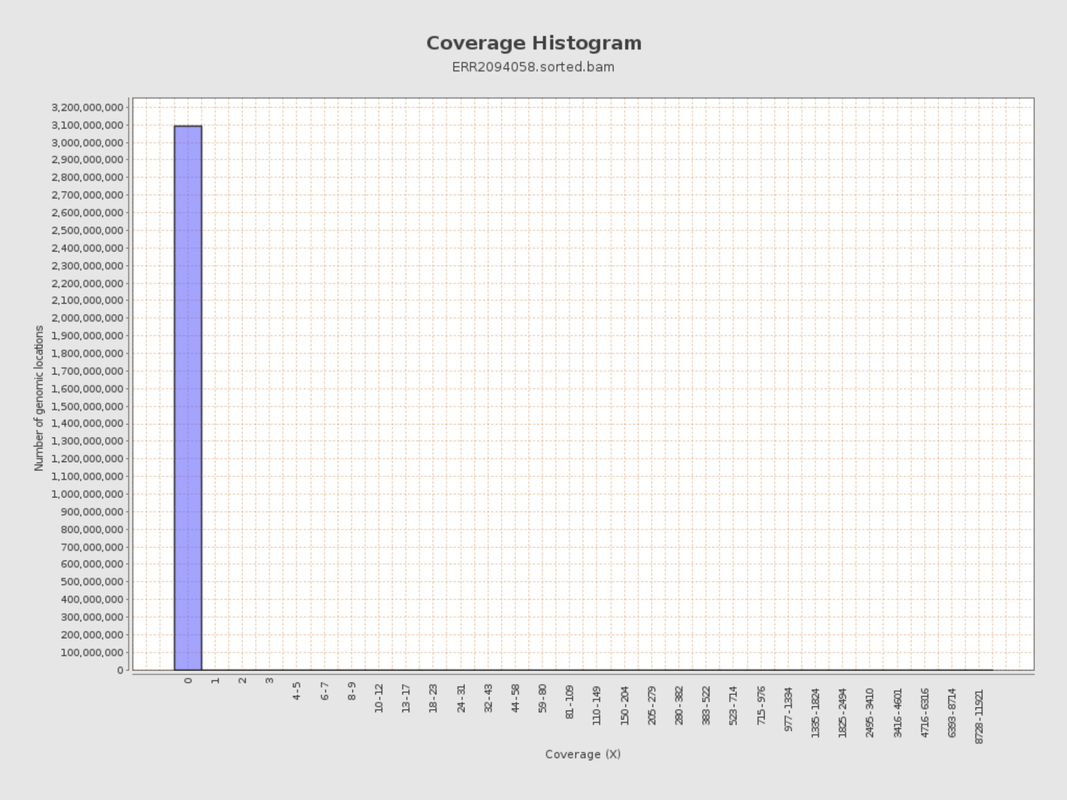
		bases	coverage	deviation
chr1	249250621	1598288	0.0064	2.7525
chr2	243199373	3645787	0.015	5.1268
chr3	198022430	2422008	0.0122	3.4681
chr4	191154276	644033	0.0034	1.4101
chr5	180915260	286960	0.0016	0.5823
chr6	171115067	1724630	0.0101	4.3364
chr7	159138663	1142249	0.0072	2.9381
chr8	146364022	1260362	0.0086	2.4395
chr9	141213431	1556874	0.011	4.4928
chr10	135534747	752685	0.0056	2.6097
chr11	135006516	1496389	0.0111	3.6989
chr12	133851895	1535411	0.0115	4.812
chr13	115169878	1758263	0.0153	4.5318
chr14	107349540	317087	0.003	0.9783
chr15	102531392	646665	0.0063	1.8477
chr16	90354753	320015	0.0035	1.2602
chr17	81195210	1307294	0.0161	4.4113
chr18	78077248	89997	0.0012	0.3244
chr19	59128983	195917	0.0033	1.0013
chr20	63025520	154532	0.0025	0.5072
chr21	48129895	790909	0.0164	6.2554
chr22	51304566	263064	0.0051	1.444
chrMT	16571	5580926	336.7887	1,415.6099
chrX	155270560	24413177	0.1572	16.0183

chrY	59373566	312524	0.0053	2.7022

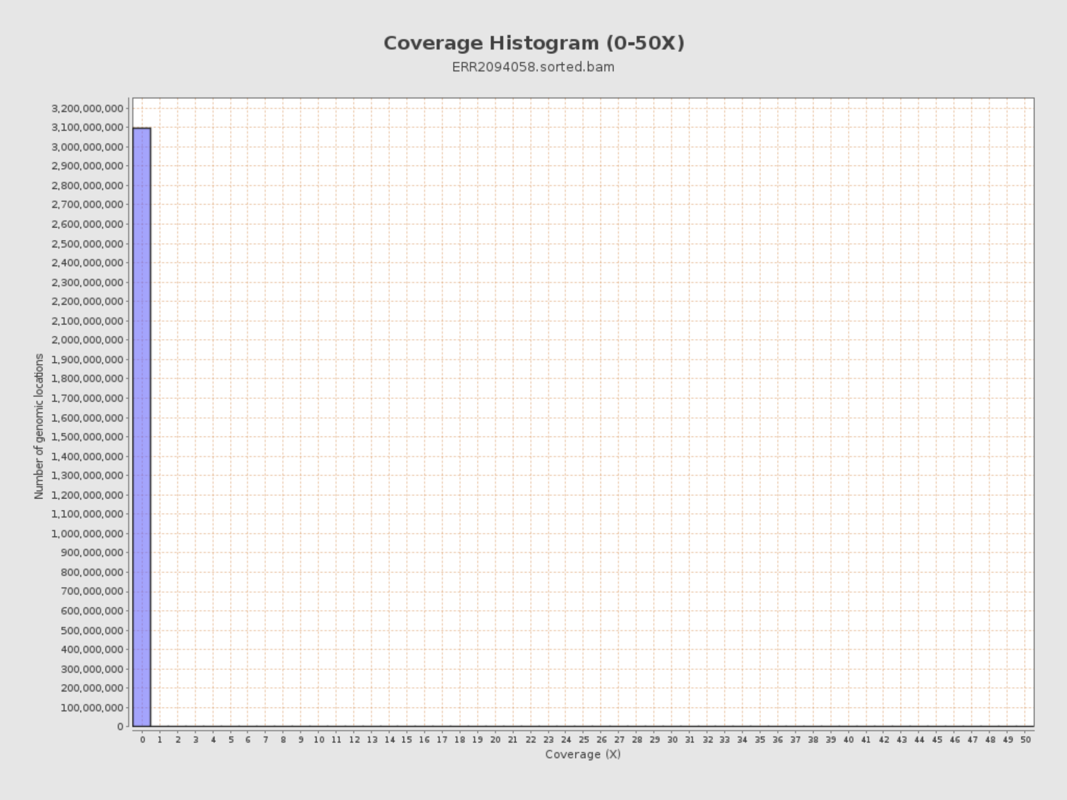
3. Results : Coverage across reference



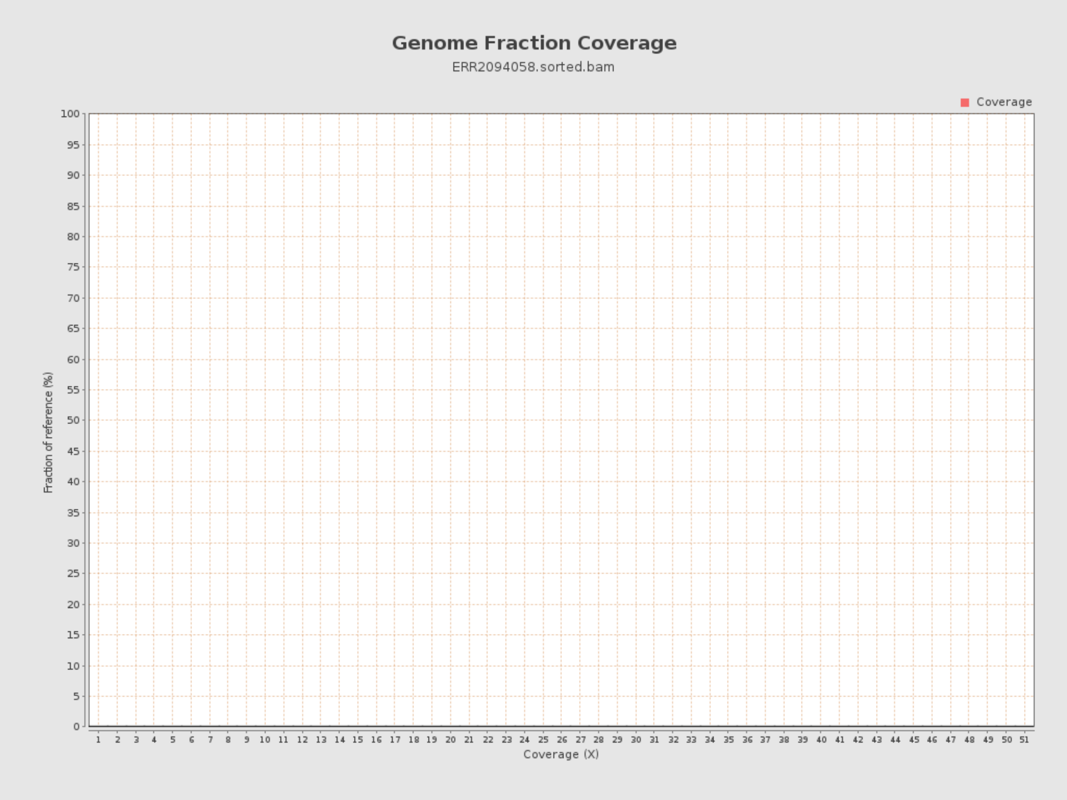
4. Results : Coverage Histogram



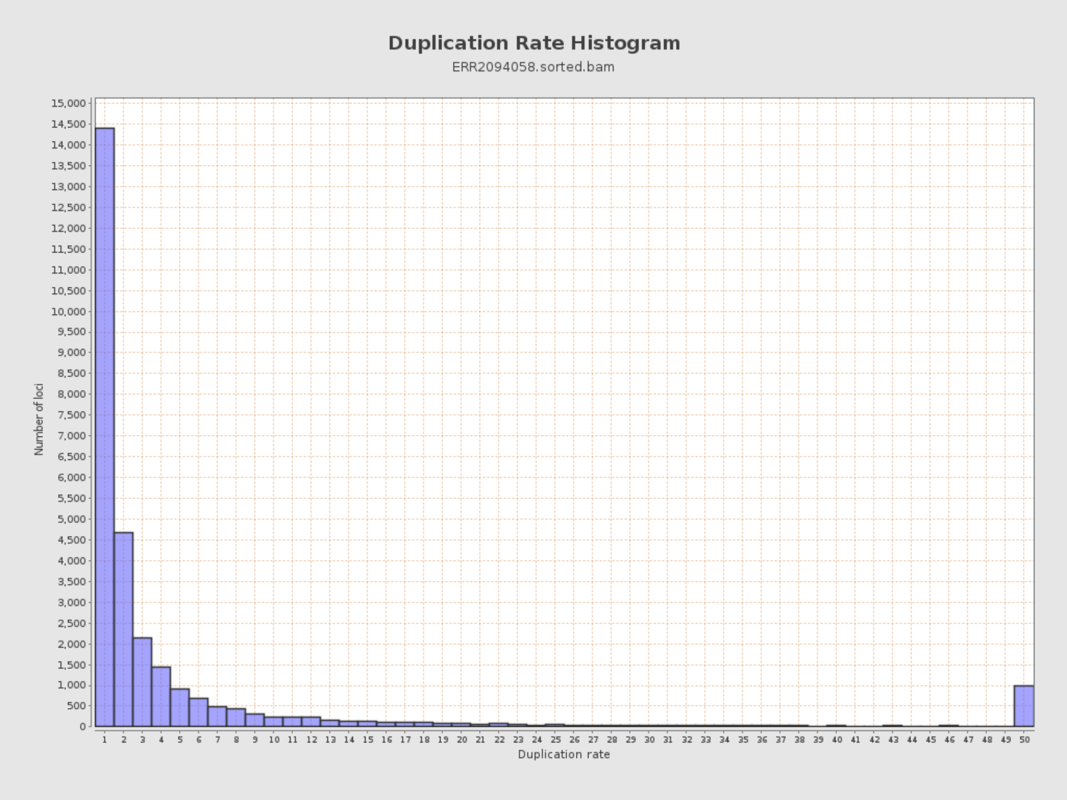
5. Results : Coverage Histogram (0-50X)



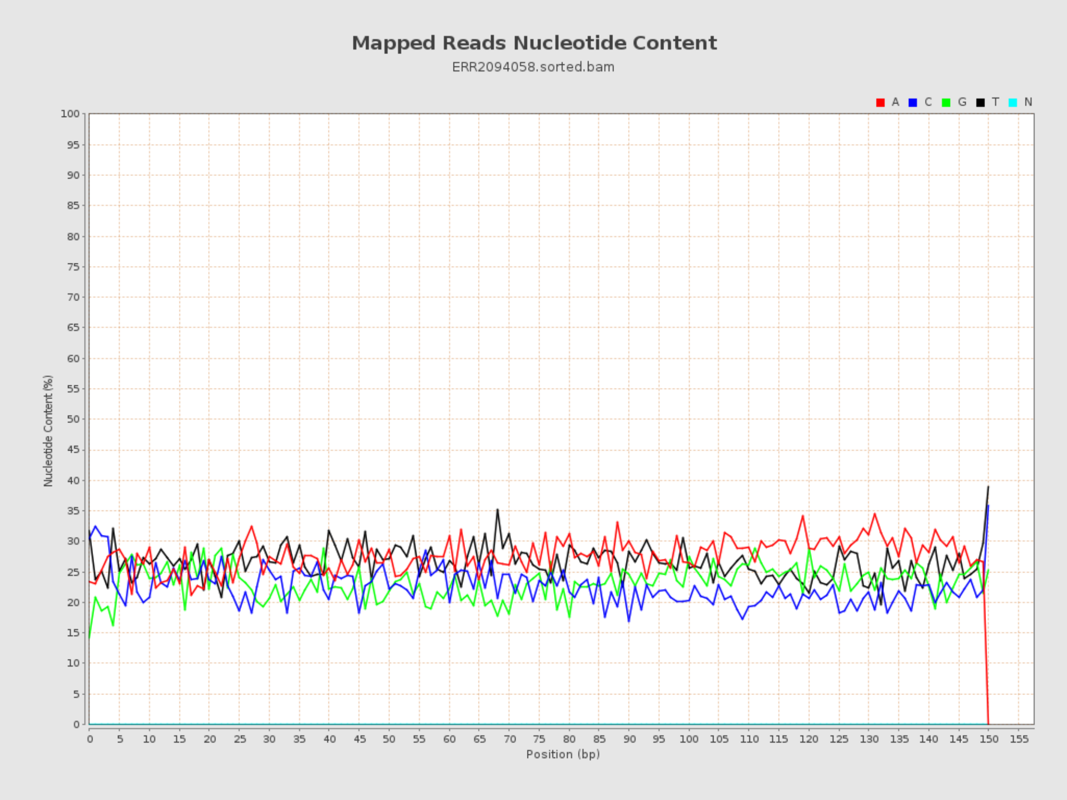
6. Results : Genome Fraction Coverage



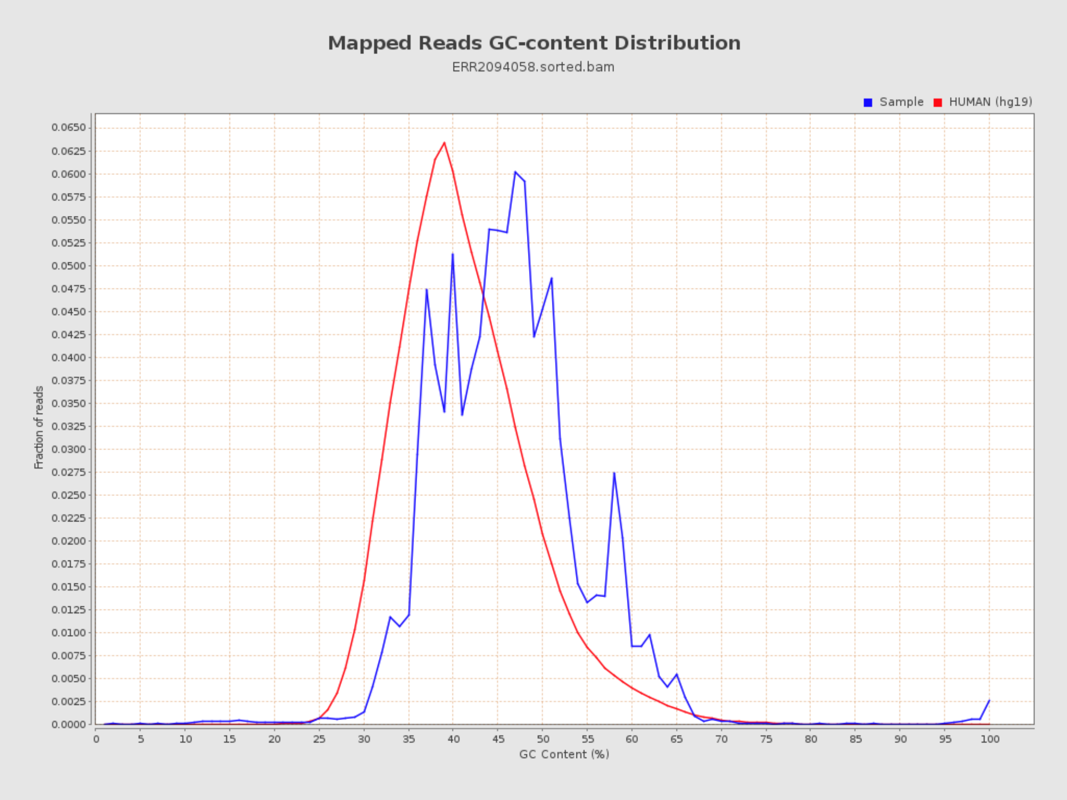
7. Results : Duplication Rate Histogram



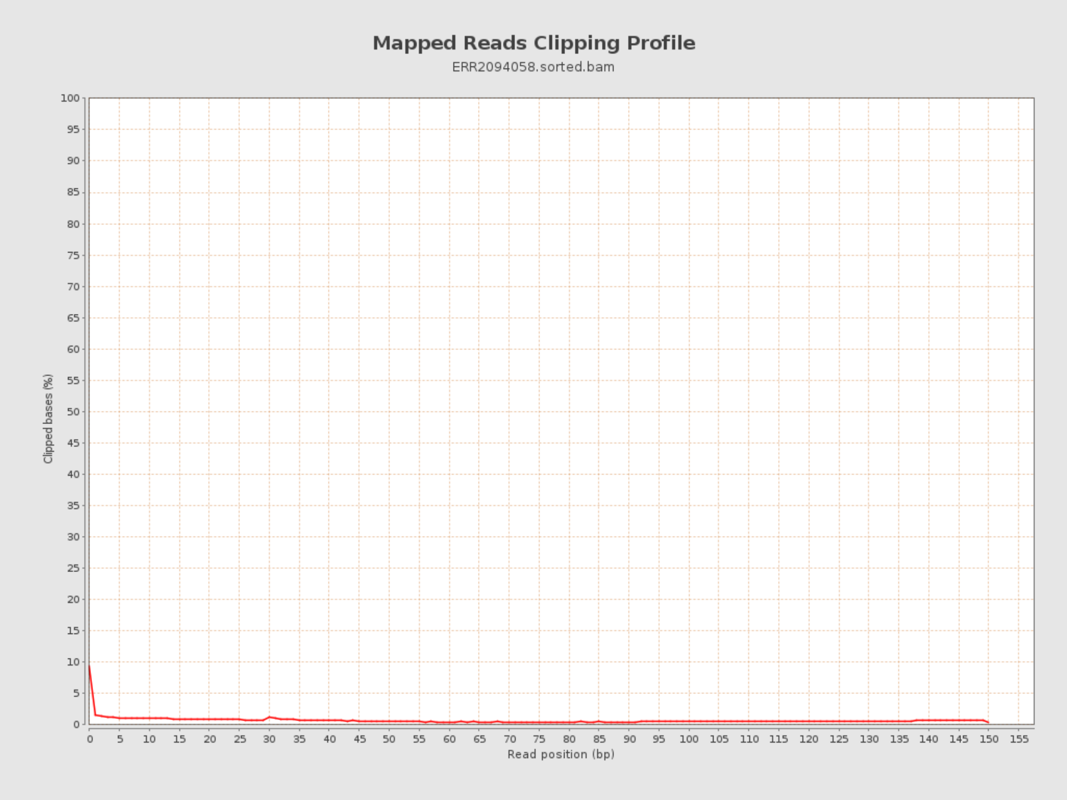
8. Results : Mapped Reads Nucleotide Content



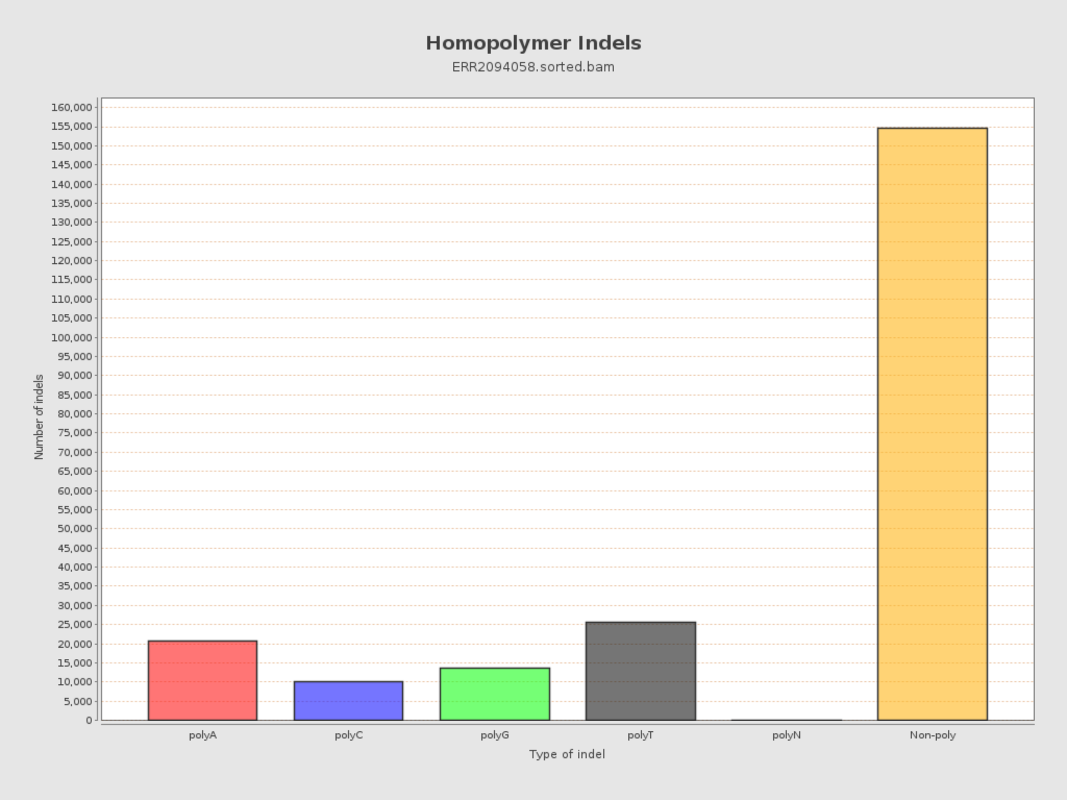
9. Results : Mapped Reads GC-content Distribution



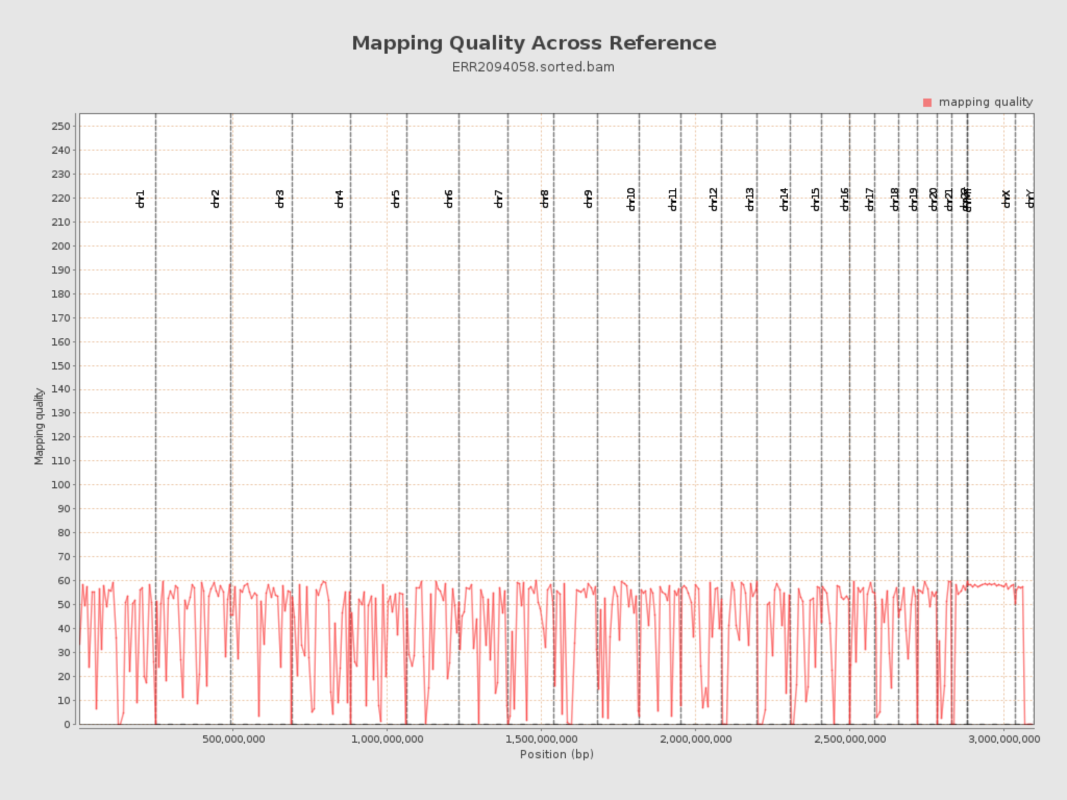
10. Results : Mapped Reads Clipping Profile



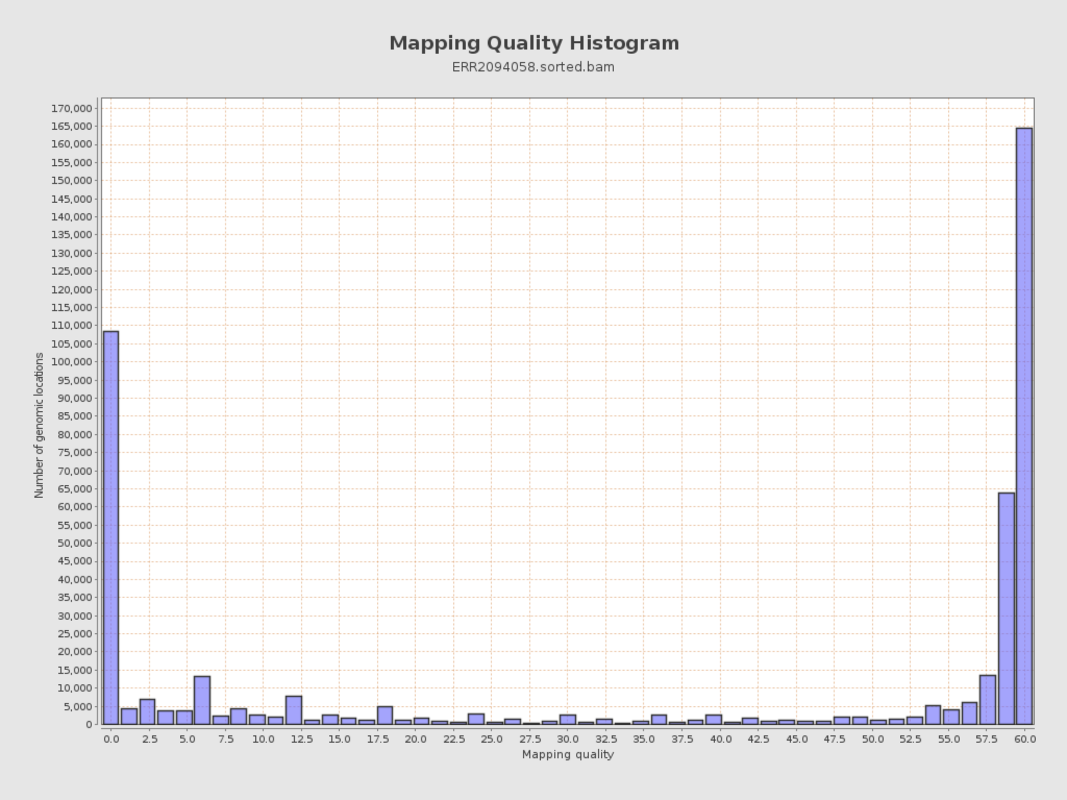
11. Results : Homopolymer Indels



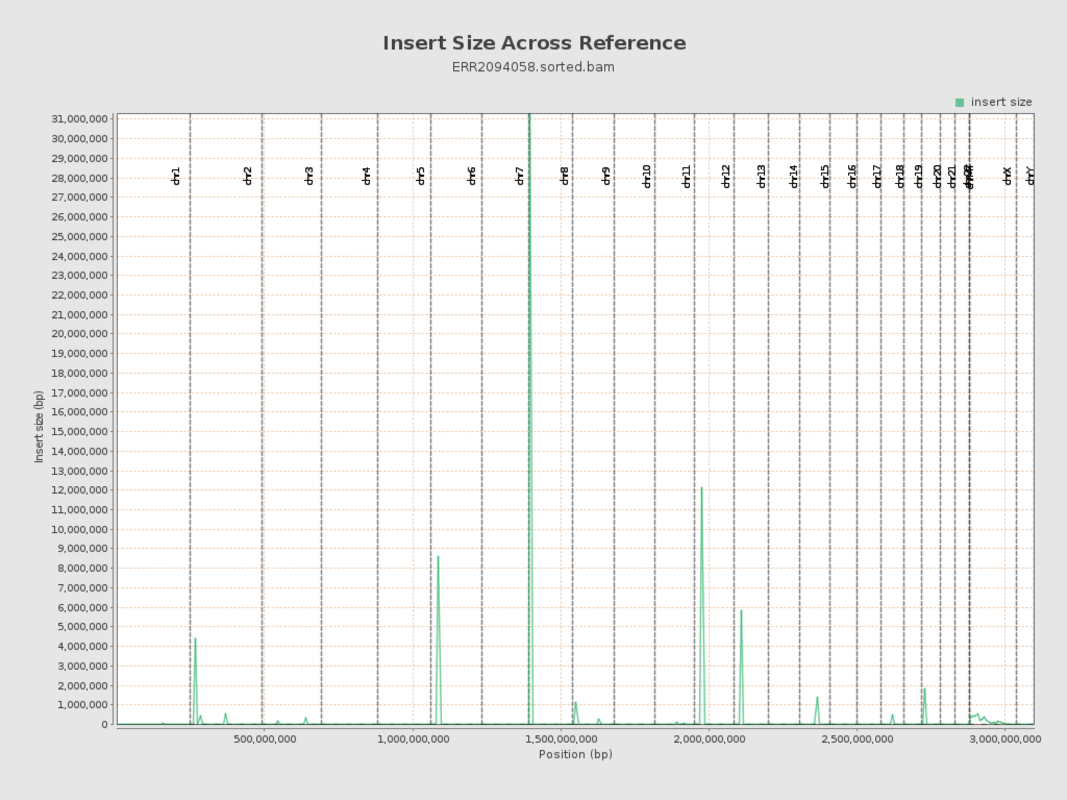
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram