Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:46:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094092.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_ERR2094092 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094092_1.fastq.gz ERR2094092_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:46:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	346,268
Mapped reads	318,518 / 91.99%
Unmapped reads	27,750 / 8.01%
Mapped paired reads	318,518 / 91.99%
Mapped reads, first in pair	159,992 / 46.2%
Mapped reads, second in pair	158,526 / 45.78%
Mapped reads, both in pair	315,864 / 91.22%
Mapped reads, singletons	2,654 / 0.77%
Secondary alignments	0
Supplementary alignments	25,831 / 7.46%
Read min/max/mean length	30 / 151 / 135.79
Duplicated reads (estimated)	297,668 / 85.96%
Duplication rate	51.94%
Clipped reads	177,647 / 51.3%

2.2. ACGT Content

Number/percentage of A's	11,267,749 / 28.84%
Number/percentage of C's	8,322,695 / 21.3%
Number/percentage of T's	10,656,278 / 27.28%
Number/percentage of G's	8,819,355 / 22.58%
Number/percentage of N's	476 / 0%

GC Percentage	43.88%

2.3. Coverage

Mean	0.0129
Standard Deviation	2.2427

2.4. Mapping Quality

Mean Mapping Quality	42.68

2.5. Insert size

Mean	1,974,935.7
Standard Deviation	12,252,018.34
P25/Median/P75	116 / 151 / 181

2.6. Mismatches and indels

General error rate	3.61%
Mismatches	1,355,297
Insertions	26,375
Mapped reads with at least one insertion	8.13%
Deletions	106,143
Mapped reads with at least one deletion	32.07%
Homopolymer indels	28.4%

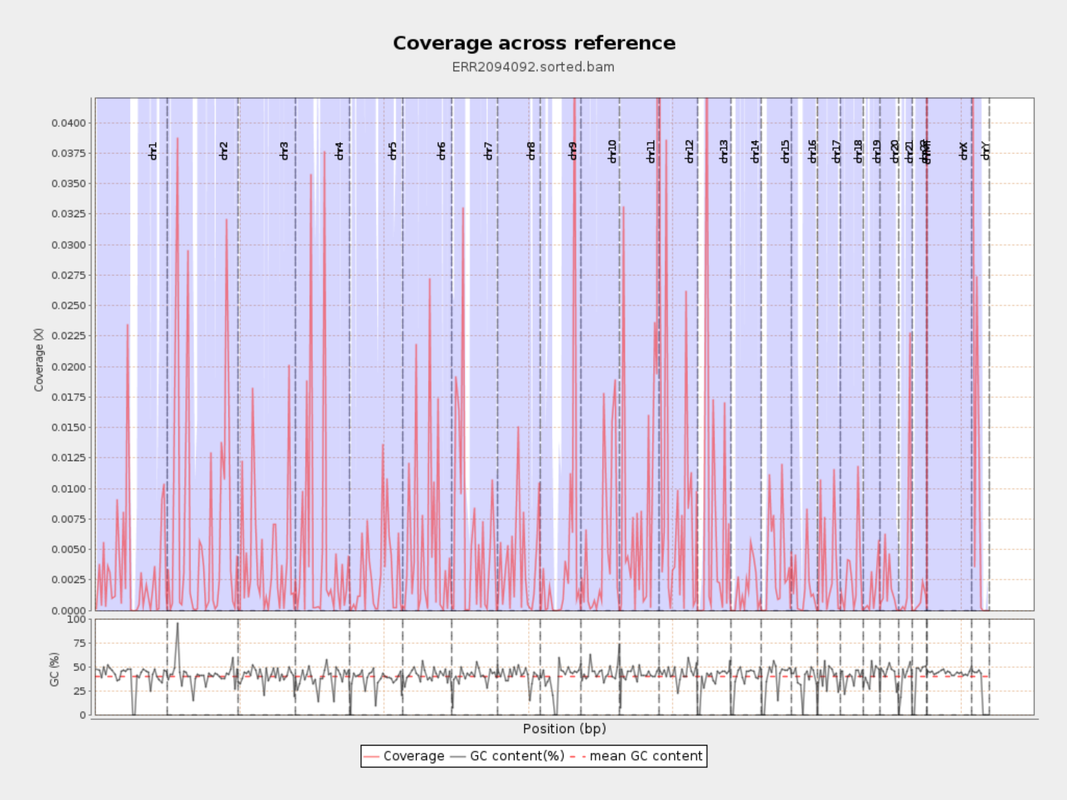
2.7. Chromosome stats

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

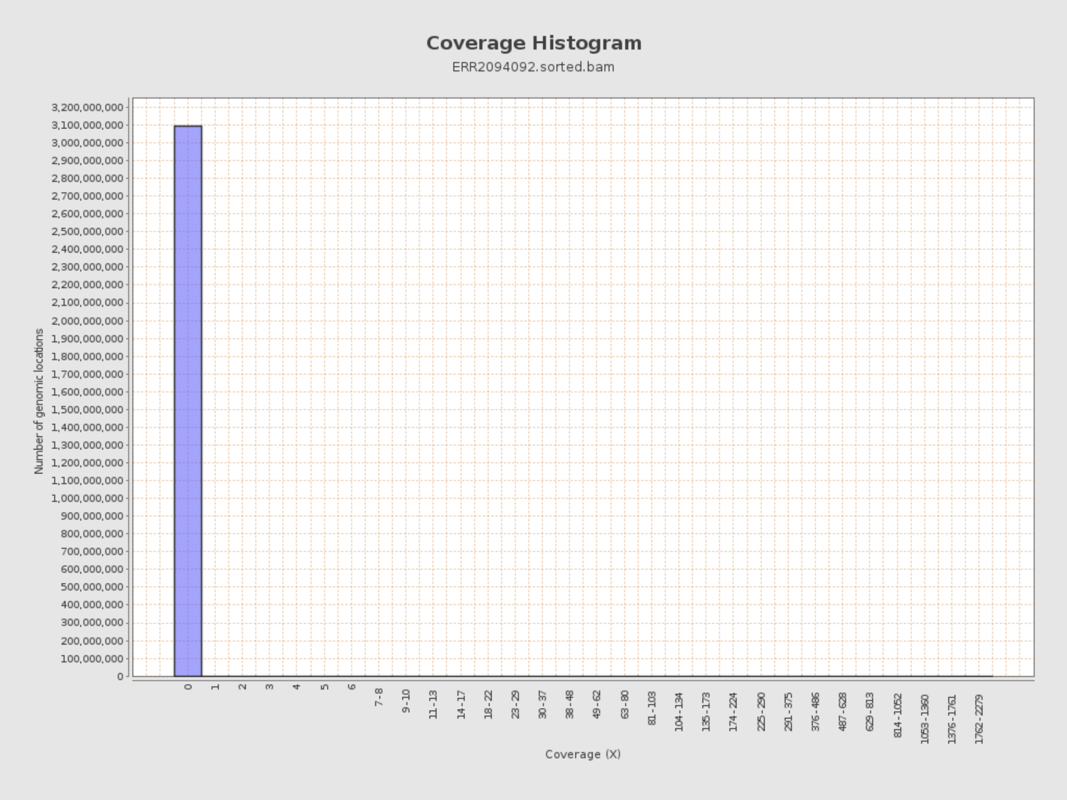
		bases	coverage	deviation
chr1	249250621	778644	0.0031	1.0016
chr2	243199373	1727321	0.0071	1.9167
chr3	198022430	827786	0.0042	1.2398
chr4	191154276	1056791	0.0055	1.5384
chr5	180915260	569760	0.0031	0.9876
chr6	171115067	942403	0.0055	1.5614
chr7	159138663	993362	0.0062	1.5681
chr8	146364022	583153	0.004	0.9409
chr9	141213431	643942	0.0046	2.0585
chr10	135534747	674649	0.005	1.4079
chr11	135006516	1242182	0.0092	2.059
chr12	133851895	1185177	0.0089	2.124
chr13	115169878	818992	0.0071	1.6285
chr14	107349540	174082	0.0016	0.5159
chr15	102531392	385619	0.0038	0.7786
chr16	90354753	187638	0.0021	0.6267
chr17	81195210	300838	0.0037	0.8876
chr18	78077248	234428	0.003	0.8149
chr19	59128983	90712	0.0015	0.4147
chr20	63025520	123706	0.002	0.543
chr21	48129895	193531	0.004	1.6001
chr22	51304566	37921	0.0007	0.1783
chrMT	16571	119666	7.2214	35.4519
chrX	155270560	25306396	0.163	7.8236

chrY	59373566	629170	0.0106	2.1785

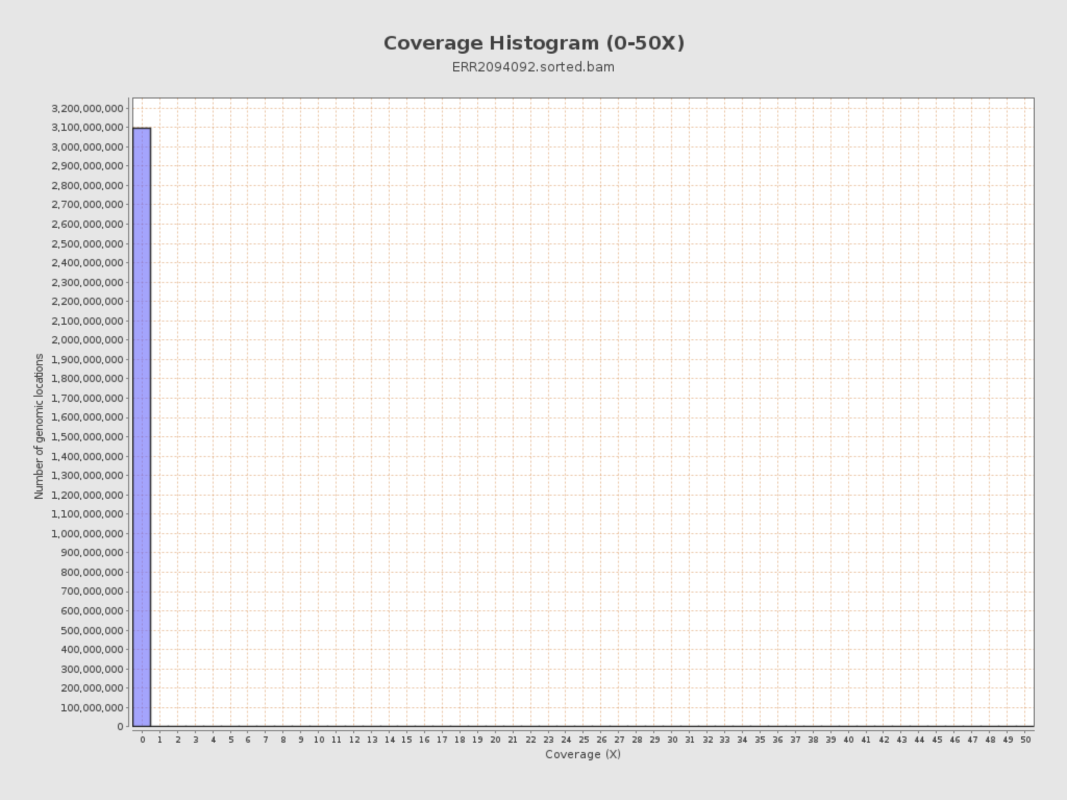
3. Results : Coverage across reference



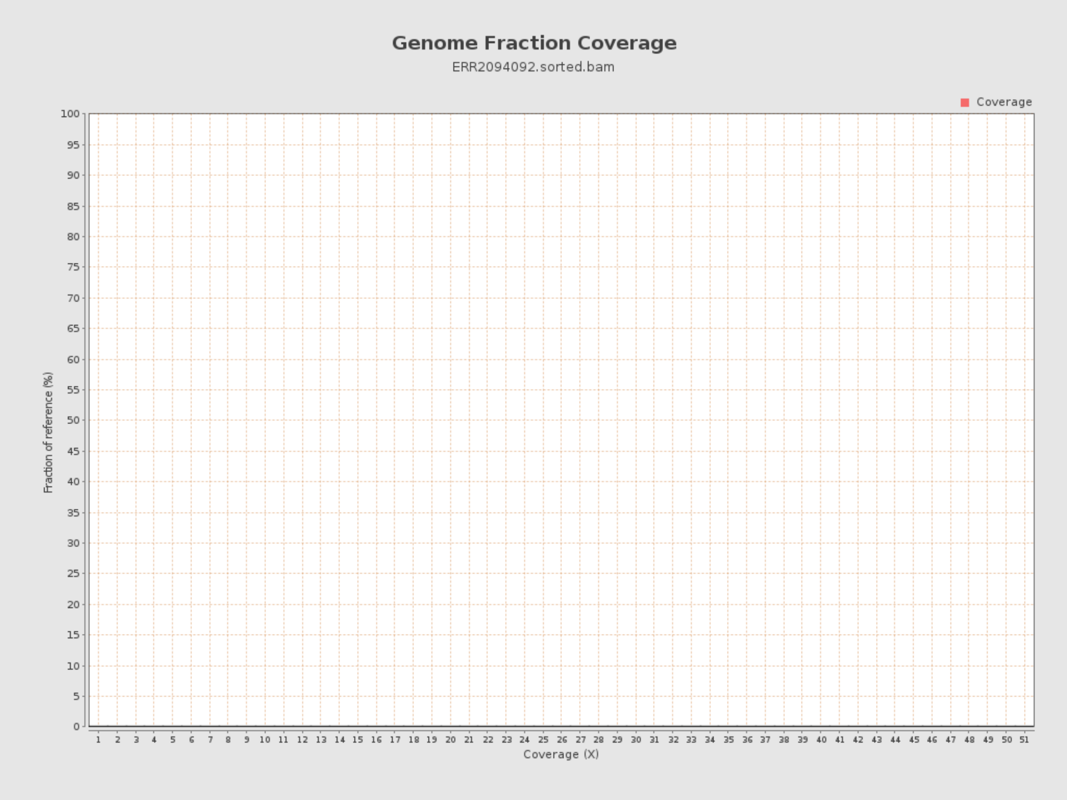
4. Results : Coverage Histogram



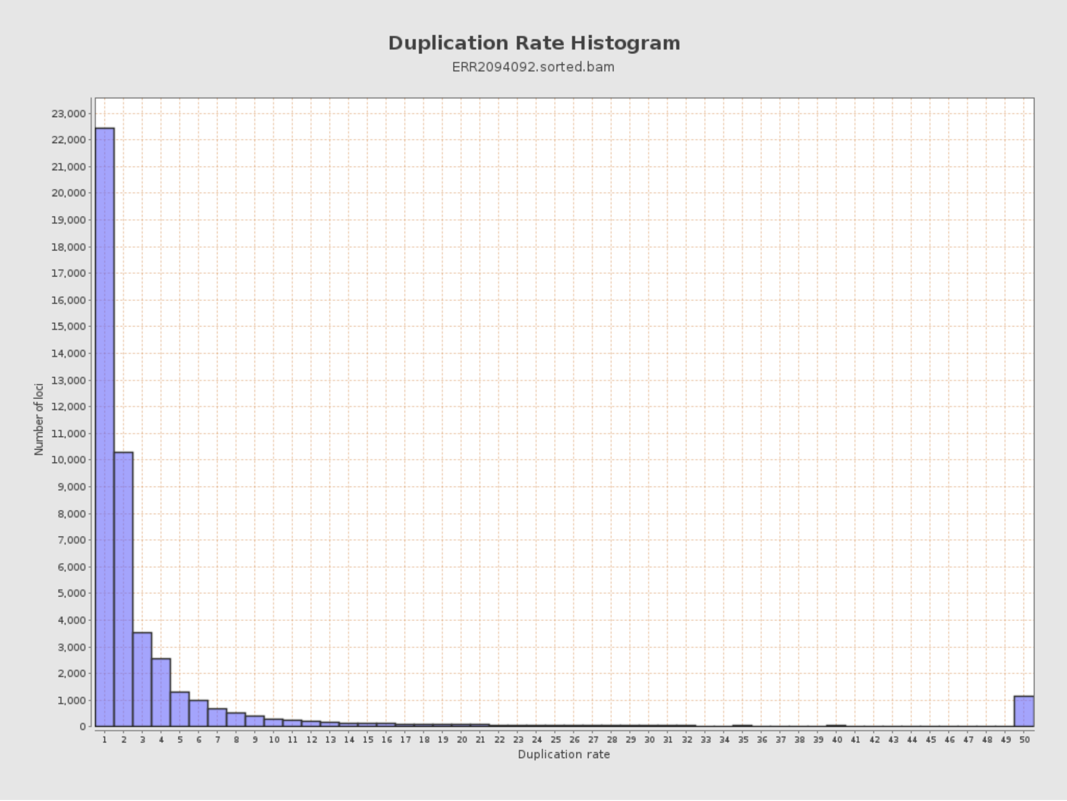
5. Results : Coverage Histogram (0-50X)



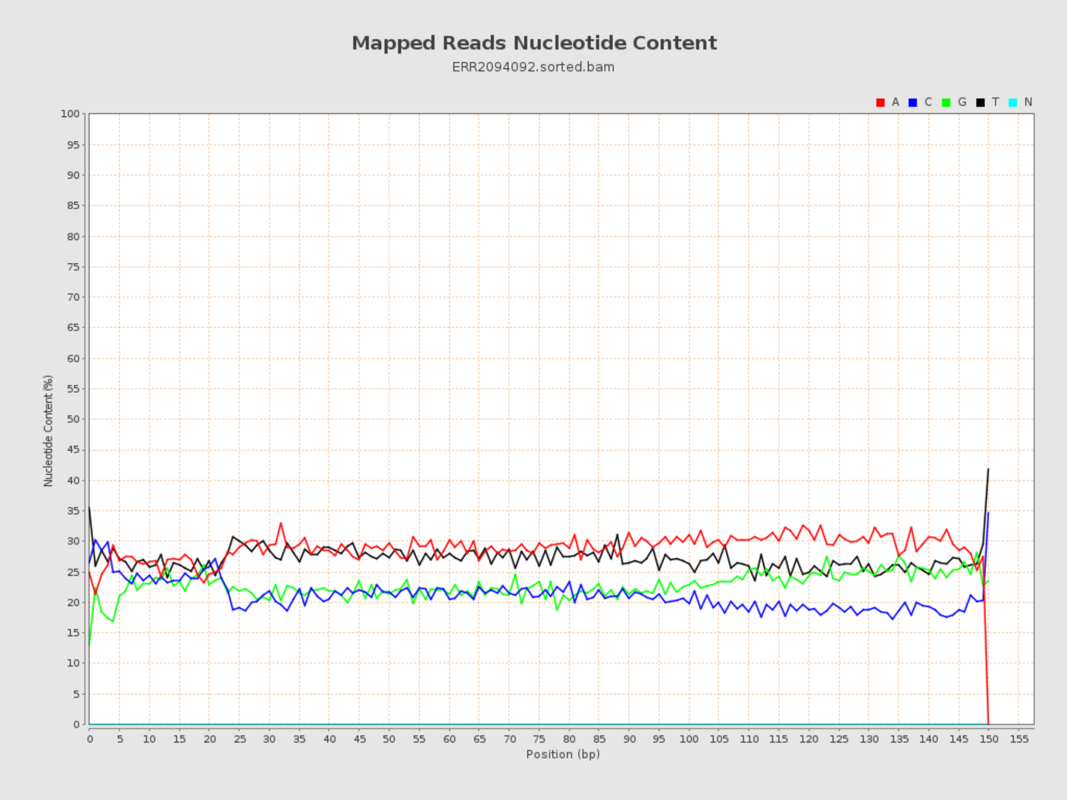
6. Results : Genome Fraction Coverage



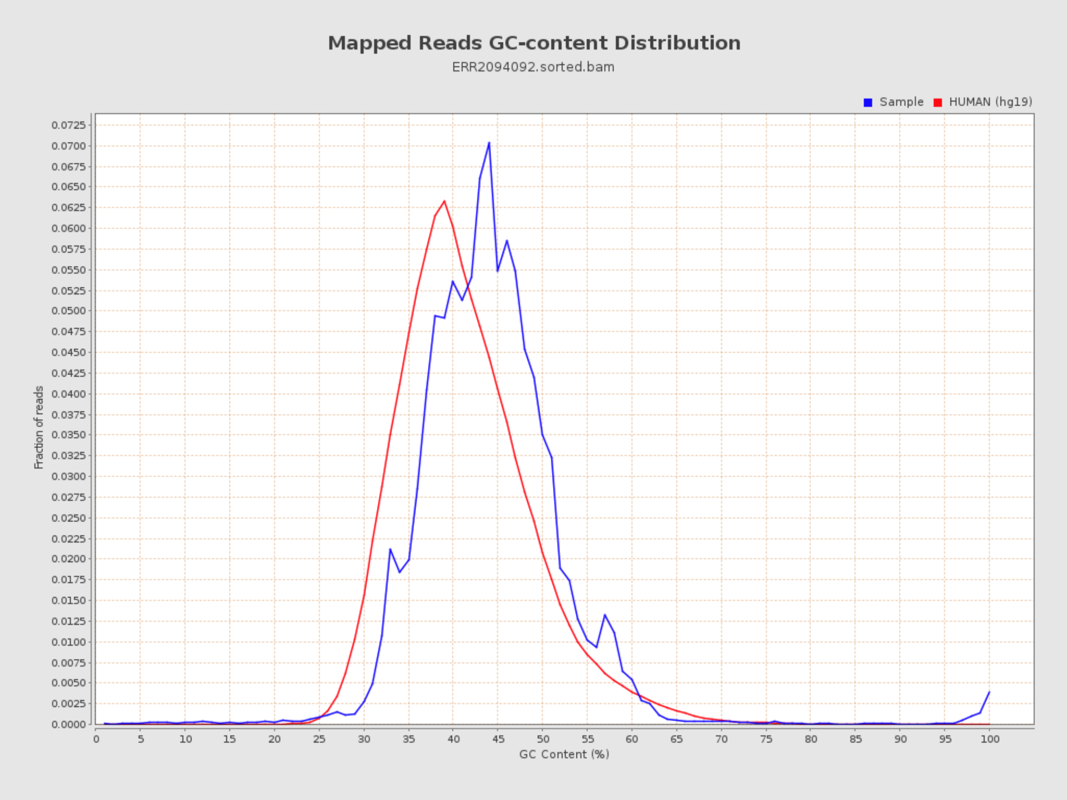
7. Results : Duplication Rate Histogram



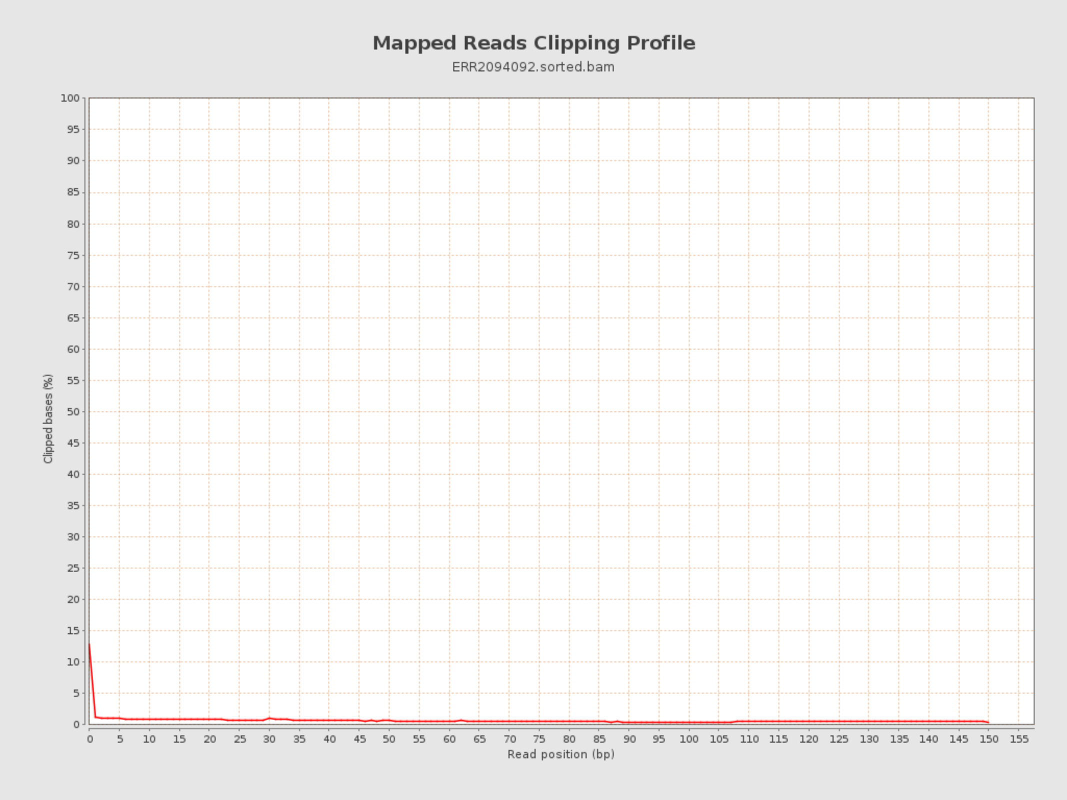
8. Results : Mapped Reads Nucleotide Content



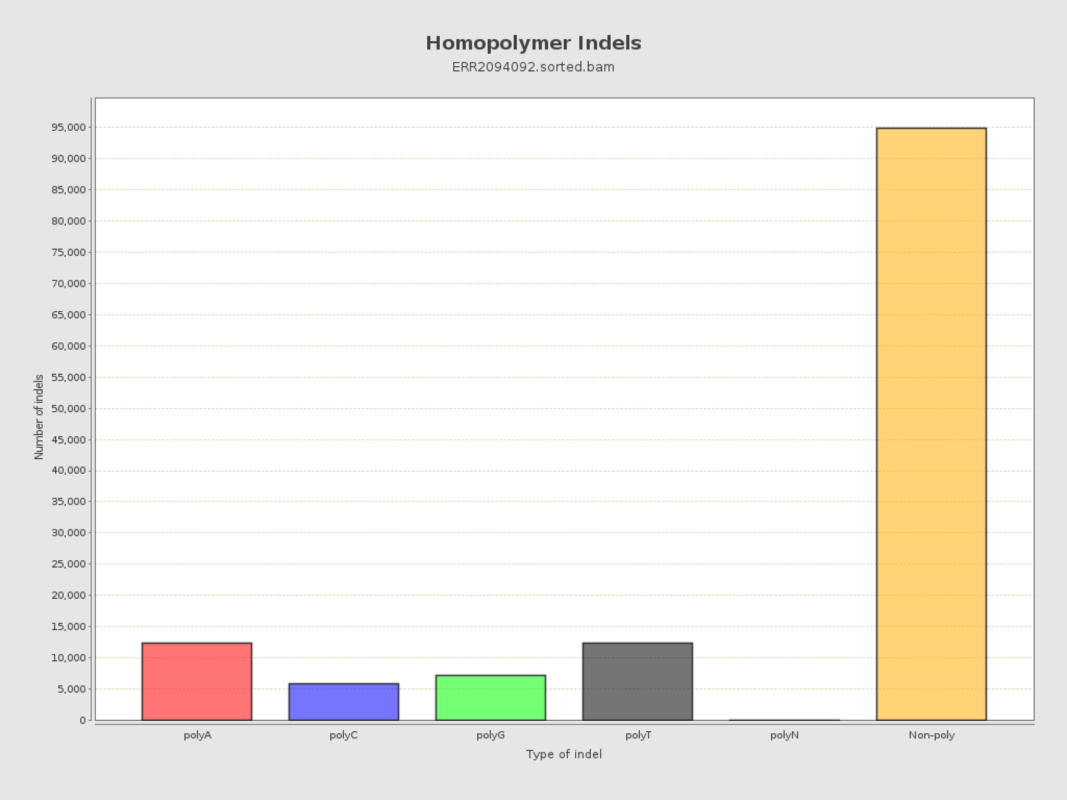
9. Results : Mapped Reads GC-content Distribution



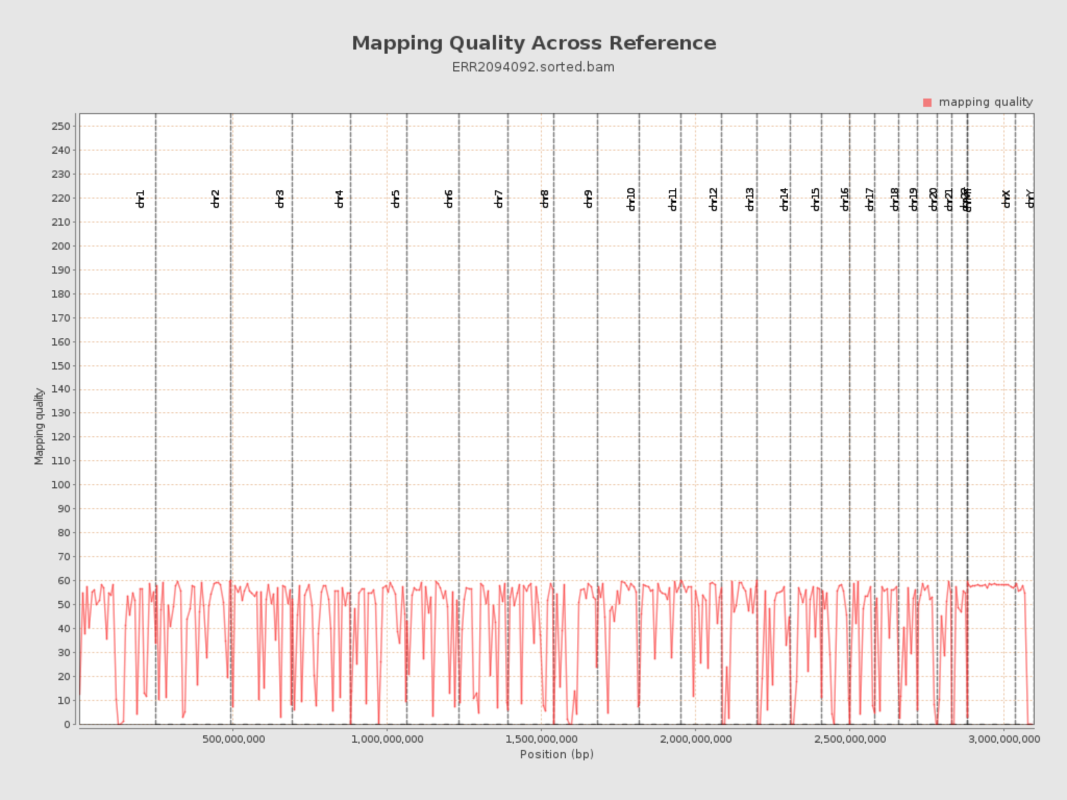
10. Results : Mapped Reads Clipping Profile



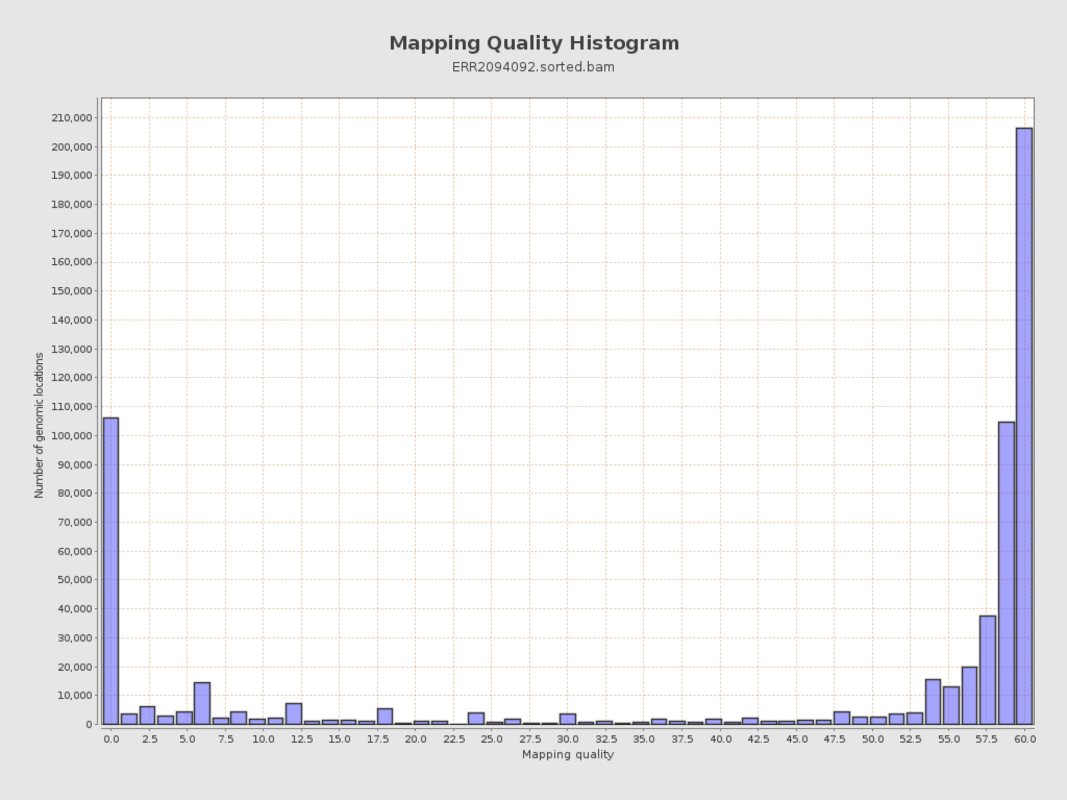
11. Results : Homopolymer Indels



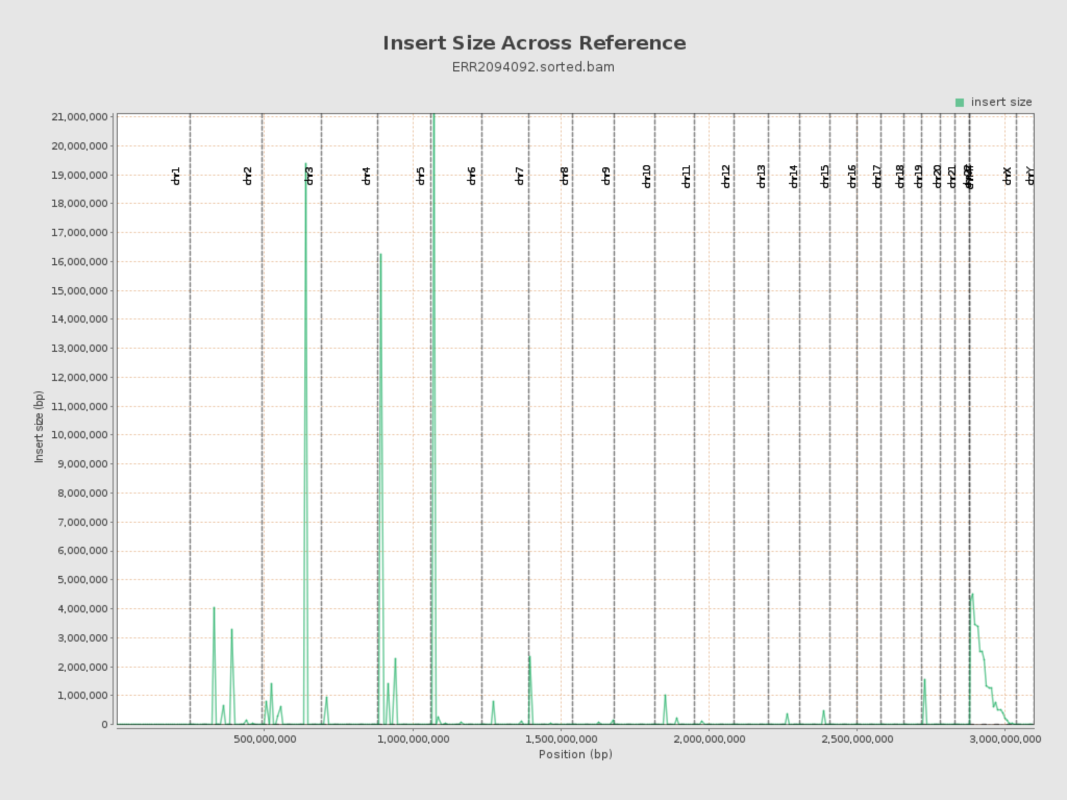
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram