Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:25:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094028.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_ERR2094028 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094028_1.fastq.gz ERR2094028_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:25:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	439,730
Mapped reads	405,957 / 92.32%
Unmapped reads	33,773 / 7.68%
Mapped paired reads	405,957 / 92.32%
Mapped reads, first in pair	204,011 / 46.39%
Mapped reads, second in pair	201,946 / 45.92%
Mapped reads, both in pair	401,370 / 91.28%
Mapped reads, singletons	4,587 / 1.04%
Secondary alignments	0
Supplementary alignments	20,359 / 4.63%
Read min/max/mean length	30 / 151 / 139.23
Duplicated reads (estimated)	377,853 / 85.93%
Duplication rate	47.08%
Clipped reads	195,518 / 44.46%

2.2. ACGT Content

Number/percentage of A's	14,252,677 / 28.02%
Number/percentage of C's	11,178,485 / 21.98%
Number/percentage of T's	13,579,483 / 26.7%
Number/percentage of G's	11,853,037 / 23.3%
Number/percentage of N's	525 / 0%

GC Percentage	45.28%

2.3. Coverage

Mean	0.0167
Standard Deviation	4.9213

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Insert size

Mean	675,749.96
Standard Deviation	7,483,986.53
P25/Median/P75	127 / 161 / 203

2.6. Mismatches and indels

General error rate	3.49%
Mismatches	1,716,457
Insertions	32,252
Mapped reads with at least one insertion	7.81%
Deletions	139,964
Mapped reads with at least one deletion	33.22%
Homopolymer indels	28.11%

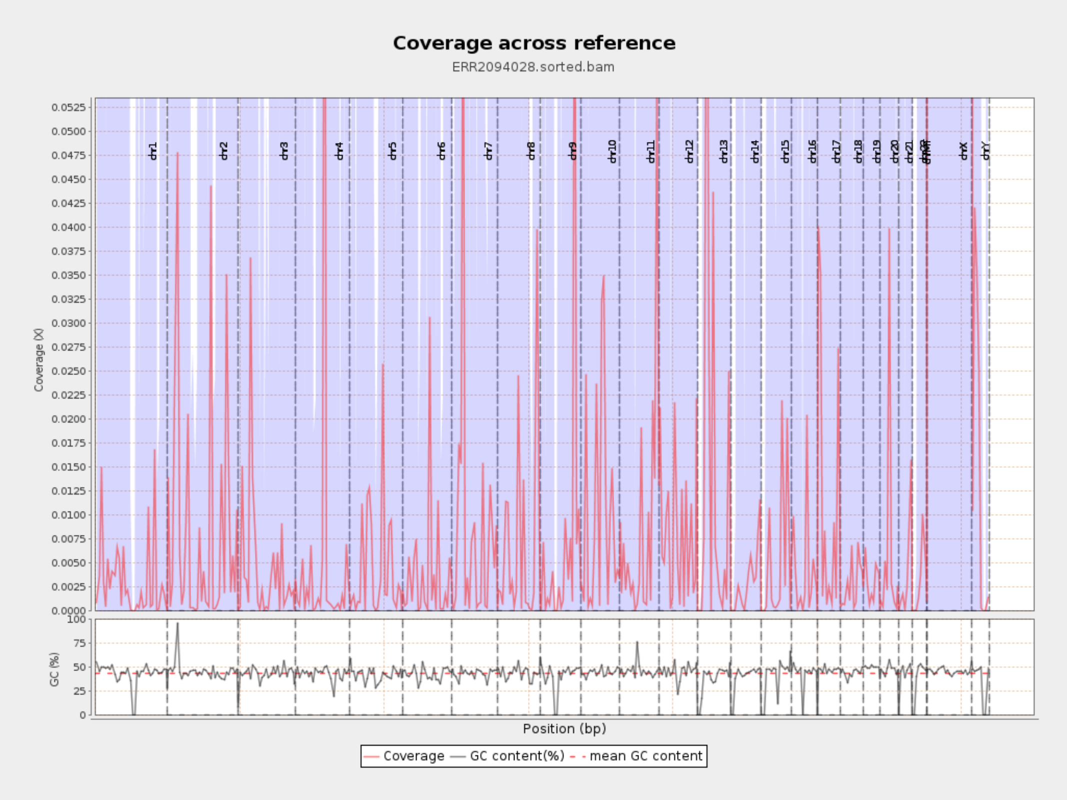
2.7. Chromosome stats

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

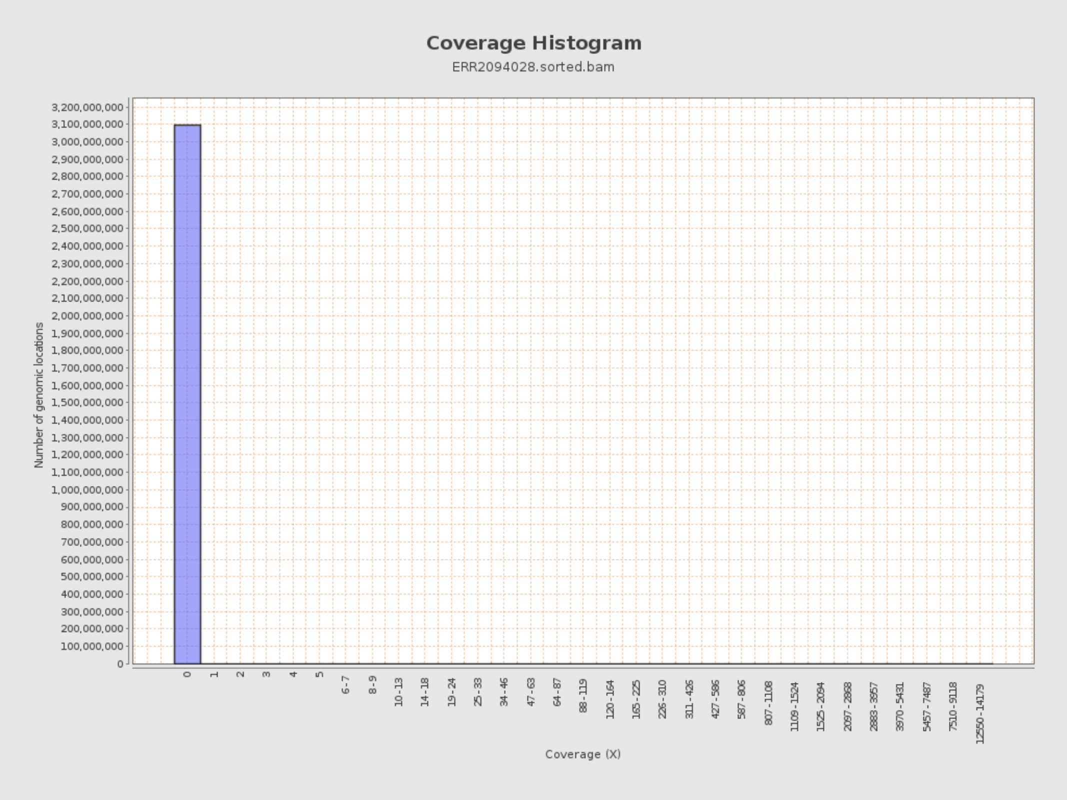
		bases	coverage	deviation
chr1	249250621	769709	0.0031	0.8714
chr2	243199373	2078631	0.0085	2.4828
chr3	198022430	924593	0.0047	1.5917
chr4	191154276	1075145	0.0056	1.9905
chr5	180915260	829580	0.0046	1.6355
chr6	171115067	657018	0.0038	1.0859
chr7	159138663	1400451	0.0088	2.6592
chr8	146364022	962269	0.0066	2.259
chr9	141213431	1063026	0.0075	2.8942
chr10	135534747	1351076	0.01	2.8702
chr11	135006516	1180486	0.0087	2.5876
chr12	133851895	1036946	0.0077	1.7153
chr13	115169878	1595742	0.0139	3.6101
chr14	107349540	332111	0.0031	0.5763
chr15	102531392	514631	0.005	1.3465
chr16	90354753	393571	0.0044	1.4906
chr17	81195210	970315	0.012	2.6855
chr18	78077248	219616	0.0028	0.6884
chr19	59128983	173154	0.0029	0.3903
chr20	63025520	412780	0.0065	2.3793
chr21	48129895	210999	0.0044	0.7112
chr22	51304566	157039	0.0031	0.4685
chrMT	16571	6027685	363.749	1,546.3736
chrX	155270560	26581292	0.1712	11.5148

chrY	59373566	864991	0.0146	2.9561

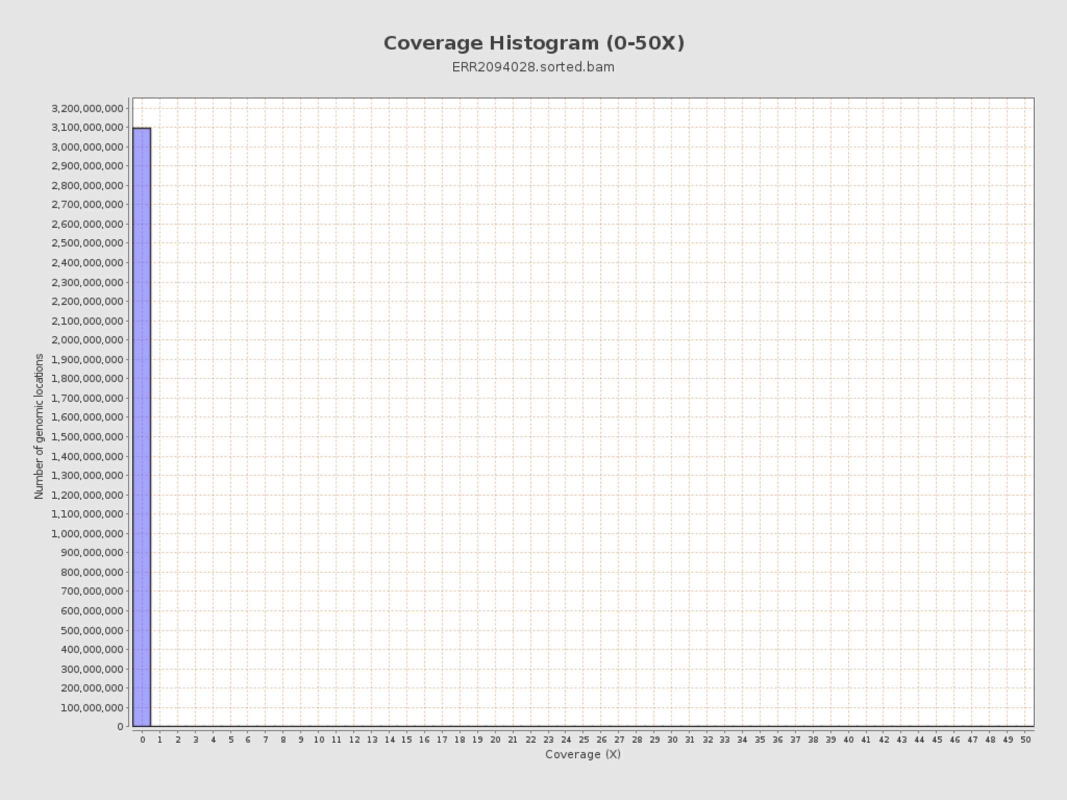
3. Results : Coverage across reference



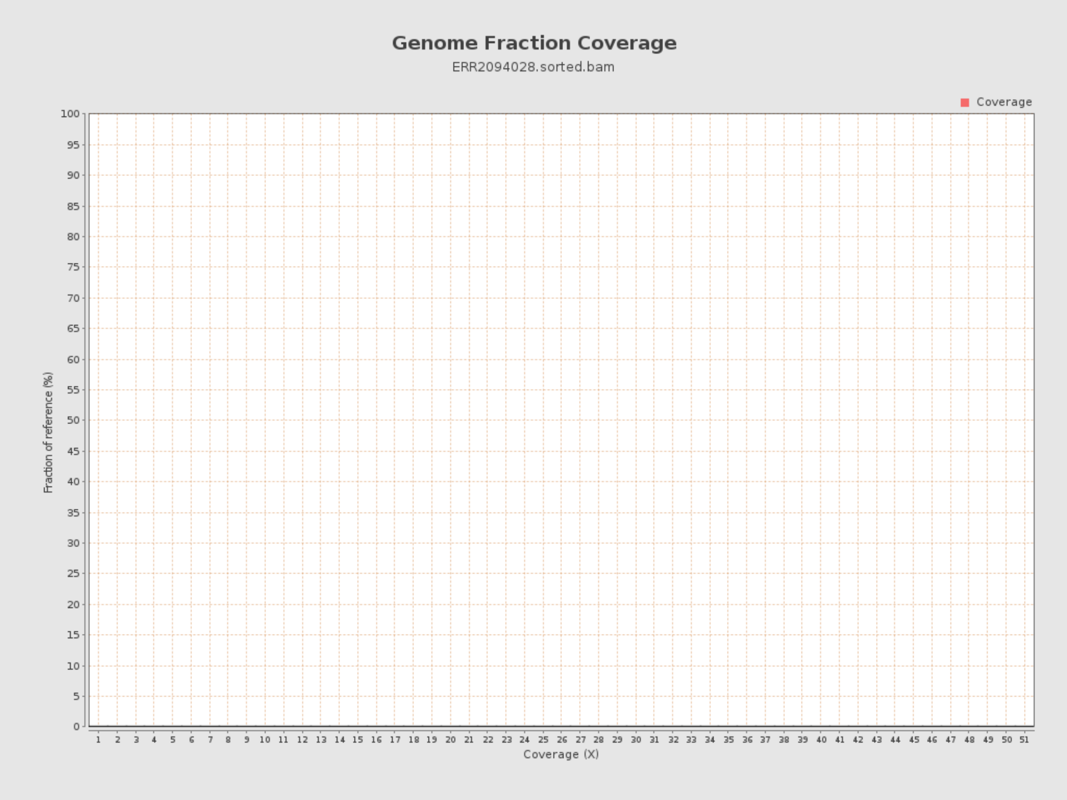
4. Results : Coverage Histogram



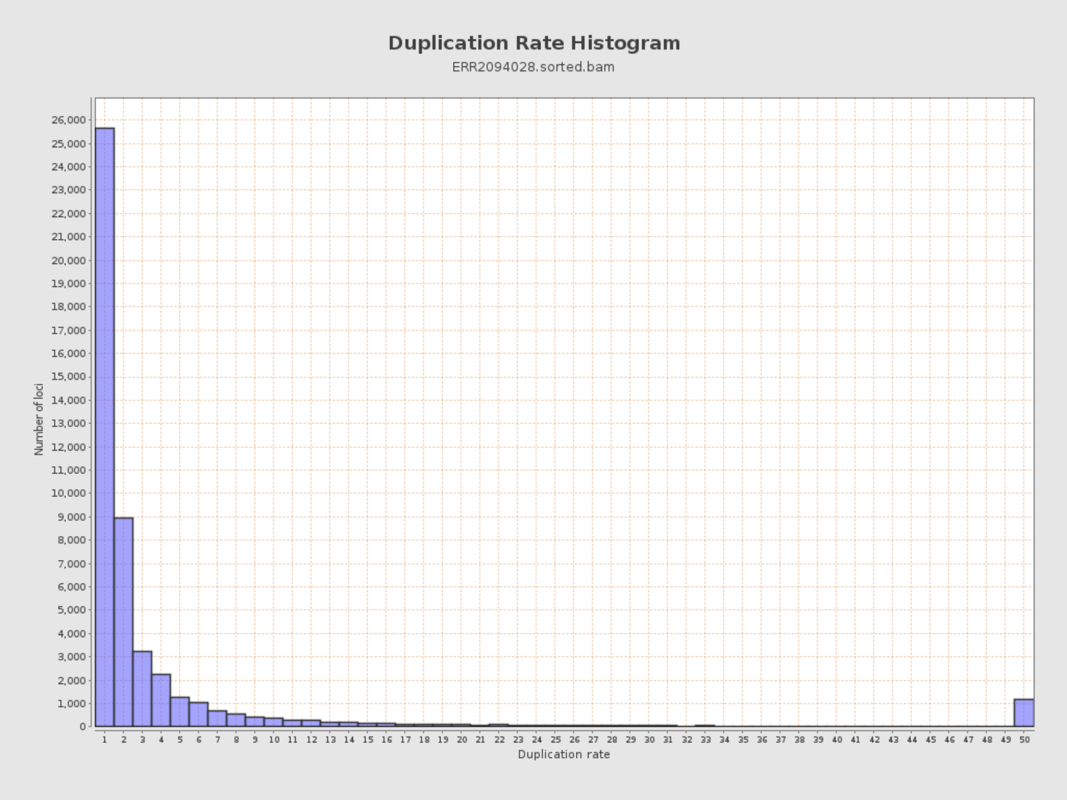
5. Results : Coverage Histogram (0-50X)



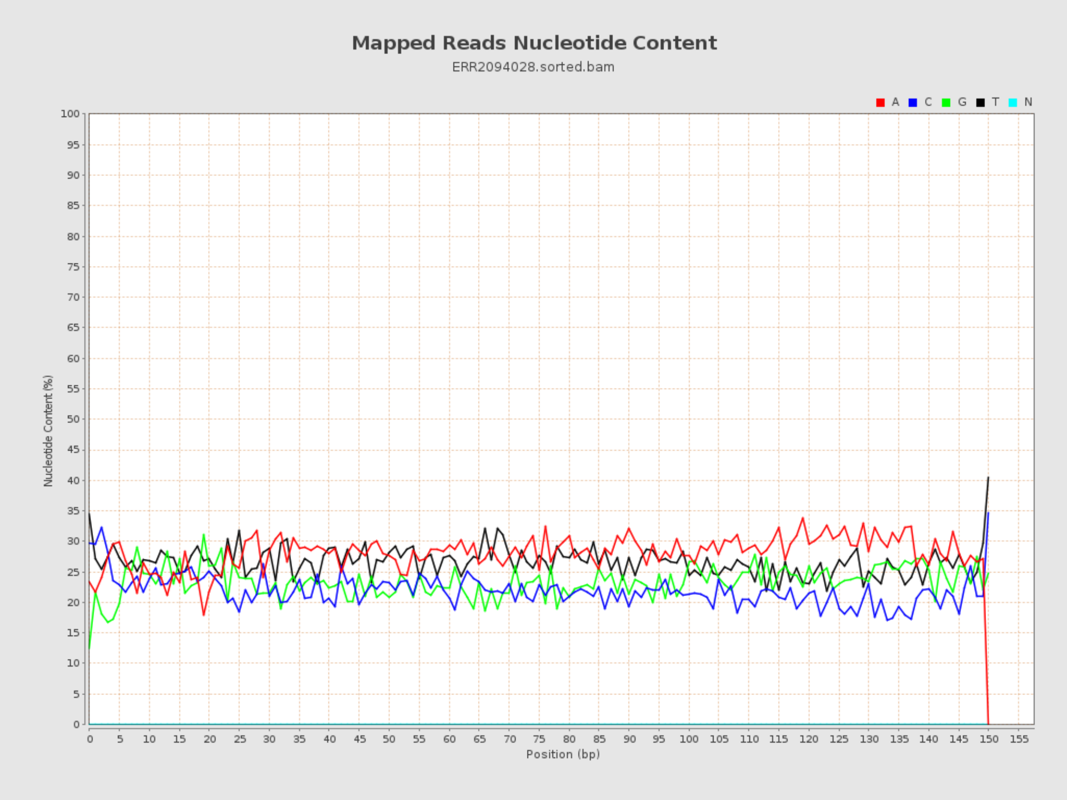
6. Results : Genome Fraction Coverage



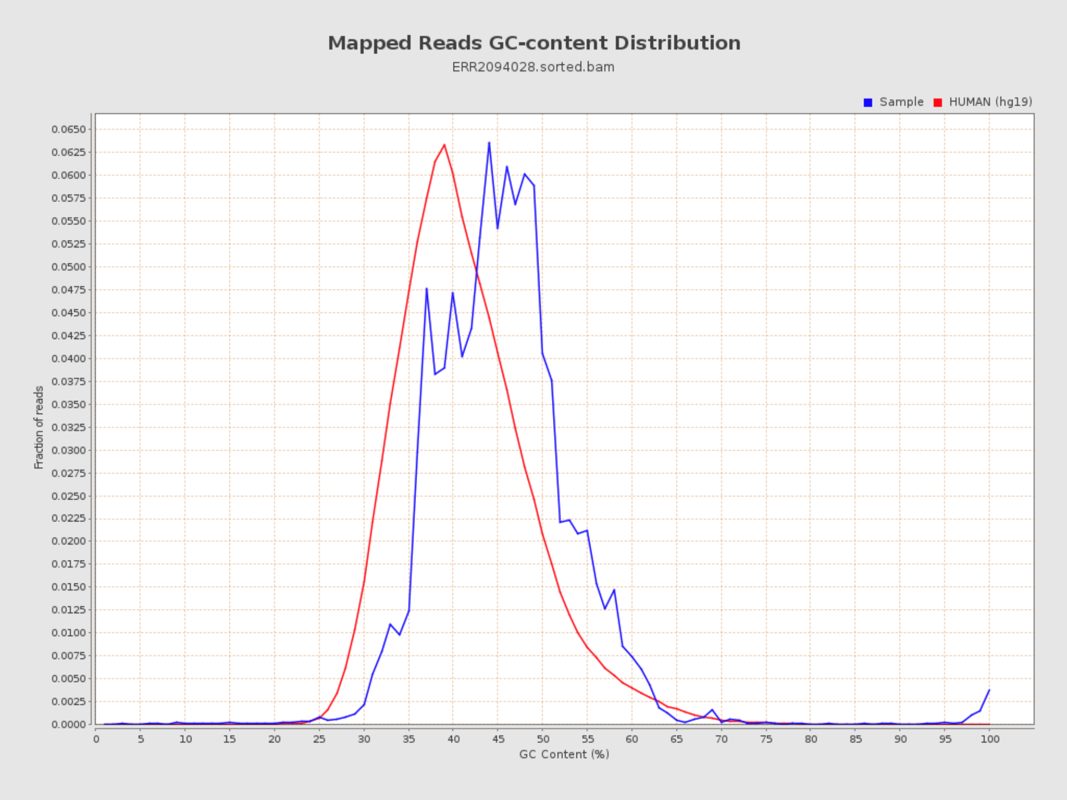
7. Results : Duplication Rate Histogram



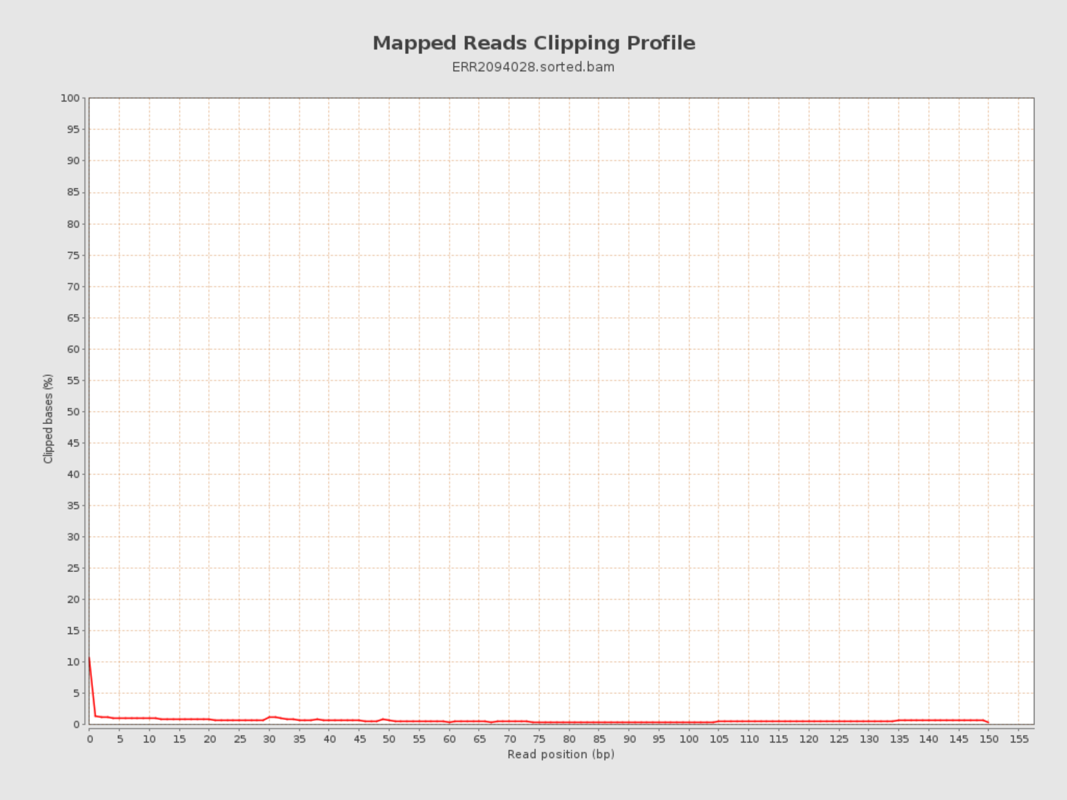
8. Results : Mapped Reads Nucleotide Content



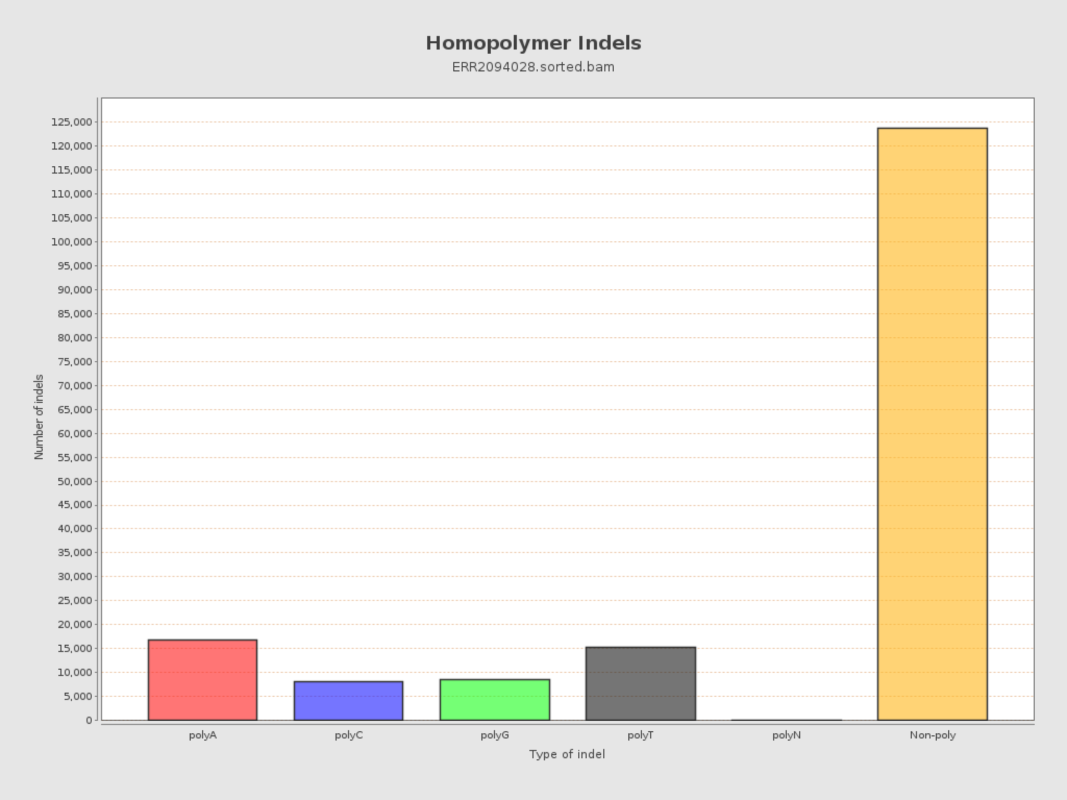
9. Results : Mapped Reads GC-content Distribution



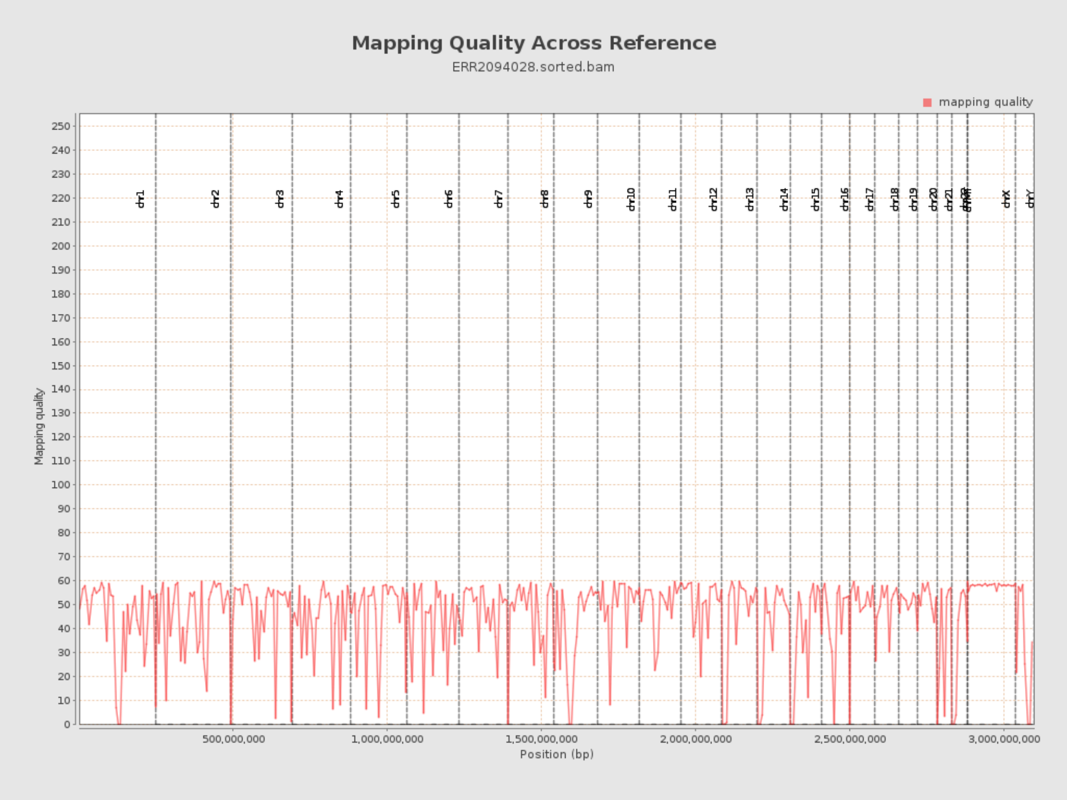
10. Results : Mapped Reads Clipping Profile



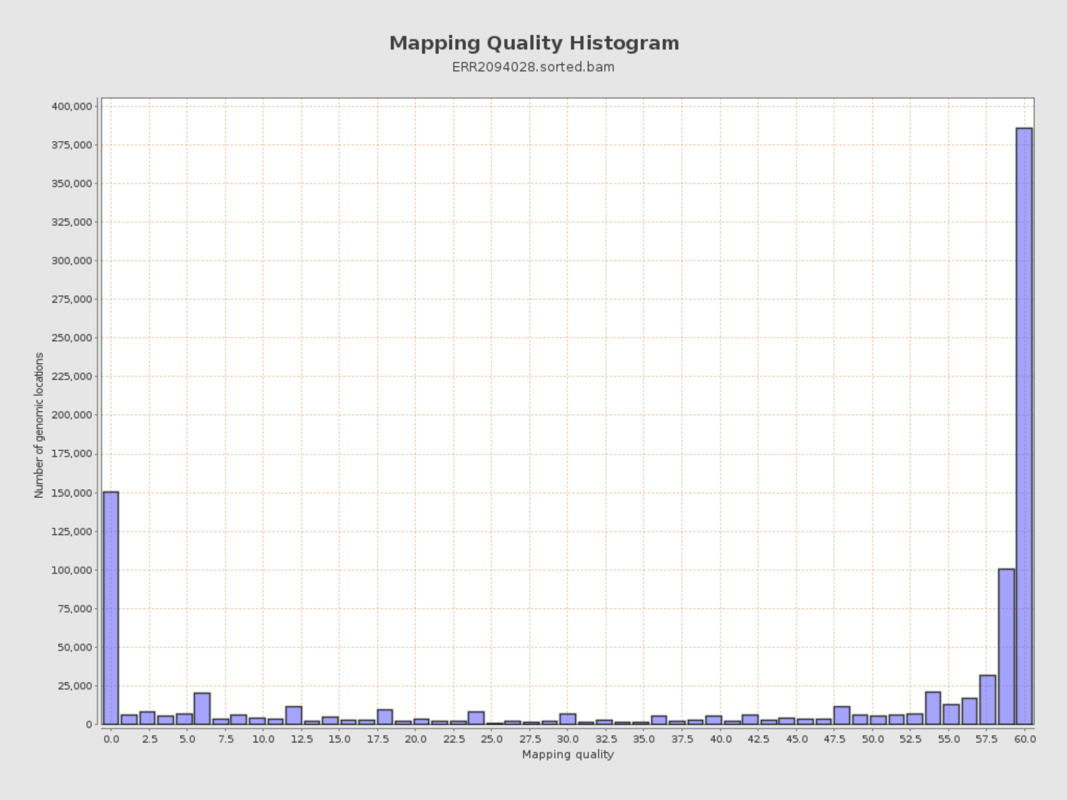
11. Results : Homopolymer Indels



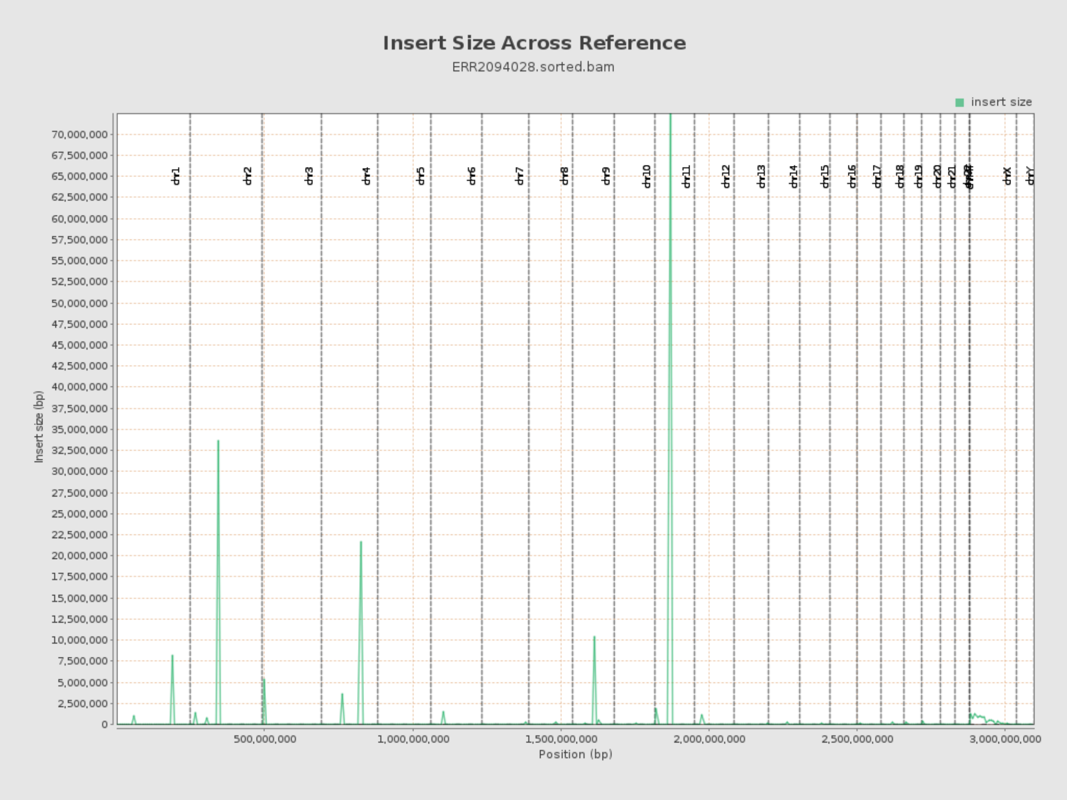
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram