Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 05:27:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094150.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_ERR2094150 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094150_1.fastq.gz ERR2094150_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 05:27:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	448,722
Mapped reads	410,674 / 91.52%
Unmapped reads	38,048 / 8.48%
Mapped paired reads	410,674 / 91.52%
Mapped reads, first in pair	206,248 / 45.96%
Mapped reads, second in pair	204,426 / 45.56%
Mapped reads, both in pair	407,556 / 90.83%
Mapped reads, singletons	3,118 / 0.69%
Secondary alignments	0
Supplementary alignments	27,807 / 6.2%
Read min/max/mean length	30 / 151 / 133.06
Duplicated reads (estimated)	393,511 / 87.7%
Duplication rate	51.12%
Clipped reads	213,781 / 47.64%

2.2. ACGT Content

Number/percentage of A's	14,387,244 / 29.13%
Number/percentage of C's	10,472,402 / 21.21%
Number/percentage of T's	13,425,276 / 27.19%
Number/percentage of G's	11,097,924 / 22.47%
Number/percentage of N's	457 / 0%

GC Percentage	43.68%

2.3. Coverage

Mean	0.0163
Standard Deviation	3.4175

2.4. Mapping Quality

Mean Mapping Quality	41.88

2.5. Insert size

Mean	1,310,978.26
Standard Deviation	10,129,601.4
P25/Median/P75	113 / 145 / 176

2.6. Mismatches and indels

General error rate	3.92%
Mismatches	1,887,782
Insertions	32,975
Mapped reads with at least one insertion	7.9%
Deletions	159,793
Mapped reads with at least one deletion	37.51%
Homopolymer indels	26.9%

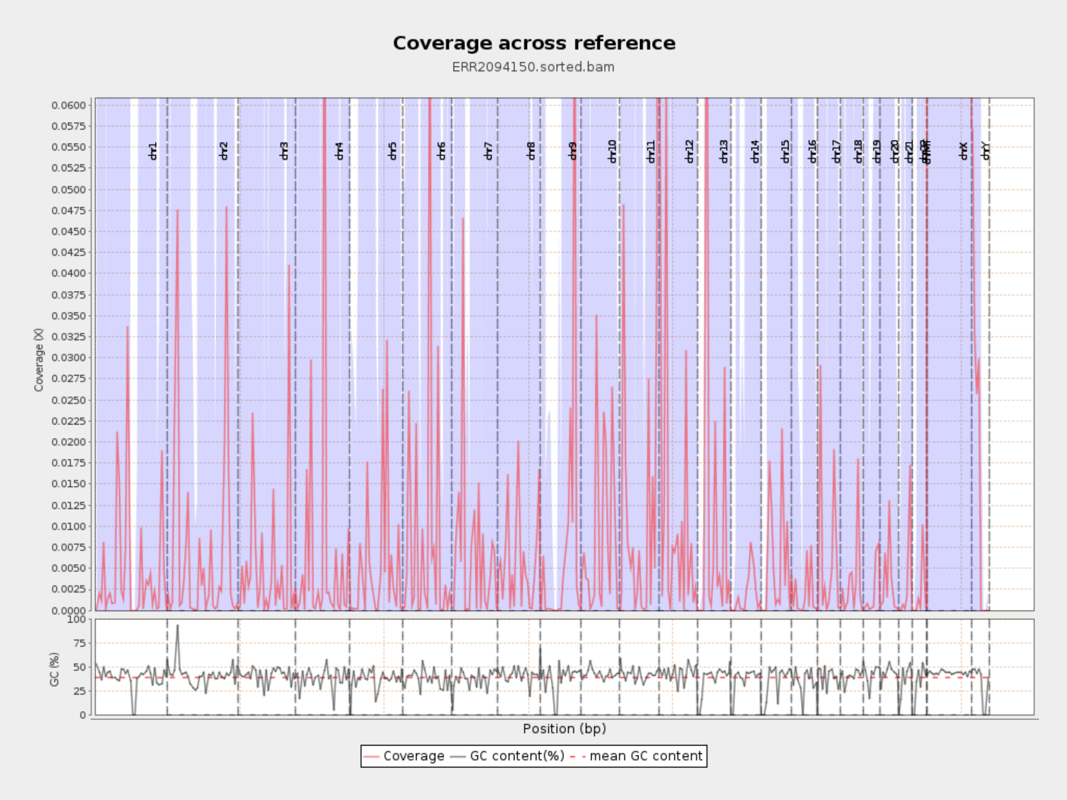
2.7. Chromosome stats

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

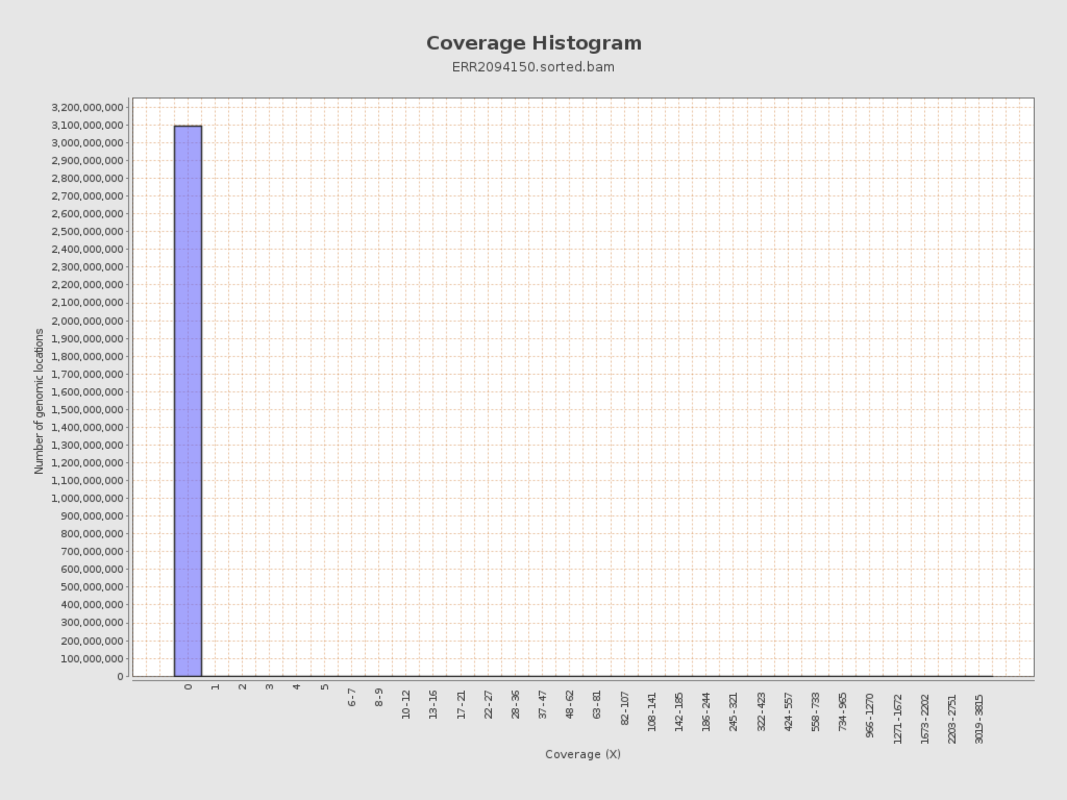
		bases	coverage	deviation
chr1	249250621	1141382	0.0046	1.6919
chr2	243199373	1721333	0.0071	2.3632
chr3	198022430	1046938	0.0053	2.1604
chr4	191154276	1384151	0.0072	1.9508
chr5	180915260	1017991	0.0056	2.1308
chr6	171115067	1550445	0.0091	2.8171
chr7	159138663	1089868	0.0068	2.0393
chr8	146364022	888376	0.0061	1.4631
chr9	141213431	1152768	0.0082	3.3571
chr10	135534747	1148398	0.0085	2.5071
chr11	135006516	1617114	0.012	2.7809
chr12	133851895	1659550	0.0124	3.4619
chr13	115169878	1219158	0.0106	3.0342
chr14	107349540	199437	0.0019	0.6662
chr15	102531392	576812	0.0056	1.3344
chr16	90354753	189984	0.0021	0.5843
chr17	81195210	521499	0.0064	1.808
chr18	78077248	279462	0.0036	1.1885
chr19	59128983	134006	0.0023	0.6952
chr20	63025520	214726	0.0034	0.9862
chr21	48129895	172619	0.0036	1.0497
chr22	51304566	97364	0.0019	0.7261
chrMT	16571	519667	31.36	182.9986
chrX	155270560	30038738	0.1935	11.5648

chrY	59373566	978256	0.0165	4.0556

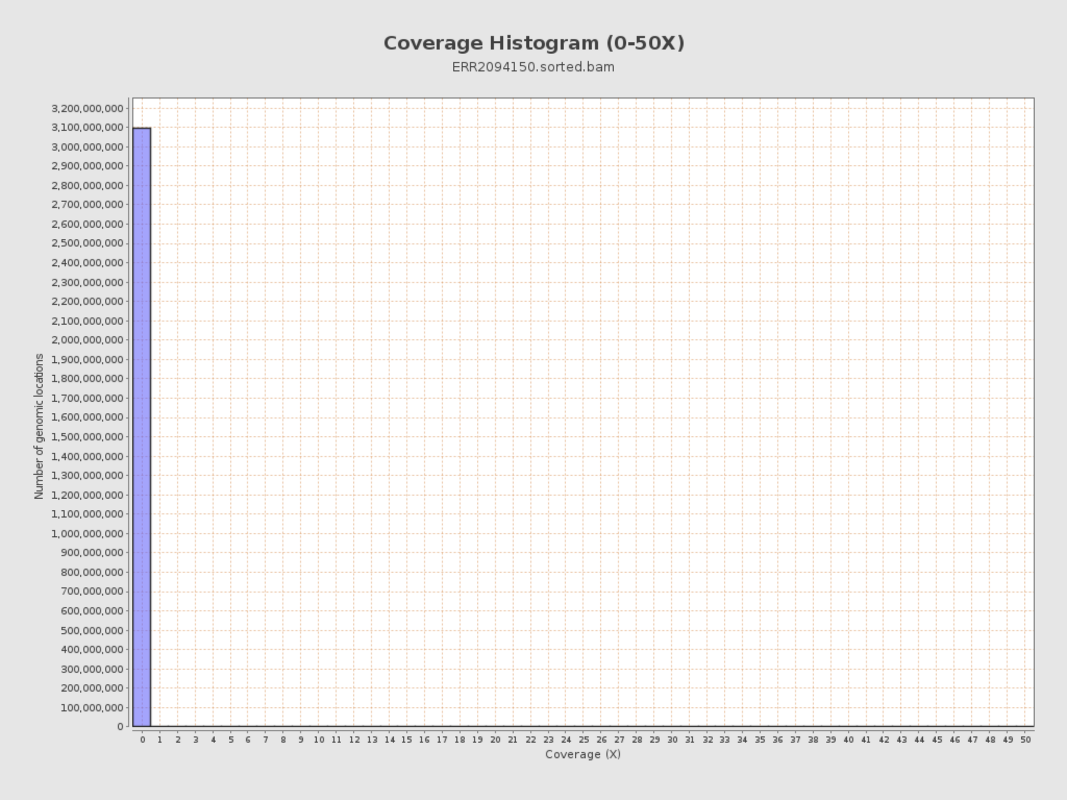
3. Results : Coverage across reference



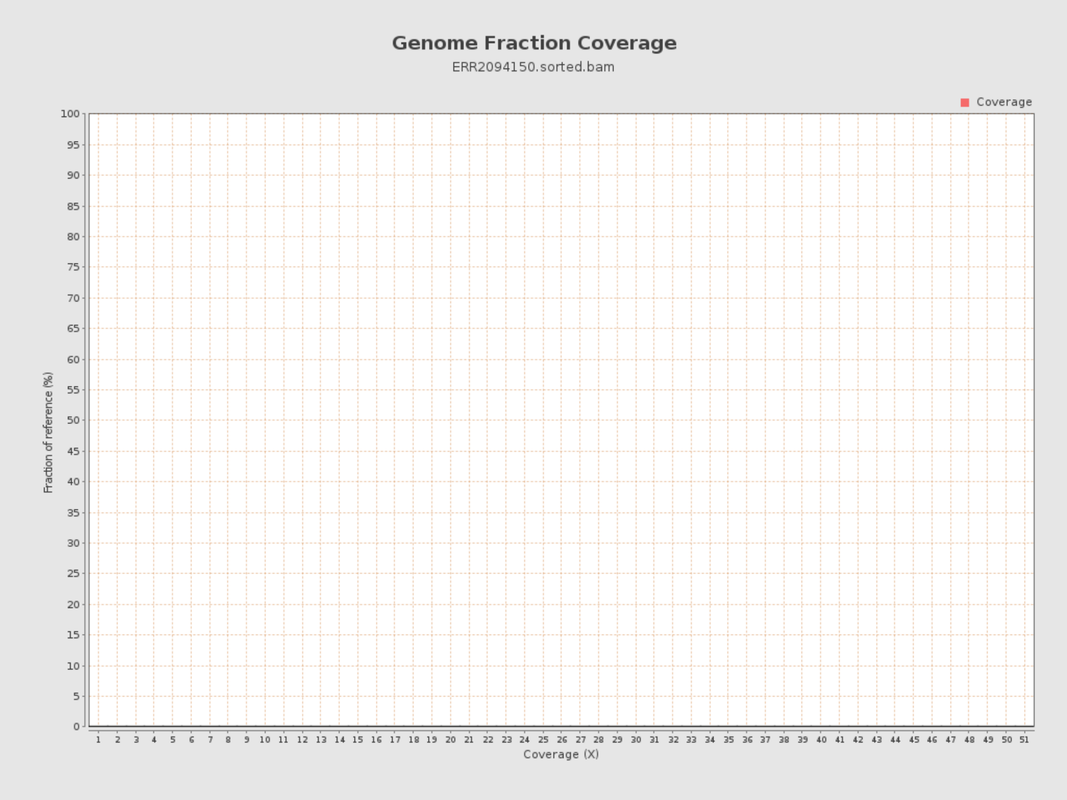
4. Results : Coverage Histogram



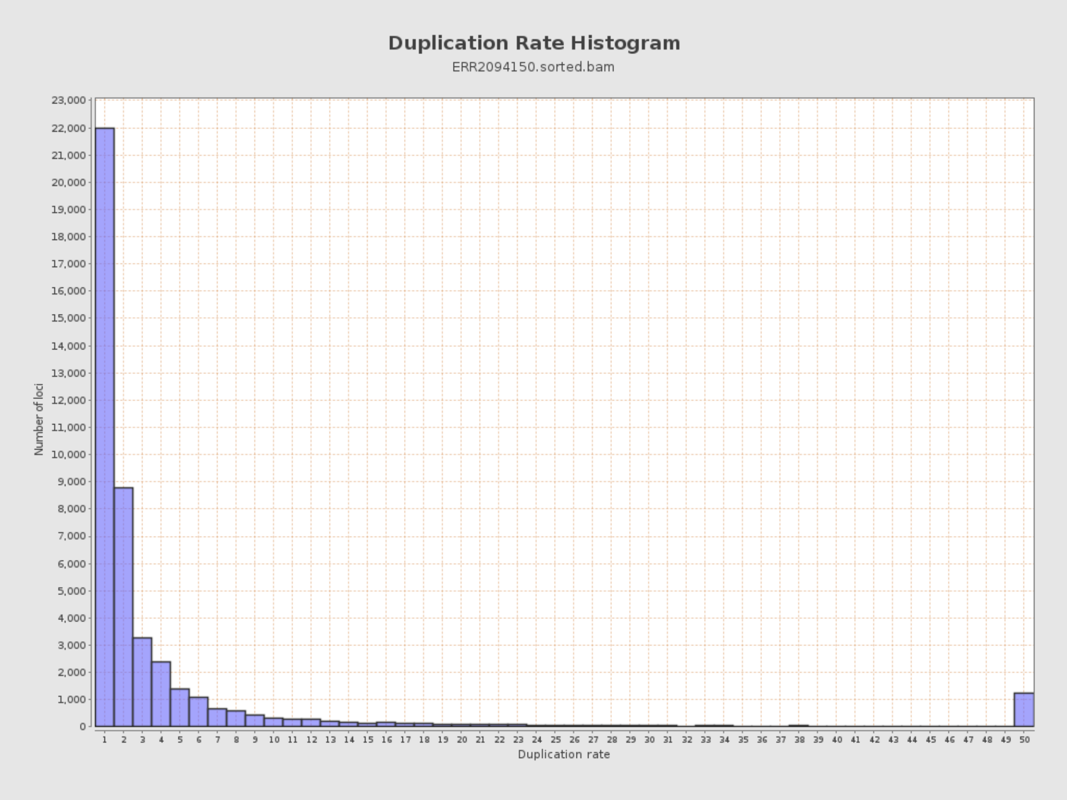
5. Results : Coverage Histogram (0-50X)



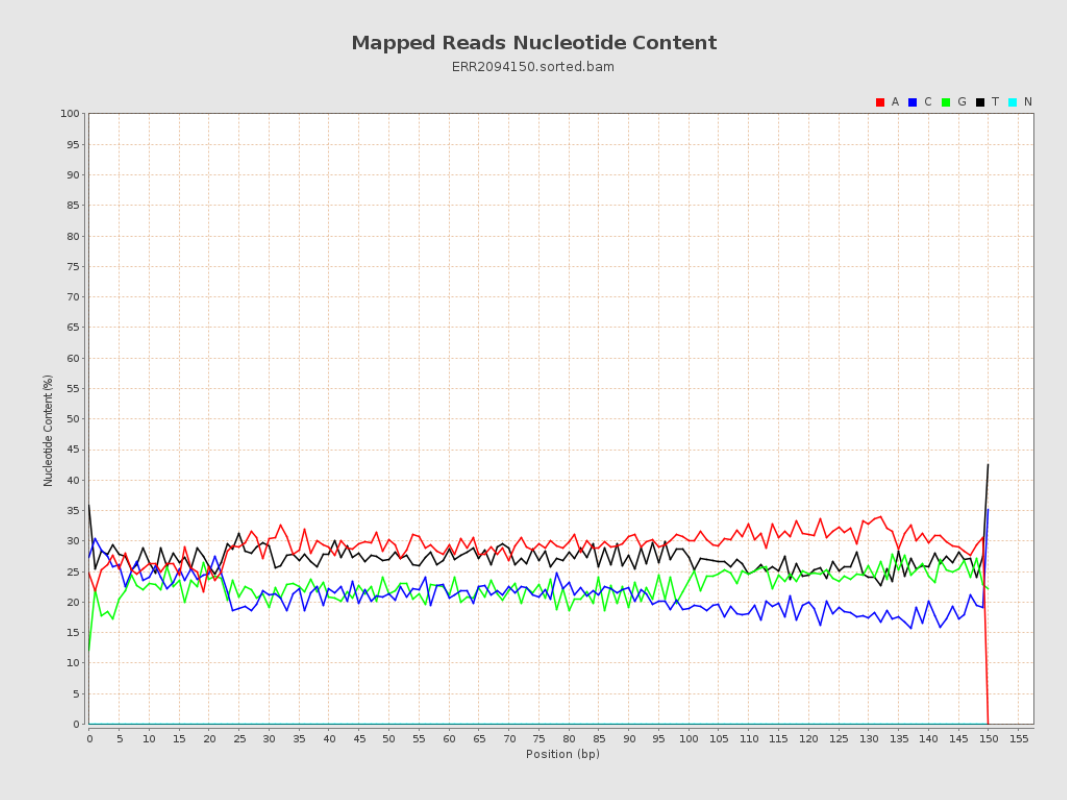
6. Results : Genome Fraction Coverage



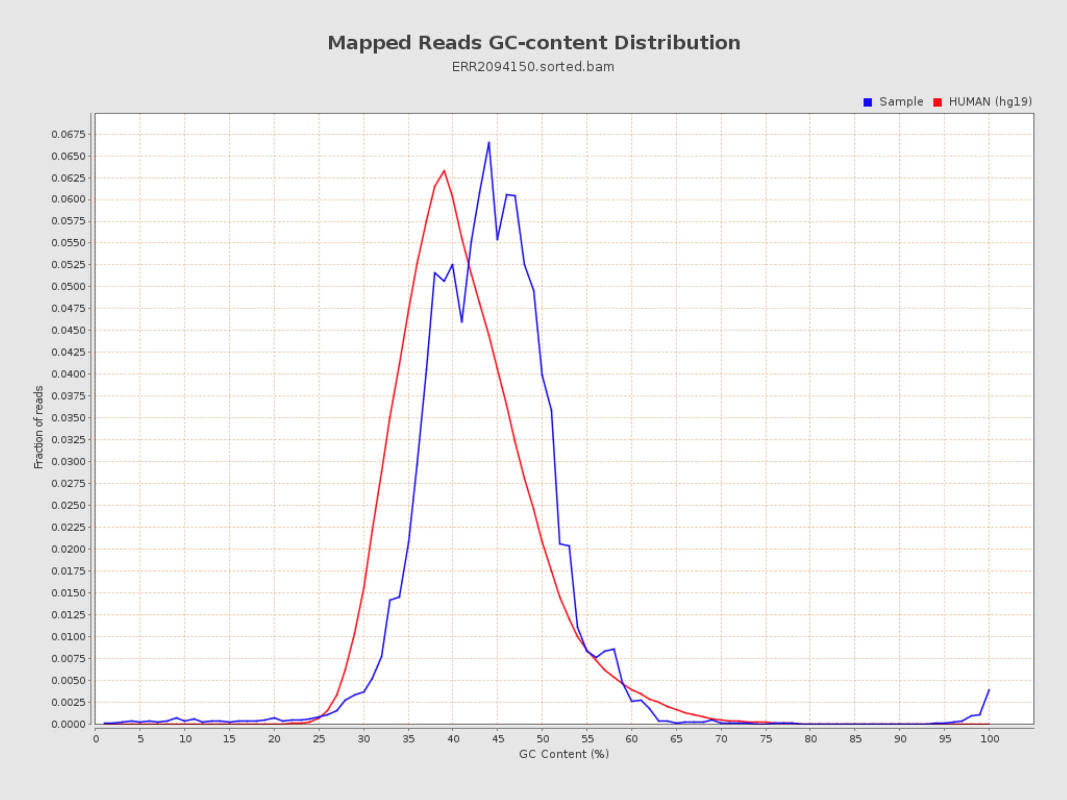
7. Results : Duplication Rate Histogram



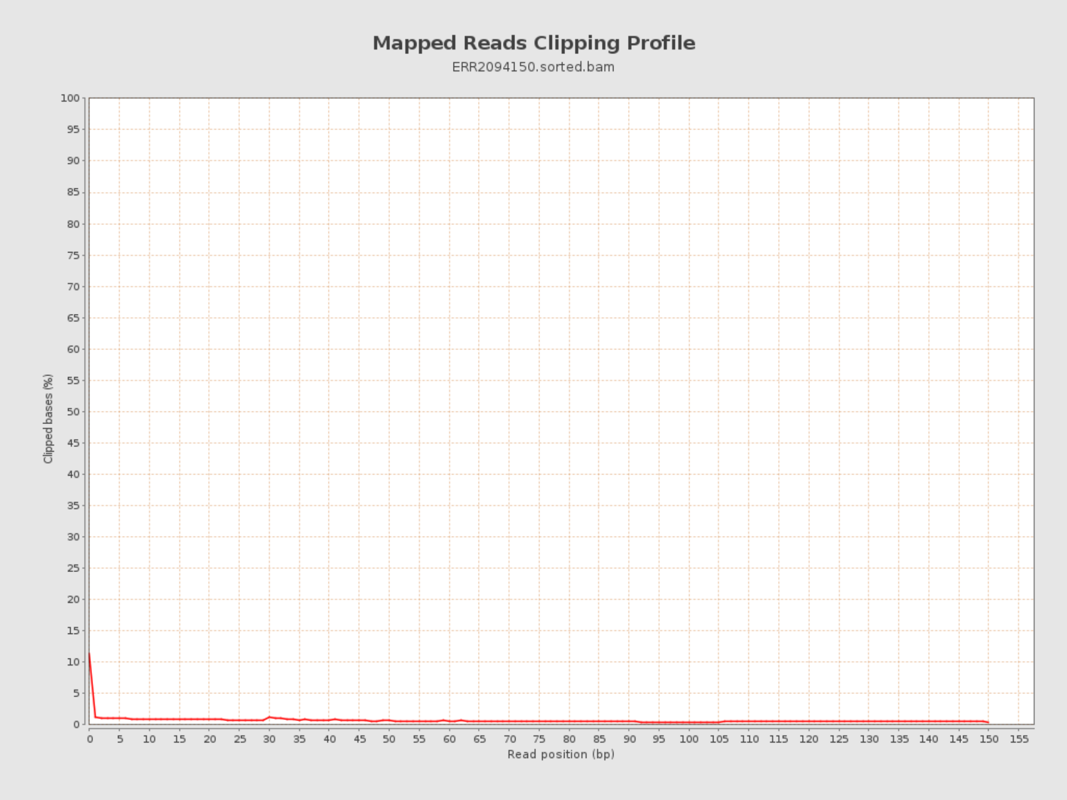
8. Results : Mapped Reads Nucleotide Content



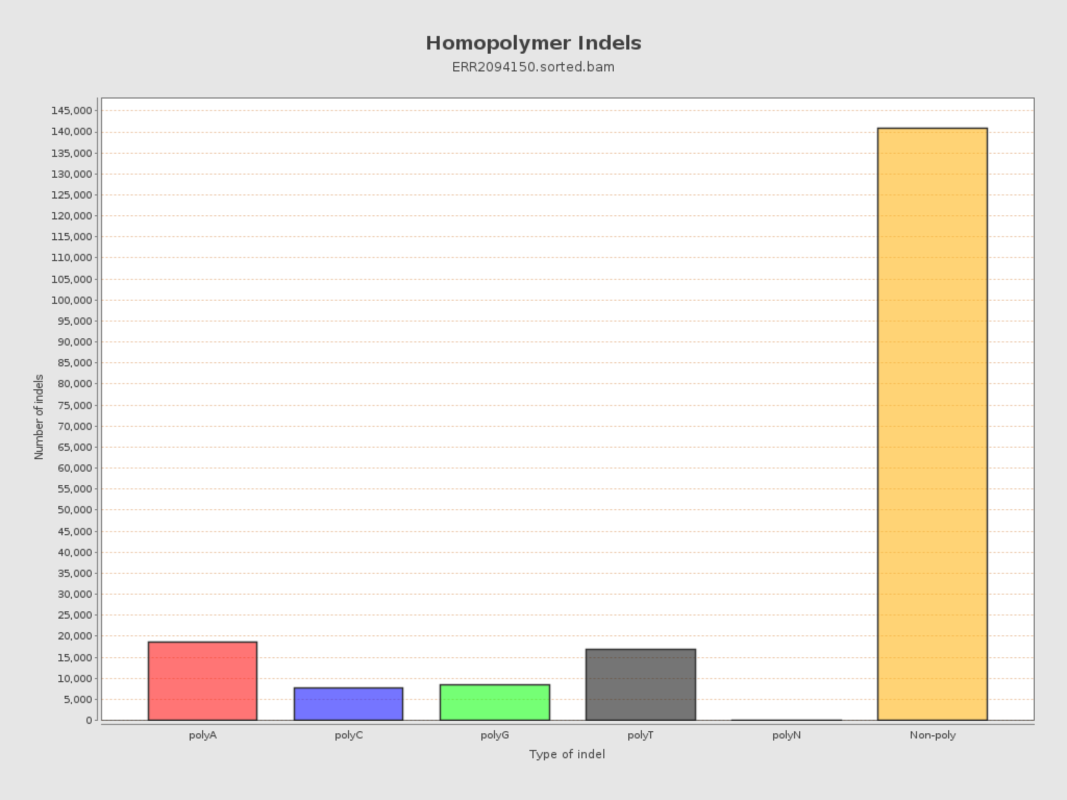
9. Results : Mapped Reads GC-content Distribution



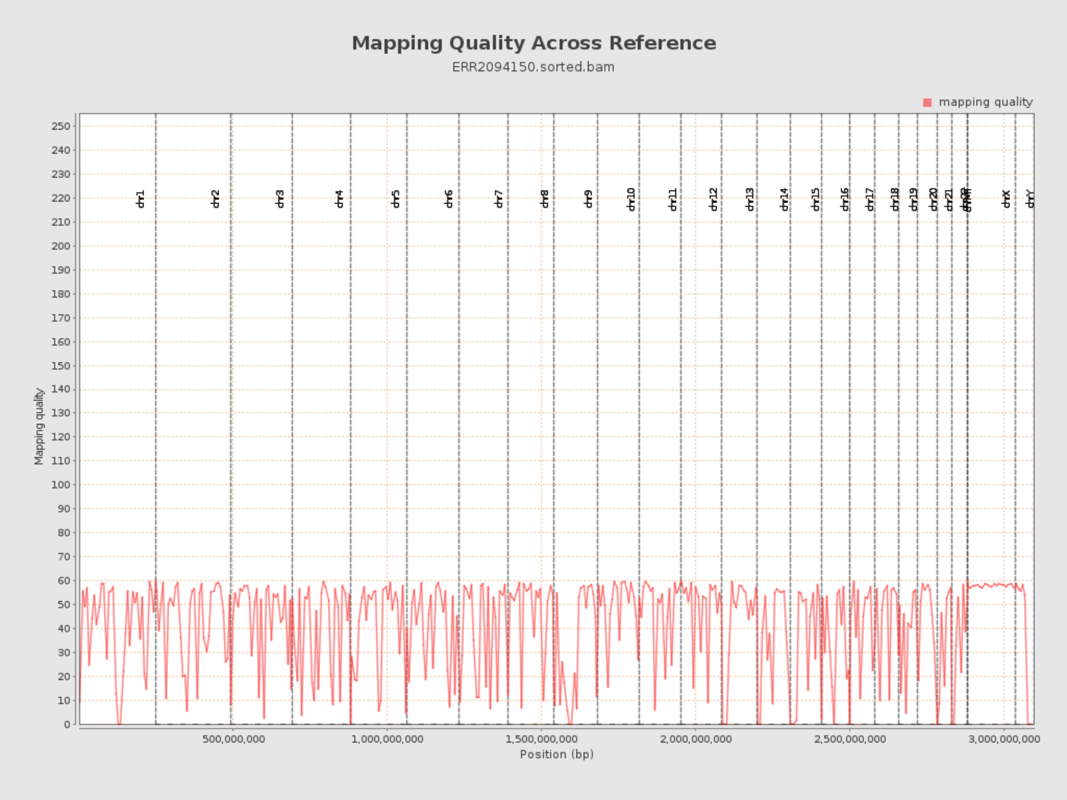
10. Results : Mapped Reads Clipping Profile



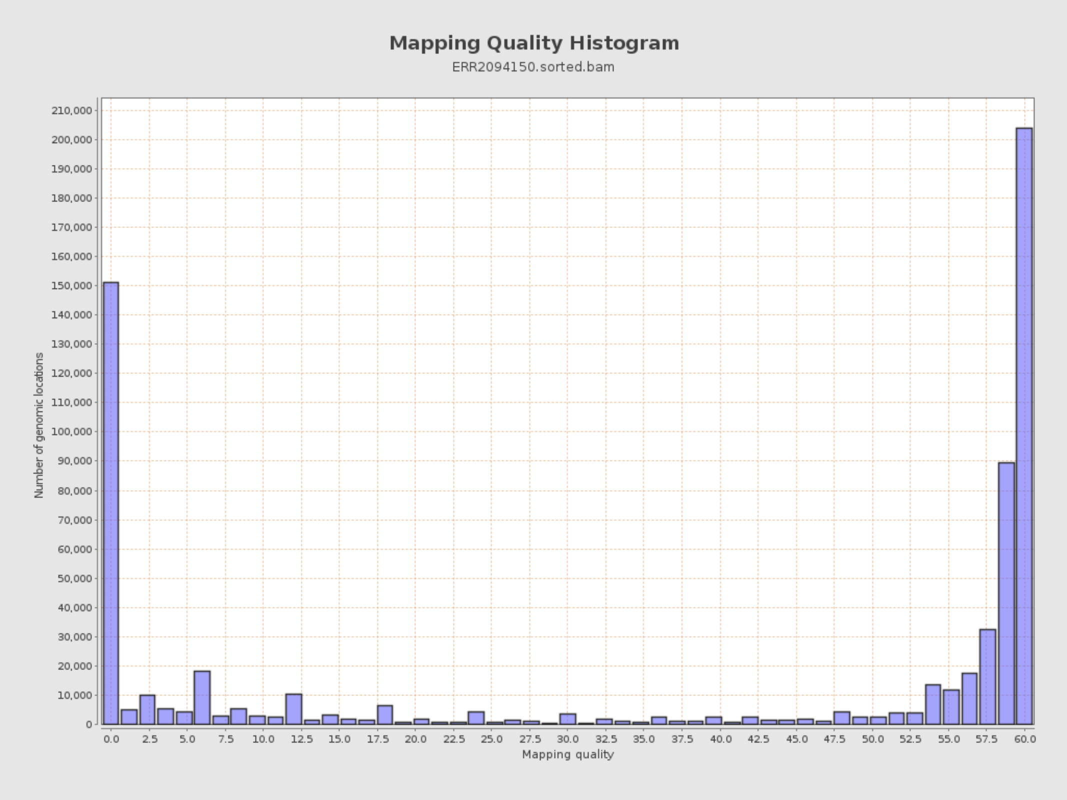
11. Results : Homopolymer Indels



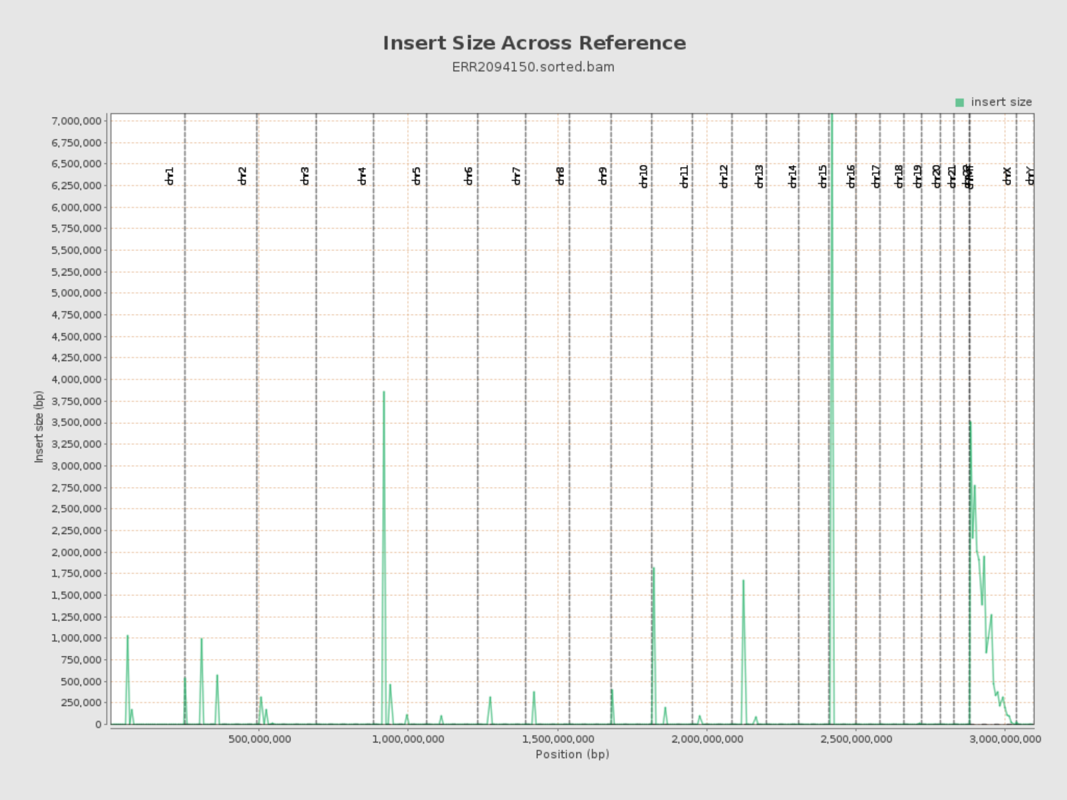
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram