Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:56:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094146.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_ERR2094146 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094146_1.fastq.gz ERR2094146_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:56:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	369,324
Mapped reads	337,492 / 91.38%
Unmapped reads	31,832 / 8.62%
Mapped paired reads	337,492 / 91.38%
Mapped reads, first in pair	169,658 / 45.94%
Mapped reads, second in pair	167,834 / 45.44%
Mapped reads, both in pair	334,196 / 90.49%
Mapped reads, singletons	3,296 / 0.89%
Secondary alignments	0
Supplementary alignments	21,860 / 5.92%
Read min/max/mean length	30 / 151 / 135.69
Duplicated reads (estimated)	308,257 / 83.47%
Duplication rate	47.53%
Clipped reads	167,489 / 45.35%

2.2. ACGT Content

Number/percentage of A's	11,567,008 / 27.52%
Number/percentage of C's	9,429,665 / 22.44%
Number/percentage of T's	10,975,731 / 26.11%
Number/percentage of G's	10,056,922 / 23.93%
Number/percentage of N's	422 / 0%

GC Percentage	46.36%

2.3. Coverage

Mean	0.0139
Standard Deviation	2.3365

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Insert size

Mean	1,468,881.7
Standard Deviation	10,881,881.12
P25/Median/P75	122 / 157 / 191

2.6. Mismatches and indels

General error rate	3.94%
Mismatches	1,604,904
Insertions	26,626
Mapped reads with at least one insertion	7.74%
Deletions	127,848
Mapped reads with at least one deletion	36.67%
Homopolymer indels	29.33%

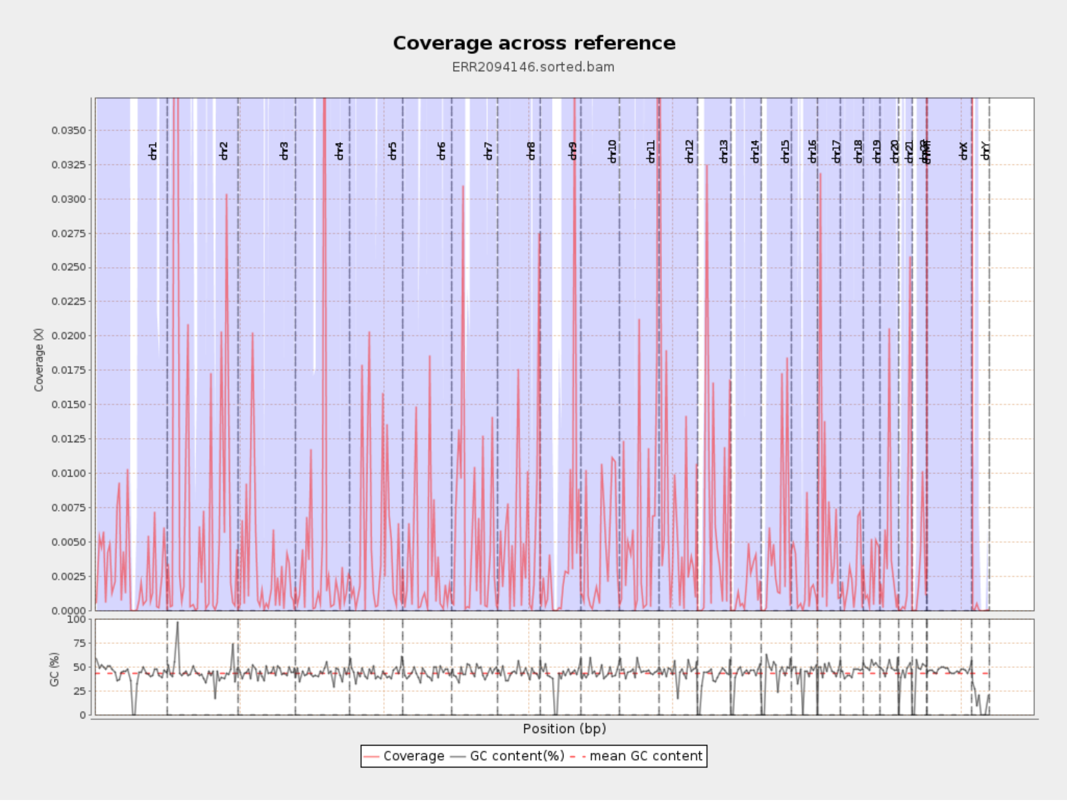
2.7. Chromosome stats

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

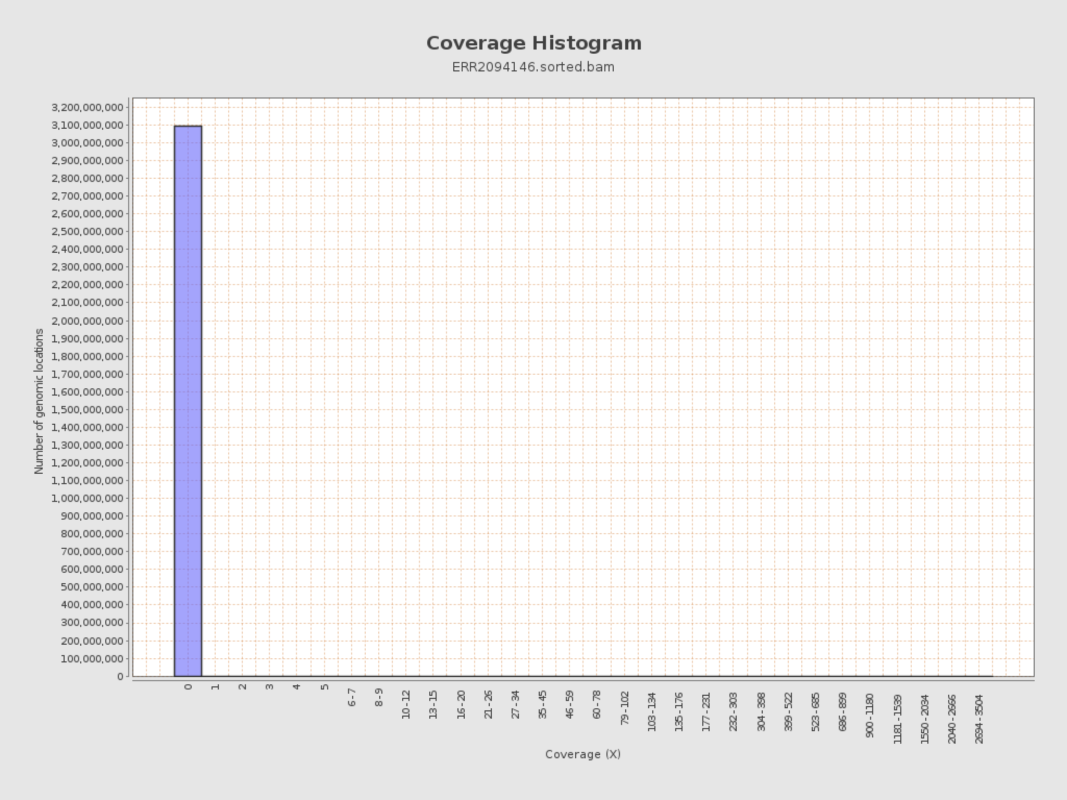
		bases	coverage	deviation
chr1	249250621	721836	0.0029	0.8135
chr2	243199373	1987702	0.0082	2.1816
chr3	198022430	626822	0.0032	0.809
chr4	191154276	832675	0.0044	1.0435
chr5	180915260	912683	0.005	1.5006
chr6	171115067	578419	0.0034	1.0187
chr7	159138663	930030	0.0058	1.4133
chr8	146364022	830278	0.0057	1.5964
chr9	141213431	640546	0.0045	1.5106
chr10	135534747	568932	0.0042	0.8821
chr11	135006516	828881	0.0061	1.4157
chr12	133851895	934636	0.007	1.556
chr13	115169878	791237	0.0069	1.4176
chr14	107349540	176371	0.0016	0.4492
chr15	102531392	476519	0.0046	1.024
chr16	90354753	205642	0.0023	0.5564
chr17	81195210	570042	0.007	1.3717
chr18	78077248	201730	0.0026	0.5951
chr19	59128983	147064	0.0025	0.5594
chr20	63025520	285541	0.0045	1.3996
chr21	48129895	261272	0.0054	1.5975
chr22	51304566	139967	0.0027	0.6433
chrMT	16571	2026278	122.2786	486.7613
chrX	155270560	27320035	0.176	7.1371

chrY	59373566	5526	0.0001	0.04

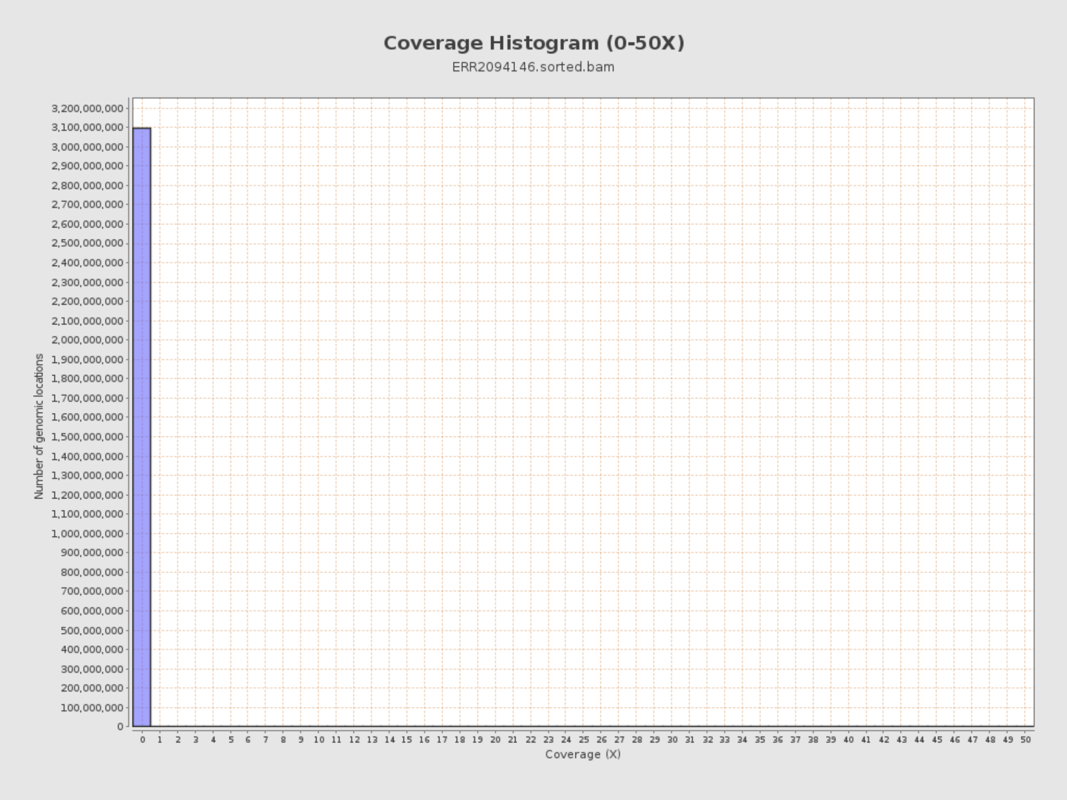
3. Results : Coverage across reference



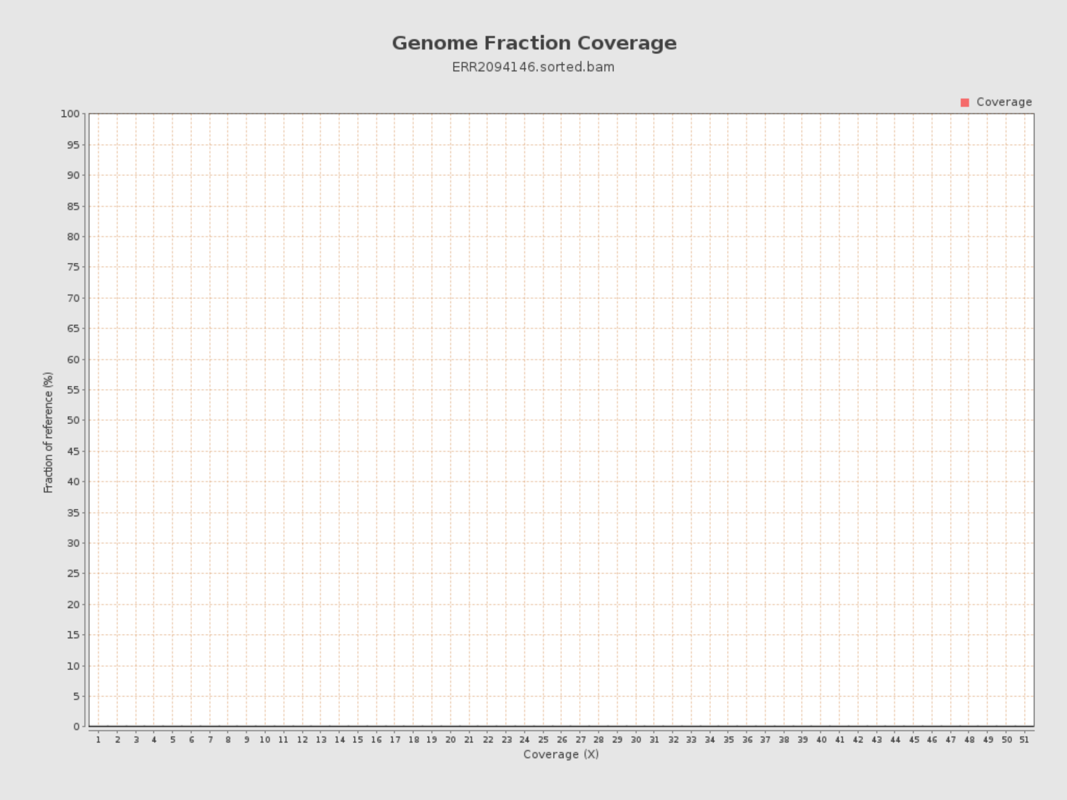
4. Results : Coverage Histogram



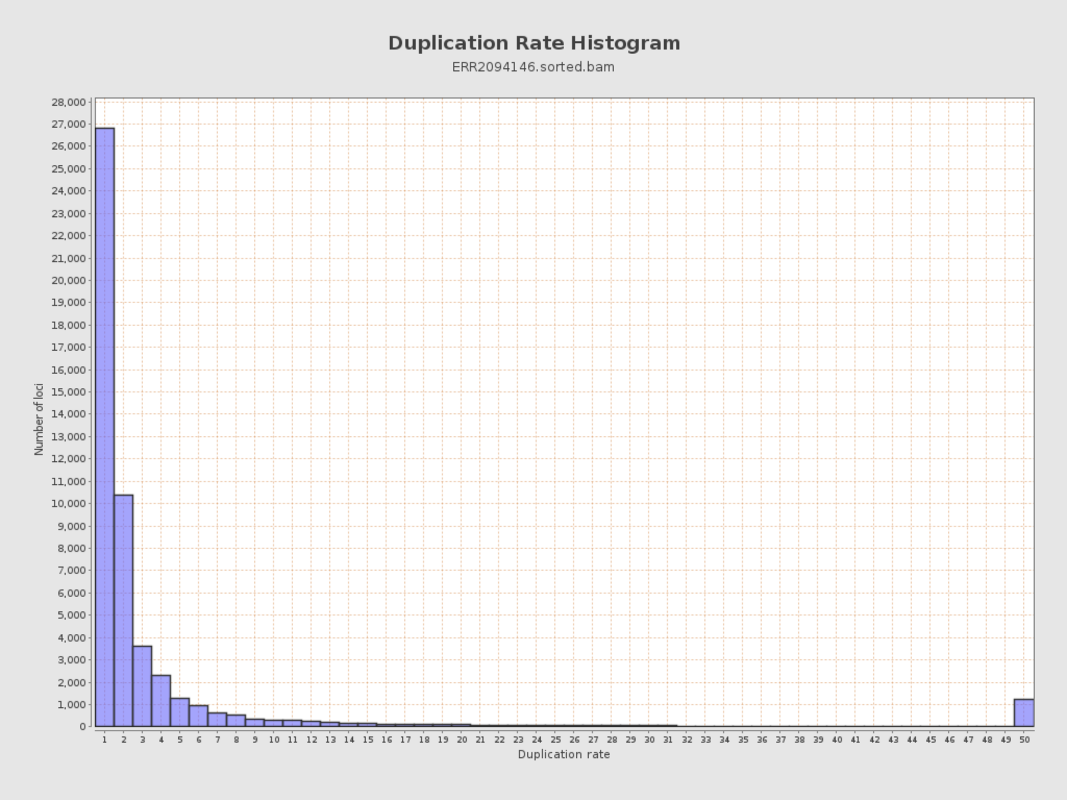
5. Results : Coverage Histogram (0-50X)



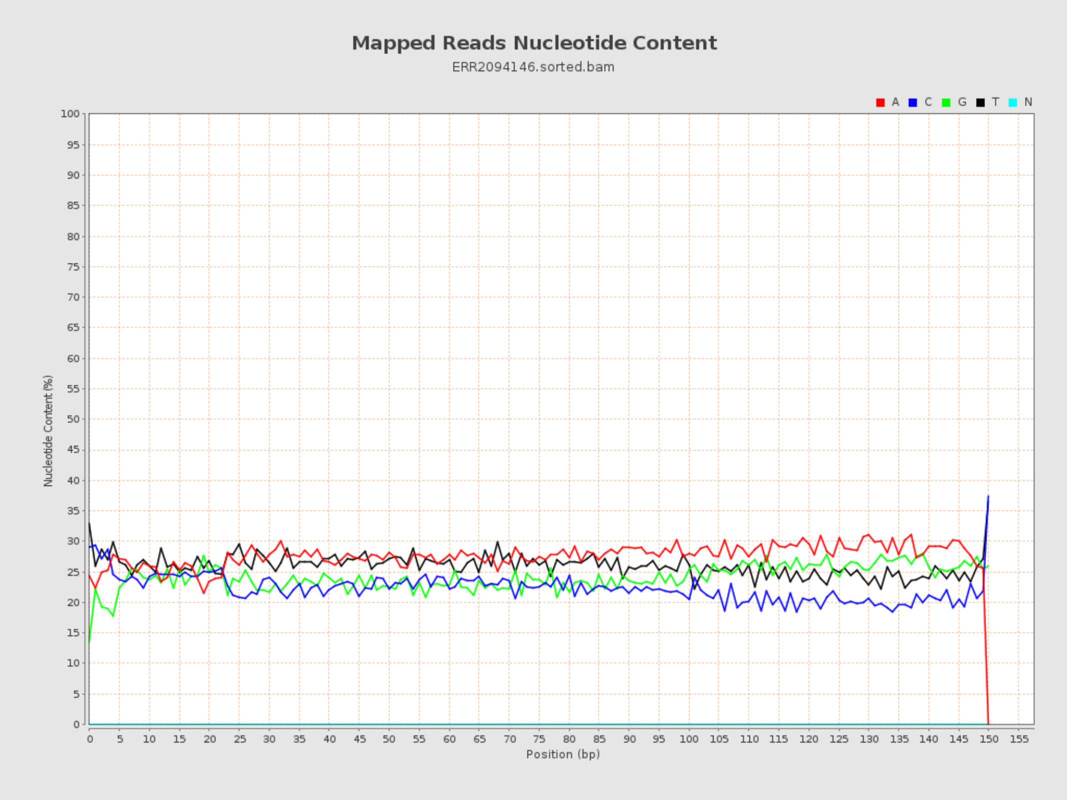
6. Results : Genome Fraction Coverage



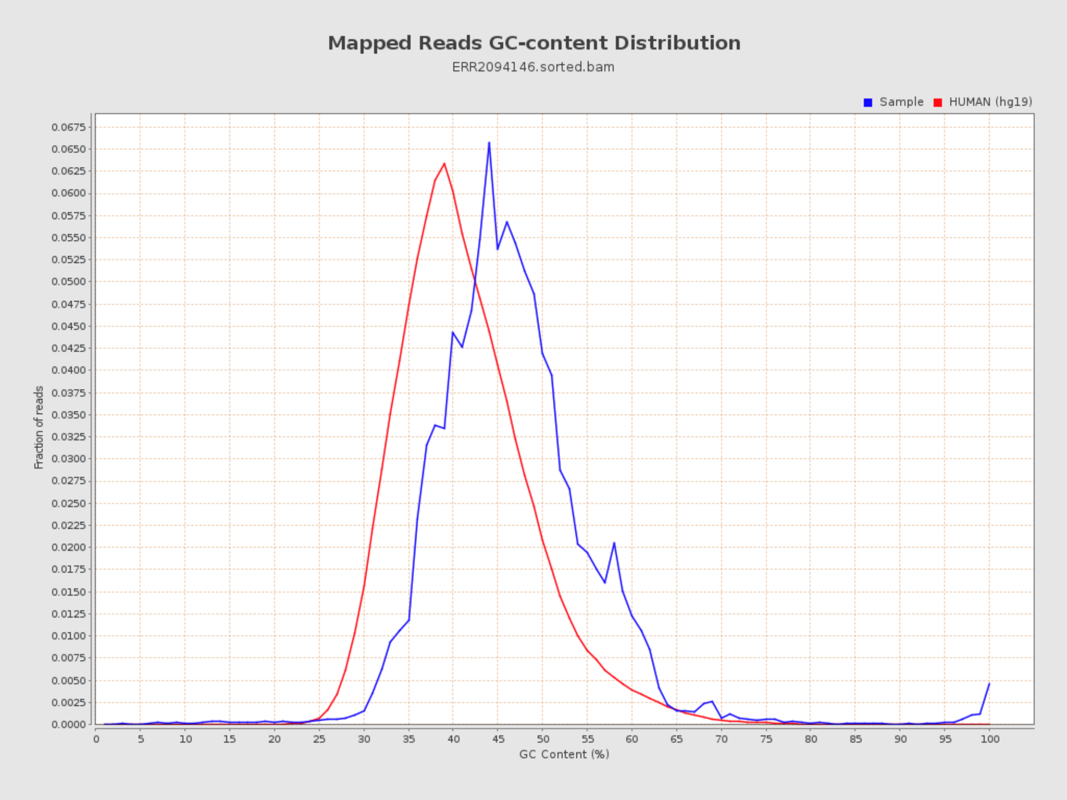
7. Results : Duplication Rate Histogram



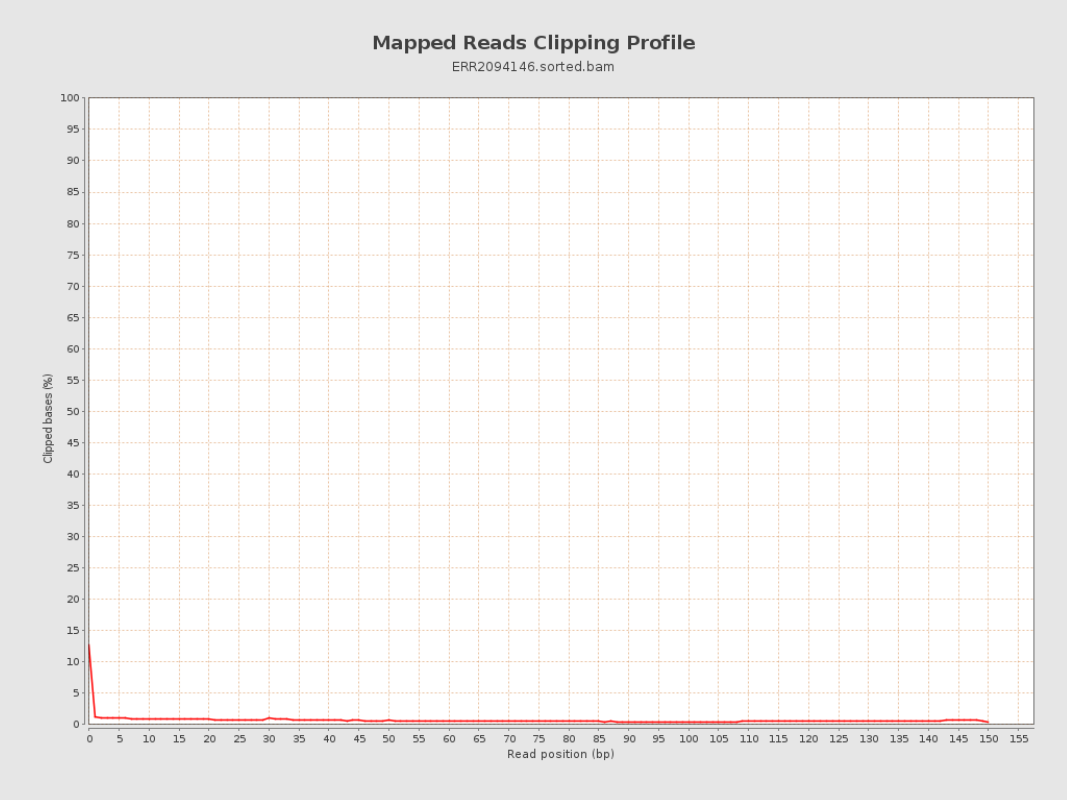
8. Results : Mapped Reads Nucleotide Content



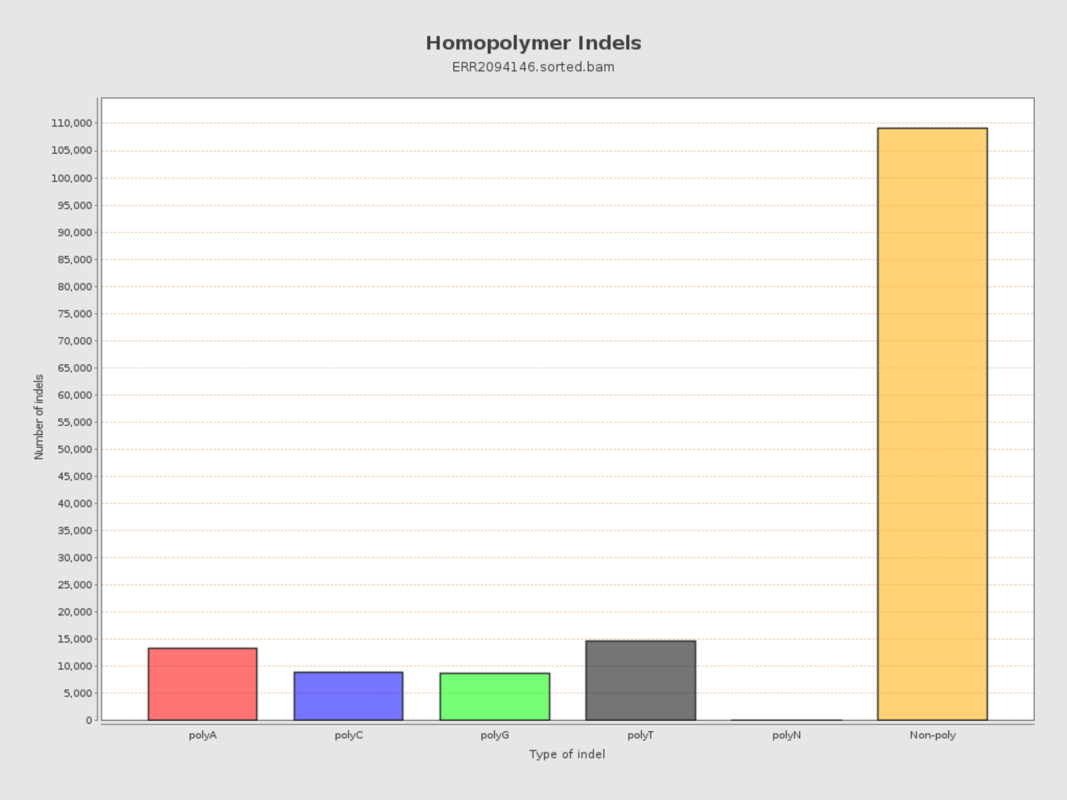
9. Results : Mapped Reads GC-content Distribution



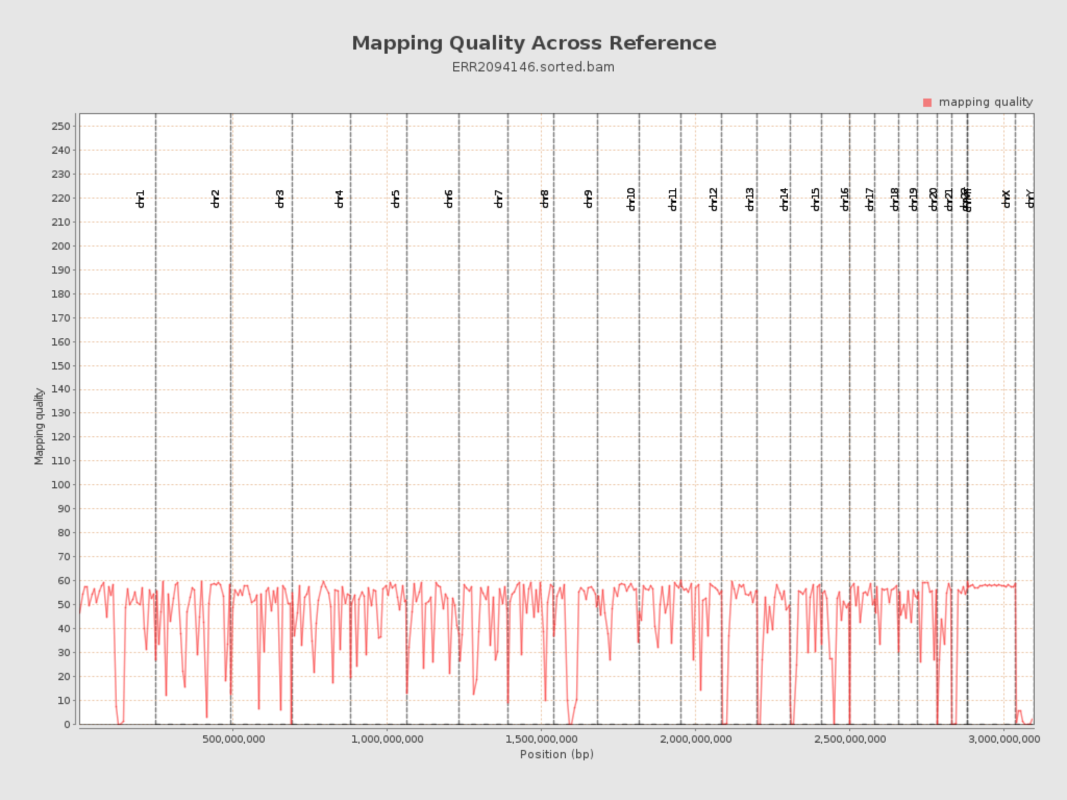
10. Results : Mapped Reads Clipping Profile



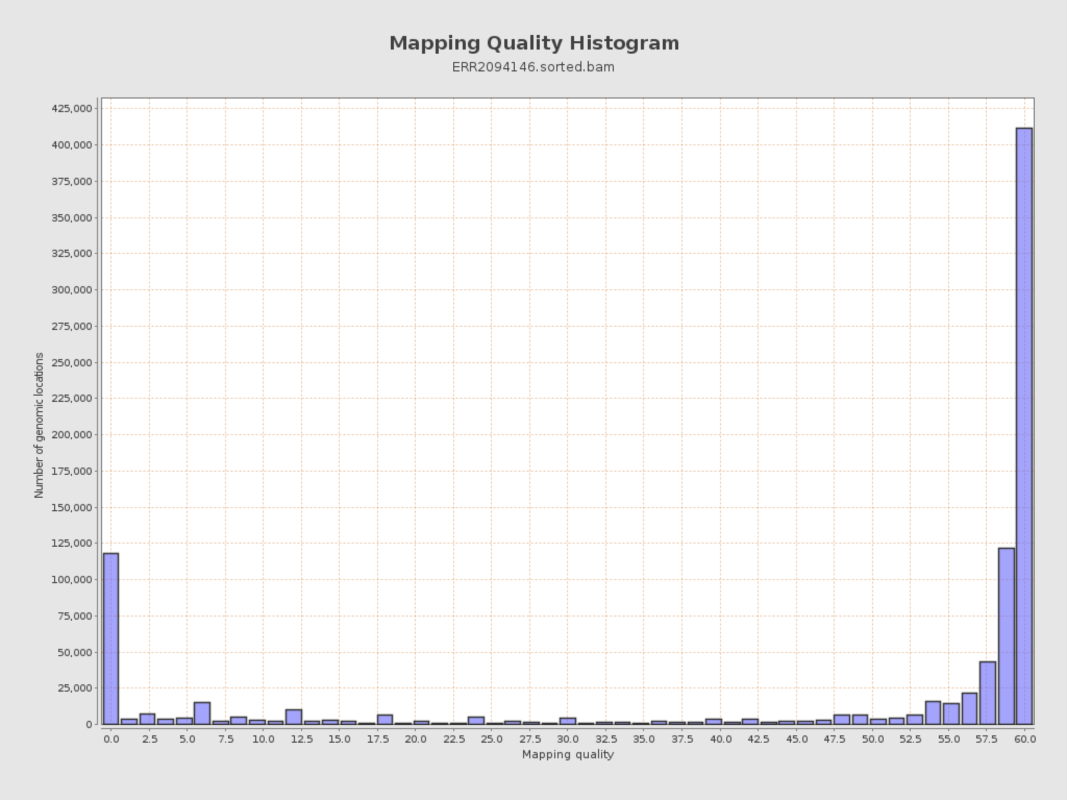
11. Results : Homopolymer Indels



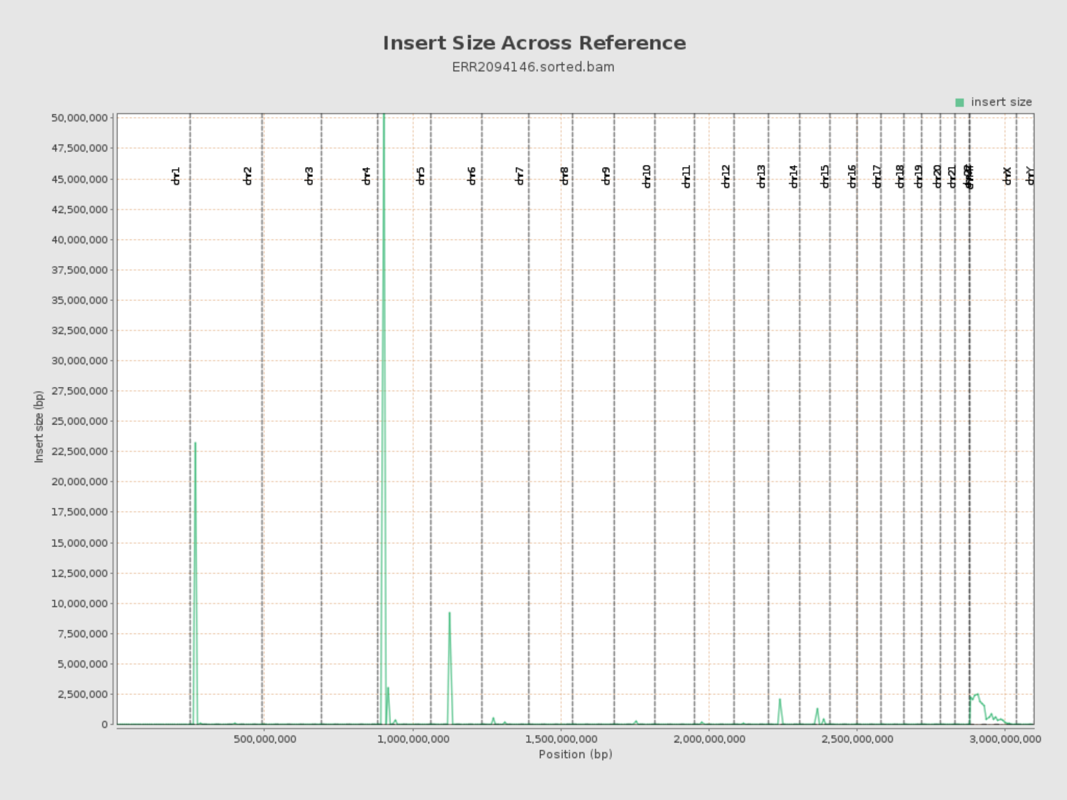
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram