Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:03:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094099.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_ERR2094099 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094099_1.fastq.gz ERR2094099_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:03:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	326,480
Mapped reads	304,371 / 93.23%
Unmapped reads	22,109 / 6.77%
Mapped paired reads	304,371 / 93.23%
Mapped reads, first in pair	152,997 / 46.86%
Mapped reads, second in pair	151,374 / 46.37%
Mapped reads, both in pair	301,396 / 92.32%
Mapped reads, singletons	2,975 / 0.91%
Secondary alignments	0
Supplementary alignments	19,663 / 6.02%
Read min/max/mean length	30 / 151 / 133.84
Duplicated reads (estimated)	287,532 / 88.07%
Duplication rate	50.43%
Clipped reads	164,231 / 50.3%

2.2. ACGT Content

Number/percentage of A's	10,283,071 / 28.82%
Number/percentage of C's	7,714,076 / 21.62%
Number/percentage of T's	9,608,969 / 26.93%
Number/percentage of G's	8,072,645 / 22.63%
Number/percentage of N's	423 / 0%

GC Percentage	44.25%

2.3. Coverage

Mean	0.0118
Standard Deviation	2.769

2.4. Mapping Quality

Mean Mapping Quality	39.7

2.5. Insert size

Mean	1,565,821.92
Standard Deviation	10,980,337.99
P25/Median/P75	109 / 138 / 167

2.6. Mismatches and indels

General error rate	3.96%
Mismatches	1,373,130
Insertions	23,176
Mapped reads with at least one insertion	7.53%
Deletions	111,057
Mapped reads with at least one deletion	35.43%
Homopolymer indels	27.86%

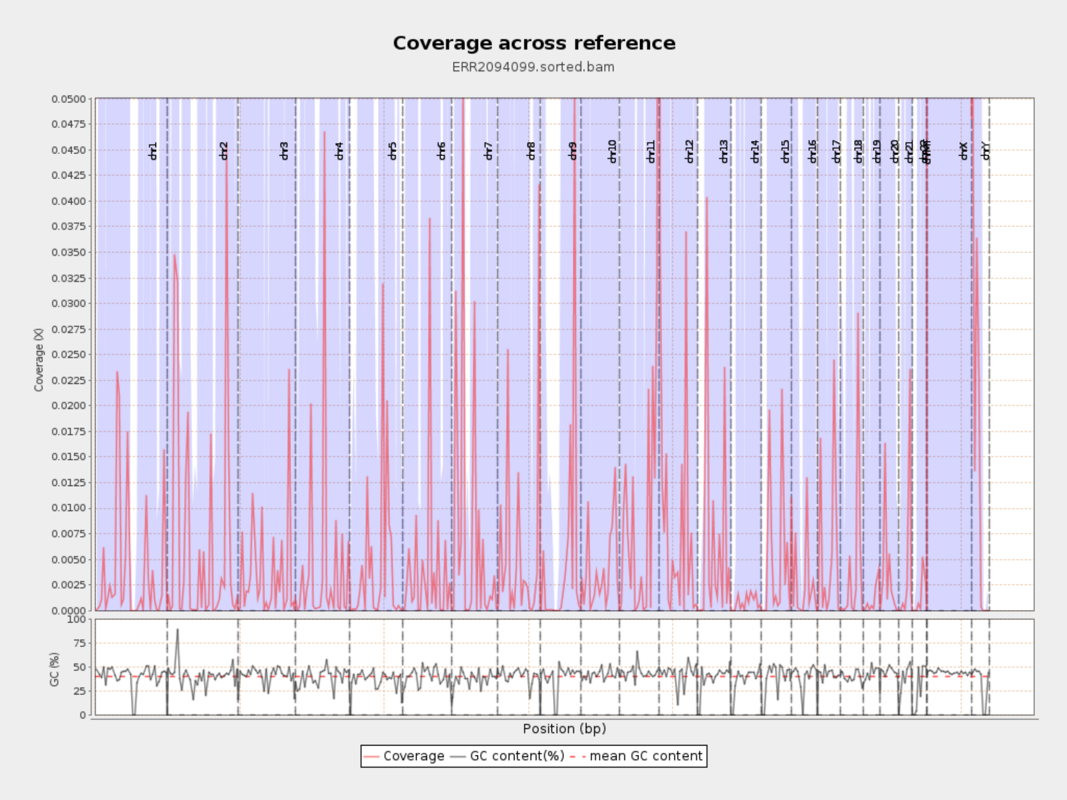
2.7. Chromosome stats

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

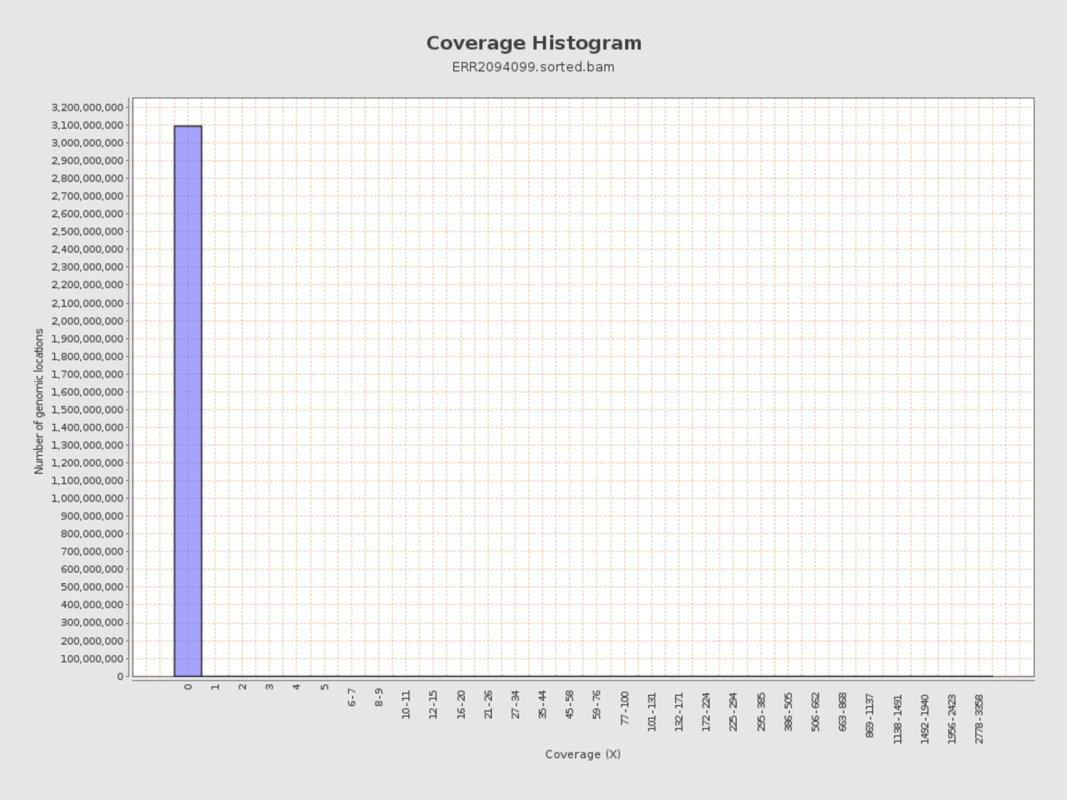
		bases	coverage	deviation
chr1	249250621	969205	0.0039	1.7192
chr2	243199373	1609132	0.0066	2.1511
chr3	198022430	725378	0.0037	1.2467
chr4	191154276	849846	0.0044	1.2459
chr5	180915260	797335	0.0044	2.0096
chr6	171115067	699549	0.0041	1.4792
chr7	159138663	1151085	0.0072	2.6882
chr8	146364022	864287	0.0059	2.25
chr9	141213431	725834	0.0051	2.8957
chr10	135534747	510639	0.0038	1.0353
chr11	135006516	1210393	0.009	2.5492
chr12	133851895	1111241	0.0083	2.169
chr13	115169878	732983	0.0064	1.7544
chr14	107349540	82817	0.0008	0.2248
chr15	102531392	481542	0.0047	1.4398
chr16	90354753	276911	0.0031	1.0693
chr17	81195210	477539	0.0059	1.7507
chr18	78077248	342395	0.0044	2.2159
chr19	59128983	63168	0.0011	0.3057
chr20	63025520	226355	0.0036	1.2159
chr21	48129895	212529	0.0044	1.5999
chr22	51304566	68588	0.0013	0.4047
chrMT	16571	53113	3.2052	22.706
chrX	155270560	21413190	0.1379	9.2618

chrY	59373566	858559	0.0145	3.0941

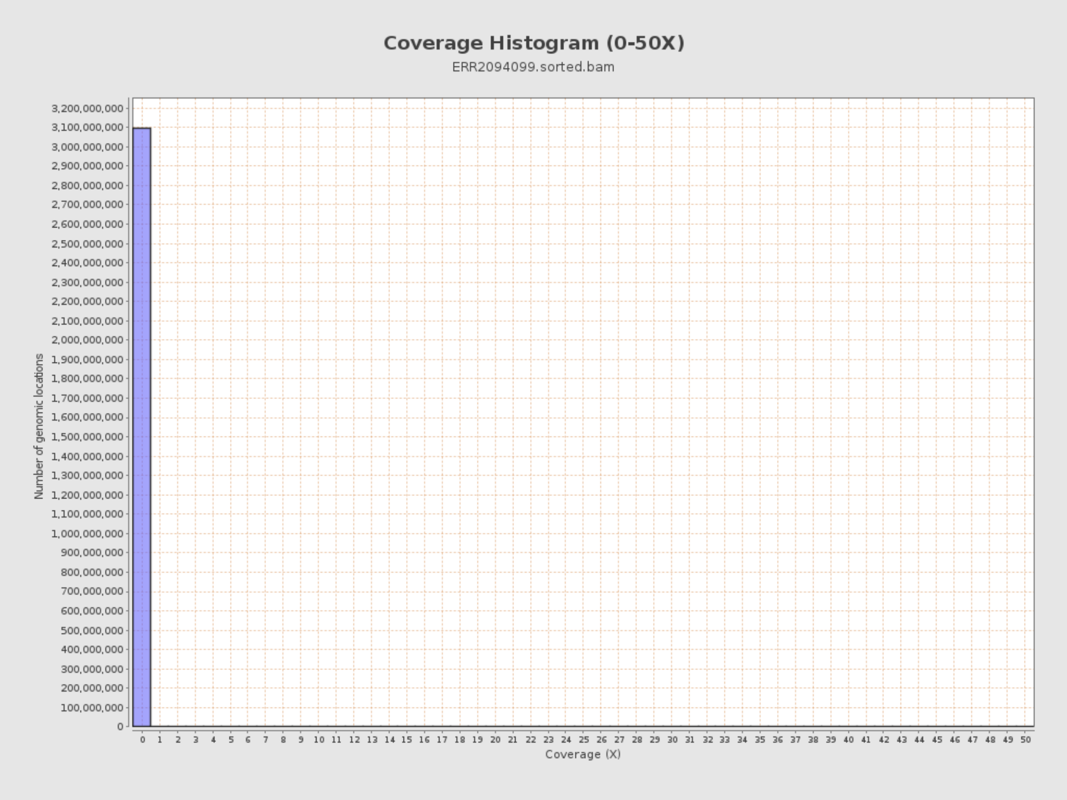
3. Results : Coverage across reference



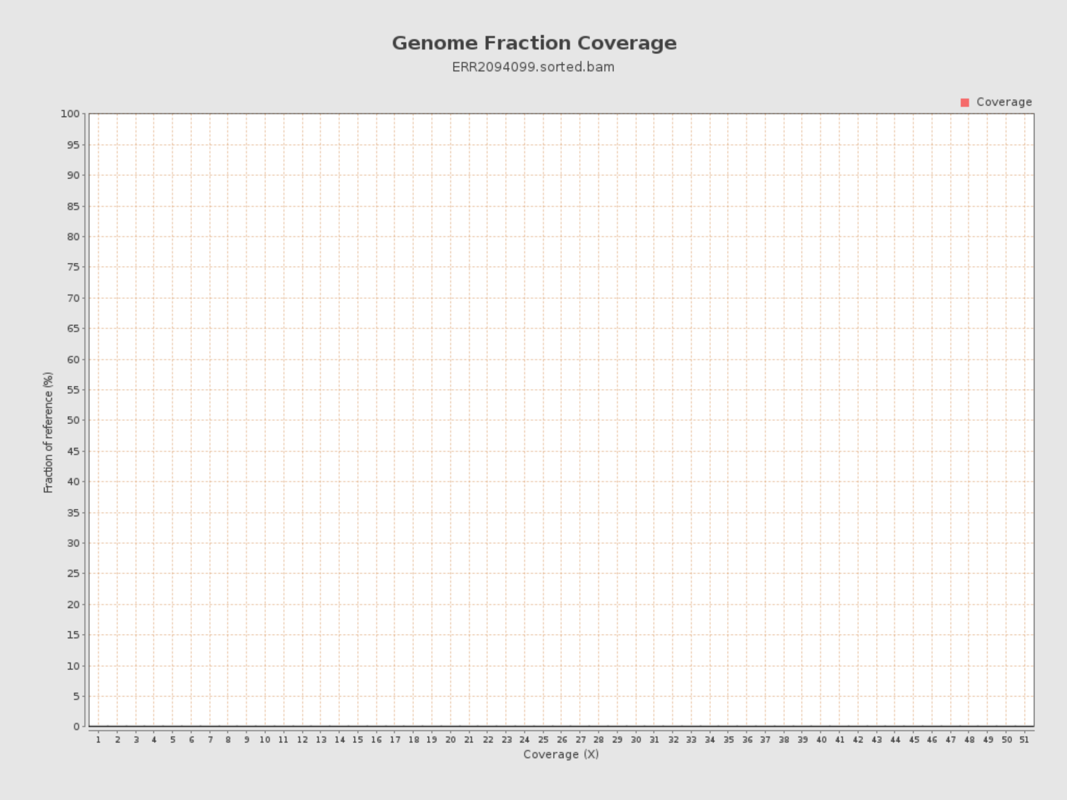
4. Results : Coverage Histogram



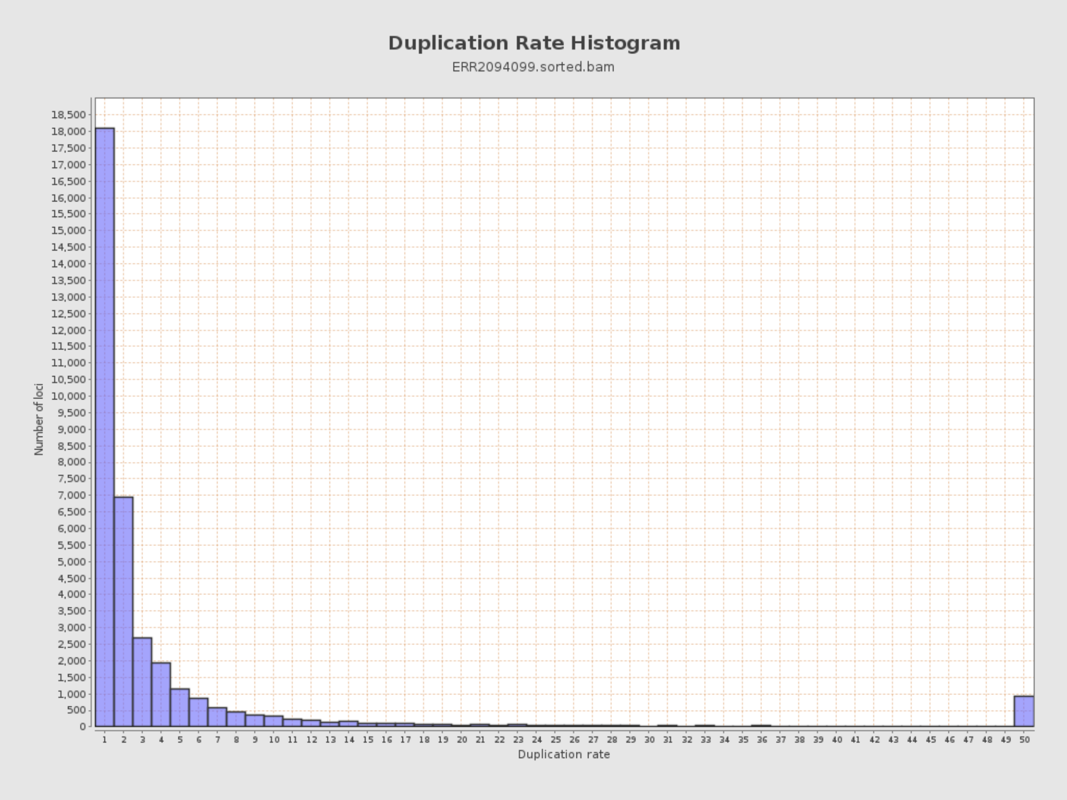
5. Results : Coverage Histogram (0-50X)



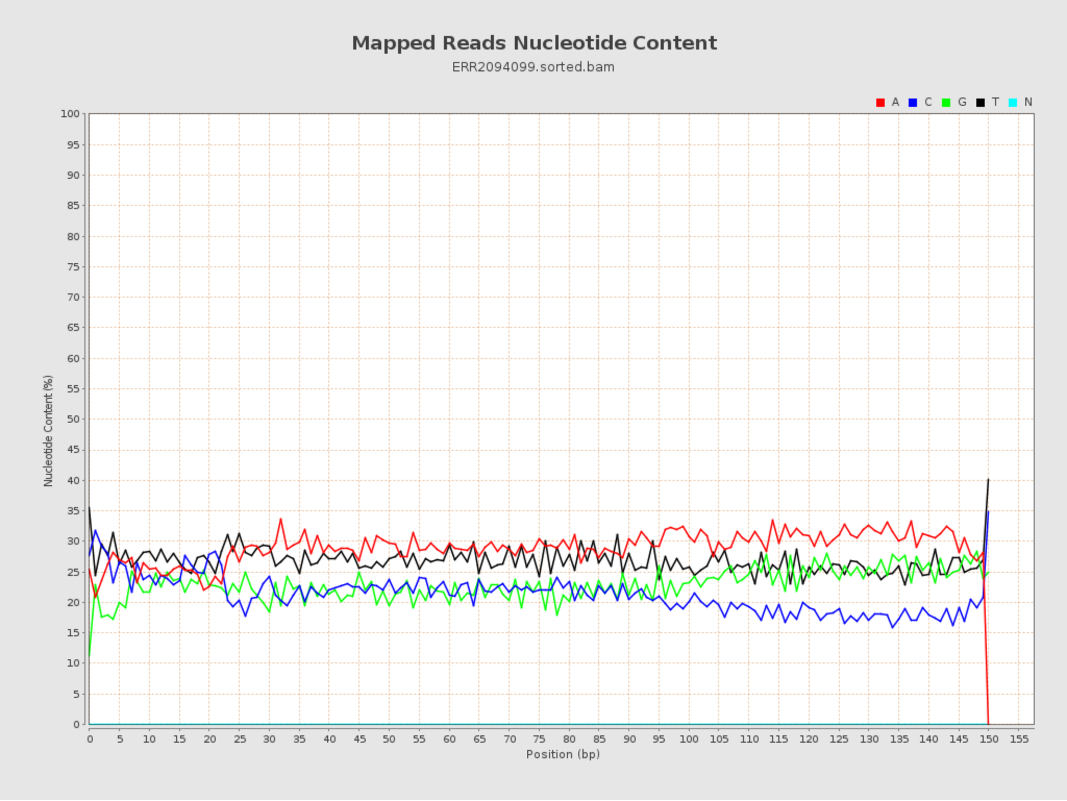
6. Results : Genome Fraction Coverage



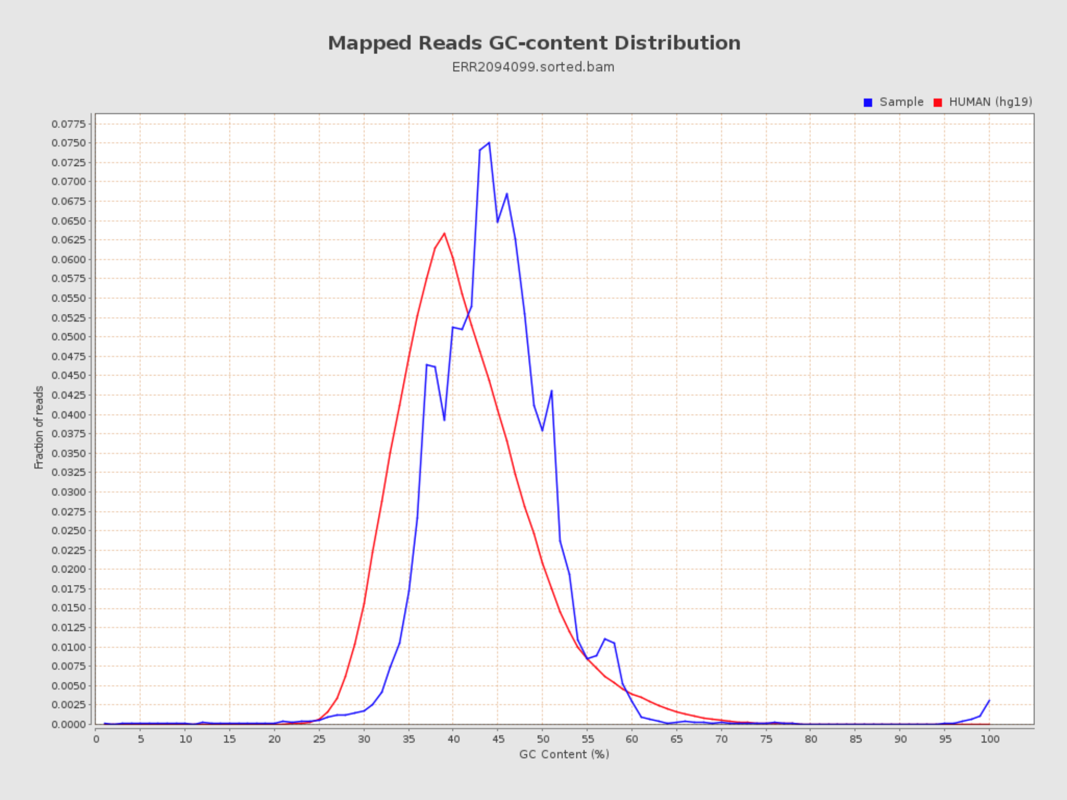
7. Results : Duplication Rate Histogram



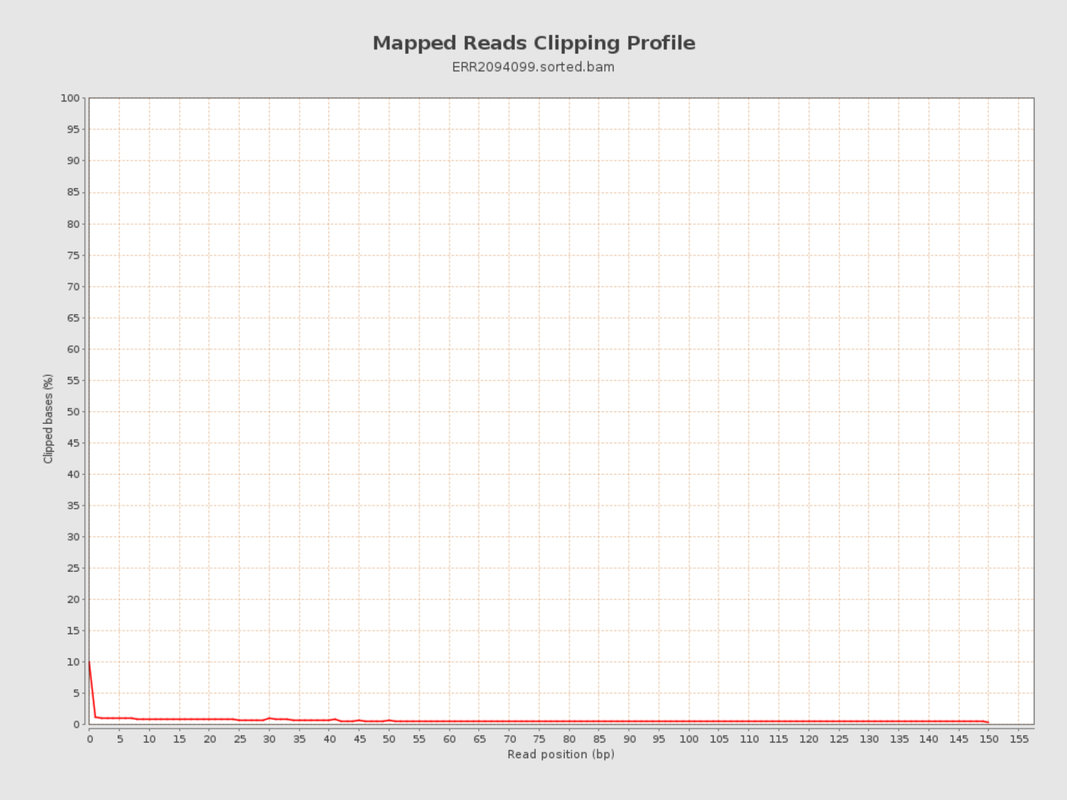
8. Results : Mapped Reads Nucleotide Content



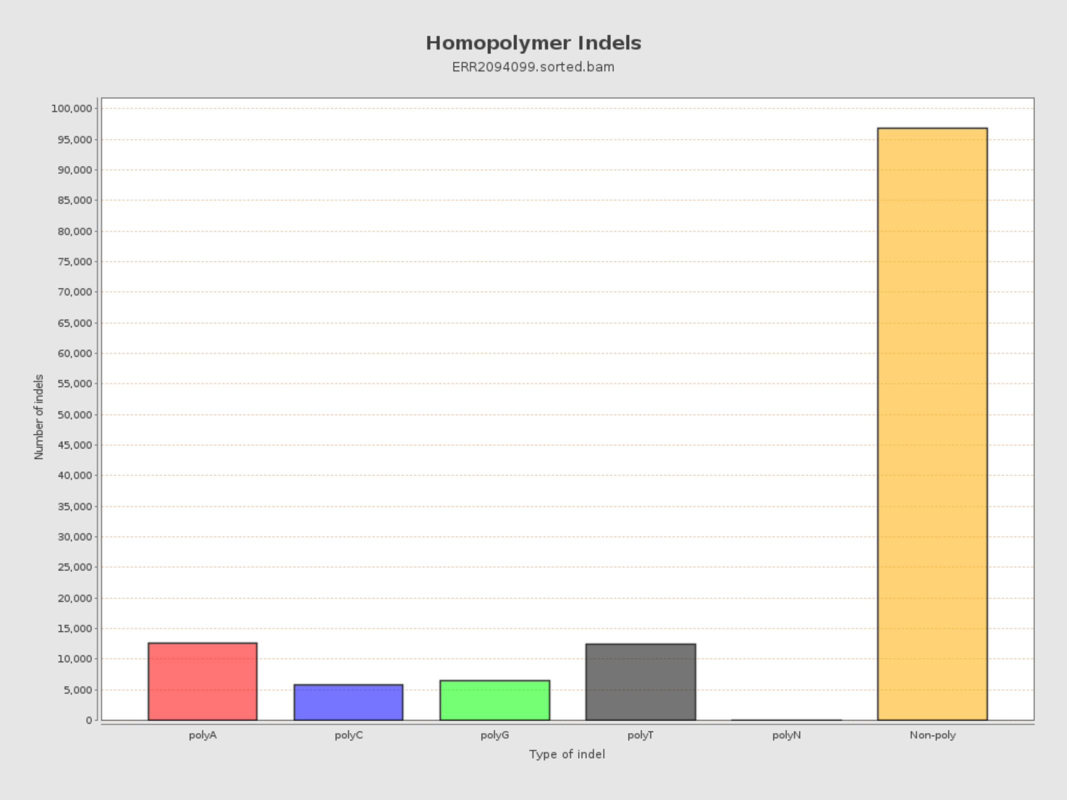
9. Results : Mapped Reads GC-content Distribution



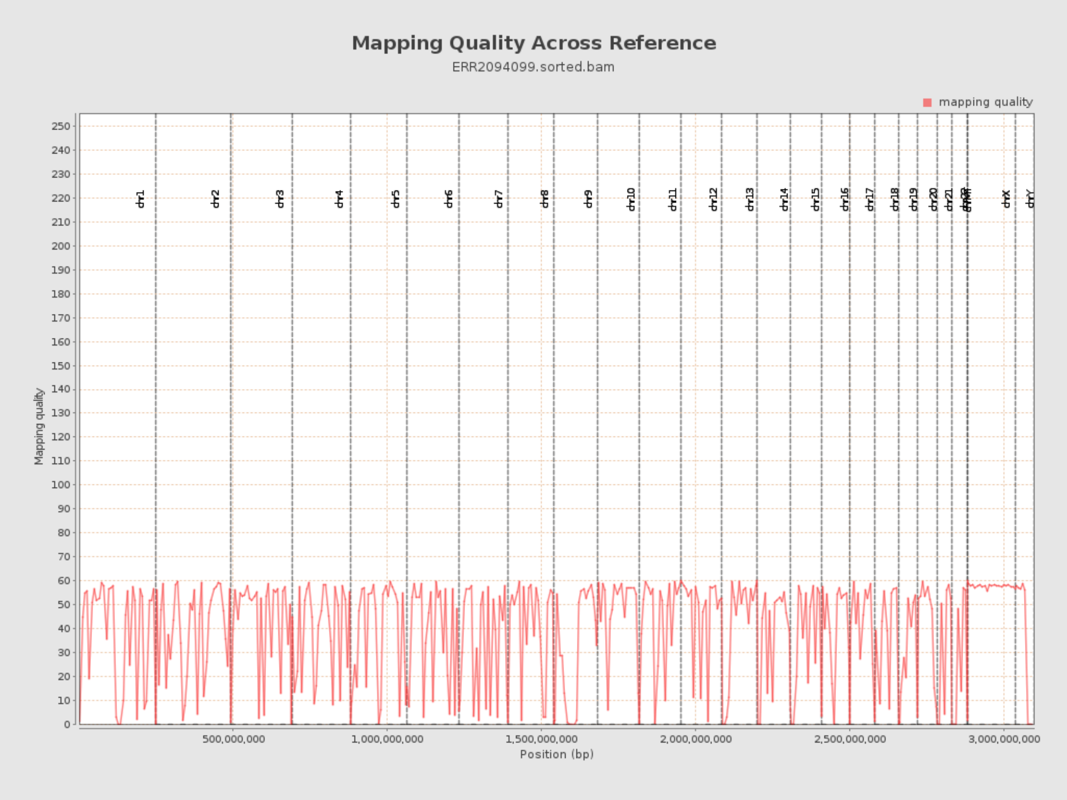
10. Results : Mapped Reads Clipping Profile



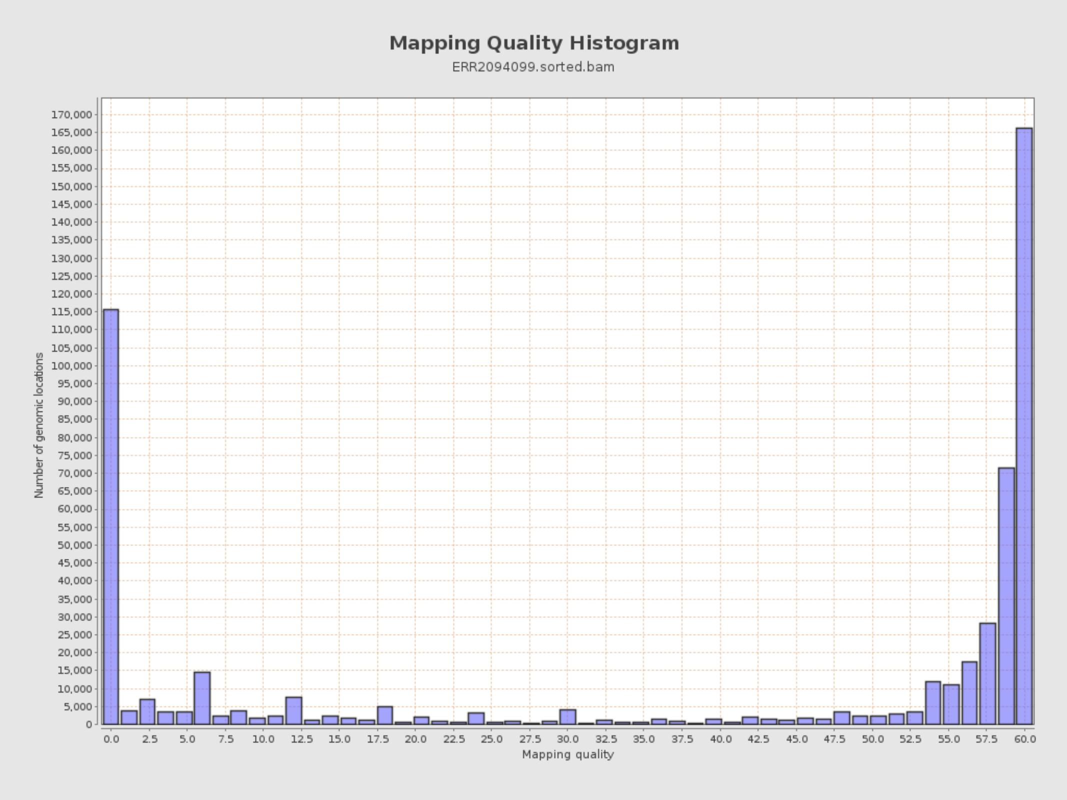
11. Results : Homopolymer Indels



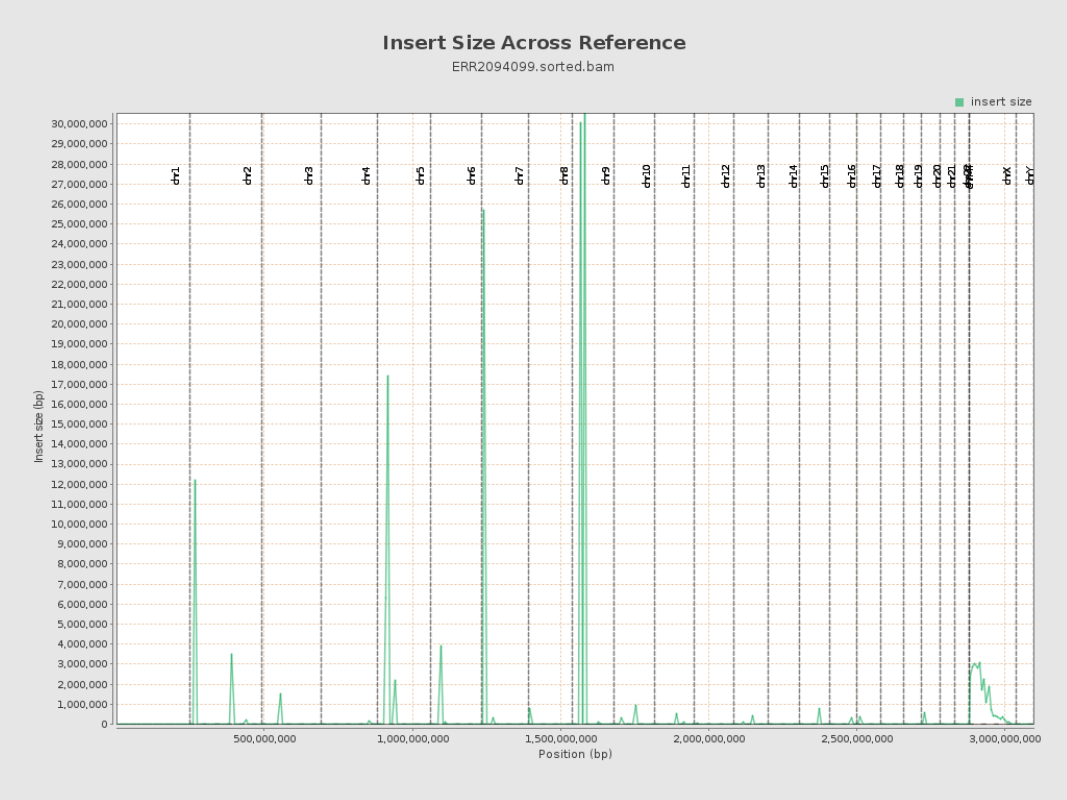
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram