Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:26:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094109.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_ERR2094109 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094109_1.fastq.gz ERR2094109_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:26:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	458,544
Mapped reads	438,470 / 95.62%
Unmapped reads	20,074 / 4.38%
Mapped paired reads	438,470 / 95.62%
Mapped reads, first in pair	220,429 / 48.07%
Mapped reads, second in pair	218,041 / 47.55%
Mapped reads, both in pair	434,930 / 94.85%
Mapped reads, singletons	3,540 / 0.77%
Secondary alignments	0
Supplementary alignments	33,393 / 7.28%
Read min/max/mean length	30 / 151 / 141.3
Duplicated reads (estimated)	423,105 / 92.27%
Duplication rate	53.17%
Clipped reads	234,415 / 51.12%

2.2. ACGT Content

Number/percentage of A's	15,809,380 / 28.79%
Number/percentage of C's	11,769,314 / 21.43%
Number/percentage of T's	14,907,055 / 27.14%
Number/percentage of G's	12,432,485 / 22.64%
Number/percentage of N's	697 / 0%

GC Percentage	44.07%

2.3. Coverage

Mean	0.0181
Standard Deviation	3.5842

2.4. Mapping Quality

Mean Mapping Quality	40.9

2.5. Insert size

Mean	1,753,434.97
Standard Deviation	11,583,689.65
P25/Median/P75	121 / 159 / 189

2.6. Mismatches and indels

General error rate	3.47%
Mismatches	1,821,392
Insertions	37,613
Mapped reads with at least one insertion	8.45%
Deletions	139,218
Mapped reads with at least one deletion	30.56%
Homopolymer indels	28.69%

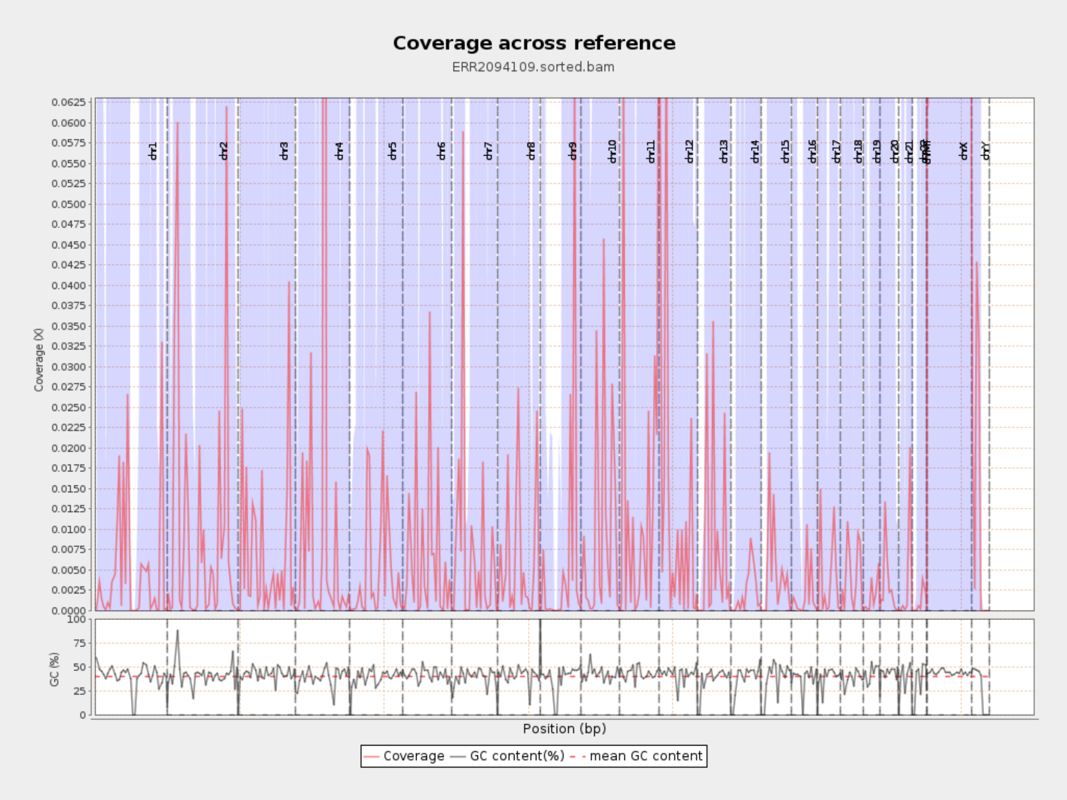
2.7. Chromosome stats

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

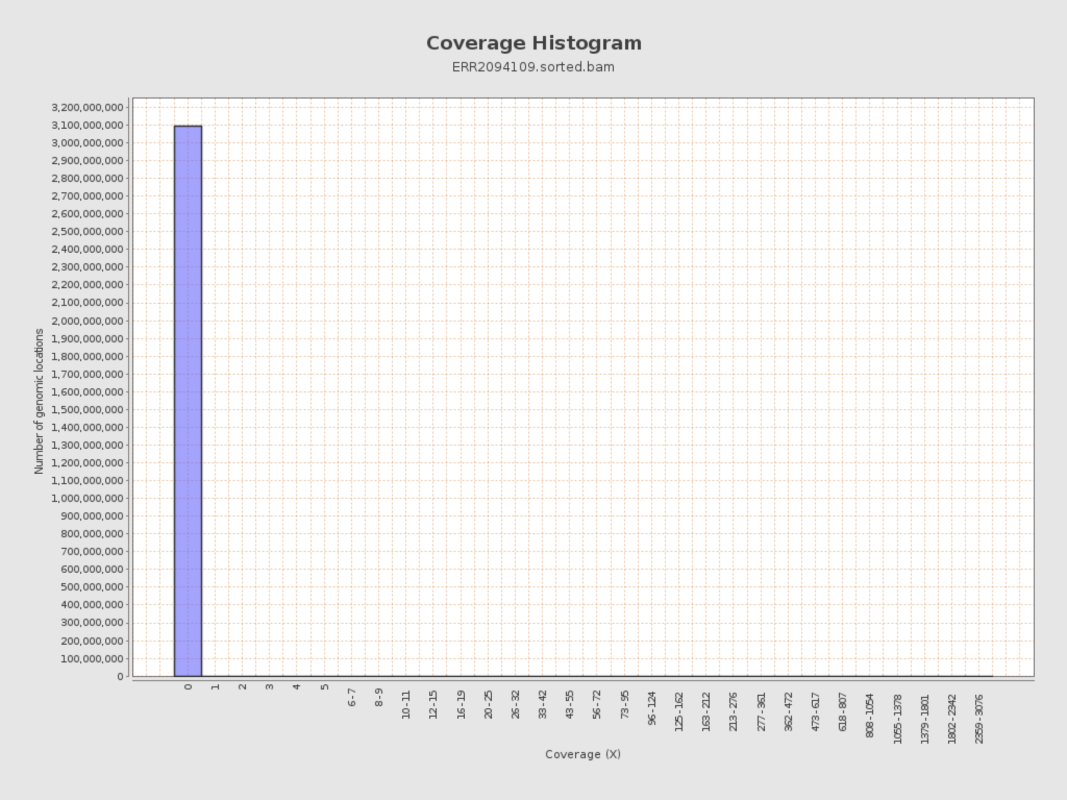
		bases	coverage	deviation
chr1	249250621	1176330	0.0047	1.8628
chr2	243199373	2362482	0.0097	3.0931
chr3	198022430	1339286	0.0068	2.3264
chr4	191154276	2676476	0.014	3.8744
chr5	180915260	943025	0.0052	1.672
chr6	171115067	1158824	0.0068	2.0028
chr7	159138663	1184725	0.0074	2.2457
chr8	146364022	915612	0.0063	1.7652
chr9	141213431	919674	0.0065	2.5652
chr10	135534747	1258987	0.0093	3.0477
chr11	135006516	1653609	0.0122	3.0118
chr12	133851895	1807057	0.0135	3.4682
chr13	115169878	899612	0.0078	2.4043
chr14	107349540	240916	0.0022	0.7721
chr15	102531392	468824	0.0046	1.1662
chr16	90354753	190679	0.0021	0.797
chr17	81195210	333682	0.0041	1.2409
chr18	78077248	334965	0.0043	0.9504
chr19	59128983	103885	0.0018	0.5236
chr20	63025520	212841	0.0034	1.1571
chr21	48129895	200381	0.0042	1.1296
chr22	51304566	54702	0.0011	0.3332
chrMT	16571	524174	31.632	138.9105
chrX	155270560	34251384	0.2206	12.2018

chrY	59373566	716079	0.0121	2.6366

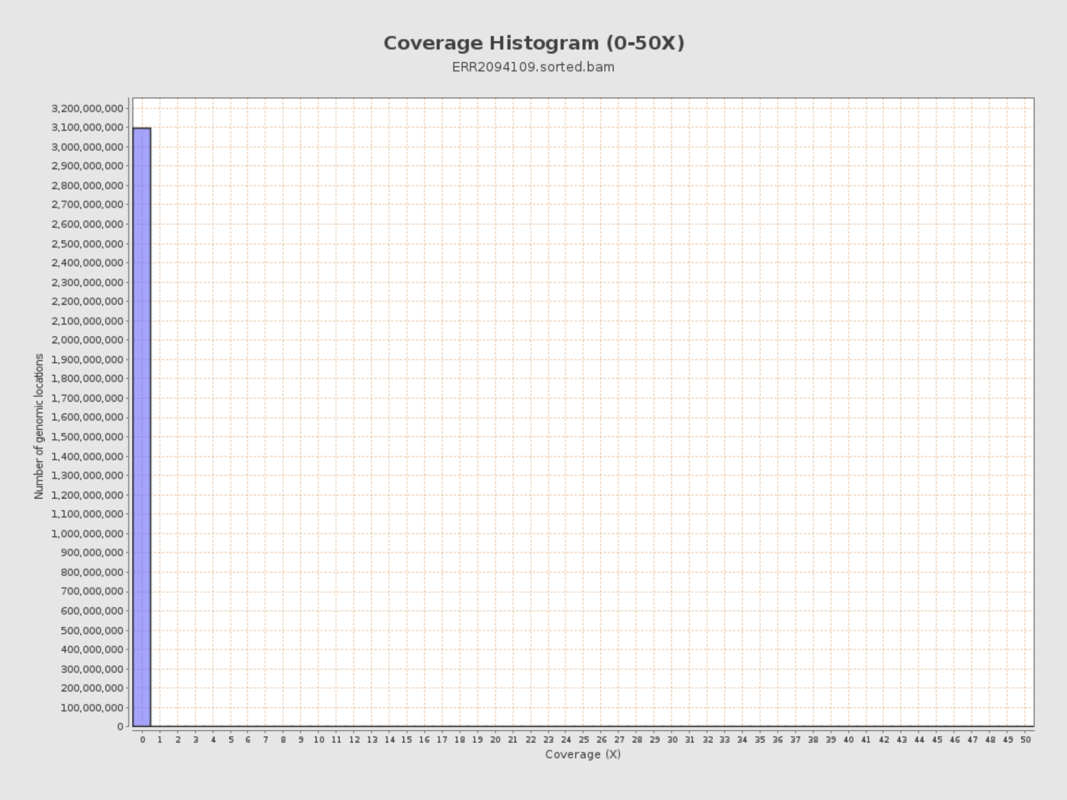
3. Results : Coverage across reference



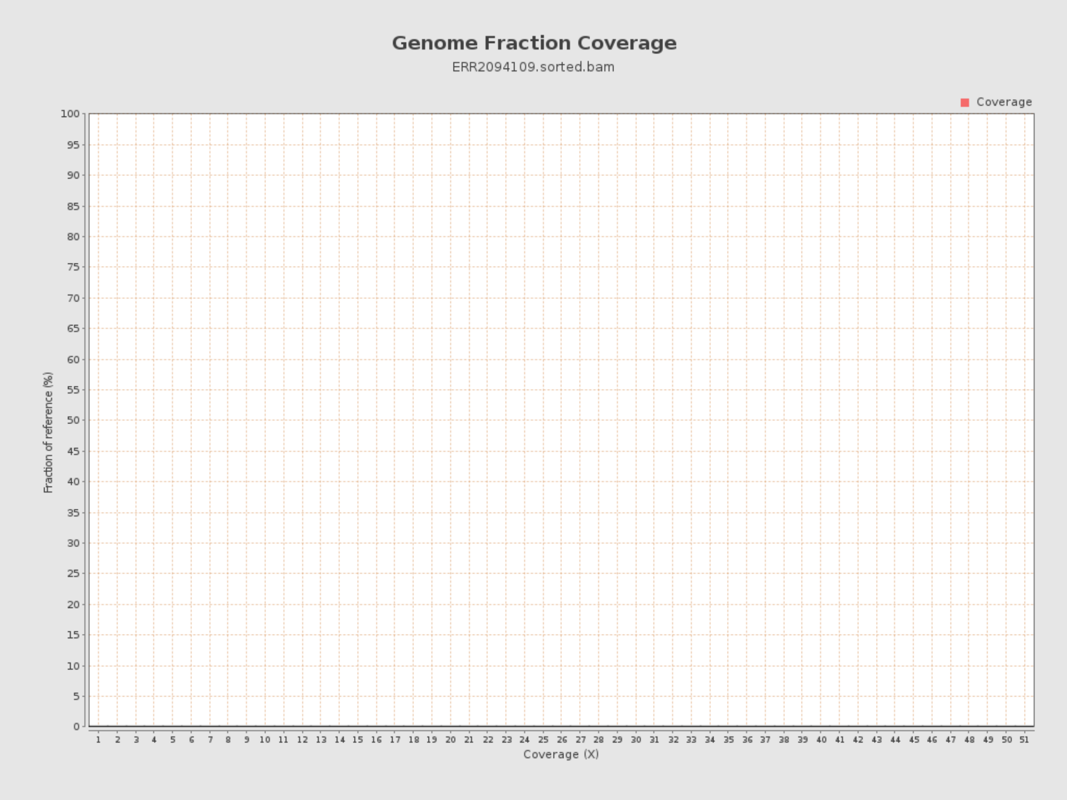
4. Results : Coverage Histogram



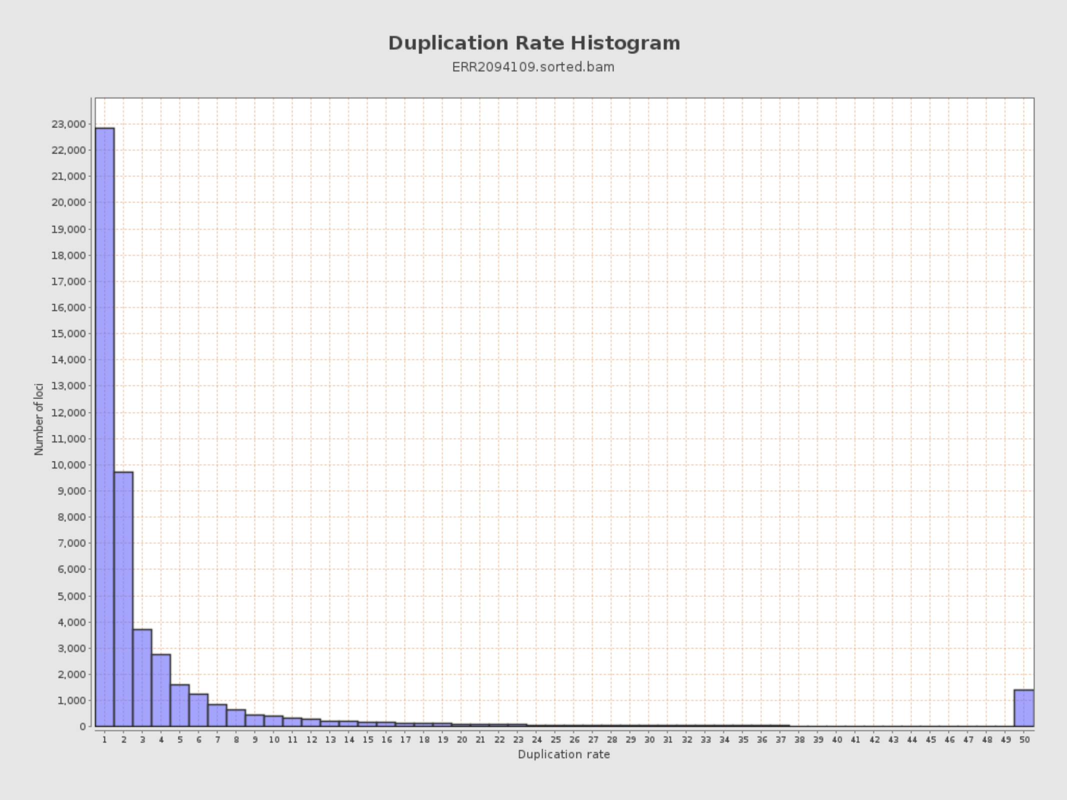
5. Results : Coverage Histogram (0-50X)



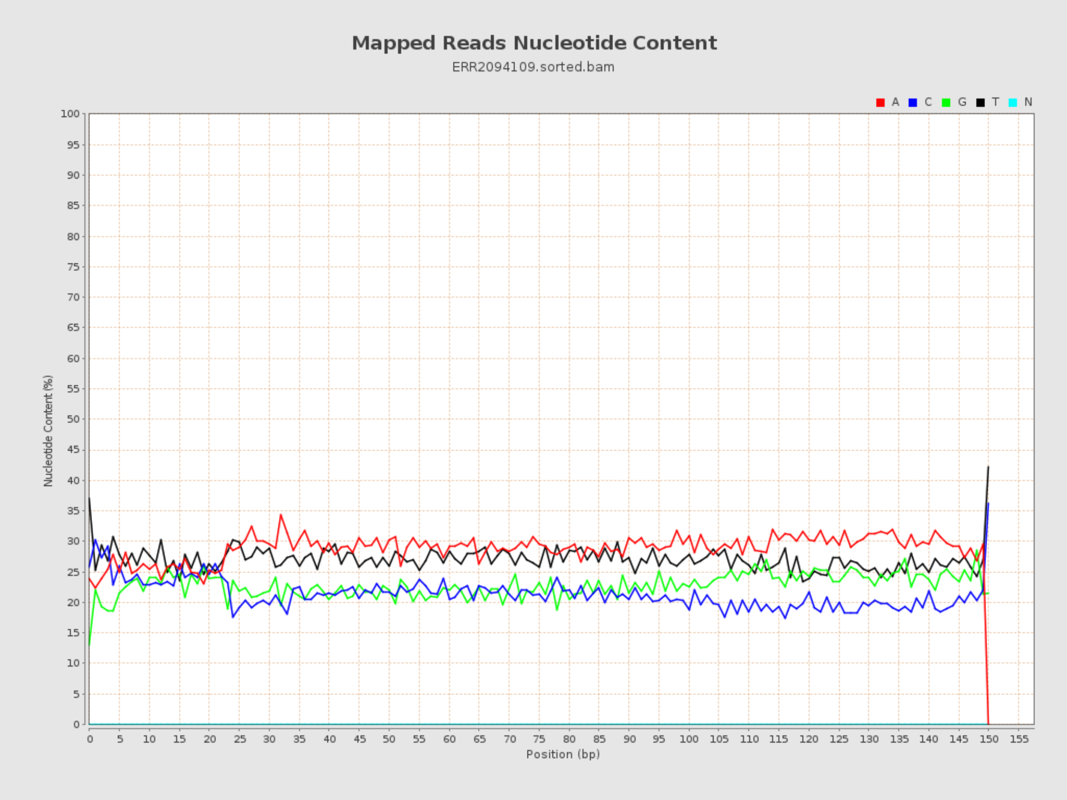
6. Results : Genome Fraction Coverage



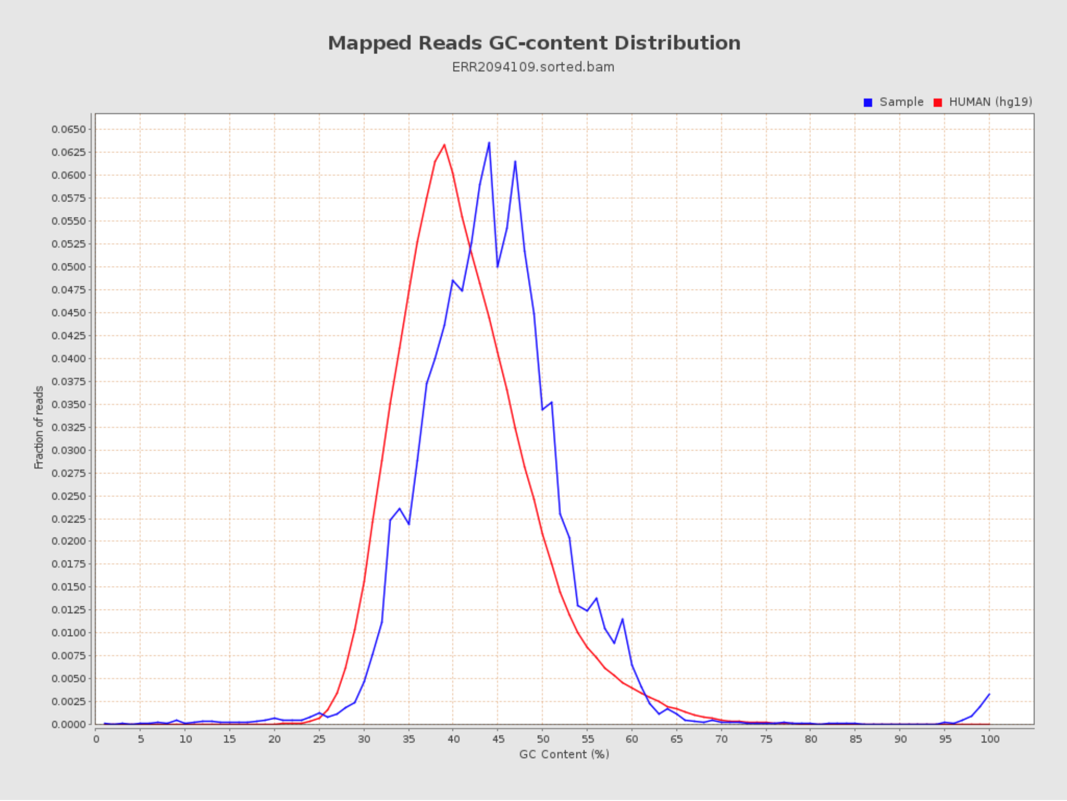
7. Results : Duplication Rate Histogram



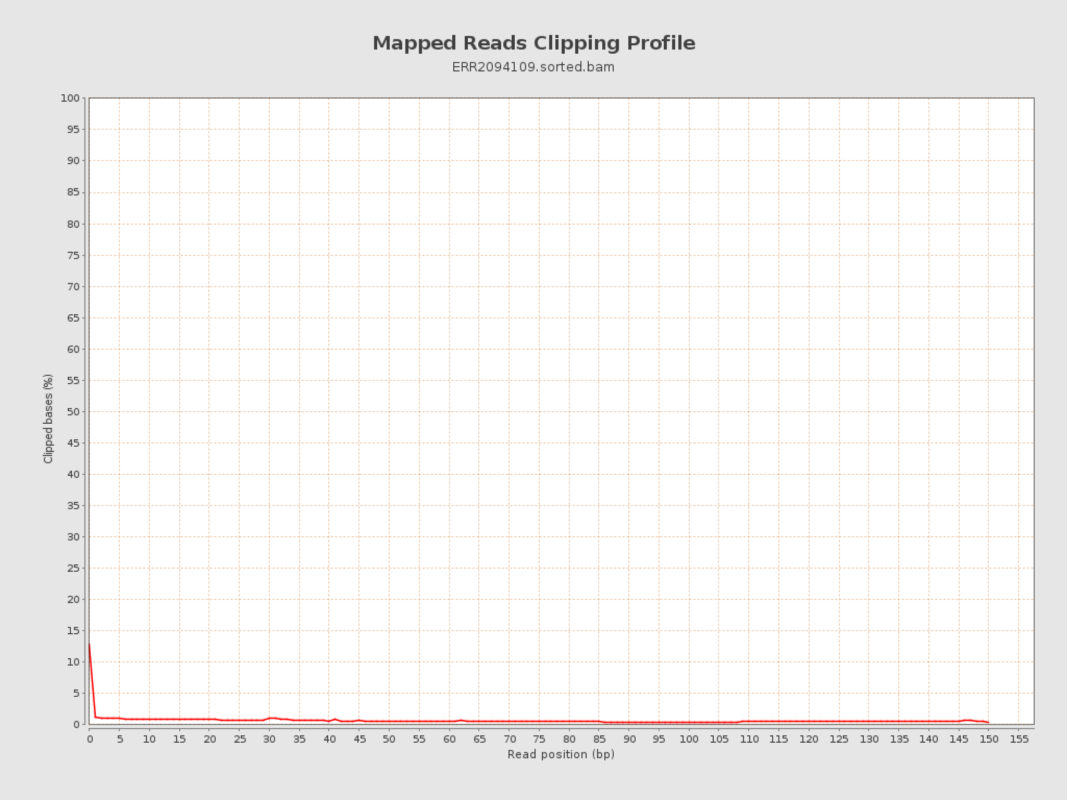
8. Results : Mapped Reads Nucleotide Content



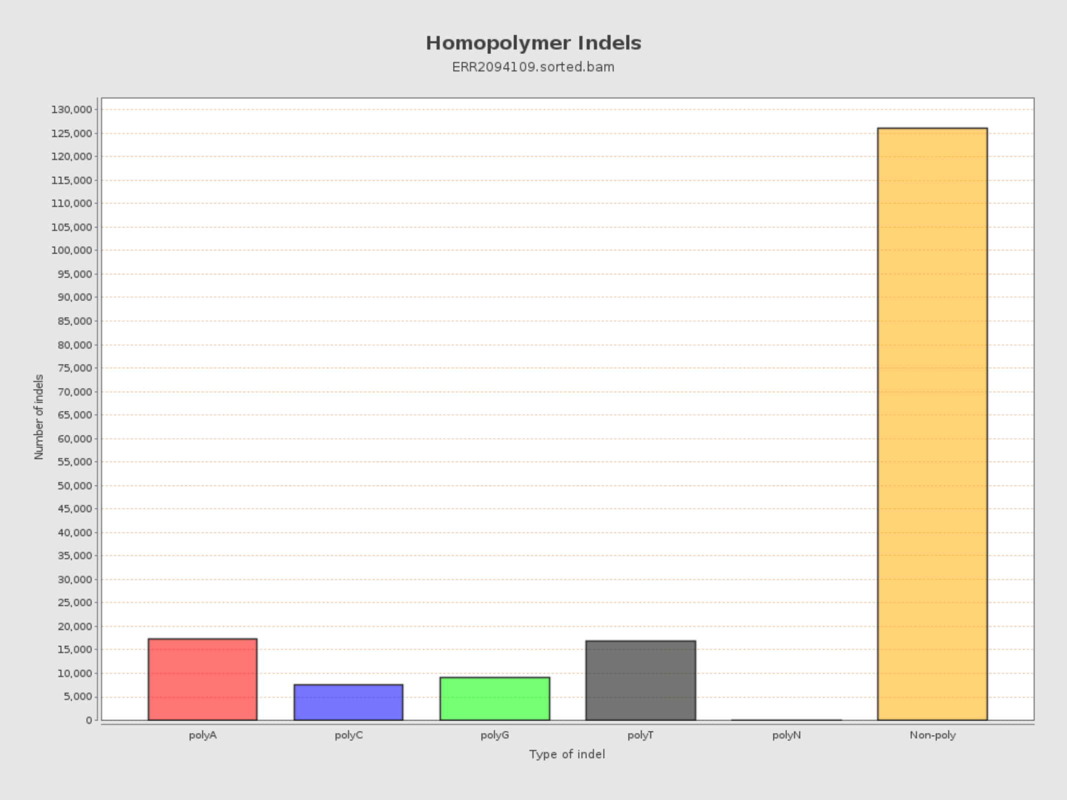
9. Results : Mapped Reads GC-content Distribution



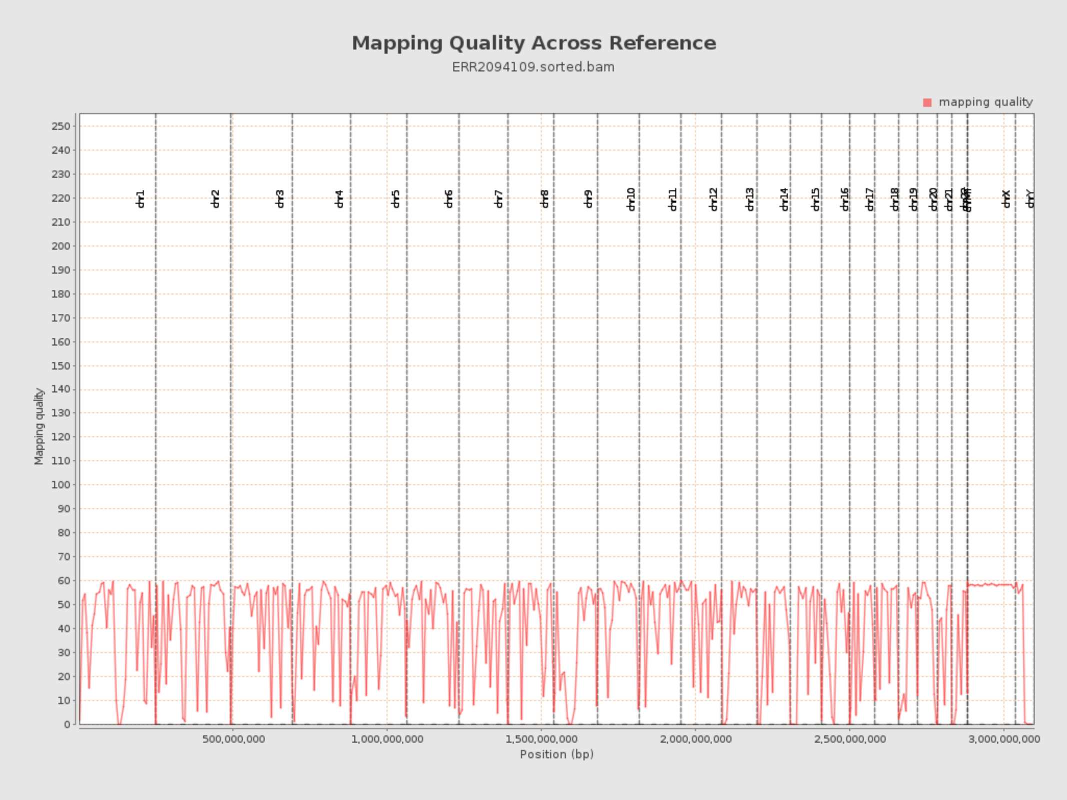
10. Results : Mapped Reads Clipping Profile



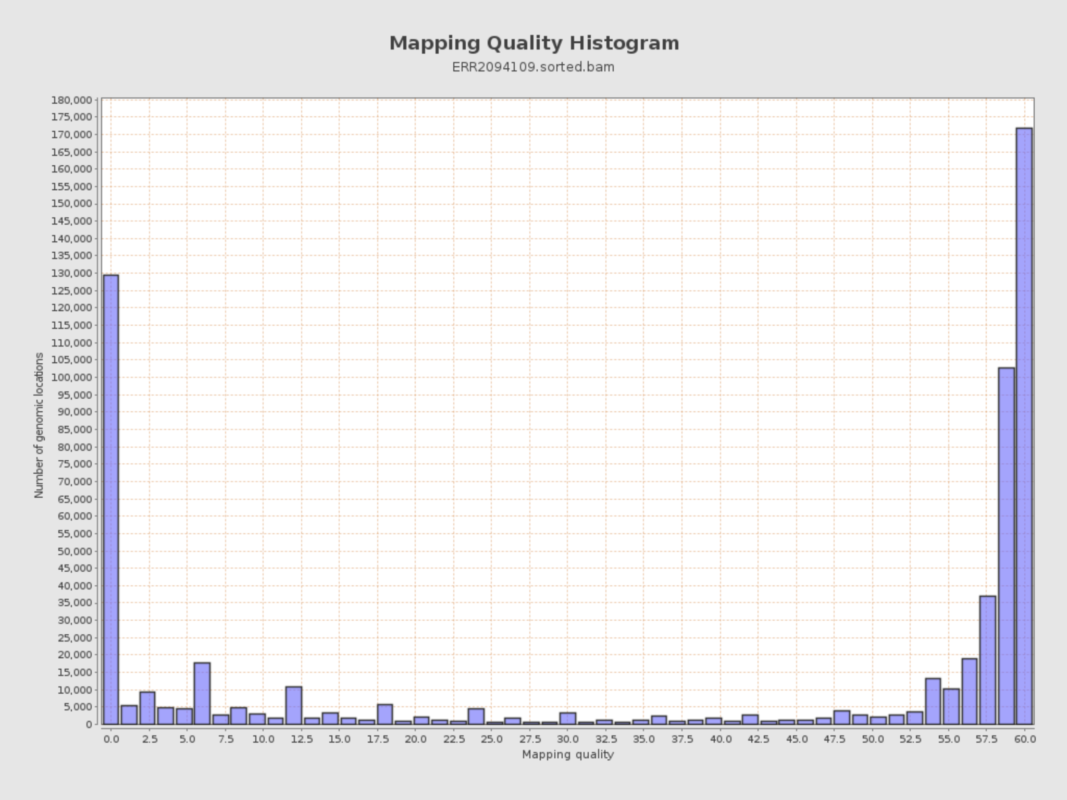
11. Results : Homopolymer Indels



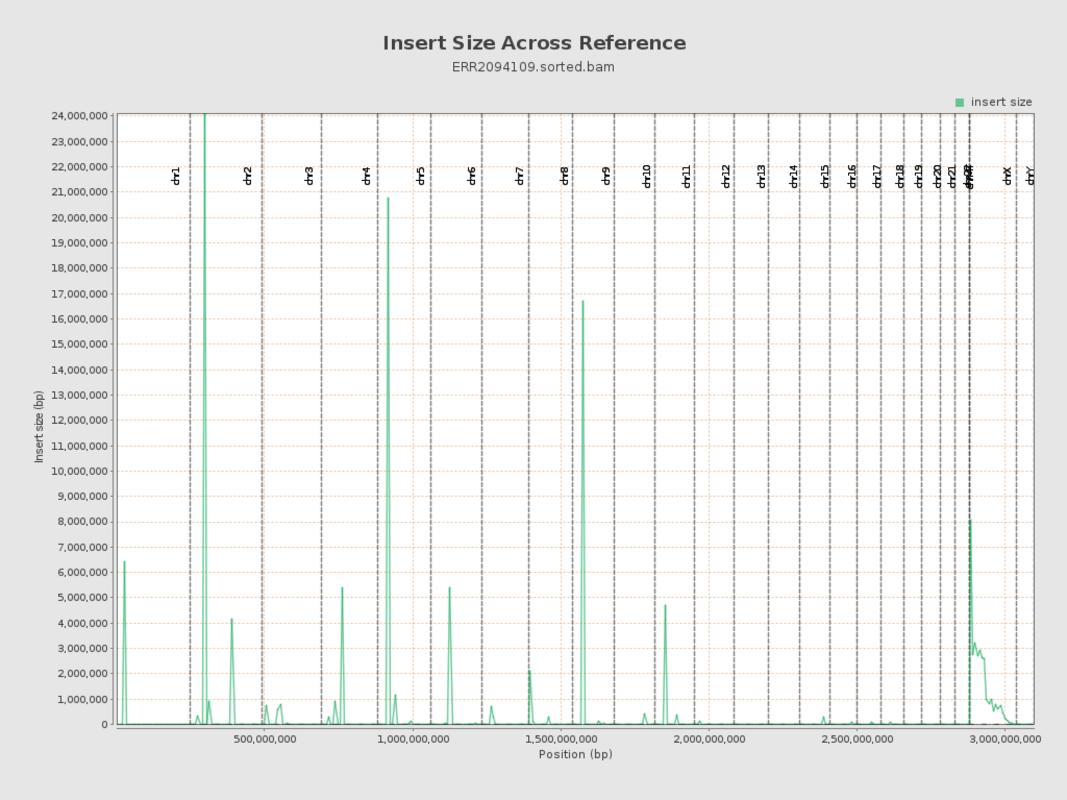
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram