Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:22:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094085.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_ERR2094085 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094085_1.fastq.gz ERR2094085_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:22:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	434,754
Mapped reads	423,507 / 97.41%
Unmapped reads	11,247 / 2.59%
Mapped paired reads	423,507 / 97.41%
Mapped reads, first in pair	212,739 / 48.93%
Mapped reads, second in pair	210,768 / 48.48%
Mapped reads, both in pair	420,702 / 96.77%
Mapped reads, singletons	2,805 / 0.65%
Secondary alignments	0
Supplementary alignments	15,165 / 3.49%
Read min/max/mean length	30 / 151 / 143.9
Duplicated reads (estimated)	405,674 / 93.31%
Duplication rate	49.84%
Clipped reads	160,490 / 36.92%

2.2. ACGT Content

Number/percentage of A's	14,768,038 / 26.53%
Number/percentage of C's	13,113,027 / 23.56%
Number/percentage of T's	14,066,401 / 25.27%
Number/percentage of G's	13,718,425 / 24.64%
Number/percentage of N's	730 / 0%

GC Percentage	48.2%

2.3. Coverage

Mean	0.0184
Standard Deviation	4.9984

2.4. Mapping Quality

Mean Mapping Quality	38.76

2.5. Insert size

Mean	366,507.81
Standard Deviation	5,503,843
P25/Median/P75	142 / 169 / 199

2.6. Mismatches and indels

General error rate	3.86%
Mismatches	2,074,187
Insertions	33,195
Mapped reads with at least one insertion	7.71%
Deletions	169,153
Mapped reads with at least one deletion	38.17%
Homopolymer indels	29.88%

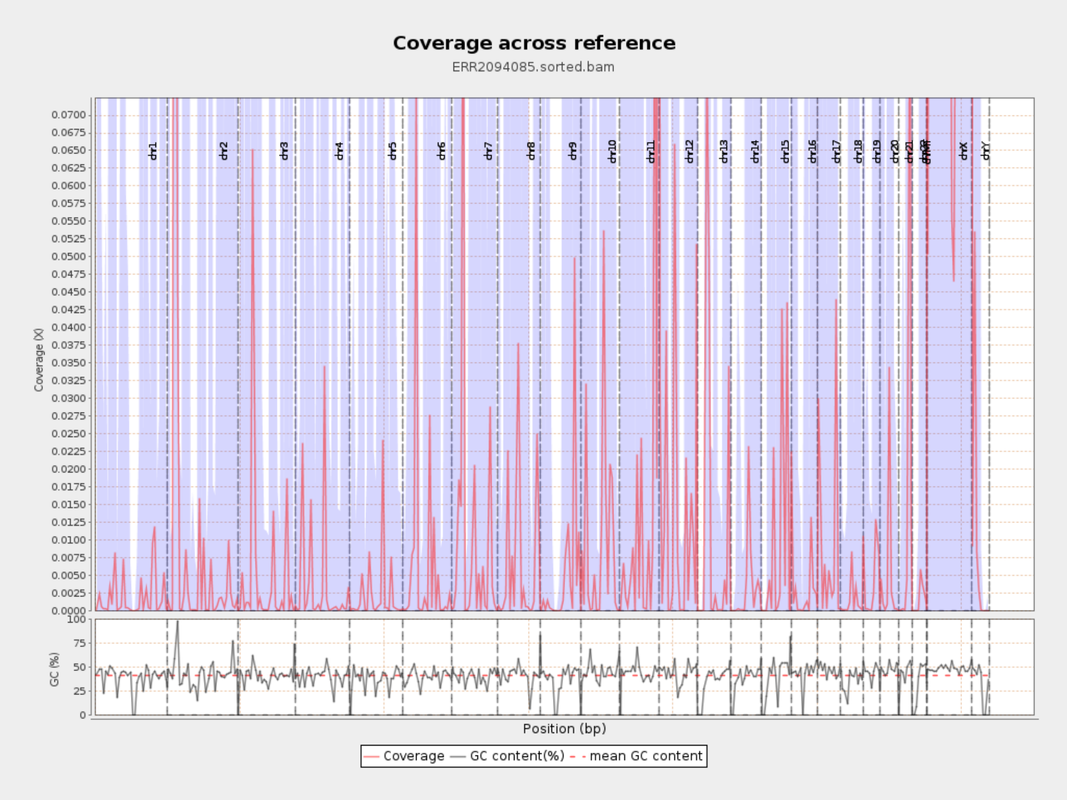
2.7. Chromosome stats

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

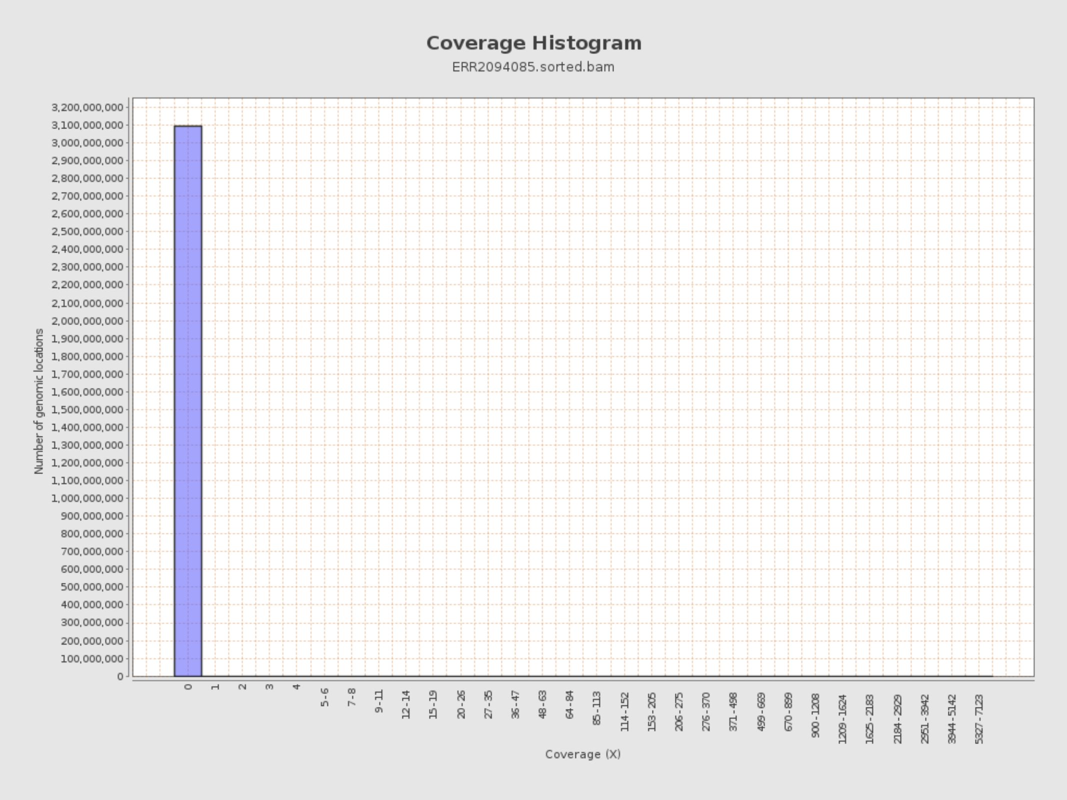
		bases	coverage	deviation
chr1	249250621	483364	0.0019	0.7014
chr2	243199373	2624232	0.0108	4.6199
chr3	198022430	963435	0.0049	2.2139
chr4	191154276	700190	0.0037	1.4909
chr5	180915260	413541	0.0023	1.29
chr6	171115067	1109265	0.0065	3.6066
chr7	159138663	1664365	0.0105	4.1437
chr8	146364022	1002296	0.0068	2.4409
chr9	141213431	722642	0.0051	2.3588
chr10	135534747	1347527	0.0099	3.3359
chr11	135006516	1863192	0.0138	3.7298
chr12	133851895	1734339	0.013	3.9525
chr13	115169878	1338201	0.0116	3.6897
chr14	107349540	366112	0.0034	1.4413
chr15	102531392	933903	0.0091	2.9333
chr16	90354753	304159	0.0034	1.2663
chr17	81195210	828161	0.0102	3.5476
chr18	78077248	109001	0.0014	0.6359
chr19	59128983	219099	0.0037	0.9915
chr20	63025520	332029	0.0053	1.8854
chr21	48129895	868057	0.018	7.4782
chr22	51304566	86709	0.0017	0.409
chrMT	16571	1682553	101.536	470.4979
chrX	155270560	34594949	0.2228	17.4081

chrY	59373566	548271	0.0092	2.8624

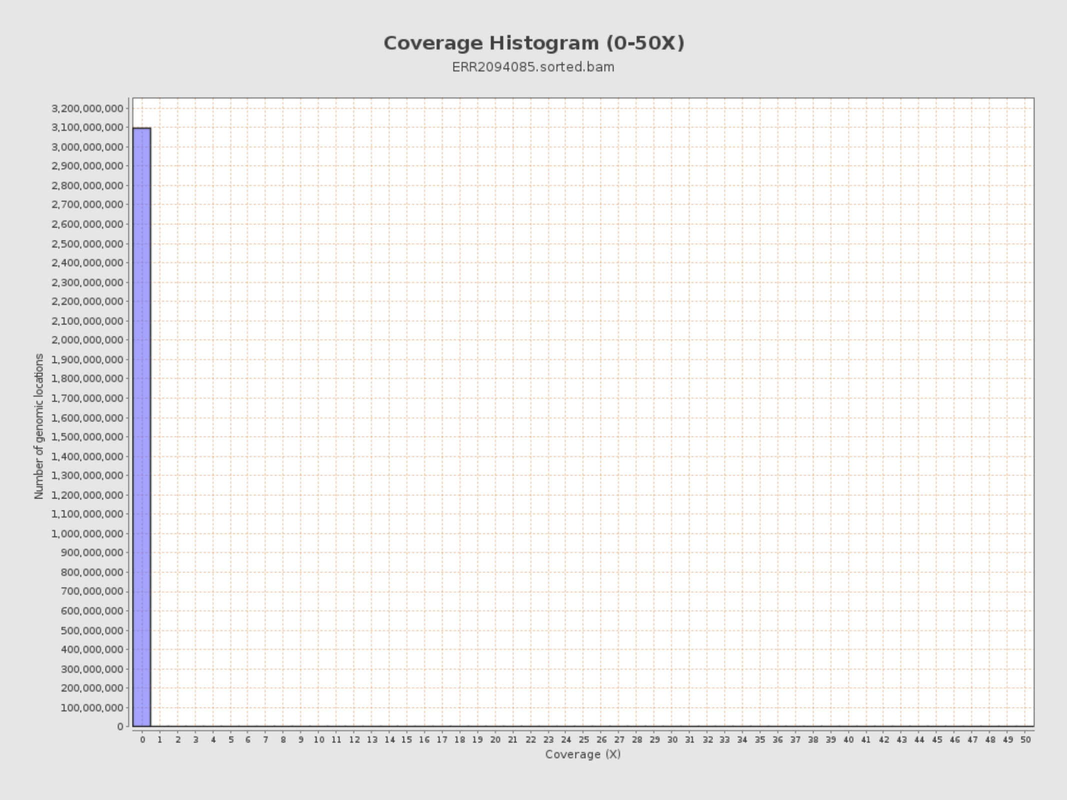
3. Results : Coverage across reference



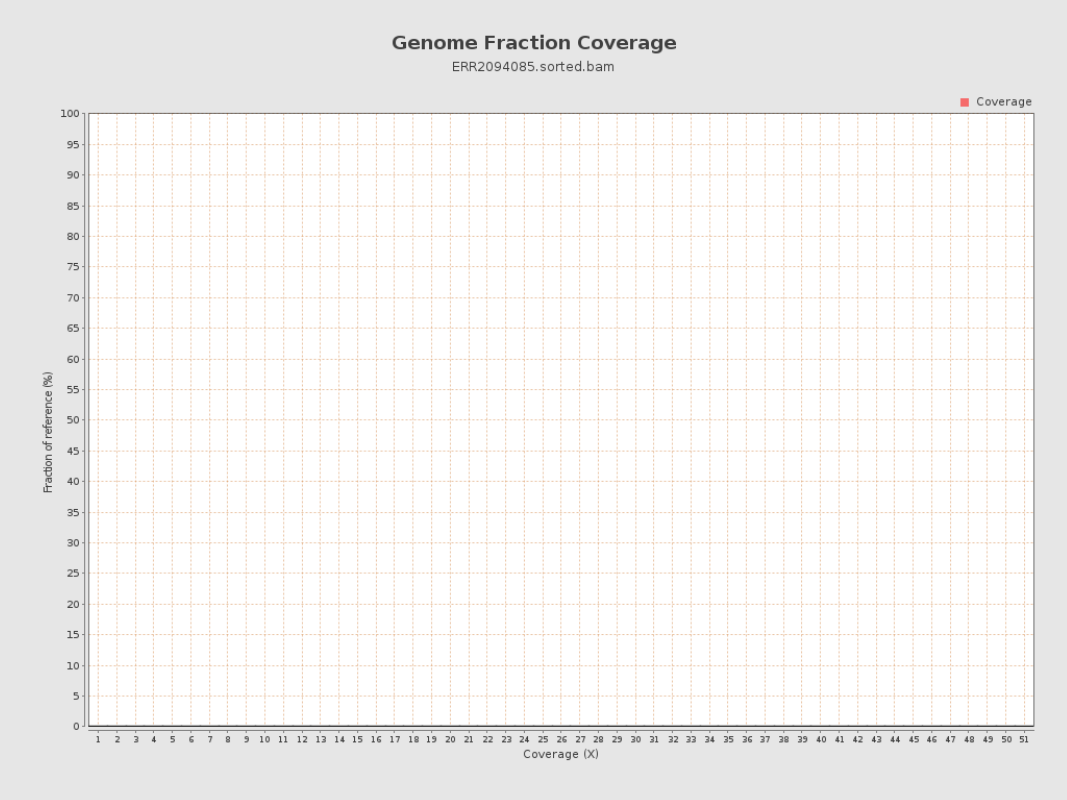
4. Results : Coverage Histogram



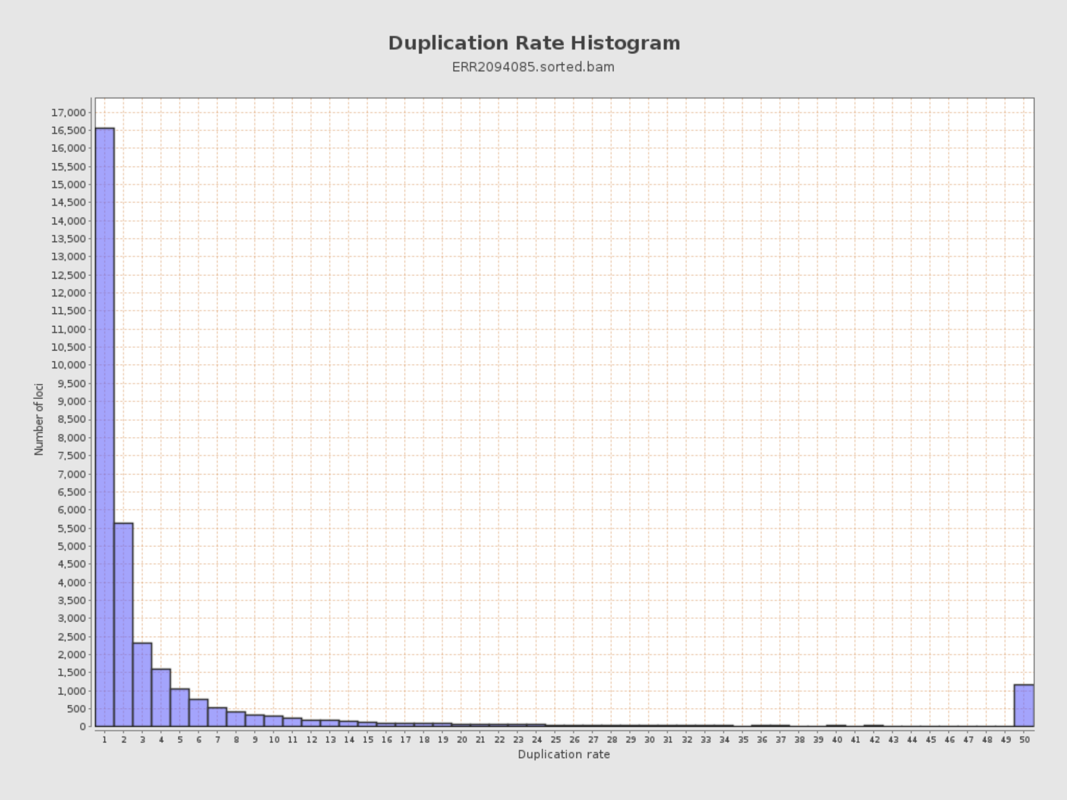
5. Results : Coverage Histogram (0-50X)



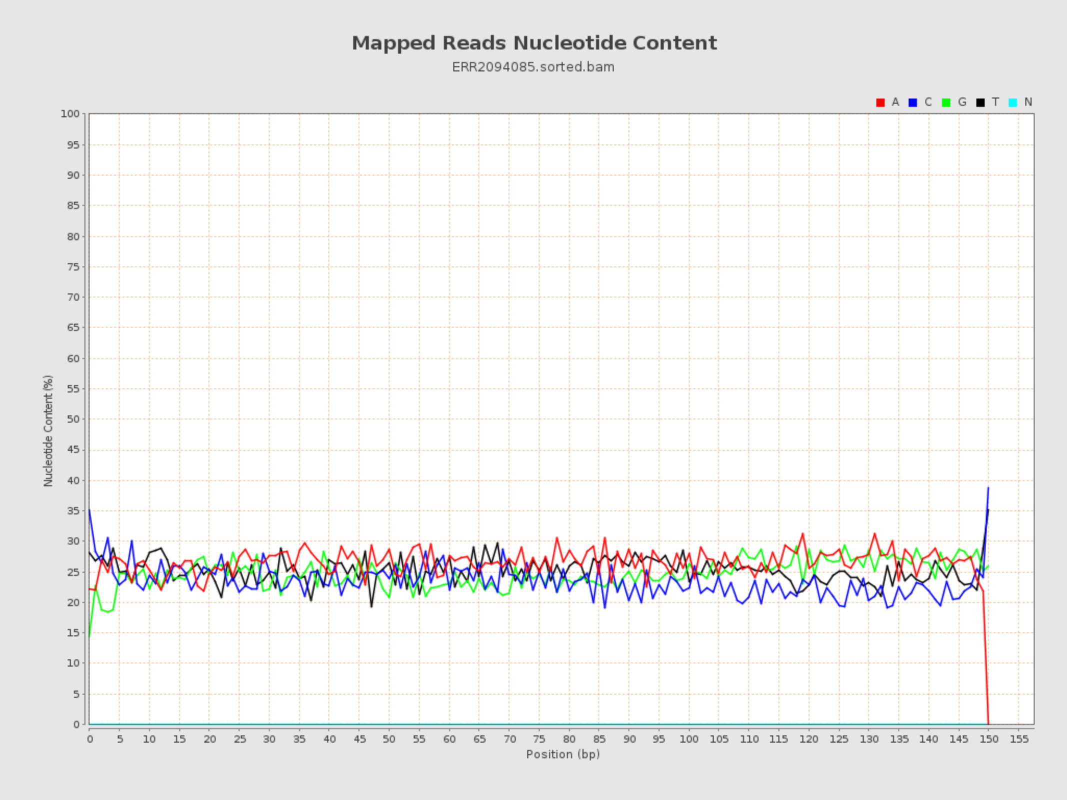
6. Results : Genome Fraction Coverage



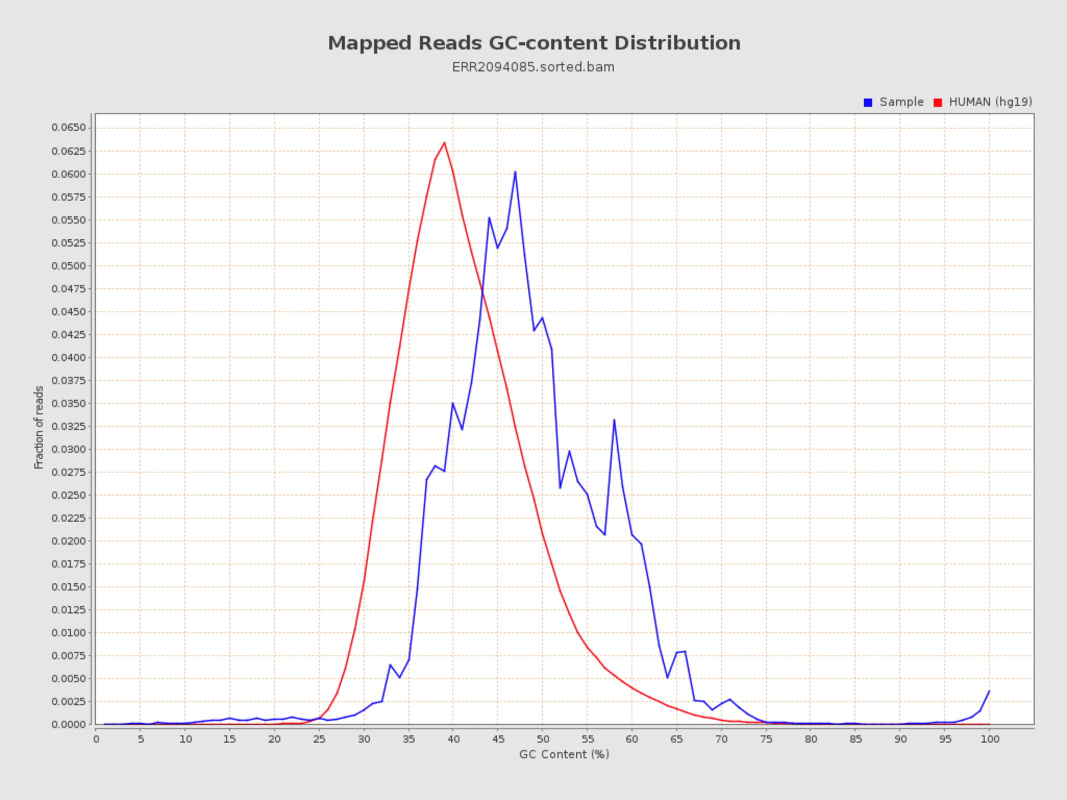
7. Results : Duplication Rate Histogram



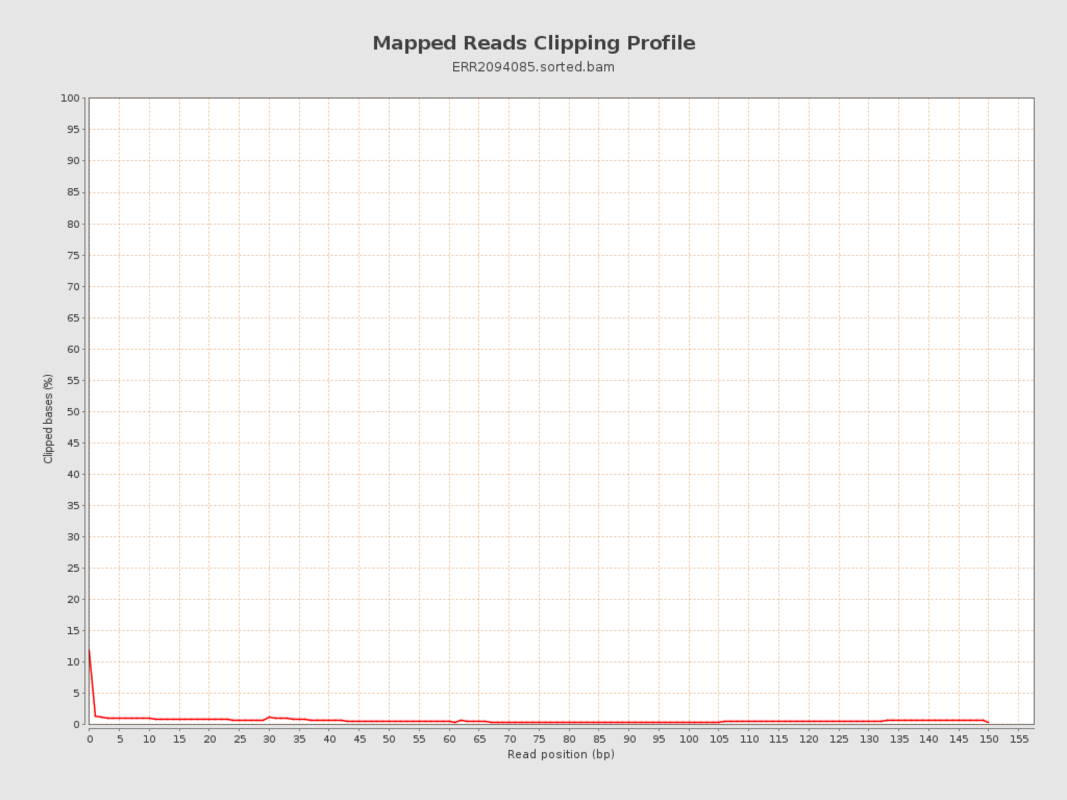
8. Results : Mapped Reads Nucleotide Content



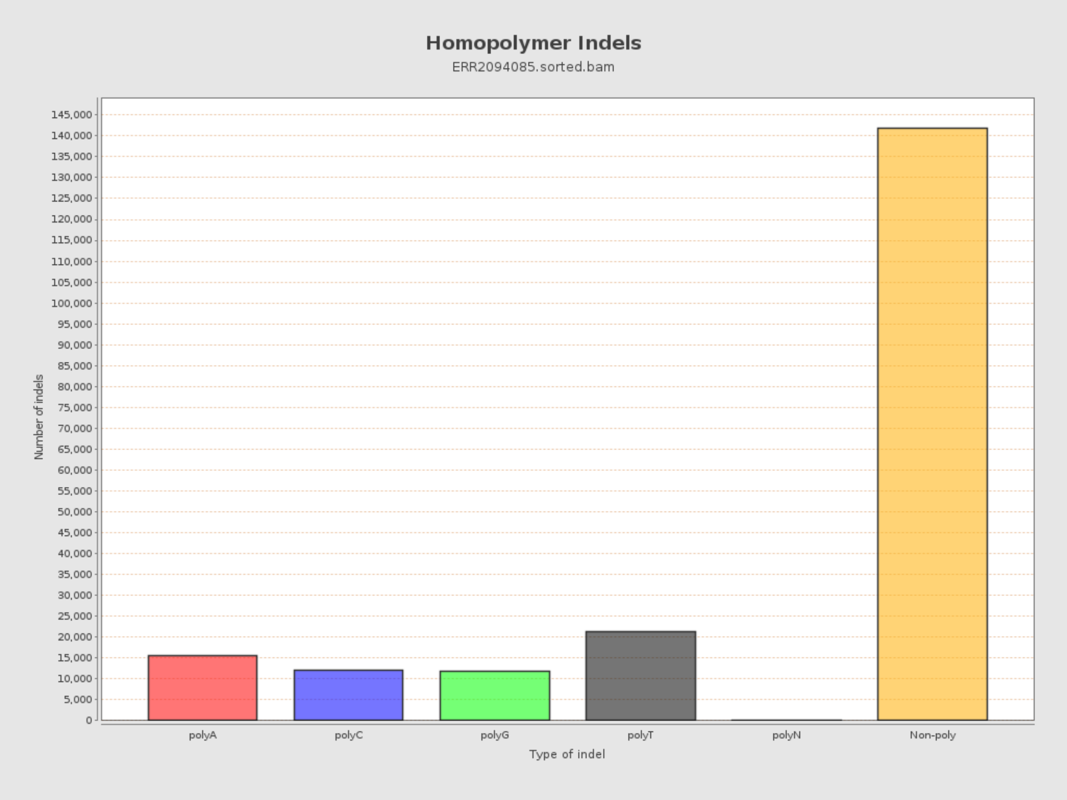
9. Results : Mapped Reads GC-content Distribution



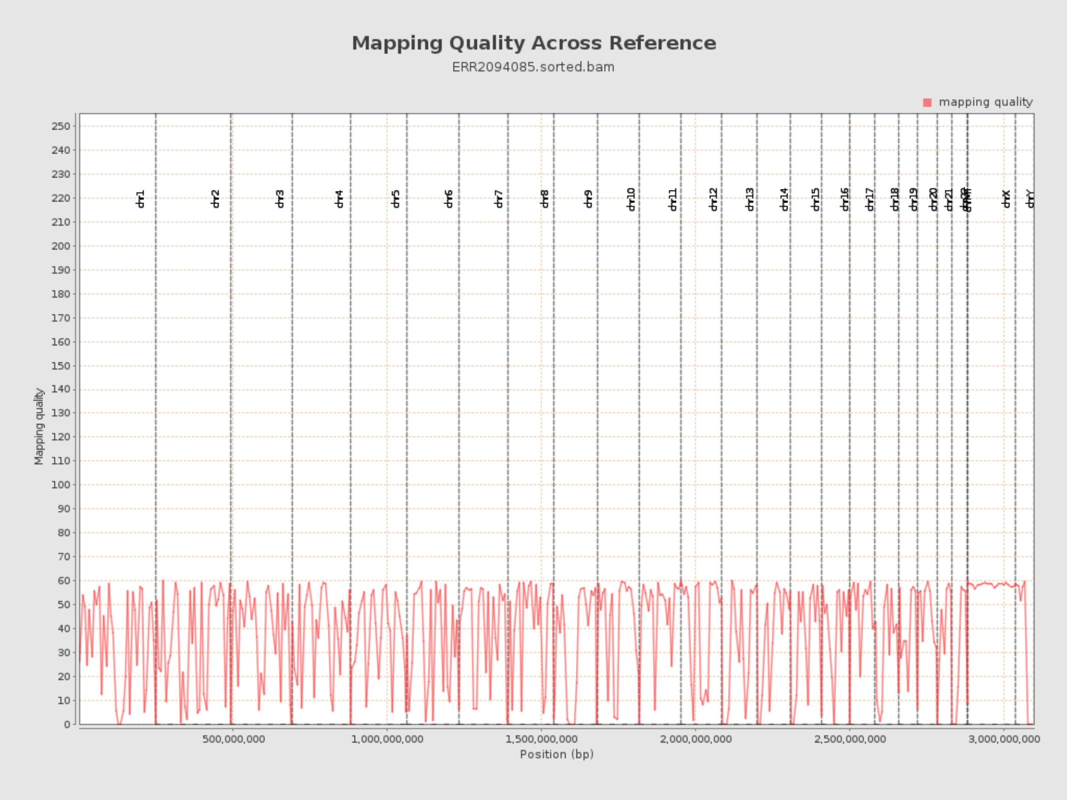
10. Results : Mapped Reads Clipping Profile



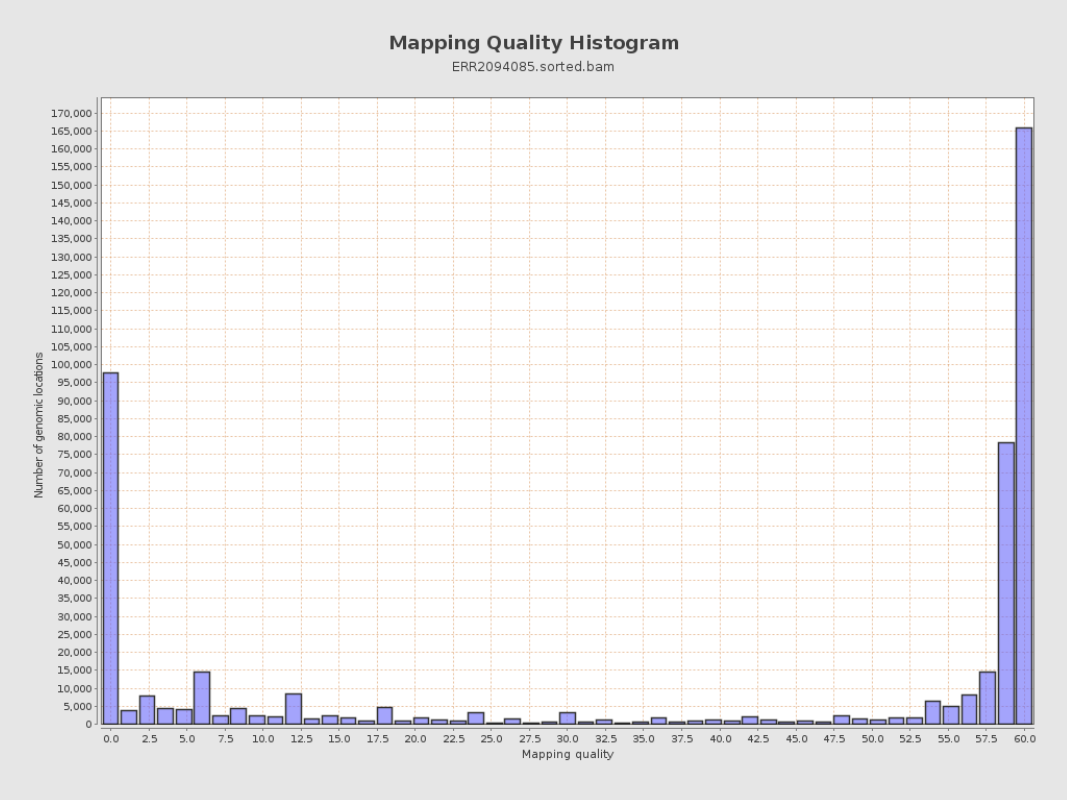
11. Results : Homopolymer Indels



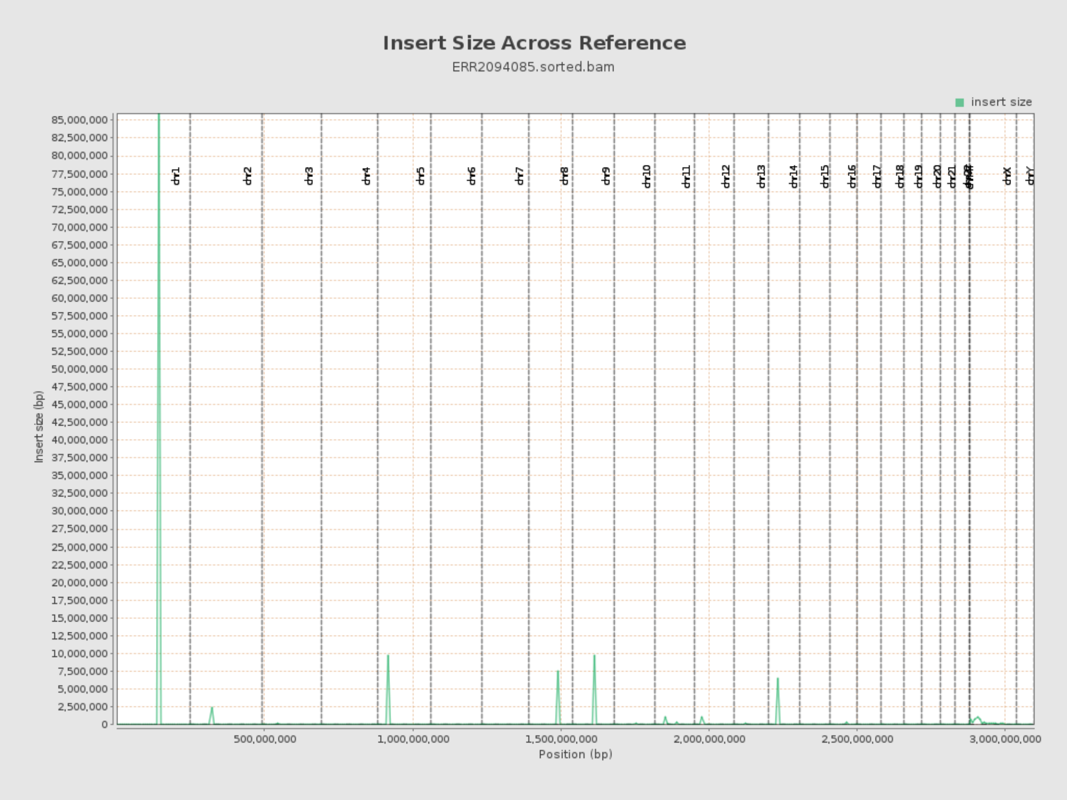
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram