Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:19:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094106.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_ERR2094106 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094106_1.fastq.gz ERR2094106_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:19:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	398,986
Mapped reads	383,158 / 96.03%
Unmapped reads	15,828 / 3.97%
Mapped paired reads	383,158 / 96.03%
Mapped reads, first in pair	192,583 / 48.27%
Mapped reads, second in pair	190,575 / 47.76%
Mapped reads, both in pair	380,160 / 95.28%
Mapped reads, singletons	2,998 / 0.75%
Secondary alignments	0
Supplementary alignments	28,992 / 7.27%
Read min/max/mean length	30 / 151 / 139.58
Duplicated reads (estimated)	367,252 / 92.05%
Duplication rate	52.33%
Clipped reads	204,180 / 51.17%

2.2. ACGT Content

Number/percentage of A's	13,450,146 / 28.74%
Number/percentage of C's	10,060,242 / 21.5%
Number/percentage of T's	12,643,330 / 27.01%
Number/percentage of G's	10,647,756 / 22.75%
Number/percentage of N's	497 / 0%

GC Percentage	44.25%

2.3. Coverage

Mean	0.0154
Standard Deviation	3.1424

2.4. Mapping Quality

Mean Mapping Quality	40.48

2.5. Insert size

Mean	1,903,414.03
Standard Deviation	12,288,719.48
P25/Median/P75	115 / 147 / 176

2.6. Mismatches and indels

General error rate	3.42%
Mismatches	1,542,101
Insertions	29,984
Mapped reads with at least one insertion	7.72%
Deletions	121,962
Mapped reads with at least one deletion	30.72%
Homopolymer indels	28.65%

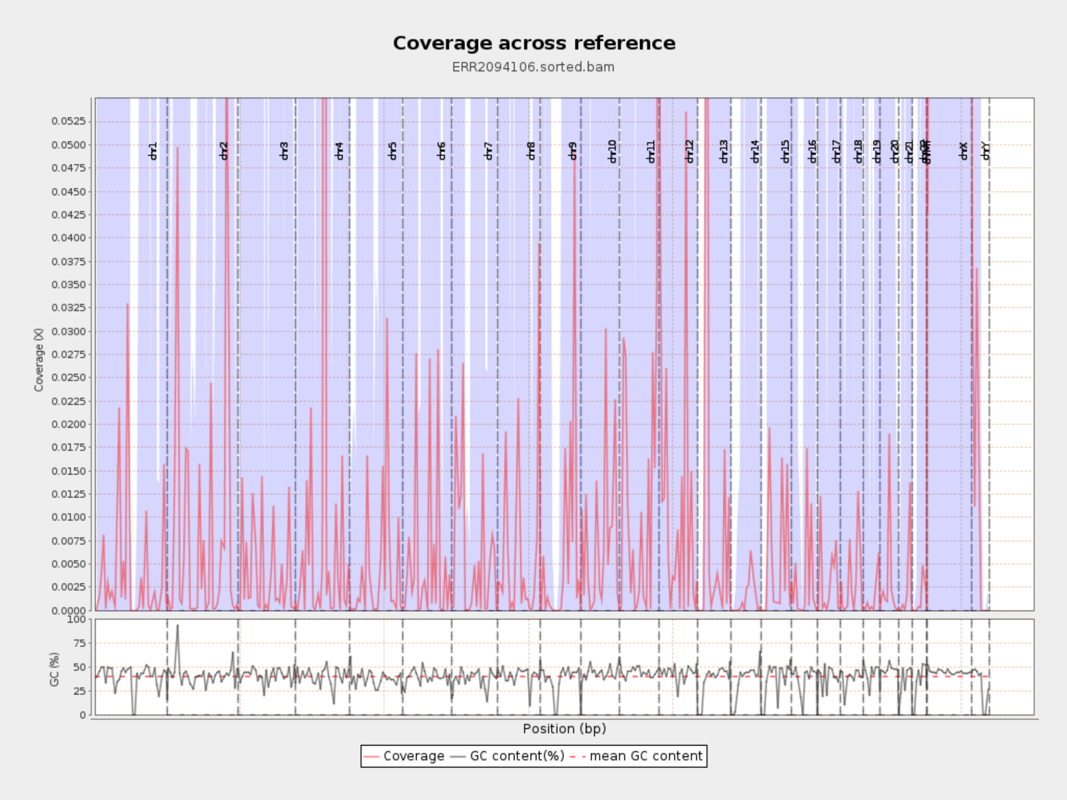
2.7. Chromosome stats

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

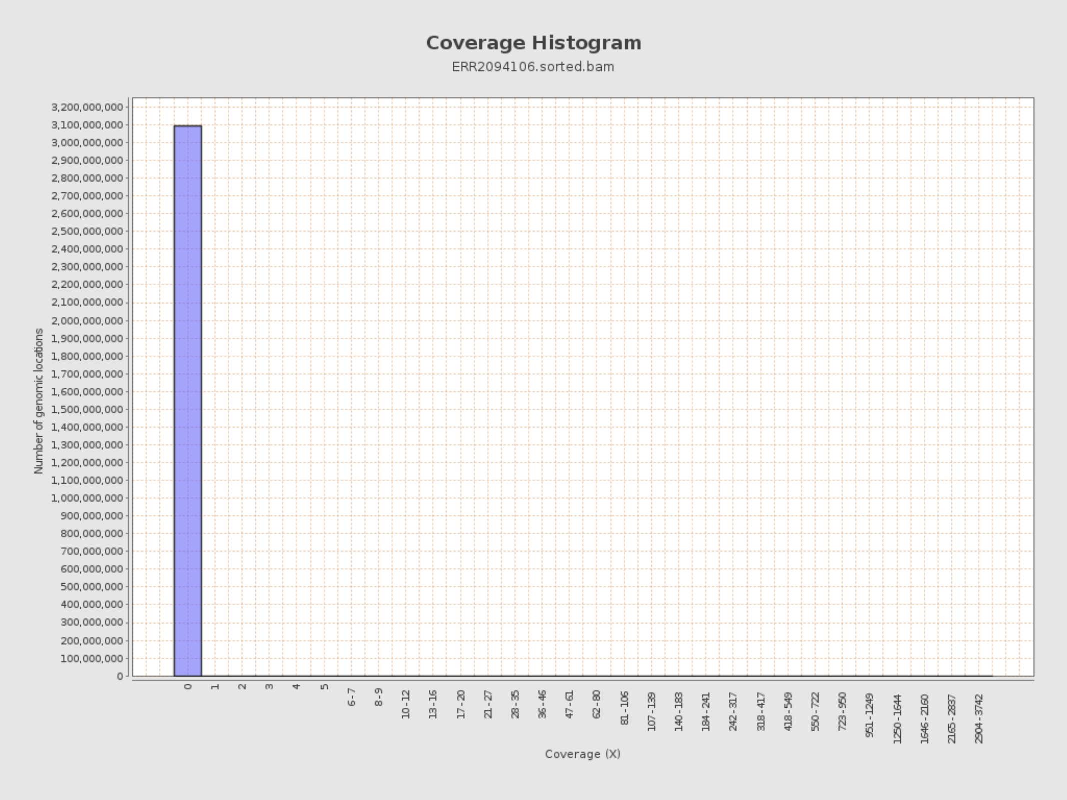
		bases	coverage	deviation
chr1	249250621	1028583	0.0041	1.7953
chr2	243199373	2147934	0.0088	3.0731
chr3	198022430	796009	0.004	1.1061
chr4	191154276	2377894	0.0124	3.9696
chr5	180915260	832899	0.0046	1.9608
chr6	171115067	963083	0.0056	1.7145
chr7	159138663	934604	0.0059	1.525
chr8	146364022	928880	0.0063	1.9963
chr9	141213431	878845	0.0062	2.3136
chr10	135534747	1005283	0.0074	2.0437
chr11	135006516	1569141	0.0116	2.9882
chr12	133851895	1574506	0.0118	2.9877
chr13	115169878	1139021	0.0099	2.6888
chr14	107349540	141917	0.0013	0.496
chr15	102531392	519558	0.0051	1.4629
chr16	90354753	305724	0.0034	1.3193
chr17	81195210	260938	0.0032	0.9981
chr18	78077248	272831	0.0035	1.0307
chr19	59128983	83358	0.0014	0.4702
chr20	63025520	208532	0.0033	1.1899
chr21	48129895	131669	0.0027	0.6484
chr22	51304566	62671	0.0012	0.4288
chrMT	16571	52272	3.1544	16.0563
chrX	155270560	28764834	0.1853	10.2989

chrY	59373566	679304	0.0114	2.3572

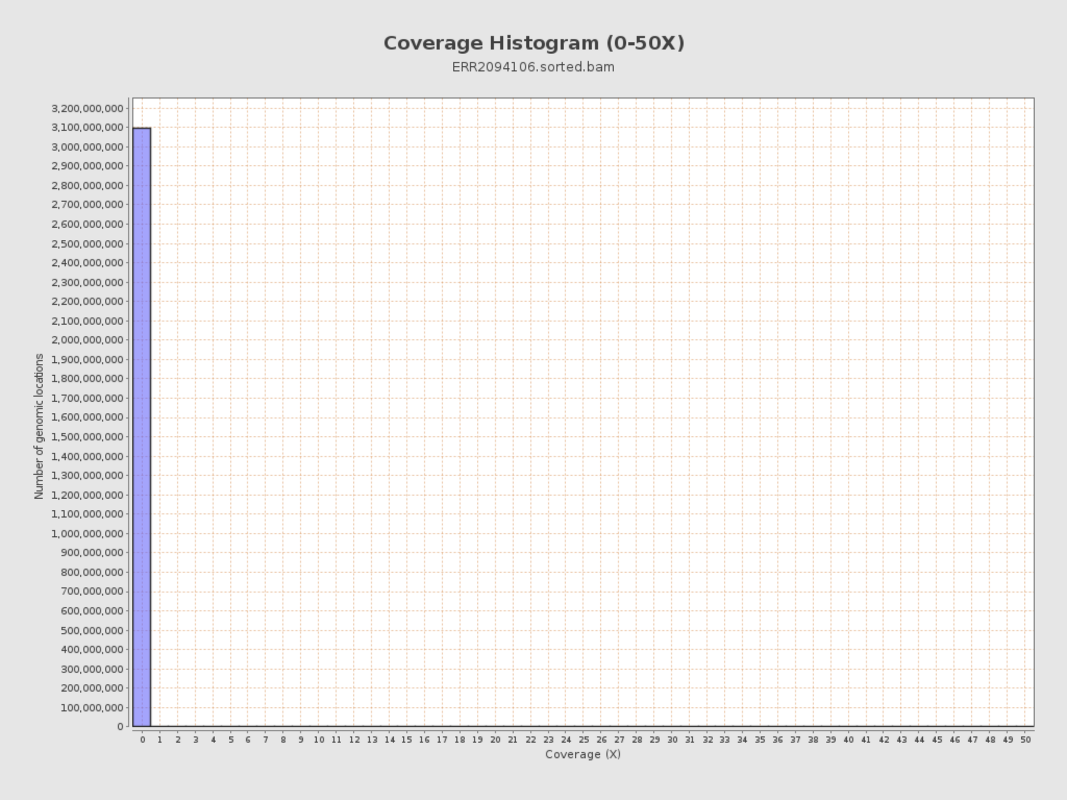
3. Results : Coverage across reference



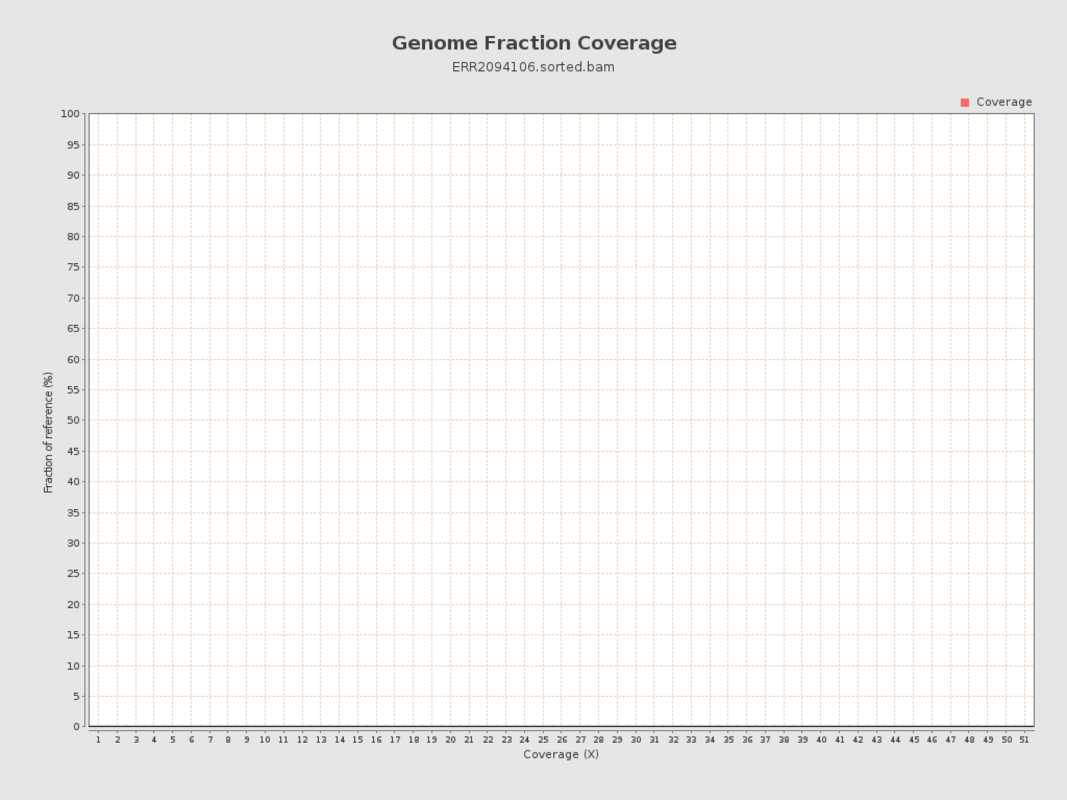
4. Results : Coverage Histogram



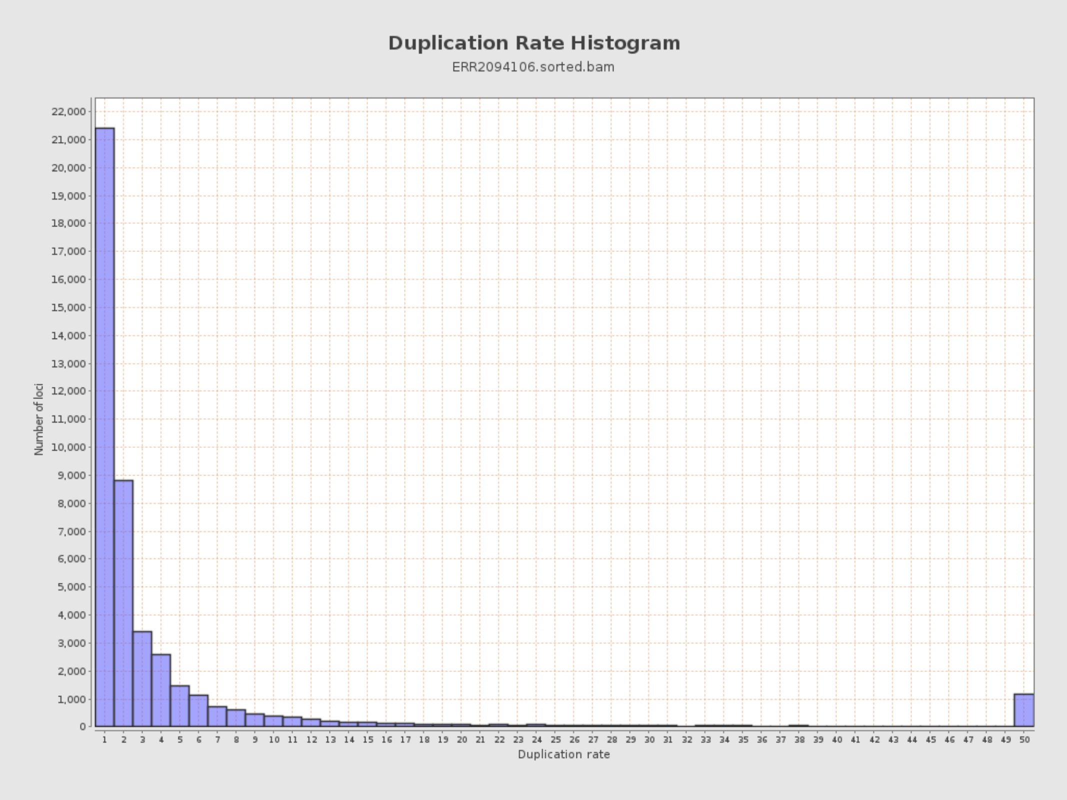
5. Results : Coverage Histogram (0-50X)



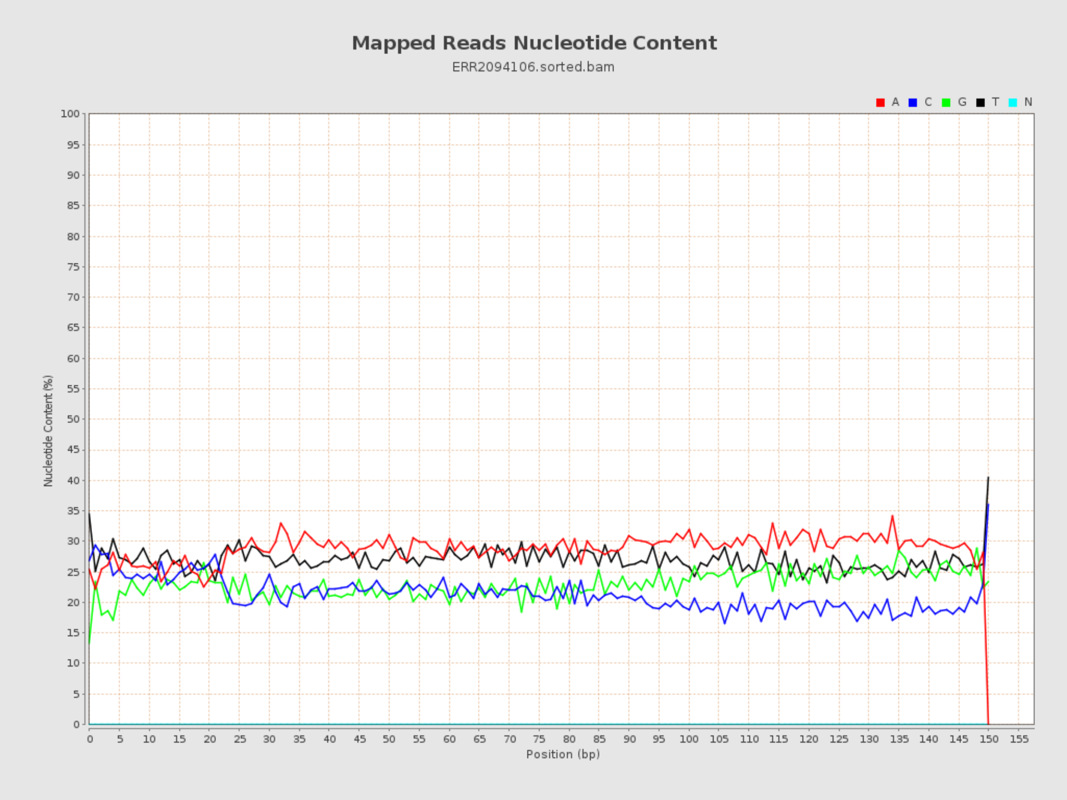
6. Results : Genome Fraction Coverage



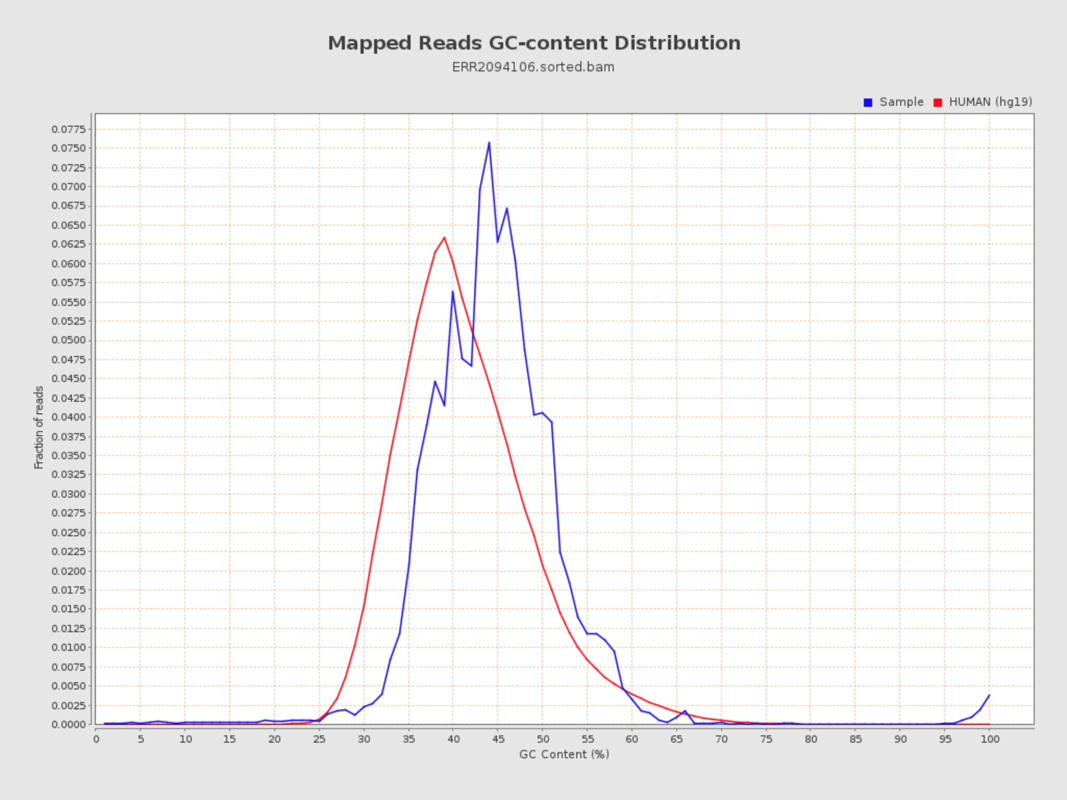
7. Results : Duplication Rate Histogram



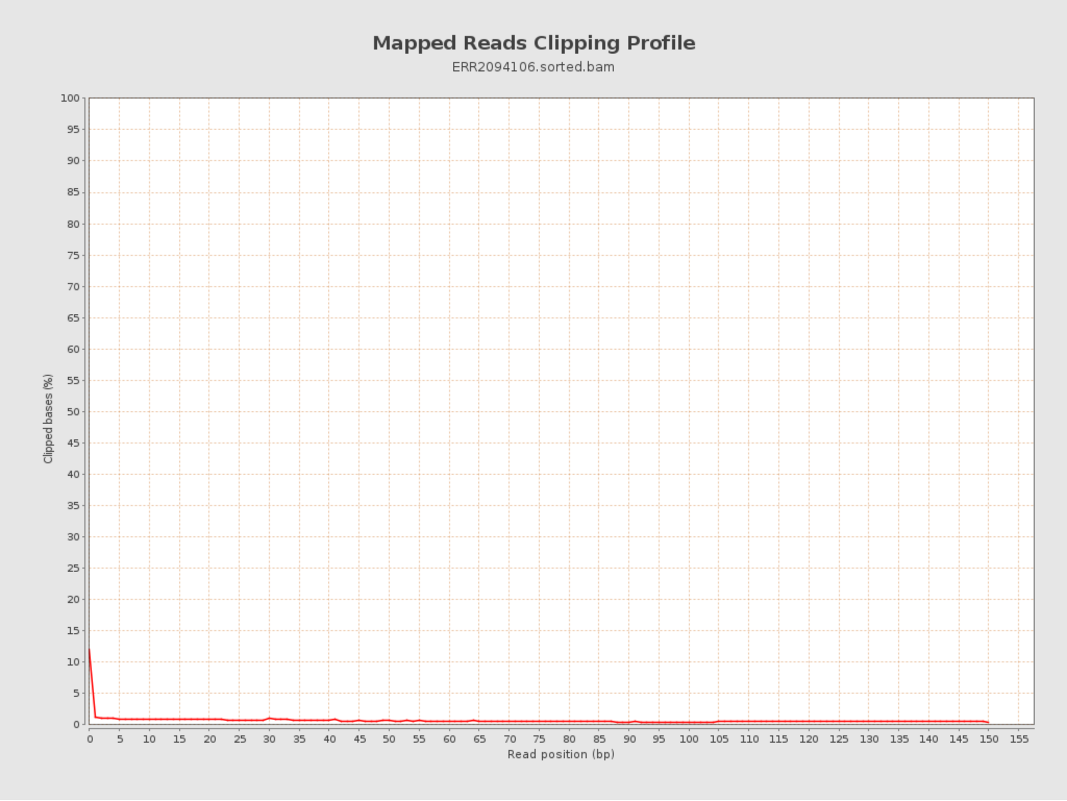
8. Results : Mapped Reads Nucleotide Content



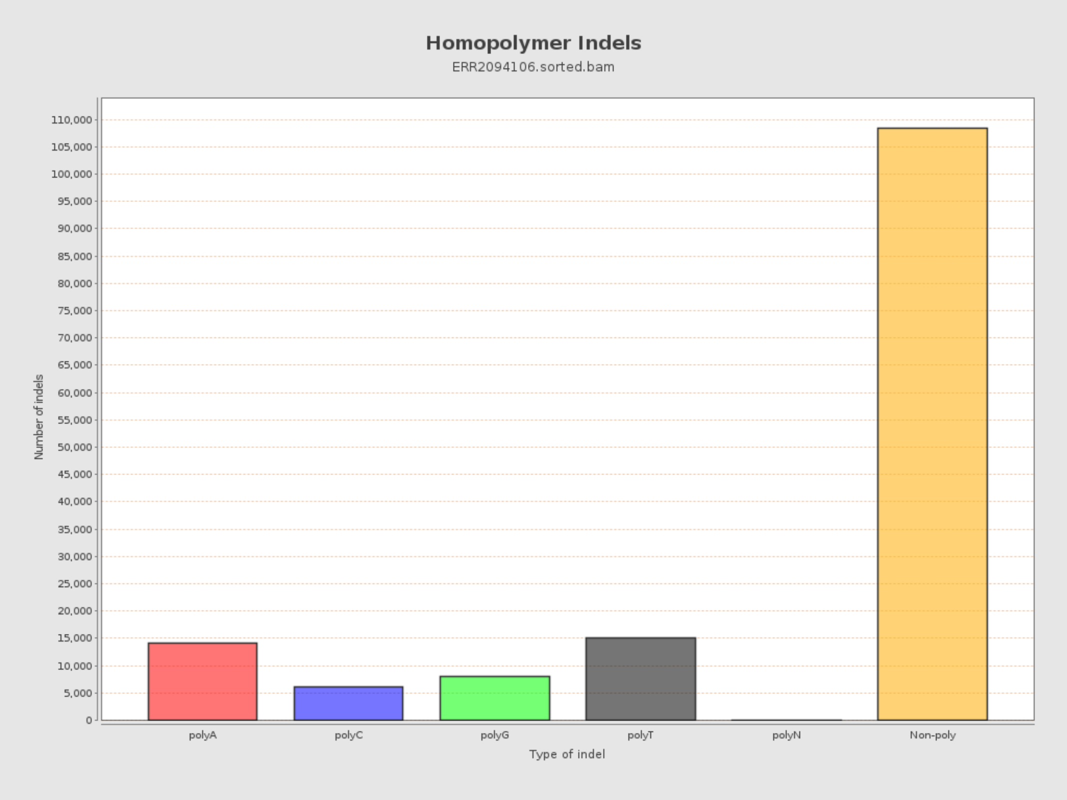
9. Results : Mapped Reads GC-content Distribution



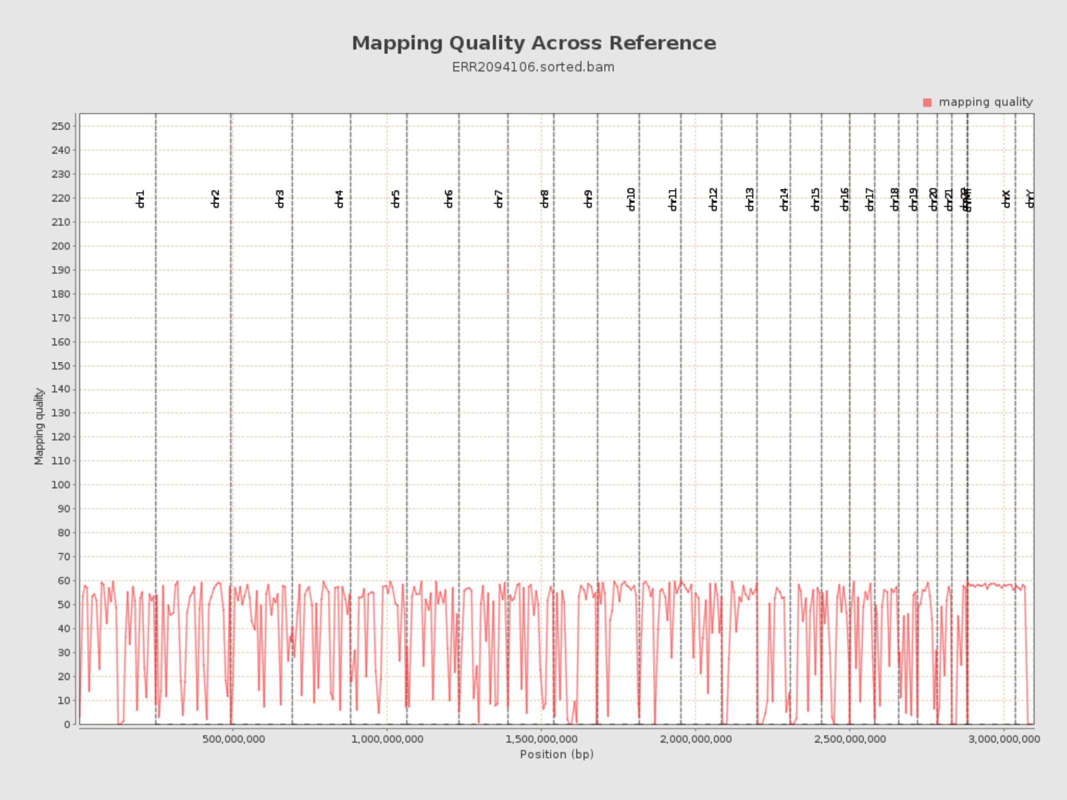
10. Results : Mapped Reads Clipping Profile



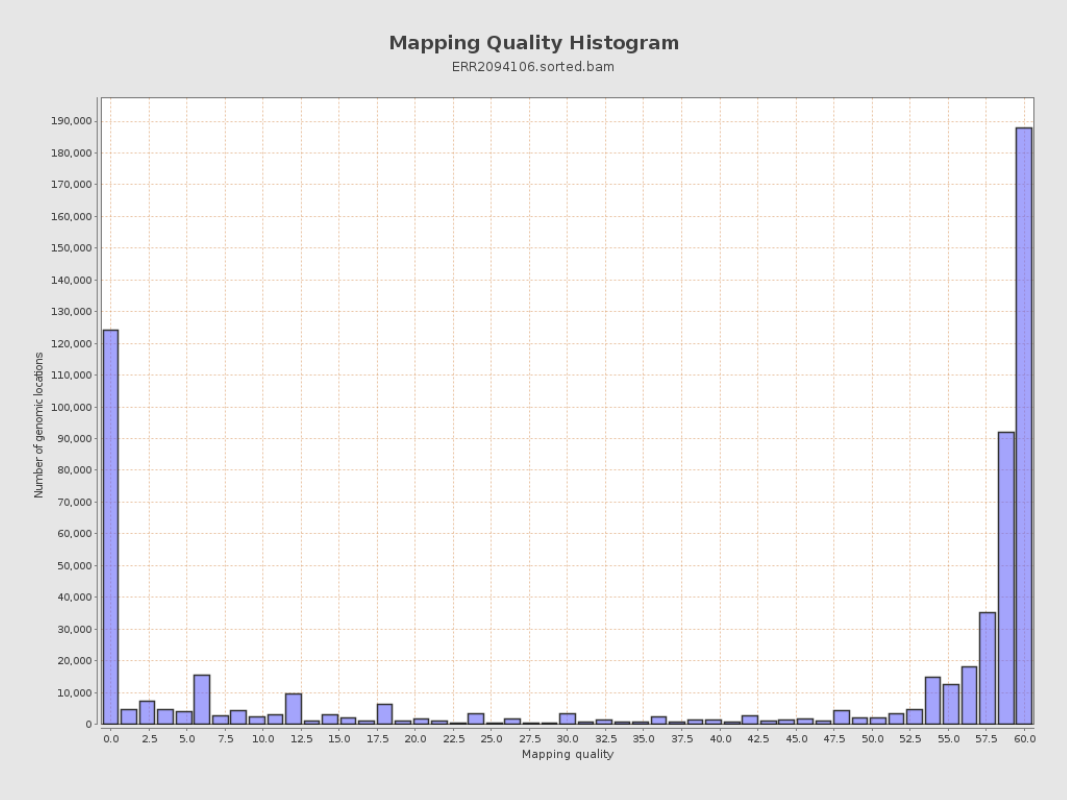
11. Results : Homopolymer Indels



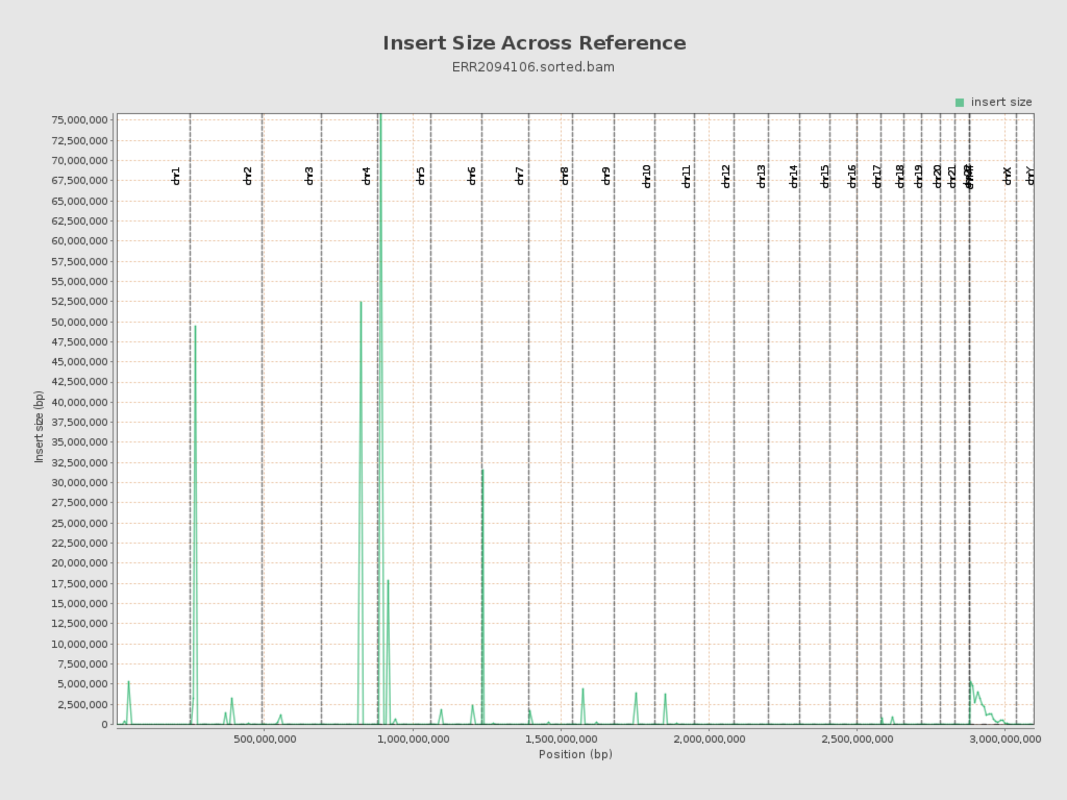
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram