Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:41:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094007.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_ERR2094007 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094007_1.fastq.gz ERR2094007_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:41:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	488,452
Mapped reads	369,286 / 75.6%
Unmapped reads	119,166 / 24.4%
Mapped paired reads	369,286 / 75.6%
Mapped reads, first in pair	185,163 / 37.91%
Mapped reads, second in pair	184,123 / 37.7%
Mapped reads, both in pair	365,018 / 74.73%
Mapped reads, singletons	4,268 / 0.87%
Secondary alignments	0
Supplementary alignments	19,381 / 3.97%
Read min/max/mean length	30 / 151 / 123.21
Duplicated reads (estimated)	368,168 / 75.37%
Duplication rate	44.43%
Clipped reads	193,300 / 39.57%

2.2. ACGT Content

Number/percentage of A's	12,645,945 / 27.43%
Number/percentage of C's	10,205,678 / 22.14%
Number/percentage of T's	11,751,604 / 25.49%
Number/percentage of G's	11,496,622 / 24.94%
Number/percentage of N's	314 / 0%

GC Percentage	47.08%

2.3. Coverage

Mean	0.0152
Standard Deviation	9.7664

2.4. Mapping Quality

Mean Mapping Quality	30.53

2.5. Insert size

Mean	741,402.62
Standard Deviation	7,978,121.03
P25/Median/P75	140 / 184 / 214

2.6. Mismatches and indels

General error rate	3.96%
Mismatches	1,782,042
Insertions	23,074
Mapped reads with at least one insertion	6.13%
Deletions	136,419
Mapped reads with at least one deletion	35.74%
Homopolymer indels	28.84%

2.7. Chromosome stats

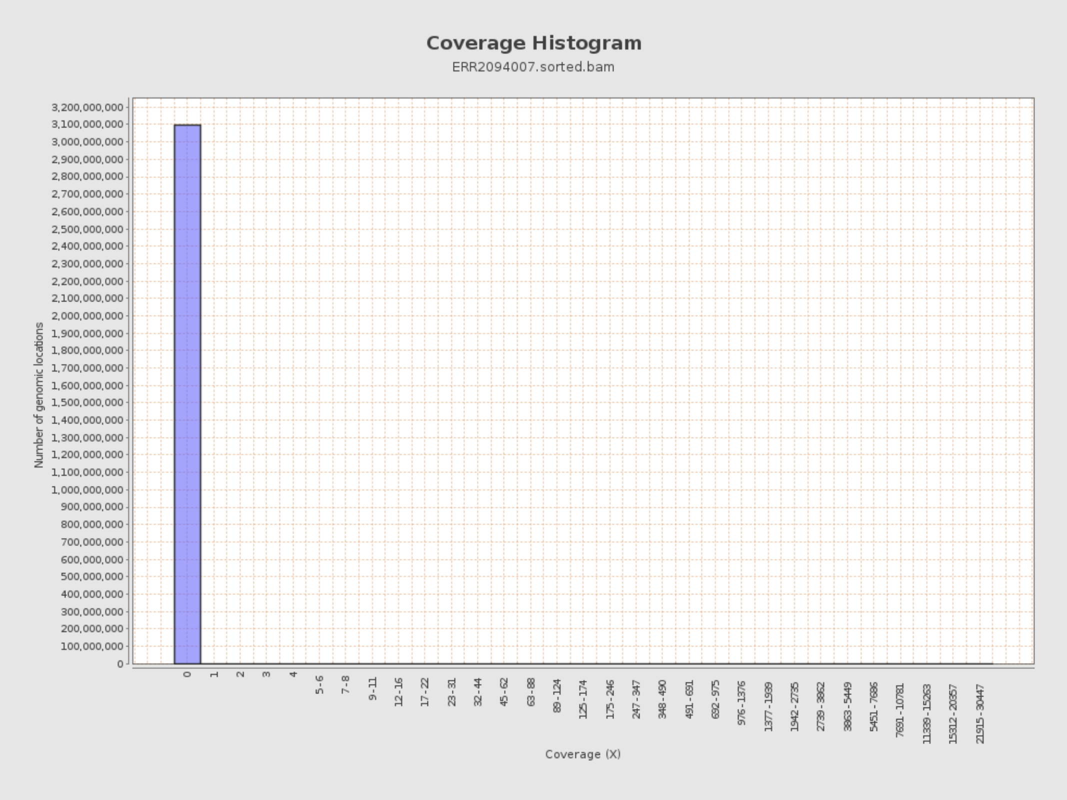
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	545172	0.0022	0.9661
chr2	243199373	3157076	0.013	10.3181
chr3	198022430	723646	0.0037	1.6254
chr4	191154276	654943	0.0034	3.1737
chr5	180915260	271014	0.0015	0.8965
chr6	171115067	1390294	0.0081	5.294
chr7	159138663	584111	0.0037	1.8888
chr8	146364022	127962	0.0009	0.3323
chr9	141213431	1054975	0.0075	3.2131
chr10	135534747	267841	0.002	1.4377
chr11	135006516	434671	0.0032	3.2436
chr12	133851895	454299	0.0034	1.3159
chr13	115169878	913283	0.0079	4.3643
chr14	107349540	240835	0.0022	0.9203
chr15	102531392	455525	0.0044	2.963
chr16	90354753	374703	0.0041	1.4333
chr17	81195210	240165	0.003	1.0619
chr18	78077248	563793	0.0072	3.3911
chr19	59128983	72361	0.0012	0.3006
chr20	63025520	29387	0.0005	0.1983
chr21	48129895	424286	0.0088	4.0238
chr22	51304566	213161	0.0042	1.4978
chrMT	16571	1710077	103.197	505.3208
chrX	155270560	31892645	0.2054	39.9572

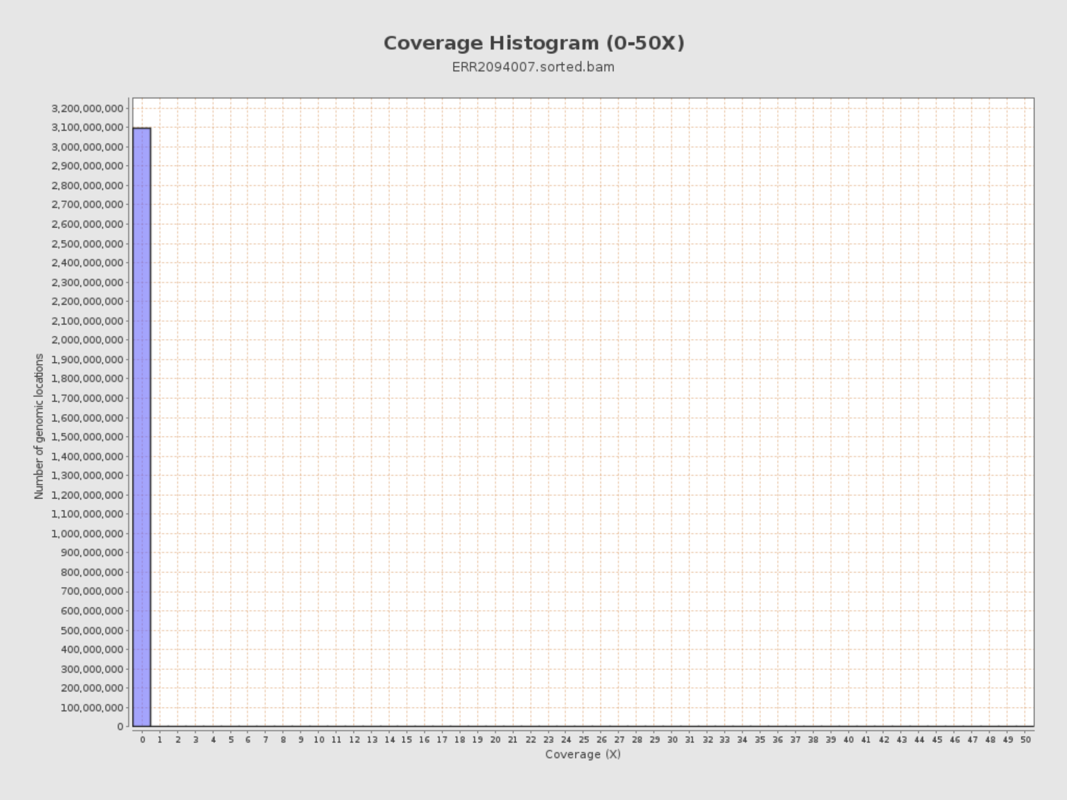
chrY	59373566	388032	0.0065	1.8933

3. Results : Coverage across reference

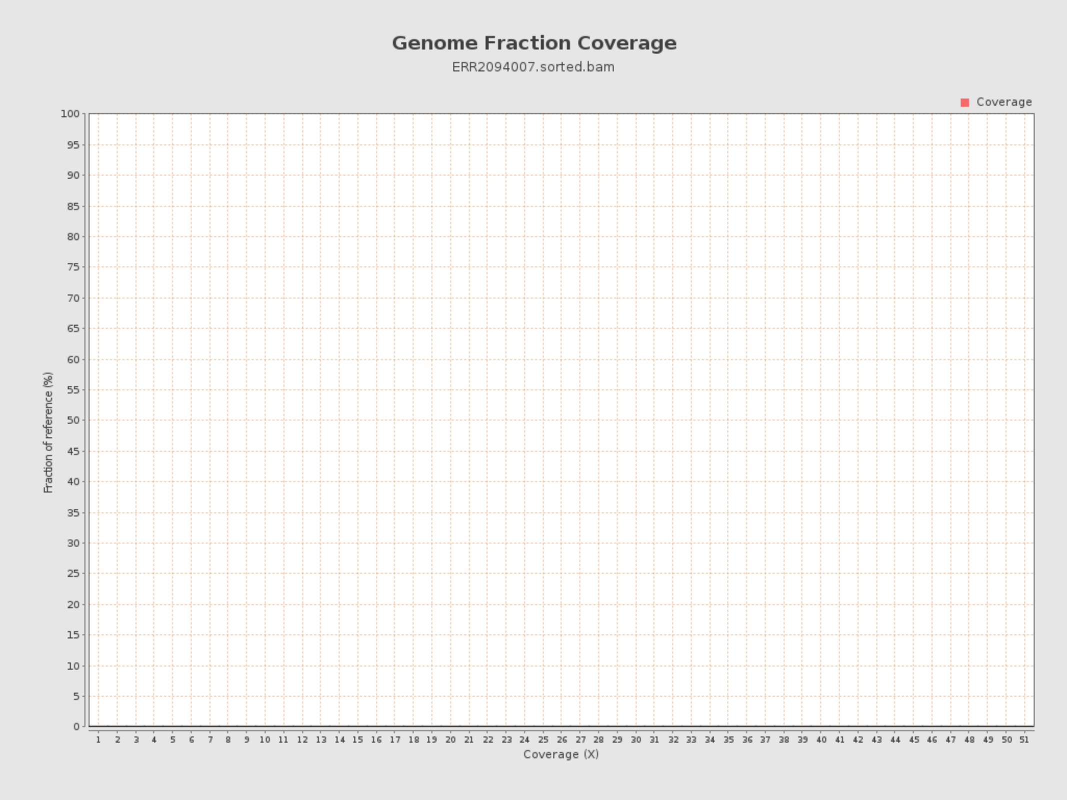
4. Results : Coverage Histogram



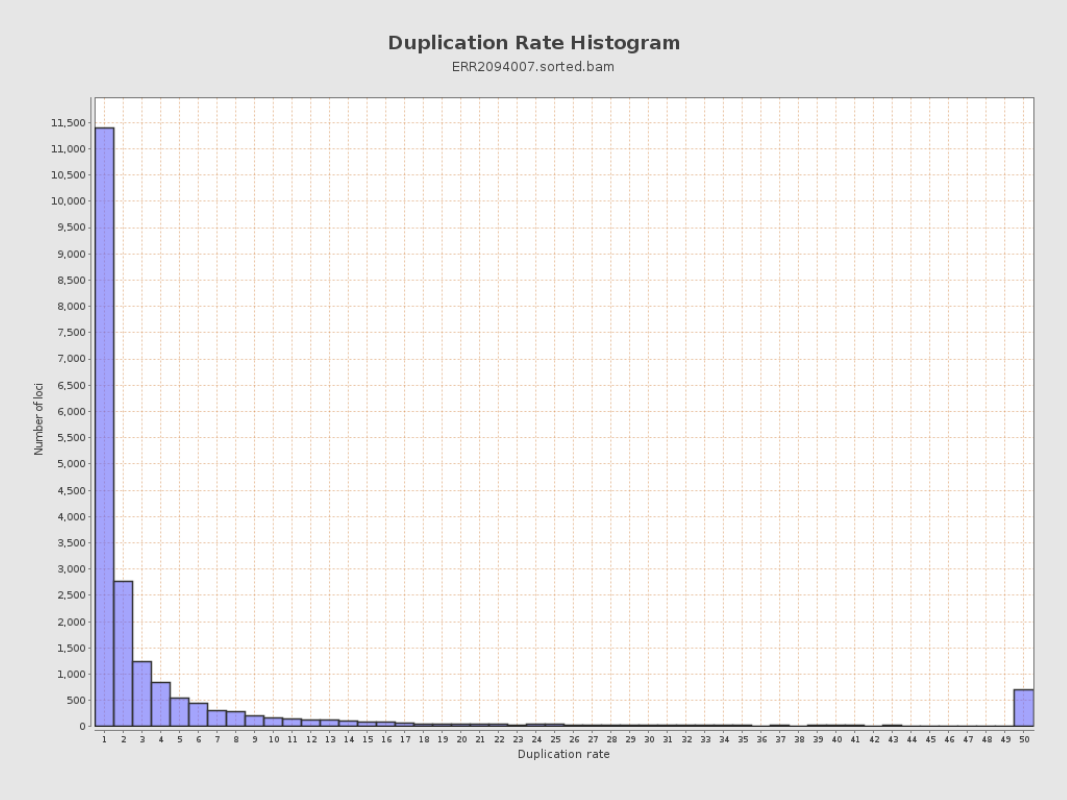
5. Results : Coverage Histogram (0-50X)



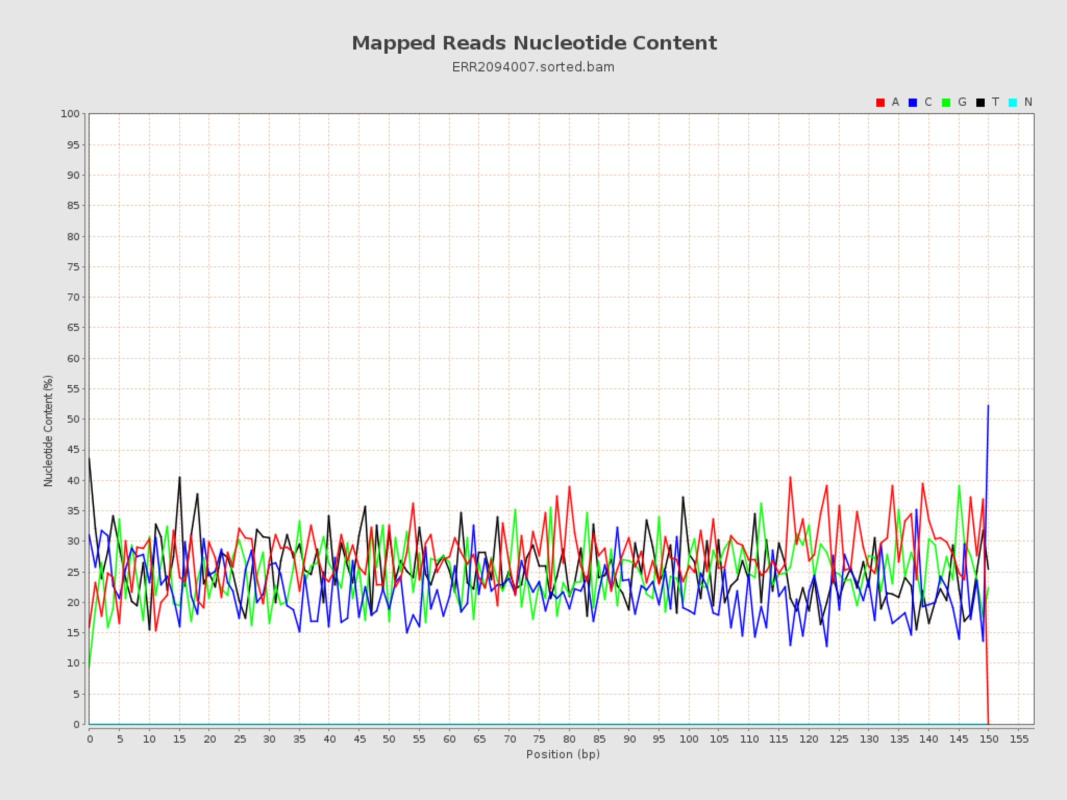
6. Results : Genome Fraction Coverage



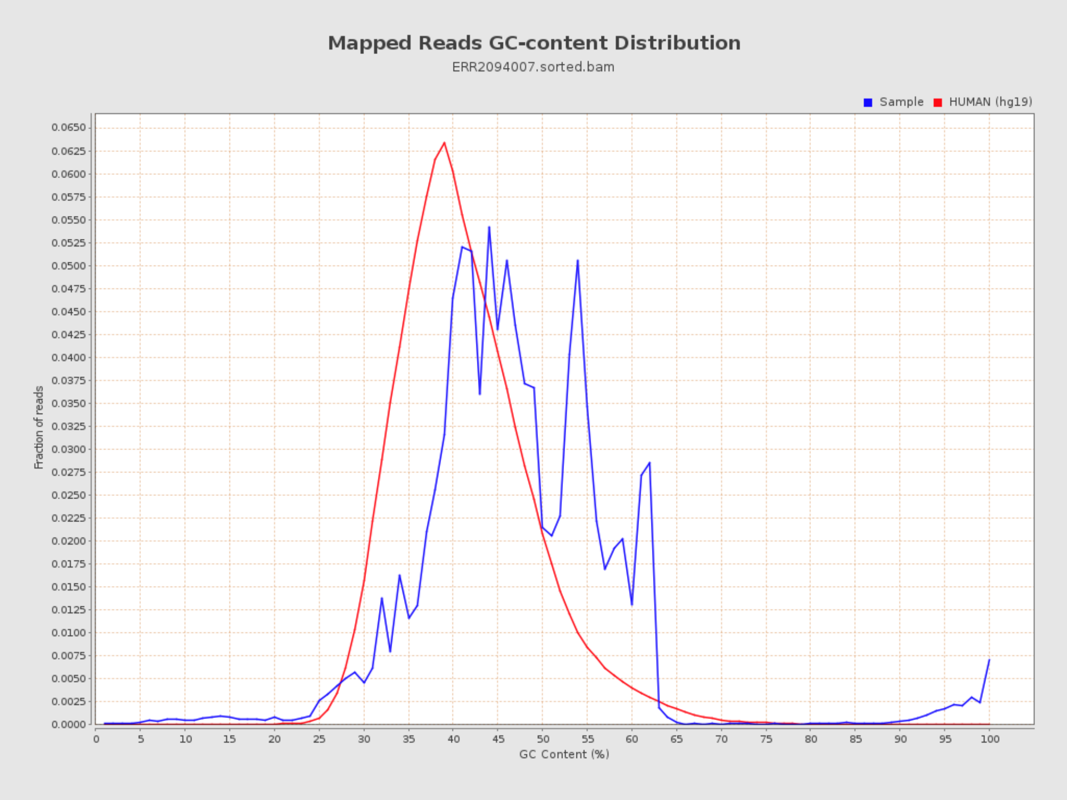
7. Results : Duplication Rate Histogram



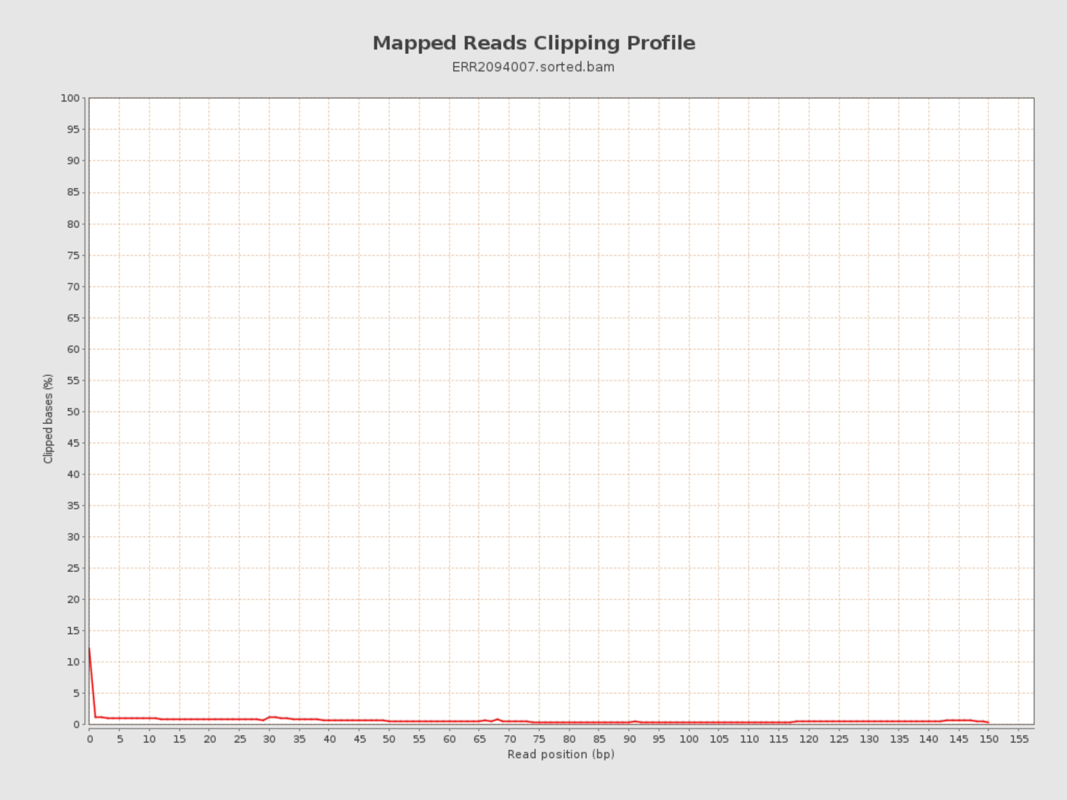
8. Results : Mapped Reads Nucleotide Content



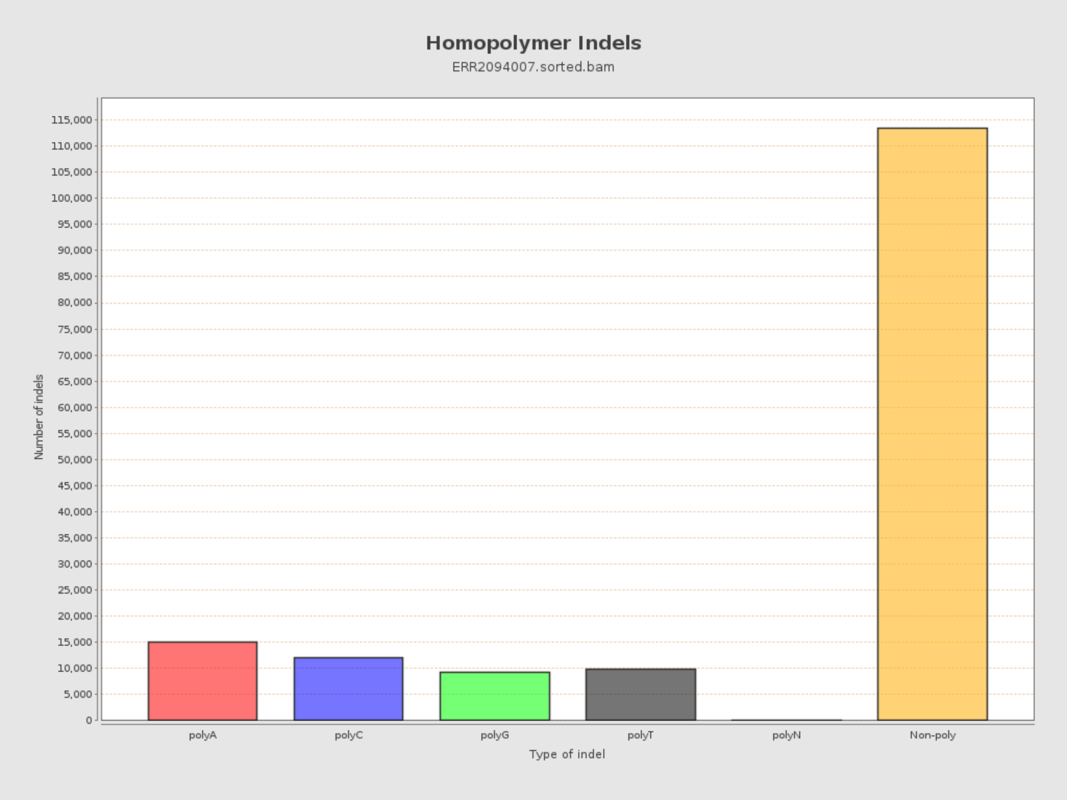
9. Results : Mapped Reads GC-content Distribution



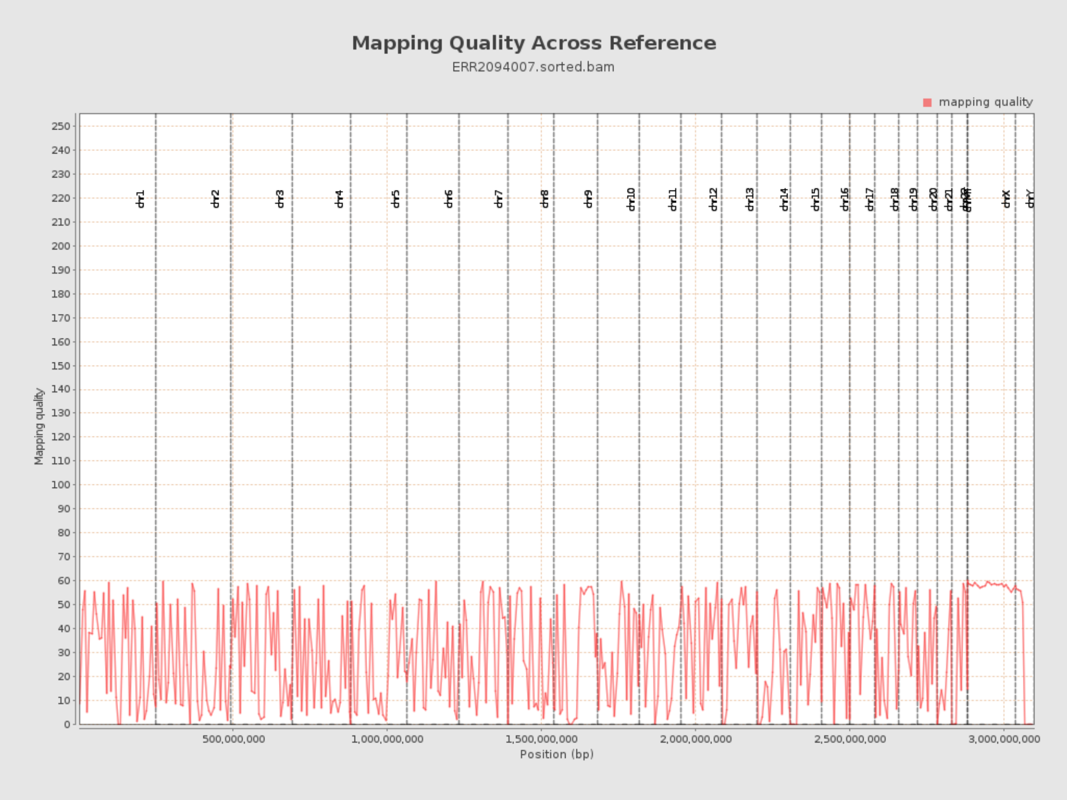
10. Results : Mapped Reads Clipping Profile



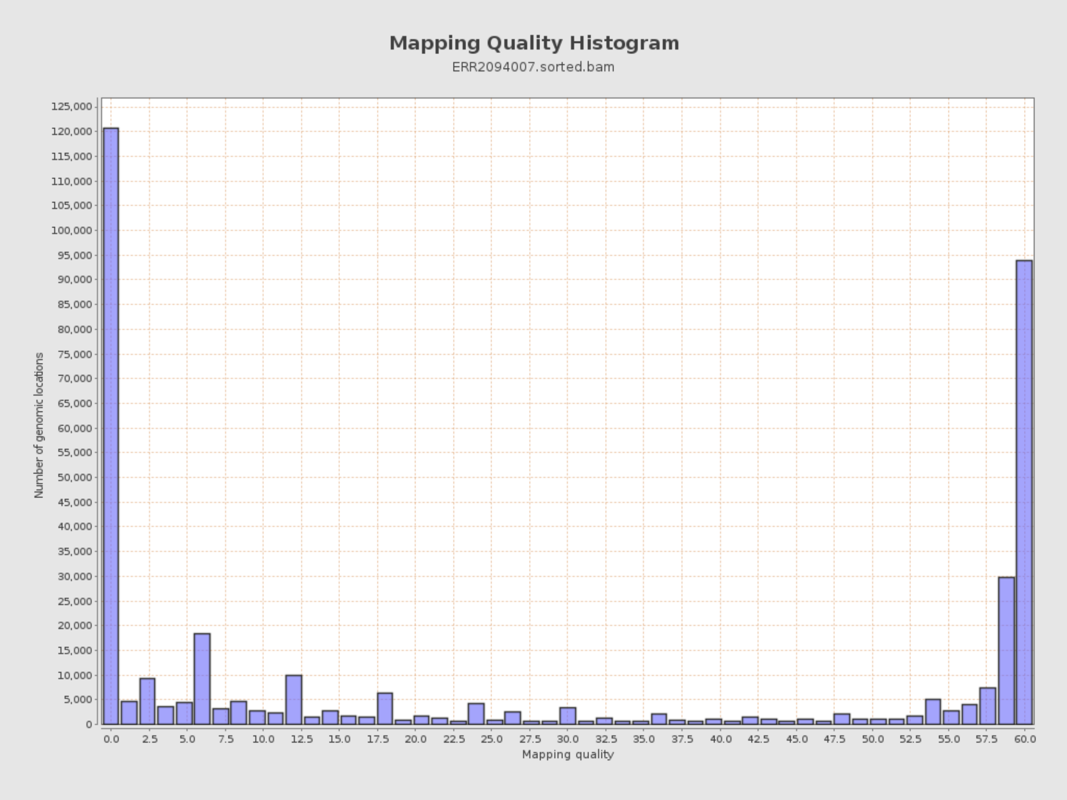
11. Results : Homopolymer Indels



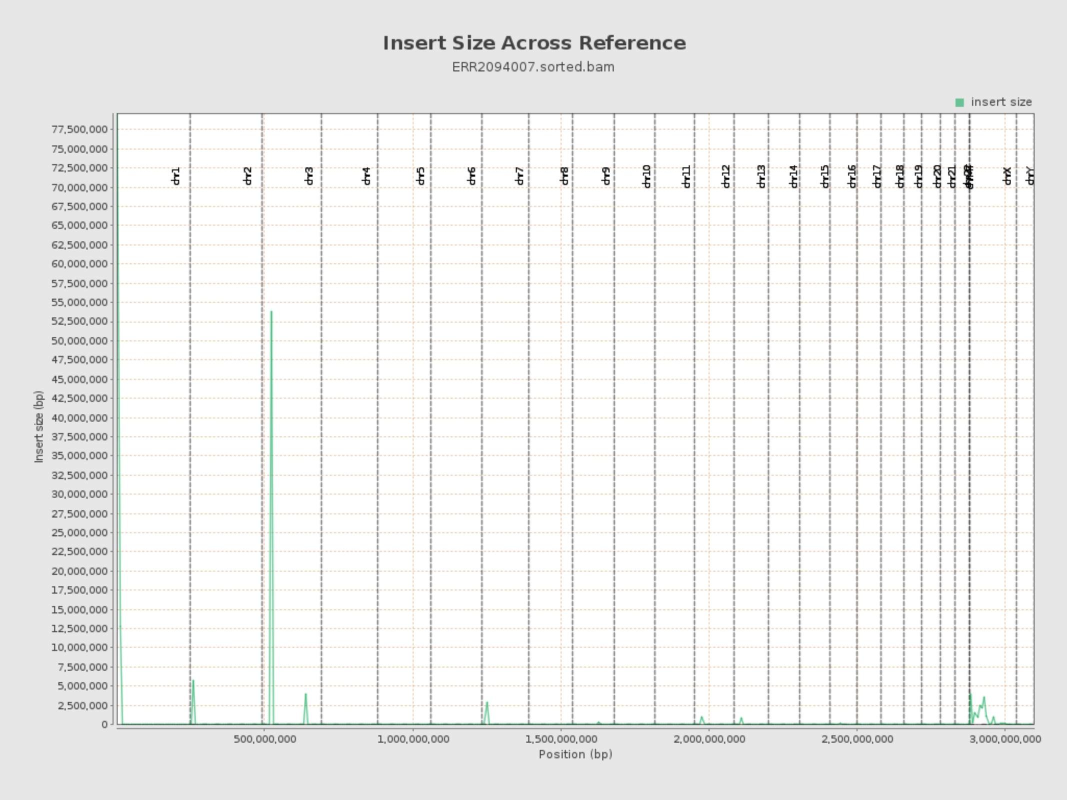
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram