Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:24:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094157.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_ERR2094157 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094157_1.fastq.gz ERR2094157_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:24:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,678
Mapped reads	670 / 4.56%
Unmapped reads	14,008 / 95.44%
Mapped paired reads	670 / 4.56%
Mapped reads, first in pair	269 / 1.83%
Mapped reads, second in pair	401 / 2.73%
Mapped reads, both in pair	462 / 3.15%
Mapped reads, singletons	208 / 1.42%
Secondary alignments	0
Supplementary alignments	25 / 0.17%
Read min/max/mean length	30 / 151 / 61.83
Duplicated reads (estimated)	456 / 3.11%
Duplication rate	18.41%
Clipped reads	524 / 3.57%

2.2. ACGT Content

Number/percentage of A's	10,124 / 15.74%
Number/percentage of C's	8,361 / 13%
Number/percentage of T's	8,942 / 13.91%
Number/percentage of G's	36,874 / 57.35%
Number/percentage of N's	0 / 0%

GC Percentage	70.35%

2.3. Coverage

Mean	0
Standard Deviation	0.0433

2.4. Mapping Quality

Mean Mapping Quality	6.5

2.5. Insert size

Mean	119.25
Standard Deviation	69.71
P25/Median/P75	65 / 114 / 176

2.6. Mismatches and indels

General error rate	2.39%
Mismatches	1,310
Insertions	38
Mapped reads with at least one insertion	4.63%
Deletions	35
Mapped reads with at least one deletion	5.07%
Homopolymer indels	46.58%

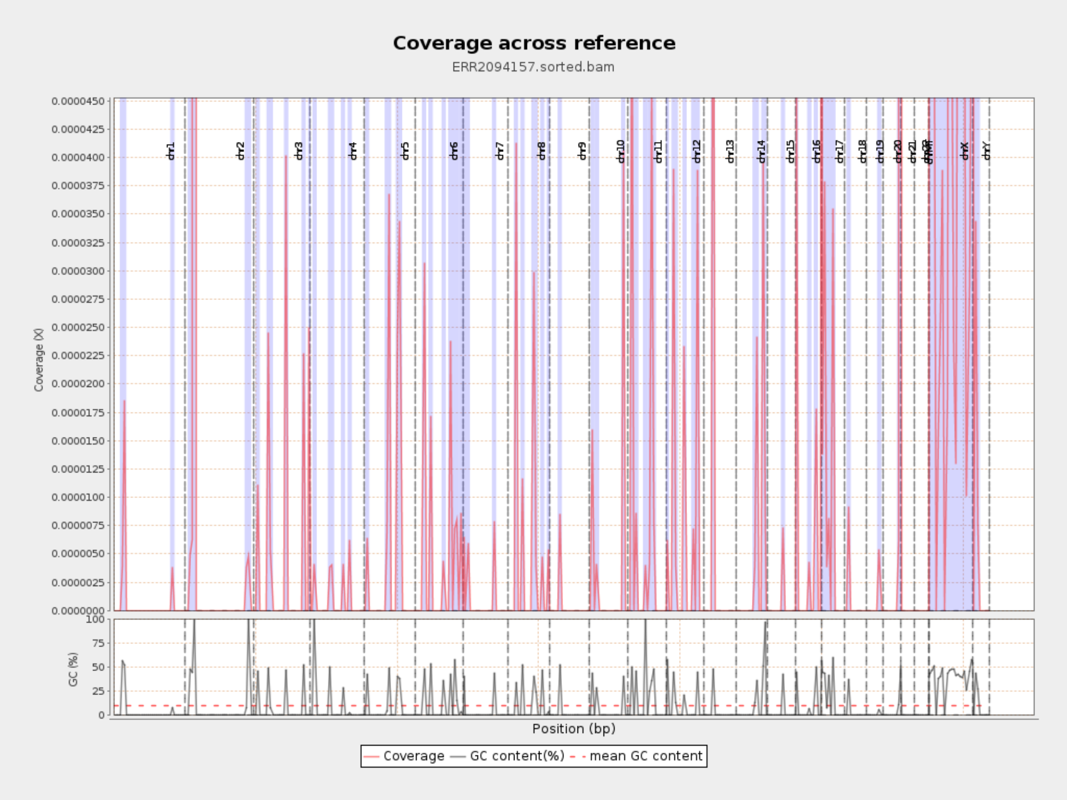
2.7. Chromosome stats

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

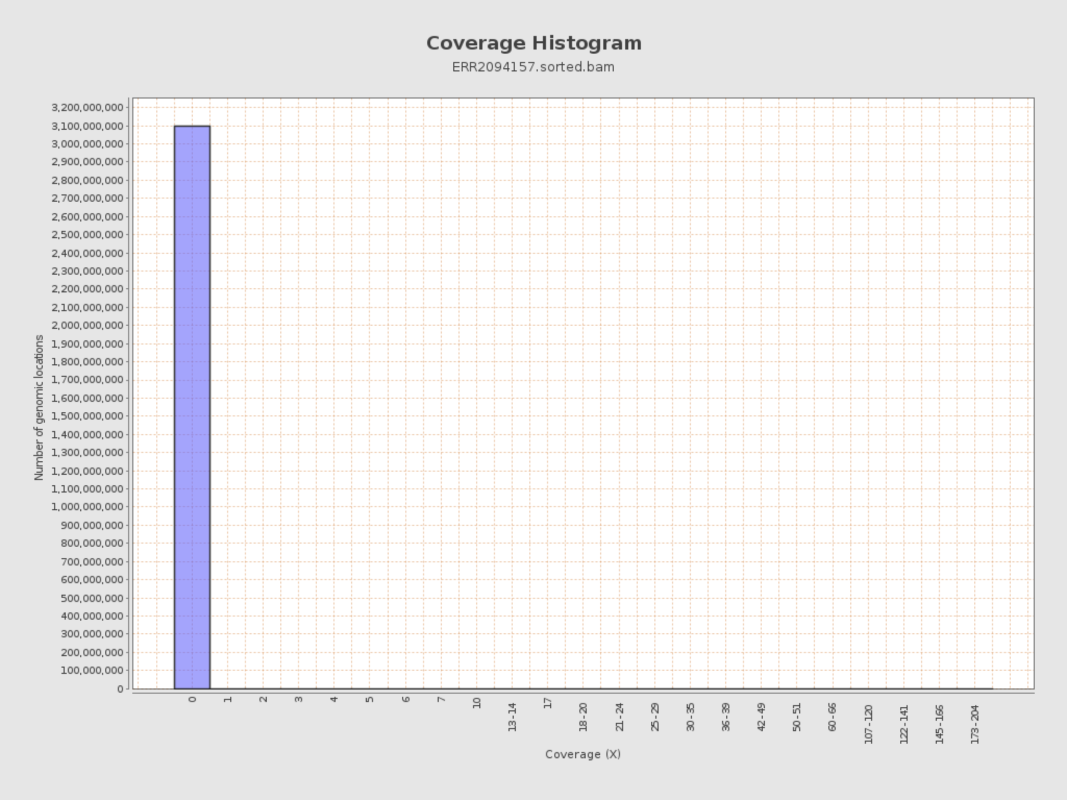
		bases	coverage	deviation
chr1	249250621	204	0	0.0016
chr2	243199373	28813	0.0001	0.1261
chr3	198022430	846	0	0.0025
chr4	191154276	173	0	0.001
chr5	180915260	846	0	0.0028
chr6	171115067	774	0	0.0024
chr7	159138663	137	0	0.0011
chr8	146364022	745	0	0.0028
chr9	141213431	66	0	0.0007
chr10	135534747	471	0	0.0025
chr11	135006516	1008	0	0.0043
chr12	133851895	916	0	0.0033
chr13	115169878	565	0	0.003
chr14	107349540	585	0	0.003
chr15	102531392	57	0	0.0007
chr16	90354753	435	0	0.0026
chr17	81195210	762	0	0.0039
chr18	78077248	71	0	0.001
chr19	59128983	42	0	0.0008
chr20	63025520	17244	0.0003	0.1709
chr21	48129895	0	0	0
chr22	51304566	0	0	0
chrMT	16571	601	0.0363	0.2296
chrX	155270560	8778	0.0001	0.0224

chrY	59373566	325	0	0.0031

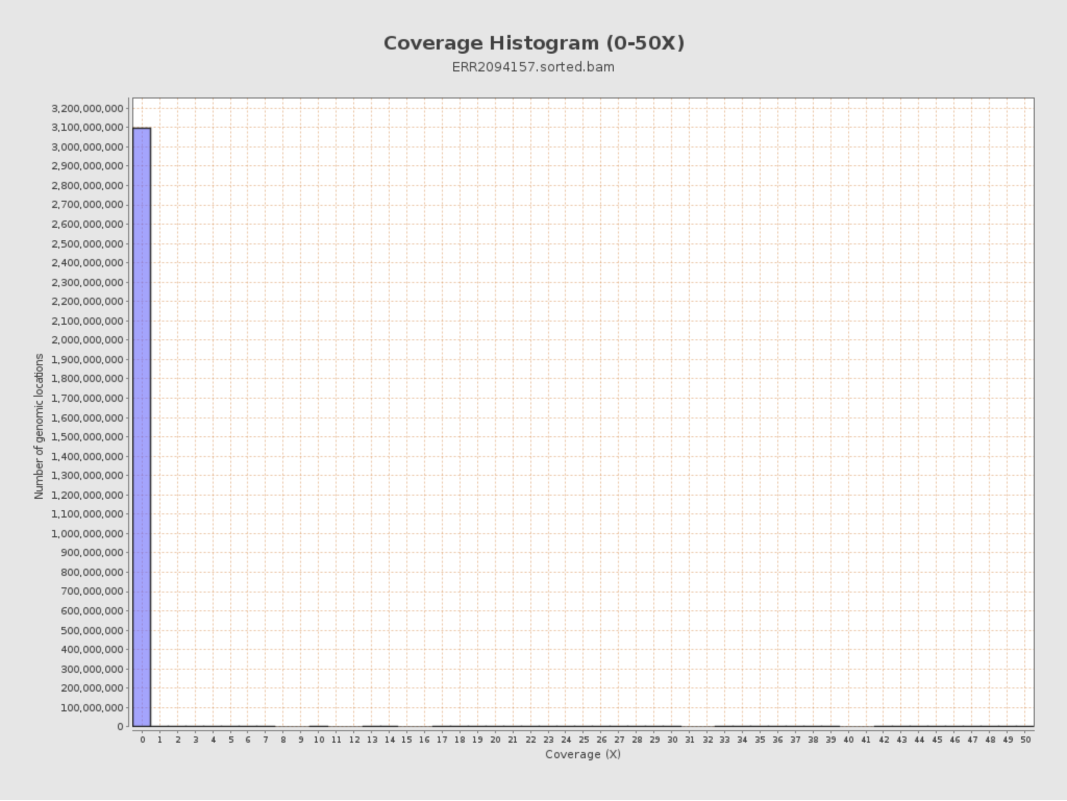
3. Results : Coverage across reference



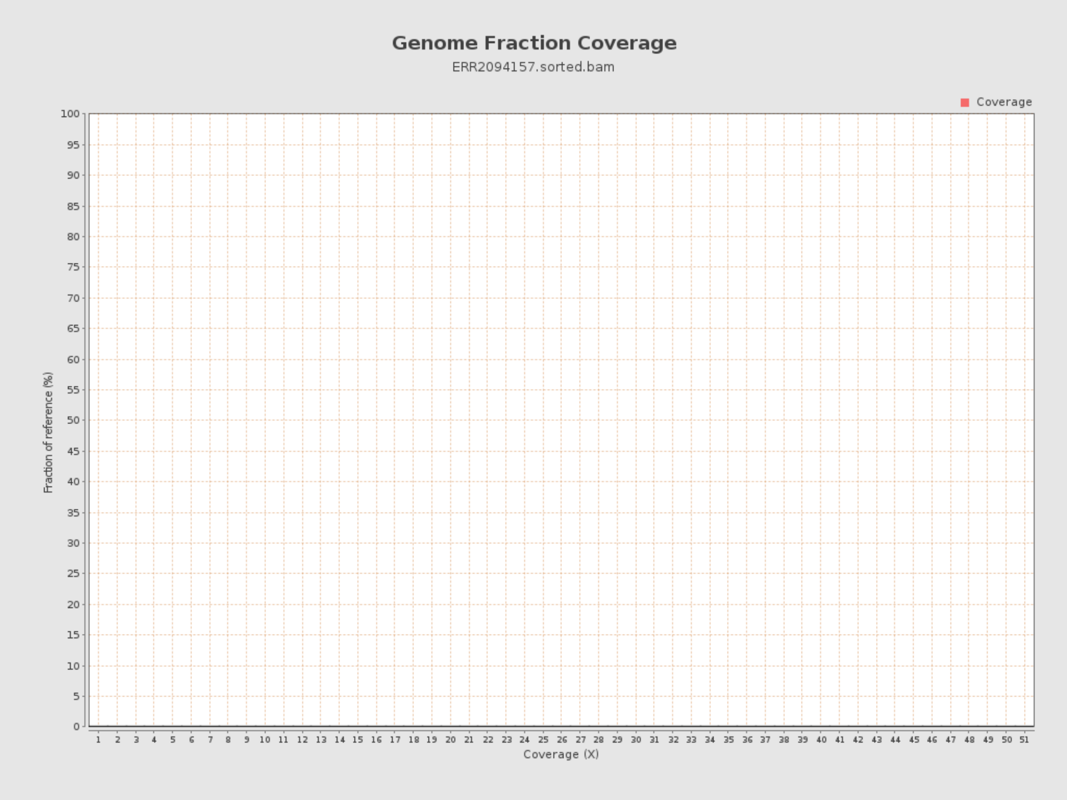
4. Results : Coverage Histogram



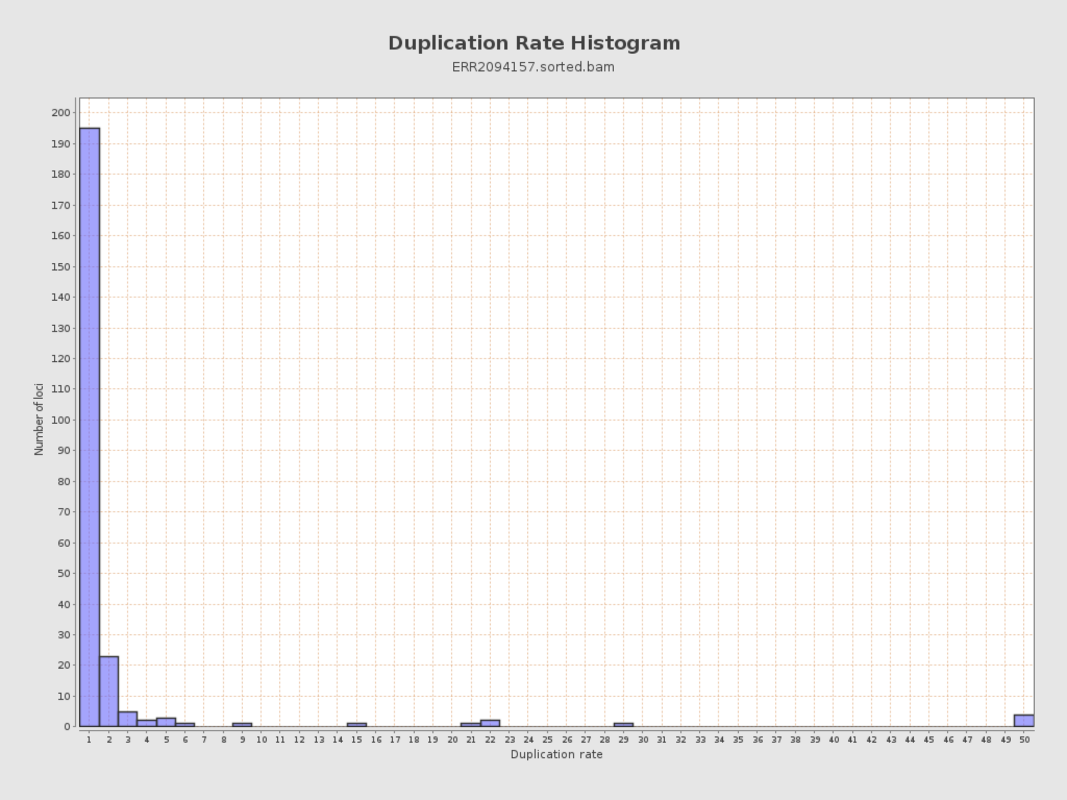
5. Results : Coverage Histogram (0-50X)



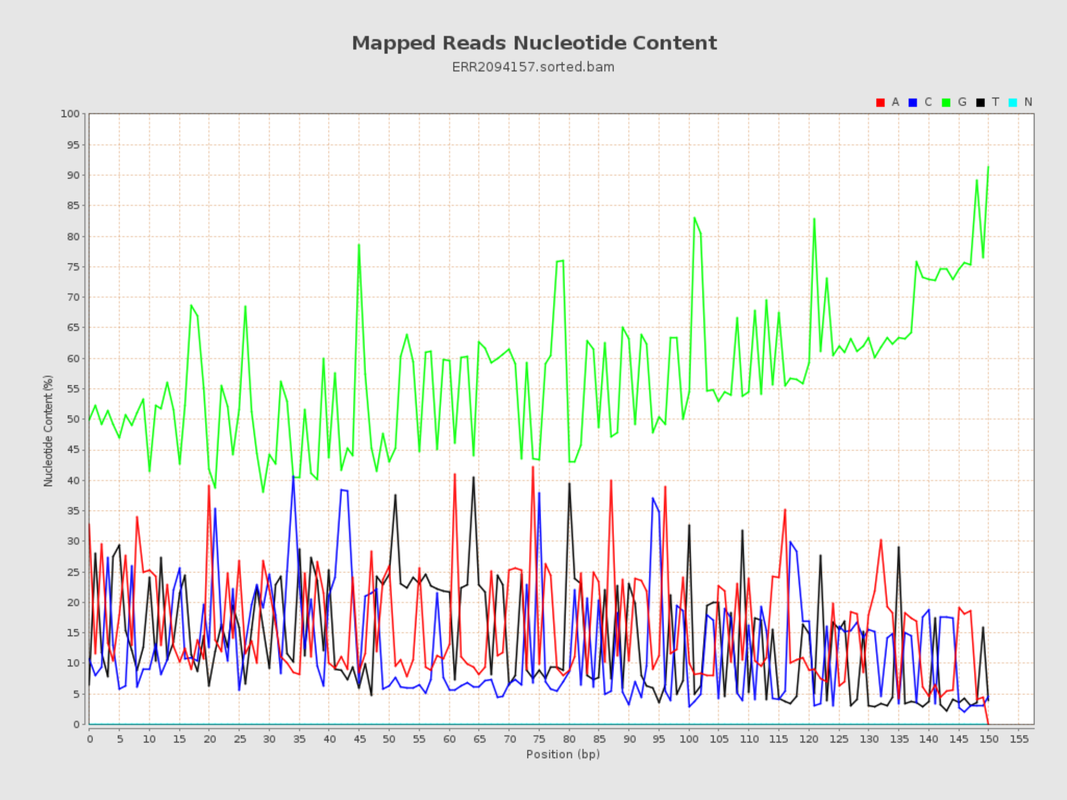
6. Results : Genome Fraction Coverage



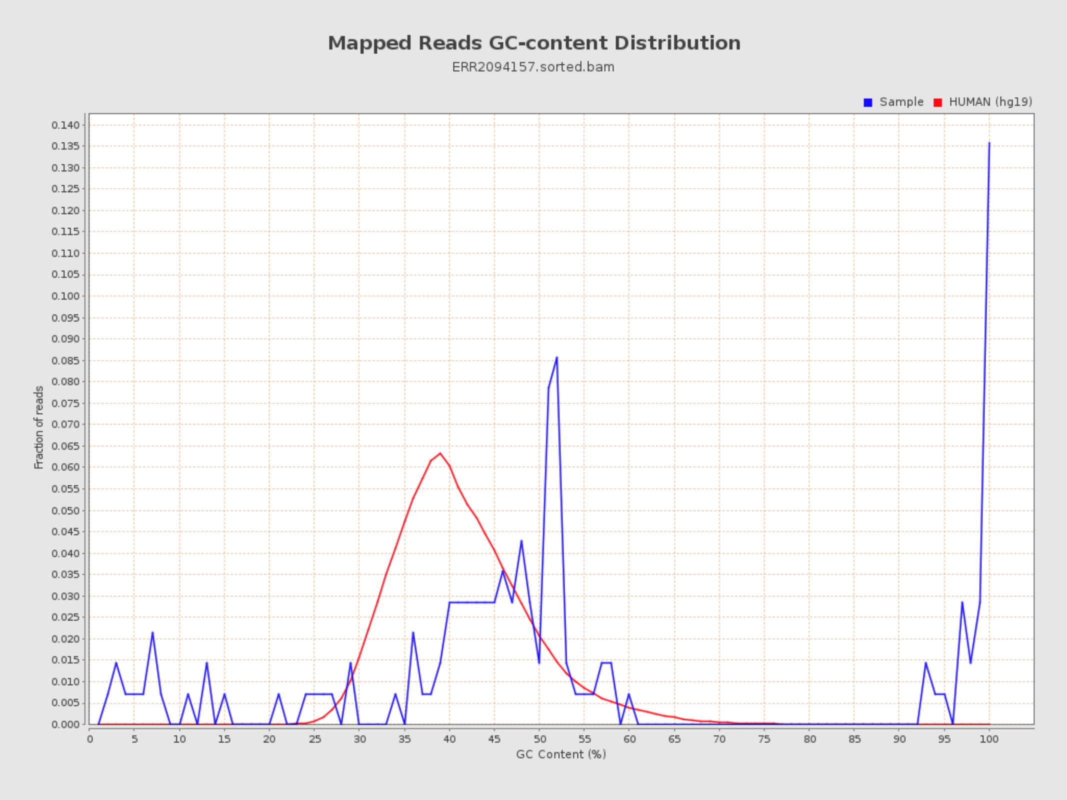
7. Results : Duplication Rate Histogram



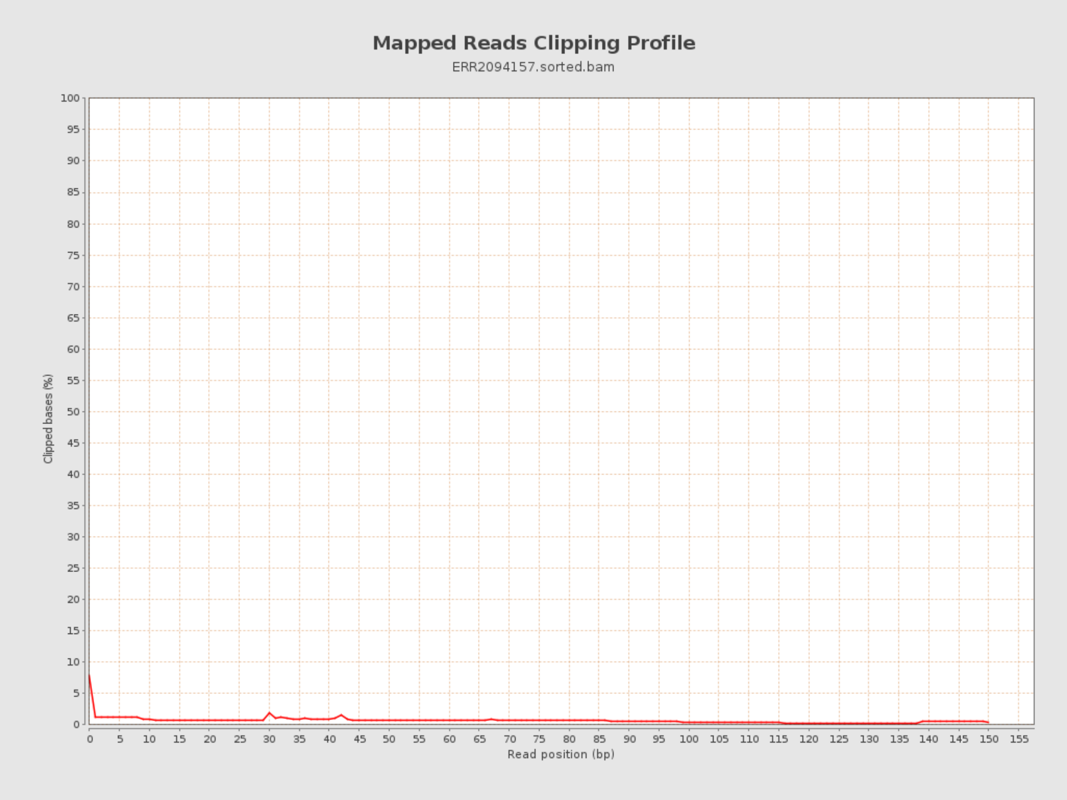
8. Results : Mapped Reads Nucleotide Content



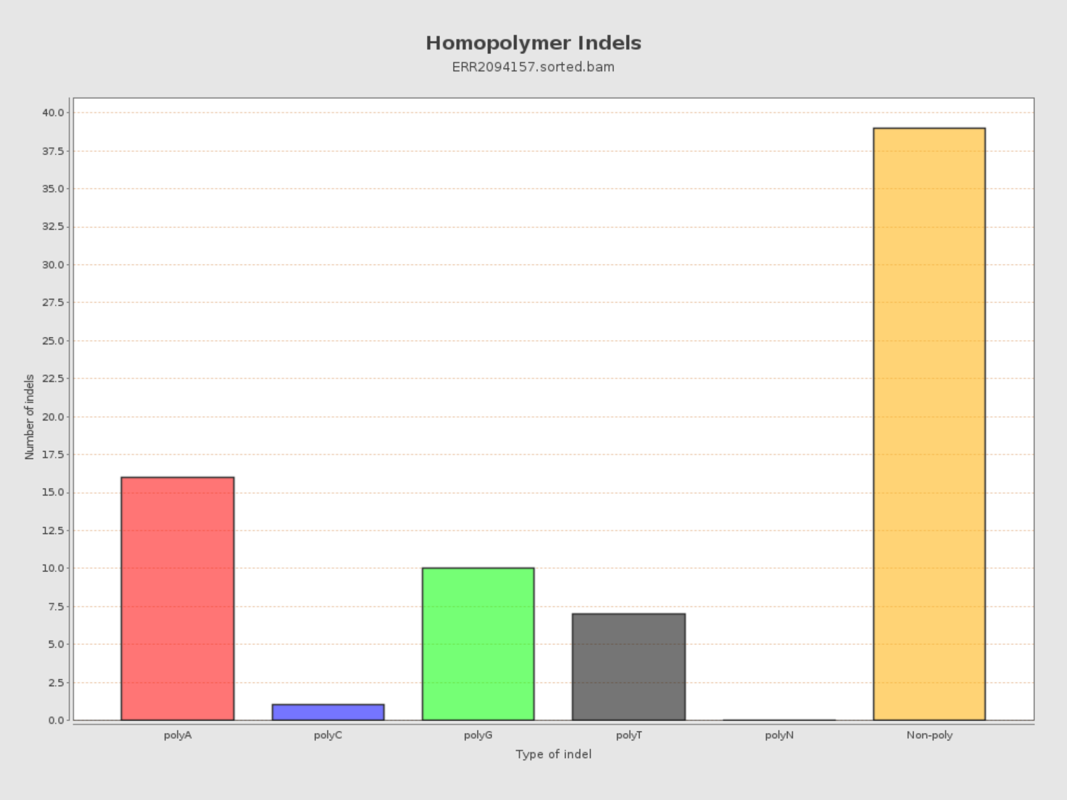
9. Results : Mapped Reads GC-content Distribution



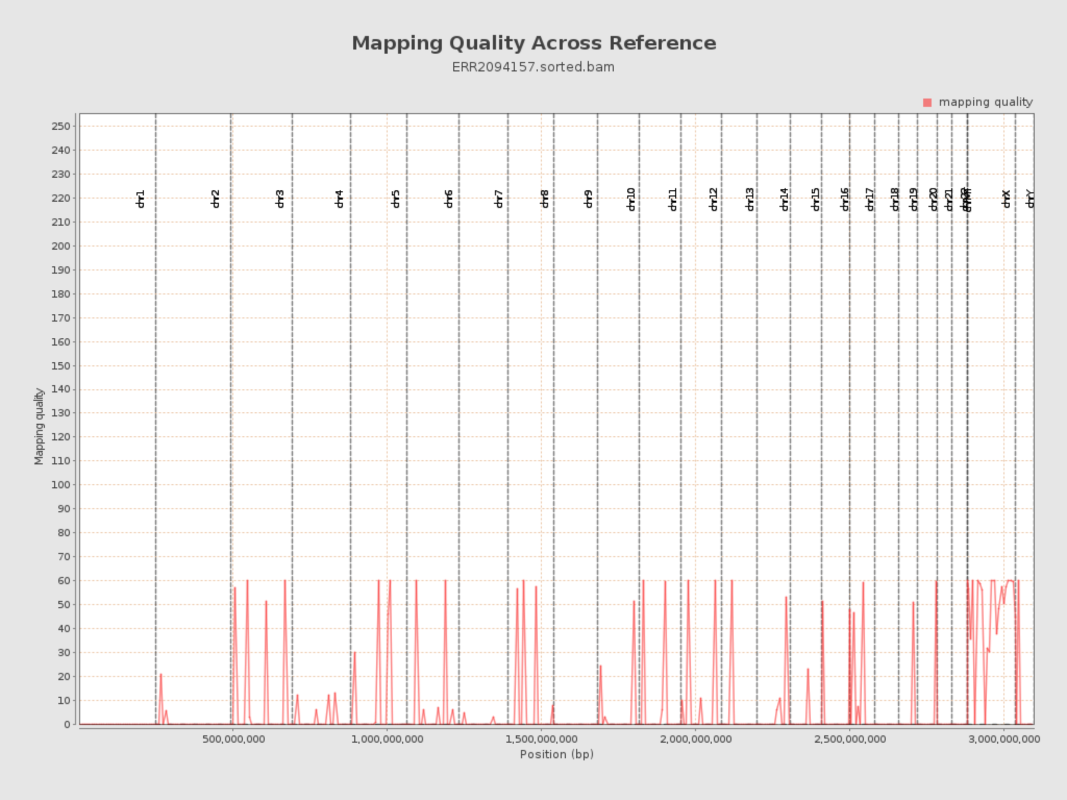
10. Results : Mapped Reads Clipping Profile



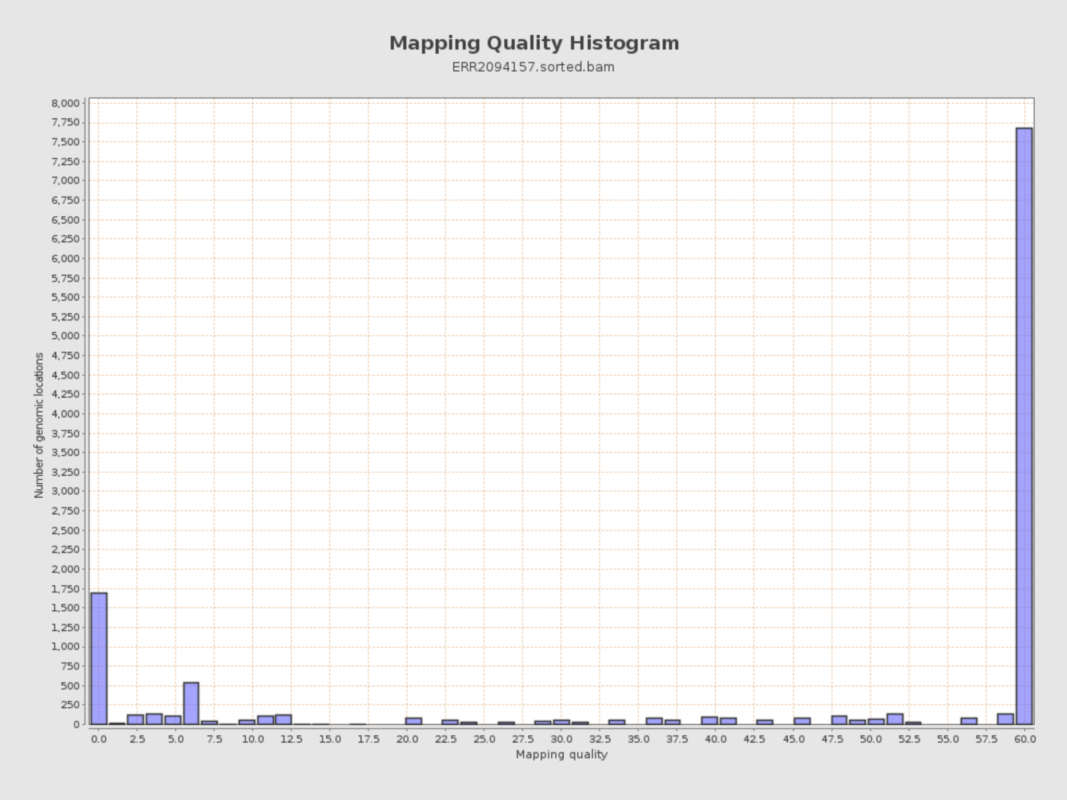
11. Results : Homopolymer Indels



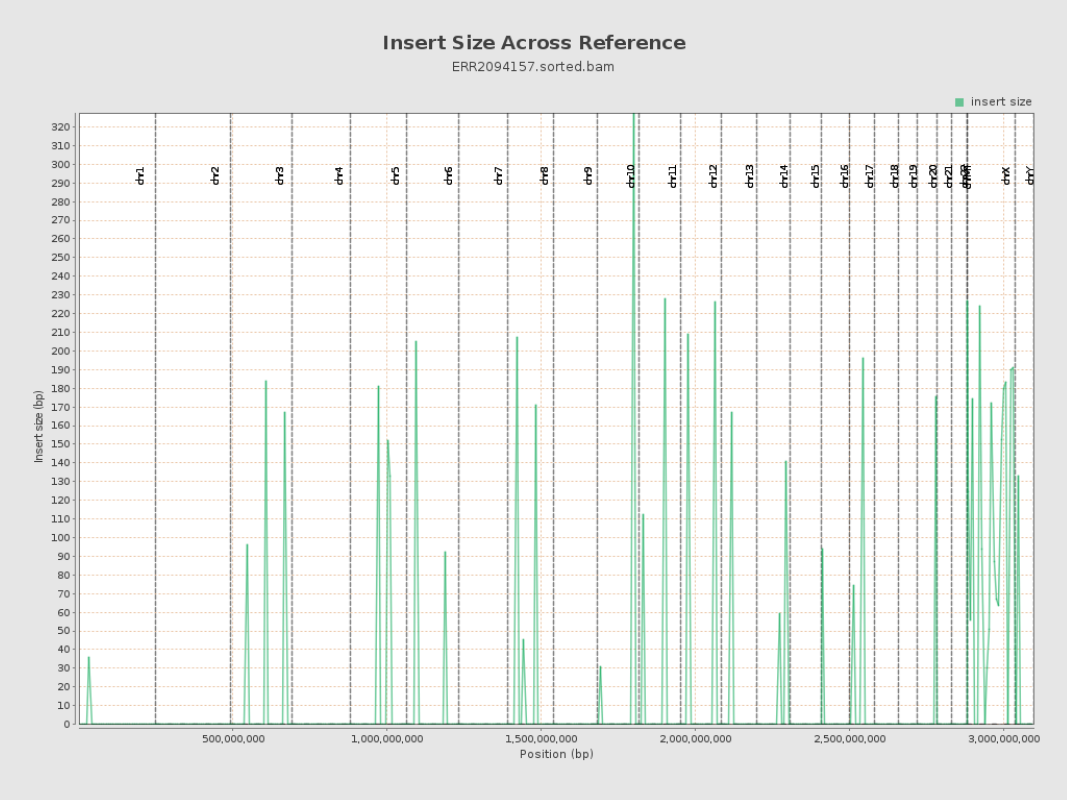
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram