Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:18:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094127.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_ERR2094127 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094127_1.fastq.gz ERR2094127_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:18:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	384,154
Mapped reads	365,771 / 95.21%
Unmapped reads	18,383 / 4.79%
Mapped paired reads	365,771 / 95.21%
Mapped reads, first in pair	183,546 / 47.78%
Mapped reads, second in pair	182,225 / 47.44%
Mapped reads, both in pair	363,758 / 94.69%
Mapped reads, singletons	2,013 / 0.52%
Secondary alignments	0
Supplementary alignments	3,941 / 1.03%
Read min/max/mean length	30 / 151 / 144.74
Duplicated reads (estimated)	364,937 / 95%
Duplication rate	58.68%
Clipped reads	89,124 / 23.2%

2.2. ACGT Content

Number/percentage of A's	14,431,418 / 27.65%
Number/percentage of C's	11,193,190 / 21.44%
Number/percentage of T's	14,890,108 / 28.53%
Number/percentage of G's	11,680,617 / 22.38%
Number/percentage of N's	510 / 0%

GC Percentage	43.82%

2.3. Coverage

Mean	0.0169
Standard Deviation	25.9256

2.4. Mapping Quality

Mean Mapping Quality	11.14

2.5. Insert size

Mean	3,277.53
Standard Deviation	510,059.19
P25/Median/P75	212 / 231 / 256

2.6. Mismatches and indels

General error rate	1.71%
Mismatches	845,652
Insertions	18,032
Mapped reads with at least one insertion	4.86%
Deletions	42,498
Mapped reads with at least one deletion	11.4%
Homopolymer indels	54.93%

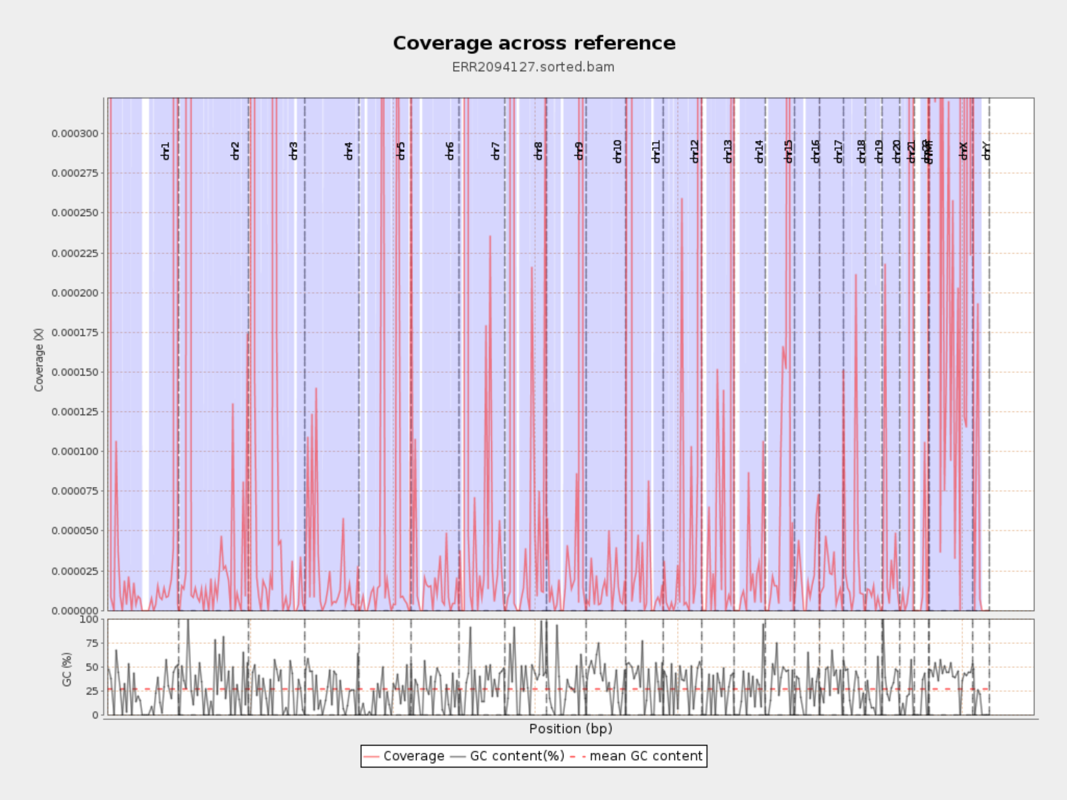
2.7. Chromosome stats

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

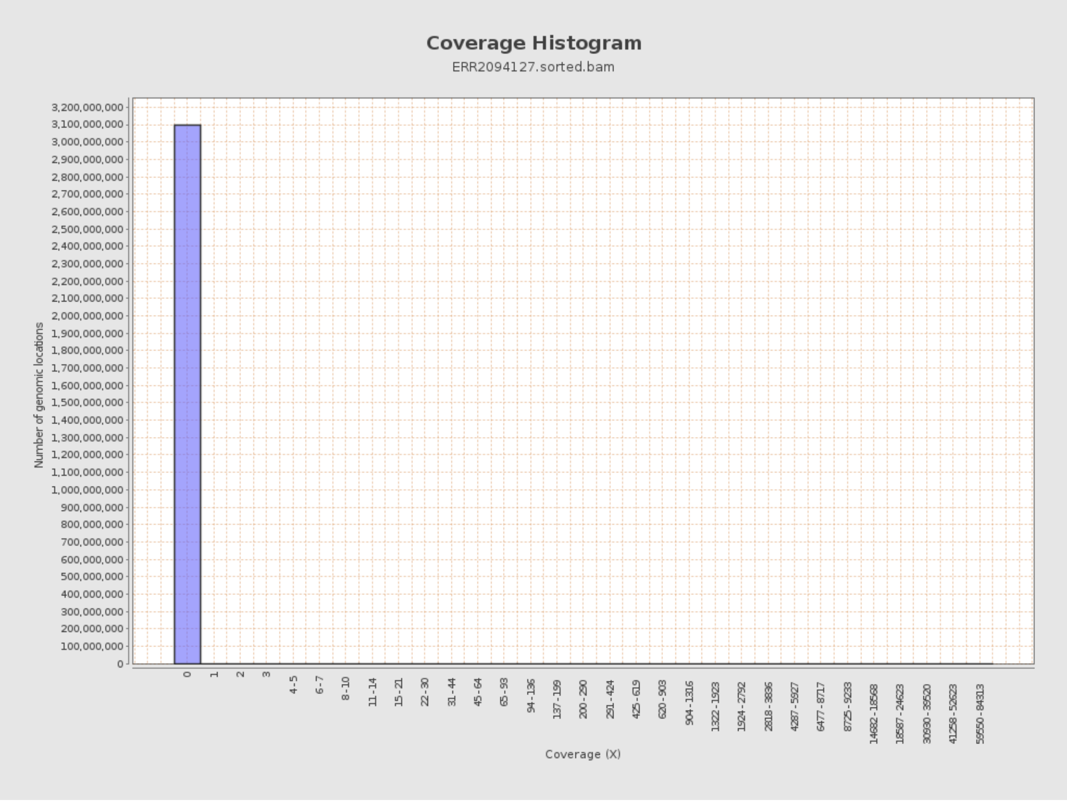
		bases	**coverage**	**deviation**
chr1	249250621	199533	0.0008	0.5093
chr2	243199373	158624	0.0007	0.6383
chr3	198022430	144769	0.0007	0.2497
chr4	191154276	5006	0	0.0111
chr5	180915260	9208	0.0001	0.034
chr6	171115067	4610	0	0.0159
chr7	159138663	170555	0.0011	1.0324
chr8	146364022	552976	0.0038	3.1797
chr9	141213431	29983	0.0002	0.1877
chr10	135534747	2014	0	0.0064
chr11	135006516	421951	0.0031	2.4046
chr12	133851895	23847	0.0002	0.1575
chr13	115169878	42192	0.0004	0.3271
chr14	107349540	2430	0	0.0145
chr15	102531392	11297	0.0001	0.0581
chr16	90354753	2280	0	0.0086
chr17	81195210	1687	0	0.0078
chr18	78077248	3091	0	0.023
chr19	59128983	460	0	0.0032
chr20	63025520	2683	0	0.017
chr21	48129895	305268	0.0063	3.2793
chr22	51304566	890	0	0.0151
chrMT	16571	48417498	2,921.8211	10,777.1539
chrX	155270560	1788384	0.0115	8.6593

chrY	59373566	1932	0	0.0122

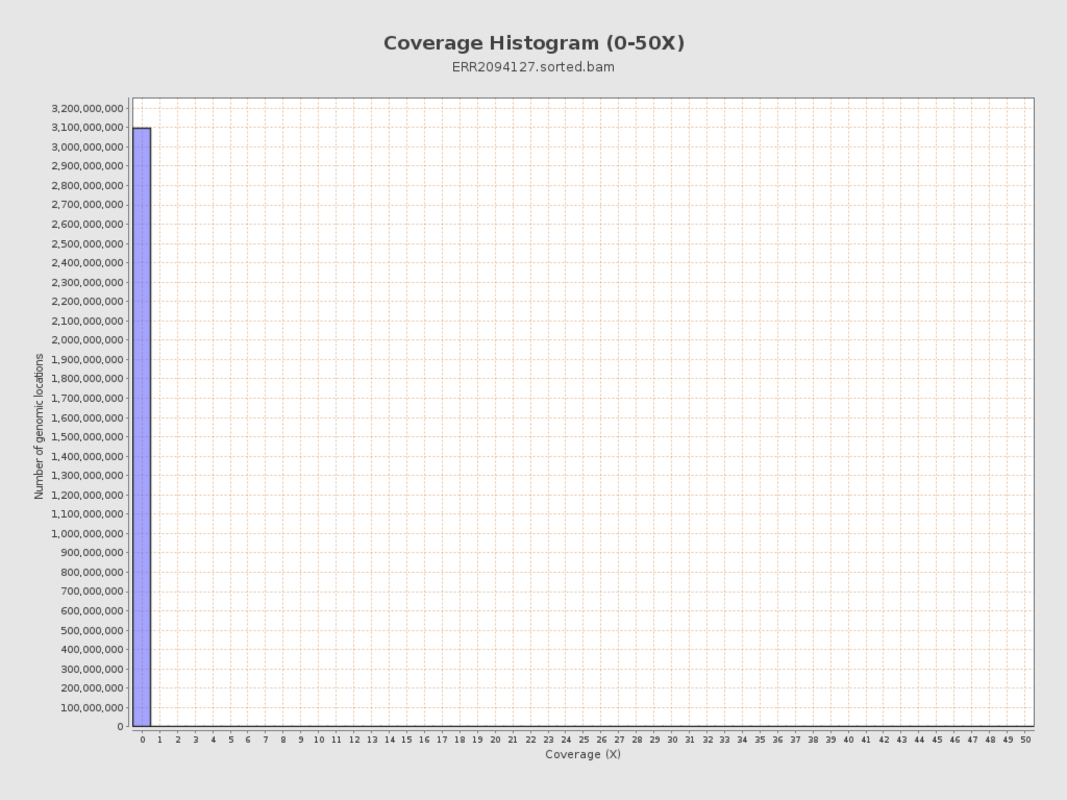
3. Results : Coverage across reference



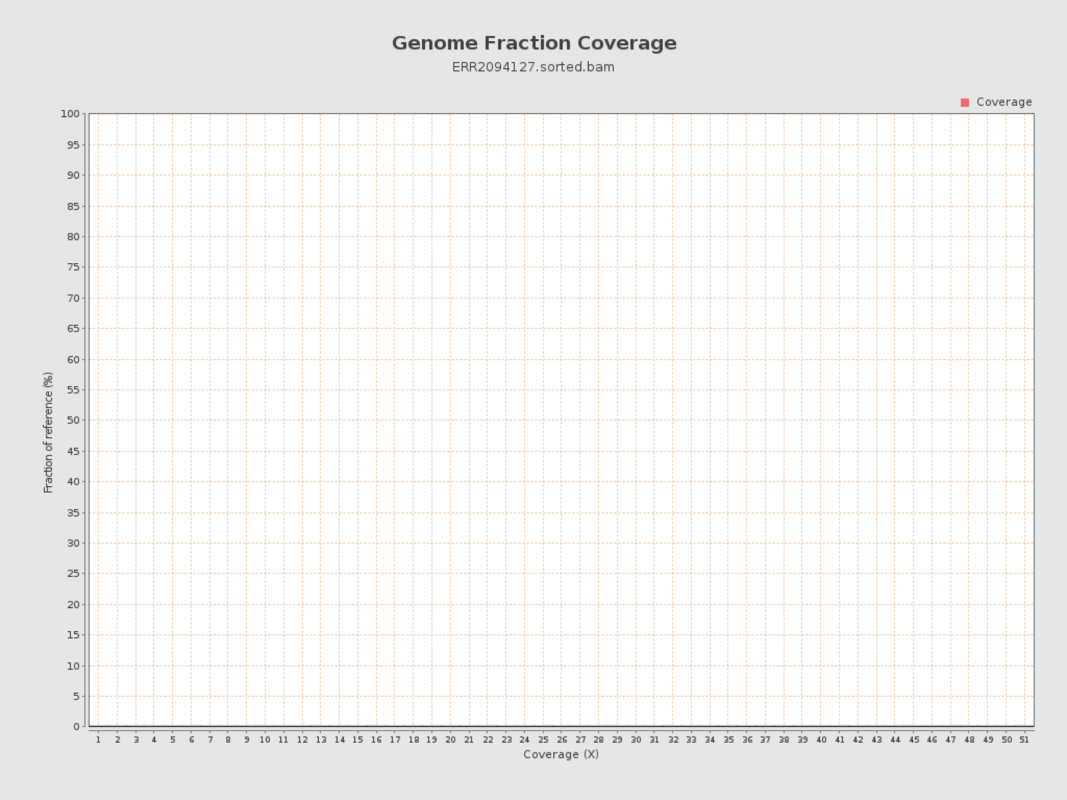
4. Results : Coverage Histogram



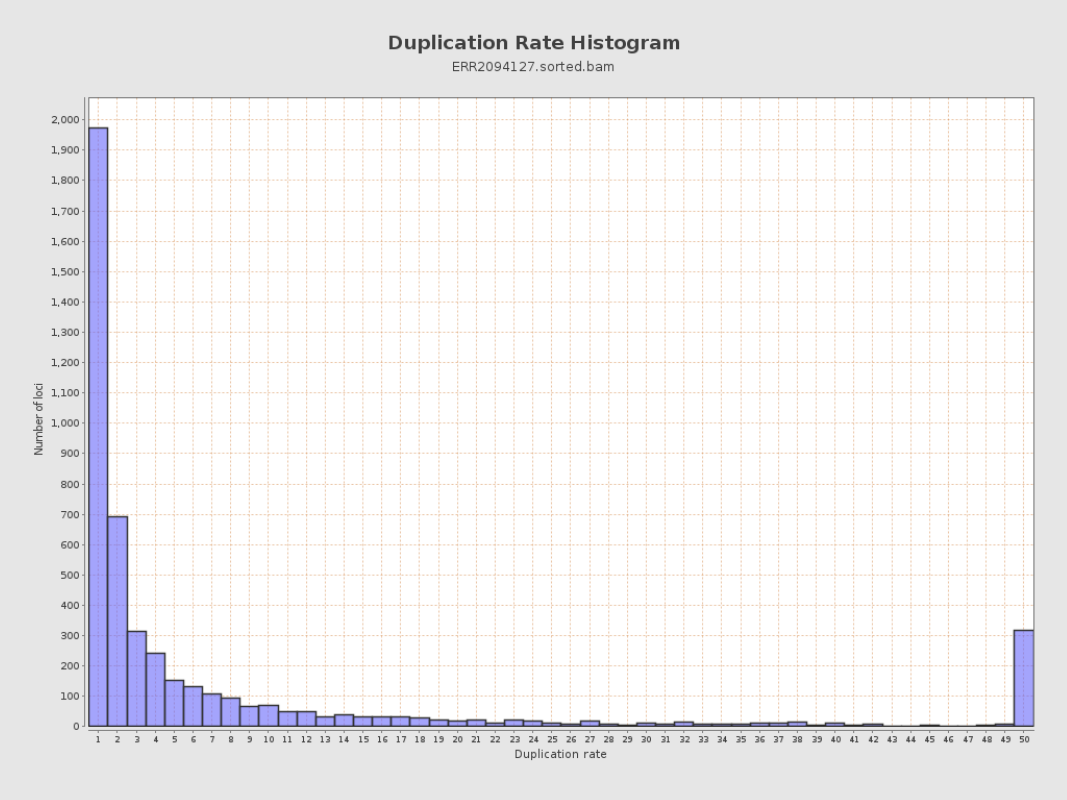
5. Results : Coverage Histogram (0-50X)



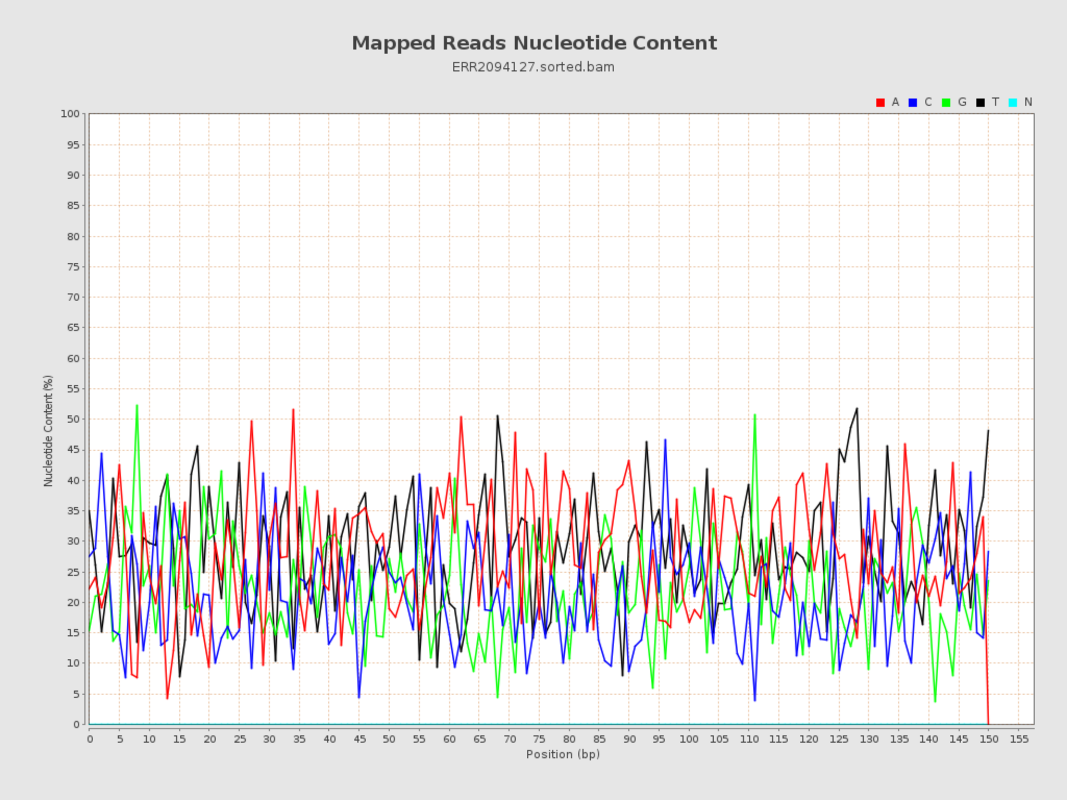
6. Results : Genome Fraction Coverage



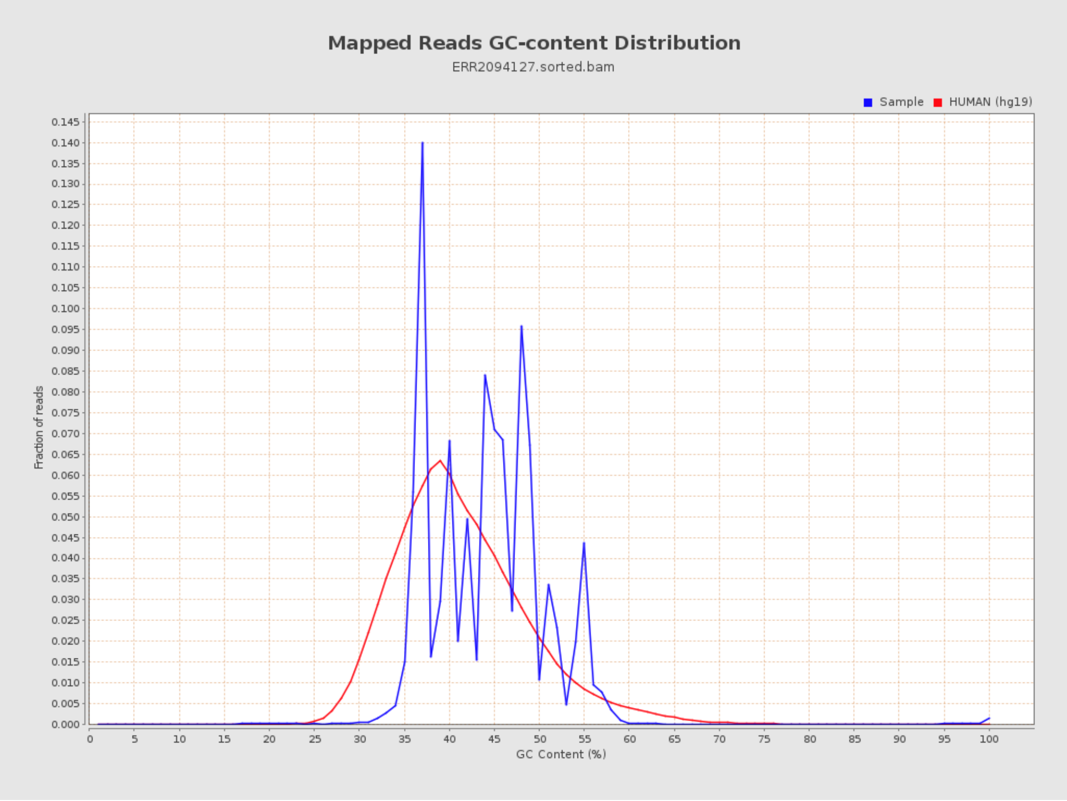
7. Results : Duplication Rate Histogram



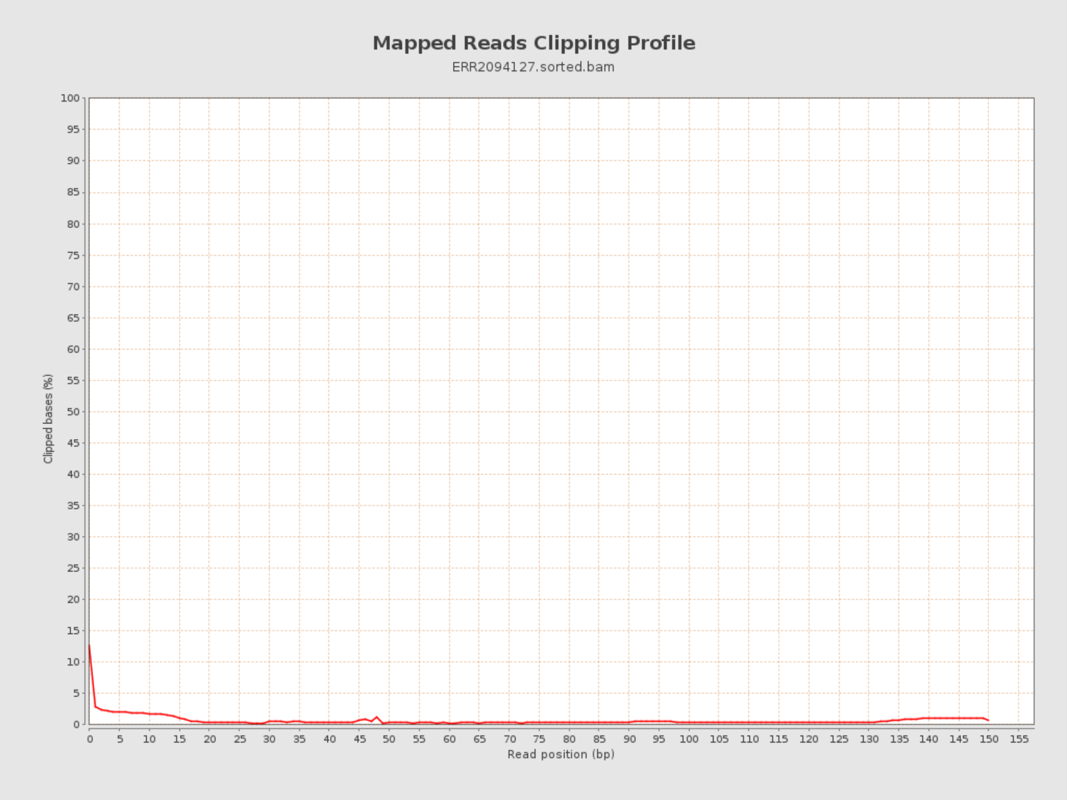
8. Results : Mapped Reads Nucleotide Content



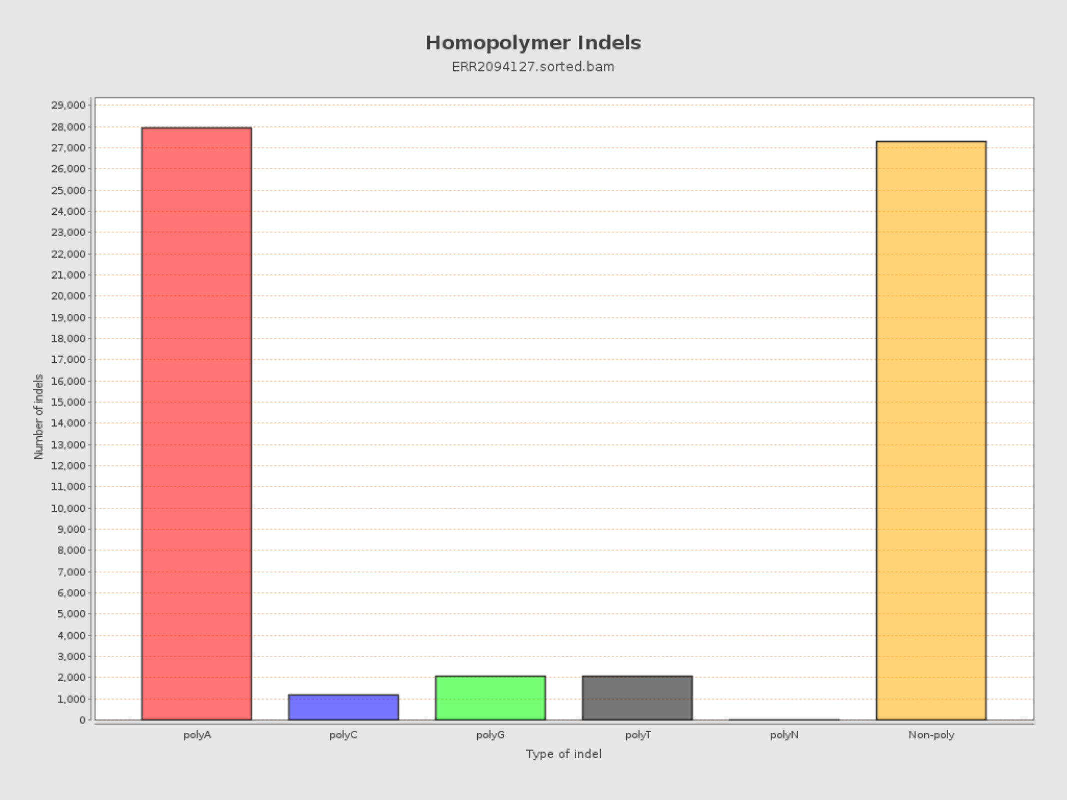
9. Results : Mapped Reads GC-content Distribution



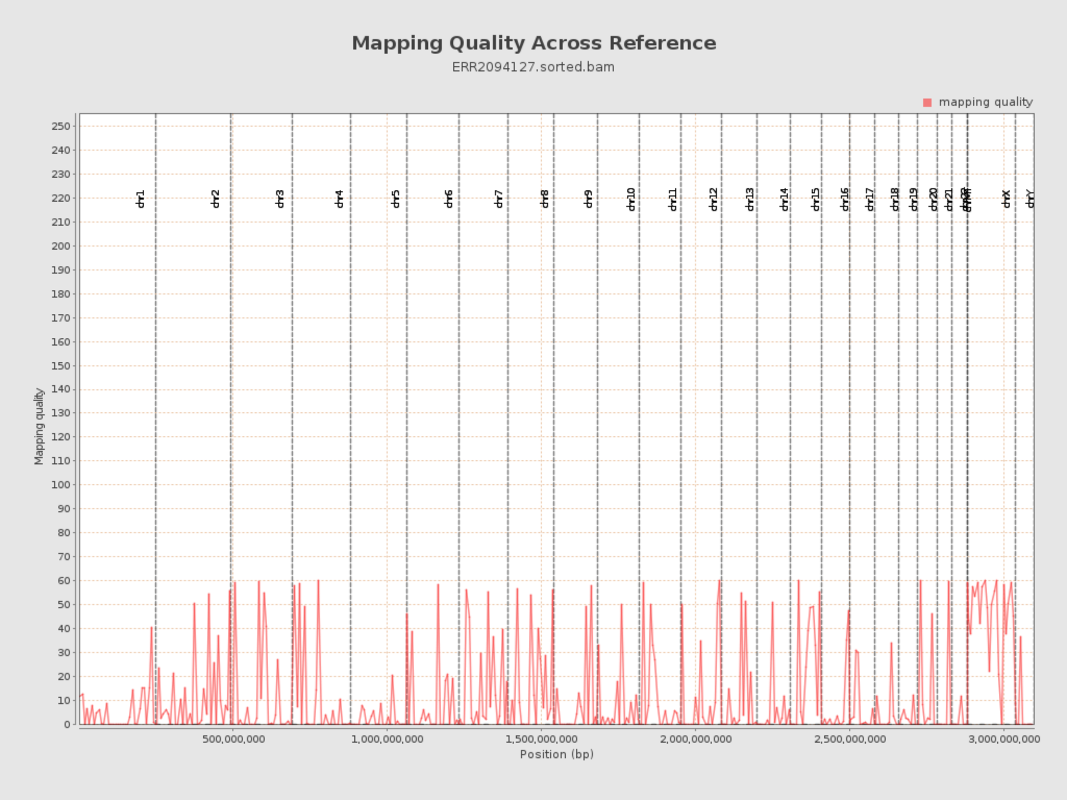
10. Results : Mapped Reads Clipping Profile



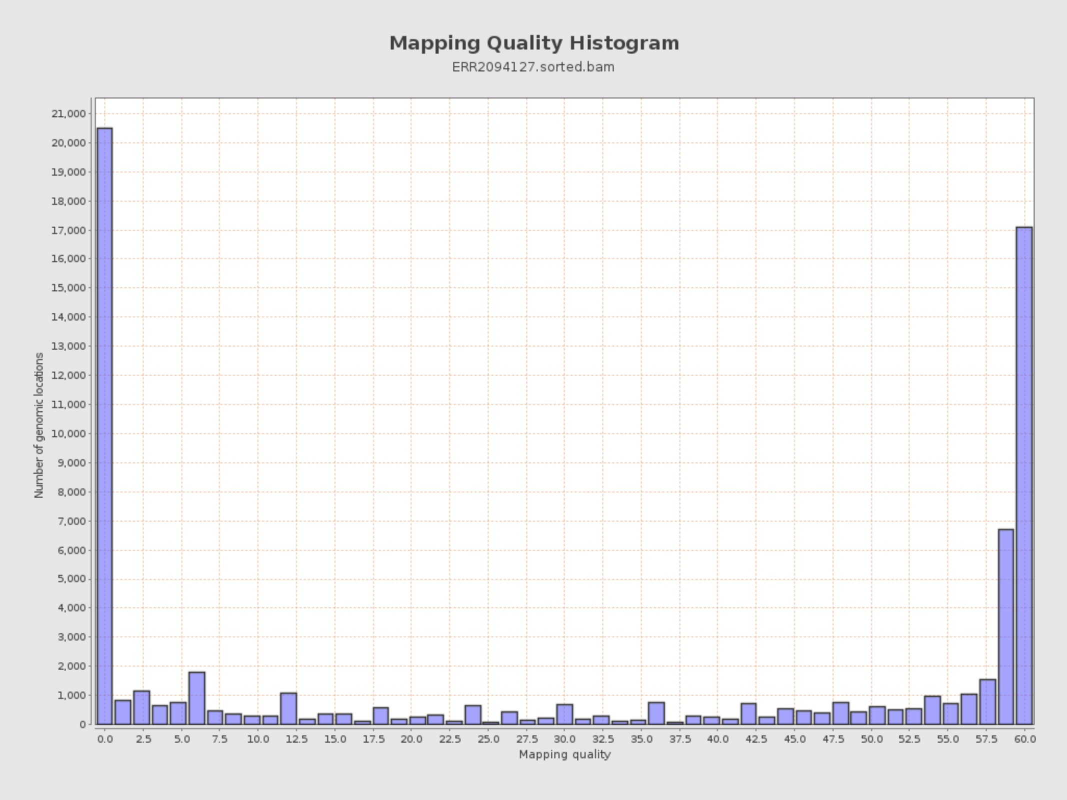
11. Results : Homopolymer Indels



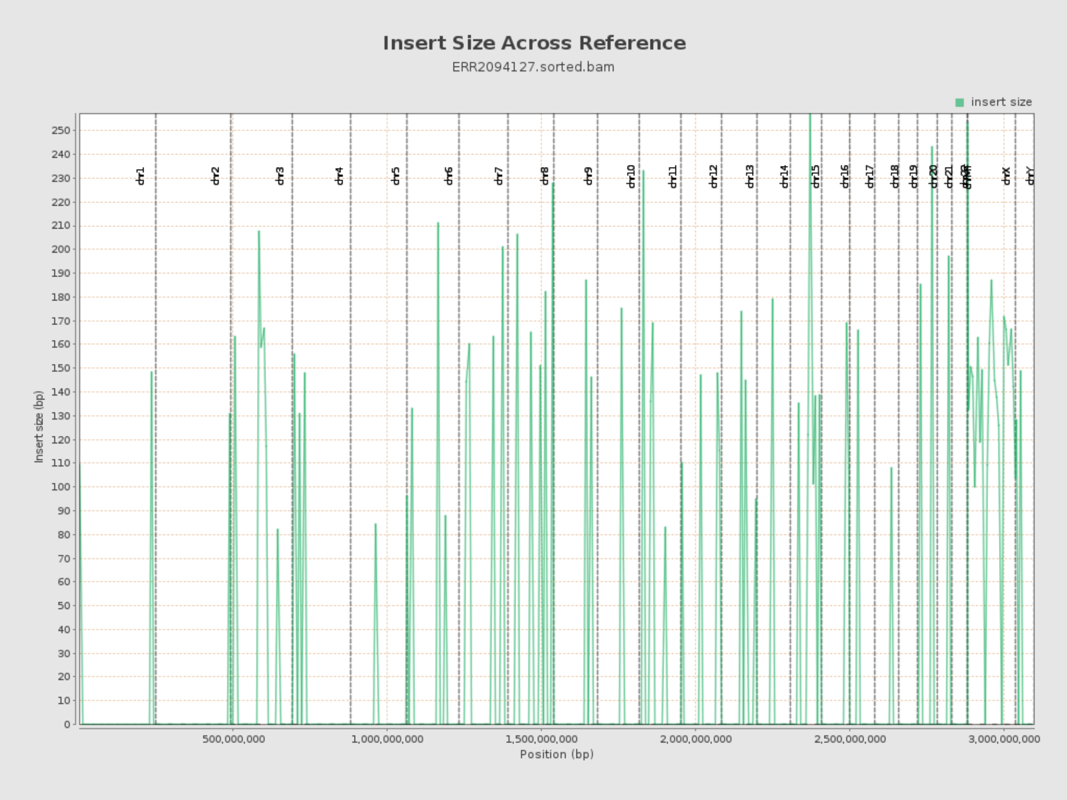
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram