Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 05:35:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094151.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_ERR2094151 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094151_1.fastq.gz ERR2094151_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 05:35:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	525,972
Mapped reads	491,601 / 93.47%
Unmapped reads	34,371 / 6.53%
Mapped paired reads	491,601 / 93.47%
Mapped reads, first in pair	246,450 / 46.86%
Mapped reads, second in pair	245,151 / 46.61%
Mapped reads, both in pair	489,380 / 93.04%
Mapped reads, singletons	2,221 / 0.42%
Secondary alignments	0
Supplementary alignments	61,096 / 11.62%
Read min/max/mean length	30 / 151 / 145.67
Duplicated reads (estimated)	526,857 / 100.17%
Duplication rate	39.6%
Clipped reads	438,464 / 83.36%

2.2. ACGT Content

Number/percentage of A's	18,747,903 / 31.22%
Number/percentage of C's	12,914,216 / 21.51%
Number/percentage of T's	15,475,748 / 25.77%
Number/percentage of G's	12,913,022 / 21.5%
Number/percentage of N's	579 / 0%

GC Percentage	43.01%

2.3. Coverage

Mean	0.0195
Standard Deviation	28.9135

2.4. Mapping Quality

Mean Mapping Quality	22.13

2.5. Insert size

Mean	262,322.11
Standard Deviation	3,513,376.02
P25/Median/P75	142 / 173 / 178

2.6. Mismatches and indels

General error rate	1.47%
Mismatches	828,531
Insertions	16,014
Mapped reads with at least one insertion	3.17%
Deletions	35,979
Mapped reads with at least one deletion	7%
Homopolymer indels	47.68%

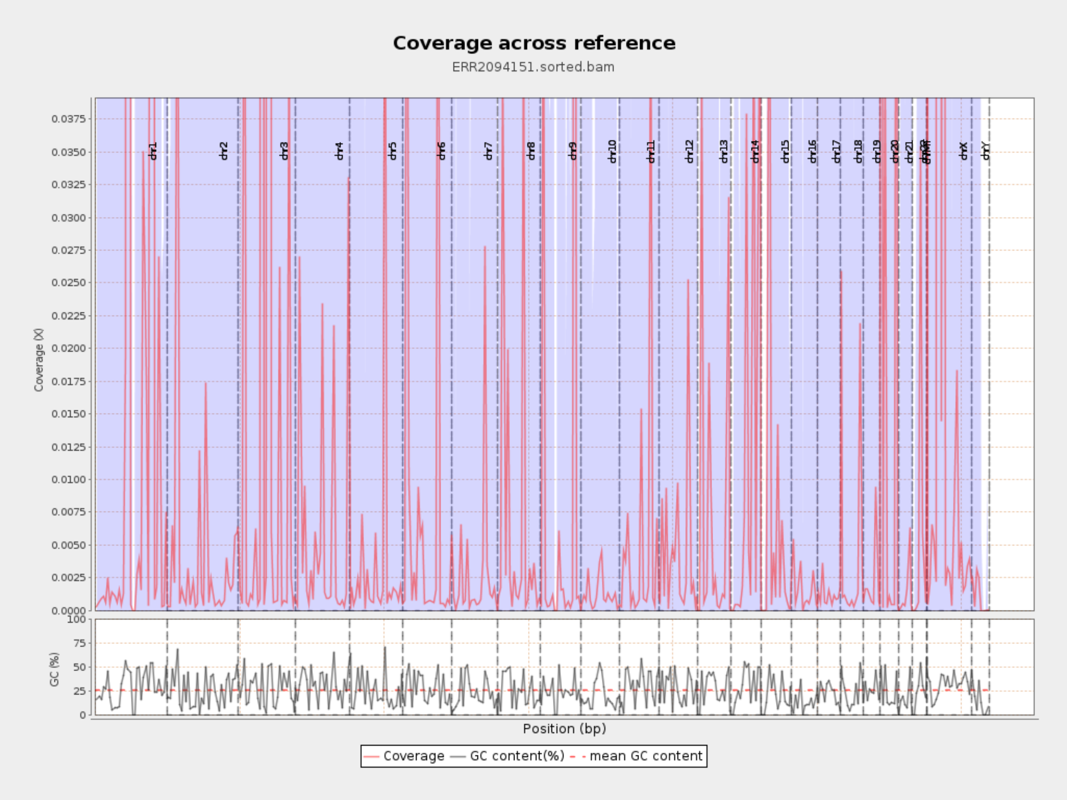
2.7. Chromosome stats

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

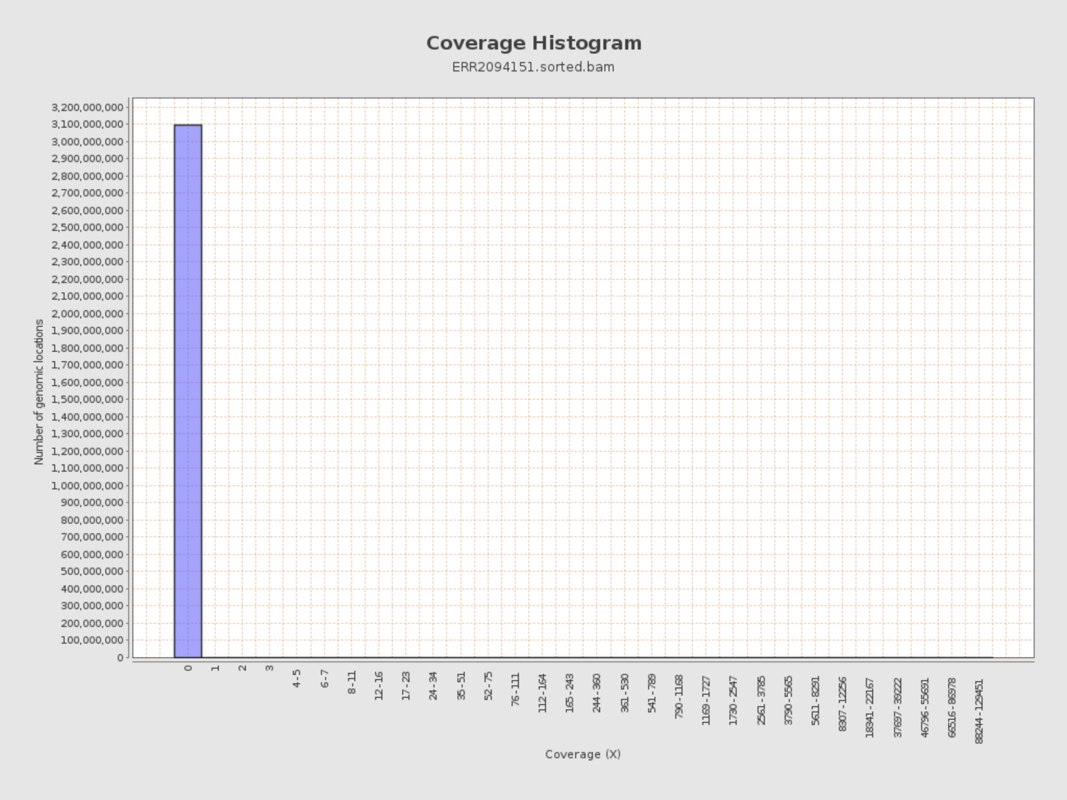
		bases	coverage	deviation
chr1	249250621	21404720	0.0859	77.3956
chr2	243199373	1070857	0.0044	1.6308
chr3	198022430	11111235	0.0561	35.8808
chr4	191154276	1112803	0.0058	1.7634
chr5	180915260	752769	0.0042	2.395
chr6	171115067	1482490	0.0087	3.5116
chr7	159138663	474164	0.003	1.4101
chr8	146364022	1037221	0.0071	2.6726
chr9	141213431	1365160	0.0097	4.1482
chr10	135534747	172861	0.0013	0.2714
chr11	135006516	753047	0.0056	1.4903
chr12	133851895	585851	0.0044	1.5835
chr13	115169878	966431	0.0084	2.9231
chr14	107349540	1401136	0.0131	3.4519
chr15	102531392	707209	0.0069	2.5706
chr16	90354753	149842	0.0017	0.5766
chr17	81195210	98285	0.0012	0.2146
chr18	78077248	325574	0.0042	1.8402
chr19	59128983	125169	0.0021	0.6087
chr20	63025520	1980081	0.0314	10.4901
chr21	48129895	72228	0.0015	0.4465
chr22	51304566	365768	0.0071	1.6987
chrMT	16571	109489	6.6073	46.0949
chrX	155270560	12632833	0.0814	72.7058

chrY	59373566	58991	0.001	0.3372

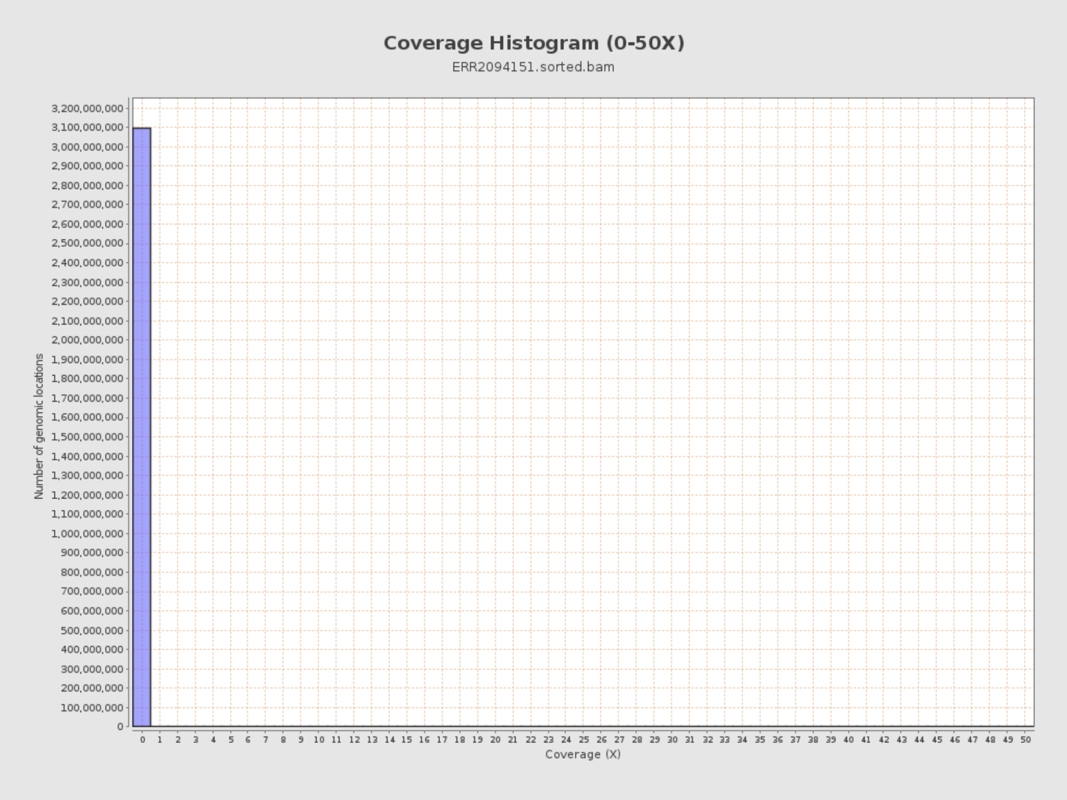
3. Results : Coverage across reference



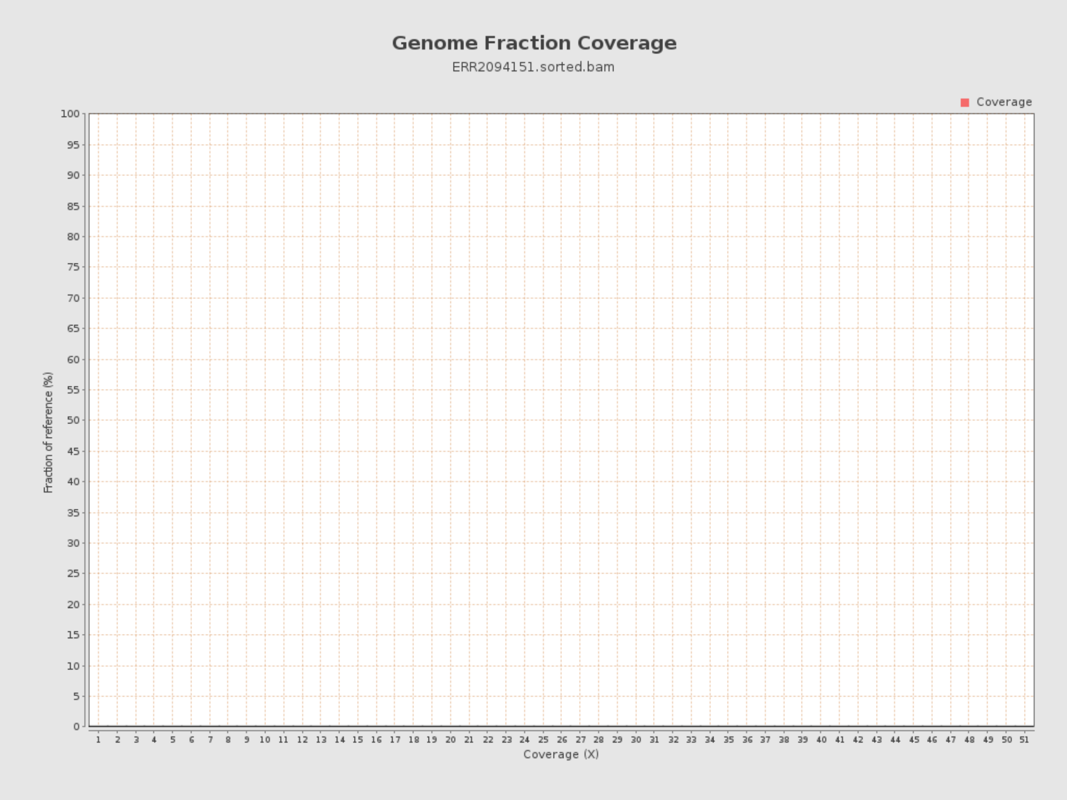
4. Results : Coverage Histogram



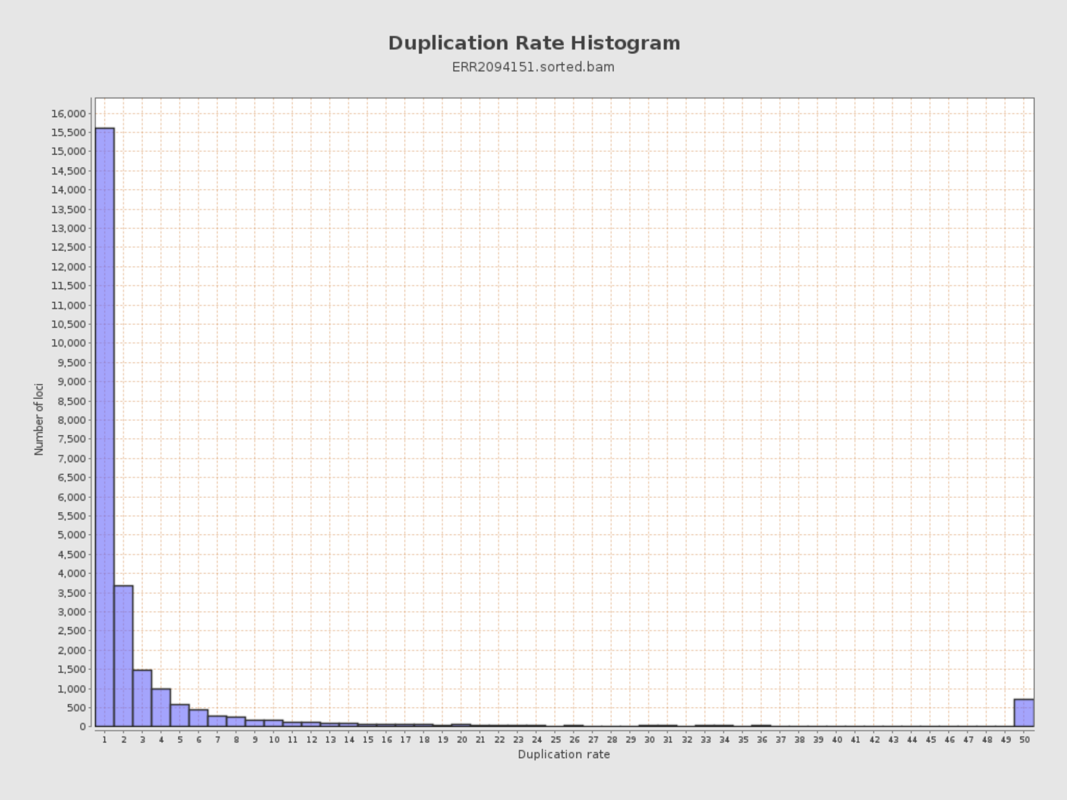
5. Results : Coverage Histogram (0-50X)



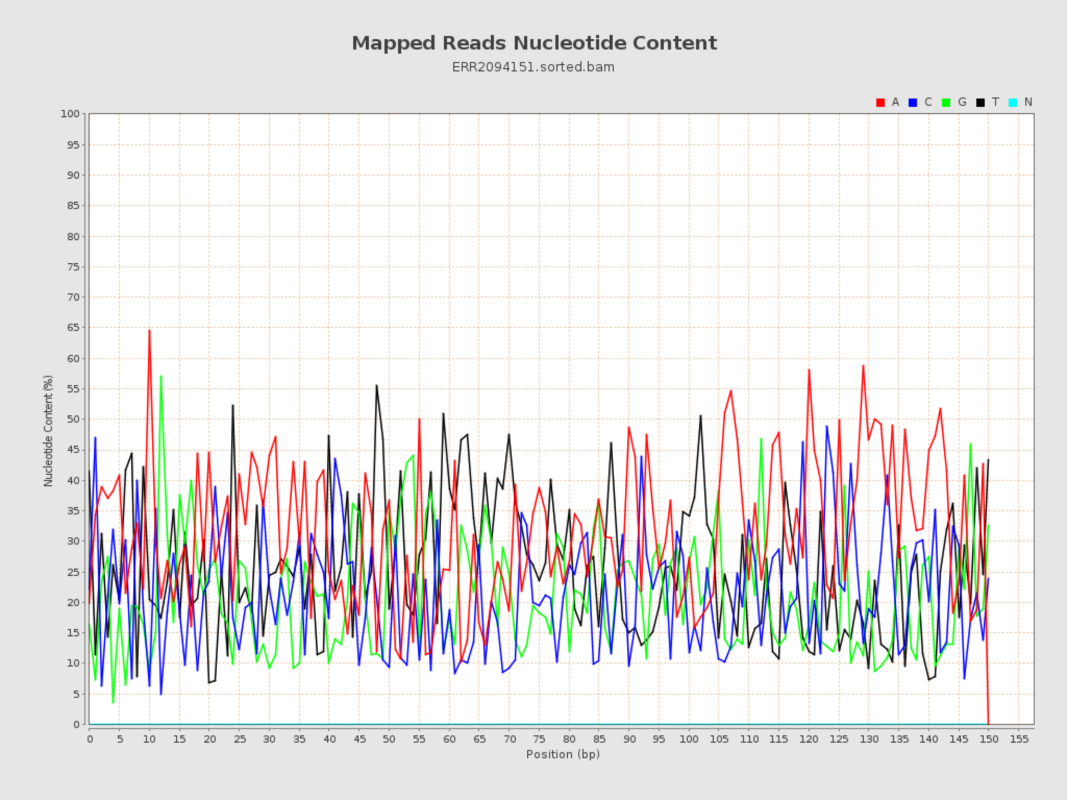
6. Results : Genome Fraction Coverage



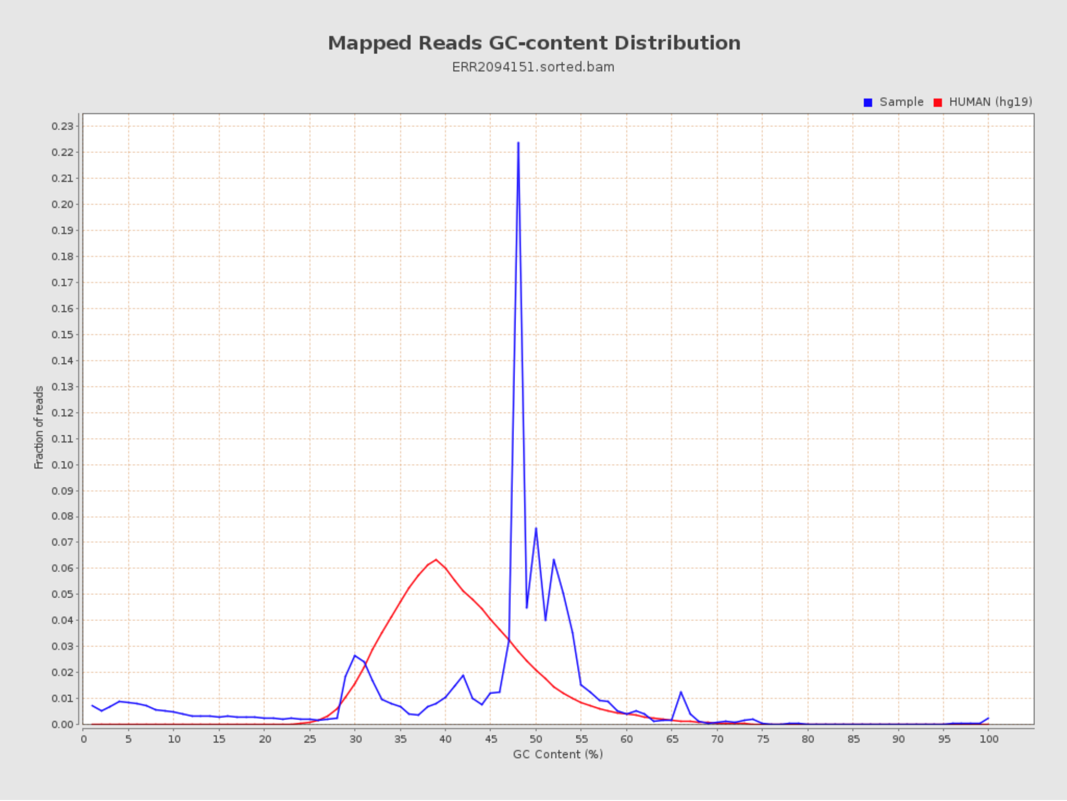
7. Results : Duplication Rate Histogram



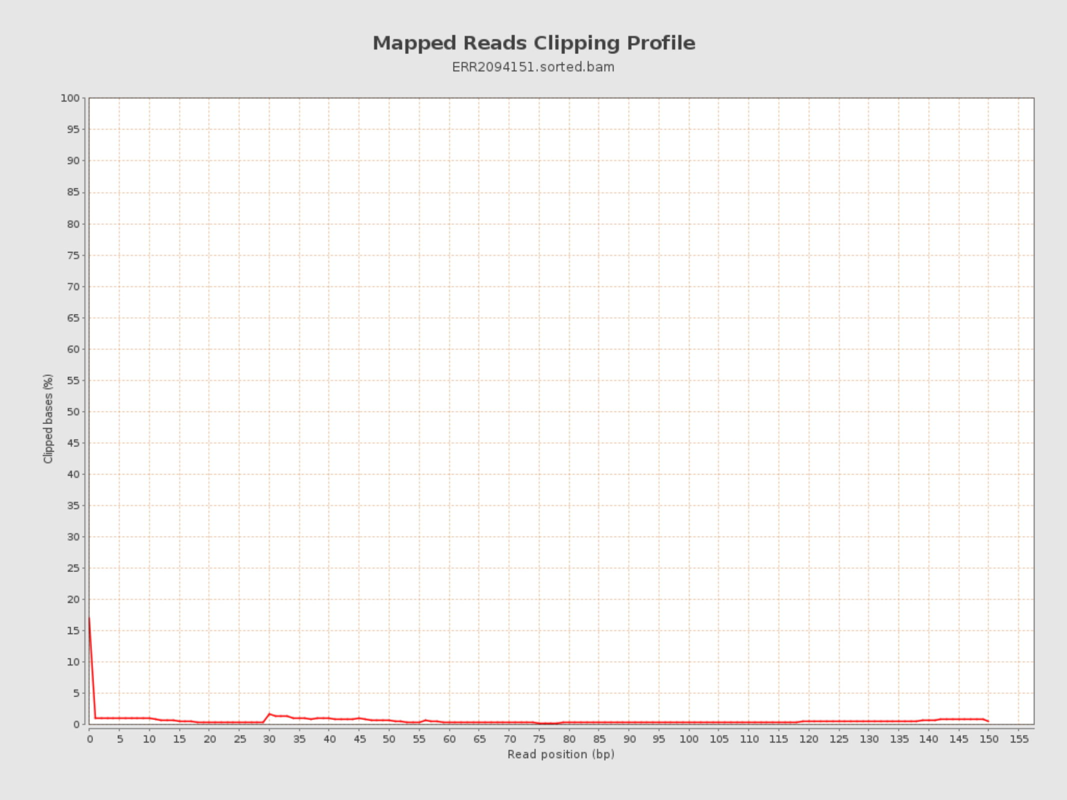
8. Results : Mapped Reads Nucleotide Content



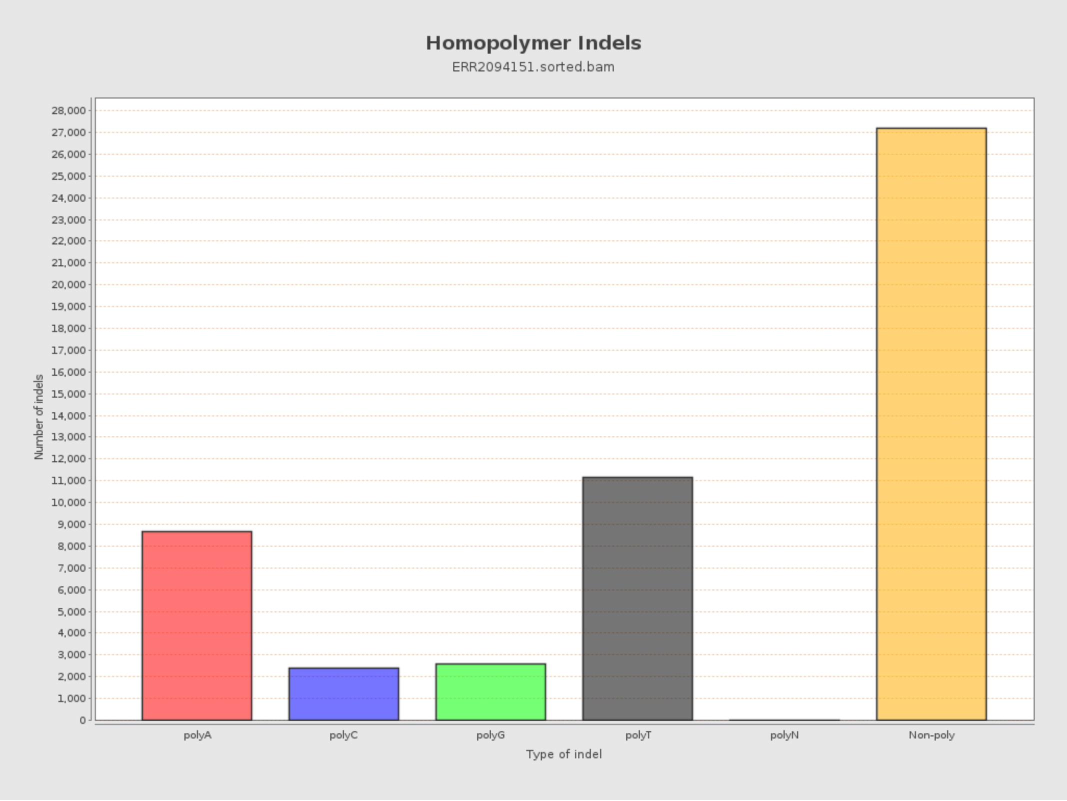
9. Results : Mapped Reads GC-content Distribution



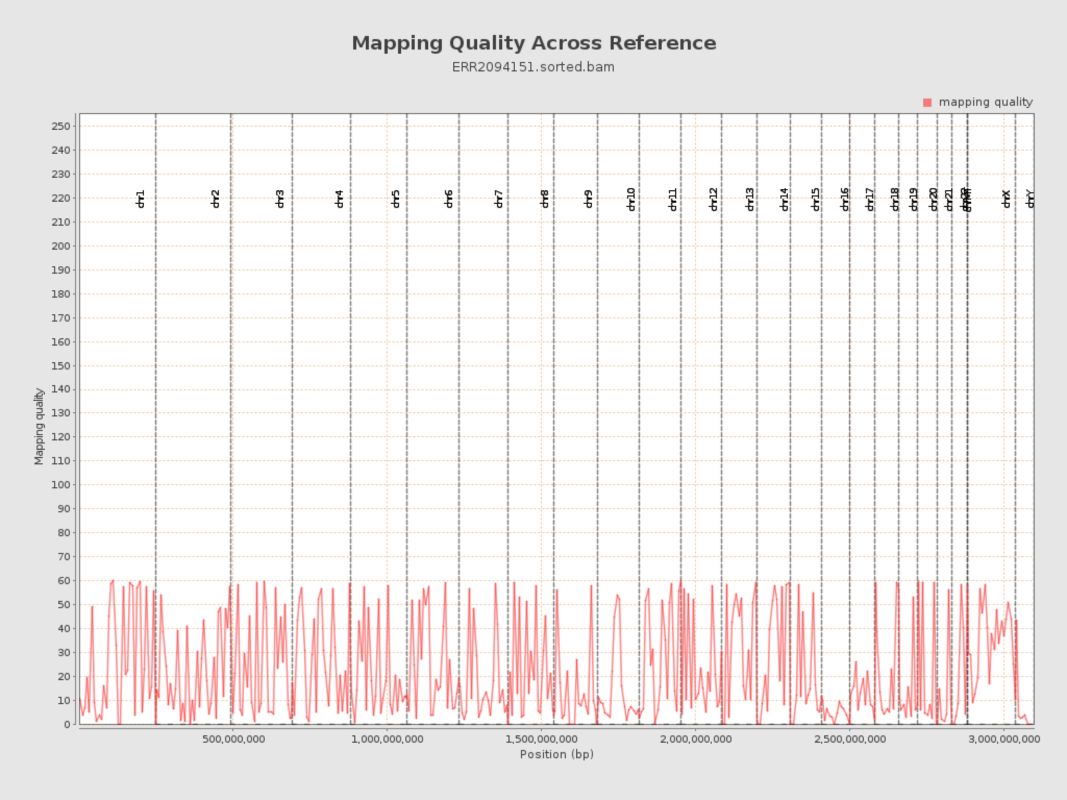
10. Results : Mapped Reads Clipping Profile



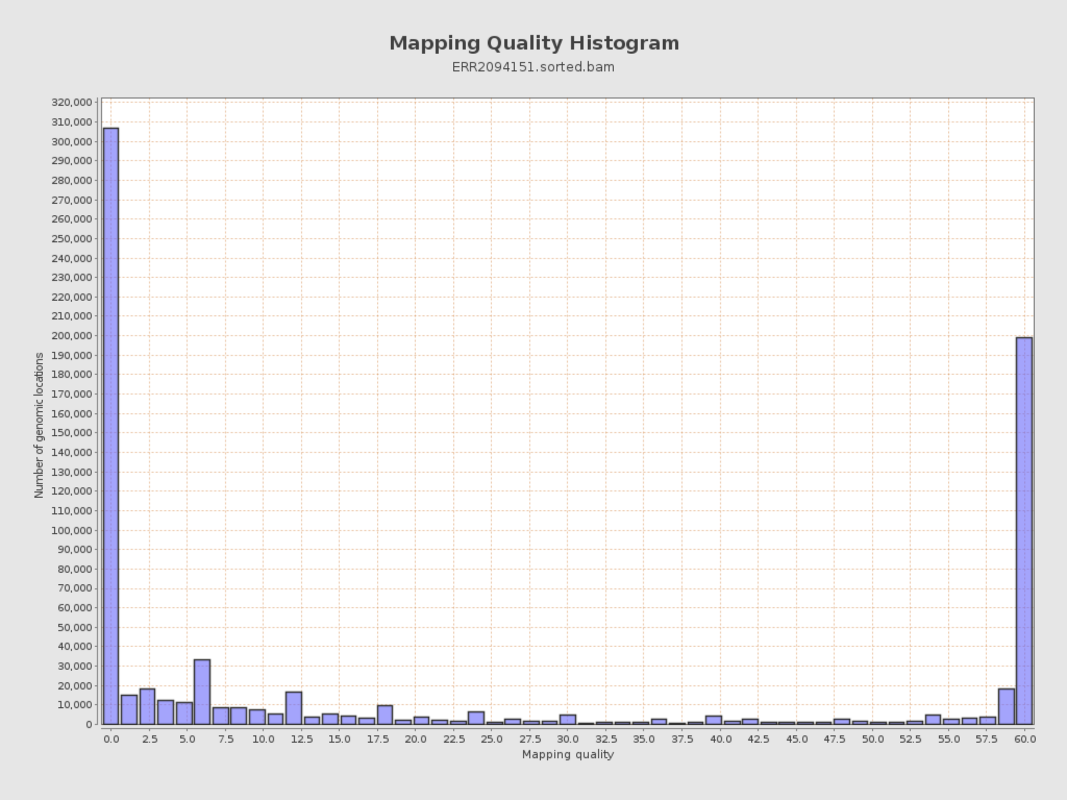
11. Results : Homopolymer Indels



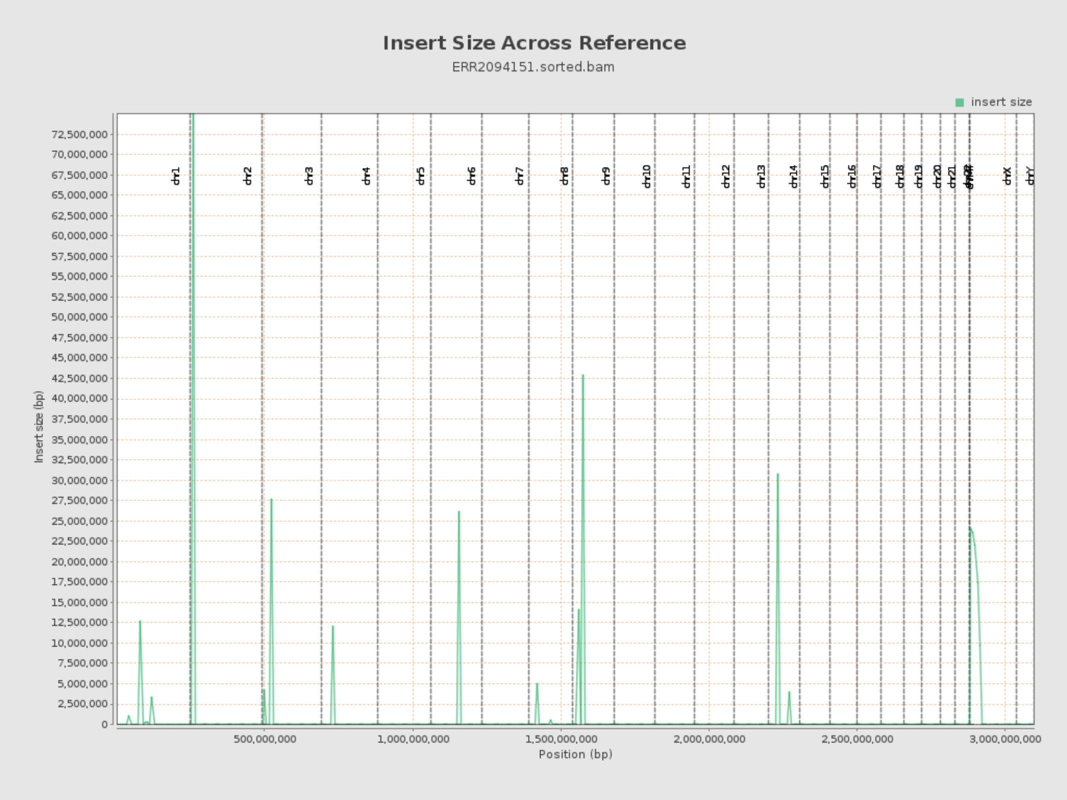
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram