Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:34:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094111.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_ERR2094111 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094111_1.fastq.gz ERR2094111_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:34:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	423,716
Mapped reads	404,799 / 95.54%
Unmapped reads	18,917 / 4.46%
Mapped paired reads	404,799 / 95.54%
Mapped reads, first in pair	203,485 / 48.02%
Mapped reads, second in pair	201,314 / 47.51%
Mapped reads, both in pair	401,396 / 94.73%
Mapped reads, singletons	3,403 / 0.8%
Secondary alignments	0
Supplementary alignments	32,341 / 7.63%
Read min/max/mean length	30 / 151 / 136.9
Duplicated reads (estimated)	393,111 / 92.78%
Duplication rate	54.4%
Clipped reads	225,173 / 53.14%

2.2. ACGT Content

Number/percentage of A's	13,858,791 / 28.86%
Number/percentage of C's	10,293,640 / 21.43%
Number/percentage of T's	12,973,339 / 27.01%
Number/percentage of G's	10,897,195 / 22.69%
Number/percentage of N's	569 / 0%

GC Percentage	44.13%

2.3. Coverage

Mean	0.0159
Standard Deviation	3.4496

2.4. Mapping Quality

Mean Mapping Quality	40.07

2.5. Insert size

Mean	1,820,800.99
Standard Deviation	11,762,390.28
P25/Median/P75	110 / 141 / 169

2.6. Mismatches and indels

General error rate	3.76%
Mismatches	1,756,417
Insertions	30,978
Mapped reads with at least one insertion	7.53%
Deletions	137,002
Mapped reads with at least one deletion	32.83%
Homopolymer indels	27.44%

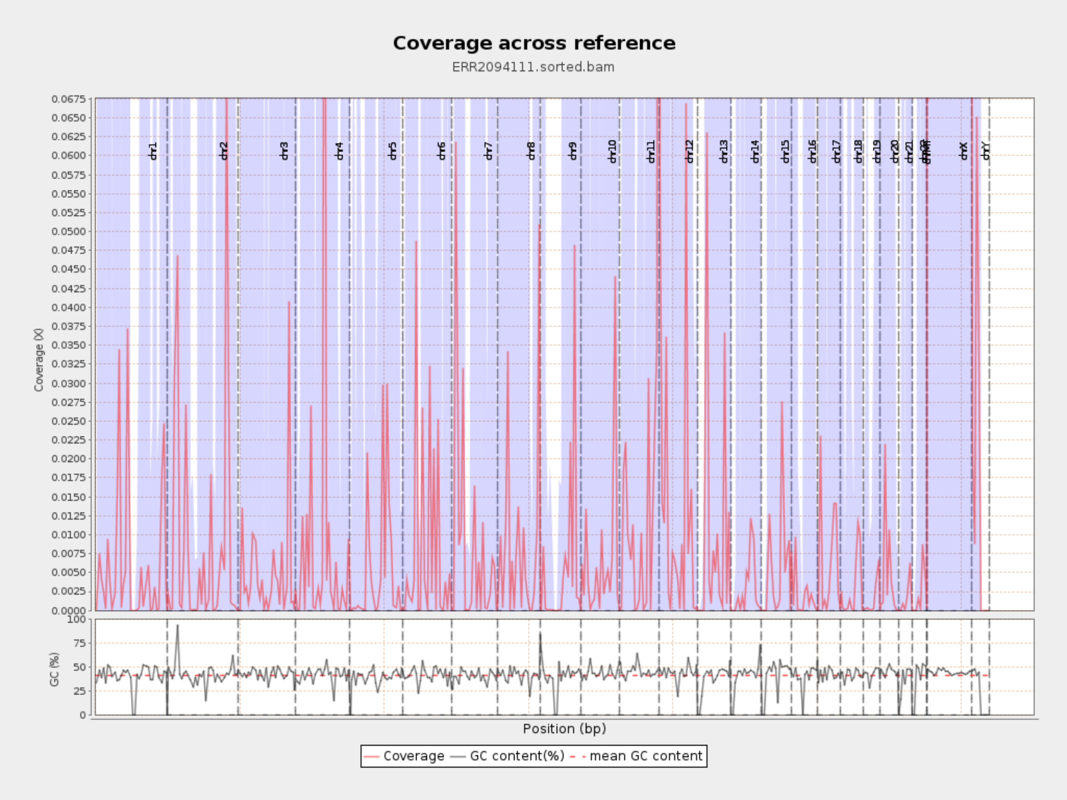
2.7. Chromosome stats

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

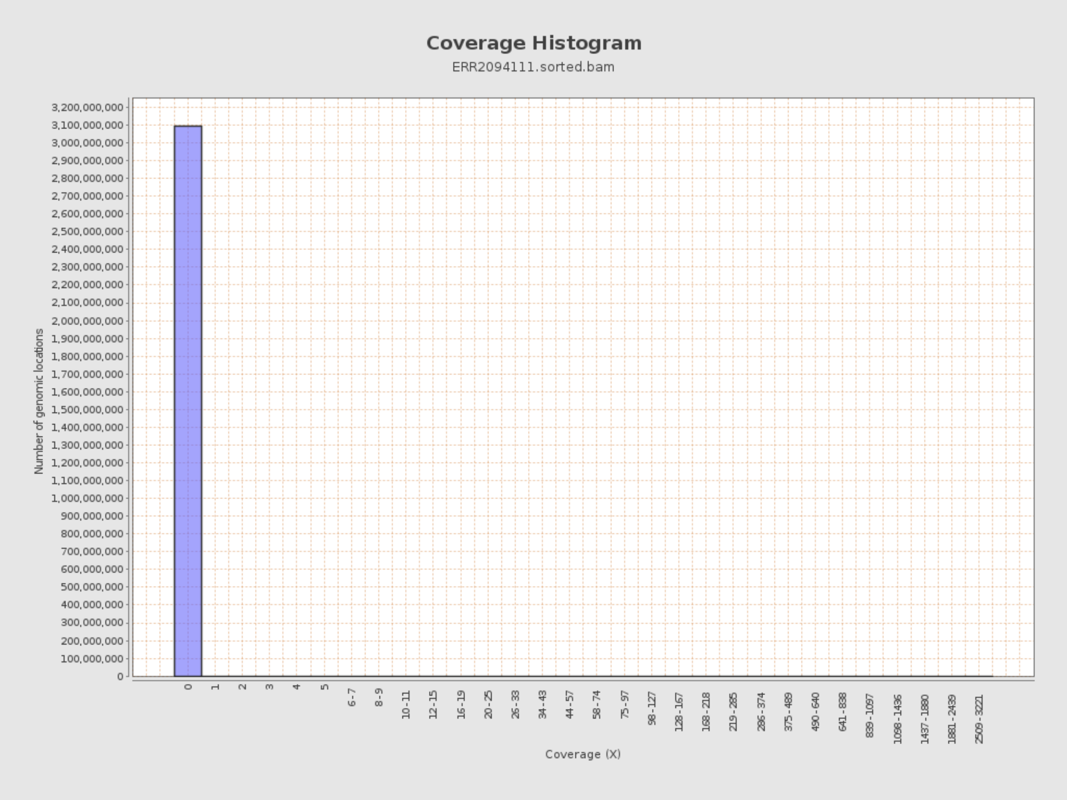
		bases	**coverage**	**deviation**
chr1	249250621	1480401	0.0059	2.3477
chr2	243199373	2177550	0.009	3.2924
chr3	198022430	994198	0.005	1.9332
chr4	191154276	1845964	0.0097	2.5414
chr5	180915260	1031420	0.0057	2.397
chr6	171115067	1409837	0.0082	3.0372
chr7	159138663	1278720	0.008	3.1441
chr8	146364022	1257818	0.0086	2.977
chr9	141213431	790962	0.0056	2.5426
chr10	135534747	859467	0.0063	2.1546
chr11	135006516	1680107	0.0124	3.4257
chr12	133851895	1813154	0.0135	3.7452
chr13	115169878	1123929	0.0098	2.4341
chr14	107349540	288106	0.0027	1.019
chr15	102531392	561929	0.0055	1.4065
chr16	90354753	198066	0.0022	0.711
chr17	81195210	516262	0.0064	1.7315
chr18	78077248	248691	0.0032	1.0329
chr19	59128983	88121	0.0015	0.5396
chr20	63025520	316702	0.005	1.7848
chr21	48129895	79715	0.0017	0.3376
chr22	51304566	110806	0.0022	0.7566
chrMT	16571	285169	17.2089	117.4251
chrX	155270560	27727431	0.1786	10.7462

chrY	59373566	933035	0.0157	3.1

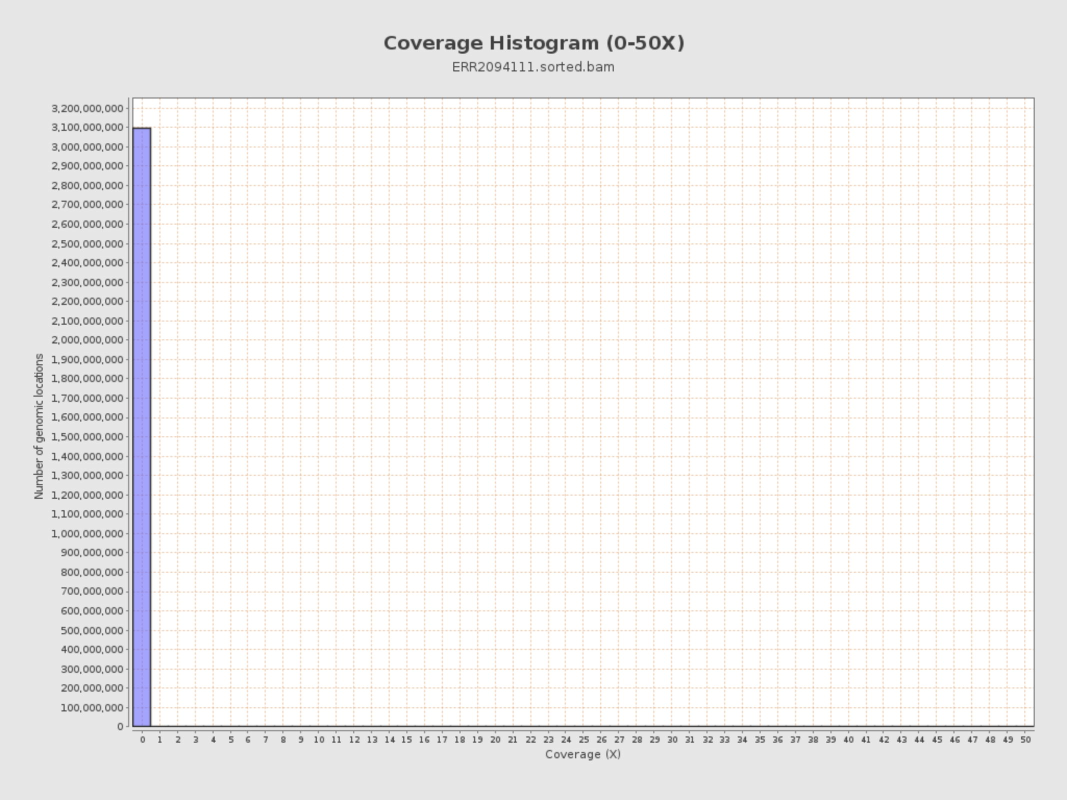
3. Results : Coverage across reference



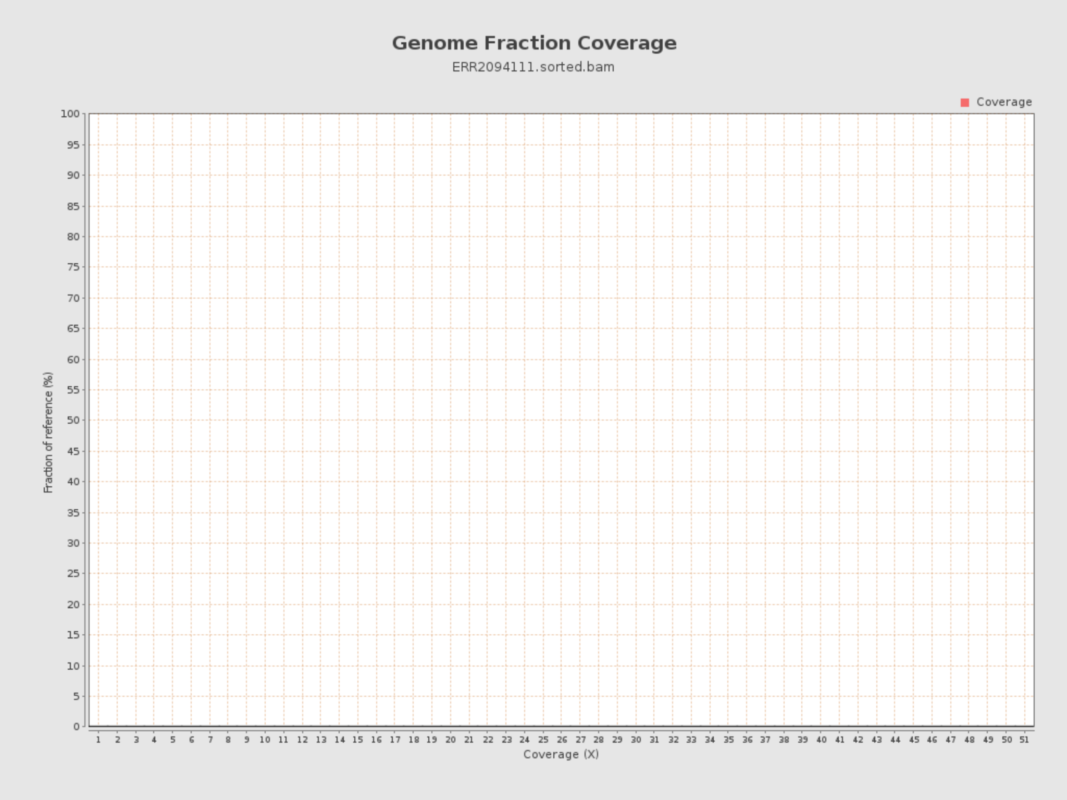
4. Results : Coverage Histogram



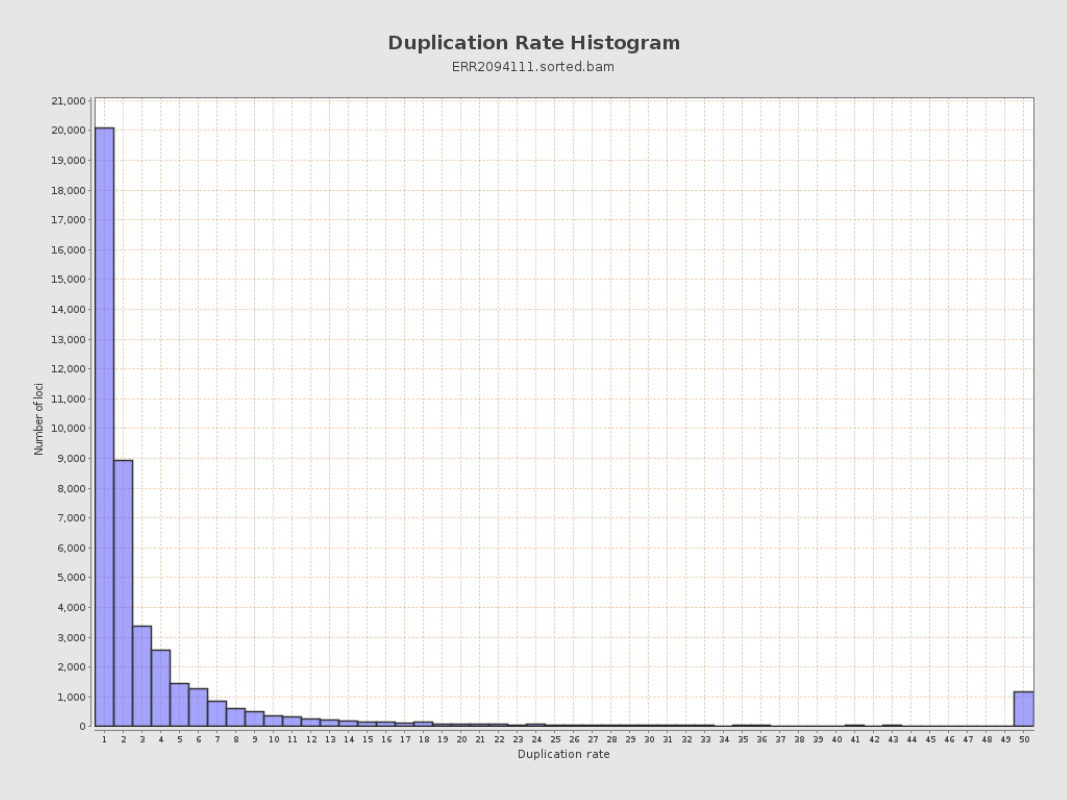
5. Results : Coverage Histogram (0-50X)



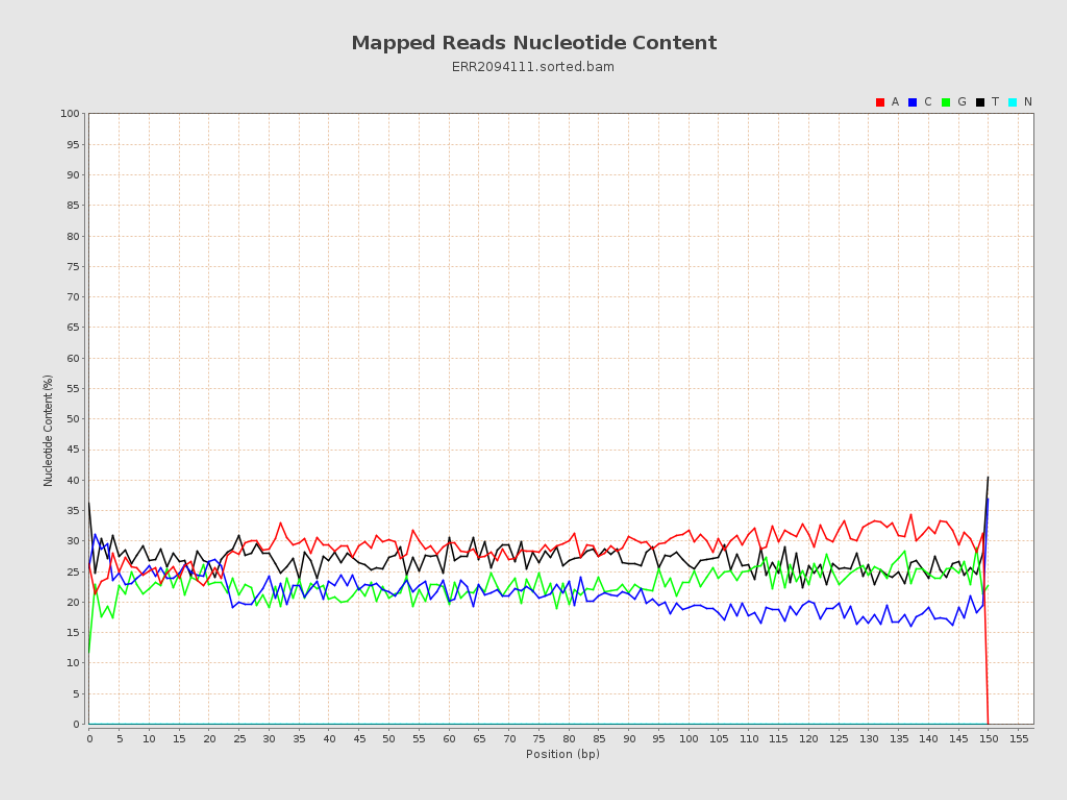
6. Results : Genome Fraction Coverage



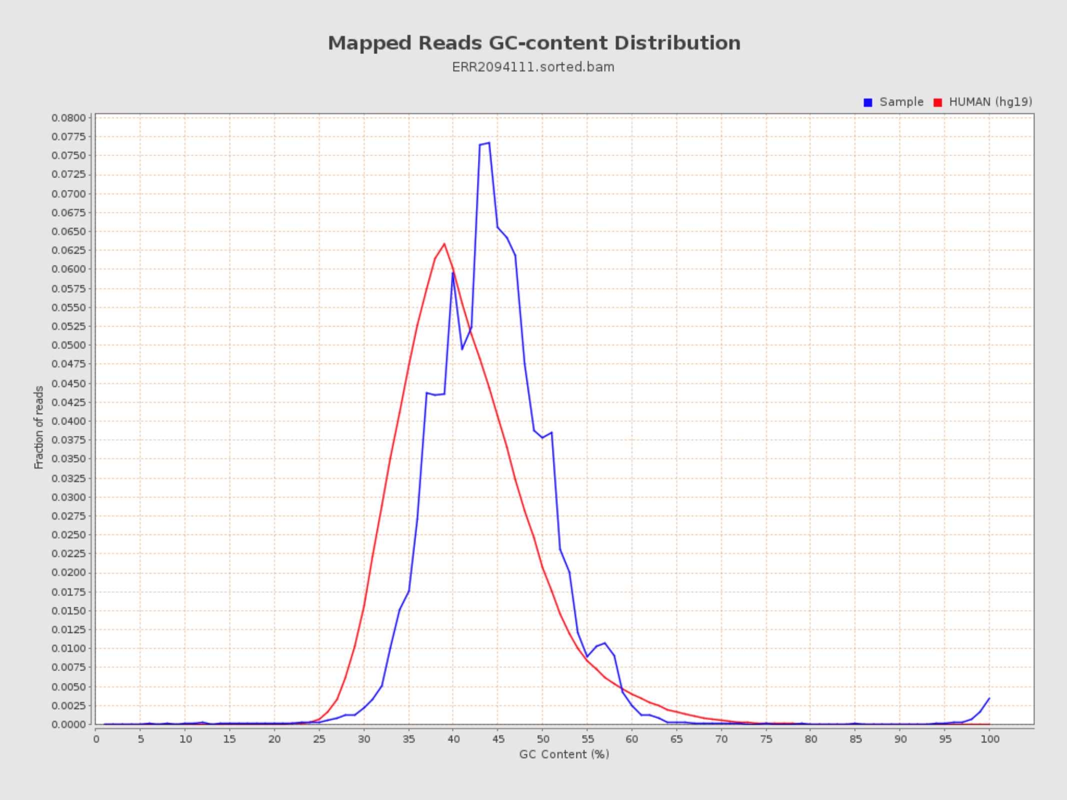
7. Results : Duplication Rate Histogram



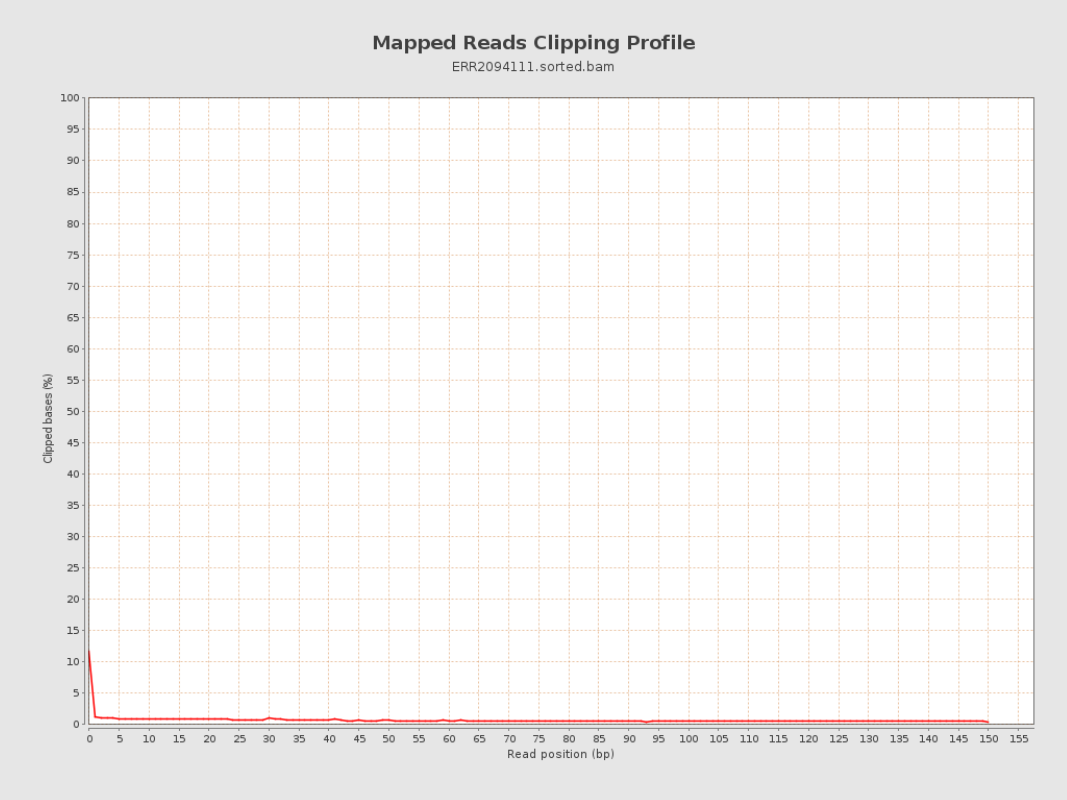
8. Results : Mapped Reads Nucleotide Content



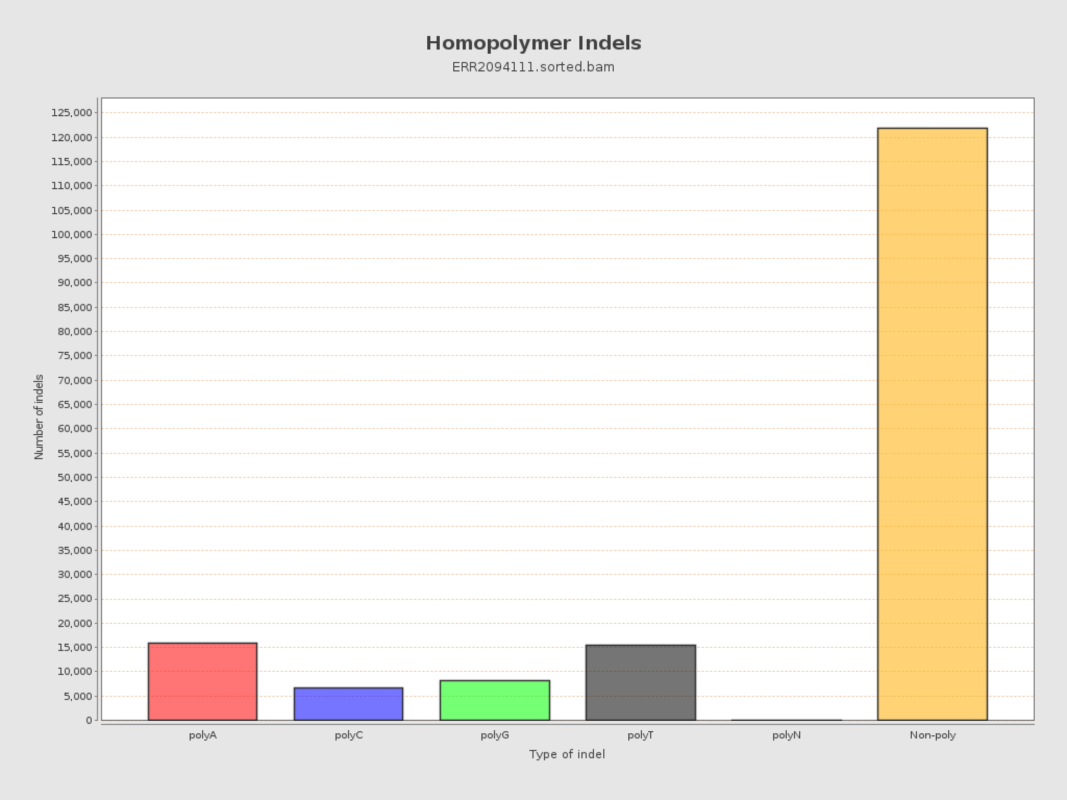
9. Results : Mapped Reads GC-content Distribution



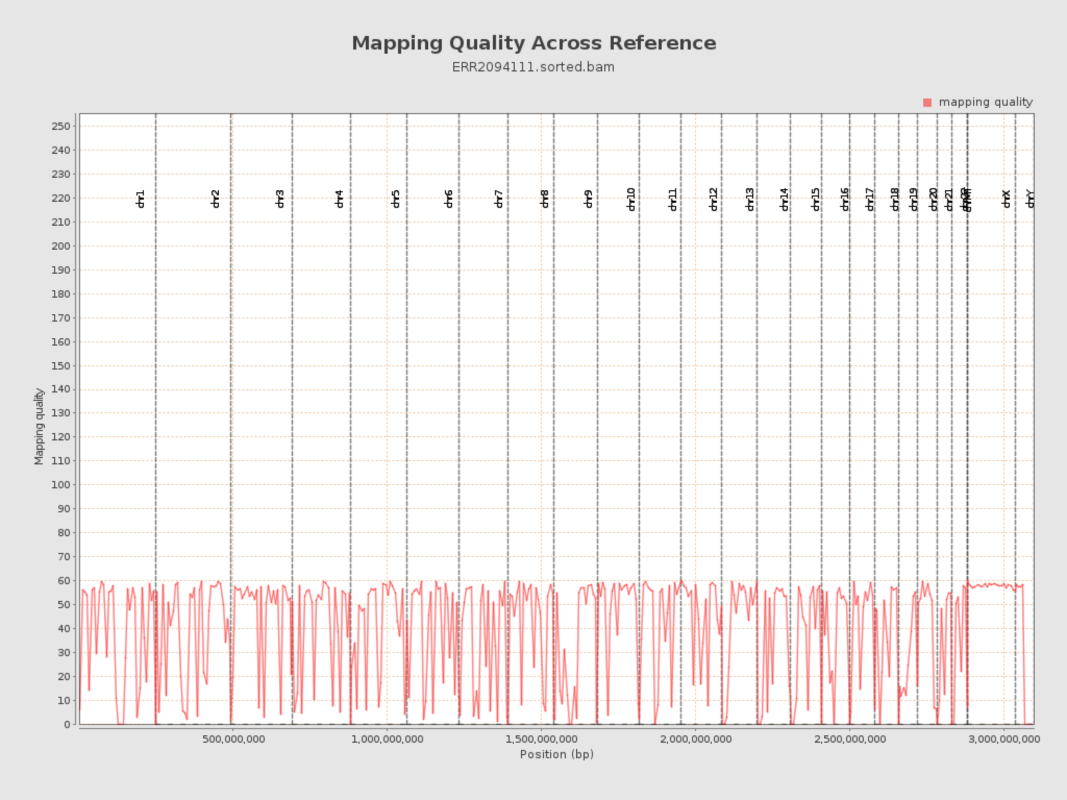
10. Results : Mapped Reads Clipping Profile



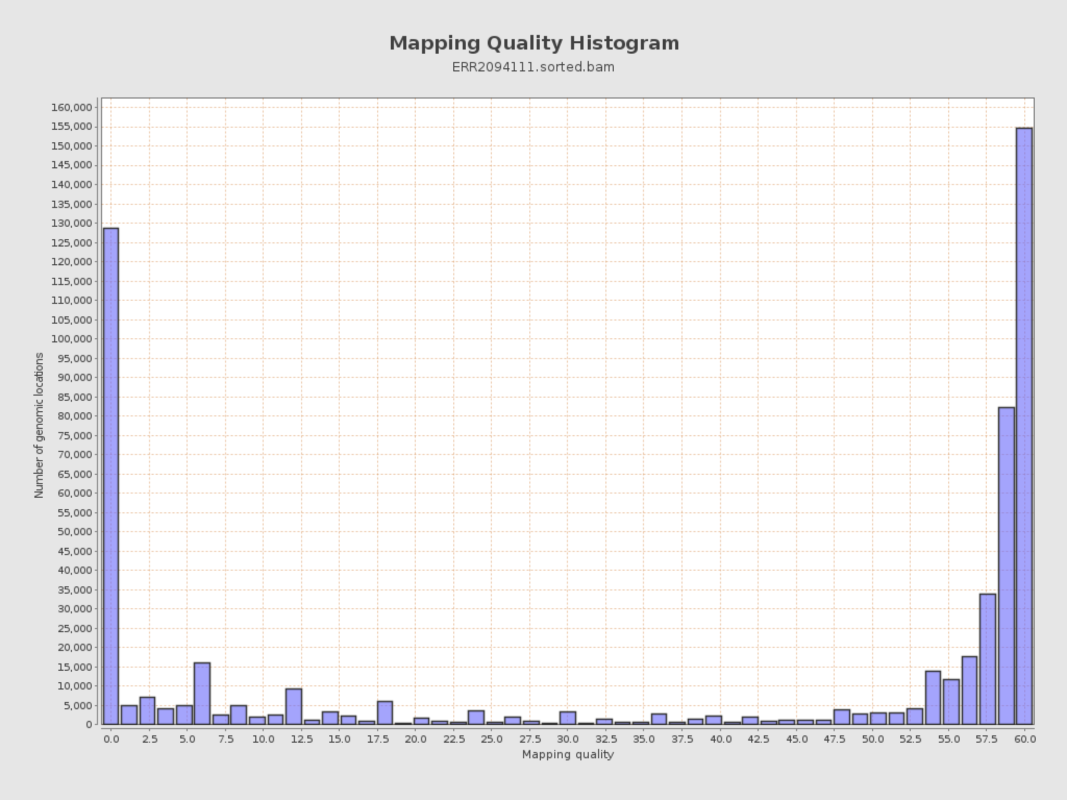
11. Results : Homopolymer Indels



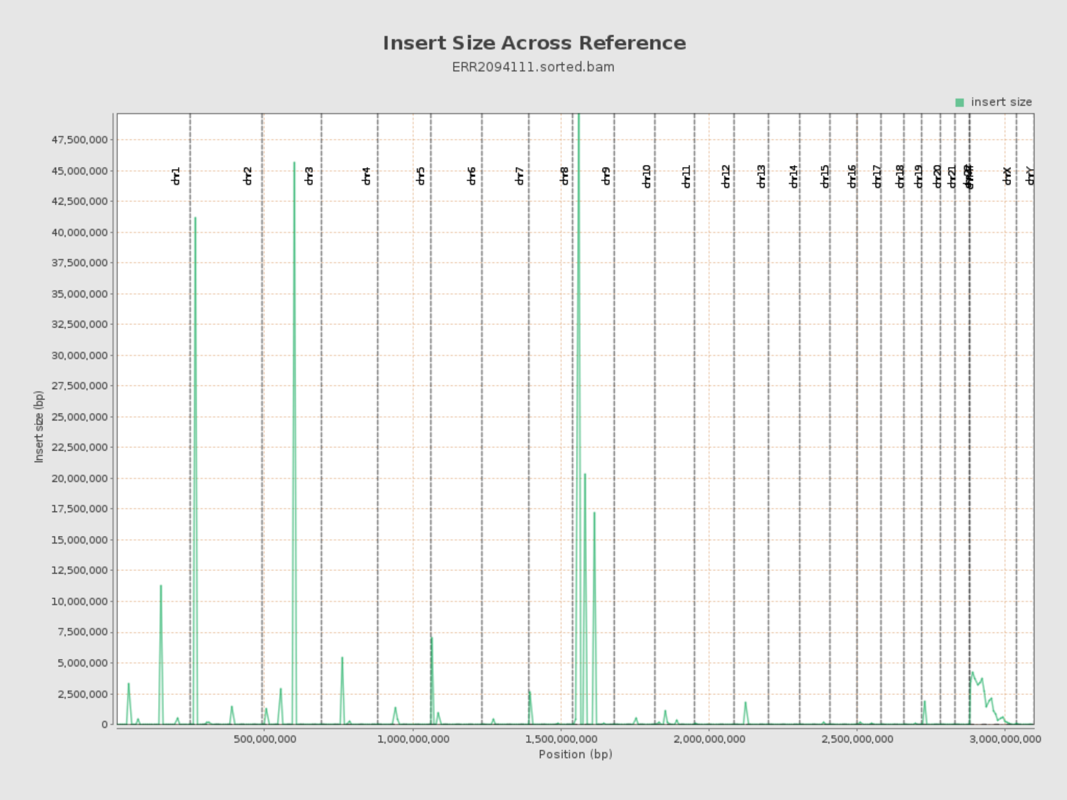
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram