Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:48:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094010.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_ERR2094010 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094010_1.fastq.gz ERR2094010_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:48:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	443,372
Mapped reads	394,946 / 89.08%
Unmapped reads	48,426 / 10.92%
Mapped paired reads	394,946 / 89.08%
Mapped reads, first in pair	197,993 / 44.66%
Mapped reads, second in pair	196,953 / 44.42%
Mapped reads, both in pair	392,534 / 88.53%
Mapped reads, singletons	2,412 / 0.54%
Secondary alignments	0
Supplementary alignments	2,772 / 0.63%
Read min/max/mean length	30 / 151 / 135.61
Duplicated reads (estimated)	387,308 / 87.36%
Duplication rate	46.24%
Clipped reads	108,806 / 24.54%

2.2. ACGT Content

Number/percentage of A's	15,057,441 / 28.07%
Number/percentage of C's	11,773,954 / 21.95%
Number/percentage of T's	14,642,142 / 27.3%
Number/percentage of G's	12,159,266 / 22.67%
Number/percentage of N's	601 / 0%

GC Percentage	44.62%

2.3. Coverage

Mean	0.0176
Standard Deviation	18.5171

2.4. Mapping Quality

Mean Mapping Quality	33.38

2.5. Insert size

Mean	54,297.9
Standard Deviation	2,164,567.64
P25/Median/P75	152 / 196 / 217

2.6. Mismatches and indels

General error rate	3.24%
Mismatches	1,731,301
Insertions	12,898
Mapped reads with at least one insertion	3.17%
Deletions	133,907
Mapped reads with at least one deletion	32.42%
Homopolymer indels	28.57%

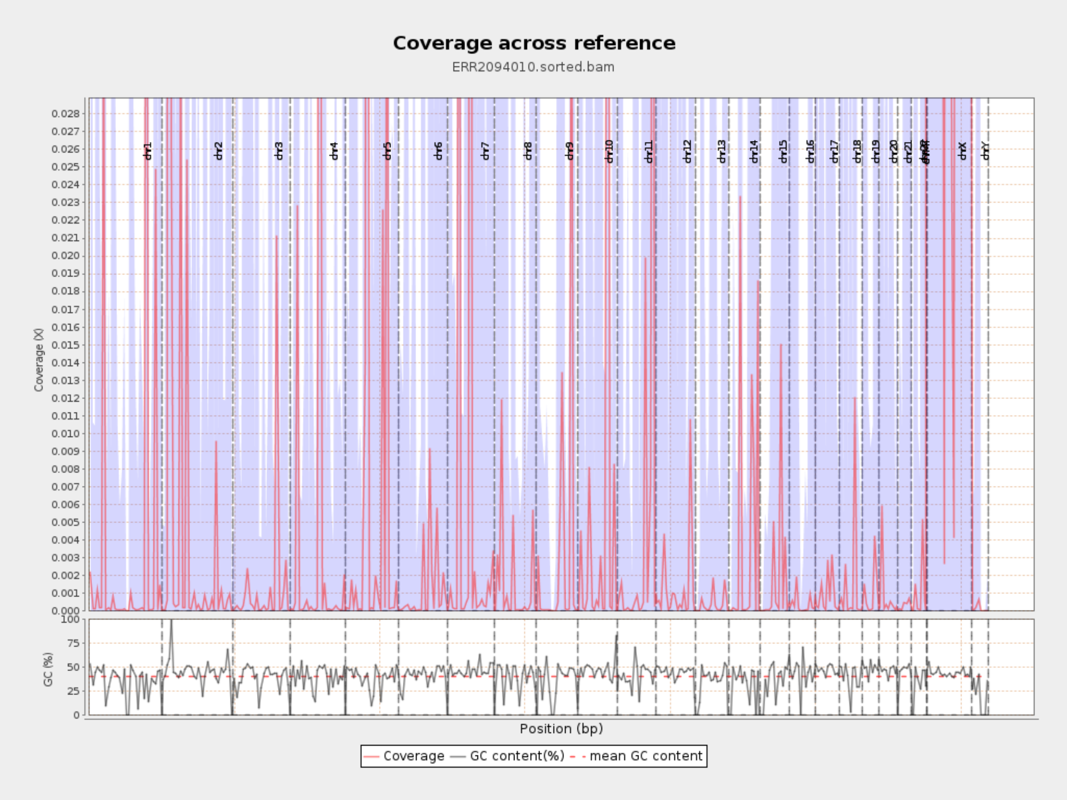
2.7. Chromosome stats

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

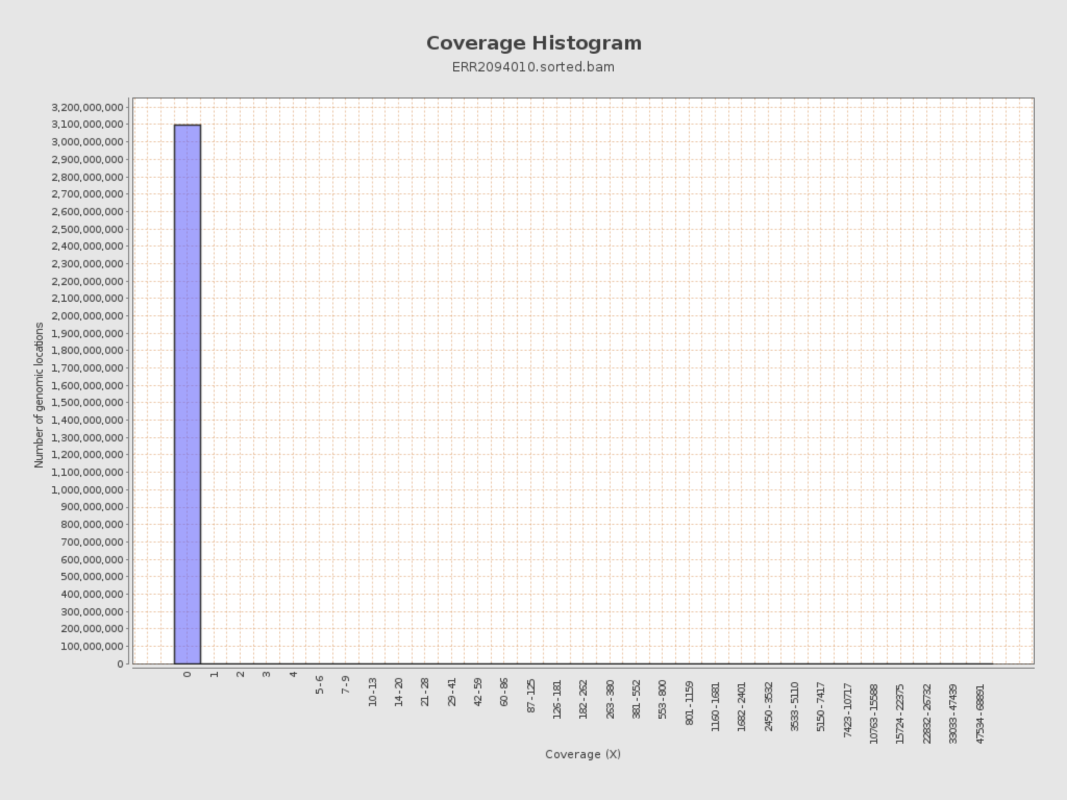
		bases	coverage	deviation
chr1	249250621	1016743	0.0041	2.9381
chr2	243199373	4273678	0.0176	16.657
chr3	198022430	255038	0.0013	1.0605
chr4	191154276	824025	0.0043	2.1381
chr5	180915260	1535225	0.0085	5.7348
chr6	171115067	209951	0.0012	0.5708
chr7	159138663	1341297	0.0084	6.5519
chr8	146364022	227434	0.0016	0.5855
chr9	141213431	497945	0.0035	2.0799
chr10	135534747	780653	0.0058	4.1039
chr11	135006516	788750	0.0058	3.5948
chr12	133851895	170282	0.0013	0.5874
chr13	115169878	48230	0.0004	0.1574
chr14	107349540	499043	0.0046	1.7441
chr15	102531392	197418	0.0019	0.8243
chr16	90354753	32999	0.0004	0.1299
chr17	81195210	70440	0.0009	0.2972
chr18	78077248	123536	0.0016	0.8258
chr19	59128983	57192	0.001	0.2881
chr20	63025520	57562	0.0009	0.498
chr21	48129895	14613	0.0003	0.0497
chr22	51304566	56470	0.0011	0.2678
chrMT	16571	21406656	1,291.8144	6,955.2156
chrX	155270560	19991038	0.1287	30.394

chrY	59373566	6833	0.0001	0.061

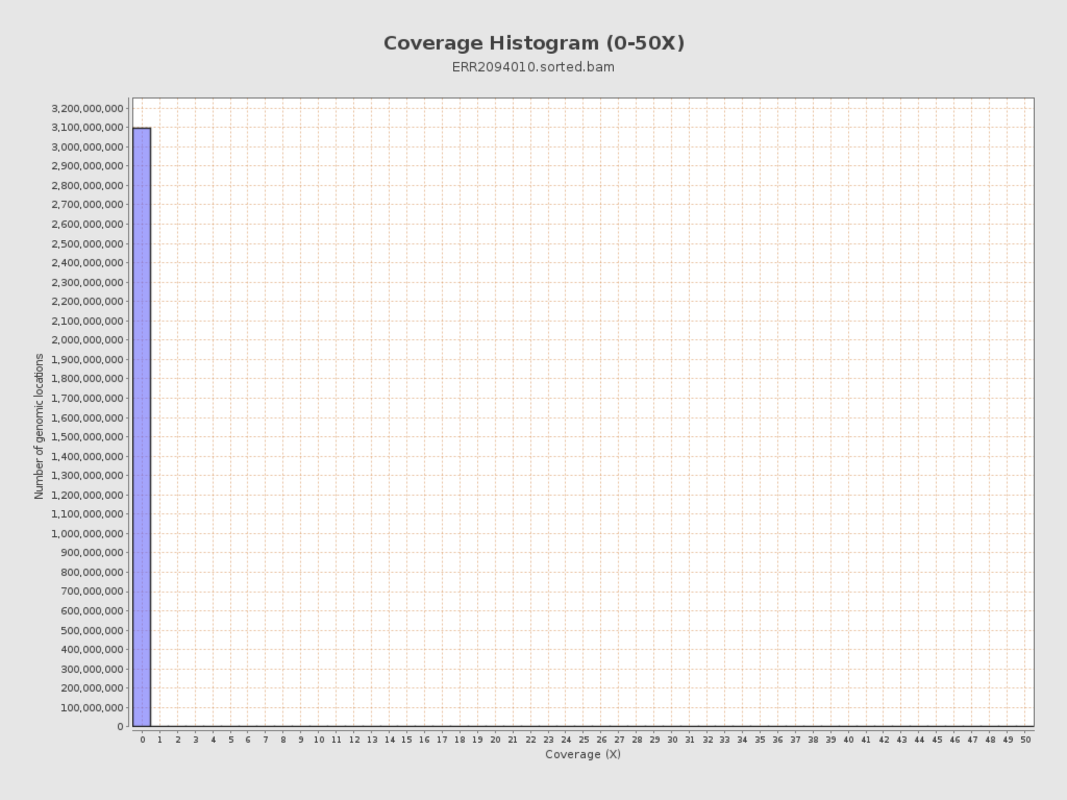
3. Results : Coverage across reference



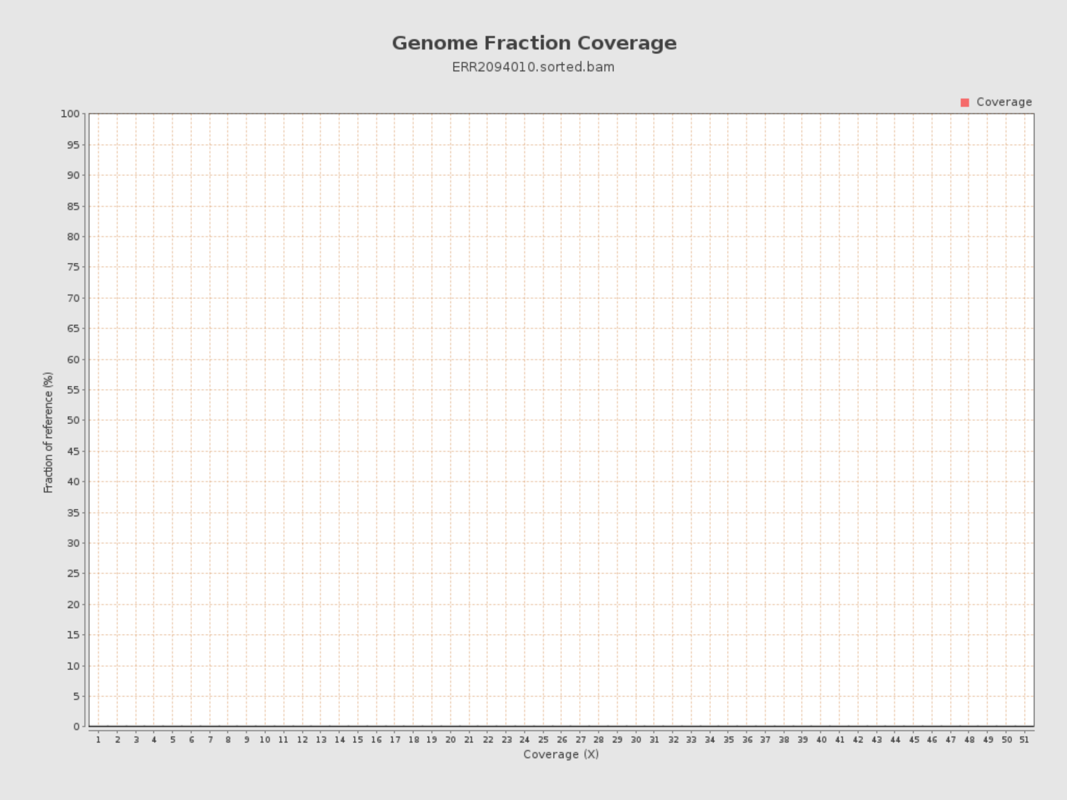
4. Results : Coverage Histogram



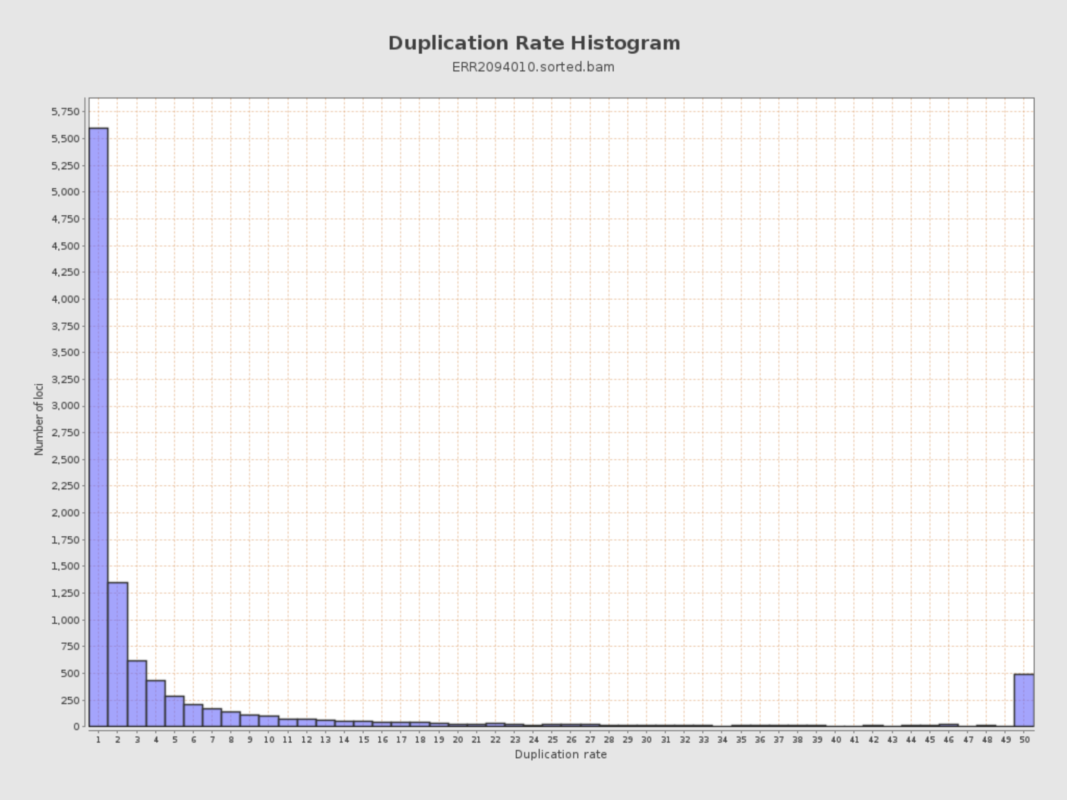
5. Results : Coverage Histogram (0-50X)



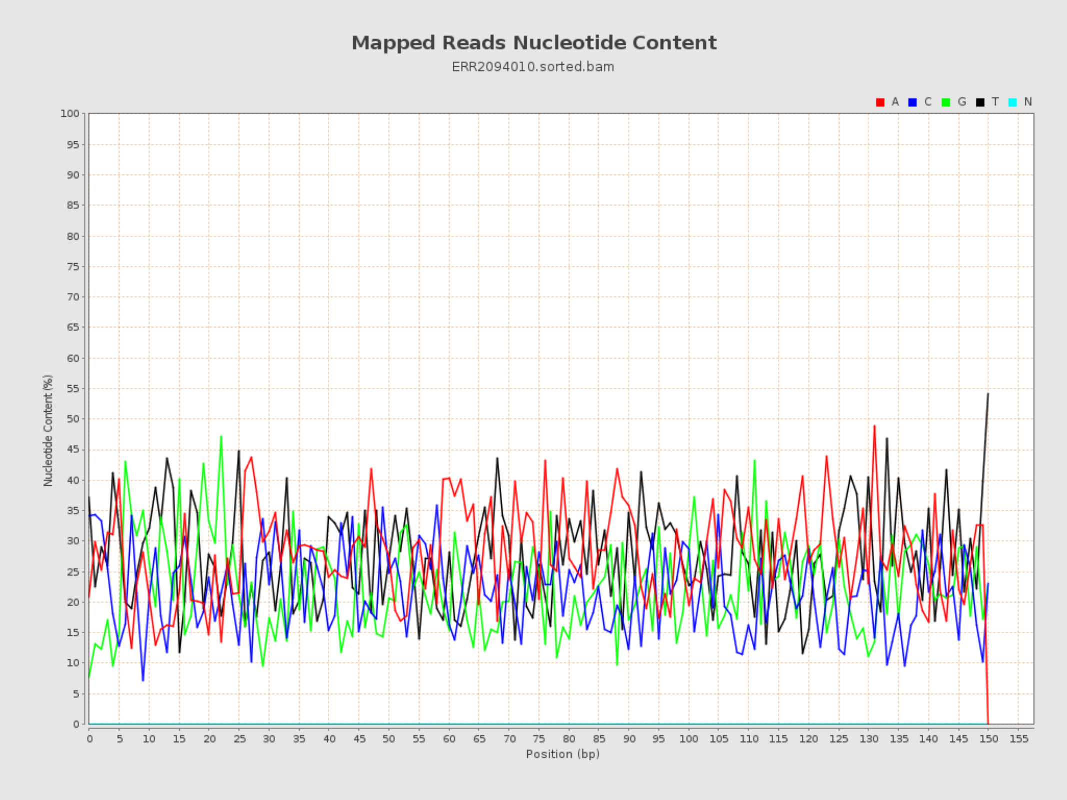
6. Results : Genome Fraction Coverage



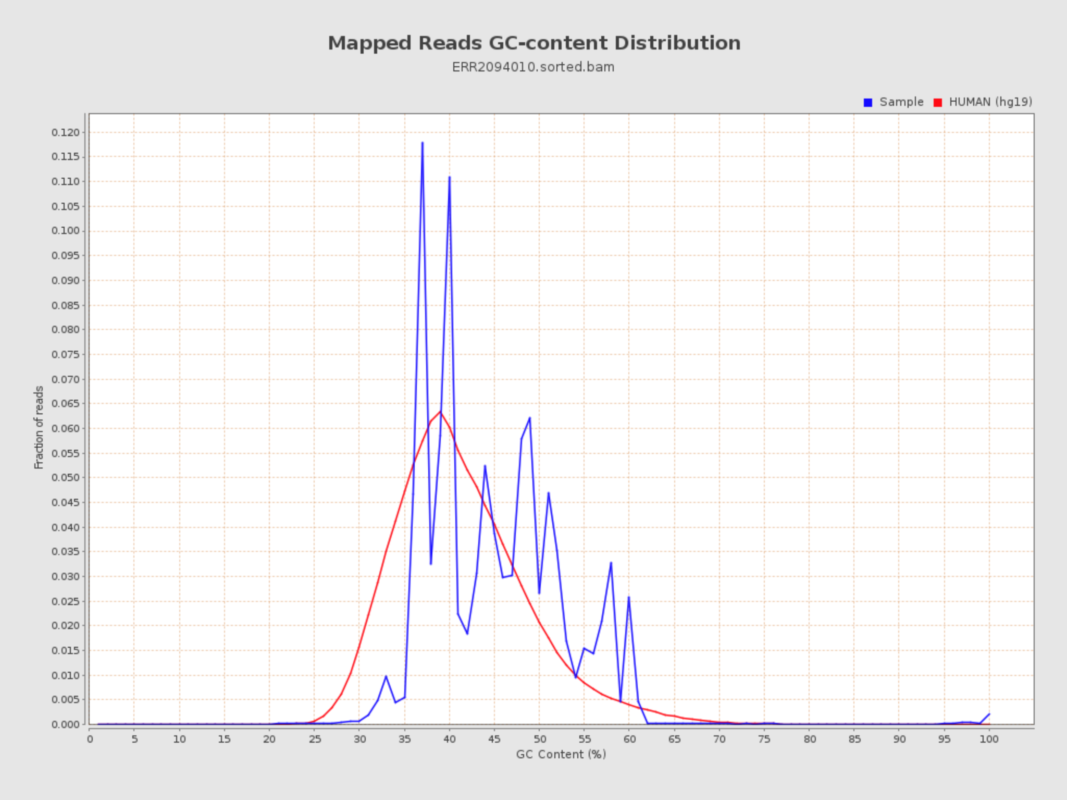
7. Results : Duplication Rate Histogram



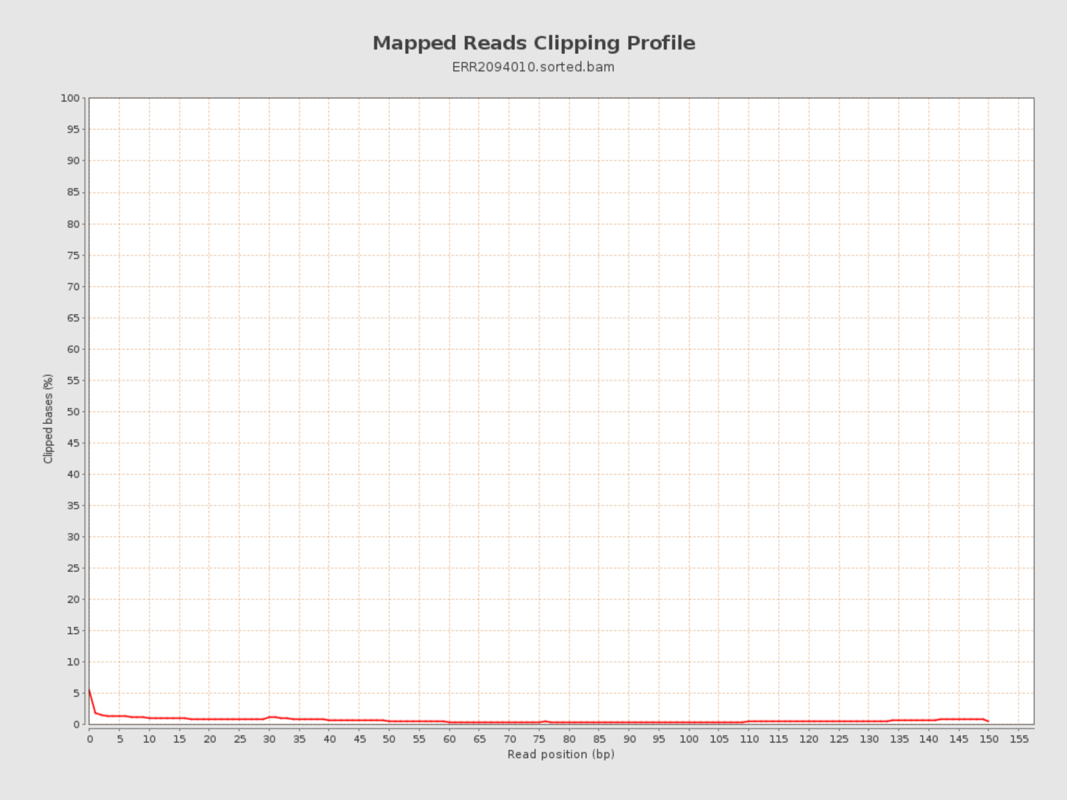
8. Results : Mapped Reads Nucleotide Content



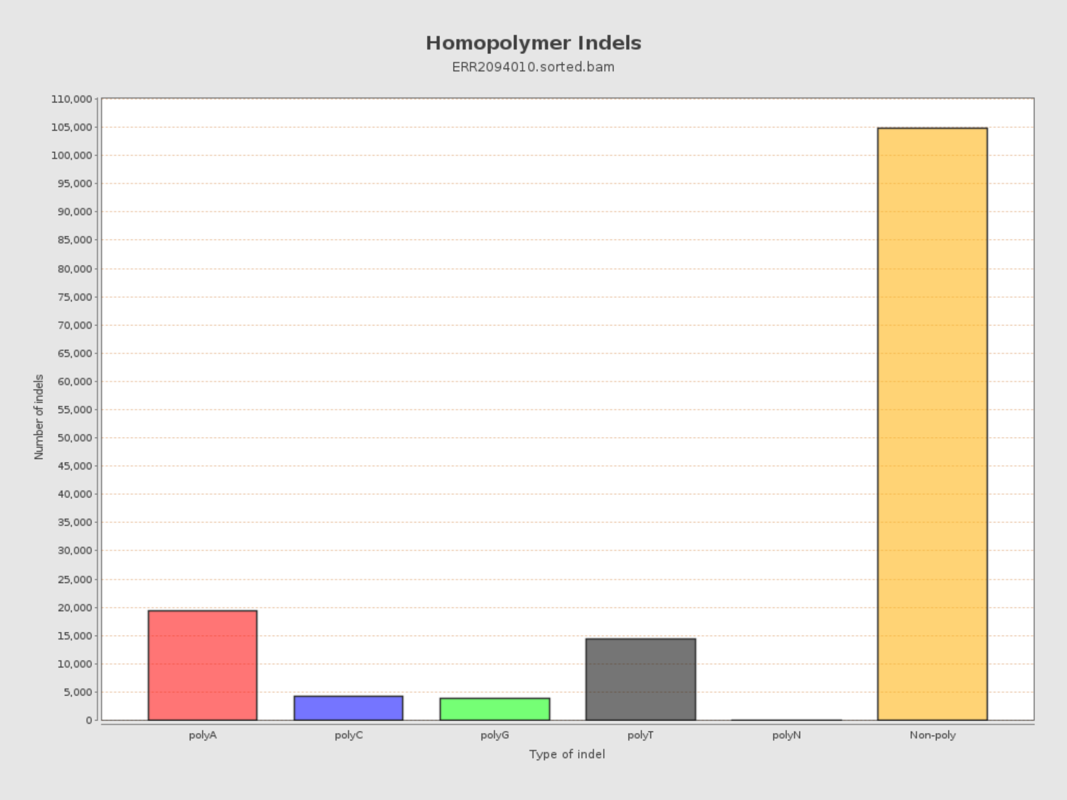
9. Results : Mapped Reads GC-content Distribution



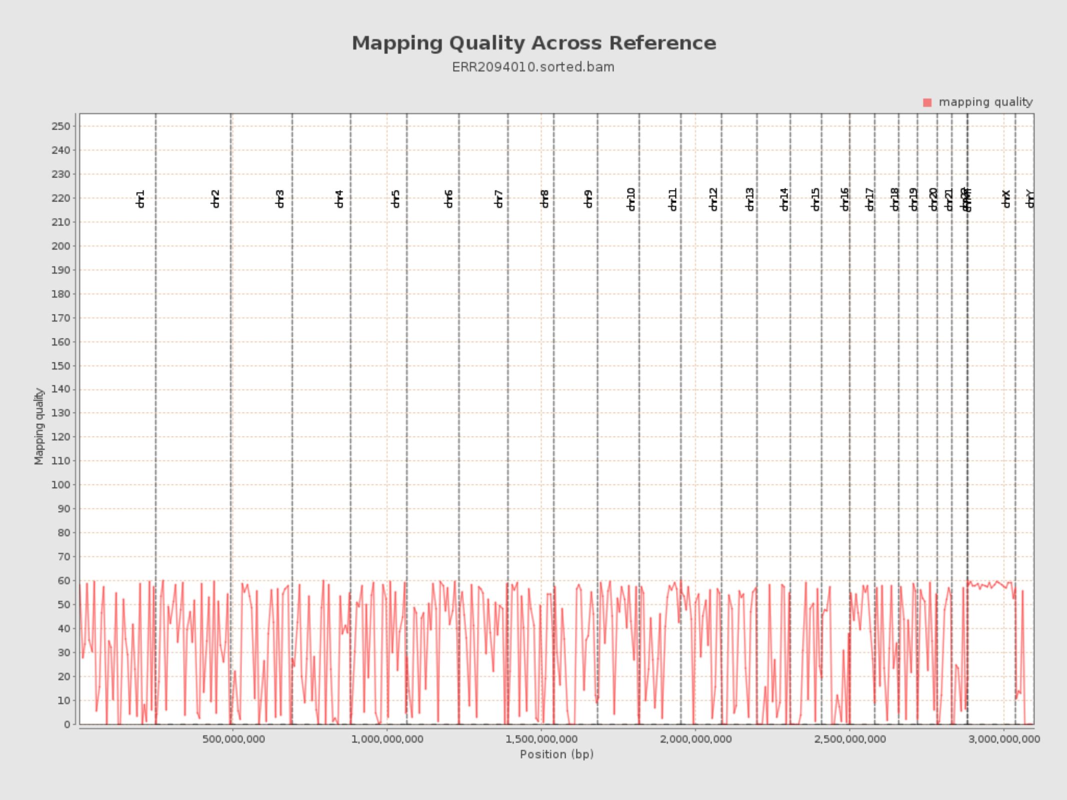
10. Results : Mapped Reads Clipping Profile



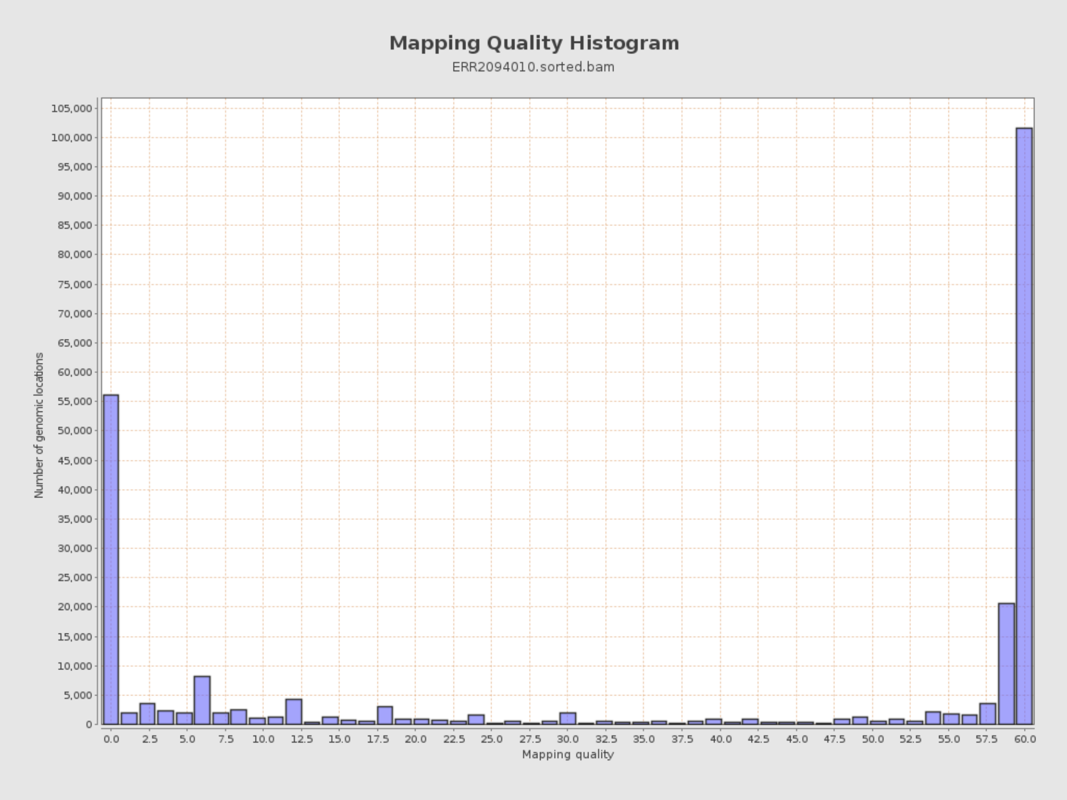
11. Results : Homopolymer Indels



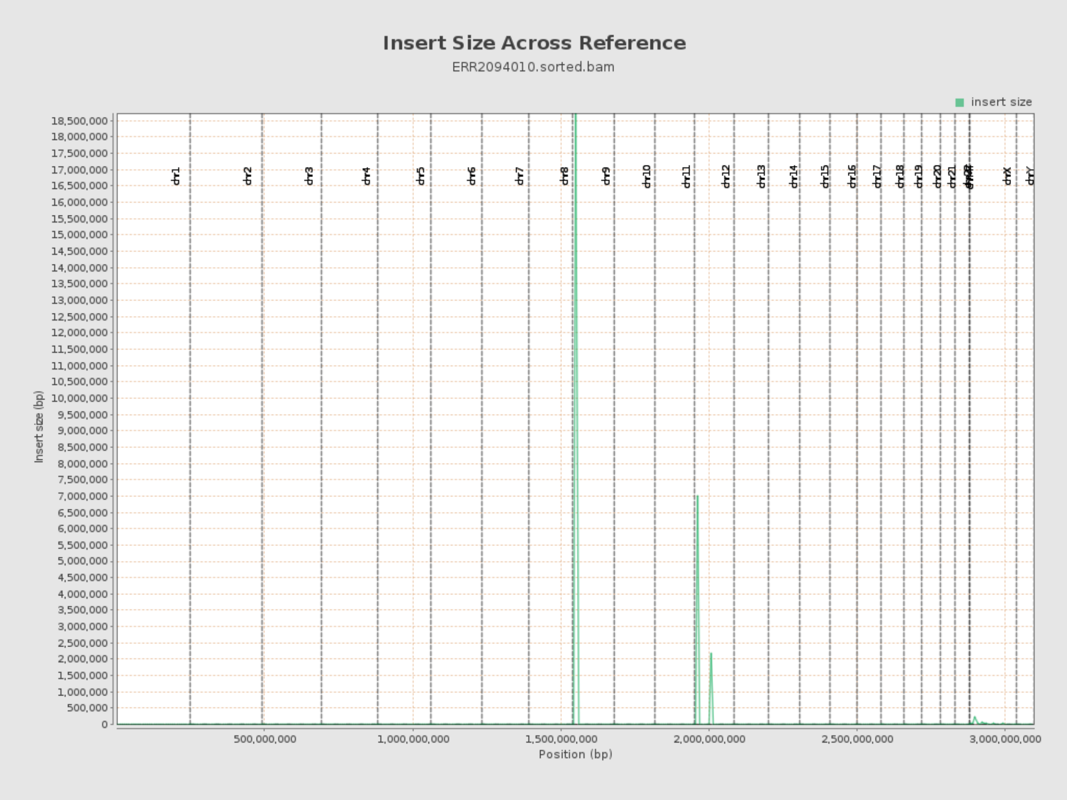
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram