Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:15:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094082.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_ERR2094082 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094082_1.fastq.gz ERR2094082_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:15:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	334,674
Mapped reads	324,611 / 96.99%
Unmapped reads	10,063 / 3.01%
Mapped paired reads	324,611 / 96.99%
Mapped reads, first in pair	163,033 / 48.71%
Mapped reads, second in pair	161,578 / 48.28%
Mapped reads, both in pair	322,584 / 96.39%
Mapped reads, singletons	2,027 / 0.61%
Secondary alignments	0
Supplementary alignments	11,701 / 3.5%
Read min/max/mean length	30 / 151 / 144.16
Duplicated reads (estimated)	308,389 / 92.15%
Duplication rate	49.22%
Clipped reads	121,190 / 36.21%

2.2. ACGT Content

Number/percentage of A's	11,193,340 / 25.98%
Number/percentage of C's	10,345,963 / 24.02%
Number/percentage of T's	10,812,154 / 25.1%
Number/percentage of G's	10,725,964 / 24.9%
Number/percentage of N's	575 / 0%

GC Percentage	48.92%

2.3. Coverage

Mean	0.0142
Standard Deviation	4.1927

2.4. Mapping Quality

Mean Mapping Quality	38.51

2.5. Insert size

Mean	490,804.72
Standard Deviation	6,388,210.86
P25/Median/P75	145 / 172 / 199

2.6. Mismatches and indels

General error rate	4.09%
Mismatches	1,710,680
Insertions	24,191
Mapped reads with at least one insertion	7.3%
Deletions	130,066
Mapped reads with at least one deletion	38.14%
Homopolymer indels	27.13%

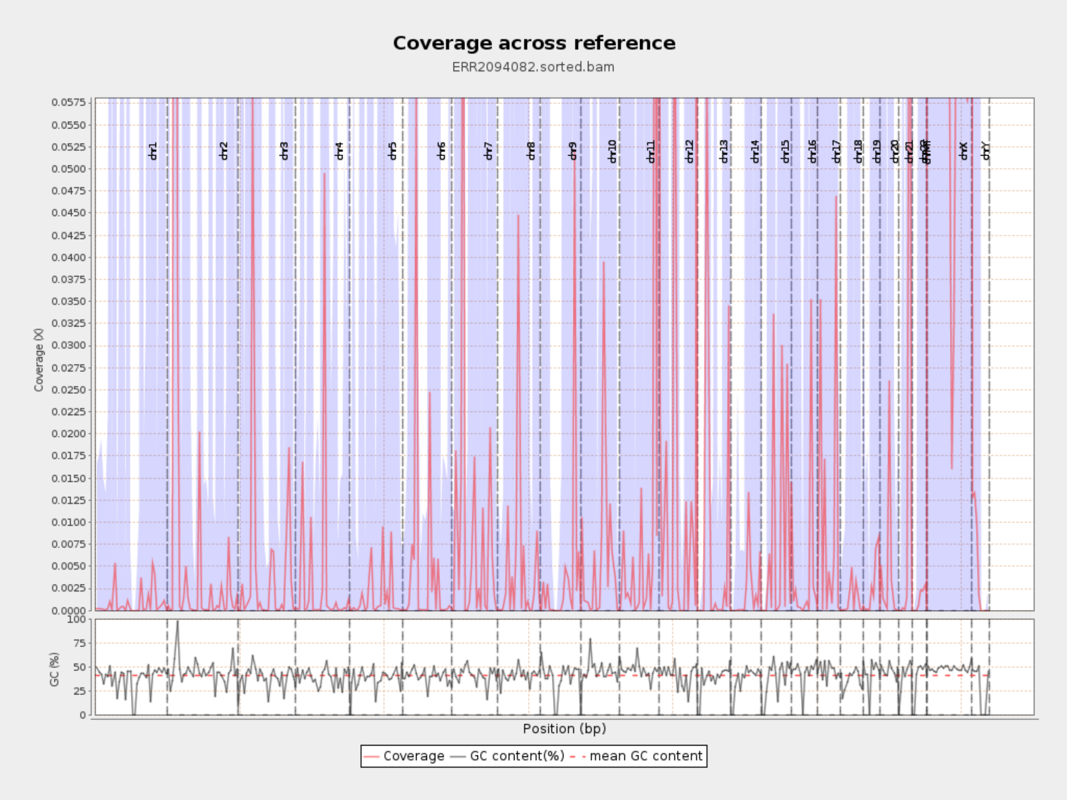
2.7. Chromosome stats

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

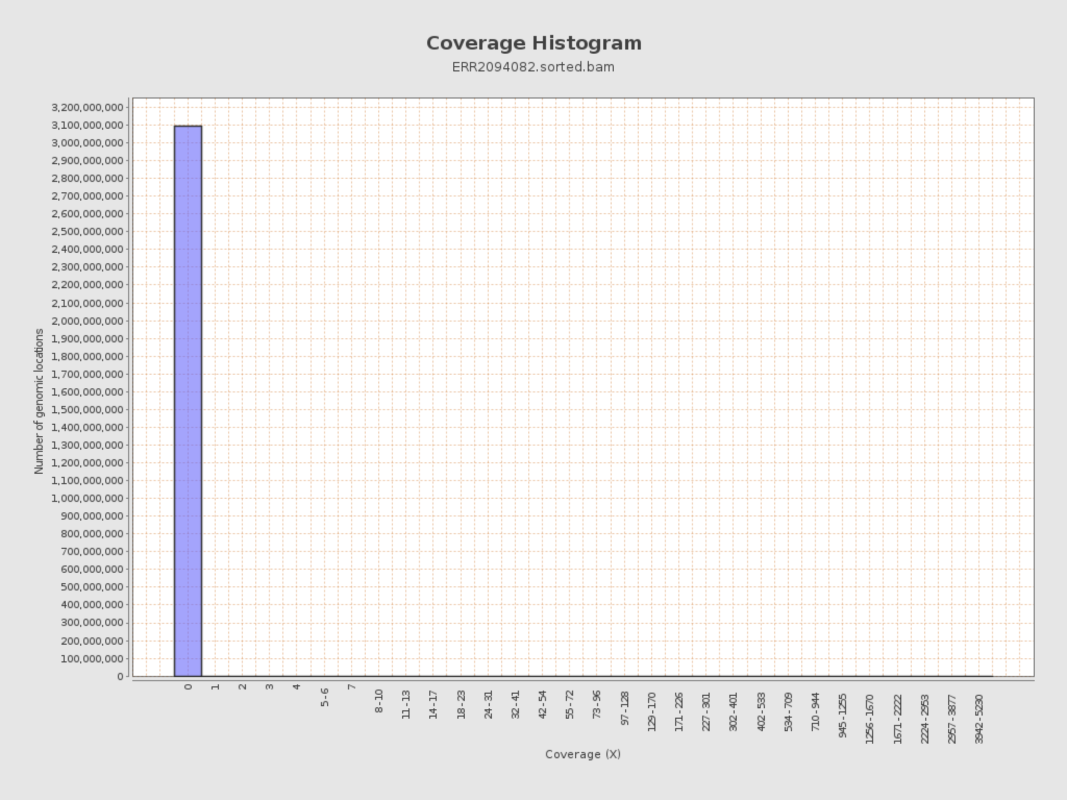
		bases	coverage	deviation
chr1	249250621	214558	0.0009	0.3391
chr2	243199373	2325184	0.0096	4.3081
chr3	198022430	919659	0.0046	2.0646
chr4	191154276	662429	0.0035	1.5501
chr5	180915260	294522	0.0016	0.7499
chr6	171115067	869737	0.0051	2.8588
chr7	159138663	1507326	0.0095	3.7669
chr8	146364022	713757	0.0049	2.0088
chr9	141213431	611766	0.0043	2.3488
chr10	135534747	866063	0.0064	2.3187
chr11	135006516	1477193	0.0109	3.6591
chr12	133851895	1611621	0.012	4.4843
chr13	115169878	961223	0.0083	2.4276
chr14	107349540	239747	0.0022	0.8987
chr15	102531392	818828	0.008	2.5007
chr16	90354753	418043	0.0046	1.8418
chr17	81195210	913293	0.0112	3.8805
chr18	78077248	99577	0.0013	0.4484
chr19	59128983	158069	0.0027	0.6305
chr20	63025520	278039	0.0044	1.2667
chr21	48129895	906521	0.0188	8.5141
chr22	51304566	61533	0.0012	0.3105
chrMT	16571	1327046	80.0824	415.2126
chrX	155270560	25577176	0.1647	13.5801

chrY	59373566	259375	0.0044	0.8652

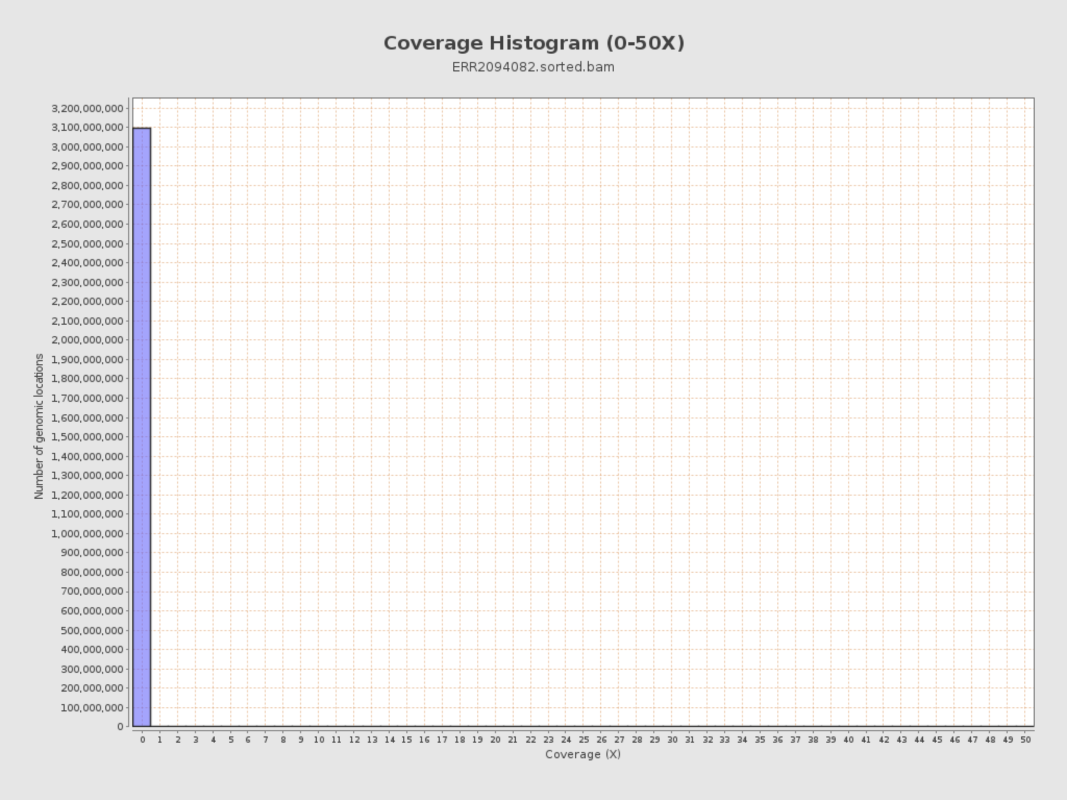
3. Results : Coverage across reference



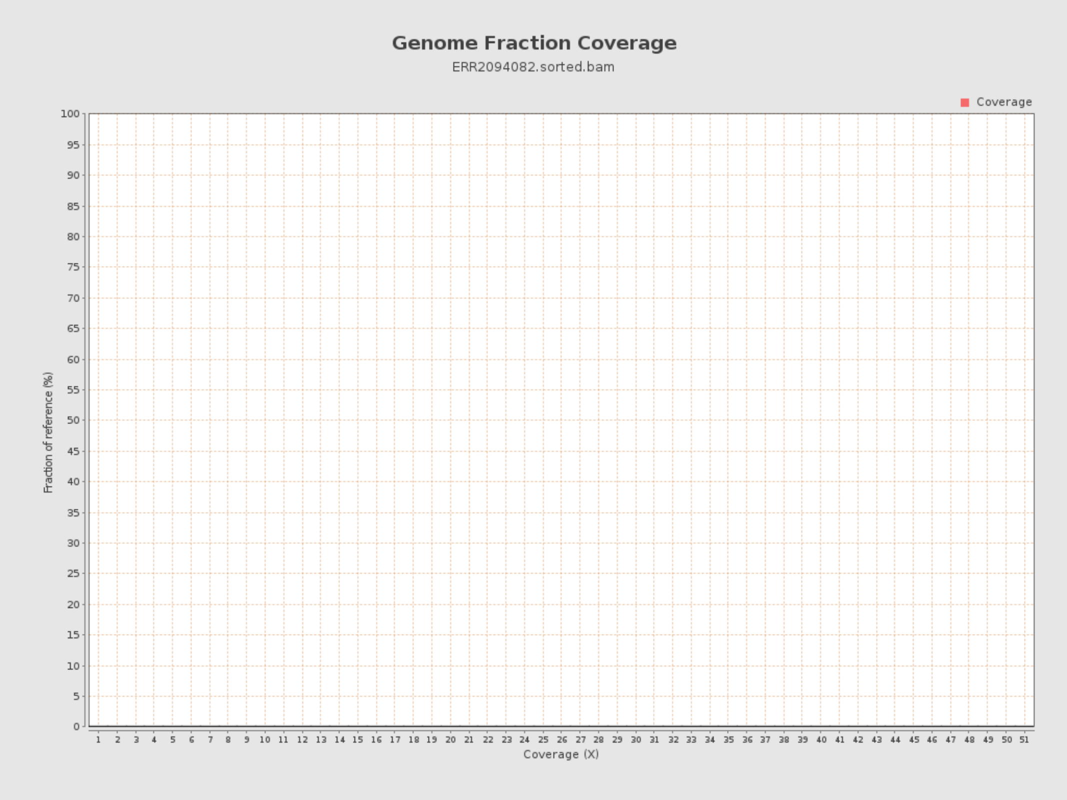
4. Results : Coverage Histogram



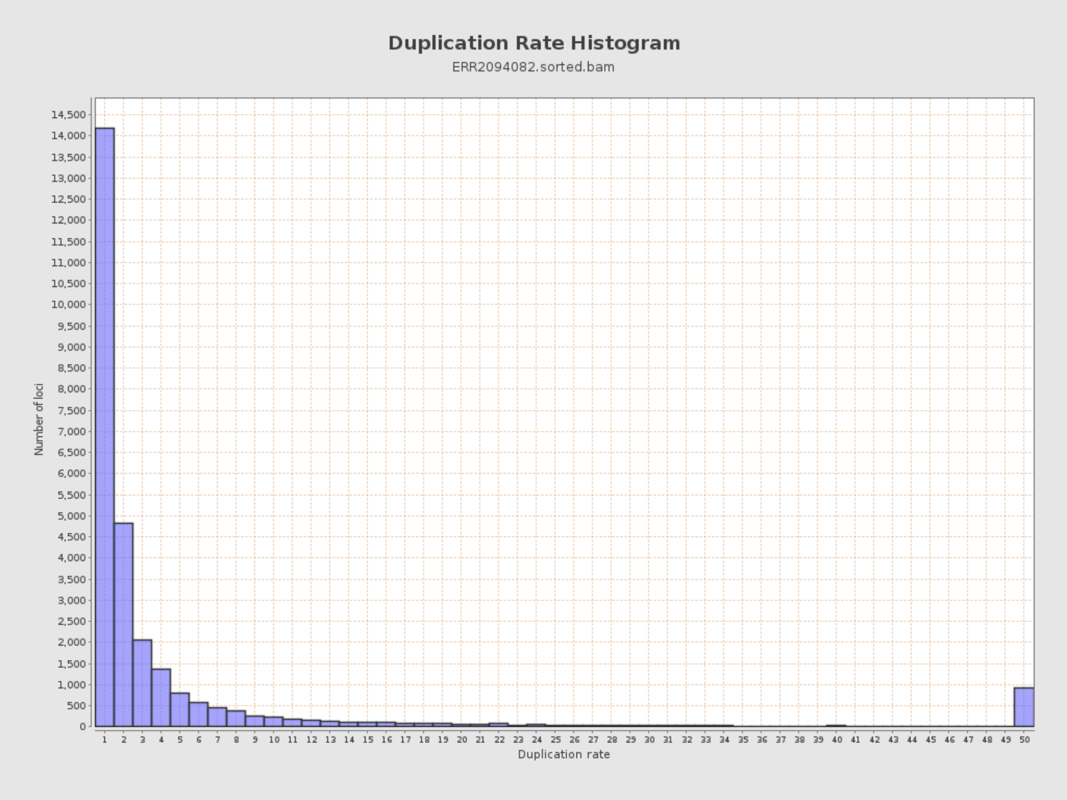
5. Results : Coverage Histogram (0-50X)



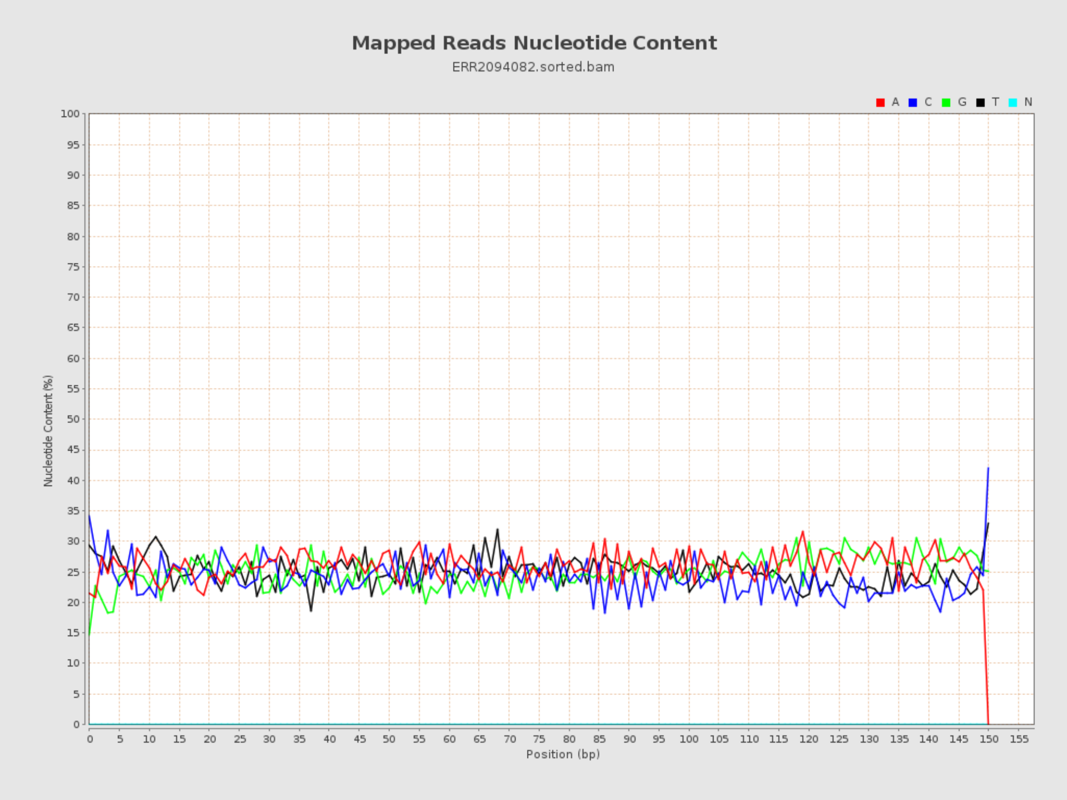
6. Results : Genome Fraction Coverage



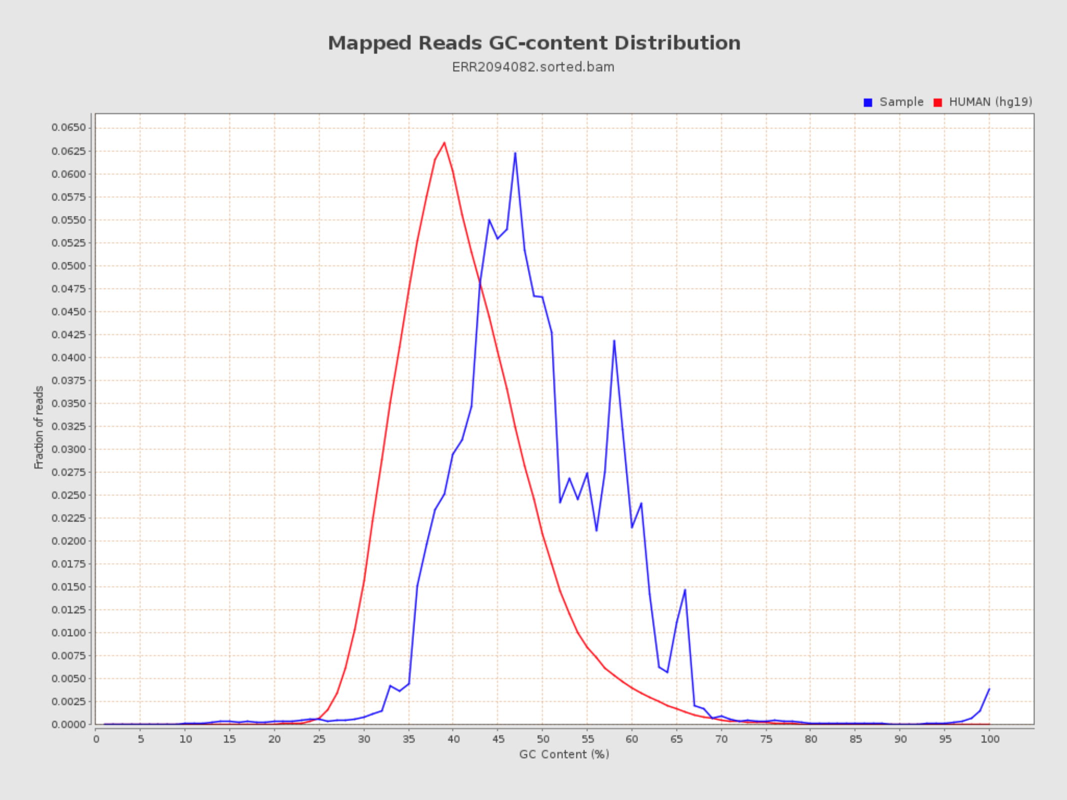
7. Results : Duplication Rate Histogram



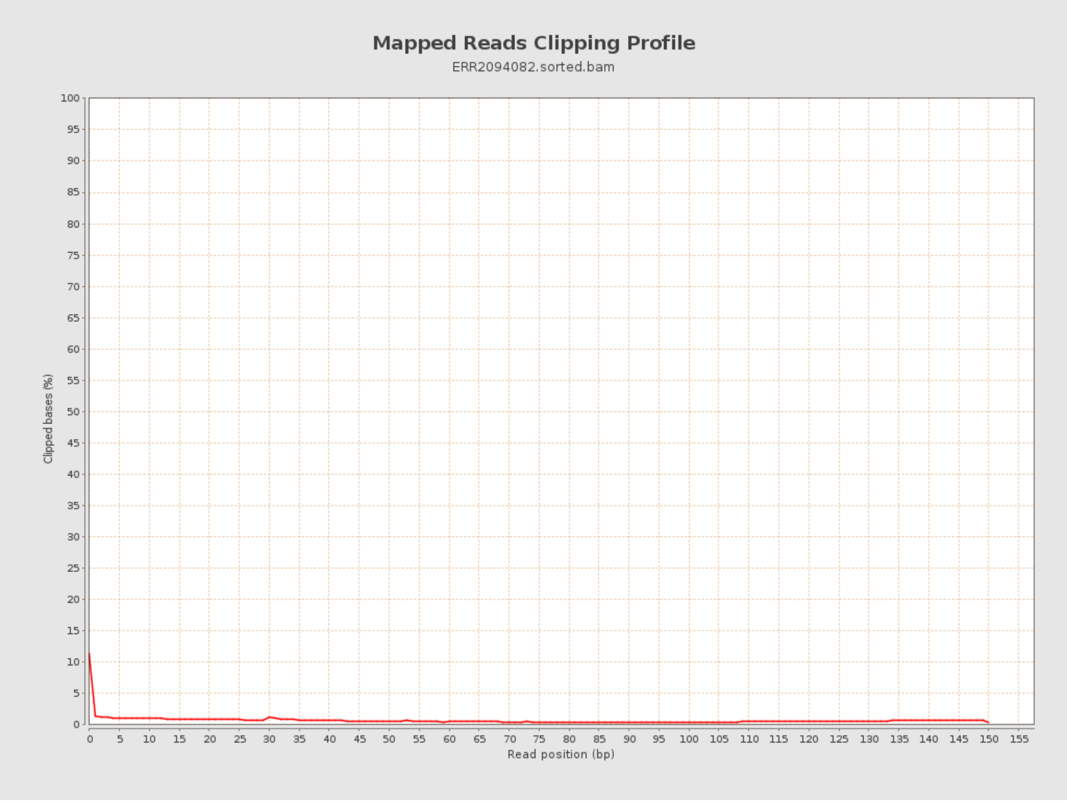
8. Results : Mapped Reads Nucleotide Content



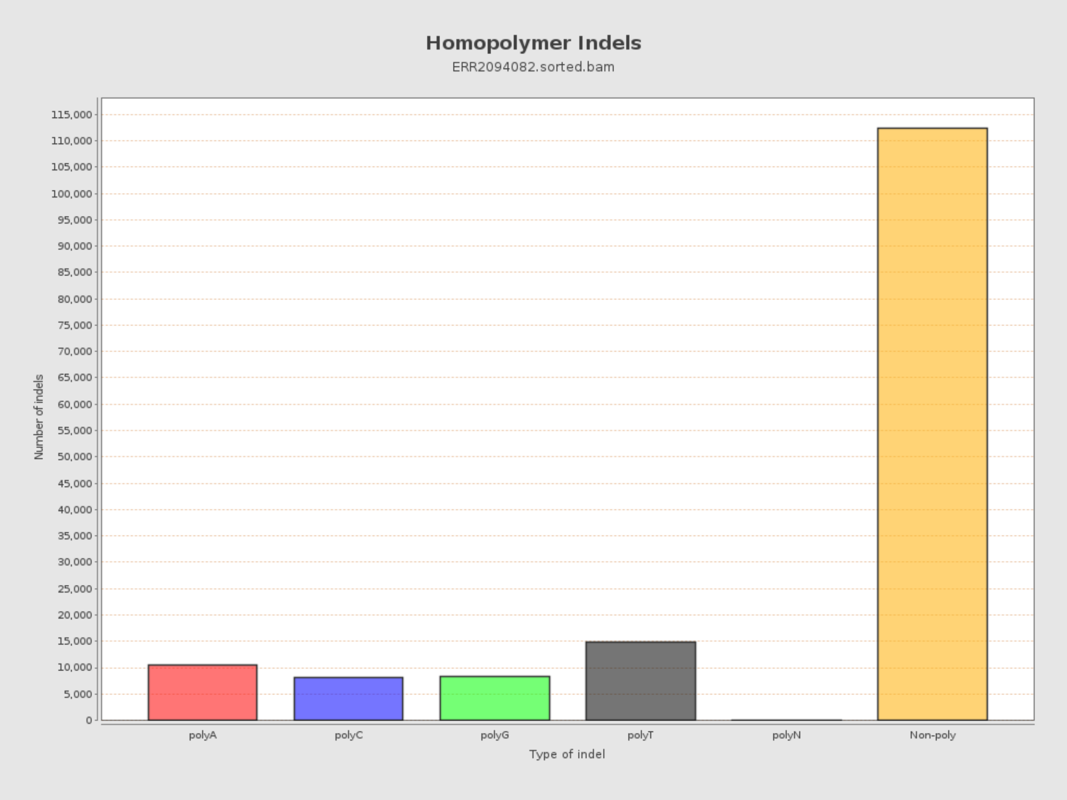
9. Results : Mapped Reads GC-content Distribution



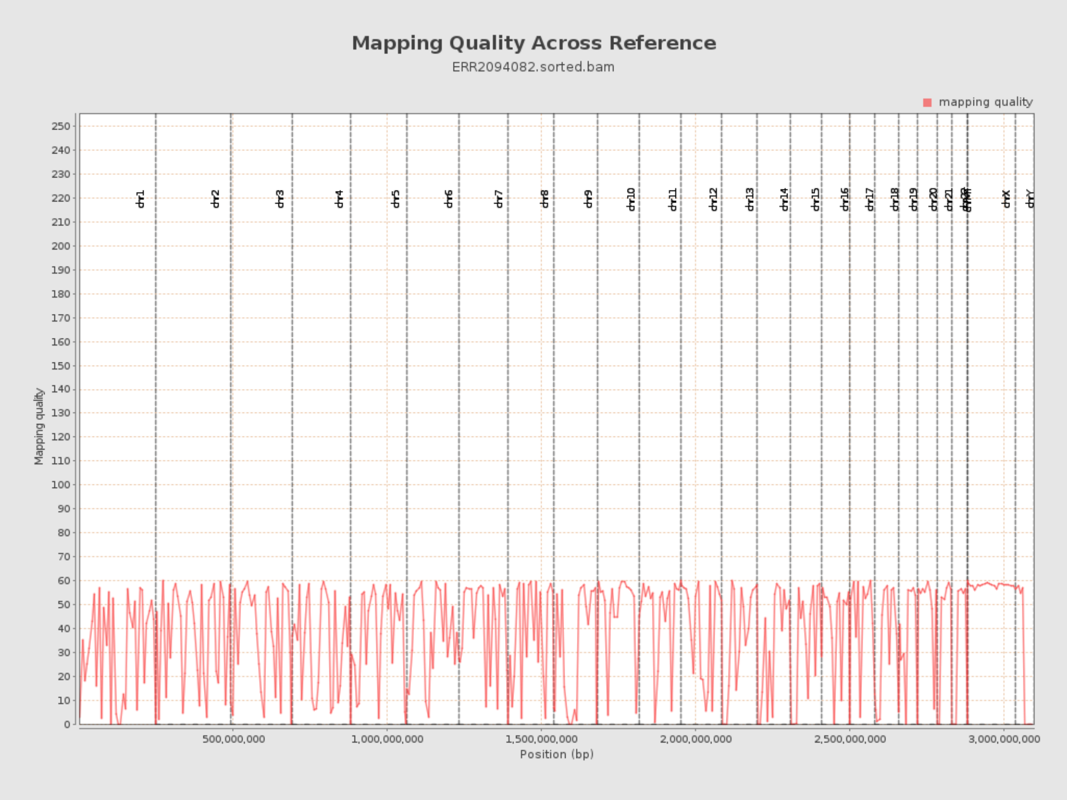
10. Results : Mapped Reads Clipping Profile



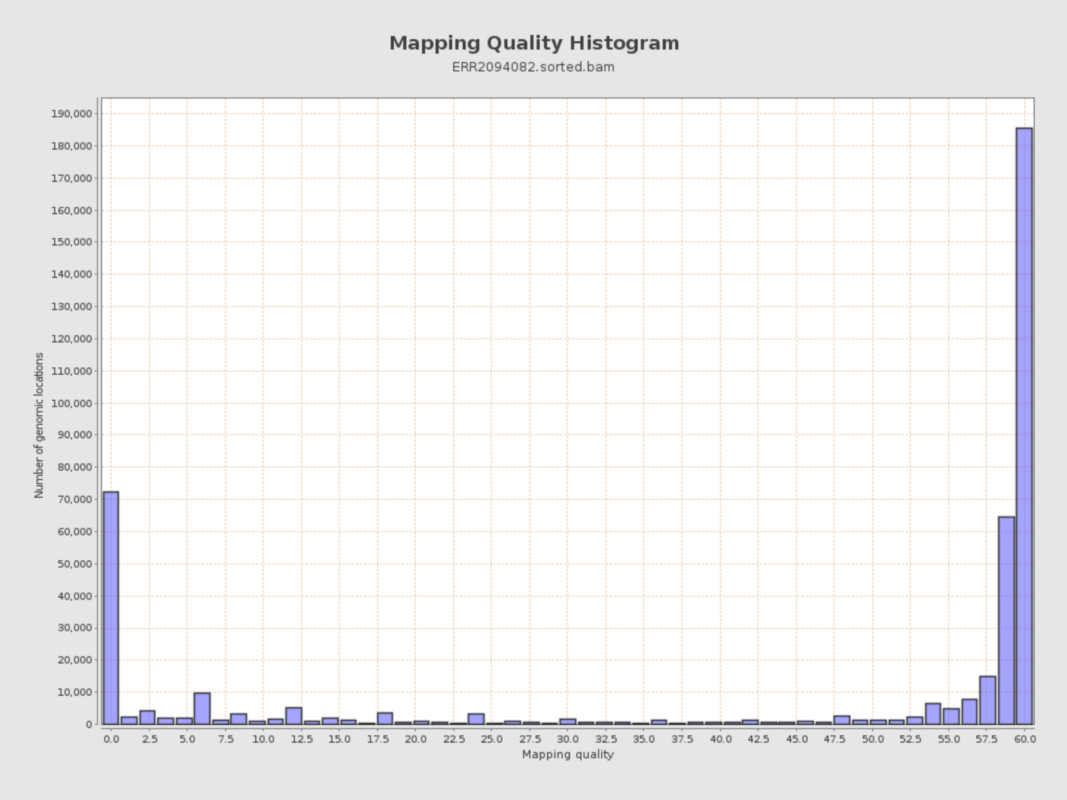
11. Results : Homopolymer Indels



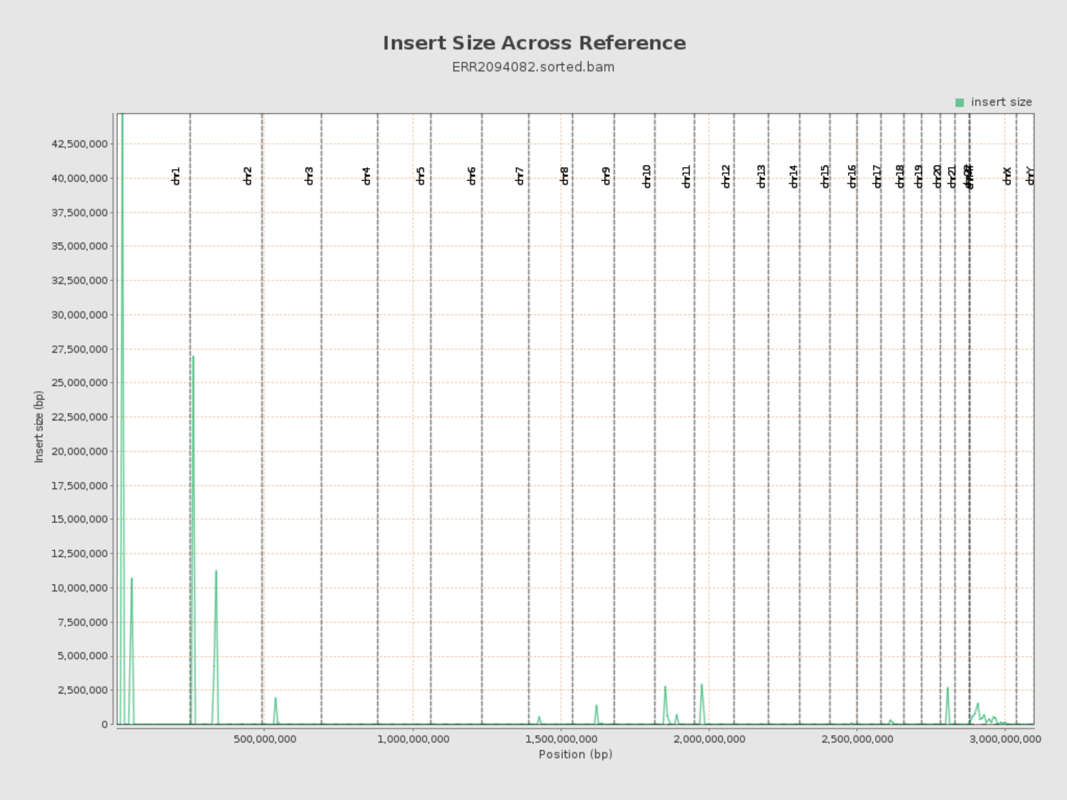
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram