Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:23:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094051.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_ERR2094051 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094051_1.fastq.gz ERR2094051_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:23:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	516,500
Mapped reads	485,731 / 94.04%
Unmapped reads	30,769 / 5.96%
Mapped paired reads	485,731 / 94.04%
Mapped reads, first in pair	243,675 / 47.18%
Mapped reads, second in pair	242,056 / 46.86%
Mapped reads, both in pair	482,554 / 93.43%
Mapped reads, singletons	3,177 / 0.62%
Secondary alignments	0
Supplementary alignments	16,495 / 3.19%
Read min/max/mean length	30 / 151 / 137.31
Duplicated reads (estimated)	465,081 / 90.04%
Duplication rate	51.69%
Clipped reads	190,560 / 36.89%

2.2. ACGT Content

Number/percentage of A's	17,235,605 / 27.78%
Number/percentage of C's	13,807,996 / 22.25%
Number/percentage of T's	16,595,646 / 26.75%
Number/percentage of G's	14,406,122 / 23.22%
Number/percentage of N's	669 / 0%

GC Percentage	45.47%

2.3. Coverage

Mean	0.0206
Standard Deviation	5.067

2.4. Mapping Quality

Mean Mapping Quality	41.27

2.5. Insert size

Mean	494,698.02
Standard Deviation	6,560,359.67
P25/Median/P75	129 / 163 / 195

2.6. Mismatches and indels

General error rate	4.52%
Mismatches	2,736,273
Insertions	41,223
Mapped reads with at least one insertion	8.31%
Deletions	230,710
Mapped reads with at least one deletion	44.46%
Homopolymer indels	29.86%

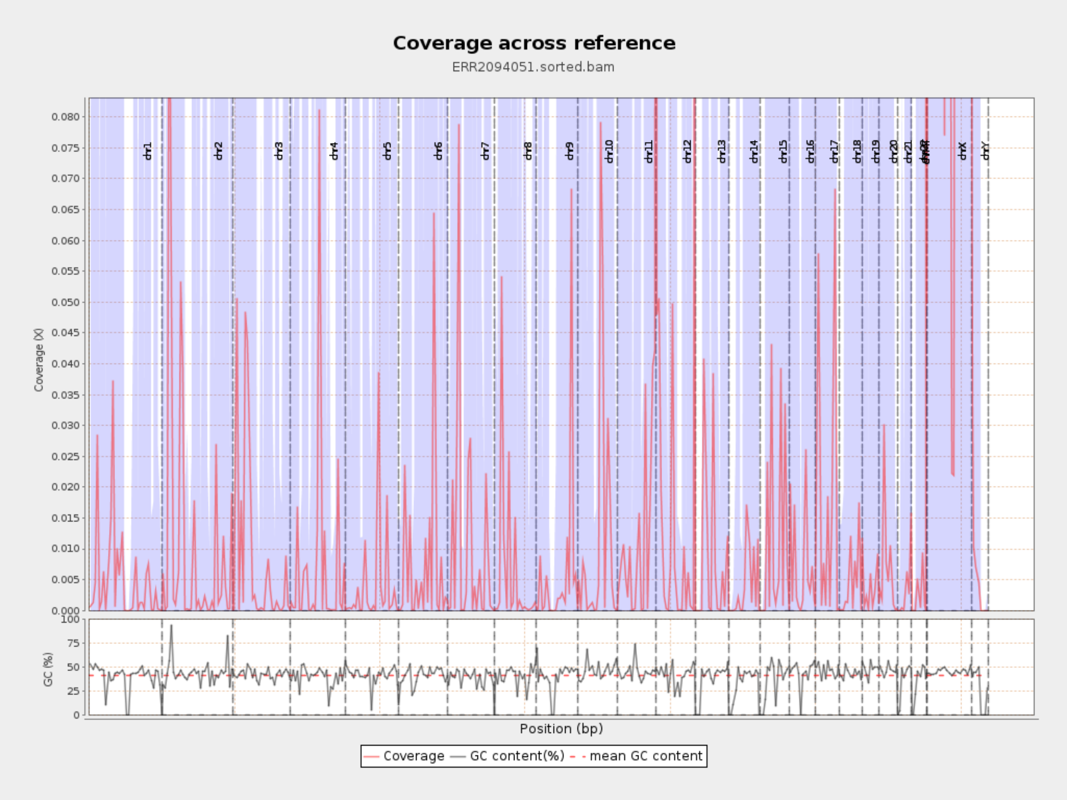
2.7. Chromosome stats

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

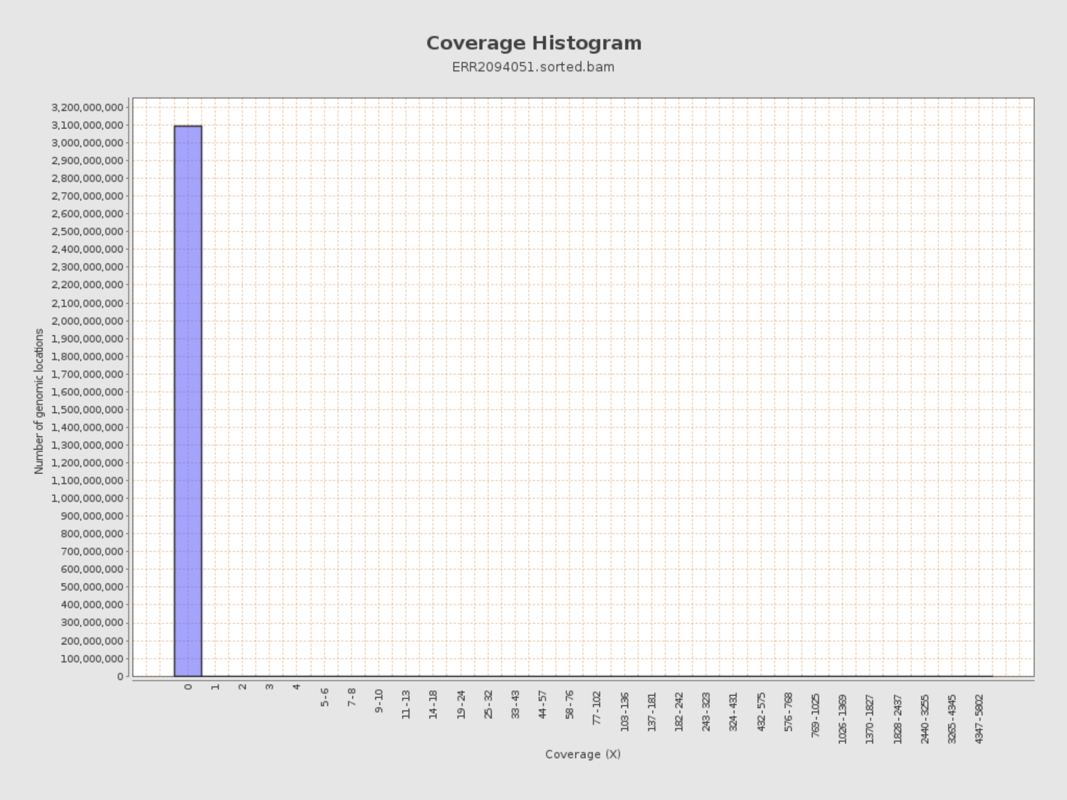
		bases	coverage	deviation
chr1	249250621	1254559	0.005	2.2412
chr2	243199373	2821483	0.0116	3.4292
chr3	198022430	1682781	0.0085	2.9656
chr4	191154276	1355921	0.0071	2.2277
chr5	180915260	692617	0.0038	2.1388
chr6	171115067	1218186	0.0071	3.6199
chr7	159138663	1769286	0.0111	3.607
chr8	146364022	895630	0.0061	2.9239
chr9	141213431	908456	0.0064	2.9814
chr10	135534747	1662880	0.0123	4.4229
chr11	135006516	1813278	0.0134	3.5454
chr12	133851895	1856678	0.0139	4.4213
chr13	115169878	948368	0.0082	2.5756
chr14	107349540	446325	0.0042	1.398
chr15	102531392	1230461	0.012	3.3266
chr16	90354753	612151	0.0068	2.2544
chr17	81195210	1463951	0.018	5.4704
chr18	78077248	345622	0.0044	1.182
chr19	59128983	203315	0.0034	0.8268
chr20	63025520	453779	0.0072	2.5318
chr21	48129895	150588	0.0031	0.6385
chr22	51304566	122962	0.0024	0.6024
chrMT	16571	3165234	191.0104	769.9318
chrX	155270560	36316587	0.2339	16.4181

chrY	59373566	340516	0.0057	1.79

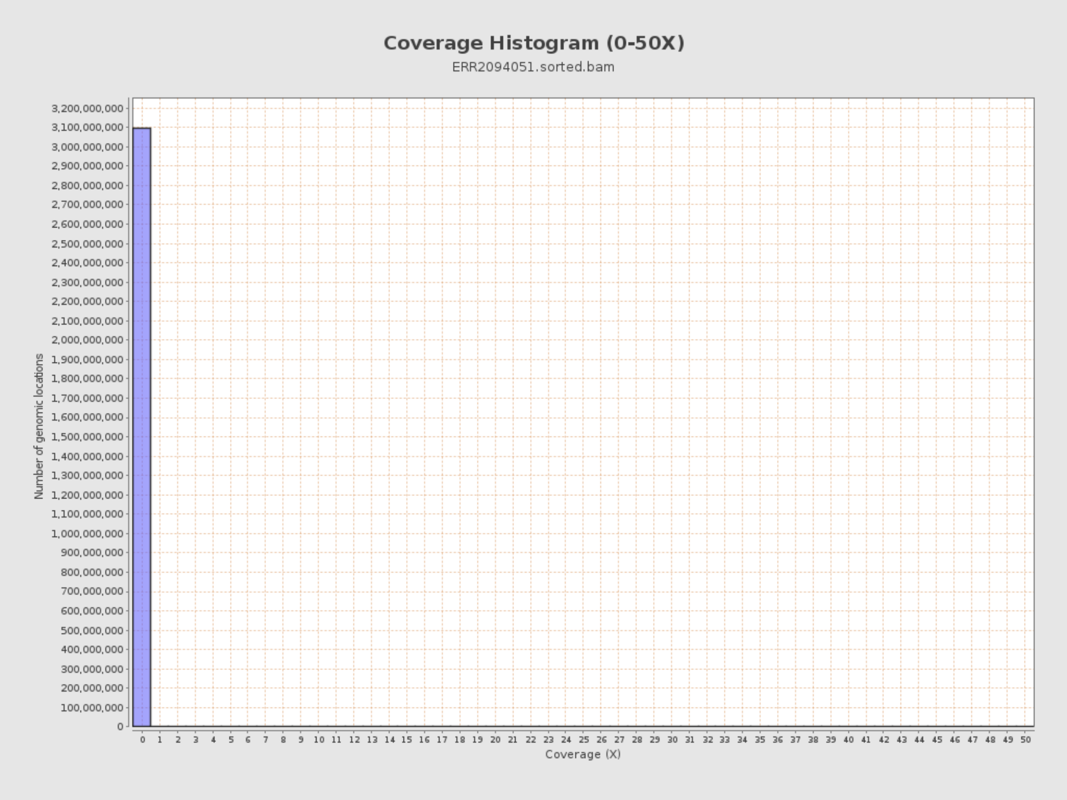
3. Results : Coverage across reference



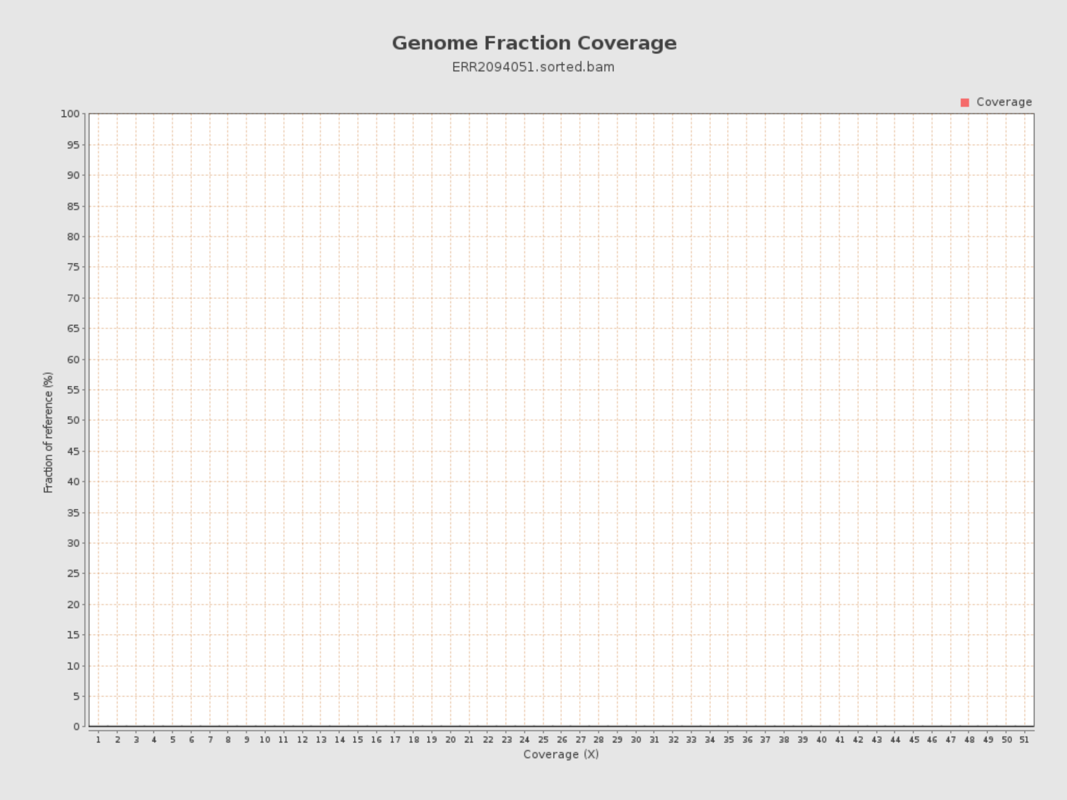
4. Results : Coverage Histogram



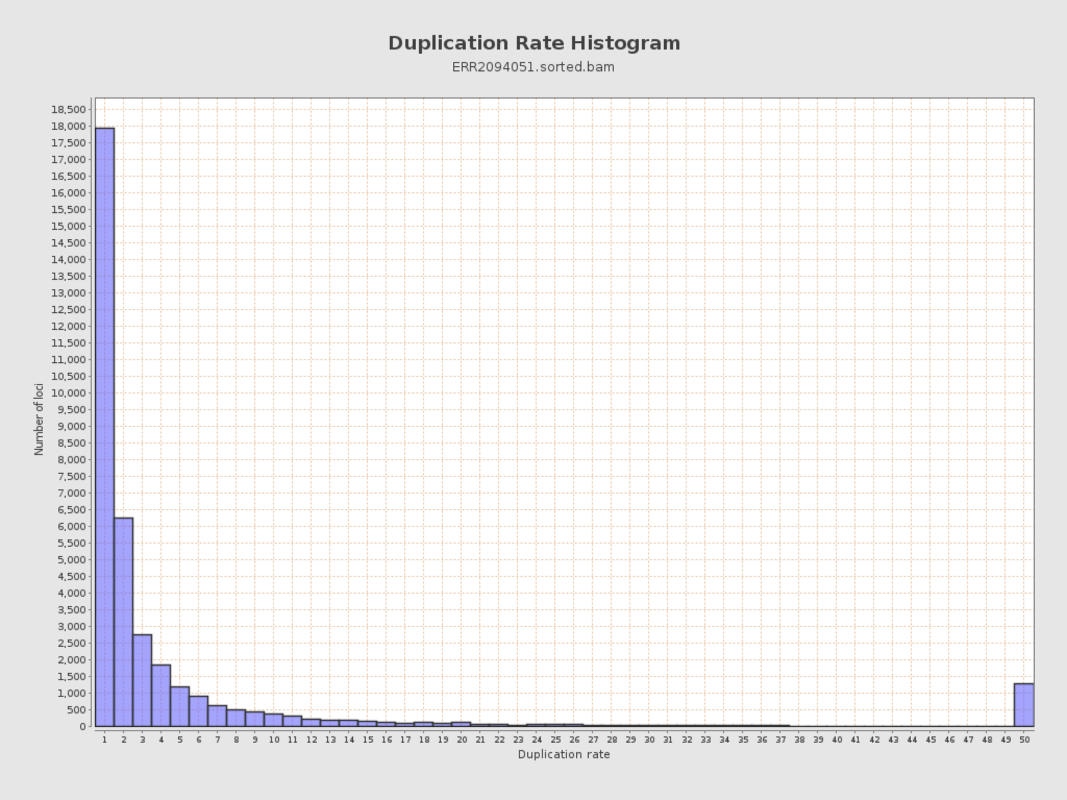
5. Results : Coverage Histogram (0-50X)



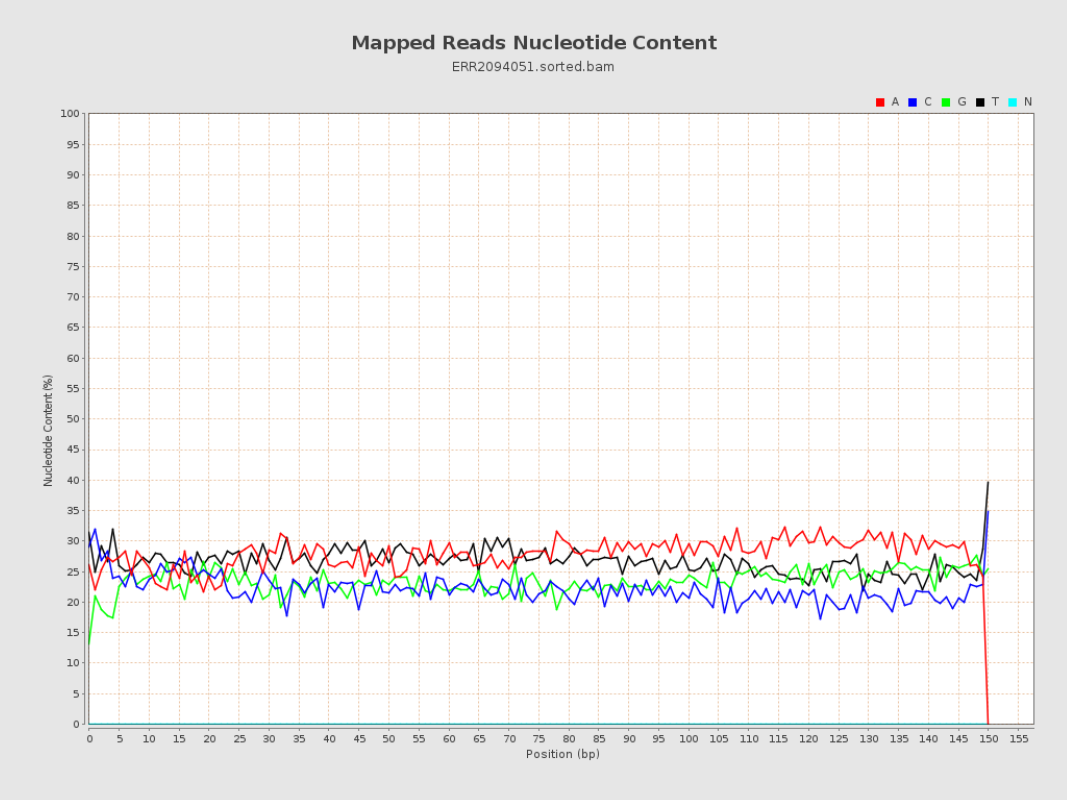
6. Results : Genome Fraction Coverage



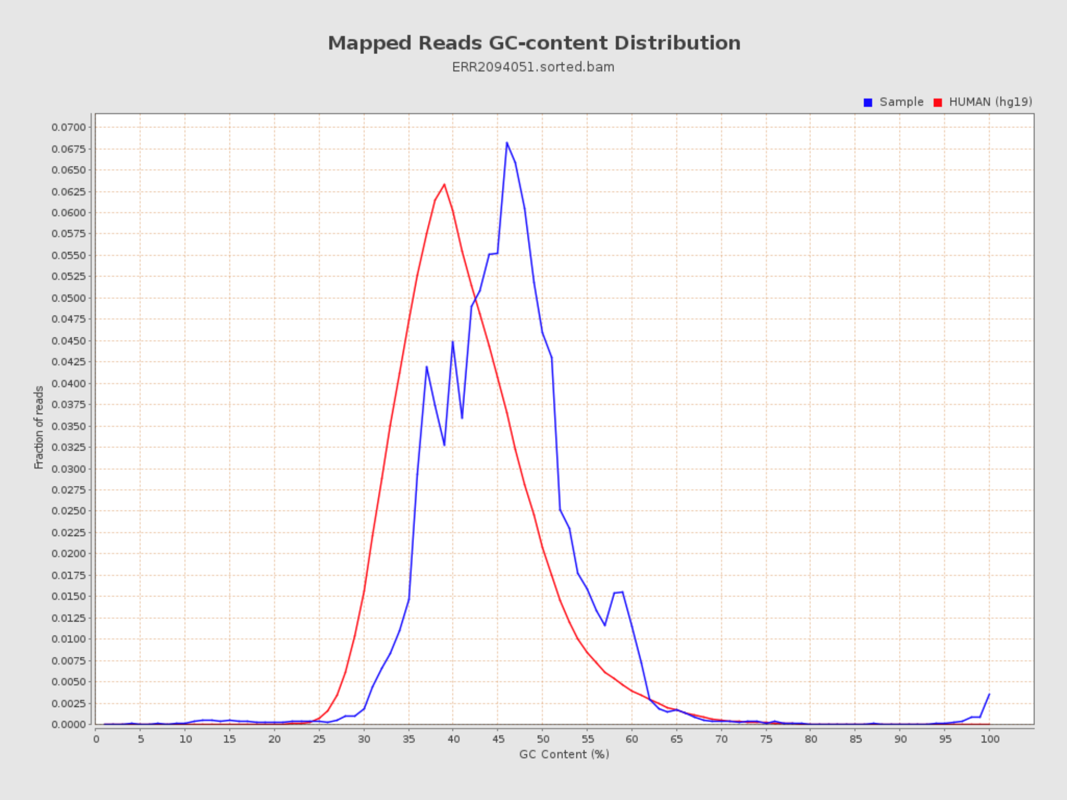
7. Results : Duplication Rate Histogram



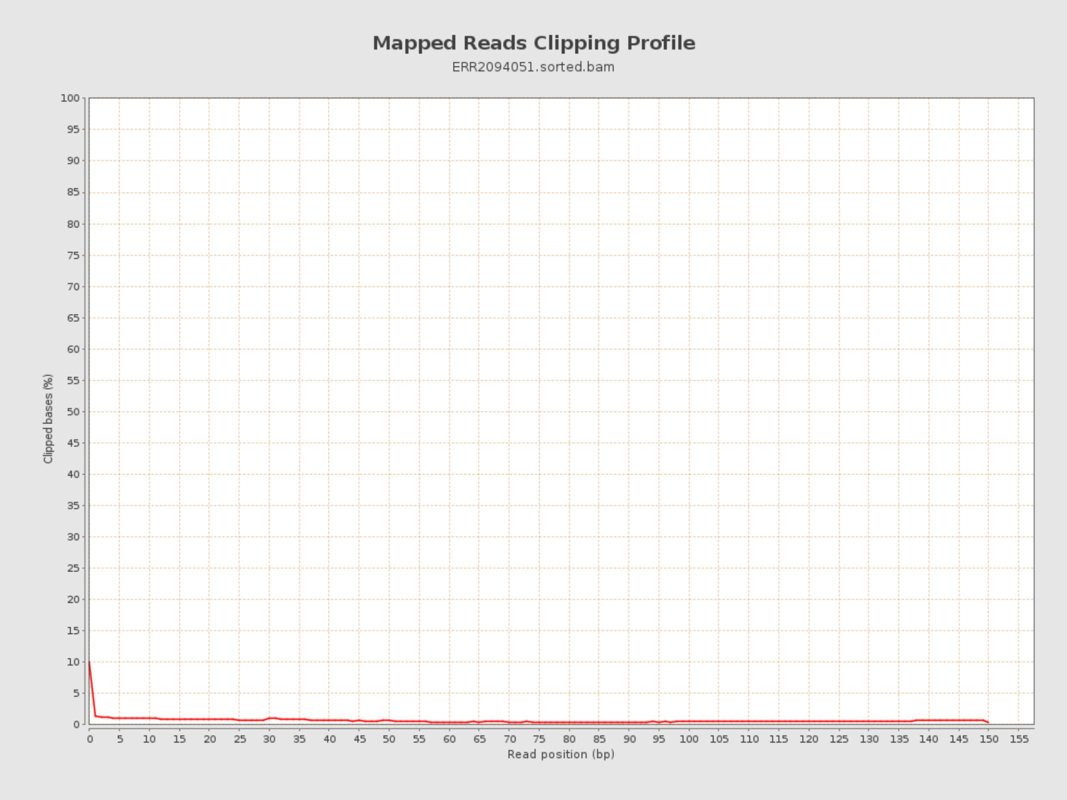
8. Results : Mapped Reads Nucleotide Content



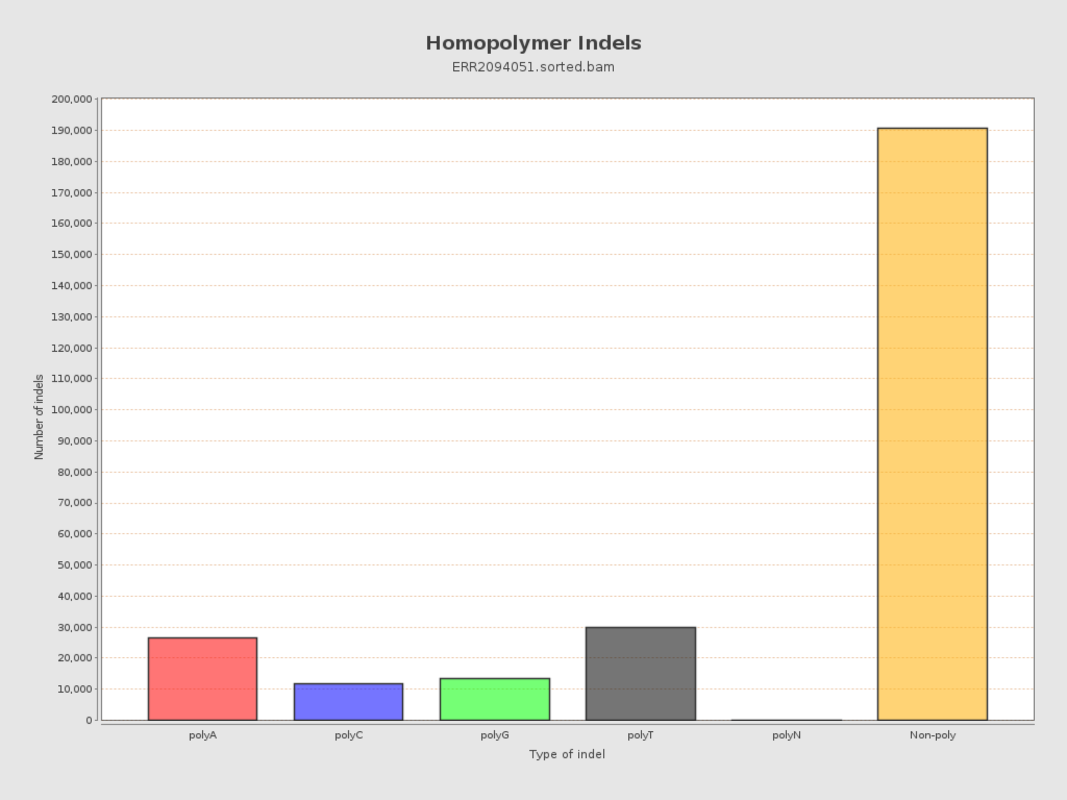
9. Results : Mapped Reads GC-content Distribution



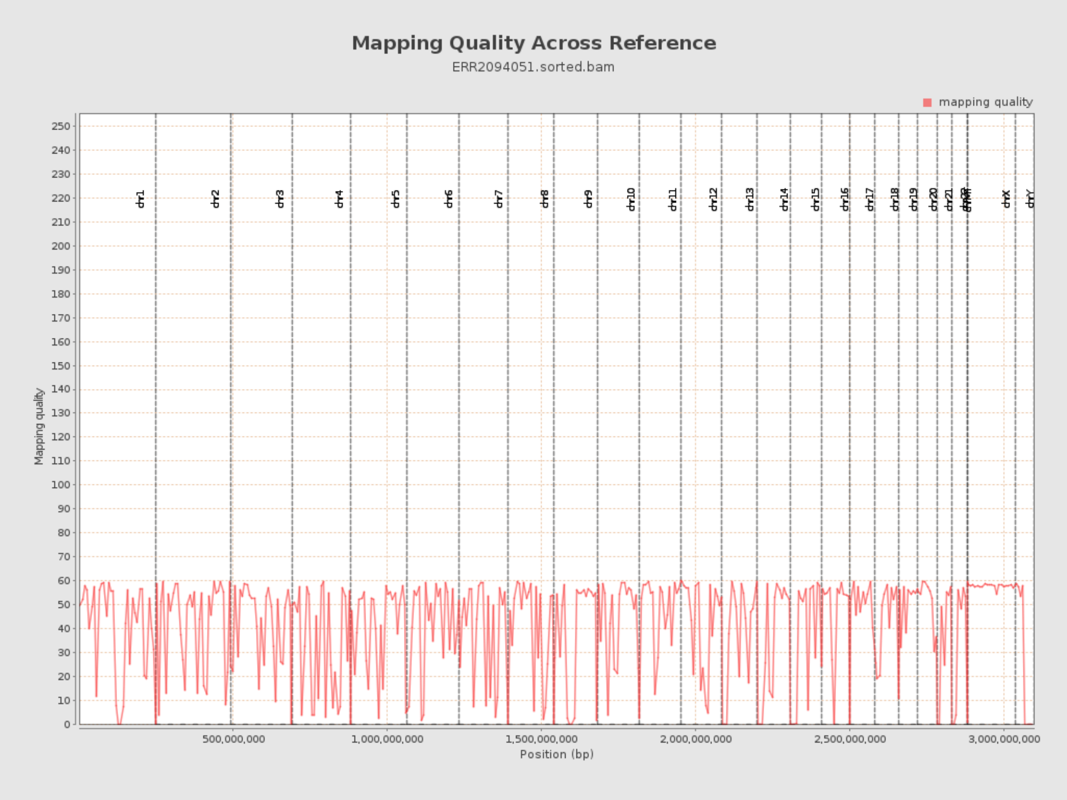
10. Results : Mapped Reads Clipping Profile



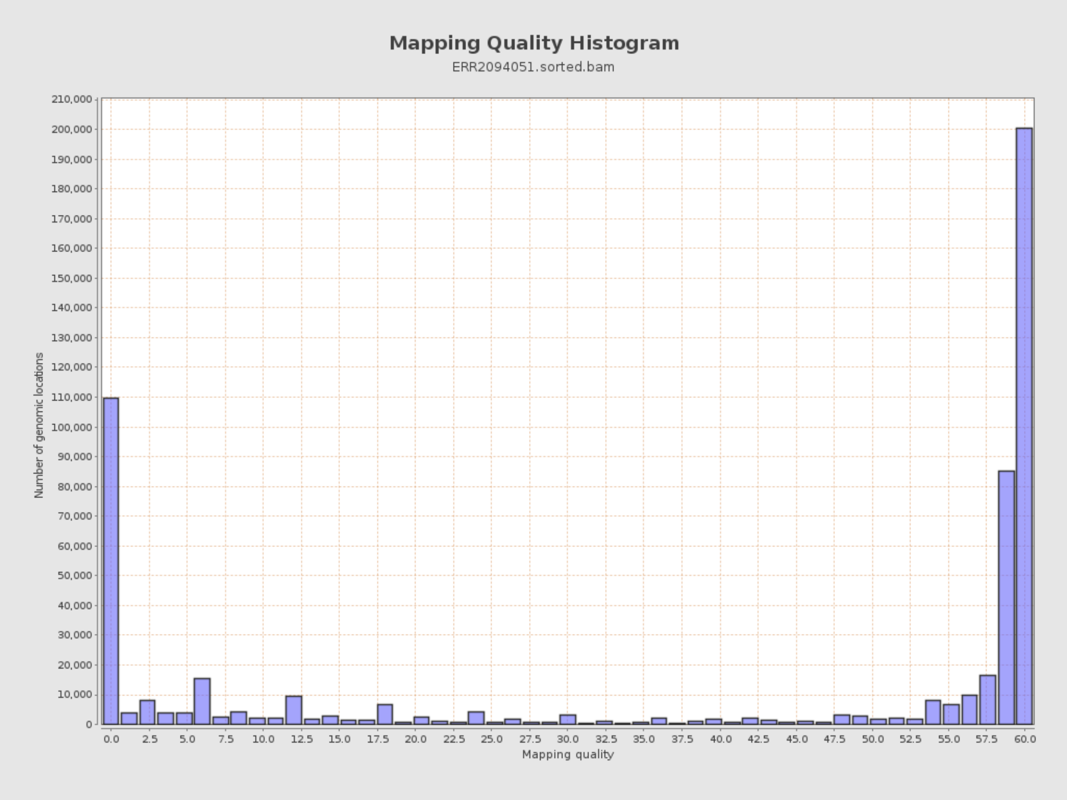
11. Results : Homopolymer Indels



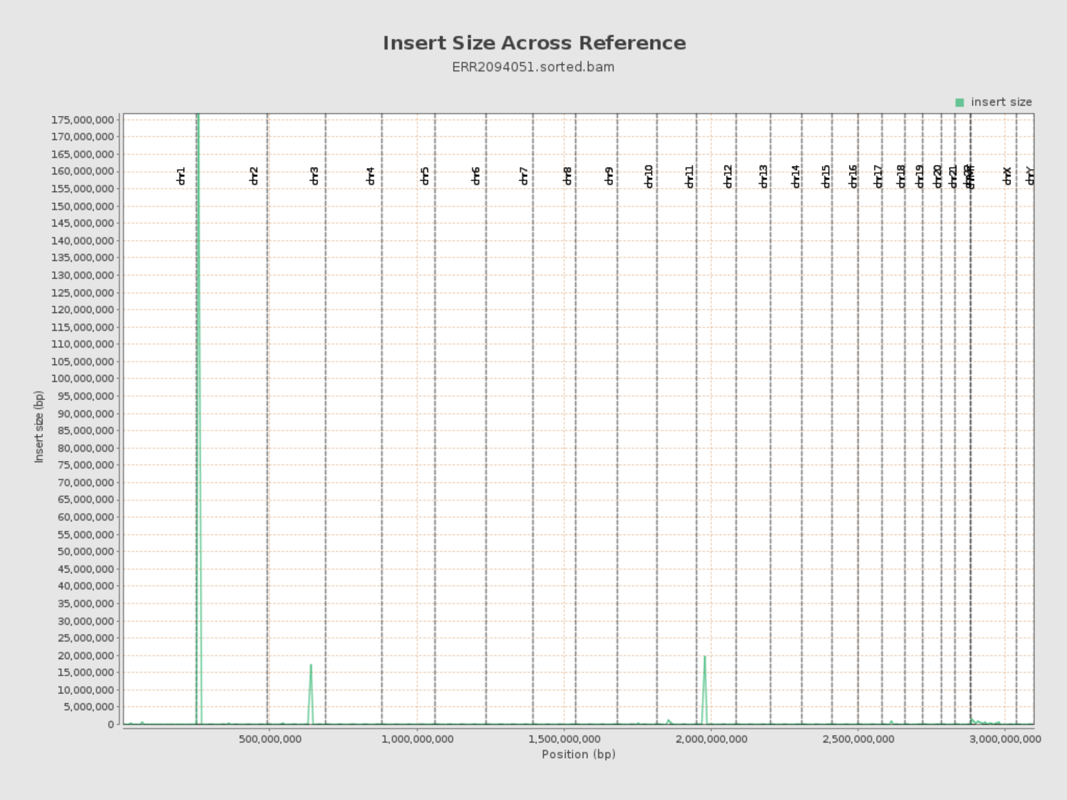
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram