Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:44:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094070.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_ERR2094070 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094070_1.fastq.gz ERR2094070_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	381,528
Mapped reads	362,164 / 94.92%
Unmapped reads	19,364 / 5.08%
Mapped paired reads	362,164 / 94.92%
Mapped reads, first in pair	181,779 / 47.64%
Mapped reads, second in pair	180,385 / 47.28%
Mapped reads, both in pair	359,820 / 94.31%
Mapped reads, singletons	2,344 / 0.61%
Secondary alignments	0
Supplementary alignments	12,194 / 3.2%
Read min/max/mean length	30 / 151 / 139.31
Duplicated reads (estimated)	344,430 / 90.28%
Duplication rate	49.6%
Clipped reads	141,835 / 37.18%

2.2. ACGT Content

Number/percentage of A's	12,281,679 / 26.35%
Number/percentage of C's	10,950,183 / 23.49%
Number/percentage of T's	11,833,912 / 25.39%
Number/percentage of G's	11,540,620 / 24.76%
Number/percentage of N's	435 / 0%

GC Percentage	48.26%

2.3. Coverage

Mean	0.0154
Standard Deviation	4.2618

2.4. Mapping Quality

Mean Mapping Quality	38.02

2.5. Insert size

Mean	391,630.63
Standard Deviation	5,598,639.13
P25/Median/P75	134 / 168 / 196

2.6. Mismatches and indels

General error rate	4.11%
Mismatches	1,840,388
Insertions	31,808
Mapped reads with at least one insertion	8.64%
Deletions	150,415
Mapped reads with at least one deletion	39.63%
Homopolymer indels	27.2%

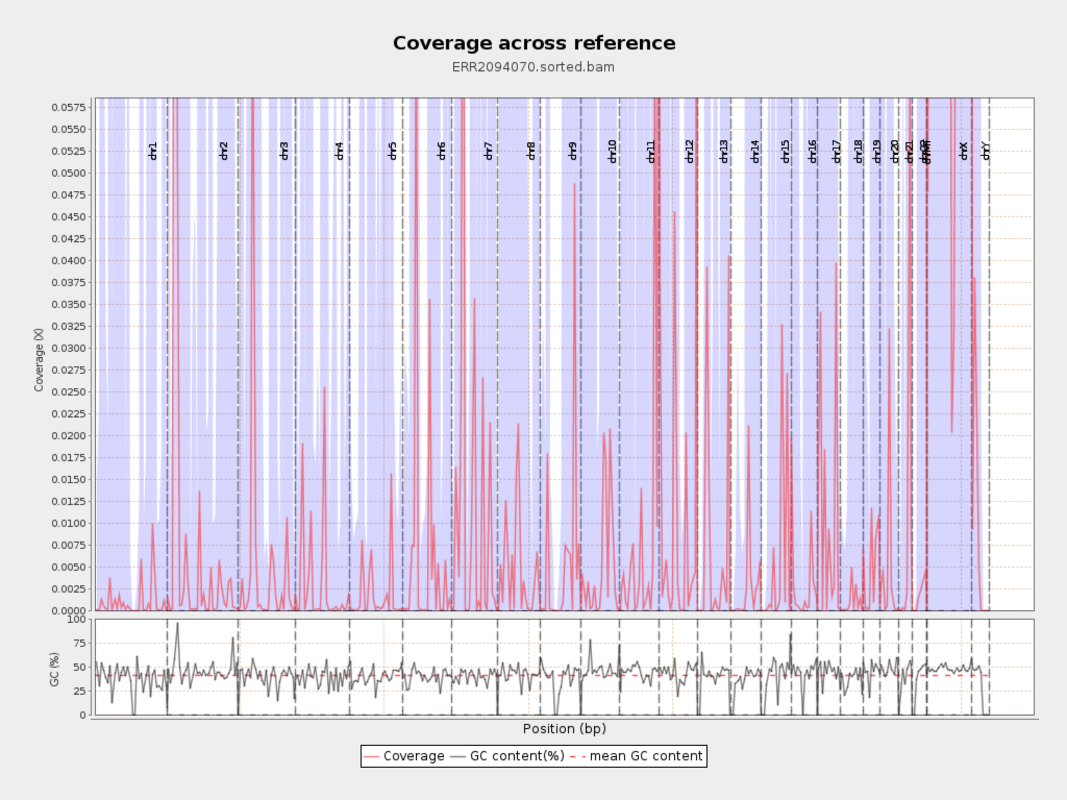
2.7. Chromosome stats

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

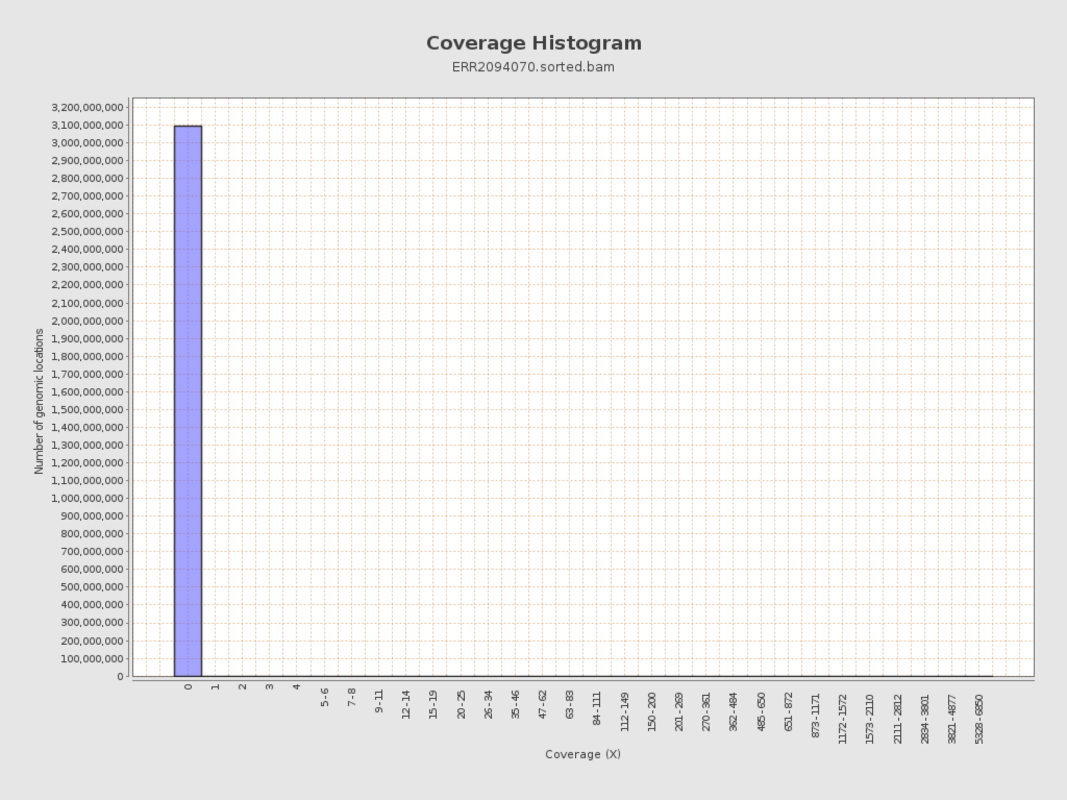
		bases	coverage	deviation
chr1	249250621	270555	0.0011	0.4912
chr2	243199373	1979567	0.0081	3.1017
chr3	198022430	932522	0.0047	1.9042
chr4	191154276	584276	0.0031	1.2288
chr5	180915260	326415	0.0018	0.9416
chr6	171115067	1176169	0.0069	3.7127
chr7	159138663	1953218	0.0123	4.4966
chr8	146364022	662594	0.0045	1.2707
chr9	141213431	779627	0.0055	2.4564
chr10	135534747	712469	0.0053	1.7777
chr11	135006516	1055432	0.0078	2.3346
chr12	133851895	1294364	0.0097	3.0417
chr13	115169878	816162	0.0071	2.238
chr14	107349540	306101	0.0029	1.2827
chr15	102531392	552608	0.0054	1.6333
chr16	90354753	271172	0.003	1.123
chr17	81195210	952109	0.0117	3.5183
chr18	78077248	82566	0.0011	0.4116
chr19	59128983	273033	0.0046	1.1148
chr20	63025520	328148	0.0052	1.9131
chr21	48129895	551021	0.0114	4.5426
chr22	51304566	89281	0.0017	0.4665
chrMT	16571	1220859	73.6744	340.5494
chrX	155270560	29948057	0.1929	15.6019

chrY	59373566	551290	0.0093	2.2993

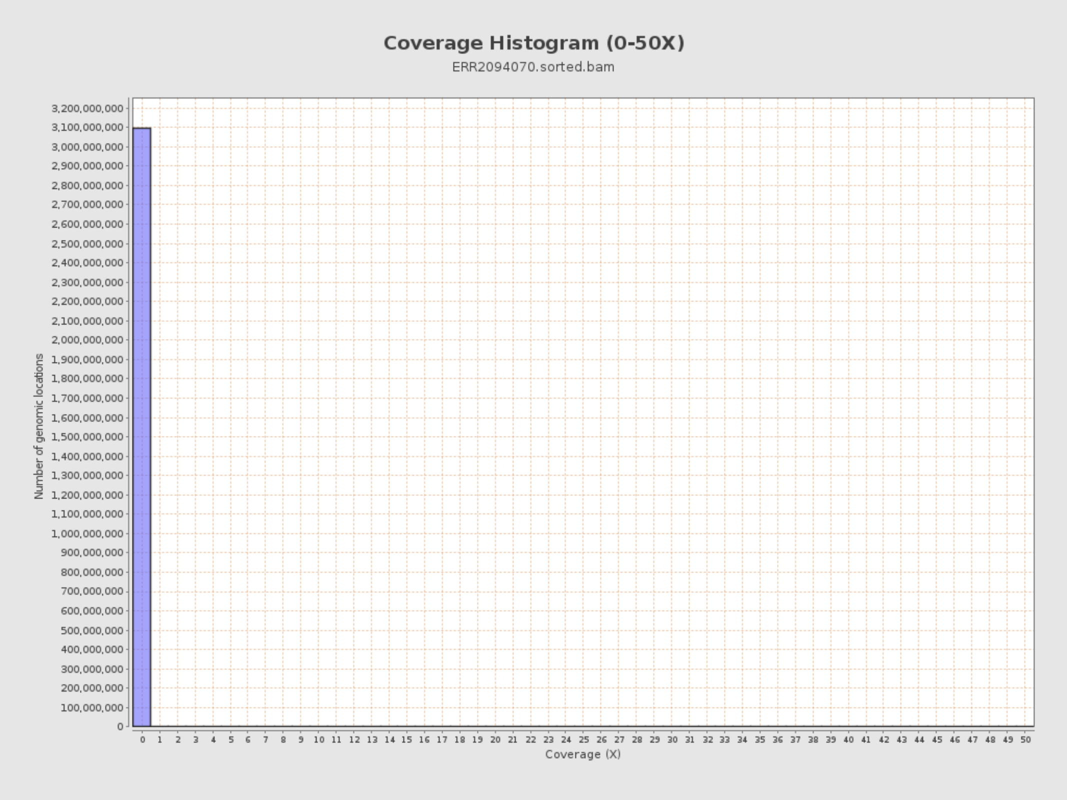
3. Results : Coverage across reference



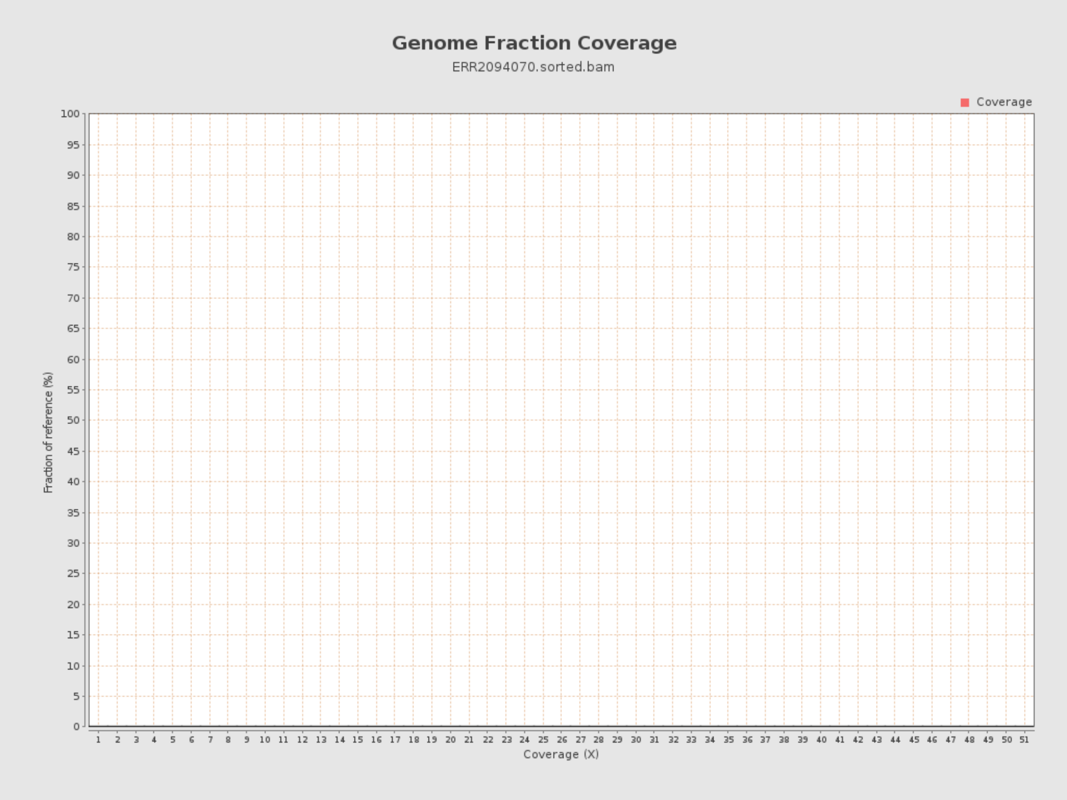
4. Results : Coverage Histogram



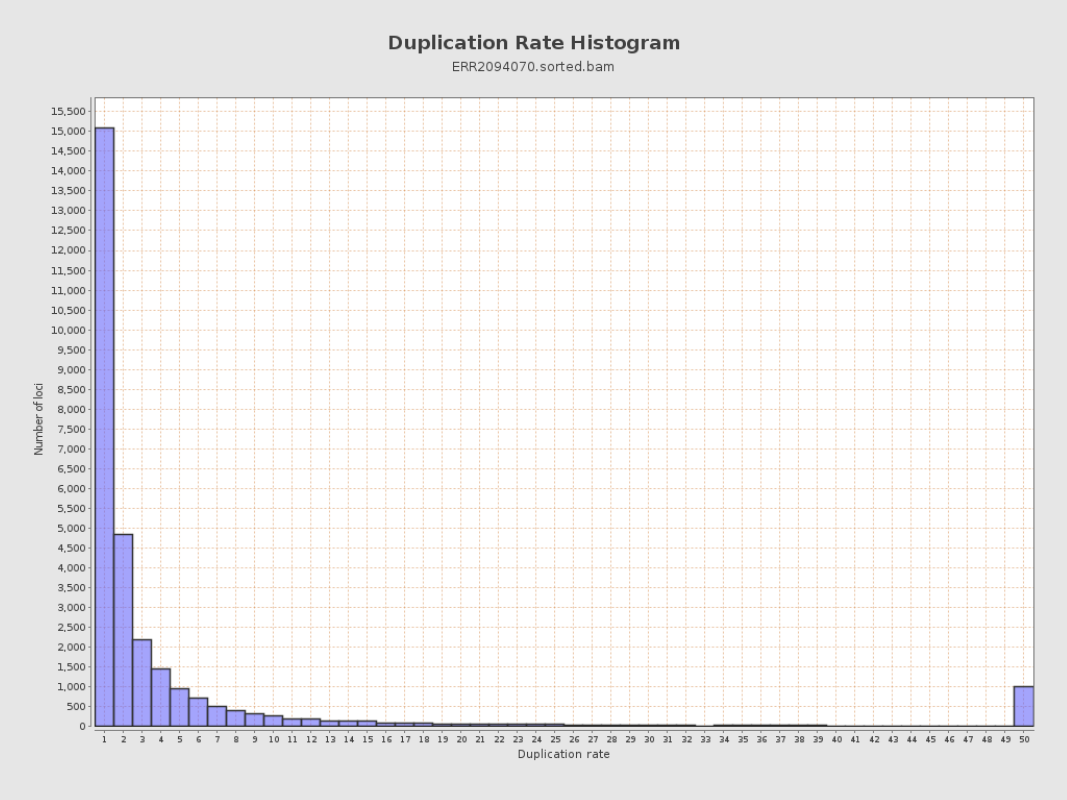
5. Results : Coverage Histogram (0-50X)



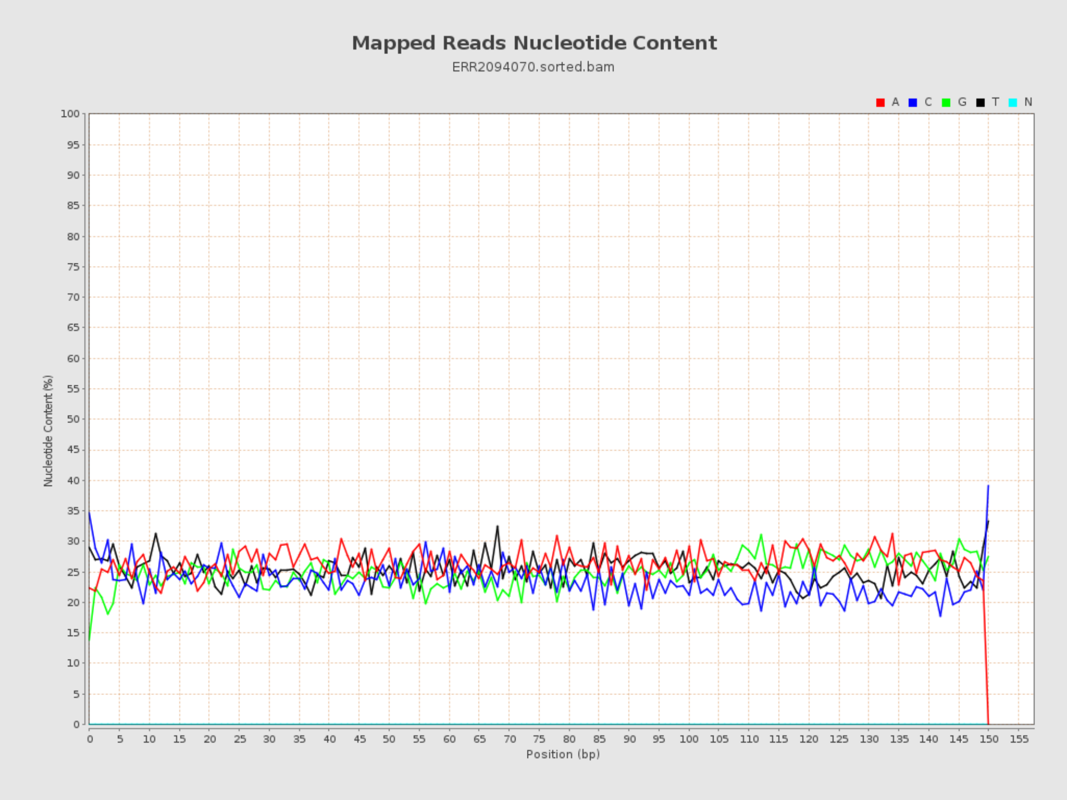
6. Results : Genome Fraction Coverage



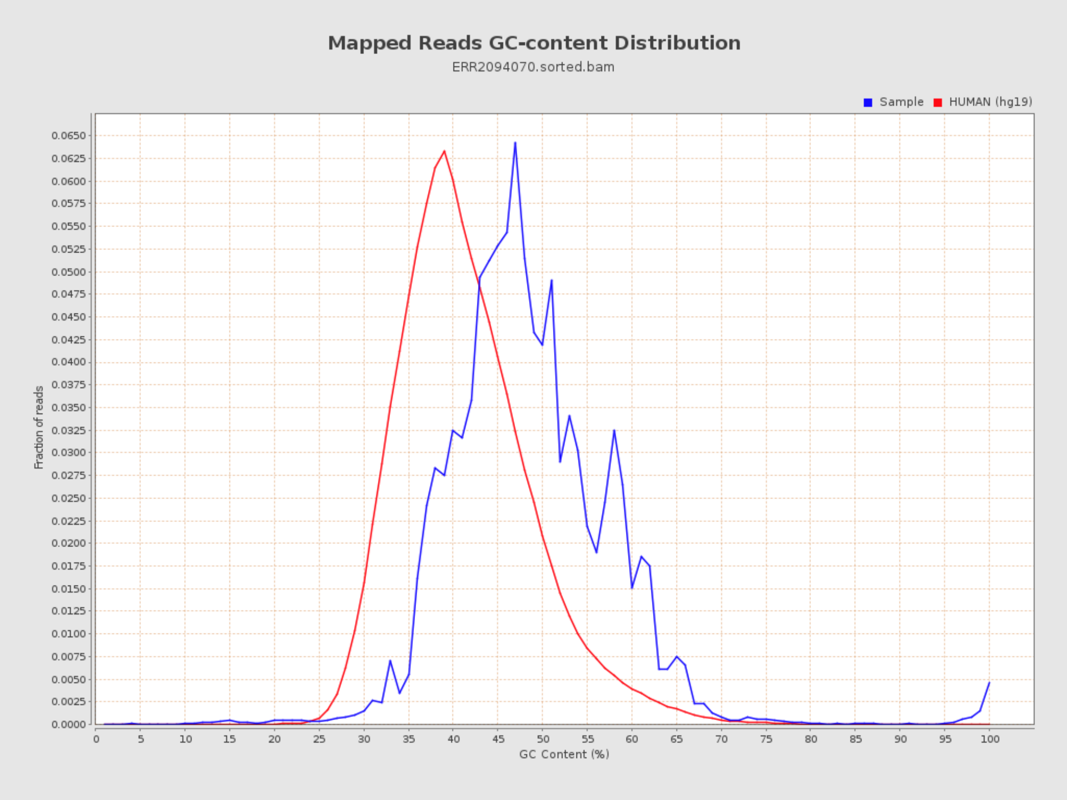
7. Results : Duplication Rate Histogram



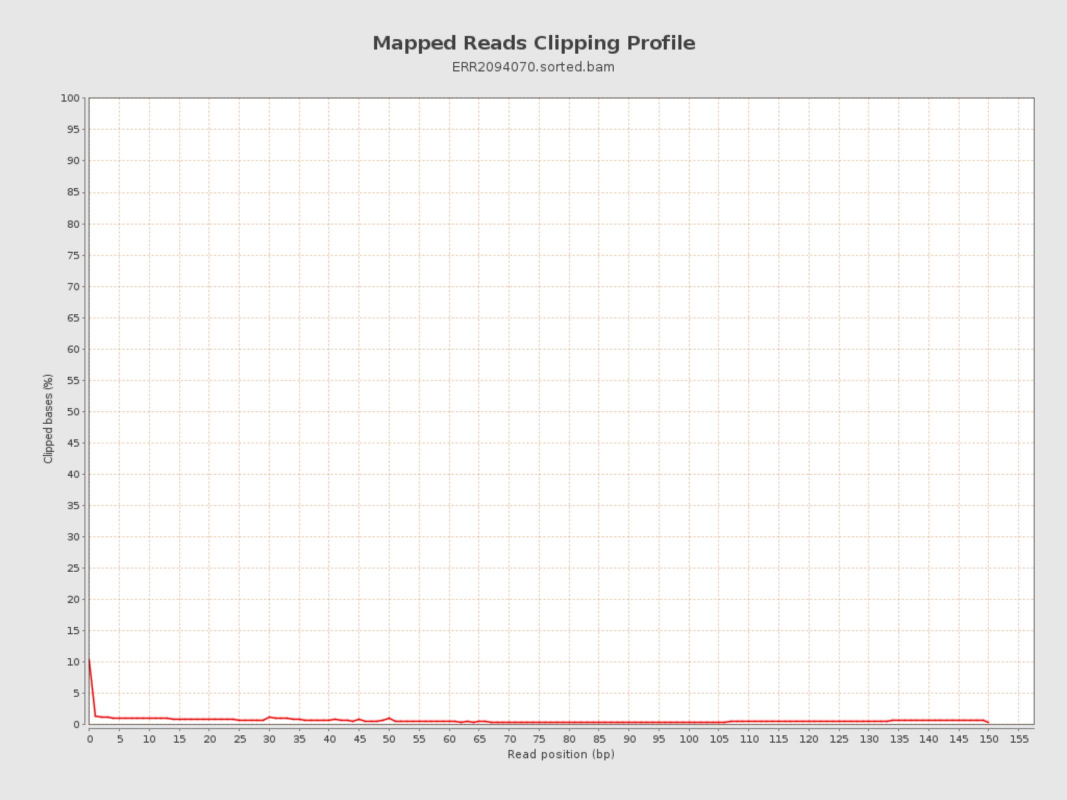
8. Results : Mapped Reads Nucleotide Content



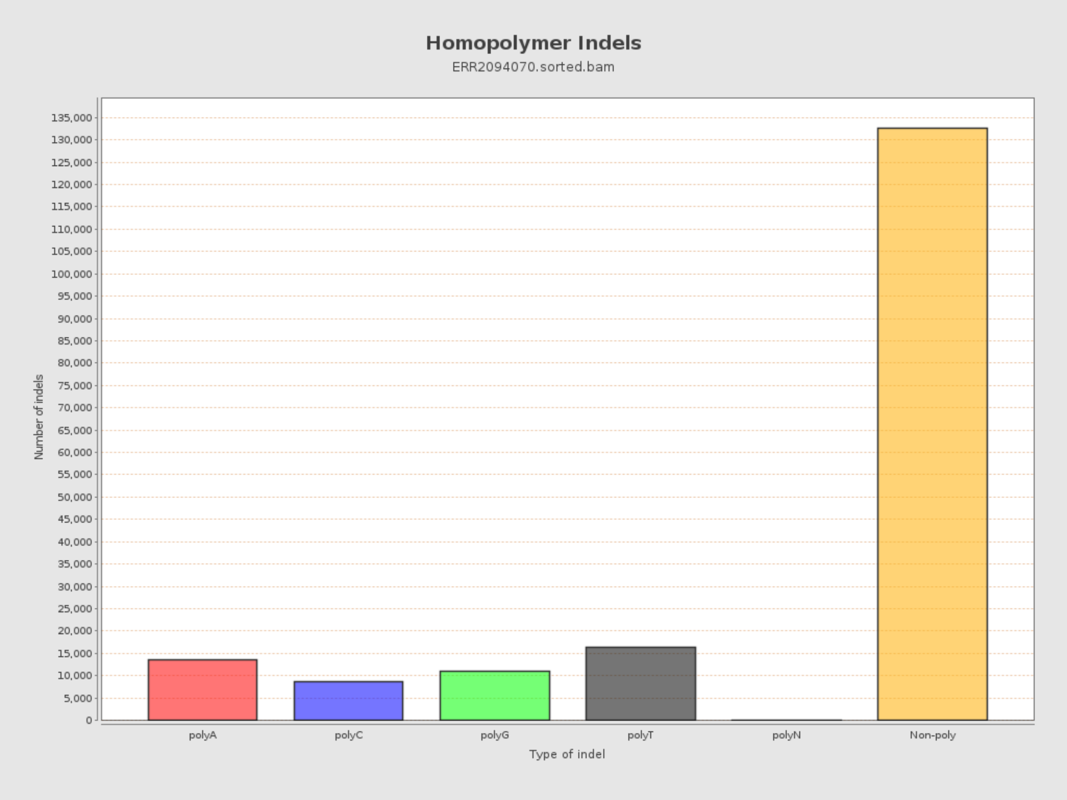
9. Results : Mapped Reads GC-content Distribution



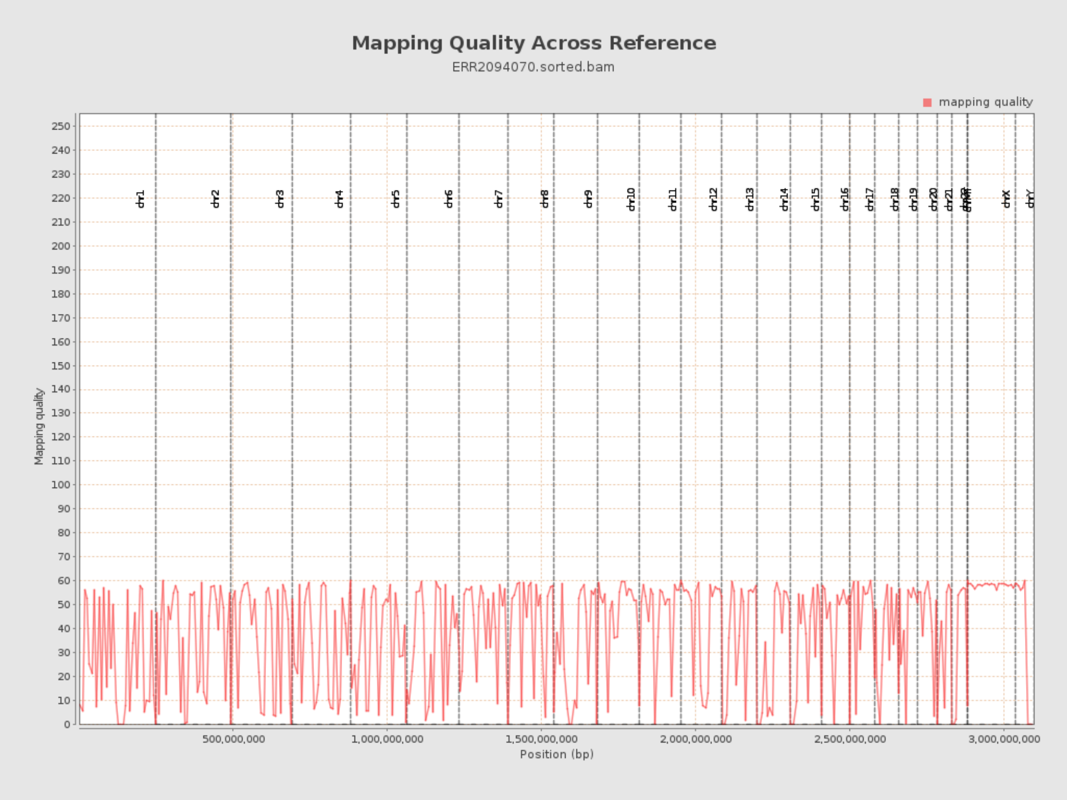
10. Results : Mapped Reads Clipping Profile



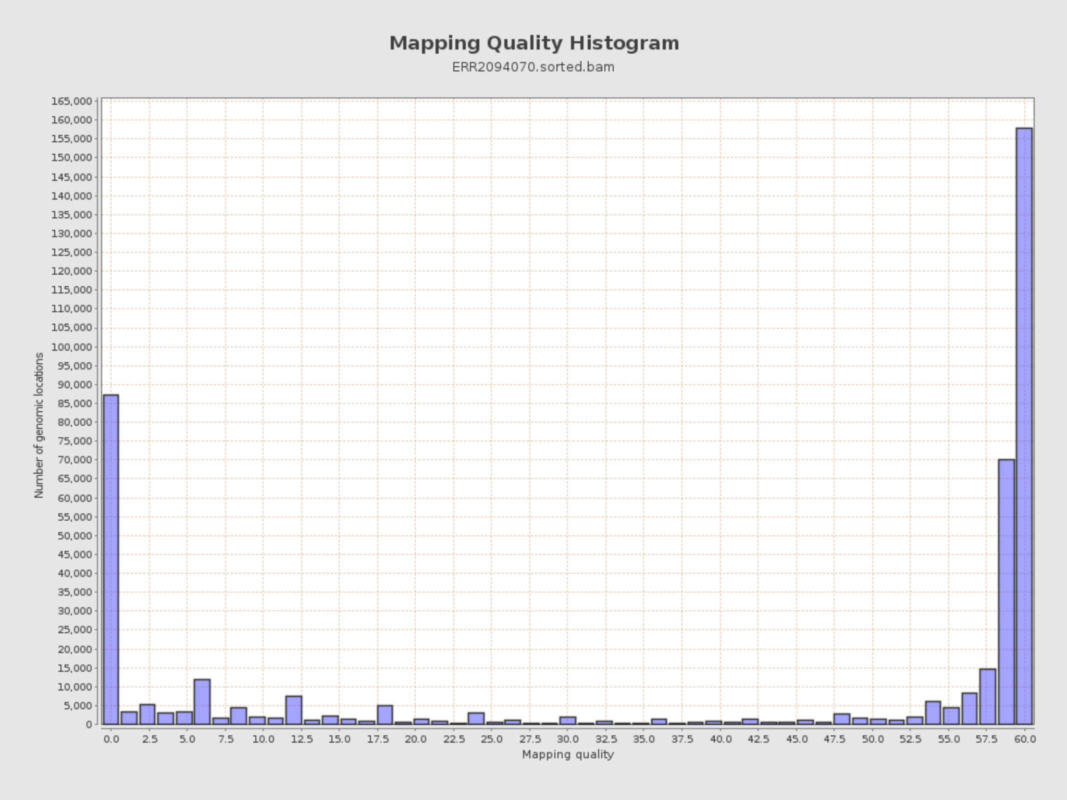
11. Results : Homopolymer Indels



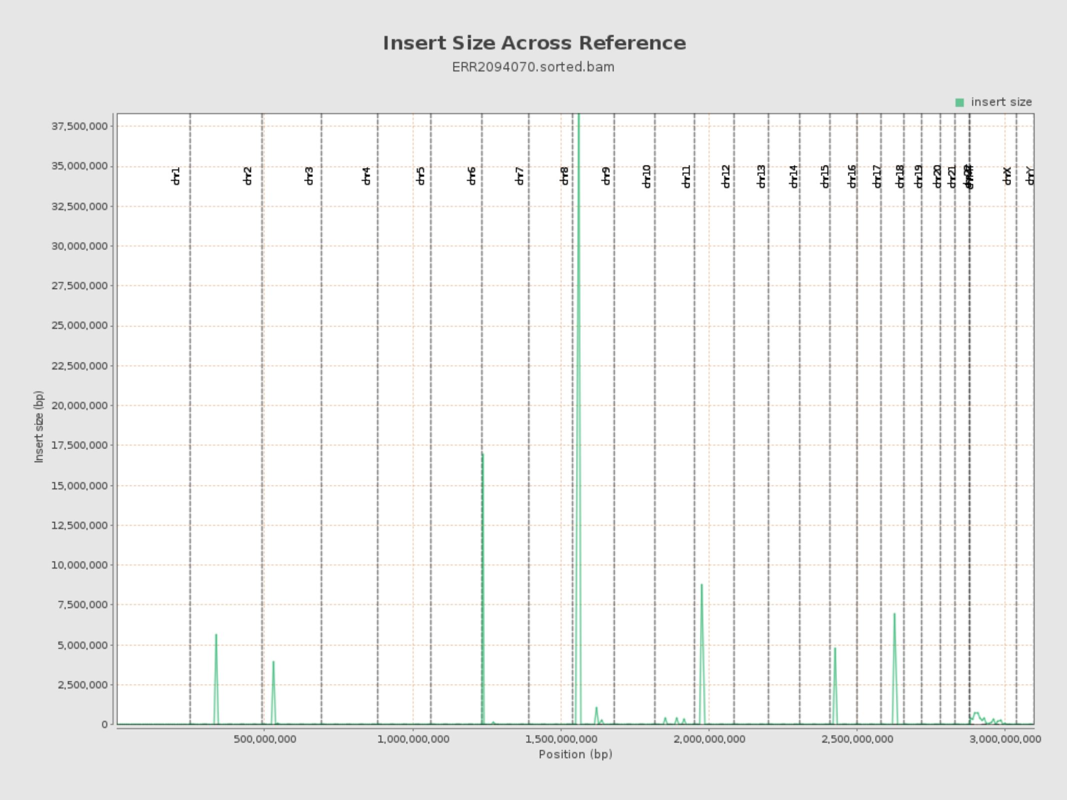
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram