Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:01:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094097.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_ERR2094097 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094097_1.fastq.gz ERR2094097_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	714
Mapped reads	478 / 66.95%
Unmapped reads	236 / 33.05%
Mapped paired reads	478 / 66.95%
Mapped reads, first in pair	251 / 35.15%
Mapped reads, second in pair	227 / 31.79%
Mapped reads, both in pair	394 / 55.18%
Mapped reads, singletons	84 / 11.76%
Secondary alignments	0
Supplementary alignments	39 / 5.46%
Read min/max/mean length	30 / 151 / 142.57
Duplicated reads (estimated)	60 / 8.4%
Duplication rate	8.32%
Clipped reads	385 / 53.92%

2.2. ACGT Content

Number/percentage of A's	16,774 / 32.97%
Number/percentage of C's	10,697 / 21.02%
Number/percentage of T's	12,520 / 24.6%
Number/percentage of G's	10,893 / 21.41%
Number/percentage of N's	0 / 0%

GC Percentage	42.43%

2.3. Coverage

Mean	0
Standard Deviation	0.0068

2.4. Mapping Quality

Mean Mapping Quality	12.45

2.5. Insert size

Mean	809,491.8
Standard Deviation	7,226,691.33
P25/Median/P75	154 / 182 / 210

2.6. Mismatches and indels

General error rate	3.58%
Mismatches	1,747
Insertions	38
Mapped reads with at least one insertion	7.53%
Deletions	111
Mapped reads with at least one deletion	22.18%
Homopolymer indels	24.16%

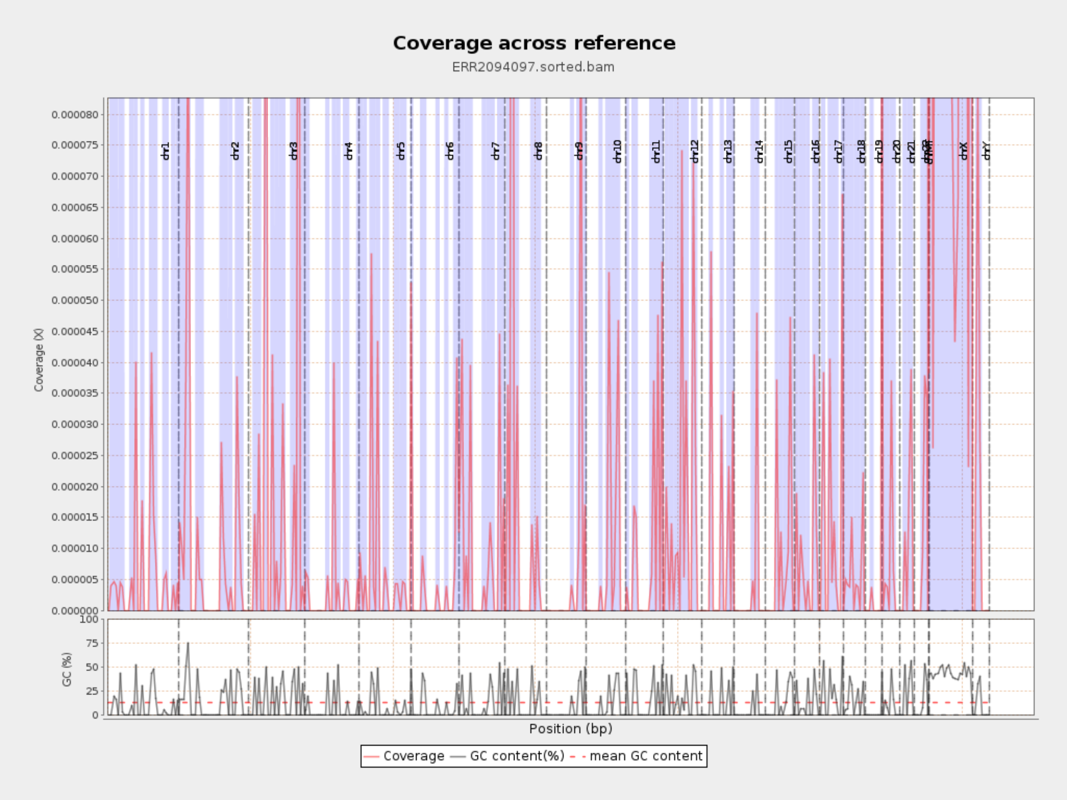
2.7. Chromosome stats

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

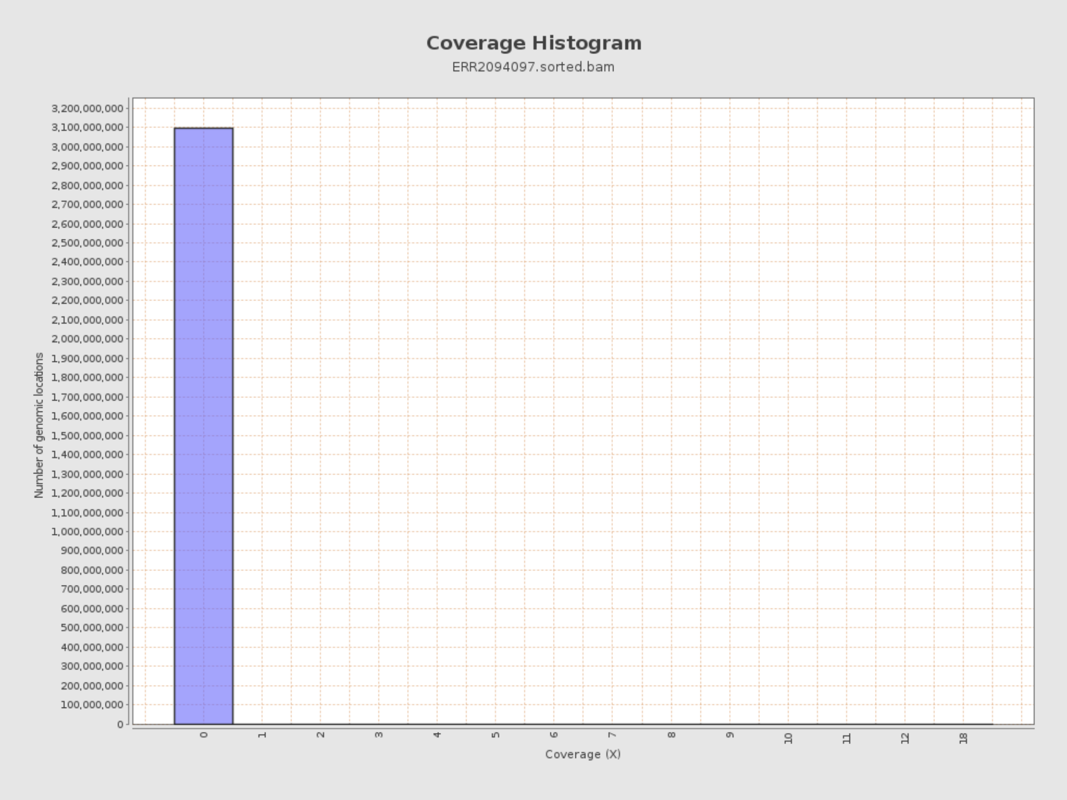
		bases	coverage	deviation
chr1	249250621	1313	0	0.0024
chr2	243199373	2301	0	0.0039
chr3	198022430	3747	0	0.0087
chr4	191154276	577	0	0.002
chr5	180915260	1151	0	0.0033
chr6	171115067	858	0	0.0024
chr7	159138663	1539	0	0.0037
chr8	146364022	3689	0	0.017
chr9	141213431	1068	0	0.0033
chr10	135534747	1062	0	0.0033
chr11	135006516	1413	0	0.0037
chr12	133851895	2058	0	0.0053
chr13	115169878	1147	0	0.0044
chr14	107349540	408	0	0.0025
chr15	102531392	894	0	0.0032
chr16	90354753	733	0	0.0032
chr17	81195210	1071	0	0.0042
chr18	78077248	452	0	0.0025
chr19	59128983	313	0	0.0023
chr20	63025520	399	0	0.0025
chr21	48129895	559	0	0.0042
chr22	51304566	628	0	0.0044
chrMT	16571	1498	0.0904	0.5543
chrX	155270560	21951	0.0001	0.0179

chrY	59373566	862	0	0.0052

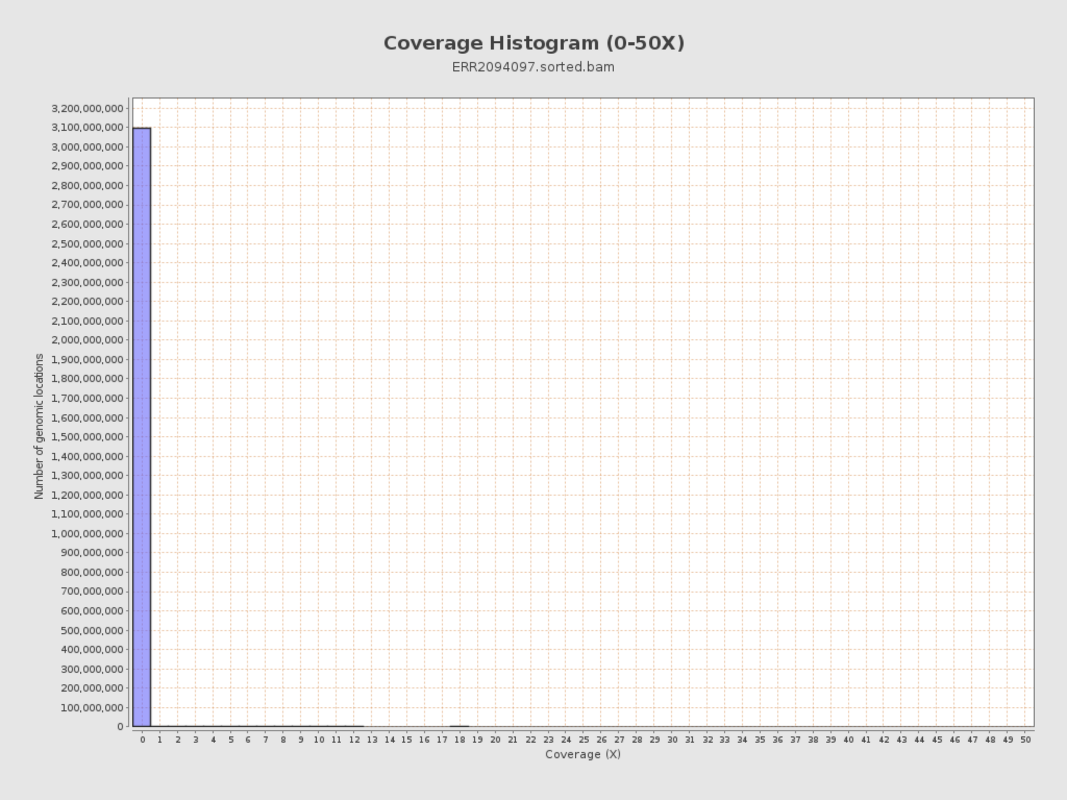
3. Results : Coverage across reference



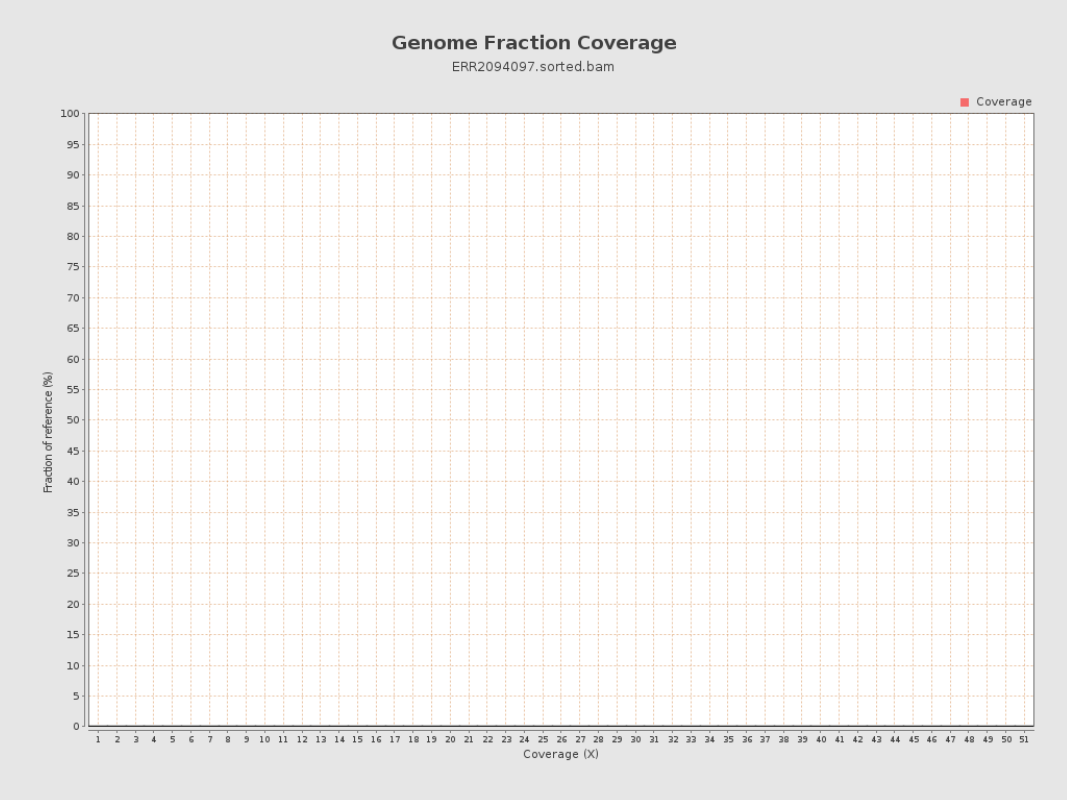
4. Results : Coverage Histogram



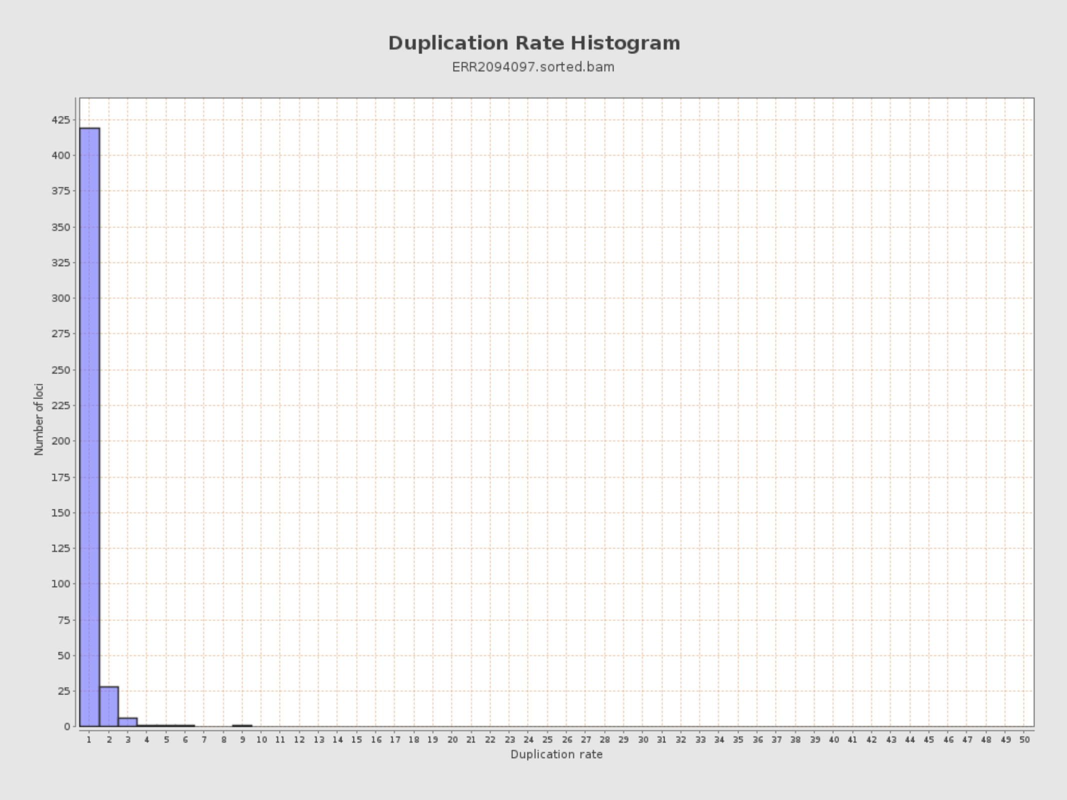
5. Results : Coverage Histogram (0-50X)



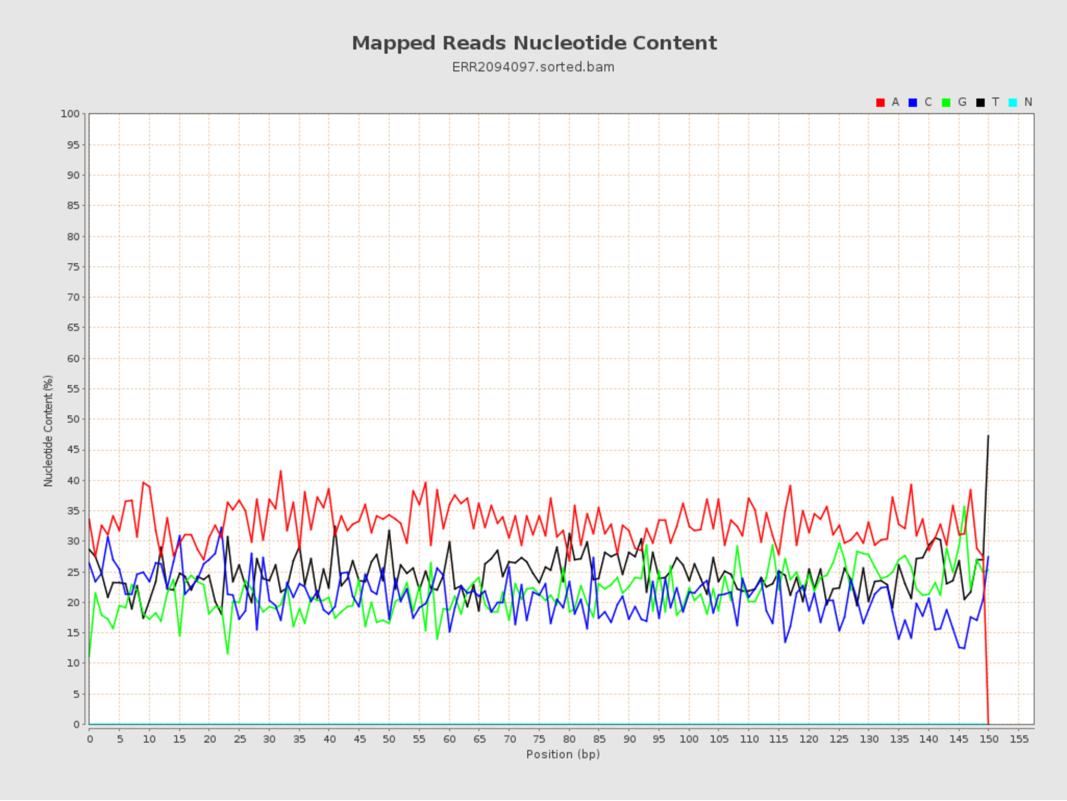
6. Results : Genome Fraction Coverage



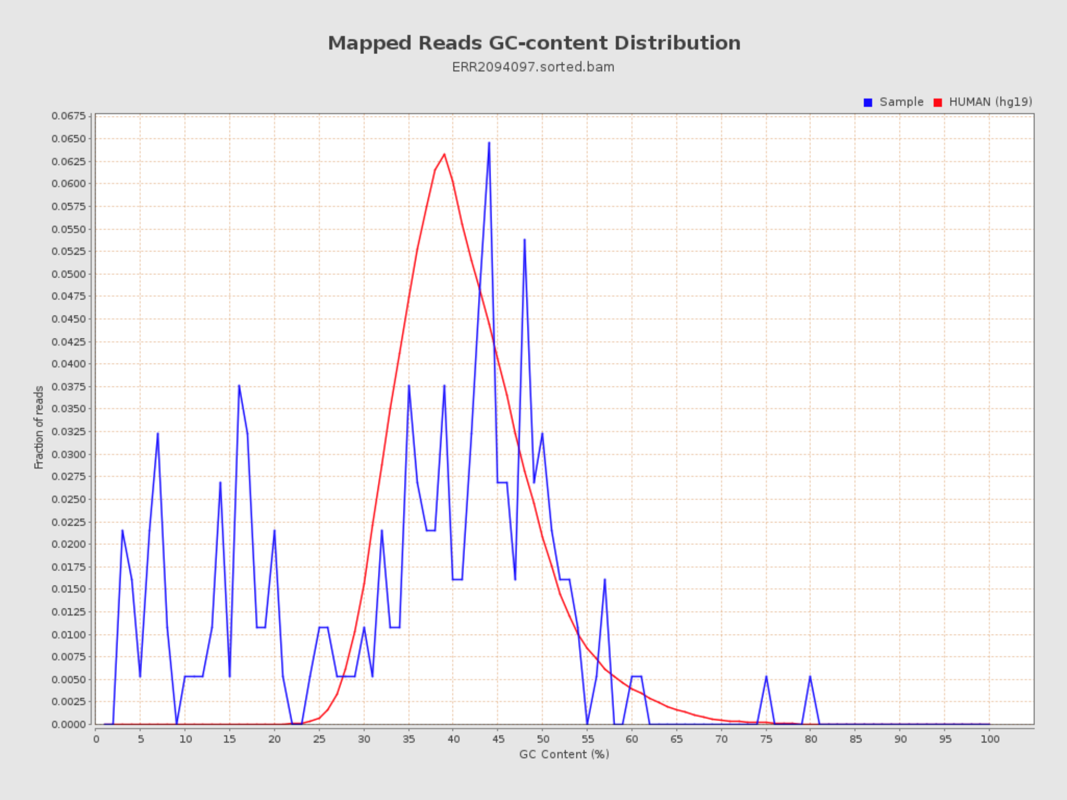
7. Results : Duplication Rate Histogram



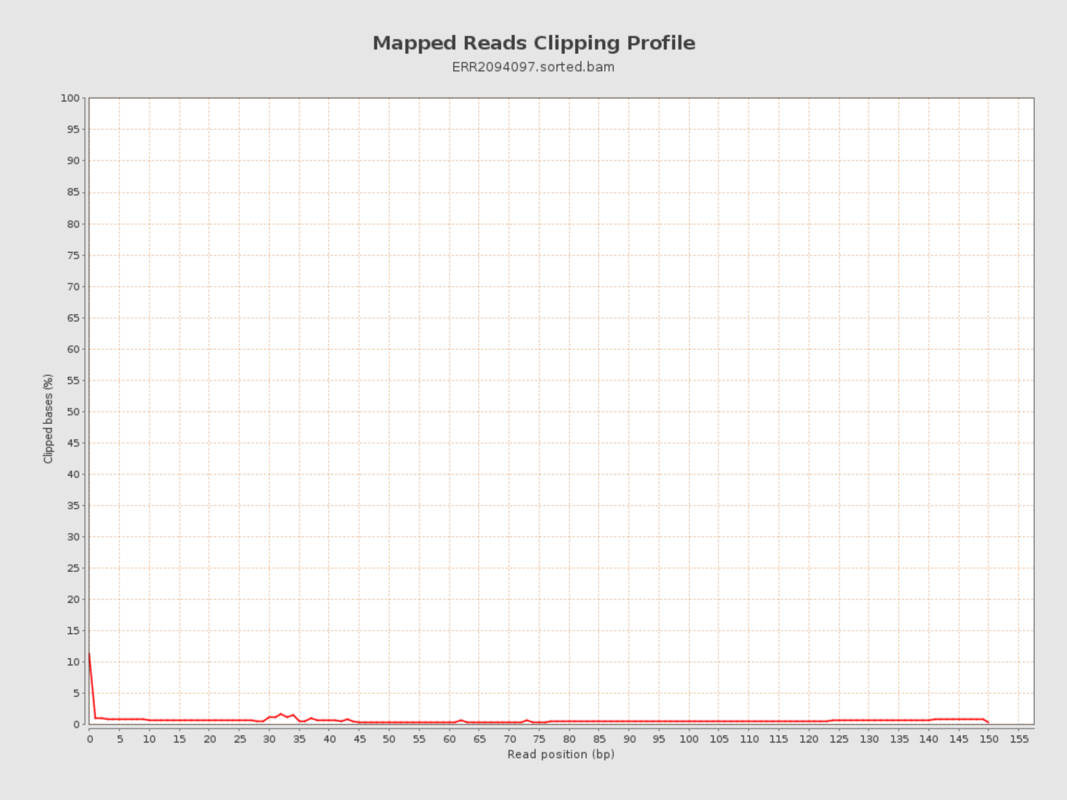
8. Results : Mapped Reads Nucleotide Content



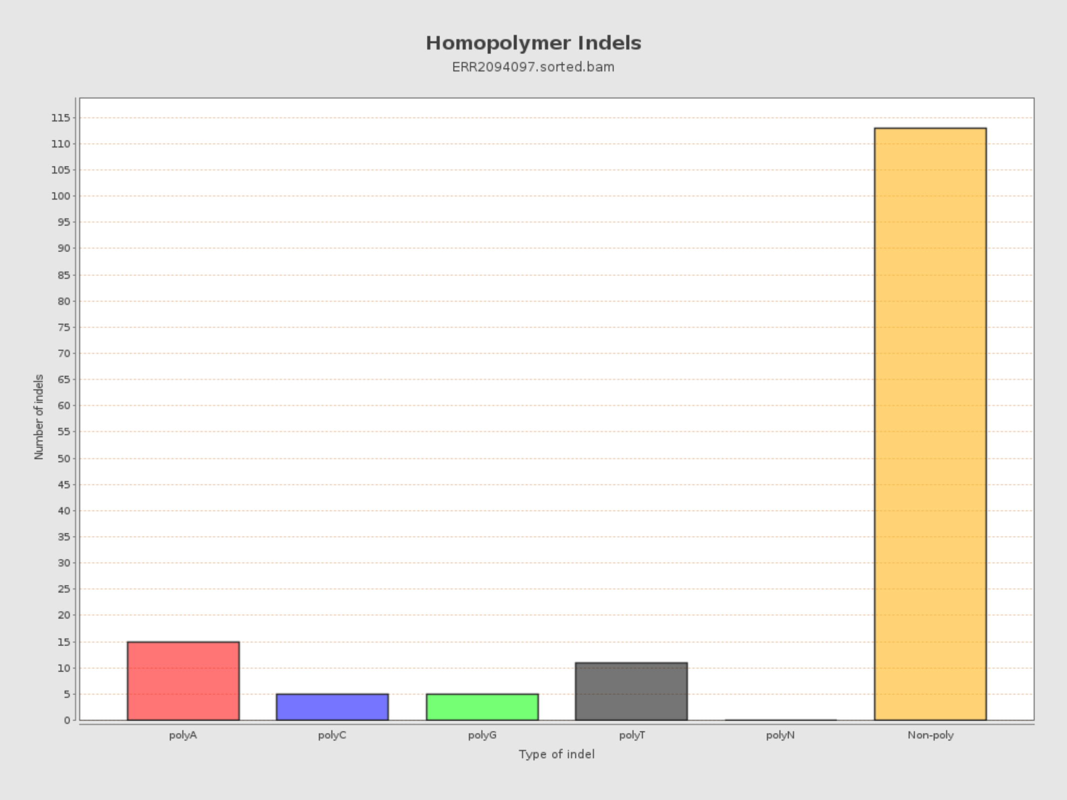
9. Results : Mapped Reads GC-content Distribution



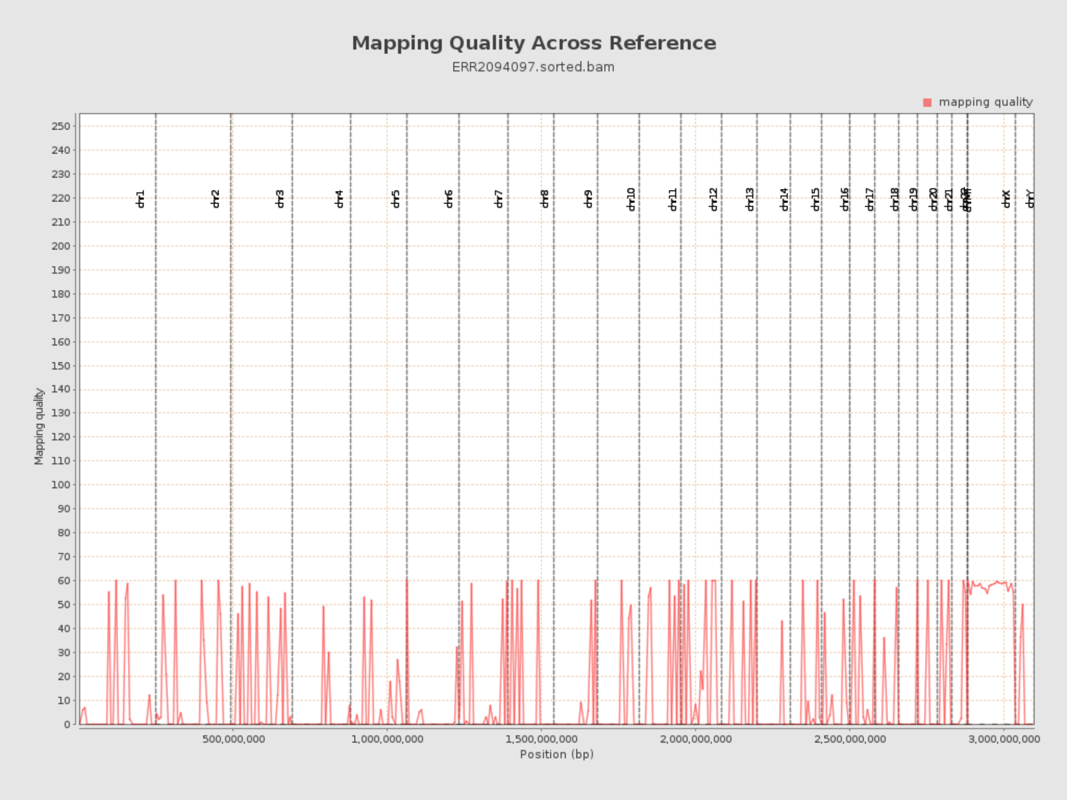
10. Results : Mapped Reads Clipping Profile



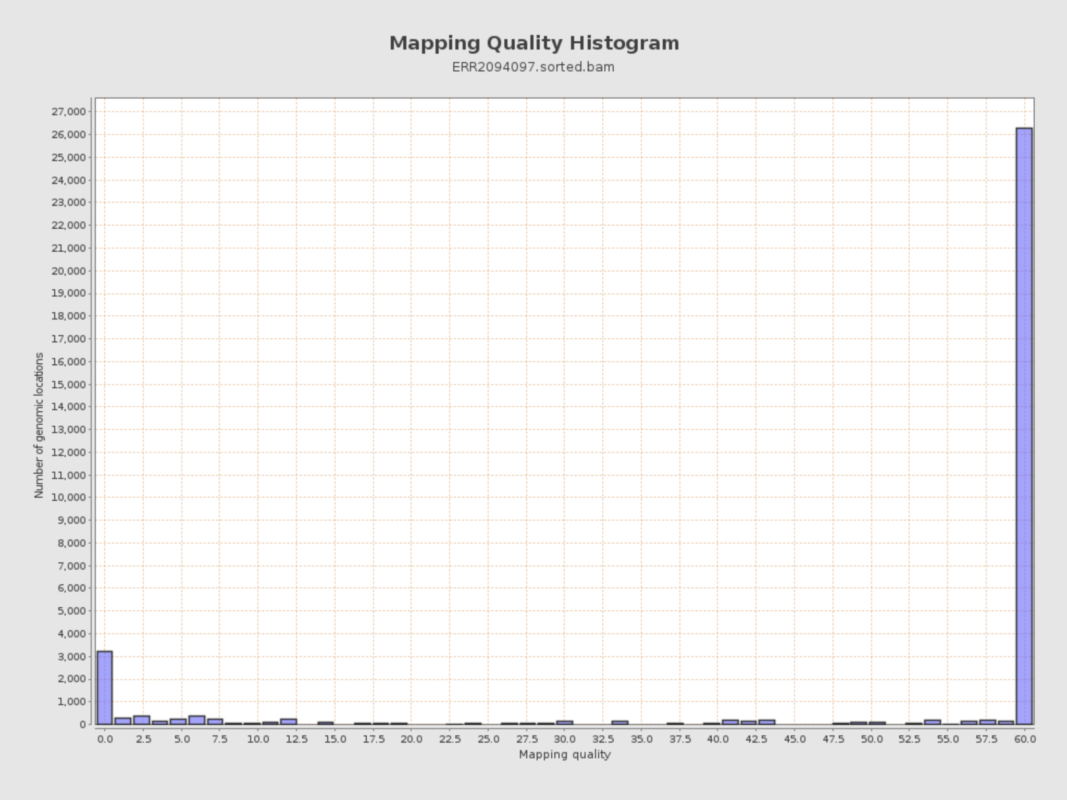
11. Results : Homopolymer Indels



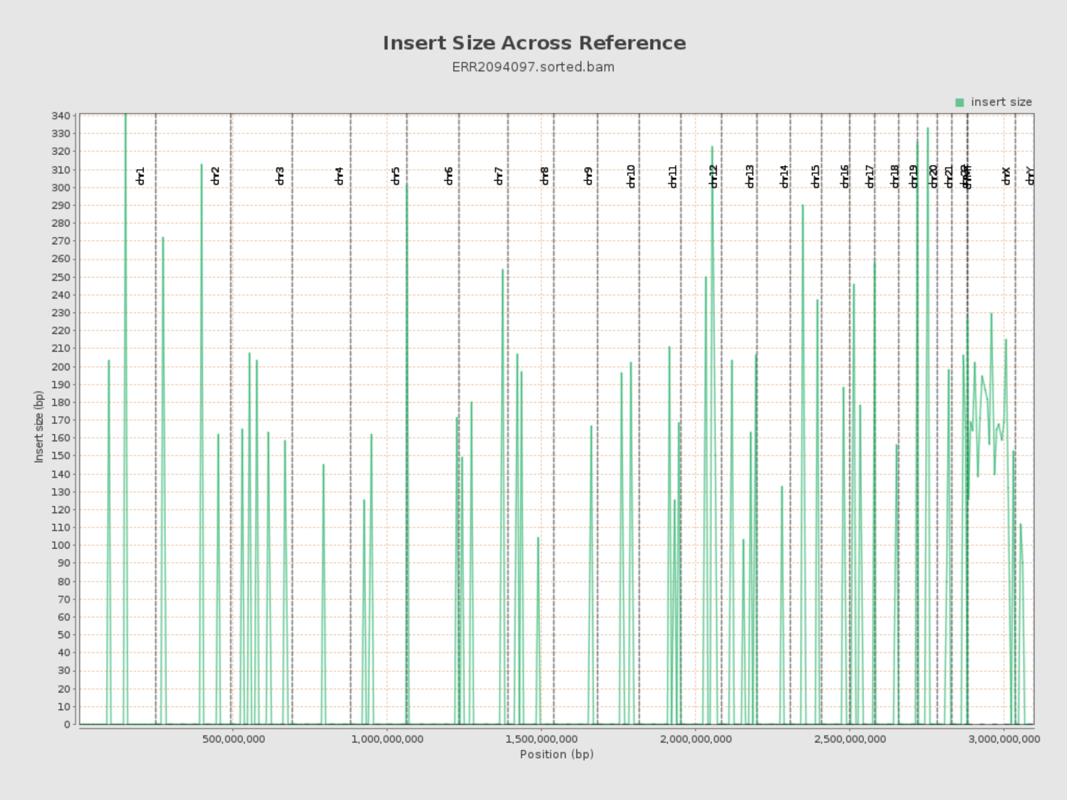
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram