Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:37:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094160.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_ERR2094160 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094160_1.fastq.gz ERR2094160_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:37:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,044
Mapped reads	900 / 2.57%
Unmapped reads	34,144 / 97.43%
Mapped paired reads	900 / 2.57%
Mapped reads, first in pair	305 / 0.87%
Mapped reads, second in pair	595 / 1.7%
Mapped reads, both in pair	484 / 1.38%
Mapped reads, singletons	416 / 1.19%
Secondary alignments	0
Supplementary alignments	22 / 0.06%
Read min/max/mean length	30 / 151 / 61.29
Duplicated reads (estimated)	641 / 1.83%
Duplication rate	24.56%
Clipped reads	735 / 2.1%

2.2. ACGT Content

Number/percentage of A's	7,582 / 12.86%
Number/percentage of C's	5,557 / 9.42%
Number/percentage of T's	6,305 / 10.69%
Number/percentage of G's	39,526 / 67.03%
Number/percentage of N's	1 / 0%

GC Percentage	76.45%

2.3. Coverage

Mean	0
Standard Deviation	0.0421

2.4. Mapping Quality

Mean Mapping Quality	3.7

2.5. Insert size

Mean	7,488.87
Standard Deviation	76,085.01
P25/Median/P75	30 / 31 / 65

2.6. Mismatches and indels

General error rate	2.96%
Mismatches	1,288
Insertions	74
Mapped reads with at least one insertion	6%
Deletions	40
Mapped reads with at least one deletion	3.78%
Homopolymer indels	61.4%

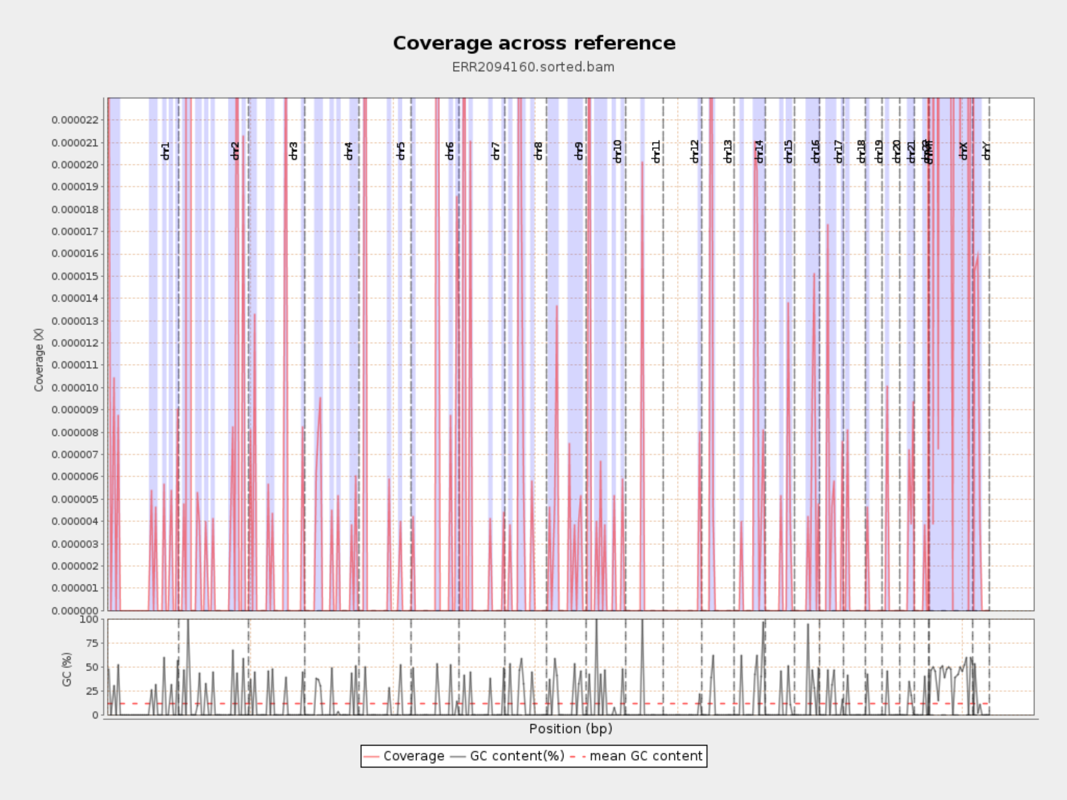
2.7. Chromosome stats

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

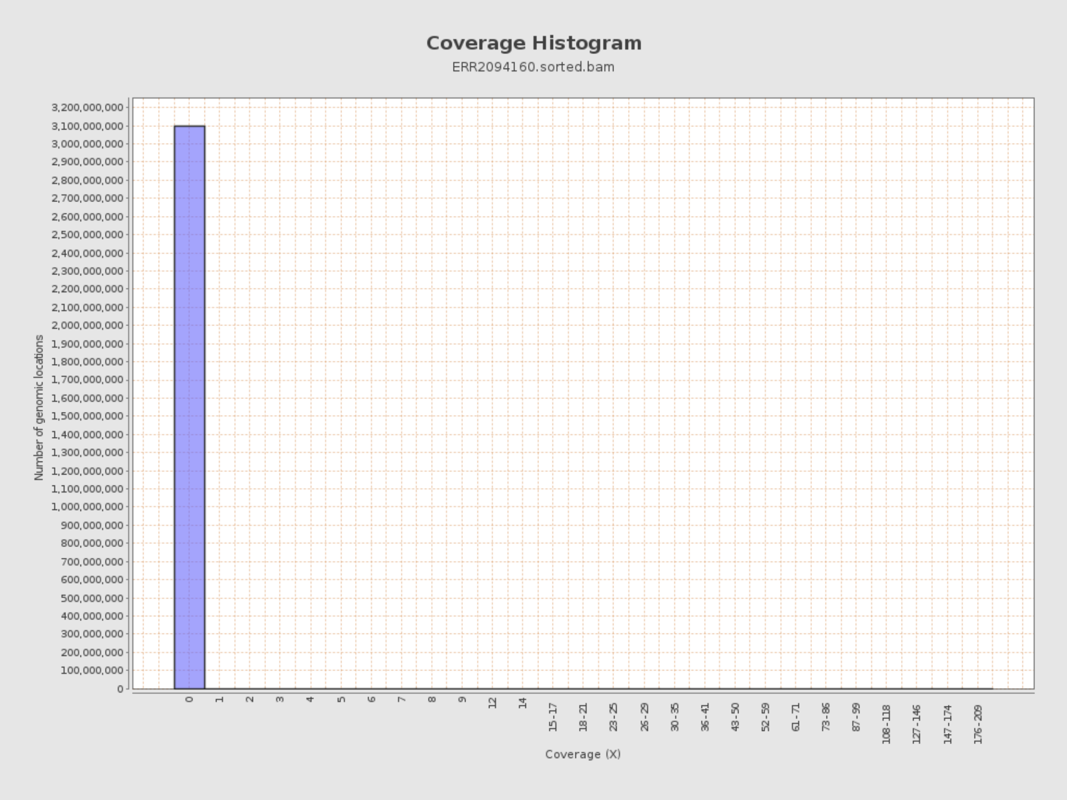
		bases	coverage	deviation
chr1	249250621	577	0	0.0019
chr2	243199373	34635	0.0001	0.1399
chr3	198022430	520	0	0.0019
chr4	191154276	337	0	0.0013
chr5	180915260	406	0	0.0036
chr6	171115067	650	0	0.0042
chr7	159138663	532	0	0.0021
chr8	146364022	559	0	0.0023
chr9	141213431	339	0	0.0017
chr10	135534747	464	0	0.0023
chr11	135006516	156	0	0.0023
chr12	133851895	62	0	0.0007
chr13	115169878	333	0	0.0023
chr14	107349540	440	0	0.0032
chr15	102531392	177	0	0.0015
chr16	90354753	260	0	0.0017
chr17	81195210	247	0	0.0028
chr18	78077248	63	0	0.0009
chr19	59128983	36	0	0.0008
chr20	63025520	78	0	0.0016
chr21	48129895	132	0	0.0017
chr22	51304566	30	0	0.0008
chrMT	16571	1873	0.113	0.5964
chrX	155270560	15961	0.0001	0.0678

chrY	59373566	271	0	0.0026

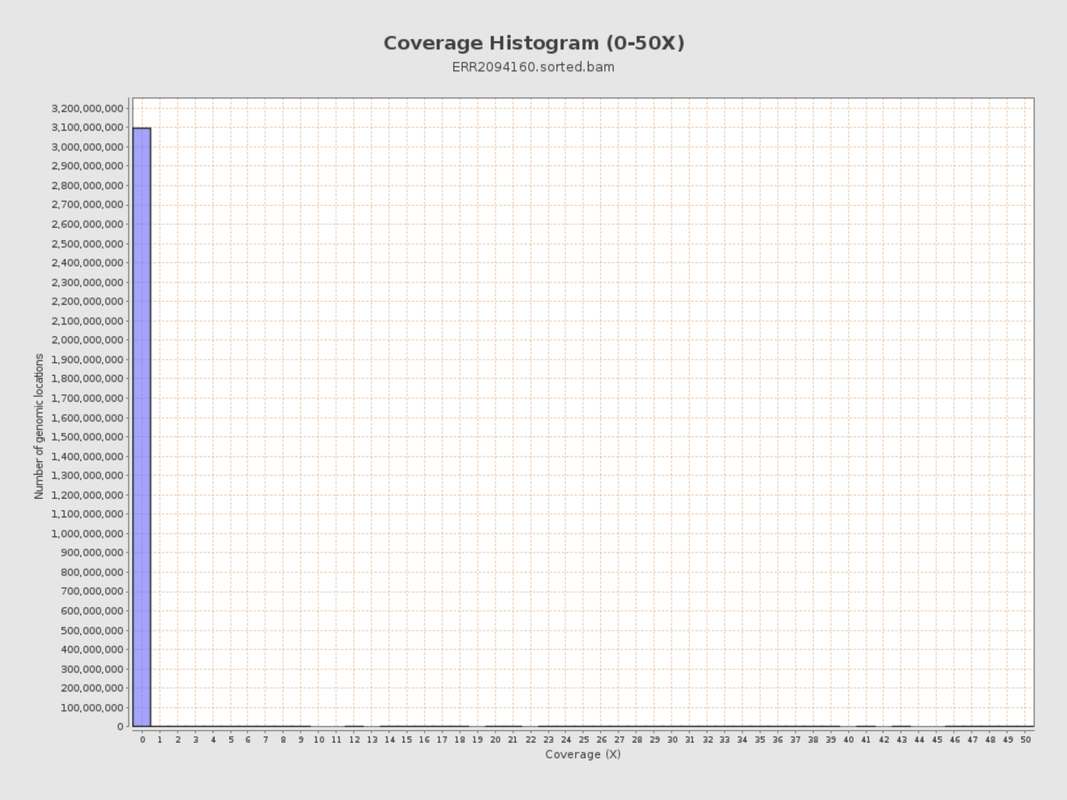
3. Results : Coverage across reference



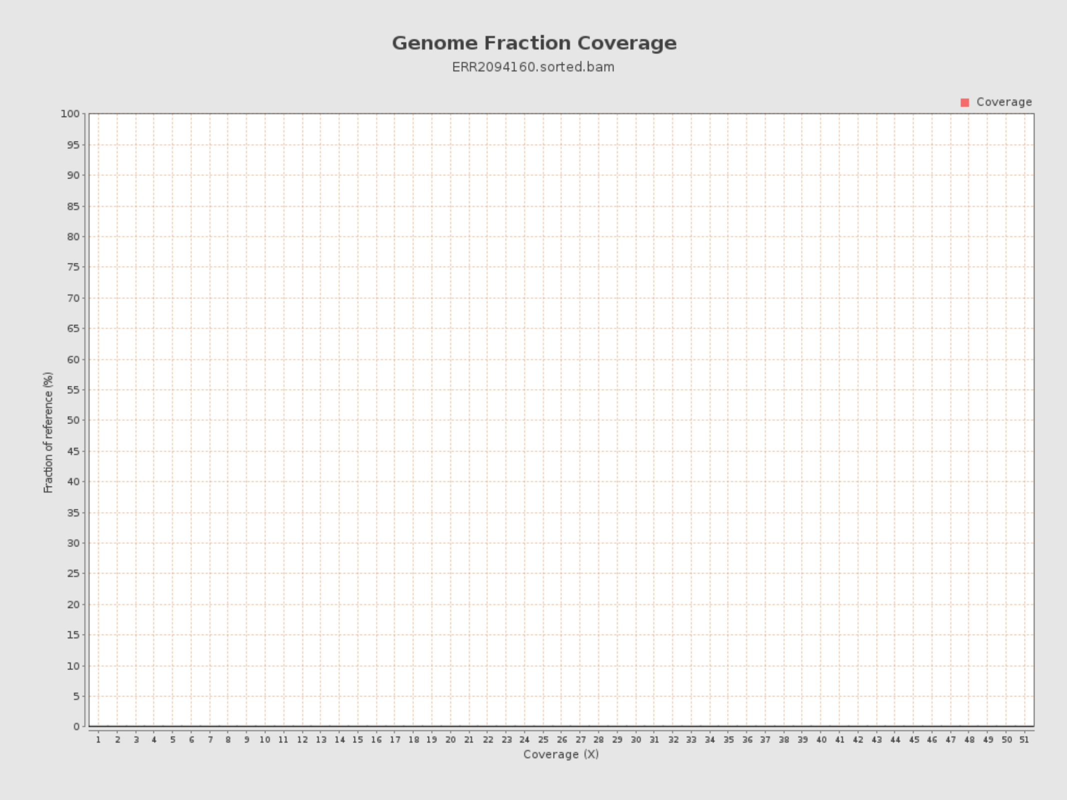
4. Results : Coverage Histogram



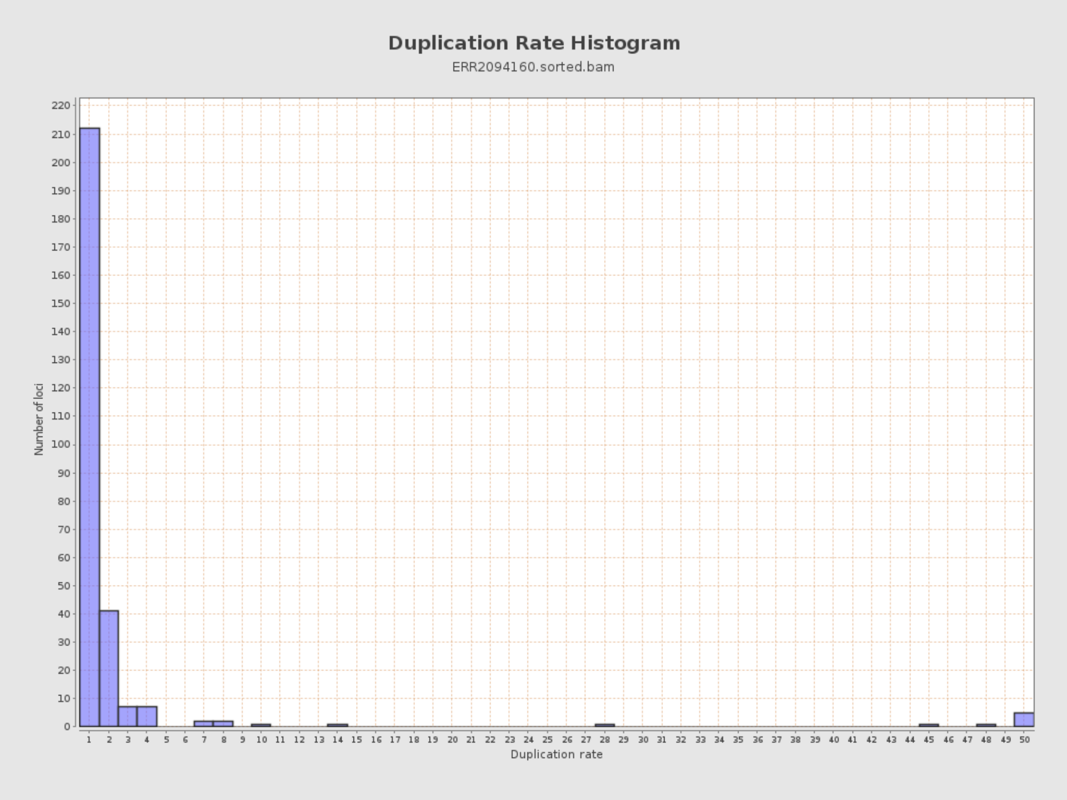
5. Results : Coverage Histogram (0-50X)



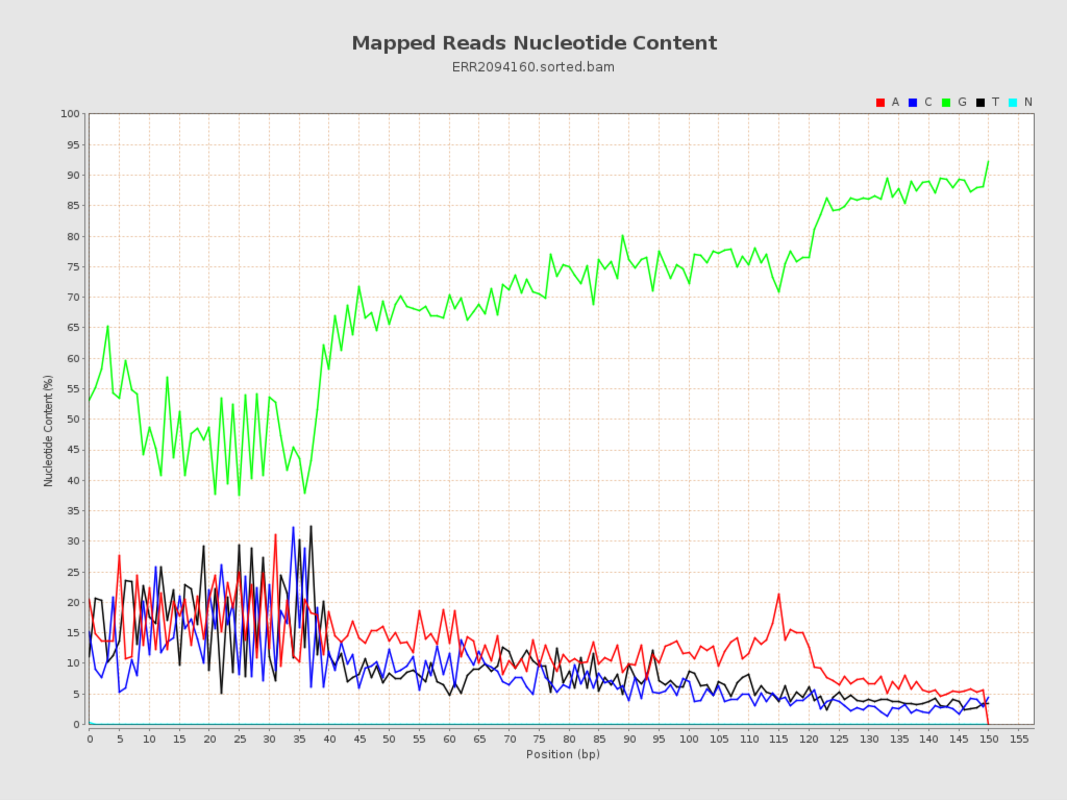
6. Results : Genome Fraction Coverage



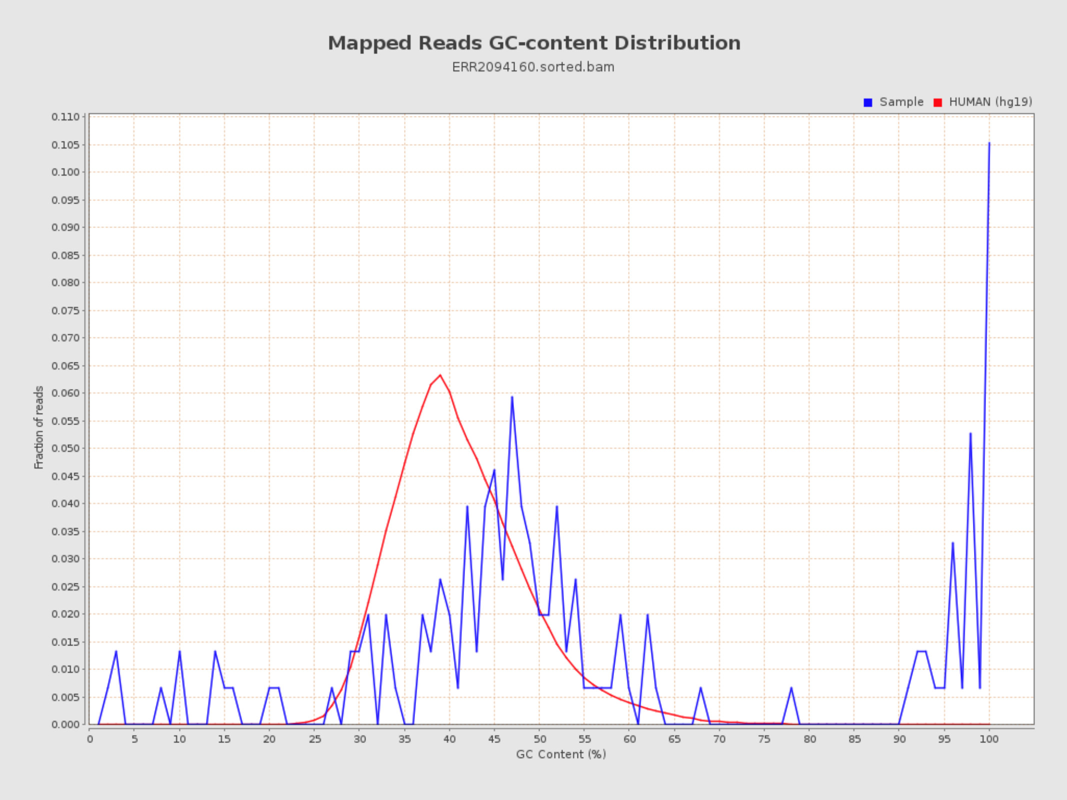
7. Results : Duplication Rate Histogram



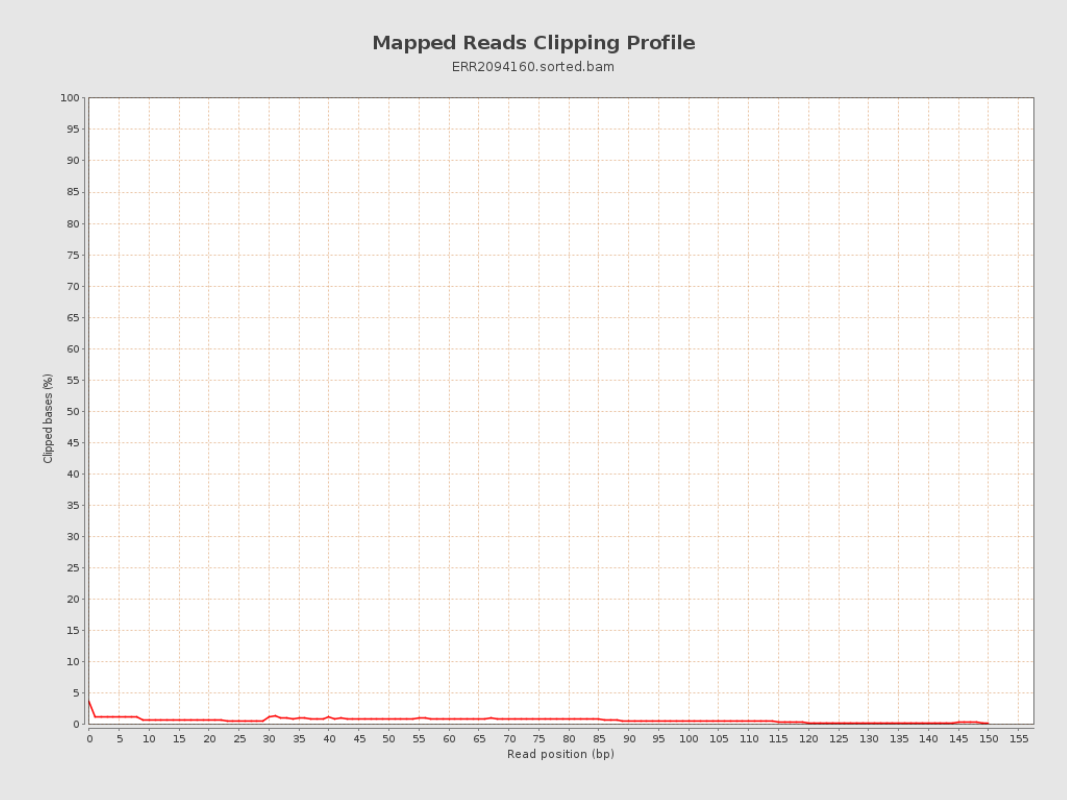
8. Results : Mapped Reads Nucleotide Content



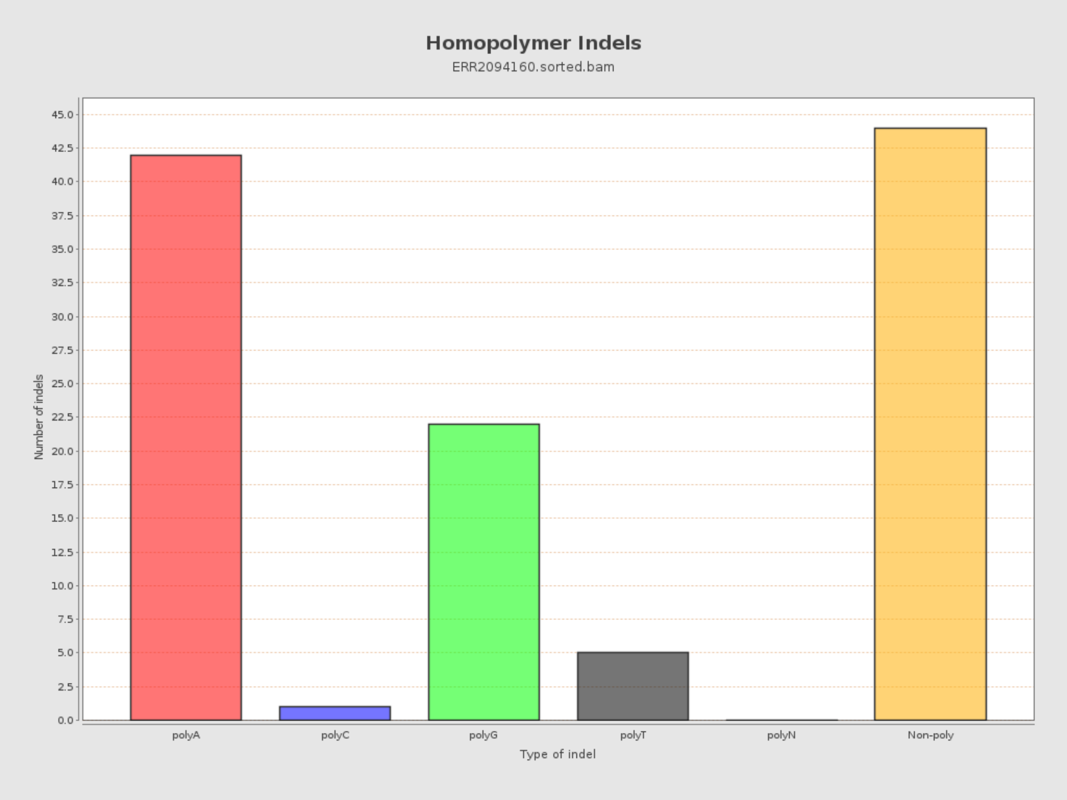
9. Results : Mapped Reads GC-content Distribution



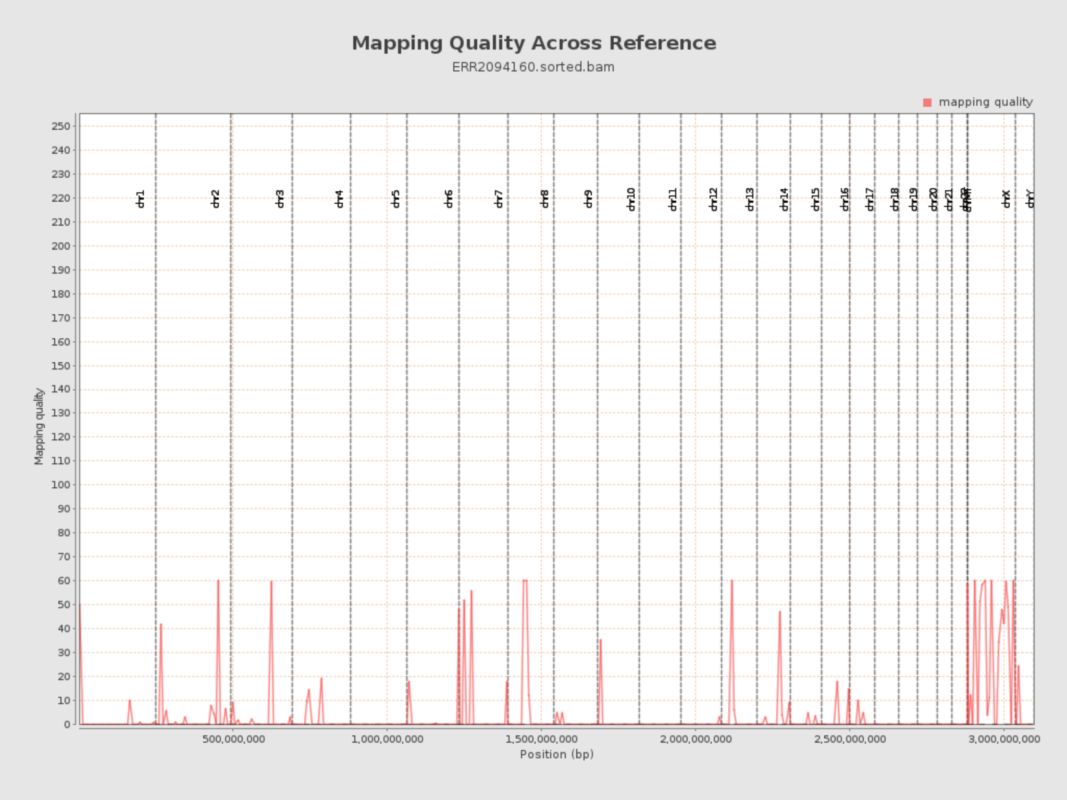
10. Results : Mapped Reads Clipping Profile



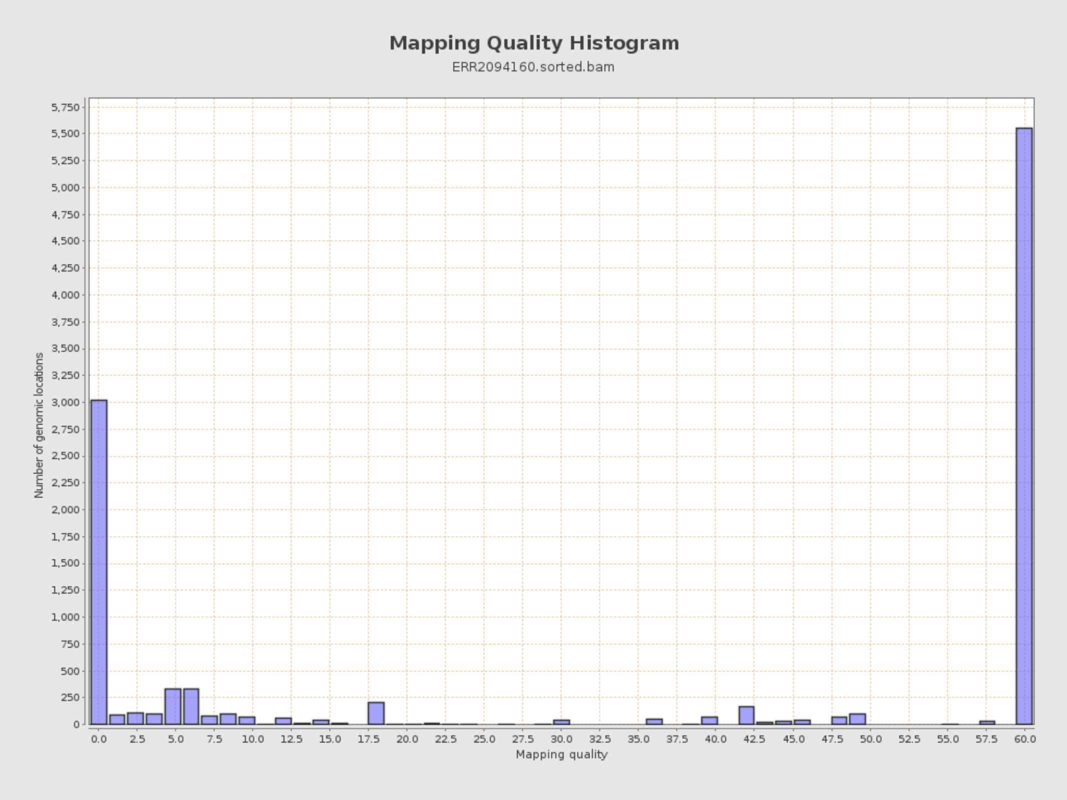
11. Results : Homopolymer Indels



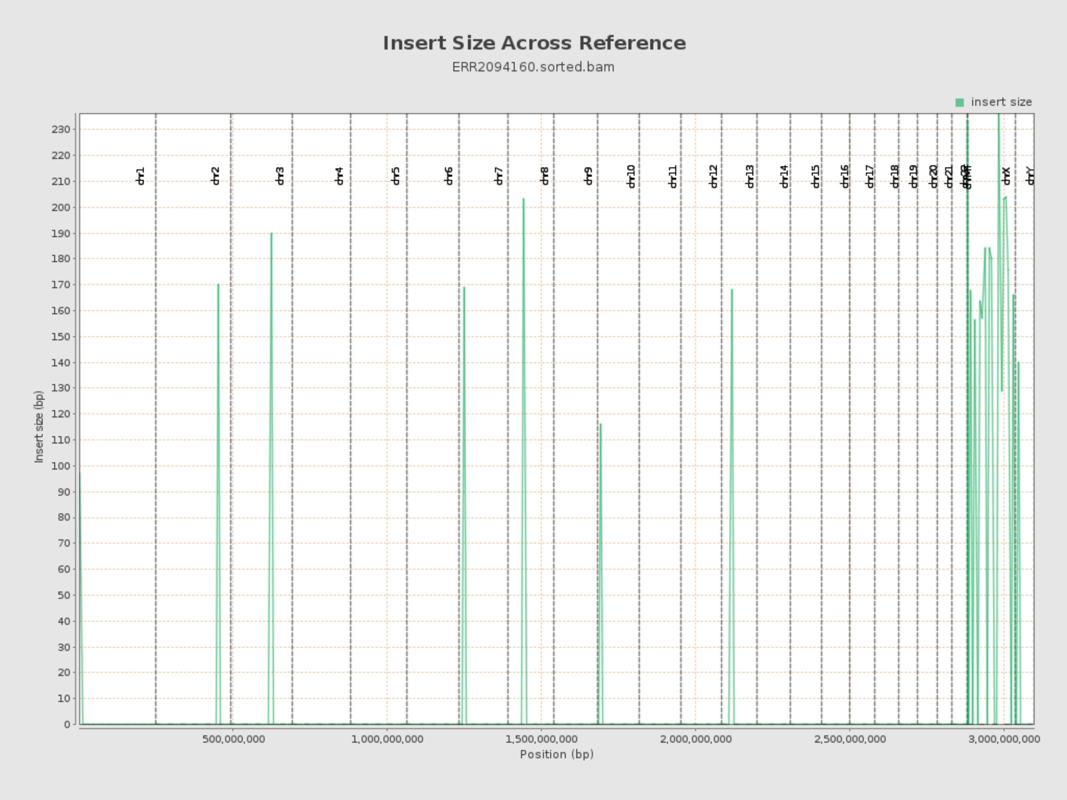
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram