Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:30:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094030.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_ERR2094030 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094030_1.fastq.gz ERR2094030_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:30:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	480,220
Mapped reads	447,555 / 93.2%
Unmapped reads	32,665 / 6.8%
Mapped paired reads	447,555 / 93.2%
Mapped reads, first in pair	225,032 / 46.86%
Mapped reads, second in pair	222,523 / 46.34%
Mapped reads, both in pair	441,178 / 91.87%
Mapped reads, singletons	6,377 / 1.33%
Secondary alignments	0
Supplementary alignments	18,031 / 3.75%
Read min/max/mean length	30 / 151 / 143.17
Duplicated reads (estimated)	419,241 / 87.3%
Duplication rate	43.96%
Clipped reads	203,470 / 42.37%

2.2. ACGT Content

Number/percentage of A's	16,028,877 / 27.88%
Number/percentage of C's	12,746,984 / 22.17%
Number/percentage of T's	15,559,962 / 27.07%
Number/percentage of G's	13,148,149 / 22.87%
Number/percentage of N's	513 / 0%

GC Percentage	45.05%

2.3. Coverage

Mean	0.0189
Standard Deviation	7.8593

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Insert size

Mean	337,507.9
Standard Deviation	5,511,759.38
P25/Median/P75	143 / 175 / 217

2.6. Mismatches and indels

General error rate	3.7%
Mismatches	2,040,545
Insertions	36,827
Mapped reads with at least one insertion	8.1%
Deletions	150,393
Mapped reads with at least one deletion	32.5%
Homopolymer indels	28.44%

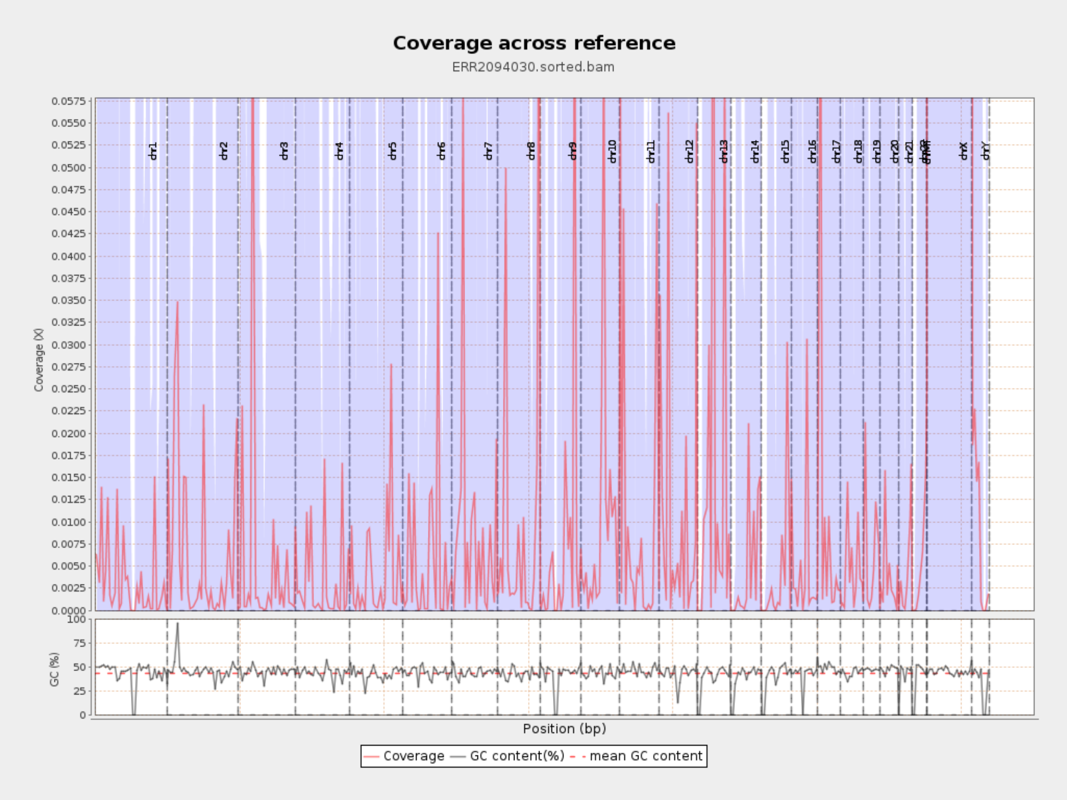
2.7. Chromosome stats

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

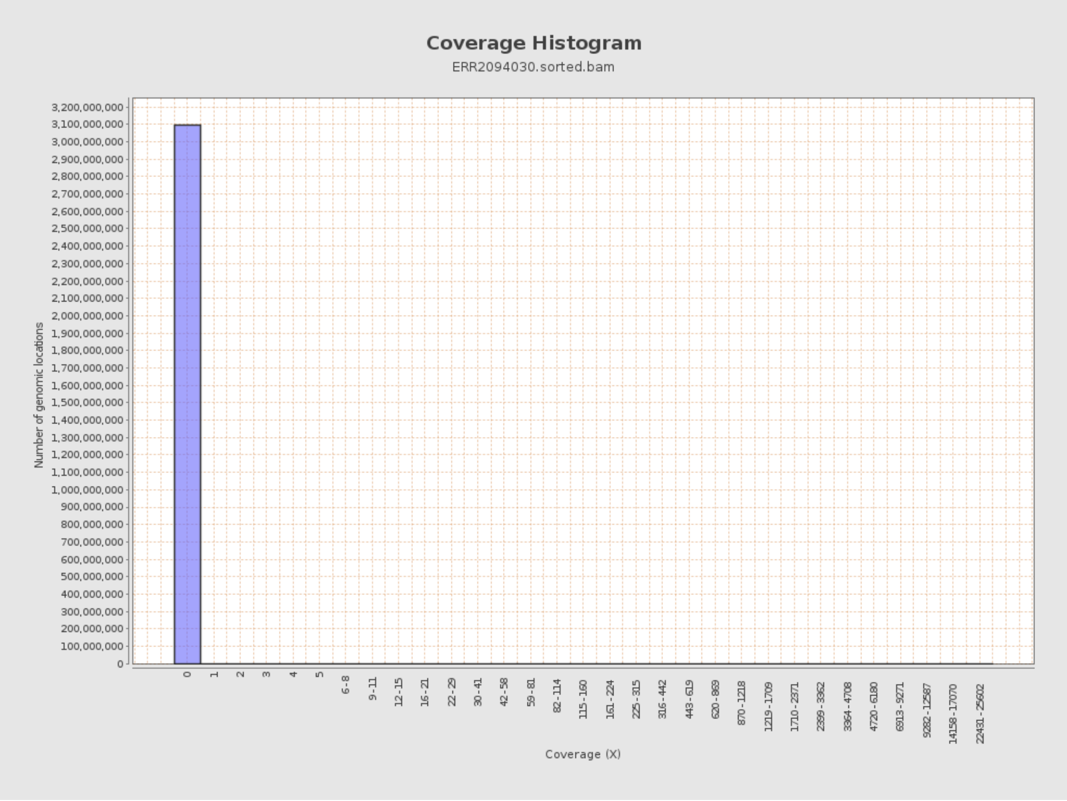
		bases	coverage	deviation
chr1	249250621	843439	0.0034	1.025
chr2	243199373	1605065	0.0066	1.6749
chr3	198022430	1071680	0.0054	1.9404
chr4	191154276	681116	0.0036	1.0685
chr5	180915260	819640	0.0045	1.6306
chr6	171115067	997828	0.0058	2.5515
chr7	159138663	1370591	0.0086	1.9578
chr8	146364022	1511721	0.0103	3.9059
chr9	141213431	1074223	0.0076	2.7264
chr10	135534747	1423220	0.0105	3.5749
chr11	135006516	1304998	0.0097	3.0237
chr12	133851895	1461590	0.0109	3.4799
chr13	115169878	1945328	0.0169	5.8449
chr14	107349540	524421	0.0049	1.3773
chr15	102531392	438776	0.0043	1.6208
chr16	90354753	451600	0.005	1.8524
chr17	81195210	1012344	0.0125	3.2432
chr18	78077248	355759	0.0046	1.258
chr19	59128983	379396	0.0064	1.0793
chr20	63025520	246305	0.0039	1.146
chr21	48129895	215897	0.0045	0.5638
chr22	51304566	269192	0.0052	0.781
chrMT	16571	10838209	654.0468	2,796.4292
chrX	155270560	27234840	0.1754	15.3284

chrY	59373566	536712	0.009	1.7979

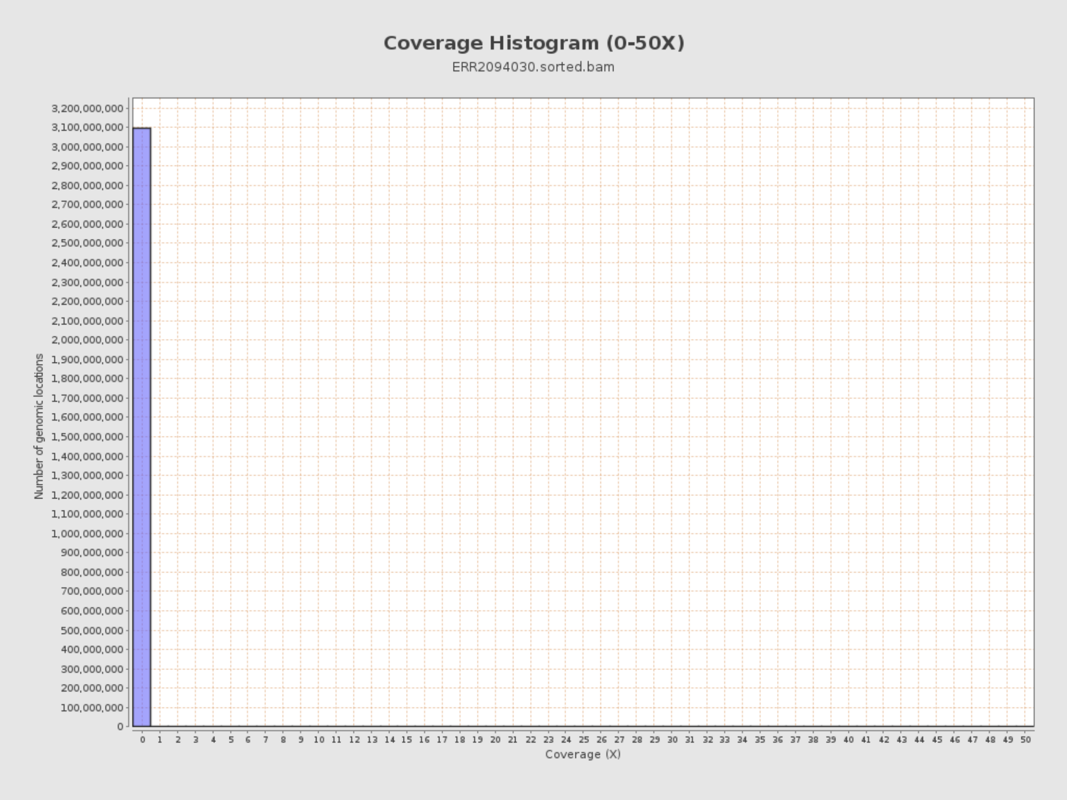
3. Results : Coverage across reference



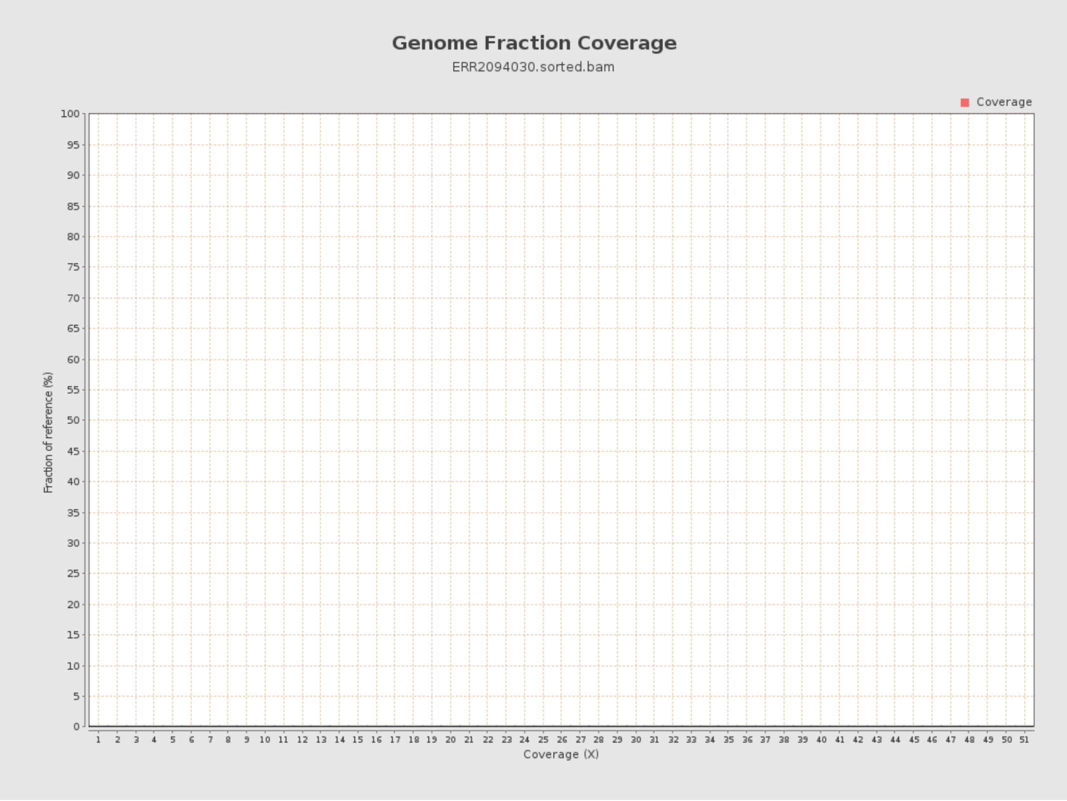
4. Results : Coverage Histogram



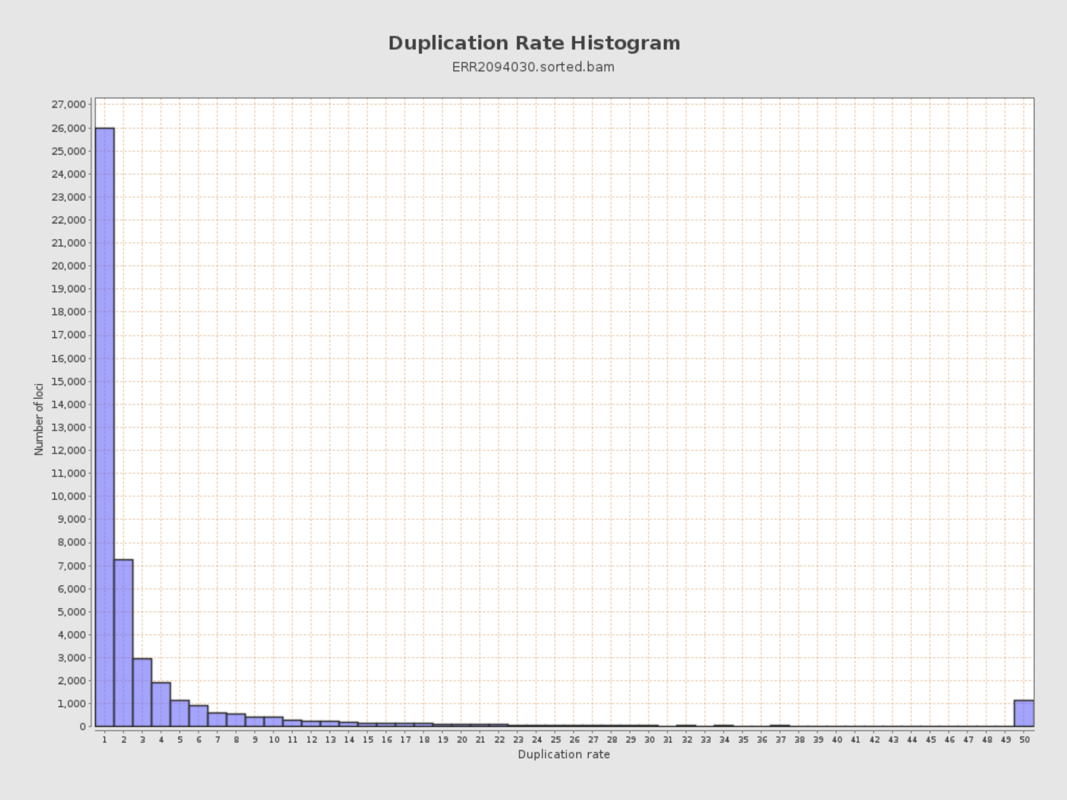
5. Results : Coverage Histogram (0-50X)



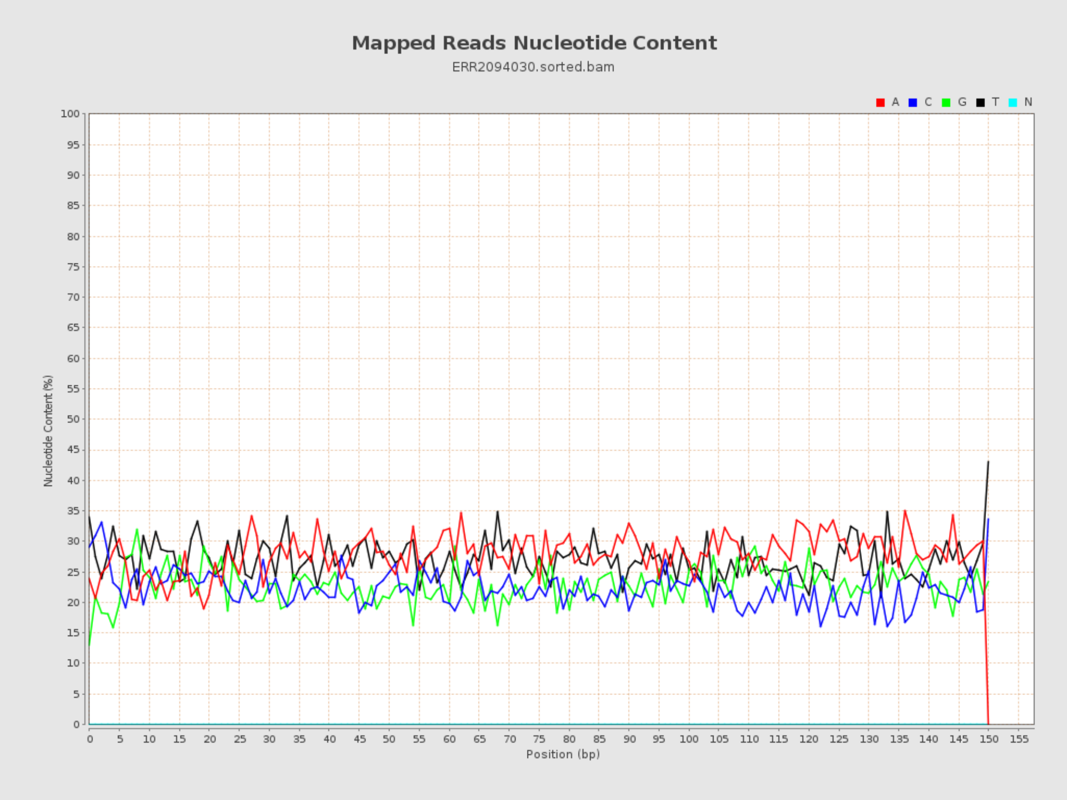
6. Results : Genome Fraction Coverage



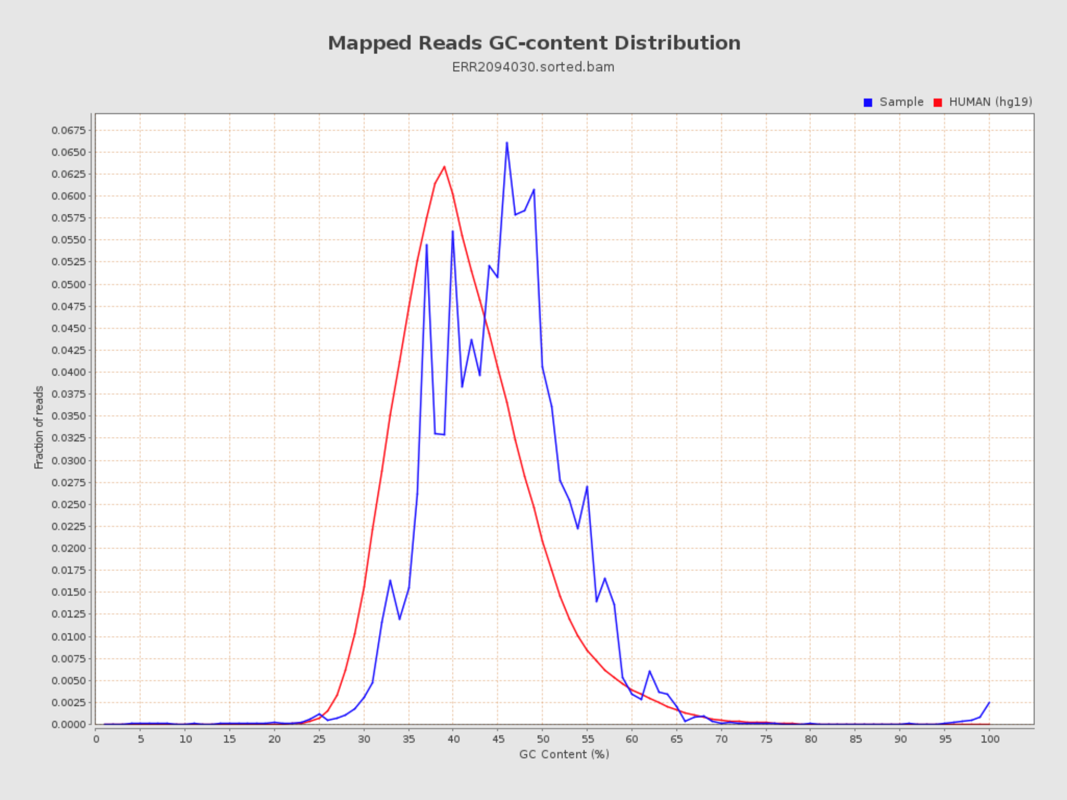
7. Results : Duplication Rate Histogram



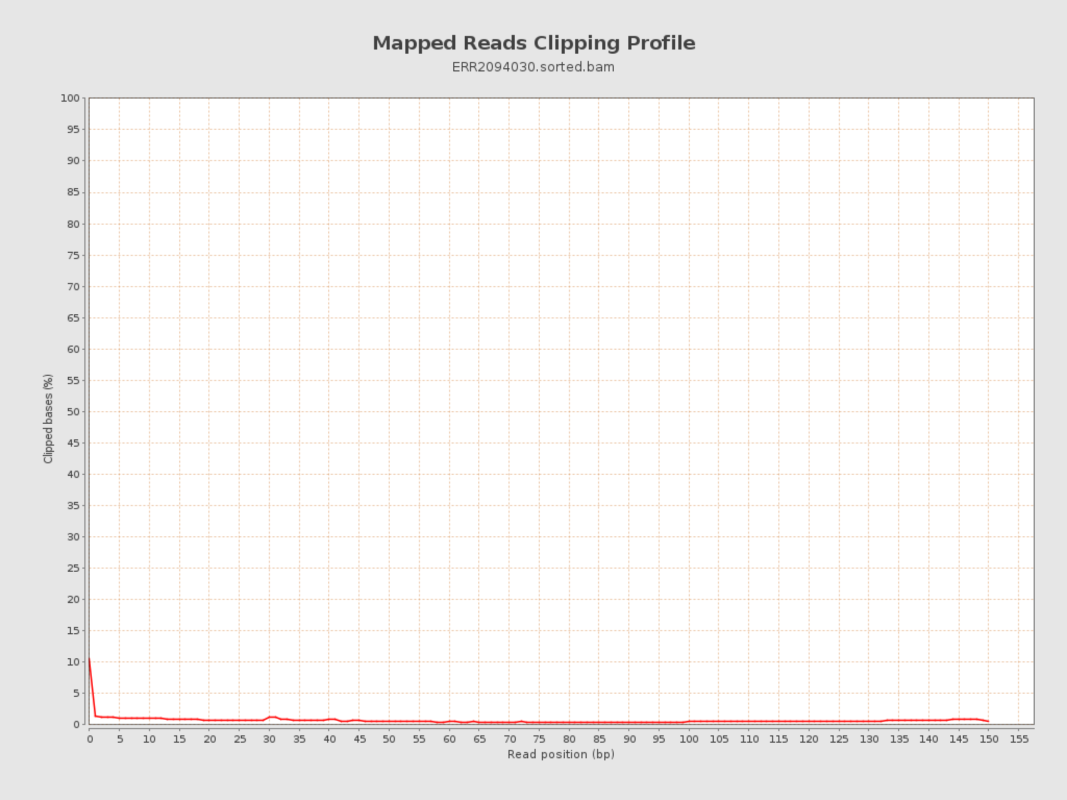
8. Results : Mapped Reads Nucleotide Content



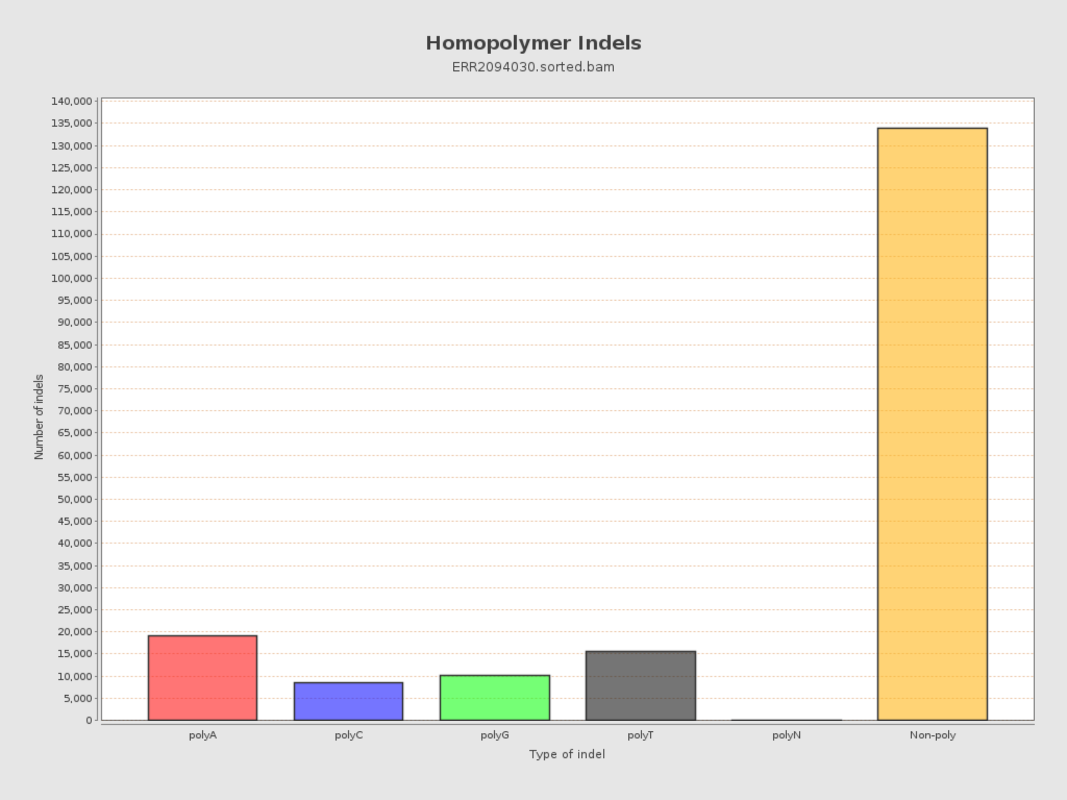
9. Results : Mapped Reads GC-content Distribution



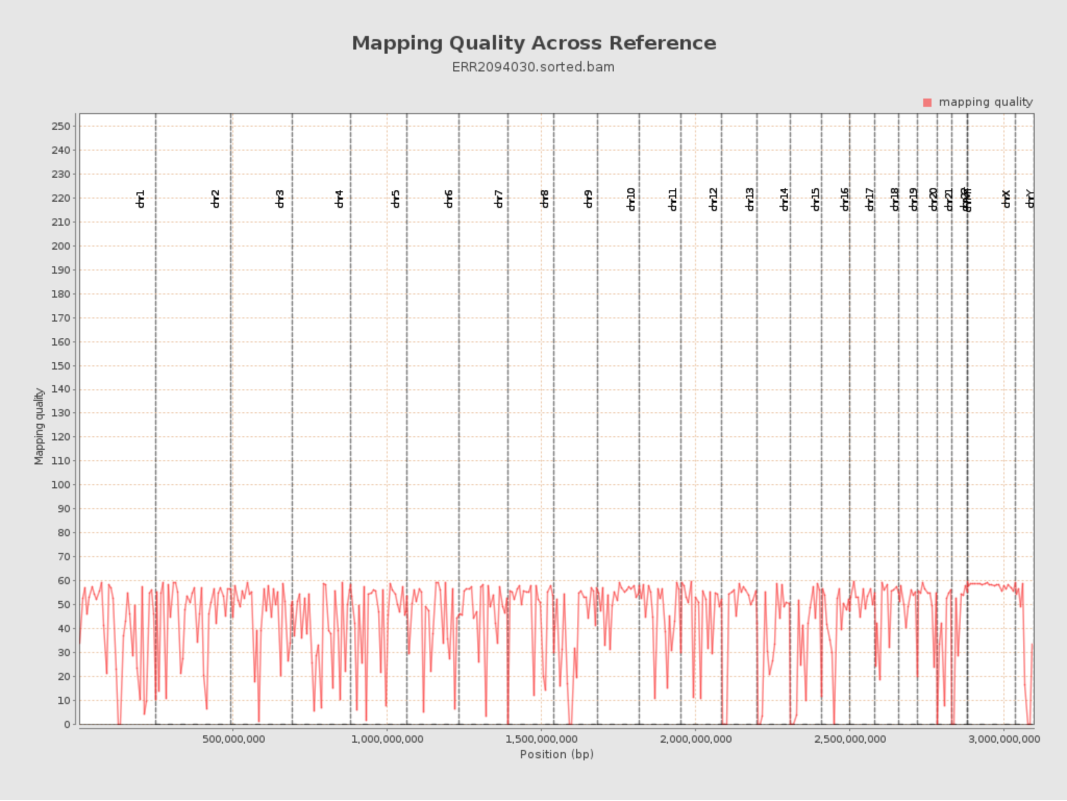
10. Results : Mapped Reads Clipping Profile



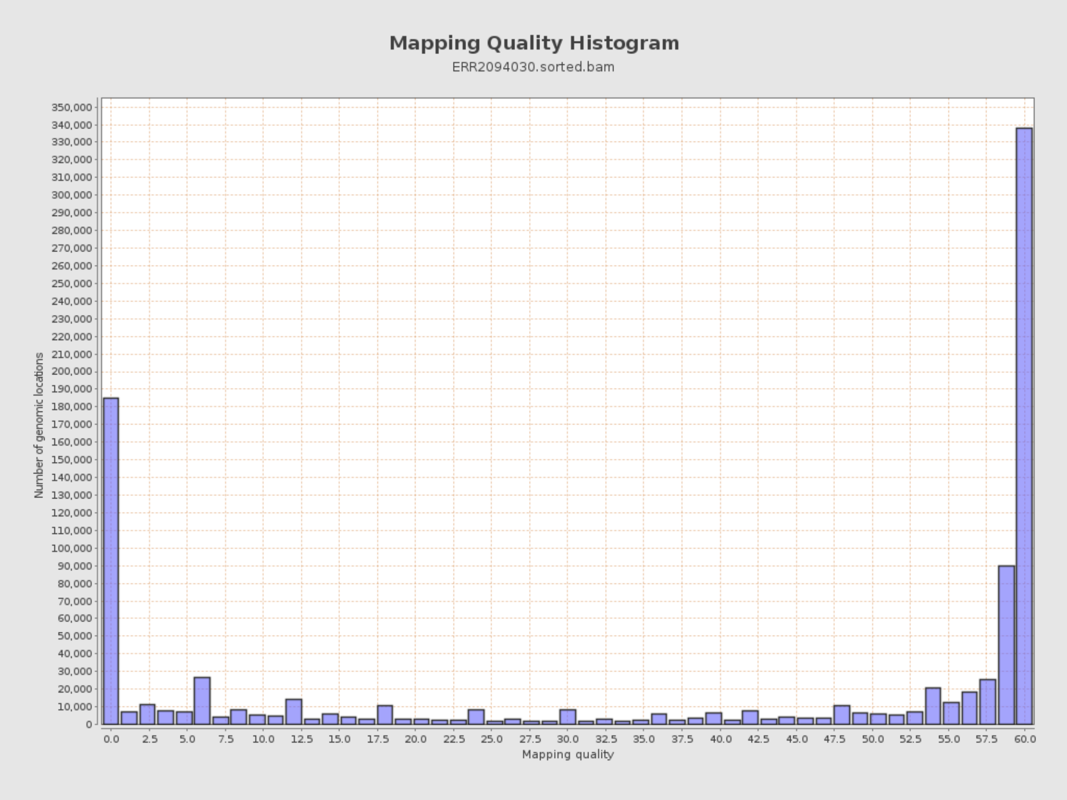
11. Results : Homopolymer Indels



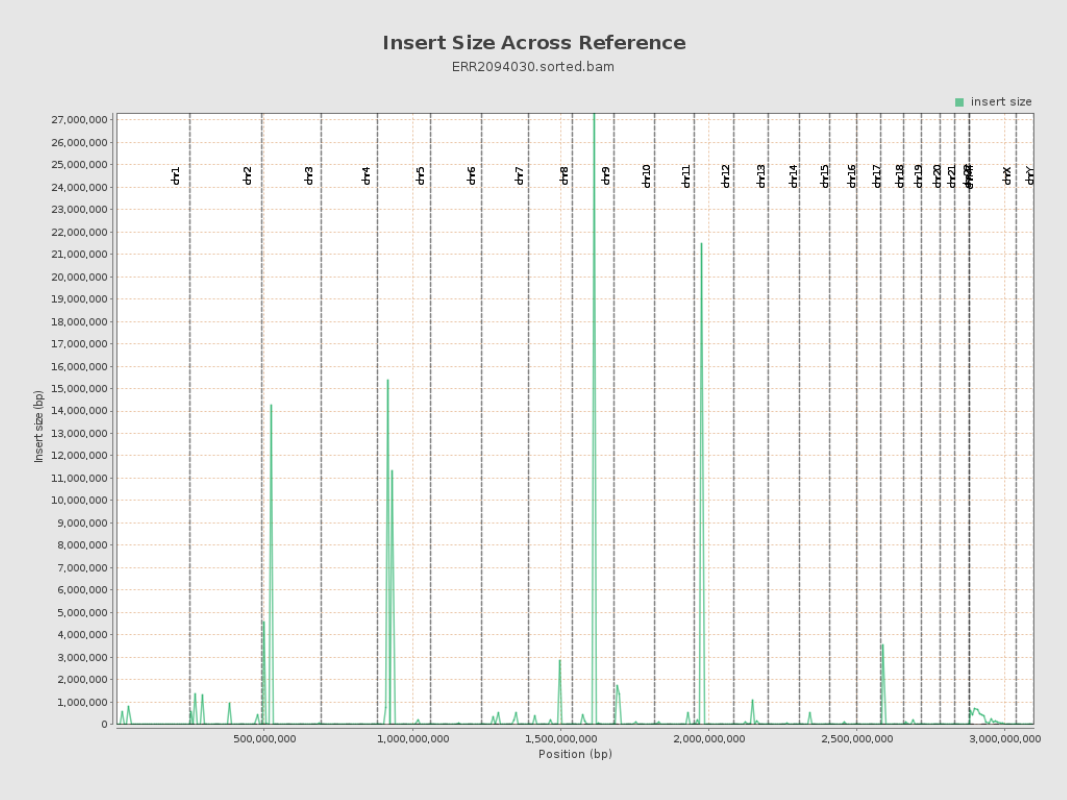
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram