Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:08:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094079.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_ERR2094079 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094079_1.fastq.gz ERR2094079_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:07:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	424,002
Mapped reads	403,845 / 95.25%
Unmapped reads	20,157 / 4.75%
Mapped paired reads	403,845 / 95.25%
Mapped reads, first in pair	202,892 / 47.85%
Mapped reads, second in pair	200,953 / 47.39%
Mapped reads, both in pair	400,994 / 94.57%
Mapped reads, singletons	2,851 / 0.67%
Secondary alignments	0
Supplementary alignments	13,395 / 3.16%
Read min/max/mean length	30 / 151 / 140.41
Duplicated reads (estimated)	387,163 / 91.31%
Duplication rate	50.03%
Clipped reads	156,351 / 36.88%

2.2. ACGT Content

Number/percentage of A's	14,356,107 / 27.4%
Number/percentage of C's	11,976,796 / 22.86%
Number/percentage of T's	13,585,929 / 25.93%
Number/percentage of G's	12,482,556 / 23.82%
Number/percentage of N's	453 / 0%

GC Percentage	46.68%

2.3. Coverage

Mean	0.0174
Standard Deviation	5.0113

2.4. Mapping Quality

Mean Mapping Quality	37.55

2.5. Insert size

Mean	383,473.11
Standard Deviation	5,776,752.95
P25/Median/P75	136 / 168 / 197

2.6. Mismatches and indels

General error rate	4.35%
Mismatches	2,206,196
Insertions	37,824
Mapped reads with at least one insertion	9.2%
Deletions	174,819
Mapped reads with at least one deletion	41.21%
Homopolymer indels	27.27%

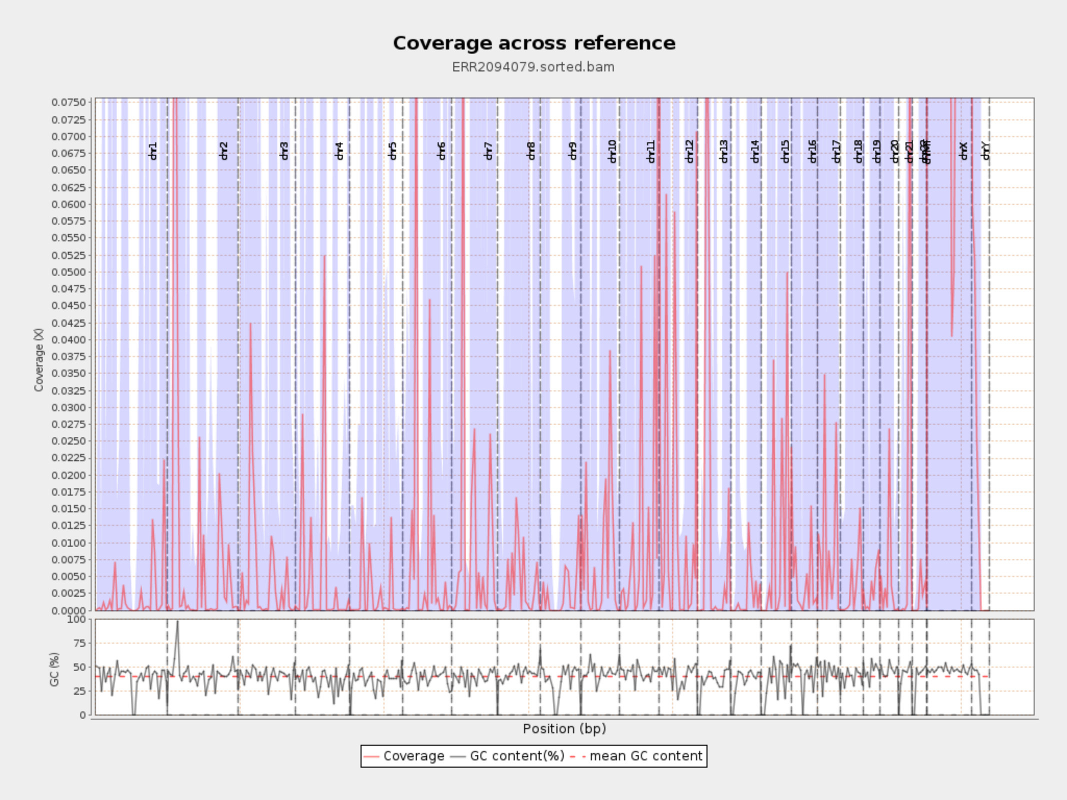
2.7. Chromosome stats

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

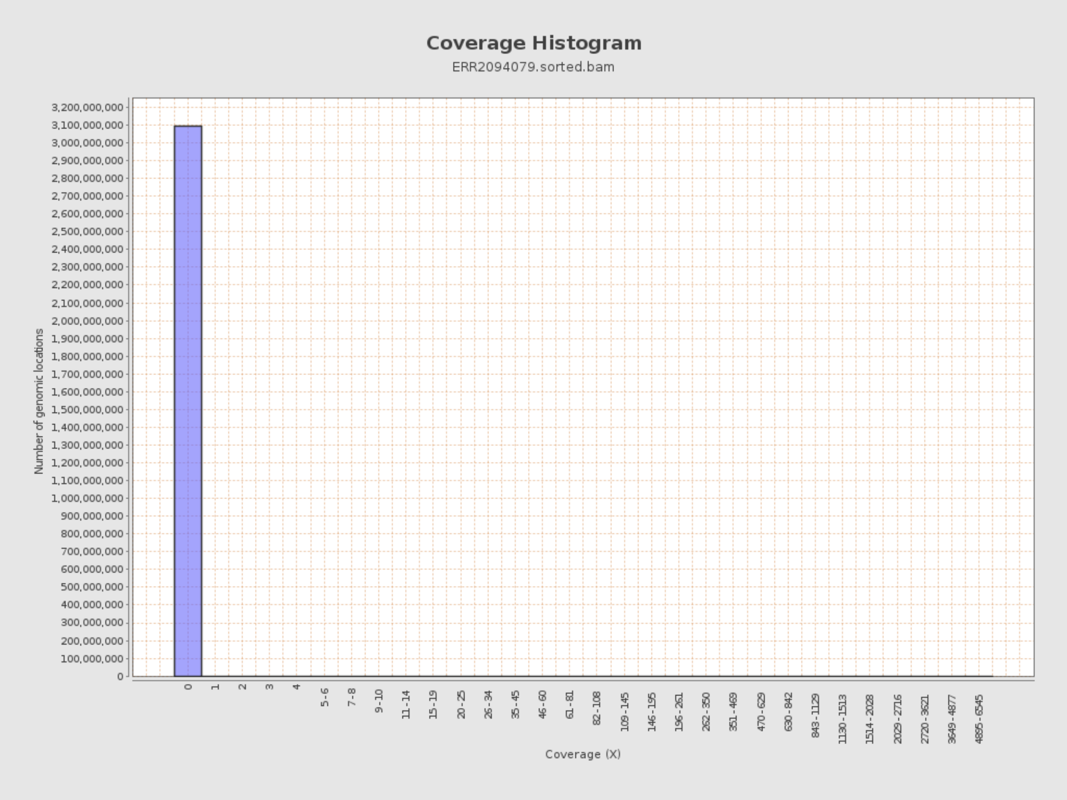
		bases	coverage	deviation
chr1	249250621	522755	0.0021	1.0011
chr2	243199373	2229051	0.0092	3.5198
chr3	198022430	940888	0.0048	2.0639
chr4	191154276	982955	0.0051	2.1447
chr5	180915260	403493	0.0022	1.0126
chr6	171115067	1458897	0.0085	4.9887
chr7	159138663	1592692	0.01	3.7059
chr8	146364022	556153	0.0038	0.9993
chr9	141213431	326307	0.0023	0.821
chr10	135534747	1089190	0.008	2.3937
chr11	135006516	1385322	0.0103	2.9675
chr12	133851895	1662636	0.0124	3.813
chr13	115169878	1375605	0.0119	4.1273
chr14	107349540	235841	0.0022	0.9233
chr15	102531392	946879	0.0092	3.2498
chr16	90354753	450738	0.005	1.5531
chr17	81195210	769878	0.0095	2.8615
chr18	78077248	275045	0.0035	1.2633
chr19	59128983	178776	0.003	0.6571
chr20	63025520	297705	0.0047	1.4734
chr21	48129895	768418	0.016	6.7245
chr22	51304566	113305	0.0022	0.6106
chrMT	16571	2077248	125.3544	608.8524
chrX	155270560	32076480	0.2066	17.5688

chrY	59373566	998474	0.0168	4.3807

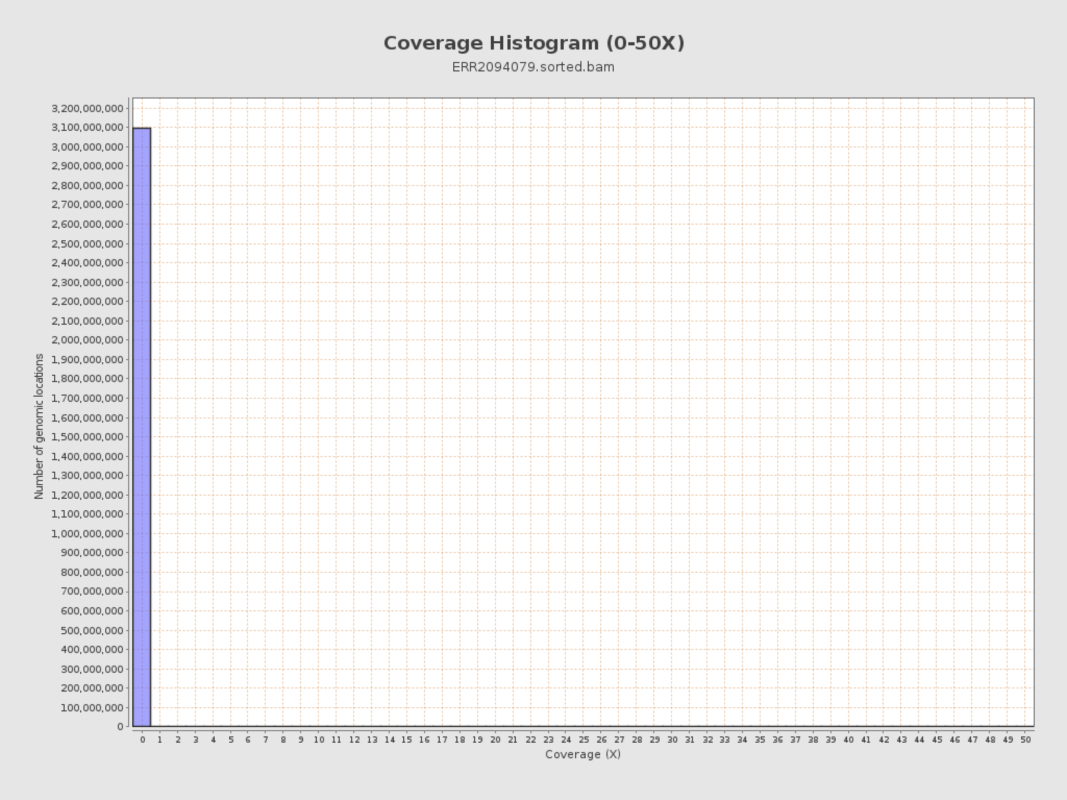
3. Results : Coverage across reference



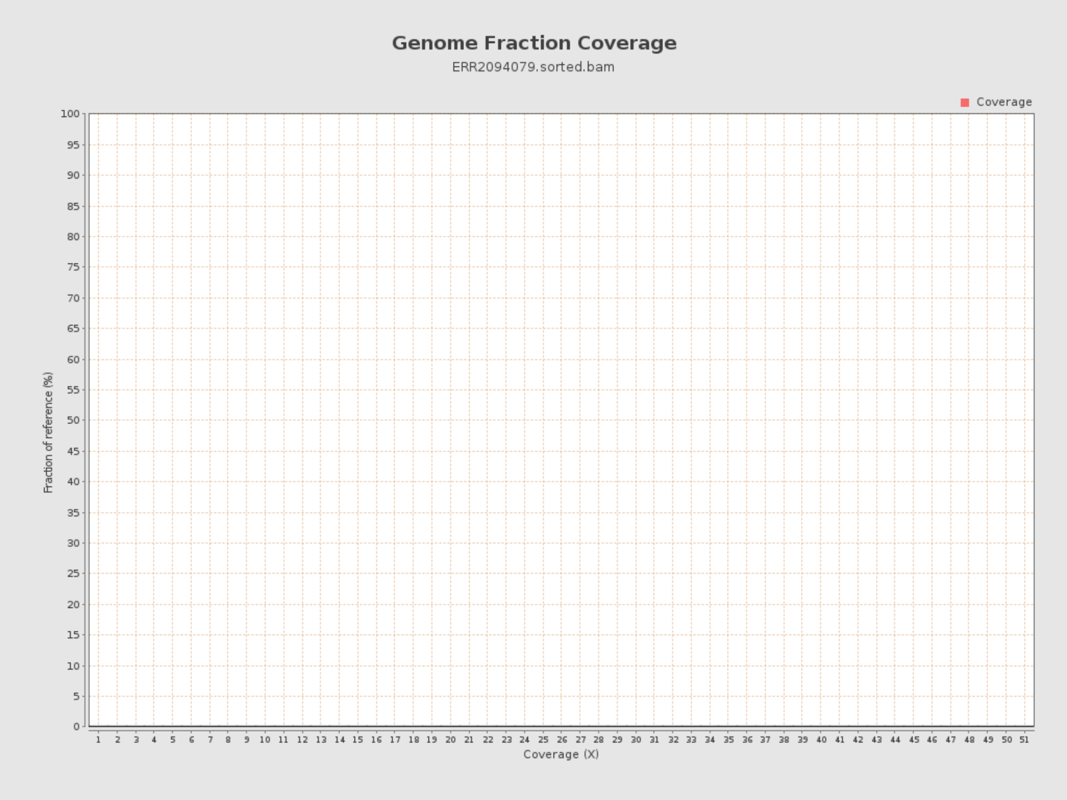
4. Results : Coverage Histogram



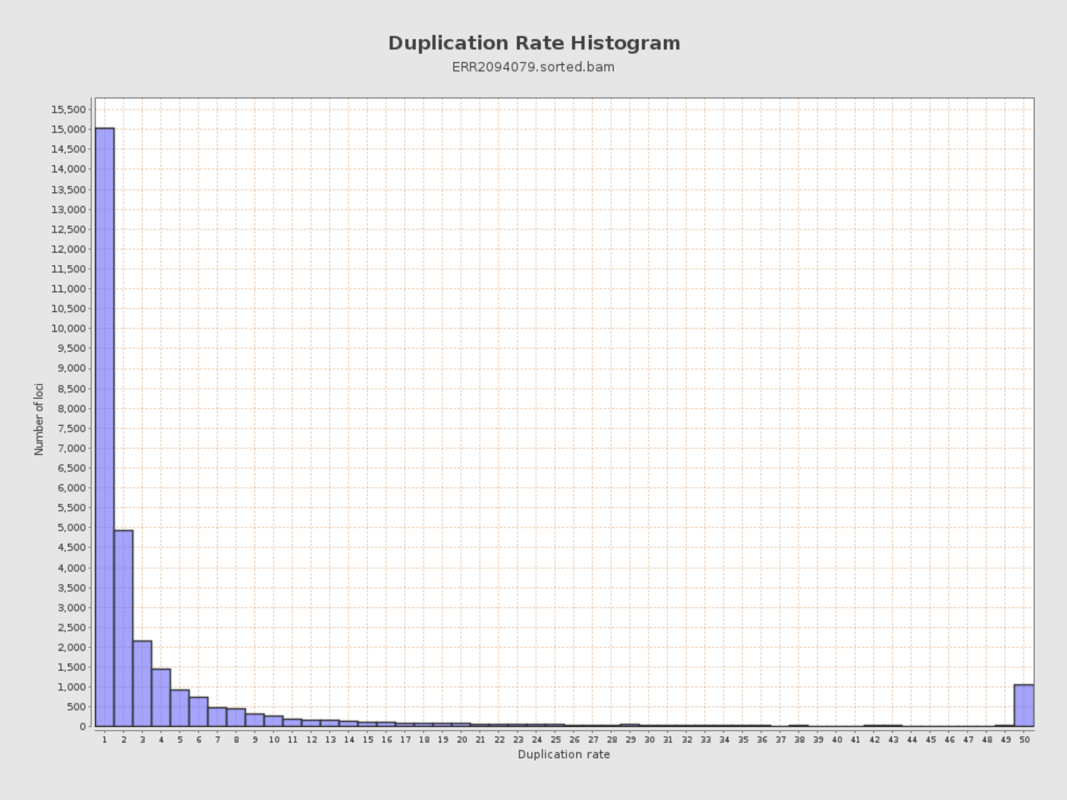
5. Results : Coverage Histogram (0-50X)



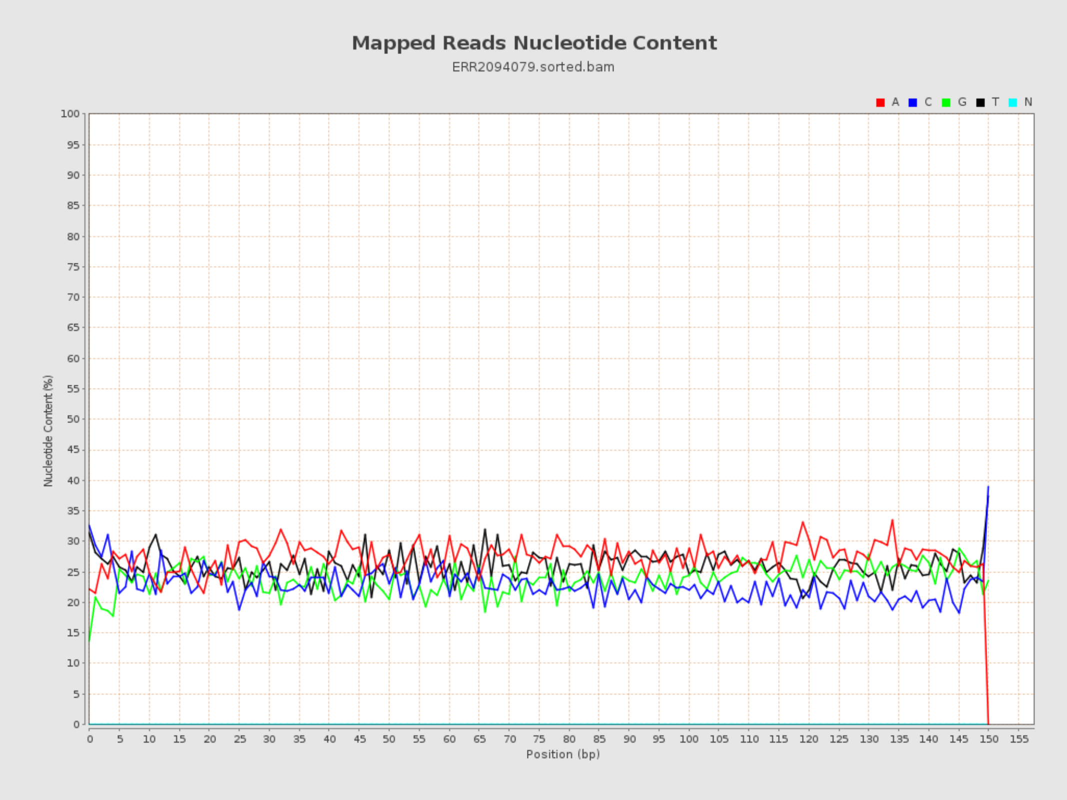
6. Results : Genome Fraction Coverage



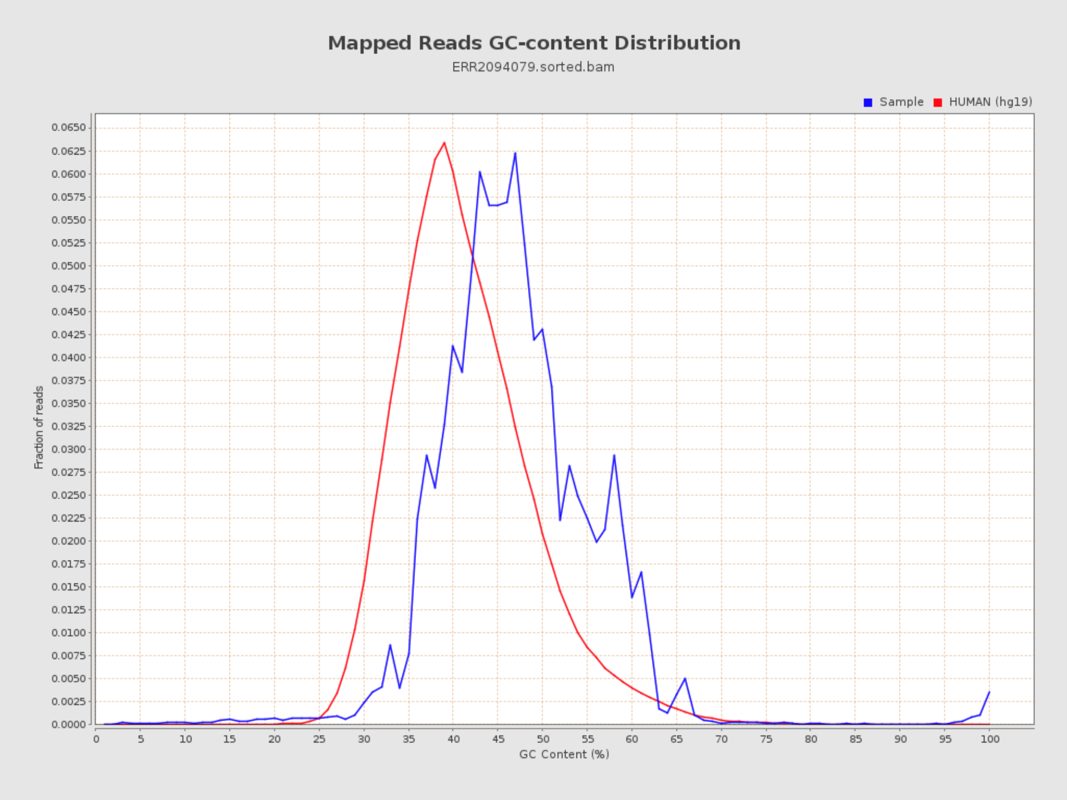
7. Results : Duplication Rate Histogram



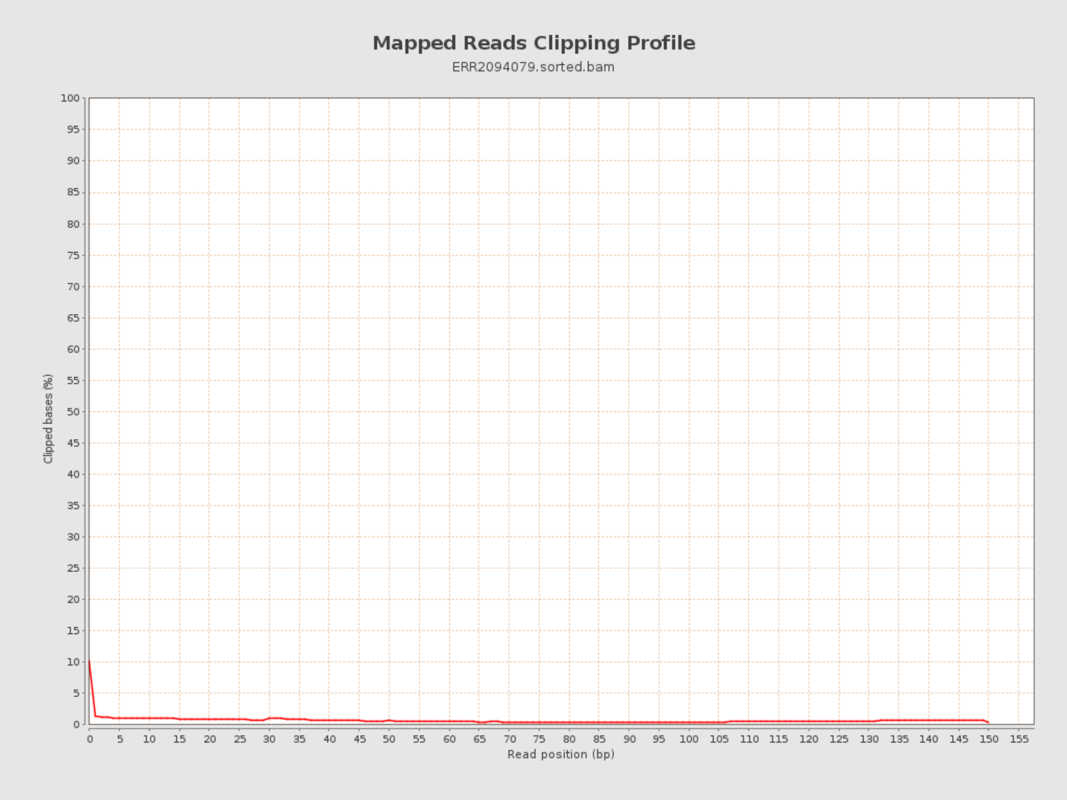
8. Results : Mapped Reads Nucleotide Content



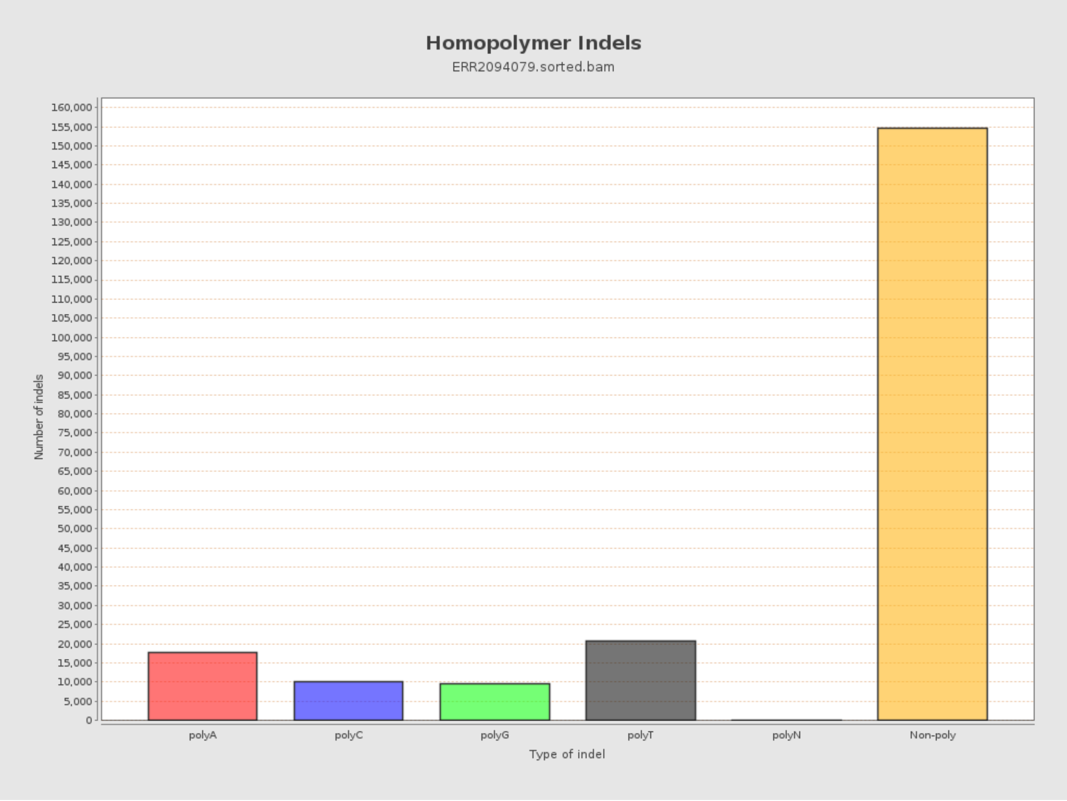
9. Results : Mapped Reads GC-content Distribution



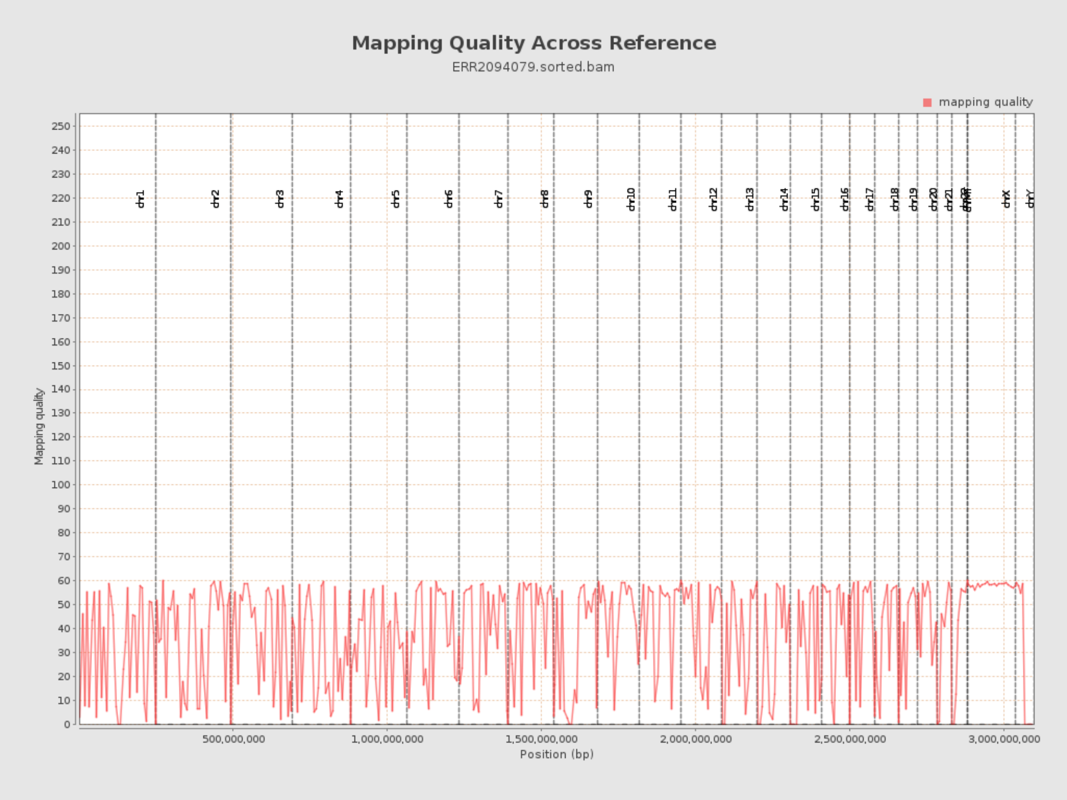
10. Results : Mapped Reads Clipping Profile



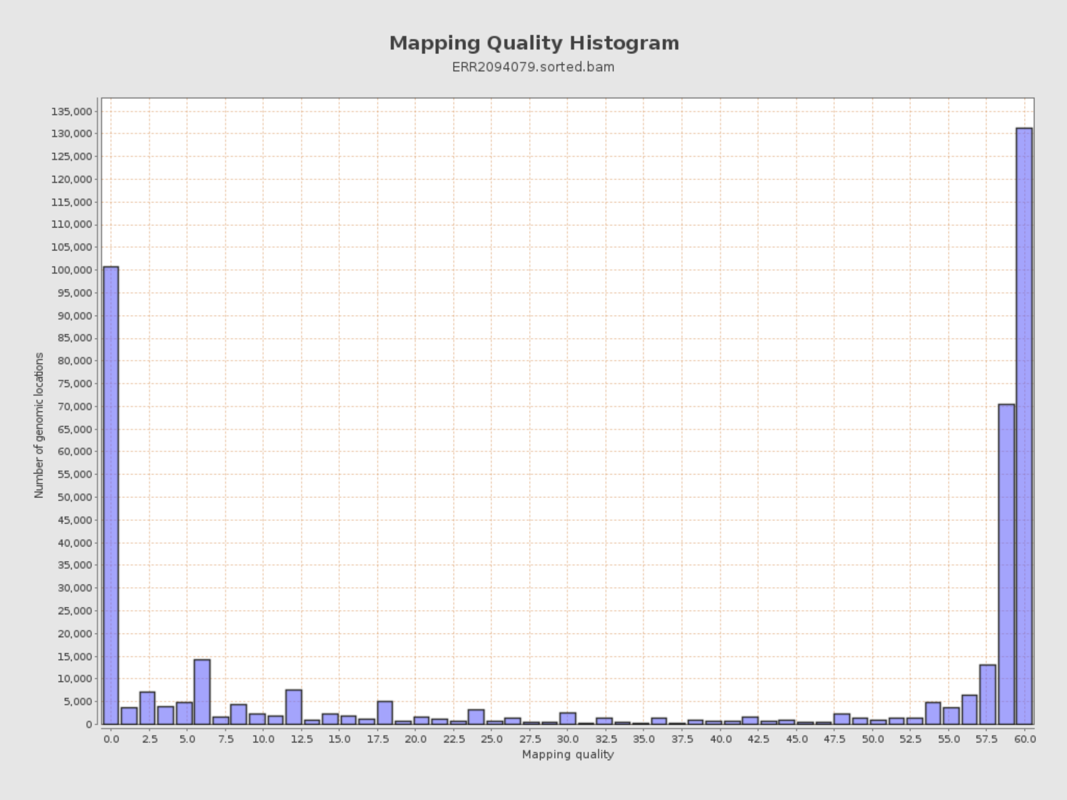
11. Results : Homopolymer Indels



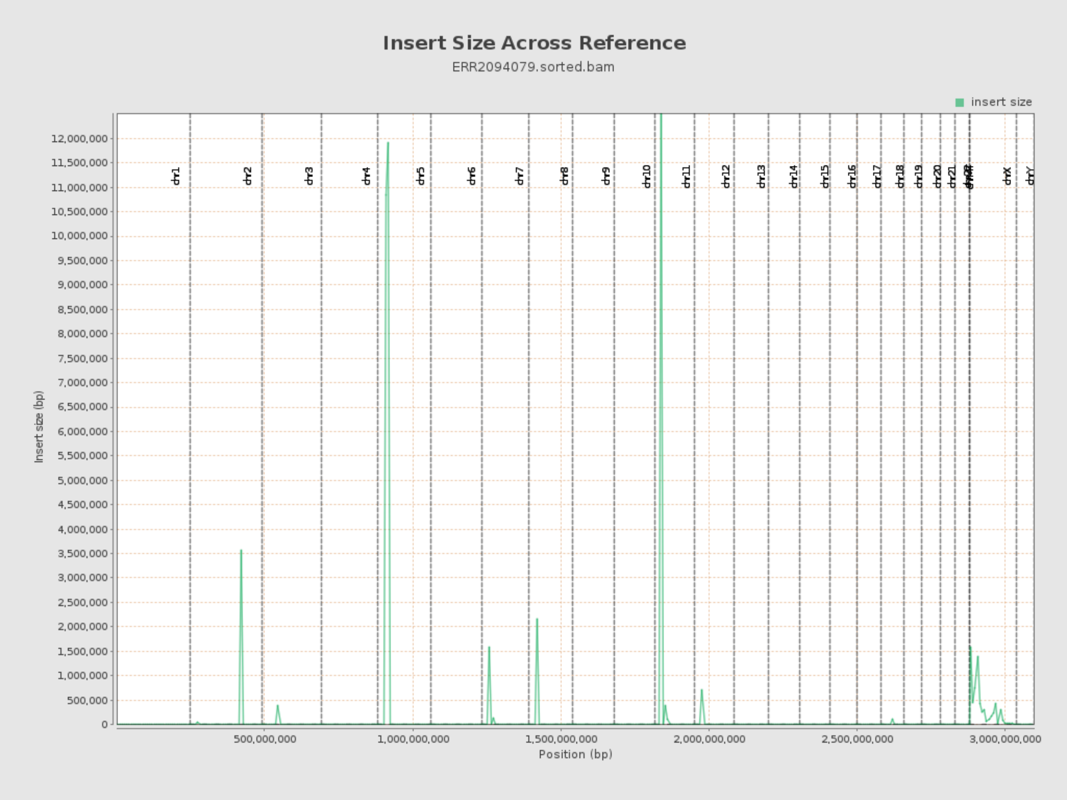
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram