Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:18:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094060.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_ERR2094060 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094060_1.fastq.gz ERR2094060_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:18:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	374,608
Mapped reads	355,592 / 94.92%
Unmapped reads	19,016 / 5.08%
Mapped paired reads	355,592 / 94.92%
Mapped reads, first in pair	178,678 / 47.7%
Mapped reads, second in pair	176,914 / 47.23%
Mapped reads, both in pair	352,950 / 94.22%
Mapped reads, singletons	2,642 / 0.71%
Secondary alignments	0
Supplementary alignments	14,250 / 3.8%
Read min/max/mean length	30 / 151 / 139.48
Duplicated reads (estimated)	332,211 / 88.68%
Duplication rate	50.58%
Clipped reads	147,851 / 39.47%

2.2. ACGT Content

Number/percentage of A's	12,756,311 / 27.93%
Number/percentage of C's	10,079,869 / 22.07%
Number/percentage of T's	12,263,339 / 26.85%
Number/percentage of G's	10,566,027 / 23.14%
Number/percentage of N's	464 / 0%

GC Percentage	45.21%

2.3. Coverage

Mean	0.0152
Standard Deviation	3.425

2.4. Mapping Quality

Mean Mapping Quality	43.87

2.5. Insert size

Mean	739,925.52
Standard Deviation	7,816,310.4
P25/Median/P75	133 / 167 / 197

2.6. Mismatches and indels

General error rate	4.63%
Mismatches	2,057,582
Insertions	34,746
Mapped reads with at least one insertion	9.58%
Deletions	162,303
Mapped reads with at least one deletion	42.69%
Homopolymer indels	29.73%

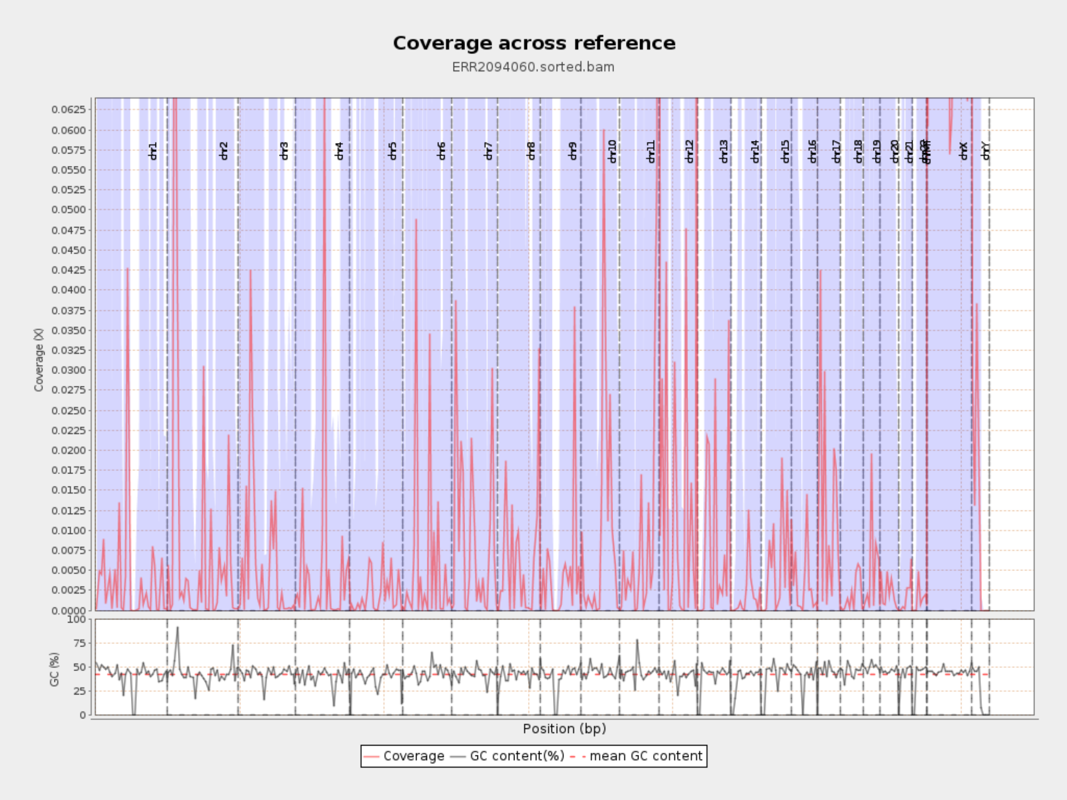
2.7. Chromosome stats

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

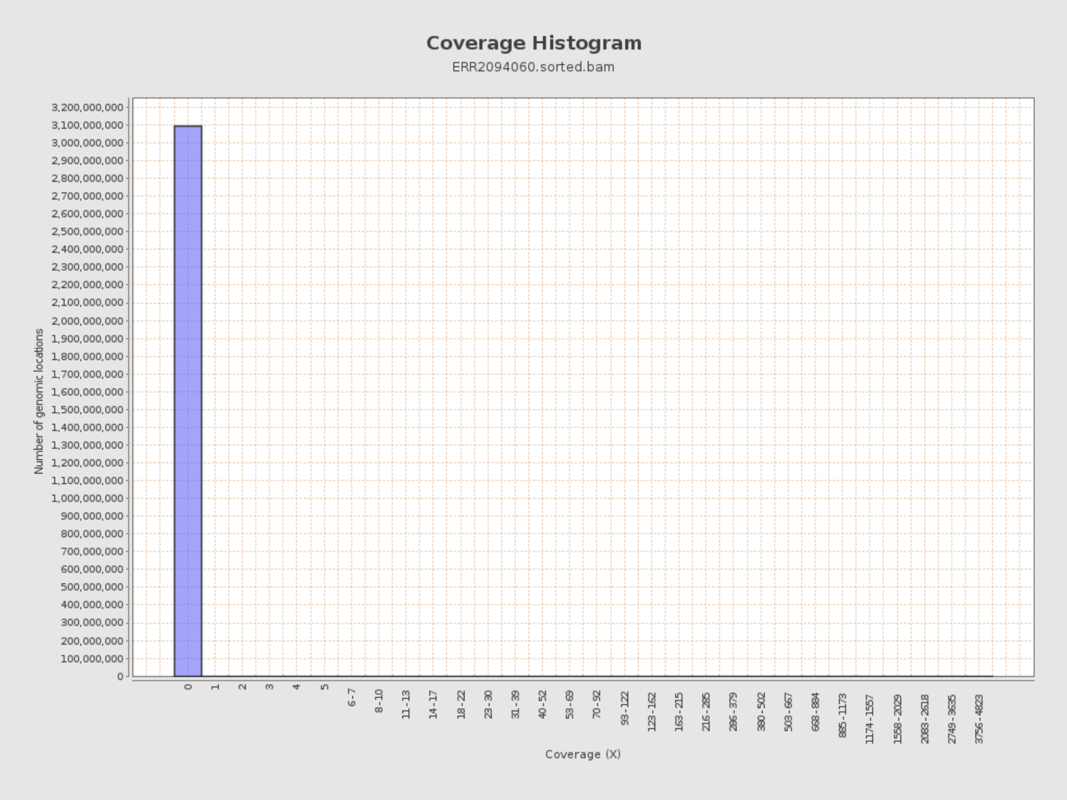
		bases	coverage	deviation
chr1	249250621	946787	0.0038	1.5403
chr2	243199373	1946551	0.008	2.3419
chr3	198022430	1124922	0.0057	1.8873
chr4	191154276	1043494	0.0055	1.5823
chr5	180915260	396966	0.0022	0.6776
chr6	171115067	1042053	0.0061	2.6164
chr7	159138663	1402087	0.0088	2.4596
chr8	146364022	898957	0.0061	1.8426
chr9	141213431	668283	0.0047	1.8276
chr10	135534747	1371688	0.0101	3.2638
chr11	135006516	1431436	0.0106	2.9614
chr12	133851895	1772314	0.0132	3.6344
chr13	115169878	972103	0.0084	2.473
chr14	107349540	216207	0.002	0.7879
chr15	102531392	527483	0.0051	1.3295
chr16	90354753	347765	0.0038	1.2171
chr17	81195210	1072339	0.0132	2.7189
chr18	78077248	161615	0.0021	0.5206
chr19	59128983	299814	0.0051	1.457
chr20	63025520	136846	0.0022	0.502
chr21	48129895	81505	0.0017	0.3645
chr22	51304566	71985	0.0014	0.335
chrMT	16571	2778766	167.6885	675.2543
chrX	155270560	25528908	0.1644	9.9354

chrY	59373566	694967	0.0117	2.6324

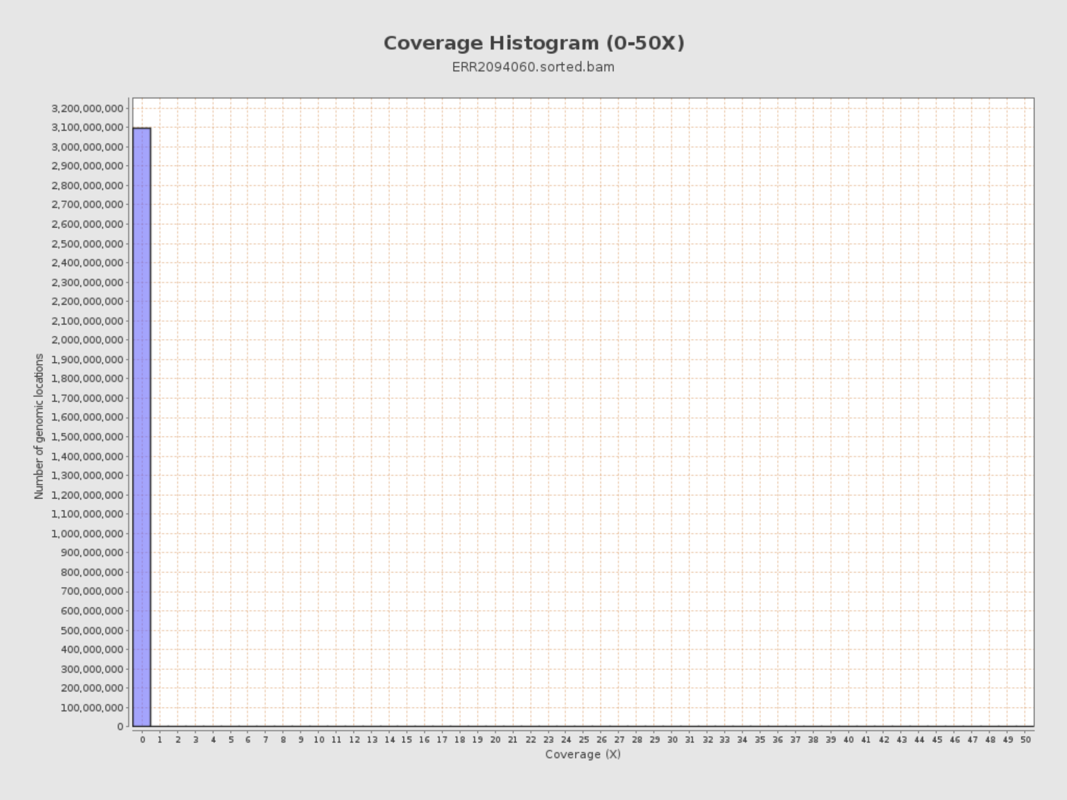
3. Results : Coverage across reference



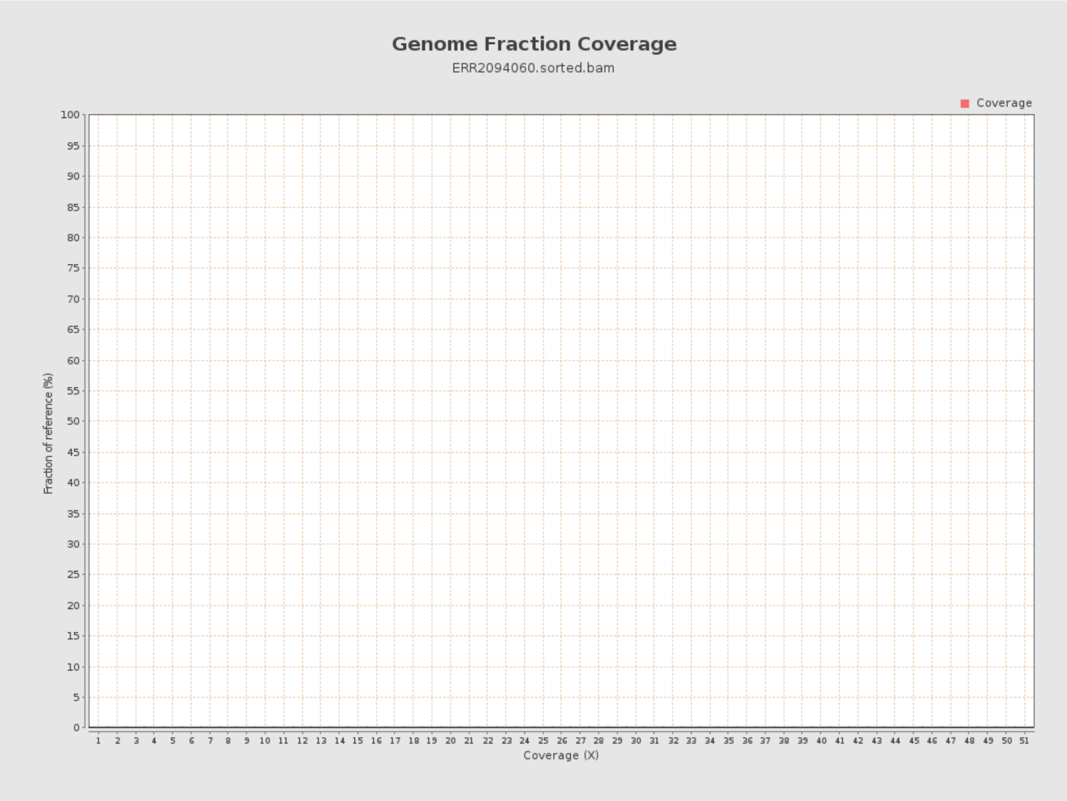
4. Results : Coverage Histogram



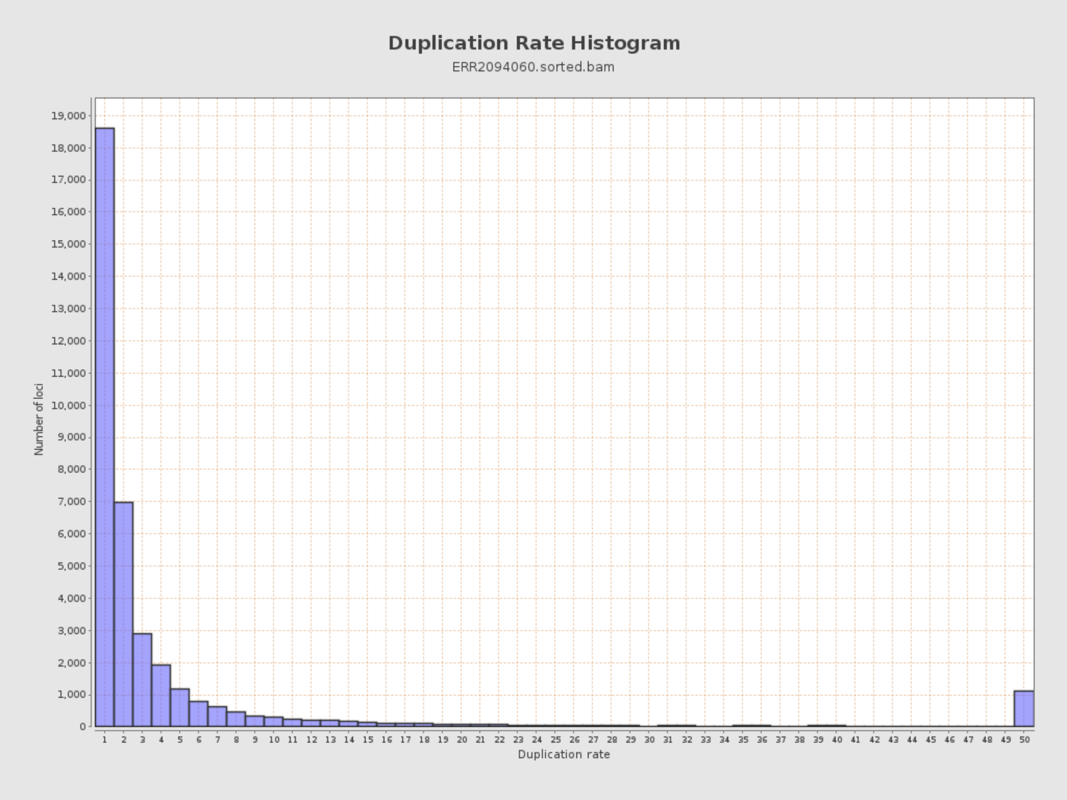
5. Results : Coverage Histogram (0-50X)



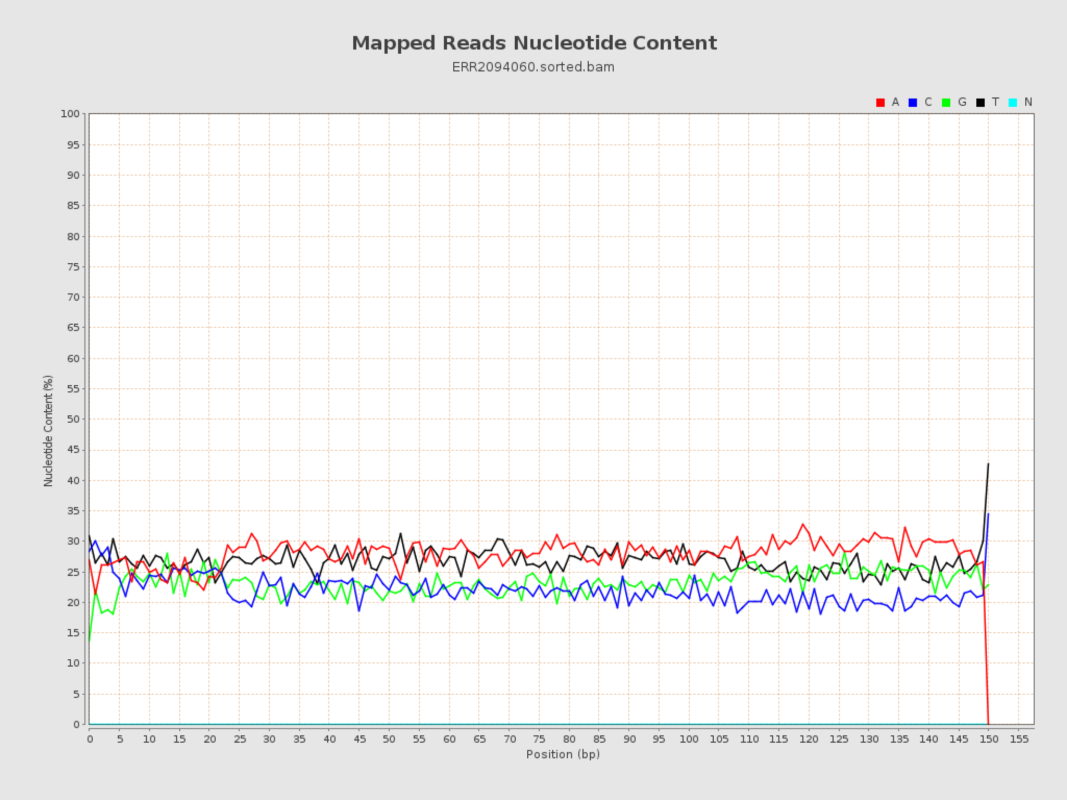
6. Results : Genome Fraction Coverage



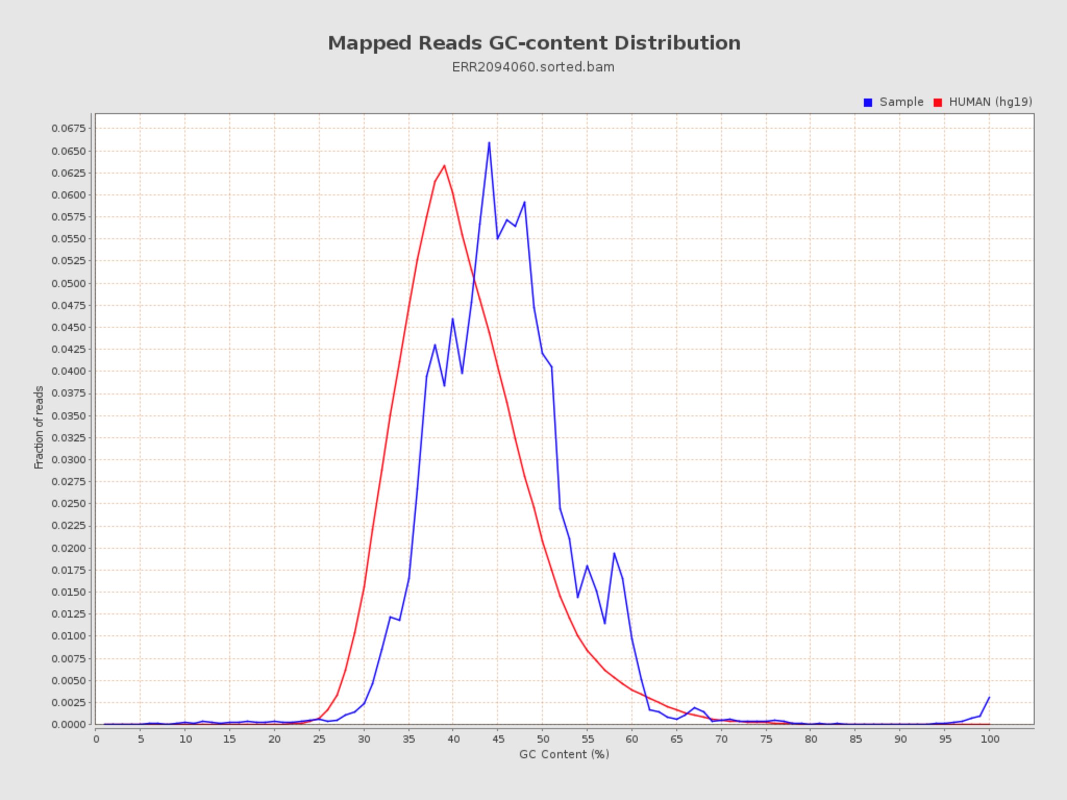
7. Results : Duplication Rate Histogram



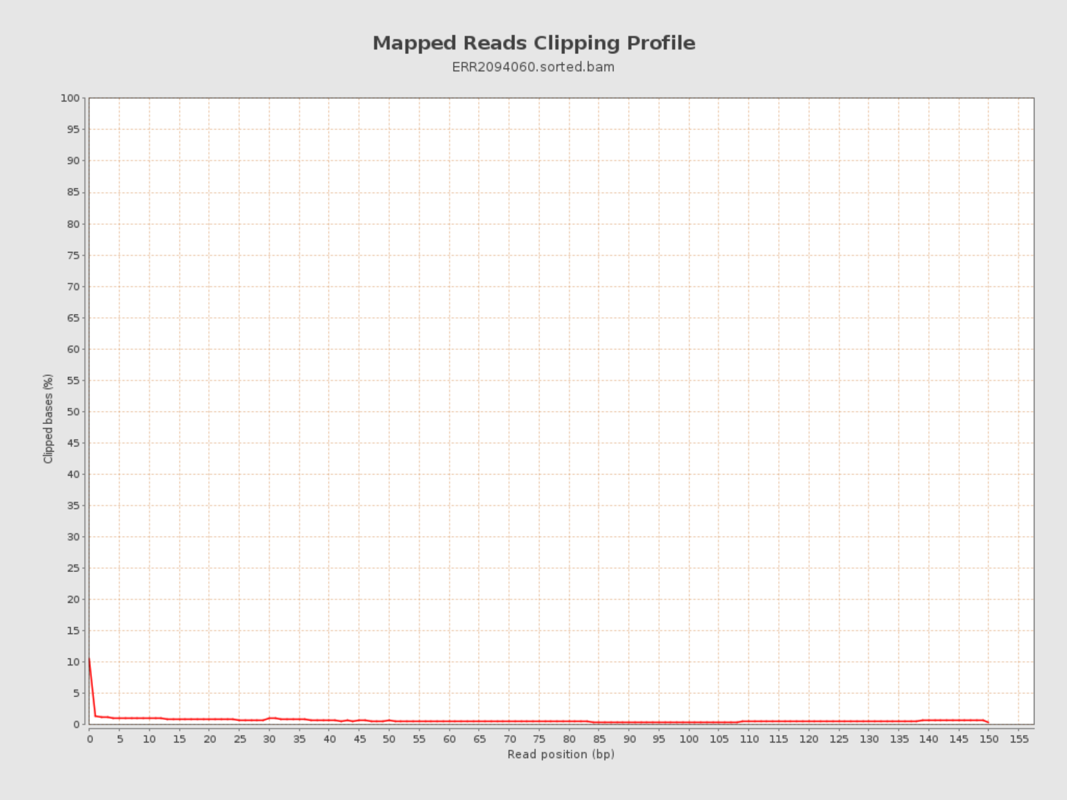
8. Results : Mapped Reads Nucleotide Content



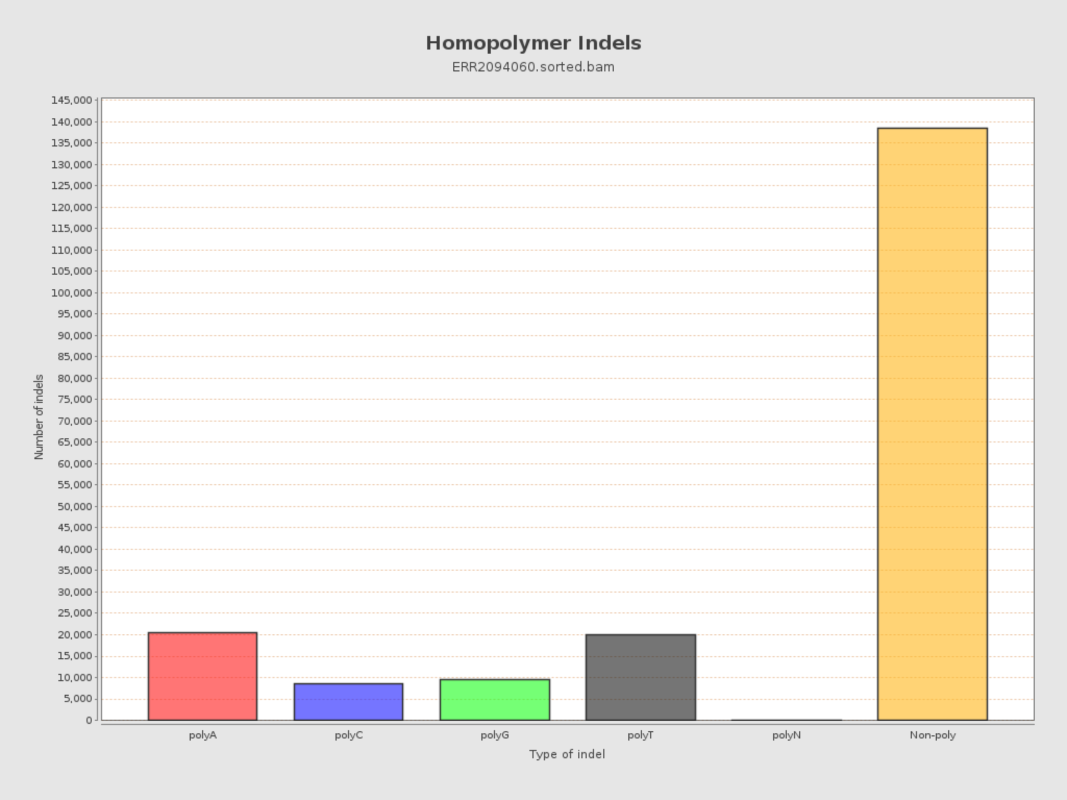
9. Results : Mapped Reads GC-content Distribution



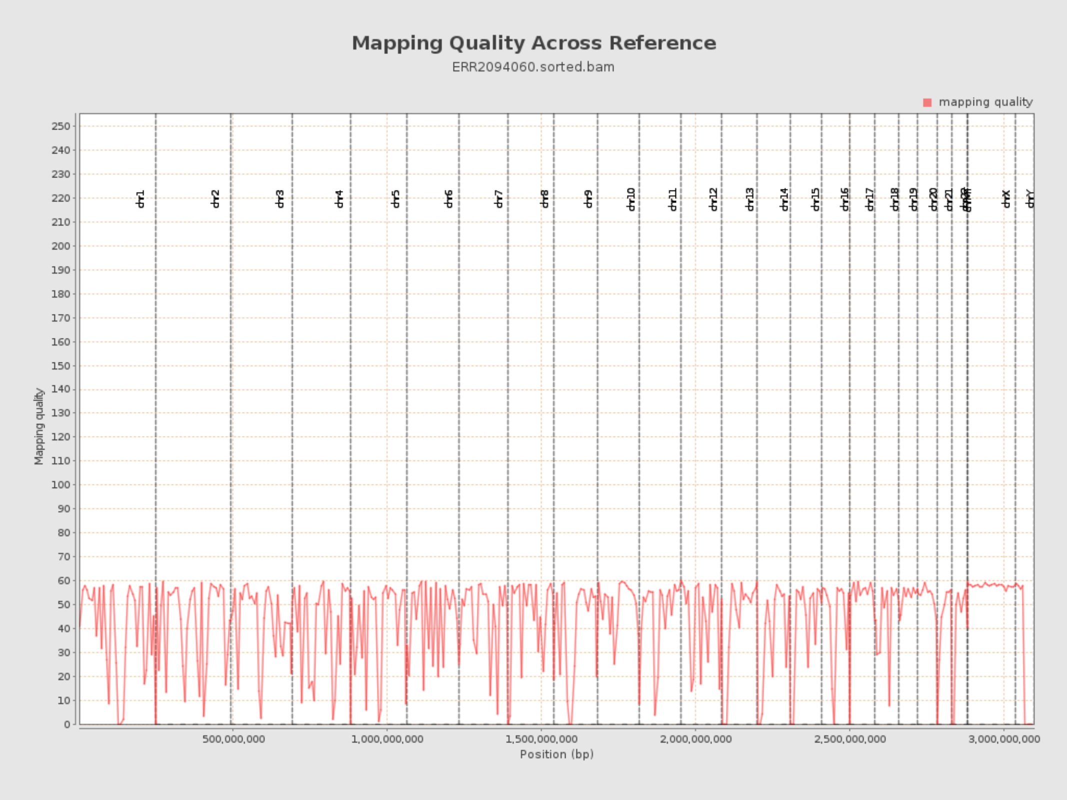
10. Results : Mapped Reads Clipping Profile



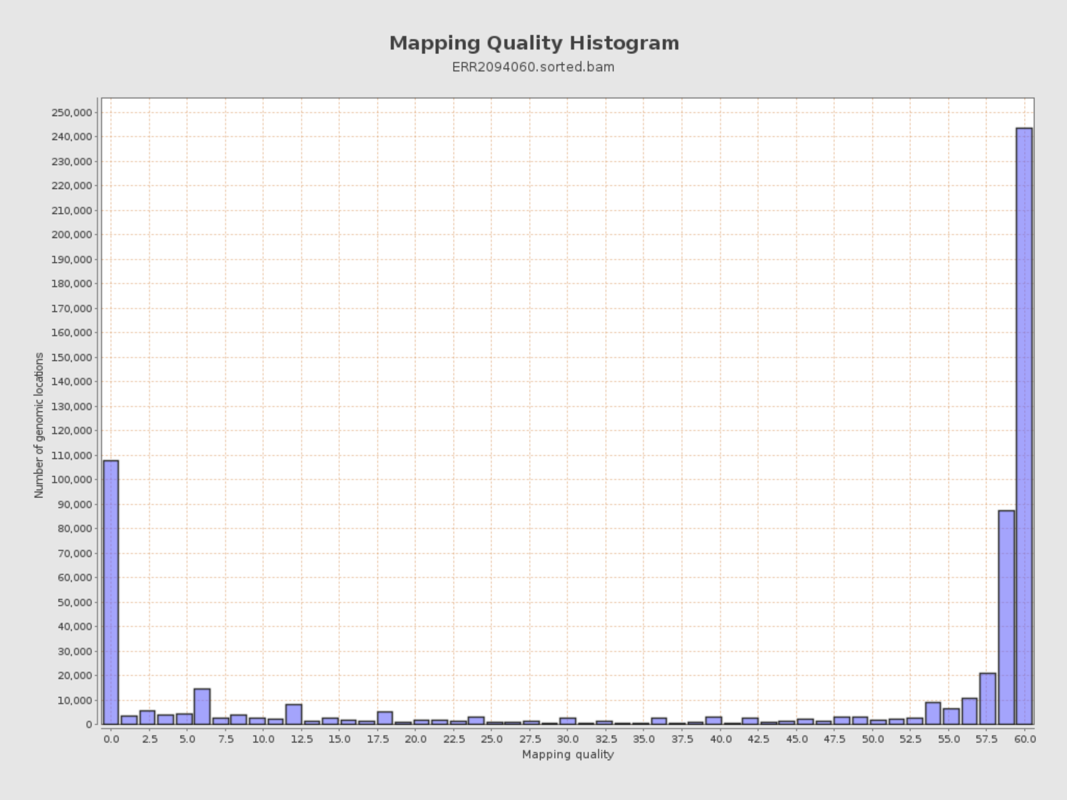
11. Results : Homopolymer Indels



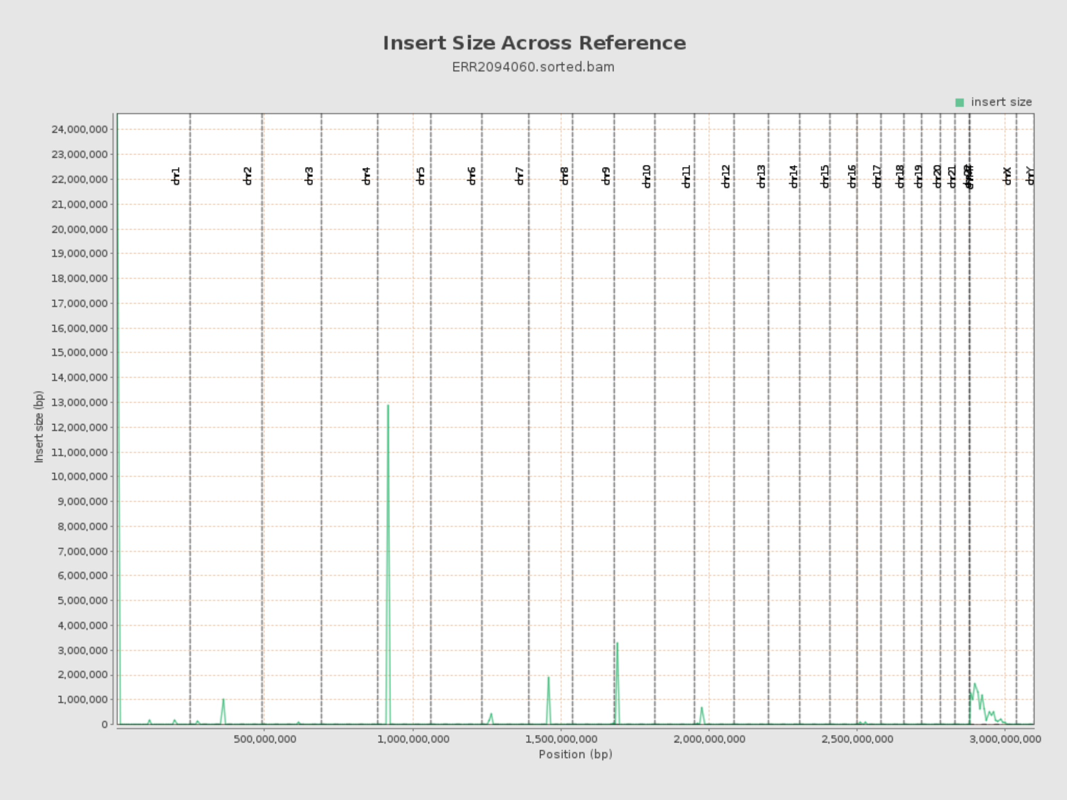
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram