Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094032.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_ERR2094032 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094032_1.fastq.gz ERR2094032_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:35:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	382,794
Mapped reads	363,426 / 94.94%
Unmapped reads	19,368 / 5.06%
Mapped paired reads	363,426 / 94.94%
Mapped reads, first in pair	182,589 / 47.7%
Mapped reads, second in pair	180,837 / 47.24%
Mapped reads, both in pair	360,134 / 94.08%
Mapped reads, singletons	3,292 / 0.86%
Secondary alignments	0
Supplementary alignments	19,517 / 5.1%
Read min/max/mean length	30 / 151 / 141.97
Duplicated reads (estimated)	337,858 / 88.26%
Duplication rate	47.3%
Clipped reads	170,554 / 44.56%

2.2. ACGT Content

Number/percentage of A's	12,743,696 / 27.69%
Number/percentage of C's	10,223,947 / 22.21%
Number/percentage of T's	12,271,941 / 26.66%
Number/percentage of G's	10,786,062 / 23.43%
Number/percentage of N's	538 / 0%

GC Percentage	45.65%

2.3. Coverage

Mean	0.0152
Standard Deviation	4.2885

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Insert size

Mean	792,703.93
Standard Deviation	8,073,090.06
P25/Median/P75	130 / 170 / 205

2.6. Mismatches and indels

General error rate	3.59%
Mismatches	1,585,822
Insertions	29,330
Mapped reads with at least one insertion	7.95%
Deletions	117,596
Mapped reads with at least one deletion	31.22%
Homopolymer indels	28.48%

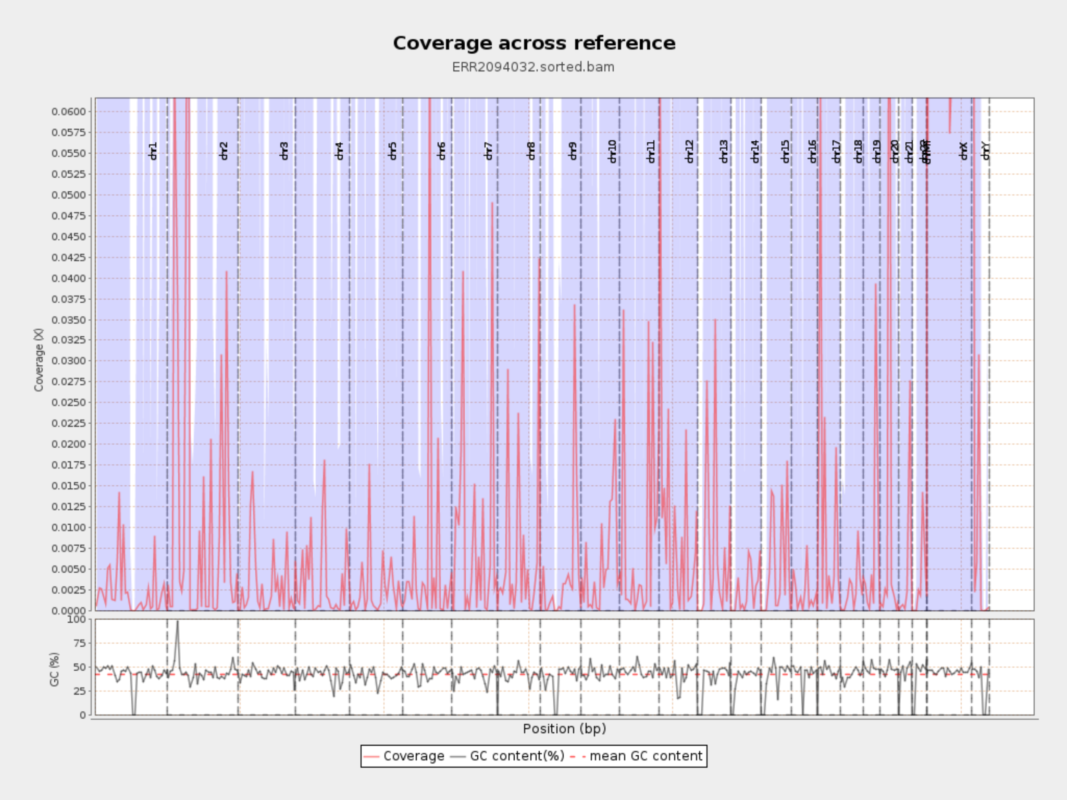
2.7. Chromosome stats

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

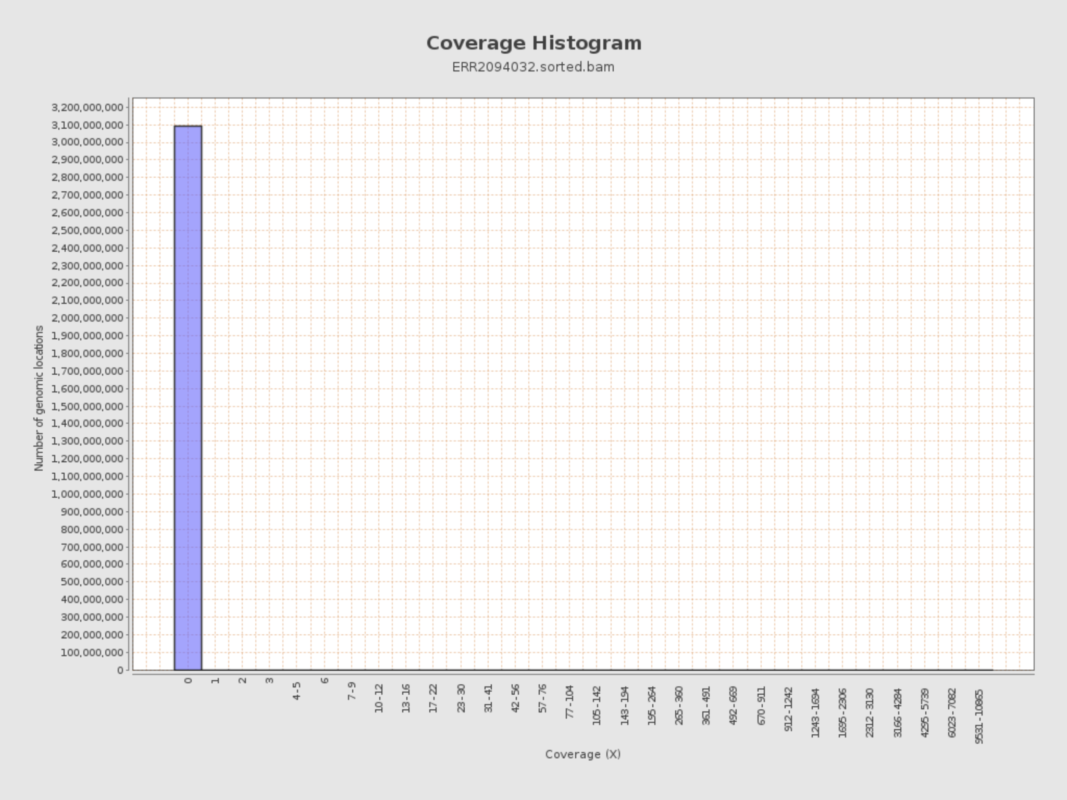
		bases	**coverage**	**deviation**
chr1	249250621	612254	0.0025	0.8826
chr2	243199373	3418509	0.0141	4.6173
chr3	198022430	606716	0.0031	0.7397
chr4	191154276	718754	0.0038	0.9237
chr5	180915260	481899	0.0027	0.855
chr6	171115067	1037598	0.0061	2.5924
chr7	159138663	1443578	0.0091	2.4911
chr8	146364022	1033463	0.0071	2.4323
chr9	141213431	637707	0.0045	1.4772
chr10	135534747	747890	0.0055	1.4221
chr11	135006516	1141119	0.0085	2.5206
chr12	133851895	1409685	0.0105	2.8074
chr13	115169878	794792	0.0069	2.1541
chr14	107349540	259137	0.0024	0.6381
chr15	102531392	577849	0.0056	1.3127
chr16	90354753	190701	0.0021	0.4635
chr17	81195210	1028692	0.0127	2.878
chr18	78077248	197057	0.0025	0.7032
chr19	59128983	433694	0.0073	2.1968
chr20	63025520	904019	0.0143	5.5097
chr21	48129895	270787	0.0056	1.8329
chr22	51304566	178710	0.0035	0.9919
chrMT	16571	4906130	296.0672	1,232.5817
chrX	155270560	22686612	0.1461	8.7819

chrY	59373566	1211889	0.0204	7.2894

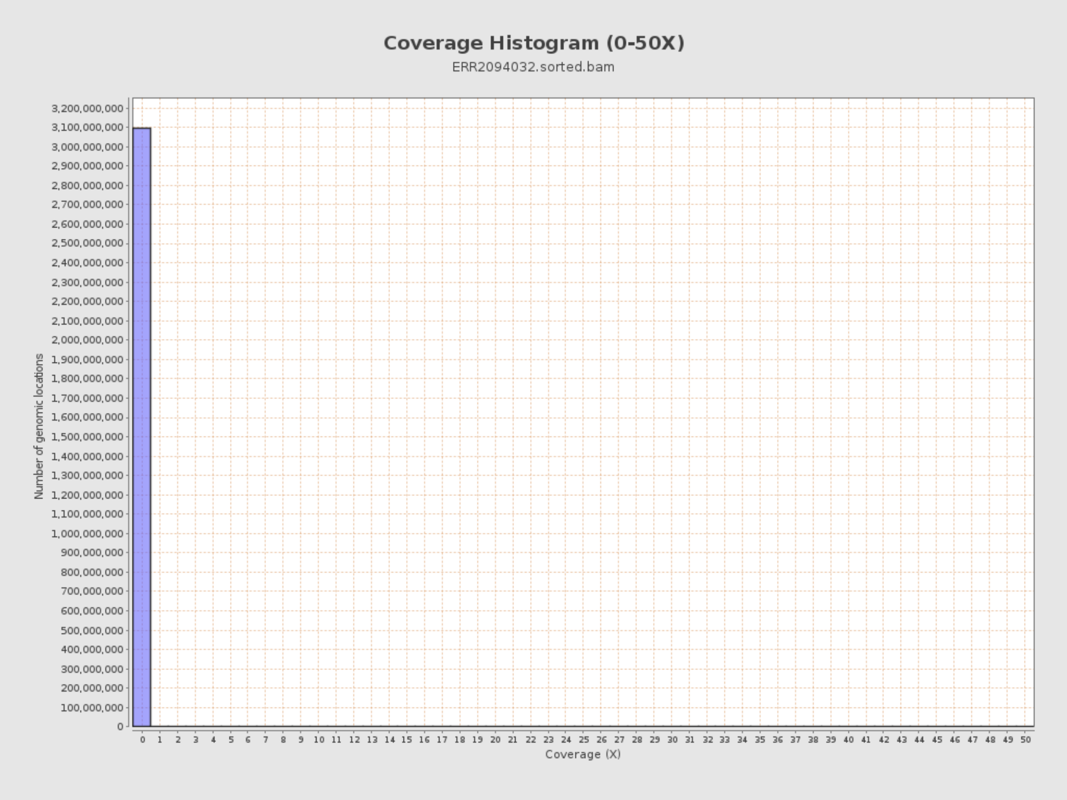
3. Results : Coverage across reference



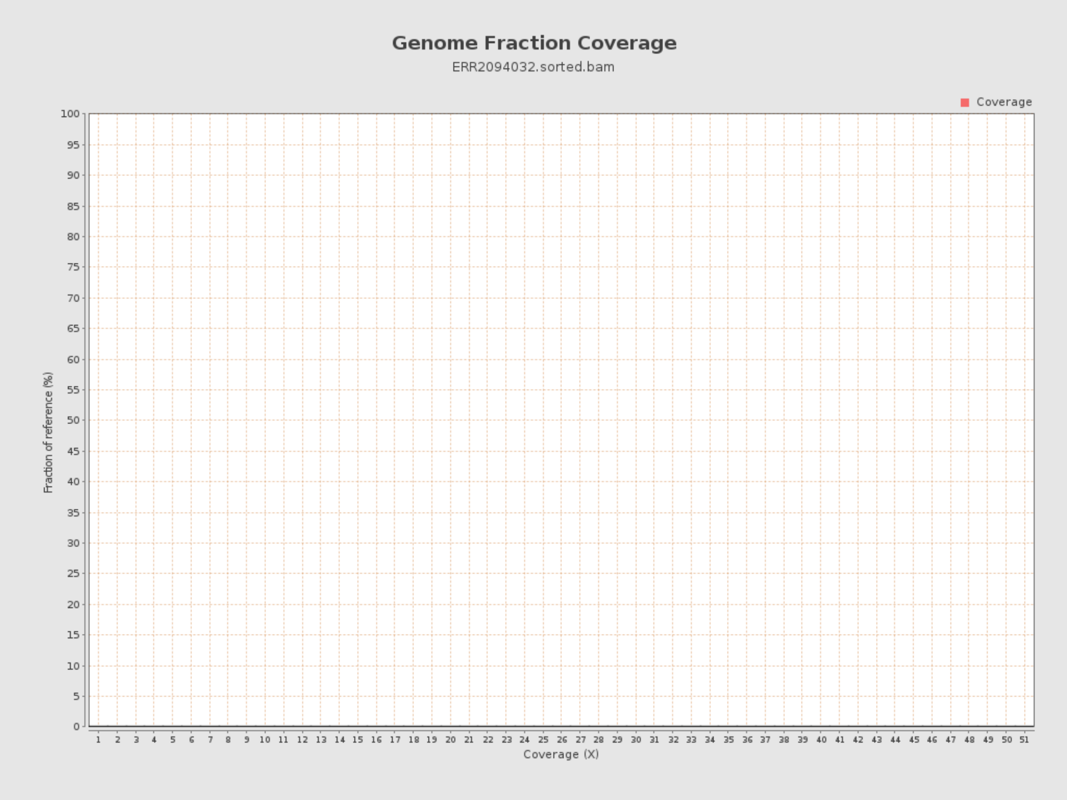
4. Results : Coverage Histogram



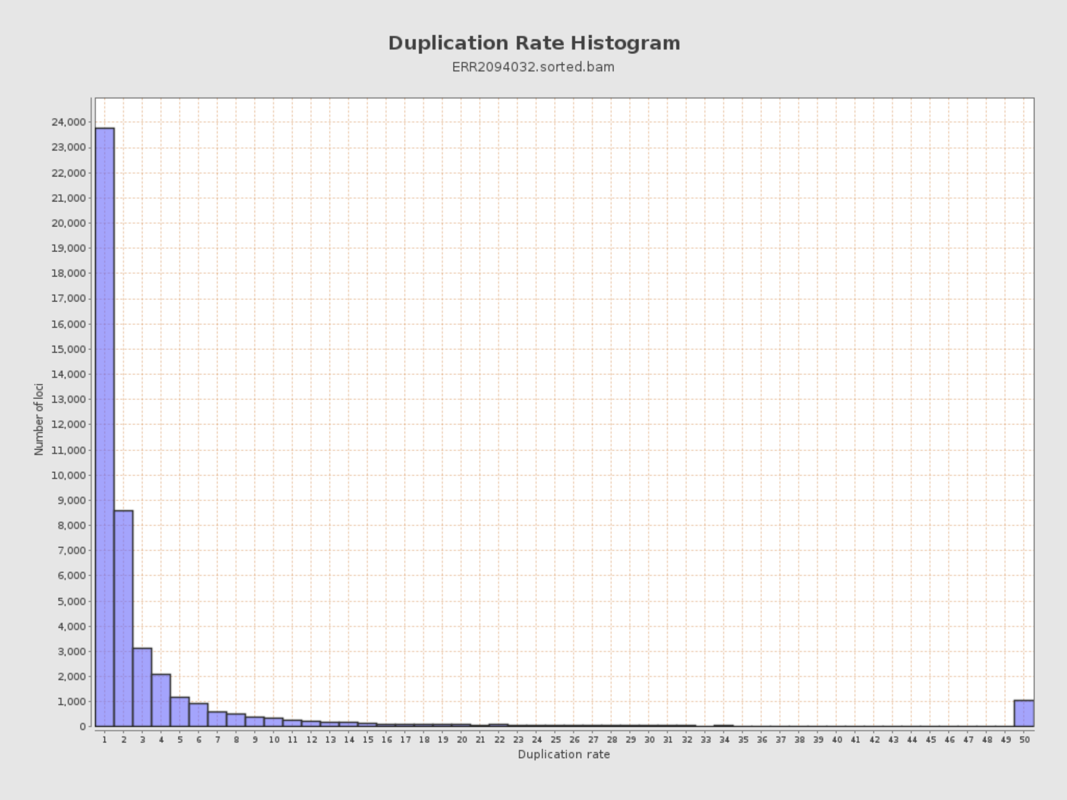
5. Results : Coverage Histogram (0-50X)



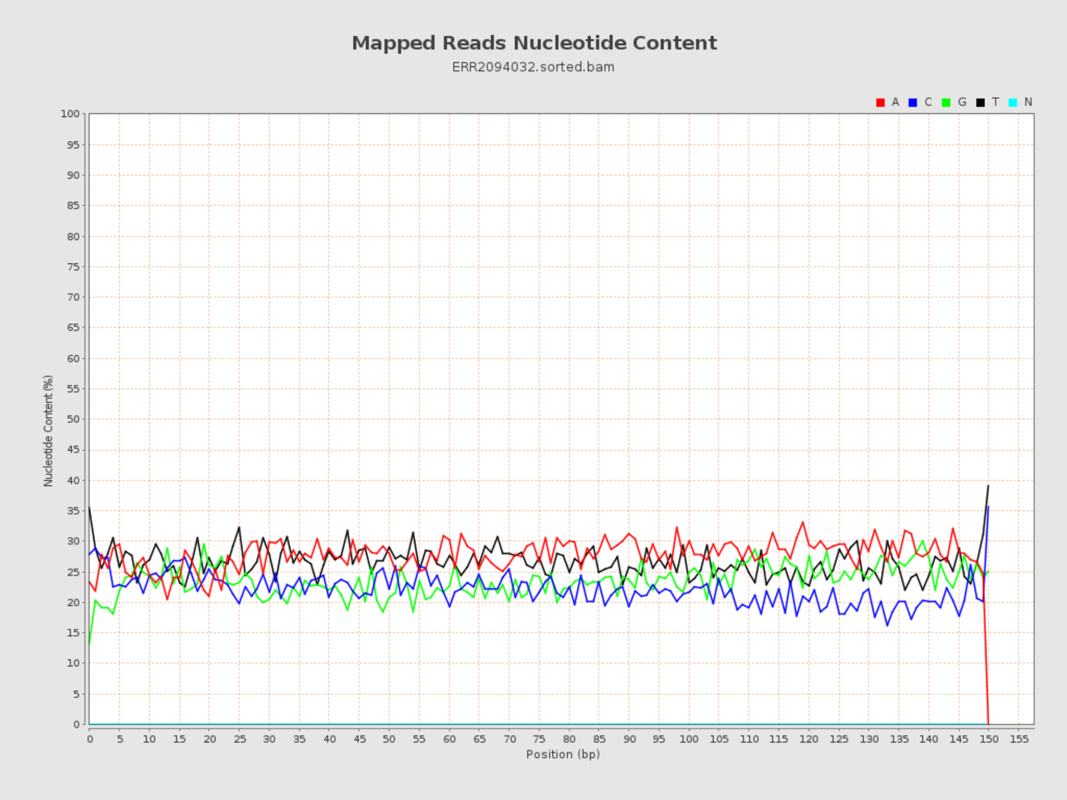
6. Results : Genome Fraction Coverage



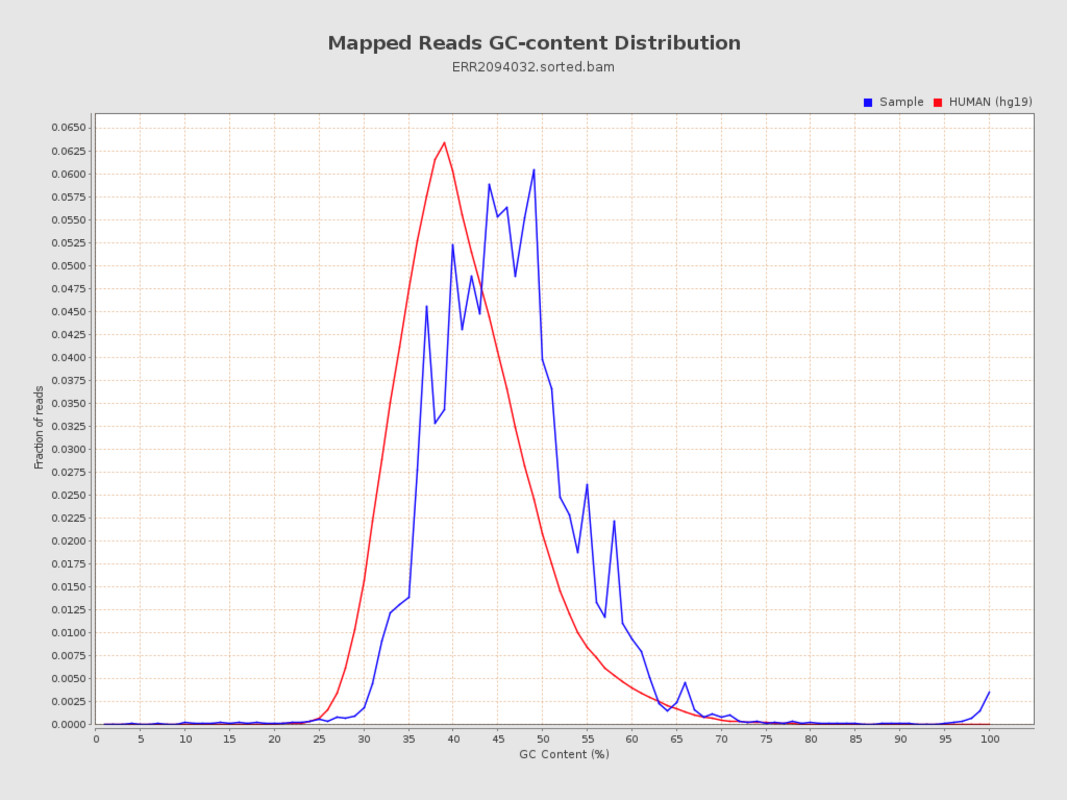
7. Results : Duplication Rate Histogram



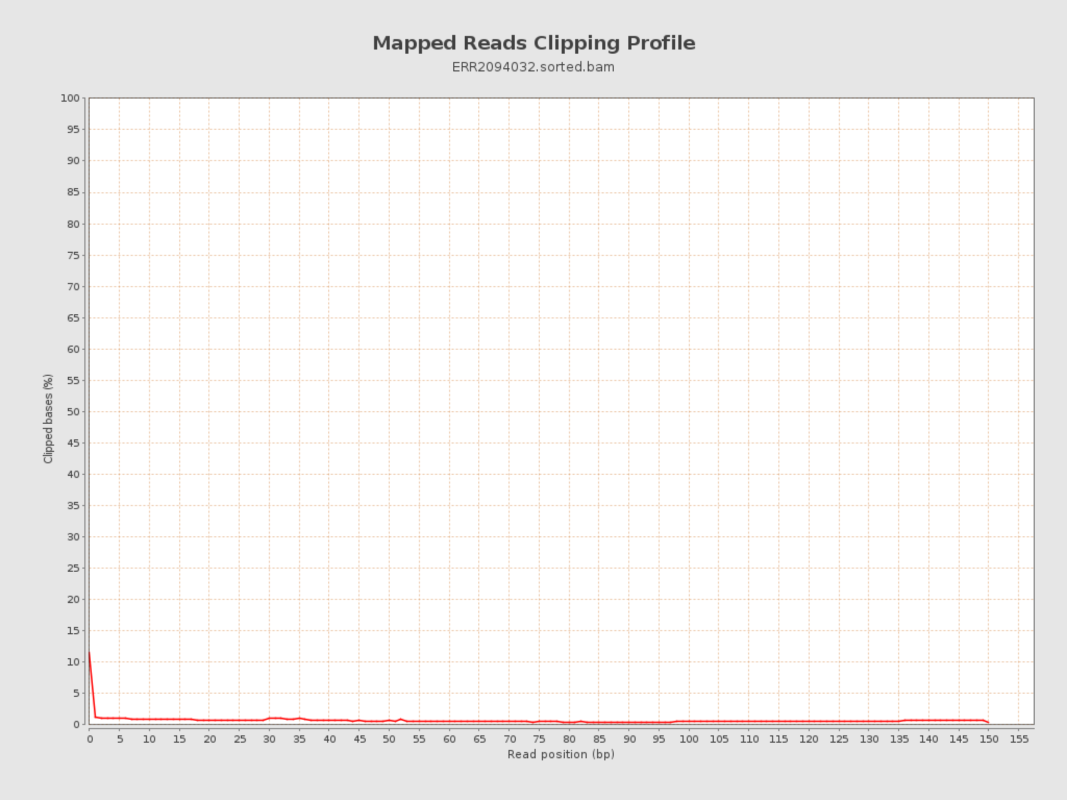
8. Results : Mapped Reads Nucleotide Content



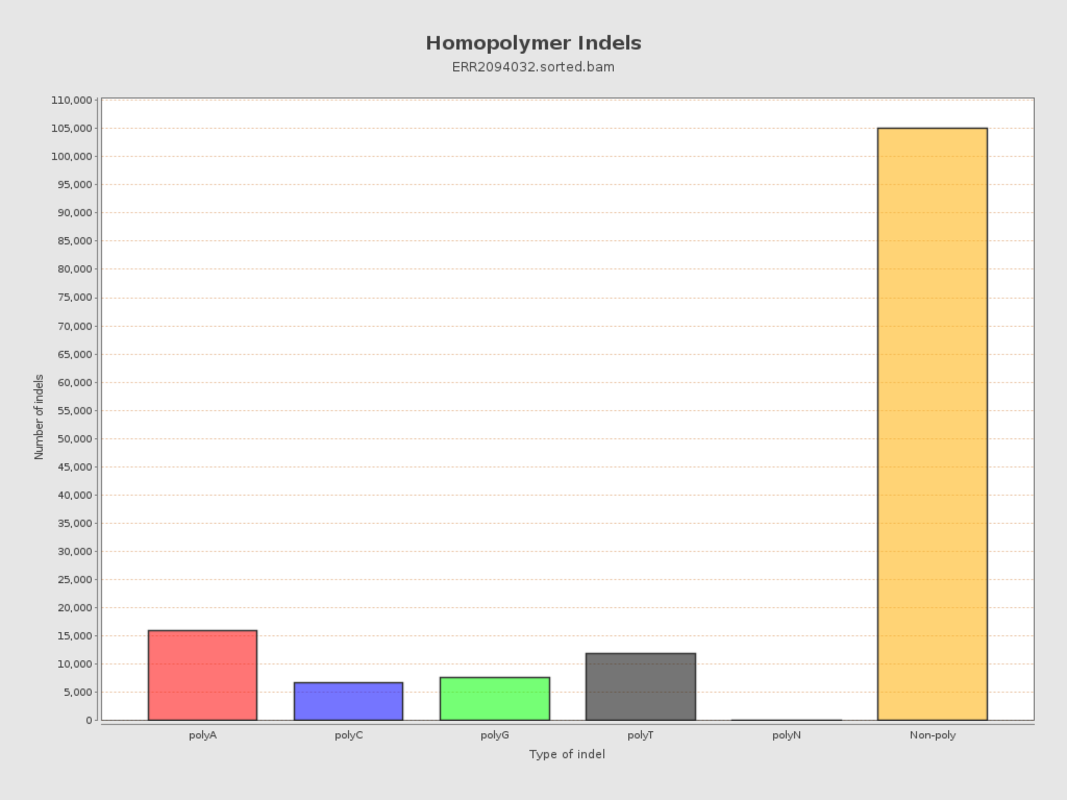
9. Results : Mapped Reads GC-content Distribution



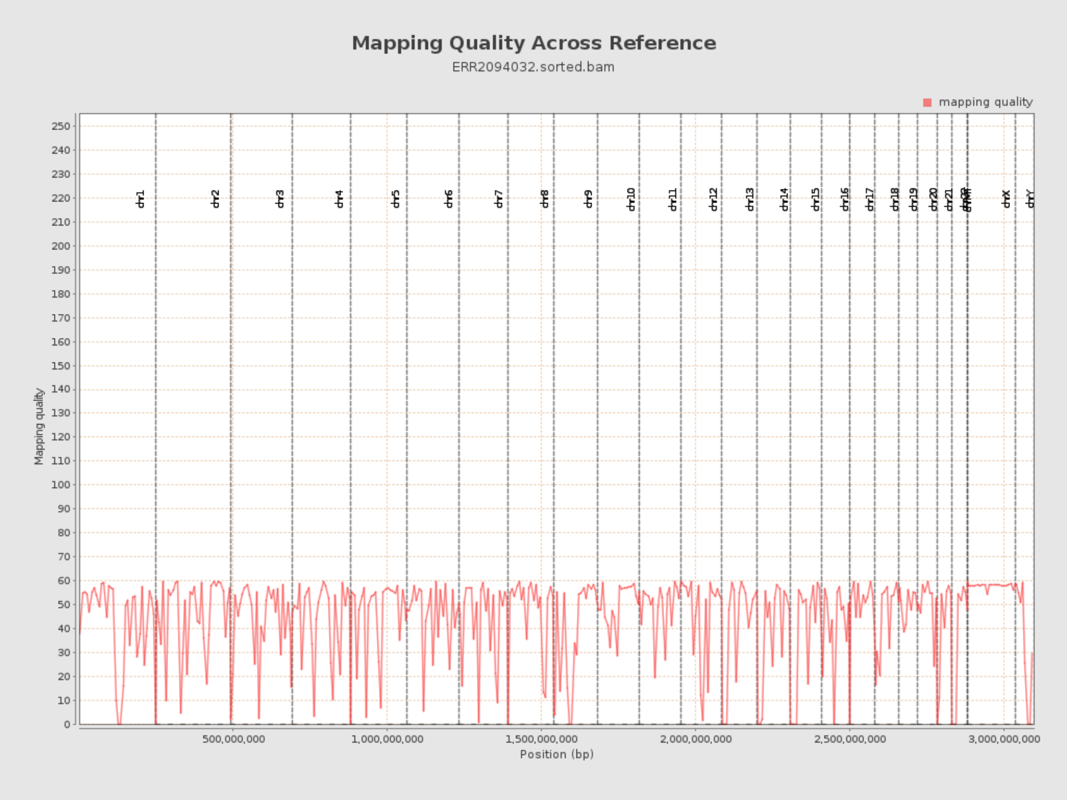
10. Results : Mapped Reads Clipping Profile



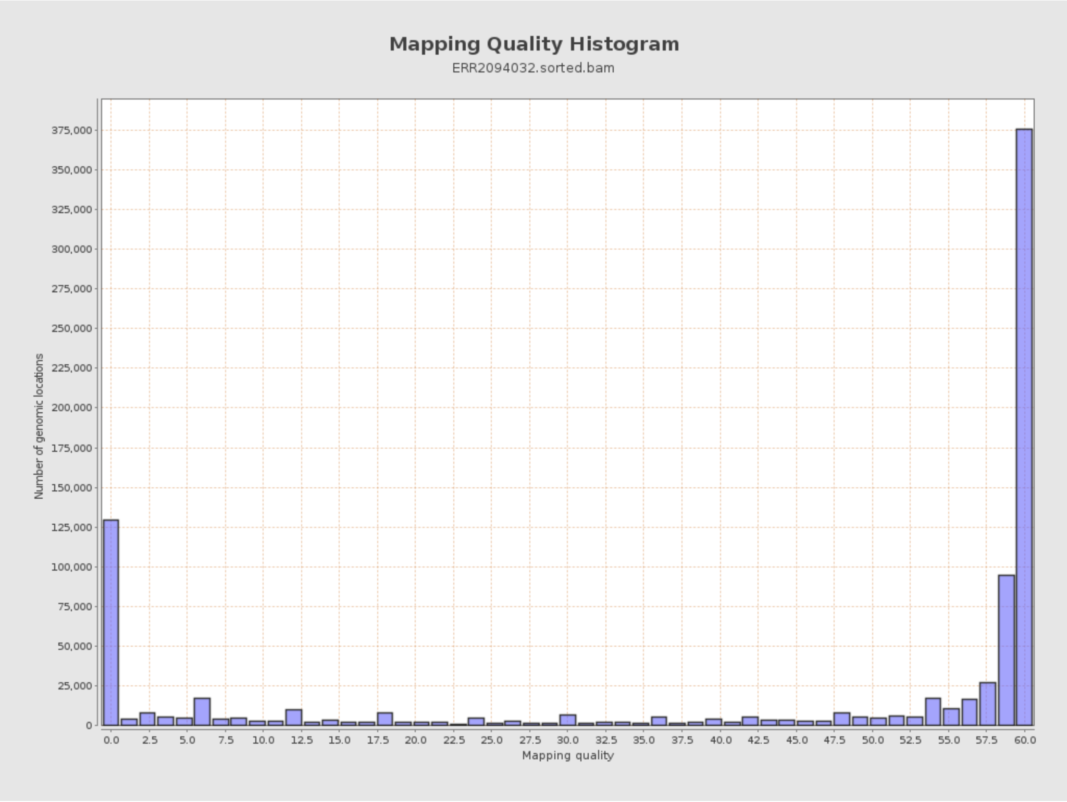
11. Results : Homopolymer Indels



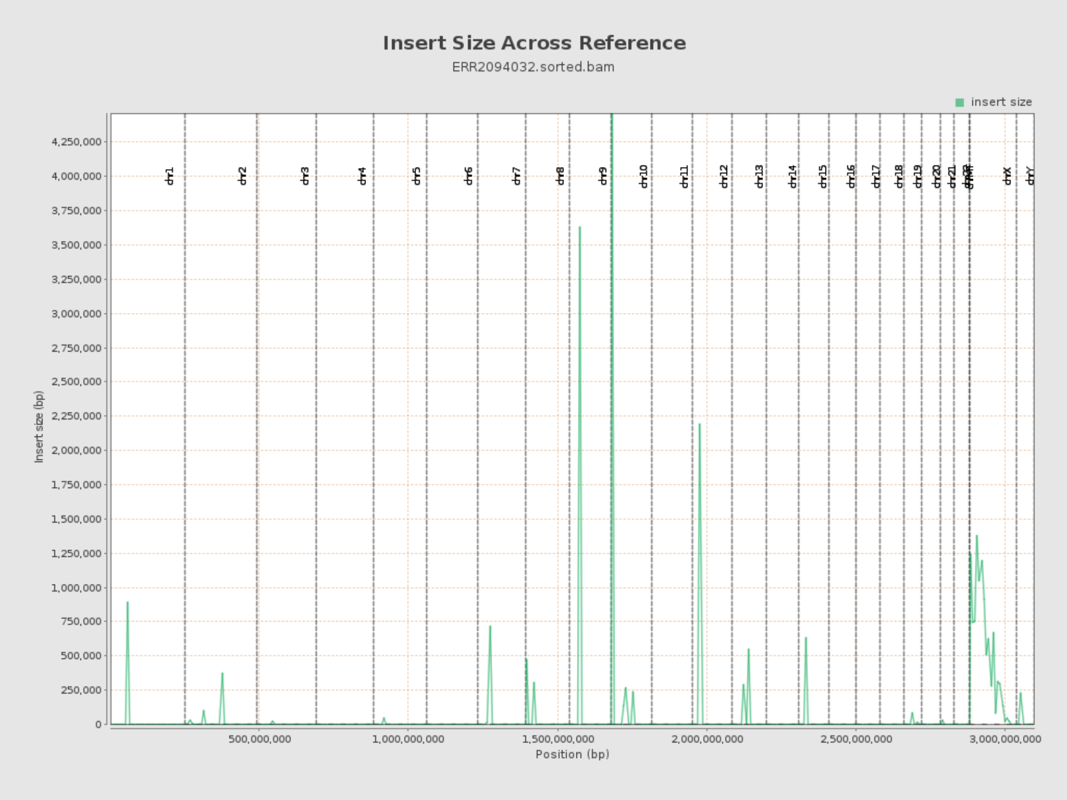
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram