Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:18:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094083.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_ERR2094083 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094083_1.fastq.gz ERR2094083_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:18:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	404,622
Mapped reads	392,774 / 97.07%
Unmapped reads	11,848 / 2.93%
Mapped paired reads	392,774 / 97.07%
Mapped reads, first in pair	197,363 / 48.78%
Mapped reads, second in pair	195,411 / 48.29%
Mapped reads, both in pair	390,116 / 96.41%
Mapped reads, singletons	2,658 / 0.66%
Secondary alignments	0
Supplementary alignments	15,073 / 3.73%
Read min/max/mean length	30 / 151 / 142.77
Duplicated reads (estimated)	375,404 / 92.78%
Duplication rate	50.98%
Clipped reads	152,006 / 37.57%

2.2. ACGT Content

Number/percentage of A's	13,326,594 / 26.03%
Number/percentage of C's	12,228,807 / 23.89%
Number/percentage of T's	12,817,066 / 25.03%
Number/percentage of G's	12,824,223 / 25.05%
Number/percentage of N's	612 / 0%

GC Percentage	48.93%

2.3. Coverage

Mean	0.0169
Standard Deviation	4.493

2.4. Mapping Quality

Mean Mapping Quality	39.5

2.5. Insert size

Mean	482,754.11
Standard Deviation	6,289,074.94
P25/Median/P75	136 / 168 / 199

2.6. Mismatches and indels

General error rate	4%
Mismatches	1,969,950
Insertions	31,732
Mapped reads with at least one insertion	7.93%
Deletions	156,667
Mapped reads with at least one deletion	38%
Homopolymer indels	28.3%

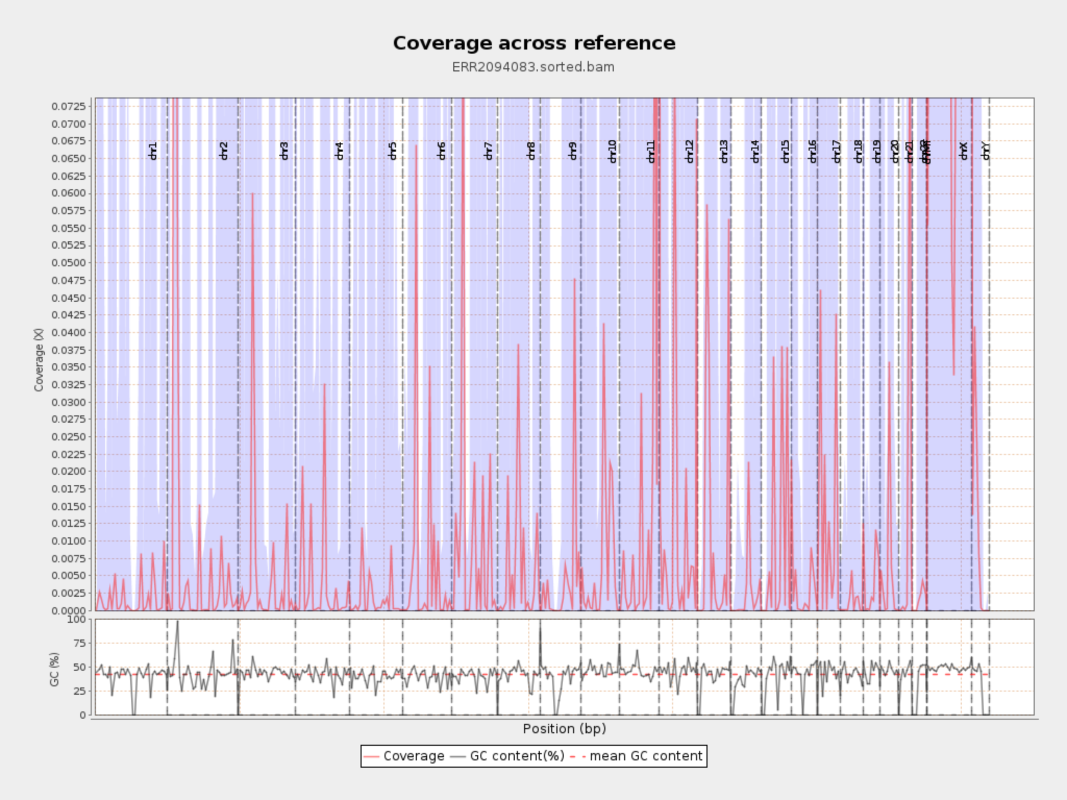
2.7. Chromosome stats

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

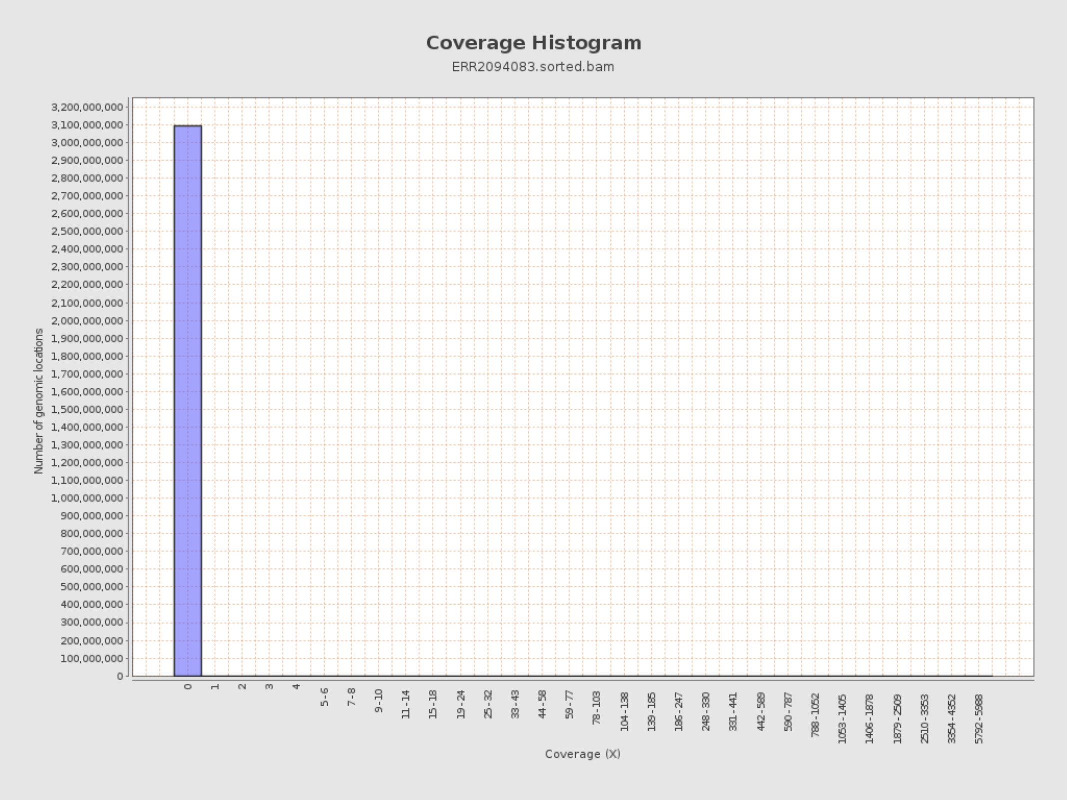
		bases	coverage	deviation
chr1	249250621	431954	0.0017	0.64
chr2	243199373	2519997	0.0104	4.447
chr3	198022430	869904	0.0044	1.8951
chr4	191154276	710762	0.0037	1.3832
chr5	180915260	315233	0.0017	0.6807
chr6	171115067	1134973	0.0066	3.4359
chr7	159138663	1593922	0.01	3.6559
chr8	146364022	865632	0.0059	2.0356
chr9	141213431	645350	0.0046	2.1163
chr10	135534747	956807	0.0071	2.6481
chr11	135006516	1929999	0.0143	4.0819
chr12	133851895	1394098	0.0104	4.1562
chr13	115169878	1319583	0.0115	3.3683
chr14	107349540	289743	0.0027	1.2653
chr15	102531392	939712	0.0092	2.9684
chr16	90354753	304692	0.0034	1.2289
chr17	81195210	1098459	0.0135	3.9269
chr18	78077248	94866	0.0012	0.4527
chr19	59128983	213018	0.0036	0.9211
chr20	63025520	384561	0.0061	1.9319
chr21	48129895	766511	0.0159	7.0855
chr22	51304566	79851	0.0016	0.3508
chrMT	16571	1534332	92.5914	438.7248
chrX	155270560	31285409	0.2015	15.0767

chrY	59373566	641099	0.0108	2.5888

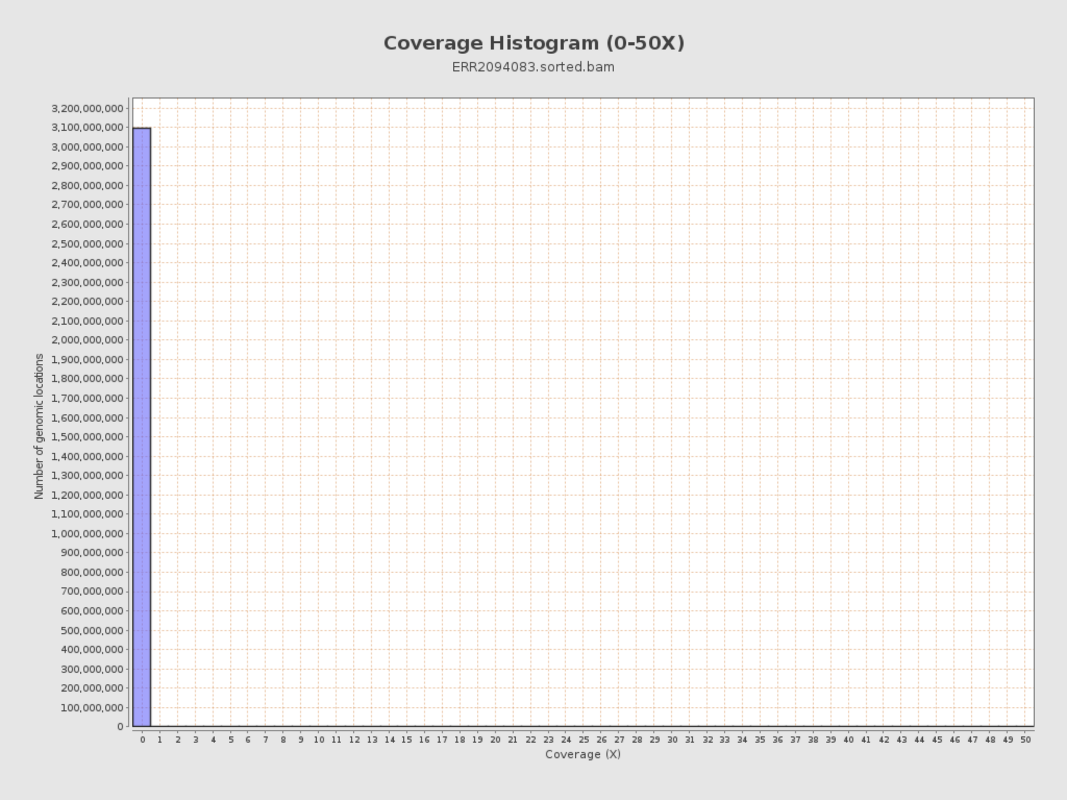
3. Results : Coverage across reference



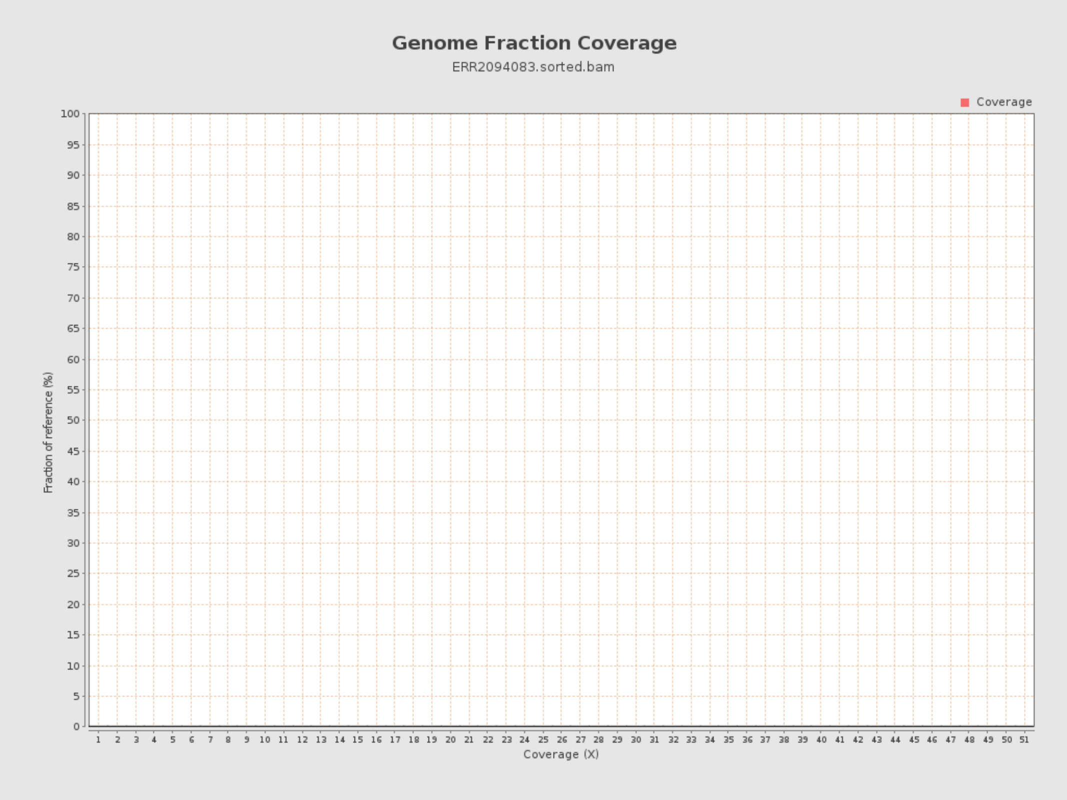
4. Results : Coverage Histogram



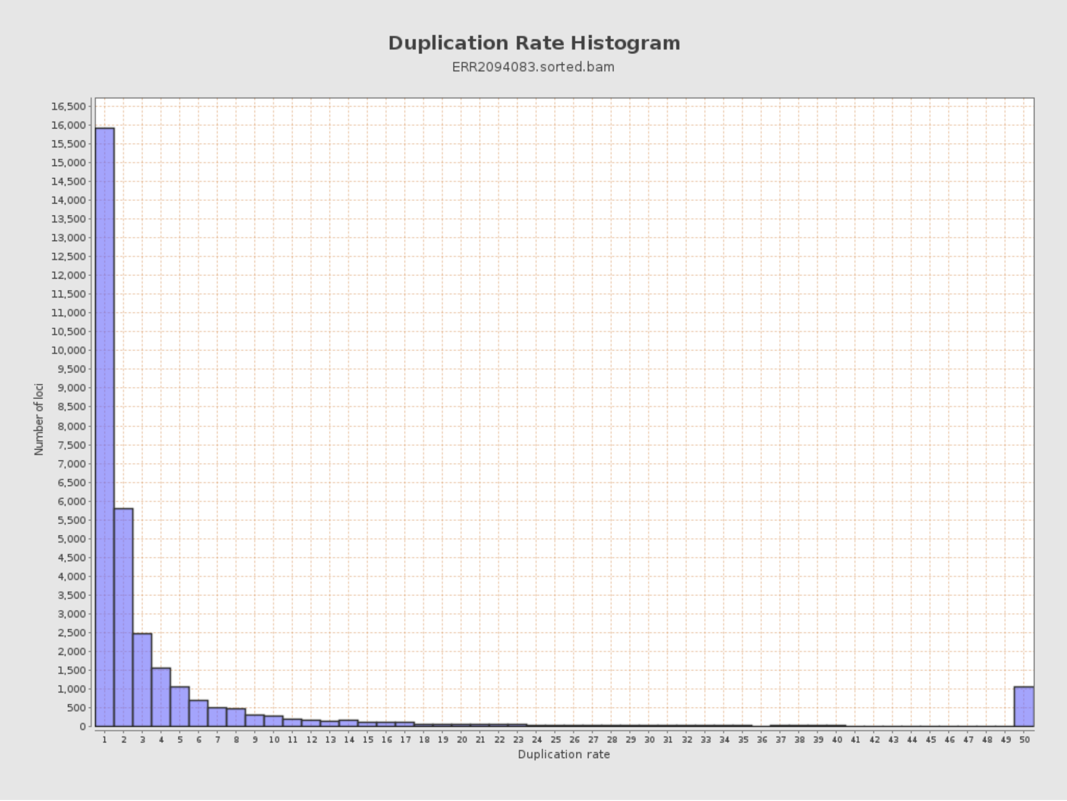
5. Results : Coverage Histogram (0-50X)



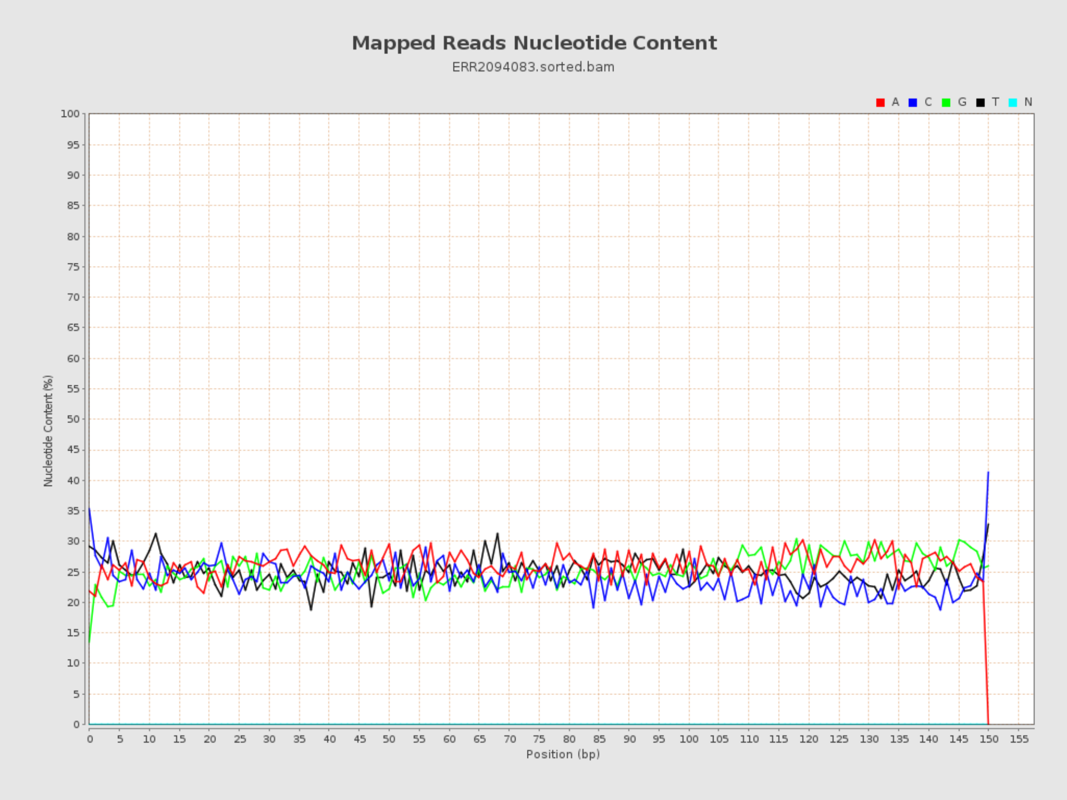
6. Results : Genome Fraction Coverage



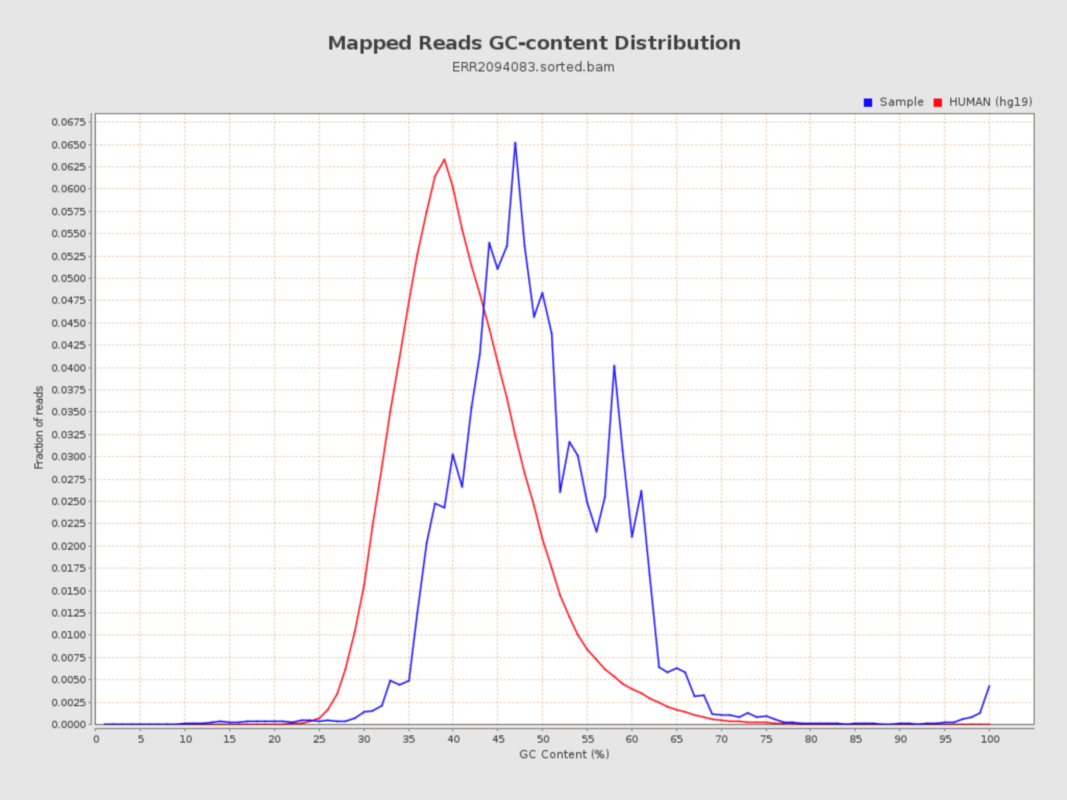
7. Results : Duplication Rate Histogram



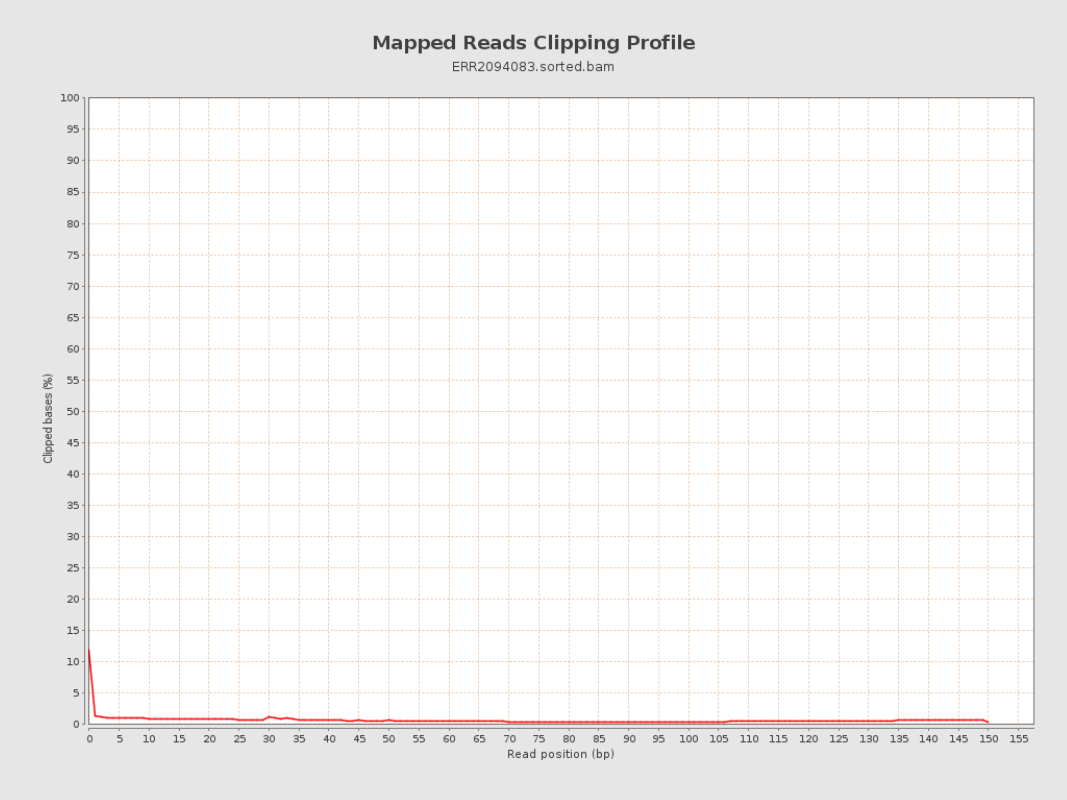
8. Results : Mapped Reads Nucleotide Content



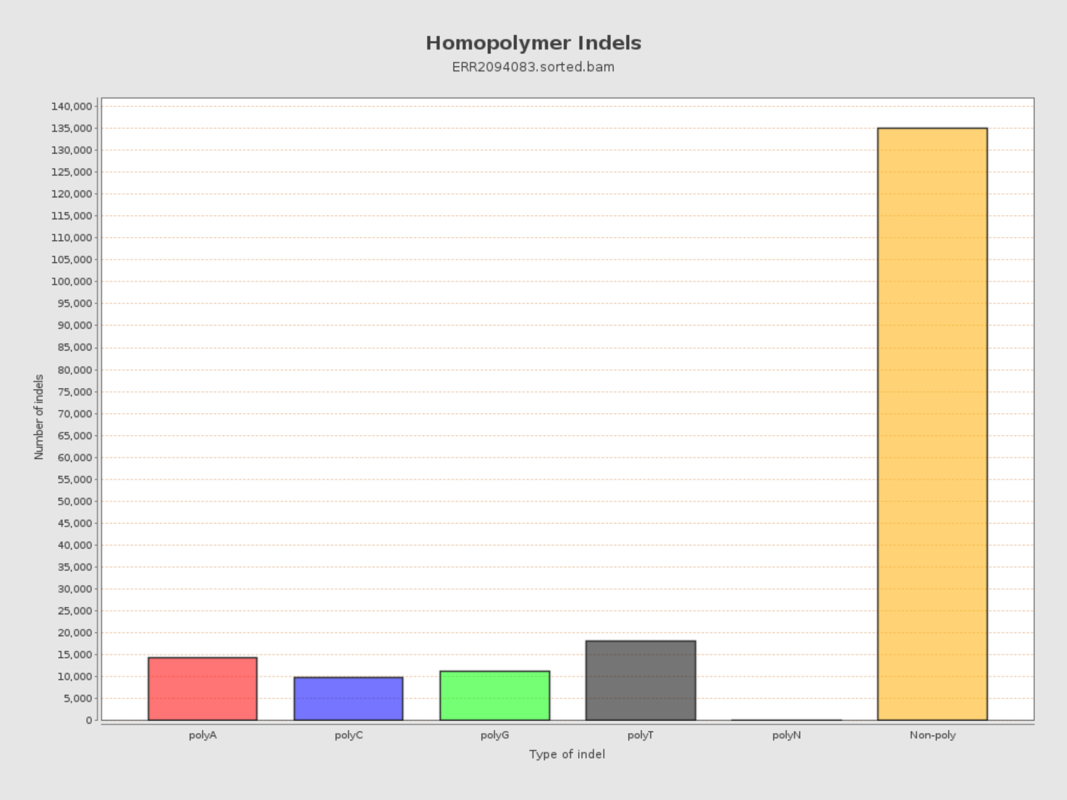
9. Results : Mapped Reads GC-content Distribution



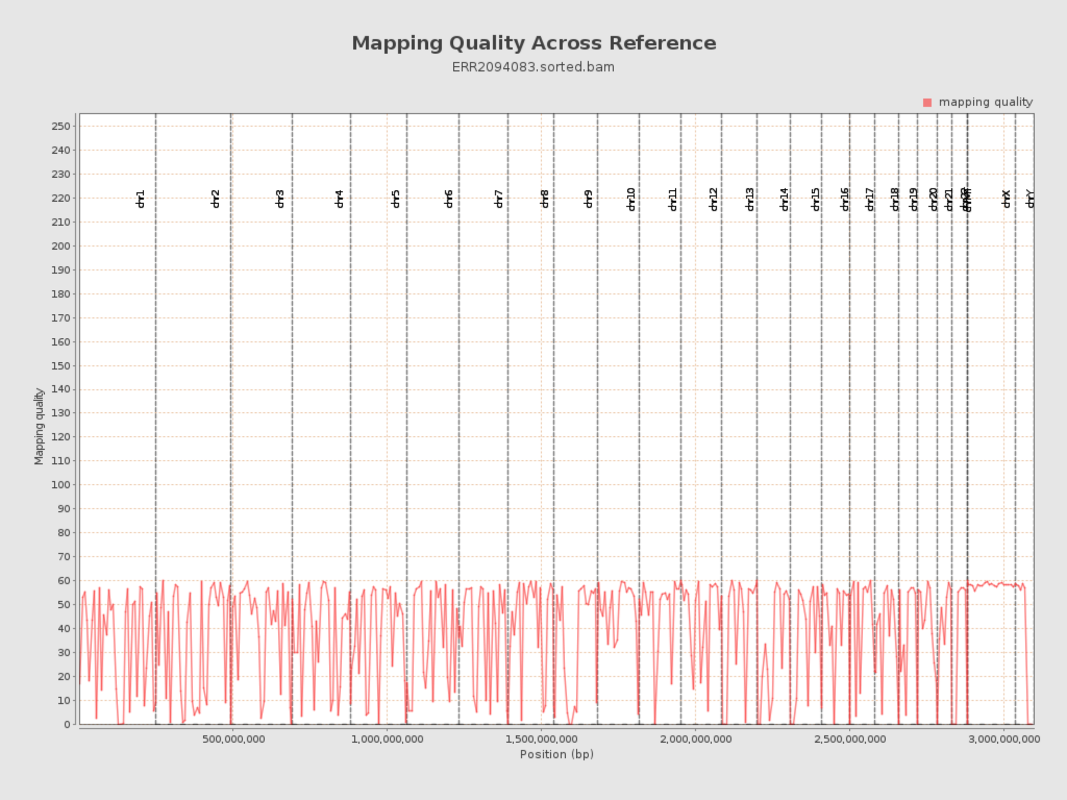
10. Results : Mapped Reads Clipping Profile



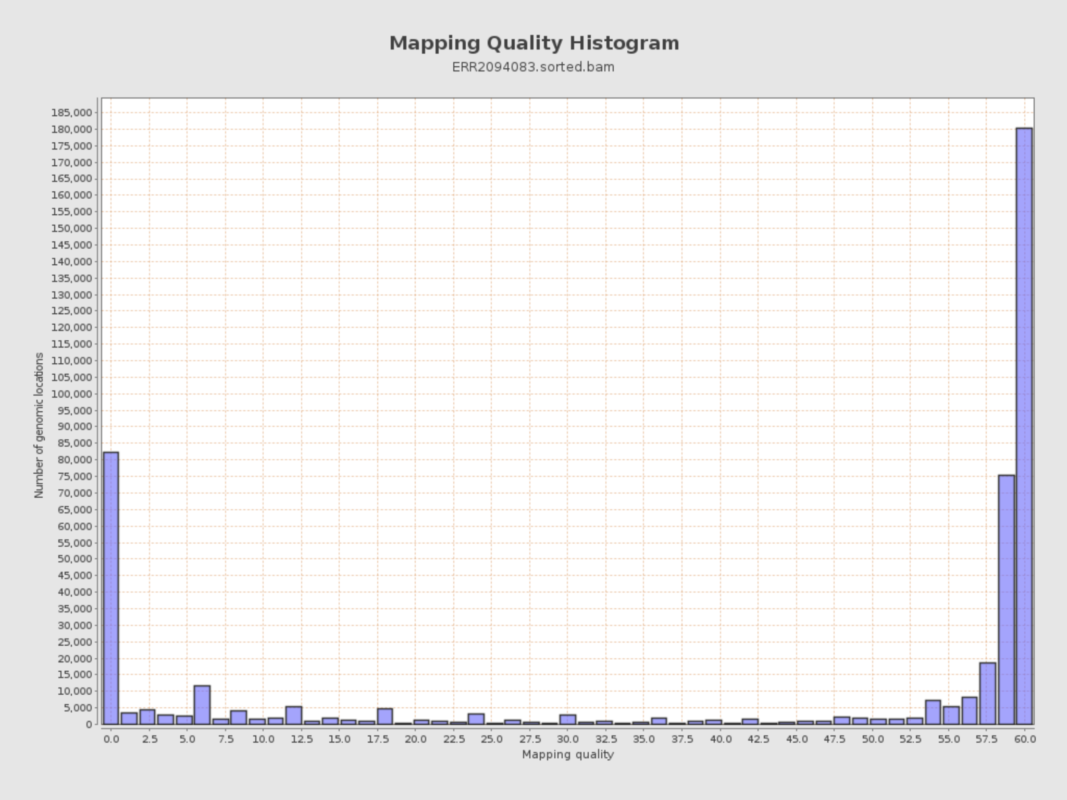
11. Results : Homopolymer Indels



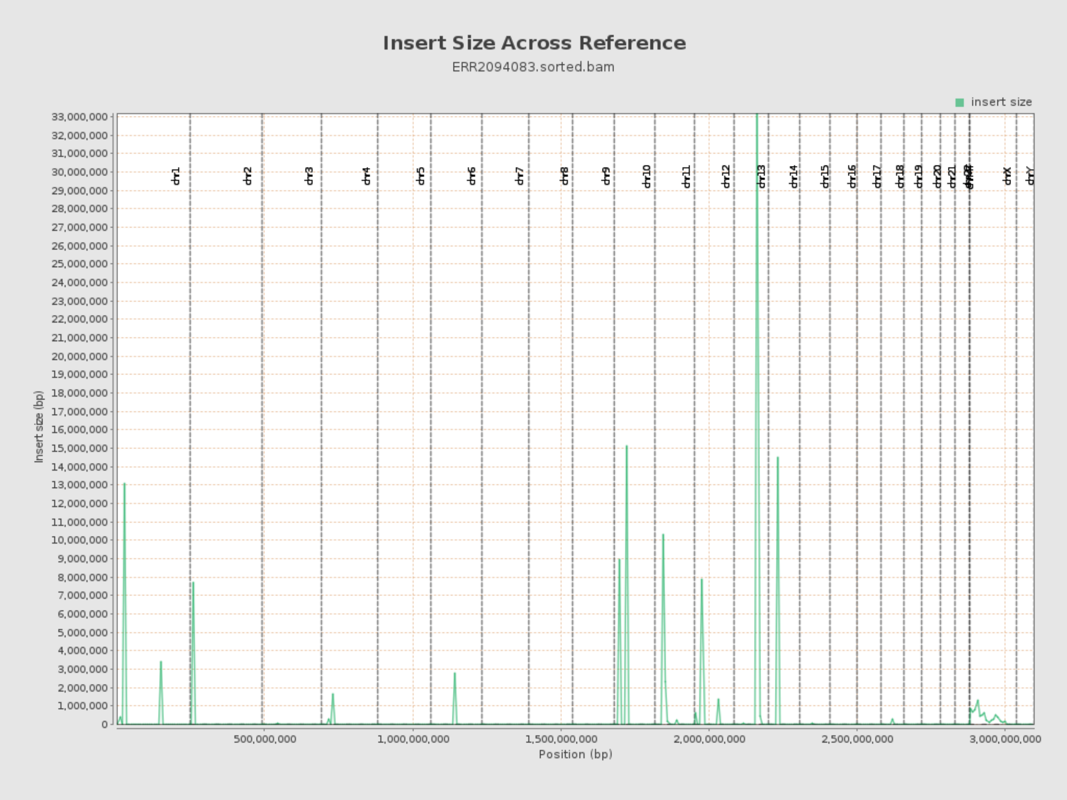
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram