

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:44:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094008.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_ERR2094008 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094008_1.fastq.gz ERR2094008_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:44:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	582,124
Mapped reads	467,749 / 80.35%
Unmapped reads	114,375 / 19.65%
Mapped paired reads	467,749 / 80.35%
Mapped reads, first in pair	234,378 / 40.26%
Mapped reads, second in pair	233,371 / 40.09%
Mapped reads, both in pair	463,806 / 79.67%
Mapped reads, singletons	3,943 / 0.68%
Secondary alignments	0
Supplementary alignments	9,702 / 1.67%
Read min/max/mean length	30 / 151 / 129.35
Duplicated reads (estimated)	461,730 / 79.32%
Duplication rate	40.35%
Clipped reads	182,315 / 31.32%

2.2. ACGT Content

Number/percentage of A's	17,701,369 / 28.23%
Number/percentage of C's	13,836,453 / 22.07%
Number/percentage of T's	16,901,540 / 26.96%
Number/percentage of G's	14,259,795 / 22.74%
Number/percentage of N's	607 / 0%

GC Percentage	44.81%
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2.3. Coverage

Mean	0.0206
Standard Deviation	16.2388

2.4. Mapping Quality

Mean Mapping Quality	32.67
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2.5. Insert size

Mean	114,654.73
Standard Deviation	2,906,607.71
P25/Median/P75	158 / 180 / 217

2.6. Mismatches and indels

General error rate	3.12%
Mismatches	1,931,426
Insertions	17,843
Mapped reads with at least one insertion	3.7%
Deletions	166,321
Mapped reads with at least one deletion	34.48%
Homopolymer indels	33.15%

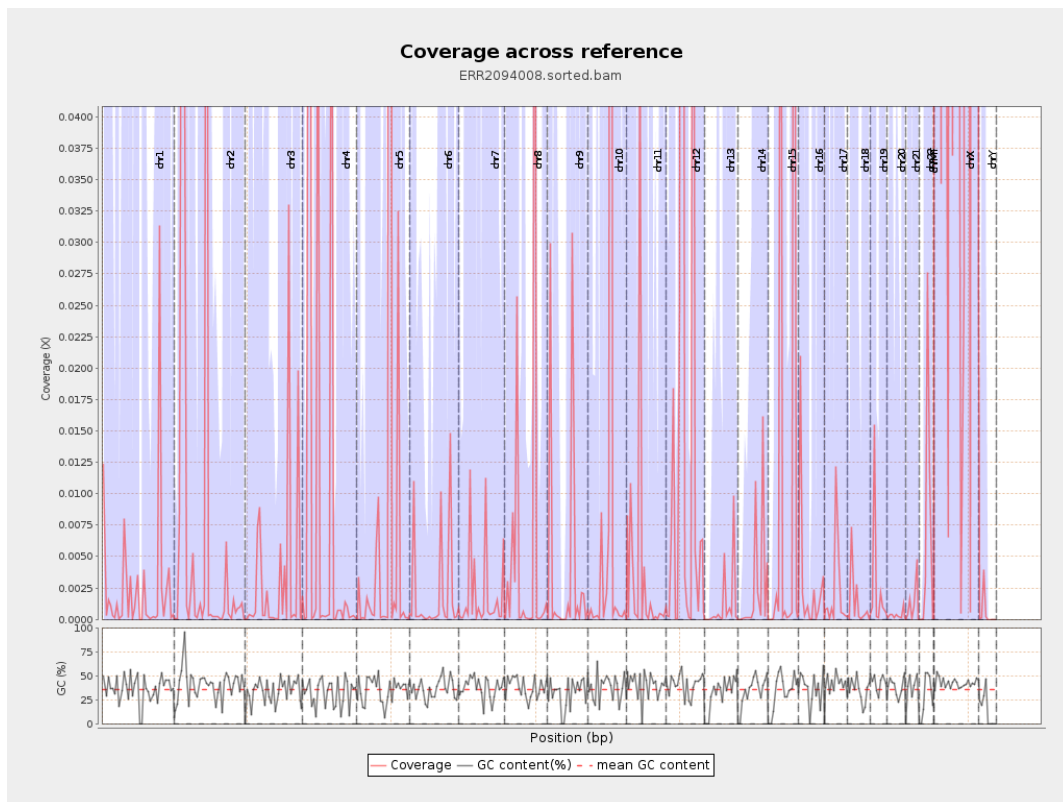
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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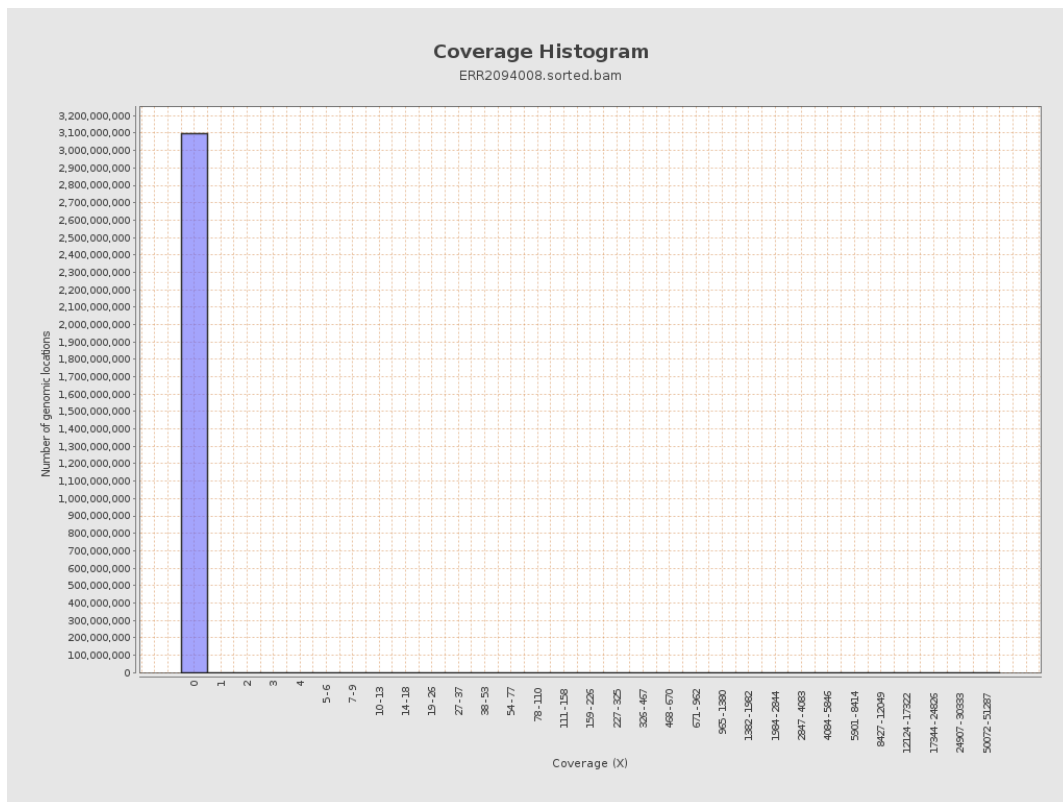
		bases	coverage	deviation
chr1	249250621	645914	0.0026	1.3552
chr2	243199373	1808641	0.0074	4.1541
chr3	198022430	663763	0.0034	1.6376
chr4	191154276	2007862	0.0105	6.8776
chr5	180915260	3860370	0.0213	20.9677
chr6	171115067	326111	0.0019	0.8603
chr7	159138663	326677	0.0021	0.7532
chr8	146364022	903890	0.0062	3.4713
chr9	141213431	534130	0.0038	2.1384
chr10	135534747	1305342	0.0096	7.5411
chr11	135006516	570565	0.0042	3.0653
chr12	133851895	2737324	0.0205	10.6587
chr13	115169878	139946	0.0012	0.6338
chr14	107349540	275803	0.0026	1.067
chr15	102531392	1404196	0.0137	7.6207
chr16	90354753	254398	0.0028	0.9558
chr17	81195210	162458	0.002	0.8064
chr18	78077248	94997	0.0012	0.4156
chr19	59128983	159869	0.0027	0.9095
chr20	63025520	23602	0.0004	0.0606
chr21	48129895	62531	0.0013	0.4017
chr22	51304566	329083	0.0064	2.4908
chrMT	16571	16578518	1,000.4537	5,077.6545
chrX	155270560	28424286	0.1831	39.7462

chrY	59373566	33366	0.0006	0.2226
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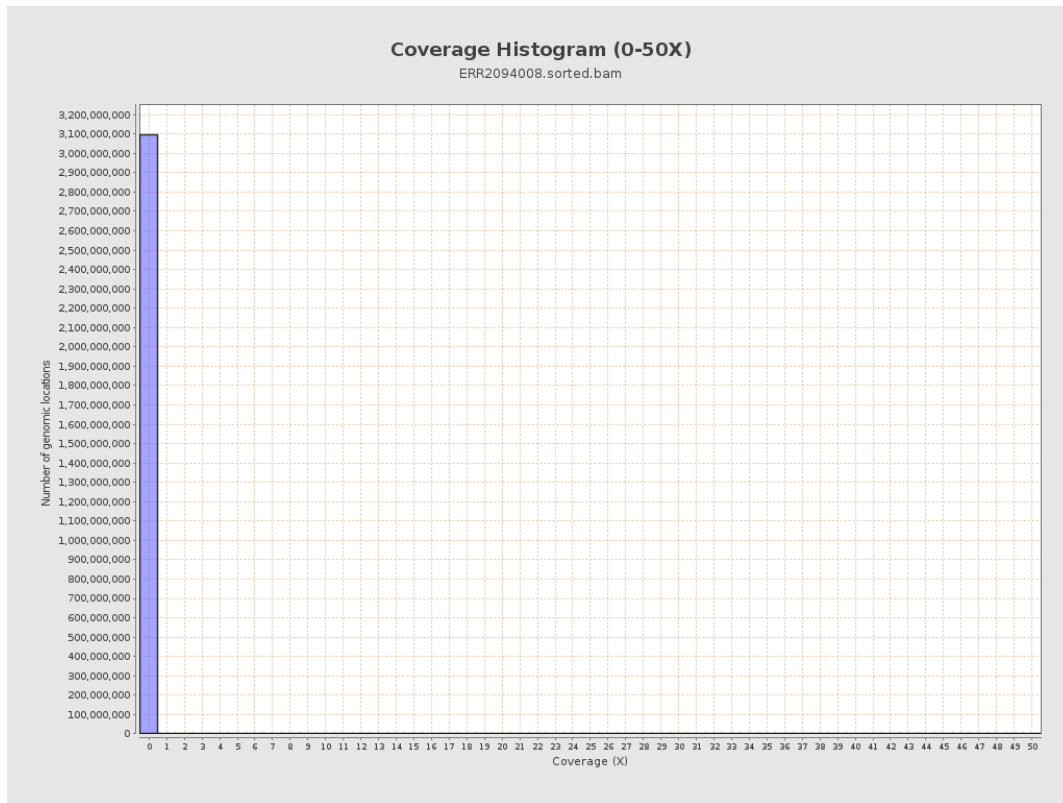
3. Results : Coverage across reference



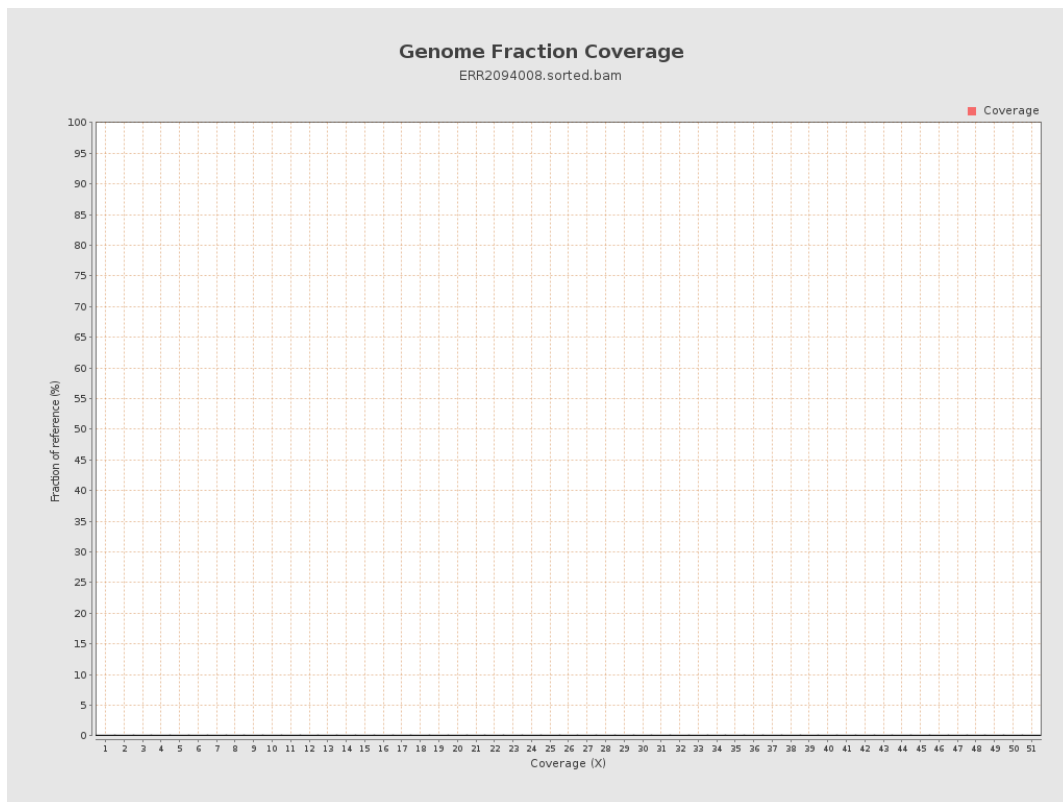
4. Results : Coverage Histogram



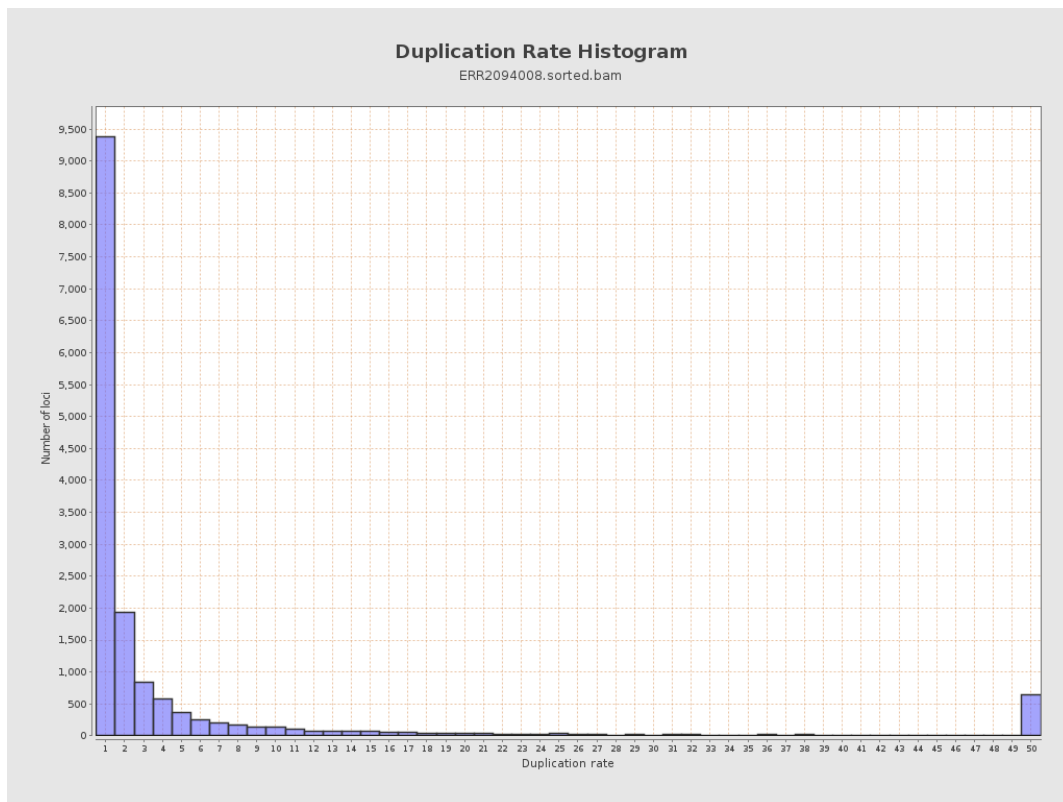
5. Results : Coverage Histogram (0-50X)



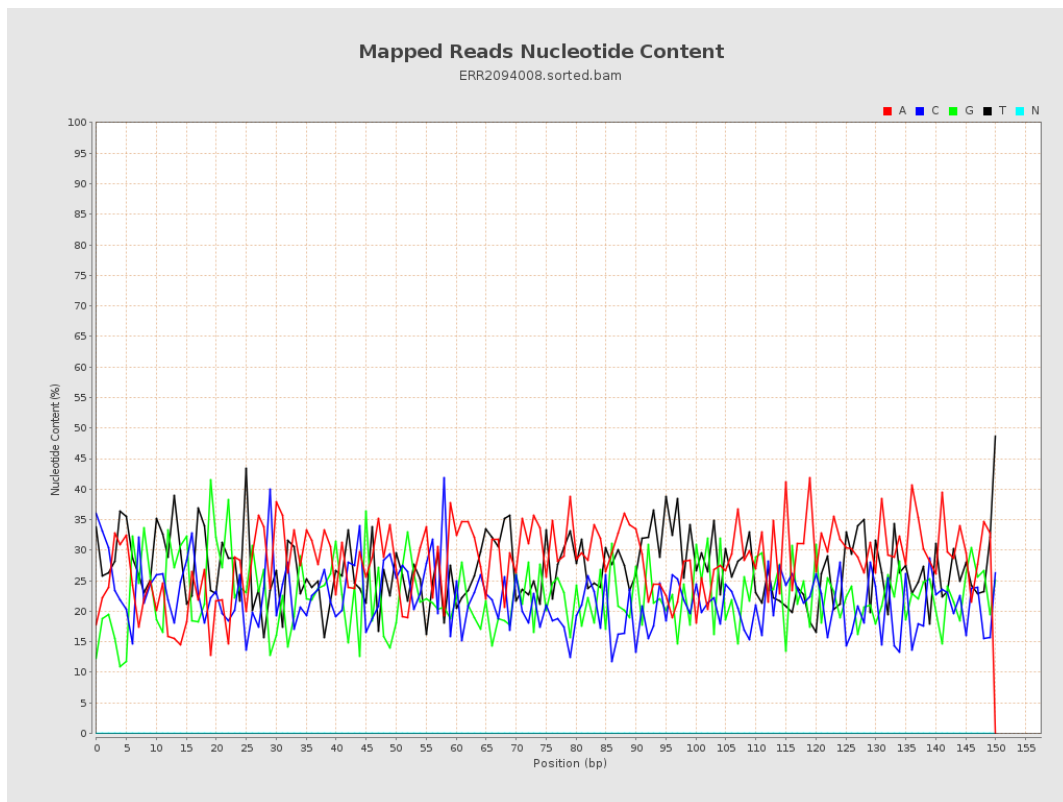
6. Results : Genome Fraction Coverage



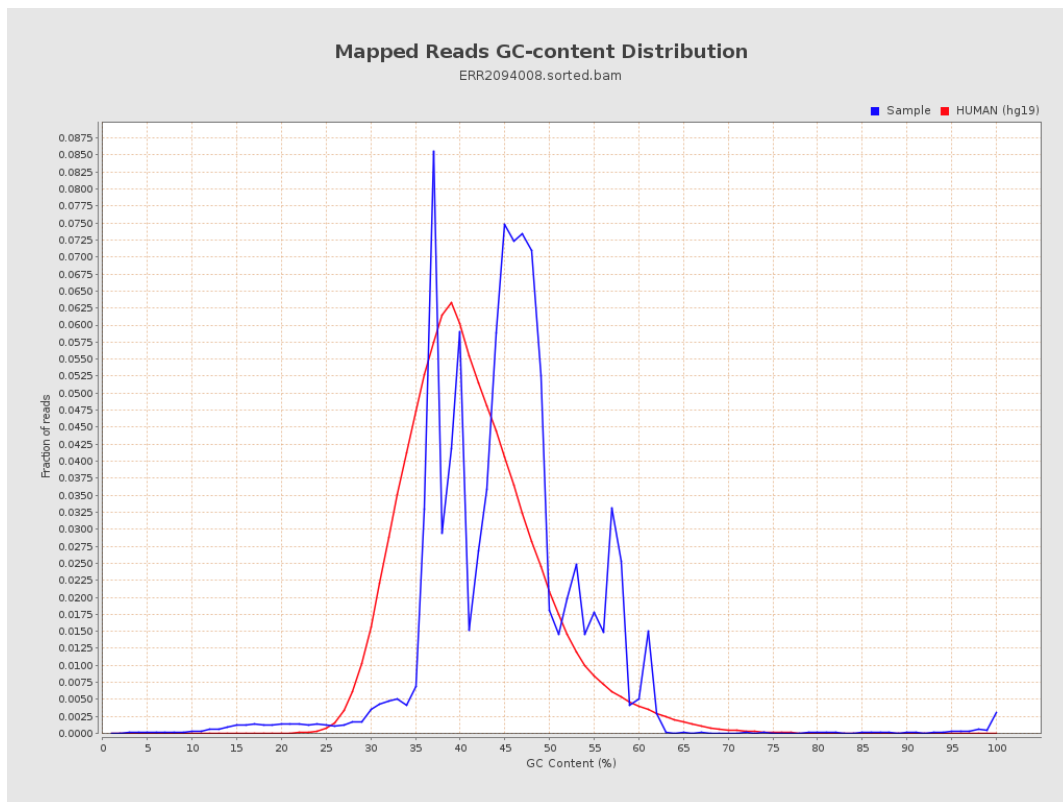
7. Results : Duplication Rate Histogram



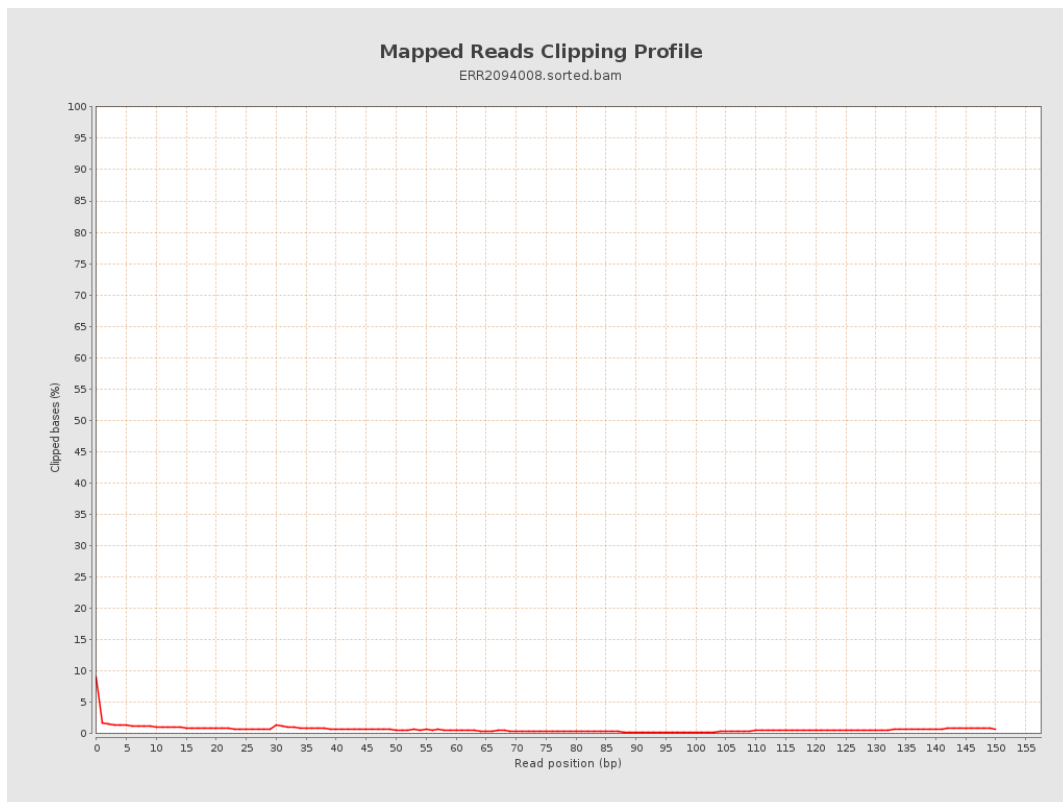
8. Results : Mapped Reads Nucleotide Content



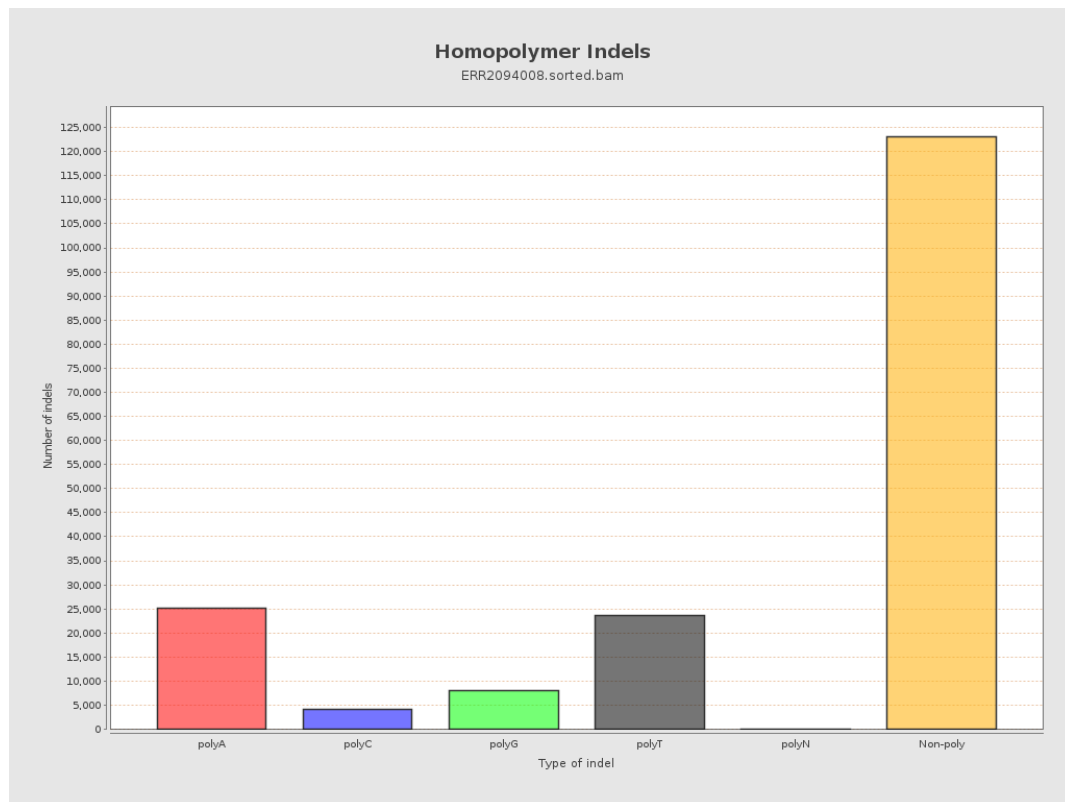
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



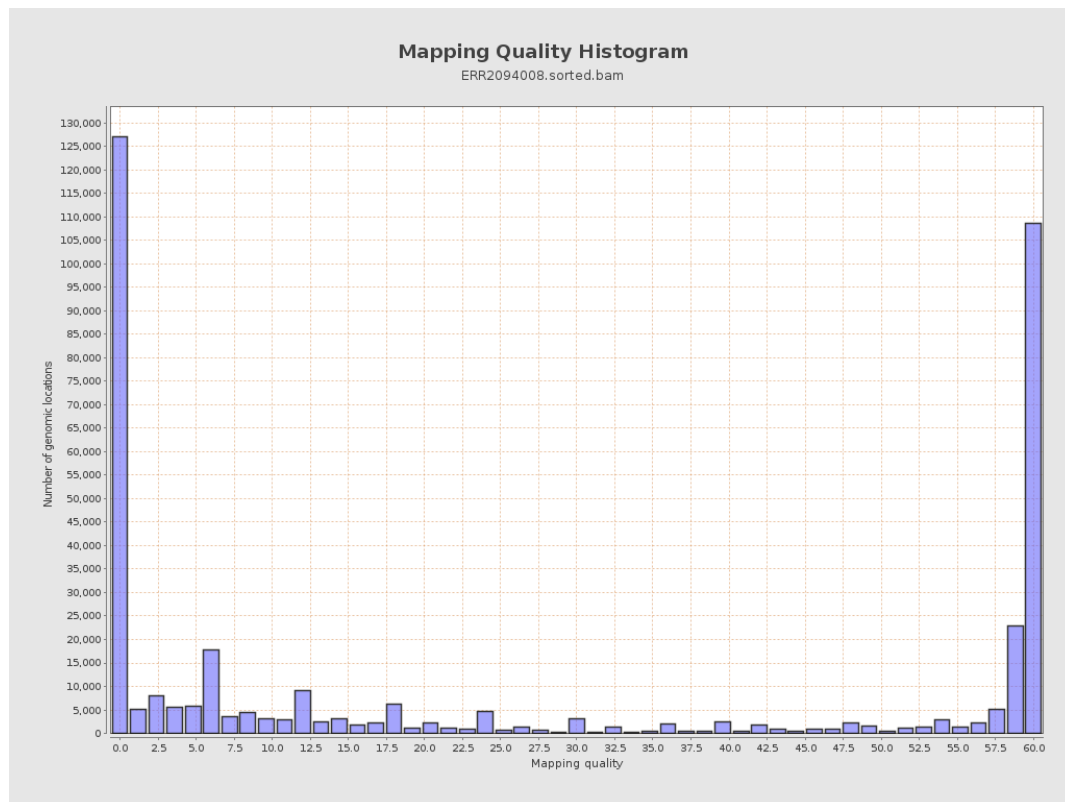
11. Results : Homopolymer Indels



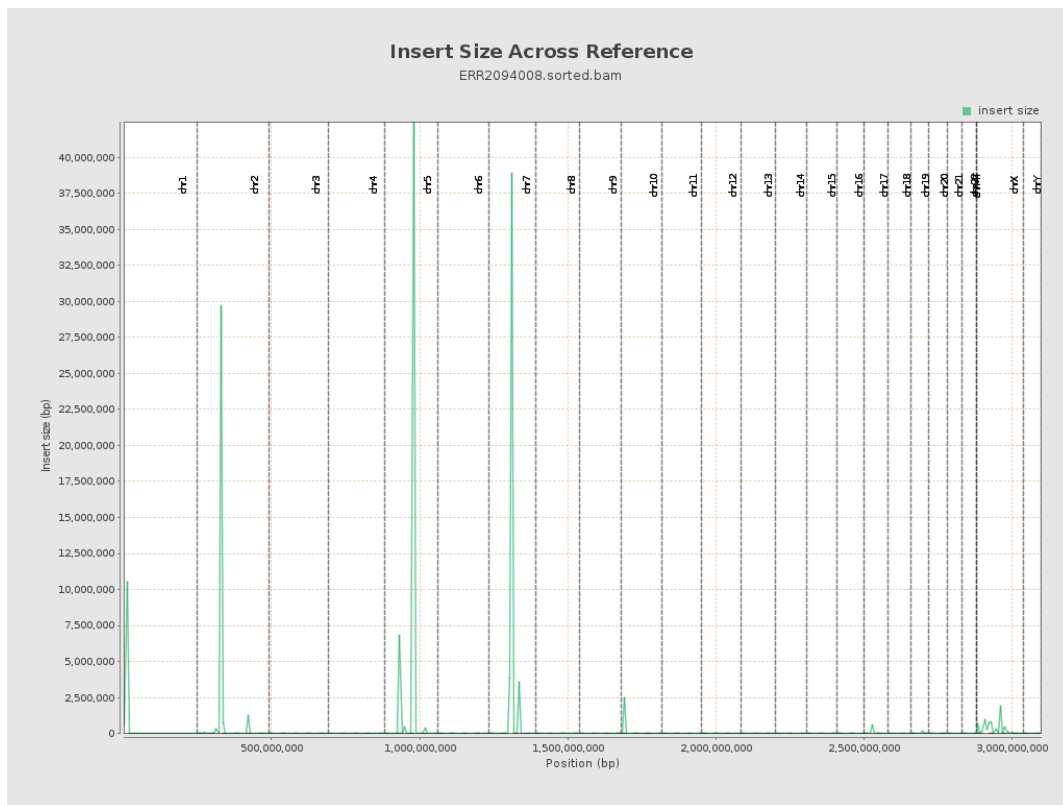
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

