

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094098.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_ERR2094098 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094098_1.fastq.gz ERR2094098_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:02:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	524
Mapped reads	309 / 58.97%
Unmapped reads	215 / 41.03%
Mapped paired reads	309 / 58.97%
Mapped reads, first in pair	163 / 31.11%
Mapped reads, second in pair	146 / 27.86%
Mapped reads, both in pair	266 / 50.76%
Mapped reads, singletons	43 / 8.21%
Secondary alignments	0
Supplementary alignments	22 / 4.2%
Read min/max/mean length	30 / 151 / 121.46
Duplicated reads (estimated)	109 / 20.8%
Duplication rate	11.26%
Clipped reads	198 / 37.79%

2.2. ACGT Content

Number/percentage of A's	11,276 / 32.53%
Number/percentage of C's	7,230 / 20.86%
Number/percentage of T's	9,055 / 26.12%
Number/percentage of G's	7,100 / 20.48%
Number/percentage of N's	0 / 0%

GC Percentage	41.34%
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2.3. Coverage

Mean	0
Standard Deviation	0.011

2.4. Mapping Quality

Mean Mapping Quality	6.73
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2.5. Insert size

Mean	787,279.45
Standard Deviation	5,688,706.99
P25/Median/P75	137 / 147 / 198

2.6. Mismatches and indels

General error rate	3.74%
Mismatches	1,233
Insertions	21
Mapped reads with at least one insertion	6.8%
Deletions	114
Mapped reads with at least one deletion	35.28%
Homopolymer indels	28.89%

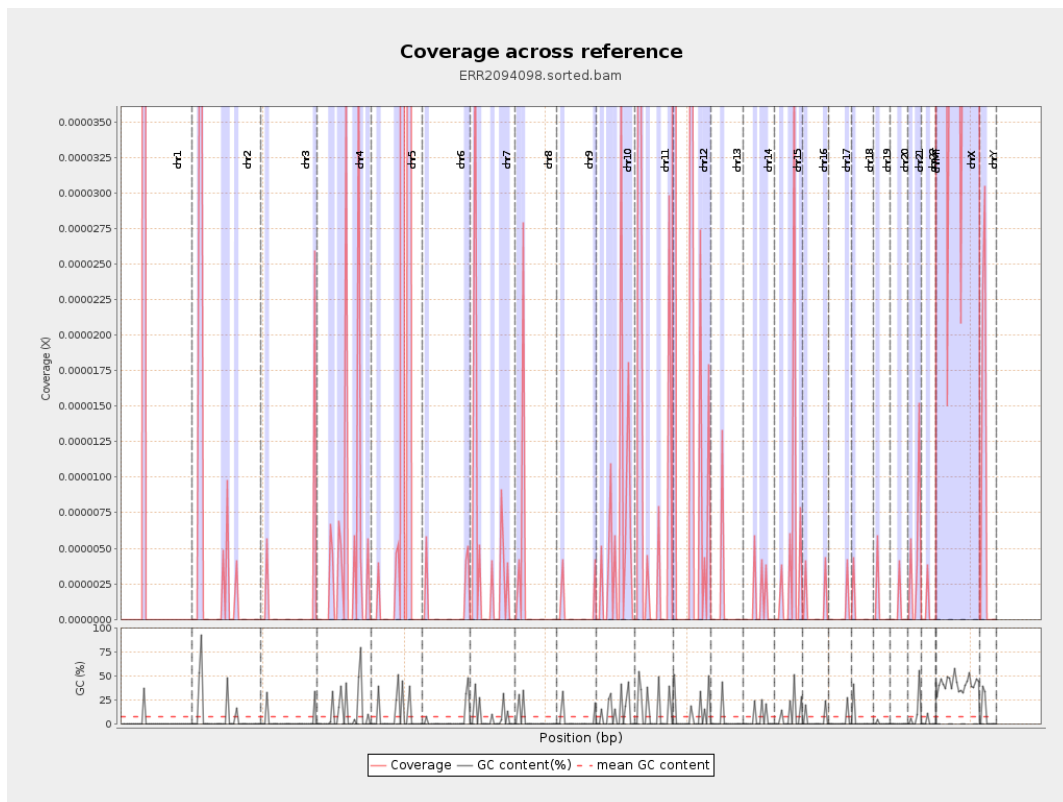
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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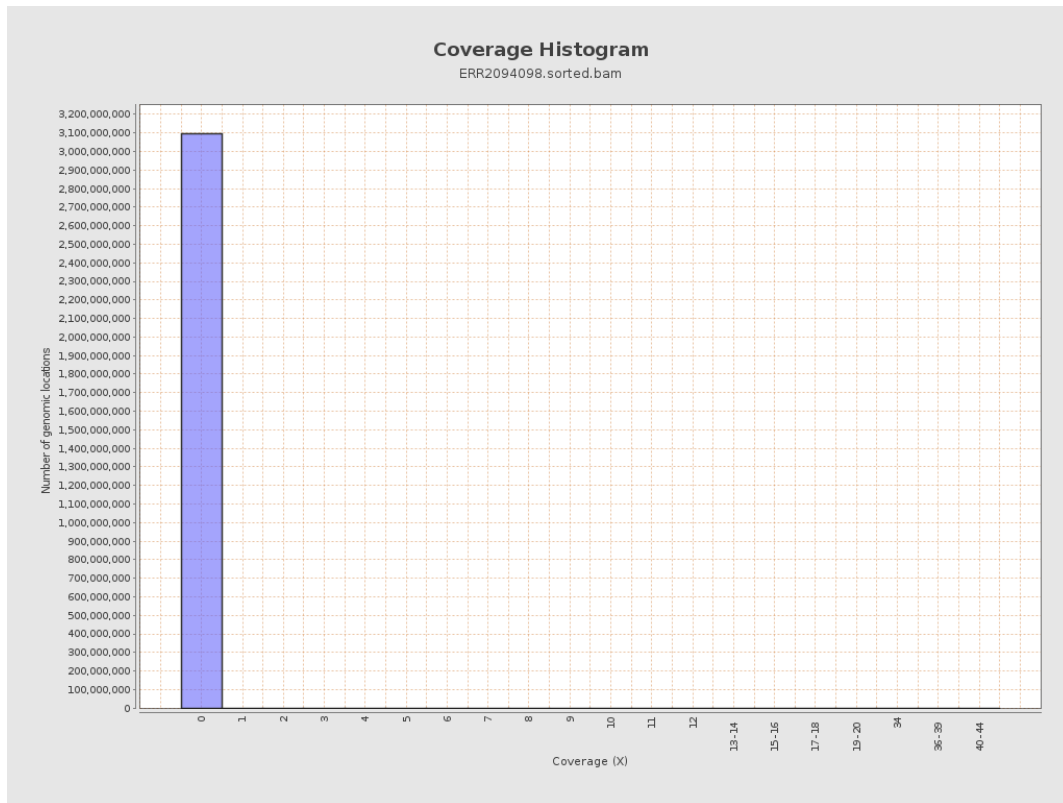
		bases	coverage	deviation
chr1	249250621	1771	0	0.0105
chr2	243199373	877	0	0.0026
chr3	198022430	245	0	0.0012
chr4	191154276	927	0	0.0026
chr5	180915260	7183	0	0.0358
chr6	171115067	117	0	0.0008
chr7	159138663	545	0	0.0023
chr8	146364022	249	0	0.0016
chr9	141213431	66	0	0.0007
chr10	135534747	729	0	0.0026
chr11	135006516	1452	0	0.0045
chr12	133851895	2599	0	0.0129
chr13	115169878	103	0	0.0009
chr14	107349540	109	0	0.001
chr15	102531392	454	0	0.0025
chr16	90354753	66	0	0.0009
chr17	81195210	33	0	0.0006
chr18	78077248	34	0	0.0007
chr19	59128983	46	0	0.0009
chr20	63025520	32	0	0.0007
chr21	48129895	193	0	0.002
chr22	51304566	30	0	0.0008
chrMT	16571	6278	0.3789	1.9423
chrX	155270560	10605	0.0001	0.0102

chrY	59373566	416	0	0.0031
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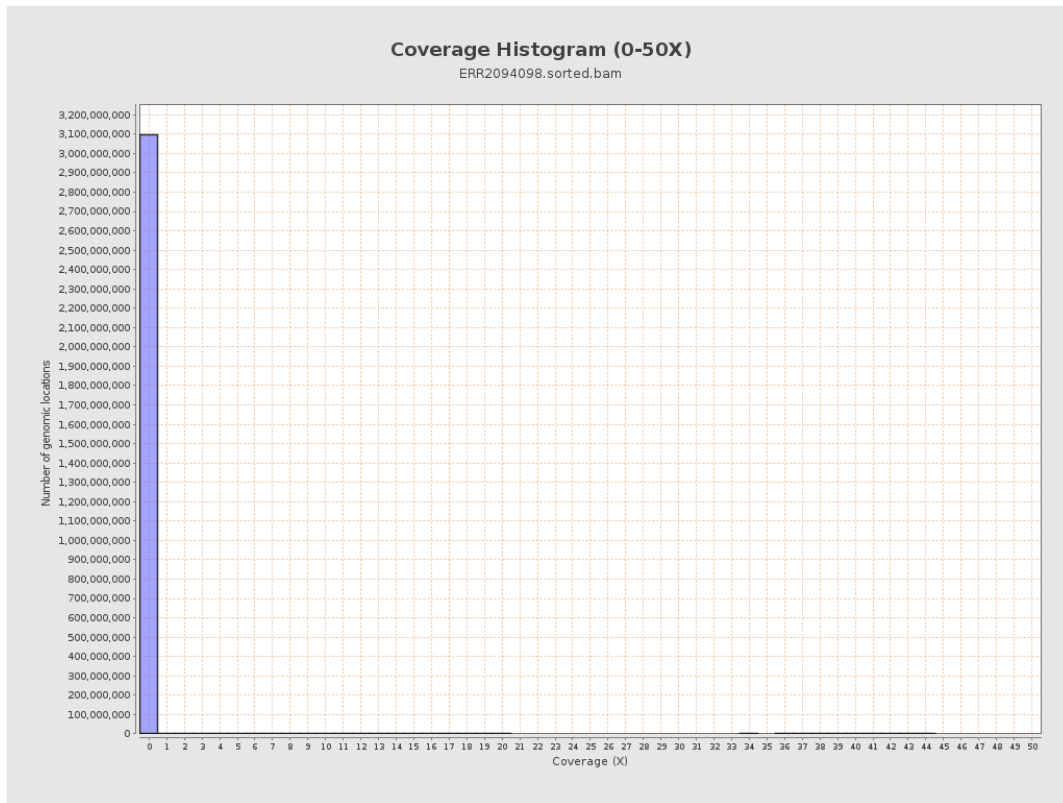
3. Results : Coverage across reference



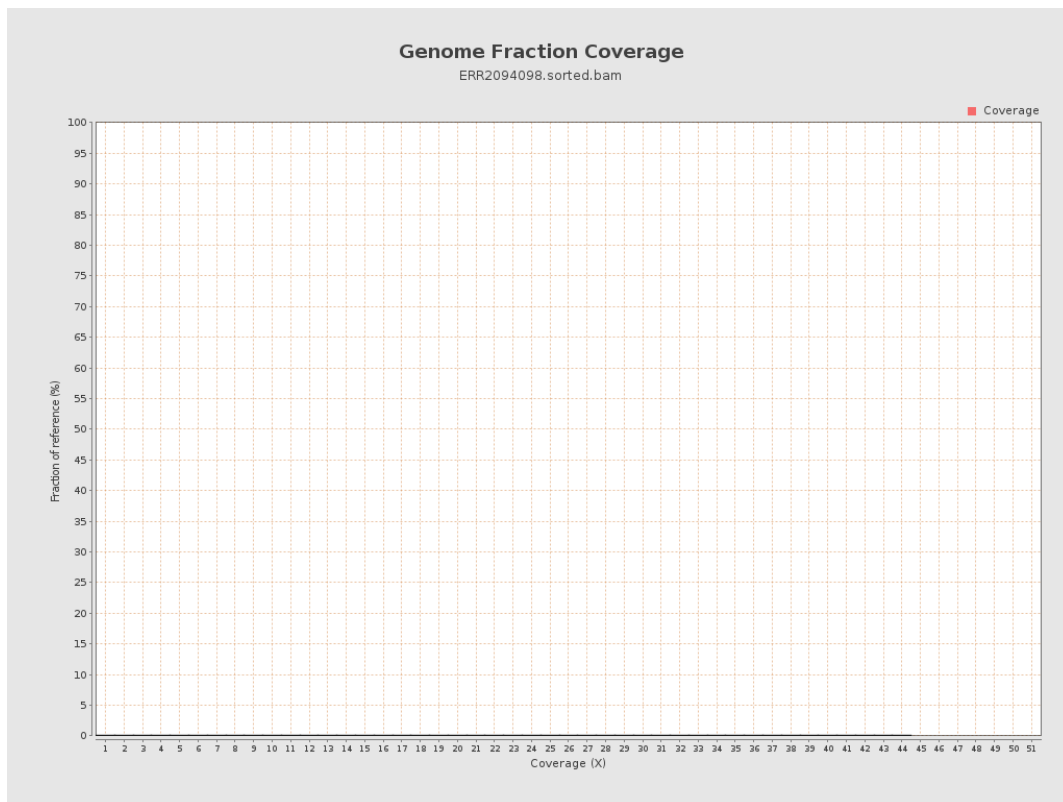
4. Results : Coverage Histogram



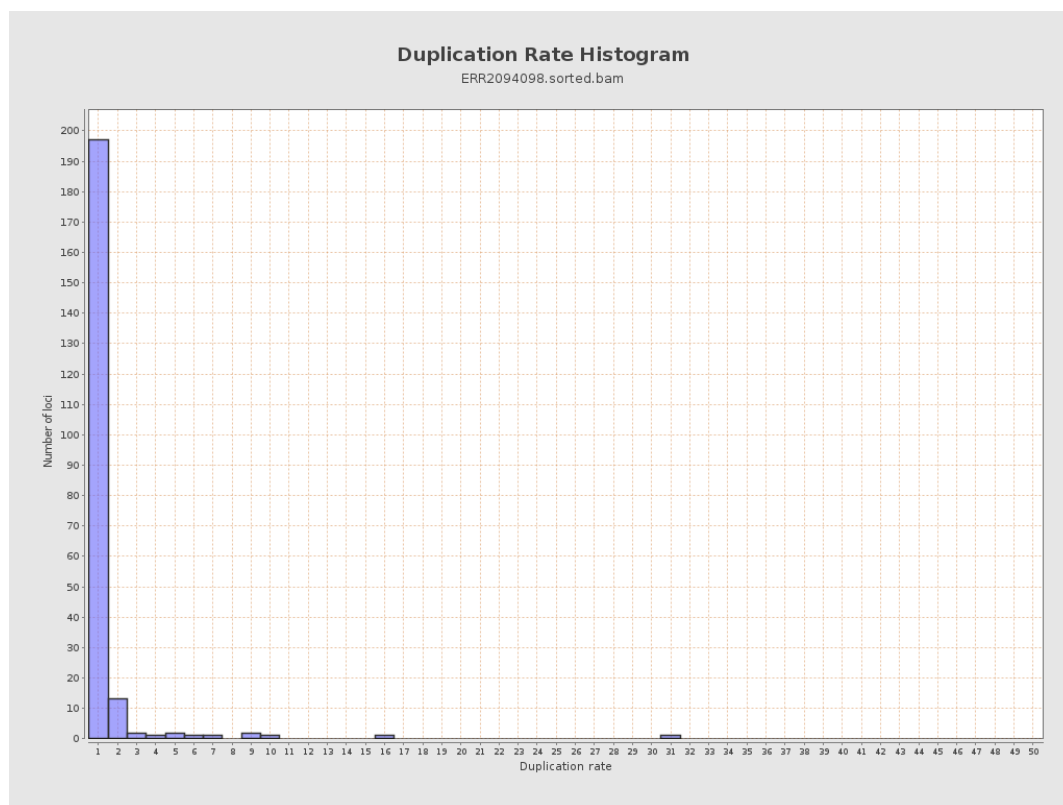
5. Results : Coverage Histogram (0-50X)



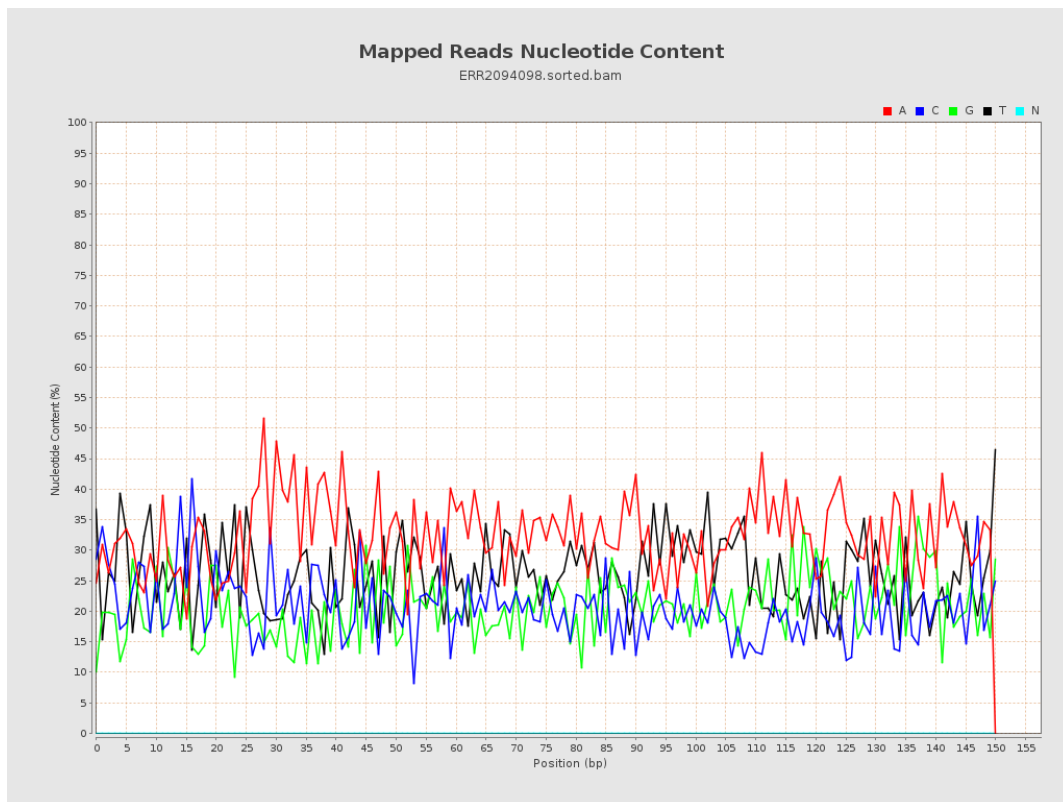
6. Results : Genome Fraction Coverage



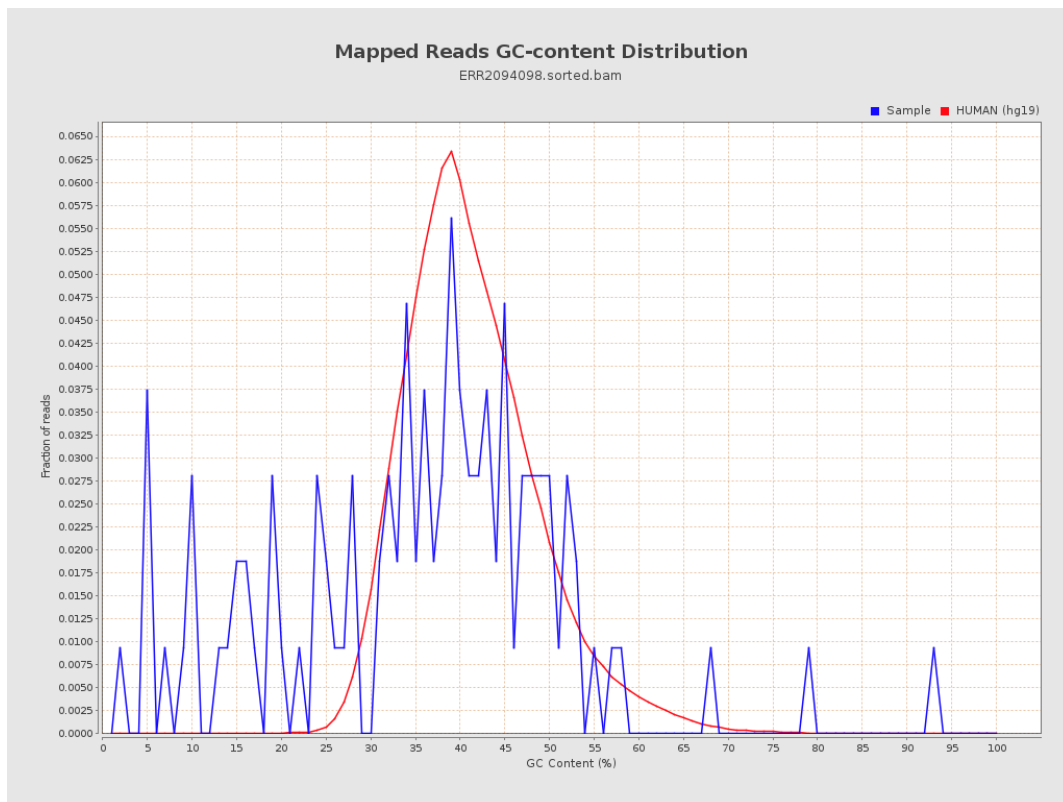
7. Results : Duplication Rate Histogram



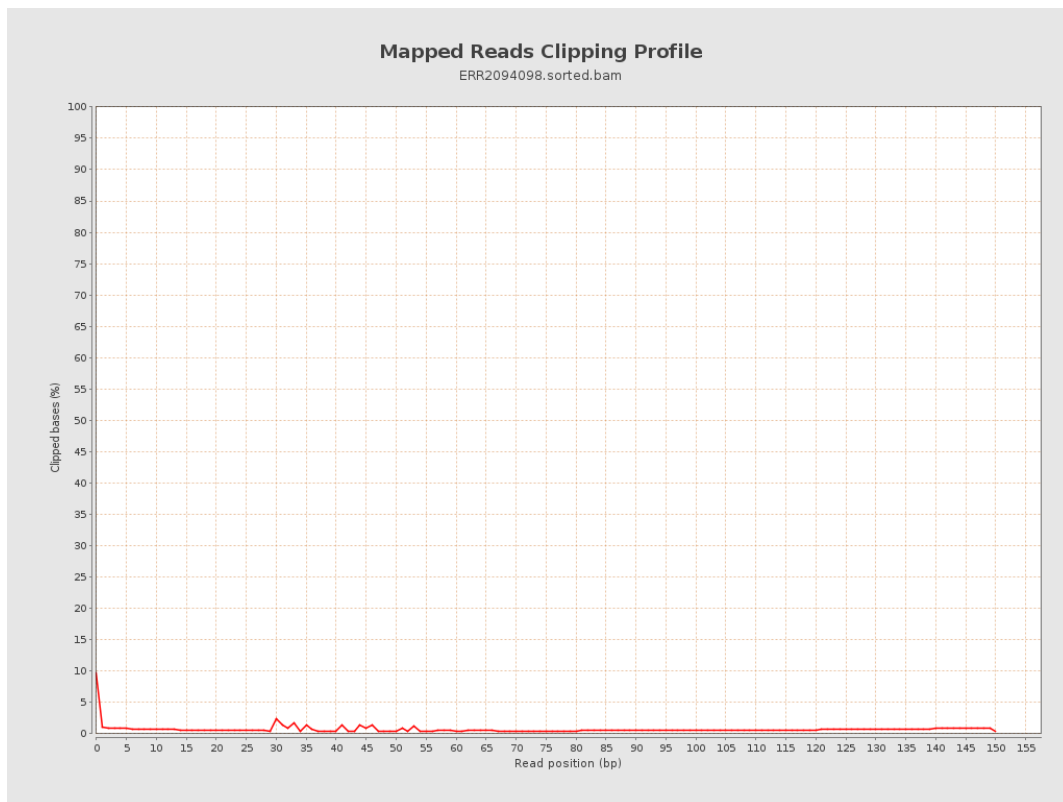
8. Results : Mapped Reads Nucleotide Content



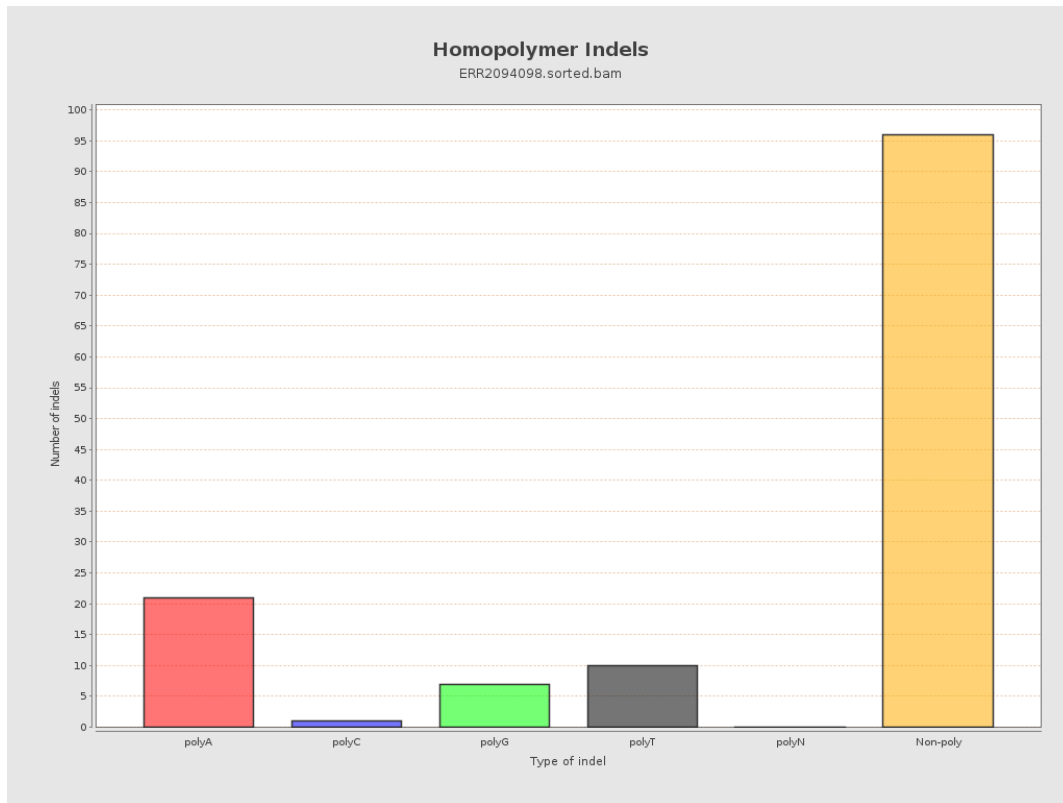
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



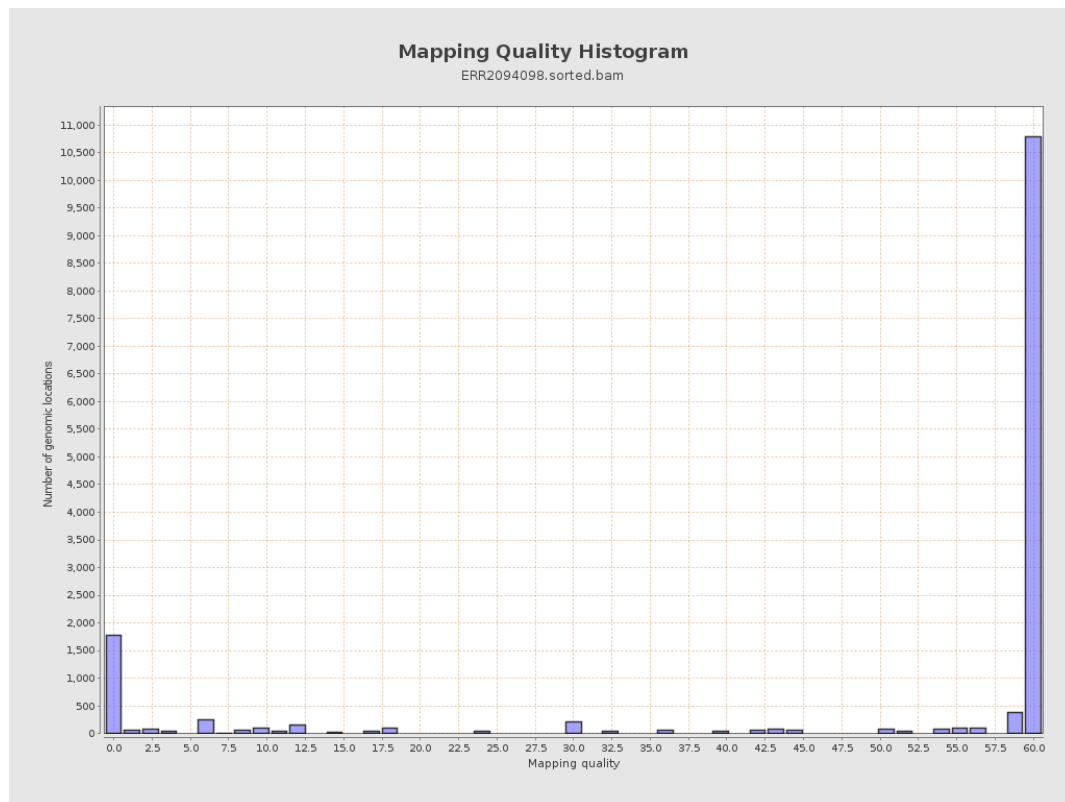
11. Results : Homopolymer Indels



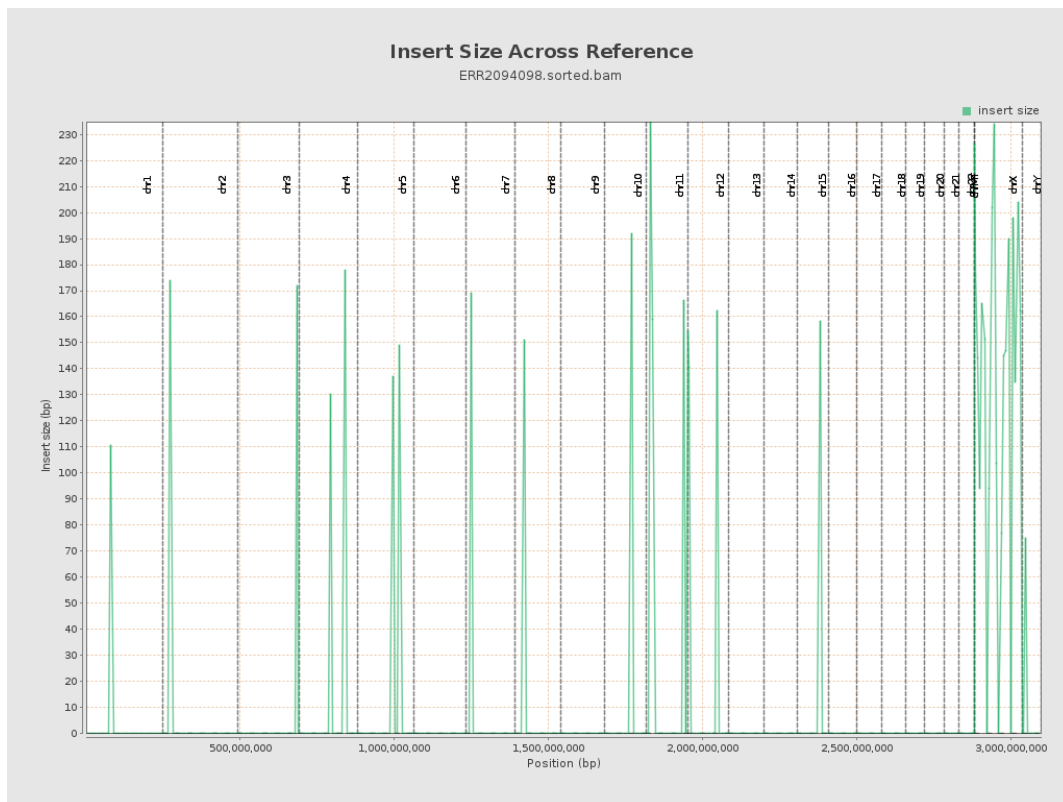
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

