

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:24:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094108.sorted.bam -c -nw 400 -hm 3
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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_ERR2094108 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094108_1.fastq.gz ERR2094108_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:24:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	374,492
Mapped reads	352,340 / 94.08%
Unmapped reads	22,152 / 5.92%
Mapped paired reads	352,340 / 94.08%
Mapped reads, first in pair	177,194 / 47.32%
Mapped reads, second in pair	175,146 / 46.77%
Mapped reads, both in pair	349,166 / 93.24%
Mapped reads, singletons	3,174 / 0.85%
Secondary alignments	0
Supplementary alignments	26,967 / 7.2%
Read min/max/mean length	30 / 151 / 134.21
Duplicated reads (estimated)	340,021 / 90.8%
Duplication rate	53.19%
Clipped reads	196,932 / 52.59%

2.2. ACGT Content

Number/percentage of A's	11,775,233 / 28.55%
Number/percentage of C's	8,934,973 / 21.67%
Number/percentage of T's	11,017,315 / 26.72%
Number/percentage of G's	9,510,119 / 23.06%
Number/percentage of N's	373 / 0%

GC Percentage	44.73%
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2.3. Coverage

Mean	0.0137
Standard Deviation	3.2446

2.4. Mapping Quality

Mean Mapping Quality	39.21
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2.5. Insert size

Mean	1,633,145.8
Standard Deviation	11,172,011.83
P25/Median/P75	111 / 135 / 166

2.6. Mismatches and indels

General error rate	4.1%
Mismatches	1,658,292
Insertions	25,533
Mapped reads with at least one insertion	7.15%
Deletions	127,890
Mapped reads with at least one deletion	35.16%
Homopolymer indels	27.44%

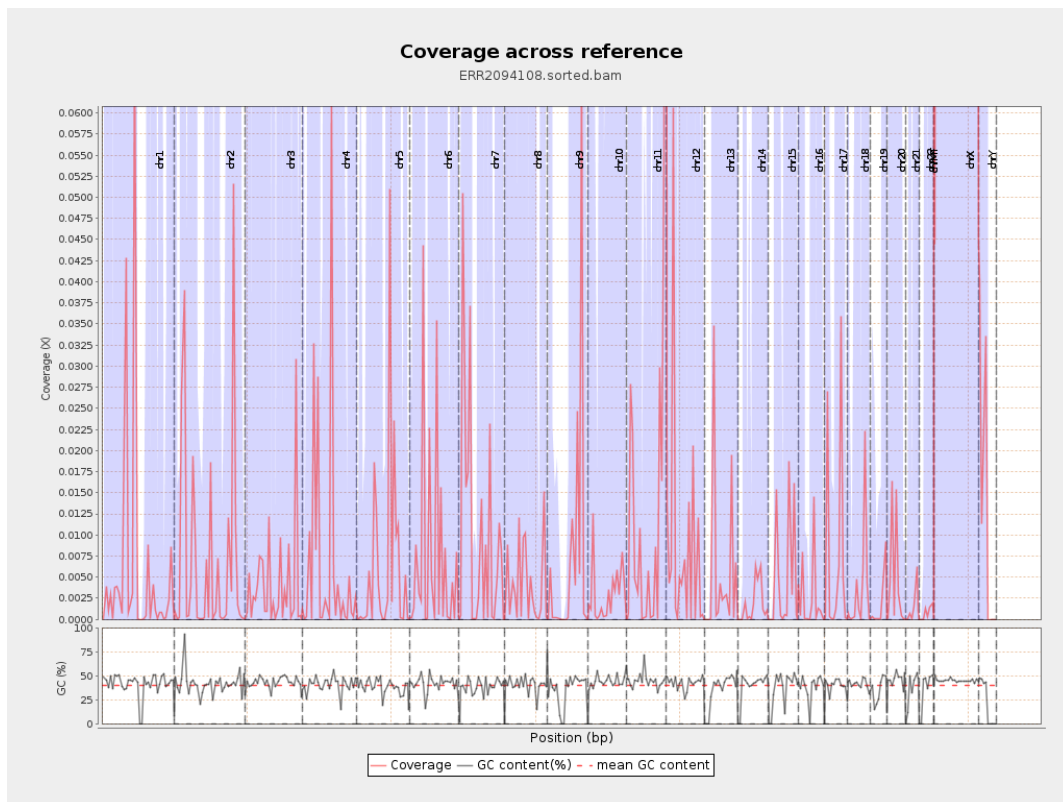
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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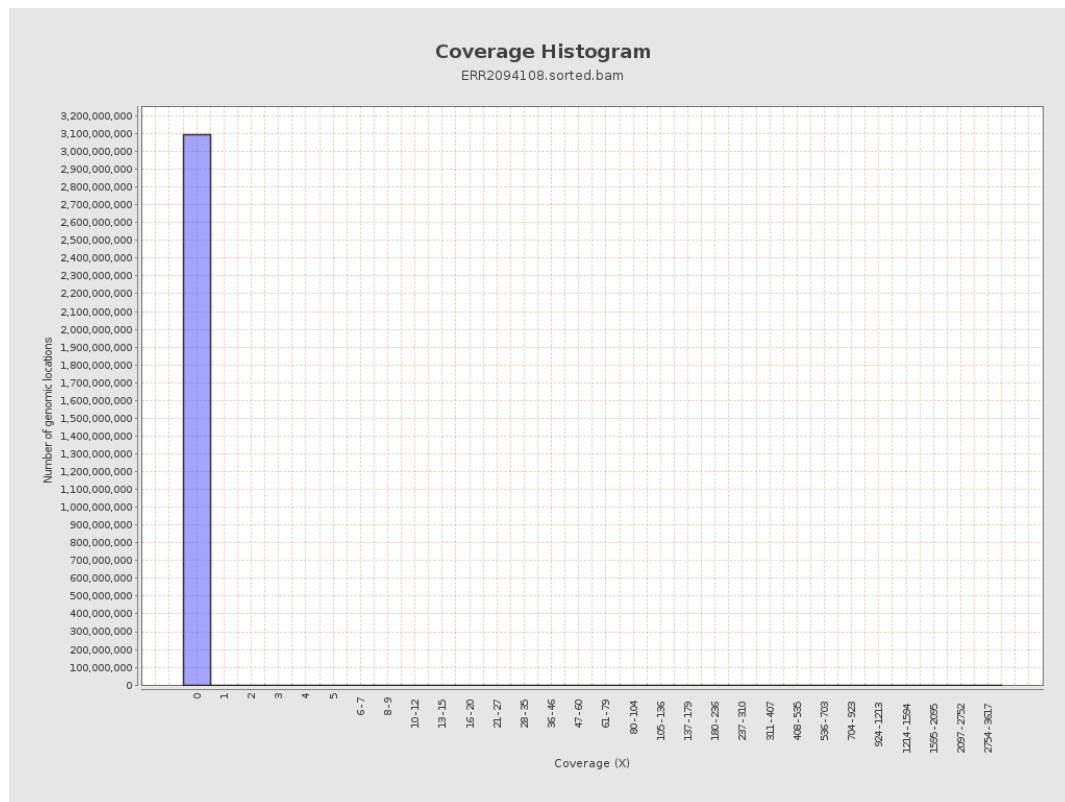
		bases	coverage	deviation
chr1	249250621	1456695	0.0058	3.1252
chr2	243199373	1685343	0.0069	2.6202
chr3	198022430	809438	0.0041	1.5565
chr4	191154276	1314869	0.0069	2.1589
chr5	180915260	1161896	0.0064	2.9963
chr6	171115067	1248182	0.0073	2.6566
chr7	159138663	1514491	0.0095	2.9067
chr8	146364022	595295	0.0041	1.1461
chr9	141213431	979636	0.0069	2.7007
chr10	135534747	404581	0.003	0.8532
chr11	135006516	1634904	0.0121	3.3054
chr12	133851895	1153929	0.0086	2.749
chr13	115169878	587517	0.0051	1.7028
chr14	107349540	190788	0.0018	0.6771
chr15	102531392	470067	0.0046	1.3428
chr16	90354753	233810	0.0026	1.1278
chr17	81195210	590332	0.0073	2.6704
chr18	78077248	303734	0.0039	1.4632
chr19	59128983	105827	0.0018	0.6525
chr20	63025520	312476	0.005	1.588
chr21	48129895	71286	0.0015	0.3684
chr22	51304566	39086	0.0008	0.222
chrMT	16571	12853	0.7756	4.7426
chrX	155270560	24660794	0.1588	10.4924

chrY	59373566	730772	0.0123	2.6327
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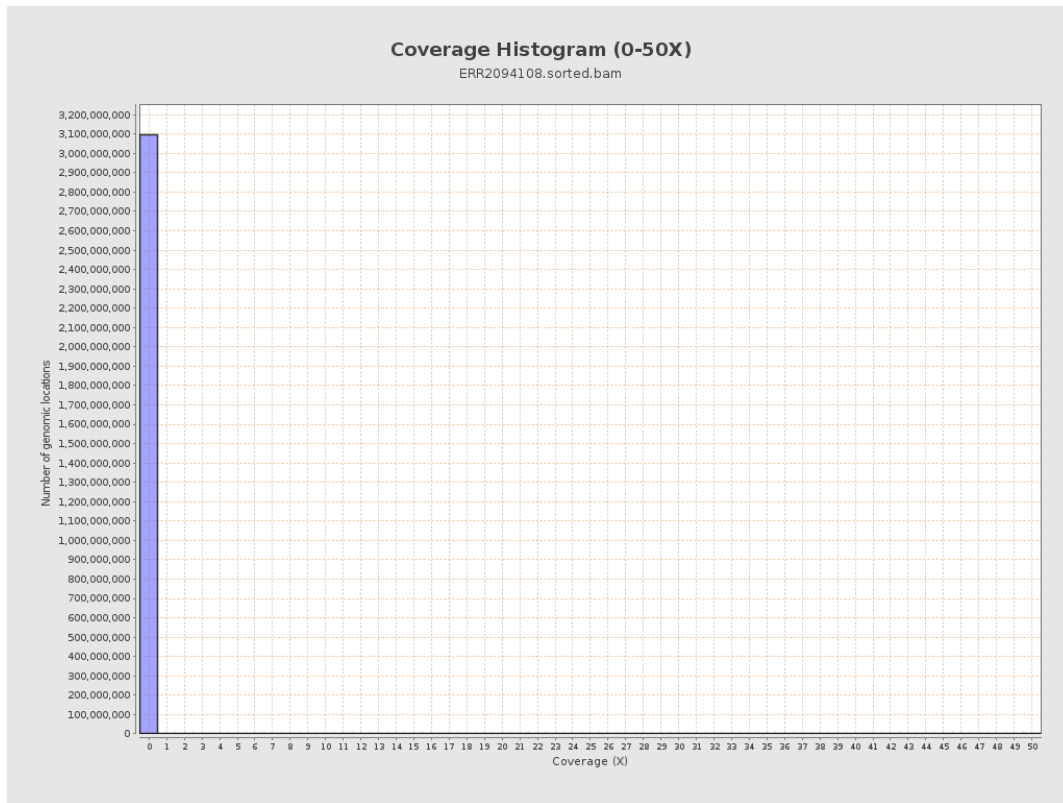
3. Results : Coverage across reference



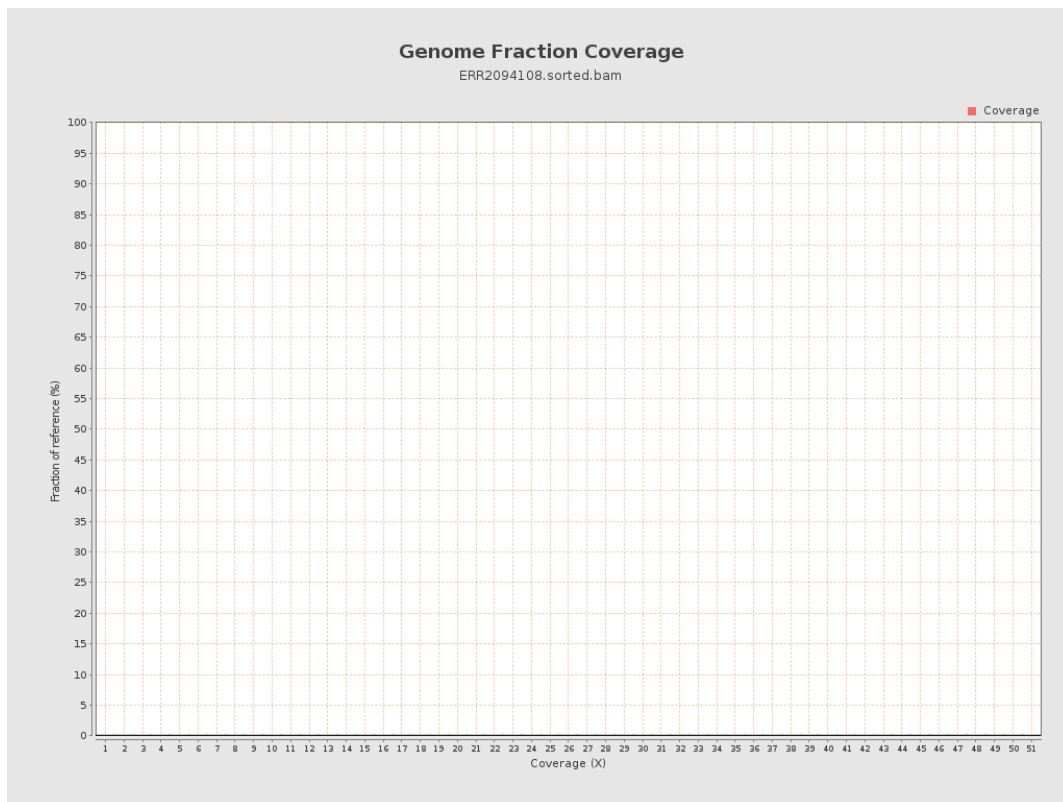
4. Results : Coverage Histogram



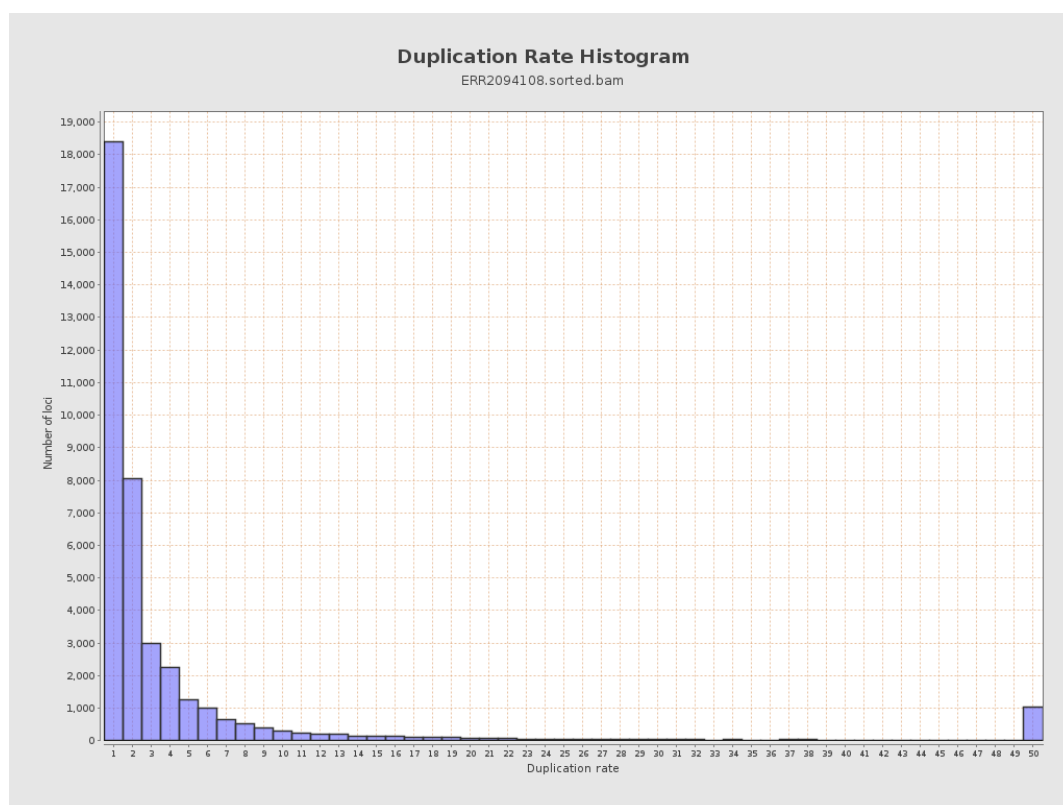
5. Results : Coverage Histogram (0-50X)



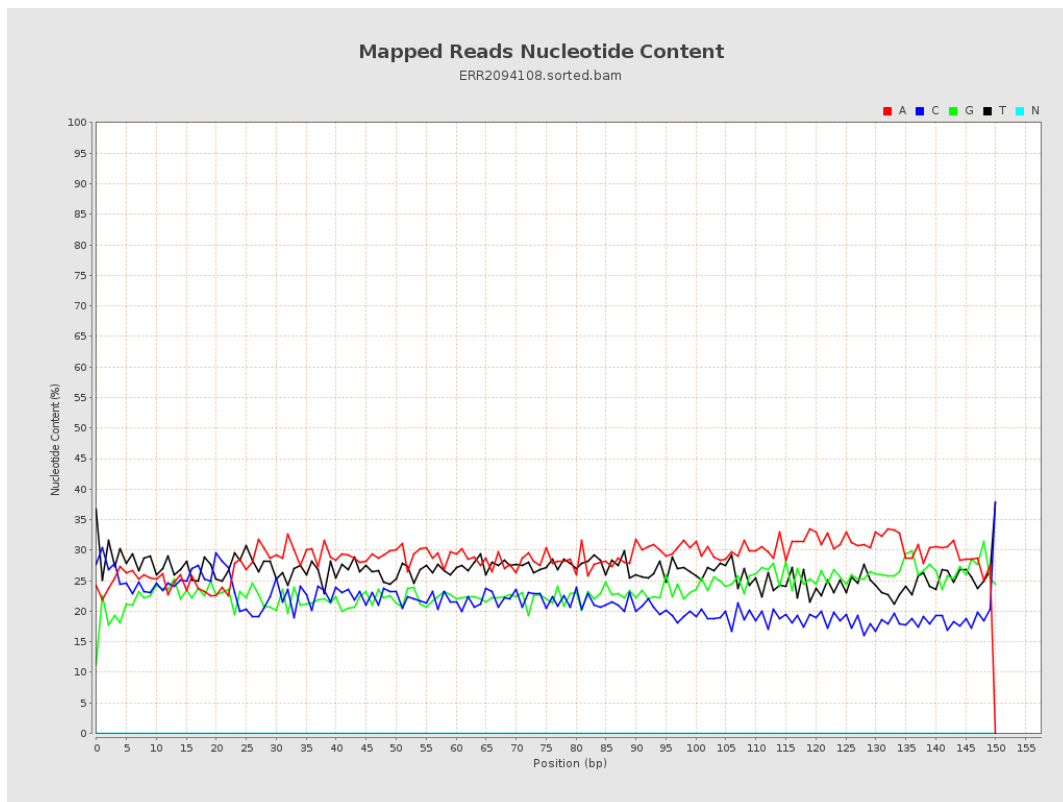
6. Results : Genome Fraction Coverage



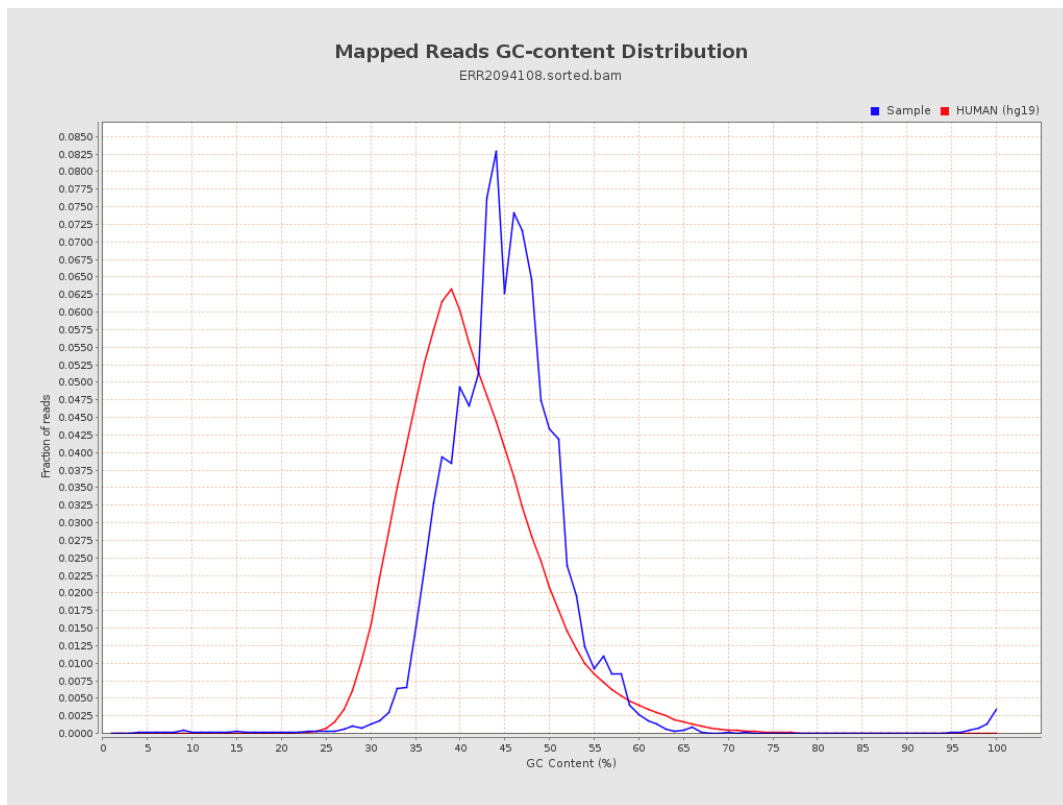
7. Results : Duplication Rate Histogram



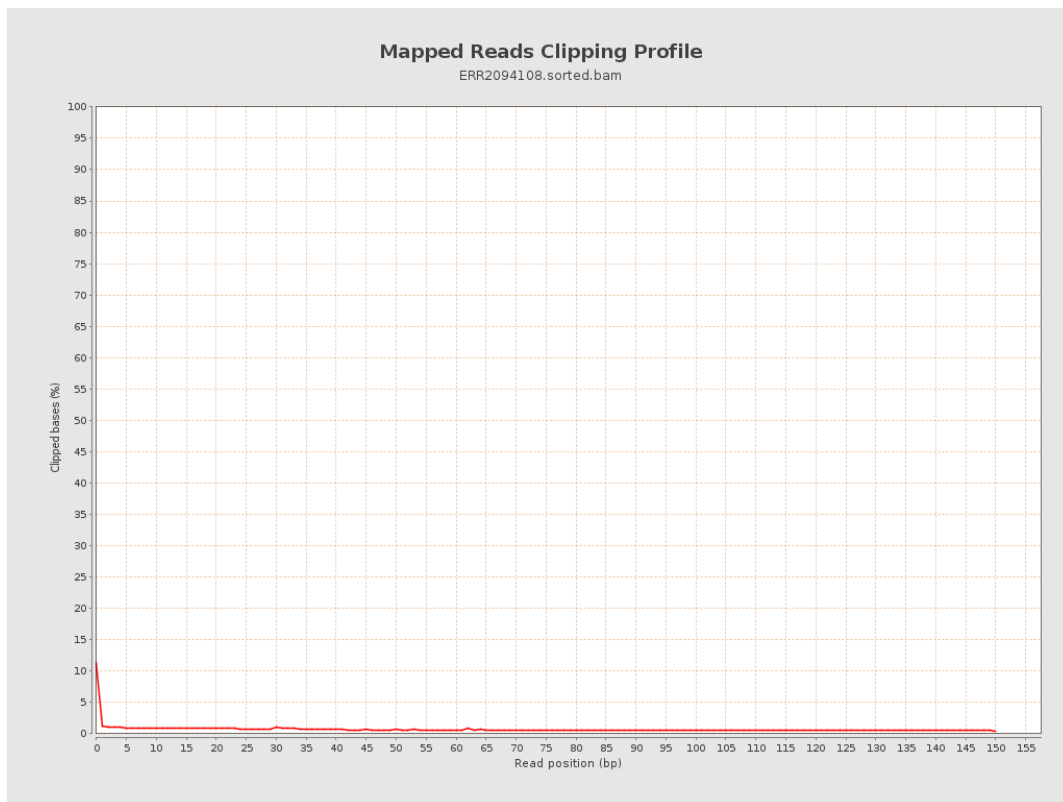
8. Results : Mapped Reads Nucleotide Content



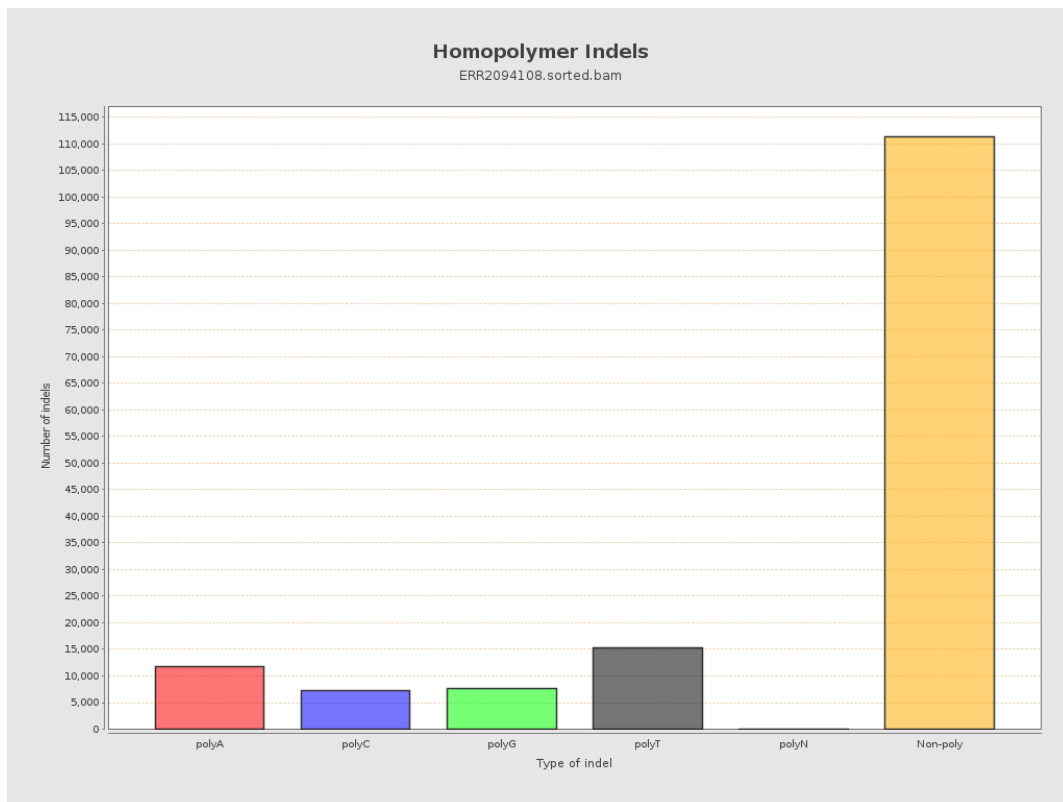
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



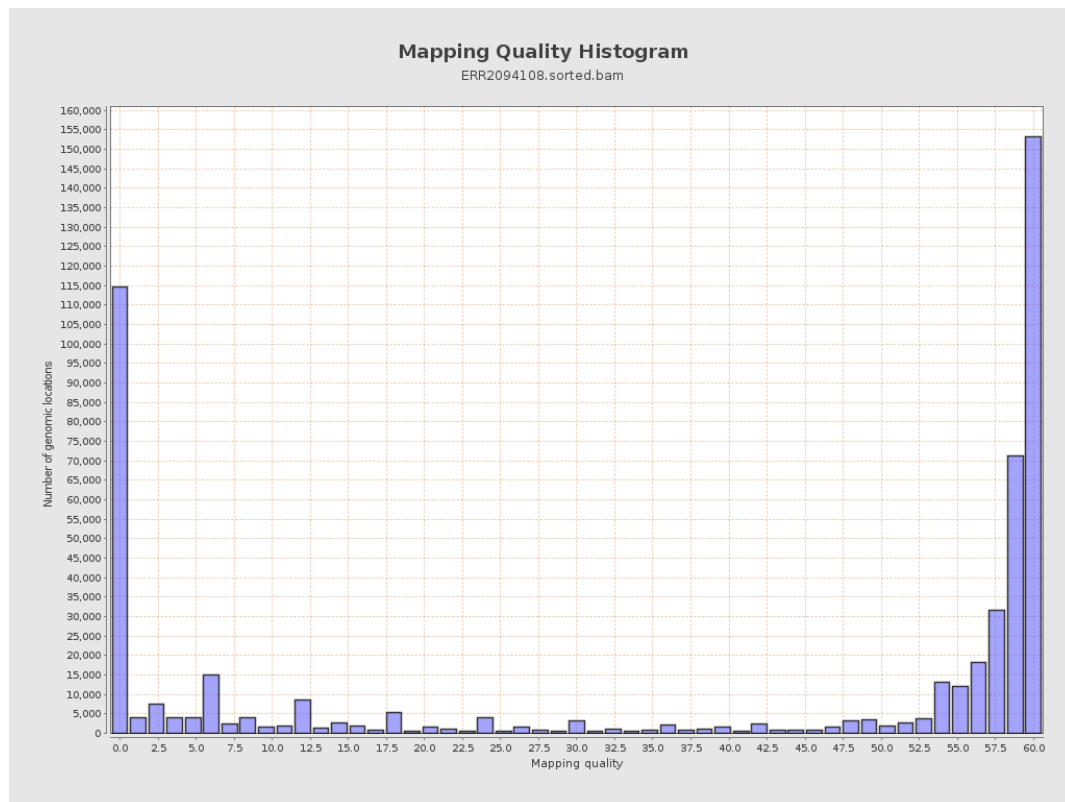
11. Results : Homopolymer Indels



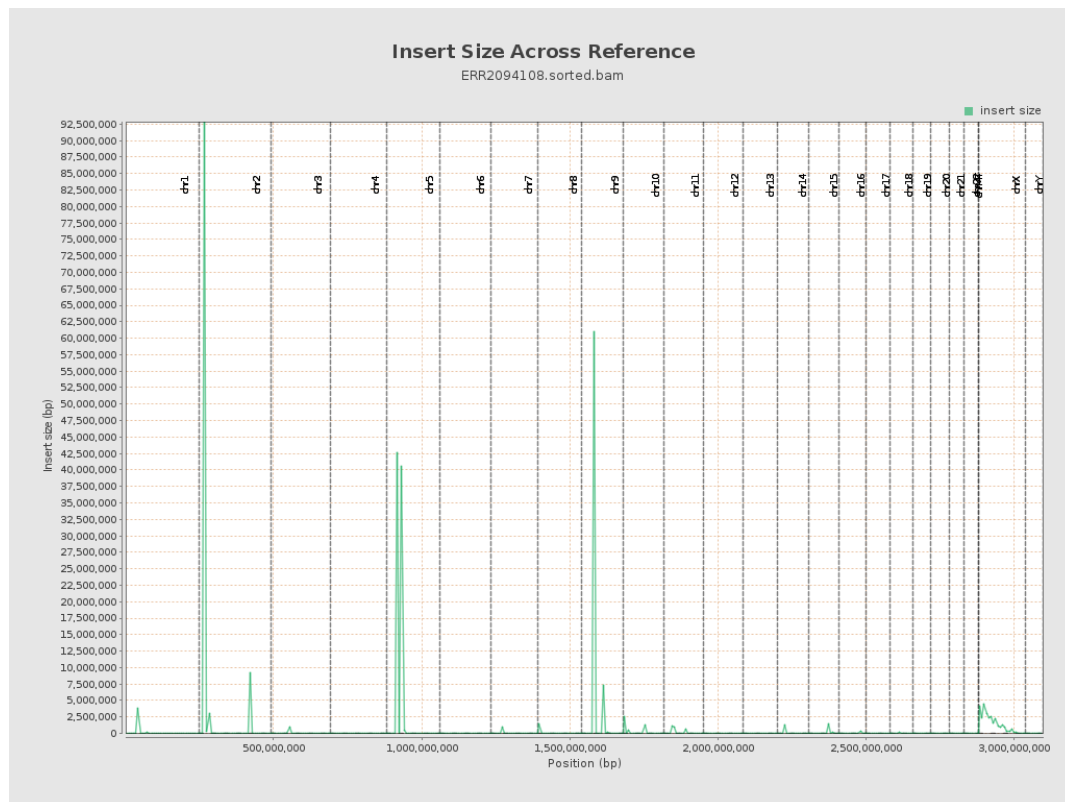
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

