

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:19:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094050.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_ERR2094050 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094050_1.fastq.gz ERR2094050_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:19:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	289,566
Mapped reads	269,858 / 93.19%
Unmapped reads	19,708 / 6.81%
Mapped paired reads	269,858 / 93.19%
Mapped reads, first in pair	135,594 / 46.83%
Mapped reads, second in pair	134,264 / 46.37%
Mapped reads, both in pair	267,788 / 92.48%
Mapped reads, singletons	2,070 / 0.71%
Secondary alignments	0
Supplementary alignments	9,074 / 3.13%
Read min/max/mean length	30 / 151 / 137.88
Duplicated reads (estimated)	251,873 / 86.98%
Duplication rate	47.6%
Clipped reads	111,154 / 38.39%

2.2. ACGT Content

Number/percentage of A's	9,647,087 / 27.88%
Number/percentage of C's	7,682,487 / 22.2%
Number/percentage of T's	9,264,503 / 26.77%
Number/percentage of G's	8,008,977 / 23.14%
Number/percentage of N's	483 / 0%

GC Percentage	45.35%
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2.3. Coverage

Mean	0.0115
Standard Deviation	3.0484

2.4. Mapping Quality

Mean Mapping Quality	41.29
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2.5. Insert size

Mean	409,419.2
Standard Deviation	5,919,861.19
P25/Median/P75	134 / 170 / 198

2.6. Mismatches and indels

General error rate	4.55%
Mismatches	1,513,487
Insertions	25,696
Mapped reads with at least one insertion	9.35%
Deletions	119,716
Mapped reads with at least one deletion	41.47%
Homopolymer indels	31%

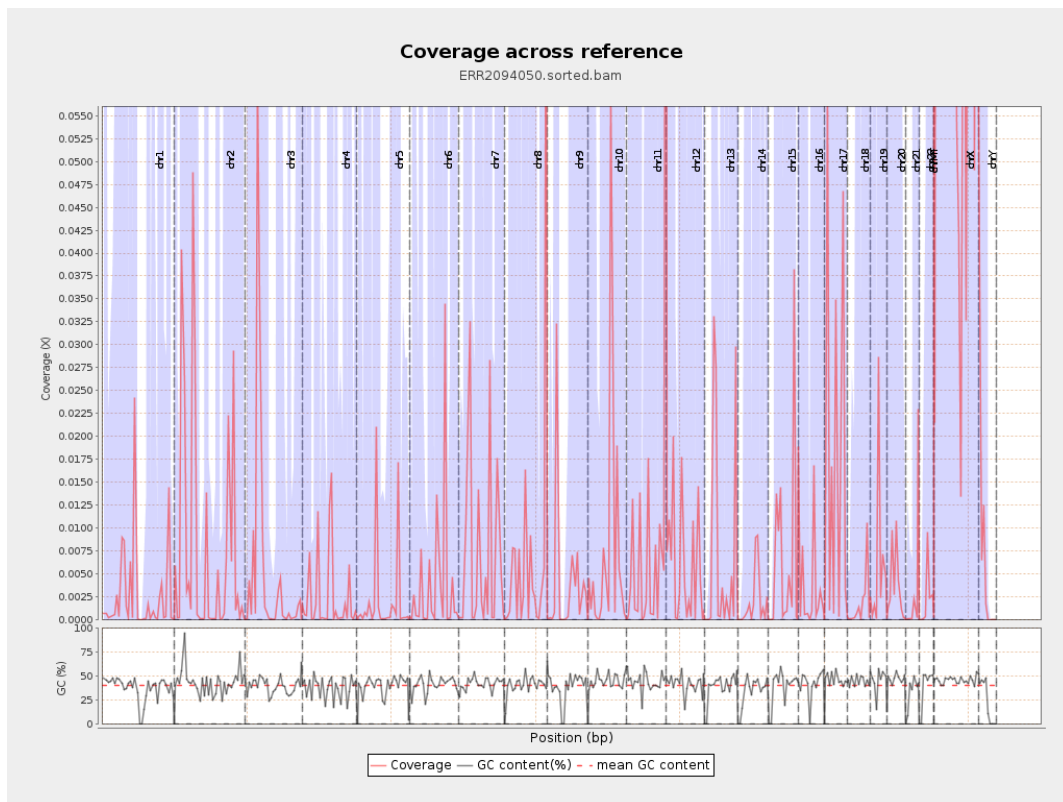
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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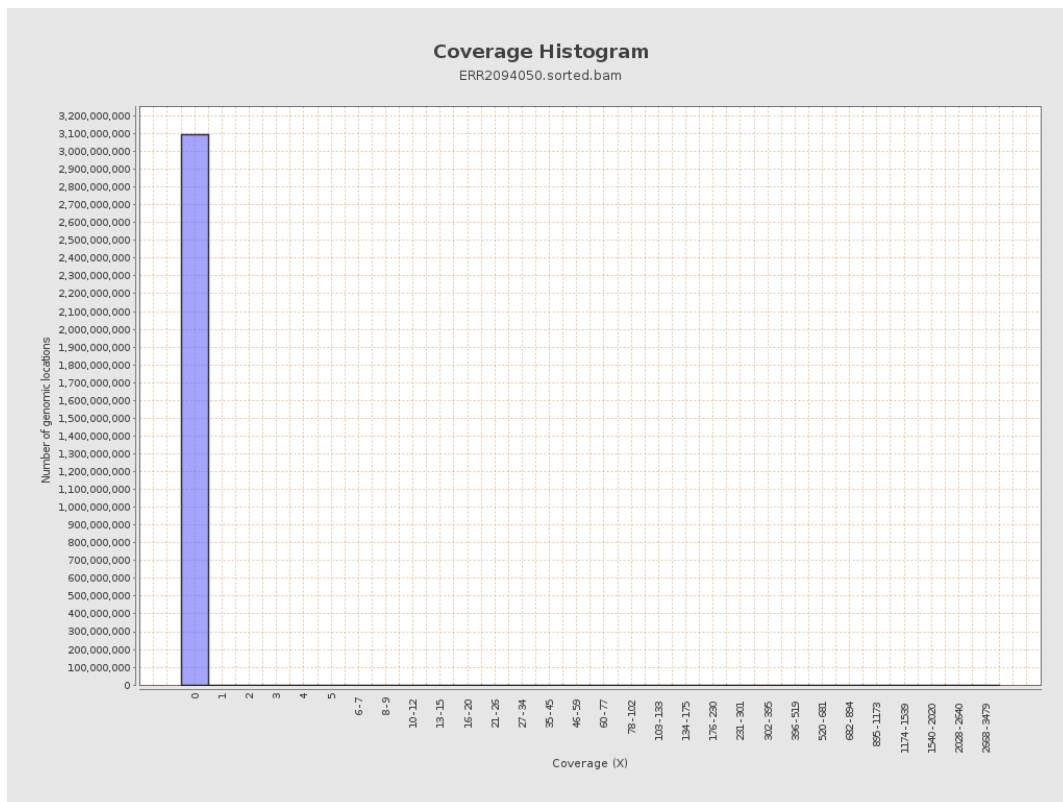
		bases	coverage	deviation
chr1	249250621	621637	0.0025	1.1097
chr2	243199373	1921125	0.0079	2.3156
chr3	198022430	1037897	0.0052	2.4911
chr4	191154276	480819	0.0025	0.8892
chr5	180915260	380184	0.0021	1.0636
chr6	171115067	656470	0.0038	1.9517
chr7	159138663	1171737	0.0074	2.2331
chr8	146364022	1060738	0.0072	3.4414
chr9	141213431	507849	0.0036	1.5983
chr10	135534747	1090548	0.008	3.0762
chr11	135006516	749076	0.0055	1.5493
chr12	133851895	784204	0.0059	1.4665
chr13	115169878	802016	0.007	2.1512
chr14	107349540	207335	0.0019	0.7803
chr15	102531392	653251	0.0064	1.9207
chr16	90354753	348699	0.0039	1.5562
chr17	81195210	1469139	0.0181	4.2291
chr18	78077248	142195	0.0018	0.5559
chr19	59128983	354135	0.006	2.0388
chr20	63025520	247144	0.0039	0.9512
chr21	48129895	132638	0.0028	0.8911
chr22	51304566	116825	0.0023	0.6959
chrMT	16571	1816912	109.6441	446.3655
chrX	155270560	18405898	0.1185	9.3091

chrY	59373566	356643	0.006	1.5465
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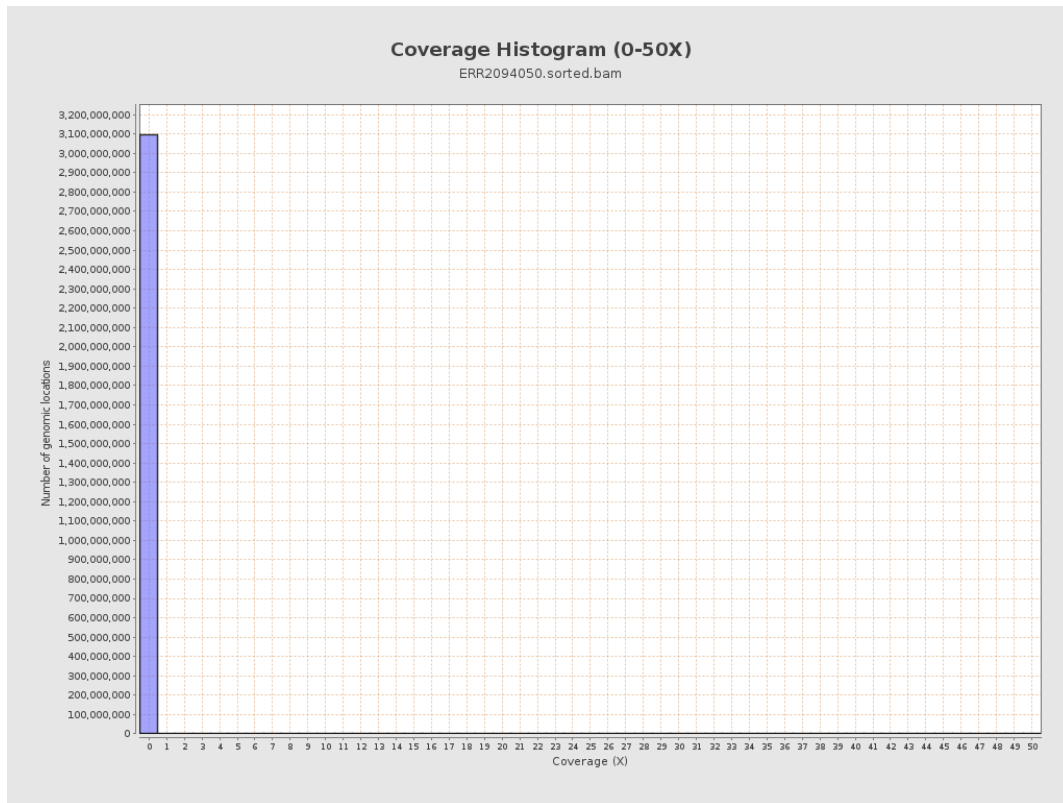
3. Results : Coverage across reference



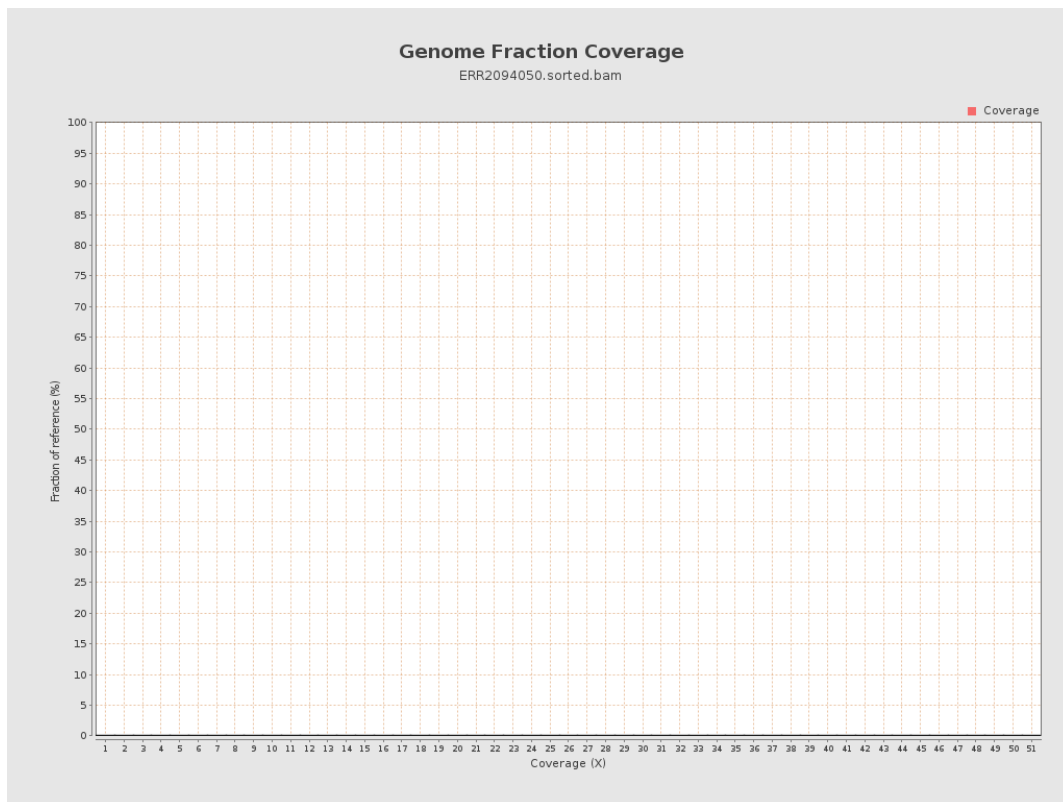
4. Results : Coverage Histogram



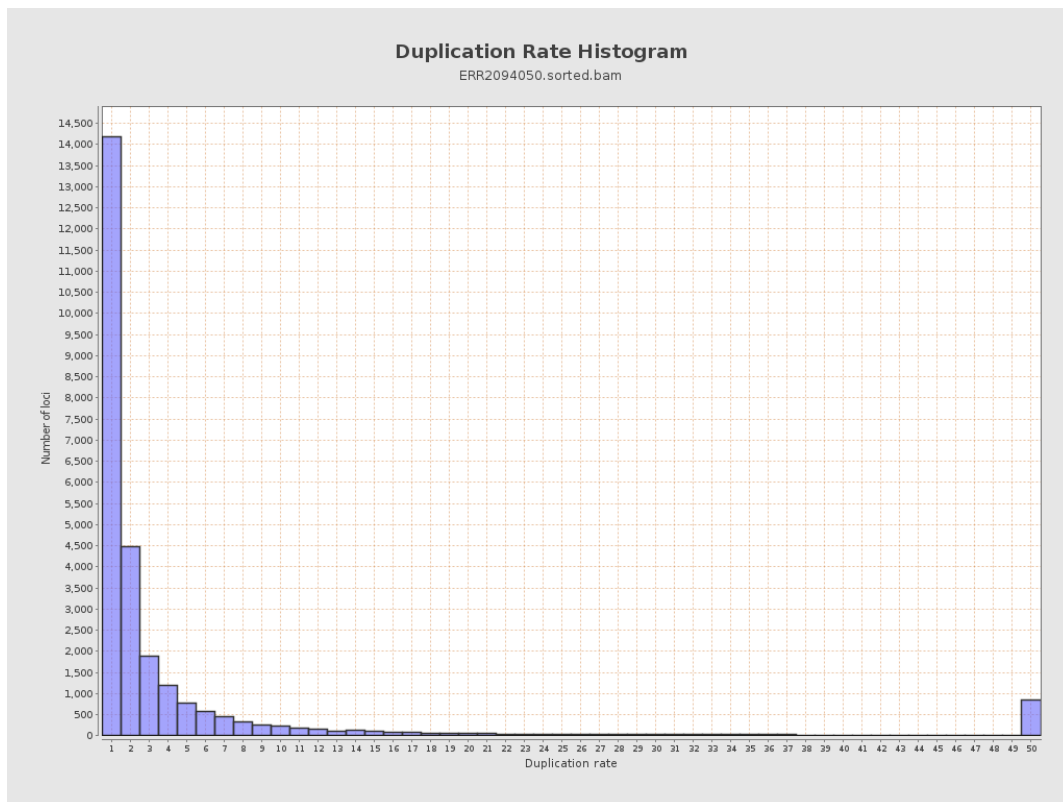
5. Results : Coverage Histogram (0-50X)



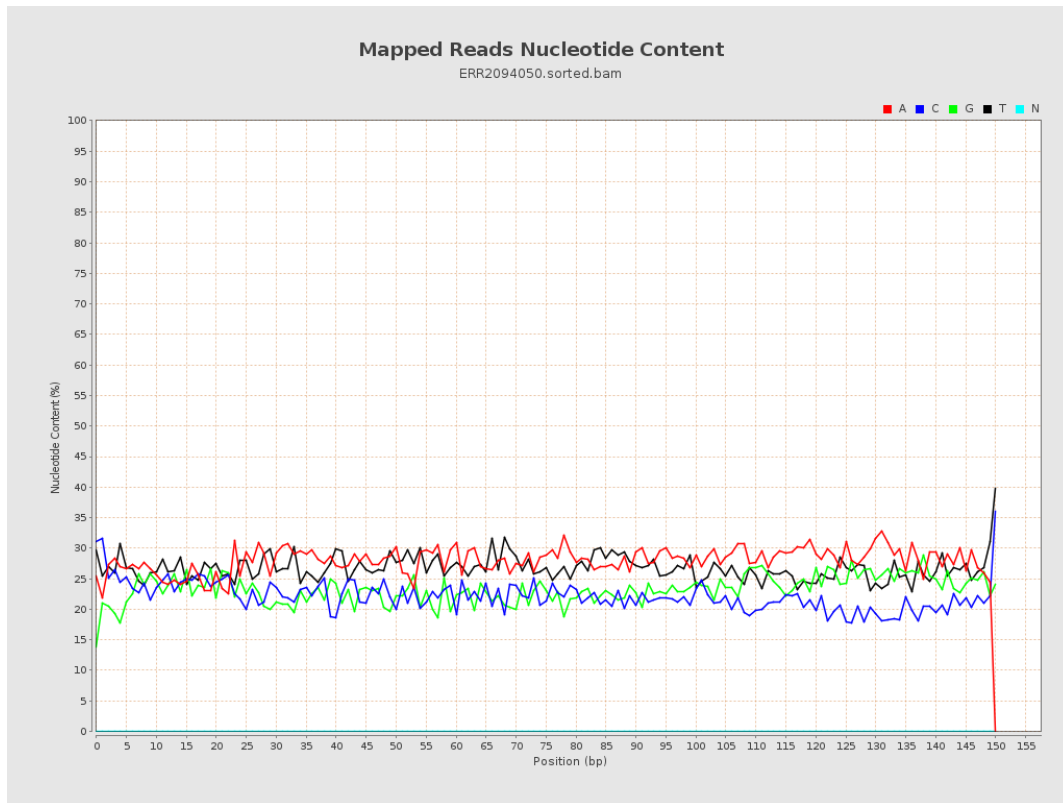
6. Results : Genome Fraction Coverage



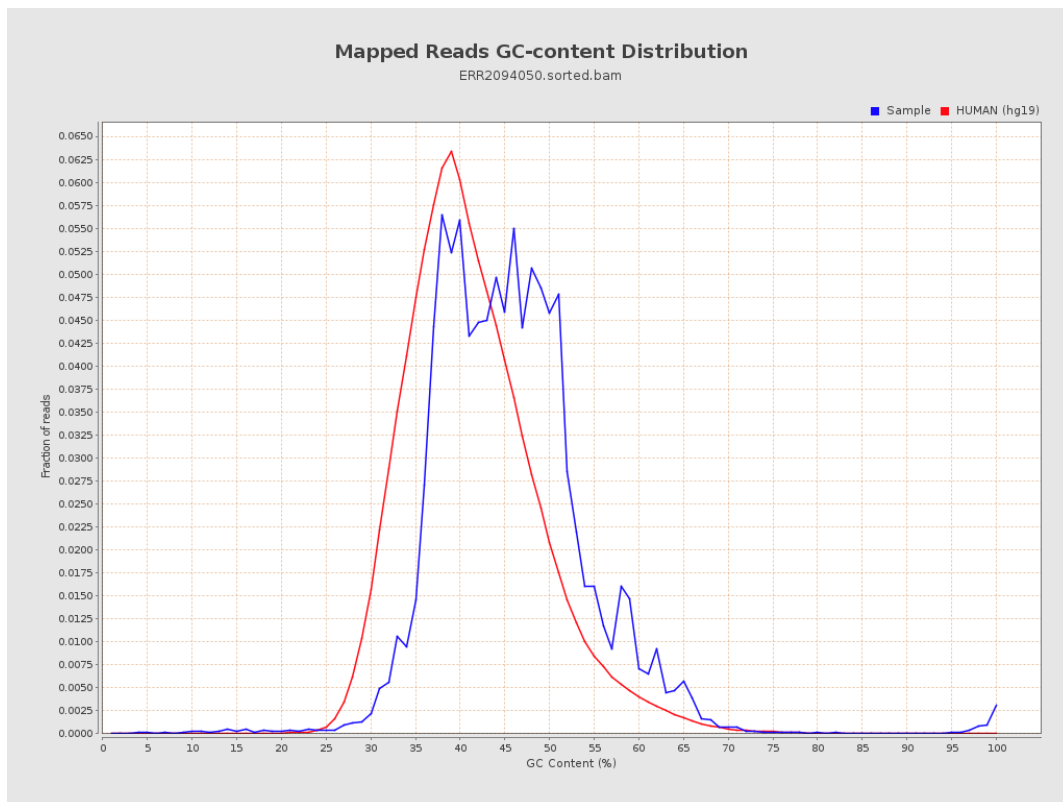
7. Results : Duplication Rate Histogram



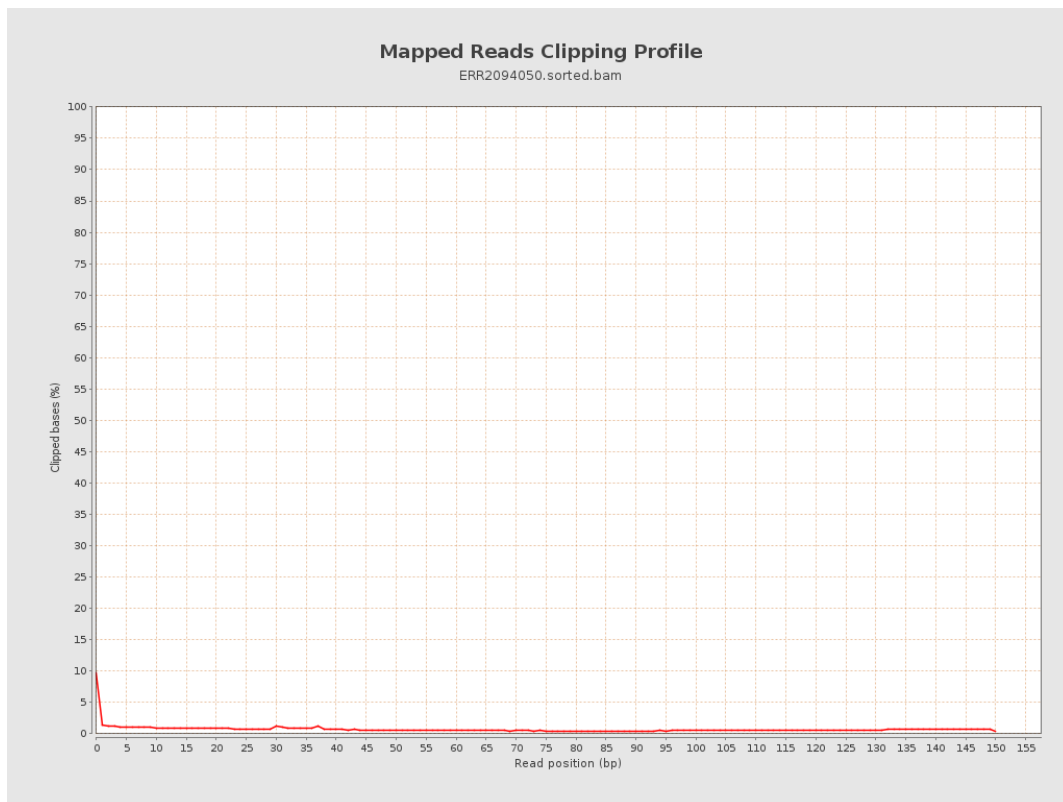
8. Results : Mapped Reads Nucleotide Content



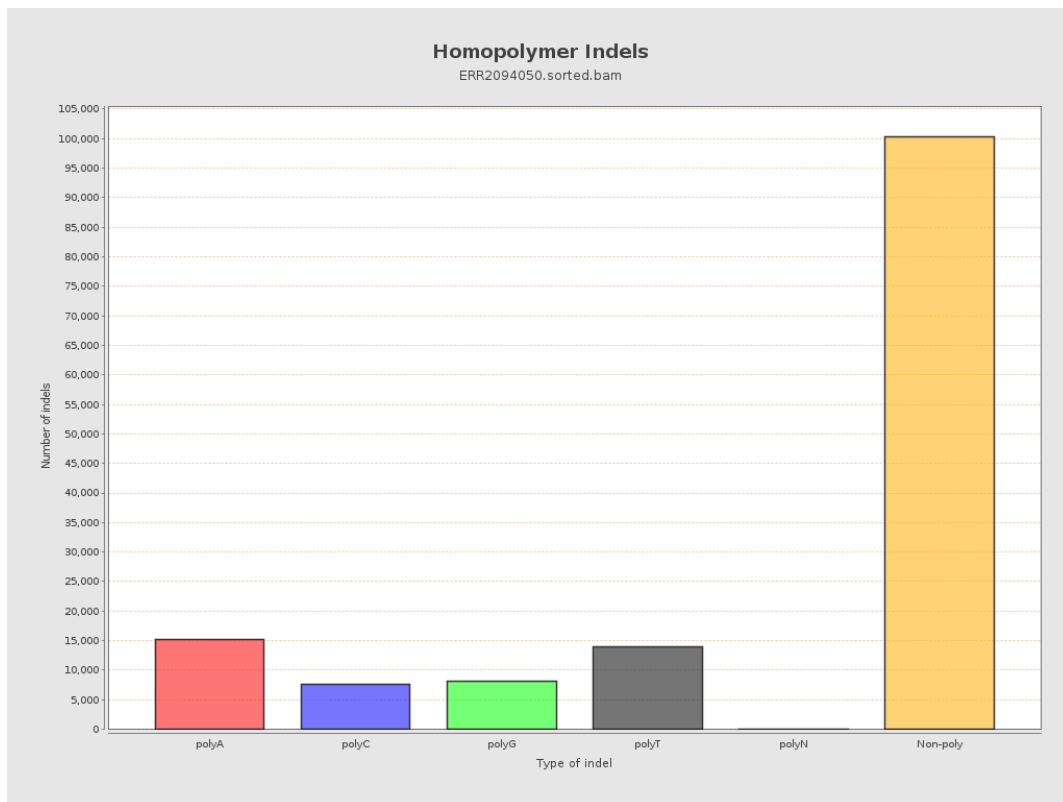
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



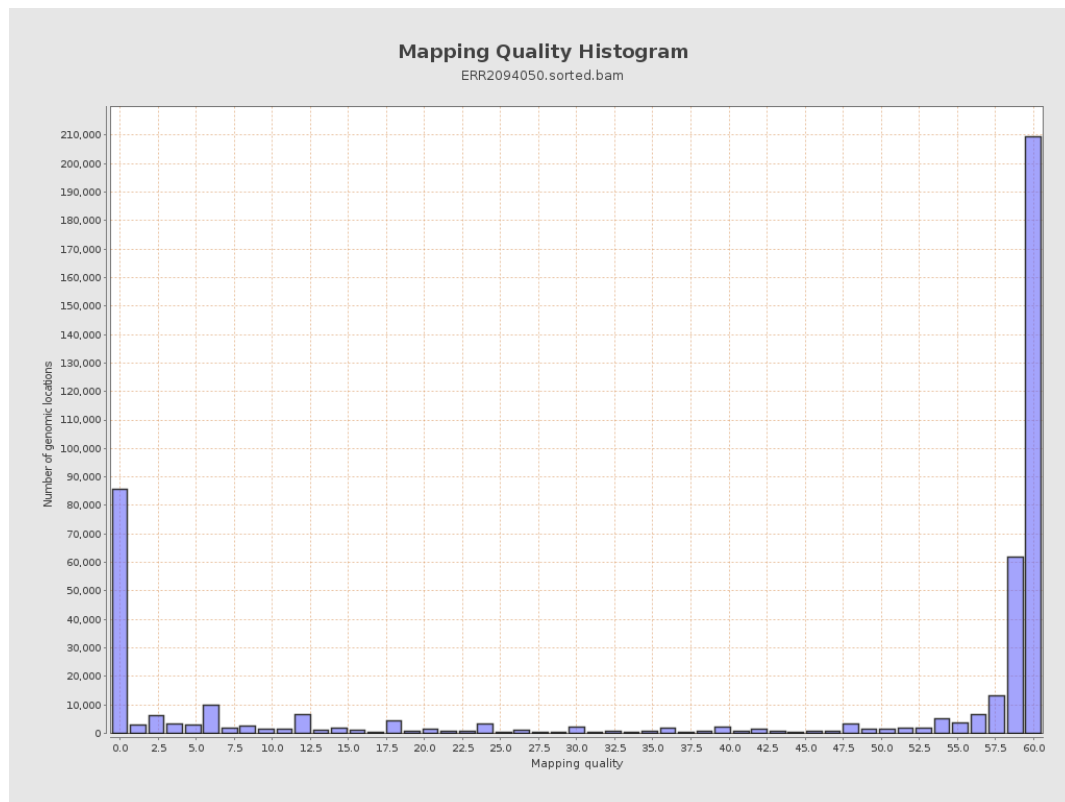
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

