

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:50:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094093.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_ERR2094093 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094093_1.fastq.gz ERR2094093_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:50:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	718,124
Mapped reads	666,335 / 92.79%
Unmapped reads	51,789 / 7.21%
Mapped paired reads	666,335 / 92.79%
Mapped reads, first in pair	334,369 / 46.56%
Mapped reads, second in pair	331,966 / 46.23%
Mapped reads, both in pair	661,478 / 92.11%
Mapped reads, singletons	4,857 / 0.68%
Secondary alignments	0
Supplementary alignments	49,106 / 6.84%
Read min/max/mean length	30 / 151 / 135.36
Duplicated reads (estimated)	655,129 / 91.23%
Duplication rate	55.06%
Clipped reads	359,814 / 50.1%

2.2. ACGT Content

Number/percentage of A's	23,379,639 / 28.95%
Number/percentage of C's	17,094,817 / 21.16%
Number/percentage of T's	22,080,777 / 27.34%
Number/percentage of G's	18,213,714 / 22.55%
Number/percentage of N's	730 / 0%

GC Percentage	43.72%
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2.3. Coverage

Mean	0.0266
Standard Deviation	5.4093

2.4. Mapping Quality

Mean Mapping Quality	41.46
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2.5. Insert size

Mean	1,728,685.71
Standard Deviation	11,553,687.39
P25/Median/P75	113 / 147 / 177

2.6. Mismatches and indels

General error rate	3.56%
Mismatches	2,784,248
Insertions	49,224
Mapped reads with at least one insertion	7.3%
Deletions	222,387
Mapped reads with at least one deletion	32.36%
Homopolymer indels	27.49%

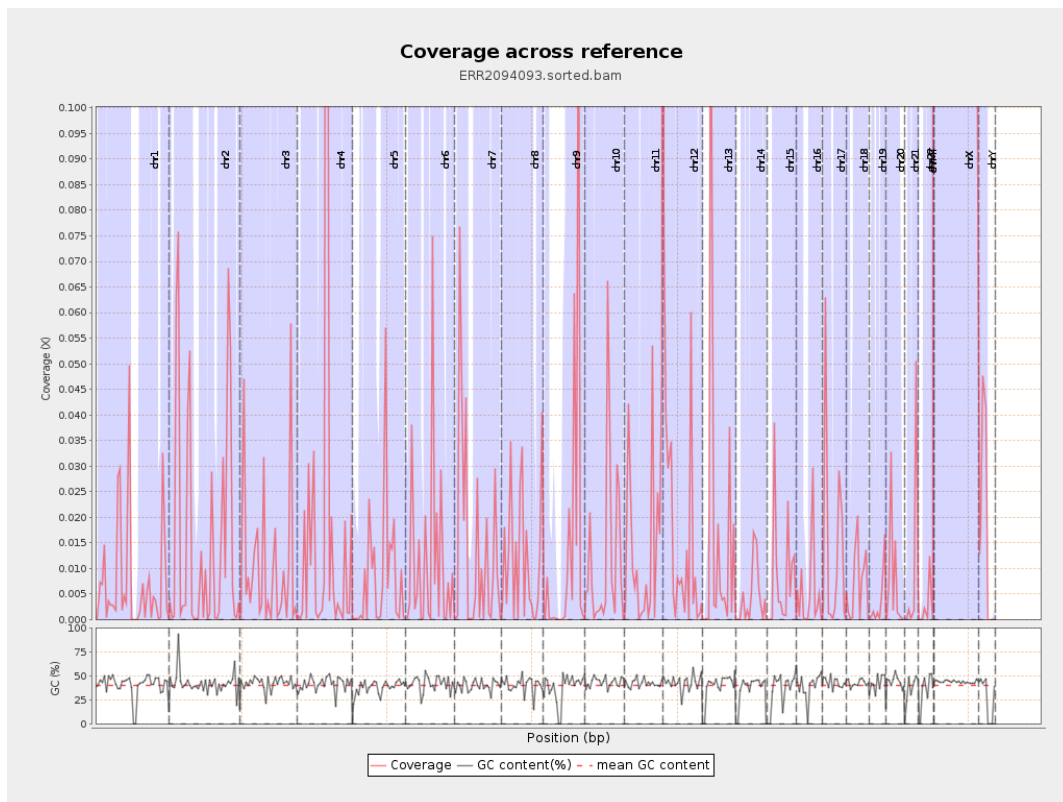
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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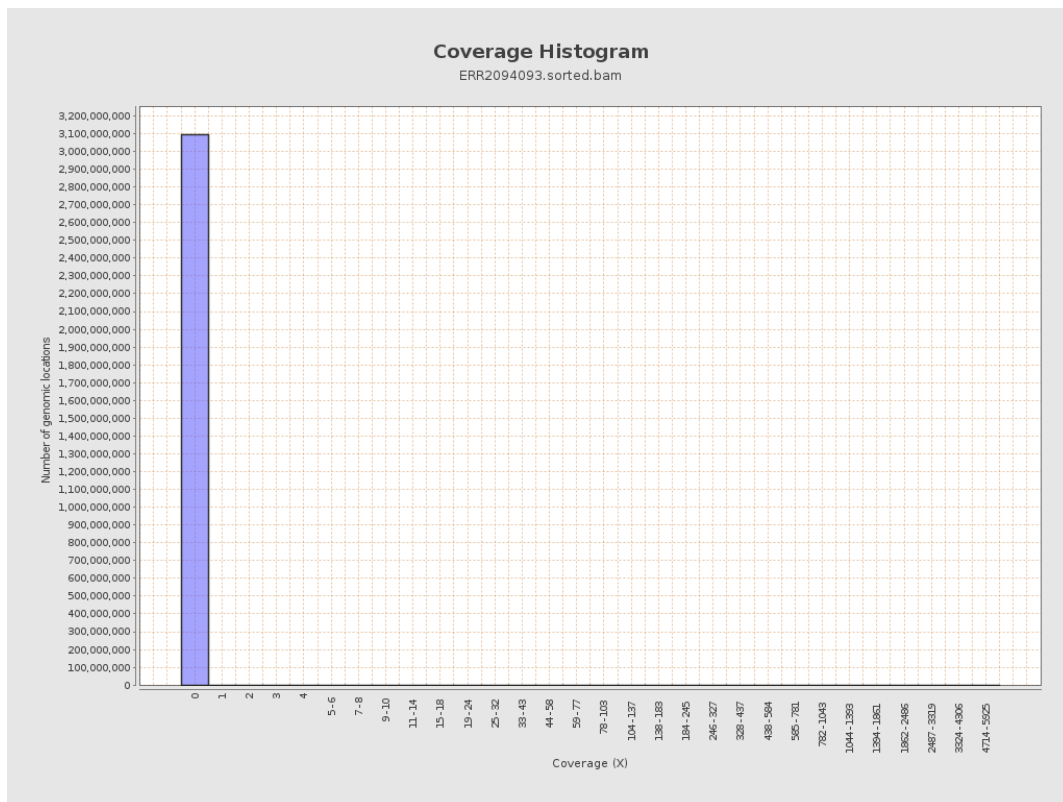
		bases	coverage	deviation
chr1	249250621	1858161	0.0075	2.7209
chr2	243199373	3764218	0.0155	4.1882
chr3	198022430	1998062	0.0101	3.4908
chr4	191154276	3454569	0.0181	4.8896
chr5	180915260	1472072	0.0081	3.3313
chr6	171115067	1828917	0.0107	3.1454
chr7	159138663	2295681	0.0144	4.3363
chr8	146364022	1749115	0.012	3.345
chr9	141213431	1981902	0.014	5.4583
chr10	135534747	1730512	0.0128	4.232
chr11	135006516	2153678	0.016	3.9144
chr12	133851895	2256013	0.0169	4.3619
chr13	115169878	1787685	0.0155	4.0884
chr14	107349540	457790	0.0043	1.4912
chr15	102531392	844837	0.0082	2.1937
chr16	90354753	434217	0.0048	1.9274
chr17	81195210	998673	0.0123	3.4393
chr18	78077248	542279	0.0069	1.9138
chr19	59128983	196608	0.0033	1.4164
chr20	63025520	463742	0.0074	2.6047
chr21	48129895	450344	0.0094	2.6533
chr22	51304566	141073	0.0027	0.7956
chrMT	16571	72675	4.3857	27.5468
chrX	155270560	48534740	0.3126	18.329

chrY	59373566	892394	0.015	3.0709
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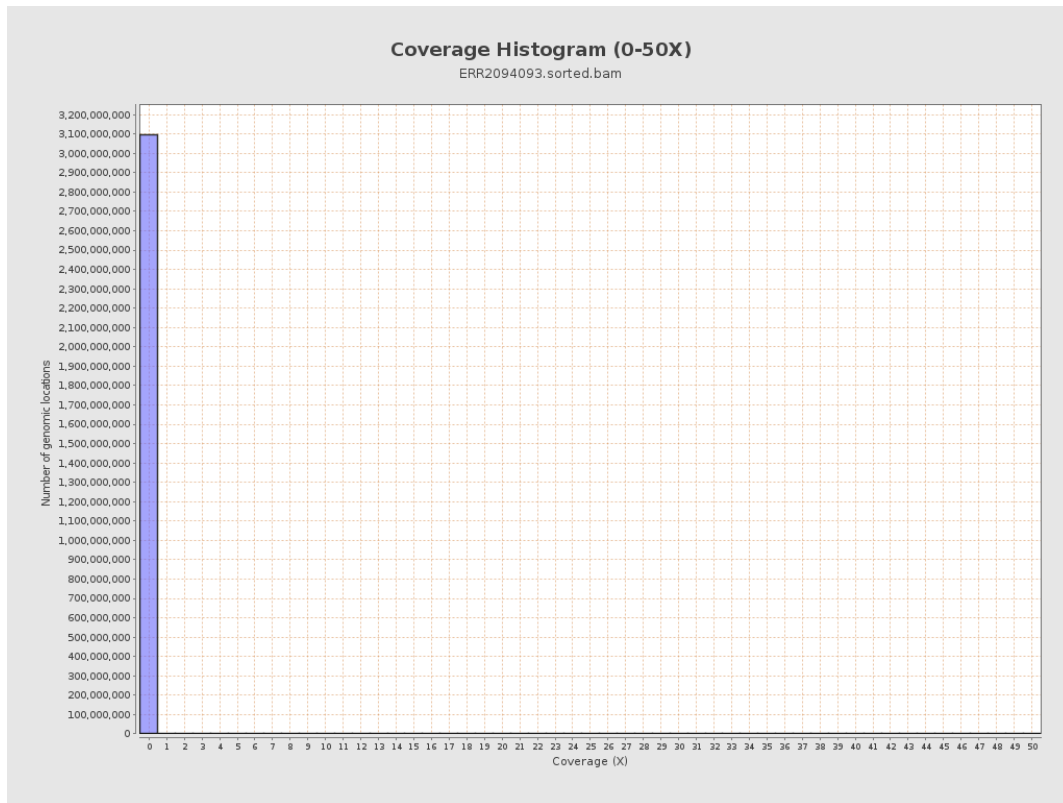
3. Results : Coverage across reference



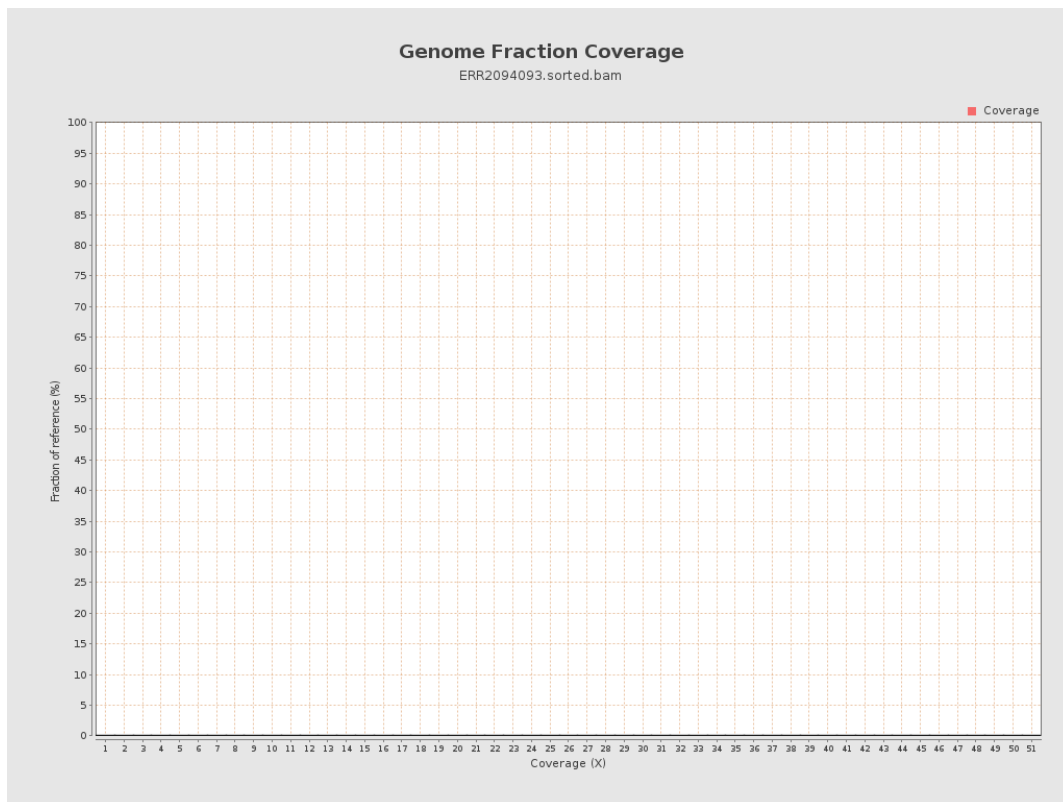
4. Results : Coverage Histogram



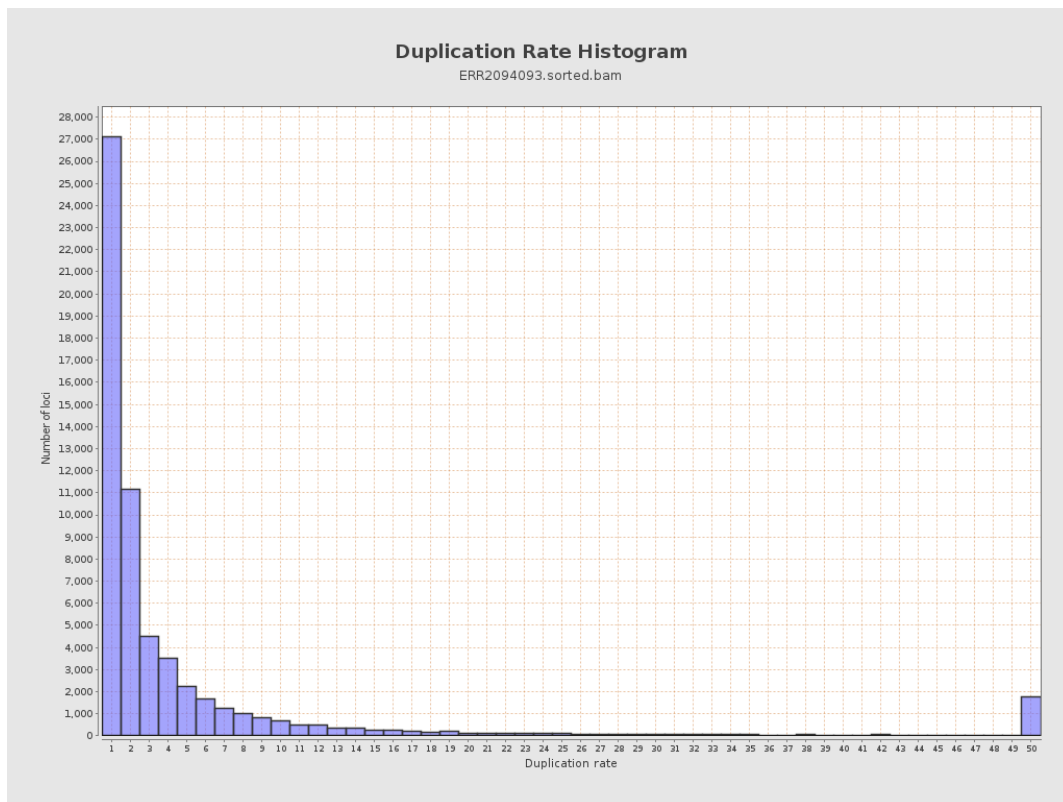
5. Results : Coverage Histogram (0-50X)



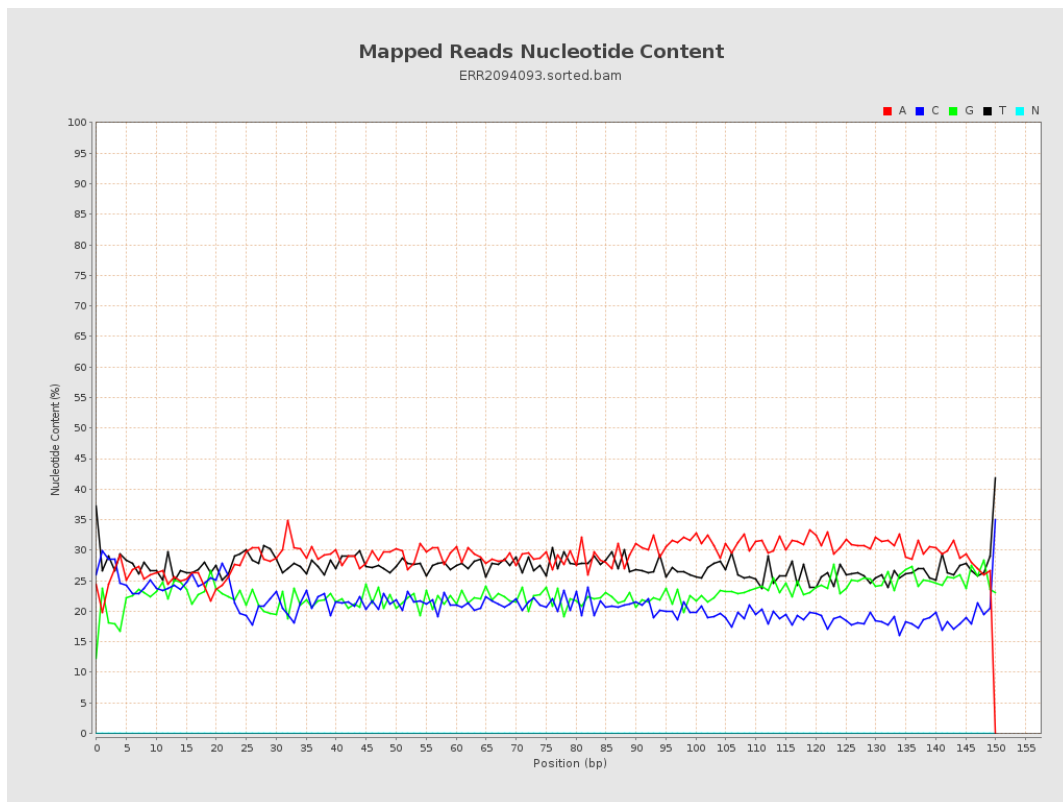
6. Results : Genome Fraction Coverage



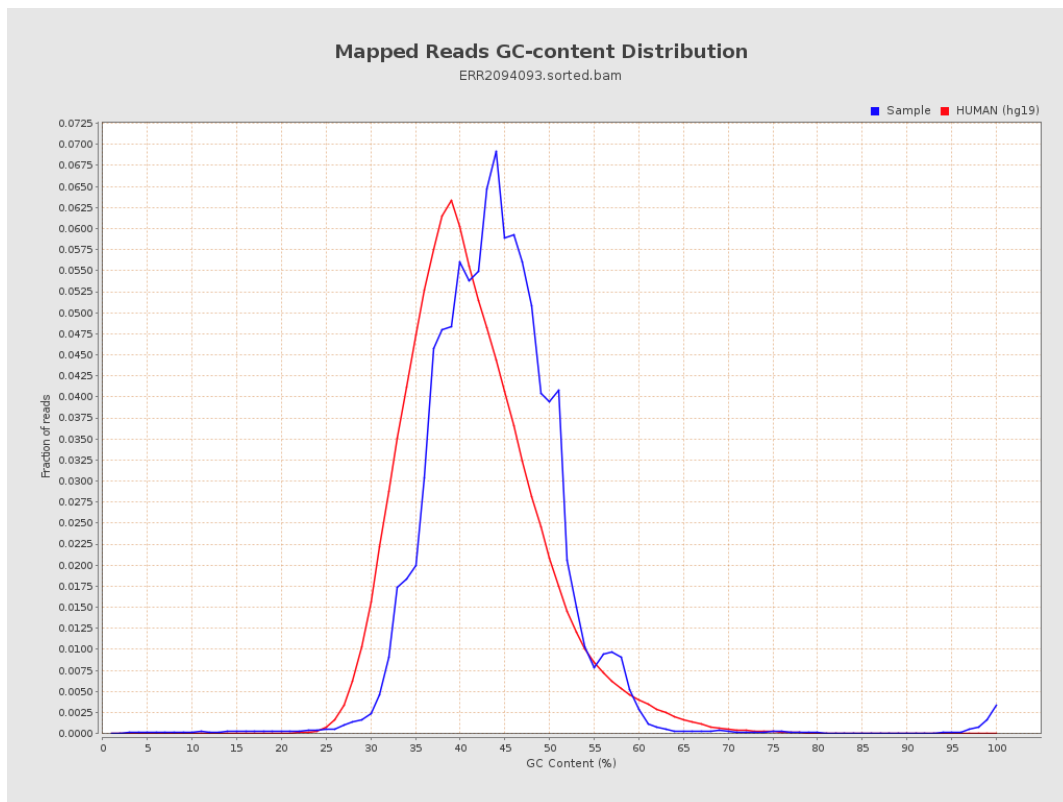
7. Results : Duplication Rate Histogram



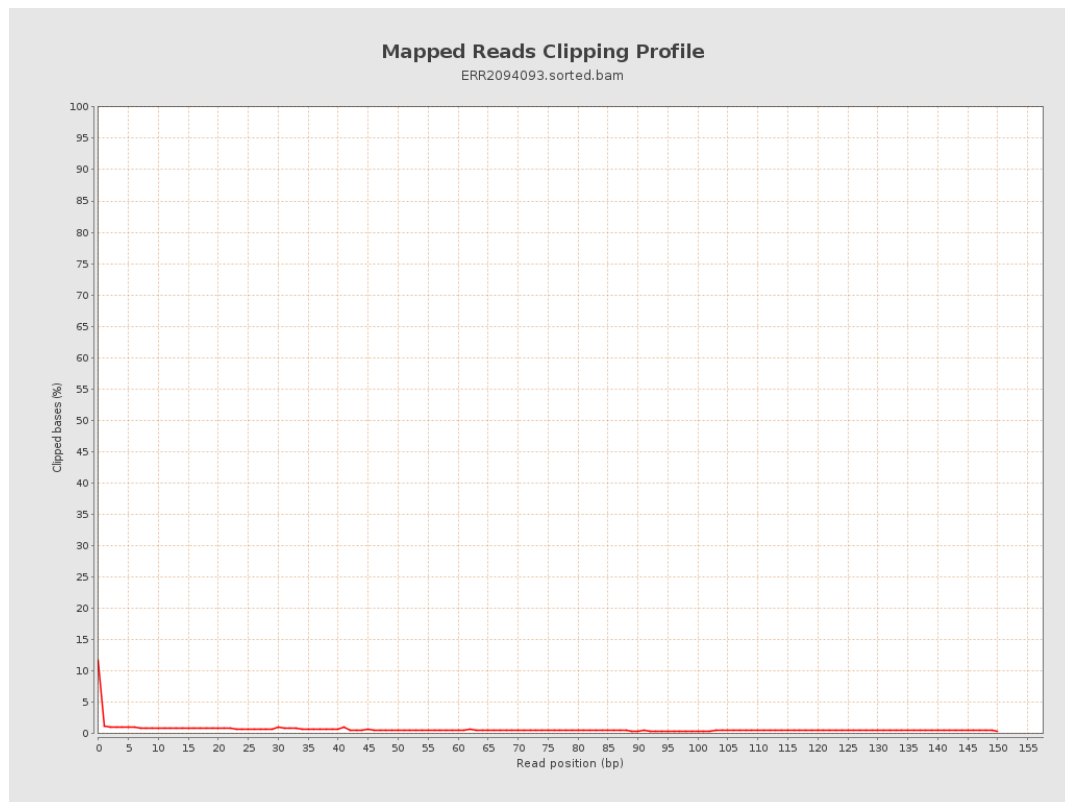
8. Results : Mapped Reads Nucleotide Content



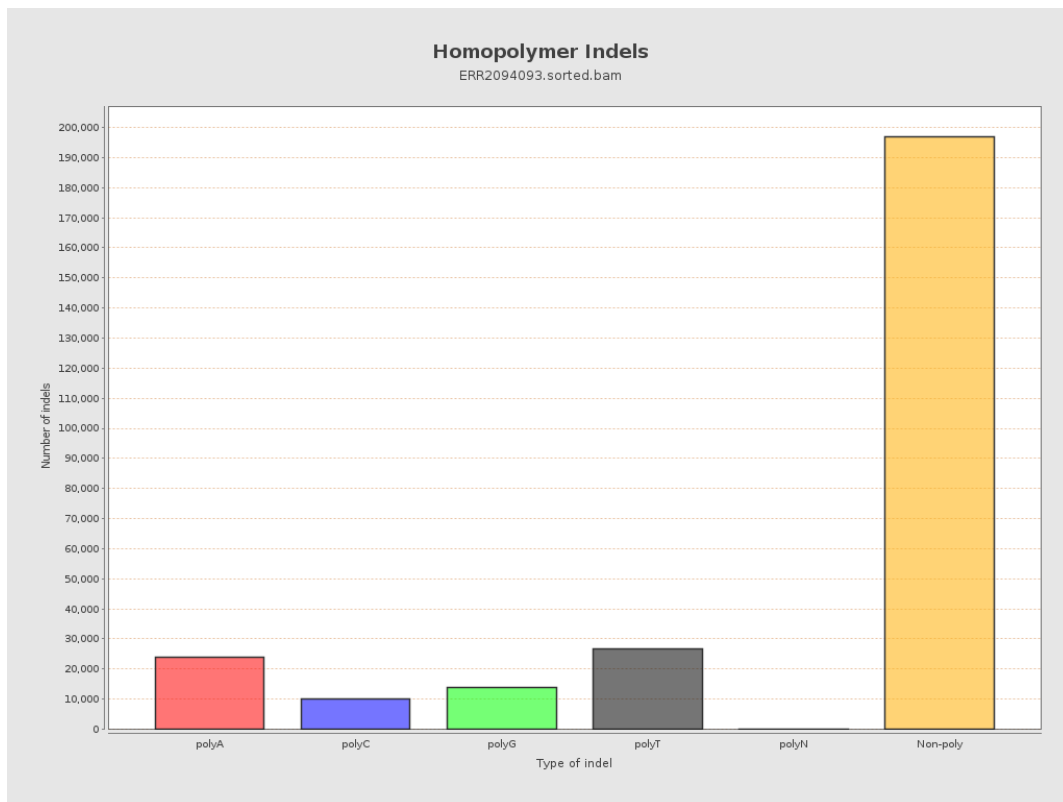
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



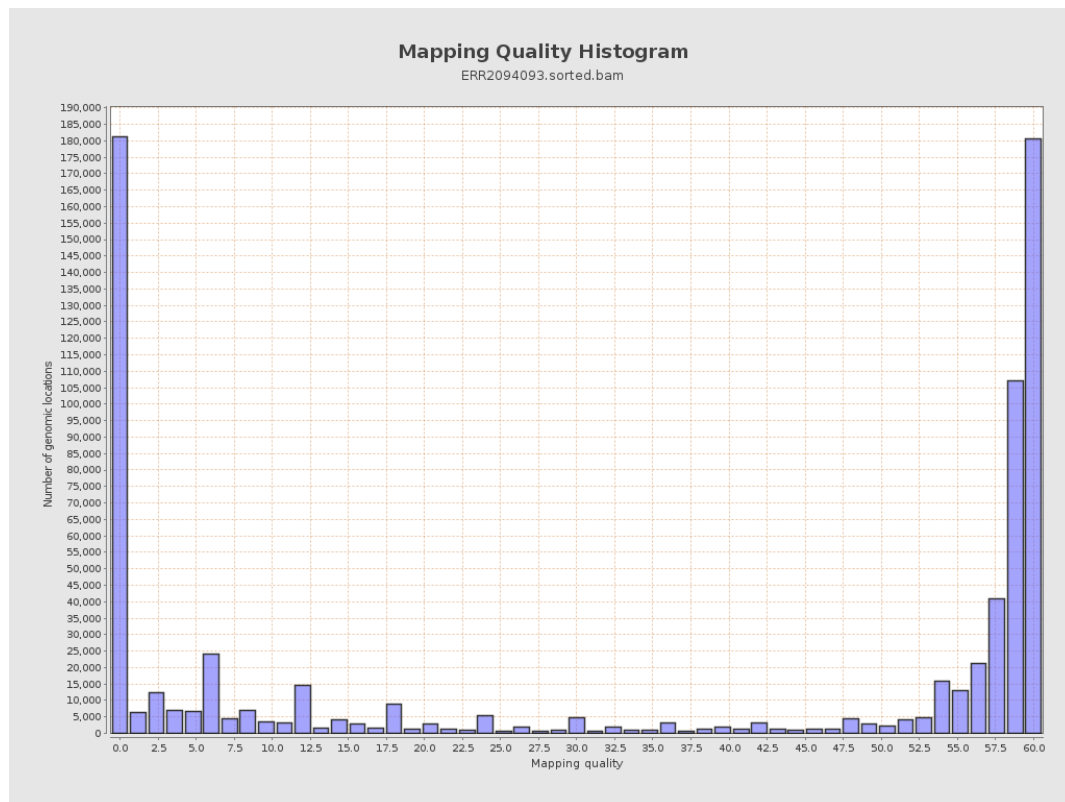
11. Results : Homopolymer Indels



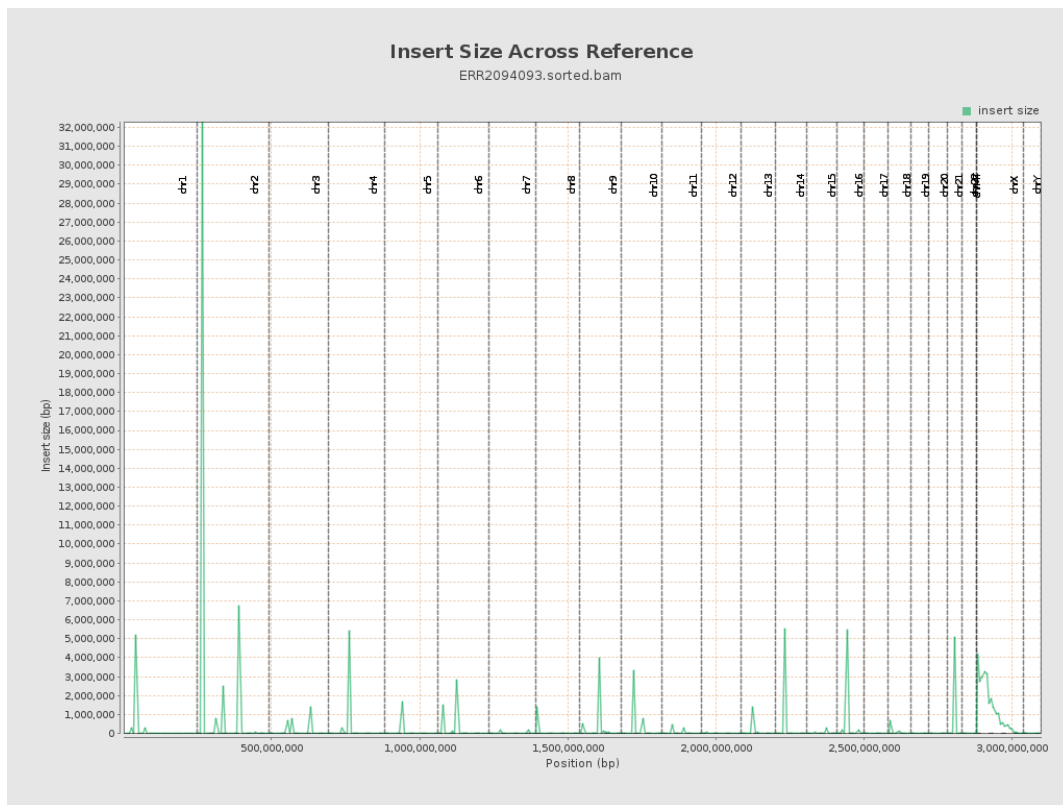
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

