

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:06:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094045.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_ERR2094045 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094045_1.fastq.gz ERR2094045_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:06:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	377,262
Mapped reads	361,564 / 95.84%
Unmapped reads	15,698 / 4.16%
Mapped paired reads	361,564 / 95.84%
Mapped reads, first in pair	181,629 / 48.14%
Mapped reads, second in pair	179,935 / 47.69%
Mapped reads, both in pair	358,974 / 95.15%
Mapped reads, singletons	2,590 / 0.69%
Secondary alignments	0
Supplementary alignments	14,354 / 3.8%
Read min/max/mean length	30 / 151 / 140.96
Duplicated reads (estimated)	337,237 / 89.39%
Duplication rate	49.94%
Clipped reads	150,647 / 39.93%

2.2. ACGT Content

Number/percentage of A's	12,909,661 / 27.69%
Number/percentage of C's	10,449,875 / 22.42%
Number/percentage of T's	12,415,390 / 26.63%
Number/percentage of G's	10,842,722 / 23.26%
Number/percentage of N's	666 / 0%

GC Percentage	45.67%
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2.3. Coverage

Mean	0.0155
Standard Deviation	3.4224

2.4. Mapping Quality

Mean Mapping Quality	44.85
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2.5. Insert size

Mean	662,759.62
Standard Deviation	7,356,451.23
P25/Median/P75	133 / 165 / 195

2.6. Mismatches and indels

General error rate	4.46%
Mismatches	2,042,870
Insertions	28,569
Mapped reads with at least one insertion	7.73%
Deletions	164,706
Mapped reads with at least one deletion	42.36%
Homopolymer indels	29.14%

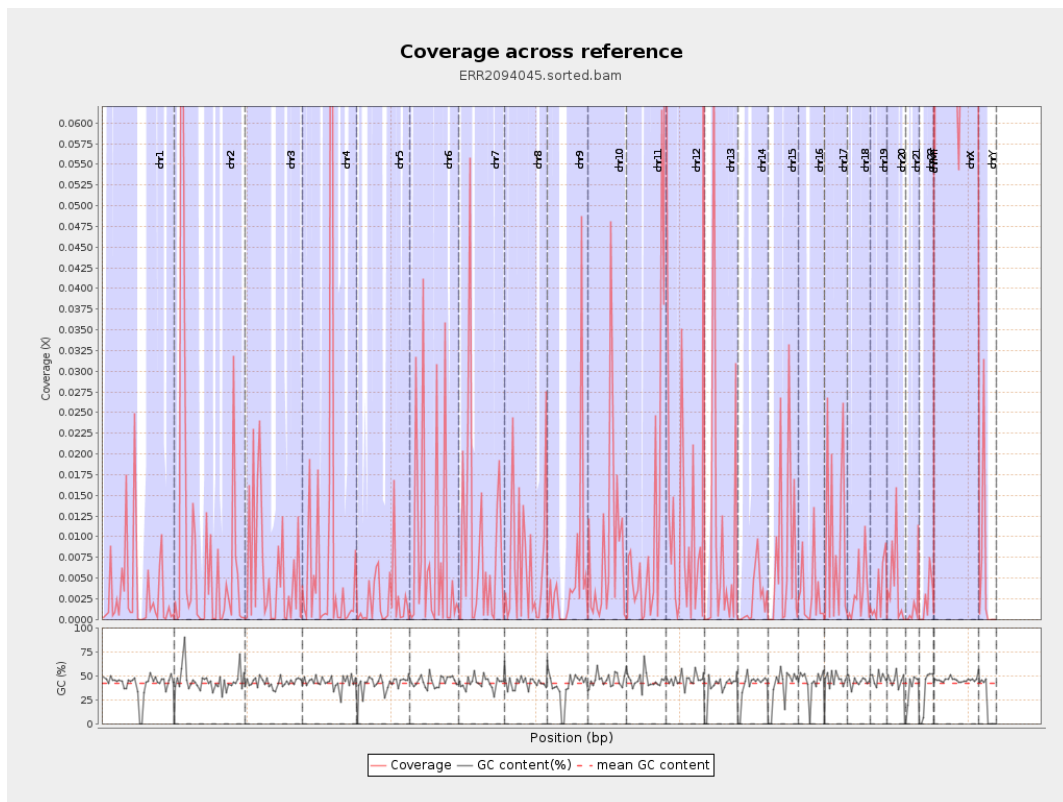
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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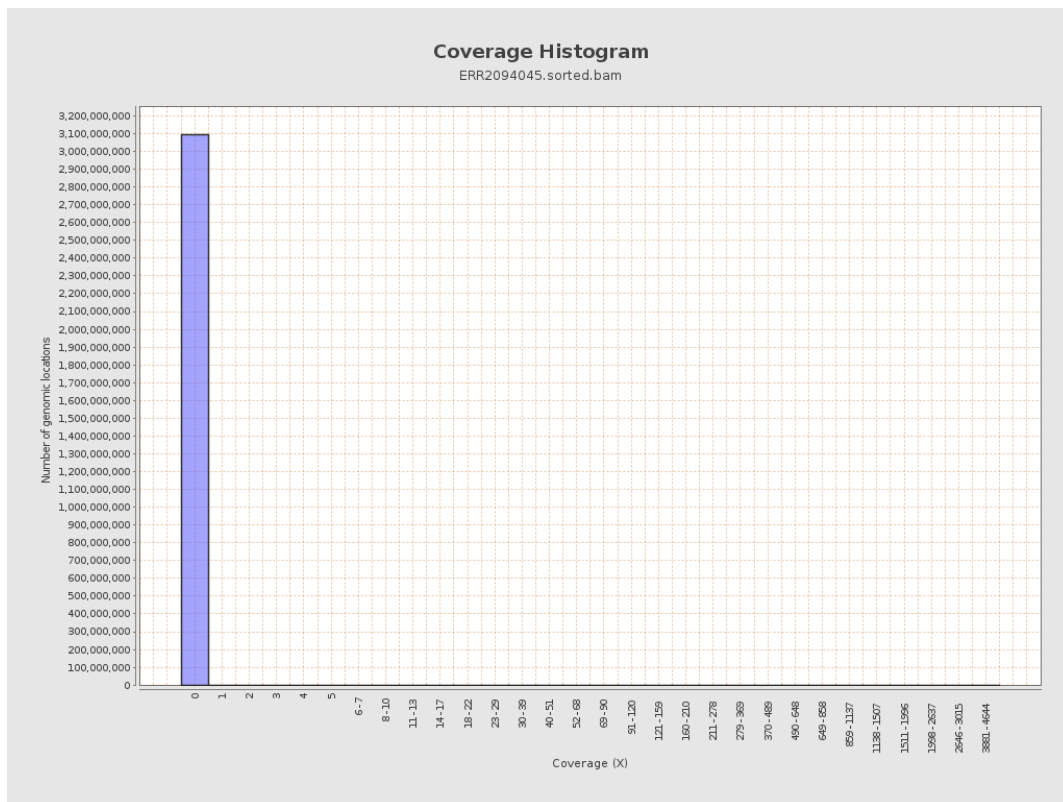
		bases	coverage	deviation
chr1	249250621	772447	0.0031	1.2346
chr2	243199373	2046760	0.0084	2.3994
chr3	198022430	1139726	0.0058	1.5596
chr4	191154276	1803985	0.0094	2.9636
chr5	180915260	447353	0.0025	0.7755
chr6	171115067	1392137	0.0081	3.2724
chr7	159138663	1408334	0.0088	2.2943
chr8	146364022	972251	0.0066	1.7812
chr9	141213431	738680	0.0052	2.2082
chr10	135534747	1200947	0.0089	2.7621
chr11	135006516	1592508	0.0118	3.1197
chr12	133851895	1663847	0.0124	3.2549
chr13	115169878	1045147	0.0091	2.4182
chr14	107349540	259095	0.0024	0.7696
chr15	102531392	775940	0.0076	1.8792
chr16	90354753	295942	0.0033	0.9882
chr17	81195210	776567	0.0096	2.2347
chr18	78077248	263957	0.0034	0.9502
chr19	59128983	191782	0.0032	0.6996
chr20	63025520	277079	0.0044	0.9374
chr21	48129895	80029	0.0017	0.3769
chr22	51304566	115836	0.0023	0.5515
chrMT	16571	2342335	141.3515	585.9929
chrX	155270560	25944083	0.1671	10.3523

chrY	59373566	312242	0.0053	1.7643
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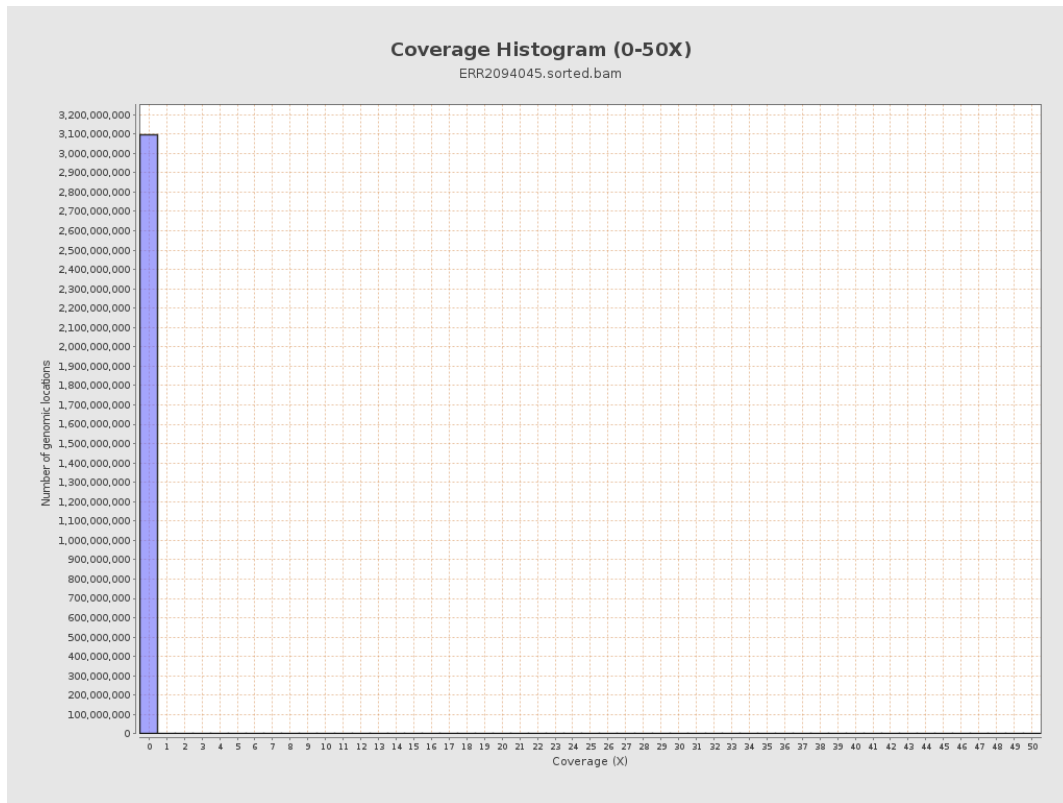
3. Results : Coverage across reference



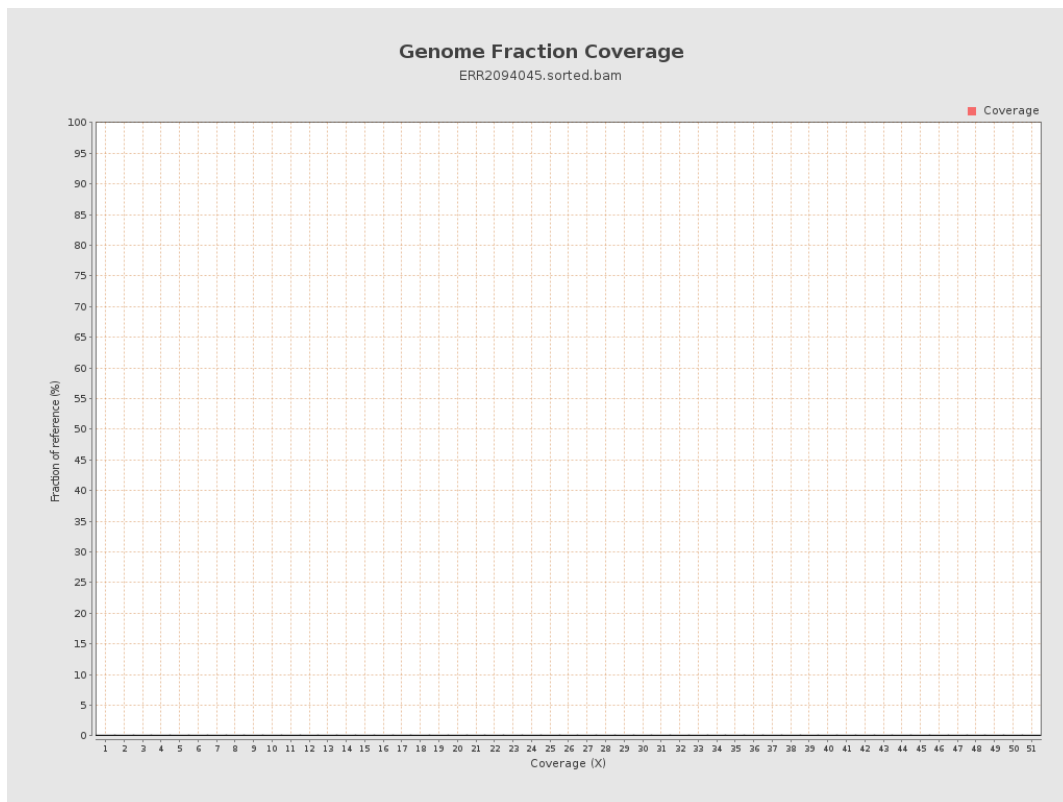
4. Results : Coverage Histogram



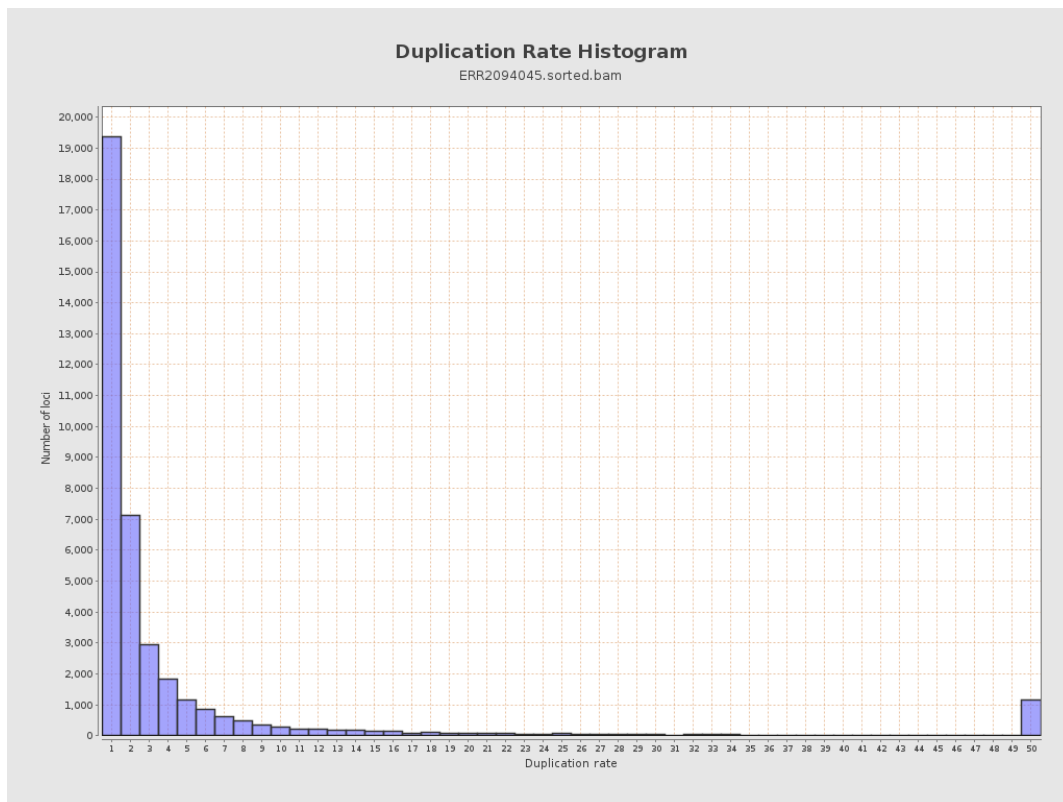
5. Results : Coverage Histogram (0-50X)



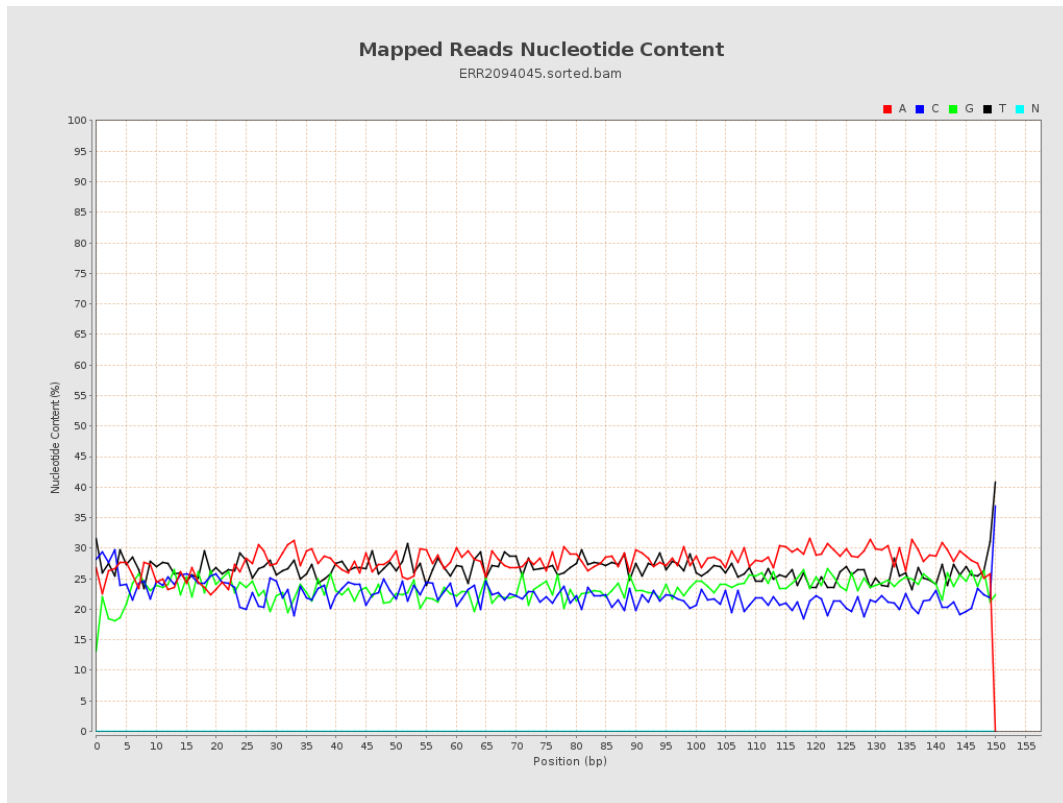
6. Results : Genome Fraction Coverage



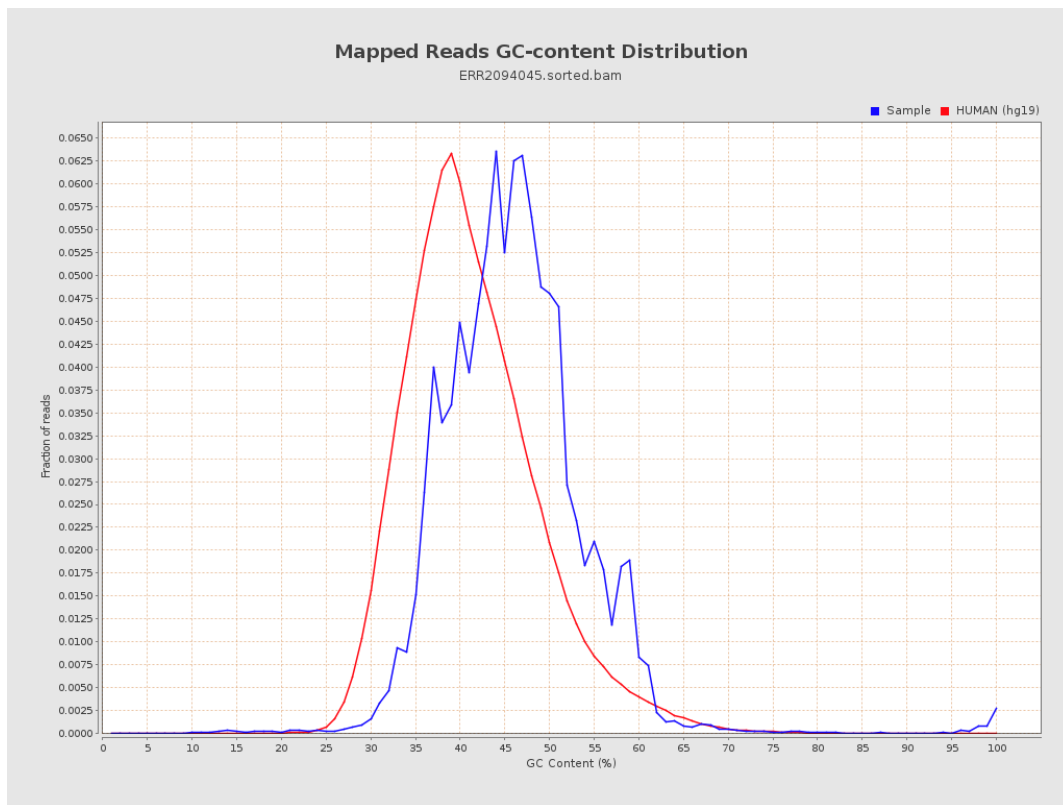
7. Results : Duplication Rate Histogram



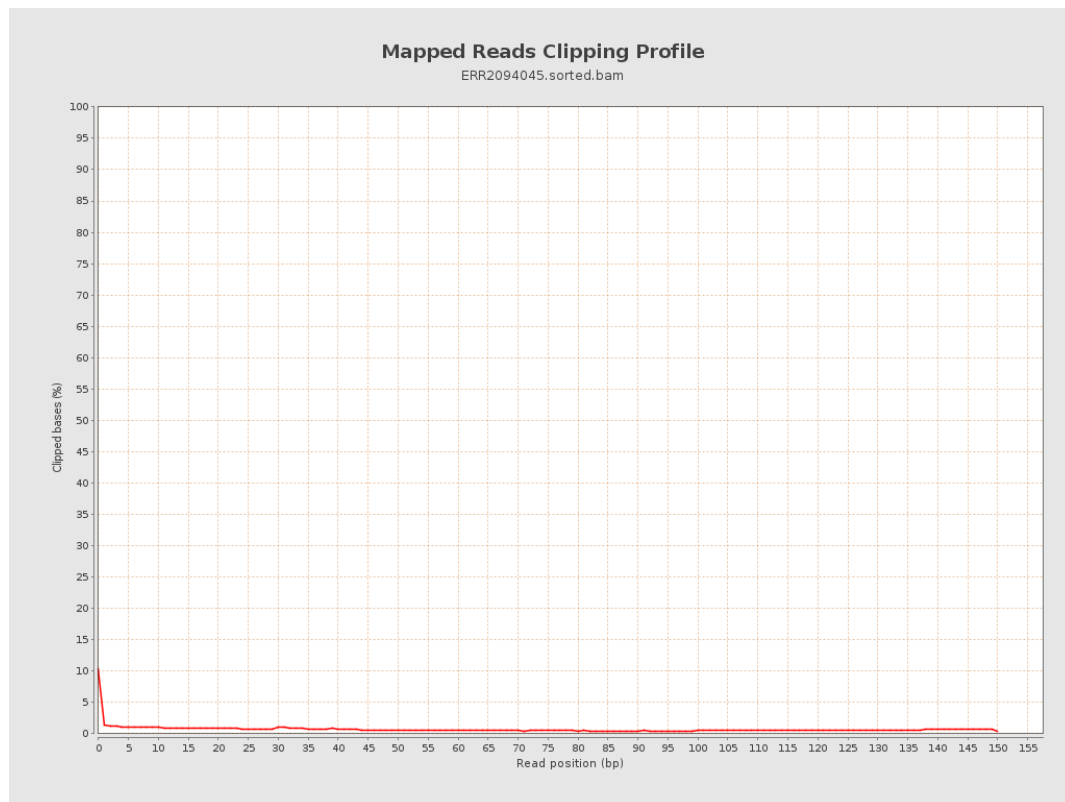
8. Results : Mapped Reads Nucleotide Content



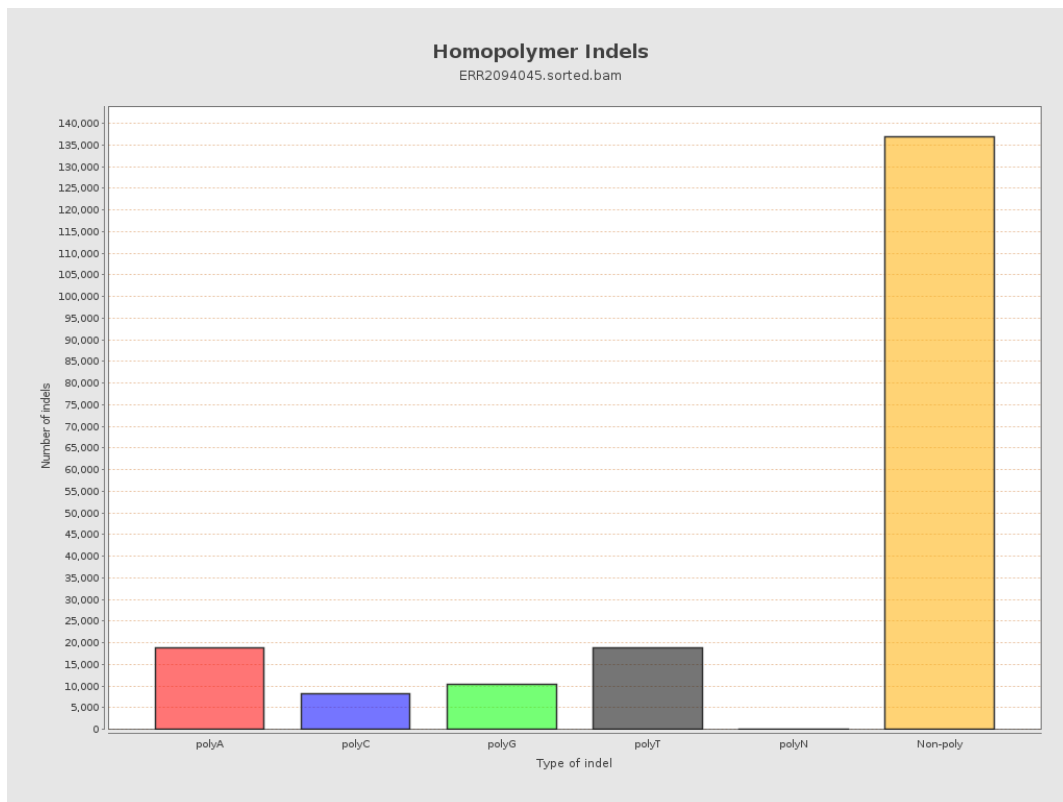
9. Results : Mapped Reads GC-content Distribution



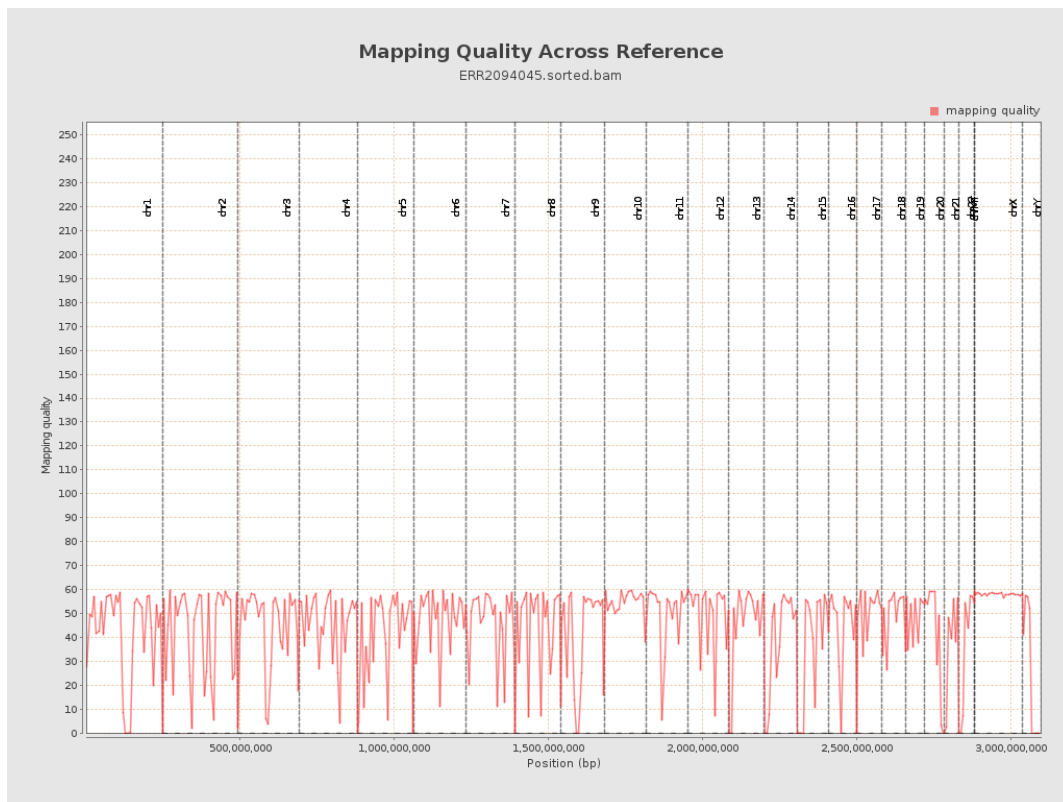
10. Results : Mapped Reads Clipping Profile



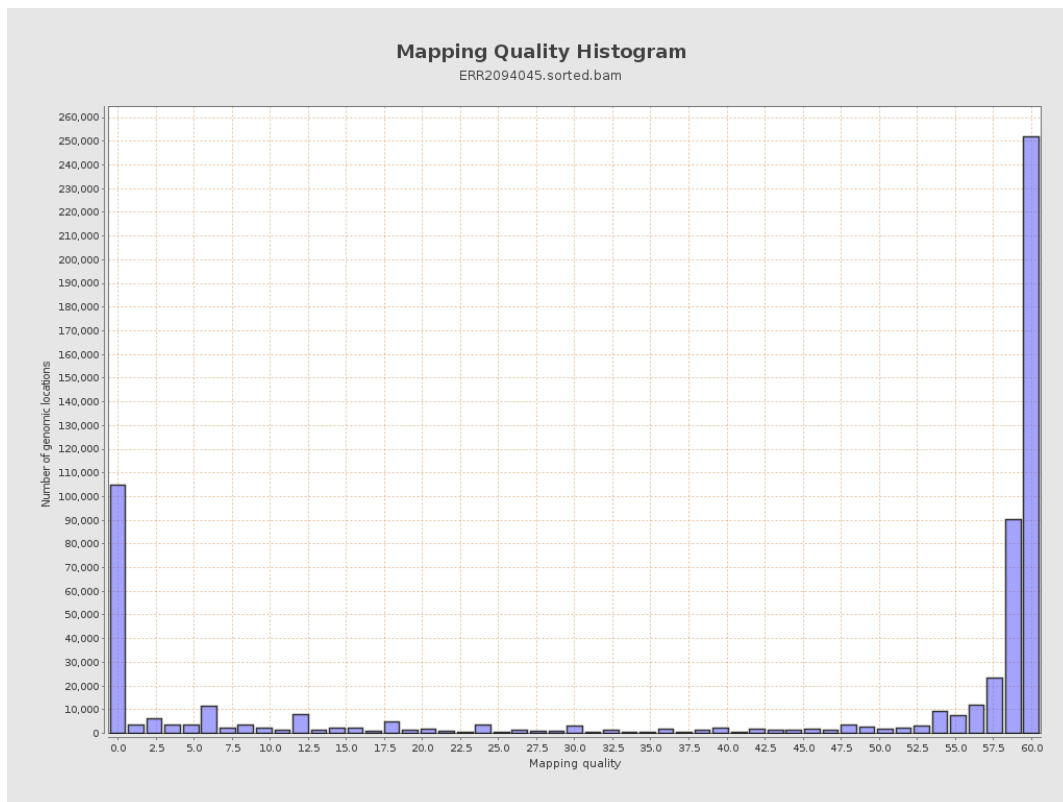
11. Results : Homopolymer Indels



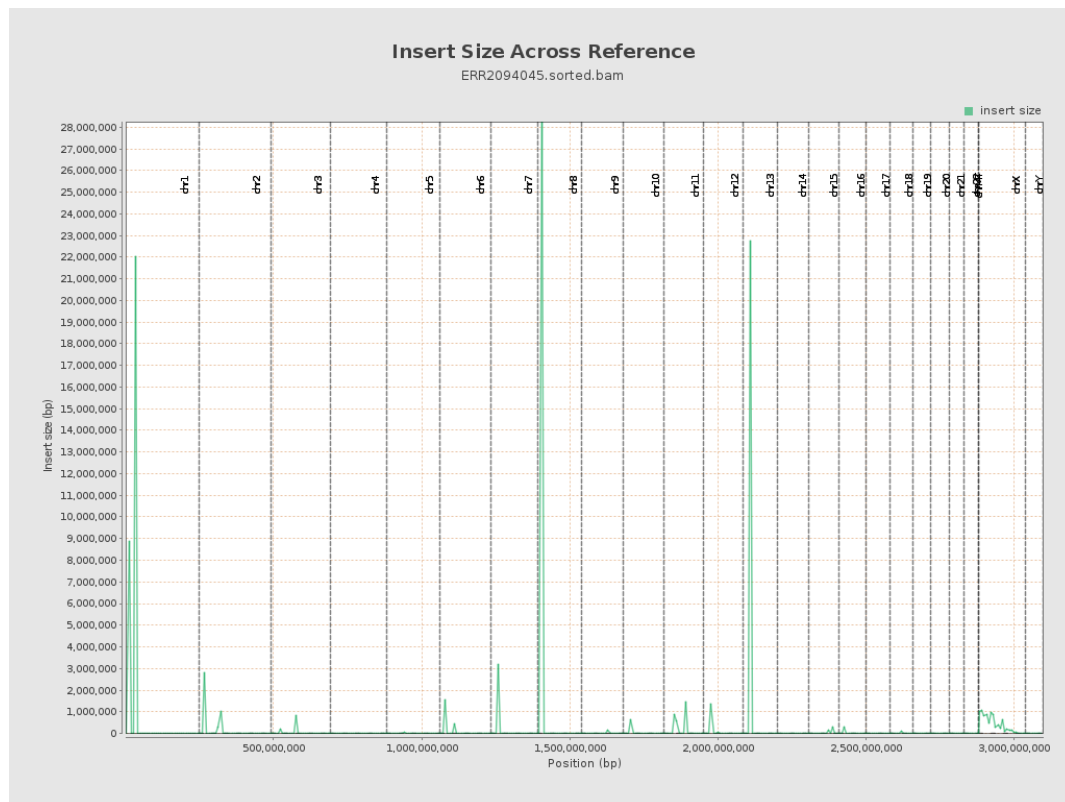
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

