

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:43:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094131.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_ERR2094131 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094131_1.fastq.gz ERR2094131_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:43:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	430,312
Mapped reads	403,445 / 93.76%
Unmapped reads	26,867 / 6.24%
Mapped paired reads	403,445 / 93.76%
Mapped reads, first in pair	202,394 / 47.03%
Mapped reads, second in pair	201,051 / 46.72%
Mapped reads, both in pair	401,204 / 93.24%
Mapped reads, singletons	2,241 / 0.52%
Secondary alignments	0
Supplementary alignments	3,724 / 0.87%
Read min/max/mean length	30 / 151 / 144.81
Duplicated reads (estimated)	400,587 / 93.09%
Duplication rate	46.64%
Clipped reads	110,825 / 25.75%

2.2. ACGT Content

Number/percentage of A's	15,806,656 / 27.32%
Number/percentage of C's	12,443,383 / 21.51%
Number/percentage of T's	16,484,895 / 28.49%
Number/percentage of G's	13,117,555 / 22.67%
Number/percentage of N's	692 / 0%

GC Percentage	44.18%
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2.3. Coverage

Mean	0.0188
Standard Deviation	25.9402

2.4. Mapping Quality

Mean Mapping Quality	26.87
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2.5. Insert size

Mean	17,854.79
Standard Deviation	1,345,050.24
P25/Median/P75	210 / 220 / 256

2.6. Mismatches and indels

General error rate	2.04%
Mismatches	1,155,988
Insertions	22,546
Mapped reads with at least one insertion	5.51%
Deletions	68,428
Mapped reads with at least one deletion	16.56%
Homopolymer indels	47.33%

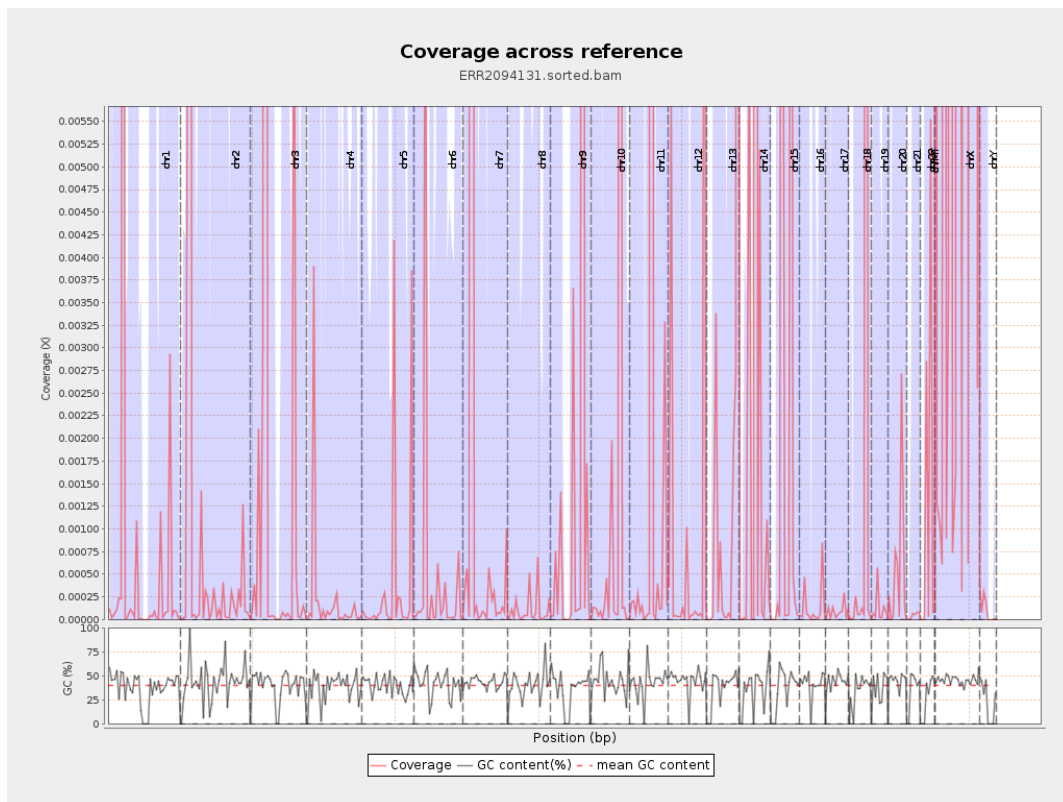
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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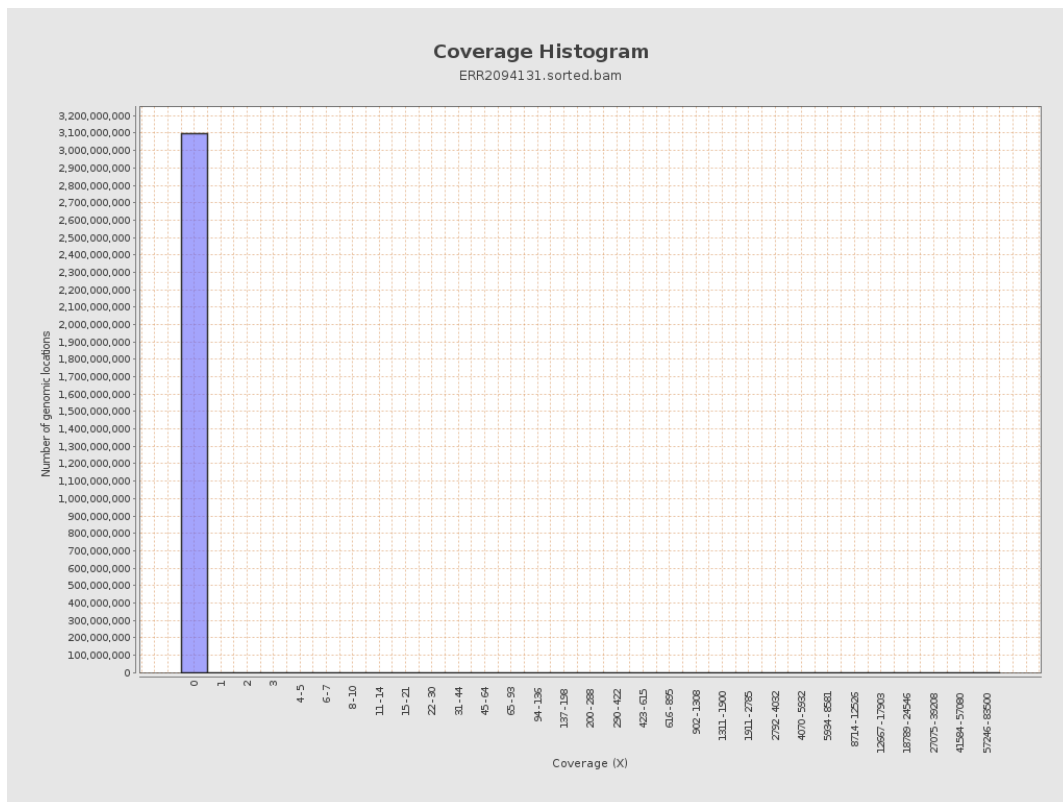
		bases	coverage	deviation
chr1	249250621	174609	0.0007	0.5781
chr2	243199373	329003	0.0014	0.9824
chr3	198022430	358857	0.0018	1.1116
chr4	191154276	43195	0.0002	0.2101
chr5	180915260	74855	0.0004	0.3155
chr6	171115067	86807	0.0005	0.2613
chr7	159138663	379749	0.0024	2.177
chr8	146364022	16995	0.0001	0.0421
chr9	141213431	537824	0.0038	2.8984
chr10	135534747	259700	0.0019	1.529
chr11	135006516	1044846	0.0077	6.0596
chr12	133851895	179049	0.0013	0.7913
chr13	115169878	1201362	0.0104	8.7355
chr14	107349540	3650125	0.034	25.9038
chr15	102531392	253295	0.0025	1.1915
chr16	90354753	13431	0.0001	0.0816
chr17	81195210	7150	0.0001	0.017
chr18	78077248	167492	0.0021	1.2403
chr19	59128983	6958	0.0001	0.0614
chr20	63025520	35257	0.0006	0.213
chr21	48129895	1907	0	0.0074
chr22	51304566	65923	0.0013	0.4695
chrMT	16571	42473168	2,563.1023	10,543.8359
chrX	155270560	6790893	0.0437	16.6697

chrY	59373566	6627	0.0001	0.0289
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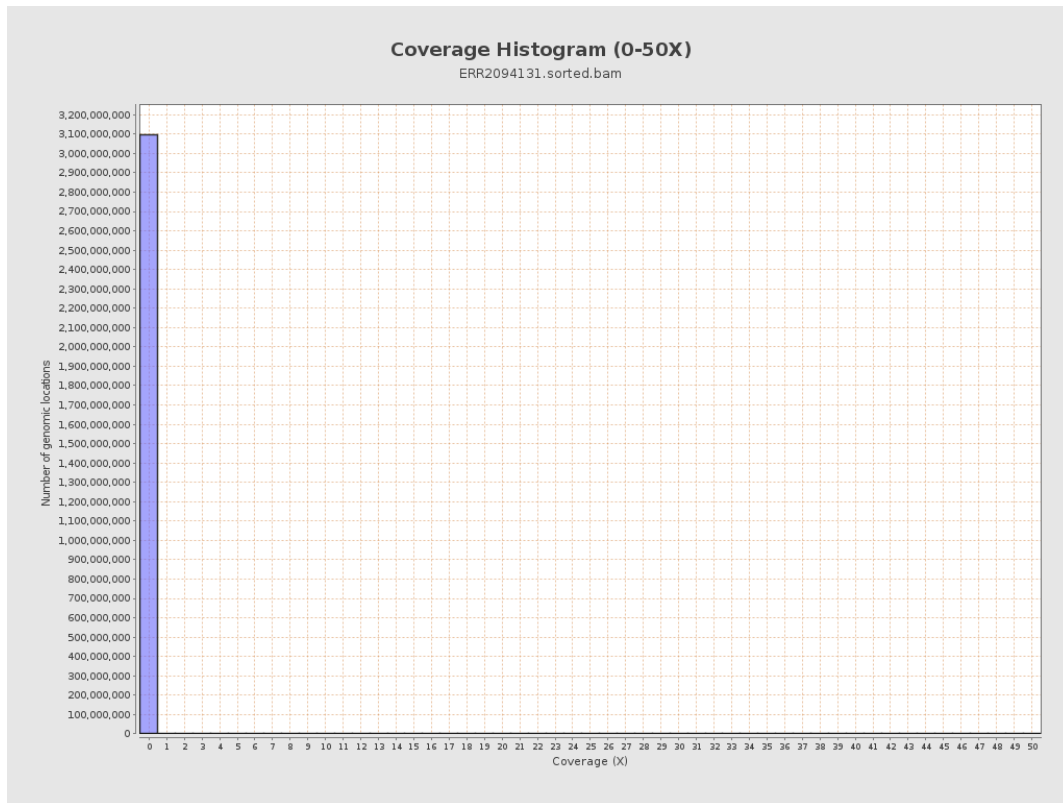
3. Results : Coverage across reference



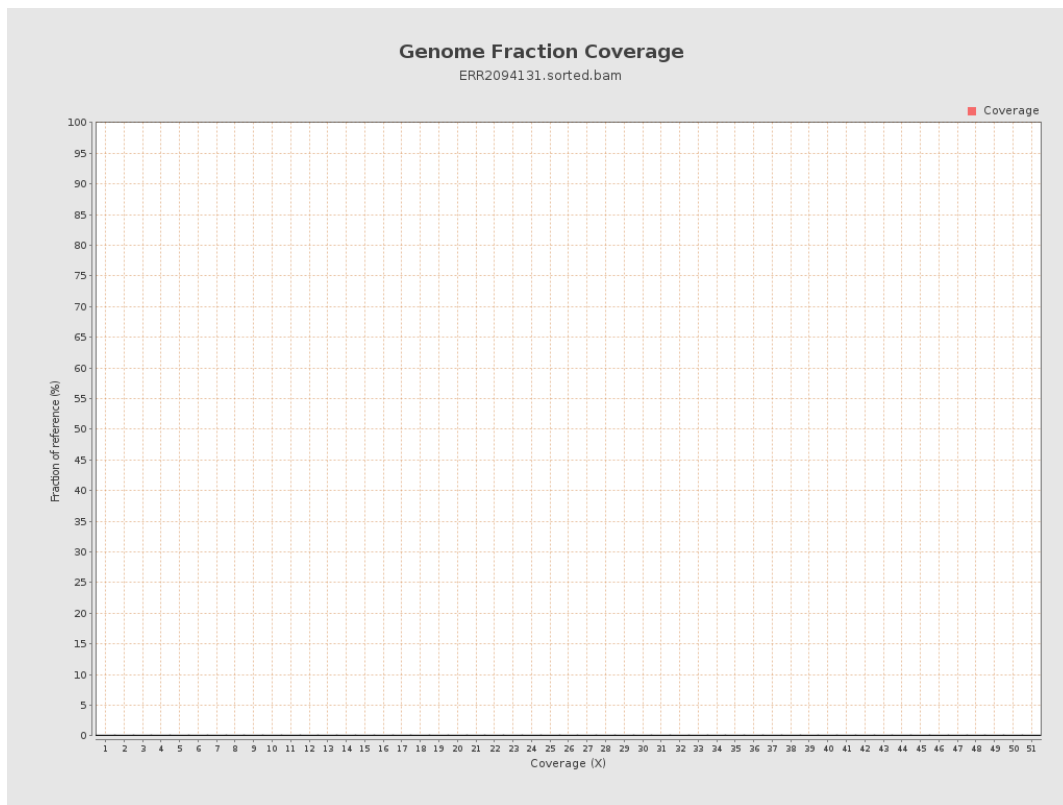
4. Results : Coverage Histogram



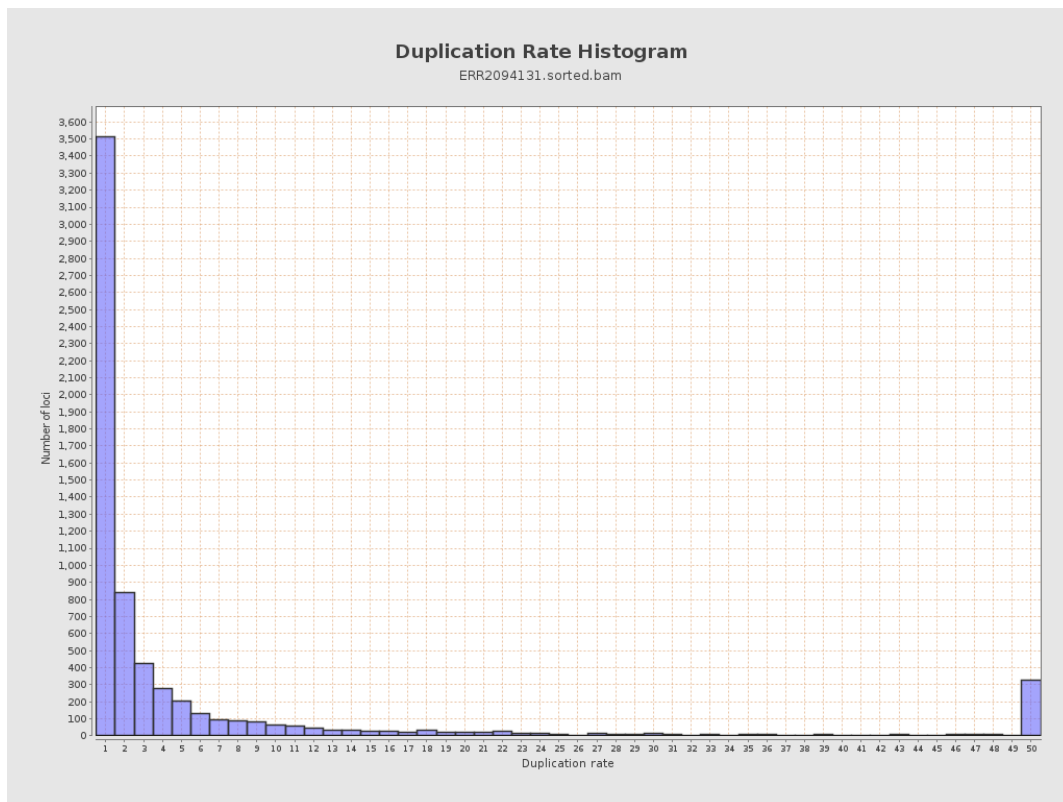
5. Results : Coverage Histogram (0-50X)



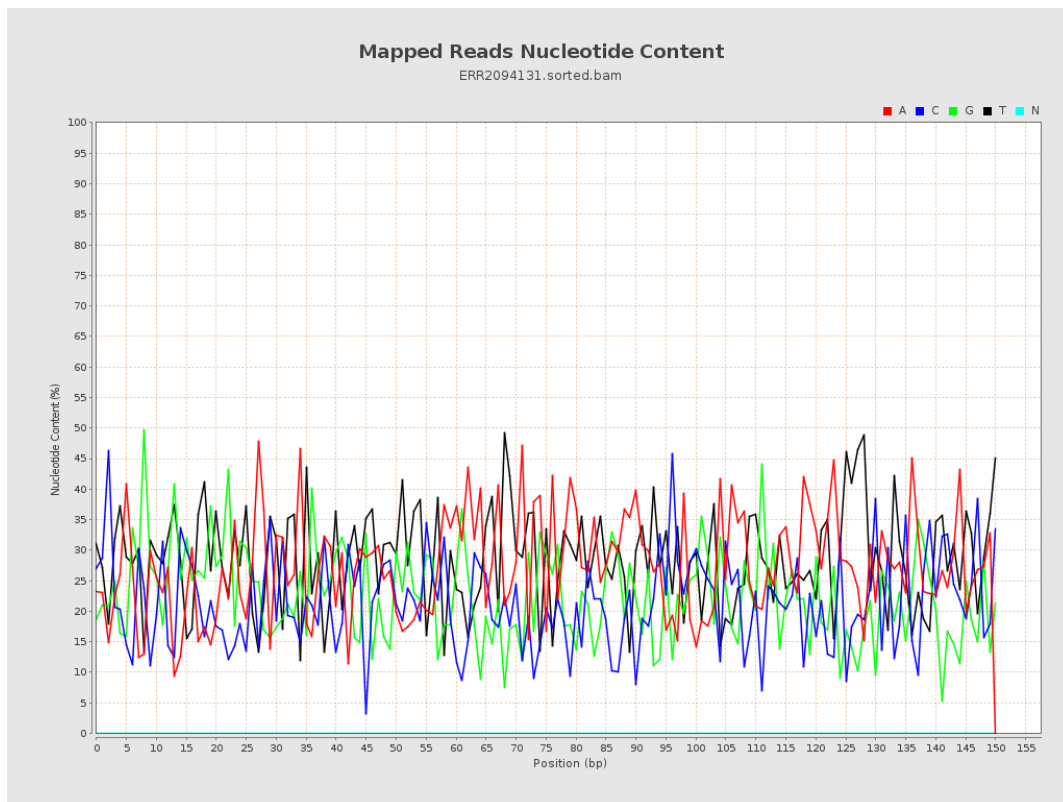
6. Results : Genome Fraction Coverage



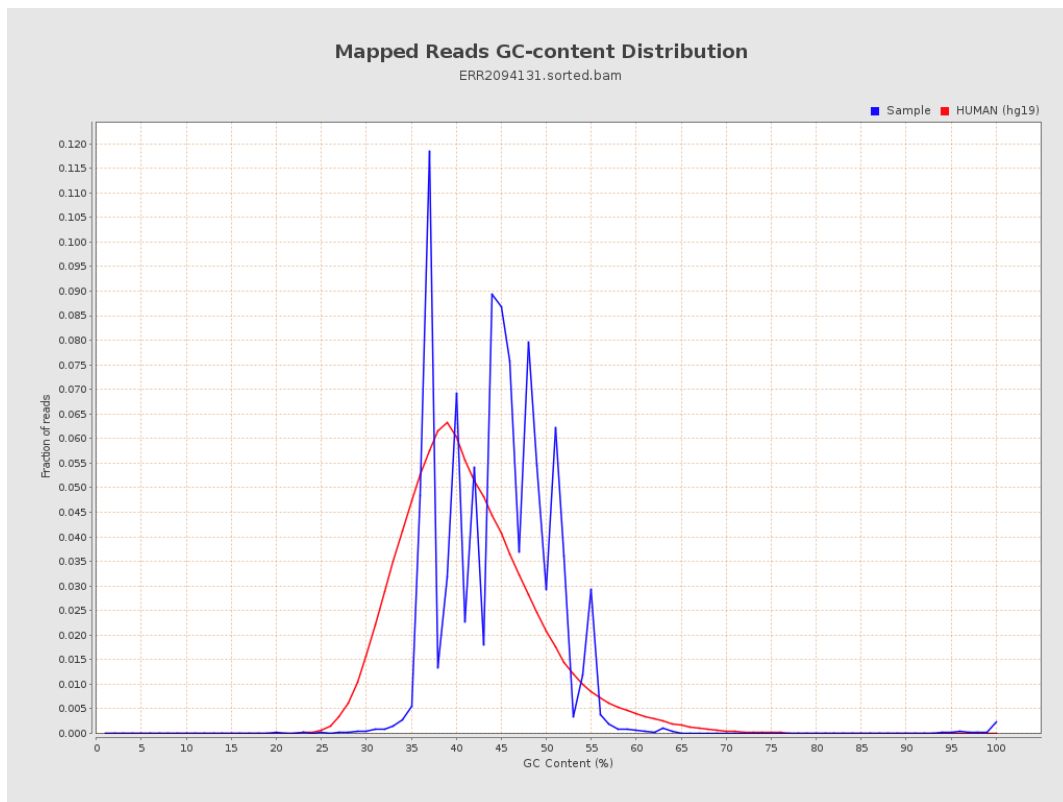
7. Results : Duplication Rate Histogram



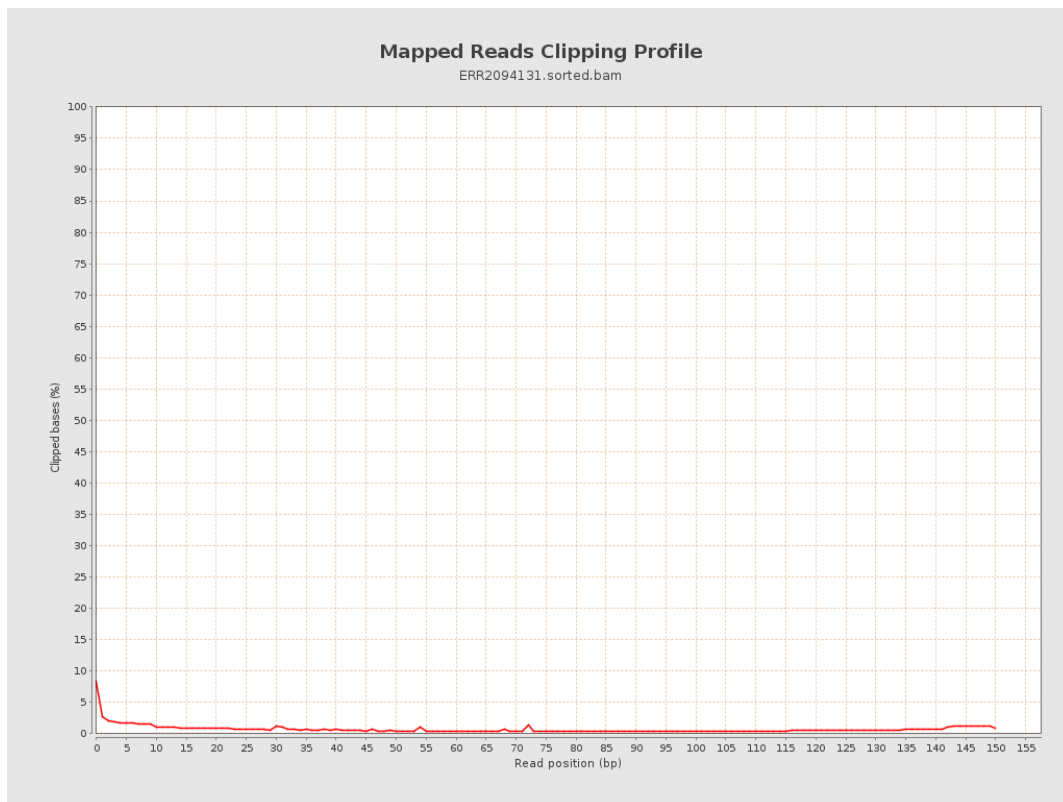
8. Results : Mapped Reads Nucleotide Content



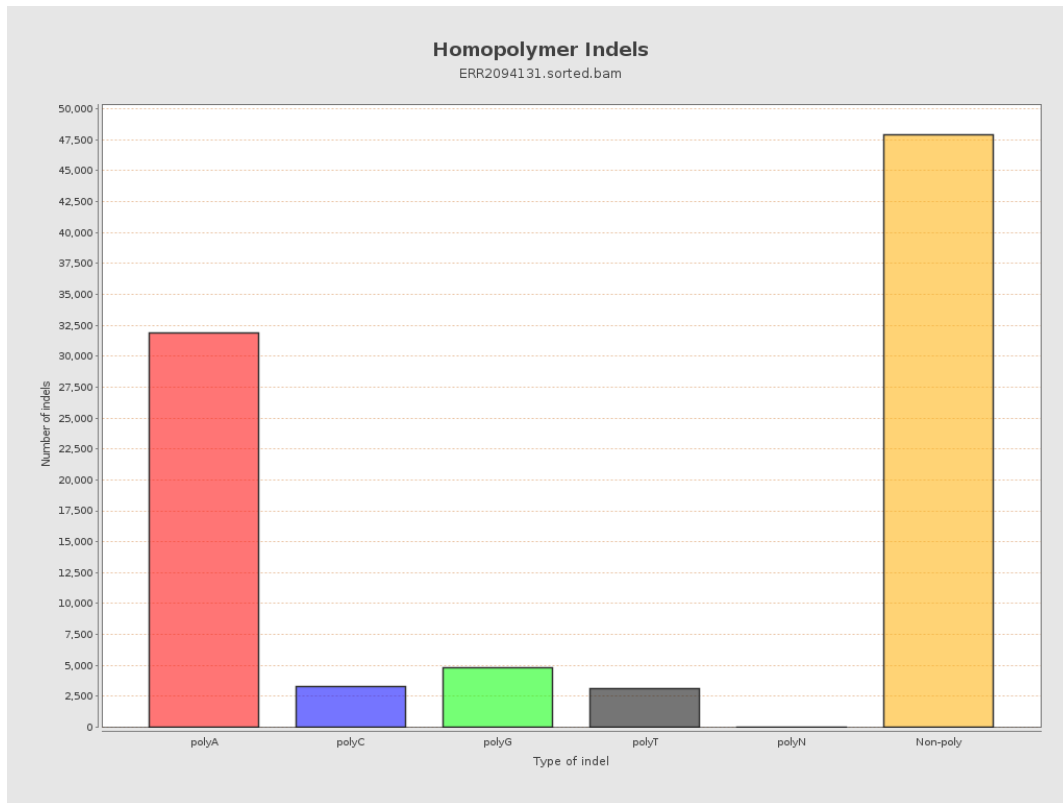
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



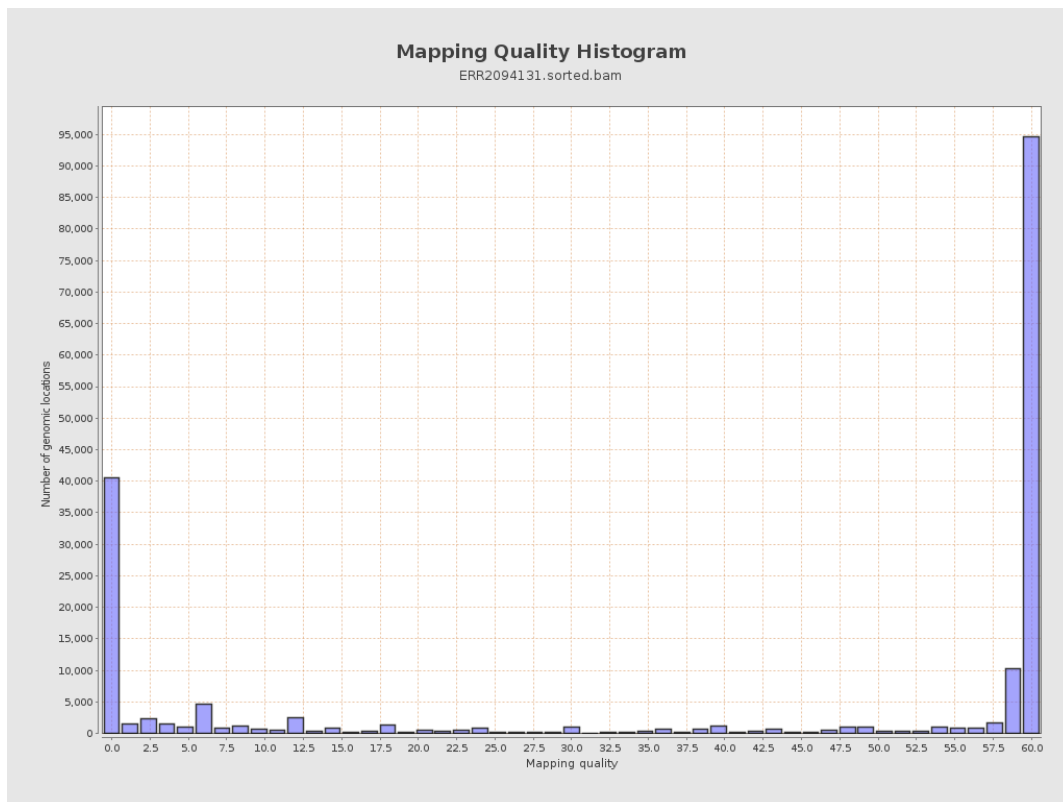
11. Results : Homopolymer Indels



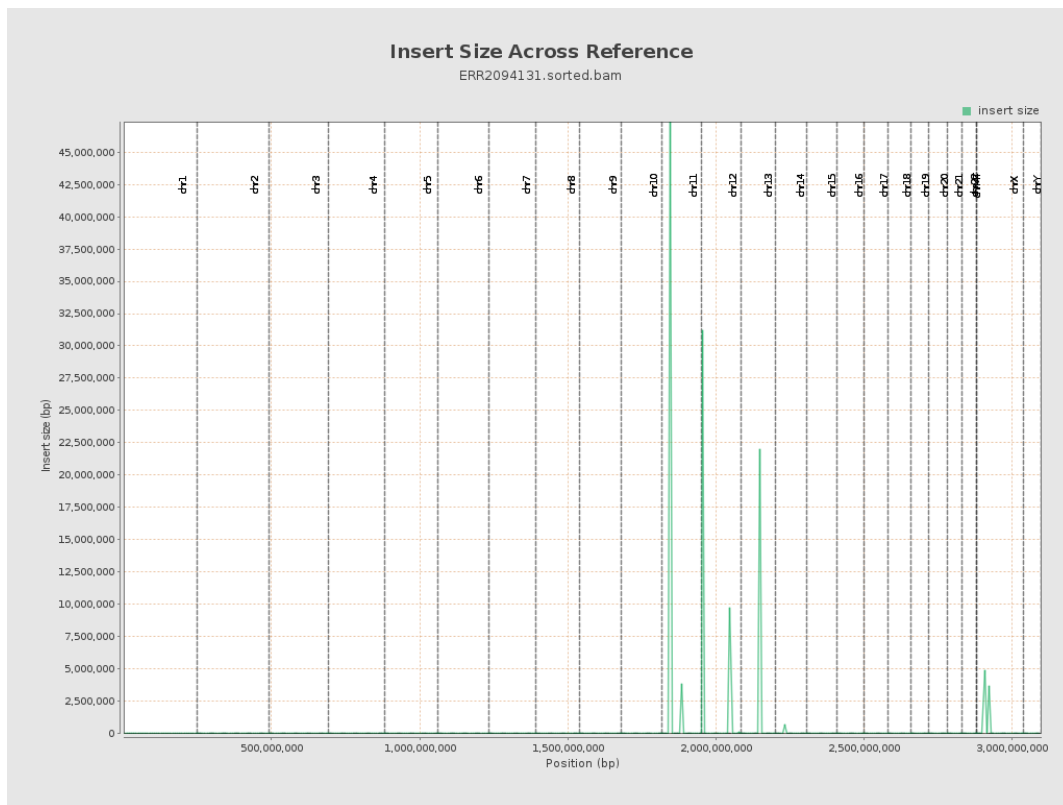
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

