

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:10:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094102.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_ERR2094102 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094102_1.fastq.gz ERR2094102_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:10:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	450,616
Mapped reads	436,673 / 96.91%
Unmapped reads	13,943 / 3.09%
Mapped paired reads	436,673 / 96.91%
Mapped reads, first in pair	219,401 / 48.69%
Mapped reads, second in pair	217,272 / 48.22%
Mapped reads, both in pair	433,124 / 96.12%
Mapped reads, singletons	3,549 / 0.79%
Secondary alignments	0
Supplementary alignments	31,538 / 7%
Read min/max/mean length	30 / 151 / 140.46
Duplicated reads (estimated)	425,543 / 94.44%
Duplication rate	53.29%
Clipped reads	227,303 / 50.44%

2.2. ACGT Content

Number/percentage of A's	15,325,701 / 28.73%
Number/percentage of C's	11,541,383 / 21.64%
Number/percentage of T's	14,295,299 / 26.8%
Number/percentage of G's	12,177,150 / 22.83%
Number/percentage of N's	580 / 0%

GC Percentage	44.47%
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2.3. Coverage

Mean	0.0175
Standard Deviation	4.2081

2.4. Mapping Quality

Mean Mapping Quality	39.82
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2.5. Insert size

Mean	1,693,681.08
Standard Deviation	11,607,936.17
P25/Median/P75	115 / 147 / 173

2.6. Mismatches and indels

General error rate	3.38%
Mismatches	1,728,908
Insertions	35,018
Mapped reads with at least one insertion	7.91%
Deletions	132,369
Mapped reads with at least one deletion	29.32%
Homopolymer indels	26.13%

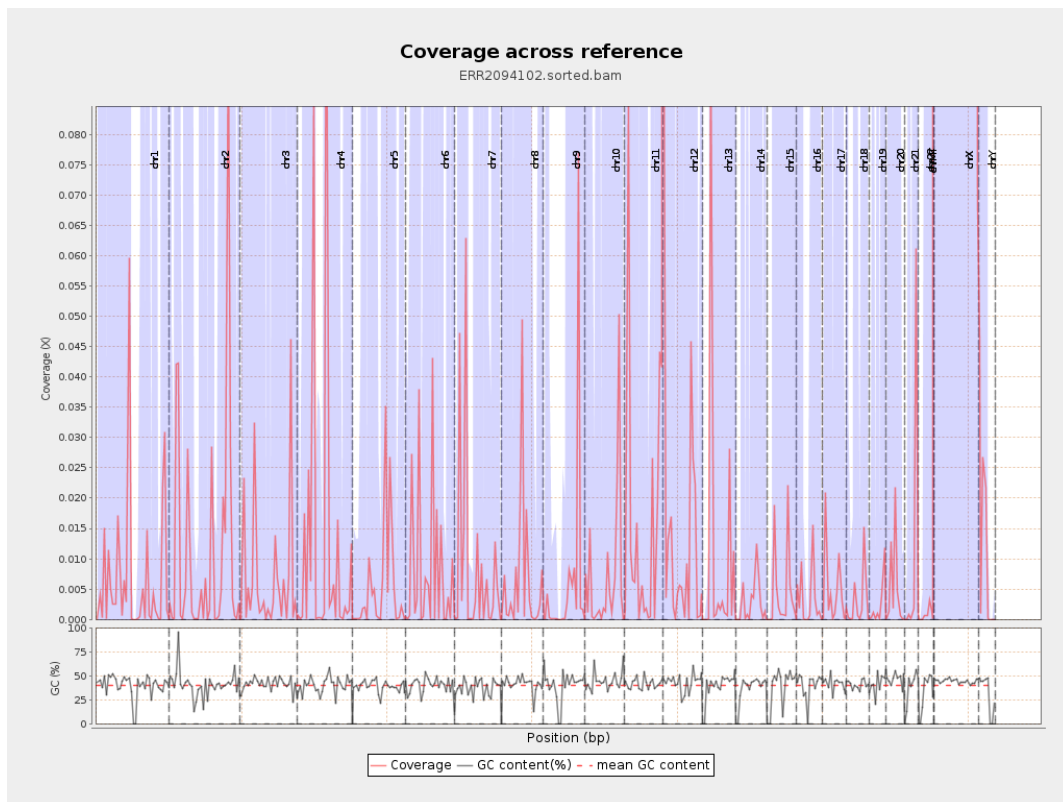
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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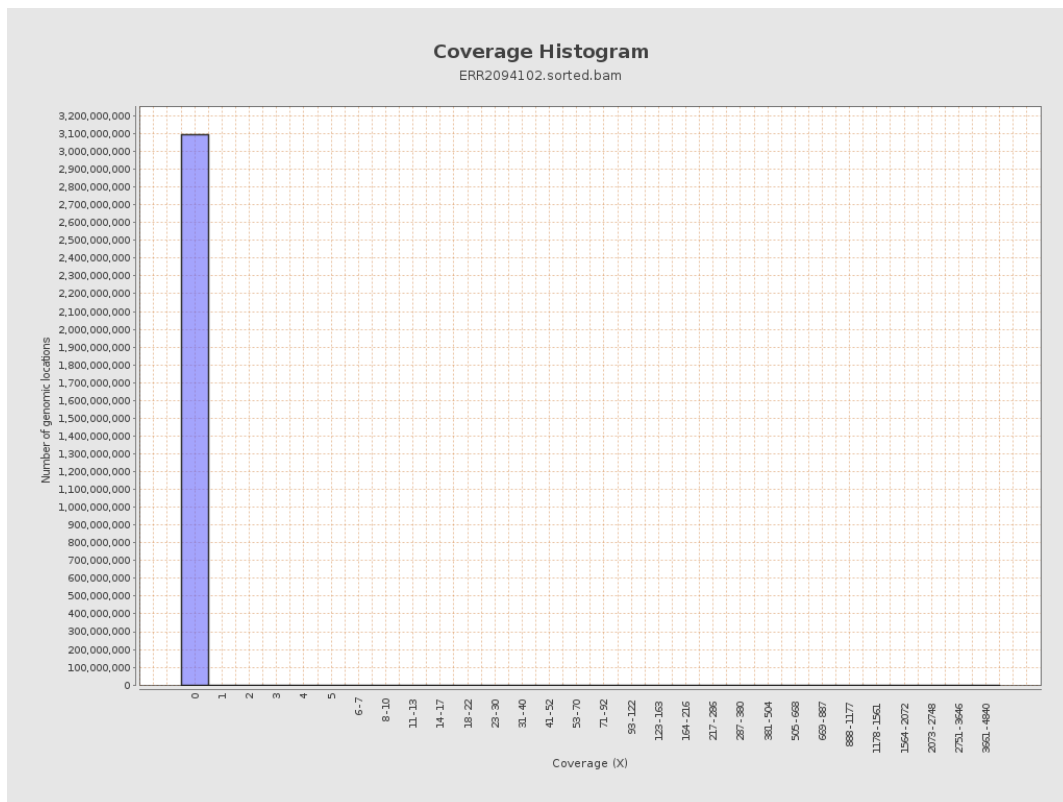
		bases	coverage	deviation
chr1	249250621	1695030	0.0068	2.6851
chr2	243199373	2697869	0.0111	4.3692
chr3	198022430	1326385	0.0067	2.5032
chr4	191154276	2321471	0.0121	3.8964
chr5	180915260	945272	0.0052	2.3207
chr6	171115067	1356682	0.0079	2.671
chr7	159138663	1414401	0.0089	2.9899
chr8	146364022	962814	0.0066	1.8727
chr9	141213431	871429	0.0062	3.5194
chr10	135534747	998851	0.0074	2.5892
chr11	135006516	2457606	0.0182	4.9367
chr12	133851895	1913716	0.0143	5.0331
chr13	115169878	1119003	0.0097	2.6899
chr14	107349540	297856	0.0028	1.0372
chr15	102531392	476833	0.0047	1.2115
chr16	90354753	286253	0.0032	1.0966
chr17	81195210	361448	0.0045	1.1451
chr18	78077248	243469	0.0031	1.1859
chr19	59128983	142930	0.0024	0.8362
chr20	63025520	335686	0.0053	1.6974
chr21	48129895	500526	0.0104	4.7327
chr22	51304566	47387	0.0009	0.2536
chrMT	16571	388777	23.4613	144.304
chrX	155270560	30533079	0.1966	13.2416

chrY	59373566	628357	0.0106	2.7617
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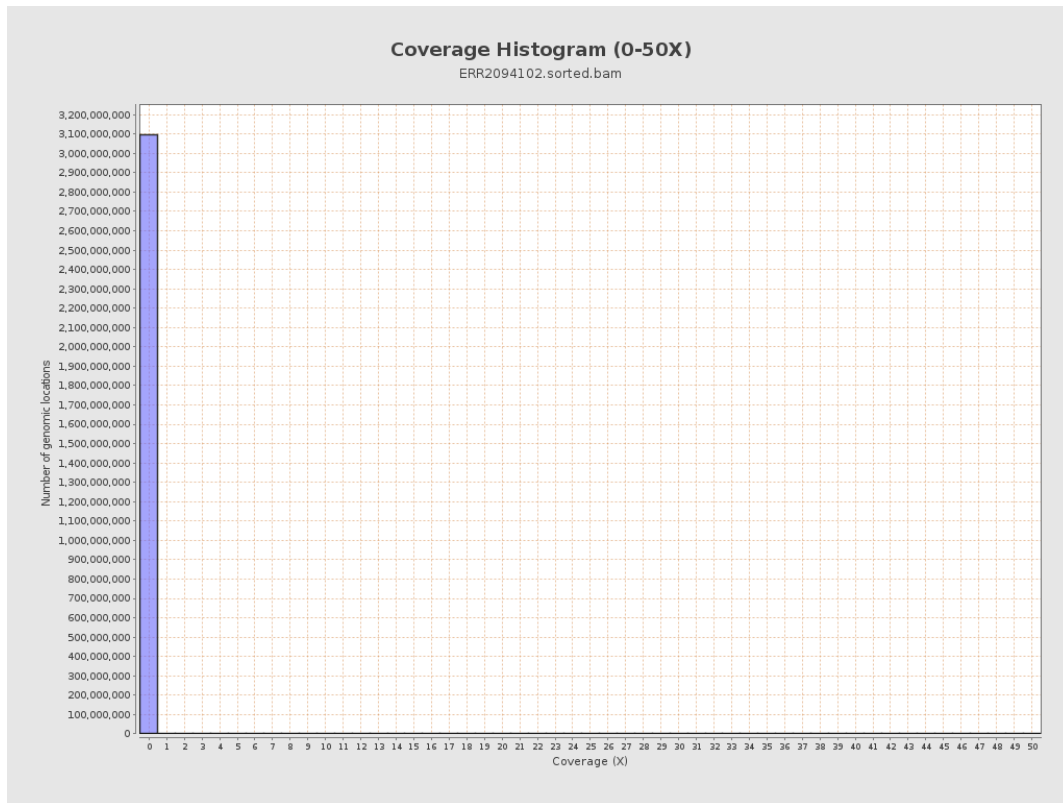
3. Results : Coverage across reference



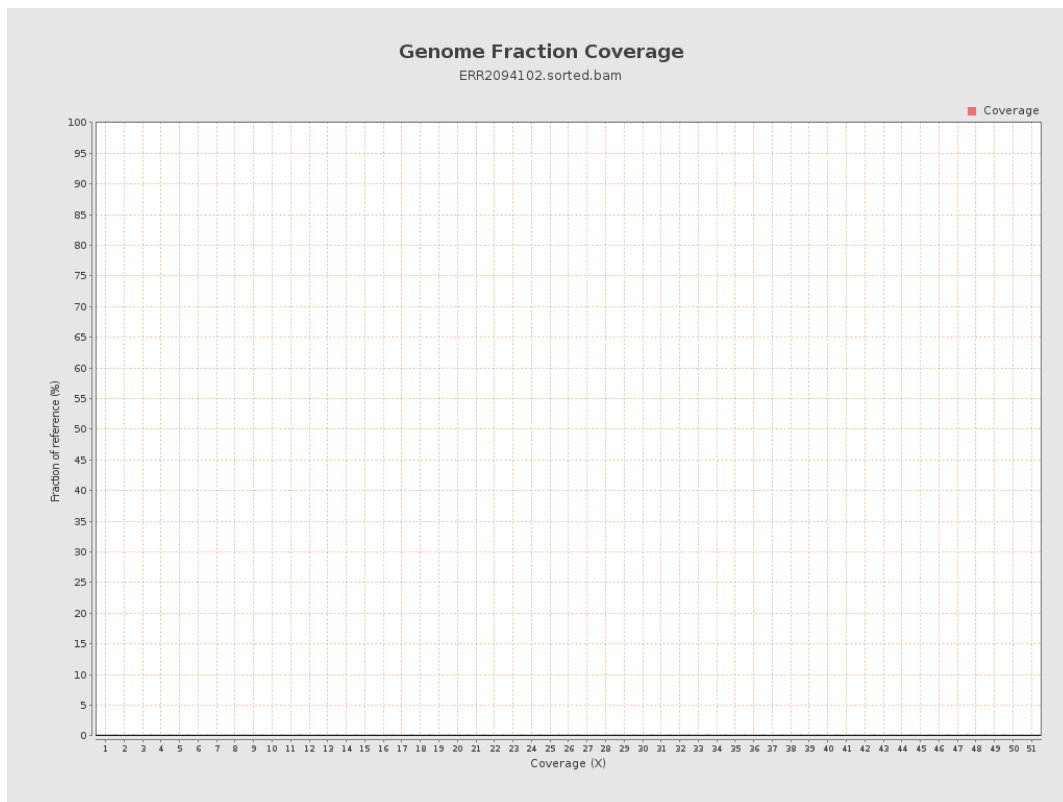
4. Results : Coverage Histogram



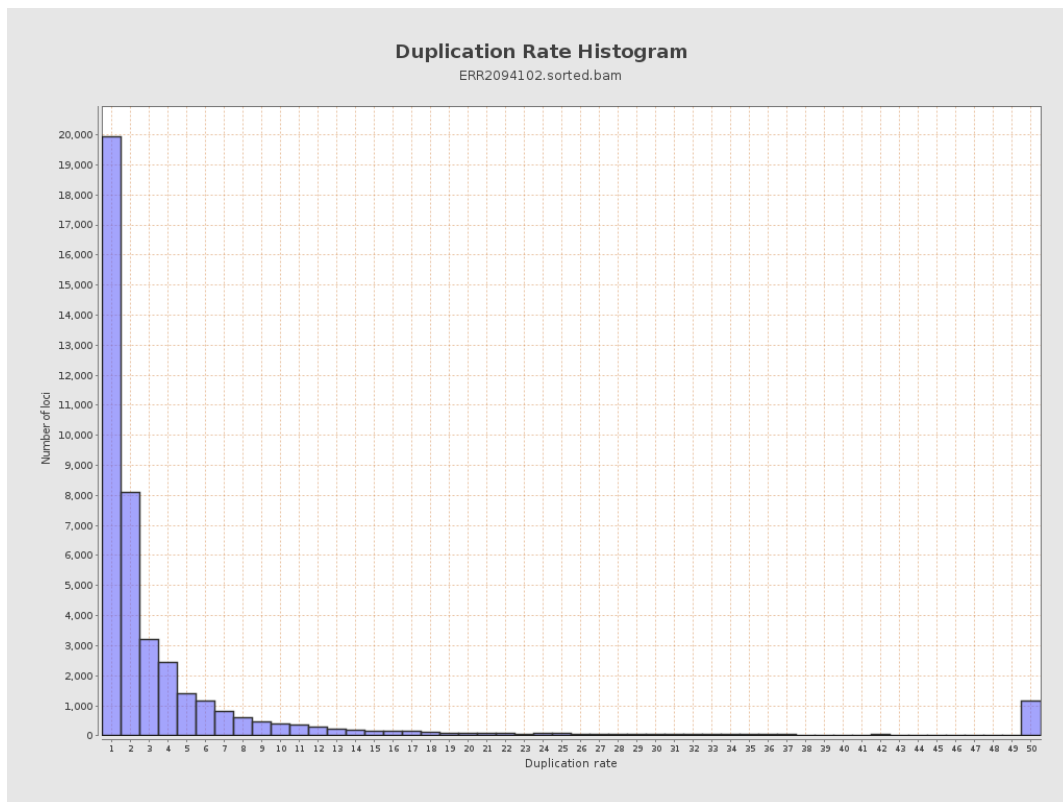
5. Results : Coverage Histogram (0-50X)



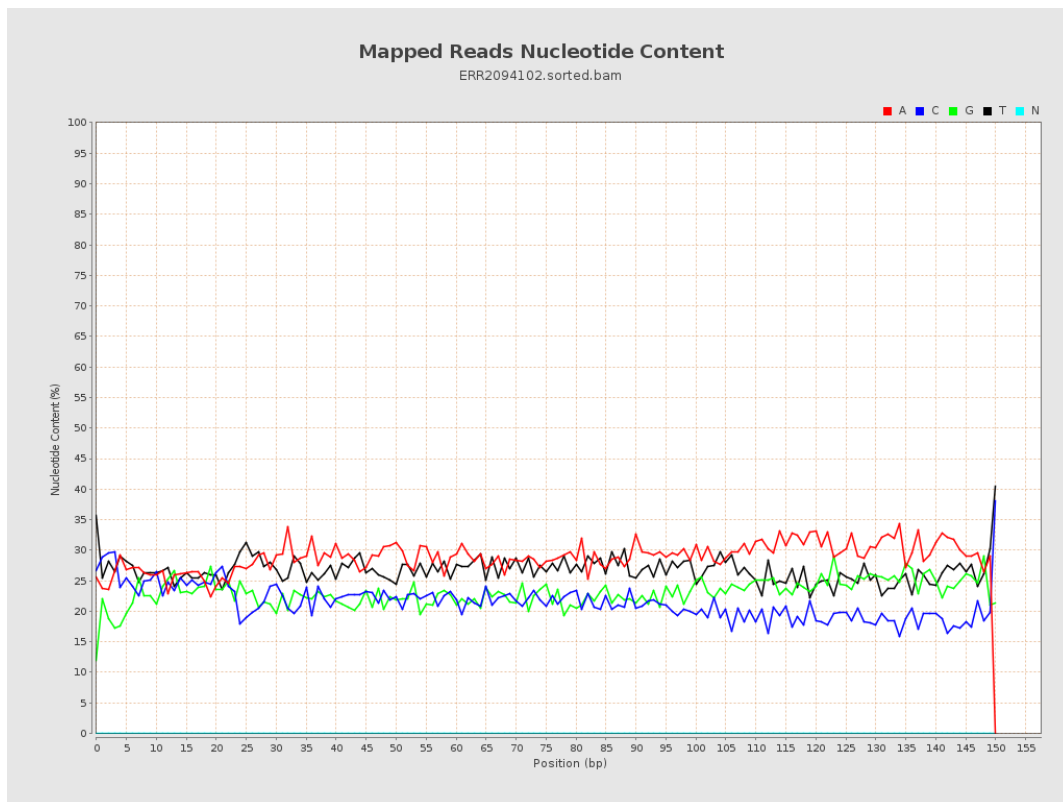
6. Results : Genome Fraction Coverage



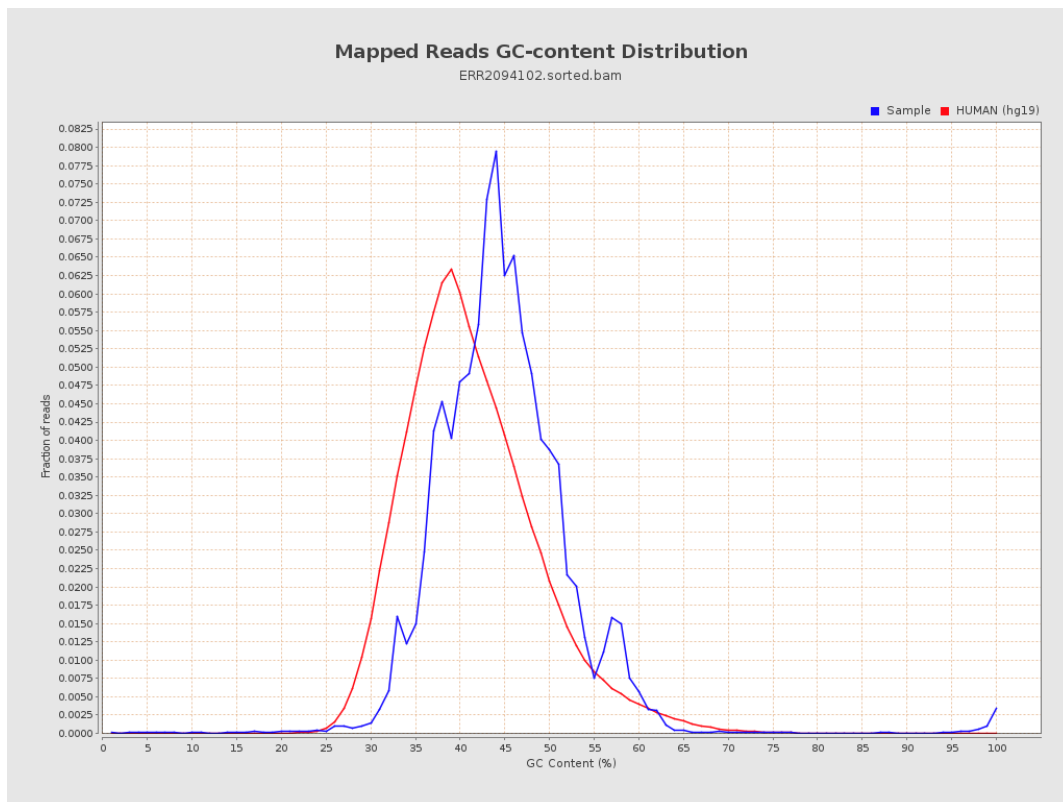
7. Results : Duplication Rate Histogram



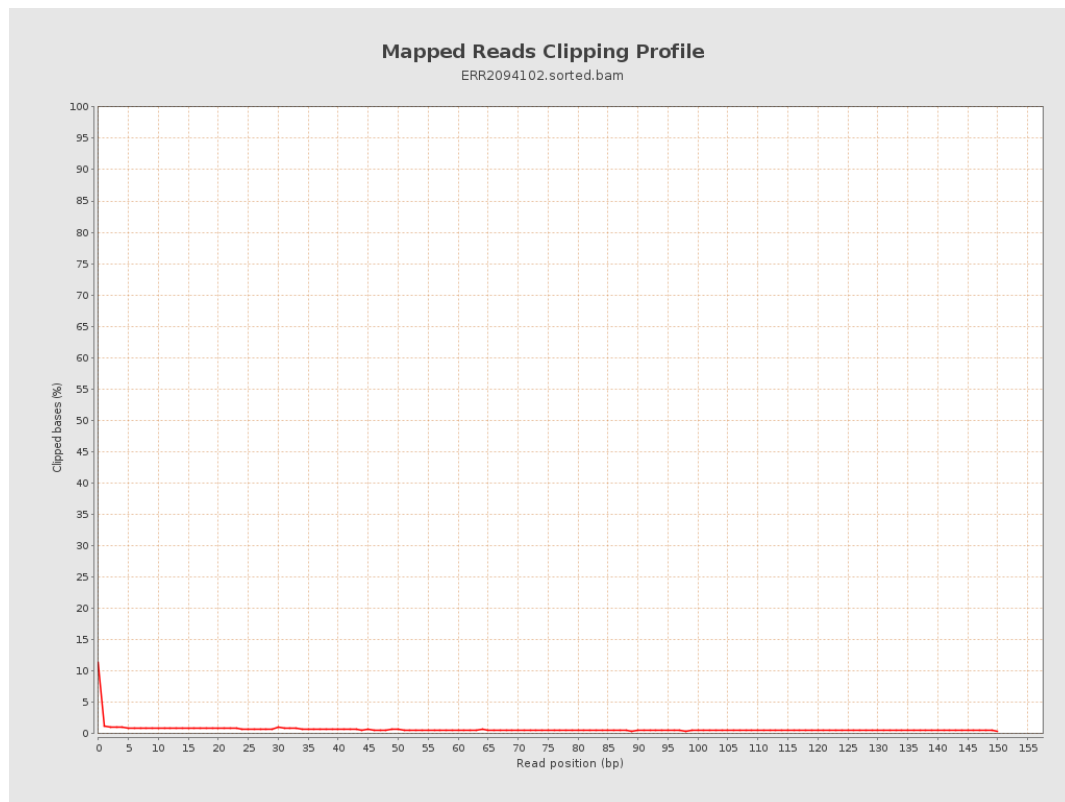
8. Results : Mapped Reads Nucleotide Content



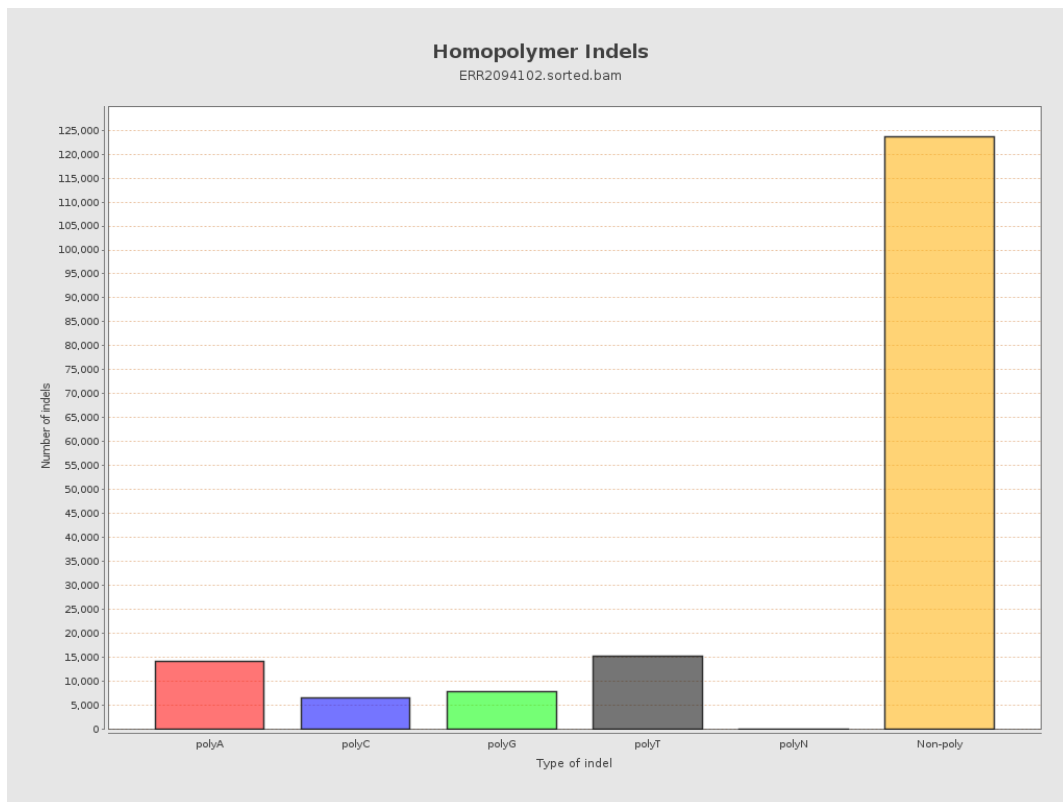
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



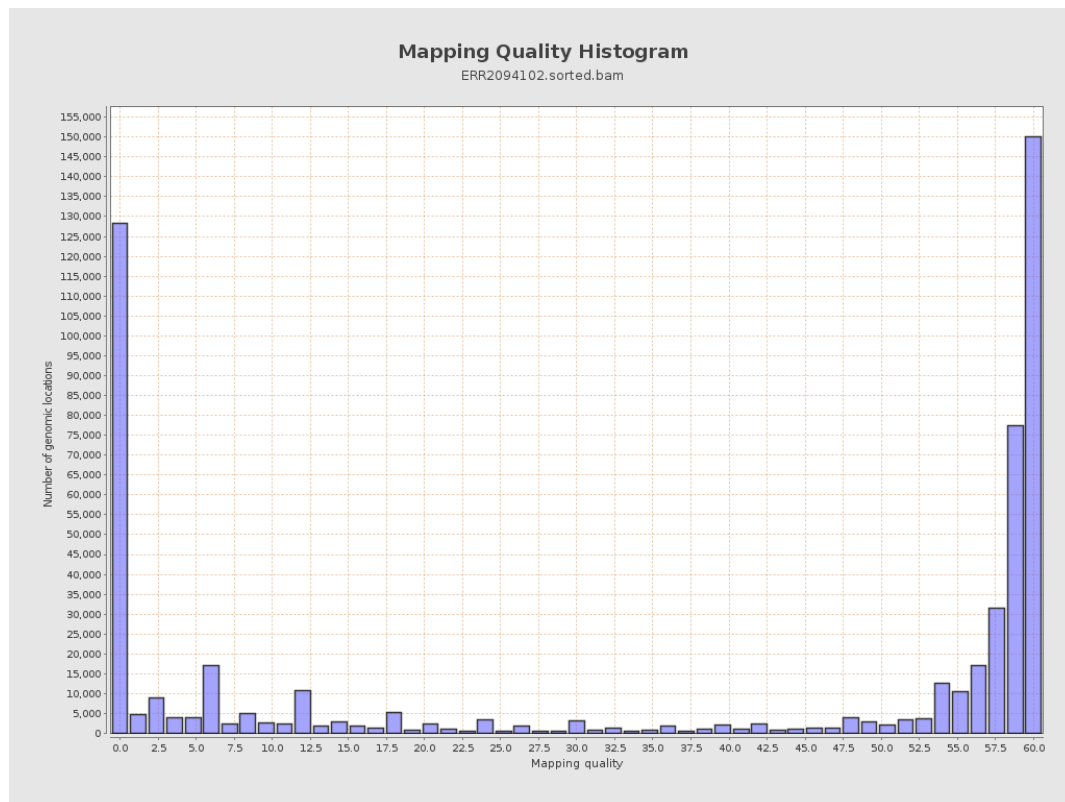
11. Results : Homopolymer Indels



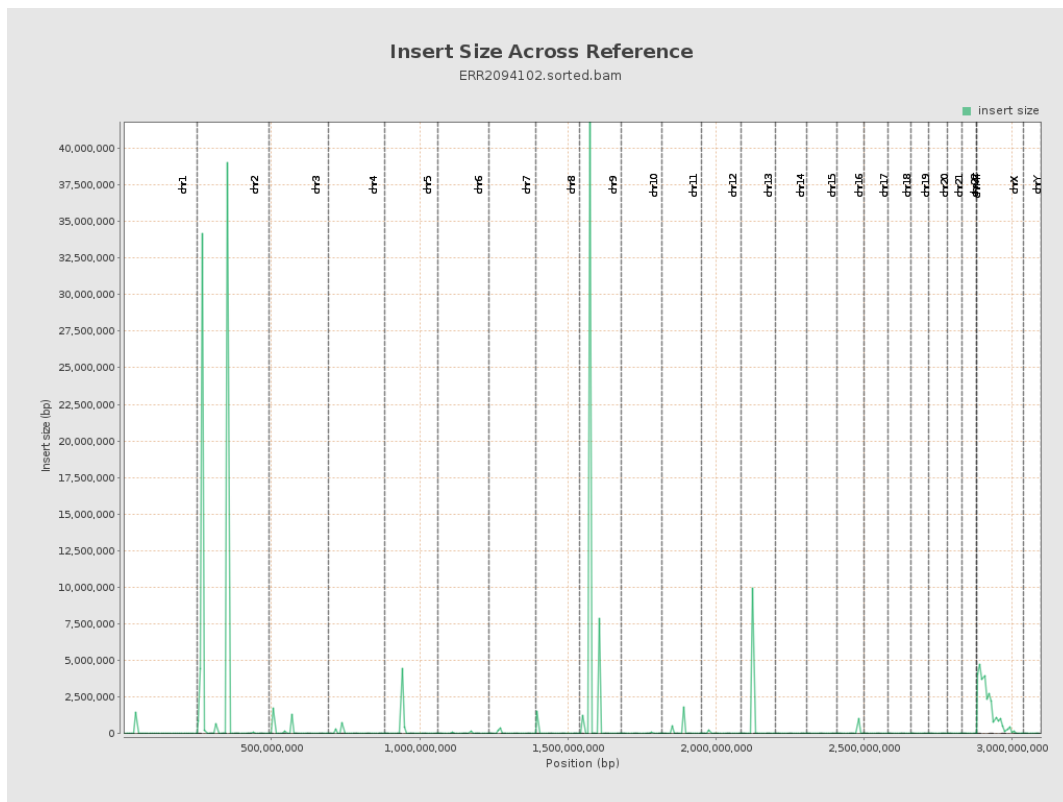
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

