

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:50:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094038.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_ERR2094038 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094038_1.fastq.gz ERR2094038_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:50:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	441,680
Mapped reads	420,893 / 95.29%
Unmapped reads	20,787 / 4.71%
Mapped paired reads	420,893 / 95.29%
Mapped reads, first in pair	211,539 / 47.89%
Mapped reads, second in pair	209,354 / 47.4%
Mapped reads, both in pair	417,738 / 94.58%
Mapped reads, singletons	3,155 / 0.71%
Secondary alignments	0
Supplementary alignments	15,942 / 3.61%
Read min/max/mean length	30 / 151 / 139.78
Duplicated reads (estimated)	399,450 / 90.44%
Duplication rate	50.79%
Clipped reads	168,906 / 38.24%

2.2. ACGT Content

Number/percentage of A's	15,006,538 / 27.69%
Number/percentage of C's	12,005,180 / 22.15%
Number/percentage of T's	14,526,565 / 26.8%
Number/percentage of G's	12,662,999 / 23.36%
Number/percentage of N's	651 / 0%

GC Percentage	45.51%
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2.3. Coverage

Mean	0.018
Standard Deviation	4.4618

2.4. Mapping Quality

Mean Mapping Quality	41.19
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2.5. Insert size

Mean	550,381.2
Standard Deviation	6,692,990.69
P25/Median/P75	132 / 166 / 196

2.6. Mismatches and indels

General error rate	4.54%
Mismatches	2,392,937
Insertions	37,868
Mapped reads with at least one insertion	8.82%
Deletions	198,389
Mapped reads with at least one deletion	43.8%
Homopolymer indels	27.95%

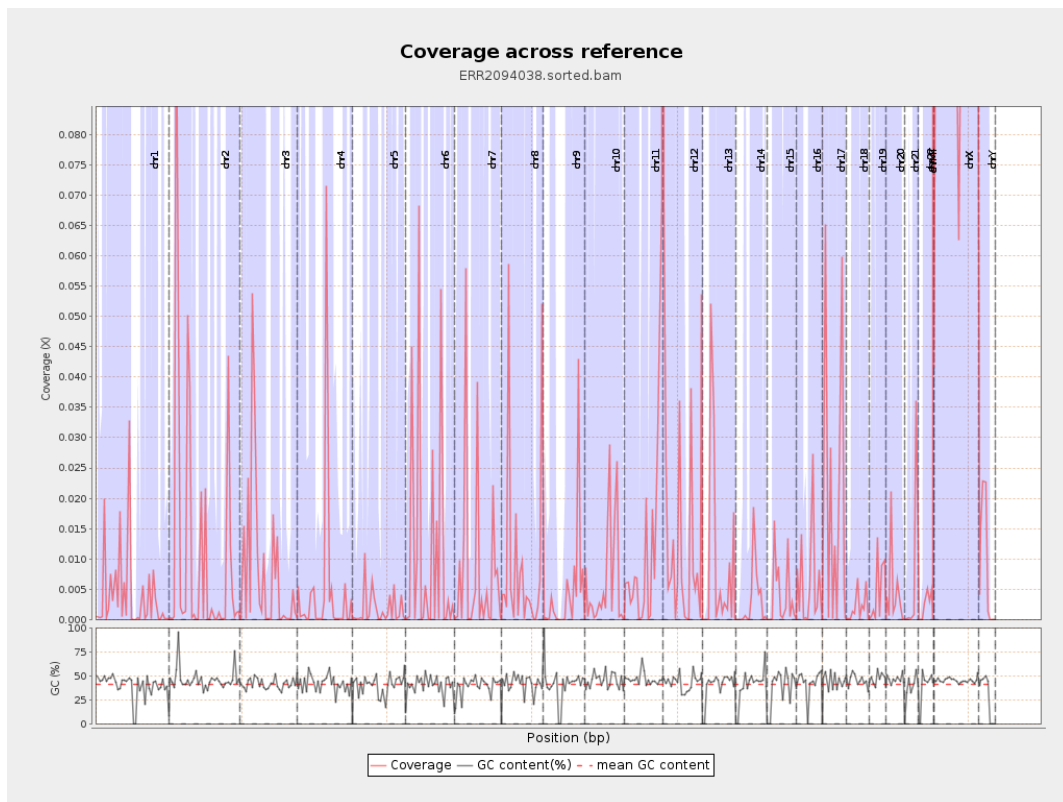
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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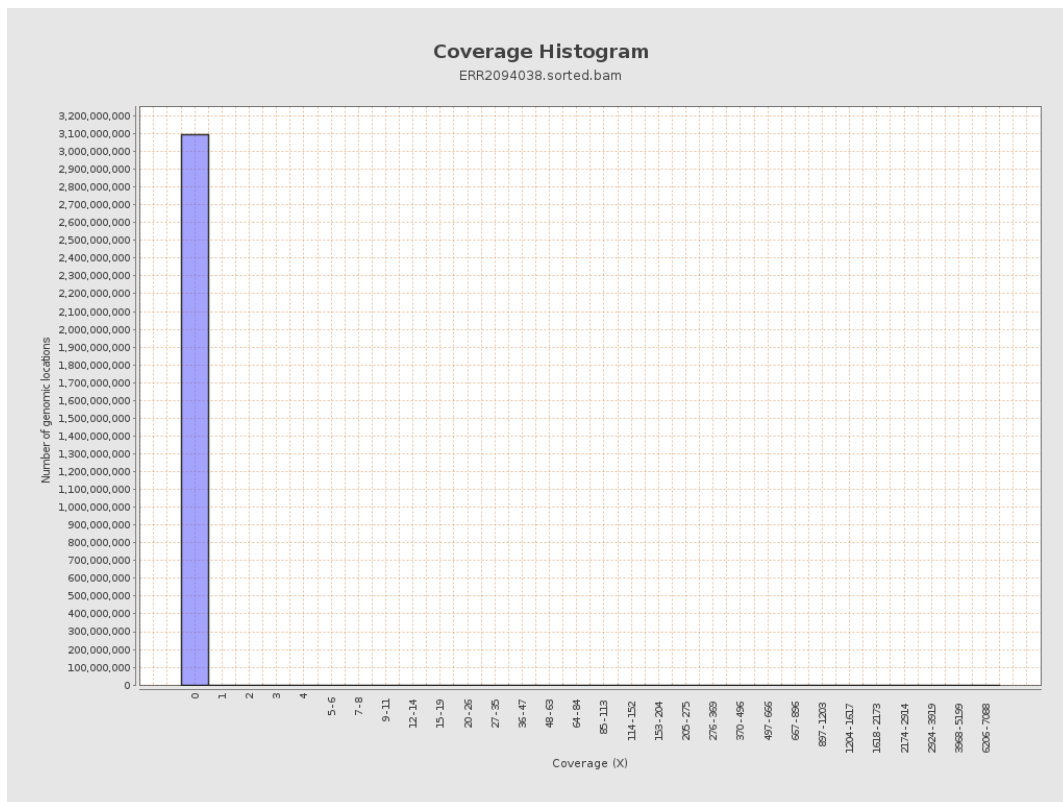
		bases	coverage	deviation
chr1	249250621	1002202	0.004	1.5301
chr2	243199373	2808256	0.0115	3.4999
chr3	198022430	1572903	0.0079	2.599
chr4	191154276	851799	0.0045	1.5677
chr5	180915260	324772	0.0018	0.59
chr6	171115067	1818992	0.0106	4.8098
chr7	159138663	1352077	0.0085	2.8186
chr8	146364022	1337241	0.0091	3.5211
chr9	141213431	660720	0.0047	1.9694
chr10	135534747	901073	0.0066	2.0236
chr11	135006516	1984108	0.0147	3.9738
chr12	133851895	1868943	0.014	3.8879
chr13	115169878	976773	0.0085	2.1962
chr14	107349540	316278	0.0029	1.2118
chr15	102531392	398252	0.0039	0.9719
chr16	90354753	516280	0.0057	2.1081
chr17	81195210	1609666	0.0198	4.8387
chr18	78077248	154519	0.002	0.605
chr19	59128983	268511	0.0045	1.2199
chr20	63025520	287711	0.0046	1.6827
chr21	48129895	359220	0.0075	2.6918
chr22	51304566	123636	0.0024	0.5301
chrMT	16571	3555860	214.5833	880.0462
chrX	155270560	30101287	0.1939	13.0139

chrY	59373566	500732	0.0084	1.9807
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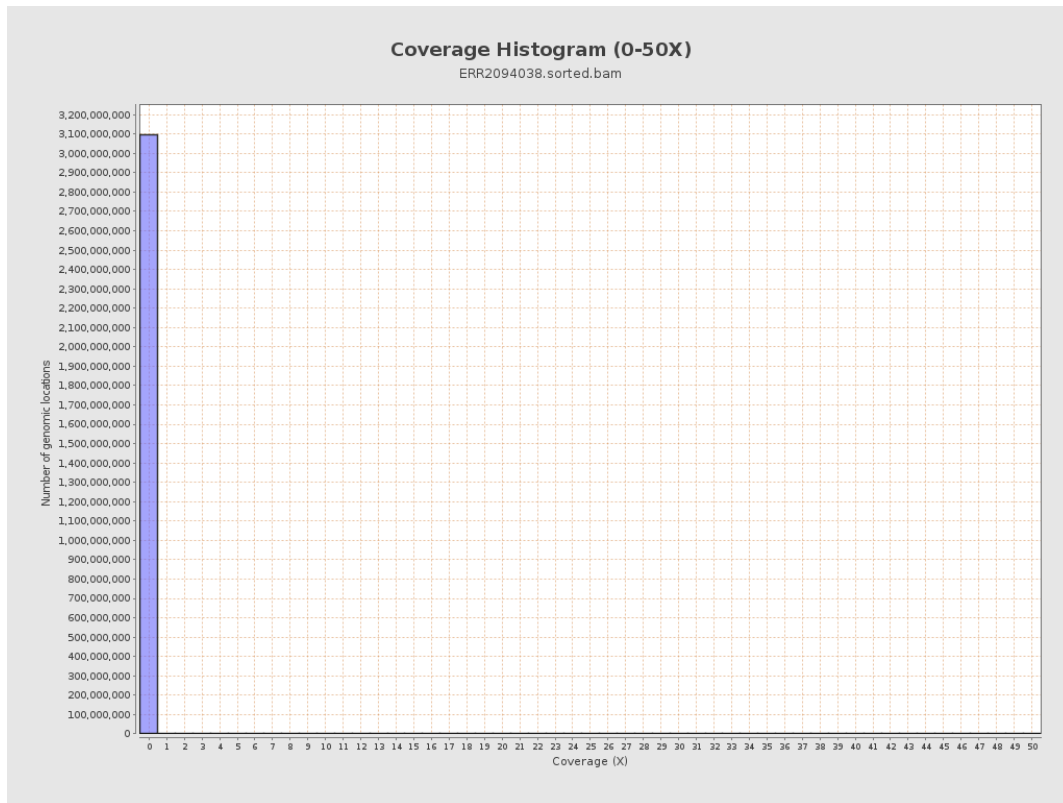
3. Results : Coverage across reference



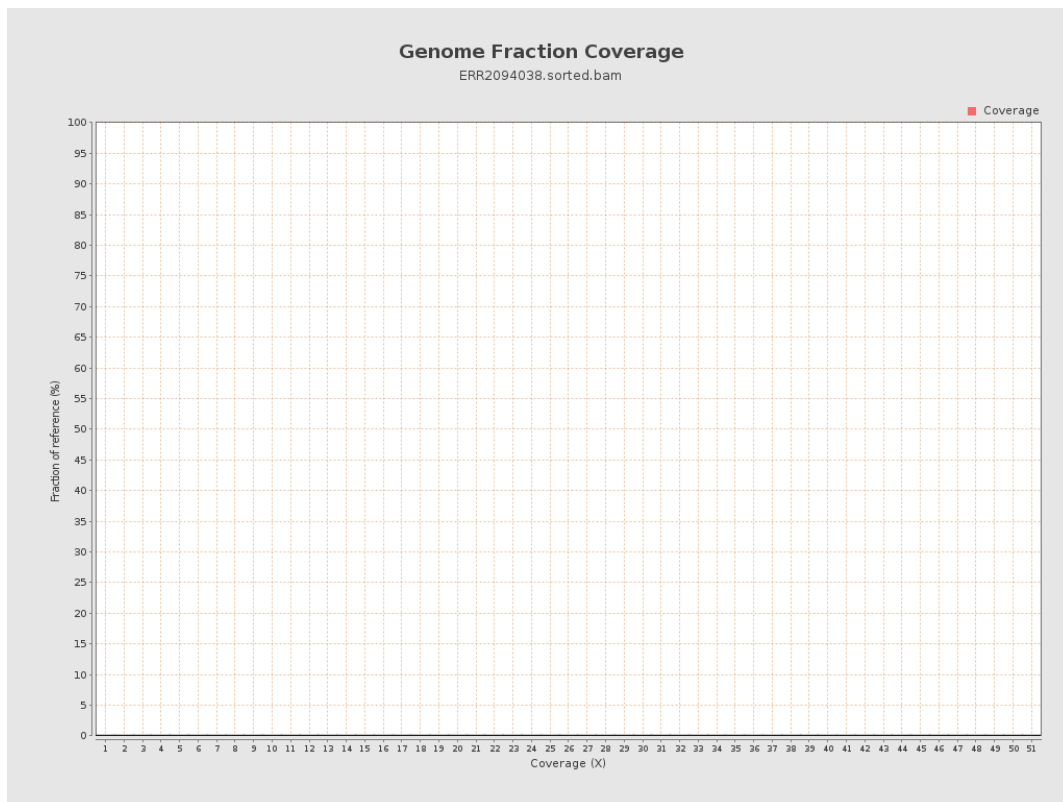
4. Results : Coverage Histogram



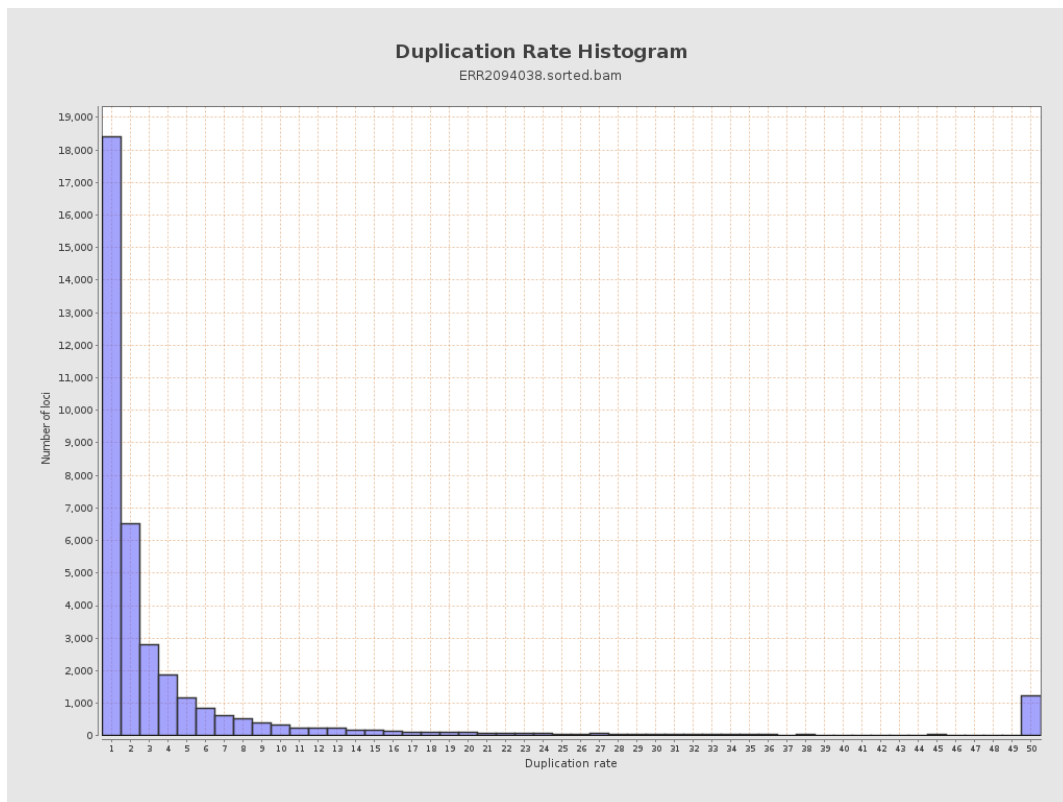
5. Results : Coverage Histogram (0-50X)



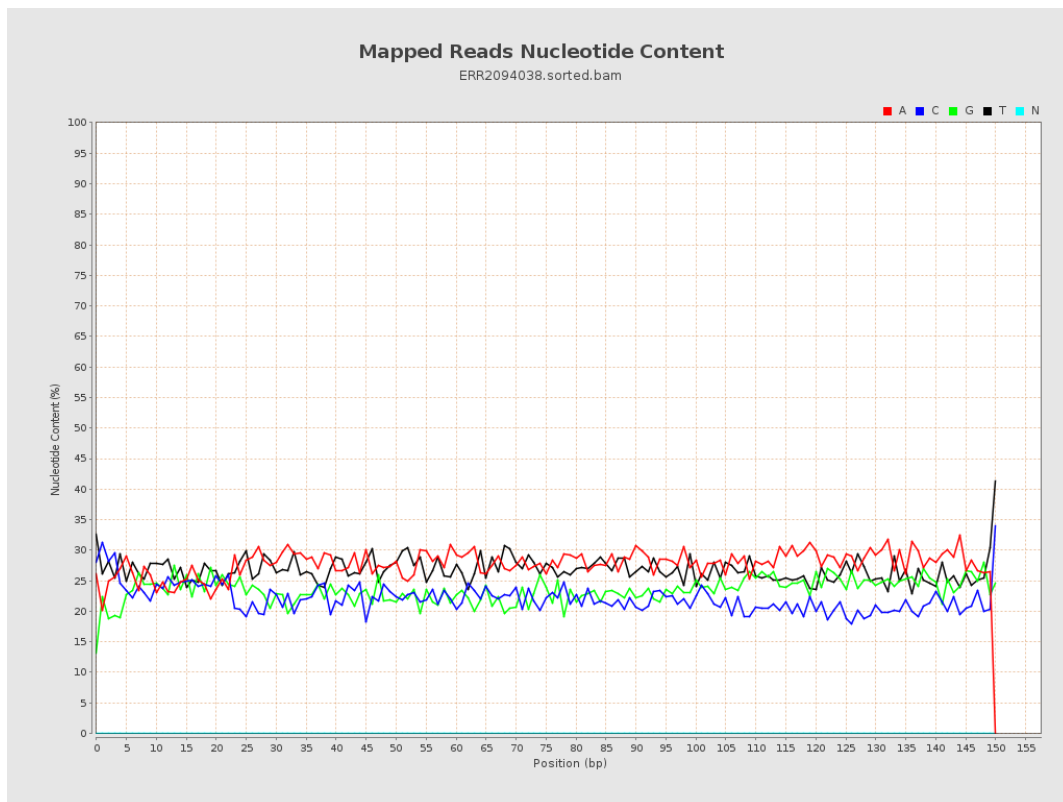
6. Results : Genome Fraction Coverage



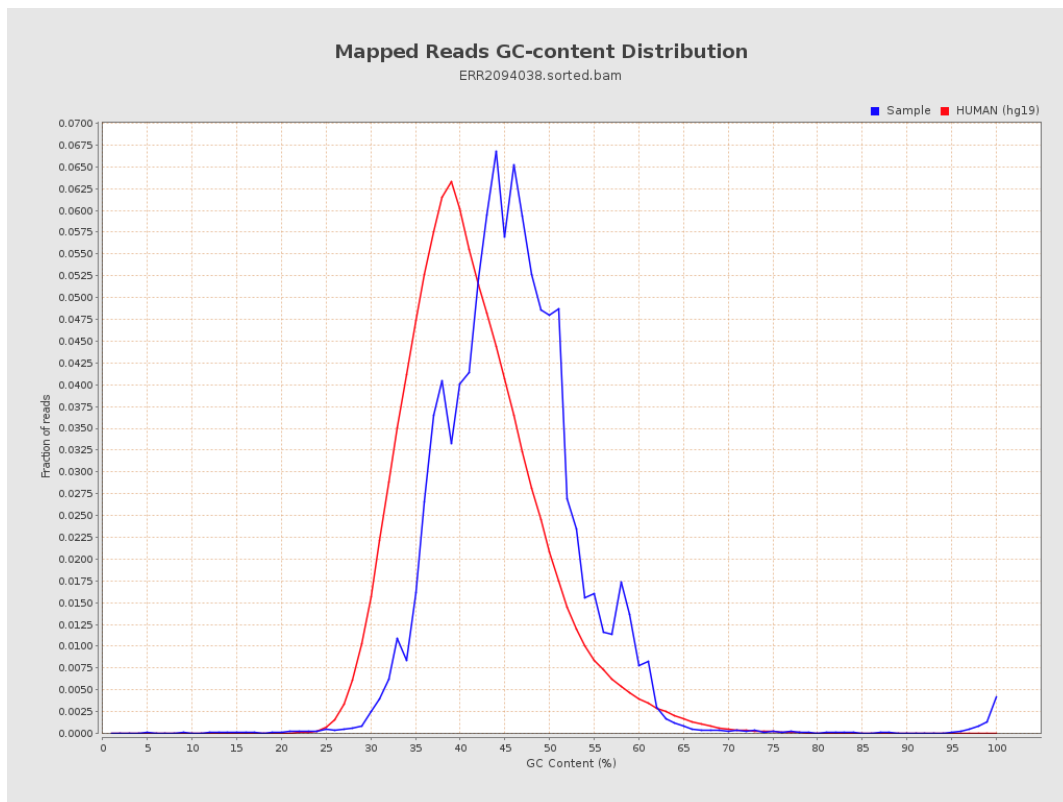
7. Results : Duplication Rate Histogram



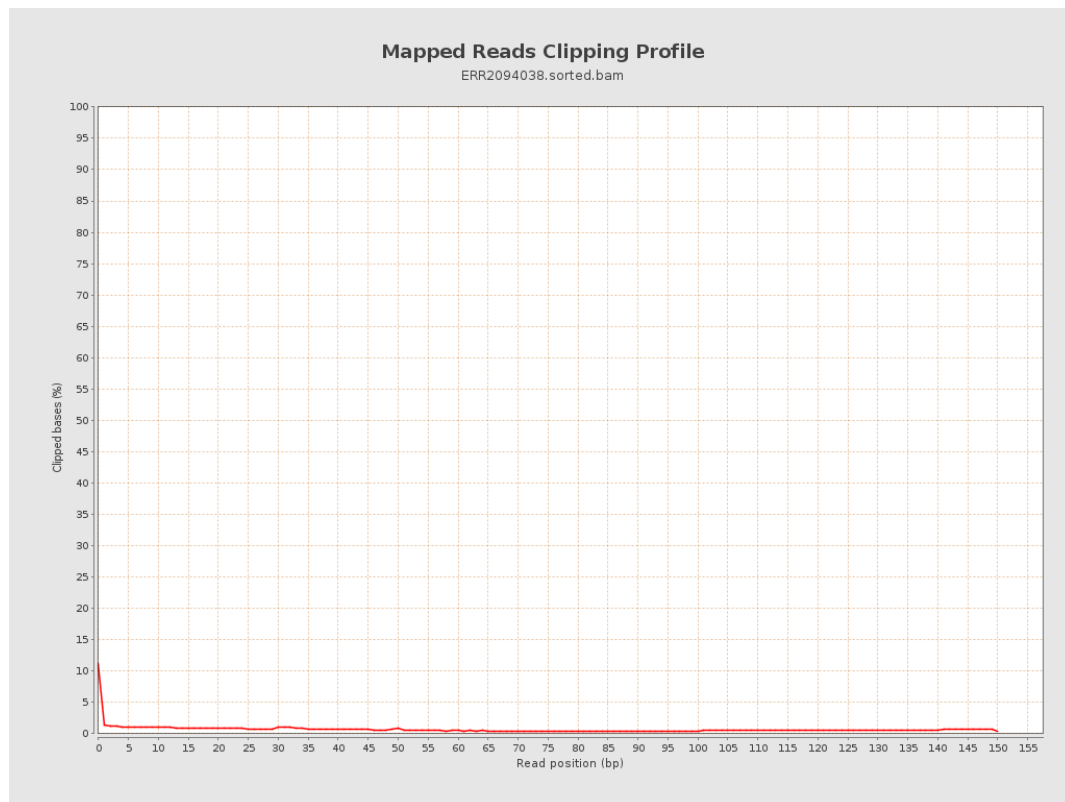
8. Results : Mapped Reads Nucleotide Content



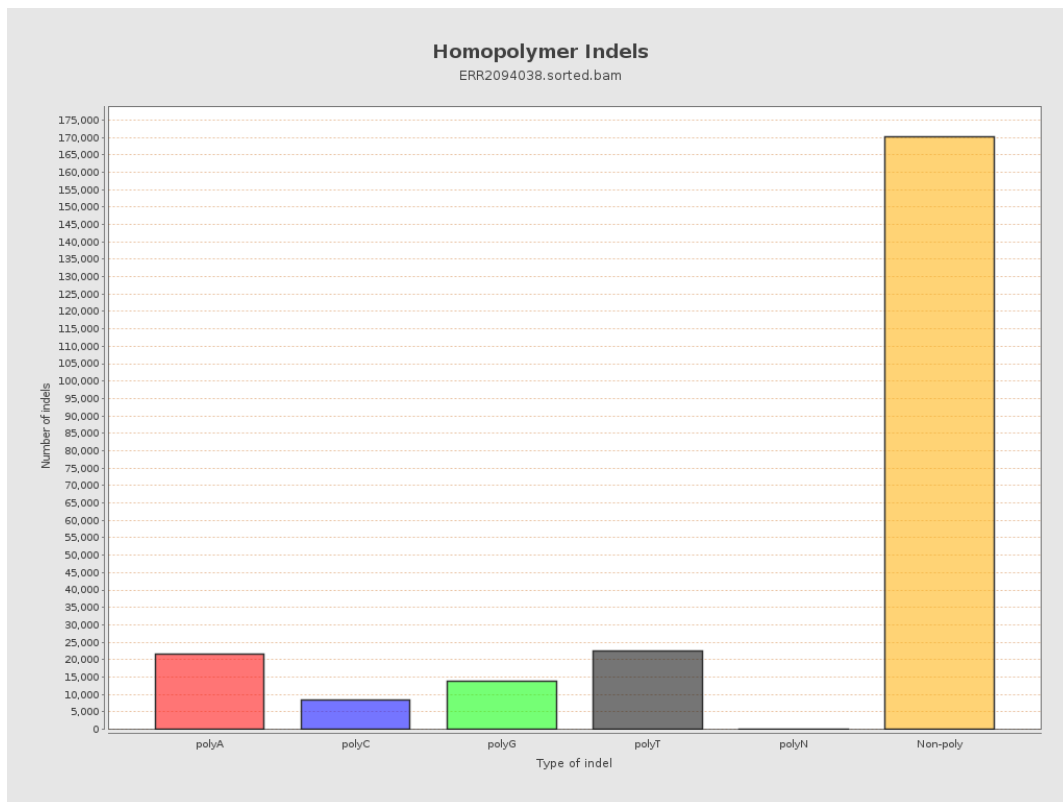
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



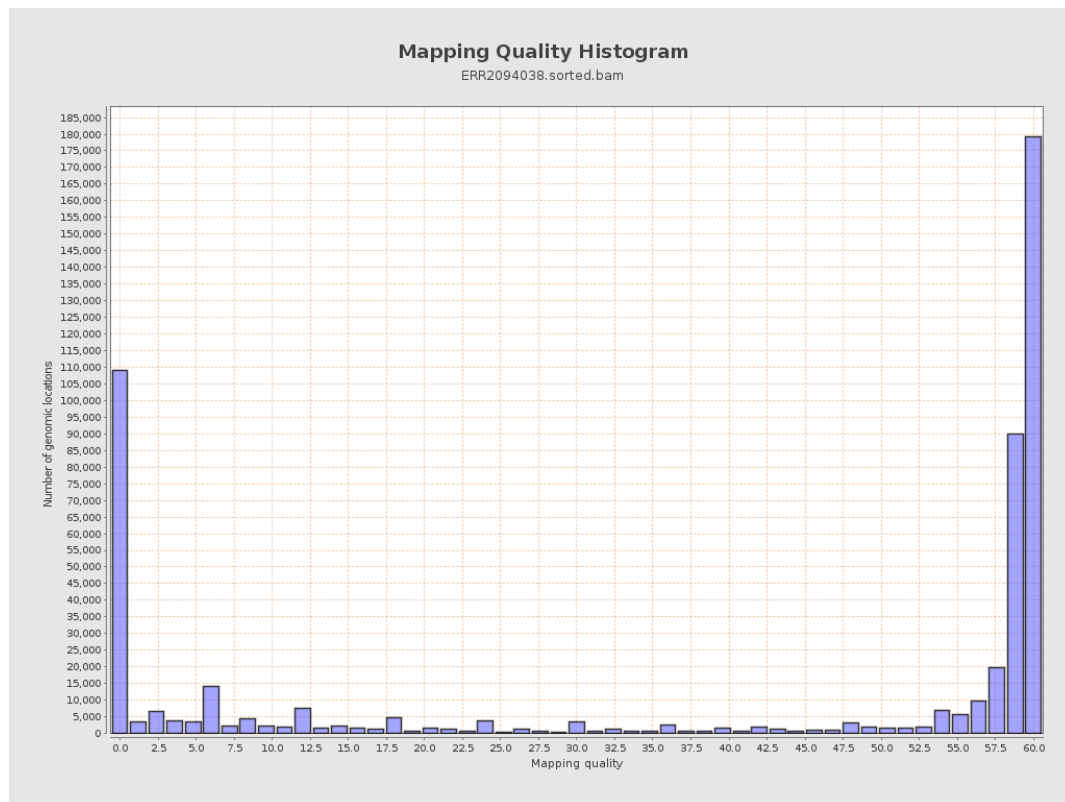
11. Results : Homopolymer Indels



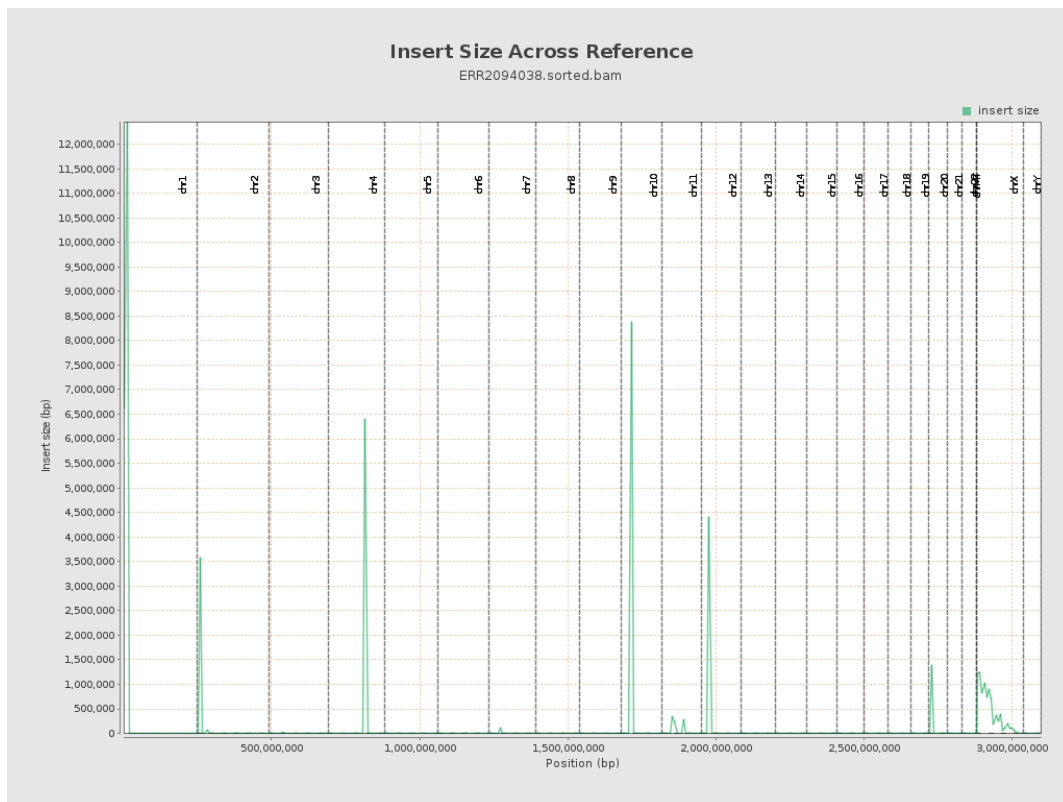
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

