

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:11:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094047.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_ERR2094047 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094047_1.fastq.gz ERR2094047_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:11:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	471,330
Mapped reads	440,186 / 93.39%
Unmapped reads	31,144 / 6.61%
Mapped paired reads	440,186 / 93.39%
Mapped reads, first in pair	221,061 / 46.9%
Mapped reads, second in pair	219,125 / 46.49%
Mapped reads, both in pair	436,950 / 92.71%
Mapped reads, singletons	3,236 / 0.69%
Secondary alignments	0
Supplementary alignments	15,403 / 3.27%
Read min/max/mean length	30 / 151 / 136.63
Duplicated reads (estimated)	416,965 / 88.47%
Duplication rate	50.37%
Clipped reads	183,921 / 39.02%

2.2. ACGT Content

Number/percentage of A's	15,655,239 / 28.09%
Number/percentage of C's	12,287,109 / 22.05%
Number/percentage of T's	14,962,855 / 26.85%
Number/percentage of G's	12,817,645 / 23%
Number/percentage of N's	565 / 0%

GC Percentage	45.05%
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2.3. Coverage

Mean	0.0185
Standard Deviation	4.507

2.4. Mapping Quality

Mean Mapping Quality	42.23
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2.5. Insert size

Mean	402,099.56
Standard Deviation	5,494,323.72
P25/Median/P75	126 / 164 / 189

2.6. Mismatches and indels

General error rate	4.7%
Mismatches	2,548,814
Insertions	41,686
Mapped reads with at least one insertion	9.33%
Deletions	205,104
Mapped reads with at least one deletion	43.52%
Homopolymer indels	29.03%

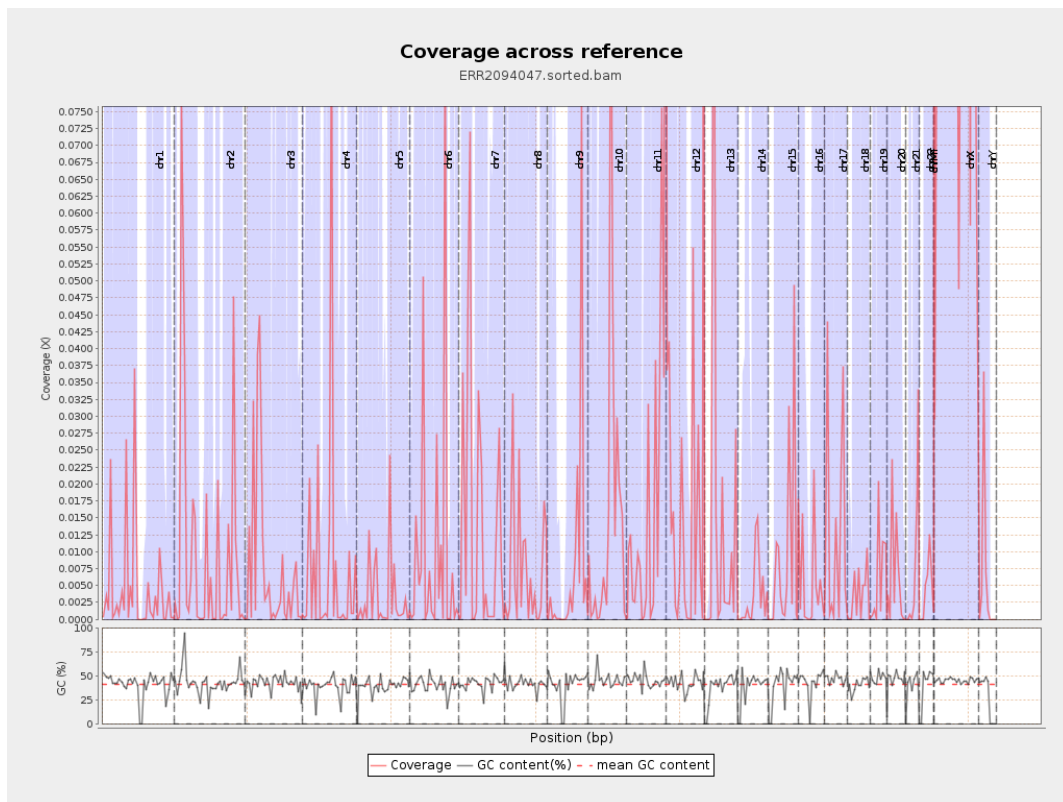
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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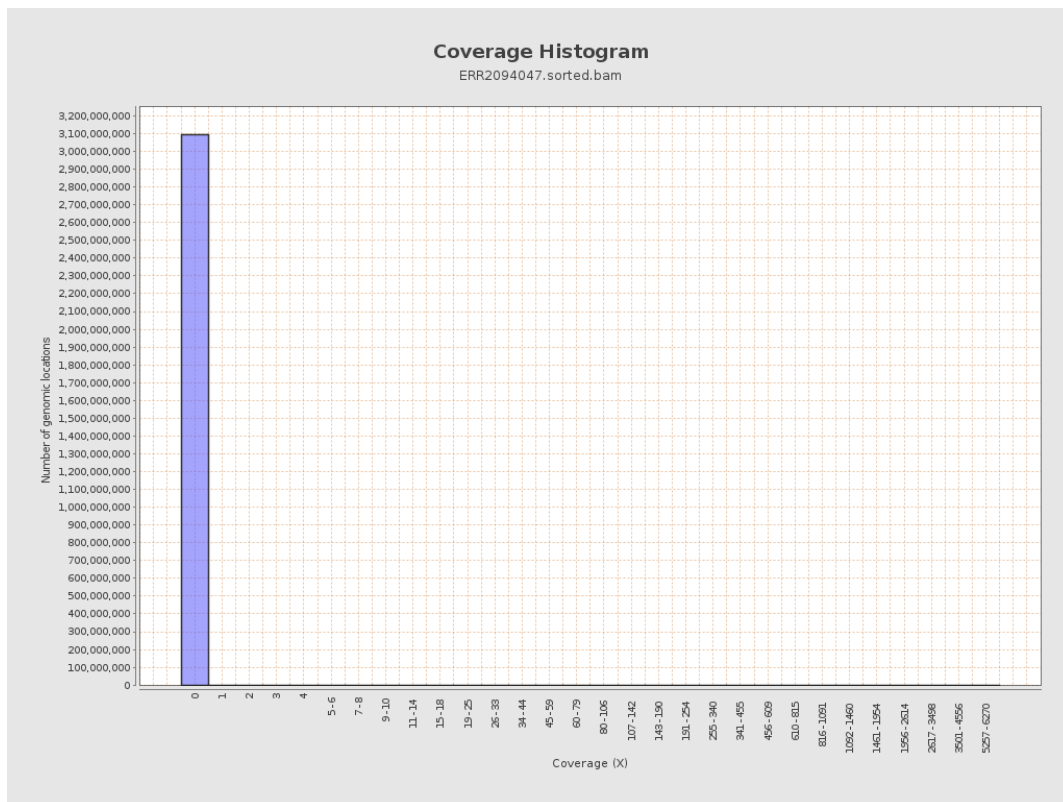
		bases	coverage	deviation
chr1	249250621	1095870	0.0044	1.9047
chr2	243199373	2248179	0.0092	2.7764
chr3	198022430	1479079	0.0075	2.3952
chr4	191154276	1529198	0.008	2.2055
chr5	180915260	597047	0.0033	1.372
chr6	171115067	1779134	0.0104	5.438
chr7	159138663	2157182	0.0136	4.0134
chr8	146364022	1041639	0.0071	2.064
chr9	141213431	1030851	0.0073	2.8879
chr10	135534747	2094804	0.0155	4.8783
chr11	135006516	2278372	0.0169	4.4283
chr12	133851895	2159099	0.0161	4.2263
chr13	115169878	1548589	0.0134	3.3993
chr14	107349540	367358	0.0034	1.2053
chr15	102531392	894638	0.0087	2.3964
chr16	90354753	507589	0.0056	1.9347
chr17	81195210	1028858	0.0127	3.1598
chr18	78077248	282079	0.0036	0.8791
chr19	59128983	359985	0.0061	1.6985
chr20	63025520	413342	0.0066	2.0316
chr21	48129895	335210	0.007	1.9288
chr22	51304566	215397	0.0042	1.1702
chrMT	16571	2305623	139.136	568.7896
chrX	155270560	29166979	0.1878	13.9274

chrY	59373566	375244	0.0063	2.0117
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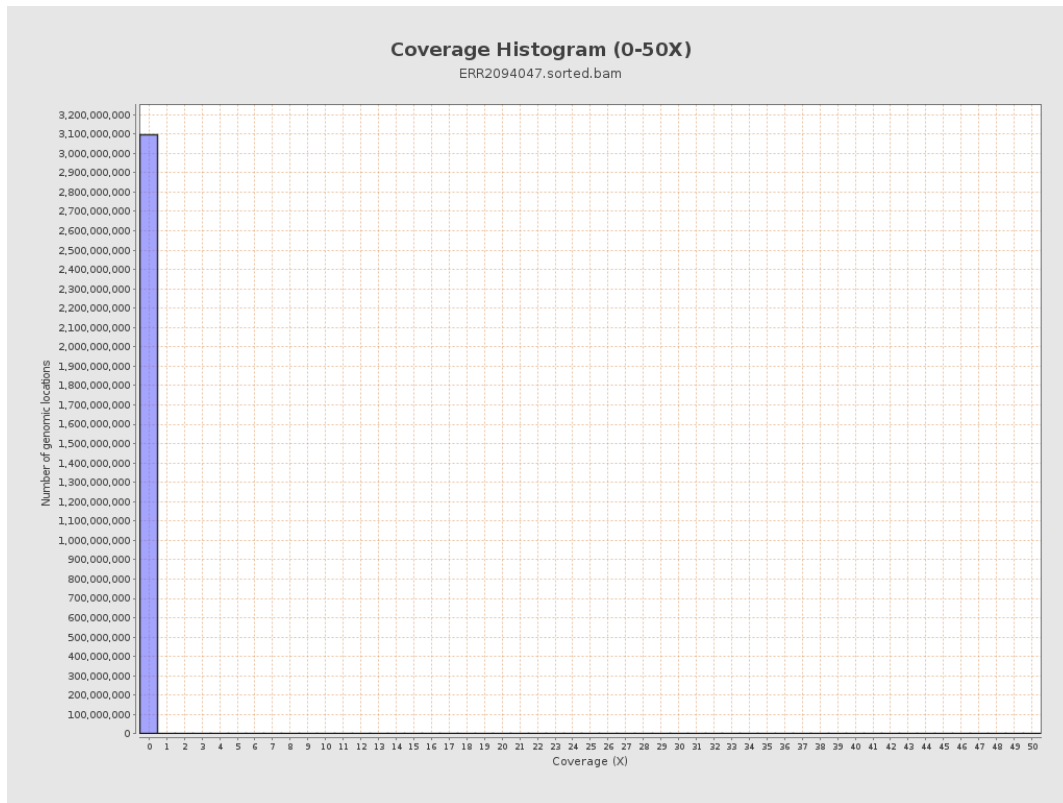
3. Results : Coverage across reference



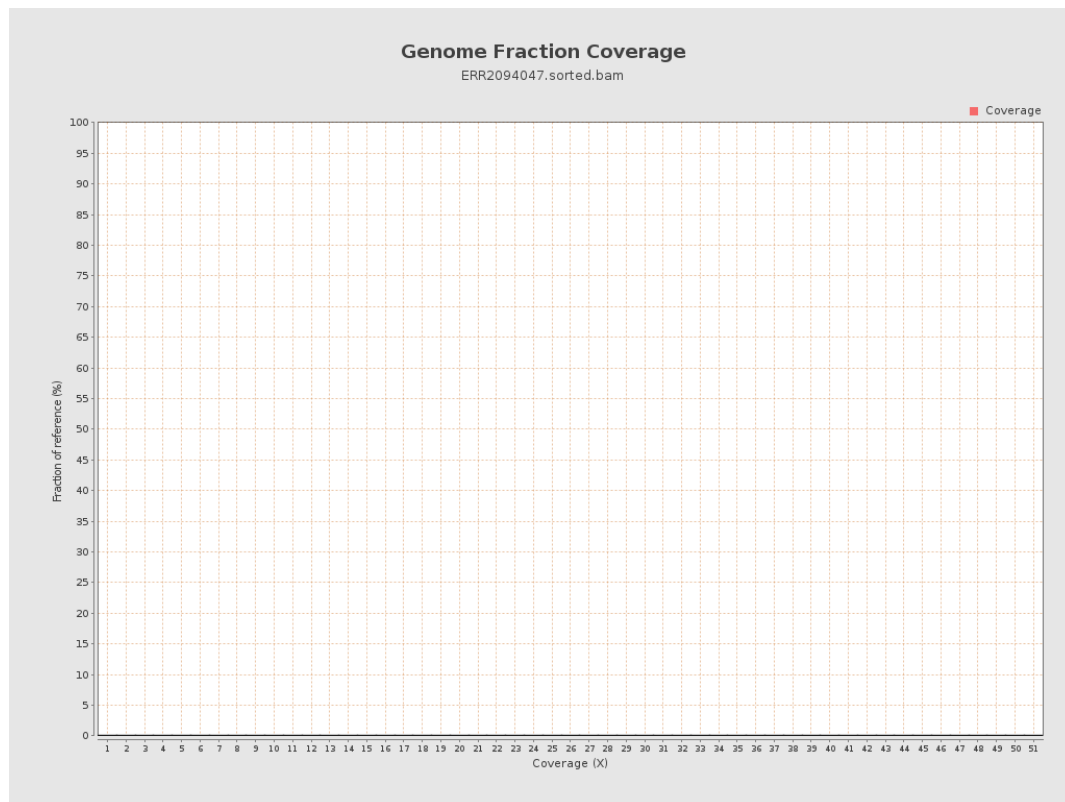
4. Results : Coverage Histogram



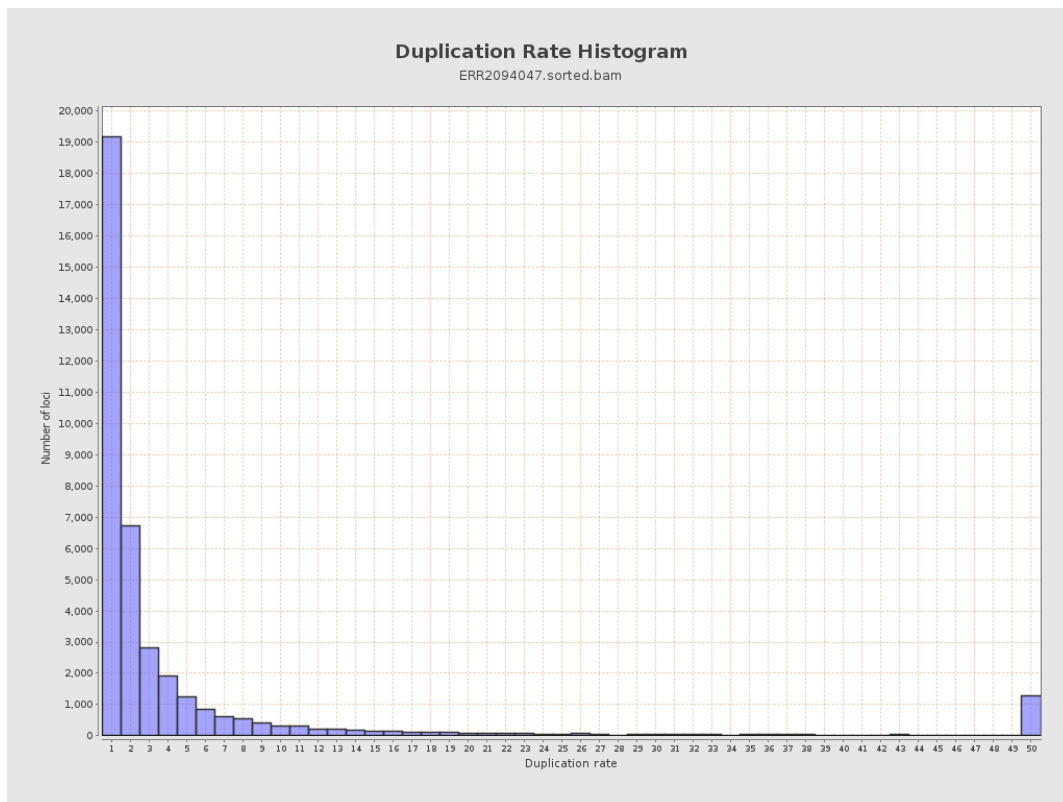
5. Results : Coverage Histogram (0-50X)



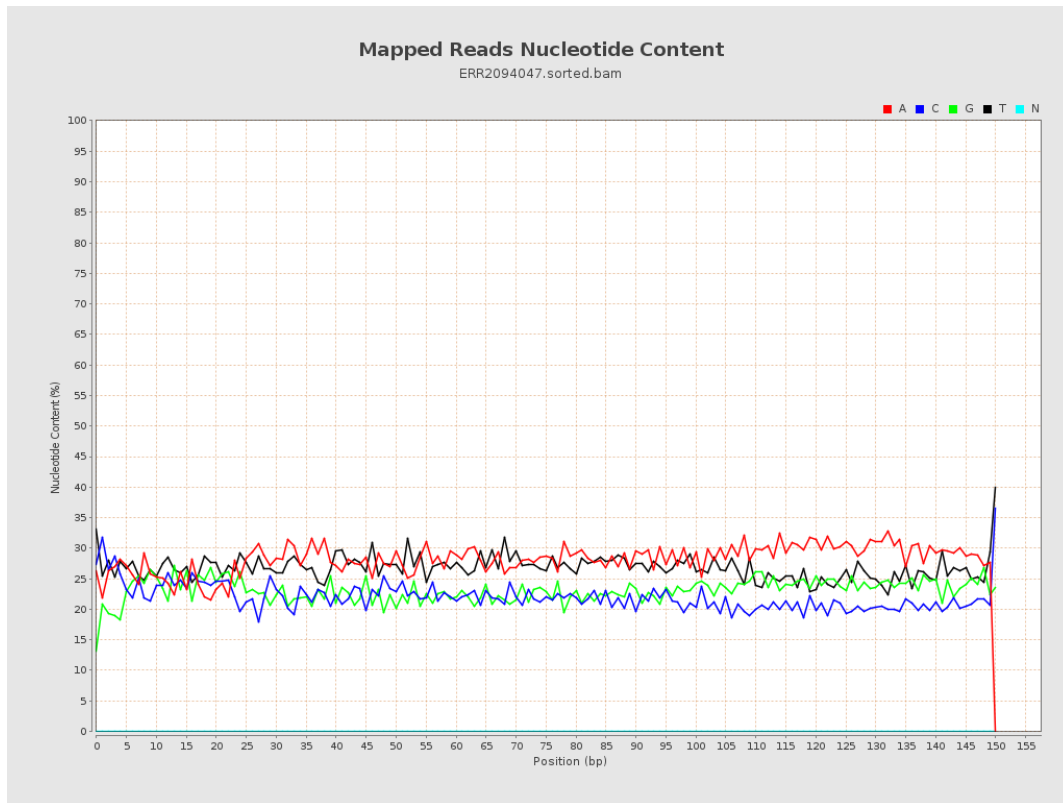
6. Results : Genome Fraction Coverage



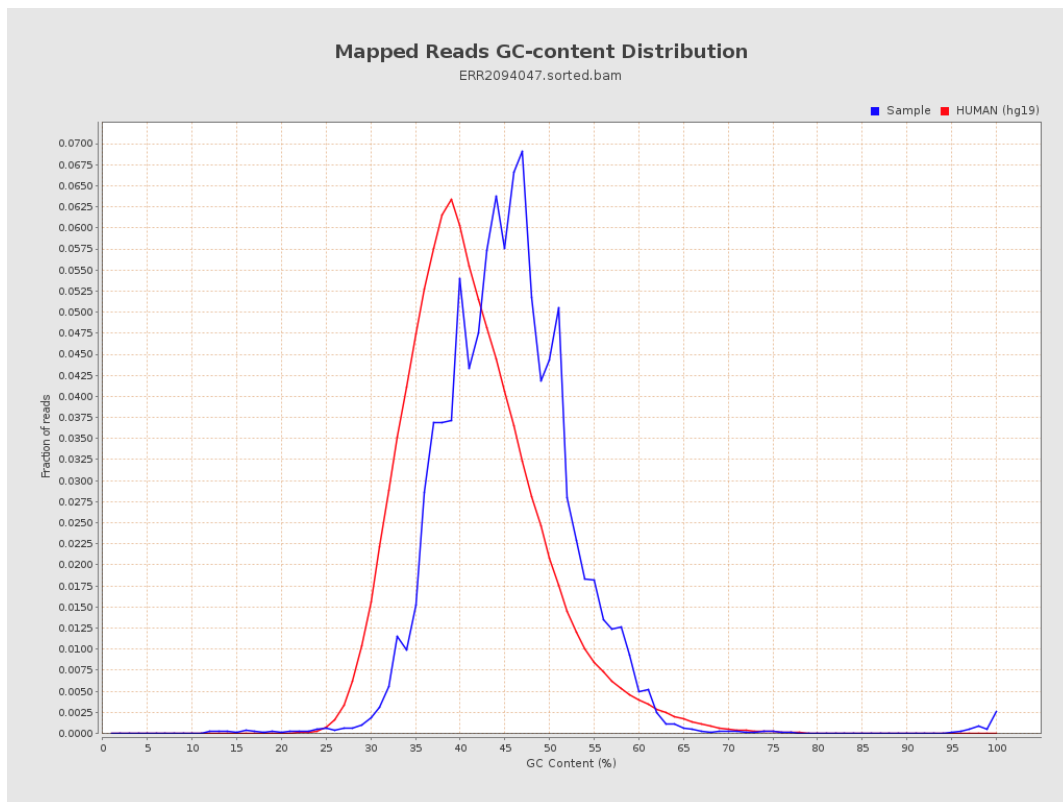
7. Results : Duplication Rate Histogram



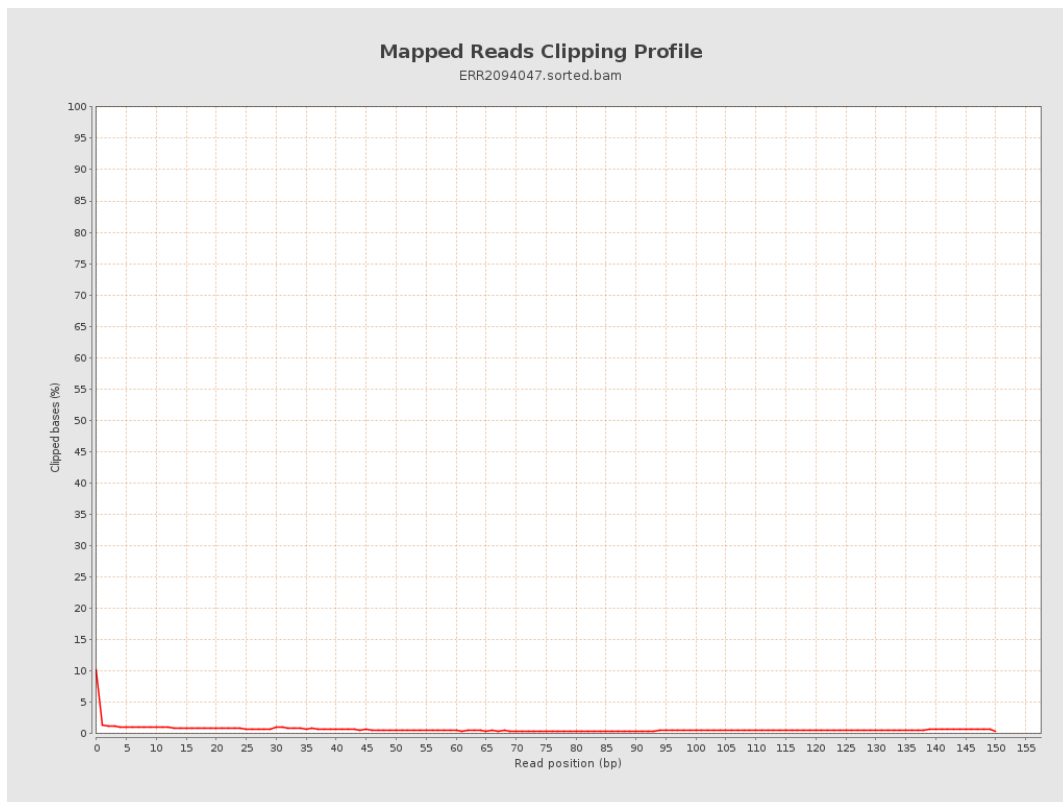
8. Results : Mapped Reads Nucleotide Content



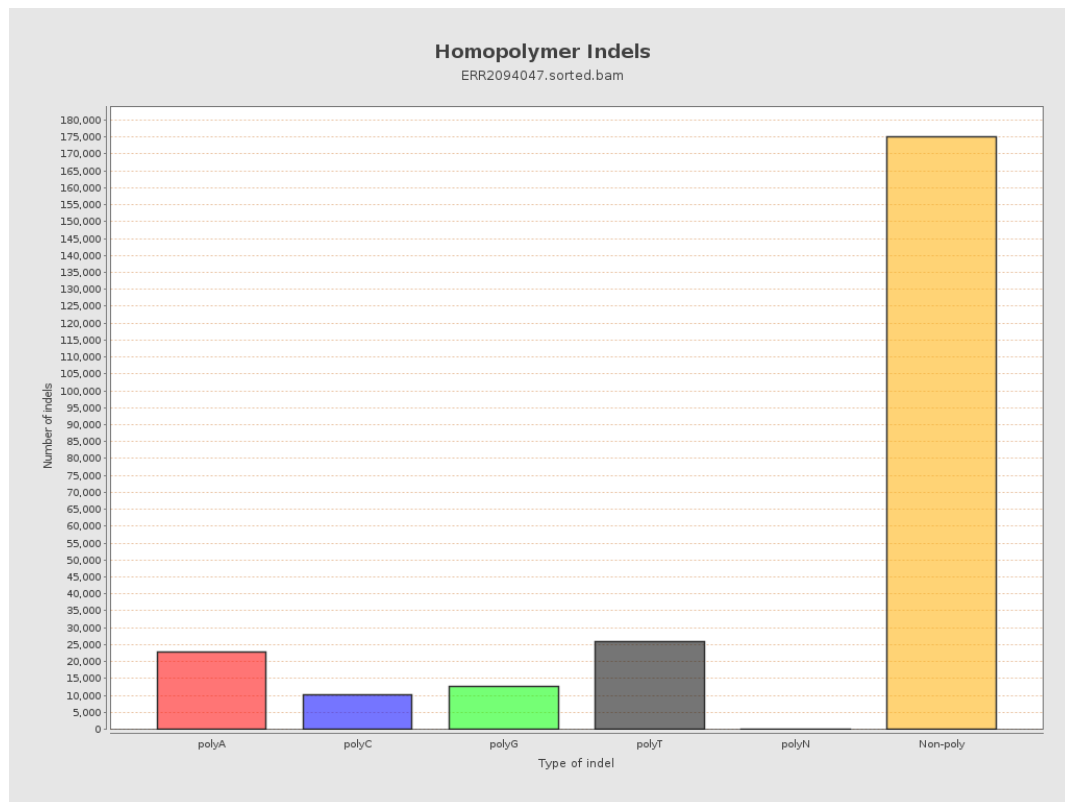
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



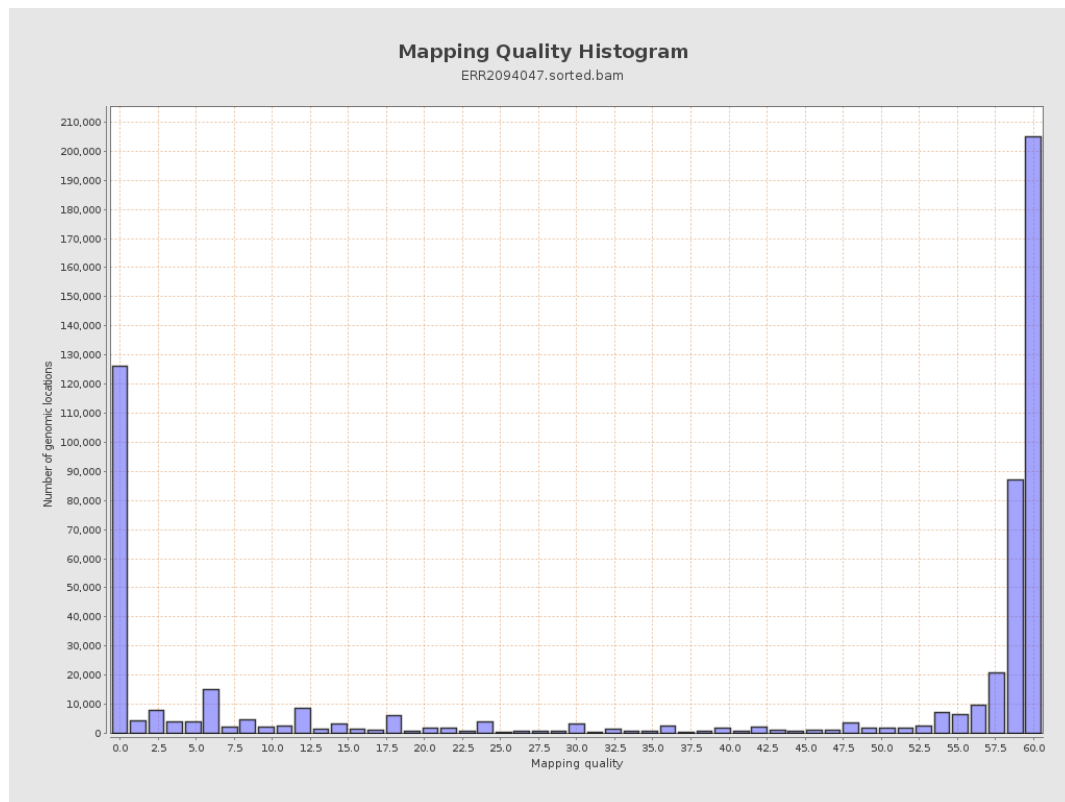
11. Results : Homopolymer Indels



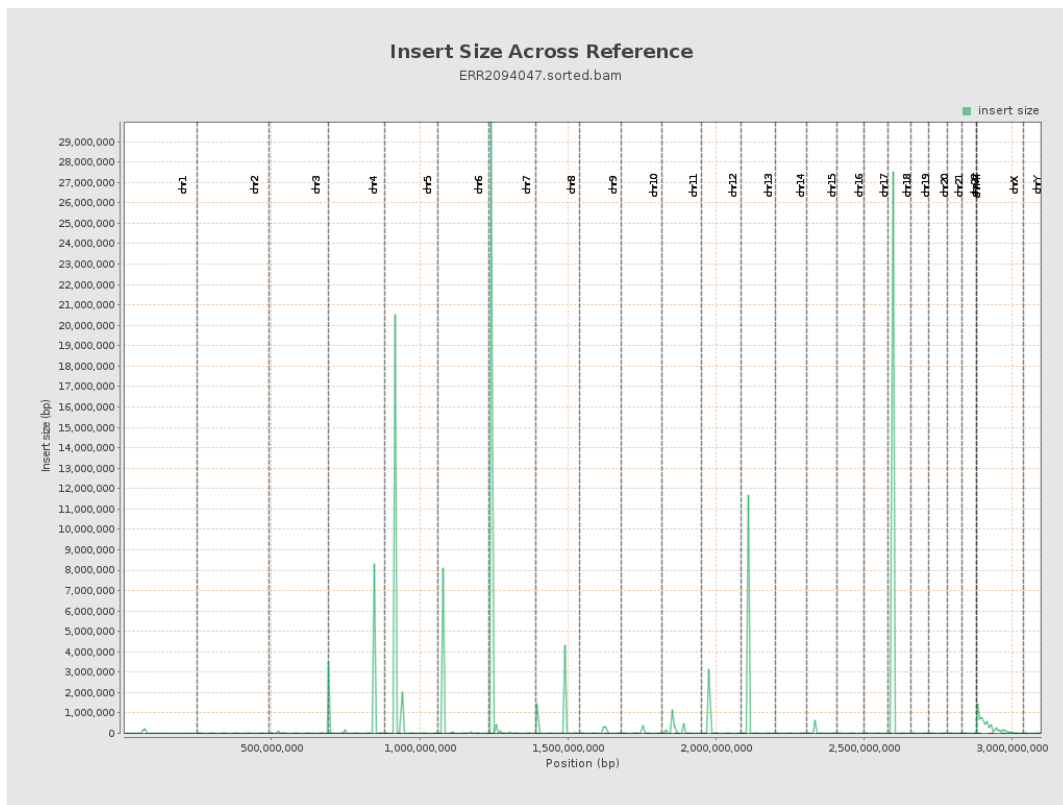
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

