

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:46:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094143.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_ERR2094143 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094143_1.fastq.gz ERR2094143_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:46:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	440,338
Mapped reads	418,980 / 95.15%
Unmapped reads	21,358 / 4.85%
Mapped paired reads	418,980 / 95.15%
Mapped reads, first in pair	210,434 / 47.79%
Mapped reads, second in pair	208,546 / 47.36%
Mapped reads, both in pair	416,022 / 94.48%
Mapped reads, singletons	2,958 / 0.67%
Secondary alignments	0
Supplementary alignments	17,158 / 3.9%
Read min/max/mean length	30 / 151 / 139.17
Duplicated reads (estimated)	391,187 / 88.84%
Duplication rate	49.59%
Clipped reads	174,414 / 39.61%

2.2. ACGT Content

Number/percentage of A's	14,517,181 / 27.2%
Number/percentage of C's	12,159,235 / 22.78%
Number/percentage of T's	13,939,509 / 26.12%
Number/percentage of G's	12,758,169 / 23.9%
Number/percentage of N's	582 / 0%

GC Percentage	46.68%
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2.3. Coverage

Mean	0.0178
Standard Deviation	3.5944

2.4. Mapping Quality

Mean Mapping Quality	43.36
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2.5. Insert size

Mean	601,812.46
Standard Deviation	6,906,074.74
P25/Median/P75	129 / 166 / 193

2.6. Mismatches and indels

General error rate	4.8%
Mismatches	2,539,555
Insertions	31,865
Mapped reads with at least one insertion	7.41%
Deletions	207,851
Mapped reads with at least one deletion	46.27%
Homopolymer indels	28.78%

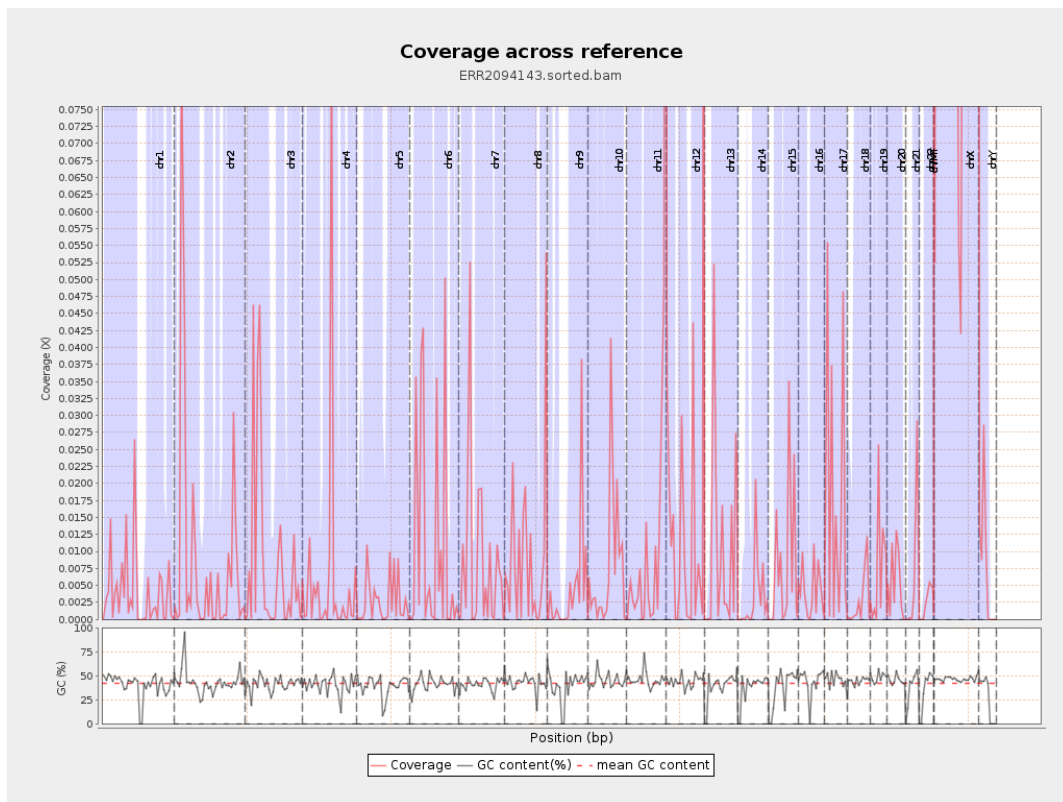
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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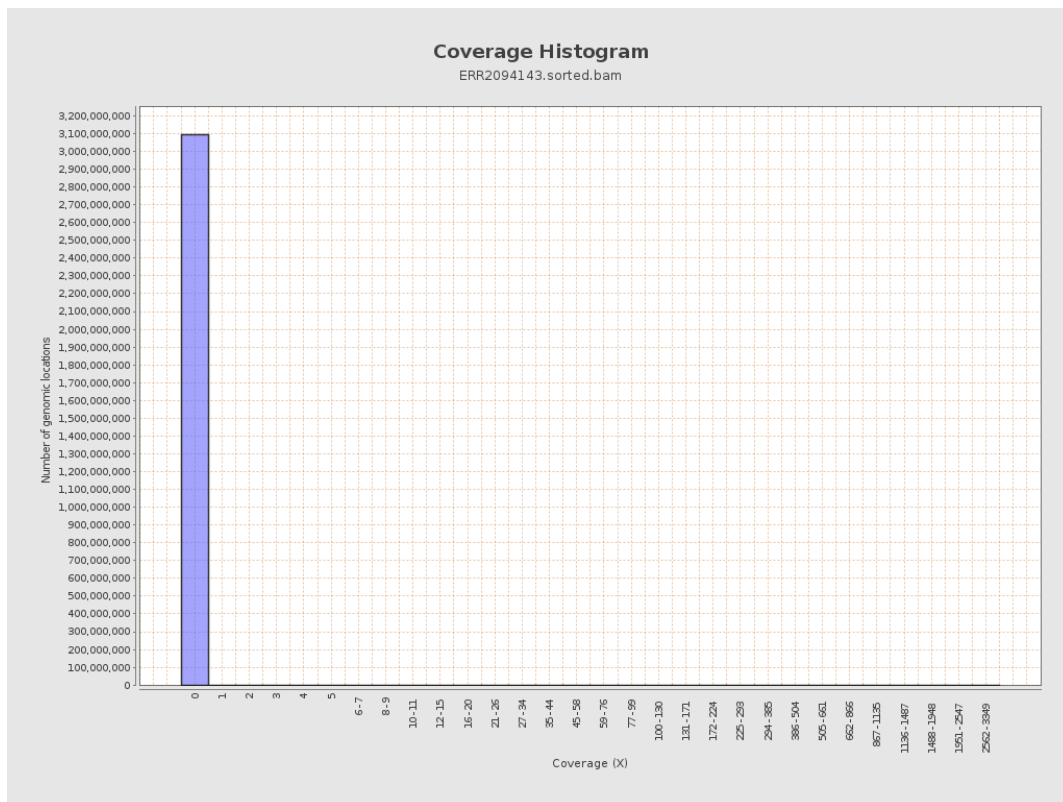
		bases	coverage	deviation
chr1	249250621	959797	0.0039	1.3753
chr2	243199373	2016895	0.0083	2.37
chr3	198022430	1597990	0.0081	2.5983
chr4	191154276	1149553	0.006	1.8327
chr5	180915260	518077	0.0029	0.8997
chr6	171115067	1826270	0.0107	3.8768
chr7	159138663	1340620	0.0084	2.4091
chr8	146364022	1302725	0.0089	2.6614
chr9	141213431	623698	0.0044	1.5892
chr10	135534747	1054120	0.0078	2.1473
chr11	135006516	1322886	0.0098	2.553
chr12	133851895	1814216	0.0136	3.6863
chr13	115169878	1174273	0.0102	2.198
chr14	107349540	347748	0.0032	1.3091
chr15	102531392	766766	0.0075	1.6612
chr16	90354753	394791	0.0044	1.1138
chr17	81195210	1457258	0.0179	4.121
chr18	78077248	235841	0.003	0.8486
chr19	59128983	417594	0.0071	1.9927
chr20	63025520	340683	0.0054	1.3322
chr21	48129895	329423	0.0068	2.162
chr22	51304566	124927	0.0024	0.503
chrMT	16571	1570012	94.7446	414.2751
chrX	155270560	31888730	0.2054	11.7621

chrY	59373566	447075	0.0075	1.7691
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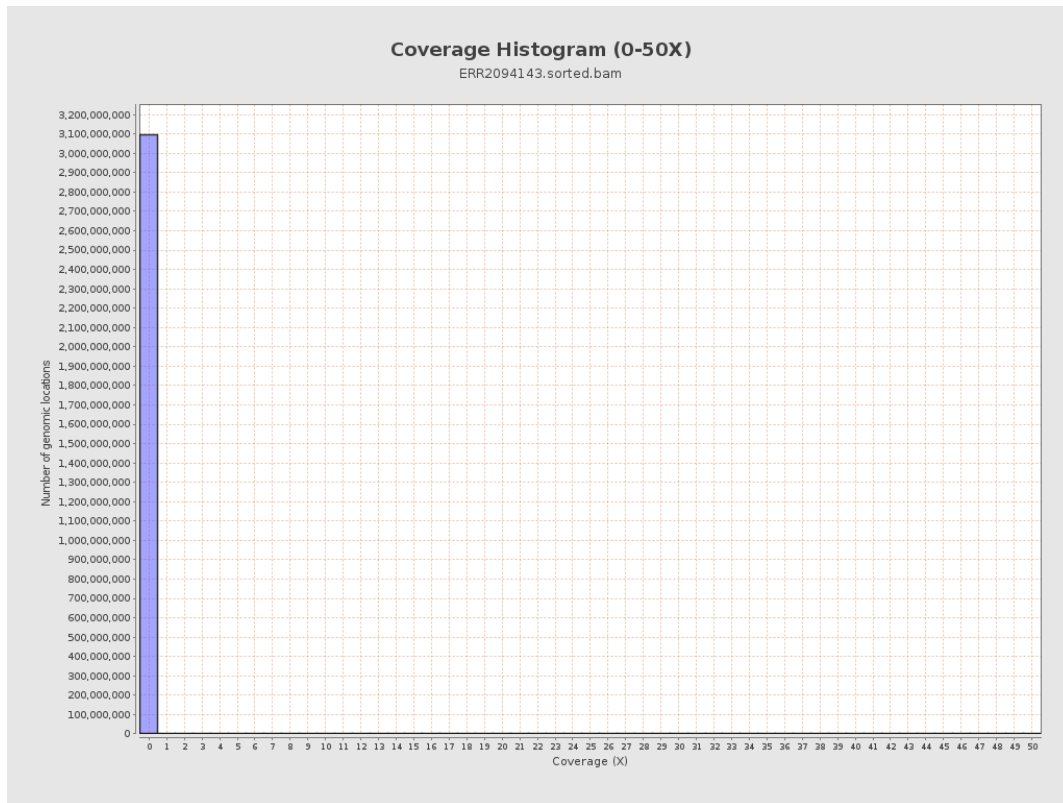
3. Results : Coverage across reference



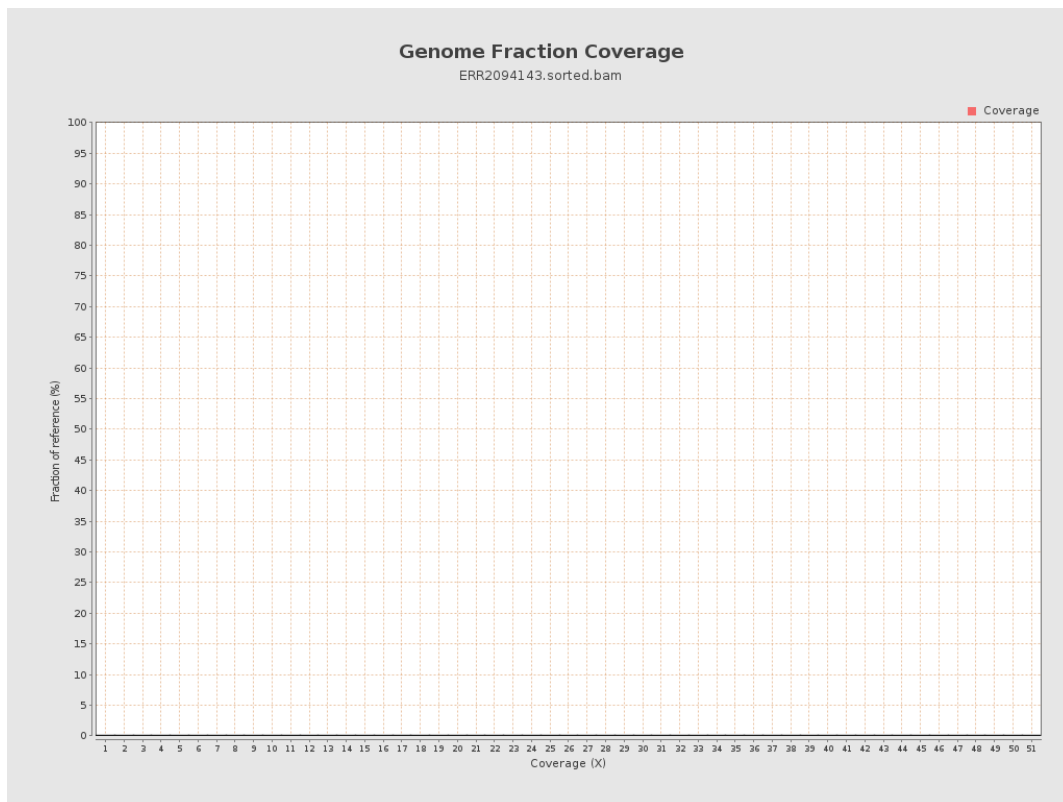
4. Results : Coverage Histogram



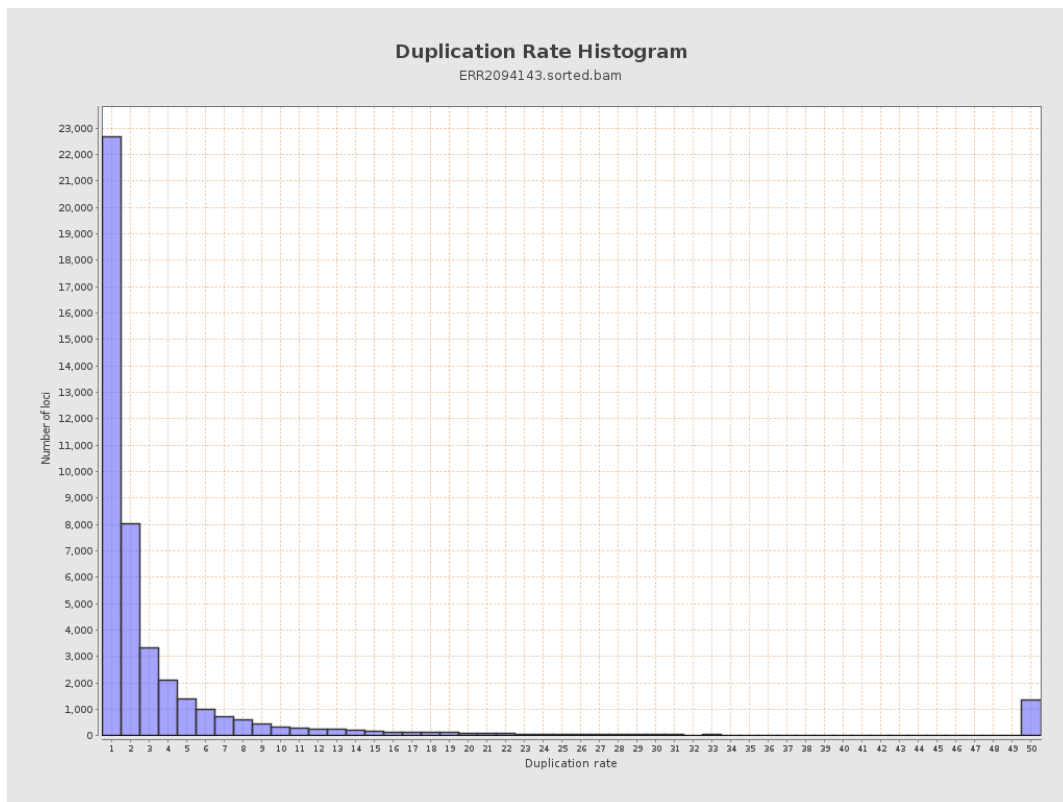
5. Results : Coverage Histogram (0-50X)



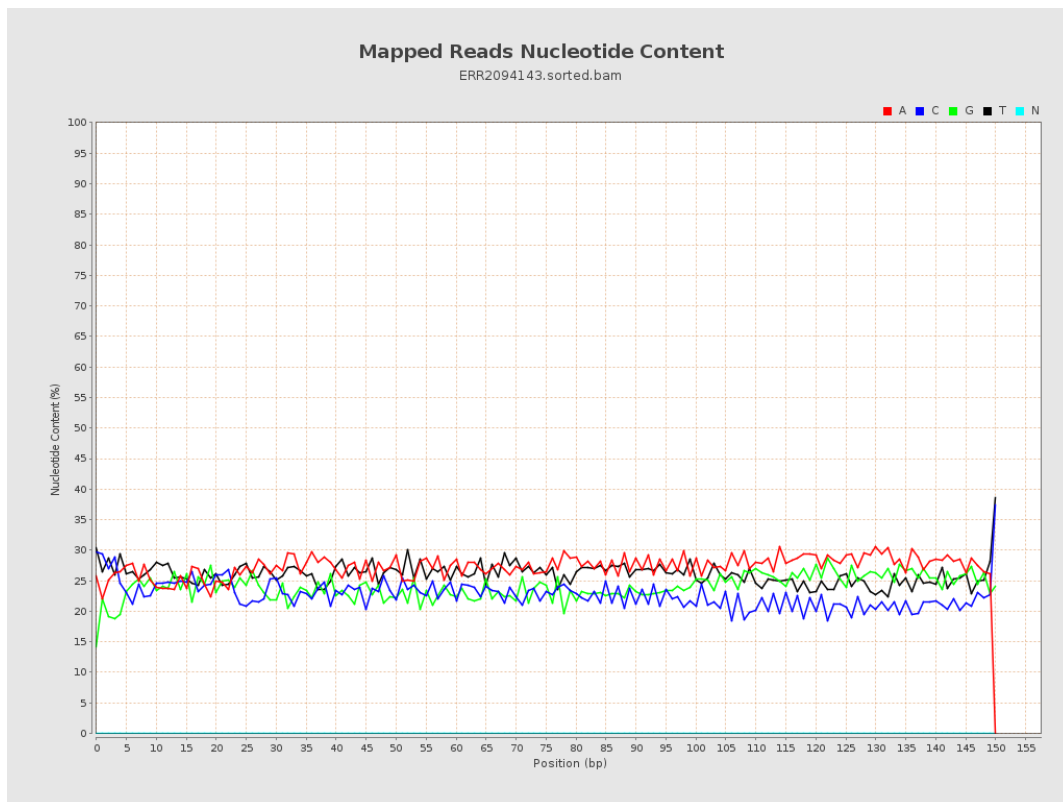
6. Results : Genome Fraction Coverage



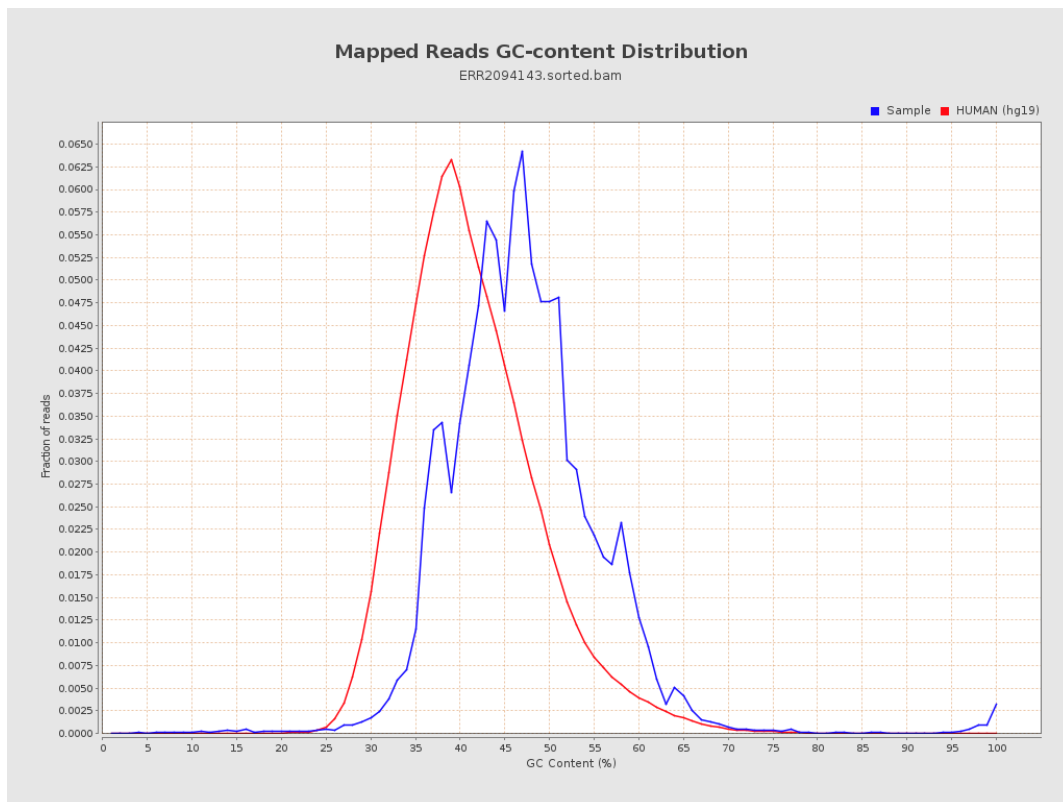
7. Results : Duplication Rate Histogram



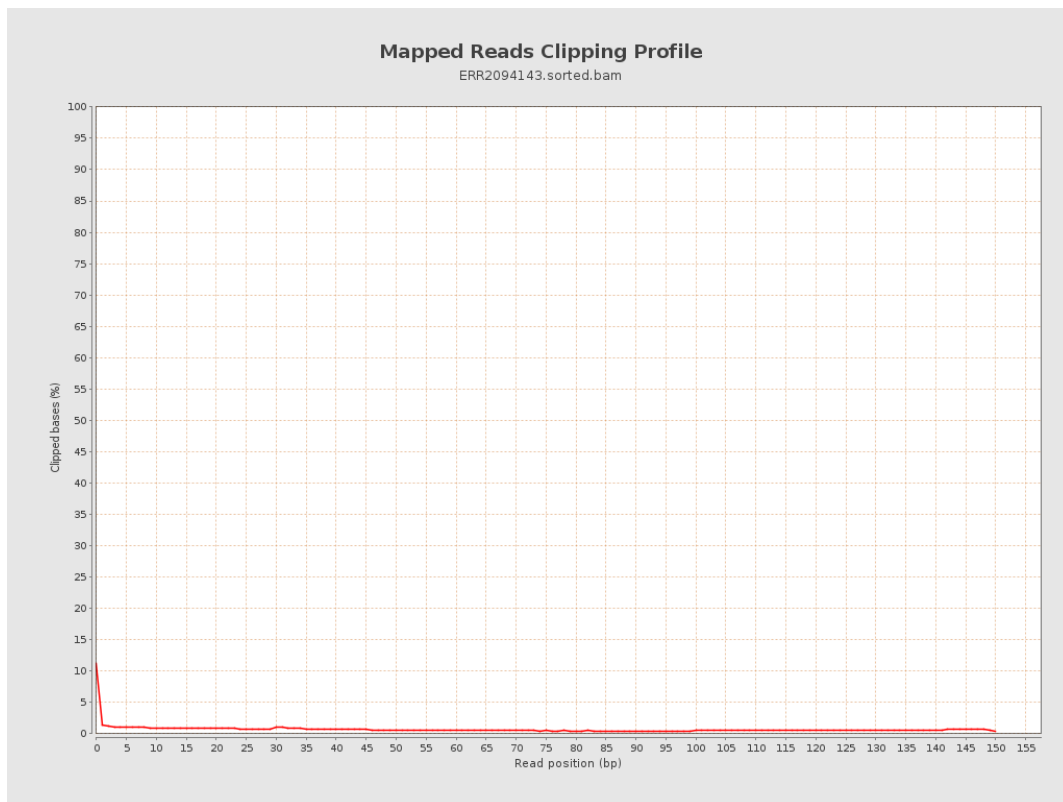
8. Results : Mapped Reads Nucleotide Content



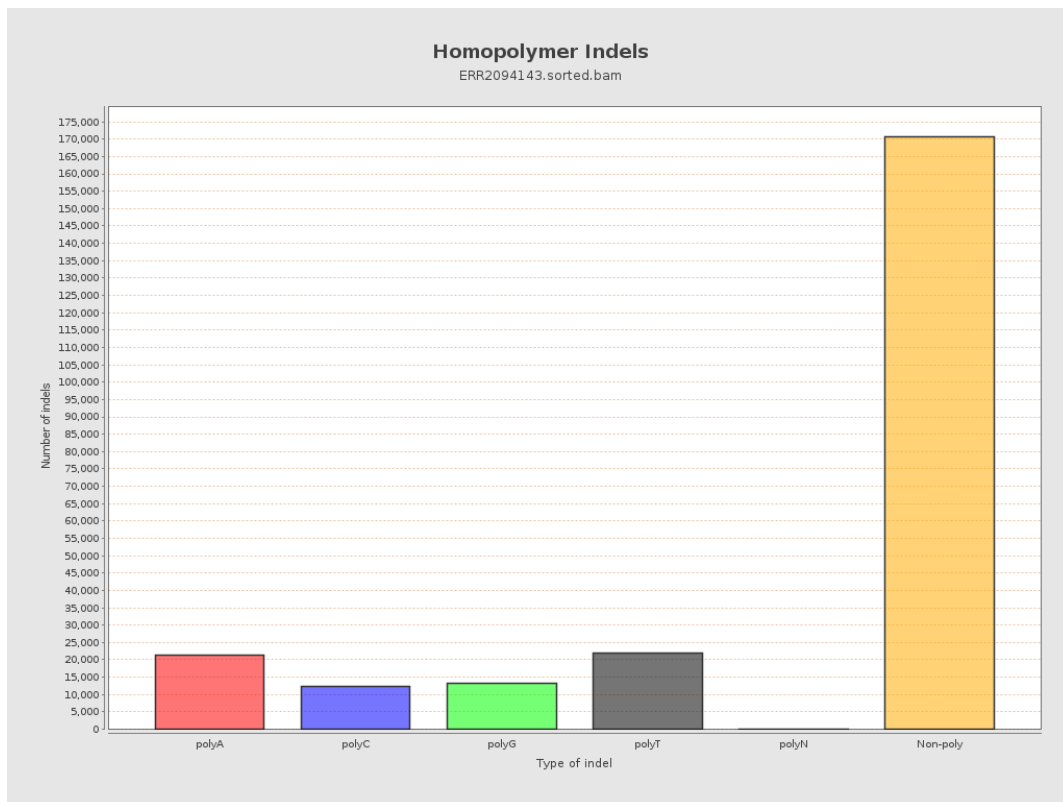
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



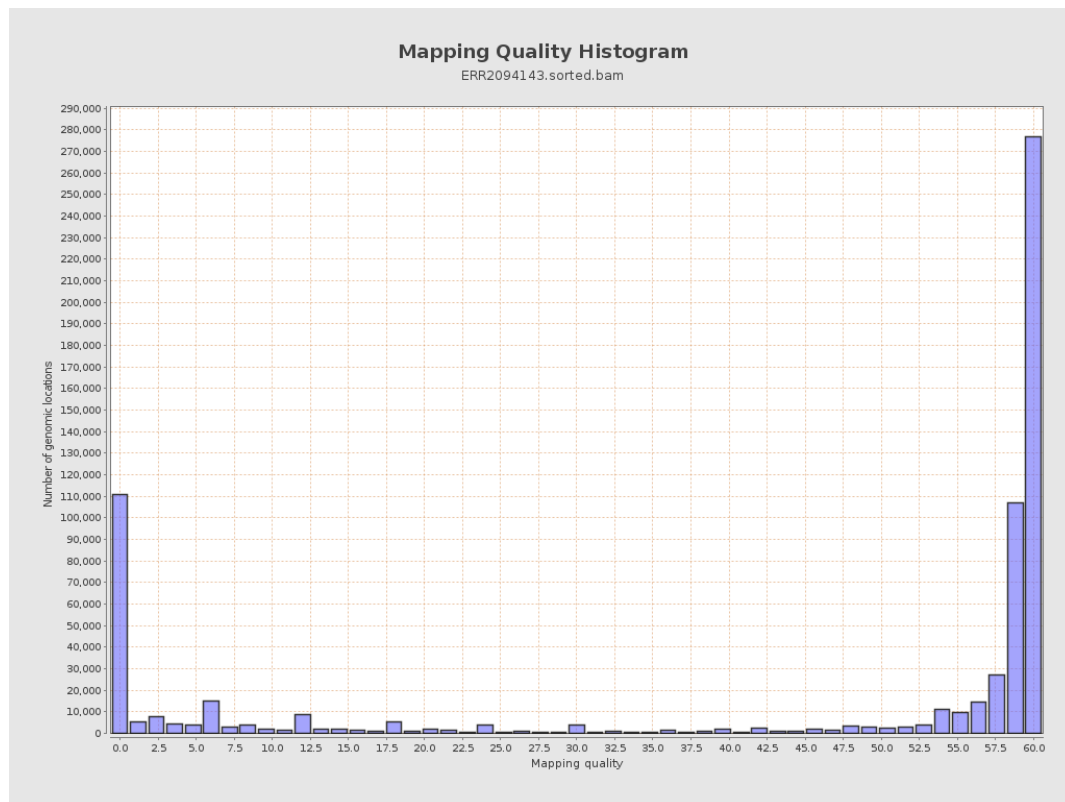
11. Results : Homopolymer Indels



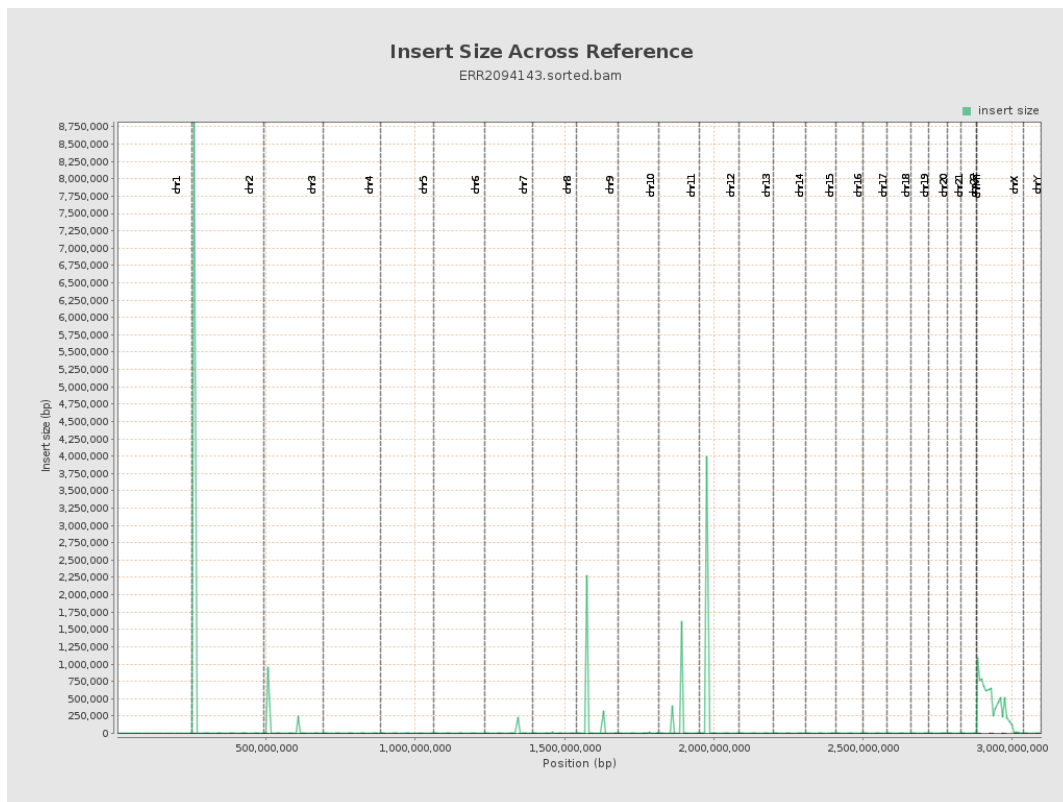
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

