

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:58:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094095.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_ERR2094095 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094095_1.fastq.gz ERR2094095_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:58:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	405,374
Mapped reads	386,534 / 95.35%
Unmapped reads	18,840 / 4.65%
Mapped paired reads	386,534 / 95.35%
Mapped reads, first in pair	194,303 / 47.93%
Mapped reads, second in pair	192,231 / 47.42%
Mapped reads, both in pair	383,184 / 94.53%
Mapped reads, singletons	3,350 / 0.83%
Secondary alignments	0
Supplementary alignments	31,353 / 7.73%
Read min/max/mean length	30 / 151 / 138.59
Duplicated reads (estimated)	369,910 / 91.25%
Duplication rate	53.3%
Clipped reads	210,861 / 52.02%

2.2. ACGT Content

Number/percentage of A's	13,552,360 / 28.71%
Number/percentage of C's	10,131,511 / 21.47%
Number/percentage of T's	12,825,996 / 27.17%
Number/percentage of G's	10,687,901 / 22.64%
Number/percentage of N's	415 / 0%

GC Percentage	44.11%
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2.3. Coverage

Mean	0.0155
Standard Deviation	3.0061

2.4. Mapping Quality

Mean Mapping Quality	41.76
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2.5. Insert size

Mean	2,119,120.71
Standard Deviation	13,016,964.36
P25/Median/P75	113 / 146 / 177

2.6. Mismatches and indels

General error rate	3.56%
Mismatches	1,620,322
Insertions	29,471
Mapped reads with at least one insertion	7.5%
Deletions	127,507
Mapped reads with at least one deletion	31.73%
Homopolymer indels	28.43%

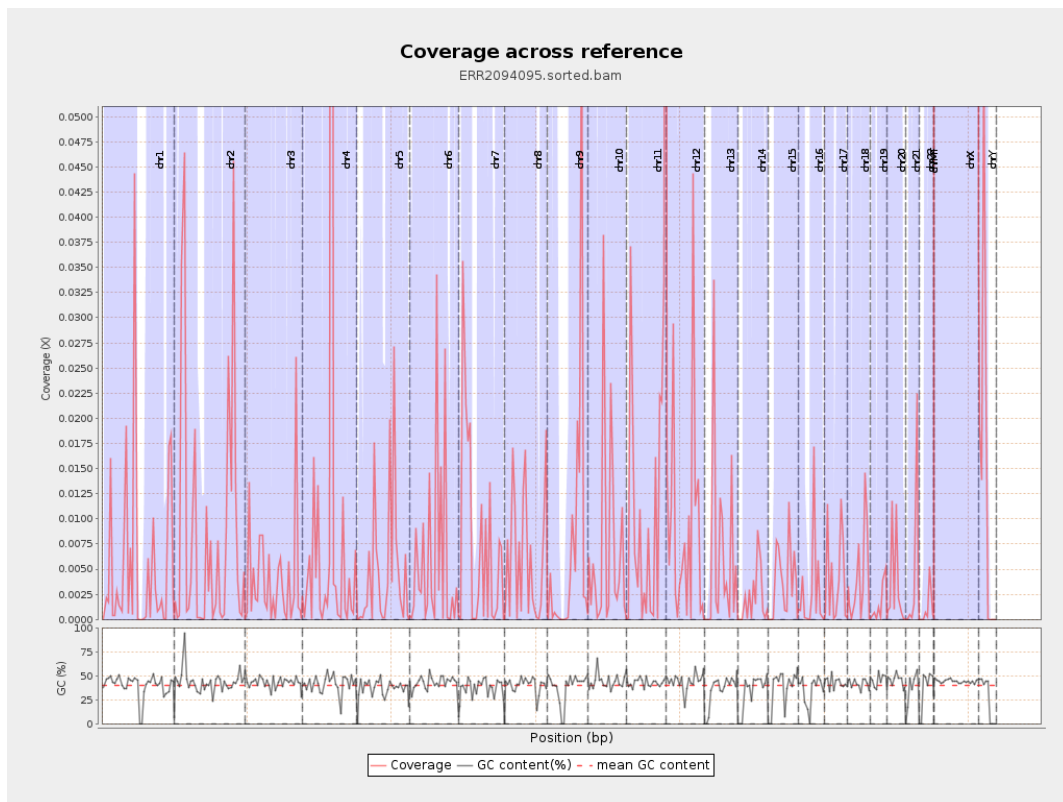
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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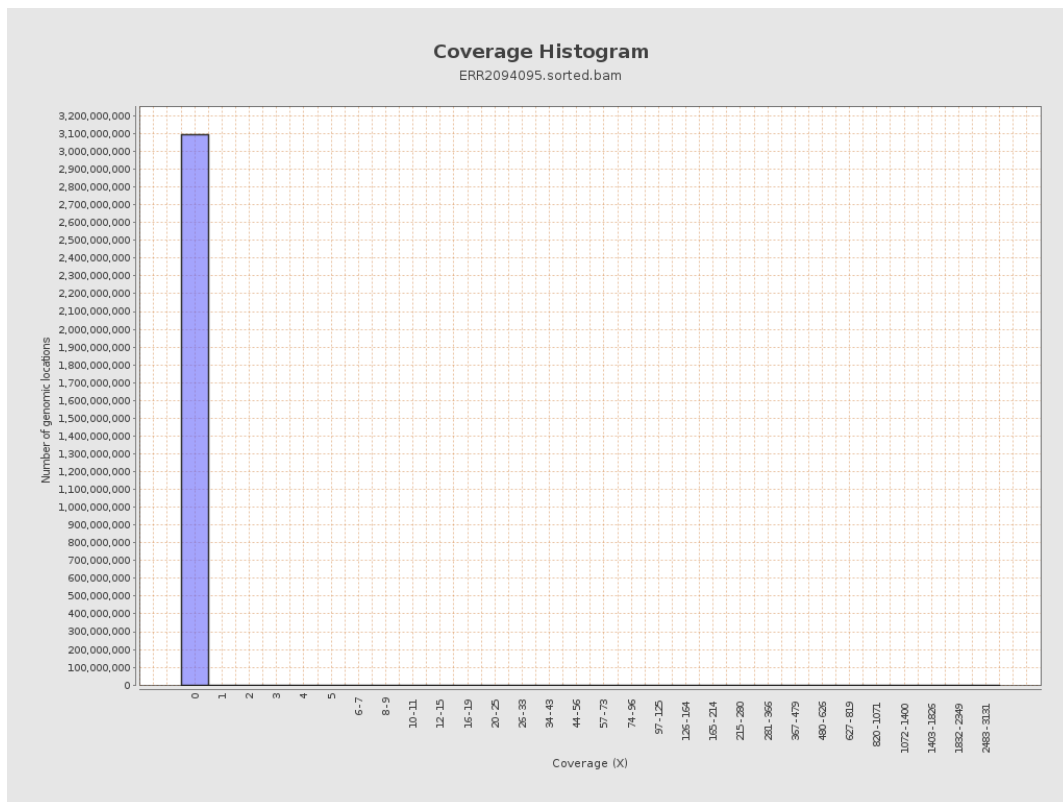
		bases	coverage	deviation
chr1	249250621	1303269	0.0052	1.997
chr2	243199373	2072458	0.0085	2.4572
chr3	198022430	801301	0.004	1.3177
chr4	191154276	2214483	0.0116	3.3285
chr5	180915260	902833	0.005	1.9153
chr6	171115067	1006419	0.0059	1.807
chr7	159138663	1155048	0.0073	2.1098
chr8	146364022	899795	0.0061	1.5486
chr9	141213431	982796	0.007	2.908
chr10	135534747	905819	0.0067	2.2857
chr11	135006516	1522194	0.0113	2.6681
chr12	133851895	1245406	0.0093	2.2045
chr13	115169878	679401	0.0059	1.4102
chr14	107349540	213790	0.002	0.7373
chr15	102531392	388819	0.0038	0.7473
chr16	90354753	252581	0.0028	1.1643
chr17	81195210	330317	0.0041	0.9296
chr18	78077248	335231	0.0043	1.1355
chr19	59128983	88973	0.0015	0.4446
chr20	63025520	226113	0.0036	1.147
chr21	48129895	208281	0.0043	1.7489
chr22	51304566	51951	0.001	0.3341
chrMT	16571	350989	21.1809	98.1277
chrX	155270560	29150175	0.1877	10.0661

chrY	59373566	831670	0.014	2.7996
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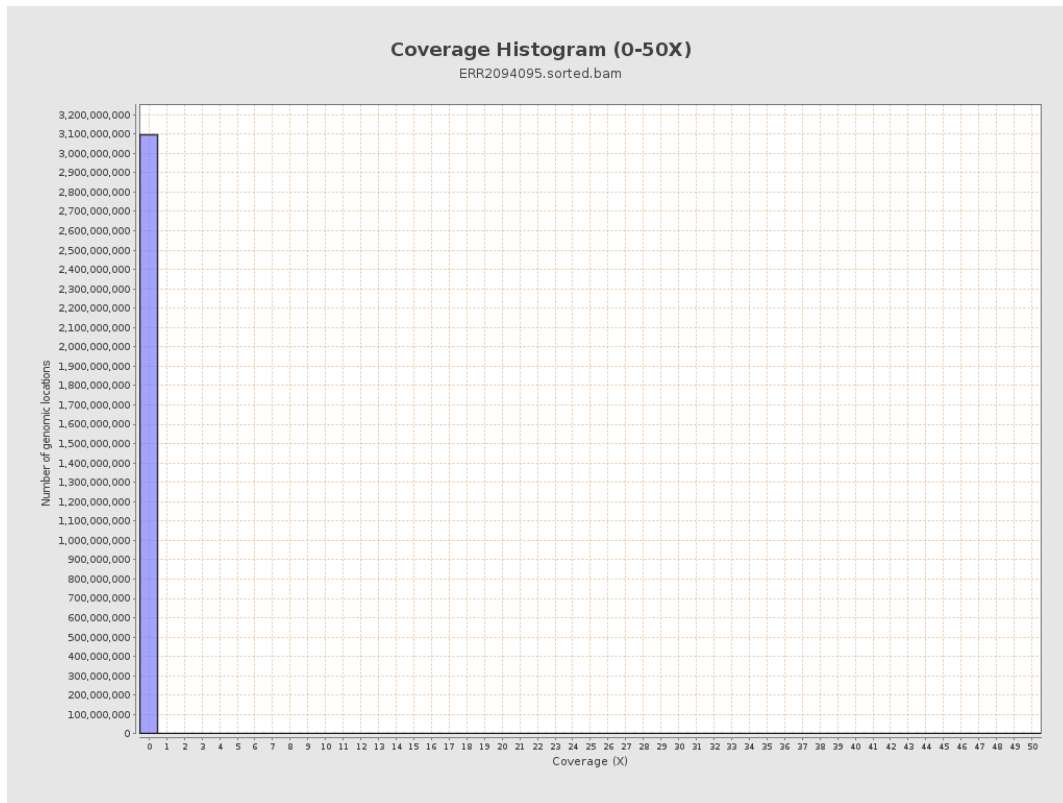
3. Results : Coverage across reference



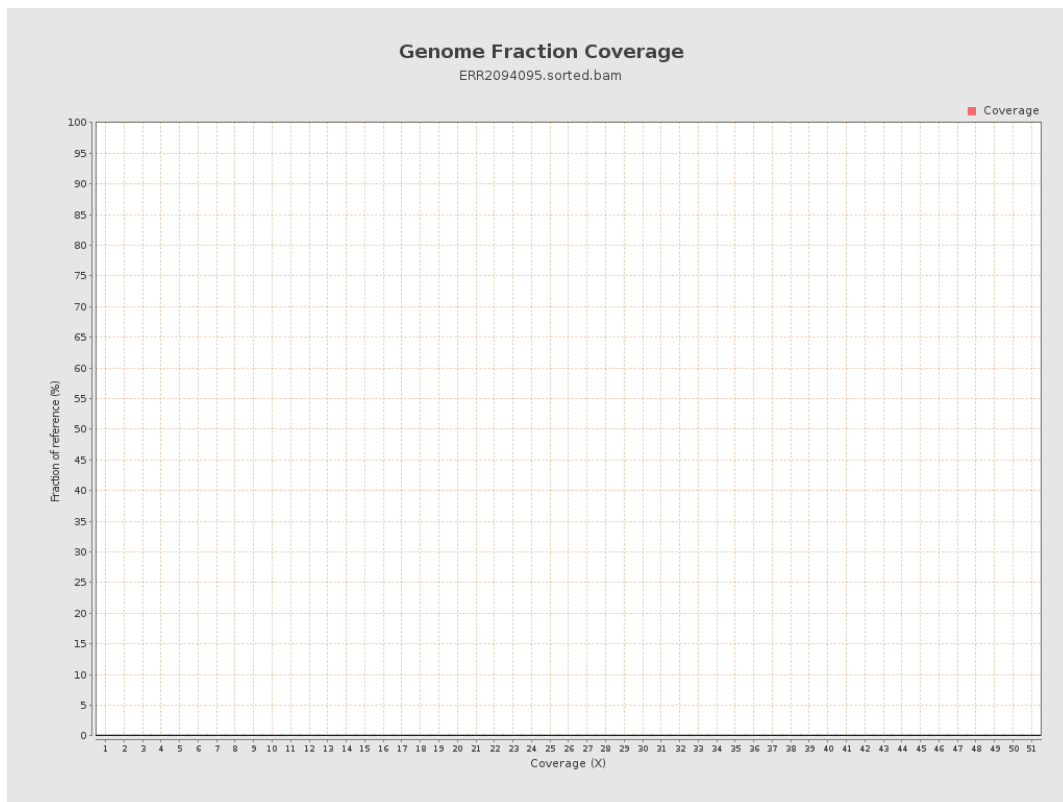
4. Results : Coverage Histogram



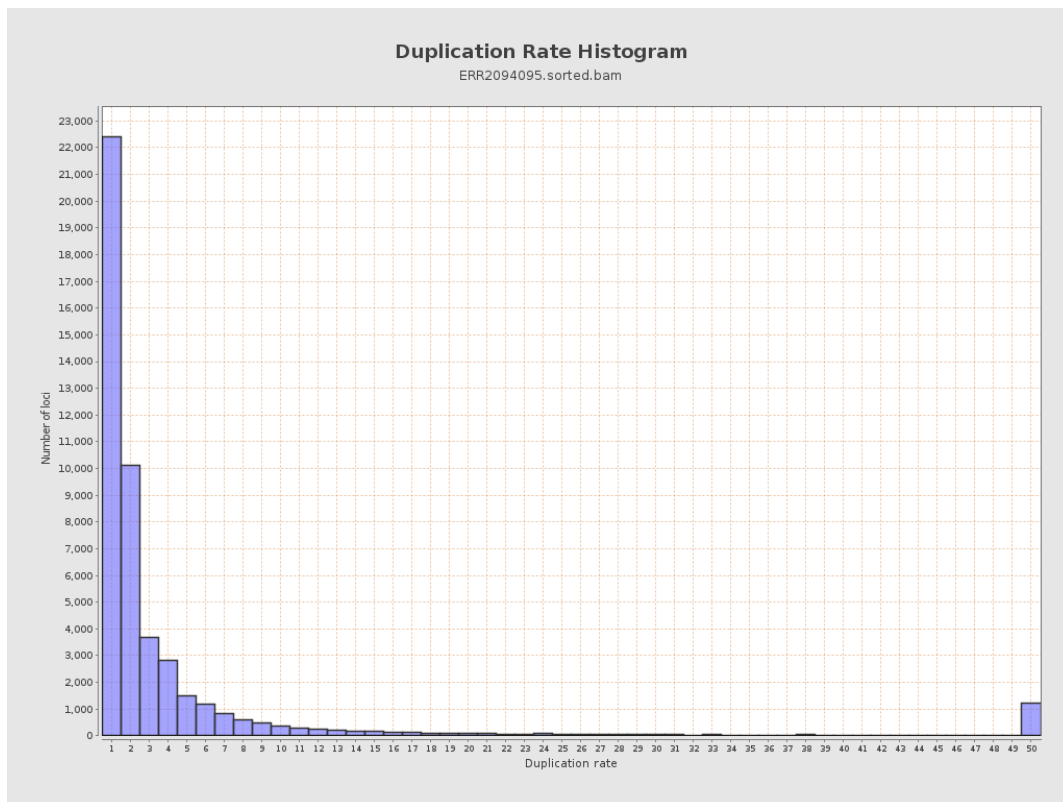
5. Results : Coverage Histogram (0-50X)



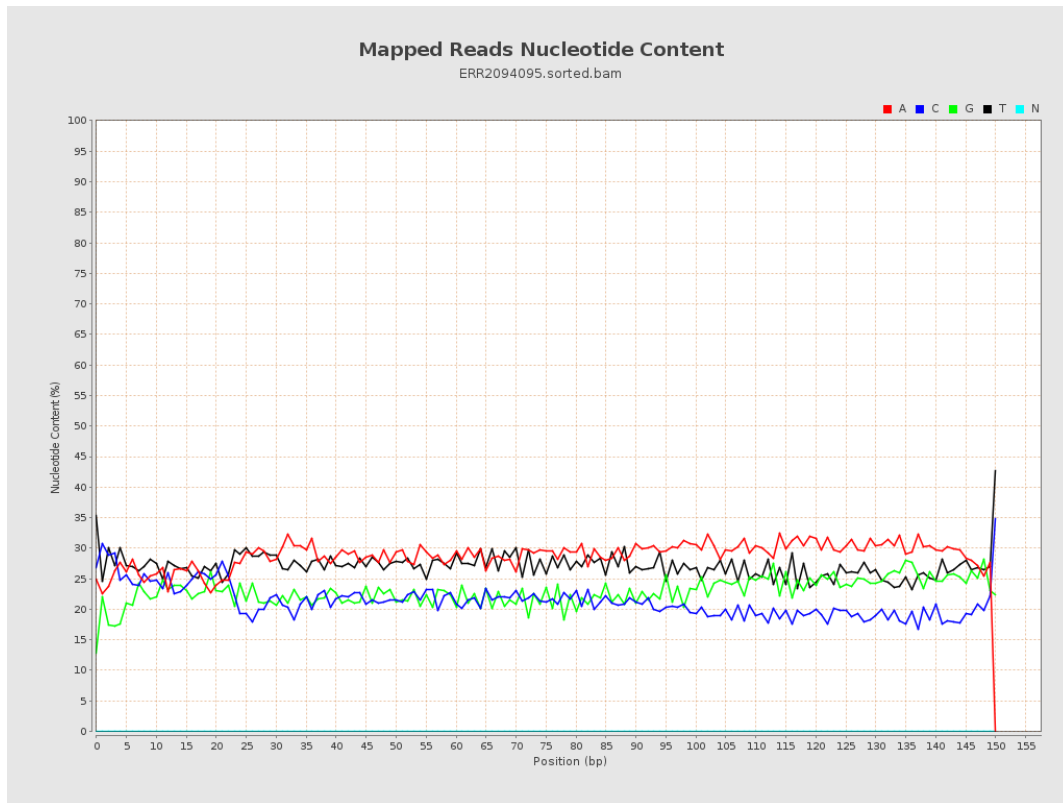
6. Results : Genome Fraction Coverage



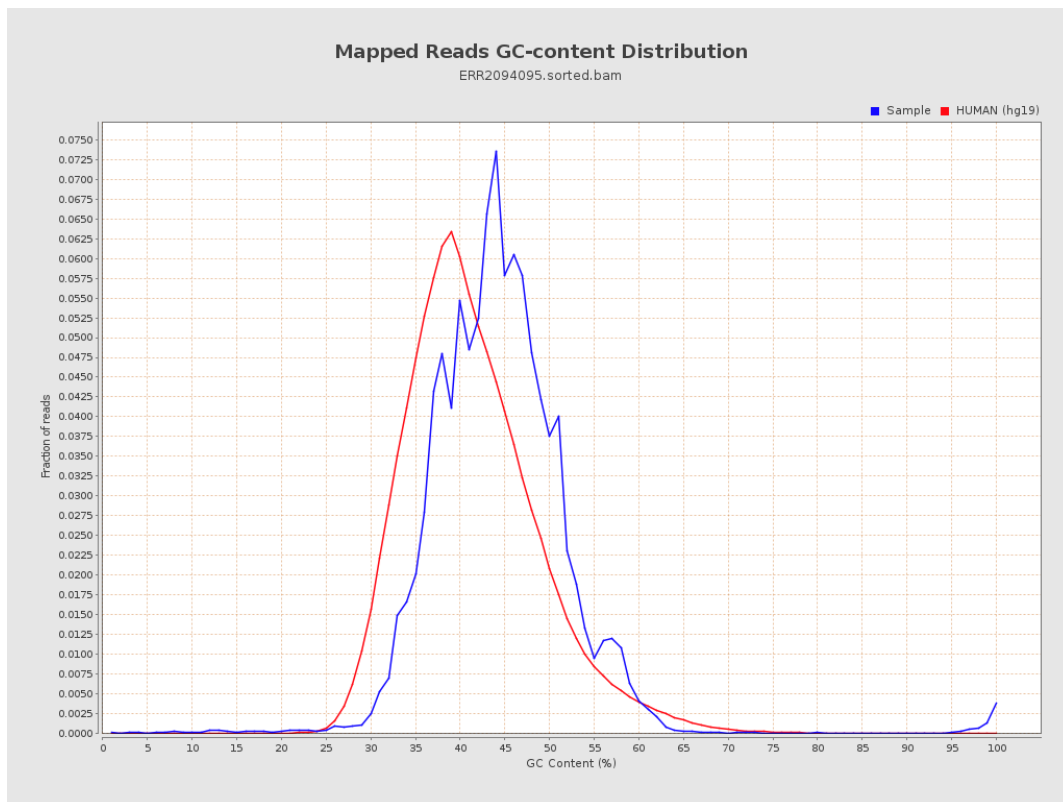
7. Results : Duplication Rate Histogram



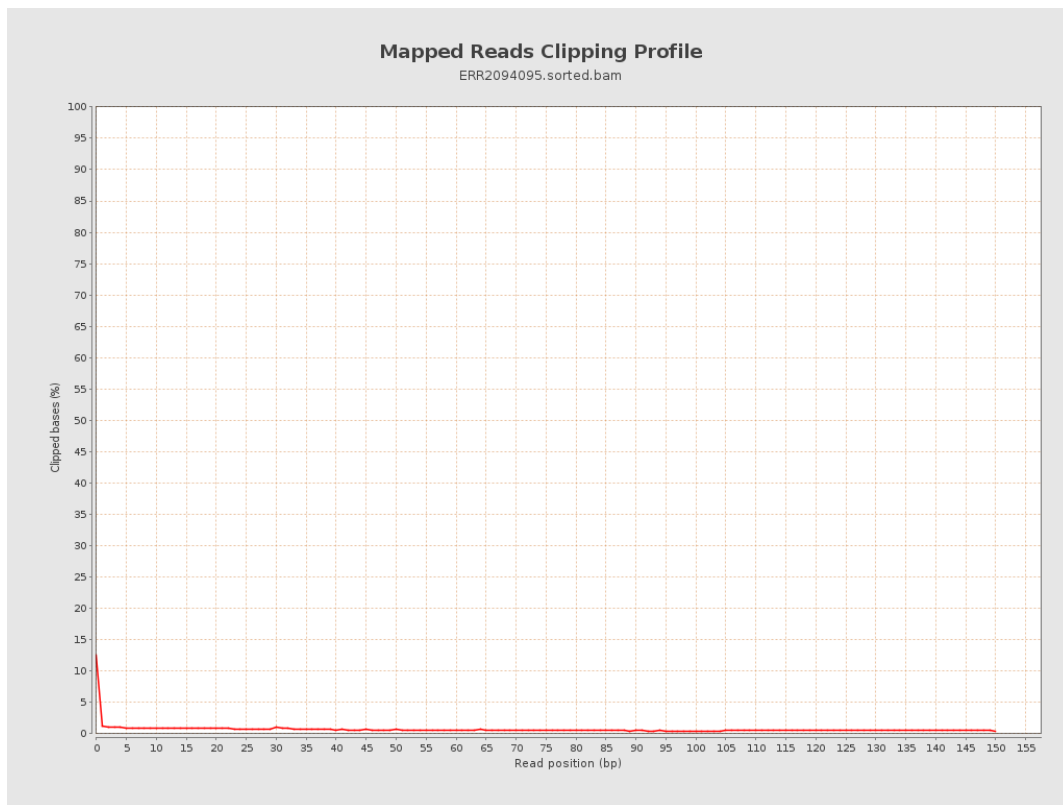
8. Results : Mapped Reads Nucleotide Content



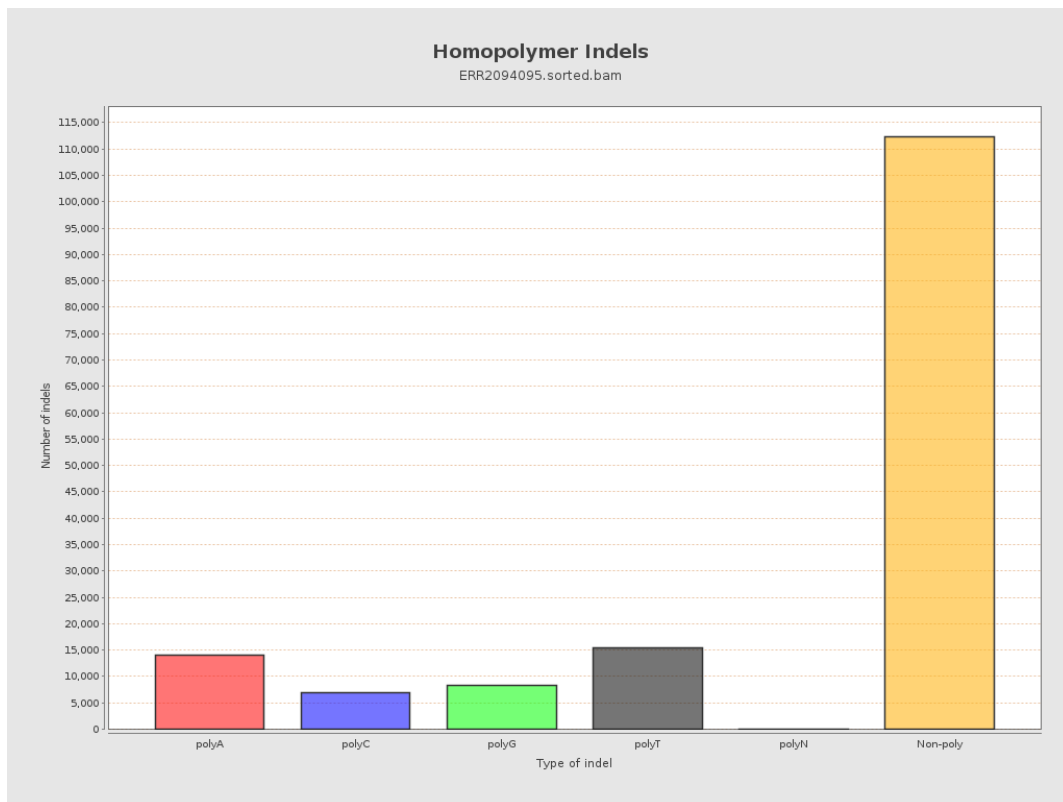
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



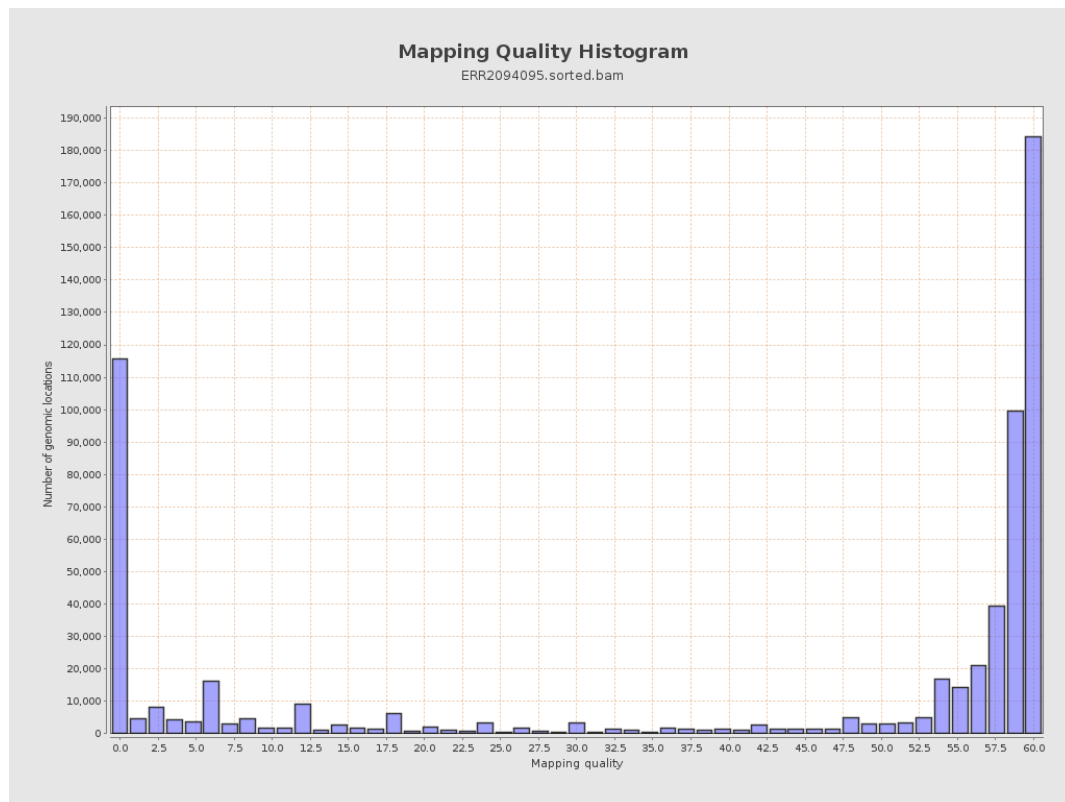
11. Results : Homopolymer Indels



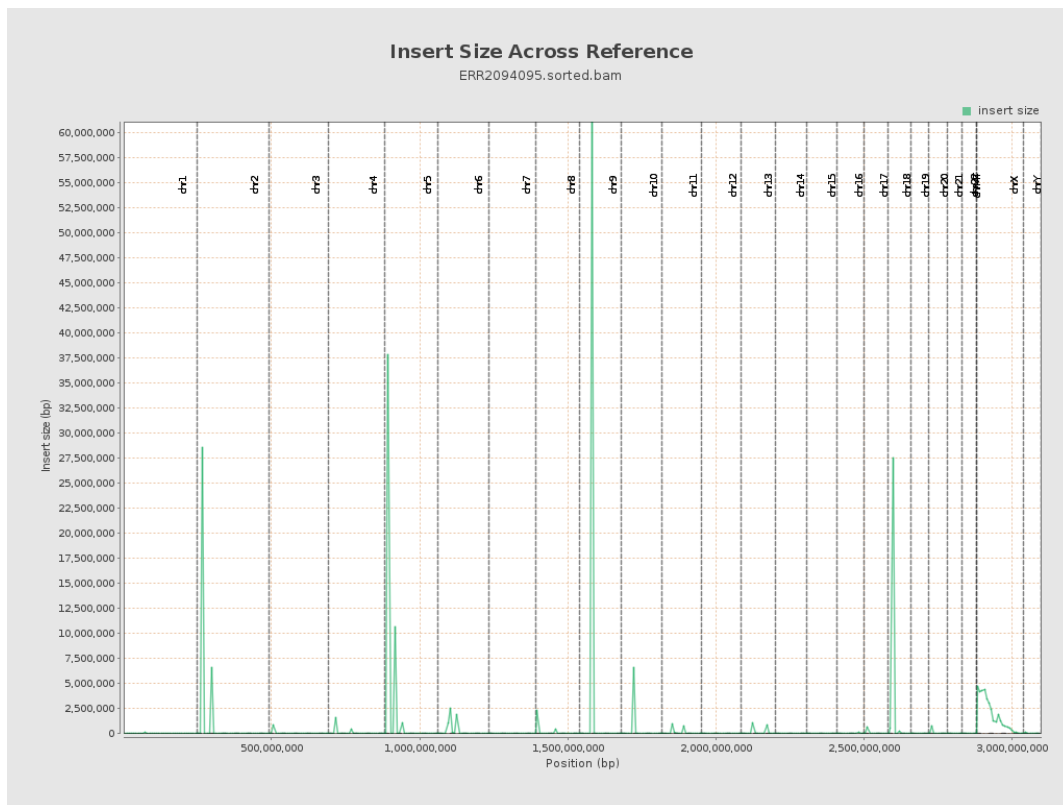
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

