

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:21:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094061.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_ERR2094061 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094061_1.fastq.gz ERR2094061_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:21:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	642,056
Mapped reads	601,500 / 93.68%
Unmapped reads	40,556 / 6.32%
Mapped paired reads	601,500 / 93.68%
Mapped reads, first in pair	302,276 / 47.08%
Mapped reads, second in pair	299,224 / 46.6%
Mapped reads, both in pair	596,240 / 92.86%
Mapped reads, singletons	5,260 / 0.82%
Secondary alignments	0
Supplementary alignments	37,511 / 5.84%
Read min/max/mean length	30 / 151 / 138.49
Duplicated reads (estimated)	568,965 / 88.62%
Duplication rate	50.93%
Clipped reads	295,607 / 46.04%

2.2. ACGT Content

Number/percentage of A's	20,882,527 / 27.74%
Number/percentage of C's	16,887,239 / 22.43%
Number/percentage of T's	19,746,936 / 26.23%
Number/percentage of G's	17,759,427 / 23.59%
Number/percentage of N's	826 / 0%

GC Percentage	46.03%
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2.3. Coverage

Mean	0.0248
Standard Deviation	4.7879

2.4. Mapping Quality

Mean Mapping Quality	46.77
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2.5. Insert size

Mean	1,294,257.56
Standard Deviation	10,245,046.74
P25/Median/P75	122 / 156 / 192

2.6. Mismatches and indels

General error rate	3.64%
Mismatches	2,668,741
Insertions	41,430
Mapped reads with at least one insertion	6.8%
Deletions	212,341
Mapped reads with at least one deletion	34.01%
Homopolymer indels	29%

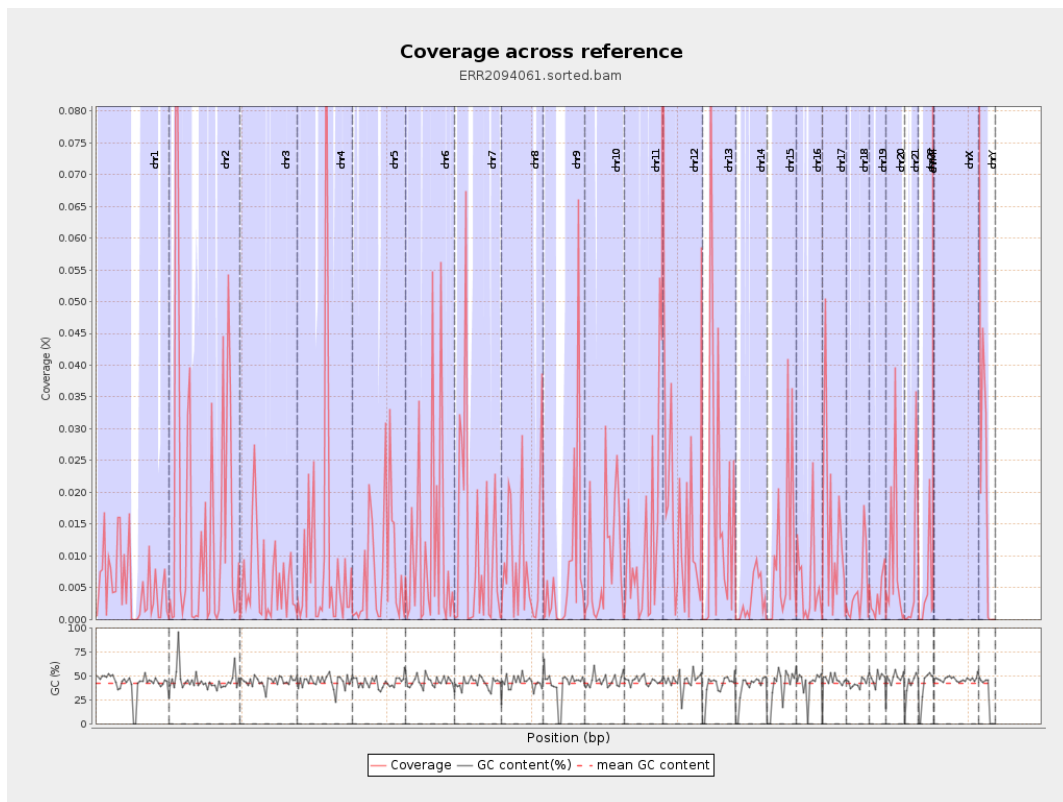
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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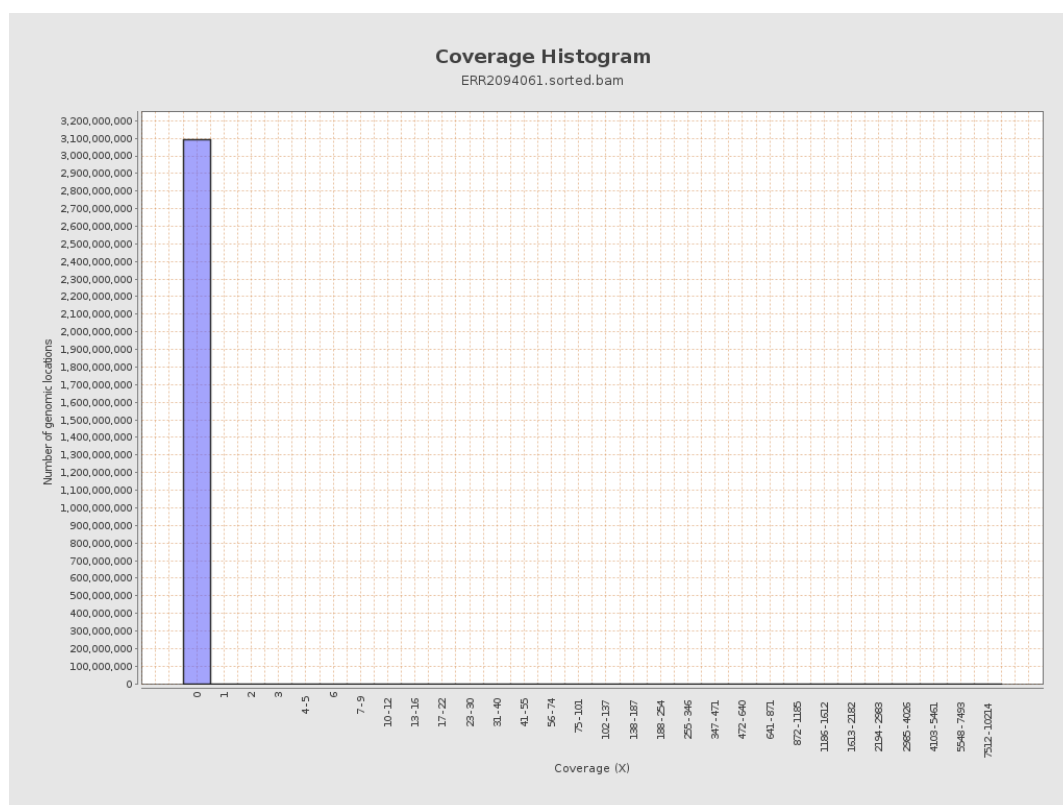
		bases	coverage	deviation
chr1	249250621	1321214	0.0053	1.504
chr2	243199373	3972485	0.0163	4.1014
chr3	198022430	1192749	0.006	1.3913
chr4	191154276	1813160	0.0095	2.172
chr5	180915260	1391930	0.0077	2.558
chr6	171115067	1876390	0.011	3.5069
chr7	159138663	1916353	0.012	3.1309
chr8	146364022	1429335	0.0098	2.5137
chr9	141213431	1127937	0.008	2.6232
chr10	135534747	1304102	0.0096	2.1768
chr11	135006516	1881619	0.0139	3.163
chr12	133851895	2111963	0.0158	3.1039
chr13	115169878	1931170	0.0168	3.8034
chr14	107349540	334455	0.0031	0.9254
chr15	102531392	1048339	0.0102	2.5413
chr16	90354753	489512	0.0054	1.6396
chr17	81195210	1123658	0.0138	2.5975
chr18	78077248	376199	0.0048	1.2306
chr19	59128983	205219	0.0035	0.7604
chr20	63025520	606129	0.0096	2.8689
chr21	48129895	371262	0.0077	2.061
chr22	51304566	235601	0.0046	1.2912
chrMT	16571	5314524	320.7123	1,293.7415
chrX	155270560	42298669	0.2724	11.5522

chrY	59373566	1121218	0.0189	3.3271
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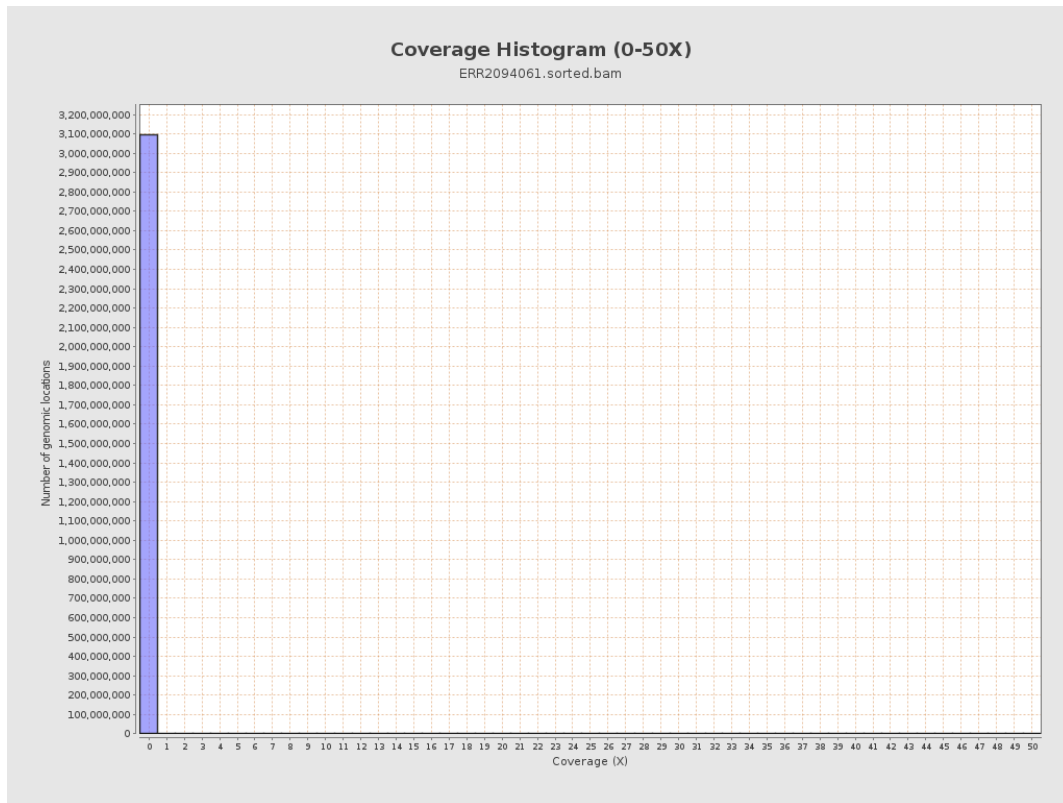
3. Results : Coverage across reference



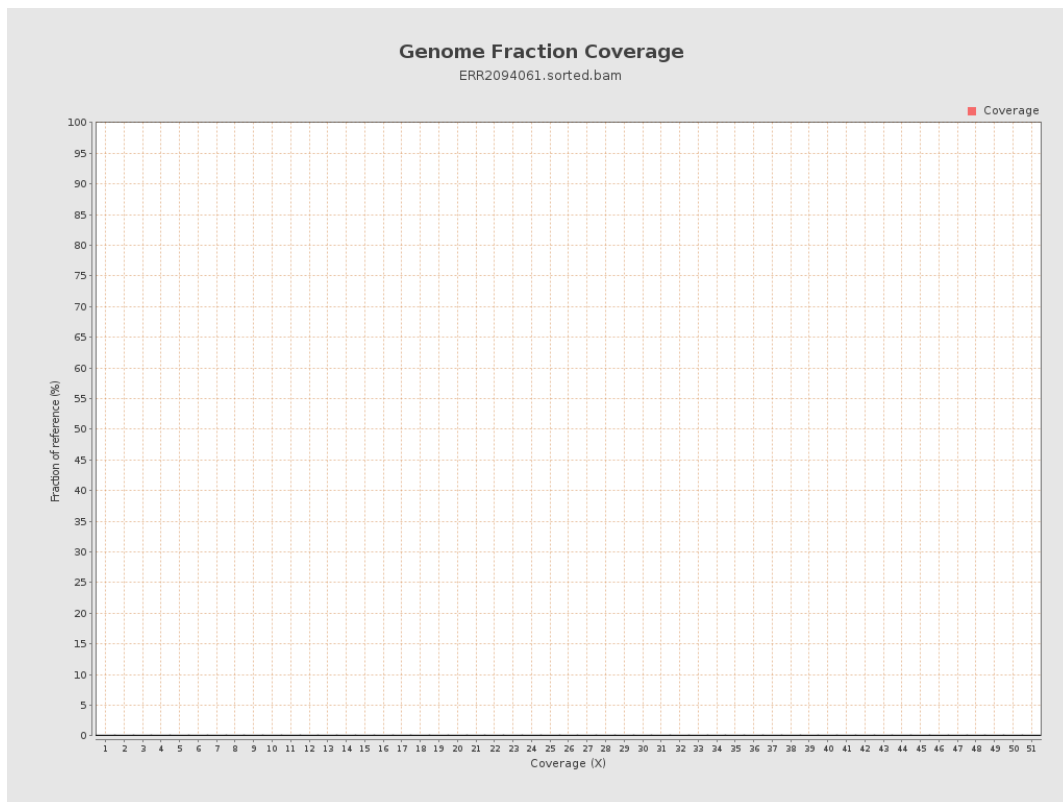
4. Results : Coverage Histogram



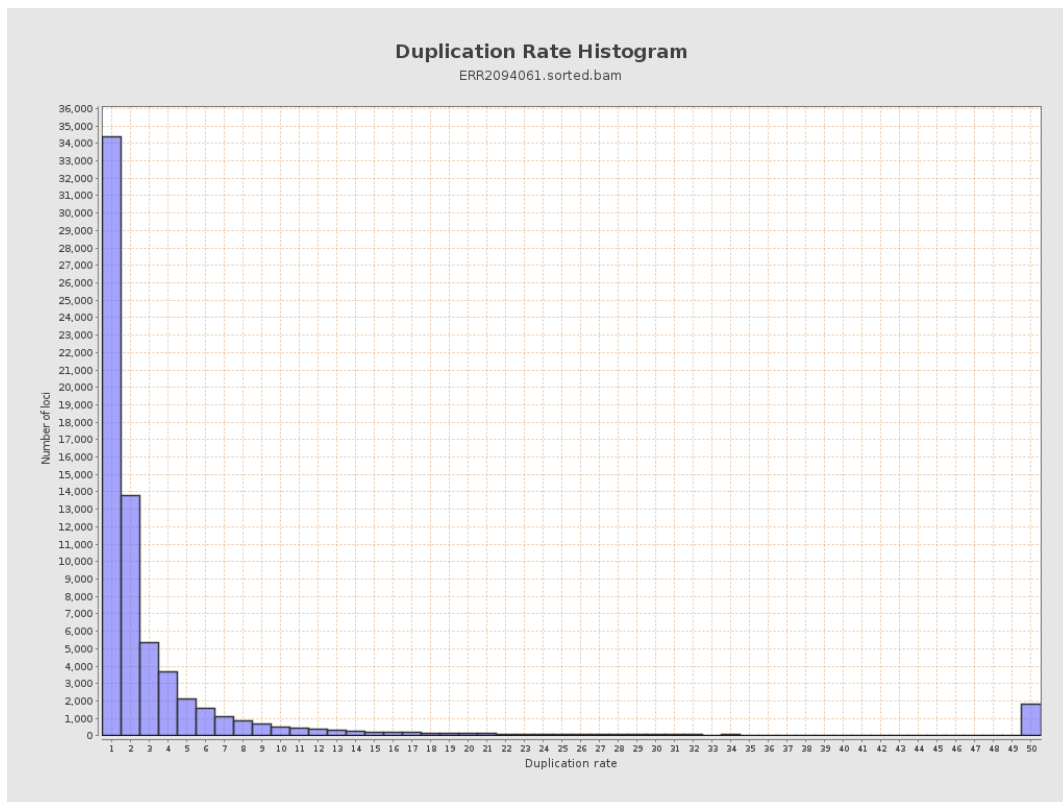
5. Results : Coverage Histogram (0-50X)



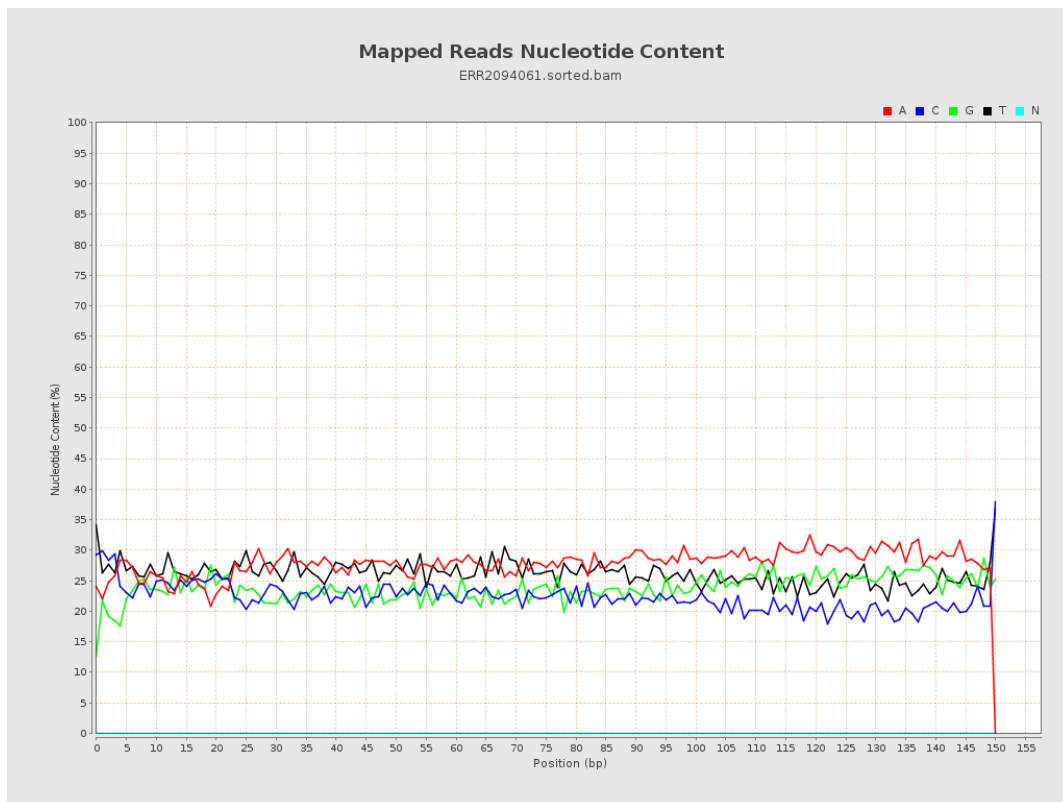
6. Results : Genome Fraction Coverage



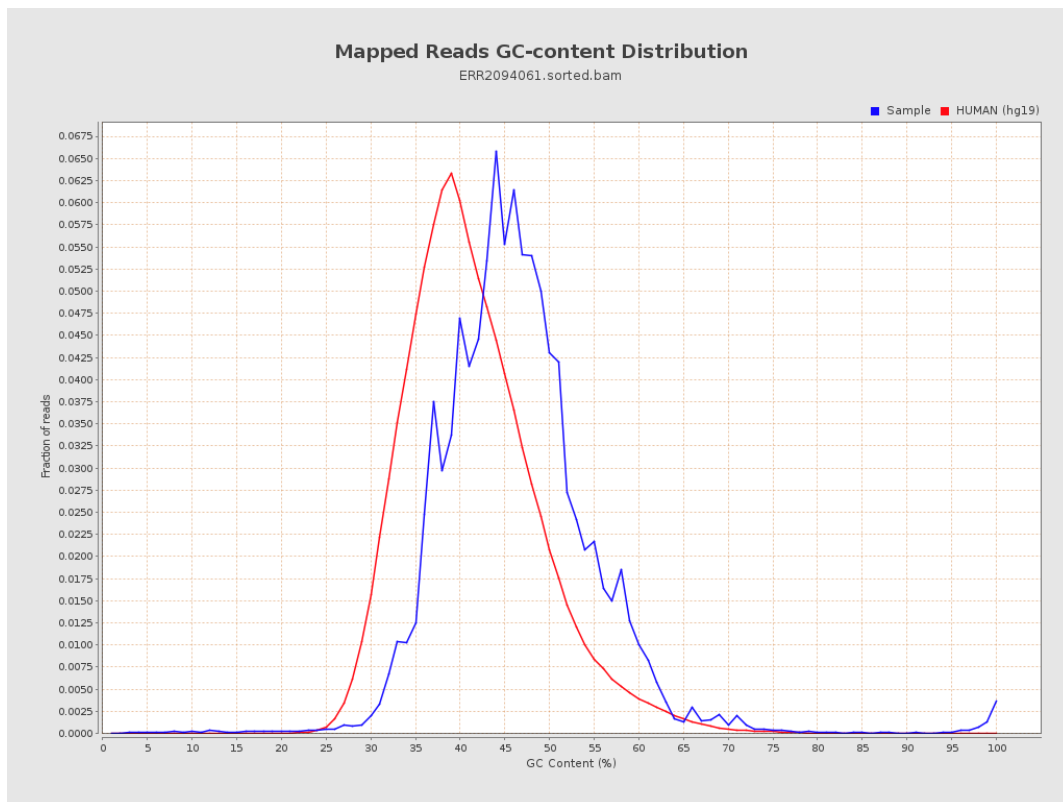
7. Results : Duplication Rate Histogram



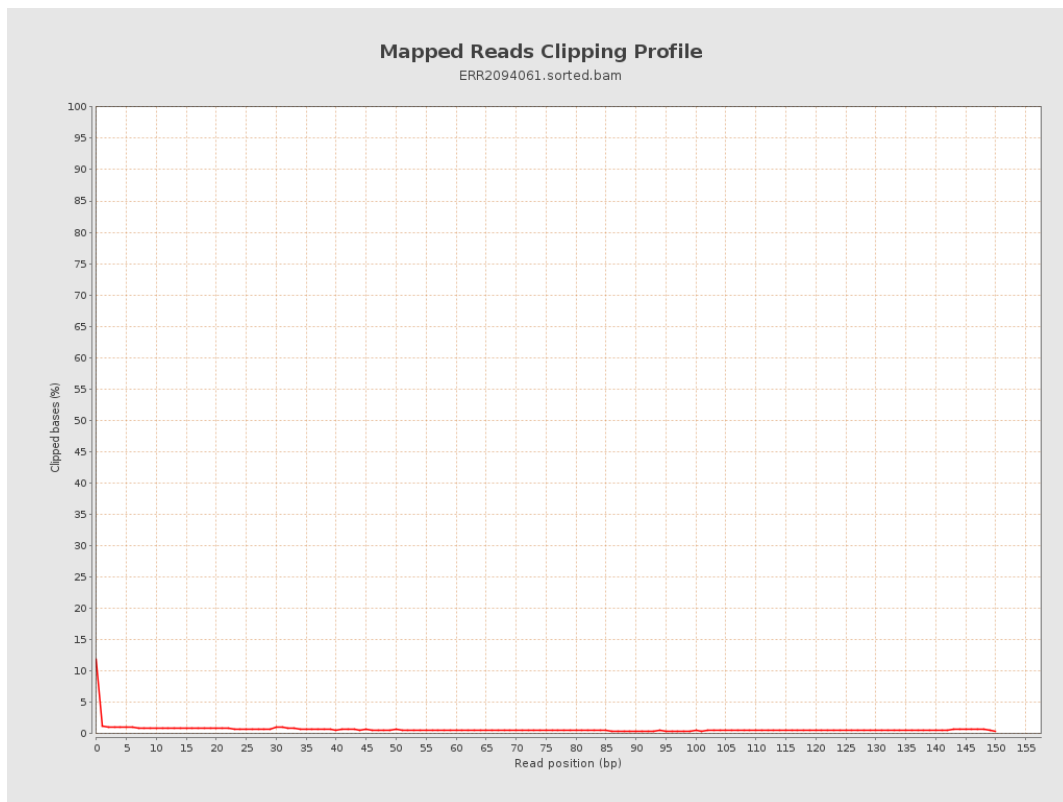
8. Results : Mapped Reads Nucleotide Content



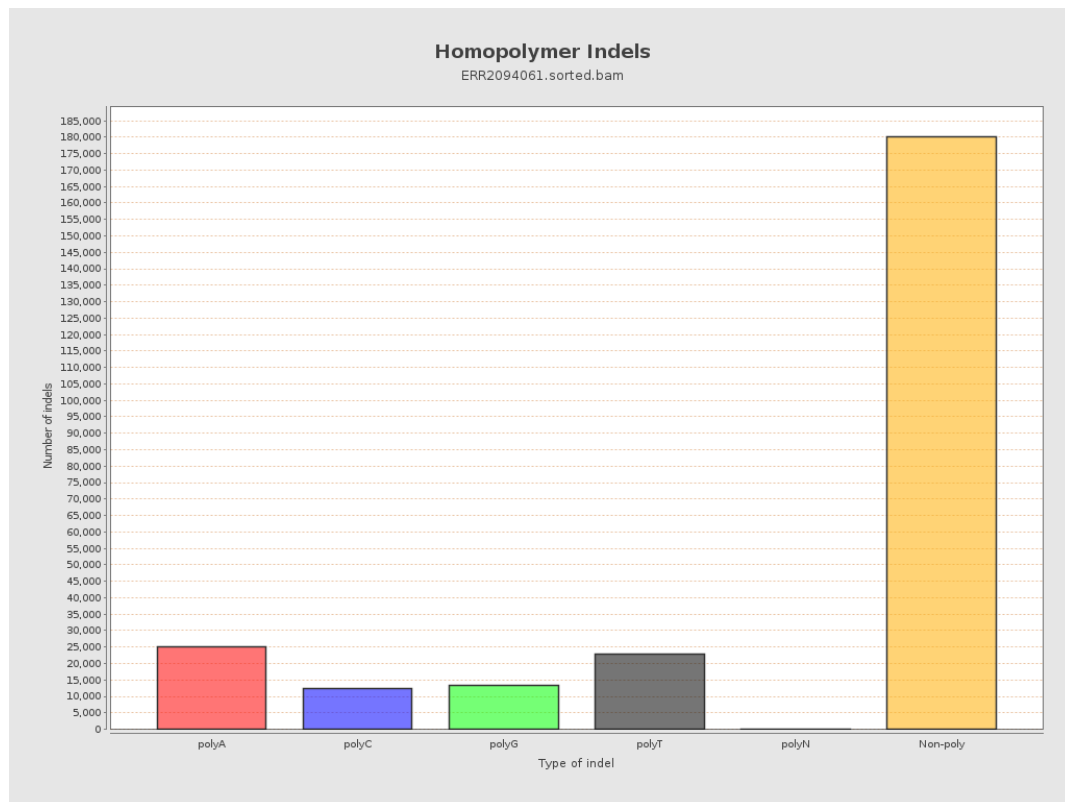
9. Results : Mapped Reads GC-content Distribution



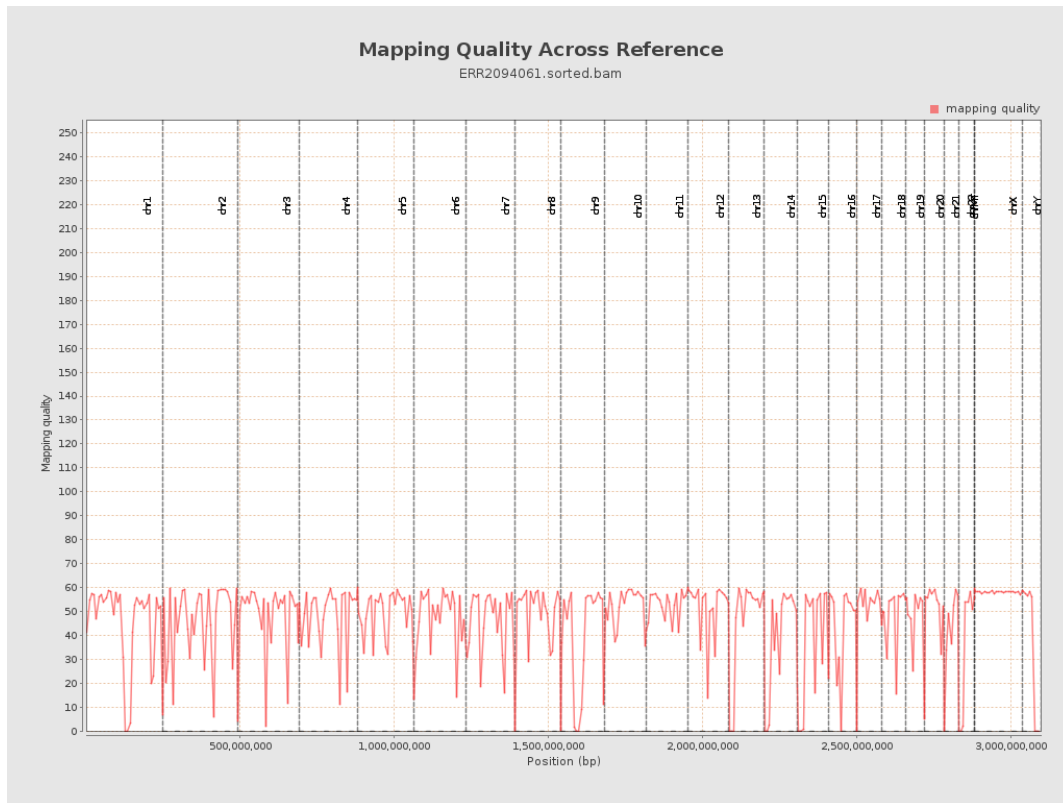
10. Results : Mapped Reads Clipping Profile



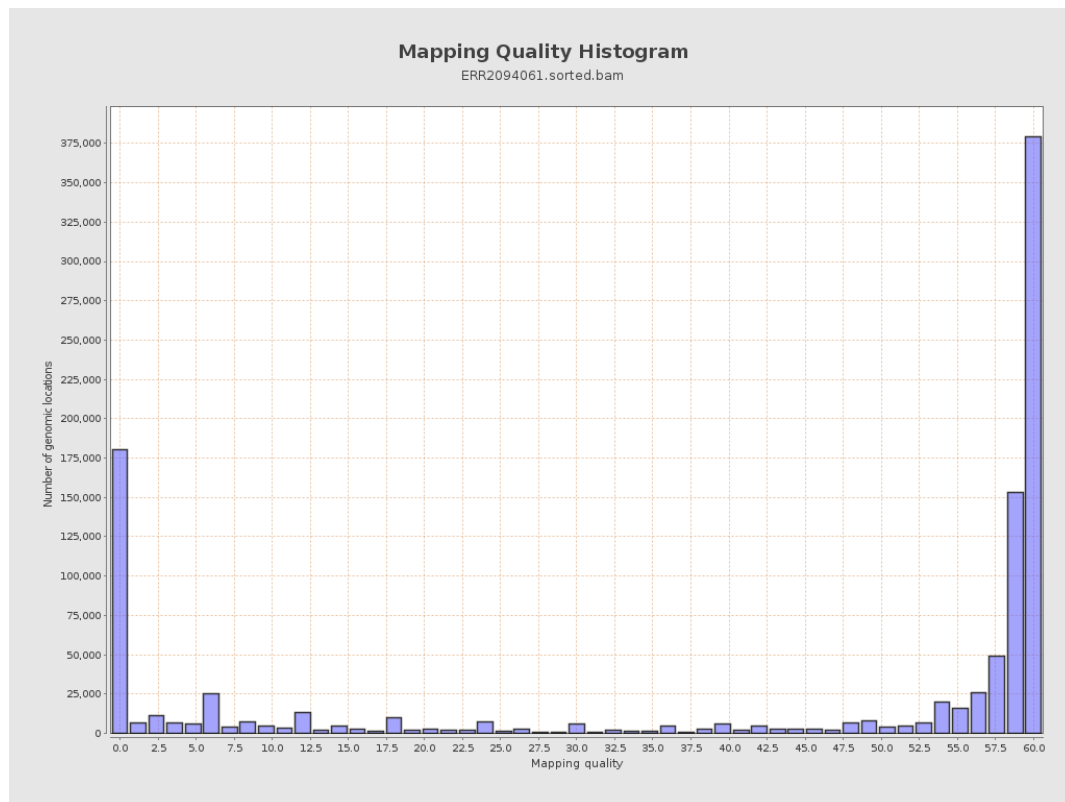
11. Results : Homopolymer Indels



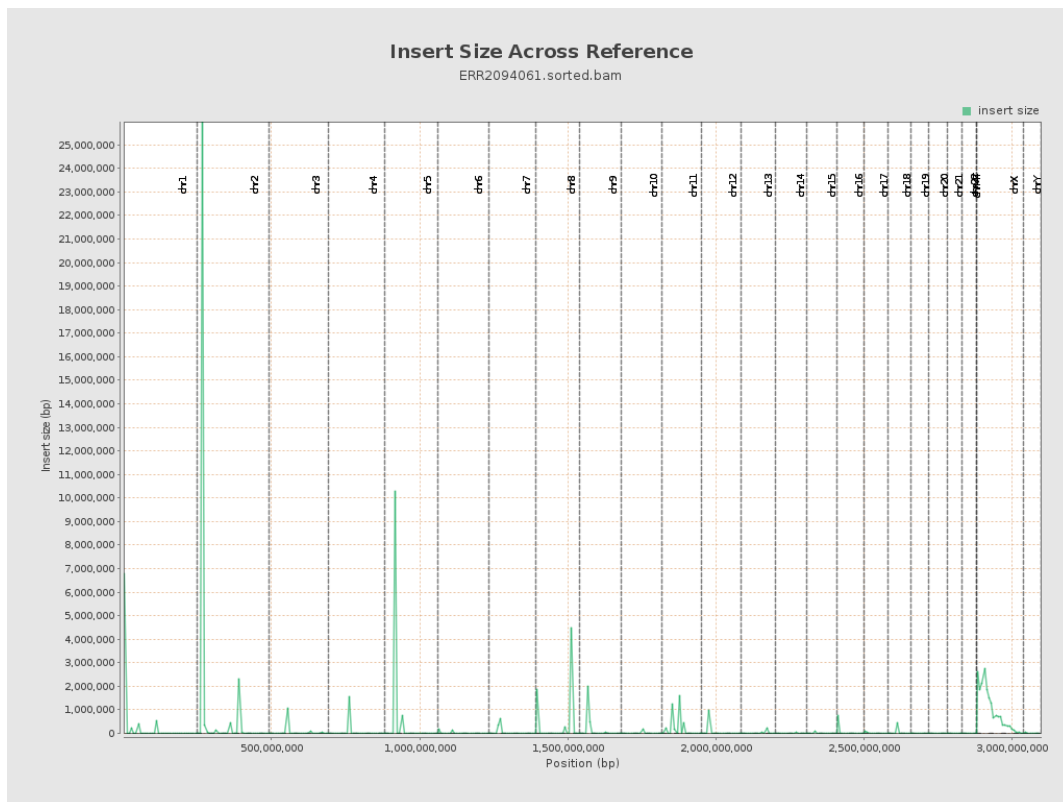
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

