

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:37:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094005.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_ERR2094005 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094005_1.fastq.gz ERR2094005_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:37:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094005.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	423,230
Mapped reads	211,030 / 49.86%
Unmapped reads	212,200 / 50.14%
Mapped paired reads	211,030 / 49.86%
Mapped reads, first in pair	105,144 / 24.84%
Mapped reads, second in pair	105,886 / 25.02%
Mapped reads, both in pair	207,470 / 49.02%
Mapped reads, singletons	3,560 / 0.84%
Secondary alignments	0
Supplementary alignments	1,117 / 0.26%
Read min/max/mean length	30 / 151 / 96.14
Duplicated reads (estimated)	206,927 / 48.89%
Duplication rate	42.84%
Clipped reads	62,789 / 14.84%

2.2. ACGT Content

Number/percentage of A's	7,652,674 / 27.63%
Number/percentage of C's	5,959,632 / 21.52%
Number/percentage of T's	7,546,710 / 27.25%
Number/percentage of G's	6,533,471 / 23.59%
Number/percentage of N's	338 / 0%

GC Percentage	45.11%
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2.3. Coverage

Mean	0.0091
Standard Deviation	11.0086

2.4. Mapping Quality

Mean Mapping Quality	18.6
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2.5. Insert size

Mean	76,809.33
Standard Deviation	2,866,121.68
P25/Median/P75	141 / 186 / 237

2.6. Mismatches and indels

General error rate	3.92%
Mismatches	1,098,222
Insertions	3,107
Mapped reads with at least one insertion	1.39%
Deletions	72,989
Mapped reads with at least one deletion	33.39%
Homopolymer indels	32.46%

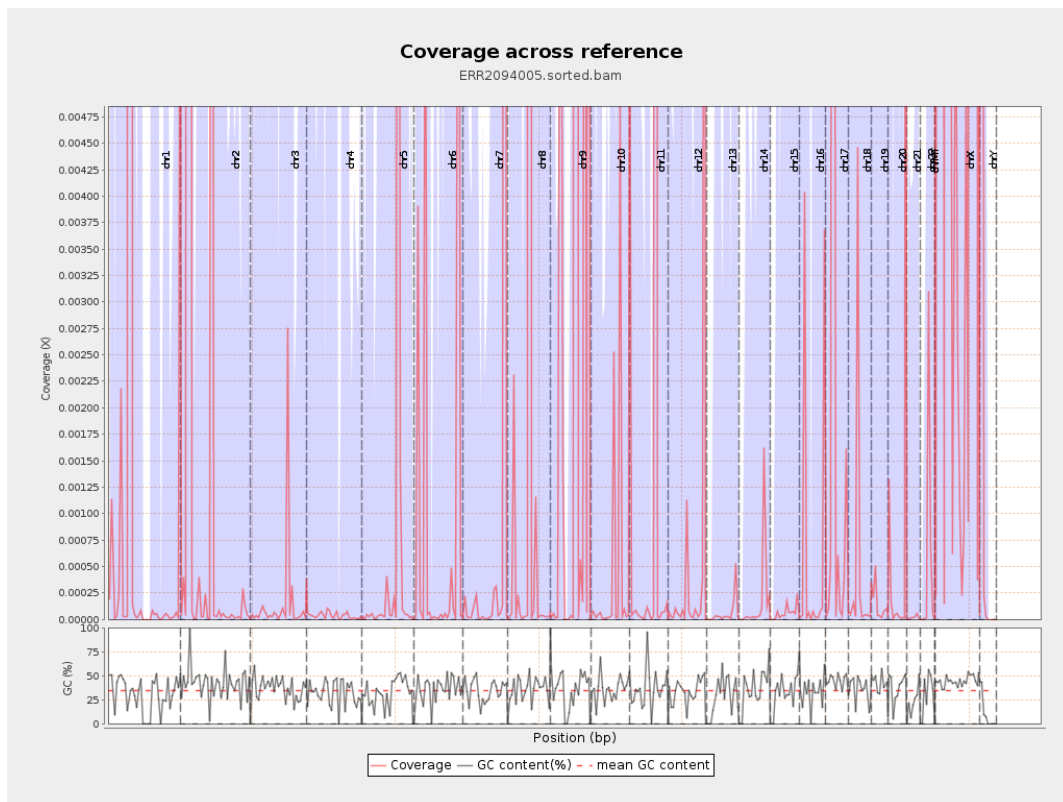
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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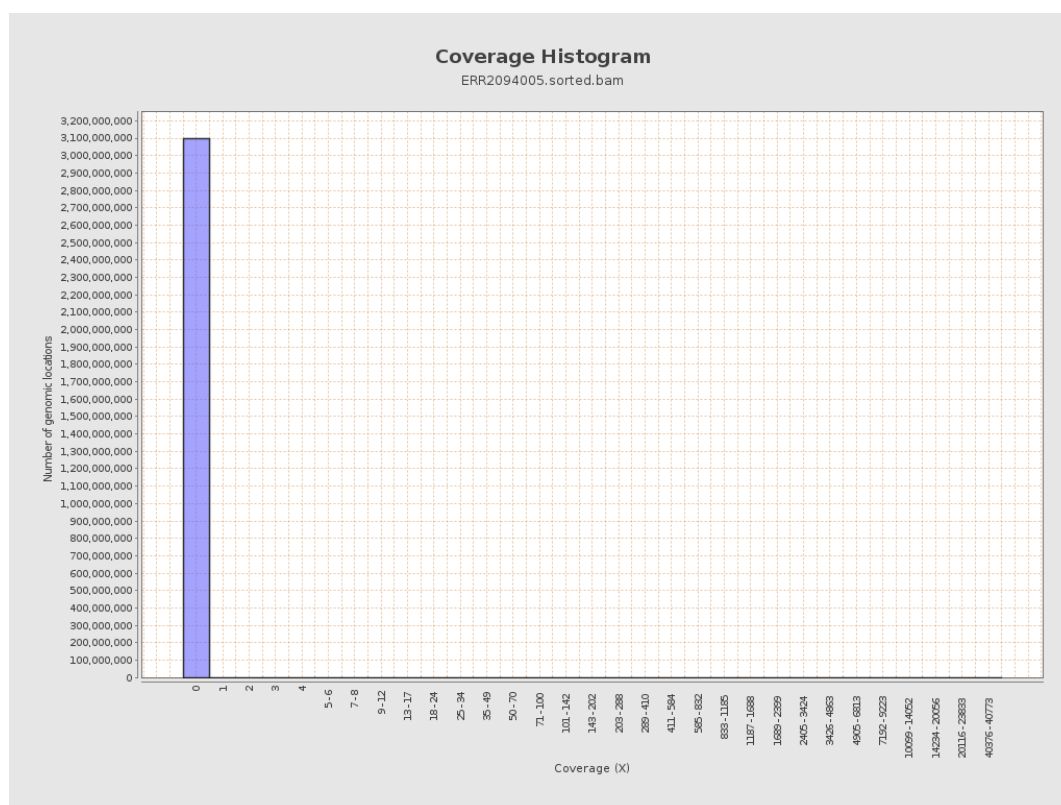
		bases	coverage	deviation
chr1	249250621	1236419	0.005	7.6704
chr2	243199373	889425	0.0037	3.0097
chr3	198022430	32081	0.0002	0.109
chr4	191154276	7006	0	0.0121
chr5	180915260	157766	0.0009	0.8022
chr6	171115067	171797	0.001	0.5262
chr7	159138663	167685	0.0011	1.0086
chr8	146364022	2011085	0.0137	10.803
chr9	141213431	991296	0.007	4.1651
chr10	135534747	61490	0.0005	0.2766
chr11	135006516	258556	0.0019	1.5823
chr12	133851895	123181	0.0009	0.6941
chr13	115169878	7058	0.0001	0.0306
chr14	107349540	17459	0.0002	0.0921
chr15	102531392	6704	0.0001	0.0185
chr16	90354753	63761	0.0007	0.3174
chr17	81195210	194572	0.0024	1.599
chr18	78077248	39338	0.0005	0.3225
chr19	59128983	8651	0.0001	0.0385
chr20	63025520	48228	0.0008	0.384
chr21	48129895	971	0	0.0049
chr22	51304566	29930	0.0006	0.2381
chrMT	16571	13207352	797.016	4,043.6024
chrX	155270560	8030642	0.0517	18.7913

chrY	59373566	465601	0.0078	5.0418
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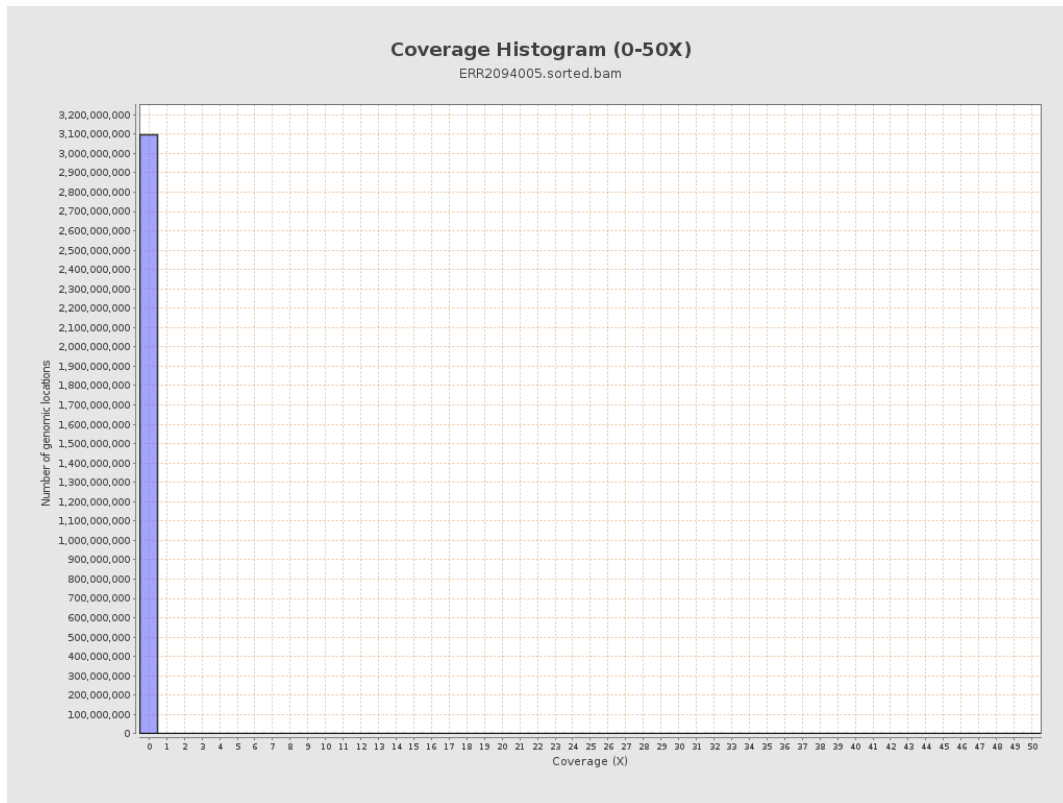
3. Results : Coverage across reference



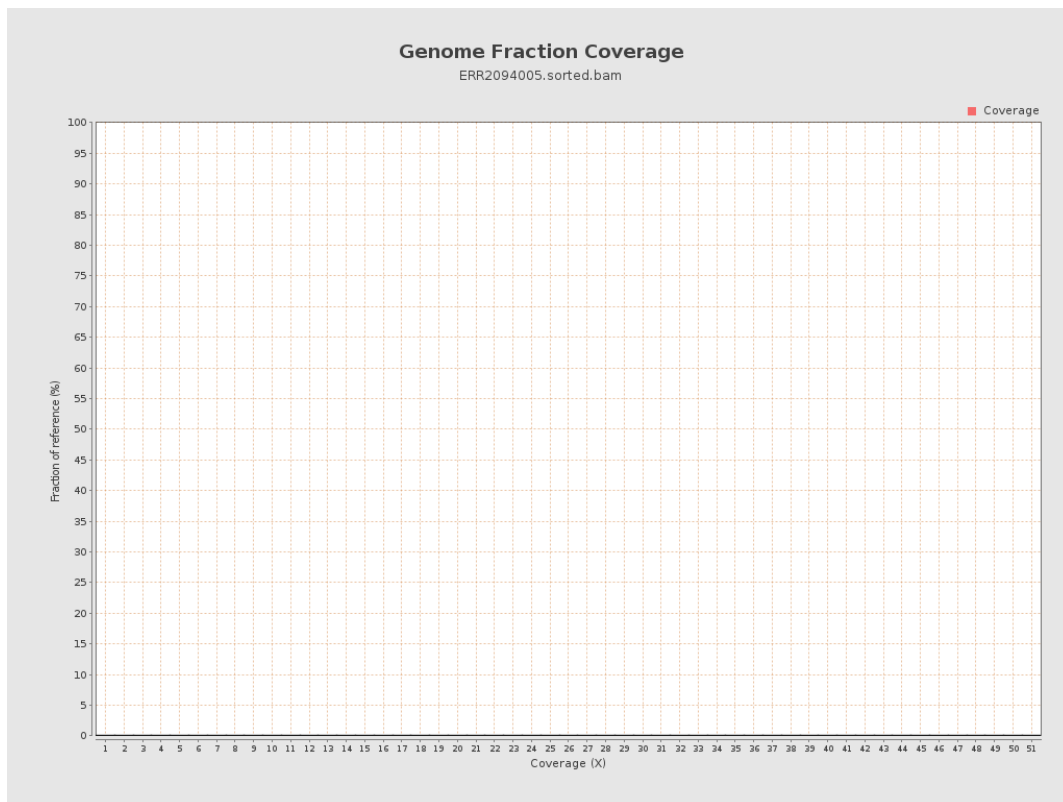
4. Results : Coverage Histogram



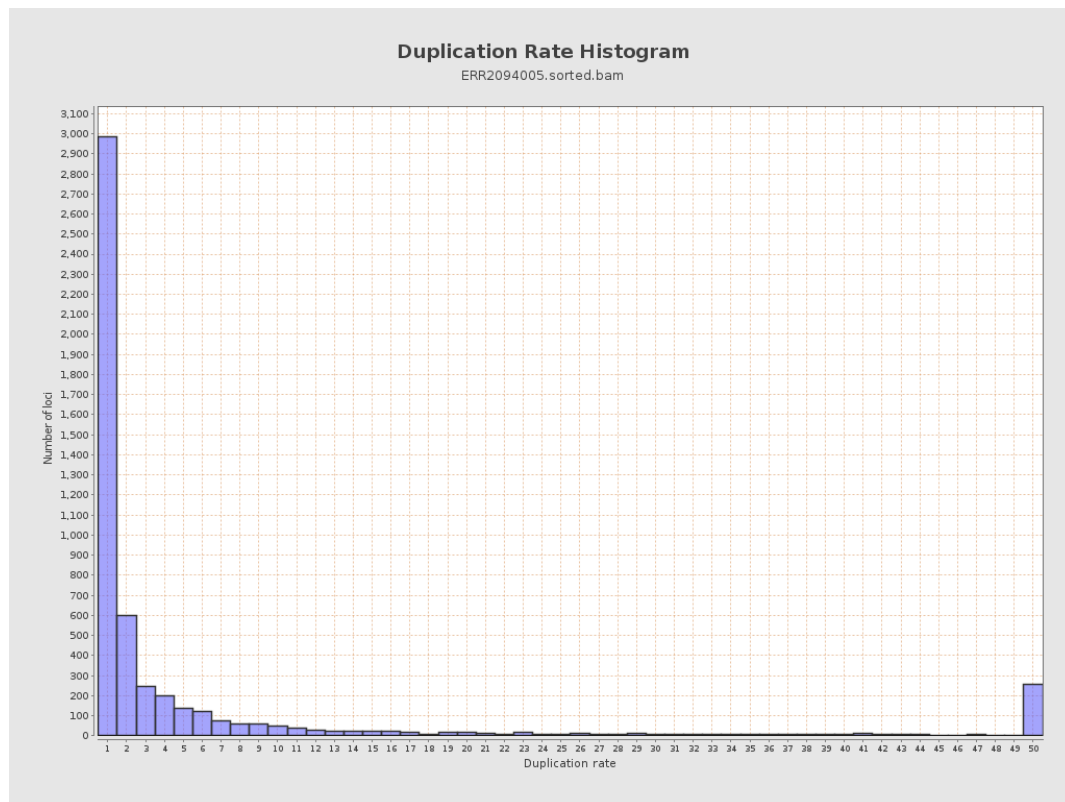
5. Results : Coverage Histogram (0-50X)



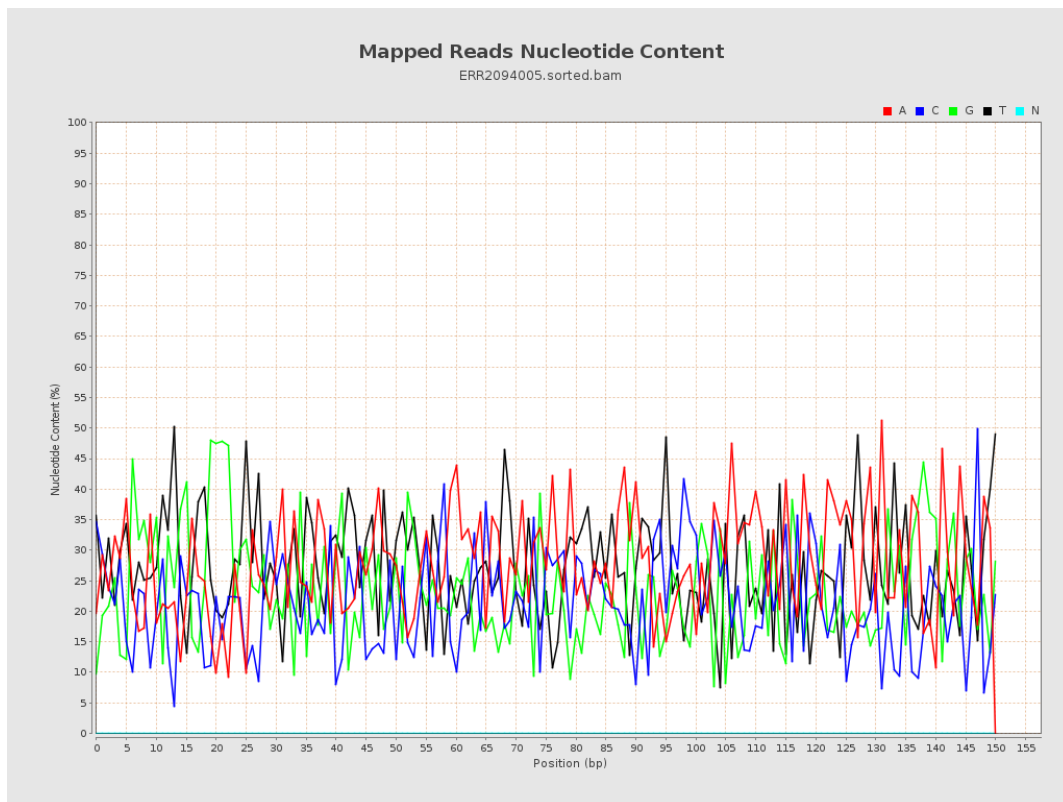
6. Results : Genome Fraction Coverage



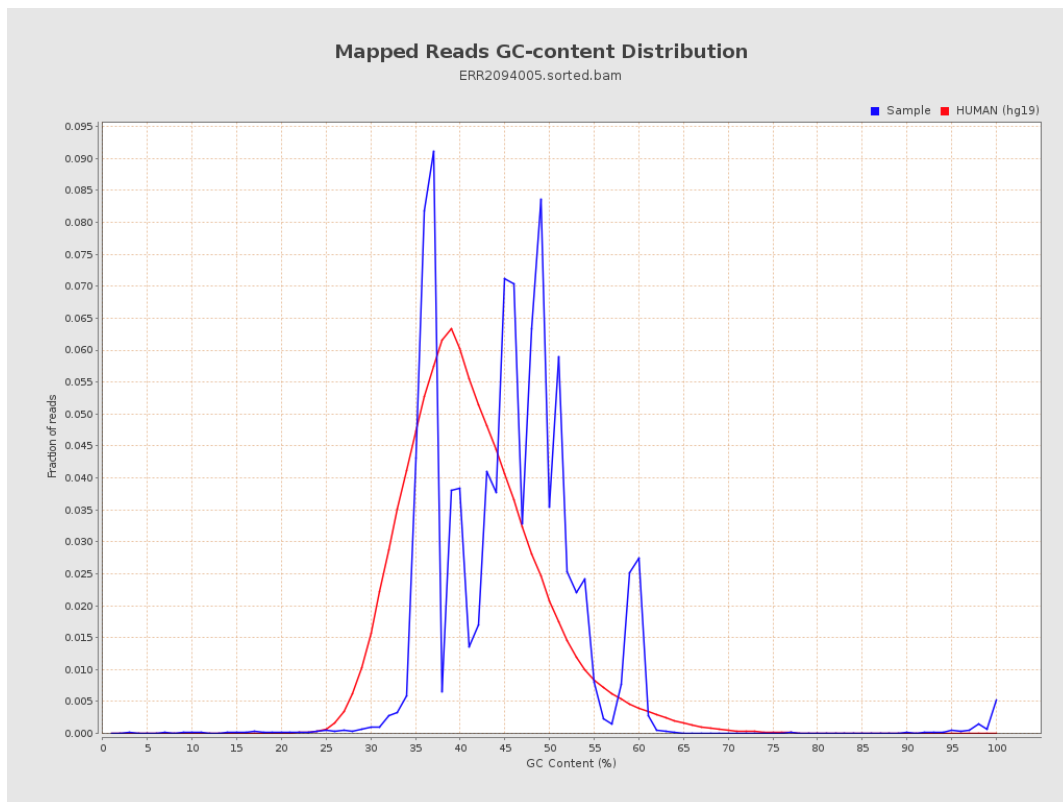
7. Results : Duplication Rate Histogram



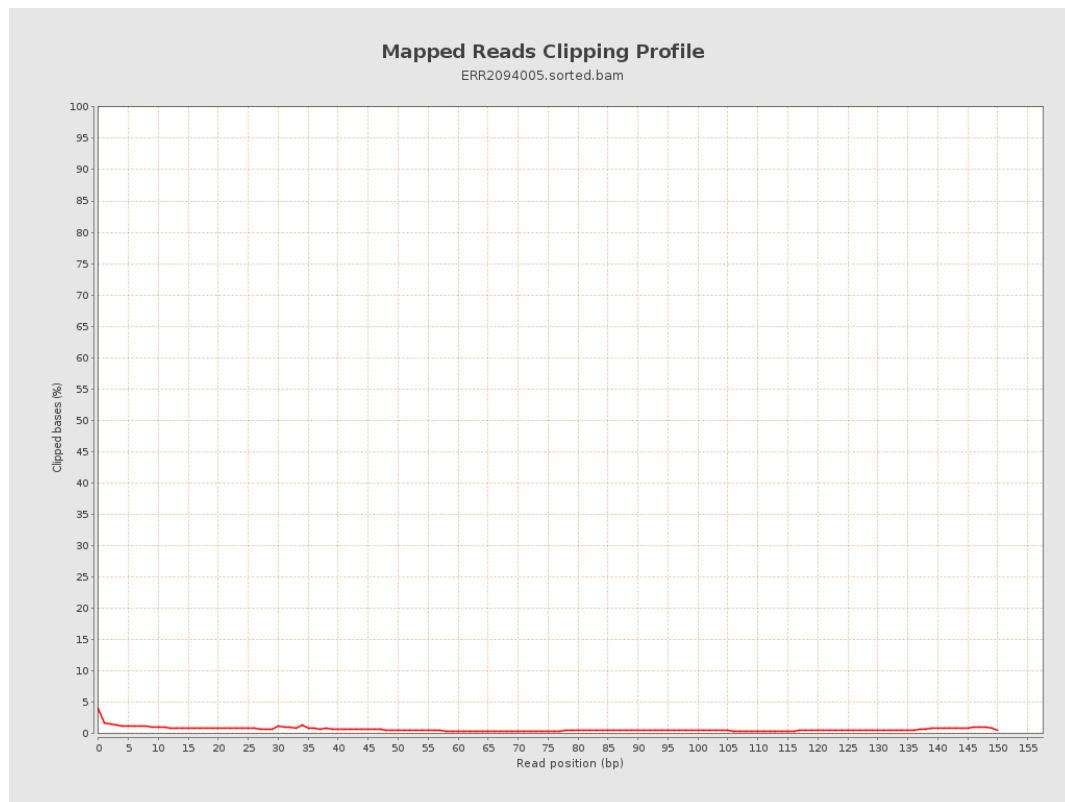
8. Results : Mapped Reads Nucleotide Content



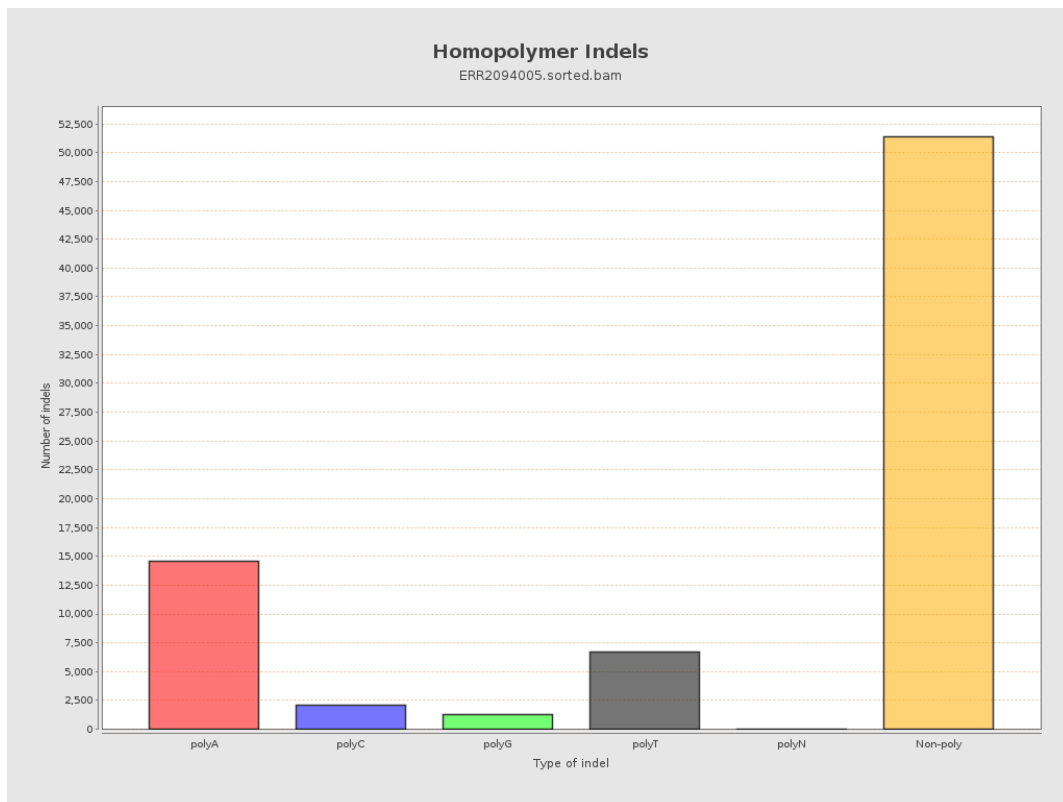
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



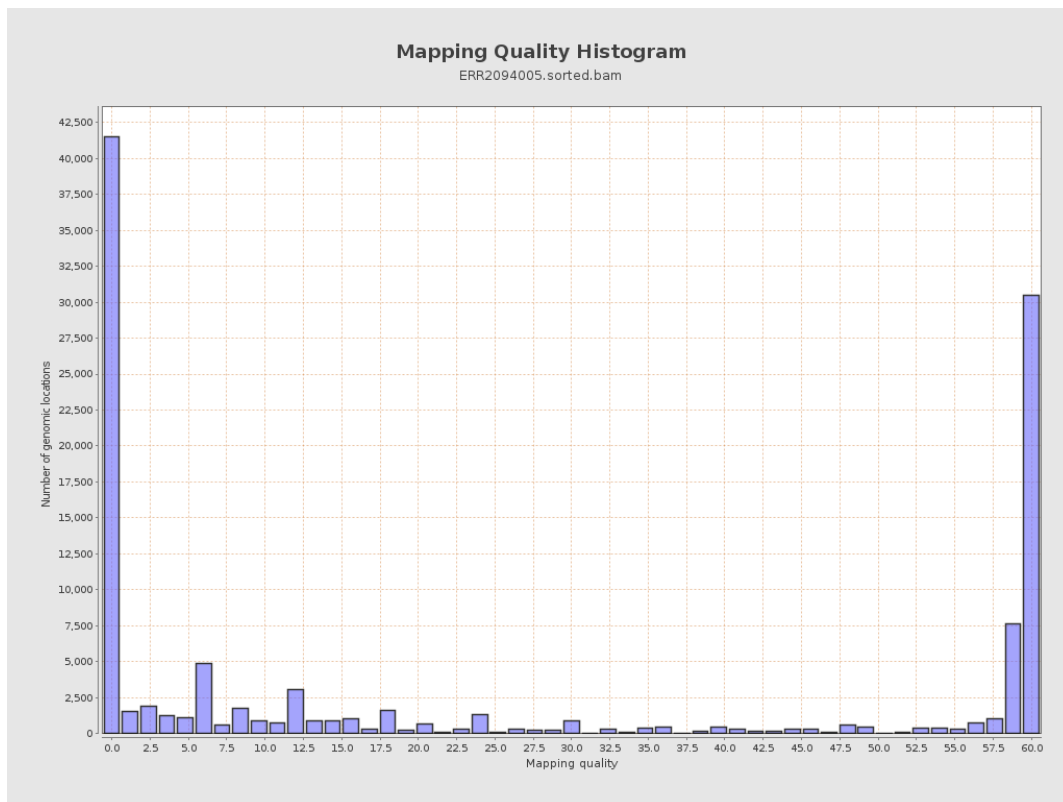
11. Results : Homopolymer Indels



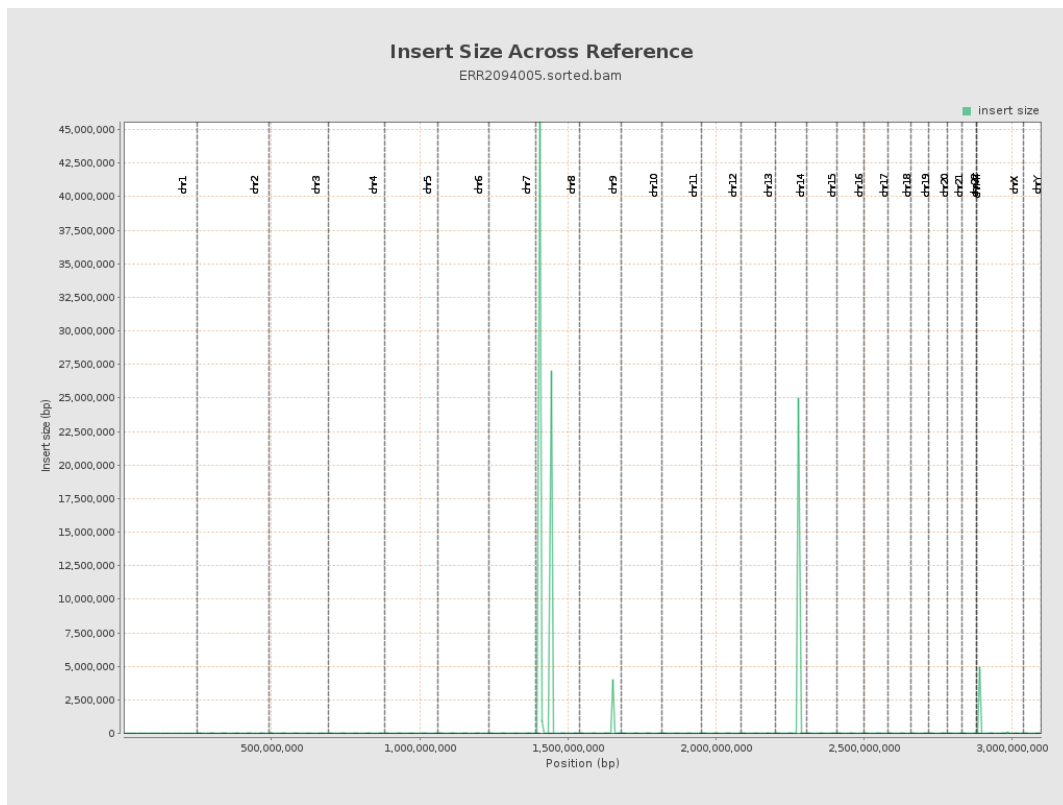
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

