

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:59:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094076.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_ERR2094076 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094076_1.fastq.gz ERR2094076_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:59:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	367,378
Mapped reads	341,336 / 92.91%
Unmapped reads	26,042 / 7.09%
Mapped paired reads	341,336 / 92.91%
Mapped reads, first in pair	171,566 / 46.7%
Mapped reads, second in pair	169,770 / 46.21%
Mapped reads, both in pair	338,396 / 92.11%
Mapped reads, singletons	2,940 / 0.8%
Secondary alignments	0
Supplementary alignments	11,647 / 3.17%
Read min/max/mean length	30 / 151 / 137.64
Duplicated reads (estimated)	325,776 / 88.68%
Duplication rate	48.49%
Clipped reads	132,605 / 36.09%

2.2. ACGT Content

Number/percentage of A's	11,572,918 / 26.37%
Number/percentage of C's	10,346,973 / 23.57%
Number/percentage of T's	11,002,984 / 25.07%
Number/percentage of G's	10,967,165 / 24.99%
Number/percentage of N's	375 / 0%

GC Percentage	48.56%
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2.3. Coverage

Mean	0.0145
Standard Deviation	4.2098

2.4. Mapping Quality

Mean Mapping Quality	36.23
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2.5. Insert size

Mean	276,817.17
Standard Deviation	4,672,389.73
P25/Median/P75	133 / 166 / 197

2.6. Mismatches and indels

General error rate	4.39%
Mismatches	1,875,991
Insertions	26,479
Mapped reads with at least one insertion	7.66%
Deletions	146,739
Mapped reads with at least one deletion	40.97%
Homopolymer indels	28.41%

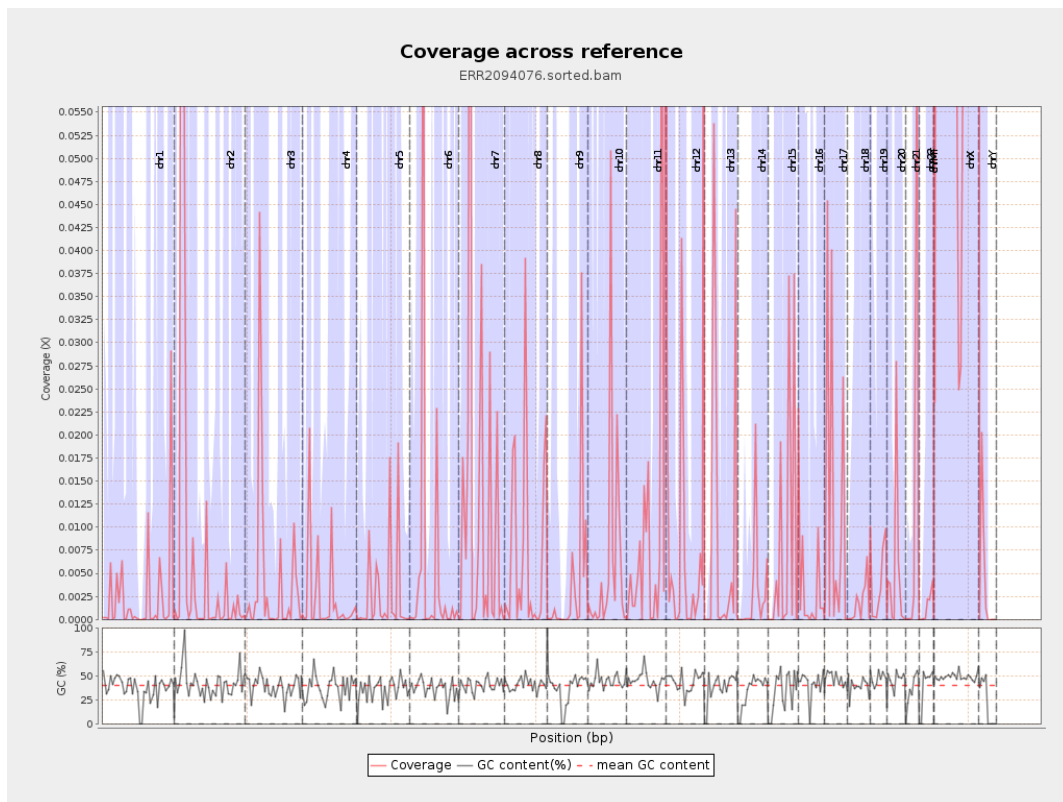
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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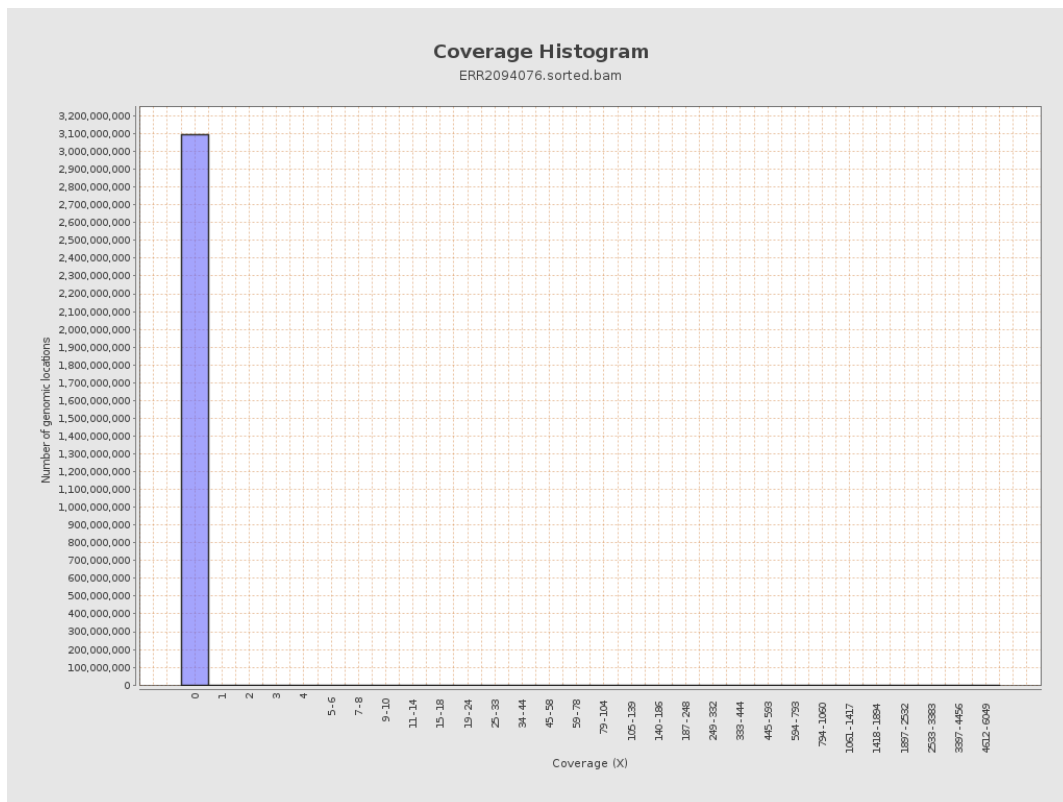
		bases	coverage	deviation
chr1	249250621	588225	0.0024	1.1732
chr2	243199373	1760117	0.0072	2.9084
chr3	198022430	727151	0.0037	1.3793
chr4	191154276	415972	0.0022	1.1219
chr5	180915260	477192	0.0026	1.3962
chr6	171115067	946565	0.0055	3.8719
chr7	159138663	2059857	0.0129	5.0096
chr8	146364022	1035497	0.0071	2.2585
chr9	141213431	505202	0.0036	1.8062
chr10	135534747	838803	0.0062	2.8772
chr11	135006516	1274018	0.0094	2.8427
chr12	133851895	1040919	0.0078	2.6952
chr13	115169878	1038516	0.009	2.7831
chr14	107349540	317171	0.003	1.3206
chr15	102531392	777155	0.0076	2.6899
chr16	90354753	299194	0.0033	1.2942
chr17	81195210	991490	0.0122	3.3215
chr18	78077248	141753	0.0018	0.5275
chr19	59128983	209686	0.0035	0.8219
chr20	63025520	326564	0.0052	1.7123
chr21	48129895	593476	0.0123	4.9438
chr22	51304566	68320	0.0013	0.3488
chrMT	16571	905294	54.6312	258.526
chrX	155270560	27438290	0.1767	15.0179

chrY	59373566	235256	0.004	1.0442
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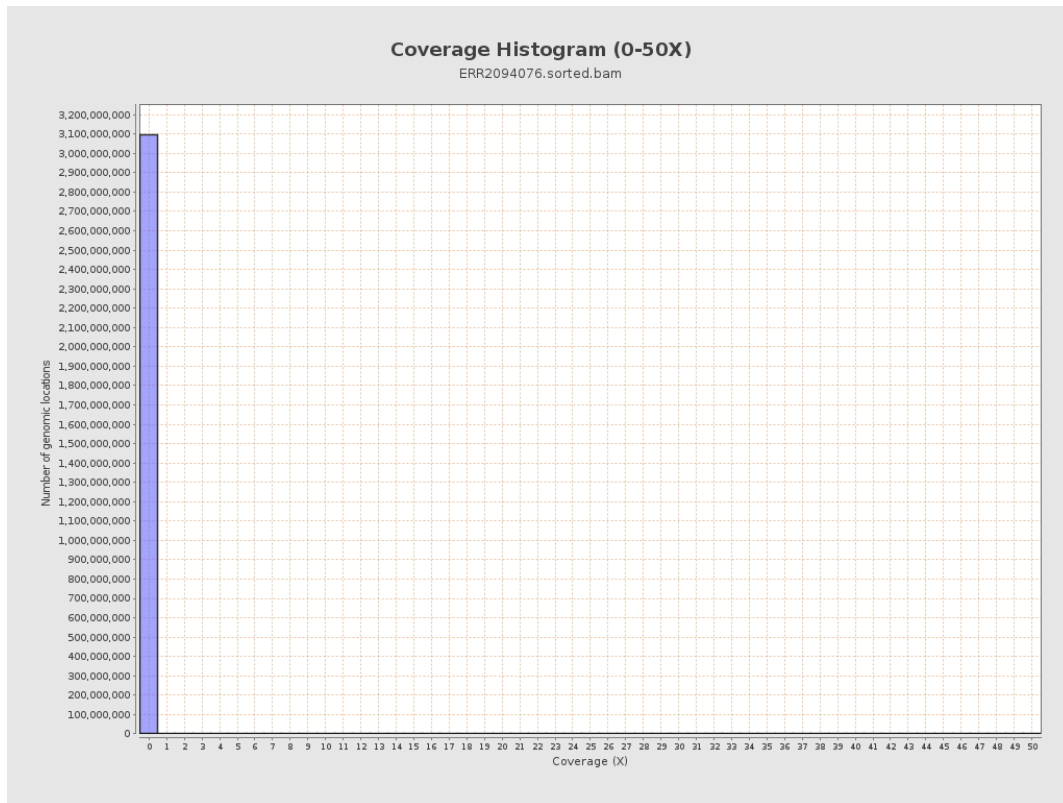
3. Results : Coverage across reference



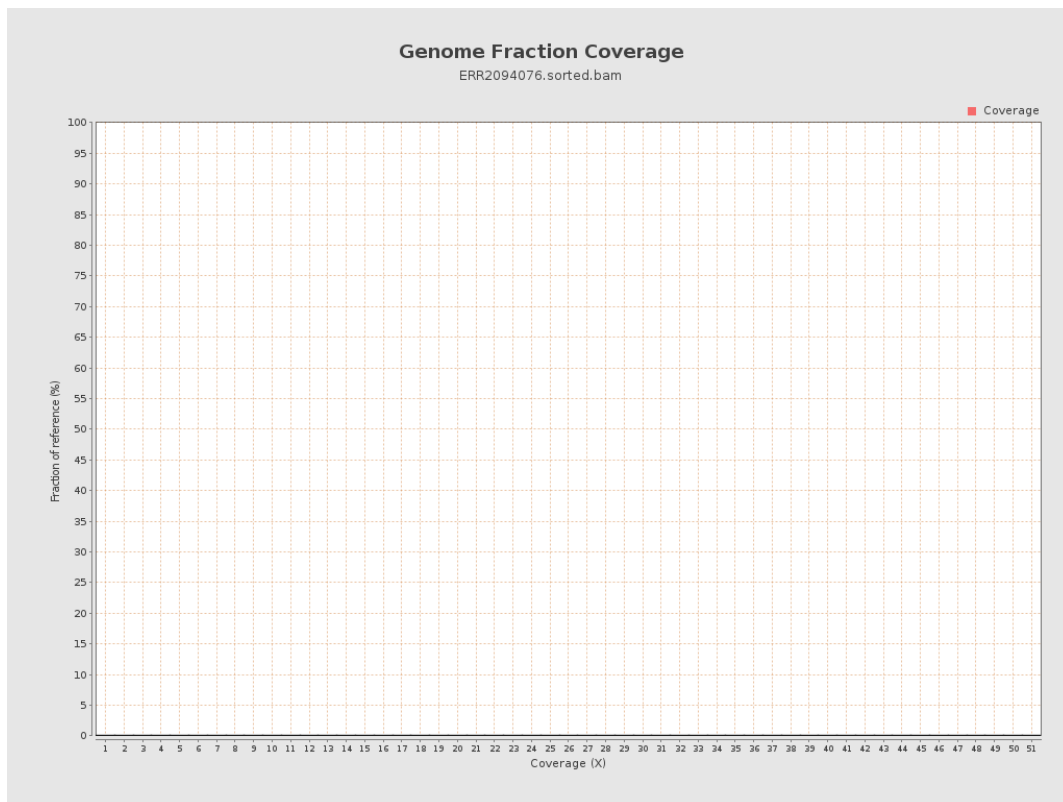
4. Results : Coverage Histogram



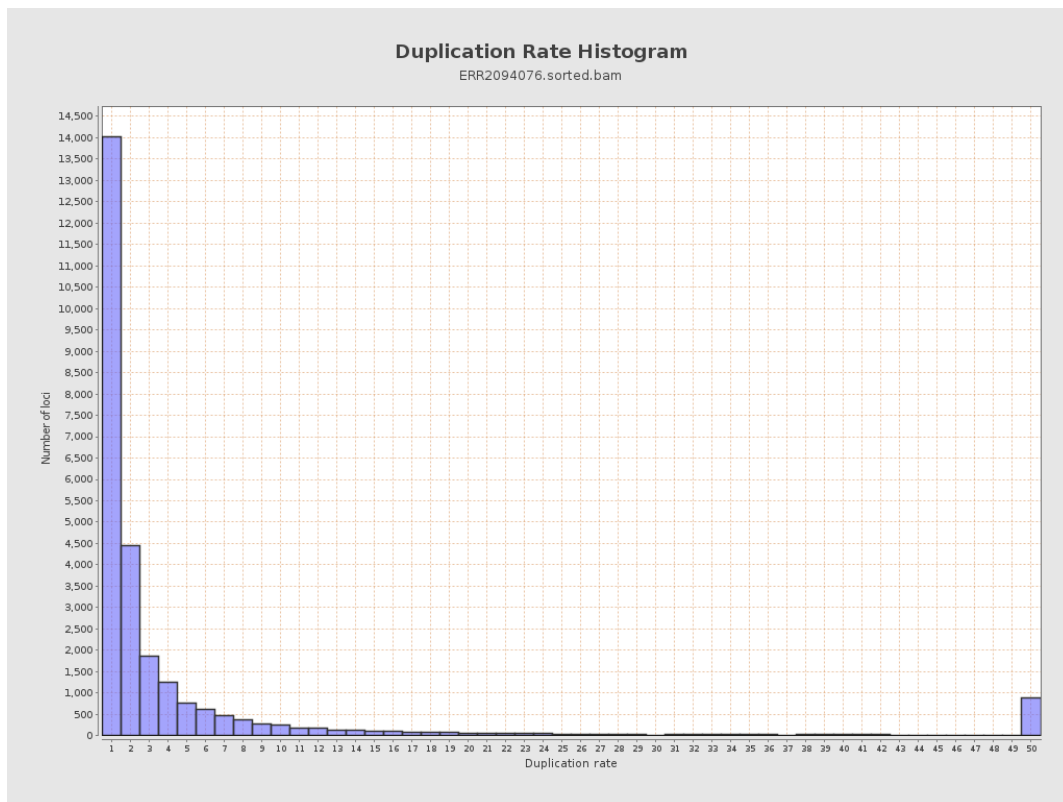
5. Results : Coverage Histogram (0-50X)



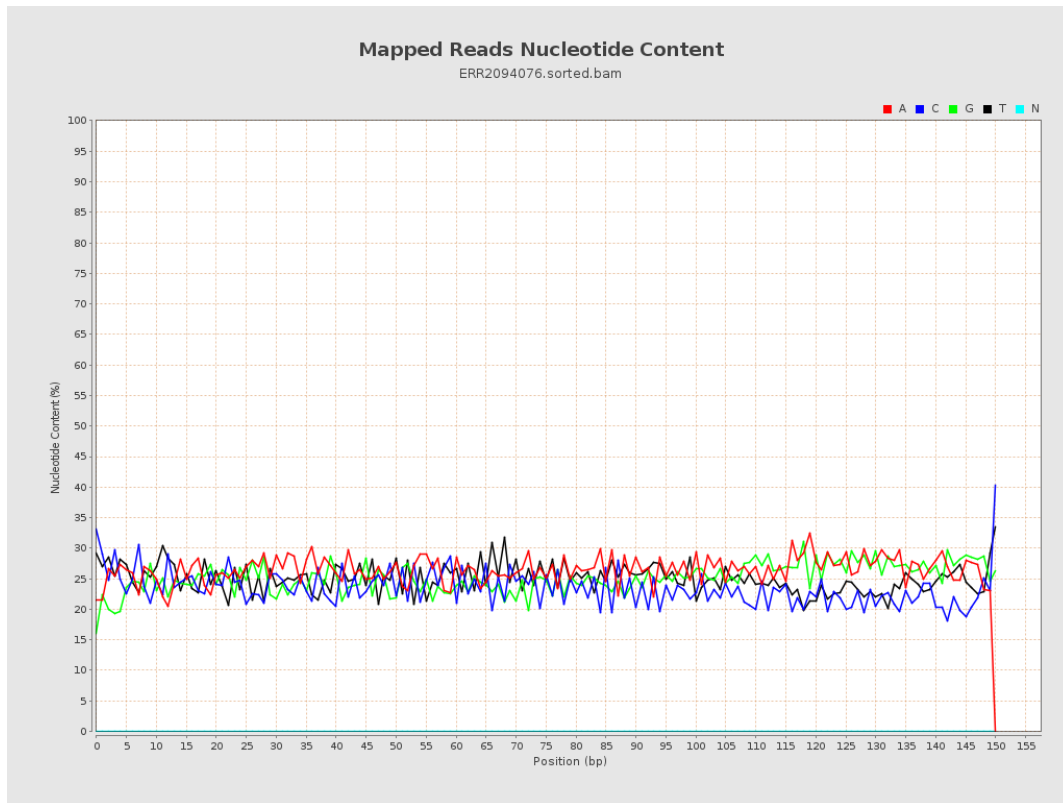
6. Results : Genome Fraction Coverage



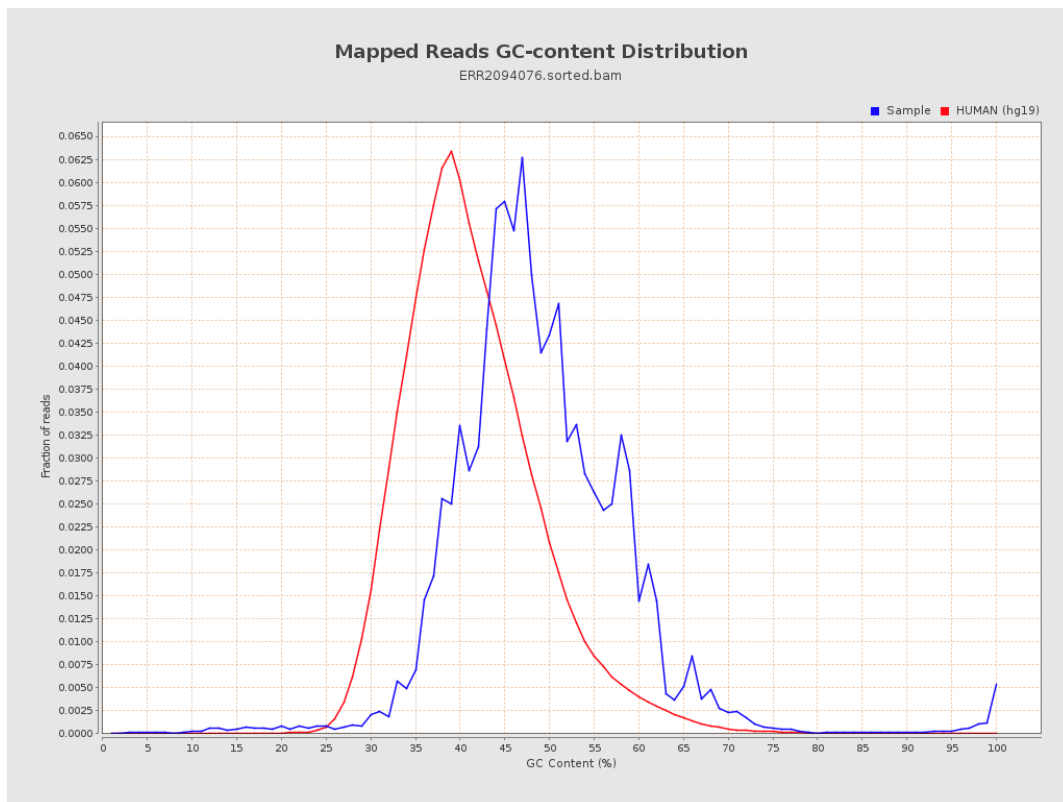
7. Results : Duplication Rate Histogram



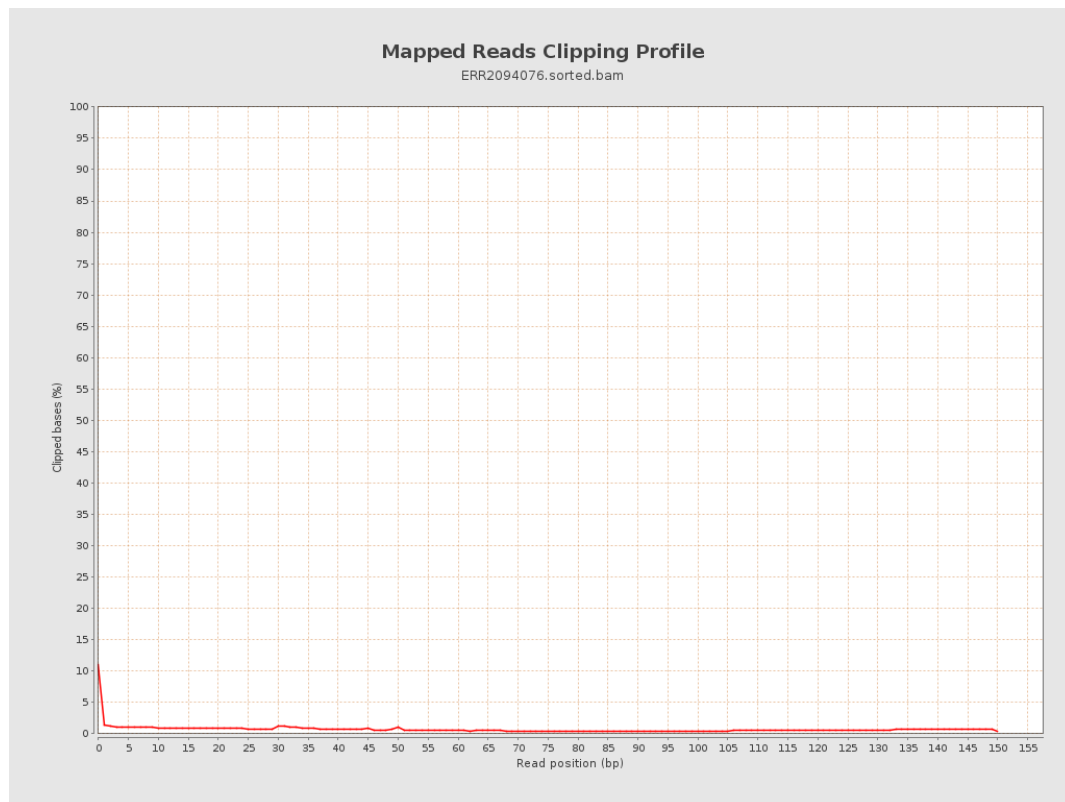
8. Results : Mapped Reads Nucleotide Content



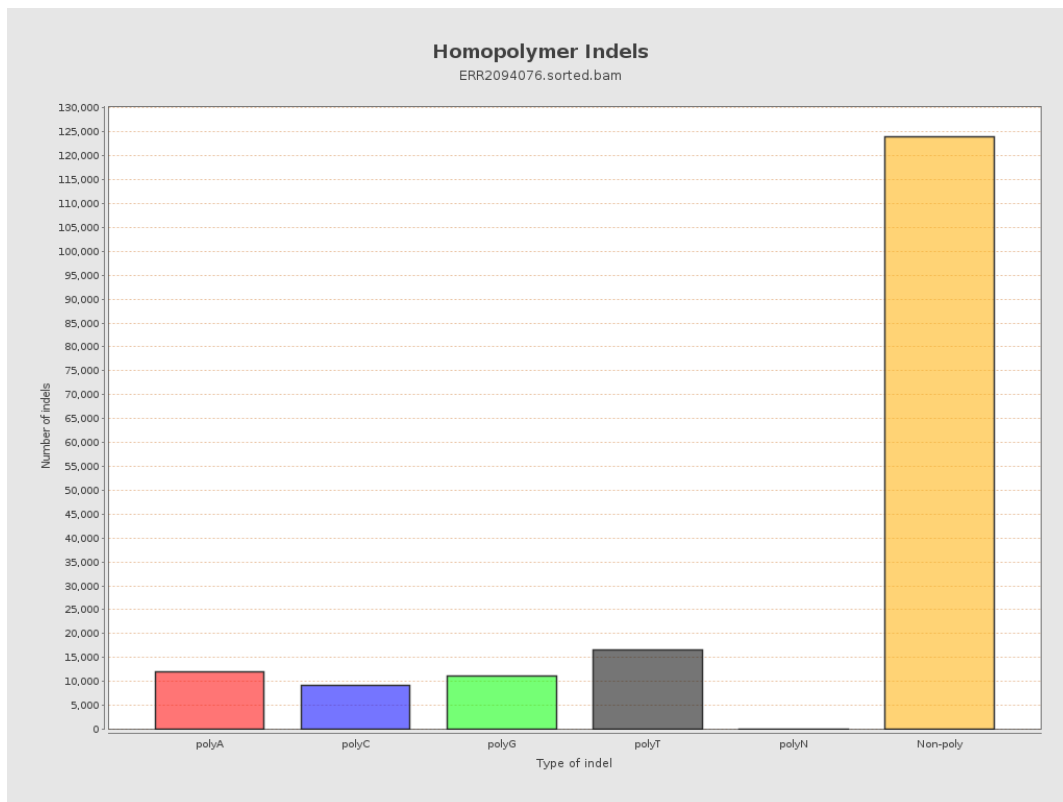
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



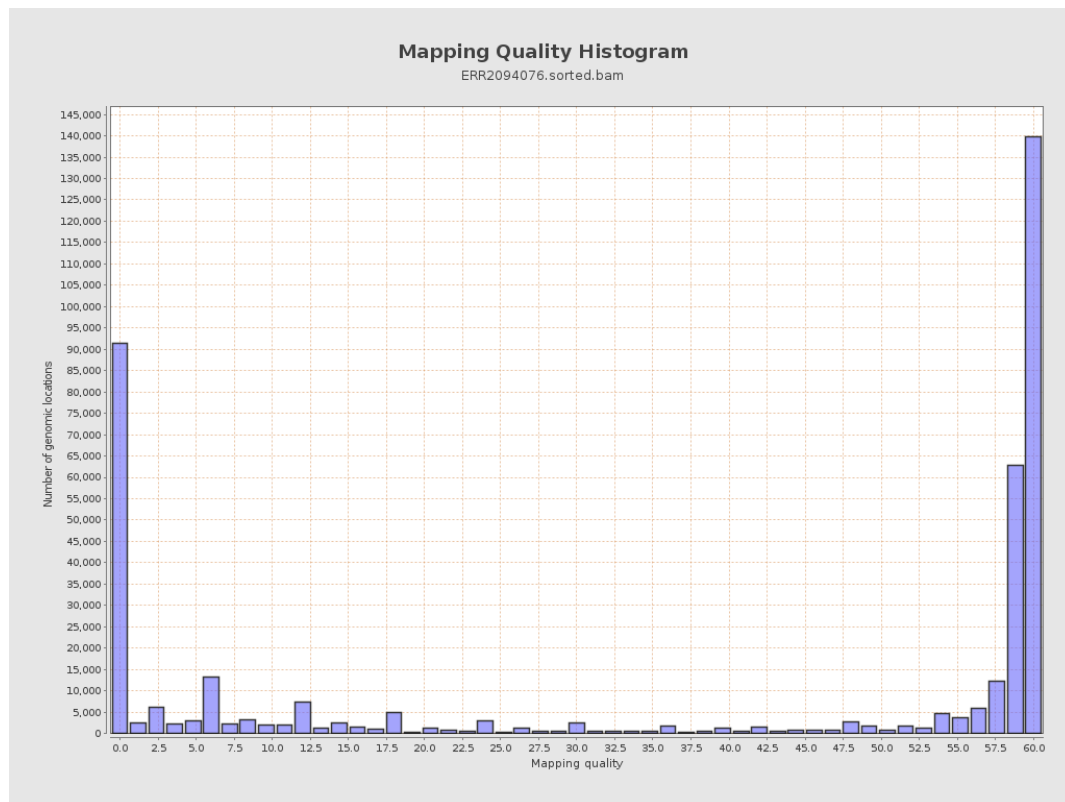
11. Results : Homopolymer Indels



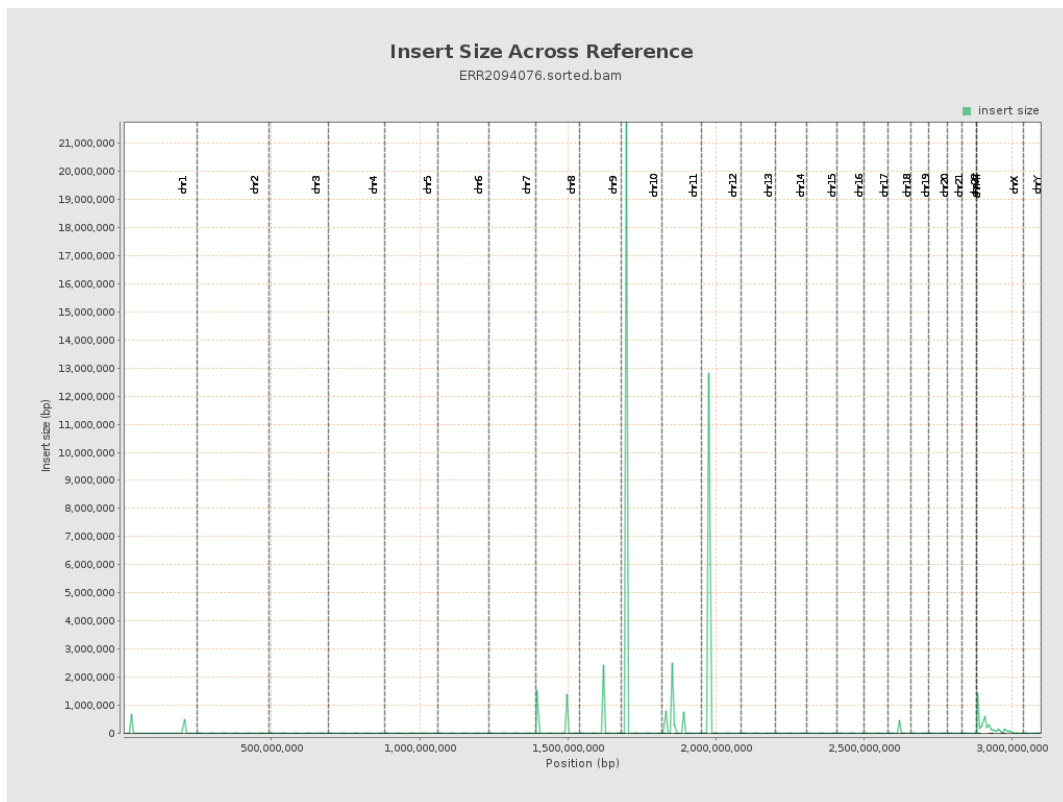
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

