

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:30:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094064.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_ERR2094064 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094064_1.fastq.gz ERR2094064_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:30:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	357,494
Mapped reads	341,789 / 95.61%
Unmapped reads	15,705 / 4.39%
Mapped paired reads	341,789 / 95.61%
Mapped reads, first in pair	171,709 / 48.03%
Mapped reads, second in pair	170,080 / 47.58%
Mapped reads, both in pair	339,318 / 94.92%
Mapped reads, singletons	2,471 / 0.69%
Secondary alignments	0
Supplementary alignments	10,927 / 3.06%
Read min/max/mean length	30 / 151 / 141.83
Duplicated reads (estimated)	322,776 / 90.29%
Duplication rate	49.32%
Clipped reads	131,353 / 36.74%

2.2. ACGT Content

Number/percentage of A's	11,855,464 / 26.47%
Number/percentage of C's	10,526,050 / 23.51%
Number/percentage of T's	11,307,740 / 25.25%
Number/percentage of G's	11,092,161 / 24.77%
Number/percentage of N's	461 / 0%

GC Percentage	48.27%
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2.3. Coverage

Mean	0.0148
Standard Deviation	3.9698

2.4. Mapping Quality

Mean Mapping Quality	38.15
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2.5. Insert size

Mean	380,988.33
Standard Deviation	5,652,359.45
P25/Median/P75	144 / 172 / 205

2.6. Mismatches and indels

General error rate	4.05%
Mismatches	1,772,653
Insertions	24,409
Mapped reads with at least one insertion	7.03%
Deletions	139,420
Mapped reads with at least one deletion	38.82%
Homopolymer indels	26.93%

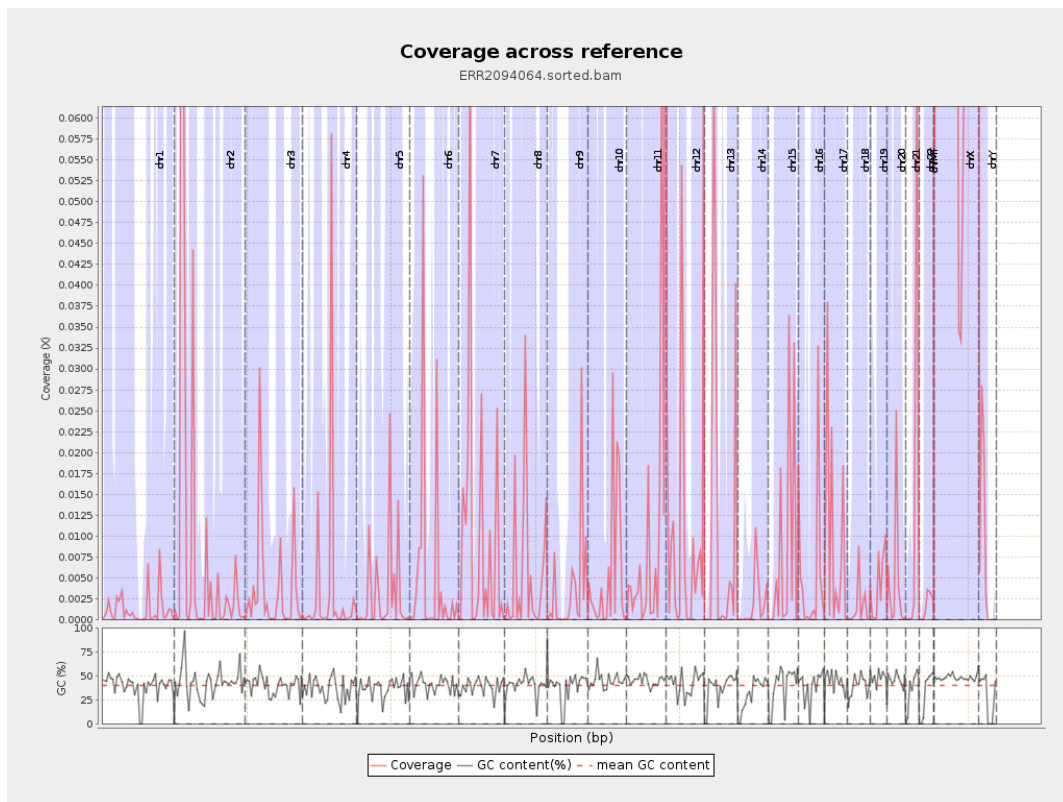
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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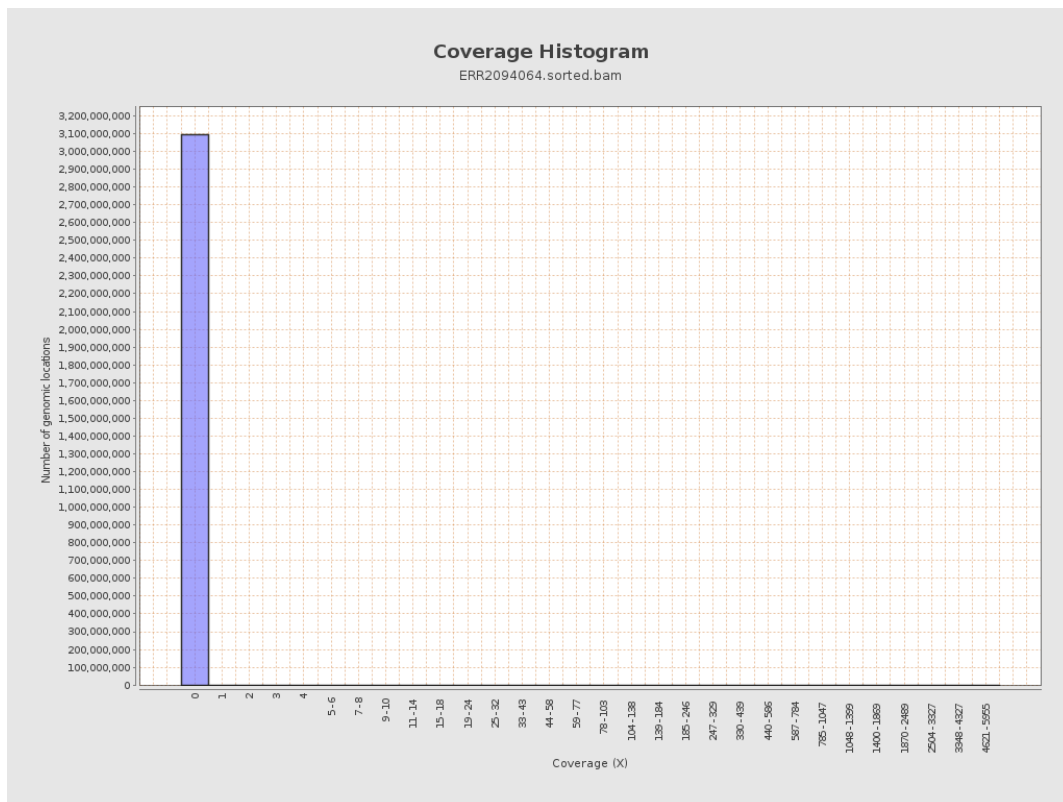
		bases	coverage	deviation
chr1	249250621	295586	0.0012	0.4607
chr2	243199373	2011591	0.0083	3.0887
chr3	198022430	685123	0.0035	1.1846
chr4	191154276	669884	0.0035	1.5709
chr5	180915260	559261	0.0031	1.497
chr6	171115067	886659	0.0052	2.6804
chr7	159138663	1479296	0.0093	3.1959
chr8	146364022	791227	0.0054	1.9575
chr9	141213431	502859	0.0036	1.5546
chr10	135534747	717391	0.0053	2.0319
chr11	135006516	1300448	0.0096	2.6393
chr12	133851895	1290415	0.0096	3.0723
chr13	115169878	1171913	0.0102	3.0727
chr14	107349540	212336	0.002	0.7695
chr15	102531392	751152	0.0073	2.6767
chr16	90354753	478314	0.0053	1.9208
chr17	81195210	767665	0.0095	2.706
chr18	78077248	120106	0.0015	0.6584
chr19	59128983	232314	0.0039	0.933
chr20	63025520	290816	0.0046	1.4775
chr21	48129895	653776	0.0136	5.2069
chr22	51304566	80614	0.0016	0.321
chrMT	16571	1371824	82.7846	392.4126
chrX	155270560	28028341	0.1805	14.2438

chrY	59373566	437577	0.0074	1.9232
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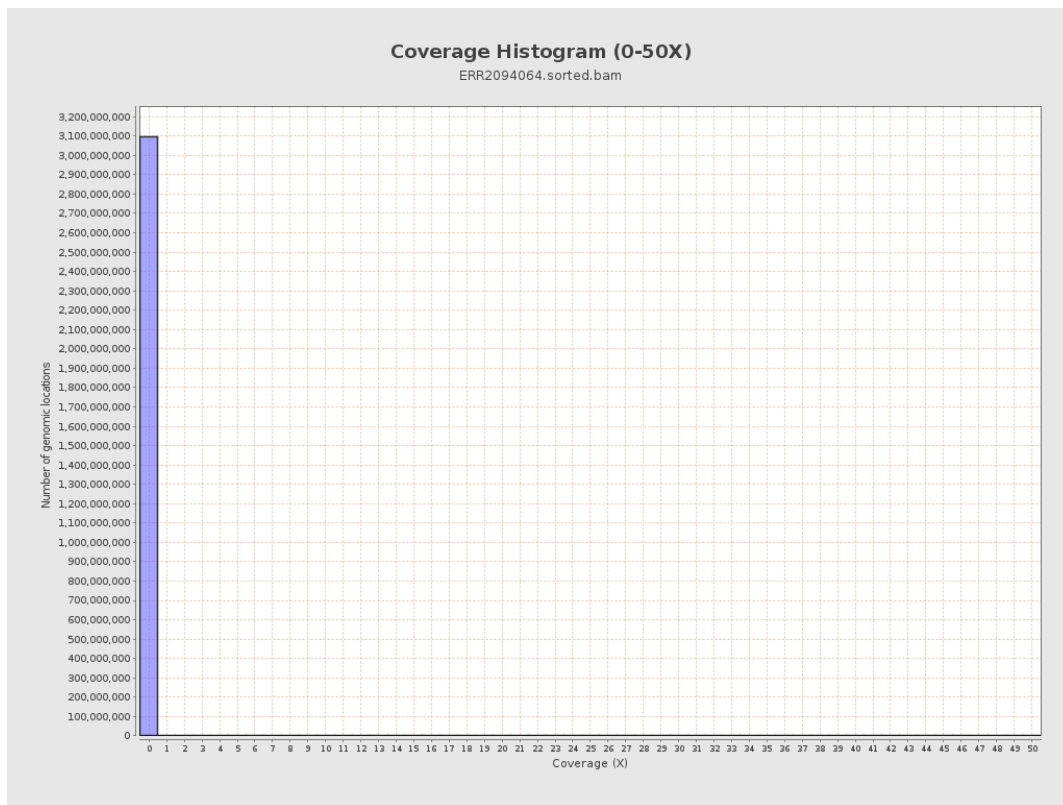
3. Results : Coverage across reference



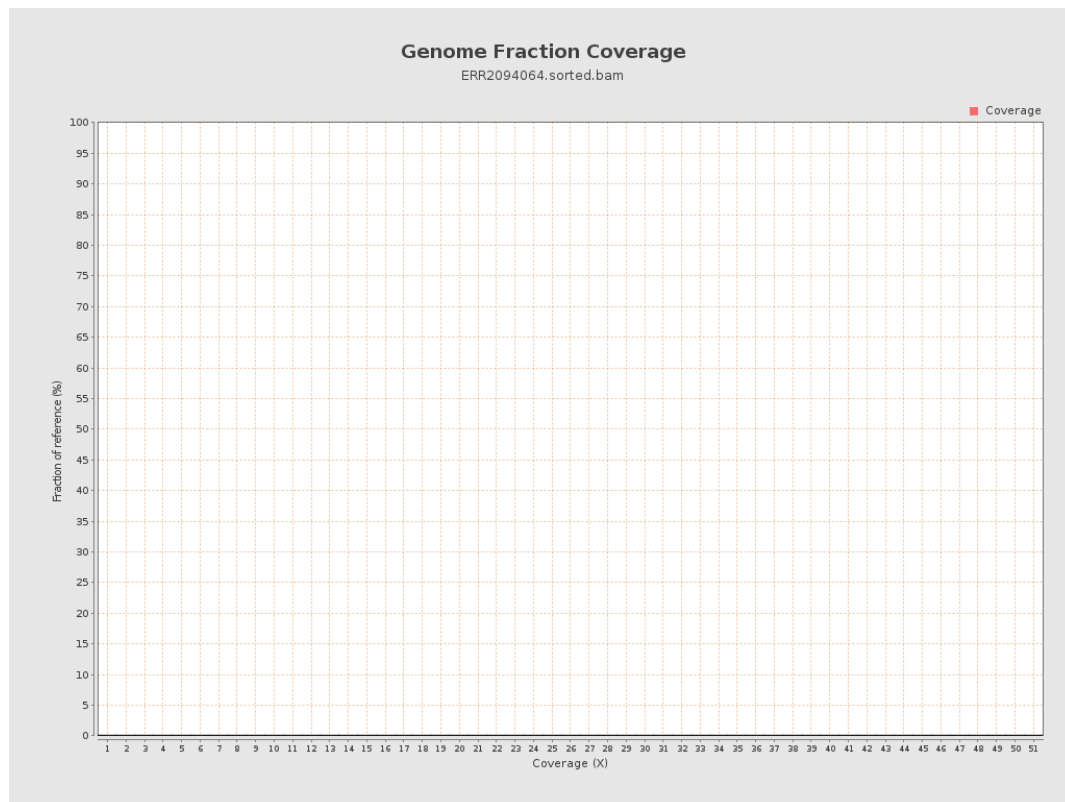
4. Results : Coverage Histogram



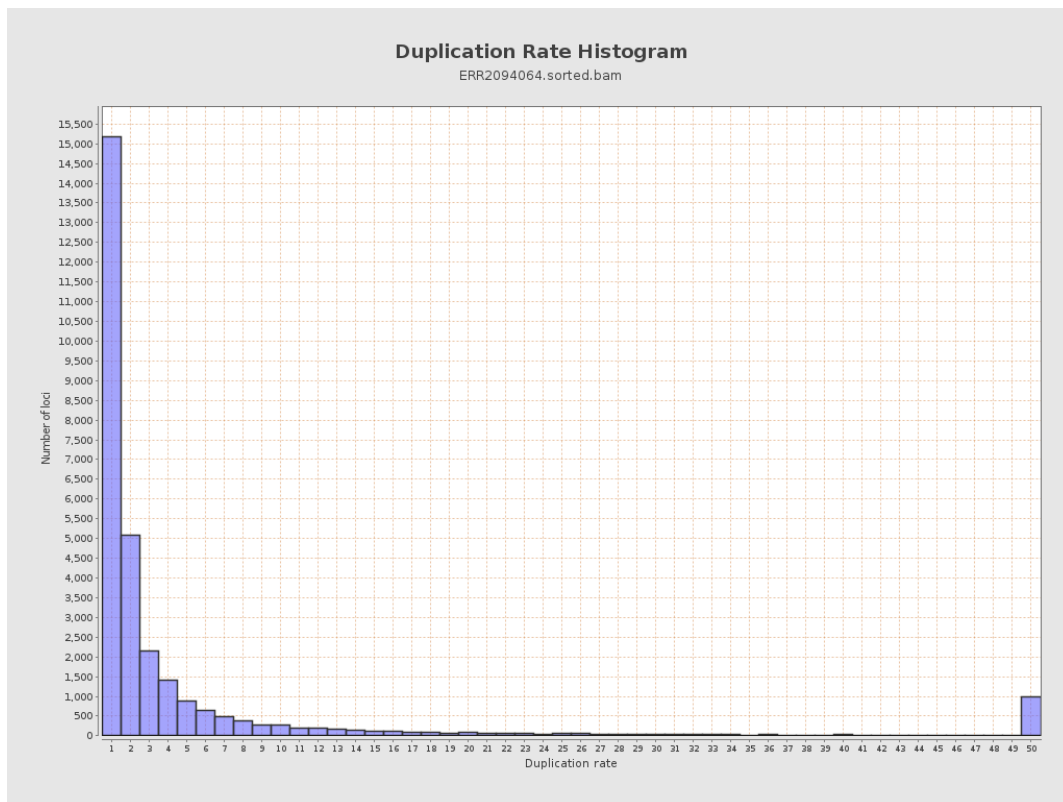
5. Results : Coverage Histogram (0-50X)



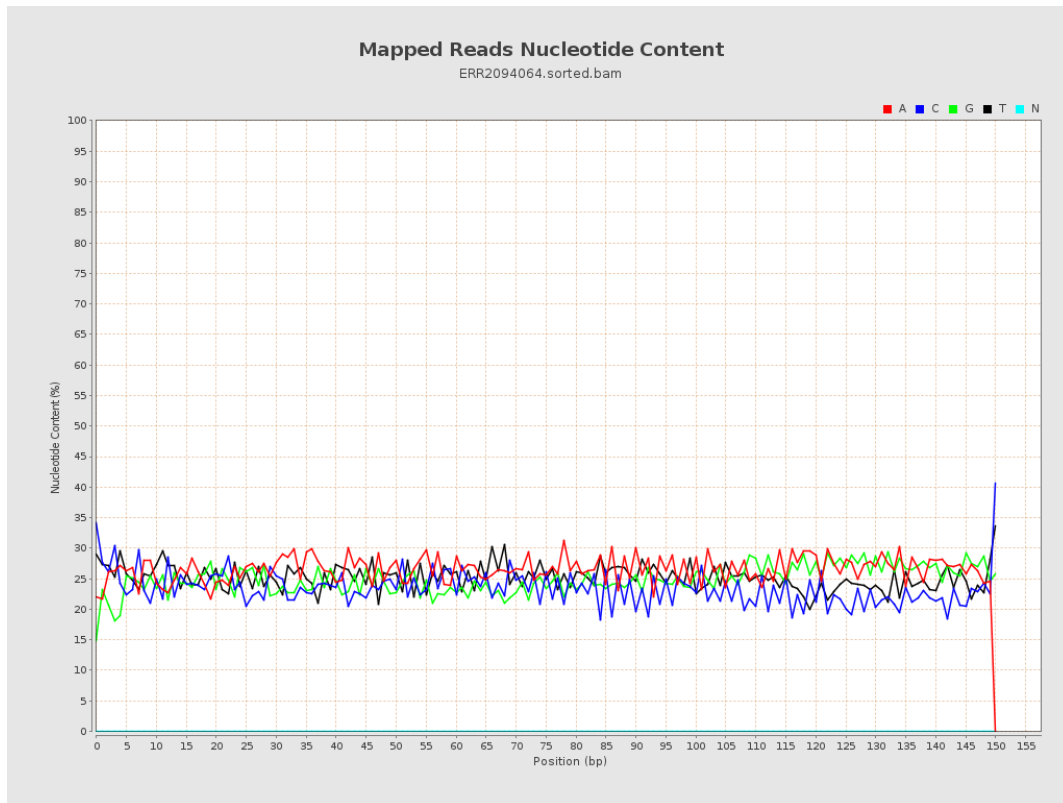
6. Results : Genome Fraction Coverage



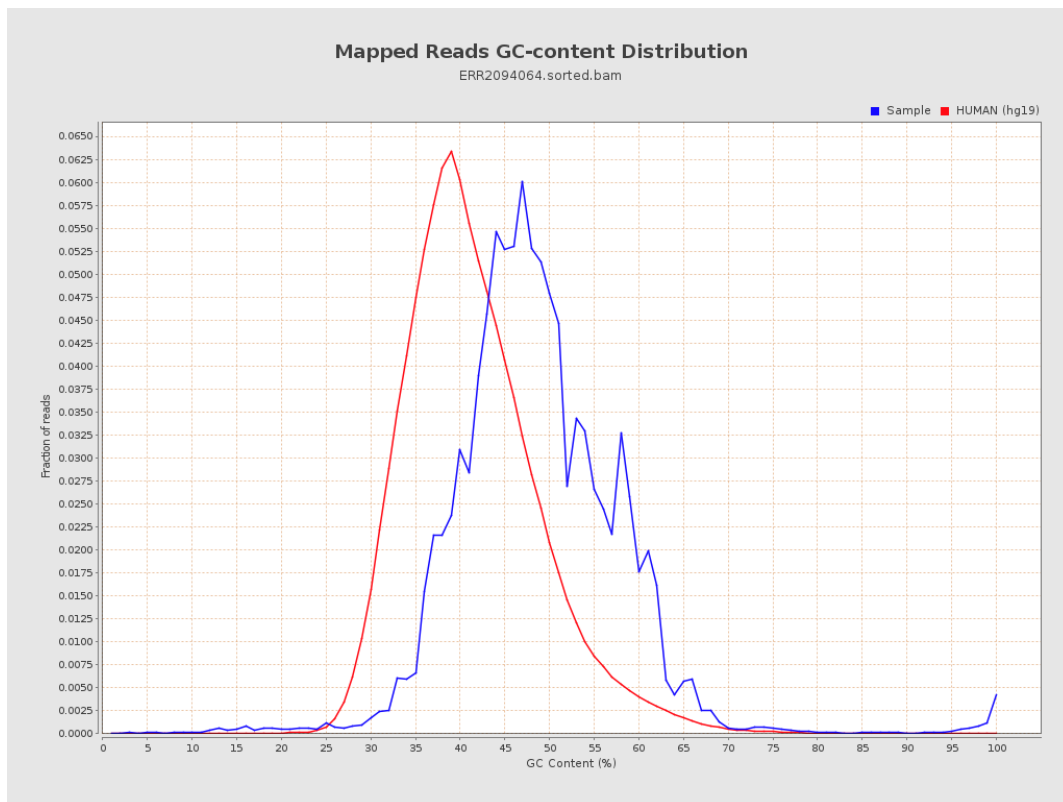
7. Results : Duplication Rate Histogram



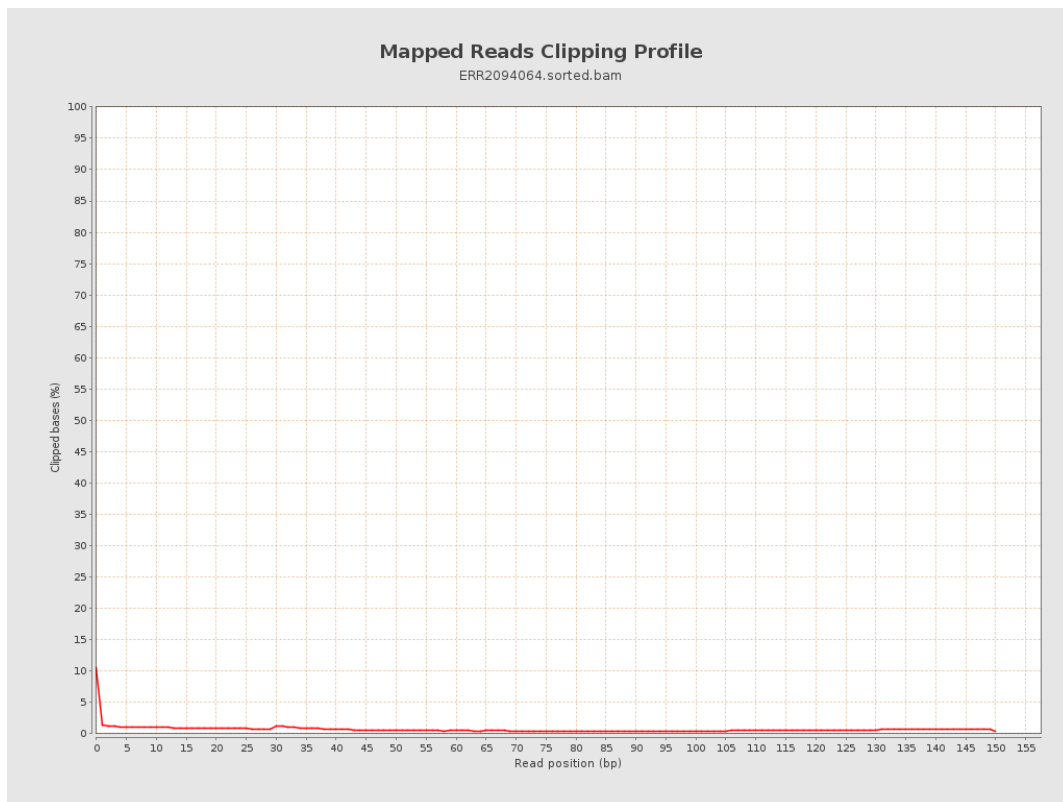
8. Results : Mapped Reads Nucleotide Content



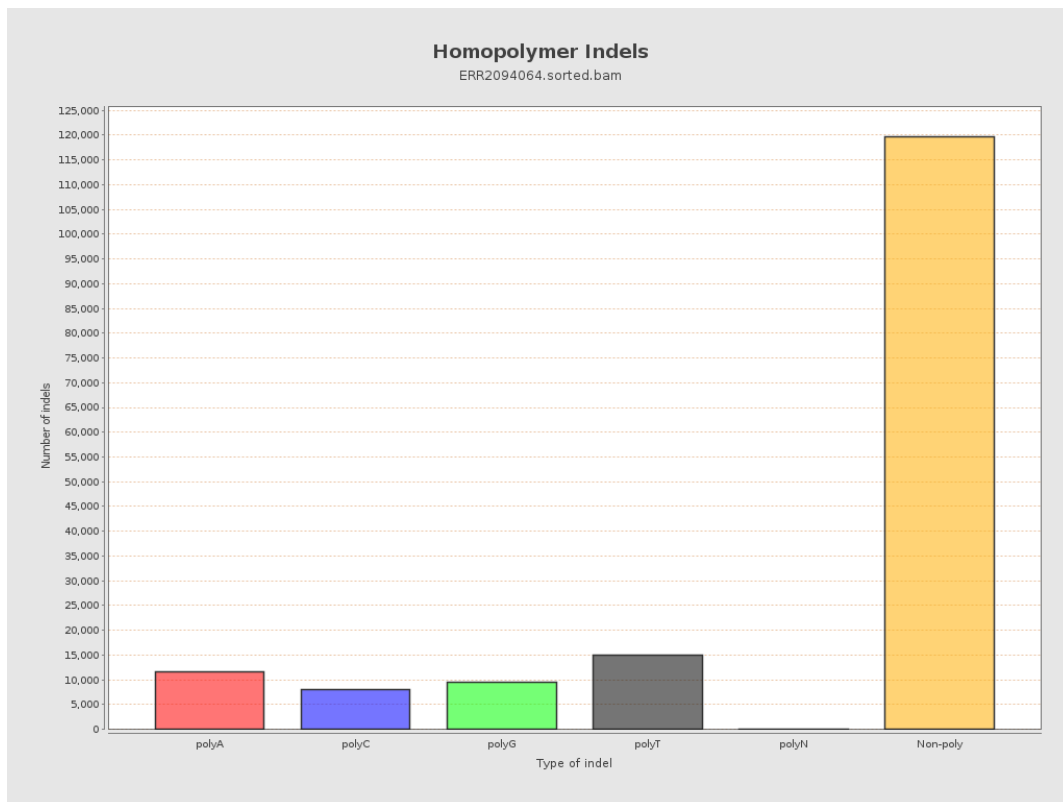
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



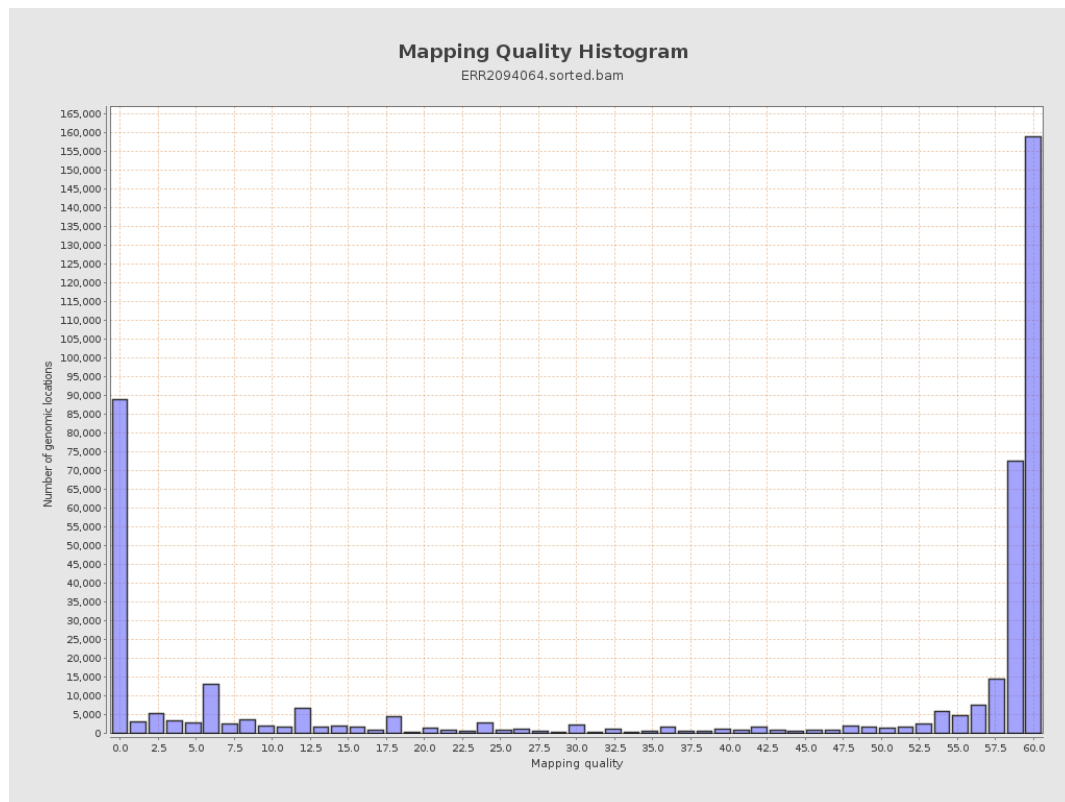
11. Results : Homopolymer Indels



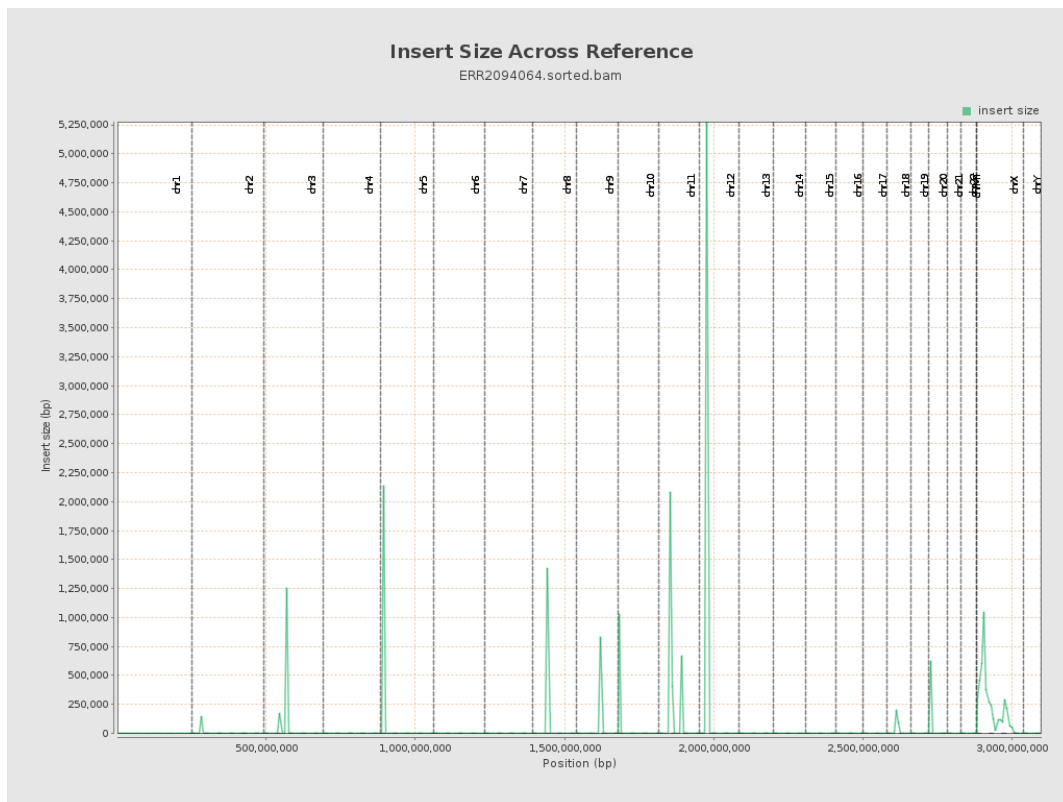
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

