

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:44:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094036.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_ERR2094036 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094036_1.fastq.gz ERR2094036_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:44:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	475,470
Mapped reads	437,886 / 92.1%
Unmapped reads	37,584 / 7.9%
Mapped paired reads	437,886 / 92.1%
Mapped reads, first in pair	220,074 / 46.29%
Mapped reads, second in pair	217,812 / 45.81%
Mapped reads, both in pair	429,540 / 90.34%
Mapped reads, singletons	8,346 / 1.76%
Secondary alignments	0
Supplementary alignments	25,005 / 5.26%
Read min/max/mean length	30 / 151 / 144.7
Duplicated reads (estimated)	412,139 / 86.68%
Duplication rate	43.06%
Clipped reads	222,400 / 46.77%

2.2. ACGT Content

Number/percentage of A's	15,766,744 / 28.35%
Number/percentage of C's	12,210,008 / 21.95%
Number/percentage of T's	14,988,119 / 26.95%
Number/percentage of G's	12,649,564 / 22.74%
Number/percentage of N's	483 / 0%

GC Percentage	44.7%
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2.3. Coverage

Mean	0.0183
Standard Deviation	8.0175

2.4. Mapping Quality

Mean Mapping Quality	43.31
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2.5. Insert size

Mean	414,884.72
Standard Deviation	6,024,303.28
P25/Median/P75	141 / 172 / 216

2.6. Mismatches and indels

General error rate	3.38%
Mismatches	1,824,417
Insertions	28,530
Mapped reads with at least one insertion	6.32%
Deletions	133,904
Mapped reads with at least one deletion	29.55%
Homopolymer indels	28.49%

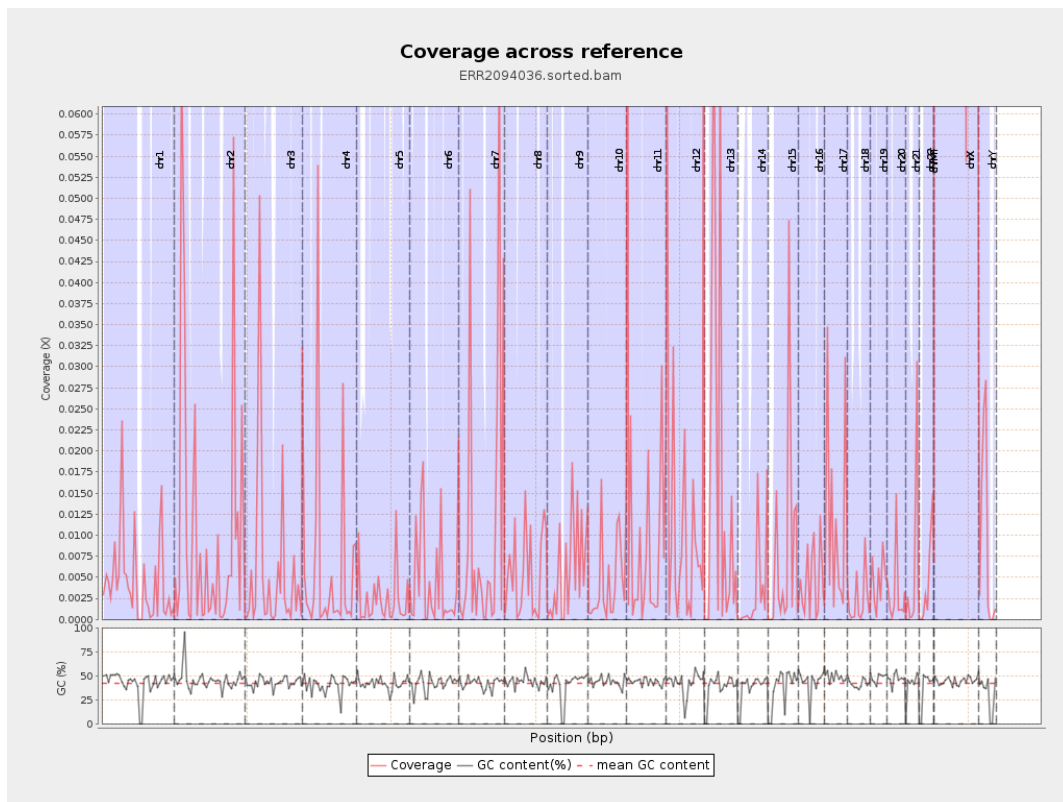
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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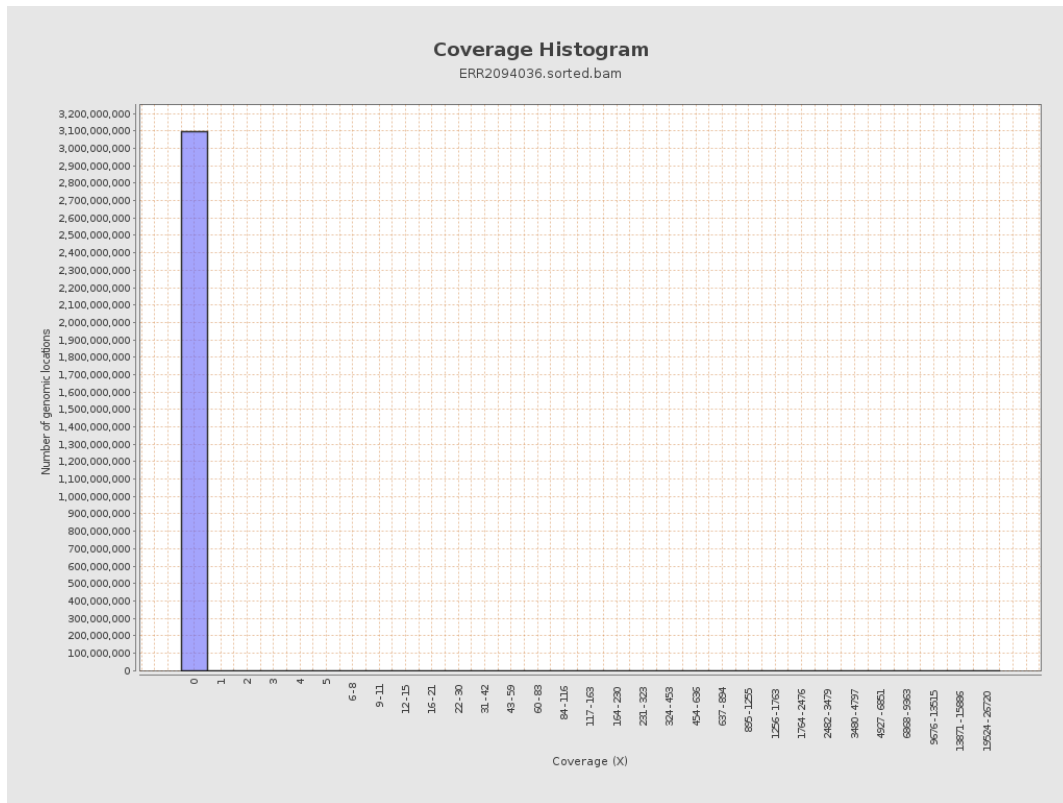
		bases	coverage	deviation
chr1	249250621	1113773	0.0045	1.1687
chr2	243199373	2486376	0.0102	2.5965
chr3	198022430	1101176	0.0056	2.0989
chr4	191154276	1268961	0.0066	2.3469
chr5	180915260	452639	0.0025	0.6542
chr6	171115067	786600	0.0046	1.286
chr7	159138663	1787460	0.0112	3.5821
chr8	146364022	780390	0.0053	1.2326
chr9	141213431	783995	0.0056	0.9982
chr10	135534747	616779	0.0046	0.8711
chr11	135006516	1395076	0.0103	2.0801
chr12	133851895	1718498	0.0128	3.8984
chr13	115169878	1874388	0.0163	4.4229
chr14	107349540	357626	0.0033	1.105
chr15	102531392	773460	0.0075	2.584
chr16	90354753	400310	0.0044	0.7582
chr17	81195210	916356	0.0113	2.0897
chr18	78077248	183068	0.0023	0.7707
chr19	59128983	266789	0.0045	0.6451
chr20	63025520	197510	0.0031	0.8854
chr21	48129895	288834	0.006	1.7011
chr22	51304566	226232	0.0044	0.4285
chrMT	16571	11365939	685.8934	2,926.298
chrX	155270560	24835763	0.16	15.1923

chrY	59373566	577489	0.0097	2.3529
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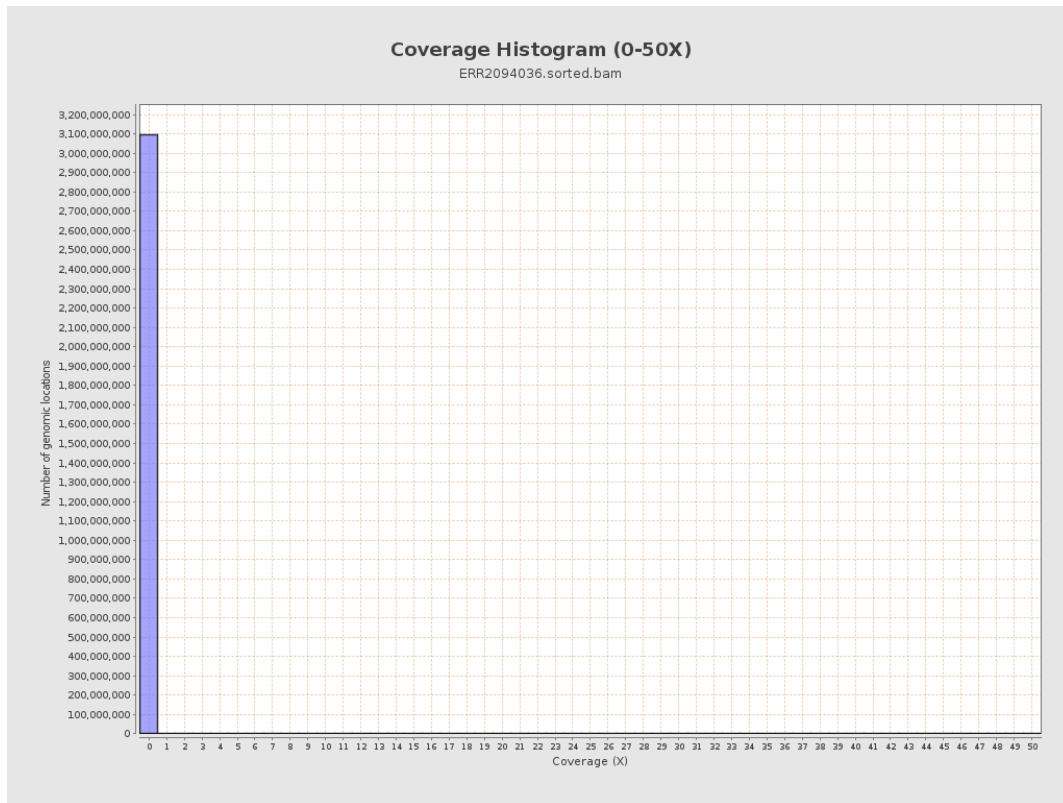
3. Results : Coverage across reference



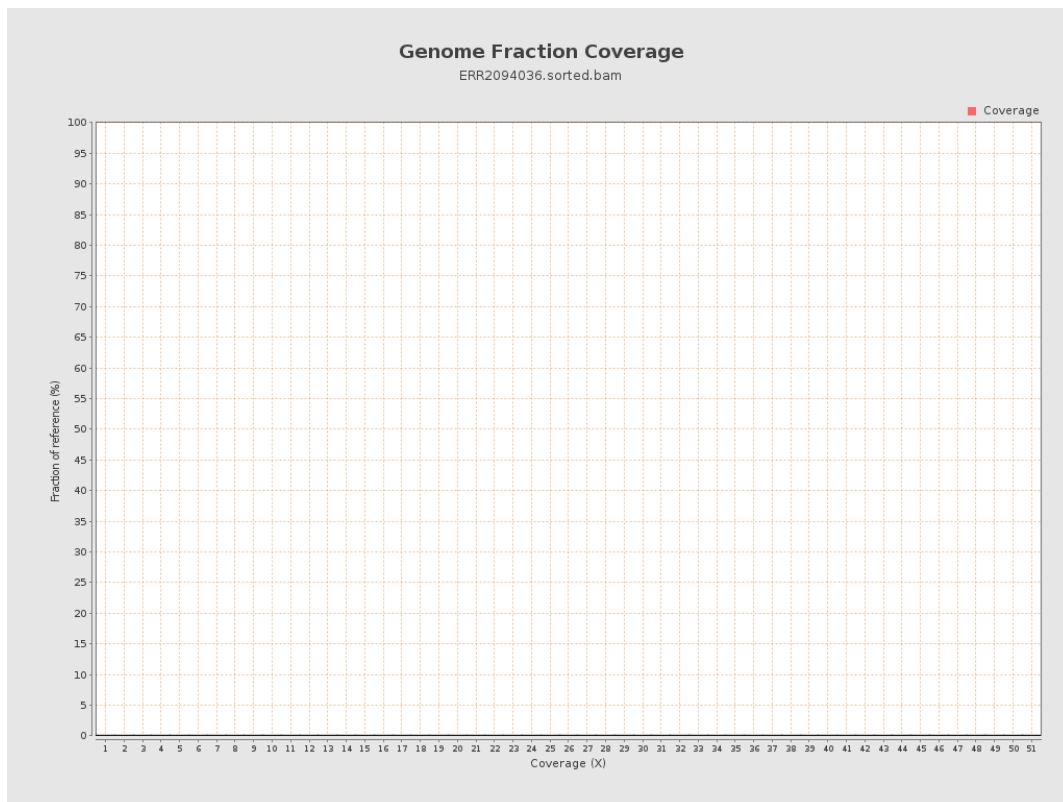
4. Results : Coverage Histogram



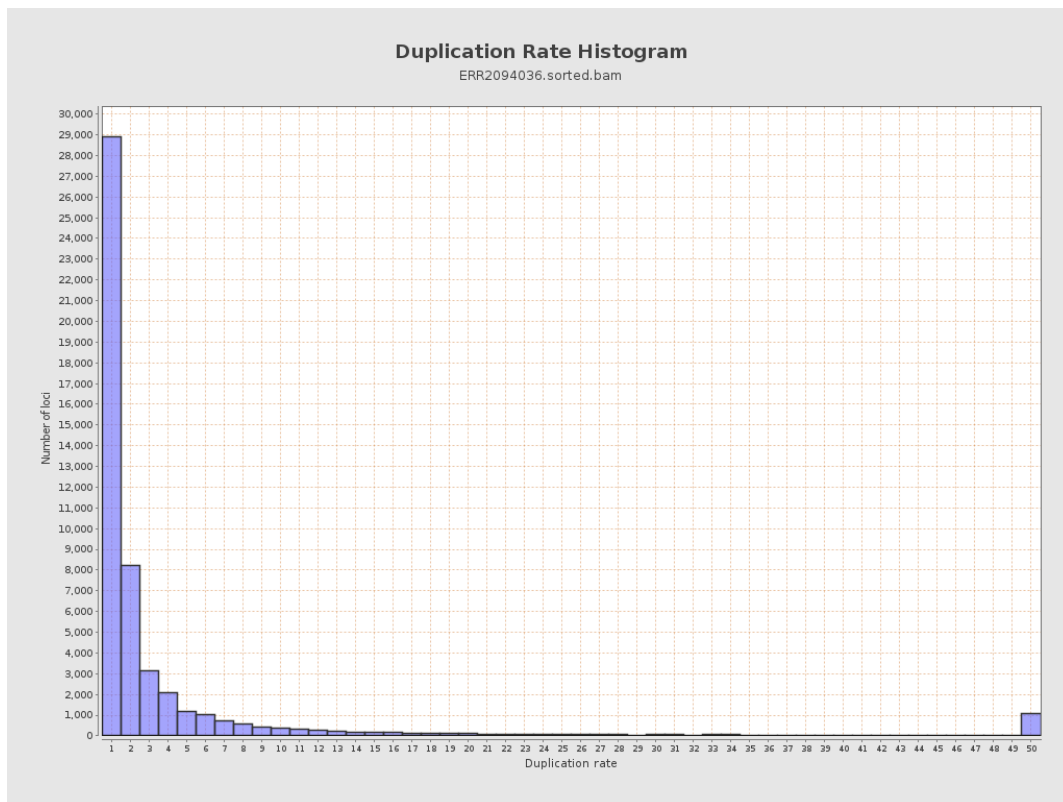
5. Results : Coverage Histogram (0-50X)



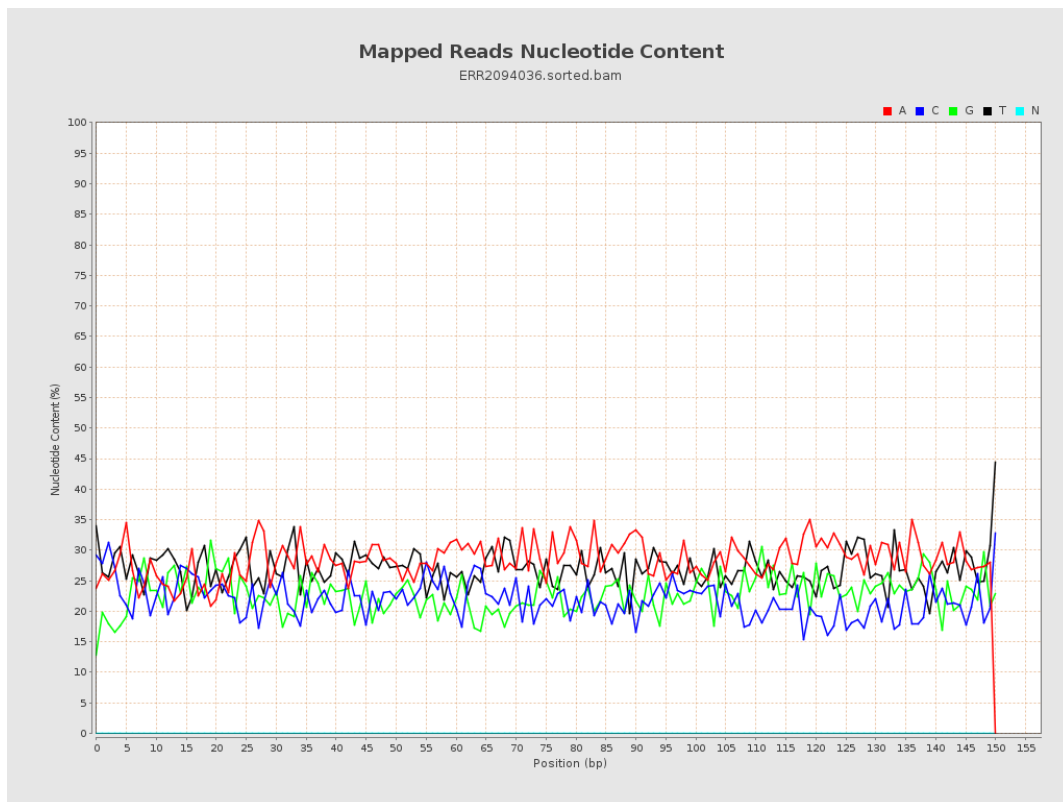
6. Results : Genome Fraction Coverage



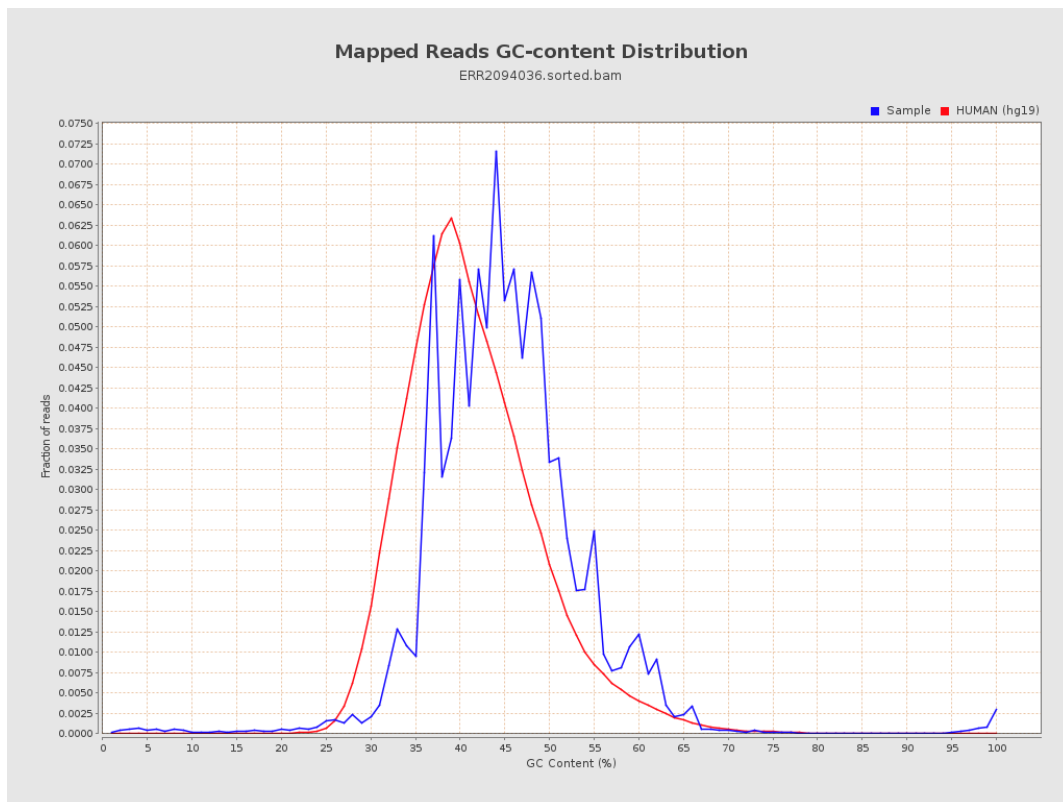
7. Results : Duplication Rate Histogram



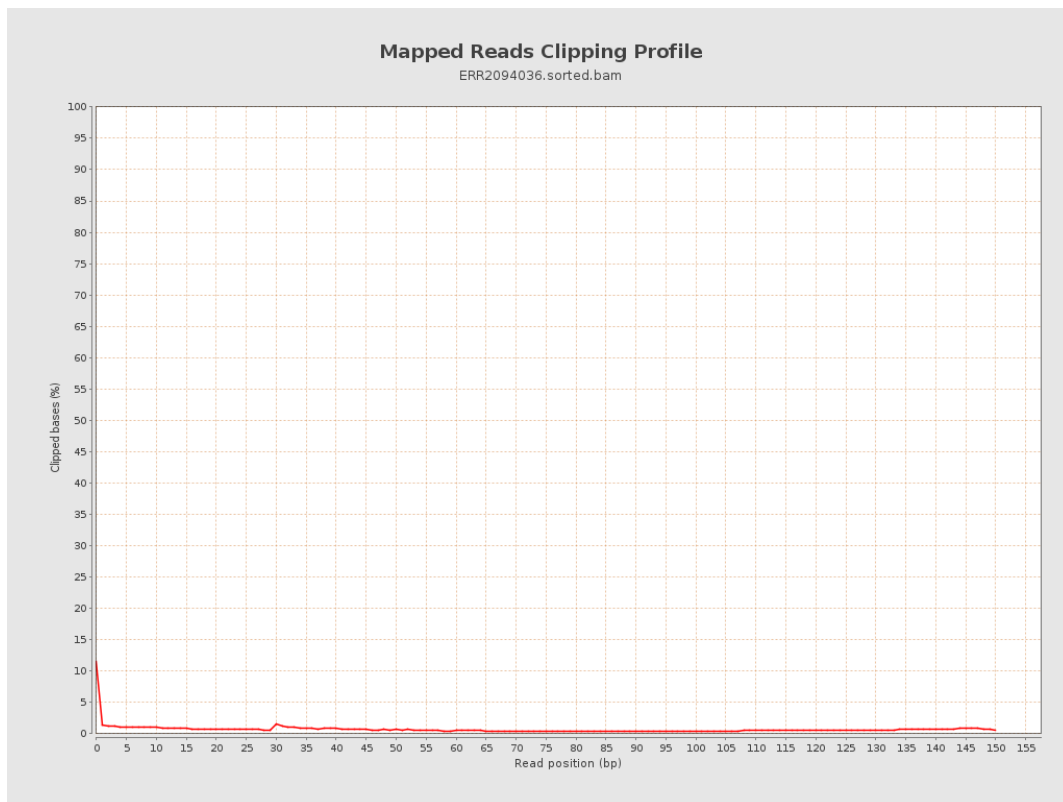
8. Results : Mapped Reads Nucleotide Content



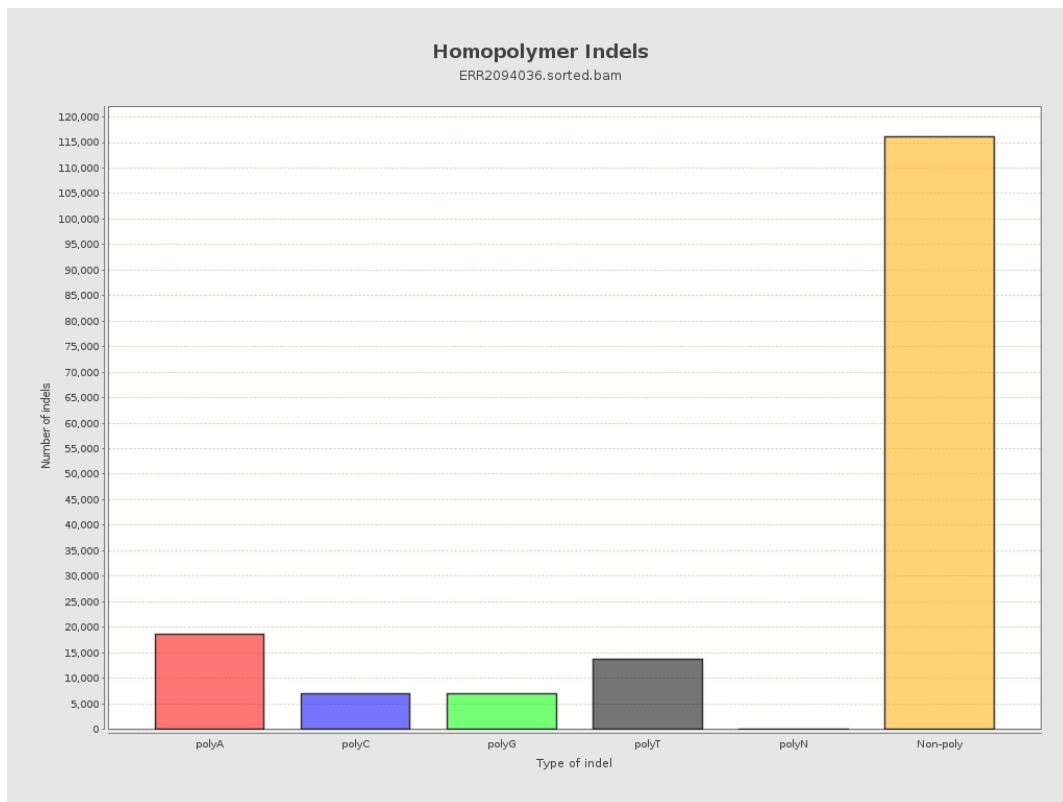
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



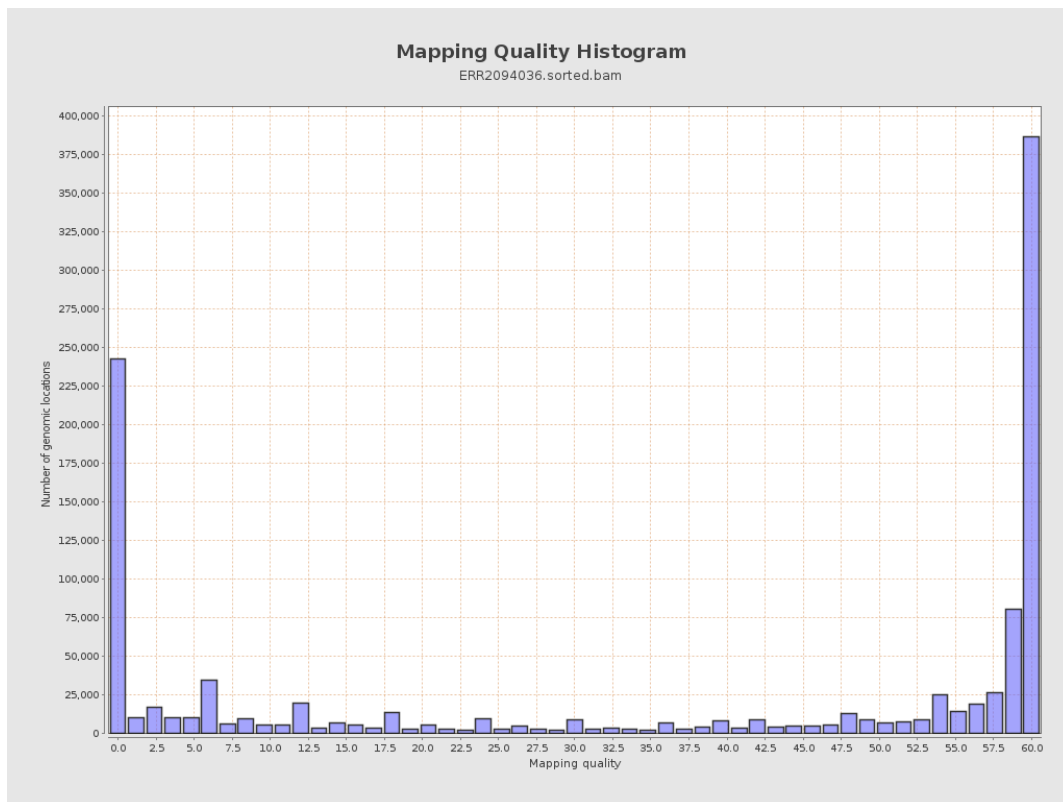
11. Results : Homopolymer Indels



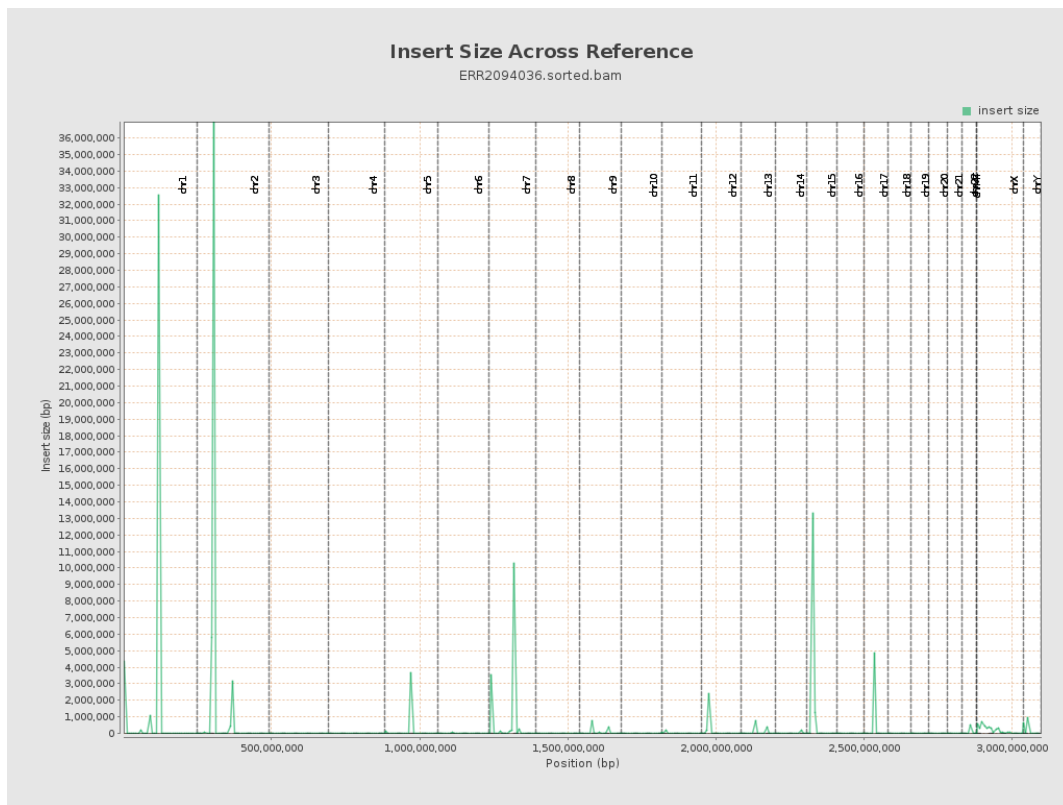
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

