

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:08:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094046.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_ERR2094046 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094046_1.fastq.gz ERR2094046_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:08:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	480,802
Mapped reads	452,375 / 94.09%
Unmapped reads	28,427 / 5.91%
Mapped paired reads	452,375 / 94.09%
Mapped reads, first in pair	227,229 / 47.26%
Mapped reads, second in pair	225,146 / 46.83%
Mapped reads, both in pair	449,184 / 93.42%
Mapped reads, singletons	3,191 / 0.66%
Secondary alignments	0
Supplementary alignments	18,237 / 3.79%
Read min/max/mean length	30 / 151 / 136.03
Duplicated reads (estimated)	431,975 / 89.84%
Duplication rate	52.93%
Clipped reads	190,153 / 39.55%

2.2. ACGT Content

Number/percentage of A's	15,563,216 / 27.41%
Number/percentage of C's	12,857,430 / 22.64%
Number/percentage of T's	14,939,651 / 26.31%
Number/percentage of G's	13,427,948 / 23.65%
Number/percentage of N's	711 / 0%

GC Percentage	46.29%
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2.3. Coverage

Mean	0.0189
Standard Deviation	4.337

2.4. Mapping Quality

Mean Mapping Quality	41.34
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2.5. Insert size

Mean	607,659.51
Standard Deviation	6,839,688.51
P25/Median/P75	122 / 159 / 189

2.6. Mismatches and indels

General error rate	4.69%
Mismatches	2,598,968
Insertions	42,815
Mapped reads with at least one insertion	9.28%
Deletions	208,023
Mapped reads with at least one deletion	42.76%
Homopolymer indels	29.07%

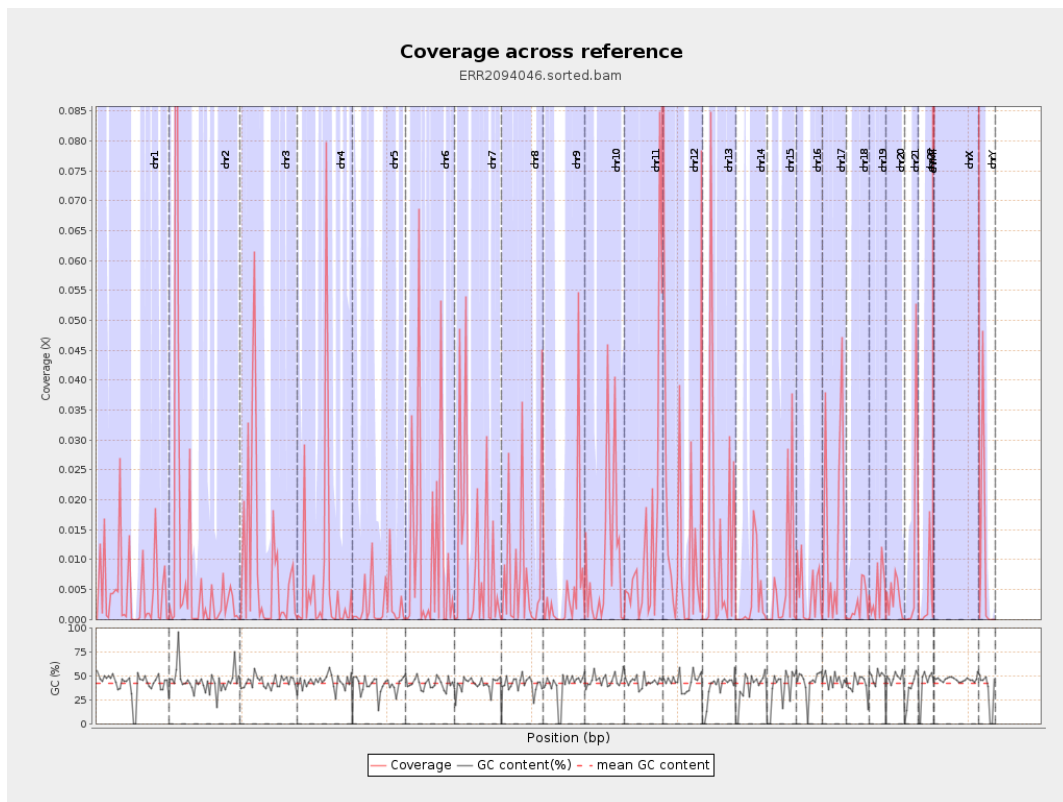
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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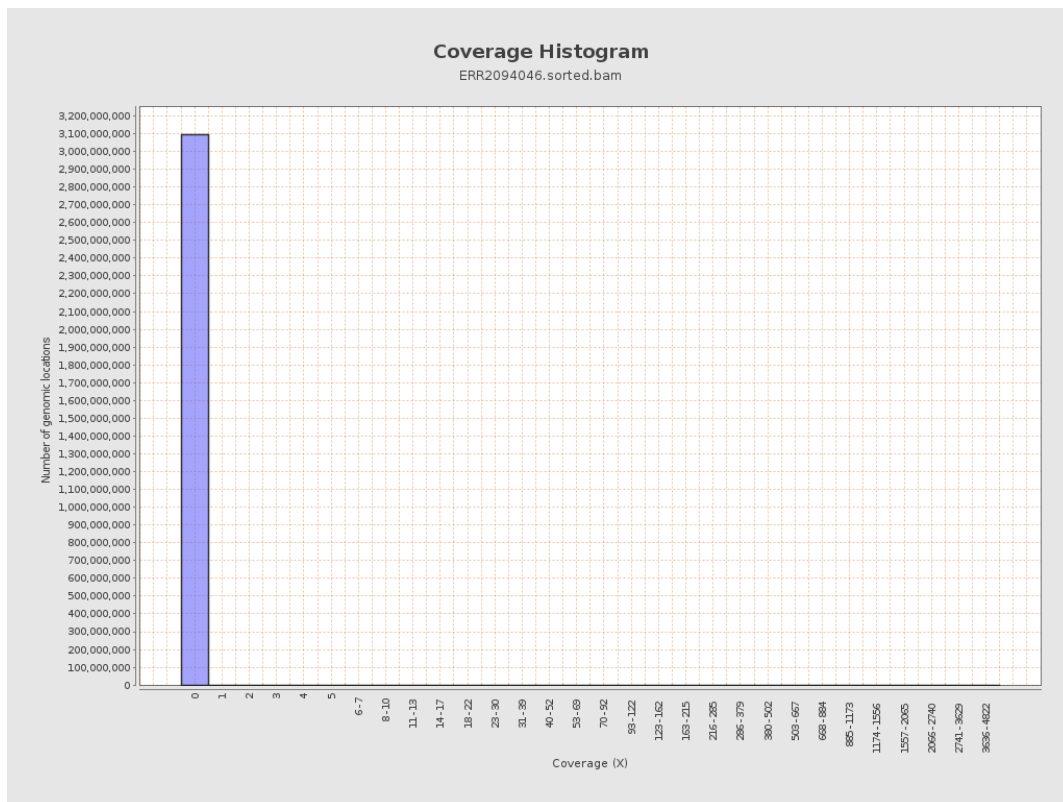
		bases	coverage	deviation
chr1	249250621	1129896	0.0045	1.7442
chr2	243199373	2202060	0.0091	3.2755
chr3	198022430	1783813	0.009	2.6476
chr4	191154276	1182776	0.0062	2.8995
chr5	180915260	434109	0.0024	0.9088
chr6	171115067	1857955	0.0109	4.7532
chr7	159138663	1732793	0.0109	3.6876
chr8	146364022	1176755	0.008	2.6396
chr9	141213431	725236	0.0051	2.1389
chr10	135534747	1399971	0.0103	3.2496
chr11	135006516	2300754	0.017	4.5474
chr12	133851895	1866751	0.0139	3.7961
chr13	115169878	1413815	0.0123	3.2408
chr14	107349540	349859	0.0033	1.3747
chr15	102531392	650513	0.0063	2.6195
chr16	90354753	382783	0.0042	1.2265
chr17	81195210	1044323	0.0129	4.0219
chr18	78077248	192938	0.0025	0.713
chr19	59128983	253729	0.0043	1.0124
chr20	63025520	228813	0.0036	0.868
chr21	48129895	505680	0.0105	3.6962
chr22	51304566	175326	0.0034	1.3958
chrMT	16571	2169618	130.9286	558.9072
chrX	155270560	32798314	0.2112	13.3275

chrY	59373566	439002	0.0074	2.4364
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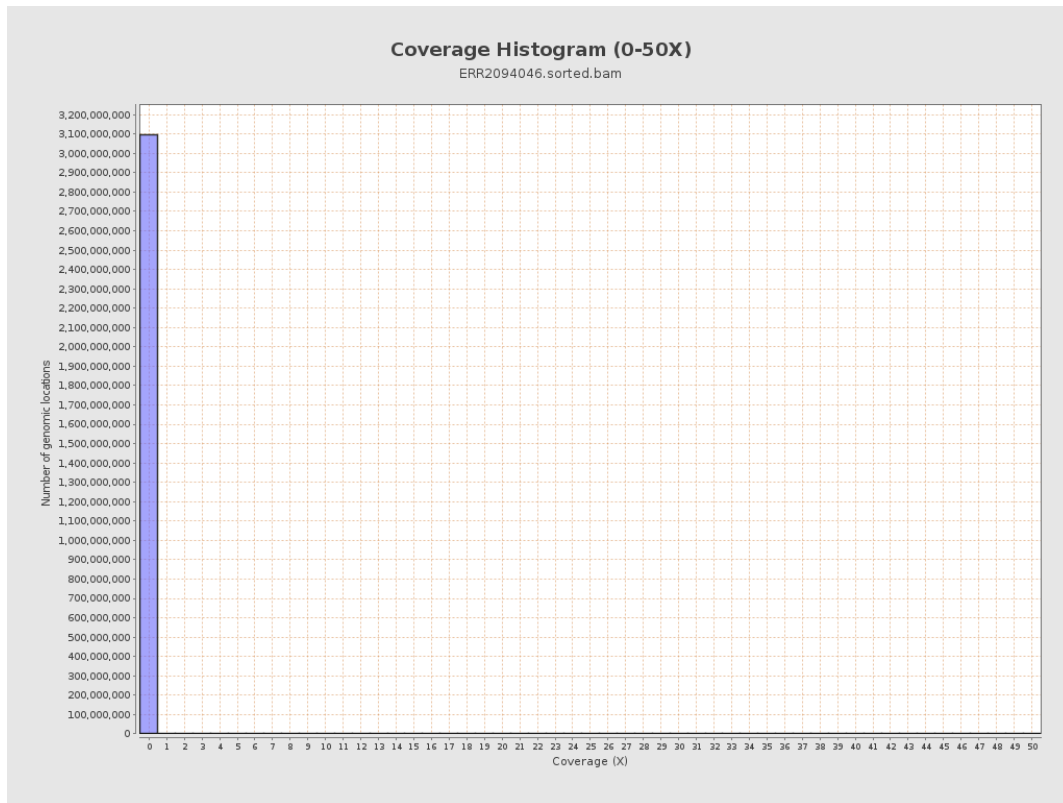
3. Results : Coverage across reference



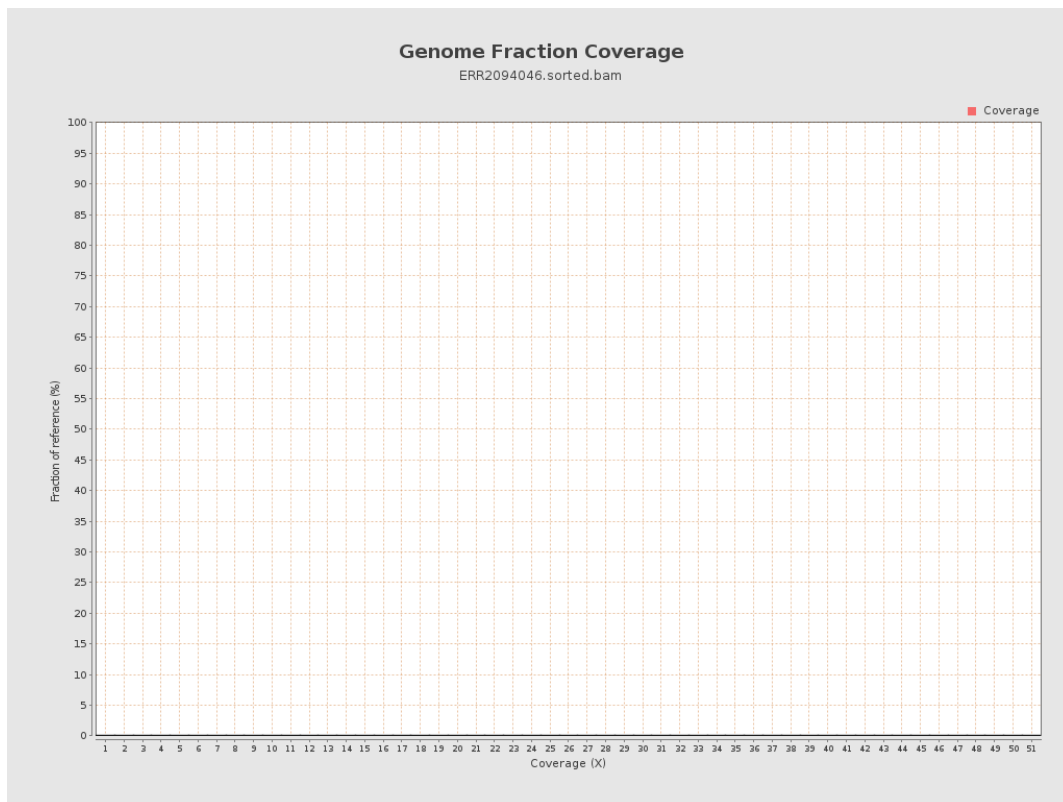
4. Results : Coverage Histogram



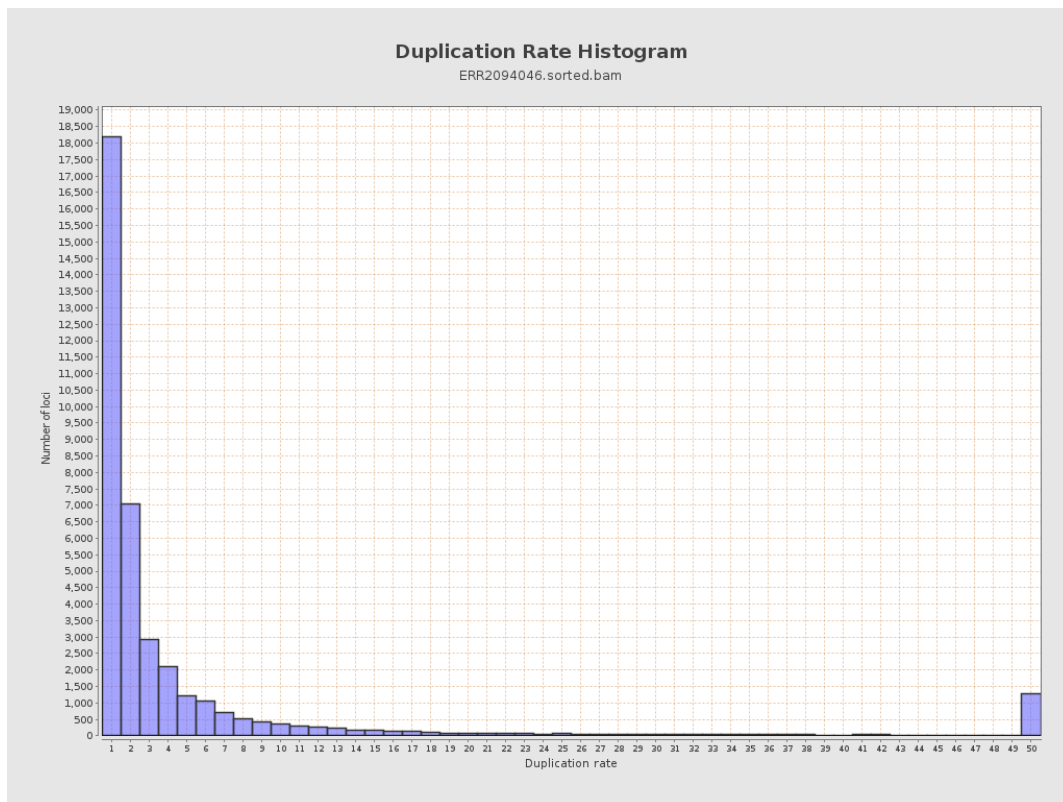
5. Results : Coverage Histogram (0-50X)



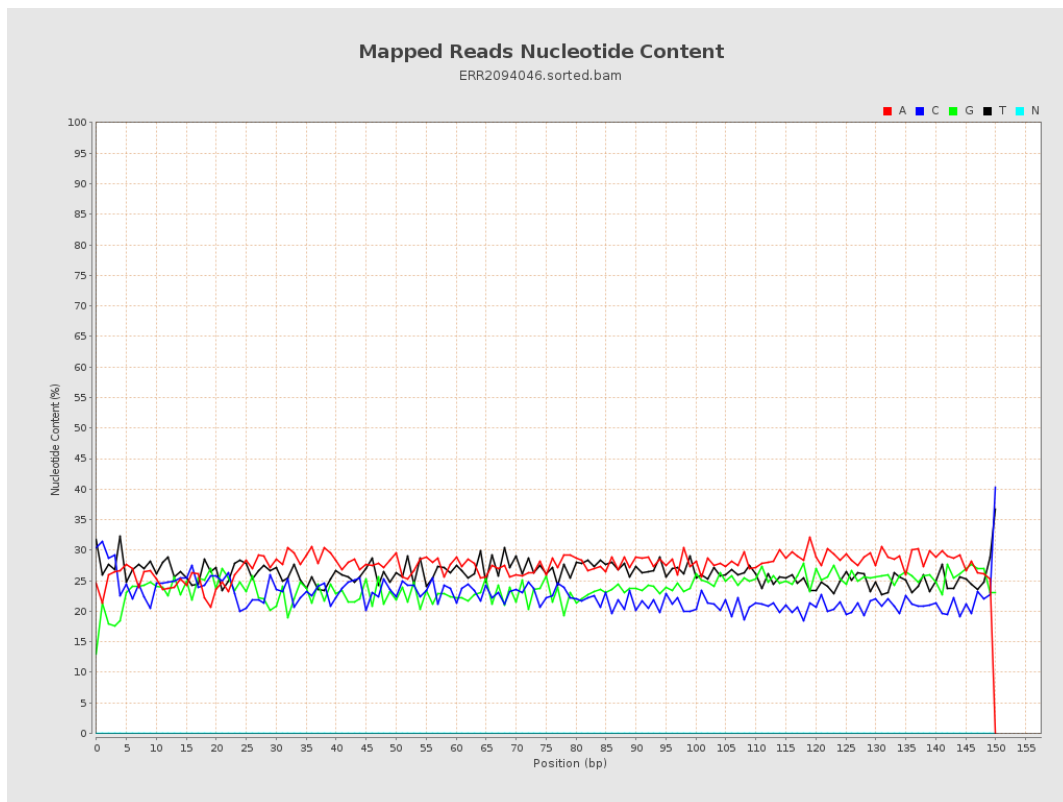
6. Results : Genome Fraction Coverage



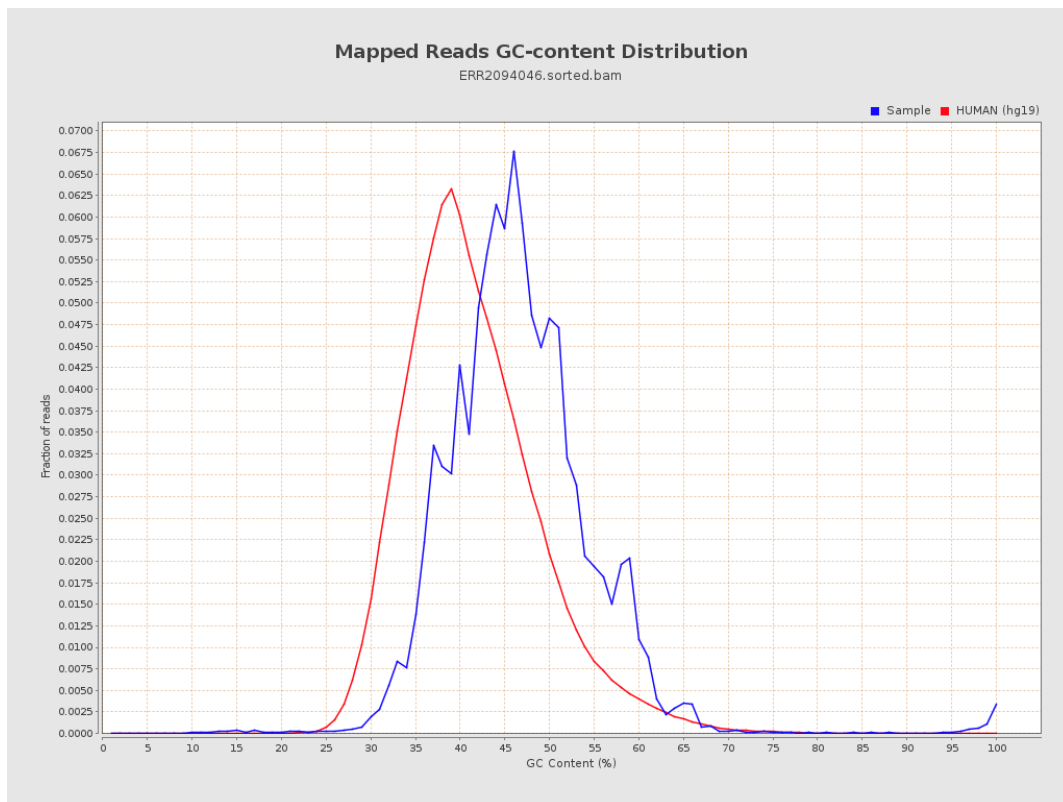
7. Results : Duplication Rate Histogram



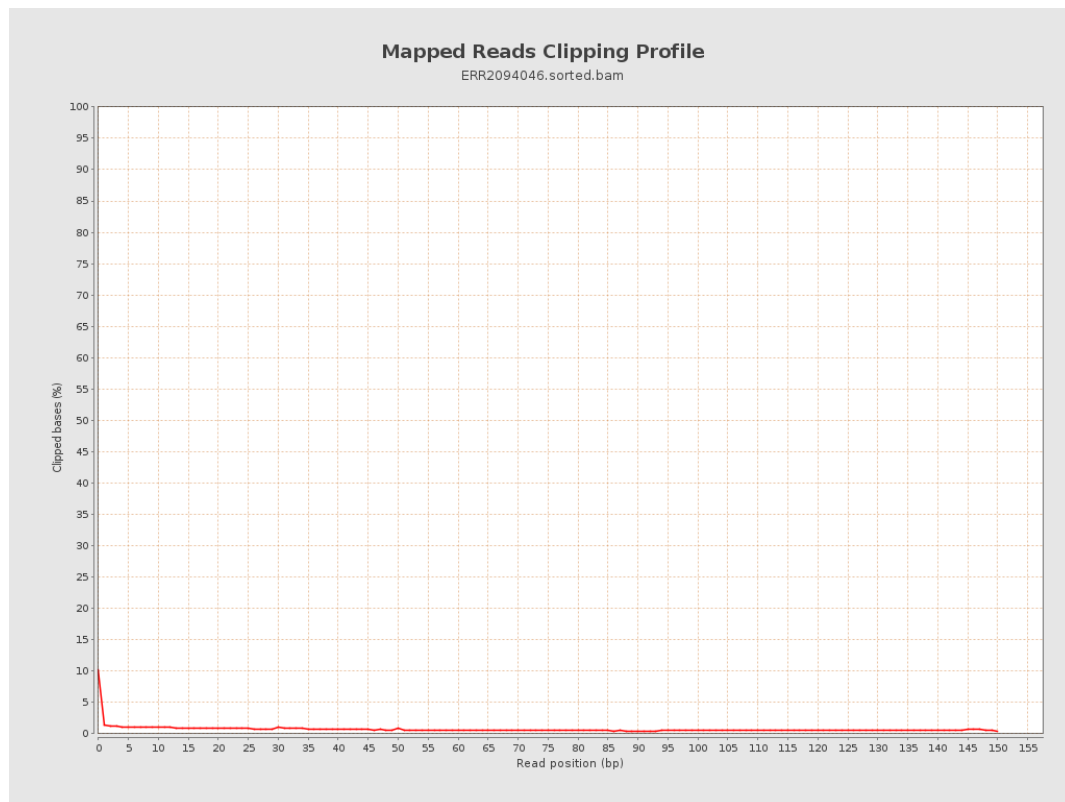
8. Results : Mapped Reads Nucleotide Content



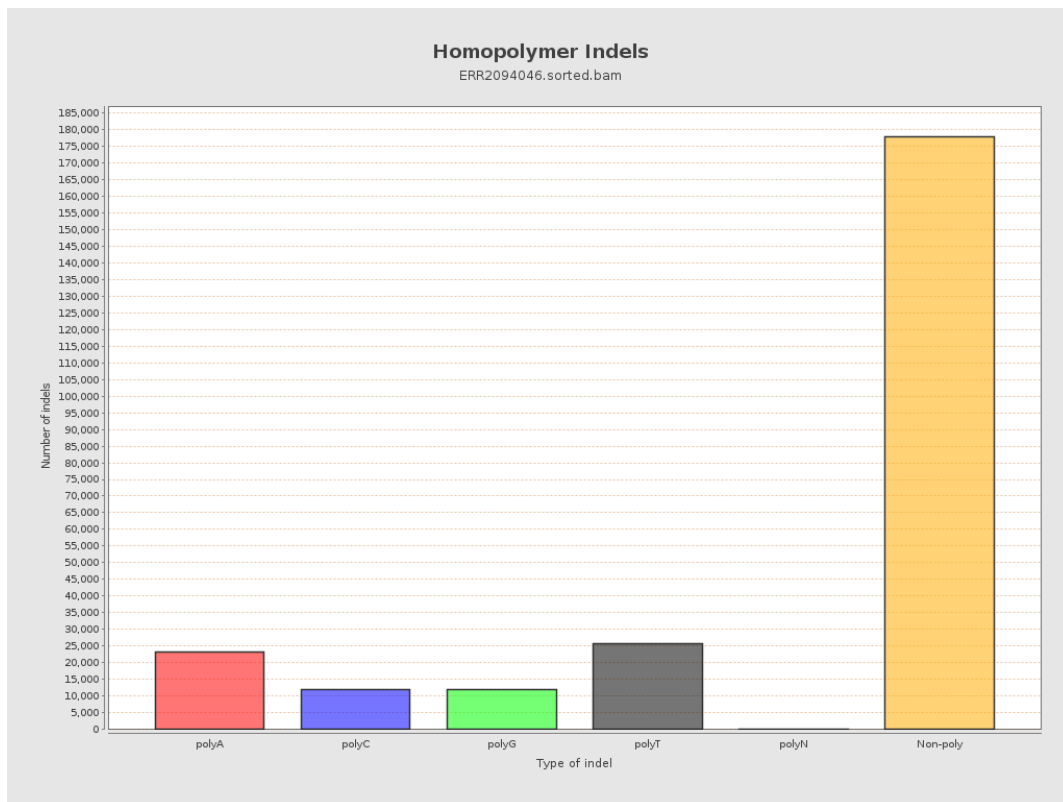
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



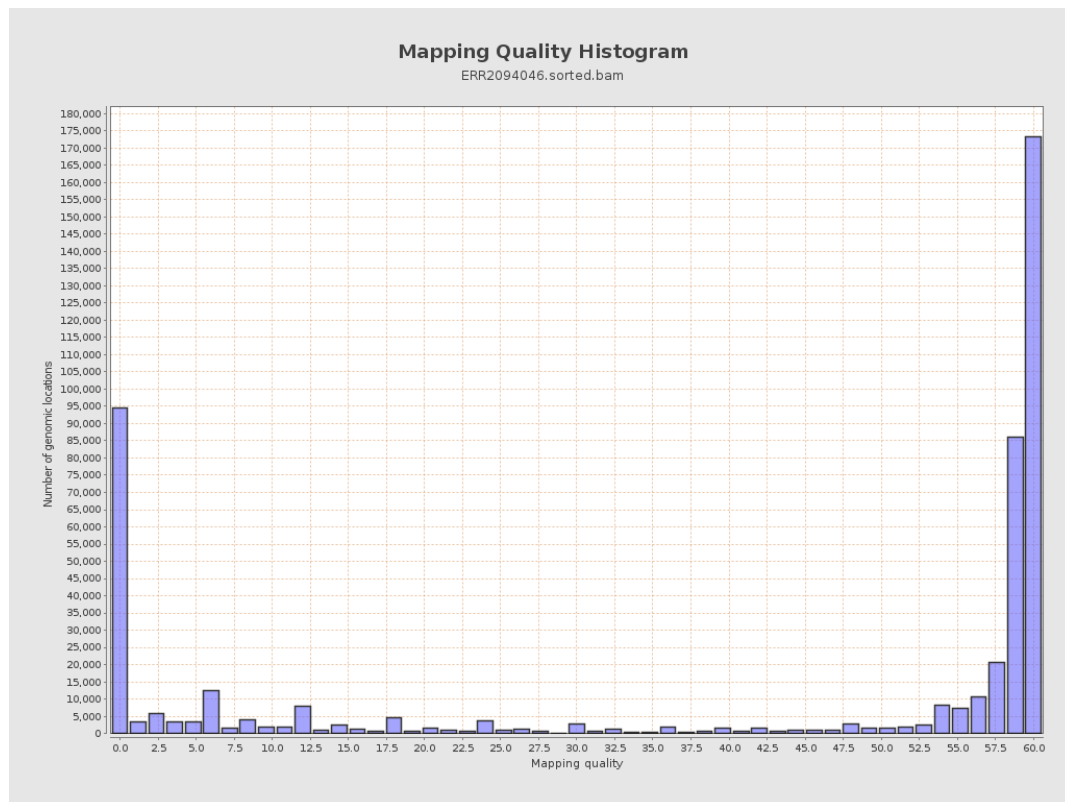
11. Results : Homopolymer Indels



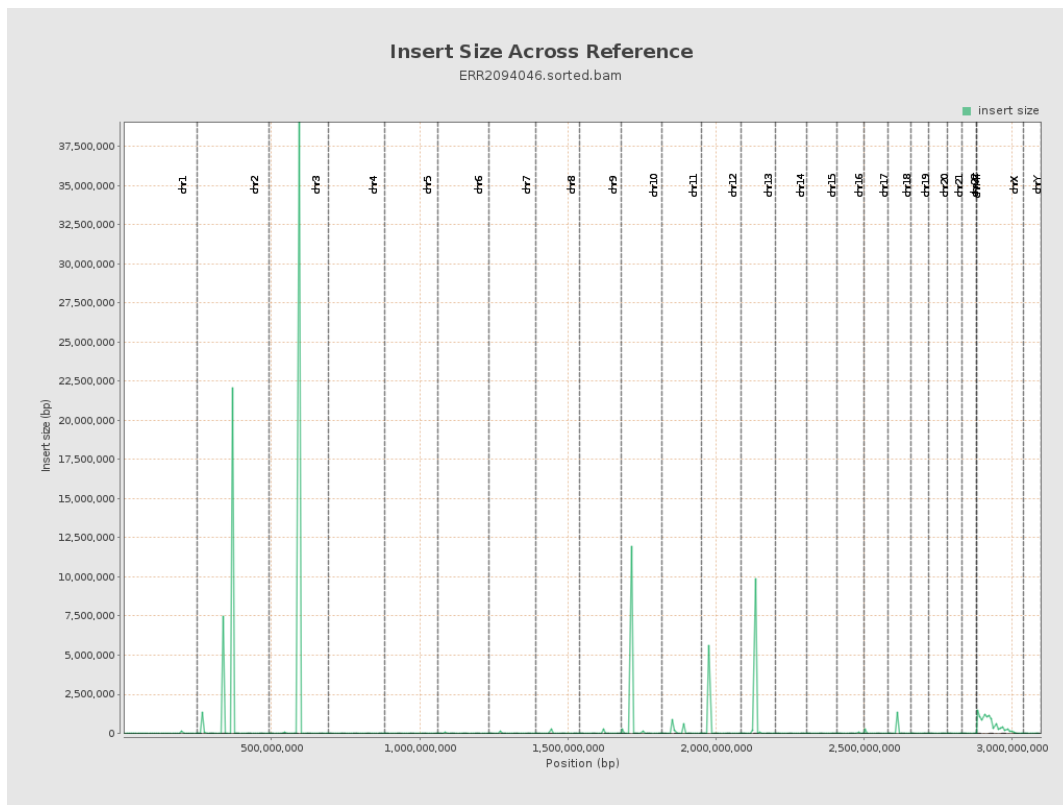
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

