

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:26:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094052.sorted.bam -c -nw 400 -hm 3
```

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_ERR2094052 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094052_1.fastq.gz ERR2094052_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:26:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	388,050
Mapped reads	362,430 / 93.4%
Unmapped reads	25,620 / 6.6%
Mapped paired reads	362,430 / 93.4%
Mapped reads, first in pair	181,990 / 46.9%
Mapped reads, second in pair	180,440 / 46.5%
Mapped reads, both in pair	359,946 / 92.76%
Mapped reads, singletons	2,484 / 0.64%
Secondary alignments	0
Supplementary alignments	15,810 / 4.07%
Read min/max/mean length	30 / 151 / 138.12
Duplicated reads (estimated)	346,752 / 89.36%
Duplication rate	49.57%
Clipped reads	153,507 / 39.56%

2.2. ACGT Content

Number/percentage of A's	12,936,402 / 27.76%
Number/percentage of C's	10,400,790 / 22.32%
Number/percentage of T's	12,356,178 / 26.52%
Number/percentage of G's	10,904,012 / 23.4%
Number/percentage of N's	636 / 0%

GC Percentage	45.72%
---------------	--------

2.3. Coverage

Mean	0.0155
Standard Deviation	4.4771

2.4. Mapping Quality

Mean Mapping Quality	44.33
----------------------	-------

2.5. Insert size

Mean	418,883.77
Standard Deviation	5,712,727.81
P25/Median/P75	133 / 167 / 195

2.6. Mismatches and indels

General error rate	4.48%
Mismatches	2,039,837
Insertions	32,940
Mapped reads with at least one insertion	8.95%
Deletions	161,538
Mapped reads with at least one deletion	41.53%
Homopolymer indels	27.8%

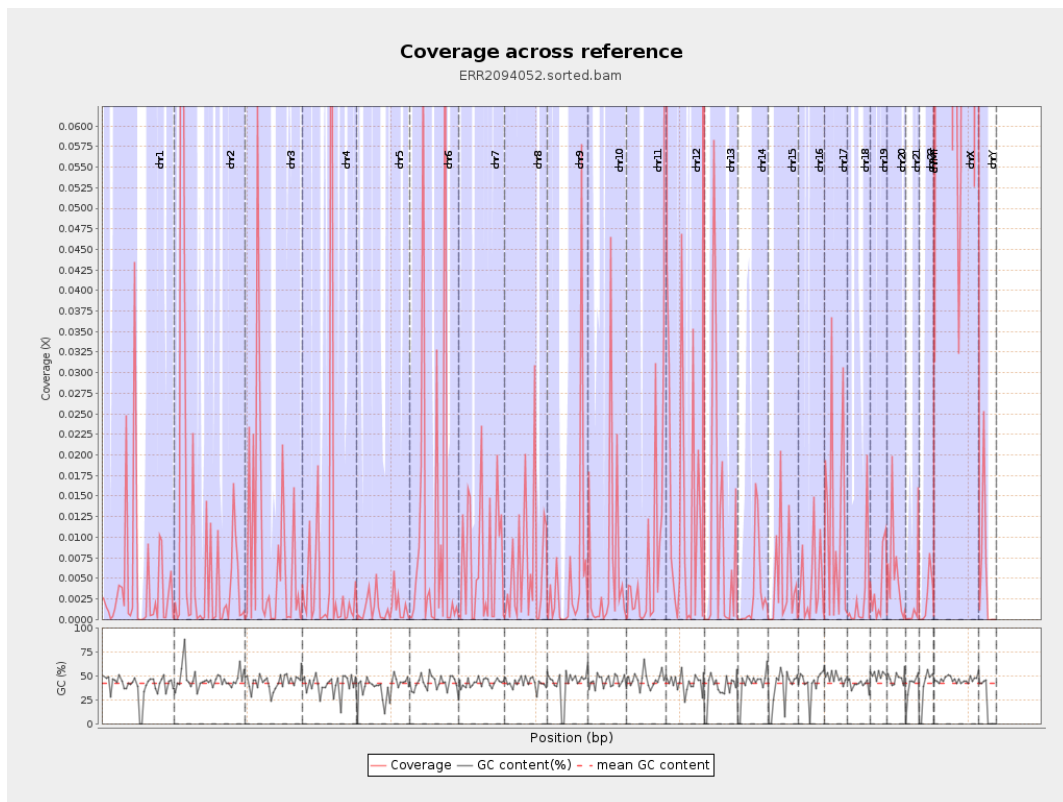
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

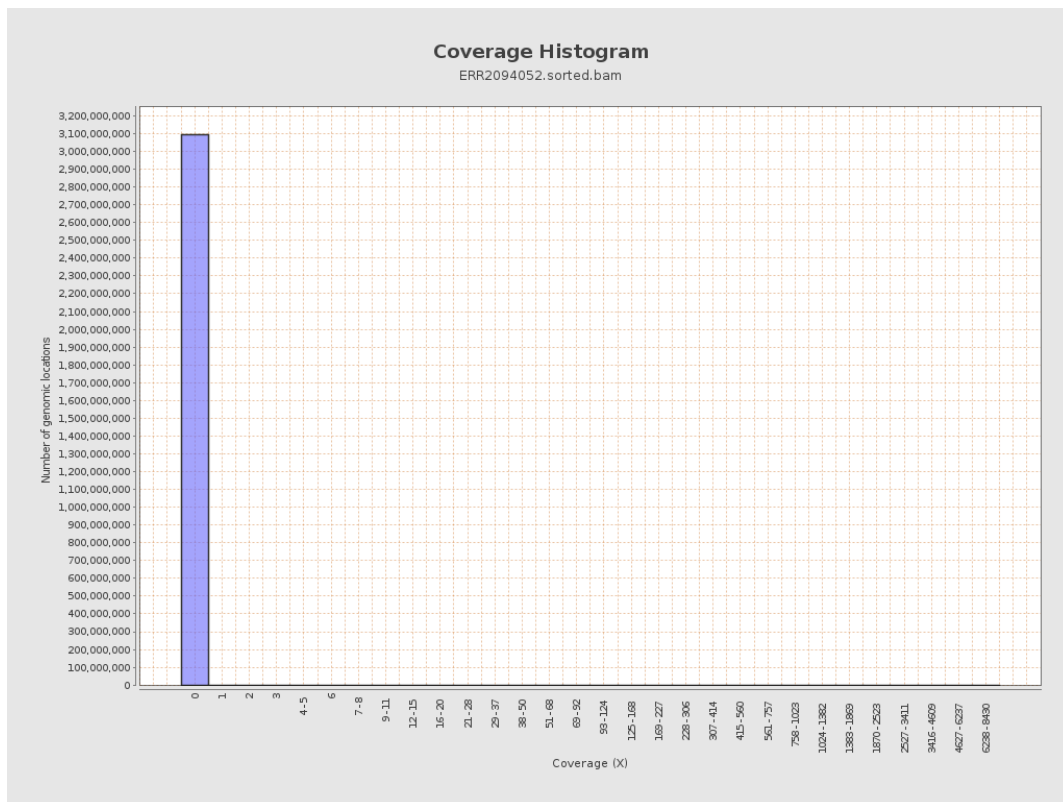
		bases	coverage	deviation
chr1	249250621	1026094	0.0041	1.9306
chr2	243199373	2174915	0.0089	3.2096
chr3	198022430	1649847	0.0083	2.8997
chr4	191154276	1352336	0.0071	2.3039
chr5	180915260	261048	0.0014	0.4451
chr6	171115067	1872338	0.0109	5.5178
chr7	159138663	1081578	0.0068	1.9947
chr8	146364022	953061	0.0065	2.2083
chr9	141213431	768100	0.0054	2.5047
chr10	135534747	844206	0.0062	2.5407
chr11	135006516	1099032	0.0081	2.4799
chr12	133851895	2228107	0.0166	4.9495
chr13	115169878	1168454	0.0101	2.8734
chr14	107349540	340091	0.0032	1.3495
chr15	102531392	454064	0.0044	1.2469
chr16	90354753	388008	0.0043	1.2944
chr17	81195210	996019	0.0123	2.972
chr18	78077248	216612	0.0028	0.9507
chr19	59128983	217702	0.0037	0.9043
chr20	63025520	354579	0.0056	1.6073
chr21	48129895	93019	0.0019	0.6524
chr22	51304566	125129	0.0024	0.4988
chrMT	16571	3928783	237.0879	998.3072
chrX	155270560	23921339	0.1541	12.2741

chrY	59373566	318799	0.0054	1.5632
------	----------	--------	--------	--------

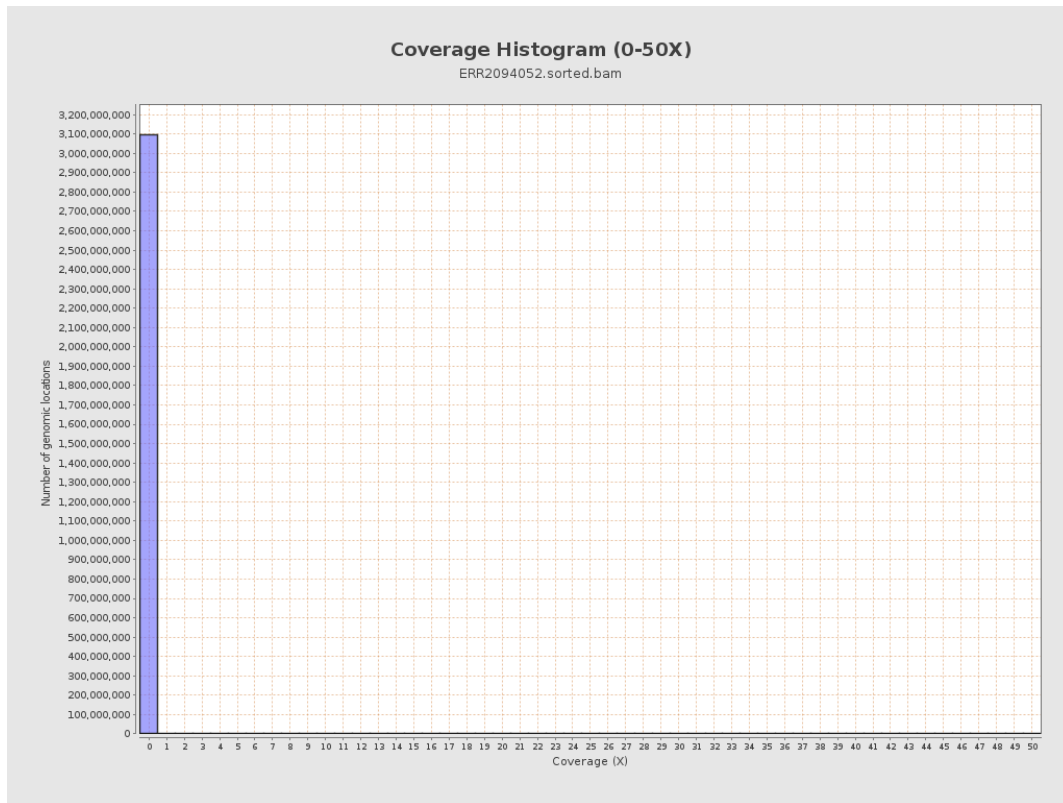
3. Results : Coverage across reference



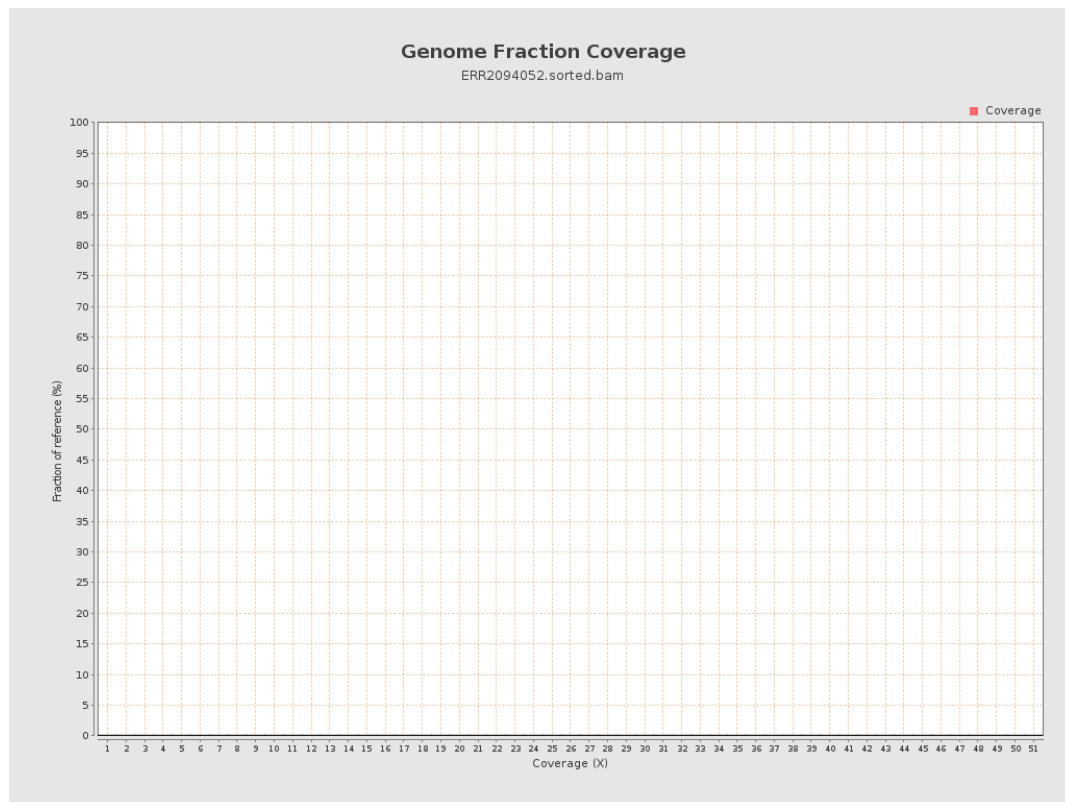
4. Results : Coverage Histogram



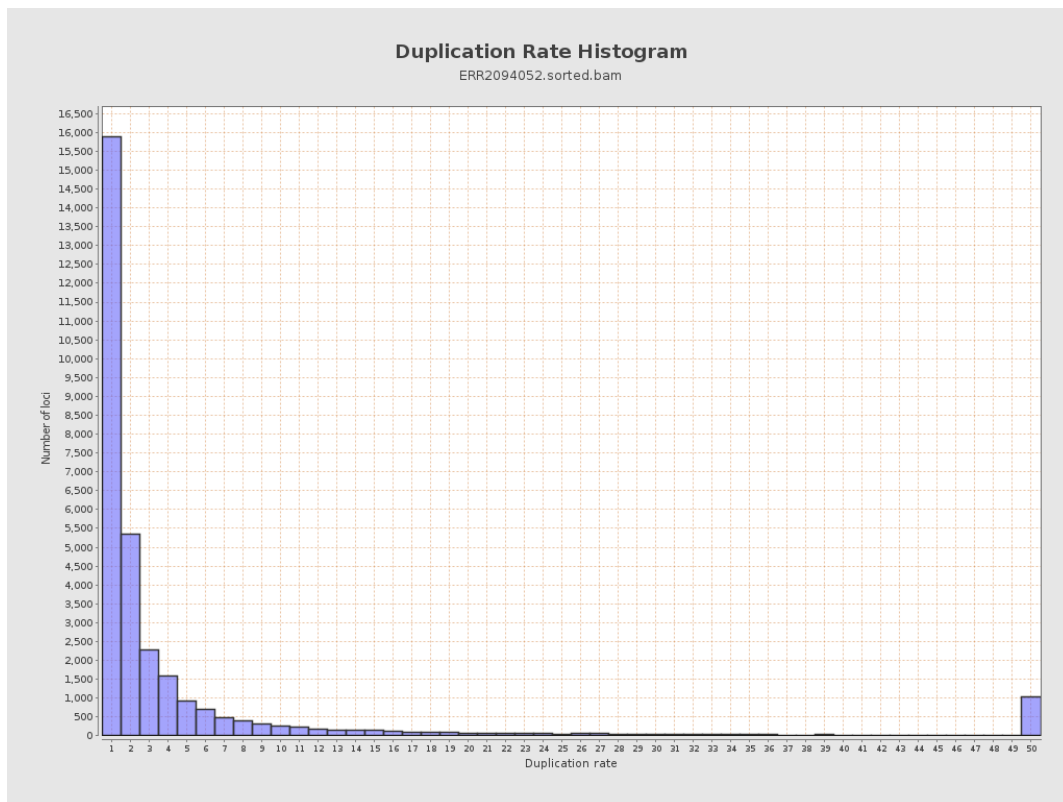
5. Results : Coverage Histogram (0-50X)



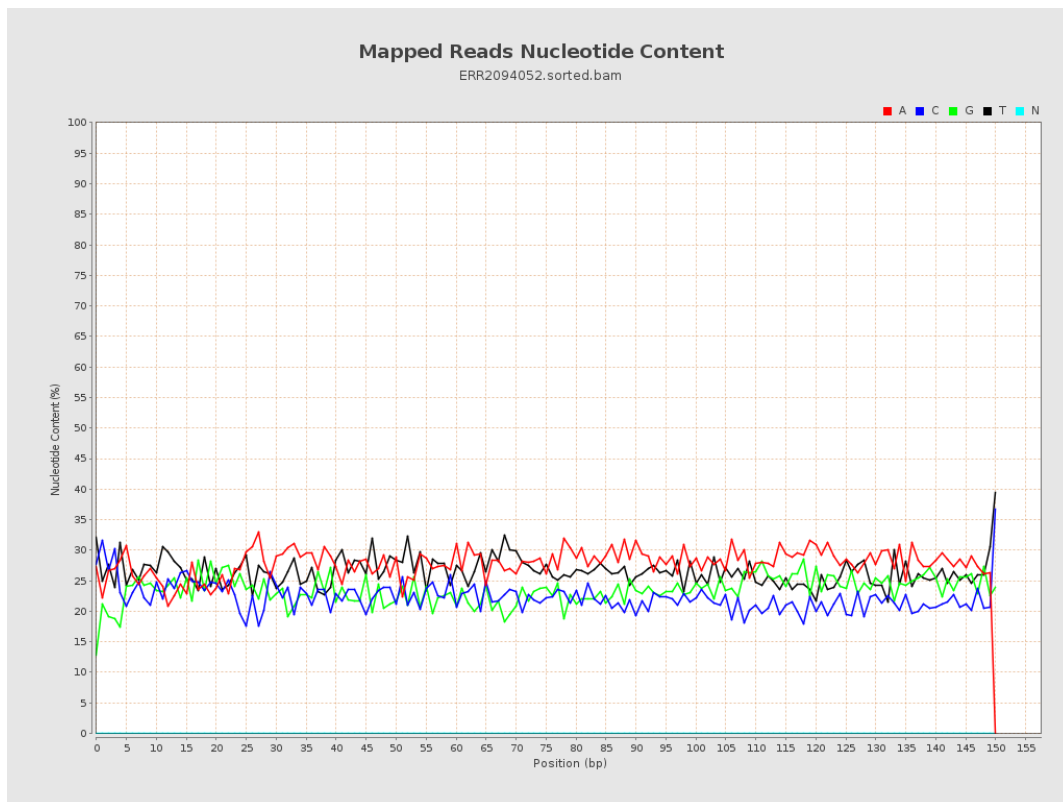
6. Results : Genome Fraction Coverage



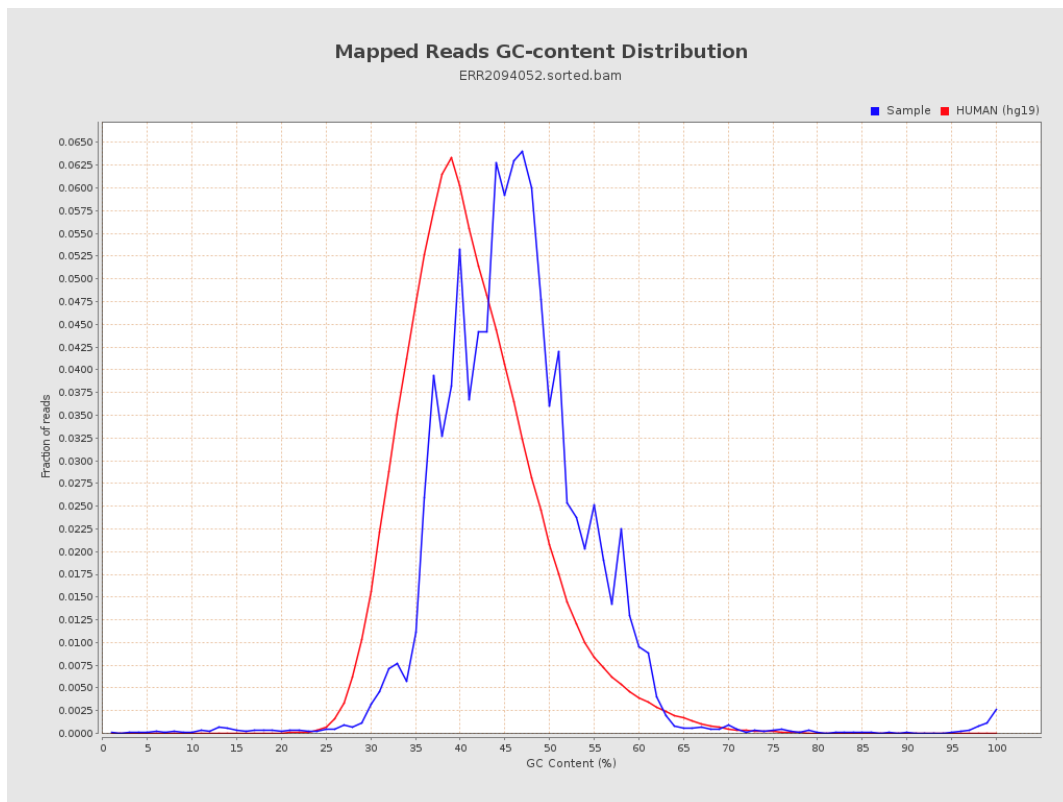
7. Results : Duplication Rate Histogram



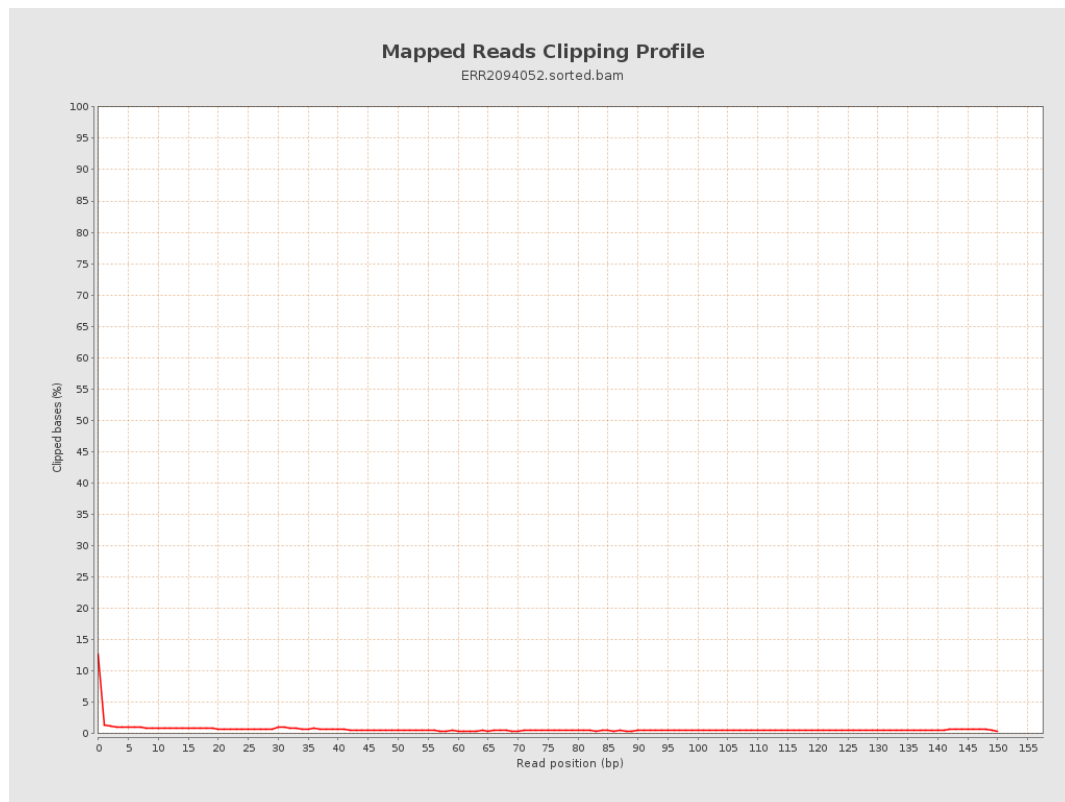
8. Results : Mapped Reads Nucleotide Content



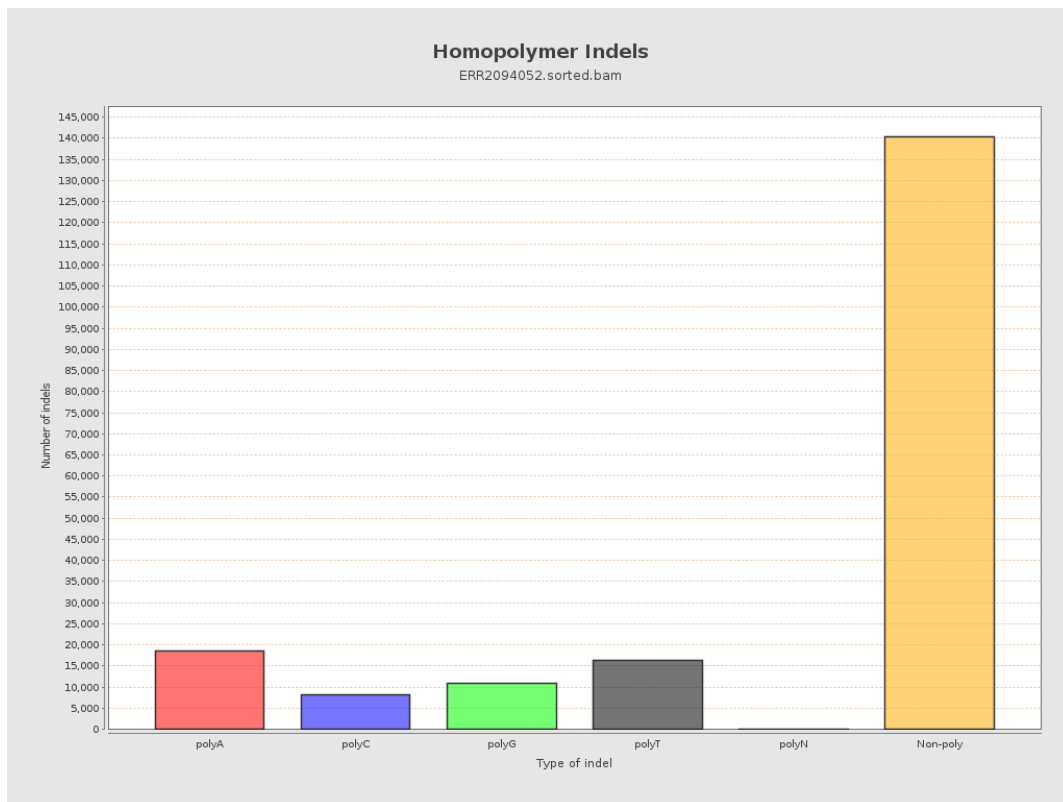
9. Results : Mapped Reads GC-content Distribution



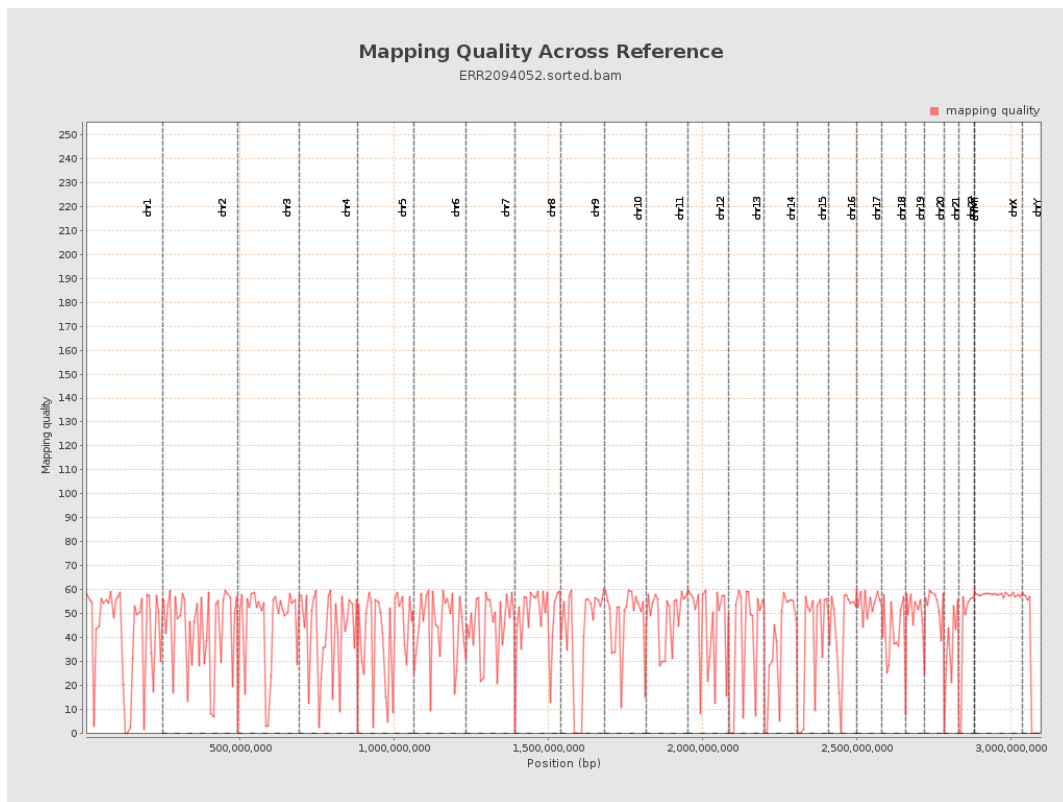
10. Results : Mapped Reads Clipping Profile



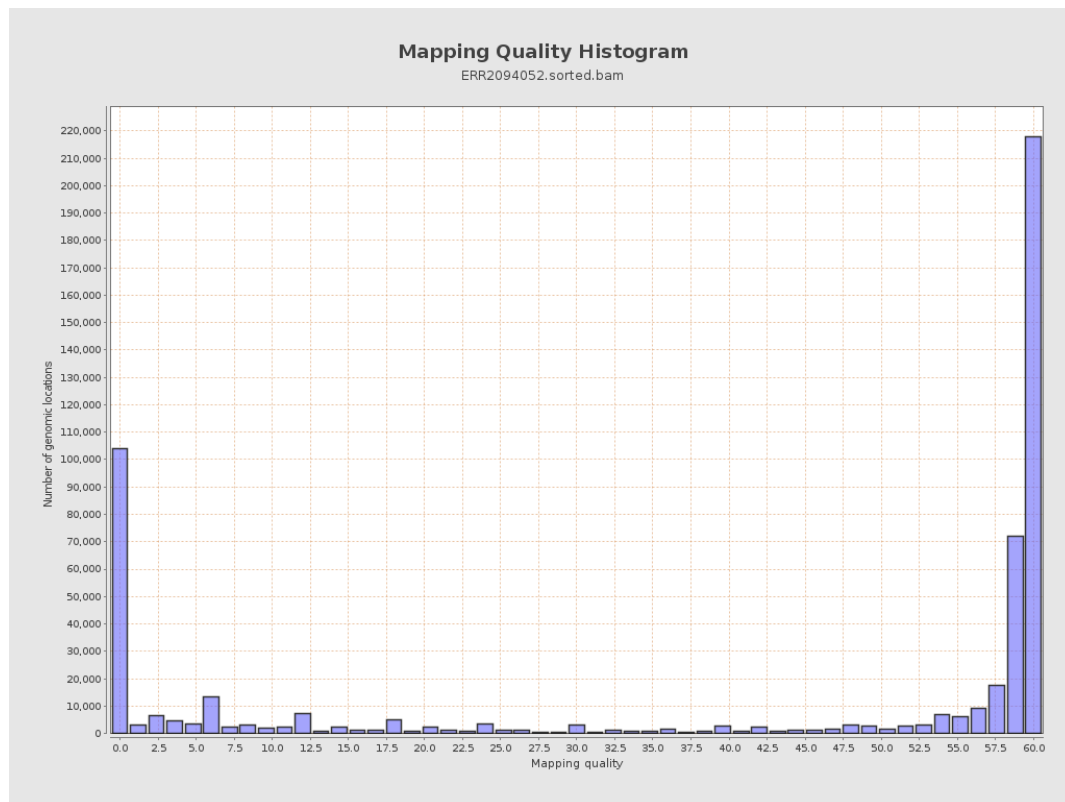
11. Results : Homopolymer Indels



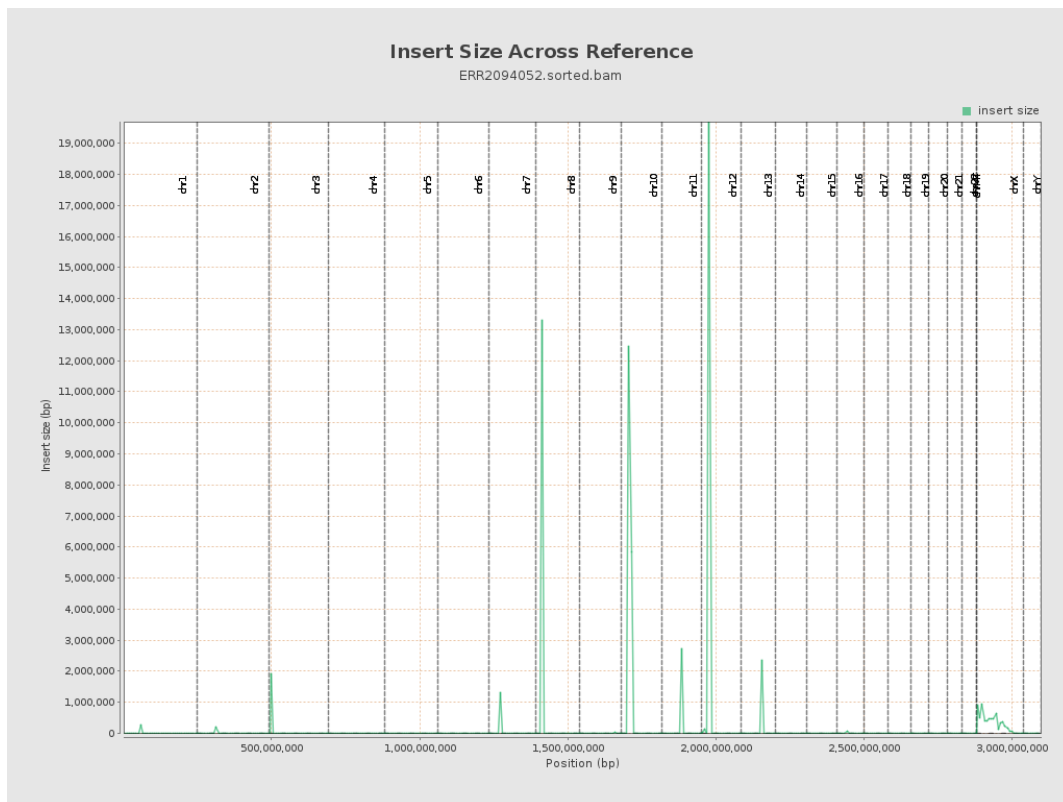
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

