

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:21:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094107.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_ERR2094107 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094107_1.fastq.gz ERR2094107_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:21:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	325,580
Mapped reads	311,761 / 95.76%
Unmapped reads	13,819 / 4.24%
Mapped paired reads	311,761 / 95.76%
Mapped reads, first in pair	156,609 / 48.1%
Mapped reads, second in pair	155,152 / 47.65%
Mapped reads, both in pair	309,562 / 95.08%
Mapped reads, singletons	2,199 / 0.68%
Secondary alignments	0
Supplementary alignments	17,992 / 5.53%
Read min/max/mean length	30 / 151 / 143.28
Duplicated reads (estimated)	301,706 / 92.67%
Duplication rate	50.42%
Clipped reads	152,879 / 46.96%

2.2. ACGT Content

Number/percentage of A's	11,726,938 / 29.29%
Number/percentage of C's	8,493,900 / 21.22%
Number/percentage of T's	10,962,353 / 27.38%
Number/percentage of G's	8,847,010 / 22.1%
Number/percentage of N's	469 / 0%

GC Percentage	43.32%
---------------	--------

2.3. Coverage

Mean	0.0132
Standard Deviation	4.3022

2.4. Mapping Quality

Mean Mapping Quality	35.54
----------------------	-------

2.5. Insert size

Mean	1,130,520.58
Standard Deviation	9,303,378.19
P25/Median/P75	133 / 165 / 198

2.6. Mismatches and indels

General error rate	3.51%
Mismatches	1,341,875
Insertions	31,003
Mapped reads with at least one insertion	9.54%
Deletions	90,792
Mapped reads with at least one deletion	28.19%
Homopolymer indels	33.04%

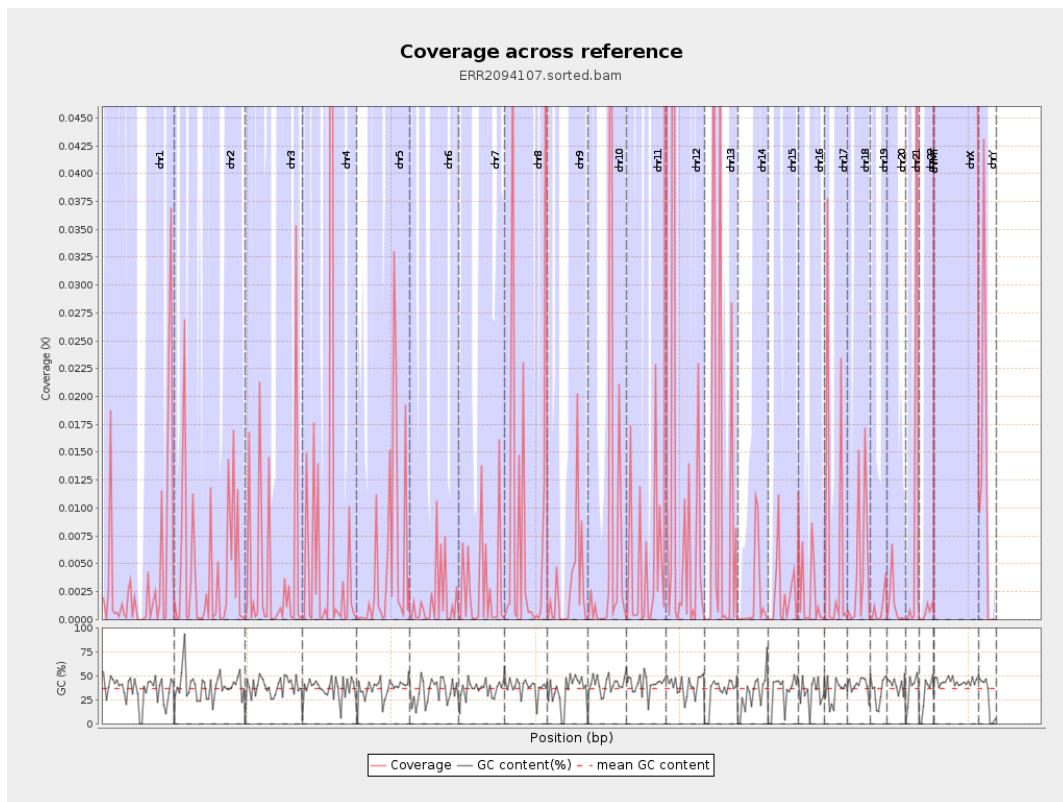
2.7. Chromosome stats

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

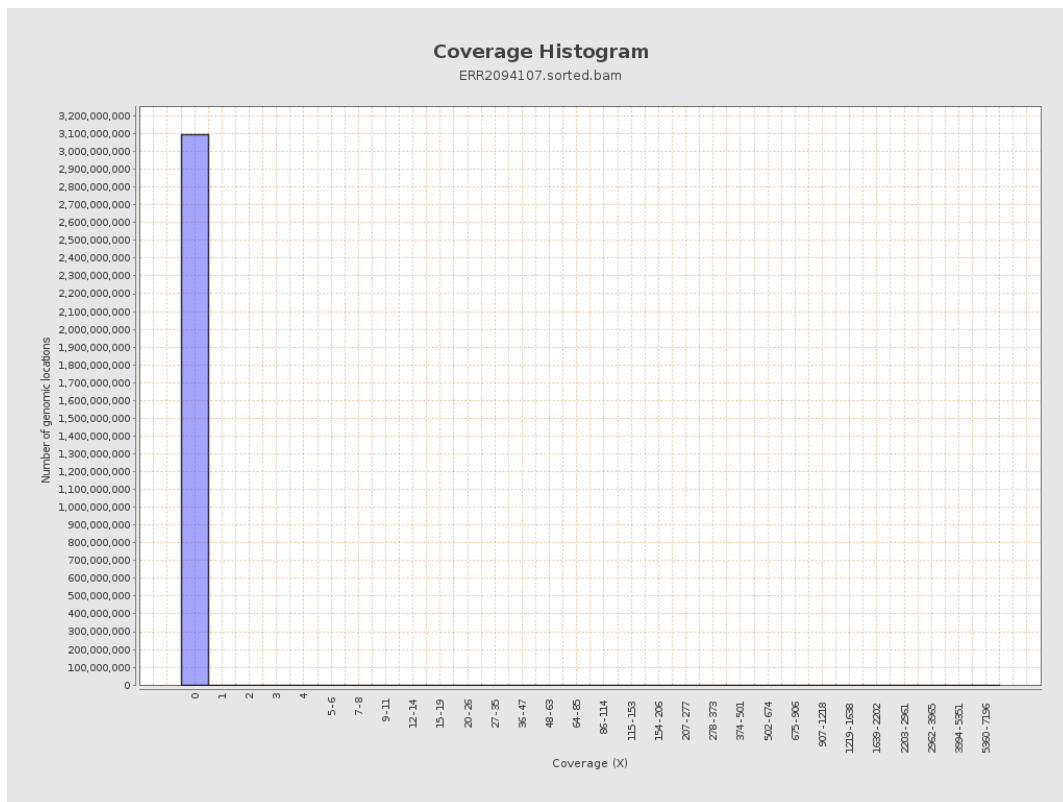
		bases	coverage	deviation
chr1	249250621	959588	0.0038	1.7543
chr2	243199373	1000141	0.0041	1.2942
chr3	198022430	806804	0.0041	1.8674
chr4	191154276	1621717	0.0085	3.6394
chr5	180915260	938530	0.0052	2.2049
chr6	171115067	293695	0.0017	0.6331
chr7	159138663	447404	0.0028	1.0591
chr8	146364022	1369022	0.0094	4.1536
chr9	141213431	396757	0.0028	0.8851
chr10	135534747	1048563	0.0077	4.8998
chr11	135006516	765373	0.0057	1.6501
chr12	133851895	1383209	0.0103	4.8419
chr13	115169878	1188165	0.0103	3.4673
chr14	107349540	185676	0.0017	0.8333
chr15	102531392	219505	0.0021	0.7166
chr16	90354753	234637	0.0026	0.9321
chr17	81195210	499902	0.0062	2.0566
chr18	78077248	385366	0.0049	1.6078
chr19	59128983	56774	0.001	0.3893
chr20	63025520	93031	0.0015	0.4937
chr21	48129895	465468	0.0097	3.5166
chr22	51304566	33371	0.0007	0.1677
chrMT	16571	2831682	170.8818	771.055
chrX	155270560	22881936	0.1474	13.6448

chrY	59373566	656694	0.0111	2.5197
------	----------	--------	--------	--------

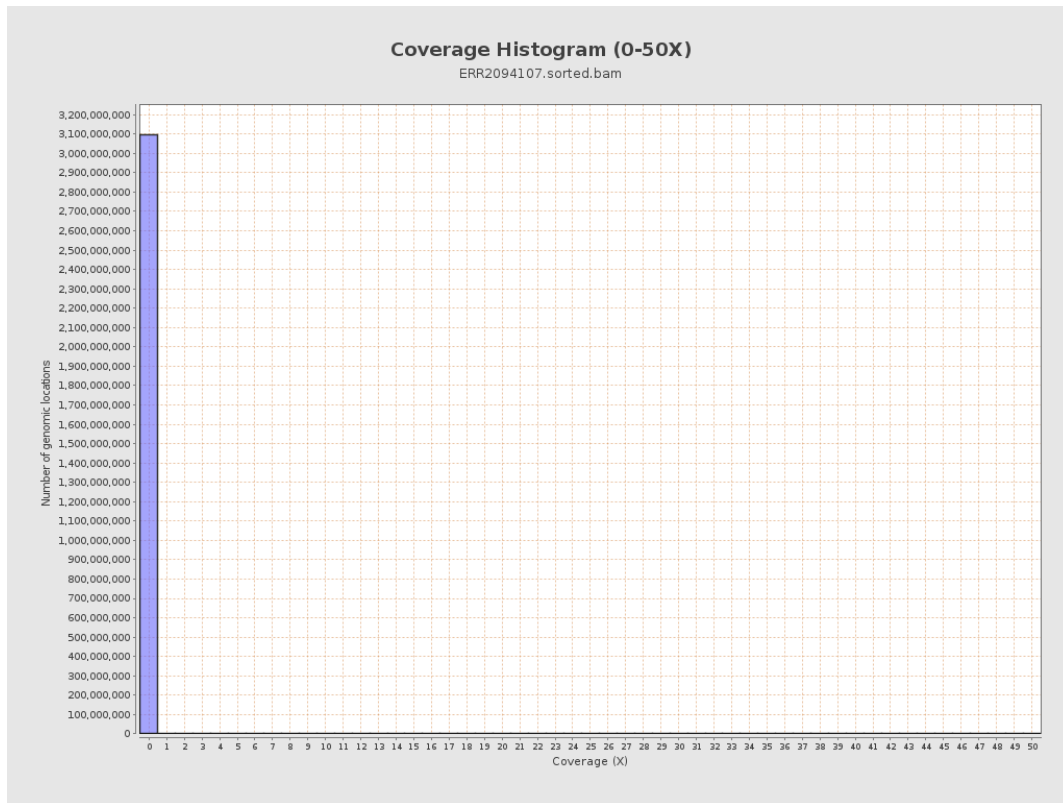
3. Results : Coverage across reference



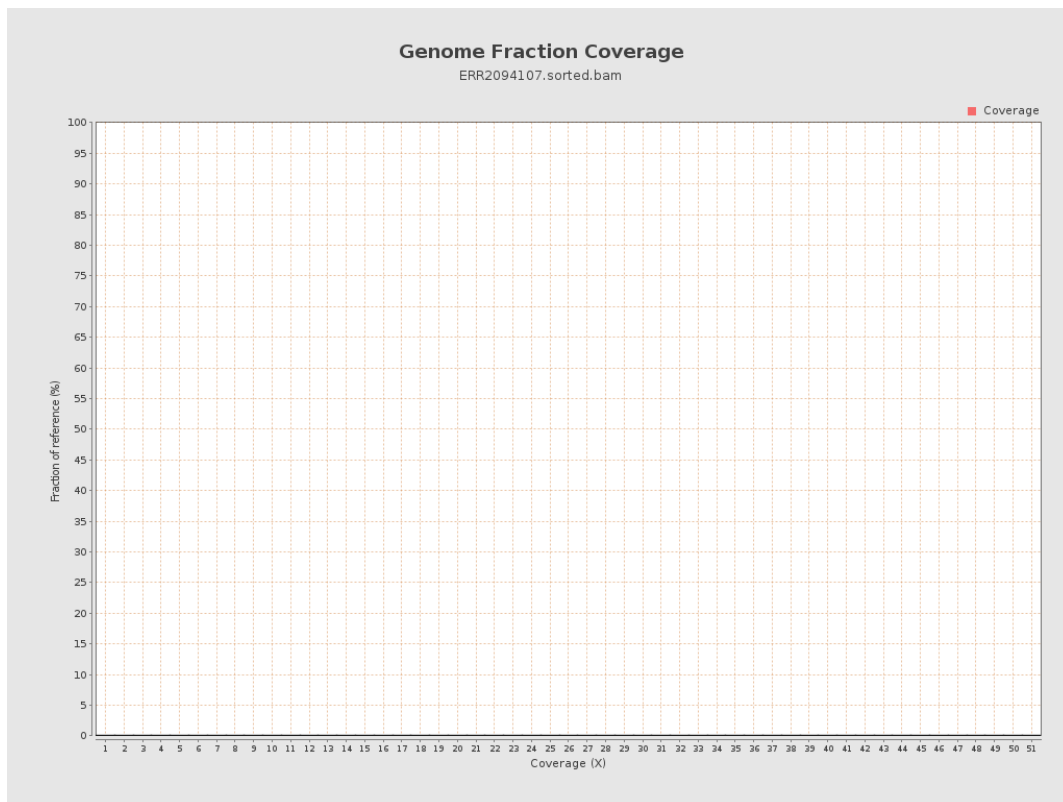
4. Results : Coverage Histogram



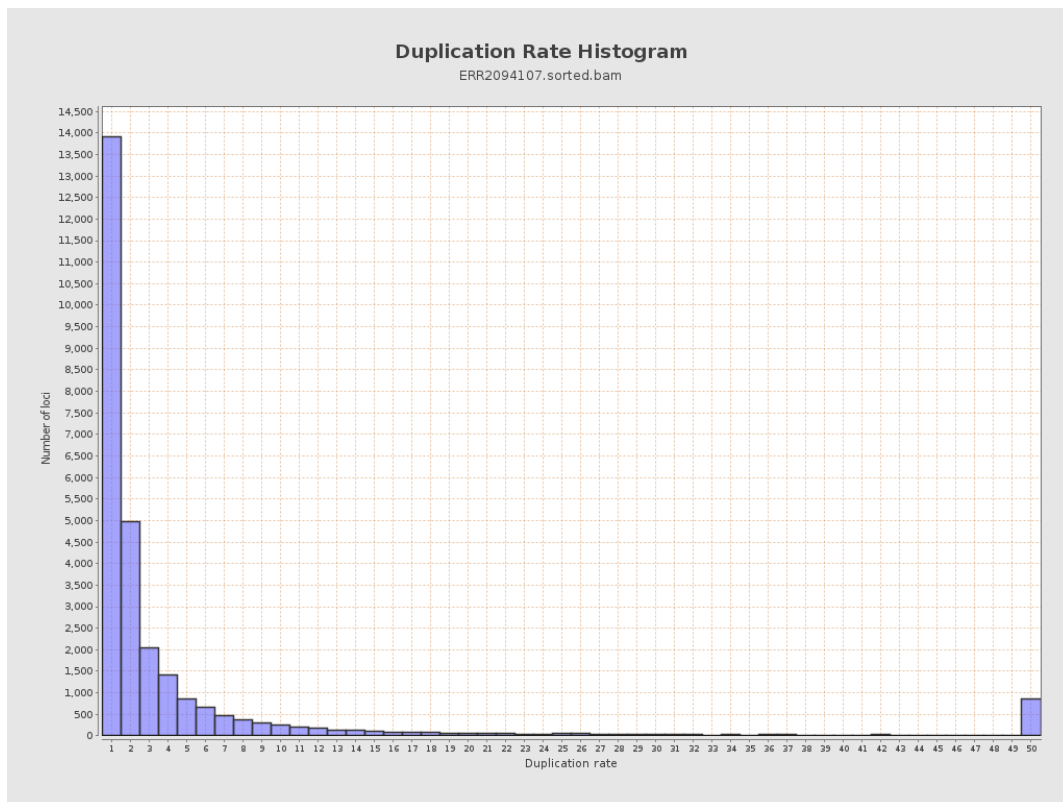
5. Results : Coverage Histogram (0-50X)



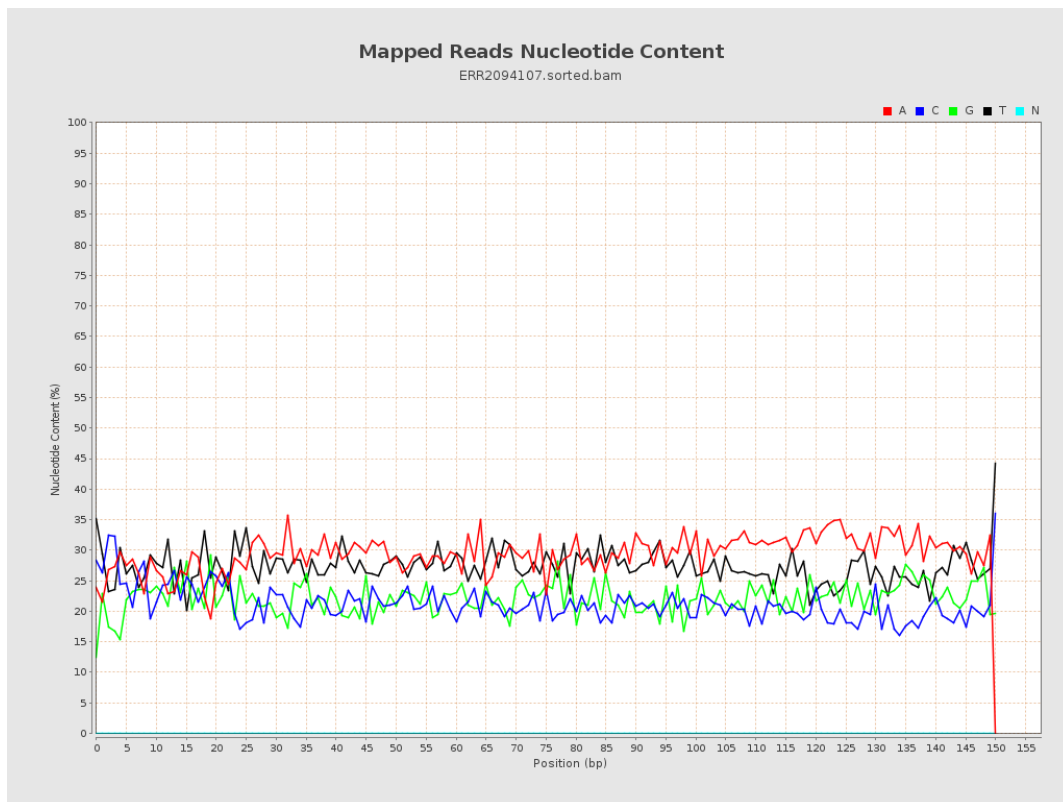
6. Results : Genome Fraction Coverage



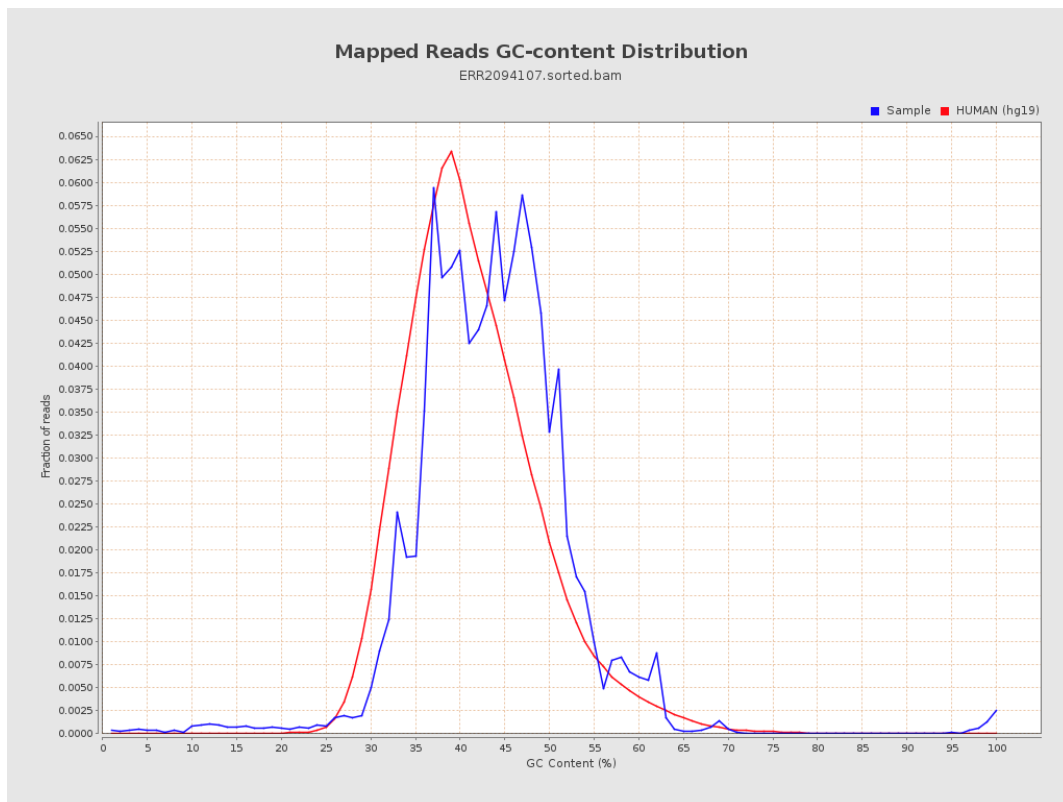
7. Results : Duplication Rate Histogram



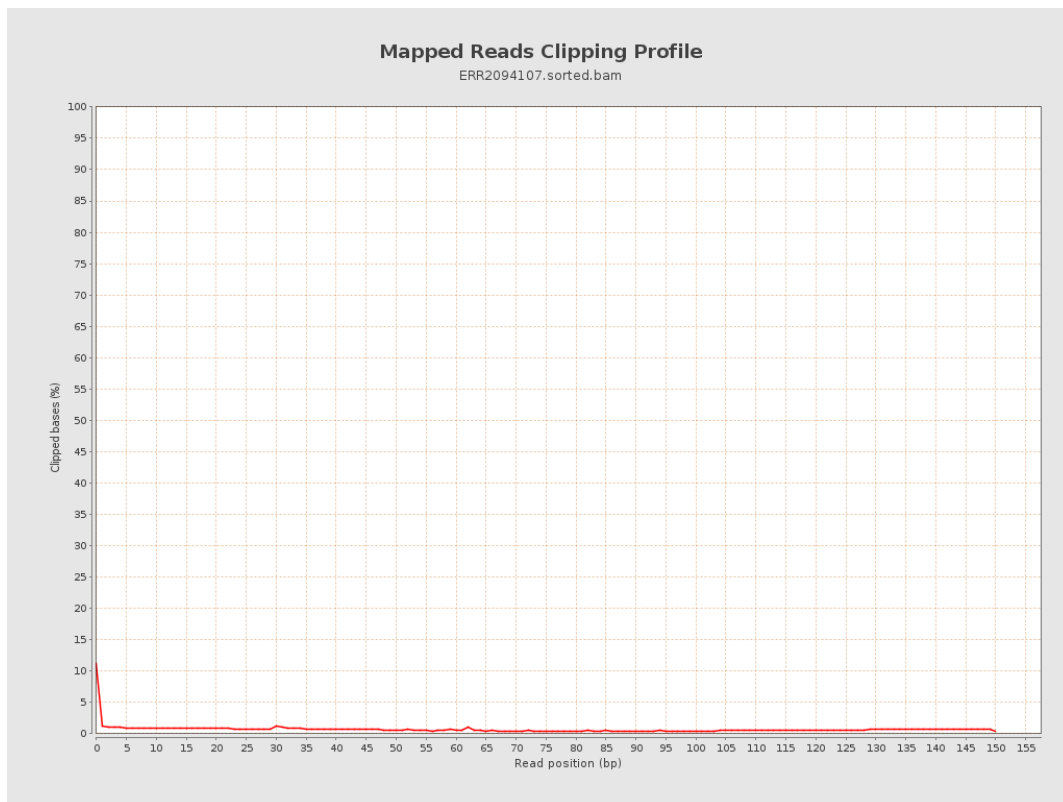
8. Results : Mapped Reads Nucleotide Content



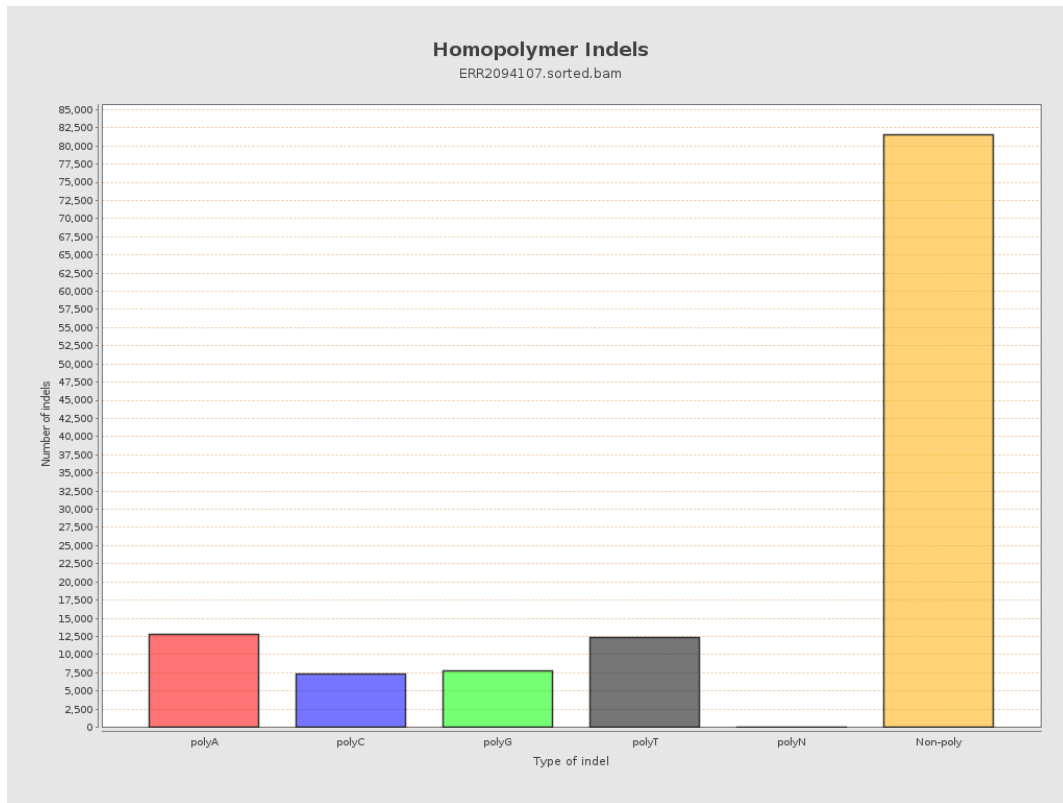
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



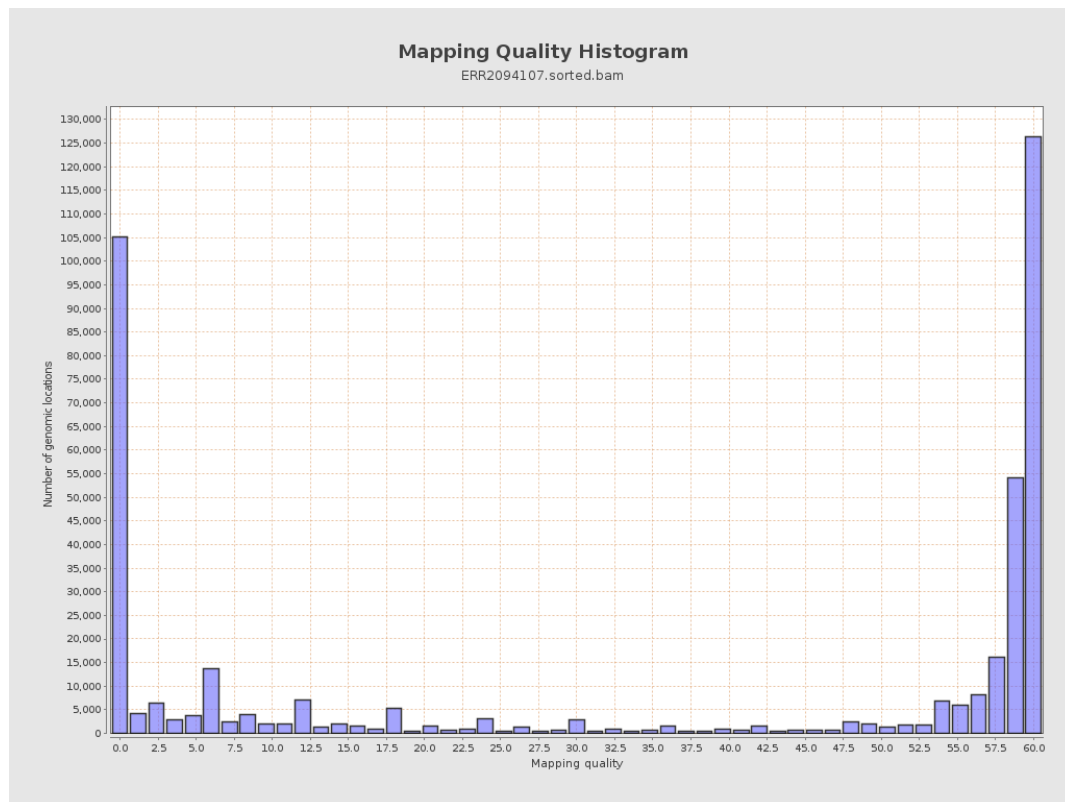
11. Results : Homopolymer Indels



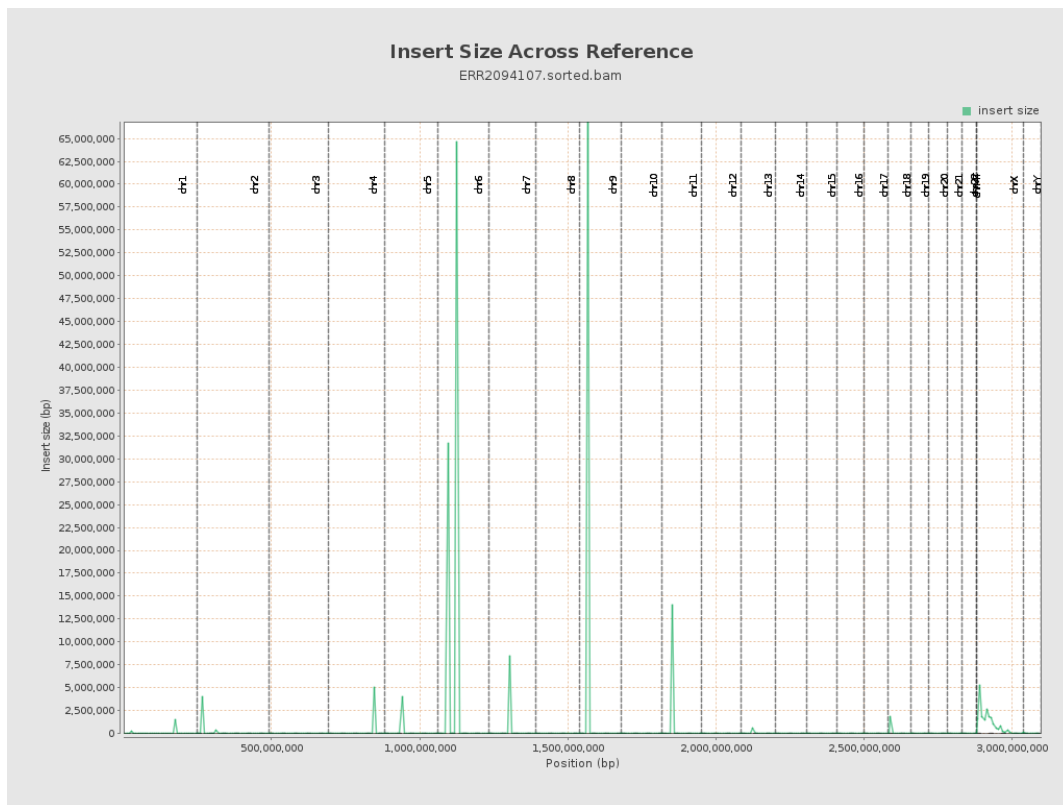
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

