

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:31:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094054.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_ERR2094054 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094054_1.fastq.gz ERR2094054_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:31:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	373,754
Mapped reads	358,104 / 95.81%
Unmapped reads	15,650 / 4.19%
Mapped paired reads	358,104 / 95.81%
Mapped reads, first in pair	179,878 / 48.13%
Mapped reads, second in pair	178,226 / 47.69%
Mapped reads, both in pair	355,642 / 95.15%
Mapped reads, singletons	2,462 / 0.66%
Secondary alignments	0
Supplementary alignments	15,223 / 4.07%
Read min/max/mean length	30 / 151 / 141.39
Duplicated reads (estimated)	335,864 / 89.86%
Duplication rate	50.88%
Clipped reads	150,909 / 40.38%

2.2. ACGT Content

Number/percentage of A's	12,852,241 / 27.62%
Number/percentage of C's	10,459,269 / 22.48%
Number/percentage of T's	12,383,606 / 26.61%
Number/percentage of G's	10,841,151 / 23.3%
Number/percentage of N's	510 / 0%

GC Percentage	45.77%
---------------	--------

2.3. Coverage

Mean	0.0154
Standard Deviation	3.4979

2.4. Mapping Quality

Mean Mapping Quality	43.09
----------------------	-------

2.5. Insert size

Mean	632,399.63
Standard Deviation	6,975,041.05
P25/Median/P75	134 / 169 / 198

2.6. Mismatches and indels

General error rate	4.52%
Mismatches	2,030,406
Insertions	34,735
Mapped reads with at least one insertion	9.49%
Deletions	162,535
Mapped reads with at least one deletion	42.13%
Homopolymer indels	28.35%

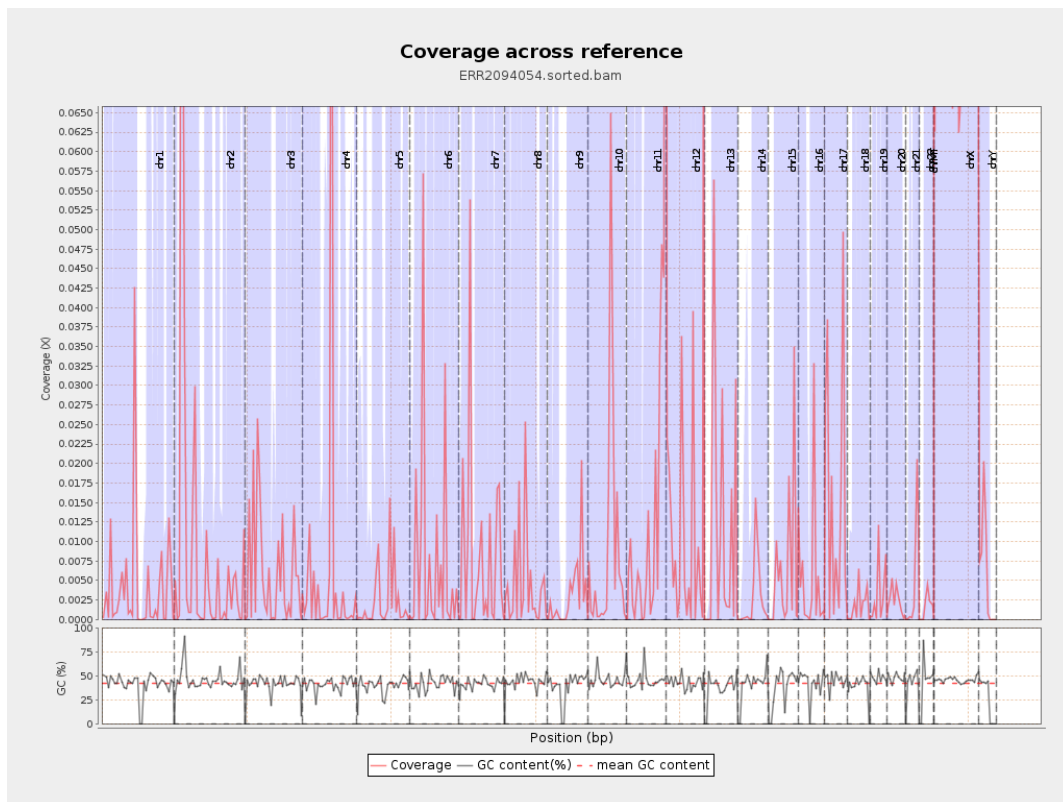
2.7. Chromosome stats

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

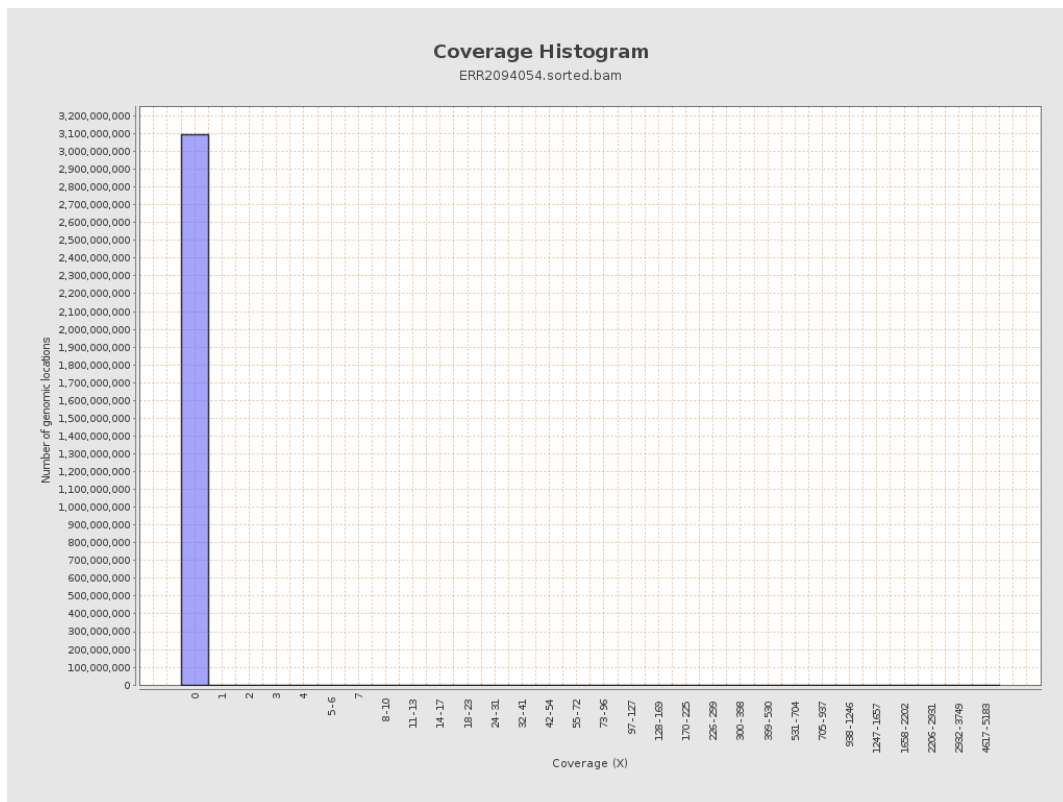
		bases	coverage	deviation
chr1	249250621	977997	0.0039	1.5533
chr2	243199373	2149212	0.0088	2.6969
chr3	198022430	1206088	0.0061	1.6725
chr4	191154276	1337651	0.007	2.4495
chr5	180915260	445520	0.0025	1.066
chr6	171115067	1274451	0.0074	3.2898
chr7	159138663	1260923	0.0079	2.1355
chr8	146364022	663422	0.0045	1.2546
chr9	141213431	441482	0.0031	1.0038
chr10	135534747	1256242	0.0093	3.177
chr11	135006516	1788501	0.0132	3.2511
chr12	133851895	1531745	0.0114	3.0644
chr13	115169878	1305363	0.0113	2.7433
chr14	107349540	288109	0.0027	1.1294
chr15	102531392	628538	0.0061	1.7378
chr16	90354753	501644	0.0056	2.0789
chr17	81195210	1282798	0.0158	3.9421
chr18	78077248	144077	0.0018	0.5401
chr19	59128983	196182	0.0033	0.9505
chr20	63025520	158883	0.0025	0.597
chr21	48129895	243813	0.0051	1.4696
chr22	51304566	88127	0.0017	0.3472
chrMT	16571	2670511	161.1557	654.8942
chrX	155270560	25534770	0.1645	10.07

chrY	59373566	362548	0.0061	1.523
------	----------	--------	--------	-------

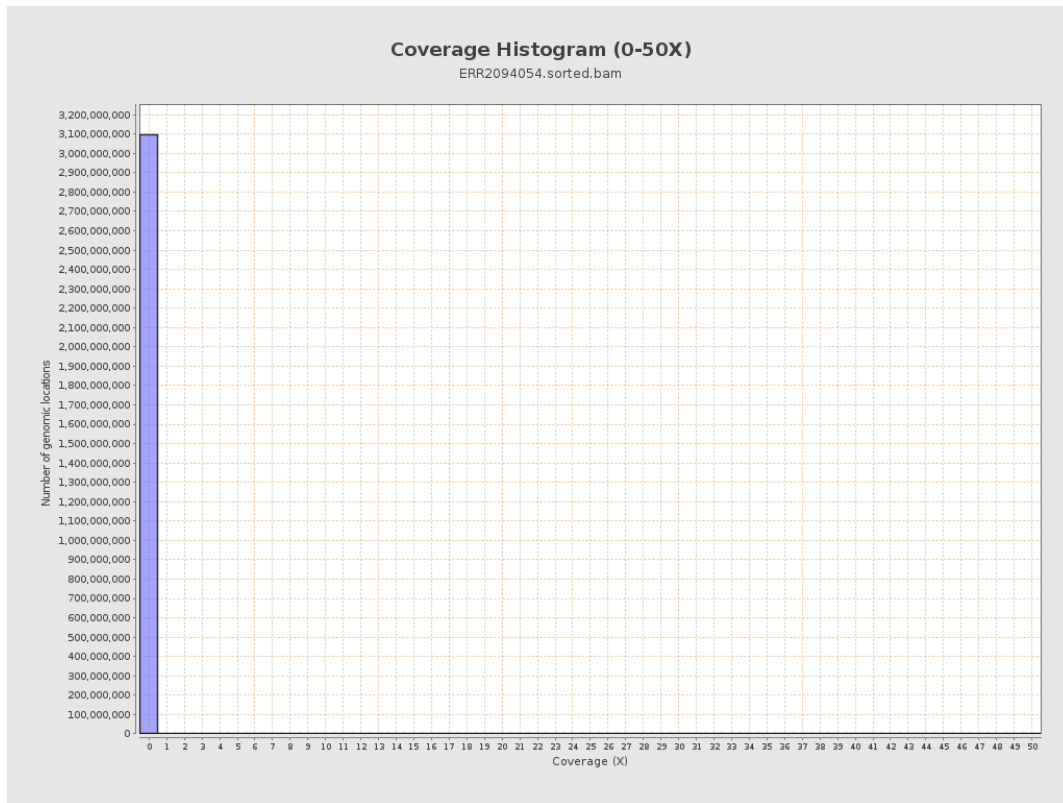
3. Results : Coverage across reference



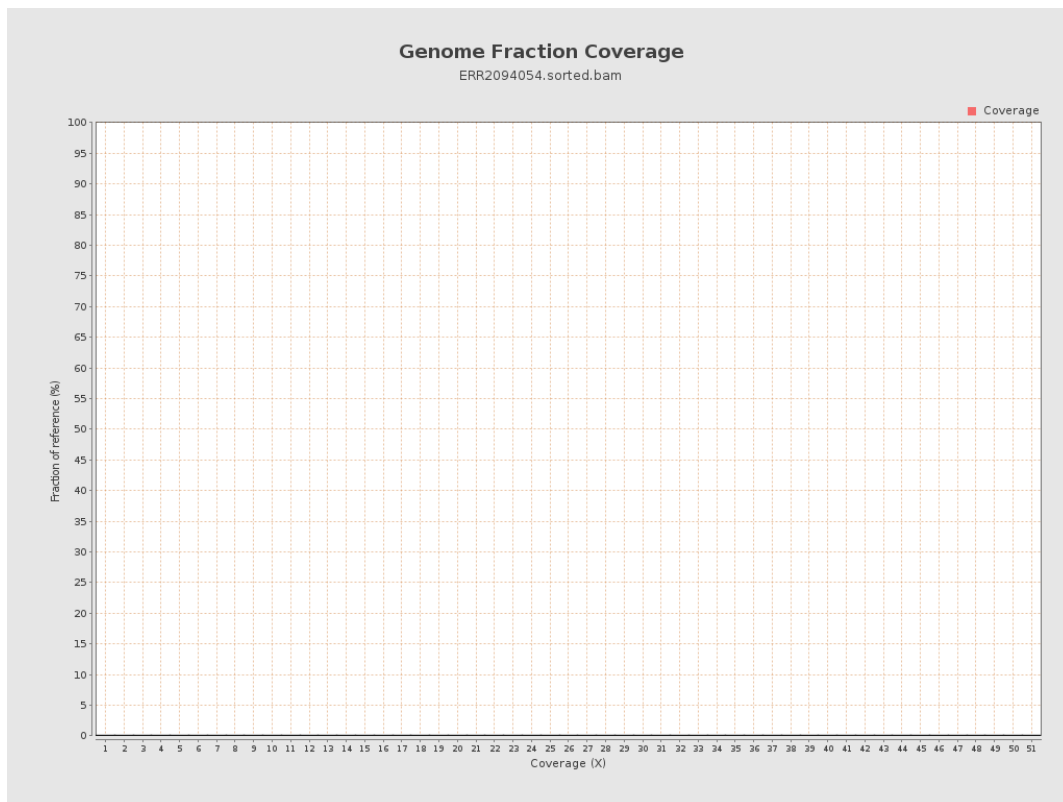
4. Results : Coverage Histogram



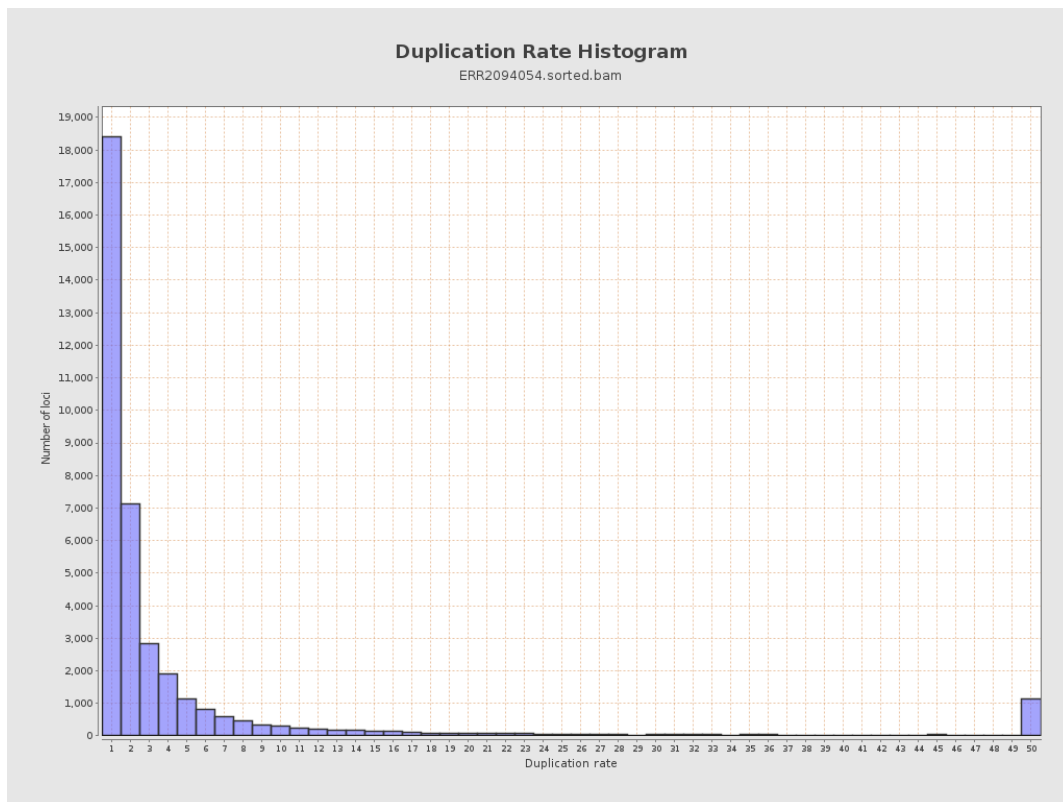
5. Results : Coverage Histogram (0-50X)



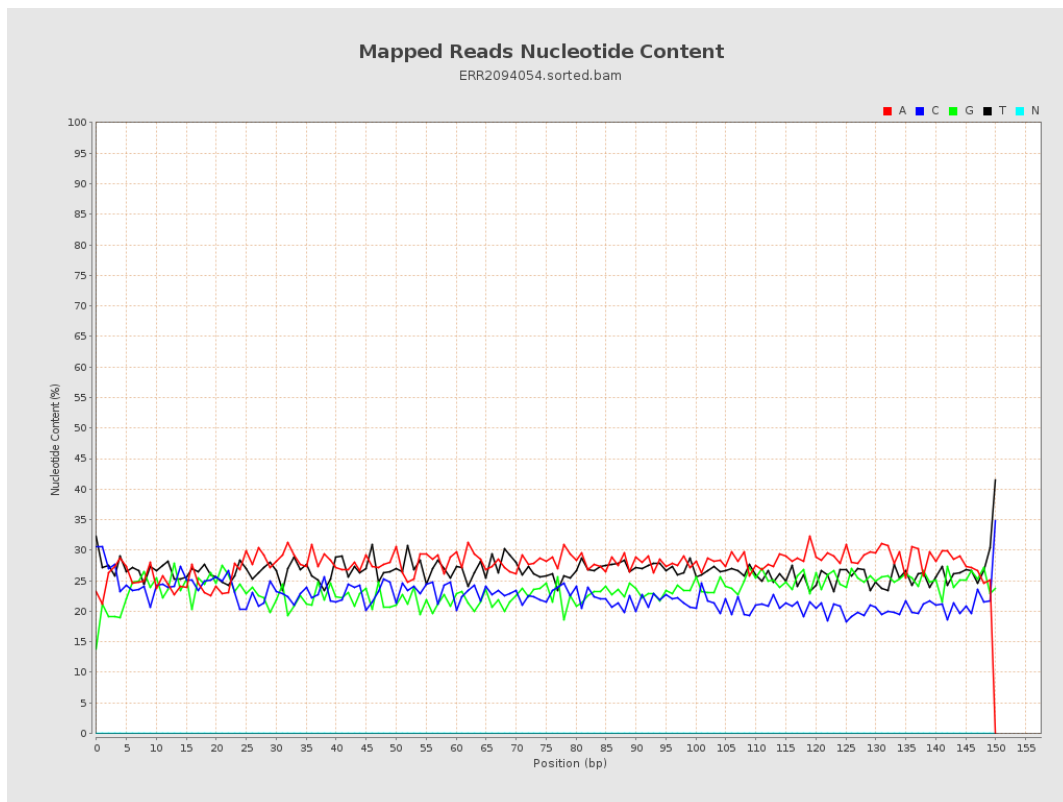
6. Results : Genome Fraction Coverage



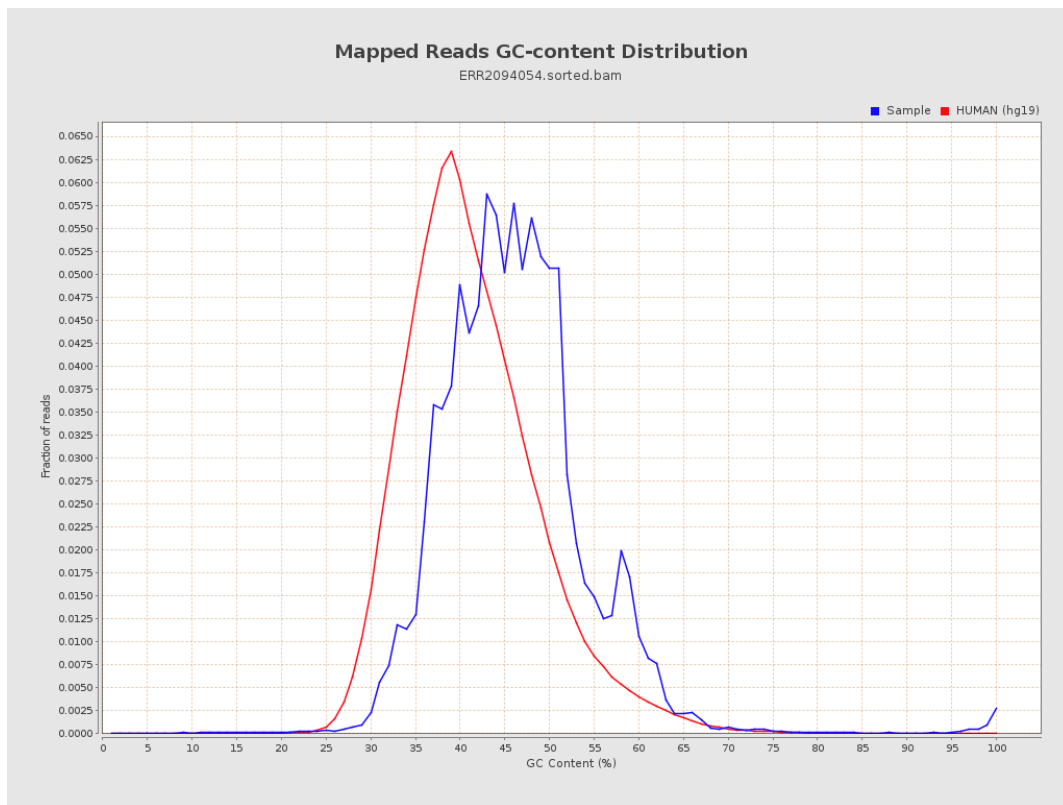
7. Results : Duplication Rate Histogram



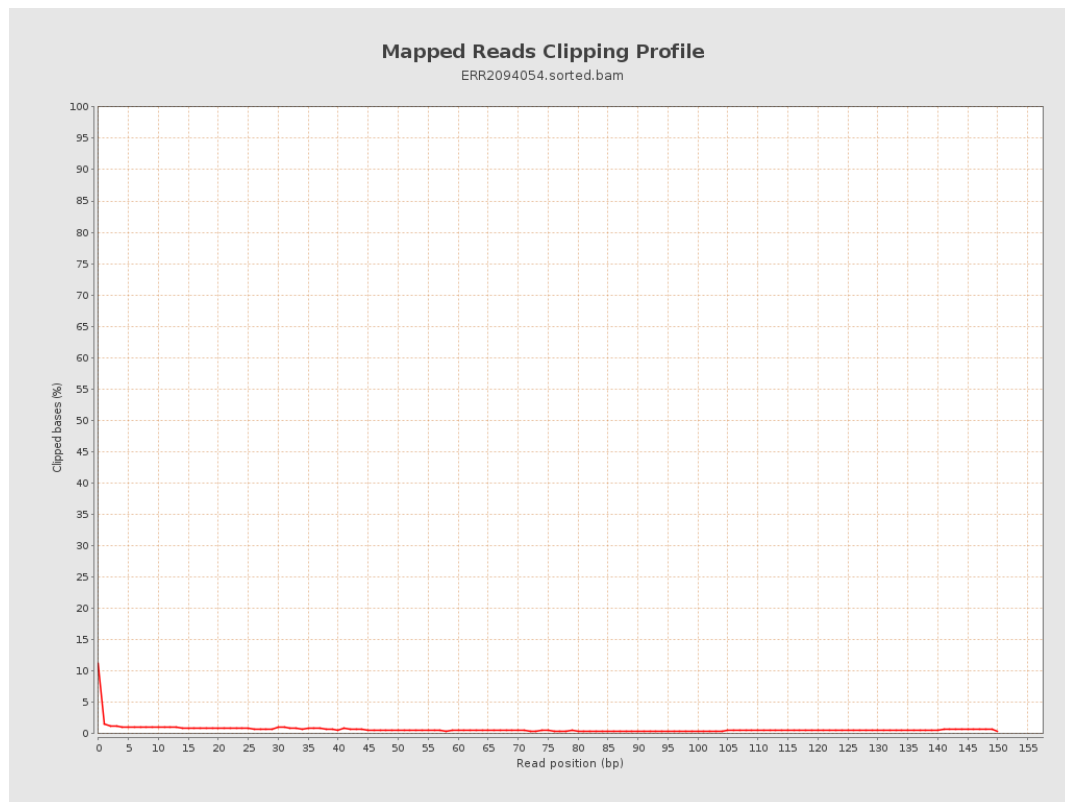
8. Results : Mapped Reads Nucleotide Content



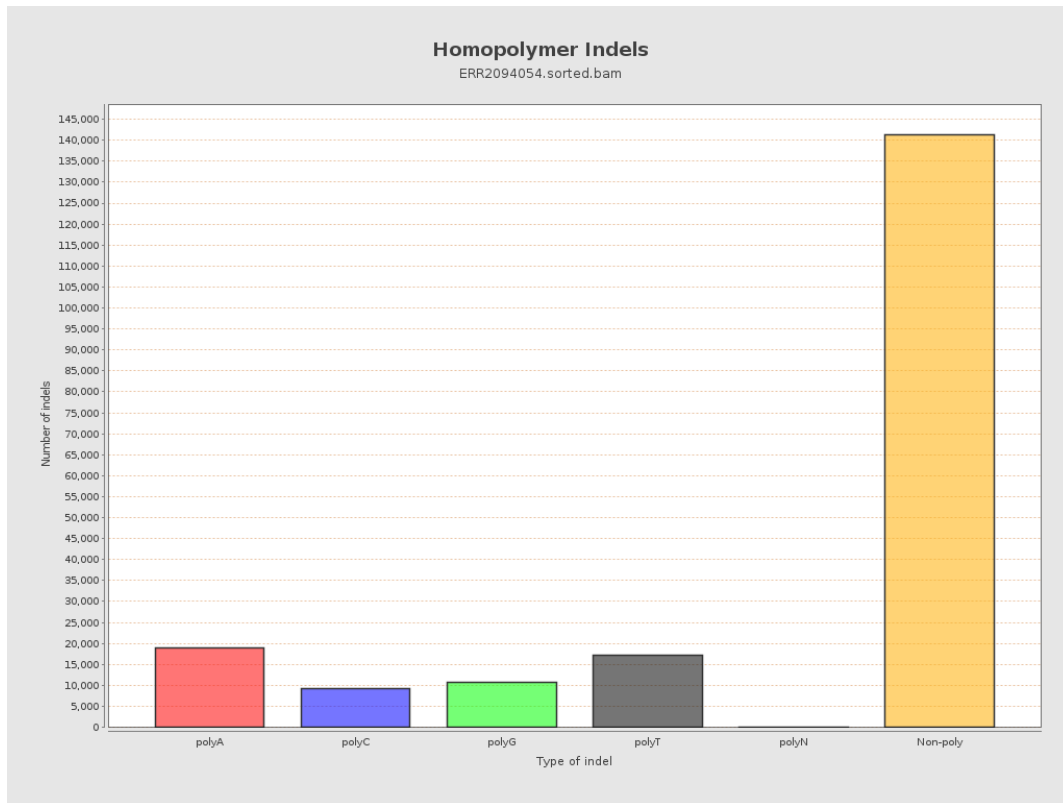
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



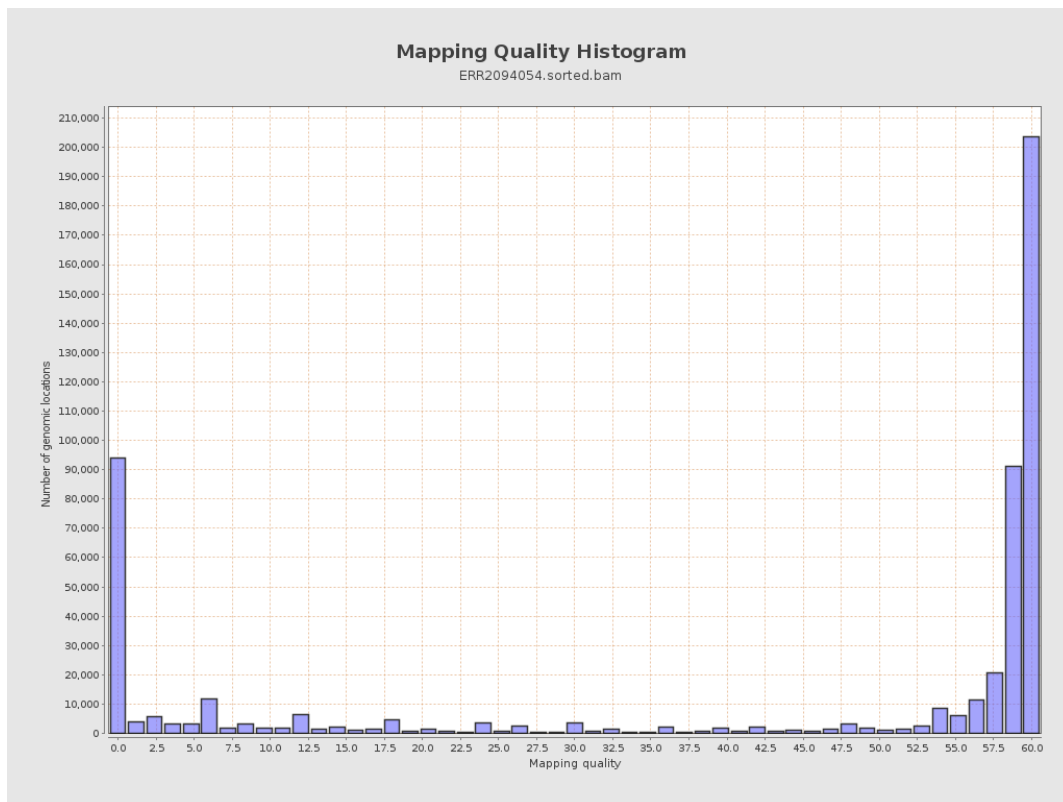
11. Results : Homopolymer Indels



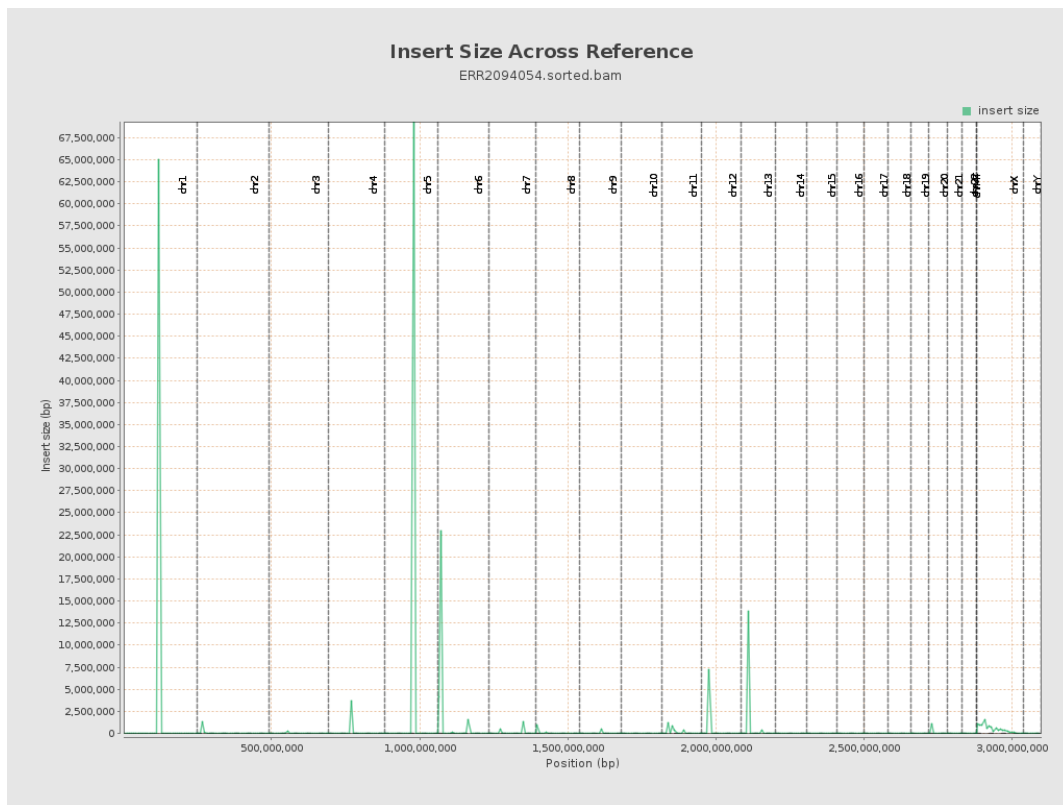
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

