

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:42:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094091.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_ERR2094091 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094091_1.fastq.gz ERR2094091_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:42:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	784,100
Mapped reads	746,368 / 95.19%
Unmapped reads	37,732 / 4.81%
Mapped paired reads	746,368 / 95.19%
Mapped reads, first in pair	375,014 / 47.83%
Mapped reads, second in pair	371,354 / 47.36%
Mapped reads, both in pair	740,356 / 94.42%
Mapped reads, singletons	6,012 / 0.77%
Secondary alignments	0
Supplementary alignments	72,301 / 9.22%
Read min/max/mean length	30 / 151 / 138.87
Duplicated reads (estimated)	742,966 / 94.75%
Duplication rate	56.4%
Clipped reads	435,658 / 55.56%

2.2. ACGT Content

Number/percentage of A's	25,745,696 / 28.46%
Number/percentage of C's	19,712,070 / 21.79%
Number/percentage of T's	24,186,554 / 26.73%
Number/percentage of G's	20,829,850 / 23.02%
Number/percentage of N's	990 / 0%

GC Percentage	44.81%
---------------	--------

2.3. Coverage

Mean	0.0298
Standard Deviation	5.2891

2.4. Mapping Quality

Mean Mapping Quality	41.58
----------------------	-------

2.5. Insert size

Mean	2,412,893.44
Standard Deviation	13,614,771.47
P25/Median/P75	111 / 144 / 178

2.6. Mismatches and indels

General error rate	3.46%
Mismatches	2,999,615
Insertions	62,637
Mapped reads with at least one insertion	8.26%
Deletions	232,967
Mapped reads with at least one deletion	30.21%
Homopolymer indels	28%

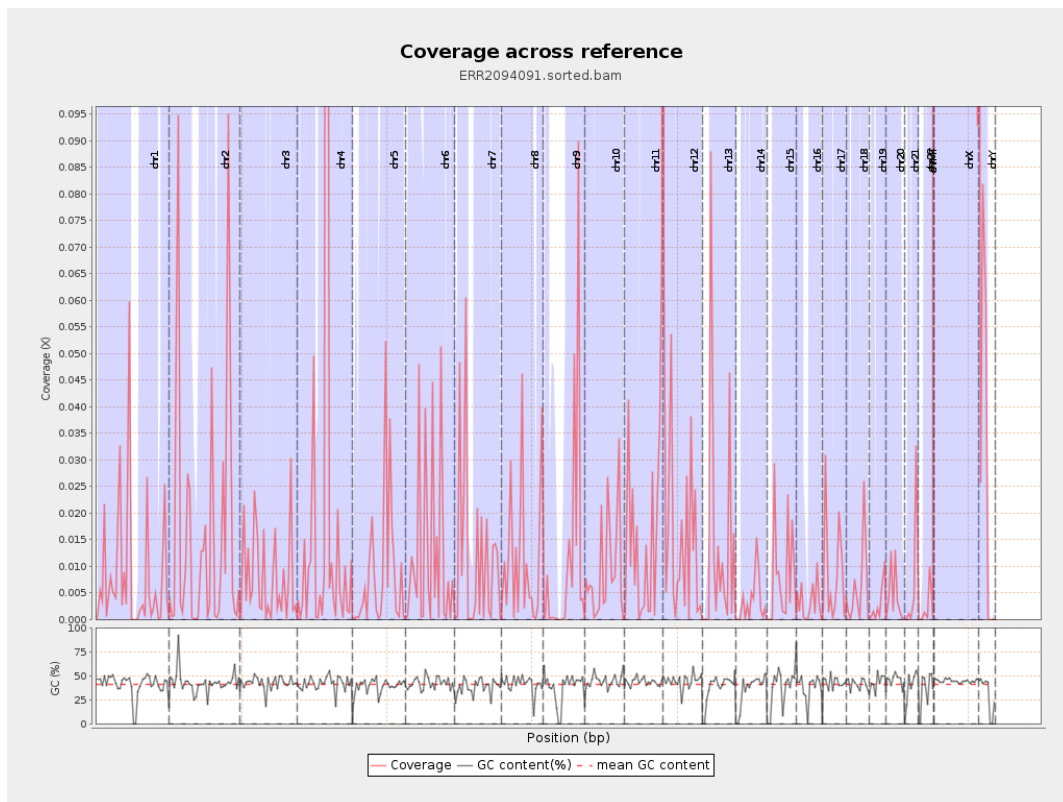
2.7. Chromosome stats

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

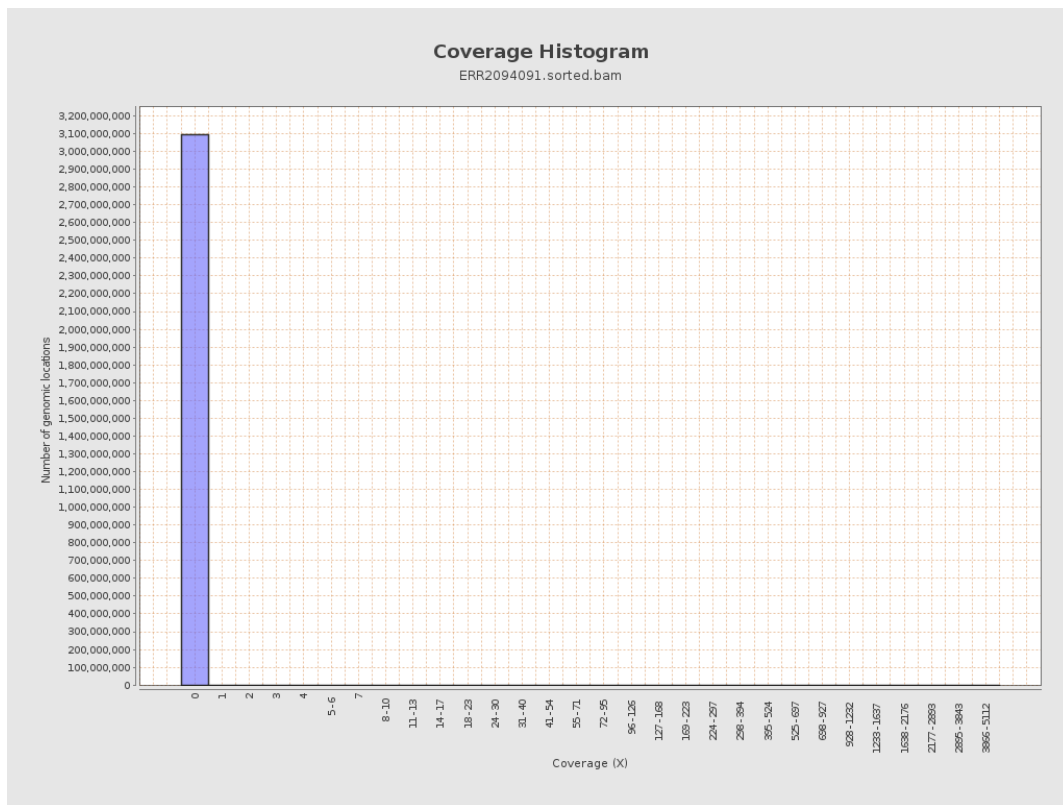
		bases	coverage	deviation
chr1	249250621	2049532	0.0082	2.955
chr2	243199373	4013881	0.0165	4.8236
chr3	198022430	1545342	0.0078	2.0919
chr4	191154276	4023472	0.021	5.7898
chr5	180915260	1524528	0.0084	3.3545
chr6	171115067	1992120	0.0116	3.4981
chr7	159138663	1915708	0.012	3.1718
chr8	146364022	1706136	0.0117	2.9088
chr9	141213431	1558697	0.011	3.9613
chr10	135534747	1343829	0.0099	2.3565
chr11	135006516	2505796	0.0186	4.4334
chr12	133851895	2197200	0.0164	3.3736
chr13	115169878	1553399	0.0135	2.9728
chr14	107349540	357249	0.0033	1.2336
chr15	102531392	854941	0.0083	1.9908
chr16	90354753	277905	0.0031	0.8153
chr17	81195210	628170	0.0077	1.8997
chr18	78077248	498289	0.0064	1.8709
chr19	59128983	168663	0.0029	0.8063
chr20	63025520	291245	0.0046	1.2587
chr21	48129895	338276	0.007	2.3709
chr22	51304566	127546	0.0025	0.8356
chrMT	16571	509560	30.7501	154.3216
chrX	155270560	58285861	0.3754	18.4266

chrY	59373566	1844090	0.0311	5.1411
------	----------	---------	--------	--------

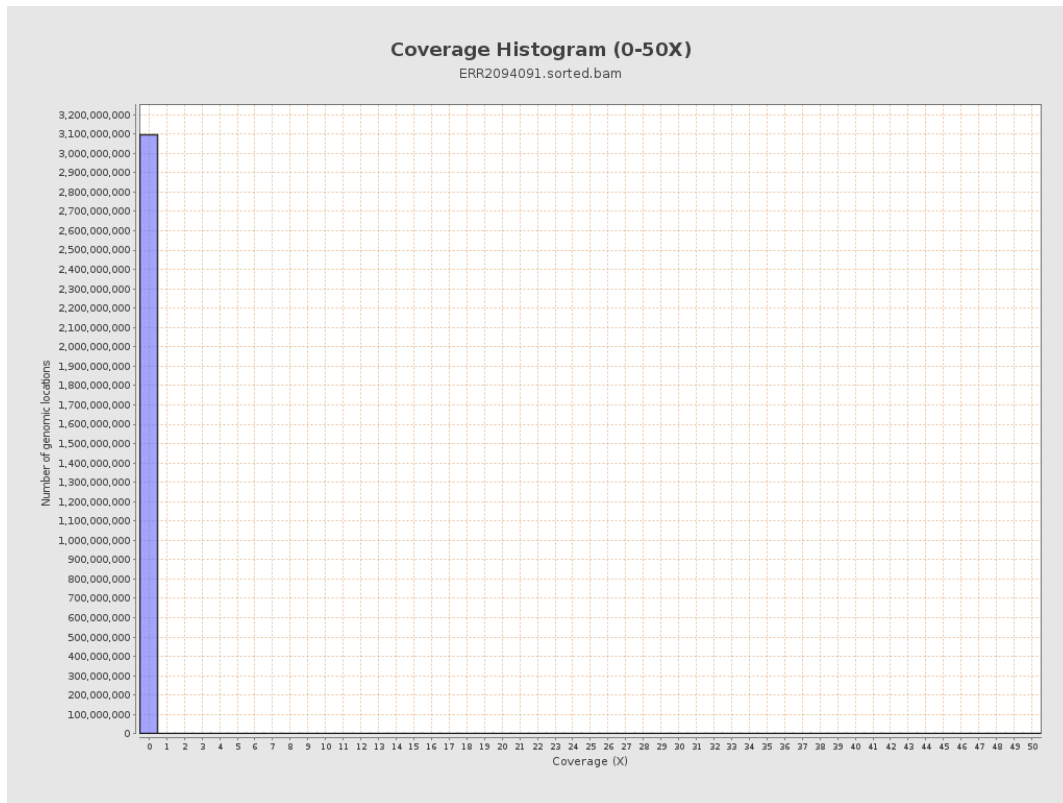
3. Results : Coverage across reference



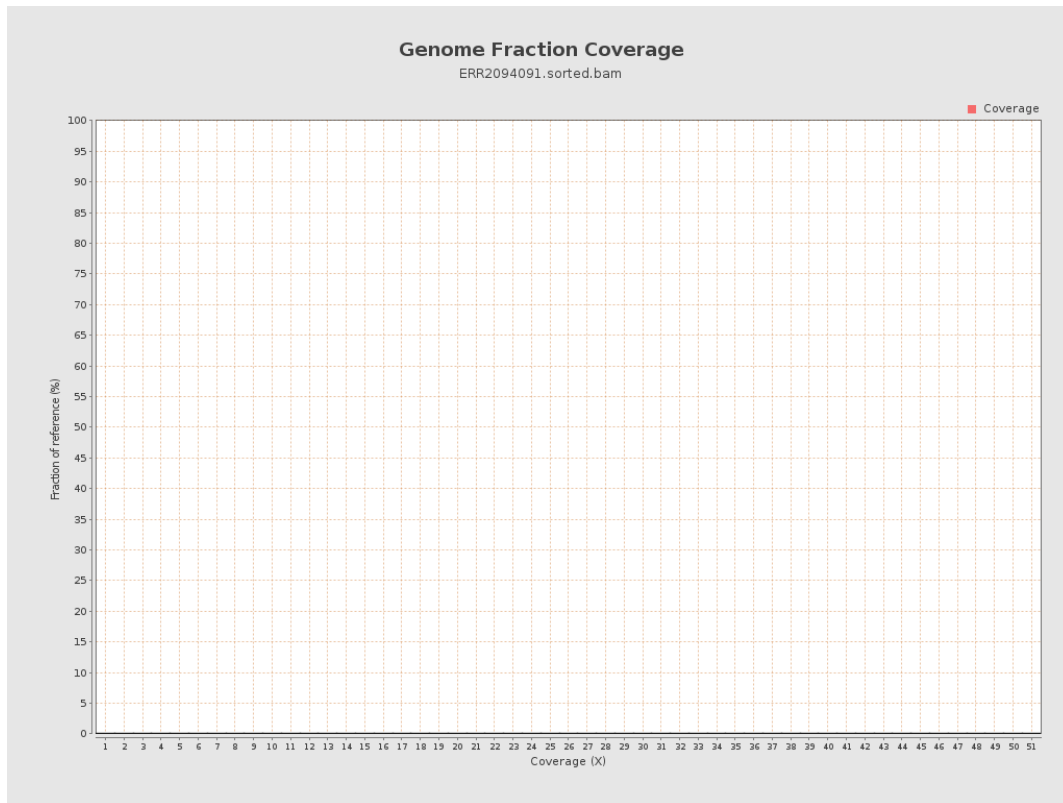
4. Results : Coverage Histogram



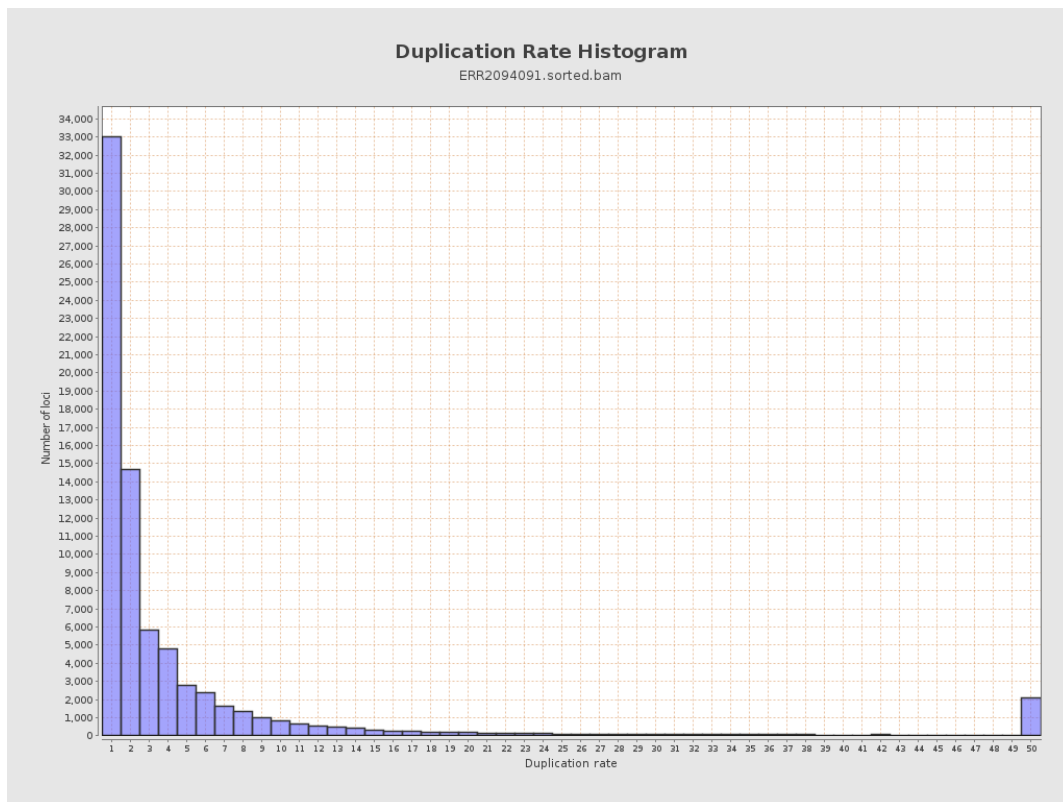
5. Results : Coverage Histogram (0-50X)



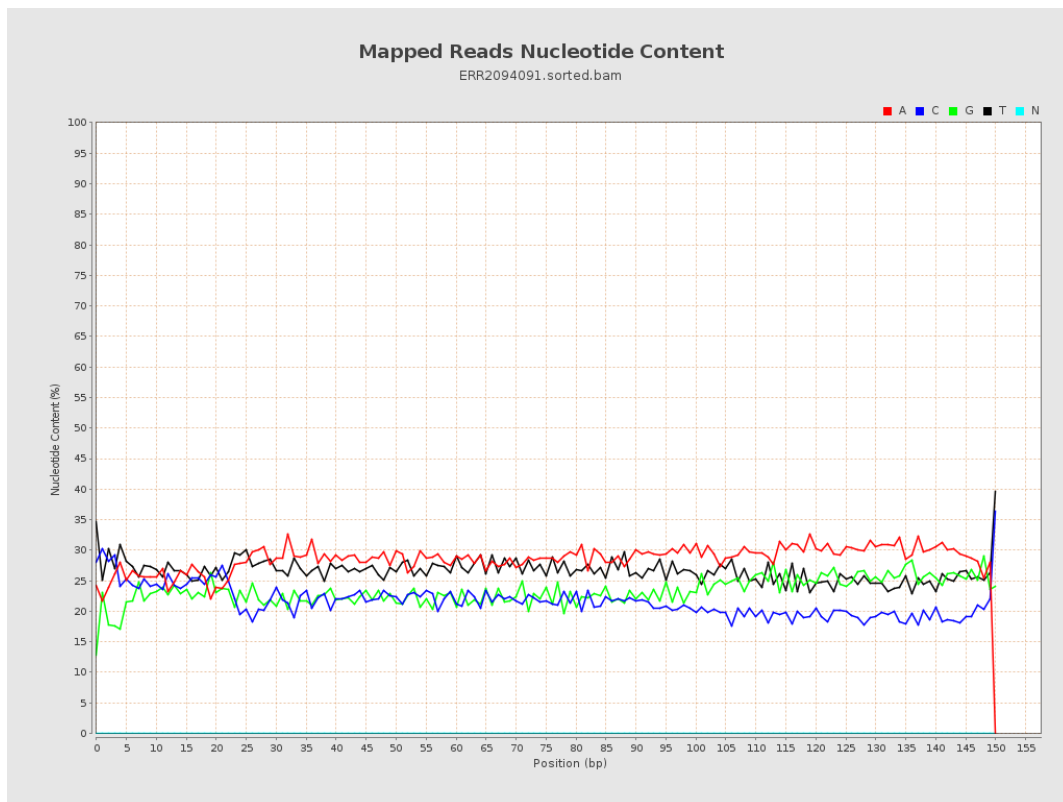
6. Results : Genome Fraction Coverage



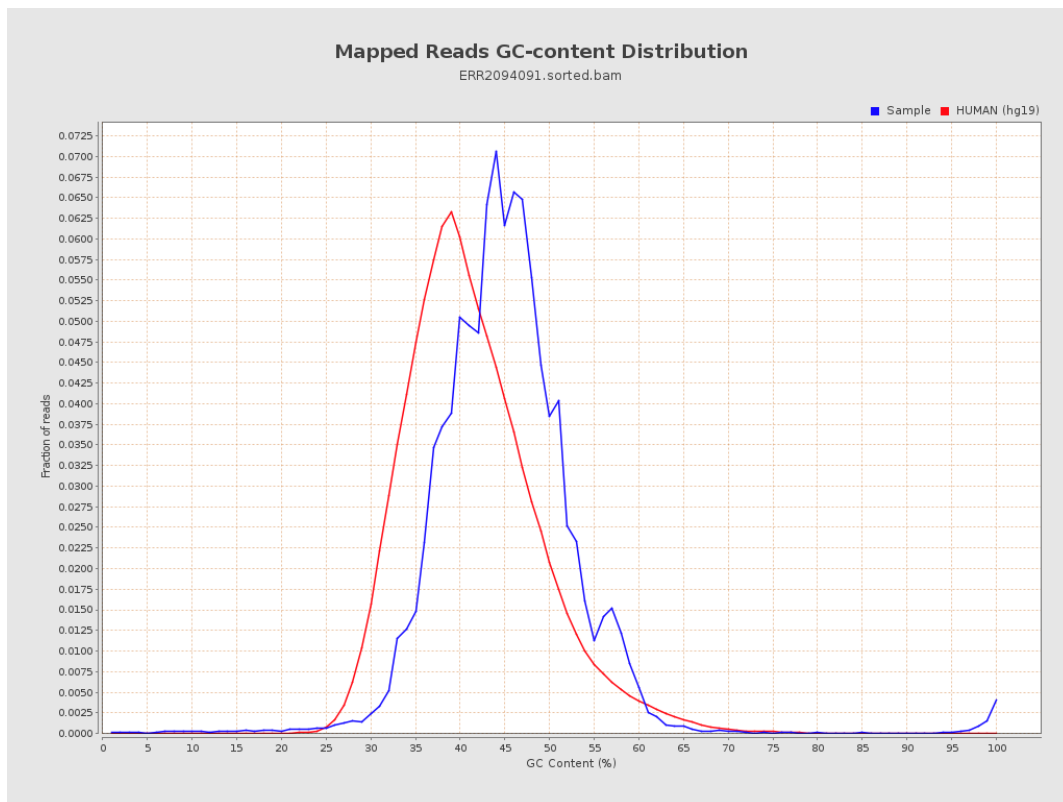
7. Results : Duplication Rate Histogram



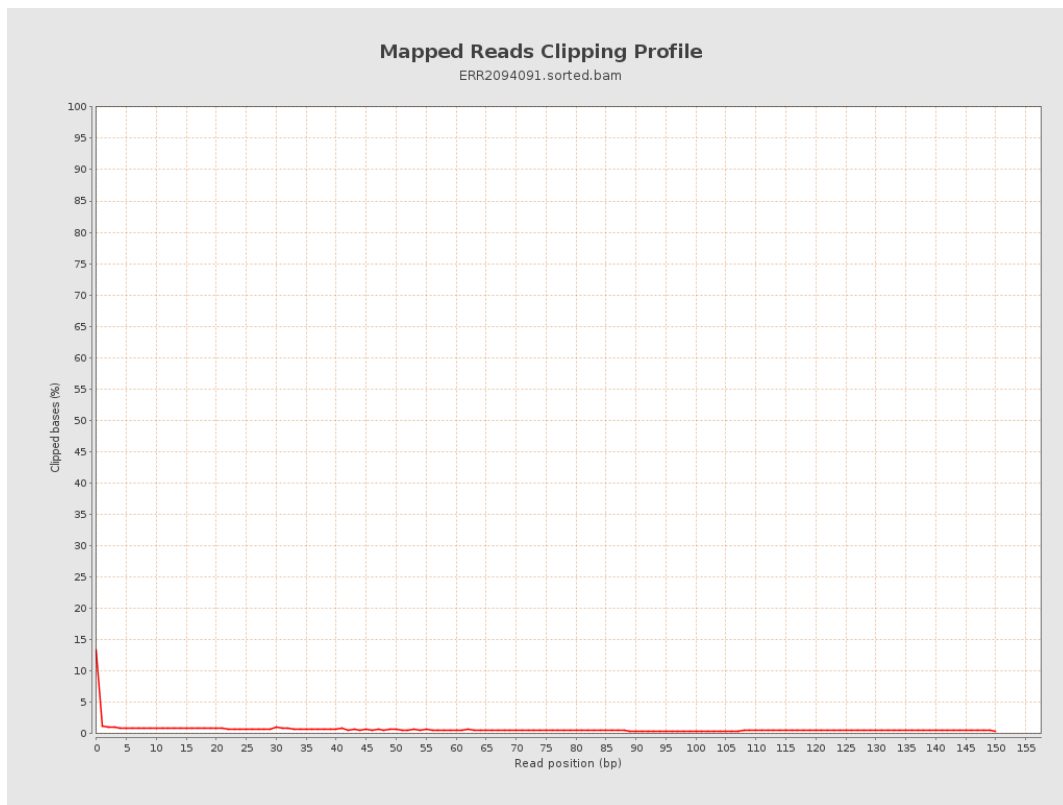
8. Results : Mapped Reads Nucleotide Content



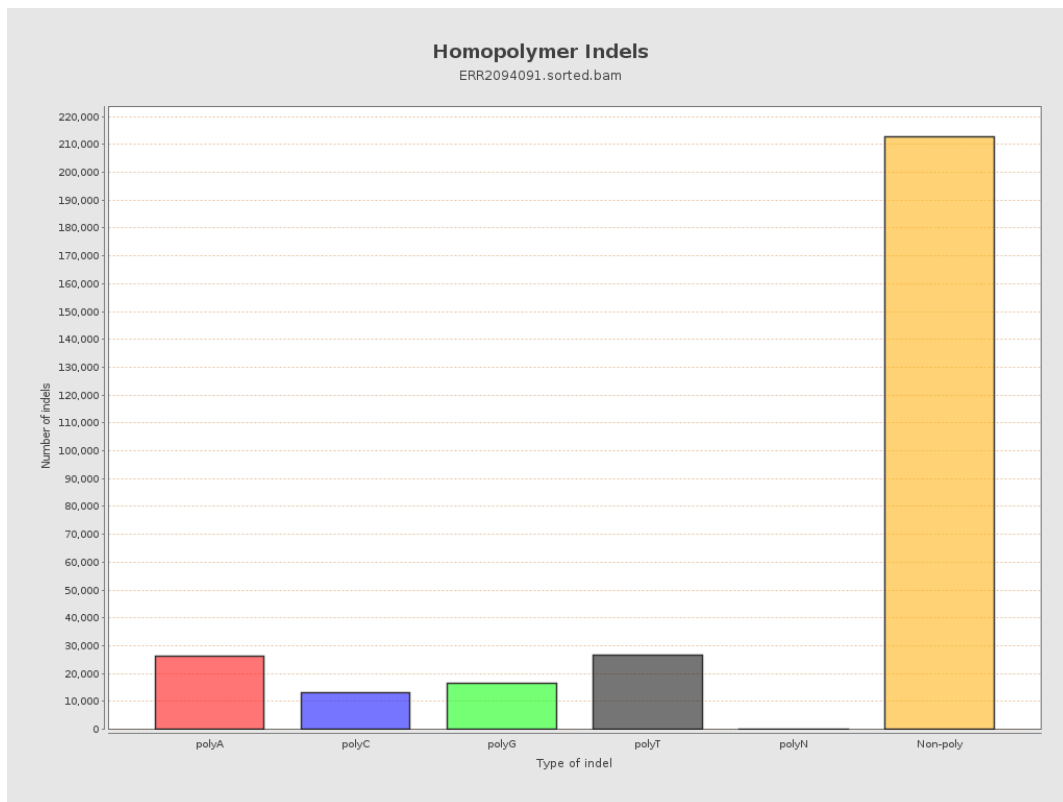
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



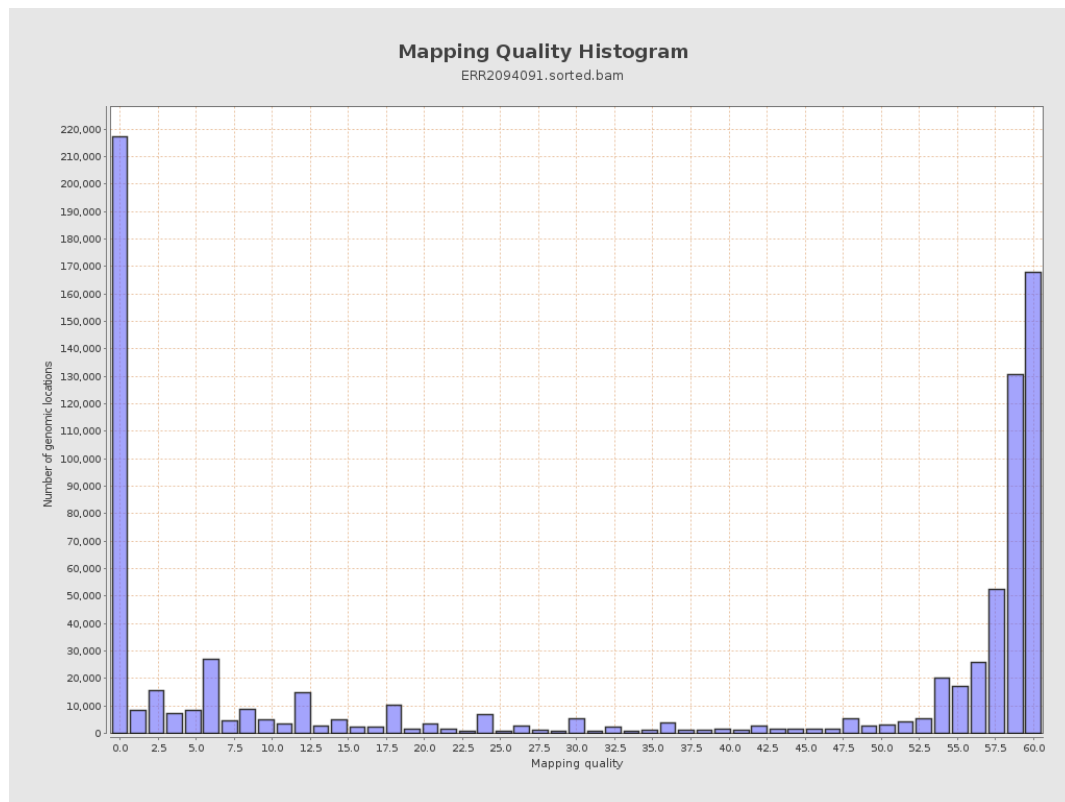
11. Results : Homopolymer Indels



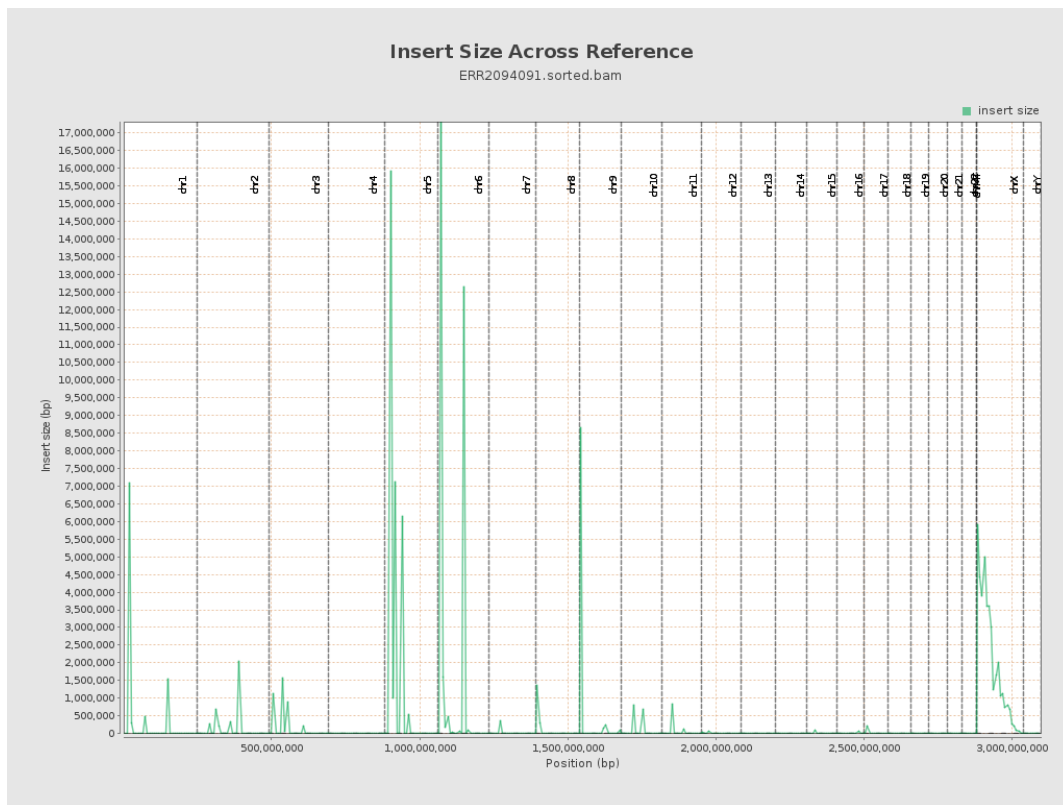
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

