

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:10:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093994.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_ERR2093994 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093994_1.fastq.gz ERR2093994_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:10:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	349,426
Mapped reads	329,386 / 94.26%
Unmapped reads	20,040 / 5.74%
Mapped paired reads	329,386 / 94.26%
Mapped reads, first in pair	165,582 / 47.39%
Mapped reads, second in pair	163,804 / 46.88%
Mapped reads, both in pair	326,412 / 93.41%
Mapped reads, singletons	2,974 / 0.85%
Secondary alignments	0
Supplementary alignments	20,336 / 5.82%
Read min/max/mean length	30 / 151 / 138.74
Duplicated reads (estimated)	309,016 / 88.44%
Duplication rate	50.17%
Clipped reads	167,801 / 48.02%

2.2. ACGT Content

Number/percentage of A's	10,664,706 / 26.22%
Number/percentage of C's	9,565,633 / 23.52%
Number/percentage of T's	10,074,851 / 24.77%
Number/percentage of G's	10,368,128 / 25.49%
Number/percentage of N's	555 / 0%

GC Percentage	49.01%
---------------	--------

2.3. Coverage

Mean	0.0134
Standard Deviation	2.5253

2.4. Mapping Quality

Mean Mapping Quality	40.58
----------------------	-------

2.5. Insert size

Mean	1,071,446.4
Standard Deviation	9,440,421.28
P25/Median/P75	121 / 161 / 197

2.6. Mismatches and indels

General error rate	3.6%
Mismatches	1,418,389
Insertions	22,934
Mapped reads with at least one insertion	6.83%
Deletions	112,460
Mapped reads with at least one deletion	32.79%
Homopolymer indels	29.69%

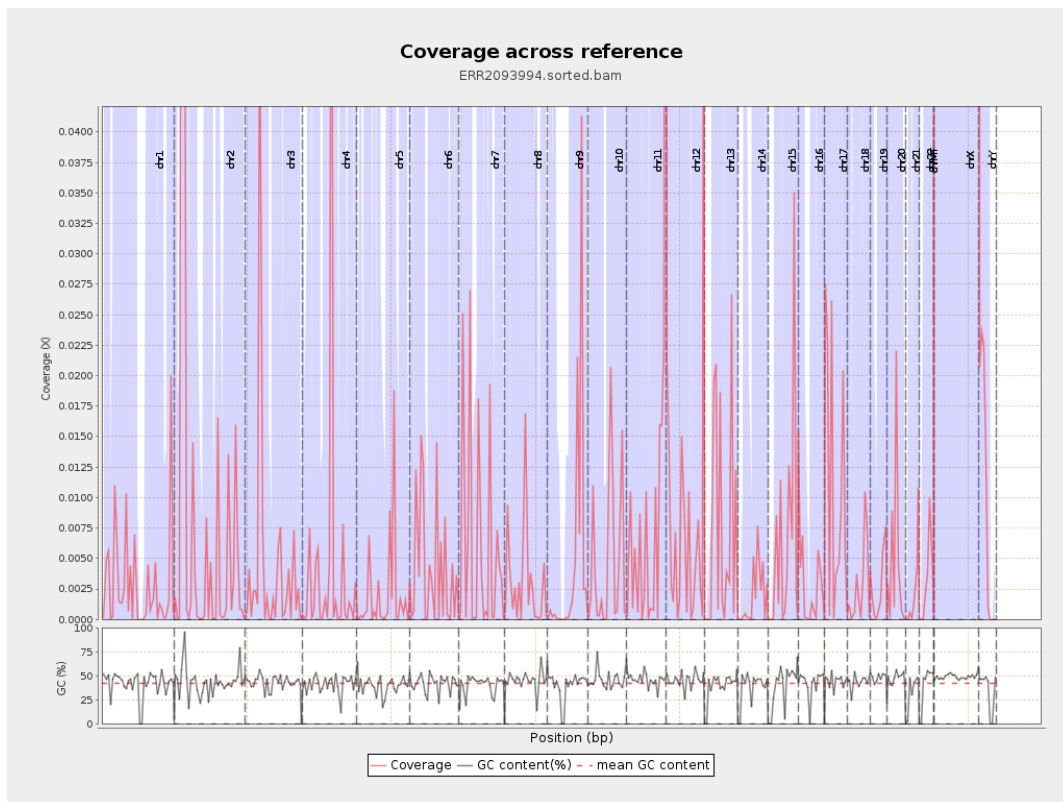
2.7. Chromosome stats

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

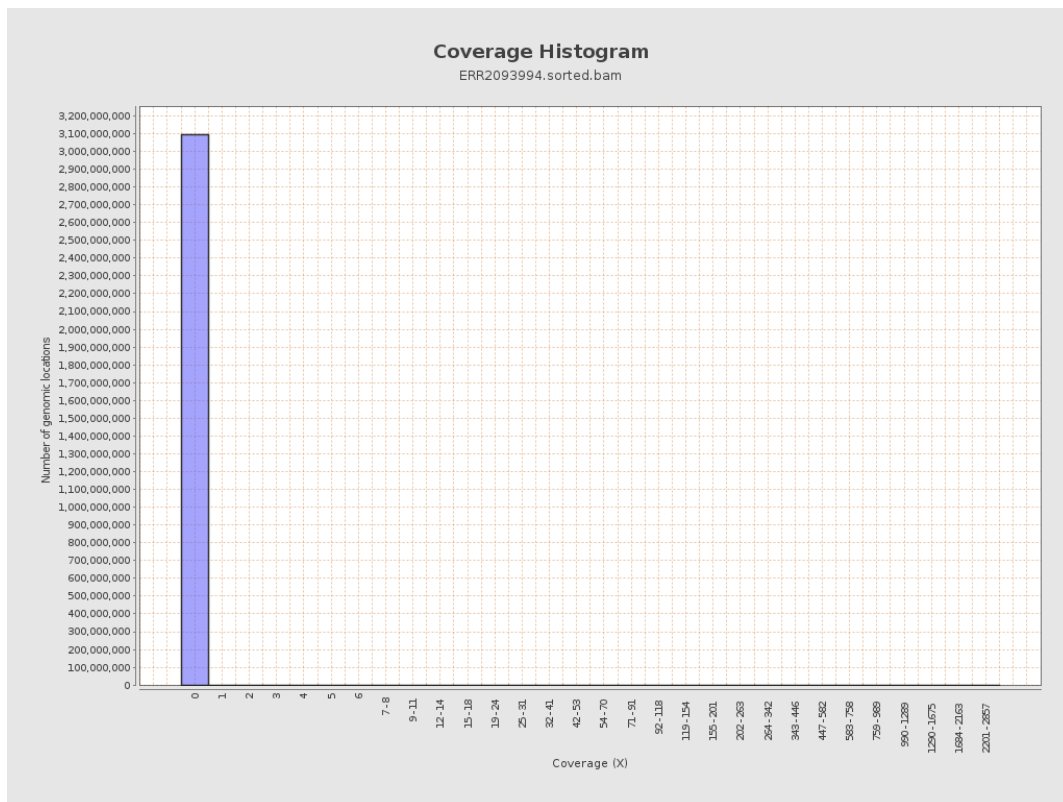
		bases	coverage	deviation
chr1	249250621	725368	0.0029	1.0284
chr2	243199373	1813197	0.0075	2.3912
chr3	198022430	815084	0.0041	1.3552
chr4	191154276	905233	0.0047	1.4582
chr5	180915260	368626	0.002	1.0657
chr6	171115067	722189	0.0042	1.1374
chr7	159138663	913952	0.0057	1.6942
chr8	146364022	453554	0.0031	0.9531
chr9	141213431	648819	0.0046	1.5124
chr10	135534747	653690	0.0048	1.333
chr11	135006516	962833	0.0071	1.6956
chr12	133851895	940980	0.007	1.7845
chr13	115169878	846345	0.0073	1.8791
chr14	107349540	198659	0.0019	0.6195
chr15	102531392	634982	0.0062	1.7241
chr16	90354753	268595	0.003	0.9092
chr17	81195210	917778	0.0113	2.7226
chr18	78077248	228430	0.0029	0.8406
chr19	59128983	147418	0.0025	0.7451
chr20	63025520	309090	0.0049	1.5646
chr21	48129895	102571	0.0021	0.4088
chr22	51304566	153994	0.003	0.7353
chrMT	16571	737611	44.5122	189.4222
chrX	155270560	26397660	0.17	8.9558

chrY	59373566	576668	0.0097	1.4839
------	----------	--------	--------	--------

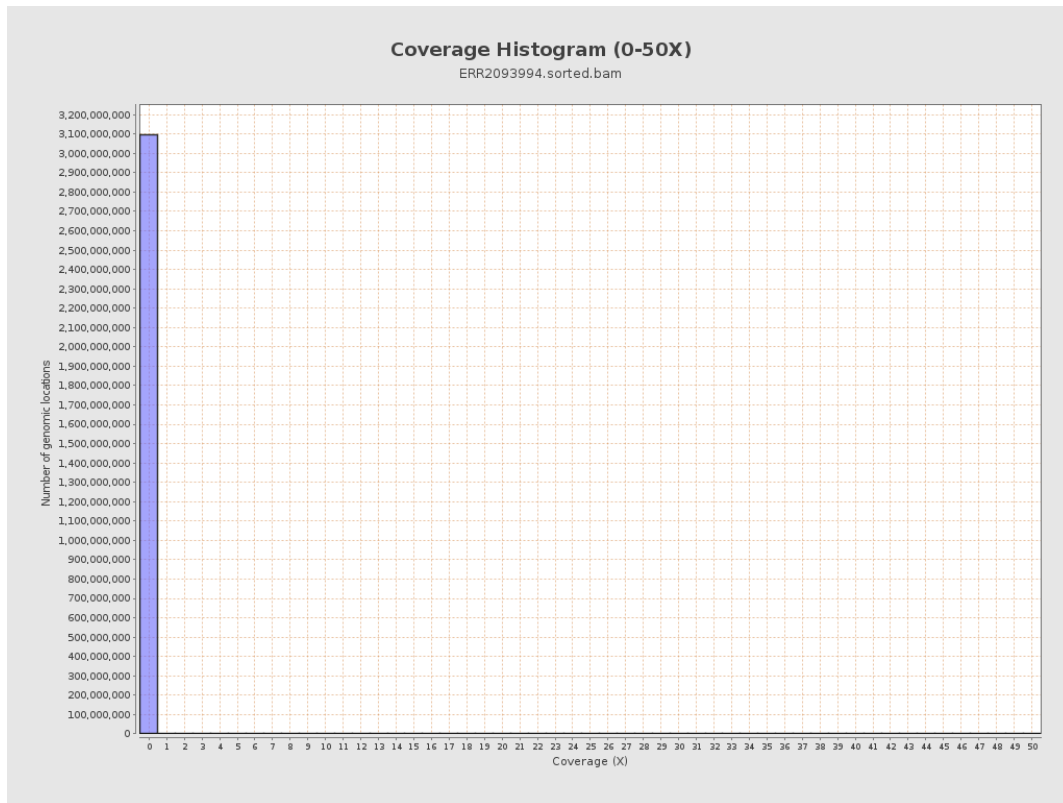
3. Results : Coverage across reference



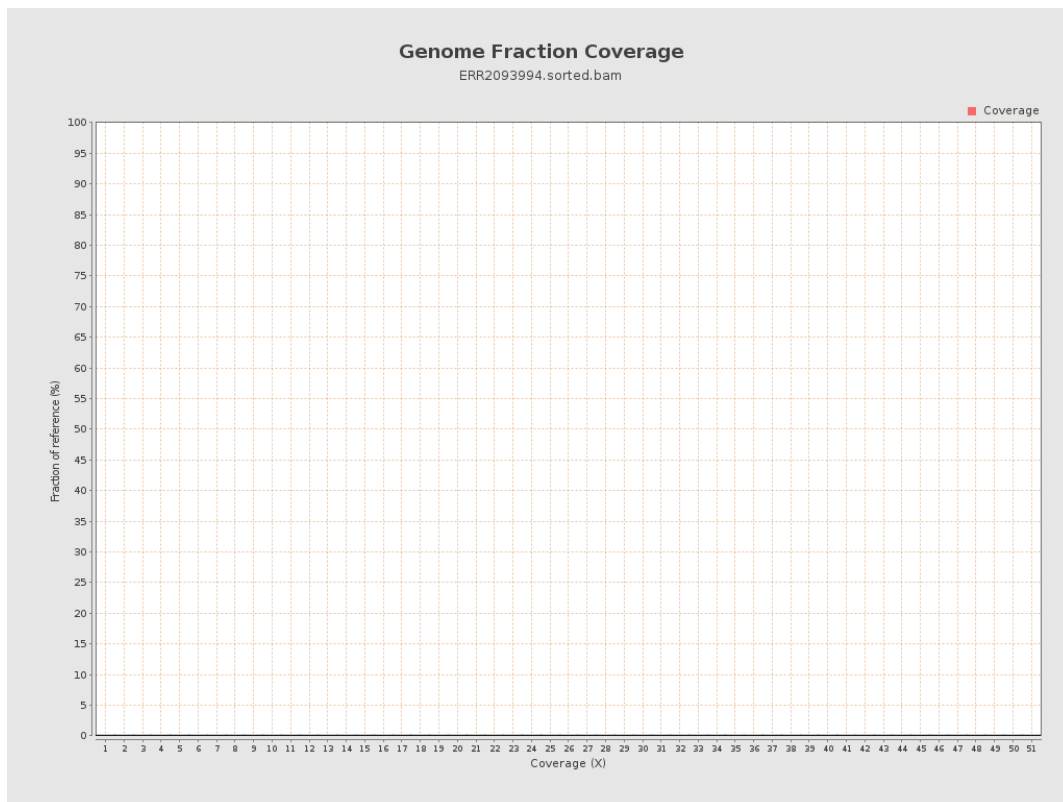
4. Results : Coverage Histogram



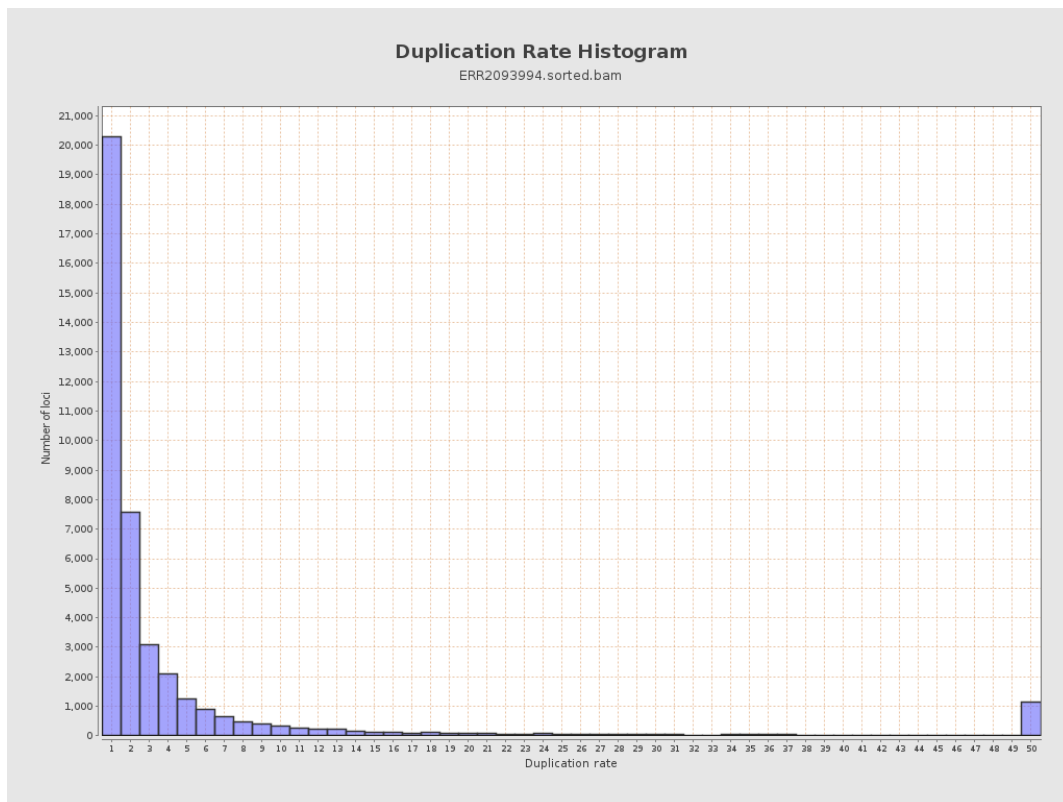
5. Results : Coverage Histogram (0-50X)



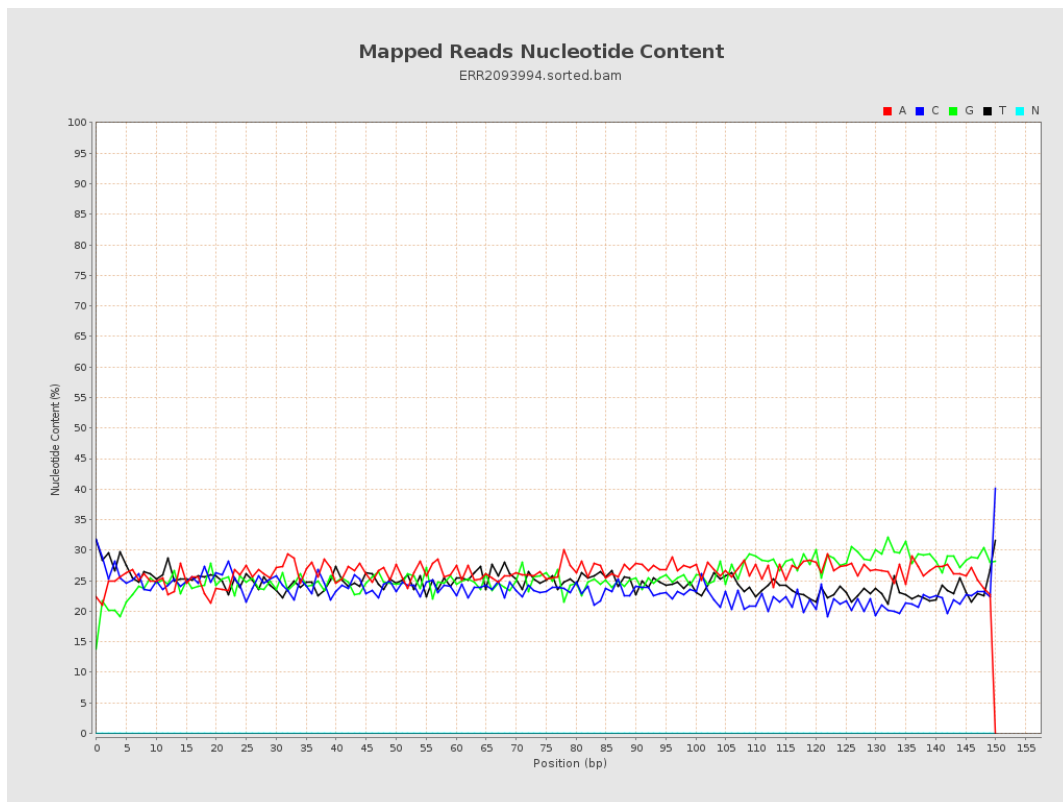
6. Results : Genome Fraction Coverage



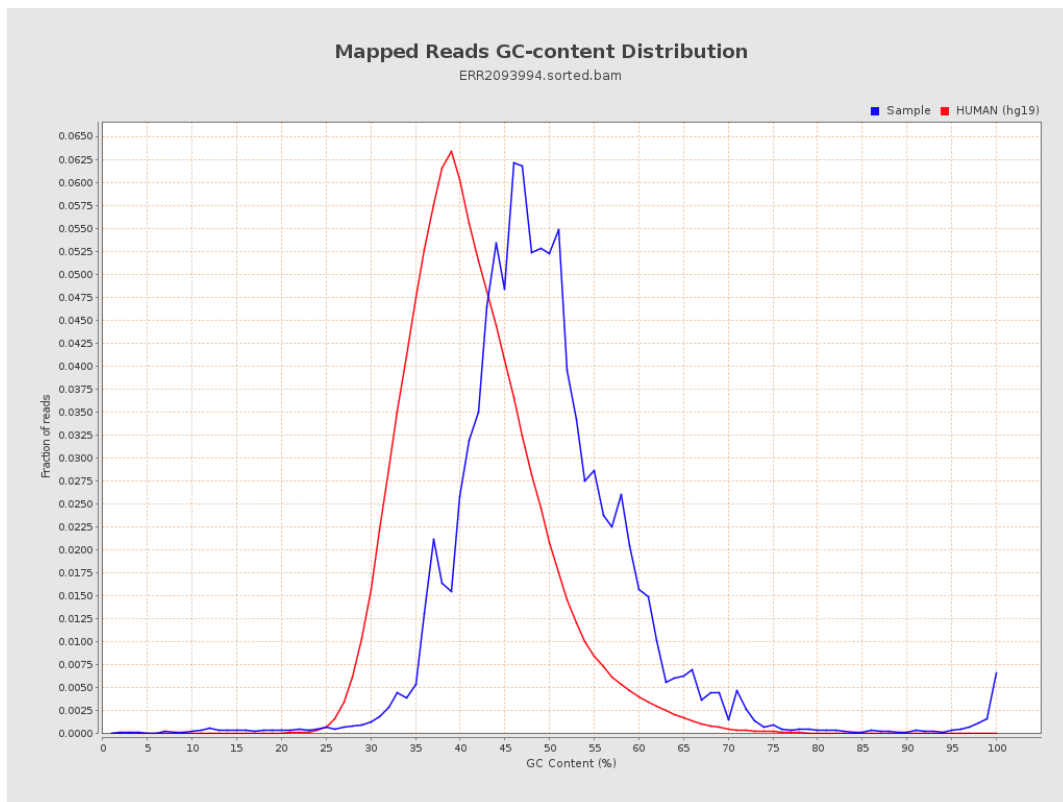
7. Results : Duplication Rate Histogram



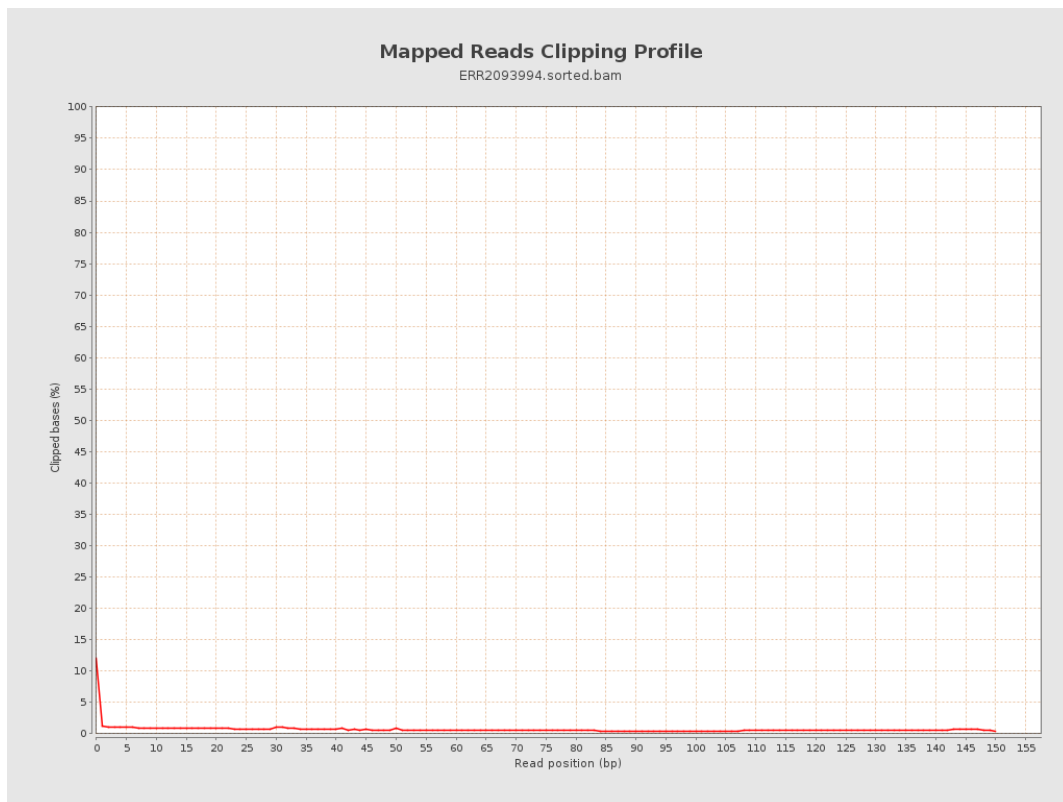
8. Results : Mapped Reads Nucleotide Content



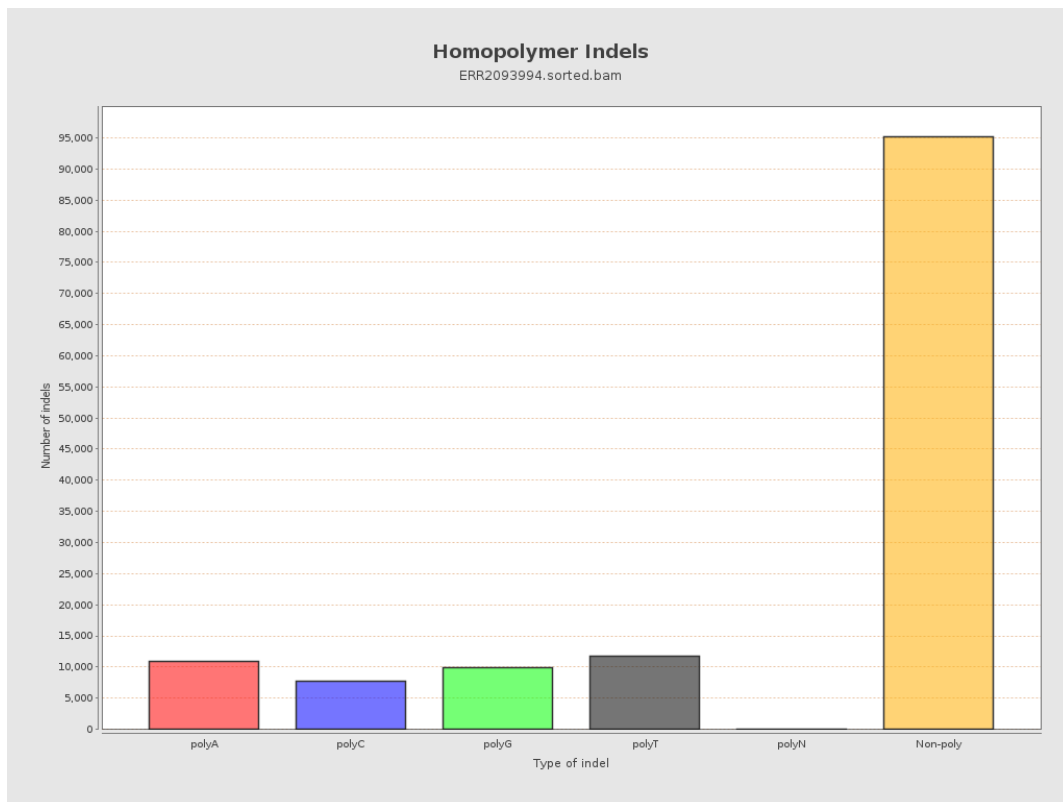
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



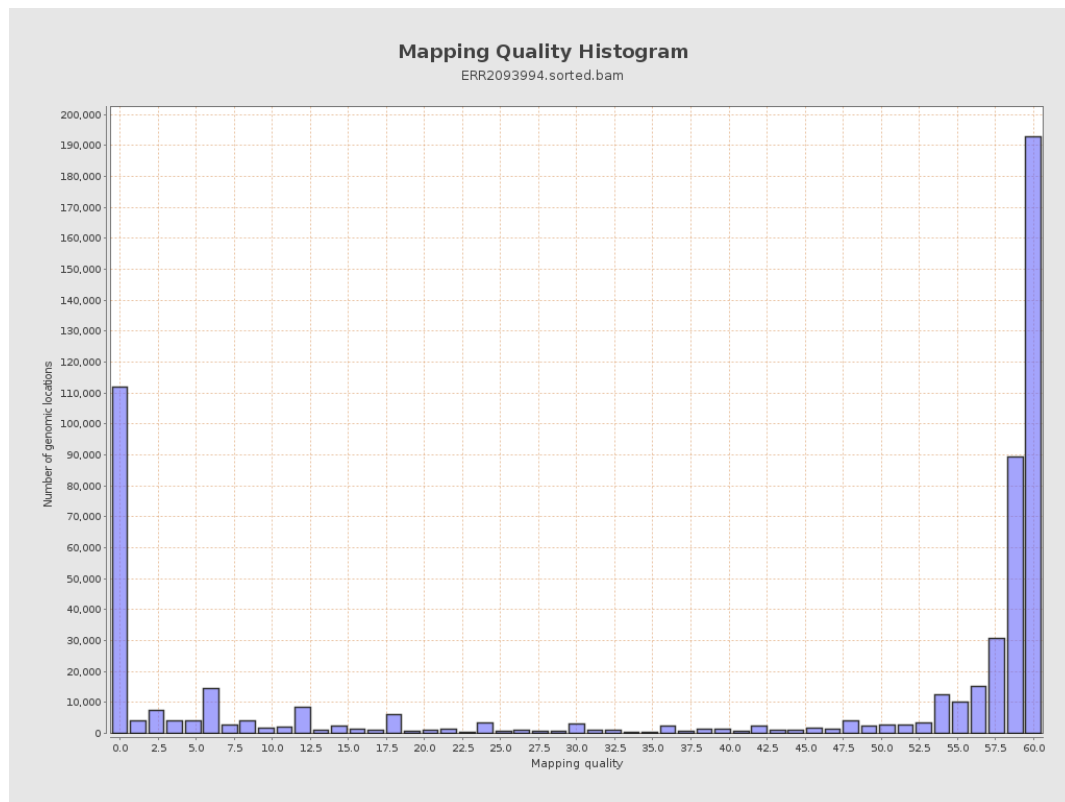
11. Results : Homopolymer Indels



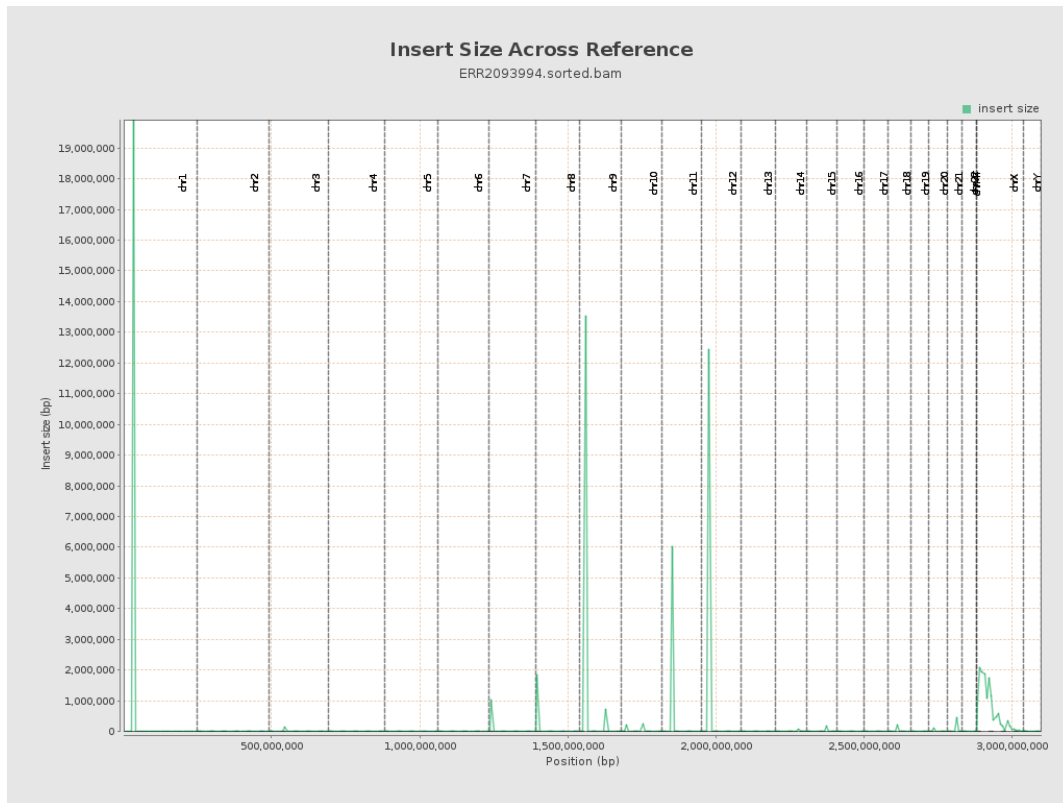
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

