Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:53:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094145.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_ERR2094145 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094145_1.fastq.gz ERR2094145_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:53:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	590,468
Mapped reads	552,487 / 93.57%
Unmapped reads	37,981 / 6.43%
Mapped paired reads	552,487 / 93.57%
Mapped reads, first in pair	277,679 / 47.03%
Mapped reads, second in pair	274,808 / 46.54%
Mapped reads, both in pair	547,358 / 92.7%
Mapped reads, singletons	5,129 / 0.87%
Secondary alignments	0
Supplementary alignments	38,089 / 6.45%
Read min/max/mean length	30 / 151 / 138.02
Duplicated reads (estimated)	522,875 / 88.55%
Duplication rate	50.55%
Clipped reads	277,659 / 47.02%

2.2. ACGT Content

Number/percentage of A's	19,042,940 / 27.65%
Number/percentage of C's	15,435,239 / 22.41%
Number/percentage of T's	18,038,845 / 26.2%
Number/percentage of G's	16,345,378 / 23.74%
Number/percentage of N's	898 / 0%

GC Percentage	46.15%

2.3. Coverage

Mean	0.0228
Standard Deviation	4.0548

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Insert size

Mean	1,546,765.16
Standard Deviation	11,133,359.82
P25/Median/P75	121 / 156 / 191

2.6. Mismatches and indels

General error rate	3.94%
Mismatches	2,623,860
Insertions	43,738
Mapped reads with at least one insertion	7.77%
Deletions	206,782
Mapped reads with at least one deletion	36.24%
Homopolymer indels	29.22%

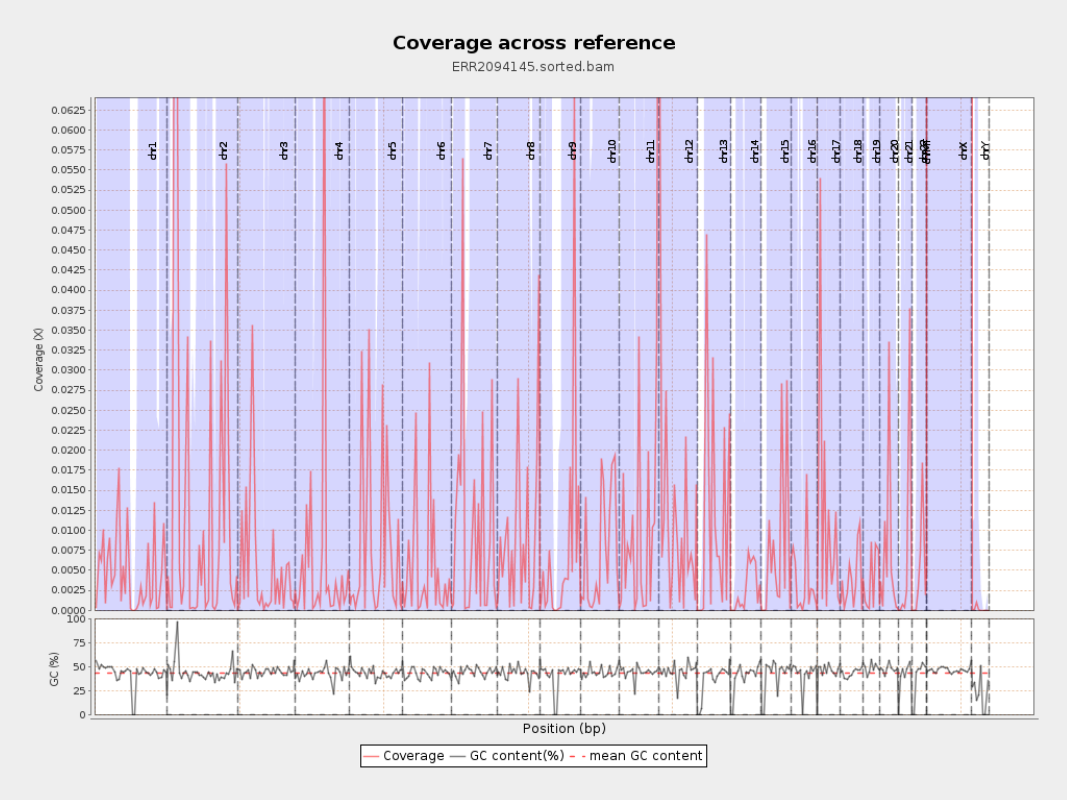
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

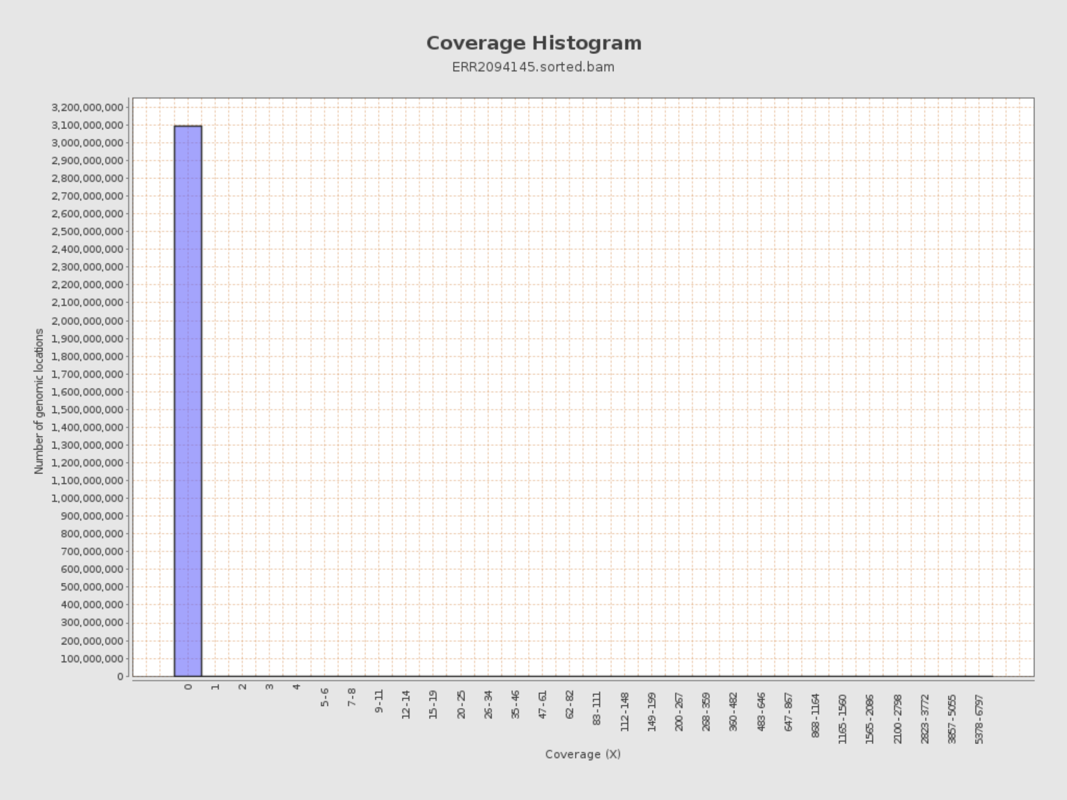
		bases	coverage	deviation
chr1	249250621	1161023	0.0047	1.3286
chr2	243199373	3169854	0.013	3.5531
chr3	198022430	1059295	0.0053	1.367
chr4	191154276	1271739	0.0067	1.585
chr5	180915260	1515703	0.0084	2.5614
chr6	171115067	936128	0.0055	1.6617
chr7	159138663	1626267	0.0102	2.5306
chr8	146364022	1361720	0.0093	2.5304
chr9	141213431	1054261	0.0075	2.4775
chr10	135534747	978981	0.0072	1.5734
chr11	135006516	1340682	0.0099	2.3346
chr12	133851895	1570873	0.0117	2.5818
chr13	115169878	1325626	0.0115	2.329
chr14	107349540	282951	0.0026	0.7688
chr15	102531392	772781	0.0075	1.6745
chr16	90354753	347690	0.0038	1.0831
chr17	81195210	953219	0.0117	2.2768
chr18	78077248	312093	0.004	0.8845
chr19	59128983	218829	0.0037	0.8591
chr20	63025520	456462	0.0072	2.3443
chr21	48129895	396407	0.0082	2.543
chr22	51304566	244094	0.0048	1.128
chrMT	16571	4071264	245.6861	973.0333
chrX	155270560	44008487	0.2834	11.6472

chrY	59373566	10041	0.0002	0.0677

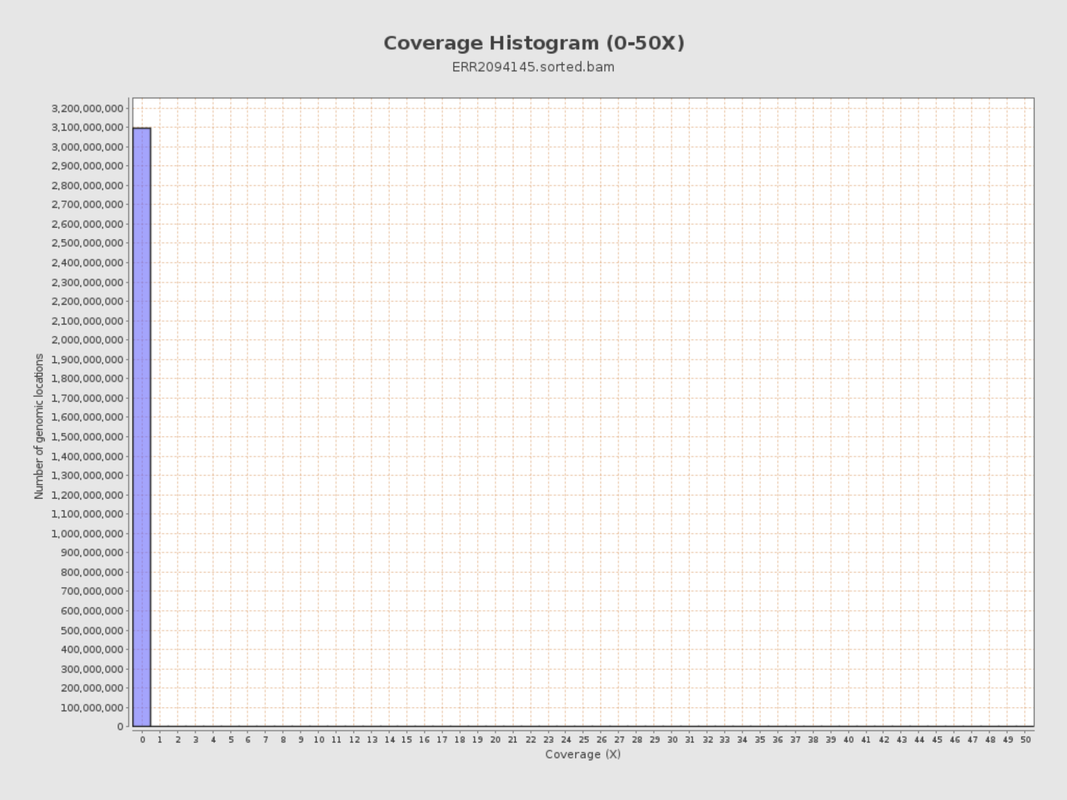
3. Results : Coverage across reference



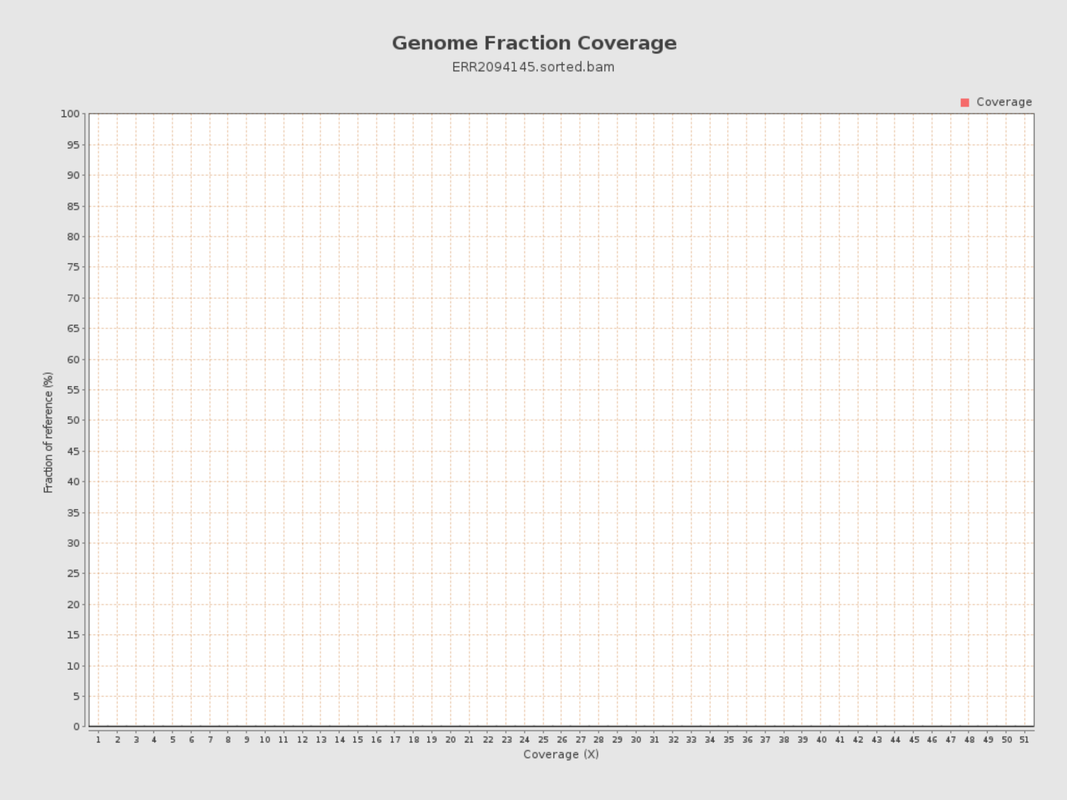
4. Results : Coverage Histogram



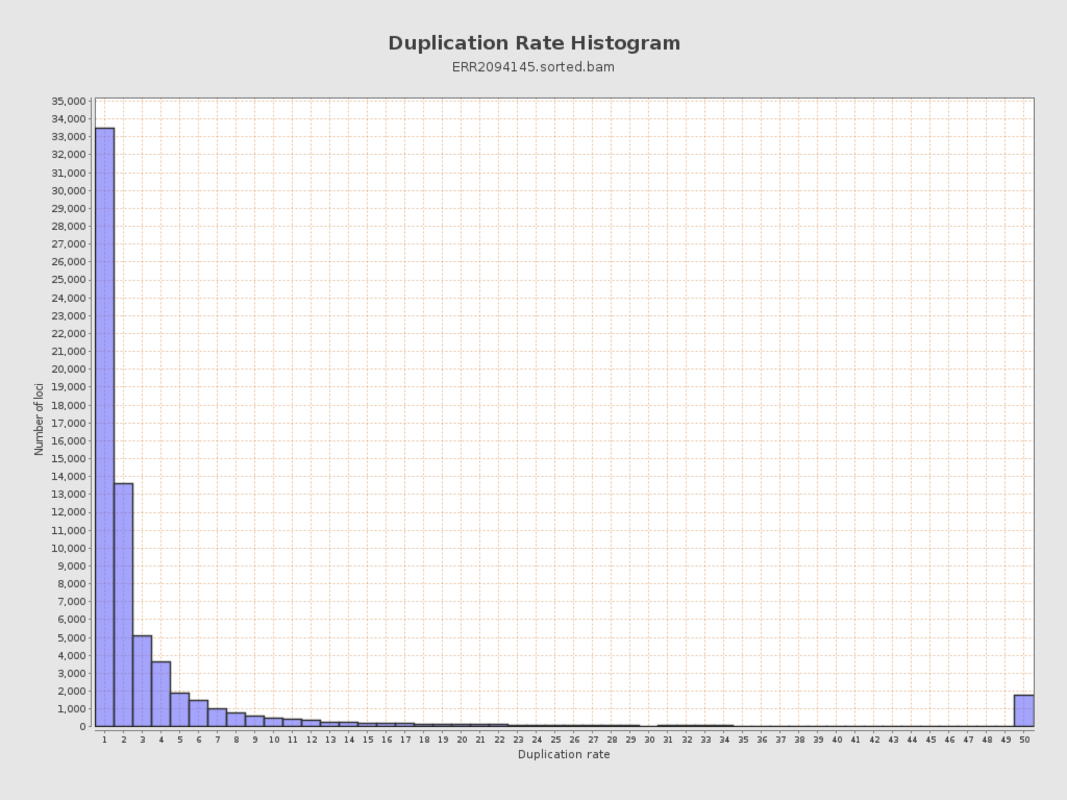
5. Results : Coverage Histogram (0-50X)



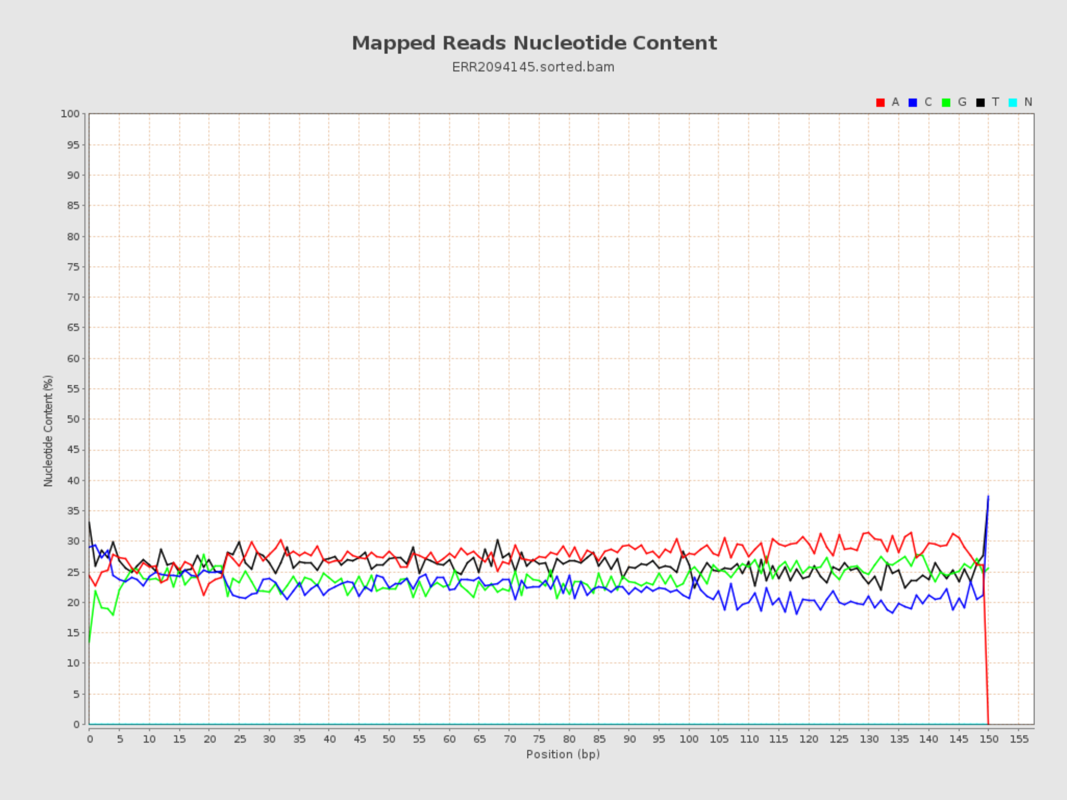
6. Results : Genome Fraction Coverage



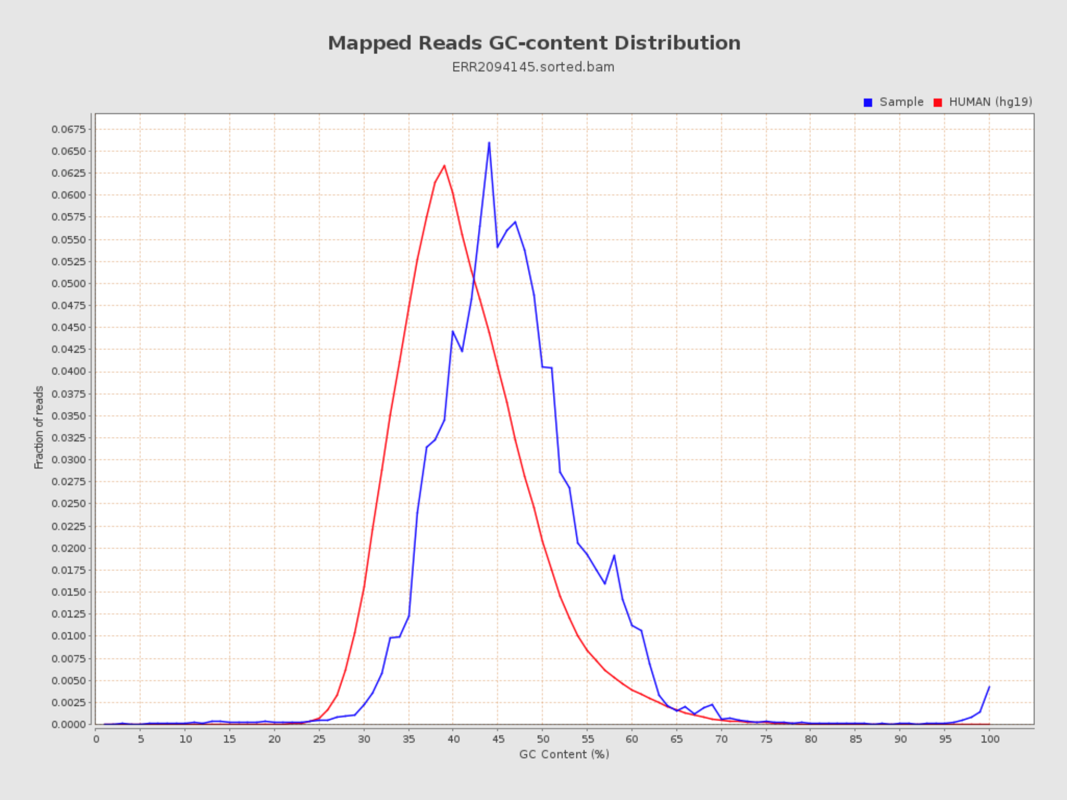
7. Results : Duplication Rate Histogram



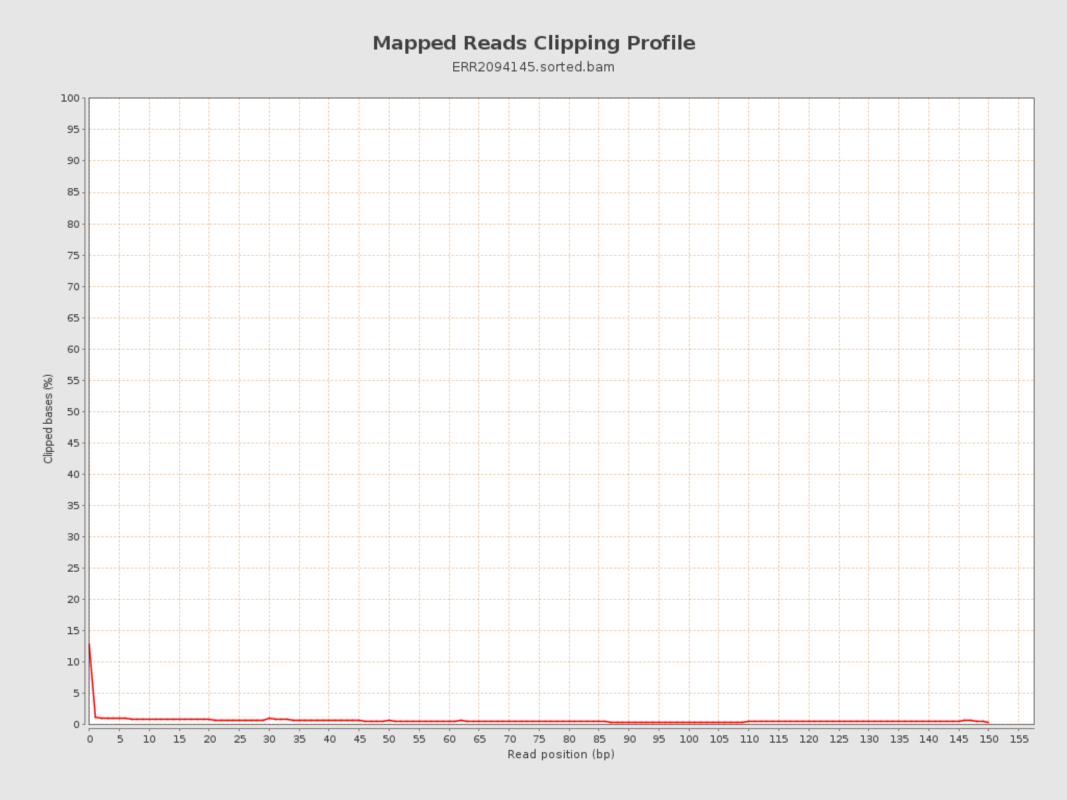
8. Results : Mapped Reads Nucleotide Content



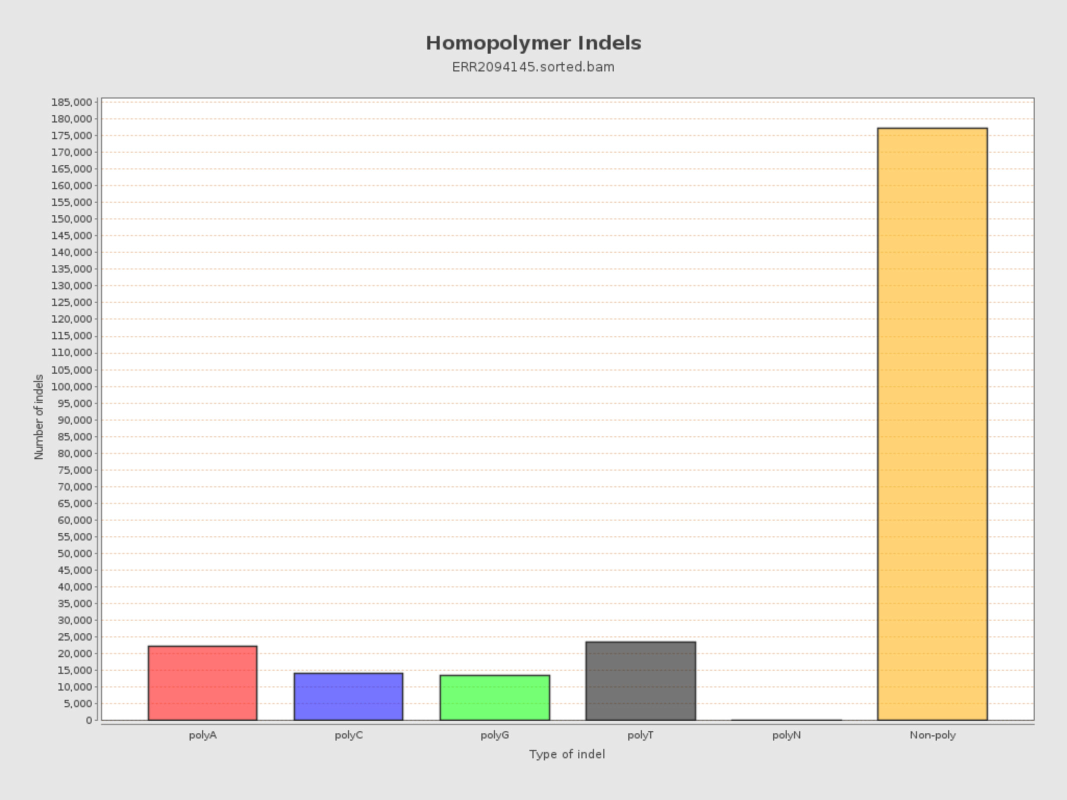
9. Results : Mapped Reads GC-content Distribution



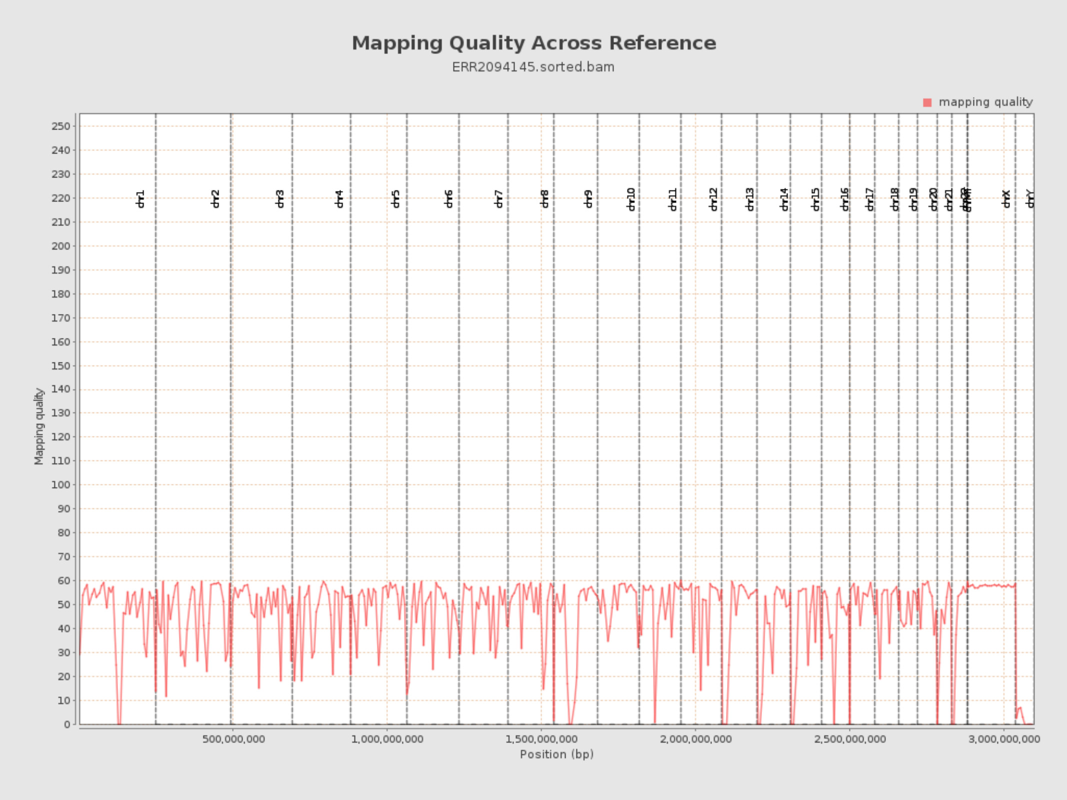
10. Results : Mapped Reads Clipping Profile



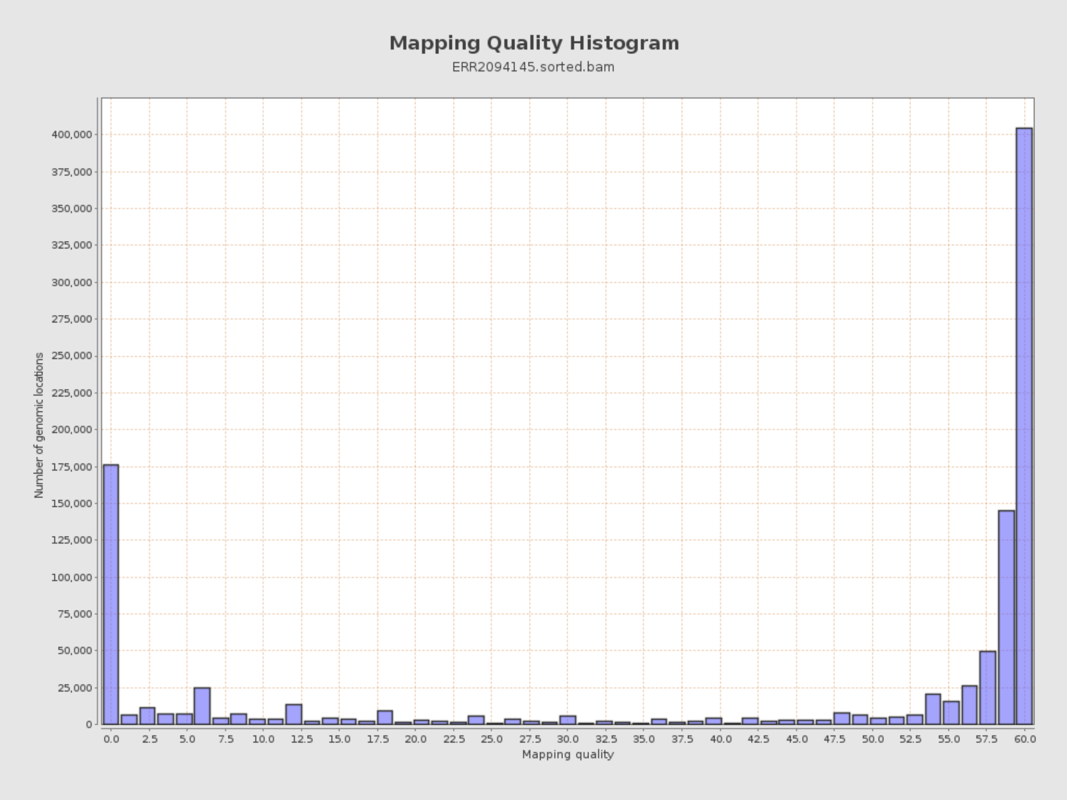
11. Results : Homopolymer Indels



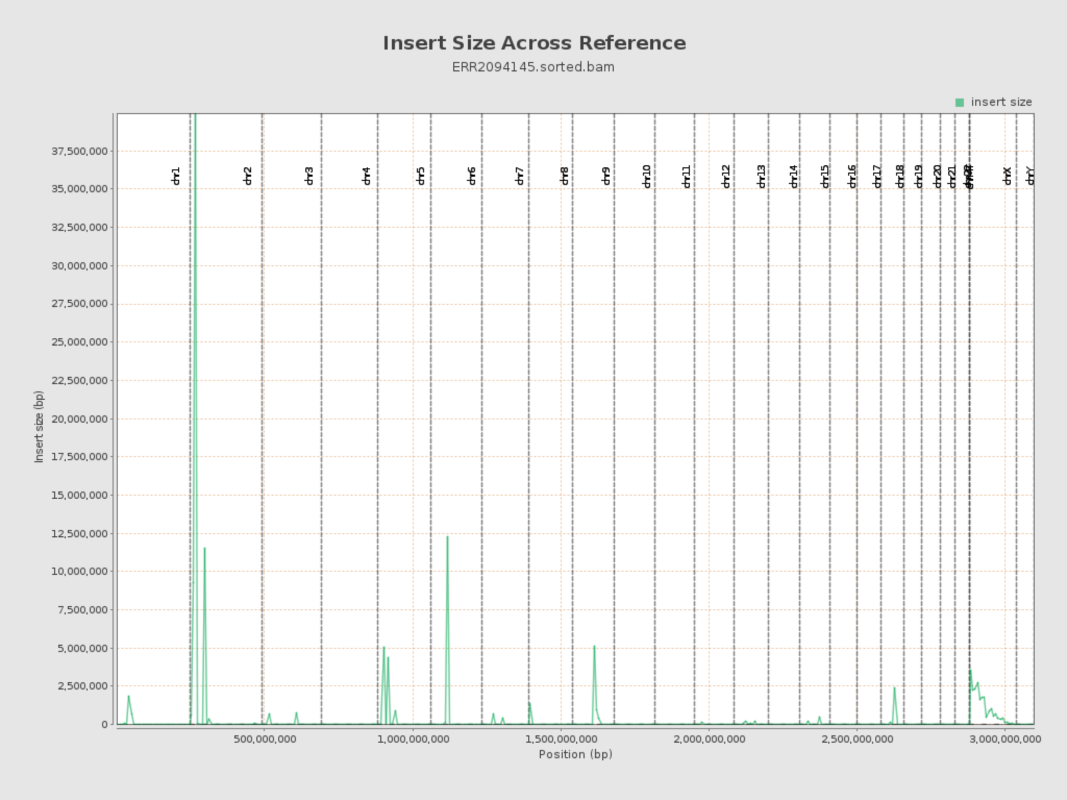
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram