Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:49:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094144.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_ERR2094144 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094144_1.fastq.gz ERR2094144_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:49:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	429,402
Mapped reads	393,441 / 91.63%
Unmapped reads	35,961 / 8.37%
Mapped paired reads	393,441 / 91.63%
Mapped reads, first in pair	197,616 / 46.02%
Mapped reads, second in pair	195,825 / 45.6%
Mapped reads, both in pair	390,006 / 90.83%
Mapped reads, singletons	3,435 / 0.8%
Secondary alignments	0
Supplementary alignments	22,415 / 5.22%
Read min/max/mean length	30 / 151 / 135.02
Duplicated reads (estimated)	364,525 / 84.89%
Duplication rate	47.89%
Clipped reads	191,129 / 44.51%

2.2. ACGT Content

Number/percentage of A's	13,381,312 / 27.48%
Number/percentage of C's	10,860,469 / 22.31%
Number/percentage of T's	12,763,515 / 26.21%
Number/percentage of G's	11,684,590 / 24%
Number/percentage of N's	576 / 0%

GC Percentage	46.3%

2.3. Coverage

Mean	0.0161
Standard Deviation	2.853

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Insert size

Mean	1,078,563.51
Standard Deviation	9,408,547.24
P25/Median/P75	122 / 157 / 191

2.6. Mismatches and indels

General error rate	3.99%
Mismatches	1,872,197
Insertions	32,112
Mapped reads with at least one insertion	8.01%
Deletions	148,708
Mapped reads with at least one deletion	36.58%
Homopolymer indels	28.98%

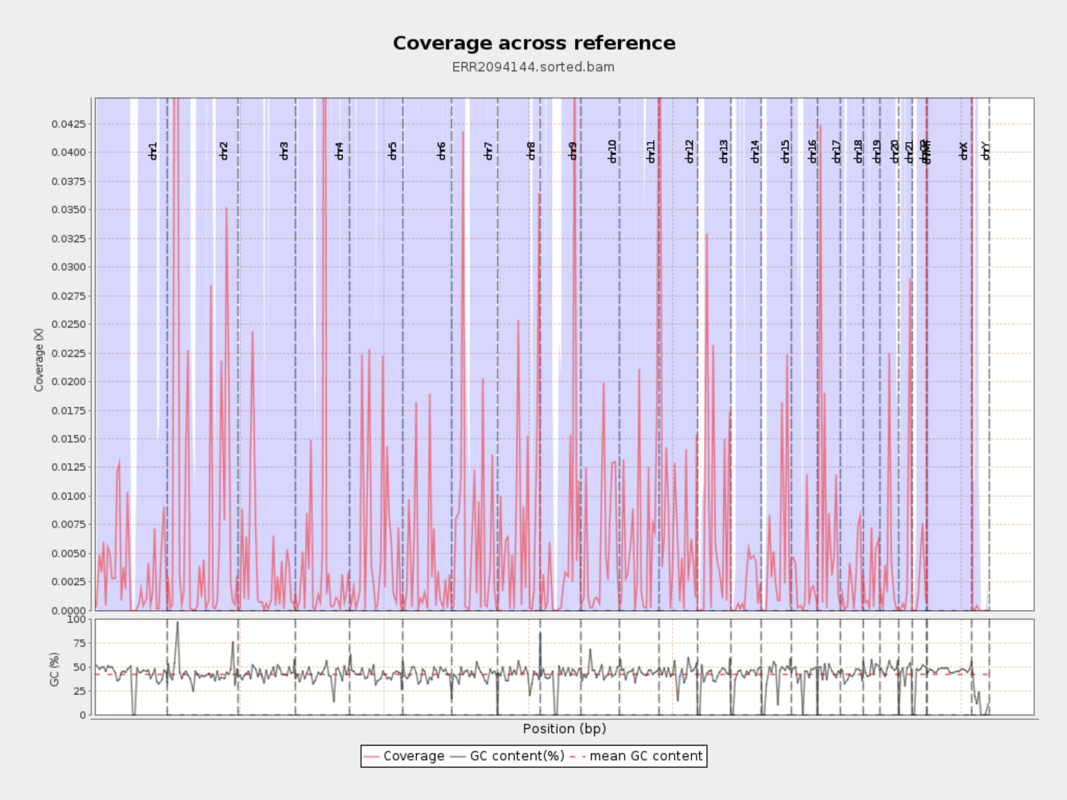
2.7. Chromosome stats

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

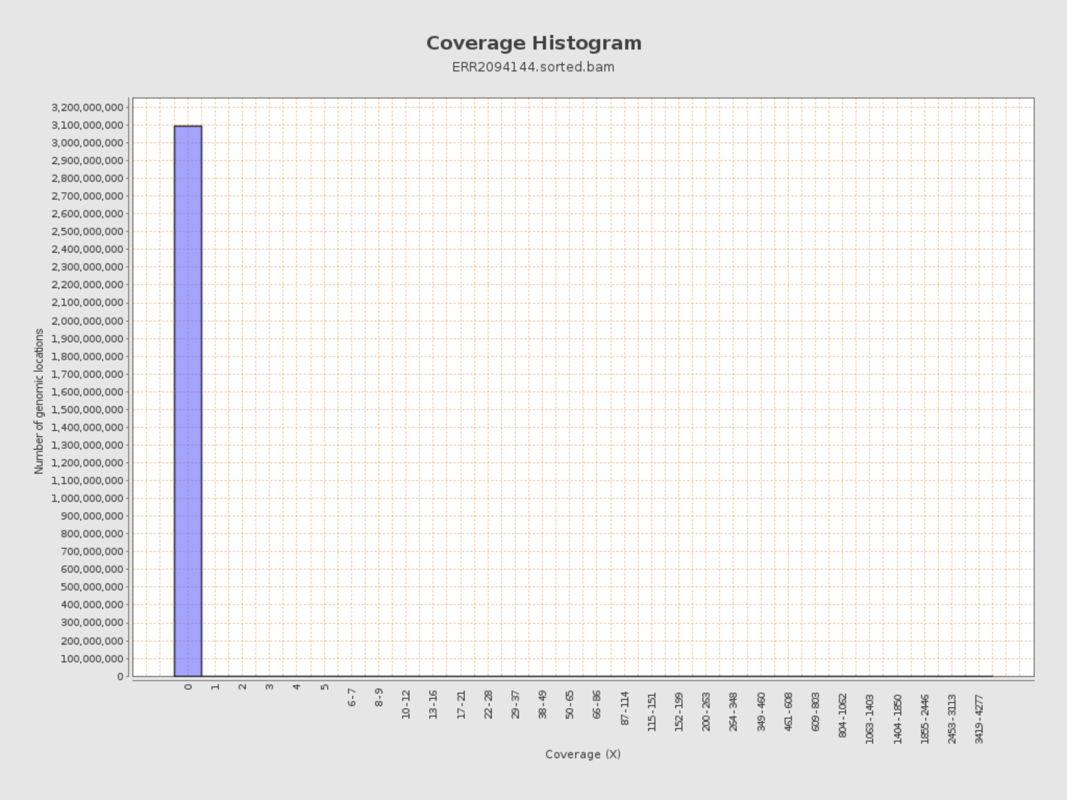
		bases	coverage	deviation
chr1	249250621	838850	0.0034	1.0451
chr2	243199373	2228062	0.0092	2.5901
chr3	198022430	725839	0.0037	0.9915
chr4	191154276	1129914	0.0059	1.5607
chr5	180915260	1052537	0.0058	1.8258
chr6	171115067	629746	0.0037	1.1278
chr7	159138663	1086626	0.0068	1.7375
chr8	146364022	1096783	0.0075	2.2351
chr9	141213431	818391	0.0058	2.133
chr10	135534747	736001	0.0054	1.2084
chr11	135006516	852694	0.0063	1.4257
chr12	133851895	1140246	0.0085	2.0146
chr13	115169878	889030	0.0077	1.5587
chr14	107349540	205822	0.0019	0.5771
chr15	102531392	520317	0.0051	1.228
chr16	90354753	235074	0.0026	0.7529
chr17	81195210	762662	0.0094	1.8297
chr18	78077248	213444	0.0027	0.695
chr19	59128983	171463	0.0029	0.7339
chr20	63025520	270518	0.0043	1.4676
chr21	48129895	294631	0.0061	1.7542
chr22	51304566	117699	0.0023	0.4531
chrMT	16571	2550057	153.8867	612.8668
chrX	155270560	31239706	0.2012	8.4797

chrY	59373566	5291	0.0001	0.032

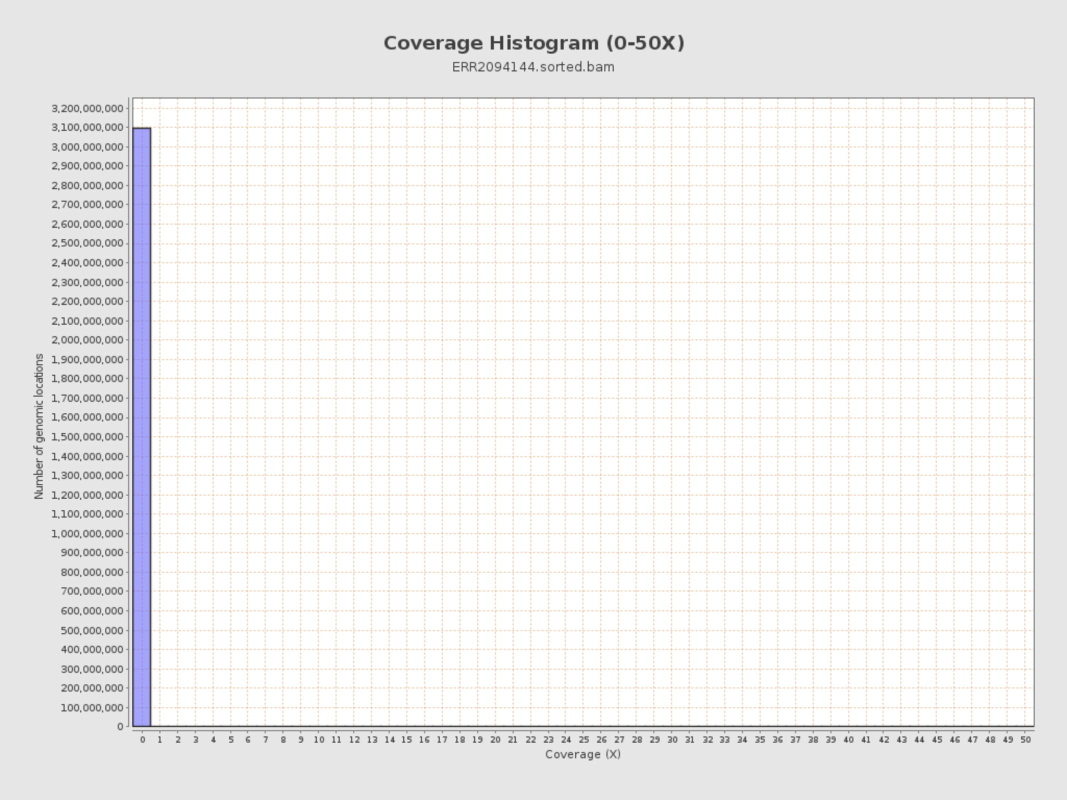
3. Results : Coverage across reference



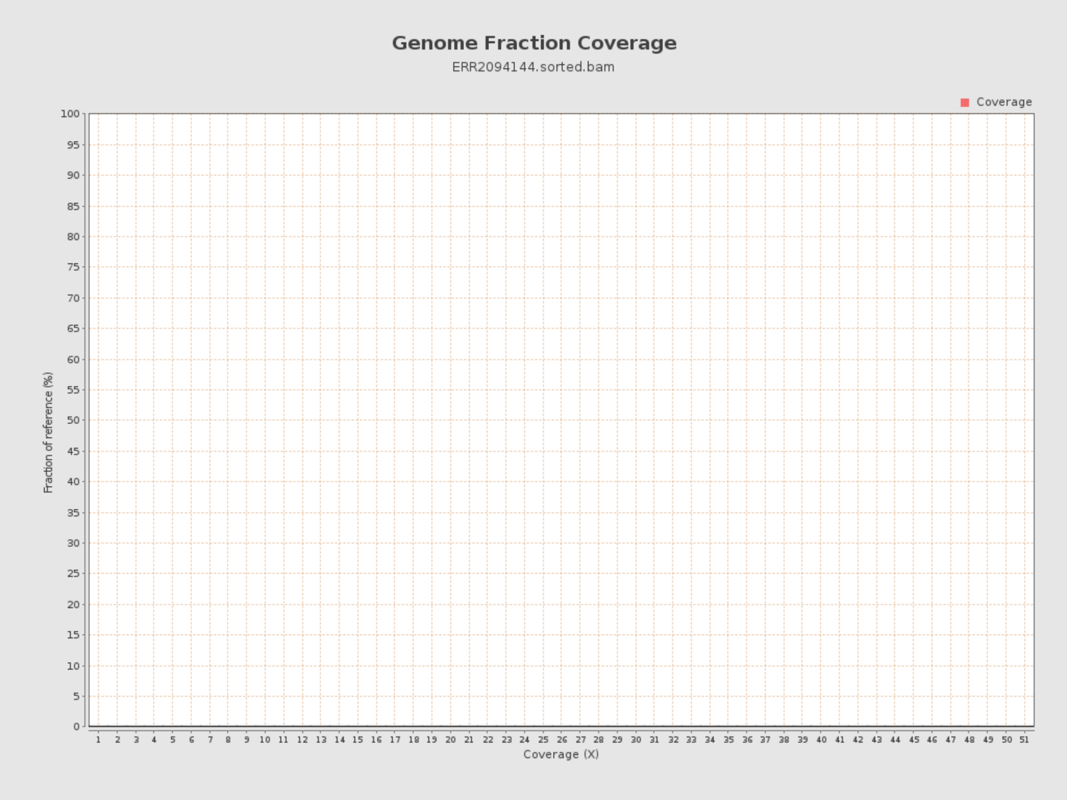
4. Results : Coverage Histogram



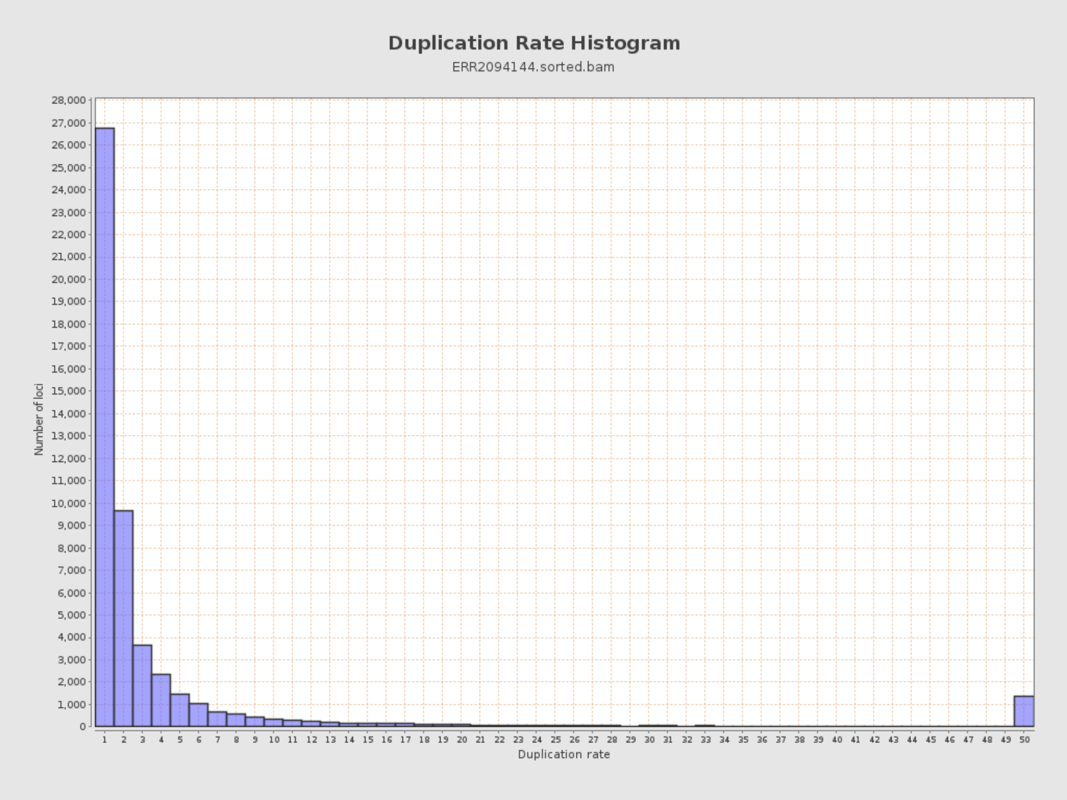
5. Results : Coverage Histogram (0-50X)



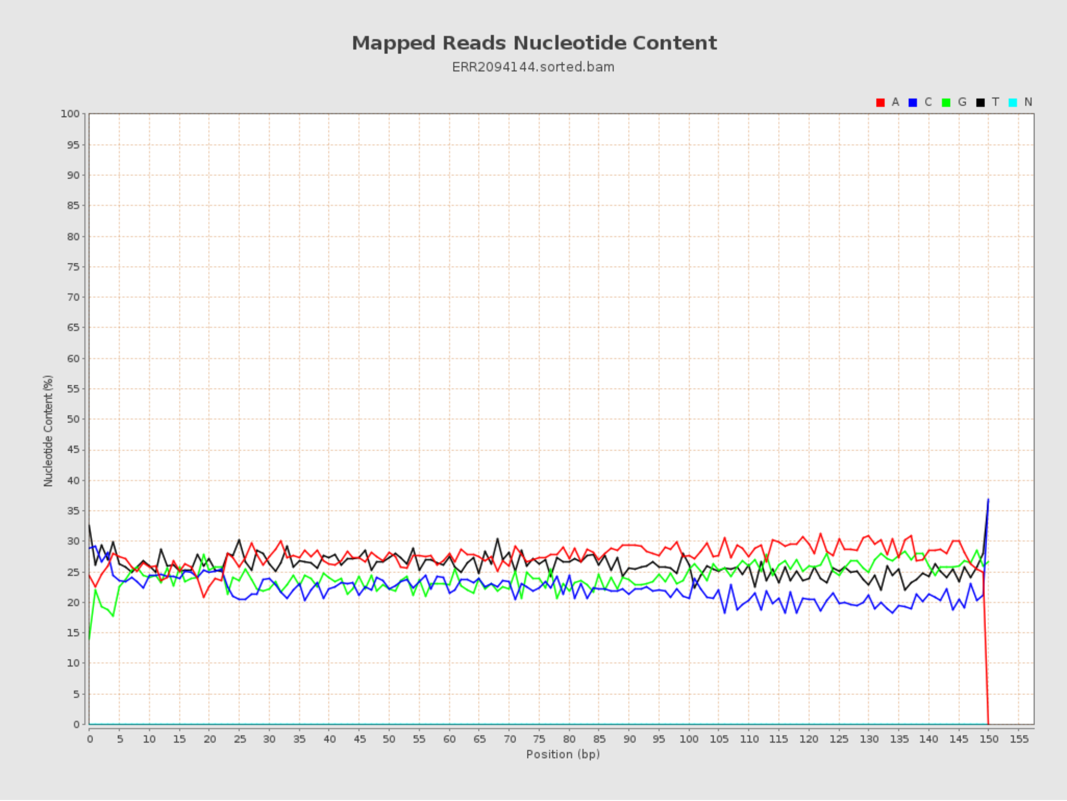
6. Results : Genome Fraction Coverage



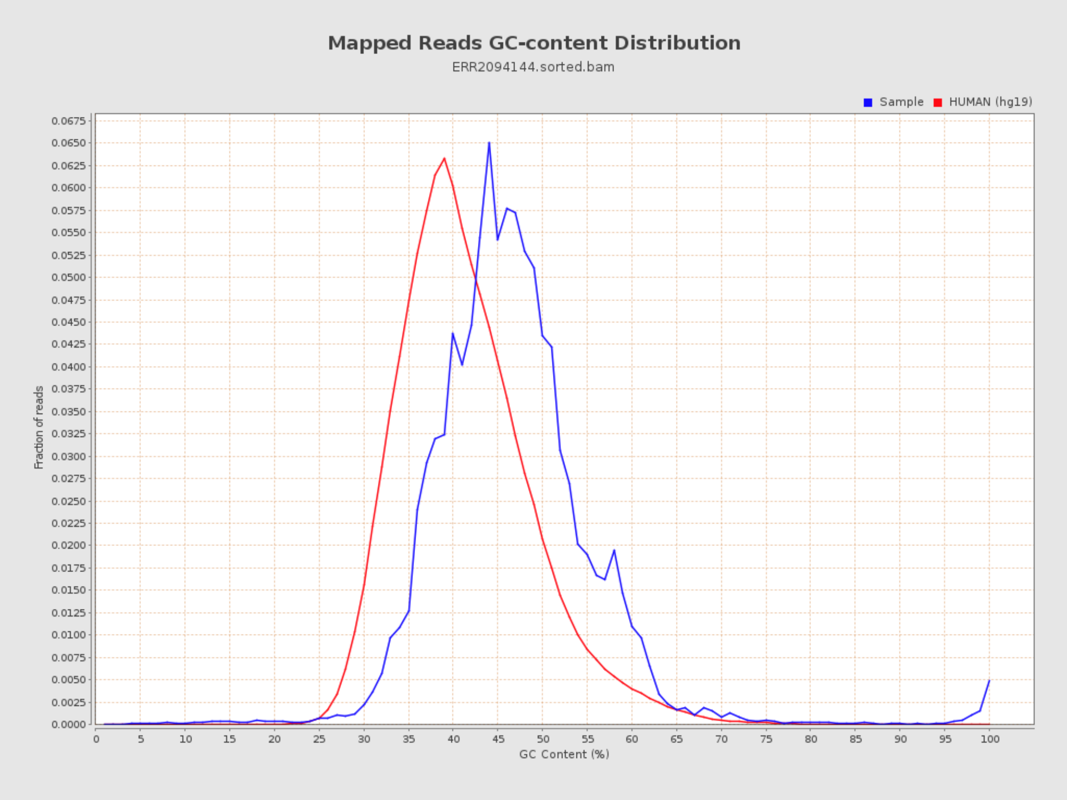
7. Results : Duplication Rate Histogram



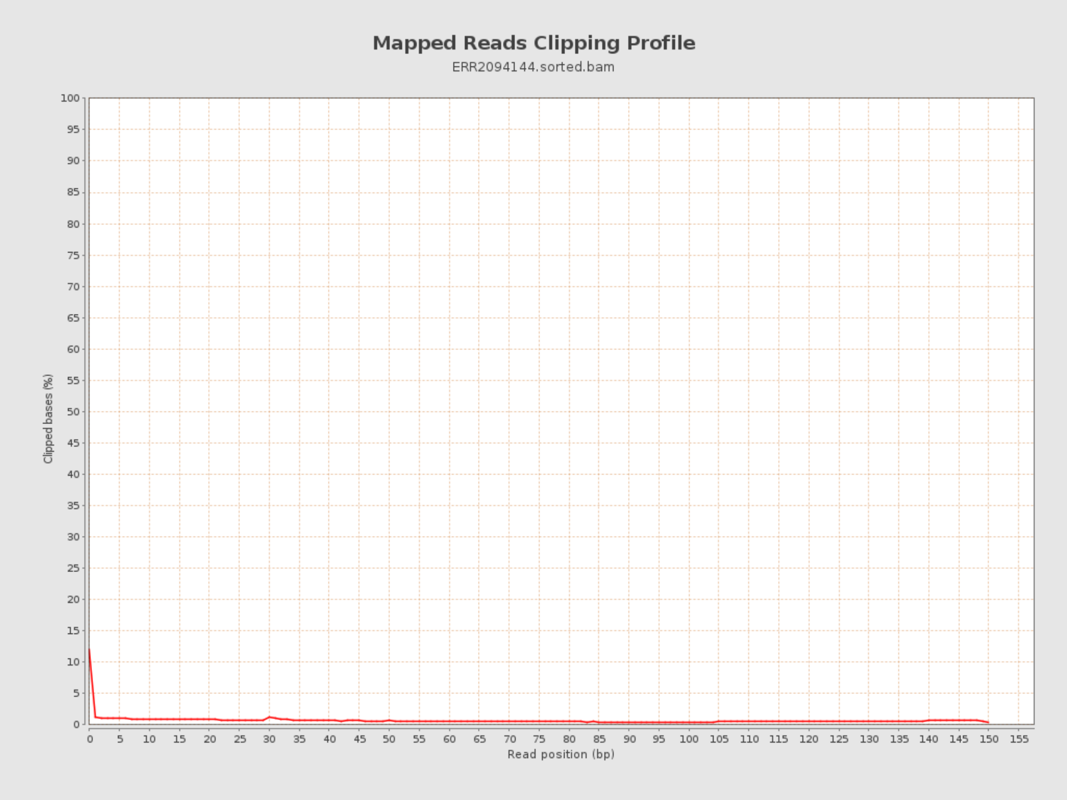
8. Results : Mapped Reads Nucleotide Content



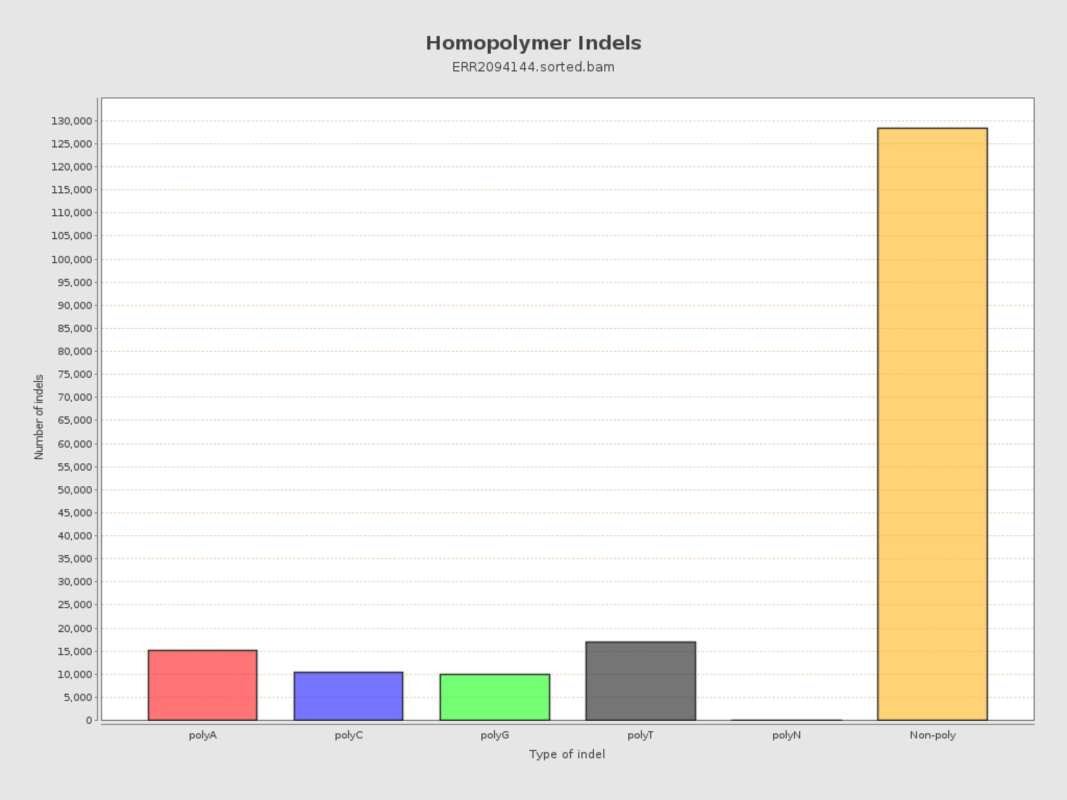
9. Results : Mapped Reads GC-content Distribution



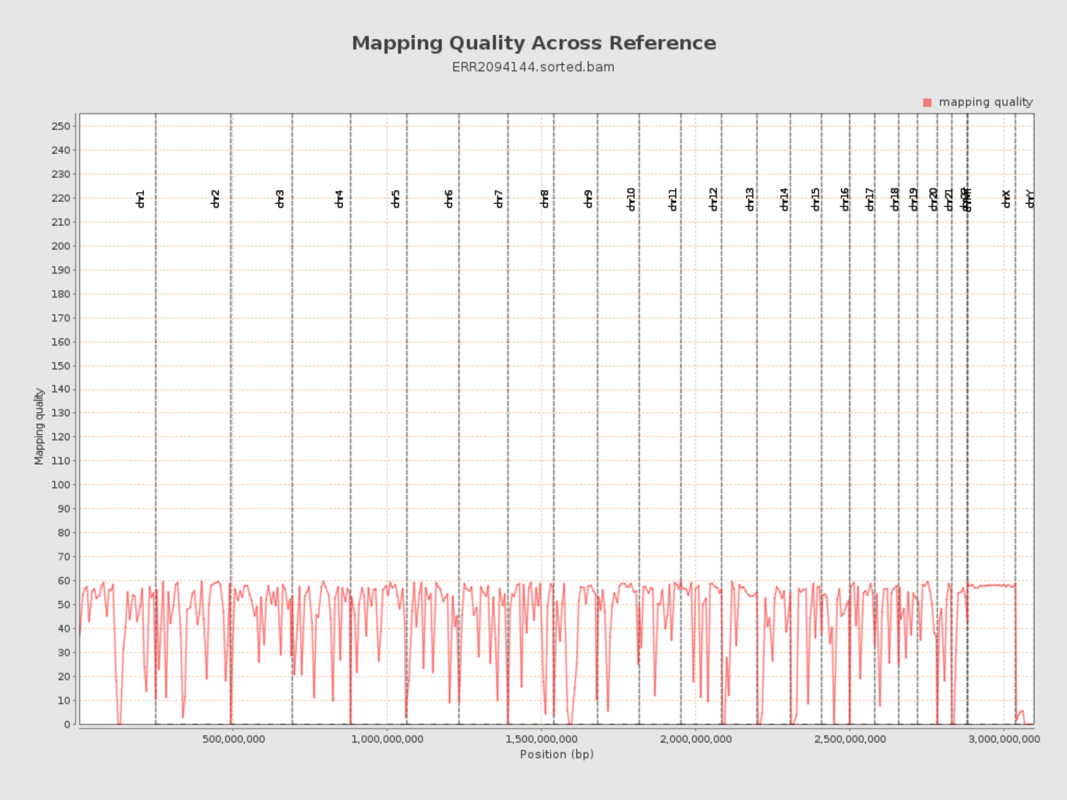
10. Results : Mapped Reads Clipping Profile



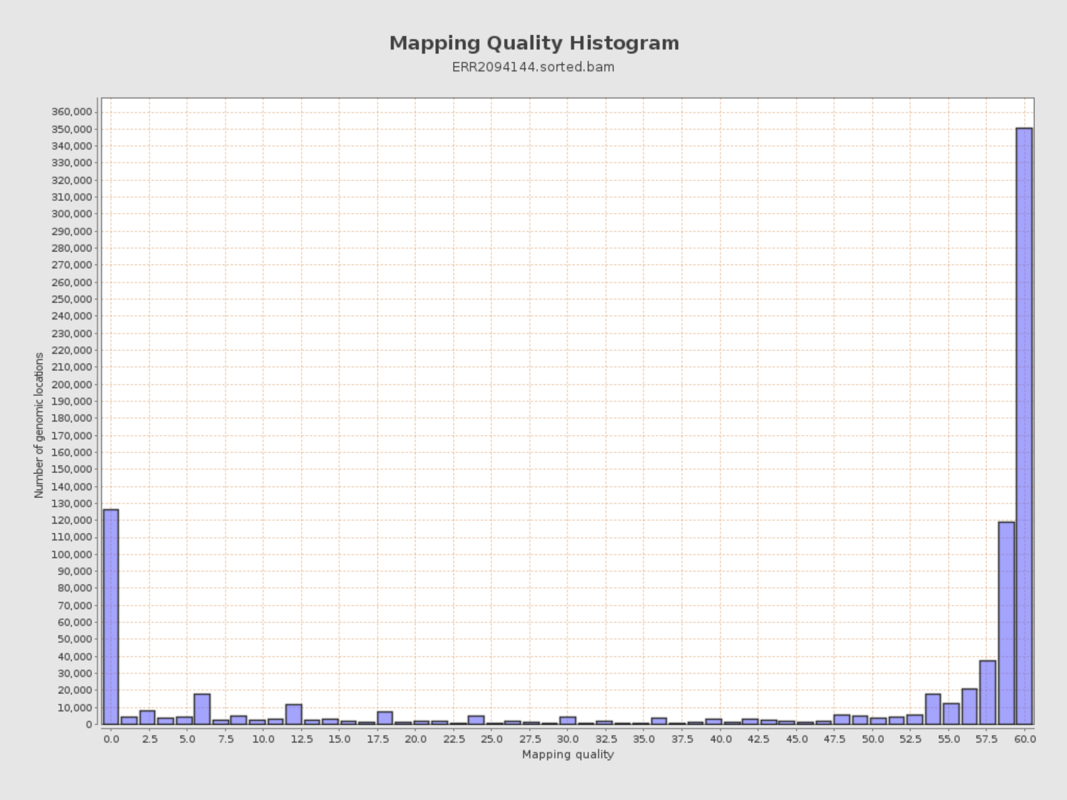
11. Results : Homopolymer Indels



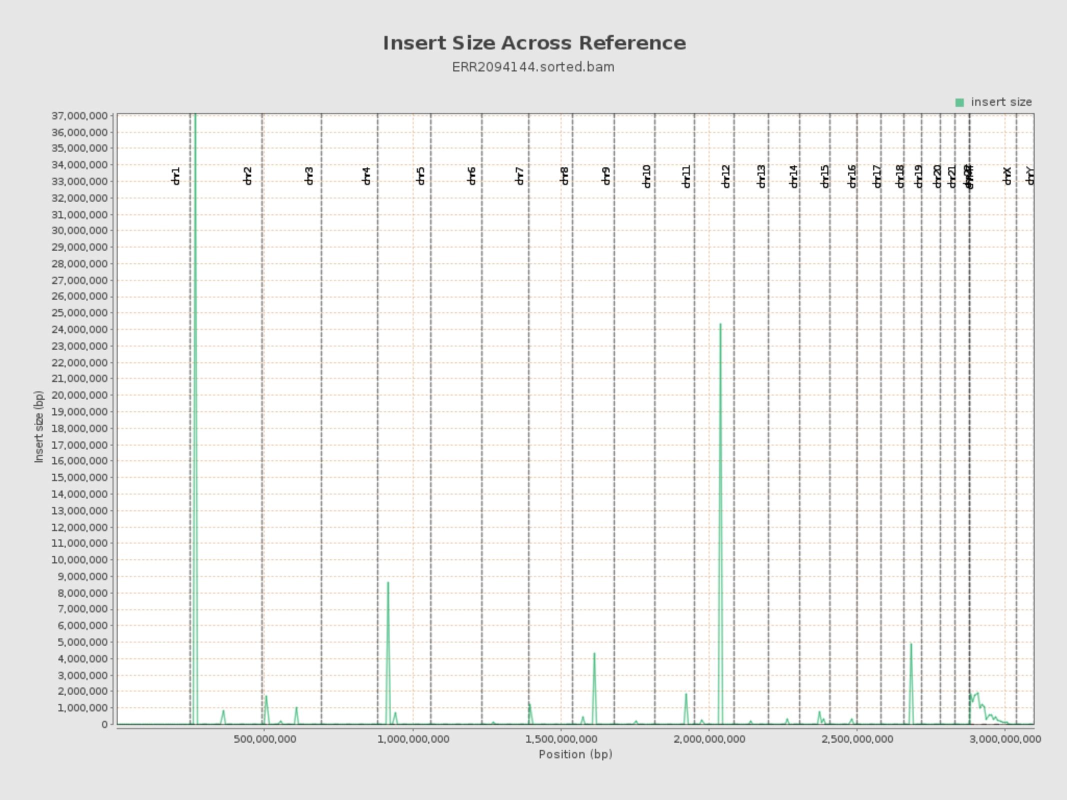
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram