Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:39:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094141.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_ERR2094141 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094141_1.fastq.gz ERR2094141_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:39:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	432,218
Mapped reads	397,070 / 91.87%
Unmapped reads	35,148 / 8.13%
Mapped paired reads	397,070 / 91.87%
Mapped reads, first in pair	199,306 / 46.11%
Mapped reads, second in pair	197,764 / 45.76%
Mapped reads, both in pair	394,358 / 91.24%
Mapped reads, singletons	2,712 / 0.63%
Secondary alignments	0
Supplementary alignments	9,036 / 2.09%
Read min/max/mean length	30 / 151 / 138.34
Duplicated reads (estimated)	383,904 / 88.82%
Duplication rate	46.4%
Clipped reads	158,836 / 36.75%

2.2. ACGT Content

Number/percentage of A's	15,088,403 / 28.95%
Number/percentage of C's	11,073,666 / 21.25%
Number/percentage of T's	14,477,976 / 27.78%
Number/percentage of G's	11,475,771 / 22.02%
Number/percentage of N's	489 / 0%

GC Percentage	43.27%

2.3. Coverage

Mean	0.0172
Standard Deviation	9.1066

2.4. Mapping Quality

Mean Mapping Quality	41.26

2.5. Insert size

Mean	236,180.89
Standard Deviation	4,679,708.7
P25/Median/P75	145 / 169 / 198

2.6. Mismatches and indels

General error rate	4.06%
Mismatches	2,108,693
Insertions	23,957
Mapped reads with at least one insertion	5.96%
Deletions	167,497
Mapped reads with at least one deletion	40.74%
Homopolymer indels	28.83%

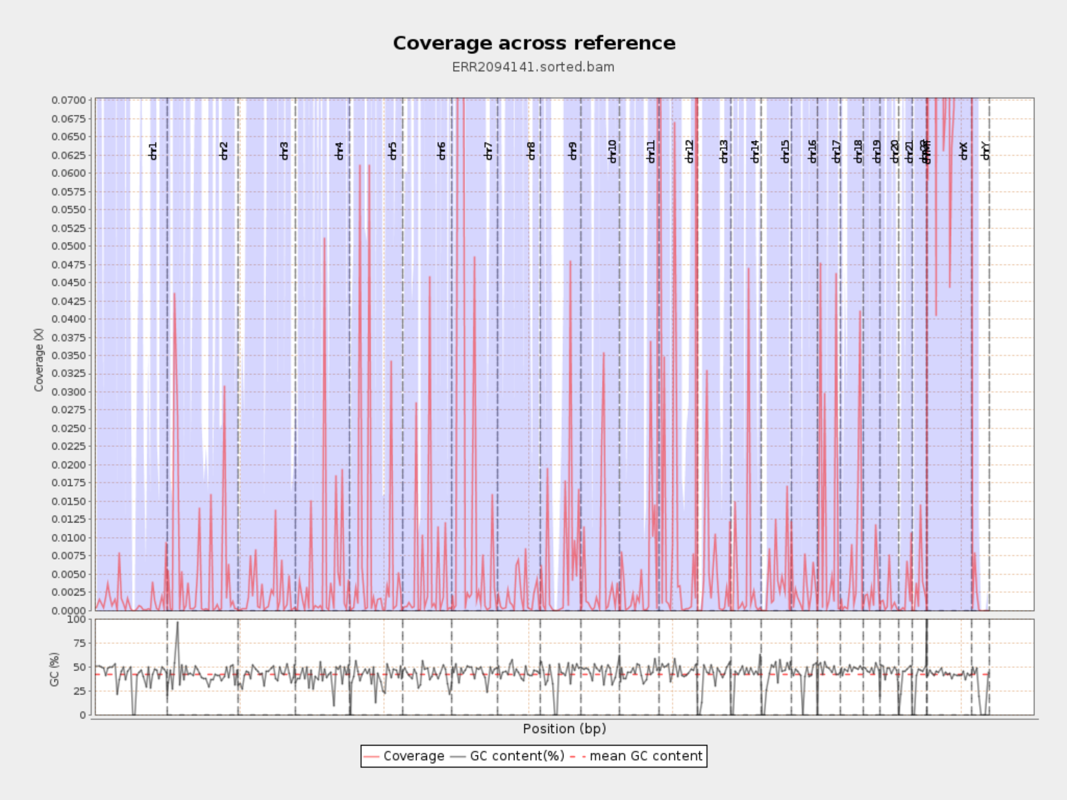
2.7. Chromosome stats

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

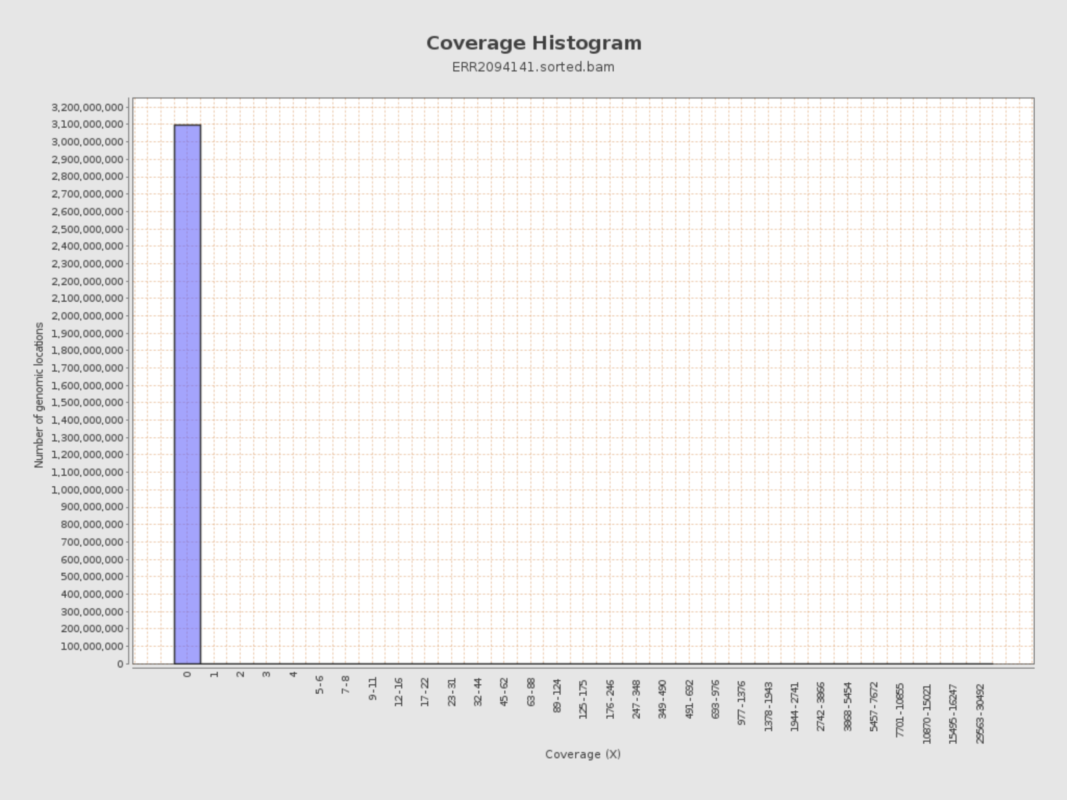
		bases	**coverage**	**deviation**
chr1	249250621	350019	0.0014	0.5301
chr2	243199373	1276076	0.0052	1.958
chr3	198022430	460992	0.0023	0.7614
chr4	191154276	1035285	0.0054	2.5497
chr5	180915260	1453286	0.008	3.5625
chr6	171115067	916687	0.0054	2.5151
chr7	159138663	3350132	0.0211	9.0569
chr8	146364022	303950	0.0021	0.6279
chr9	141213431	1006294	0.0071	2.5178
chr10	135534747	669174	0.0049	2.2074
chr11	135006516	831411	0.0062	2.2818
chr12	133851895	2634659	0.0197	7.2977
chr13	115169878	561216	0.0049	1.862
chr14	107349540	536191	0.005	2.9489
chr15	102531392	425142	0.0041	1.1353
chr16	90354753	278398	0.0031	0.7255
chr17	81195210	1043052	0.0128	4.3276
chr18	78077248	590233	0.0076	3.0678
chr19	59128983	177099	0.003	0.829
chr20	63025520	97180	0.0015	0.5002
chr21	48129895	118880	0.0025	0.5566
chr22	51304566	191259	0.0037	0.9286
chrMT	16571	8603517	519.1912	2,833.623
chrX	155270560	26401207	0.17	23.6789

chrY	59373566	83398	0.0014	0.6585

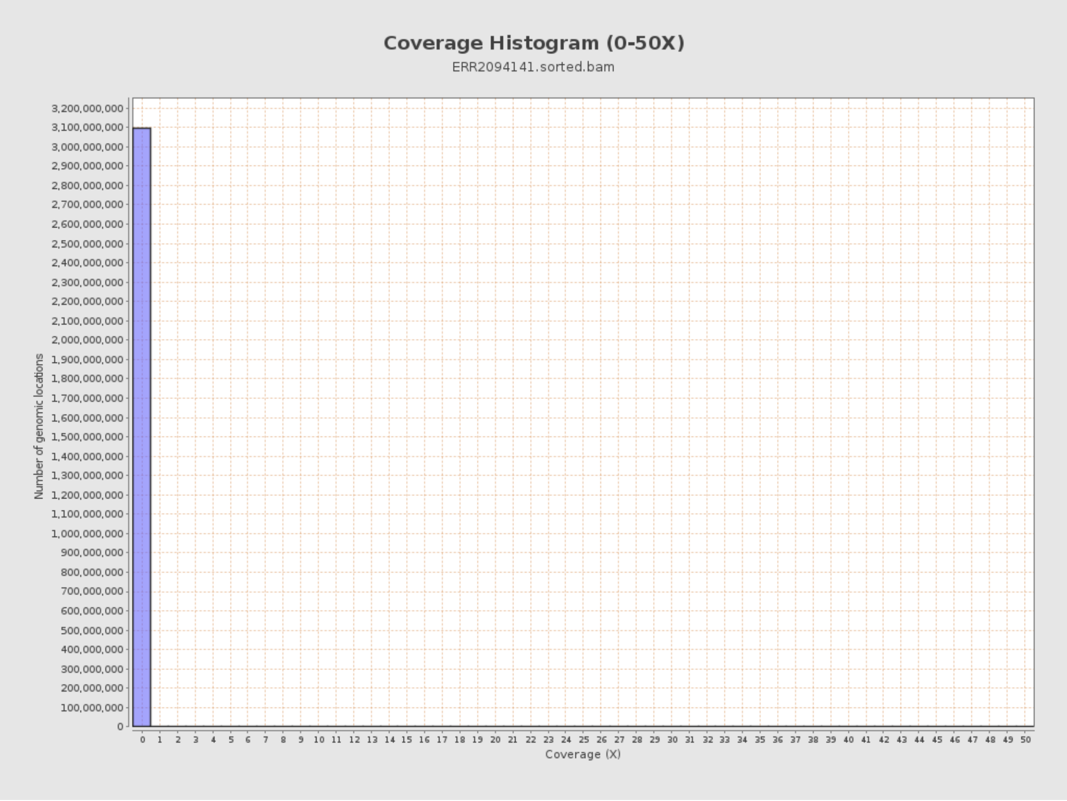
3. Results : Coverage across reference



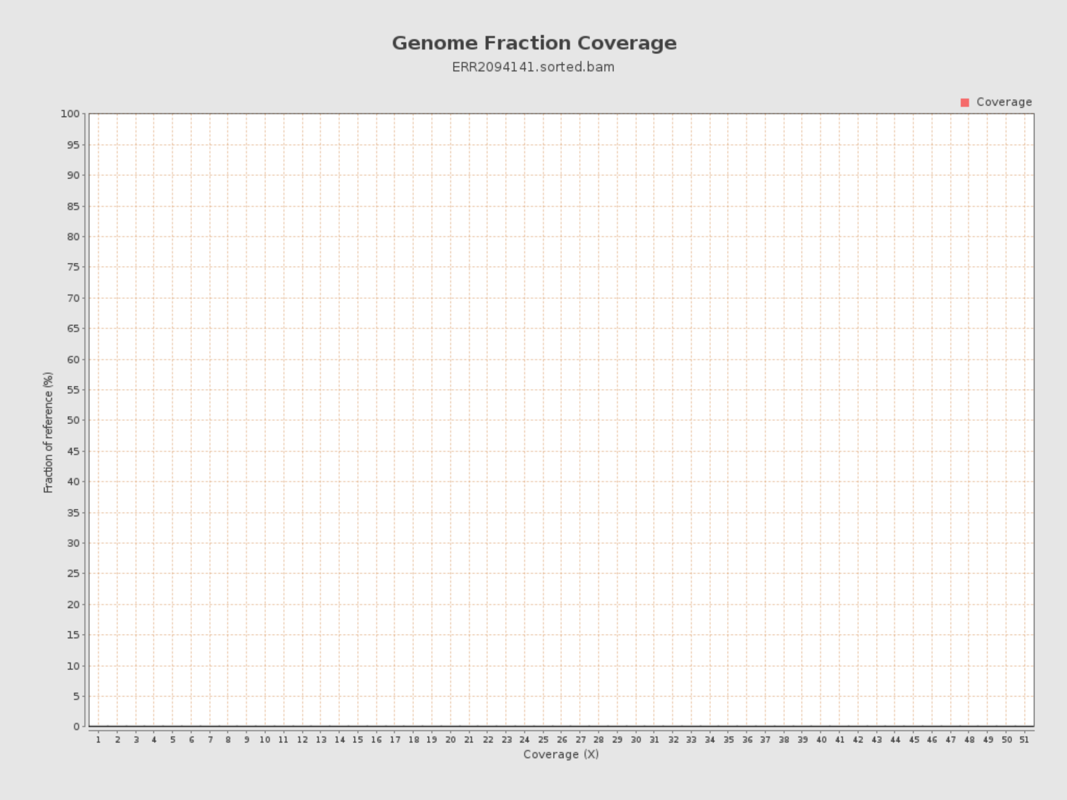
4. Results : Coverage Histogram



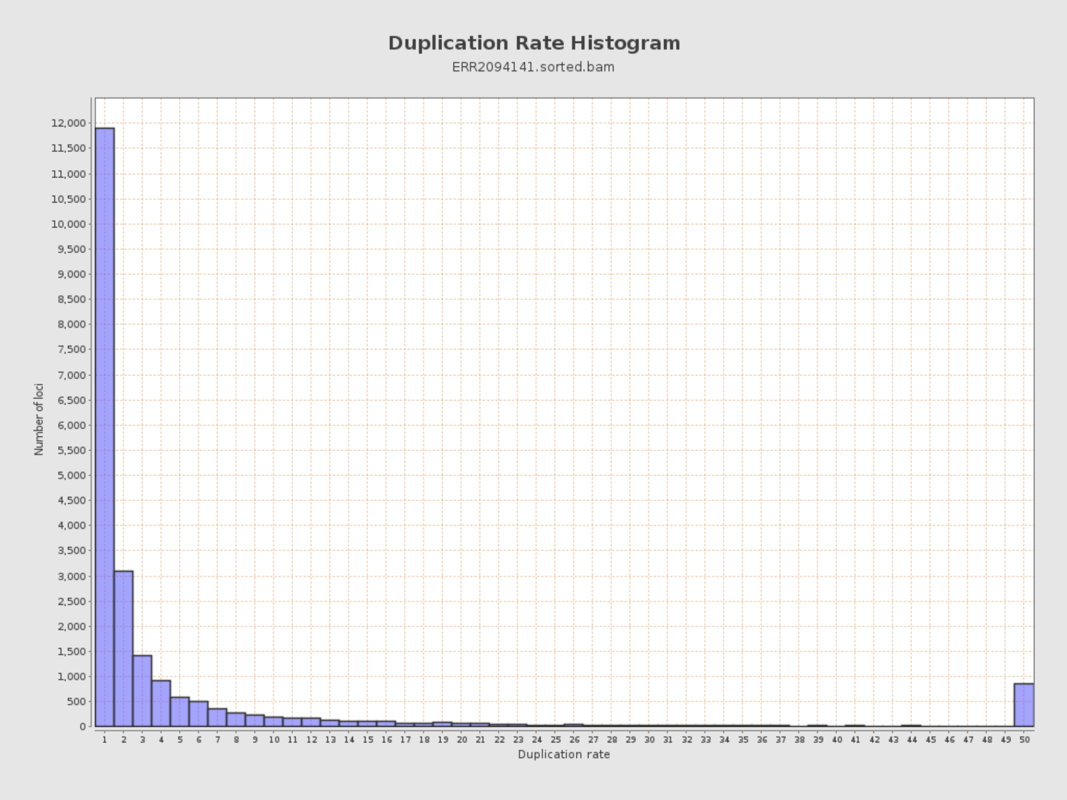
5. Results : Coverage Histogram (0-50X)



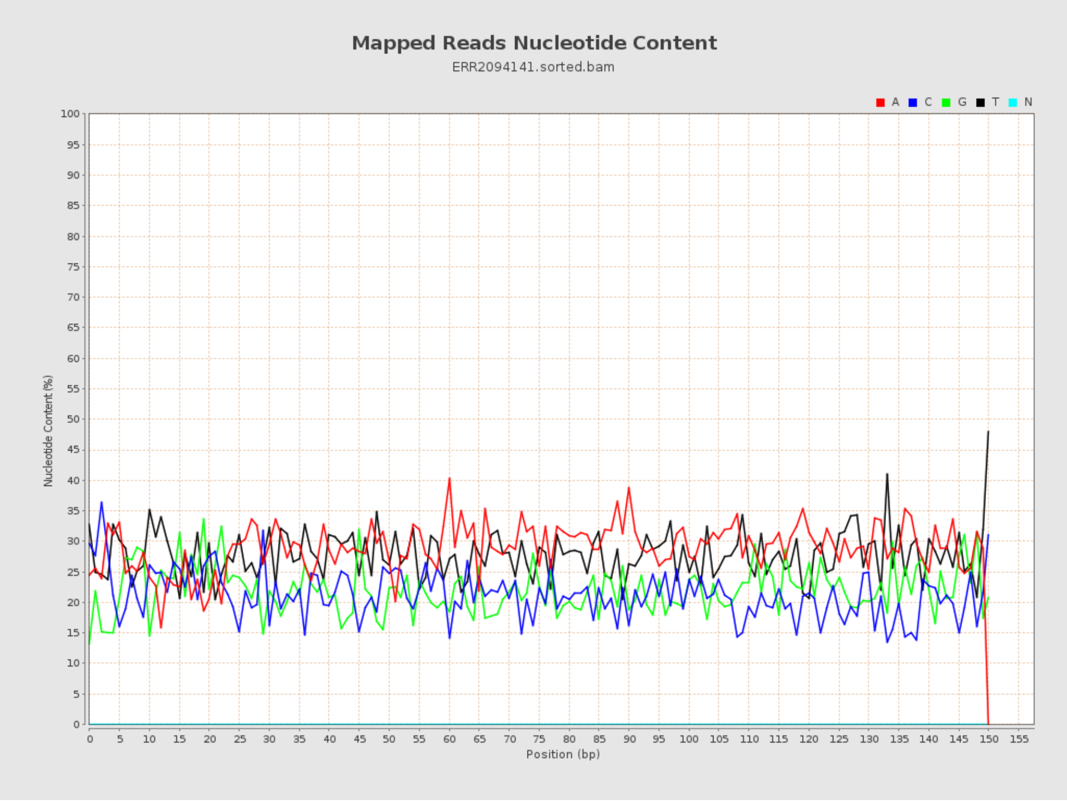
6. Results : Genome Fraction Coverage



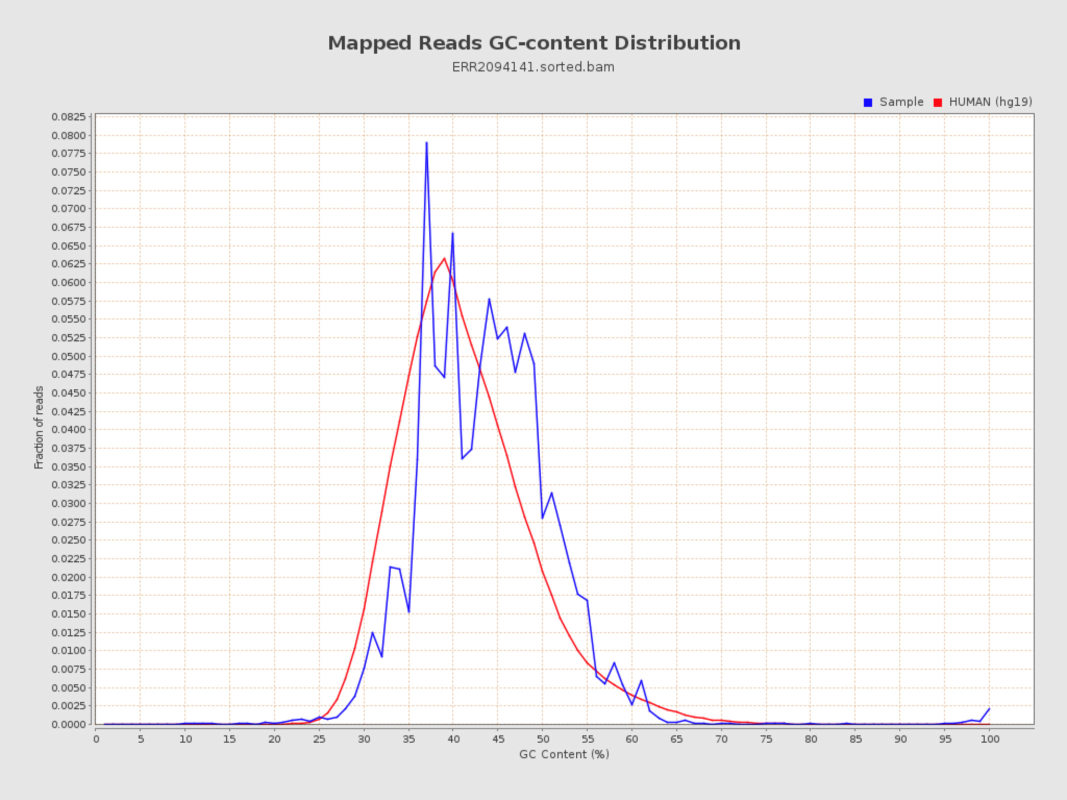
7. Results : Duplication Rate Histogram



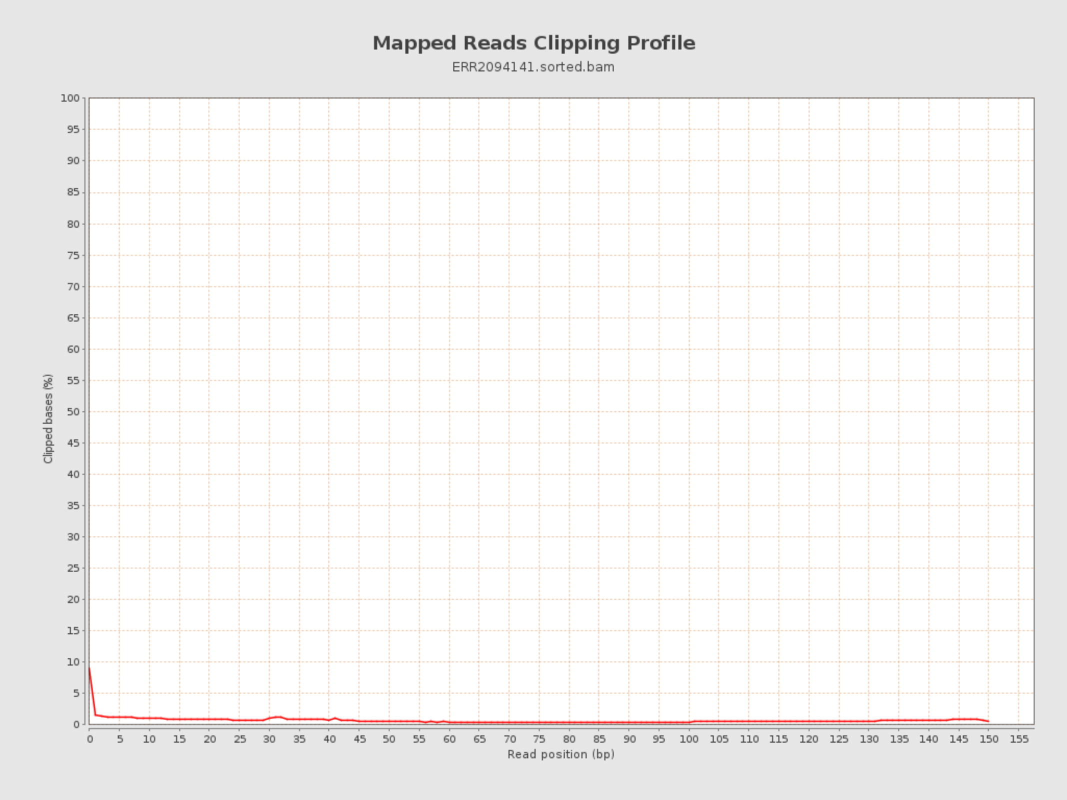
8. Results : Mapped Reads Nucleotide Content



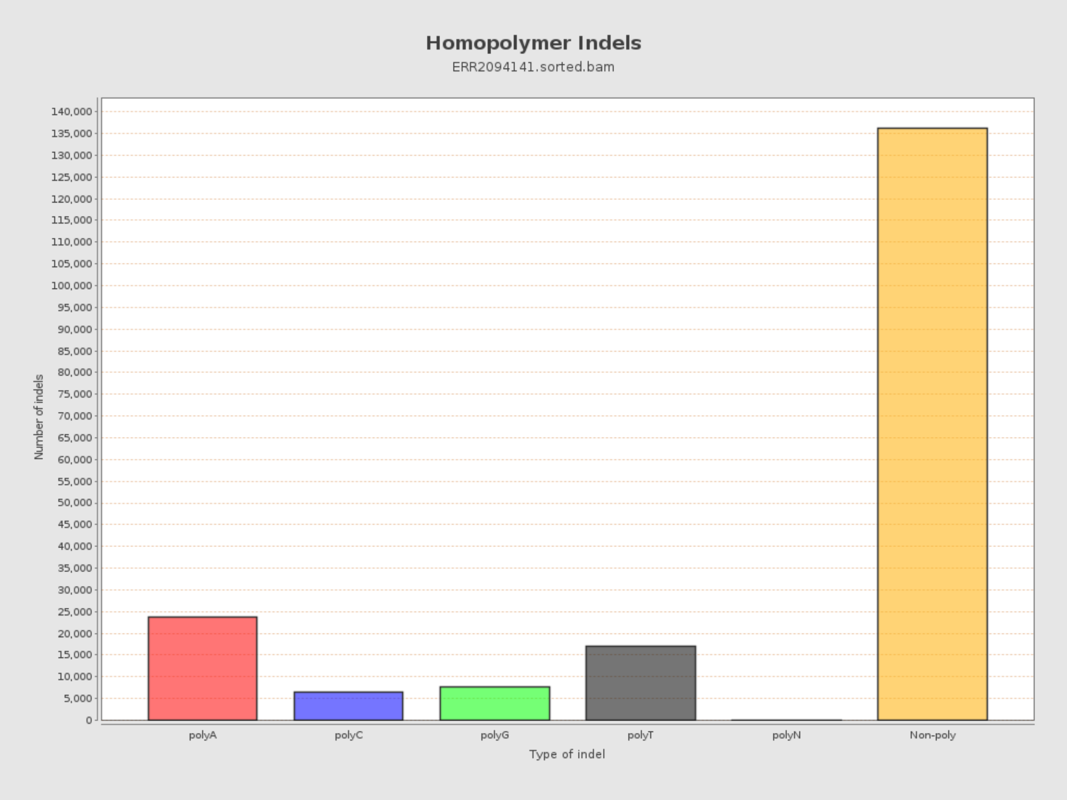
9. Results : Mapped Reads GC-content Distribution



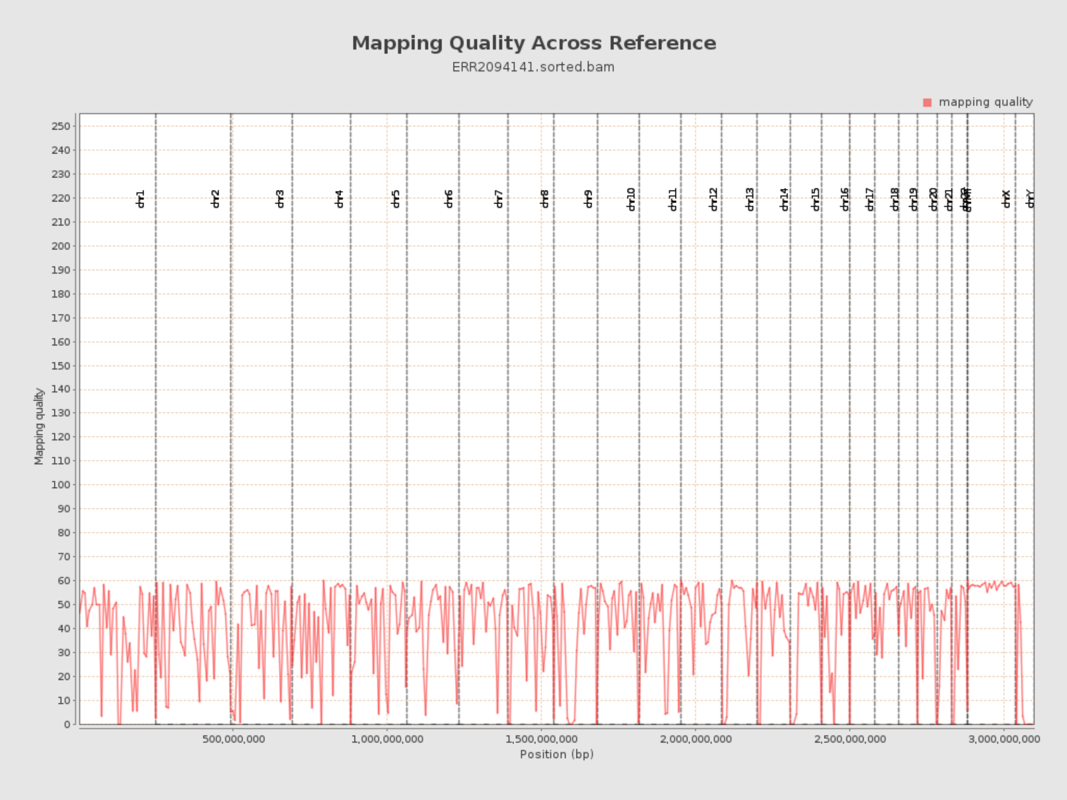
10. Results : Mapped Reads Clipping Profile



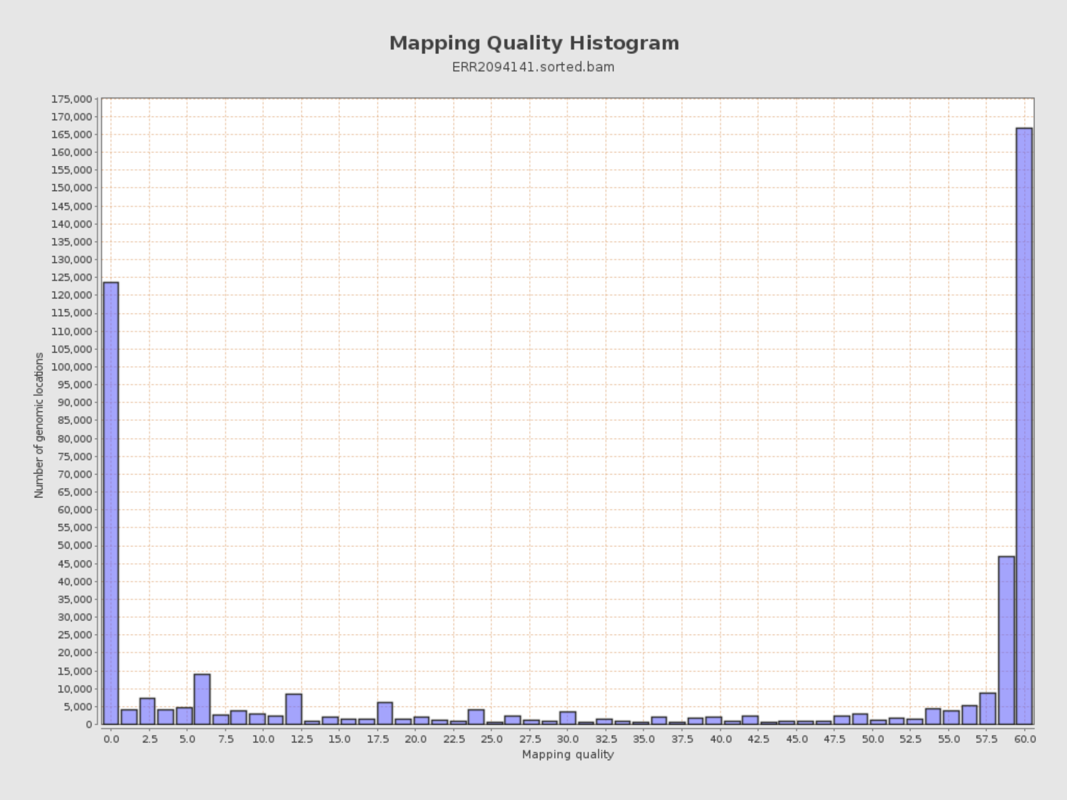
11. Results : Homopolymer Indels



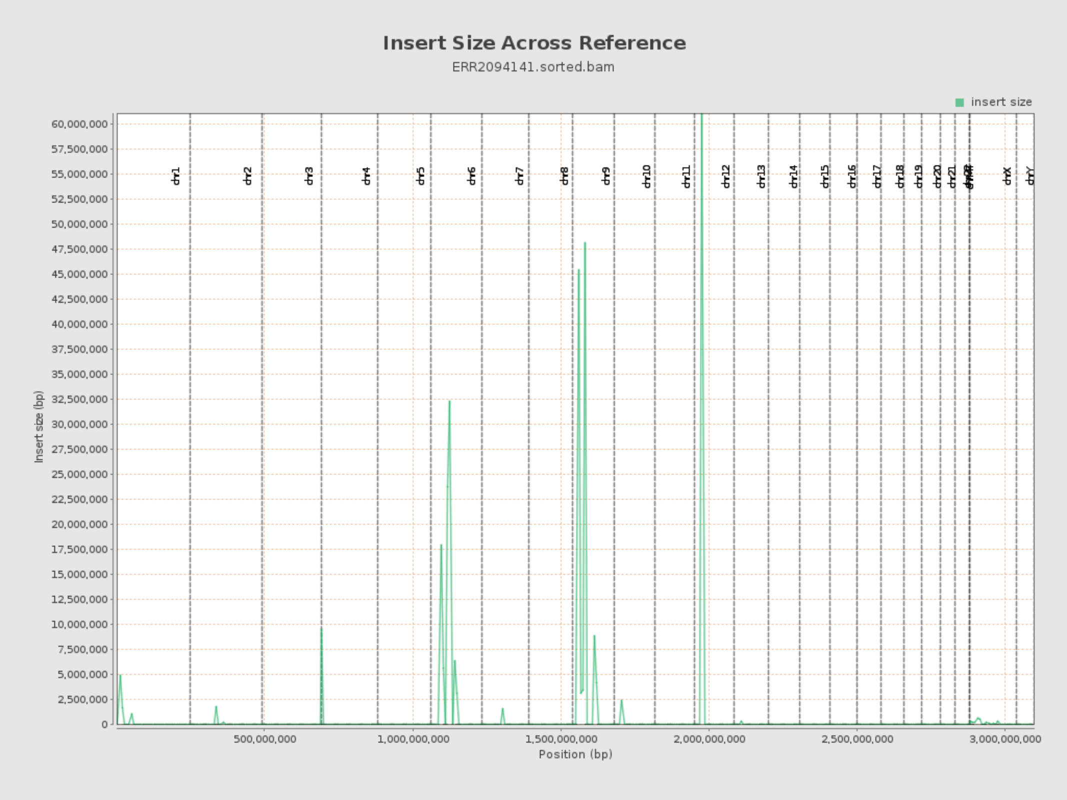
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram