Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:34:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094140.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_ERR2094140 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094140_1.fastq.gz ERR2094140_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:34:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,434
Mapped reads	2,175 / 89.36%
Unmapped reads	259 / 10.64%
Mapped paired reads	2,175 / 89.36%
Mapped reads, first in pair	1,107 / 45.48%
Mapped reads, second in pair	1,068 / 43.88%
Mapped reads, both in pair	2,098 / 86.2%
Mapped reads, singletons	77 / 3.16%
Secondary alignments	0
Supplementary alignments	166 / 6.82%
Read min/max/mean length	30 / 151 / 143.7
Duplicated reads (estimated)	996 / 40.92%
Duplication rate	28.48%
Clipped reads	1,147 / 47.12%

2.2. ACGT Content

Number/percentage of A's	81,058 / 29.9%
Number/percentage of C's	61,395 / 22.65%
Number/percentage of T's	65,738 / 24.25%
Number/percentage of G's	62,893 / 23.2%
Number/percentage of N's	0 / 0%

GC Percentage	45.85%

2.3. Coverage

Mean	0.0001
Standard Deviation	0.0328

2.4. Mapping Quality

Mean Mapping Quality	21.93

2.5. Insert size

Mean	769,828.88
Standard Deviation	7,015,153.4
P25/Median/P75	141 / 169 / 208

2.6. Mismatches and indels

General error rate	3.76%
Mismatches	9,742
Insertions	138
Mapped reads with at least one insertion	6.11%
Deletions	756
Mapped reads with at least one deletion	33.33%
Homopolymer indels	28.97%

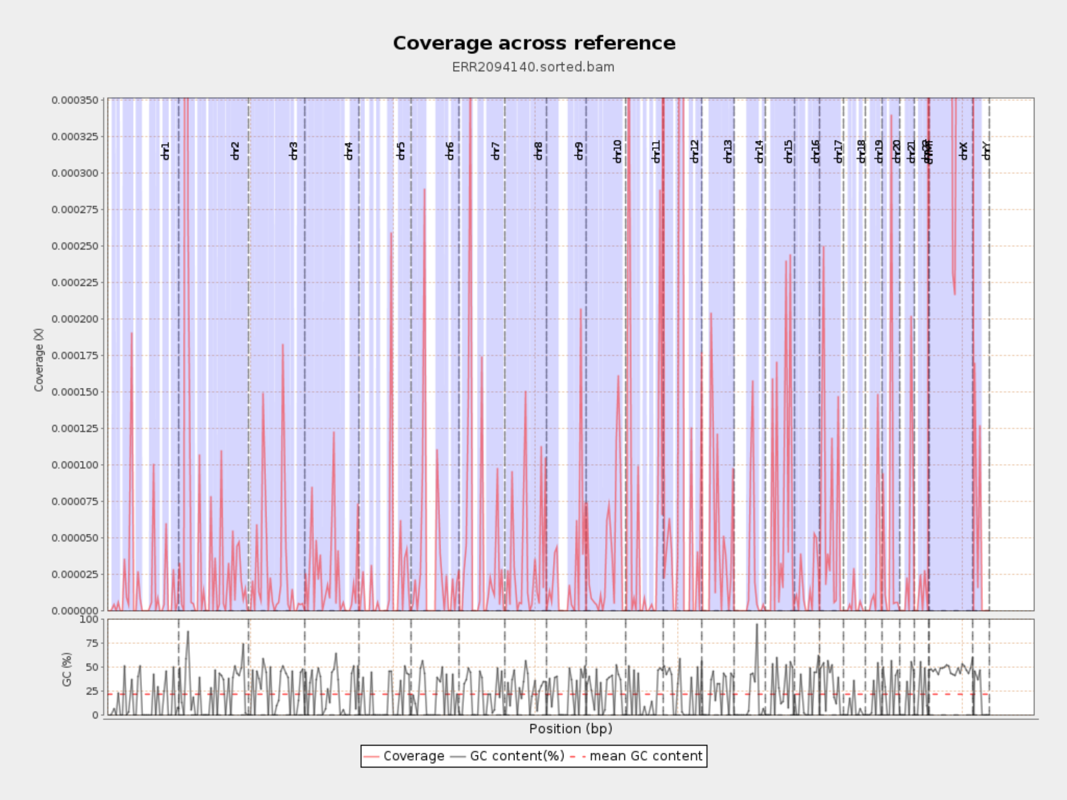
2.7. Chromosome stats

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

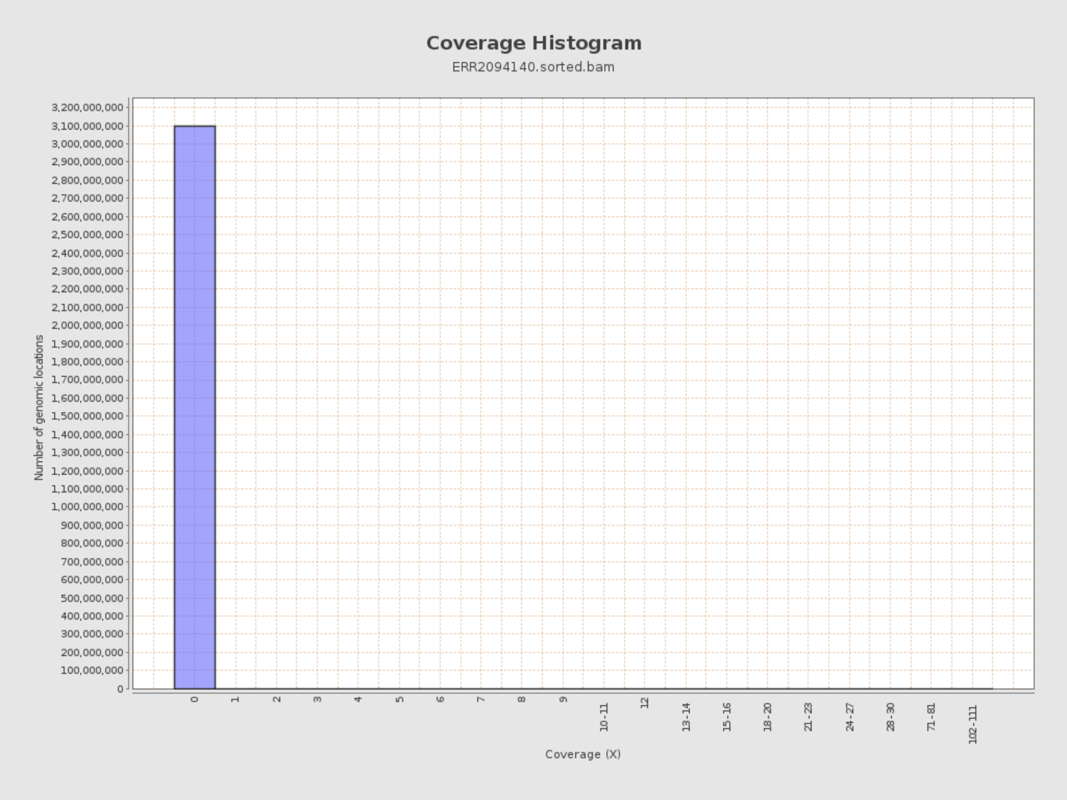
		bases	coverage	deviation
chr1	249250621	3874	0	0.01
chr2	243199373	14903	0.0001	0.0224
chr3	198022430	4802	0	0.0085
chr4	191154276	4761	0	0.0075
chr5	180915260	3725	0	0.013
chr6	171115067	5259	0	0.0142
chr7	159138663	7460	0	0.0174
chr8	146364022	5304	0	0.0104
chr9	141213431	3953	0	0.0103
chr10	135534747	5233	0	0.0119
chr11	135006516	8215	0.0001	0.022
chr12	133851895	17604	0.0001	0.0947
chr13	115169878	5506	0	0.0139
chr14	107349540	2268	0	0.0107
chr15	102531392	7231	0.0001	0.0208
chr16	90354753	1572	0	0.0055
chr17	81195210	5078	0.0001	0.018
chr18	78077248	304	0	0.0024
chr19	59128983	1283	0	0.0095
chr20	63025520	3367	0.0001	0.021
chr21	48129895	2156	0	0.0145
chr22	51304566	471	0	0.004
chrMT	16571	6693	0.4039	2.4269
chrX	155270560	153277	0.001	0.0973

chrY	59373566	2422	0	0.0118

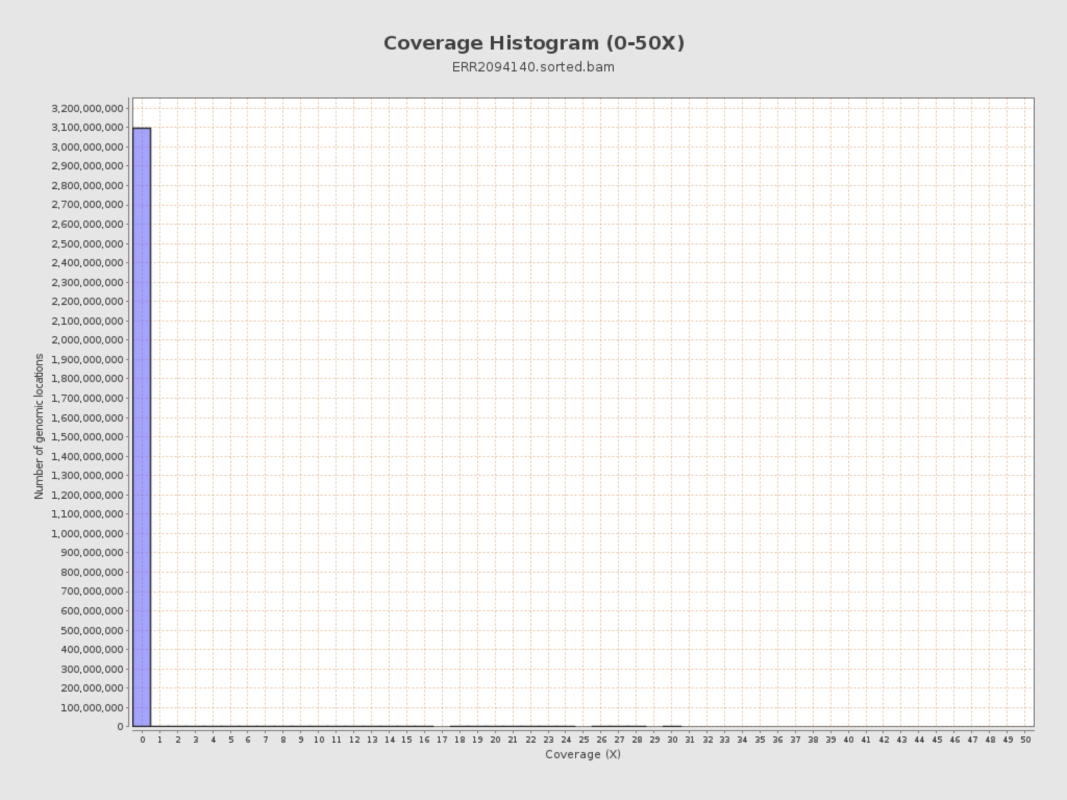
3. Results : Coverage across reference



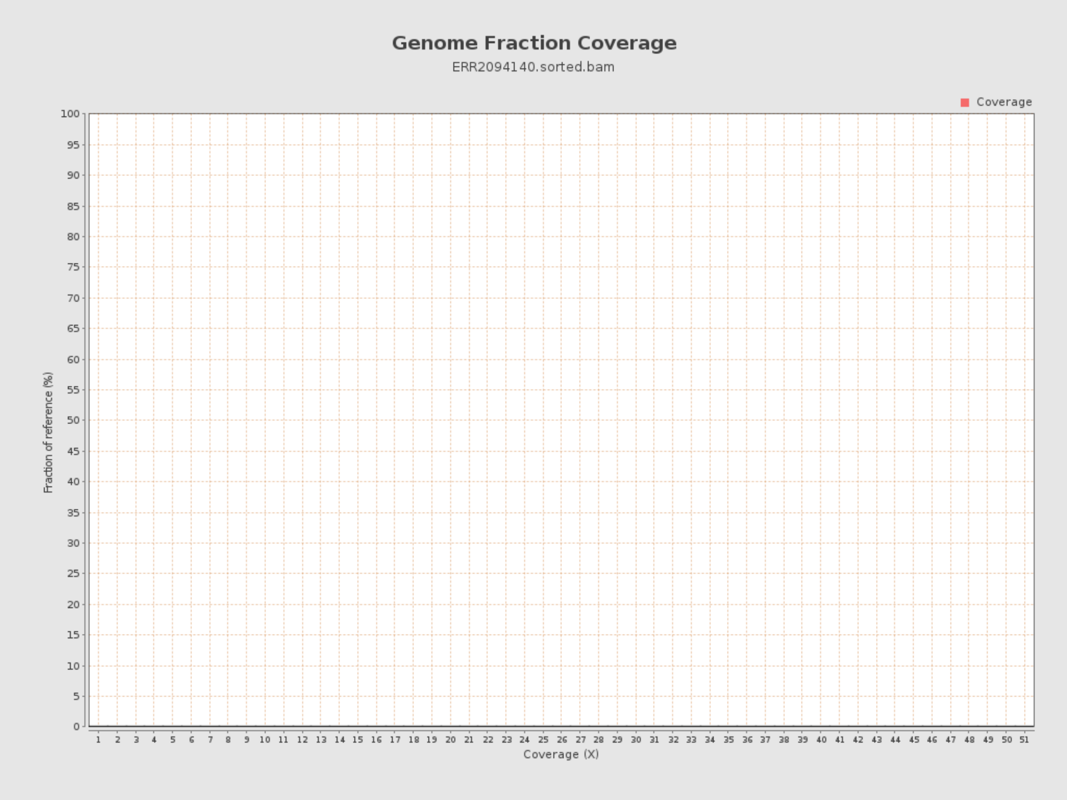
4. Results : Coverage Histogram



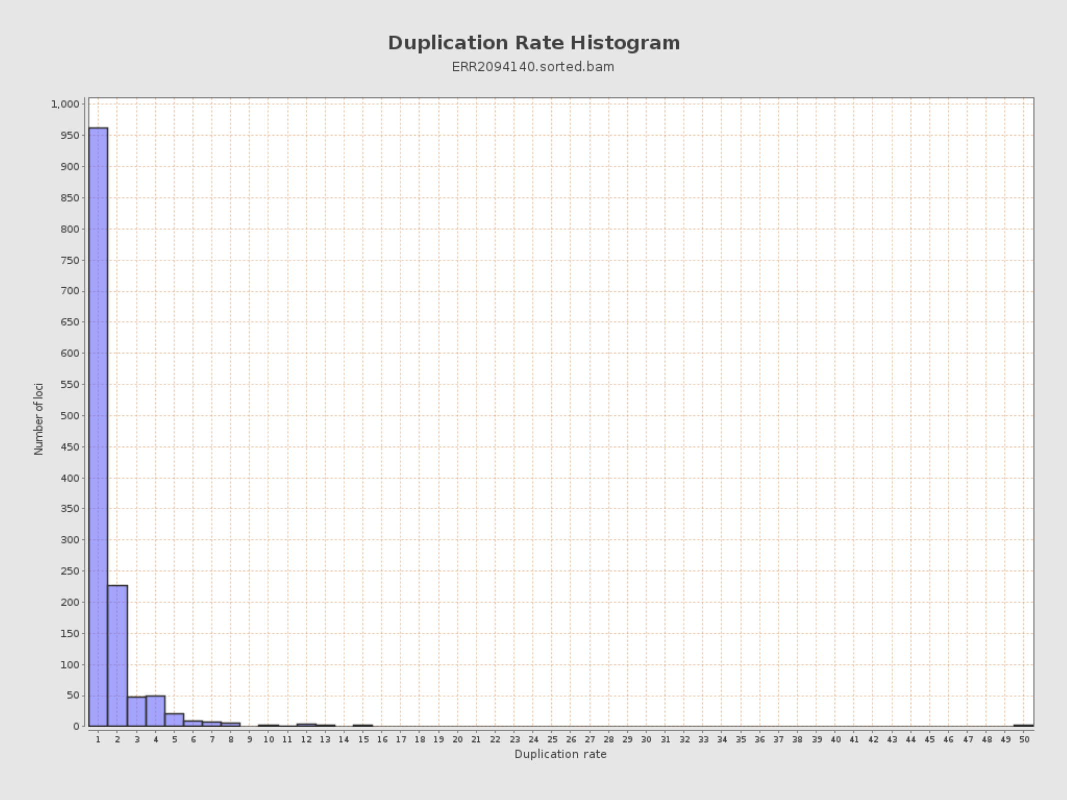
5. Results : Coverage Histogram (0-50X)



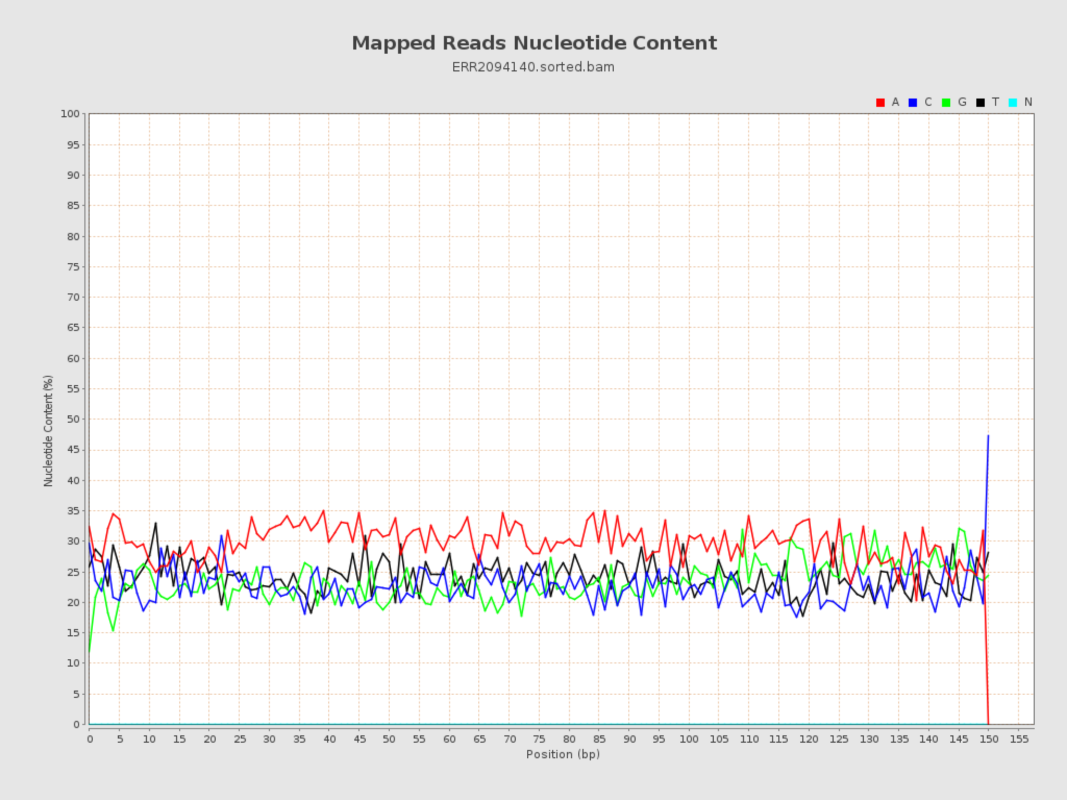
6. Results : Genome Fraction Coverage



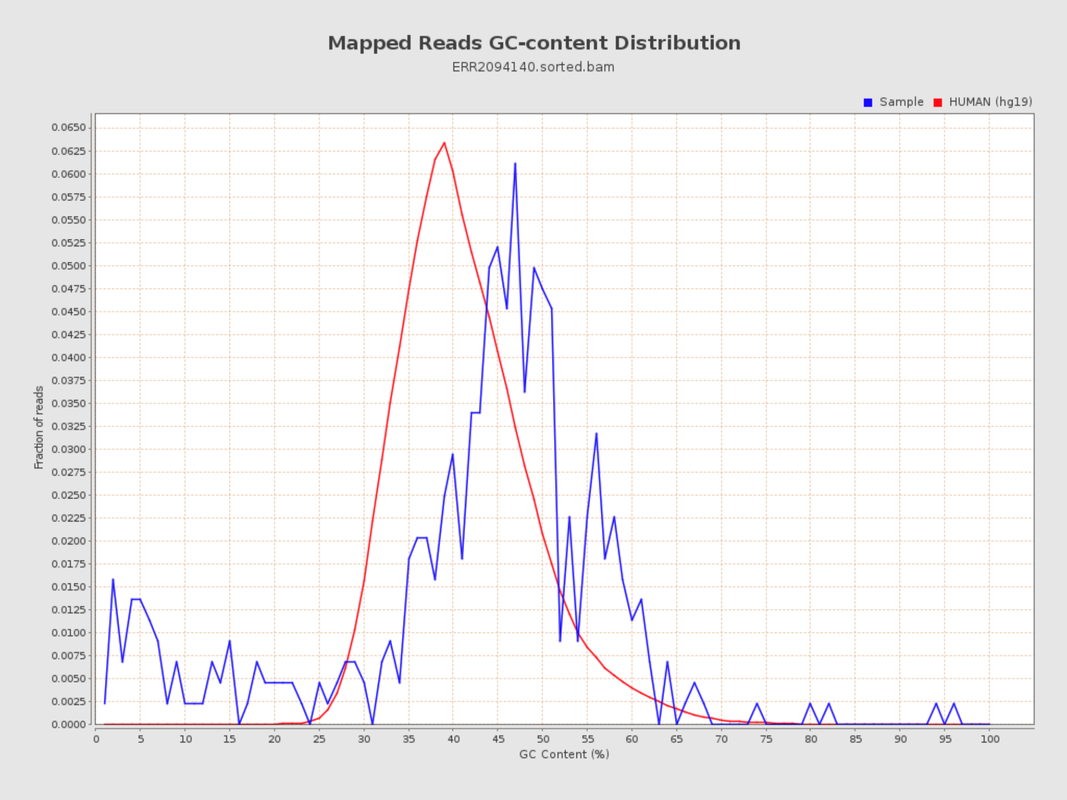
7. Results : Duplication Rate Histogram



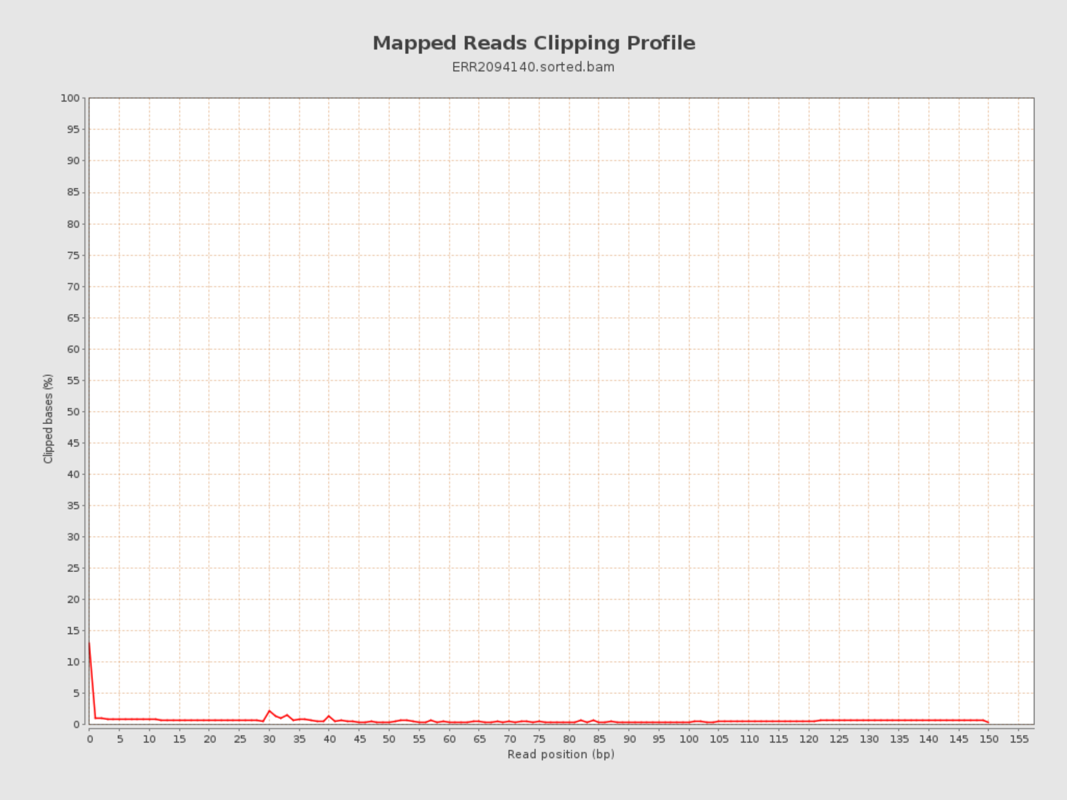
8. Results : Mapped Reads Nucleotide Content



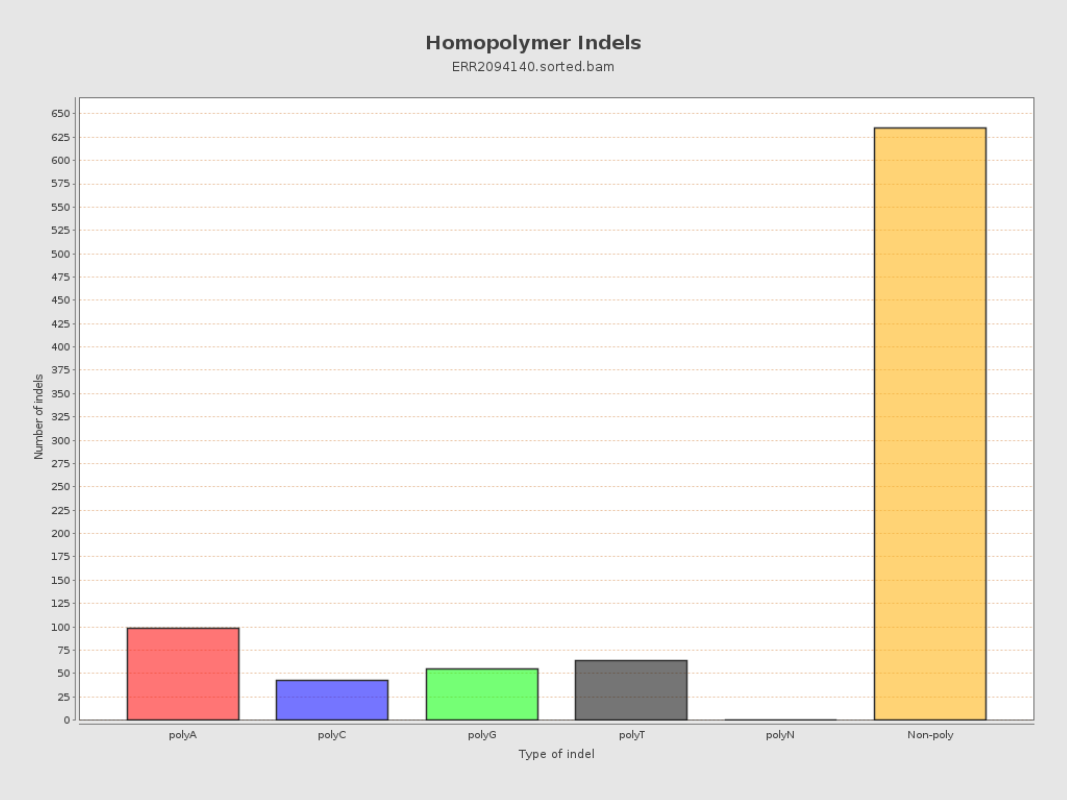
9. Results : Mapped Reads GC-content Distribution



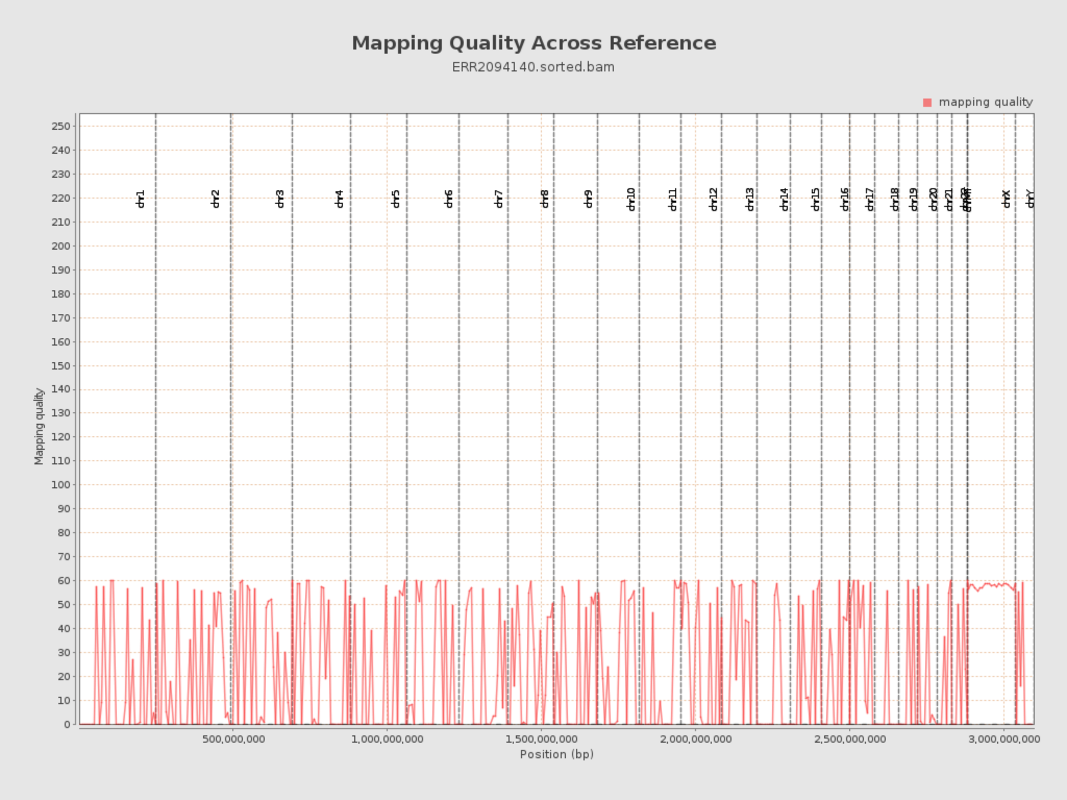
10. Results : Mapped Reads Clipping Profile



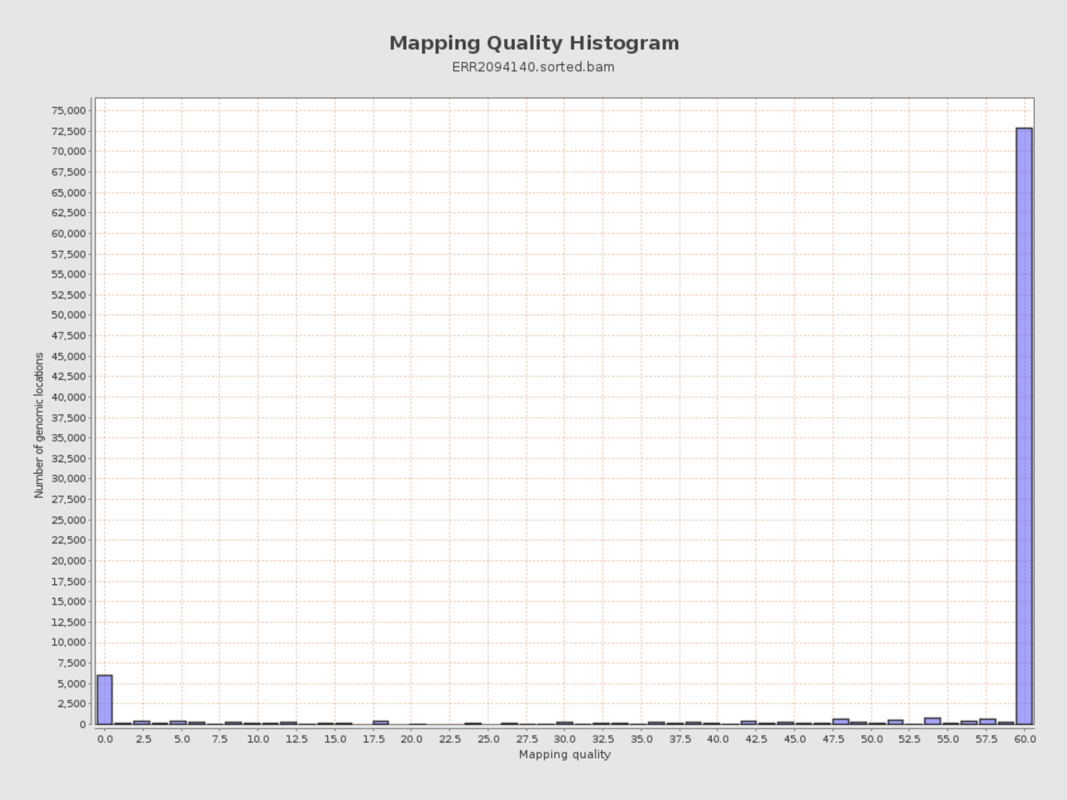
11. Results : Homopolymer Indels



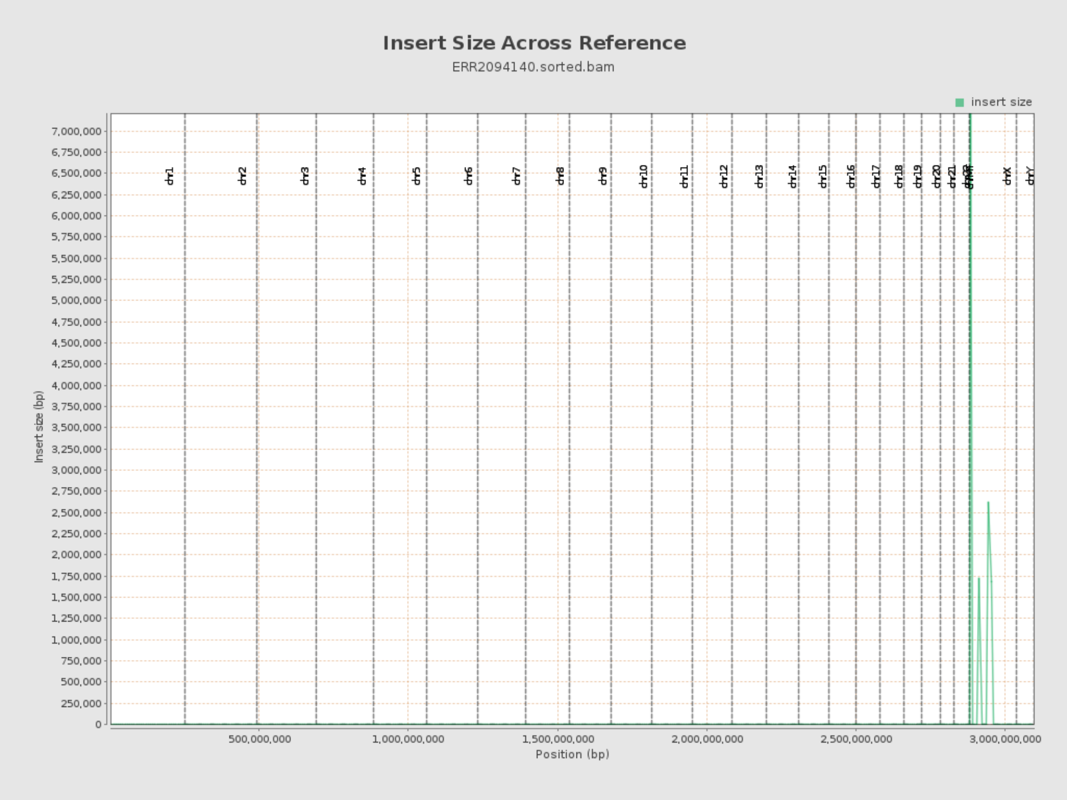
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram