Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 03:00:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094135.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_ERR2094135 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094135_1.fastq.gz ERR2094135_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 03:00:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	530,136
Mapped reads	507,967 / 95.82%
Unmapped reads	22,169 / 4.18%
Mapped paired reads	507,967 / 95.82%
Mapped reads, first in pair	254,879 / 48.08%
Mapped reads, second in pair	253,088 / 47.74%
Mapped reads, both in pair	505,426 / 95.34%
Mapped reads, singletons	2,541 / 0.48%
Secondary alignments	0
Supplementary alignments	3,789 / 0.71%
Read min/max/mean length	30 / 151 / 145.81
Duplicated reads (estimated)	503,860 / 95.04%
Duplication rate	41.44%
Clipped reads	119,118 / 22.47%

2.2. ACGT Content

Number/percentage of A's	20,298,830 / 27.78%
Number/percentage of C's	15,760,283 / 21.57%
Number/percentage of T's	20,710,221 / 28.34%
Number/percentage of G's	16,303,248 / 22.31%
Number/percentage of N's	974 / 0%

GC Percentage	43.88%

2.3. Coverage

Mean	0.0237
Standard Deviation	34.9781

2.4. Mapping Quality

Mean Mapping Quality	33.57

2.5. Insert size

Mean	21,554.59
Standard Deviation	1,047,992.74
P25/Median/P75	212 / 217 / 256

2.6. Mismatches and indels

General error rate	1.91%
Mismatches	1,266,270
Insertions	42,039
Mapped reads with at least one insertion	8.18%
Deletions	66,636
Mapped reads with at least one deletion	12.79%
Homopolymer indels	55.96%

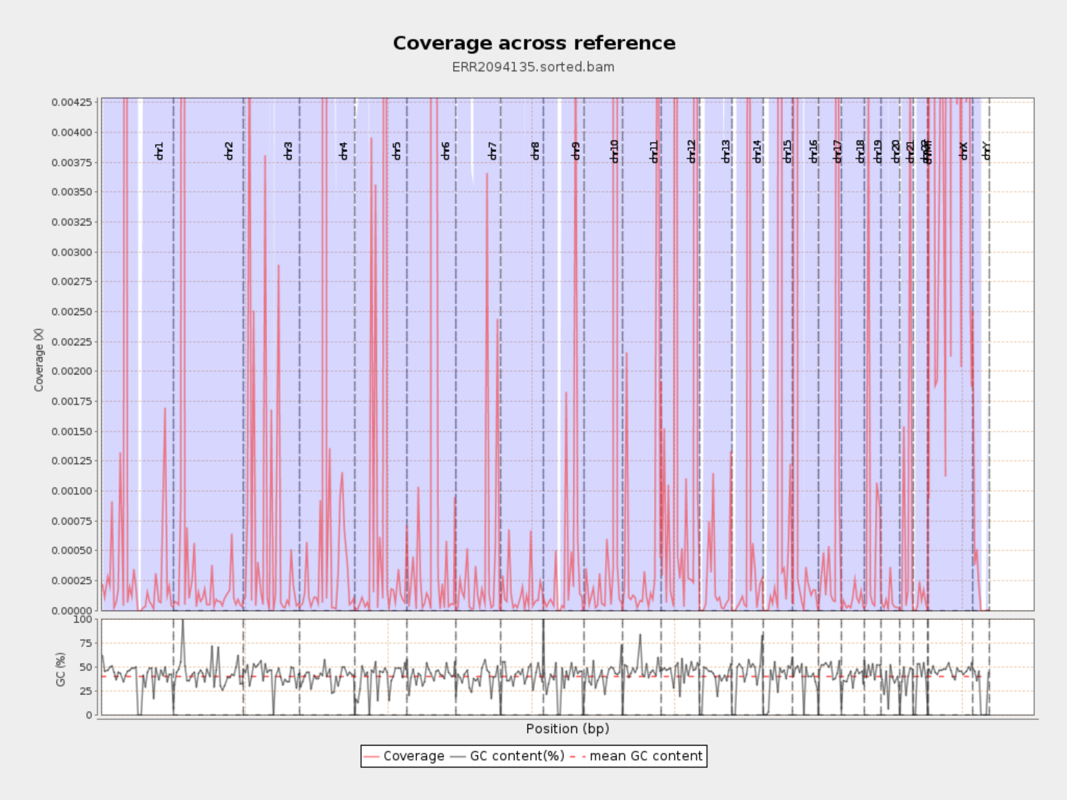
2.7. Chromosome stats

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

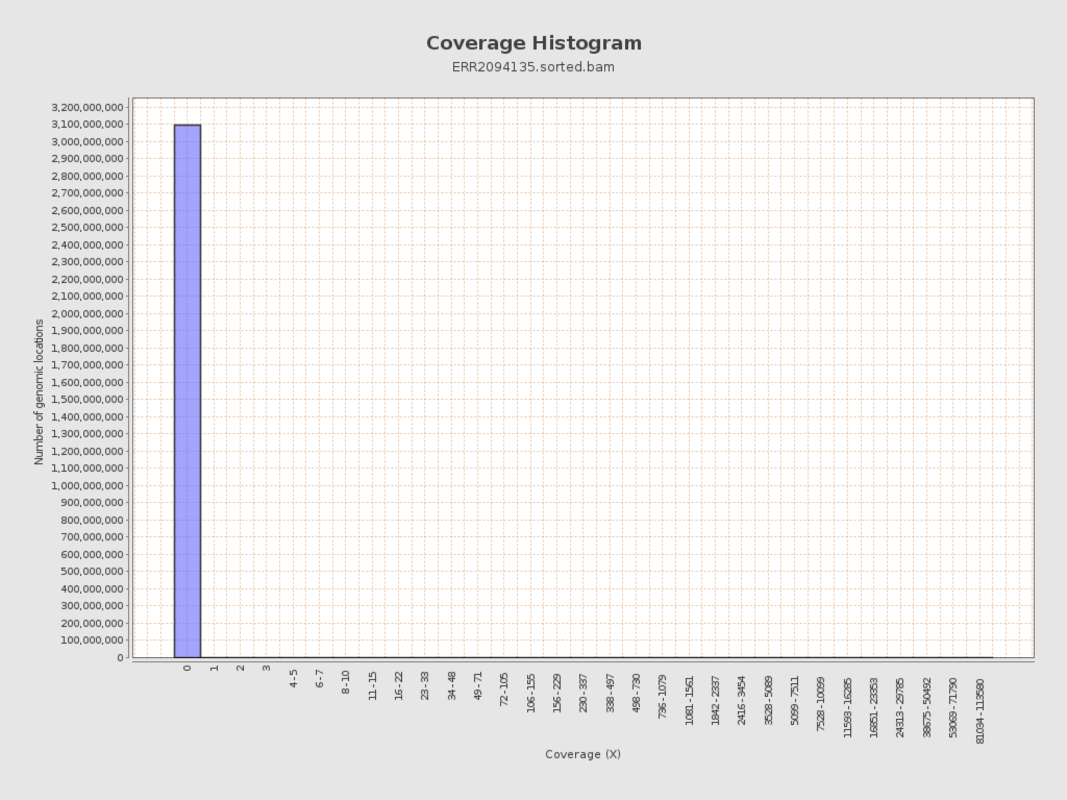
		bases	coverage	deviation
chr1	249250621	171786	0.0007	0.4506
chr2	243199373	255608	0.0011	0.8779
chr3	198022430	148100	0.0007	0.3341
chr4	191154276	3083124	0.0161	18.6973
chr5	180915260	193827	0.0011	0.6793
chr6	171115067	2817620	0.0165	16.5241
chr7	159138663	67678	0.0004	0.1651
chr8	146364022	24313	0.0002	0.0471
chr9	141213431	71408	0.0005	0.2082
chr10	135534747	1126855	0.0083	6.5968
chr11	135006516	88347	0.0007	0.3469
chr12	133851895	287020	0.0021	1.0869
chr13	115169878	31926	0.0003	0.0836
chr14	107349540	100313	0.0009	0.647
chr15	102531392	433672	0.0042	3.1333
chr16	90354753	565167	0.0063	4.0376
chr17	81195210	108466	0.0013	0.7532
chr18	78077248	7049	0.0001	0.0168
chr19	59128983	51348	0.0009	0.2952
chr20	63025520	5070	0.0001	0.0169
chr21	48129895	48561	0.001	0.3077
chr22	51304566	4550	0.0001	0.0155
chrMT	16571	57629142	3,477.7106	14,321.0713
chrX	155270560	5916230	0.0381	20.6532

chrY	59373566	21529	0.0004	0.13

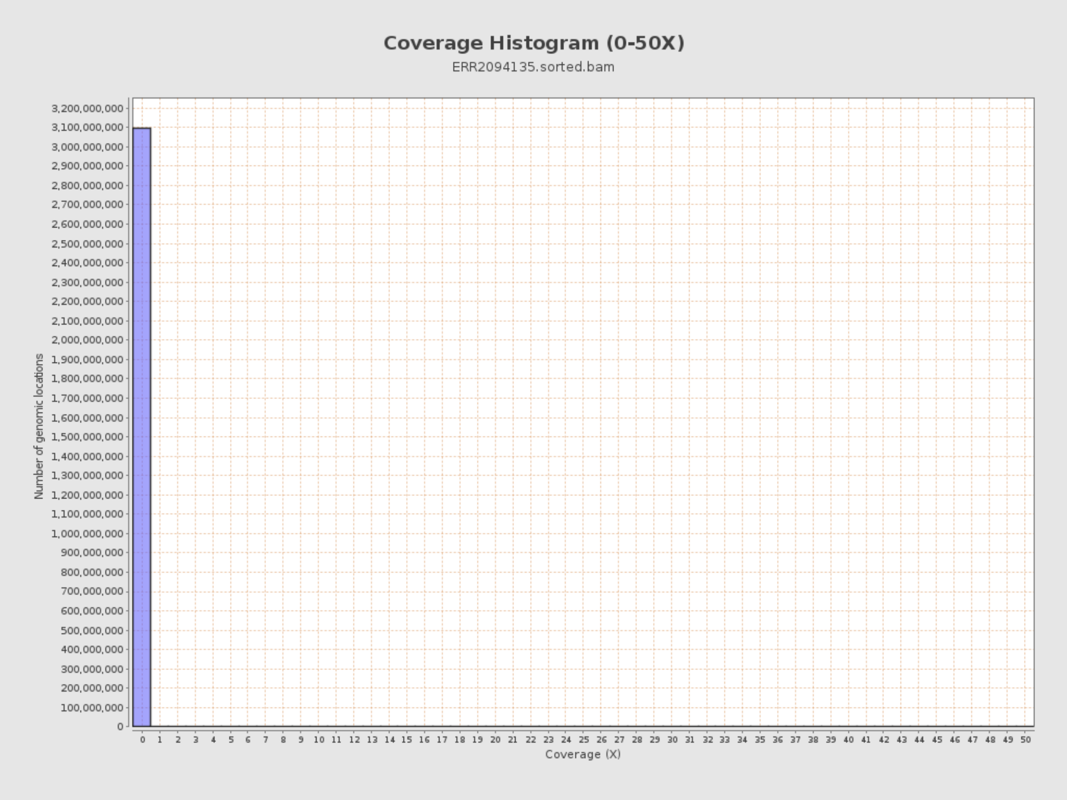
3. Results : Coverage across reference



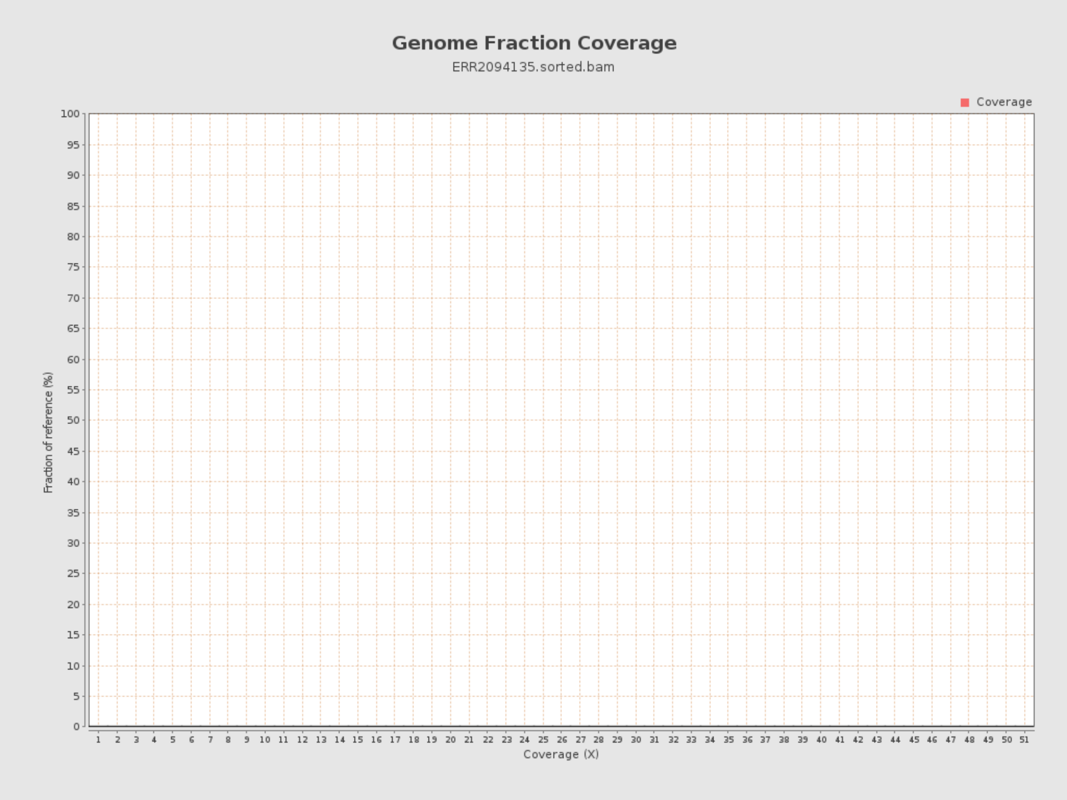
4. Results : Coverage Histogram



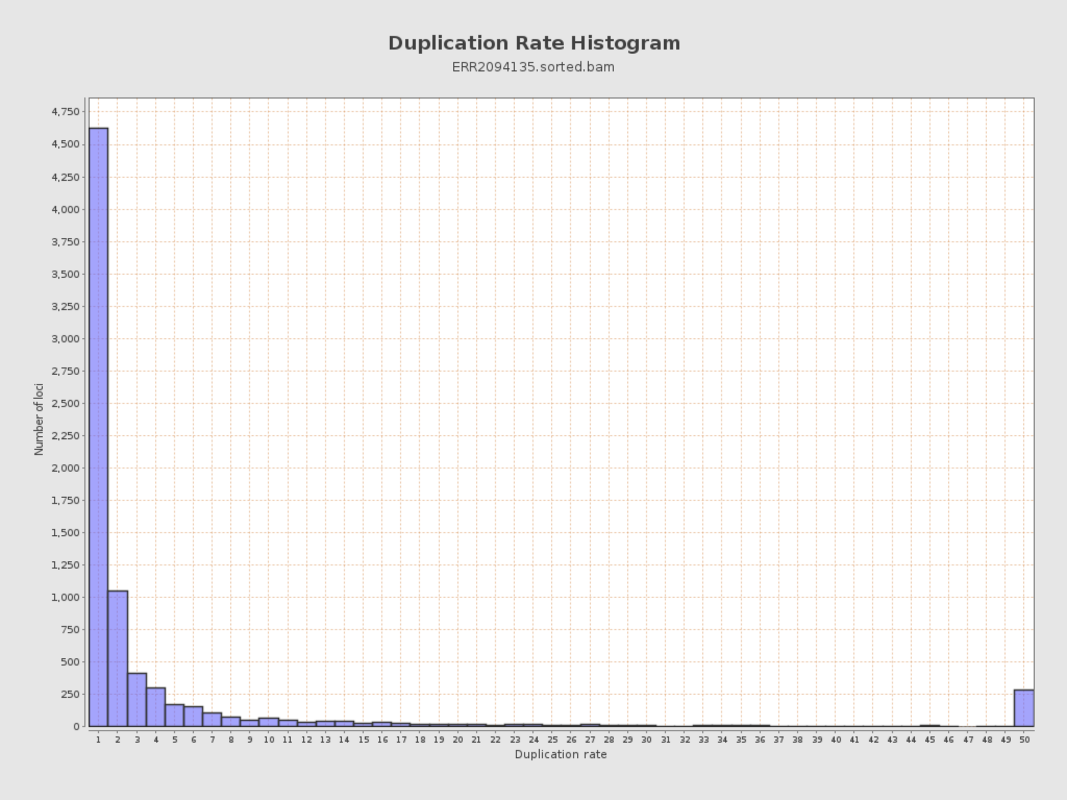
5. Results : Coverage Histogram (0-50X)



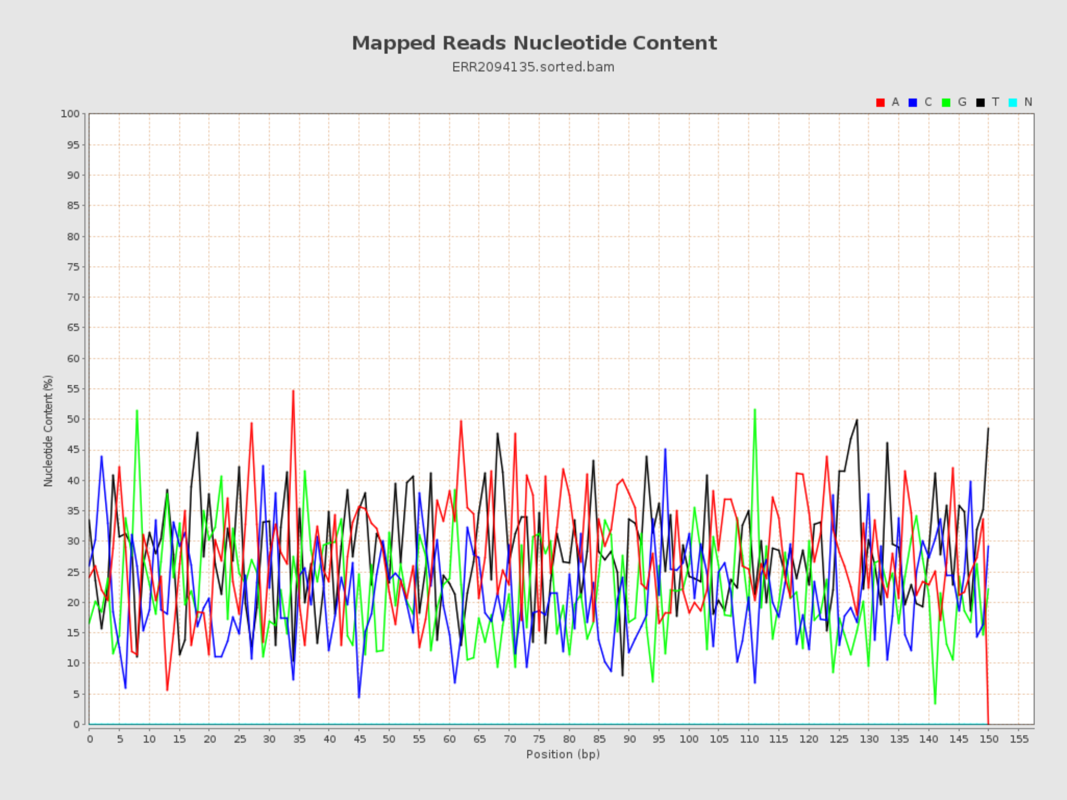
6. Results : Genome Fraction Coverage



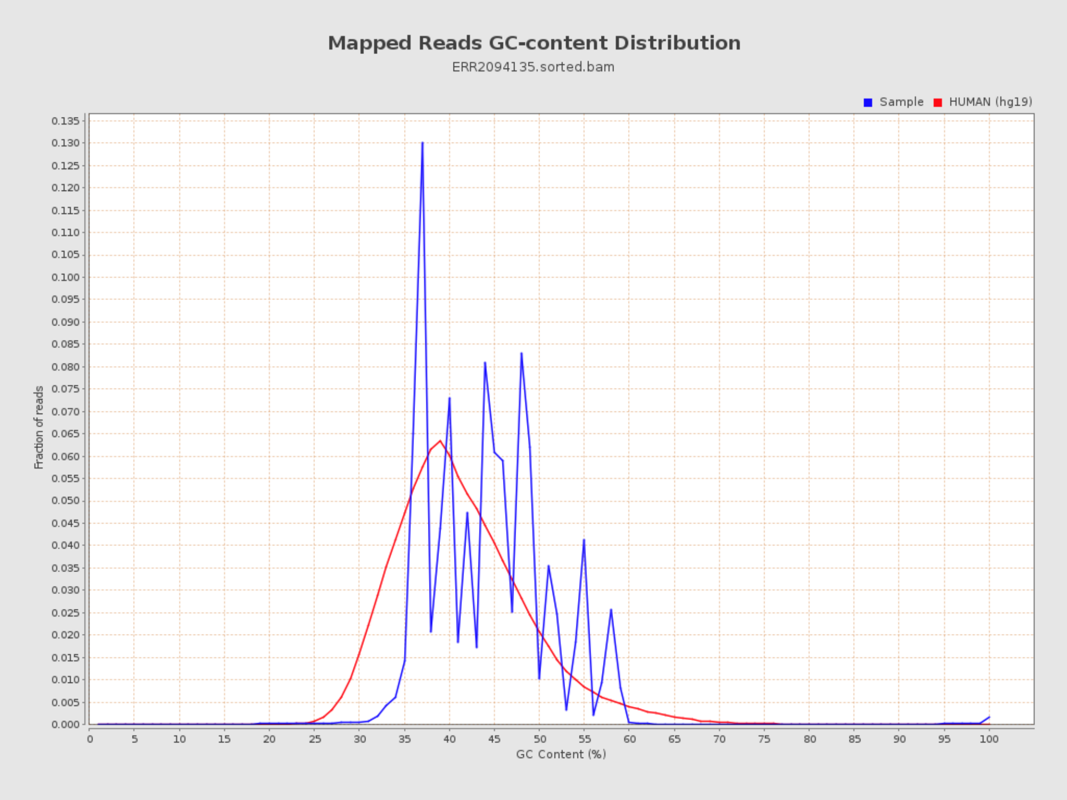
7. Results : Duplication Rate Histogram



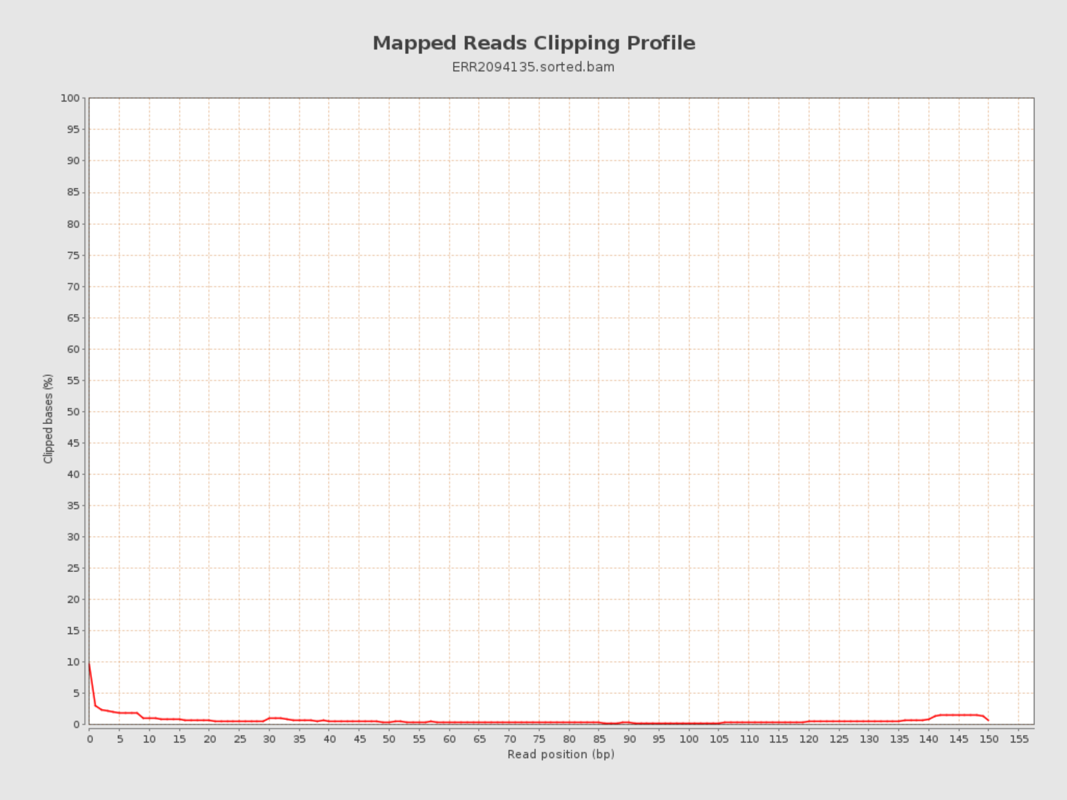
8. Results : Mapped Reads Nucleotide Content



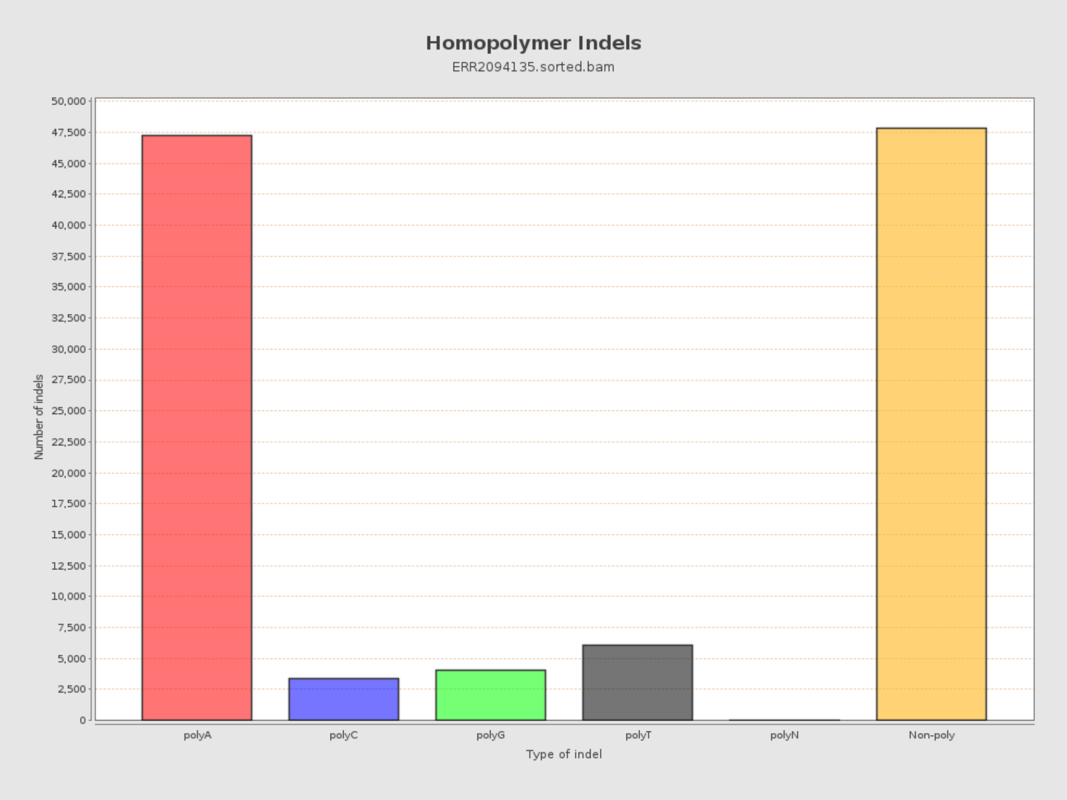
9. Results : Mapped Reads GC-content Distribution



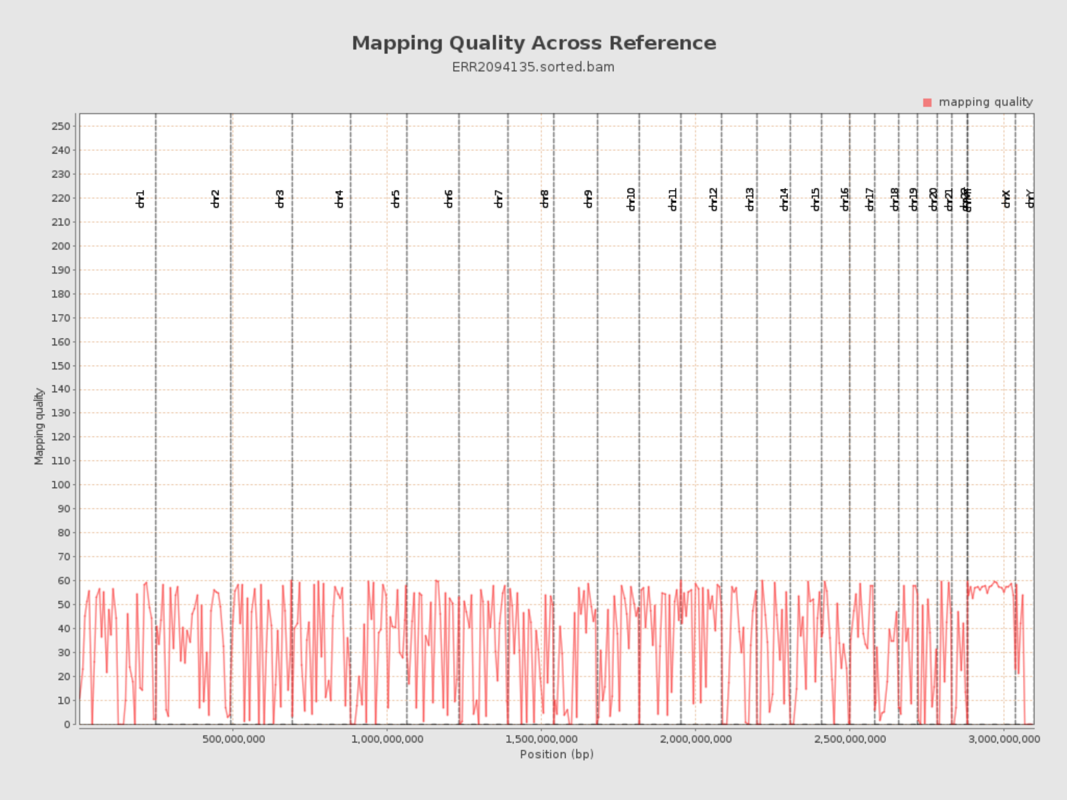
10. Results : Mapped Reads Clipping Profile



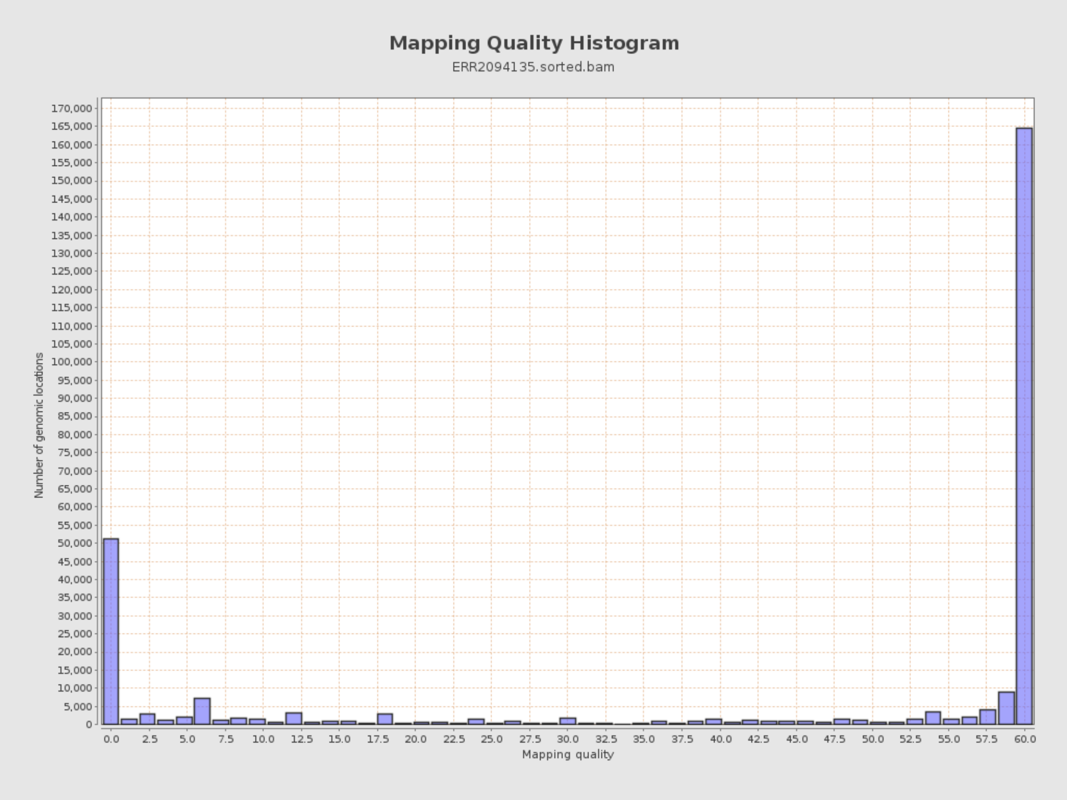
11. Results : Homopolymer Indels



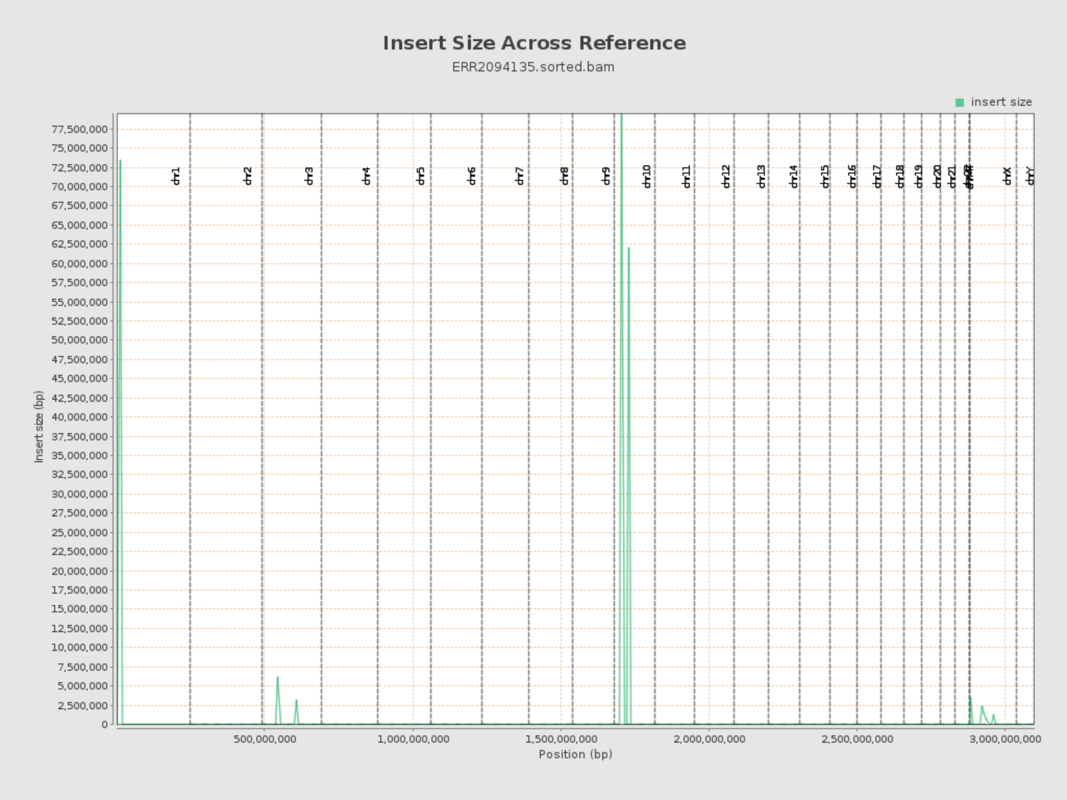
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram