Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:10:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094022.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_ERR2094022 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094022_1.fastq.gz ERR2094022_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:10:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	720,980
Mapped reads	662,202 / 91.85%
Unmapped reads	58,778 / 8.15%
Mapped paired reads	662,202 / 91.85%
Mapped reads, first in pair	332,803 / 46.16%
Mapped reads, second in pair	329,399 / 45.69%
Mapped reads, both in pair	654,854 / 90.83%
Mapped reads, singletons	7,348 / 1.02%
Secondary alignments	0
Supplementary alignments	32,715 / 4.54%
Read min/max/mean length	30 / 151 / 137.97
Duplicated reads (estimated)	629,662 / 87.33%
Duplication rate	48.17%
Clipped reads	323,411 / 44.86%

2.2. ACGT Content

Number/percentage of A's	22,844,282 / 27.76%
Number/percentage of C's	18,395,215 / 22.35%
Number/percentage of T's	21,727,299 / 26.4%
Number/percentage of G's	19,321,294 / 23.48%
Number/percentage of N's	844 / 0%

GC Percentage	45.83%

2.3. Coverage

Mean	0.0272
Standard Deviation	7.117

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Insert size

Mean	602,526.62
Standard Deviation	7,050,990.24
P25/Median/P75	126 / 160 / 201

2.6. Mismatches and indels

General error rate	3.9%
Mismatches	3,114,288
Insertions	50,170
Mapped reads with at least one insertion	7.46%
Deletions	242,061
Mapped reads with at least one deletion	35.22%
Homopolymer indels	29.05%

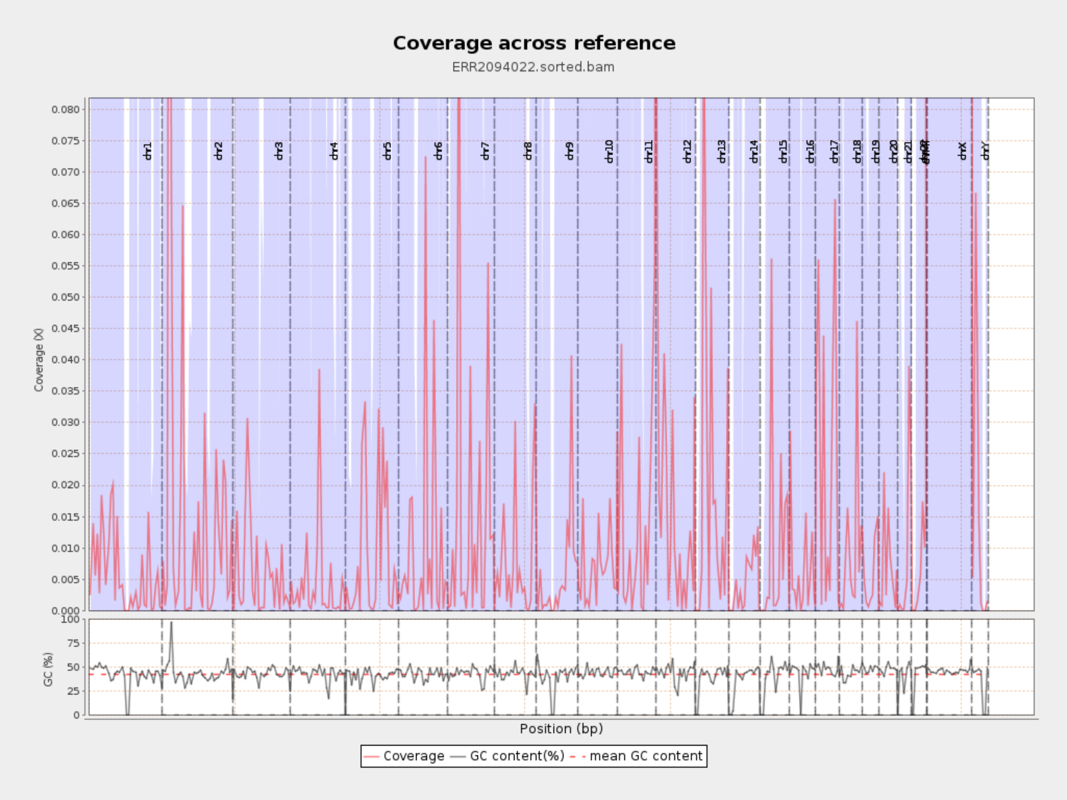
2.7. Chromosome stats

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

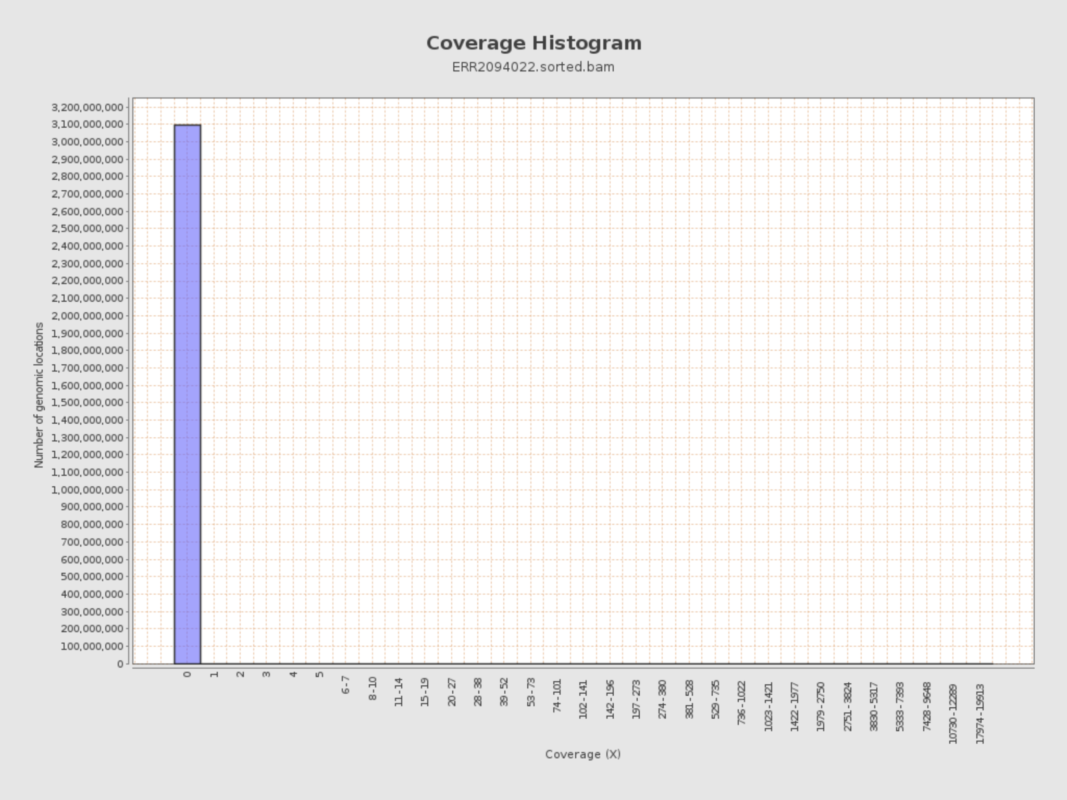
		bases	coverage	deviation
chr1	249250621	1480566	0.0059	1.7472
chr2	243199373	4341140	0.0179	4.4225
chr3	198022430	1196710	0.006	1.6204
chr4	191154276	800145	0.0042	1.0855
chr5	180915260	1609007	0.0089	3.0751
chr6	171115067	1653398	0.0097	3.5511
chr7	159138663	2594919	0.0163	4.3676
chr8	146364022	1167608	0.008	1.9913
chr9	141213431	835561	0.0059	1.3685
chr10	135534747	928578	0.0069	1.3633
chr11	135006516	2263971	0.0168	3.6341
chr12	133851895	2091662	0.0156	3.6042
chr13	115169878	2139116	0.0186	4.2796
chr14	107349540	510528	0.0048	0.9882
chr15	102531392	1003843	0.0098	2.9999
chr16	90354753	532293	0.0059	1.5759
chr17	81195210	2035251	0.0251	5.0408
chr18	78077248	747143	0.0096	3.1685
chr19	59128983	331250	0.0056	1.2288
chr20	63025520	446556	0.0071	1.9494
chr21	48129895	462412	0.0096	2.8594
chr22	51304566	299519	0.0058	1.0057
chrMT	16571	8195217	494.5517	2,139.3573
chrX	155270560	45641994	0.294	18.1645

chrY	59373566	808953	0.0136	3.899

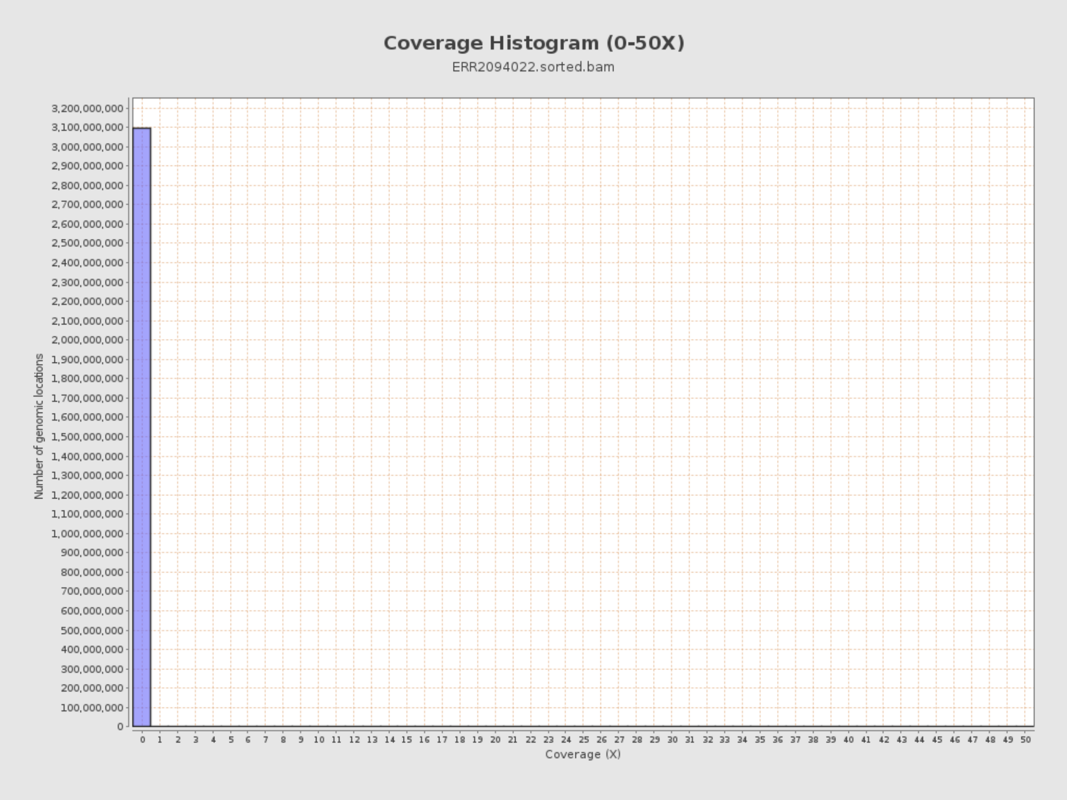
3. Results : Coverage across reference



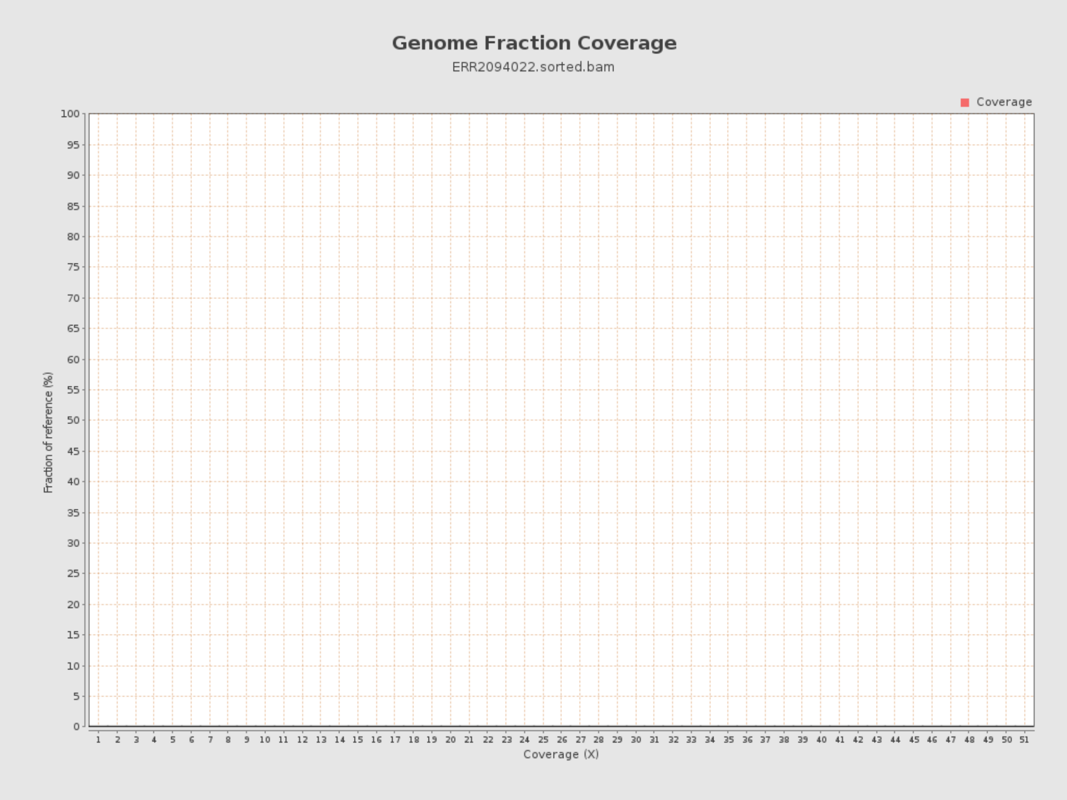
4. Results : Coverage Histogram



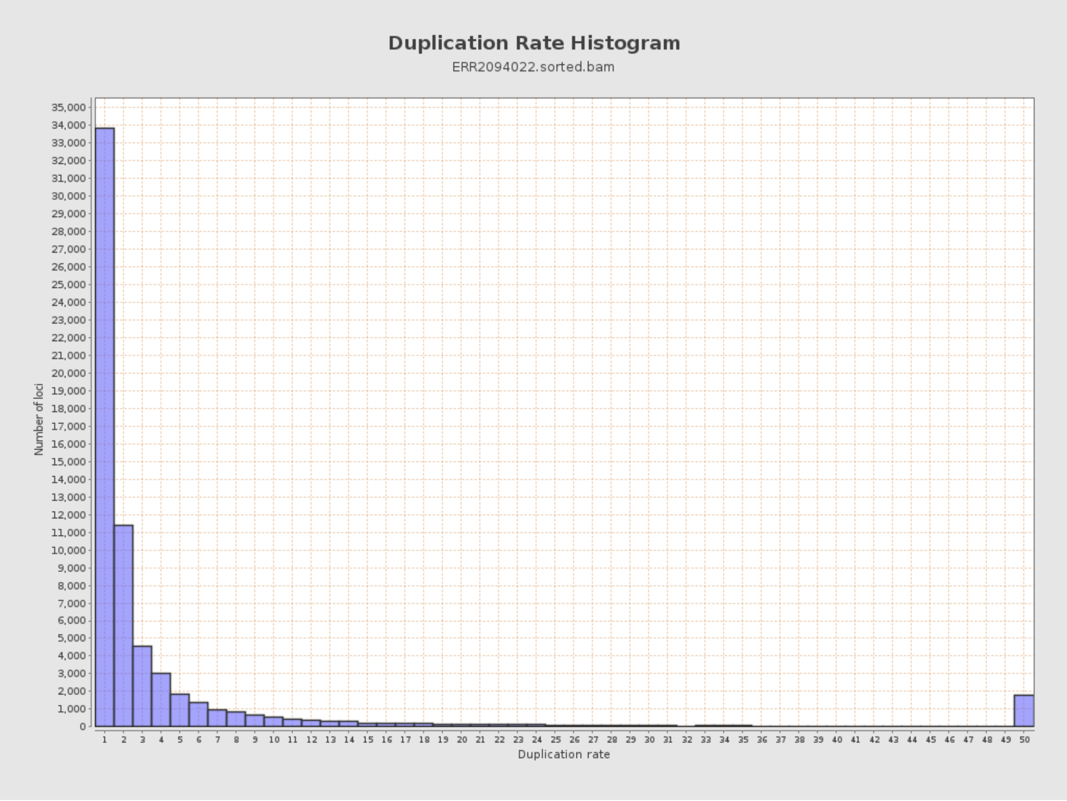
5. Results : Coverage Histogram (0-50X)



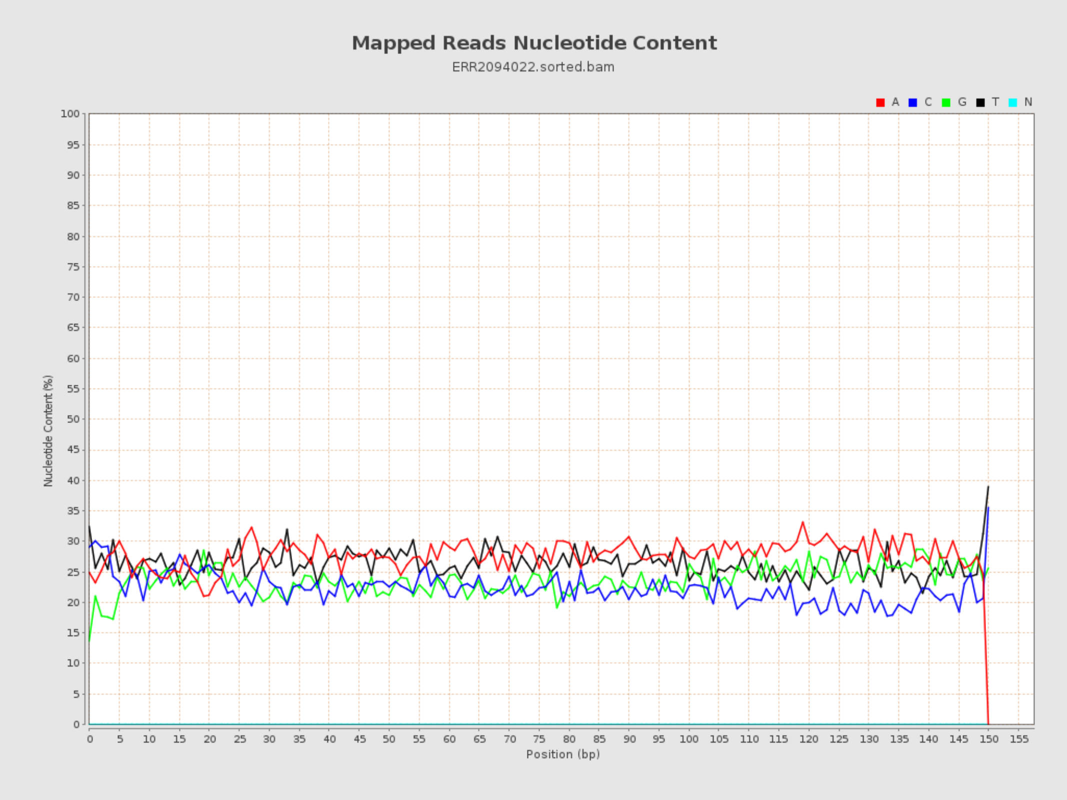
6. Results : Genome Fraction Coverage



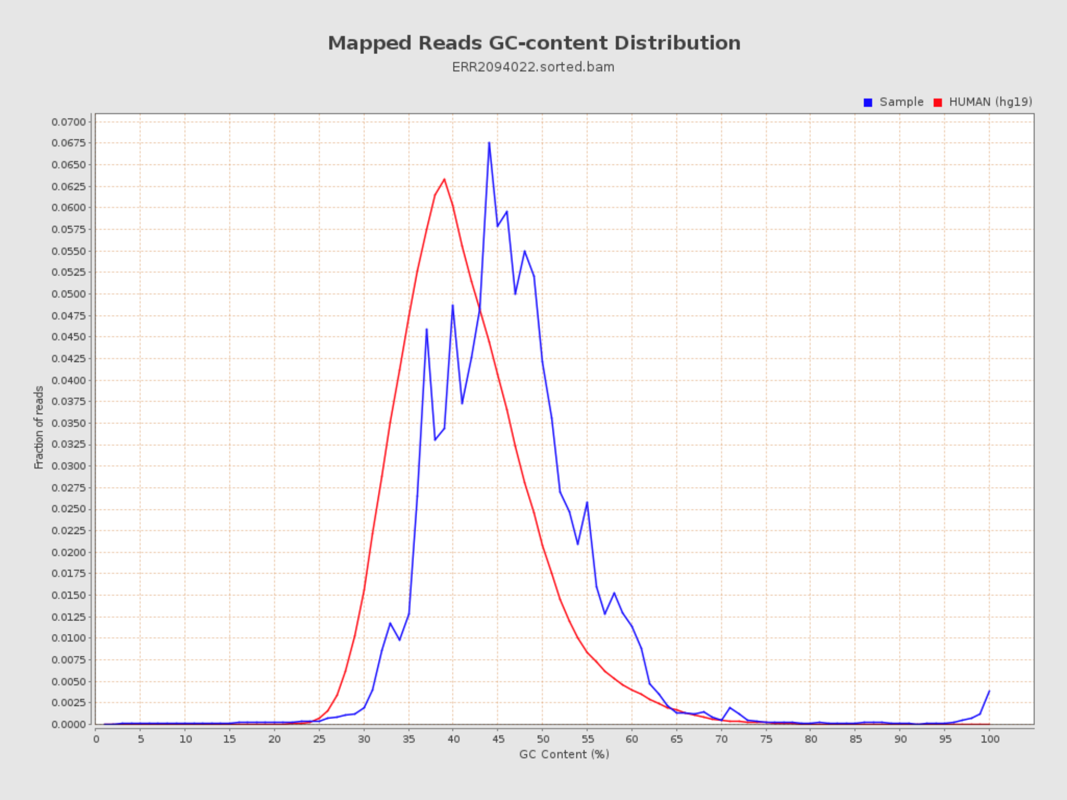
7. Results : Duplication Rate Histogram



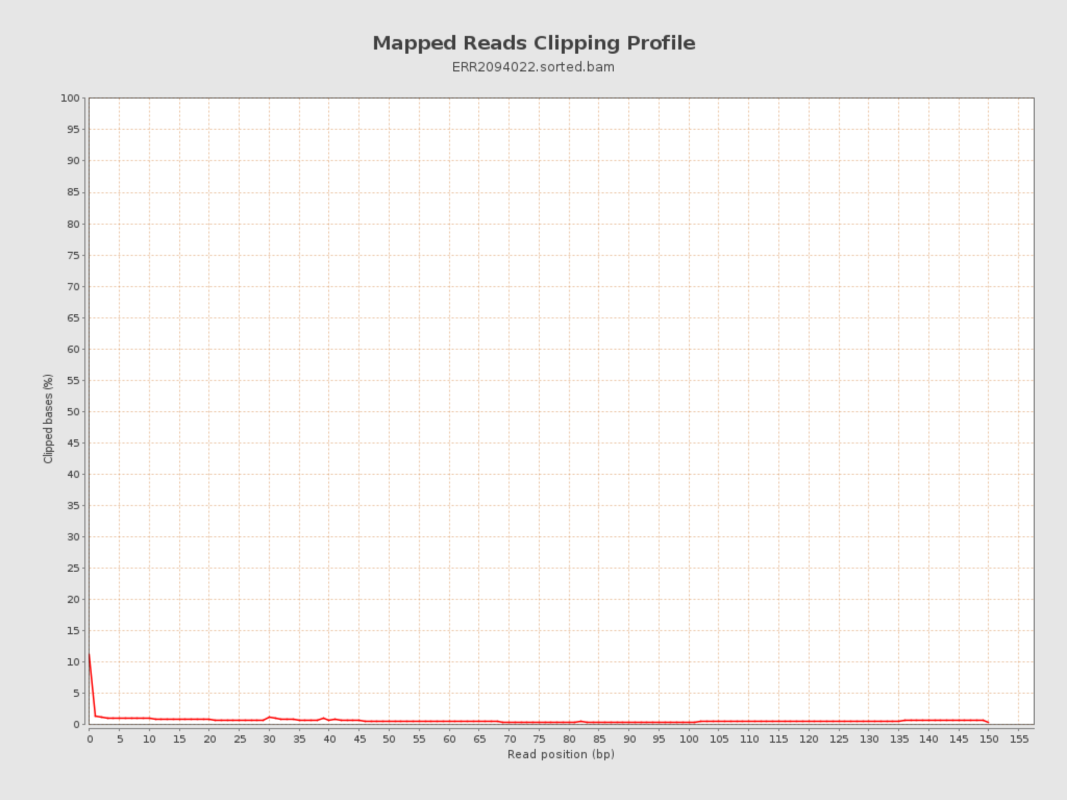
8. Results : Mapped Reads Nucleotide Content



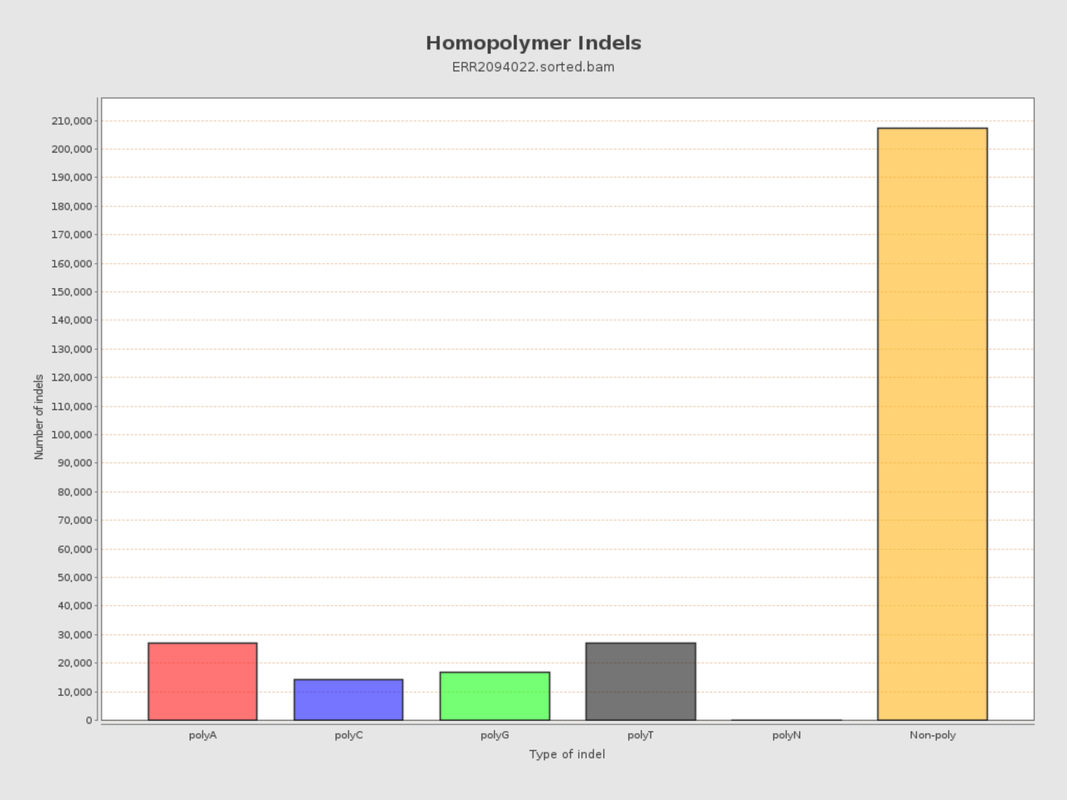
9. Results : Mapped Reads GC-content Distribution



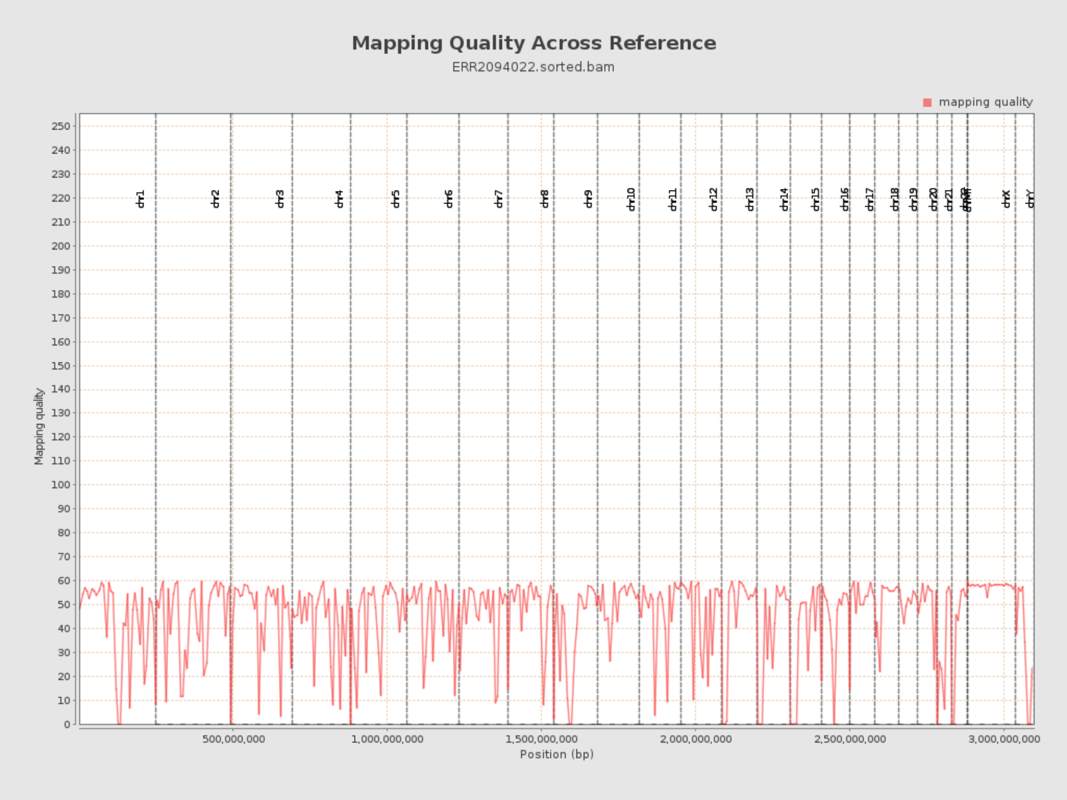
10. Results : Mapped Reads Clipping Profile



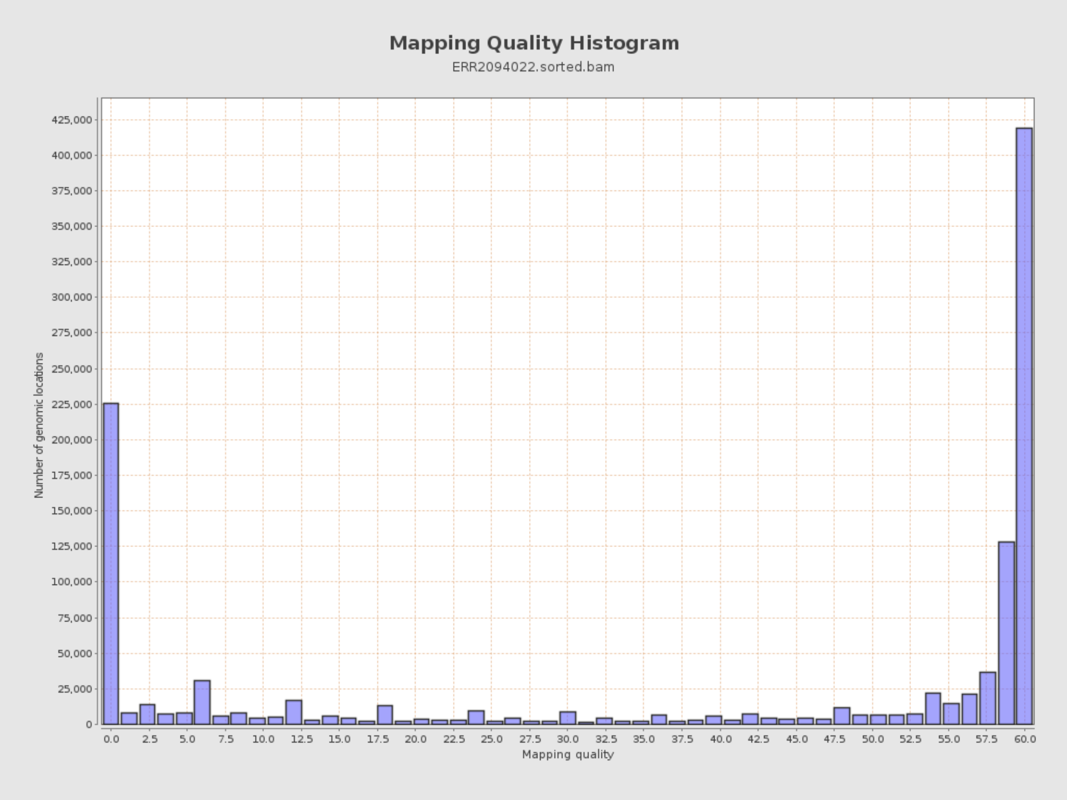
11. Results : Homopolymer Indels



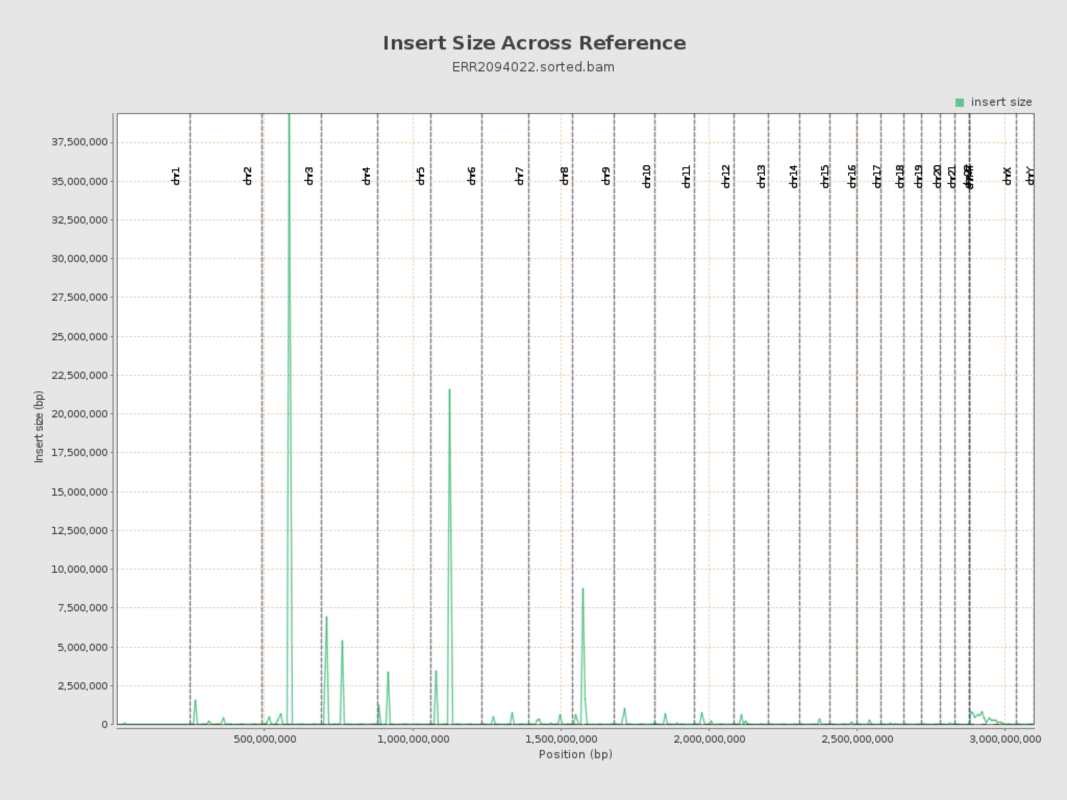
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram