Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:33:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094004.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_ERR2094004 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094004_1.fastq.gz ERR2094004_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:33:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	491,890
Mapped reads	413,426 / 84.05%
Unmapped reads	78,464 / 15.95%
Mapped paired reads	413,426 / 84.05%
Mapped reads, first in pair	207,130 / 42.11%
Mapped reads, second in pair	206,296 / 41.94%
Mapped reads, both in pair	410,548 / 83.46%
Mapped reads, singletons	2,878 / 0.59%
Secondary alignments	0
Supplementary alignments	957 / 0.19%
Read min/max/mean length	30 / 151 / 134.83
Duplicated reads (estimated)	408,377 / 83.02%
Duplication rate	46.17%
Clipped reads	91,231 / 18.55%

2.2. ACGT Content

Number/percentage of A's	17,166,364 / 29.04%
Number/percentage of C's	12,135,702 / 20.53%
Number/percentage of T's	16,928,000 / 28.64%
Number/percentage of G's	12,878,628 / 21.79%
Number/percentage of N's	604 / 0%

GC Percentage	42.32%

2.3. Coverage

Mean	0.0192
Standard Deviation	29.9144

2.4. Mapping Quality

Mean Mapping Quality	26.23

2.5. Insert size

Mean	26,463.88
Standard Deviation	1,908,372.43
P25/Median/P75	181 / 217 / 237

2.6. Mismatches and indels

General error rate	2.38%
Mismatches	1,398,352
Insertions	6,799
Mapped reads with at least one insertion	1.6%
Deletions	82,647
Mapped reads with at least one deletion	19.55%
Homopolymer indels	31.91%

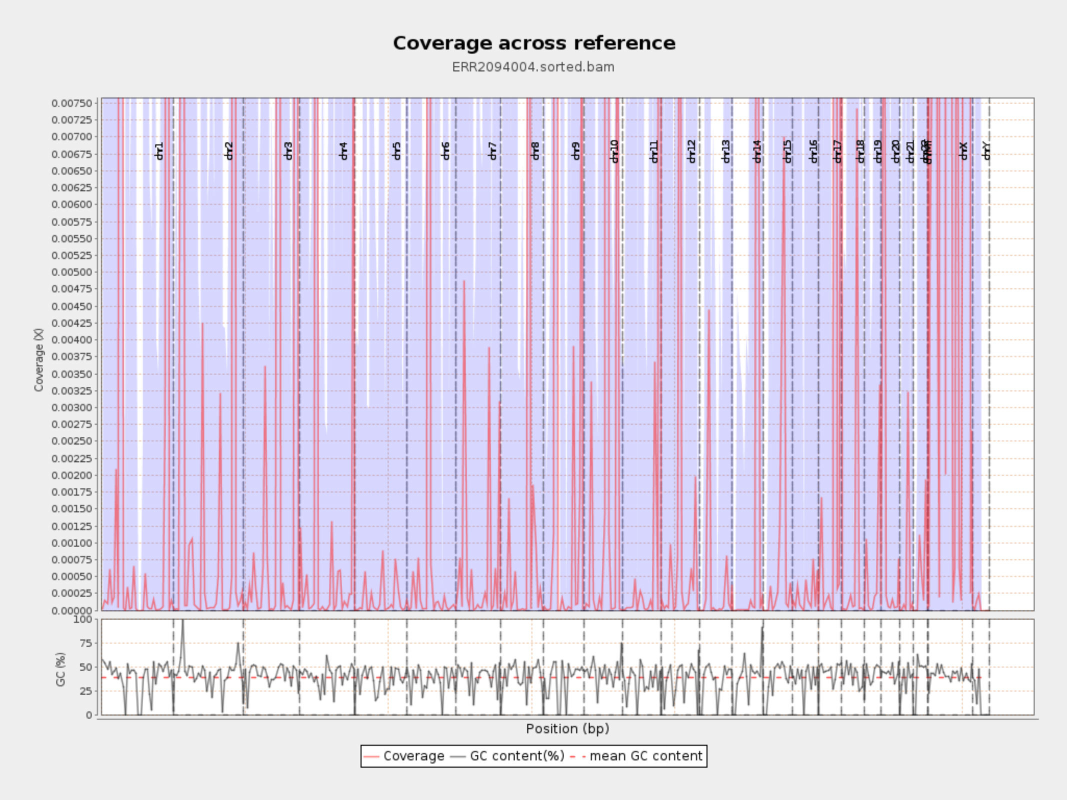
2.7. Chromosome stats

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

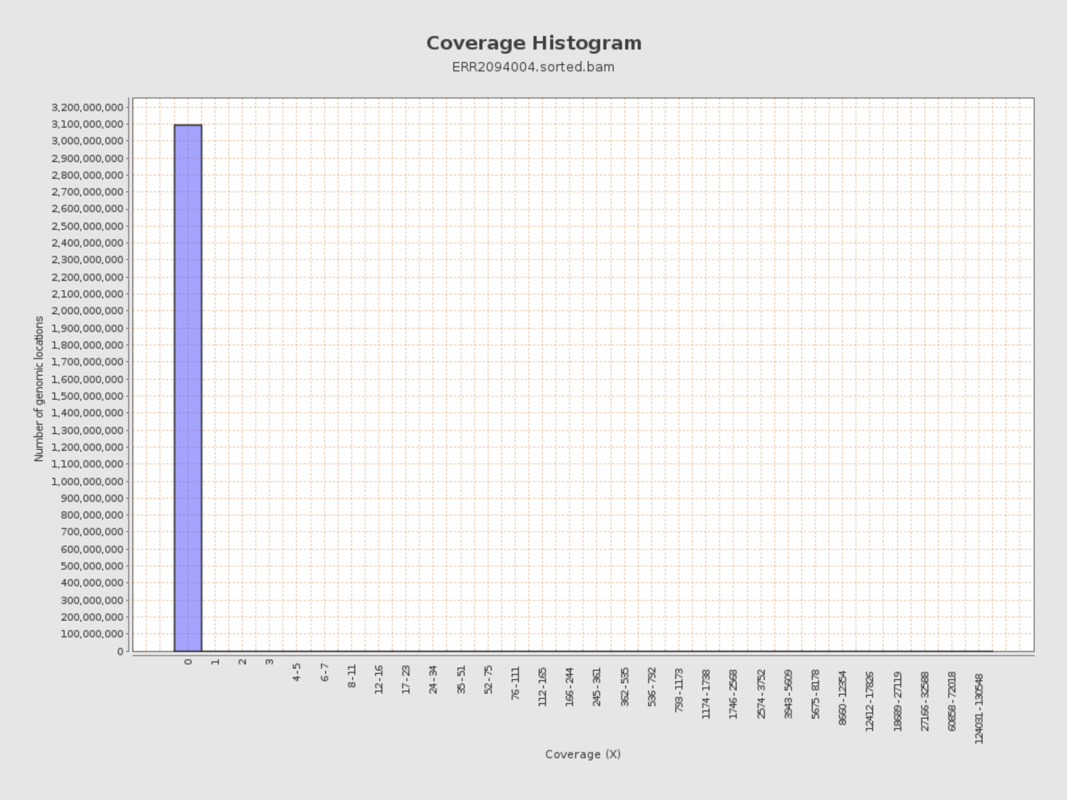
		bases	**coverage**	**deviation**
chr1	249250621	944367	0.0038	3.0249
chr2	243199373	971849	0.004	2.5705
chr3	198022430	521997	0.0026	1.9174
chr4	191154276	337081	0.0018	1.2511
chr5	180915260	26156	0.0001	0.053
chr6	171115067	358075	0.0021	2.0763
chr7	159138663	116433	0.0007	0.3576
chr8	146364022	221583	0.0015	1.3697
chr9	141213431	1075246	0.0076	4.4121
chr10	135534747	2250432	0.0166	13.5927
chr11	135006516	904226	0.0067	5.7035
chr12	133851895	154587	0.0012	0.9703
chr13	115169878	45183	0.0004	0.2421
chr14	107349540	134911	0.0013	1.017
chr15	102531392	109374	0.0011	0.496
chr16	90354753	21073	0.0002	0.0645
chr17	81195210	621762	0.0077	4.2039
chr18	78077248	61873	0.0008	0.6197
chr19	59128983	38535	0.0007	0.2676
chr20	63025520	124236	0.002	1.1417
chr21	48129895	26516	0.0006	0.2785
chr22	51304566	29271	0.0006	0.1604
chrMT	16571	36919934	2,227.9847	12,135.8354
chrX	155270560	13519219	0.0871	36.5614

chrY	59373566	3511	0.0001	0.0196

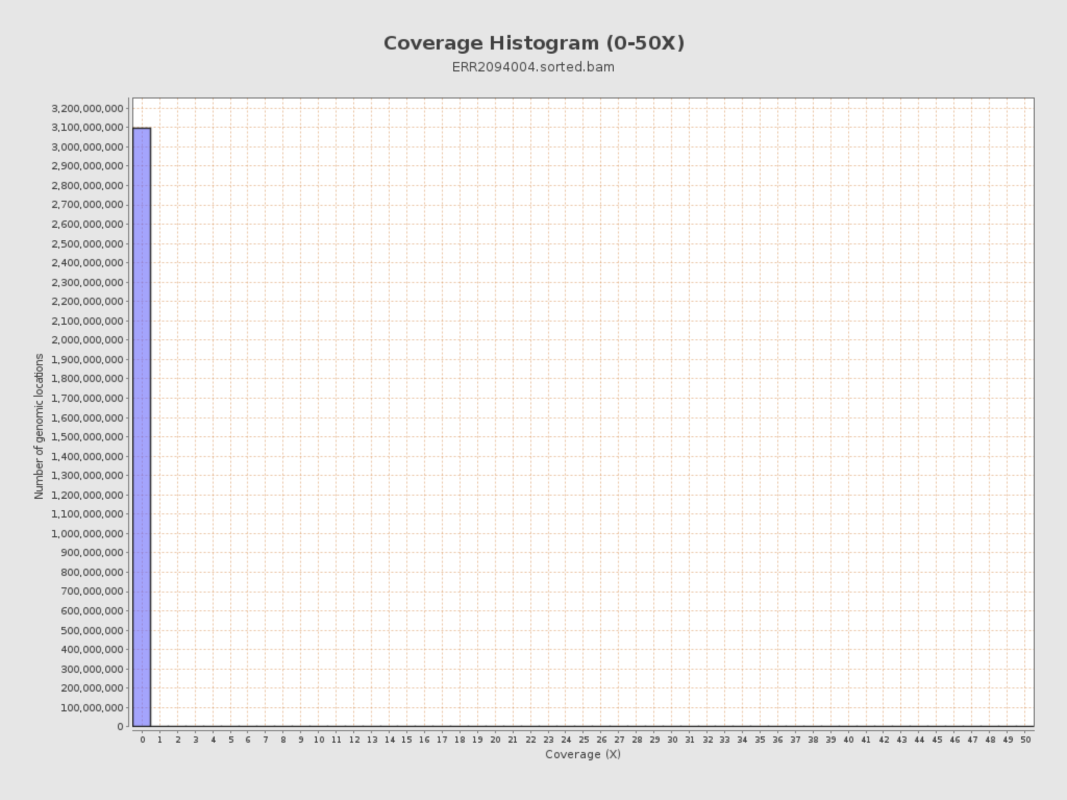
3. Results : Coverage across reference



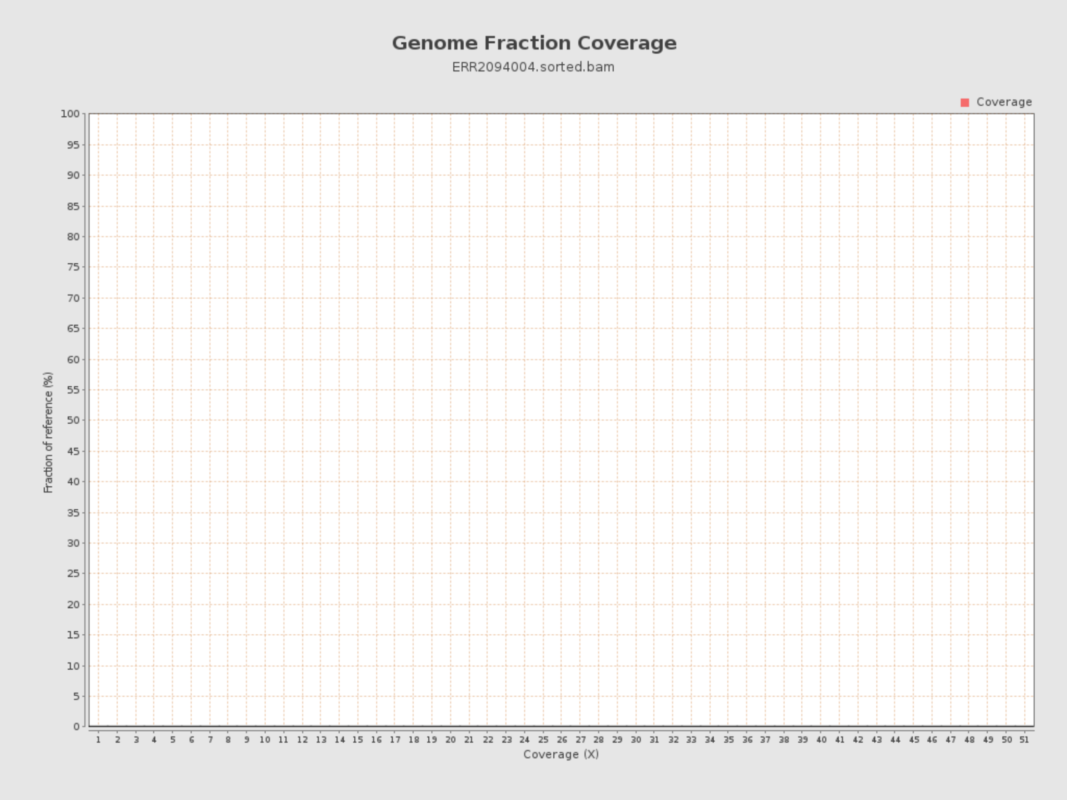
4. Results : Coverage Histogram



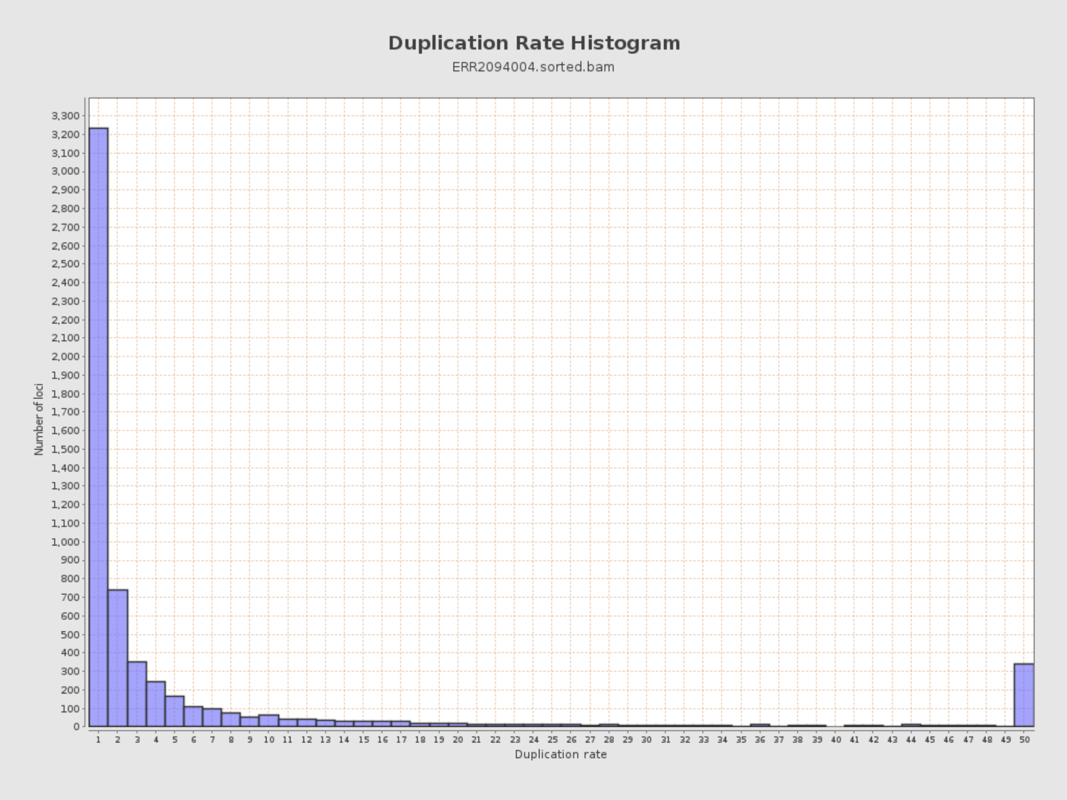
5. Results : Coverage Histogram (0-50X)



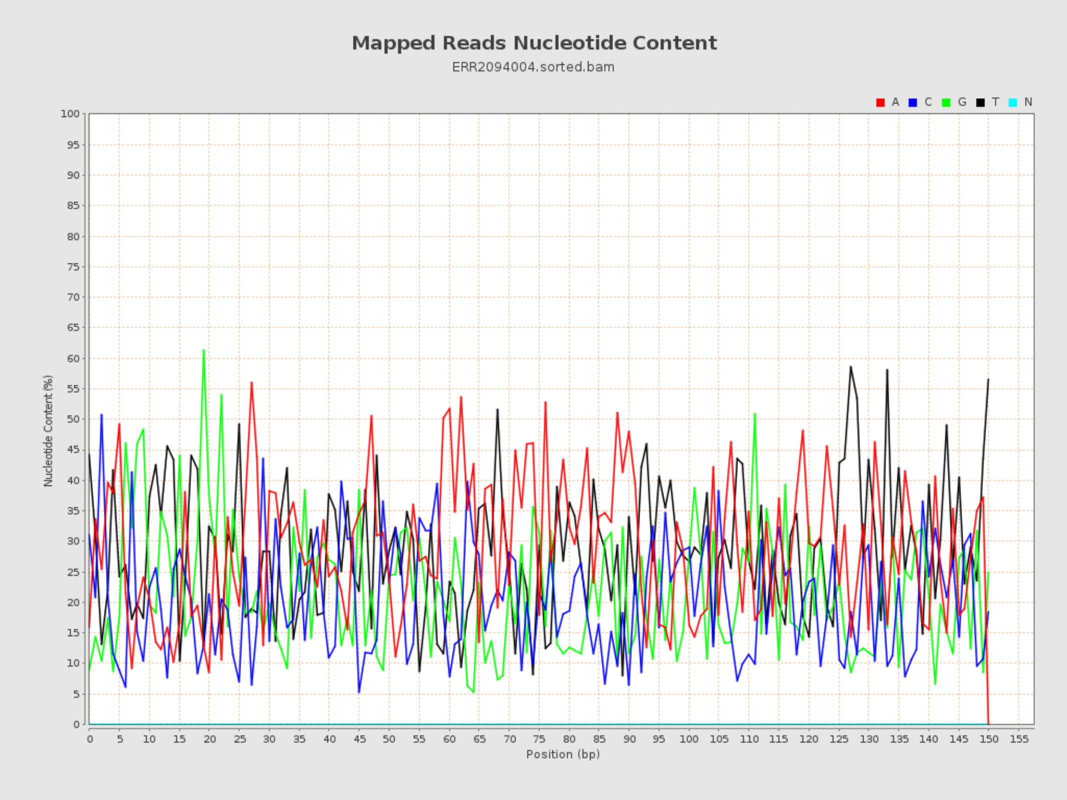
6. Results : Genome Fraction Coverage



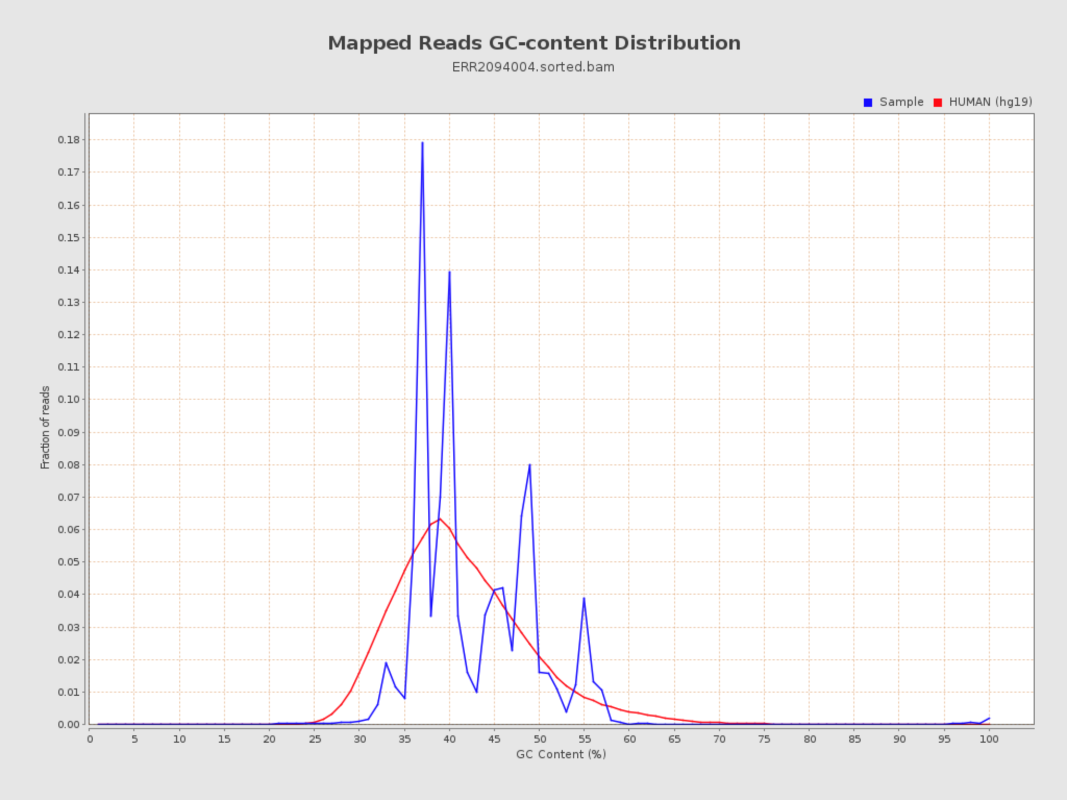
7. Results : Duplication Rate Histogram



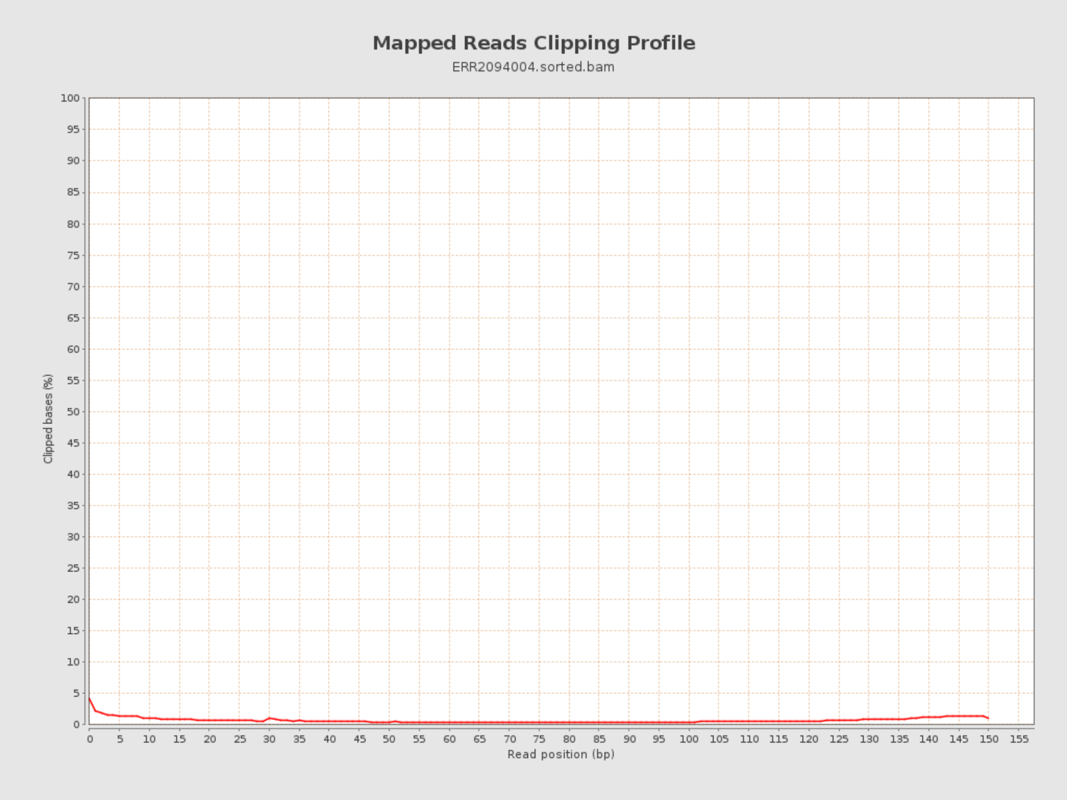
8. Results : Mapped Reads Nucleotide Content



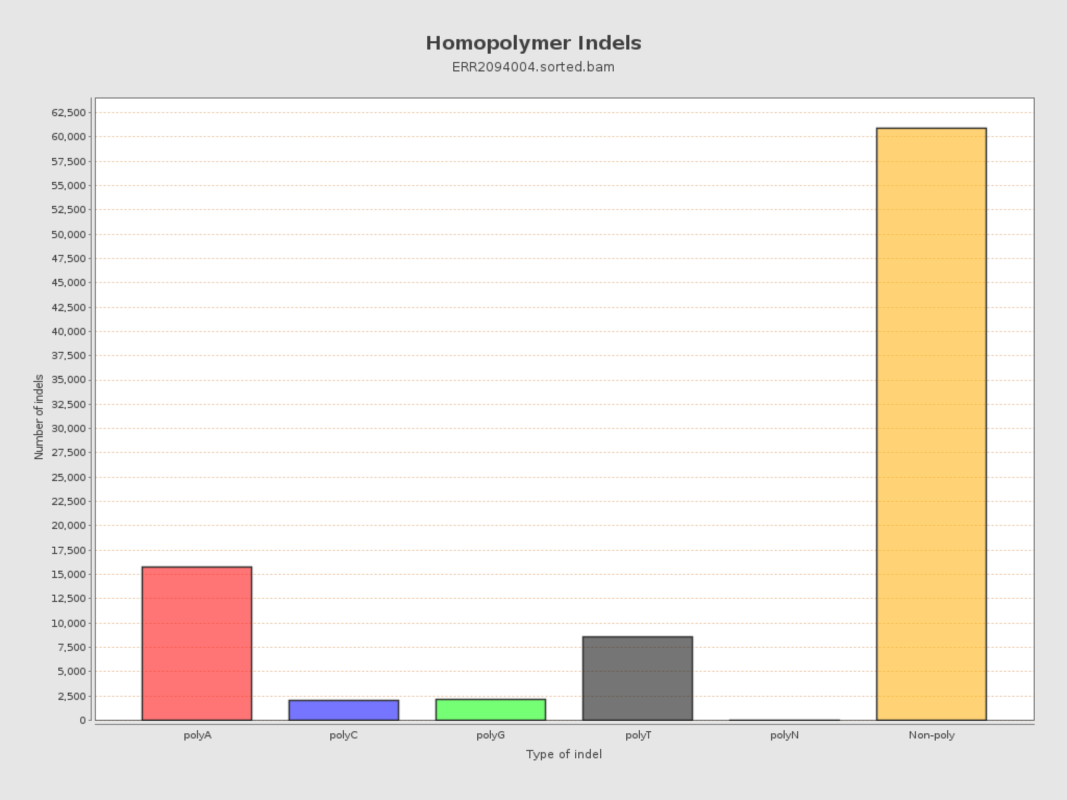
9. Results : Mapped Reads GC-content Distribution



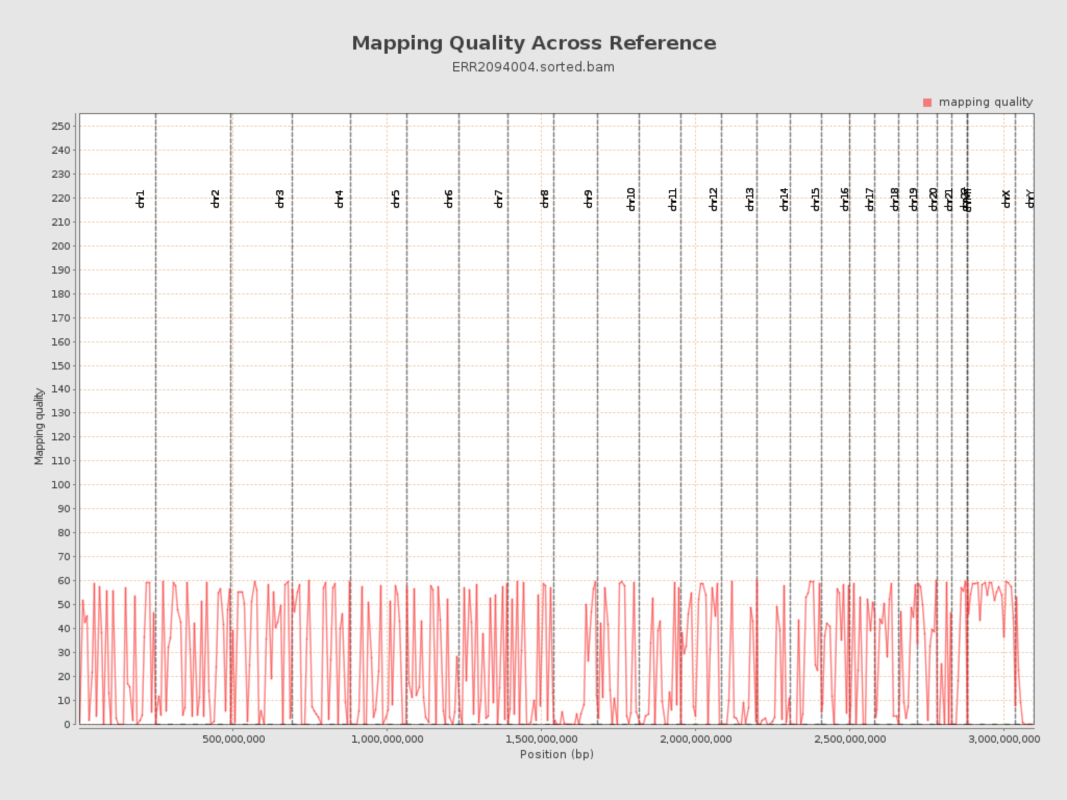
10. Results : Mapped Reads Clipping Profile



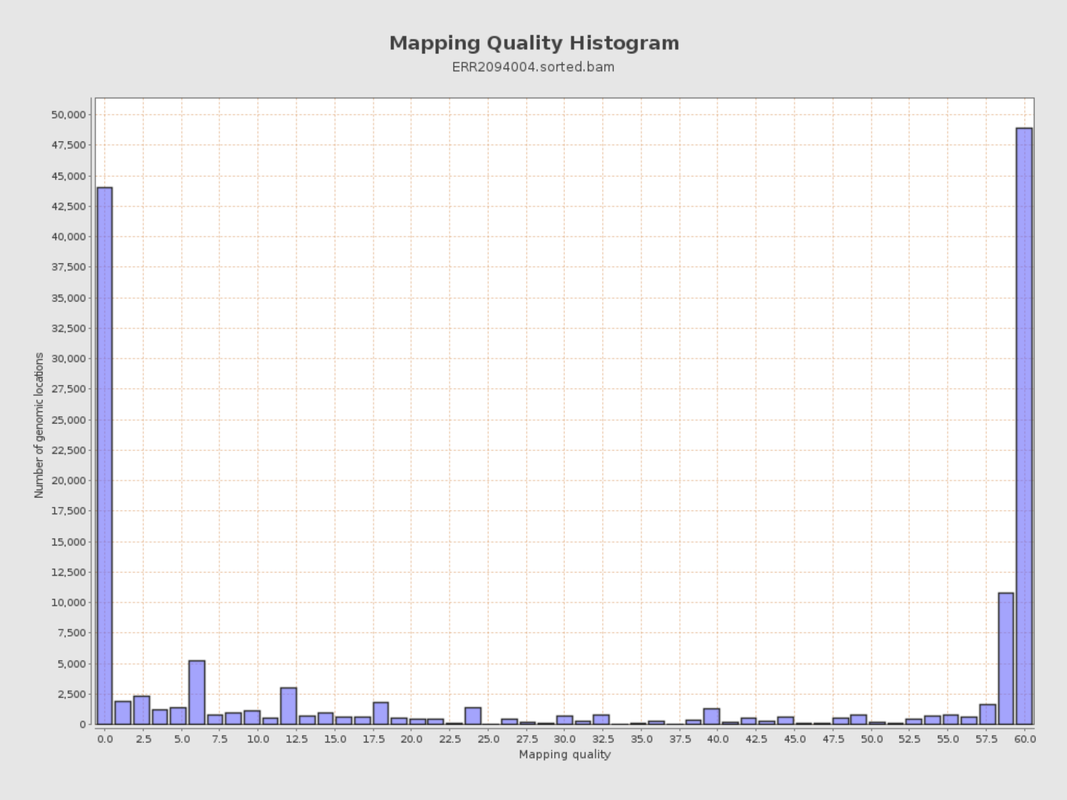
11. Results : Homopolymer Indels



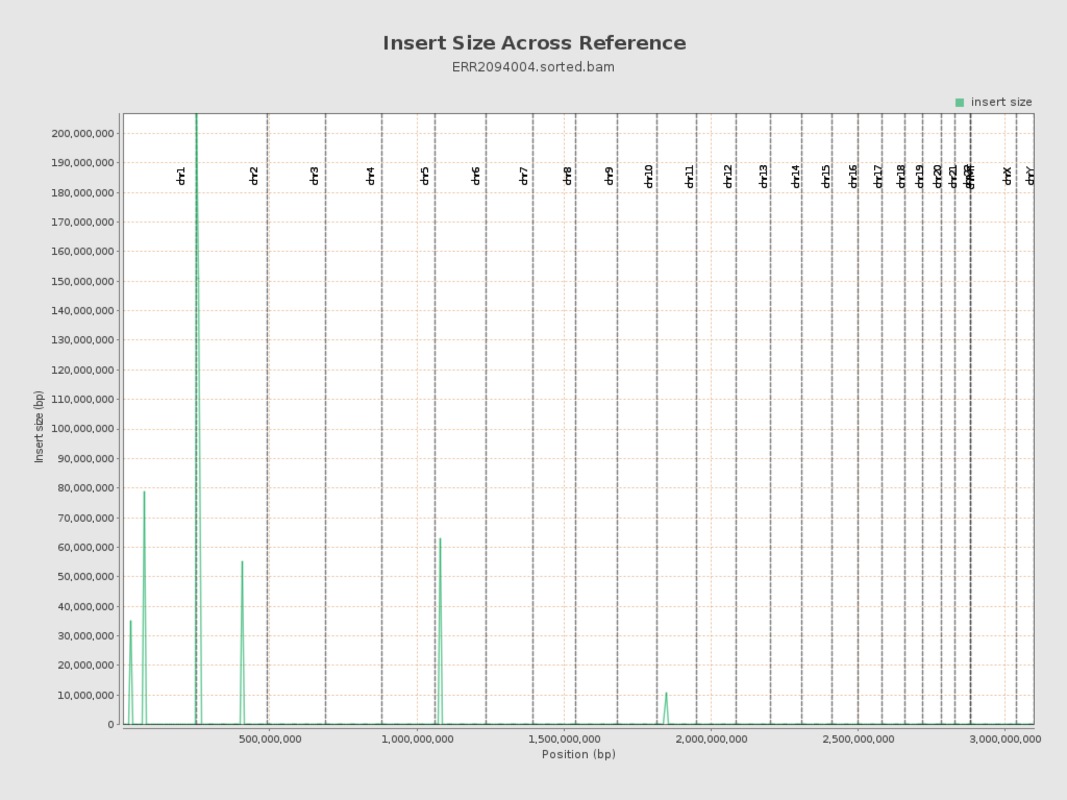
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram