Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:56:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714064.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_ERR9714064 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:56:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	426,634
Mapped reads	183,171 / 42.93%
Unmapped reads	243,463 / 57.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,913 / 1.62%
Read min/max/mean length	30 / 151 / 93.97
Duplicated reads (estimated)	174,271 / 40.85%
Duplication rate	36.67%
Clipped reads	163,956 / 38.43%

2.2. ACGT Content

Number/percentage of A's	5,656,655 / 25.49%
Number/percentage of C's	4,158,750 / 18.74%
Number/percentage of T's	5,494,225 / 24.76%
Number/percentage of G's	6,883,458 / 31.02%
Number/percentage of N's	385 / 0%
GC Percentage	49.75%

2.3. Coverage

Mean	0.0073

Standard Deviation	6.9781

2.4. Mapping Quality

Mean Mapping Quality	36.03

2.5. Mismatches and indels

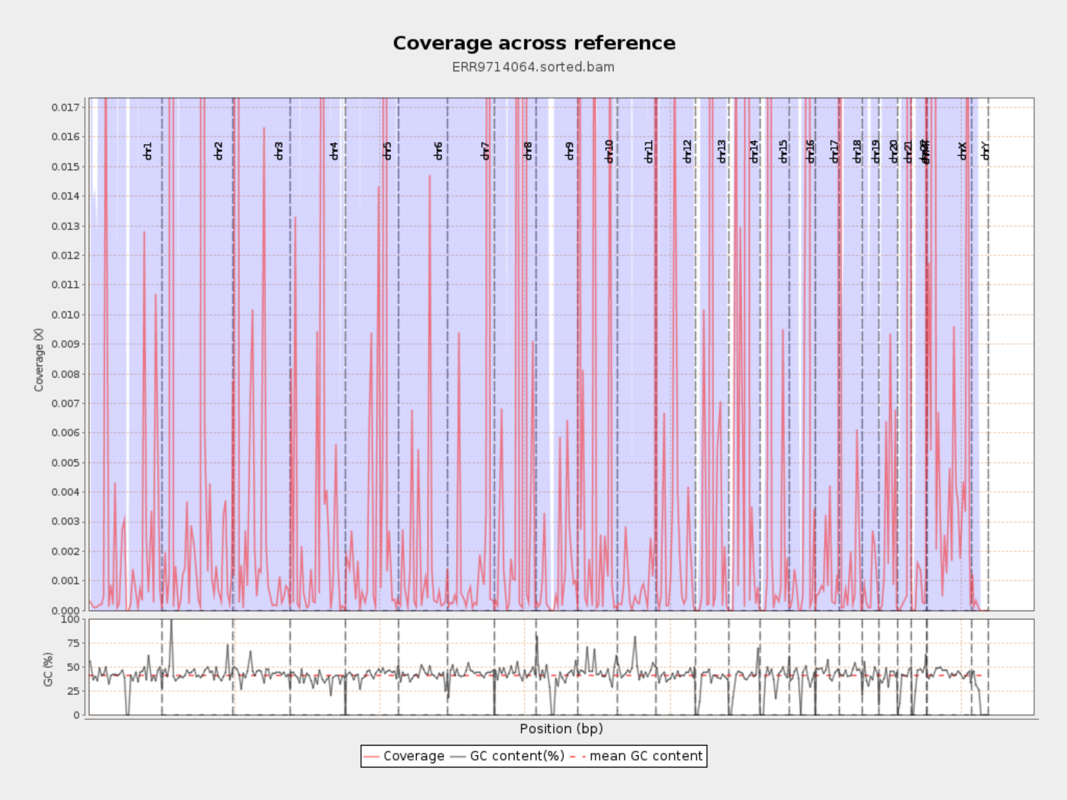
General error rate	3.86%
Mismatches	769,236
Insertions	25,398
Mapped reads with at least one insertion	13.22%
Deletions	63,532
Mapped reads with at least one deletion	33.32%
Homopolymer indels	27.31%

2.6. Chromosome stats

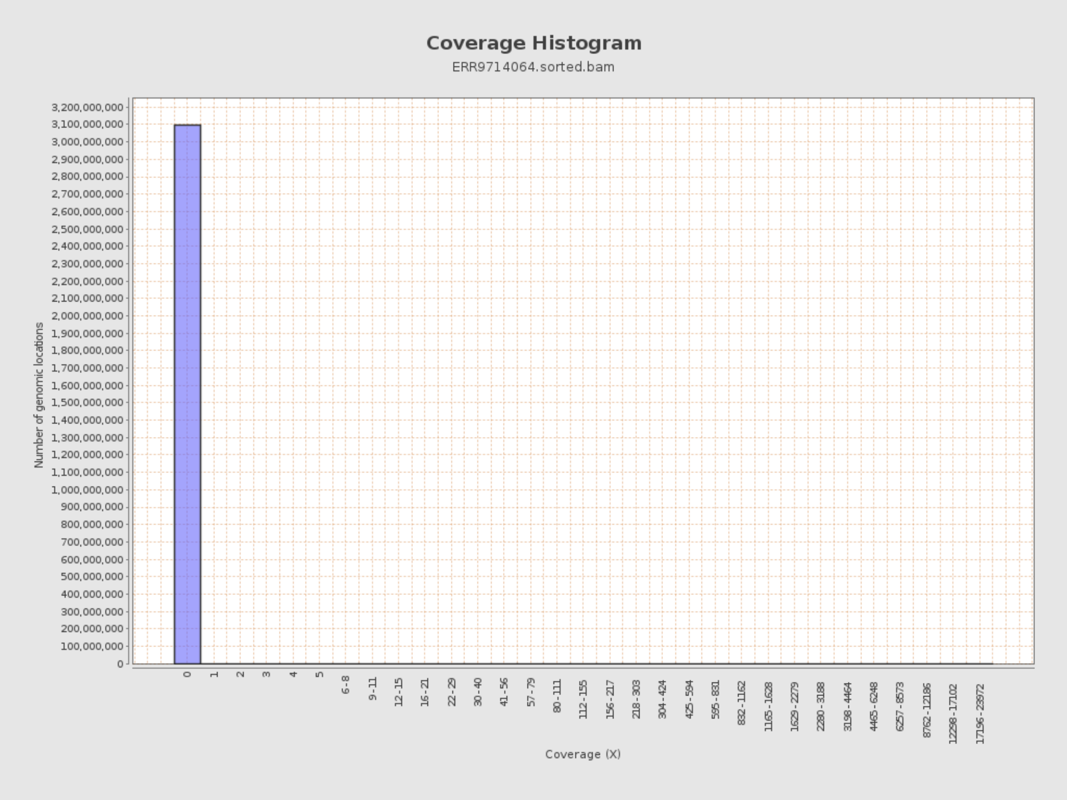
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	565381	0.0023	0.9299
chr2	243199373	4018766	0.0165	12.5713
chr3	198022430	1201145	0.0061	4.3728
chr4	191154276	711403	0.0037	1.4225
chr5	180915260	1062111	0.0059	3.8538
chr6	171115067	301735	0.0018	0.7895
chr7	159138663	606807	0.0038	2.5255

chr8	146364022	4312614	0.0295	23.1855
chr9	141213431	200462	0.0014	0.3862
chr10	135534747	865685	0.0064	2.4267
chr11	135006516	476656	0.0035	2.5101
chr12	133851895	350910	0.0026	0.6655
chr13	115169878	652671	0.0057	3
chr14	107349540	1320395	0.0123	7.2447
chr15	102531392	839185	0.0082	4.0144
chr16	90354753	1293720	0.0143	7.0543
chr17	81195210	100273	0.0012	0.3199
chr18	78077248	438502	0.0056	3.0638
chr19	59128983	53192	0.0009	0.2345
chr20	63025520	203941	0.0032	0.738
chr21	48129895	1241062	0.0258	13.7431
chr22	51304566	29374	0.0006	0.1347
chrMT	16571	298211	17.996	145.0018
chrX	155270560	1394877	0.009	2.0556
chrY	59373566	10151	0.0002	0.0602

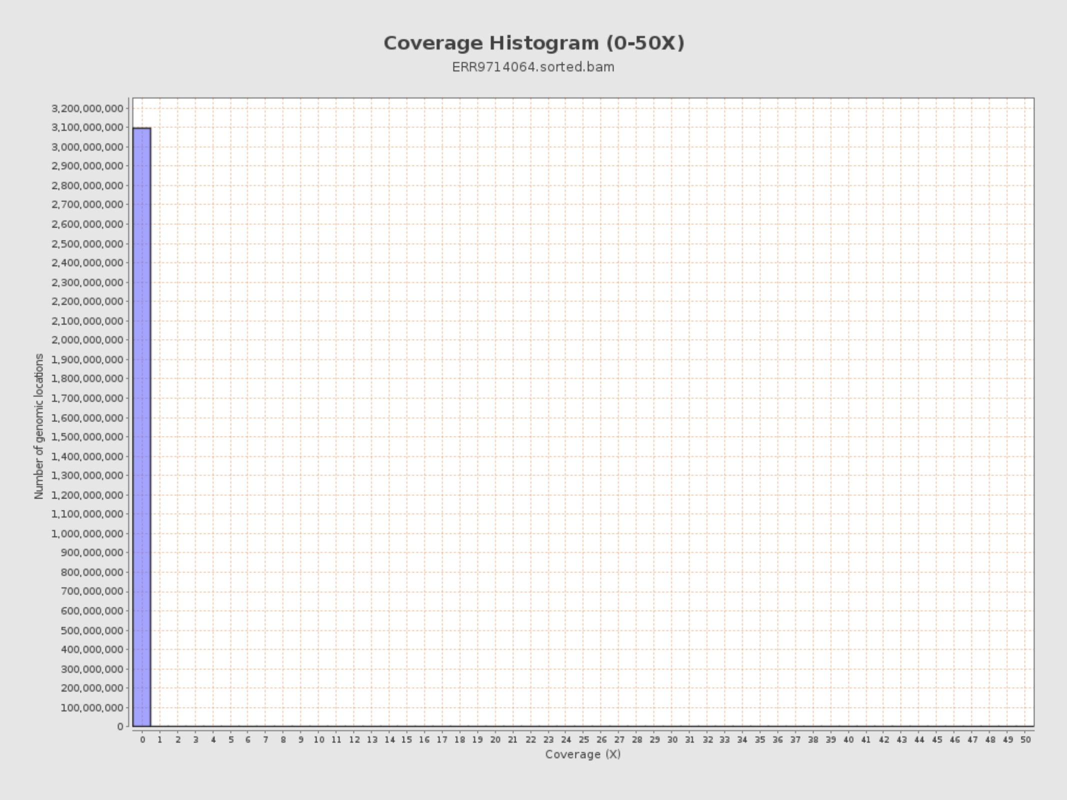
3. Results : Coverage across reference



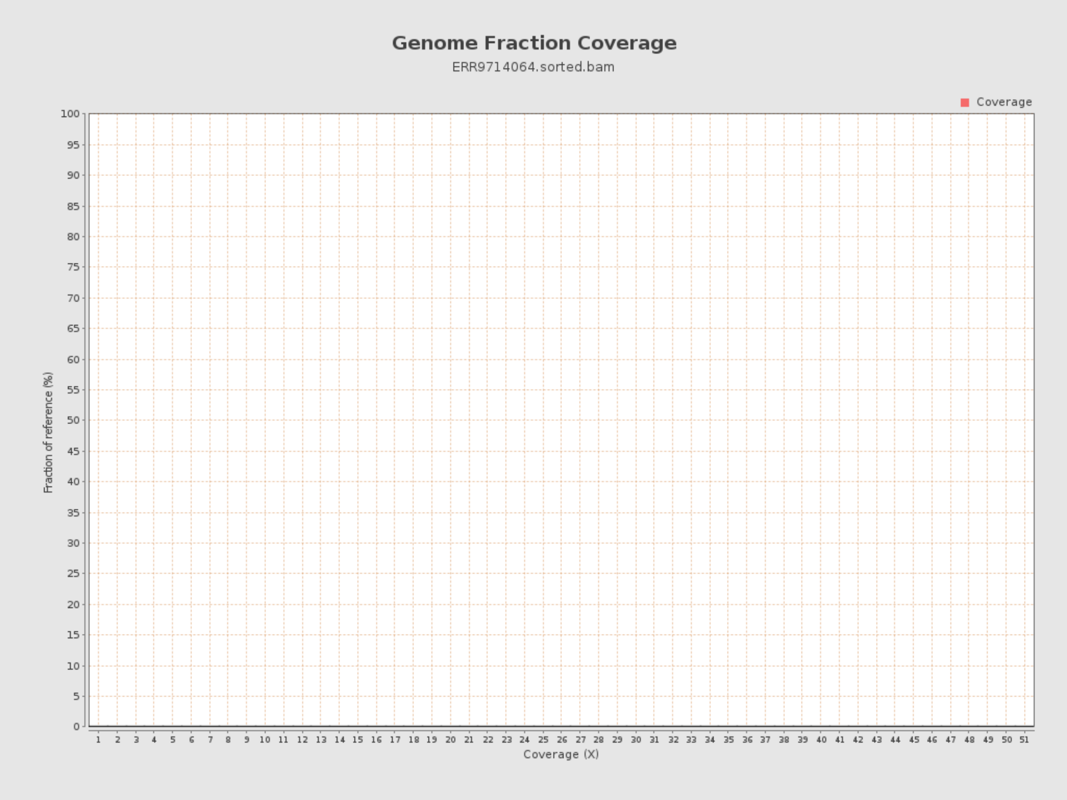
4. Results : Coverage Histogram



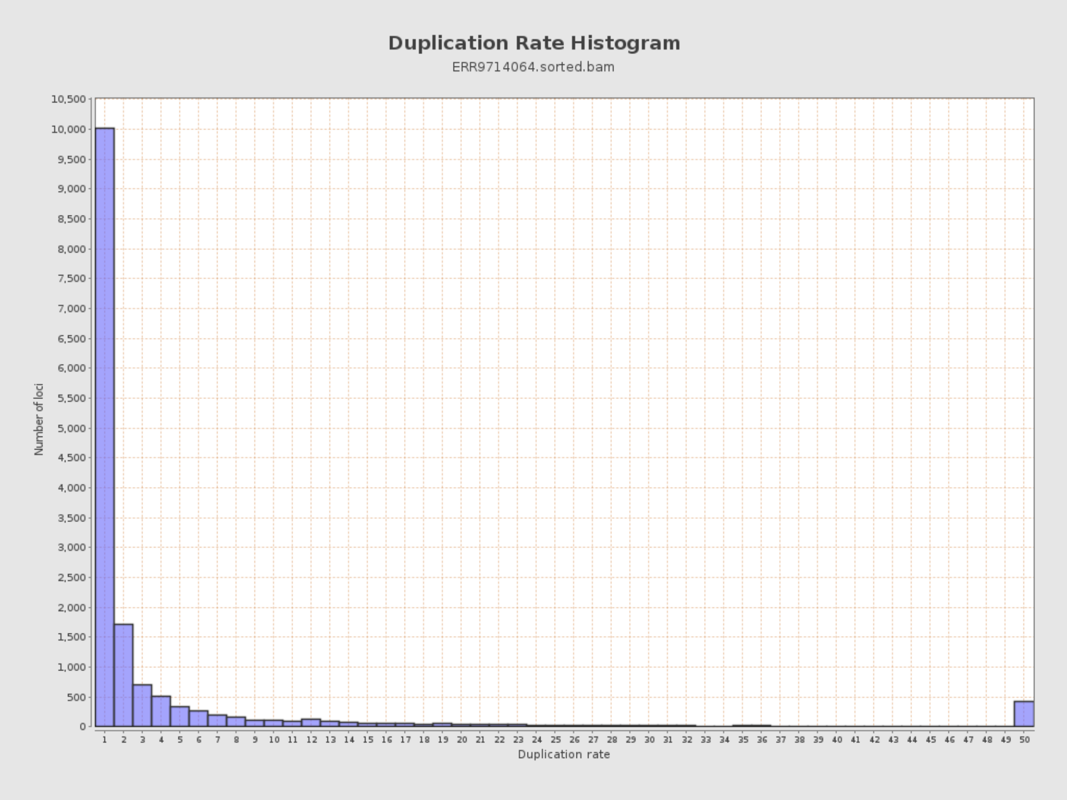
5. Results : Coverage Histogram (0-50X)



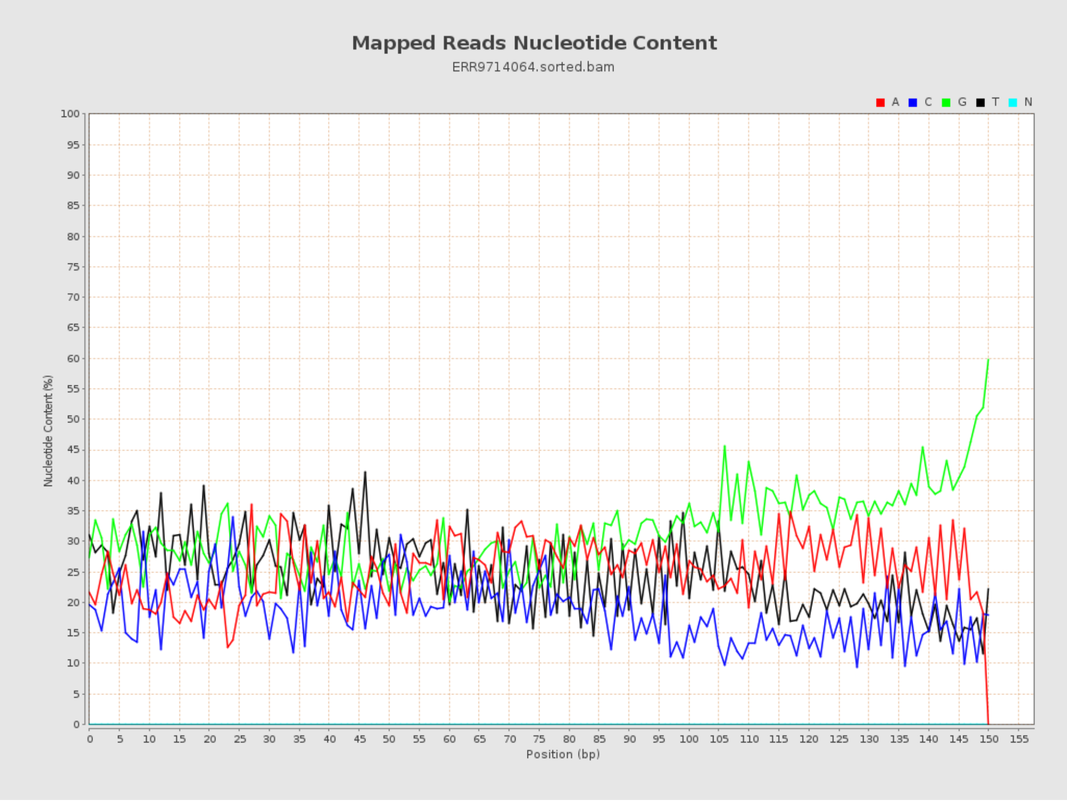
6. Results : Genome Fraction Coverage



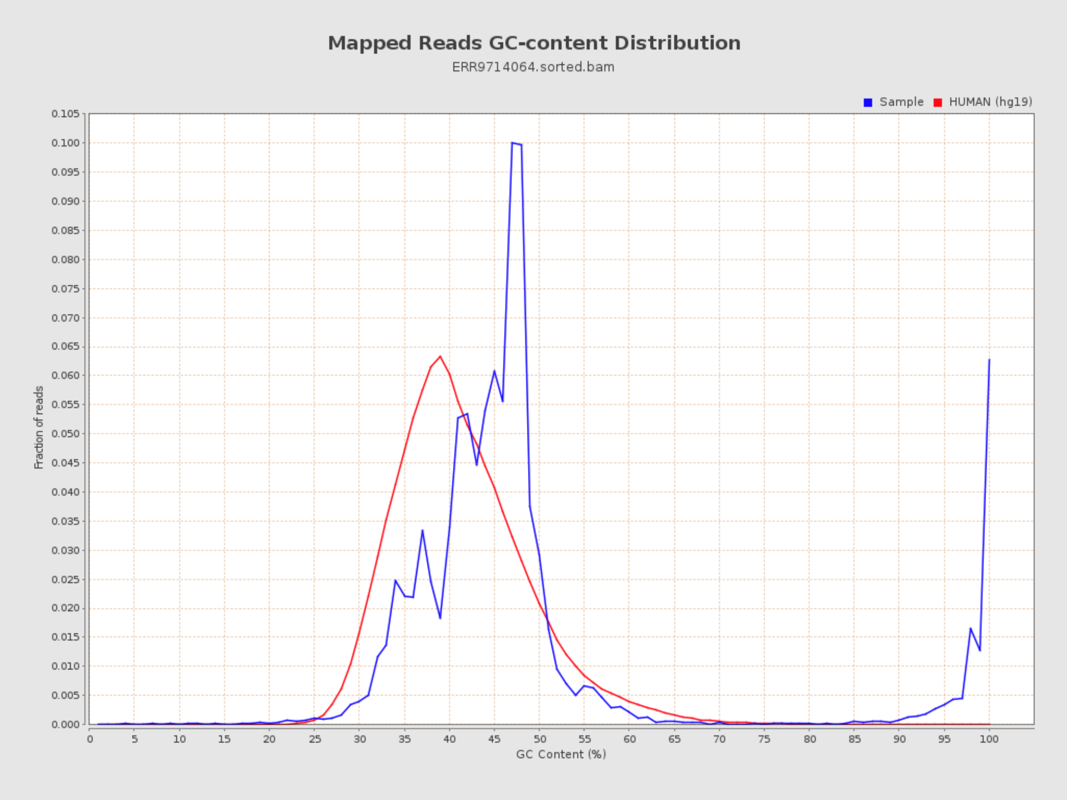
7. Results : Duplication Rate Histogram



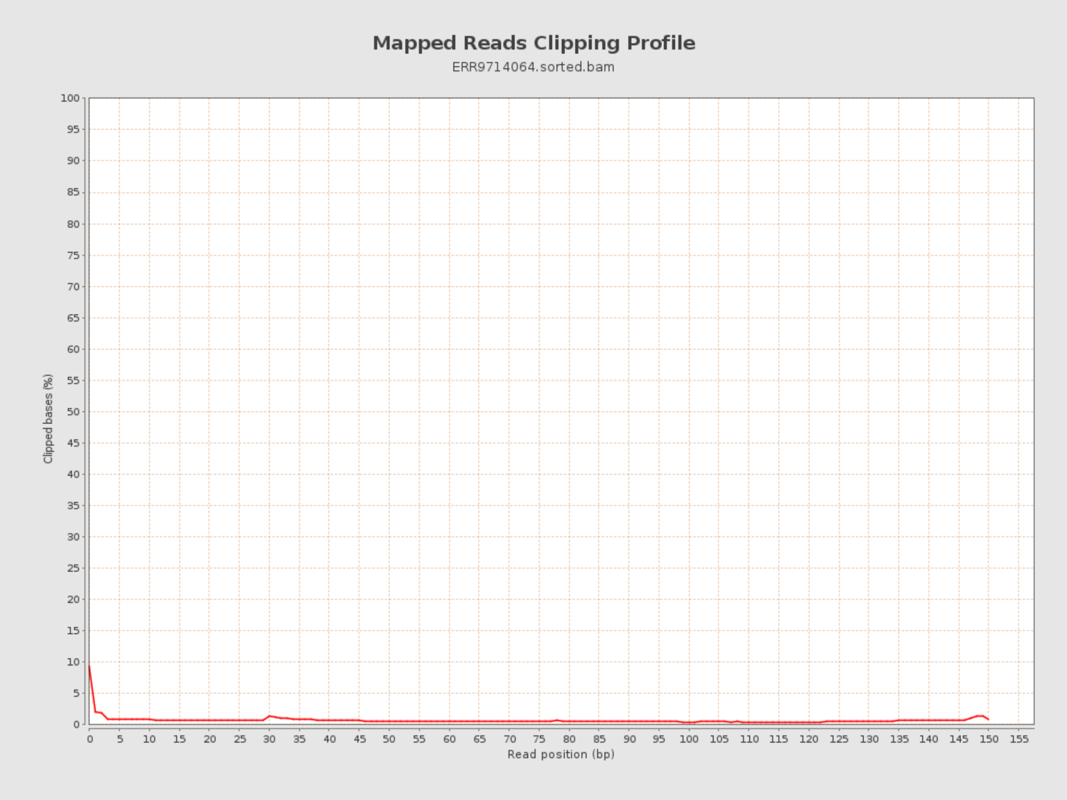
8. Results : Mapped Reads Nucleotide Content



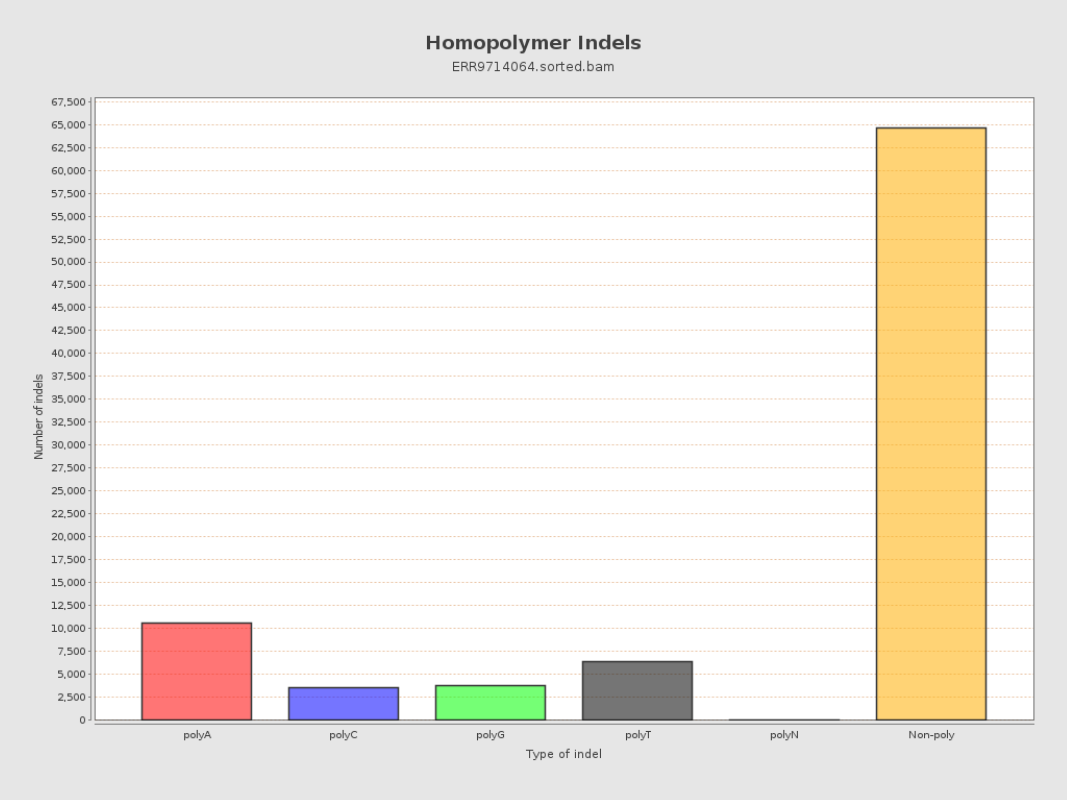
9. Results : Mapped Reads GC-content Distribution



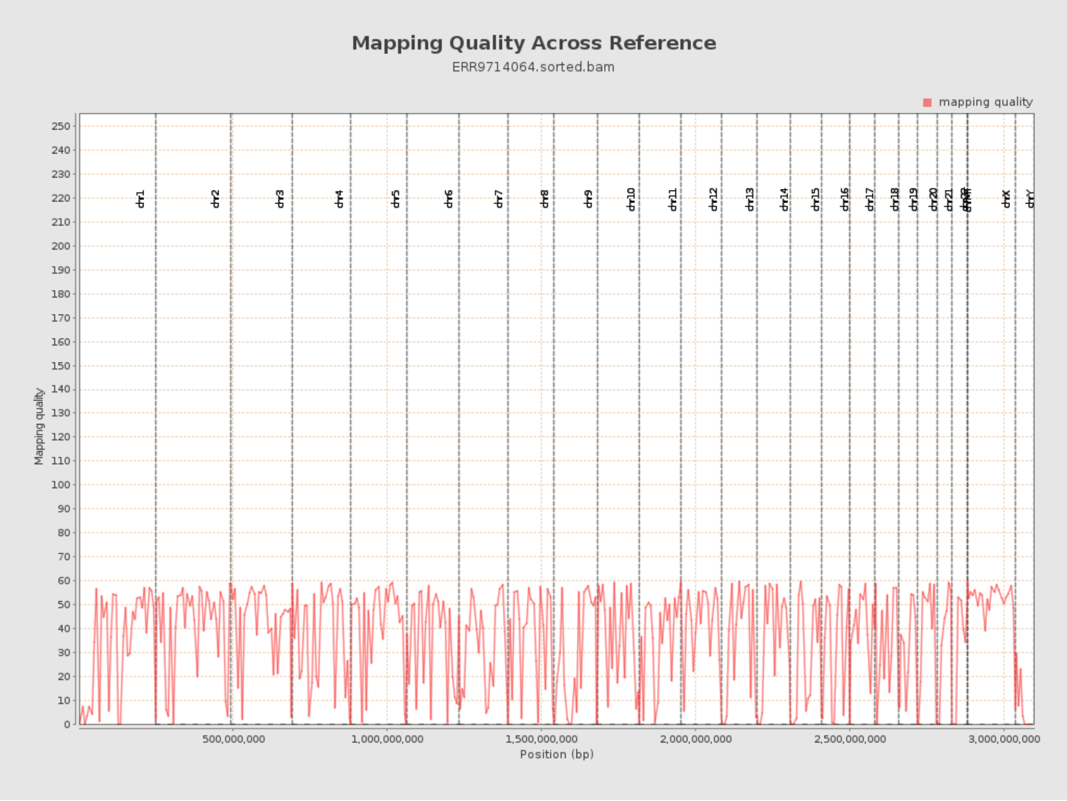
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram