Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:25:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714050.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_ERR9714050 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:25:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	413,978
Mapped reads	99,635 / 24.07%
Unmapped reads	314,343 / 75.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,335 / 0.81%
Read min/max/mean length	30 / 151 / 72.37
Duplicated reads (estimated)	91,308 / 22.06%
Duplication rate	29.61%
Clipped reads	79,226 / 19.14%

2.2. ACGT Content

Number/percentage of A's	1,897,326 / 18.33%
Number/percentage of C's	1,274,124 / 12.31%
Number/percentage of T's	1,592,297 / 15.38%
Number/percentage of G's	5,586,367 / 53.97%
Number/percentage of N's	334 / 0%
GC Percentage	66.28%

2.3. Coverage

Mean	0.0034

Standard Deviation	6.0135

2.4. Mapping Quality

Mean Mapping Quality	27.47

2.5. Mismatches and indels

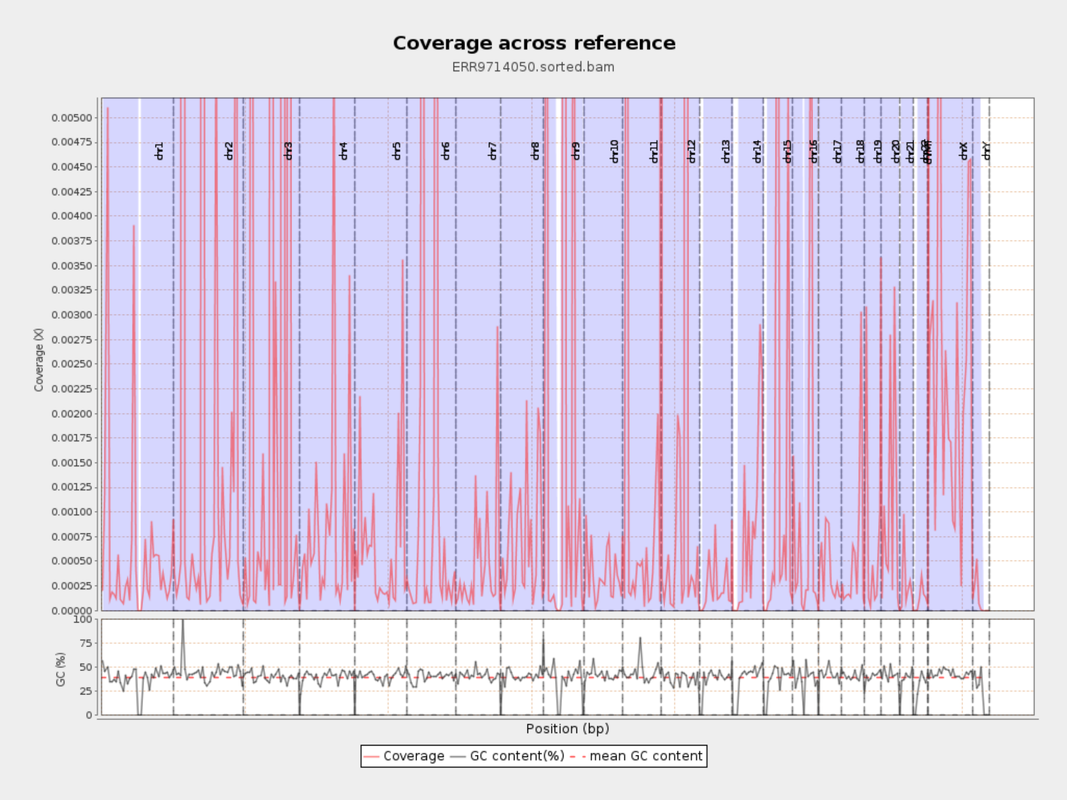
General error rate	3.42%
Mismatches	305,447
Insertions	9,539
Mapped reads with at least one insertion	7.85%
Deletions	20,562
Mapped reads with at least one deletion	19.57%
Homopolymer indels	29.22%

2.6. Chromosome stats

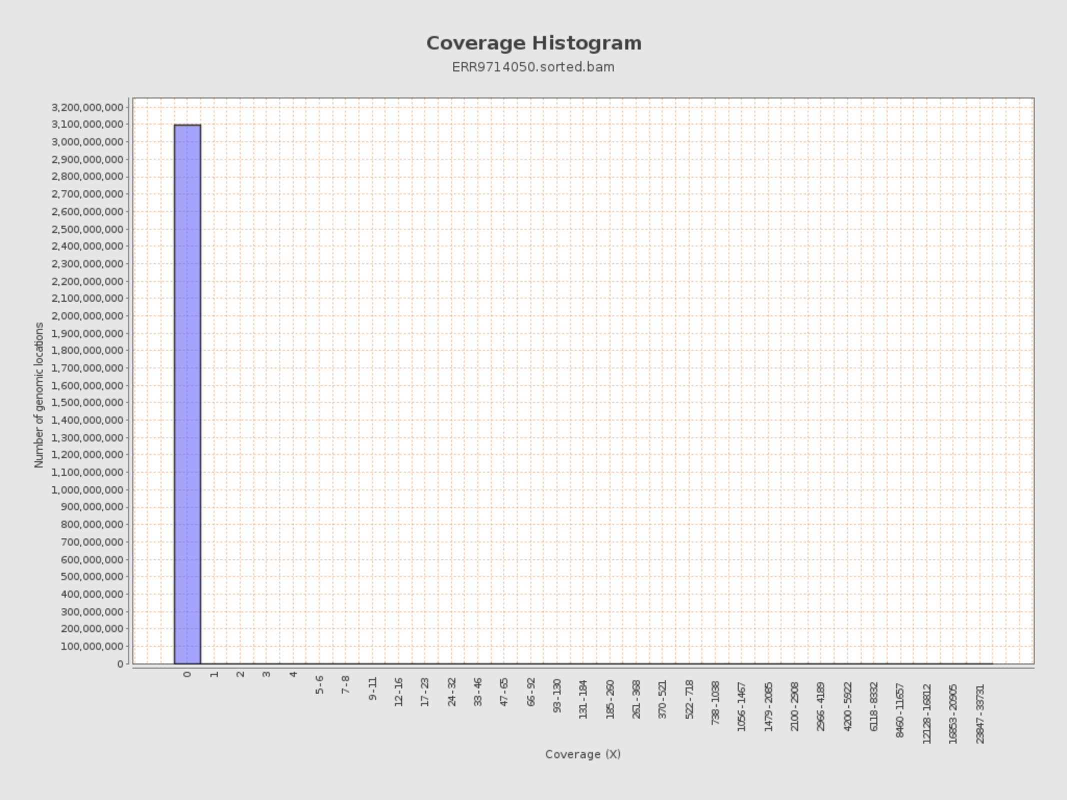
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	147676	0.0006	0.1546
chr2	243199373	4930320	0.0203	19.9707
chr3	198022430	2312915	0.0117	8.3144
chr4	191154276	173700	0.0009	0.2785
chr5	180915260	123748	0.0007	0.1798
chr6	171115067	336359	0.002	1.017
chr7	159138663	77274	0.0005	0.1818

chr8	146364022	110975	0.0008	0.1774
chr9	141213431	488687	0.0035	1.7747
chr10	135534747	49435	0.0004	0.0732
chr11	135006516	239030	0.0018	0.8666
chr12	133851895	335454	0.0025	1.5865
chr13	115169878	27343	0.0002	0.0447
chr14	107349540	85773	0.0008	0.1788
chr15	102531392	142440	0.0014	0.5709
chr16	90354753	88924	0.001	0.2876
chr17	81195210	31510	0.0004	0.1243
chr18	78077248	48234	0.0006	0.2213
chr19	59128983	46348	0.0008	0.2001
chr20	63025520	65666	0.001	0.2864
chr21	48129895	13230	0.0003	0.0666
chr22	51304566	6223	0.0001	0.0244
chrMT	16571	172650	10.4188	74.8526
chrX	155270560	401749	0.0026	0.293
chrY	59373566	7194	0.0001	0.0305

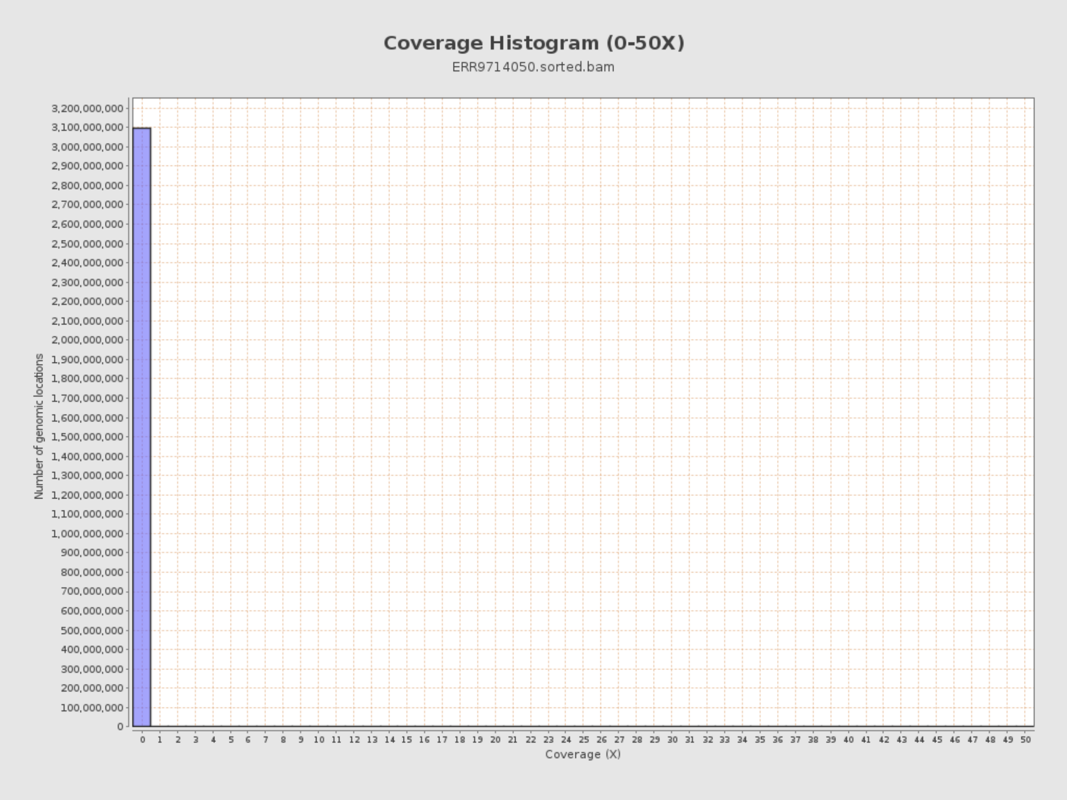
3. Results : Coverage across reference



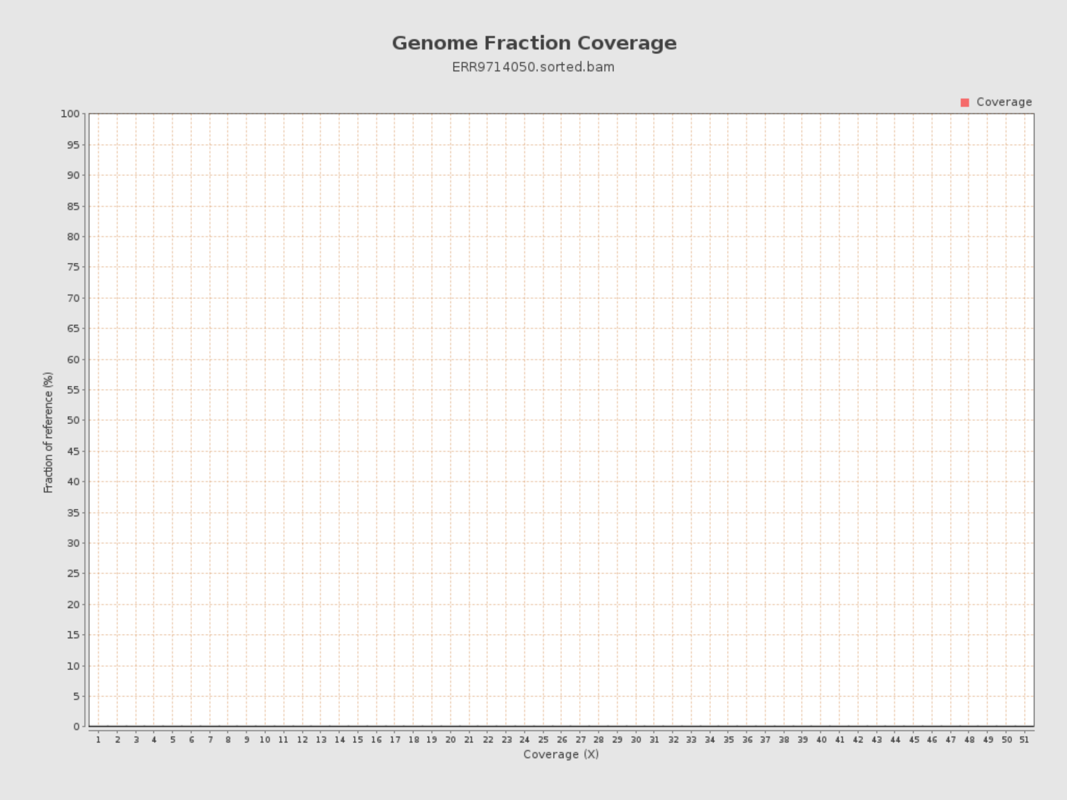
4. Results : Coverage Histogram



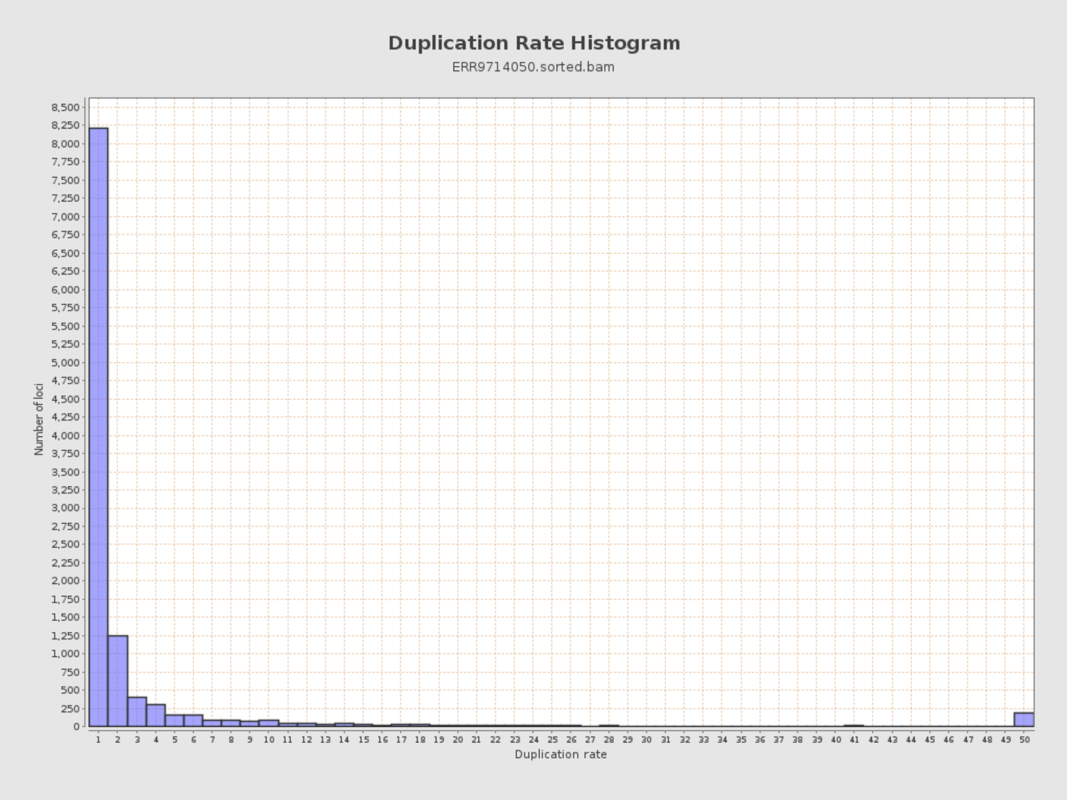
5. Results : Coverage Histogram (0-50X)



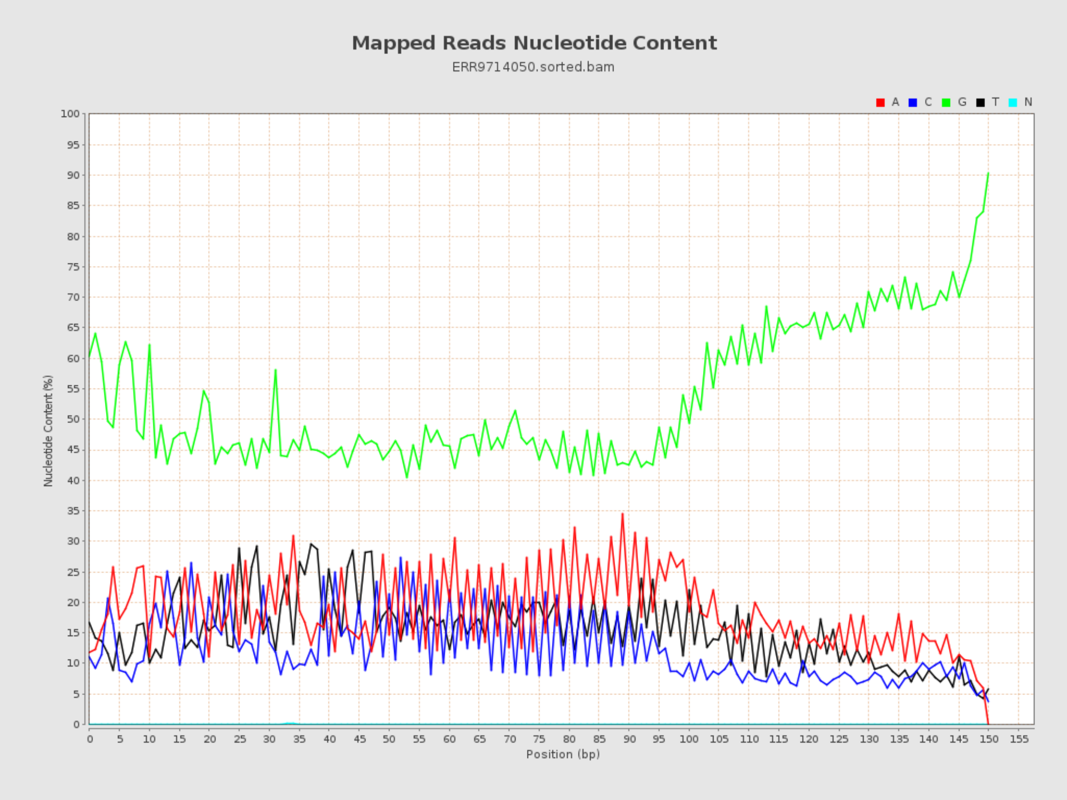
6. Results : Genome Fraction Coverage



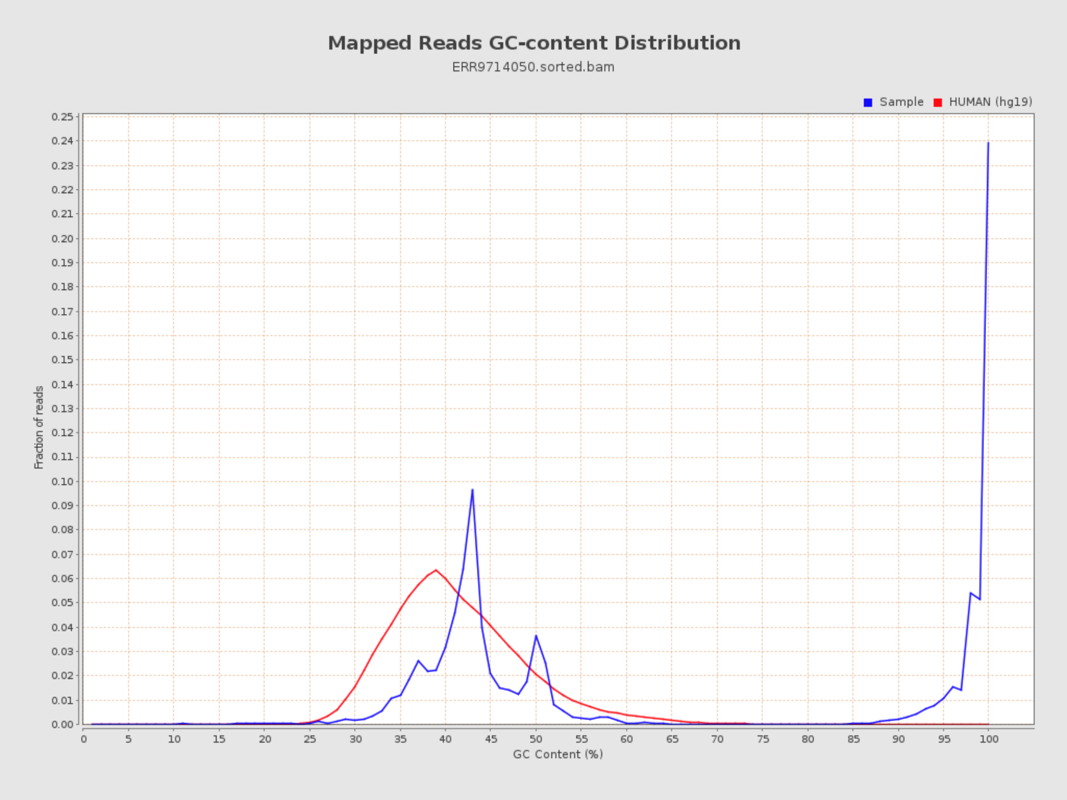
7. Results : Duplication Rate Histogram



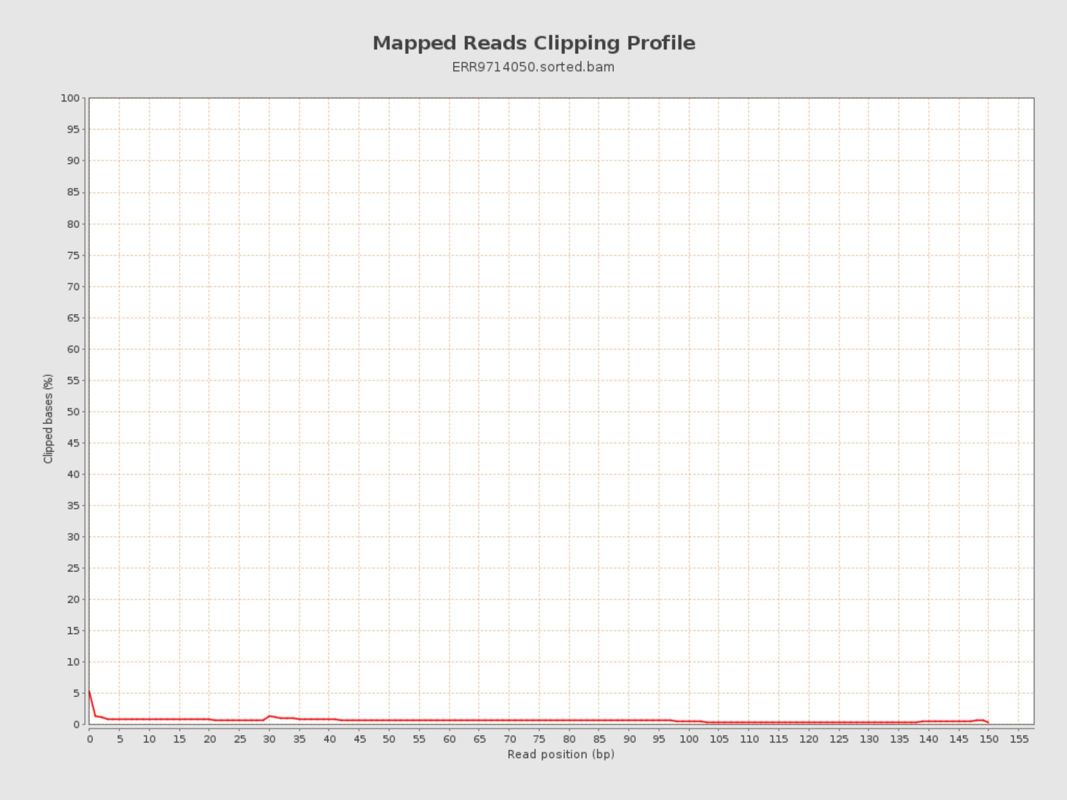
8. Results : Mapped Reads Nucleotide Content



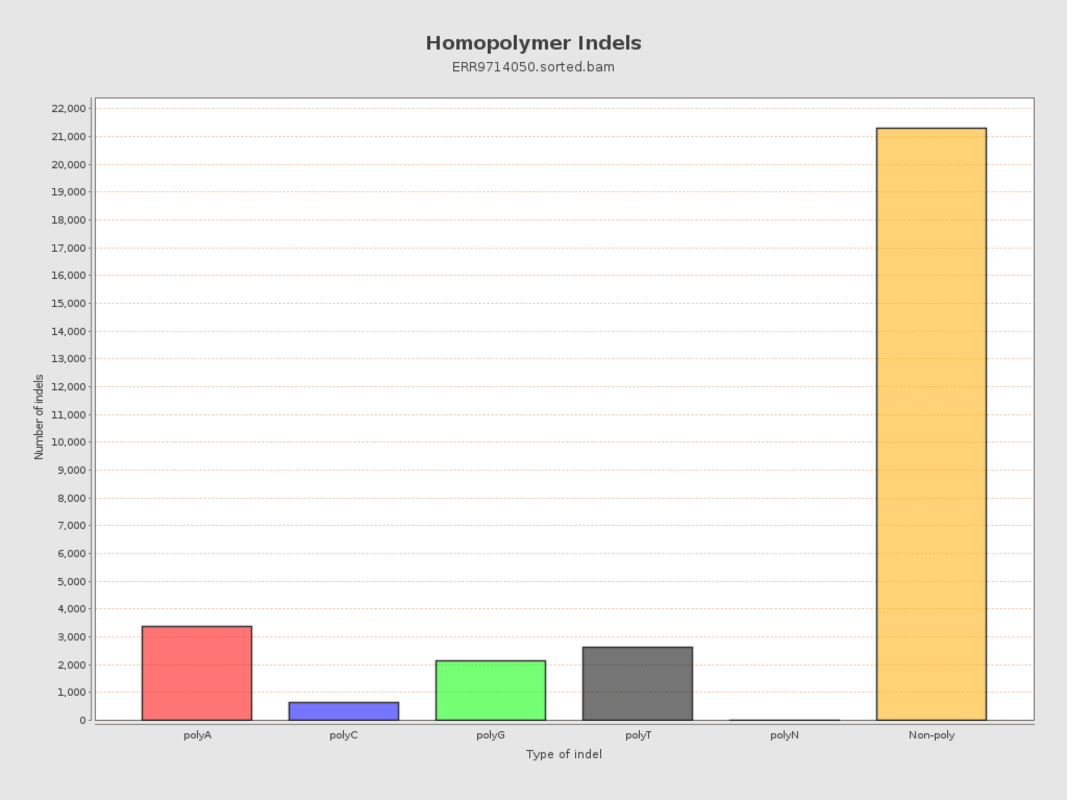
9. Results : Mapped Reads GC-content Distribution



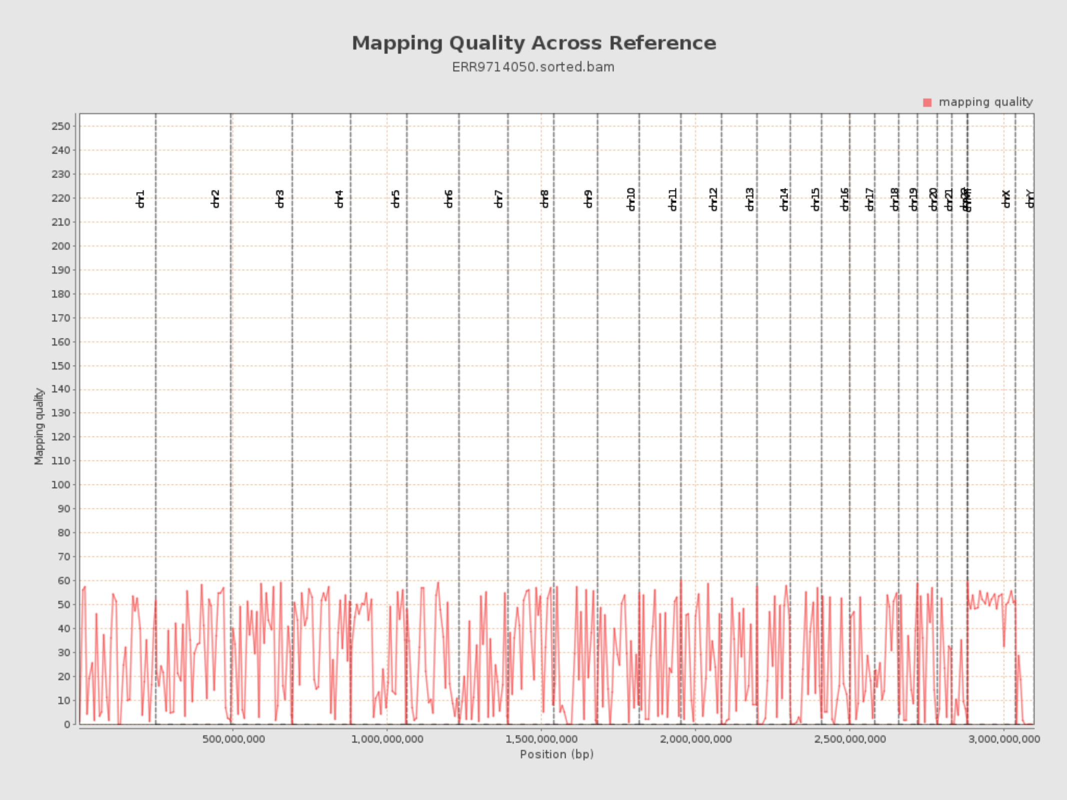
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram