Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:57:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714236.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_ERR9714236 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714236.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:57:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,570
Mapped reads	1,520 / 23.14%
Unmapped reads	5,050 / 76.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	87 / 1.32%
Read min/max/mean length	30 / 151 / 79.12
Duplicated reads (estimated)	797 / 12.13%
Duplication rate	38.77%
Clipped reads	1,207 / 18.37%

2.2. ACGT Content

Number/percentage of A's	35,182 / 20.95%
Number/percentage of C's	27,362 / 16.29%
Number/percentage of T's	32,556 / 19.39%
Number/percentage of G's	72,818 / 43.37%
Number/percentage of N's	0 / 0%
GC Percentage	59.66%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0548

2.4. Mapping Quality

Mean Mapping Quality	17.07

2.5. Mismatches and indels

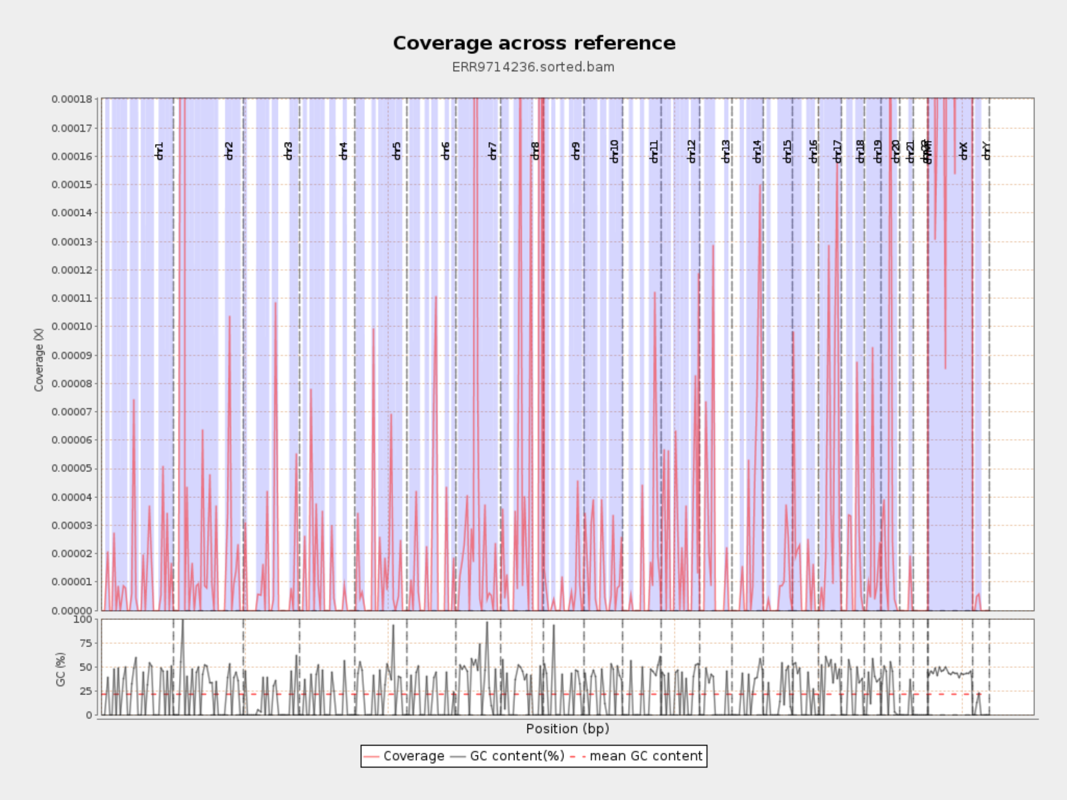
General error rate	3.9%
Mismatches	5,720
Insertions	136
Mapped reads with at least one insertion	6.58%
Deletions	394
Mapped reads with at least one deletion	25.26%
Homopolymer indels	37.92%

2.6. Chromosome stats

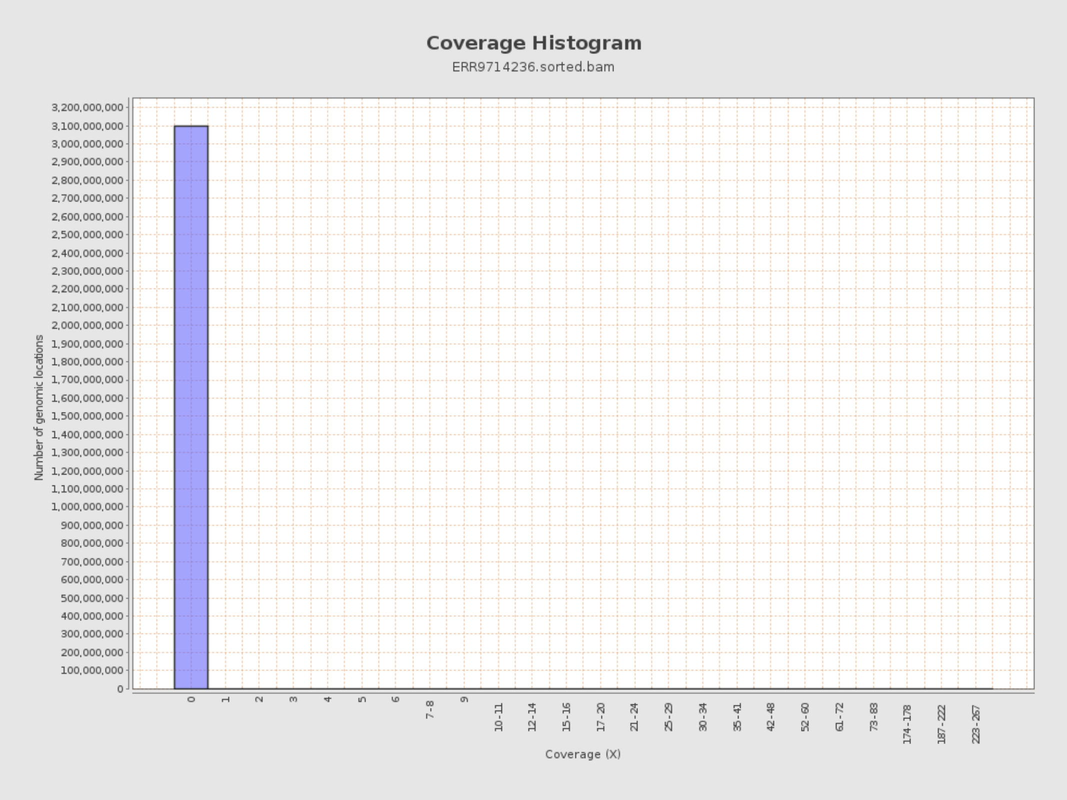
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2757	0	0.0048
chr2	243199373	50776	0.0002	0.1872
chr3	198022430	2139	0	0.0054
chr4	191154276	1772	0	0.0043
chr5	180915260	2467	0	0.0062
chr6	171115067	2558	0	0.0072
chr7	159138663	5868	0	0.0232

chr8	146364022	7663	0.0001	0.0262
chr9	141213431	1058	0	0.0039
chr10	135534747	1901	0	0.0063
chr11	135006516	1677	0	0.0043
chr12	133851895	3711	0	0.0087
chr13	115169878	1962	0	0.0082
chr14	107349540	3067	0	0.0113
chr15	102531392	771	0	0.0044
chr16	90354753	1291	0	0.0052
chr17	81195210	3786	0	0.0141
chr18	78077248	1461	0	0.0085
chr19	59128983	1114	0	0.0068
chr20	63025520	2689	0	0.0177
chr21	48129895	150	0	0.0025
chr22	51304566	0	0	0
chrMT	16571	301	0.0182	0.1335
chrX	155270560	69946	0.0005	0.054
chrY	59373566	85	0	0.0012

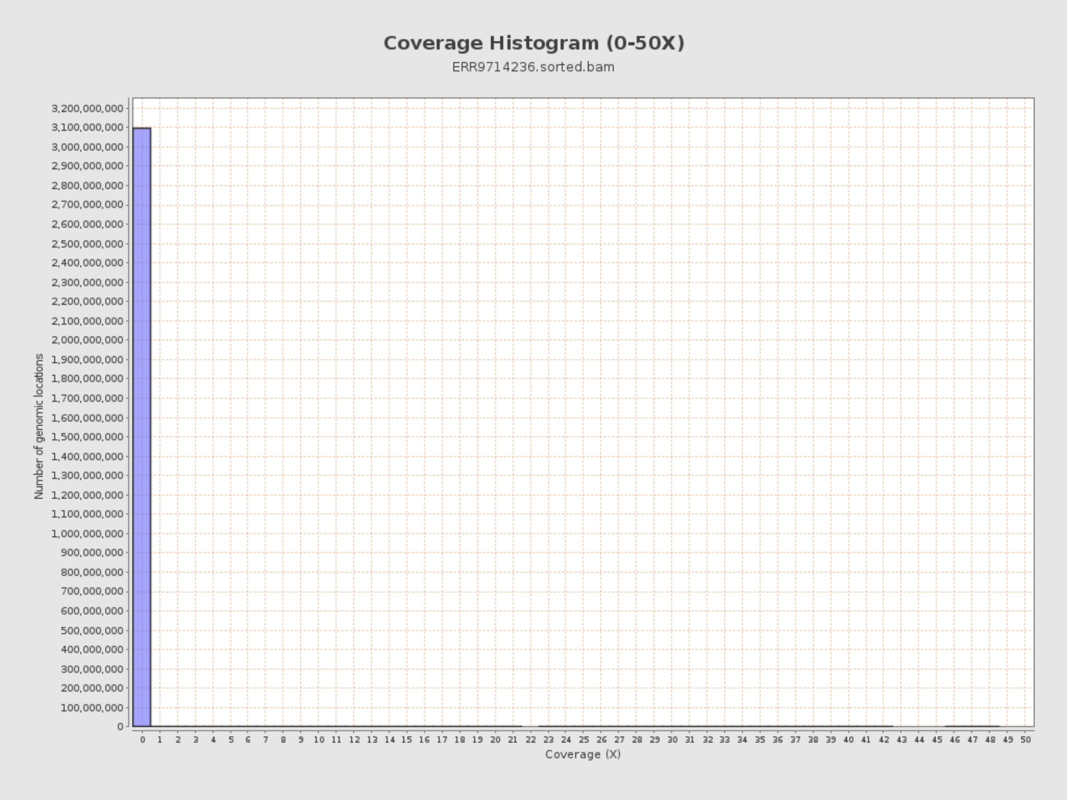
3. Results : Coverage across reference



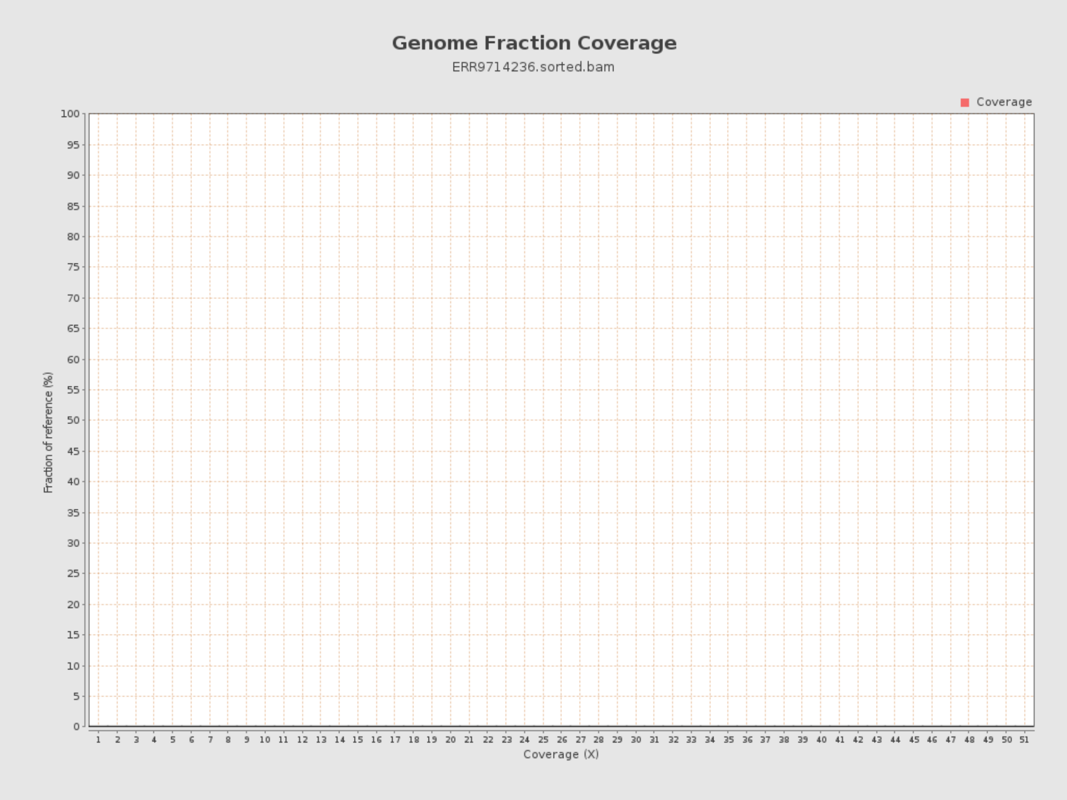
4. Results : Coverage Histogram



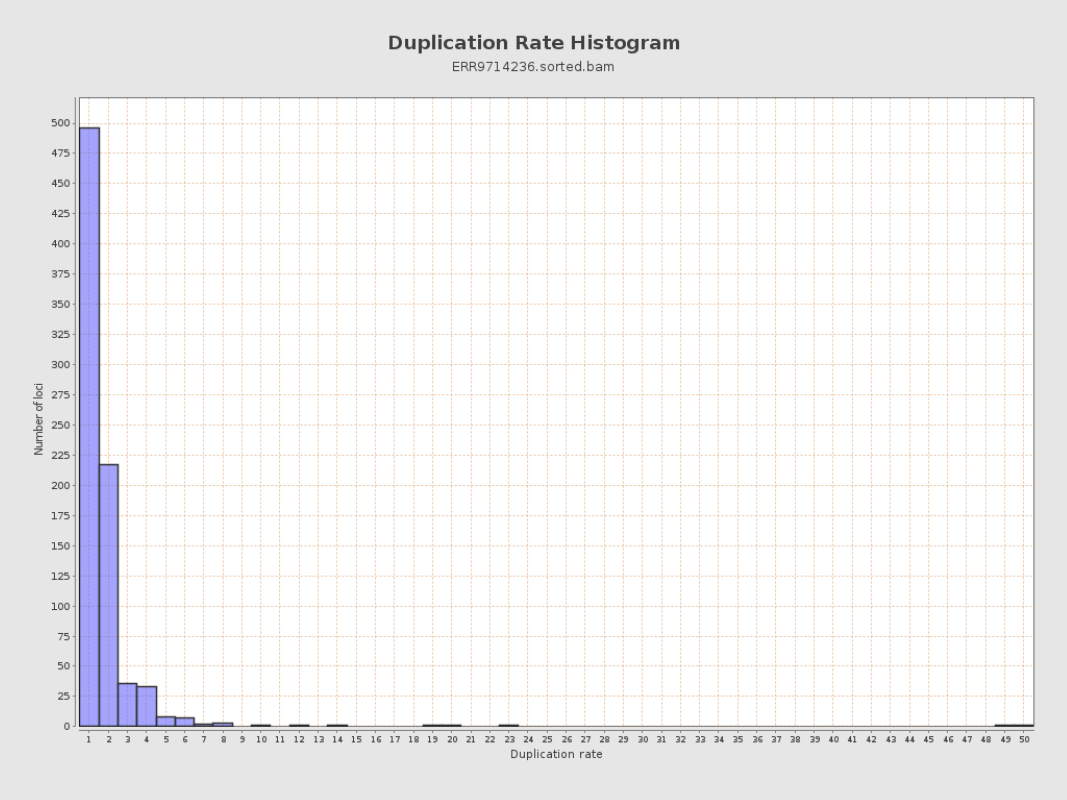
5. Results : Coverage Histogram (0-50X)



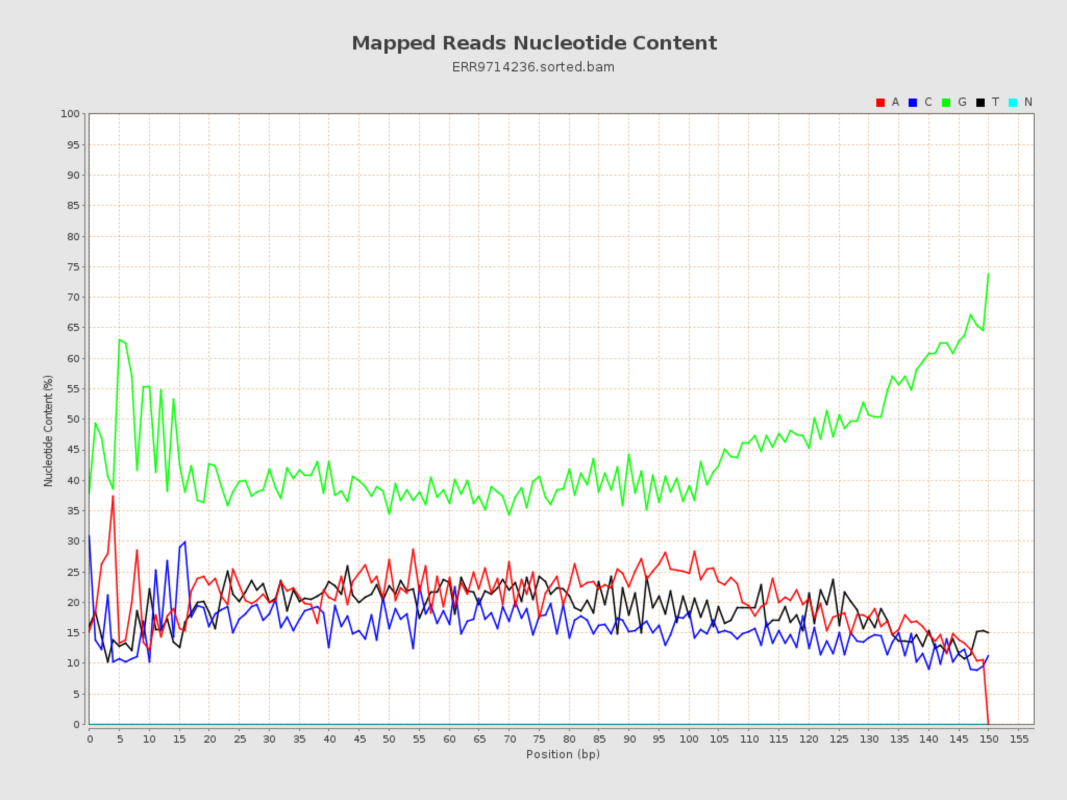
6. Results : Genome Fraction Coverage



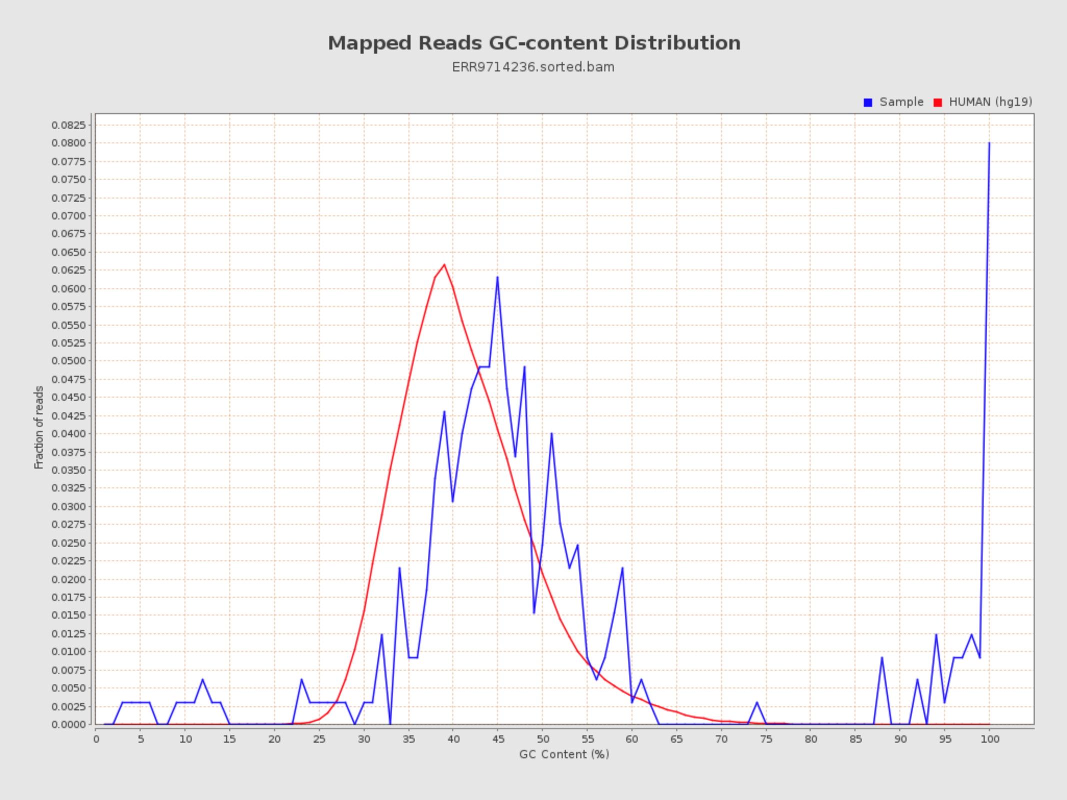
7. Results : Duplication Rate Histogram



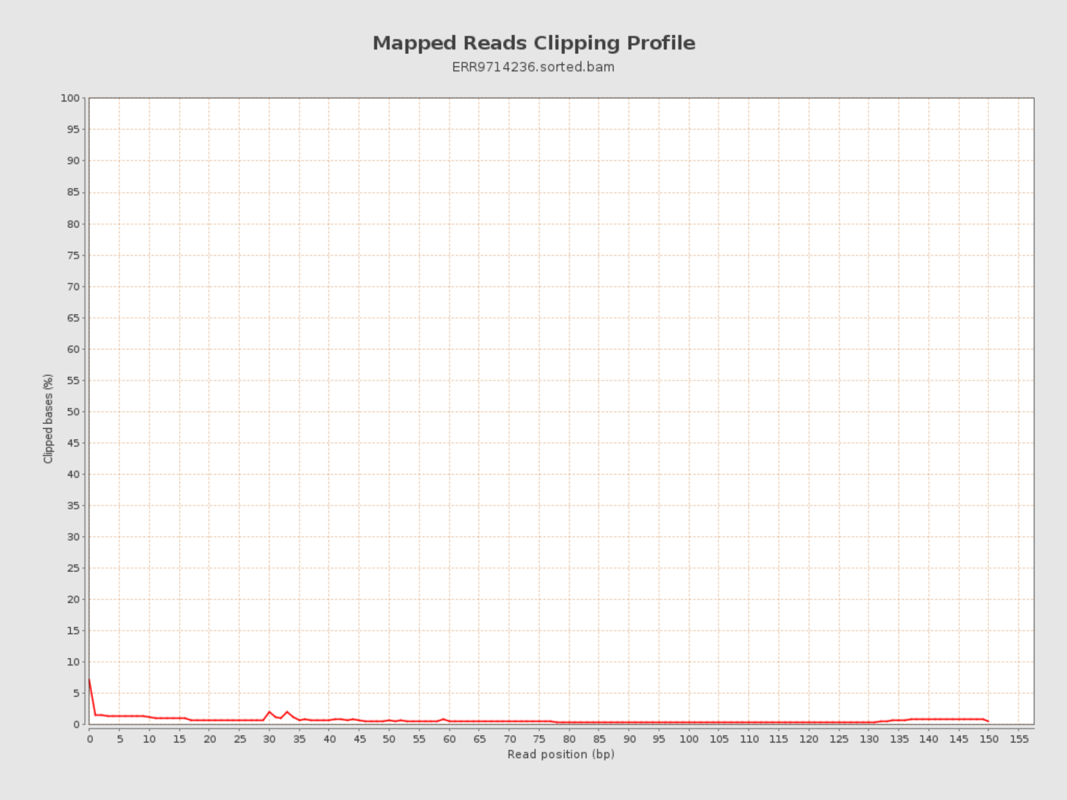
8. Results : Mapped Reads Nucleotide Content



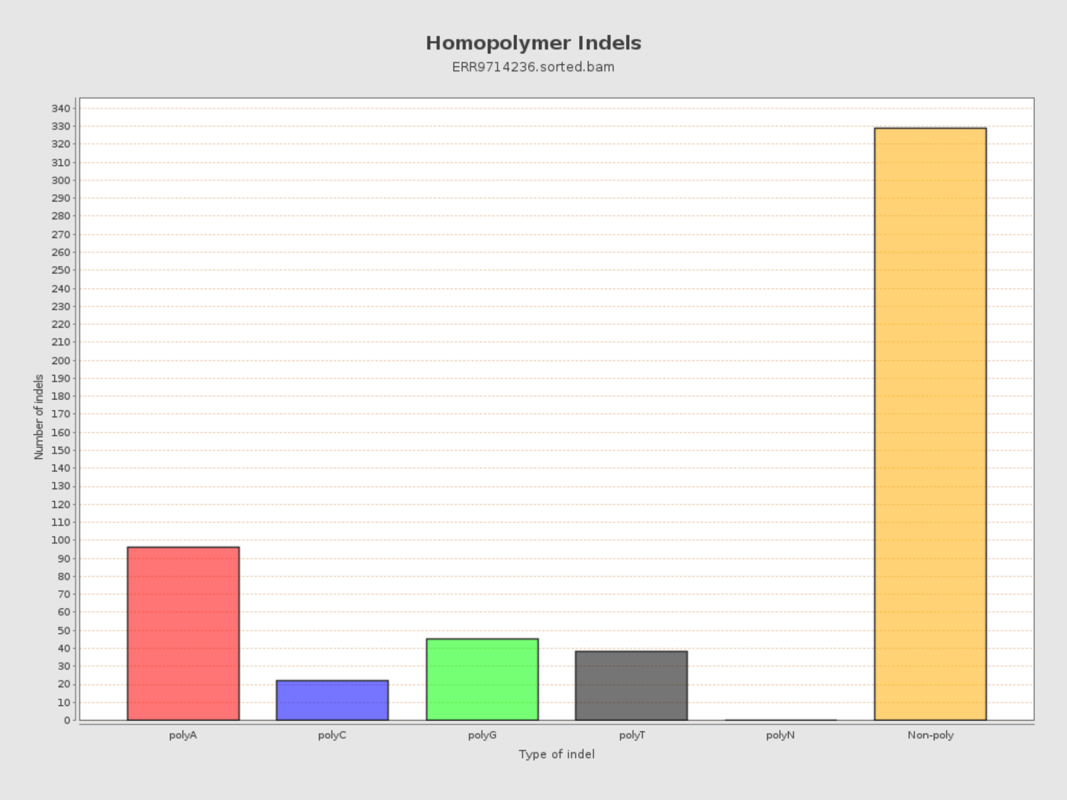
9. Results : Mapped Reads GC-content Distribution



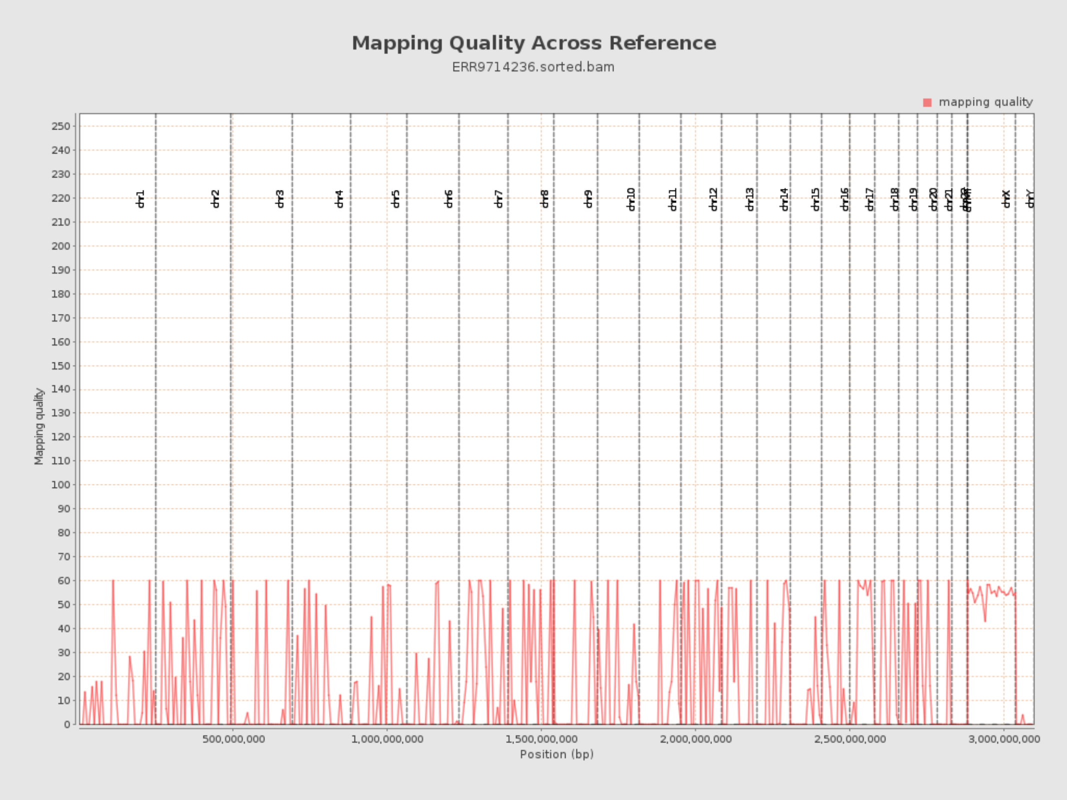
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram