Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:18:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714141.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_ERR9714141 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:18:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	884,440
Mapped reads	399,401 / 45.16%
Unmapped reads	485,039 / 54.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,921 / 1.57%
Read min/max/mean length	30 / 151 / 94.88
Duplicated reads (estimated)	324,749 / 36.72%
Duplication rate	42.6%
Clipped reads	374,106 / 42.3%

2.2. ACGT Content

Number/percentage of A's	13,255,028 / 26.78%
Number/percentage of C's	10,460,299 / 21.13%
Number/percentage of T's	12,554,734 / 25.36%
Number/percentage of G's	13,231,884 / 26.73%
Number/percentage of N's	365 / 0%
GC Percentage	47.86%

2.3. Coverage

Mean	0.0163

Standard Deviation	3.2455

2.4. Mapping Quality

Mean Mapping Quality	52.39

2.5. Mismatches and indels

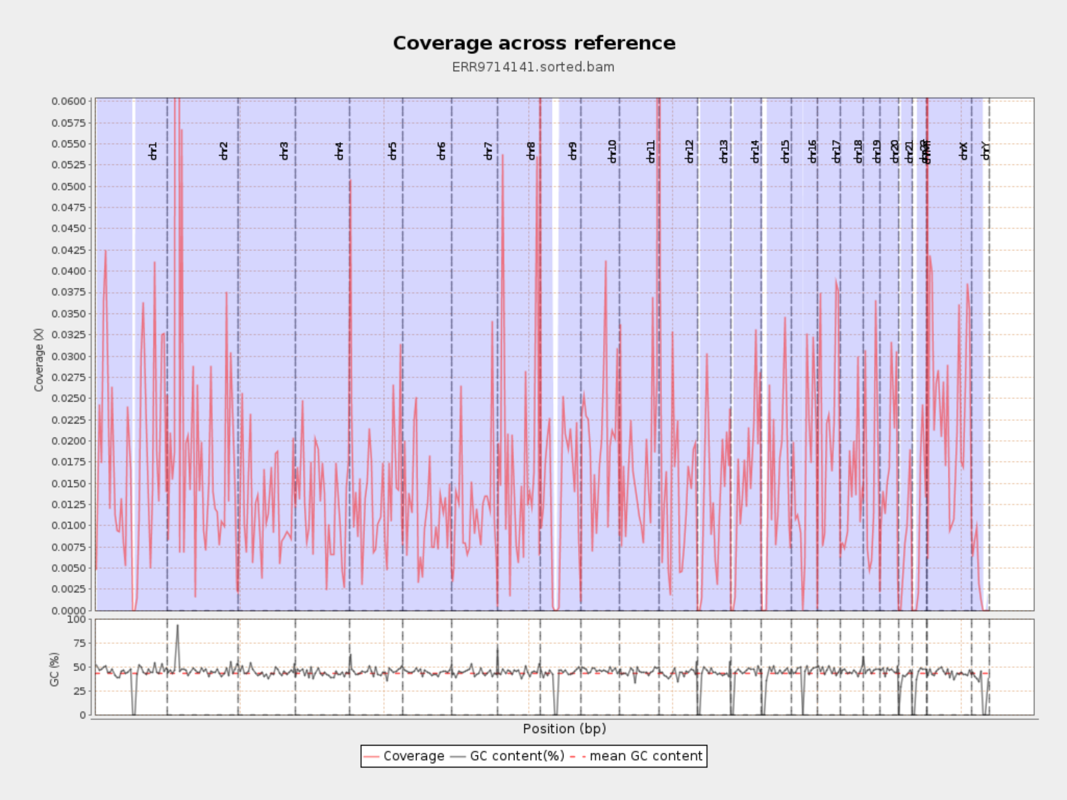
General error rate	4.24%
Mismatches	1,922,576
Insertions	53,392
Mapped reads with at least one insertion	12.64%
Deletions	166,575
Mapped reads with at least one deletion	39.9%
Homopolymer indels	29.38%

2.6. Chromosome stats

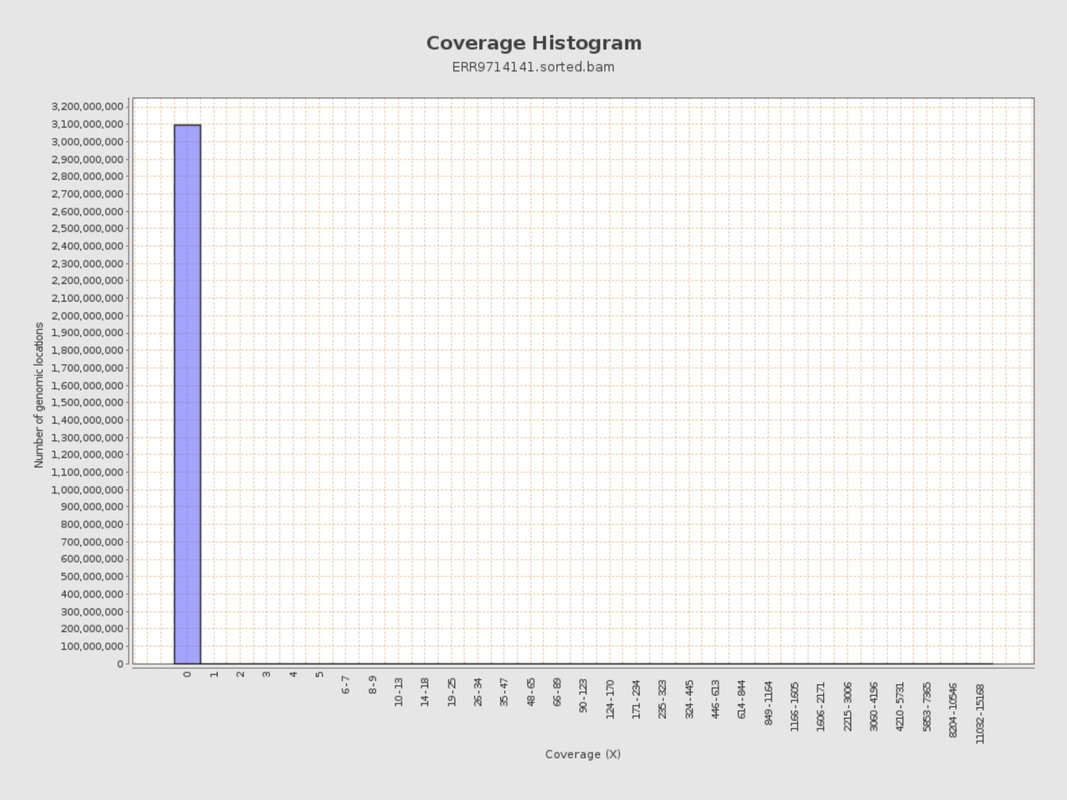
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4487780	0.018	2.0237
chr2	243199373	6799922	0.028	9.8739
chr3	198022430	2437859	0.0123	1.2045
chr4	191154276	2377251	0.0124	1.3756
chr5	180915260	2558036	0.0141	1.3138
chr6	171115067	1968097	0.0115	1.1354
chr7	159138663	1896521	0.0119	1.2583

chr8	146364022	2565954	0.0175	2.3067
chr9	141213431	1967728	0.0139	1.5405
chr10	135534747	2762180	0.0204	1.9778
chr11	135006516	2428266	0.018	2.3208
chr12	133851895	1960094	0.0146	1.641
chr13	115169878	1430839	0.0124	1.5424
chr14	107349540	1640377	0.0153	1.6002
chr15	102531392	1427614	0.0139	1.581
chr16	90354753	1466834	0.0162	1.7035
chr17	81195210	1856259	0.0229	2.4464
chr18	78077248	1109817	0.0142	1.3404
chr19	59128983	892564	0.0151	1.6318
chr20	63025520	1160653	0.0184	1.4843
chr21	48129895	371491	0.0077	0.9106
chr22	51304566	512099	0.01	1.0862
chrMT	16571	491947	29.6872	273.7877
chrX	155270560	3720909	0.024	1.5051
chrY	59373566	207302	0.0035	0.468

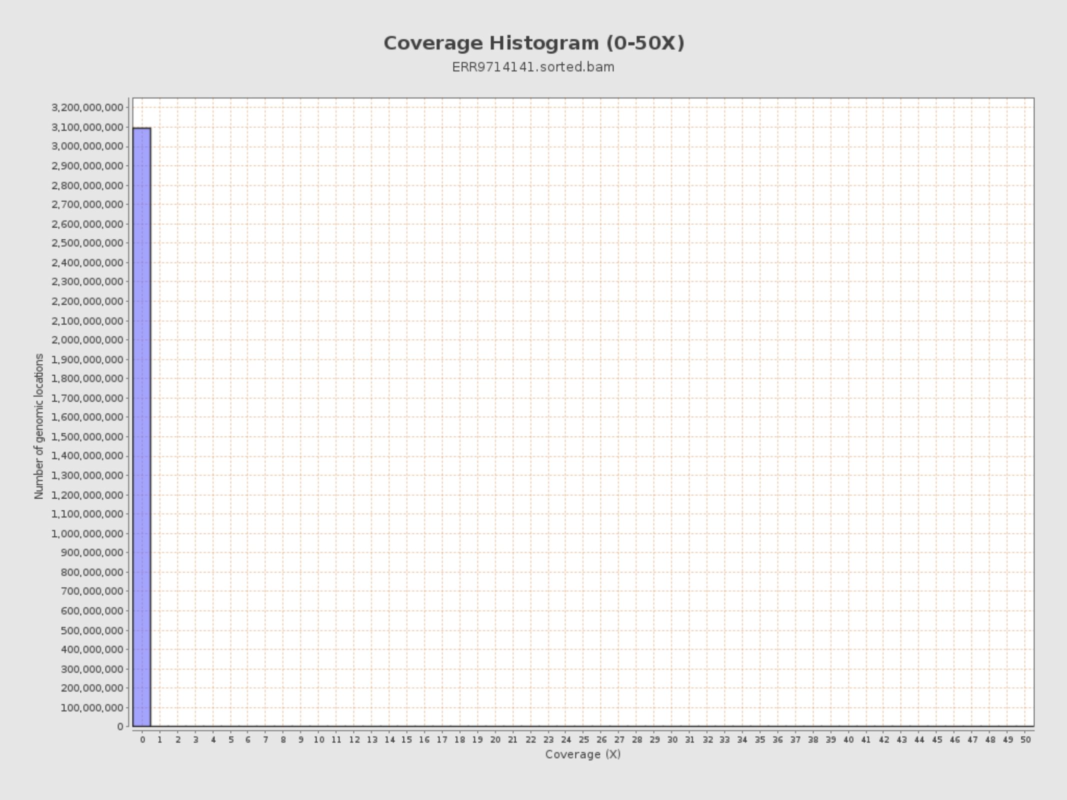
3. Results : Coverage across reference



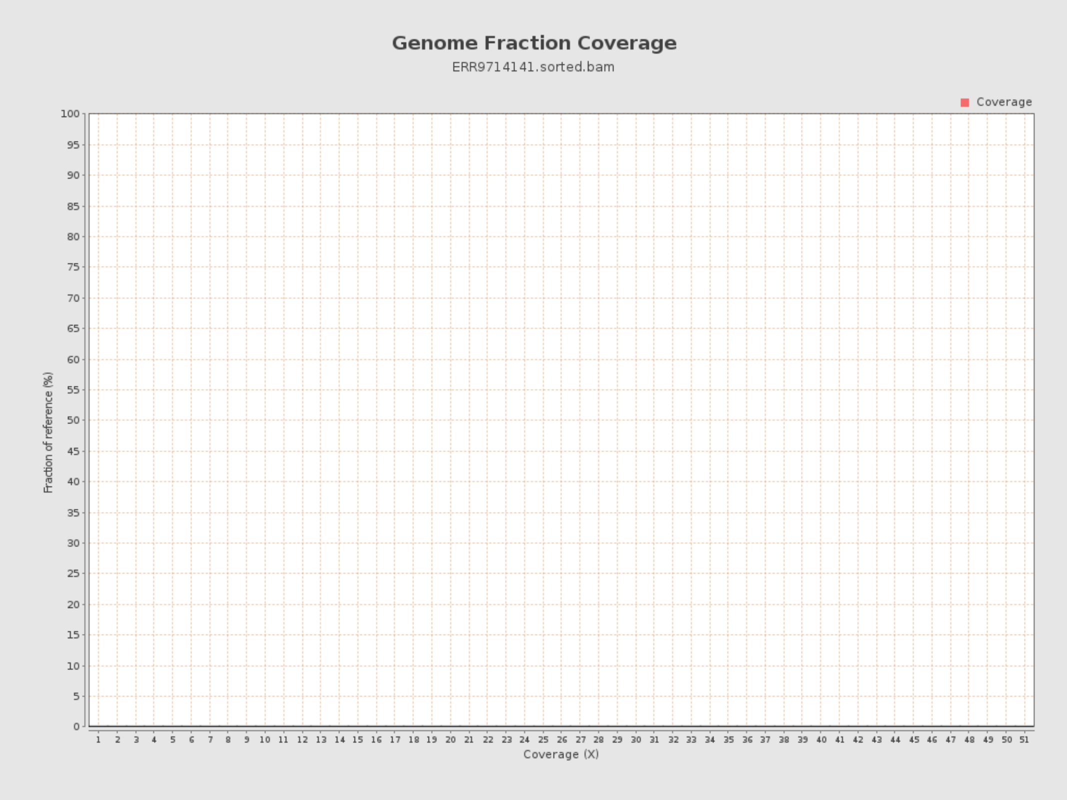
4. Results : Coverage Histogram



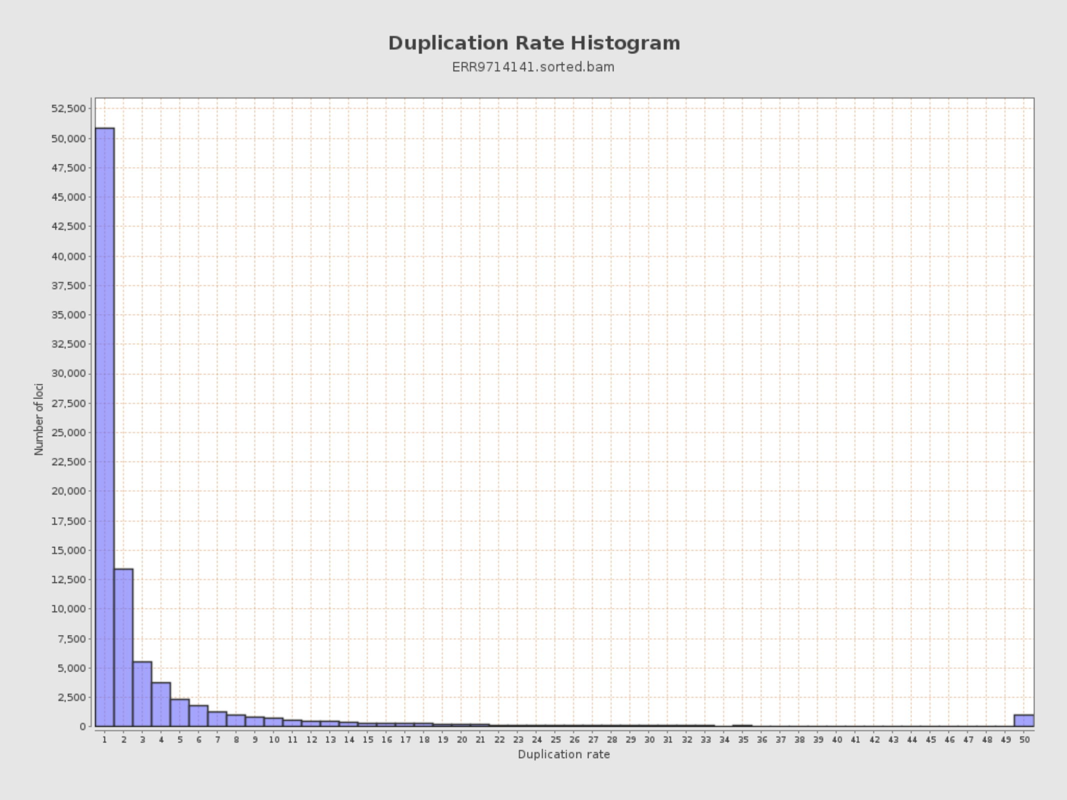
5. Results : Coverage Histogram (0-50X)



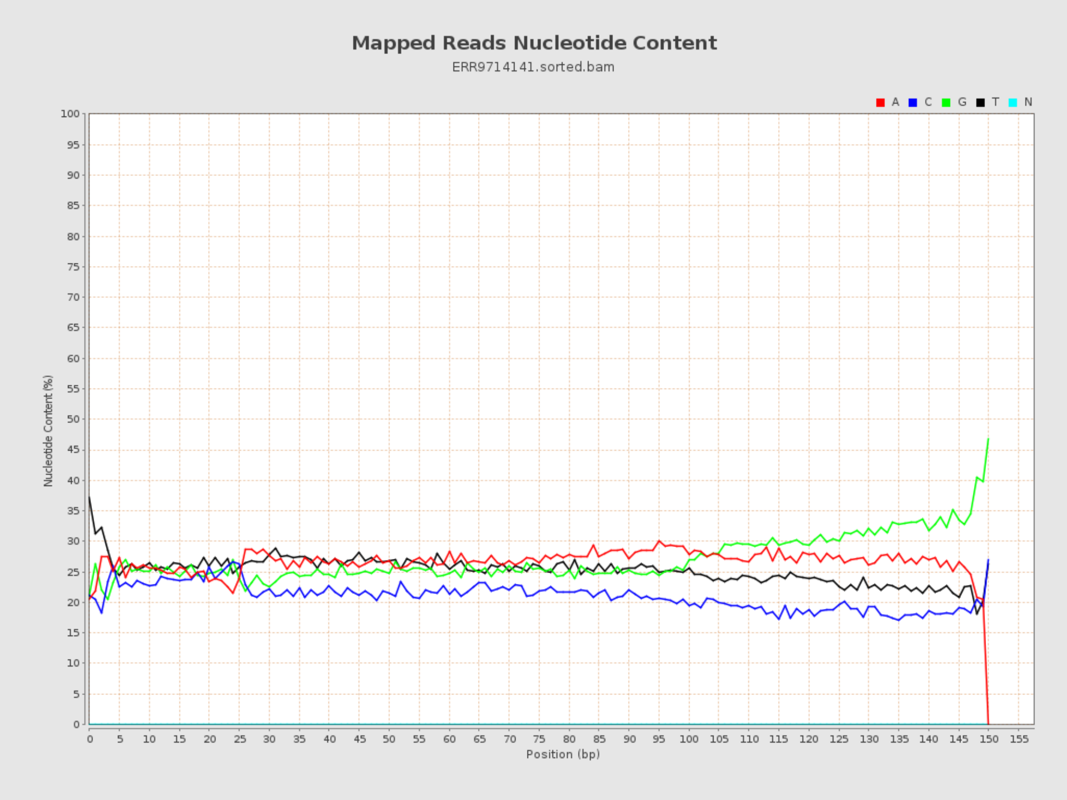
6. Results : Genome Fraction Coverage



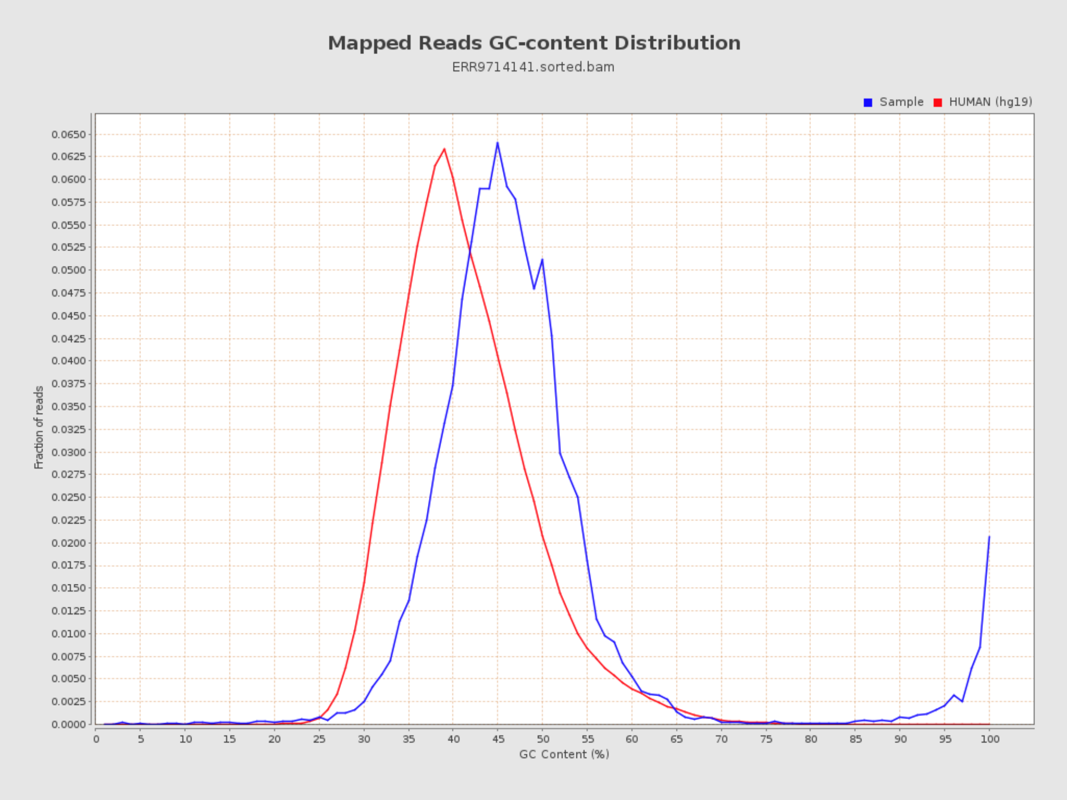
7. Results : Duplication Rate Histogram



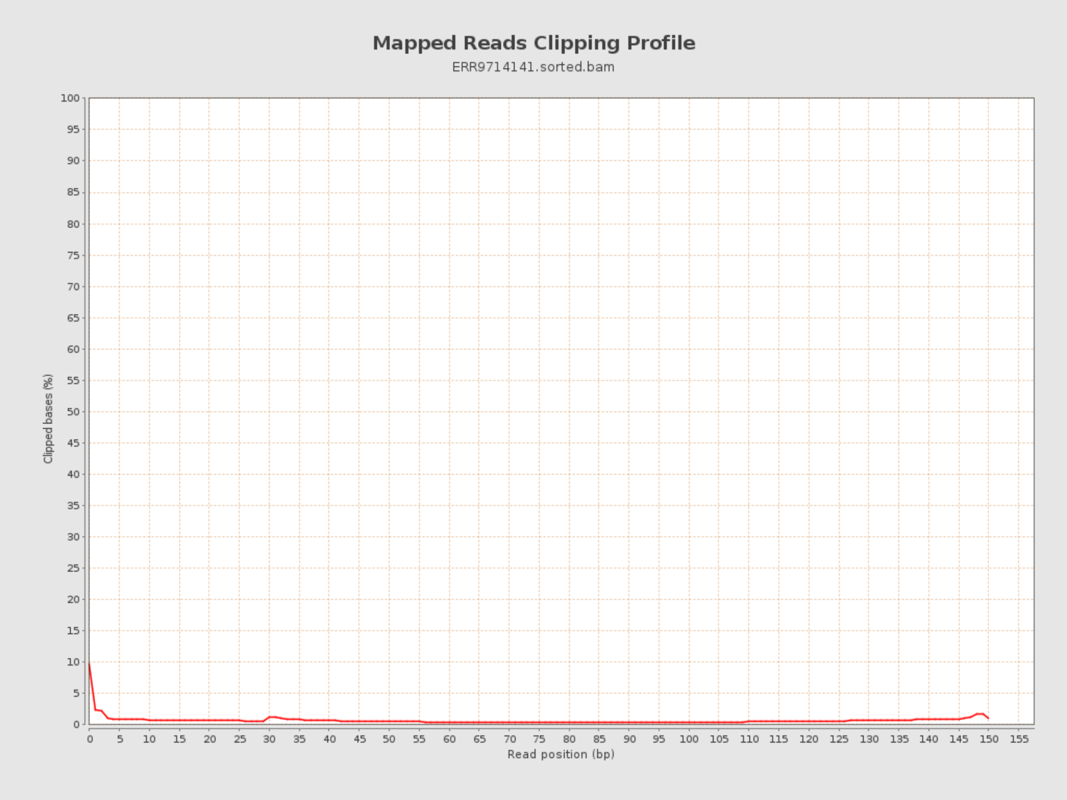
8. Results : Mapped Reads Nucleotide Content



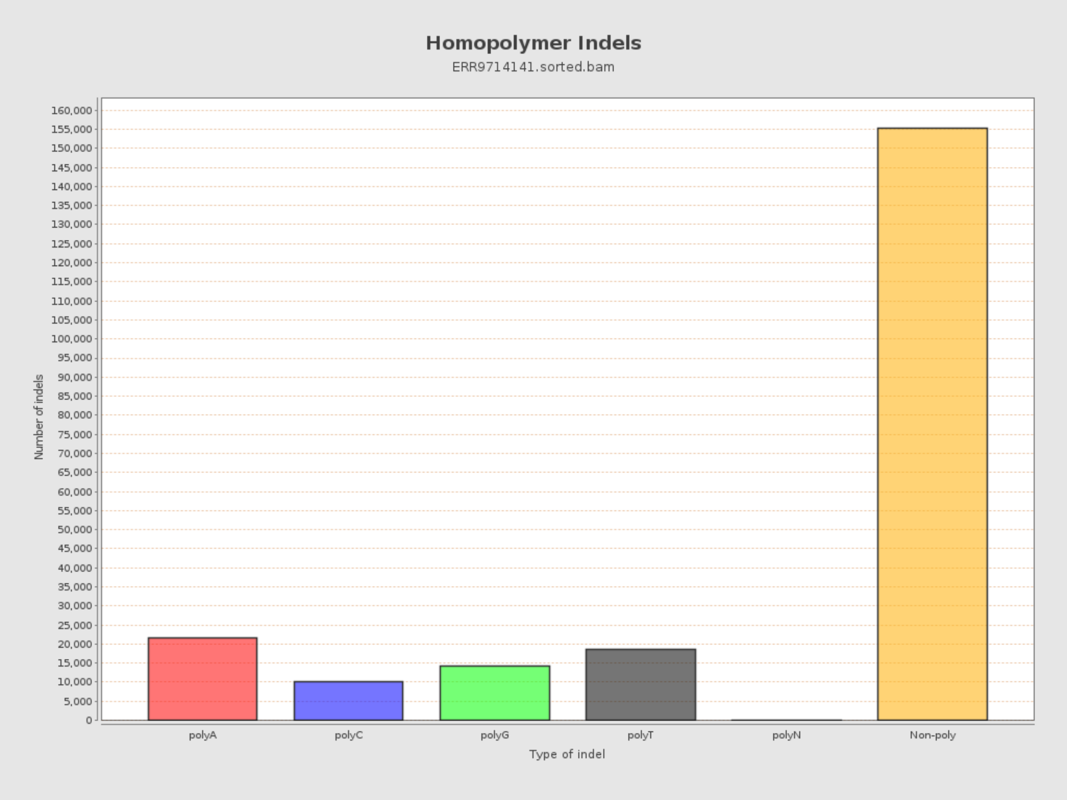
9. Results : Mapped Reads GC-content Distribution



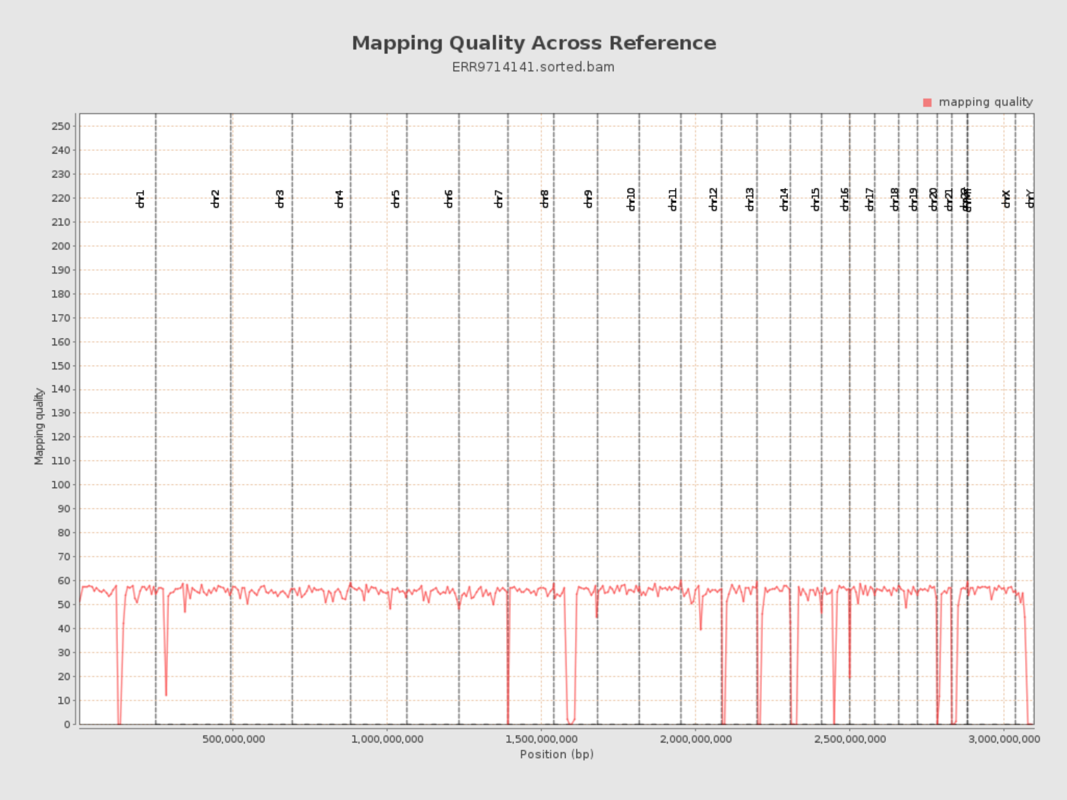
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram