Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:35:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714147.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_ERR9714147 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:35:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	756,984
Mapped reads	537,778 / 71.04%
Unmapped reads	219,206 / 28.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,399 / 2.3%
Read min/max/mean length	30 / 151 / 123.29
Duplicated reads (estimated)	478,929 / 63.27%
Duplication rate	43.85%
Clipped reads	497,575 / 65.73%

2.2. ACGT Content

Number/percentage of A's	18,654,036 / 27.34%
Number/percentage of C's	13,861,246 / 20.32%
Number/percentage of T's	17,736,898 / 26%
Number/percentage of G's	17,967,218 / 26.34%
Number/percentage of N's	816 / 0%
GC Percentage	46.66%

2.3. Coverage

Mean	0.0226

Standard Deviation	6.238

2.4. Mapping Quality

Mean Mapping Quality	51.29

2.5. Mismatches and indels

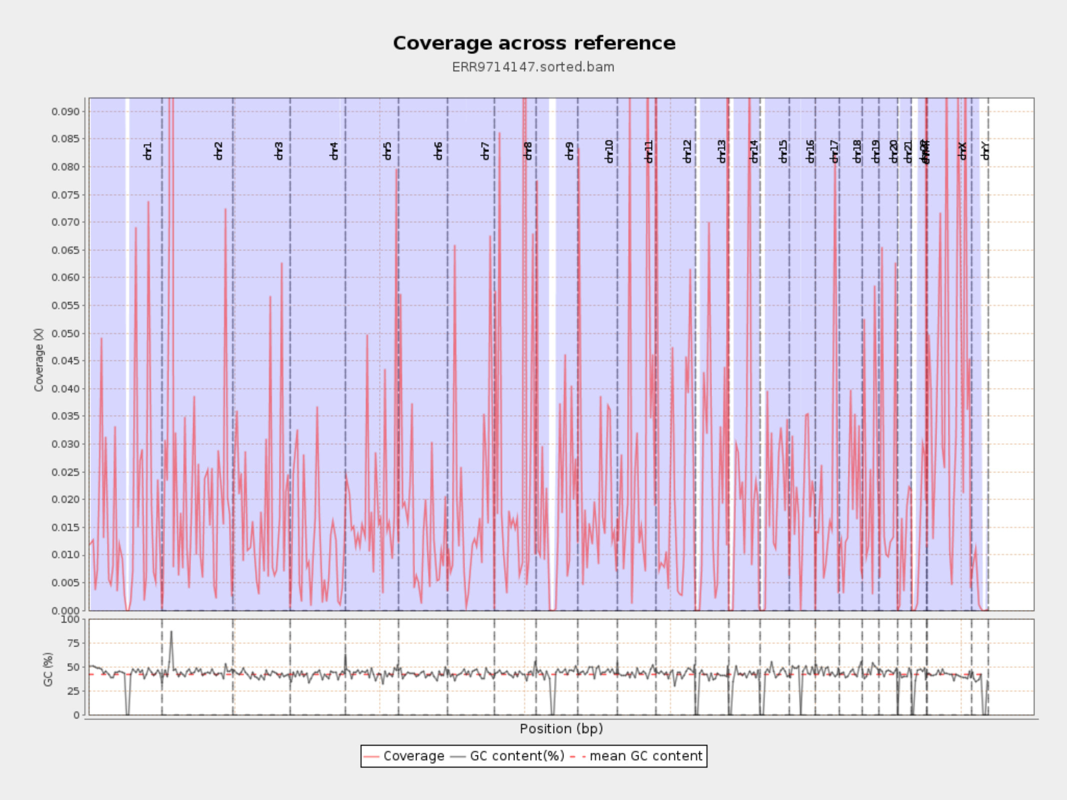
General error rate	4.76%
Mismatches	3,065,446
Insertions	71,228
Mapped reads with at least one insertion	12.65%
Deletions	270,821
Mapped reads with at least one deletion	46.53%
Homopolymer indels	31.14%

2.6. Chromosome stats

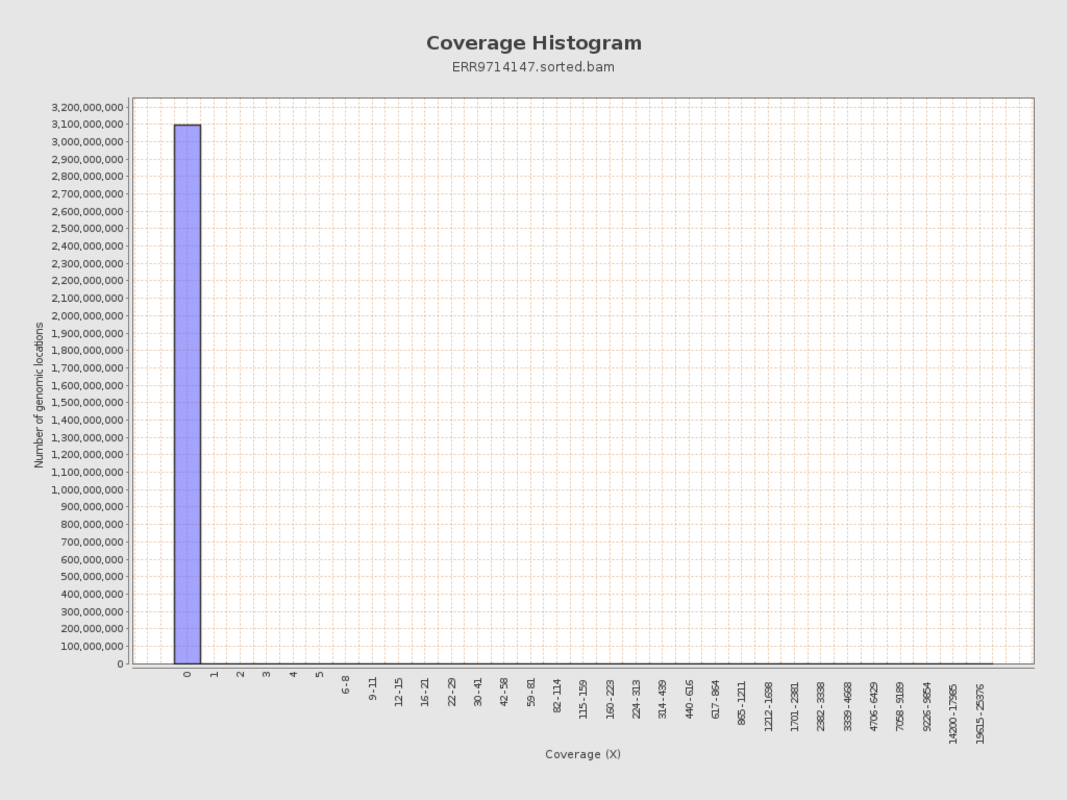
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4099449	0.0164	3.0398
chr2	243199373	9469067	0.0389	16.6183
chr3	198022430	3685213	0.0186	3.4402
chr4	191154276	2290286	0.012	2.0553
chr5	180915260	3681098	0.0203	3.3306
chr6	171115067	2640147	0.0154	2.3926
chr7	159138663	3019237	0.019	3.5824

chr8	146364022	4852896	0.0332	10.311
chr9	141213431	2400968	0.017	2.339
chr10	135534747	2959635	0.0218	3.1947
chr11	135006516	3836517	0.0284	6.2111
chr12	133851895	3074327	0.023	3.6533
chr13	115169878	2797856	0.0243	5.4449
chr14	107349540	2452090	0.0228	5.448
chr15	102531392	1972860	0.0192	2.5849
chr16	90354753	1850539	0.0205	2.5226
chr17	81195210	1711587	0.0211	3.9321
chr18	78077248	1502012	0.0192	3.005
chr19	59128983	1475799	0.025	4.2309
chr20	63025520	1549813	0.0246	5.3862
chr21	48129895	588936	0.0122	1.8192
chr22	51304566	631195	0.0123	2.0441
chrMT	16571	560276	33.8106	261.404
chrX	155270560	6661553	0.0429	4.9752
chrY	59373566	205521	0.0035	0.6773

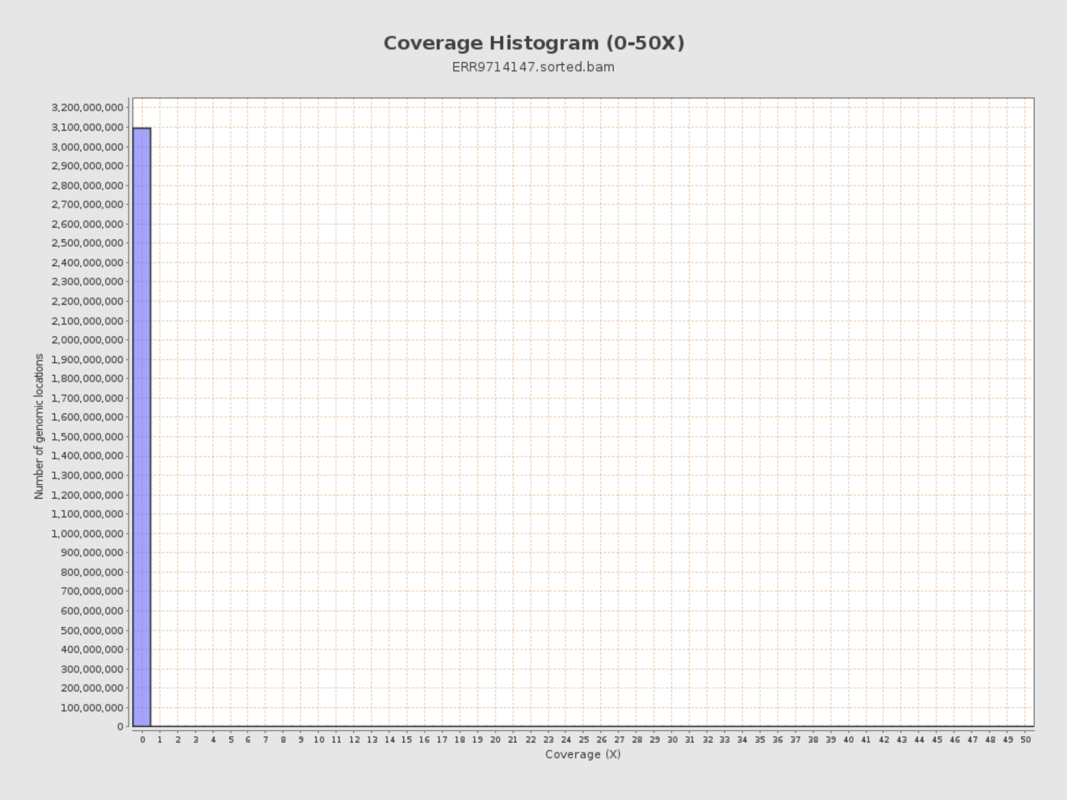
3. Results : Coverage across reference



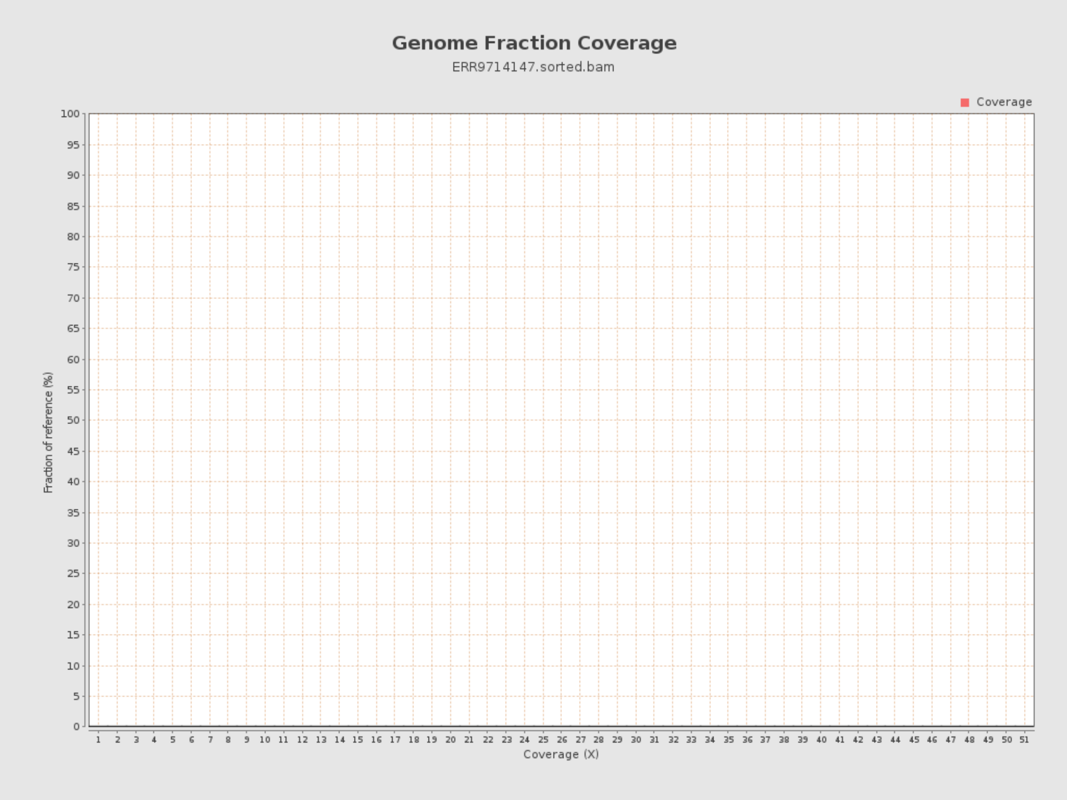
4. Results : Coverage Histogram



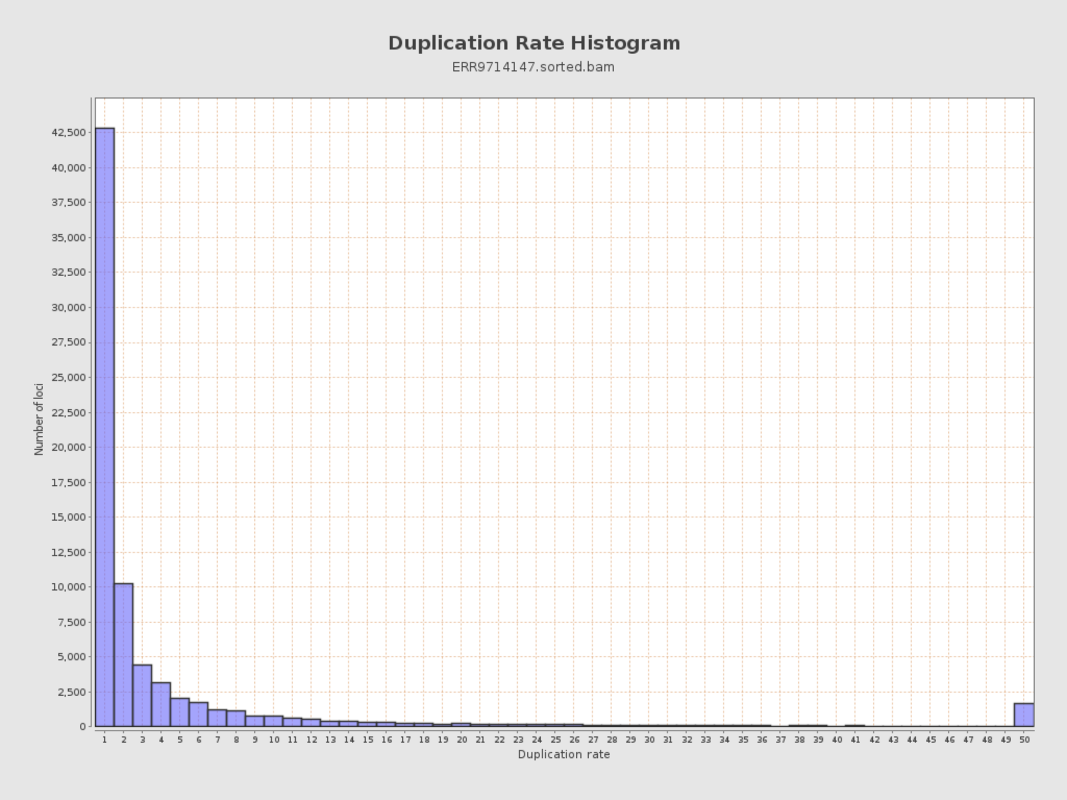
5. Results : Coverage Histogram (0-50X)



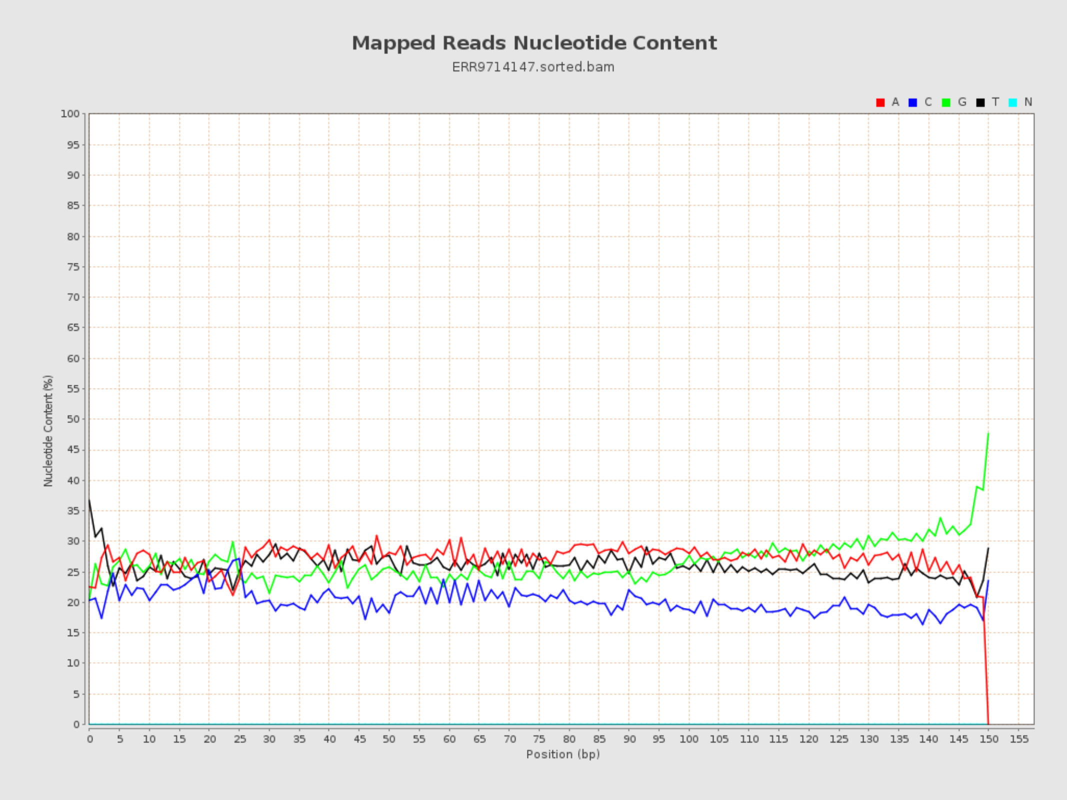
6. Results : Genome Fraction Coverage



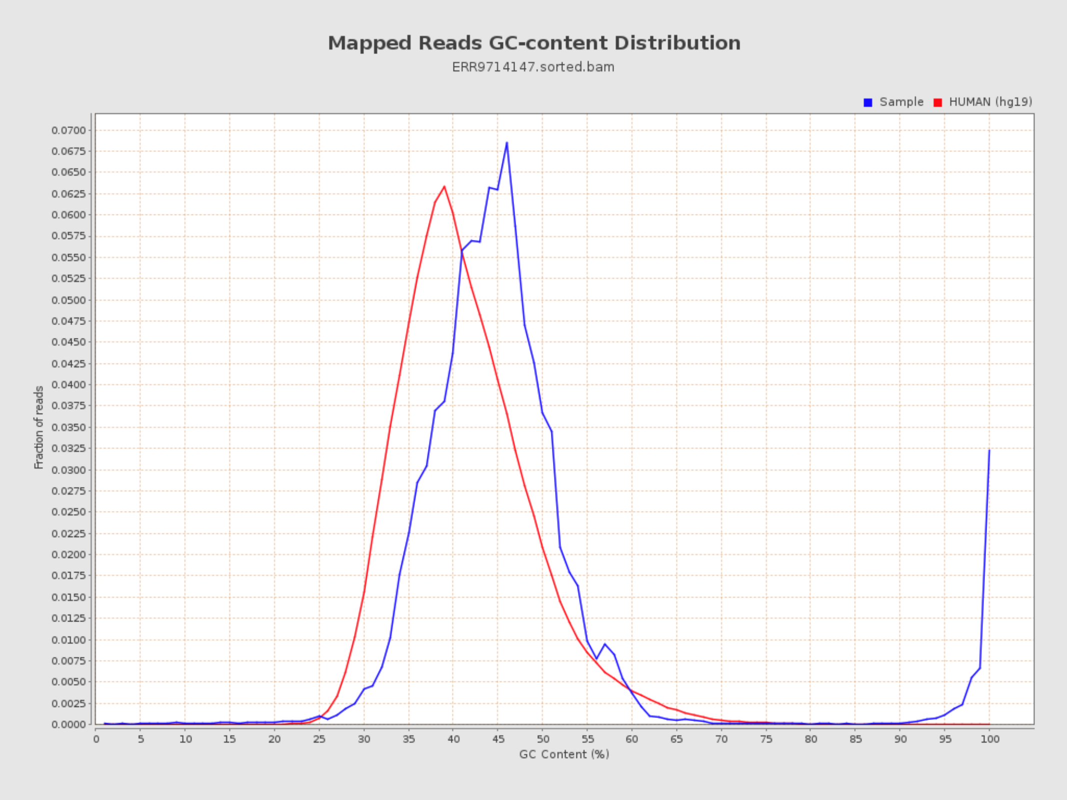
7. Results : Duplication Rate Histogram



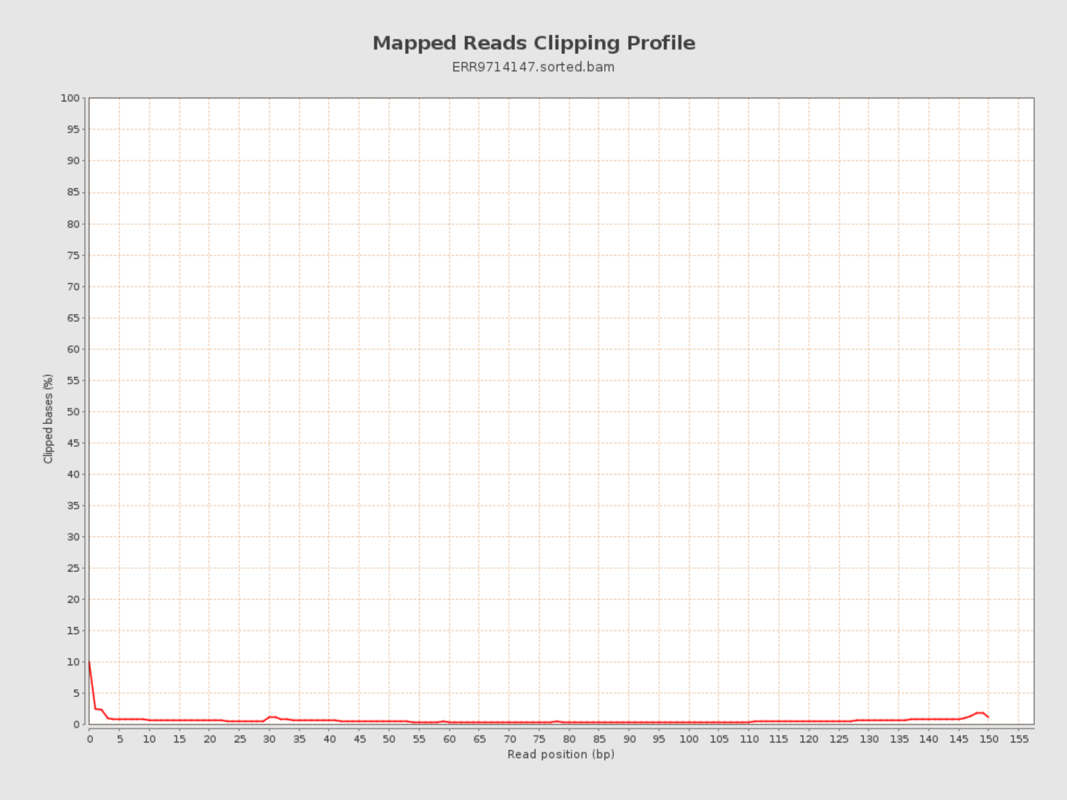
8. Results : Mapped Reads Nucleotide Content



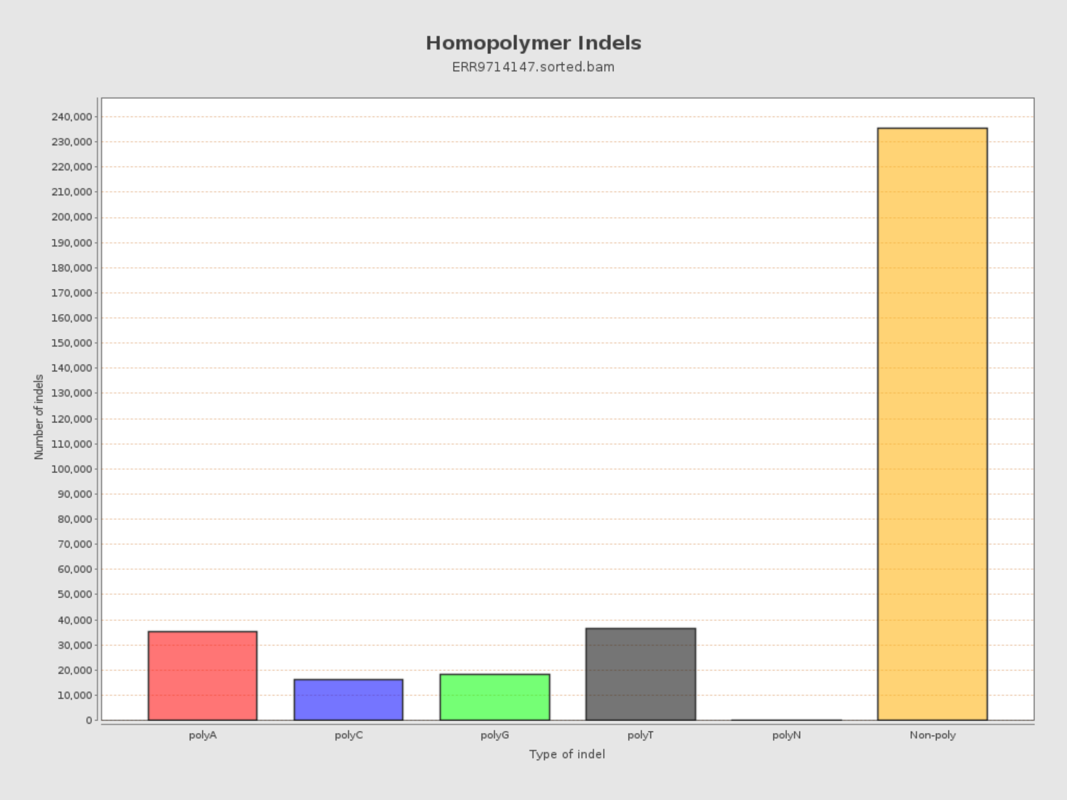
9. Results : Mapped Reads GC-content Distribution



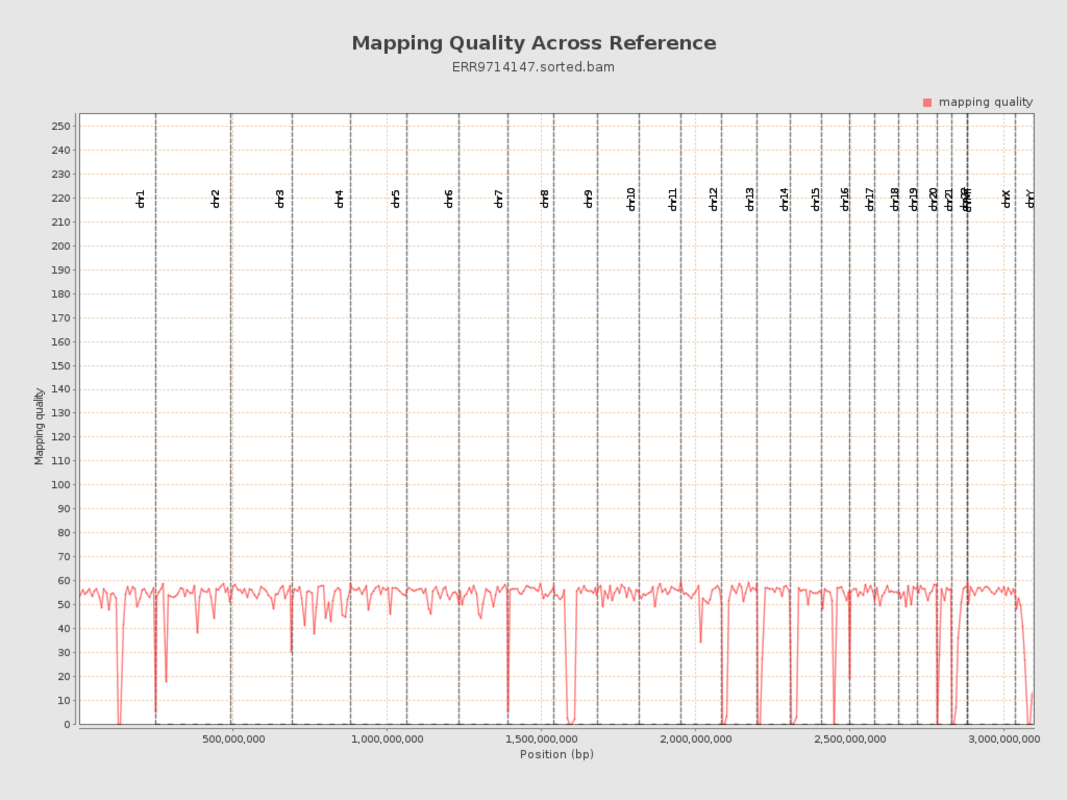
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram