Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:32:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714146.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_ERR9714146 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714146.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:32:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	667,136
Mapped reads	623,300 / 93.43%
Unmapped reads	43,836 / 6.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,120 / 3.77%
Read min/max/mean length	30 / 151 / 144.34
Duplicated reads (estimated)	556,653 / 83.44%
Duplication rate	42.16%
Clipped reads	594,386 / 89.1%

2.2. ACGT Content

Number/percentage of A's	23,596,644 / 29.78%
Number/percentage of C's	15,834,141 / 19.99%
Number/percentage of T's	22,196,156 / 28.02%
Number/percentage of G's	17,597,189 / 22.21%
Number/percentage of N's	545 / 0%
GC Percentage	42.2%

2.3. Coverage

Mean	0.026

Standard Deviation	5.5818

2.4. Mapping Quality

Mean Mapping Quality	50.72

2.5. Mismatches and indels

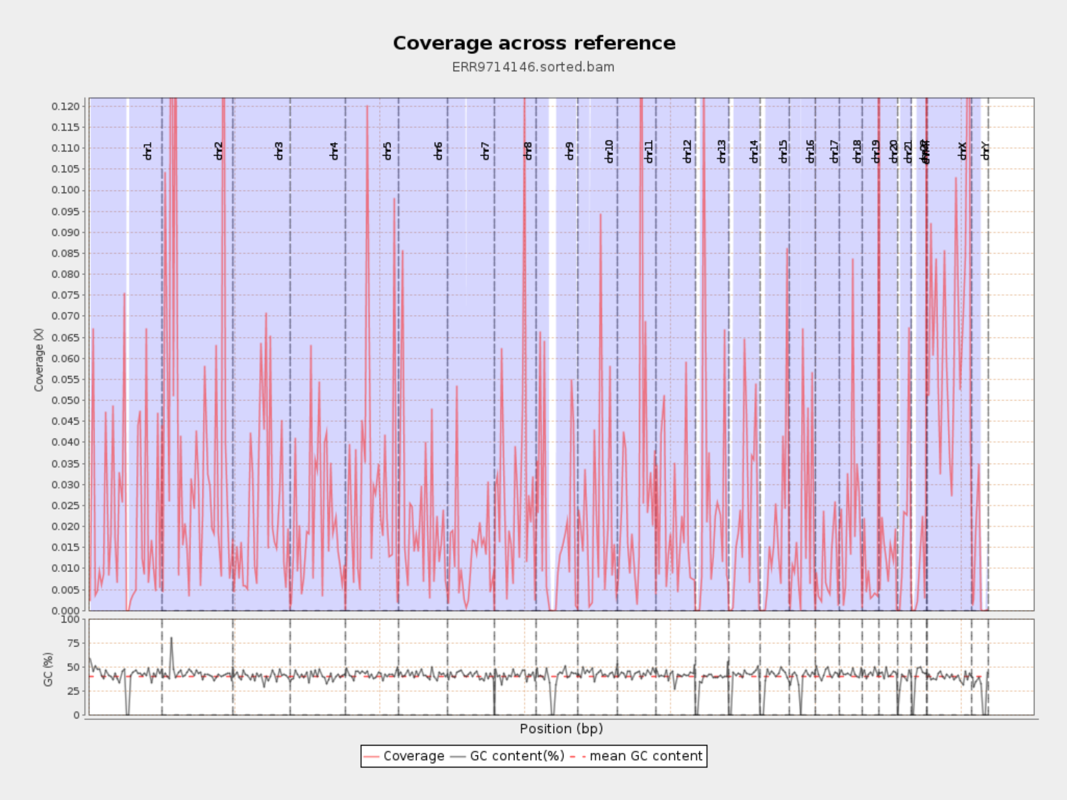
General error rate	3.96%
Mismatches	2,848,143
Insertions	96,721
Mapped reads with at least one insertion	15.11%
Deletions	250,467
Mapped reads with at least one deletion	38.43%
Homopolymer indels	27.13%

2.6. Chromosome stats

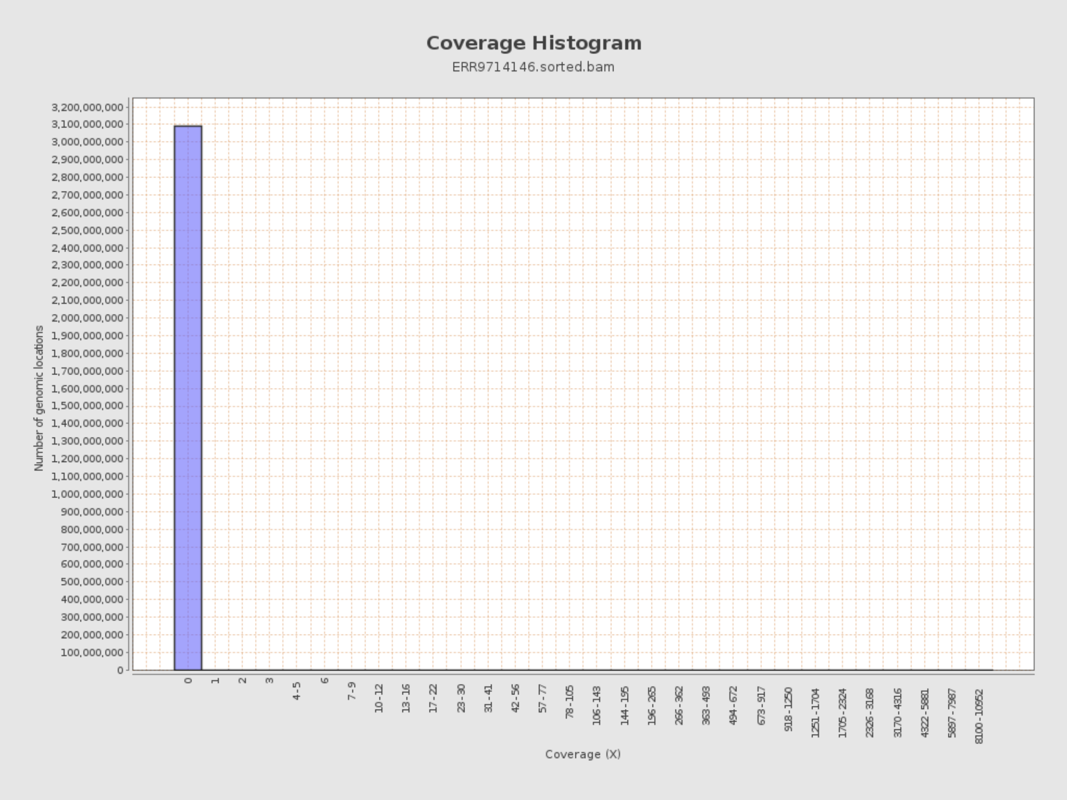
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5210036	0.0209	4.0932
chr2	243199373	10747469	0.0442	10.8155
chr3	198022430	4767086	0.0241	3.9917
chr4	191154276	4211876	0.022	3.6182
chr5	180915260	5728664	0.0317	5.7989
chr6	171115067	3796633	0.0222	4.6925
chr7	159138663	2231075	0.014	1.9853

chr8	146364022	4374607	0.0299	6.883
chr9	141213431	2787932	0.0197	4.2615
chr10	135534747	3269616	0.0241	3.1626
chr11	135006516	4462681	0.0331	9.7258
chr12	133851895	2822691	0.0211	3.5069
chr13	115169878	2906495	0.0252	6.0661
chr14	107349540	2533463	0.0236	3.7473
chr15	102531392	1883388	0.0184	4.4608
chr16	90354753	1850457	0.0205	4.3531
chr17	81195210	802847	0.0099	1.7238
chr18	78077248	1993991	0.0255	5.4267
chr19	59128983	815345	0.0138	4.6572
chr20	63025520	835500	0.0133	1.4576
chr21	48129895	959981	0.0199	5.2189
chr22	51304566	380312	0.0074	1.1736
chrMT	16571	4020	0.2426	1.9362
chrX	155270560	10789075	0.0695	6.8623
chrY	59373566	444649	0.0075	2.1402

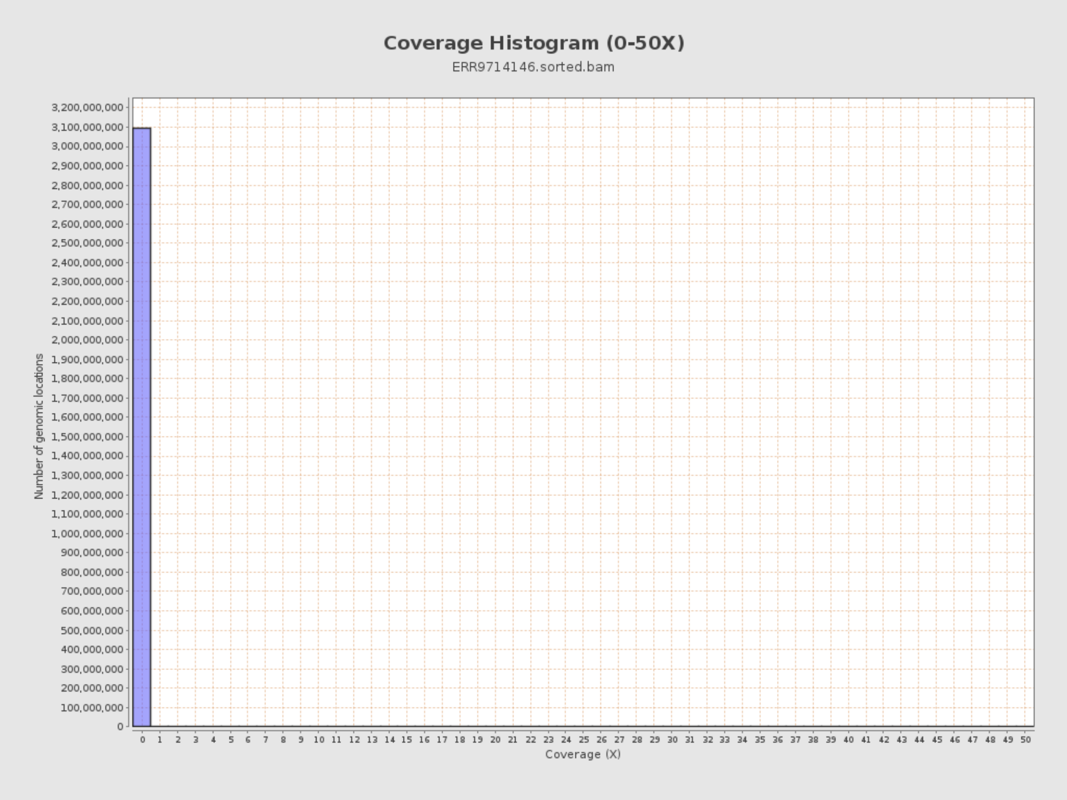
3. Results : Coverage across reference



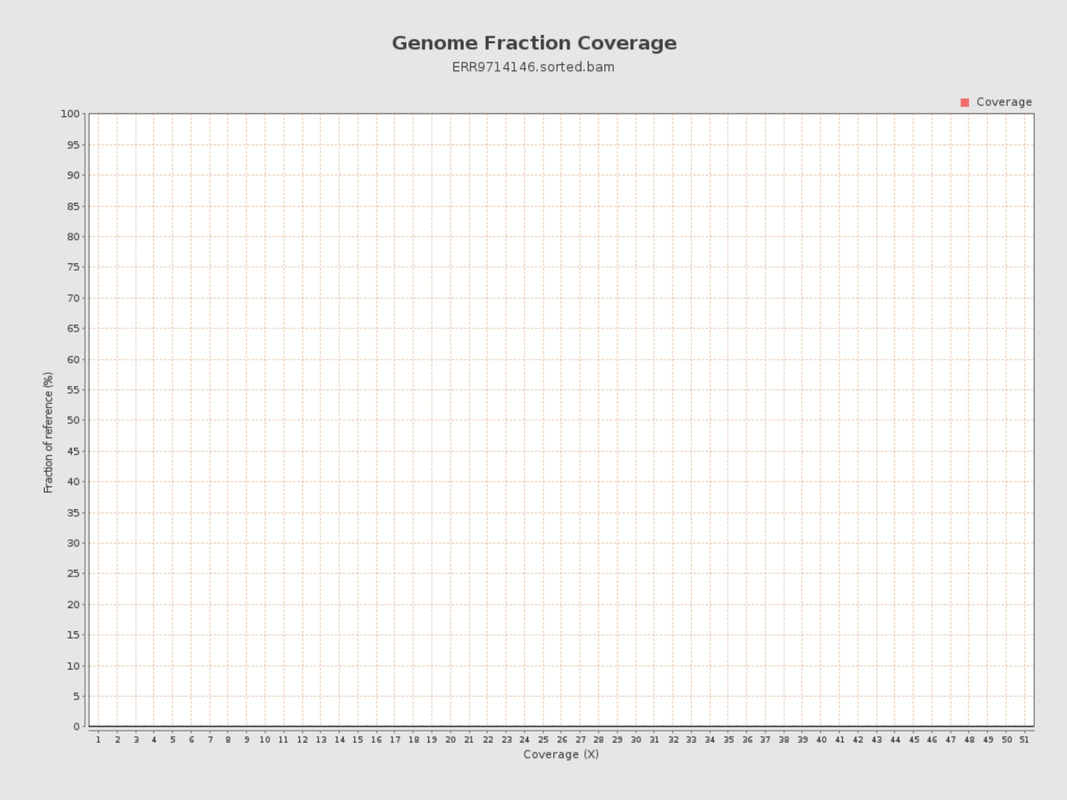
4. Results : Coverage Histogram



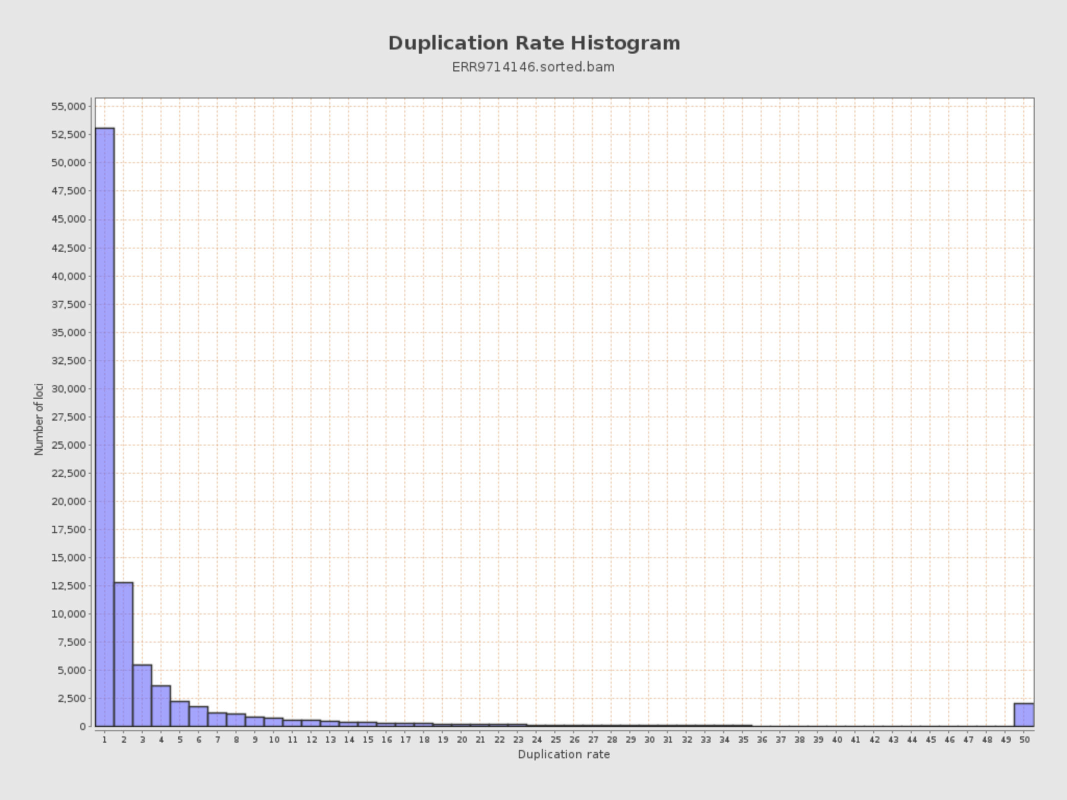
5. Results : Coverage Histogram (0-50X)



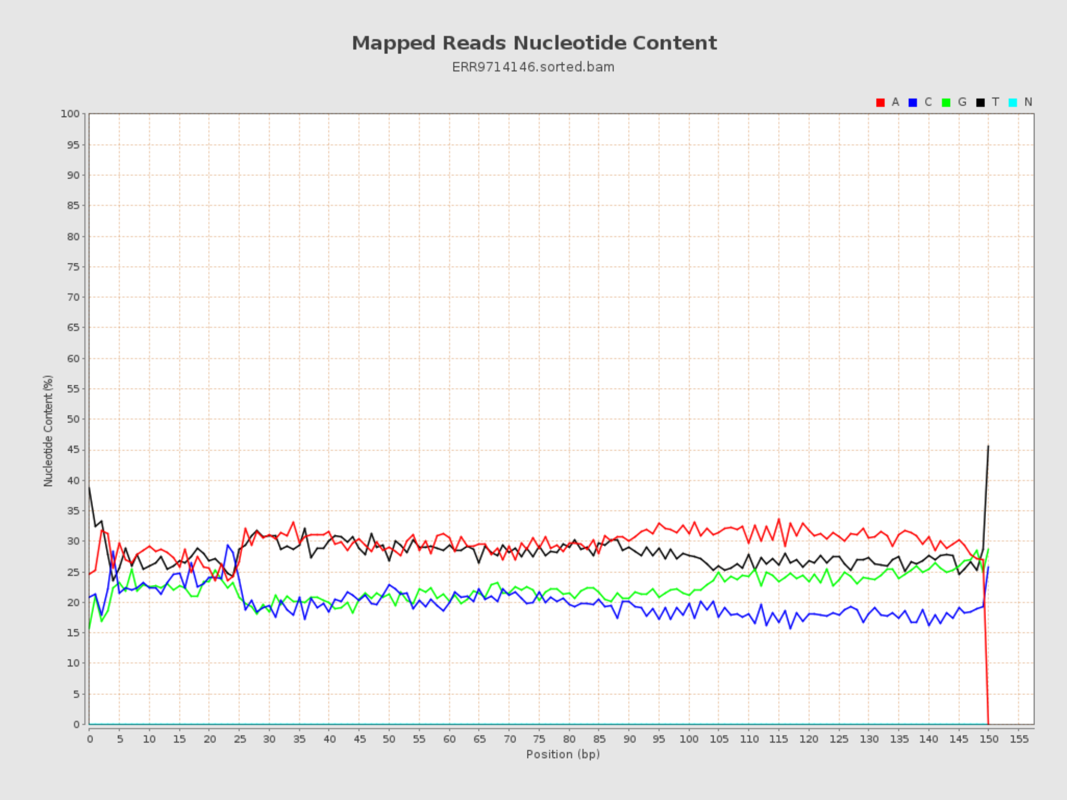
6. Results : Genome Fraction Coverage



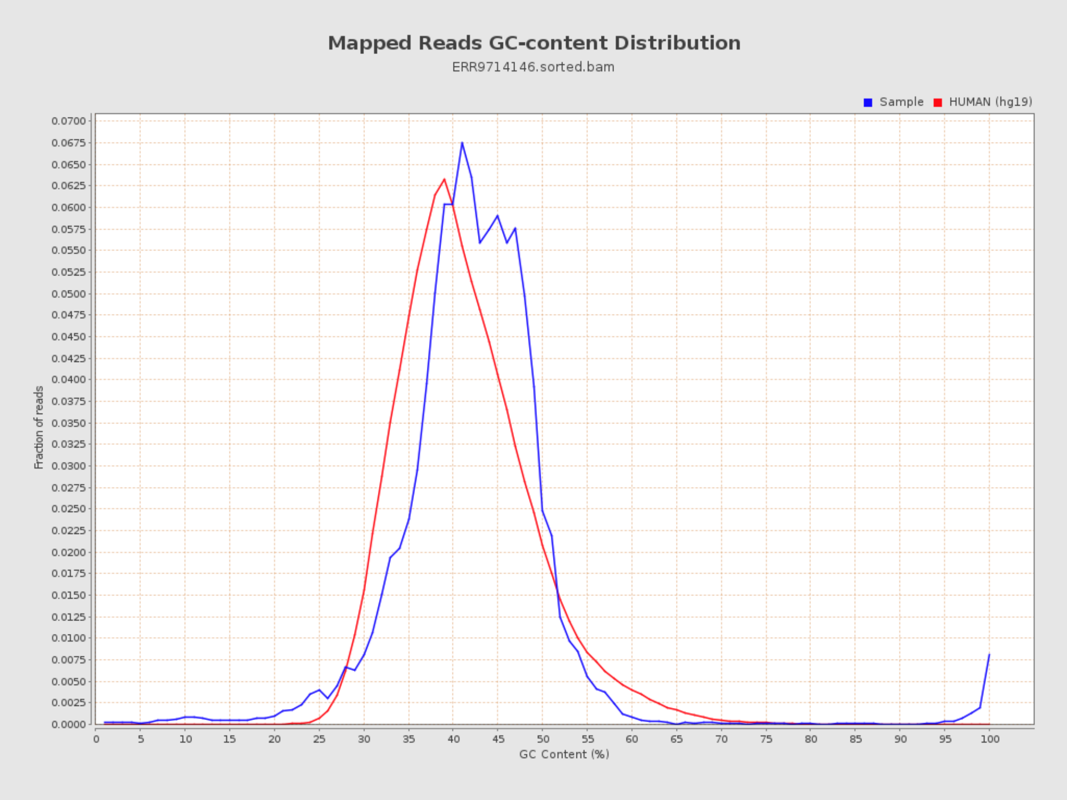
7. Results : Duplication Rate Histogram



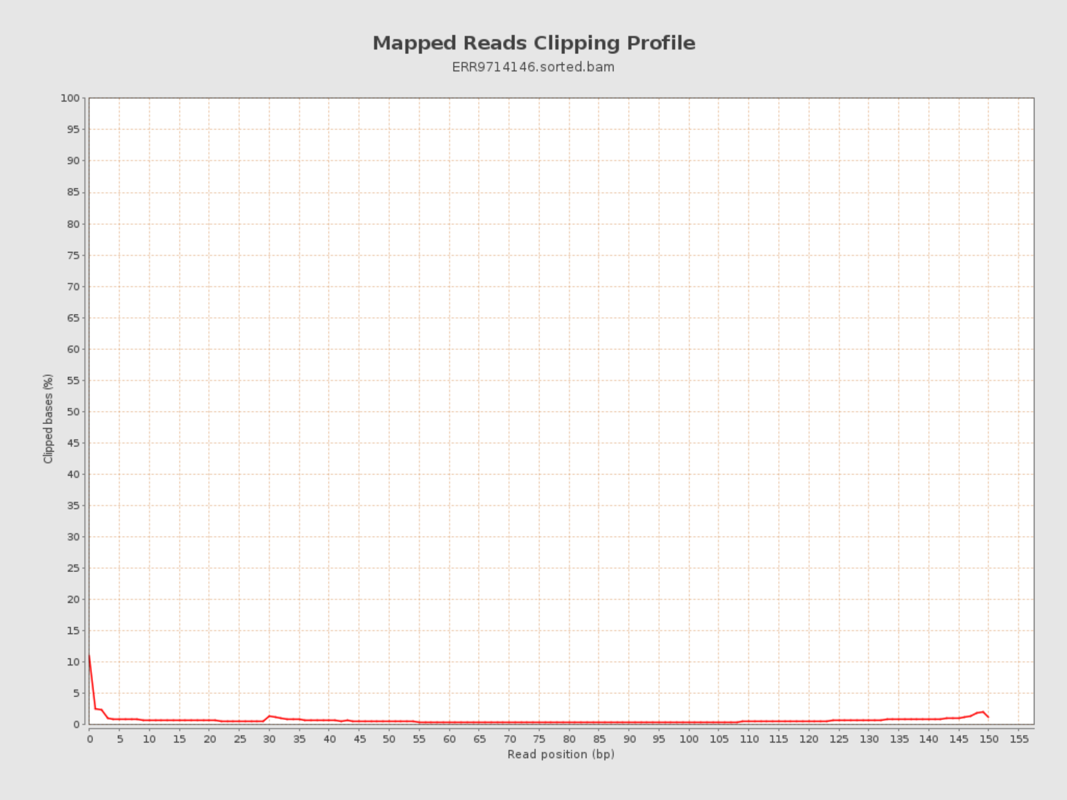
8. Results : Mapped Reads Nucleotide Content



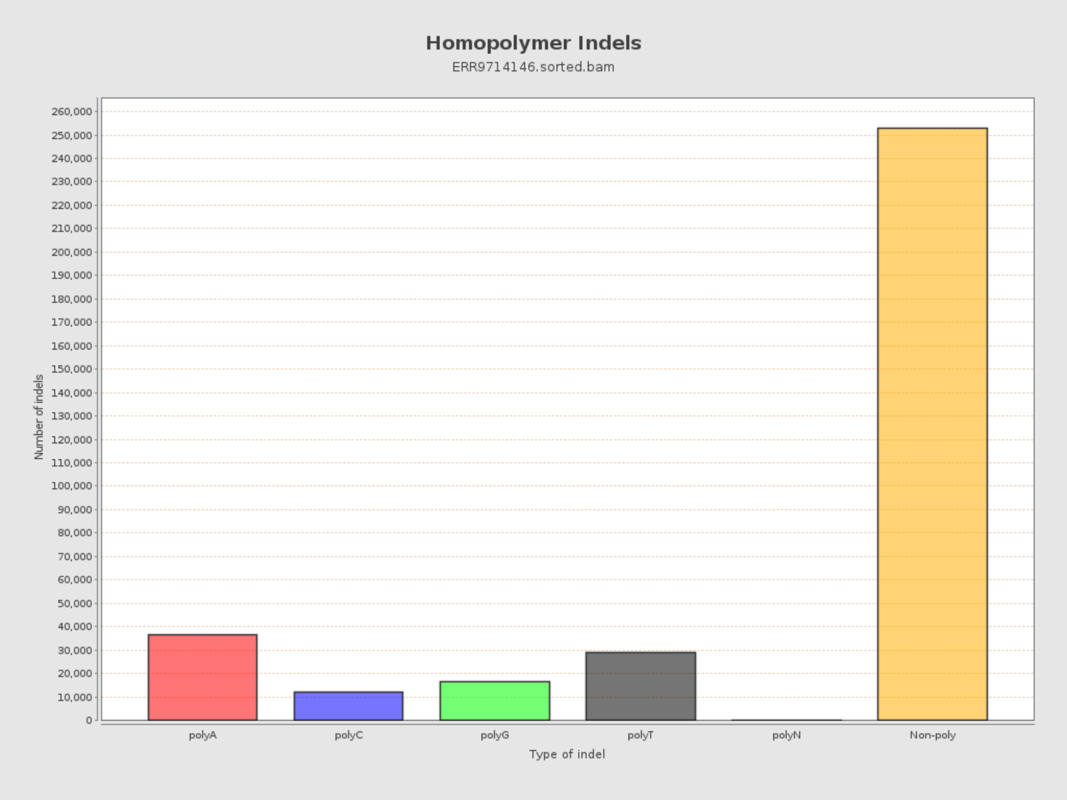
9. Results : Mapped Reads GC-content Distribution



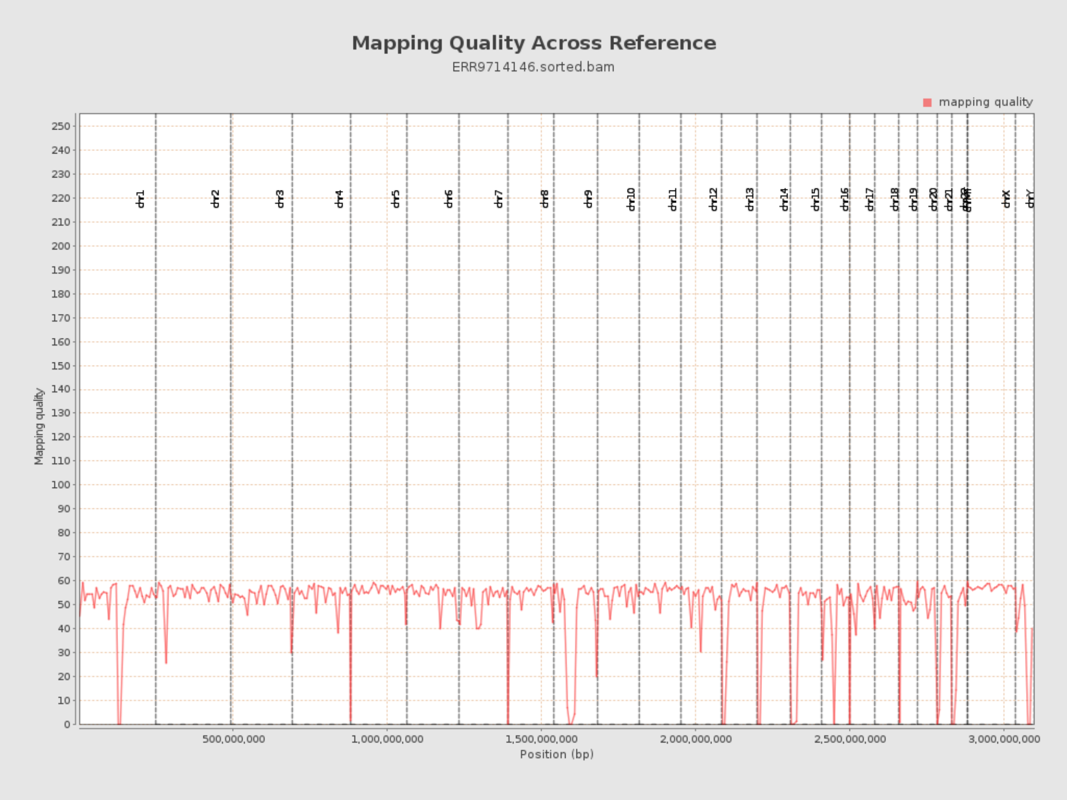
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram