Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:16:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714098.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_ERR9714098 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714098.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:16:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	535,102
Mapped reads	384,874 / 71.93%
Unmapped reads	150,228 / 28.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,815 / 2.21%
Read min/max/mean length	30 / 151 / 130.34
Duplicated reads (estimated)	326,242 / 60.97%
Duplication rate	43.73%
Clipped reads	357,871 / 66.88%

2.2. ACGT Content

Number/percentage of A's	13,948,310 / 28.24%
Number/percentage of C's	10,269,954 / 20.79%
Number/percentage of T's	13,262,331 / 26.85%
Number/percentage of G's	11,906,647 / 24.11%
Number/percentage of N's	431 / 0%
GC Percentage	44.9%

2.3. Coverage

Mean	0.0163

Standard Deviation	3.1084

2.4. Mapping Quality

Mean Mapping Quality	51.54

2.5. Mismatches and indels

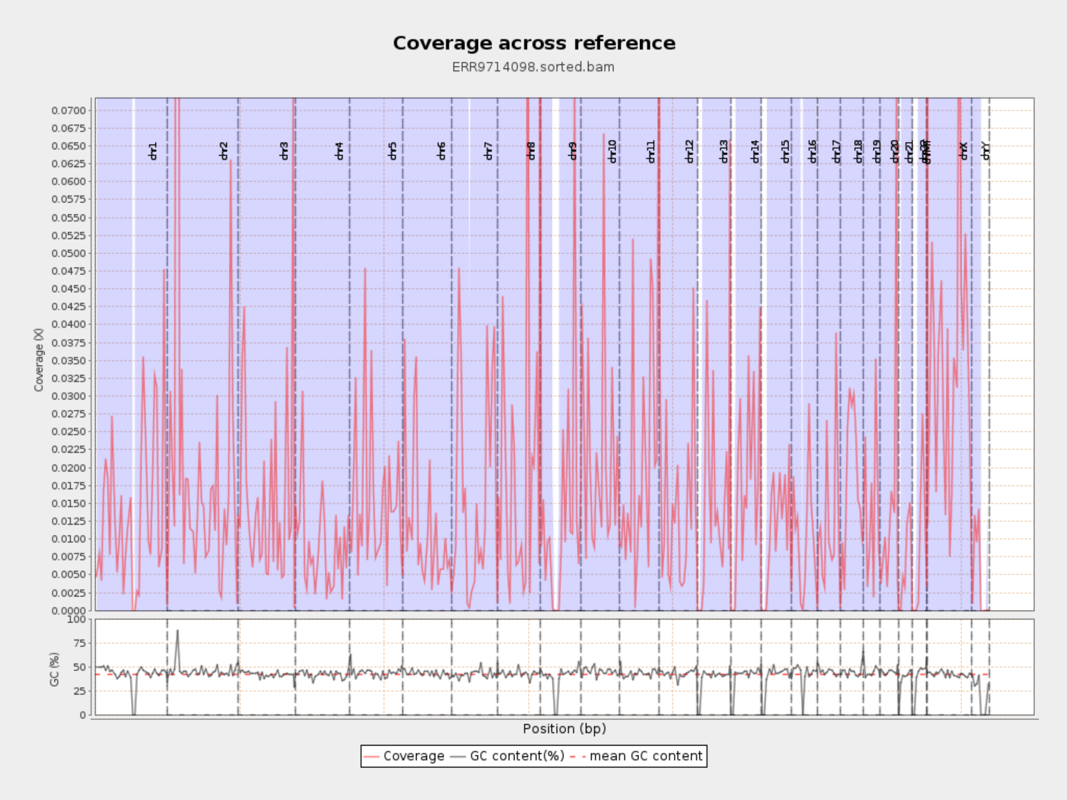
General error rate	4.72%
Mismatches	2,175,782
Insertions	56,088
Mapped reads with at least one insertion	13.99%
Deletions	196,187
Mapped reads with at least one deletion	47.29%
Homopolymer indels	30.31%

2.6. Chromosome stats

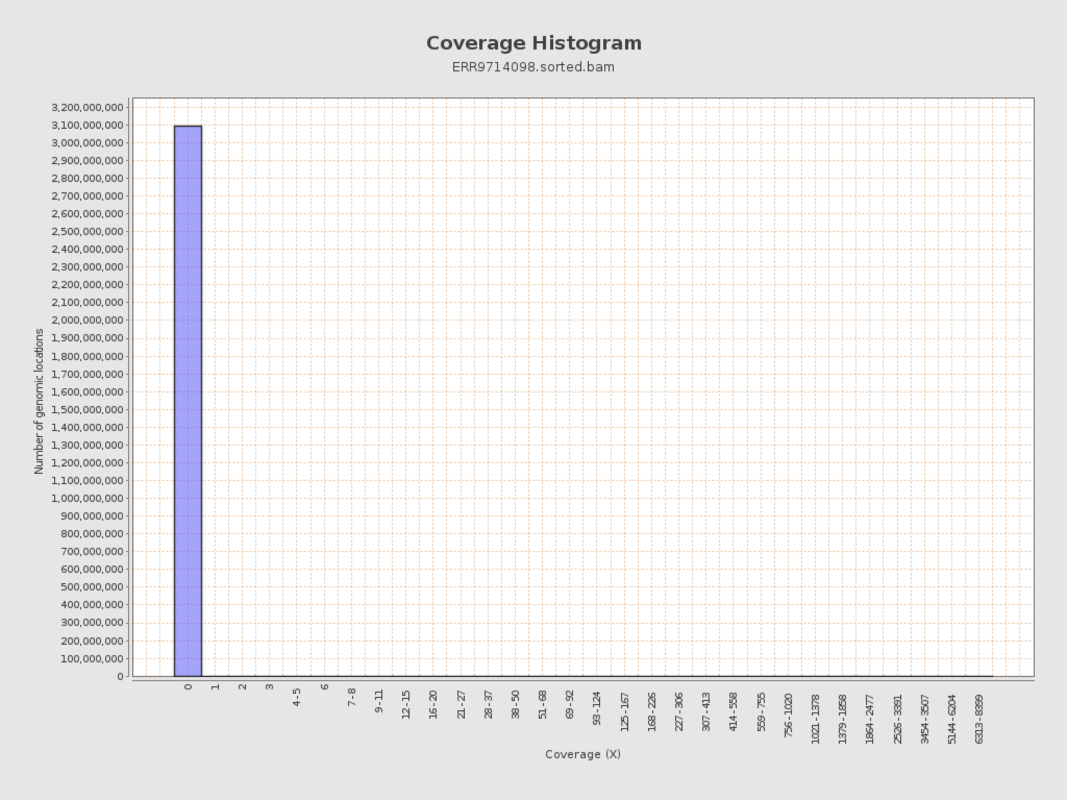
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3427218	0.0138	2.1555
chr2	243199373	5530701	0.0227	6.1265
chr3	198022430	3364394	0.017	3.4561
chr4	191154276	1743274	0.0091	1.1901
chr5	180915260	2912843	0.0161	2.9645
chr6	171115067	2005930	0.0117	1.6745
chr7	159138663	2546608	0.016	2.8201

chr8	146364022	2808097	0.0192	3.9673
chr9	141213431	2017958	0.0143	2.8867
chr10	135534747	2960026	0.0218	2.914
chr11	135006516	2650785	0.0196	3.4955
chr12	133851895	1912891	0.0143	1.855
chr13	115169878	1669624	0.0145	2.2466
chr14	107349540	1907041	0.0178	3.0575
chr15	102531392	1189010	0.0116	1.4007
chr16	90354753	939395	0.0104	1.1892
chr17	81195210	1035611	0.0128	2.2538
chr18	78077248	1476122	0.0189	2.6901
chr19	59128983	813615	0.0138	1.9713
chr20	63025520	1081266	0.0172	3.9477
chr21	48129895	319343	0.0066	0.8187
chr22	51304566	419754	0.0082	1.4744
chrMT	16571	183785	11.0908	88.0629
chrX	155270560	5401565	0.0348	3.9612
chrY	59373566	293691	0.0049	1.2822

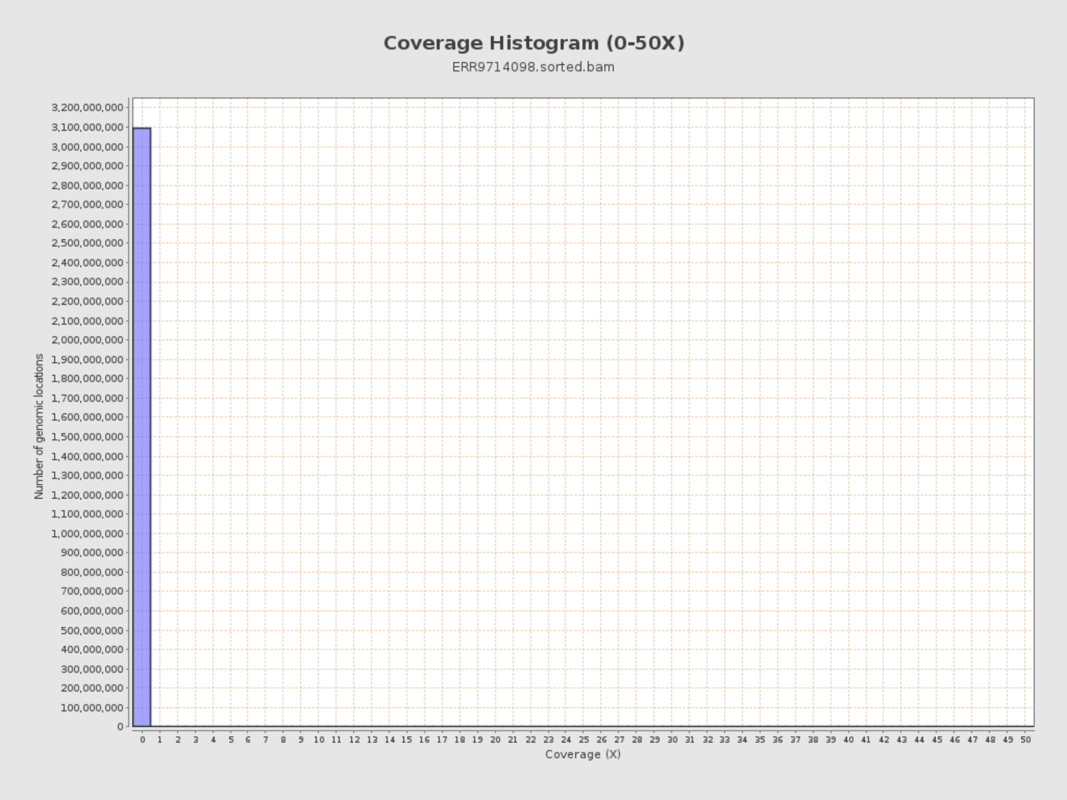
3. Results : Coverage across reference



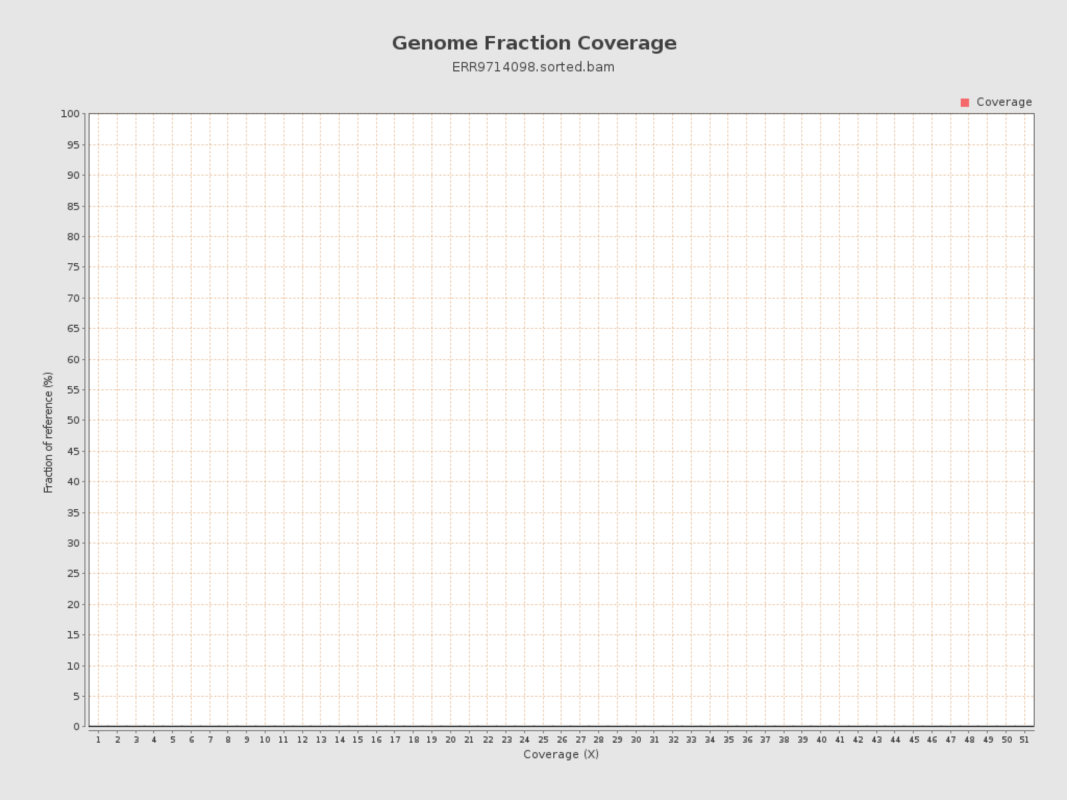
4. Results : Coverage Histogram



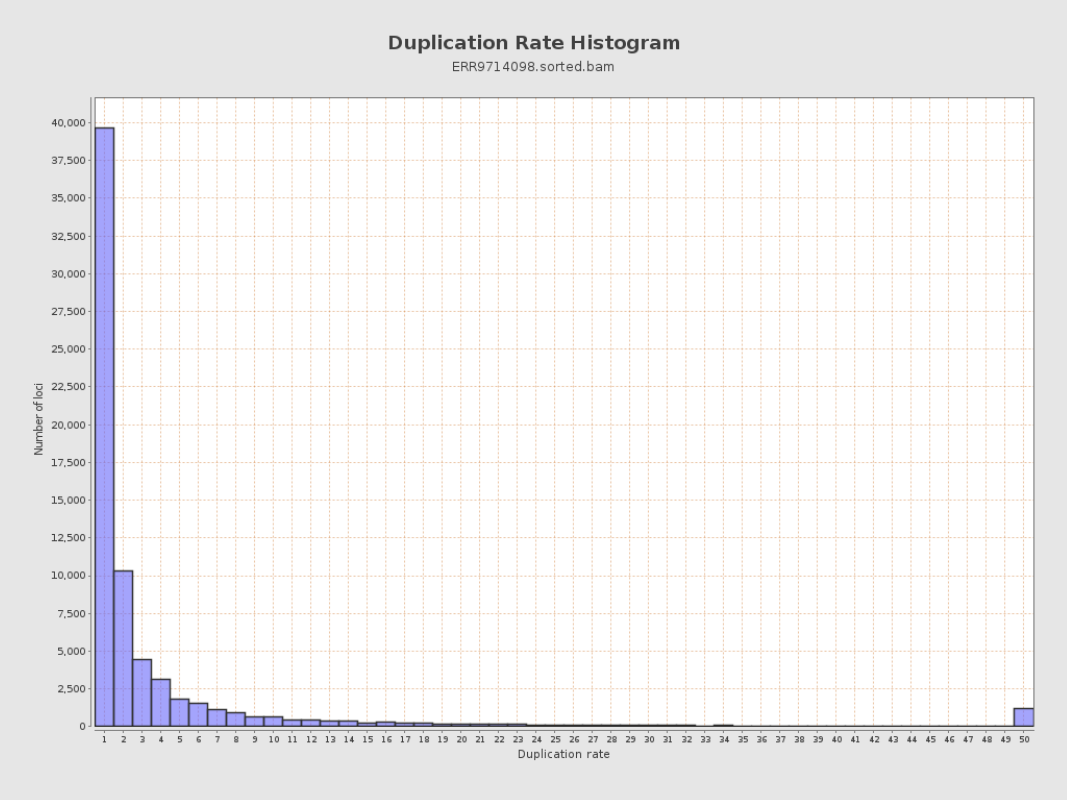
5. Results : Coverage Histogram (0-50X)



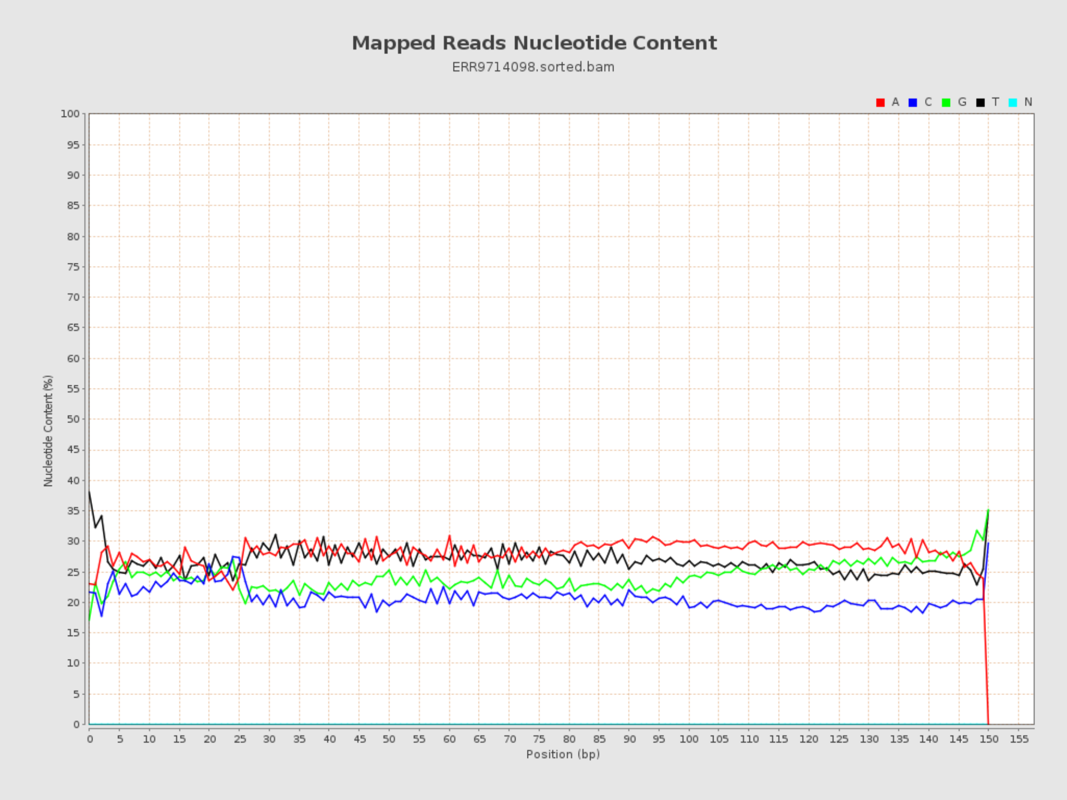
6. Results : Genome Fraction Coverage



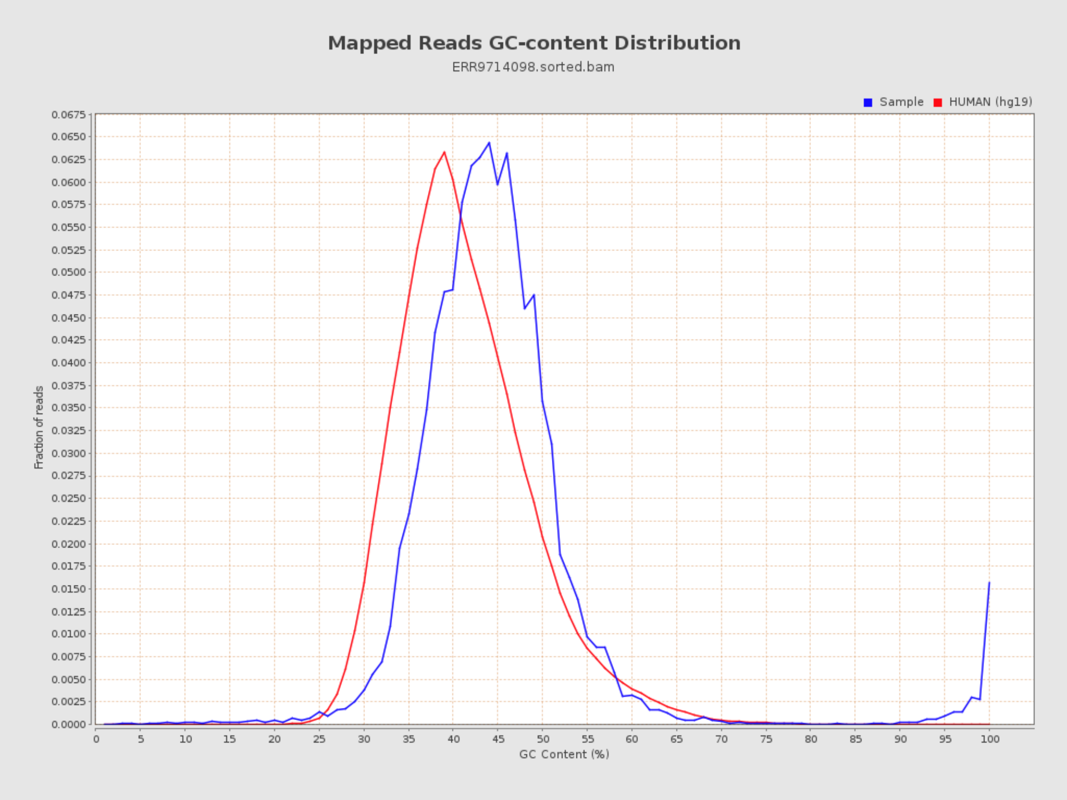
7. Results : Duplication Rate Histogram



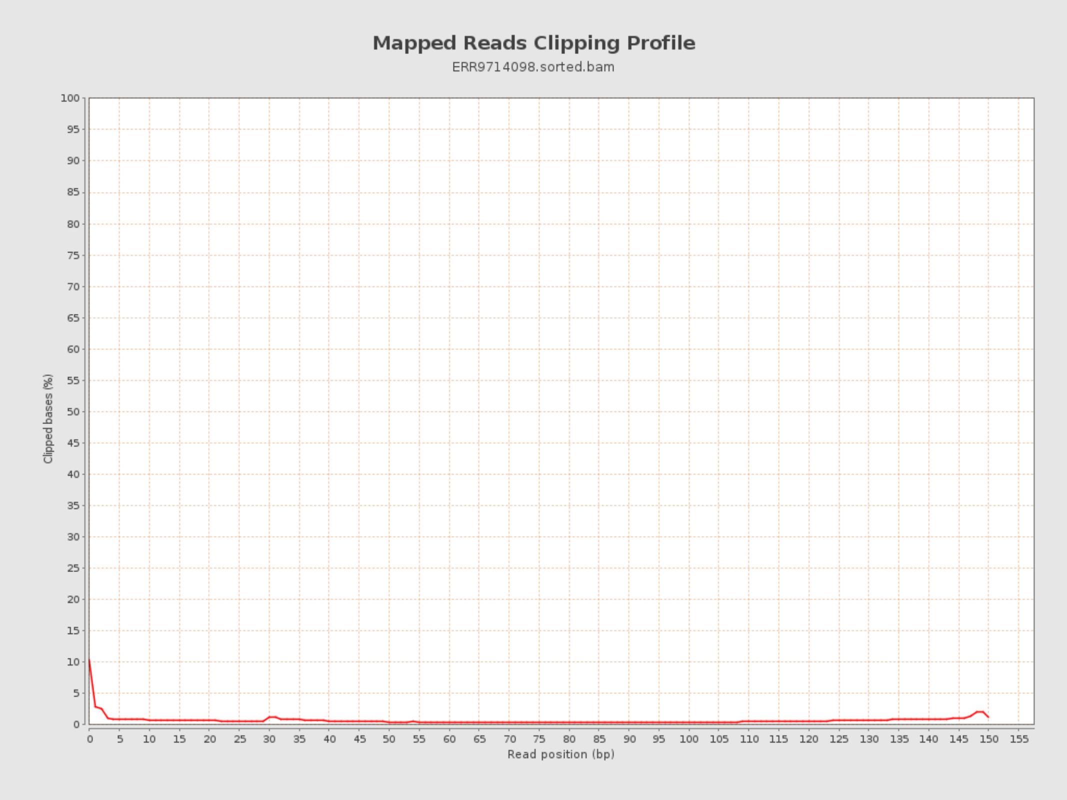
8. Results : Mapped Reads Nucleotide Content



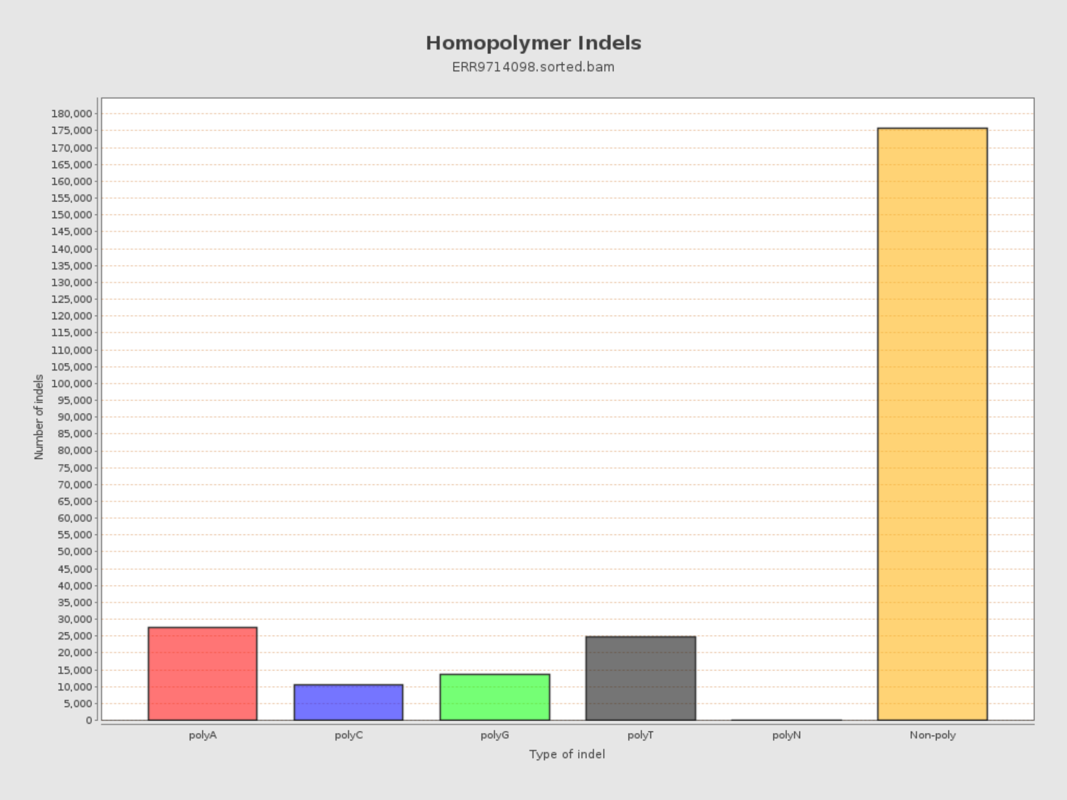
9. Results : Mapped Reads GC-content Distribution



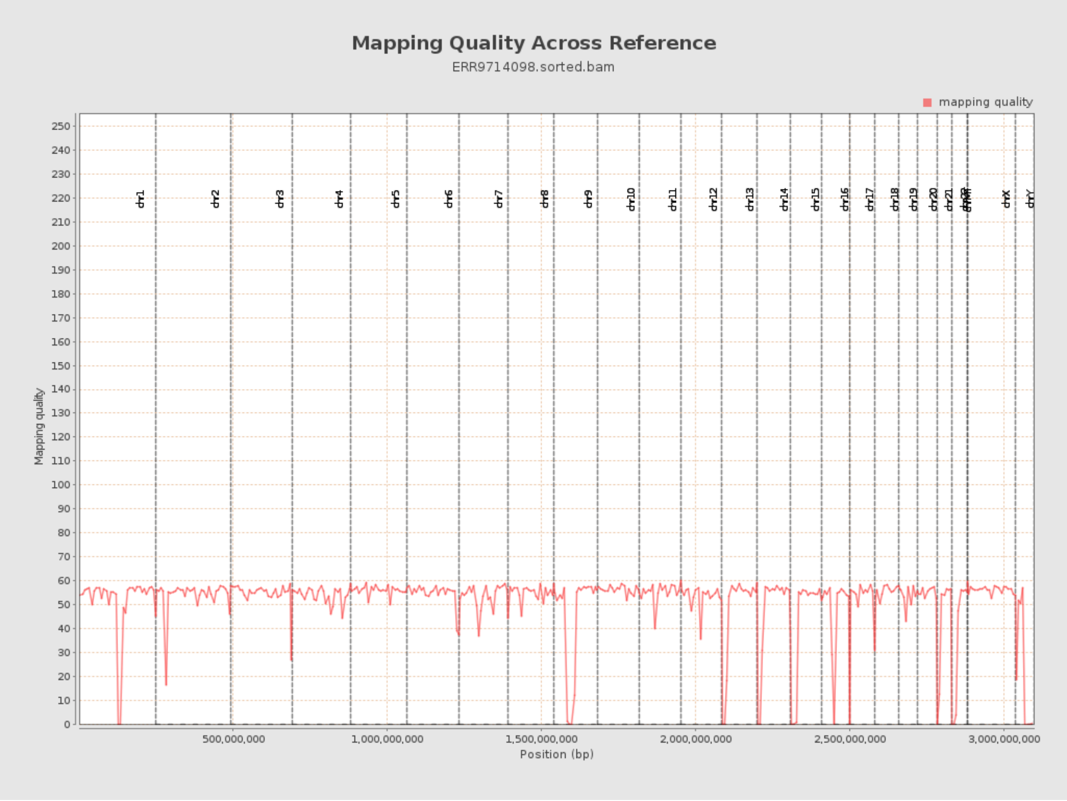
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram