Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:50:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714110.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_ERR9714110 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:50:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	609,844
Mapped reads	450,724 / 73.91%
Unmapped reads	159,120 / 26.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,970 / 2.45%
Read min/max/mean length	30 / 151 / 125.61
Duplicated reads (estimated)	391,038 / 64.12%
Duplication rate	44.02%
Clipped reads	421,718 / 69.15%

2.2. ACGT Content

Number/percentage of A's	15,793,597 / 27.78%
Number/percentage of C's	11,753,798 / 20.67%
Number/percentage of T's	14,912,453 / 26.23%
Number/percentage of G's	14,391,792 / 25.31%
Number/percentage of N's	413 / 0%
GC Percentage	45.99%

2.3. Coverage

Mean	0.0188

Standard Deviation	4.2166

2.4. Mapping Quality

Mean Mapping Quality	51.43

2.5. Mismatches and indels

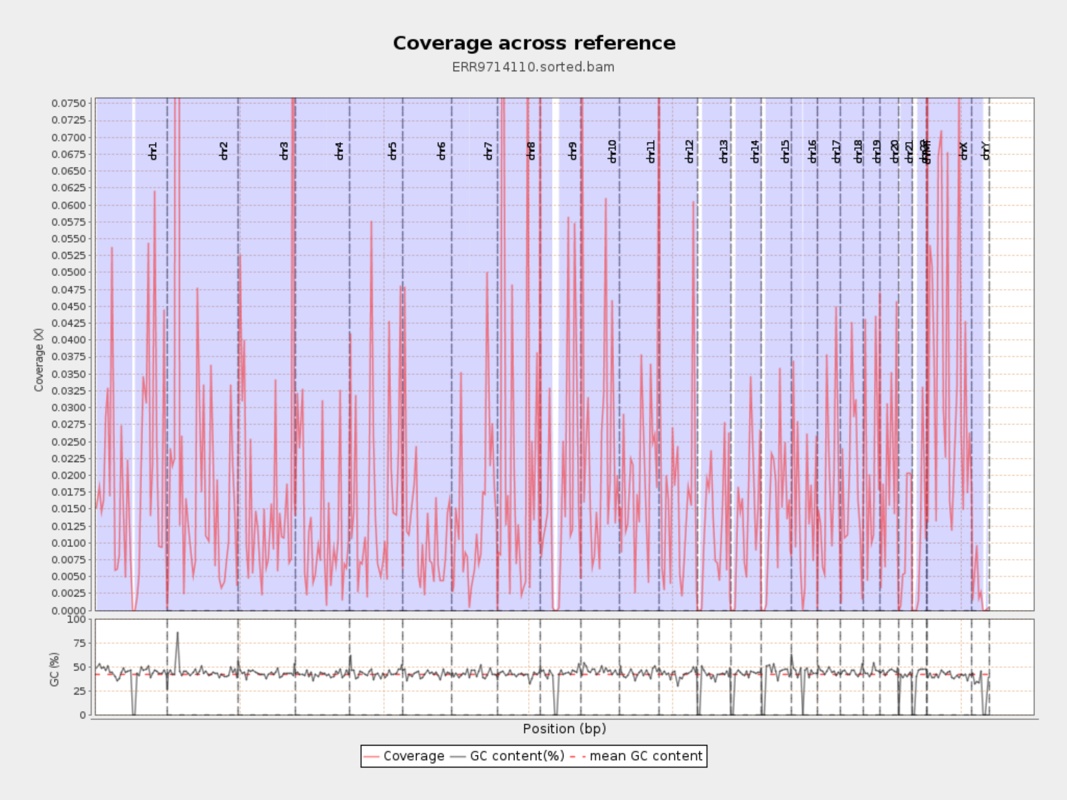
General error rate	4.83%
Mismatches	2,583,947
Insertions	62,743
Mapped reads with at least one insertion	13.27%
Deletions	230,472
Mapped reads with at least one deletion	47.36%
Homopolymer indels	30.78%

2.6. Chromosome stats

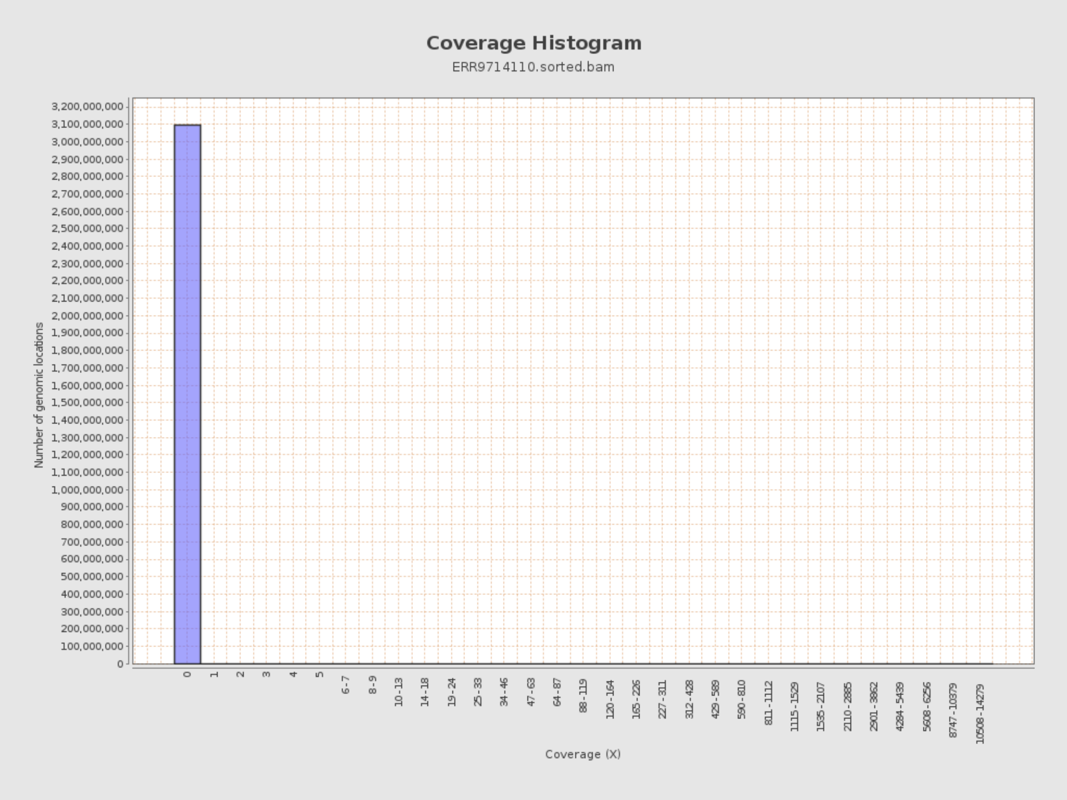
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4916264	0.0197	2.9865
chr2	243199373	6863619	0.0282	10.0957
chr3	198022430	4051542	0.0205	5.6773
chr4	191154276	2337393	0.0122	2.0508
chr5	180915260	3185592	0.0176	3.0196
chr6	171115067	2029604	0.0119	1.6322
chr7	159138663	2244788	0.0141	2.1033

chr8	146364022	3474288	0.0237	6.0028
chr9	141213431	2544687	0.018	2.8416
chr10	135534747	3449805	0.0255	4.4893
chr11	135006516	2618191	0.0194	2.6736
chr12	133851895	2244515	0.0168	2.5607
chr13	115169878	1388718	0.0121	2.088
chr14	107349540	1430633	0.0133	2.2623
chr15	102531392	1513909	0.0148	1.7792
chr16	90354753	1386417	0.0153	2.6544
chr17	81195210	1552989	0.0191	2.586
chr18	78077248	1547905	0.0198	2.9549
chr19	59128983	1306688	0.0221	2.5538
chr20	63025520	1334638	0.0212	3.2217
chr21	48129895	502025	0.0104	1.4416
chr22	51304566	487001	0.0095	1.5771
chrMT	16571	204231	12.3246	95.4509
chrX	155270560	5546393	0.0357	3.9068
chrY	59373566	165489	0.0028	0.5109

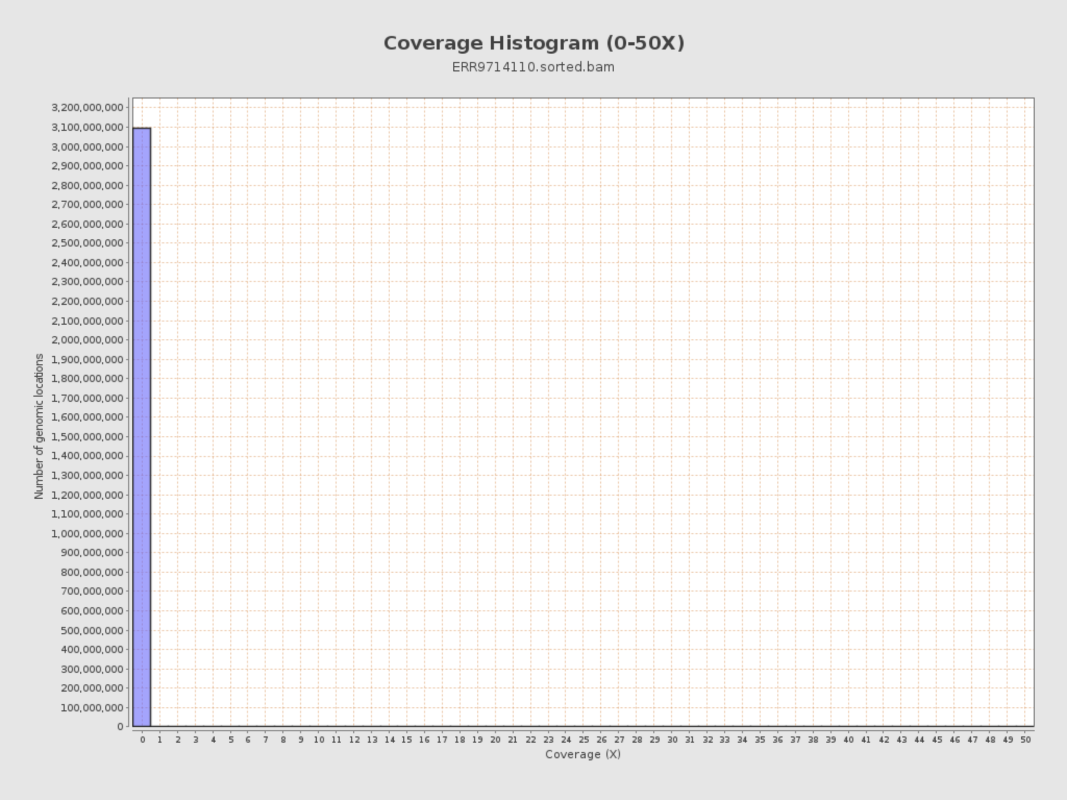
3. Results : Coverage across reference



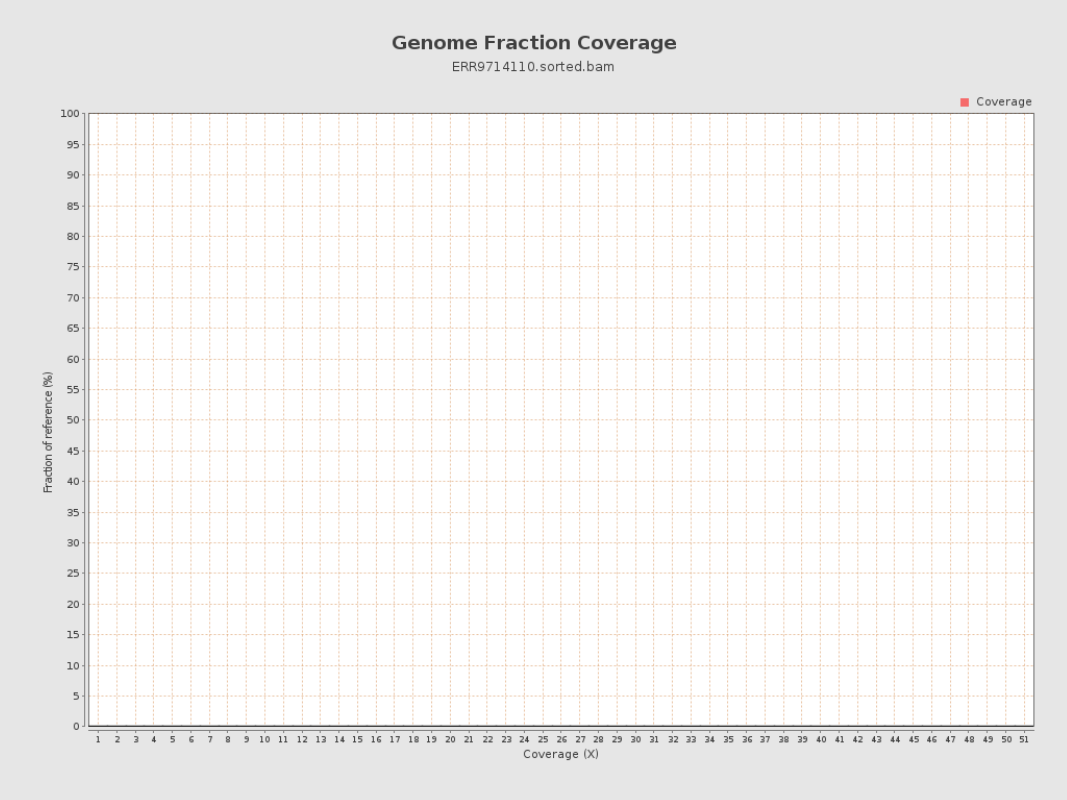
4. Results : Coverage Histogram



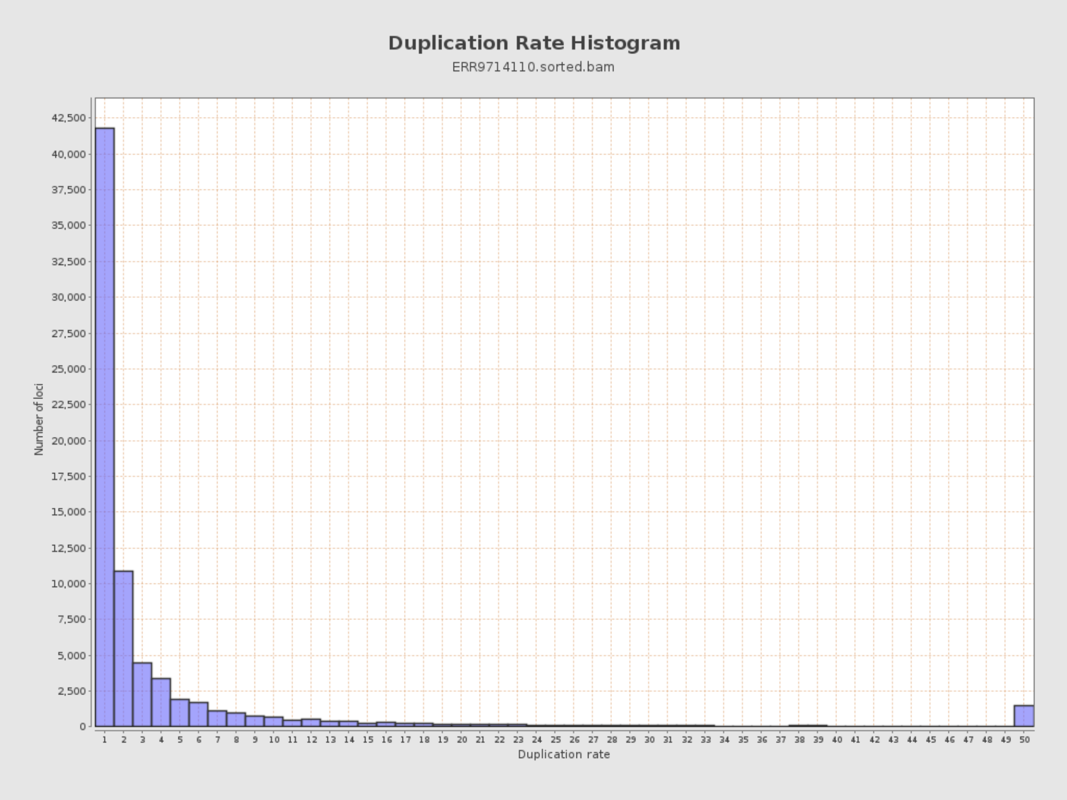
5. Results : Coverage Histogram (0-50X)



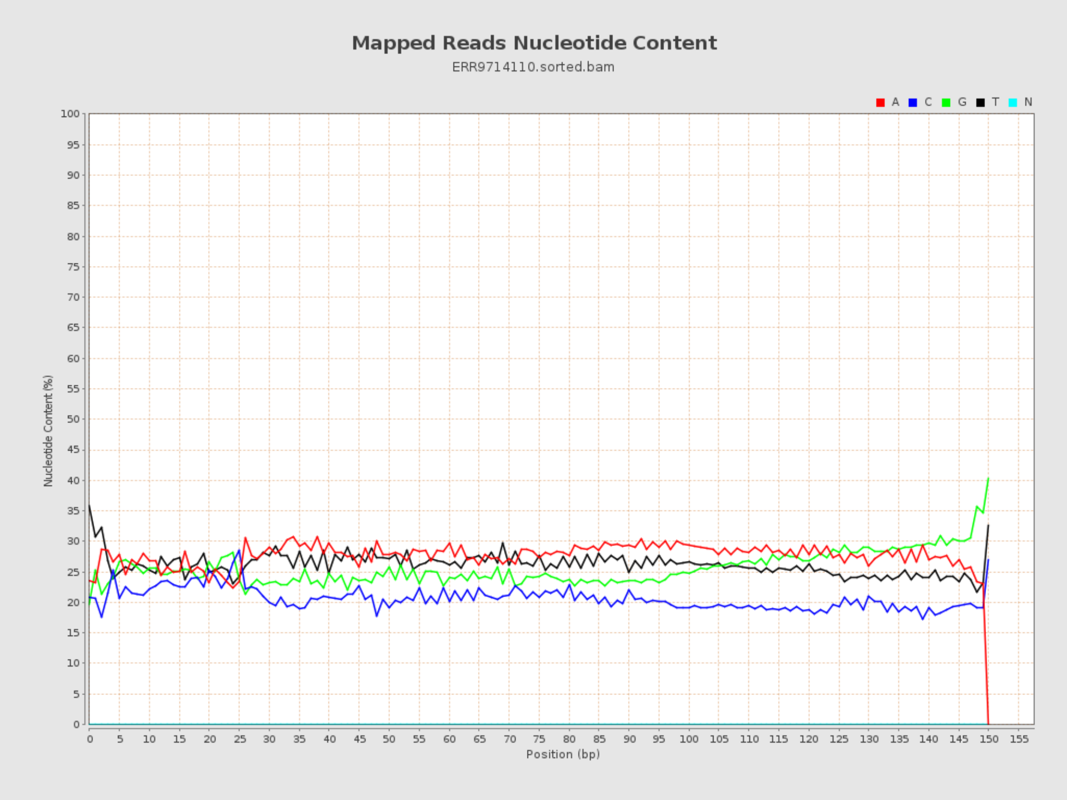
6. Results : Genome Fraction Coverage



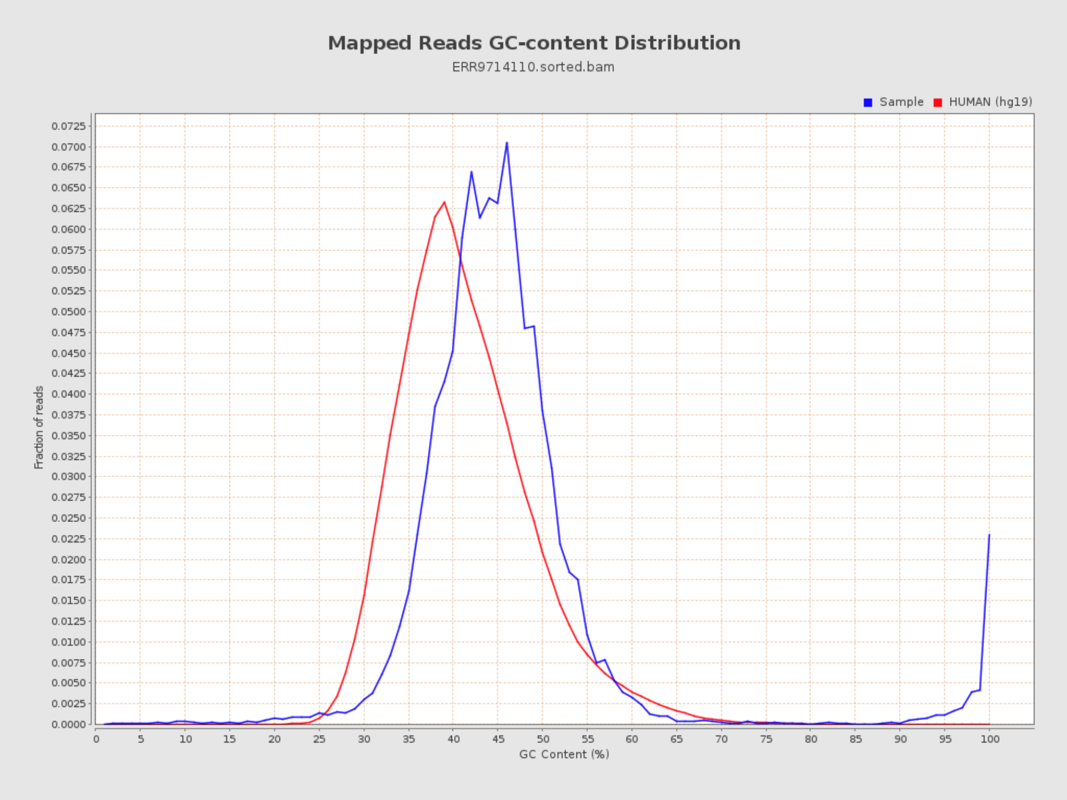
7. Results : Duplication Rate Histogram



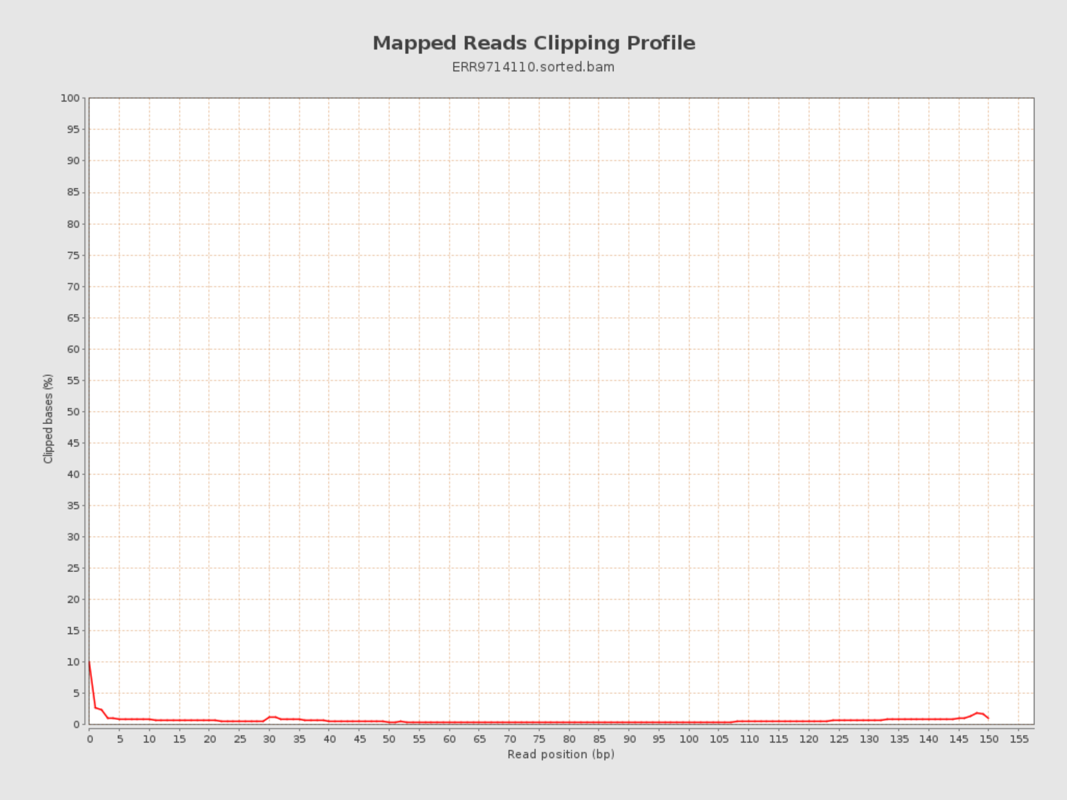
8. Results : Mapped Reads Nucleotide Content



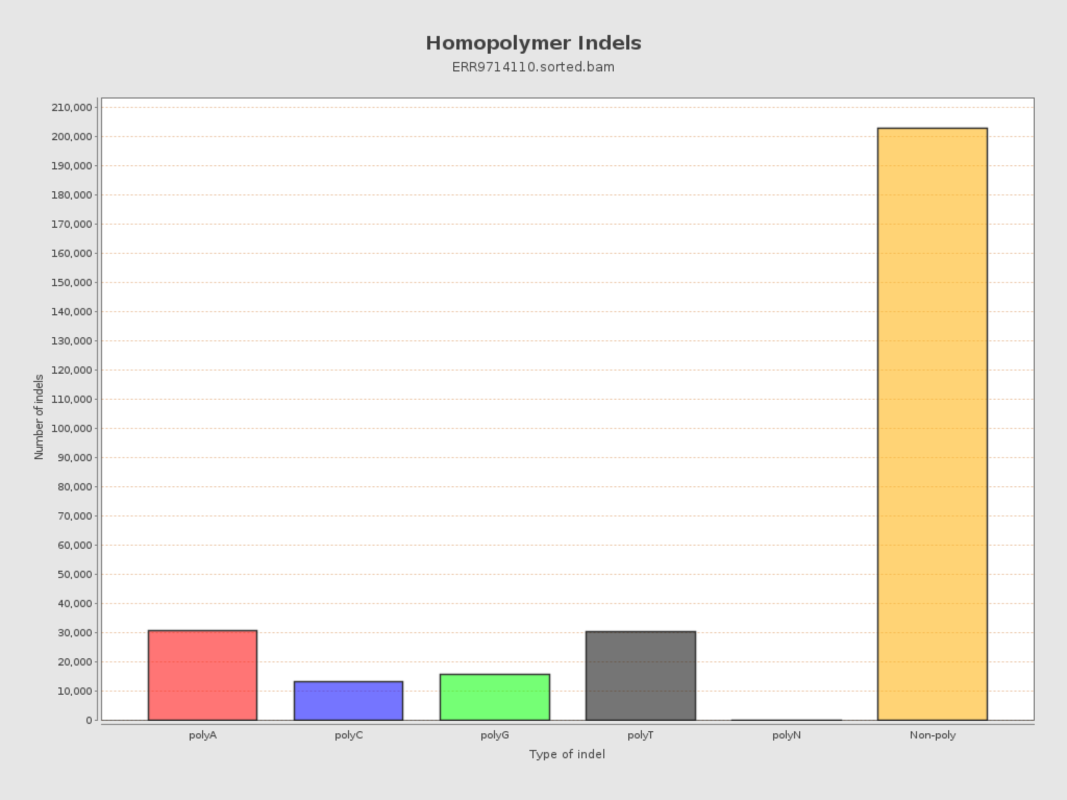
9. Results : Mapped Reads GC-content Distribution



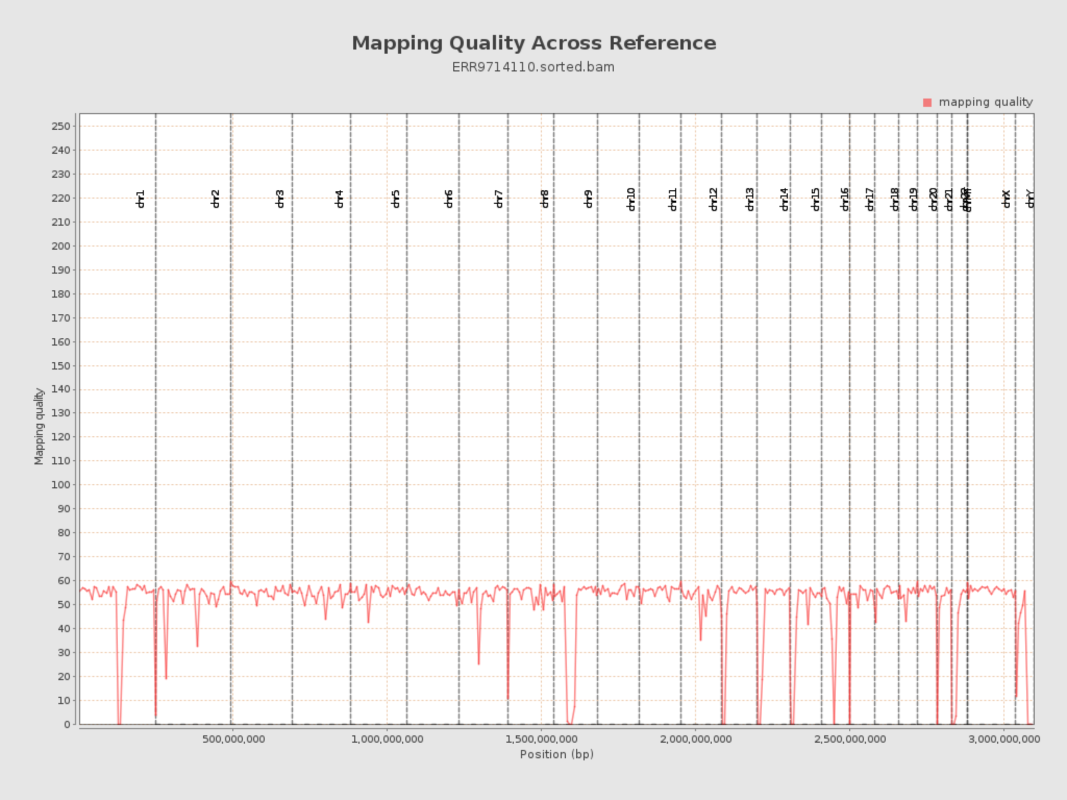
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram