Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:48:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714151.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_ERR9714151 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:48:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	747,678
Mapped reads	597,683 / 79.94%
Unmapped reads	149,995 / 20.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,400 / 1.93%
Read min/max/mean length	30 / 151 / 129.99
Duplicated reads (estimated)	538,081 / 71.97%
Duplication rate	45.37%
Clipped reads	558,650 / 74.72%

2.2. ACGT Content

Number/percentage of A's	19,904,990 / 26.24%
Number/percentage of C's	16,882,771 / 22.26%
Number/percentage of T's	19,009,051 / 25.06%
Number/percentage of G's	20,052,280 / 26.44%
Number/percentage of N's	596 / 0%
GC Percentage	48.7%

2.3. Coverage

Mean	0.0251

Standard Deviation	10.1066

2.4. Mapping Quality

Mean Mapping Quality	51.29

2.5. Mismatches and indels

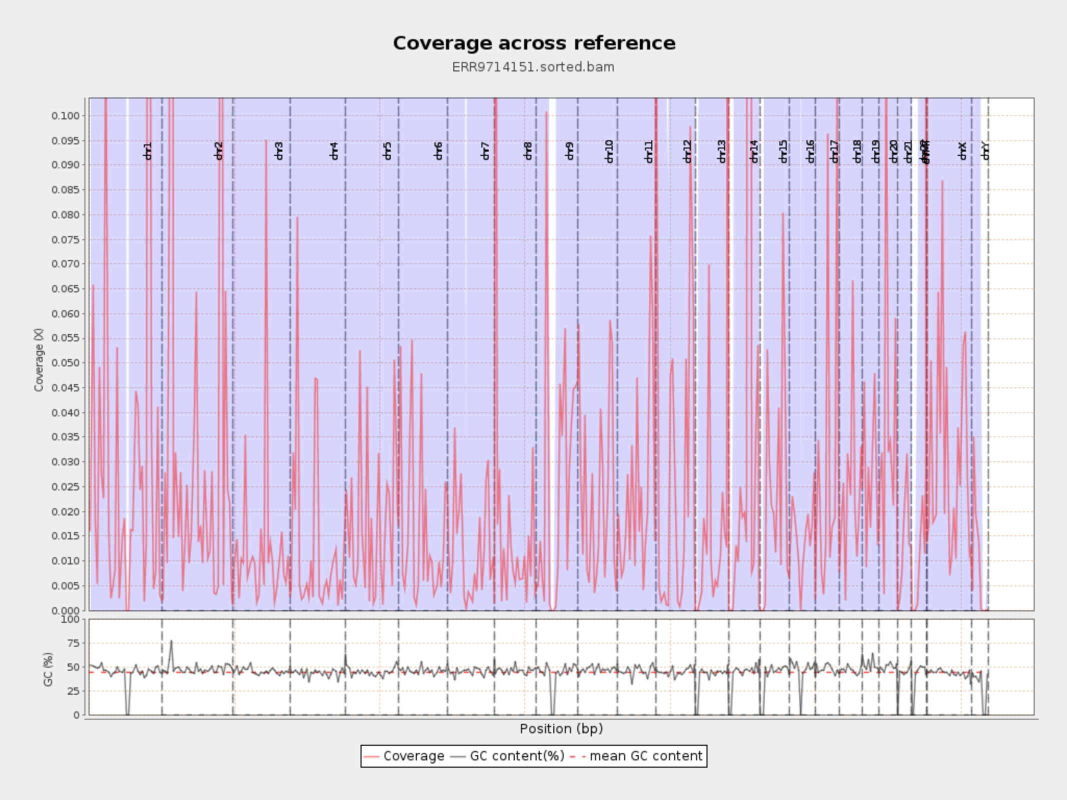
General error rate	4.52%
Mismatches	3,238,141
Insertions	77,688
Mapped reads with at least one insertion	12.49%
Deletions	287,057
Mapped reads with at least one deletion	45.65%
Homopolymer indels	28.17%

2.6. Chromosome stats

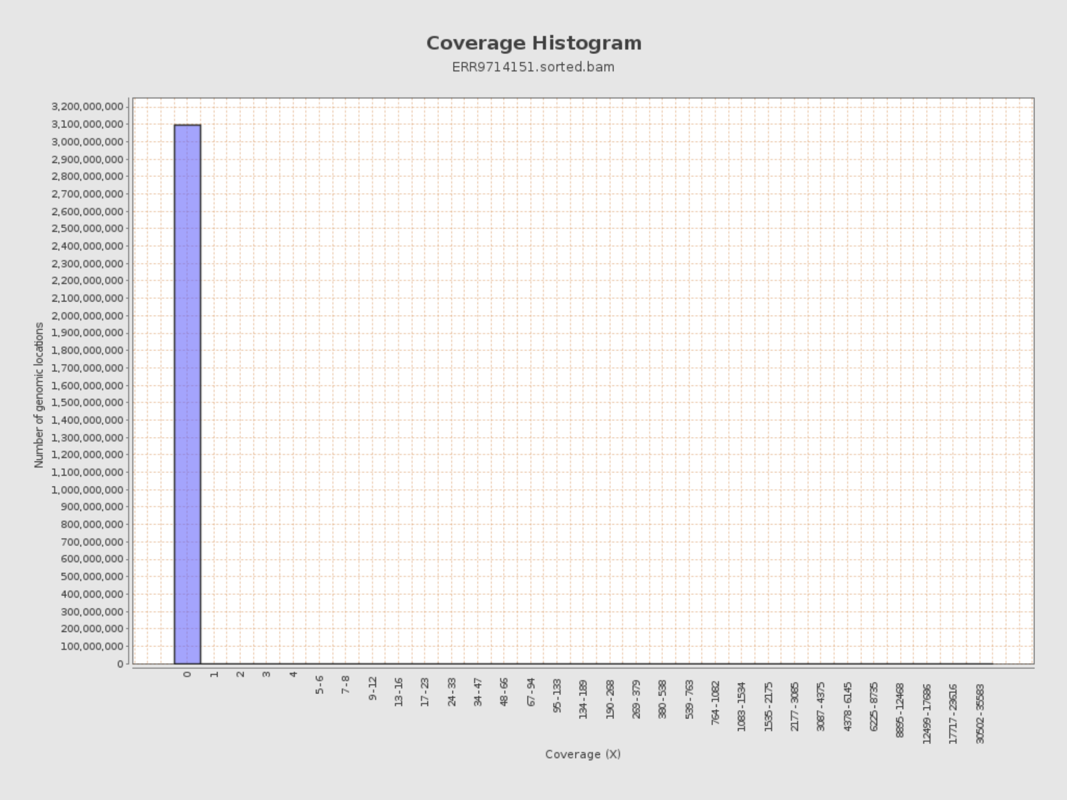
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7656647	0.0307	8.2715
chr2	243199373	11295765	0.0464	17.0848
chr3	198022430	2560404	0.0129	2.8465
chr4	191154276	2557157	0.0134	3.1485
chr5	180915260	3326599	0.0184	3.8253
chr6	171115067	2826086	0.0165	3.1792
chr7	159138663	1947342	0.0122	2.1239

chr8	146364022	3122613	0.0213	9.5145
chr9	141213431	3466913	0.0246	6.4639
chr10	135534747	3239826	0.0239	3.9535
chr11	135006516	3272910	0.0242	4.1414
chr12	133851895	3700940	0.0276	4.9947
chr13	115169878	2048368	0.0178	5.4248
chr14	107349540	7230795	0.0674	40.1559
chr15	102531392	2505932	0.0244	4.2415
chr16	90354753	1387976	0.0154	1.8
chr17	81195210	2647224	0.0326	7.1262
chr18	78077248	1879867	0.0241	4.9429
chr19	59128983	1618302	0.0274	3.1399
chr20	63025520	2595006	0.0412	8.6283
chr21	48129895	628168	0.0131	2.2775
chr22	51304566	453099	0.0088	1.2856
chrMT	16571	255423	15.4139	131.2966
chrX	155270560	4909796	0.0316	3.5348
chrY	59373566	551541	0.0093	1.5748

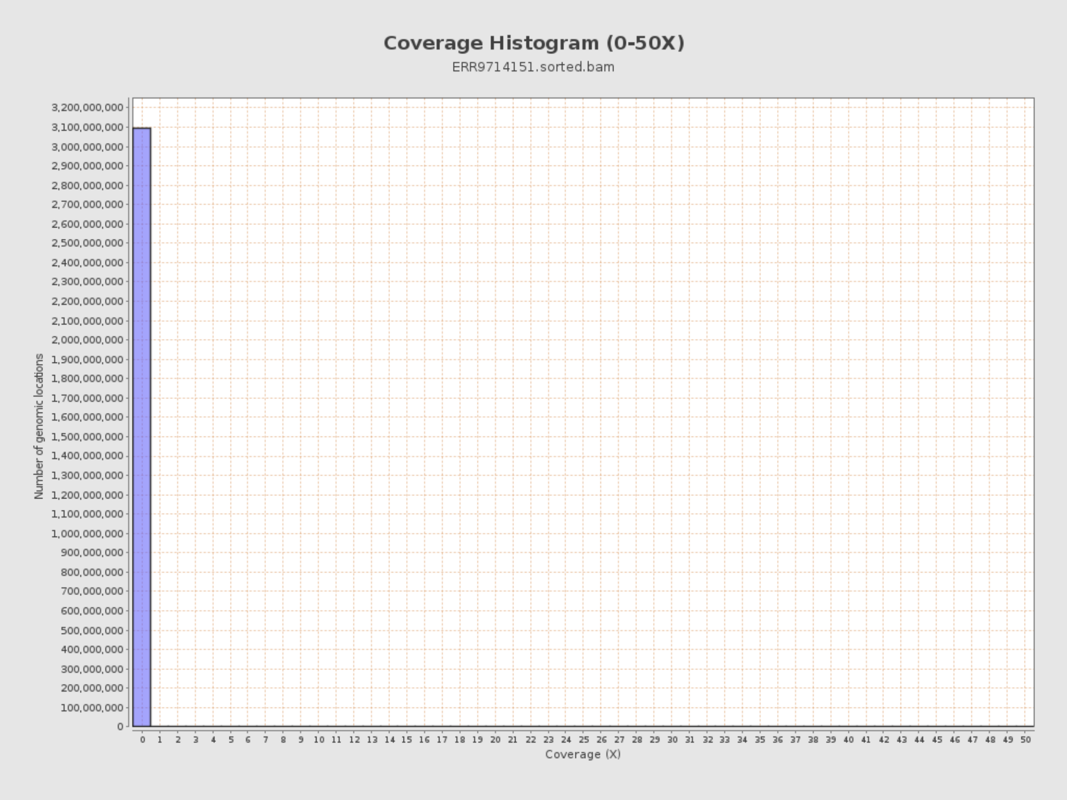
3. Results : Coverage across reference



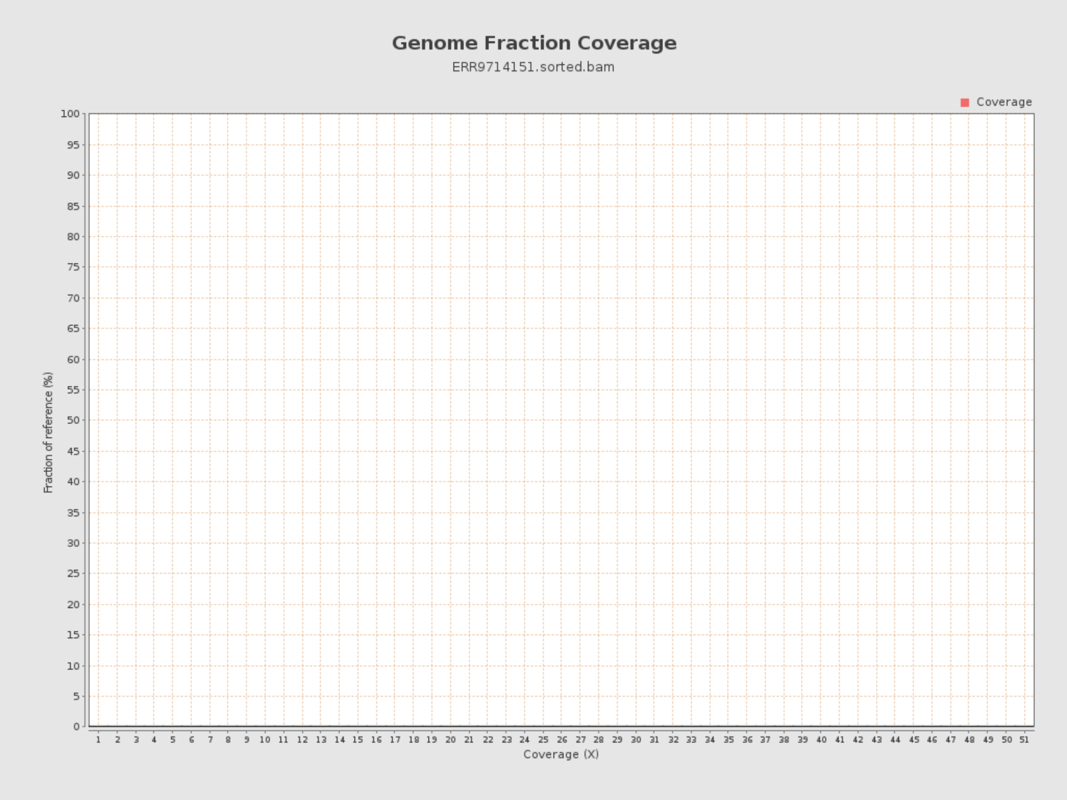
4. Results : Coverage Histogram



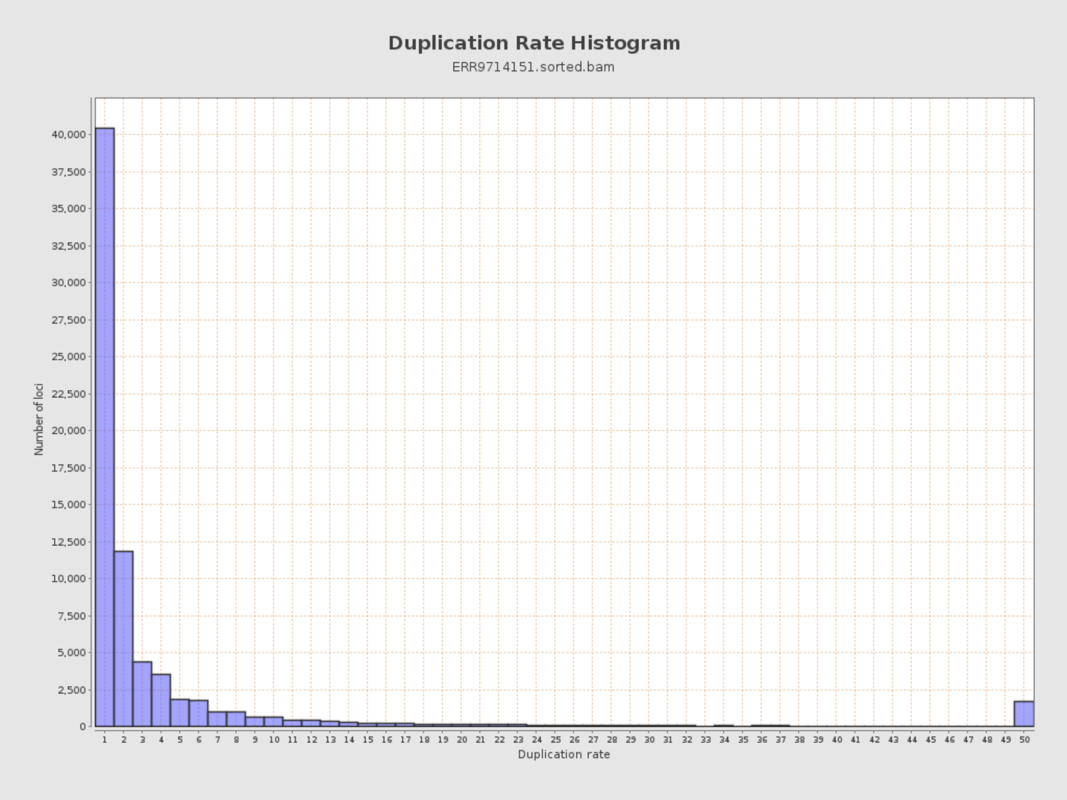
5. Results : Coverage Histogram (0-50X)



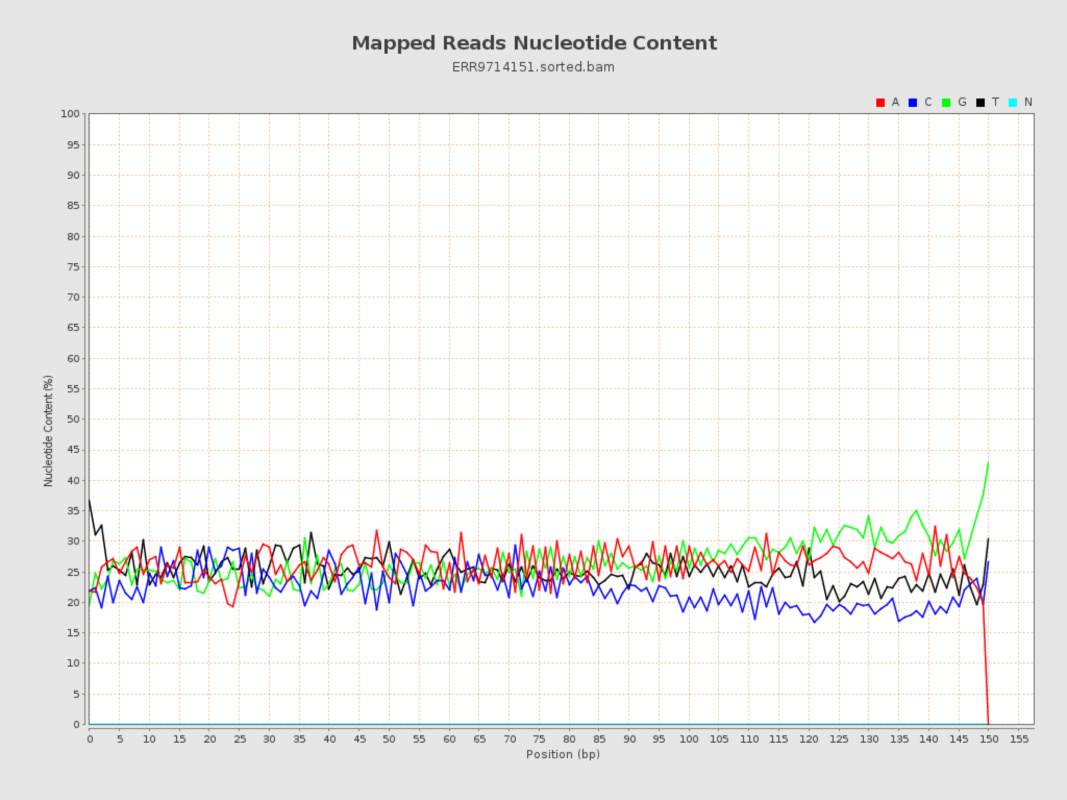
6. Results : Genome Fraction Coverage



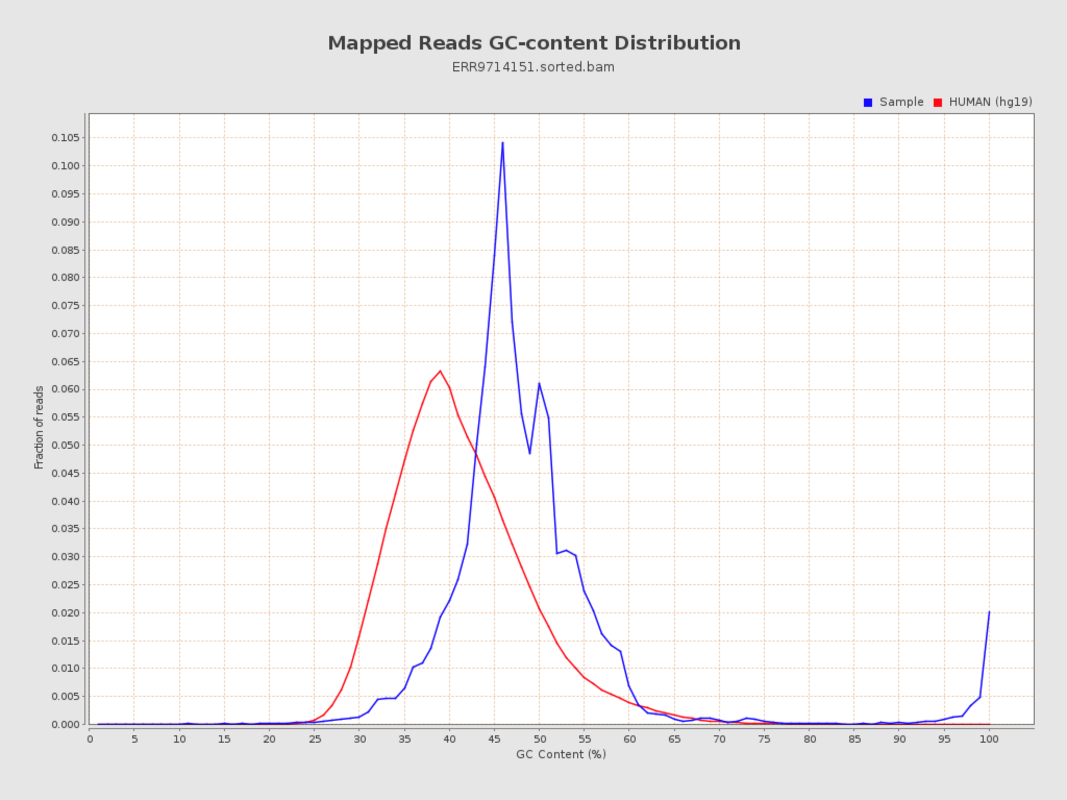
7. Results : Duplication Rate Histogram



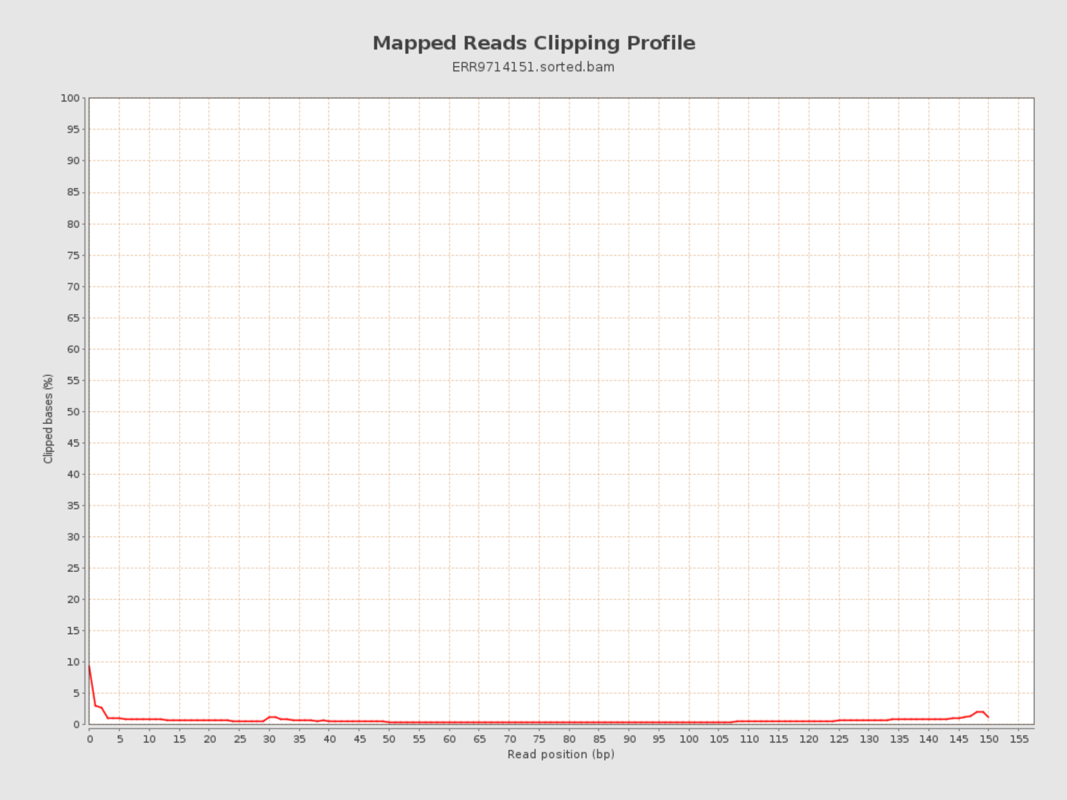
8. Results : Mapped Reads Nucleotide Content



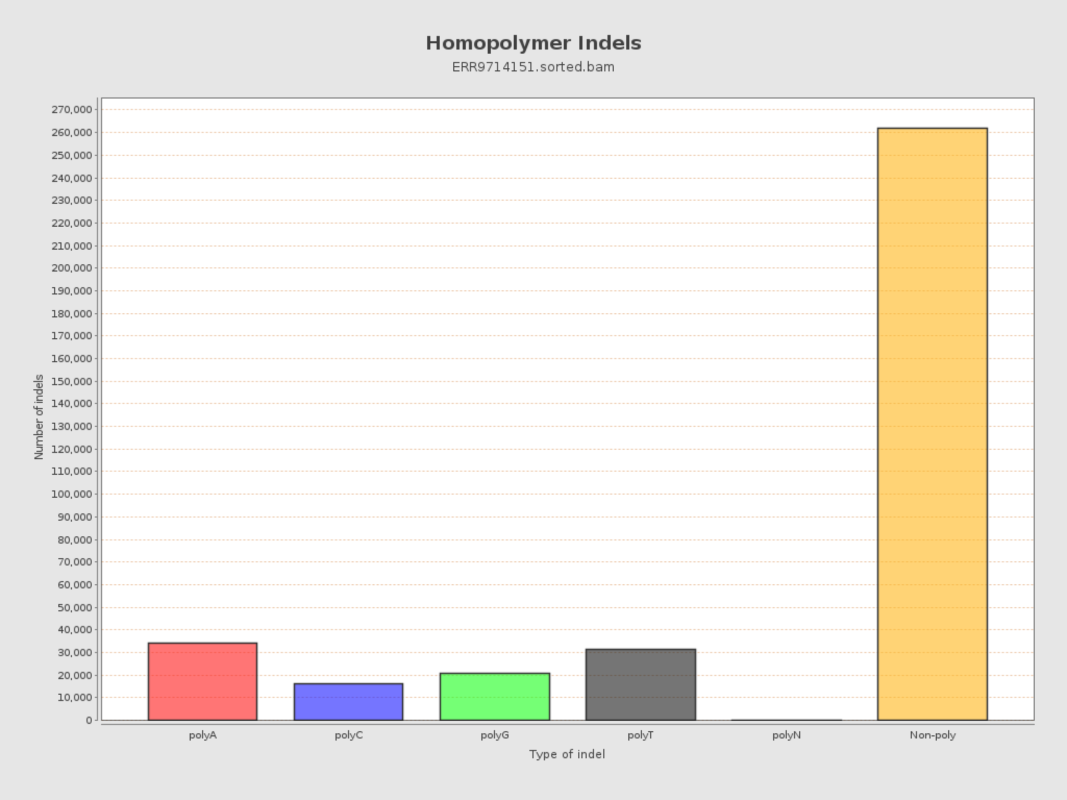
9. Results : Mapped Reads GC-content Distribution



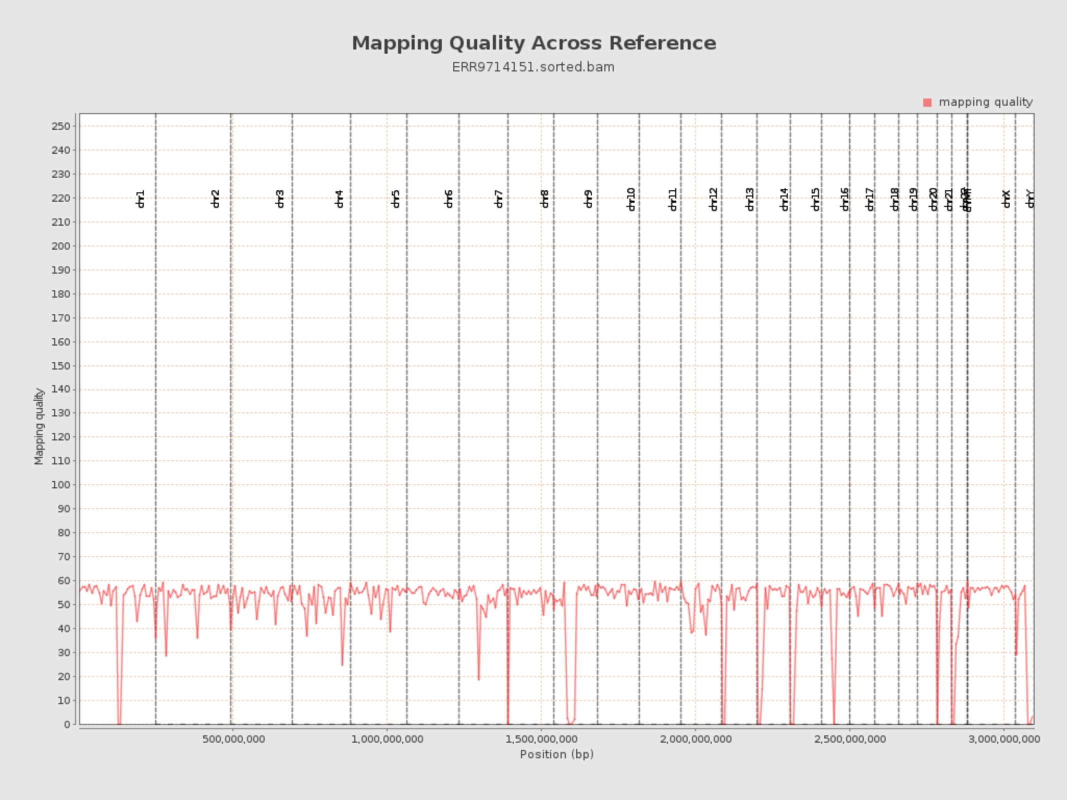
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram