Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:40:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714107.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_ERR9714107 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:40:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	605,996
Mapped reads	364,406 / 60.13%
Unmapped reads	241,590 / 39.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,211 / 1.85%
Read min/max/mean length	30 / 151 / 121.25
Duplicated reads (estimated)	311,400 / 51.39%
Duplication rate	43.78%
Clipped reads	333,546 / 55.04%

2.2. ACGT Content

Number/percentage of A's	12,545,339 / 27.13%
Number/percentage of C's	9,408,914 / 20.35%
Number/percentage of T's	11,977,109 / 25.9%
Number/percentage of G's	12,303,115 / 26.61%
Number/percentage of N's	450 / 0%
GC Percentage	46.96%

2.3. Coverage

Mean	0.0153

Standard Deviation	4.1975

2.4. Mapping Quality

Mean Mapping Quality	51.47

2.5. Mismatches and indels

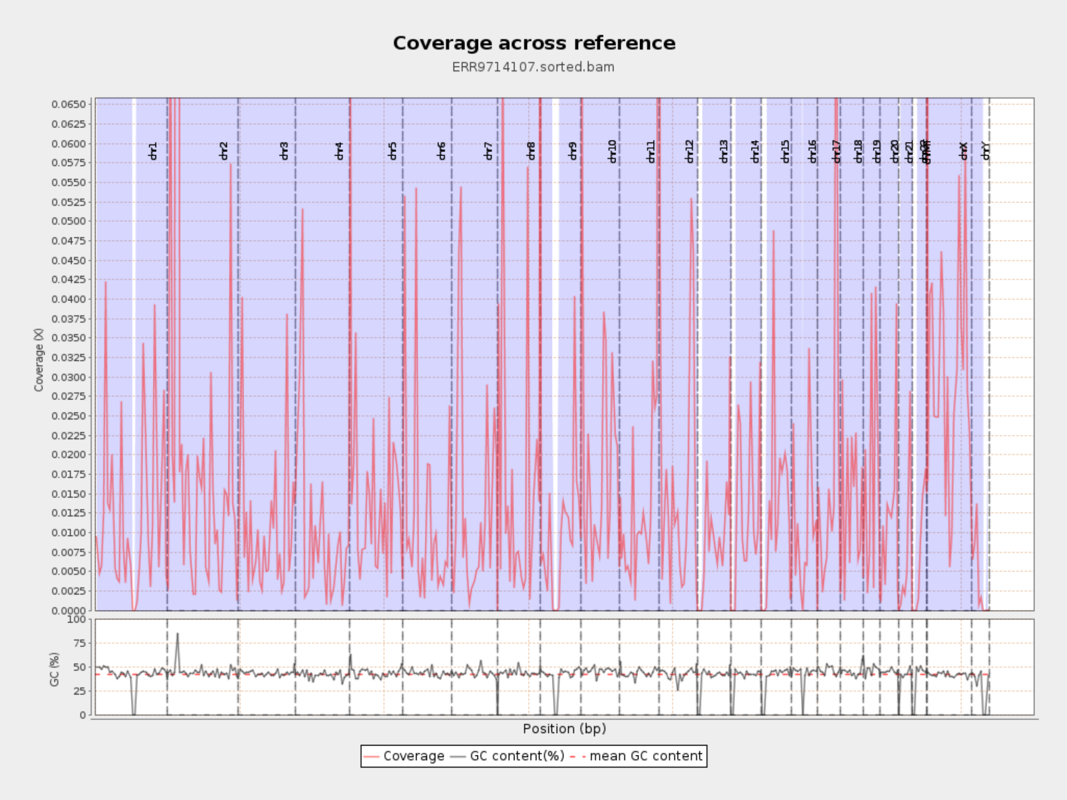
General error rate	4.65%
Mismatches	1,986,809
Insertions	52,181
Mapped reads with at least one insertion	13.65%
Deletions	179,449
Mapped reads with at least one deletion	45.66%
Homopolymer indels	30.67%

2.6. Chromosome stats

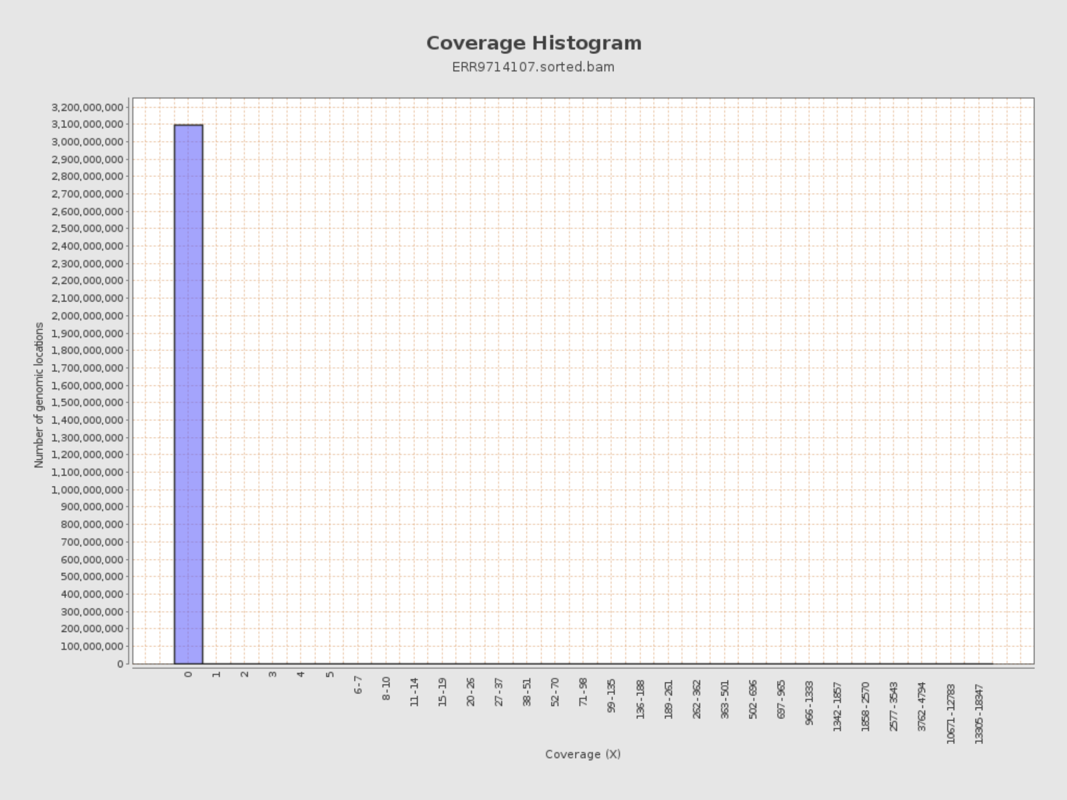
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3085964	0.0124	1.7762
chr2	243199373	7382846	0.0304	12.4868
chr3	198022430	2154029	0.0109	2.3416
chr4	191154276	1961084	0.0103	1.8083
chr5	180915260	2488103	0.0138	2.1065
chr6	171115067	2114756	0.0124	2.5027
chr7	159138663	2161373	0.0136	2.4268

chr8	146364022	2390503	0.0163	3.3921
chr9	141213431	1491391	0.0106	1.6627
chr10	135534747	2591081	0.0191	3.5331
chr11	135006516	1842298	0.0136	1.9142
chr12	133851895	2146239	0.016	2.6718
chr13	115169878	1002559	0.0087	1.1899
chr14	107349540	1348527	0.0126	2.1235
chr15	102531392	1378097	0.0134	1.7646
chr16	90354753	1019889	0.0113	1.5062
chr17	81195210	1575063	0.0194	4.1192
chr18	78077248	1149105	0.0147	2.059
chr19	59128983	1018870	0.0172	3.3931
chr20	63025520	850112	0.0135	1.8468
chr21	48129895	359272	0.0075	1.8399
chr22	51304566	370709	0.0072	0.9718
chrMT	16571	516083	31.1437	239.5426
chrX	155270560	4685958	0.0302	2.6825
chrY	59373566	227219	0.0038	0.6555

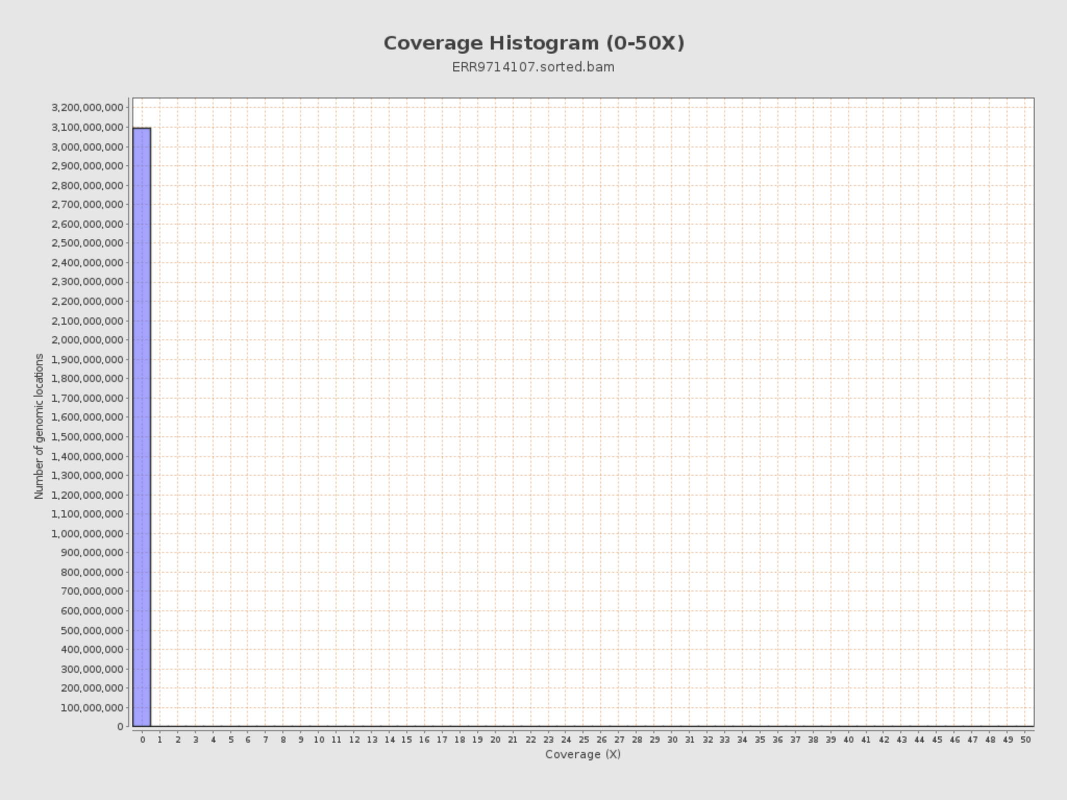
3. Results : Coverage across reference



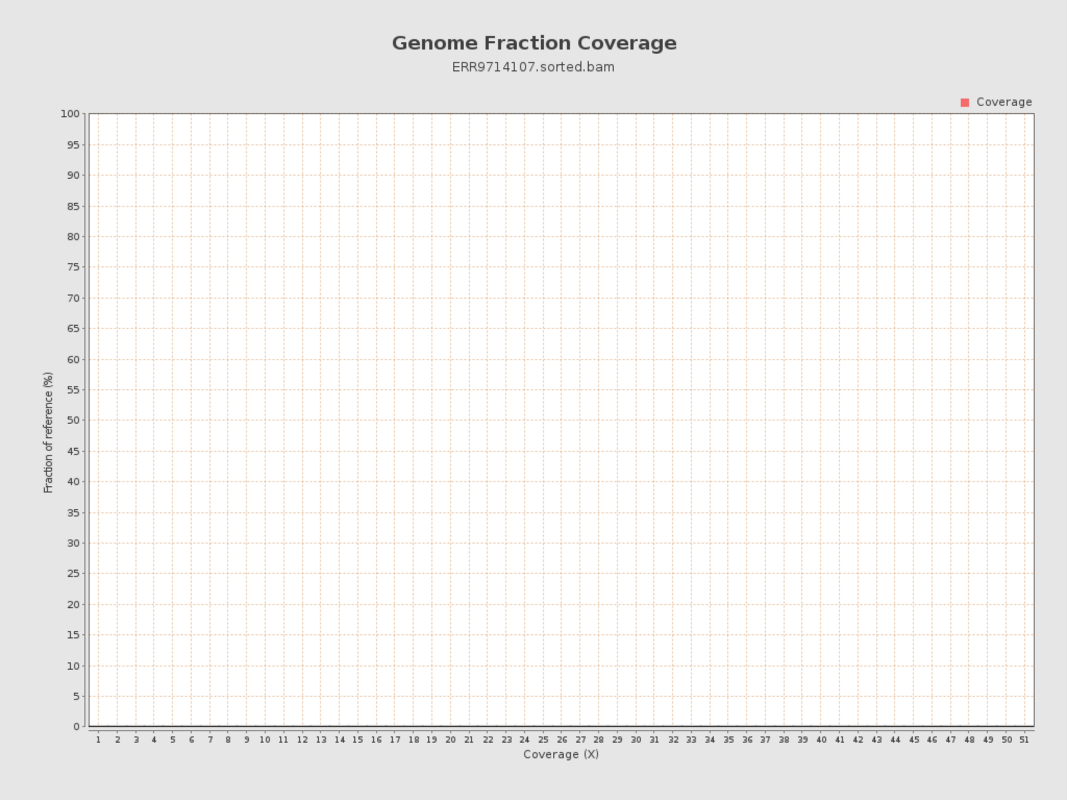
4. Results : Coverage Histogram



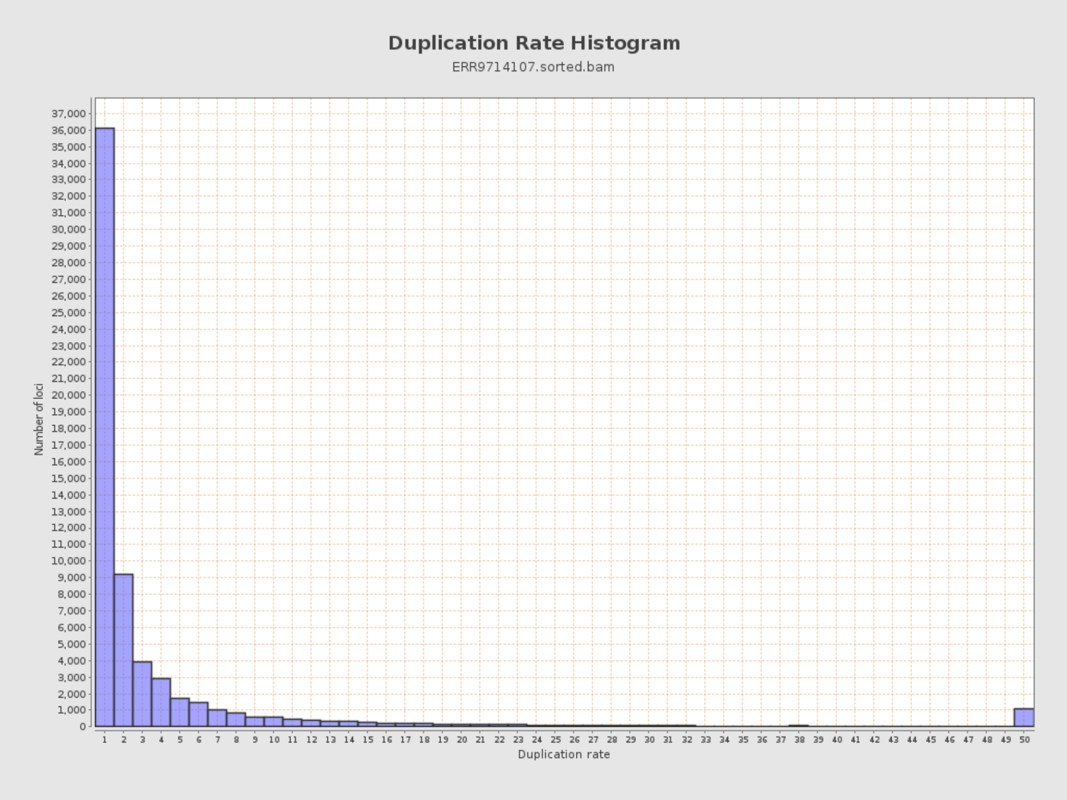
5. Results : Coverage Histogram (0-50X)



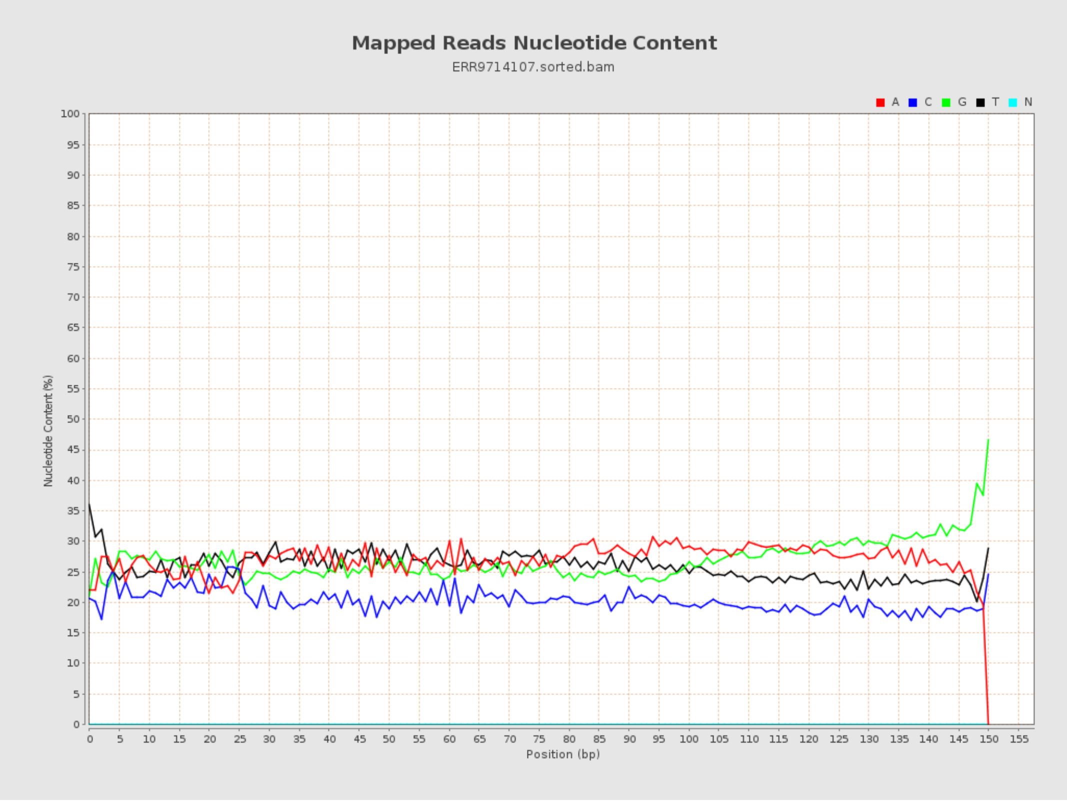
6. Results : Genome Fraction Coverage



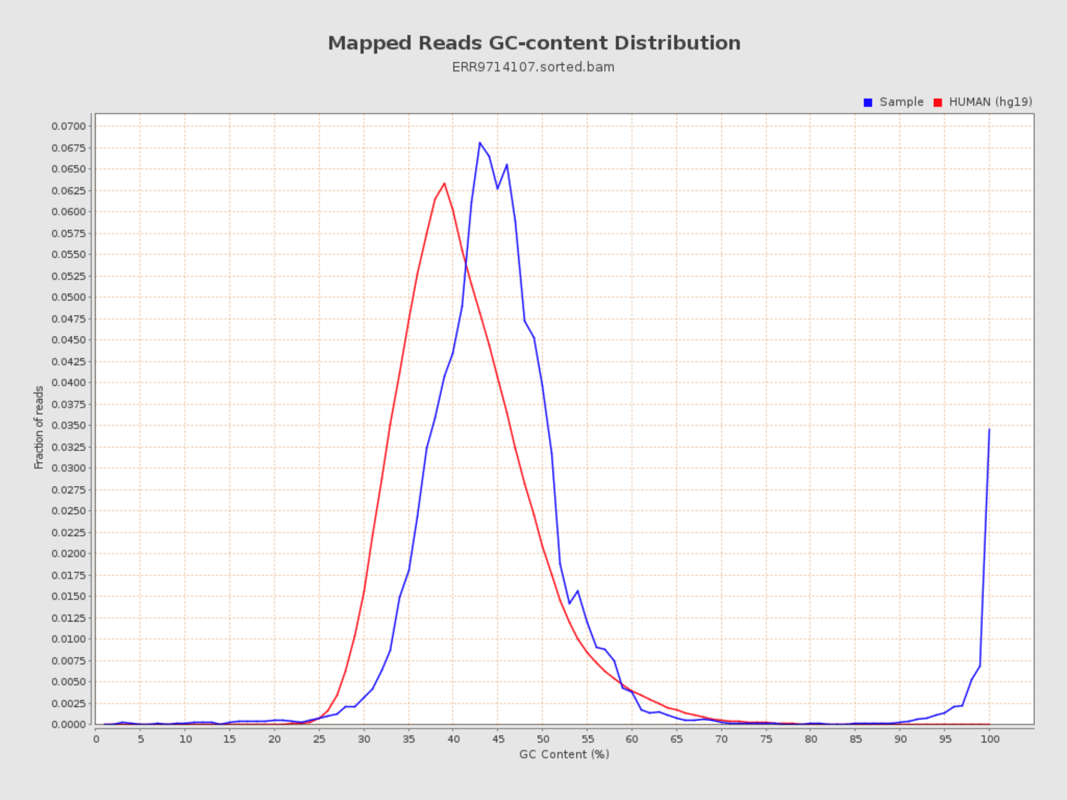
7. Results : Duplication Rate Histogram



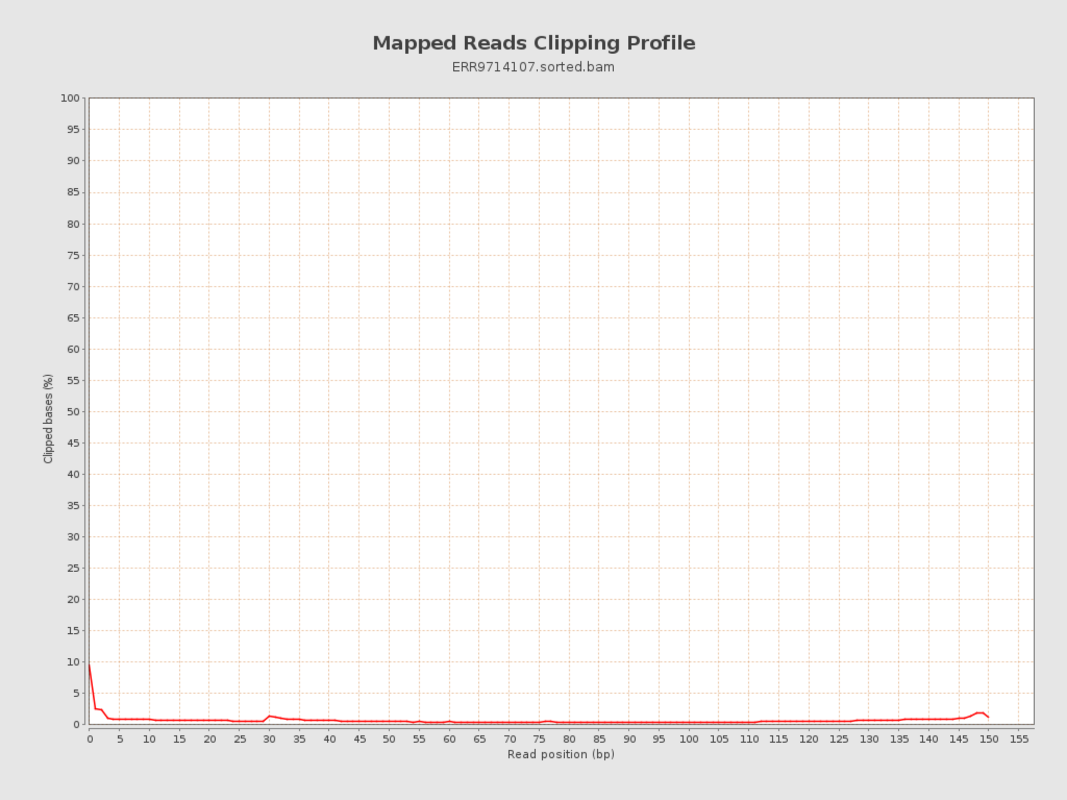
8. Results : Mapped Reads Nucleotide Content



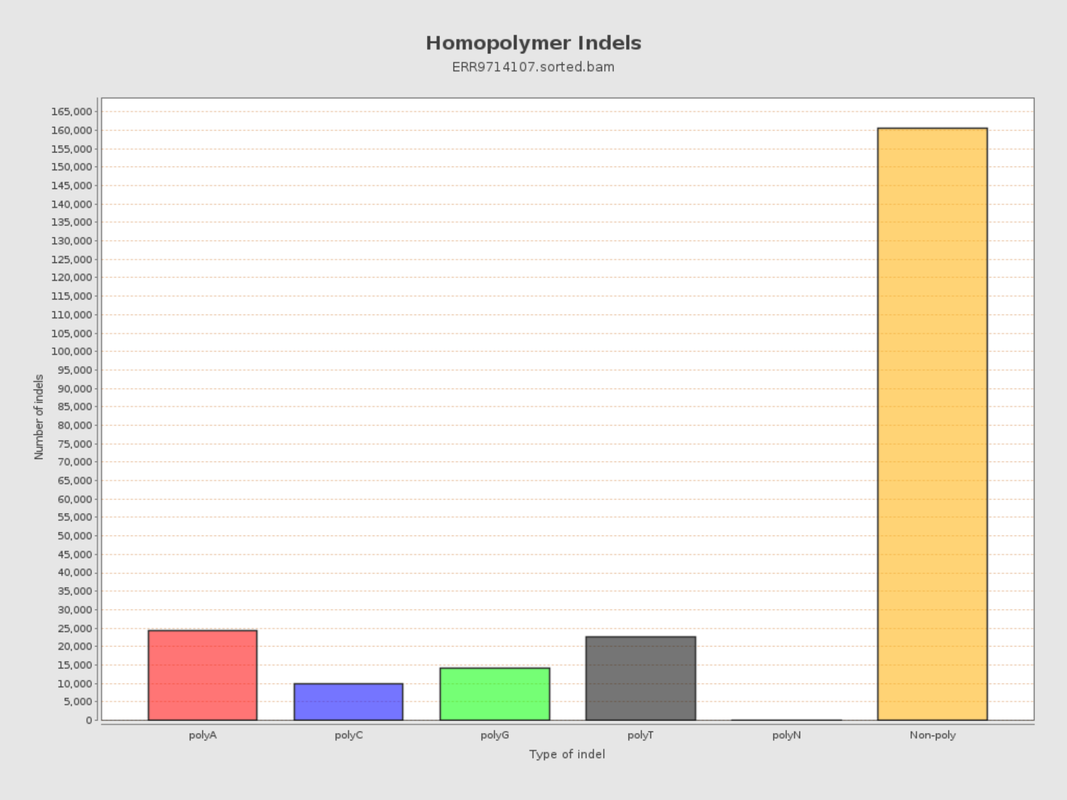
9. Results : Mapped Reads GC-content Distribution



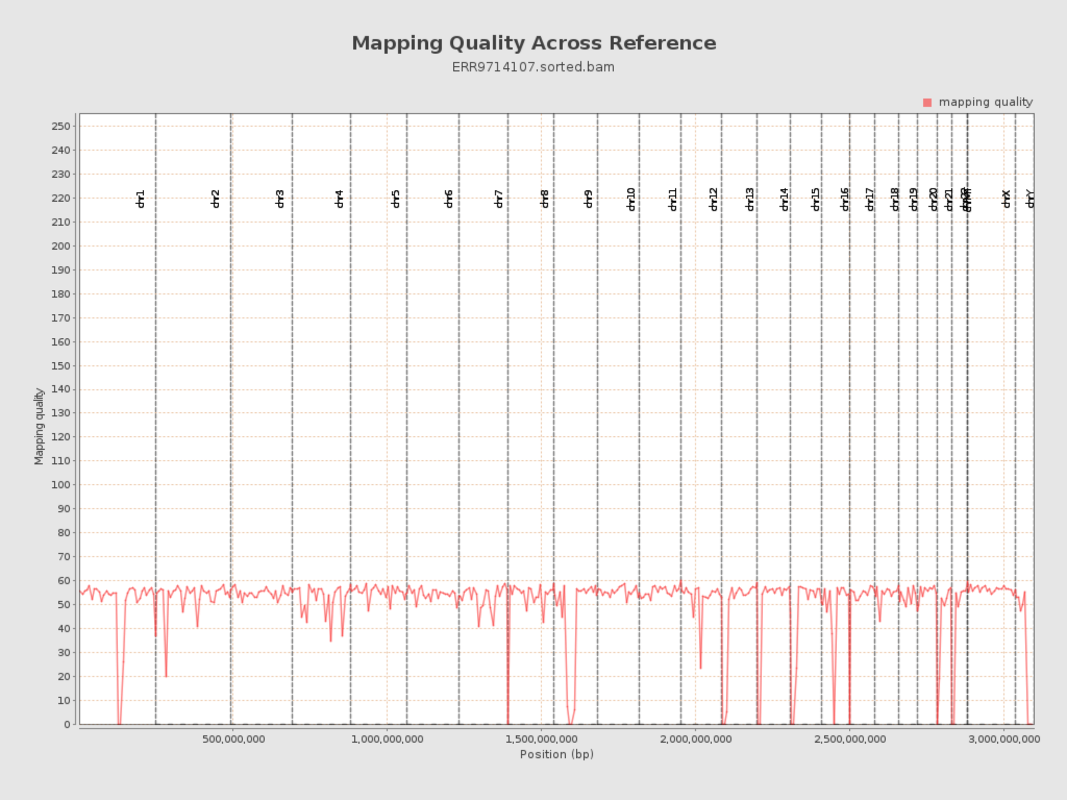
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram