Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:10:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714096.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_ERR9714096 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:10:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	523,720
Mapped reads	424,740 / 81.1%
Unmapped reads	98,980 / 18.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,814 / 2.83%
Read min/max/mean length	30 / 151 / 131.97
Duplicated reads (estimated)	369,288 / 70.51%
Duplication rate	42.79%
Clipped reads	398,993 / 76.18%

2.2. ACGT Content

Number/percentage of A's	15,217,816 / 28.21%
Number/percentage of C's	11,091,773 / 20.56%
Number/percentage of T's	14,382,476 / 26.67%
Number/percentage of G's	13,242,922 / 24.55%
Number/percentage of N's	343 / 0%
GC Percentage	45.12%

2.3. Coverage

Mean	0.0179

Standard Deviation	3.4256

2.4. Mapping Quality

Mean Mapping Quality	51.24

2.5. Mismatches and indels

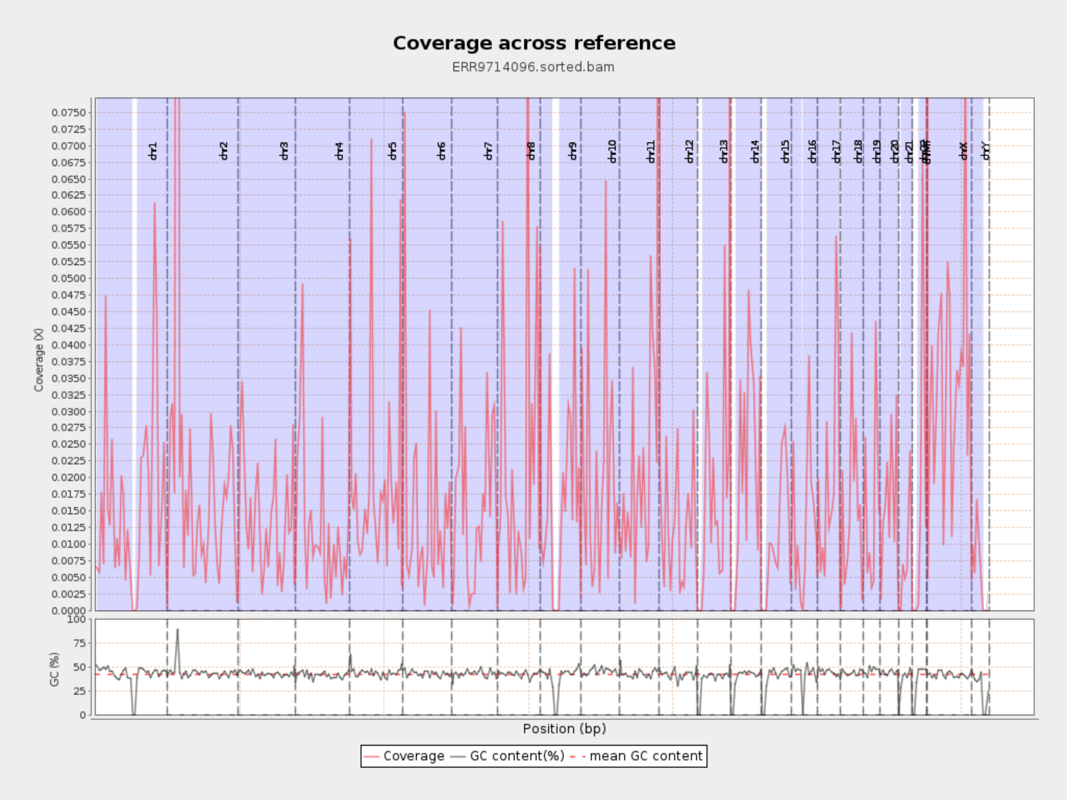
General error rate	4.83%
Mismatches	2,446,984
Insertions	61,375
Mapped reads with at least one insertion	13.9%
Deletions	218,814
Mapped reads with at least one deletion	47.77%
Homopolymer indels	30.01%

2.6. Chromosome stats

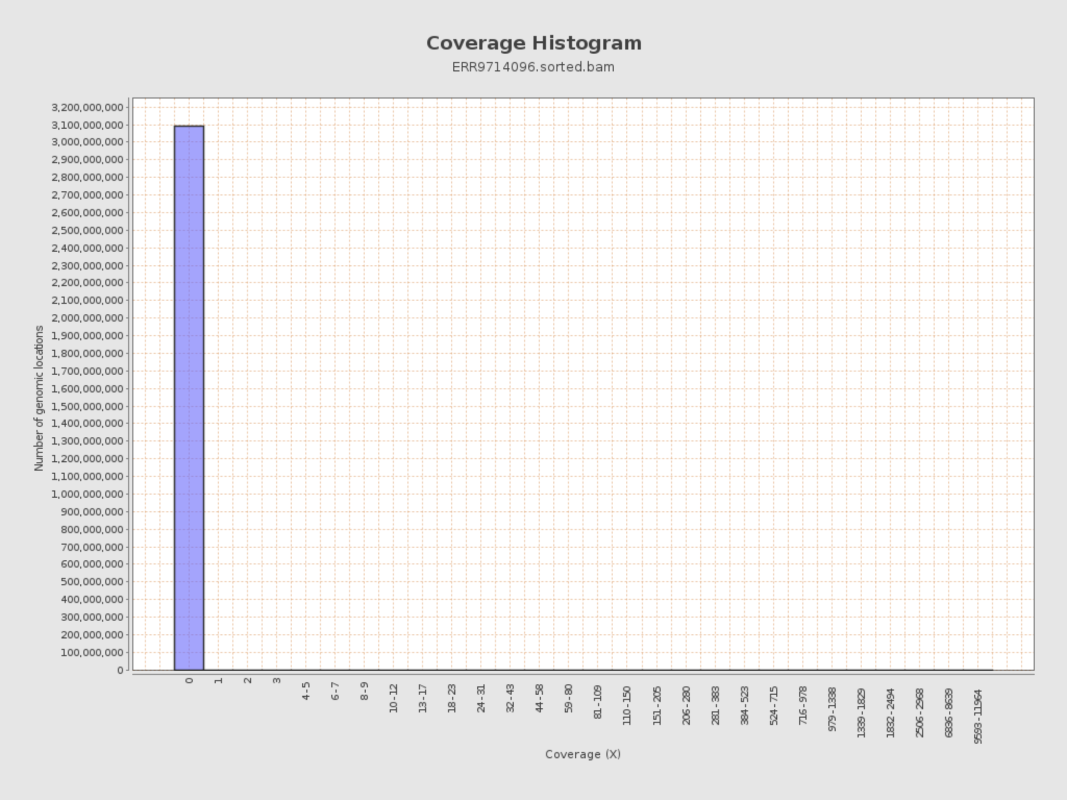
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4042903	0.0162	2.8465
chr2	243199373	5862265	0.0241	7.7638
chr3	198022430	2808923	0.0142	1.9356
chr4	191154276	2298722	0.012	1.8163
chr5	180915260	3520272	0.0195	3.3787
chr6	171115067	2621828	0.0153	2.4285
chr7	159138663	2524947	0.0159	2.2301

chr8	146364022	3118677	0.0213	3.8649
chr9	141213431	2293989	0.0162	2.4913
chr10	135534747	2768724	0.0204	3.749
chr11	135006516	2869394	0.0213	3.4743
chr12	133851895	1696707	0.0127	1.9909
chr13	115169878	2021713	0.0176	2.9093
chr14	107349540	2273601	0.0212	3.1589
chr15	102531392	1142889	0.0111	1.2794
chr16	90354753	1225734	0.0136	1.7806
chr17	81195210	1638635	0.0202	3.1544
chr18	78077248	1293926	0.0166	1.9866
chr19	59128983	871725	0.0147	1.688
chr20	63025520	1068523	0.017	2.2675
chr21	48129895	399763	0.0083	1.2684
chr22	51304566	845958	0.0165	3.2677
chrMT	16571	467994	28.2417	222.3502
chrX	155270560	5288294	0.0341	3.2609
chrY	59373566	349110	0.0059	1.0424

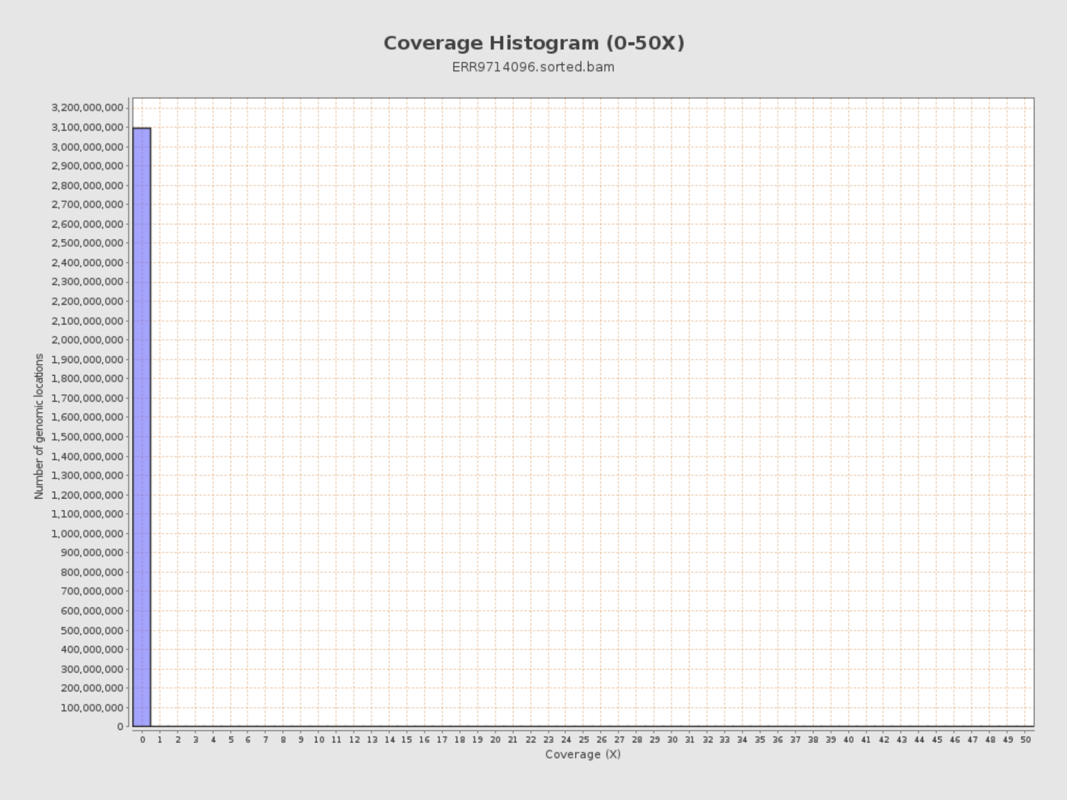
3. Results : Coverage across reference



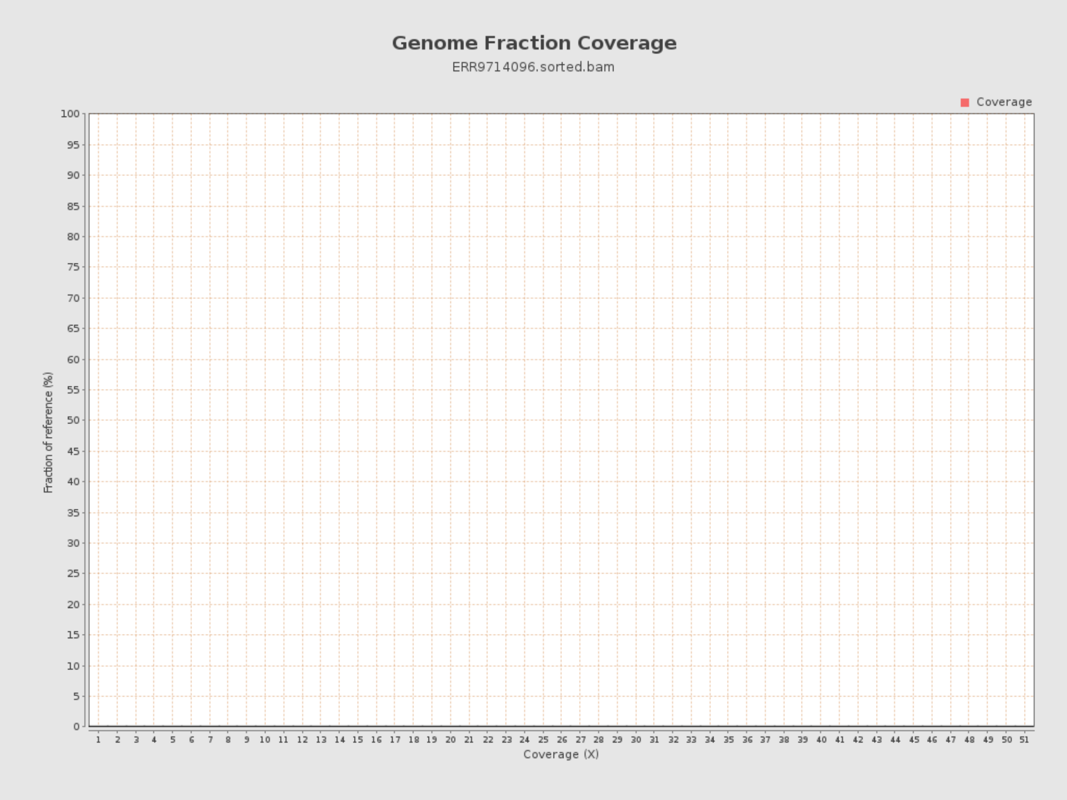
4. Results : Coverage Histogram



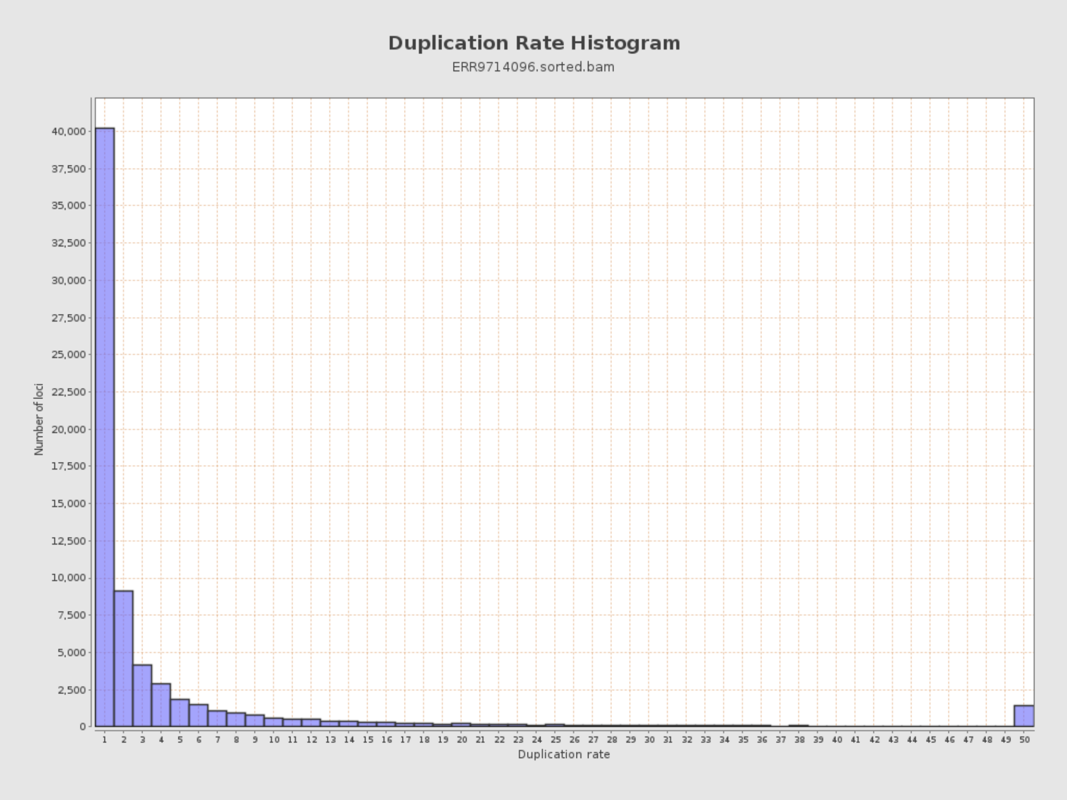
5. Results : Coverage Histogram (0-50X)



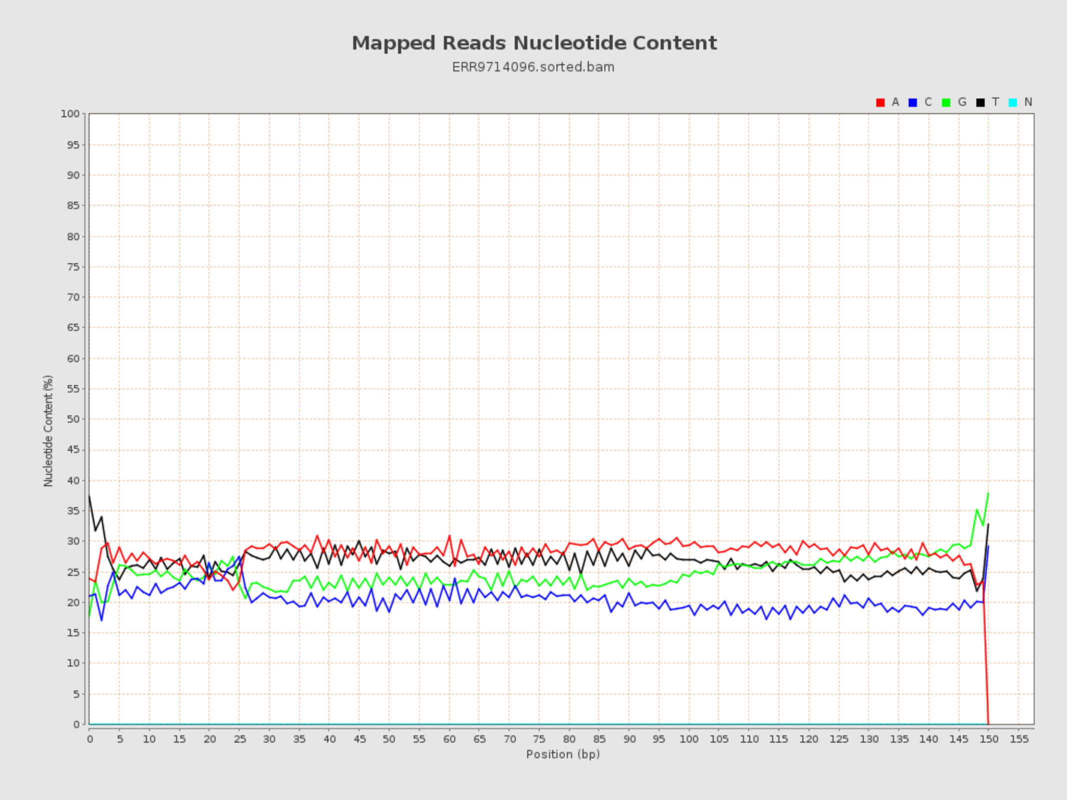
6. Results : Genome Fraction Coverage



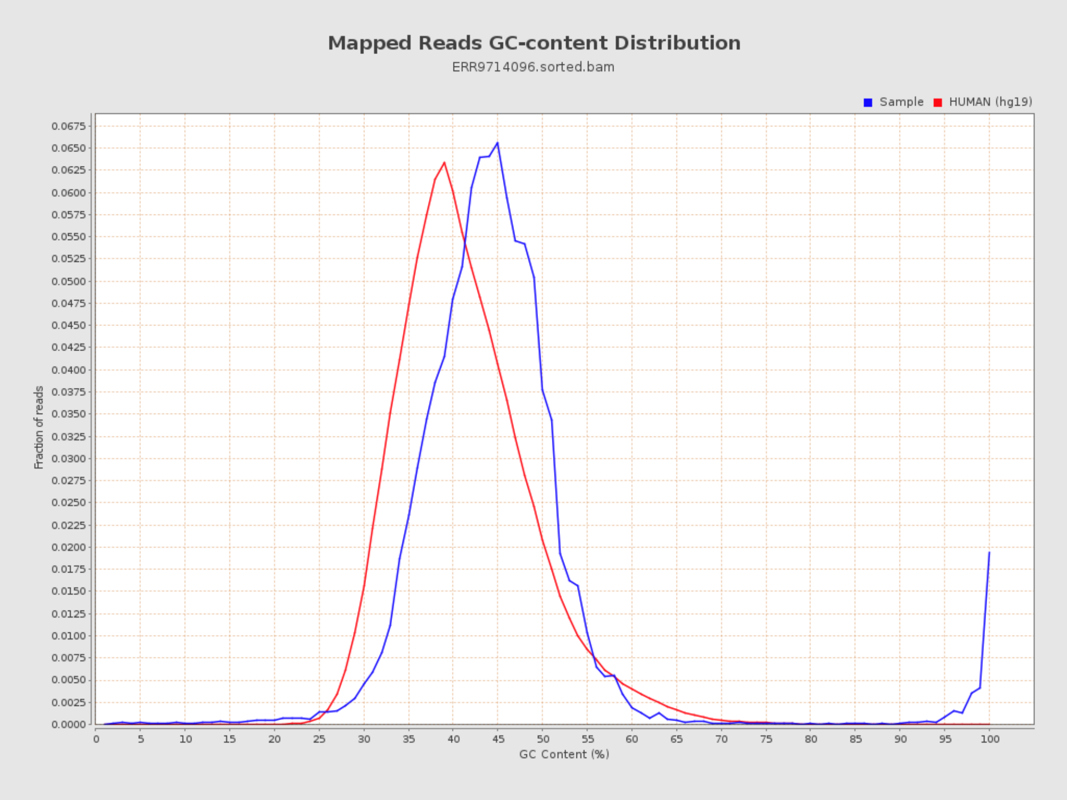
7. Results : Duplication Rate Histogram



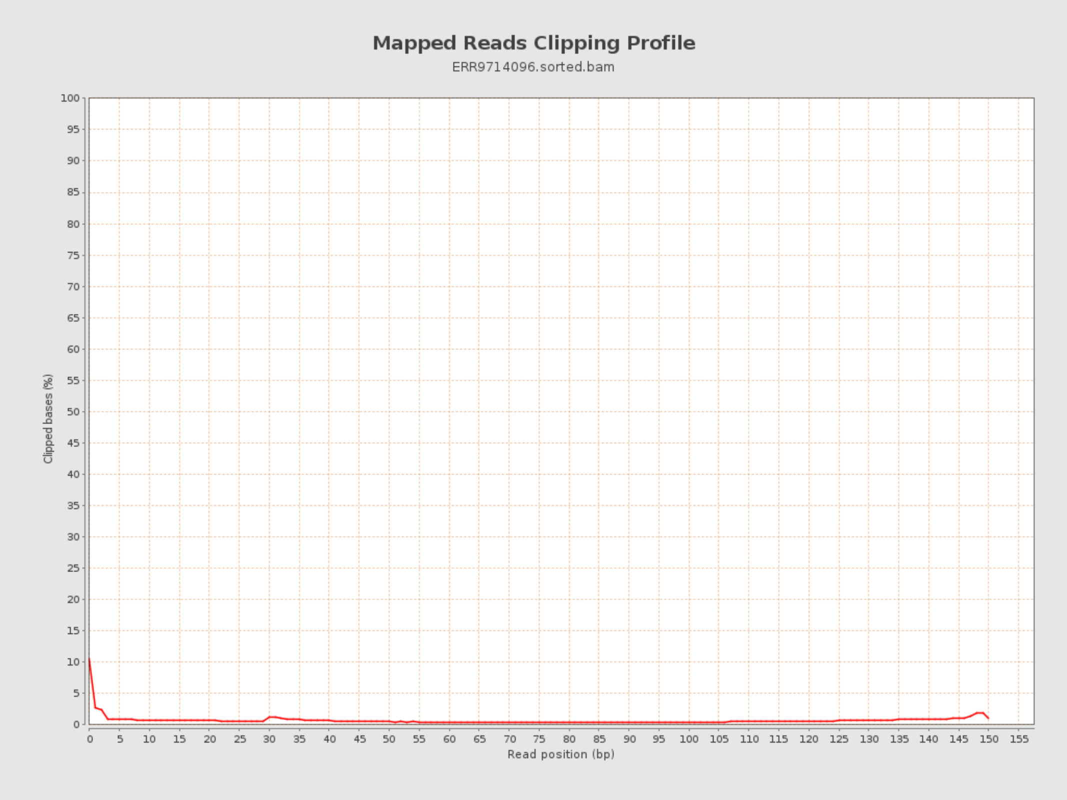
8. Results : Mapped Reads Nucleotide Content



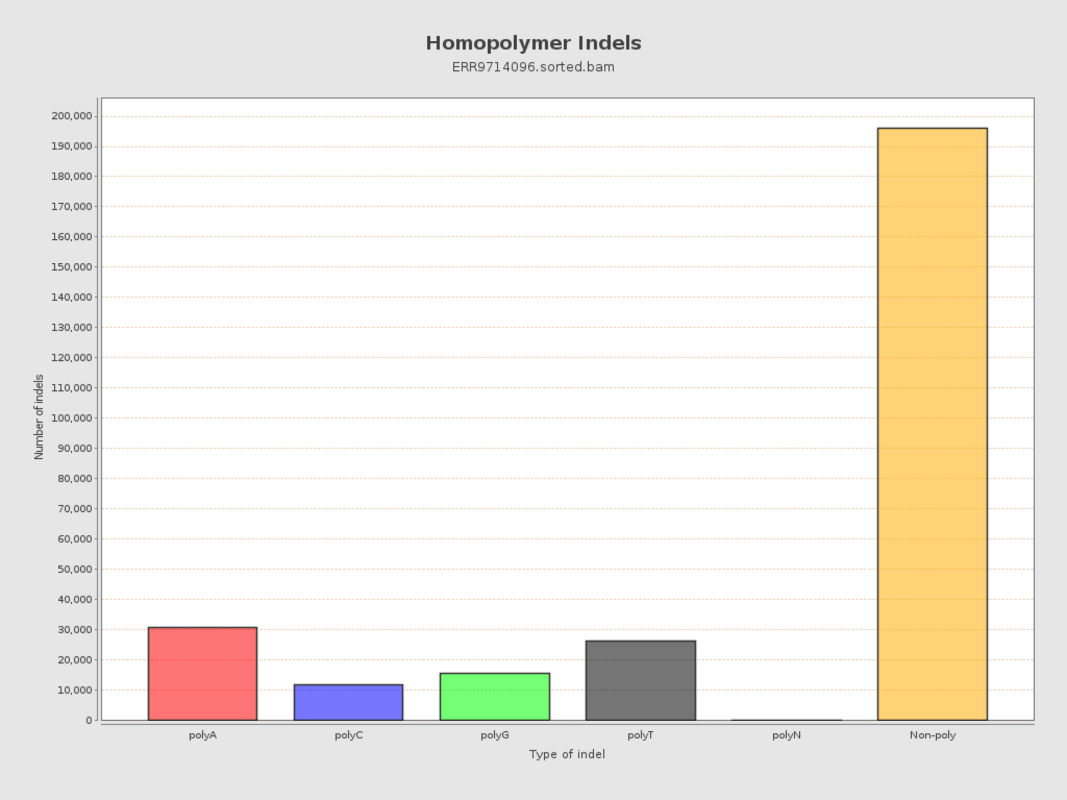
9. Results : Mapped Reads GC-content Distribution



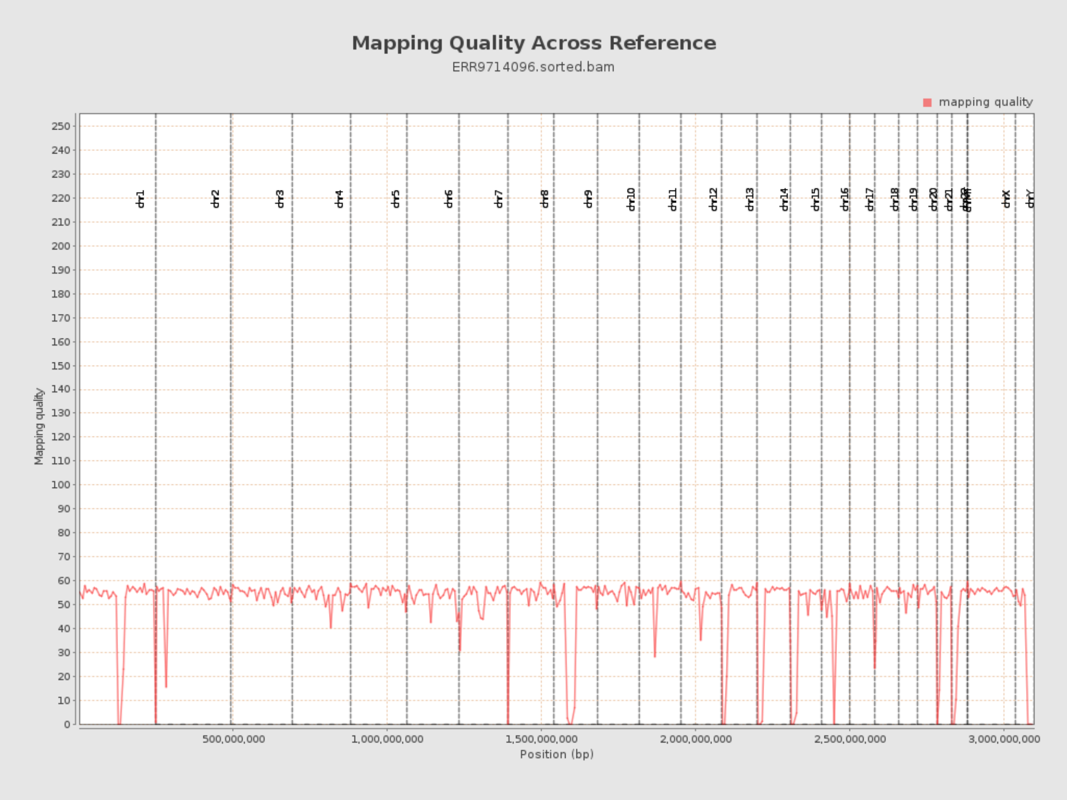
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram