Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:16:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714210.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_ERR9714210 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:16:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	141,016
Mapped reads	16,226 / 11.51%
Unmapped reads	124,790 / 88.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	683 / 0.48%
Read min/max/mean length	30 / 151 / 58.43
Duplicated reads (estimated)	15,371 / 10.9%
Duplication rate	33.75%
Clipped reads	9,597 / 6.81%

2.2. ACGT Content

Number/percentage of A's	86,646 / 5.2%
Number/percentage of C's	45,373 / 2.72%
Number/percentage of T's	51,476 / 3.09%
Number/percentage of G's	1,484,242 / 89%
Number/percentage of N's	31 / 0%
GC Percentage	91.72%

2.3. Coverage

Mean	0.0005

Standard Deviation	1.77

2.4. Mapping Quality

Mean Mapping Quality	9.46

2.5. Mismatches and indels

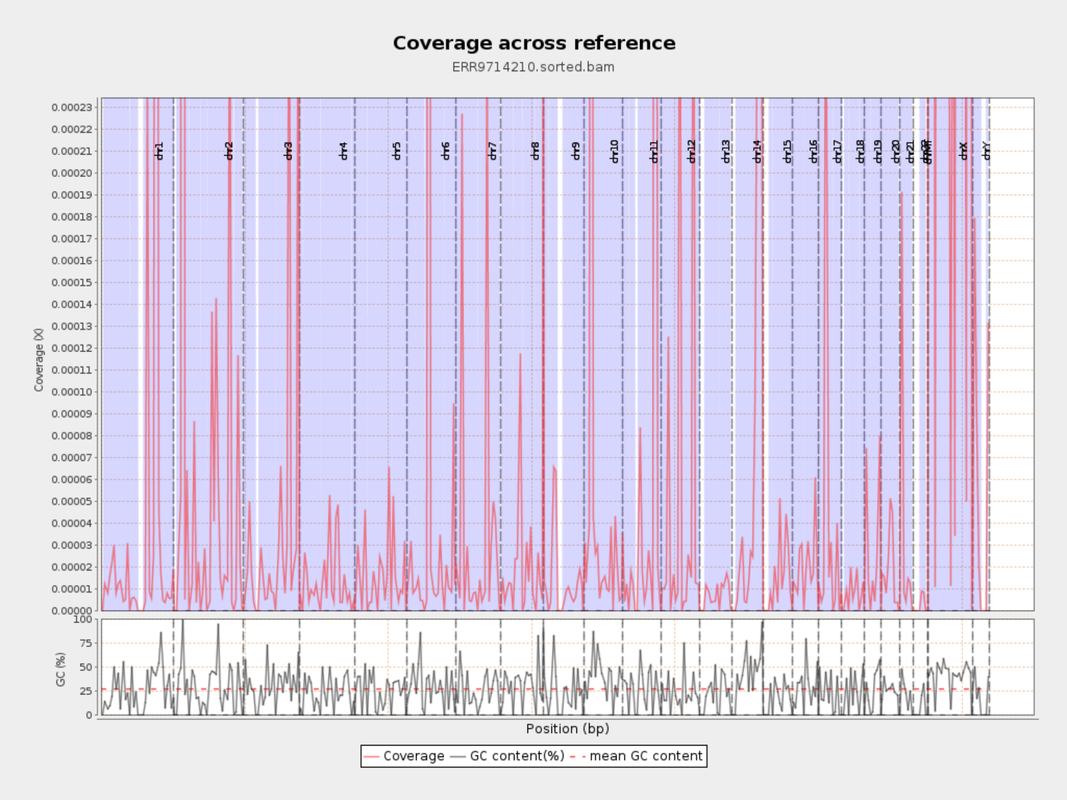
General error rate	3.88%
Mismatches	44,910
Insertions	2,546
Mapped reads with at least one insertion	10.28%
Deletions	1,331
Mapped reads with at least one deletion	7.95%
Homopolymer indels	67.5%

2.6. Chromosome stats

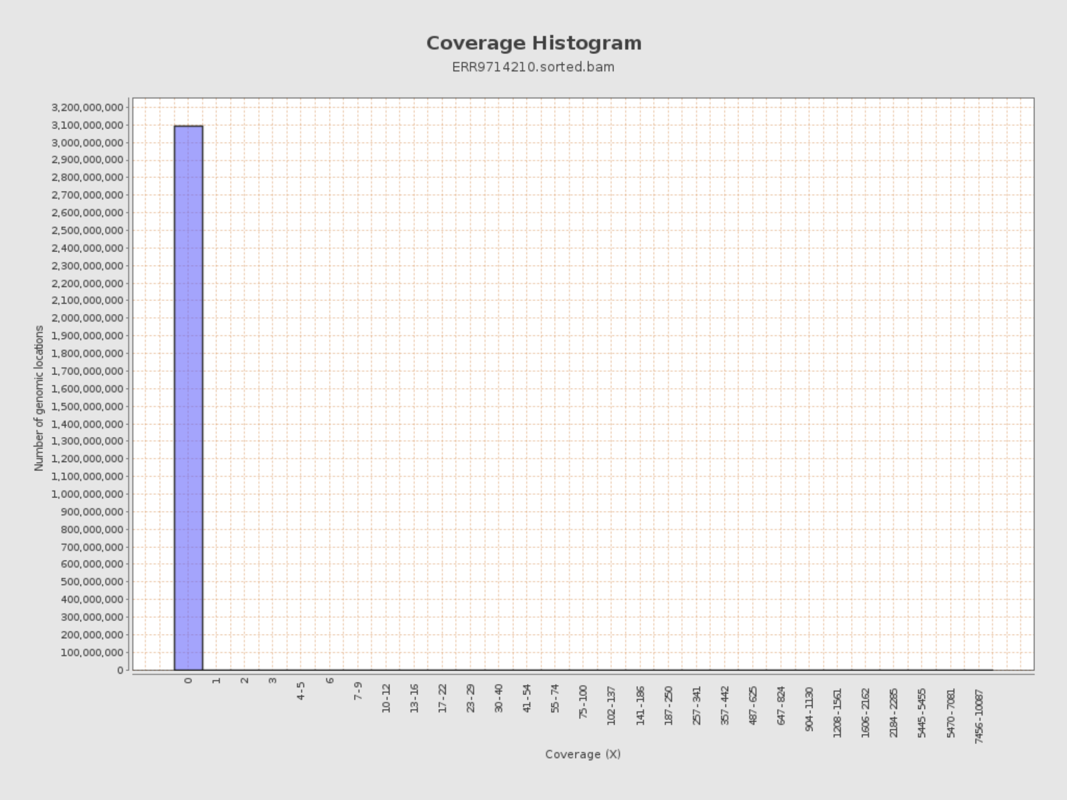
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12462	0	0.0938
chr2	243199373	1465549	0.006	6.3122
chr3	198022430	8622	0	0.0249
chr4	191154276	2522	0	0.0055
chr5	180915260	2982	0	0.006
chr6	171115067	9741	0.0001	0.0506
chr7	159138663	5857	0	0.0296

chr8	146364022	2749	0	0.0075
chr9	141213431	2142	0	0.0075
chr10	135534747	10241	0.0001	0.1178
chr11	135006516	8525	0.0001	0.0467
chr12	133851895	7947	0.0001	0.0332
chr13	115169878	751	0	0.0028
chr14	107349540	11371	0.0001	0.0566
chr15	102531392	1516	0	0.0066
chr16	90354753	1872	0	0.006
chr17	81195210	3382	0	0.0425
chr18	78077248	595	0	0.0036
chr19	59128983	1593	0	0.0129
chr20	63025520	1257	0	0.0055
chr21	48129895	1789	0	0.02
chr22	51304566	135	0	0.0016
chrMT	16571	151	0.0091	0.0947
chrX	155270560	107848	0.0007	0.14
chrY	59373566	3295	0.0001	0.0192

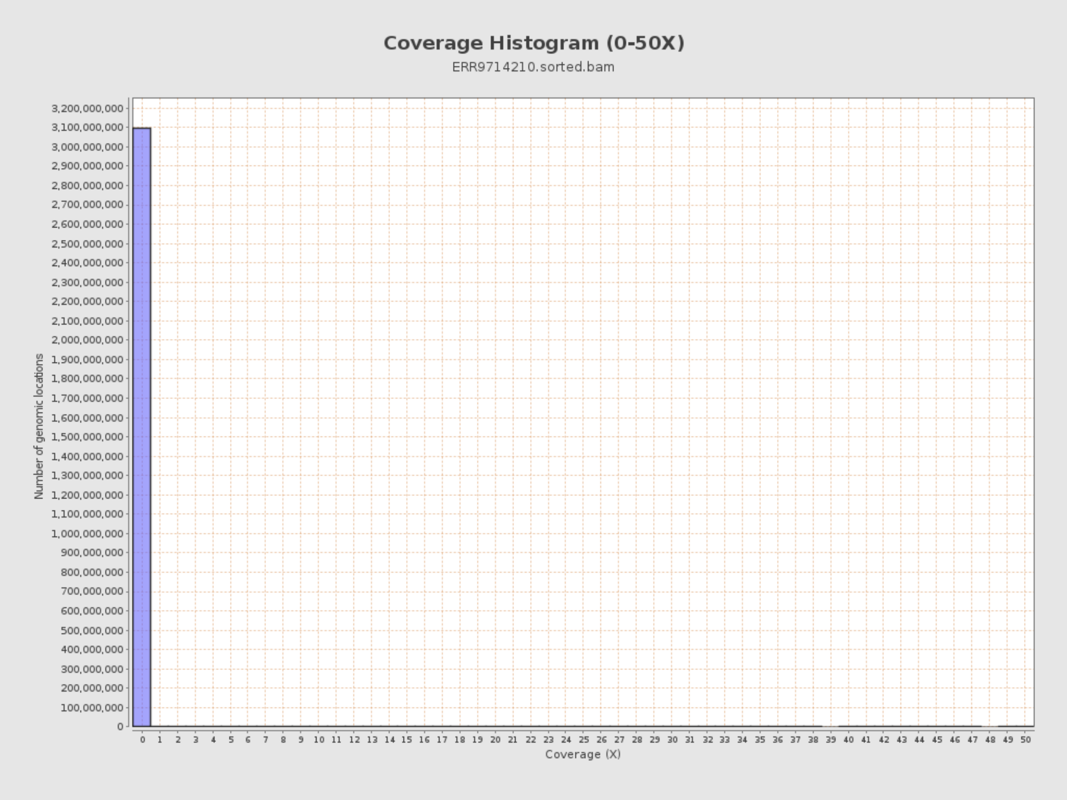
3. Results : Coverage across reference



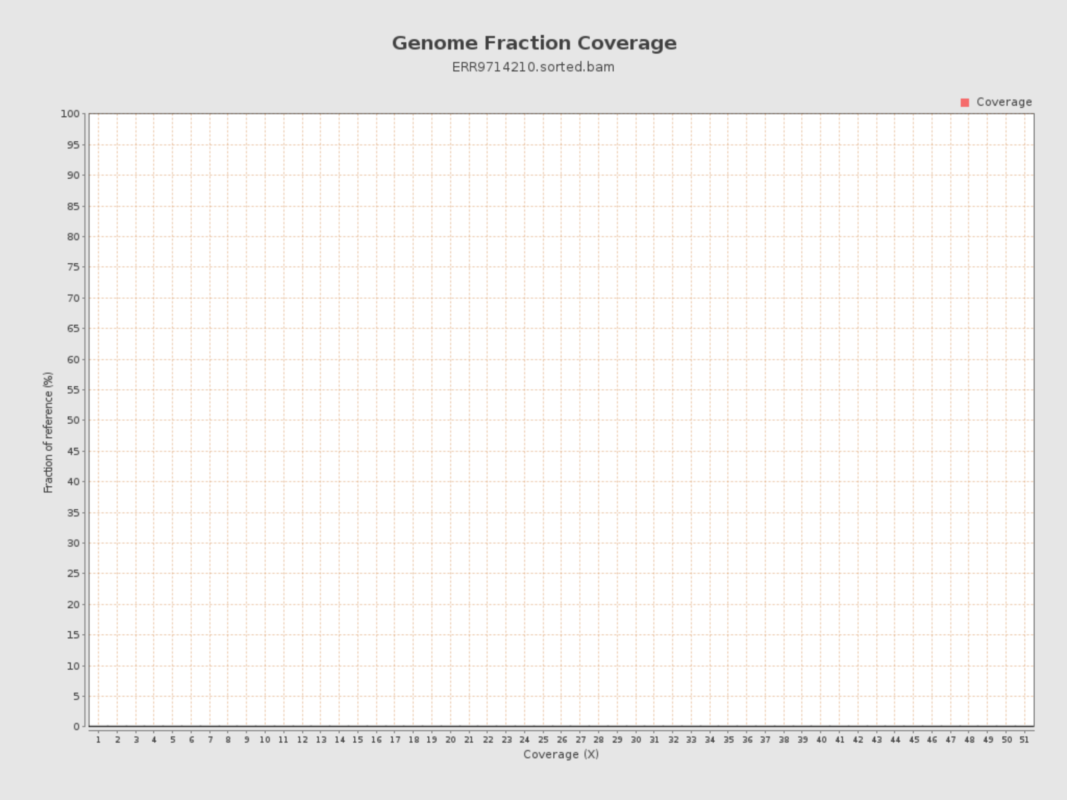
4. Results : Coverage Histogram



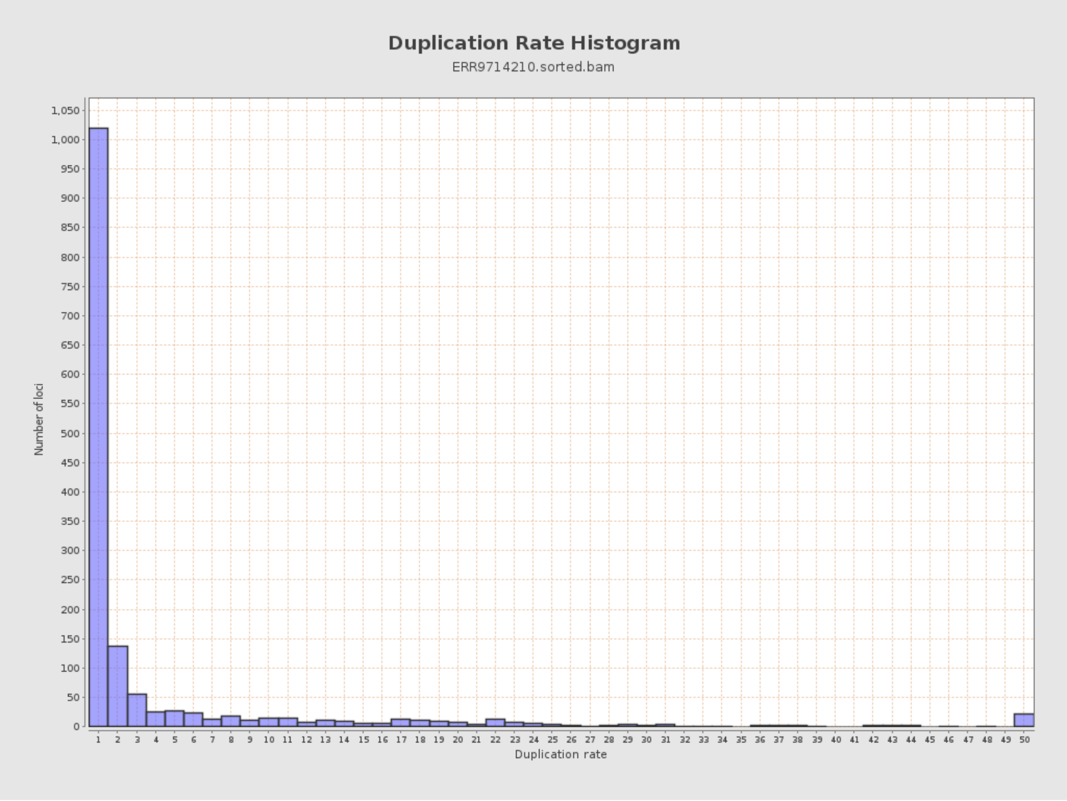
5. Results : Coverage Histogram (0-50X)



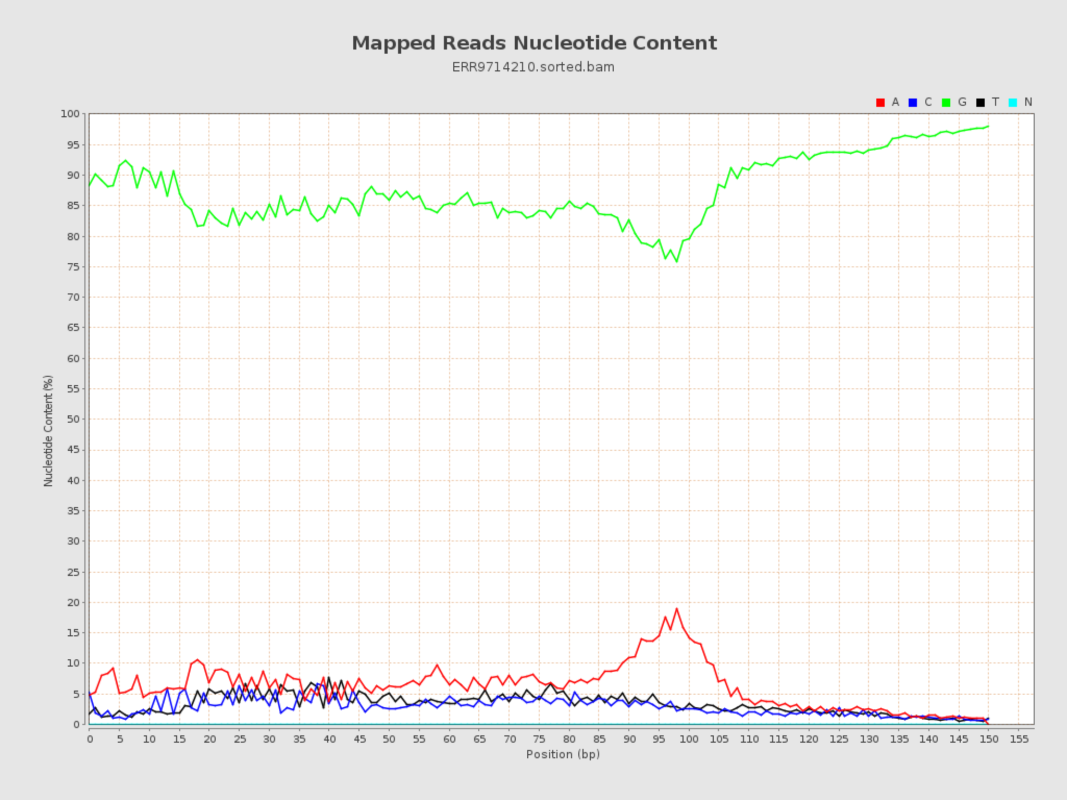
6. Results : Genome Fraction Coverage



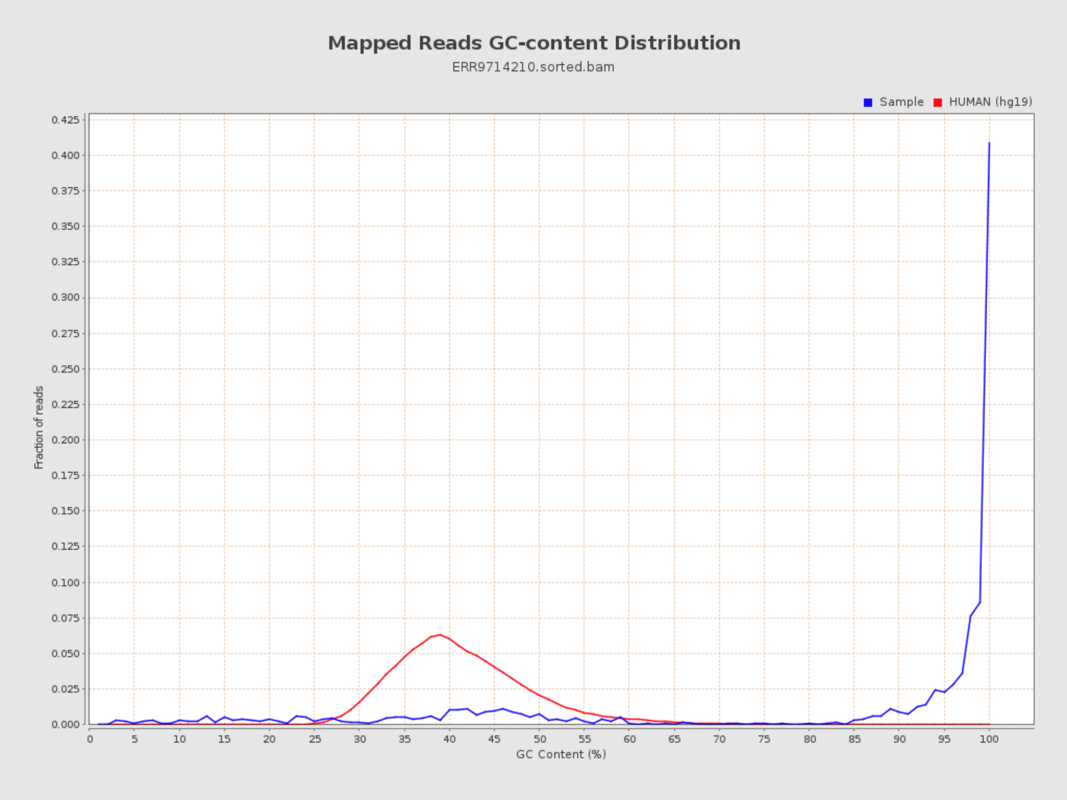
7. Results : Duplication Rate Histogram



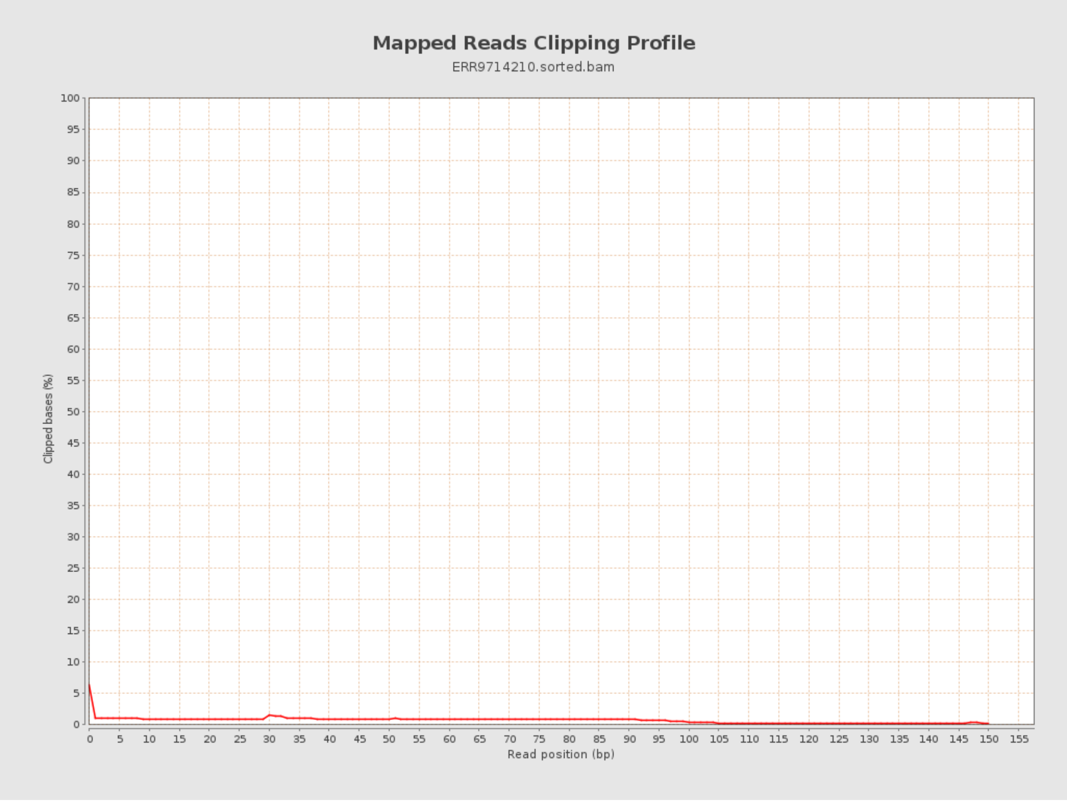
8. Results : Mapped Reads Nucleotide Content



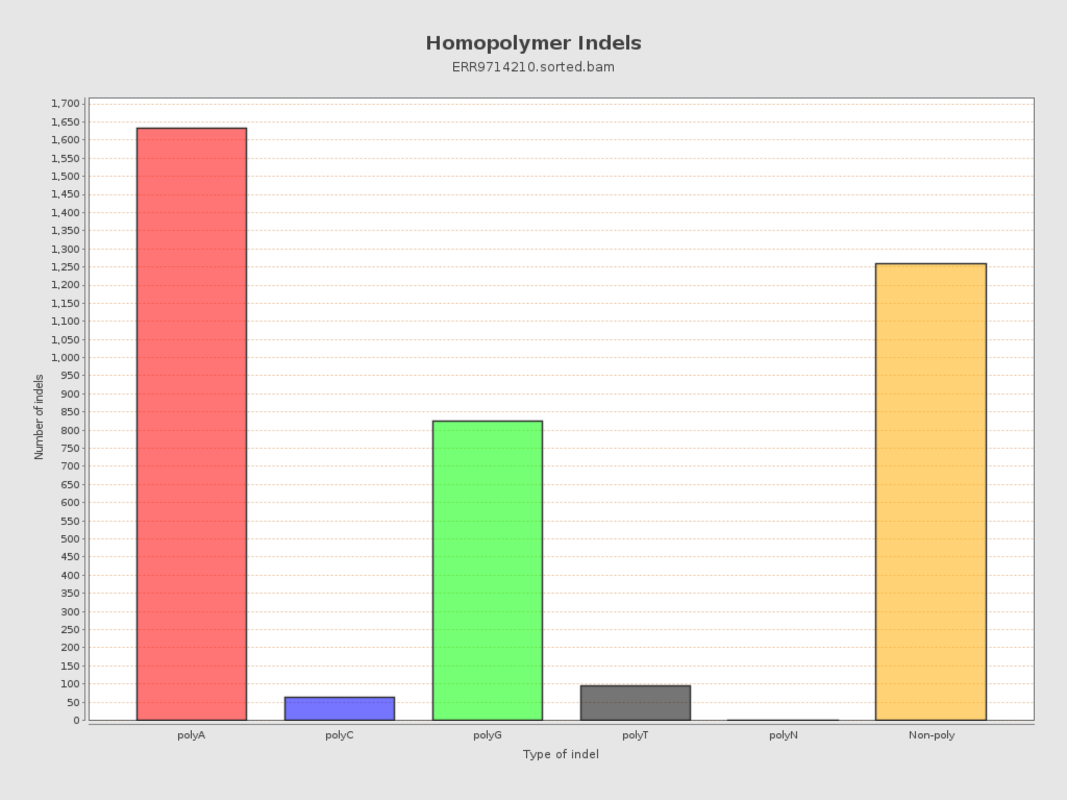
9. Results : Mapped Reads GC-content Distribution



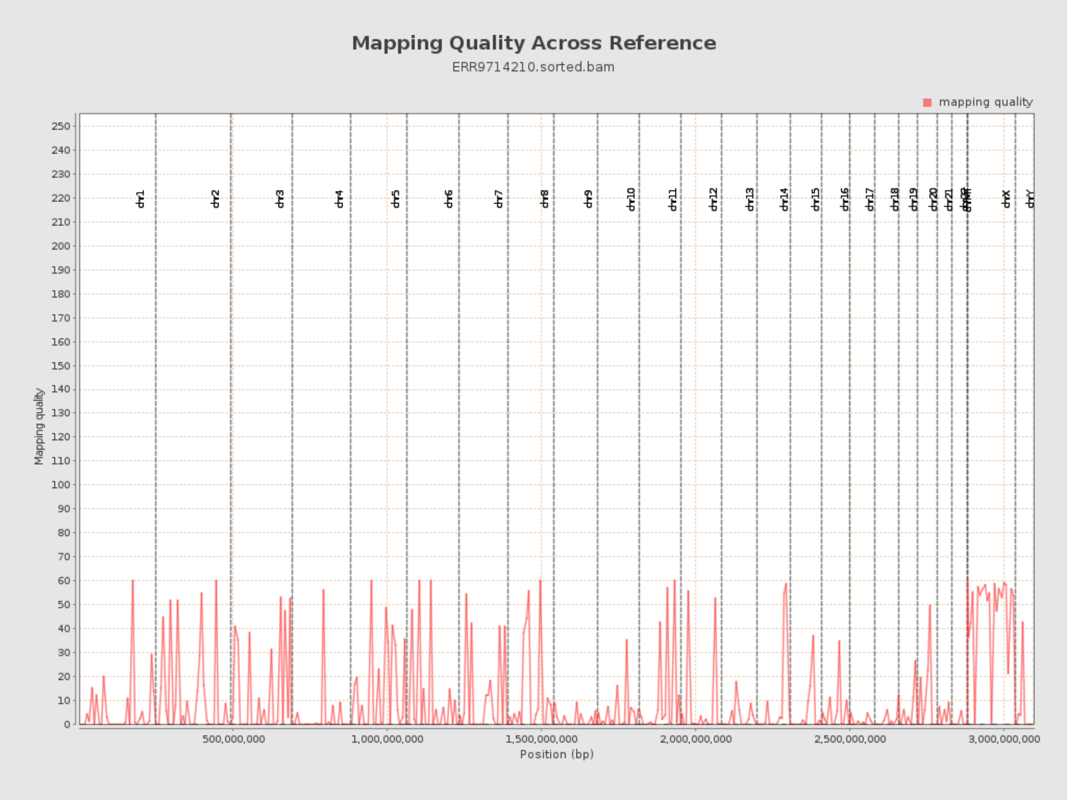
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram