Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:38:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714225.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_ERR9714225 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:38:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,554
Mapped reads	1,540 / 27.73%
Unmapped reads	4,014 / 72.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	82 / 1.48%
Read min/max/mean length	30 / 151 / 86.38
Duplicated reads (estimated)	751 / 13.52%
Duplication rate	34.79%
Clipped reads	1,274 / 22.94%

2.2. ACGT Content

Number/percentage of A's	38,778 / 22.5%
Number/percentage of C's	31,212 / 18.11%
Number/percentage of T's	35,853 / 20.8%
Number/percentage of G's	66,527 / 38.6%
Number/percentage of N's	2 / 0%
GC Percentage	56.7%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0459

2.4. Mapping Quality

Mean Mapping Quality	20.94

2.5. Mismatches and indels

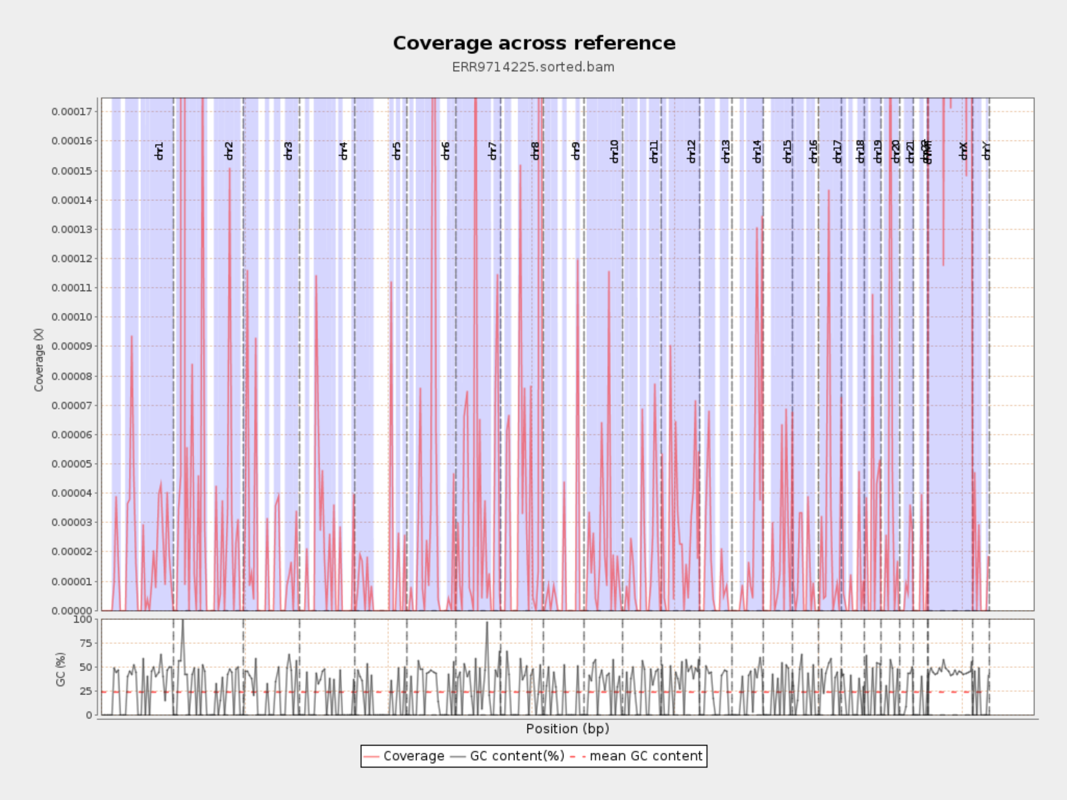
General error rate	3.77%
Mismatches	6,023
Insertions	101
Mapped reads with at least one insertion	4.81%
Deletions	402
Mapped reads with at least one deletion	25.19%
Homopolymer indels	33.2%

2.6. Chromosome stats

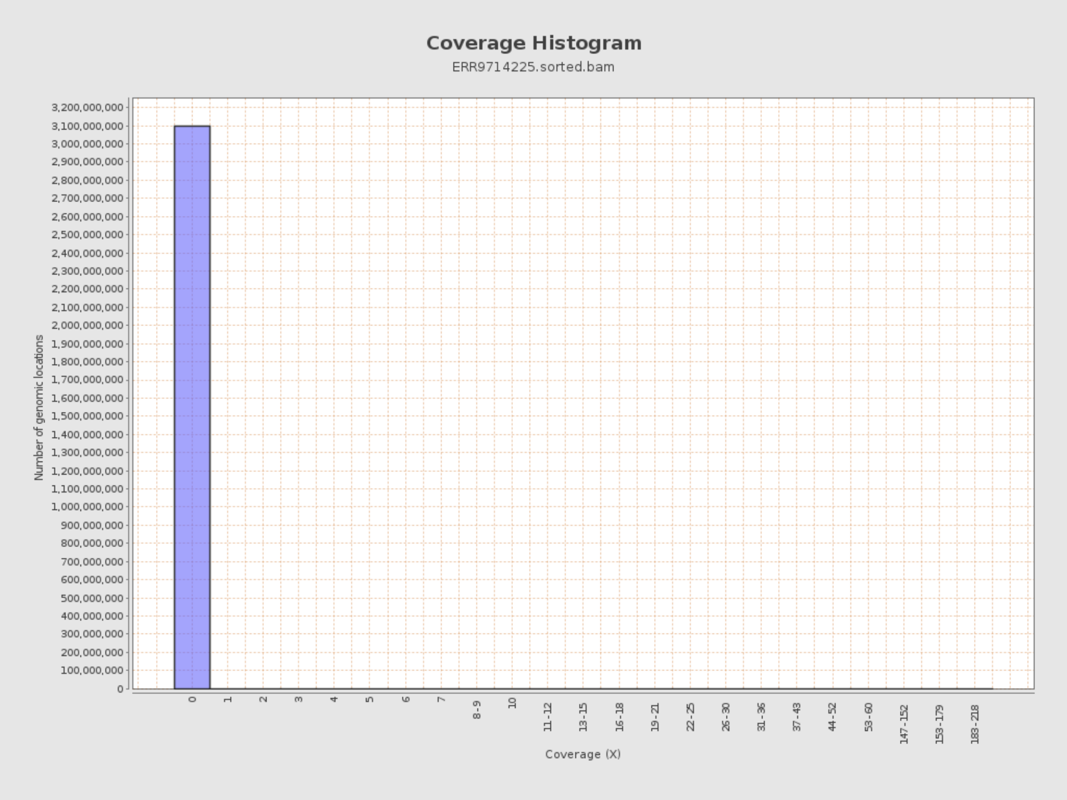
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4254	0	0.0056
chr2	243199373	42053	0.0002	0.1519
chr3	198022430	3427	0	0.0061
chr4	191154276	3252	0	0.0065
chr5	180915260	1819	0	0.0059
chr6	171115067	4706	0	0.0096
chr7	159138663	5914	0	0.0151

chr8	146364022	8836	0.0001	0.0352
chr9	141213431	1464	0	0.0044
chr10	135534747	2675	0	0.0073
chr11	135006516	2200	0	0.0063
chr12	133851895	3828	0	0.0081
chr13	115169878	1225	0	0.0043
chr14	107349540	3075	0	0.0116
chr15	102531392	1802	0	0.0066
chr16	90354753	978	0	0.0041
chr17	81195210	2105	0	0.0077
chr18	78077248	692	0	0.0039
chr19	59128983	1867	0	0.0085
chr20	63025520	2468	0	0.0176
chr21	48129895	528	0	0.0042
chr22	51304566	346	0	0.0034
chrMT	16571	0	0	0
chrX	155270560	75473	0.0005	0.0607
chrY	59373566	734	0	0.0041

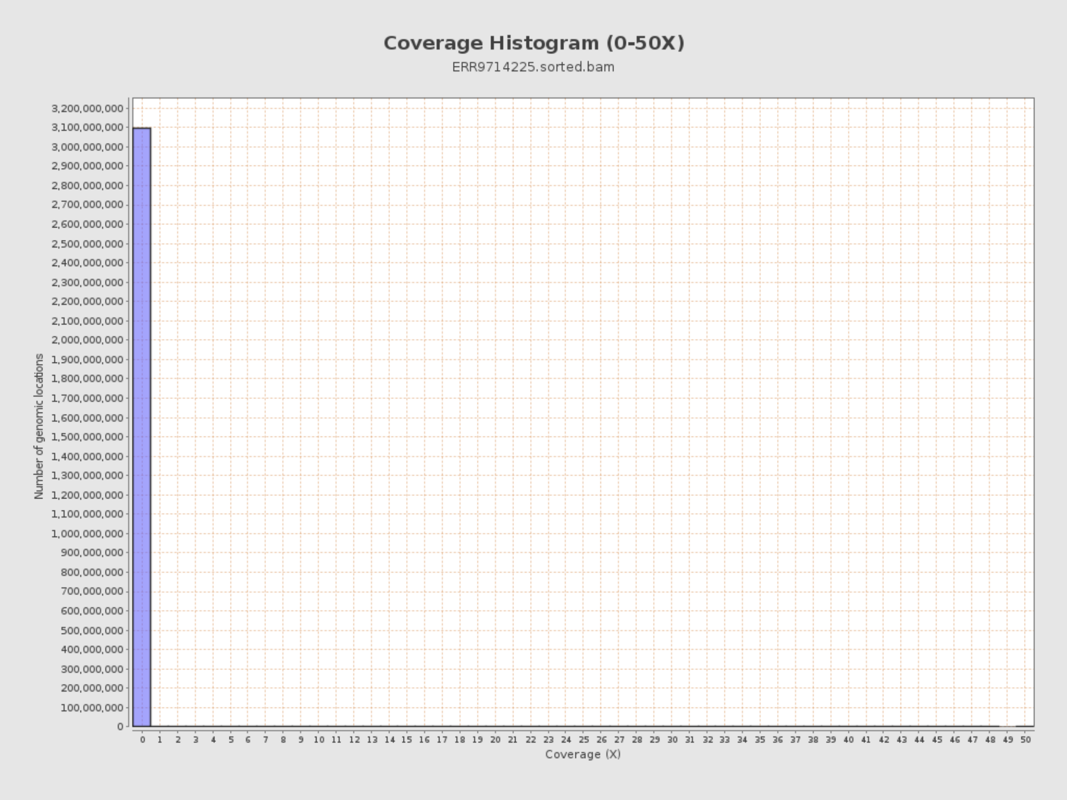
3. Results : Coverage across reference



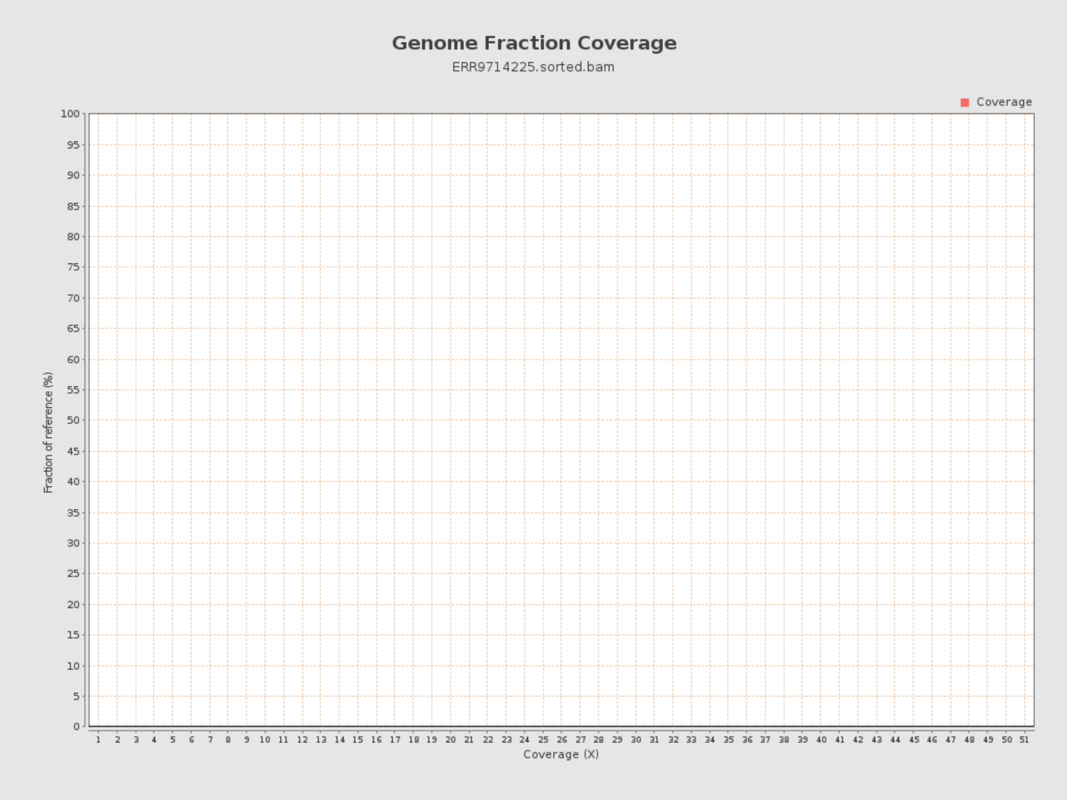
4. Results : Coverage Histogram



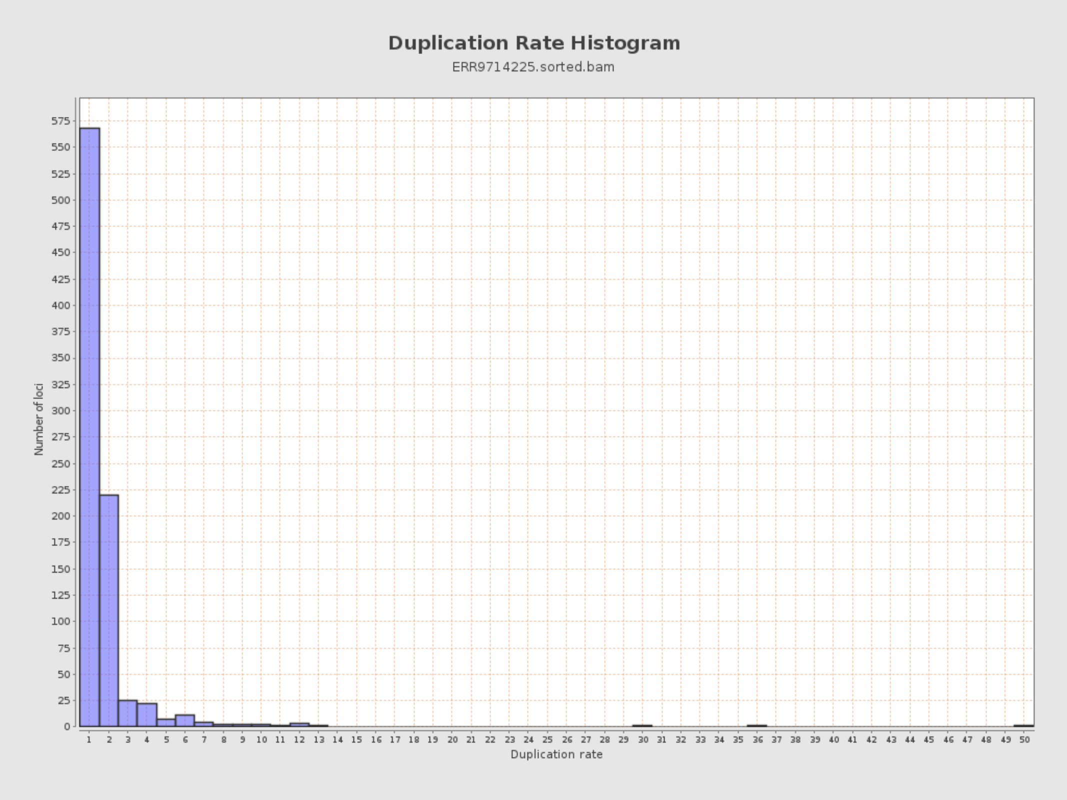
5. Results : Coverage Histogram (0-50X)



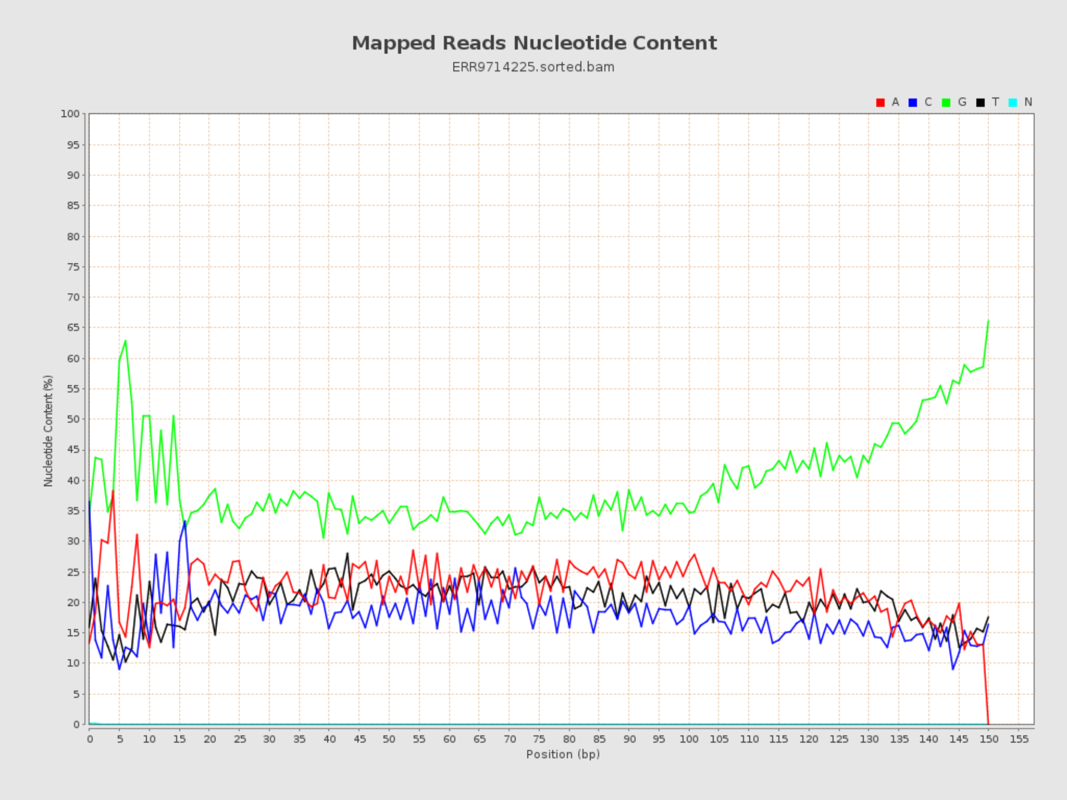
6. Results : Genome Fraction Coverage



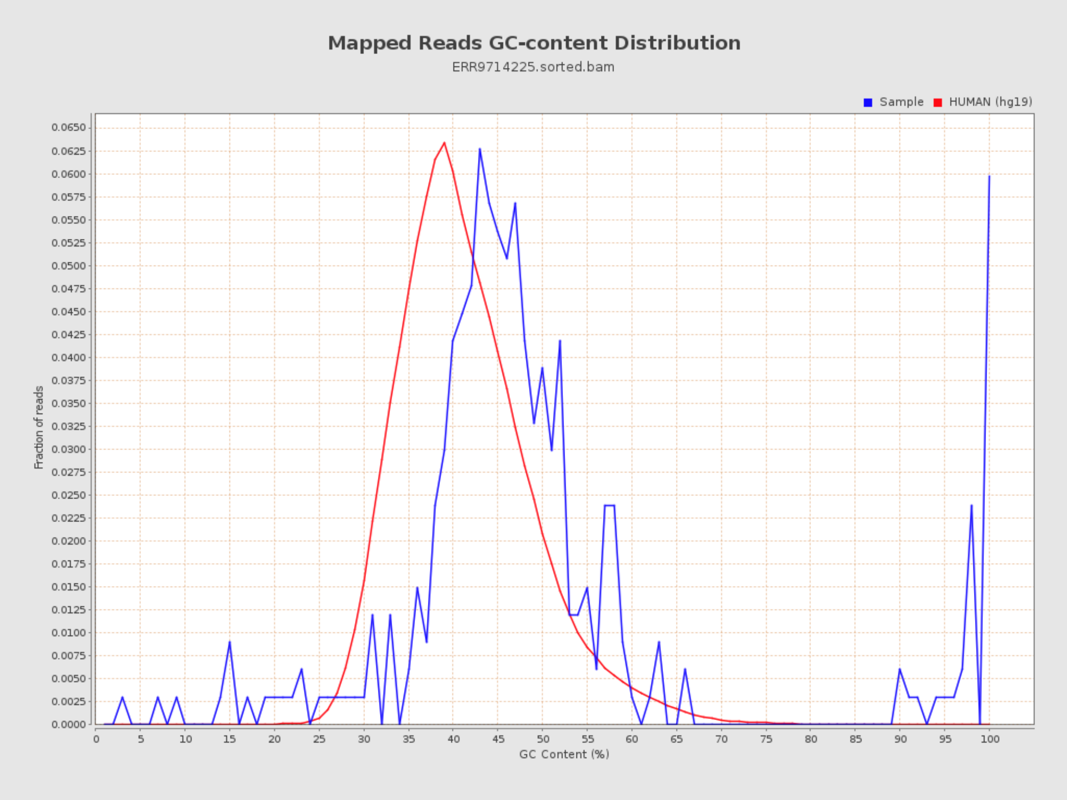
7. Results : Duplication Rate Histogram



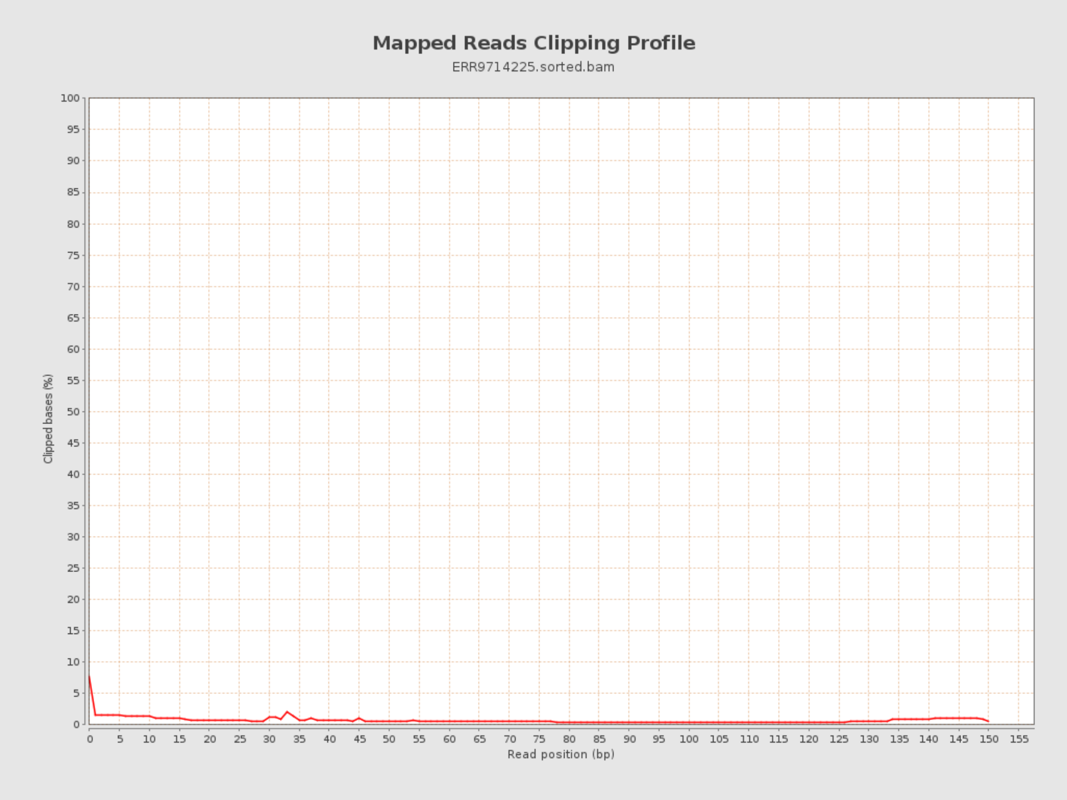
8. Results : Mapped Reads Nucleotide Content



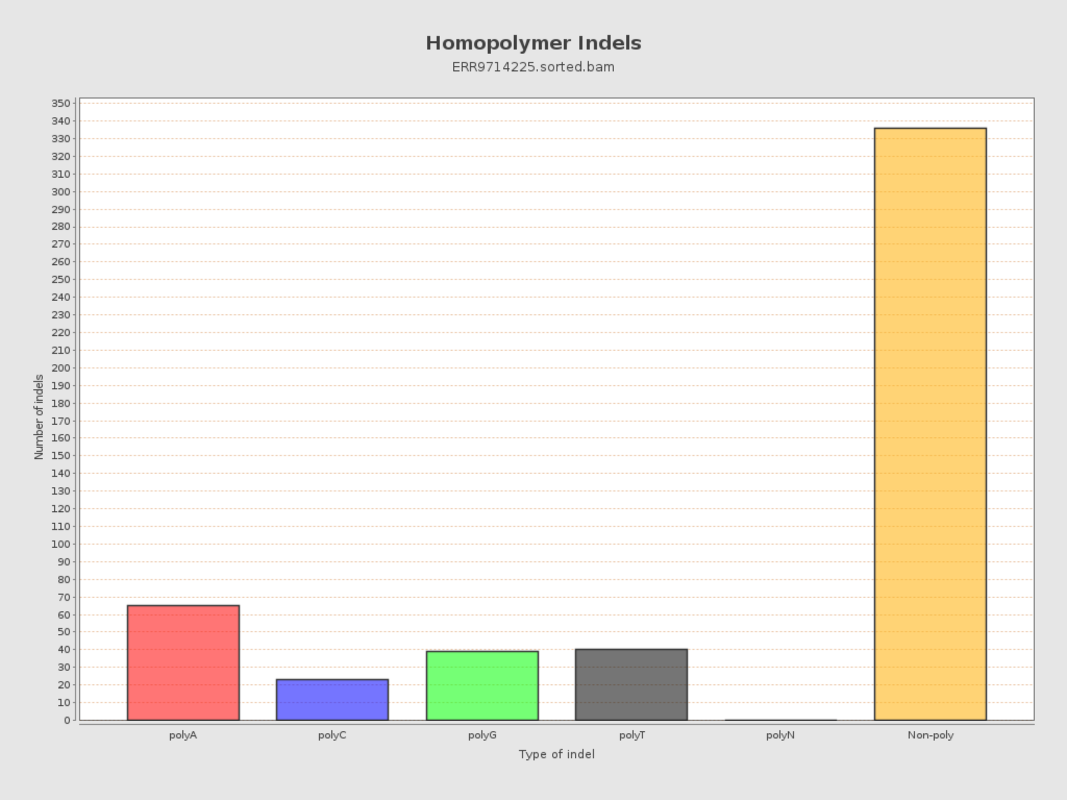
9. Results : Mapped Reads GC-content Distribution



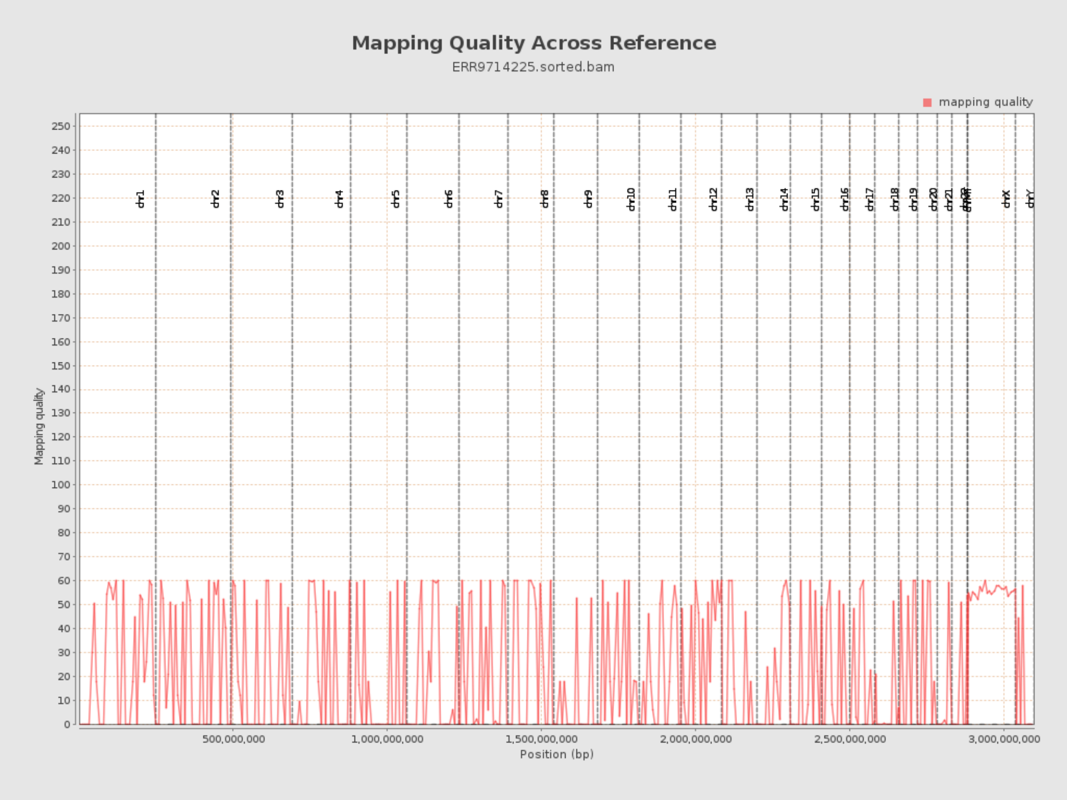
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram