Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:34:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714222.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_ERR9714222 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:34:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	226,286
Mapped reads	21,247 / 9.39%
Unmapped reads	205,039 / 90.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	624 / 0.28%
Read min/max/mean length	30 / 151 / 58.81
Duplicated reads (estimated)	17,814 / 7.87%
Duplication rate	38.9%
Clipped reads	18,350 / 8.11%

2.2. ACGT Content

Number/percentage of A's	474,523 / 21.66%
Number/percentage of C's	328,189 / 14.98%
Number/percentage of T's	432,040 / 19.72%
Number/percentage of G's	955,838 / 43.63%
Number/percentage of N's	85 / 0%
GC Percentage	58.61%

2.3. Coverage

Mean	0.0007

Standard Deviation	0.7518

2.4. Mapping Quality

Mean Mapping Quality	32.5

2.5. Mismatches and indels

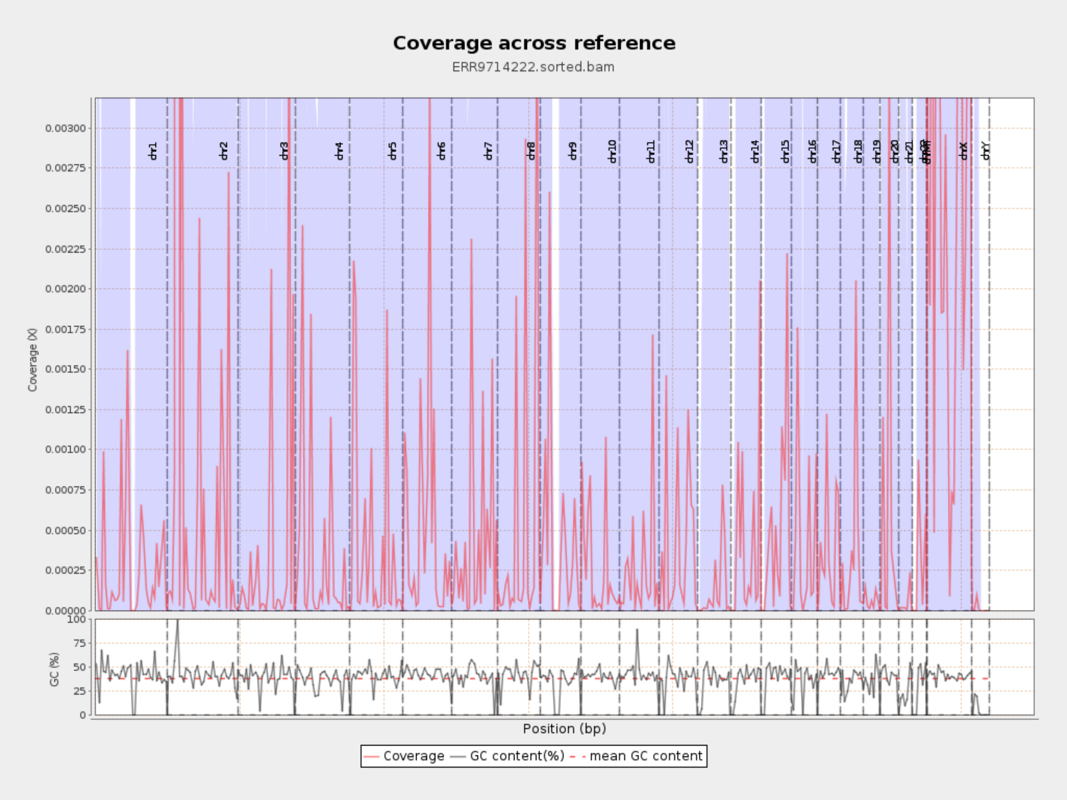
General error rate	3.79%
Mismatches	73,075
Insertions	2,202
Mapped reads with at least one insertion	9.13%
Deletions	5,767
Mapped reads with at least one deletion	26.09%
Homopolymer indels	31.69%

2.6. Chromosome stats

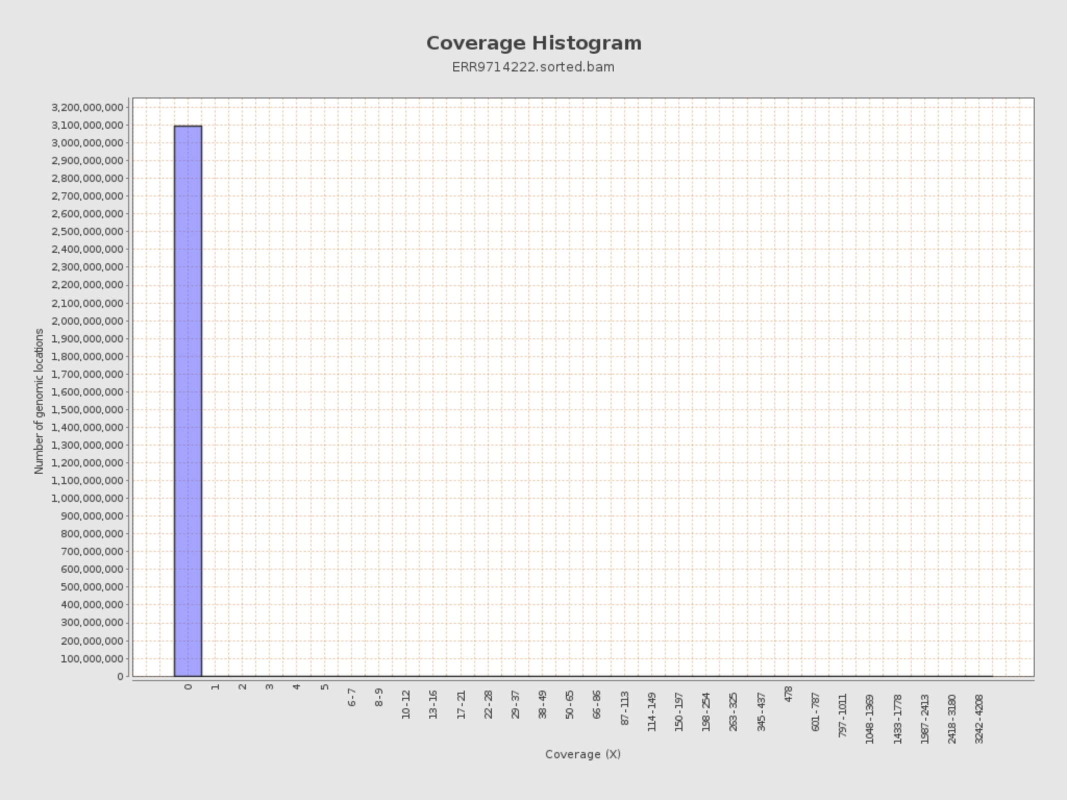
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	67815	0.0003	0.0794
chr2	243199373	763875	0.0031	2.6134
chr3	198022430	77892	0.0004	0.1805
chr4	191154276	63301	0.0003	0.1431
chr5	180915260	76706	0.0004	0.1703
chr6	171115067	91786	0.0005	0.1433
chr7	159138663	68724	0.0004	0.1554

chr8	146364022	81086	0.0006	0.2562
chr9	141213431	60004	0.0004	0.1169
chr10	135534747	37391	0.0003	0.0822
chr11	135006516	34819	0.0003	0.1059
chr12	133851895	51290	0.0004	0.104
chr13	115169878	14560	0.0001	0.0379
chr14	107349540	44022	0.0004	0.122
chr15	102531392	51544	0.0005	0.125
chr16	90354753	36175	0.0004	0.1193
chr17	81195210	31776	0.0004	0.1028
chr18	78077248	29213	0.0004	0.1441
chr19	59128983	3539	0.0001	0.0131
chr20	63025520	41706	0.0007	0.2104
chr21	48129895	2453	0.0001	0.0177
chr22	51304566	15715	0.0003	0.1071
chrMT	16571	648	0.0391	0.334
chrX	155270560	479241	0.0031	0.4965
chrY	59373566	891	0	0.0061

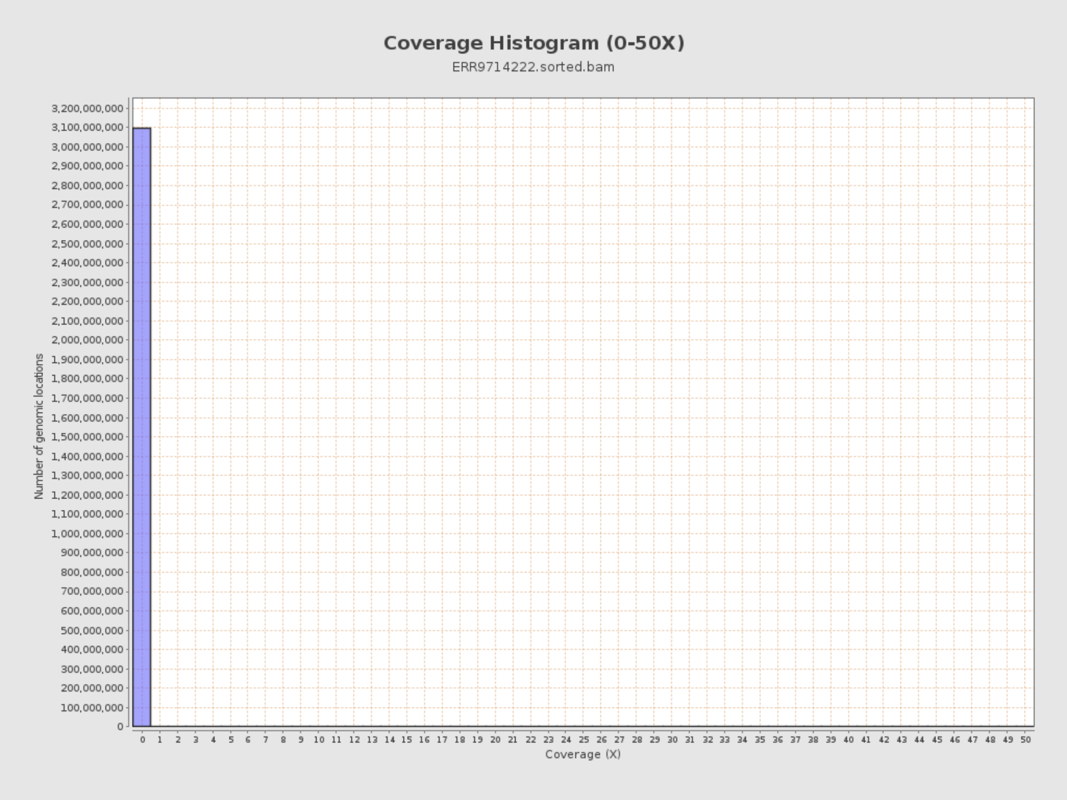
3. Results : Coverage across reference



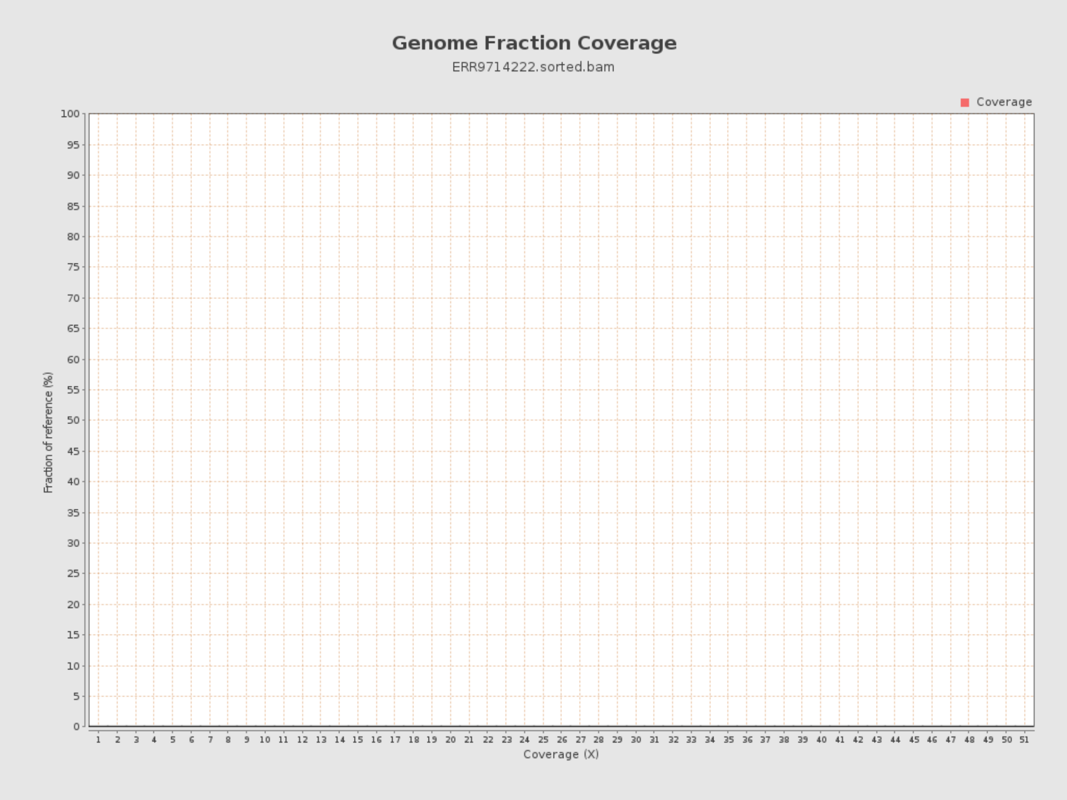
4. Results : Coverage Histogram



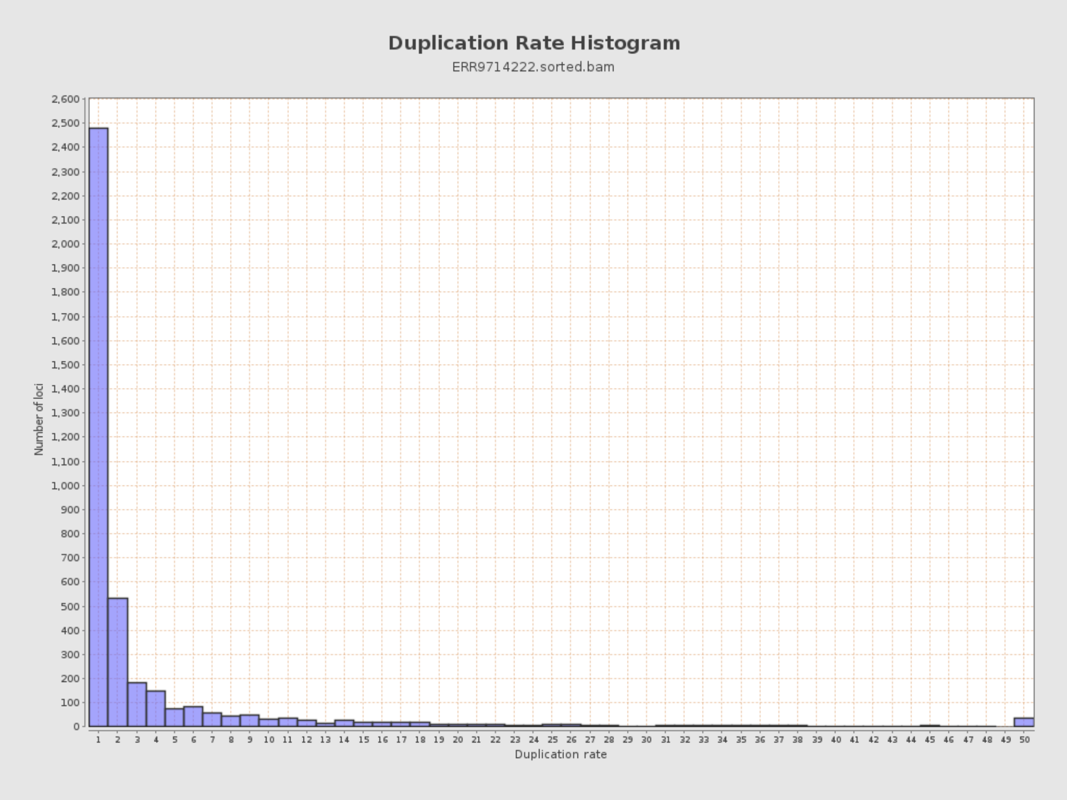
5. Results : Coverage Histogram (0-50X)



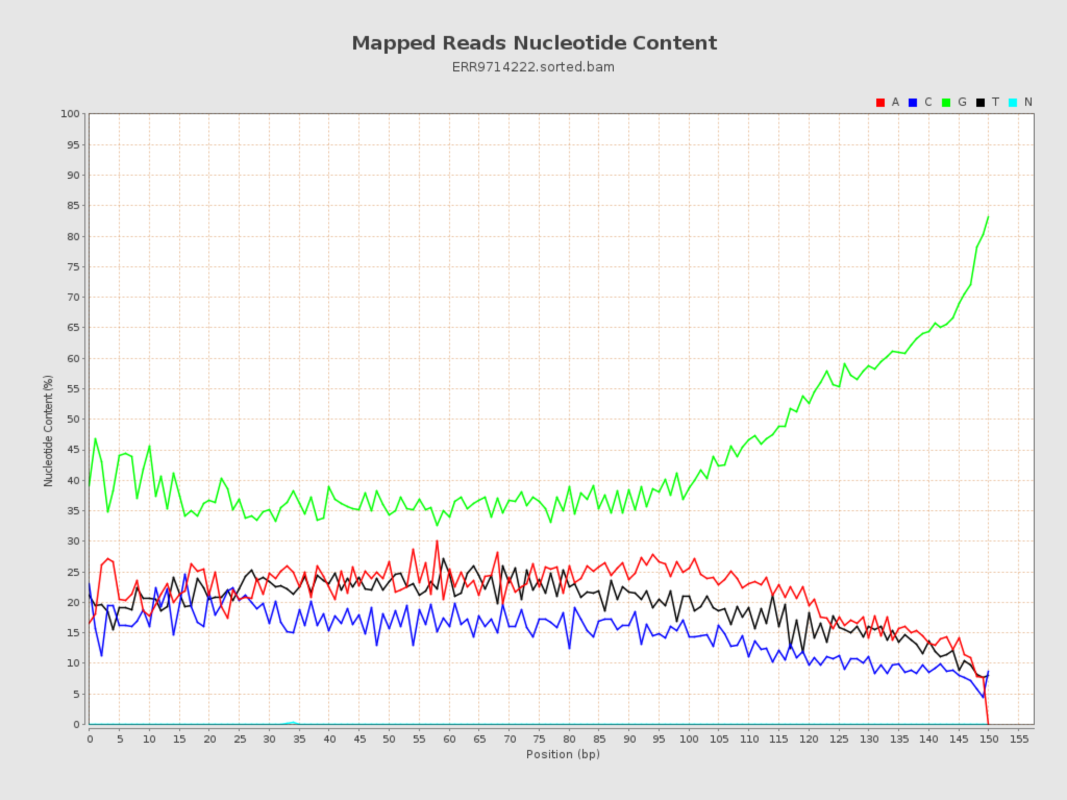
6. Results : Genome Fraction Coverage



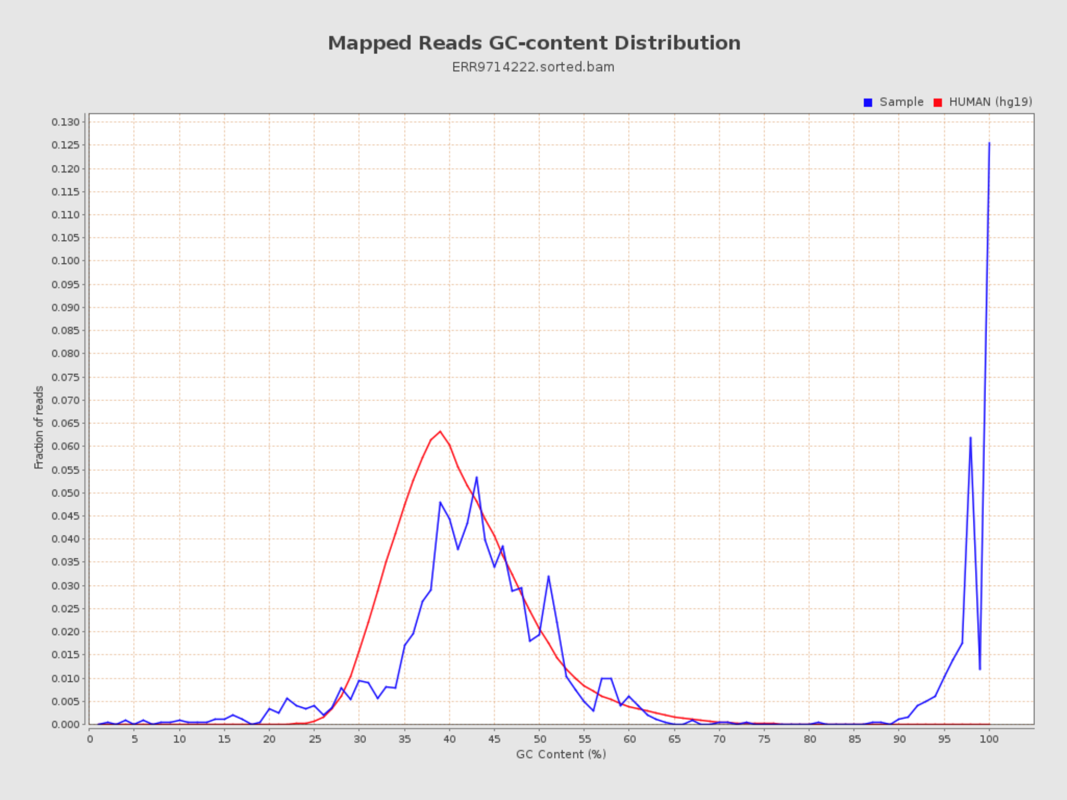
7. Results : Duplication Rate Histogram



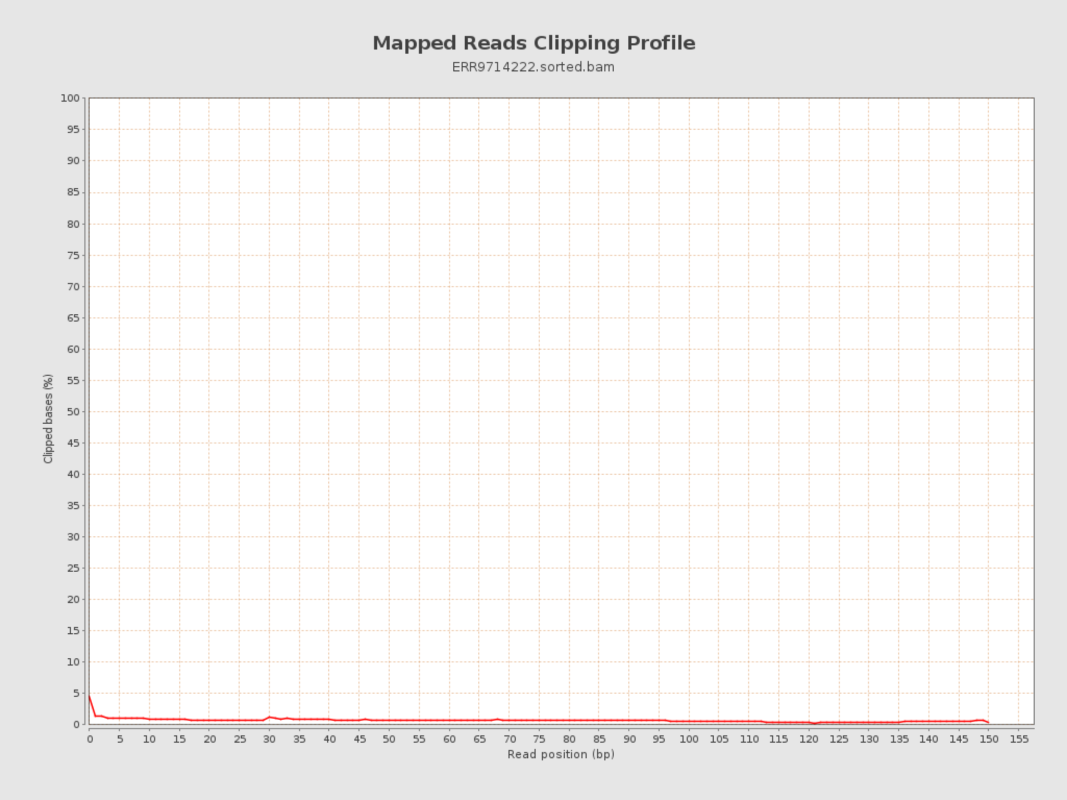
8. Results : Mapped Reads Nucleotide Content



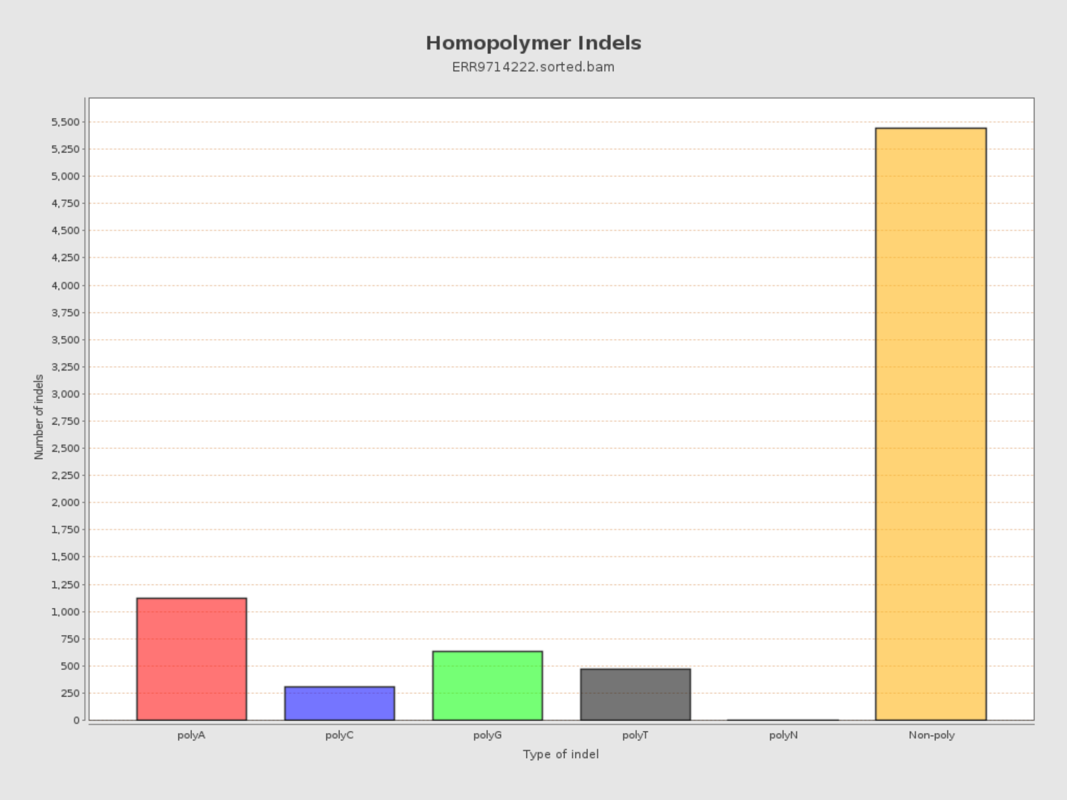
9. Results : Mapped Reads GC-content Distribution



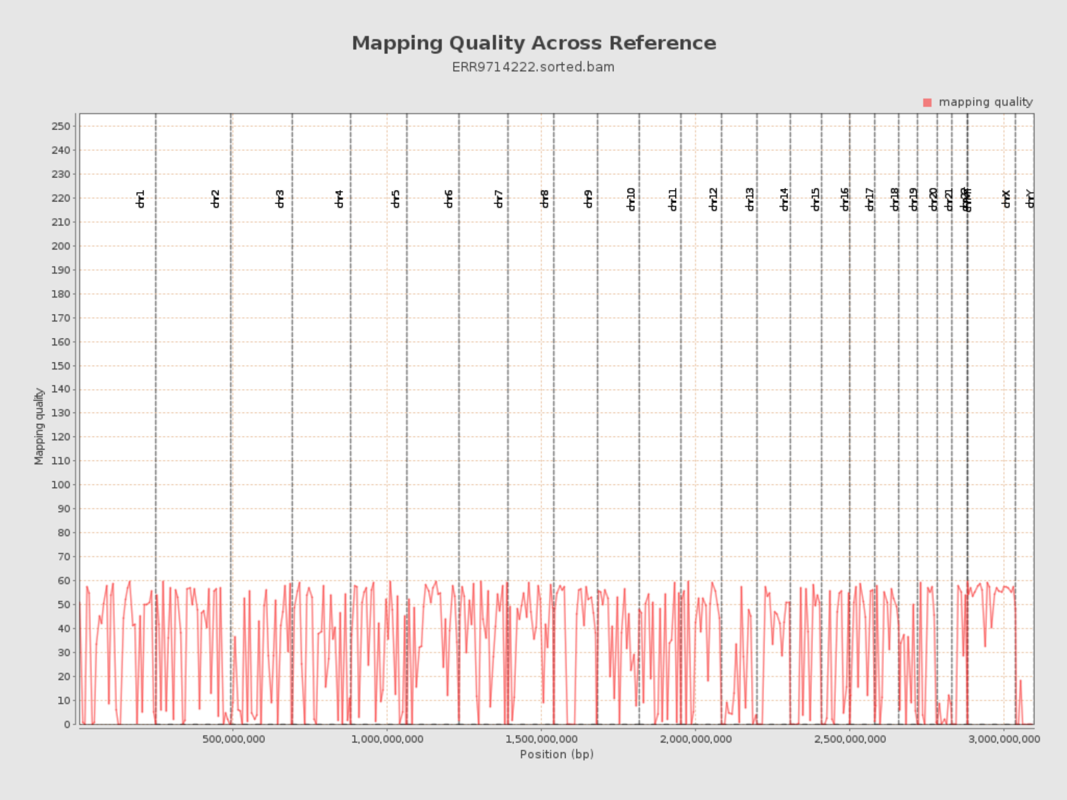
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram