Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:34:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714054.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_ERR9714054 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:34:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	485,008
Mapped reads	78,941 / 16.28%
Unmapped reads	406,067 / 83.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,490 / 0.31%
Read min/max/mean length	30 / 151 / 62.44
Duplicated reads (estimated)	78,000 / 16.08%
Duplication rate	31.84%
Clipped reads	43,419 / 8.95%

2.2. ACGT Content

Number/percentage of A's	177,890 / 2.26%
Number/percentage of C's	65,760 / 0.84%
Number/percentage of T's	87,666 / 1.12%
Number/percentage of G's	7,528,707 / 95.78%
Number/percentage of N's	226 / 0%
GC Percentage	96.62%

2.3. Coverage

Mean	0.0025

Standard Deviation	9.709

2.4. Mapping Quality

Mean Mapping Quality	7.79

2.5. Mismatches and indels

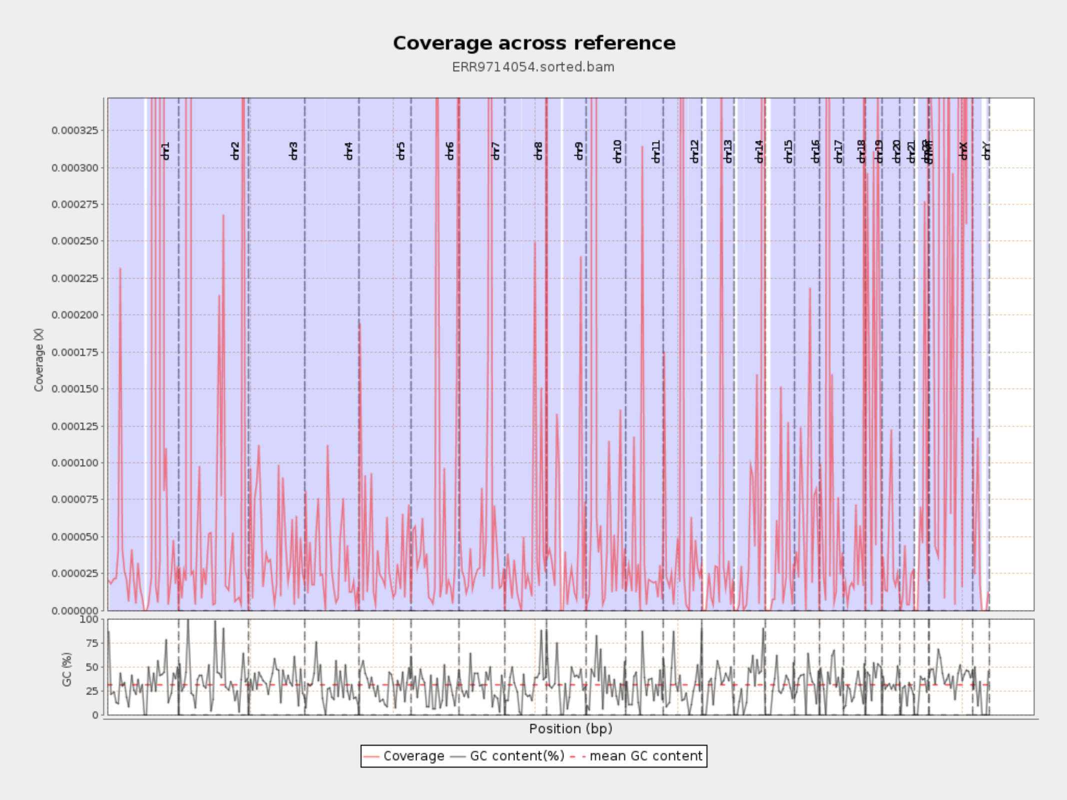
General error rate	3.11%
Mismatches	188,910
Insertions	8,305
Mapped reads with at least one insertion	7.05%
Deletions	3,339
Mapped reads with at least one deletion	4.07%
Homopolymer indels	62.25%

2.6. Chromosome stats

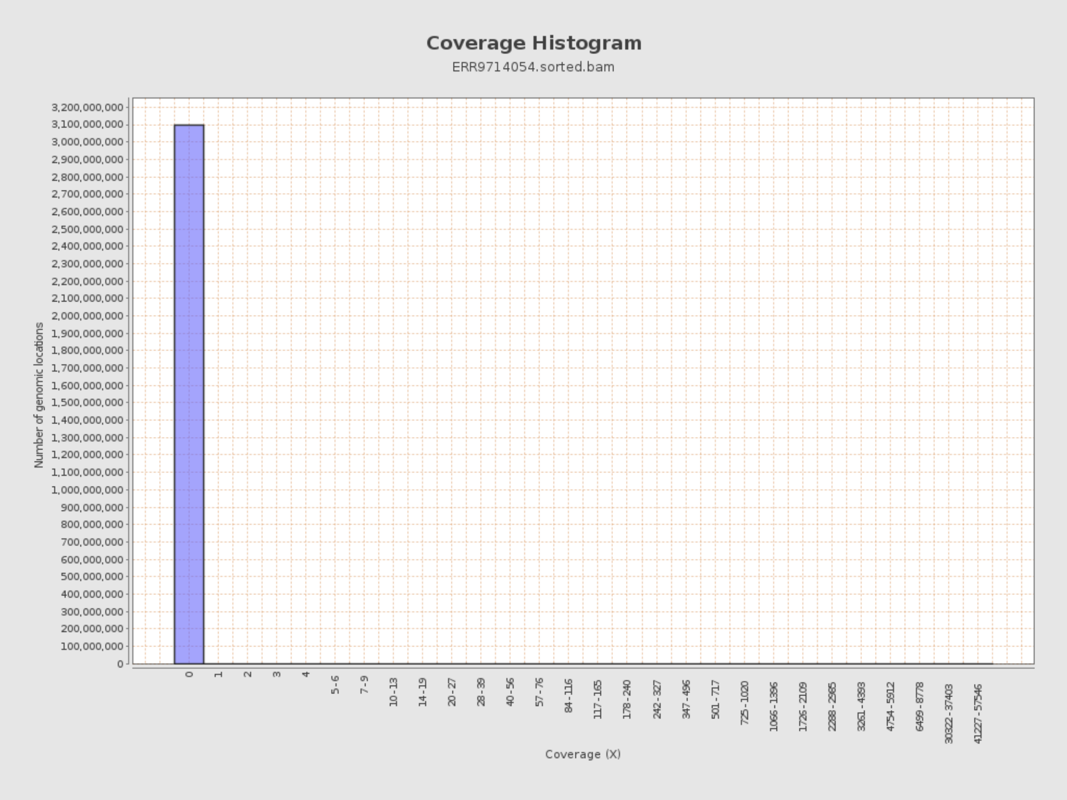
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	80101	0.0003	0.5551
chr2	243199373	7542326	0.031	34.631
chr3	198022430	8626	0	0.0164
chr4	191154276	6283	0	0.0106
chr5	180915260	7207	0	0.0109
chr6	171115067	11261	0.0001	0.0307
chr7	159138663	13987	0.0001	0.1059

chr8	146364022	5932	0	0.018
chr9	141213431	7177	0.0001	0.0176
chr10	135534747	46718	0.0003	0.6453
chr11	135006516	5463	0	0.0305
chr12	133851895	10559	0.0001	0.0575
chr13	115169878	4512	0	0.0221
chr14	107349540	12851	0.0001	0.1281
chr15	102531392	3433	0	0.0179
chr16	90354753	6155	0.0001	0.0212
chr17	81195210	11594	0.0001	0.1459
chr18	78077248	5803	0.0001	0.0779
chr19	59128983	9542	0.0002	0.0413
chr20	63025520	2437	0	0.0137
chr21	48129895	801	0	0.0061
chr22	51304566	3444	0.0001	0.0247
chrMT	16571	151	0.0091	0.0947
chrX	155270560	66026	0.0004	0.1036
chrY	59373566	1589	0	0.0098

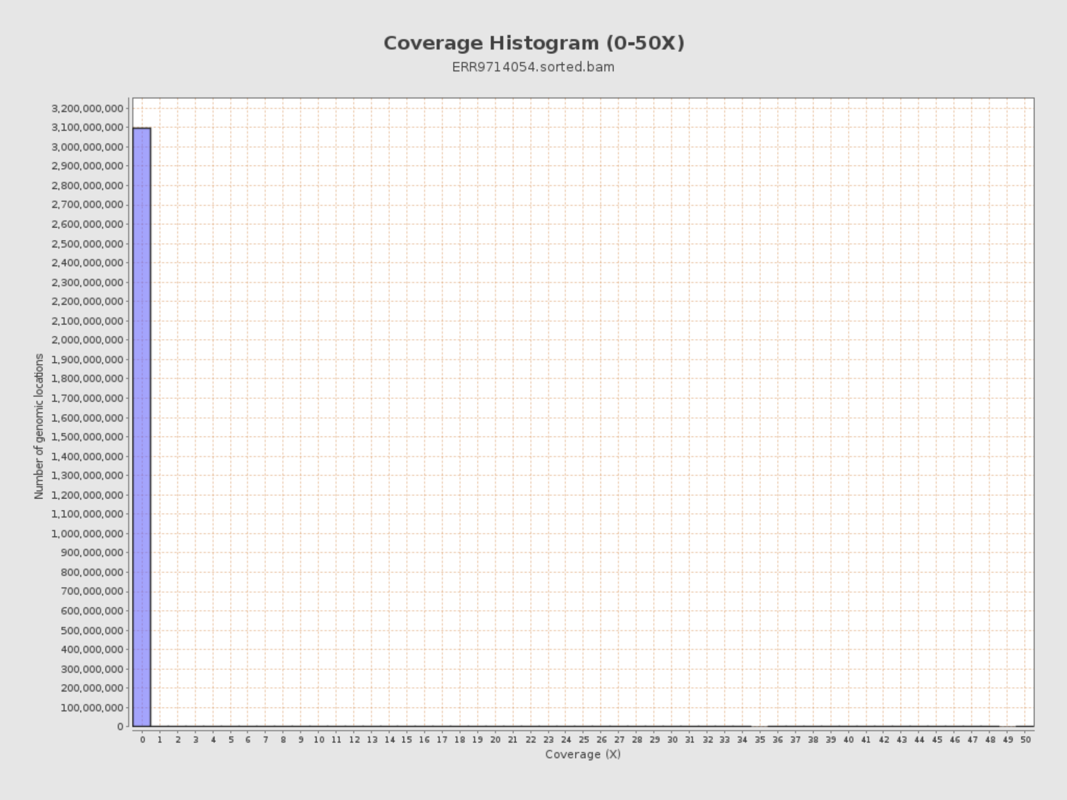
3. Results : Coverage across reference



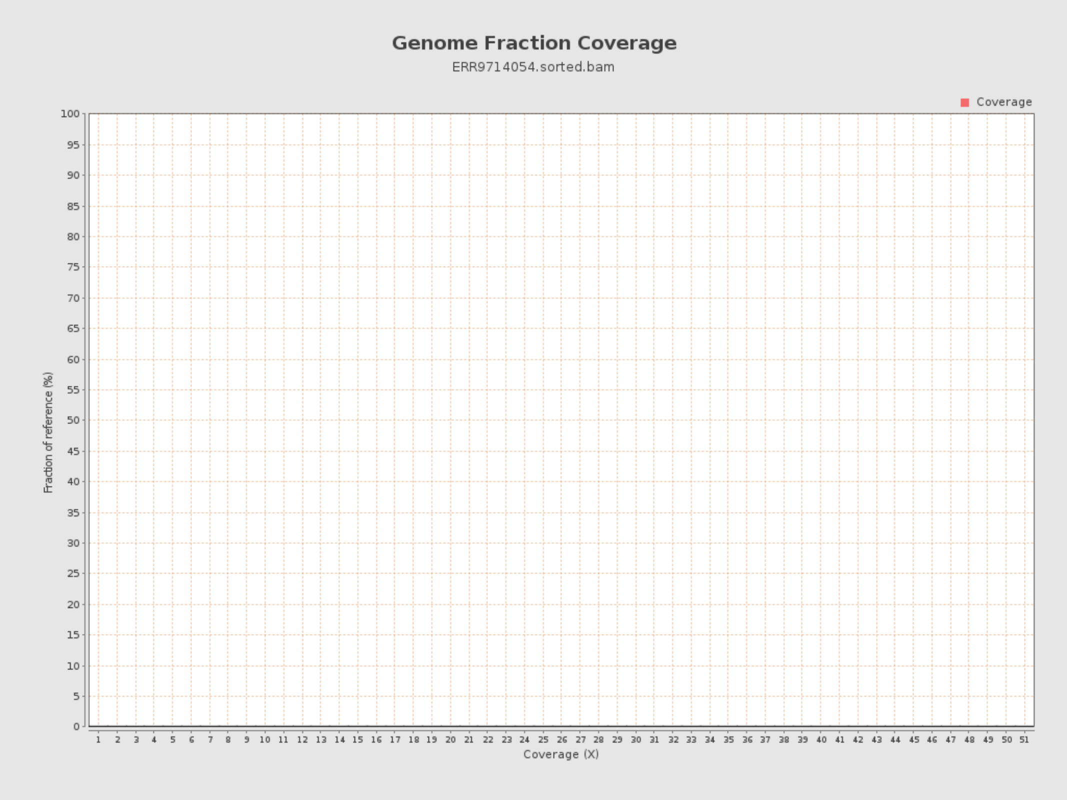
4. Results : Coverage Histogram



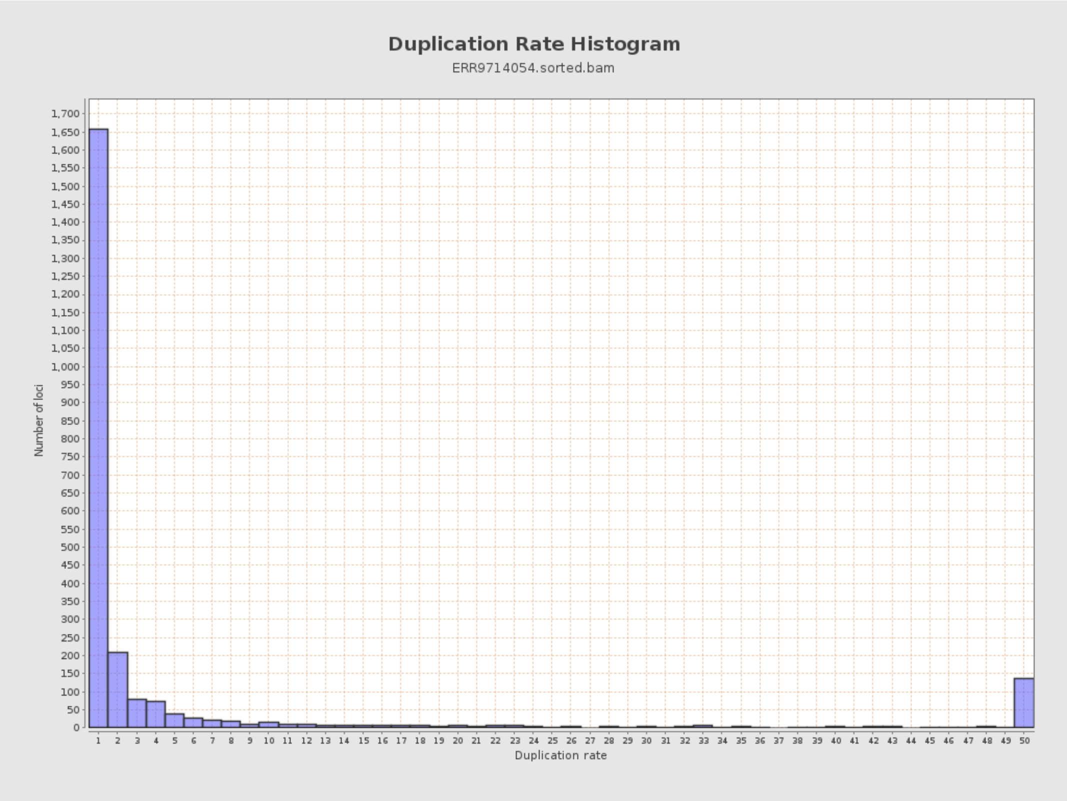
5. Results : Coverage Histogram (0-50X)



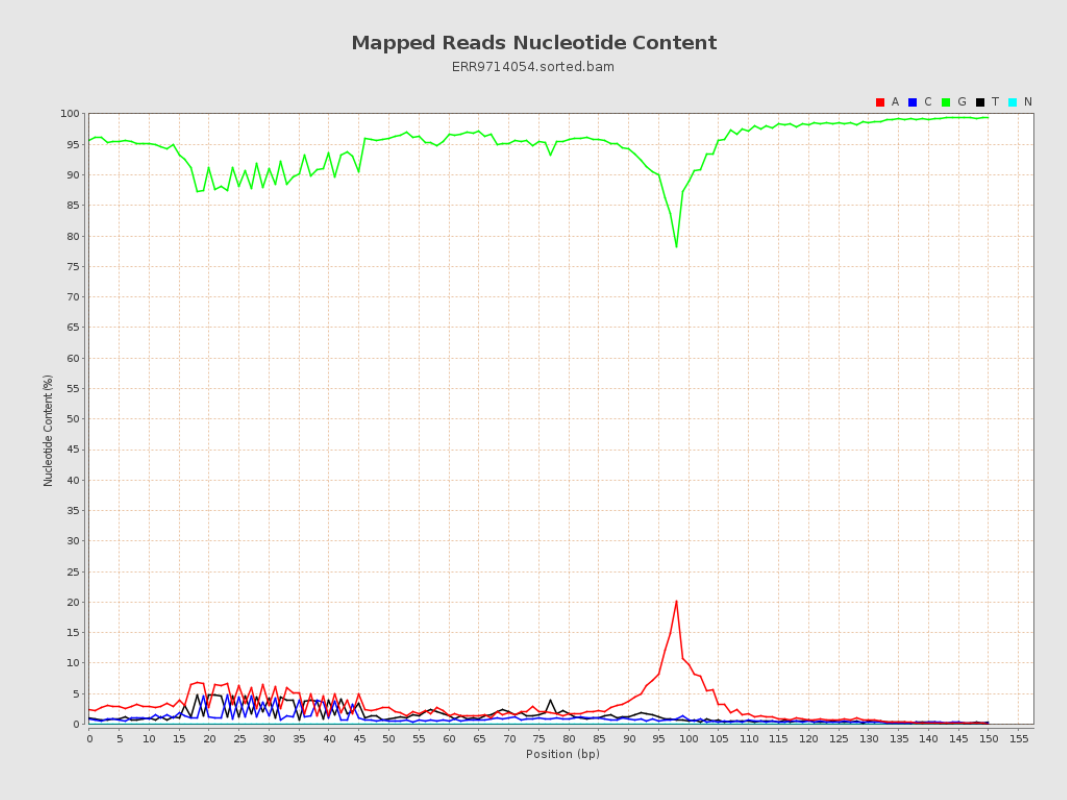
6. Results : Genome Fraction Coverage



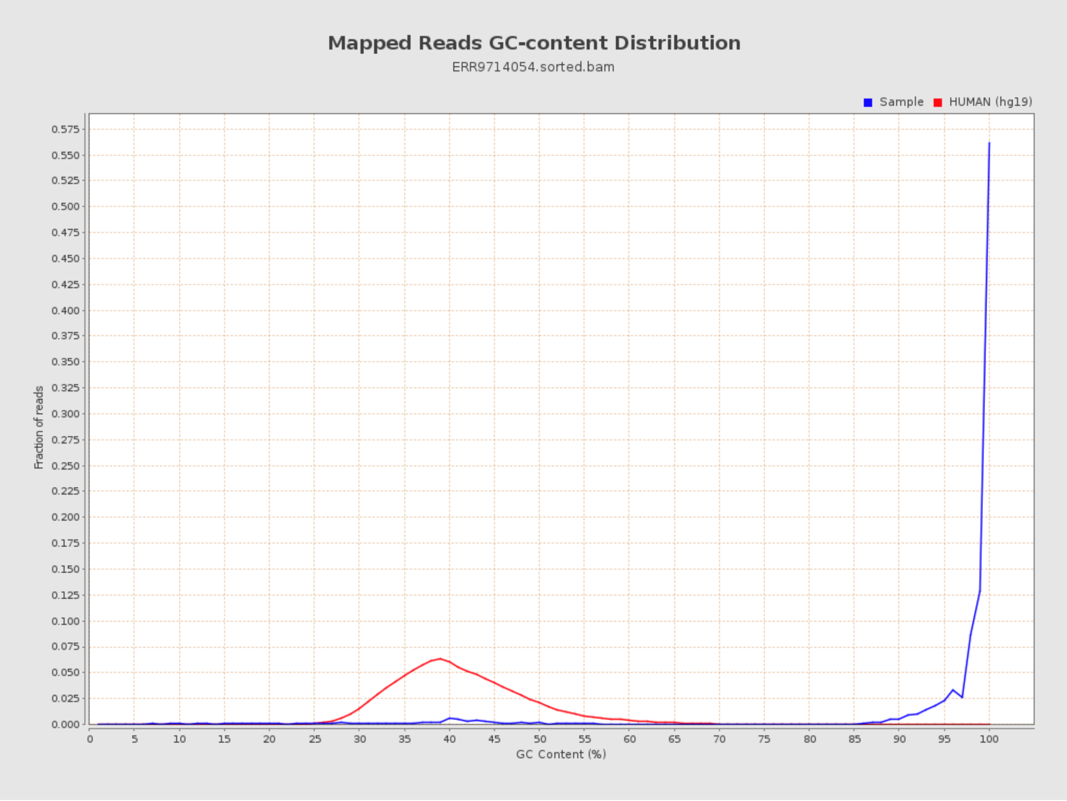
7. Results : Duplication Rate Histogram



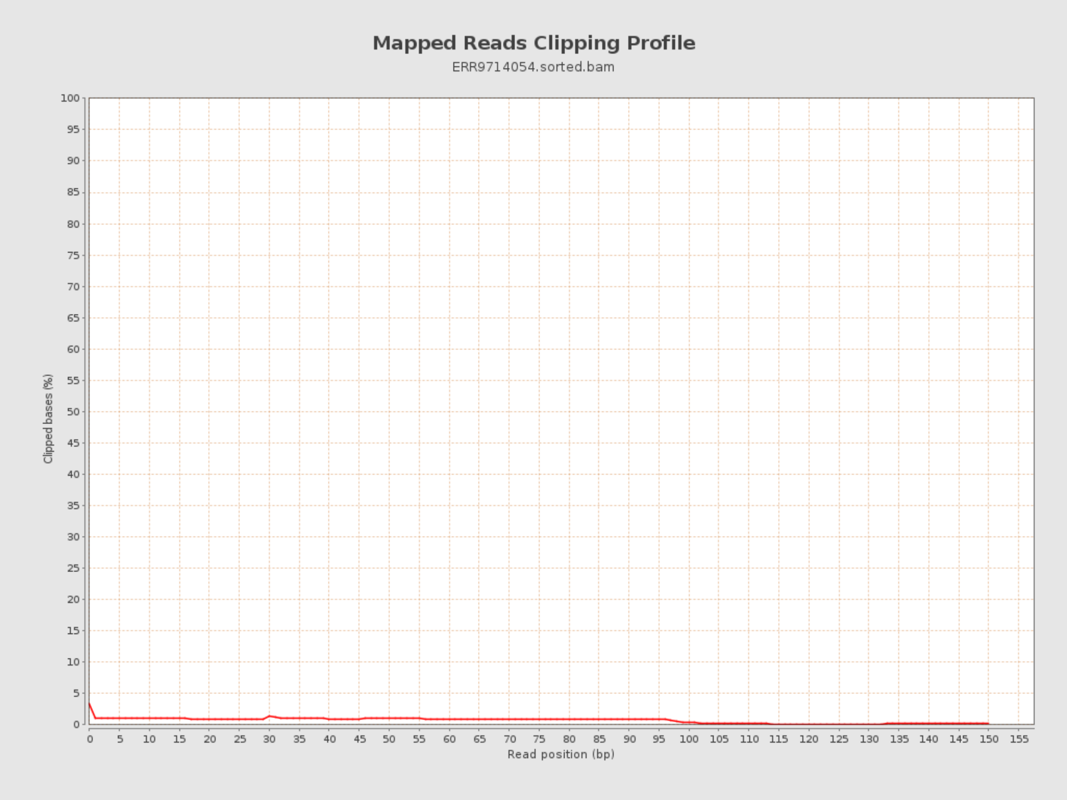
8. Results : Mapped Reads Nucleotide Content



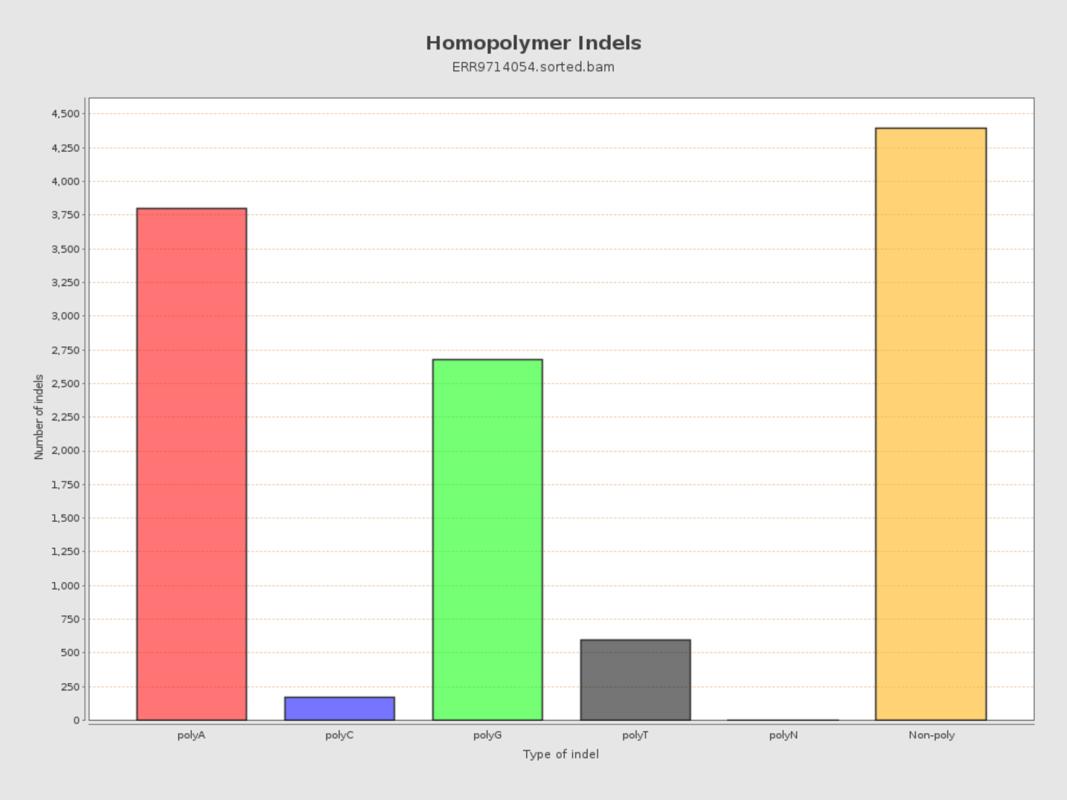
9. Results : Mapped Reads GC-content Distribution



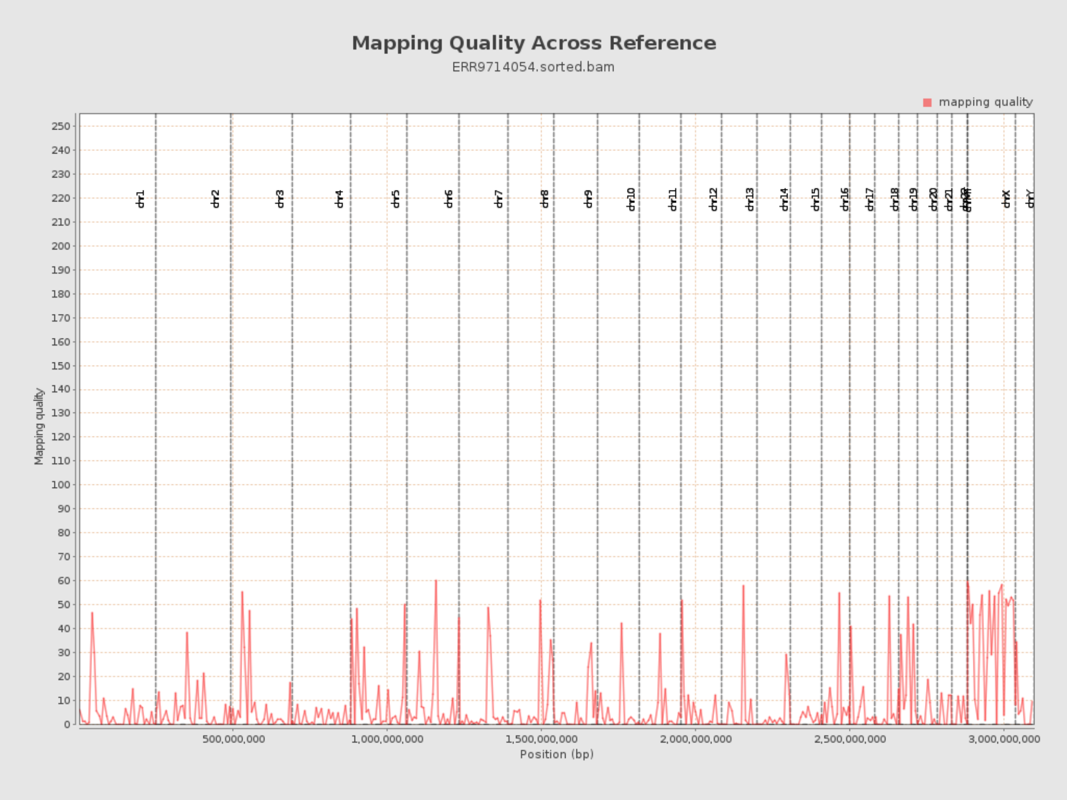
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram