Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:15:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714046.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_ERR9714046 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:15:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,562
Mapped reads	3,448 / 27.45%
Unmapped reads	9,114 / 72.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	107 / 0.85%
Read min/max/mean length	30 / 151 / 80.22
Duplicated reads (estimated)	2,589 / 20.61%
Duplication rate	45.65%
Clipped reads	2,578 / 20.52%

2.2. ACGT Content

Number/percentage of A's	73,449 / 18.67%
Number/percentage of C's	61,563 / 15.65%
Number/percentage of T's	67,956 / 17.27%
Number/percentage of G's	190,475 / 48.41%
Number/percentage of N's	13 / 0%
GC Percentage	64.06%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.1705

2.4. Mapping Quality

Mean Mapping Quality	18.76

2.5. Mismatches and indels

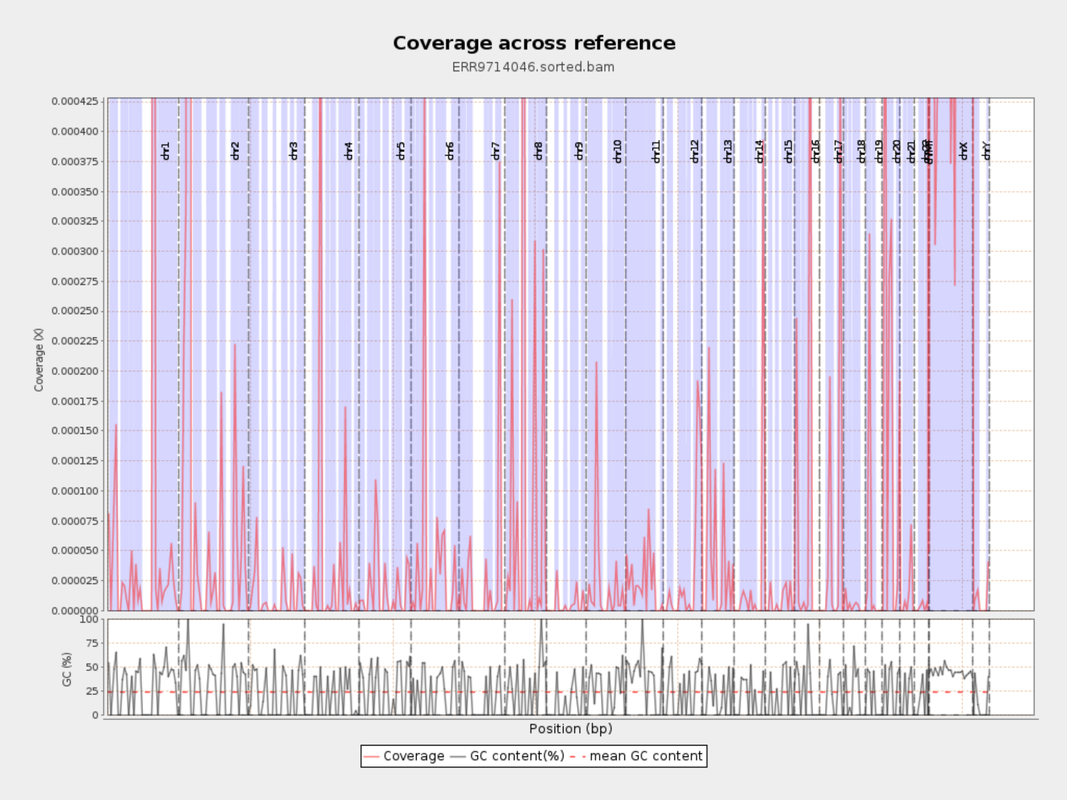
General error rate	3.61%
Mismatches	13,024
Insertions	228
Mapped reads with at least one insertion	5.57%
Deletions	792
Mapped reads with at least one deletion	21.72%
Homopolymer indels	34.22%

2.6. Chromosome stats

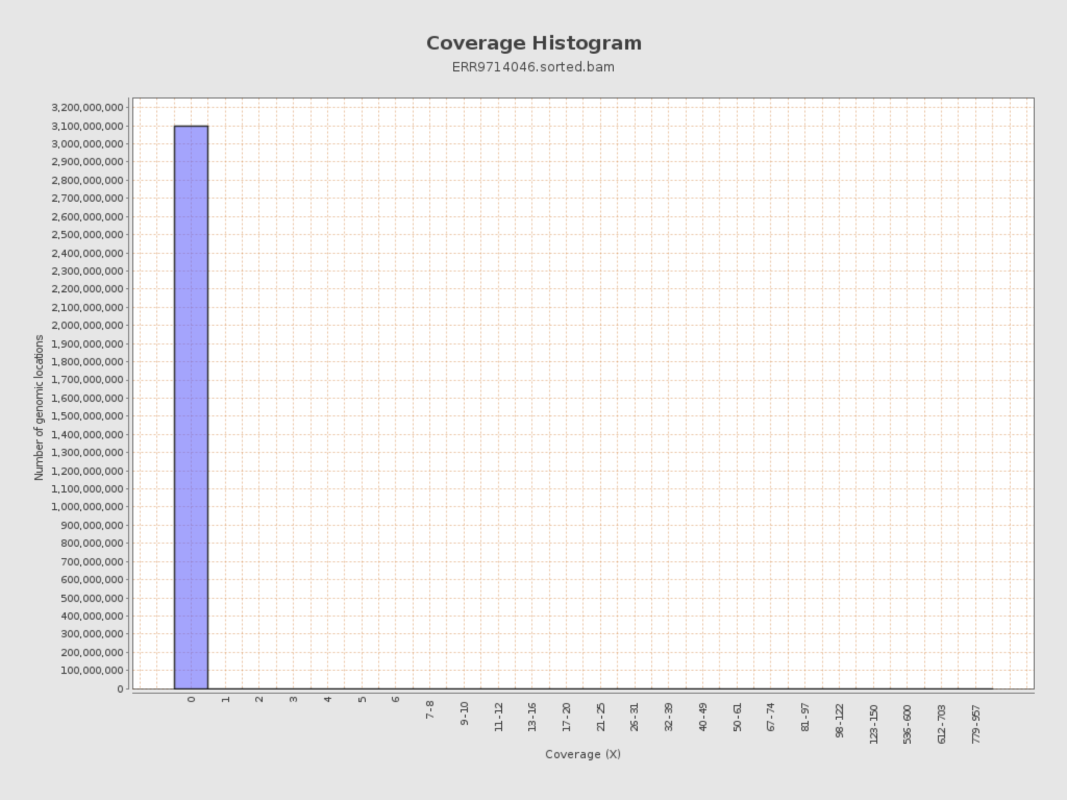
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16929	0.0001	0.0438
chr2	243199373	140518	0.0006	0.5923
chr3	198022430	2494	0	0.0056
chr4	191154276	7345	0	0.0285
chr5	180915260	3470	0	0.008
chr6	171115067	6808	0	0.0224
chr7	159138663	4564	0	0.0181

chr8	146364022	15966	0.0001	0.0554
chr9	141213431	689	0	0.0033
chr10	135534747	3024	0	0.0095
chr11	135006516	3061	0	0.0081
chr12	133851895	4266	0	0.0145
chr13	115169878	4629	0	0.0166
chr14	107349540	3485	0	0.0209
chr15	102531392	737	0	0.0036
chr16	90354753	6872	0.0001	0.0349
chr17	81195210	5411	0.0001	0.0277
chr18	78077248	311	0	0.002
chr19	59128983	2592	0	0.0284
chr20	63025520	11036	0.0002	0.0619
chr21	48129895	745	0	0.008
chr22	51304566	144	0	0.002
chrMT	16571	150	0.0091	0.0947
chrX	155270560	153932	0.001	0.1351
chrY	59373566	513	0	0.0029

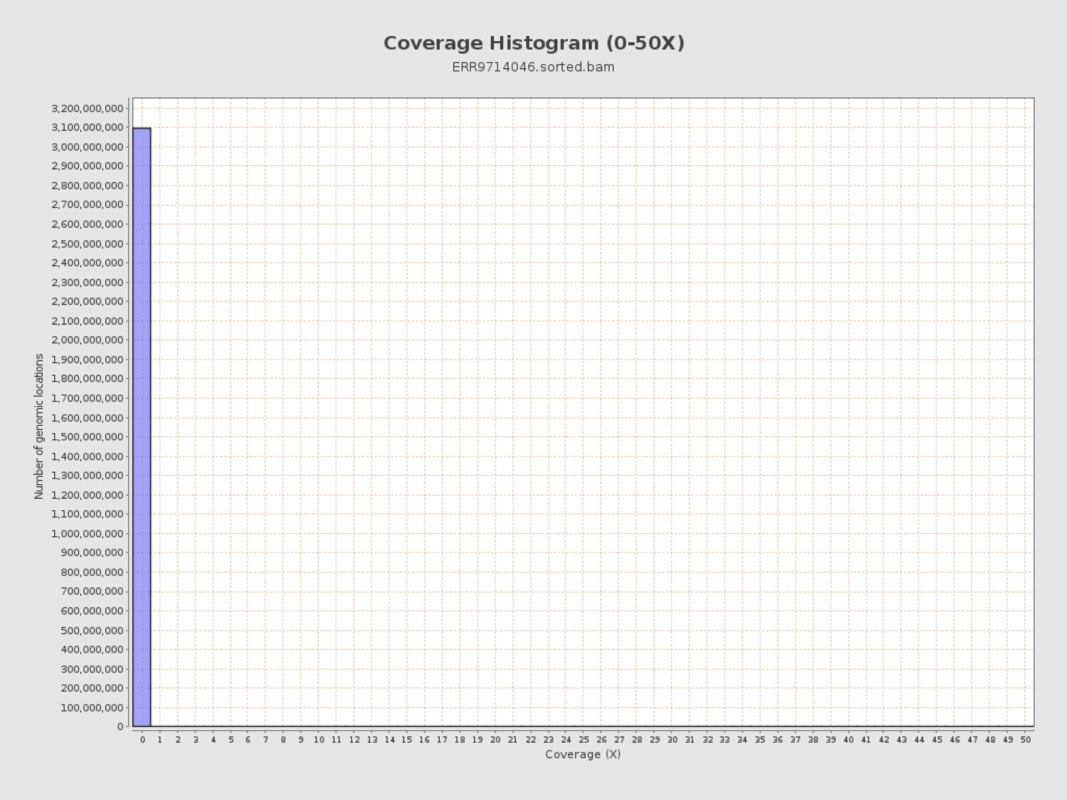
3. Results : Coverage across reference



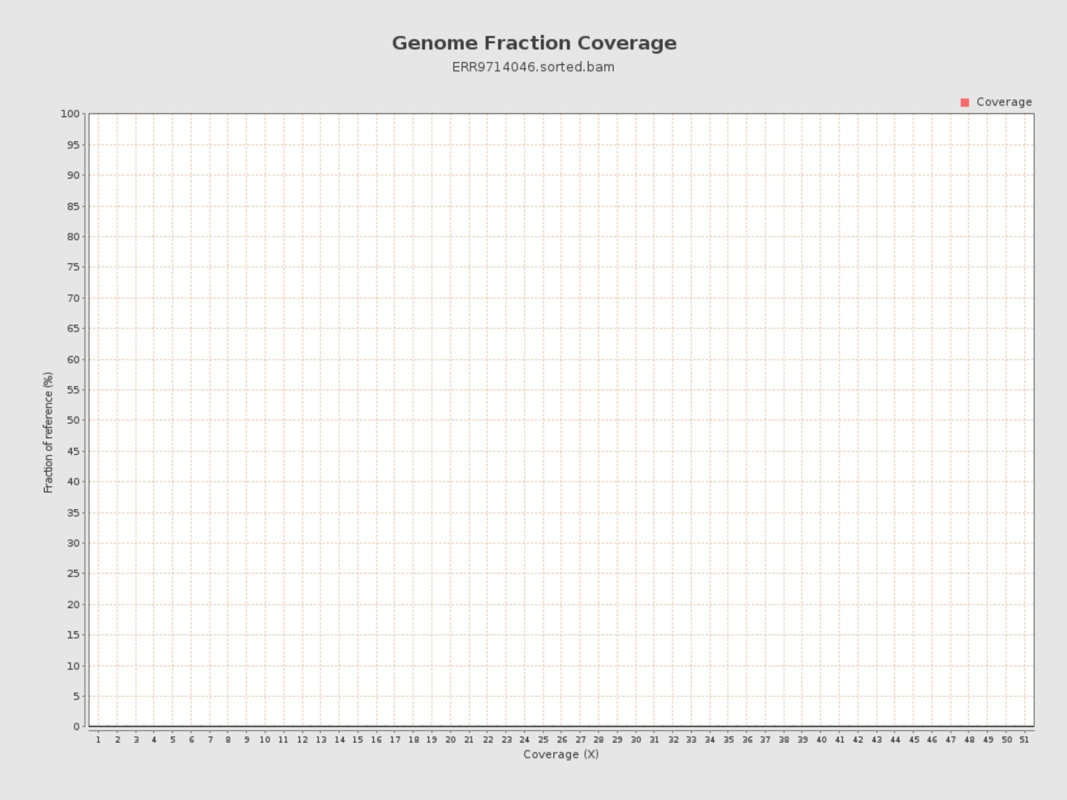
4. Results : Coverage Histogram



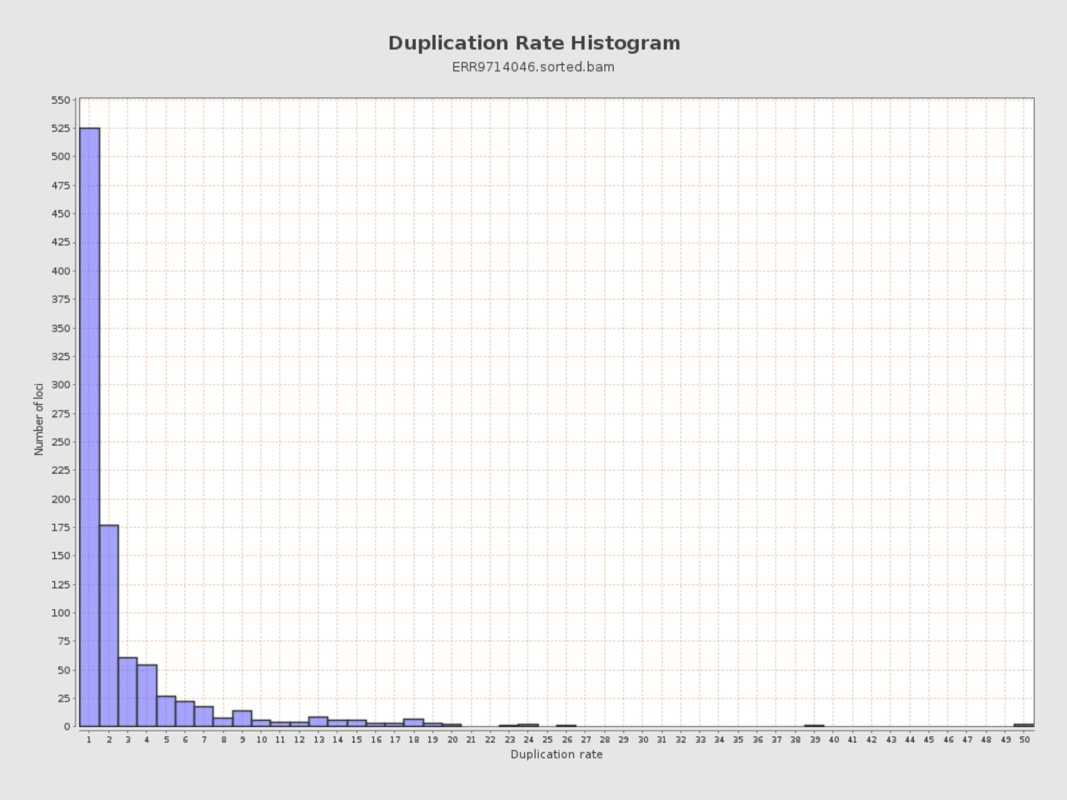
5. Results : Coverage Histogram (0-50X)



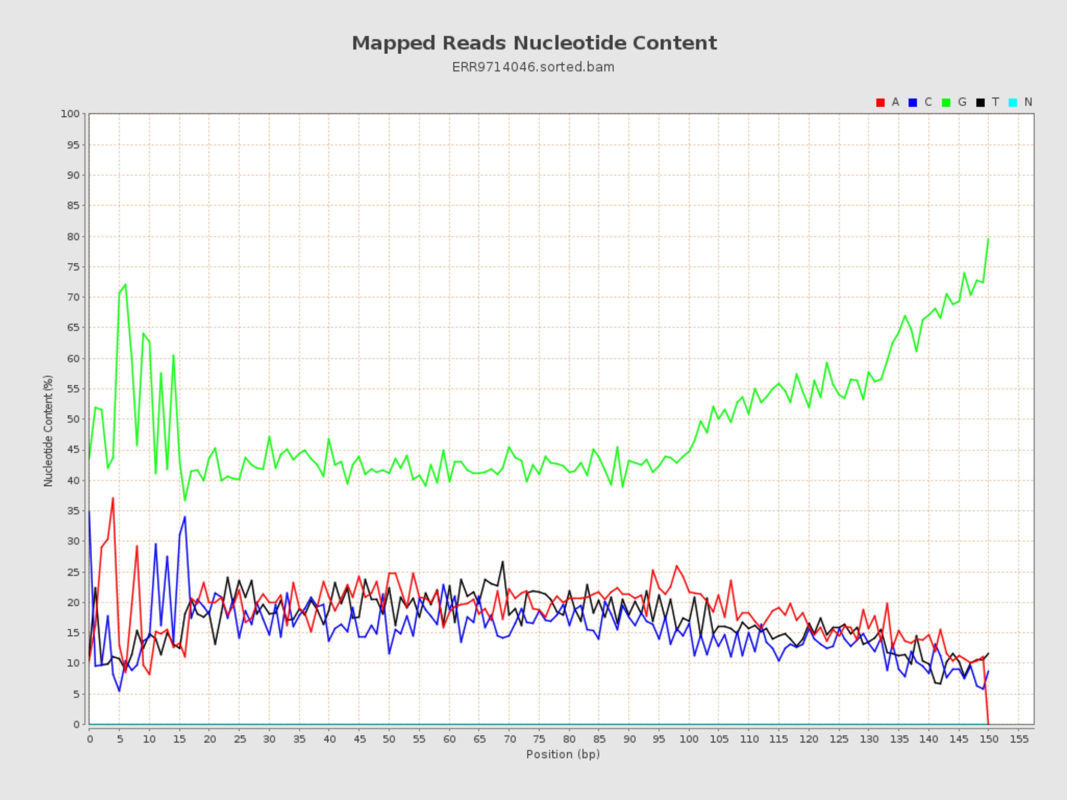
6. Results : Genome Fraction Coverage



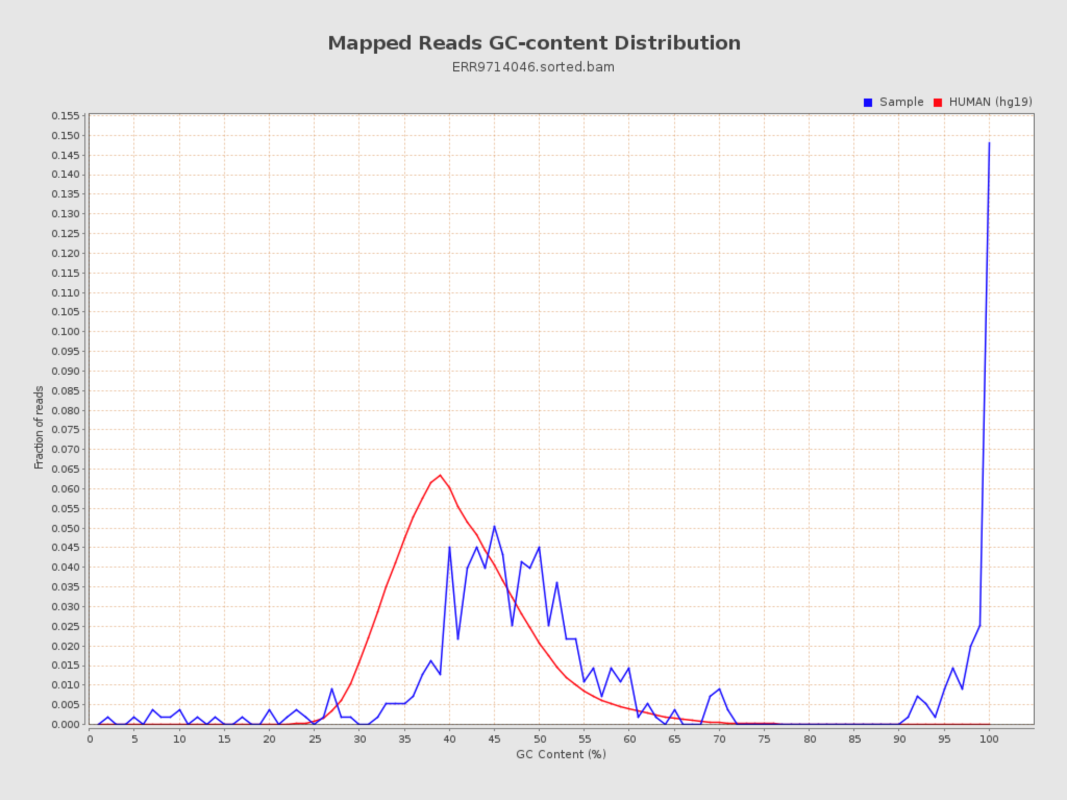
7. Results : Duplication Rate Histogram



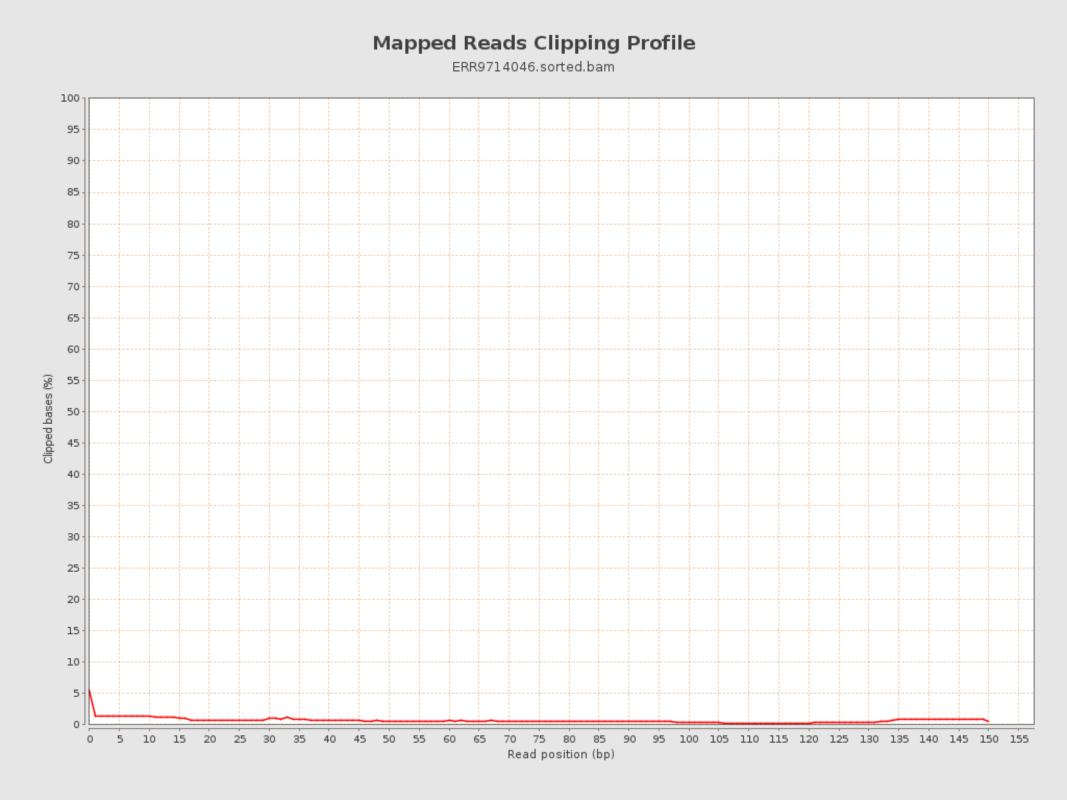
8. Results : Mapped Reads Nucleotide Content



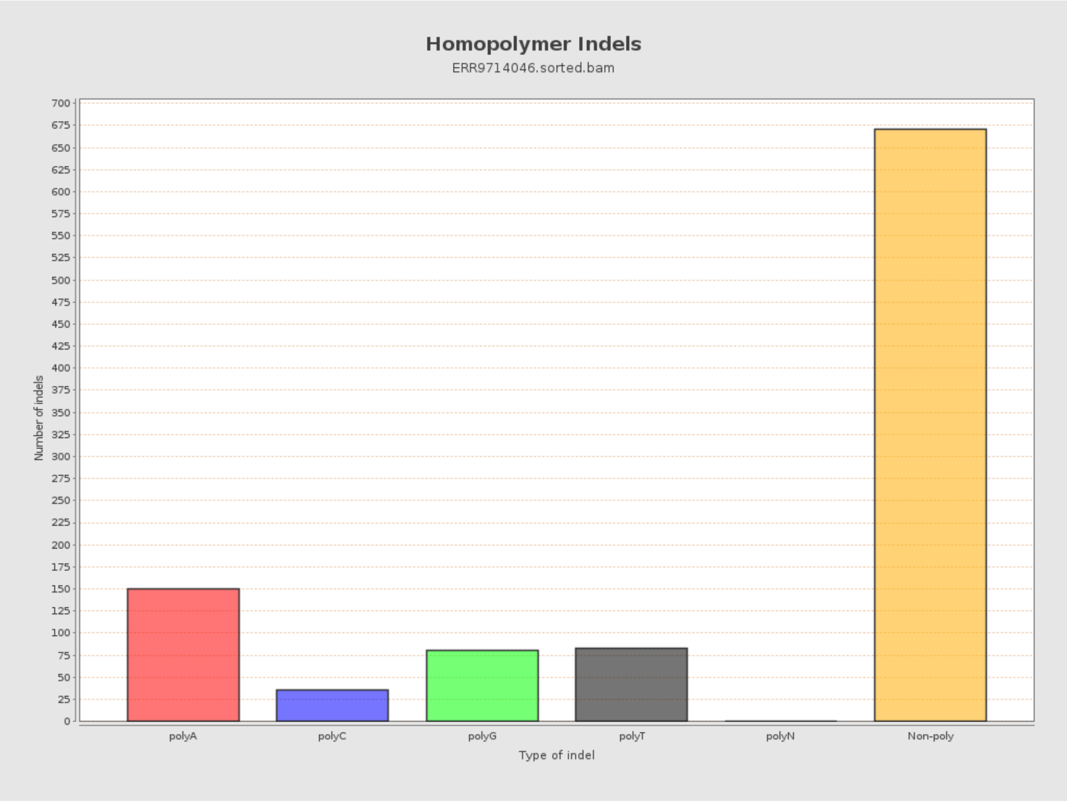
9. Results : Mapped Reads GC-content Distribution



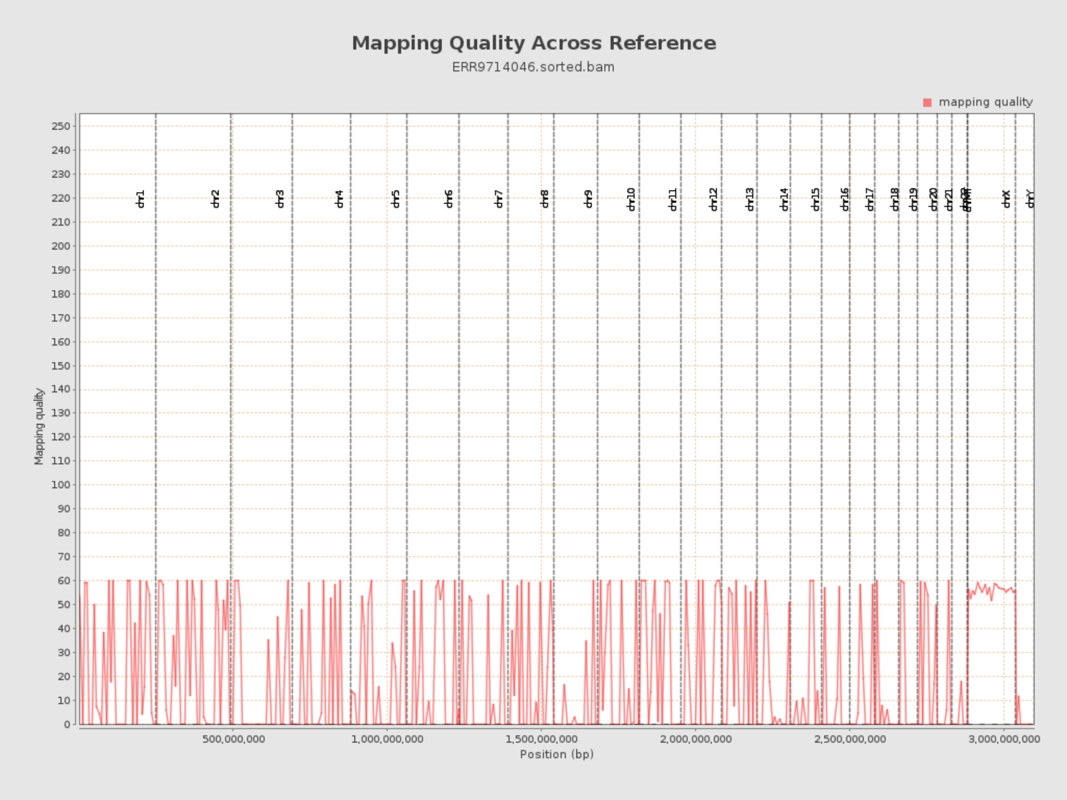
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram