Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:46:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714130.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_ERR9714130 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714130.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:46:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	742,628
Mapped reads	456,185 / 61.43%
Unmapped reads	286,443 / 38.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,890 / 2.01%
Read min/max/mean length	30 / 151 / 110.99
Duplicated reads (estimated)	375,763 / 50.6%
Duplication rate	43.23%
Clipped reads	429,392 / 57.82%

2.2. ACGT Content

Number/percentage of A's	16,066,690 / 27.98%
Number/percentage of C's	12,024,371 / 20.94%
Number/percentage of T's	15,244,829 / 26.55%
Number/percentage of G's	14,092,130 / 24.54%
Number/percentage of N's	371 / 0%
GC Percentage	45.48%

2.3. Coverage

Mean	0.0189

Standard Deviation	2.6994

2.4. Mapping Quality

Mean Mapping Quality	52.47

2.5. Mismatches and indels

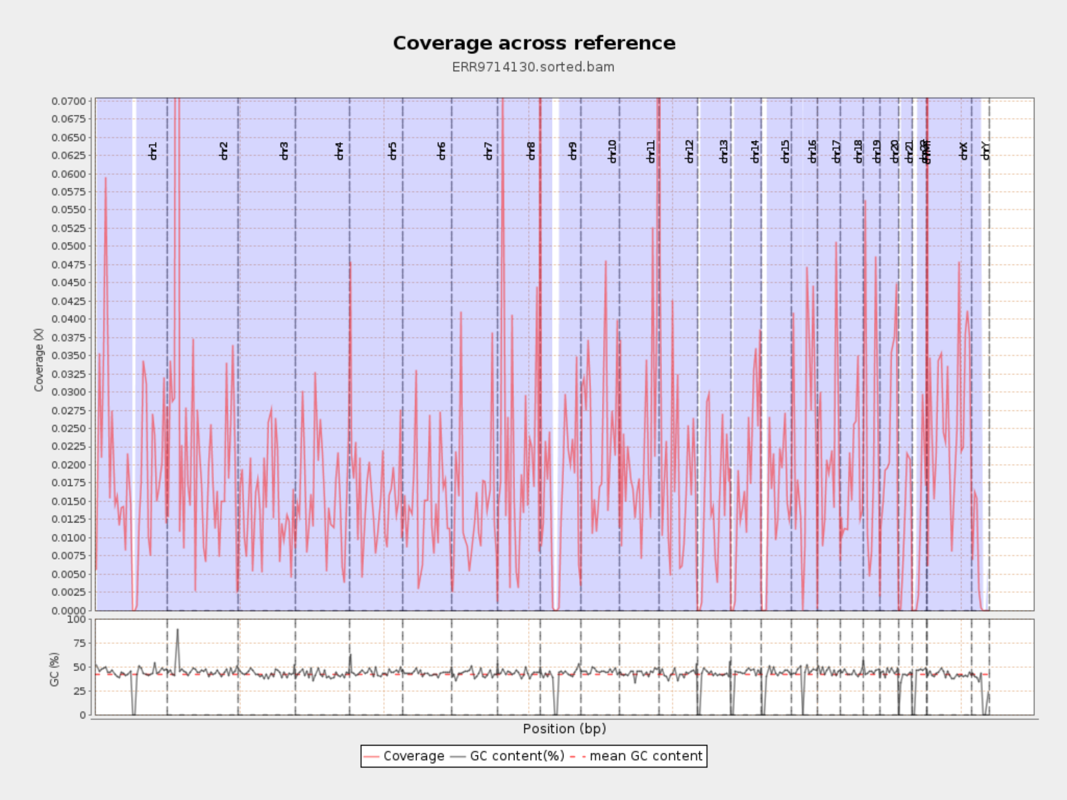
General error rate	4.27%
Mismatches	2,250,363
Insertions	64,169
Mapped reads with at least one insertion	13.43%
Deletions	195,538
Mapped reads with at least one deletion	40.88%
Homopolymer indels	28.9%

2.6. Chromosome stats

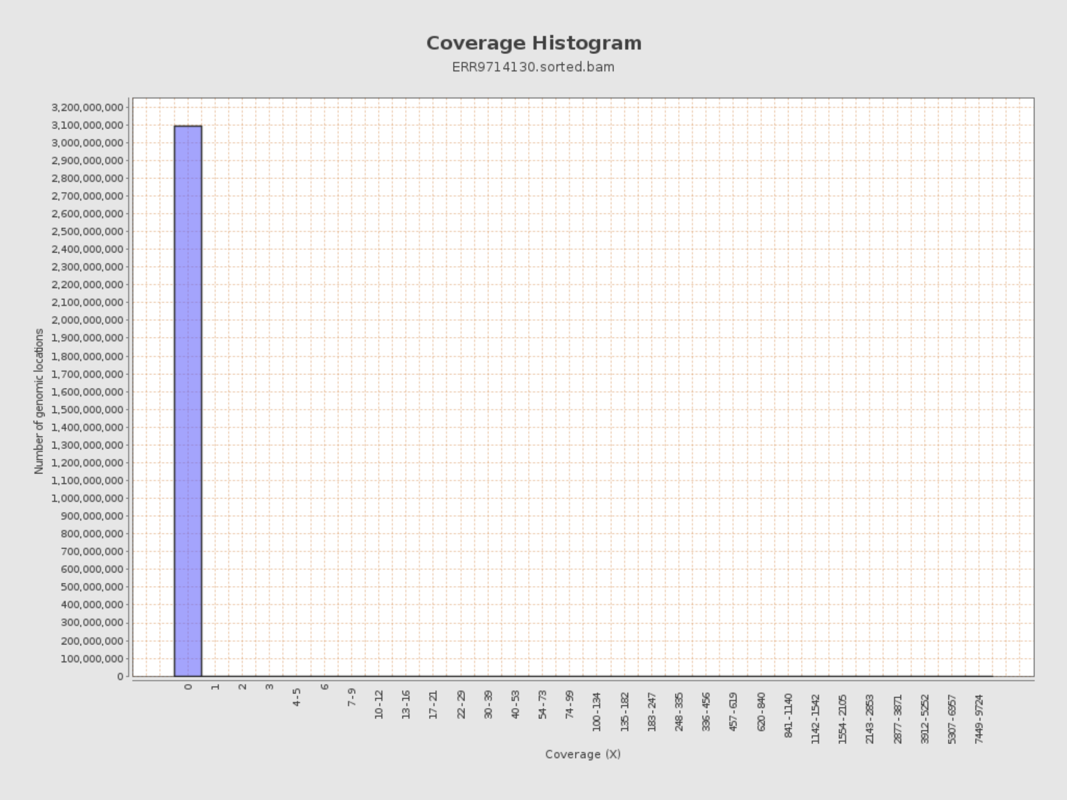
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4783977	0.0192	2.1144
chr2	243199373	6614763	0.0272	6.7172
chr3	198022430	2914753	0.0147	1.3486
chr4	191154276	3030997	0.0159	1.7095
chr5	180915260	2850884	0.0158	1.4141
chr6	171115067	2427392	0.0142	1.4604
chr7	159138663	2315501	0.0146	1.5086

chr8	146364022	3117072	0.0213	2.8294
chr9	141213431	2238602	0.0159	1.8586
chr10	135534747	3381761	0.025	2.3575
chr11	135006516	2964108	0.022	2.1223
chr12	133851895	2514509	0.0188	2.0927
chr13	115169878	1637550	0.0142	1.5244
chr14	107349540	1943916	0.0181	1.8243
chr15	102531392	1461100	0.0143	1.5274
chr16	90354753	2157815	0.0239	2.5988
chr17	81195210	1816793	0.0224	2.5624
chr18	78077248	1420354	0.0182	1.8695
chr19	59128983	1340197	0.0227	2.4161
chr20	63025520	1588705	0.0252	2.1344
chr21	48129895	544874	0.0113	1.0357
chr22	51304566	591144	0.0115	1.4597
chrMT	16571	493542	29.7835	274.7543
chrX	155270560	4115442	0.0265	1.7525
chrY	59373566	305348	0.0051	0.8089

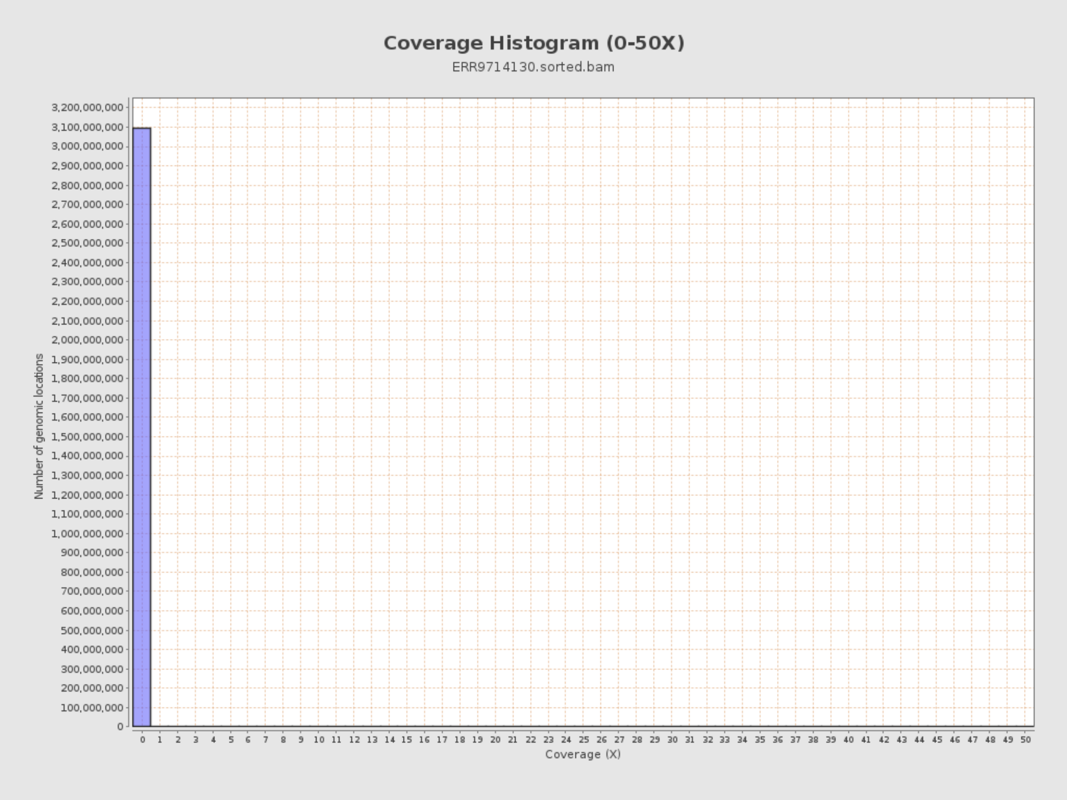
3. Results : Coverage across reference



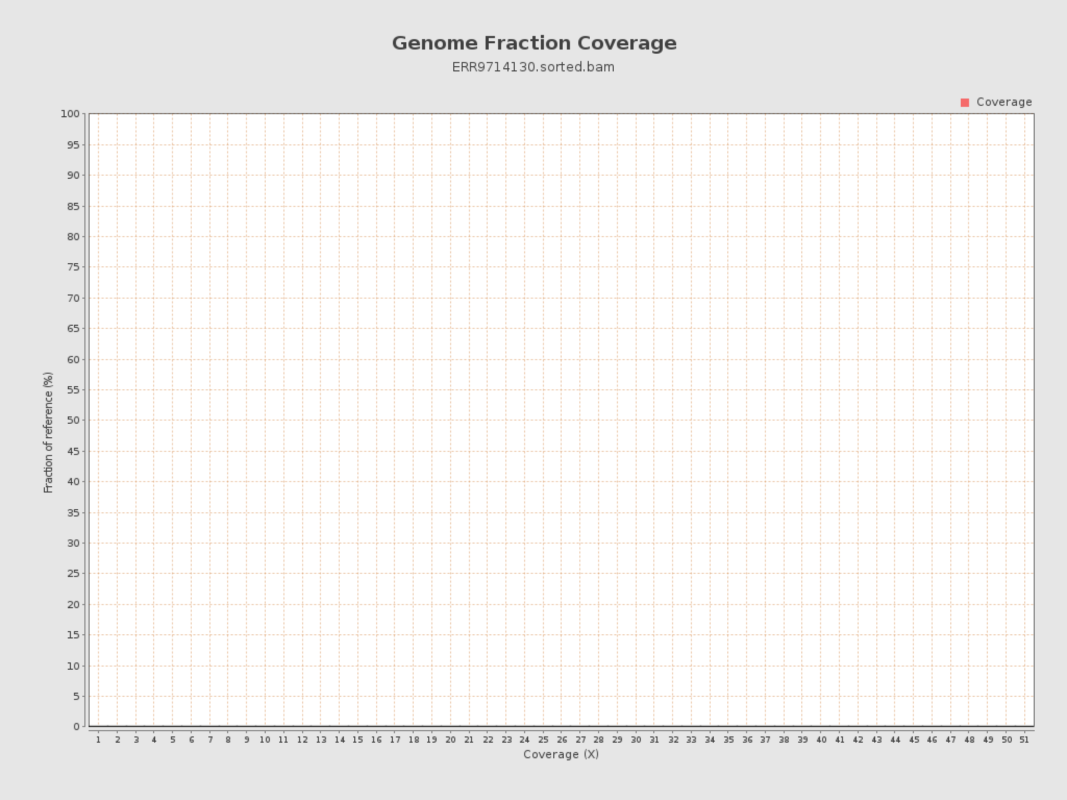
4. Results : Coverage Histogram



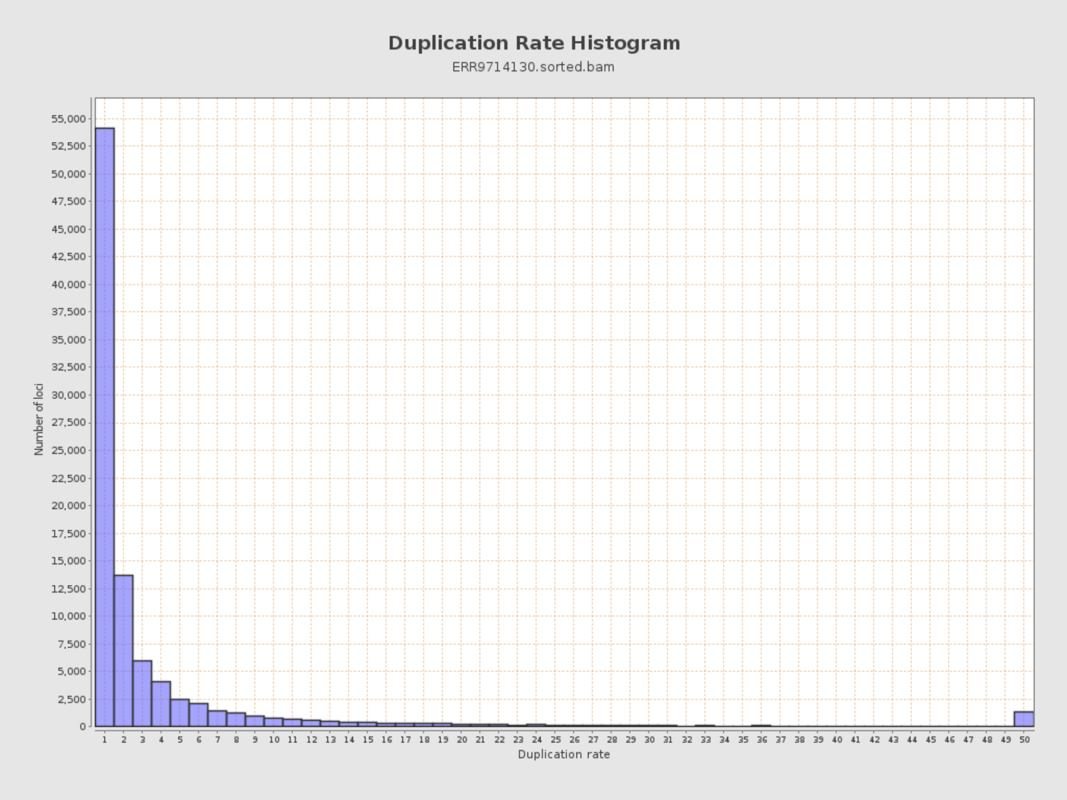
5. Results : Coverage Histogram (0-50X)



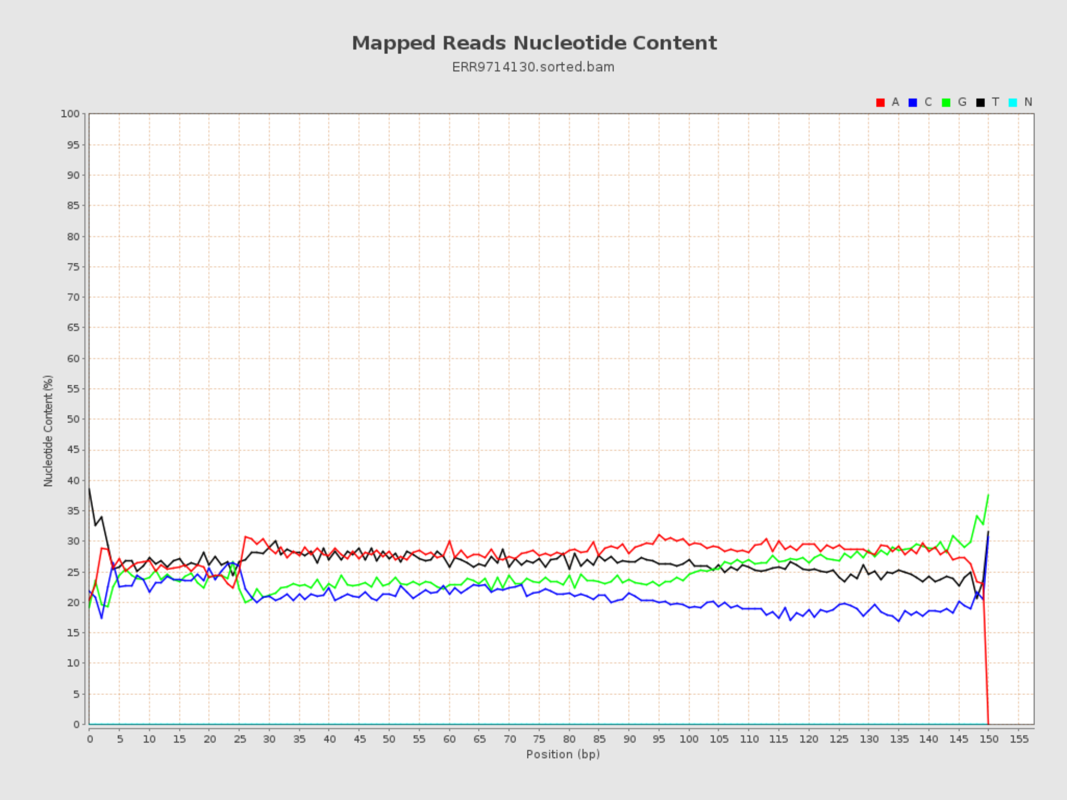
6. Results : Genome Fraction Coverage



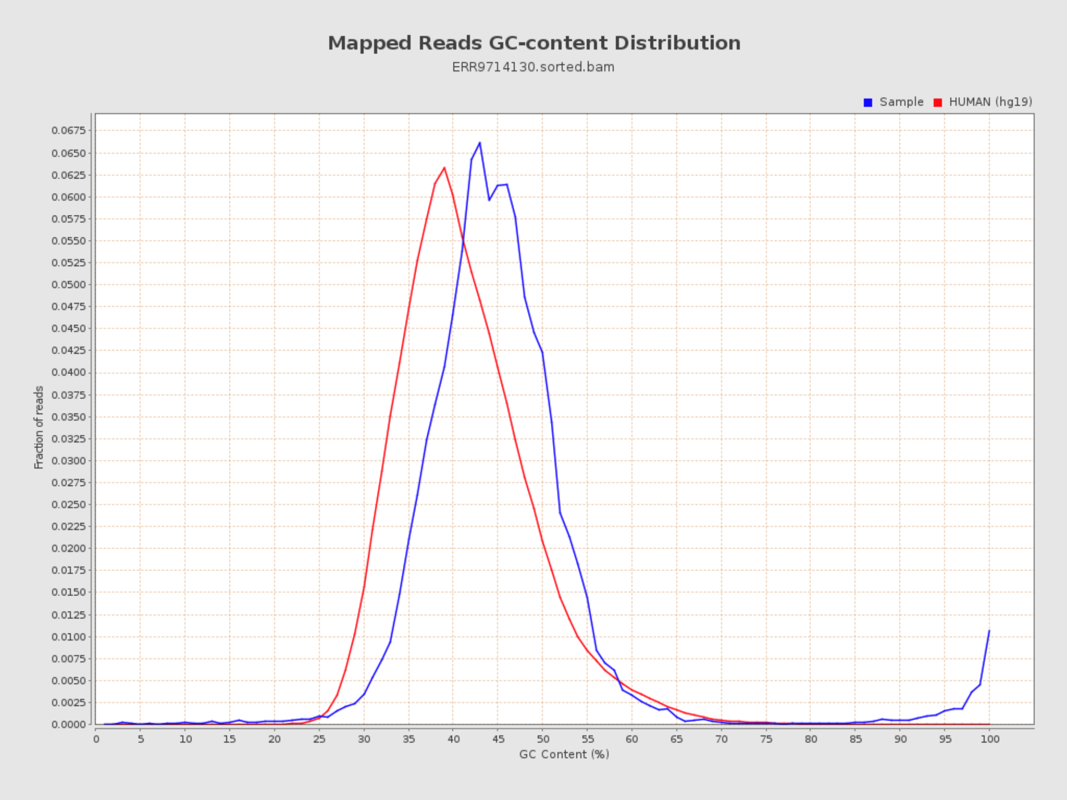
7. Results : Duplication Rate Histogram



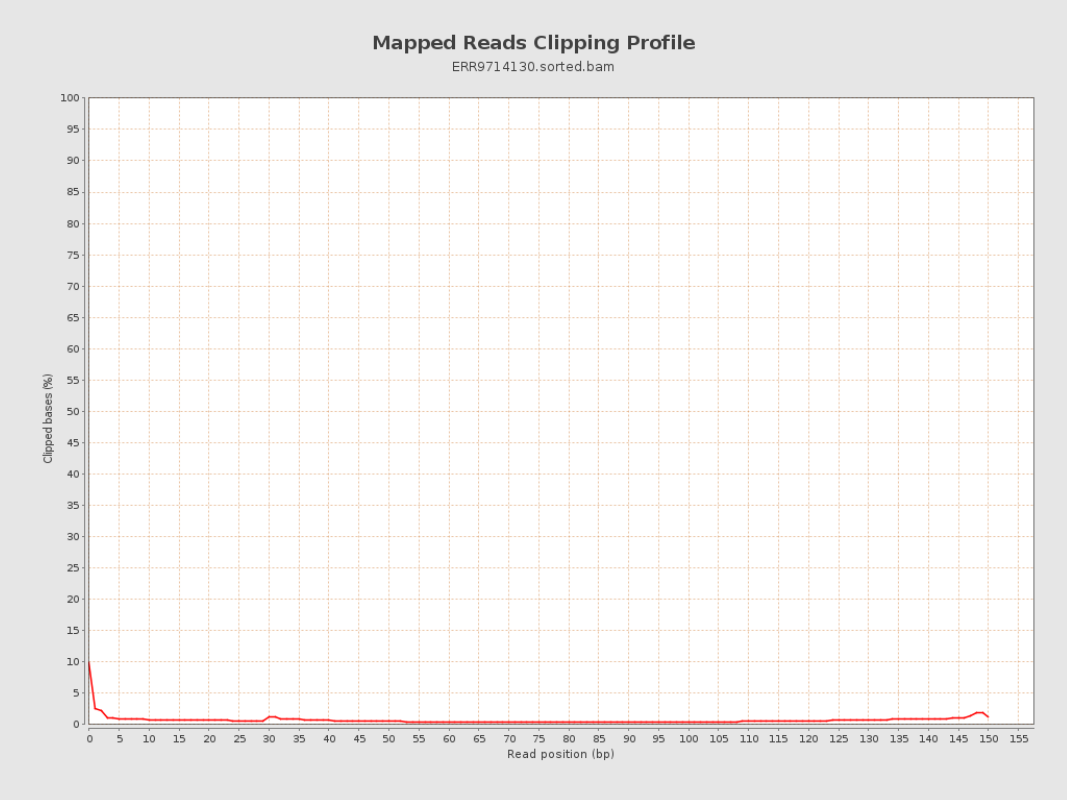
8. Results : Mapped Reads Nucleotide Content



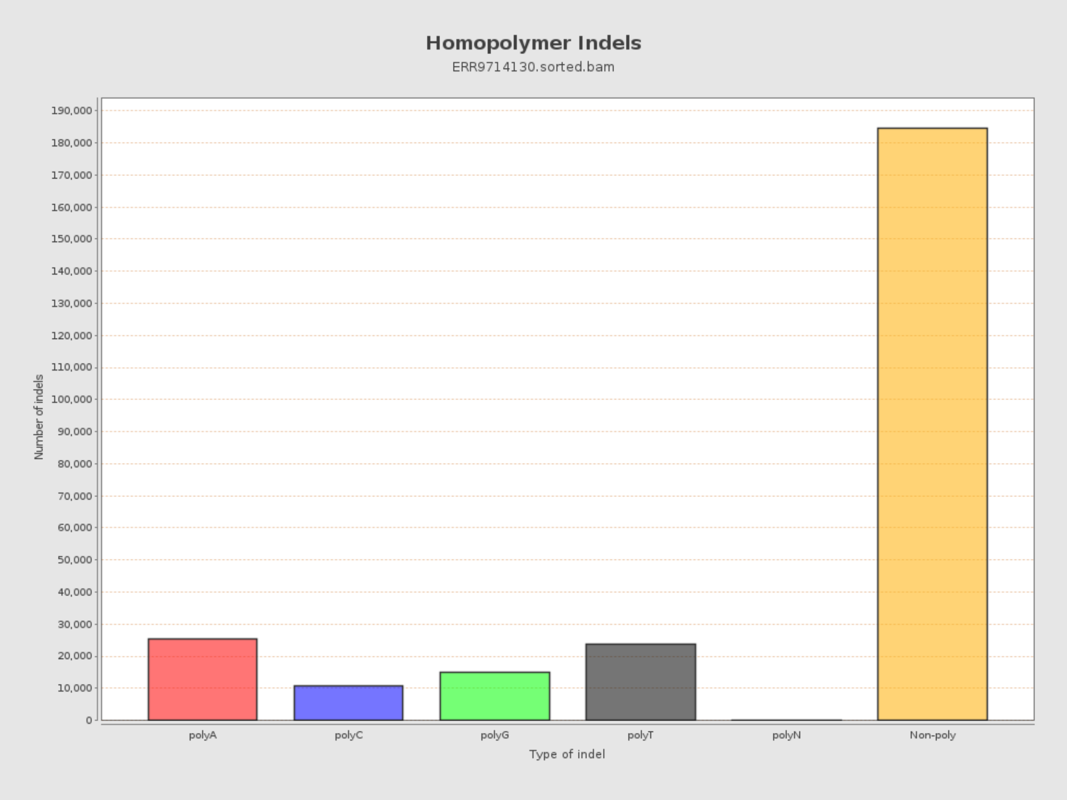
9. Results : Mapped Reads GC-content Distribution



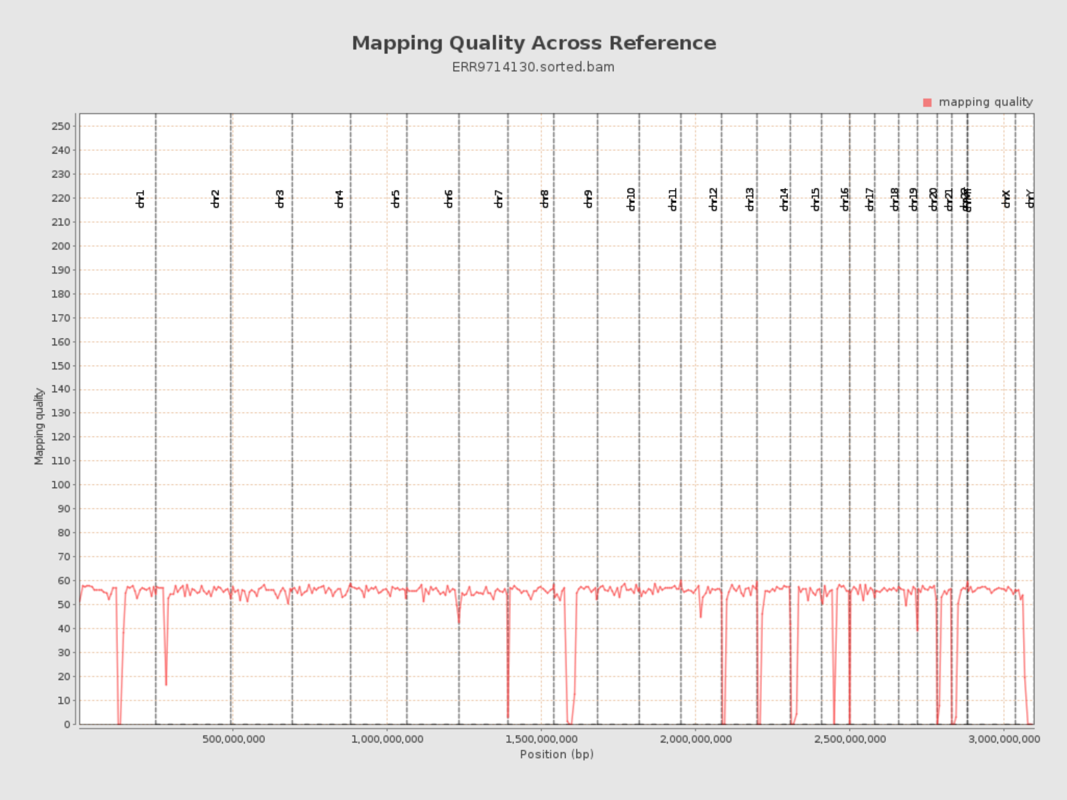
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram