Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:08:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714070.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_ERR9714070 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:08:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	352,028
Mapped reads	287,513 / 81.67%
Unmapped reads	64,515 / 18.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,539 / 2.14%
Read min/max/mean length	30 / 151 / 132.08
Duplicated reads (estimated)	254,685 / 72.35%
Duplication rate	43.41%
Clipped reads	271,590 / 77.15%

2.2. ACGT Content

Number/percentage of A's	9,838,331 / 27.09%
Number/percentage of C's	7,952,438 / 21.9%
Number/percentage of T's	9,235,862 / 25.43%
Number/percentage of G's	9,291,967 / 25.58%
Number/percentage of N's	271 / 0%
GC Percentage	47.48%

2.3. Coverage

Mean	0.012

Standard Deviation	3.9191

2.4. Mapping Quality

Mean Mapping Quality	50.87

2.5. Mismatches and indels

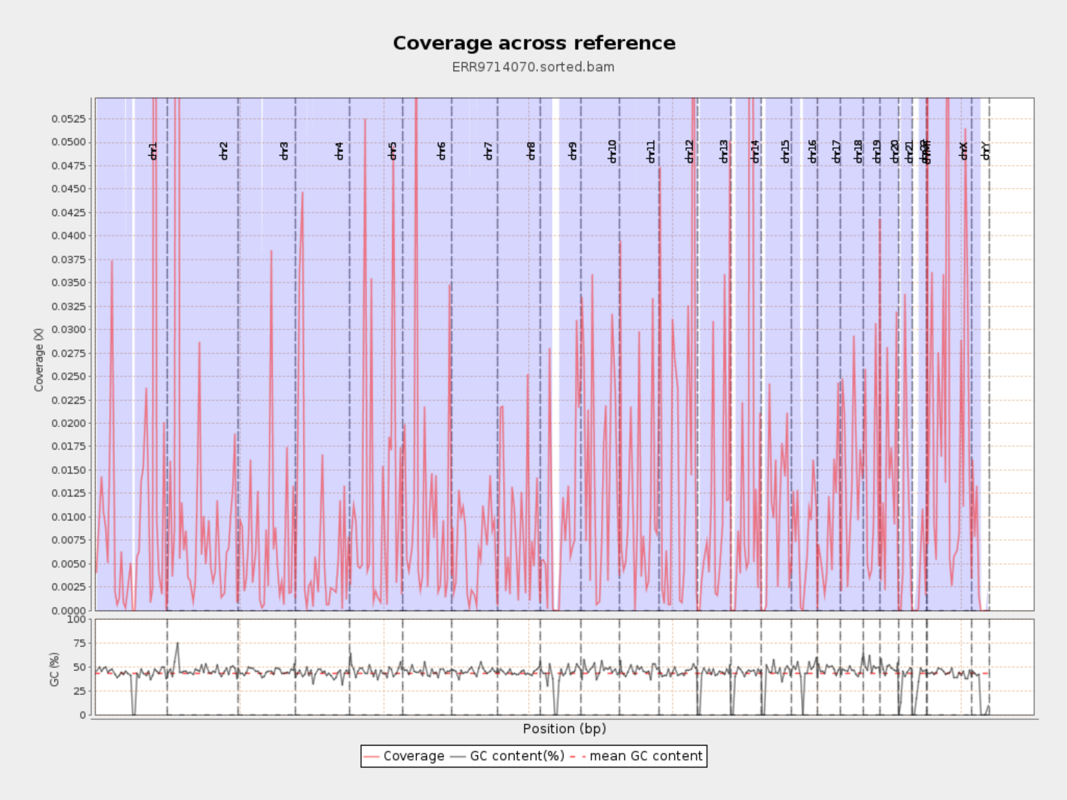
General error rate	4.69%
Mismatches	1,606,423
Insertions	40,021
Mapped reads with at least one insertion	13.5%
Deletions	136,585
Mapped reads with at least one deletion	45.25%
Homopolymer indels	29.1%

2.6. Chromosome stats

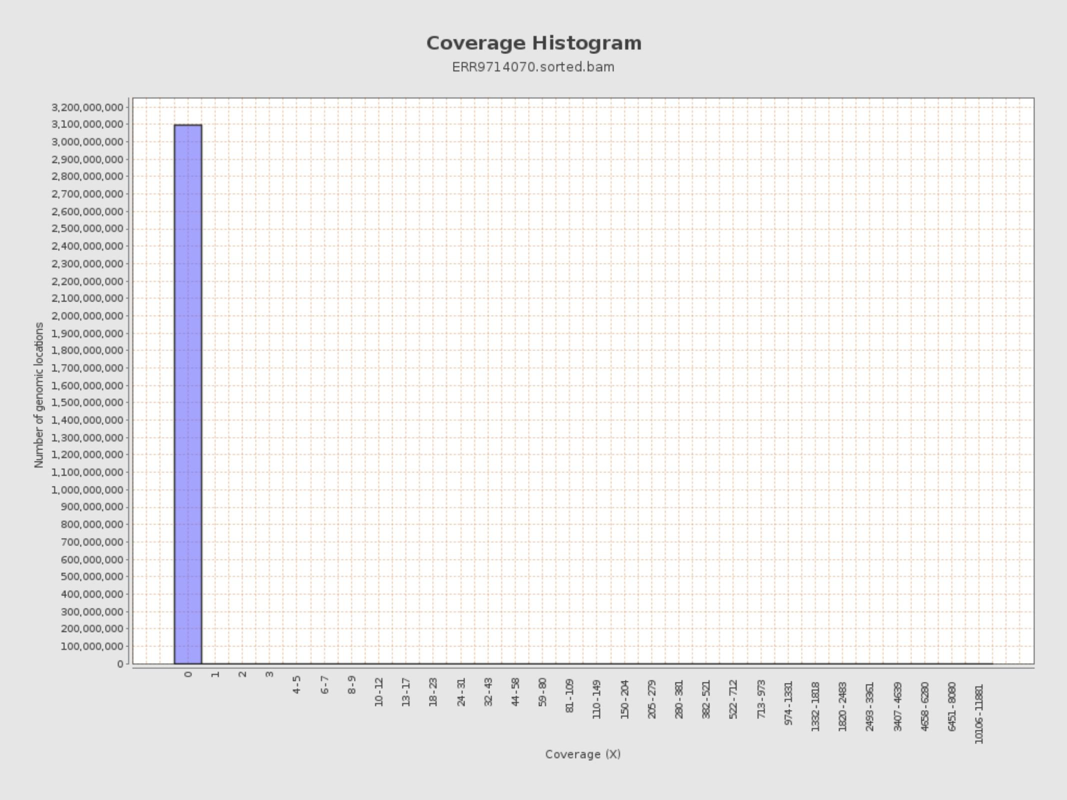
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3069474	0.0123	4.1345
chr2	243199373	3808783	0.0157	6.0154
chr3	198022430	1422630	0.0072	1.6531
chr4	191154276	1470633	0.0077	2.3714
chr5	180915260	2200301	0.0122	3.3789
chr6	171115067	2038091	0.0119	2.5391
chr7	159138663	1036204	0.0065	1.0195

chr8	146364022	1310210	0.009	1.6326
chr9	141213431	1234392	0.0087	2.0778
chr10	135534747	2146899	0.0158	3.1611
chr11	135006516	1470039	0.0109	2.2187
chr12	133851895	2401863	0.0179	4.18
chr13	115169878	1170581	0.0102	2.4183
chr14	107349540	2542873	0.0237	13.4297
chr15	102531392	1035506	0.0101	1.6786
chr16	90354753	711036	0.0079	1.2487
chr17	81195210	729729	0.009	1.4648
chr18	78077248	1190278	0.0152	3.087
chr19	59128983	778050	0.0132	1.7319
chr20	63025520	923515	0.0147	2.383
chr21	48129895	500333	0.0104	2.3914
chr22	51304566	175517	0.0034	0.4988
chrMT	16571	222894	13.4508	115.4774
chrX	155270560	3390076	0.0218	3.2772
chrY	59373566	259115	0.0044	1.1669

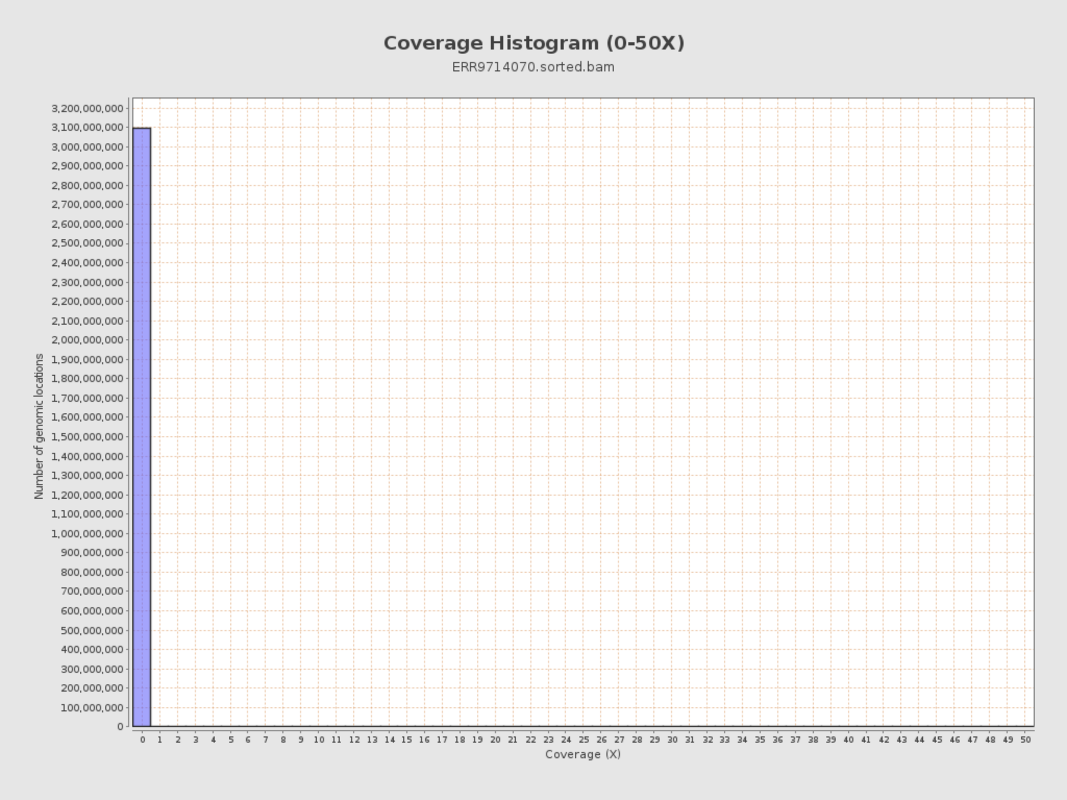
3. Results : Coverage across reference



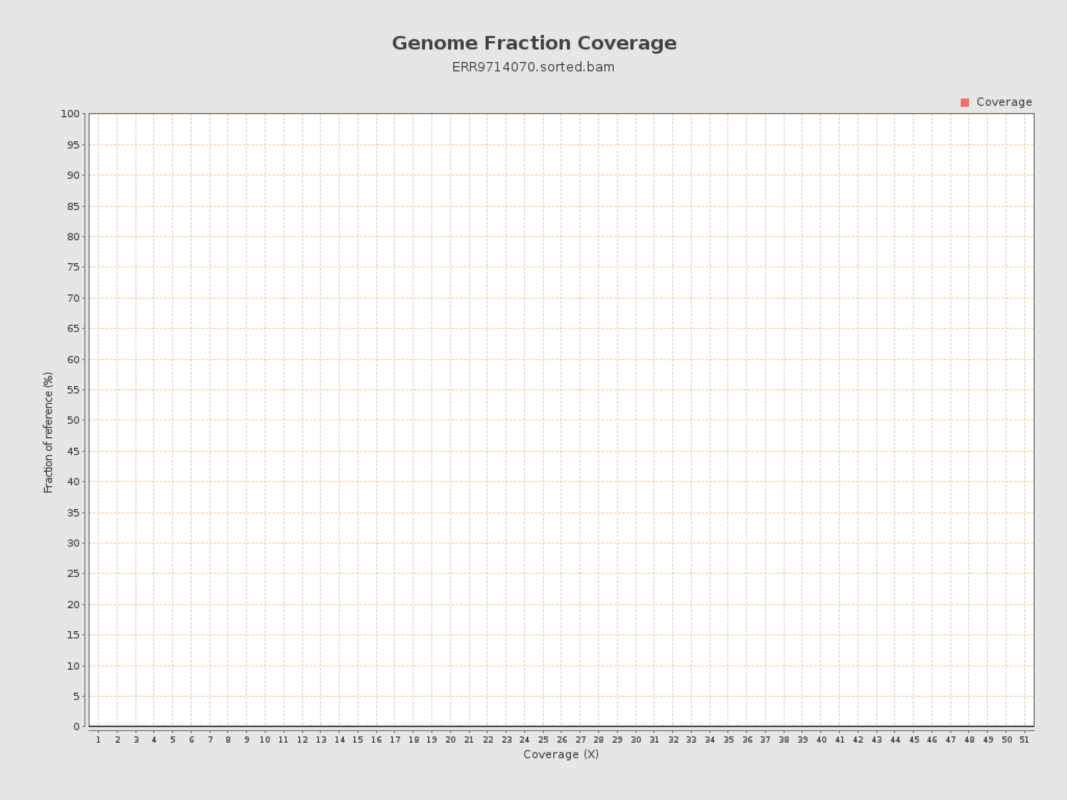
4. Results : Coverage Histogram



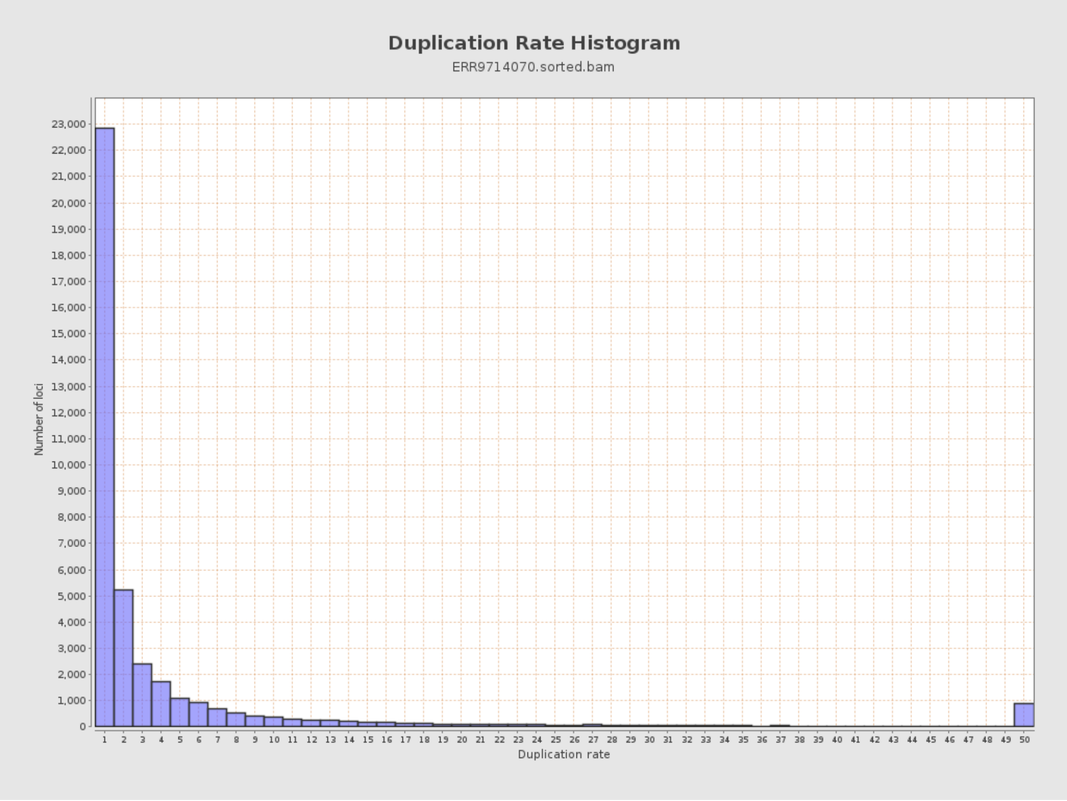
5. Results : Coverage Histogram (0-50X)



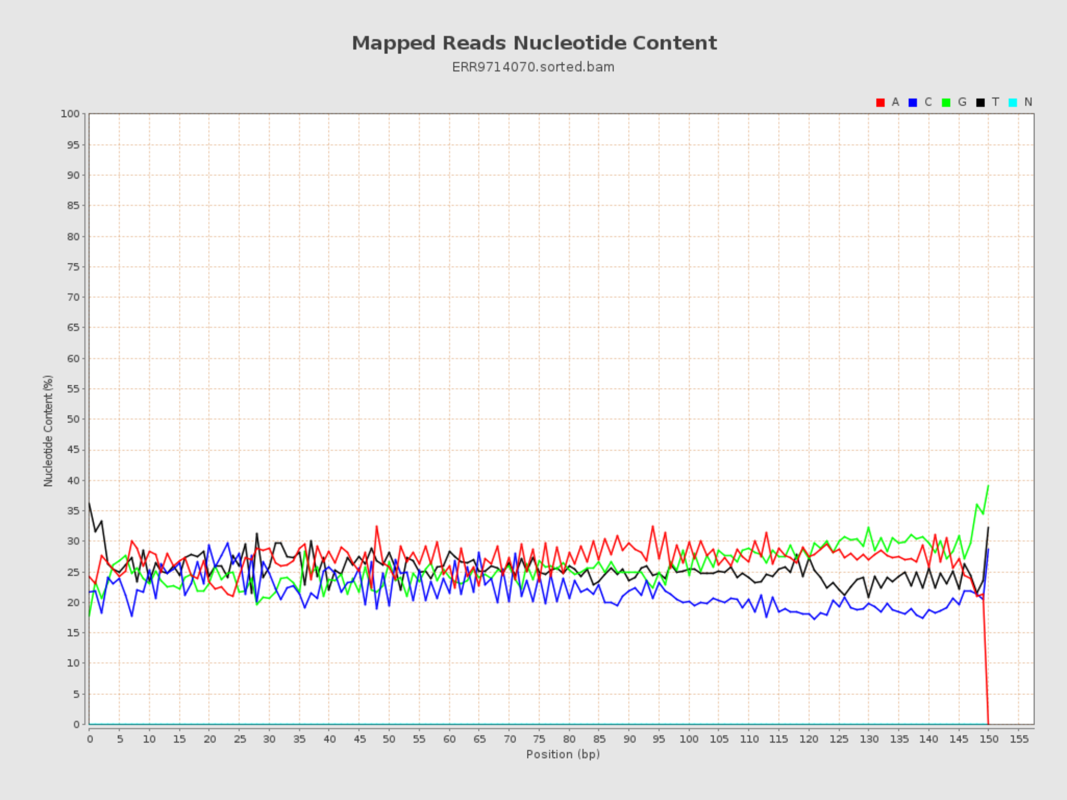
6. Results : Genome Fraction Coverage



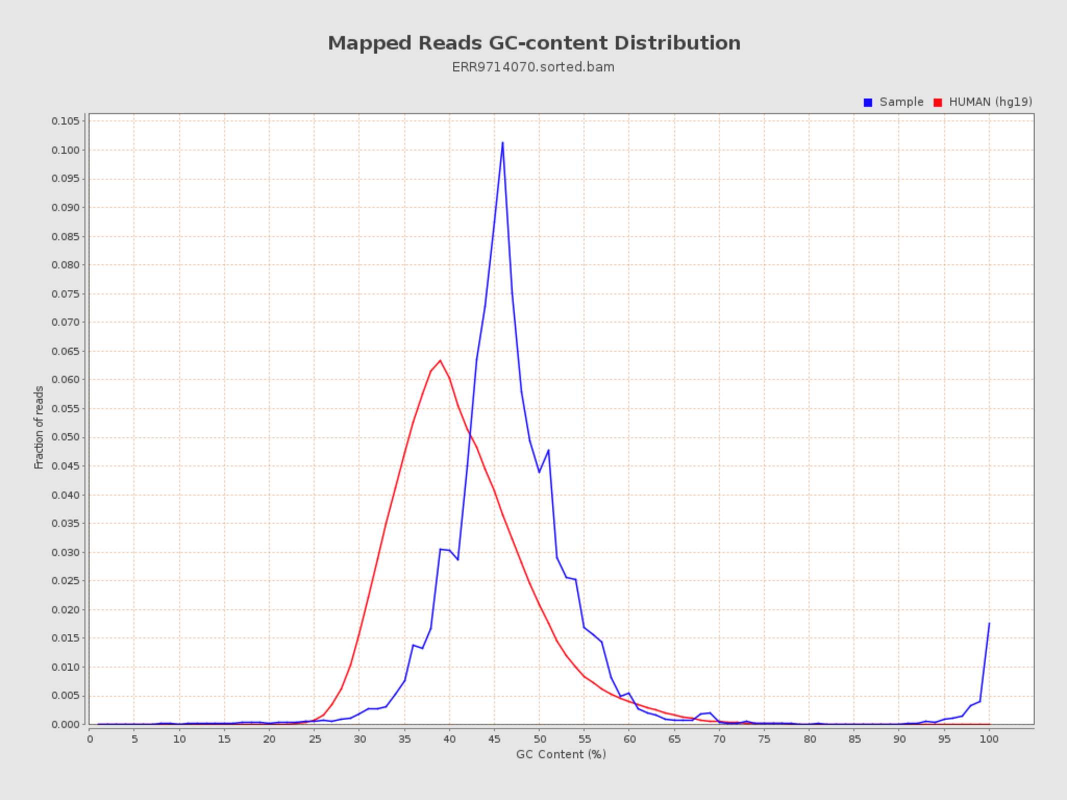
7. Results : Duplication Rate Histogram



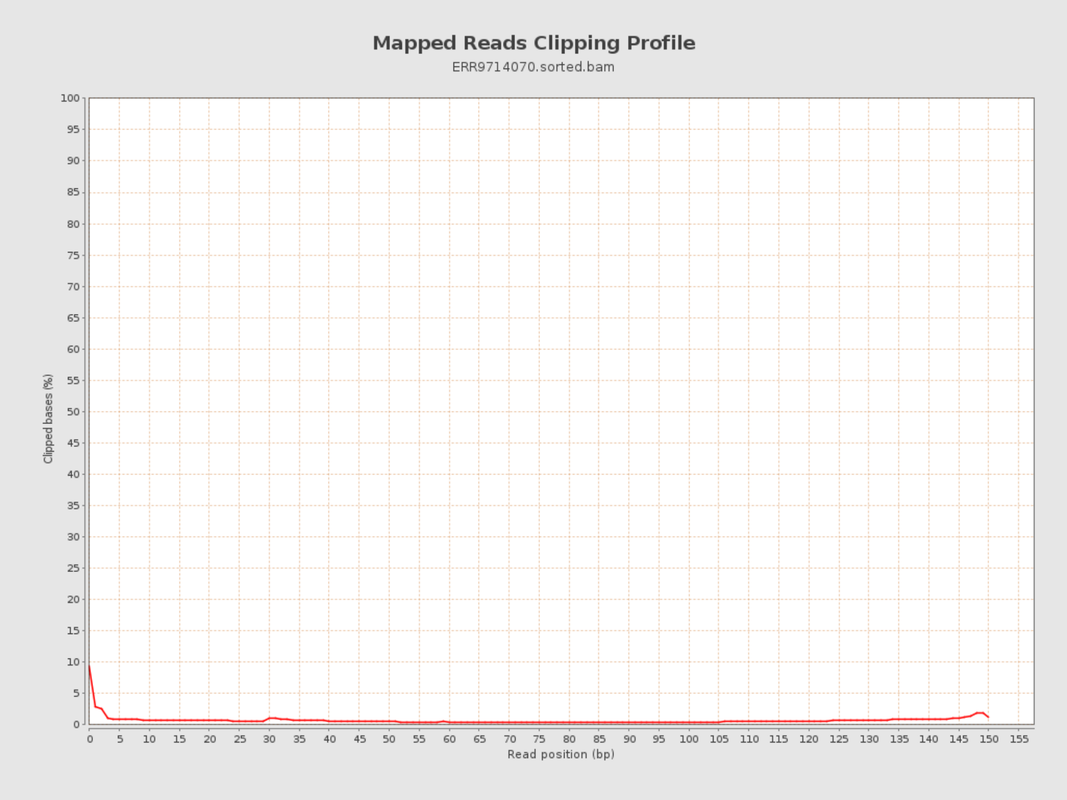
8. Results : Mapped Reads Nucleotide Content



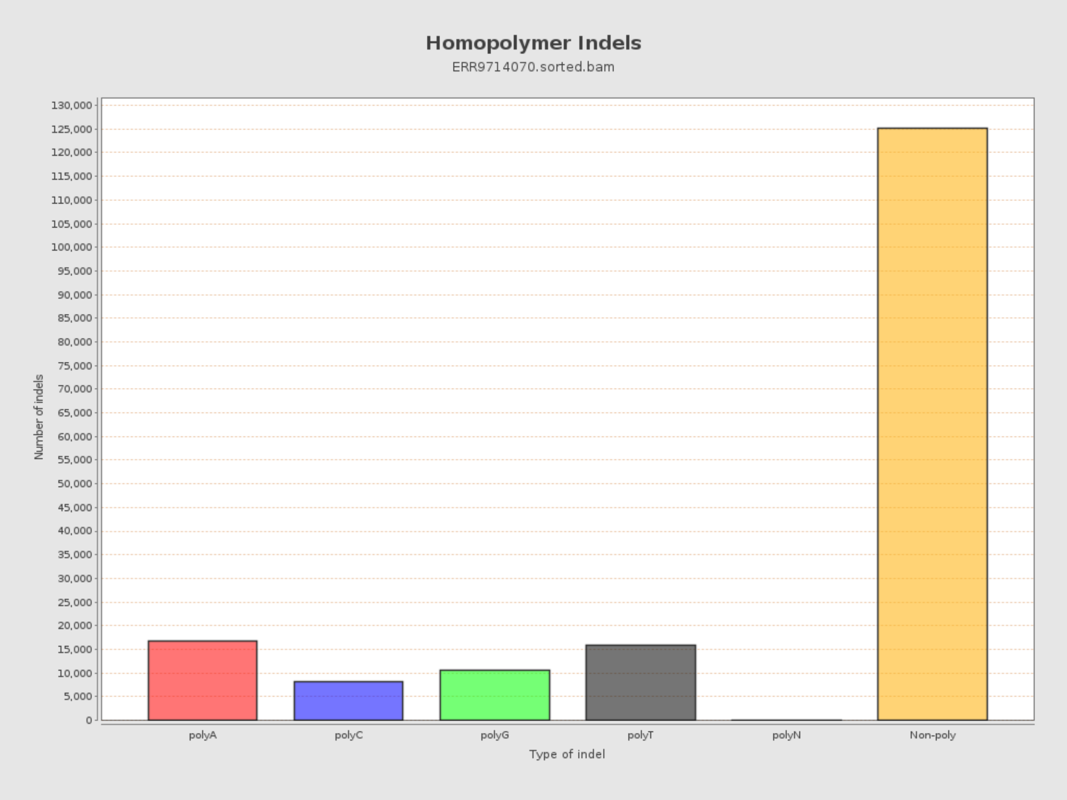
9. Results : Mapped Reads GC-content Distribution



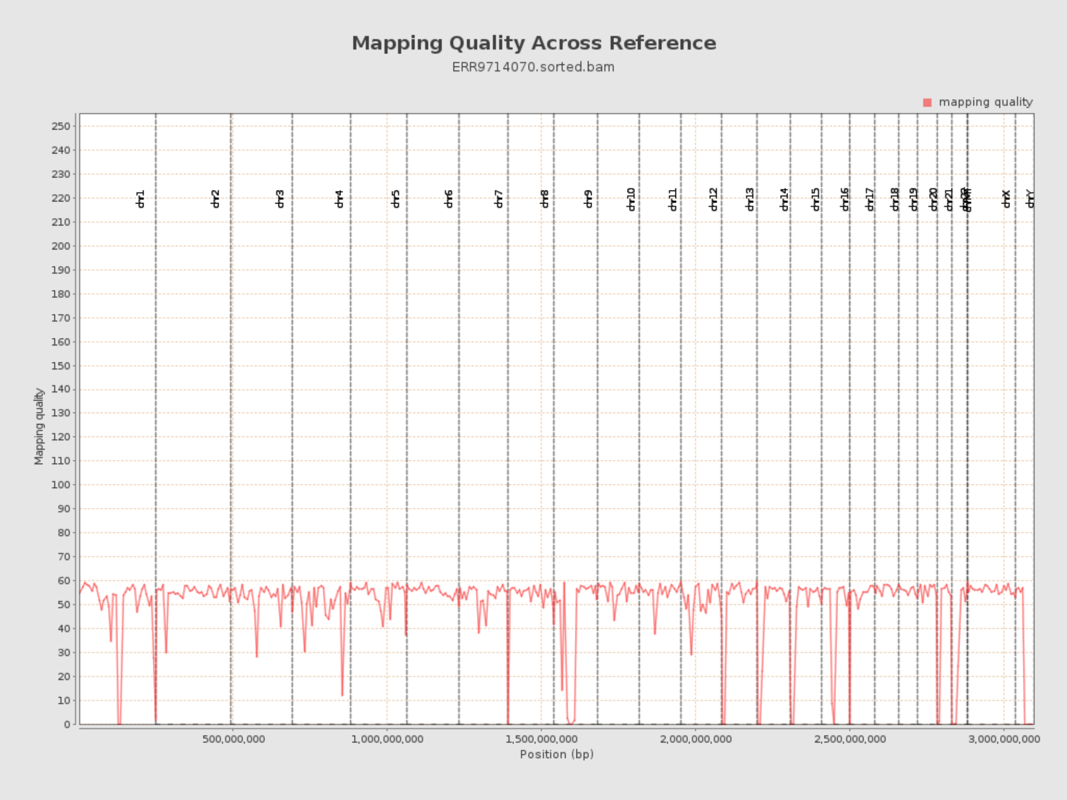
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram