Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:32:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714080.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_ERR9714080 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:32:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	412,198
Mapped reads	299,716 / 72.71%
Unmapped reads	112,482 / 27.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,016 / 2.67%
Read min/max/mean length	30 / 151 / 124.48
Duplicated reads (estimated)	234,916 / 56.99%
Duplication rate	42.85%
Clipped reads	284,439 / 69.01%

2.2. ACGT Content

Number/percentage of A's	10,349,264 / 27.46%
Number/percentage of C's	8,114,759 / 21.53%
Number/percentage of T's	9,804,122 / 26.01%
Number/percentage of G's	9,420,736 / 25%
Number/percentage of N's	262 / 0%
GC Percentage	46.53%

2.3. Coverage

Mean	0.0124

Standard Deviation	1.6152

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Mismatches and indels

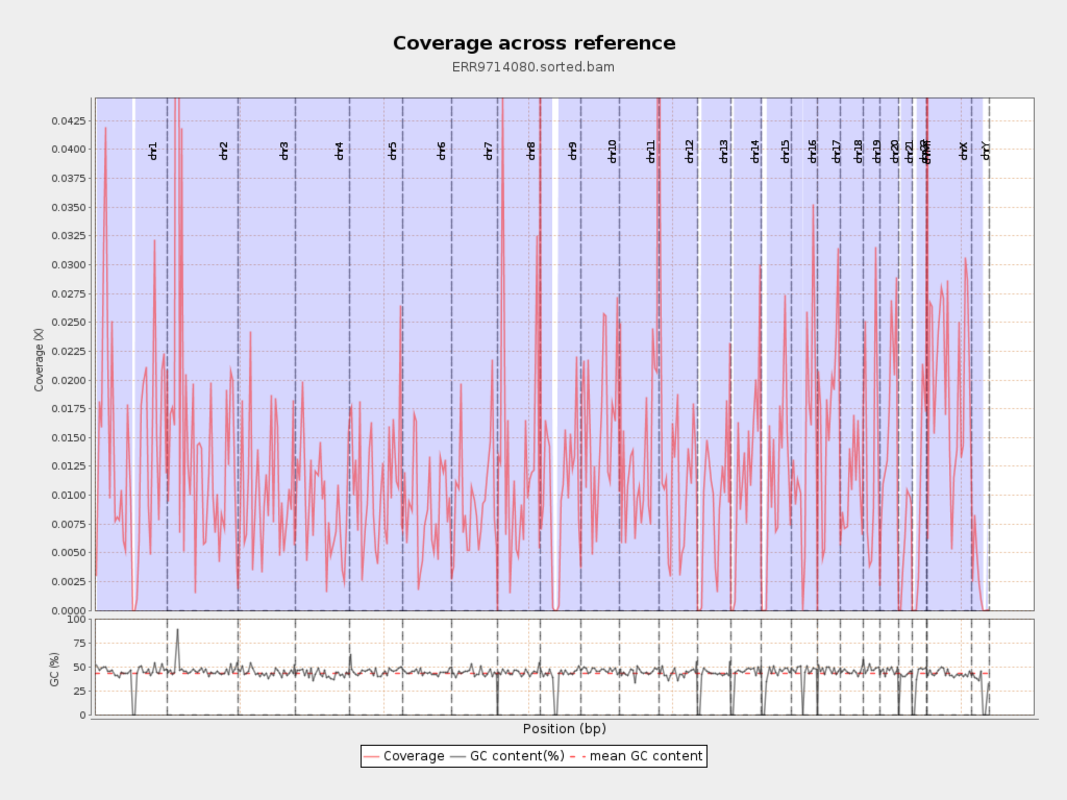
General error rate	4.21%
Mismatches	1,459,550
Insertions	41,322
Mapped reads with at least one insertion	13.35%
Deletions	127,405
Mapped reads with at least one deletion	40.45%
Homopolymer indels	28.54%

2.6. Chromosome stats

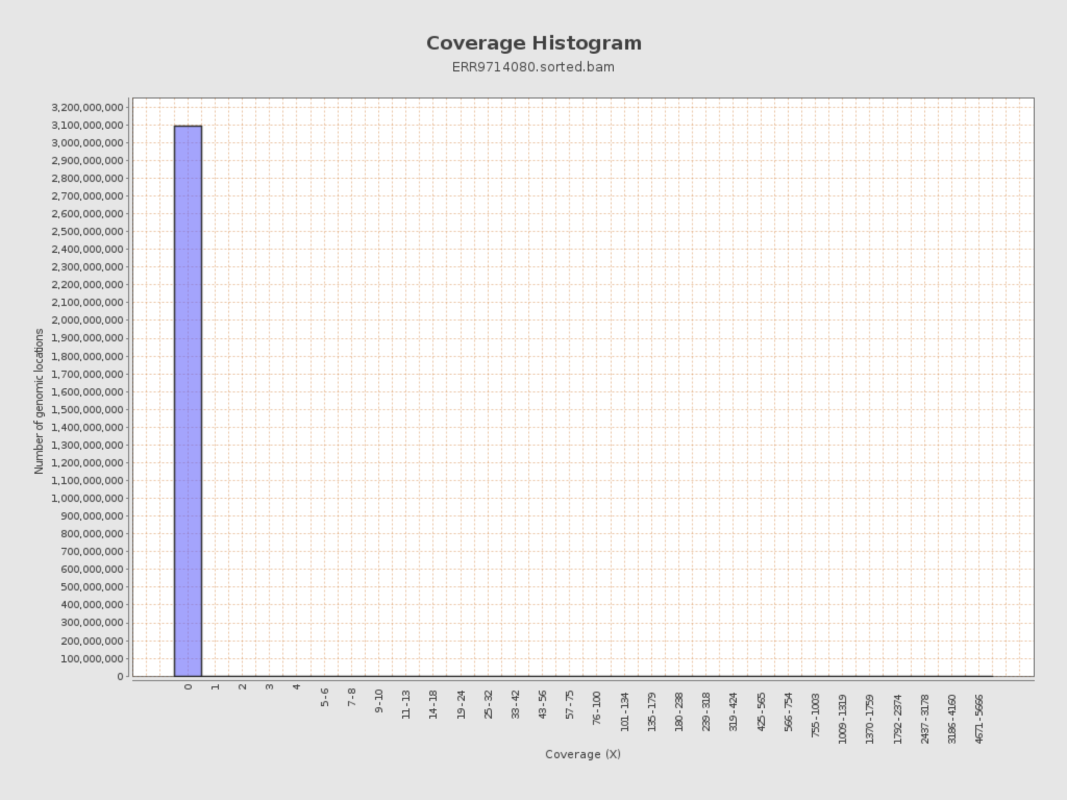
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3491574	0.014	1.4718
chr2	243199373	4191839	0.0172	3.902
chr3	198022430	2093046	0.0106	1.0183
chr4	191154276	1751203	0.0092	1.0089
chr5	180915260	2034587	0.0112	1.0276
chr6	171115067	1496859	0.0087	0.782
chr7	159138663	1497209	0.0094	0.8642

chr8	146364022	1844389	0.0126	1.3101
chr9	141213431	1439994	0.0102	1.0773
chr10	135534747	2182020	0.0161	1.4648
chr11	135006516	1770429	0.0131	1.2149
chr12	133851895	1601021	0.012	1.1421
chr13	115169878	1009811	0.0088	0.9375
chr14	107349540	1297533	0.0121	1.3828
chr15	102531392	1100199	0.0107	0.9597
chr16	90354753	1269316	0.014	1.566
chr17	81195210	1379483	0.017	1.611
chr18	78077248	849910	0.0109	0.94
chr19	59128983	752213	0.0127	1.302
chr20	63025520	1066943	0.0169	1.4471
chr21	48129895	278973	0.0058	0.4897
chr22	51304566	490645	0.0096	1.0635
chrMT	16571	308731	18.6308	171.5056
chrX	155270560	3086982	0.0199	1.2264
chrY	59373566	143665	0.0024	0.3789

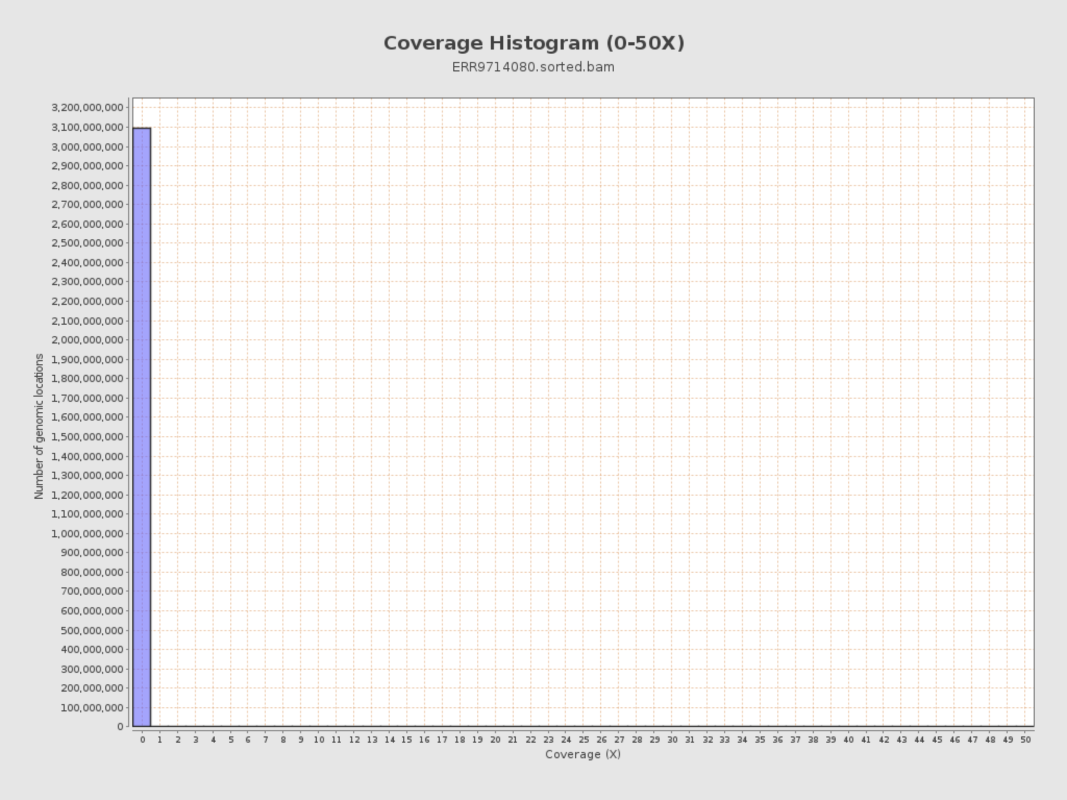
3. Results : Coverage across reference



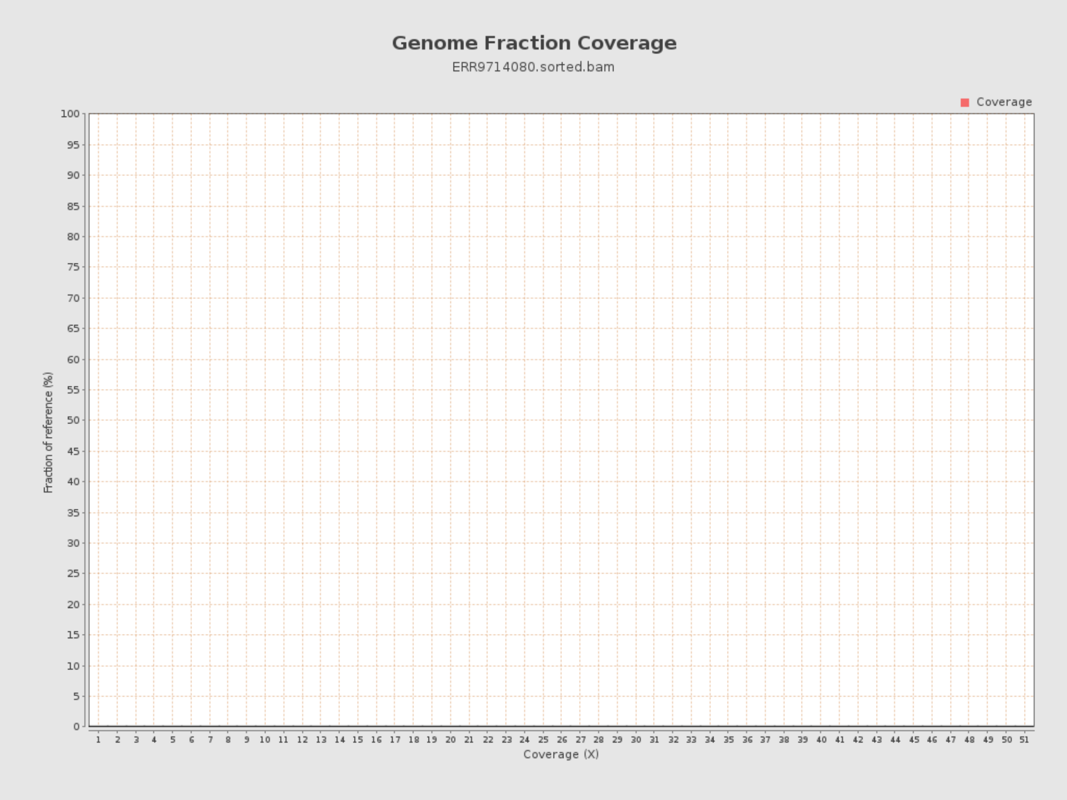
4. Results : Coverage Histogram



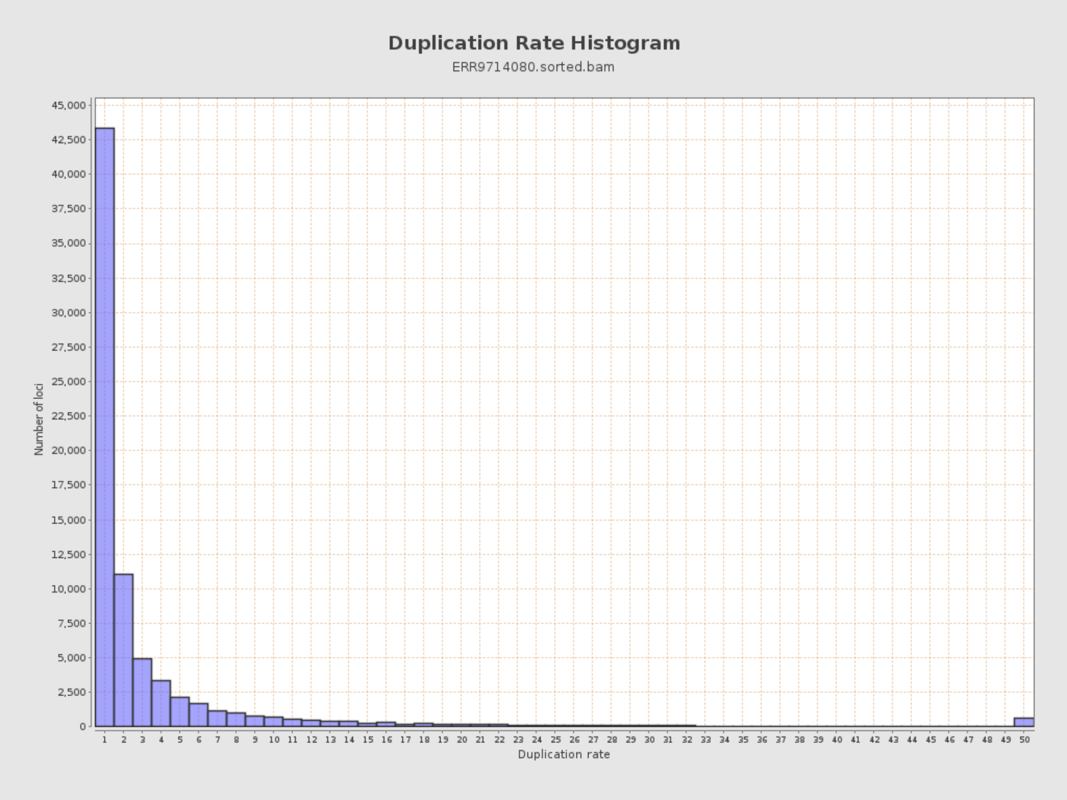
5. Results : Coverage Histogram (0-50X)



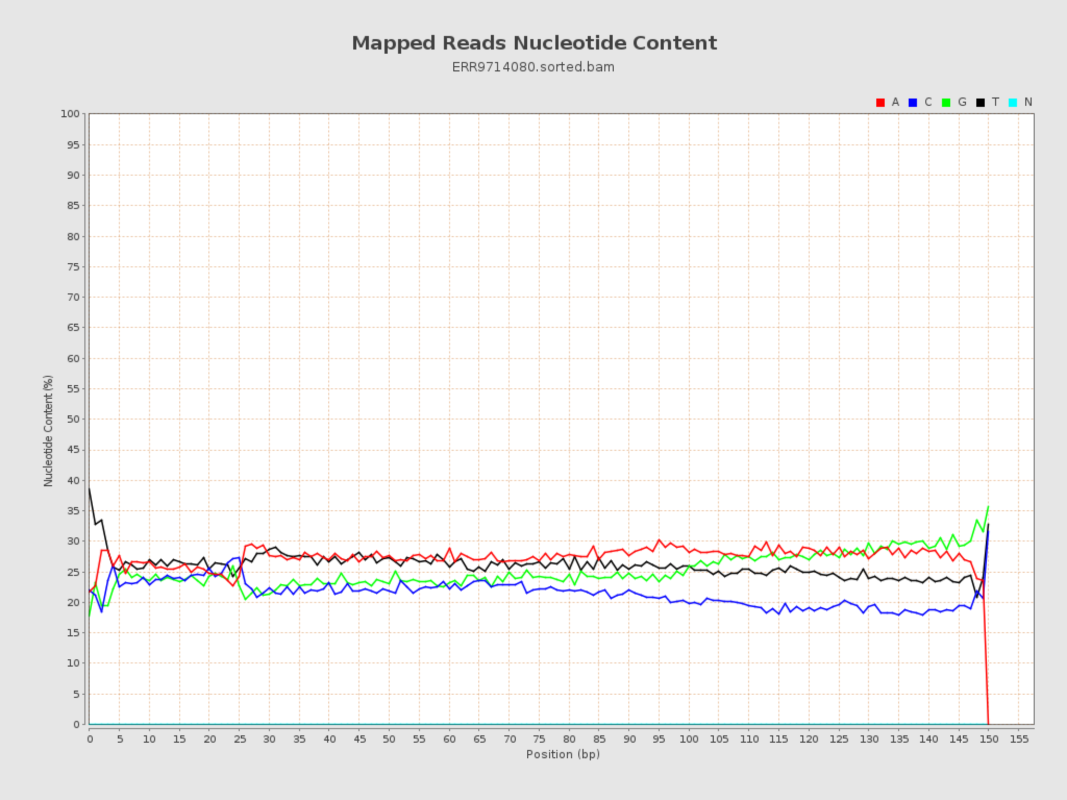
6. Results : Genome Fraction Coverage



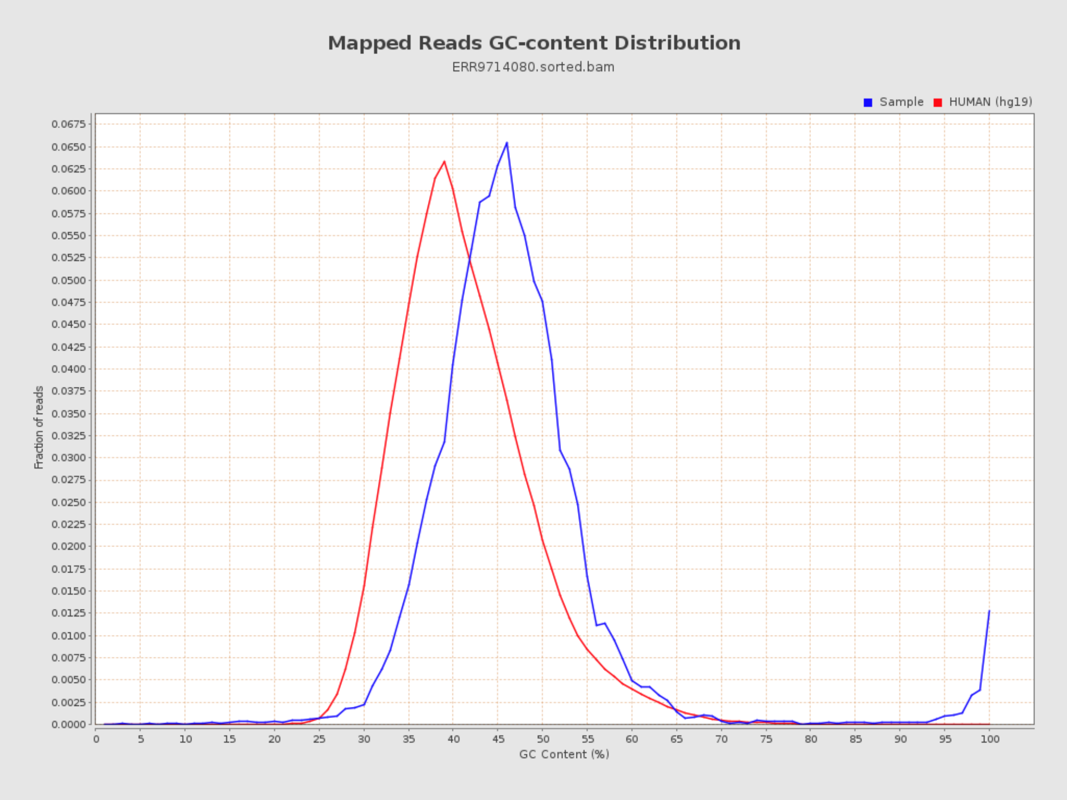
7. Results : Duplication Rate Histogram



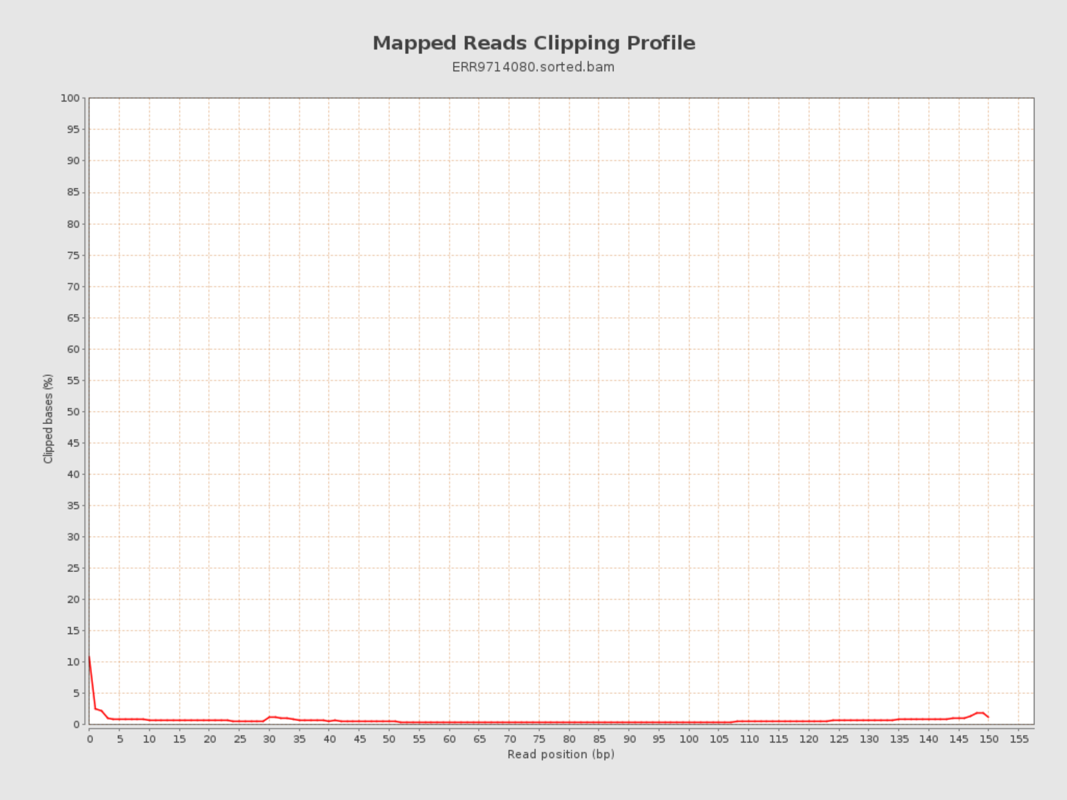
8. Results : Mapped Reads Nucleotide Content



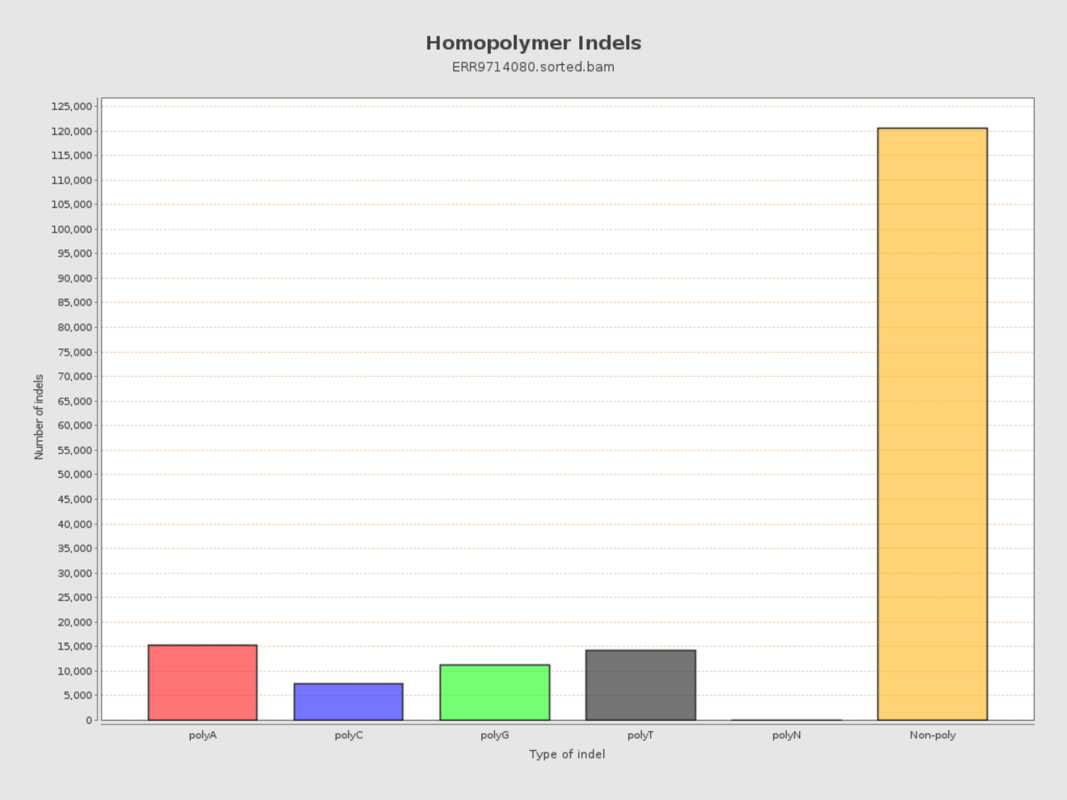
9. Results : Mapped Reads GC-content Distribution



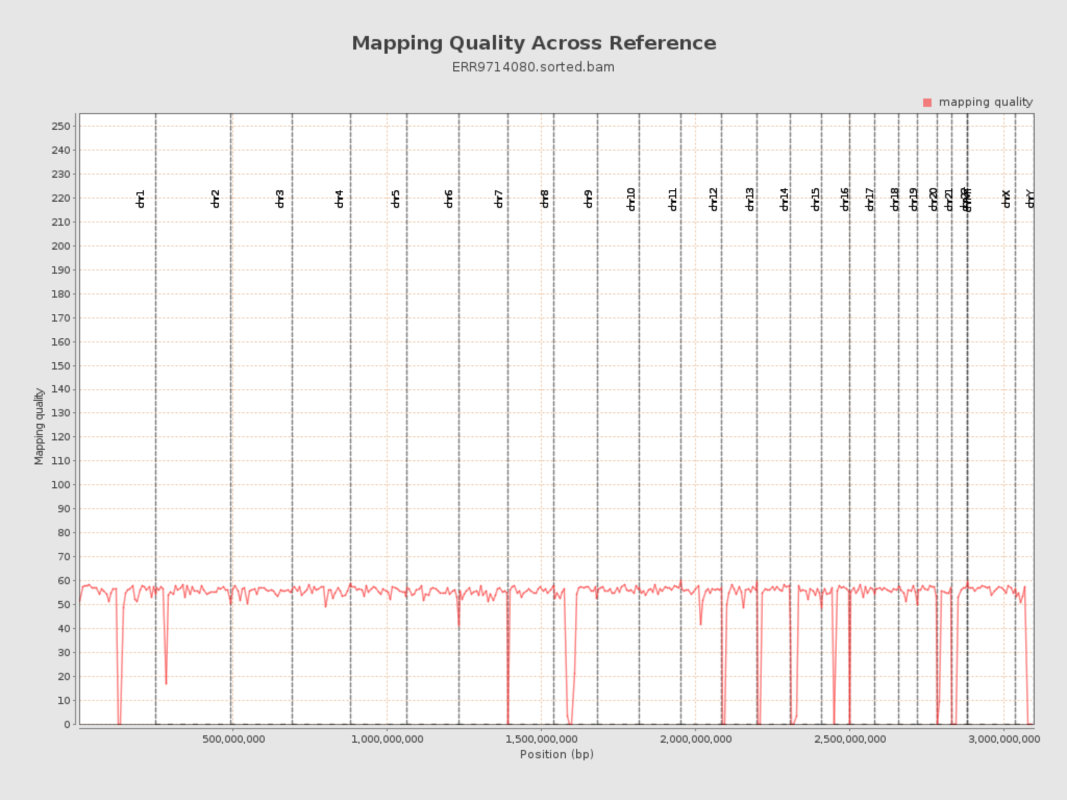
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram