Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:20:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714075.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_ERR9714075 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:20:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	347,218
Mapped reads	335,552 / 96.64%
Unmapped reads	11,666 / 3.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,810 / 4.27%
Read min/max/mean length	30 / 151 / 147.25
Duplicated reads (estimated)	278,297 / 80.15%
Duplication rate	42.11%
Clipped reads	322,107 / 92.77%

2.2. ACGT Content

Number/percentage of A's	12,765,245 / 29.84%
Number/percentage of C's	8,603,691 / 20.12%
Number/percentage of T's	11,966,483 / 27.98%
Number/percentage of G's	9,436,546 / 22.06%
Number/percentage of N's	264 / 0%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0141

Standard Deviation	2.1059

2.4. Mapping Quality

Mean Mapping Quality	51.15

2.5. Mismatches and indels

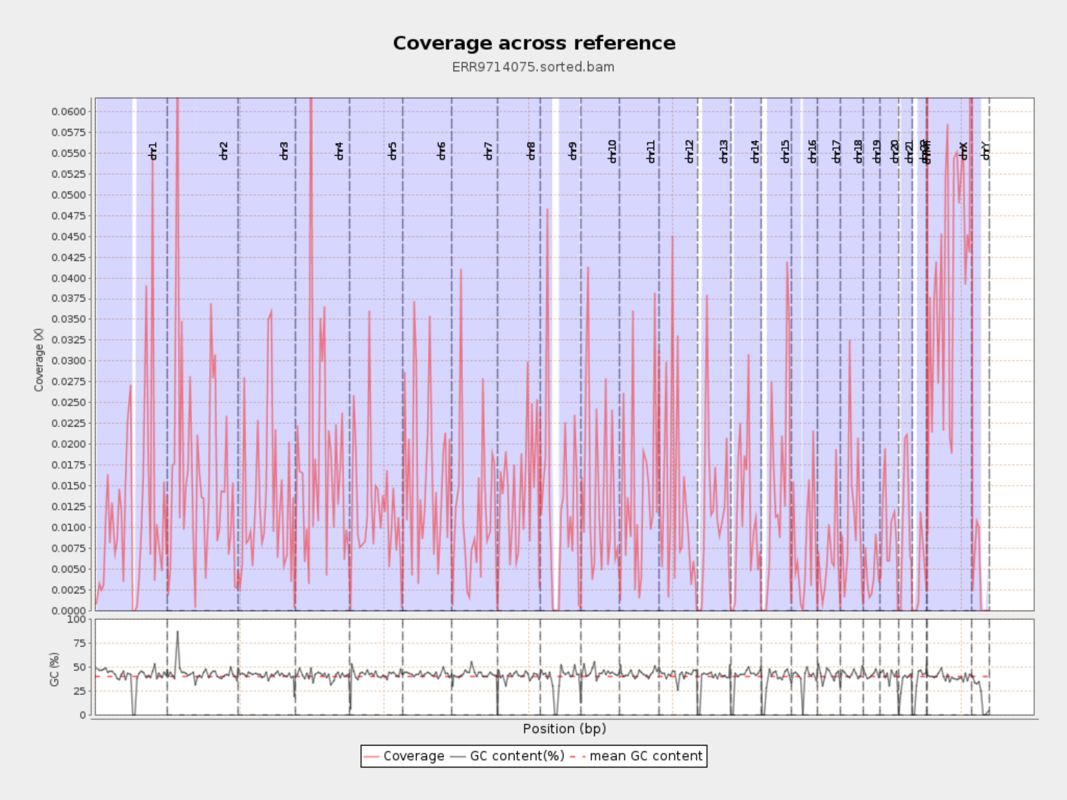
General error rate	3.86%
Mismatches	1,519,069
Insertions	45,874
Mapped reads with at least one insertion	13.23%
Deletions	131,245
Mapped reads with at least one deletion	37.38%
Homopolymer indels	27.08%

2.6. Chromosome stats

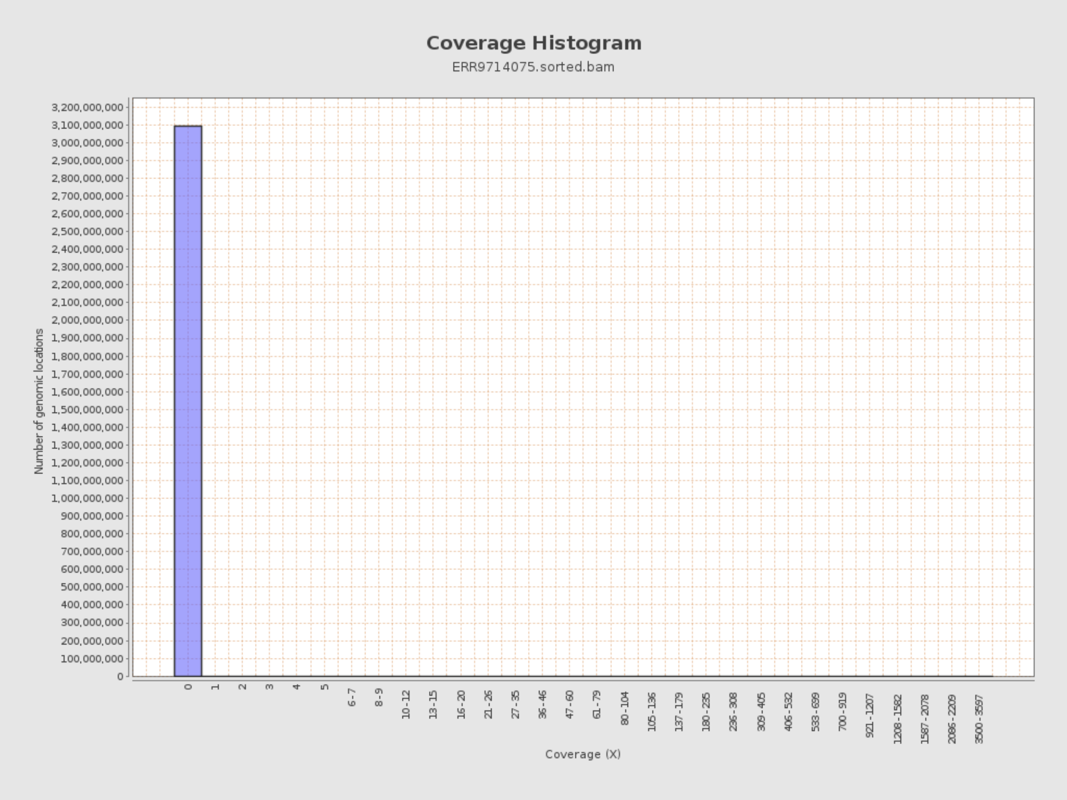
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2844622	0.0114	2.1259
chr2	243199373	4014303	0.0165	2.363
chr3	198022430	2596627	0.0131	1.4813
chr4	191154276	3495451	0.0183	3.7109
chr5	180915260	2251347	0.0124	1.5598
chr6	171115067	2741290	0.016	2.33
chr7	159138663	1846914	0.0116	1.6901

chr8	146364022	2058153	0.0141	1.5887
chr9	141213431	1737502	0.0123	1.7355
chr10	135534747	1939665	0.0143	2.002
chr11	135006516	1908411	0.0141	2.1726
chr12	133851895	1734166	0.013	2.1345
chr13	115169878	1354880	0.0118	1.2776
chr14	107349540	1207007	0.0112	1.4831
chr15	102531392	1496401	0.0146	2.0307
chr16	90354753	664853	0.0074	0.9483
chr17	81195210	507107	0.0062	0.9802
chr18	78077248	940782	0.012	1.5263
chr19	59128983	249297	0.0042	0.4963
chr20	63025520	616550	0.0098	1.2452
chr21	48129895	491027	0.0102	2.0365
chr22	51304566	196258	0.0038	0.6113
chrMT	16571	2236	0.1349	0.734
chrX	155270560	6446766	0.0415	3.7868
chrY	59373566	225049	0.0038	0.6168

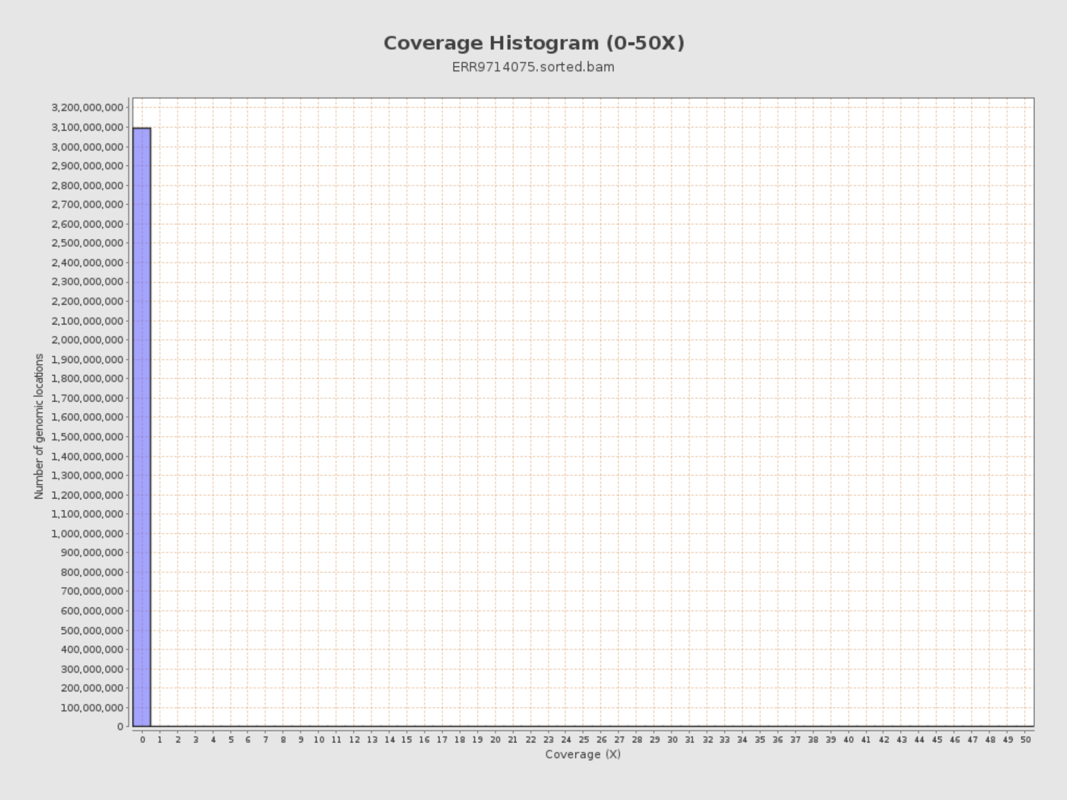
3. Results : Coverage across reference



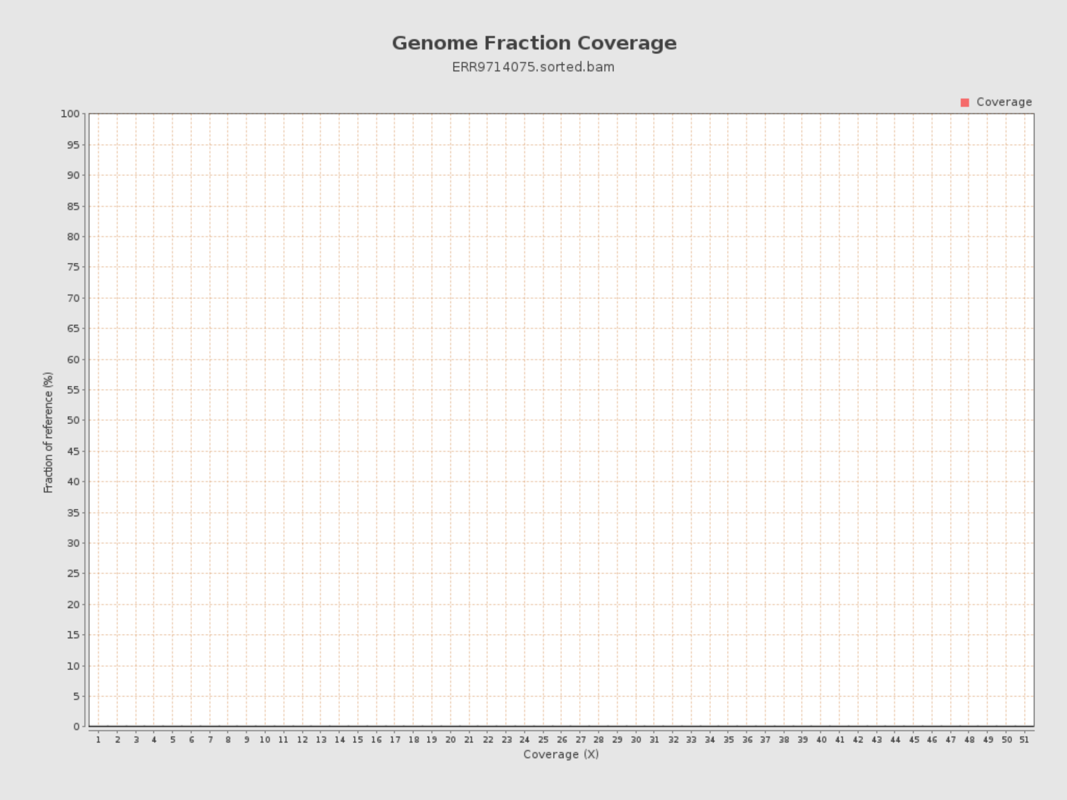
4. Results : Coverage Histogram



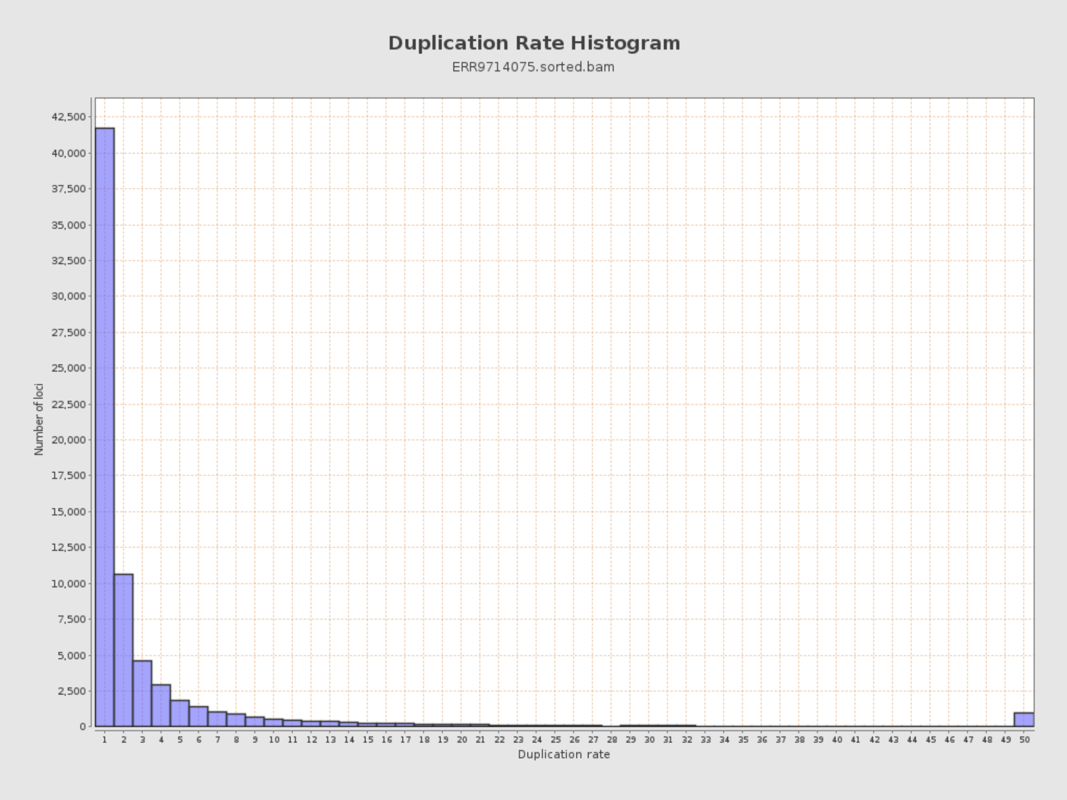
5. Results : Coverage Histogram (0-50X)



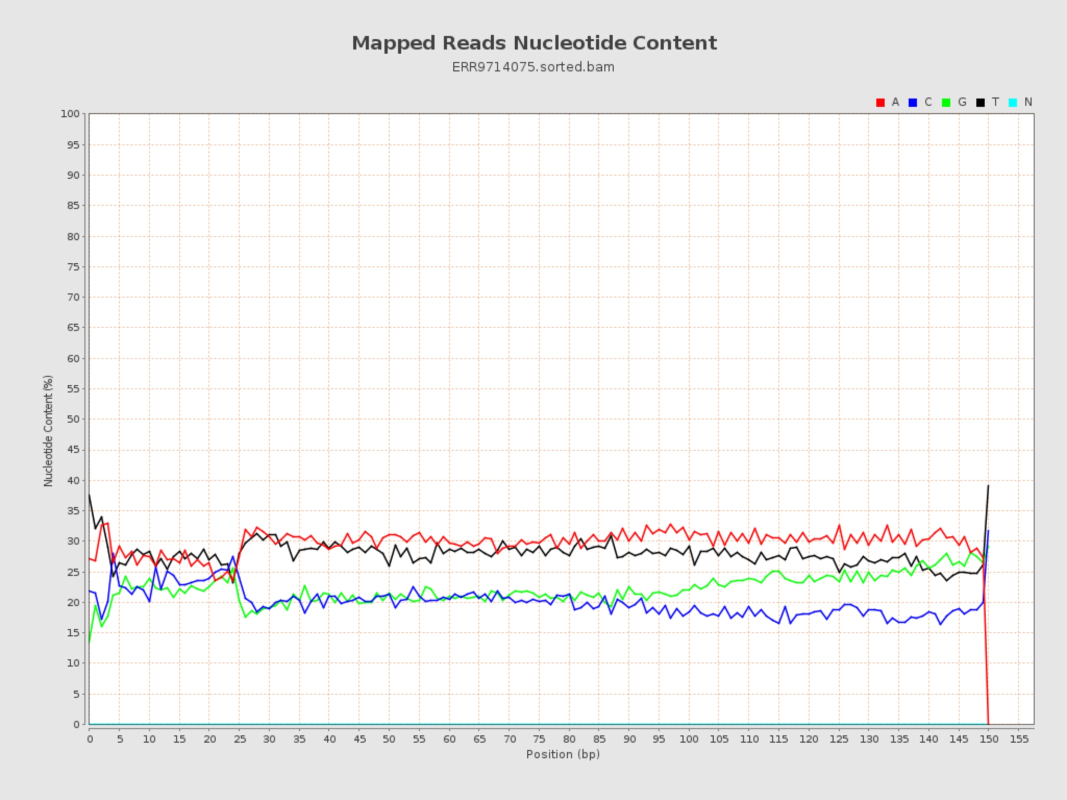
6. Results : Genome Fraction Coverage



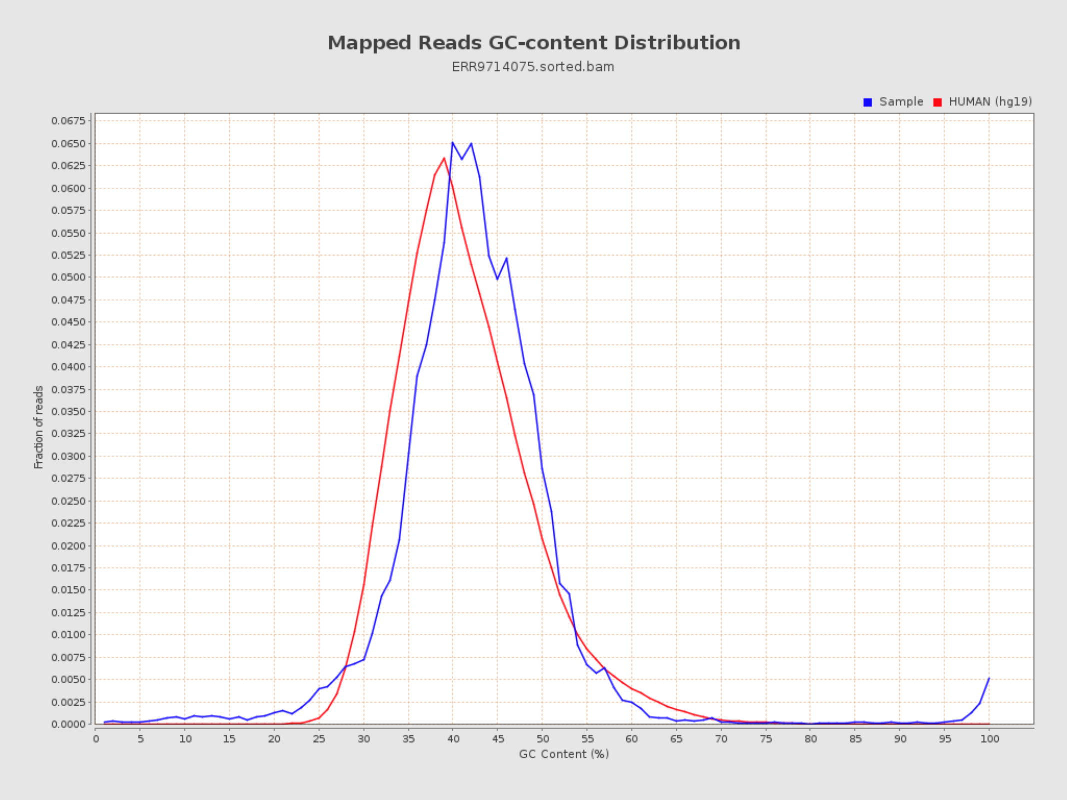
7. Results : Duplication Rate Histogram



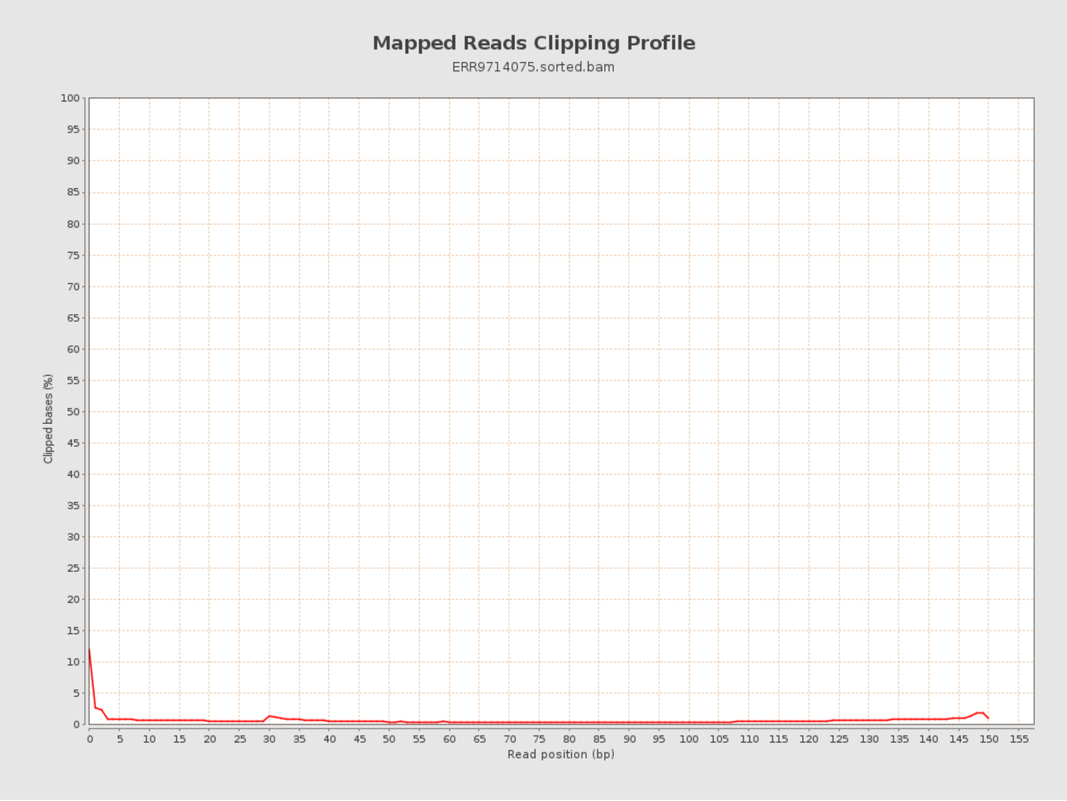
8. Results : Mapped Reads Nucleotide Content



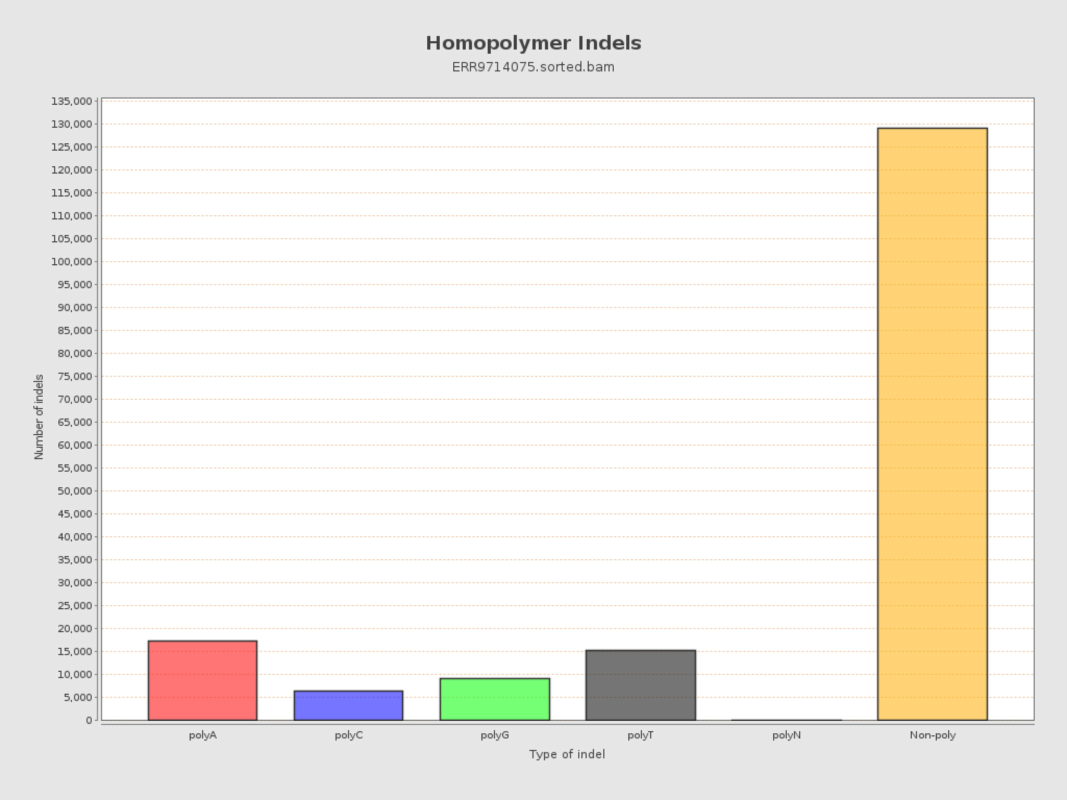
9. Results : Mapped Reads GC-content Distribution



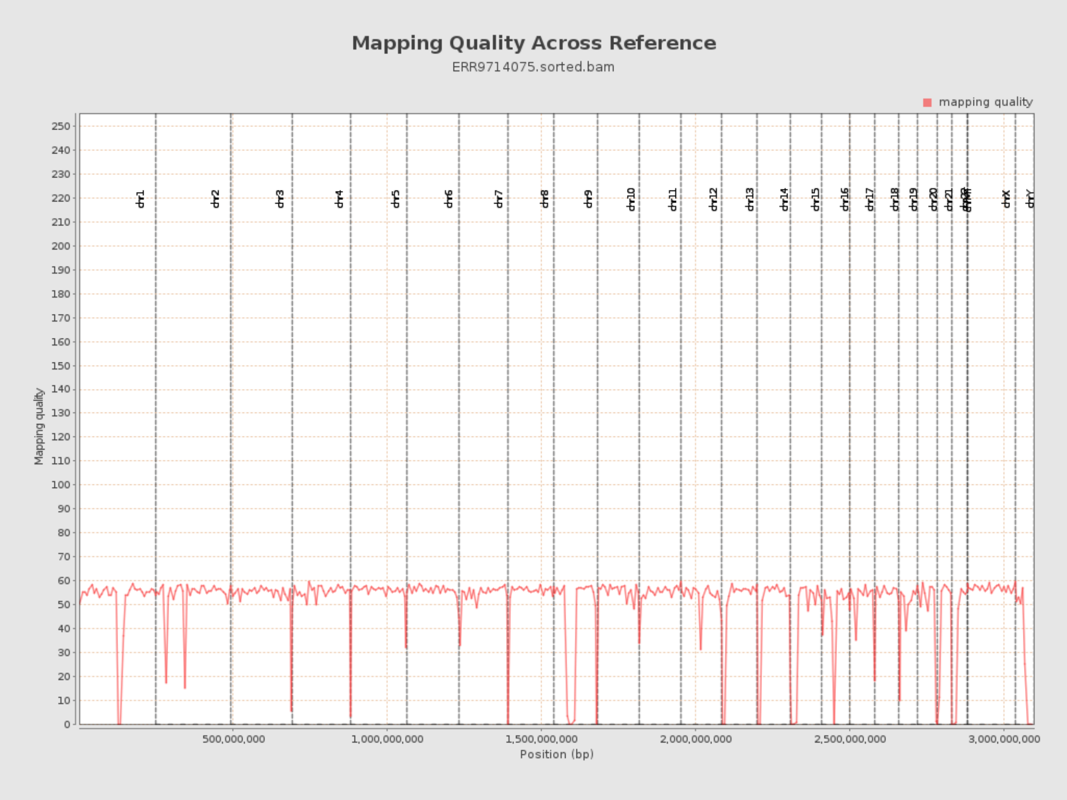
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram