Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:22:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714076.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_ERR9714076 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:22:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	431,922
Mapped reads	280,286 / 64.89%
Unmapped reads	151,636 / 35.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,829 / 2.04%
Read min/max/mean length	30 / 151 / 115.17
Duplicated reads (estimated)	222,082 / 51.42%
Duplication rate	42.37%
Clipped reads	262,613 / 60.8%

2.2. ACGT Content

Number/percentage of A's	9,913,539 / 28.01%
Number/percentage of C's	7,416,737 / 20.95%
Number/percentage of T's	9,392,985 / 26.54%
Number/percentage of G's	8,671,444 / 24.5%
Number/percentage of N's	294 / 0%
GC Percentage	45.45%

2.3. Coverage

Mean	0.0117

Standard Deviation	1.6875

2.4. Mapping Quality

Mean Mapping Quality	52.34

2.5. Mismatches and indels

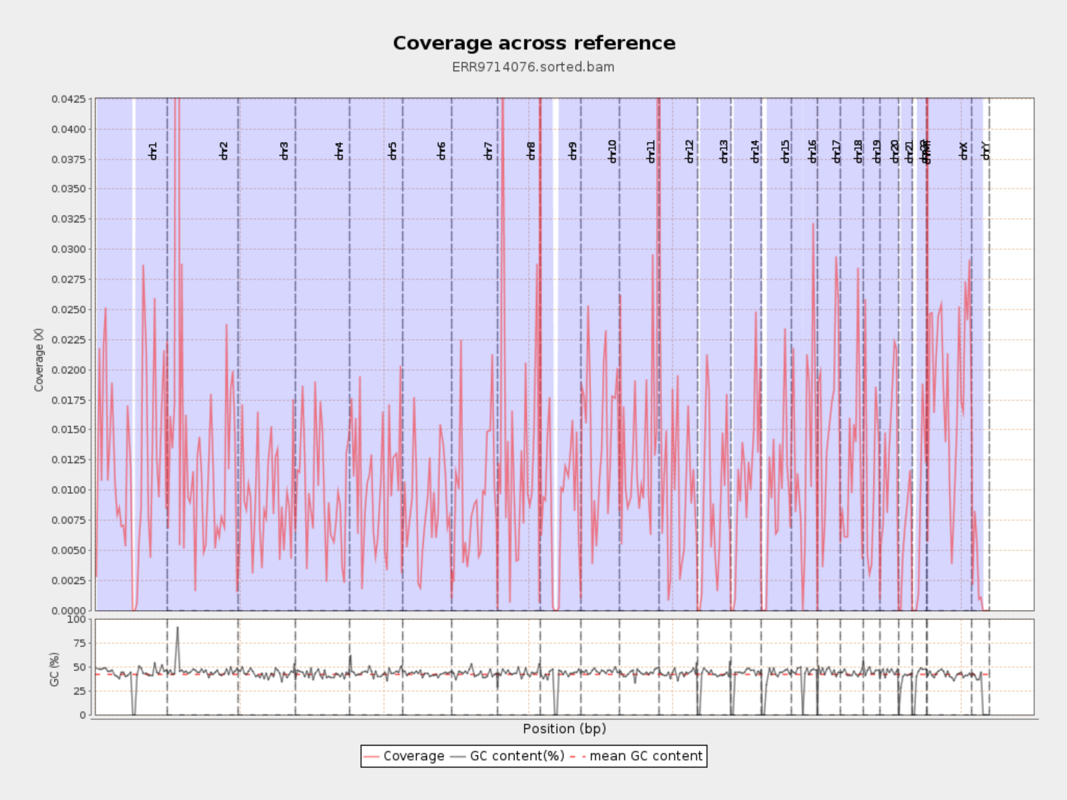
General error rate	4.29%
Mismatches	1,391,026
Insertions	39,100
Mapped reads with at least one insertion	13.35%
Deletions	119,352
Mapped reads with at least one deletion	40.64%
Homopolymer indels	29.21%

2.6. Chromosome stats

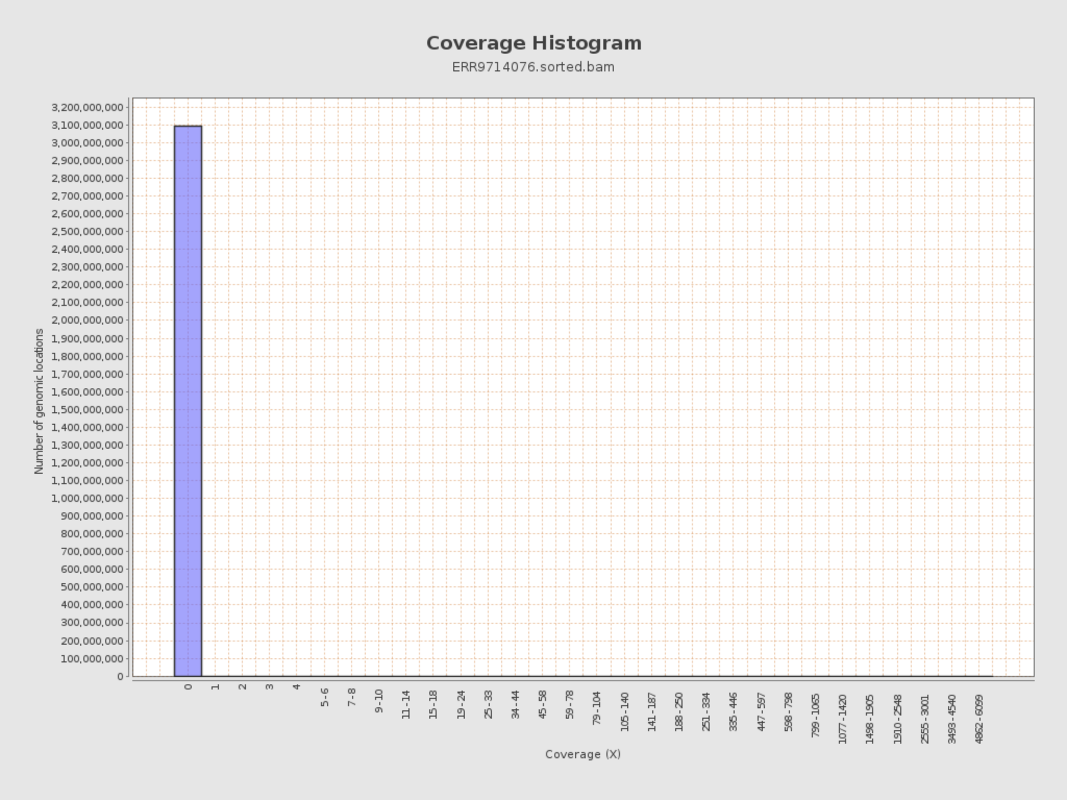
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3045834	0.0122	1.2805
chr2	243199373	3941790	0.0162	4.1891
chr3	198022430	1858594	0.0094	0.8878
chr4	191154276	1854742	0.0097	1.1093
chr5	180915260	1955057	0.0108	1.0918
chr6	171115067	1464740	0.0086	0.8547
chr7	159138663	1472528	0.0093	0.9548

chr8	146364022	1858375	0.0127	1.7201
chr9	141213431	1309419	0.0093	1.0664
chr10	135534747	2014698	0.0149	1.407
chr11	135006516	1821645	0.0135	1.5825
chr12	133851895	1371539	0.0102	1.1113
chr13	115169878	1000779	0.0087	1.0775
chr14	107349540	1171857	0.0109	1.1222
chr15	102531392	936693	0.0091	0.9021
chr16	90354753	1209621	0.0134	1.5021
chr17	81195210	1320534	0.0163	1.7887
chr18	78077248	966210	0.0124	1.3812
chr19	59128983	644216	0.0109	1.0648
chr20	63025520	858637	0.0136	1.1077
chr21	48129895	289427	0.006	0.521
chr22	51304566	374074	0.0073	0.8684
chrMT	16571	301988	18.2239	168.3658
chrX	155270560	2920619	0.0188	1.2665
chrY	59373566	136492	0.0023	0.4247

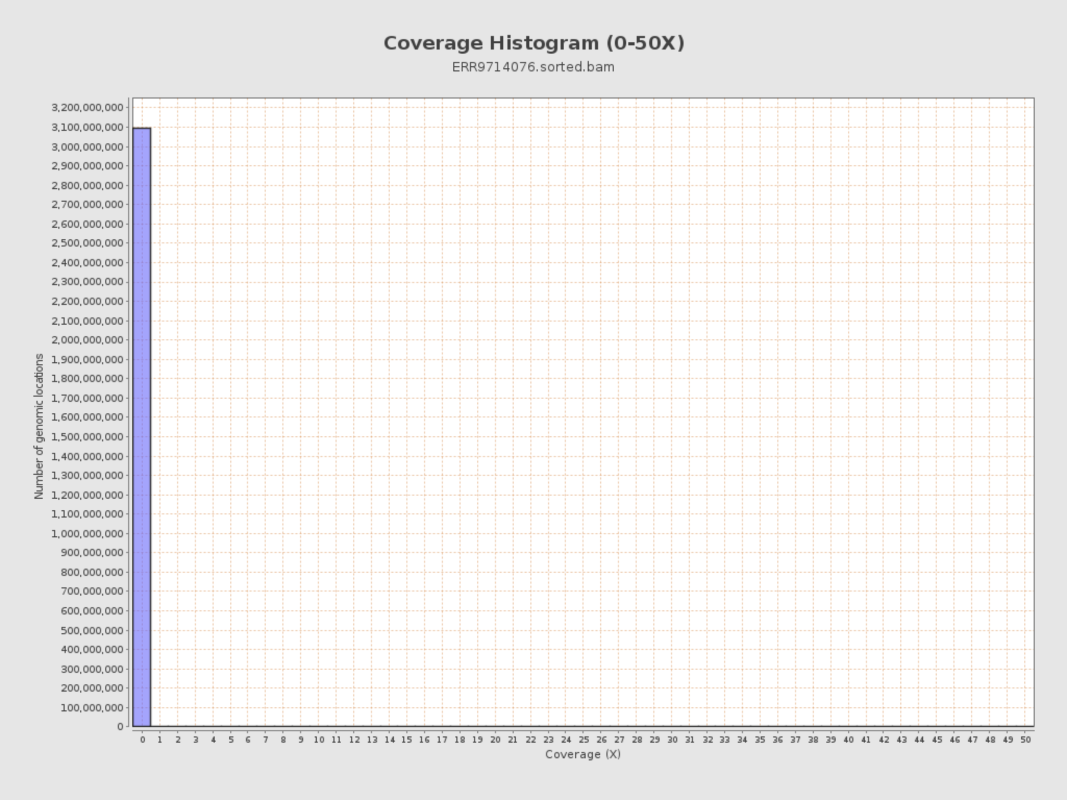
3. Results : Coverage across reference



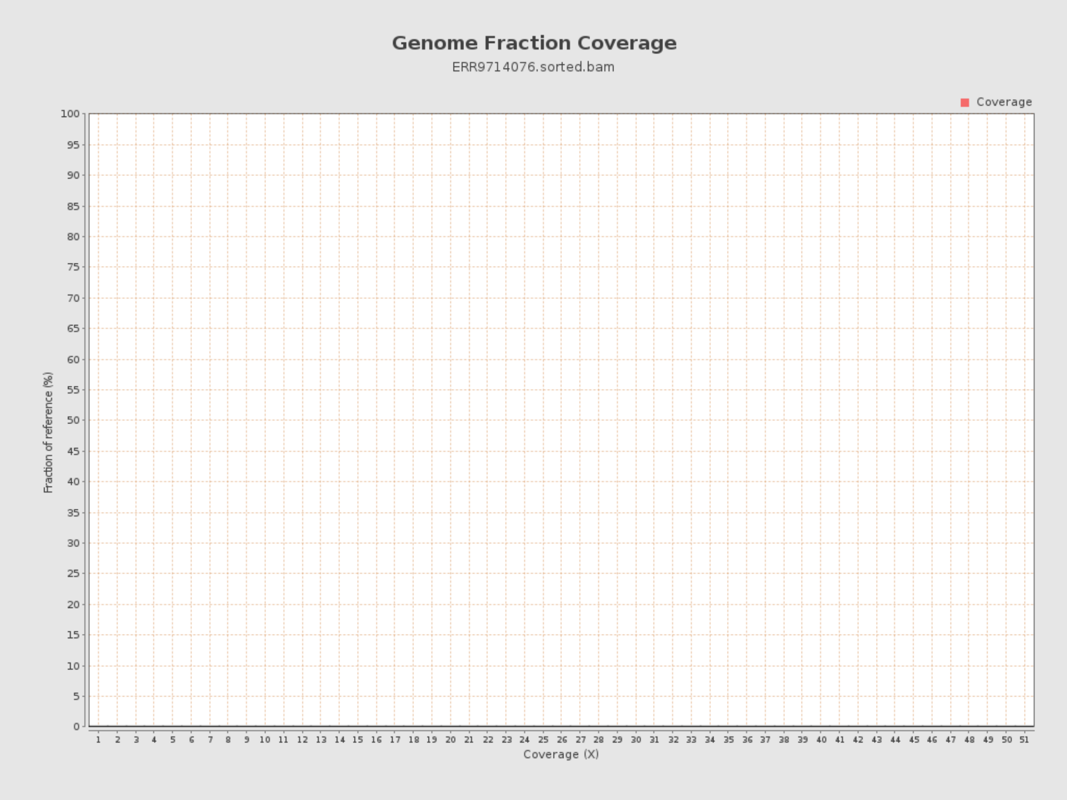
4. Results : Coverage Histogram



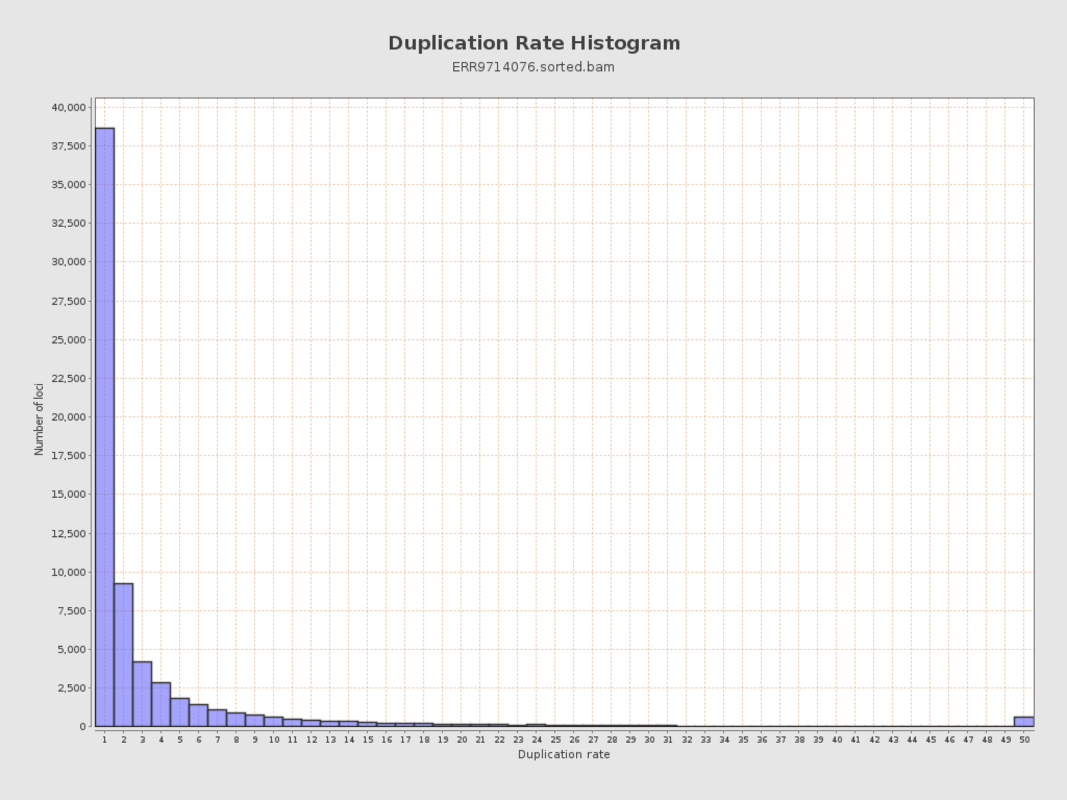
5. Results : Coverage Histogram (0-50X)



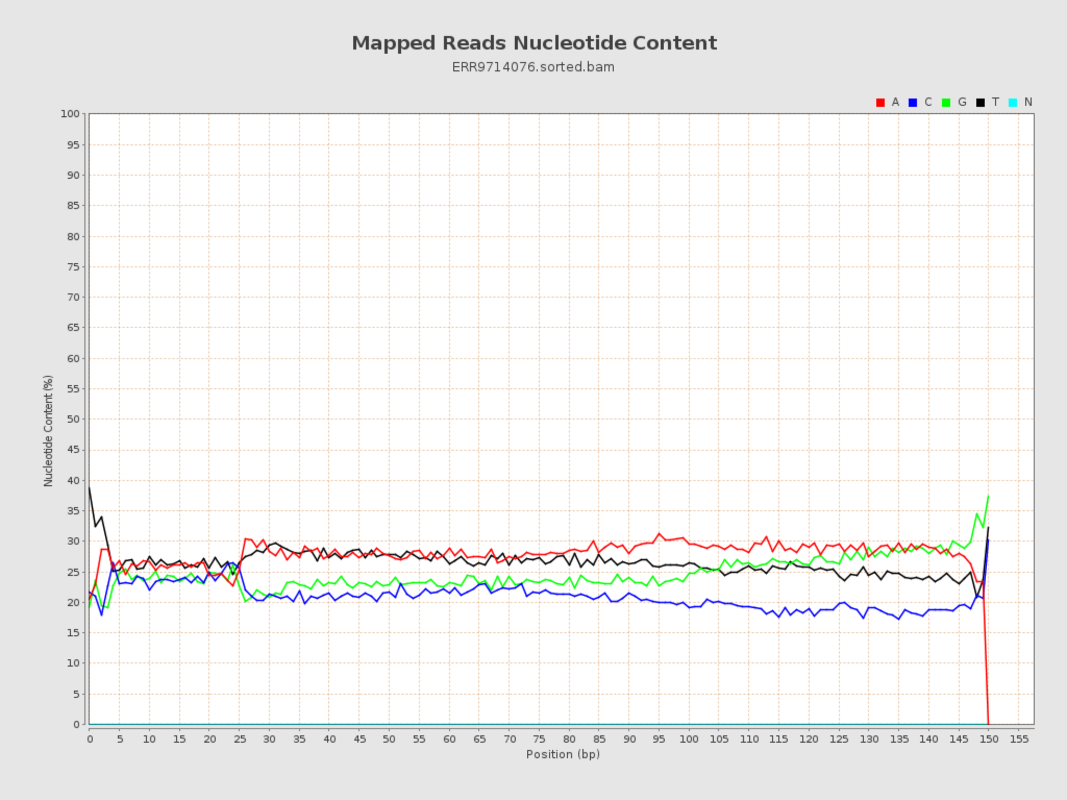
6. Results : Genome Fraction Coverage



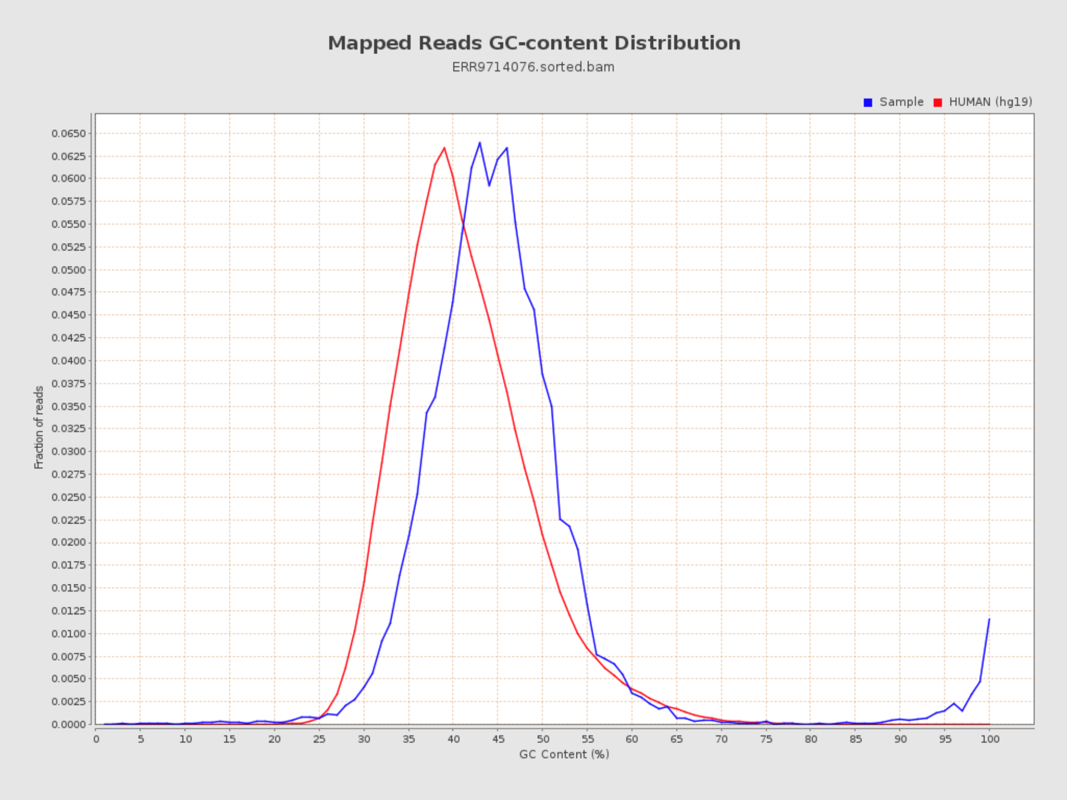
7. Results : Duplication Rate Histogram



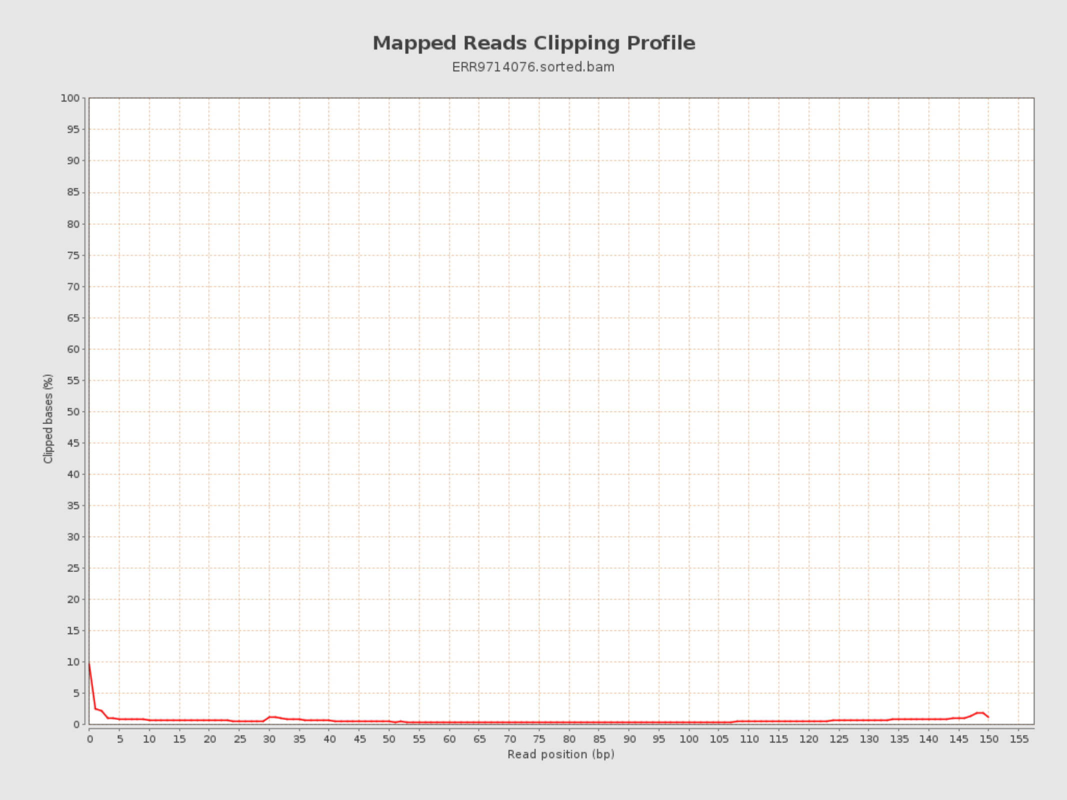
8. Results : Mapped Reads Nucleotide Content



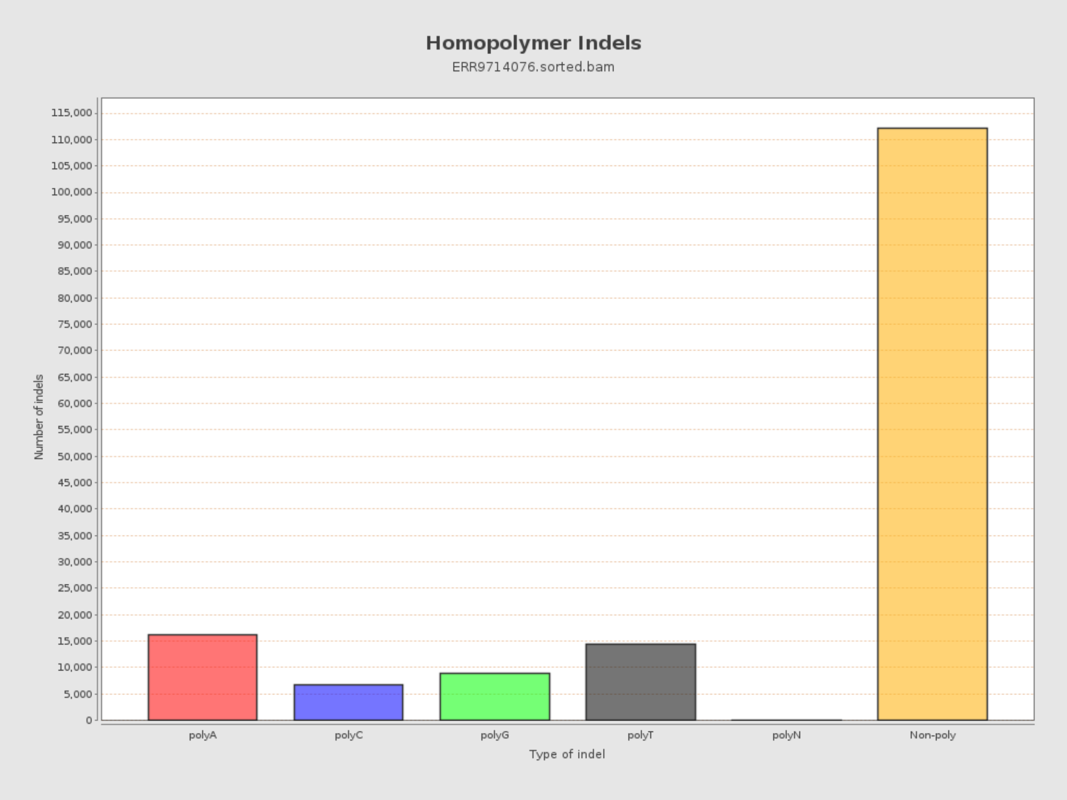
9. Results : Mapped Reads GC-content Distribution



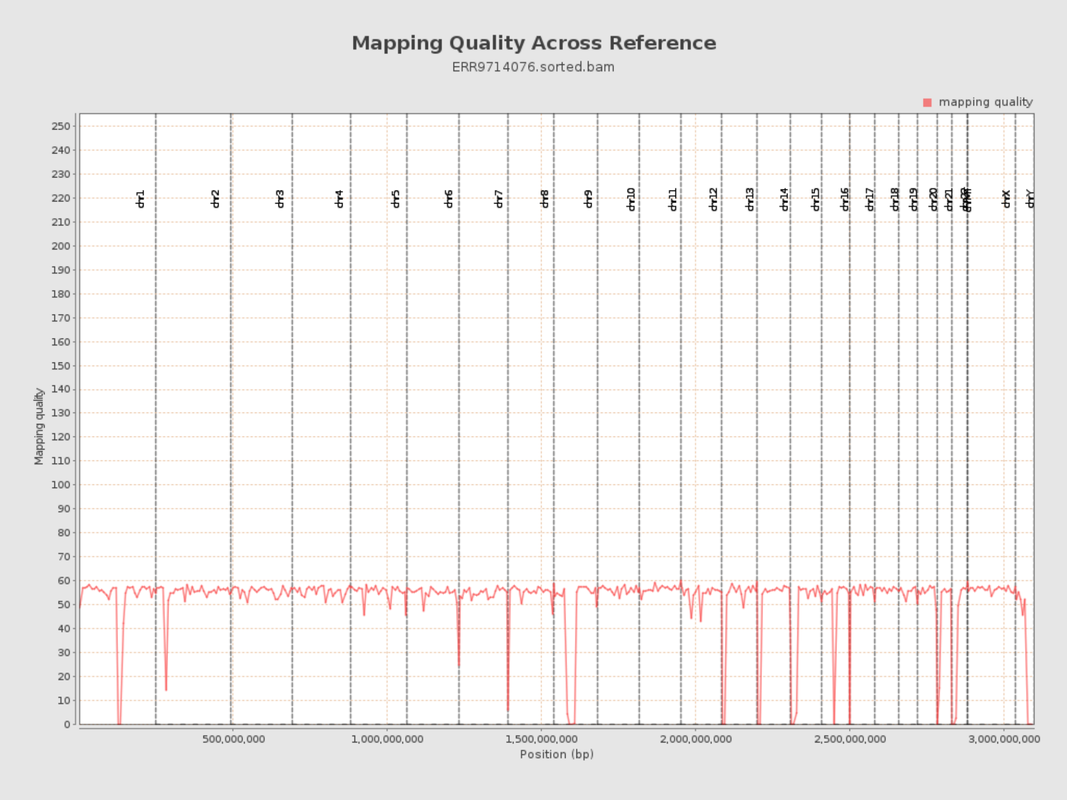
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram