Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:53:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714111.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_ERR9714111 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:53:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	586,750
Mapped reads	462,104 / 78.76%
Unmapped reads	124,646 / 21.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,550 / 2.82%
Read min/max/mean length	30 / 151 / 132.17
Duplicated reads (estimated)	387,313 / 66.01%
Duplication rate	43.46%
Clipped reads	438,387 / 74.71%

2.2. ACGT Content

Number/percentage of A's	16,448,141 / 28.09%
Number/percentage of C's	12,458,855 / 21.28%
Number/percentage of T's	15,591,581 / 26.62%
Number/percentage of G's	14,061,585 / 24.01%
Number/percentage of N's	468 / 0%
GC Percentage	45.29%

2.3. Coverage

Mean	0.0193

Standard Deviation	2.3369

2.4. Mapping Quality

Mean Mapping Quality	52.54

2.5. Mismatches and indels

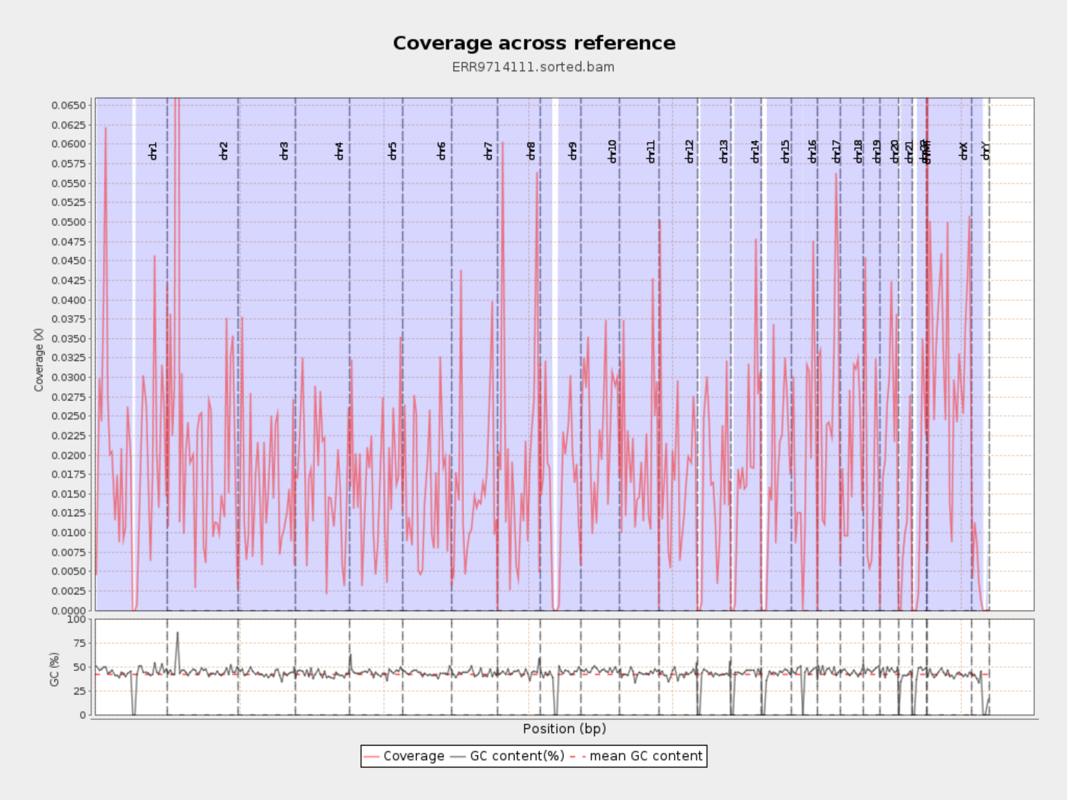
General error rate	4.19%
Mismatches	2,232,952
Insertions	67,830
Mapped reads with at least one insertion	14.27%
Deletions	194,755
Mapped reads with at least one deletion	40.26%
Homopolymer indels	28.82%

2.6. Chromosome stats

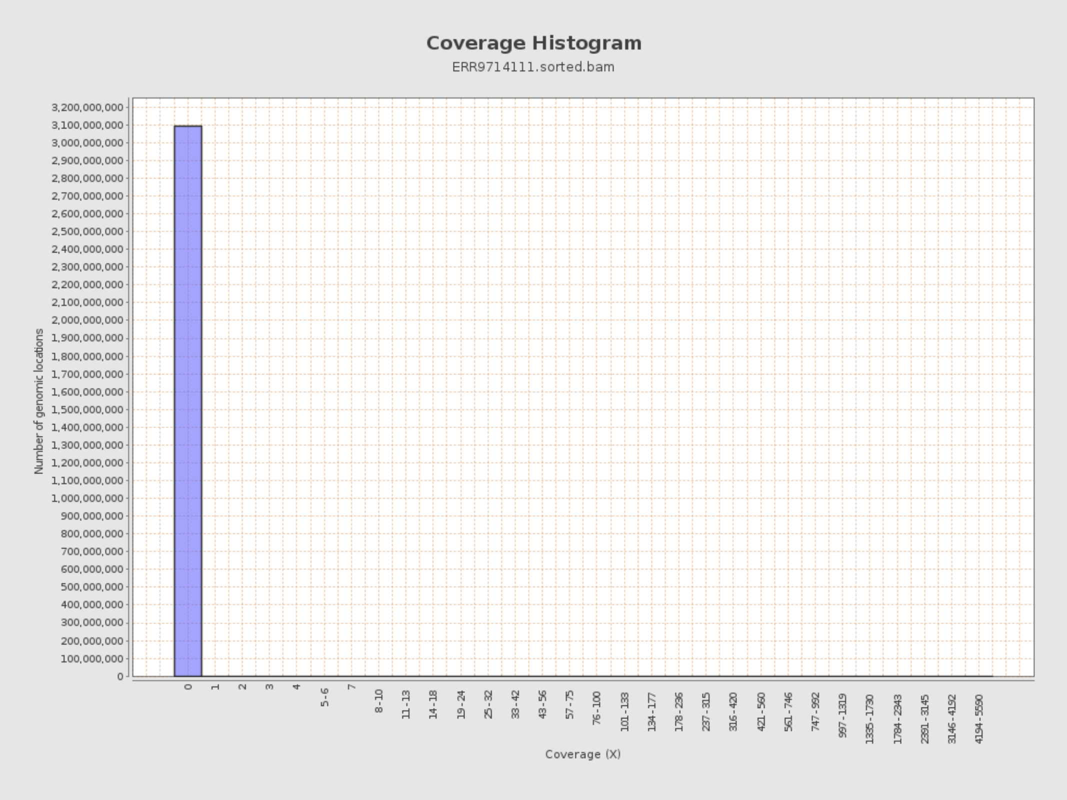
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4988036	0.02	2.1228
chr2	243199373	5944139	0.0244	4.539
chr3	198022430	3145931	0.0159	1.4619
chr4	191154276	3219430	0.0168	1.8712
chr5	180915260	3074908	0.017	1.5974
chr6	171115067	2597587	0.0152	1.482
chr7	159138663	2504457	0.0157	1.5955

chr8	146364022	2816185	0.0192	2.1727
chr9	141213431	2191786	0.0155	1.8701
chr10	135534747	3262871	0.0241	2.1632
chr11	135006516	2677902	0.0198	1.8885
chr12	133851895	2414557	0.018	1.706
chr13	115169878	1738572	0.0151	1.5502
chr14	107349540	2011270	0.0187	1.945
chr15	102531392	1729891	0.0169	1.7262
chr16	90354753	1802693	0.02	2.1116
chr17	81195210	2281755	0.0281	2.9935
chr18	78077248	1676231	0.0215	2.1102
chr19	59128983	1027187	0.0174	1.8459
chr20	63025520	1590977	0.0252	2.2927
chr21	48129895	496480	0.0103	1.0359
chr22	51304566	660342	0.0129	1.575
chrMT	16571	597442	36.0535	332.7162
chrX	155270560	4997064	0.0322	2.1017
chrY	59373566	216071	0.0036	0.682

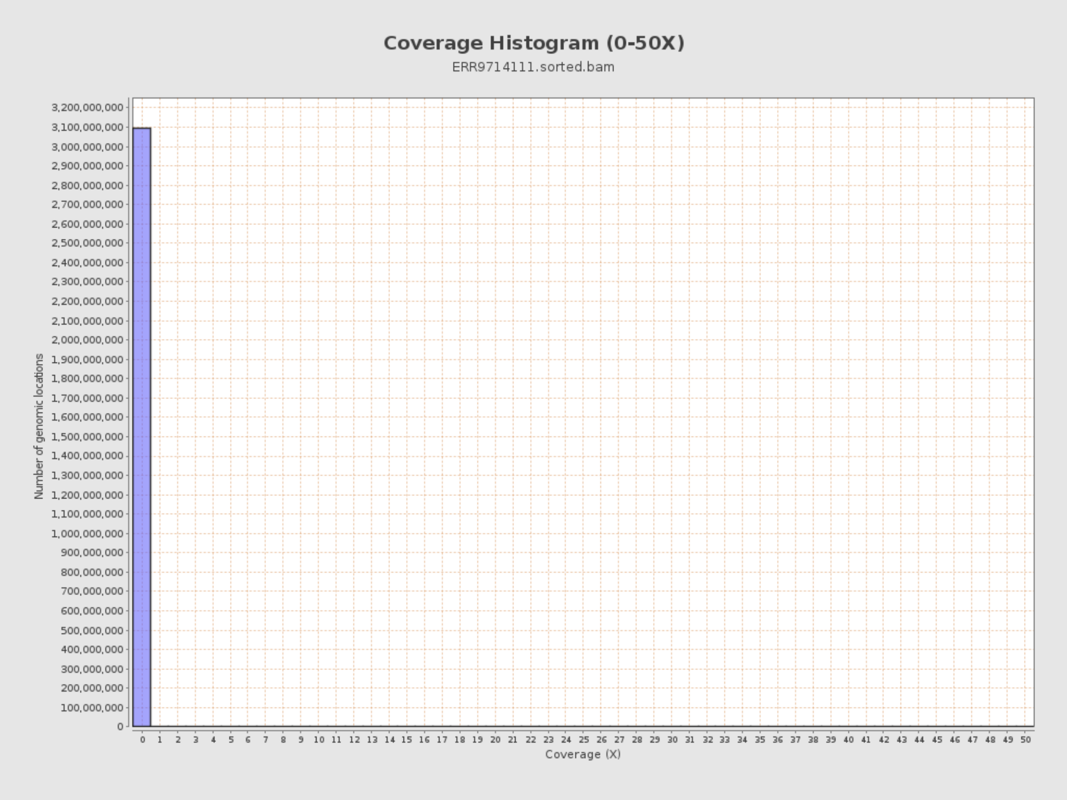
3. Results : Coverage across reference



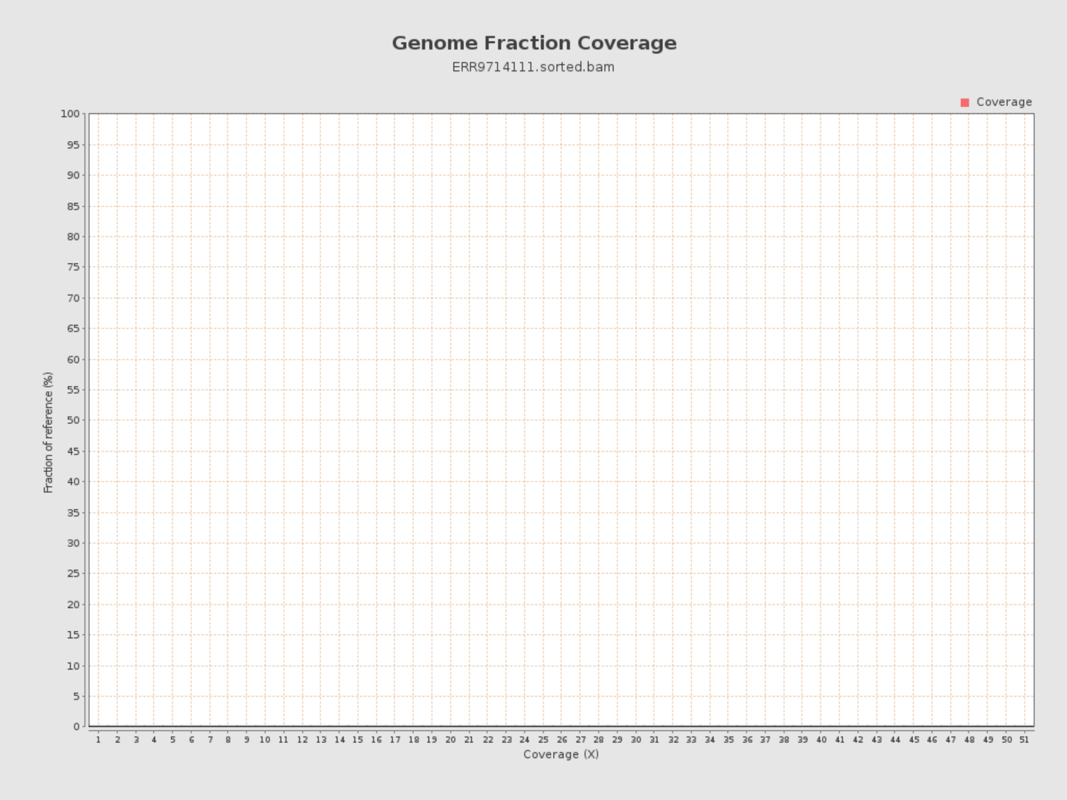
4. Results : Coverage Histogram



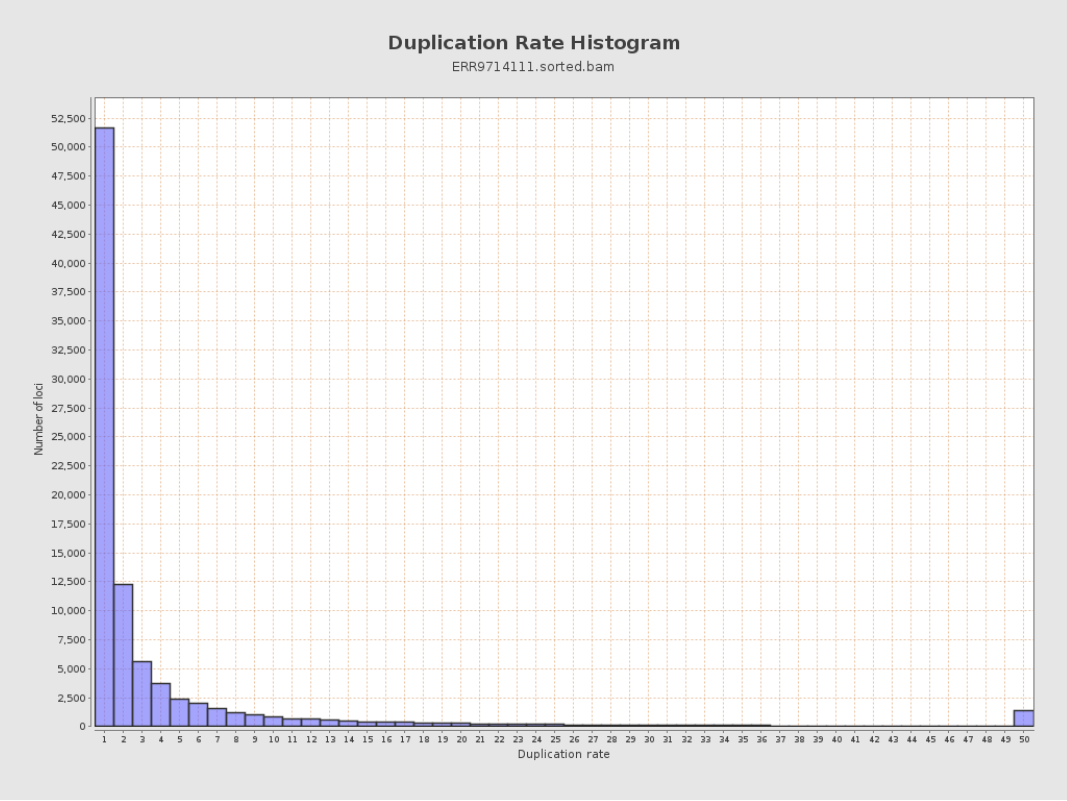
5. Results : Coverage Histogram (0-50X)



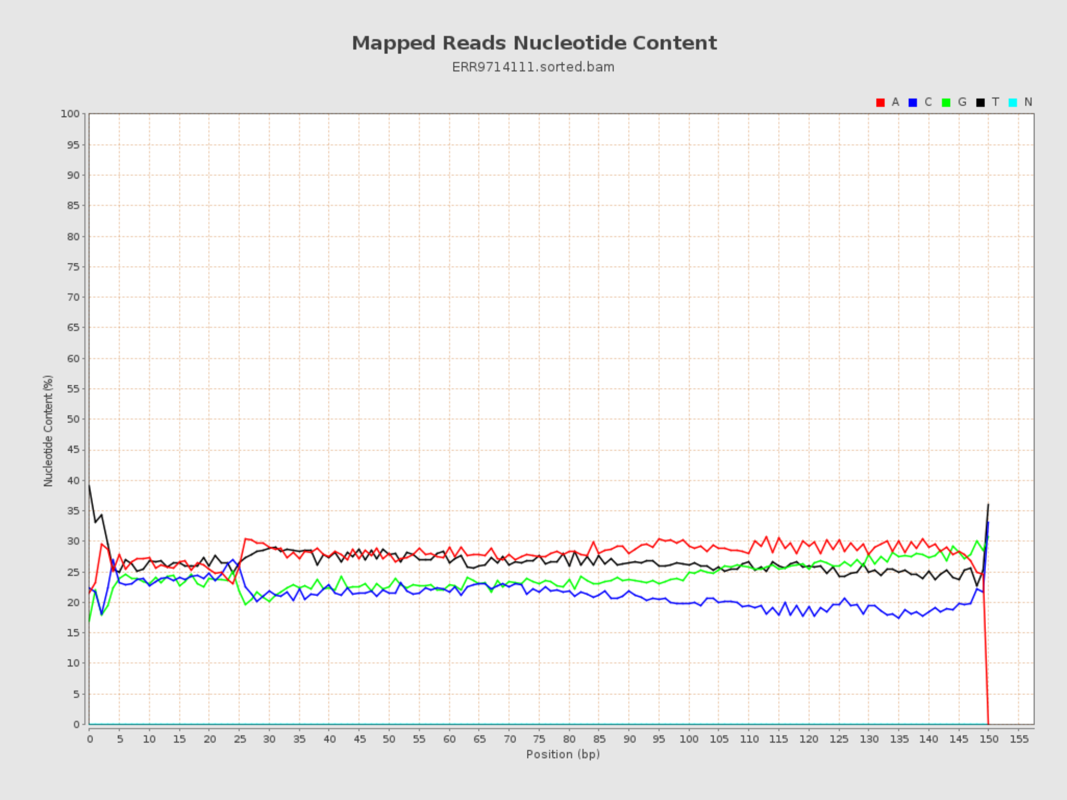
6. Results : Genome Fraction Coverage



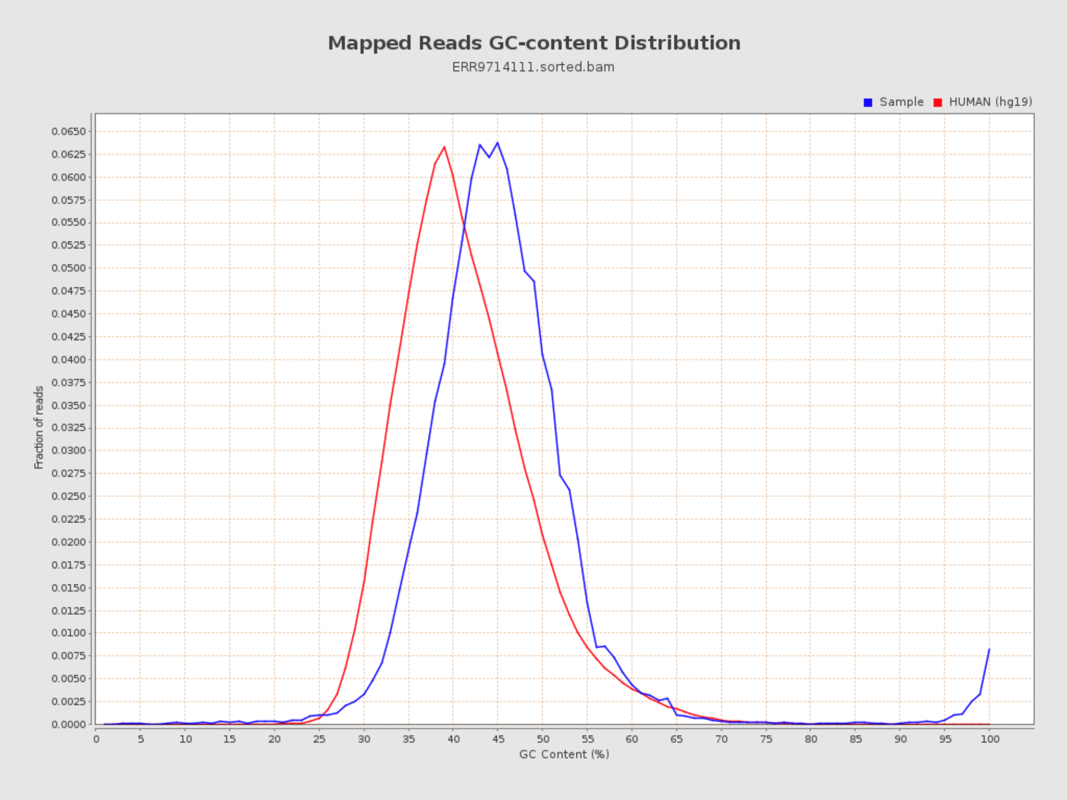
7. Results : Duplication Rate Histogram



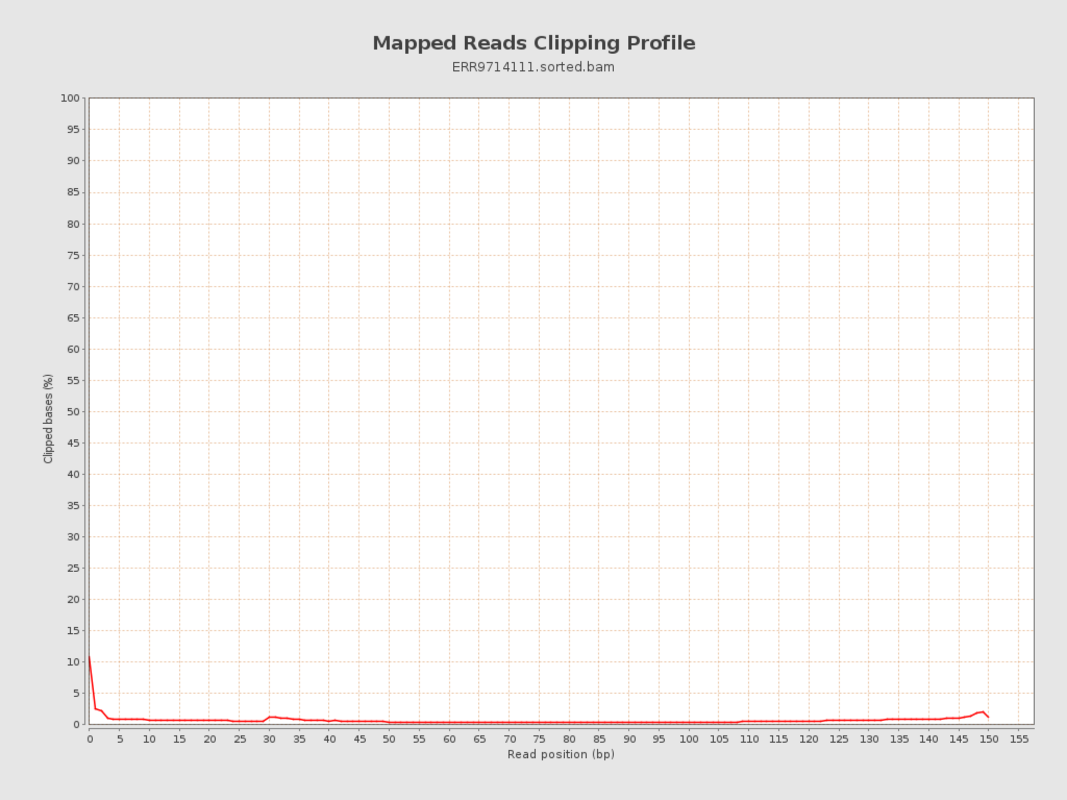
8. Results : Mapped Reads Nucleotide Content



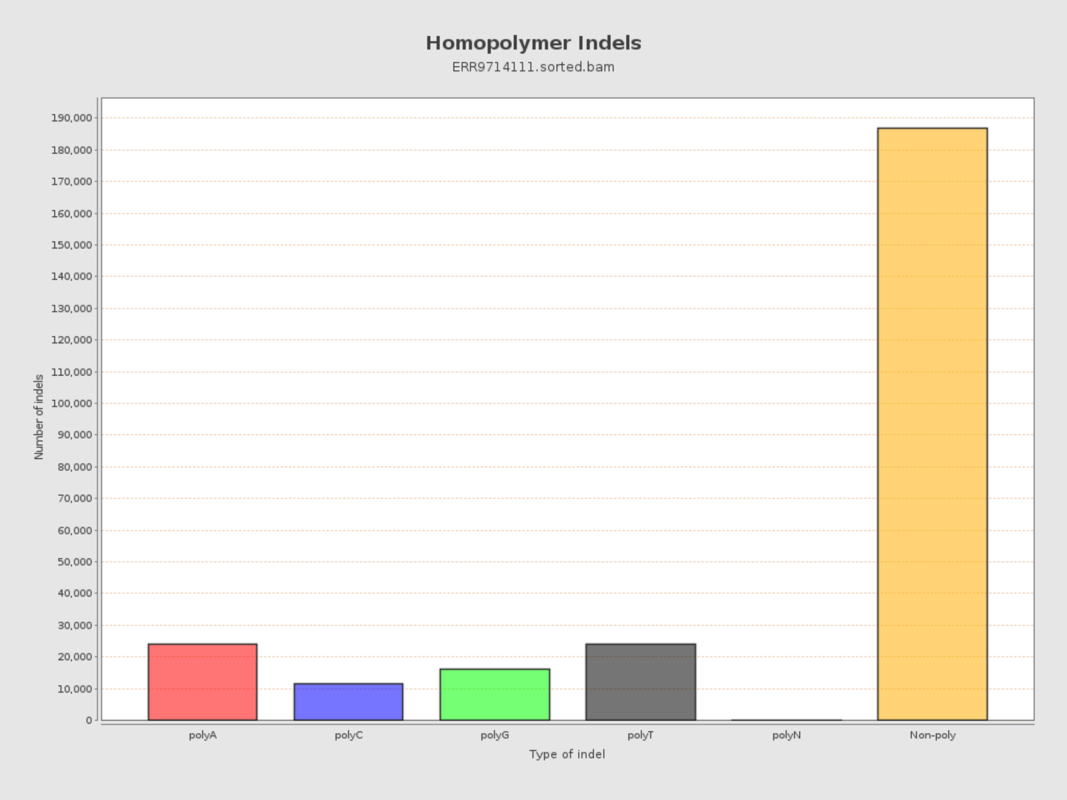
9. Results : Mapped Reads GC-content Distribution



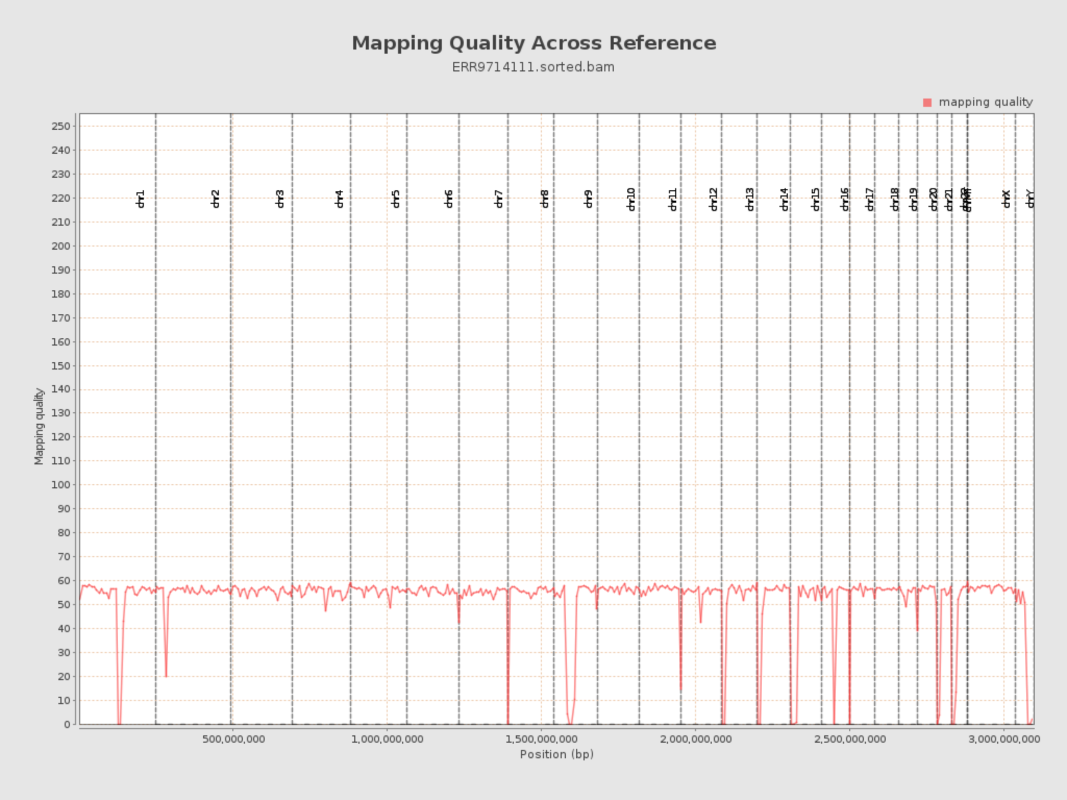
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram