Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:08:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714177.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_ERR9714177 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:08:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,627,748
Mapped reads	1,562,181 / 95.97%
Unmapped reads	65,567 / 4.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,516 / 3.96%
Read min/max/mean length	30 / 151 / 146.02
Duplicated reads (estimated)	1,454,706 / 89.37%
Duplication rate	44.16%
Clipped reads	1,490,625 / 91.58%

2.2. ACGT Content

Number/percentage of A's	59,376,823 / 29.67%
Number/percentage of C's	40,602,336 / 20.29%
Number/percentage of T's	56,200,179 / 28.08%
Number/percentage of G's	43,952,247 / 21.96%
Number/percentage of N's	1,523 / 0%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0659

Standard Deviation	10.3744

2.4. Mapping Quality

Mean Mapping Quality	51.28

2.5. Mismatches and indels

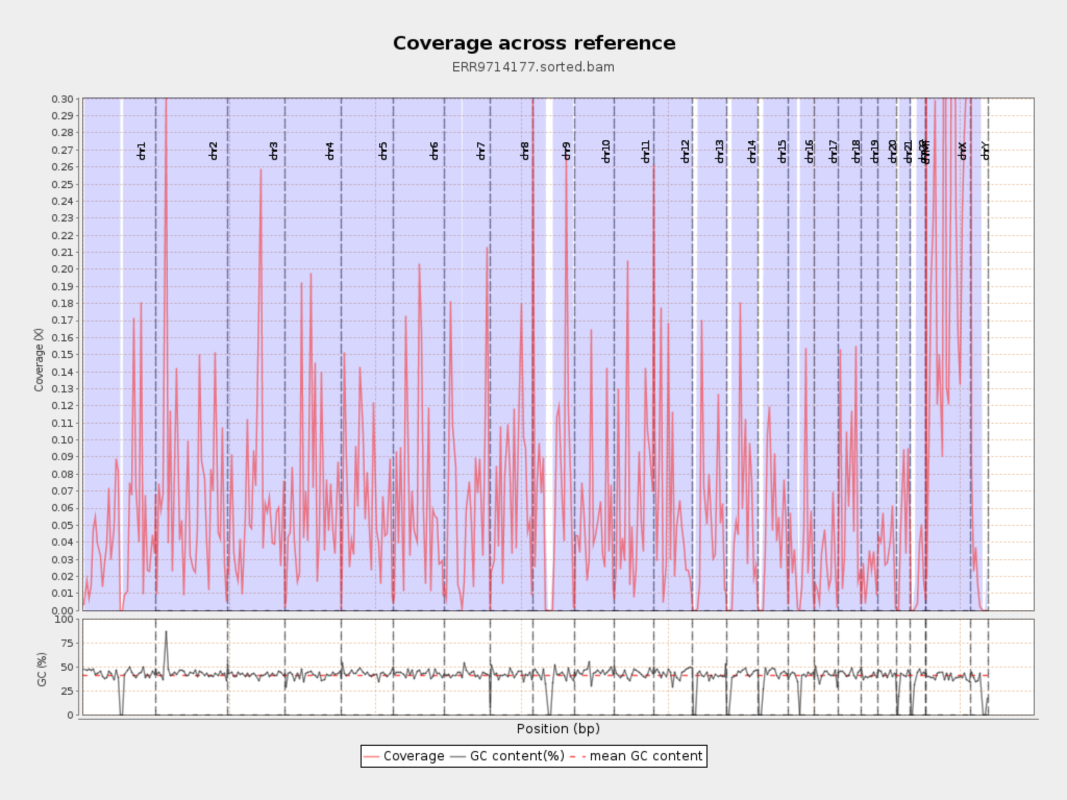
General error rate	3.85%
Mismatches	7,158,350
Insertions	202,872
Mapped reads with at least one insertion	12.63%
Deletions	638,251
Mapped reads with at least one deletion	39.03%
Homopolymer indels	26.38%

2.6. Chromosome stats

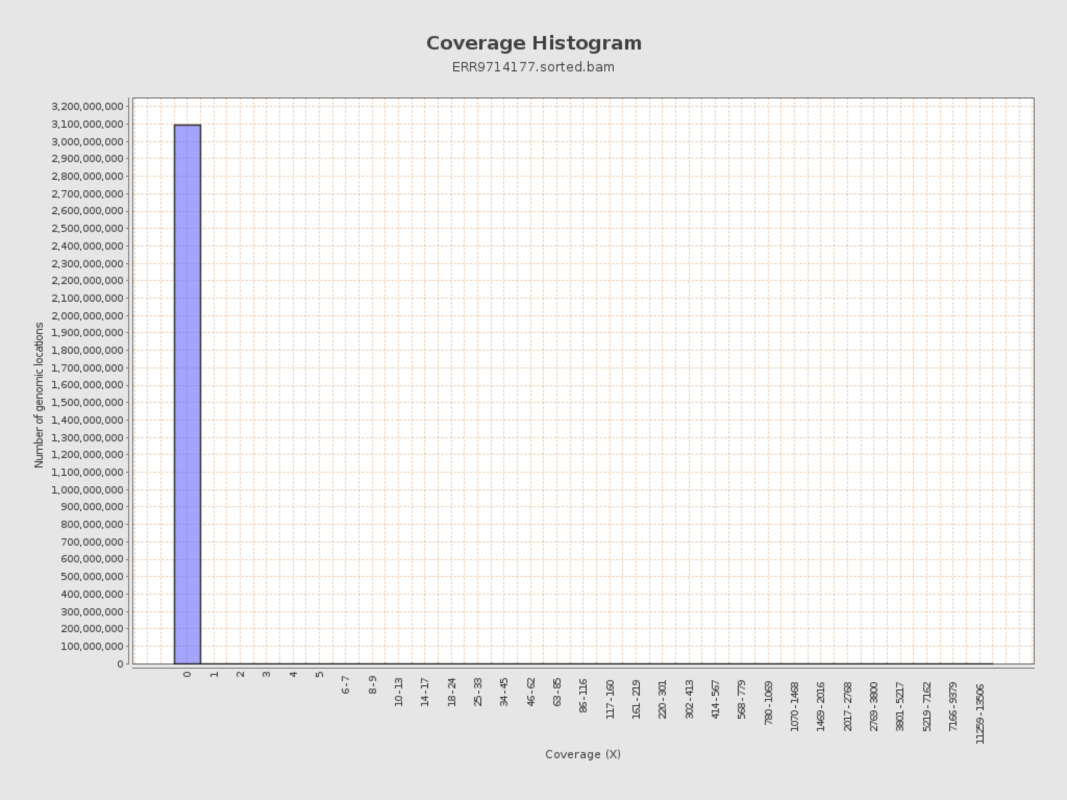
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11307948	0.0454	7.2374
chr2	243199373	17029159	0.07	11.0415
chr3	198022430	12698041	0.0641	8.3545
chr4	191154276	12942849	0.0677	11.1666
chr5	180915260	11273796	0.0623	7.805
chr6	171115067	11717832	0.0685	11.0944
chr7	159138663	10475351	0.0658	10.5982

chr8	146364022	10375469	0.0709	9.958
chr9	141213431	9695744	0.0687	15.1686
chr10	135534747	7548195	0.0557	7.3982
chr11	135006516	9045462	0.067	11.6502
chr12	133851895	7900996	0.059	8.9373
chr13	115169878	5898342	0.0512	7.047
chr14	107349540	5712677	0.0532	8.3646
chr15	102531392	5039428	0.0492	6.7119
chr16	90354753	3255734	0.036	5.035
chr17	81195210	2082566	0.0256	3.3421
chr18	78077248	5592352	0.0716	9.8151
chr19	59128983	1255724	0.0212	3.2177
chr20	63025520	2389187	0.0379	4.3395
chr21	48129895	2326142	0.0483	9.855
chr22	51304566	877765	0.0171	2.2925
chrMT	16571	14096	0.8506	5.883
chrX	155270560	36405308	0.2345	23.2058
chrY	59373566	1025035	0.0173	2.8807

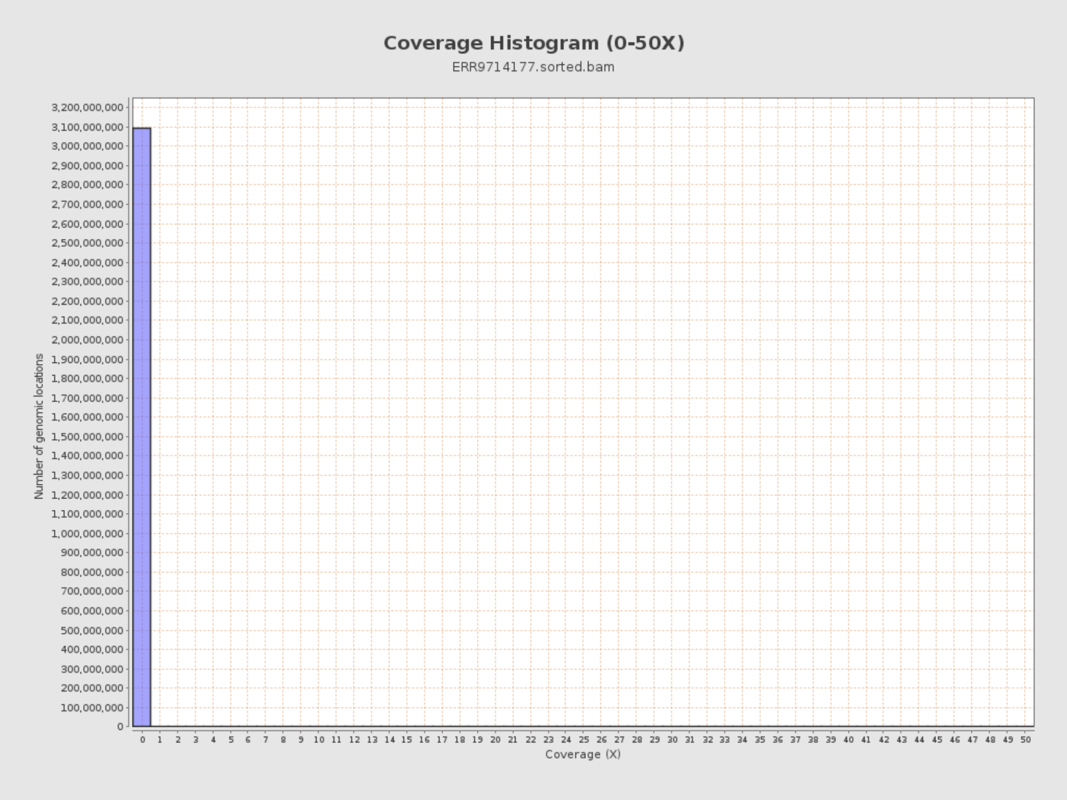
3. Results : Coverage across reference



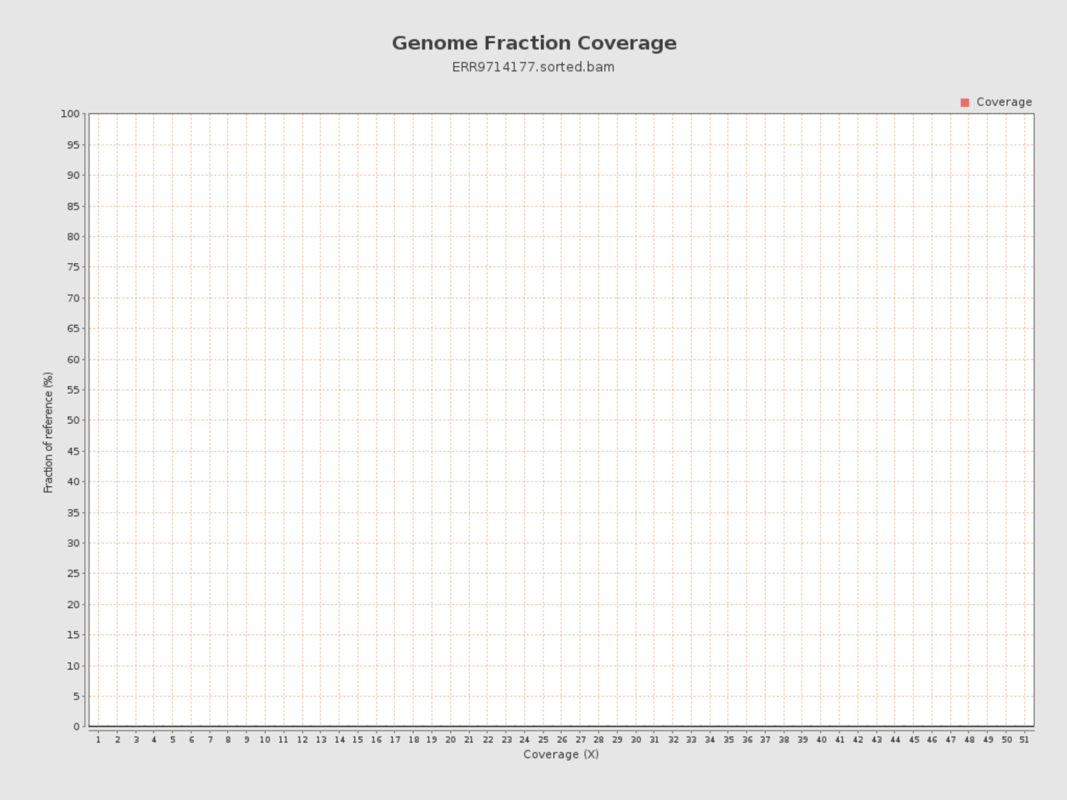
4. Results : Coverage Histogram



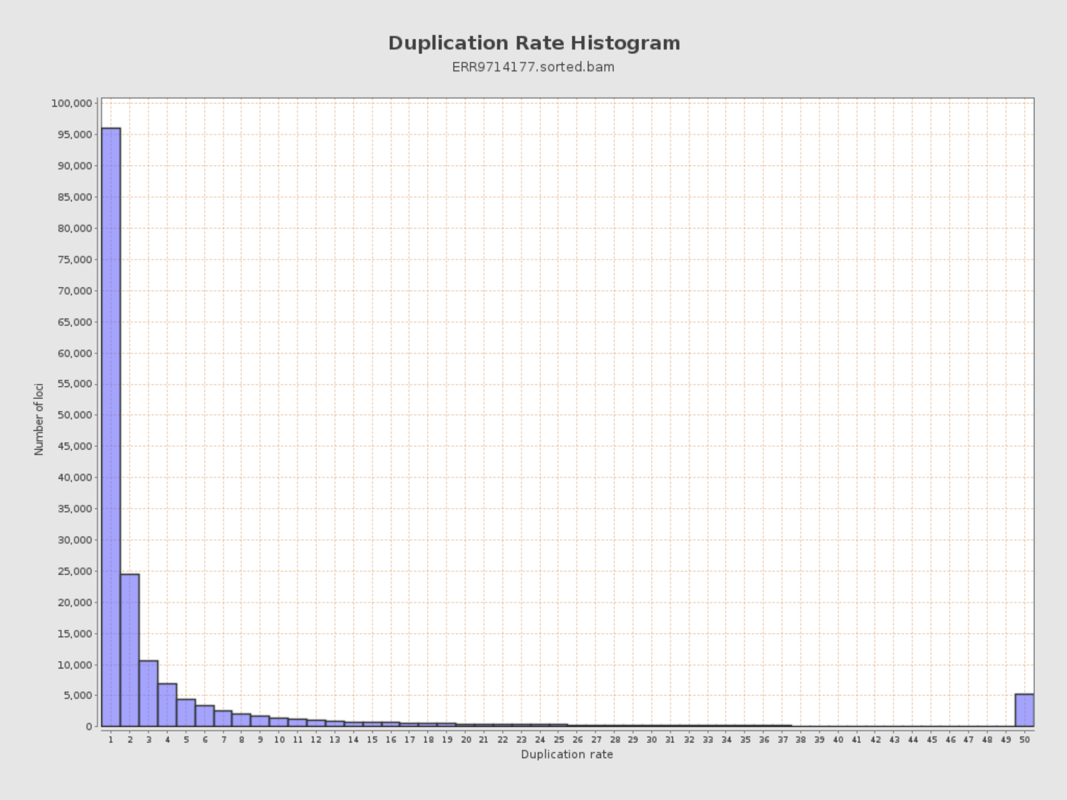
5. Results : Coverage Histogram (0-50X)



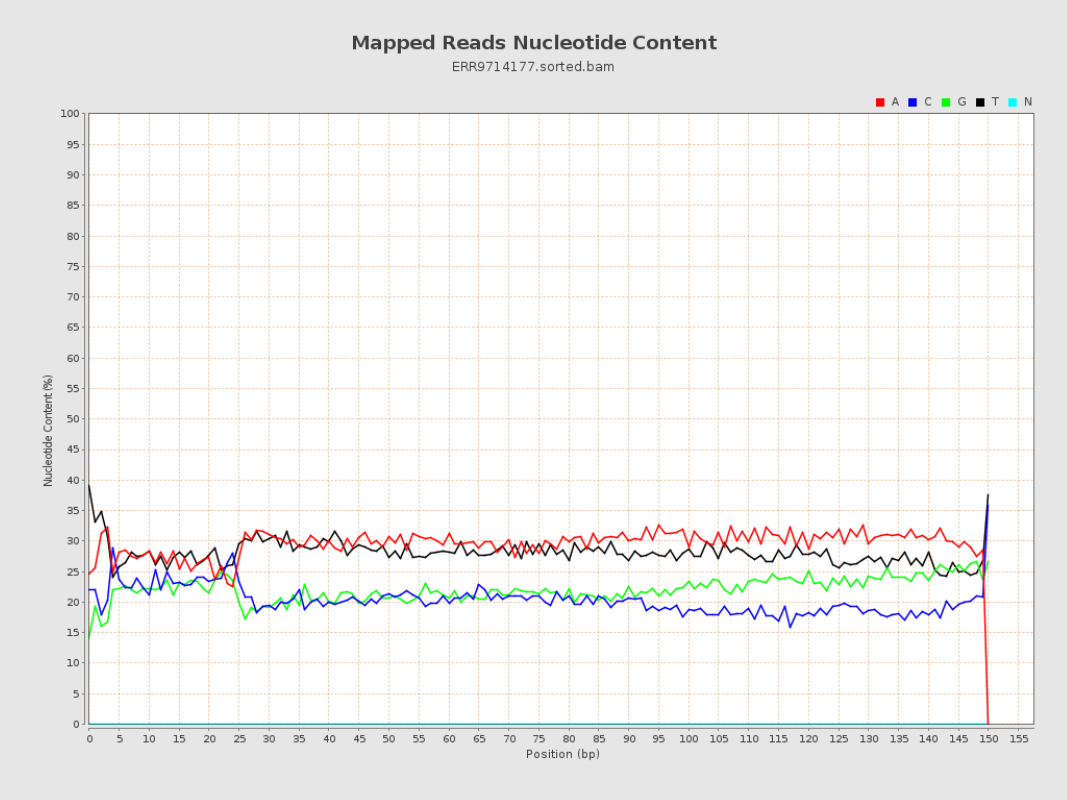
6. Results : Genome Fraction Coverage



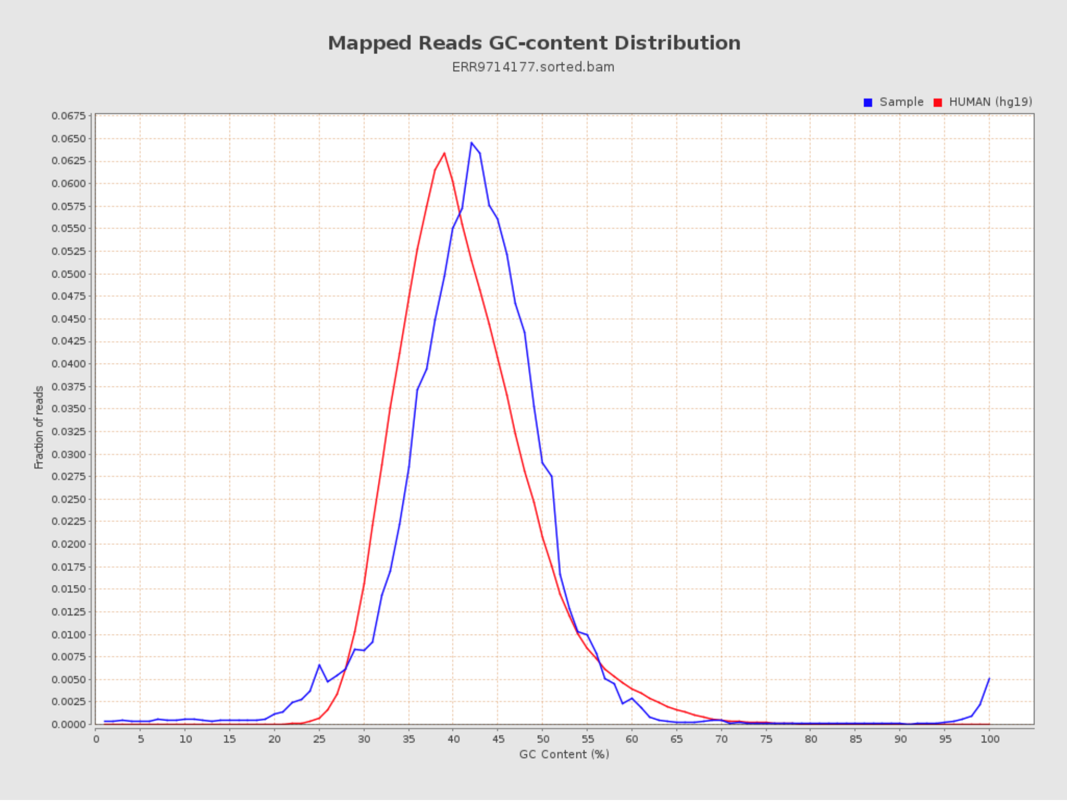
7. Results : Duplication Rate Histogram



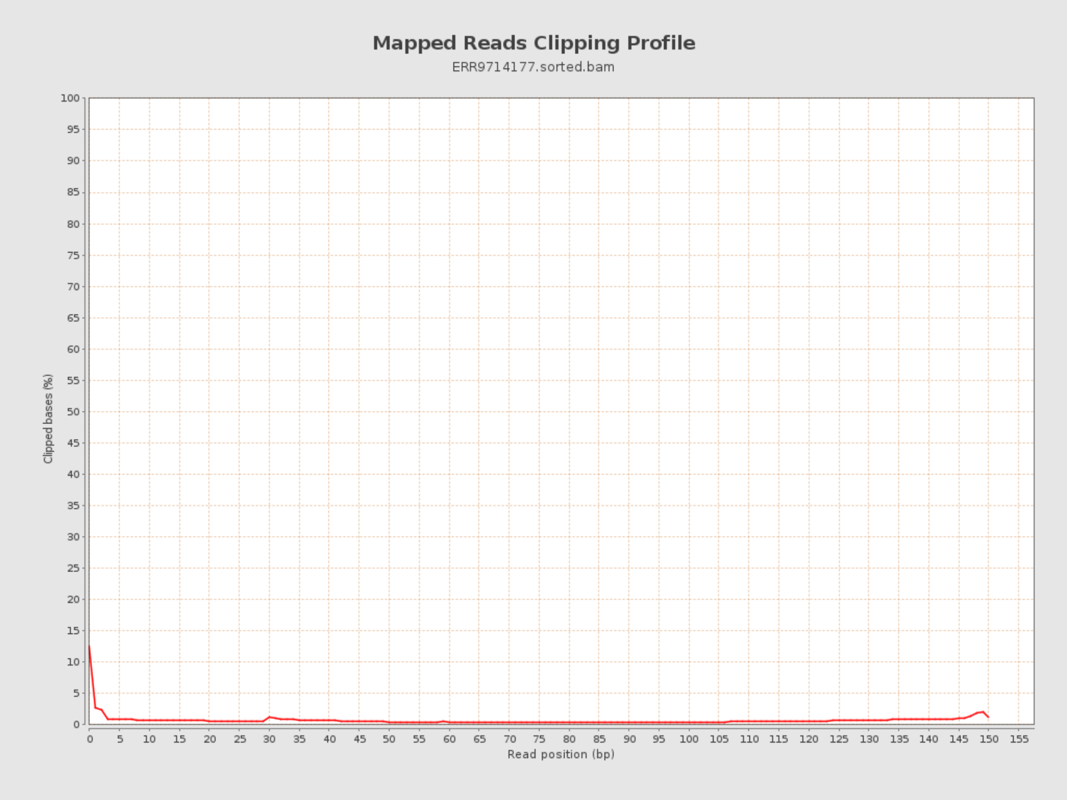
8. Results : Mapped Reads Nucleotide Content



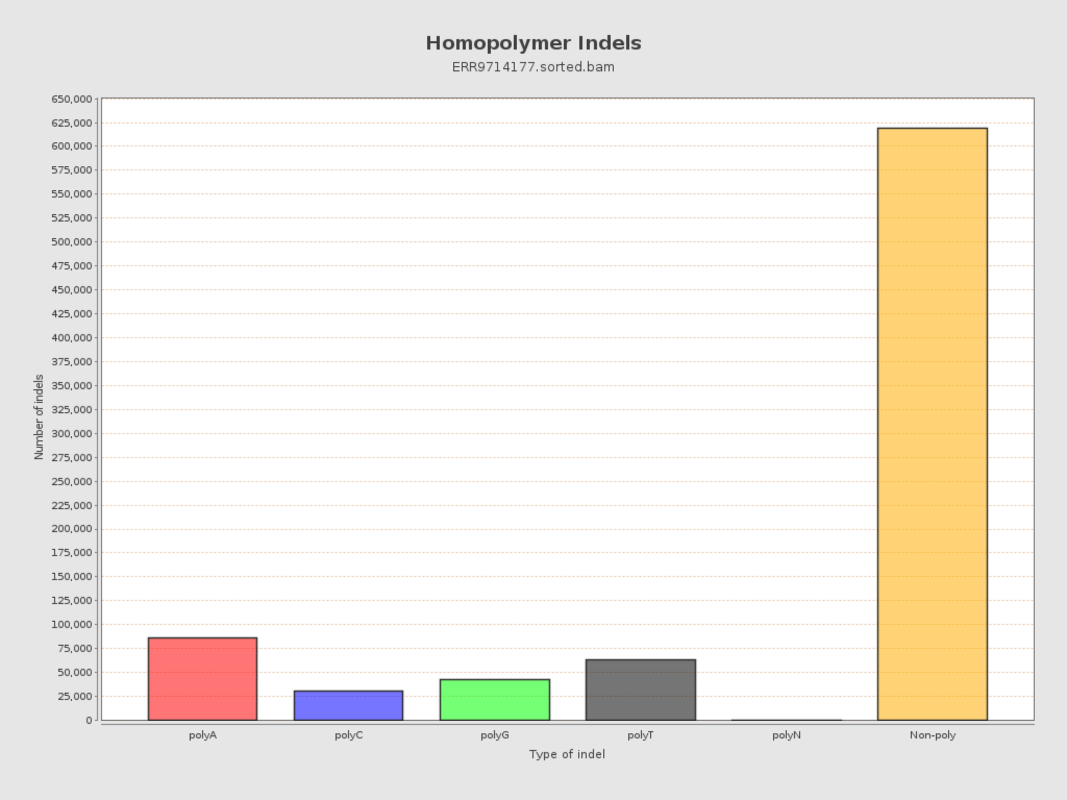
9. Results : Mapped Reads GC-content Distribution



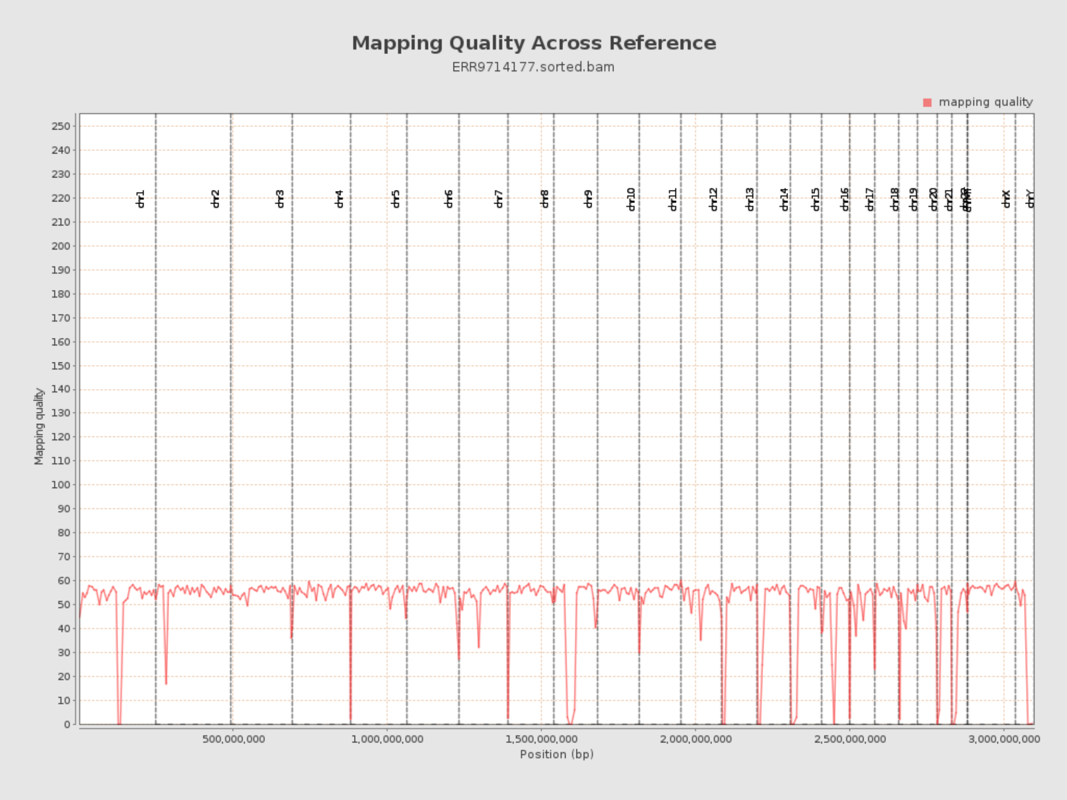
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram