Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:43:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714129.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_ERR9714129 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:43:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	676,534
Mapped reads	500,400 / 73.97%
Unmapped reads	176,134 / 26.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,379 / 2.13%
Read min/max/mean length	30 / 151 / 125.92
Duplicated reads (estimated)	439,384 / 64.95%
Duplication rate	44.12%
Clipped reads	461,372 / 68.2%

2.2. ACGT Content

Number/percentage of A's	17,202,039 / 27.14%
Number/percentage of C's	13,015,476 / 20.53%
Number/percentage of T's	16,377,452 / 25.84%
Number/percentage of G's	16,794,883 / 26.49%
Number/percentage of N's	458 / 0%
GC Percentage	47.03%

2.3. Coverage

Mean	0.021

Standard Deviation	5.7836

2.4. Mapping Quality

Mean Mapping Quality	51.46

2.5. Mismatches and indels

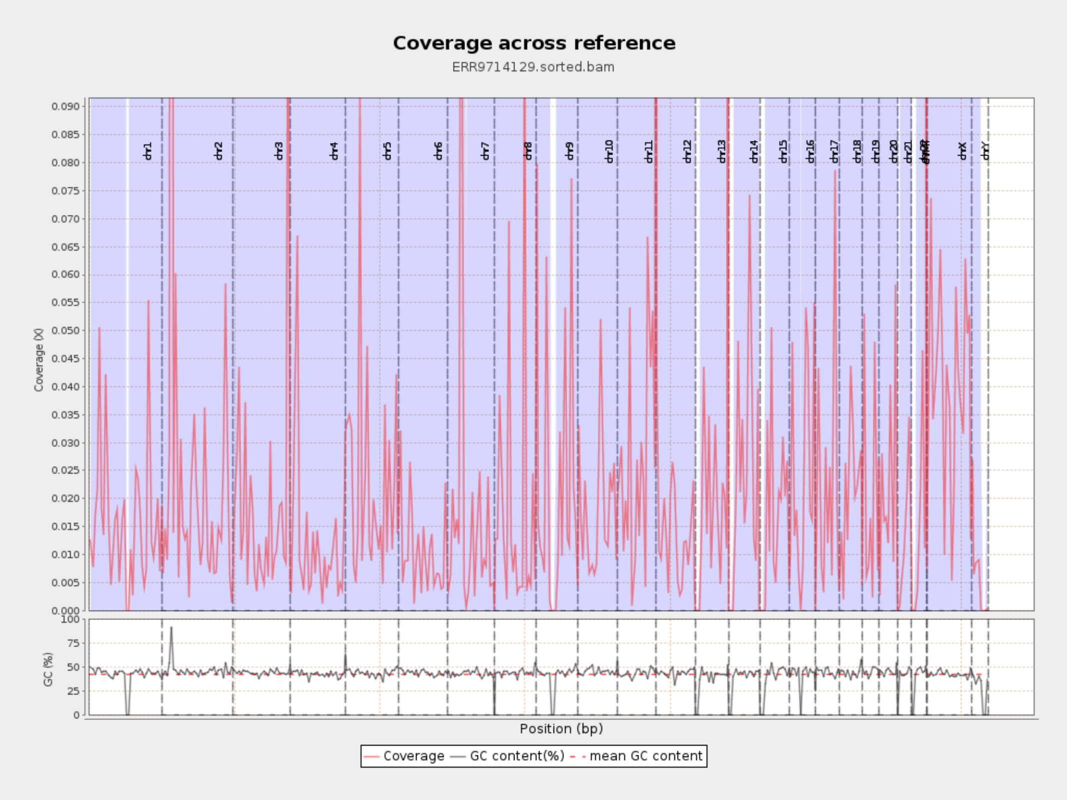
General error rate	4.7%
Mismatches	2,745,990
Insertions	74,984
Mapped reads with at least one insertion	14.33%
Deletions	247,935
Mapped reads with at least one deletion	45.28%
Homopolymer indels	31.98%

2.6. Chromosome stats

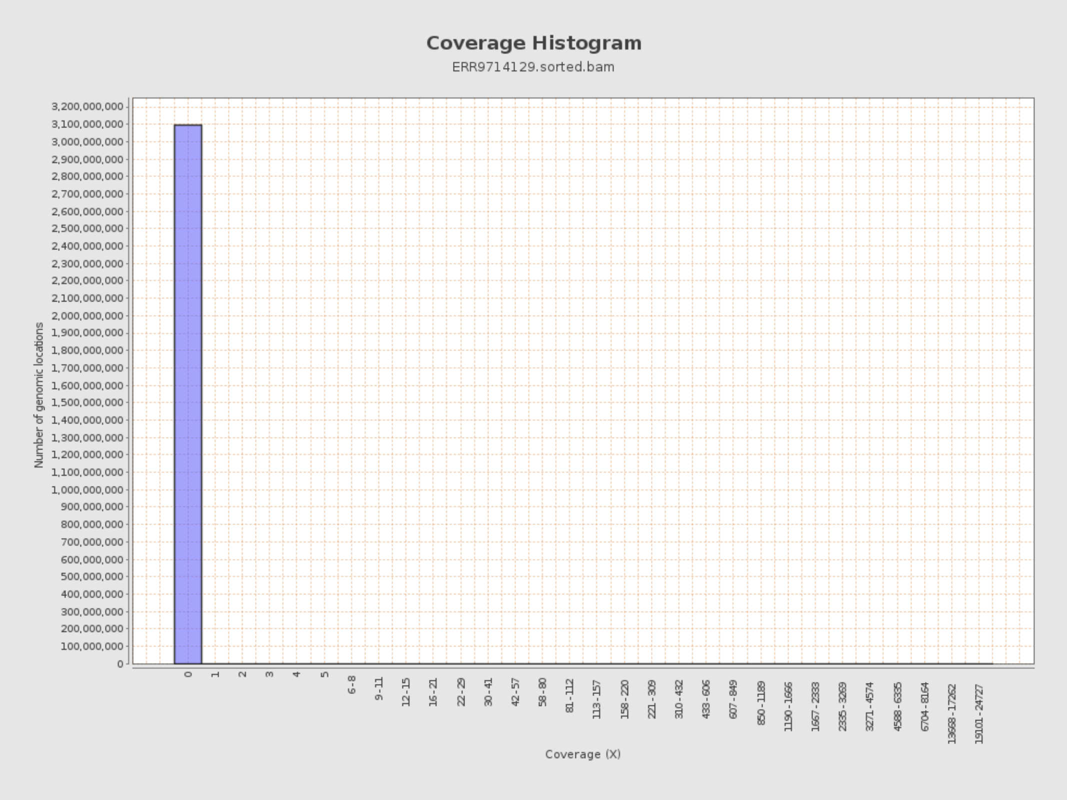
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3957541	0.0159	2.2899
chr2	243199373	8341963	0.0343	15.5605
chr3	198022430	3833713	0.0194	4.2042
chr4	191154276	2400096	0.0126	2.0699
chr5	180915260	4241184	0.0234	4.8556
chr6	171115067	1855924	0.0108	1.6084
chr7	159138663	2785264	0.0175	7.4698

chr8	146364022	2867456	0.0196	5.3294
chr9	141213431	2807209	0.0199	3.8744
chr10	135534747	2564068	0.0189	2.5908
chr11	135006516	3772070	0.0279	4.8334
chr12	133851895	1906869	0.0142	1.8603
chr13	115169878	2268760	0.0197	3.9848
chr14	107349540	2634368	0.0245	4.9331
chr15	102531392	1780851	0.0174	2.4221
chr16	90354753	2240865	0.0248	4.2845
chr17	81195210	1846319	0.0227	5.1636
chr18	78077248	1703109	0.0218	3.1519
chr19	59128983	1159091	0.0196	2.9231
chr20	63025520	1466984	0.0233	3.8299
chr21	48129895	619124	0.0129	2.0527
chr22	51304566	681626	0.0133	2.688
chrMT	16571	536852	32.3971	248.3604
chrX	155270560	6292597	0.0405	3.4838
chrY	59373566	330929	0.0056	1.1559

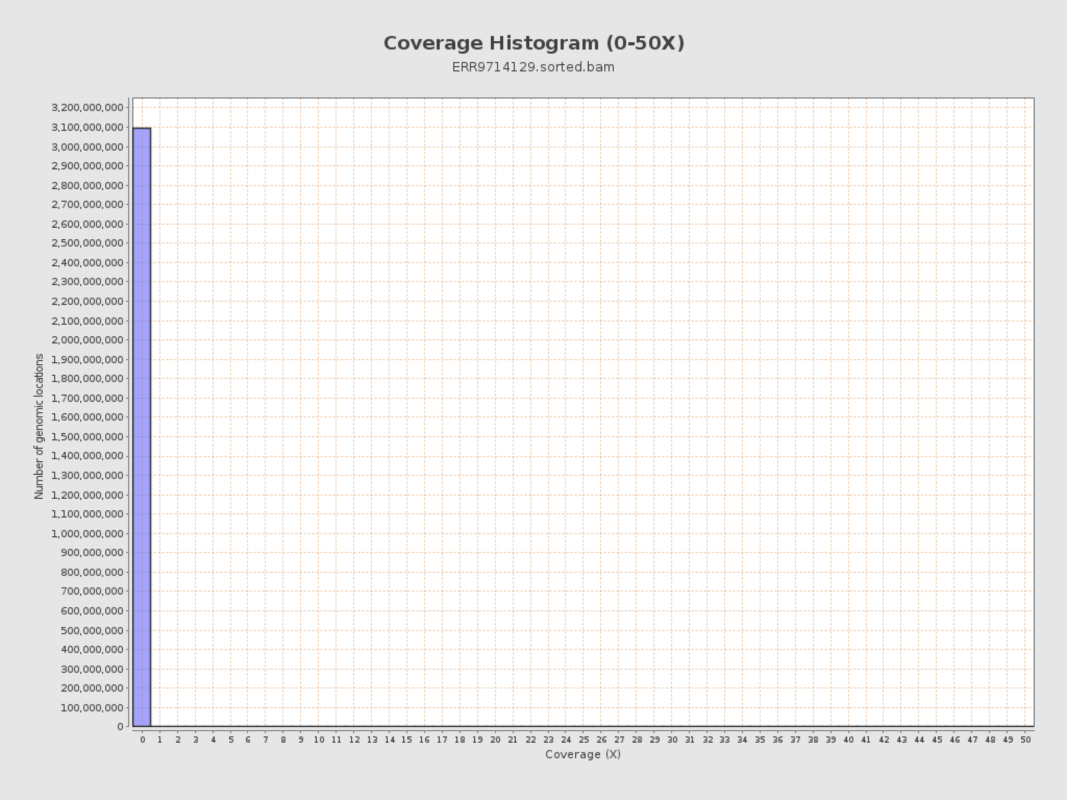
3. Results : Coverage across reference



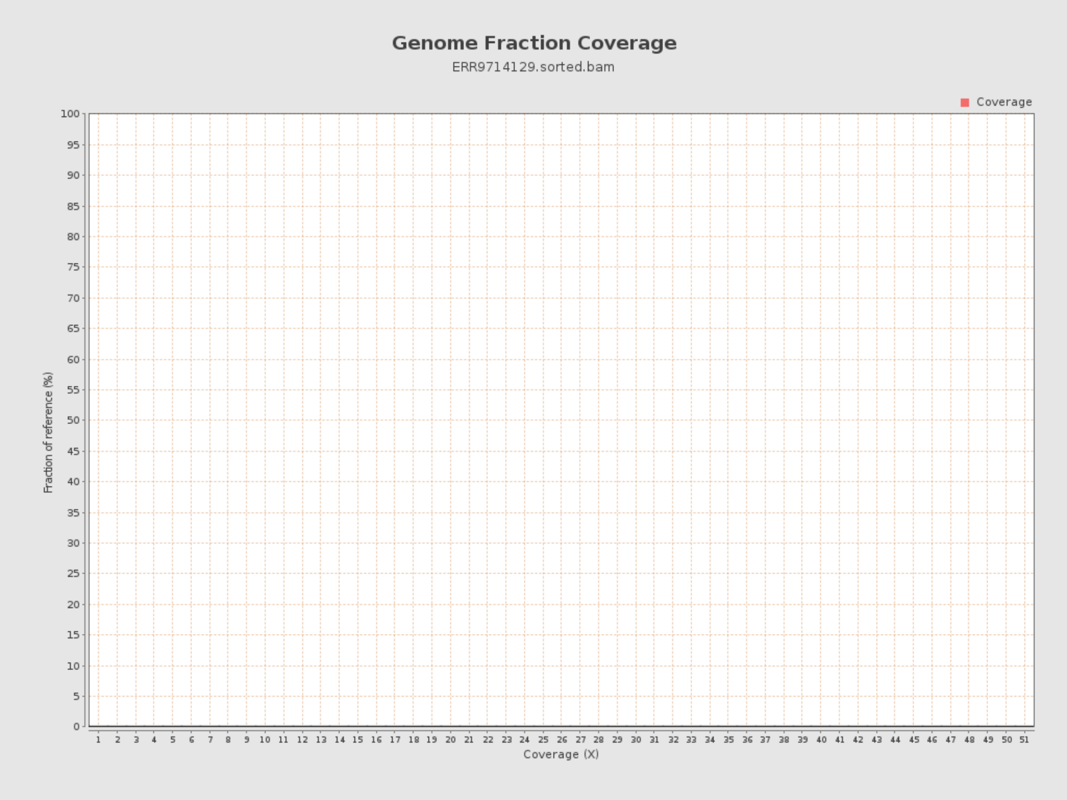
4. Results : Coverage Histogram



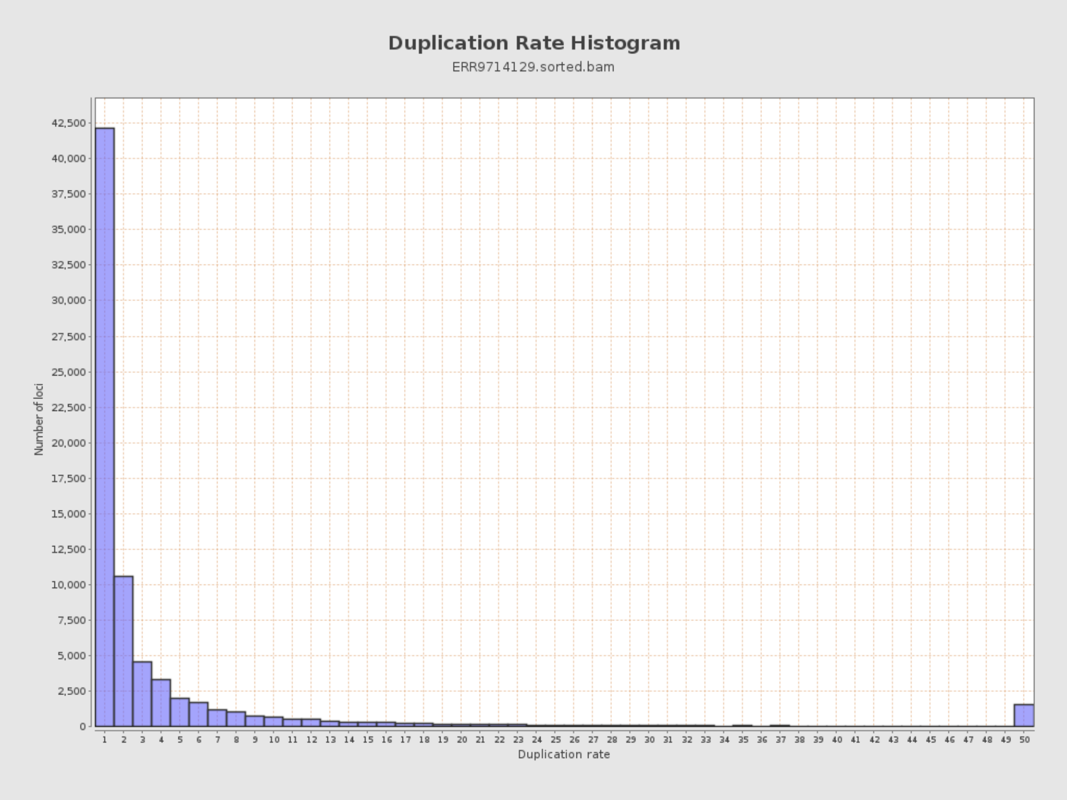
5. Results : Coverage Histogram (0-50X)



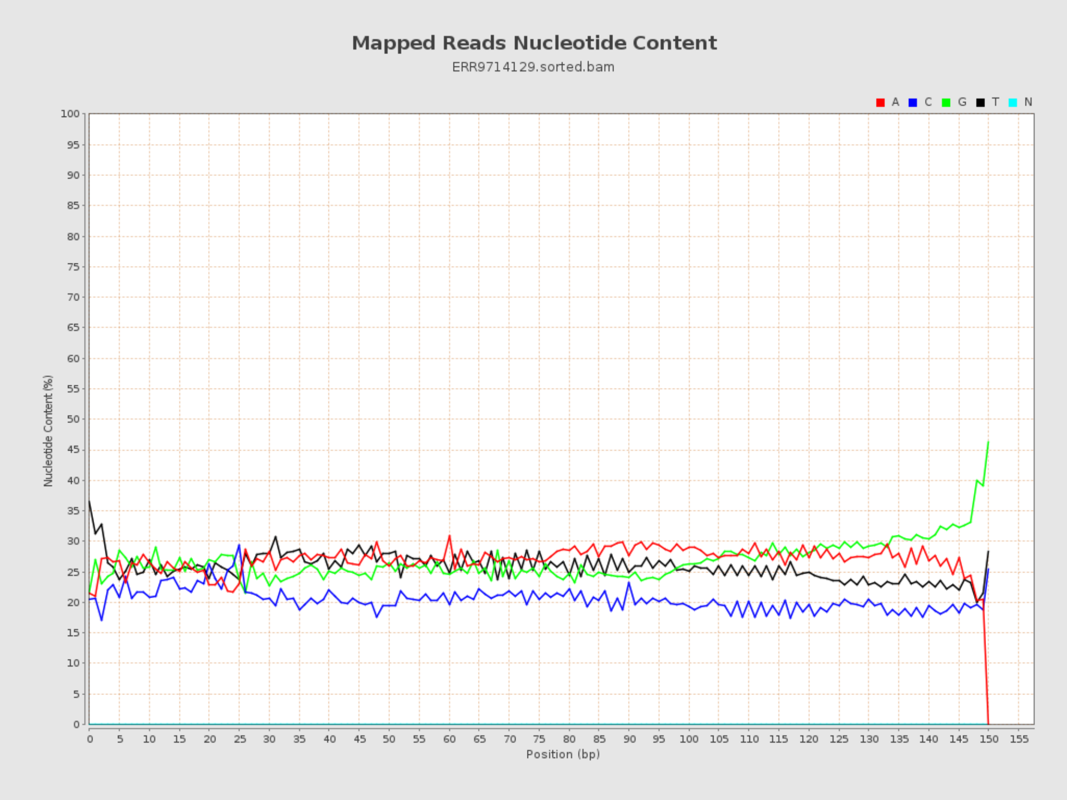
6. Results : Genome Fraction Coverage



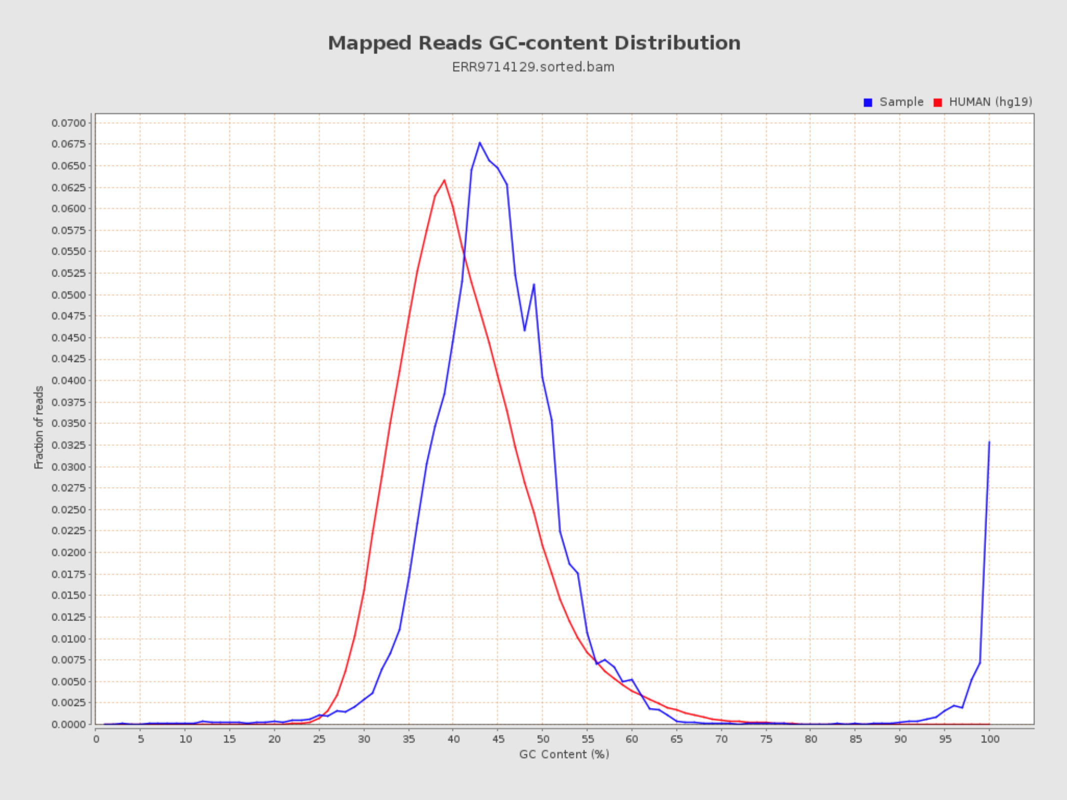
7. Results : Duplication Rate Histogram



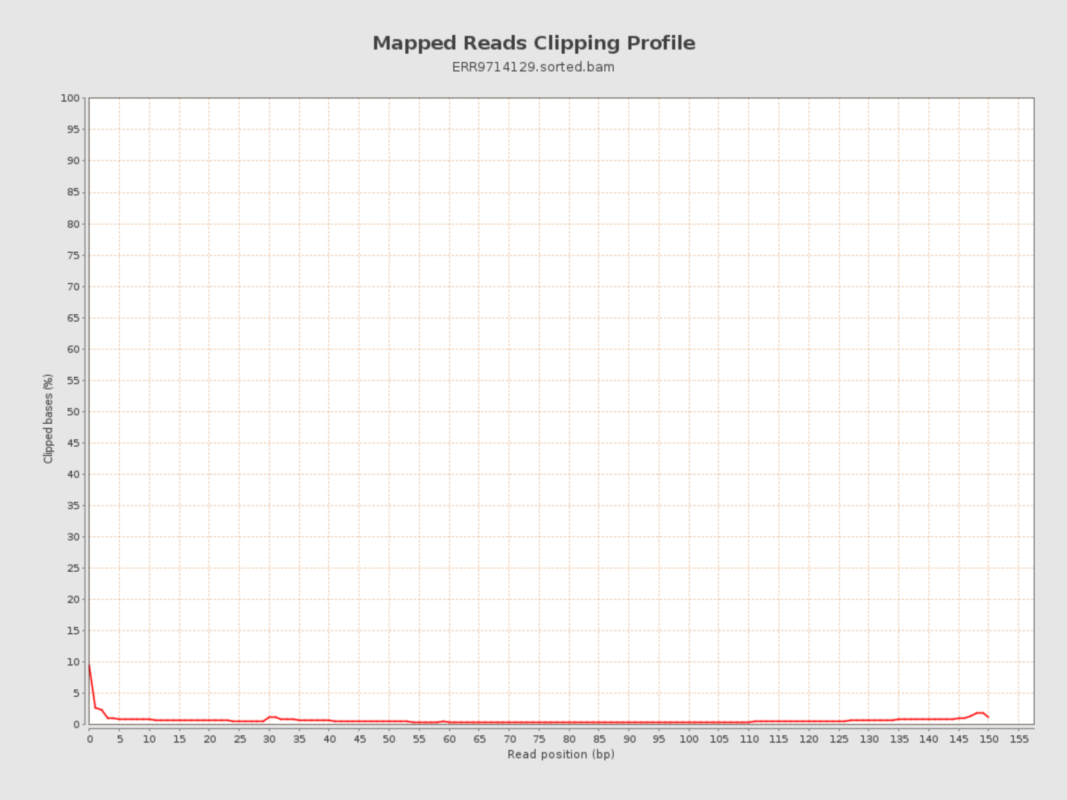
8. Results : Mapped Reads Nucleotide Content



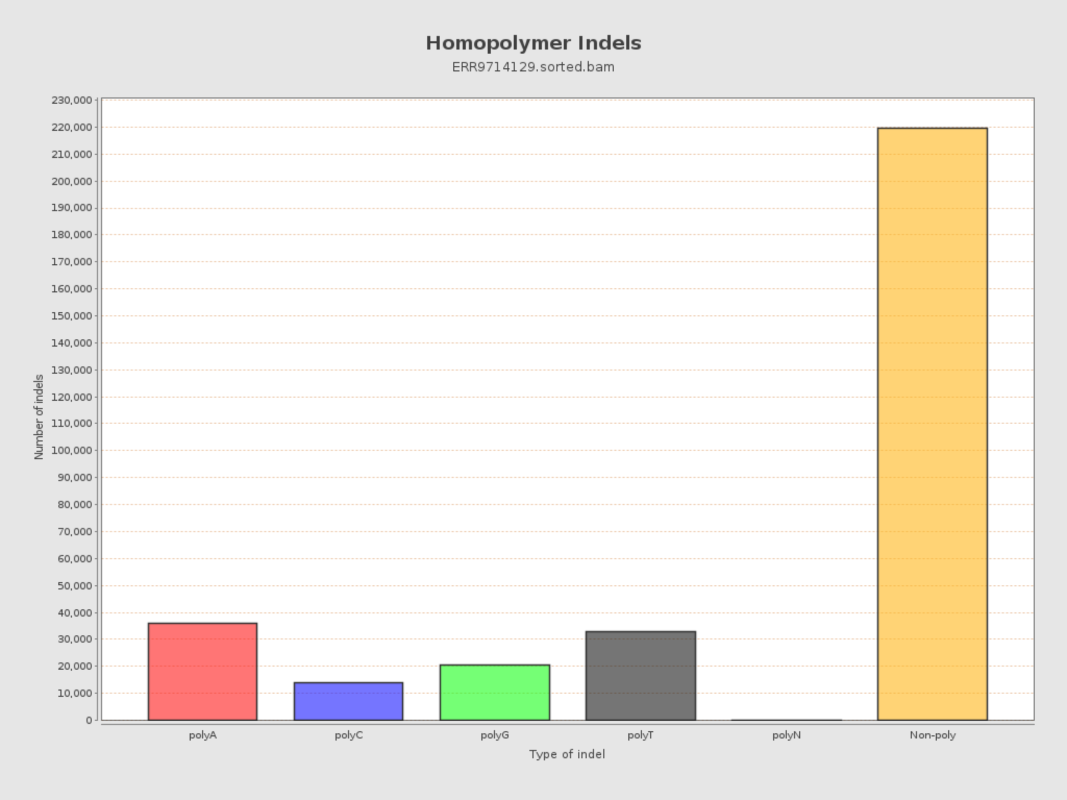
9. Results : Mapped Reads GC-content Distribution



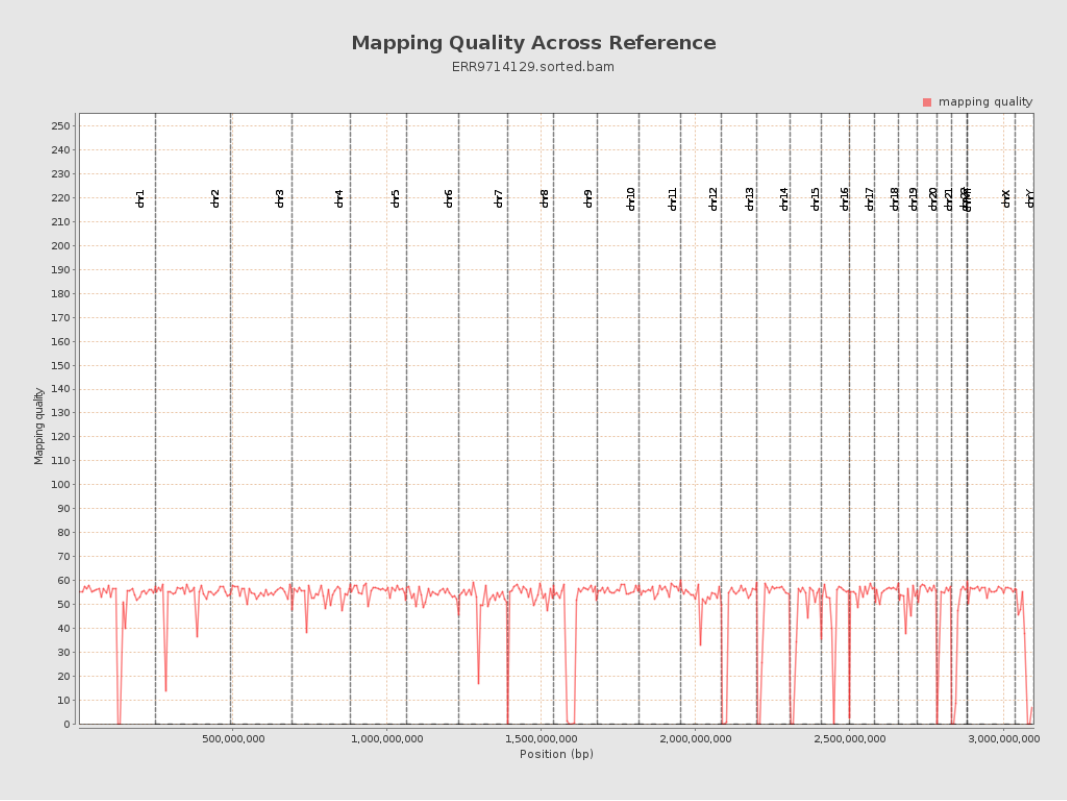
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram