Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:23:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714101.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_ERR9714101 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:23:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,220
Mapped reads	3,592 / 14.24%
Unmapped reads	21,628 / 85.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	150 / 0.59%
Read min/max/mean length	30 / 151 / 61.74
Duplicated reads (estimated)	2,383 / 9.45%
Duplication rate	39.51%
Clipped reads	3,291 / 13.05%

2.2. ACGT Content

Number/percentage of A's	105,184 / 25.8%
Number/percentage of C's	73,187 / 17.95%
Number/percentage of T's	98,260 / 24.11%
Number/percentage of G's	130,986 / 32.13%
Number/percentage of N's	3 / 0%
GC Percentage	50.09%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0749

2.4. Mapping Quality

Mean Mapping Quality	28.44

2.5. Mismatches and indels

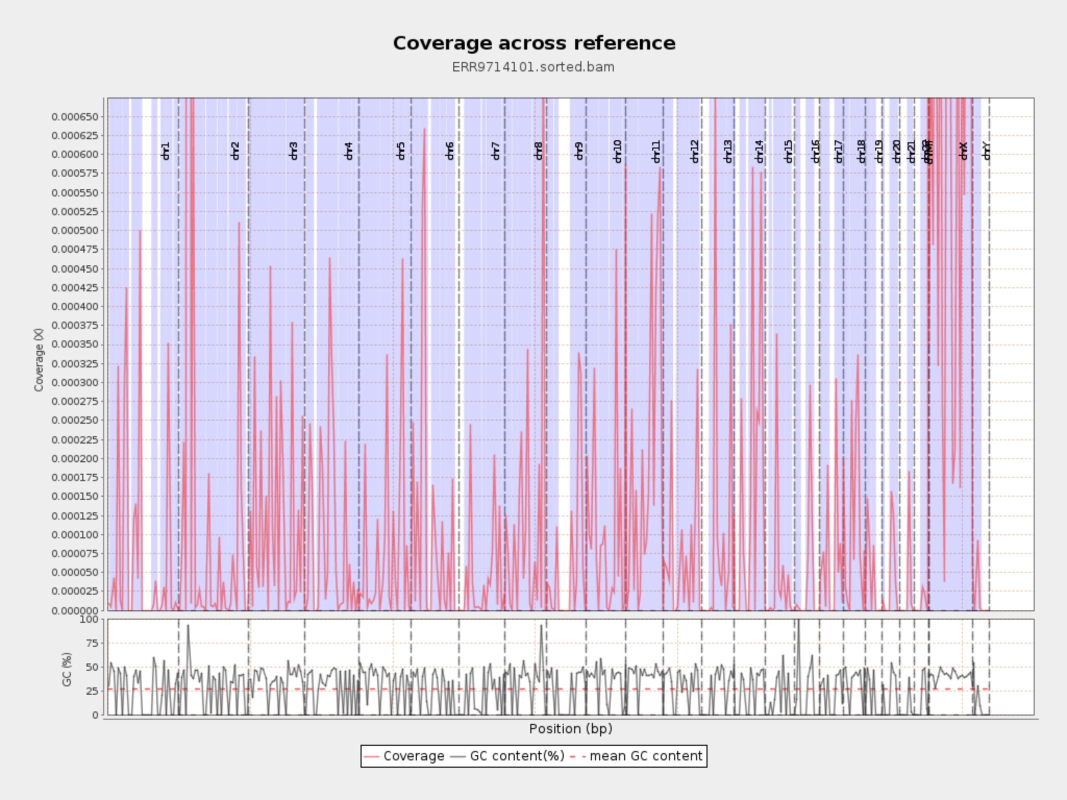
General error rate	4.13%
Mismatches	16,079
Insertions	275
Mapped reads with at least one insertion	7.1%
Deletions	1,372
Mapped reads with at least one deletion	36.8%
Homopolymer indels	33.03%

2.6. Chromosome stats

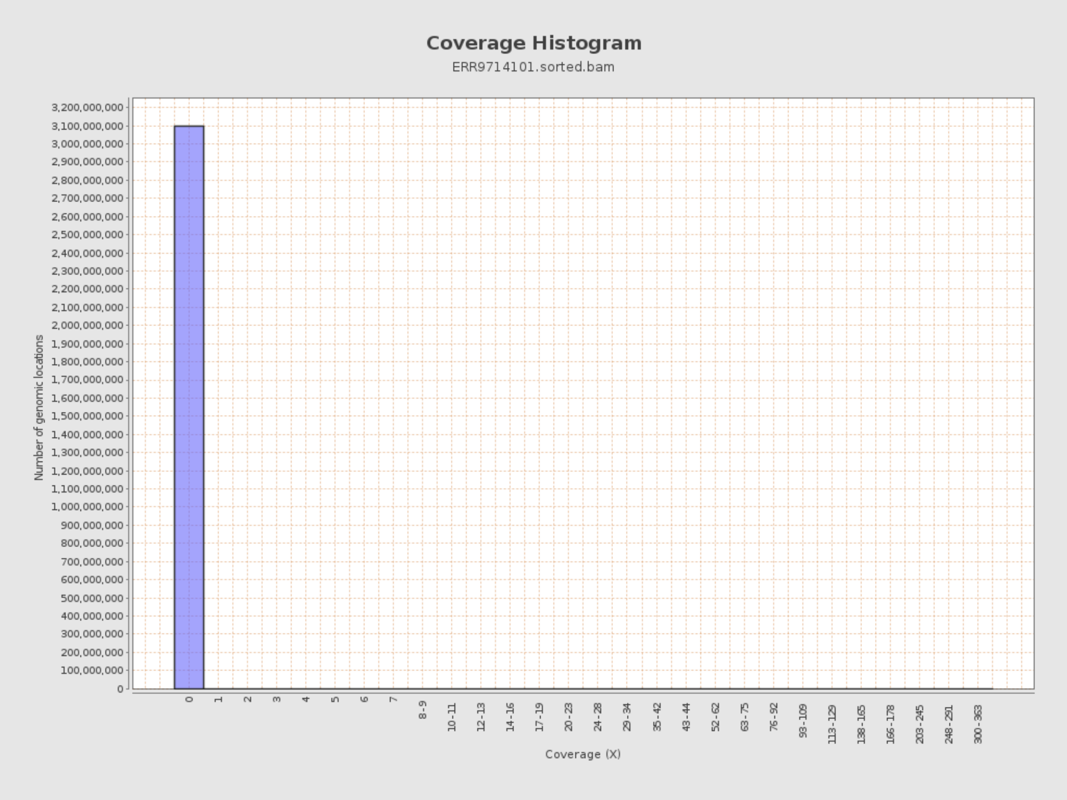
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18408	0.0001	0.0318
chr2	243199373	81051	0.0003	0.2338
chr3	198022430	24918	0.0001	0.0378
chr4	191154276	18397	0.0001	0.0316
chr5	180915260	14672	0.0001	0.0281
chr6	171115067	17964	0.0001	0.0419
chr7	159138663	6997	0	0.0179

chr8	146364022	17705	0.0001	0.0357
chr9	141213431	8207	0.0001	0.0207
chr10	135534747	13957	0.0001	0.0291
chr11	135006516	27416	0.0002	0.0501
chr12	133851895	9866	0.0001	0.0232
chr13	115169878	11224	0.0001	0.0463
chr14	107349540	18155	0.0002	0.0505
chr15	102531392	4097	0	0.0198
chr16	90354753	3801	0	0.0209
chr17	81195210	5945	0.0001	0.0258
chr18	78077248	9198	0.0001	0.033
chr19	59128983	2500	0	0.0146
chr20	63025520	2562	0	0.012
chr21	48129895	1489	0	0.0154
chr22	51304566	450	0	0.0038
chrMT	16571	1494	0.0902	0.8371
chrX	155270560	95907	0.0006	0.0906
chrY	59373566	837	0	0.0066

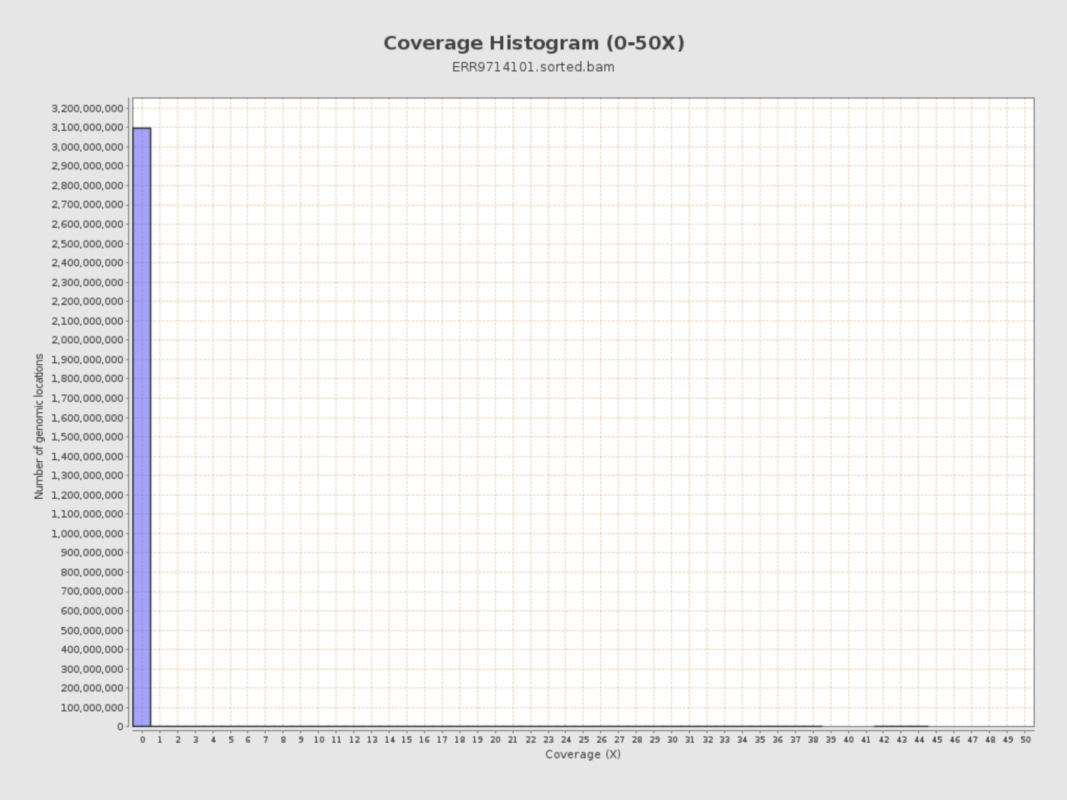
3. Results : Coverage across reference



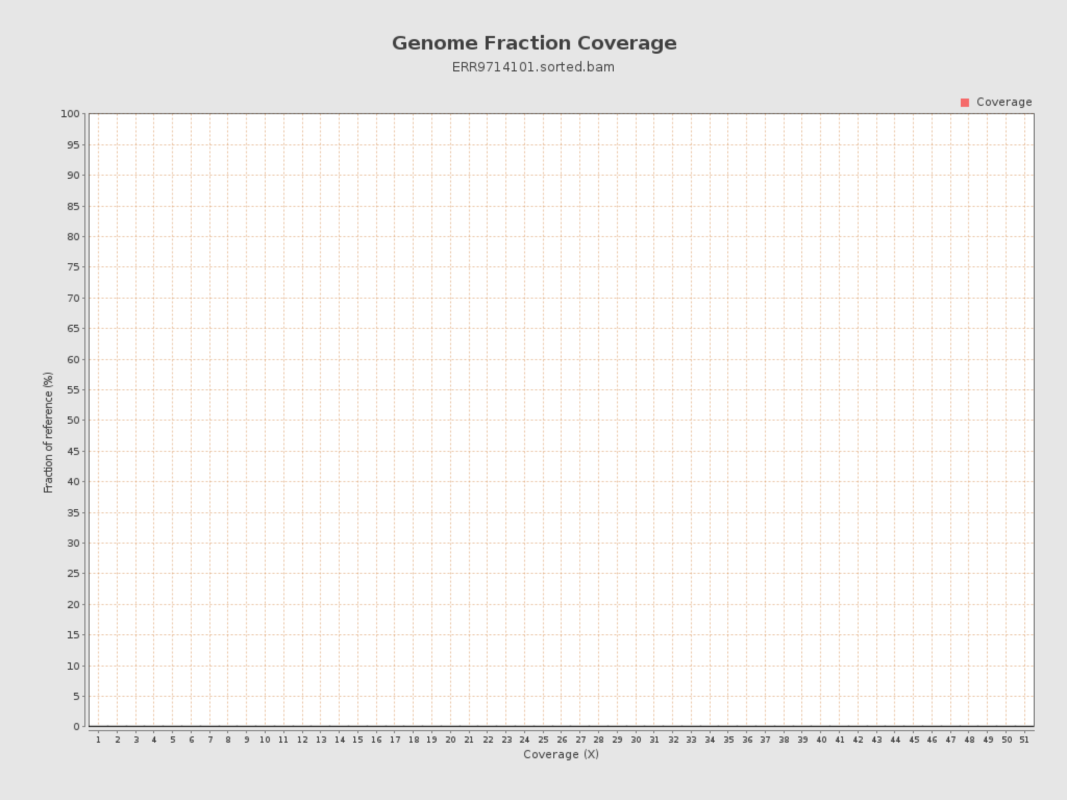
4. Results : Coverage Histogram



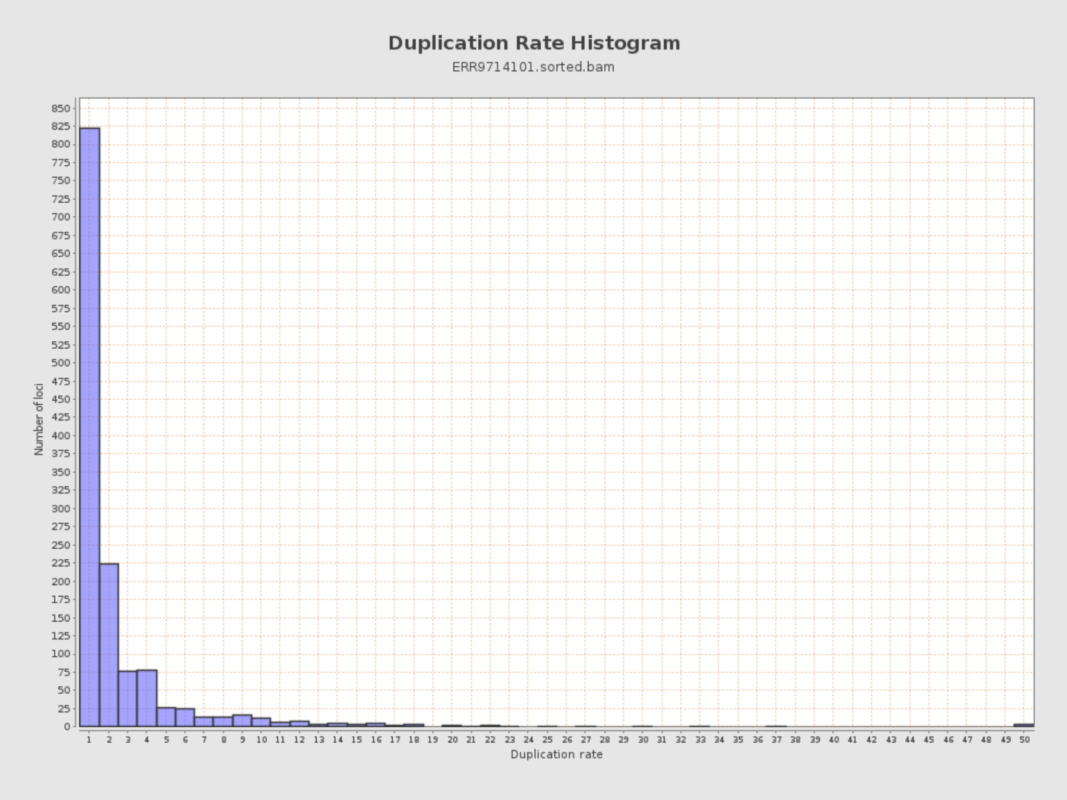
5. Results : Coverage Histogram (0-50X)



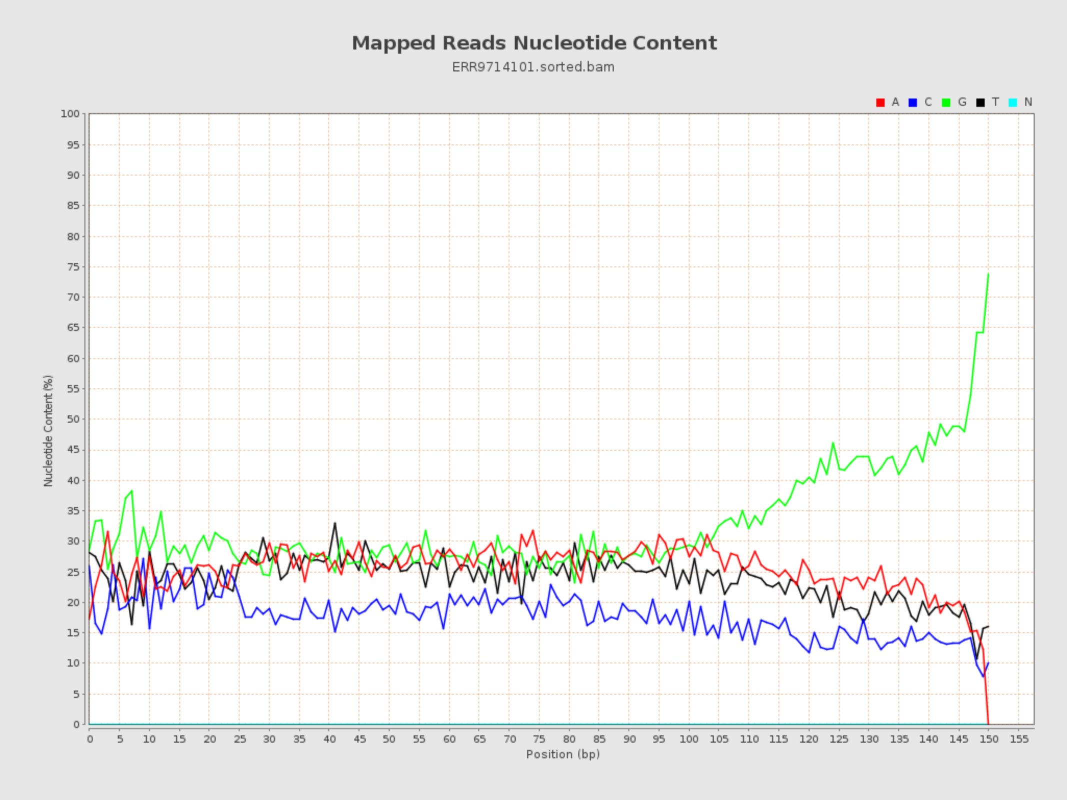
6. Results : Genome Fraction Coverage



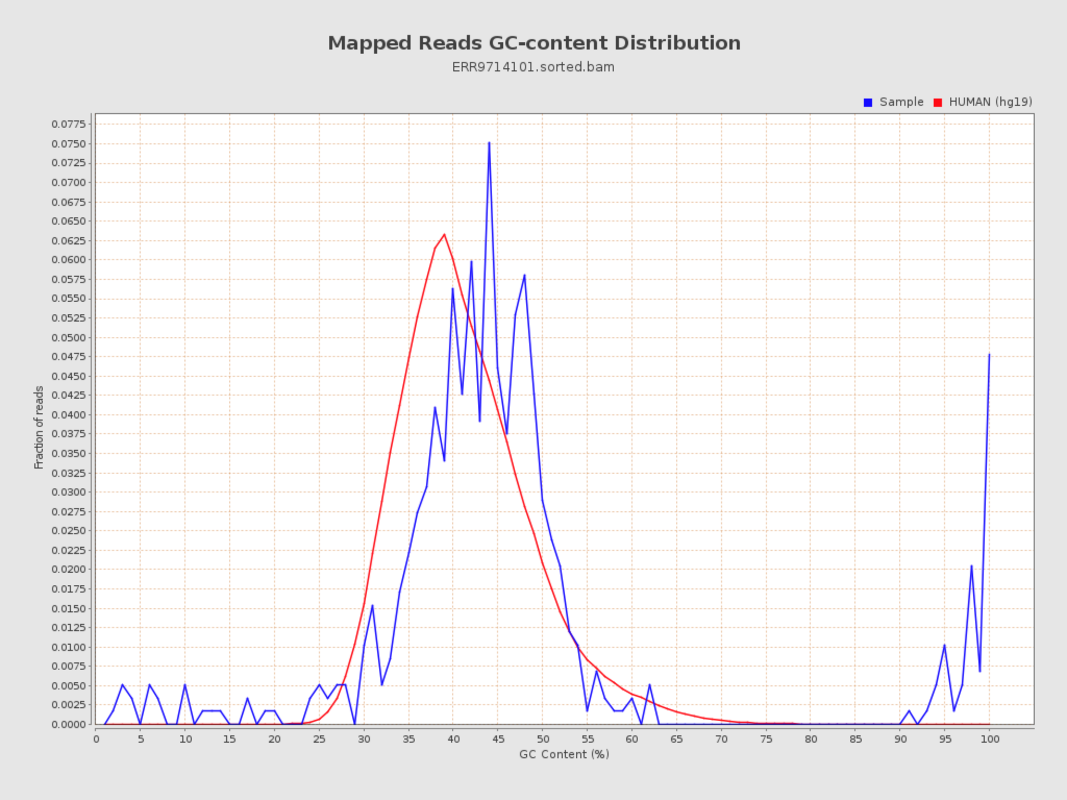
7. Results : Duplication Rate Histogram



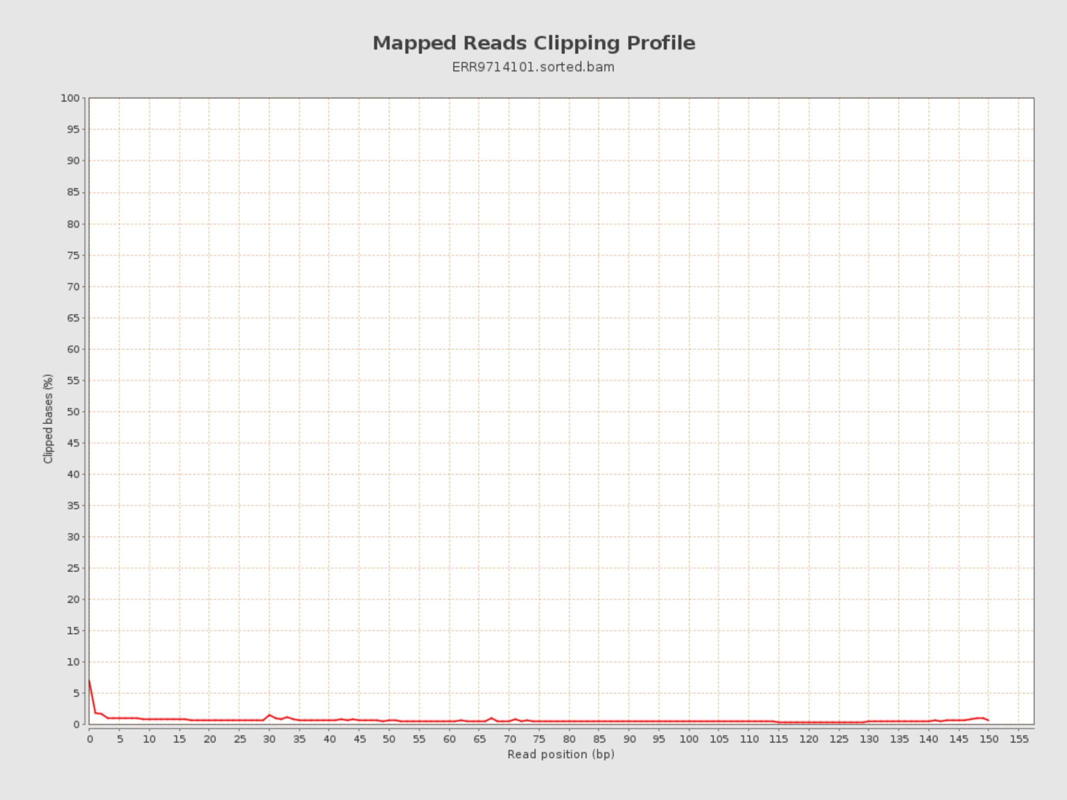
8. Results : Mapped Reads Nucleotide Content



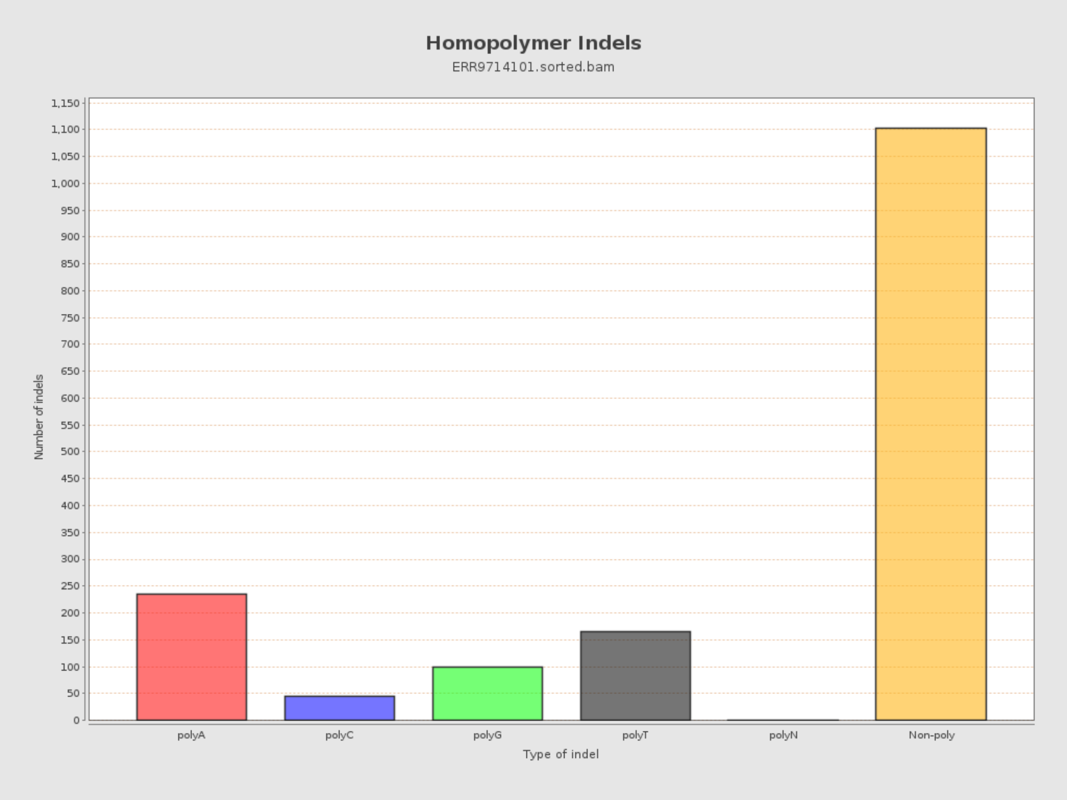
9. Results : Mapped Reads GC-content Distribution



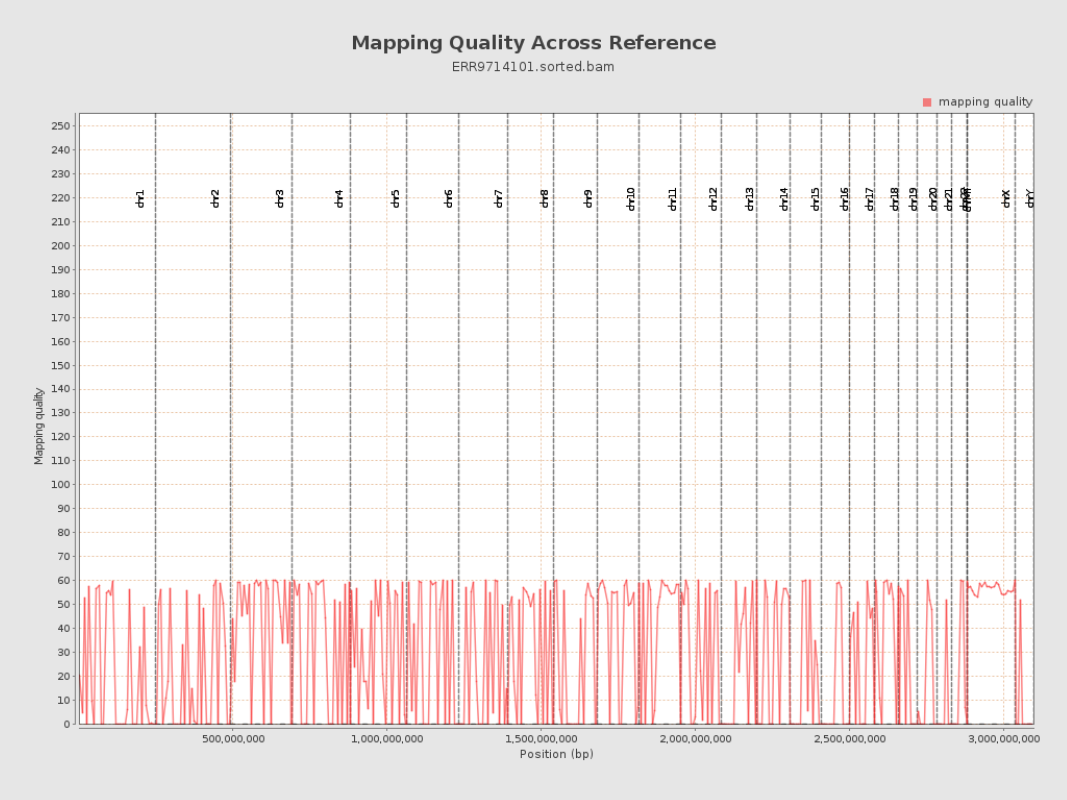
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram