Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:24:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714250.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_ERR9714250 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:24:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	389,104
Mapped reads	24,050 / 6.18%
Unmapped reads	365,054 / 93.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	467 / 0.12%
Read min/max/mean length	30 / 151 / 56.07
Duplicated reads (estimated)	21,158 / 5.44%
Duplication rate	37.72%
Clipped reads	19,452 / 5%

2.2. ACGT Content

Number/percentage of A's	370,061 / 16.3%
Number/percentage of C's	255,718 / 11.27%
Number/percentage of T's	324,664 / 14.3%
Number/percentage of G's	1,319,370 / 58.12%
Number/percentage of N's	89 / 0%
GC Percentage	69.39%

2.3. Coverage

Mean	0.0007

Standard Deviation	1.2588

2.4. Mapping Quality

Mean Mapping Quality	24.92

2.5. Mismatches and indels

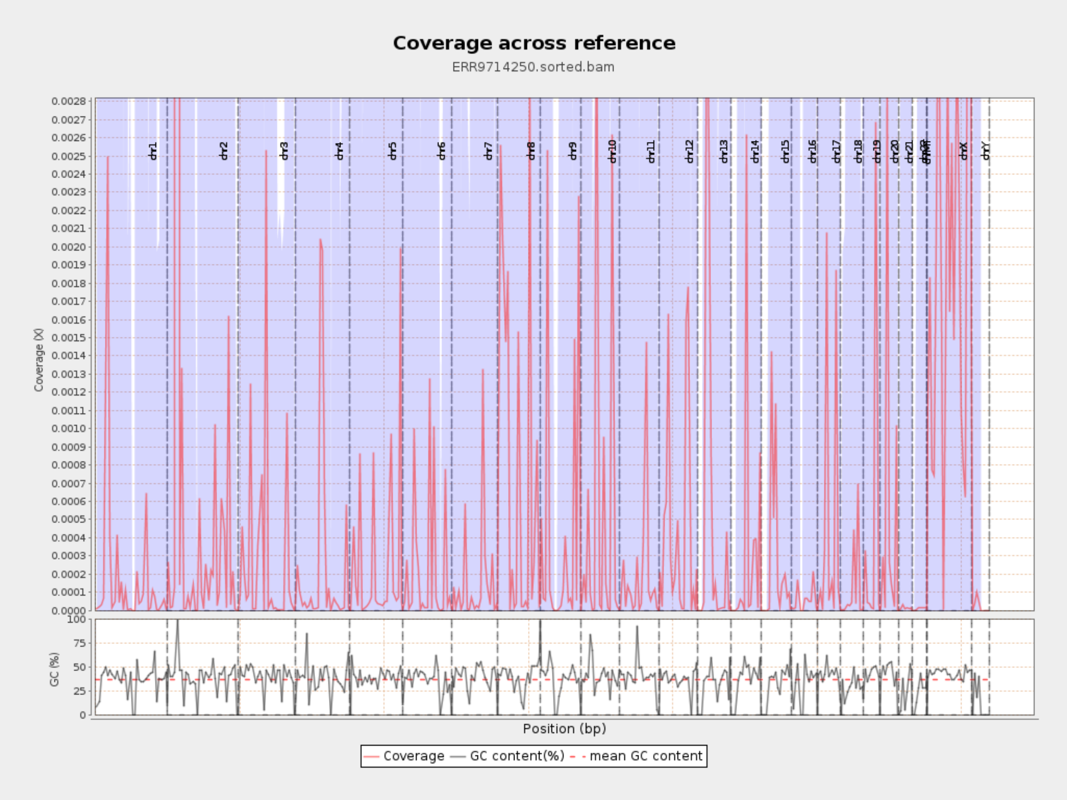
General error rate	3.48%
Mismatches	66,547
Insertions	2,658
Mapped reads with at least one insertion	9%
Deletions	4,381
Mapped reads with at least one deletion	17.4%
Homopolymer indels	34.69%

2.6. Chromosome stats

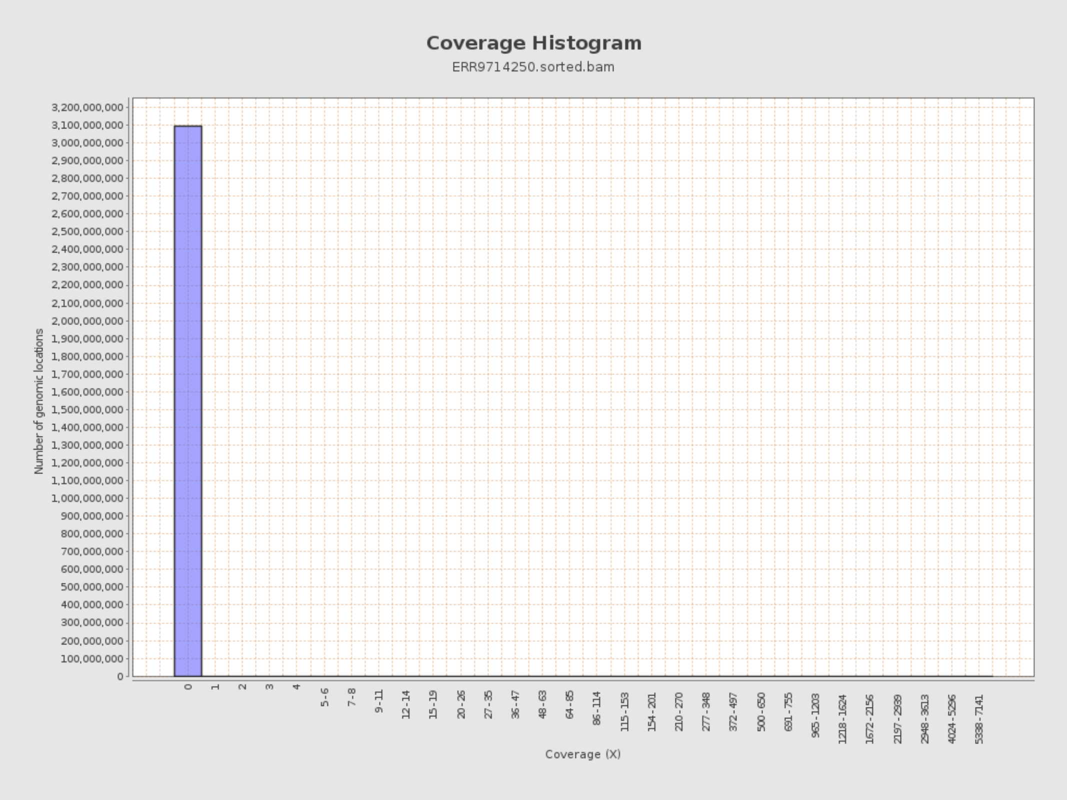
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	50478	0.0002	0.1146
chr2	243199373	1127894	0.0046	4.4567
chr3	198022430	59944	0.0003	0.1415
chr4	191154276	47762	0.0002	0.1319
chr5	180915260	51614	0.0003	0.0948
chr6	171115067	41405	0.0002	0.0902
chr7	159138663	25208	0.0002	0.1412

chr8	146364022	116362	0.0008	0.2396
chr9	141213431	60452	0.0004	0.1677
chr10	135534747	66199	0.0005	0.2018
chr11	135006516	25548	0.0002	0.0869
chr12	133851895	59464	0.0004	0.1402
chr13	115169878	59166	0.0005	0.2508
chr14	107349540	34563	0.0003	0.1537
chr15	102531392	28855	0.0003	0.1141
chr16	90354753	5143	0.0001	0.0191
chr17	81195210	37234	0.0005	0.2147
chr18	78077248	10056	0.0001	0.0539
chr19	59128983	24429	0.0004	0.2125
chr20	63025520	36621	0.0006	0.2326
chr21	48129895	718	0	0.0044
chr22	51304566	564	0	0.0035
chrMT	16571	0	0	0
chrX	155270560	323287	0.0021	0.316
chrY	59373566	1475	0	0.0123

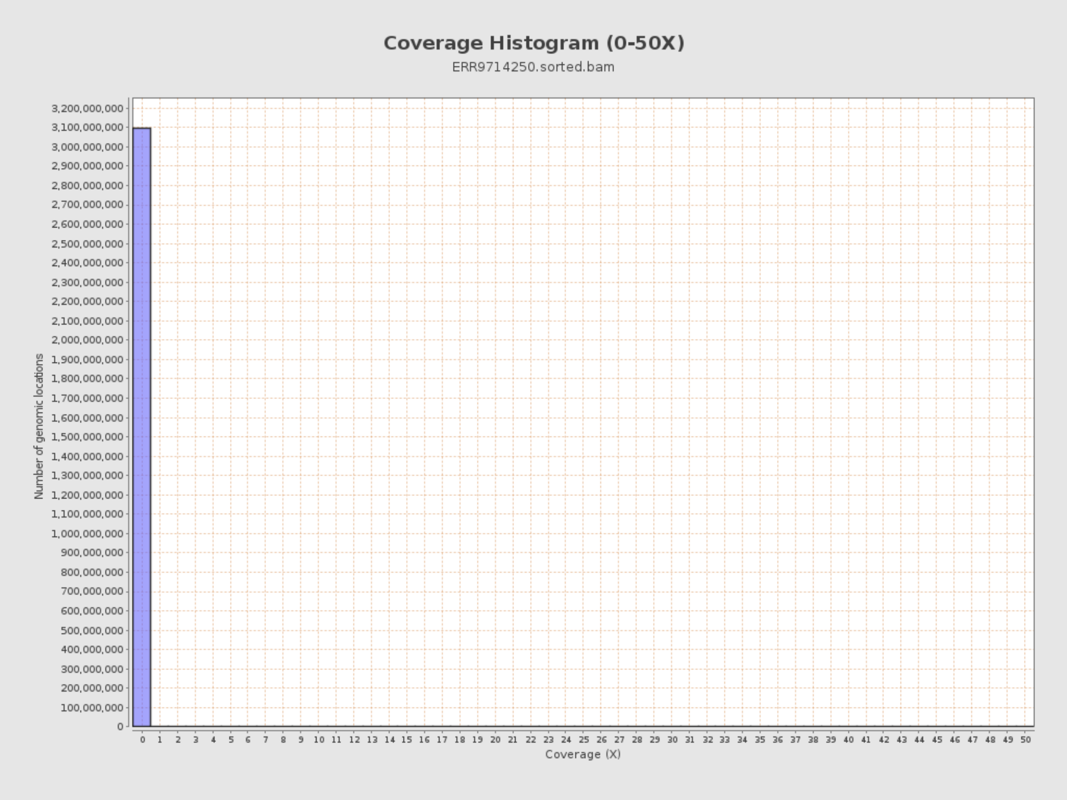
3. Results : Coverage across reference



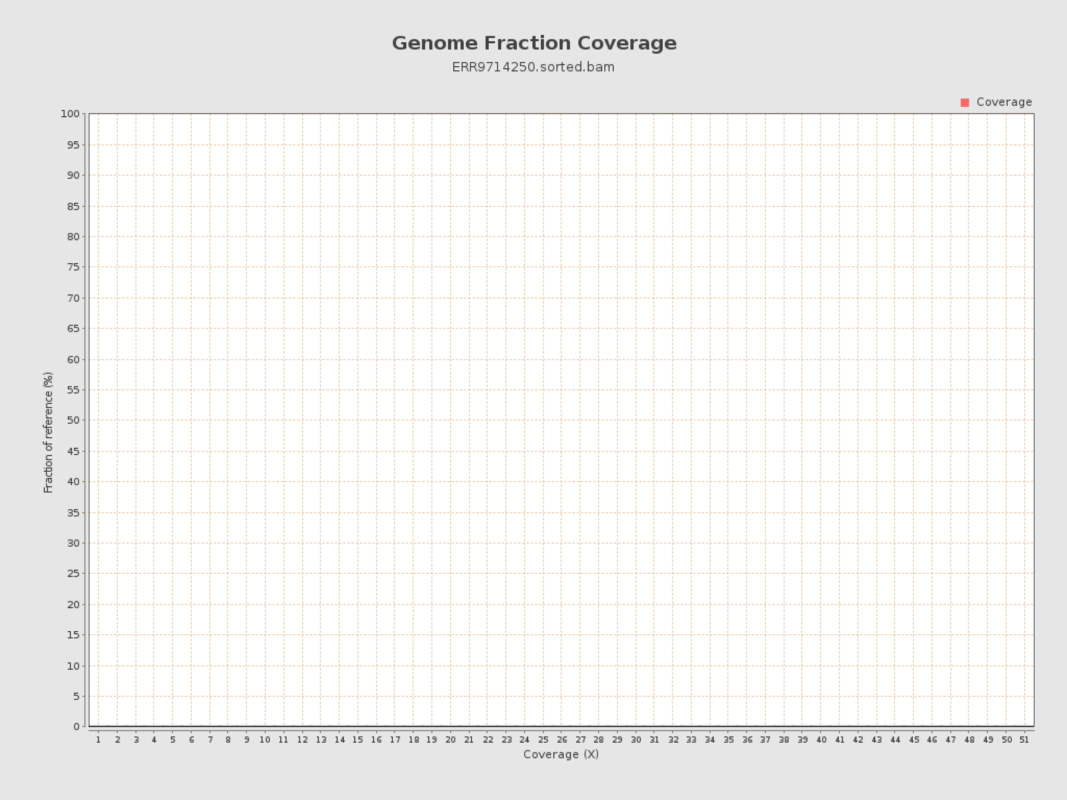
4. Results : Coverage Histogram



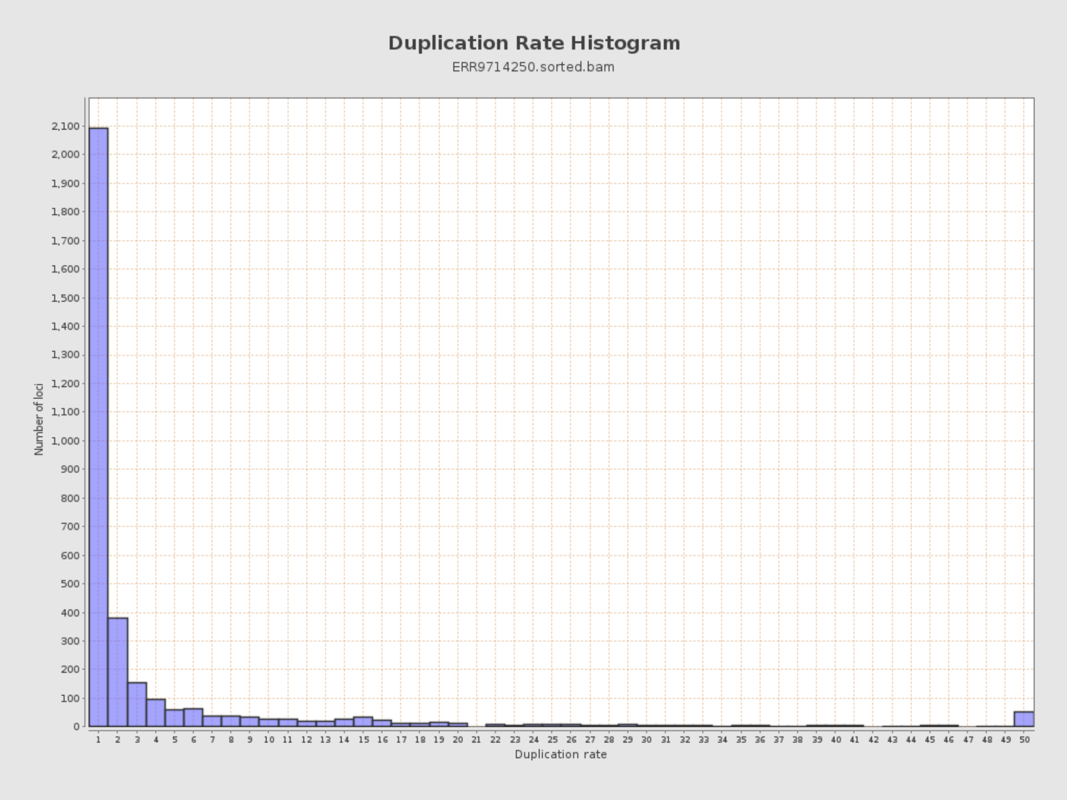
5. Results : Coverage Histogram (0-50X)



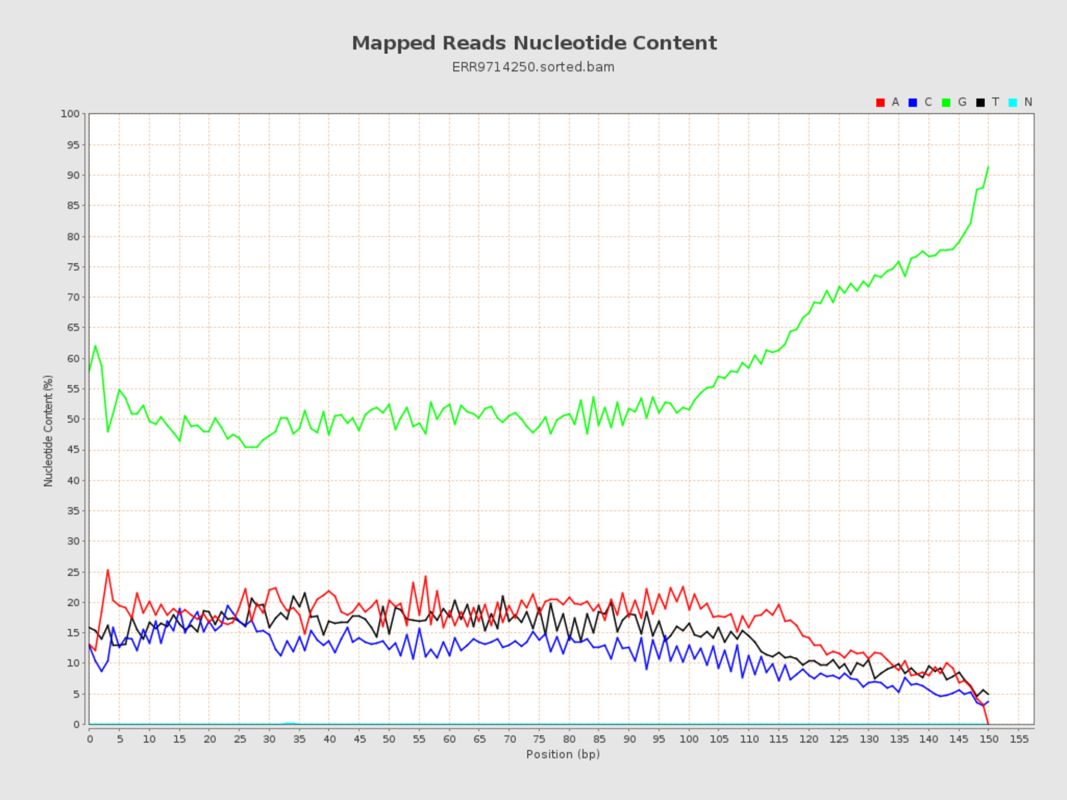
6. Results : Genome Fraction Coverage



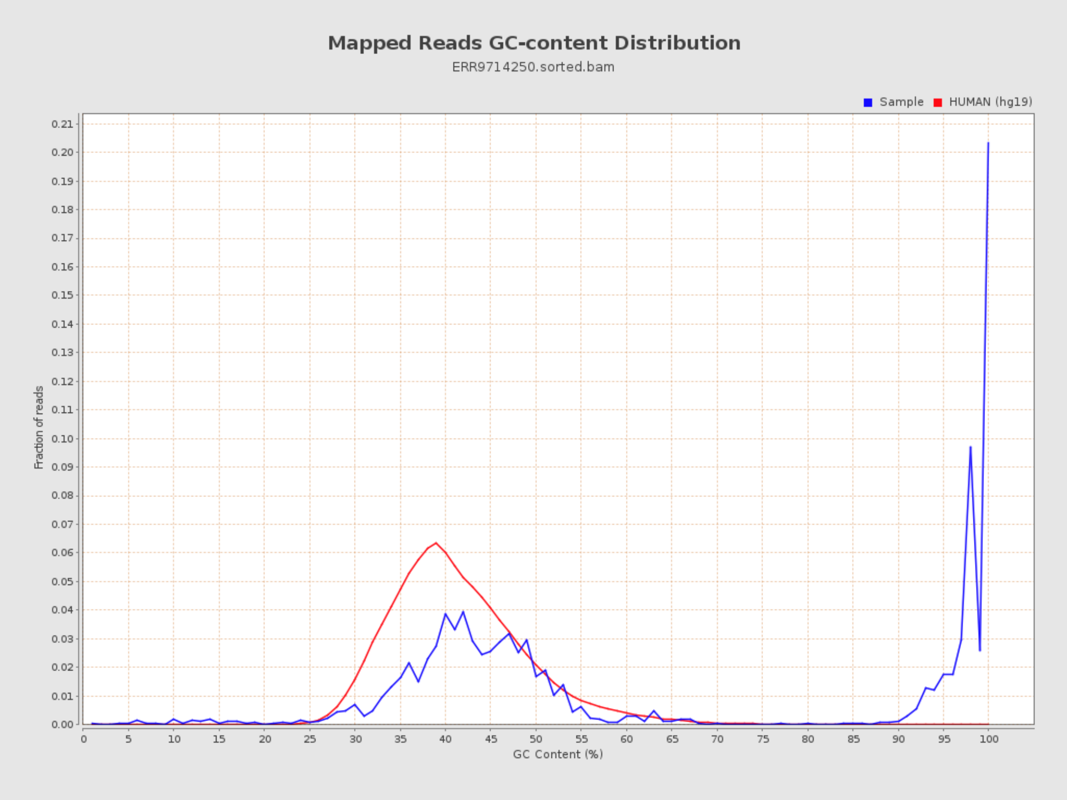
7. Results : Duplication Rate Histogram



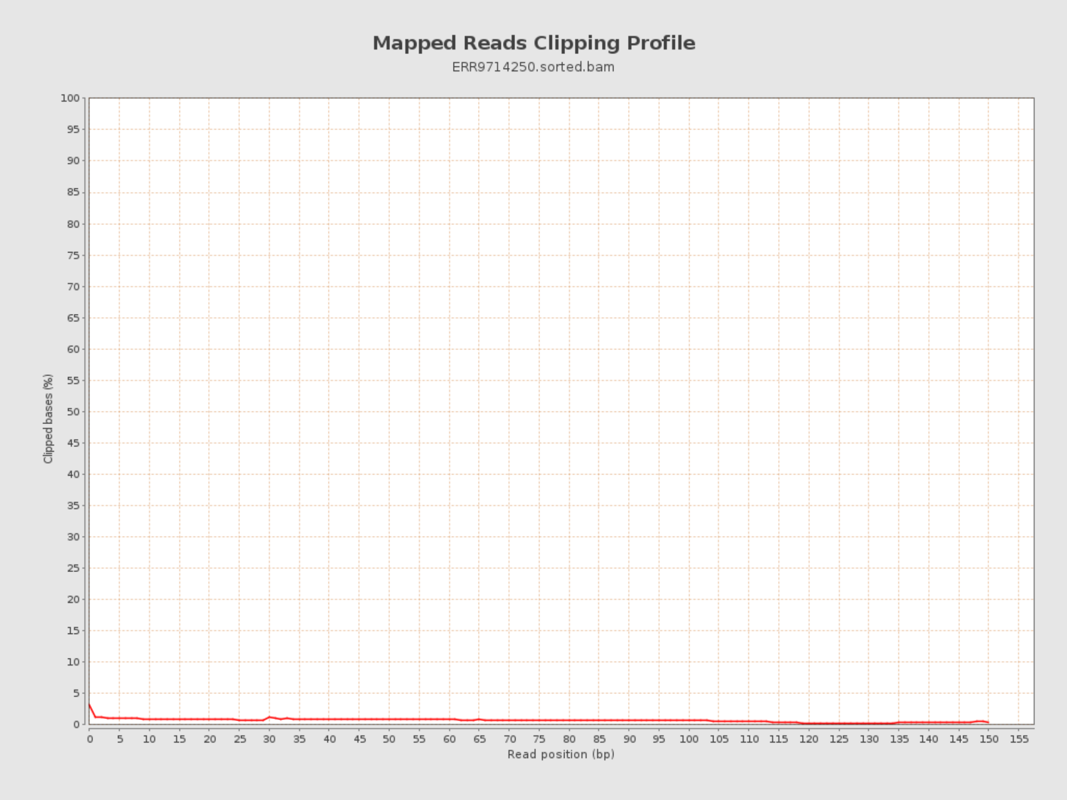
8. Results : Mapped Reads Nucleotide Content



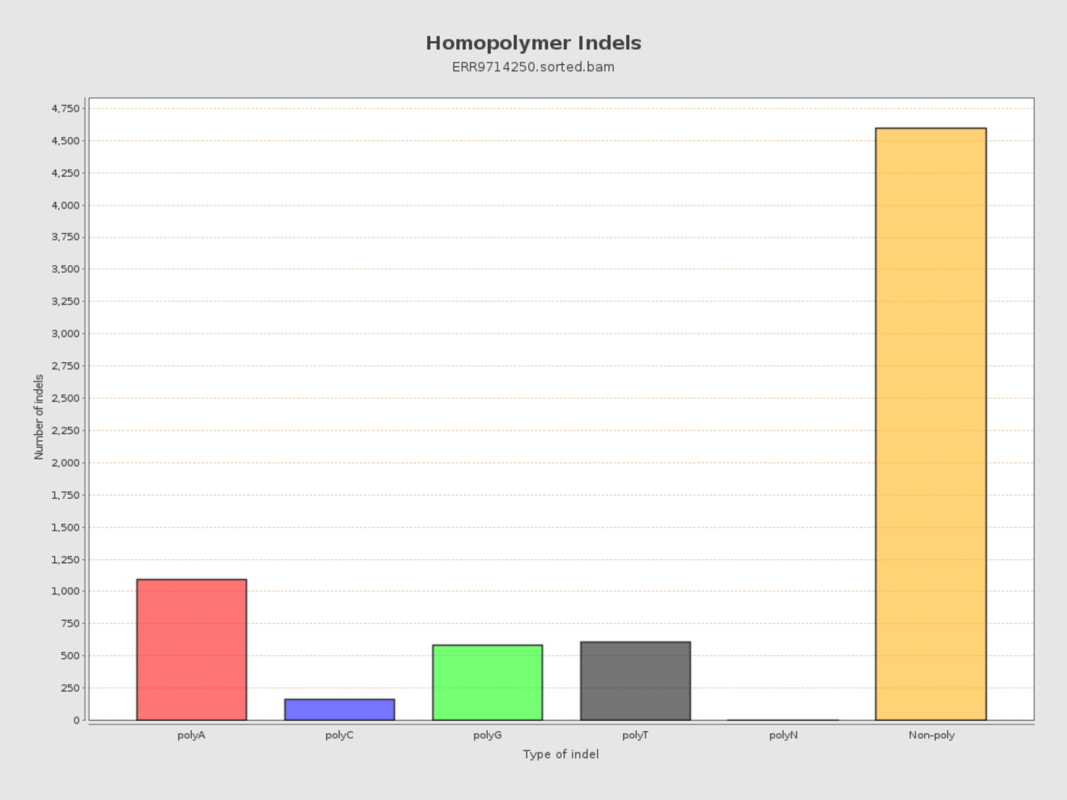
9. Results : Mapped Reads GC-content Distribution



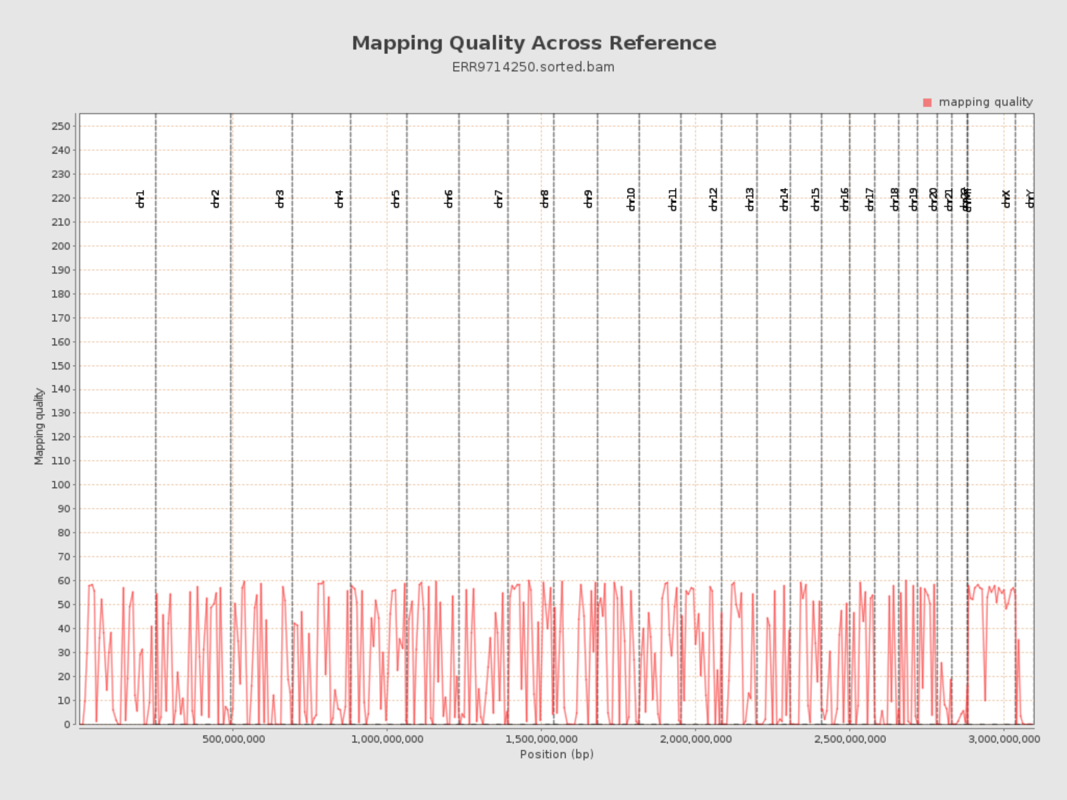
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram