Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:26:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714051.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_ERR9714051 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:26:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	453,376
Mapped reads	37,436 / 8.26%
Unmapped reads	415,940 / 91.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,170 / 0.26%
Read min/max/mean length	30 / 151 / 65.66
Duplicated reads (estimated)	31,228 / 6.89%
Duplication rate	34.18%
Clipped reads	31,395 / 6.92%

2.2. ACGT Content

Number/percentage of A's	805,306 / 20.12%
Number/percentage of C's	561,274 / 14.02%
Number/percentage of T's	780,040 / 19.49%
Number/percentage of G's	1,855,750 / 46.37%
Number/percentage of N's	43 / 0%
GC Percentage	60.39%

2.3. Coverage

Mean	0.0013

Standard Deviation	1.8966

2.4. Mapping Quality

Mean Mapping Quality	38.71

2.5. Mismatches and indels

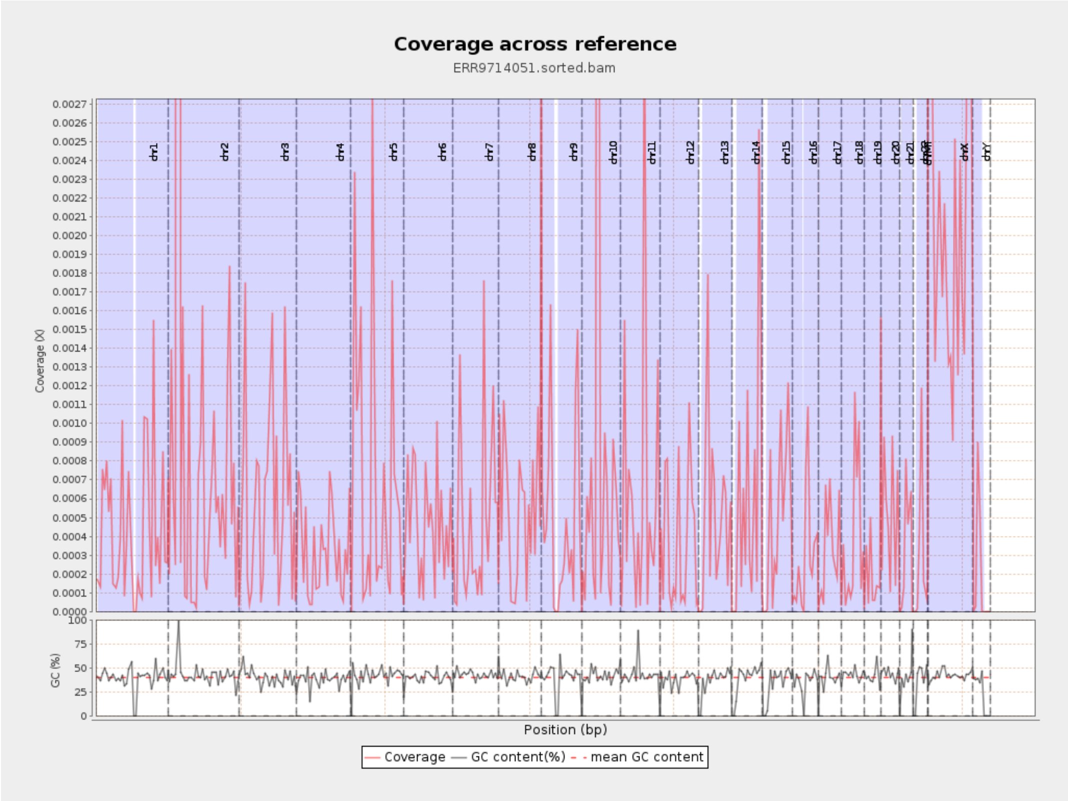
General error rate	3.5%
Mismatches	123,337
Insertions	3,867
Mapped reads with at least one insertion	8.71%
Deletions	9,176
Mapped reads with at least one deletion	23.5%
Homopolymer indels	50.66%

2.6. Chromosome stats

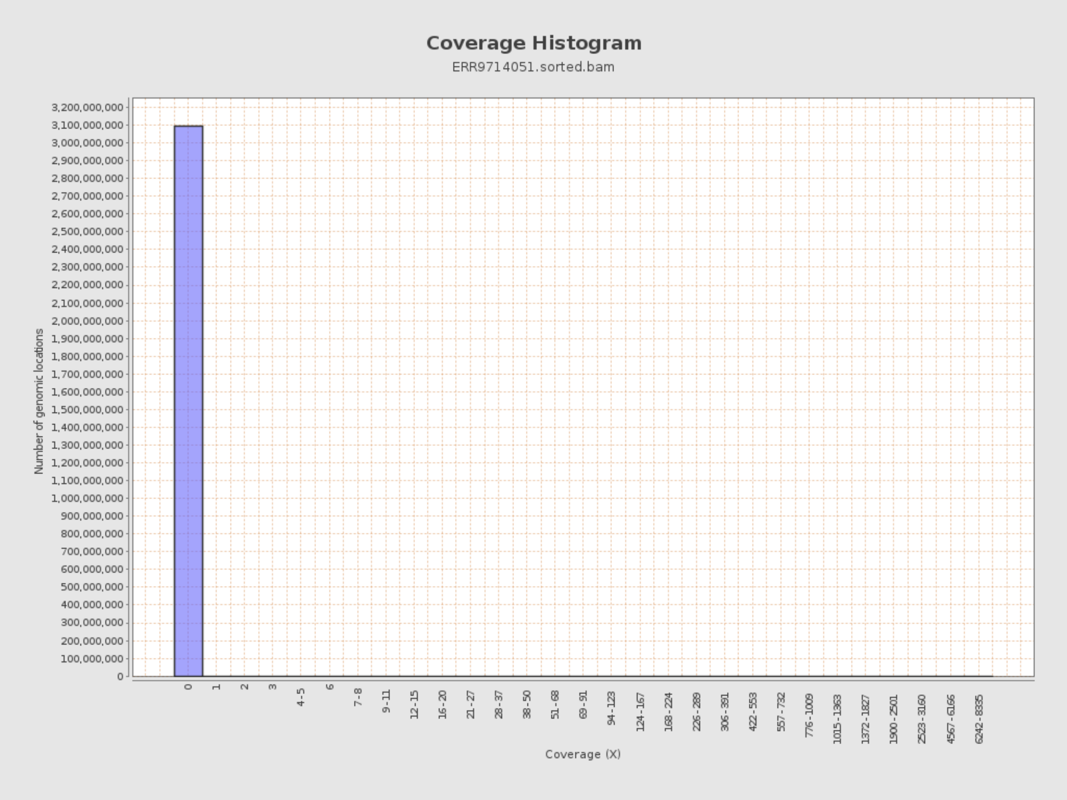
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	107113	0.0004	0.0931
chr2	243199373	1433399	0.0059	5.3788
chr3	198022430	116953	0.0006	0.11
chr4	191154276	61056	0.0003	0.066
chr5	180915260	134298	0.0007	0.1779
chr6	171115067	78151	0.0005	0.0913
chr7	159138663	77390	0.0005	0.1716

chr8	146364022	75655	0.0005	0.0924
chr9	141213431	70179	0.0005	0.0915
chr10	135534747	110087	0.0008	0.1092
chr11	135006516	84927	0.0006	0.1629
chr12	133851895	48077	0.0004	0.0833
chr13	115169878	55626	0.0005	0.1147
chr14	107349540	66937	0.0006	0.1702
chr15	102531392	50919	0.0005	0.0844
chr16	90354753	27228	0.0003	0.0585
chr17	81195210	26091	0.0003	0.0858
chr18	78077248	31207	0.0004	0.0859
chr19	59128983	13219	0.0002	0.0564
chr20	63025520	32964	0.0005	0.0975
chr21	48129895	16008	0.0003	0.0746
chr22	51304566	14854	0.0003	0.073
chrMT	16571	947061	57.1517	491.4376
chrX	155270560	349688	0.0023	0.2502
chrY	59373566	11500	0.0002	0.0672

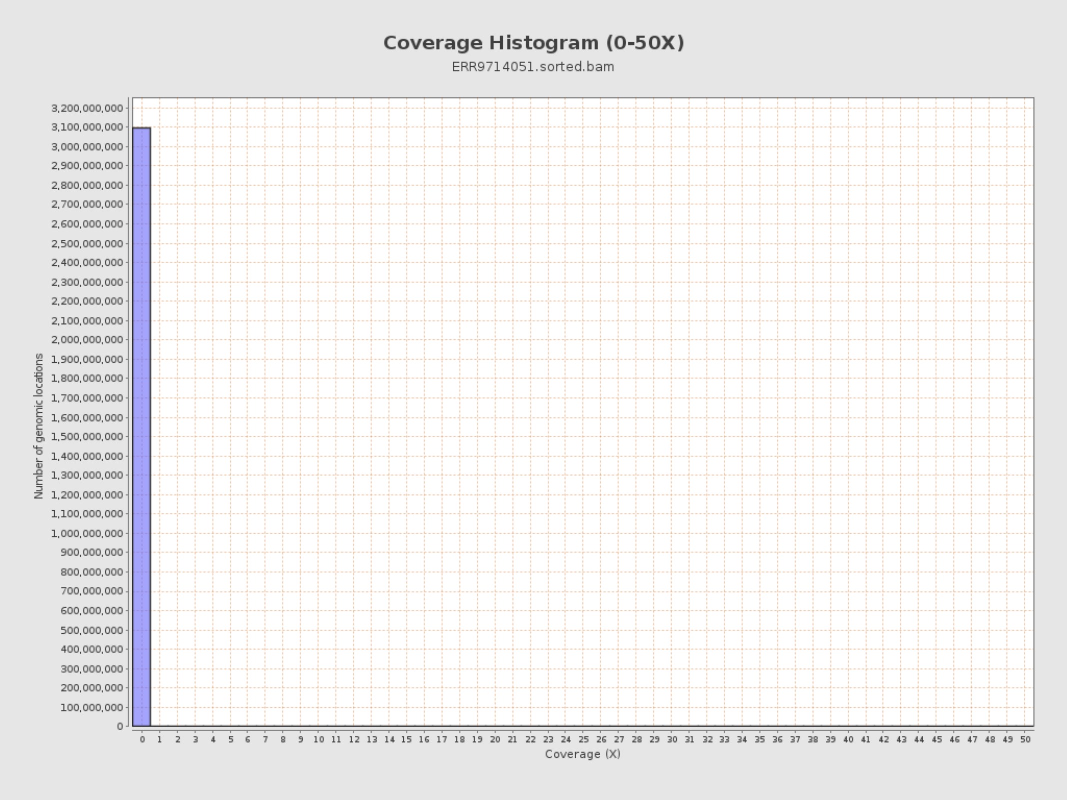
3. Results : Coverage across reference



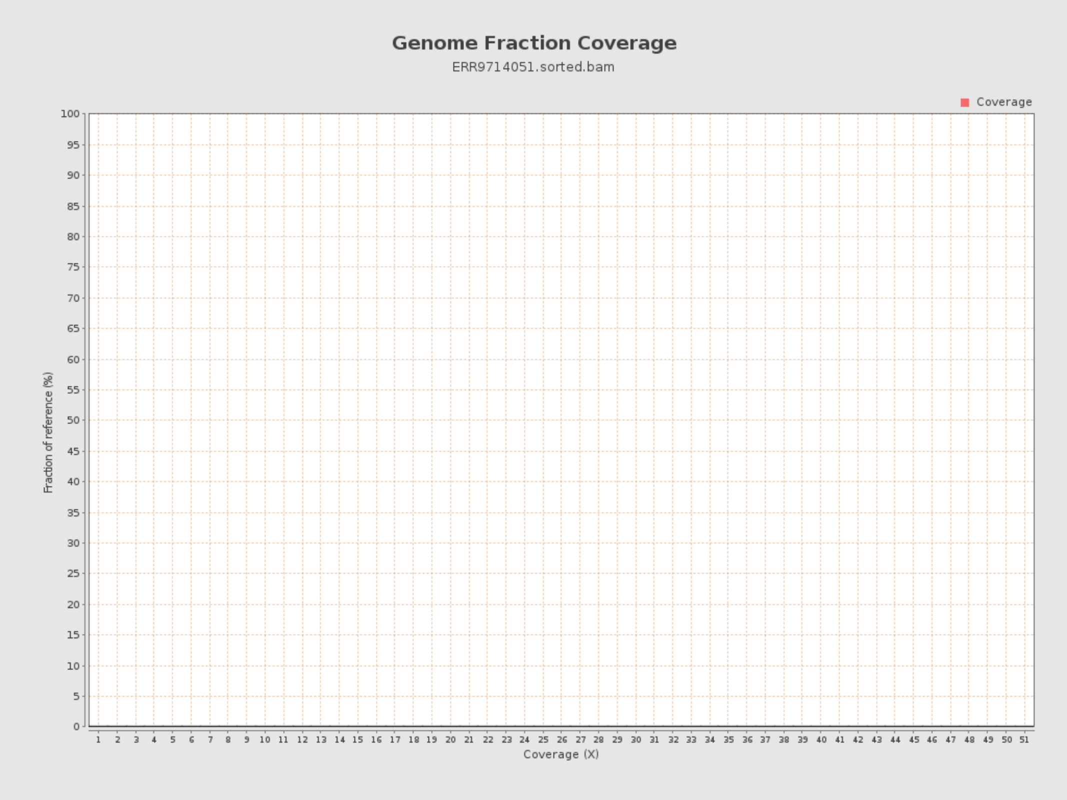
4. Results : Coverage Histogram



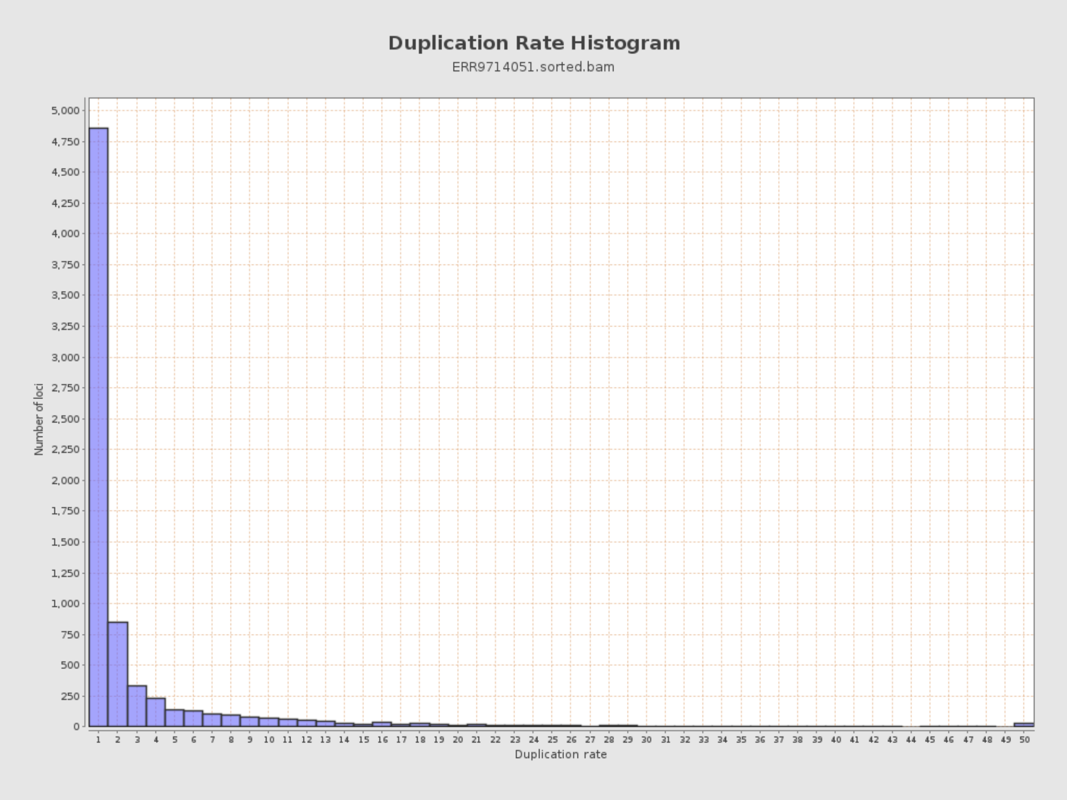
5. Results : Coverage Histogram (0-50X)



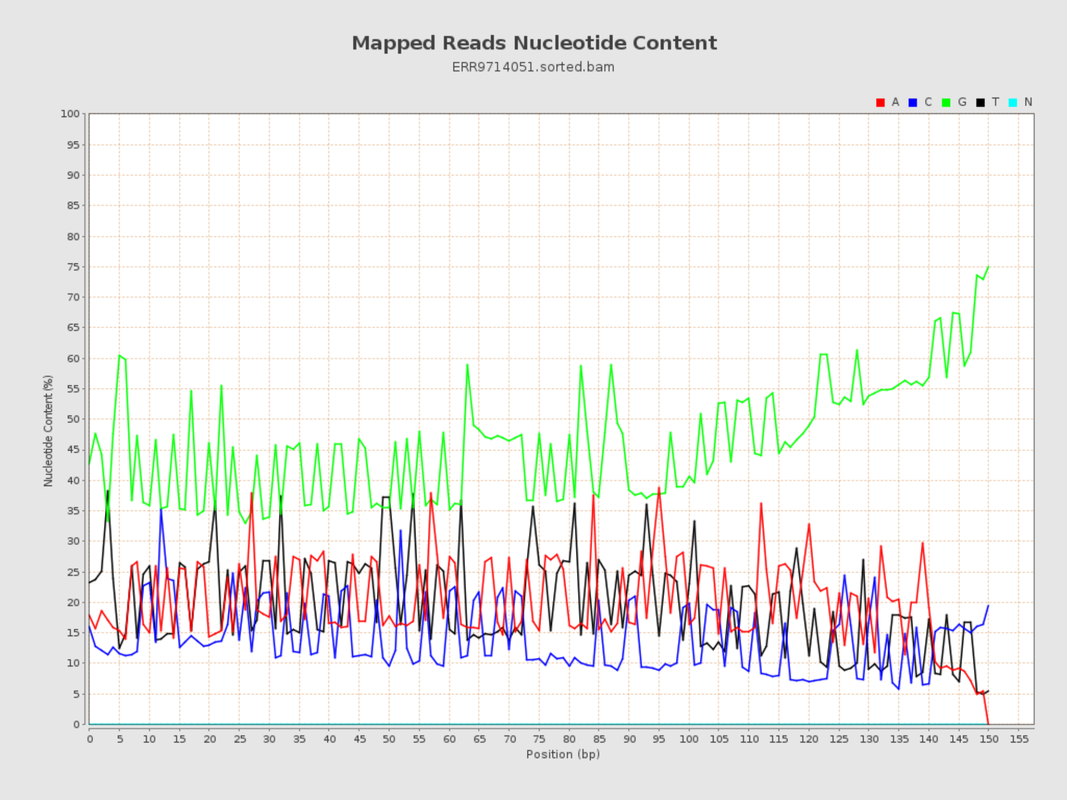
6. Results : Genome Fraction Coverage



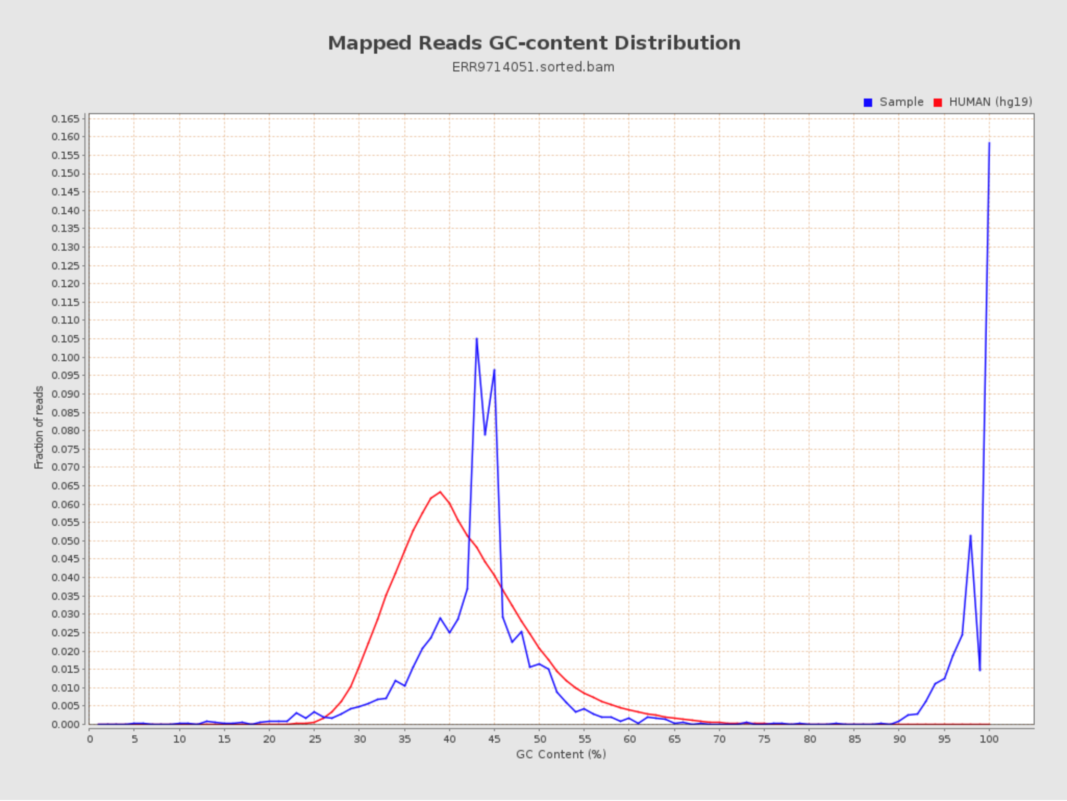
7. Results : Duplication Rate Histogram



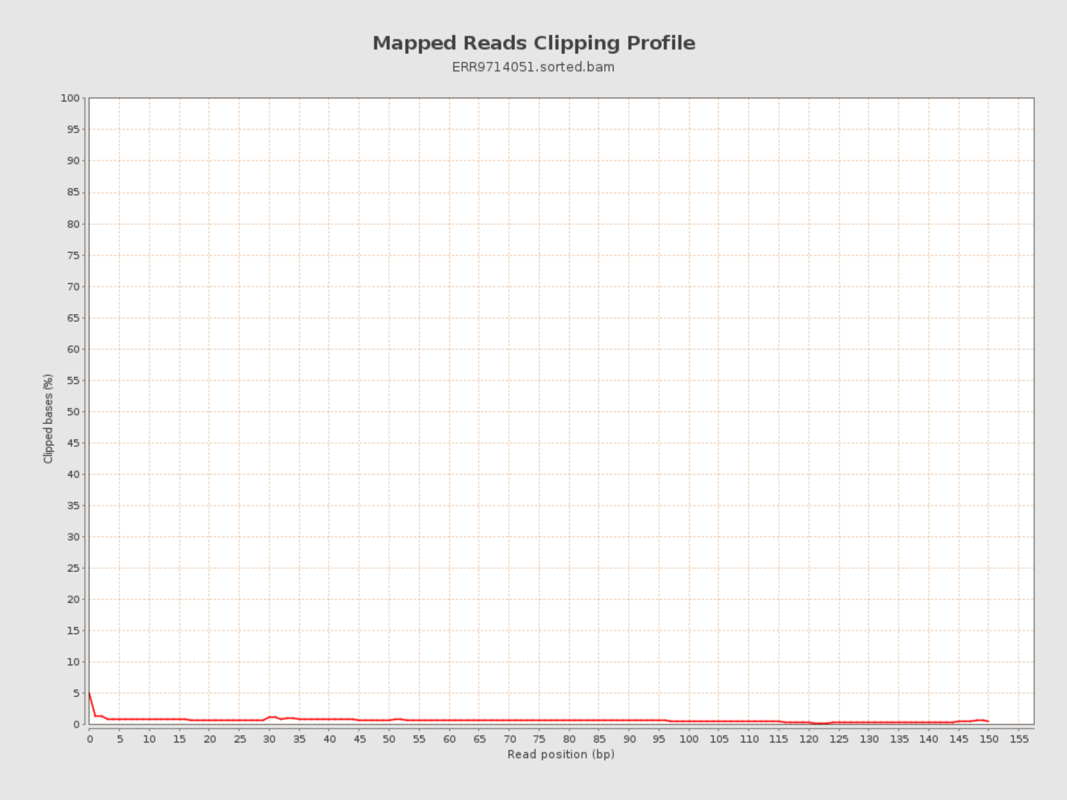
8. Results : Mapped Reads Nucleotide Content



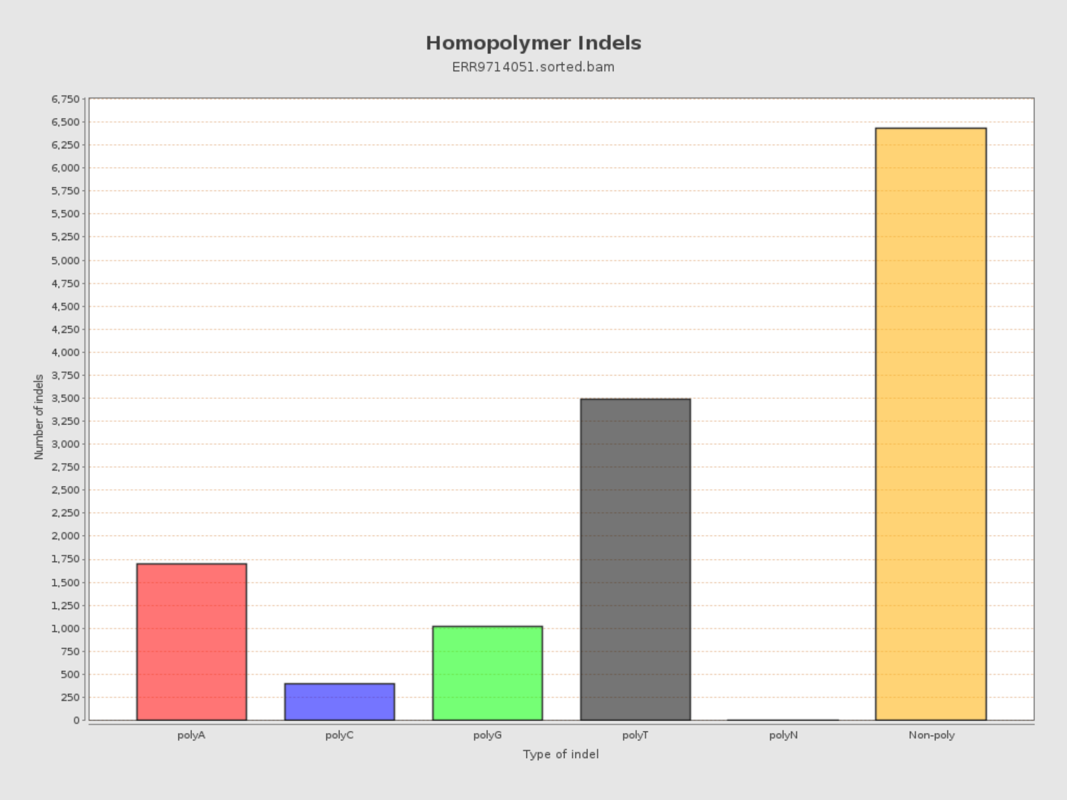
9. Results : Mapped Reads GC-content Distribution



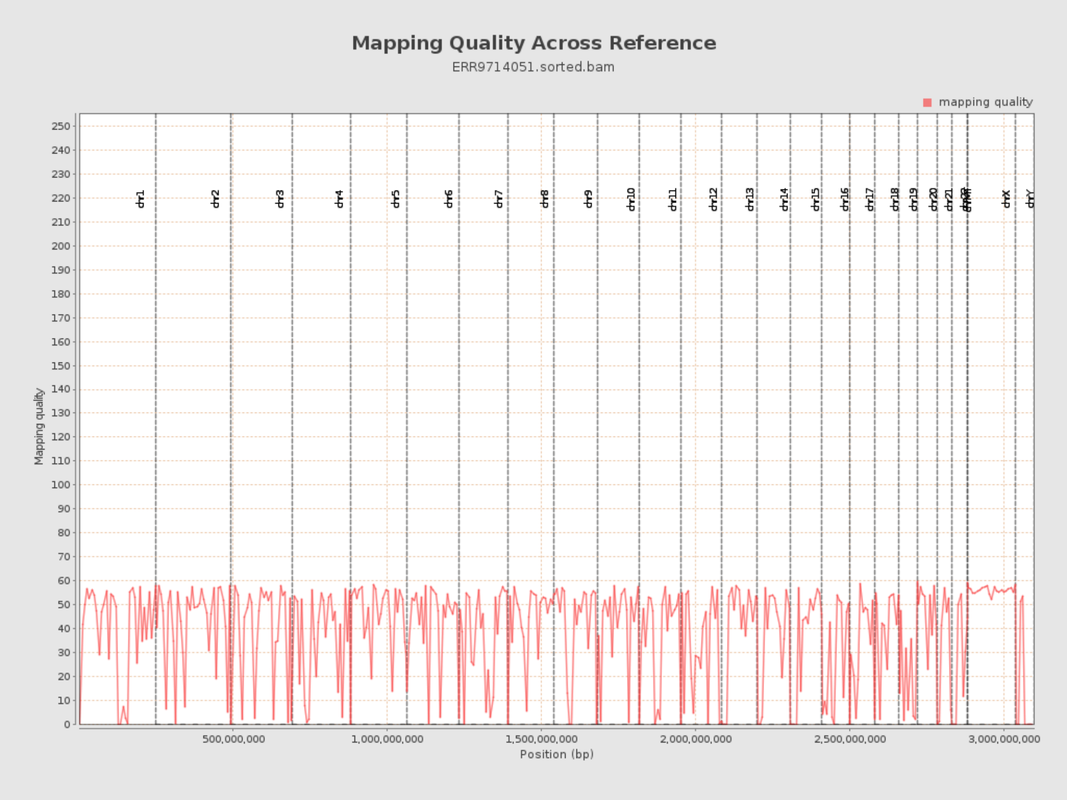
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram