Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:44:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714086.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_ERR9714086 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:44:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	803,272
Mapped reads	59,401 / 7.39%
Unmapped reads	743,871 / 92.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,495 / 0.19%
Read min/max/mean length	30 / 151 / 54.33
Duplicated reads (estimated)	54,308 / 6.76%
Duplication rate	38.62%
Clipped reads	46,501 / 5.79%

2.2. ACGT Content

Number/percentage of A's	783,252 / 14.24%
Number/percentage of C's	531,869 / 9.67%
Number/percentage of T's	695,001 / 12.63%
Number/percentage of G's	3,491,078 / 63.45%
Number/percentage of N's	562 / 0.01%
GC Percentage	73.12%

2.3. Coverage

Mean	0.0018

Standard Deviation	3.5456

2.4. Mapping Quality

Mean Mapping Quality	30.95

2.5. Mismatches and indels

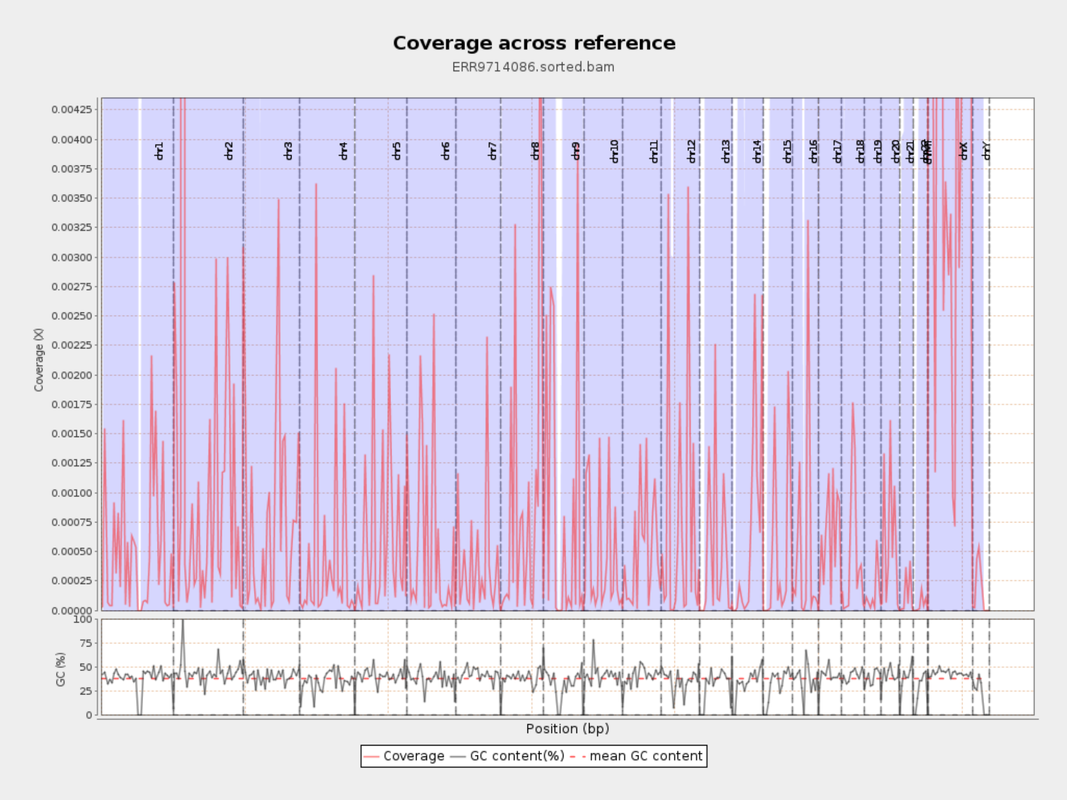
General error rate	3.43%
Mismatches	163,904
Insertions	5,053
Mapped reads with at least one insertion	6.54%
Deletions	9,349
Mapped reads with at least one deletion	15.1%
Homopolymer indels	36.74%

2.6. Chromosome stats

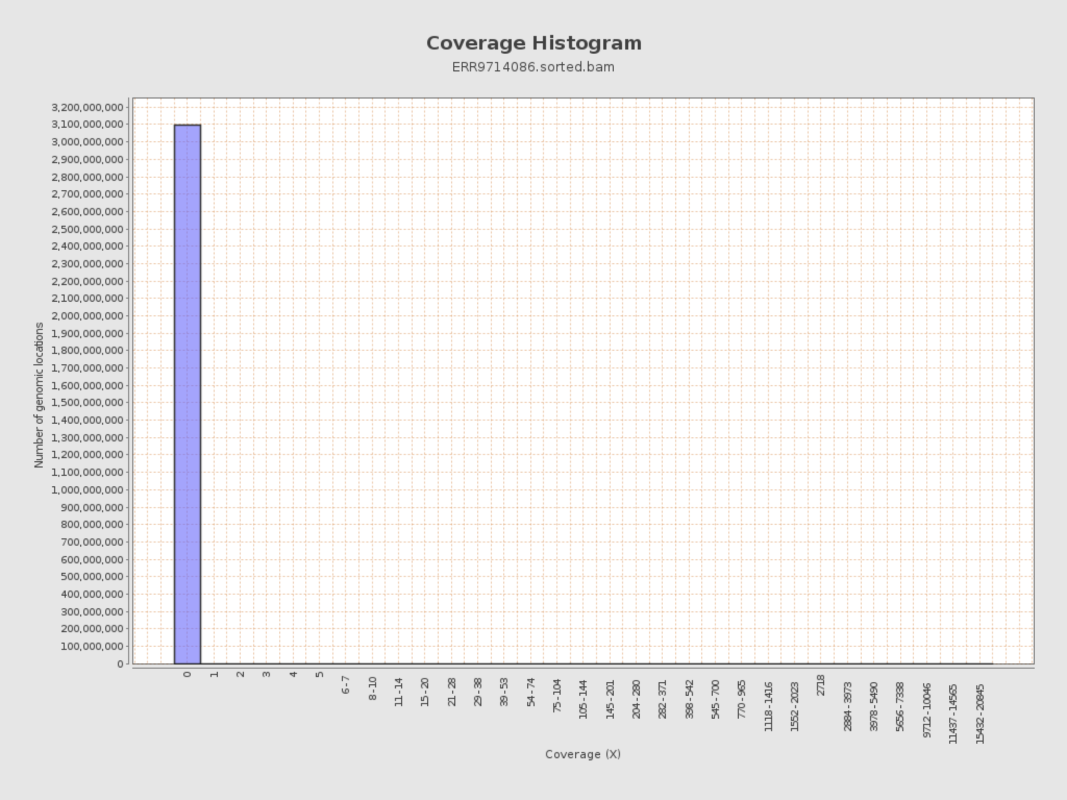
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	127149	0.0005	0.141
chr2	243199373	3177168	0.0131	12.6165
chr3	198022430	153591	0.0008	0.2051
chr4	191154276	84670	0.0004	0.2005
chr5	180915260	114039	0.0006	0.1765
chr6	171115067	98731	0.0006	0.1754
chr7	159138663	62576	0.0004	0.253

chr8	146364022	150955	0.001	0.3727
chr9	141213431	115906	0.0008	0.241
chr10	135534747	62790	0.0005	0.129
chr11	135006516	66754	0.0005	0.1245
chr12	133851895	99683	0.0007	0.271
chr13	115169878	51628	0.0004	0.1594
chr14	107349540	75177	0.0007	0.3279
chr15	102531392	49101	0.0005	0.1323
chr16	90354753	45549	0.0005	0.2089
chr17	81195210	49568	0.0006	0.1502
chr18	78077248	39528	0.0005	0.1389
chr19	59128983	8367	0.0001	0.0453
chr20	63025520	38802	0.0006	0.1538
chr21	48129895	6952	0.0001	0.0498
chr22	51304566	2764	0.0001	0.0104
chrMT	16571	10657	0.6431	5.8727
chrX	155270560	867444	0.0056	0.782
chrY	59373566	10282	0.0002	0.0546

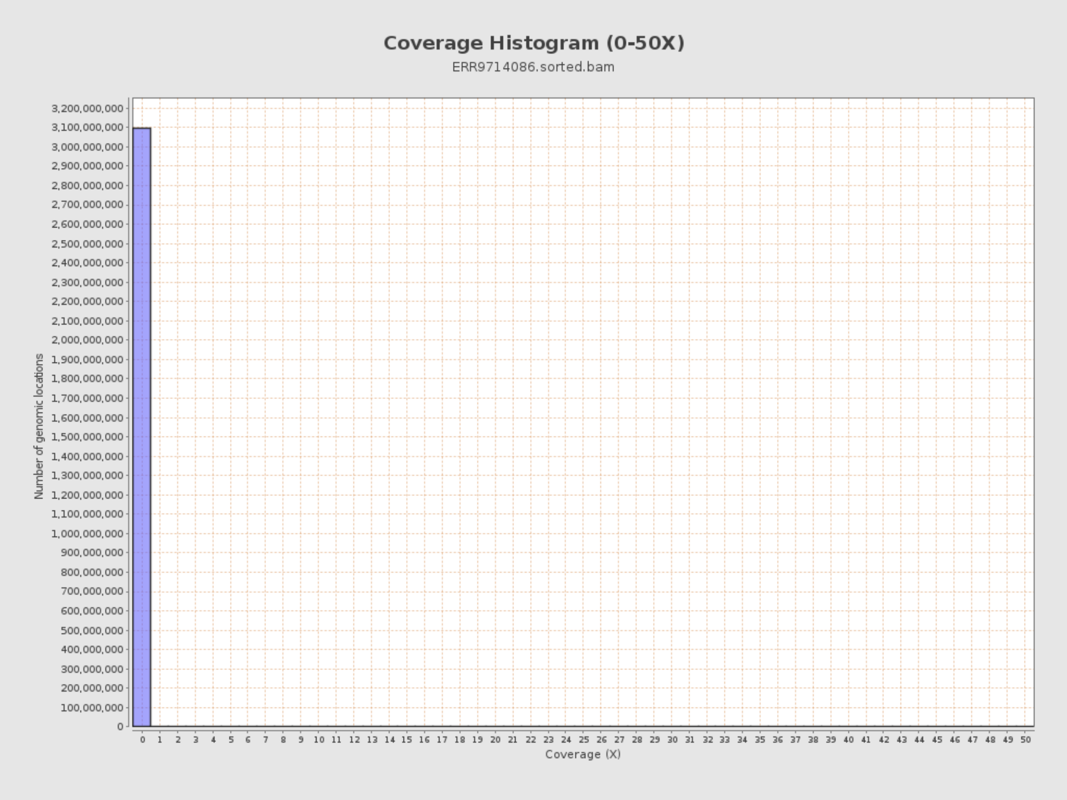
3. Results : Coverage across reference



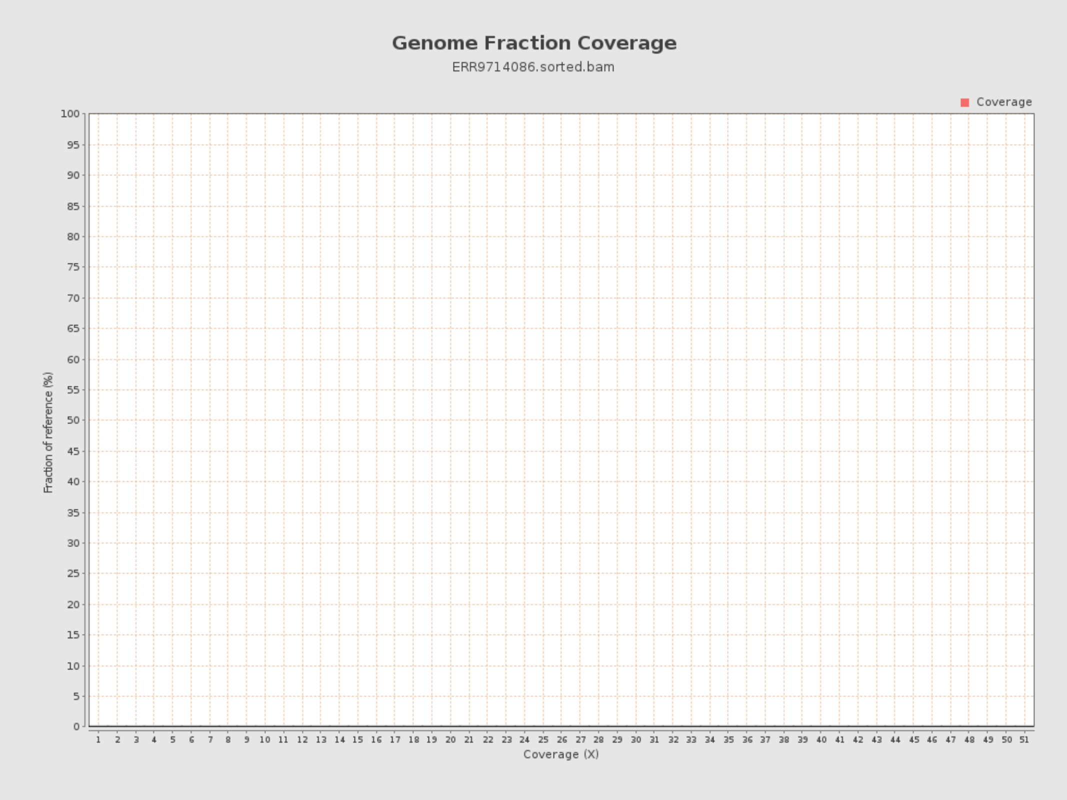
4. Results : Coverage Histogram



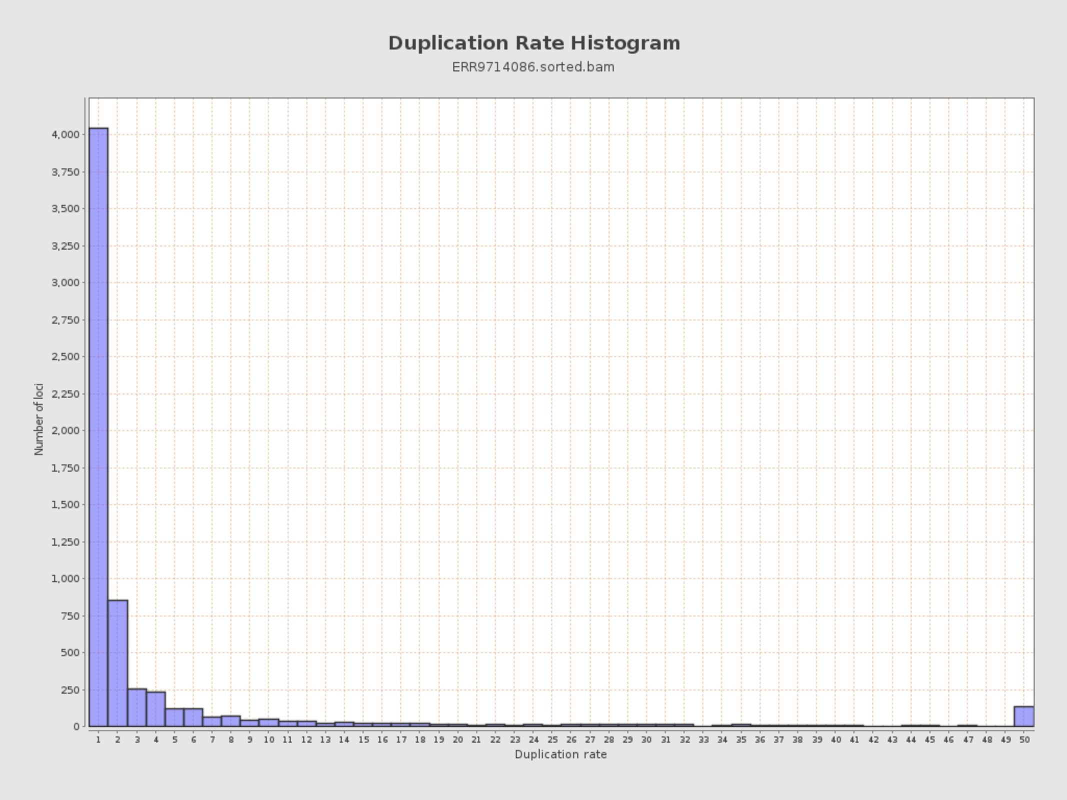
5. Results : Coverage Histogram (0-50X)



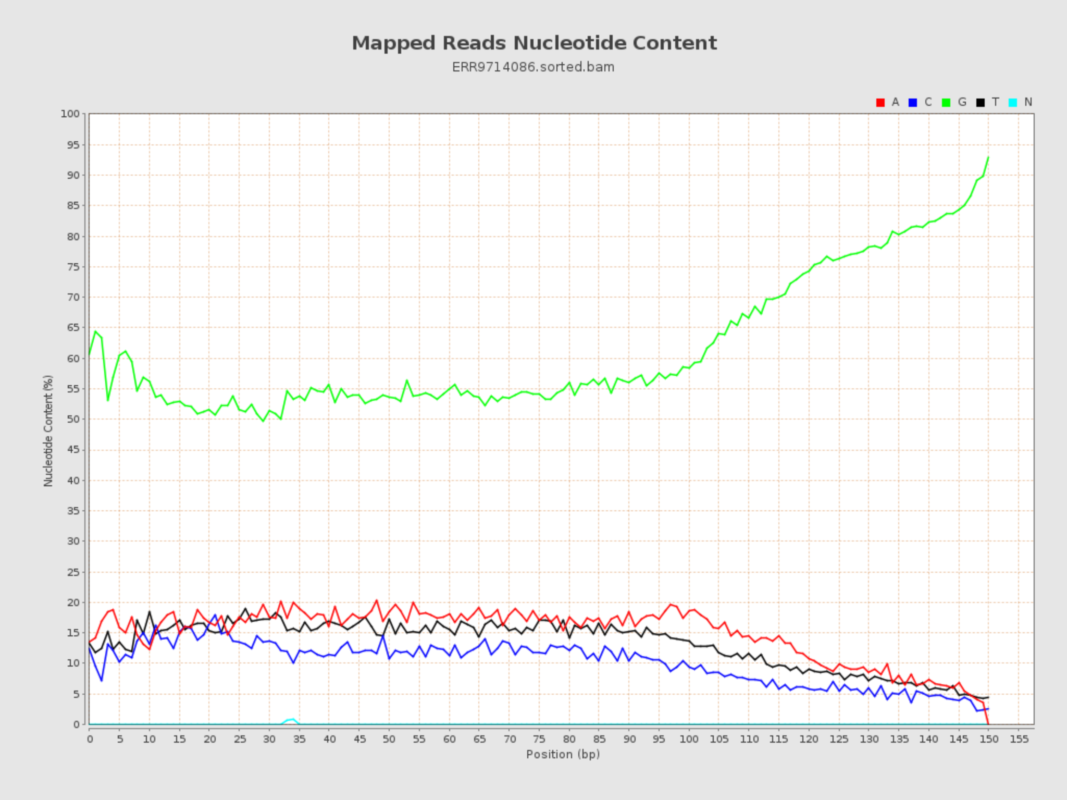
6. Results : Genome Fraction Coverage



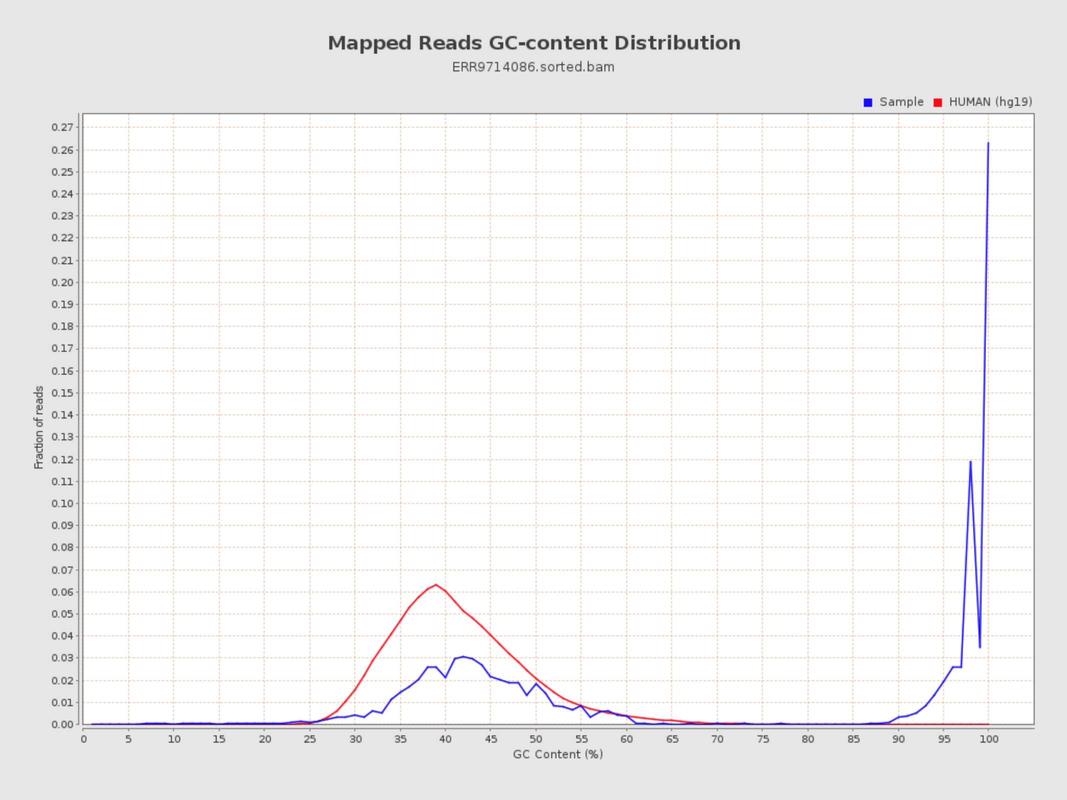
7. Results : Duplication Rate Histogram



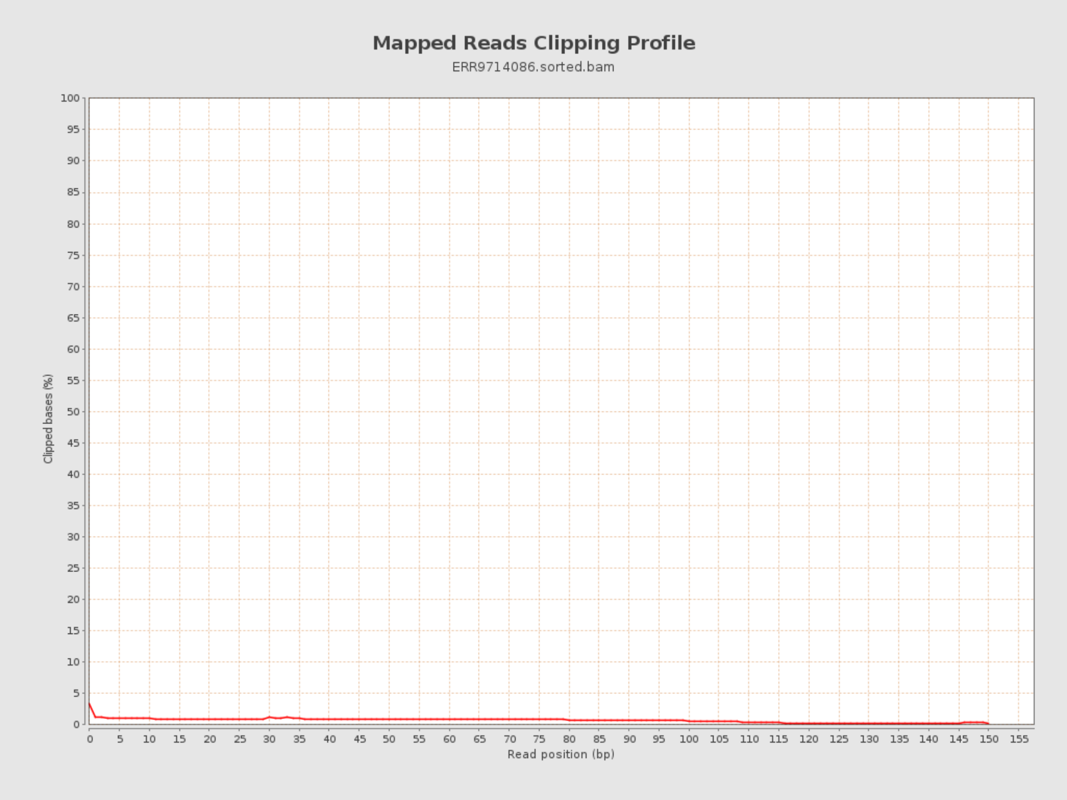
8. Results : Mapped Reads Nucleotide Content



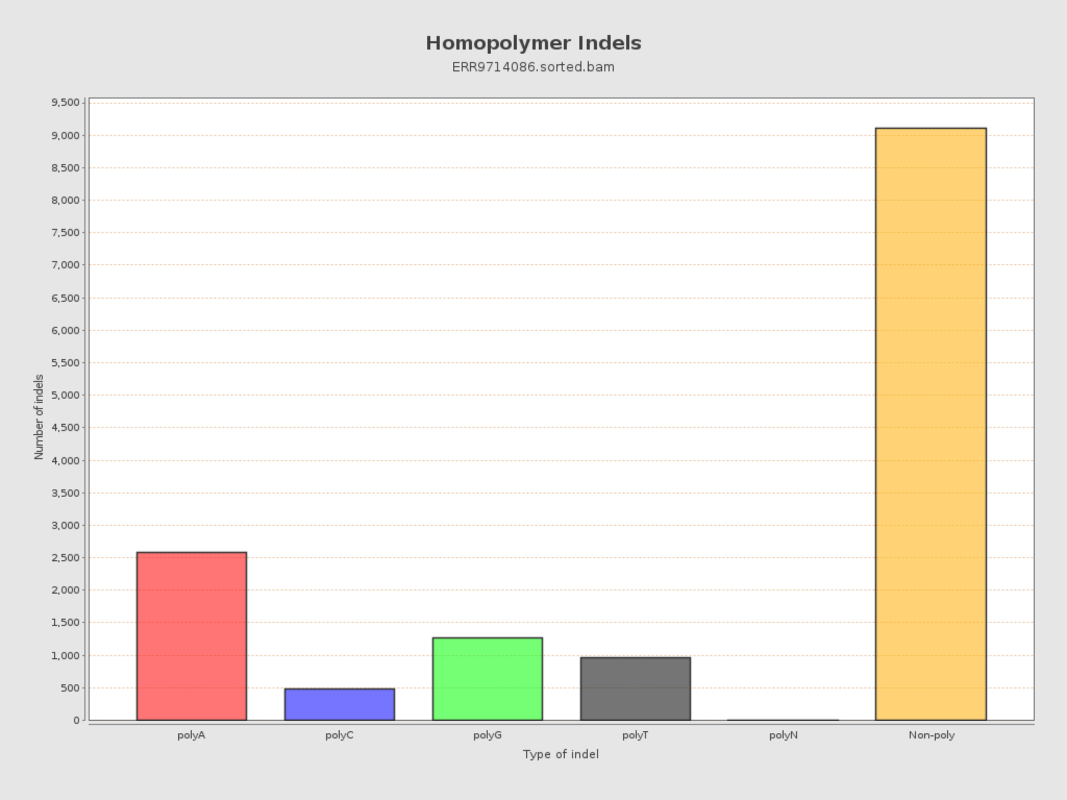
9. Results : Mapped Reads GC-content Distribution



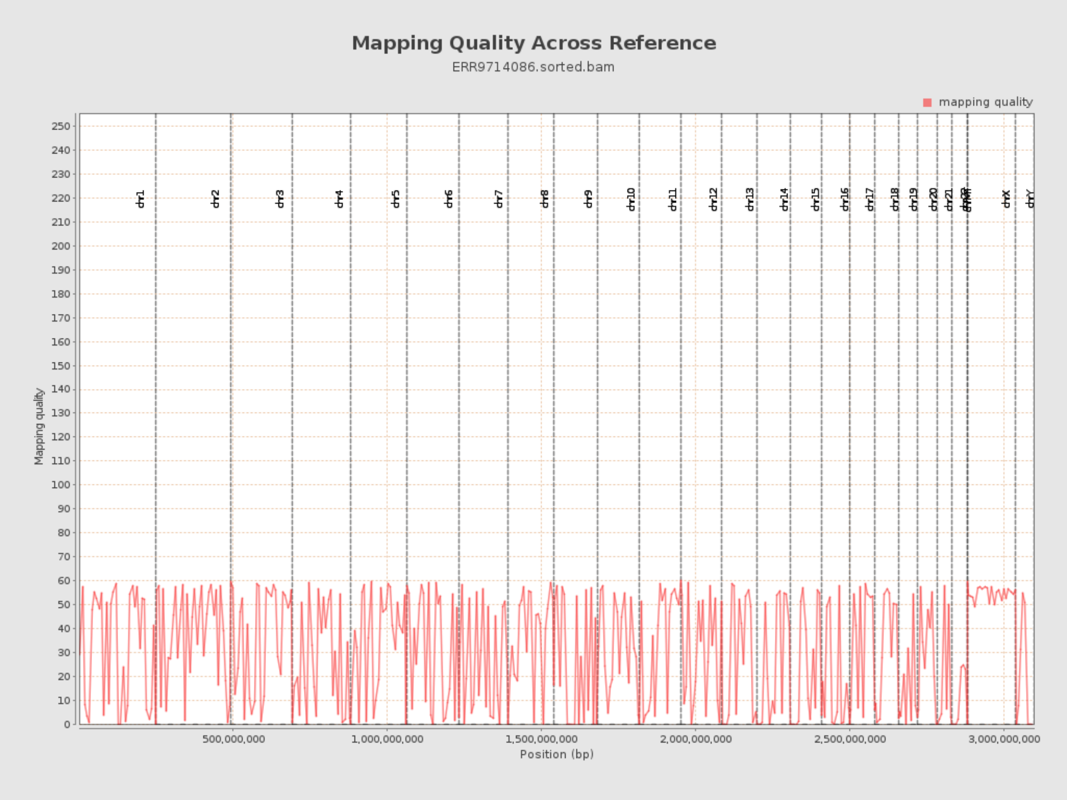
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram