

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:07:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714095.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_ERR9714095 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:07:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	544,062
Mapped reads	392,331 / 72.11%
Unmapped reads	151,731 / 27.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,330 / 2.63%
Read min/max/mean length	30 / 151 / 124.28
Duplicated reads (estimated)	339,289 / 62.36%
Duplication rate	43.52%
Clipped reads	364,195 / 66.94%

2.2. ACGT Content

Number/percentage of A's	13,801,444 / 27.71%
Number/percentage of C's	10,049,554 / 20.18%
Number/percentage of T's	13,049,831 / 26.2%
Number/percentage of G's	12,903,630 / 25.91%
Number/percentage of N's	427 / 0%
GC Percentage	46.09%

2.3. Coverage

Mean	0.0165

Standard Deviation	4.1658
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	51.1
----------------------	------

2.5. Mismatches and indels

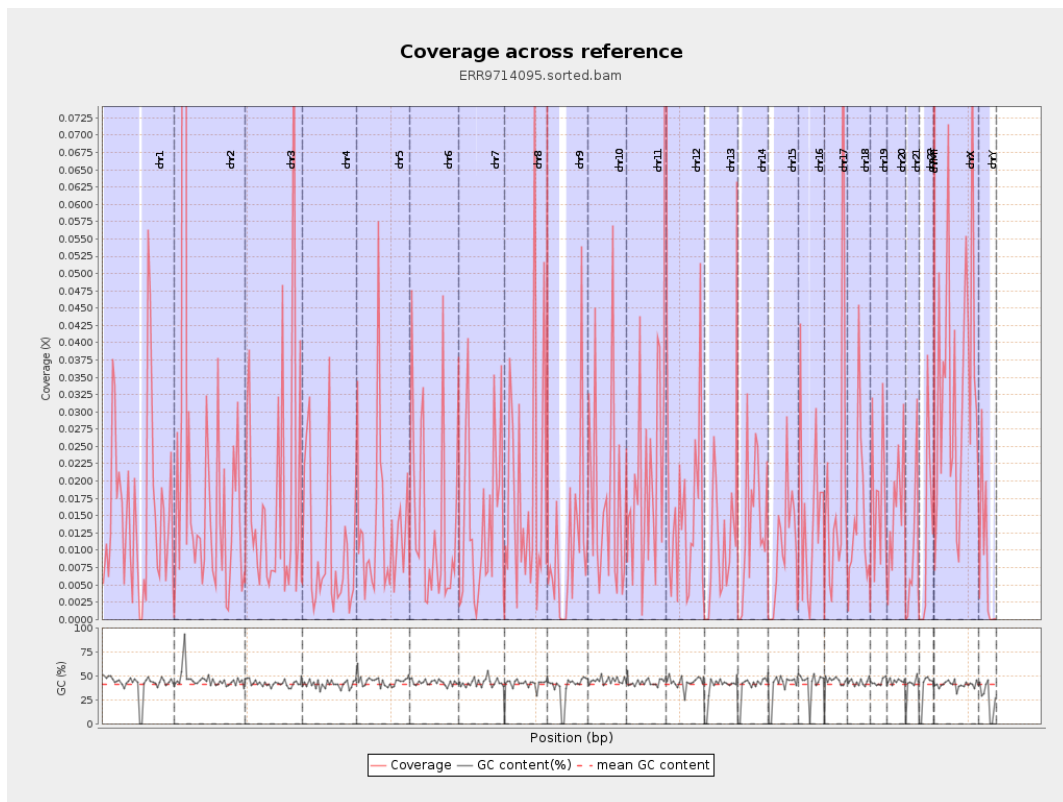
General error rate	4.66%
Mismatches	2,166,619
Insertions	56,600
Mapped reads with at least one insertion	13.81%
Deletions	191,853
Mapped reads with at least one deletion	45.11%
Homopolymer indels	29.65%

2.6. Chromosome stats

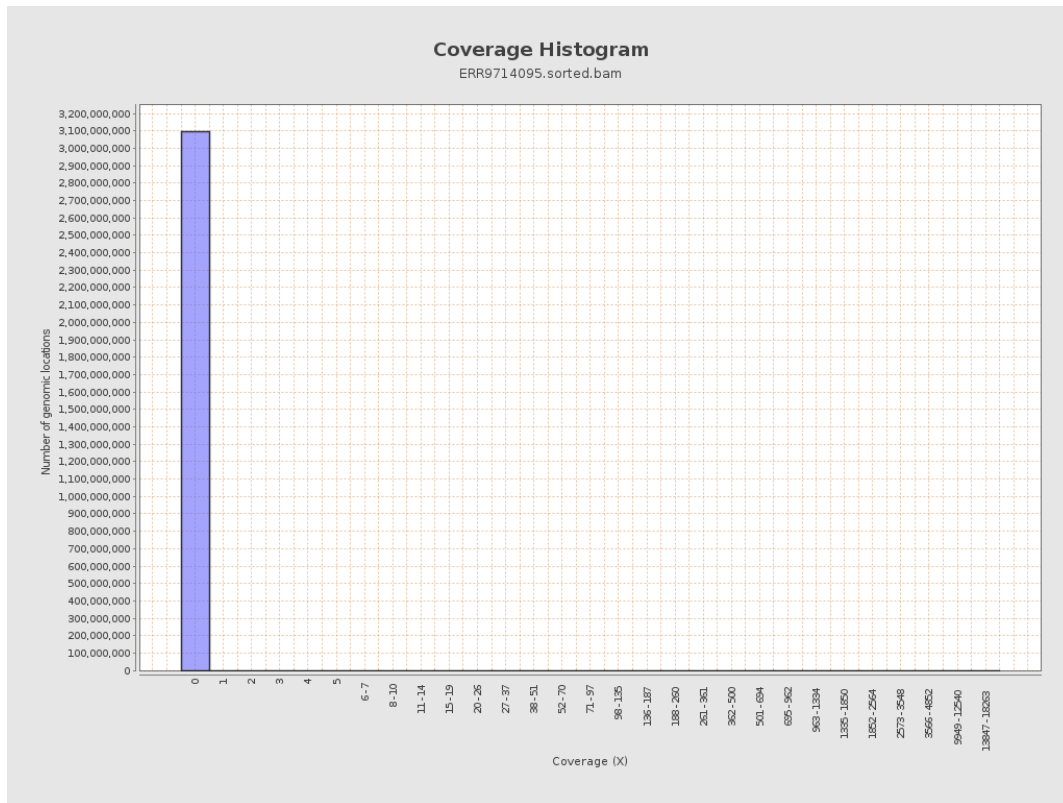
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3749200	0.015	2.4228
chr2	243199373	6303575	0.0259	11.3933
chr3	198022430	3496280	0.0177	4.5884
chr4	191154276	1932666	0.0101	1.7207
chr5	180915260	2346218	0.013	2.5124
chr6	171115067	2404037	0.014	2.7256
chr7	159138663	2191473	0.0138	2.3303

chr8	146364022	2676398	0.0183	3.9941
chr9	141213431	1477119	0.0105	2.0101
chr10	135534747	2414535	0.0178	3.1392
chr11	135006516	2728072	0.0202	2.9253
chr12	133851895	2065865	0.0154	2.5539
chr13	115169878	1232899	0.0107	1.6711
chr14	107349540	1484870	0.0138	2.0755
chr15	102531392	1068661	0.0104	1.1491
chr16	90354753	1337046	0.0148	2.0555
chr17	81195210	1652563	0.0204	3.9172
chr18	78077248	1210119	0.0155	2.2646
chr19	59128983	996892	0.0169	2.3582
chr20	63025520	1047002	0.0166	2.2197
chr21	48129895	447616	0.0093	2.1893
chr22	51304566	638938	0.0125	2.199
chrMT	16571	299007	18.044	142.1709
chrX	155270560	5303605	0.0342	3.2069
chrY	59373566	487846	0.0082	2.6171

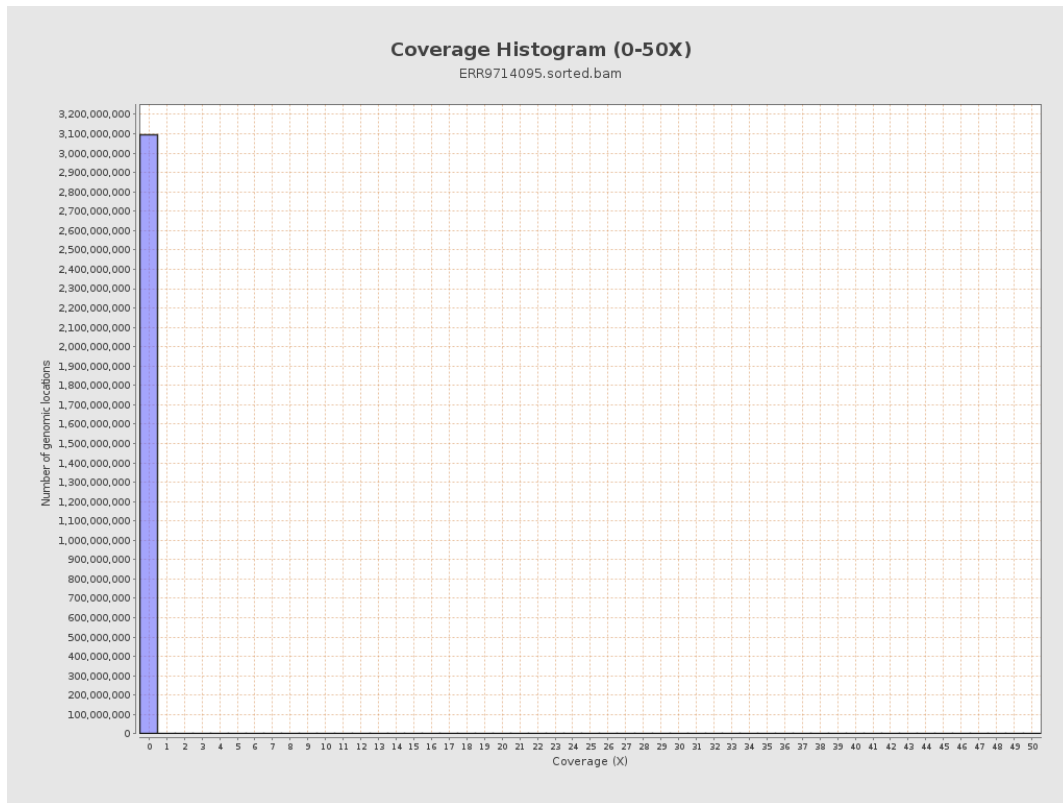
3. Results : Coverage across reference



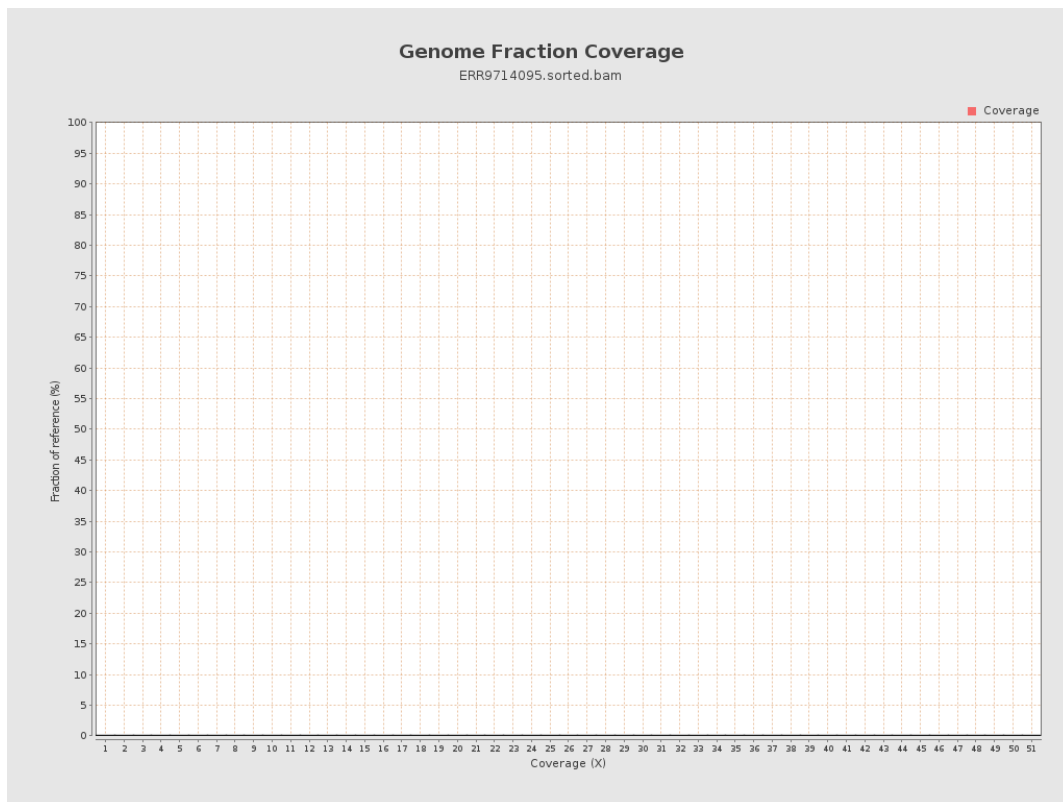
4. Results : Coverage Histogram



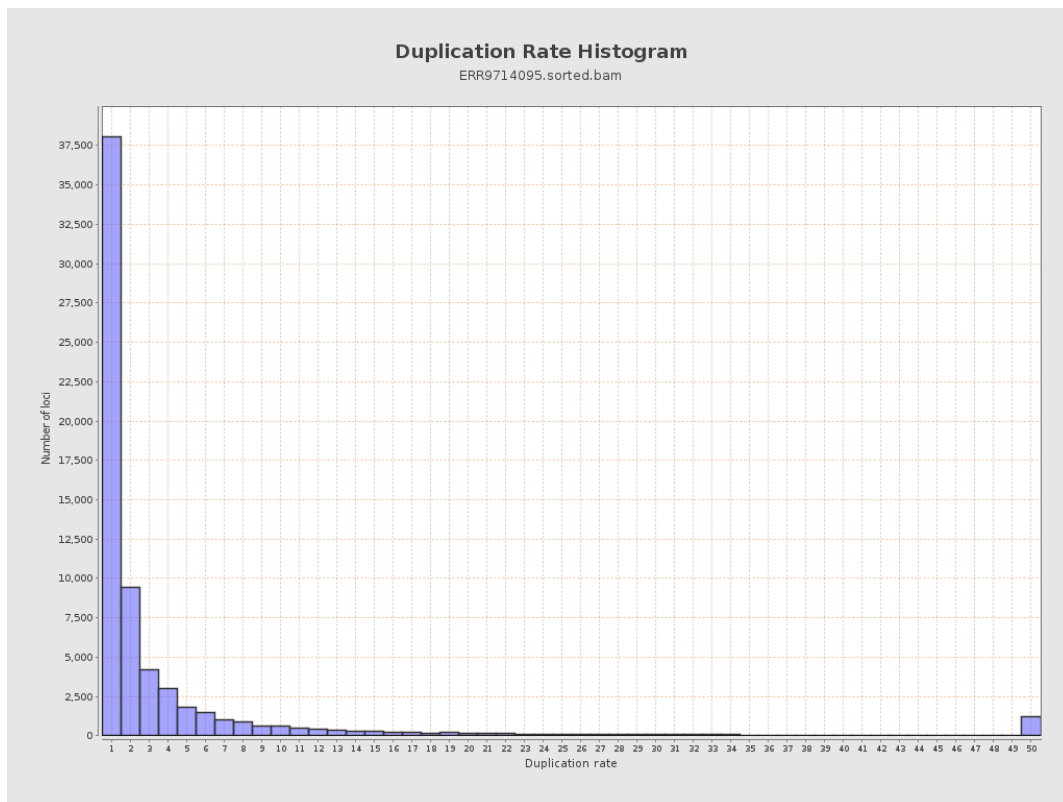
5. Results : Coverage Histogram (0-50X)



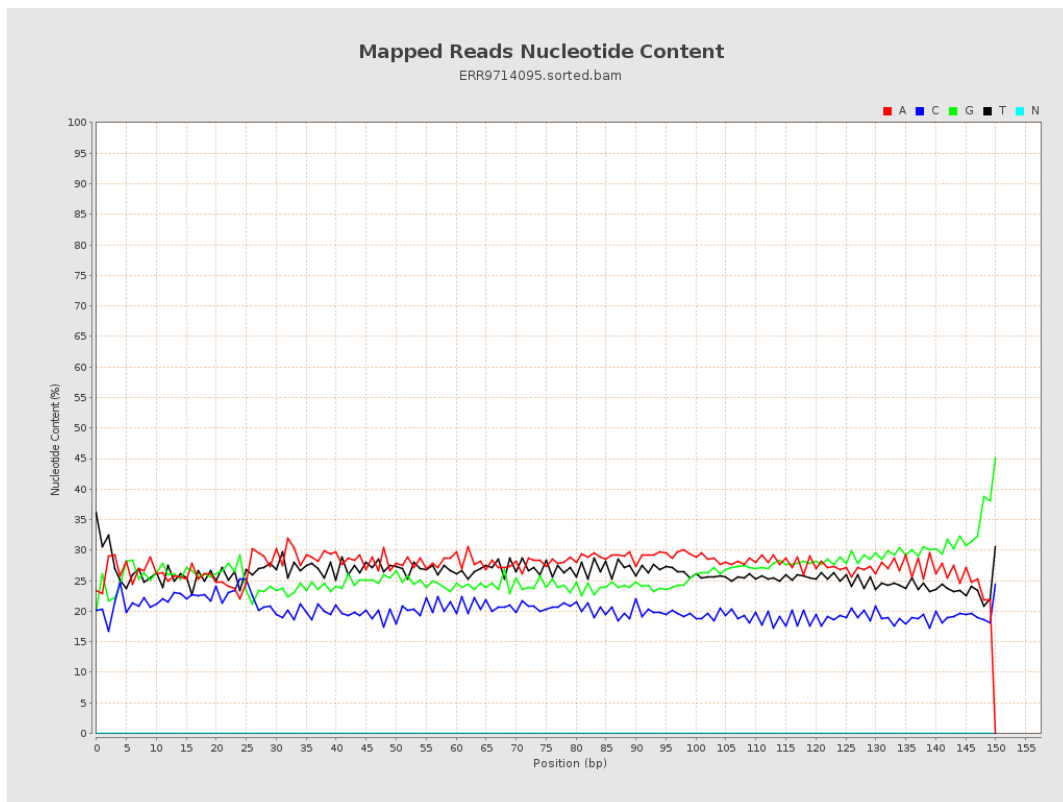
6. Results : Genome Fraction Coverage



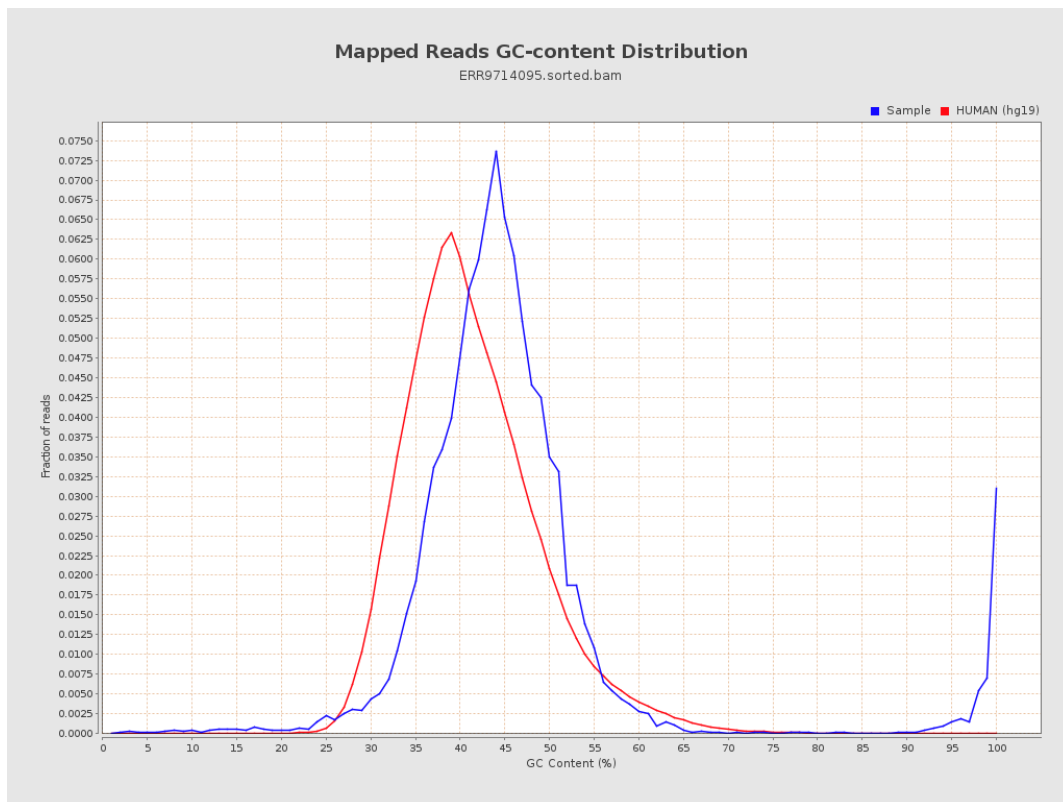
7. Results : Duplication Rate Histogram



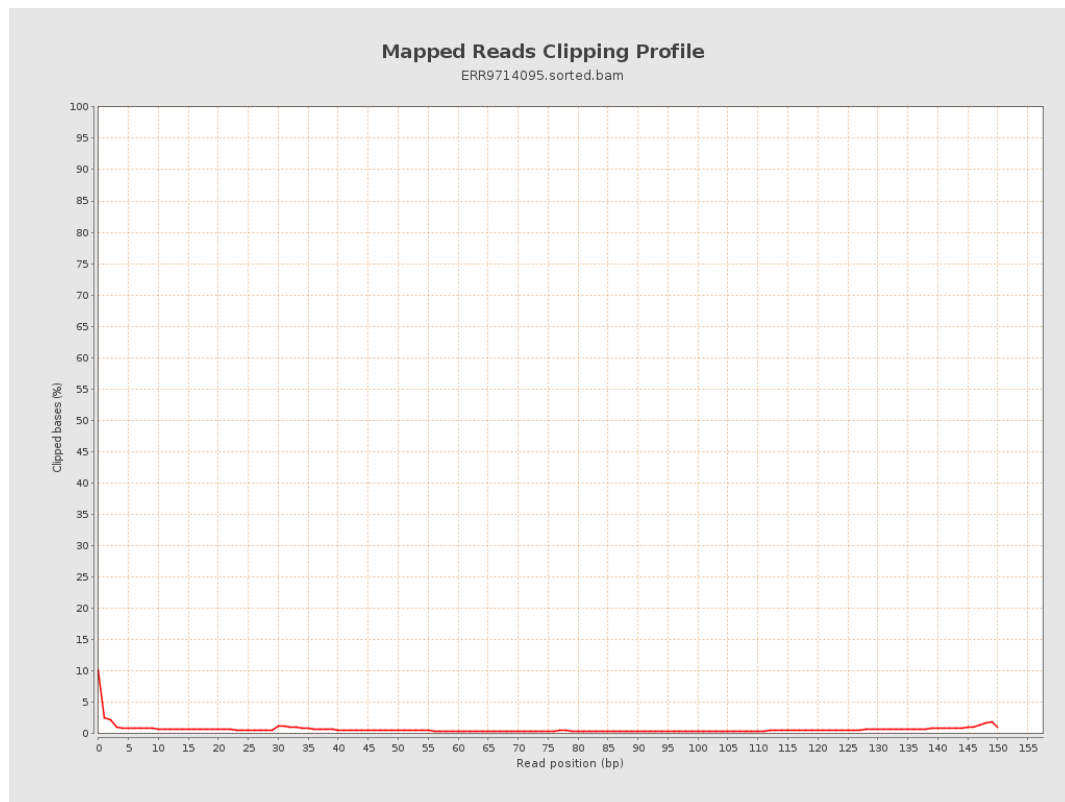
8. Results : Mapped Reads Nucleotide Content



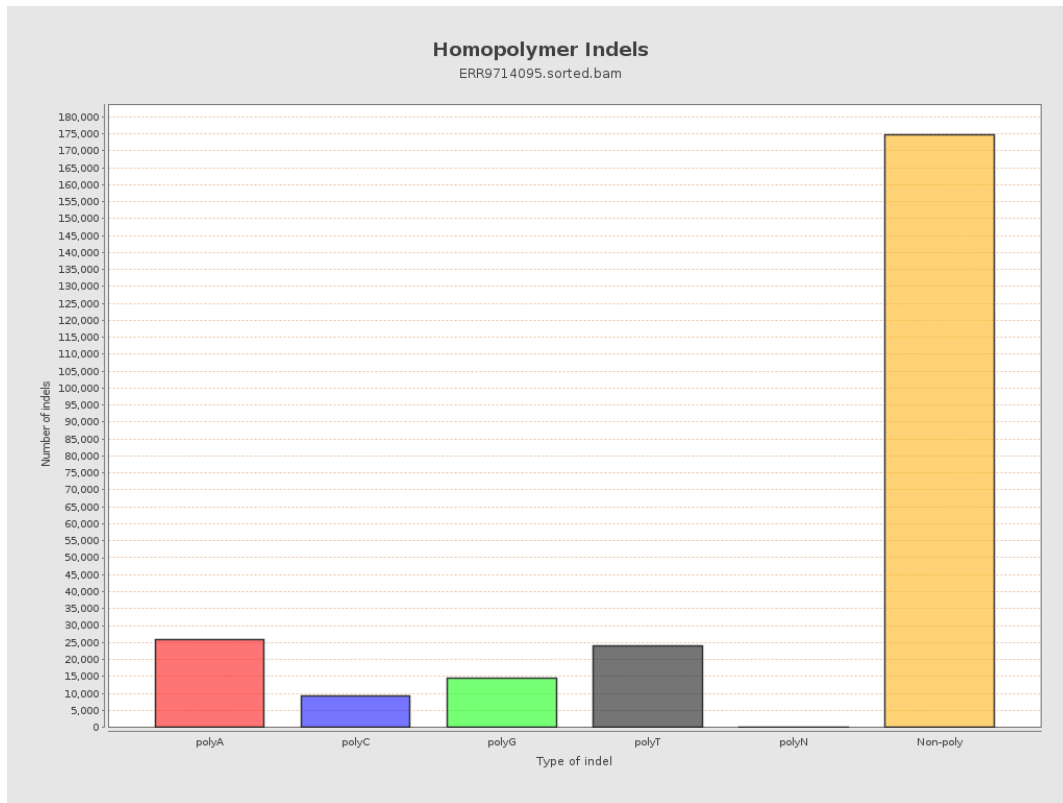
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

