

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:38:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714083.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_ERR9714083 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:38:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	431,778
Mapped reads	321,331 / 74.42%
Unmapped reads	110,447 / 25.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,909 / 2.76%
Read min/max/mean length	30 / 151 / 127.48
Duplicated reads (estimated)	261,750 / 60.62%
Duplication rate	42.05%
Clipped reads	306,212 / 70.92%

2.2. ACGT Content

Number/percentage of A's	11,200,199 / 27.73%
Number/percentage of C's	8,655,191 / 21.43%
Number/percentage of T's	10,600,490 / 26.24%
Number/percentage of G's	9,934,748 / 24.6%
Number/percentage of N's	311 / 0%
GC Percentage	46.03%

2.3. Coverage

Mean	0.0133

Standard Deviation	1.687
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2.4. Mapping Quality

Mean Mapping Quality	52.39
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2.5. Mismatches and indels

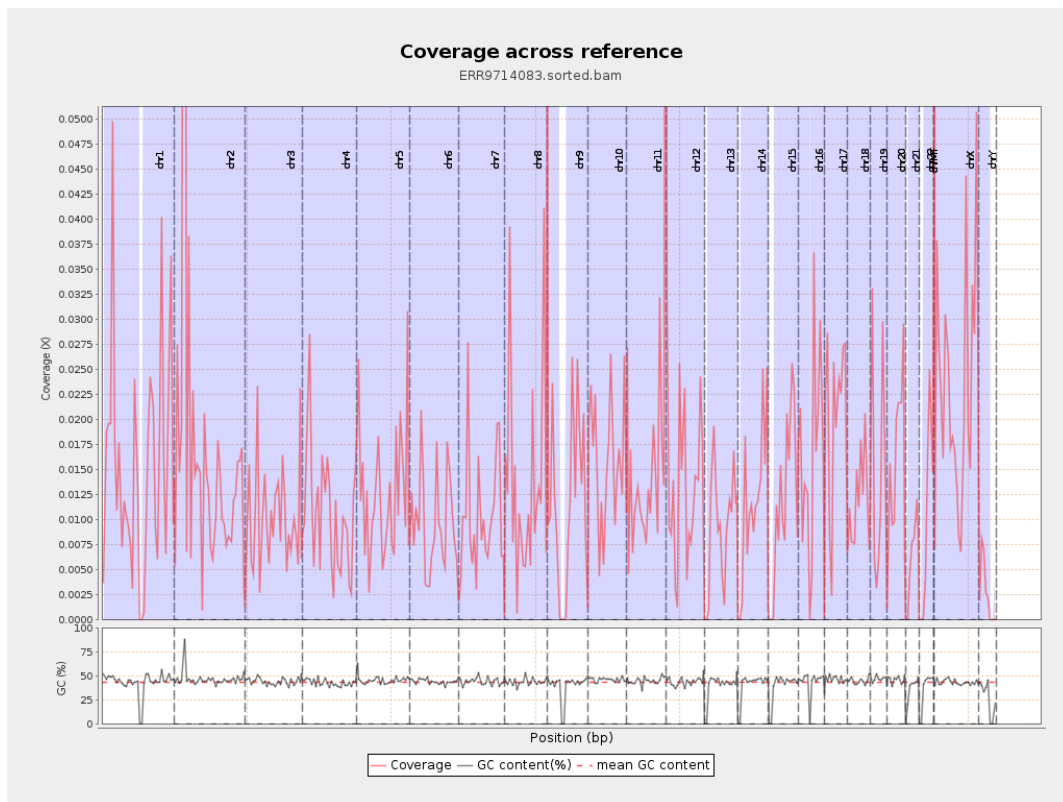
General error rate	4.34%
Mismatches	1,618,626
Insertions	44,272
Mapped reads with at least one insertion	13.35%
Deletions	139,491
Mapped reads with at least one deletion	41.47%
Homopolymer indels	28.39%

2.6. Chromosome stats

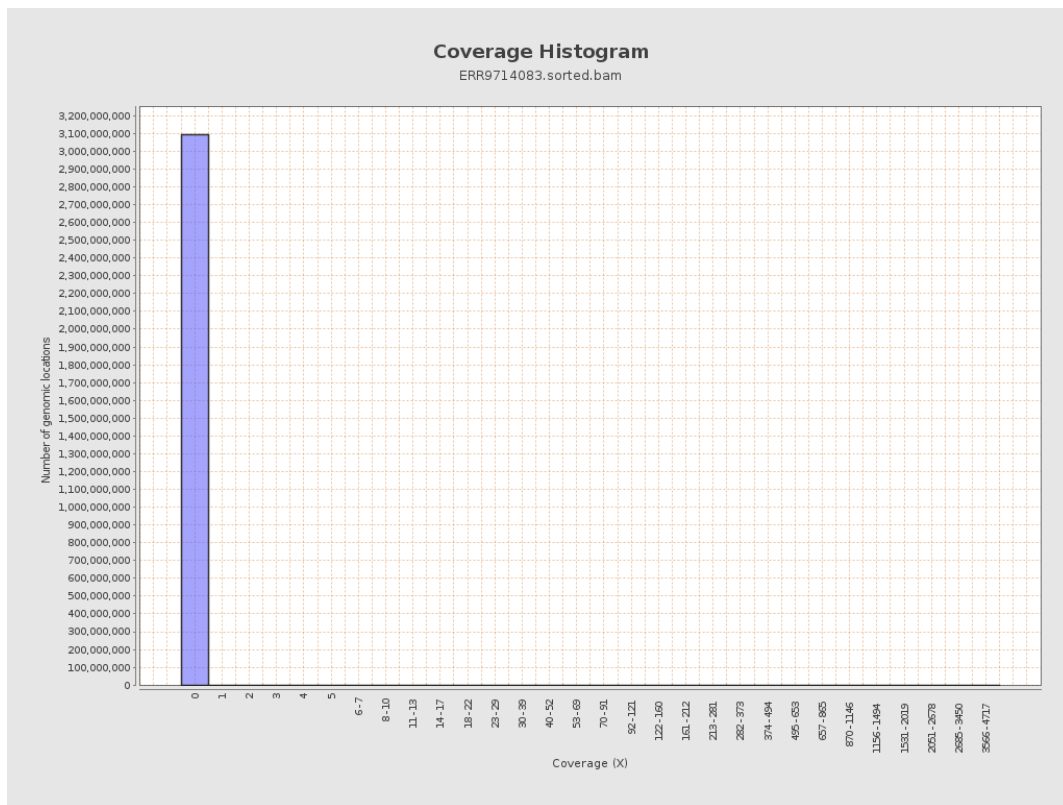
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3787634	0.0152	1.7608
chr2	243199373	4211419	0.0173	3.5374
chr3	198022430	2040221	0.0103	0.9476
chr4	191154276	2004350	0.0105	1.1865
chr5	180915260	2312066	0.0128	1.225
chr6	171115067	1624918	0.0095	0.9009
chr7	159138663	1609712	0.0101	1.0864

chr8	146364022	1951077	0.0133	1.5115
chr9	141213431	1687650	0.012	1.567
chr10	135534747	2167226	0.016	1.5559
chr11	135006516	1850375	0.0137	1.4371
chr12	133851895	1799392	0.0134	1.4343
chr13	115169878	1031180	0.009	0.9775
chr14	107349540	1239807	0.0115	1.2452
chr15	102531392	1189358	0.0116	1.1049
chr16	90354753	1467601	0.0162	1.8162
chr17	81195210	1628675	0.0201	2.1596
chr18	78077248	967526	0.0124	1.1379
chr19	59128983	804253	0.0136	1.3872
chr20	63025520	1038628	0.0165	1.5544
chr21	48129895	292275	0.0061	0.5886
chr22	51304566	541645	0.0106	1.1842
chrMT	16571	250889	15.1402	140.2831
chrX	155270560	3569437	0.023	1.8067
chrY	59373566	164421	0.0028	0.4922

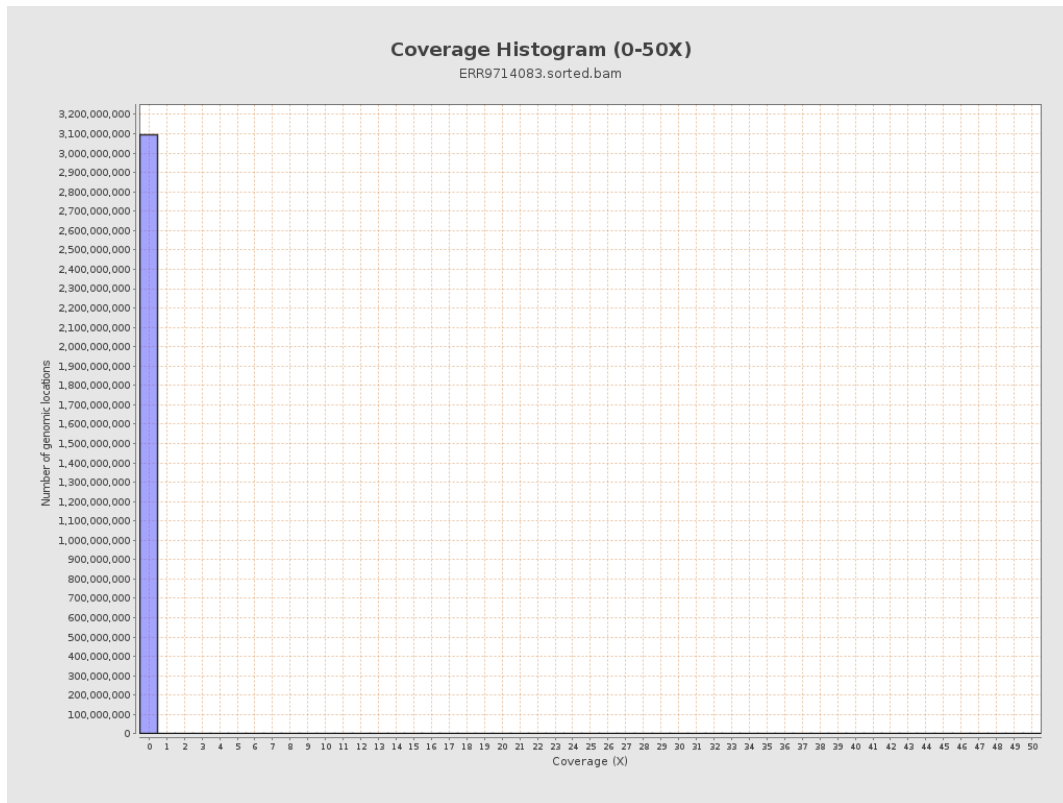
3. Results : Coverage across reference



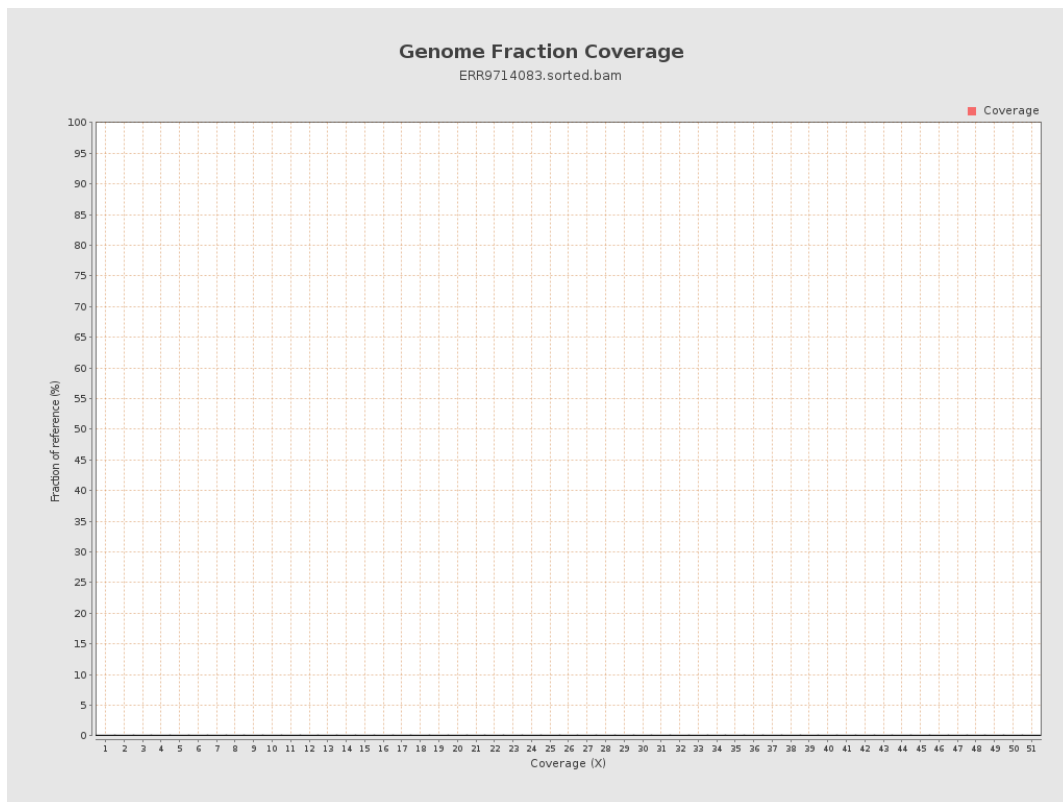
4. Results : Coverage Histogram



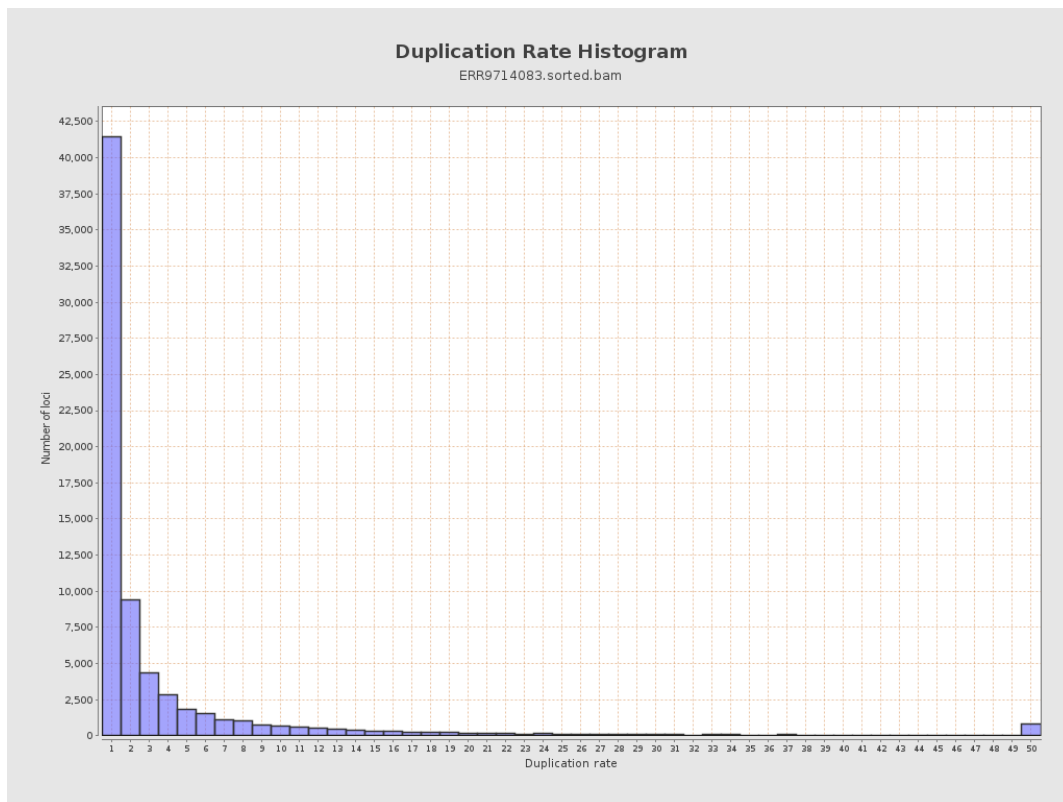
5. Results : Coverage Histogram (0-50X)



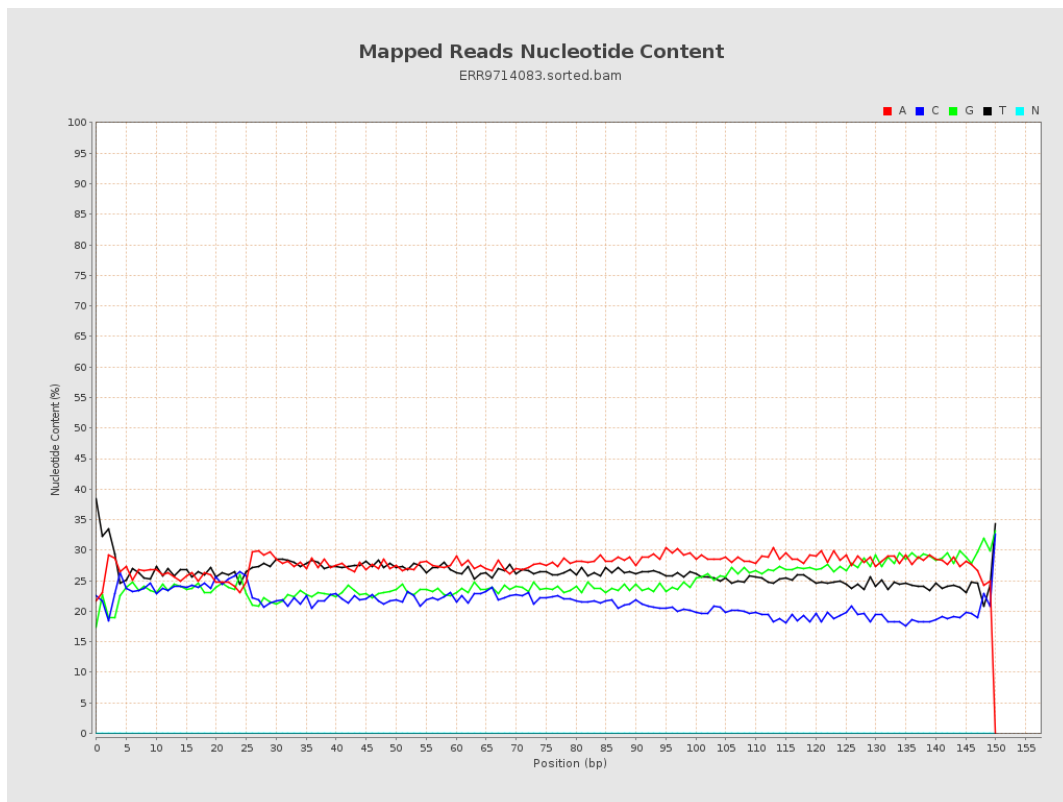
6. Results : Genome Fraction Coverage



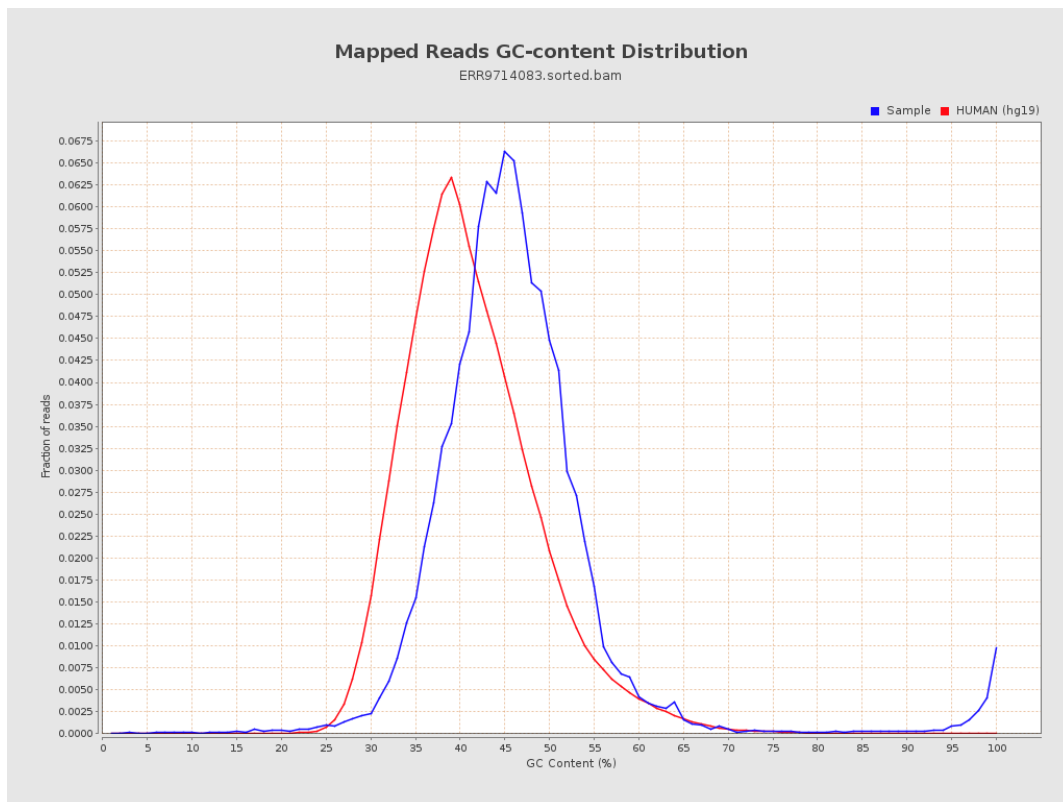
7. Results : Duplication Rate Histogram



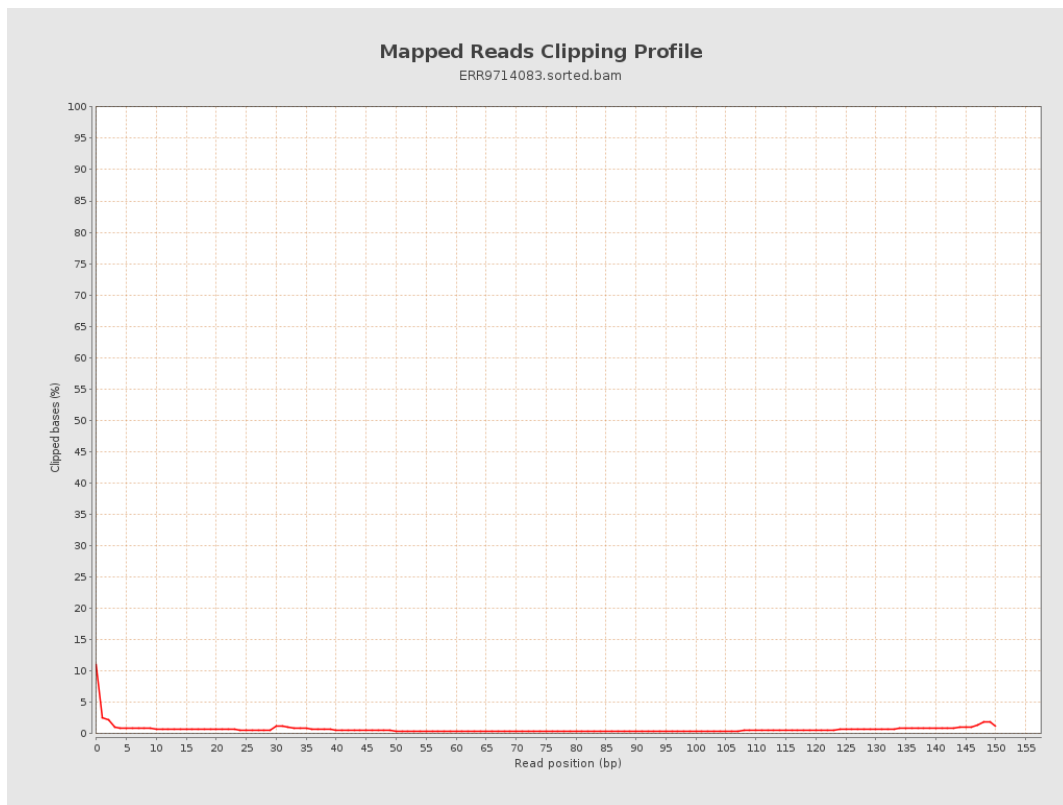
8. Results : Mapped Reads Nucleotide Content



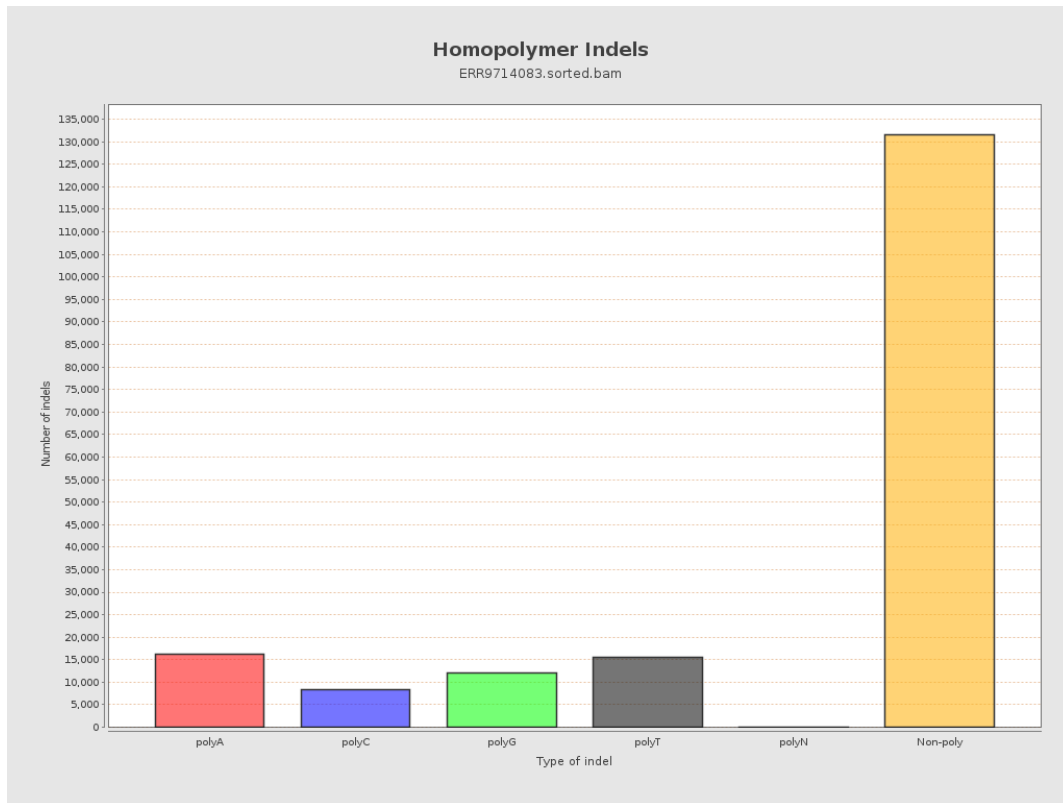
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

