

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:52:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714062.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_ERR9714062 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:52:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	328,750
Mapped reads	231,745 / 70.49%
Unmapped reads	97,005 / 29.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,978 / 2.43%
Read min/max/mean length	30 / 151 / 123.96
Duplicated reads (estimated)	179,060 / 54.47%
Duplication rate	42.4%
Clipped reads	219,318 / 66.71%

2.2. ACGT Content

Number/percentage of A's	8,104,941 / 27.82%
Number/percentage of C's	6,148,567 / 21.11%
Number/percentage of T's	7,678,674 / 26.36%
Number/percentage of G's	7,196,091 / 24.7%
Number/percentage of N's	164 / 0%
GC Percentage	45.81%

2.3. Coverage

Mean	0.0096

Standard Deviation	1.312
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2.4. Mapping Quality

Mean Mapping Quality	52.24
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2.5. Mismatches and indels

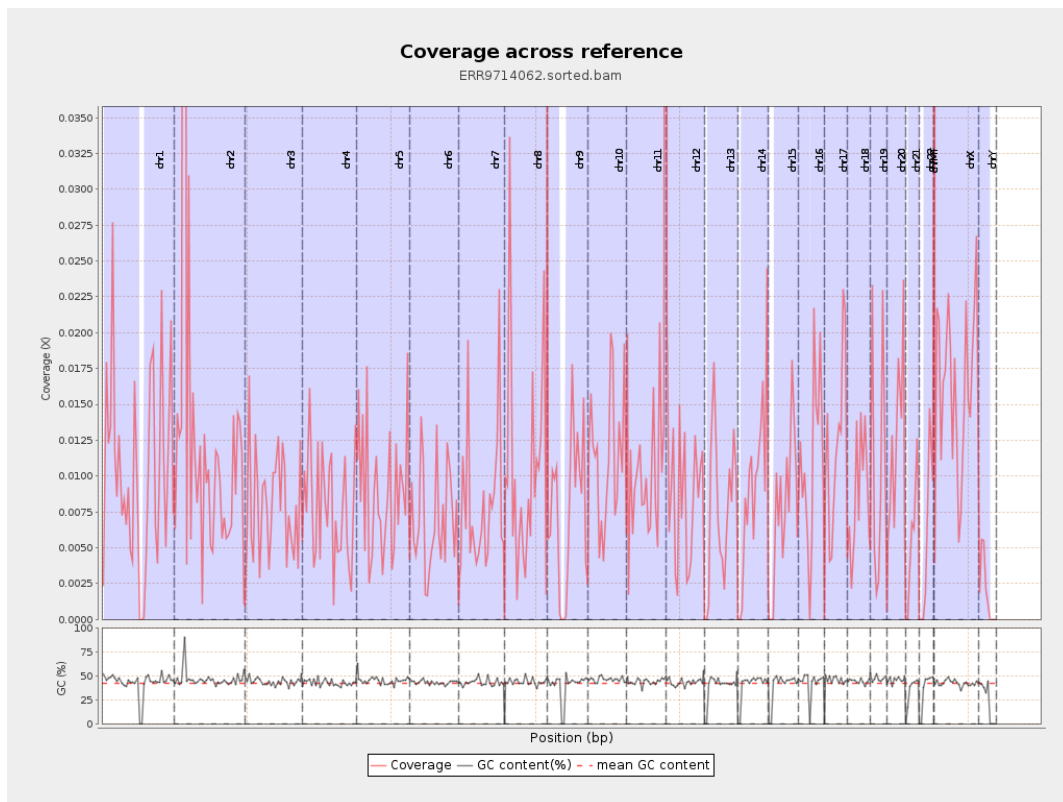
General error rate	4.29%
Mismatches	1,141,998
Insertions	33,814
Mapped reads with at least one insertion	14.11%
Deletions	98,796
Mapped reads with at least one deletion	40.6%
Homopolymer indels	28.22%

2.6. Chromosome stats

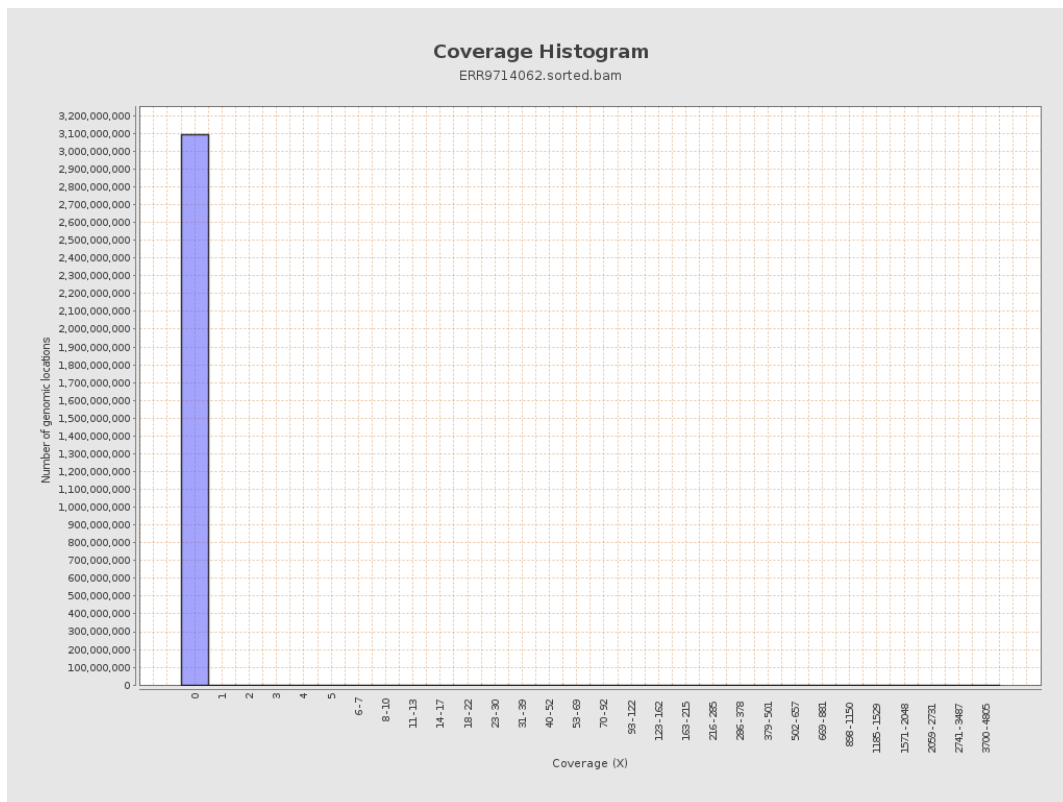
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2531393	0.0102	1.0513
chr2	243199373	3318959	0.0136	3.3158
chr3	198022430	1595936	0.0081	0.7365
chr4	191154276	1472776	0.0077	0.841
chr5	180915260	1618342	0.0089	0.8571
chr6	171115067	1170898	0.0068	0.6641
chr7	159138663	1259232	0.0079	0.8156

chr8	146364022	1478208	0.0101	1.1256
chr9	141213431	1094130	0.0077	0.8469
chr10	135534747	1533380	0.0113	0.9536
chr11	135006516	1421707	0.0105	1.1738
chr12	133851895	1171042	0.0087	0.891
chr13	115169878	862816	0.0075	0.8476
chr14	107349540	985198	0.0092	1.0821
chr15	102531392	781353	0.0076	0.7293
chr16	90354753	977938	0.0108	1.0731
chr17	81195210	965687	0.0119	1.2251
chr18	78077248	705553	0.009	0.7745
chr19	59128983	563073	0.0095	1.1557
chr20	63025520	788382	0.0125	1.0955
chr21	48129895	271573	0.0056	0.6431
chr22	51304566	327608	0.0064	0.7841
chrMT	16571	190188	11.4772	104.5393
chrX	155270560	2503306	0.0161	1.0995
chrY	59373566	120135	0.002	0.3535

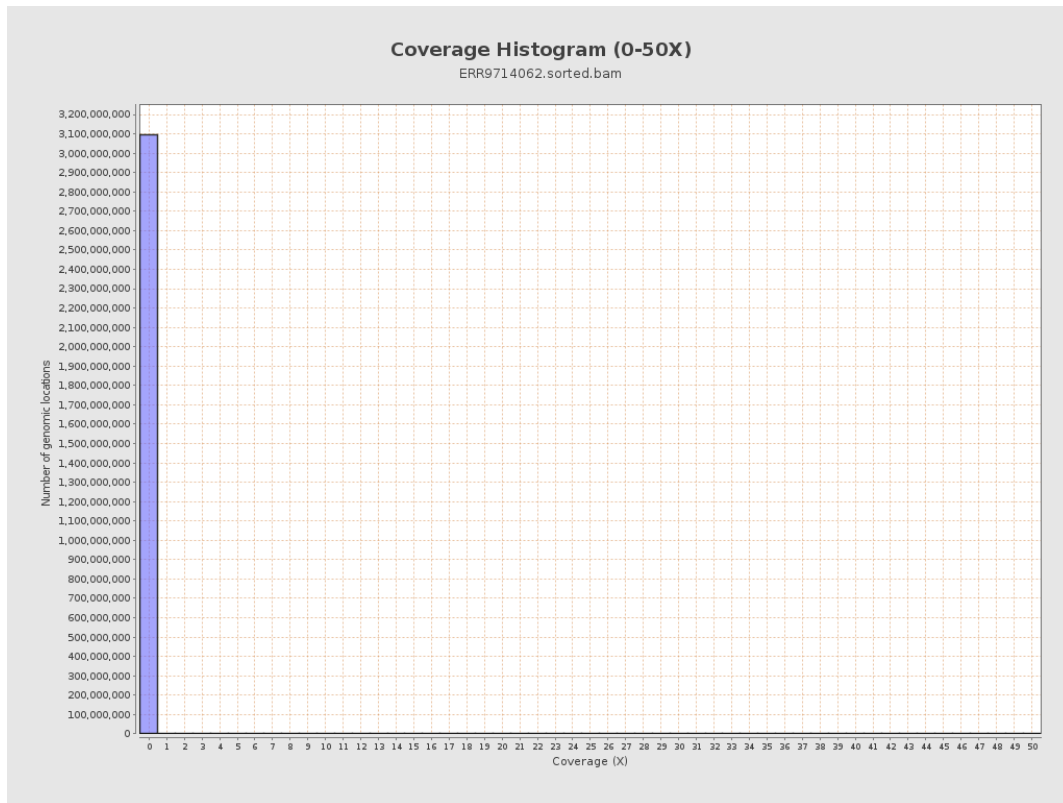
3. Results : Coverage across reference



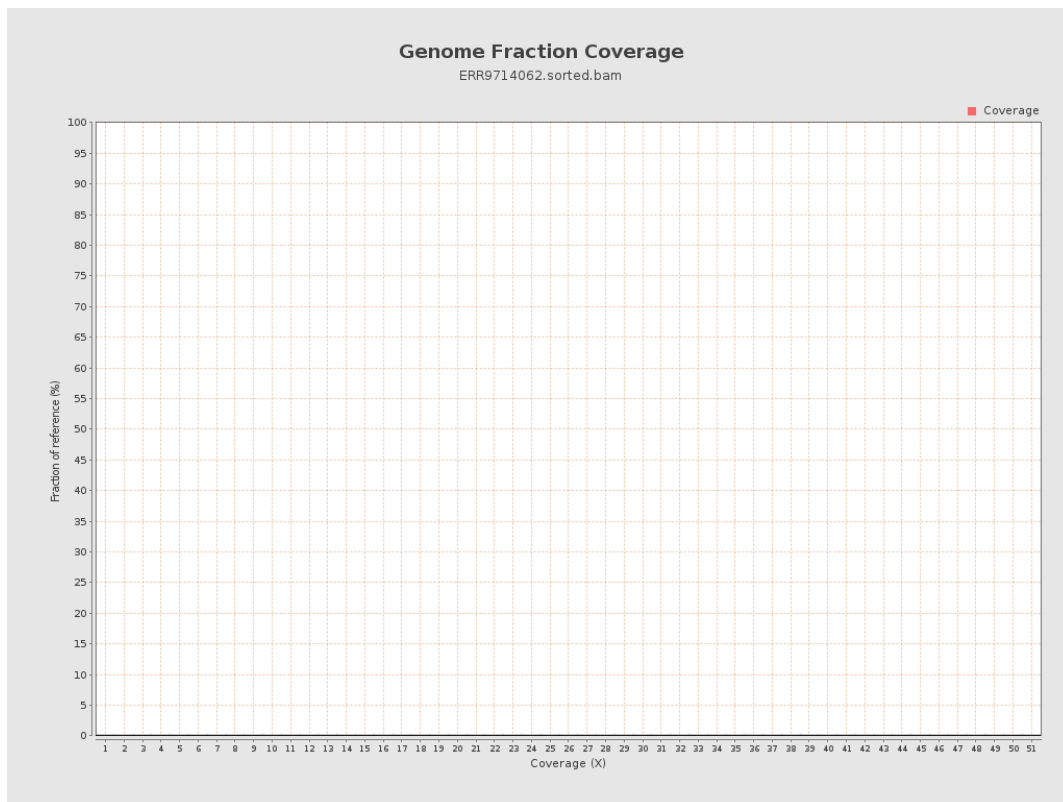
4. Results : Coverage Histogram



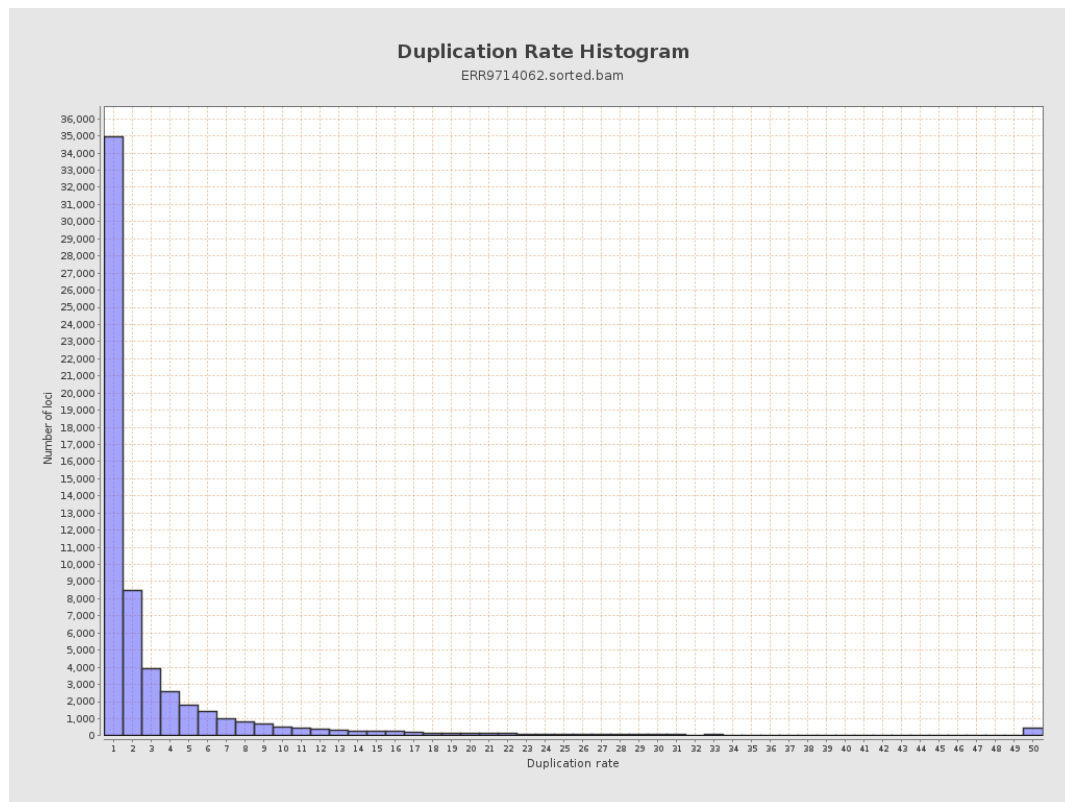
5. Results : Coverage Histogram (0-50X)



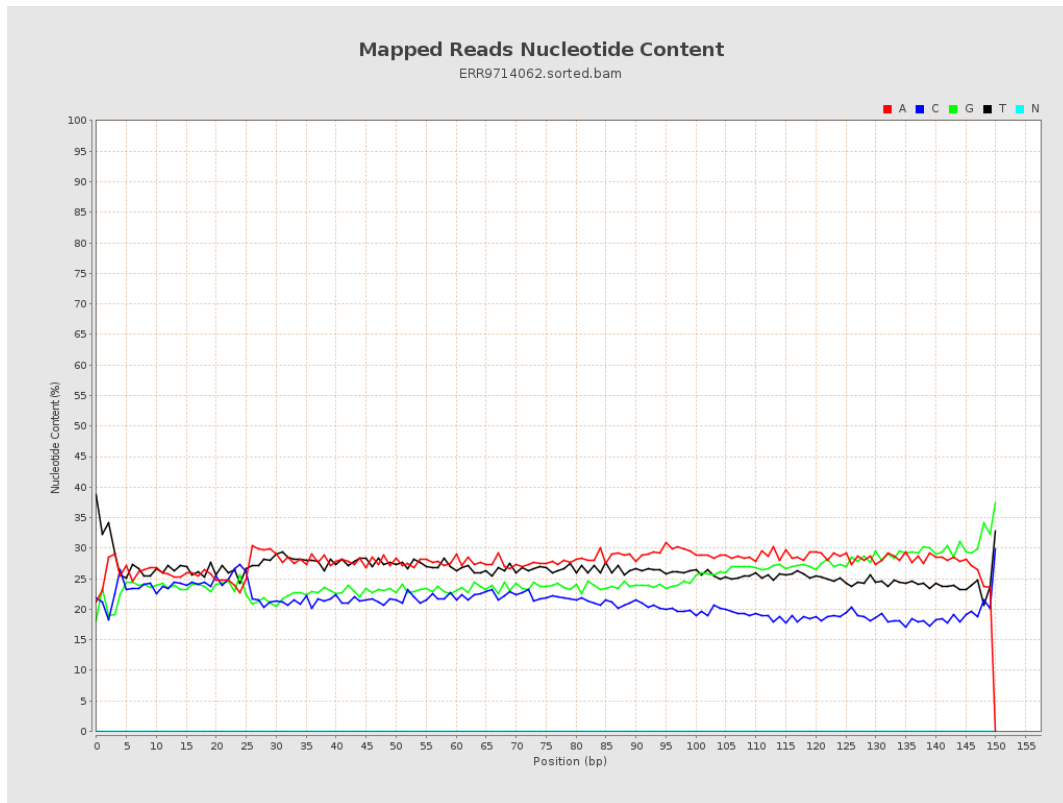
6. Results : Genome Fraction Coverage



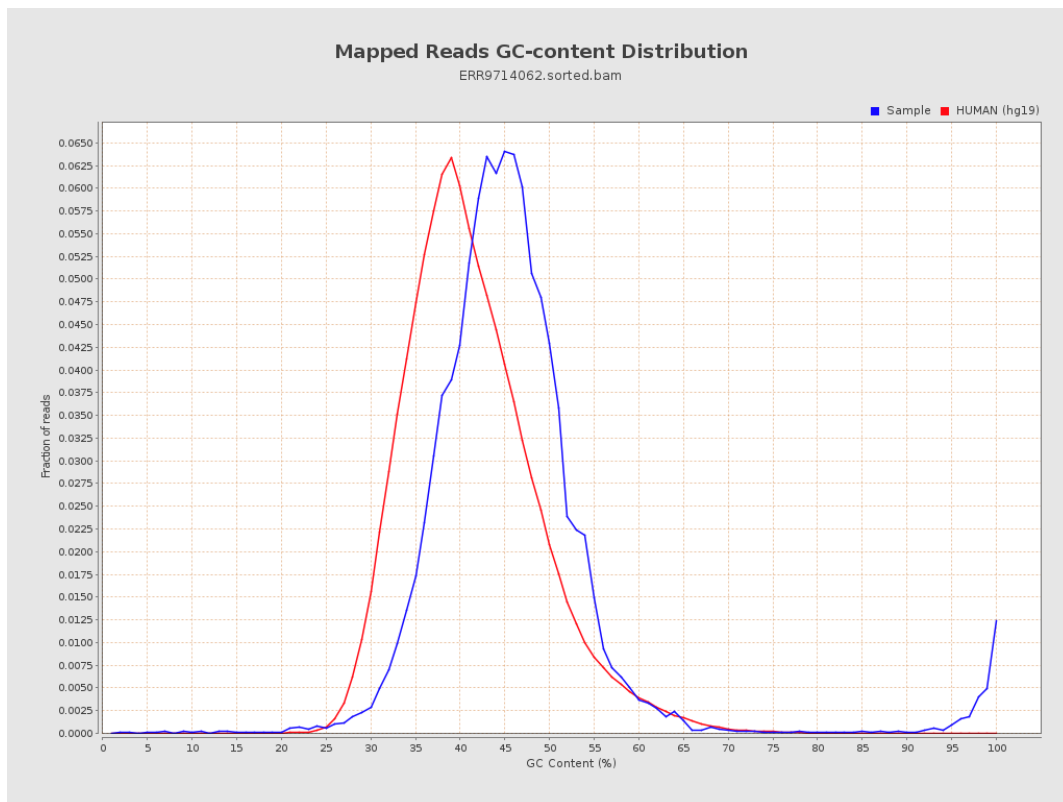
7. Results : Duplication Rate Histogram



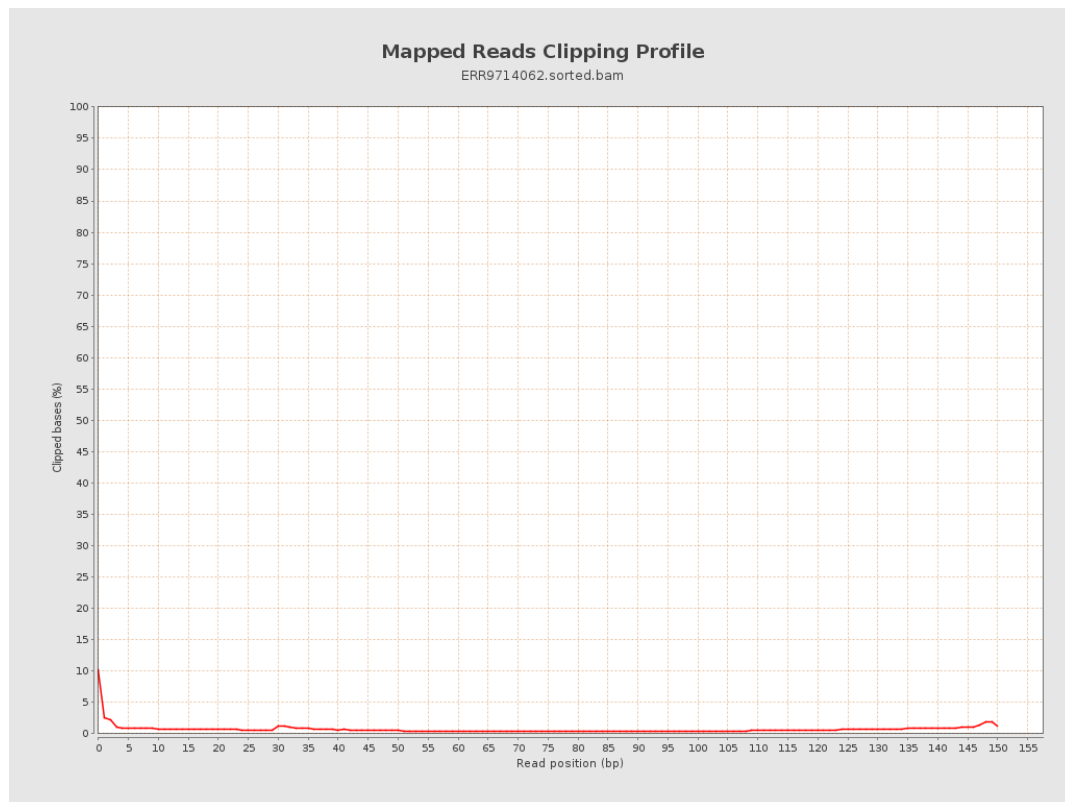
8. Results : Mapped Reads Nucleotide Content



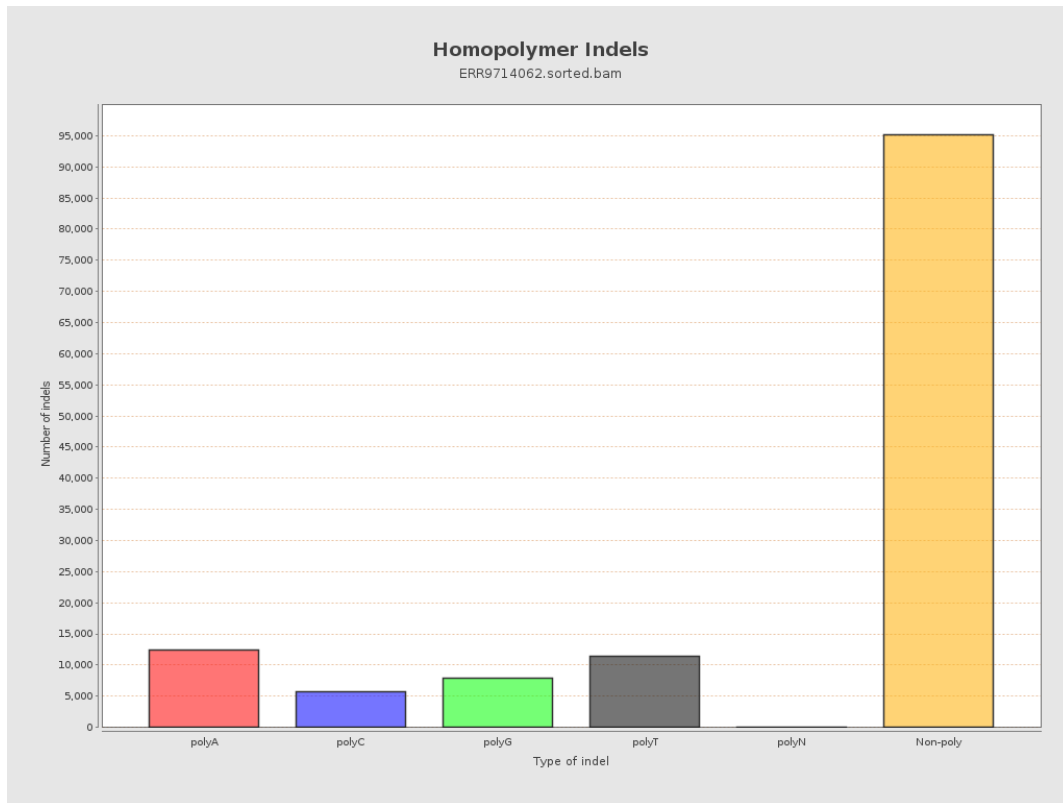
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

