

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:13:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714097.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_ERR9714097 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:13:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	548,872
Mapped reads	386,010 / 70.33%
Unmapped reads	162,862 / 29.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,614 / 2.3%
Read min/max/mean length	30 / 151 / 122.71
Duplicated reads (estimated)	314,174 / 57.24%
Duplication rate	43.55%
Clipped reads	364,581 / 66.42%

2.2. ACGT Content

Number/percentage of A's	13,555,652 / 27.86%
Number/percentage of C's	10,308,658 / 21.19%
Number/percentage of T's	12,889,623 / 26.5%
Number/percentage of G's	11,893,742 / 24.45%
Number/percentage of N's	420 / 0%
GC Percentage	45.64%

2.3. Coverage

Mean	0.016

Standard Deviation	2.133
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2.4. Mapping Quality

Mean Mapping Quality	52.5
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2.5. Mismatches and indels

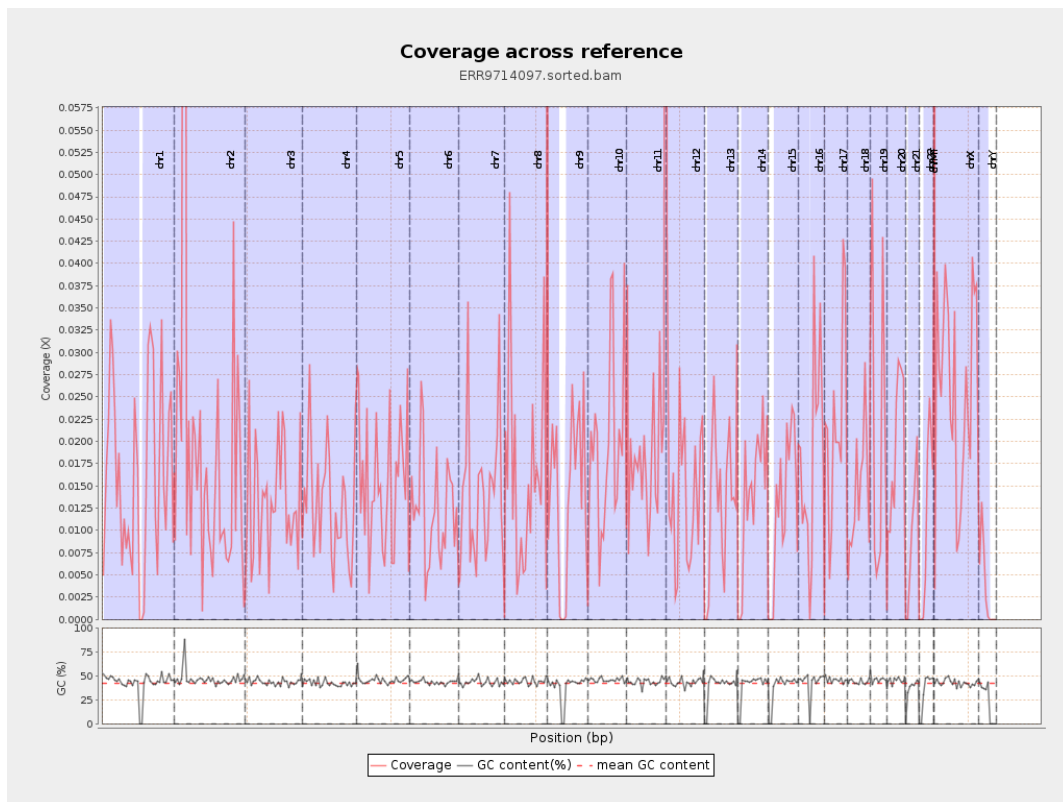
General error rate	4.2%
Mismatches	1,873,582
Insertions	54,579
Mapped reads with at least one insertion	13.69%
Deletions	162,695
Mapped reads with at least one deletion	40.22%
Homopolymer indels	29.11%

2.6. Chromosome stats

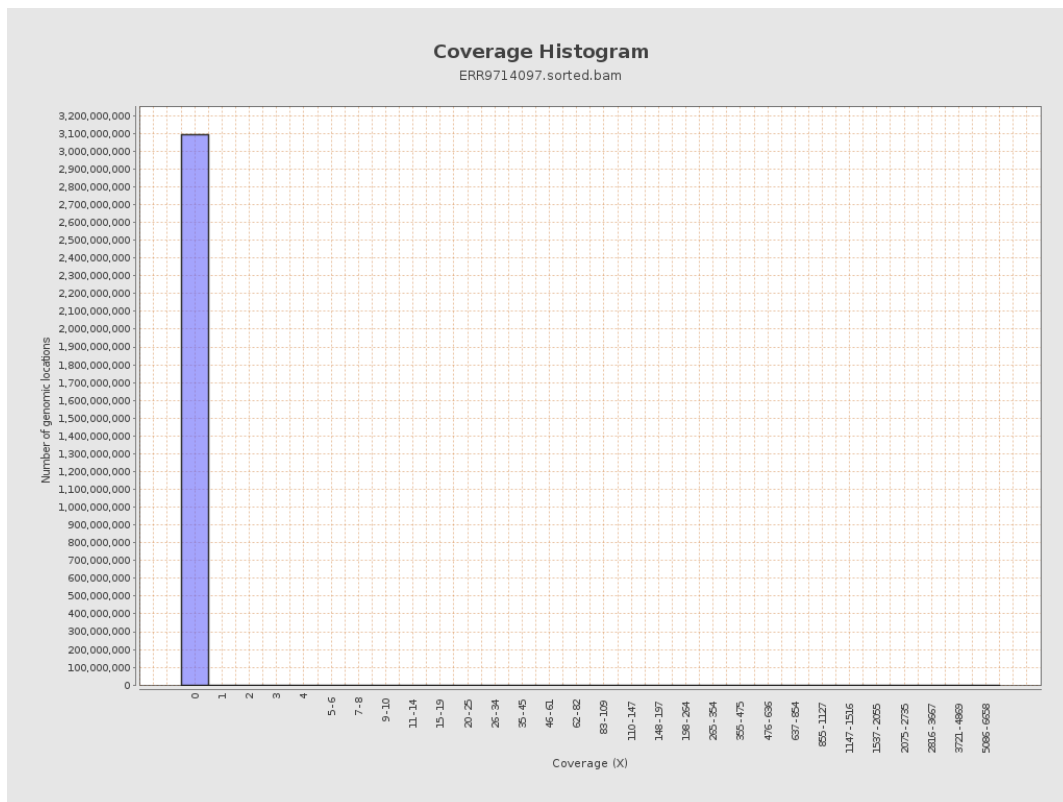
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4000445	0.016	1.8226
chr2	243199373	5101168	0.021	4.9436
chr3	198022430	2666161	0.0135	1.2398
chr4	191154276	2444362	0.0128	1.3995
chr5	180915260	2787495	0.0154	1.531
chr6	171115067	2053093	0.012	1.1741
chr7	159138663	2224932	0.014	1.4201

chr8	146364022	2292794	0.0157	1.7338
chr9	141213431	2076884	0.0147	1.6692
chr10	135534747	2641365	0.0195	1.98
chr11	135006516	2510807	0.0186	1.87
chr12	133851895	2007841	0.015	1.514
chr13	115169878	1468135	0.0127	1.5504
chr14	107349540	1483629	0.0138	1.3109
chr15	102531392	1303289	0.0127	1.2148
chr16	90354753	1645680	0.0182	1.9063
chr17	81195210	1745164	0.0215	2.3274
chr18	78077248	1147624	0.0147	1.6781
chr19	59128983	1123042	0.019	2.2833
chr20	63025520	1224602	0.0194	1.5726
chr21	48129895	433634	0.009	1.0055
chr22	51304566	587937	0.0115	1.194
chrMT	16571	404912	24.435	223.8396
chrX	155270560	3987246	0.0257	1.7299
chrY	59373566	218149	0.0037	0.547

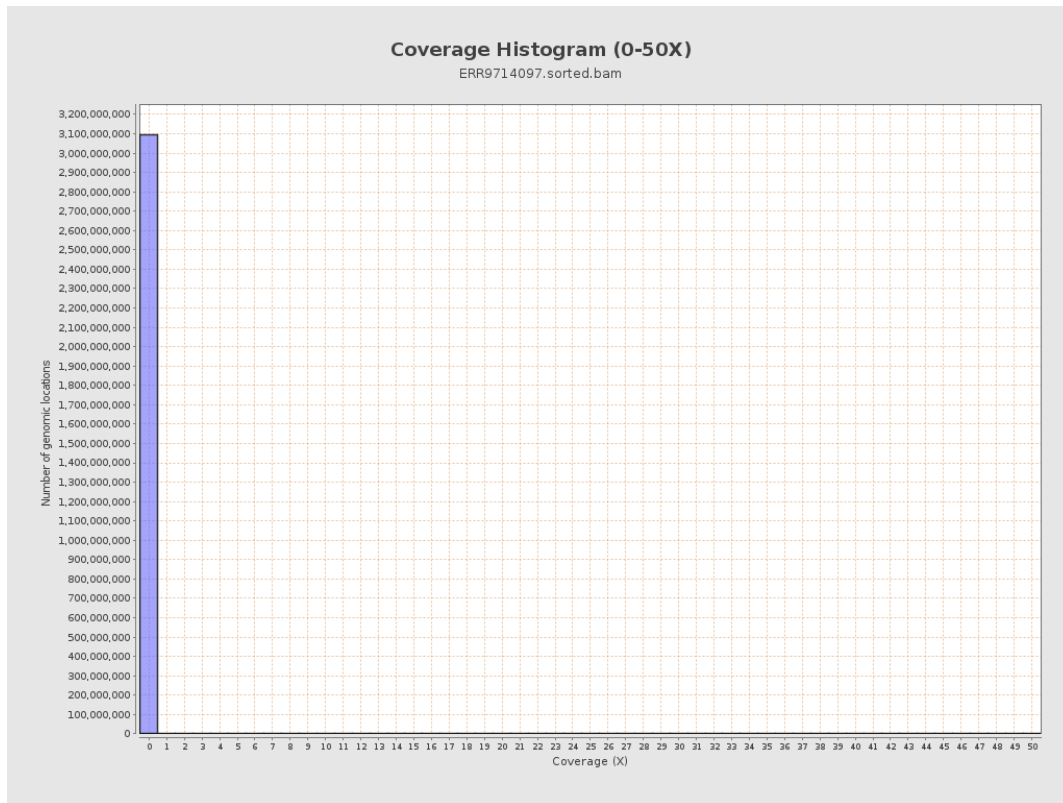
3. Results : Coverage across reference



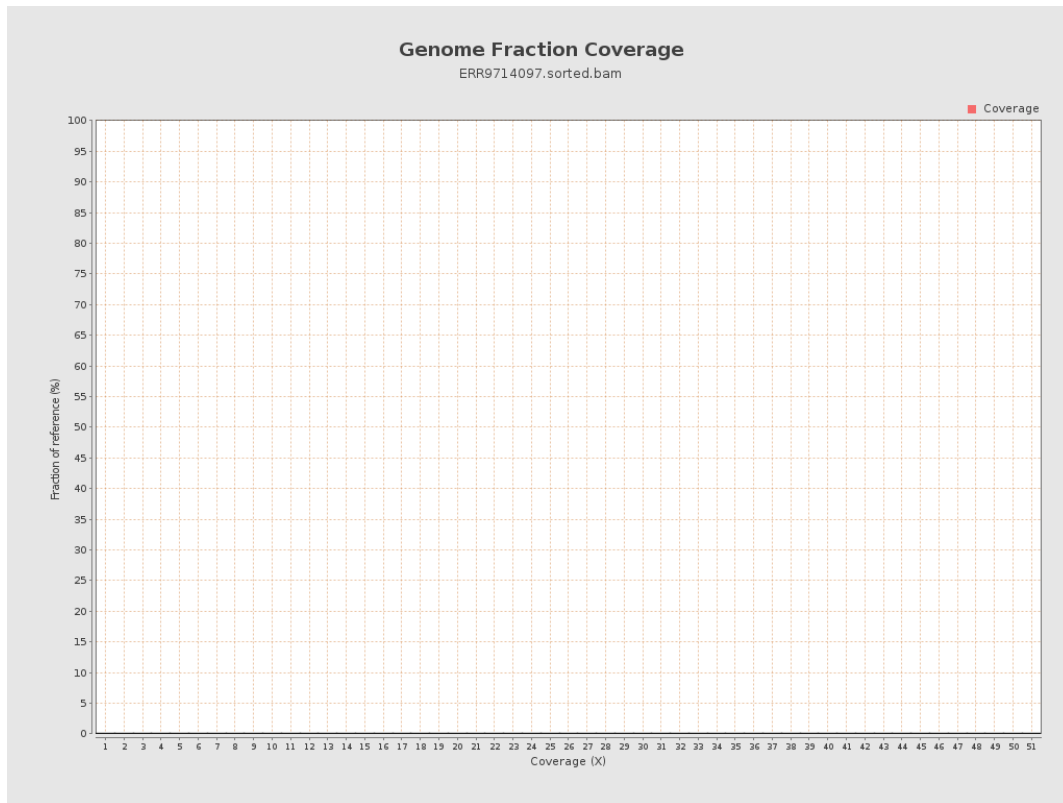
4. Results : Coverage Histogram



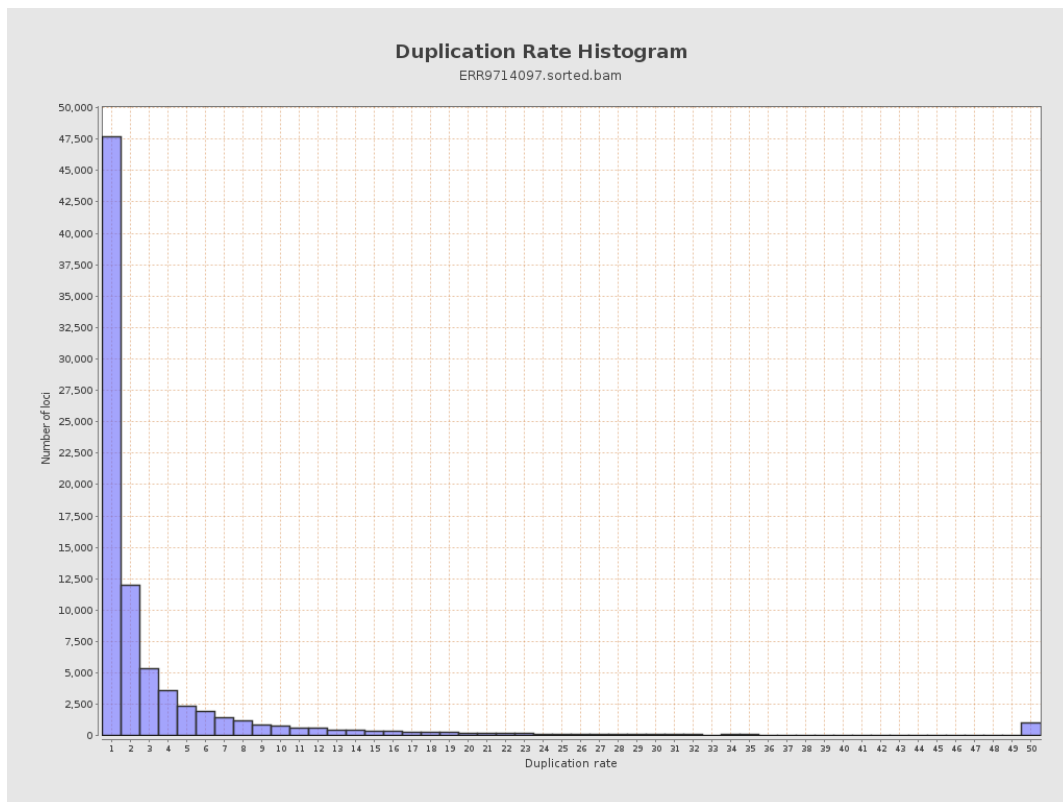
5. Results : Coverage Histogram (0-50X)



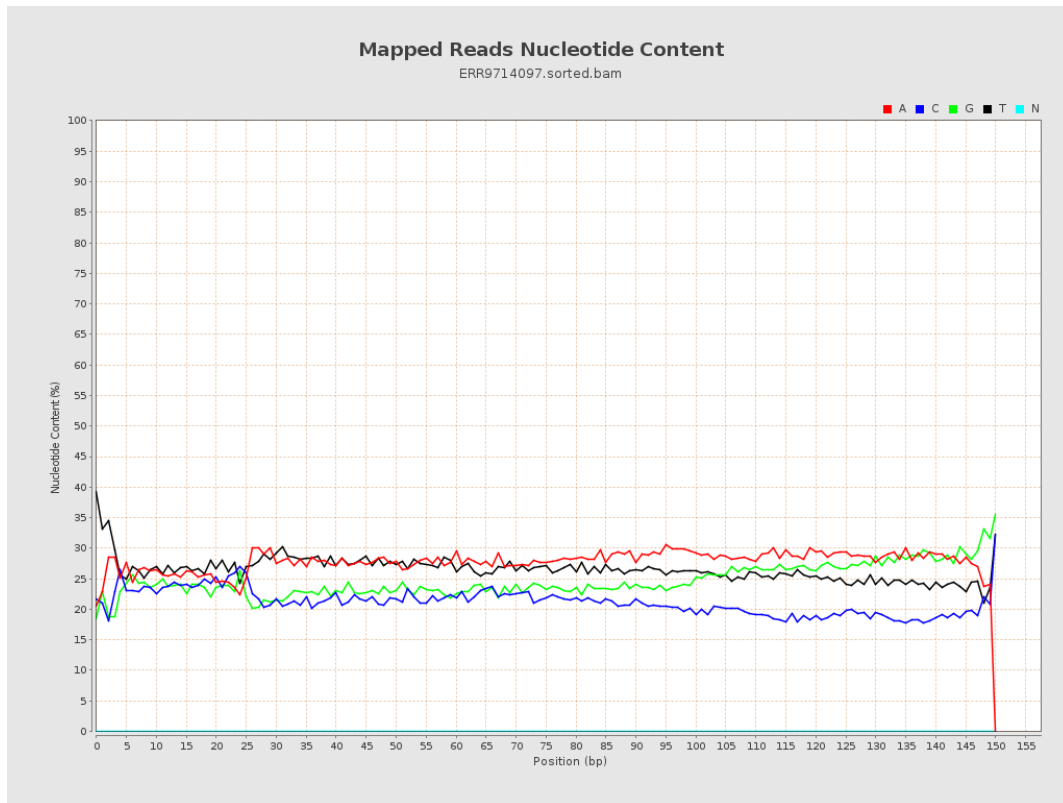
6. Results : Genome Fraction Coverage



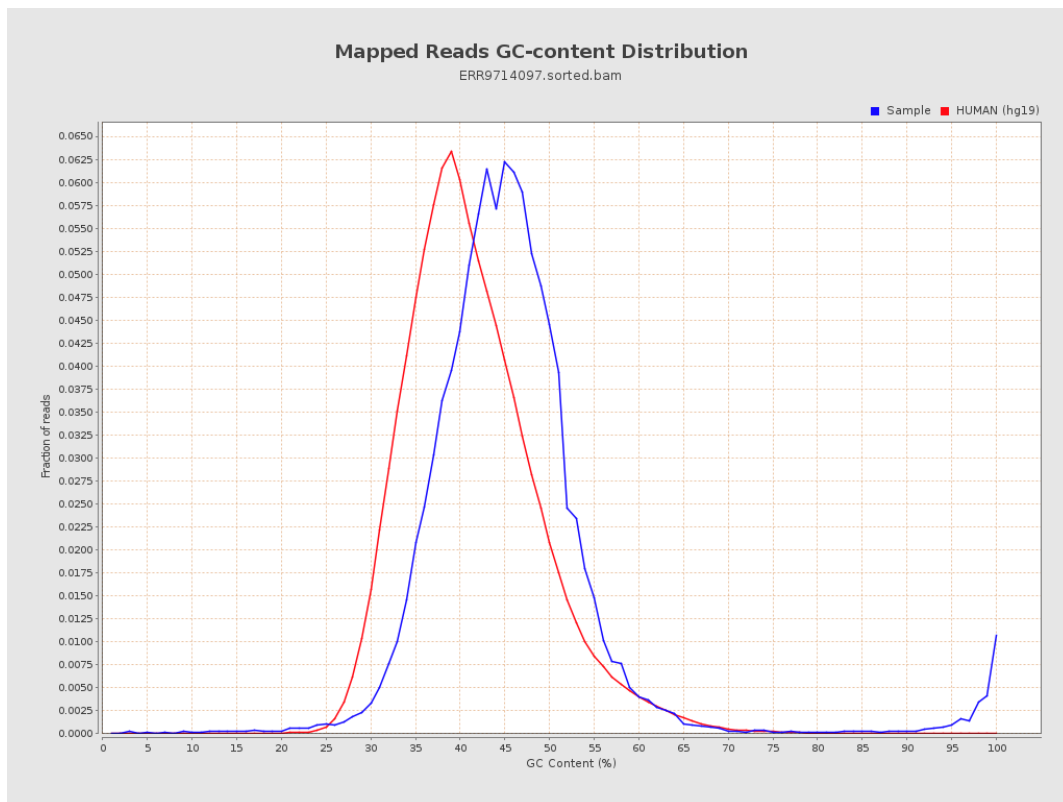
7. Results : Duplication Rate Histogram



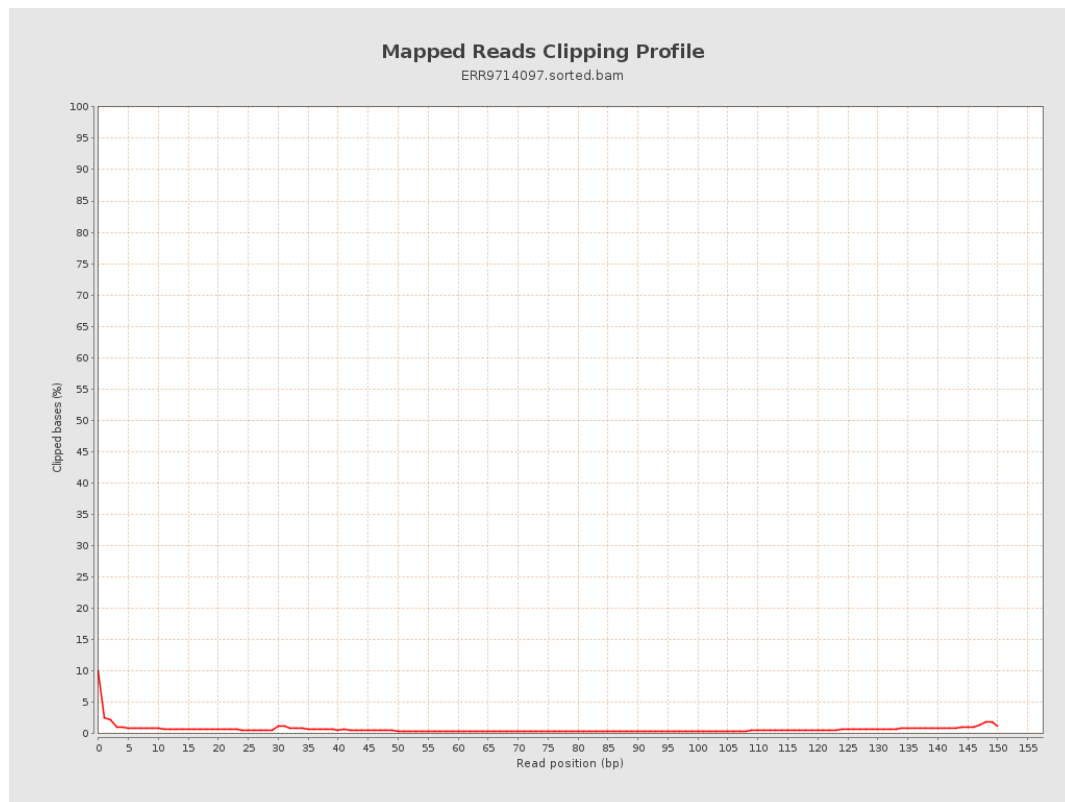
8. Results : Mapped Reads Nucleotide Content



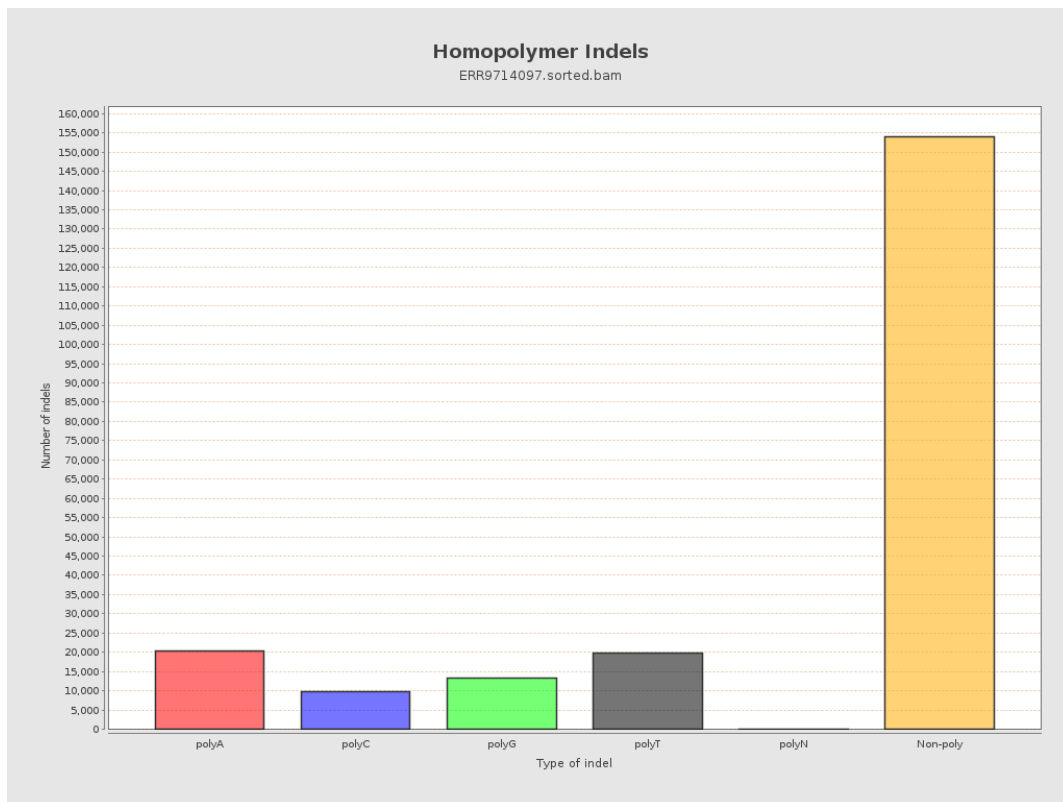
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

