

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:17:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714047.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_ERR9714047 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:17:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	250,452
Mapped reads	220,944 / 88.22%
Unmapped reads	29,508 / 11.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,089 / 2.83%
Read min/max/mean length	30 / 151 / 138.74
Duplicated reads (estimated)	184,580 / 73.7%
Duplication rate	42.9%
Clipped reads	209,801 / 83.77%

2.2. ACGT Content

Number/percentage of A's	7,499,042 / 26.74%
Number/percentage of C's	6,305,954 / 22.49%
Number/percentage of T's	7,097,502 / 25.31%
Number/percentage of G's	7,138,213 / 25.46%
Number/percentage of N's	278 / 0%
GC Percentage	47.94%

2.3. Coverage

Mean	0.0093

Standard Deviation	2.5385
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2.4. Mapping Quality

Mean Mapping Quality	51.38
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2.5. Mismatches and indels

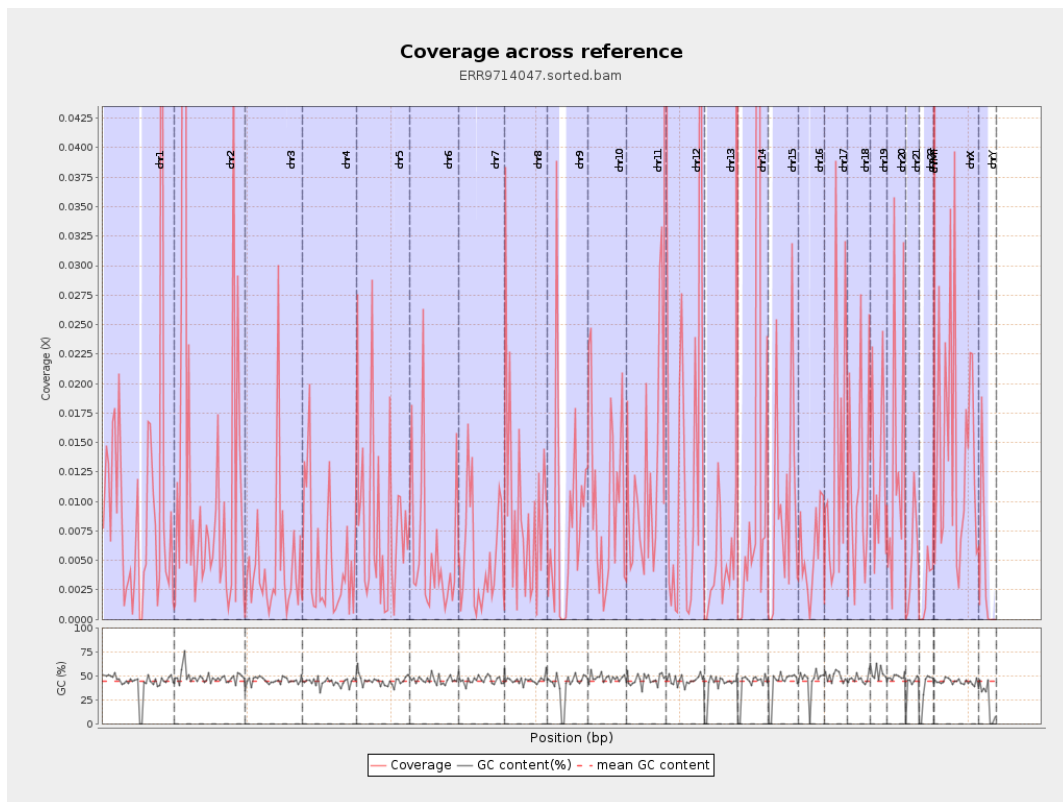
General error rate	4.4%
Mismatches	1,151,073
Insertions	30,144
Mapped reads with at least one insertion	13.17%
Deletions	101,747
Mapped reads with at least one deletion	43.77%
Homopolymer indels	30.18%

2.6. Chromosome stats

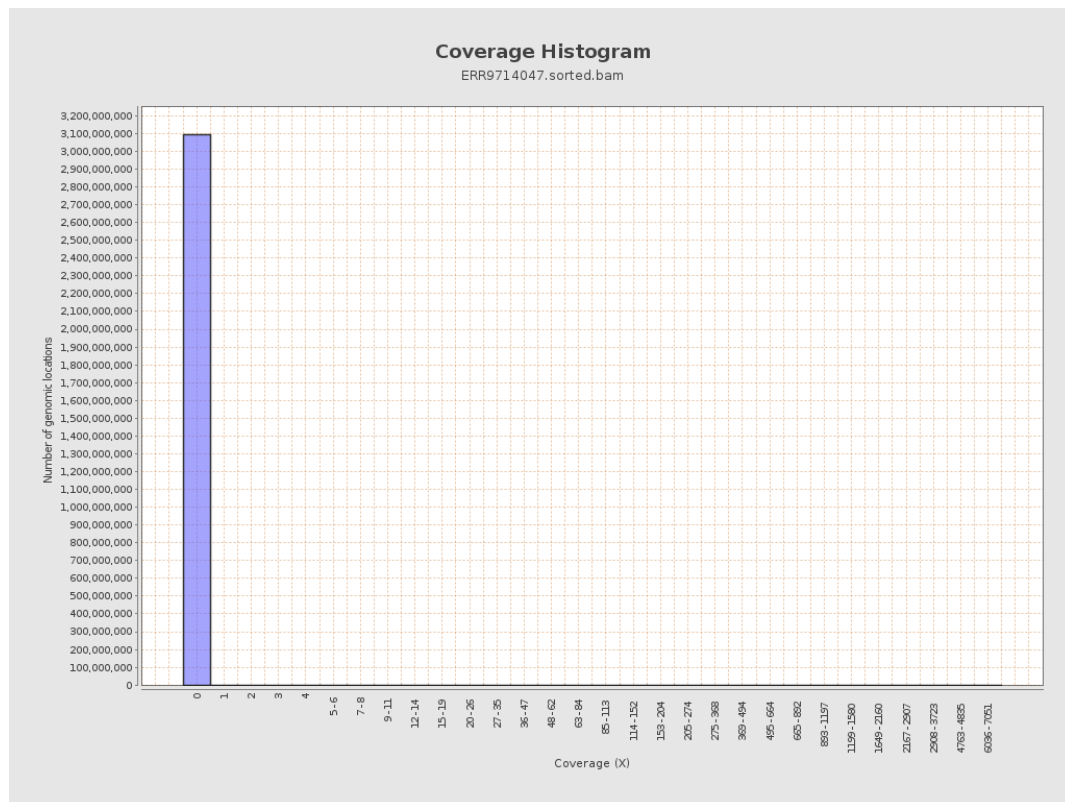
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2458534	0.0099	2.4775
chr2	243199373	3252205	0.0134	3.8306
chr3	198022430	903715	0.0046	0.9206
chr4	191154276	945183	0.0049	0.9239
chr5	180915260	1358423	0.0075	1.7232
chr6	171115067	1016963	0.0059	1.2016
chr7	159138663	835404	0.0052	1.0736

chr8	146364022	1388797	0.0095	1.9538
chr9	141213431	1073751	0.0076	2.0205
chr10	135534747	1359956	0.01	1.4975
chr11	135006516	1649404	0.0122	2.0172
chr12	133851895	1849195	0.0138	3.6006
chr13	115169878	787184	0.0068	2.2394
chr14	107349540	1700127	0.0158	8.0033
chr15	102531392	953987	0.0093	1.5962
chr16	90354753	513620	0.0057	0.6921
chr17	81195210	1090636	0.0134	2.7207
chr18	78077248	898336	0.0115	2.4749
chr19	59128983	743368	0.0126	1.3494
chr20	63025520	878295	0.0139	2.3015
chr21	48129895	239217	0.005	0.9103
chr22	51304566	154239	0.003	0.3445
chrMT	16571	85107	5.1359	44.4207
chrX	155270560	2297076	0.0148	1.6263
chrY	59373566	242694	0.0041	1.0018

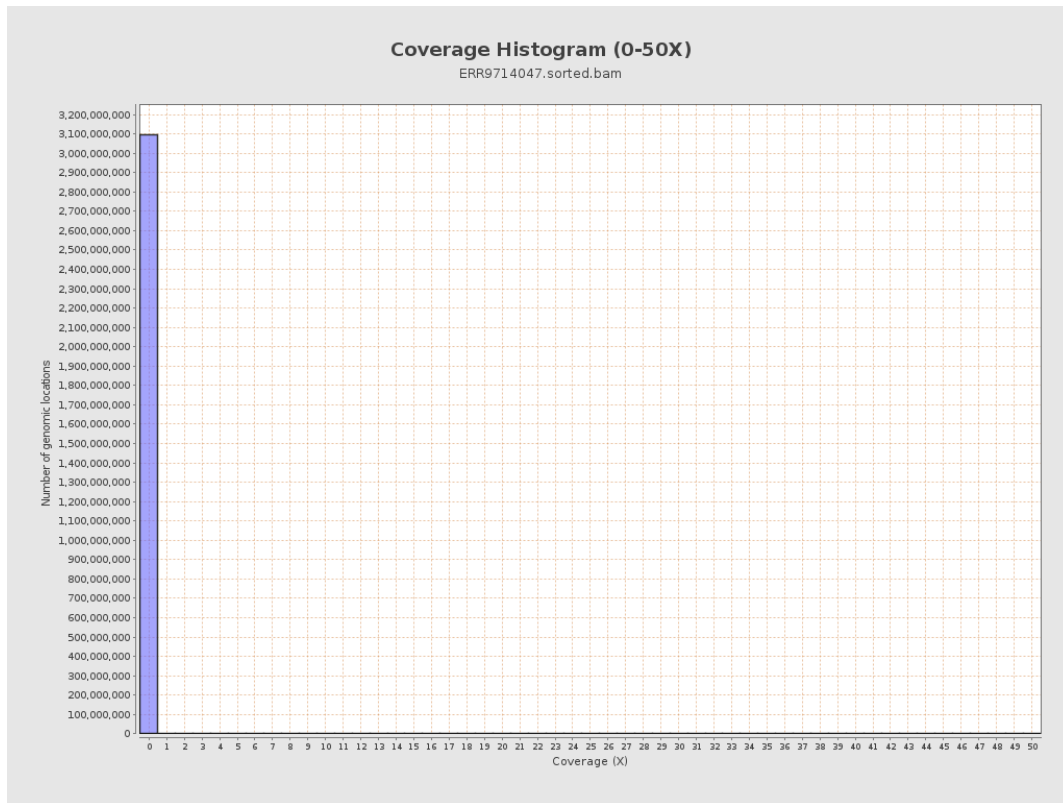
3. Results : Coverage across reference



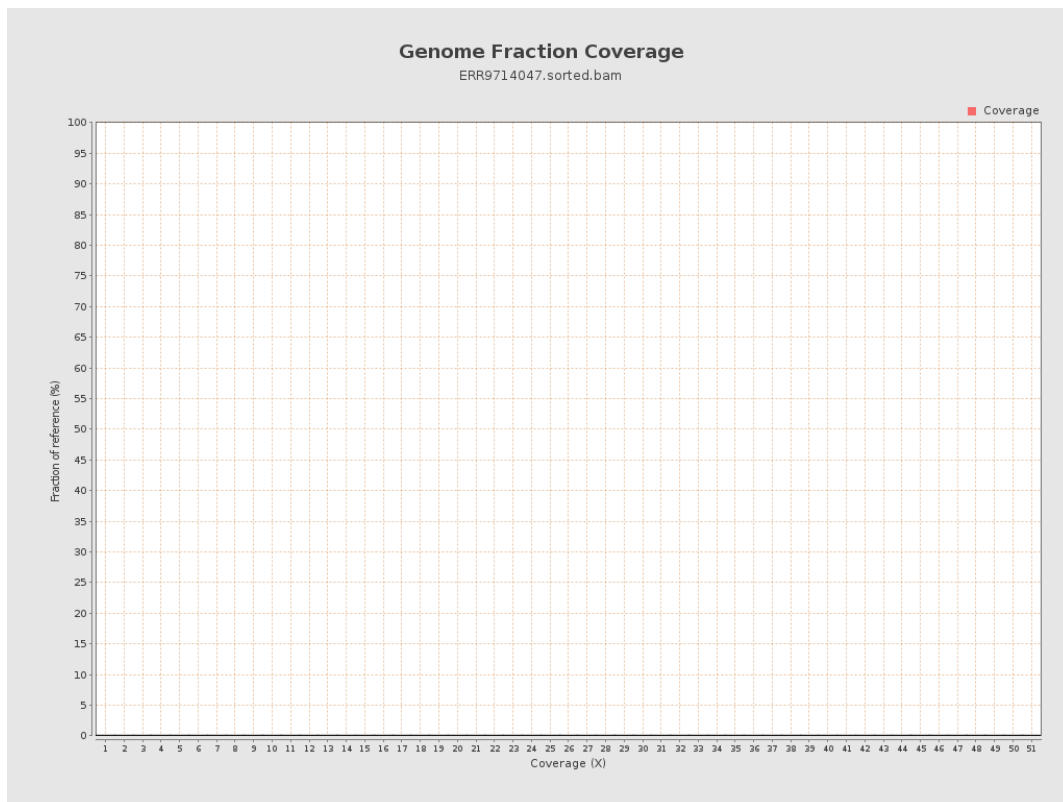
4. Results : Coverage Histogram



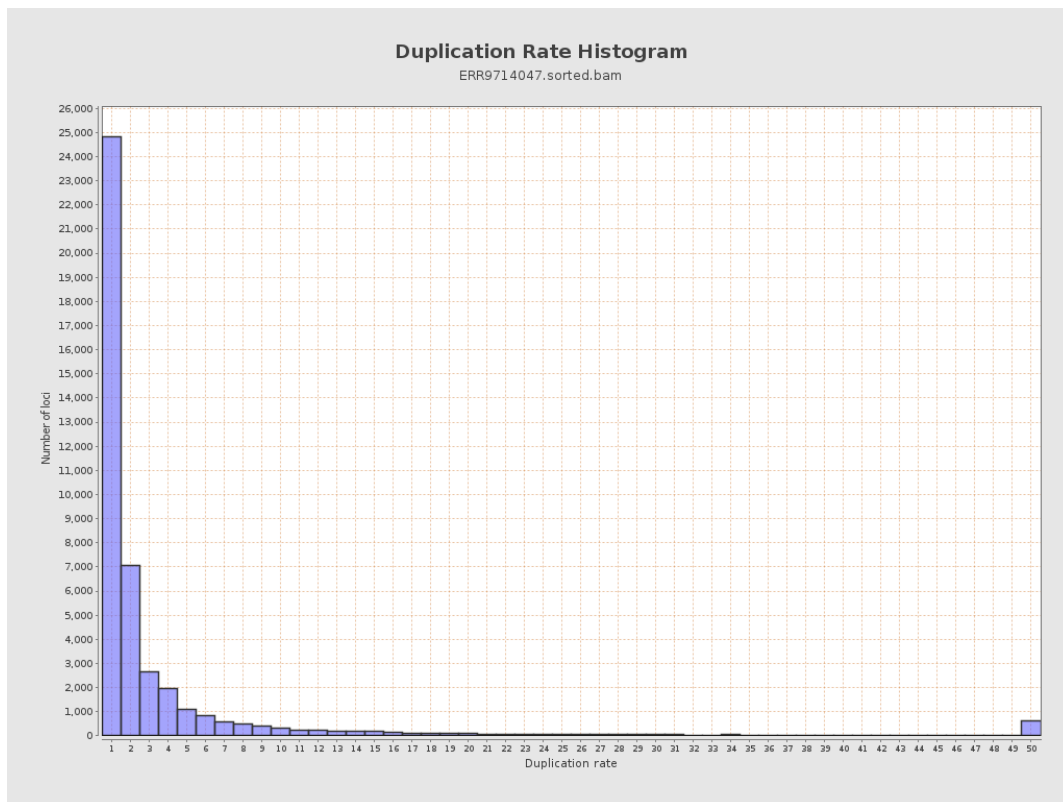
5. Results : Coverage Histogram (0-50X)



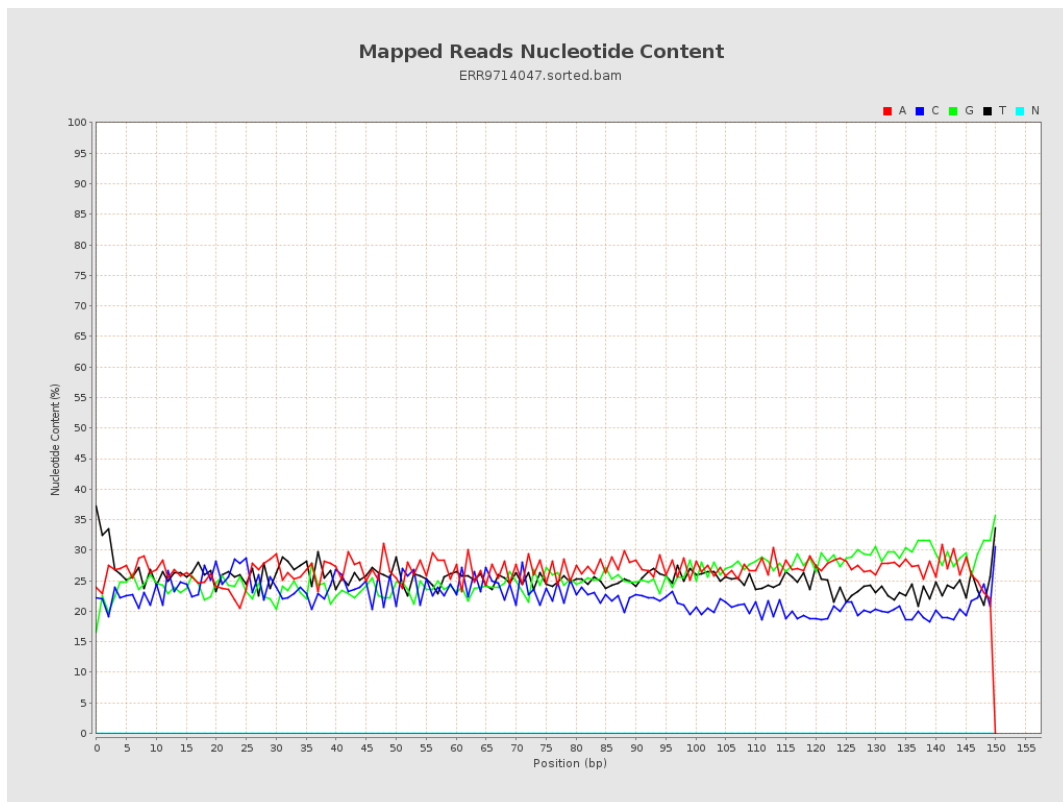
6. Results : Genome Fraction Coverage



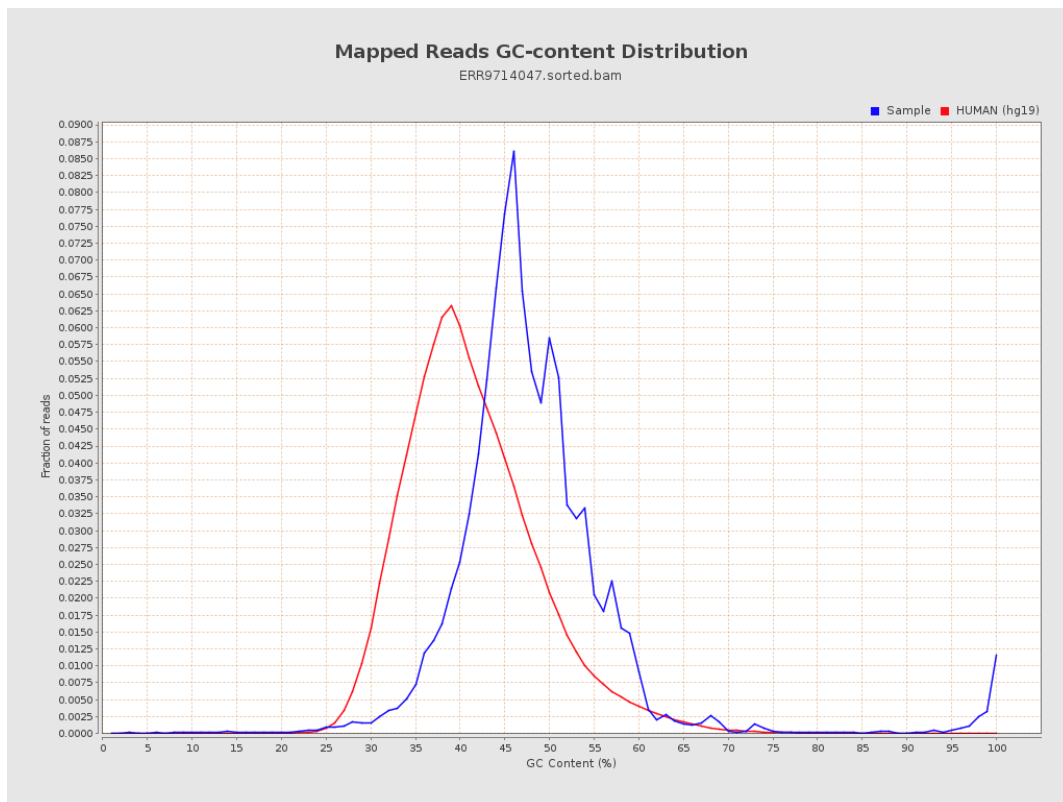
7. Results : Duplication Rate Histogram



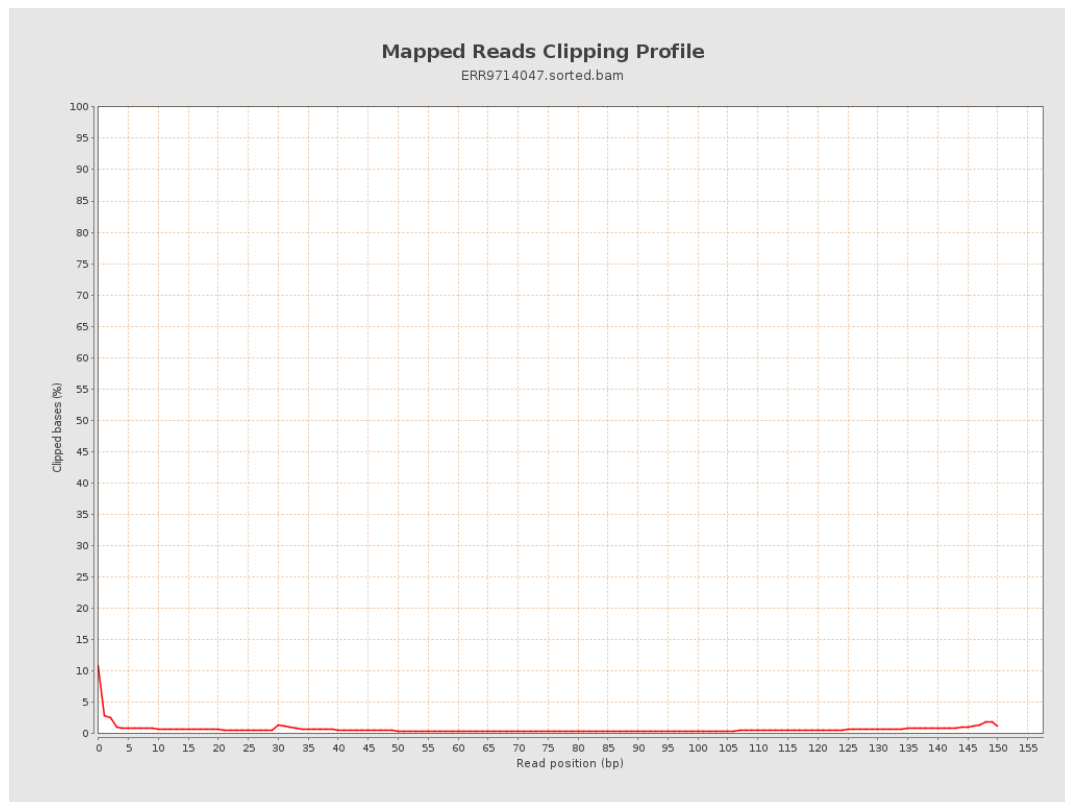
8. Results : Mapped Reads Nucleotide Content



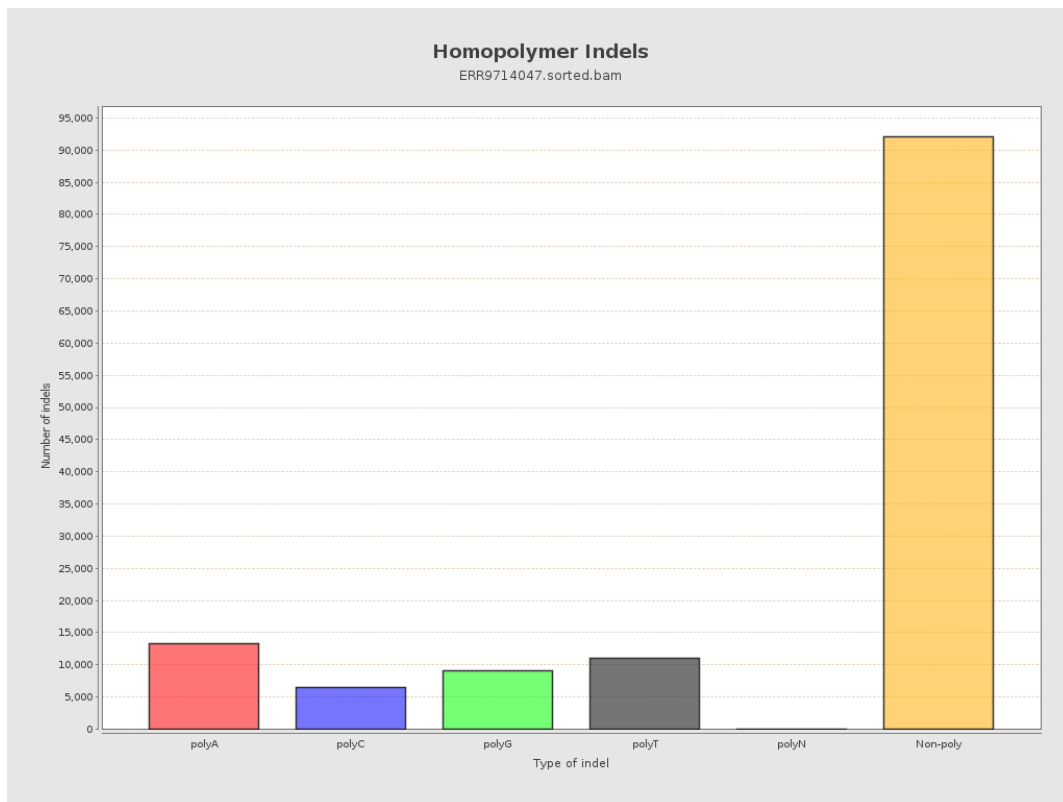
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

