

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:14:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714119.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_ERR9714119 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:14:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	614,468
Mapped reads	513,215 / 83.52%
Unmapped reads	101,253 / 16.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,669 / 2.71%
Read min/max/mean length	30 / 151 / 134.86
Duplicated reads (estimated)	500,263 / 81.41%
Duplication rate	34.8%
Clipped reads	491,727 / 80.02%

2.2. ACGT Content

Number/percentage of A's	18,005,943 / 28.23%
Number/percentage of C's	13,141,673 / 20.6%
Number/percentage of T's	17,350,028 / 27.2%
Number/percentage of G's	15,289,535 / 23.97%
Number/percentage of N's	468 / 0%
GC Percentage	44.57%

2.3. Coverage

Mean	0.021

Standard Deviation	20.6572
--------------------	---------

2.4. Mapping Quality

Mean Mapping Quality	27.15
----------------------	-------

2.5. Mismatches and indels

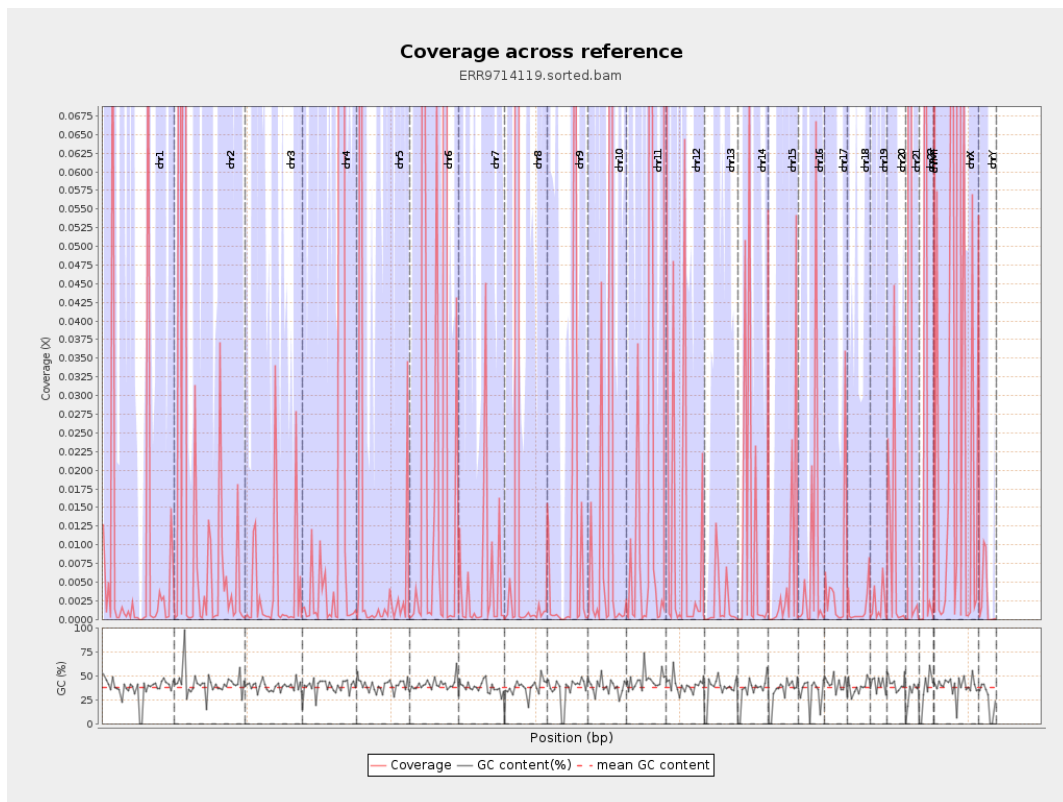
General error rate	4.33%
Mismatches	2,513,049
Insertions	87,033
Mapped reads with at least one insertion	16.61%
Deletions	162,960
Mapped reads with at least one deletion	30.53%
Homopolymer indels	25.4%

2.6. Chromosome stats

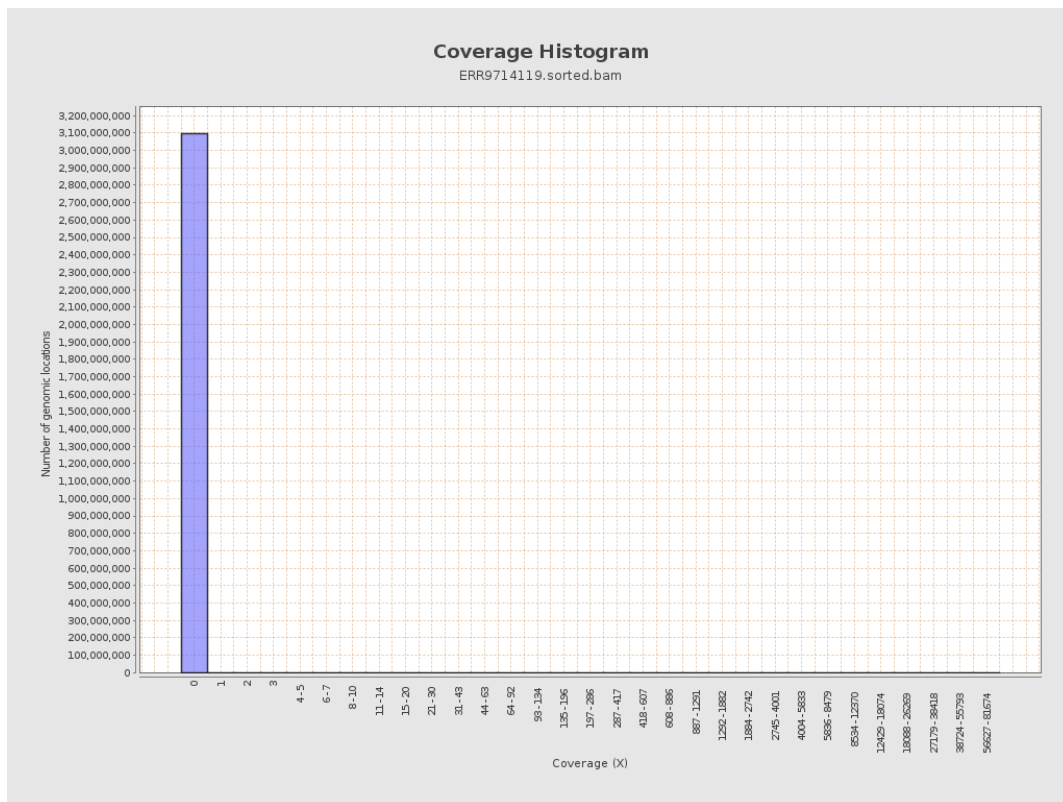
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1939423	0.0078	4.6305
chr2	243199373	3942408	0.0162	7.9311
chr3	198022430	815521	0.0041	1.74
chr4	191154276	5058568	0.0265	17.9716
chr5	180915260	1666442	0.0092	4.6352
chr6	171115067	16211778	0.0947	66.3196
chr7	159138663	887838	0.0056	2.3165

chr8	146364022	8593984	0.0587	44.4245
chr9	141213431	1315686	0.0093	5.9214
chr10	135534747	3062955	0.0226	14.8538
chr11	135006516	2981858	0.0221	12.668
chr12	133851895	1460047	0.0109	4.6356
chr13	115169878	245390	0.0021	0.6391
chr14	107349540	1245490	0.0116	3.9956
chr15	102531392	696148	0.0068	3.0759
chr16	90354753	753218	0.0083	2.7967
chr17	81195210	441464	0.0054	1.6252
chr18	78077248	107047	0.0014	0.3911
chr19	59128983	112394	0.0019	0.6002
chr20	63025520	612623	0.0097	2.9219
chr21	48129895	2487226	0.0517	25.3305
chr22	51304566	1202579	0.0234	12.8516
chrMT	16571	191190	11.5376	97.3357
chrX	155270560	8756775	0.0564	23.8913
chrY	59373566	171258	0.0029	0.8094

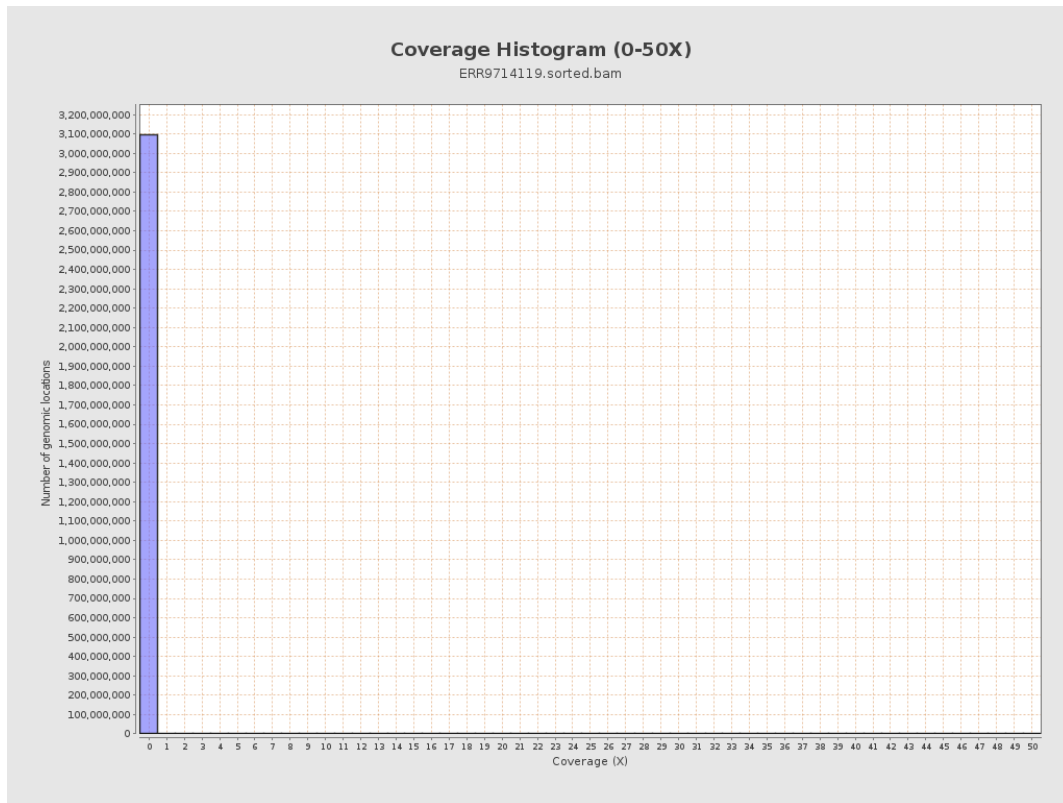
3. Results : Coverage across reference



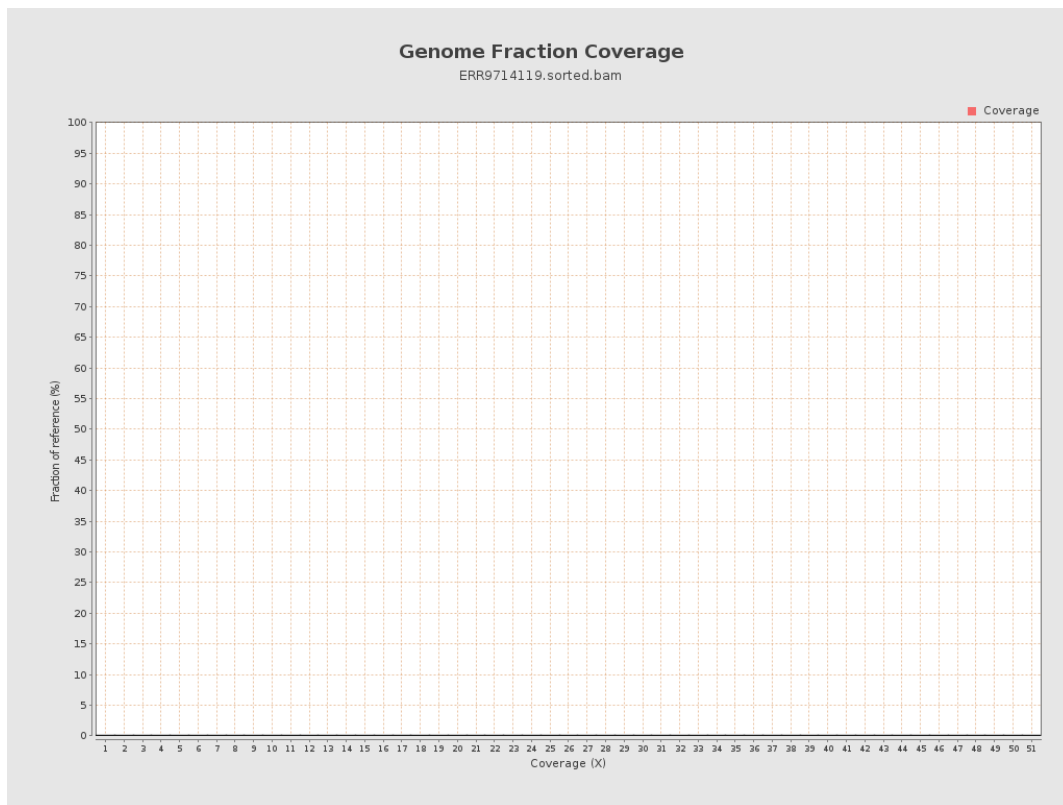
4. Results : Coverage Histogram



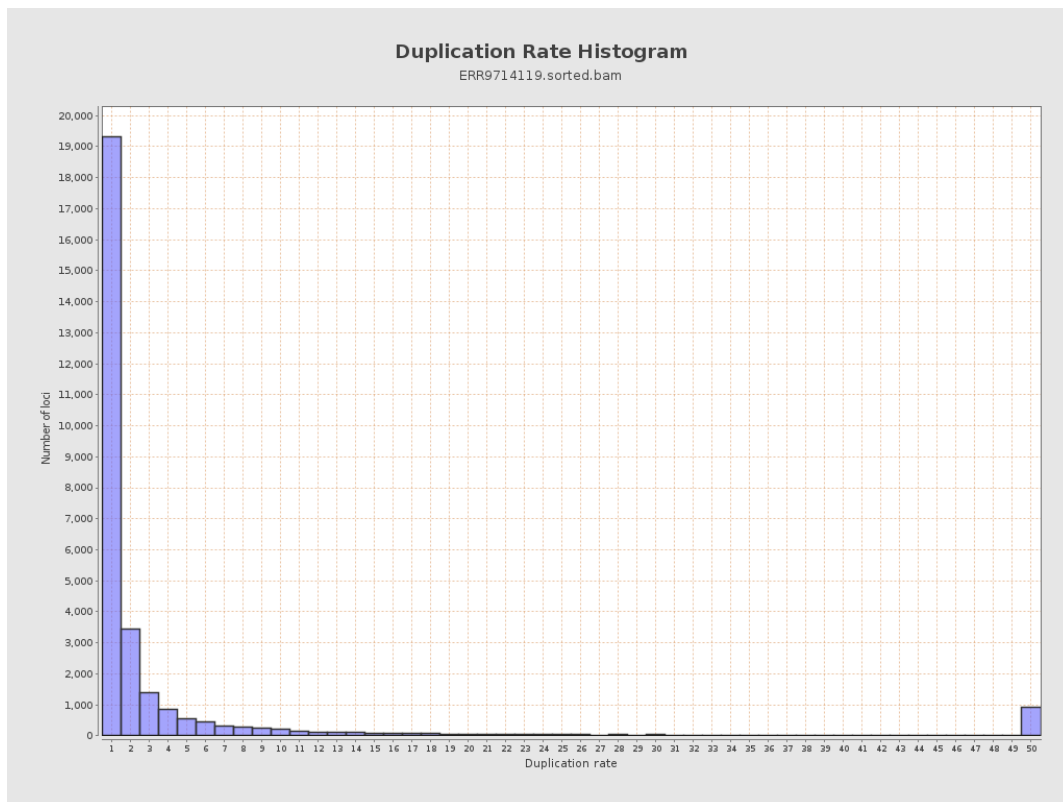
5. Results : Coverage Histogram (0-50X)



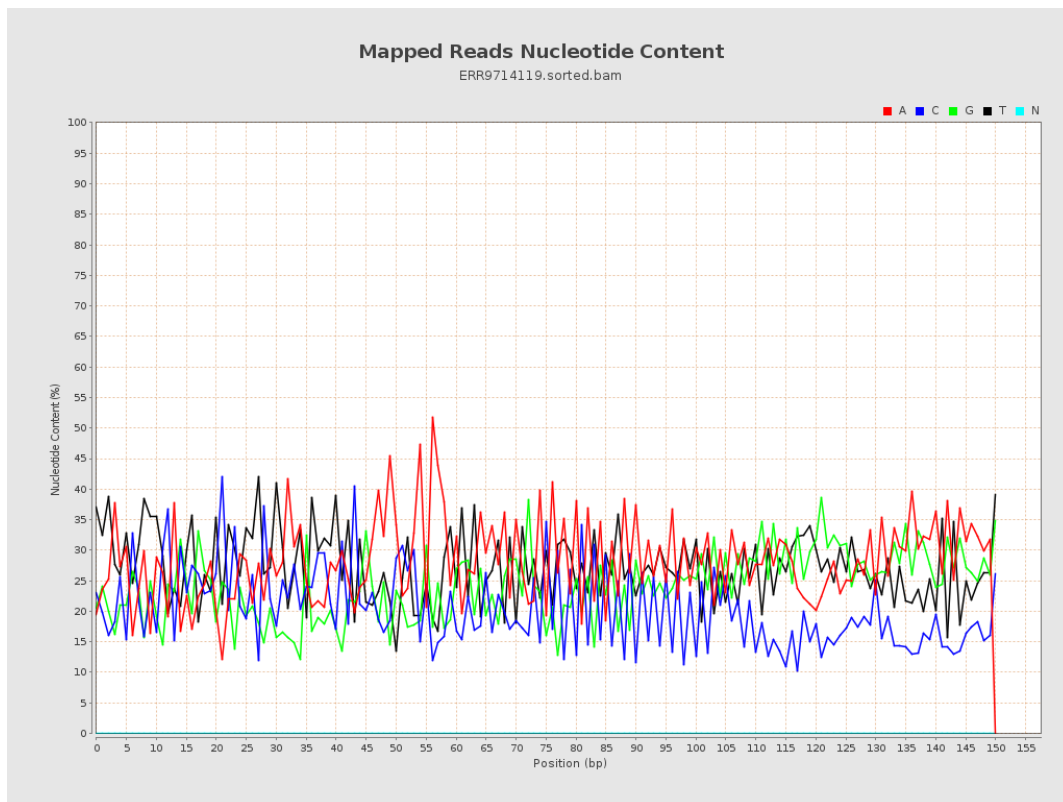
6. Results : Genome Fraction Coverage



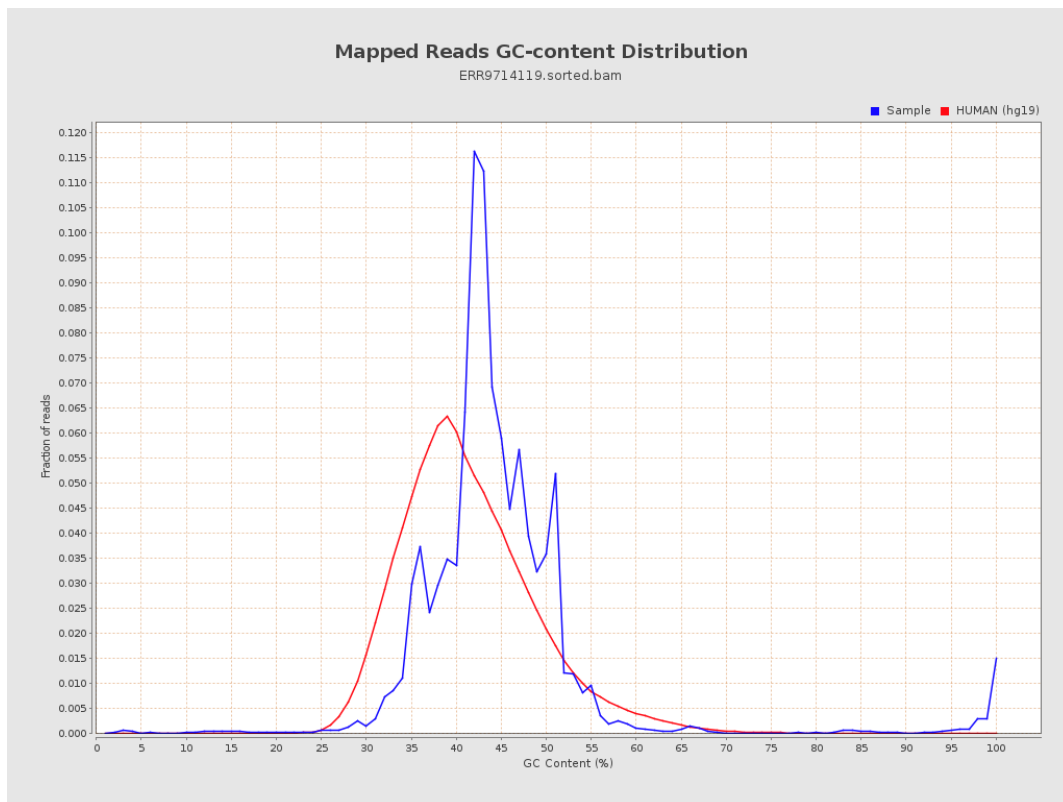
7. Results : Duplication Rate Histogram



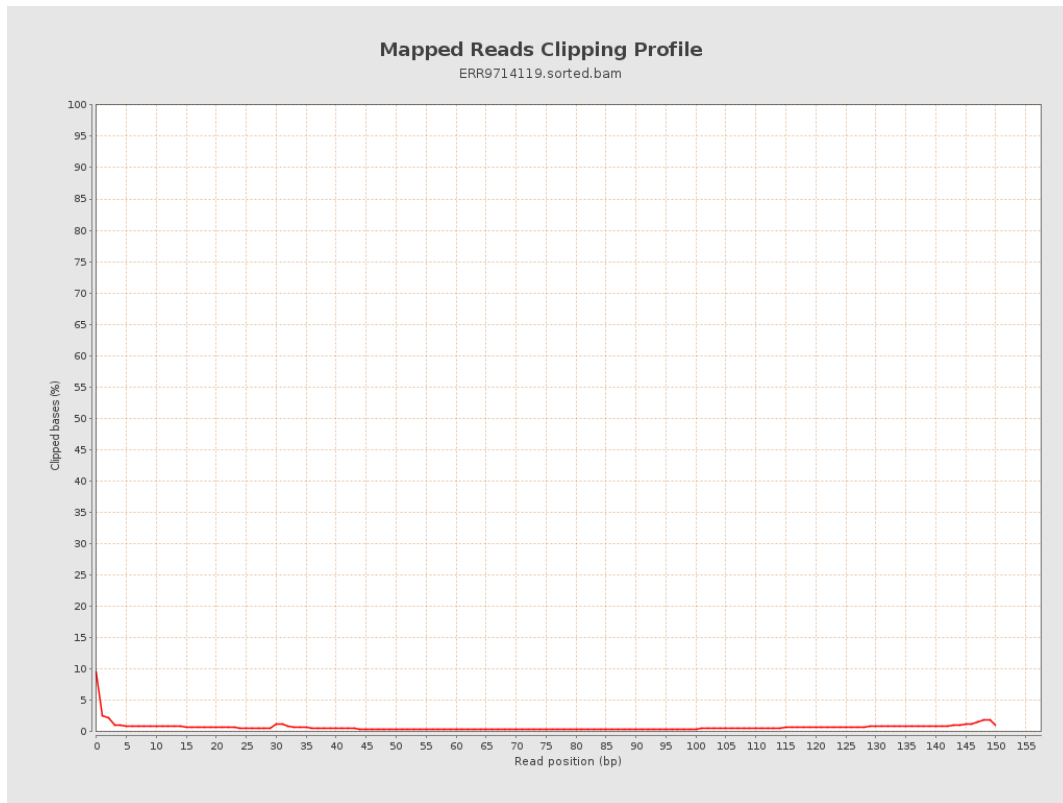
8. Results : Mapped Reads Nucleotide Content



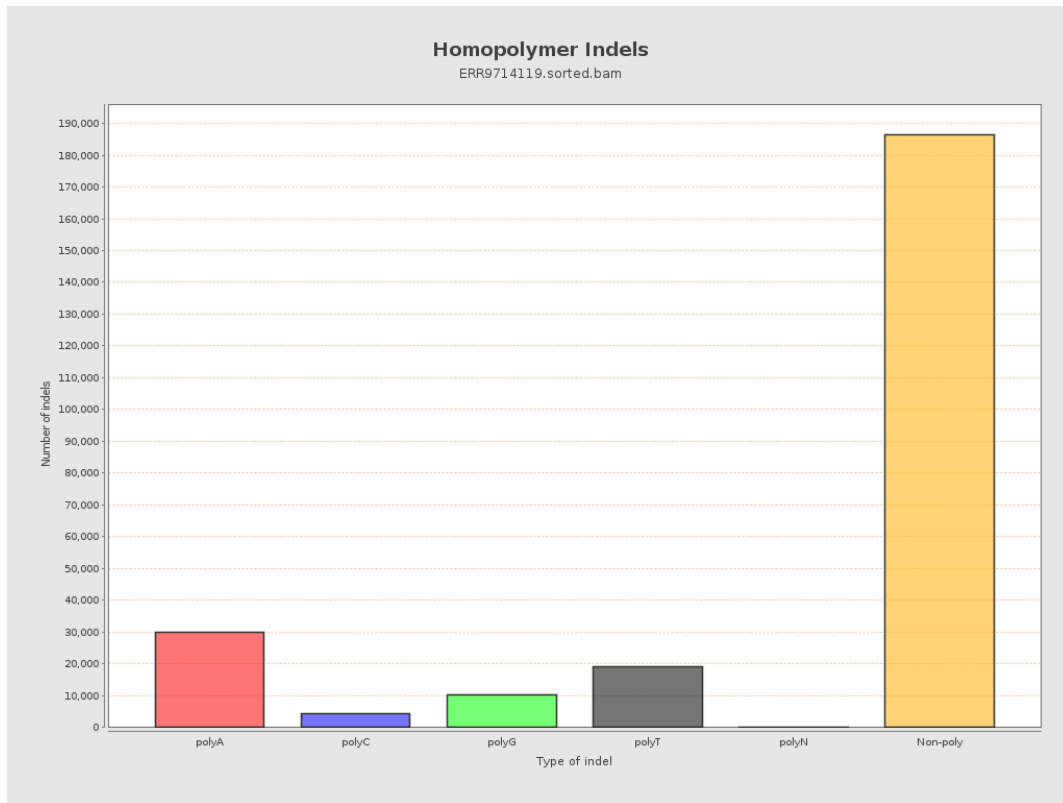
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

