

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:30:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714079.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_ERR9714079 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:30:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,022
Mapped reads	3,774 / 18.85%
Unmapped reads	16,248 / 81.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	112 / 0.56%
Read min/max/mean length	30 / 151 / 69.15
Duplicated reads (estimated)	2,998 / 14.97%
Duplication rate	49.89%
Clipped reads	2,601 / 12.99%

2.2. ACGT Content

Number/percentage of A's	61,335 / 14.65%
Number/percentage of C's	49,751 / 11.89%
Number/percentage of T's	55,282 / 13.21%
Number/percentage of G's	252,166 / 60.25%
Number/percentage of N's	13 / 0%
GC Percentage	72.13%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.256
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2.4. Mapping Quality

Mean Mapping Quality	13.67
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2.5. Mismatches and indels

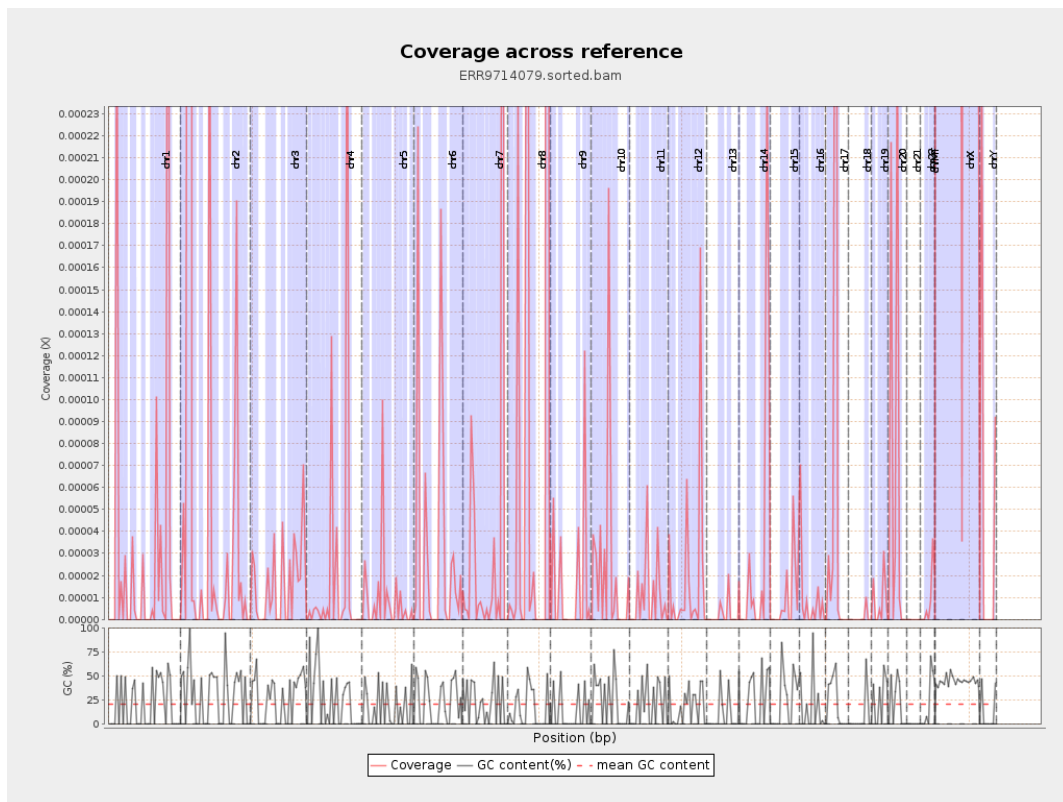
General error rate	3.71%
Mismatches	13,122
Insertions	386
Mapped reads with at least one insertion	7.18%
Deletions	797
Mapped reads with at least one deletion	20.19%
Homopolymer indels	42.6%

2.6. Chromosome stats

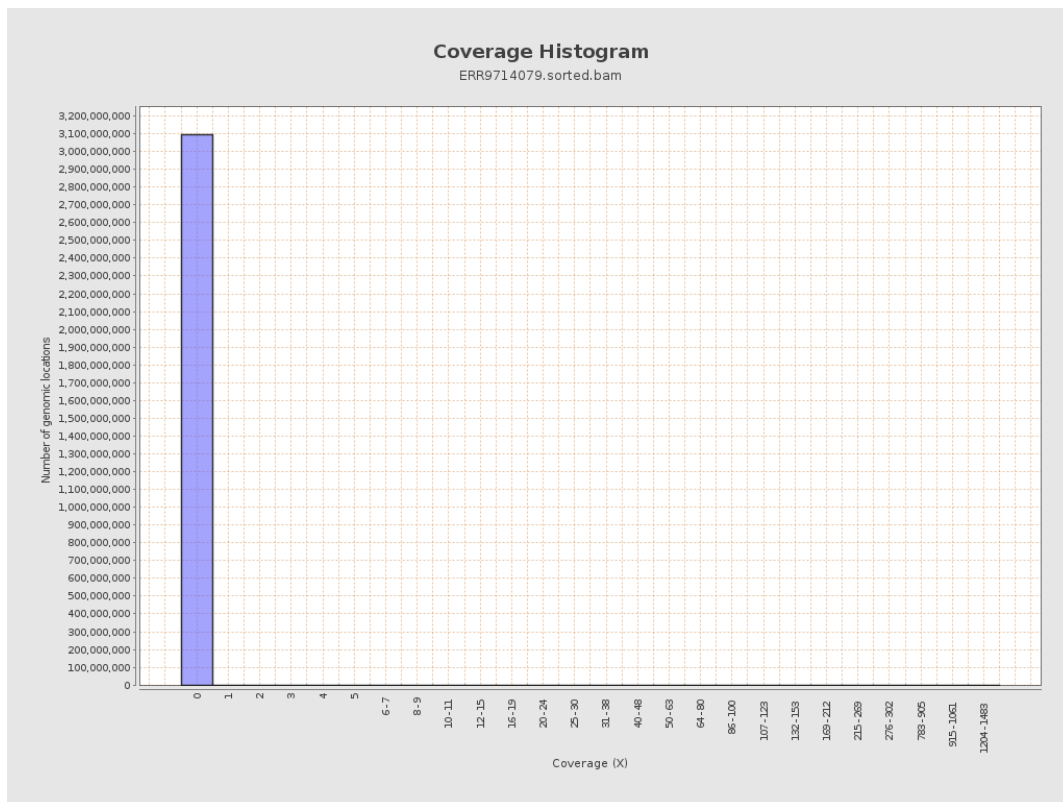
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8259	0	0.0231
chr2	243199373	213845	0.0009	0.9041
chr3	198022430	3128	0	0.0056
chr4	191154276	4225	0	0.016
chr5	180915260	1729	0	0.0055
chr6	171115067	5458	0	0.0153
chr7	159138663	5920	0	0.0214

chr8	146364022	17823	0.0001	0.0815
chr9	141213431	2059	0	0.0076
chr10	135534747	2938	0	0.0156
chr11	135006516	1428	0	0.0051
chr12	133851895	2643	0	0.0108
chr13	115169878	288	0	0.0027
chr14	107349540	3253	0	0.0156
chr15	102531392	1077	0	0.0049
chr16	90354753	656	0	0.0043
chr17	81195210	4155	0.0001	0.0343
chr18	78077248	79	0	0.001
chr19	59128983	453	0	0.0035
chr20	63025520	4156	0.0001	0.0241
chr21	48129895	0	0	0
chr22	51304566	418	0	0.0037
chrMT	16571	0	0	0
chrX	155270560	137595	0.0009	0.1303
chrY	59373566	2764	0	0.0207

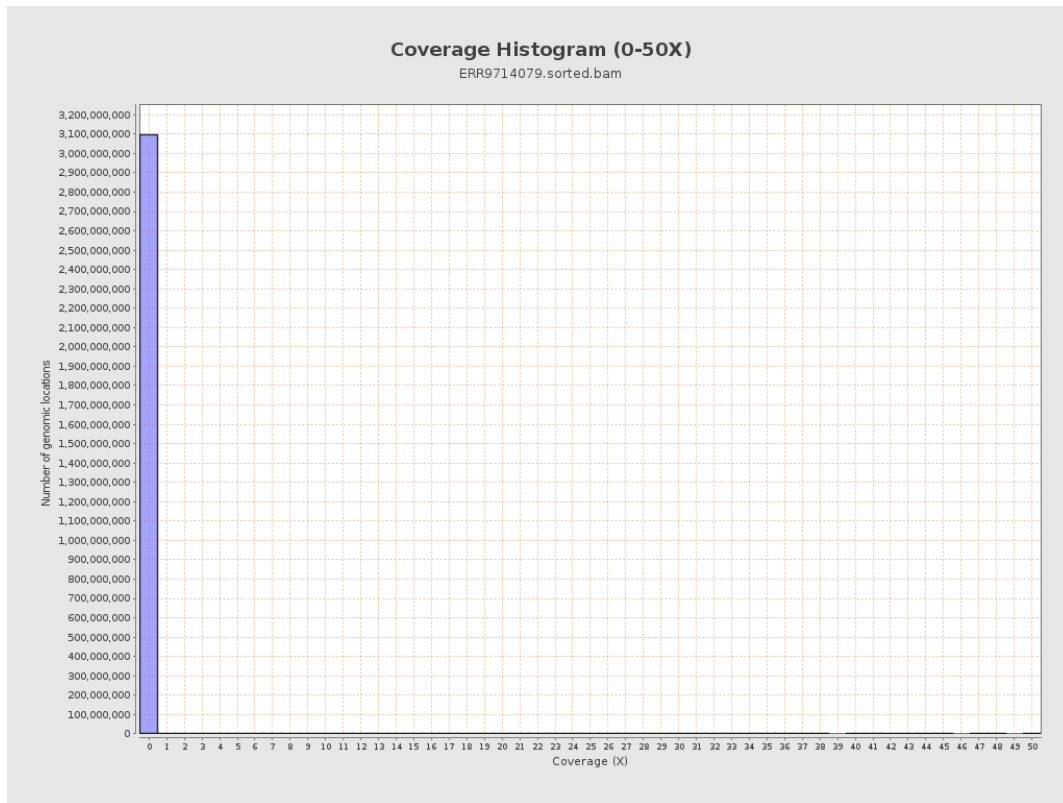
3. Results : Coverage across reference



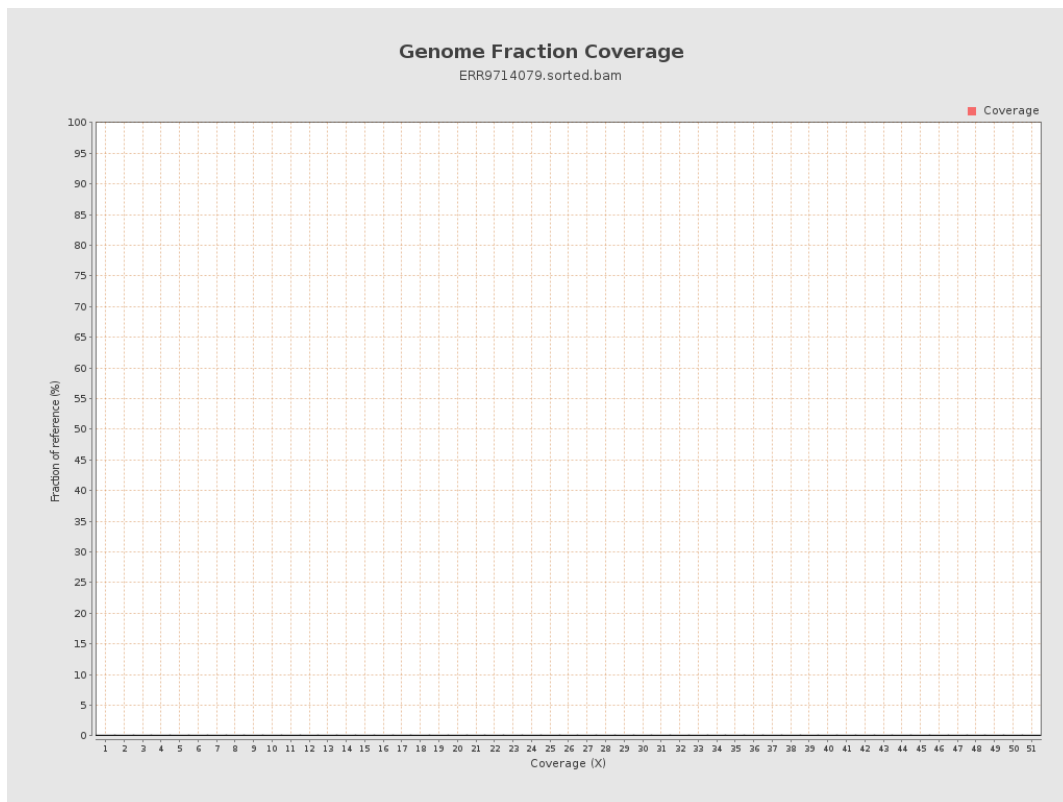
4. Results : Coverage Histogram



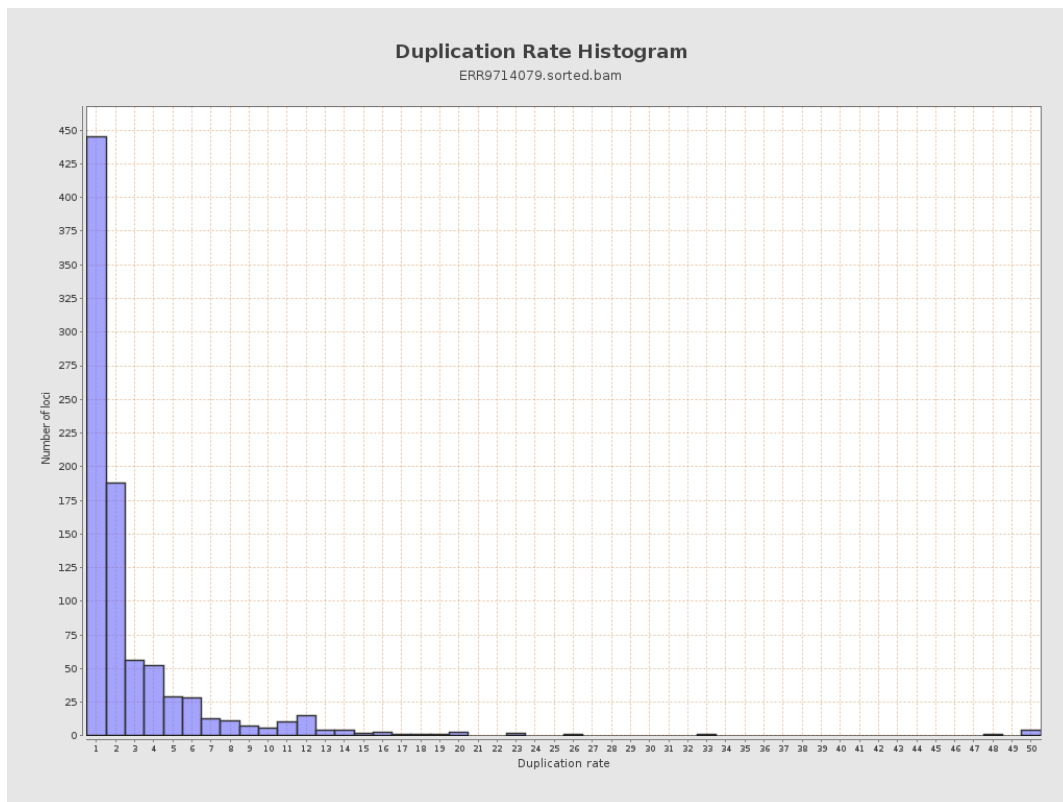
5. Results : Coverage Histogram (0-50X)



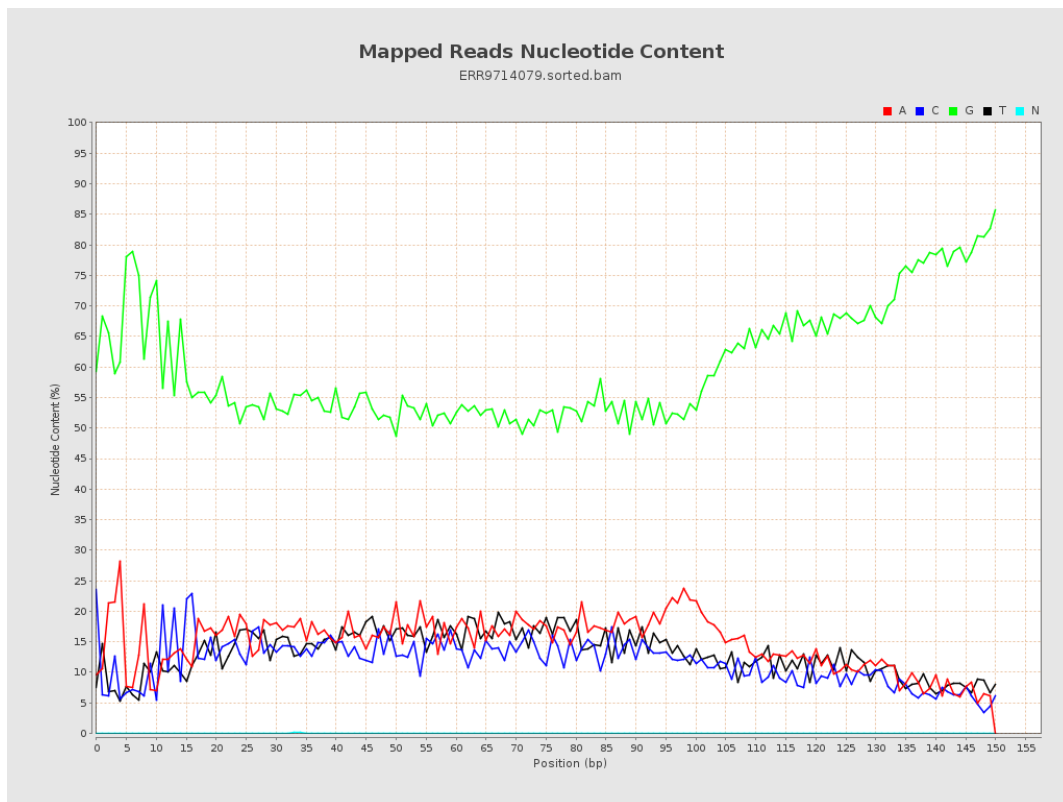
6. Results : Genome Fraction Coverage



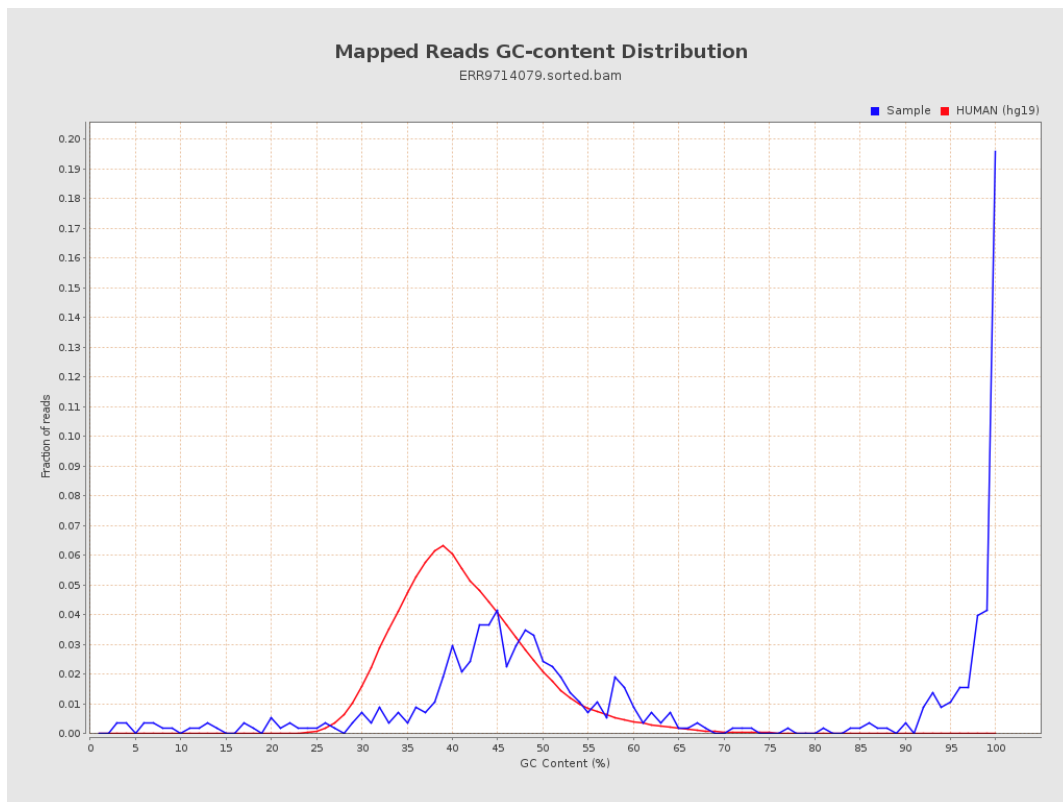
7. Results : Duplication Rate Histogram



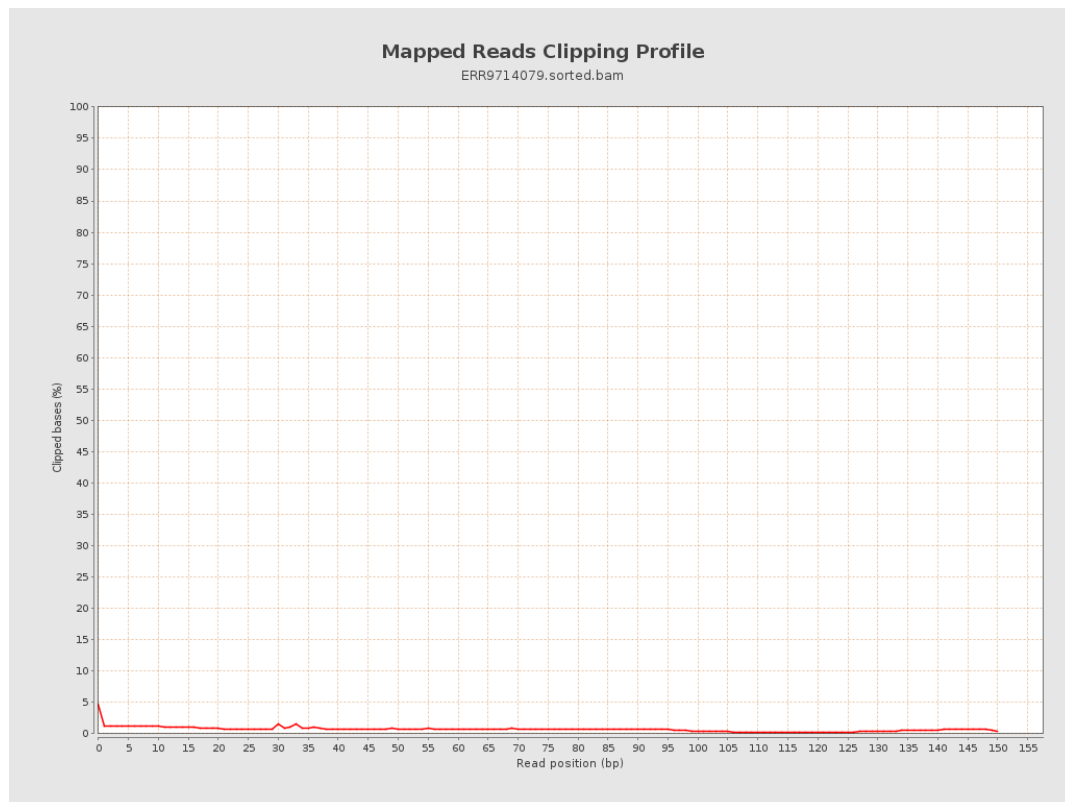
8. Results : Mapped Reads Nucleotide Content



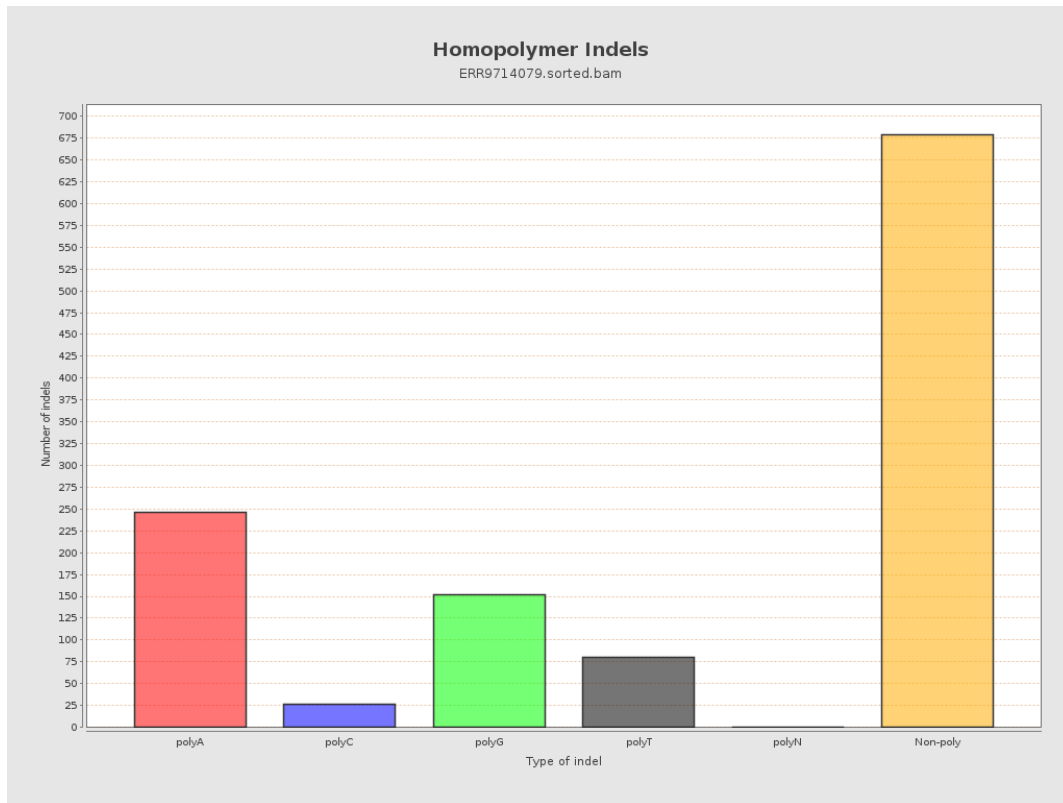
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

