

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:06:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714069.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_ERR9714069 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:06:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	614,302
Mapped reads	46,148 / 7.51%
Unmapped reads	568,154 / 92.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	918 / 0.15%
Read min/max/mean length	30 / 151 / 57.4
Duplicated reads (estimated)	41,081 / 6.69%
Duplication rate	36.39%
Clipped reads	38,330 / 6.24%

2.2. ACGT Content

Number/percentage of A's	679,858 / 16.1%
Number/percentage of C's	459,596 / 10.88%
Number/percentage of T's	604,455 / 14.31%
Number/percentage of G's	2,479,457 / 58.71%
Number/percentage of N's	84 / 0%
GC Percentage	69.59%

2.3. Coverage

Mean	0.0014

Standard Deviation	2.3516
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2.4. Mapping Quality

Mean Mapping Quality	35.57
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2.5. Mismatches and indels

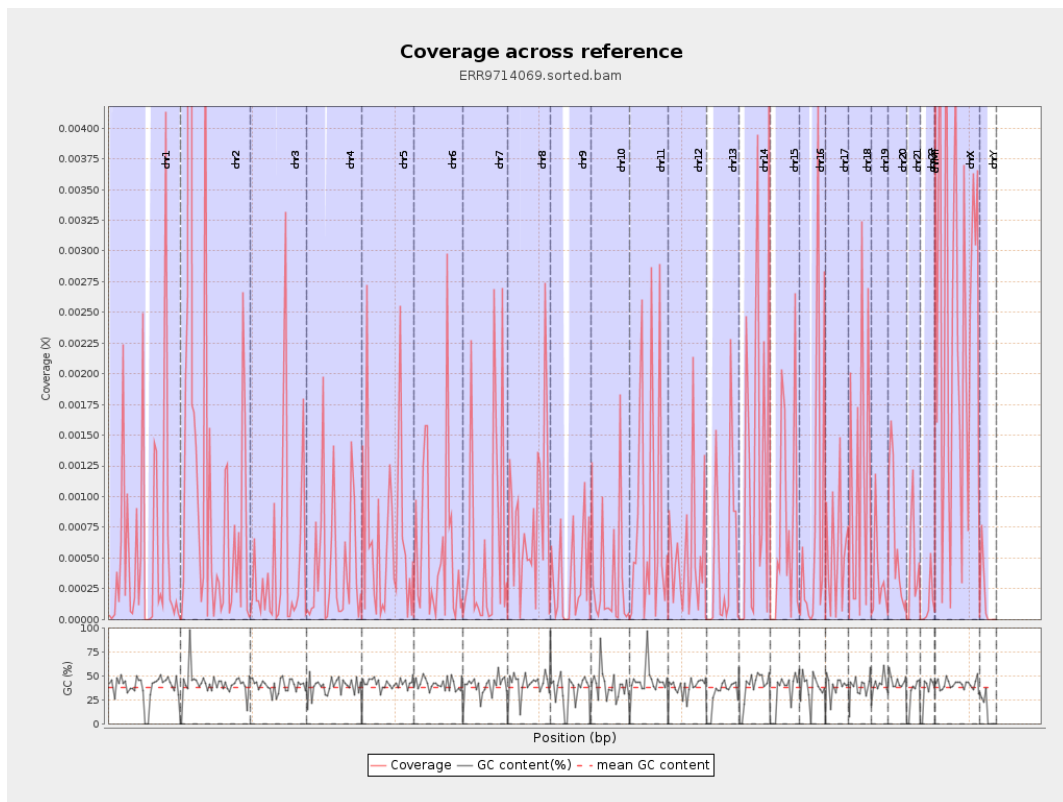
General error rate	3.5%
Mismatches	128,822
Insertions	4,341
Mapped reads with at least one insertion	7.63%
Deletions	8,326
Mapped reads with at least one deletion	17.32%
Homopolymer indels	33.5%

2.6. Chromosome stats

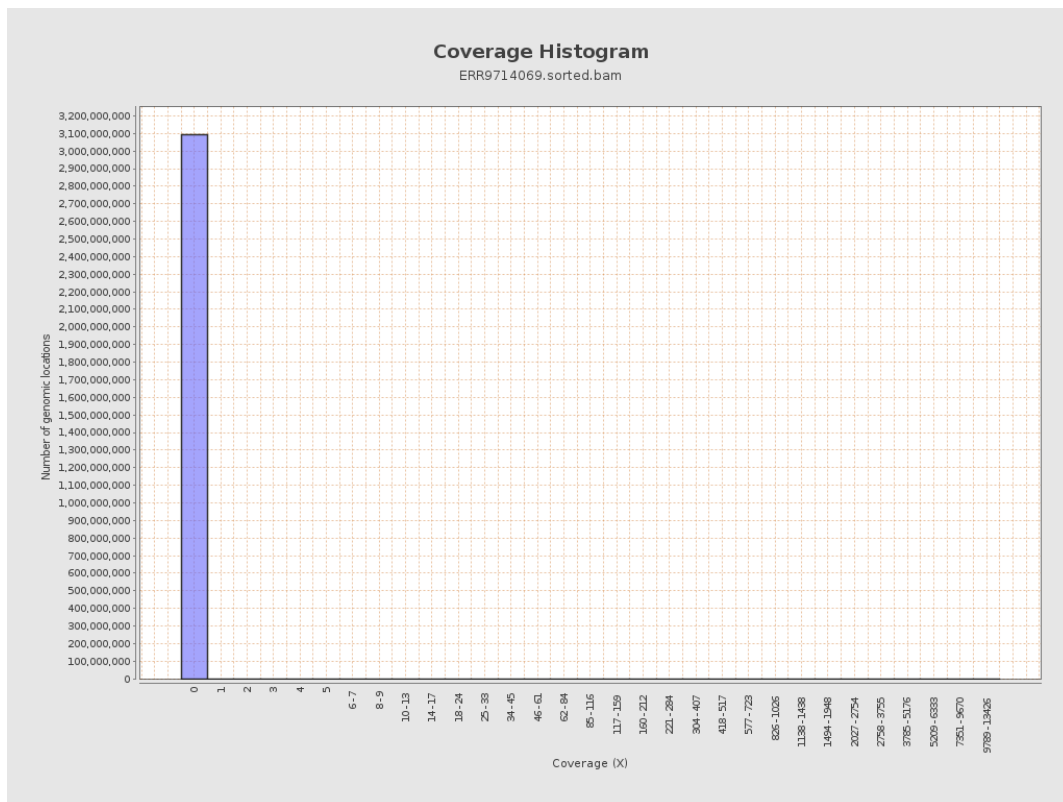
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	136303	0.0005	0.2055
chr2	243199373	2267953	0.0093	8.3626
chr3	198022430	84171	0.0004	0.169
chr4	191154276	83593	0.0004	0.1333
chr5	180915260	122347	0.0007	0.159
chr6	171115067	99798	0.0006	0.1613
chr7	159138663	97766	0.0006	0.3139

chr8	146364022	120273	0.0008	0.1915
chr9	141213431	49379	0.0003	0.0841
chr10	135534747	46883	0.0003	0.1012
chr11	135006516	120870	0.0009	0.2122
chr12	133851895	72588	0.0005	0.1214
chr13	115169878	52735	0.0005	0.131
chr14	107349540	143399	0.0013	0.3138
chr15	102531392	72963	0.0007	0.2109
chr16	90354753	70708	0.0008	0.2616
chr17	81195210	46615	0.0006	0.1484
chr18	78077248	92645	0.0012	0.2349
chr19	59128983	19934	0.0003	0.0934
chr20	63025520	41962	0.0007	0.1547
chr21	48129895	21530	0.0004	0.0973
chr22	51304566	6291	0.0001	0.0335
chrMT	16571	9496	0.573	3.9204
chrX	155270560	384536	0.0025	0.3558
chrY	59373566	9470	0.0002	0.067

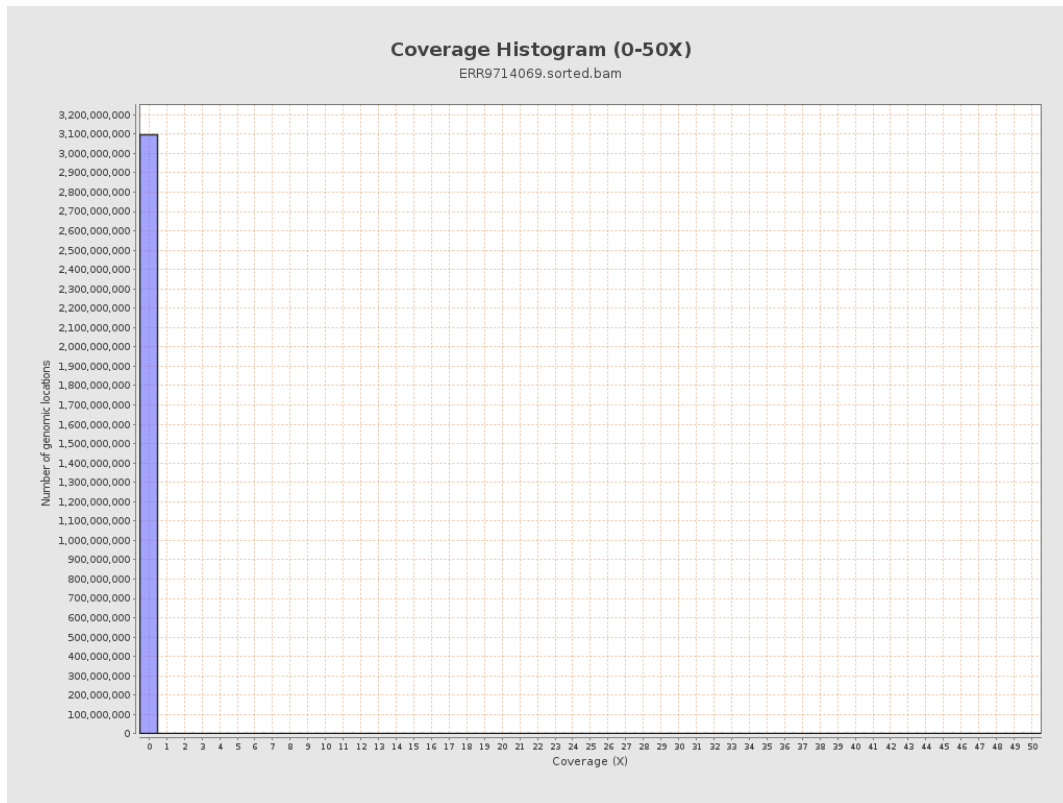
3. Results : Coverage across reference



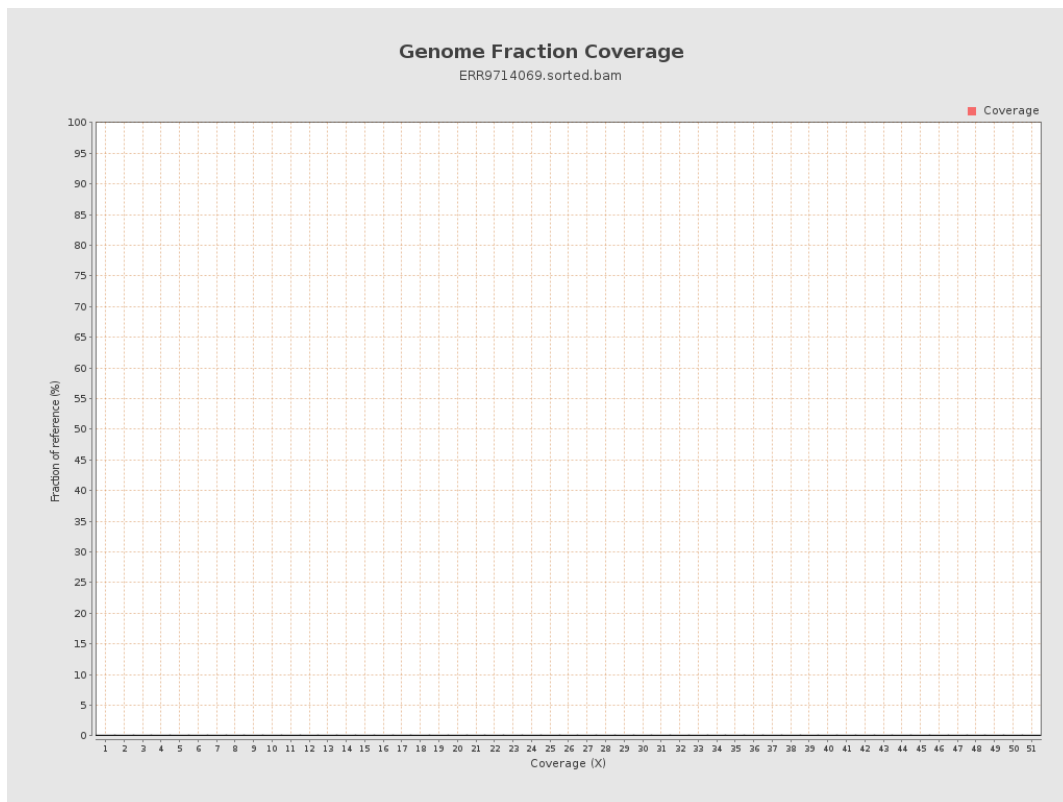
4. Results : Coverage Histogram



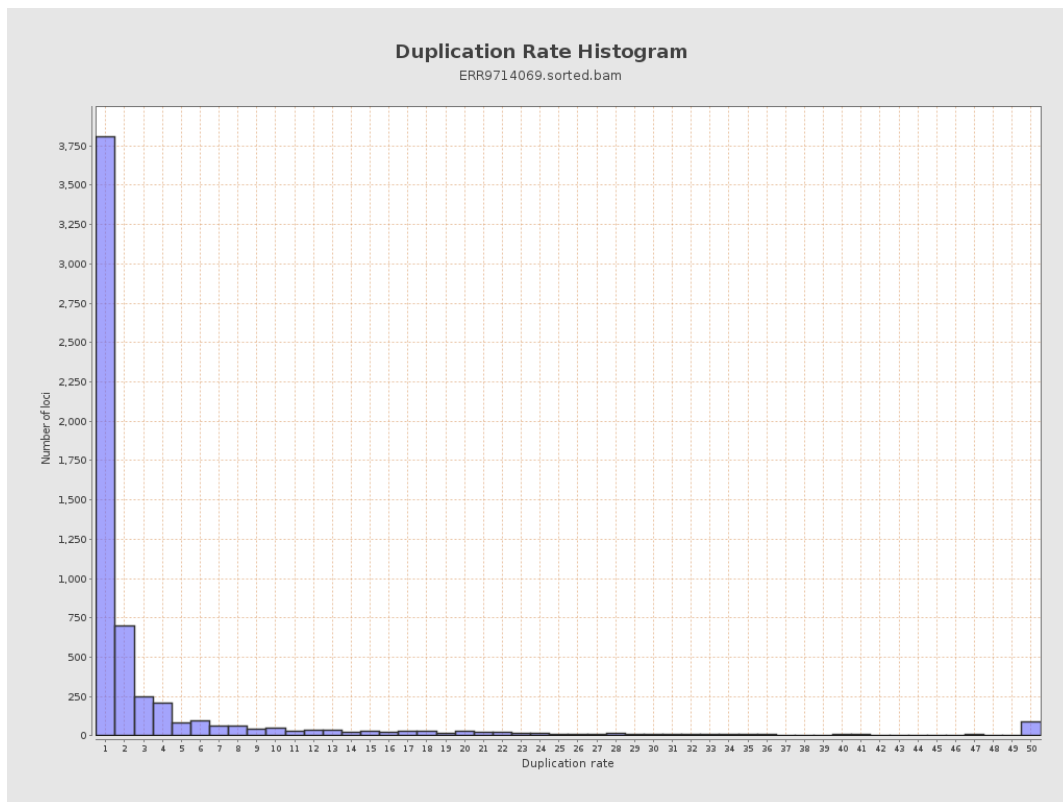
5. Results : Coverage Histogram (0-50X)



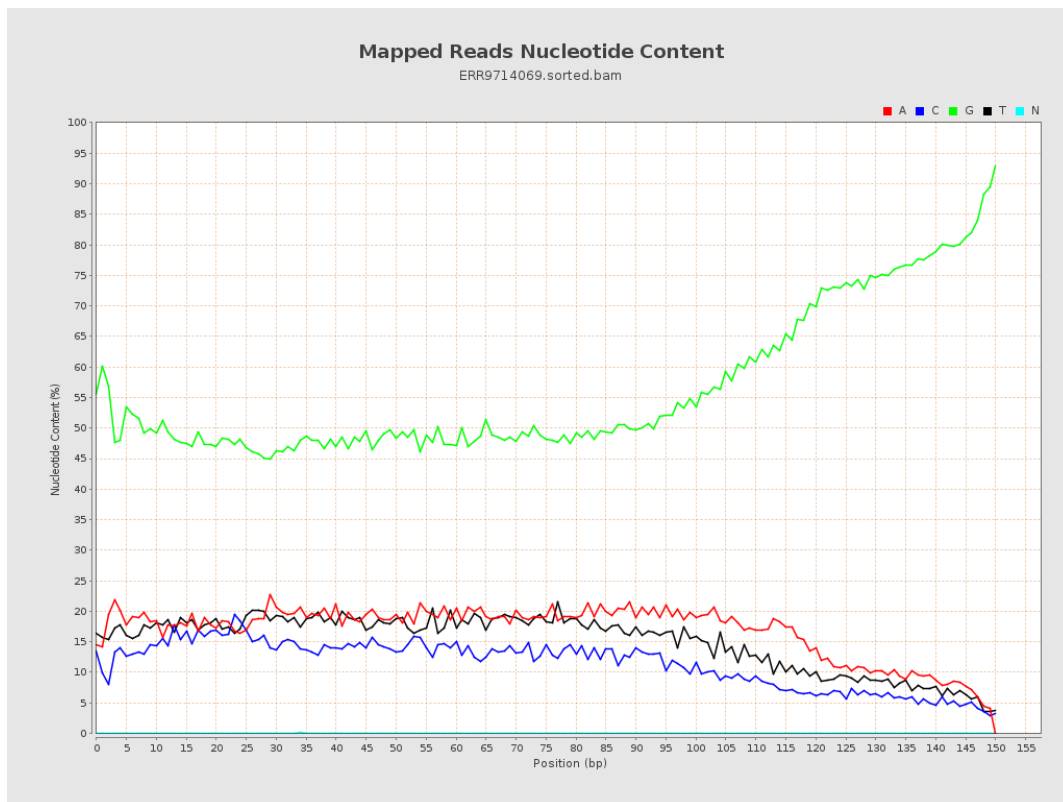
6. Results : Genome Fraction Coverage



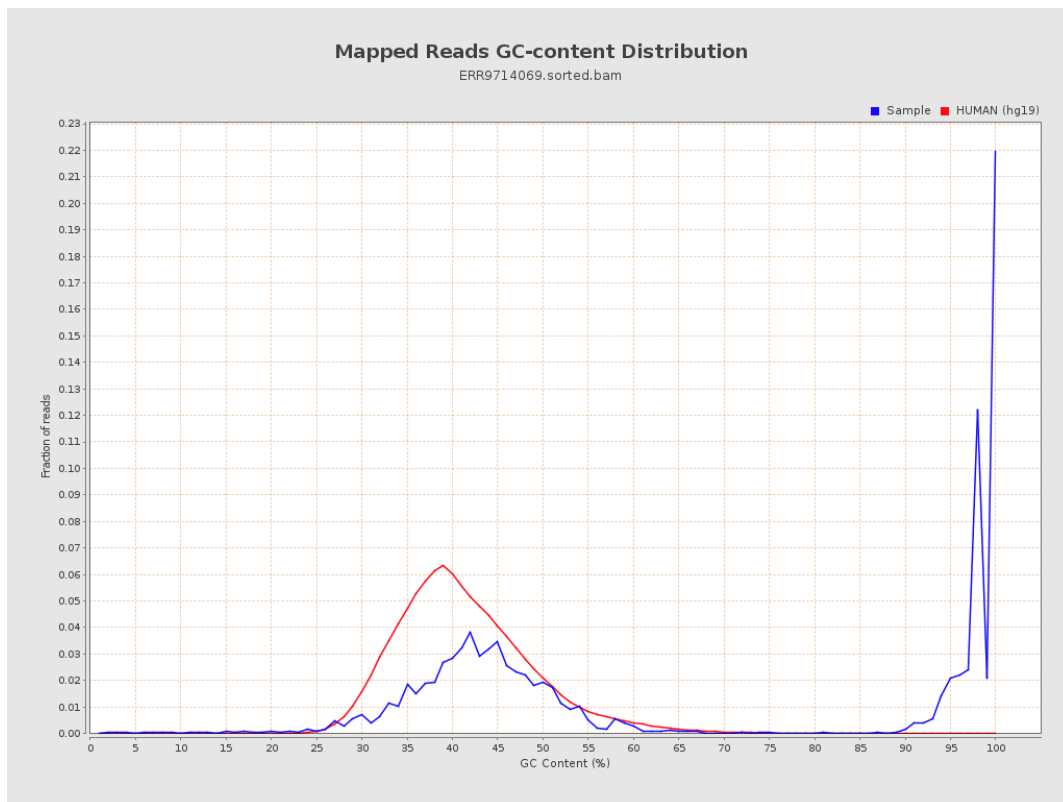
7. Results : Duplication Rate Histogram



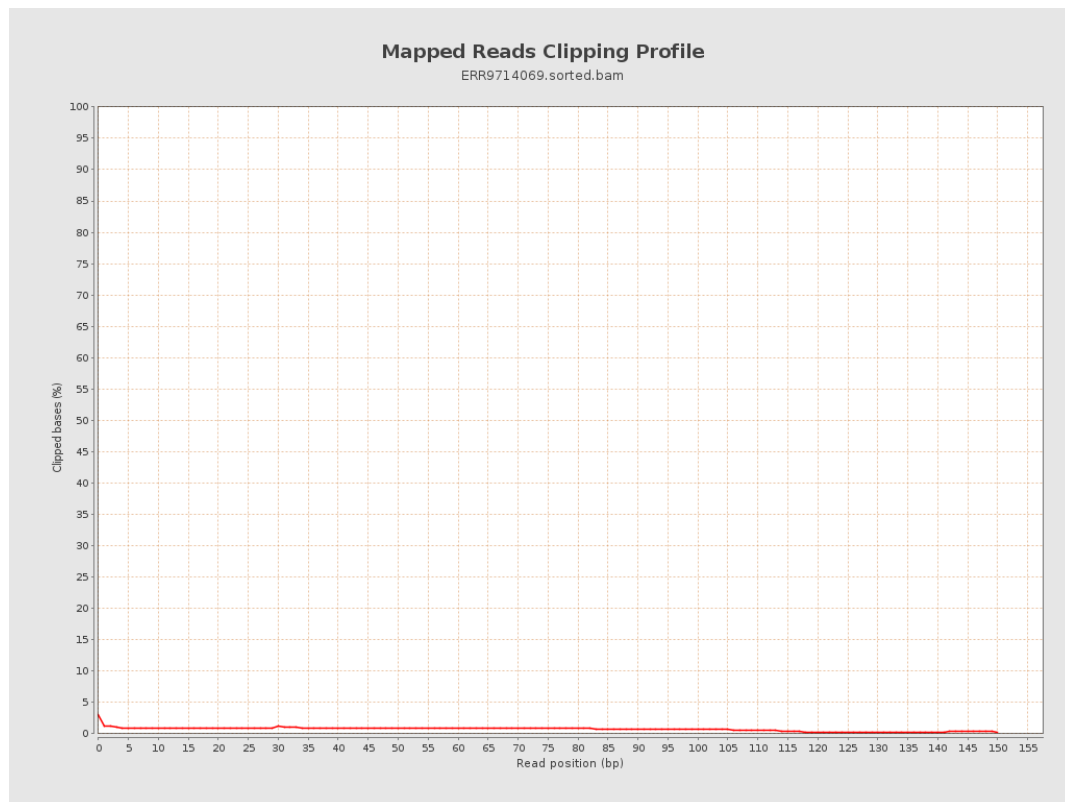
8. Results : Mapped Reads Nucleotide Content



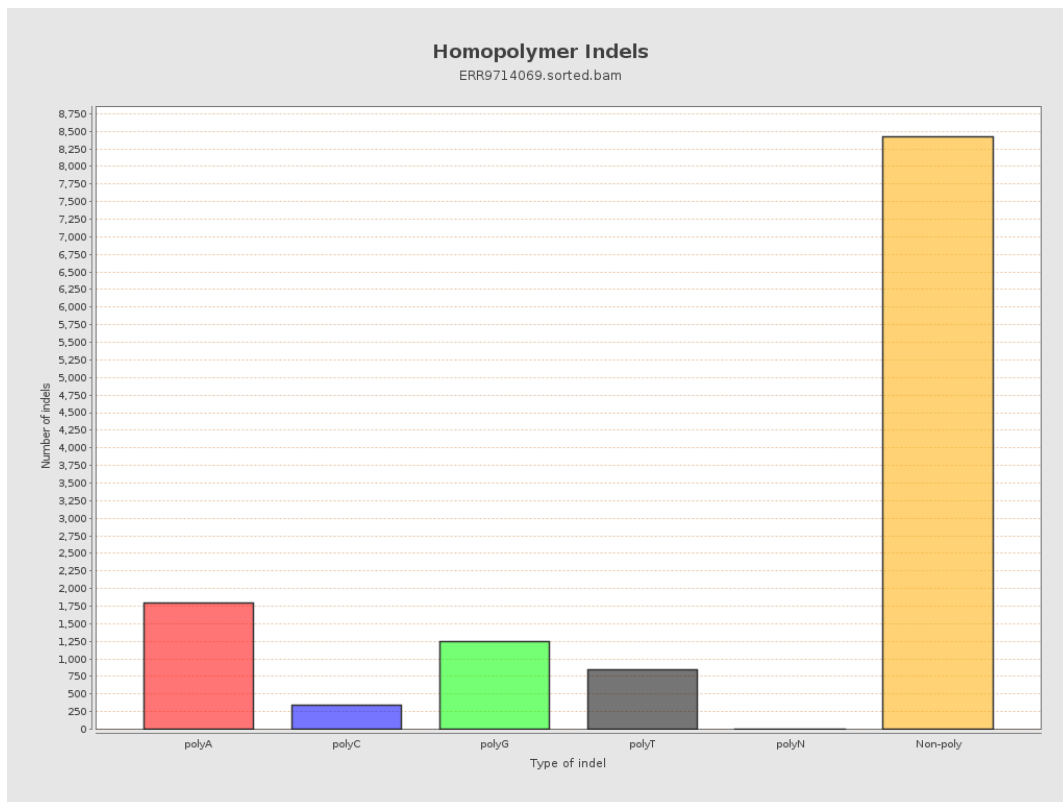
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

