

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:37:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714224.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_ERR9714224 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714224.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:37:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	229,552
Mapped reads	34,645 / 15.09%
Unmapped reads	194,907 / 84.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	716 / 0.31%
Read min/max/mean length	30 / 151 / 61.38
Duplicated reads (estimated)	33,834 / 14.74%
Duplication rate	34.58%
Clipped reads	17,811 / 7.76%

2.2. ACGT Content

Number/percentage of A's	85,452 / 2.38%
Number/percentage of C's	28,869 / 0.8%
Number/percentage of T's	41,028 / 1.14%
Number/percentage of G's	3,437,342 / 95.67%
Number/percentage of N's	94 / 0%
GC Percentage	96.48%

2.3. Coverage

Mean	0.0012

Standard Deviation	4.3905
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2.4. Mapping Quality

Mean Mapping Quality	7.21
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2.5. Mismatches and indels

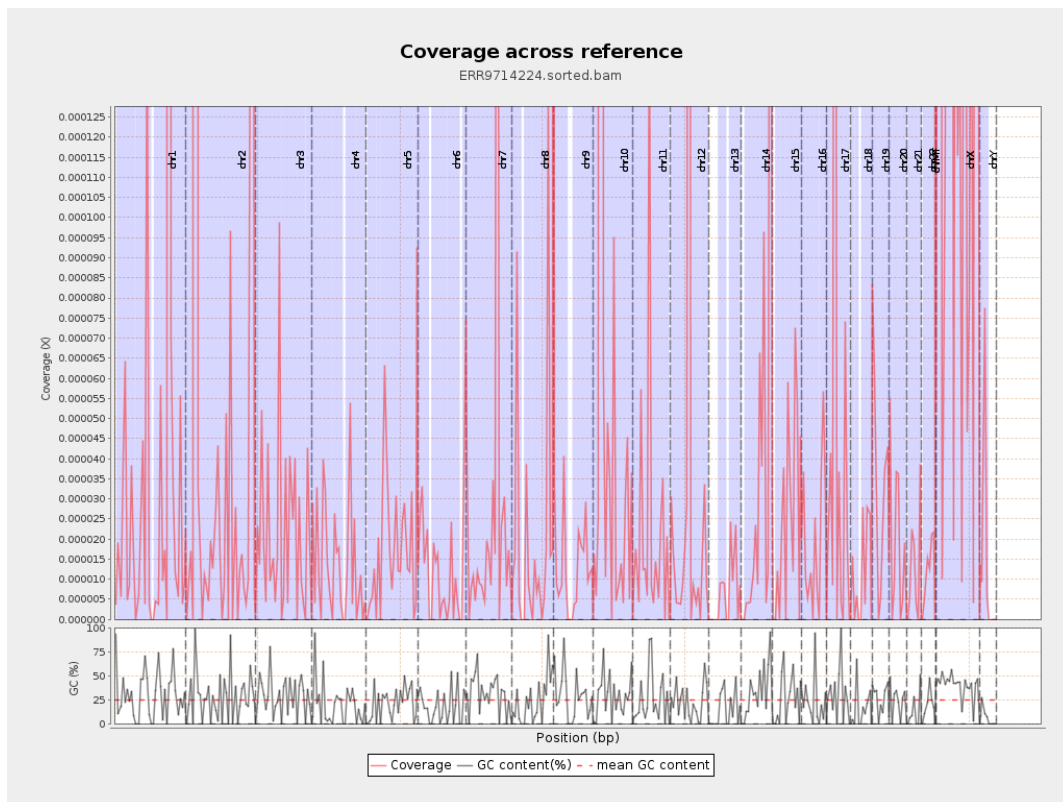
General error rate	3.36%
Mismatches	89,672
Insertions	4,328
Mapped reads with at least one insertion	8.35%
Deletions	1,666
Mapped reads with at least one deletion	4.61%
Homopolymer indels	64.25%

2.6. Chromosome stats

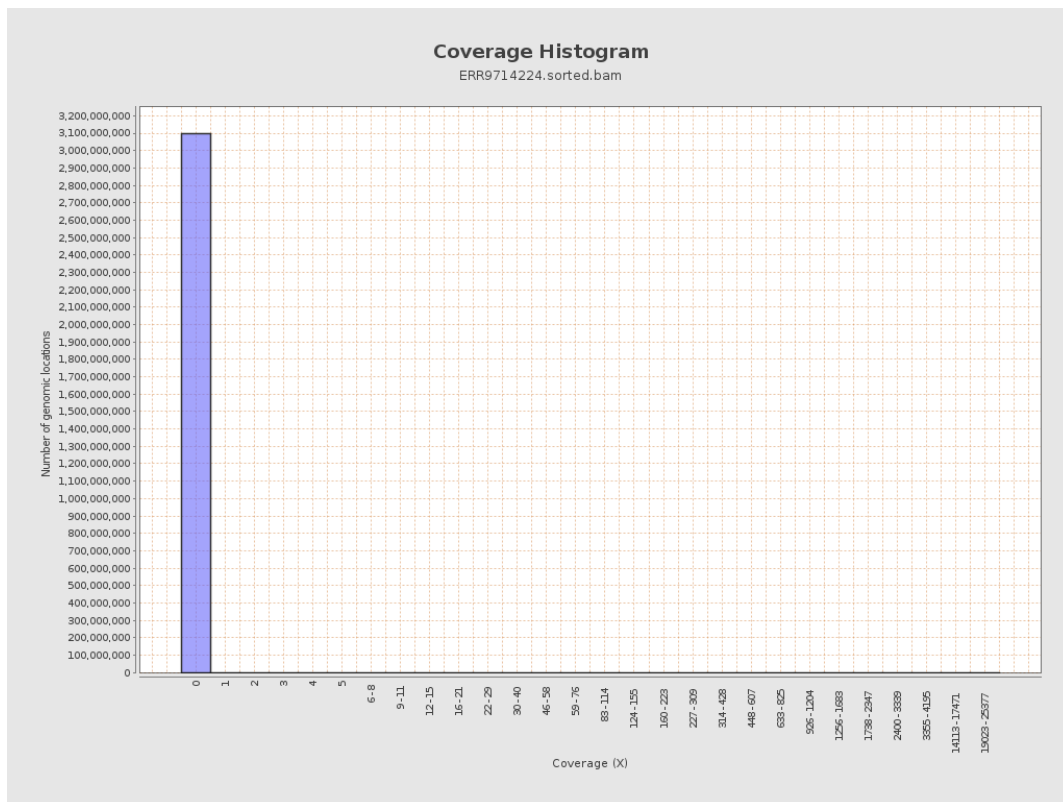
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29053	0.0001	0.2697
chr2	243199373	3450159	0.0142	15.6596
chr3	198022430	4333	0	0.0081
chr4	191154276	2641	0	0.0059
chr5	180915260	3206	0	0.0059
chr6	171115067	2116	0	0.0051
chr7	159138663	5073	0	0.0377

chr8	146364022	3018	0	0.014
chr9	141213431	2290	0	0.0079
chr10	135534747	26431	0.0002	0.361
chr11	135006516	3028	0	0.017
chr12	133851895	4886	0	0.0303
chr13	115169878	722	0	0.0028
chr14	107349540	4398	0	0.0385
chr15	102531392	2493	0	0.0096
chr16	90354753	1814	0	0.0073
chr17	81195210	4793	0.0001	0.0582
chr18	78077248	834	0	0.0036
chr19	59128983	1834	0	0.0097
chr20	63025520	1120	0	0.0077
chr21	48129895	591	0	0.0057
chr22	51304566	588	0	0.0036
chrMT	16571	4951	0.2988	1.3041
chrX	155270560	38673	0.0002	0.0529
chrY	59373566	791	0	0.0066

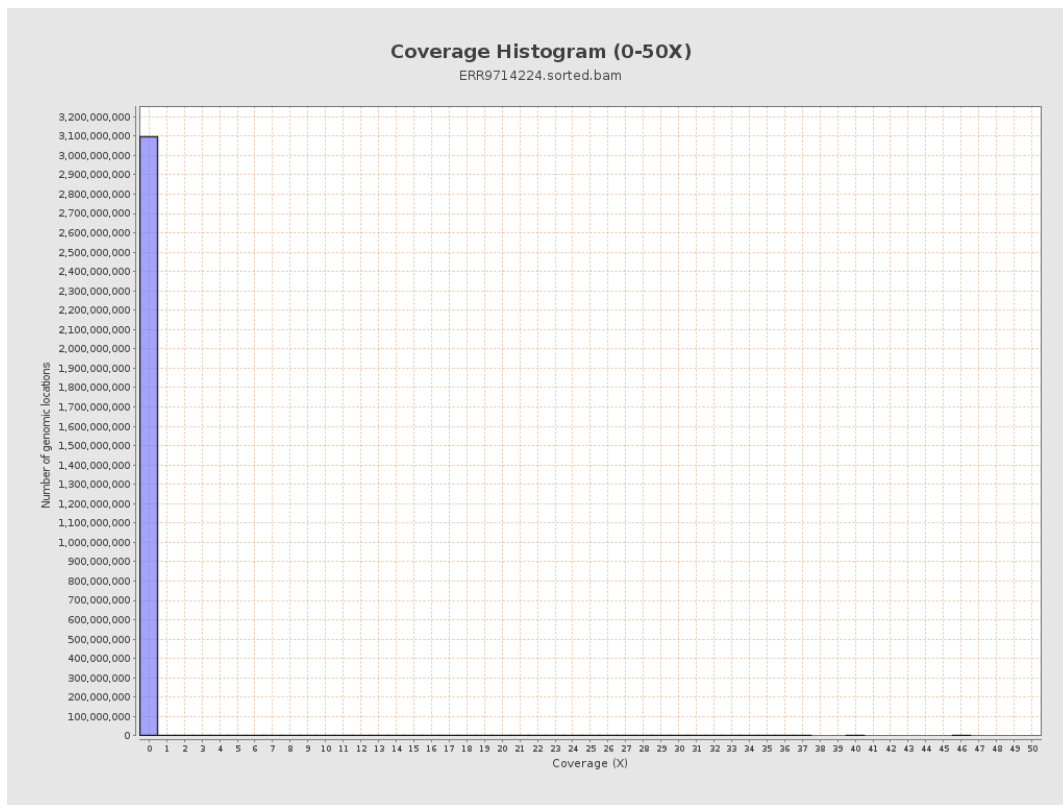
3. Results : Coverage across reference



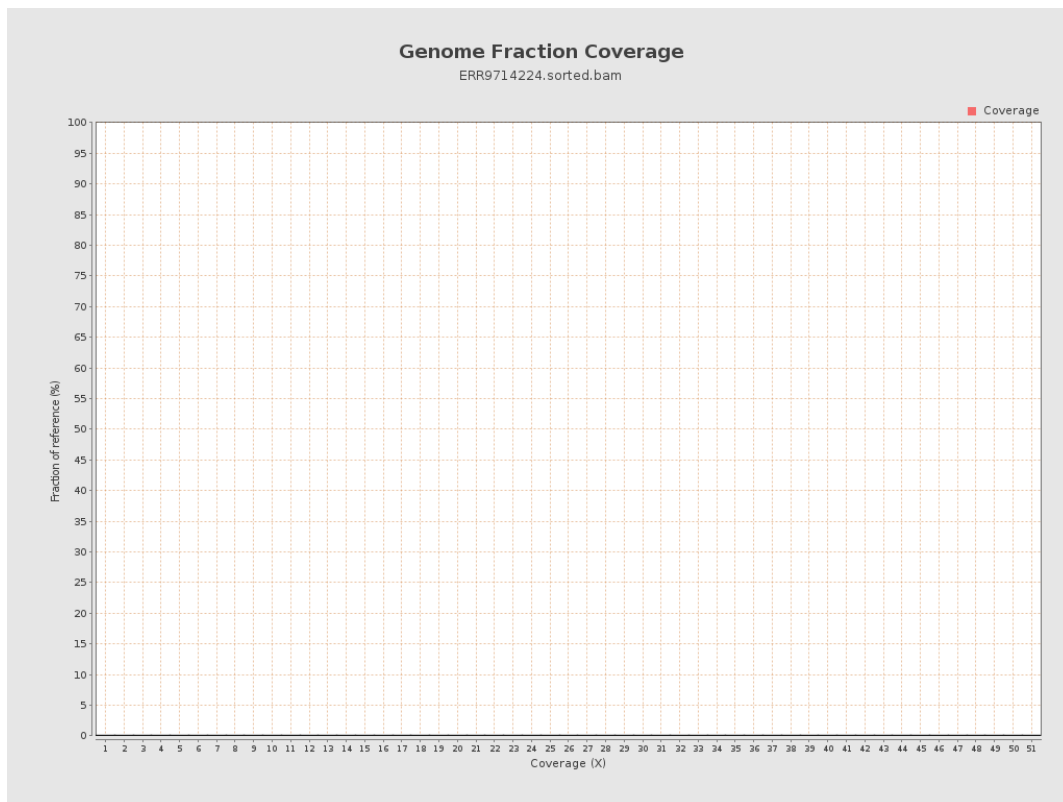
4. Results : Coverage Histogram



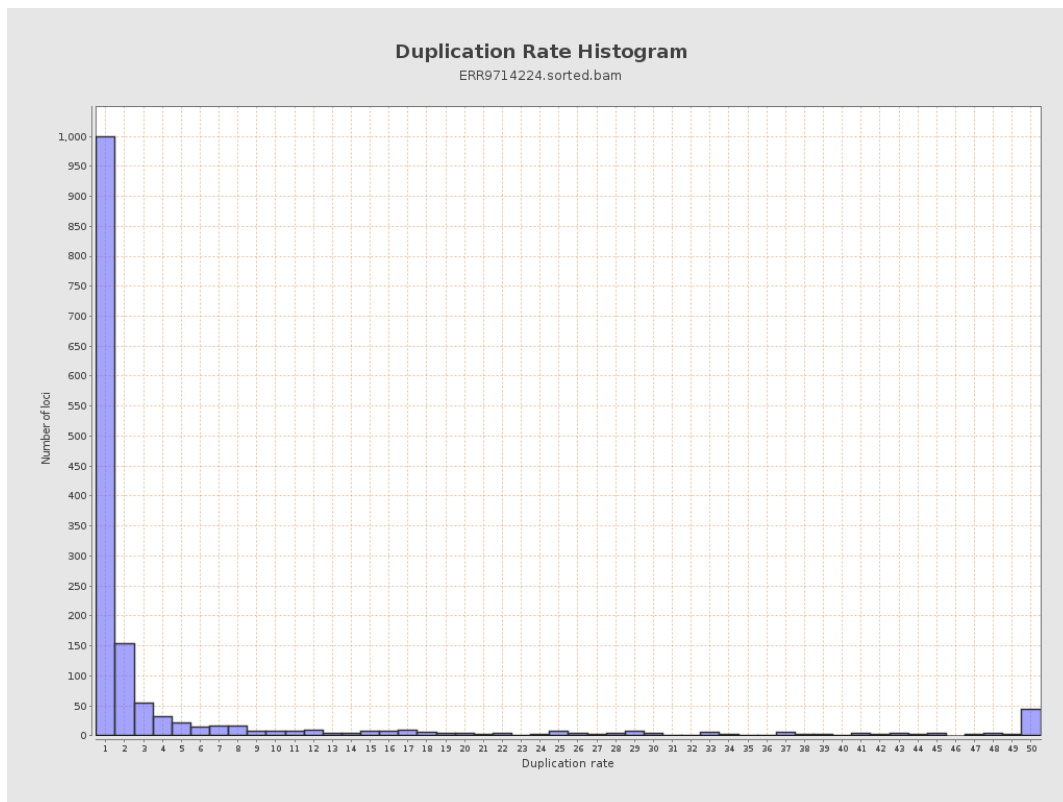
5. Results : Coverage Histogram (0-50X)



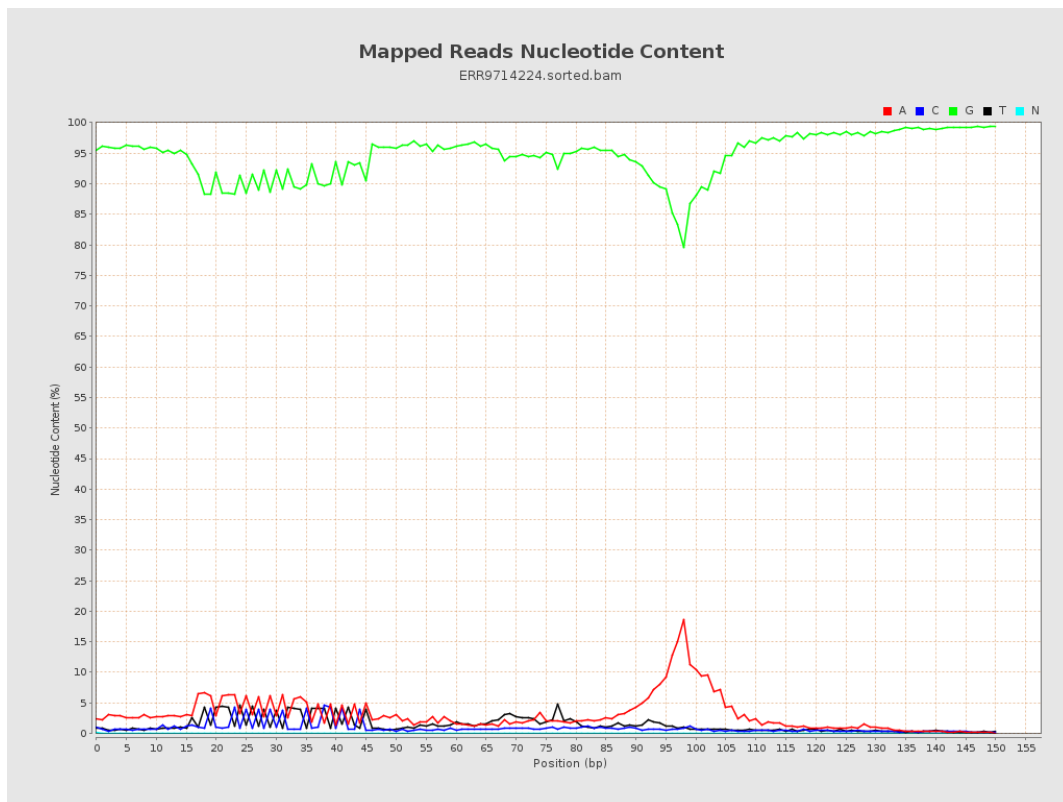
6. Results : Genome Fraction Coverage



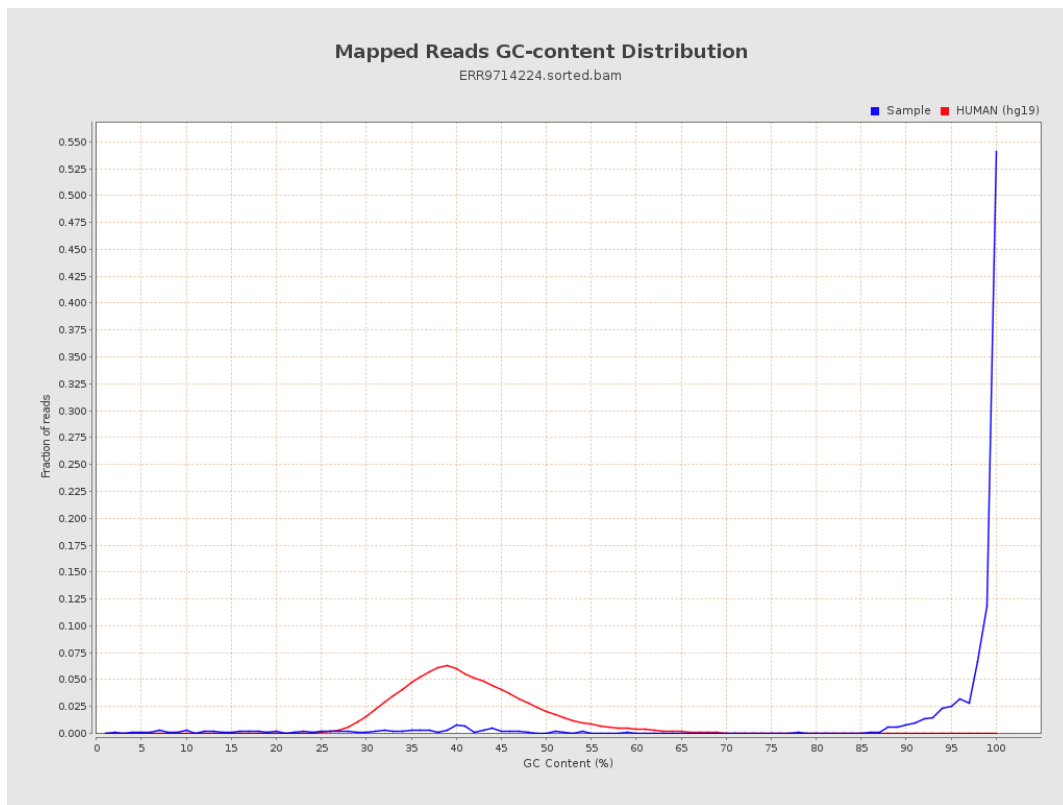
7. Results : Duplication Rate Histogram



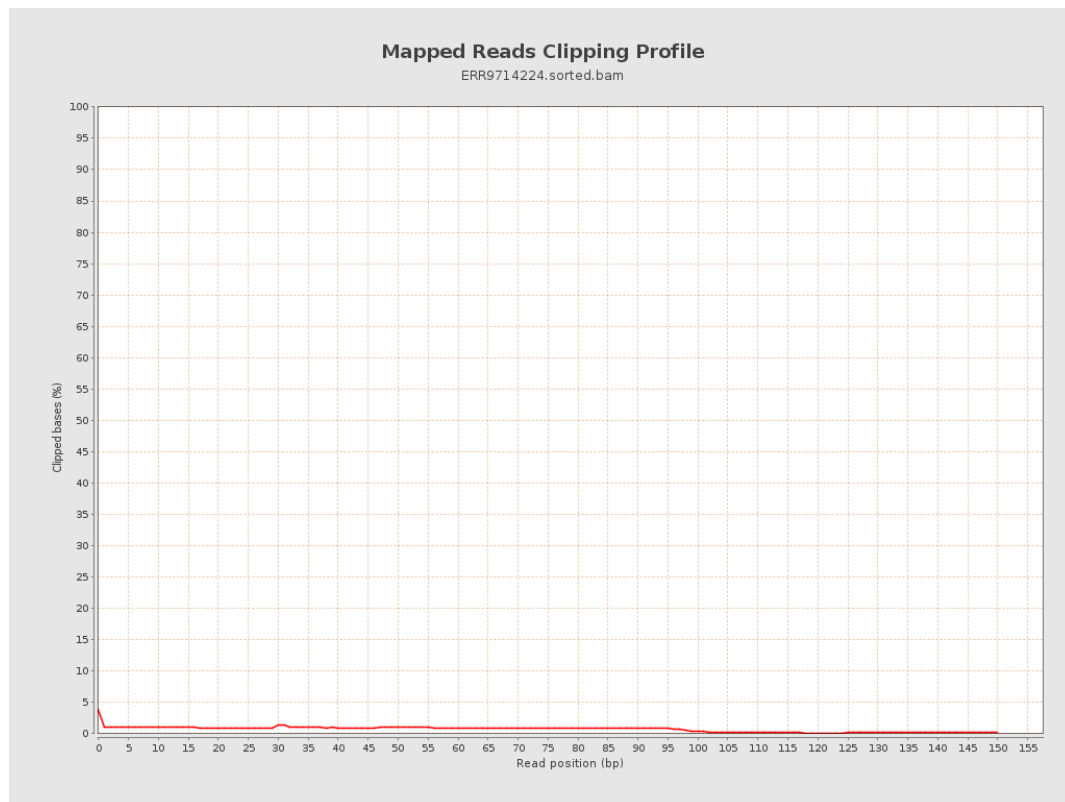
8. Results : Mapped Reads Nucleotide Content



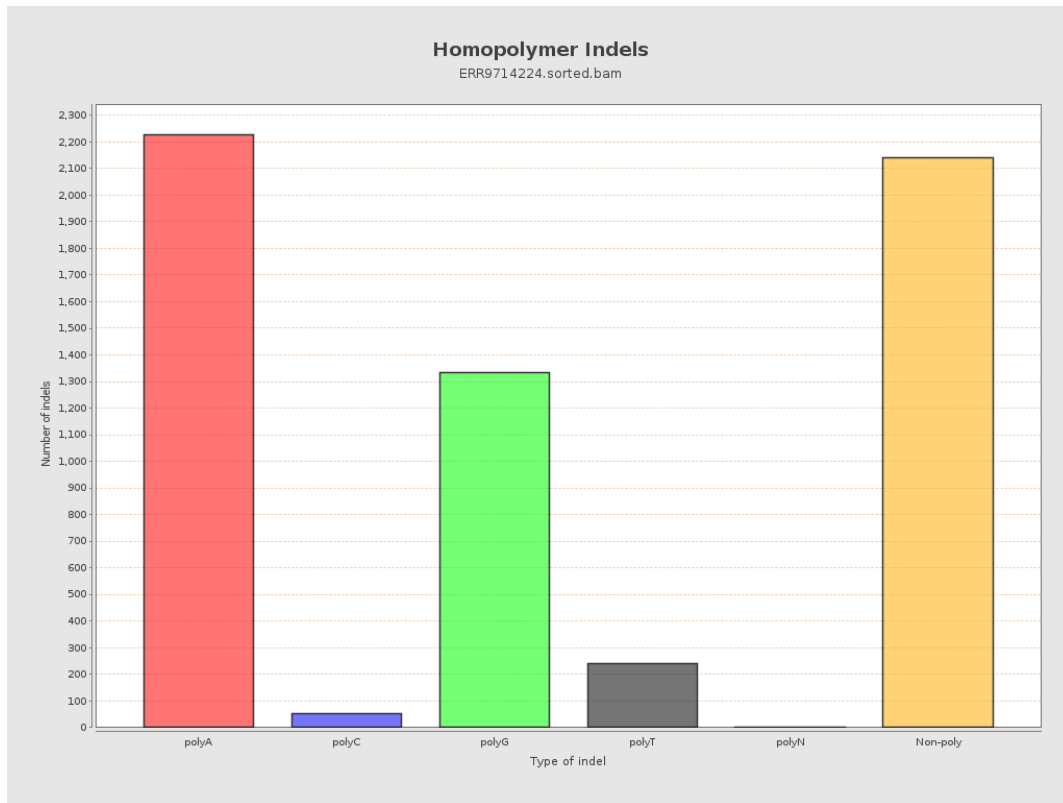
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

