

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:56:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714196.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_ERR9714196 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714196.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:56:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	110,906
Mapped reads	18,862 / 17.01%
Unmapped reads	92,044 / 82.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	681 / 0.61%
Read min/max/mean length	30 / 151 / 64.56
Duplicated reads (estimated)	16,427 / 14.81%
Duplication rate	46.12%
Clipped reads	12,000 / 10.82%

2.2. ACGT Content

Number/percentage of A's	227,200 / 10.97%
Number/percentage of C's	176,194 / 8.51%
Number/percentage of T's	198,895 / 9.61%
Number/percentage of G's	1,468,368 / 70.91%
Number/percentage of N's	50 / 0%
GC Percentage	79.42%

2.3. Coverage

Mean	0.0007

Standard Deviation	1.5984
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2.4. Mapping Quality

Mean Mapping Quality	30.01
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2.5. Mismatches and indels

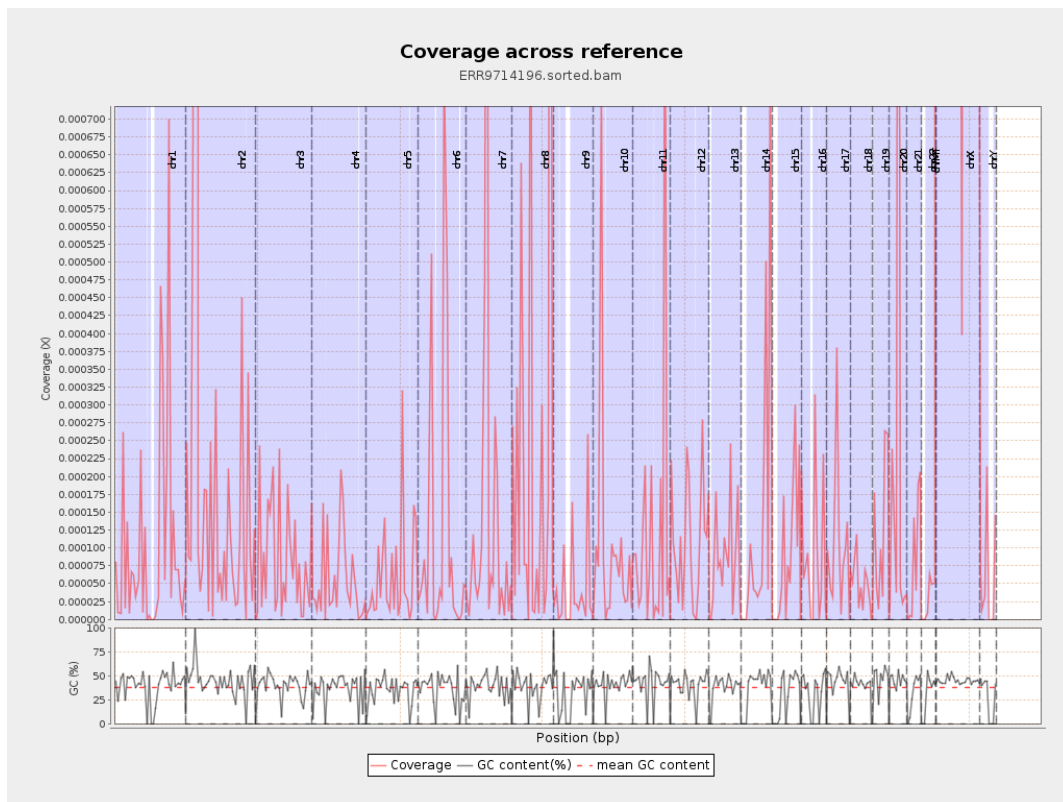
General error rate	3.76%
Mismatches	62,646
Insertions	2,182
Mapped reads with at least one insertion	7.91%
Deletions	2,881
Mapped reads with at least one deletion	14.88%
Homopolymer indels	49.36%

2.6. Chromosome stats

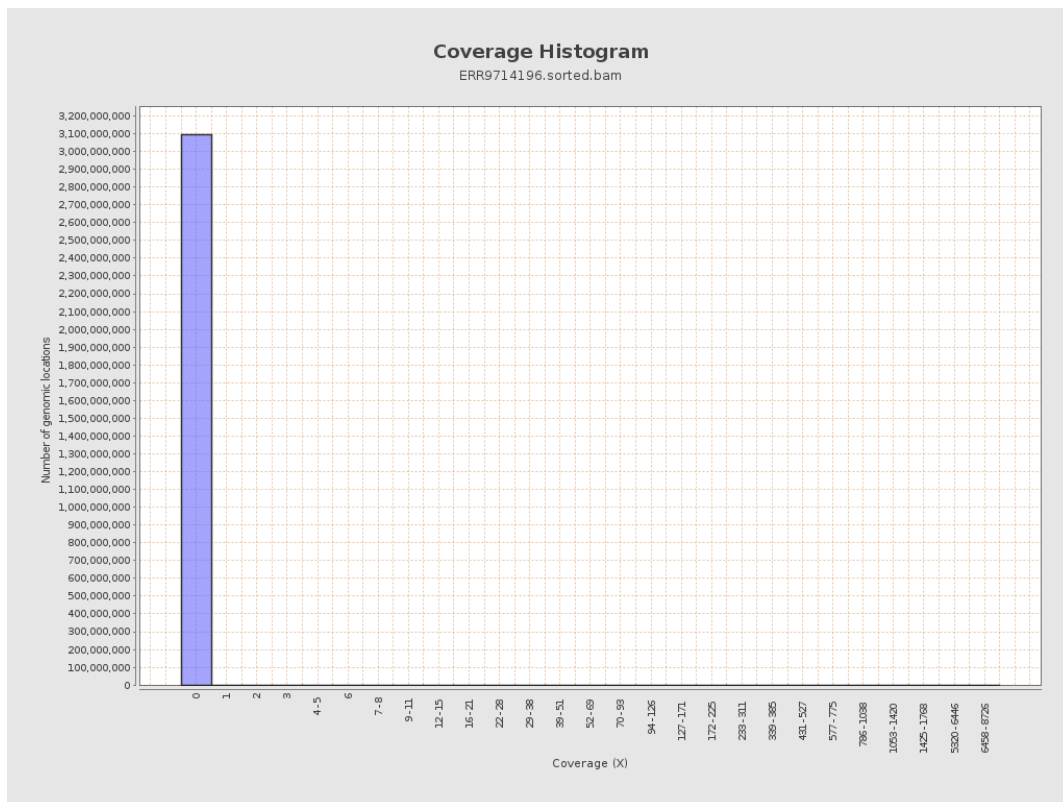
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26129	0.0001	0.0689
chr2	243199373	1333827	0.0055	5.6918
chr3	198022430	16062	0.0001	0.0197
chr4	191154276	10871	0.0001	0.0145
chr5	180915260	11324	0.0001	0.0191
chr6	171115067	19921	0.0001	0.0353
chr7	159138663	25009	0.0002	0.0819

chr8	146364022	41948	0.0003	0.1188
chr9	141213431	5778	0	0.0142
chr10	135534747	13259	0.0001	0.086
chr11	135006516	17225	0.0001	0.0461
chr12	133851895	14947	0.0001	0.0249
chr13	115169878	9628	0.0001	0.0196
chr14	107349540	14905	0.0001	0.0517
chr15	102531392	9237	0.0001	0.0237
chr16	90354753	8166	0.0001	0.0258
chr17	81195210	8909	0.0001	0.0359
chr18	78077248	3938	0.0001	0.0107
chr19	59128983	6910	0.0001	0.0252
chr20	63025520	17971	0.0003	0.1151
chr21	48129895	3970	0.0001	0.0214
chr22	51304566	1438	0	0.0077
chrMT	16571	696	0.042	0.3139
chrX	155270560	466186	0.003	0.3812
chrY	59373566	3456	0.0001	0.0111

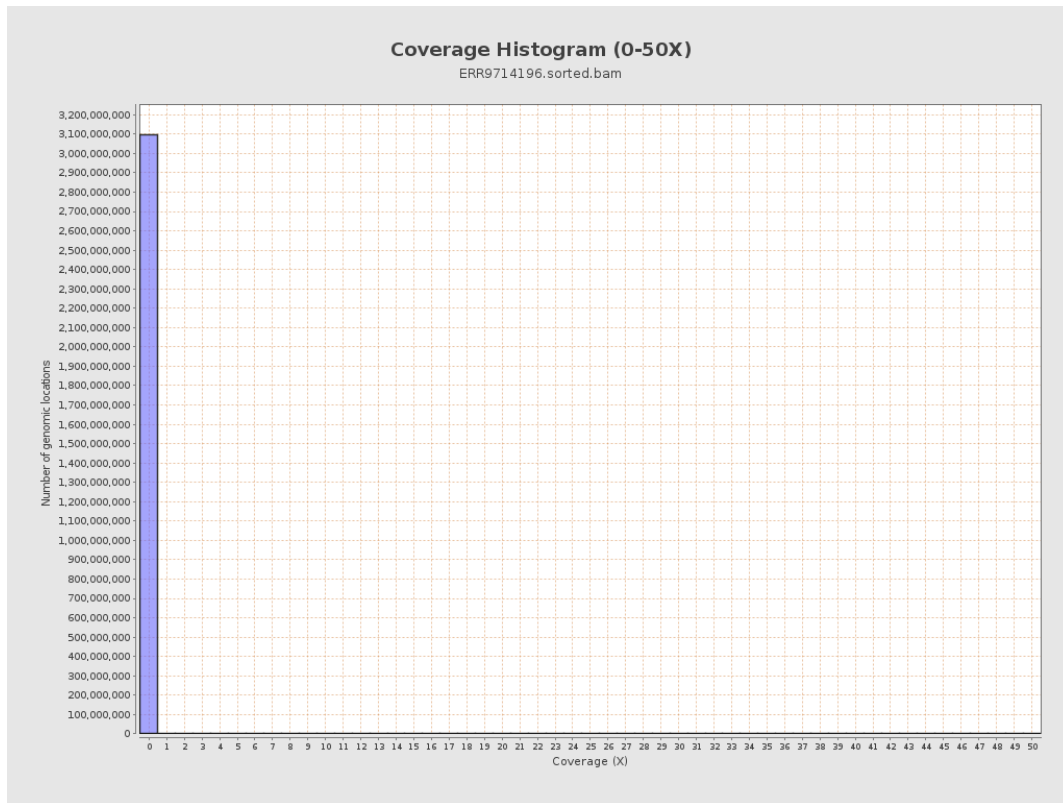
3. Results : Coverage across reference



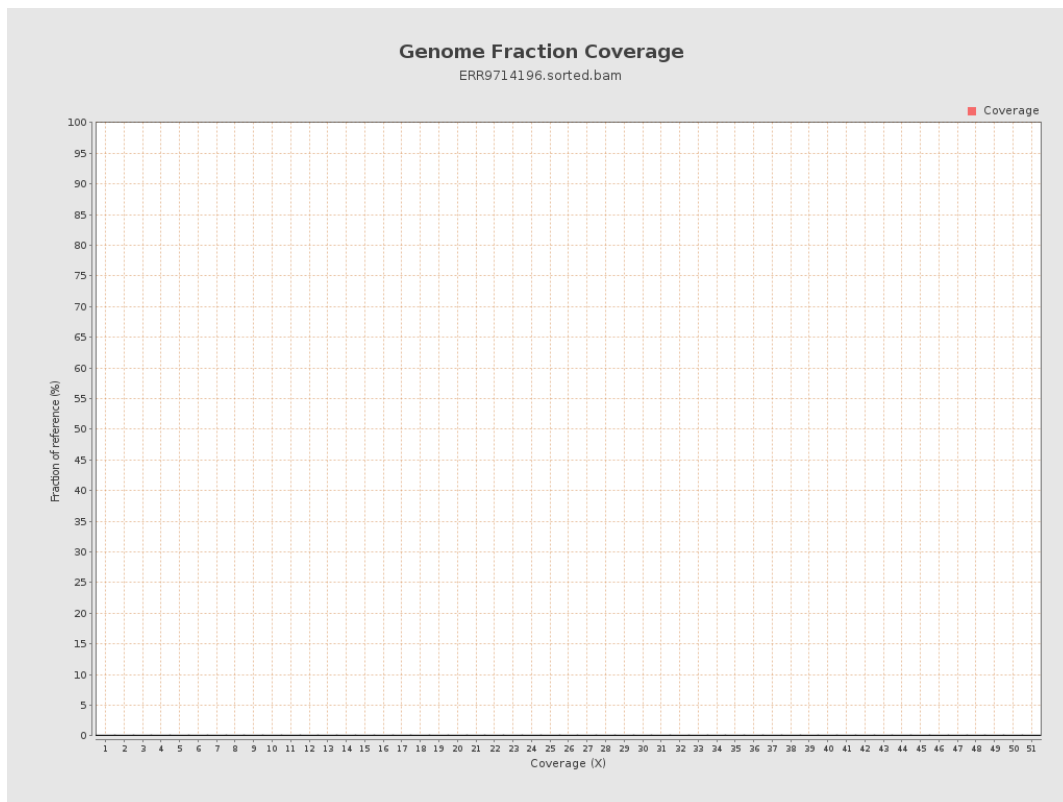
4. Results : Coverage Histogram



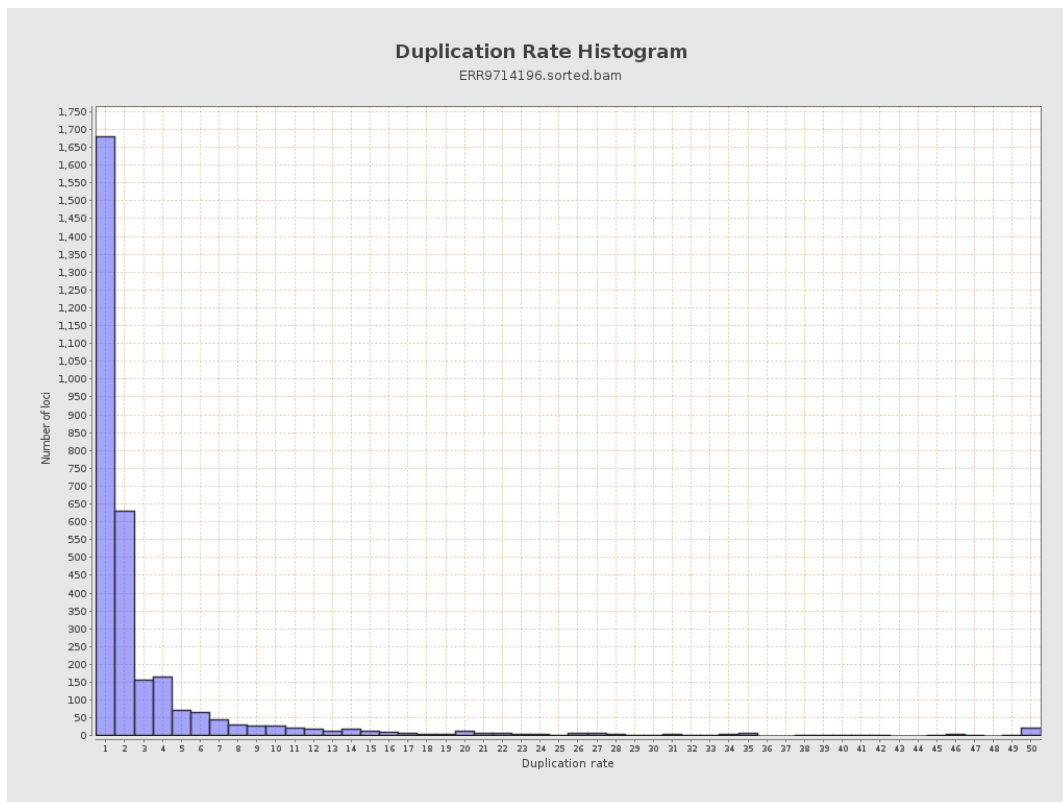
5. Results : Coverage Histogram (0-50X)



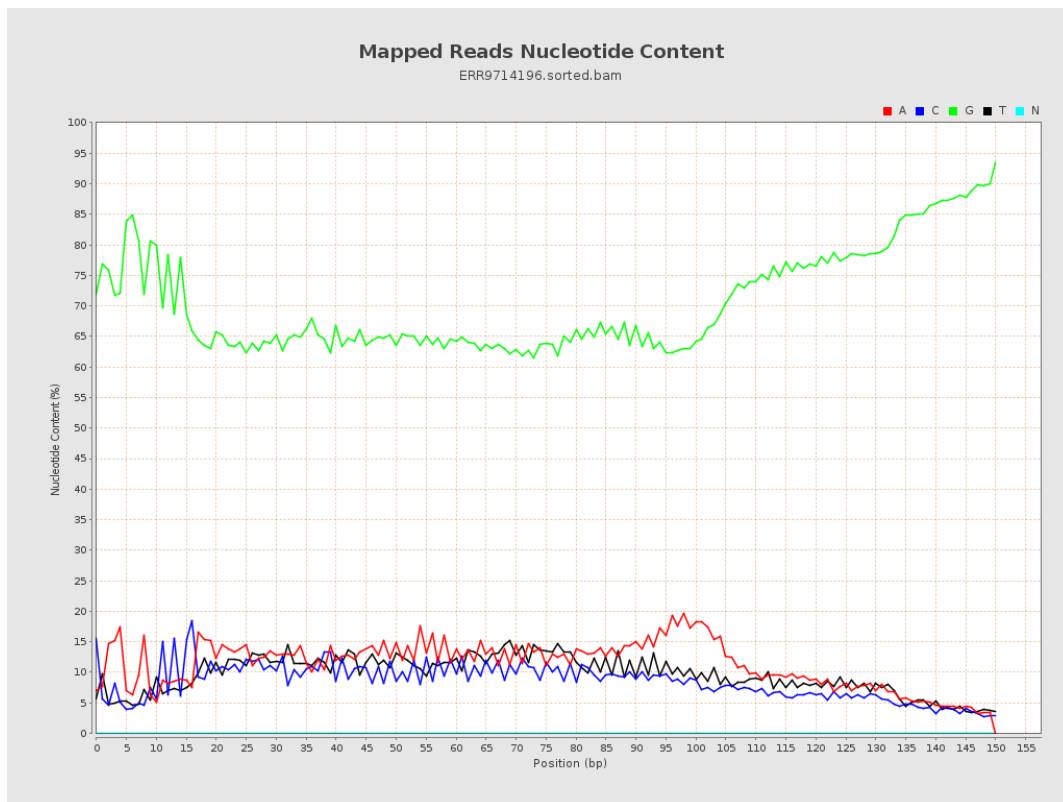
6. Results : Genome Fraction Coverage



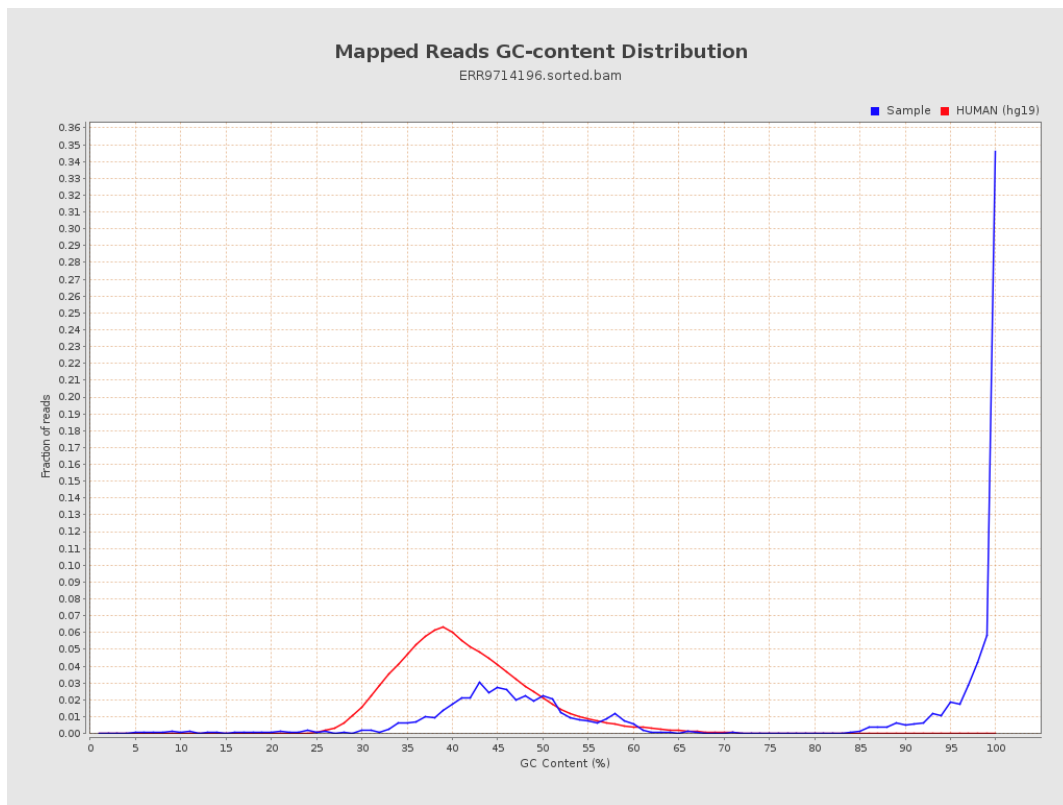
7. Results : Duplication Rate Histogram



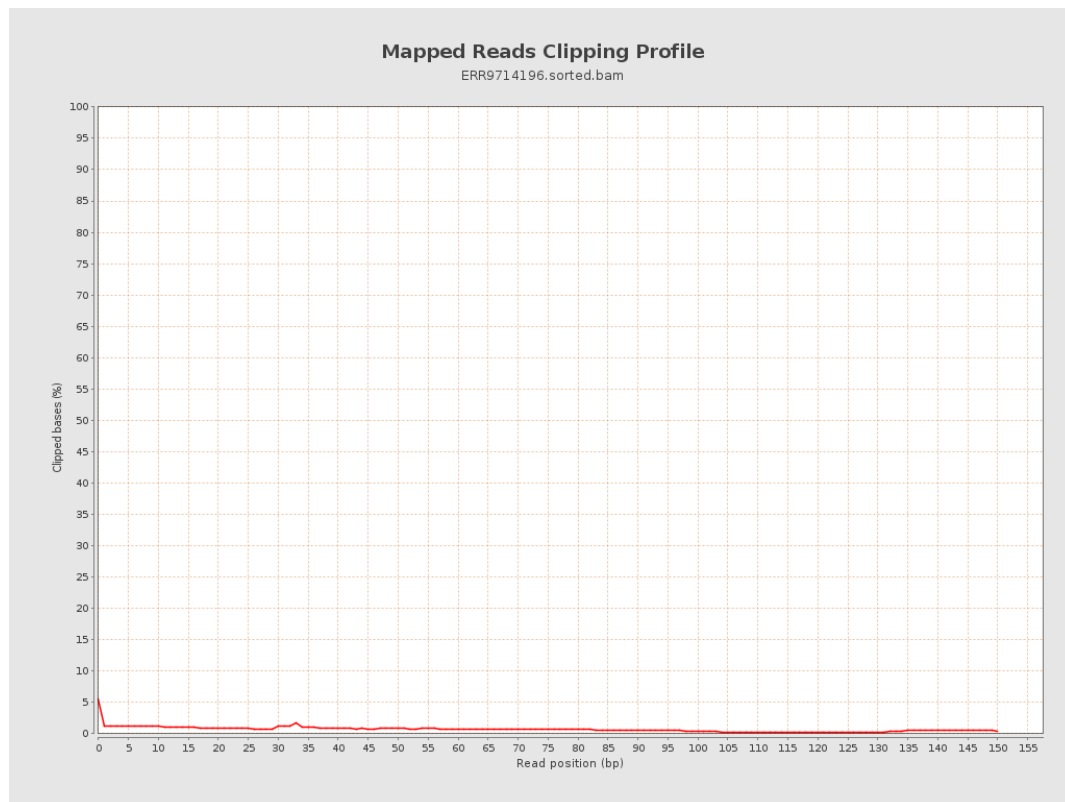
8. Results : Mapped Reads Nucleotide Content



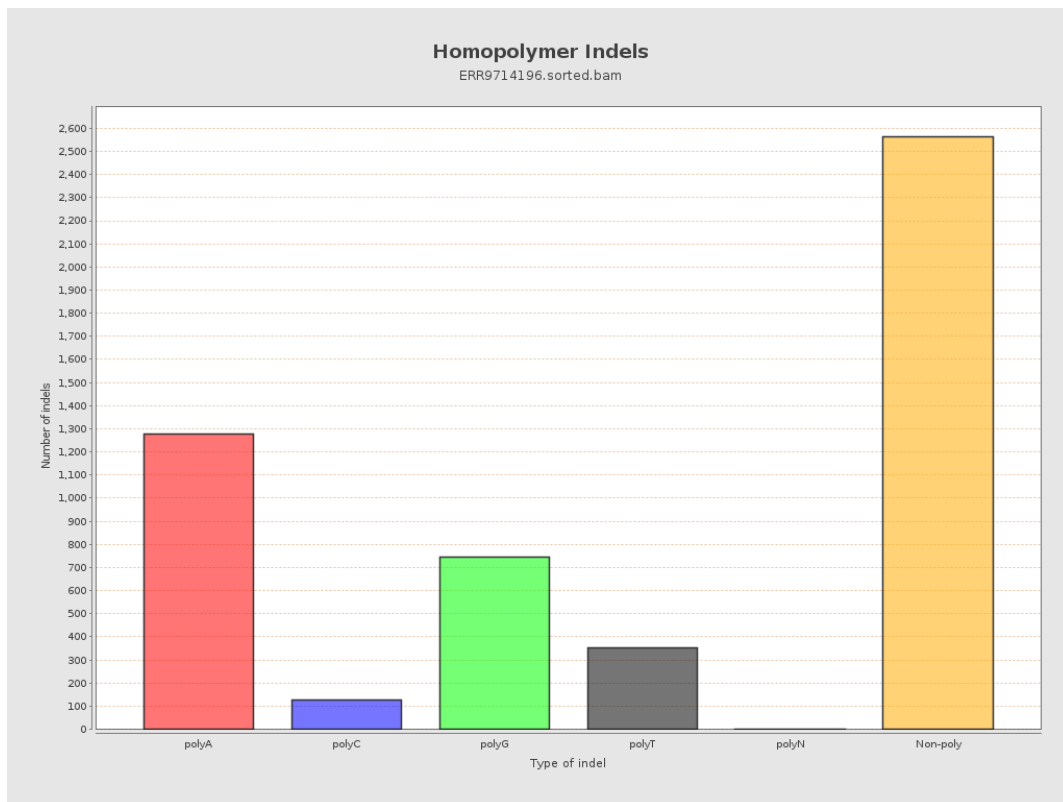
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

