

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:32:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714104.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_ERR9714104 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:32:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	569,368
Mapped reads	399,166 / 70.11%
Unmapped reads	170,202 / 29.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,647 / 2.57%
Read min/max/mean length	30 / 151 / 124.23
Duplicated reads (estimated)	333,859 / 58.64%
Duplication rate	42.08%
Clipped reads	379,567 / 66.66%

2.2. ACGT Content

Number/percentage of A's	13,784,552 / 27.49%
Number/percentage of C's	10,788,980 / 21.51%
Number/percentage of T's	13,079,141 / 26.08%
Number/percentage of G's	12,499,034 / 24.92%
Number/percentage of N's	351 / 0%
GC Percentage	46.43%

2.3. Coverage

Mean	0.0165

Standard Deviation	2.2557
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2.4. Mapping Quality

Mean Mapping Quality	52.39
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2.5. Mismatches and indels

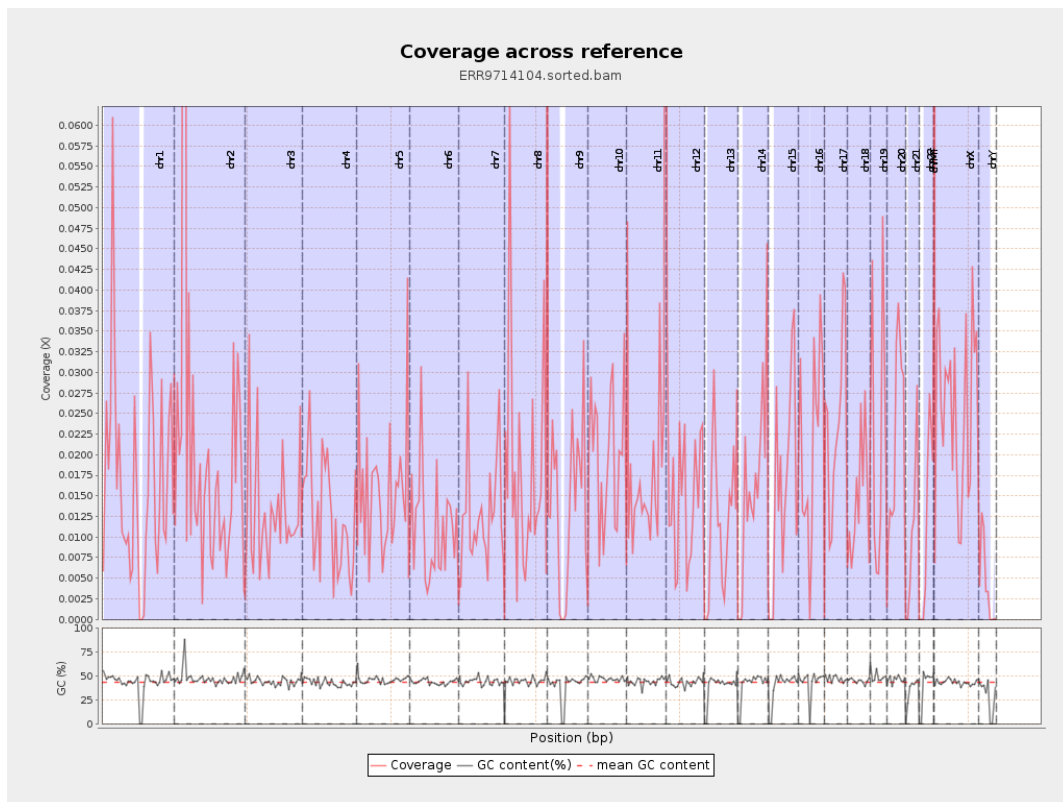
General error rate	4.17%
Mismatches	1,908,741
Insertions	58,106
Mapped reads with at least one insertion	14.1%
Deletions	164,358
Mapped reads with at least one deletion	39.17%
Homopolymer indels	28.25%

2.6. Chromosome stats

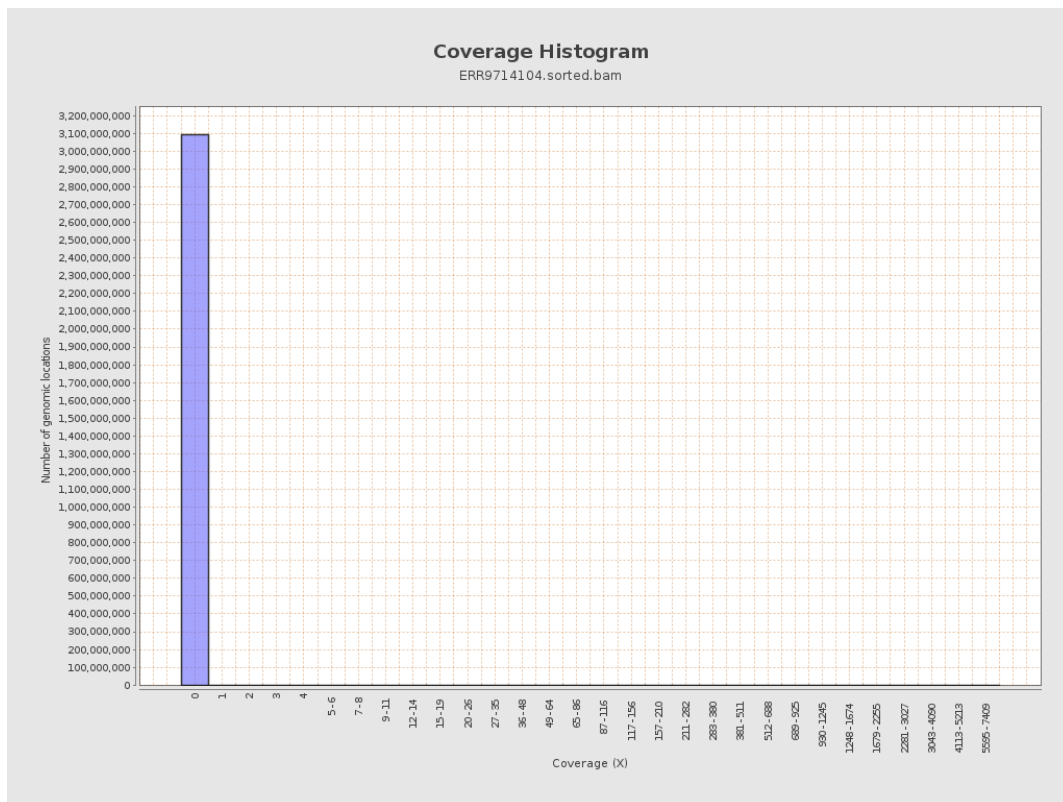
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4127380	0.0166	1.8244
chr2	243199373	5396438	0.0222	5.1888
chr3	198022430	2620499	0.0132	1.3691
chr4	191154276	2376850	0.0124	1.4023
chr5	180915260	2888550	0.016	1.5973
chr6	171115067	1866302	0.0109	1.0313
chr7	159138663	1993860	0.0125	1.3301

chr8	146364022	2588150	0.0177	2.3976
chr9	141213431	2039163	0.0144	1.6854
chr10	135534747	2685116	0.0198	1.8085
chr11	135006516	2371348	0.0176	1.8081
chr12	133851895	2054108	0.0153	1.6122
chr13	115169878	1322725	0.0115	1.4519
chr14	107349540	1765592	0.0164	1.862
chr15	102531392	1607867	0.0157	1.78
chr16	90354753	1903558	0.0211	2.3304
chr17	81195210	1899414	0.0234	2.4299
chr18	78077248	1175232	0.0151	1.4687
chr19	59128983	1199211	0.0203	2.1724
chr20	63025520	1415558	0.0225	1.9923
chr21	48129895	497236	0.0103	1.1562
chr22	51304566	626876	0.0122	1.3416
chrMT	16571	456707	27.5606	247.5544
chrX	155270560	3955303	0.0255	1.6035
chrY	59373566	261032	0.0044	0.7782

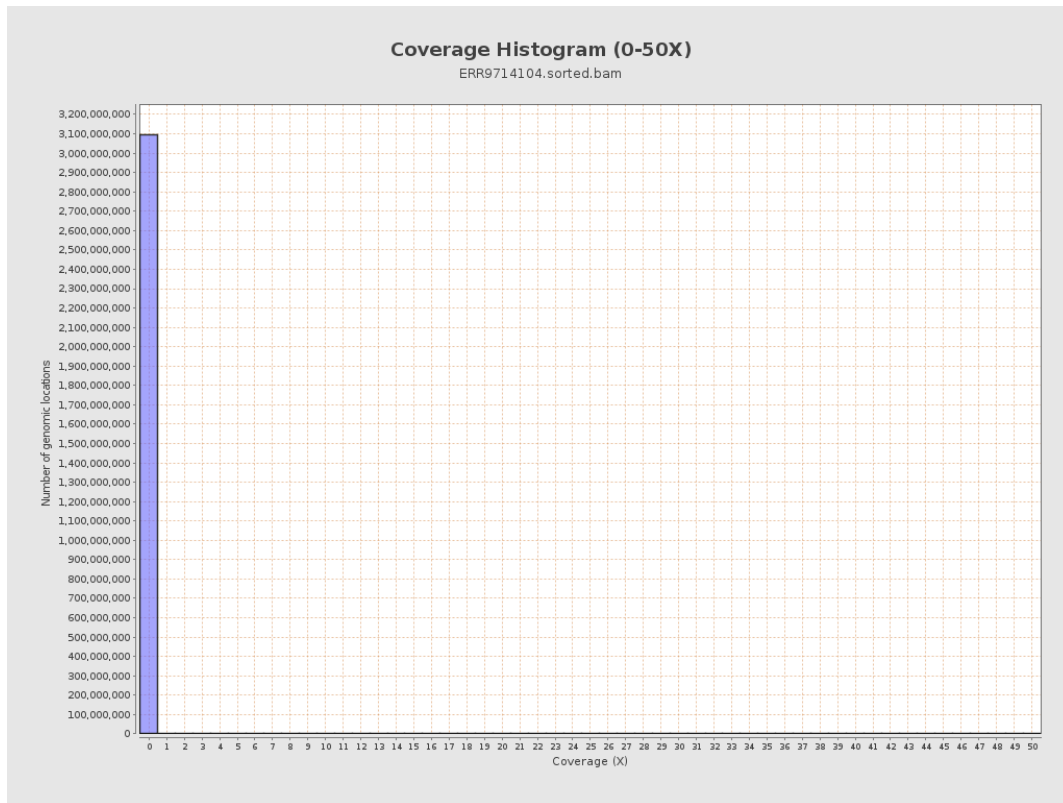
3. Results : Coverage across reference



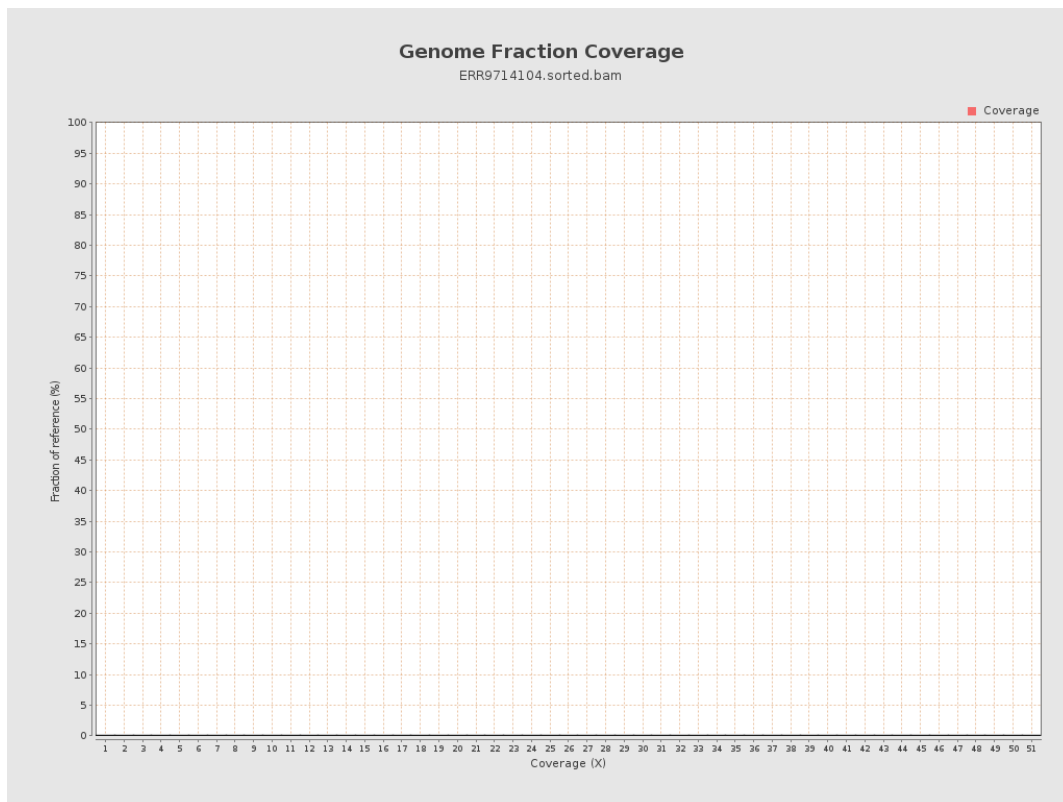
4. Results : Coverage Histogram



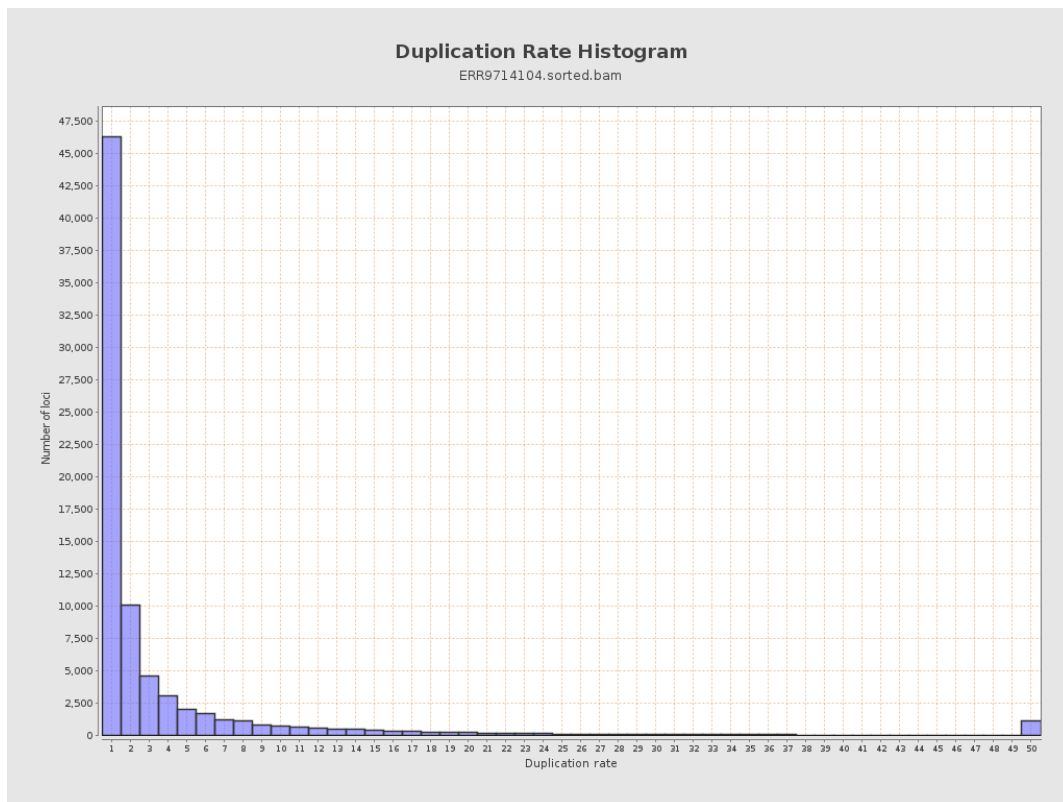
5. Results : Coverage Histogram (0-50X)



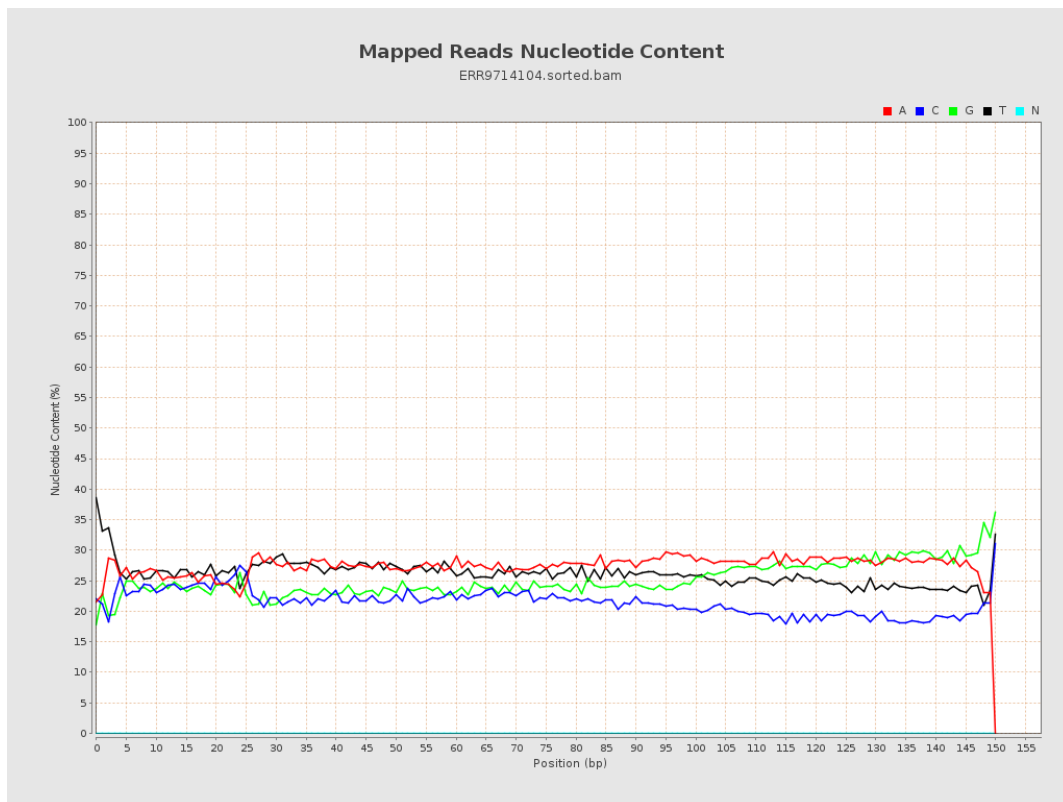
6. Results : Genome Fraction Coverage



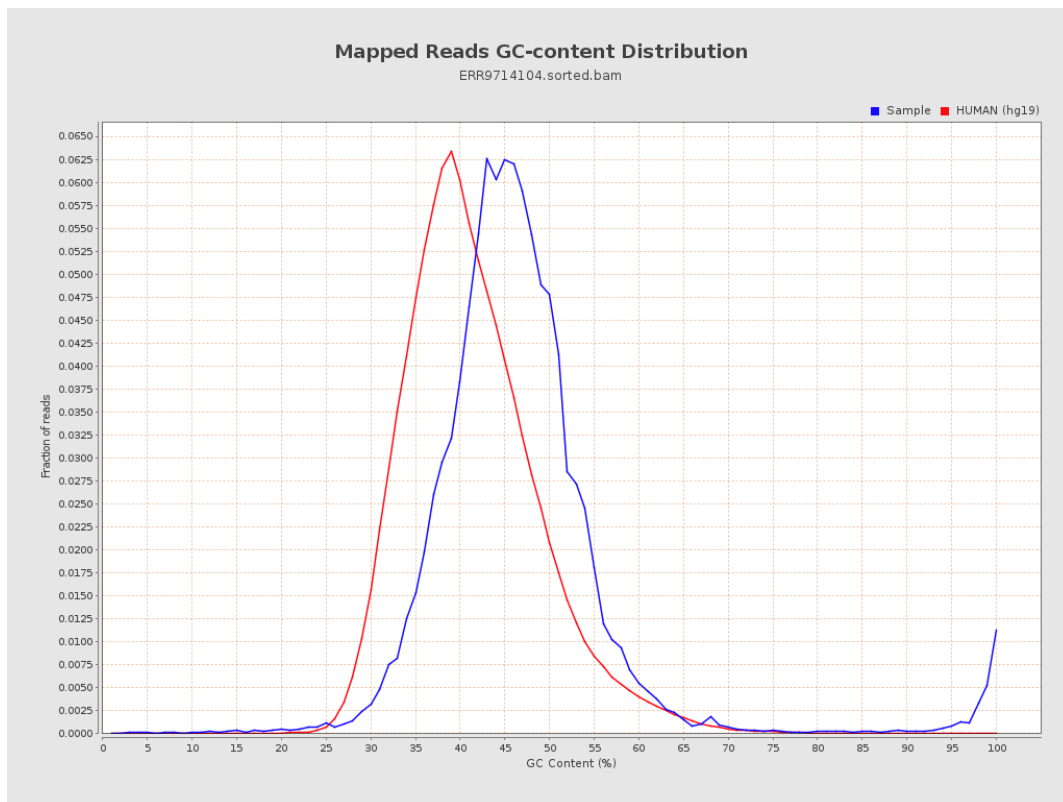
7. Results : Duplication Rate Histogram



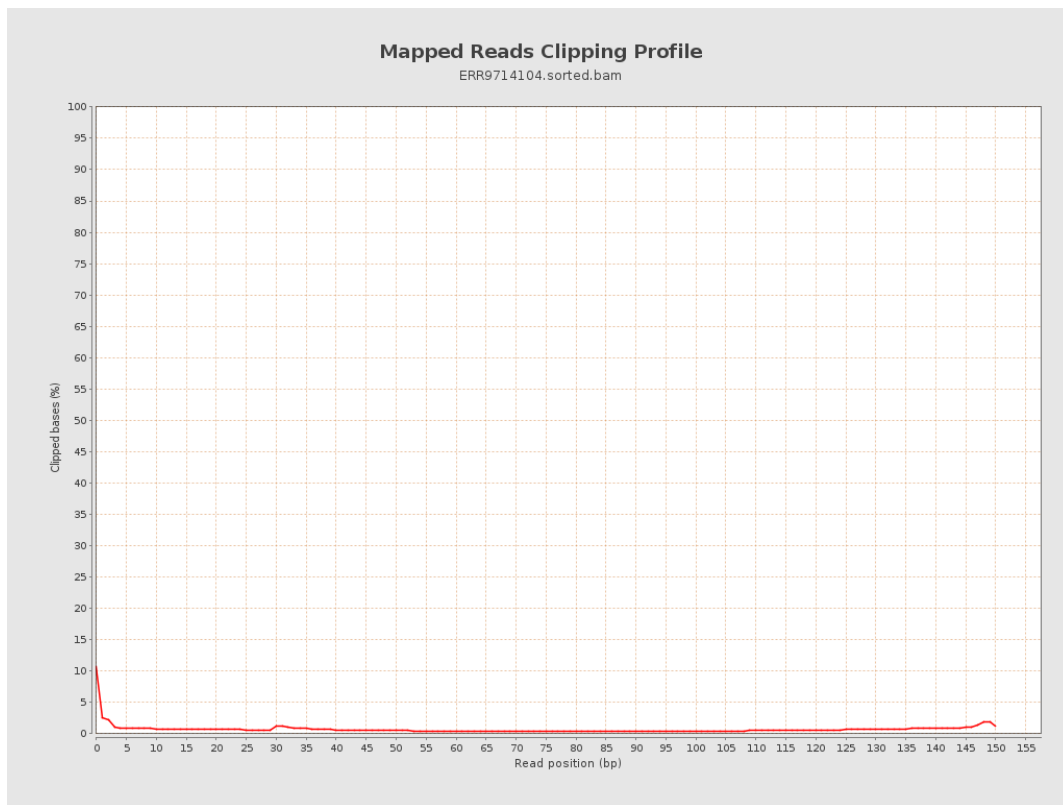
8. Results : Mapped Reads Nucleotide Content



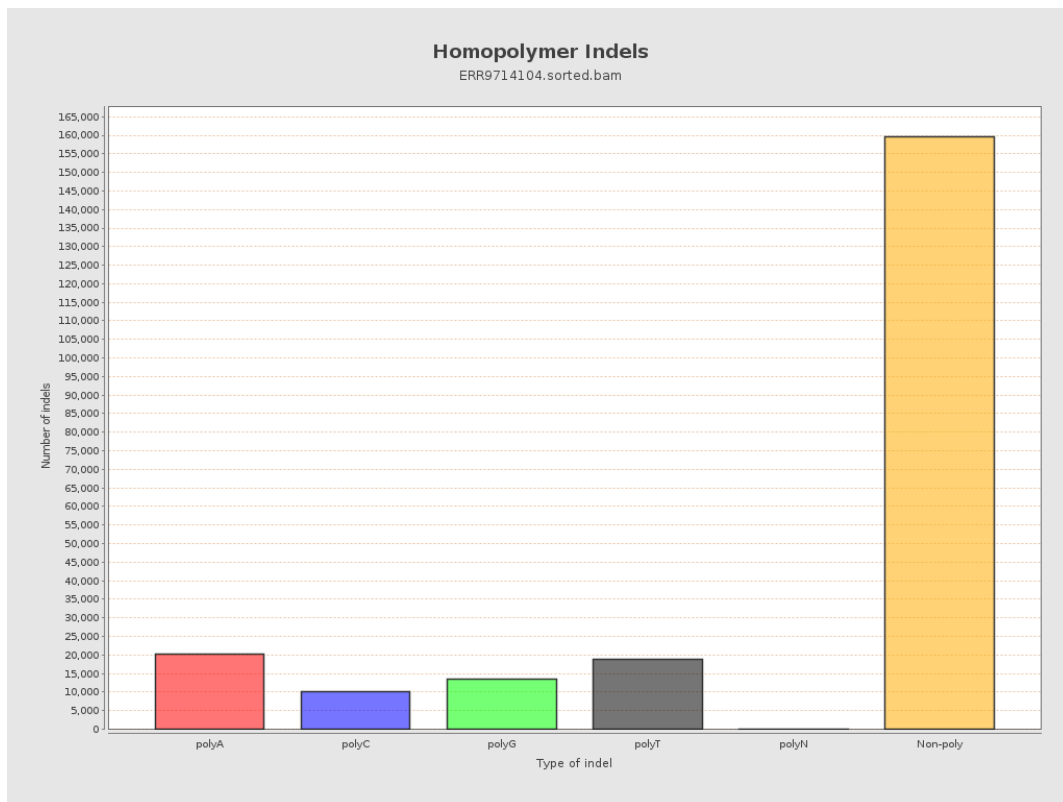
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

