

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:56:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714174.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_ERR9714174 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:56:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,149,386
Mapped reads	888,240 / 77.28%
Unmapped reads	261,146 / 22.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,702 / 2.67%
Read min/max/mean length	30 / 151 / 127.63
Duplicated reads (estimated)	777,797 / 67.67%
Duplication rate	44.27%
Clipped reads	840,302 / 73.11%

2.2. ACGT Content

Number/percentage of A's	31,071,118 / 27.62%
Number/percentage of C's	24,327,284 / 21.63%
Number/percentage of T's	29,555,938 / 26.28%
Number/percentage of G's	27,531,186 / 24.48%
Number/percentage of N's	731 / 0%
GC Percentage	46.1%

2.3. Coverage

Mean	0.037

Standard Deviation	4.854
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2.4. Mapping Quality

Mean Mapping Quality	52.52
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2.5. Mismatches and indels

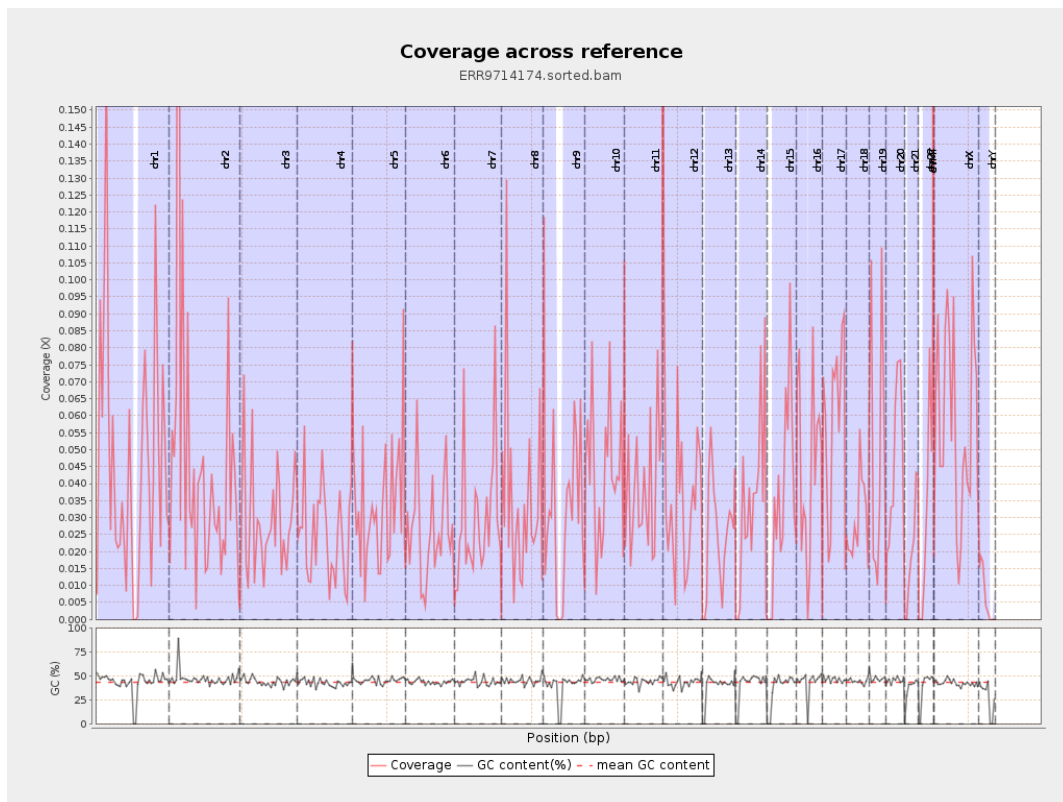
General error rate	4.15%
Mismatches	4,268,387
Insertions	123,908
Mapped reads with at least one insertion	13.48%
Deletions	373,002
Mapped reads with at least one deletion	40.09%
Homopolymer indels	28.47%

2.6. Chromosome stats

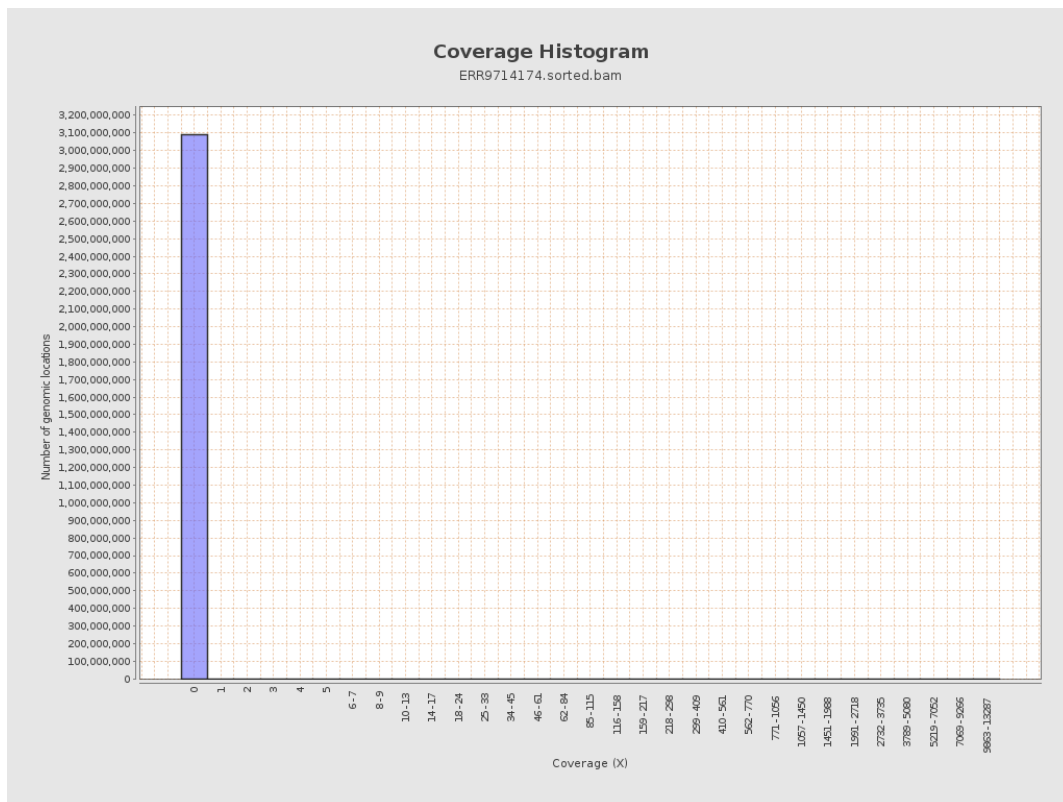
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11485097	0.0461	5.4019
chr2	243199373	11878417	0.0488	10.0773
chr3	198022430	5662848	0.0286	3.0156
chr4	191154276	4771792	0.025	2.7523
chr5	180915260	6019136	0.0333	3.4942
chr6	171115067	4451271	0.026	2.7275
chr7	159138663	4774858	0.03	3.3564

chr8	146364022	5026358	0.0343	4.2203
chr9	141213431	4232296	0.03	3.575
chr10	135534747	5982762	0.0441	4.5482
chr11	135006516	5481060	0.0406	4.1528
chr12	133851895	4866054	0.0364	4.1712
chr13	115169878	2771072	0.0241	2.9048
chr14	107349540	3731534	0.0348	3.8946
chr15	102531392	3610628	0.0352	3.5623
chr16	90354753	3986275	0.0441	5.3025
chr17	81195210	4870793	0.06	6.2624
chr18	78077248	2327882	0.0298	2.9026
chr19	59128983	2785357	0.0471	5.3023
chr20	63025520	2956352	0.0469	3.8819
chr21	48129895	945327	0.0196	2.0563
chr22	51304566	1586121	0.0309	3.4858
chrMT	16571	940249	56.7406	520.4649
chrX	155270560	9100527	0.0586	3.8052
chrY	59373566	401640	0.0068	0.9893

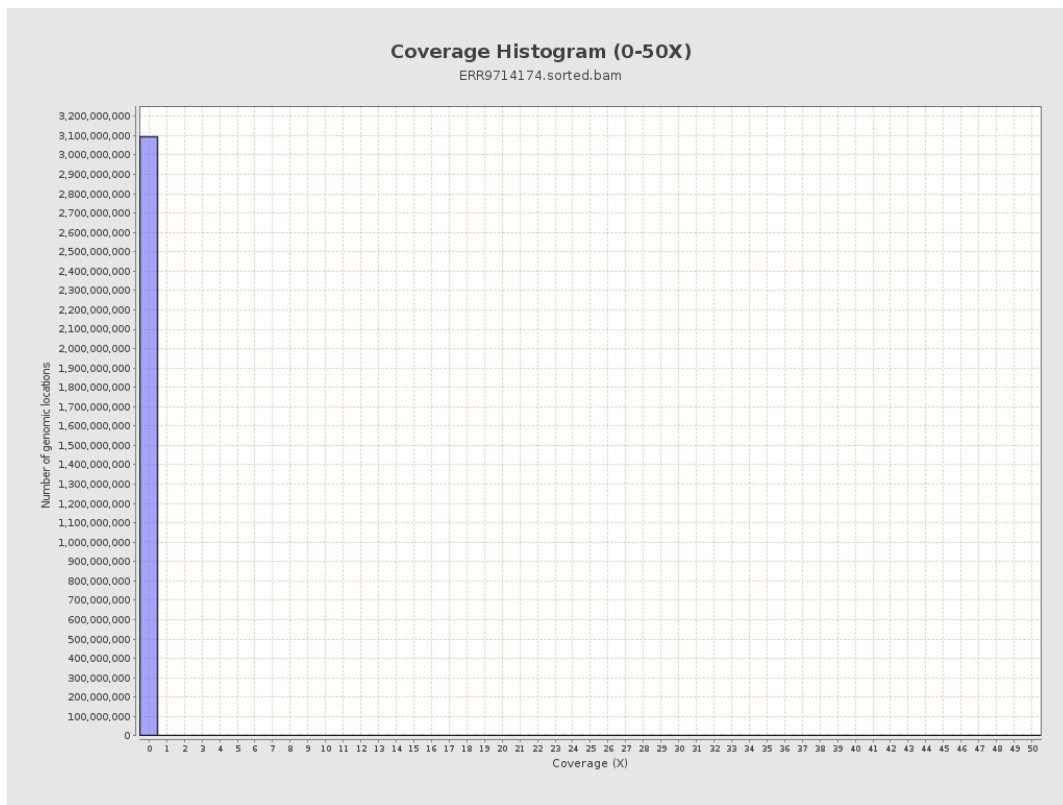
3. Results : Coverage across reference



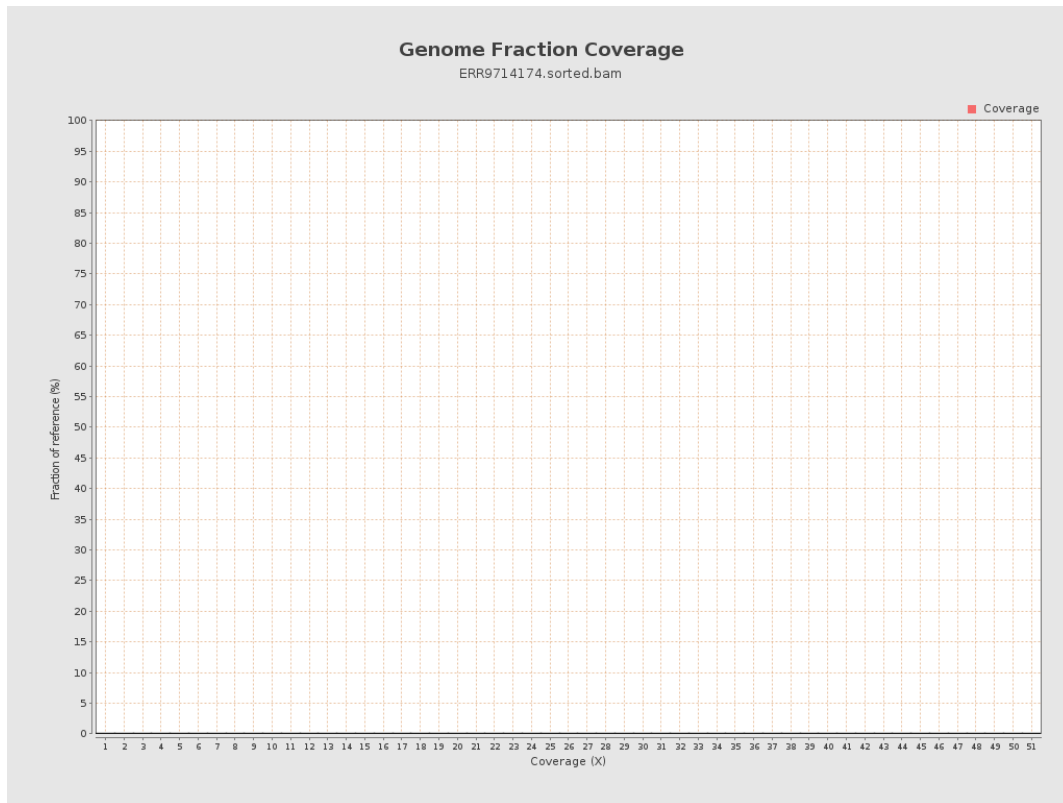
4. Results : Coverage Histogram



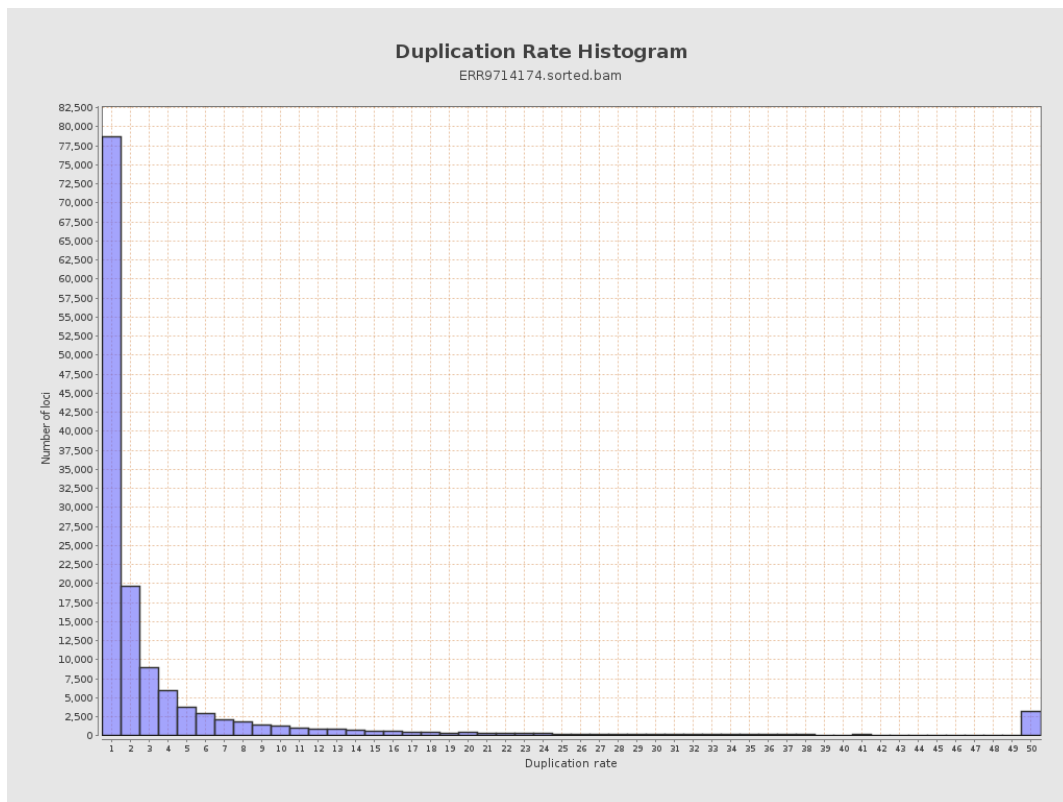
5. Results : Coverage Histogram (0-50X)



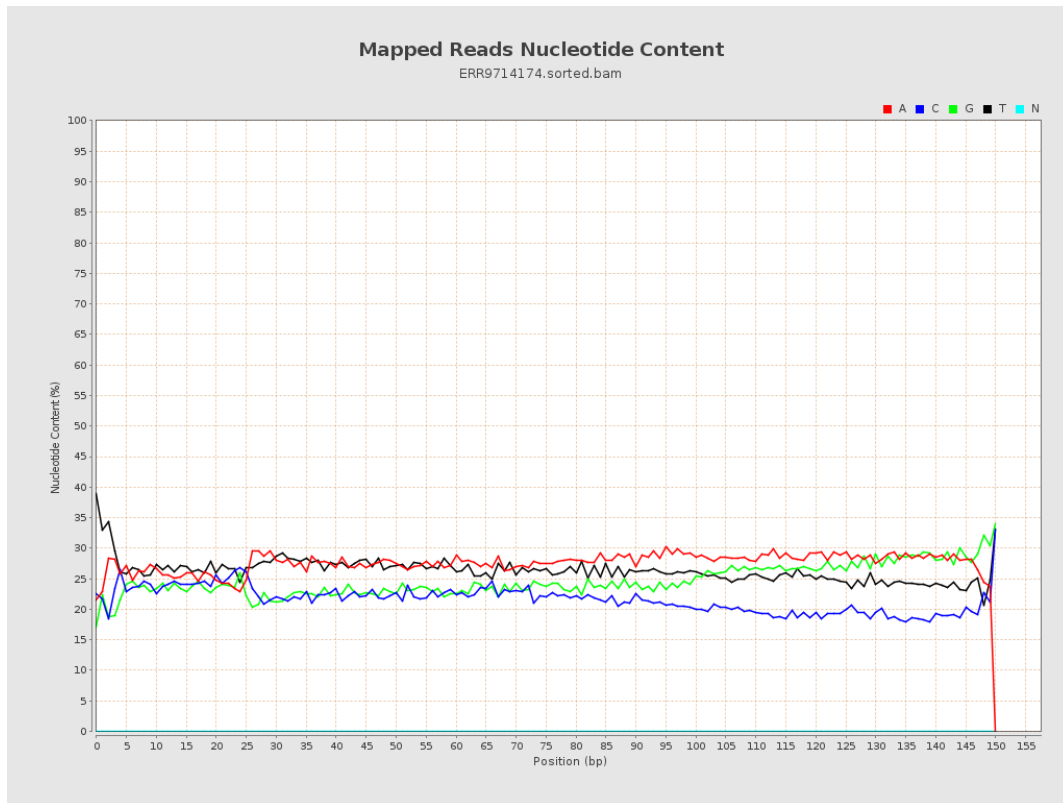
6. Results : Genome Fraction Coverage



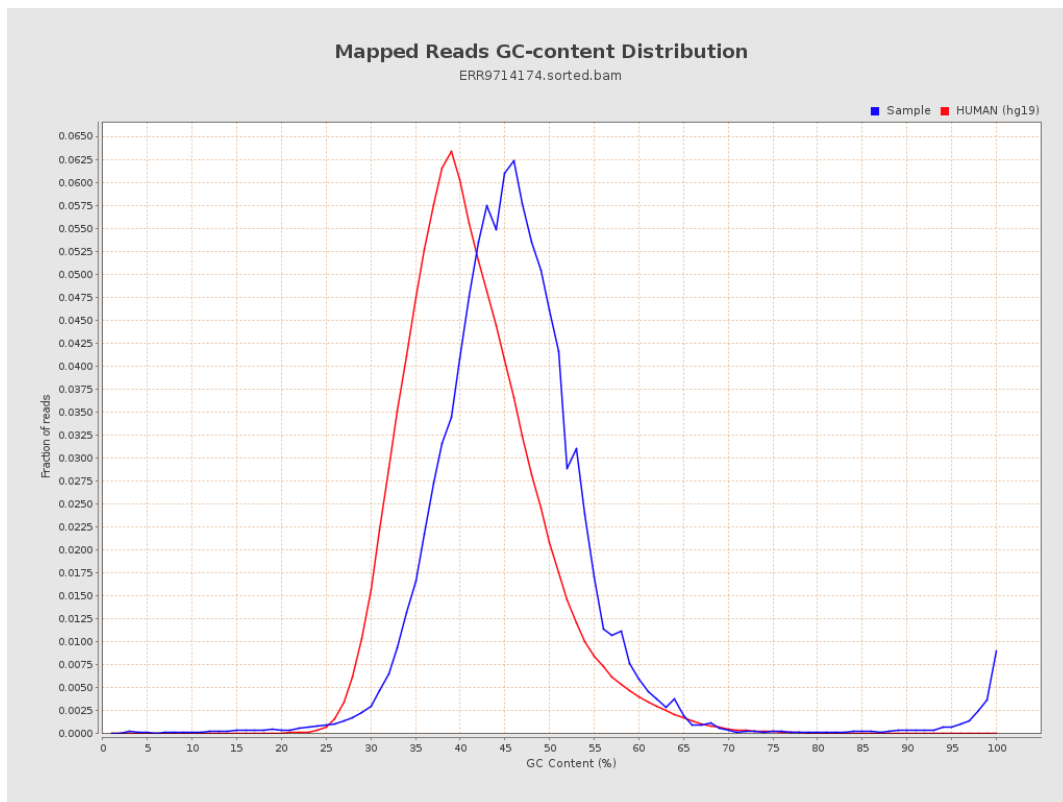
7. Results : Duplication Rate Histogram



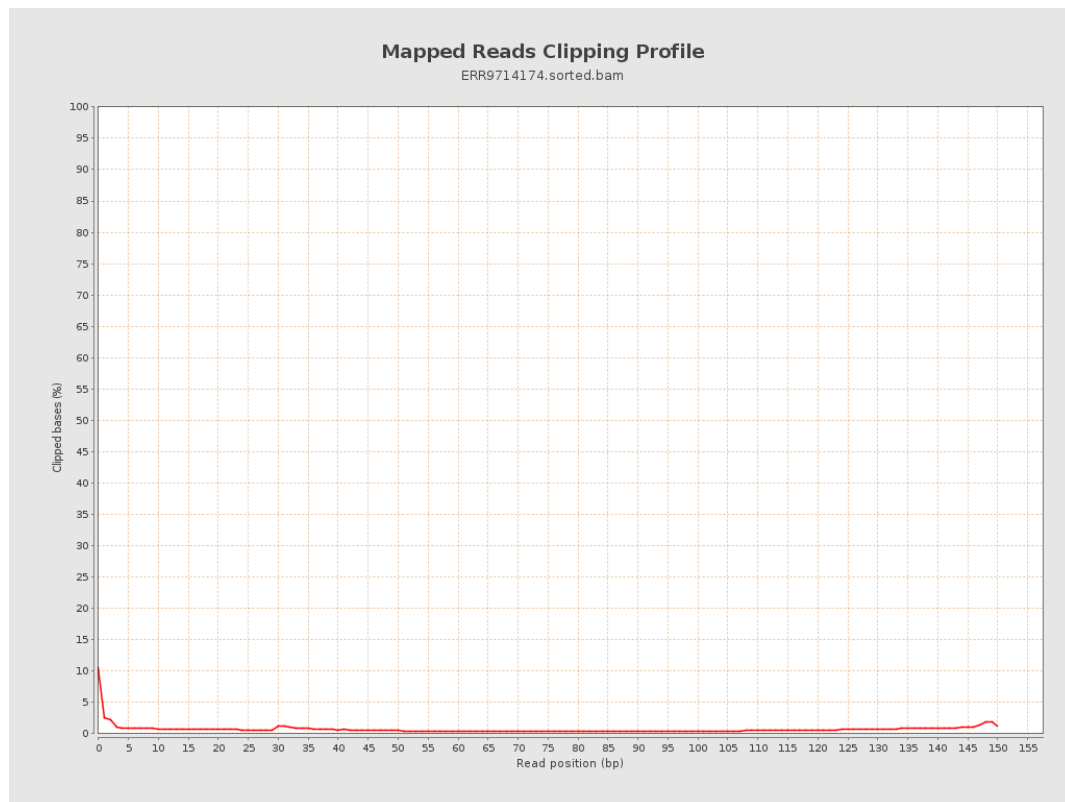
8. Results : Mapped Reads Nucleotide Content



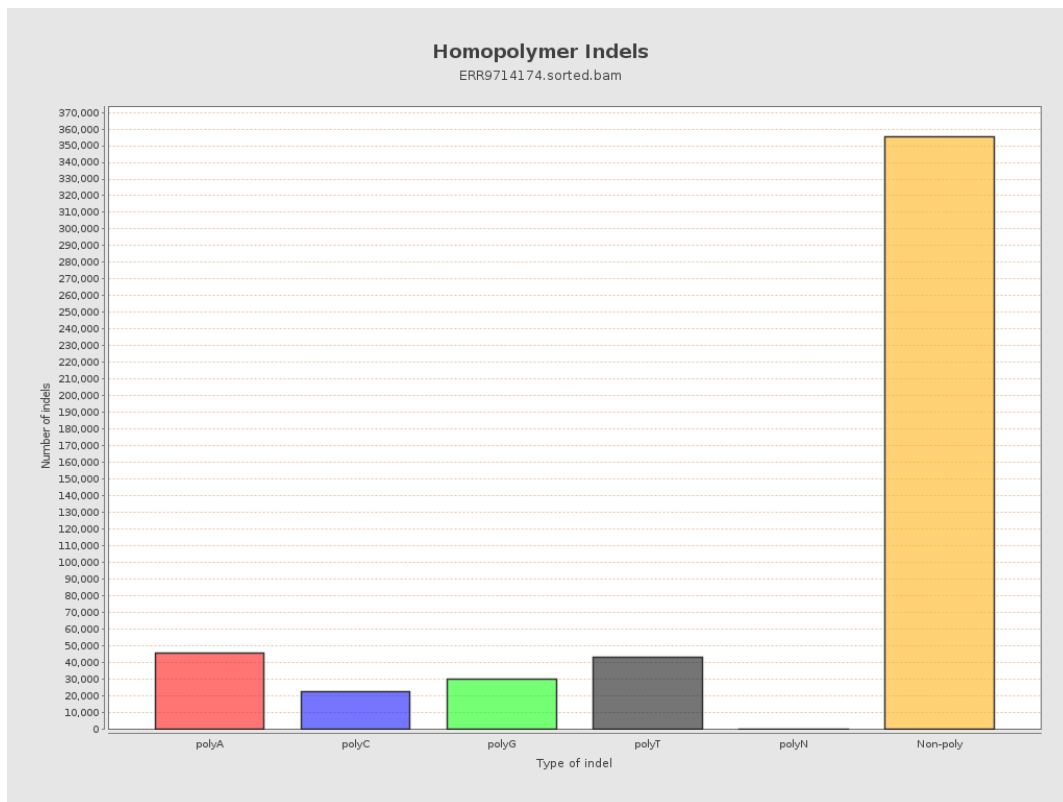
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

