

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:53:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716494.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_SRR9716494 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716494.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:53:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716494.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,385,870
Mapped reads	1,222,495 / 88.21%
Unmapped reads	163,375 / 11.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,546 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	39,426 / 2.84%
Duplication rate	2.32%
Clipped reads	1,224,499 / 88.36%

2.2. ACGT Content

Number/percentage of A's	17,937,495 / 25.61%
Number/percentage of C's	12,873,851 / 18.38%
Number/percentage of T's	22,724,112 / 32.45%
Number/percentage of G's	16,499,321 / 23.56%
Number/percentage of N's	1,898 / 0%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2499
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2.4. Mapping Quality

Mean Mapping Quality	44.34
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2.5. Mismatches and indels

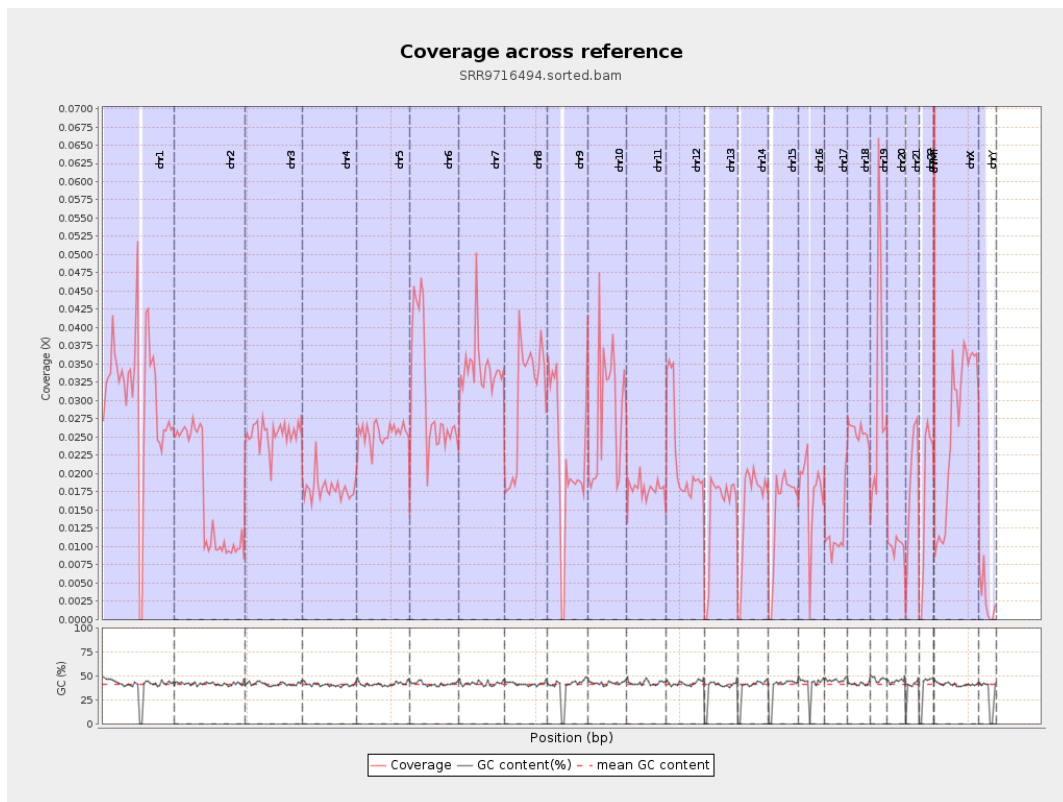
General error rate	0.52%
Mismatches	351,763
Insertions	5,270
Mapped reads with at least one insertion	0.43%
Deletions	12,895
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.62%

2.6. Chromosome stats

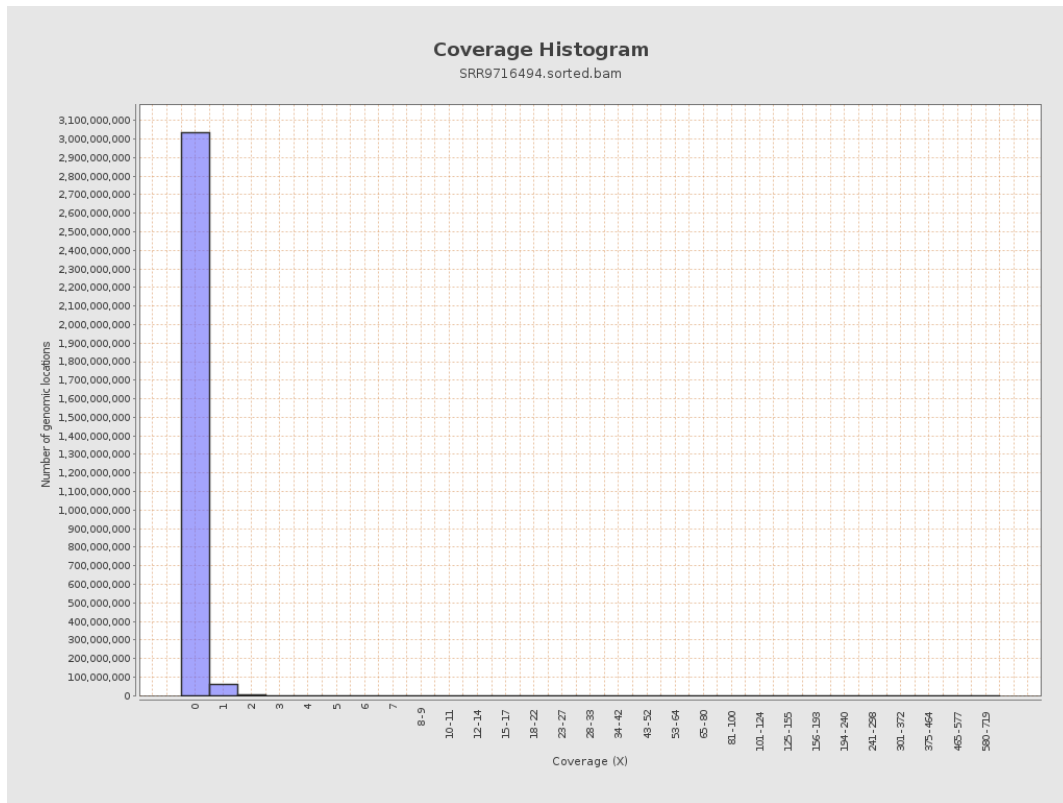
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7555968	0.0303	0.5236
chr2	243199373	4006116	0.0165	0.2789
chr3	198022430	5040659	0.0255	0.1722
chr4	191154276	3433064	0.018	0.1499
chr5	180915260	4633940	0.0256	0.1736
chr6	171115067	5130372	0.03	0.2081
chr7	159138663	5499190	0.0346	0.365

chr8	146364022	4407453	0.0301	0.2111
chr9	141213431	3065482	0.0217	0.1963
chr10	135534747	3805246	0.0281	0.2412
chr11	135006516	2424960	0.018	0.1793
chr12	133851895	2988650	0.0223	0.1641
chr13	115169878	1704830	0.0148	0.1318
chr14	107349540	1689520	0.0157	0.1406
chr15	102531392	1523903	0.0149	0.1322
chr16	90354753	1550978	0.0172	0.1534
chr17	81195210	969897	0.0119	0.1211
chr18	78077248	2008908	0.0257	0.3147
chr19	59128983	1829586	0.0309	0.3418
chr20	63025520	635632	0.0101	0.1109
chr21	48129895	913465	0.019	0.1557
chr22	51304566	878764	0.0171	0.1403
chrMT	16571	108646	6.5564	3.9974
chrX	155270560	4085870	0.0263	0.1936
chrY	59373566	165211	0.0028	0.0751

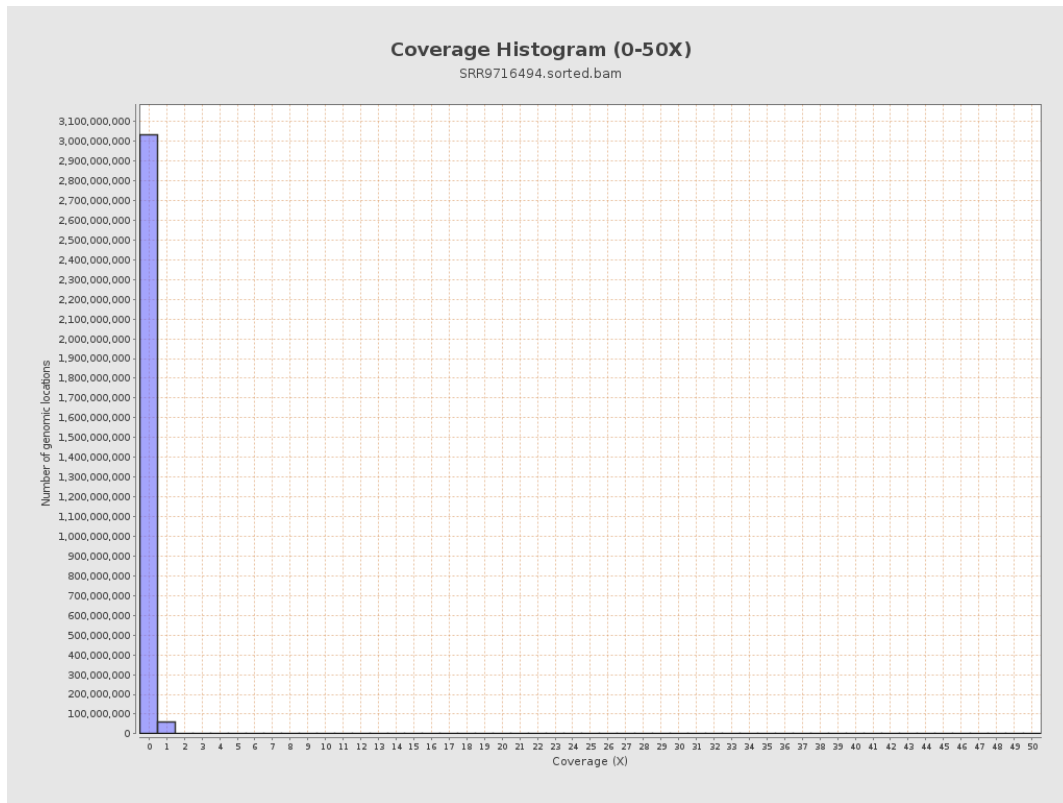
3. Results : Coverage across reference



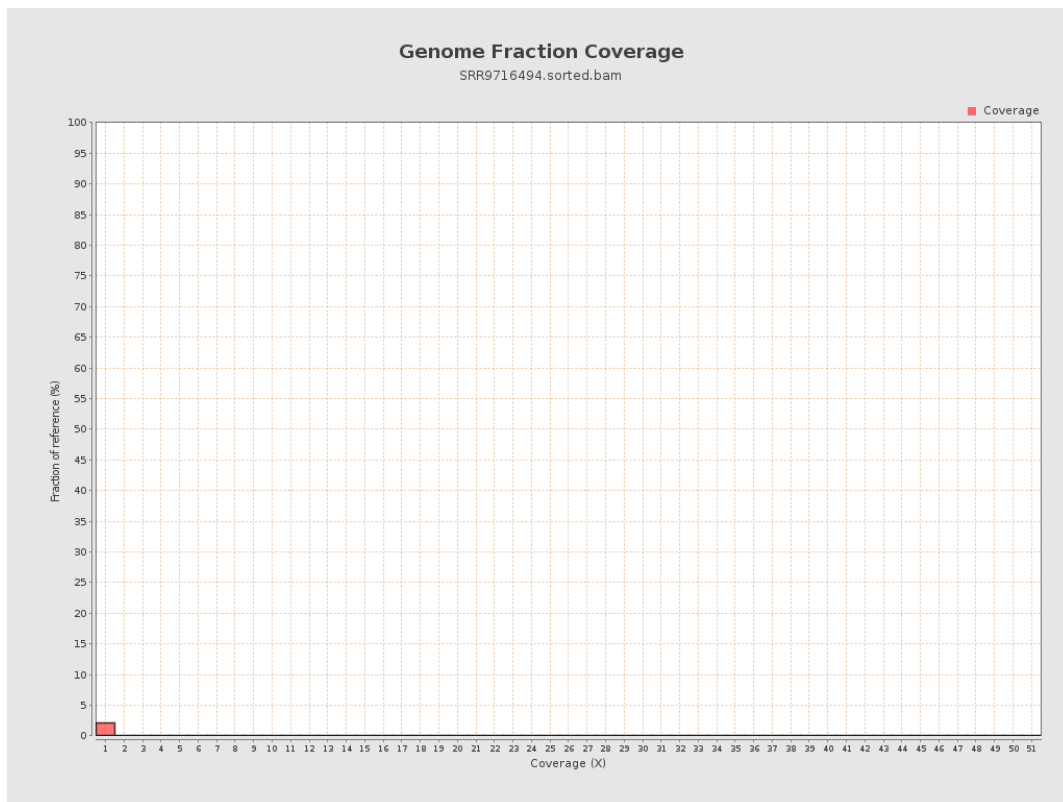
4. Results : Coverage Histogram



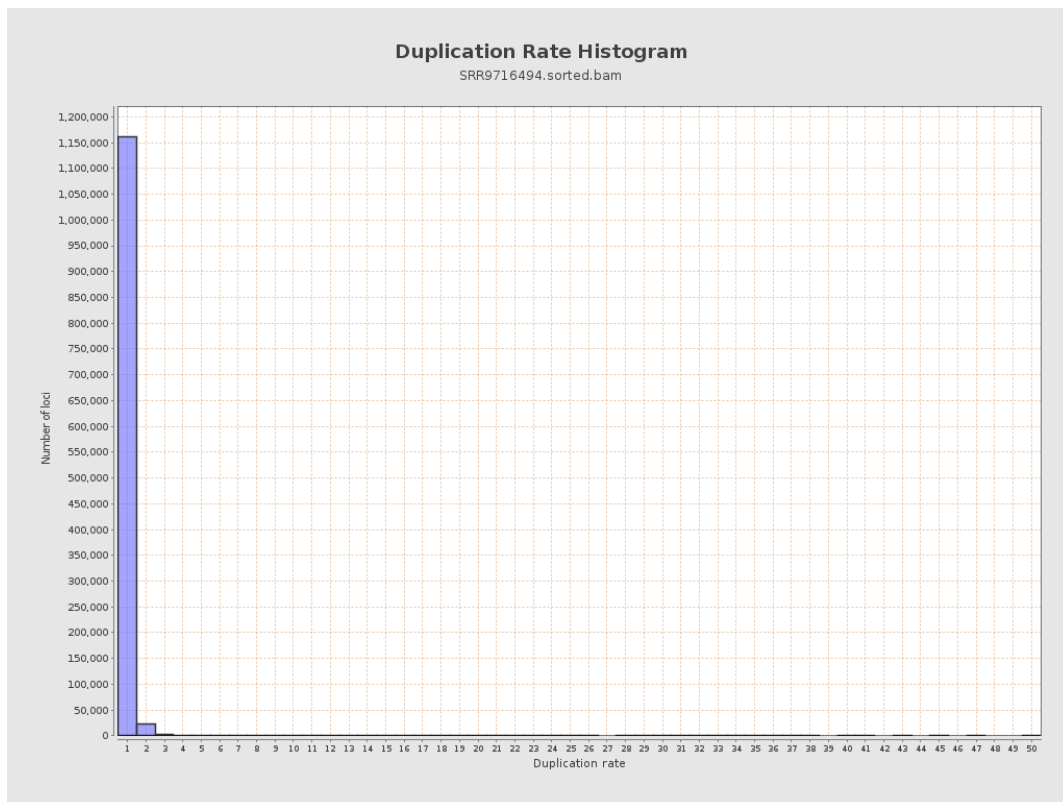
5. Results : Coverage Histogram (0-50X)



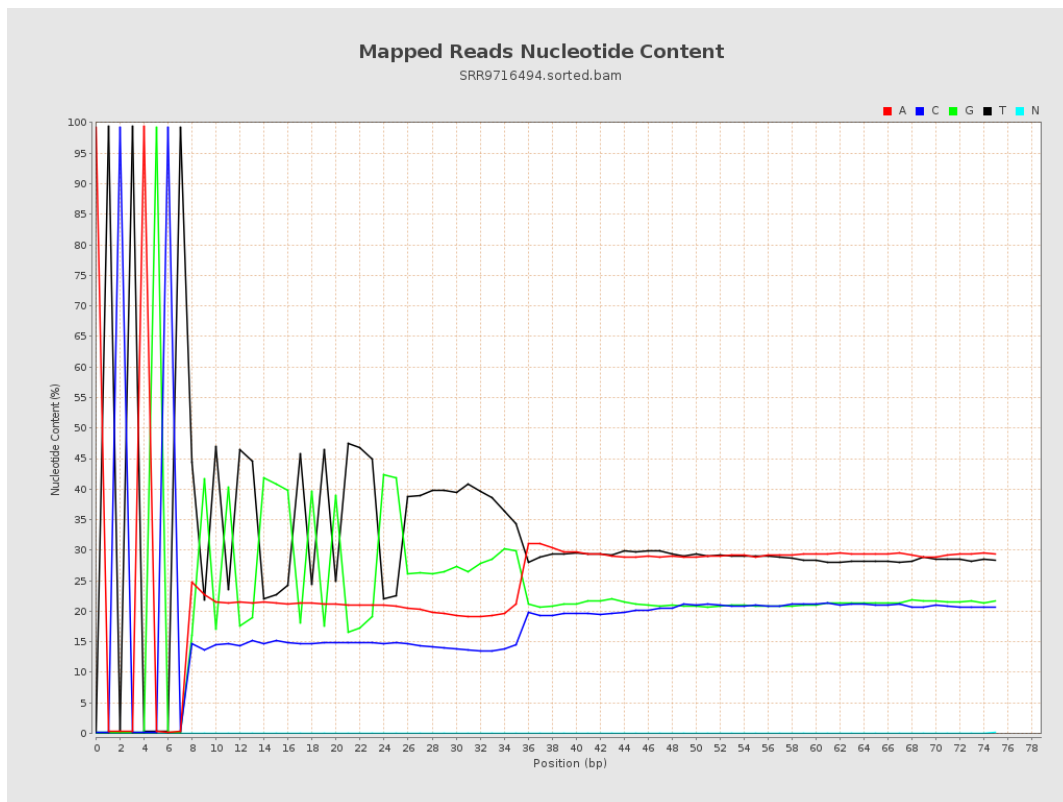
6. Results : Genome Fraction Coverage



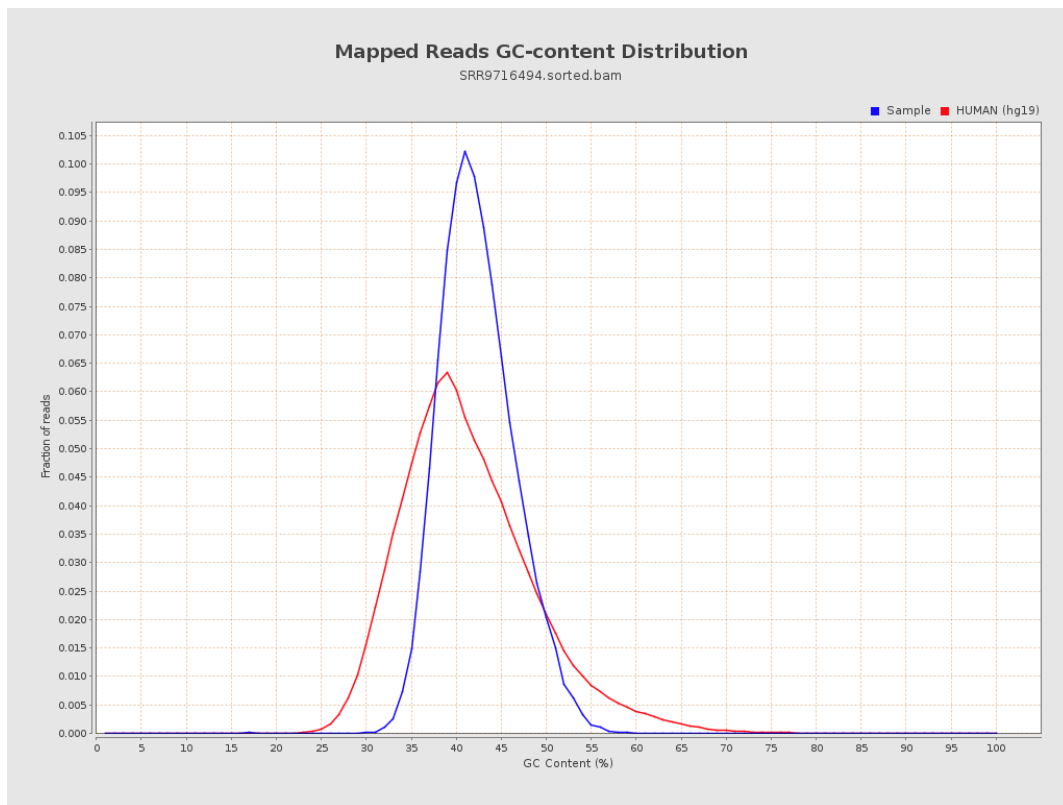
7. Results : Duplication Rate Histogram



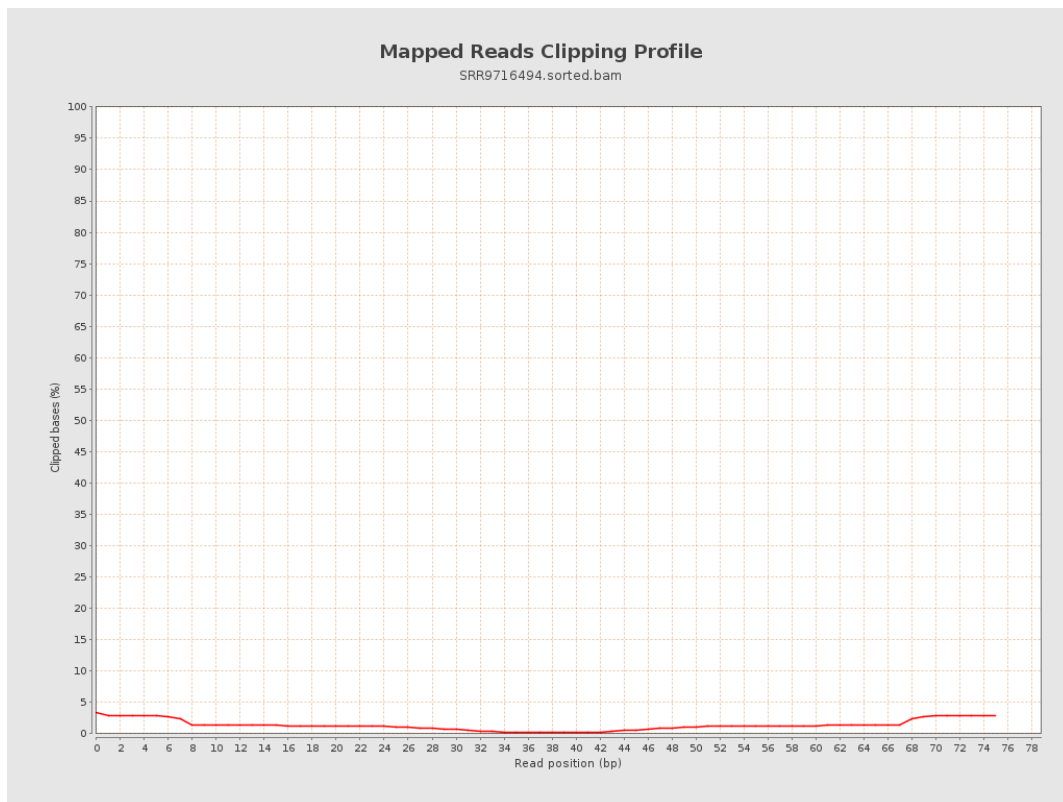
8. Results : Mapped Reads Nucleotide Content



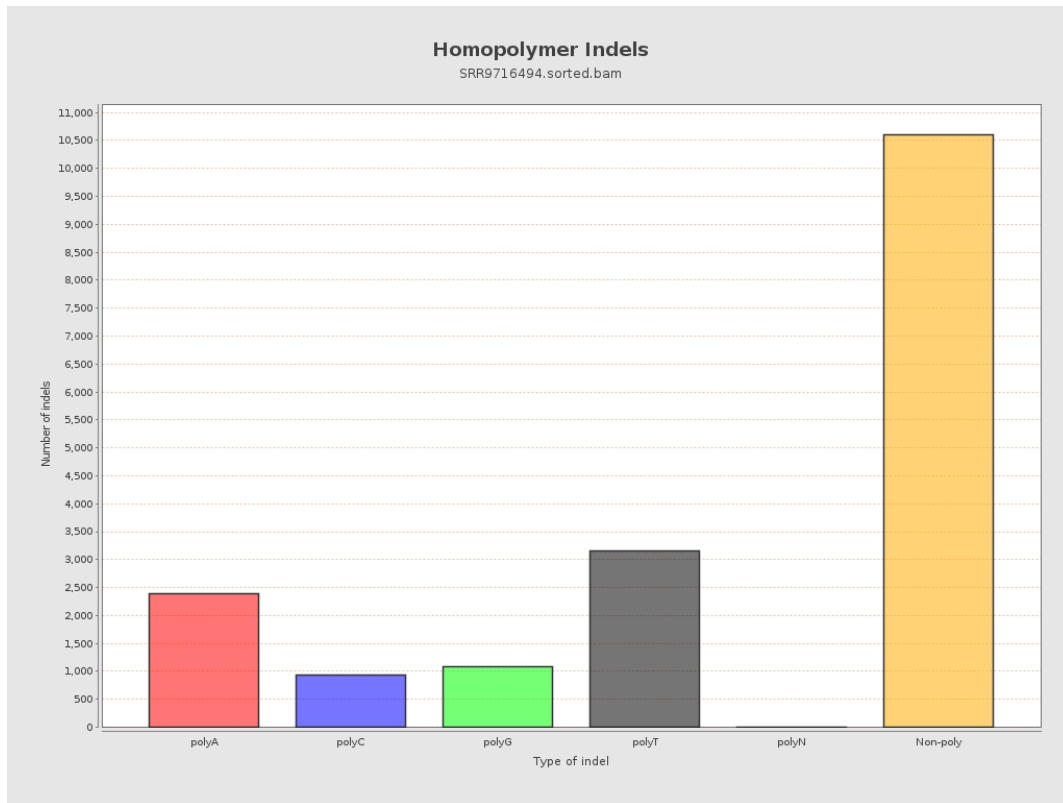
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

