

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:02:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240198.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_SRR6240198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:02:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,111,658
Mapped reads	843,185 / 75.85%
Unmapped reads	268,473 / 24.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,067 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	60,094 / 5.41%
Duplication rate	5.69%
Clipped reads	505,999 / 45.52%

2.2. ACGT Content

Number/percentage of A's	14,330,031 / 27.13%
Number/percentage of C's	9,277,179 / 17.56%
Number/percentage of T's	17,101,674 / 32.38%
Number/percentage of G's	12,098,517 / 22.91%
Number/percentage of N's	12,979 / 0.02%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.2003
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2.4. Mapping Quality

Mean Mapping Quality	45.74
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2.5. Mismatches and indels

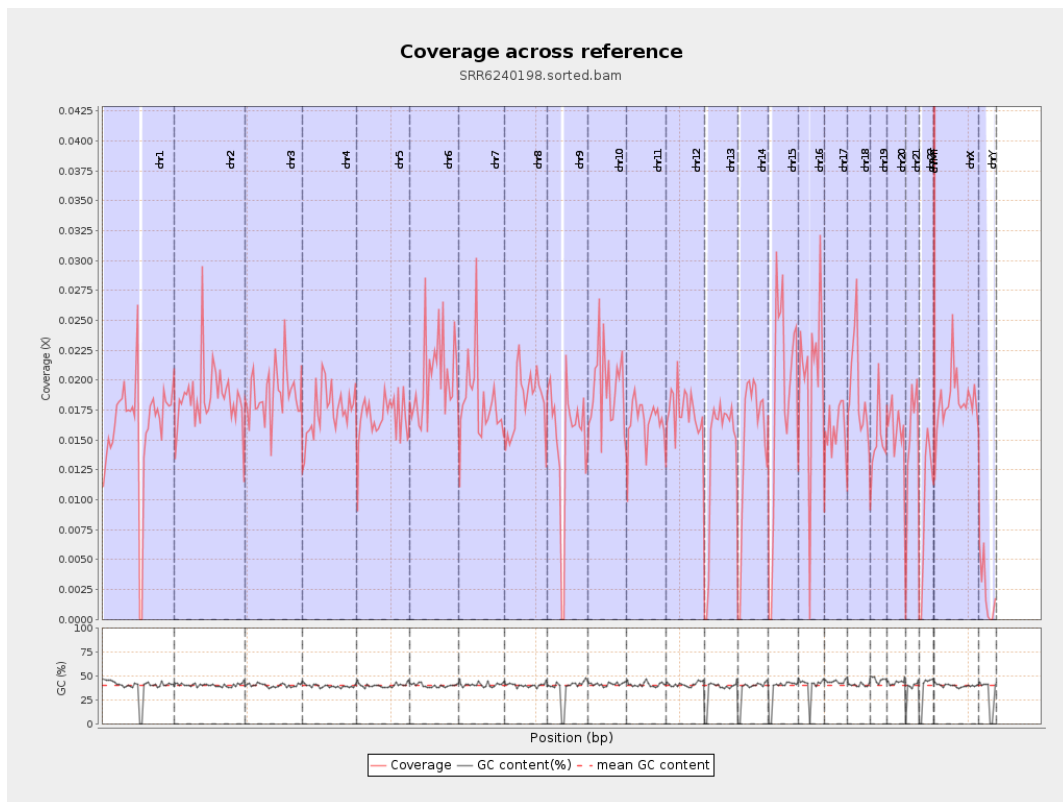
General error rate	0.87%
Mismatches	454,621
Insertions	3,849
Mapped reads with at least one insertion	0.45%
Deletions	14,500
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.9%

2.6. Chromosome stats

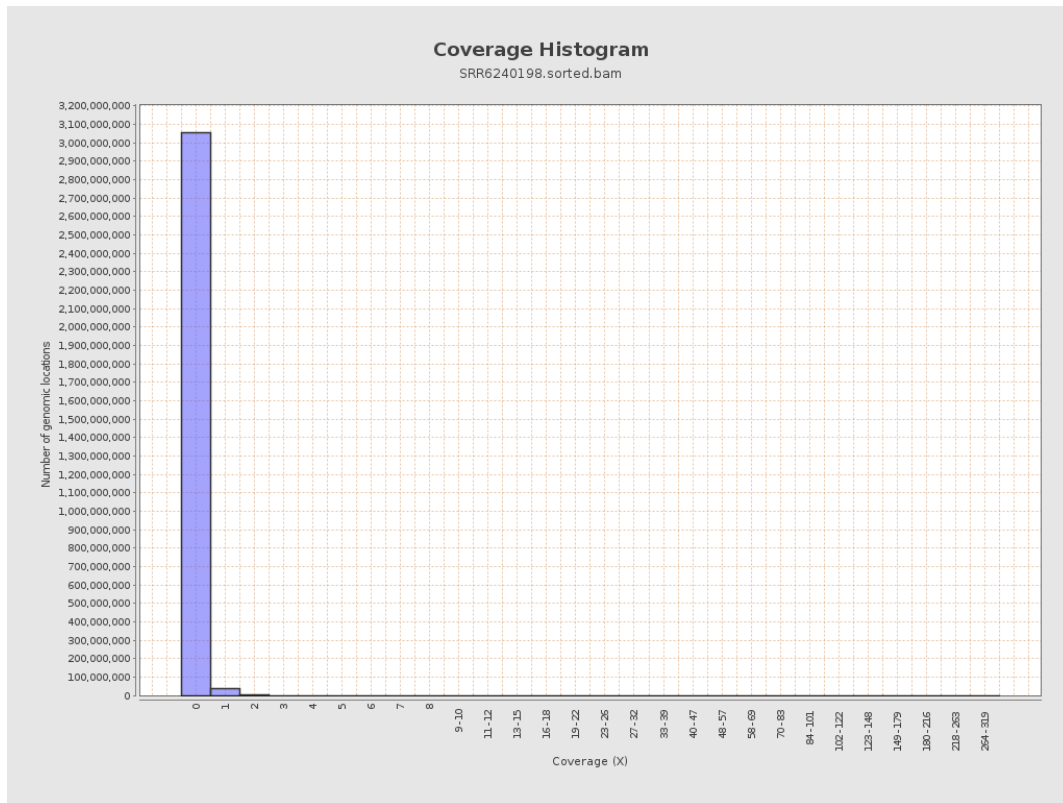
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4012726	0.0161	0.2936
chr2	243199373	4508095	0.0185	0.2181
chr3	198022430	3728565	0.0188	0.1673
chr4	191154276	3321522	0.0174	0.1854
chr5	180915260	3074619	0.017	0.1593
chr6	171115067	3463479	0.0202	0.1925
chr7	159138663	2898606	0.0182	0.2381

chr8	146364022	2666749	0.0182	0.2287
chr9	141213431	2136884	0.0151	0.1884
chr10	135534747	2609546	0.0193	0.1938
chr11	135006516	2255786	0.0167	0.1782
chr12	133851895	2329710	0.0174	0.1612
chr13	115169878	1602368	0.0139	0.1431
chr14	107349540	1609498	0.015	0.1533
chr15	102531392	1905209	0.0186	0.2487
chr16	90354753	1805811	0.02	0.1867
chr17	81195210	1288999	0.0159	0.1556
chr18	78077248	1493421	0.0191	0.2785
chr19	59128983	891928	0.0151	0.2201
chr20	63025520	997839	0.0158	0.1538
chr21	48129895	730052	0.0152	0.1535
chr22	51304566	498554	0.0097	0.1177
chrMT	16571	37987	2.2924	2.4322
chrX	155270560	2843189	0.0183	0.1689
chrY	59373566	134555	0.0023	0.0734

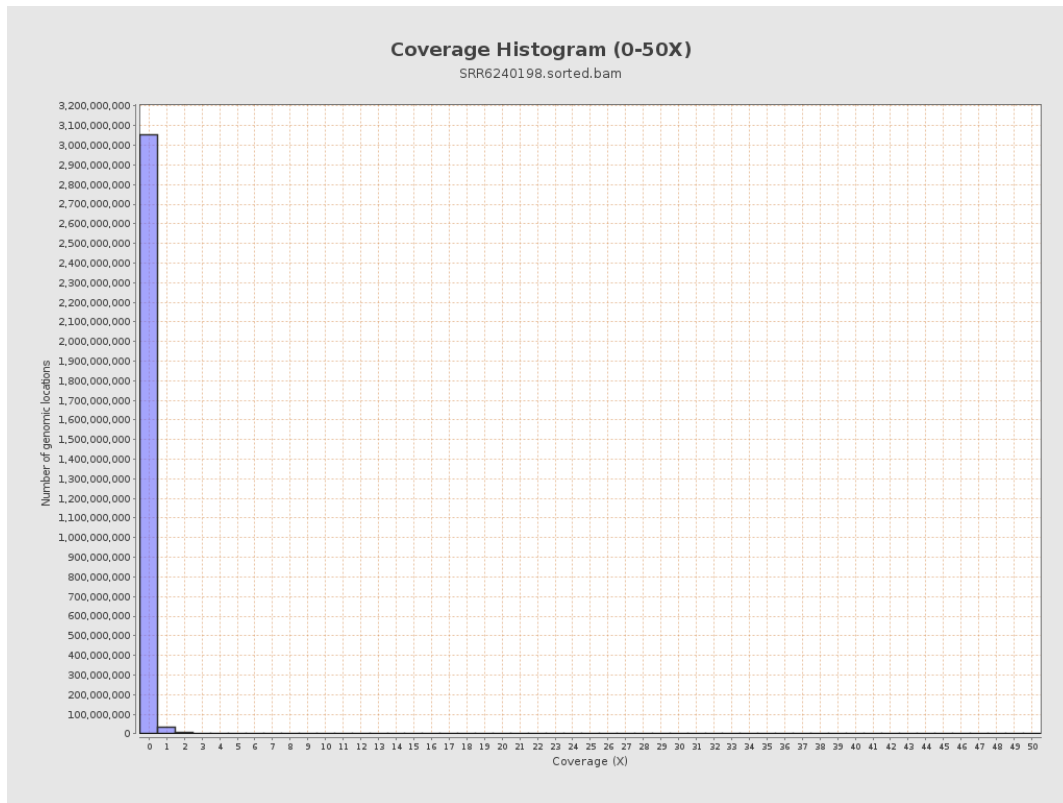
3. Results : Coverage across reference



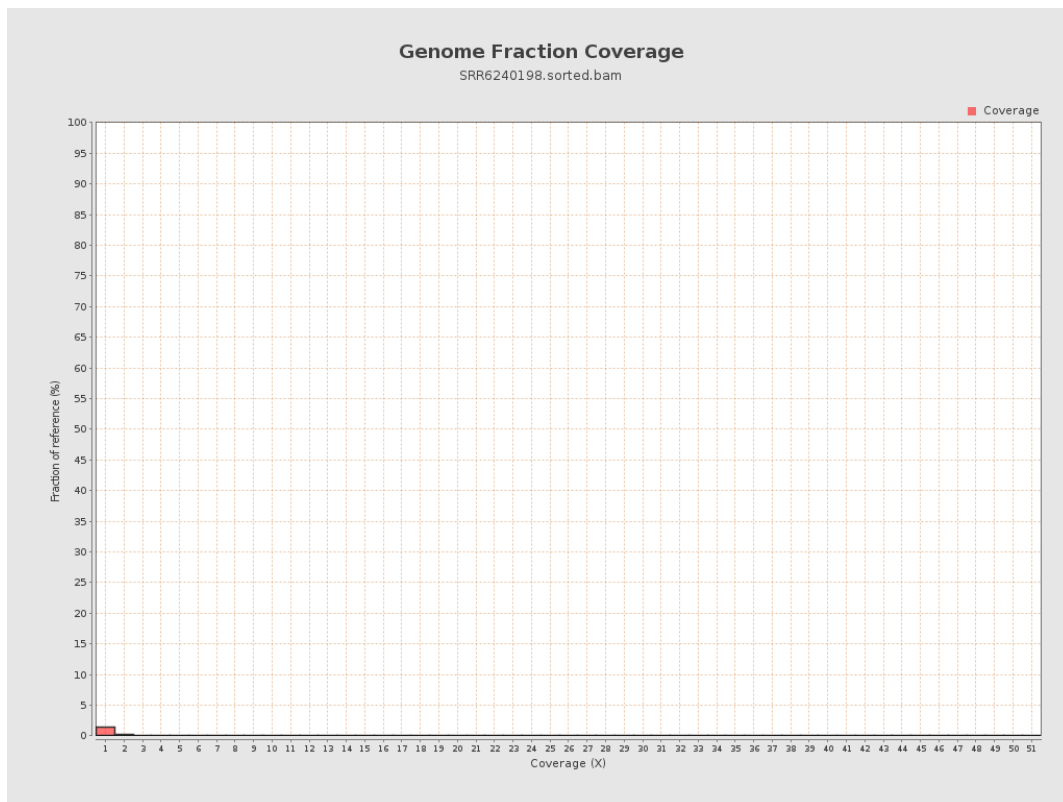
4. Results : Coverage Histogram



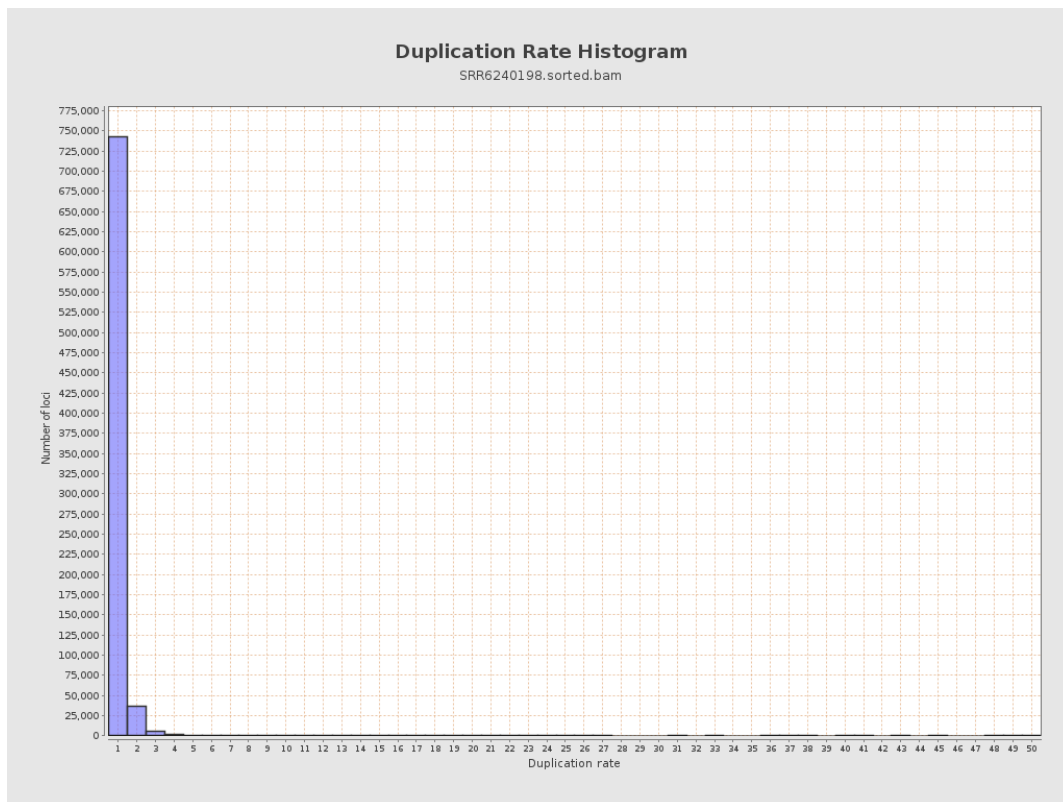
5. Results : Coverage Histogram (0-50X)



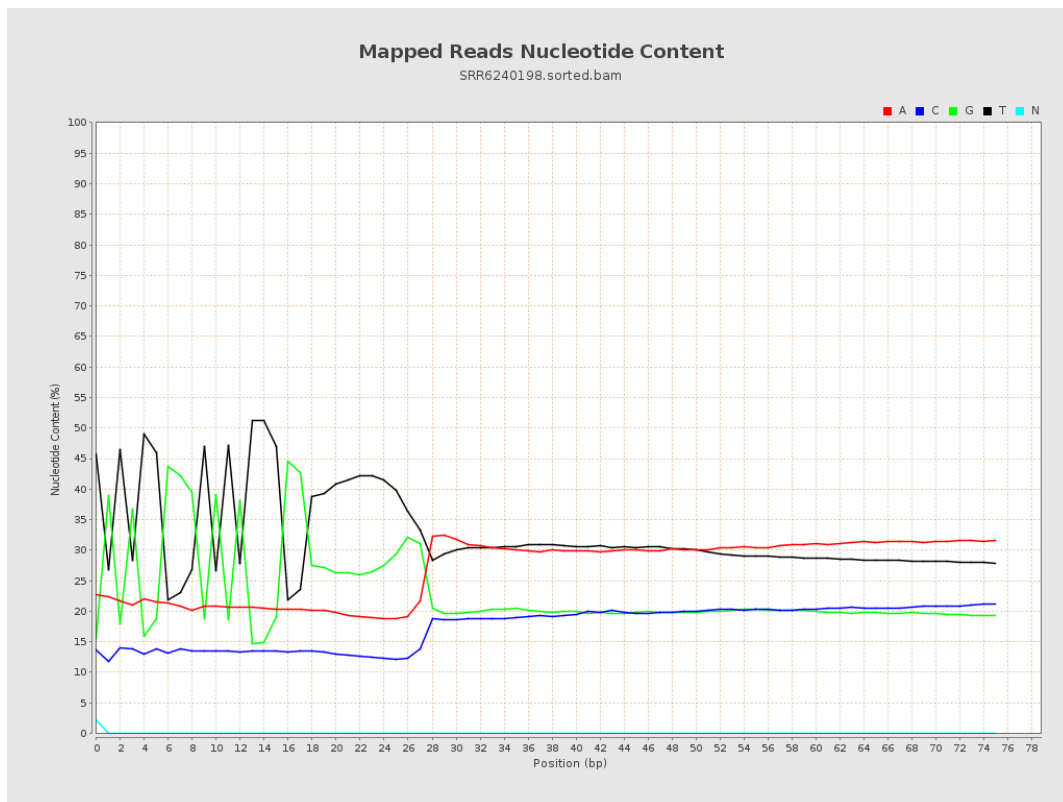
6. Results : Genome Fraction Coverage



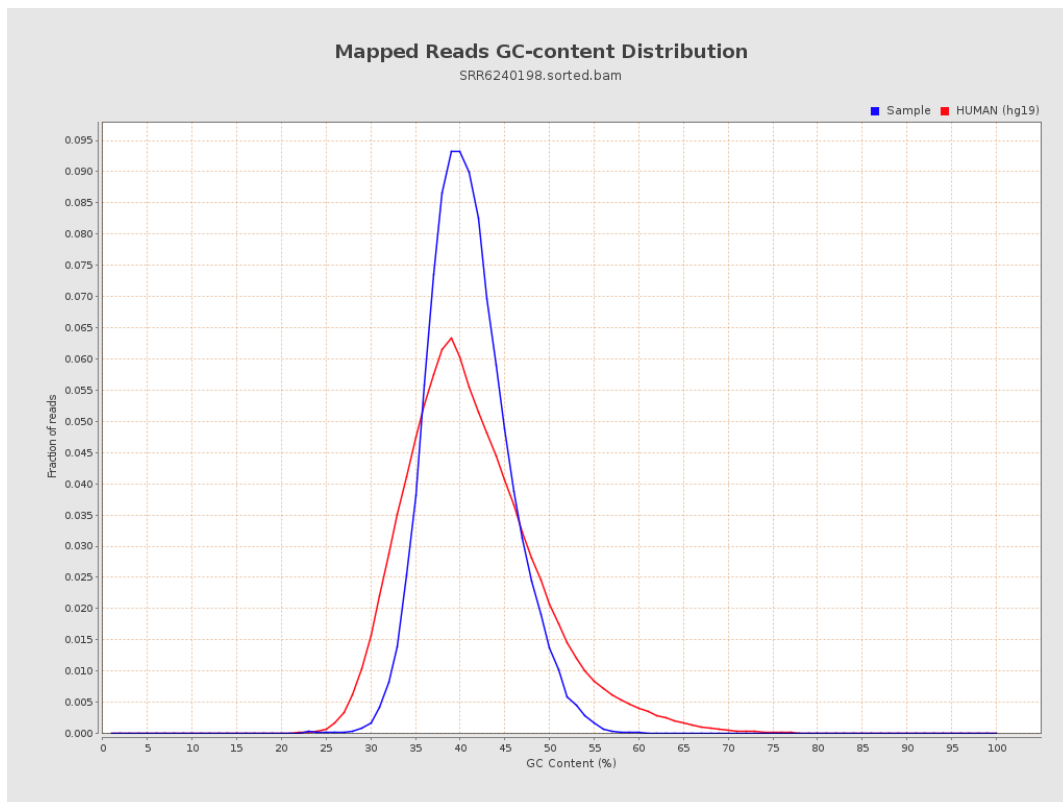
7. Results : Duplication Rate Histogram



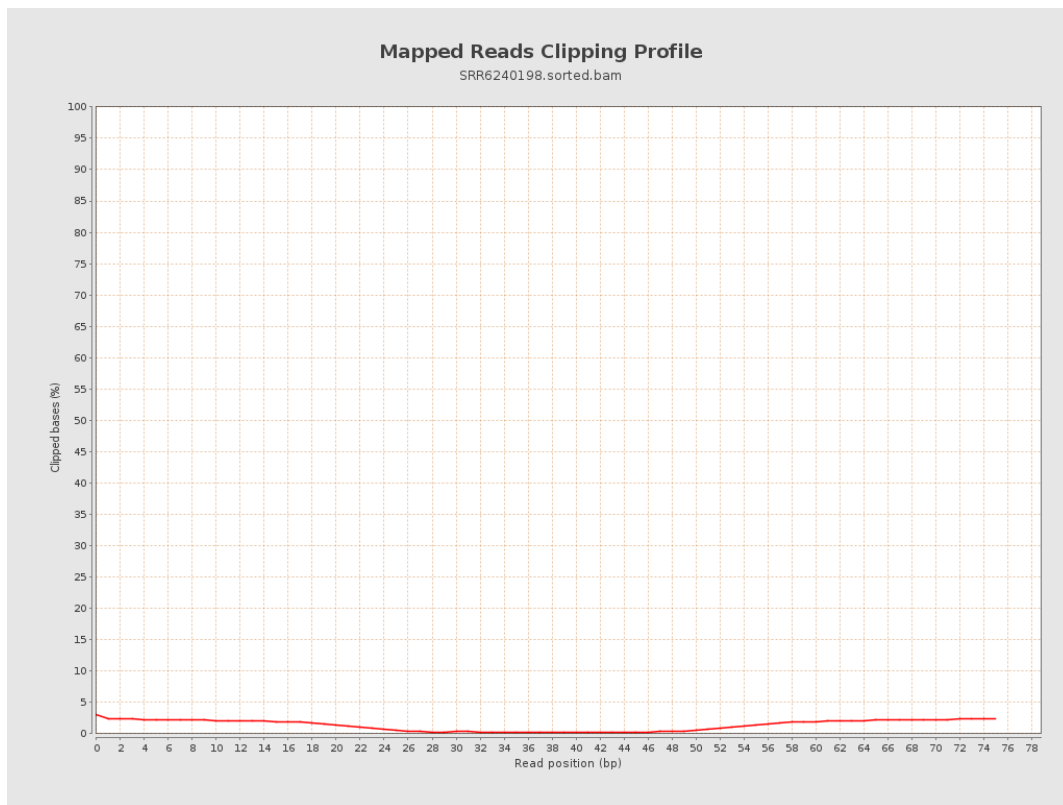
8. Results : Mapped Reads Nucleotide Content



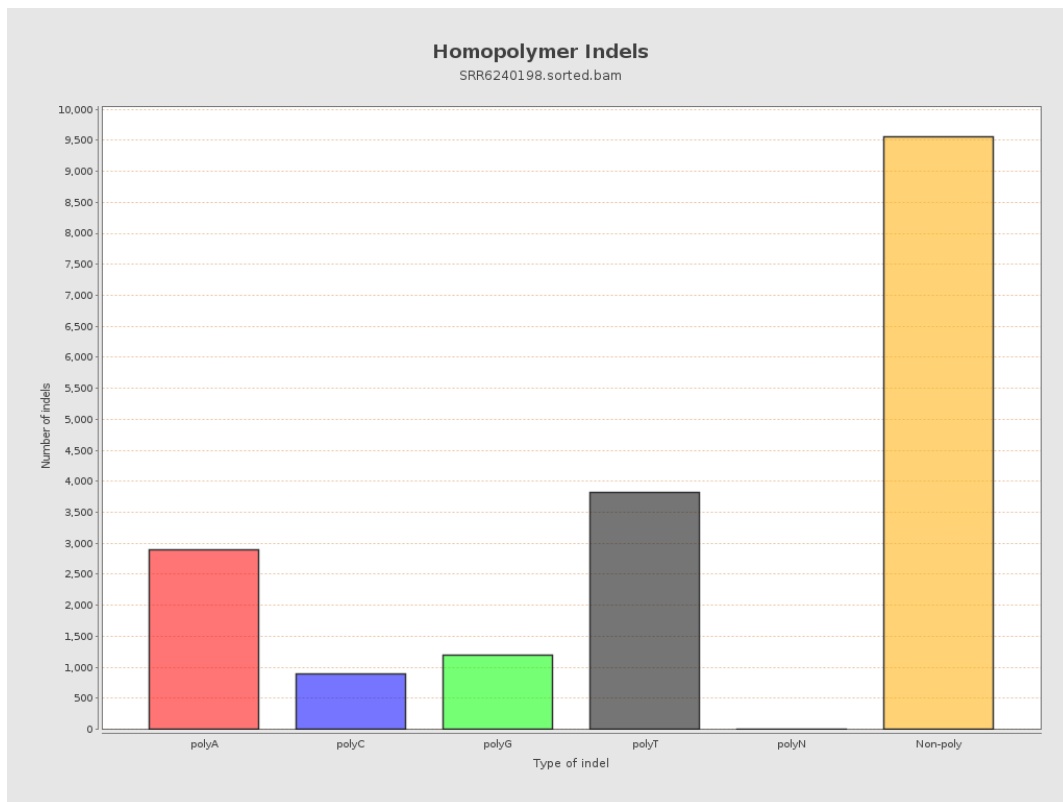
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

