Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 08:26:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR4012102.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_SRR4012102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR4012102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 08:26:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR4012102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	330,389,873
Mapped reads	245,744,614 / 74.38%
Unmapped reads	84,645,259 / 25.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,599 / 0.01%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	181,961,977 / 55.07%
Duplication rate	49.91%
Clipped reads	16,173,752 / 4.9%

2.2. ACGT Content

Number/percentage of A's	3,644,665,702 / 30.05%
Number/percentage of C's	2,432,912,591 / 20.06%
Number/percentage of T's	3,627,546,933 / 29.91%
Number/percentage of G's	2,423,125,543 / 19.98%
Number/percentage of N's	58,007 / 0%
GC Percentage	40.04%

2.3. Coverage

Mean	3.919

Standard Deviation	43.42

2.4. Mapping Quality

Mean Mapping Quality	42.99

2.5. Mismatches and indels

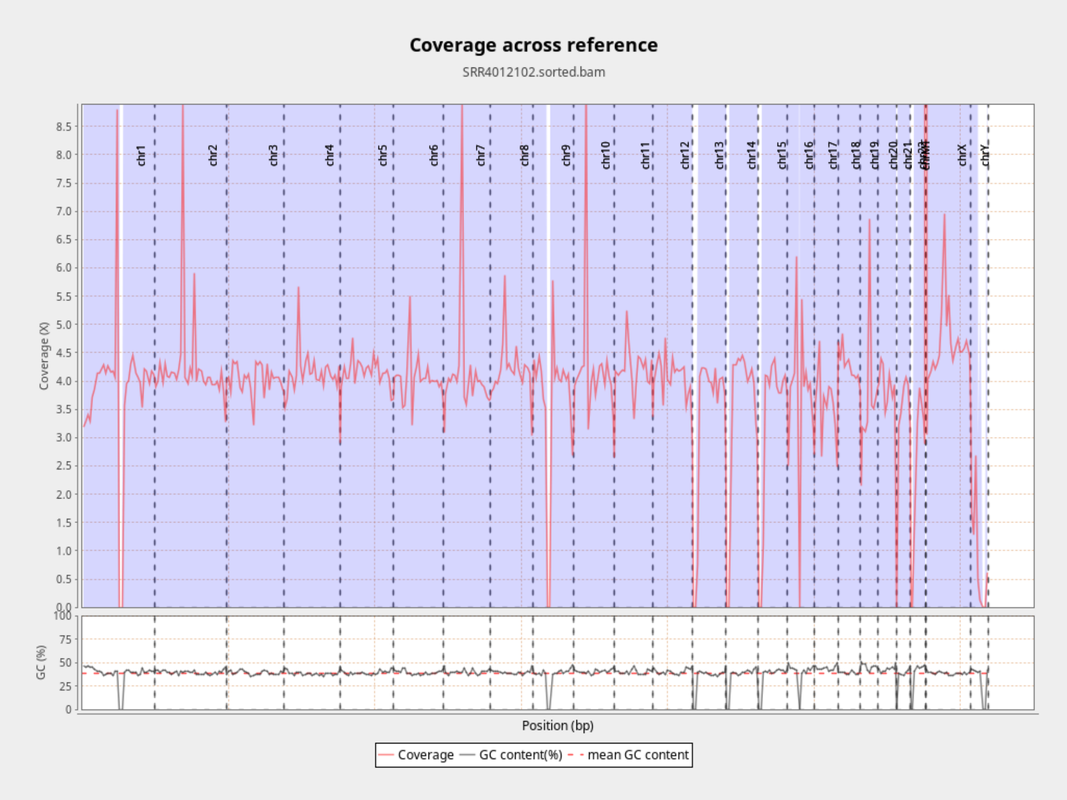
General error rate	0.57%
Mismatches	67,999,201
Insertions	782,161
Mapped reads with at least one insertion	0.32%
Deletions	2,548,015
Mapped reads with at least one deletion	1.03%
Homopolymer indels	47.24%

2.6. Chromosome stats

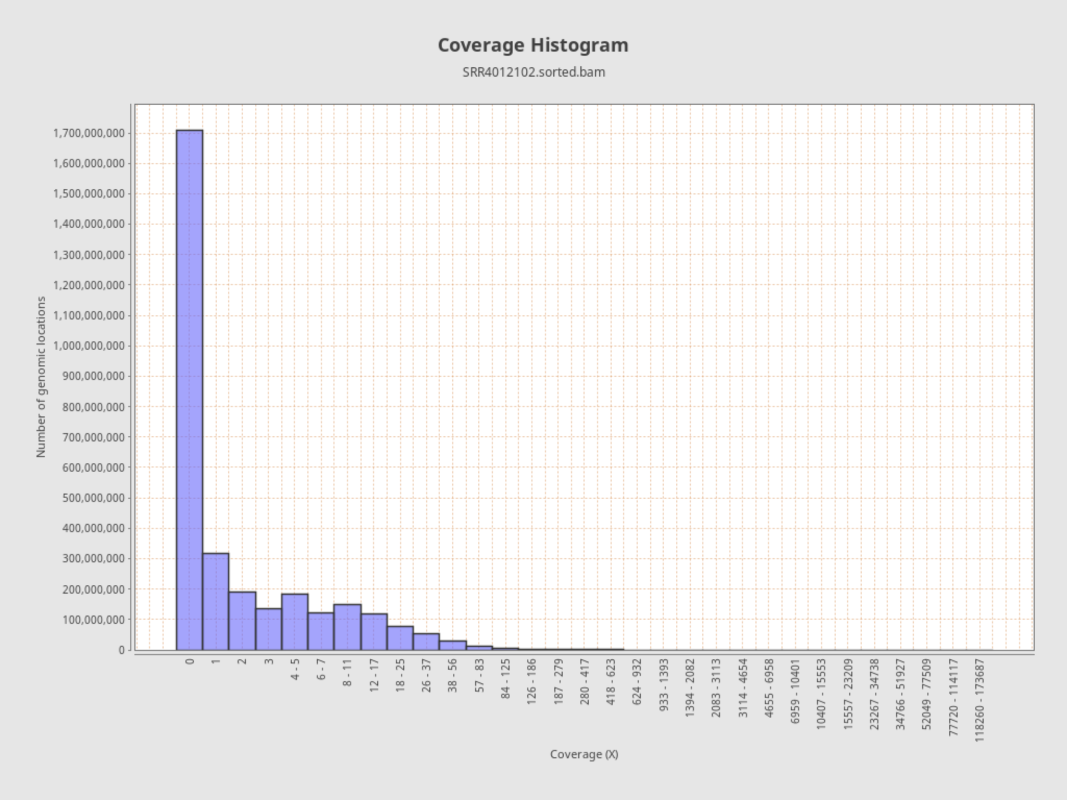
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	964845927	3.871	103.1816
chr2	243199373	1039076143	4.2725	43.9304
chr3	198022430	801169595	4.0459	10.9688
chr4	191154276	795454208	4.1613	16.5173
chr5	180915260	755166652	4.1741	18.5765
chr6	171115067	692996973	4.0499	20.8843
chr7	159138663	662520435	4.1632	65.8071

chr8	146364022	616028716	4.2089	27.7058
chr9	141213431	508438387	3.6005	31.1906
chr10	135534747	585370484	4.319	45.6726
chr11	135006516	565571249	4.1892	34.0182
chr12	133851895	547505400	4.0904	15.237
chr13	115169878	384739598	3.3406	8.957
chr14	107349540	373516602	3.4794	19.5236
chr15	102531392	331779434	3.2359	9.857
chr16	90354753	343702419	3.8039	32.1844
chr17	81195210	294780380	3.6305	19.5365
chr18	78077248	333428174	4.2705	53.0302
chr19	59128983	224964057	3.8046	89.9117
chr20	63025520	243050927	3.8564	14.3814
chr21	48129895	159608421	3.3162	16.9052
chr22	51304566	125718655	2.4504	9.8139
chrMT	16571	15855479	956.8209	666.2898
chrX	155270560	717775666	4.6227	24.5132
chrY	59373566	48872621	0.8231	31.9498

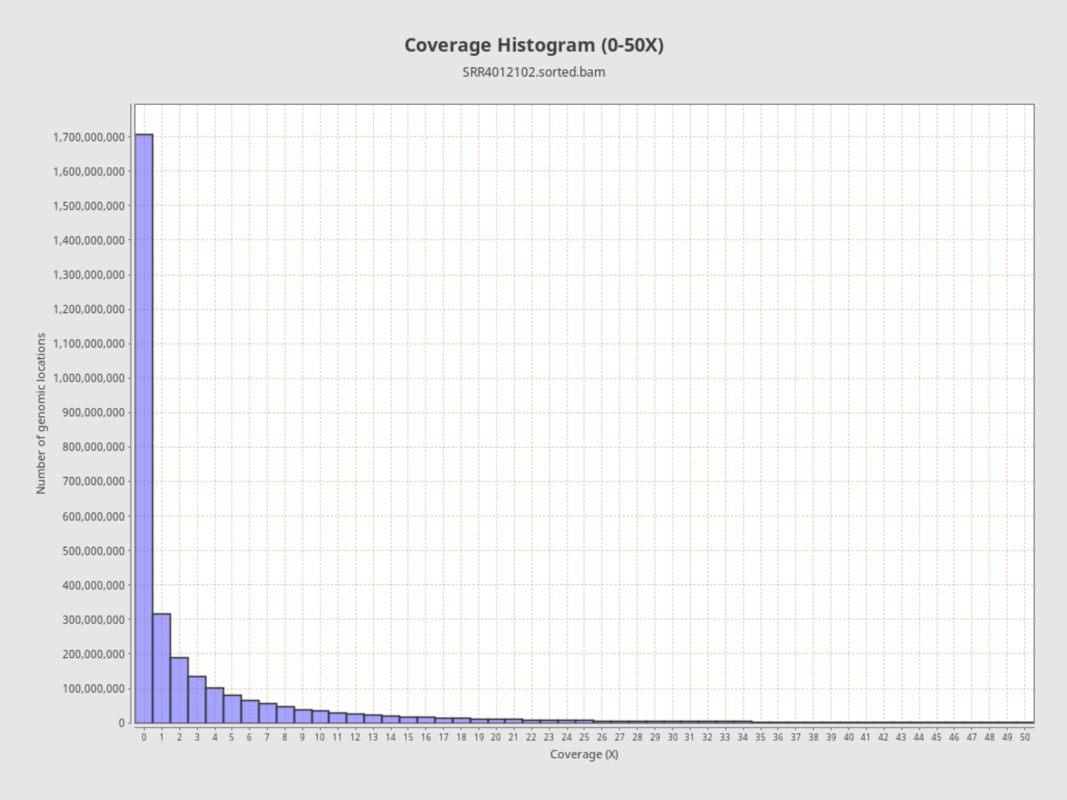
3. Results : Coverage across reference



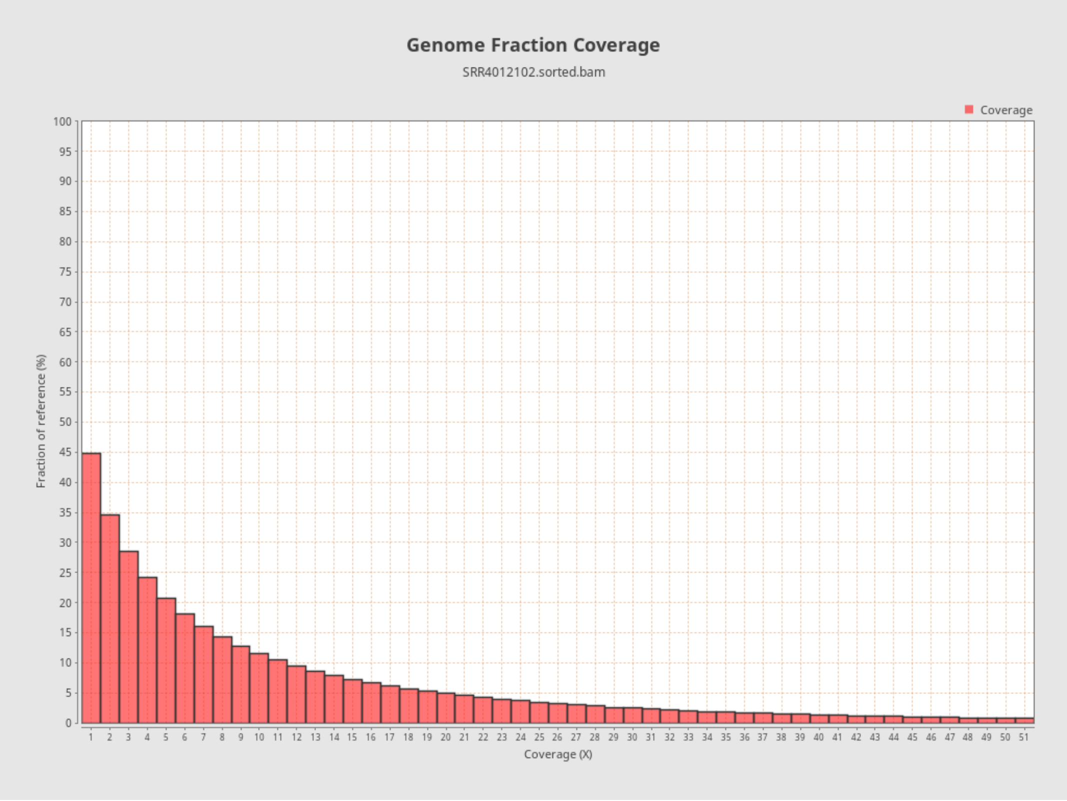
4. Results : Coverage Histogram



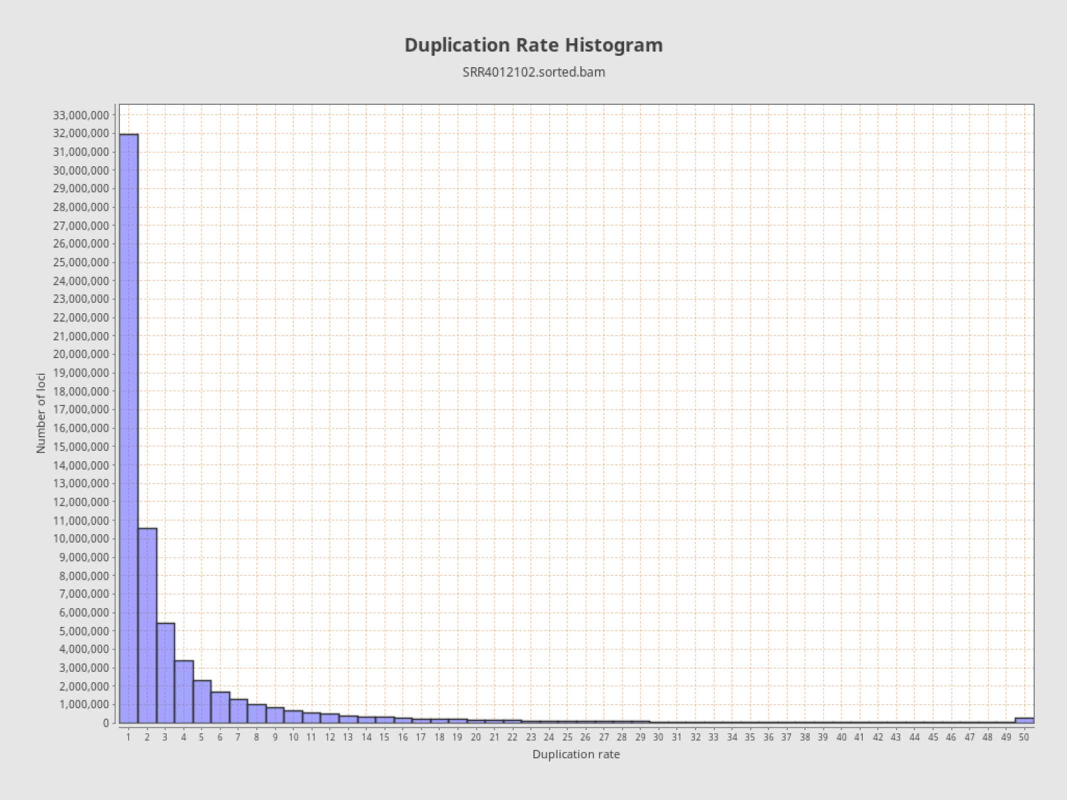
5. Results : Coverage Histogram (0-50X)



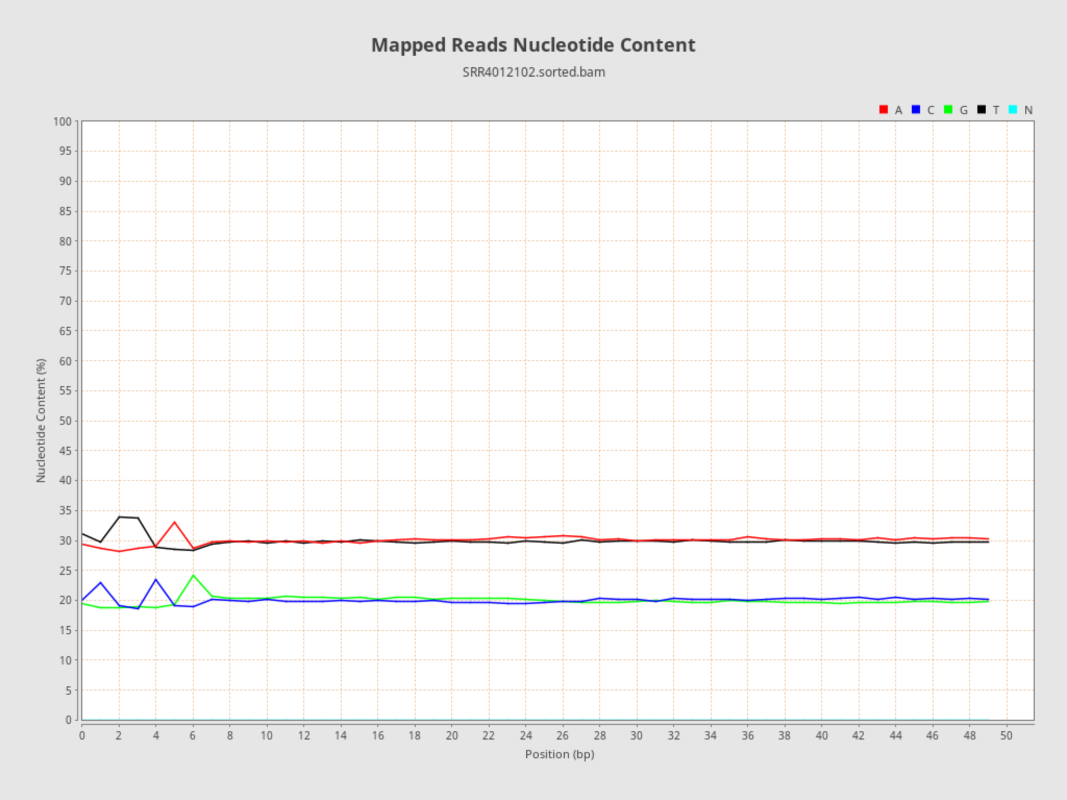
6. Results : Genome Fraction Coverage



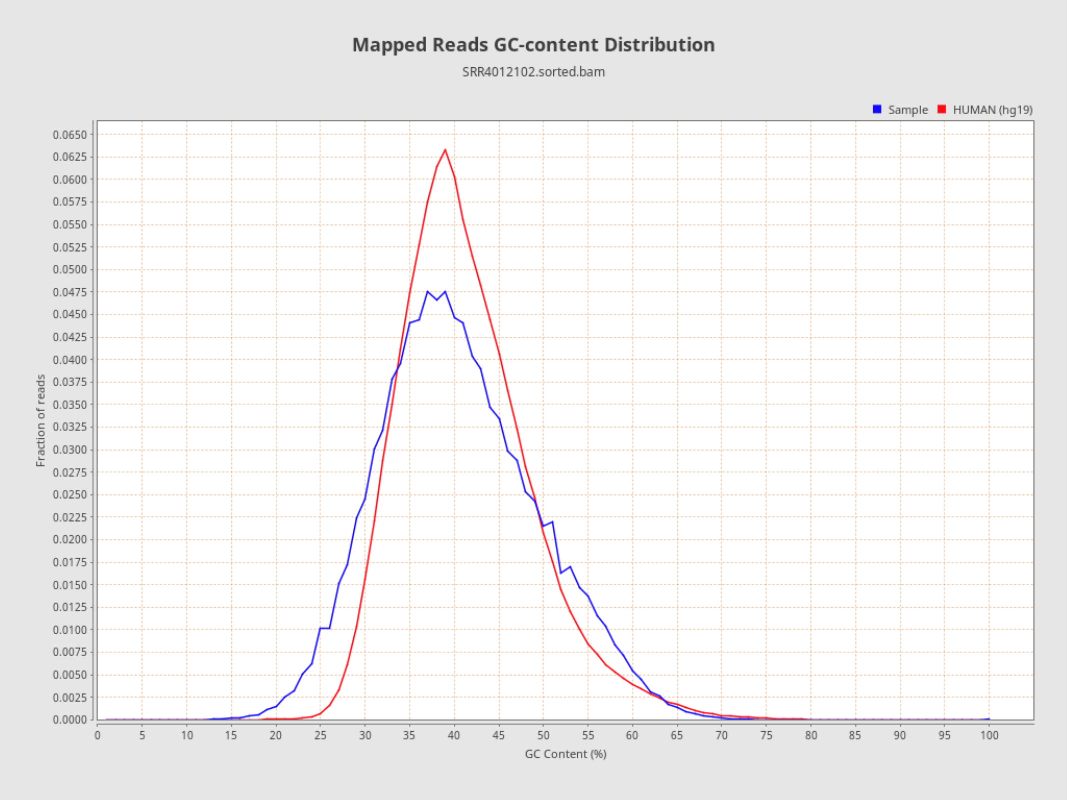
7. Results : Duplication Rate Histogram



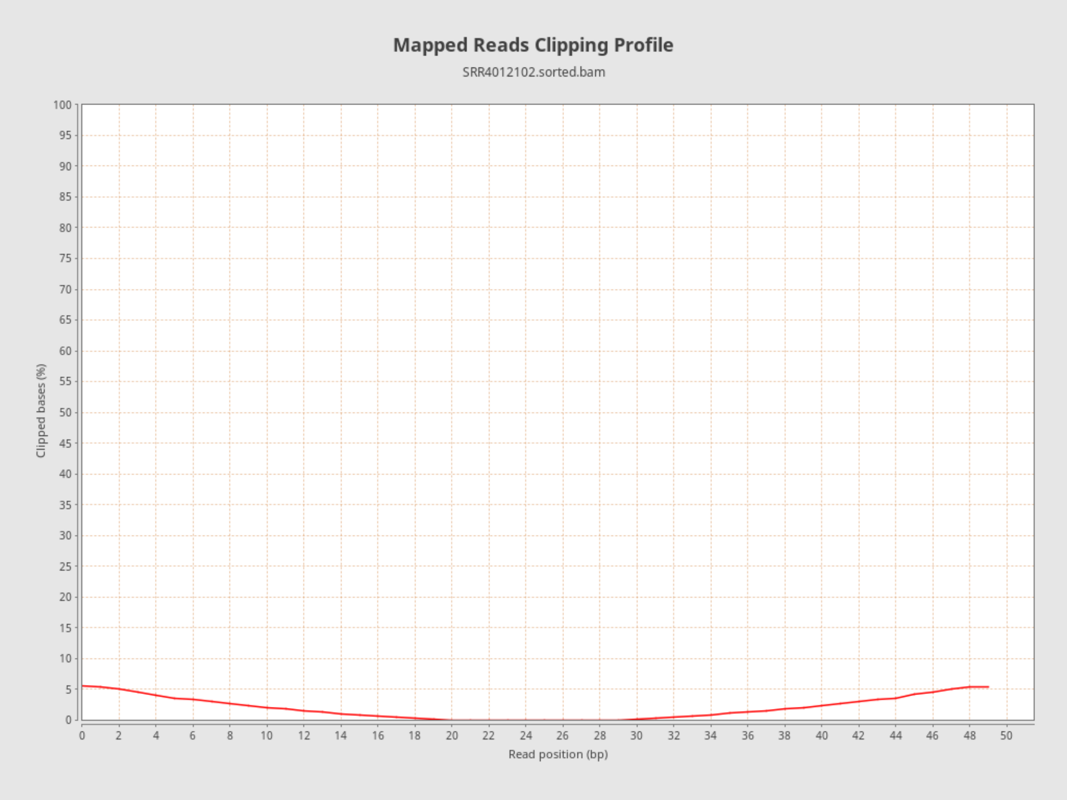
8. Results : Mapped Reads Nucleotide Content



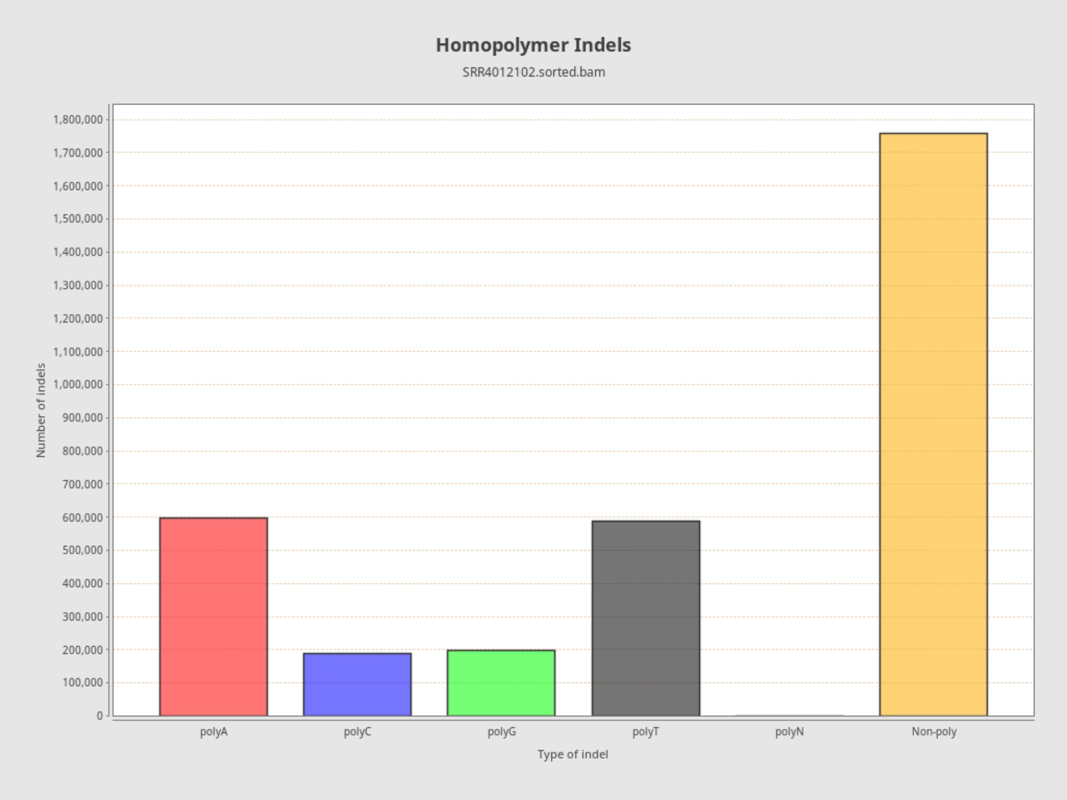
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram