Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 01:18:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975256.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_SRR975256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975256_1.fastq.gz SRR975256_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 01:18:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,552,378
Mapped reads	162,034,198 / 99.68%
Unmapped reads	518,180 / 0.32%
Mapped paired reads	162,034,198 / 99.68%
Mapped reads, first in pair	81,011,320 / 49.84%
Mapped reads, second in pair	81,022,878 / 49.84%
Mapped reads, both in pair	161,816,332 / 99.55%
Mapped reads, singletons	217,866 / 0.13%
Secondary alignments	0
Supplementary alignments	307,428 / 0.19%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	110,682,230 / 68.09%
Duplication rate	47.89%
Clipped reads	102,382,338 / 62.98%

2.2. ACGT Content

Number/percentage of A's	3,839,844,475 / 25.87%
Number/percentage of C's	3,317,819,076 / 22.36%
Number/percentage of T's	4,042,467,814 / 27.24%
Number/percentage of G's	3,639,814,993 / 24.53%
Number/percentage of N's	412,642 / 0%

GC Percentage	46.88%

2.3. Coverage

Mean	4.7954
Standard Deviation	61.7645

2.4. Mapping Quality

Mean Mapping Quality	55.85

2.5. Insert size

Mean	74,356.5
Standard Deviation	2,697,009.47
P25/Median/P75	145 / 182 / 231

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	95,586,438
Insertions	1,294,016
Mapped reads with at least one insertion	0.79%
Deletions	3,359,866
Mapped reads with at least one deletion	2.05%
Homopolymer indels	48.23%

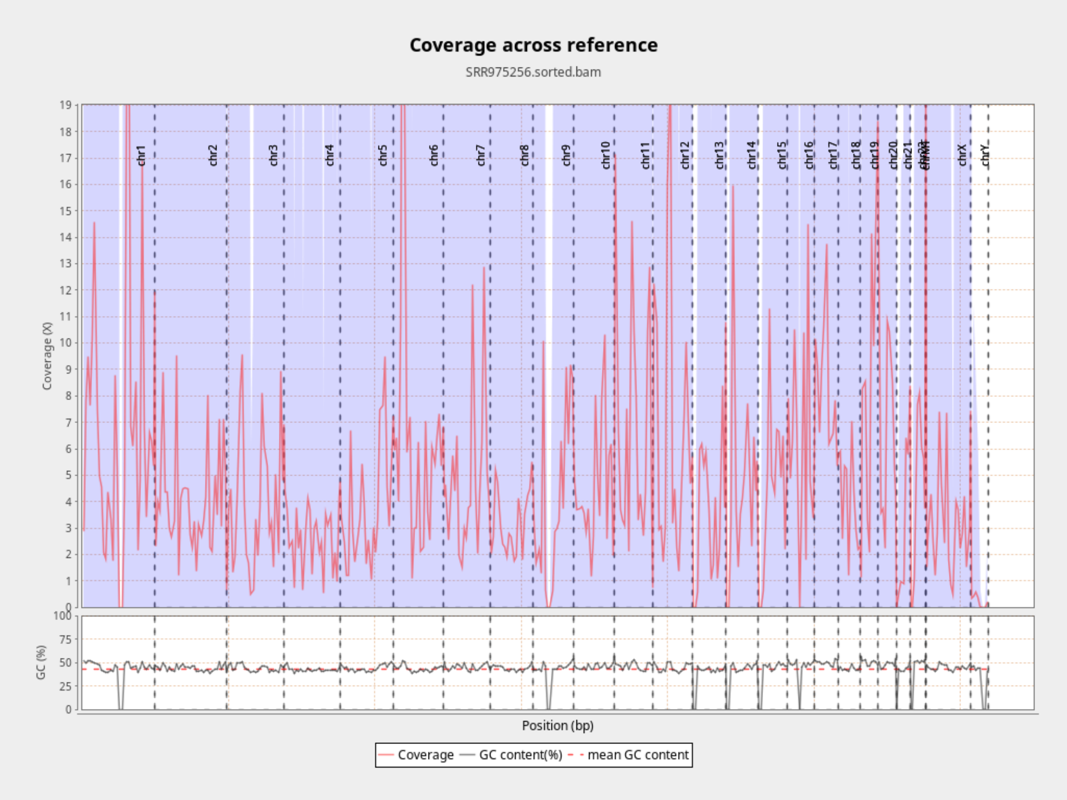
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

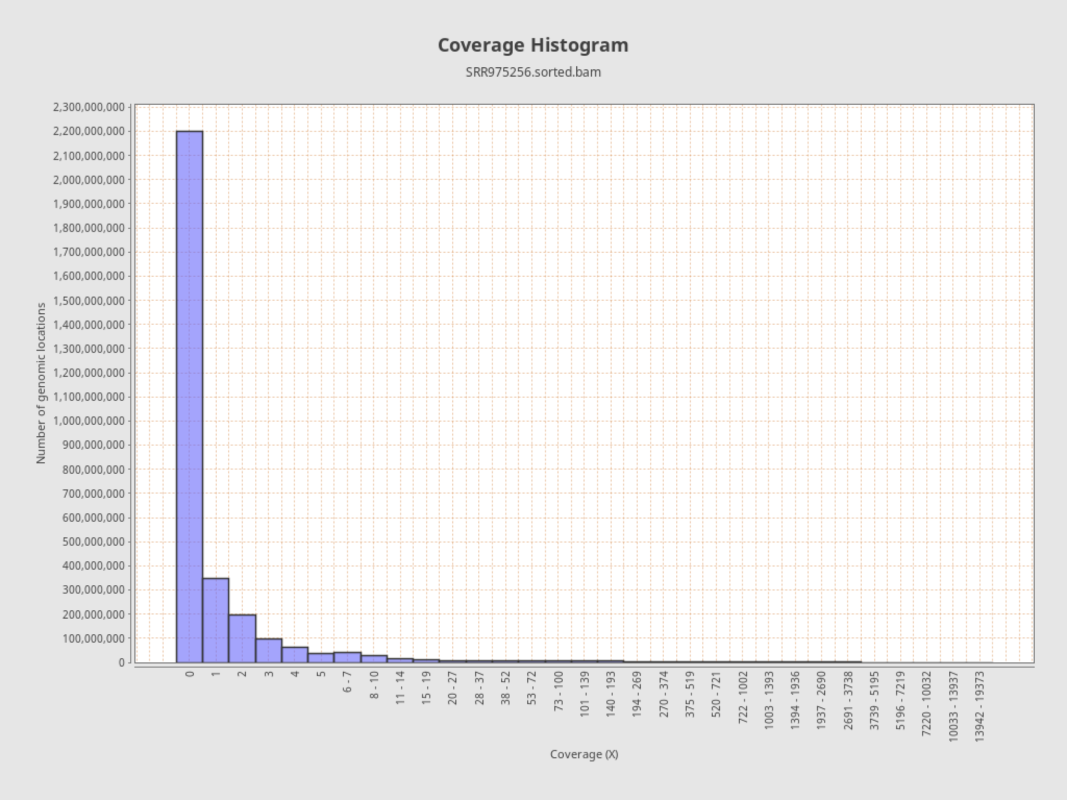
		bases	**coverage**	**deviation**
chr1	249250621	1724494626	6.9187	81.0478
chr2	243199373	996255311	4.0965	51.1826
chr3	198022430	779515472	3.9365	49.6838
chr4	191154276	494335201	2.5861	38.8465
chr5	180915260	685273866	3.7878	49.8601
chr6	171115067	1184849469	6.9243	87.4687
chr7	159138663	761244273	4.7835	64.534
chr8	146364022	463805107	3.1688	40.8283
chr9	141213431	567126088	4.0161	50.5047
chr10	135534747	618914497	4.5665	58.8684
chr11	135006516	922891303	6.8359	76.7263
chr12	133851895	893576951	6.6759	77.8542
chr13	115169878	408181307	3.5442	52.4044
chr14	107349540	494214147	4.6038	61.1307
chr15	102531392	449846690	4.3874	53.3297
chr16	90354753	569352804	6.3013	71.8919
chr17	81195210	685490735	8.4425	84.5067
chr18	78077248	315991950	4.0472	55.8169
chr19	59128983	510819675	8.6391	80.5648
chr20	63025520	430682234	6.8335	78.6723
chr21	48129895	153749499	3.1945	49.5339
chr22	51304566	228770961	4.4591	54.8206
chrMT	16571	329617	19.8912	19.8033
chrX	155270560	490986761	3.1621	43.9619

chrY	59373566	14446517	0.2433	5.4083

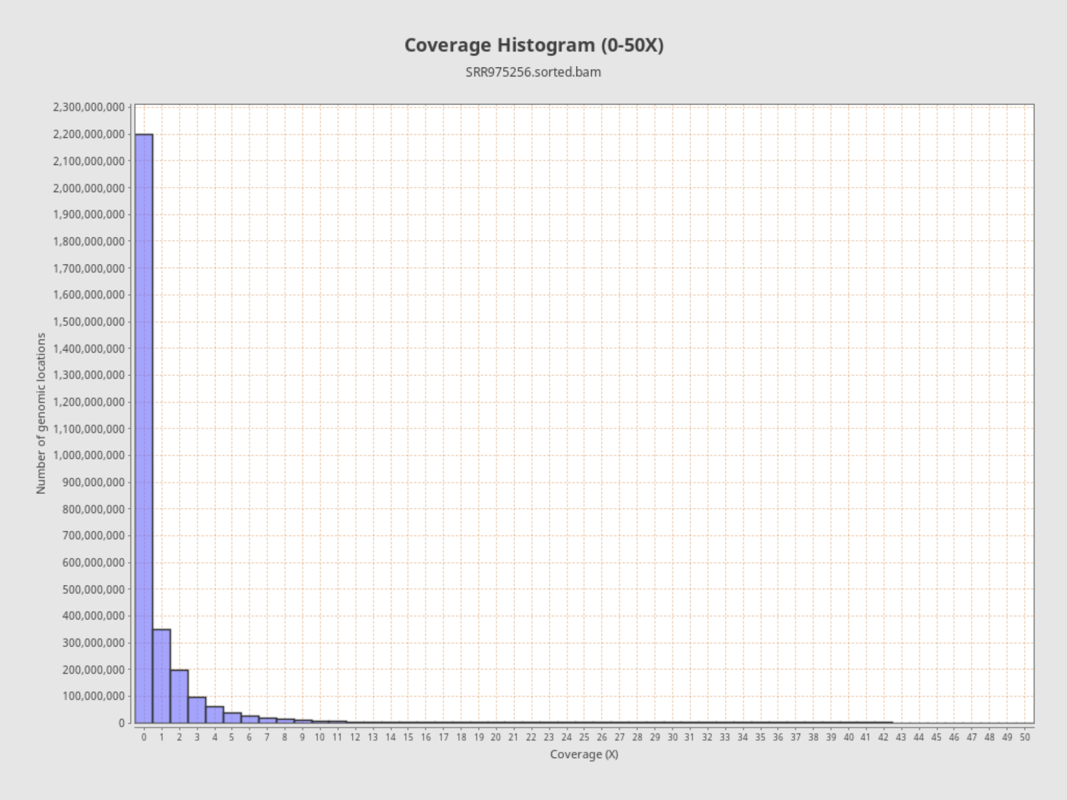
3. Results : Coverage across reference



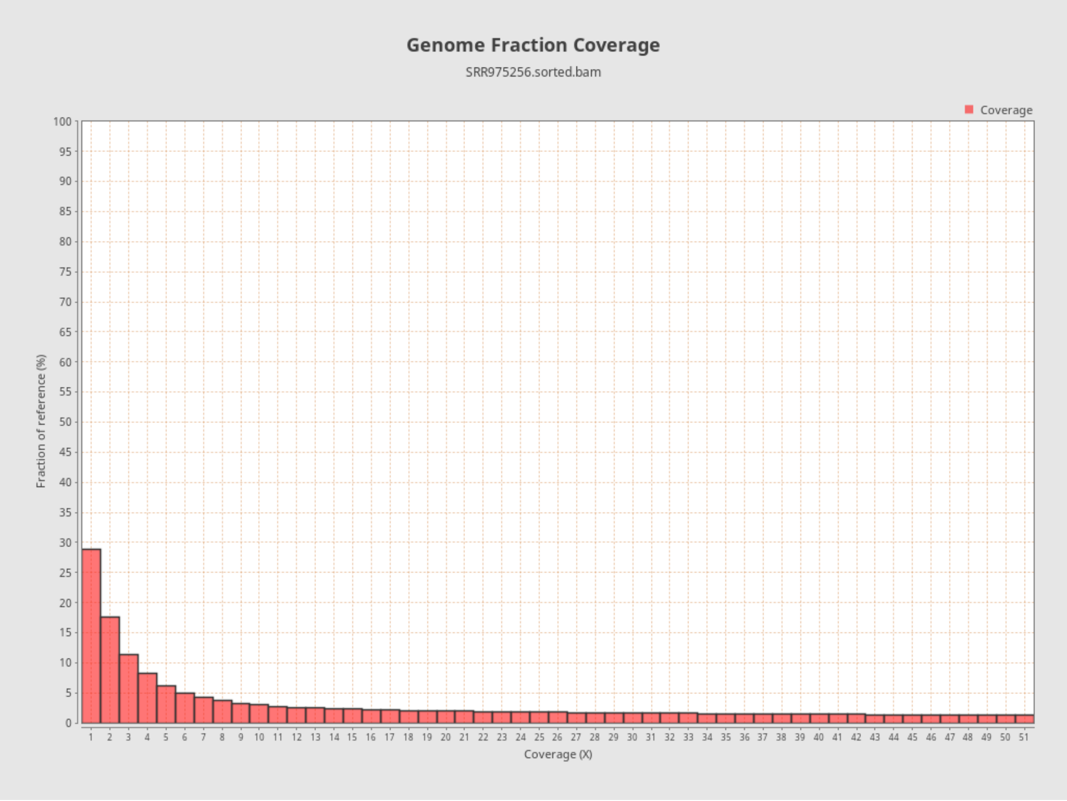
4. Results : Coverage Histogram



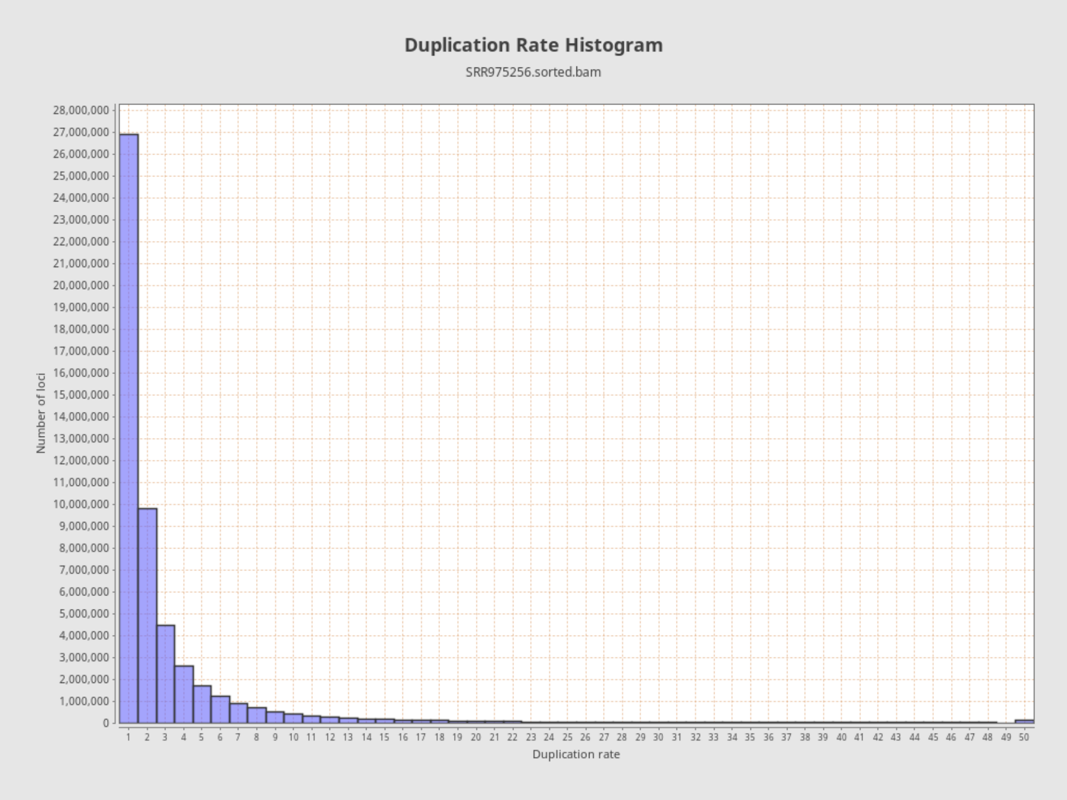
5. Results : Coverage Histogram (0-50X)



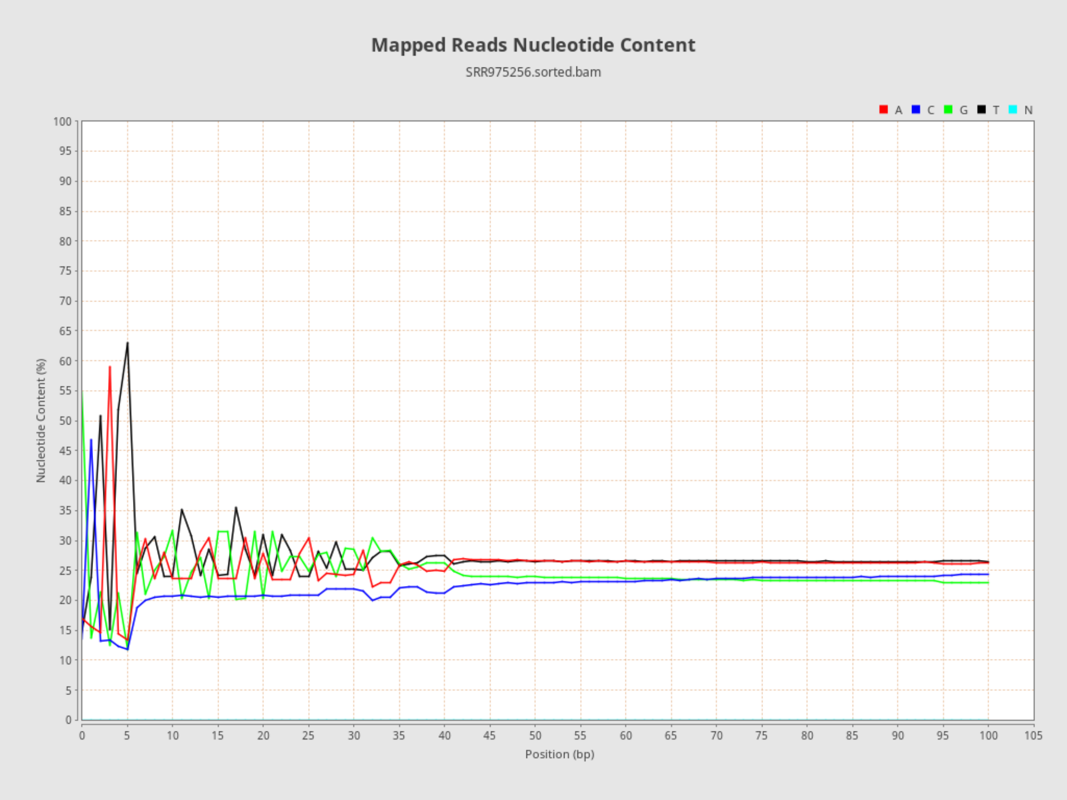
6. Results : Genome Fraction Coverage



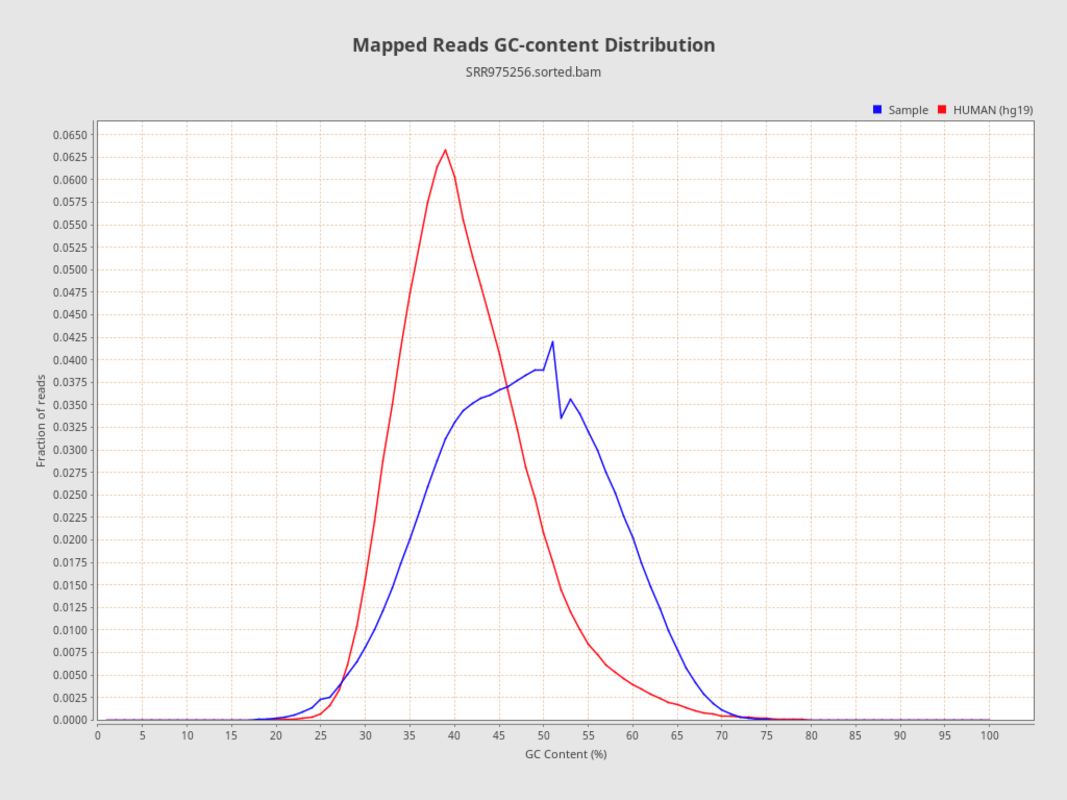
7. Results : Duplication Rate Histogram



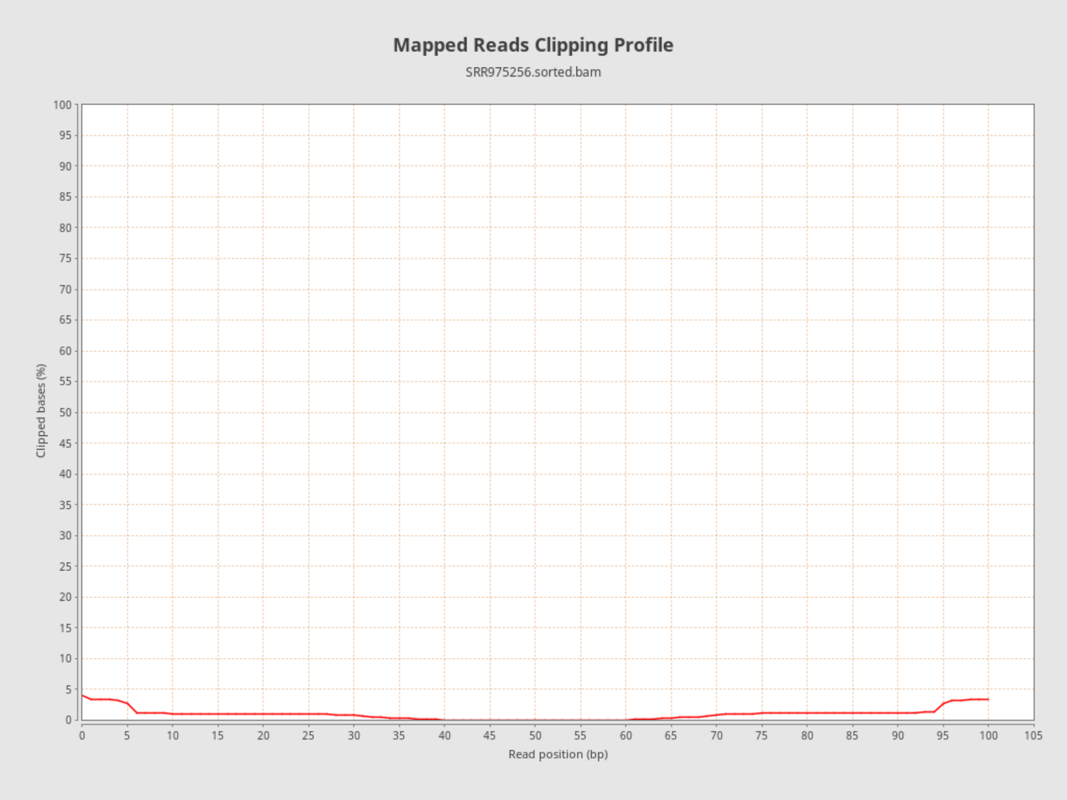
8. Results : Mapped Reads Nucleotide Content



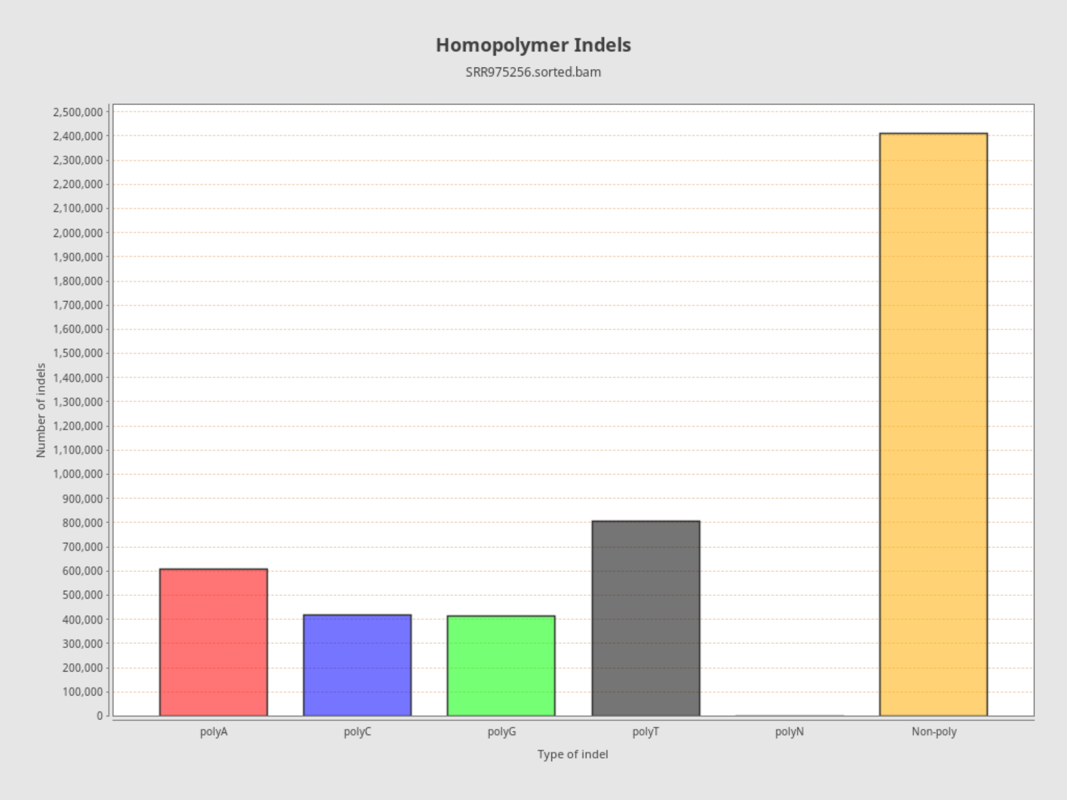
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

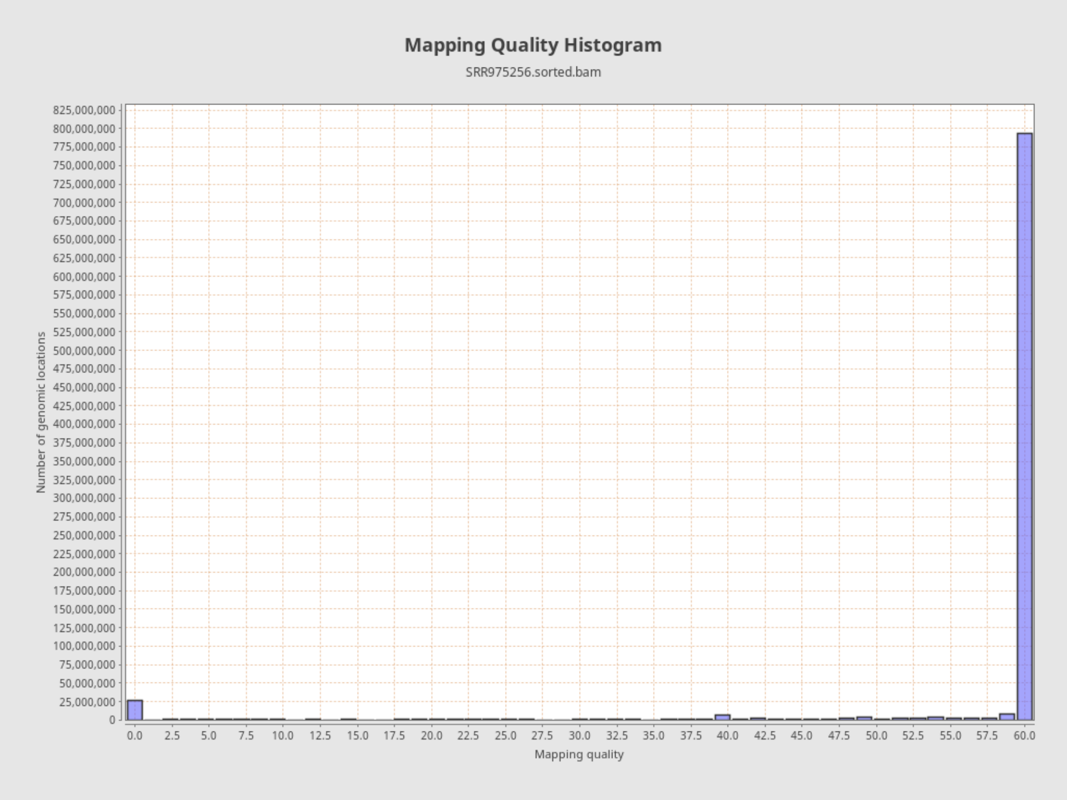


11. Results : Homopolymer Indels

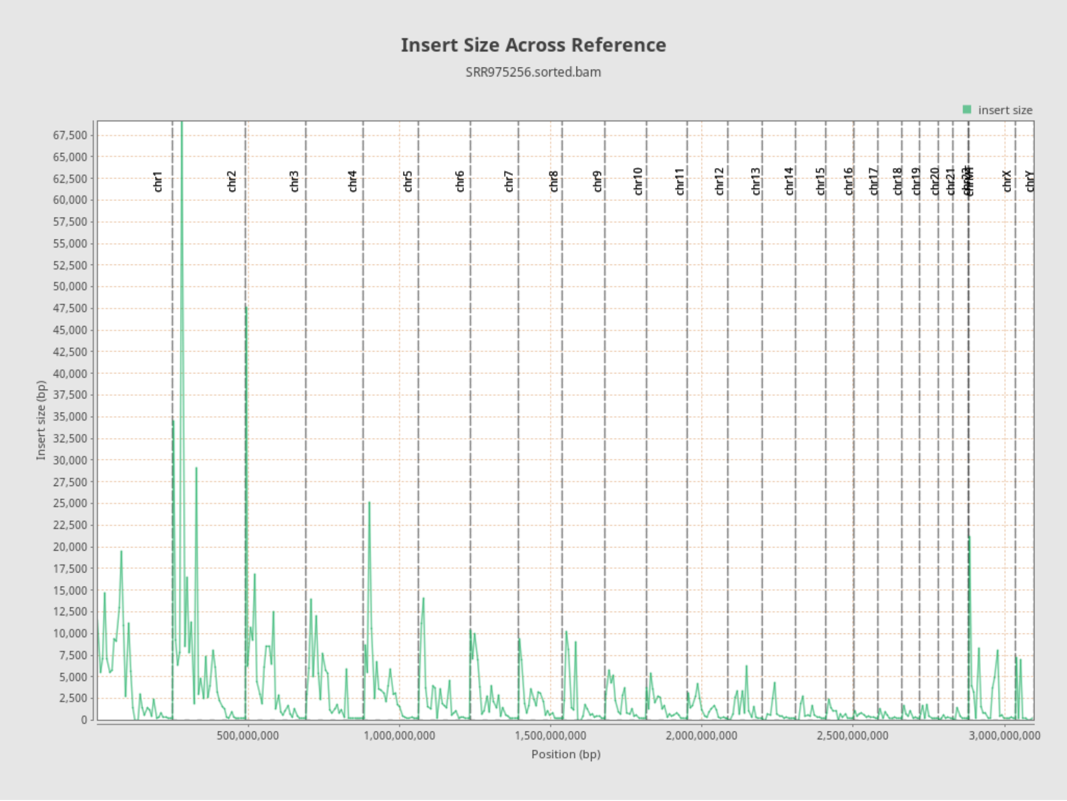


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram