Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 17:34:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975266.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_SRR975266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975266_1.fastq.gz SRR975266_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 17:34:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,471,474
Mapped reads	5,342,573 / 97.64%
Unmapped reads	128,901 / 2.36%
Mapped paired reads	5,342,573 / 97.64%
Mapped reads, first in pair	2,687,228 / 49.11%
Mapped reads, second in pair	2,655,345 / 48.53%
Mapped reads, both in pair	5,295,368 / 96.78%
Mapped reads, singletons	47,205 / 0.86%
Secondary alignments	0
Supplementary alignments	63,345 / 1.16%
Read min/max/mean length	30 / 151 / 151.58
Duplicated reads (estimated)	670,913 / 12.26%
Duplication rate	9.68%
Clipped reads	2,357,203 / 43.08%

2.2. ACGT Content

Number/percentage of A's	214,477,625 / 29.11%
Number/percentage of C's	147,538,312 / 20.03%
Number/percentage of T's	216,323,055 / 29.36%
Number/percentage of G's	158,353,275 / 21.49%
Number/percentage of N's	62,260 / 0.01%

GC Percentage	41.52%

2.3. Coverage

Mean	0.2382
Standard Deviation	3.0841

2.4. Mapping Quality

Mean Mapping Quality	53.54

2.5. Insert size

Mean	44,827.9
Standard Deviation	1,990,611.32
P25/Median/P75	155 / 200 / 265

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	8,533,689
Insertions	124,354
Mapped reads with at least one insertion	2.2%
Deletions	266,459
Mapped reads with at least one deletion	4.8%
Homopolymer indels	47.66%

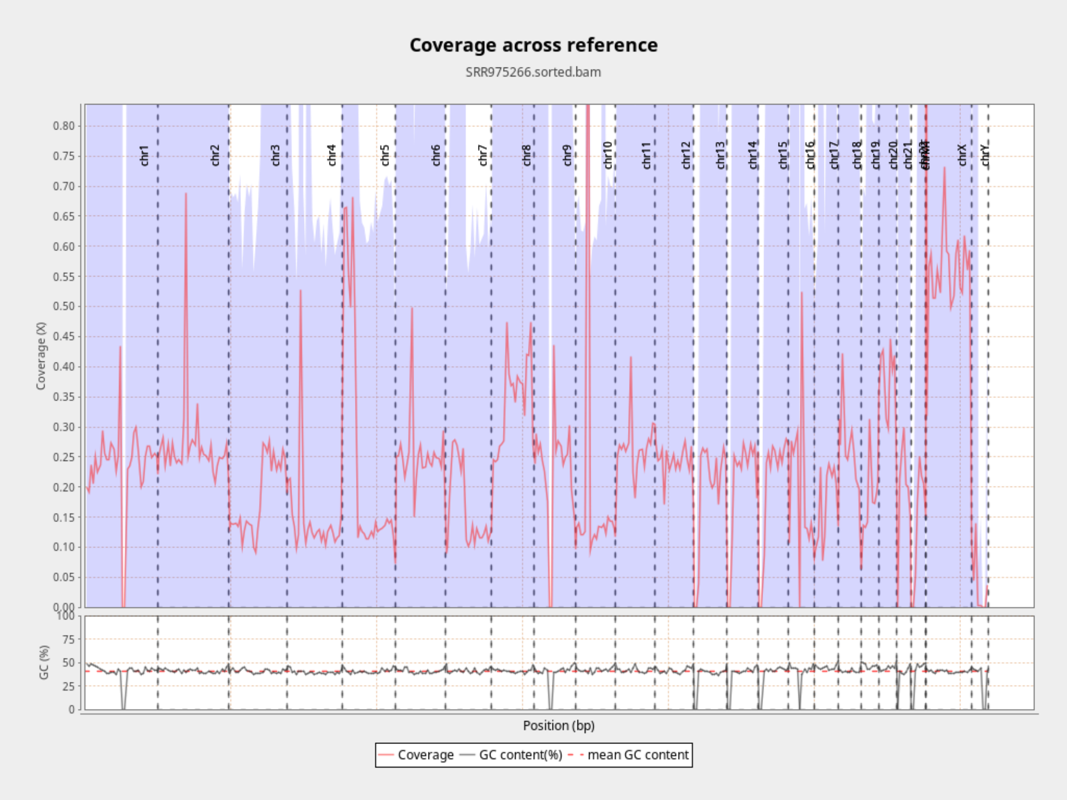
2.7. Chromosome stats

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

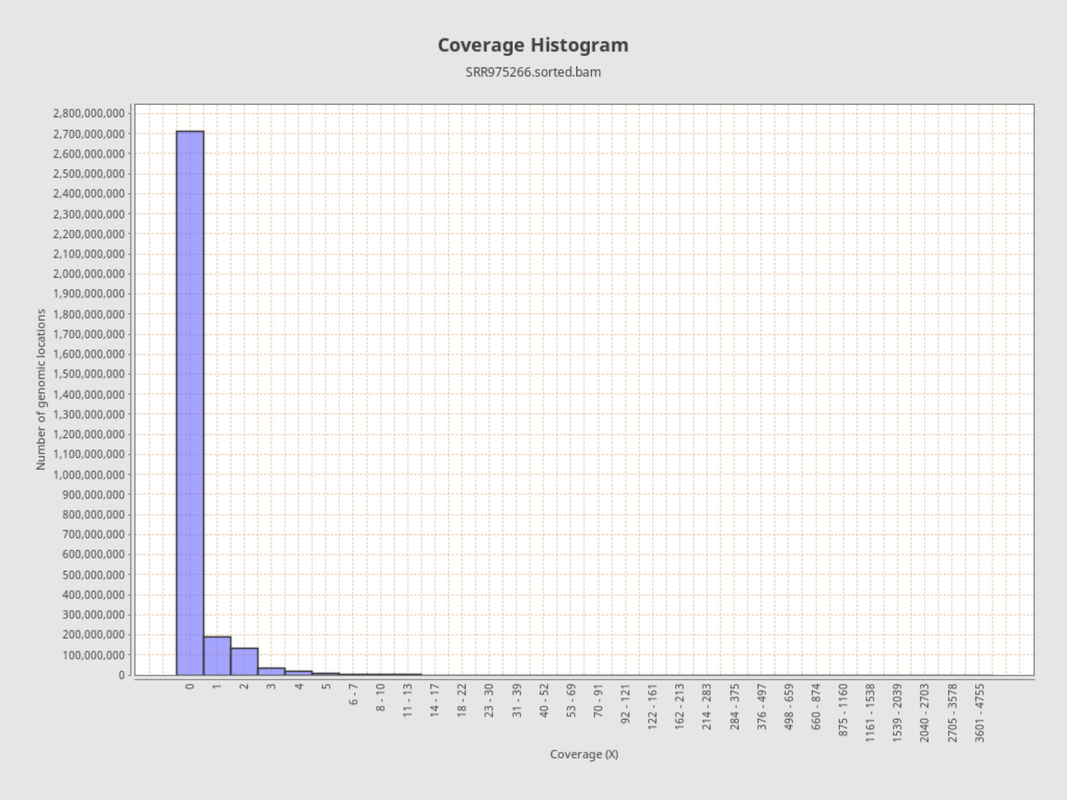
		bases	coverage	deviation
chr1	249250621	58812480	0.236	3.321
chr2	243199373	65799276	0.2706	2.8541
chr3	198022430	36376712	0.1837	0.6776
chr4	191154276	28100354	0.147	2.5294
chr5	180915260	44867576	0.248	0.8056
chr6	171115067	43405346	0.2537	2.9538
chr7	159138663	25696256	0.1615	1.9938
chr8	146364022	50283905	0.3436	1.3364
chr9	141213431	31952091	0.2263	4.2579
chr10	135534747	25542922	0.1885	9.5735
chr11	135006516	35561805	0.2634	3.6461
chr12	133851895	32548849	0.2432	0.7285
chr13	115169878	22299519	0.1936	0.6456
chr14	107349540	21961229	0.2046	0.708
chr15	102531392	21058459	0.2054	0.6784
chr16	90354753	17968827	0.1989	2.6415
chr17	81195210	14112064	0.1738	1.7917
chr18	78077248	20460325	0.2621	4.6014
chr19	59128983	10395708	0.1758	1.999
chr20	63025520	23795884	0.3776	1.2448
chr21	48129895	9876137	0.2052	1.2751
chr22	51304566	7297829	0.1422	0.57
chrMT	16571	106286	6.414	4.0406
chrX	155270560	86687647	0.5583	2.039

chrY	59373566	2293846	0.0386	2.0678

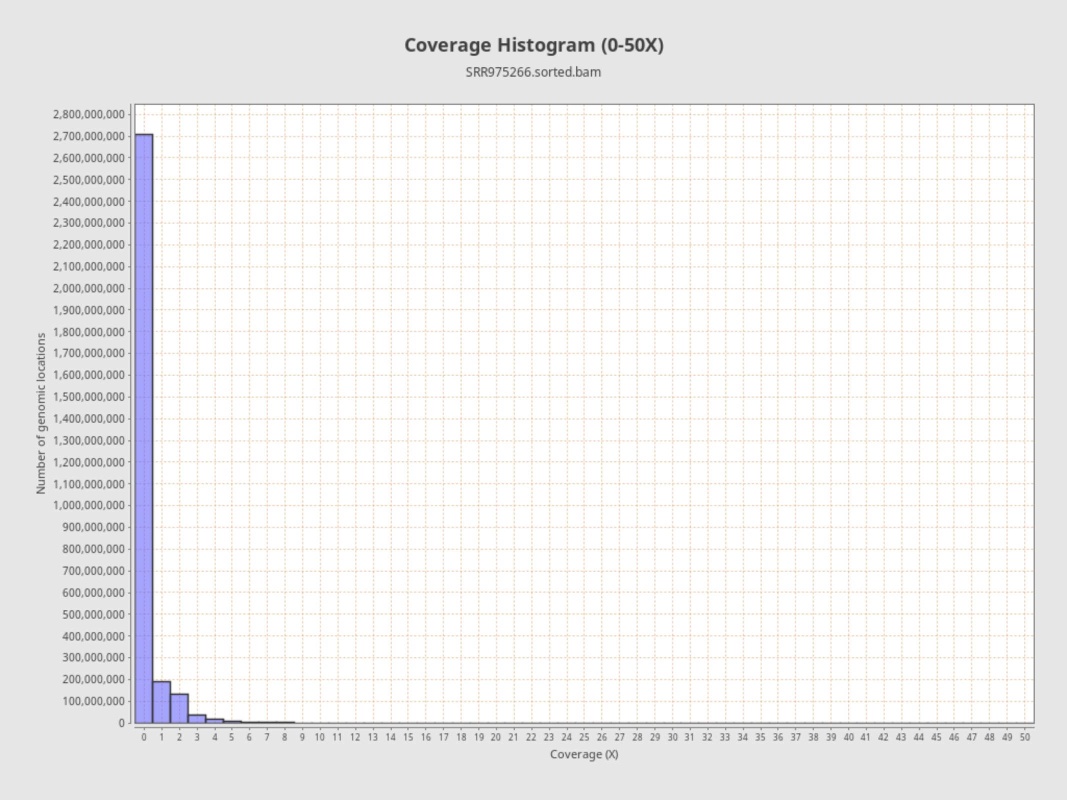
3. Results : Coverage across reference



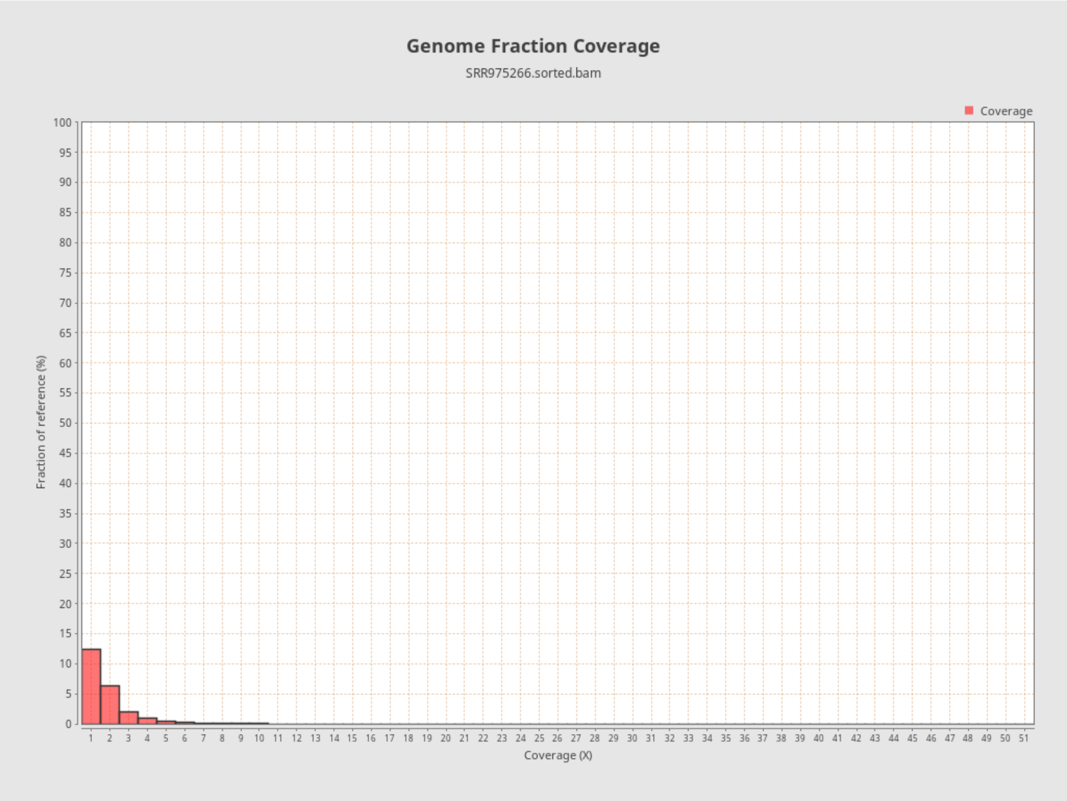
4. Results : Coverage Histogram



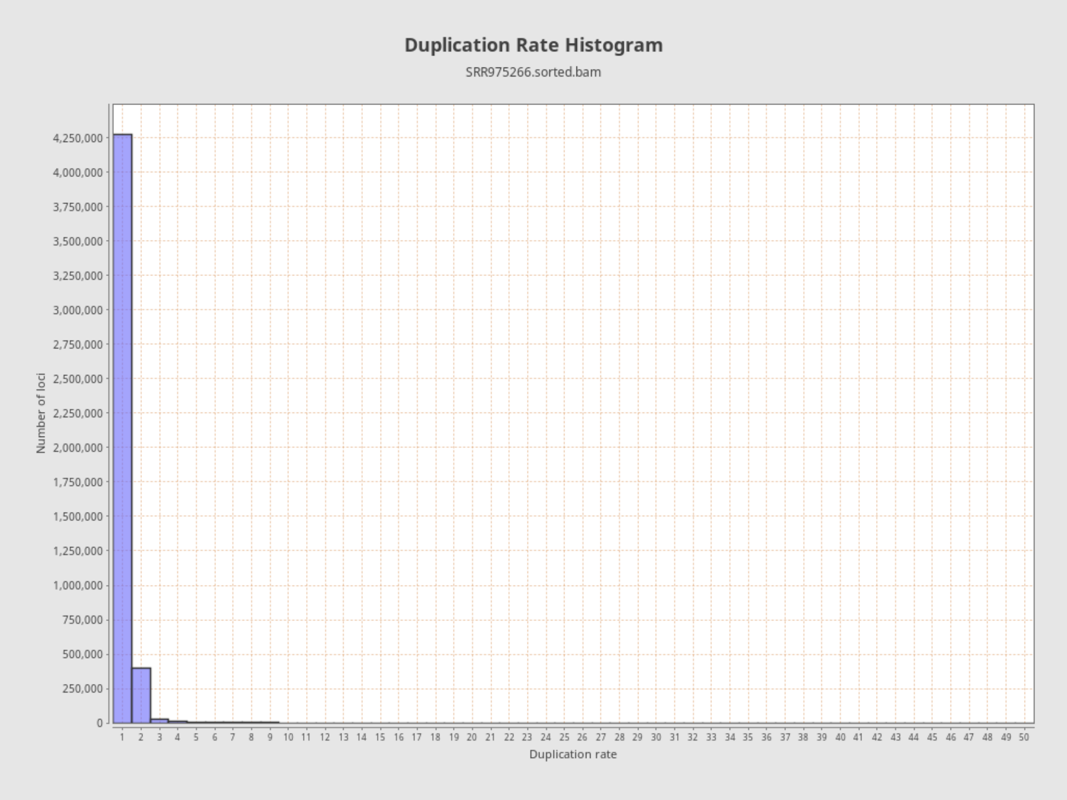
5. Results : Coverage Histogram (0-50X)



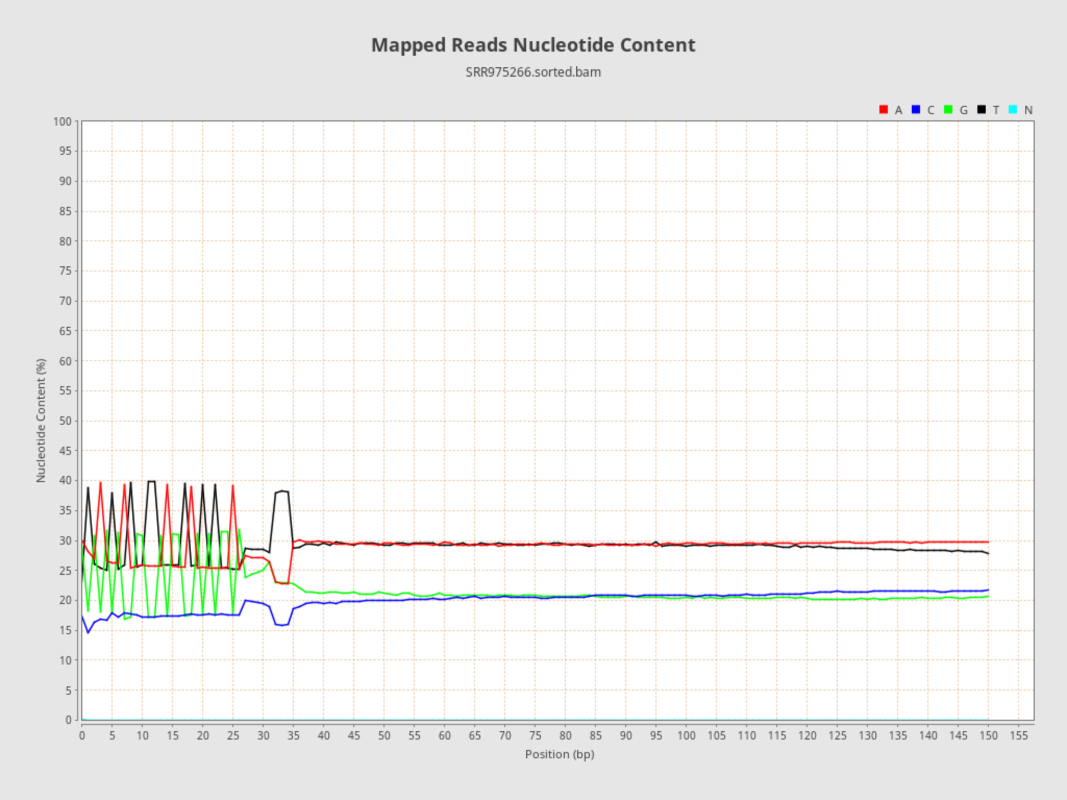
6. Results : Genome Fraction Coverage



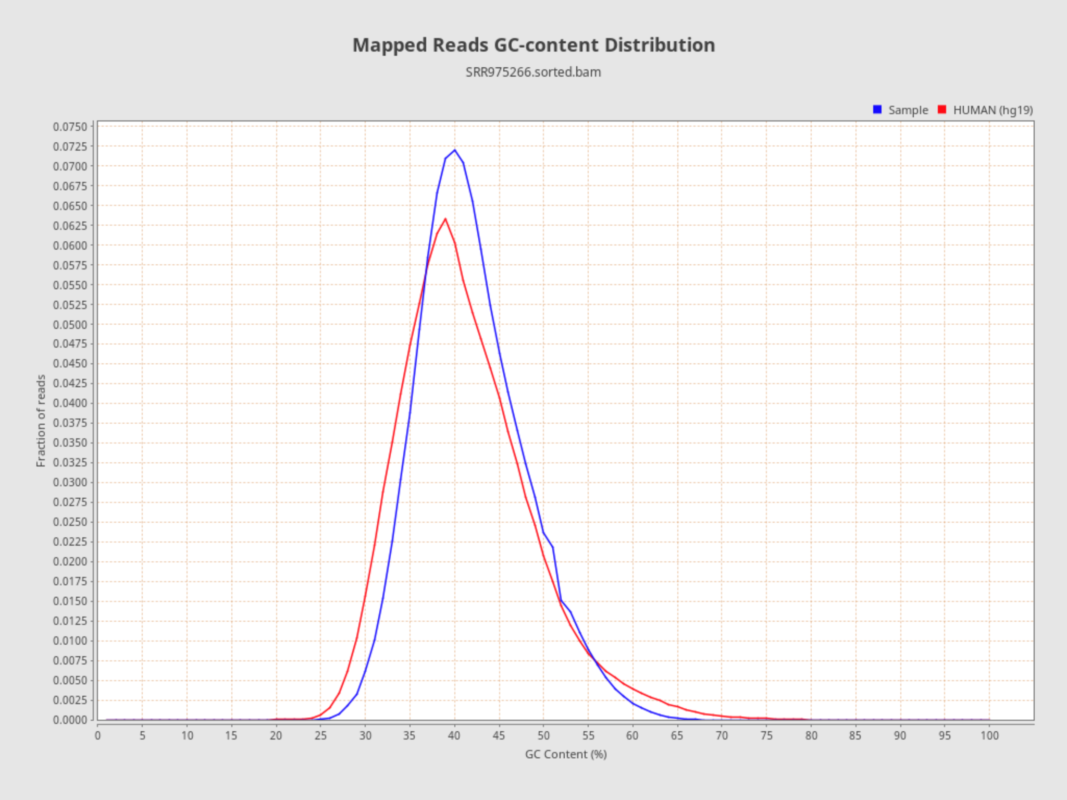
7. Results : Duplication Rate Histogram



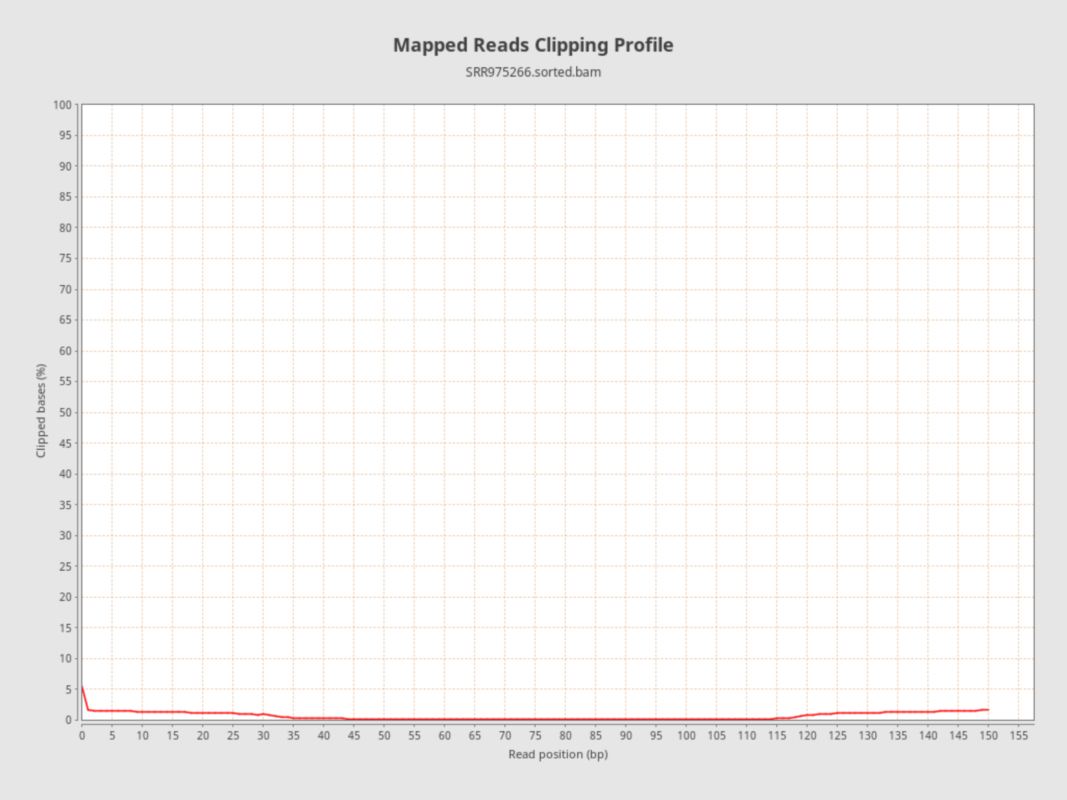
8. Results : Mapped Reads Nucleotide Content



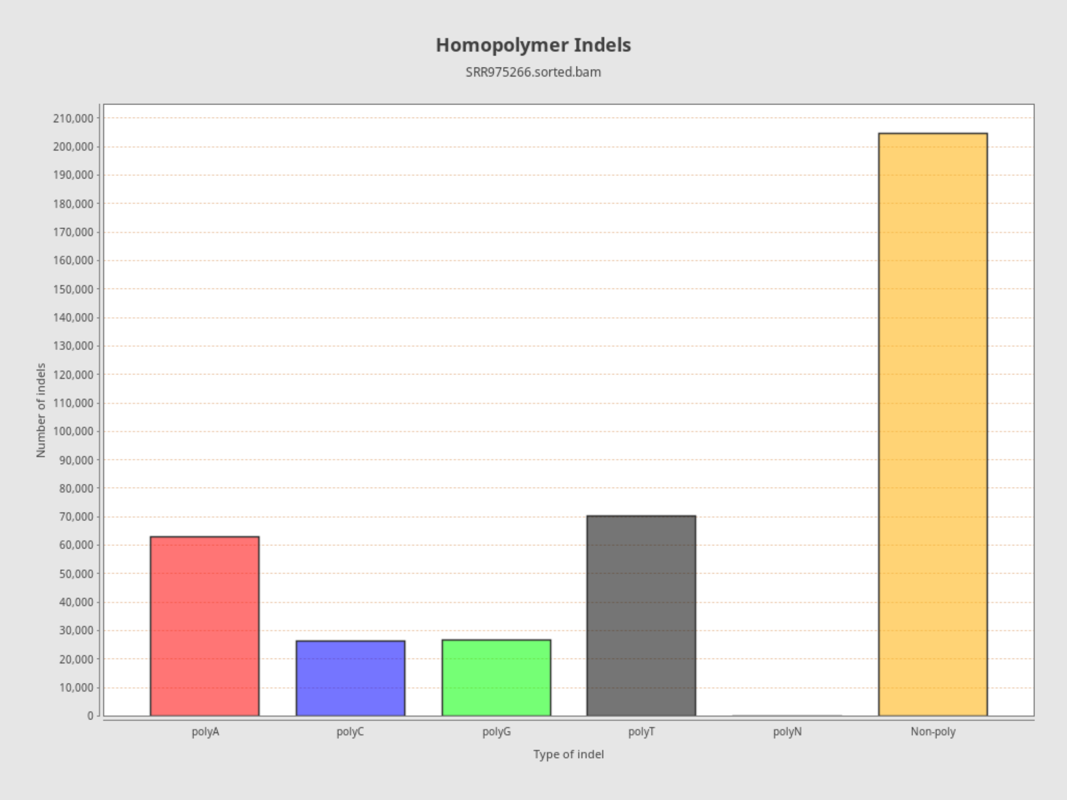
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

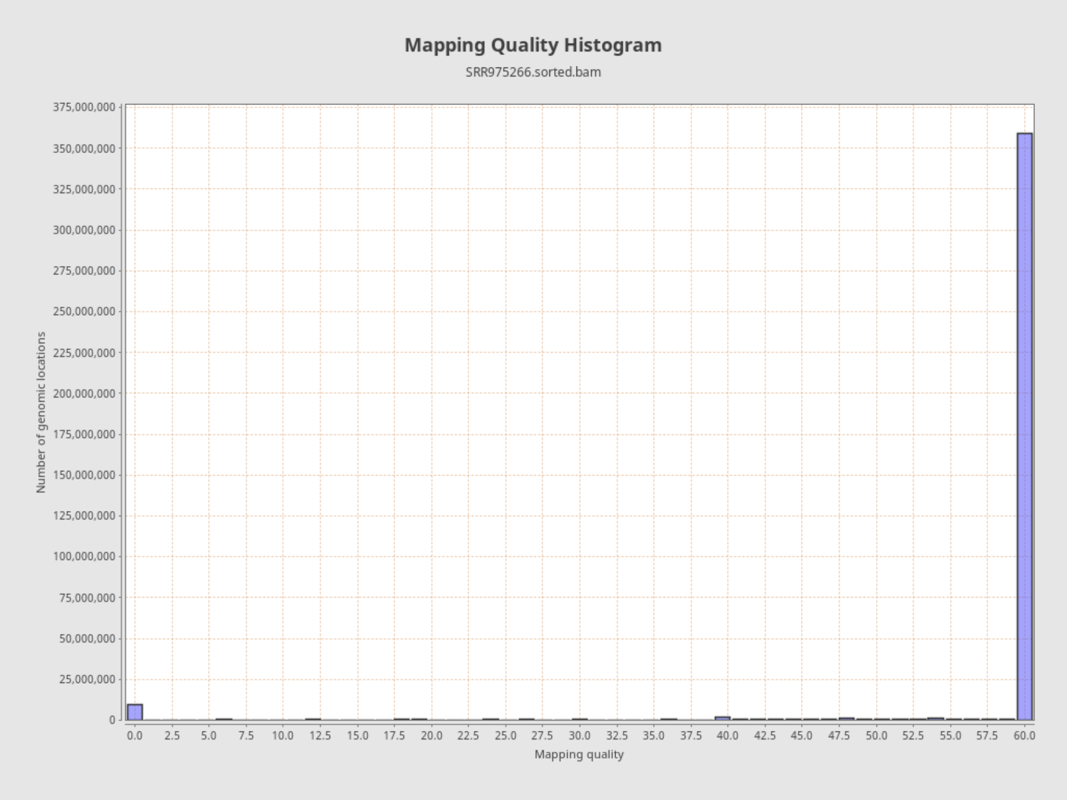


11. Results : Homopolymer Indels

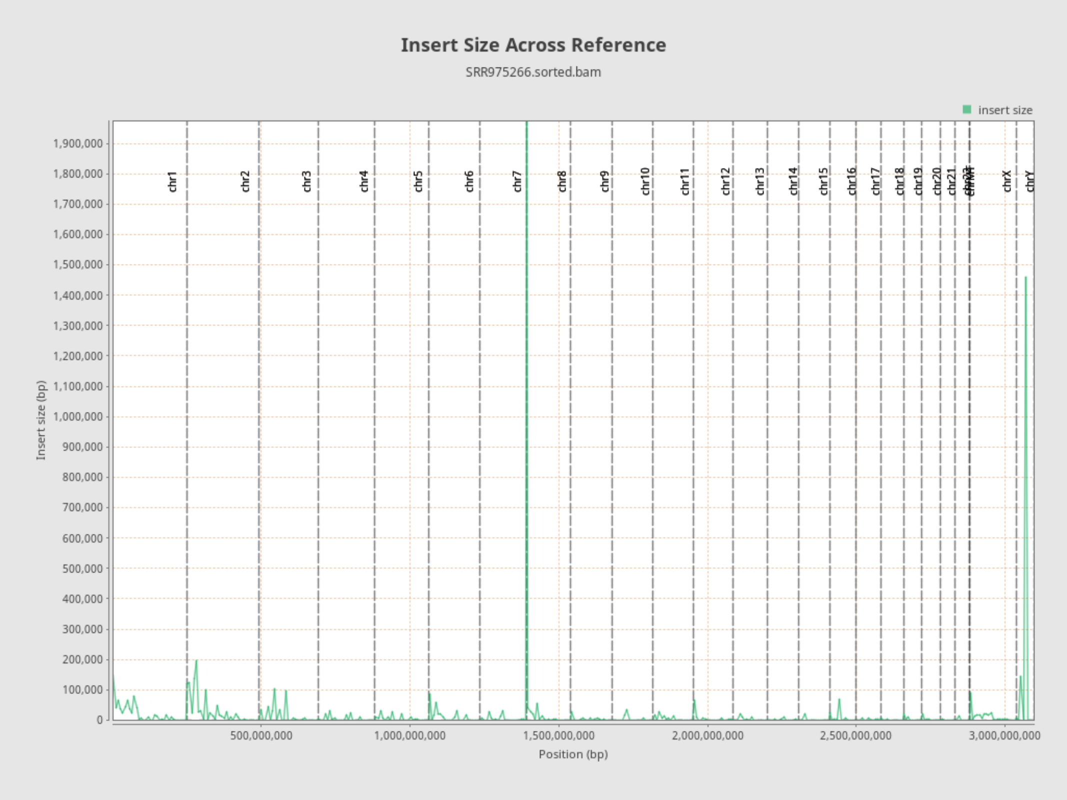


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram