Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 20:54:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975282.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_SRR975282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975282_1.fastq.gz SRR975282_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 20:54:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,208,050
Mapped reads	5,156,541 / 99.01%
Unmapped reads	51,509 / 0.99%
Mapped paired reads	5,156,541 / 99.01%
Mapped reads, first in pair	2,577,358 / 49.49%
Mapped reads, second in pair	2,579,183 / 49.52%
Mapped reads, both in pair	5,131,730 / 98.53%
Mapped reads, singletons	24,811 / 0.48%
Secondary alignments	0
Supplementary alignments	30,518 / 0.59%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	467,463 / 8.98%
Duplication rate	3.92%
Clipped reads	3,115,150 / 59.81%

2.2. ACGT Content

Number/percentage of A's	143,763,151 / 29.59%
Number/percentage of C's	96,233,338 / 19.81%
Number/percentage of T's	146,621,711 / 30.18%
Number/percentage of G's	99,185,400 / 20.42%
Number/percentage of N's	12,754 / 0%

GC Percentage	40.22%

2.3. Coverage

Mean	0.157
Standard Deviation	2.6185

2.4. Mapping Quality

Mean Mapping Quality	52.61

2.5. Insert size

Mean	65,695.98
Standard Deviation	2,359,220.24
P25/Median/P75	144 / 177 / 223

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	4,009,903
Insertions	76,566
Mapped reads with at least one insertion	1.45%
Deletions	143,396
Mapped reads with at least one deletion	2.72%
Homopolymer indels	45.74%

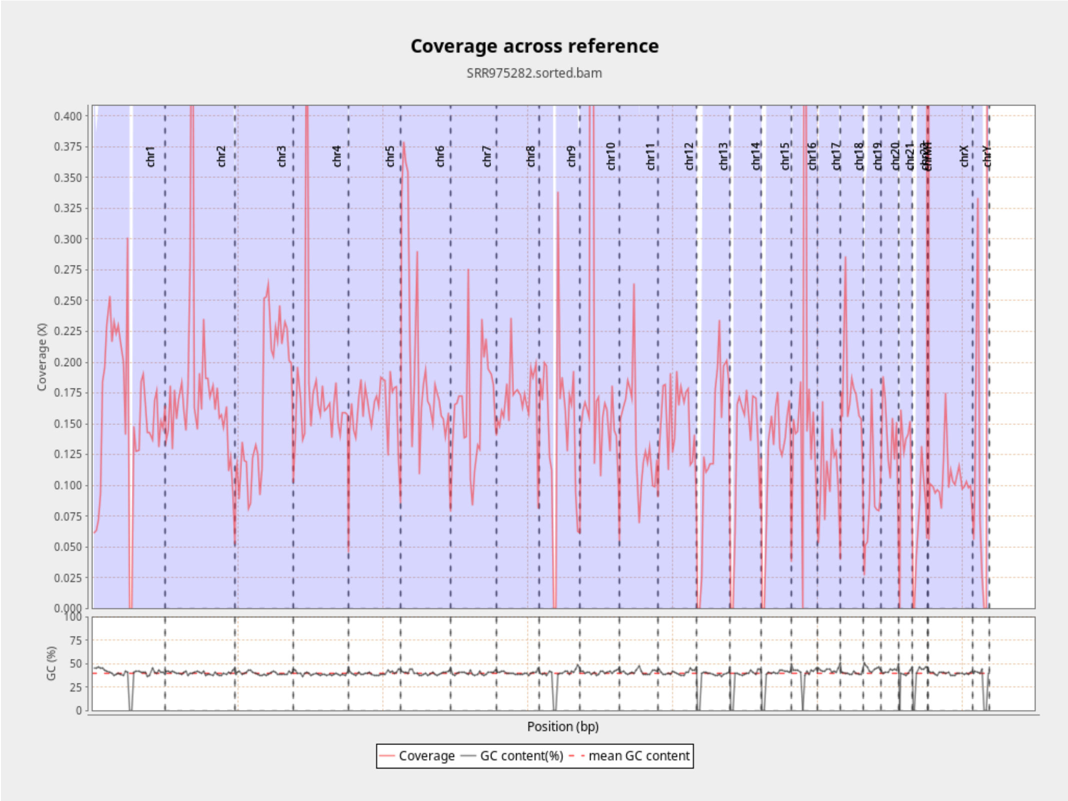
2.7. Chromosome stats

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

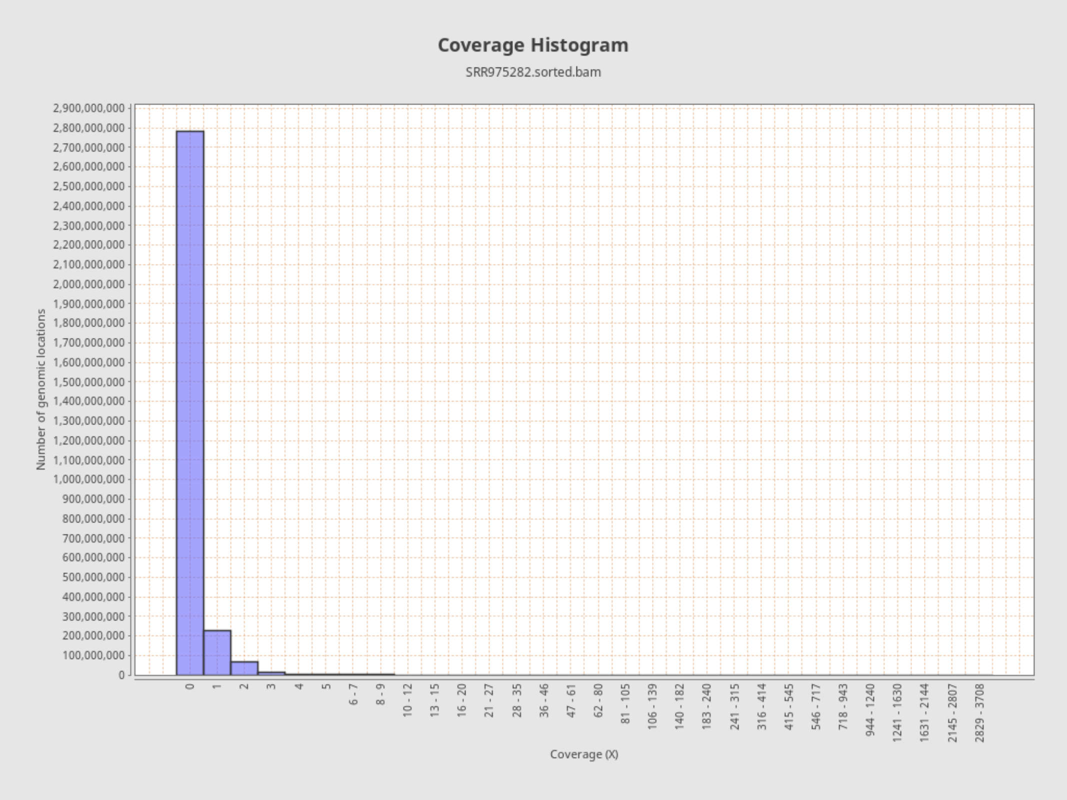
		bases	coverage	deviation
chr1	249250621	39423311	0.1582	2.3915
chr2	243199373	43305797	0.1781	2.6772
chr3	198022430	33773666	0.1706	0.6725
chr4	191154276	33846489	0.1771	2.4696
chr5	180915260	29632701	0.1638	0.5325
chr6	171115067	34436600	0.2012	1.534
chr7	159138663	25866366	0.1625	1.9554
chr8	146364022	24798917	0.1694	0.9451
chr9	141213431	20779271	0.1471	3.5583
chr10	135534747	28557996	0.2107	7.8295
chr11	135006516	18784945	0.1391	1.86
chr12	133851895	20634897	0.1542	0.5199
chr13	115169878	15235081	0.1323	0.4686
chr14	107349540	13670164	0.1273	0.5543
chr15	102531392	12396845	0.1209	0.4515
chr16	90354753	17012263	0.1883	4.1927
chr17	81195210	8628220	0.1063	1.4861
chr18	78077248	13723053	0.1758	3.5036
chr19	59128983	4999112	0.0845	1.3723
chr20	63025520	8614909	0.1367	0.7063
chr21	48129895	5883792	0.1222	1.0129
chr22	51304566	3589178	0.07	0.3582
chrMT	16571	64898	3.9164	6.0068
chrX	155270560	15942746	0.1027	0.8654

chrY	59373566	12499143	0.2105	5.6344

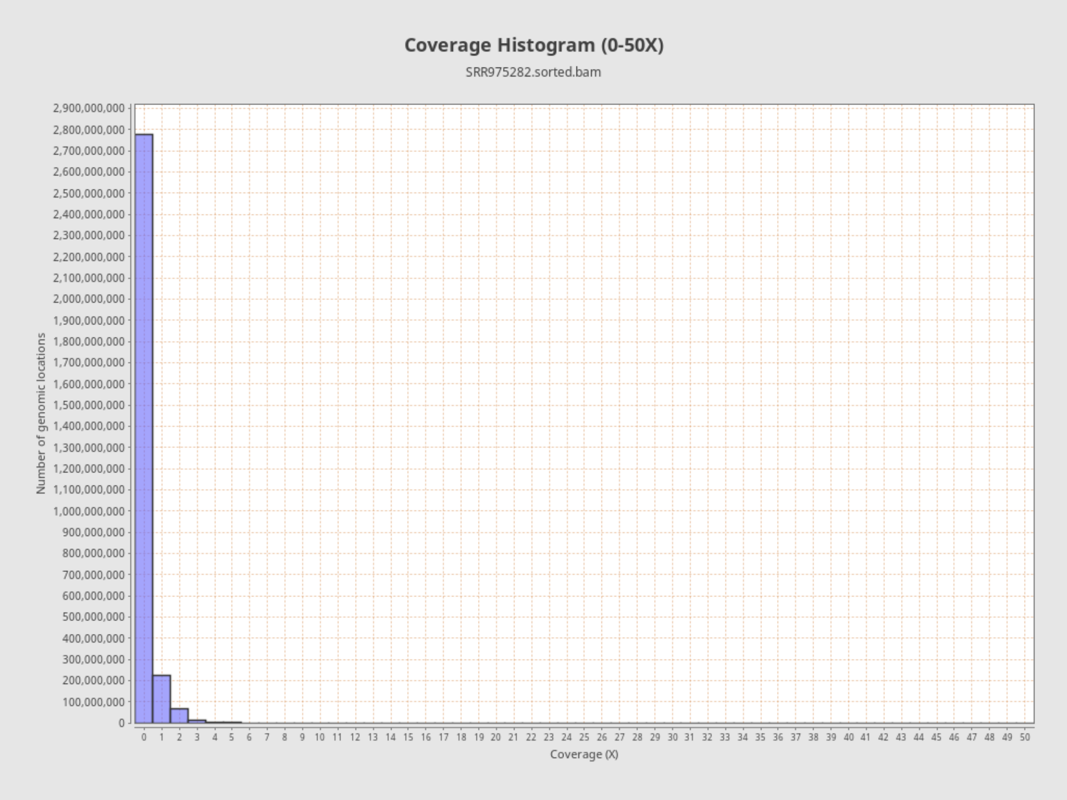
3. Results : Coverage across reference



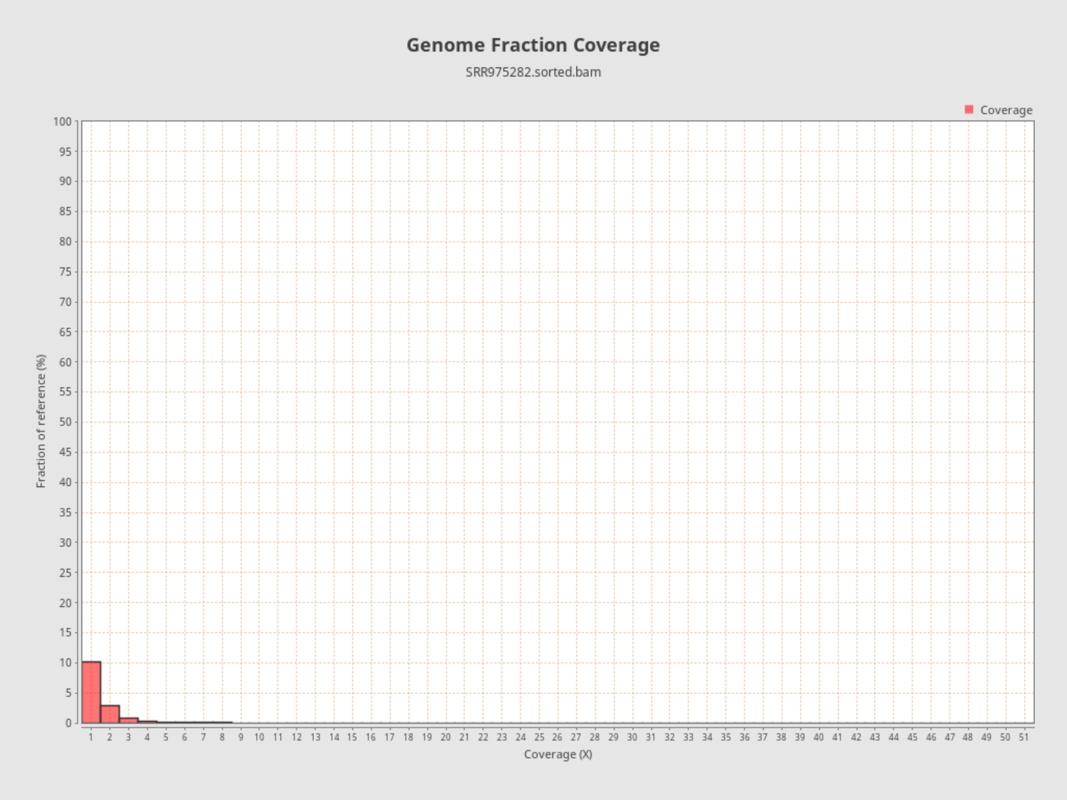
4. Results : Coverage Histogram



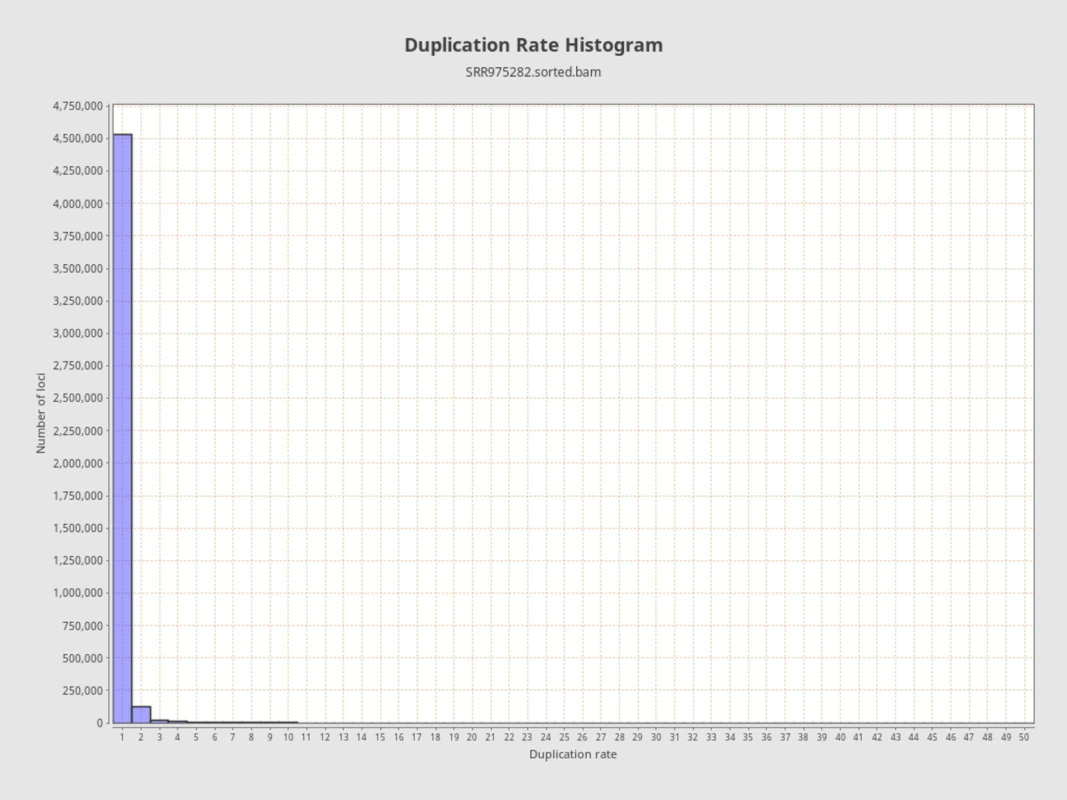
5. Results : Coverage Histogram (0-50X)



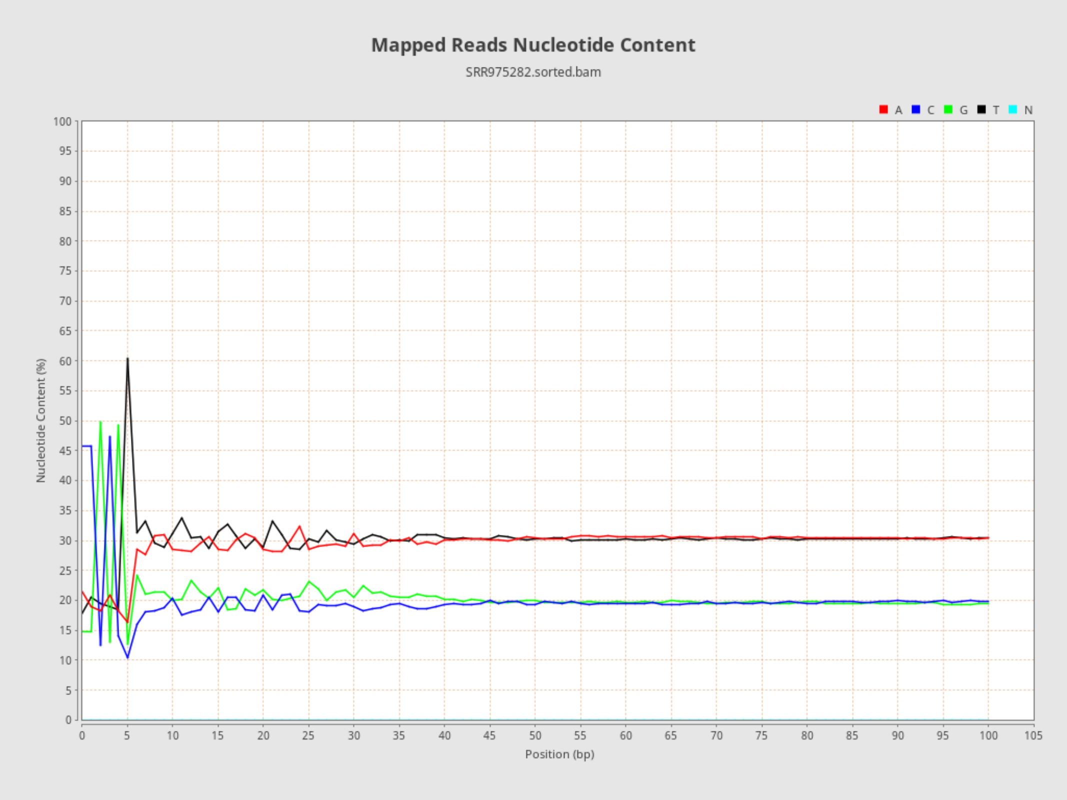
6. Results : Genome Fraction Coverage



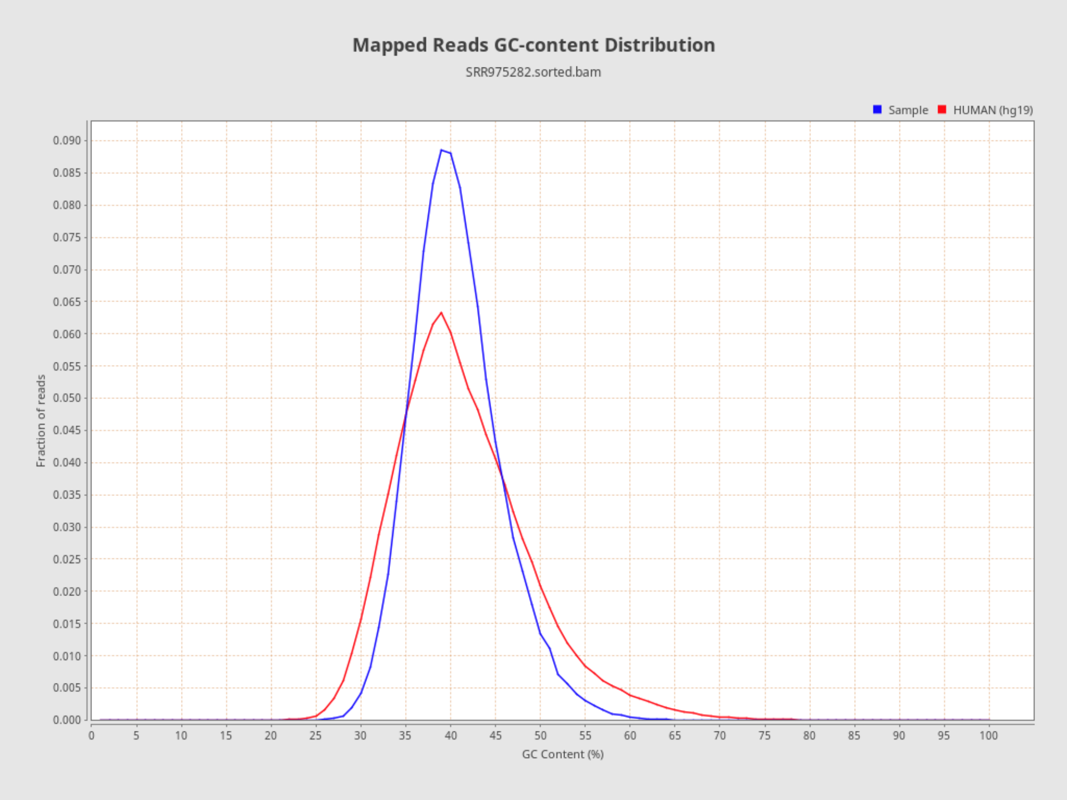
7. Results : Duplication Rate Histogram



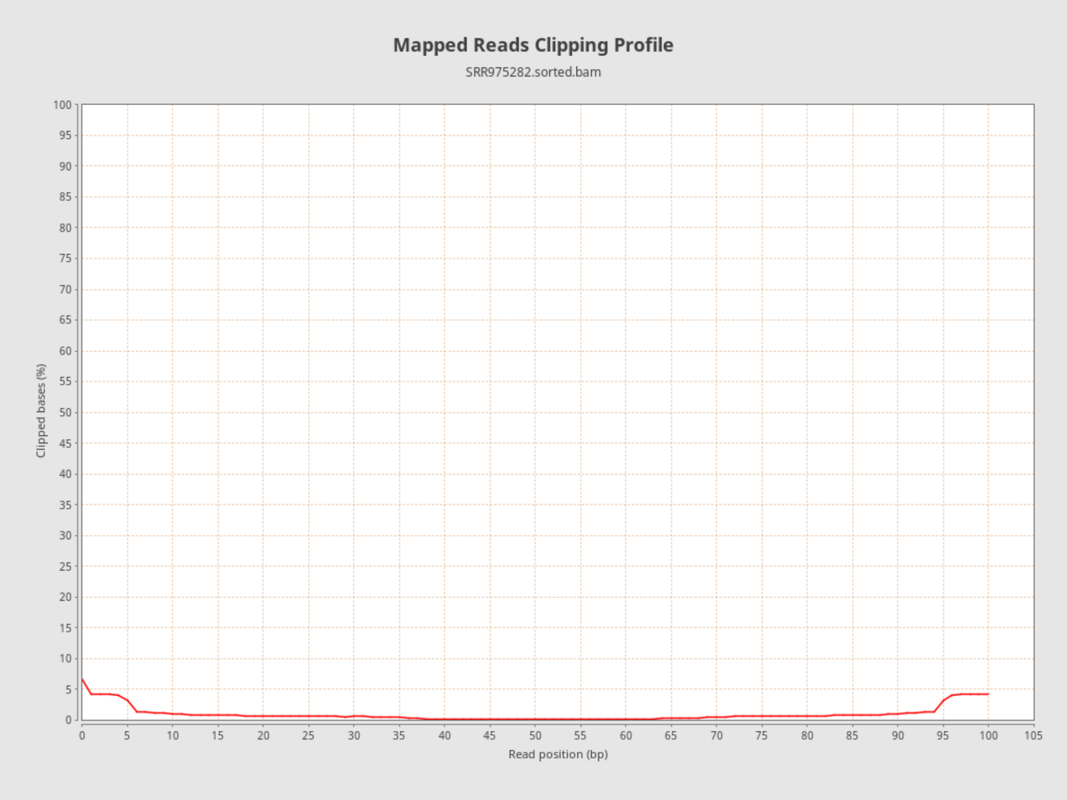
8. Results : Mapped Reads Nucleotide Content



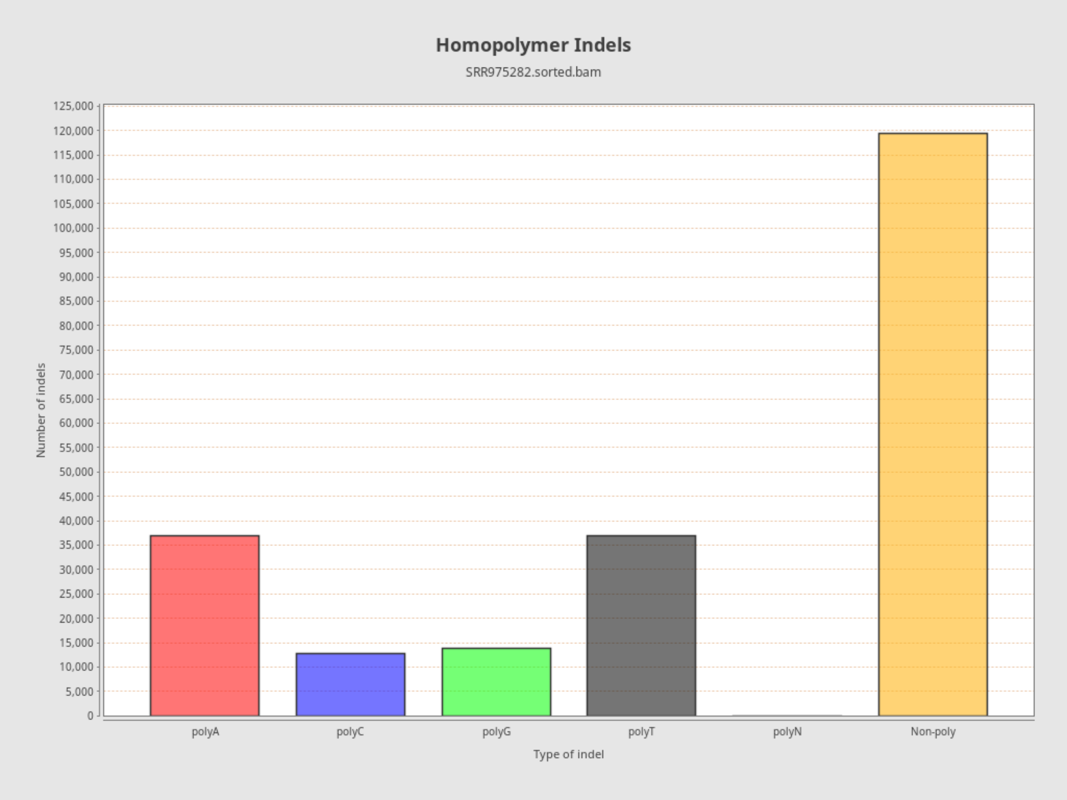
9. Results : Mapped Reads GC-content Distribution



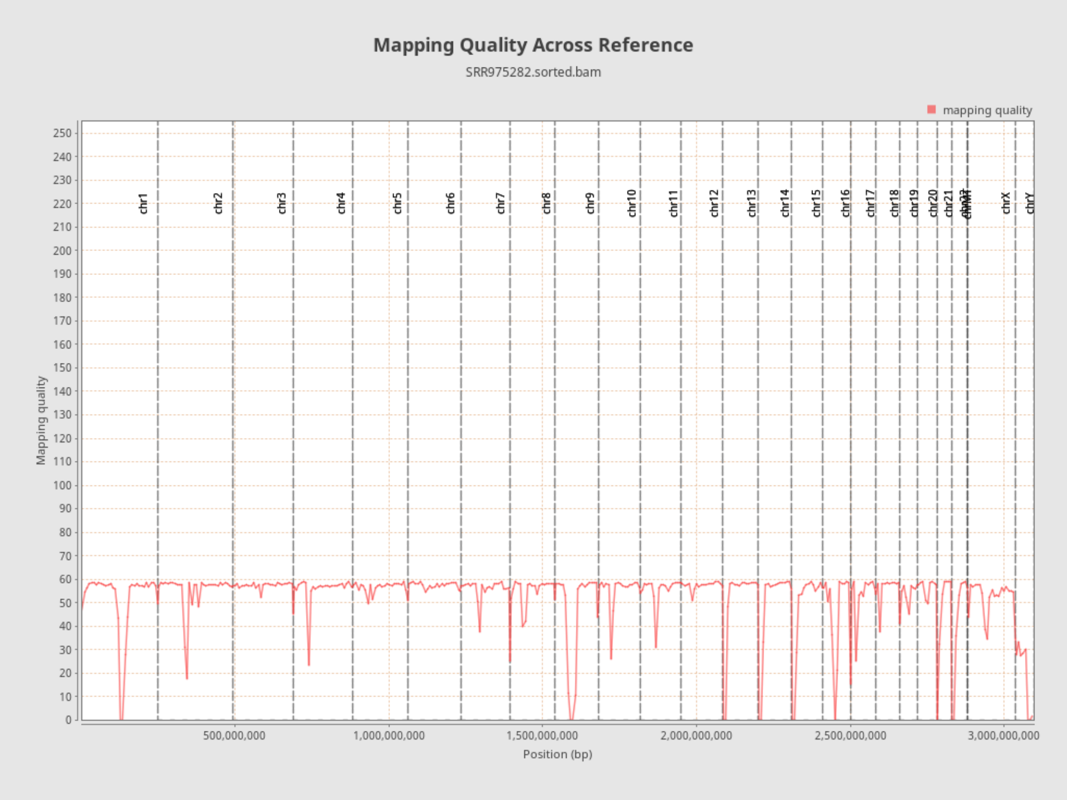
10. Results : Mapped Reads Clipping Profile



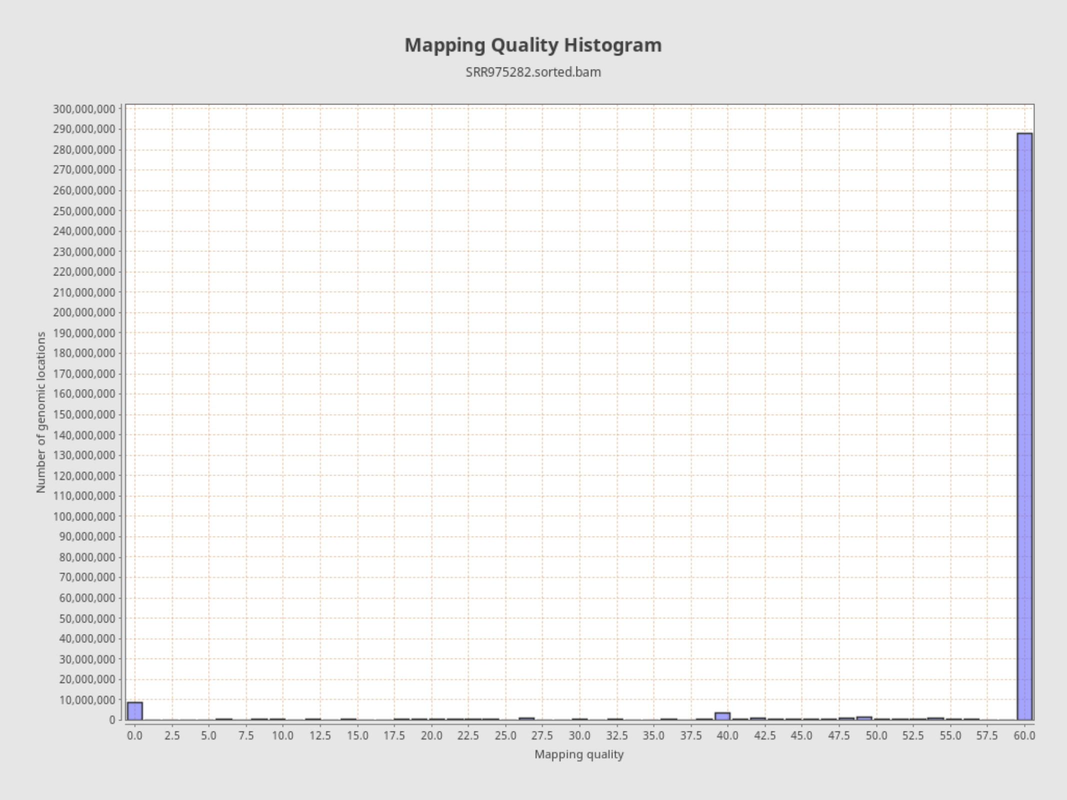
11. Results : Homopolymer Indels



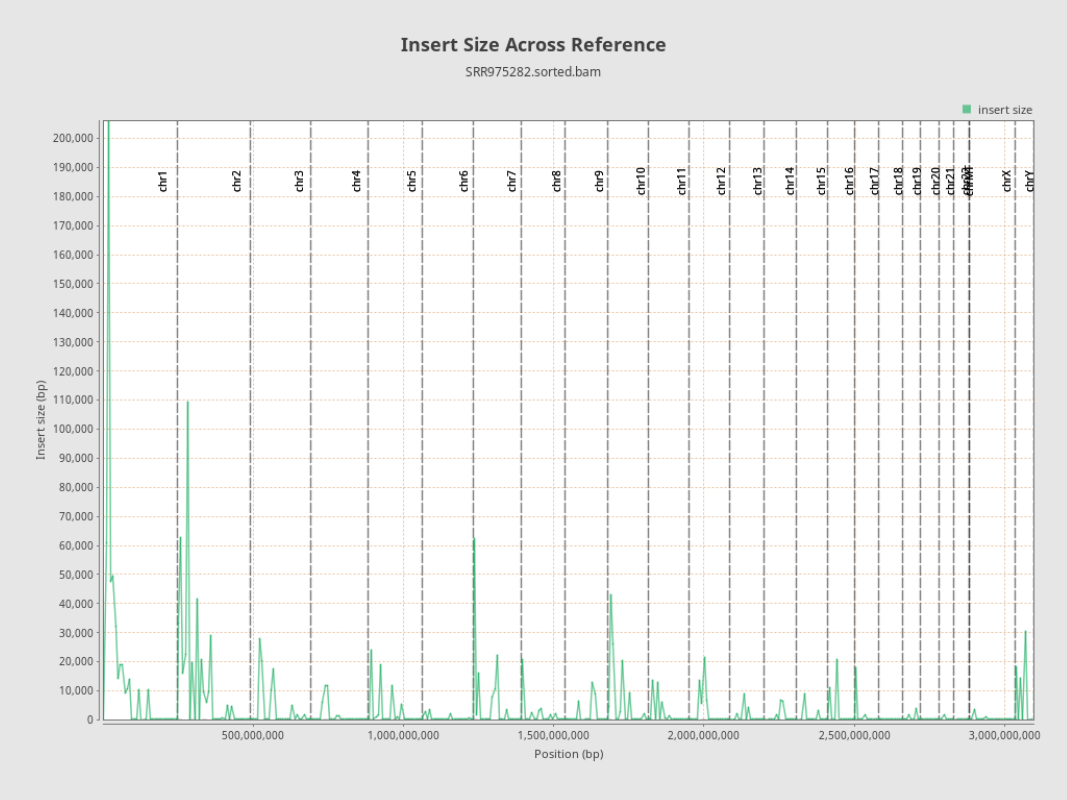
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram