Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 10:52:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975277.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_SRR975277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975277_1.fastq.gz SRR975277_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 10:52:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	65,653,560
Mapped reads	65,512,127 / 99.78%
Unmapped reads	141,433 / 0.22%
Mapped paired reads	65,512,127 / 99.78%
Mapped reads, first in pair	32,769,623 / 49.91%
Mapped reads, second in pair	32,742,504 / 49.87%
Mapped reads, both in pair	65,451,120 / 99.69%
Mapped reads, singletons	61,007 / 0.09%
Secondary alignments	0
Supplementary alignments	108,326 / 0.16%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	41,166,741 / 62.7%
Duplication rate	48.21%
Clipped reads	36,593,527 / 55.74%

2.2. ACGT Content

Number/percentage of A's	1,680,520,304 / 27.76%
Number/percentage of C's	1,286,039,495 / 21.25%
Number/percentage of T's	1,694,535,388 / 28%
Number/percentage of G's	1,391,523,291 / 22.99%
Number/percentage of N's	267,951 / 0%

GC Percentage	44.24%

2.3. Coverage

Mean	1.9558
Standard Deviation	27.3758

2.4. Mapping Quality

Mean Mapping Quality	56.21

2.5. Insert size

Mean	59,568.07
Standard Deviation	2,328,680.97
P25/Median/P75	148 / 184 / 232

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	30,649,331
Insertions	595,210
Mapped reads with at least one insertion	0.9%
Deletions	1,150,771
Mapped reads with at least one deletion	1.73%
Homopolymer indels	47.26%

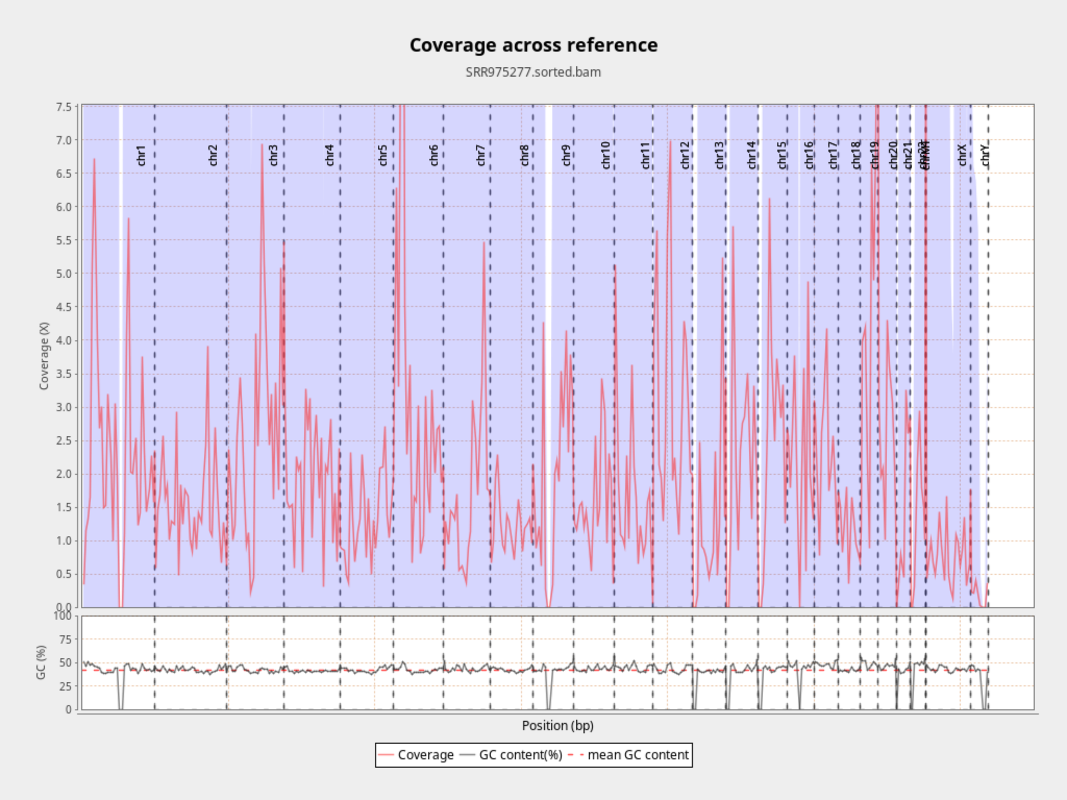
2.7. Chromosome stats

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

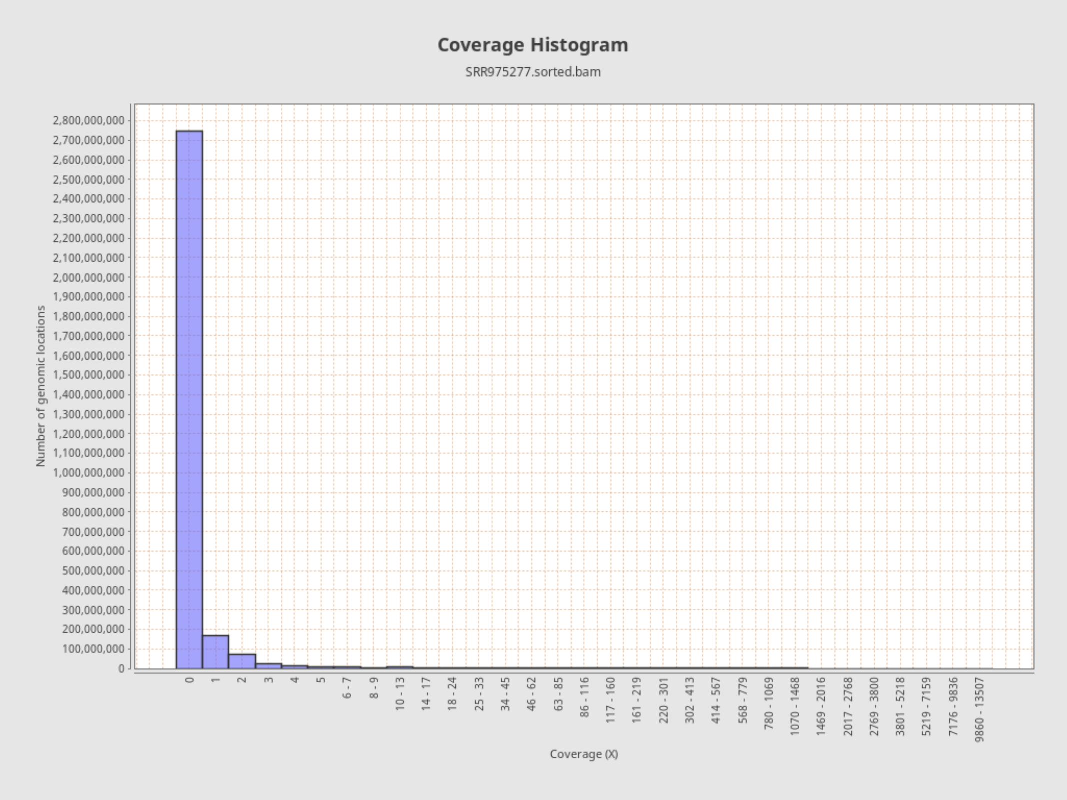
		bases	coverage	deviation
chr1	249250621	576003270	2.3109	28.3354
chr2	243199373	376246655	1.5471	20.8561
chr3	198022430	521348275	2.6328	34.3149
chr4	191154276	363143140	1.8997	27.7124
chr5	180915260	241968256	1.3375	19.0176
chr6	171115067	594824803	3.4762	47.6414
chr7	159138663	268284339	1.6859	24.4474
chr8	146364022	178161246	1.2172	18.4586
chr9	141213431	275776415	1.9529	27.4732
chr10	135534747	217945912	1.608	21.9996
chr11	135006516	221402773	1.6399	22.1108
chr12	133851895	409309997	3.0579	33.2786
chr13	115169878	144525250	1.2549	25.7452
chr14	107349540	239486601	2.2309	29.1417
chr15	102531392	250196082	2.4402	30.3678
chr16	90354753	205310142	2.2723	26.8254
chr17	81195210	185328192	2.2825	25.302
chr18	78077248	91049895	1.1662	18.7089
chr19	59128983	258220417	4.3671	40.6402
chr20	63025520	162981304	2.586	32.8405
chr21	48129895	71870258	1.4933	23.7546
chr22	51304566	69773324	1.36	18.9178
chrMT	16571	152670	9.2131	19.3887
chrX	155270560	120897235	0.7786	13.4889

chrY	59373566	10458972	0.1762	4.6046

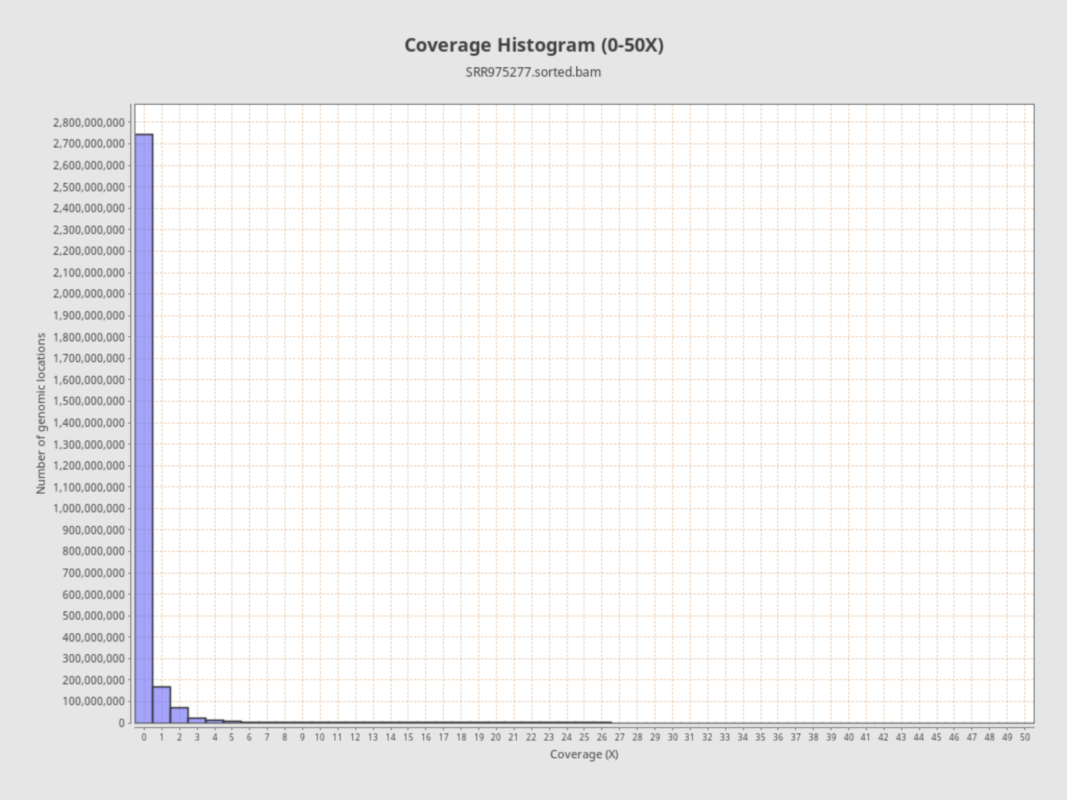
3. Results : Coverage across reference



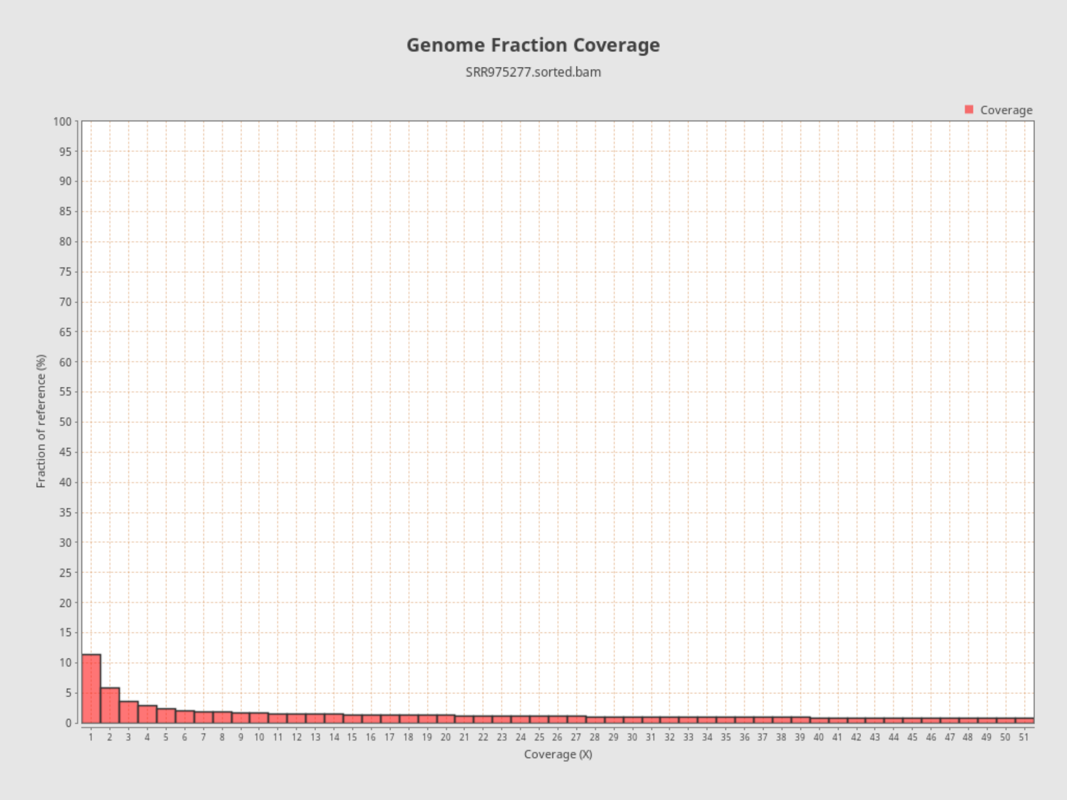
4. Results : Coverage Histogram



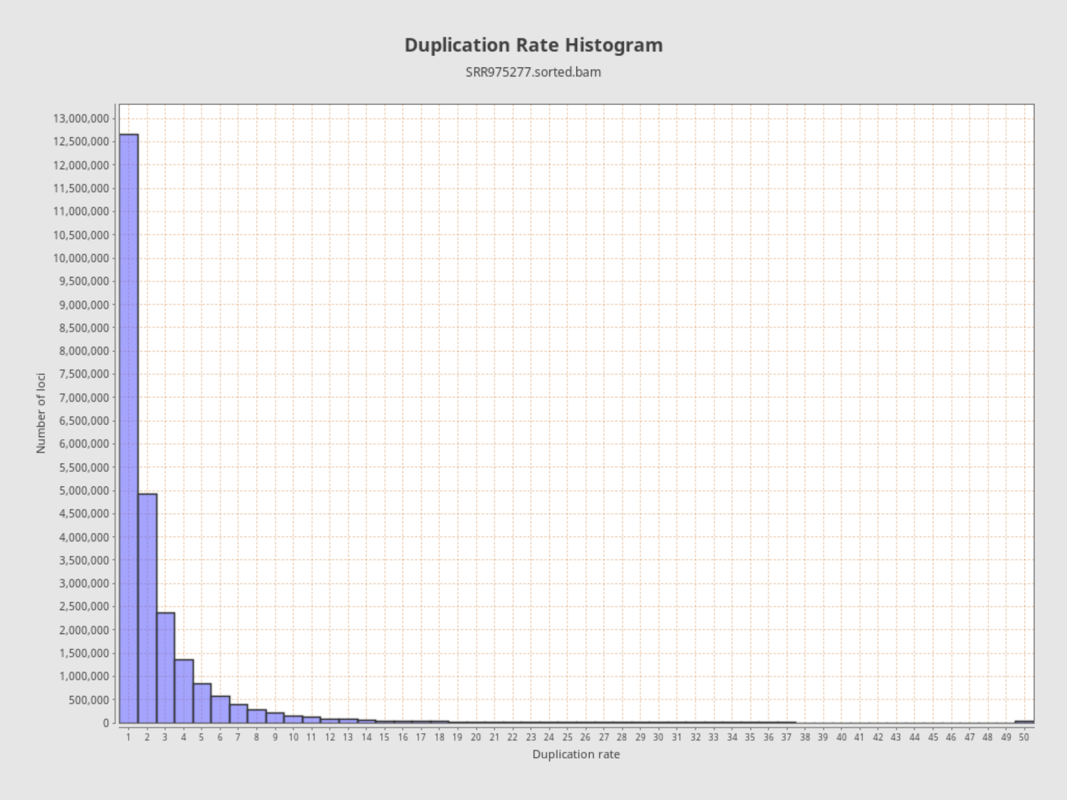
5. Results : Coverage Histogram (0-50X)



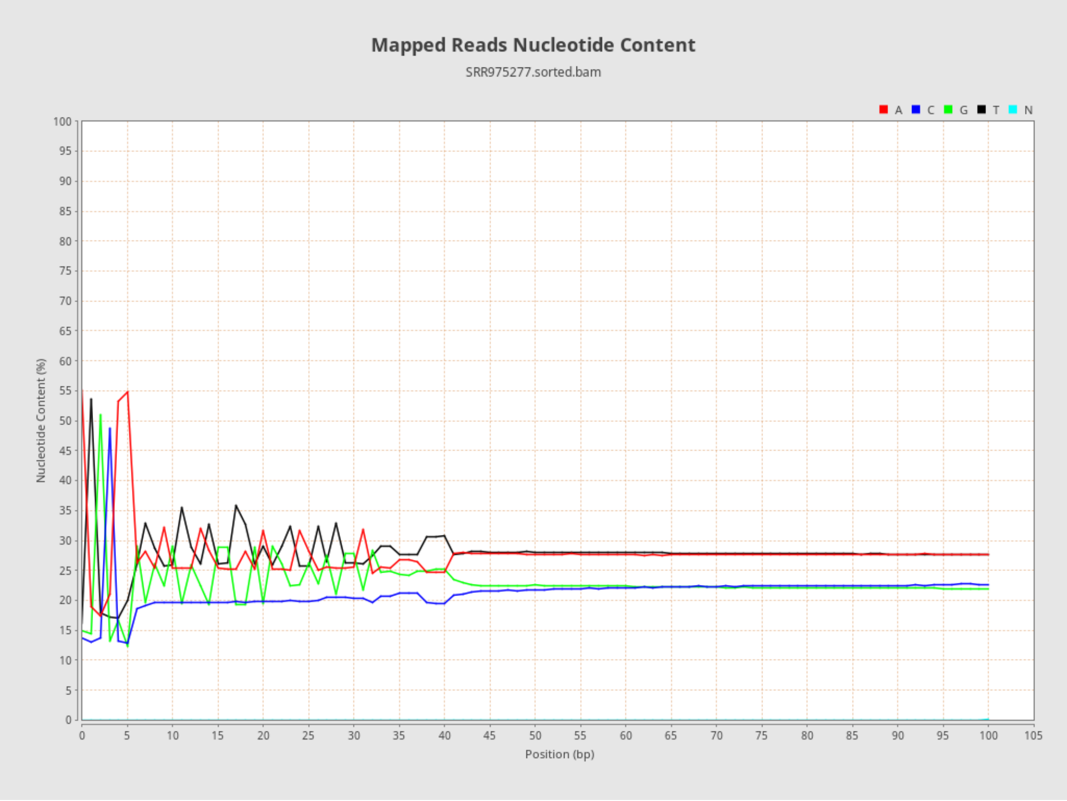
6. Results : Genome Fraction Coverage



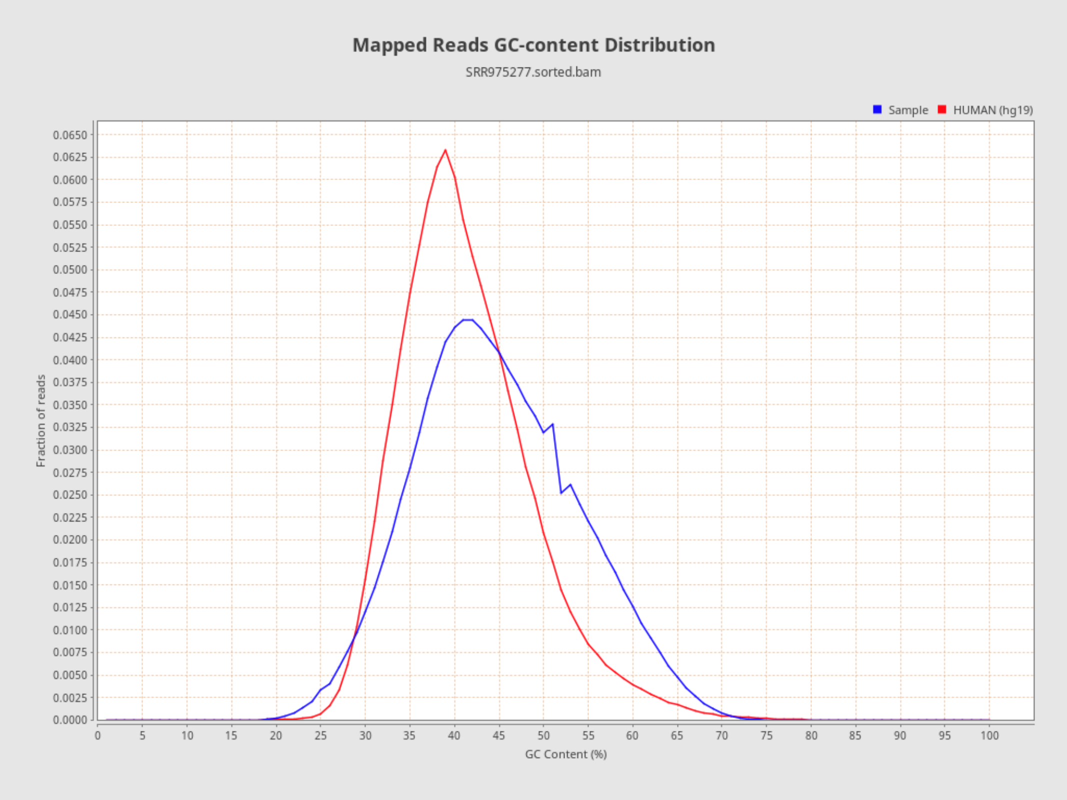
7. Results : Duplication Rate Histogram



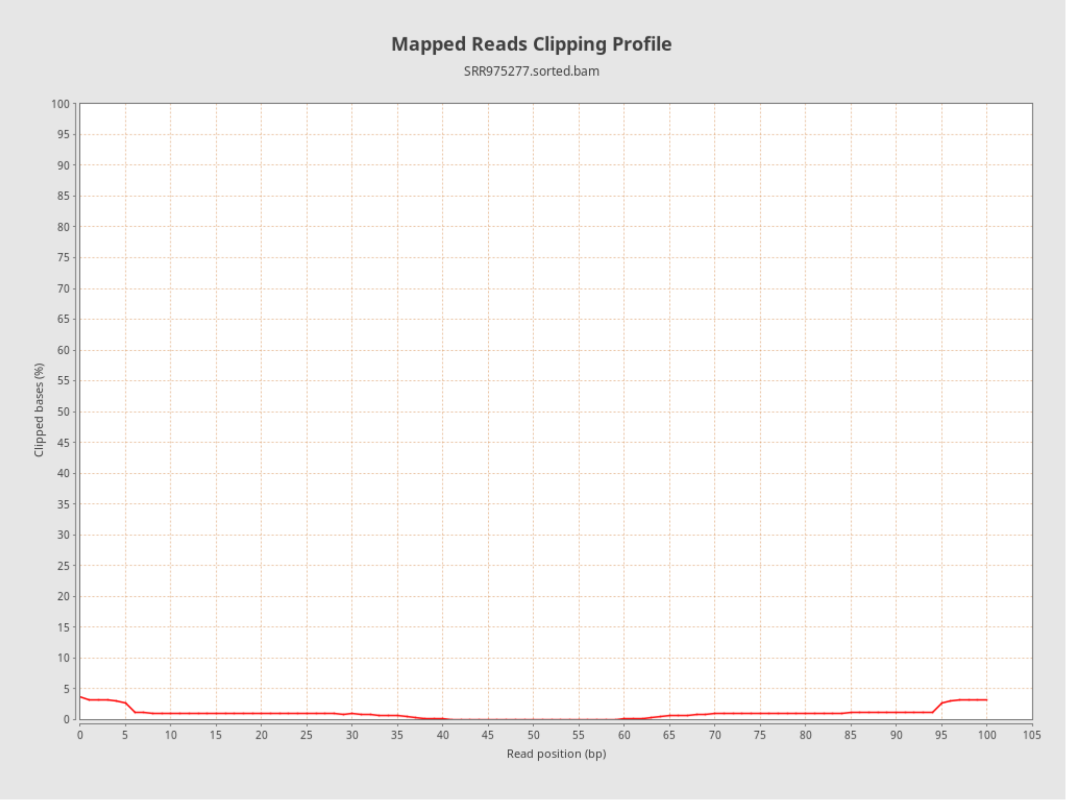
8. Results : Mapped Reads Nucleotide Content



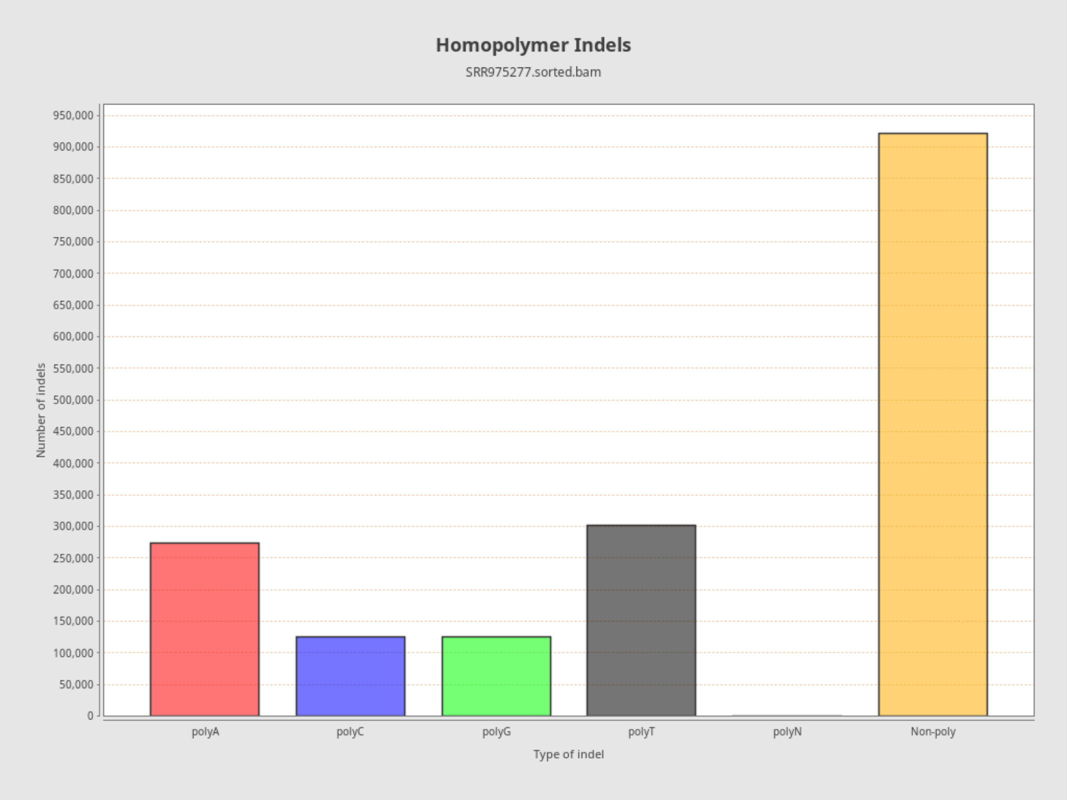
9. Results : Mapped Reads GC-content Distribution



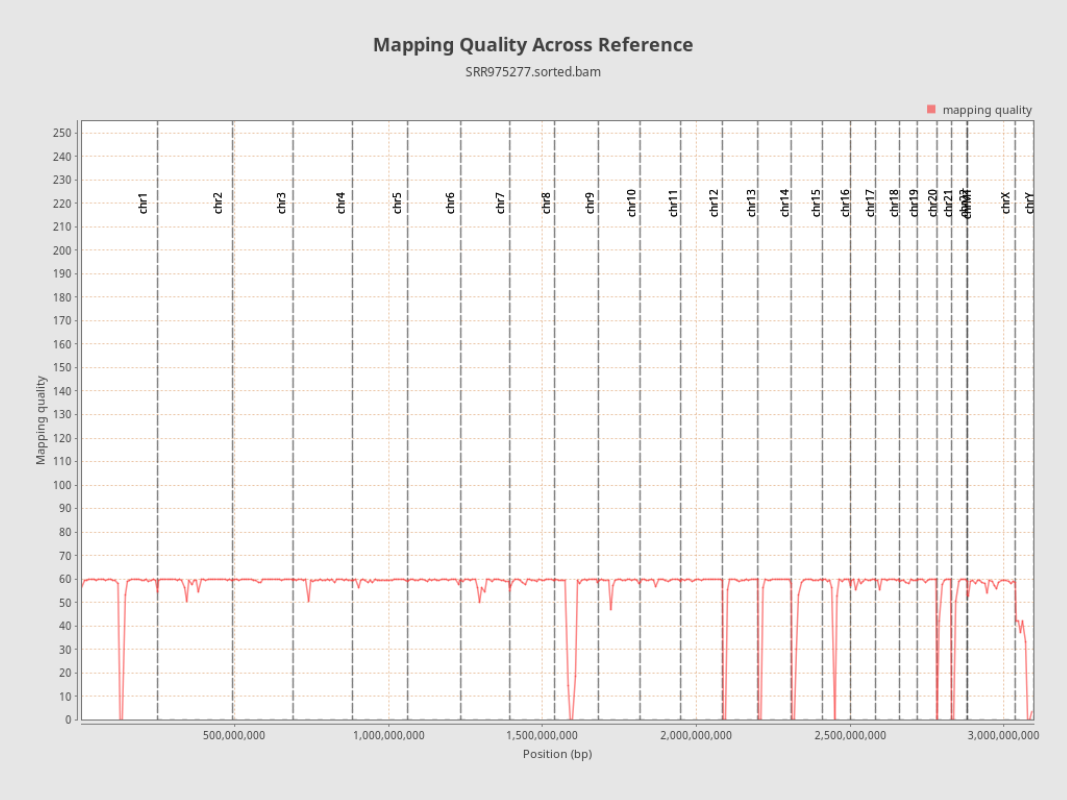
10. Results : Mapped Reads Clipping Profile



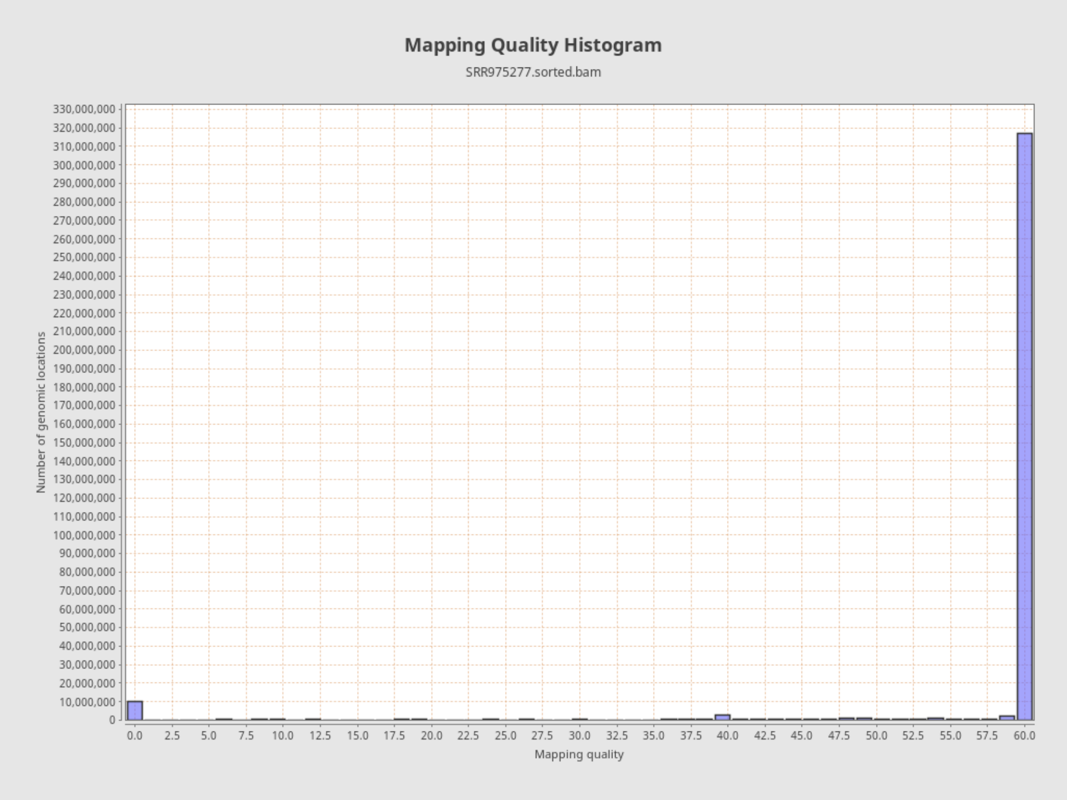
11. Results : Homopolymer Indels



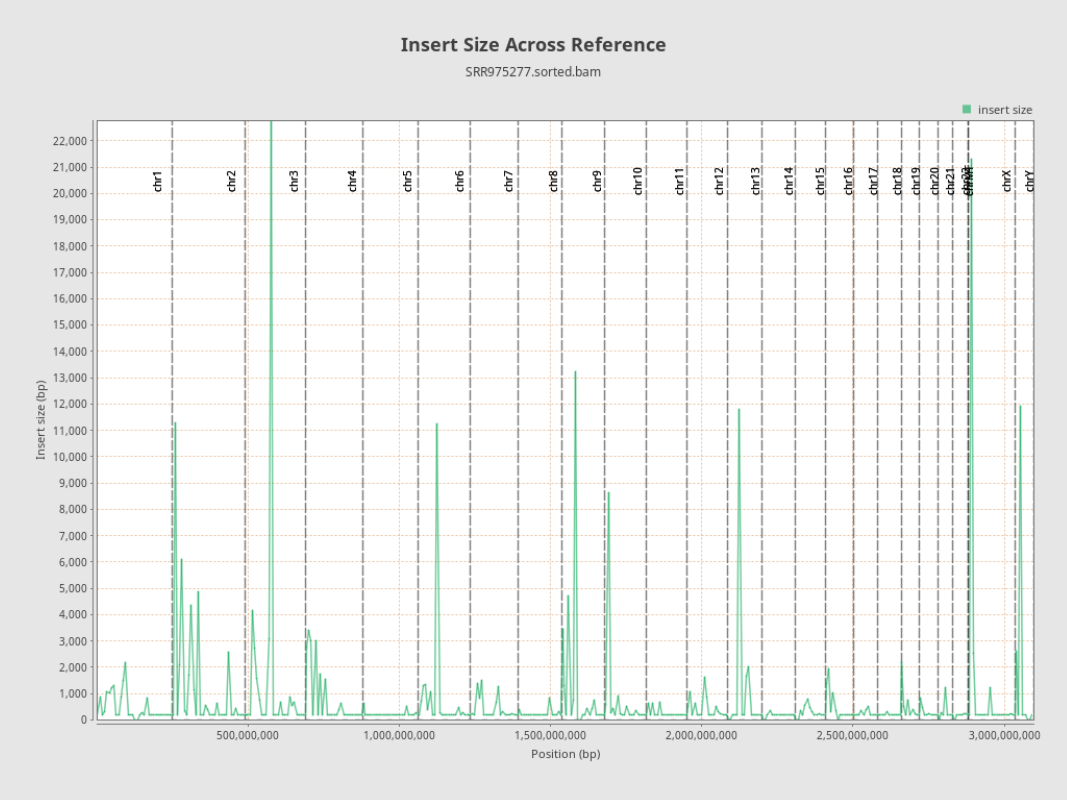
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram