Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 20:34:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975281.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_SRR975281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975281_1.fastq.gz SRR975281_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 20:34:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,482,636
Mapped reads	30,331,599 / 99.5%
Unmapped reads	151,037 / 0.5%
Mapped paired reads	30,331,599 / 99.5%
Mapped reads, first in pair	15,207,334 / 49.89%
Mapped reads, second in pair	15,124,265 / 49.62%
Mapped reads, both in pair	30,211,672 / 99.11%
Mapped reads, singletons	119,927 / 0.39%
Secondary alignments	0
Supplementary alignments	58,725 / 0.19%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	19,047,292 / 62.49%
Duplication rate	56.63%
Clipped reads	18,038,466 / 59.18%

2.2. ACGT Content

Number/percentage of A's	798,162,514 / 27.72%
Number/percentage of C's	614,886,898 / 21.35%
Number/percentage of T's	830,968,643 / 28.86%
Number/percentage of G's	635,079,151 / 22.05%
Number/percentage of N's	592,998 / 0.02%

GC Percentage	43.41%

2.3. Coverage

Mean	0.9305
Standard Deviation	13.9505

2.4. Mapping Quality

Mean Mapping Quality	56.19

2.5. Insert size

Mean	104,843.11
Standard Deviation	3,168,232.75
P25/Median/P75	191 / 234 / 284

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	20,454,722
Insertions	255,880
Mapped reads with at least one insertion	0.83%
Deletions	584,004
Mapped reads with at least one deletion	1.9%
Homopolymer indels	48.14%

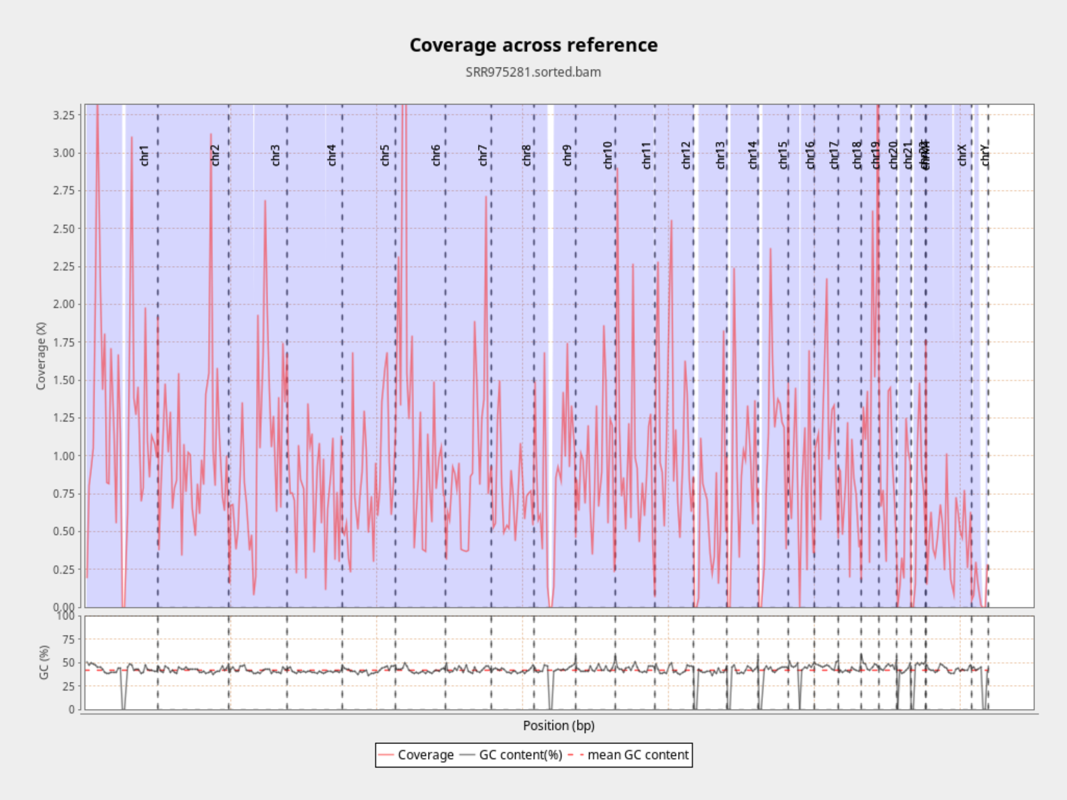
2.7. Chromosome stats

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

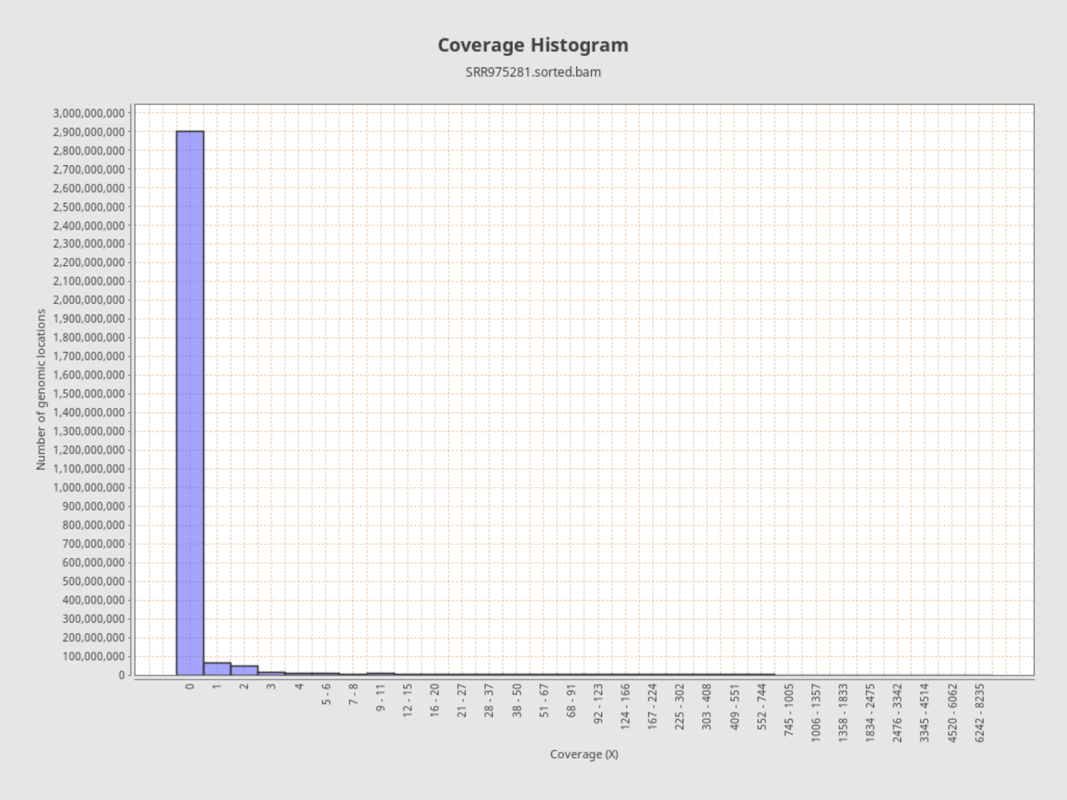
		bases	coverage	deviation
chr1	249250621	311683591	1.2505	16.1177
chr2	243199373	245451185	1.0093	14.0112
chr3	198022430	204188343	1.0311	14.9252
chr4	191154276	145558427	0.7615	11.6305
chr5	180915260	152752784	0.8443	12.8914
chr6	171115067	237826514	1.3899	21.4622
chr7	159138663	149832324	0.9415	14.1335
chr8	146364022	110021717	0.7517	11.5661
chr9	141213431	115063604	0.8148	11.8418
chr10	135534747	126885548	0.9362	13.8241
chr11	135006516	138560095	1.0263	13.6662
chr12	133851895	161111975	1.2037	14.5984
chr13	115169878	65982353	0.5729	10.611
chr14	107349540	92367745	0.8604	12.3837
chr15	102531392	104309368	1.0173	15.843
chr16	90354753	72517300	0.8026	10.3584
chr17	81195210	96146554	1.1841	14.9888
chr18	78077248	57492195	0.7364	12.8312
chr19	59128983	91356398	1.545	22.6667
chr20	63025520	58330660	0.9255	14.8887
chr21	48129895	27374452	0.5688	9.5349
chr22	51304566	34794057	0.6782	9.8147
chrMT	16571	29290	1.7675	6.1185
chrX	155270560	74257015	0.4782	8.0243

chrY	59373566	6716572	0.1131	2.8055

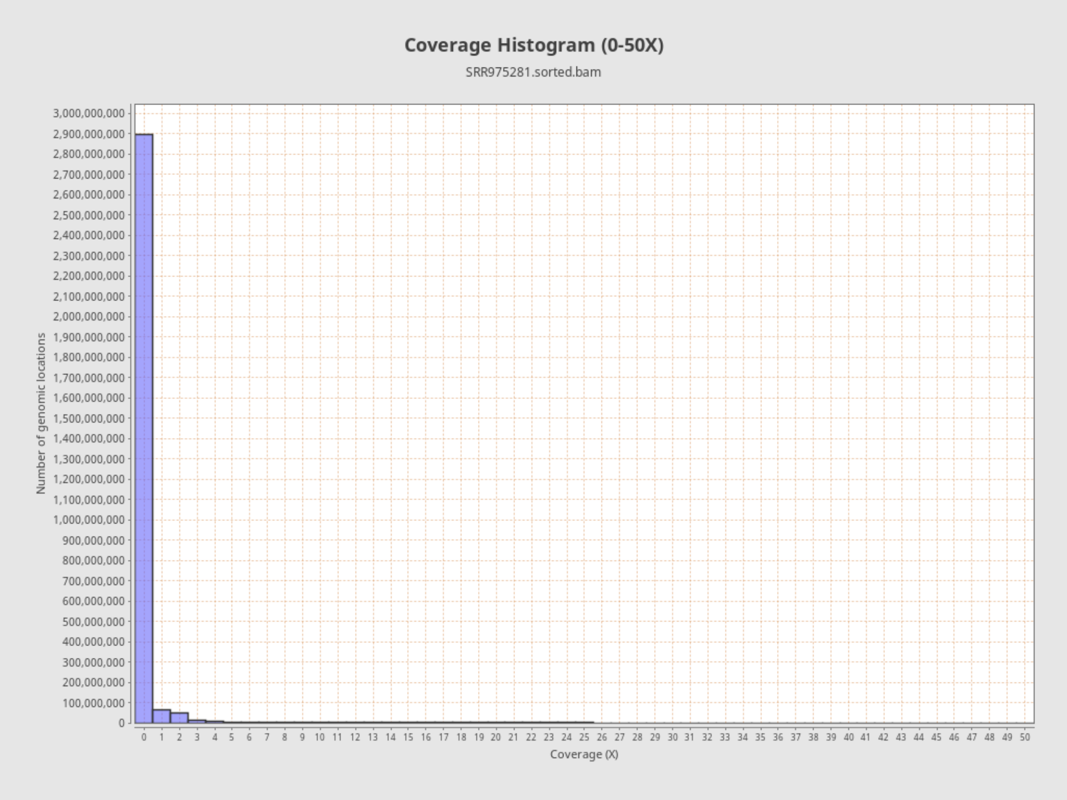
3. Results : Coverage across reference



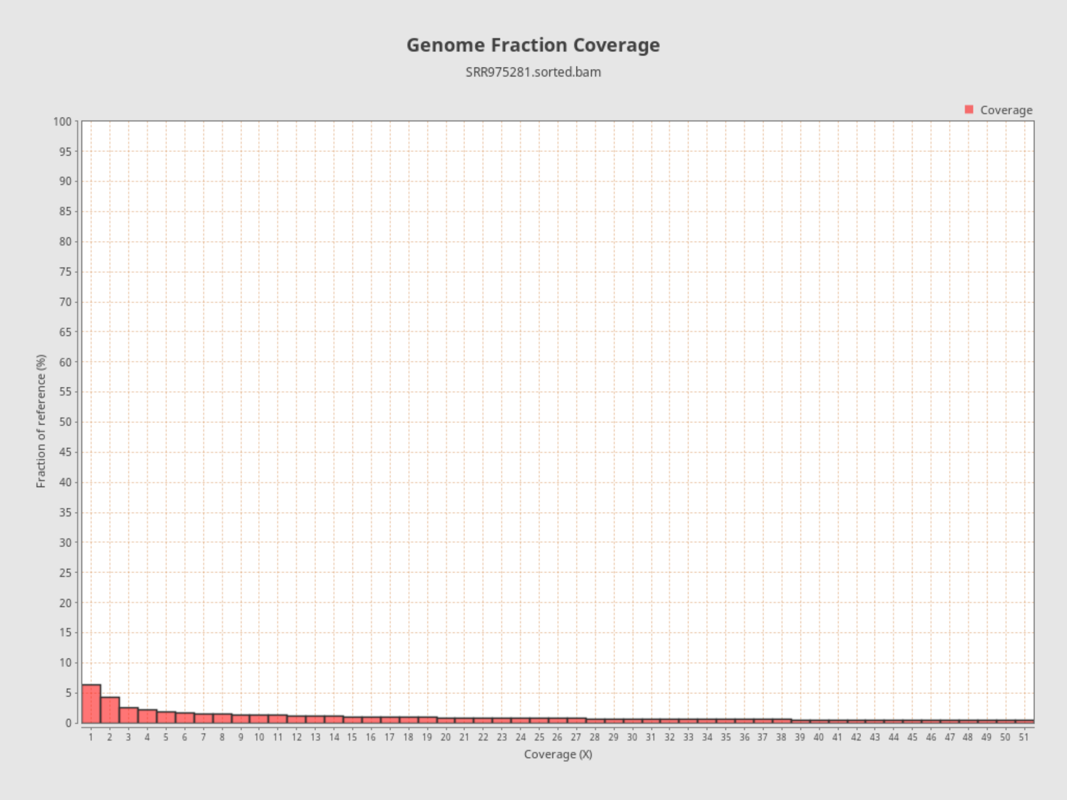
4. Results : Coverage Histogram



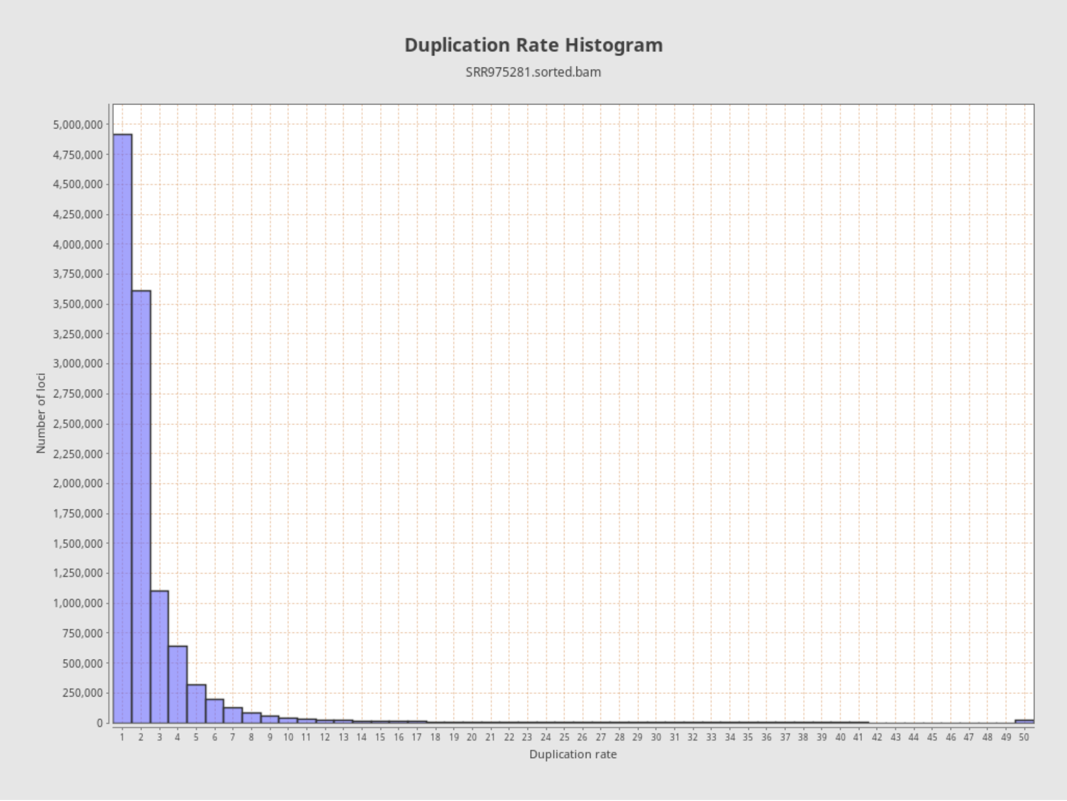
5. Results : Coverage Histogram (0-50X)



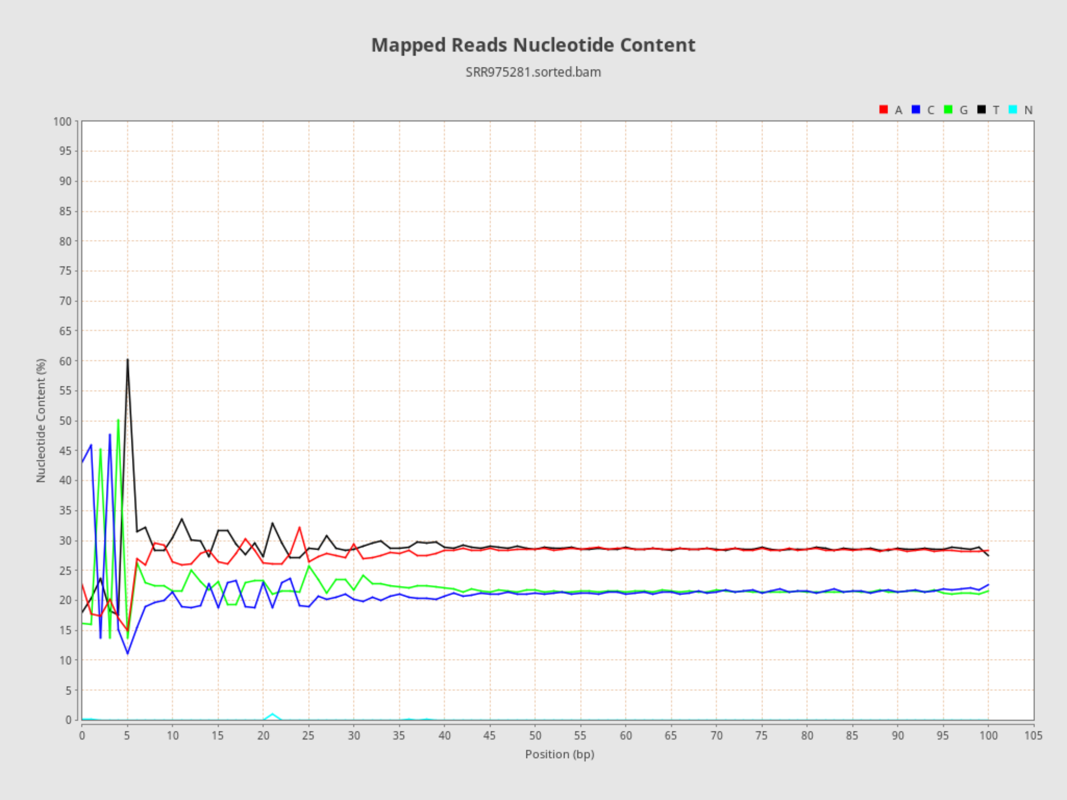
6. Results : Genome Fraction Coverage



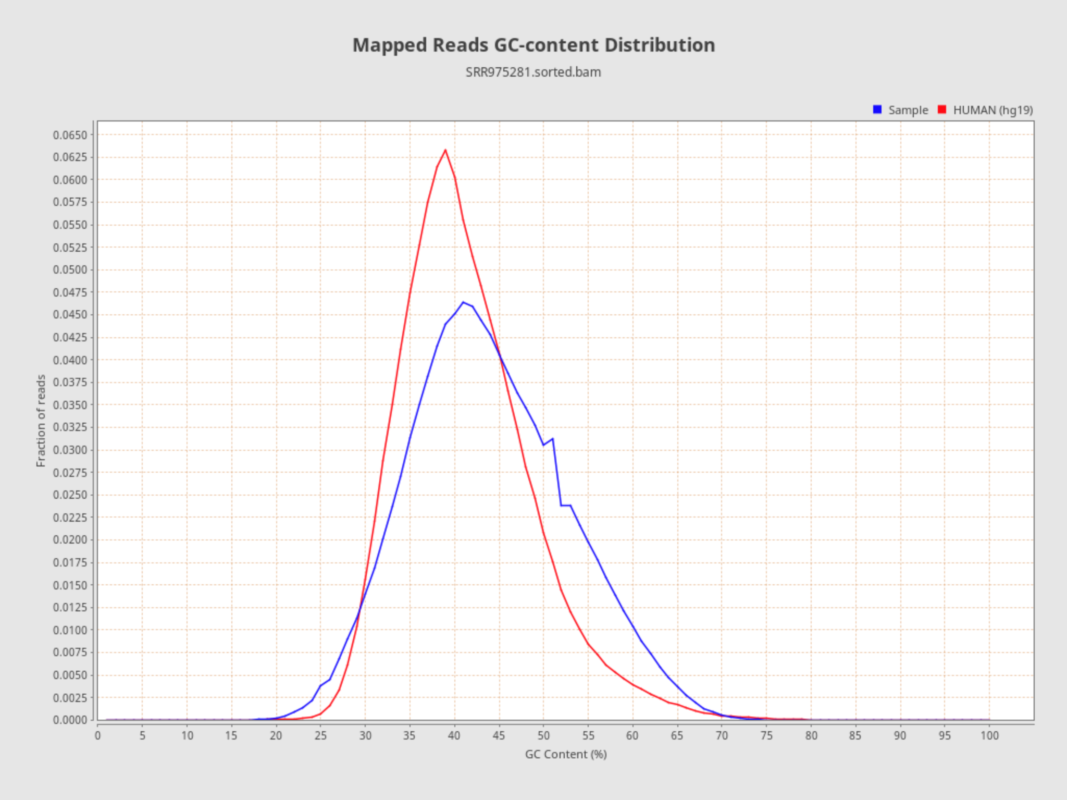
7. Results : Duplication Rate Histogram



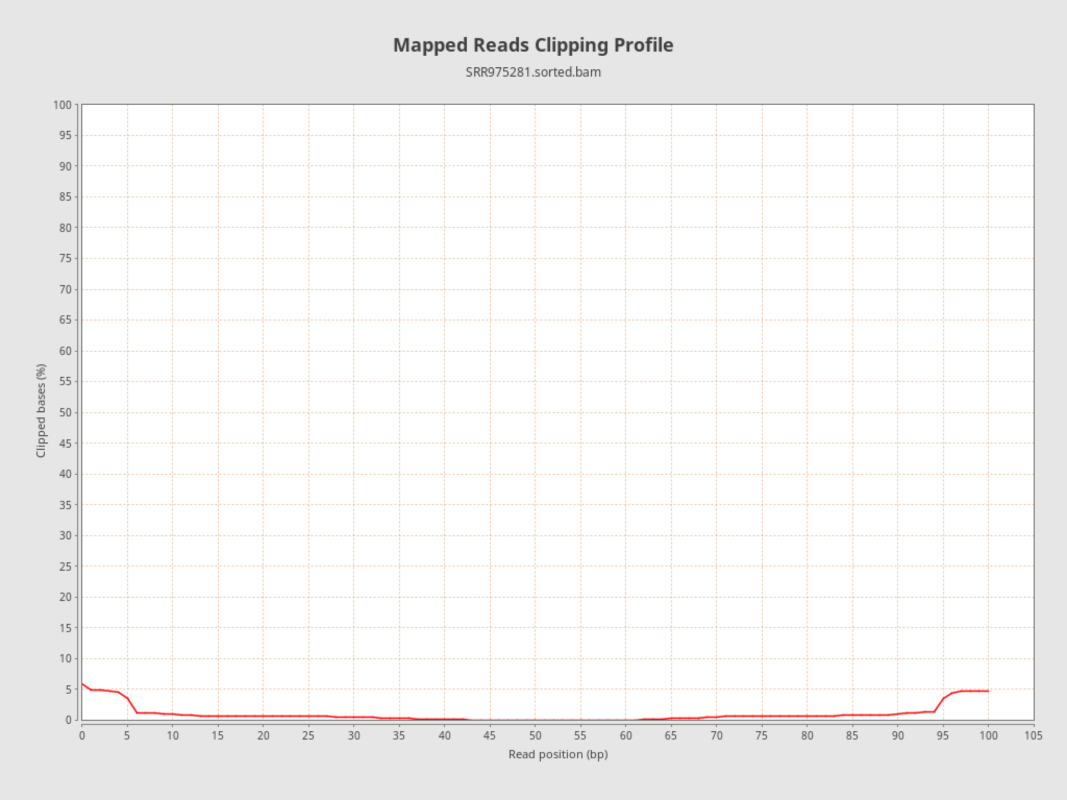
8. Results : Mapped Reads Nucleotide Content



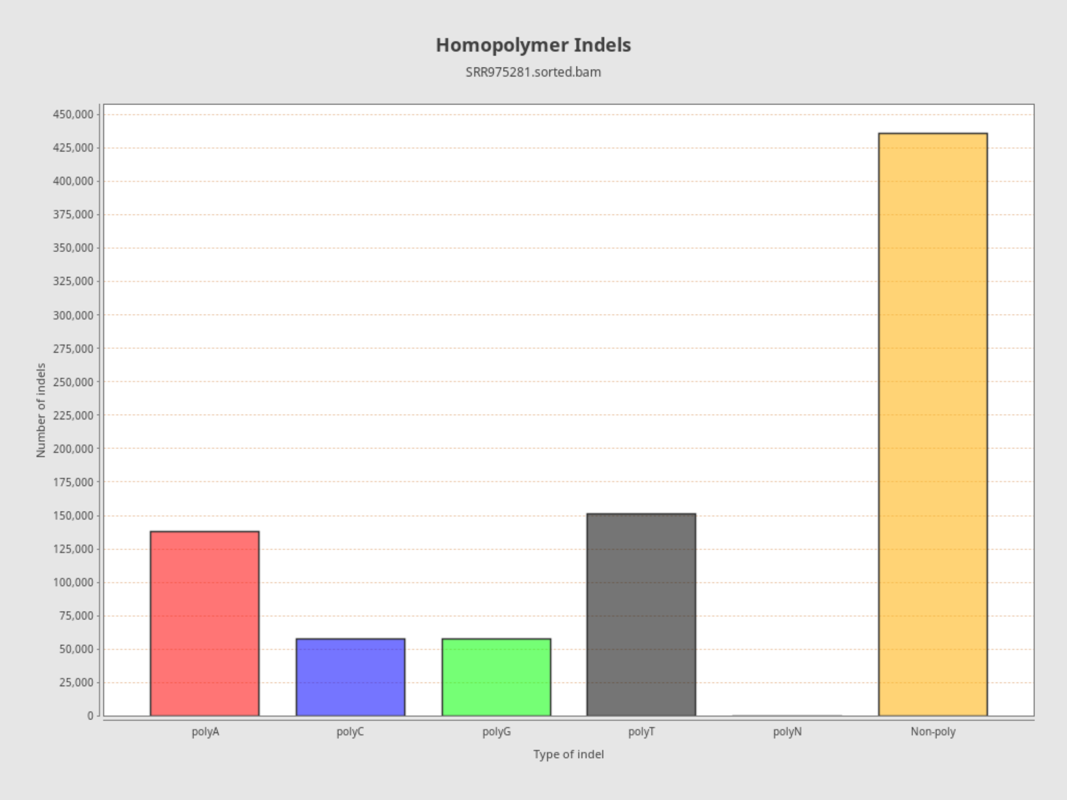
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

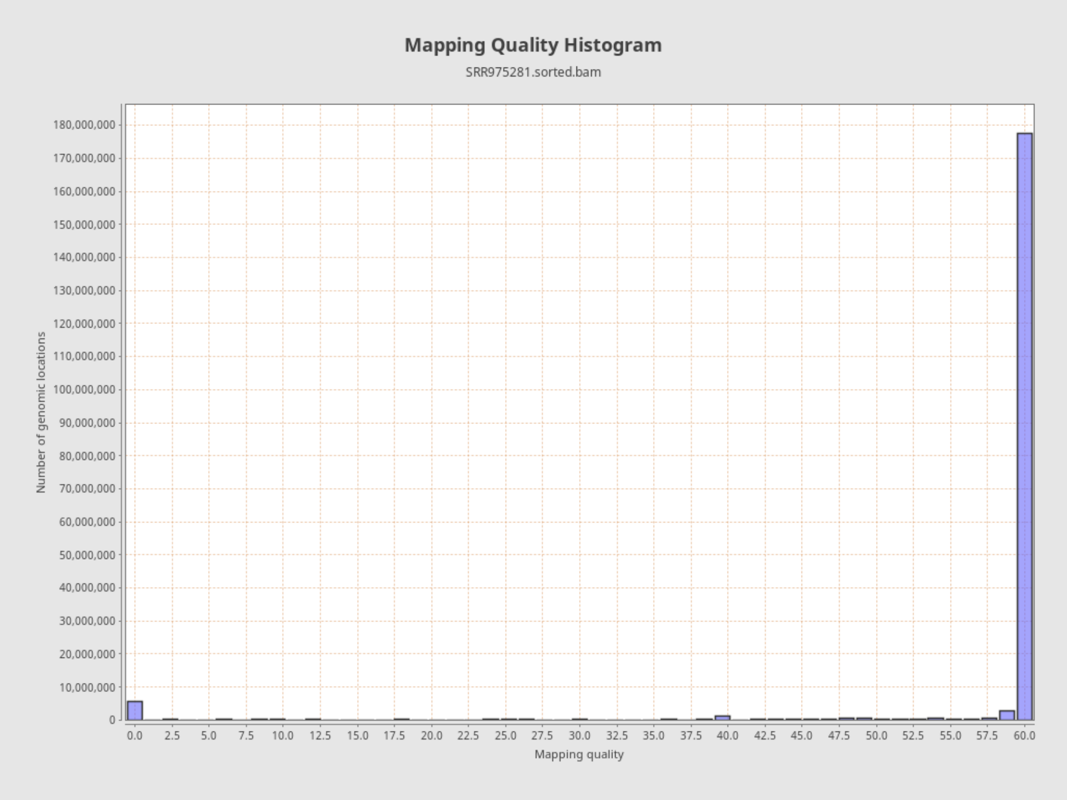


11. Results : Homopolymer Indels

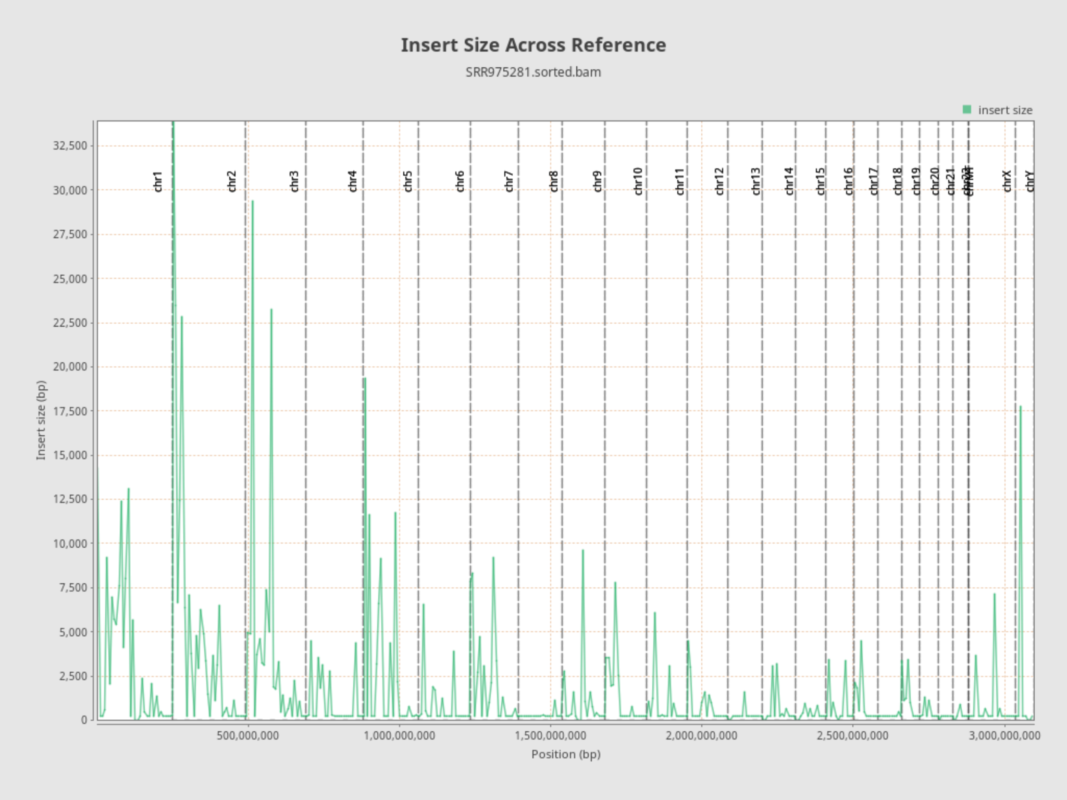


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram