Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 12:02:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975279.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_SRR975279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975279_1.fastq.gz SRR975279_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 12:02:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,656,372
Mapped reads	62,477,314 / 99.71%
Unmapped reads	179,058 / 0.29%
Mapped paired reads	62,477,314 / 99.71%
Mapped reads, first in pair	31,262,059 / 49.89%
Mapped reads, second in pair	31,215,255 / 49.82%
Mapped reads, both in pair	62,383,292 / 99.56%
Mapped reads, singletons	94,022 / 0.15%
Secondary alignments	0
Supplementary alignments	142,689 / 0.23%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	35,708,851 / 56.99%
Duplication rate	43.36%
Clipped reads	34,809,471 / 55.56%

2.2. ACGT Content

Number/percentage of A's	1,546,107,425 / 27.1%
Number/percentage of C's	1,235,724,495 / 21.66%
Number/percentage of T's	1,598,525,971 / 28.02%
Number/percentage of G's	1,324,841,260 / 23.22%
Number/percentage of N's	256,108 / 0%

GC Percentage	44.88%

2.3. Coverage

Mean	1.8436
Standard Deviation	22.7575

2.4. Mapping Quality

Mean Mapping Quality	55.83

2.5. Insert size

Mean	95,997.53
Standard Deviation	3,017,156.48
P25/Median/P75	149 / 186 / 235

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	30,105,980
Insertions	562,438
Mapped reads with at least one insertion	0.89%
Deletions	1,129,797
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.94%

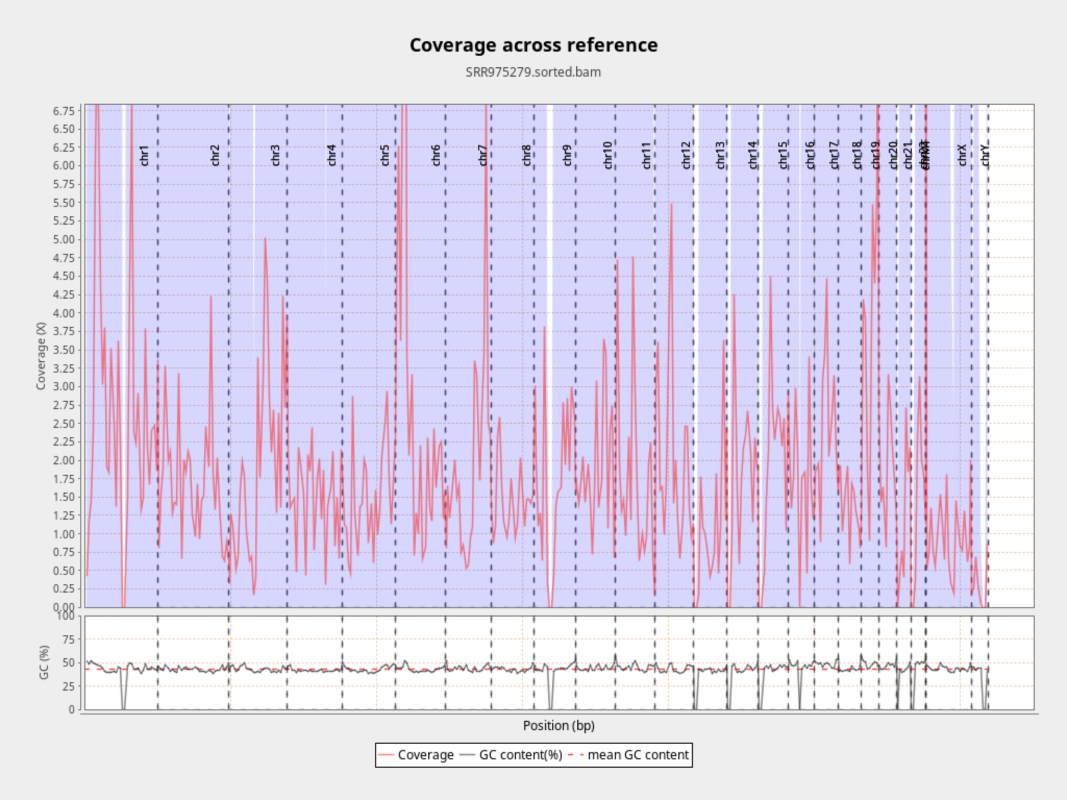
2.7. Chromosome stats

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

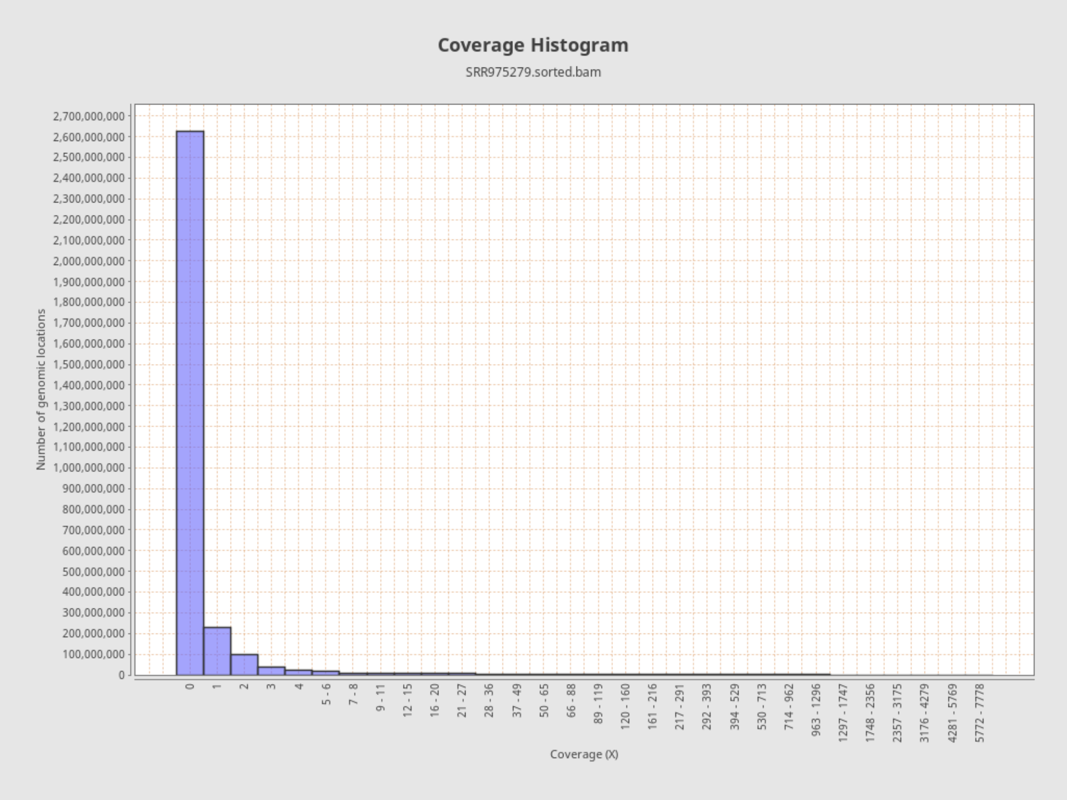
		bases	coverage	deviation
chr1	249250621	665158095	2.6686	28.5113
chr2	243199373	410241642	1.6869	20.5476
chr3	198022430	390091578	1.9699	24.4218
chr4	191154276	285215435	1.4921	20.5854
chr5	180915260	266886010	1.4752	18.378
chr6	171115067	520465253	3.0416	37.373
chr7	159138663	316549150	1.9891	25.0059
chr8	146364022	212507167	1.4519	18.2644
chr9	141213431	230343866	1.6312	20.0817
chr10	135534747	260306608	1.9206	22.9657
chr11	135006516	248051568	1.8373	21.225
chr12	133851895	280523595	2.0958	21.7882
chr13	115169878	118929173	1.0326	16.769
chr14	107349540	186327484	1.7357	20.4086
chr15	102531392	199180220	1.9426	22.0065
chr16	90354753	155039744	1.7159	19.3062
chr17	81195210	204072210	2.5134	24.5671
chr18	78077248	109042373	1.3966	19.1539
chr19	59128983	226980679	3.8387	34.1065
chr20	63025520	124662369	1.978	23.0574
chr21	48129895	58324643	1.2118	16.7277
chr22	51304566	76703040	1.4951	18.0042
chrMT	16571	201045	12.1323	20.7267
chrX	155270560	143828580	0.9263	12.3292

chrY	59373566	17611436	0.2966	6.3295

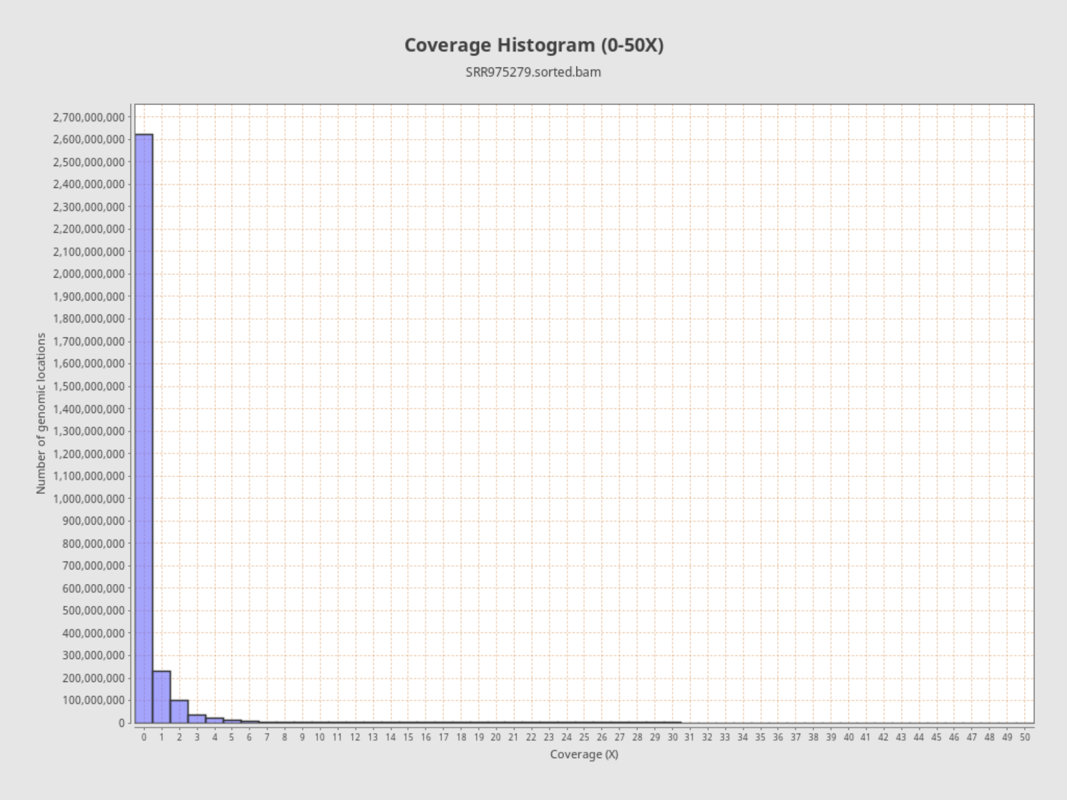
3. Results : Coverage across reference



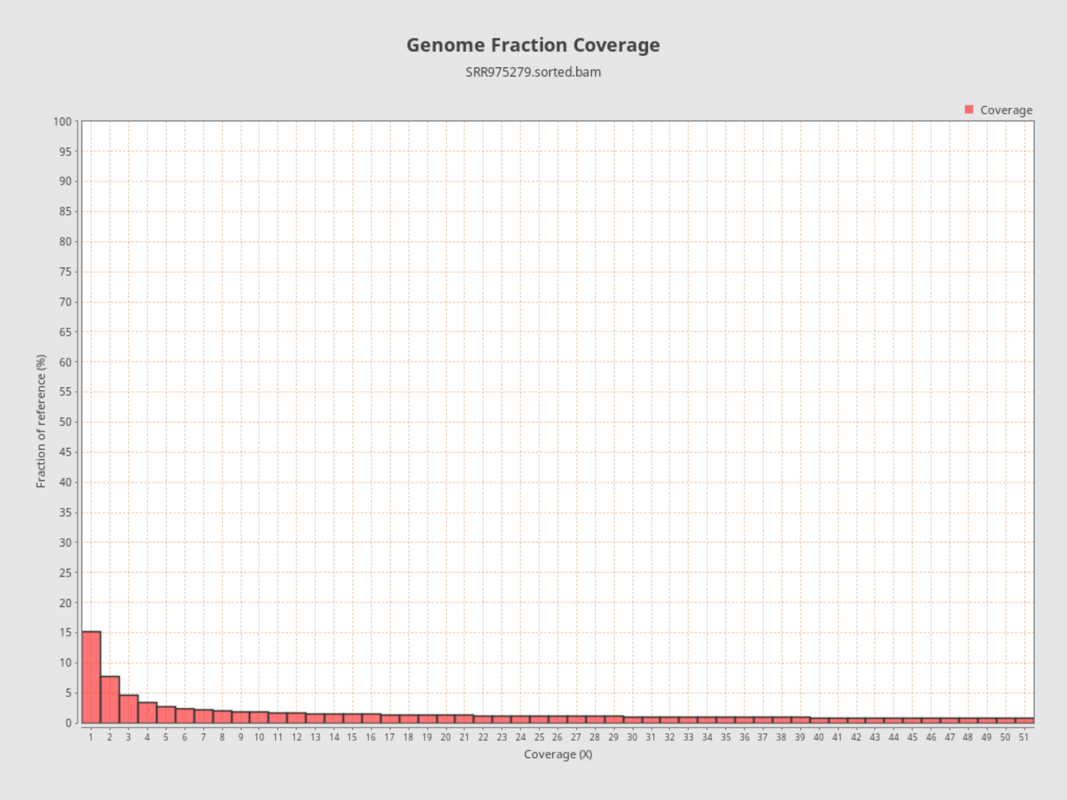
4. Results : Coverage Histogram



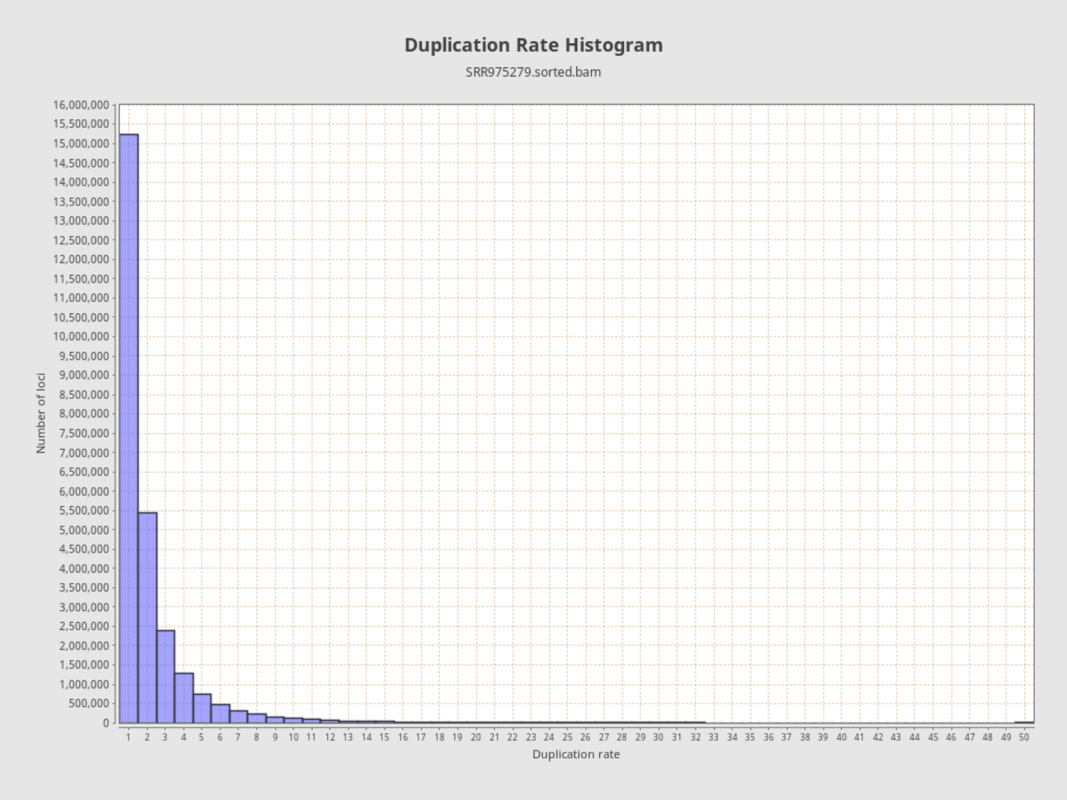
5. Results : Coverage Histogram (0-50X)



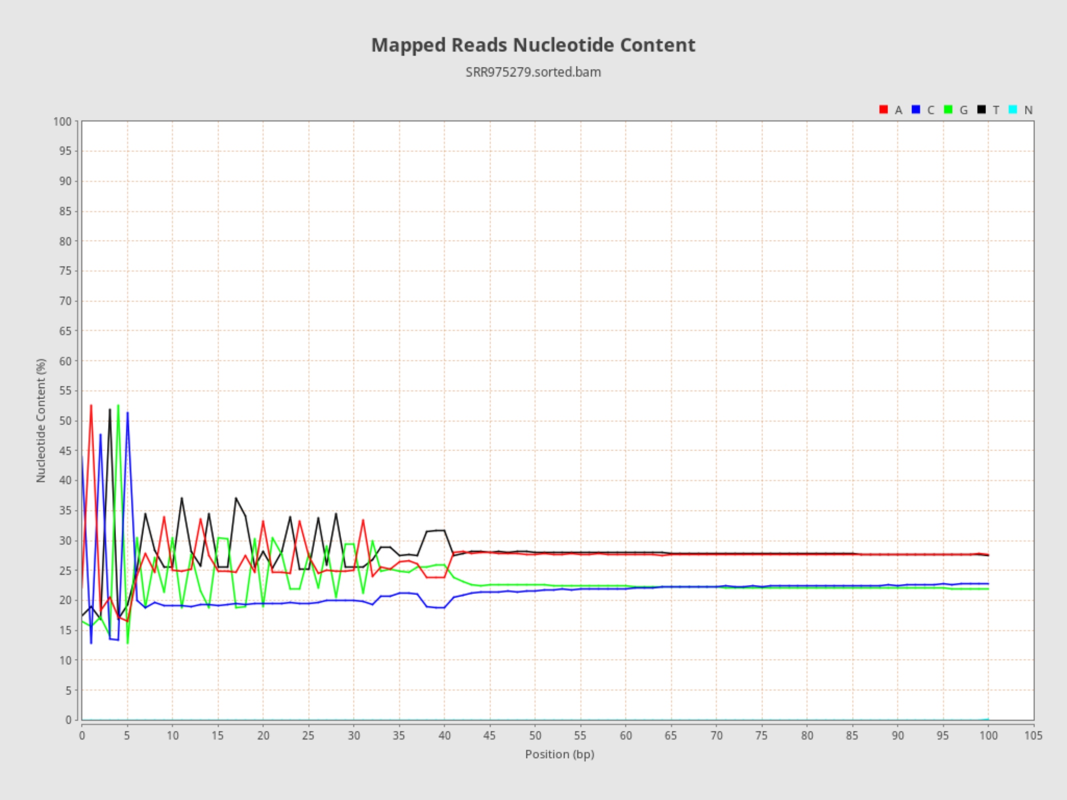
6. Results : Genome Fraction Coverage



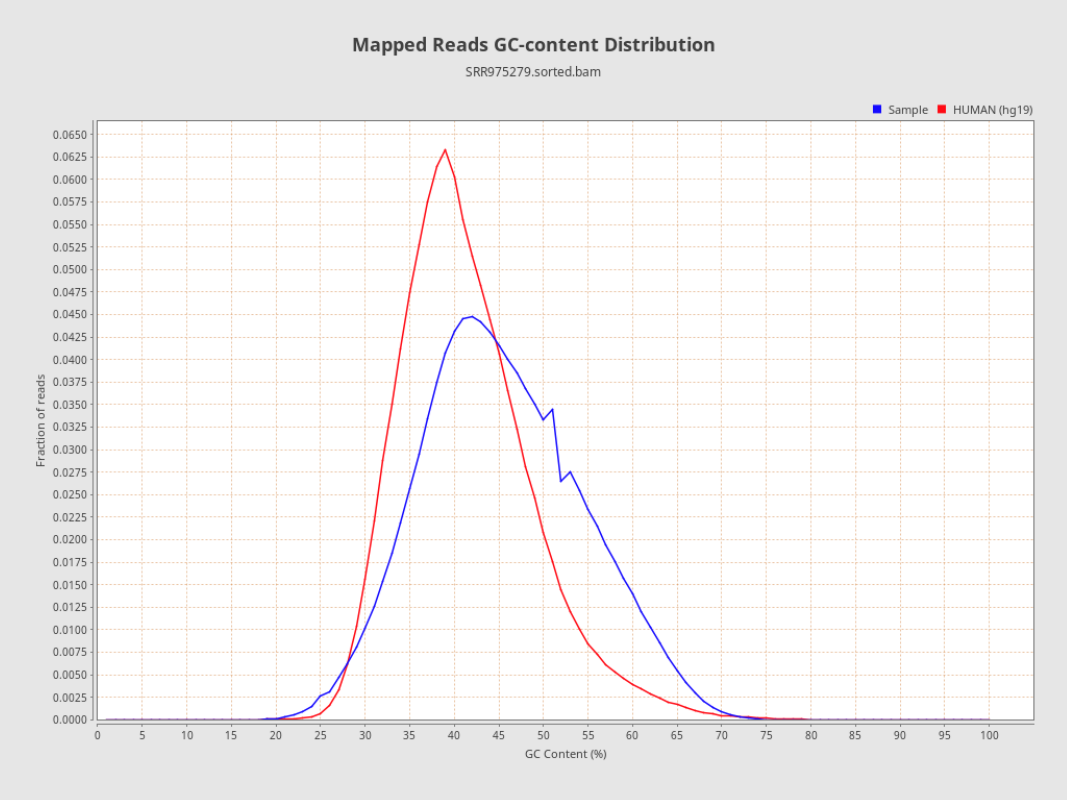
7. Results : Duplication Rate Histogram



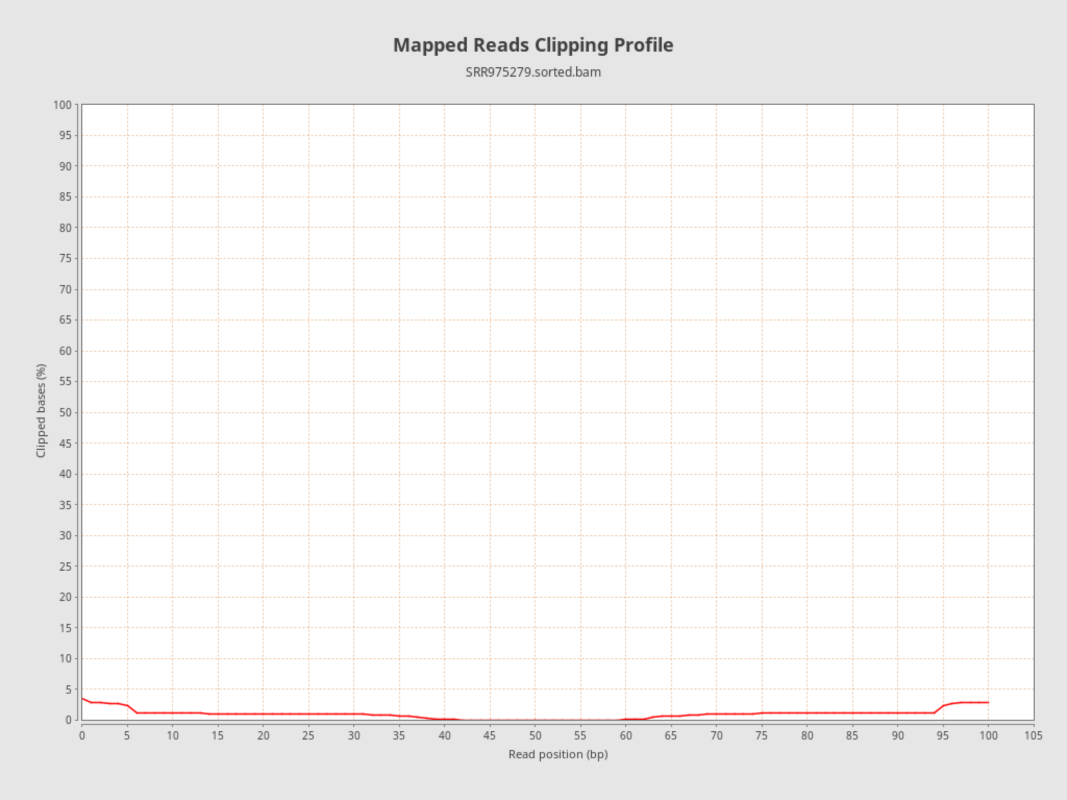
8. Results : Mapped Reads Nucleotide Content



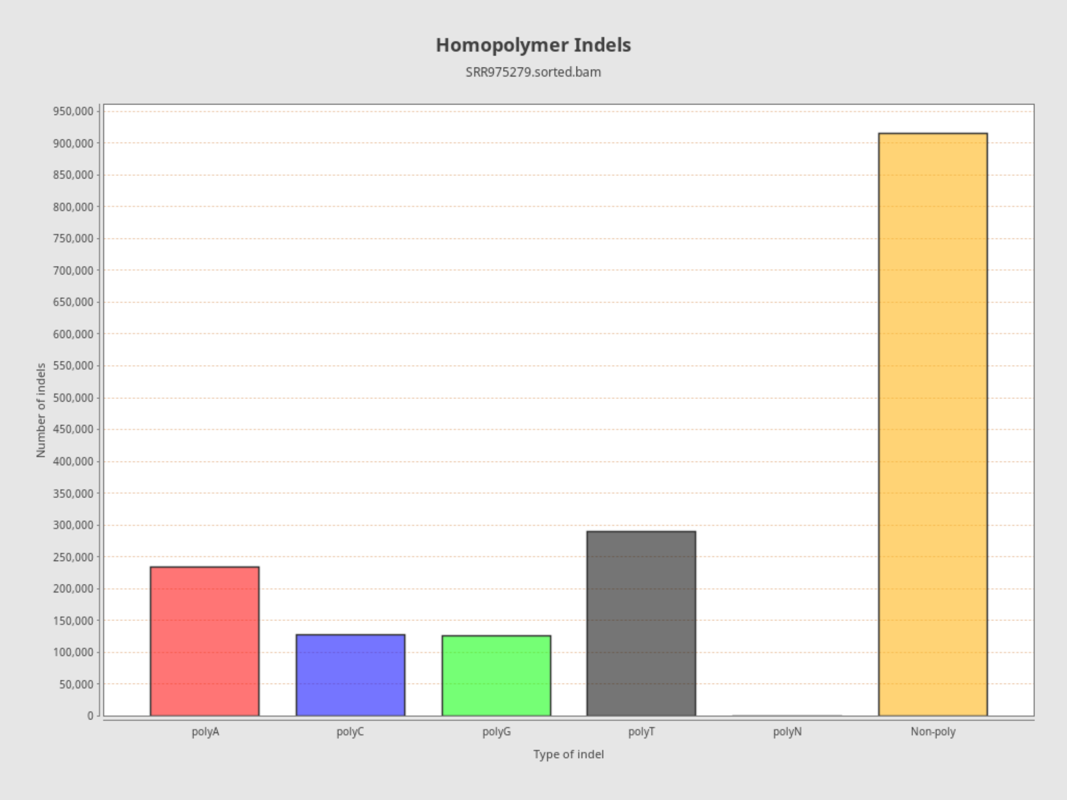
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

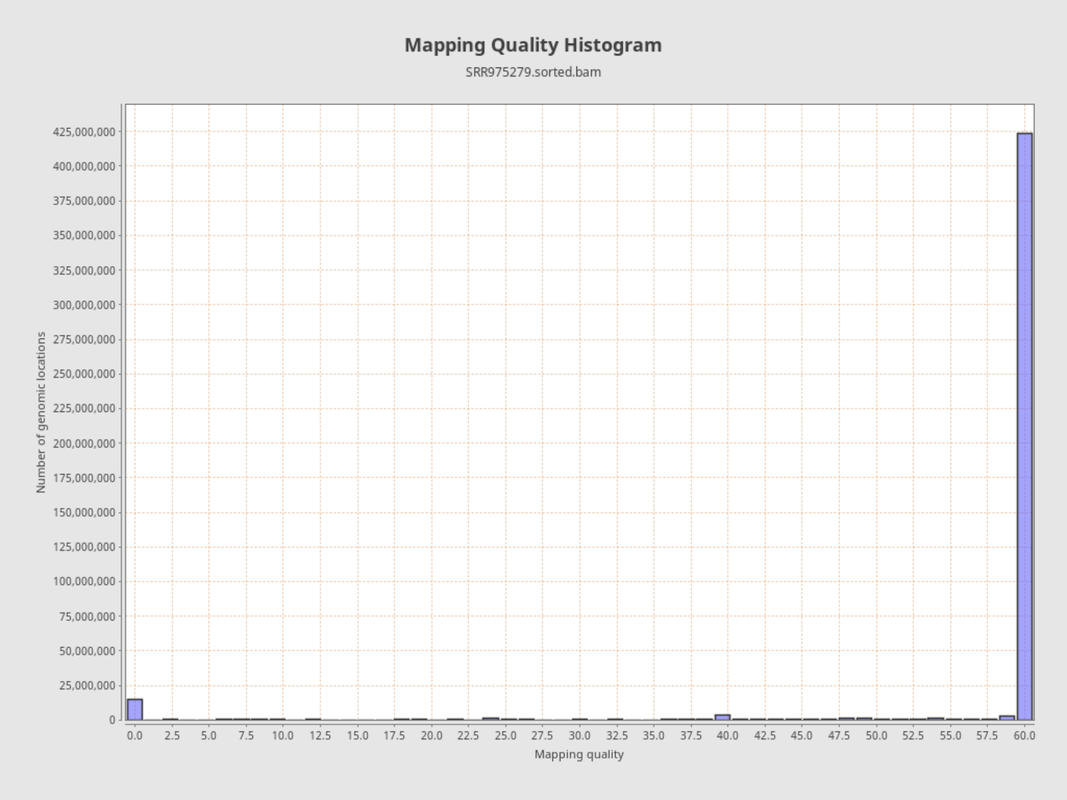


11. Results : Homopolymer Indels

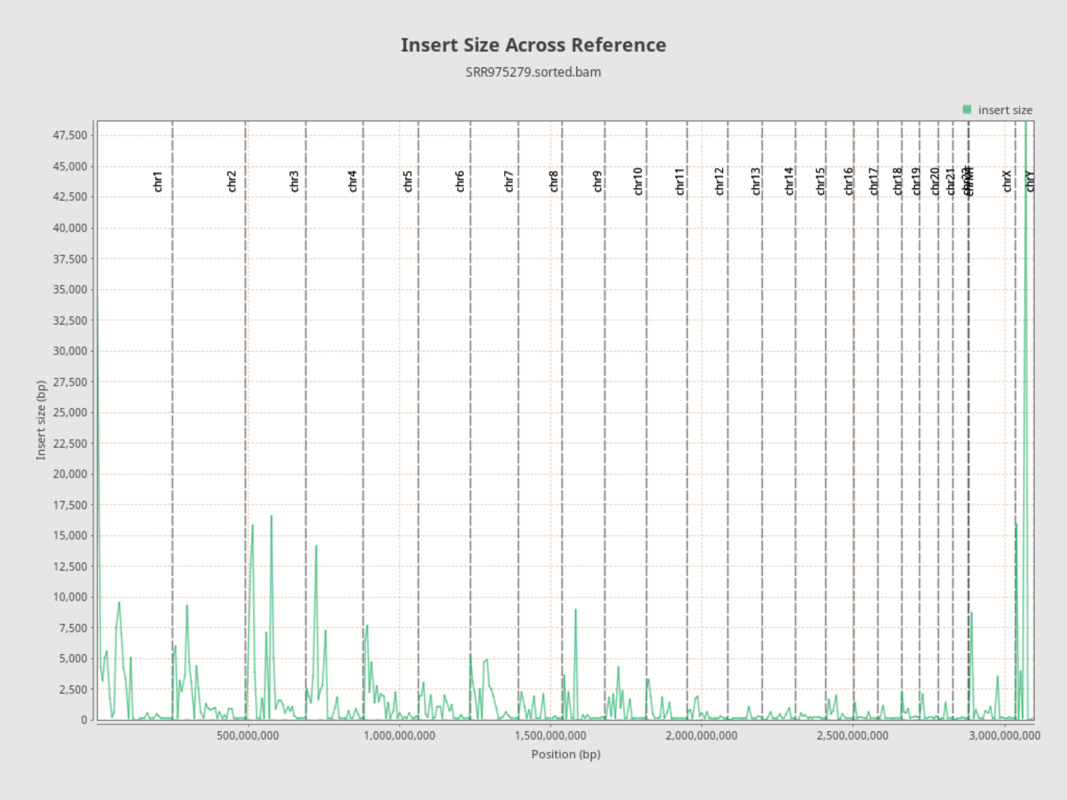


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram