Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 04:49:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975324.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_SRR975324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975324_1.fastq.gz SRR975324_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 04:49:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,335,530
Mapped reads	4,289,848 / 98.95%
Unmapped reads	45,682 / 1.05%
Mapped paired reads	4,289,848 / 98.95%
Mapped reads, first in pair	2,144,227 / 49.46%
Mapped reads, second in pair	2,145,621 / 49.49%
Mapped reads, both in pair	4,273,656 / 98.57%
Mapped reads, singletons	16,192 / 0.37%
Secondary alignments	0
Supplementary alignments	23,418 / 0.54%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	333,323 / 7.69%
Duplication rate	3.36%
Clipped reads	2,546,860 / 58.74%

2.2. ACGT Content

Number/percentage of A's	118,664,171 / 29.37%
Number/percentage of C's	79,873,855 / 19.77%
Number/percentage of T's	121,992,672 / 30.19%
Number/percentage of G's	83,534,451 / 20.67%
Number/percentage of N's	8,685 / 0%

GC Percentage	40.44%

2.3. Coverage

Mean	0.1306
Standard Deviation	2.7553

2.4. Mapping Quality

Mean Mapping Quality	52.72

2.5. Insert size

Mean	76,447.19
Standard Deviation	2,587,678.83
P25/Median/P75	143 / 176 / 223

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	3,257,362
Insertions	67,857
Mapped reads with at least one insertion	1.55%
Deletions	136,854
Mapped reads with at least one deletion	3.12%
Homopolymer indels	46.85%

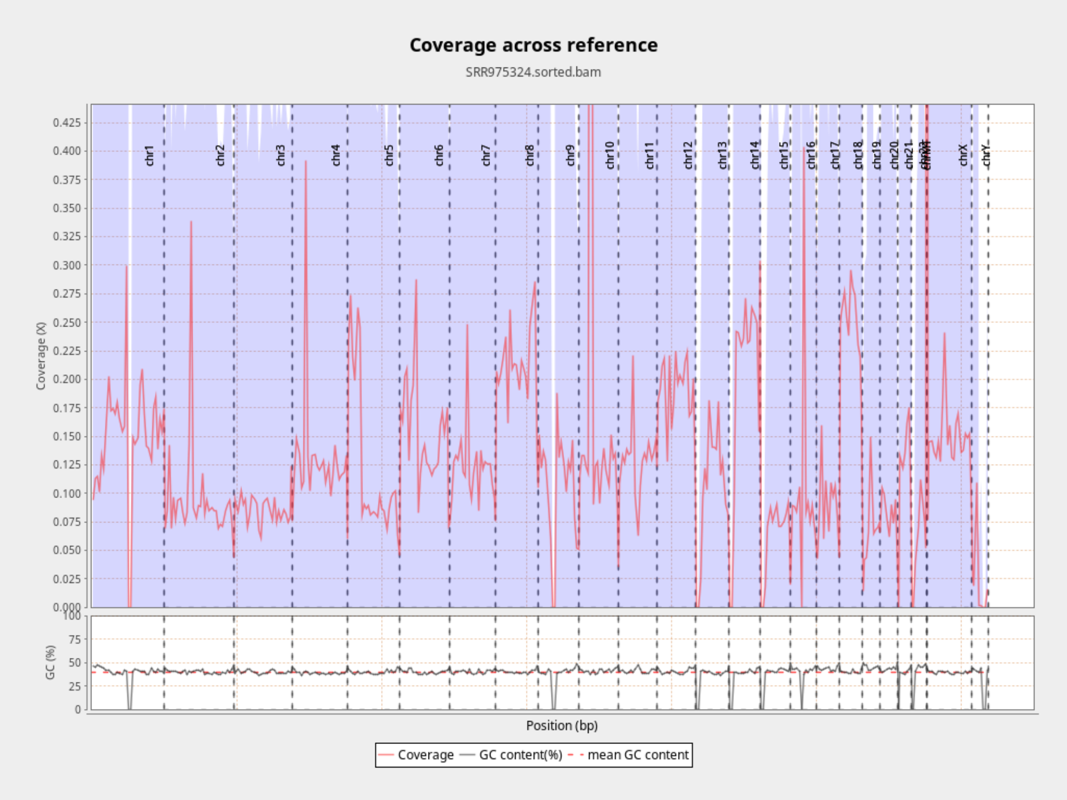
2.7. Chromosome stats

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

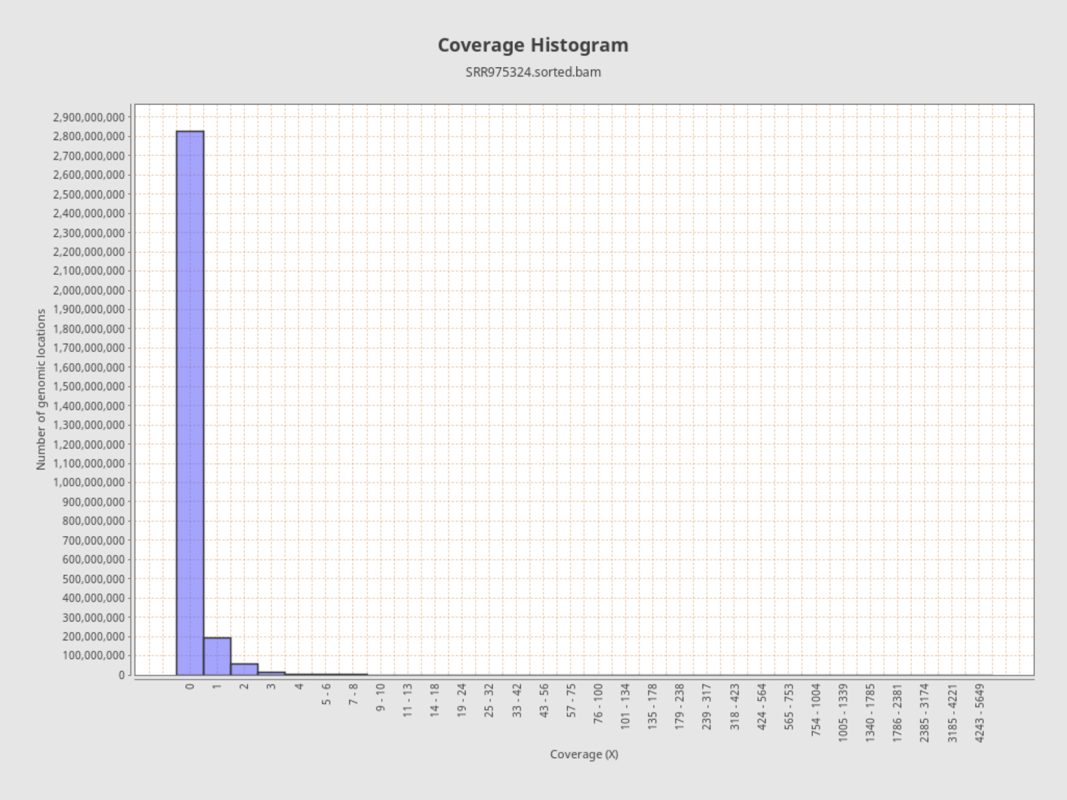
		bases	coverage	deviation
chr1	249250621	37041997	0.1486	2.2178
chr2	243199373	23203666	0.0954	1.6111
chr3	198022430	16872464	0.0852	0.7734
chr4	191154276	25141061	0.1315	1.5739
chr5	180915260	22548233	0.1246	0.4616
chr6	171115067	26256879	0.1534	1.7696
chr7	159138663	19642679	0.1234	2.2745
chr8	146364022	31245559	0.2135	0.8564
chr9	141213431	14890181	0.1054	1.9972
chr10	135534747	25966874	0.1916	11.1787
chr11	135006516	17327148	0.1283	1.7753
chr12	133851895	25599228	0.1913	0.5755
chr13	115169878	12058294	0.1047	0.4088
chr14	107349540	21158231	0.1971	0.6114
chr15	102531392	6522201	0.0636	0.3132
chr16	90354753	9192453	0.1017	2.0052
chr17	81195210	7292673	0.0898	1.4332
chr18	78077248	19795940	0.2535	2.7948
chr19	59128983	4100496	0.0693	1.1334
chr20	63025520	5110531	0.0811	0.5163
chr21	48129895	5993327	0.1245	0.7046
chr22	51304566	3122834	0.0609	0.3213
chrMT	16571	93739	5.6568	5.3146
chrX	155270560	22854853	0.1472	0.8977

chrY	59373566	1279865	0.0216	1.3854

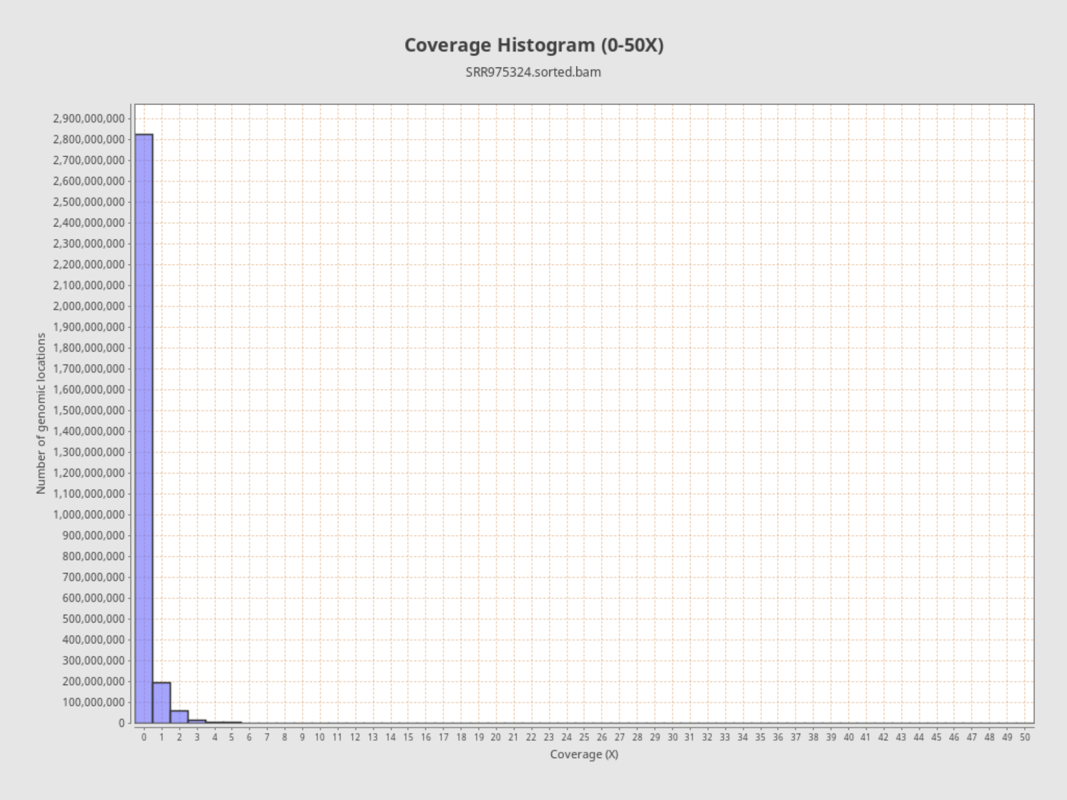
3. Results : Coverage across reference



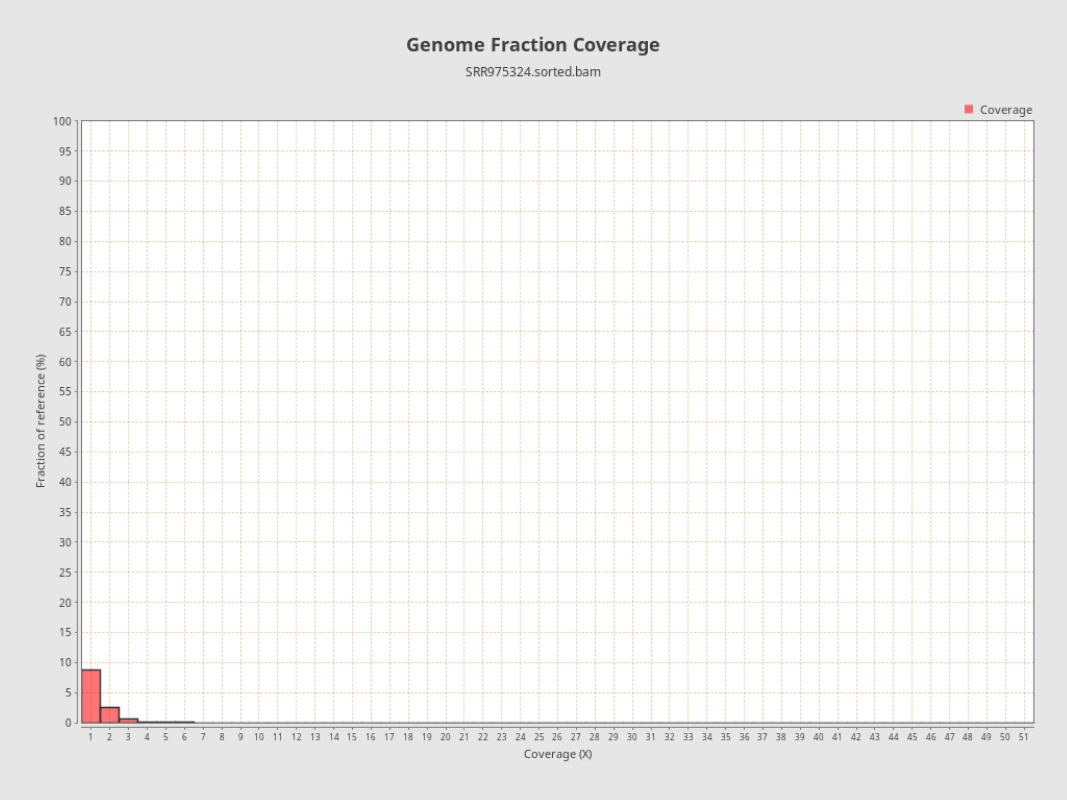
4. Results : Coverage Histogram



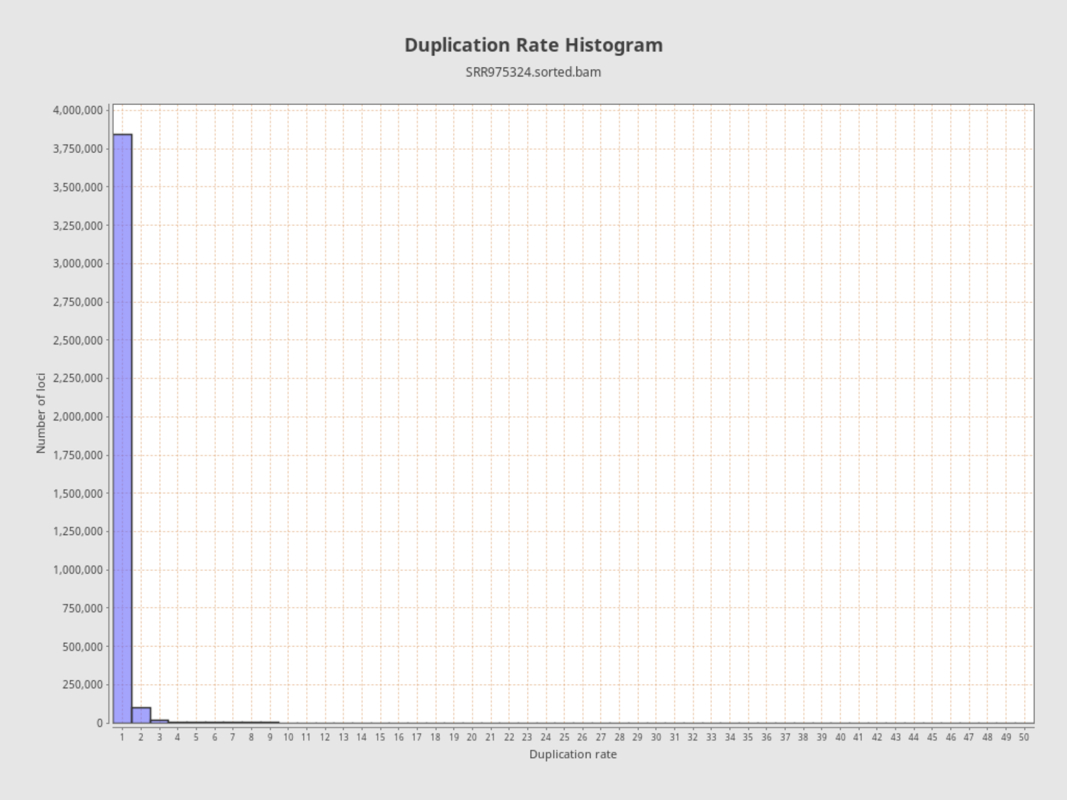
5. Results : Coverage Histogram (0-50X)



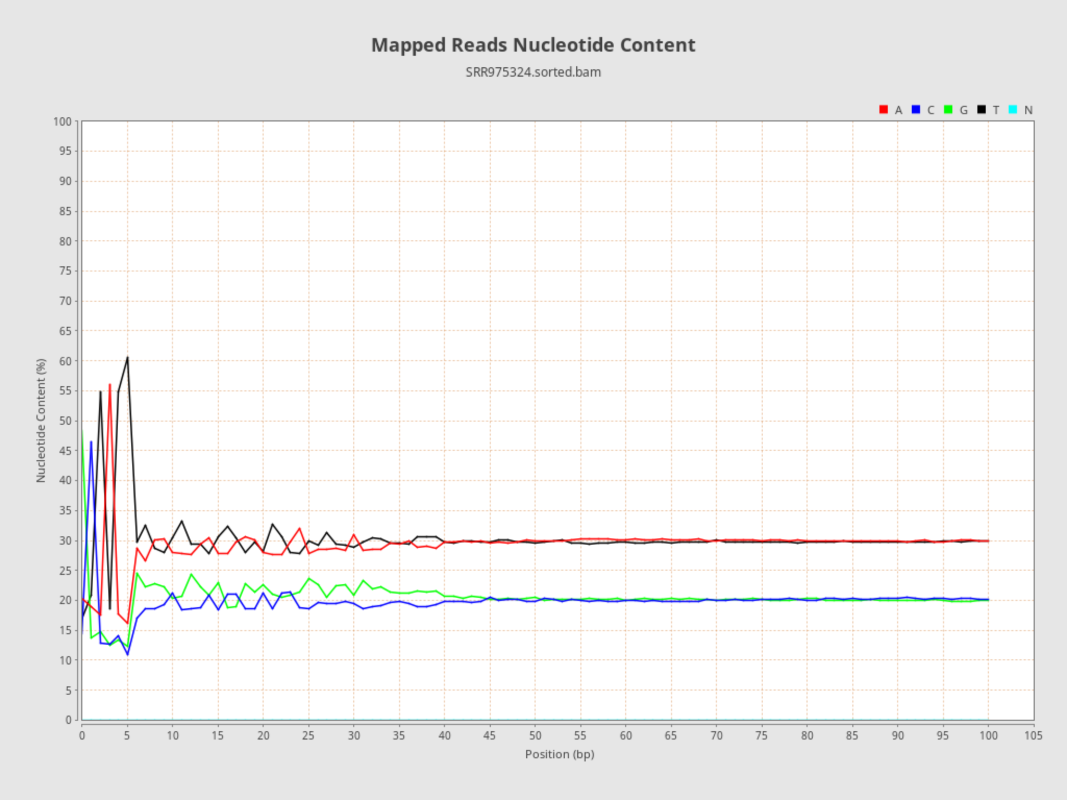
6. Results : Genome Fraction Coverage



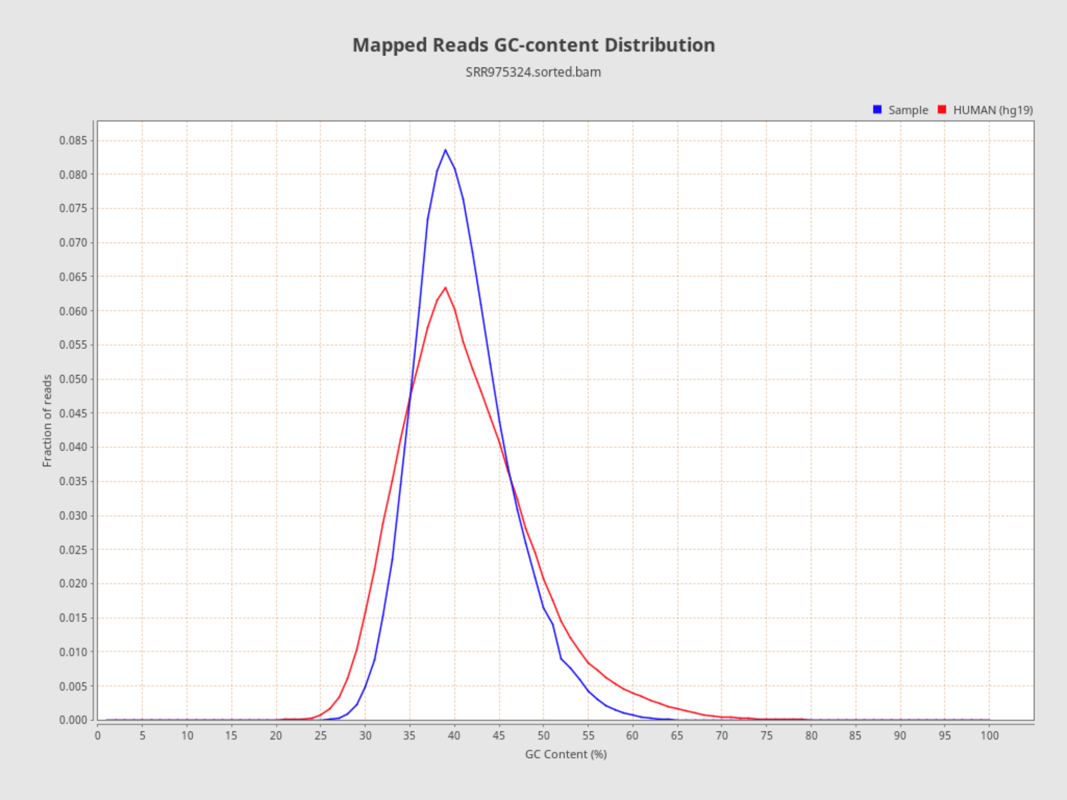
7. Results : Duplication Rate Histogram



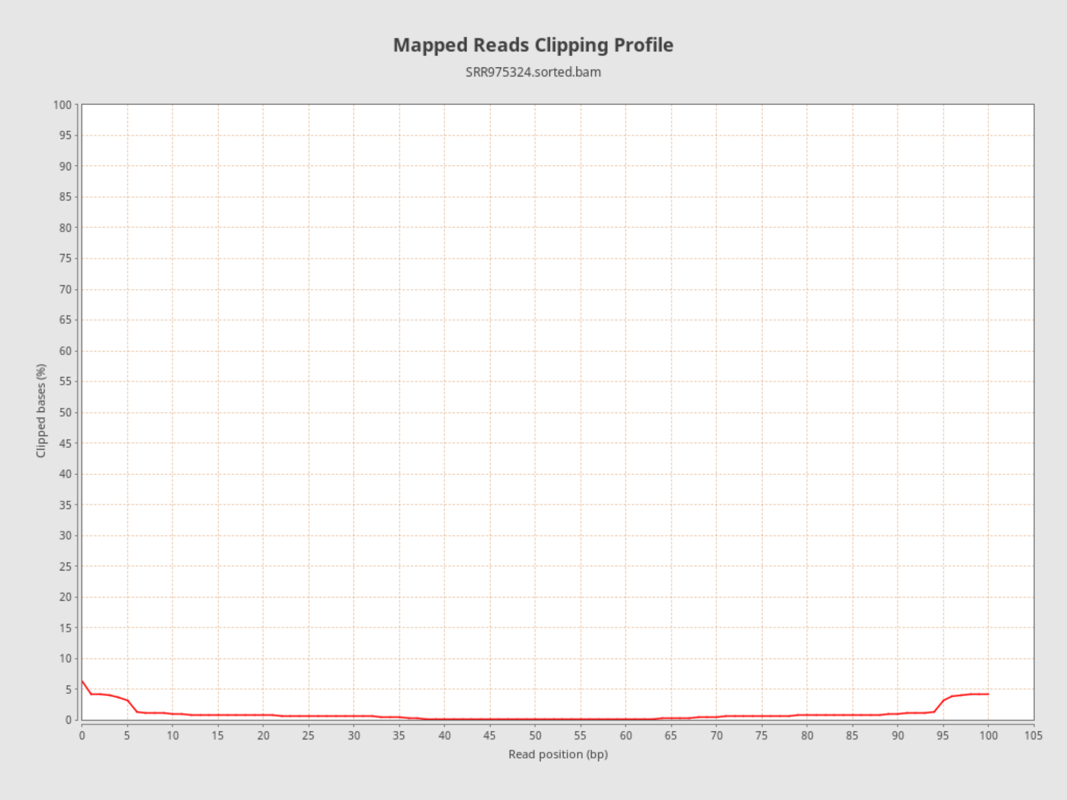
8. Results : Mapped Reads Nucleotide Content



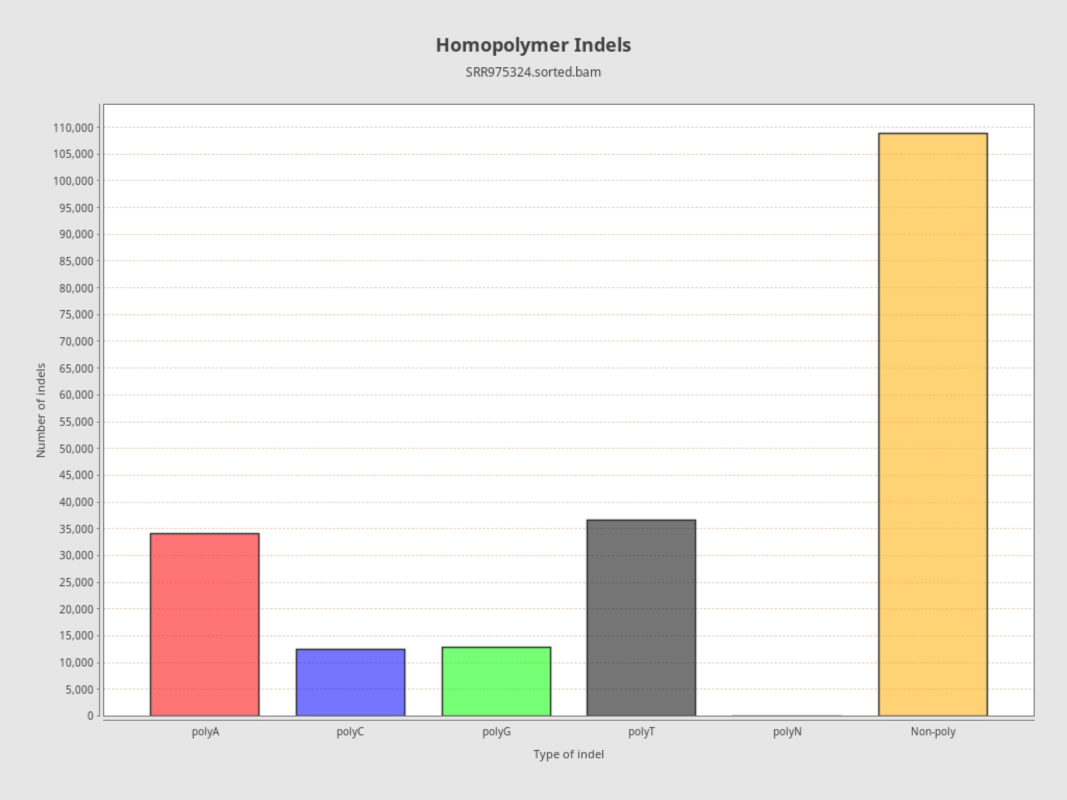
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

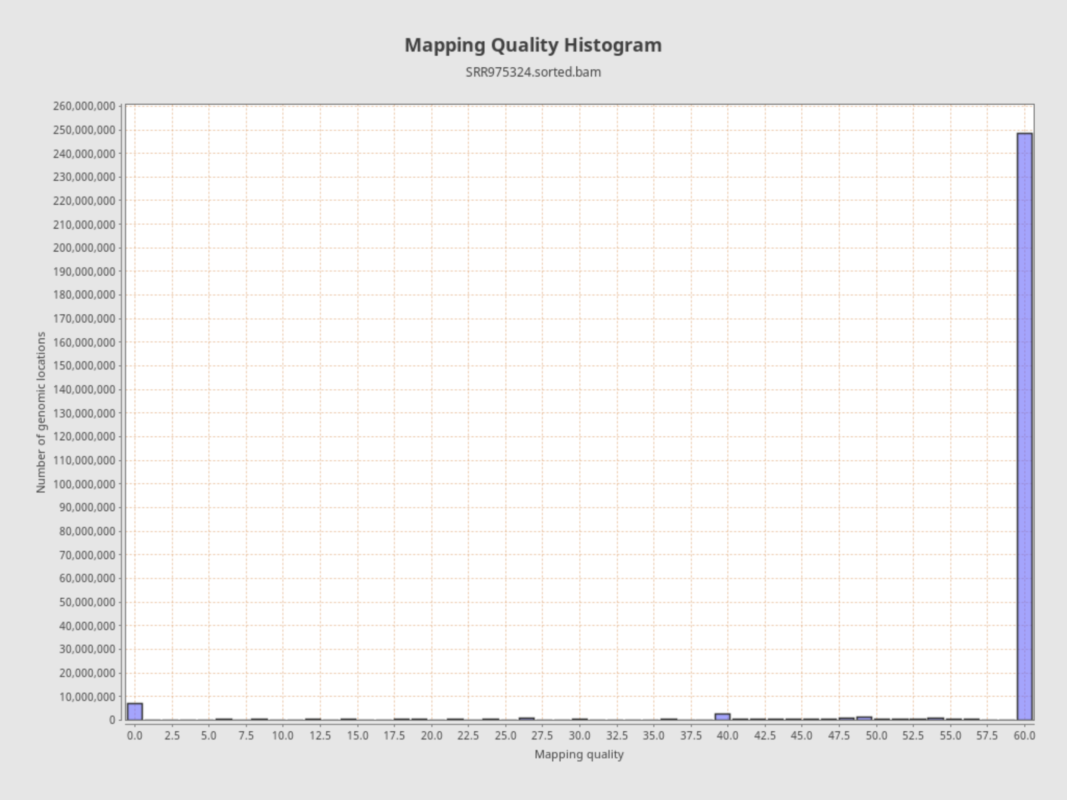


11. Results : Homopolymer Indels

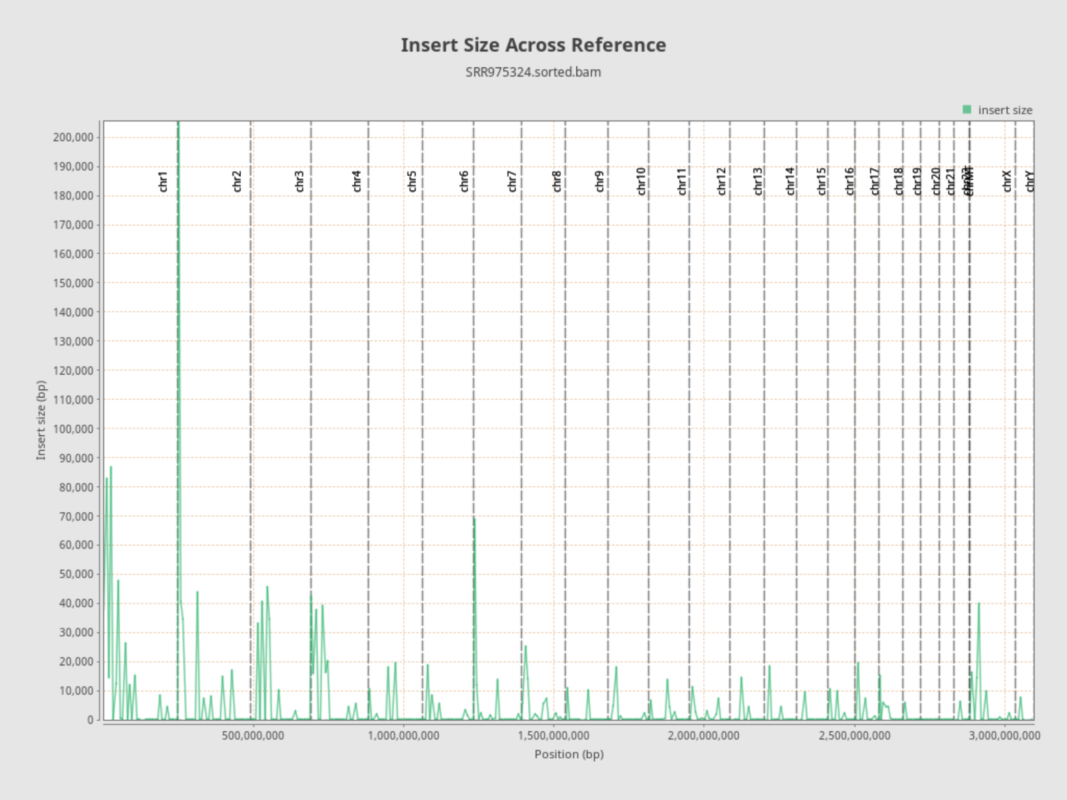


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram