Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 06:19:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975336.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_SRR975336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975336_1.fastq.gz SRR975336_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 06:19:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,285,660
Mapped reads	4,186,676 / 97.69%
Unmapped reads	98,984 / 2.31%
Mapped paired reads	4,186,676 / 97.69%
Mapped reads, first in pair	2,091,305 / 48.8%
Mapped reads, second in pair	2,095,371 / 48.89%
Mapped reads, both in pair	4,154,014 / 96.93%
Mapped reads, singletons	32,662 / 0.76%
Secondary alignments	0
Supplementary alignments	24,502 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	265,789 / 6.2%
Duplication rate	2.9%
Clipped reads	2,579,141 / 60.18%

2.2. ACGT Content

Number/percentage of A's	112,379,668 / 29.52%
Number/percentage of C's	72,170,003 / 18.96%
Number/percentage of T's	116,719,643 / 30.66%
Number/percentage of G's	79,454,023 / 20.87%
Number/percentage of N's	7,427 / 0%

GC Percentage	39.82%

2.3. Coverage

Mean	0.1231
Standard Deviation	1.582

2.4. Mapping Quality

Mean Mapping Quality	52.58

2.5. Insert size

Mean	80,651.27
Standard Deviation	2,677,383.33
P25/Median/P75	137 / 170 / 217

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	2,977,032
Insertions	75,462
Mapped reads with at least one insertion	1.75%
Deletions	128,738
Mapped reads with at least one deletion	3%
Homopolymer indels	43.75%

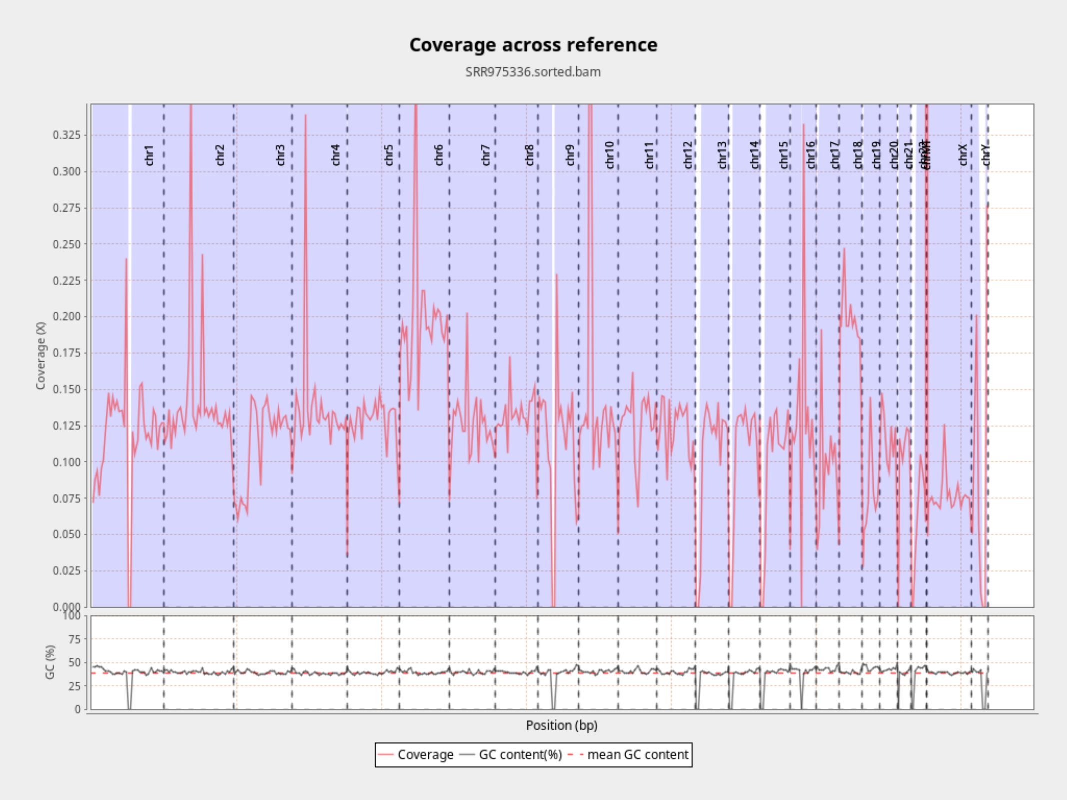
2.7. Chromosome stats

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

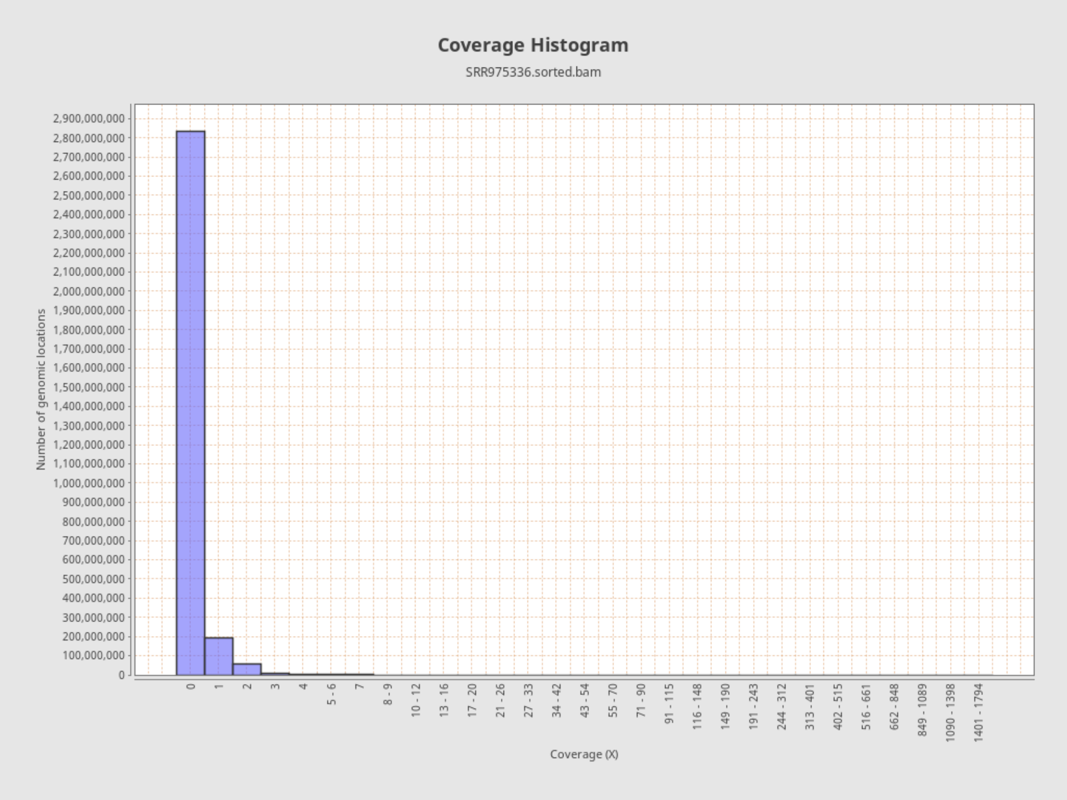
		bases	coverage	deviation
chr1	249250621	29087687	0.1167	1.805
chr2	243199373	34110636	0.1403	1.9663
chr3	198022430	22266828	0.1124	0.4489
chr4	191154276	26161780	0.1369	1.3856
chr5	180915260	23311149	0.1289	0.4928
chr6	171115067	33846455	0.1978	2.2274
chr7	159138663	19912655	0.1251	1.528
chr8	146364022	19093566	0.1305	0.6686
chr9	141213431	16008526	0.1134	2.5057
chr10	135534747	19951462	0.1472	3.4006
chr11	135006516	17145248	0.127	1.0544
chr12	133851895	16360008	0.1222	0.4499
chr13	115169878	11887500	0.1032	0.4026
chr14	107349540	10918884	0.1017	0.4906
chr15	102531392	9953389	0.0971	0.3926
chr16	90354753	11309835	0.1252	1.7352
chr17	81195210	7657727	0.0943	1.6432
chr18	78077248	15375976	0.1969	2.6378
chr19	59128983	4496605	0.076	1.0576
chr20	63025520	7130941	0.1131	0.5457
chr21	48129895	4810019	0.0999	0.6568
chr22	51304566	3154475	0.0615	0.3903
chrMT	16571	73748	4.4504	3.8977
chrX	155270560	11767702	0.0758	0.5773

chrY	59373566	5178101	0.0872	2.4751

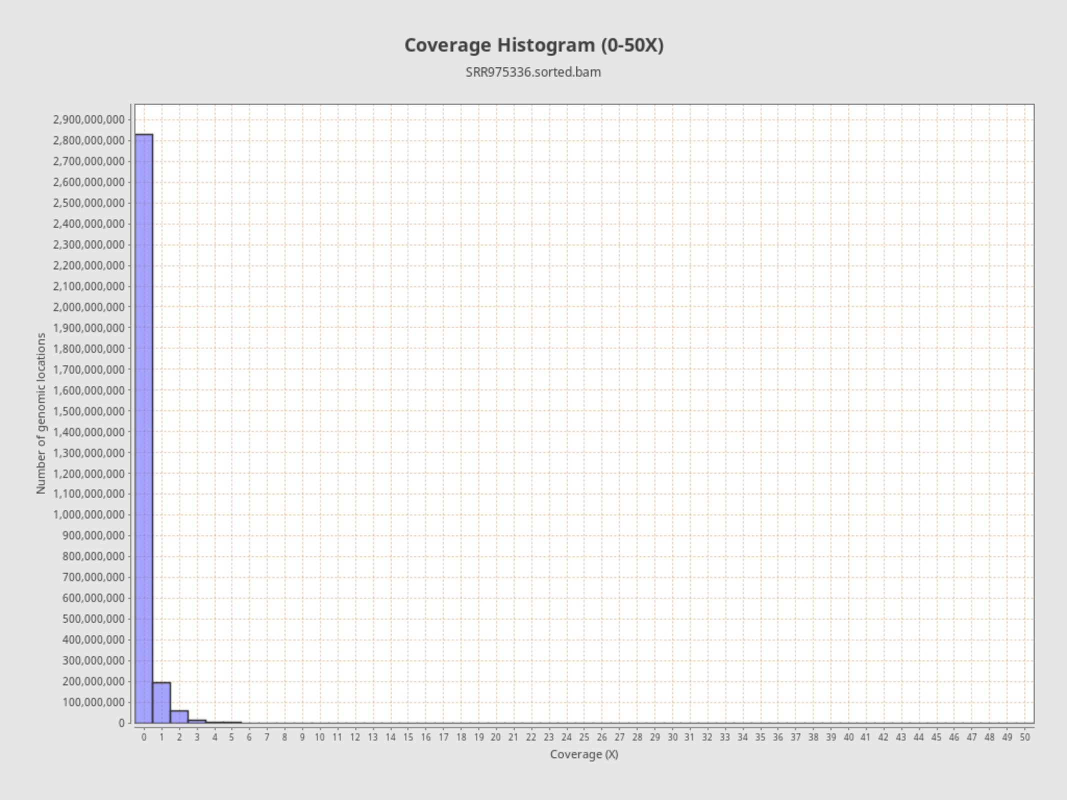
3. Results : Coverage across reference



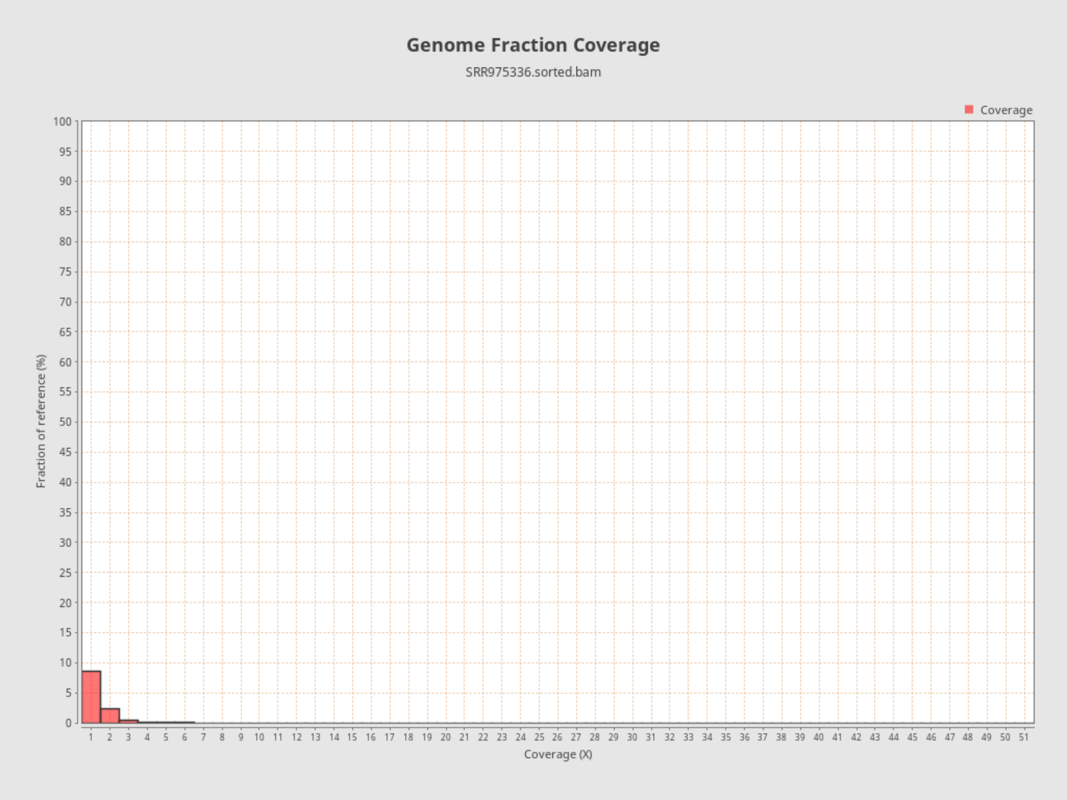
4. Results : Coverage Histogram



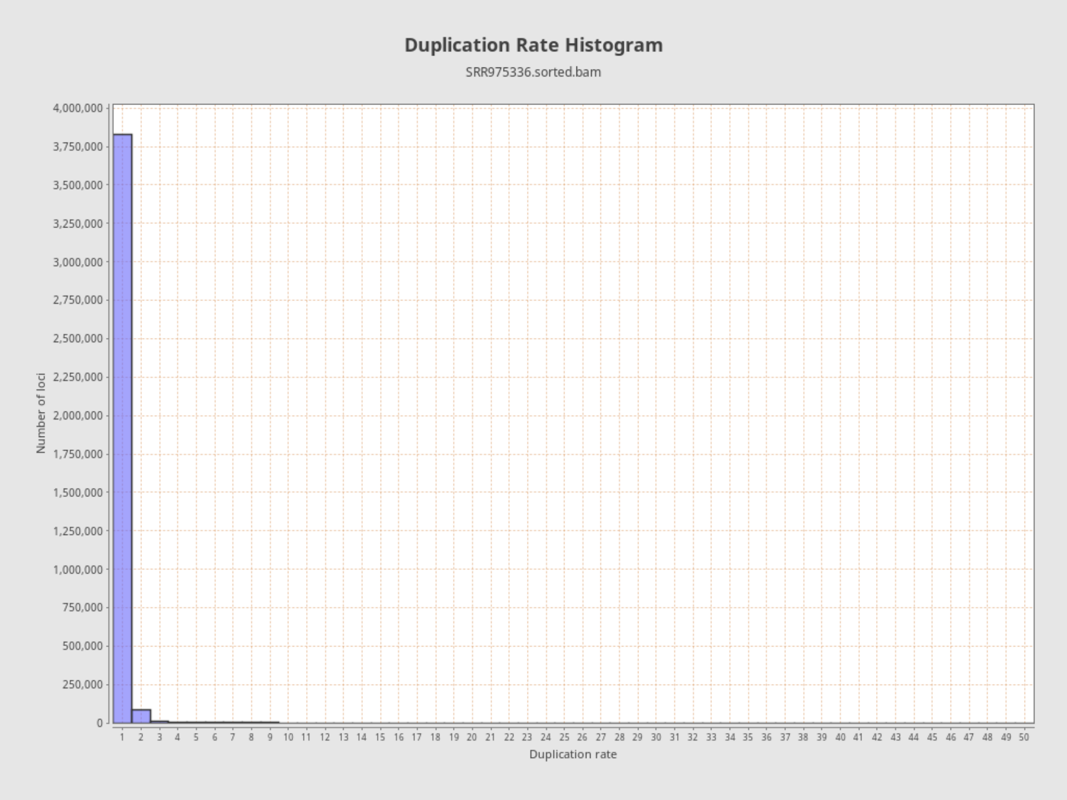
5. Results : Coverage Histogram (0-50X)



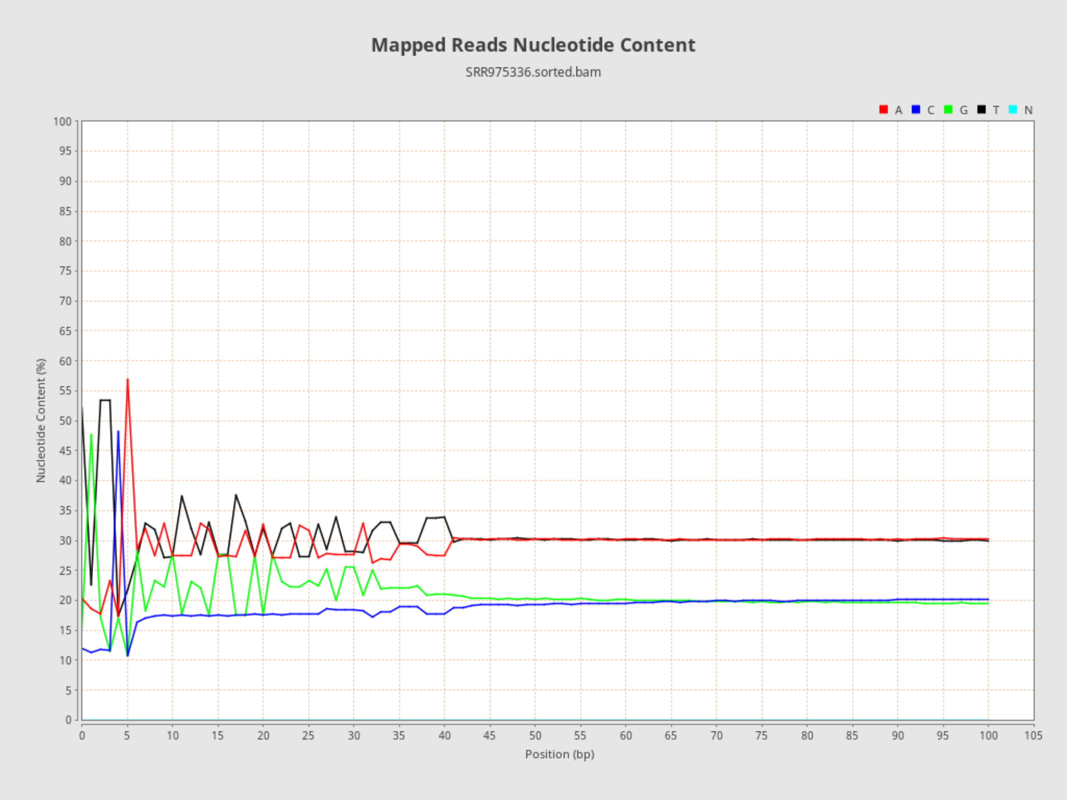
6. Results : Genome Fraction Coverage



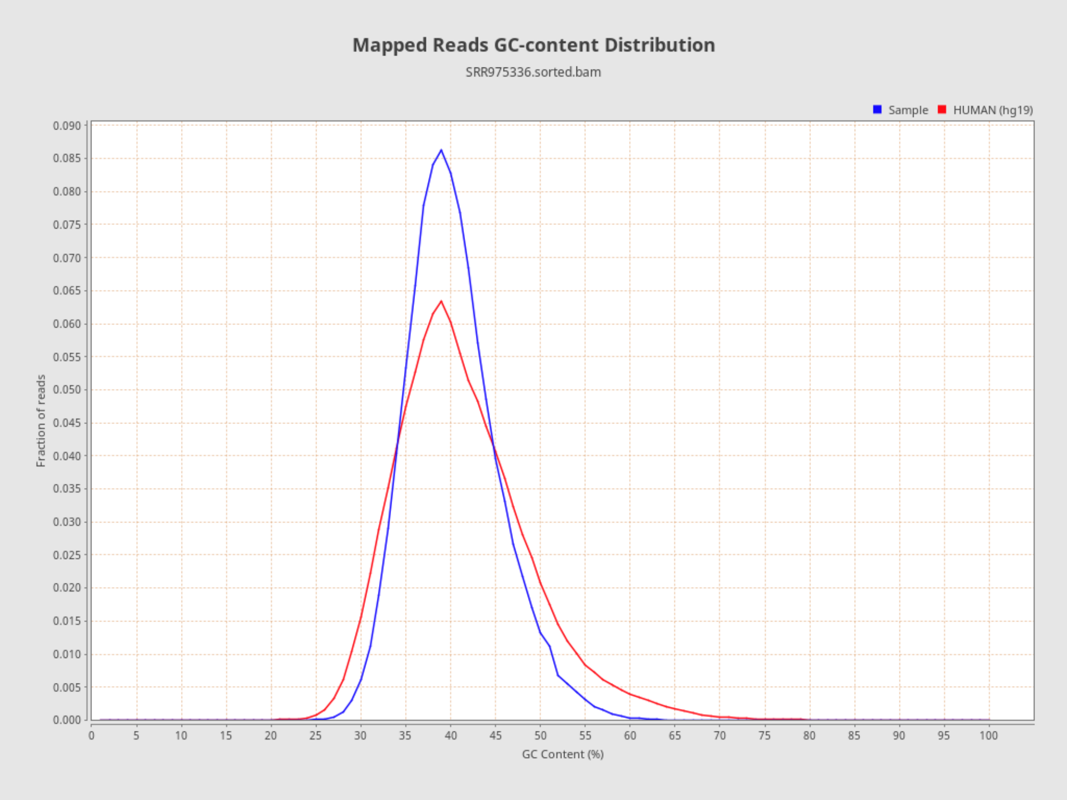
7. Results : Duplication Rate Histogram



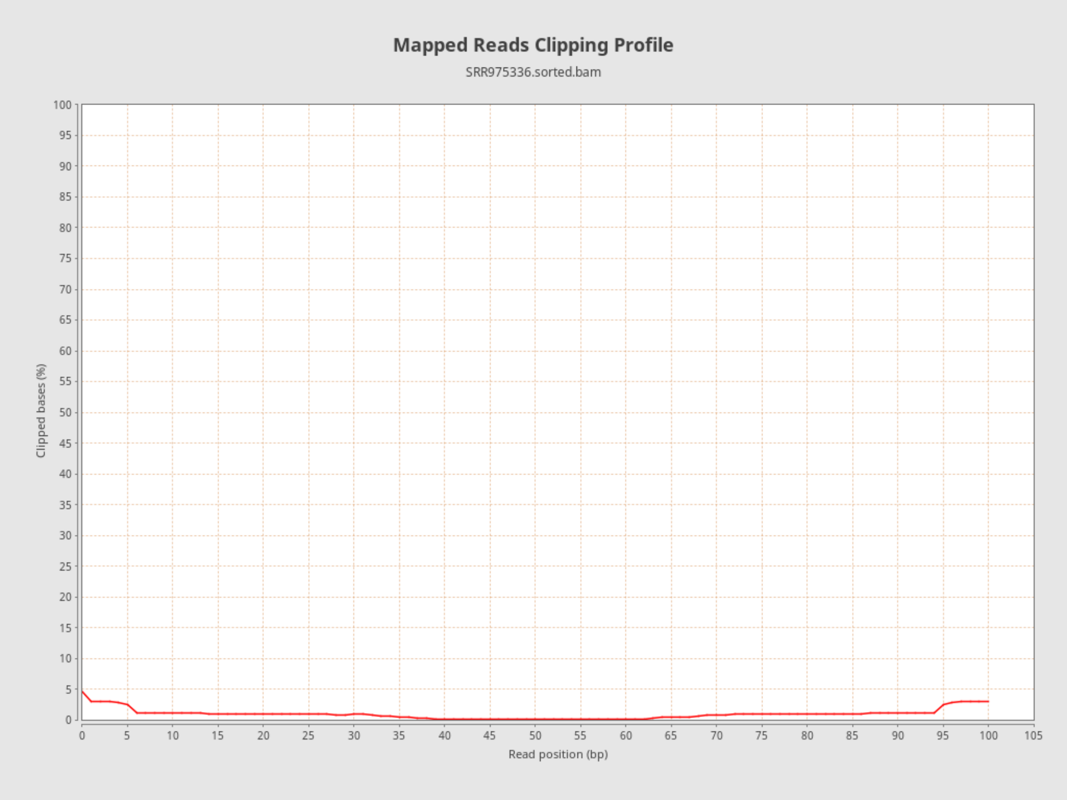
8. Results : Mapped Reads Nucleotide Content



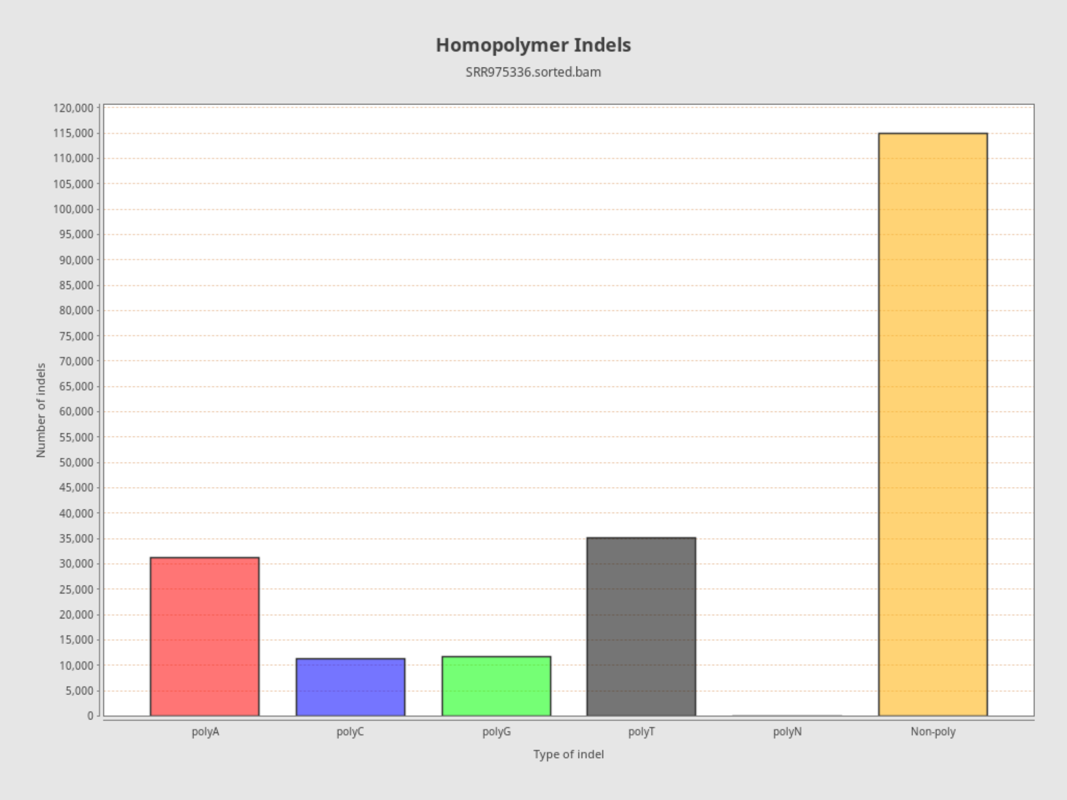
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

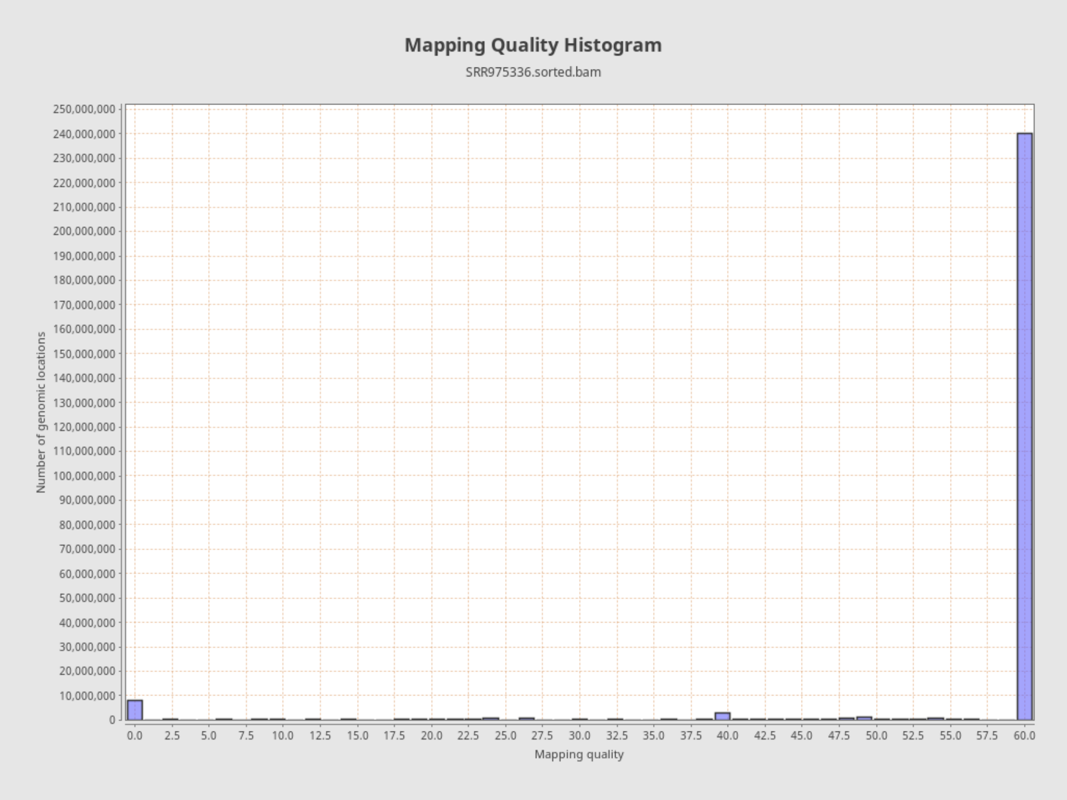


11. Results : Homopolymer Indels

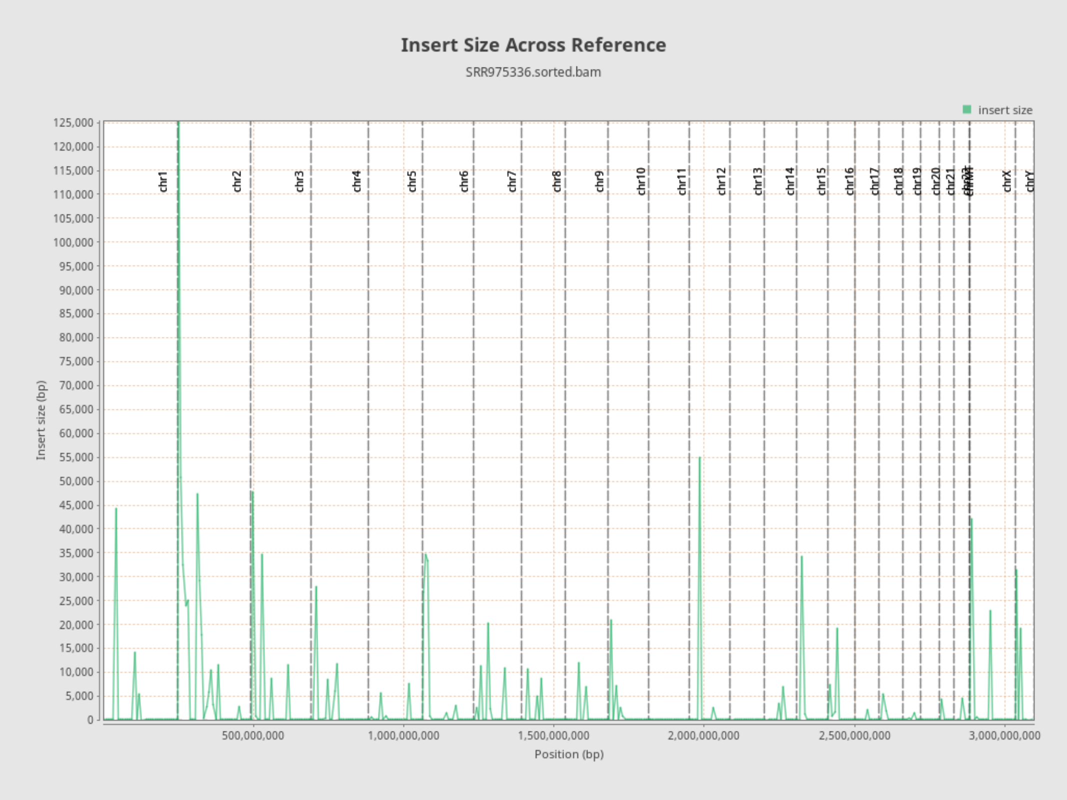


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram