Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 06:11:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975335.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_SRR975335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975335_1.fastq.gz SRR975335_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 06:11:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,716,378
Mapped reads	4,613,542 / 97.82%
Unmapped reads	102,836 / 2.18%
Mapped paired reads	4,613,542 / 97.82%
Mapped reads, first in pair	2,305,063 / 48.87%
Mapped reads, second in pair	2,308,479 / 48.95%
Mapped reads, both in pair	4,577,276 / 97.05%
Mapped reads, singletons	36,266 / 0.77%
Secondary alignments	0
Supplementary alignments	28,043 / 0.59%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	318,036 / 6.74%
Duplication rate	3.01%
Clipped reads	2,866,498 / 60.78%

2.2. ACGT Content

Number/percentage of A's	125,318,522 / 29.83%
Number/percentage of C's	79,578,502 / 18.94%
Number/percentage of T's	126,966,846 / 30.22%
Number/percentage of G's	88,229,144 / 21%
Number/percentage of N's	8,800 / 0%

GC Percentage	39.94%

2.3. Coverage

Mean	0.1358
Standard Deviation	1.8189

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	86,392.28
Standard Deviation	2,771,180.09
P25/Median/P75	136 / 168 / 214

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	3,301,583
Insertions	83,801
Mapped reads with at least one insertion	1.76%
Deletions	139,950
Mapped reads with at least one deletion	2.96%
Homopolymer indels	43.09%

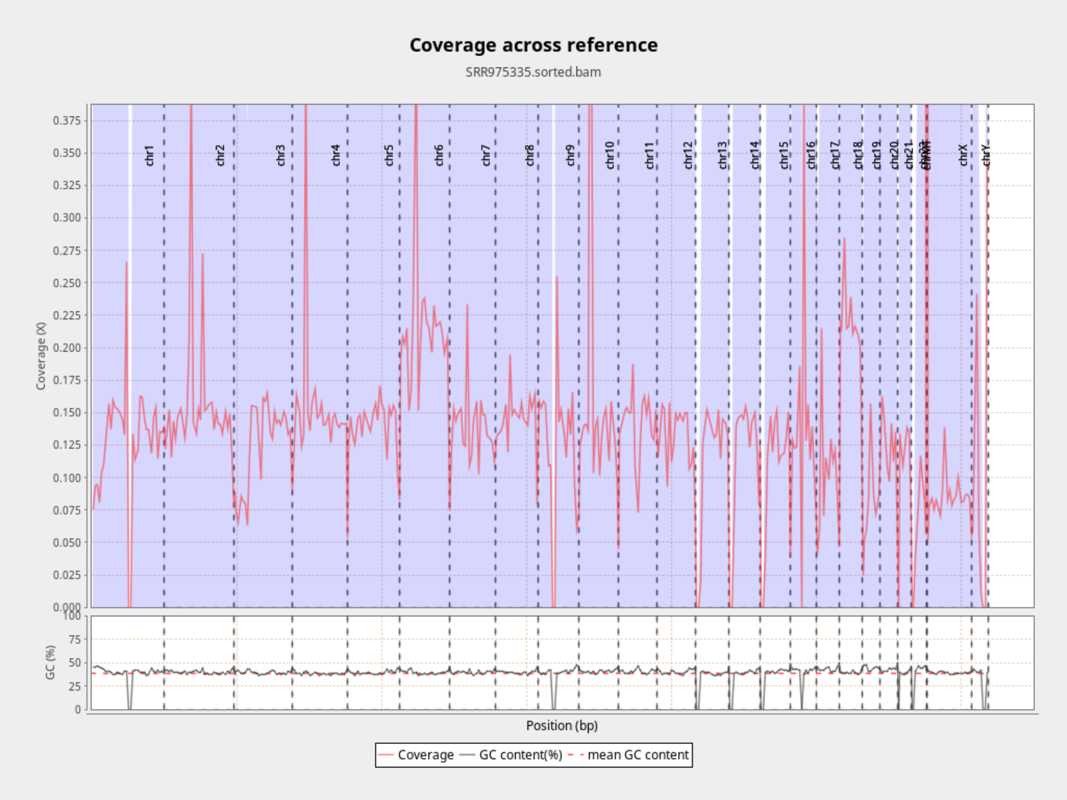
2.7. Chromosome stats

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

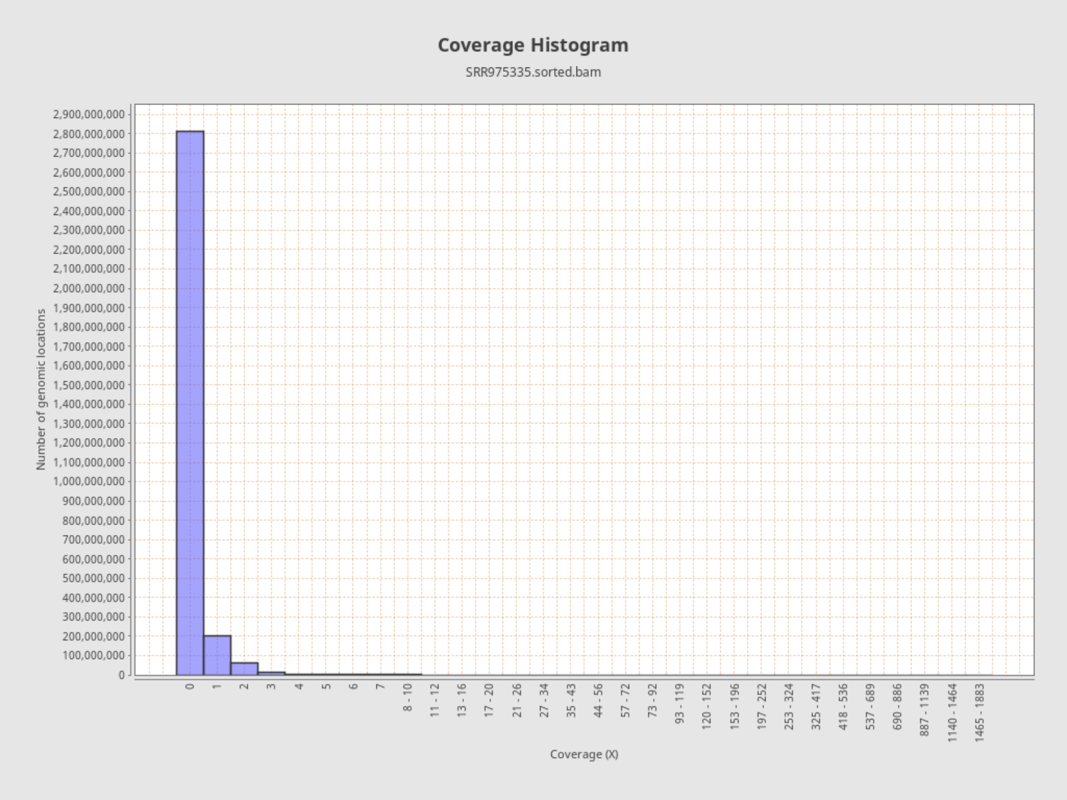
		bases	coverage	deviation
chr1	249250621	31653210	0.127	1.9878
chr2	243199373	37932114	0.156	2.3629
chr3	198022430	24845754	0.1255	0.4805
chr4	191154276	29420064	0.1539	1.7859
chr5	180915260	25675997	0.1419	0.5321
chr6	171115067	36936064	0.2159	2.4578
chr7	159138663	21945195	0.1379	1.7838
chr8	146364022	21259480	0.1453	0.7518
chr9	141213431	17607871	0.1247	2.7778
chr10	135534747	22018664	0.1625	3.8462
chr11	135006516	18936488	0.1403	1.1792
chr12	133851895	17712310	0.1323	0.4767
chr13	115169878	13059042	0.1134	0.4688
chr14	107349540	12240160	0.114	0.5457
chr15	102531392	10747024	0.1048	0.4126
chr16	90354753	12366919	0.1369	2.012
chr17	81195210	8306665	0.1023	1.9324
chr18	78077248	17096438	0.219	3.0204
chr19	59128983	4817971	0.0815	1.1437
chr20	63025520	7750481	0.123	0.6007
chr21	48129895	5287558	0.1099	0.7612
chr22	51304566	3325046	0.0648	0.4091
chrMT	16571	170993	10.3188	51.1759
chrX	155270560	13088709	0.0843	0.6074

chrY	59373566	6168779	0.1039	3.0675

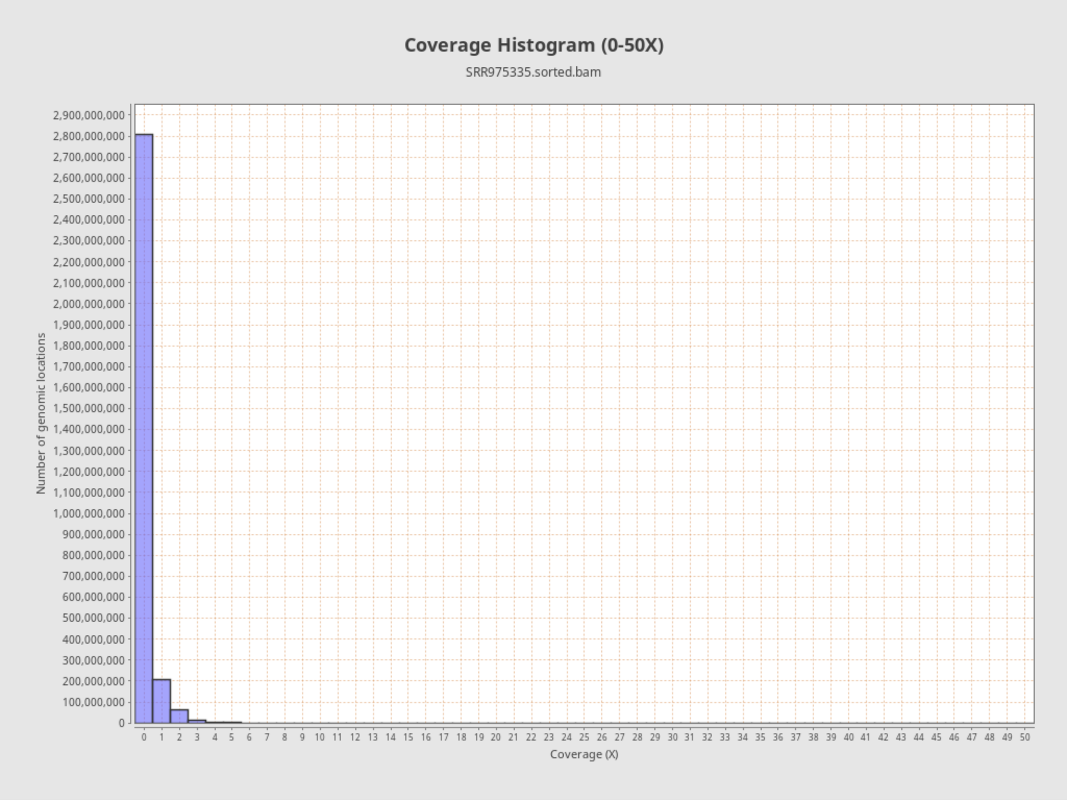
3. Results : Coverage across reference



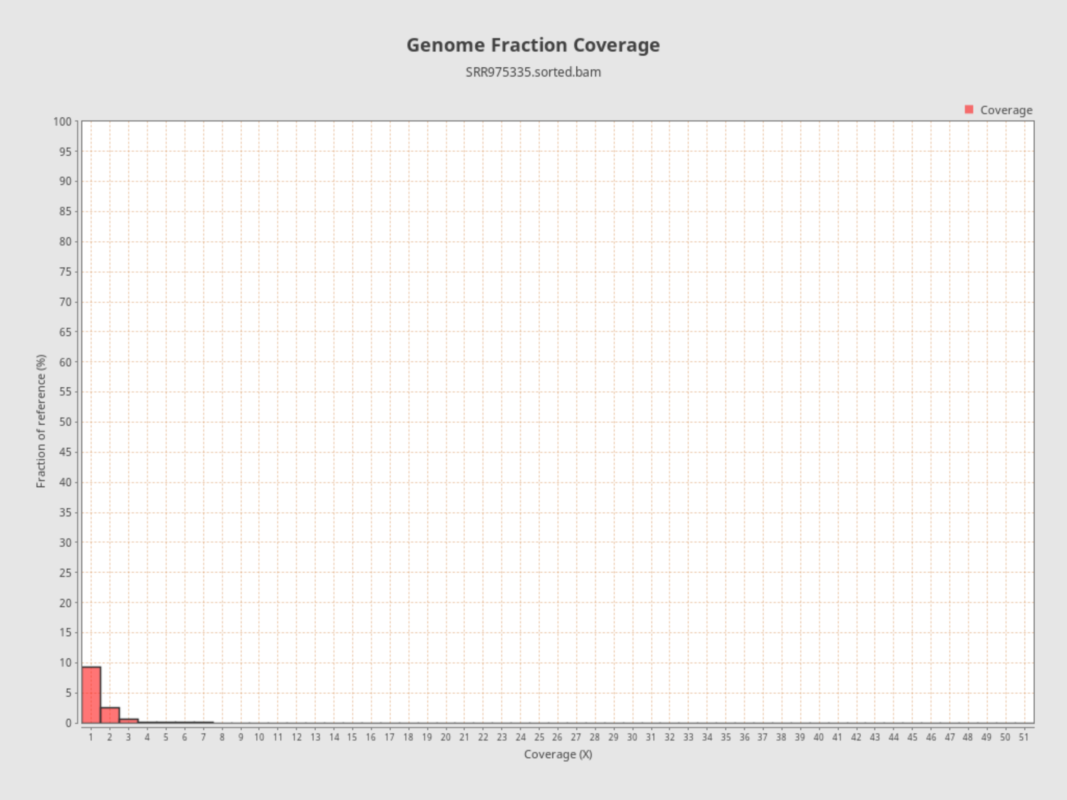
4. Results : Coverage Histogram



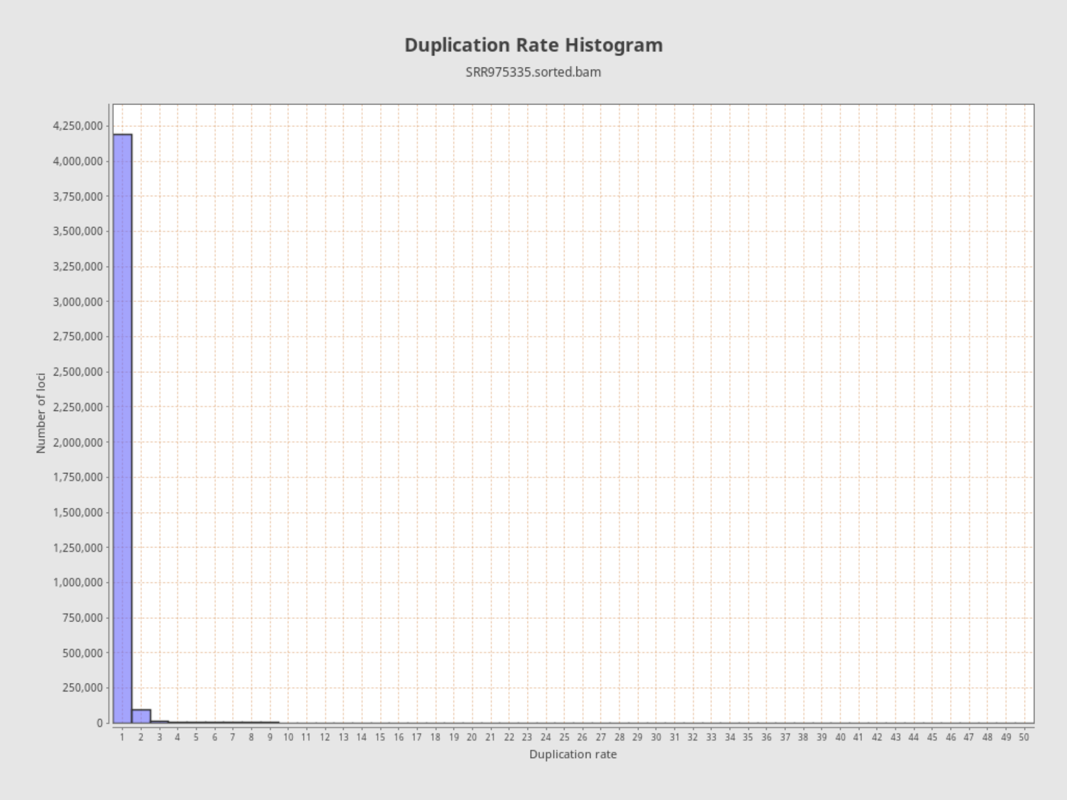
5. Results : Coverage Histogram (0-50X)



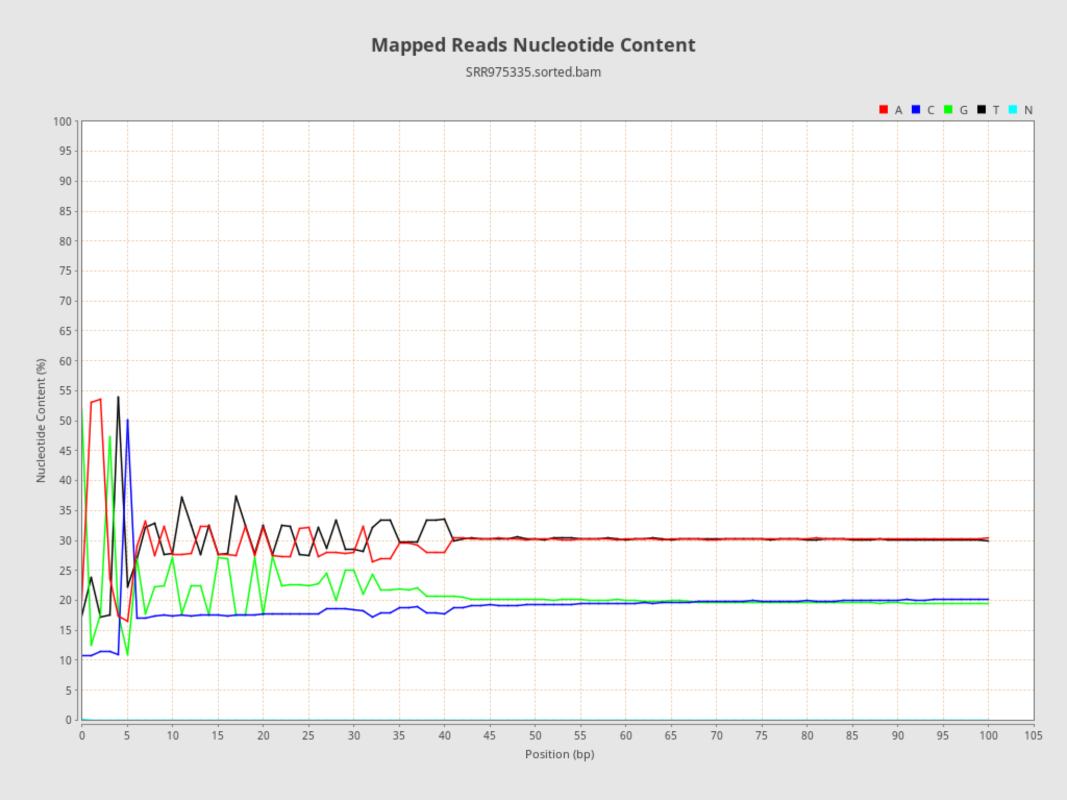
6. Results : Genome Fraction Coverage



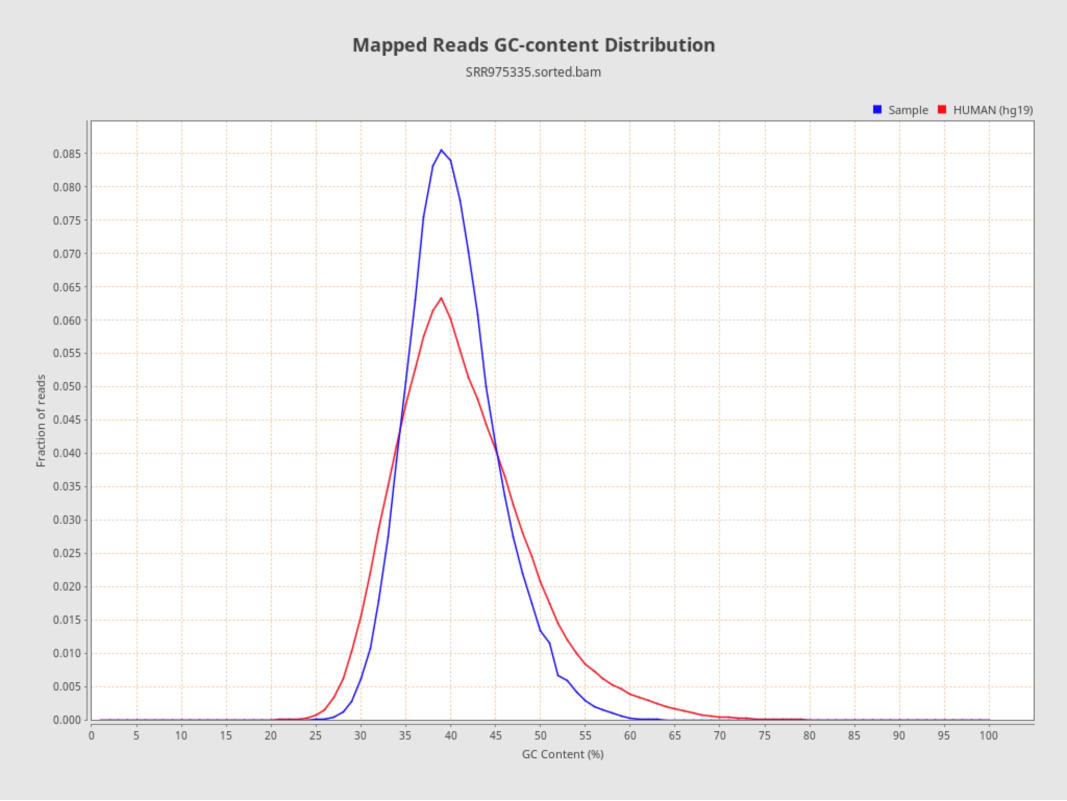
7. Results : Duplication Rate Histogram



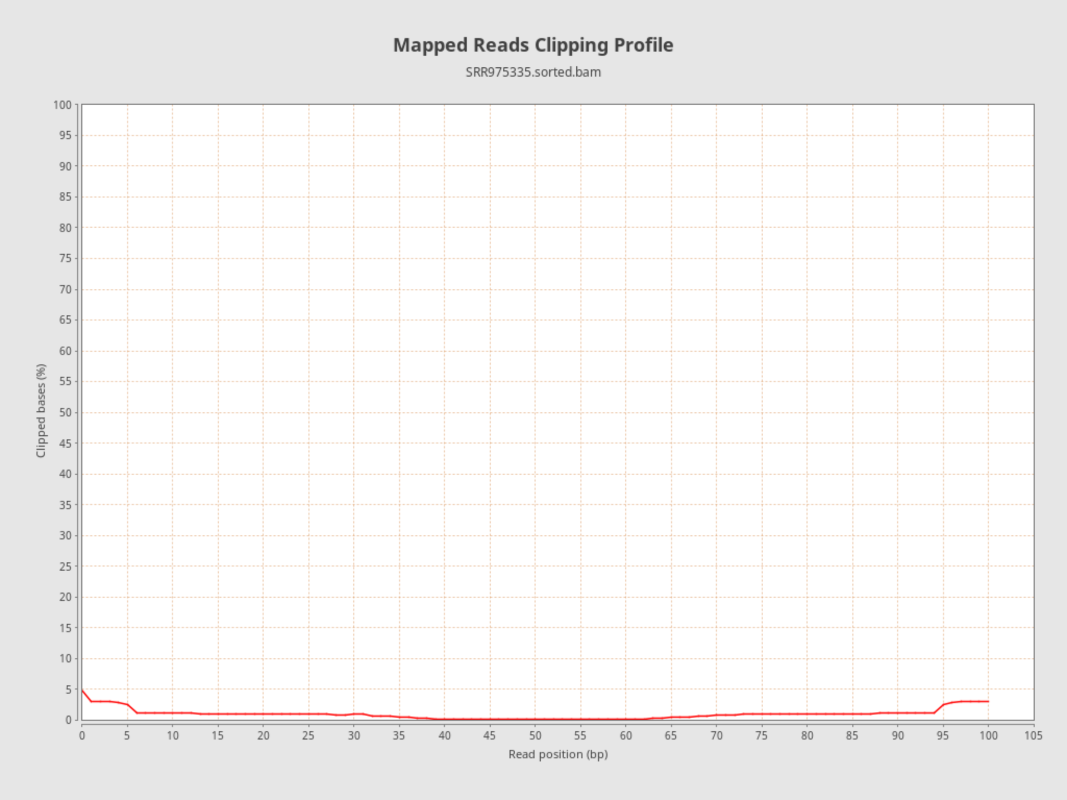
8. Results : Mapped Reads Nucleotide Content



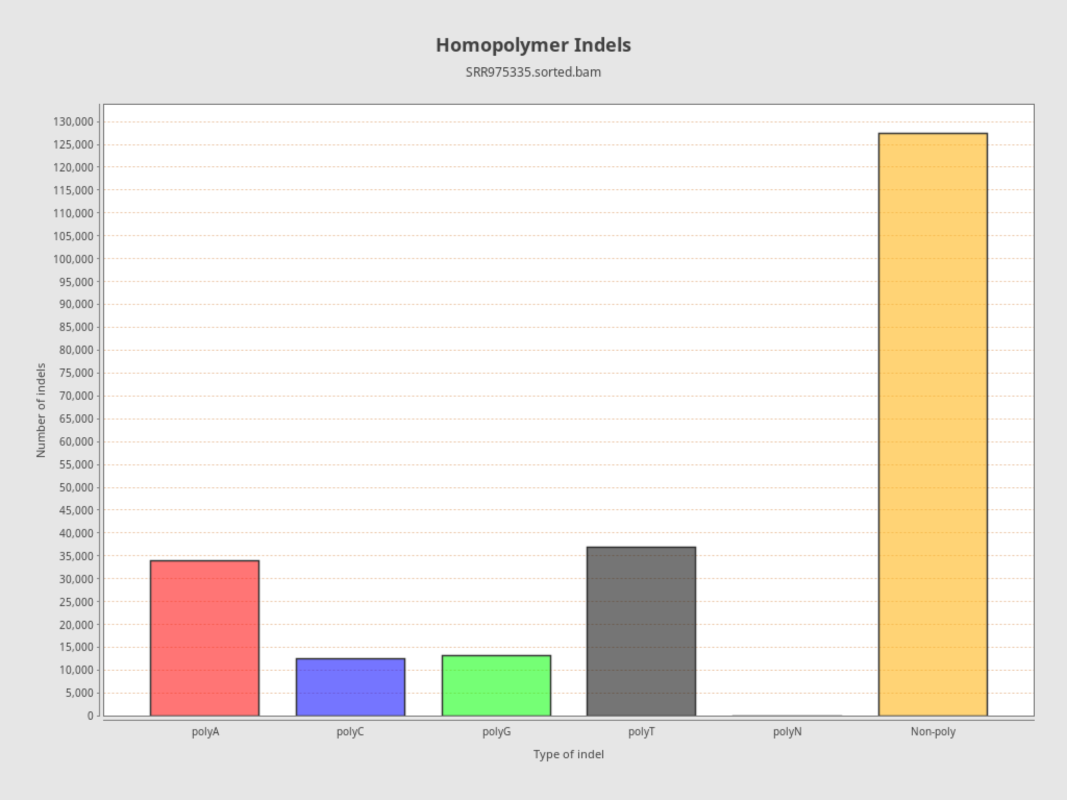
9. Results : Mapped Reads GC-content Distribution



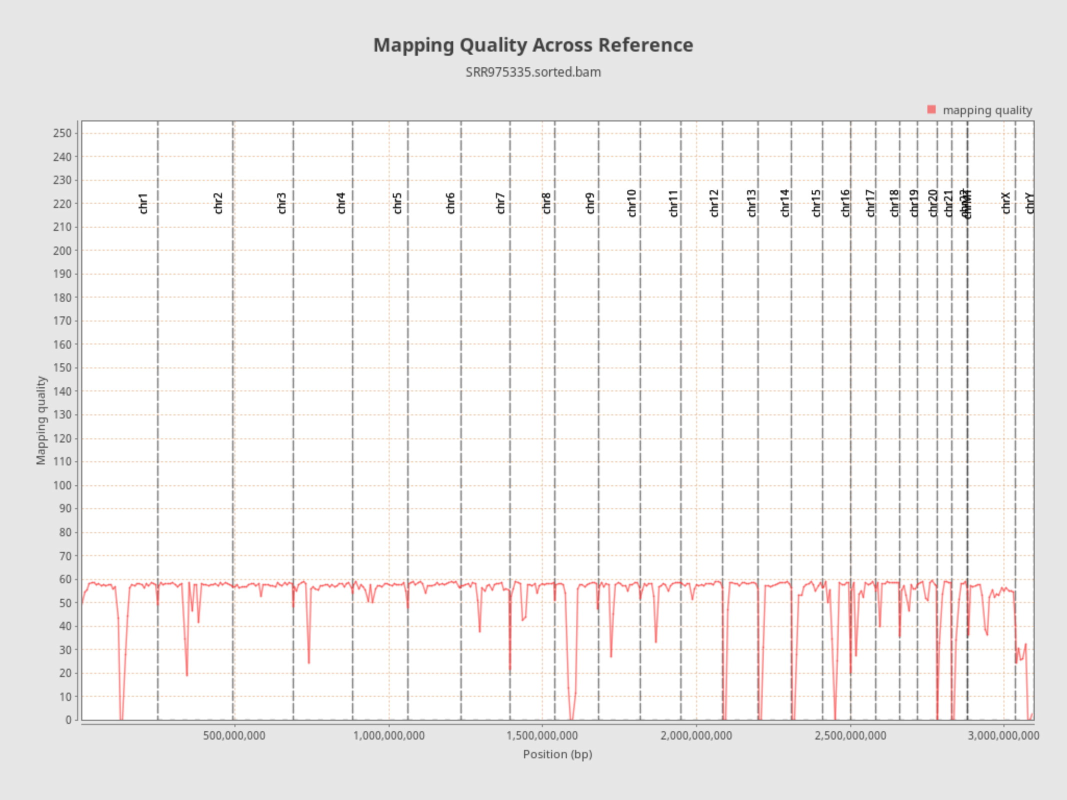
10. Results : Mapped Reads Clipping Profile



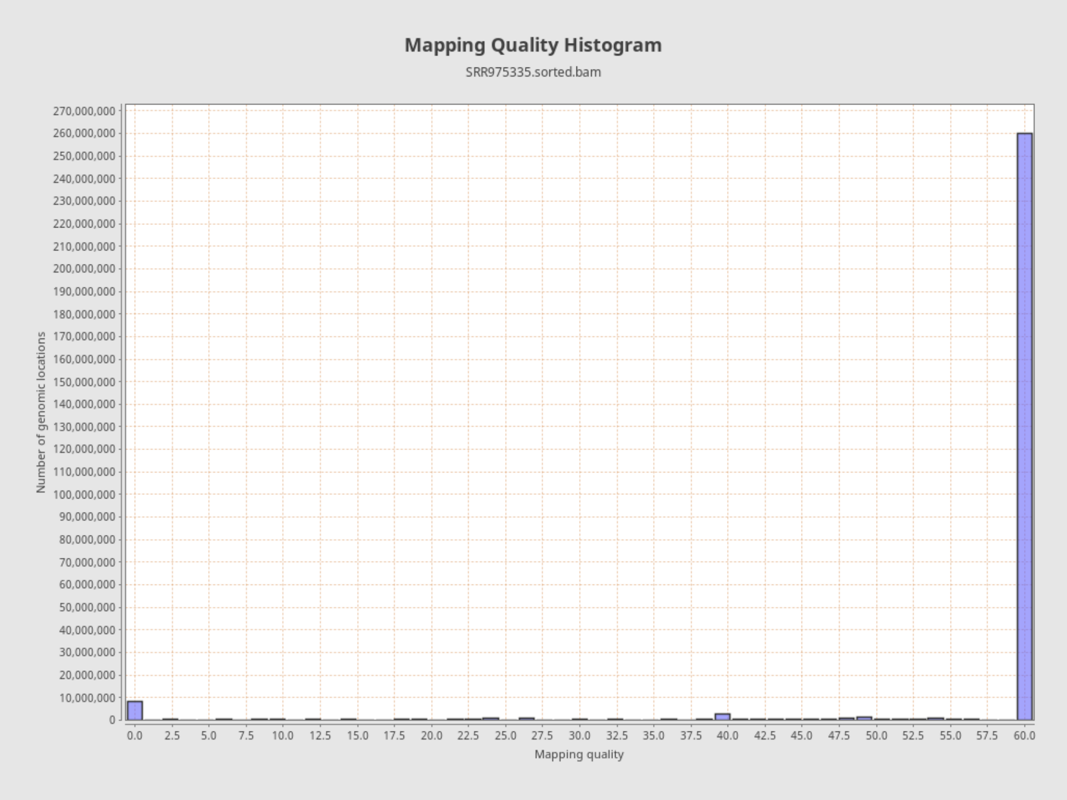
11. Results : Homopolymer Indels



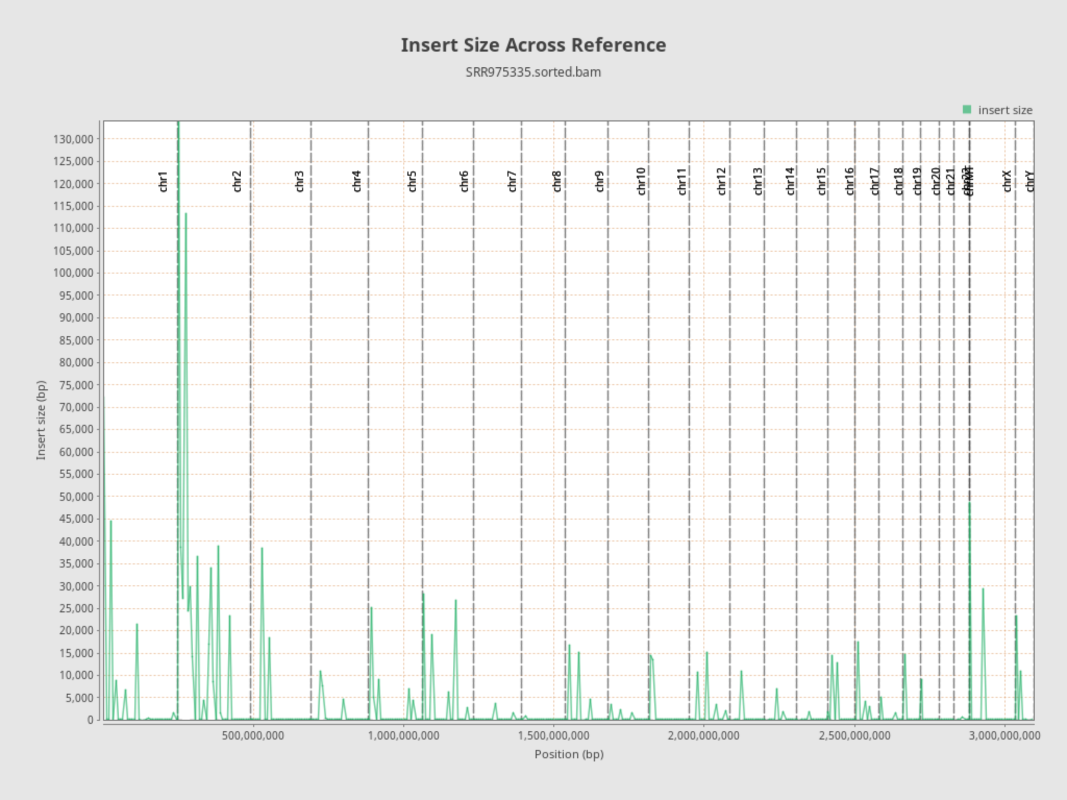
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram