Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/09 01:13:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975313.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_SRR975313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975313_1.fastq.gz SRR975313_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 09 01:13:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	77,739,668
Mapped reads	77,576,453 / 99.79%
Unmapped reads	163,215 / 0.21%
Mapped paired reads	77,576,453 / 99.79%
Mapped reads, first in pair	38,809,468 / 49.92%
Mapped reads, second in pair	38,766,985 / 49.87%
Mapped reads, both in pair	77,494,964 / 99.69%
Mapped reads, singletons	81,489 / 0.1%
Secondary alignments	0
Supplementary alignments	129,989 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	45,181,884 / 58.12%
Duplication rate	44.95%
Clipped reads	42,253,459 / 54.35%

2.2. ACGT Content

Number/percentage of A's	1,871,409,116 / 26.06%
Number/percentage of C's	1,612,116,360 / 22.45%
Number/percentage of T's	1,964,025,721 / 27.35%
Number/percentage of G's	1,734,460,978 / 24.15%
Number/percentage of N's	318,435 / 0%

GC Percentage	46.59%

2.3. Coverage

Mean	2.3209
Standard Deviation	26.5766

2.4. Mapping Quality

Mean Mapping Quality	56.03

2.5. Insert size

Mean	85,902.39
Standard Deviation	2,891,427.97
P25/Median/P75	150 / 188 / 237

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	44,215,796
Insertions	687,857
Mapped reads with at least one insertion	0.88%
Deletions	1,670,364
Mapped reads with at least one deletion	2.12%
Homopolymer indels	47.19%

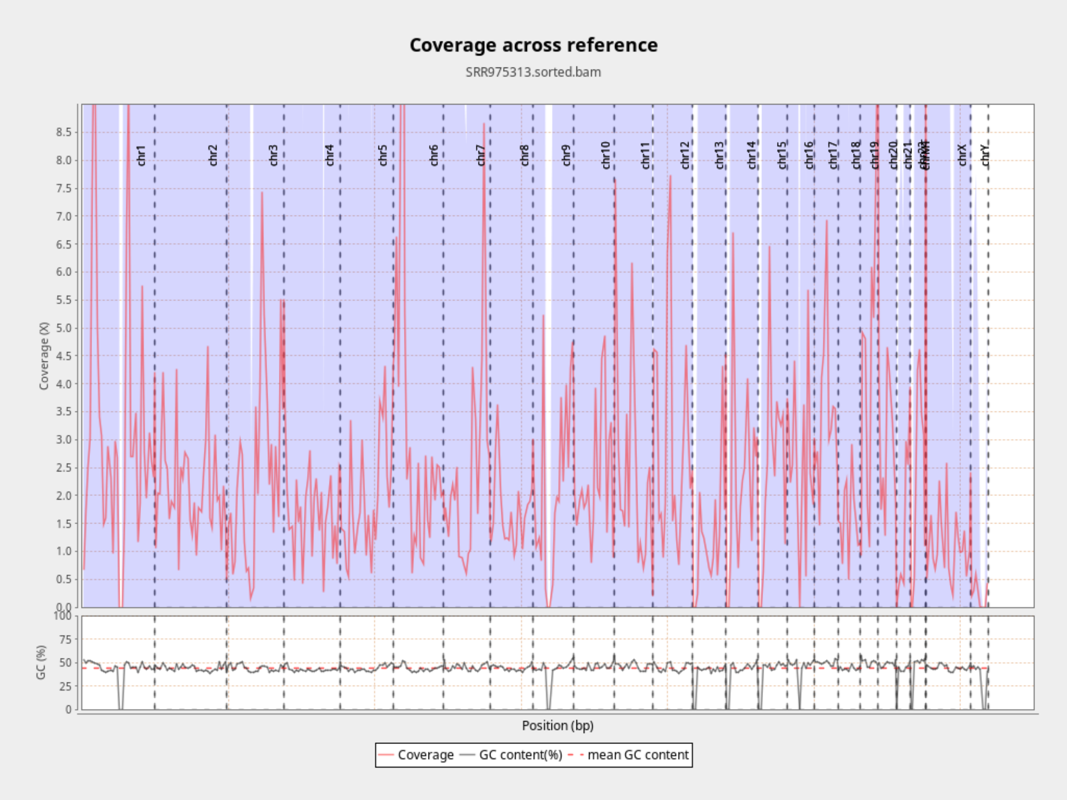
2.7. Chromosome stats

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

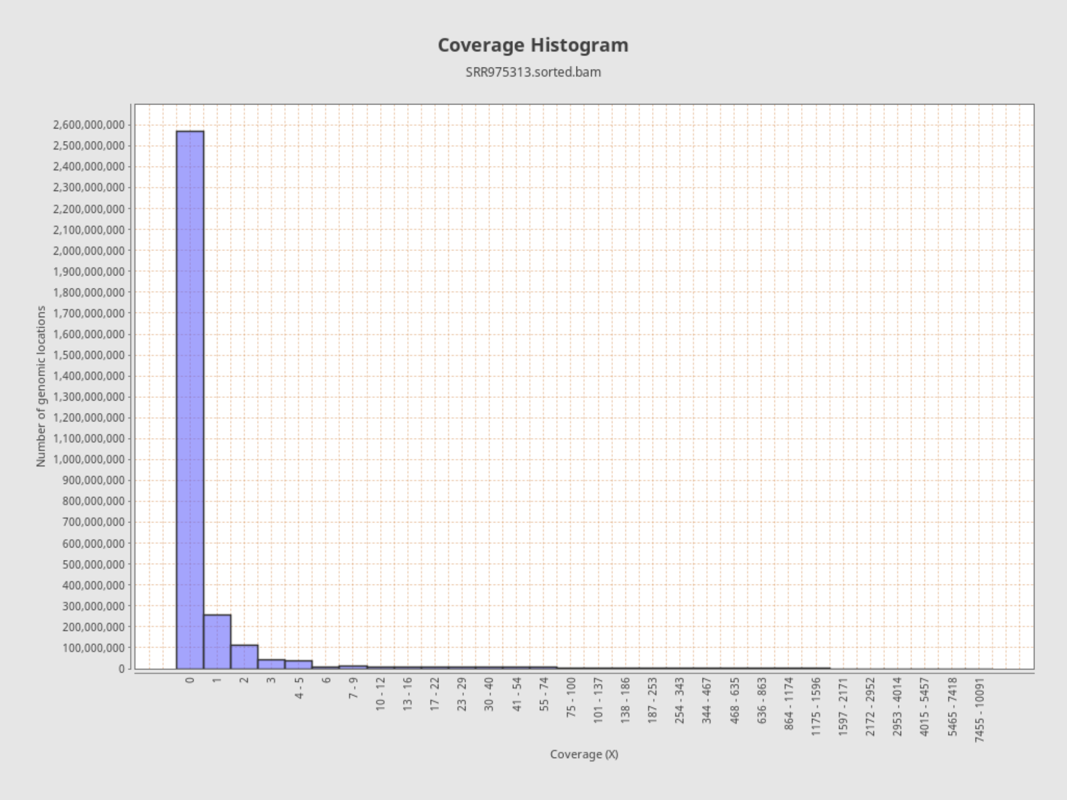
		bases	coverage	deviation
chr1	249250621	790044855	3.1697	32.9427
chr2	243199373	527110408	2.1674	23.7345
chr3	198022430	484986053	2.4491	28.6133
chr4	191154276	320520561	1.6768	21.4923
chr5	180915260	354352790	1.9587	23.2069
chr6	171115067	603899991	3.5292	41.0956
chr7	159138663	378419283	2.3779	28.3187
chr8	146364022	248499453	1.6978	20.0334
chr9	141213431	303633948	2.1502	24.5756
chr10	135534747	317849711	2.3452	25.4715
chr11	135006516	334689630	2.4791	25.4377
chr12	133851895	390602715	2.9182	28.1816
chr13	115169878	148413352	1.2886	19.607
chr14	107349540	239790186	2.2337	25.1225
chr15	102531392	259403862	2.53	26.6896
chr16	90354753	233816932	2.5878	26.378
chr17	81195210	285653207	3.5181	30.4597
chr18	78077248	124624656	1.5962	21.5466
chr19	59128983	269025465	4.5498	36.326
chr20	63025520	183520562	2.9118	33.071
chr21	48129895	72887117	1.5144	18.9309
chr22	51304566	125519253	2.4466	25.0429
chrMT	16571	165534	9.9894	13.9256
chrX	155270560	173495937	1.1174	13.9488

chrY	59373566	13794627	0.2323	4.2298

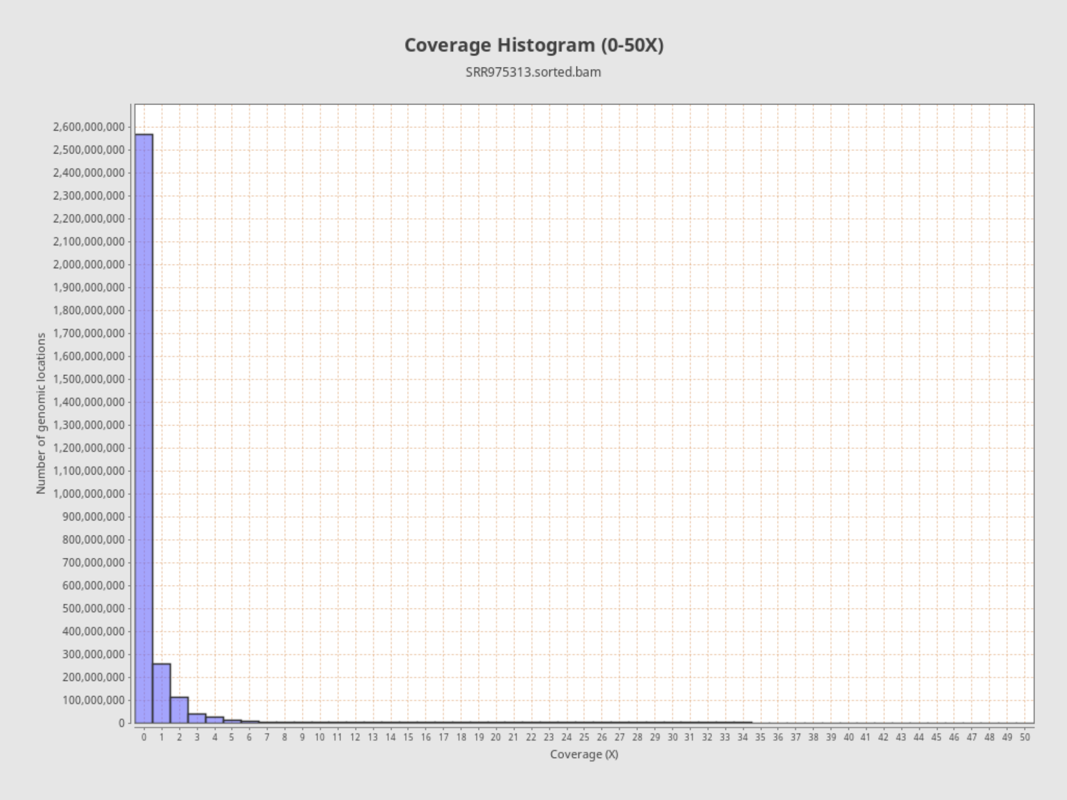
3. Results : Coverage across reference



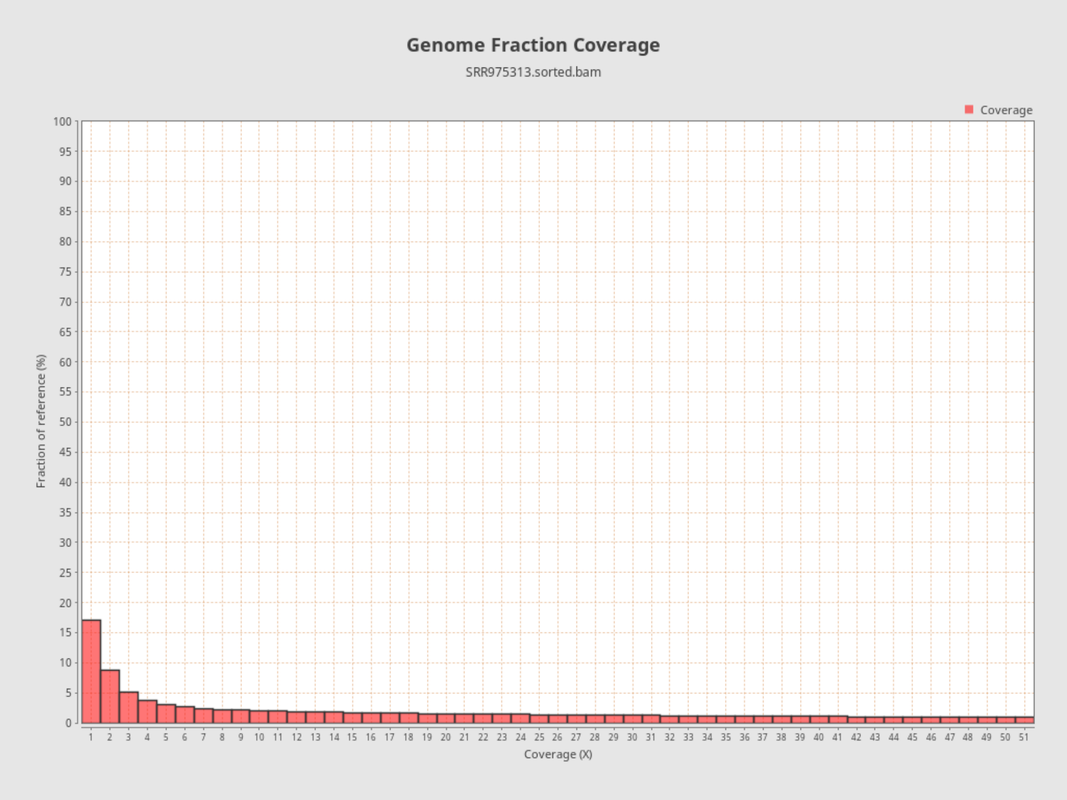
4. Results : Coverage Histogram



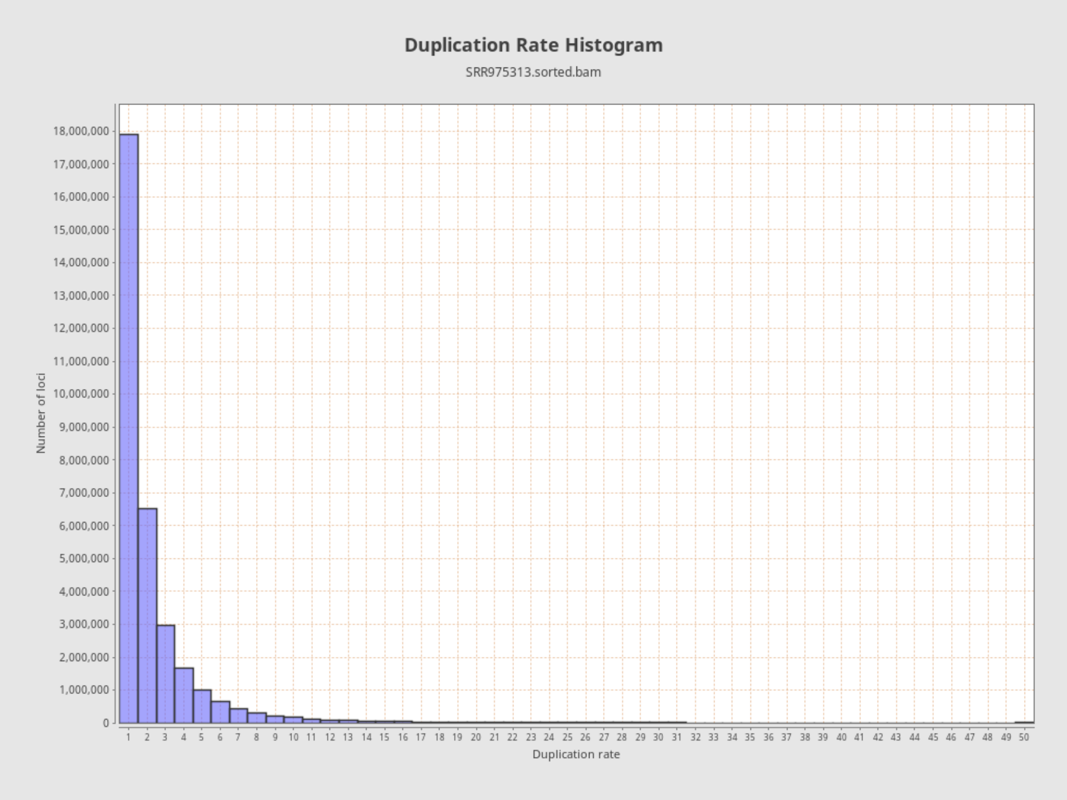
5. Results : Coverage Histogram (0-50X)



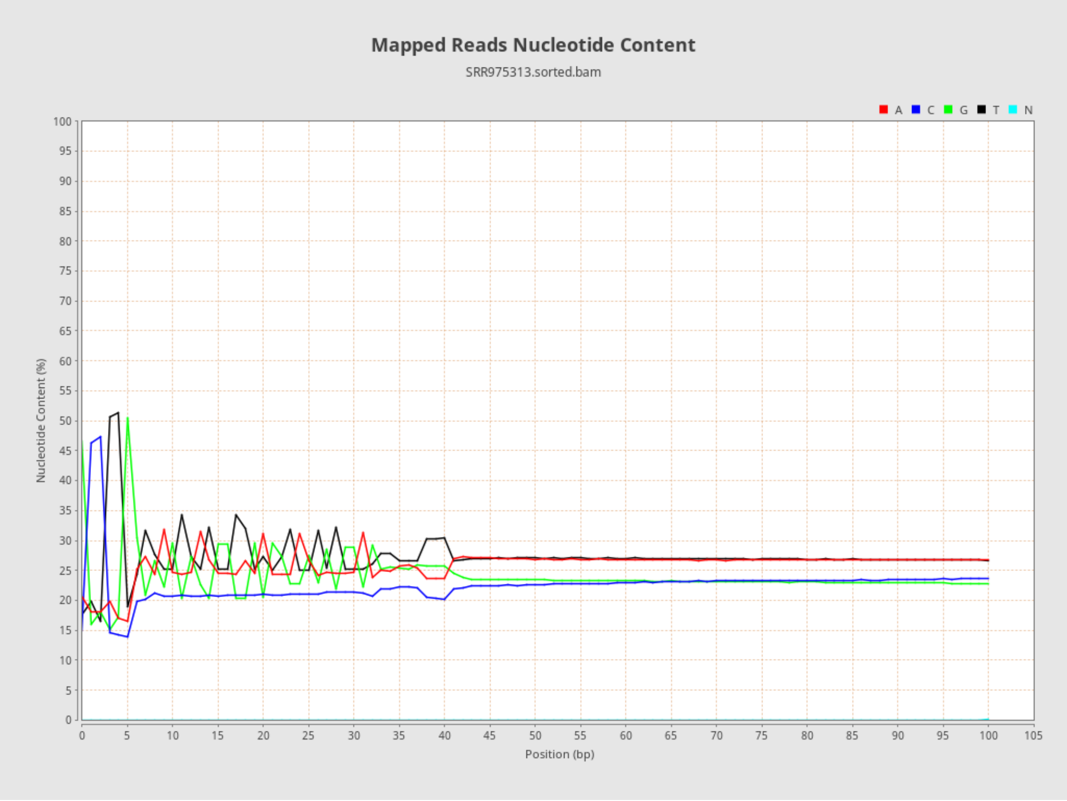
6. Results : Genome Fraction Coverage



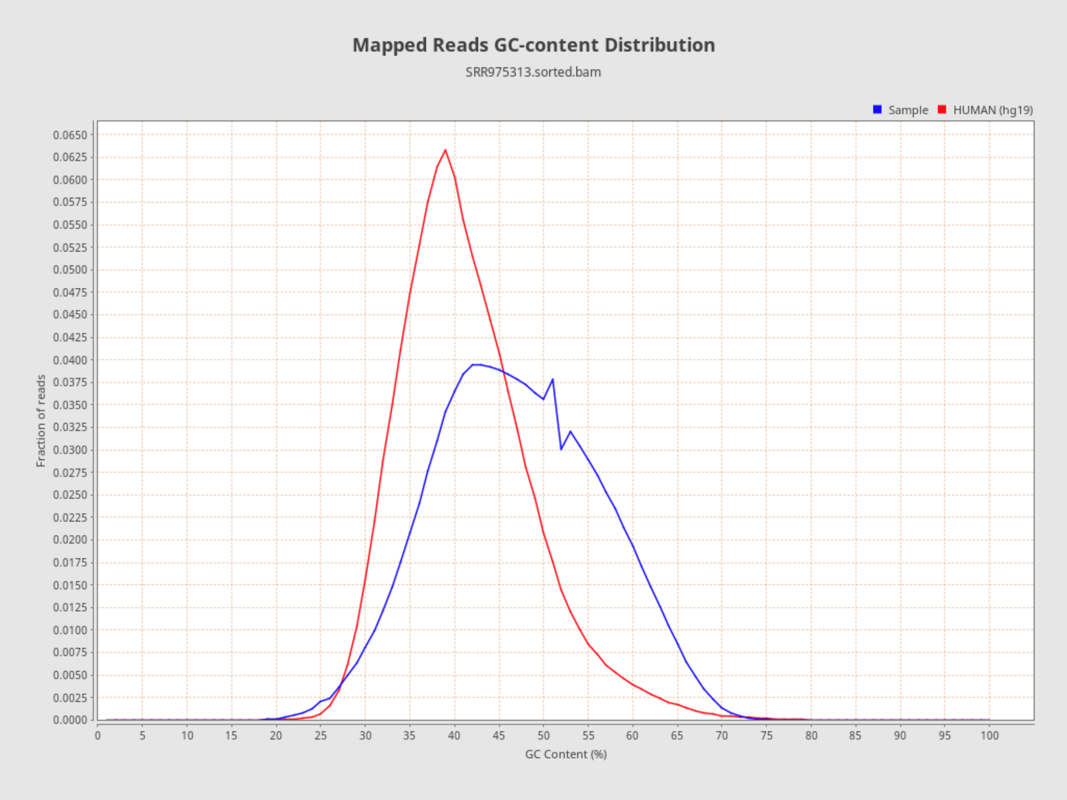
7. Results : Duplication Rate Histogram



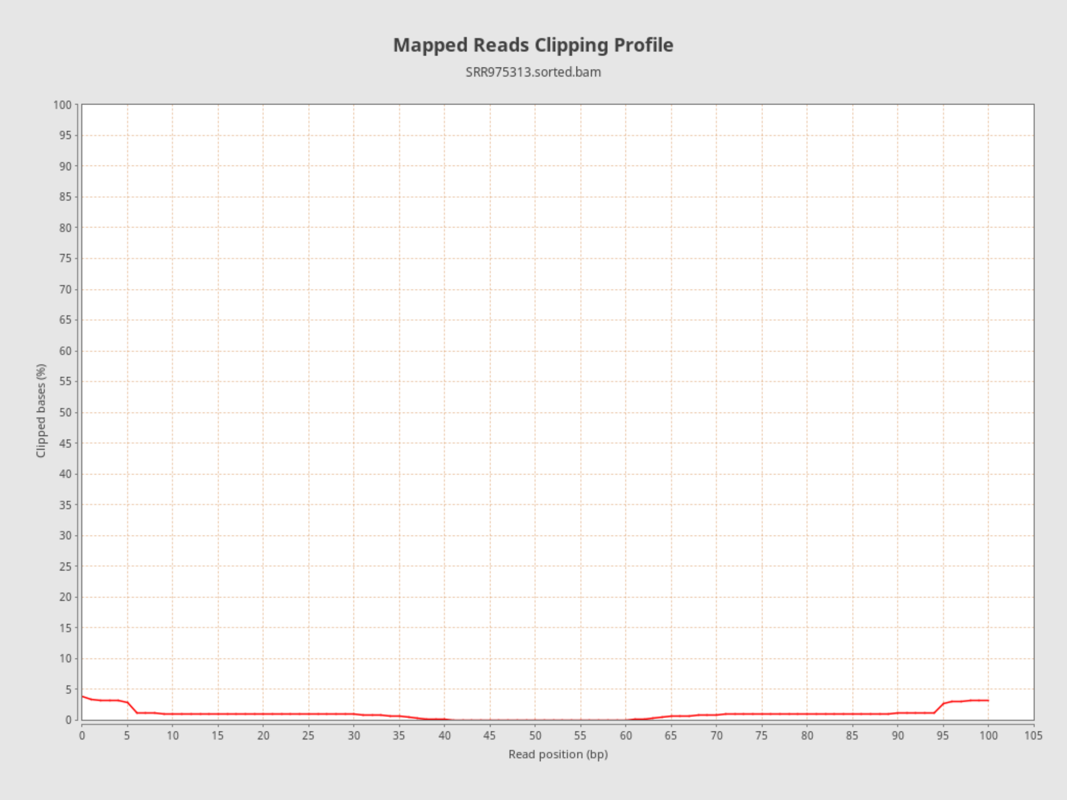
8. Results : Mapped Reads Nucleotide Content



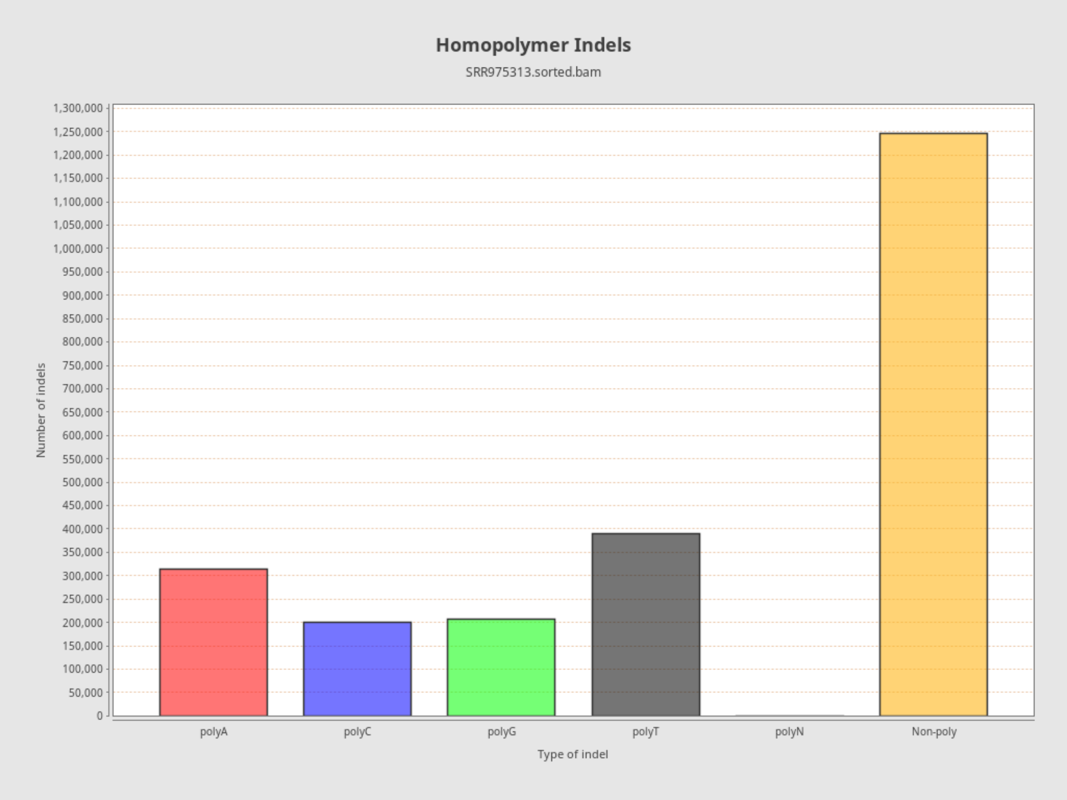
9. Results : Mapped Reads GC-content Distribution



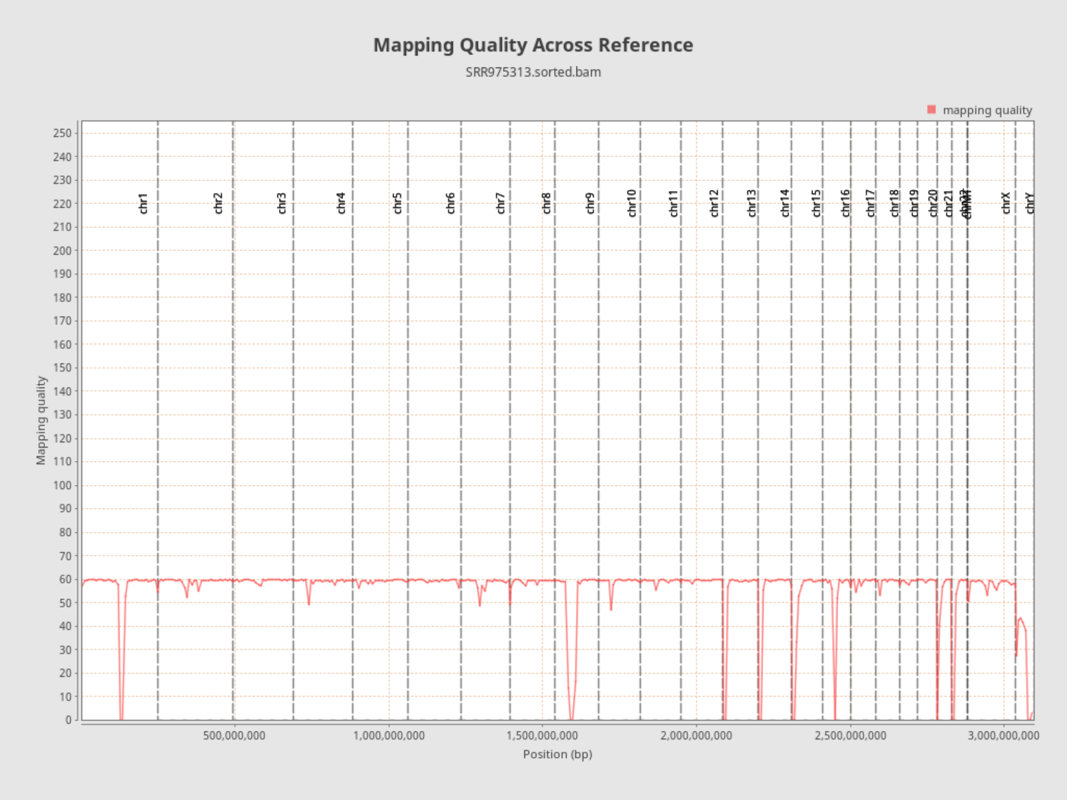
10. Results : Mapped Reads Clipping Profile



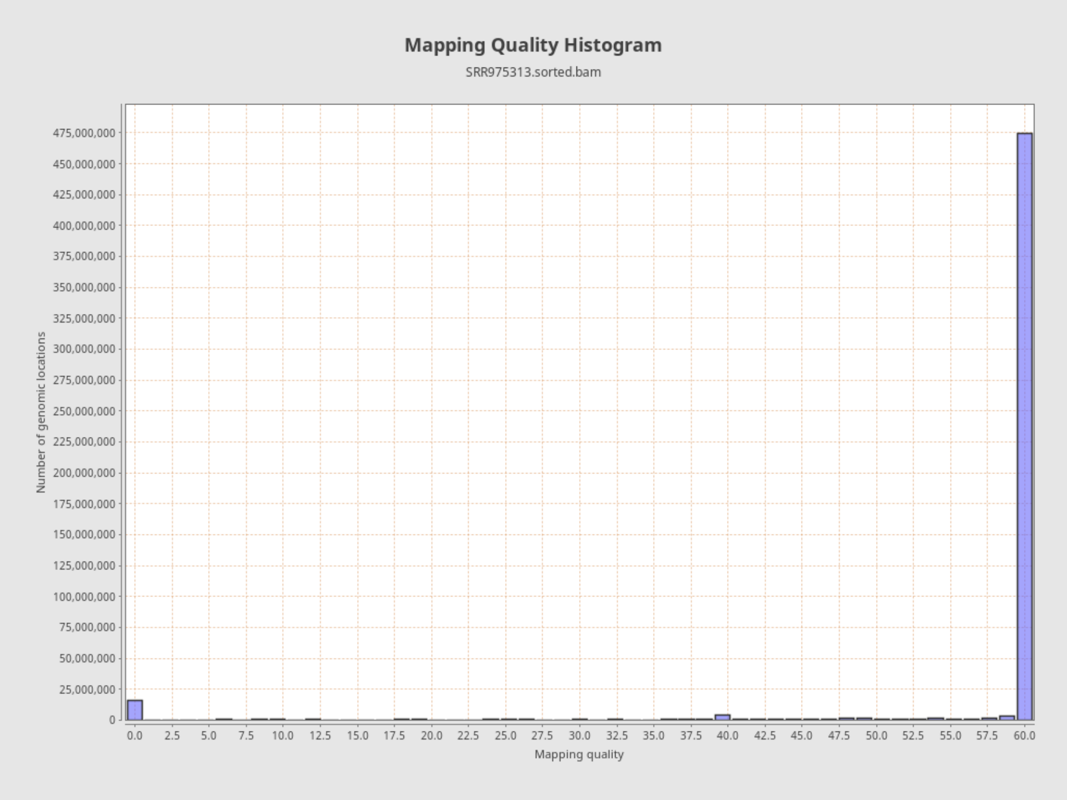
11. Results : Homopolymer Indels



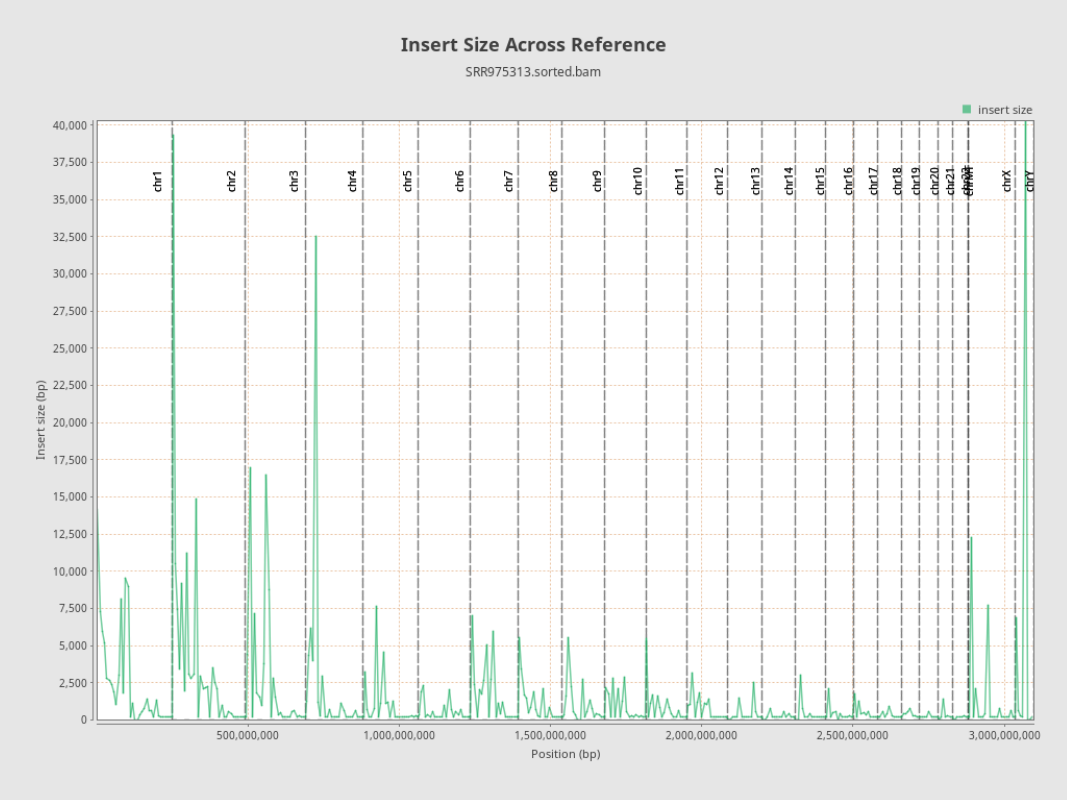
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram