Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:59:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975226.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_SRR975226 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975226_1.fastq.gz SRR975226_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:59:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,337,872
Mapped reads	38,280,939 / 99.85%
Unmapped reads	56,933 / 0.15%
Mapped paired reads	38,280,939 / 99.85%
Mapped reads, first in pair	19,142,522 / 49.93%
Mapped reads, second in pair	19,138,417 / 49.92%
Mapped reads, both in pair	38,245,472 / 99.76%
Mapped reads, singletons	35,467 / 0.09%
Secondary alignments	0
Supplementary alignments	114,893 / 0.3%
Read min/max/mean length	30 / 101 / 101.12
Duplicated reads (estimated)	14,338,587 / 37.4%
Duplication rate	35.87%
Clipped reads	19,390,345 / 50.58%

2.2. ACGT Content

Number/percentage of A's	976,397,877 / 26.08%
Number/percentage of C's	879,294,090 / 23.49%
Number/percentage of T's	1,007,505,676 / 26.91%
Number/percentage of G's	880,693,254 / 23.52%
Number/percentage of N's	96,380 / 0%

GC Percentage	47.01%

2.3. Coverage

Mean	1.2096
Standard Deviation	9.2909

2.4. Mapping Quality

Mean Mapping Quality	56.25

2.5. Insert size

Mean	203,691.34
Standard Deviation	4,465,648.76
P25/Median/P75	192 / 233 / 280

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	14,508,404
Insertions	231,026
Mapped reads with at least one insertion	0.6%
Deletions	216,626
Mapped reads with at least one deletion	0.56%
Homopolymer indels	37.34%

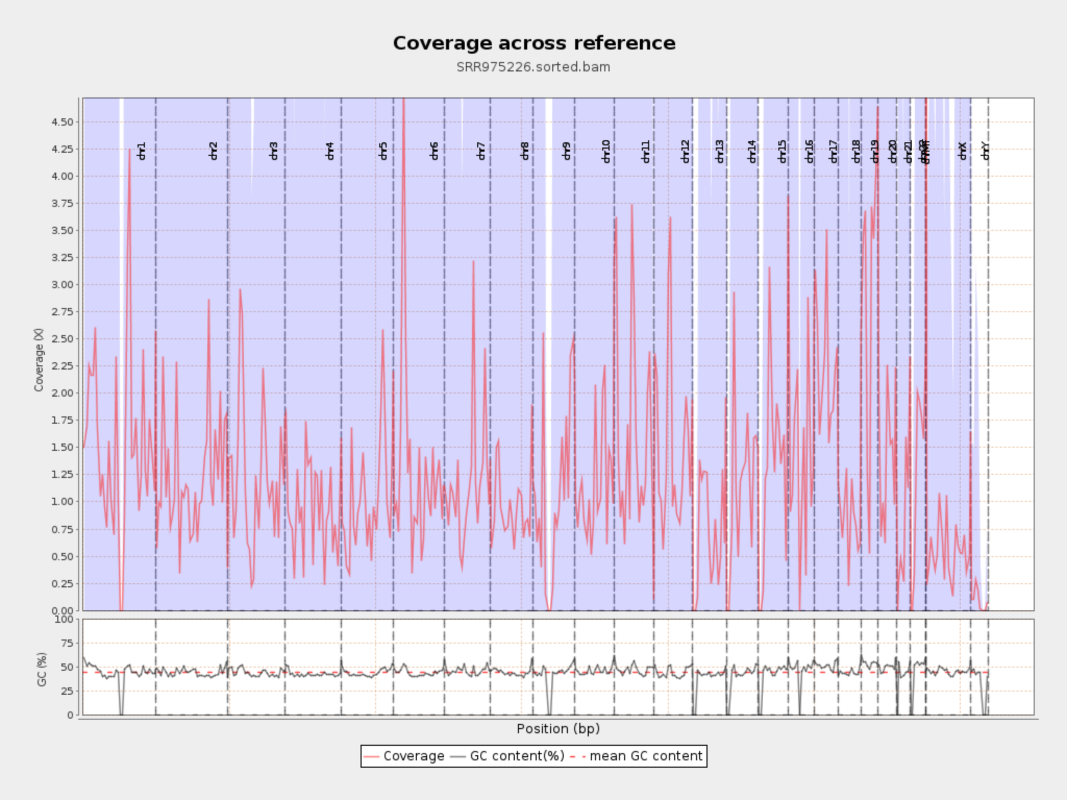
2.7. Chromosome stats

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

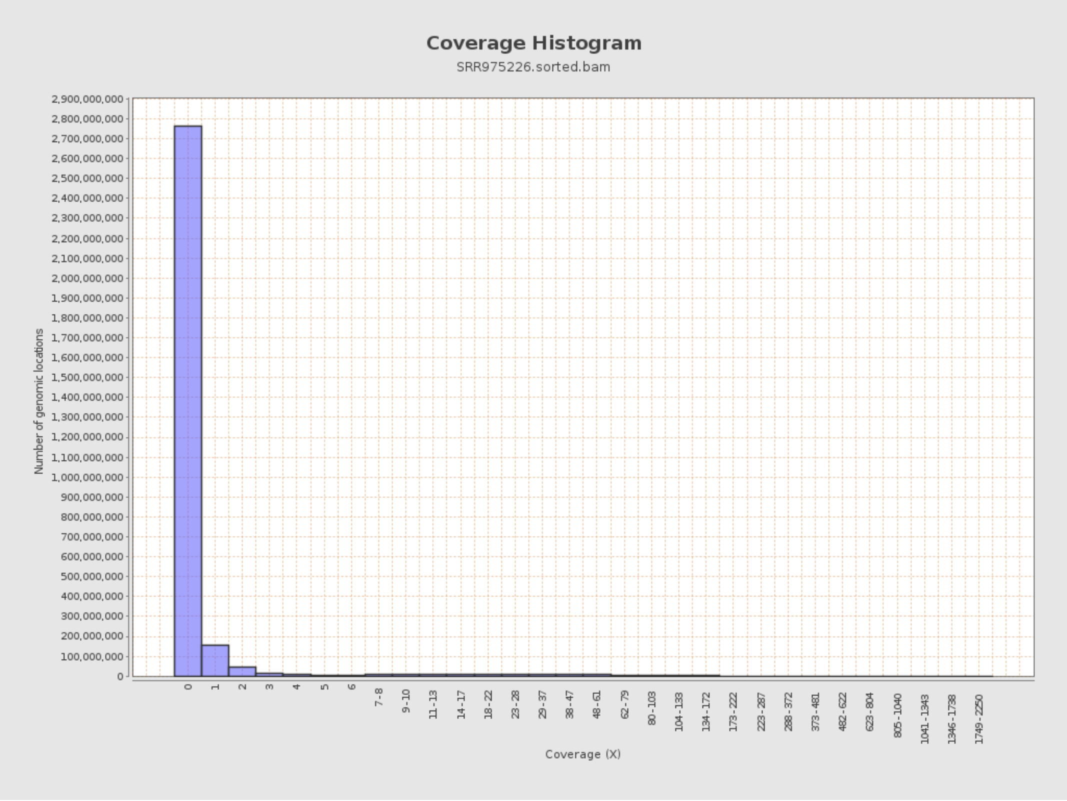
		bases	coverage	deviation
chr1	249250621	382870092	1.5361	10.8544
chr2	243199373	300525641	1.2357	9.3673
chr3	198022430	240139022	1.2127	9.1764
chr4	191154276	178795252	0.9353	8.4282
chr5	180915260	190851398	1.0549	8.5559
chr6	171115067	221071034	1.2919	10.2153
chr7	159138663	187524886	1.1784	9.5981
chr8	146364022	138925502	0.9492	7.8422
chr9	141213431	148289085	1.0501	8.4444
chr10	135534747	156197229	1.1525	8.9487
chr11	135006516	223963355	1.6589	11.4993
chr12	133851895	207965795	1.5537	10.6282
chr13	115169878	81794285	0.7102	7.2576
chr14	107349540	124690920	1.1615	9.2019
chr15	102531392	127759255	1.2461	9.3315
chr16	90354753	128030340	1.417	9.4844
chr17	81195210	183668383	2.2621	12.422
chr18	78077248	65873238	0.8437	7.608
chr19	59128983	174299942	2.9478	13.8274
chr20	63025520	85075931	1.3499	9.5428
chr21	48129895	40445034	0.8403	8.0027
chr22	51304566	64000719	1.2475	8.4004
chrMT	16571	400928	24.1946	39.9573
chrX	155270560	85614495	0.5514	4.9898

chrY	59373566	5694208	0.0959	1.5071

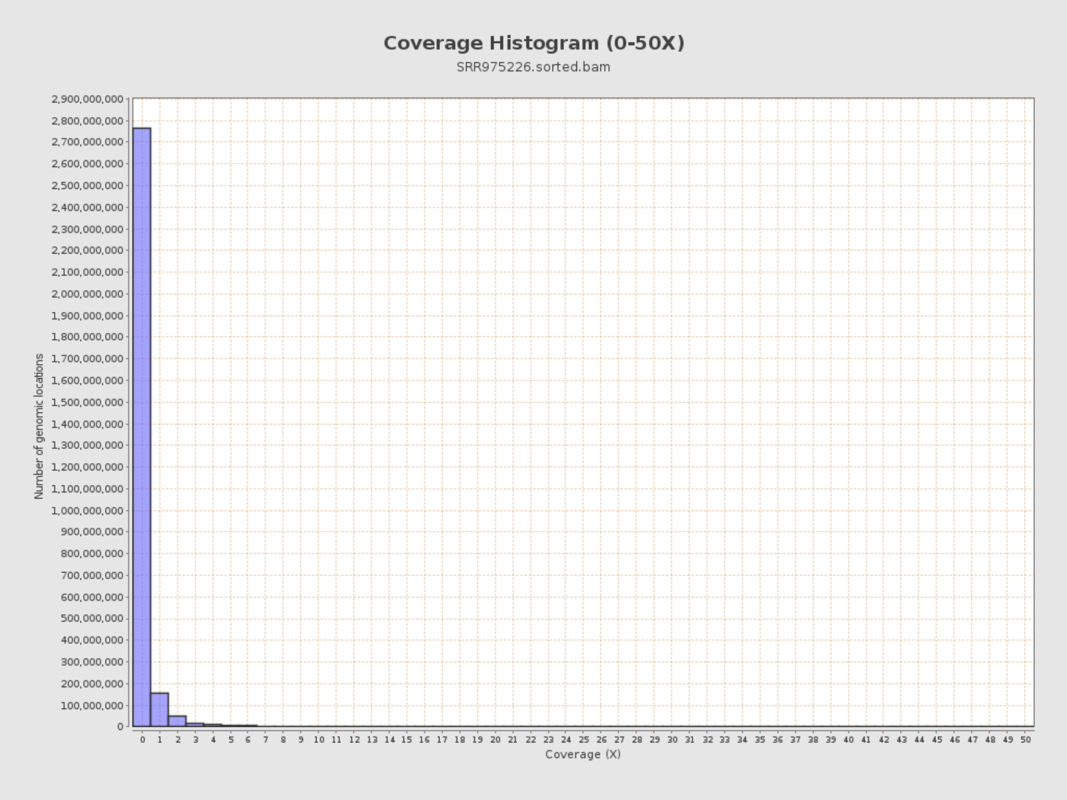
3. Results : Coverage across reference



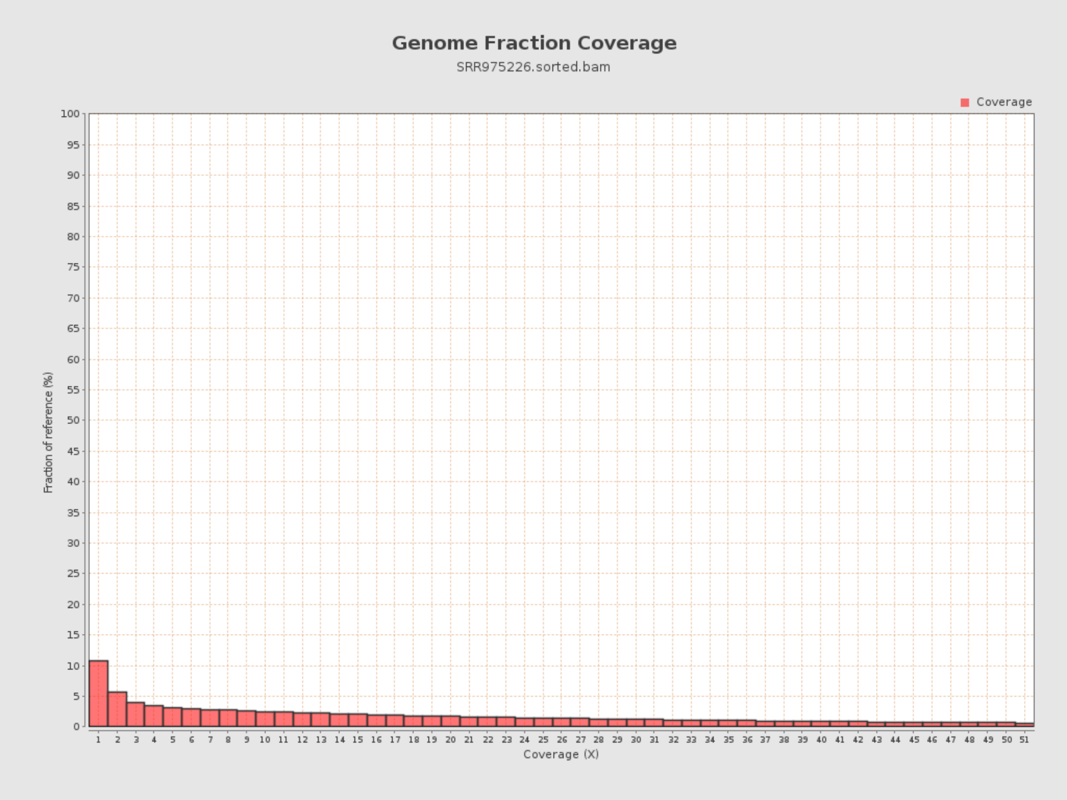
4. Results : Coverage Histogram



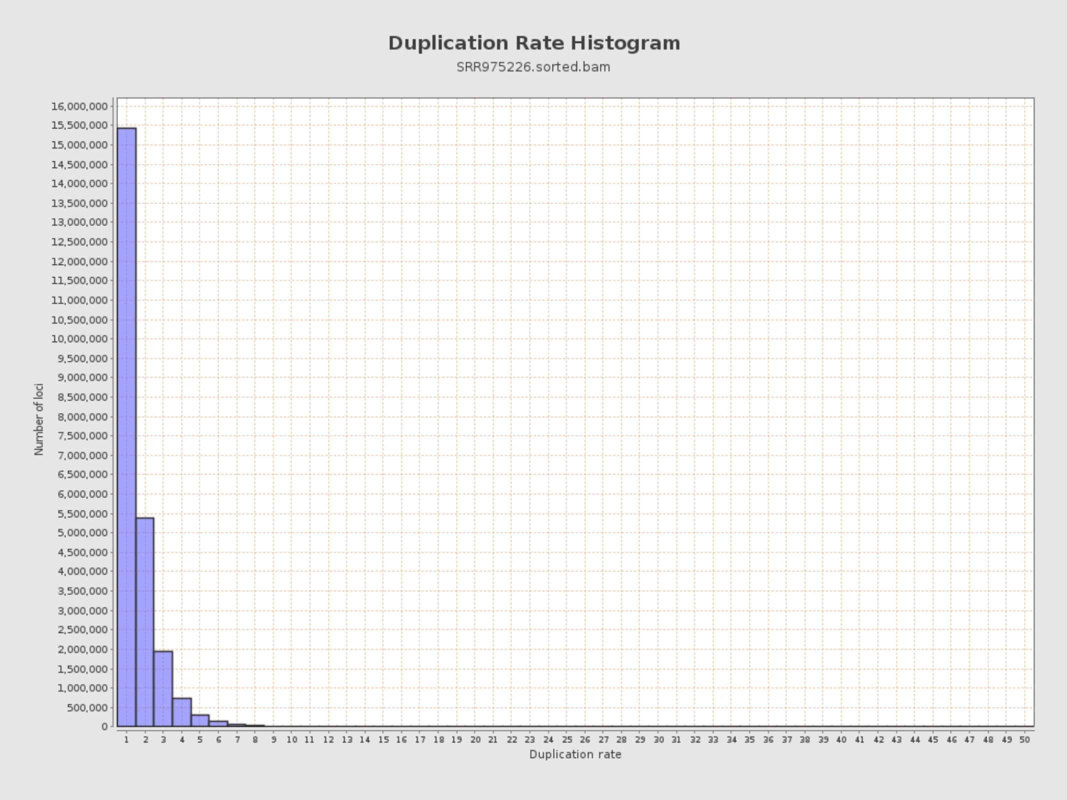
5. Results : Coverage Histogram (0-50X)



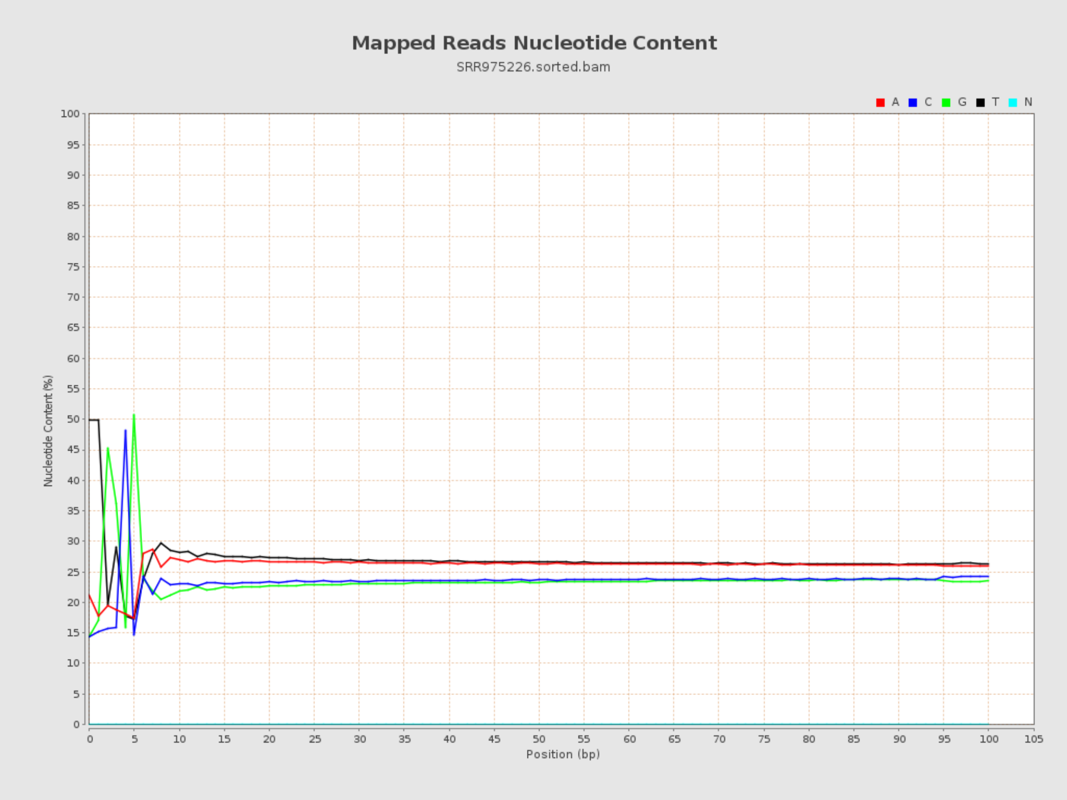
6. Results : Genome Fraction Coverage



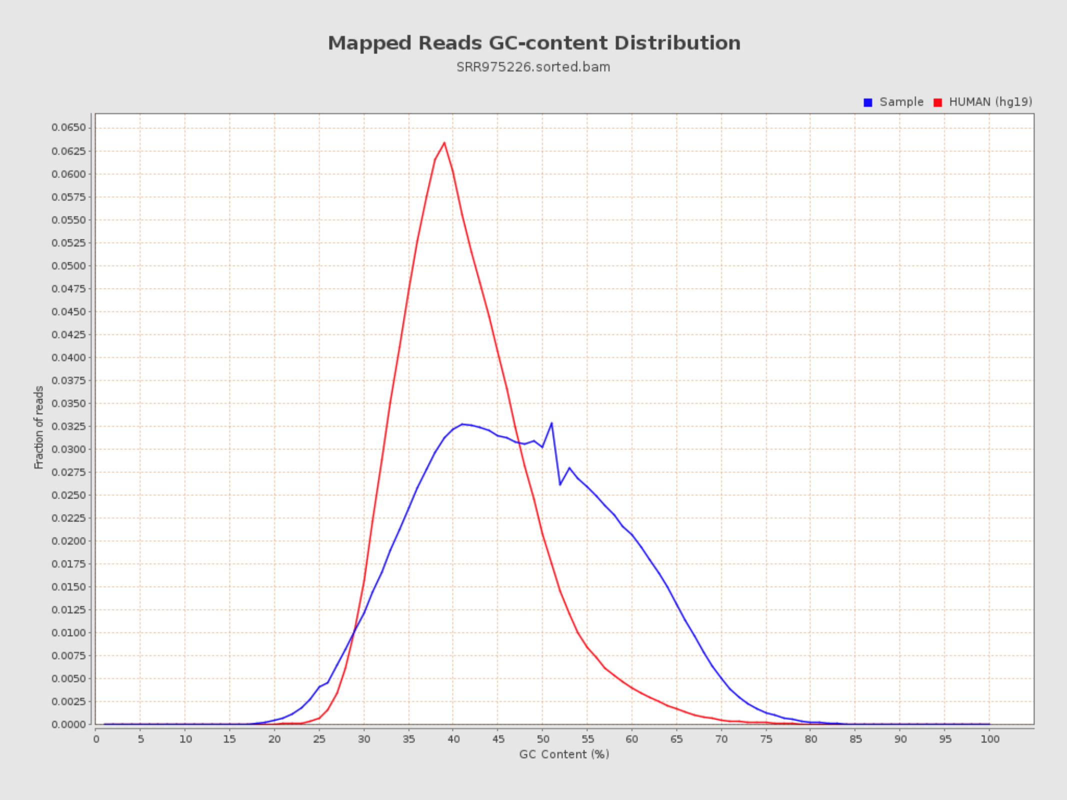
7. Results : Duplication Rate Histogram



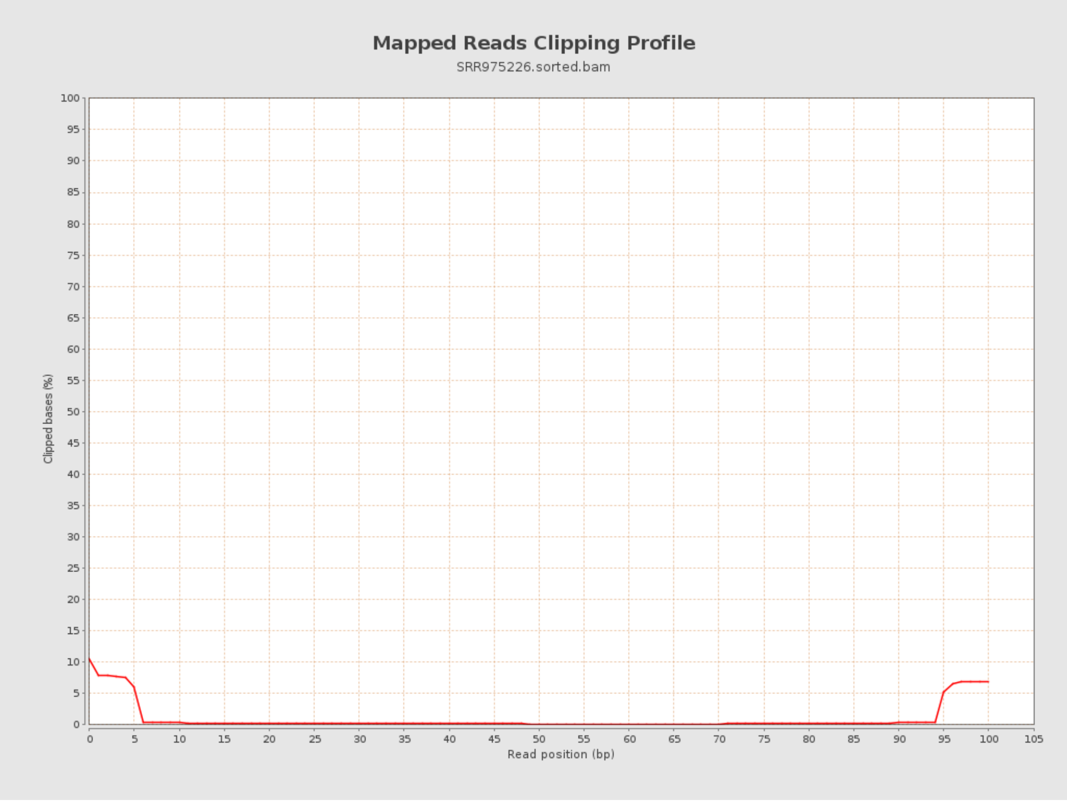
8. Results : Mapped Reads Nucleotide Content



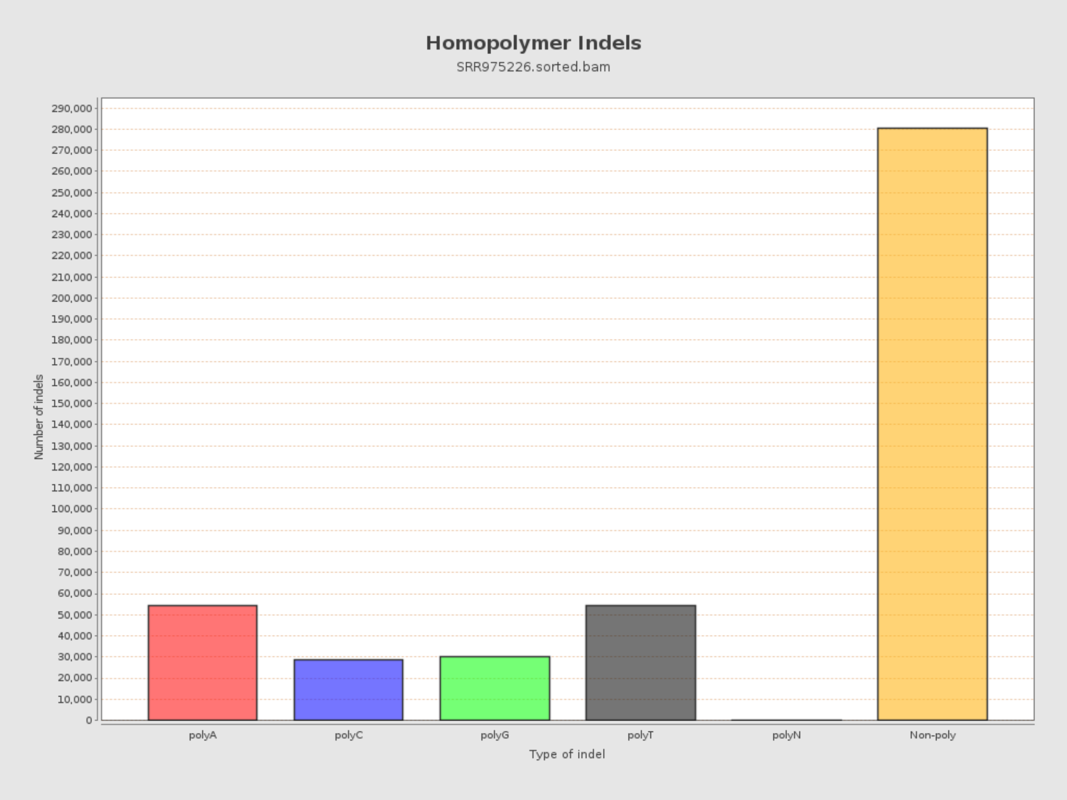
9. Results : Mapped Reads GC-content Distribution



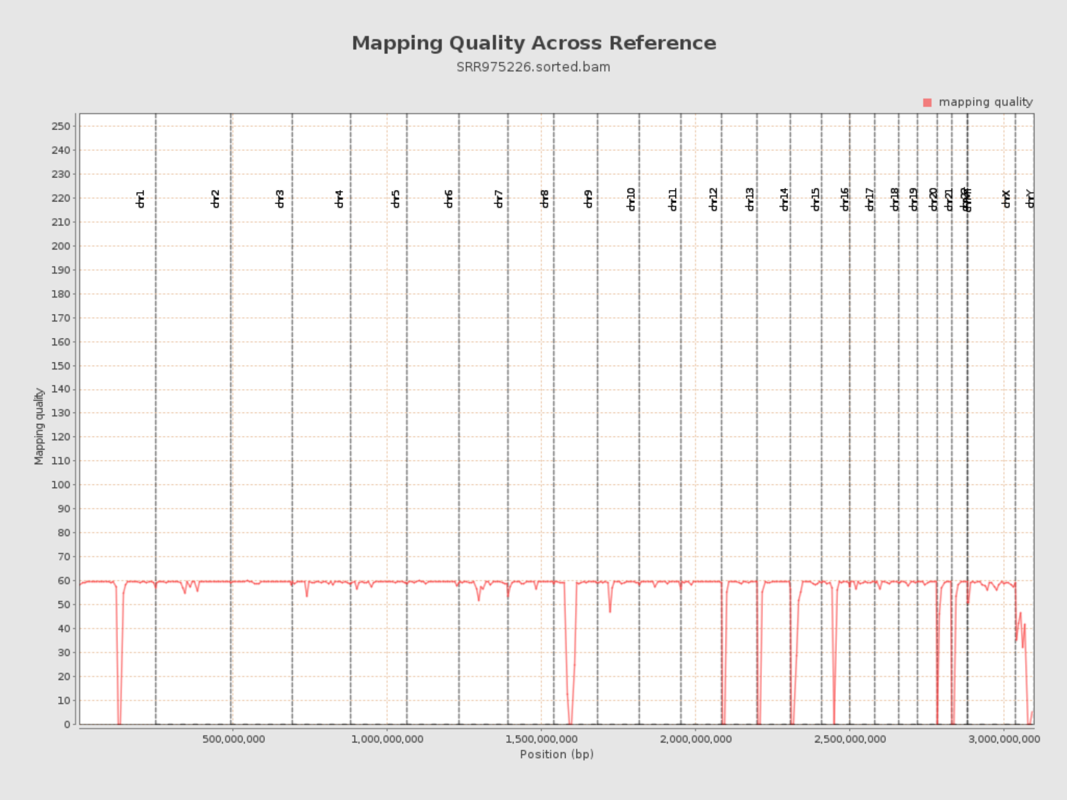
10. Results : Mapped Reads Clipping Profile



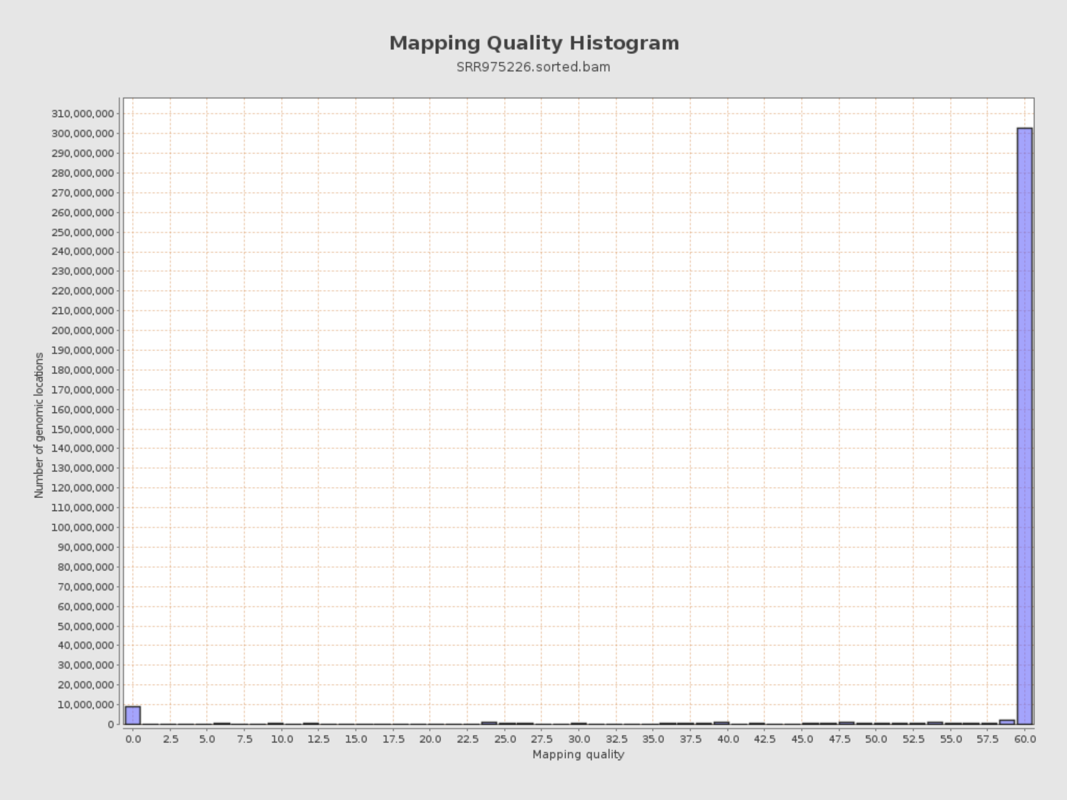
11. Results : Homopolymer Indels



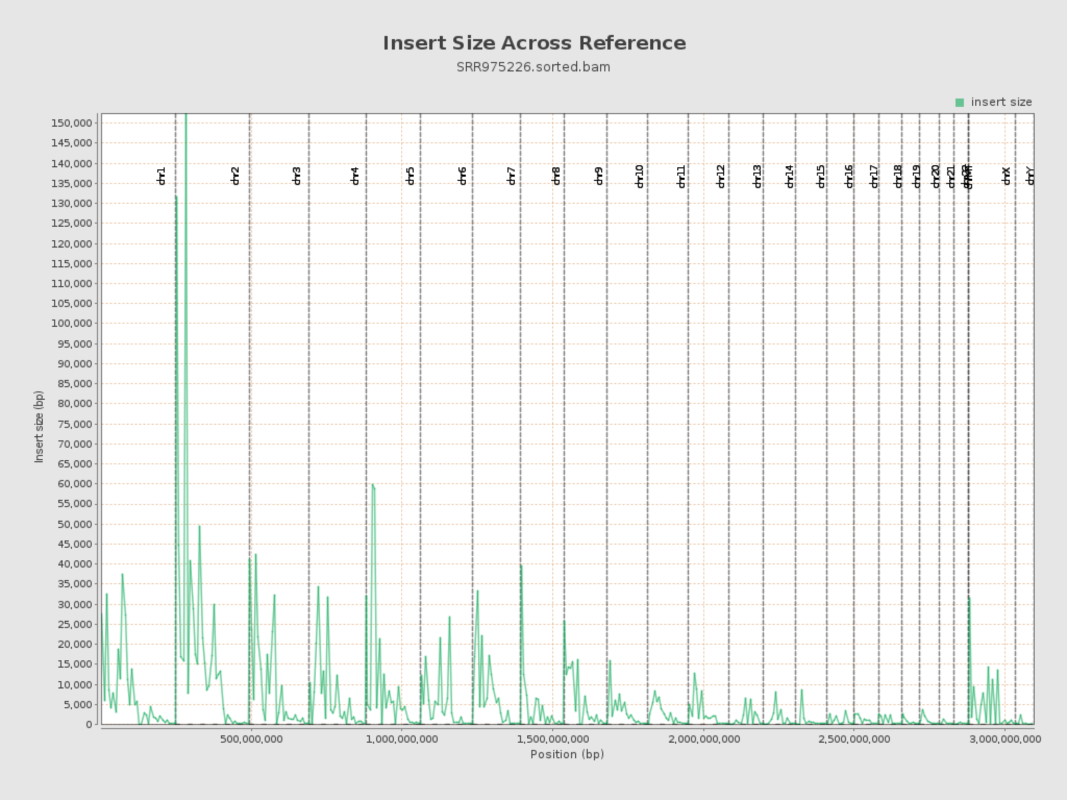
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram