Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:37:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975224.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_SRR975224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975224_1.fastq.gz SRR975224_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:37:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	128,470,164
Mapped reads	128,004,436 / 99.64%
Unmapped reads	465,728 / 0.36%
Mapped paired reads	128,004,436 / 99.64%
Mapped reads, first in pair	63,994,164 / 49.81%
Mapped reads, second in pair	64,010,272 / 49.83%
Mapped reads, both in pair	127,808,424 / 99.48%
Mapped reads, singletons	196,012 / 0.15%
Secondary alignments	0
Supplementary alignments	281,419 / 0.22%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	87,289,641 / 67.95%
Duplication rate	49.78%
Clipped reads	79,780,283 / 62.1%

2.2. ACGT Content

Number/percentage of A's	3,153,176,626 / 26.9%
Number/percentage of C's	2,562,838,629 / 21.87%
Number/percentage of T's	3,187,861,787 / 27.2%
Number/percentage of G's	2,816,583,606 / 24.03%
Number/percentage of N's	351,164 / 0%

GC Percentage	45.9%

2.3. Coverage

Mean	3.7875
Standard Deviation	51.7621

2.4. Mapping Quality

Mean Mapping Quality	55.89

2.5. Insert size

Mean	63,639.42
Standard Deviation	2,494,992.63
P25/Median/P75	146 / 182 / 229

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	70,655,074
Insertions	1,188,150
Mapped reads with at least one insertion	0.92%
Deletions	2,662,462
Mapped reads with at least one deletion	2.05%
Homopolymer indels	46.24%

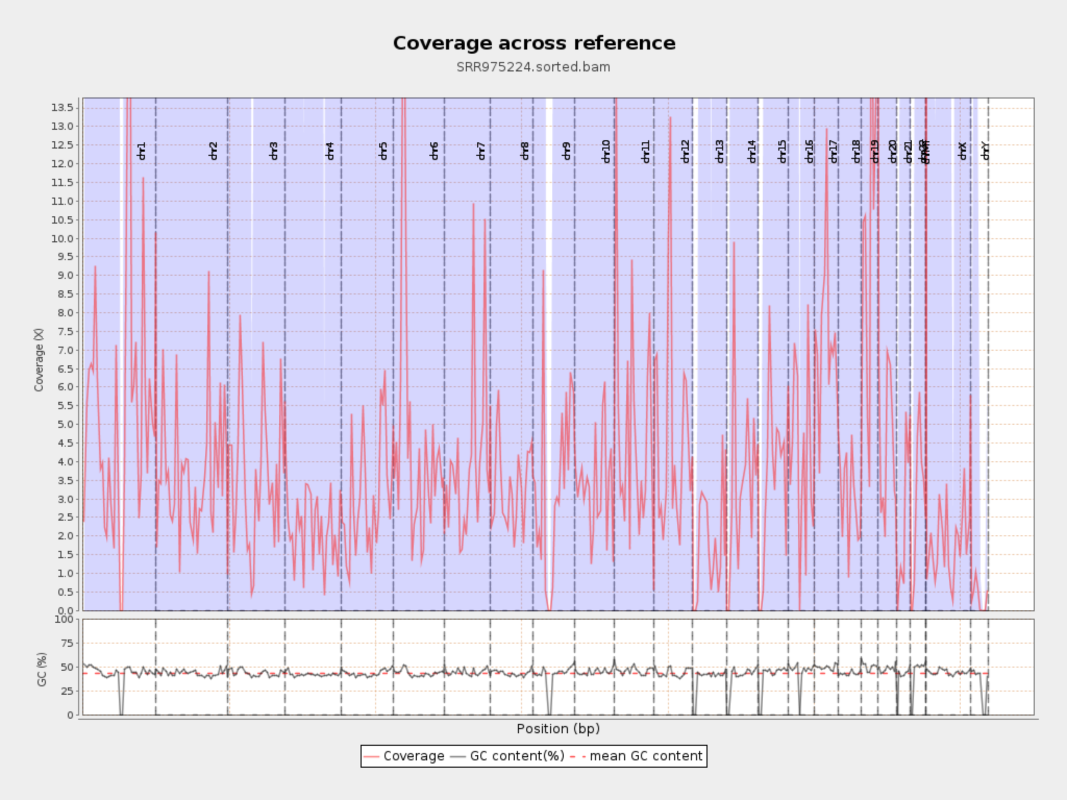
2.7. Chromosome stats

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

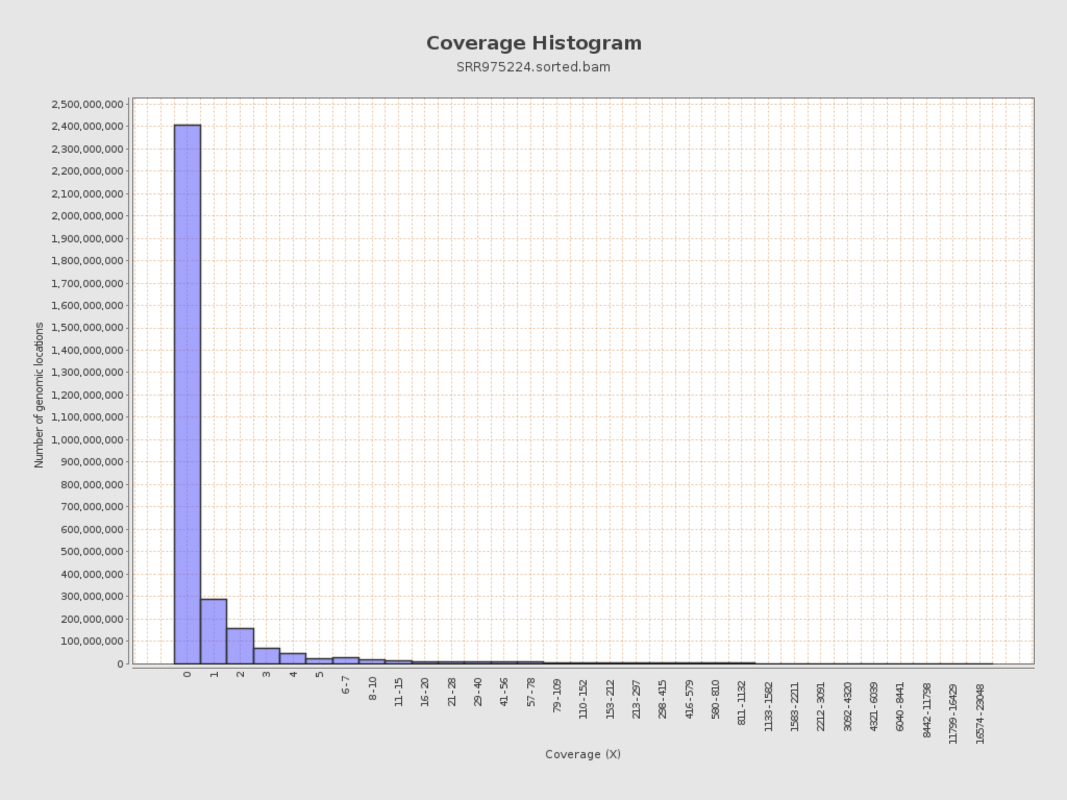
		bases	**coverage**	**deviation**
chr1	249250621	1371124168	5.501	67.0645
chr2	243199373	903257257	3.7141	48.2599
chr3	198022430	710698023	3.589	46.8534
chr4	191154276	425345459	2.2251	34.6288
chr5	180915260	564042207	3.1177	45.7965
chr6	171115067	779111748	4.5531	60.6029
chr7	159138663	633485729	3.9807	56.888
chr8	146364022	488285818	3.3361	44.3475
chr9	141213431	457204751	3.2377	44.4217
chr10	135534747	460063665	3.3944	44.0152
chr11	135006516	661572772	4.9003	63.0715
chr12	133851895	649377845	4.8515	61.5177
chr13	115169878	204056308	1.7718	34.2156
chr14	107349540	369357024	3.4407	45.969
chr15	102531392	344643210	3.3613	45.9914
chr16	90354753	367680054	4.0693	49.4859
chr17	81195210	607127217	7.4774	74.766
chr18	78077248	238275746	3.0518	46.4092
chr19	59128983	635320504	10.7447	101.4632
chr20	63025520	276115455	4.381	58.2658
chr21	48129895	116609512	2.4228	41.1325
chr22	51304566	150517746	2.9338	38.842
chrMT	16571	744902	44.9521	73.7531
chrX	155270560	288469676	1.8579	28.8228

chrY	59373566	22335974	0.3762	10.9453

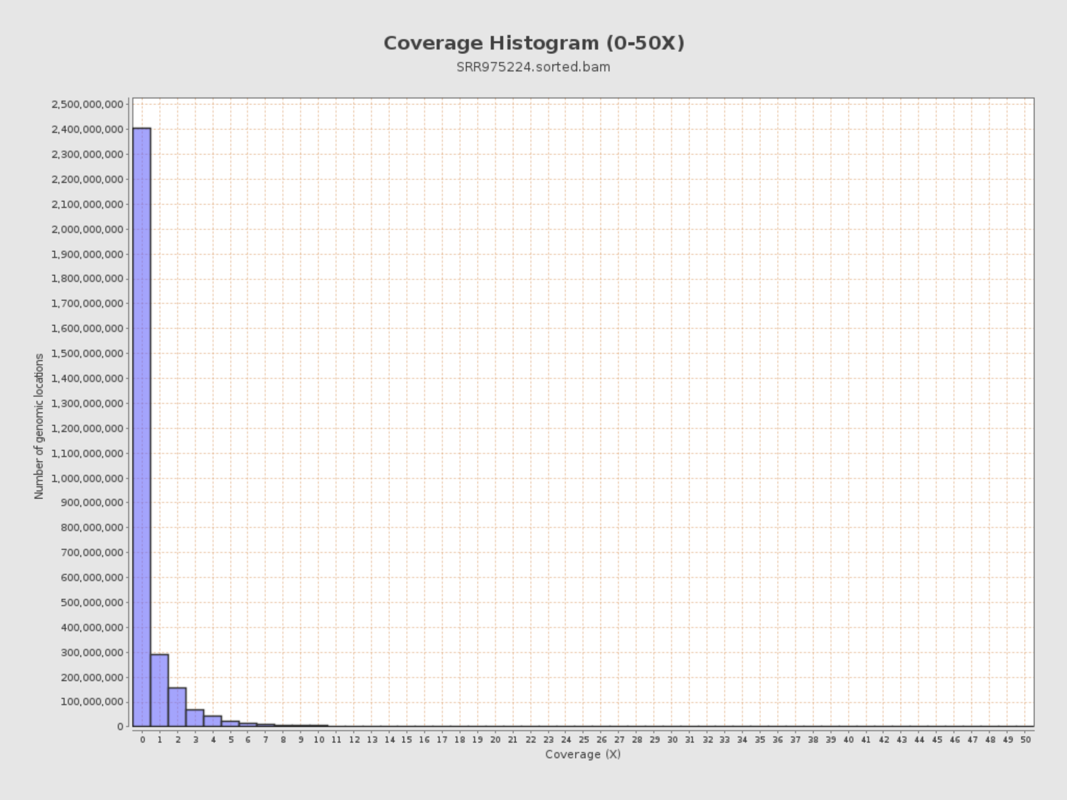
3. Results : Coverage across reference



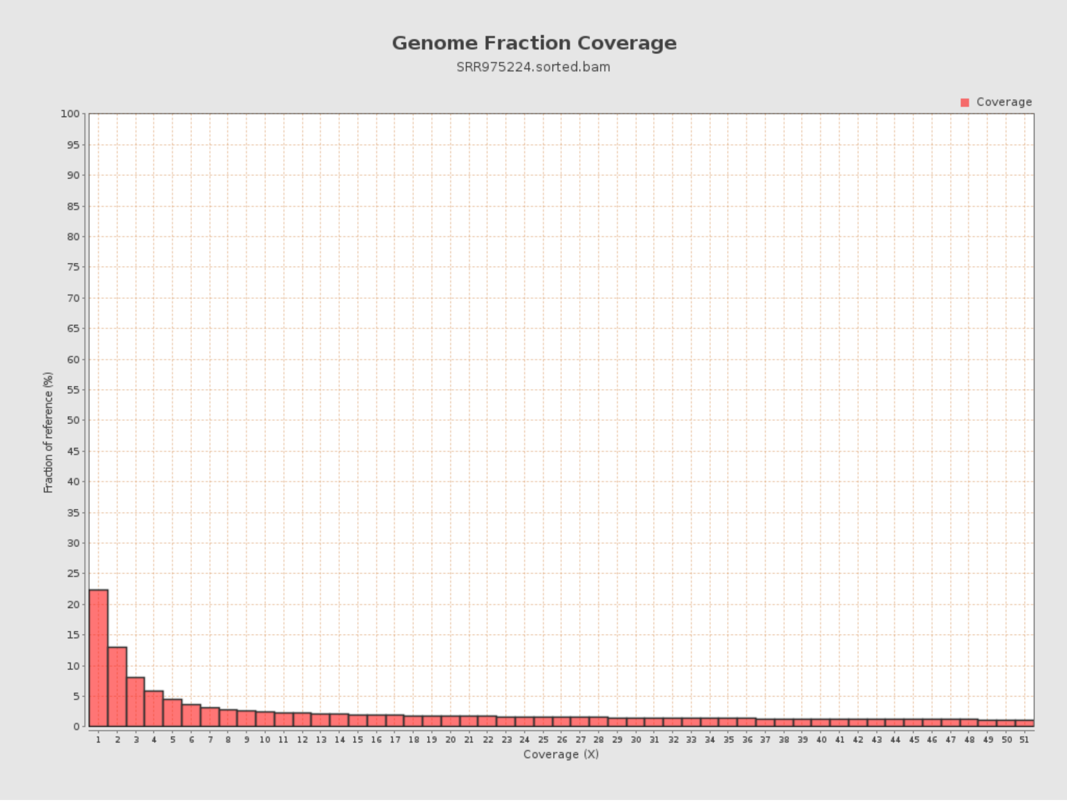
4. Results : Coverage Histogram



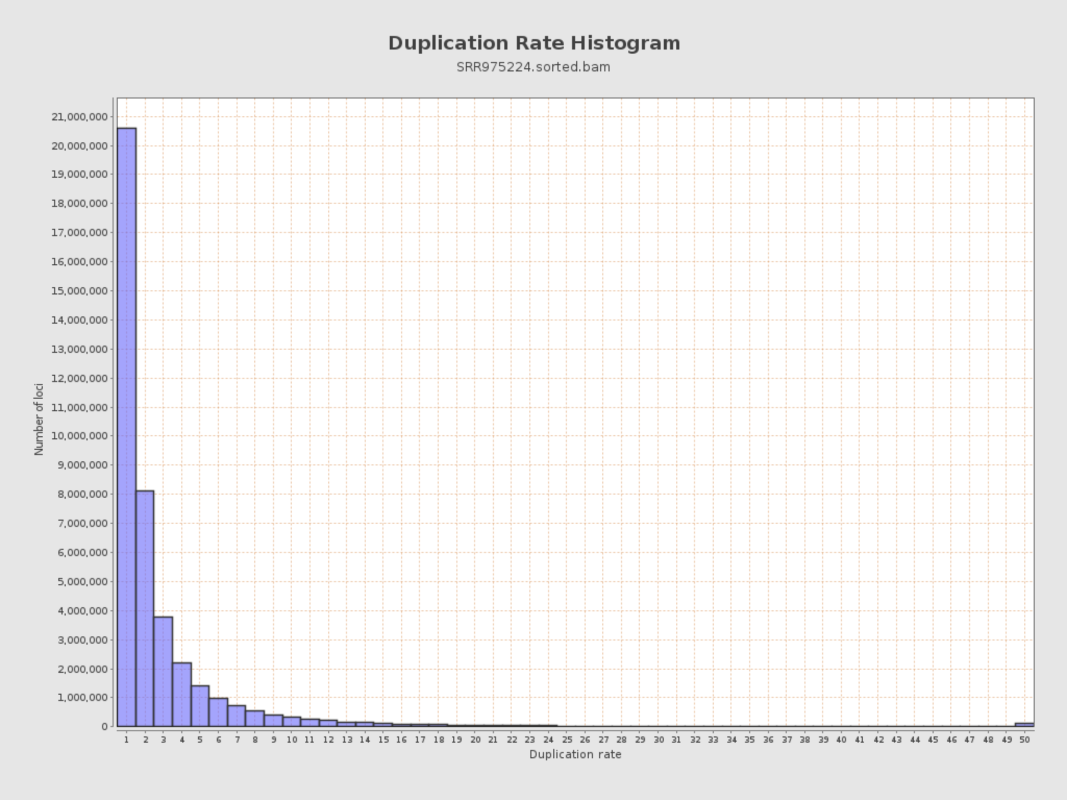
5. Results : Coverage Histogram (0-50X)



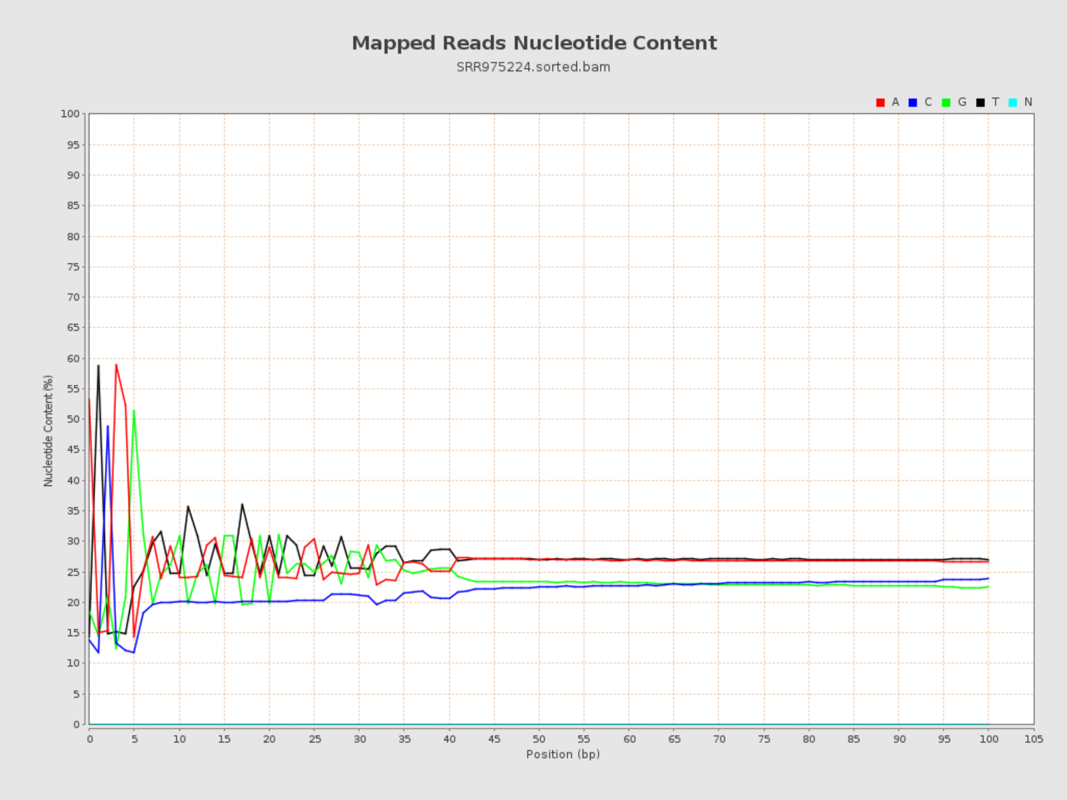
6. Results : Genome Fraction Coverage



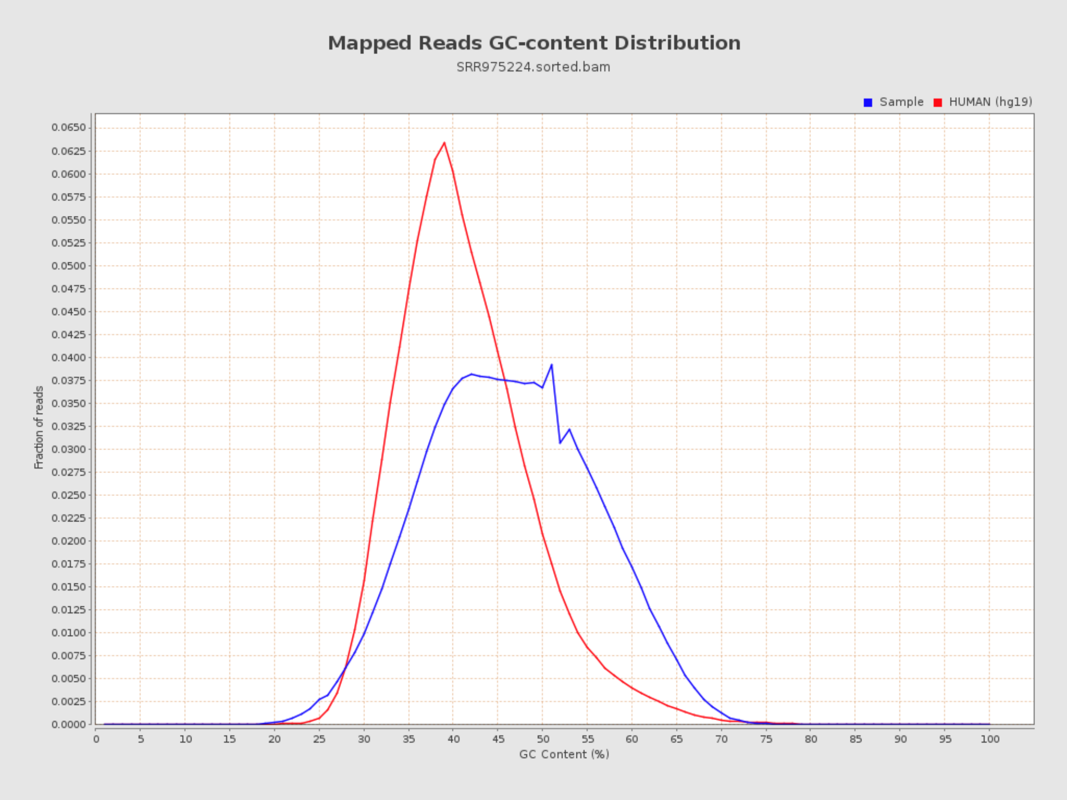
7. Results : Duplication Rate Histogram



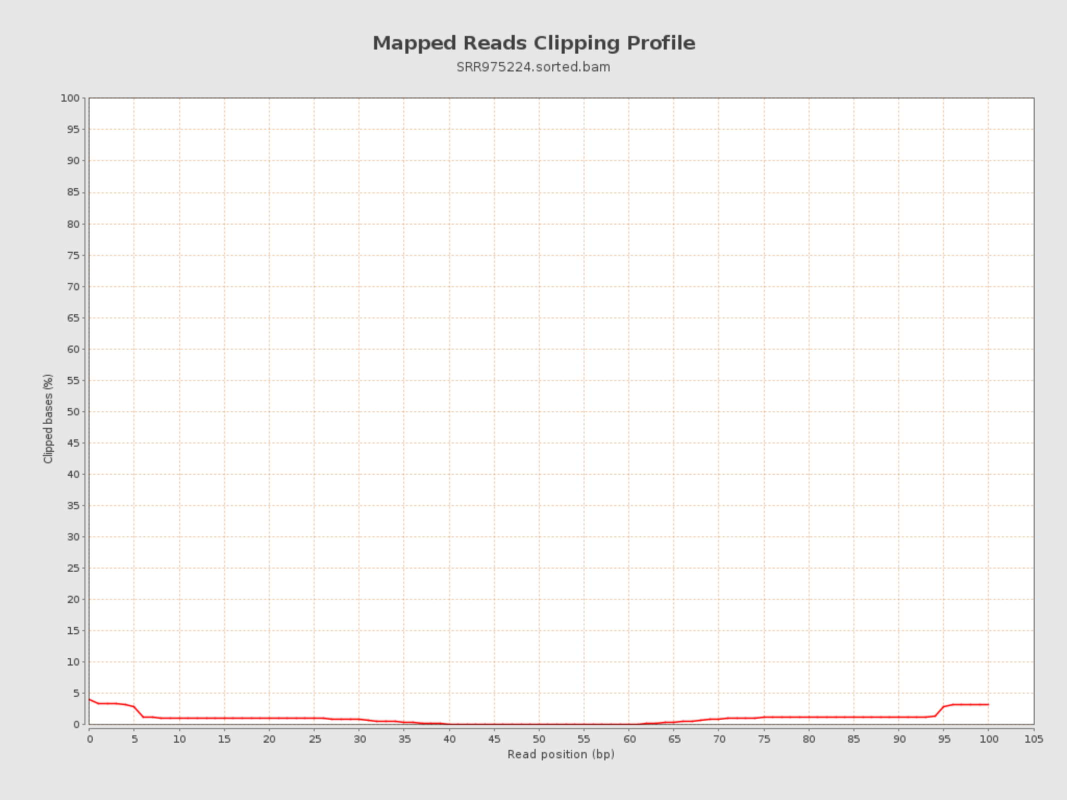
8. Results : Mapped Reads Nucleotide Content



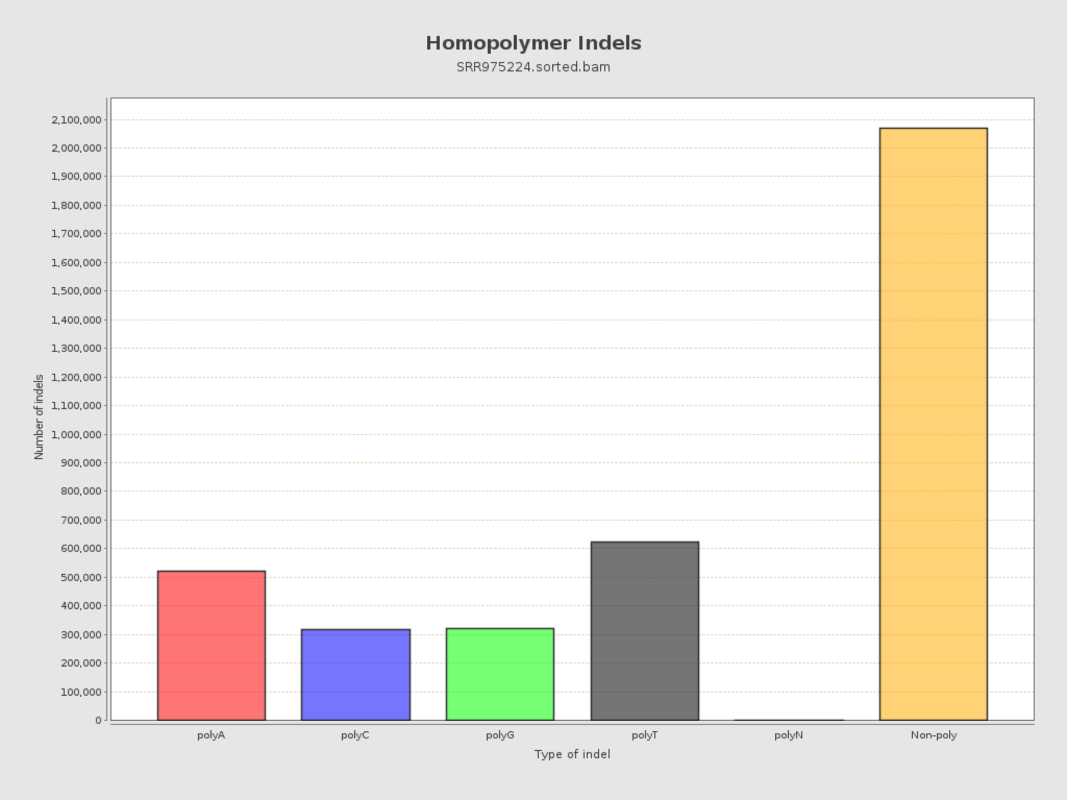
9. Results : Mapped Reads GC-content Distribution



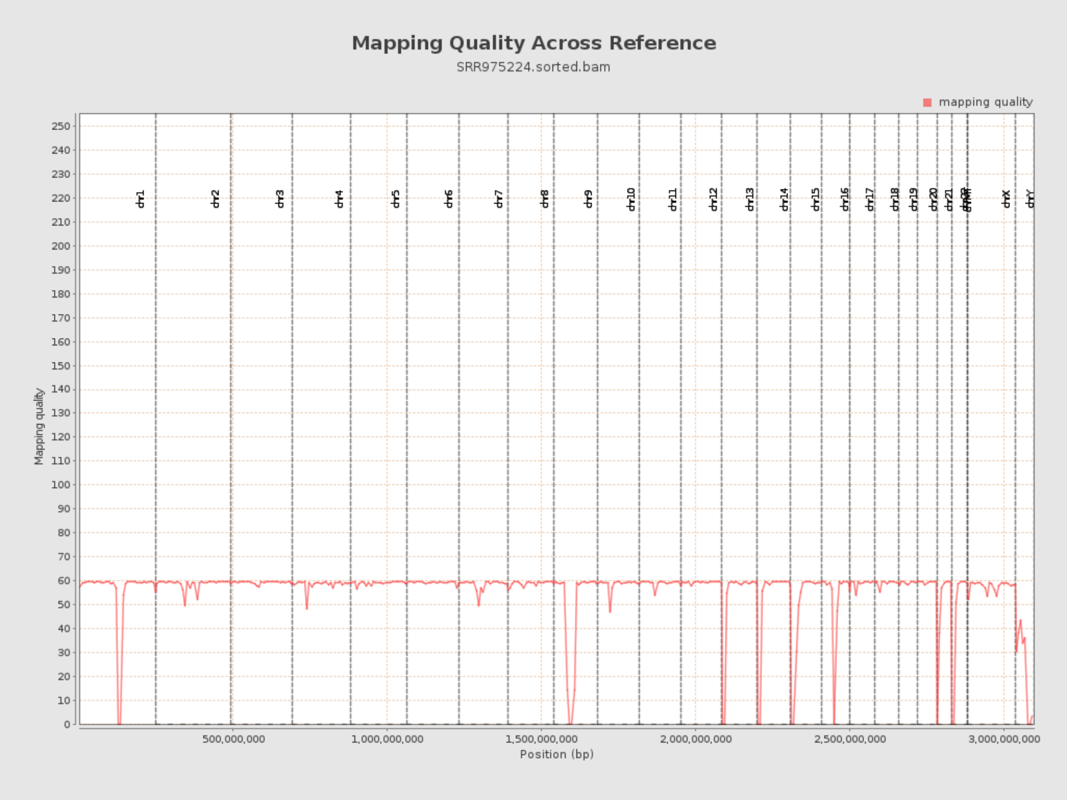
10. Results : Mapped Reads Clipping Profile



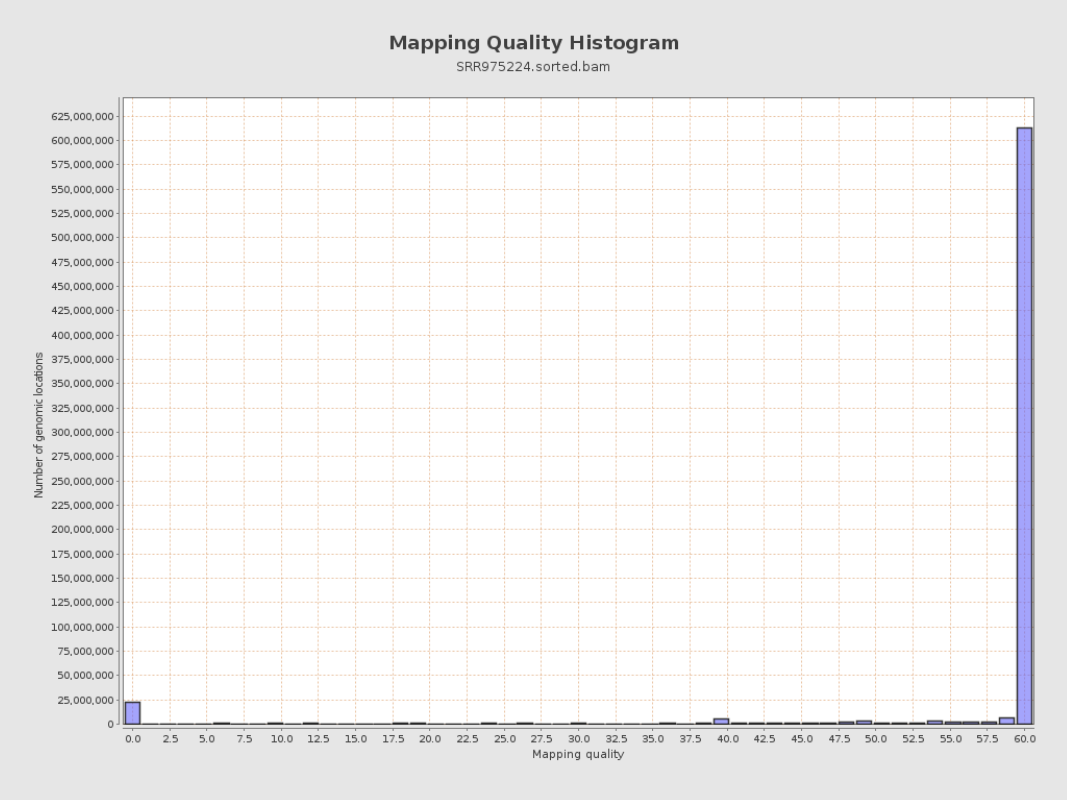
11. Results : Homopolymer Indels



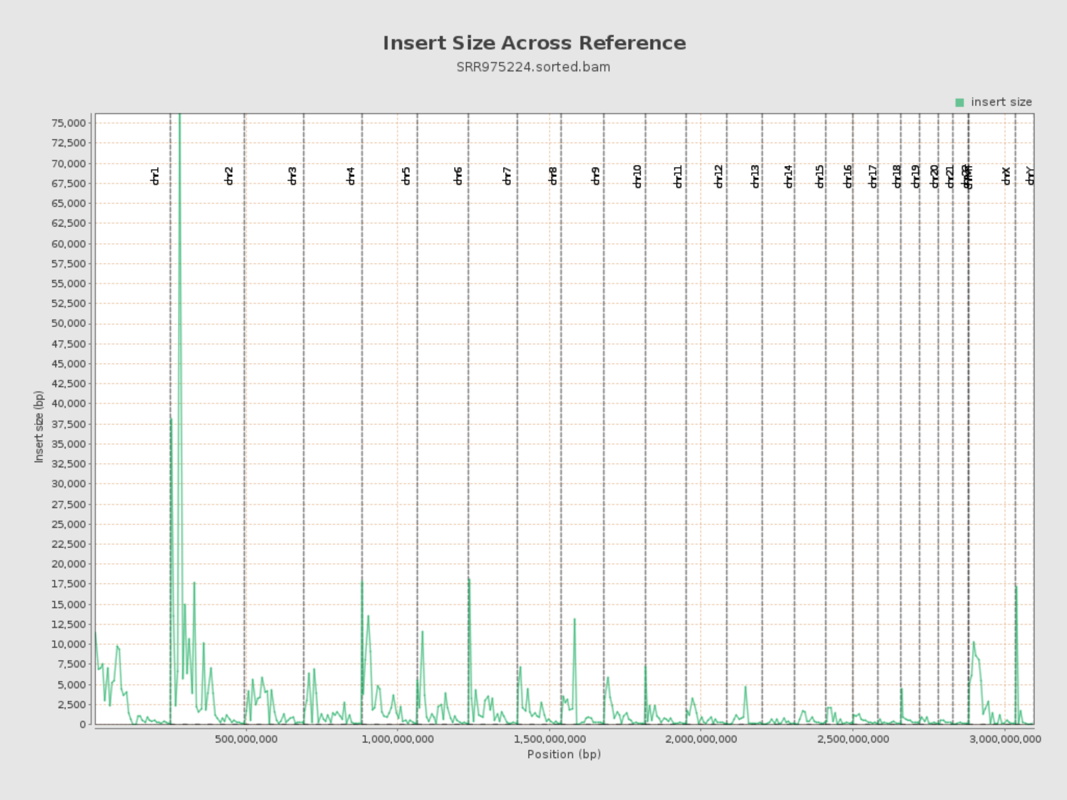
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram