Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:39:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975225.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_SRR975225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975225_1.fastq.gz SRR975225_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:39:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,523,284
Mapped reads	3,478,122 / 98.72%
Unmapped reads	45,162 / 1.28%
Mapped paired reads	3,478,122 / 98.72%
Mapped reads, first in pair	1,738,359 / 49.34%
Mapped reads, second in pair	1,739,763 / 49.38%
Mapped reads, both in pair	3,462,964 / 98.29%
Mapped reads, singletons	15,158 / 0.43%
Secondary alignments	0
Supplementary alignments	16,728 / 0.47%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	171,787 / 4.88%
Duplication rate	2.47%
Clipped reads	2,152,527 / 61.09%

2.2. ACGT Content

Number/percentage of A's	93,861,347 / 29.74%
Number/percentage of C's	60,281,857 / 19.1%
Number/percentage of T's	94,038,899 / 29.8%
Number/percentage of G's	67,407,294 / 21.36%
Number/percentage of N's	4,658 / 0%

GC Percentage	40.46%

2.3. Coverage

Mean	0.102
Standard Deviation	1.1187

2.4. Mapping Quality

Mean Mapping Quality	52.54

2.5. Insert size

Mean	50,792.31
Standard Deviation	2,156,056.44
P25/Median/P75	139 / 172 / 217

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	2,627,522
Insertions	56,885
Mapped reads with at least one insertion	1.58%
Deletions	104,808
Mapped reads with at least one deletion	2.94%
Homopolymer indels	44.18%

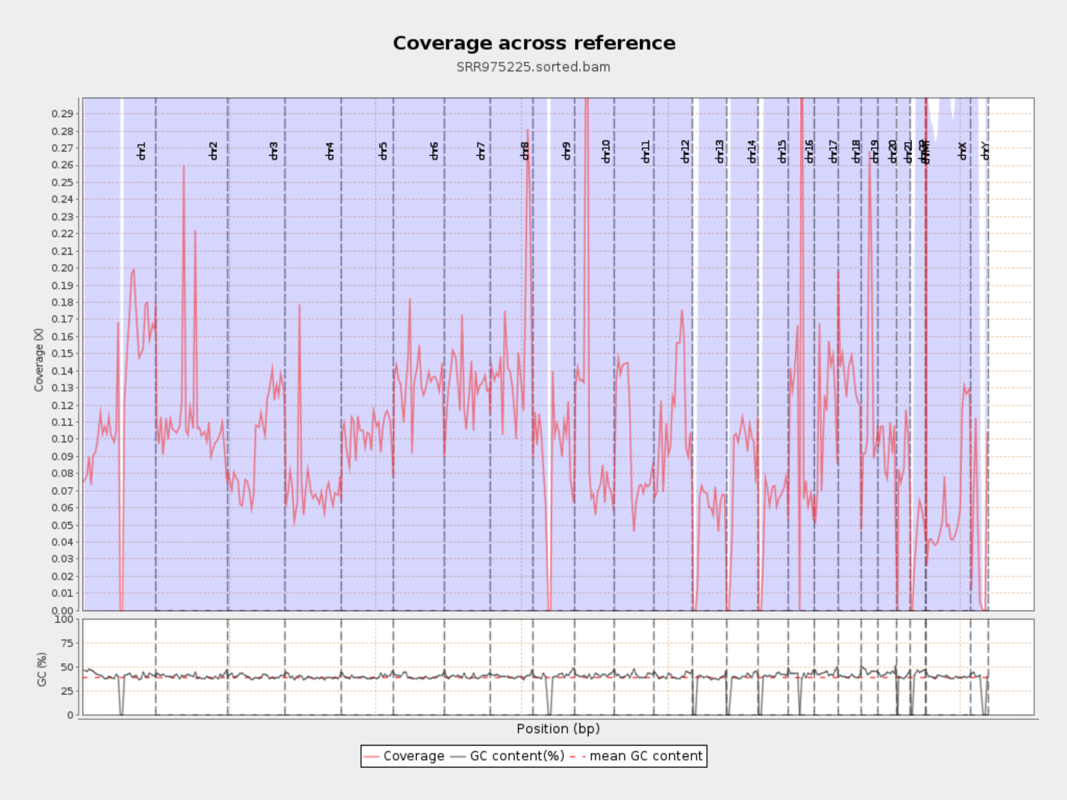
2.7. Chromosome stats

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

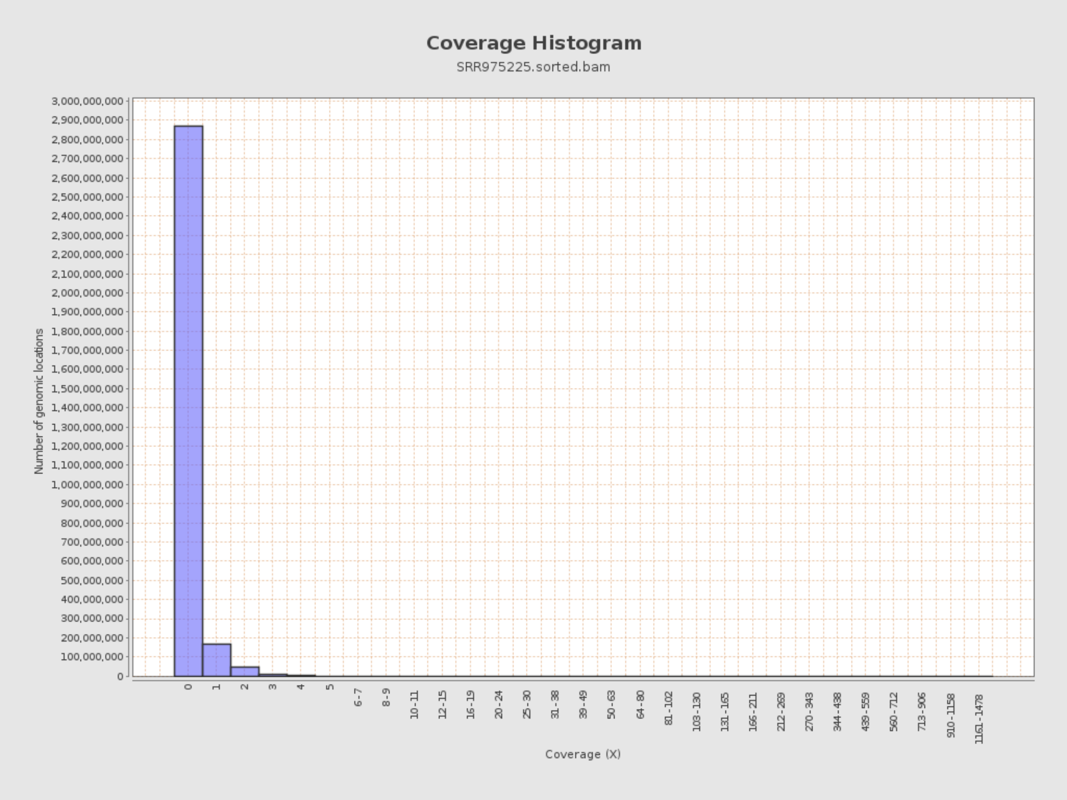
		bases	coverage	deviation
chr1	249250621	30764133	0.1234	1.0726
chr2	243199373	27390970	0.1126	1.6236
chr3	198022430	19278865	0.0974	0.4032
chr4	191154276	13831018	0.0724	0.7686
chr5	180915260	18717057	0.1035	0.4227
chr6	171115067	23081726	0.1349	0.6512
chr7	159138663	20760072	0.1305	1.2446
chr8	146364022	22172457	0.1515	0.5972
chr9	141213431	12545322	0.0888	1.1234
chr10	135534747	15020411	0.1108	2.7394
chr11	135006516	13107805	0.0971	0.787
chr12	133851895	14880925	0.1112	0.4248
chr13	115169878	6152549	0.0534	0.2831
chr14	107349540	8948527	0.0834	0.413
chr15	102531392	5860224	0.0572	0.2928
chr16	90354753	10773169	0.1192	2.5075
chr17	81195210	9454267	0.1164	1.3299
chr18	78077248	10831878	0.1387	1.2469
chr19	59128983	7699043	0.1302	0.8106
chr20	63025520	5995372	0.0951	0.432
chr21	48129895	3898411	0.081	0.4776
chr22	51304566	2033536	0.0396	0.3497
chrMT	16571	110936	6.6946	4.6172
chrX	155270560	9810368	0.0632	0.4334

chrY	59373566	2664561	0.0449	1.4497

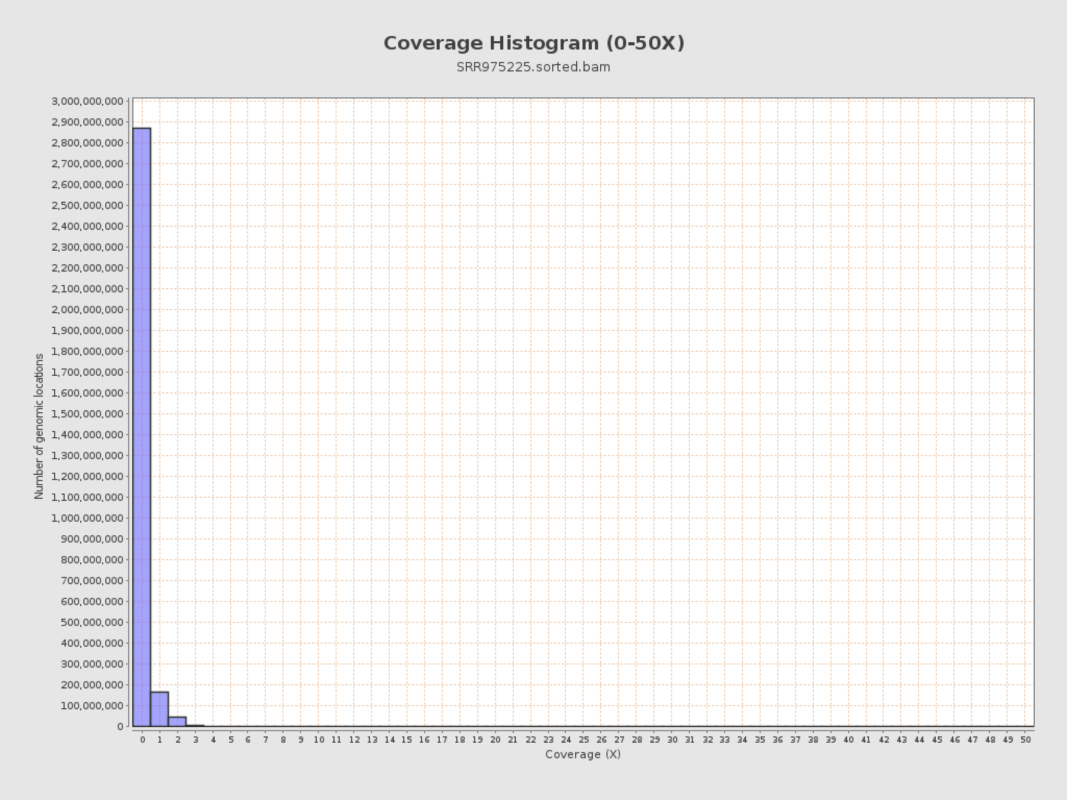
3. Results : Coverage across reference



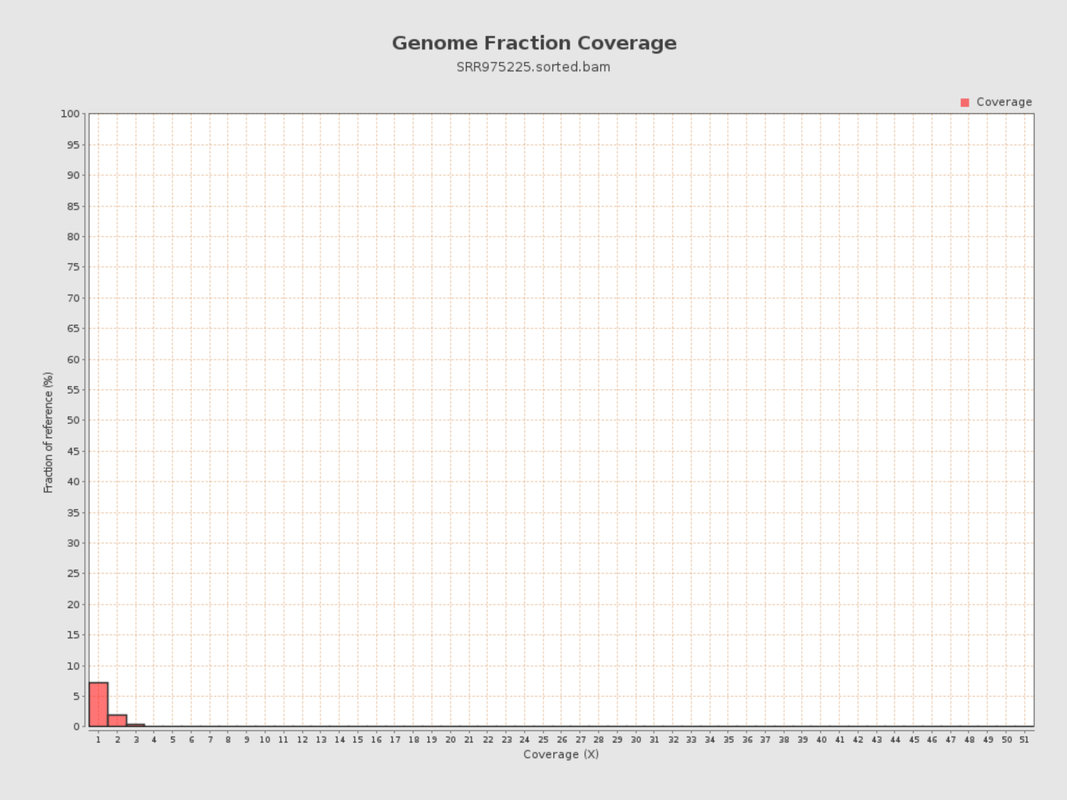
4. Results : Coverage Histogram



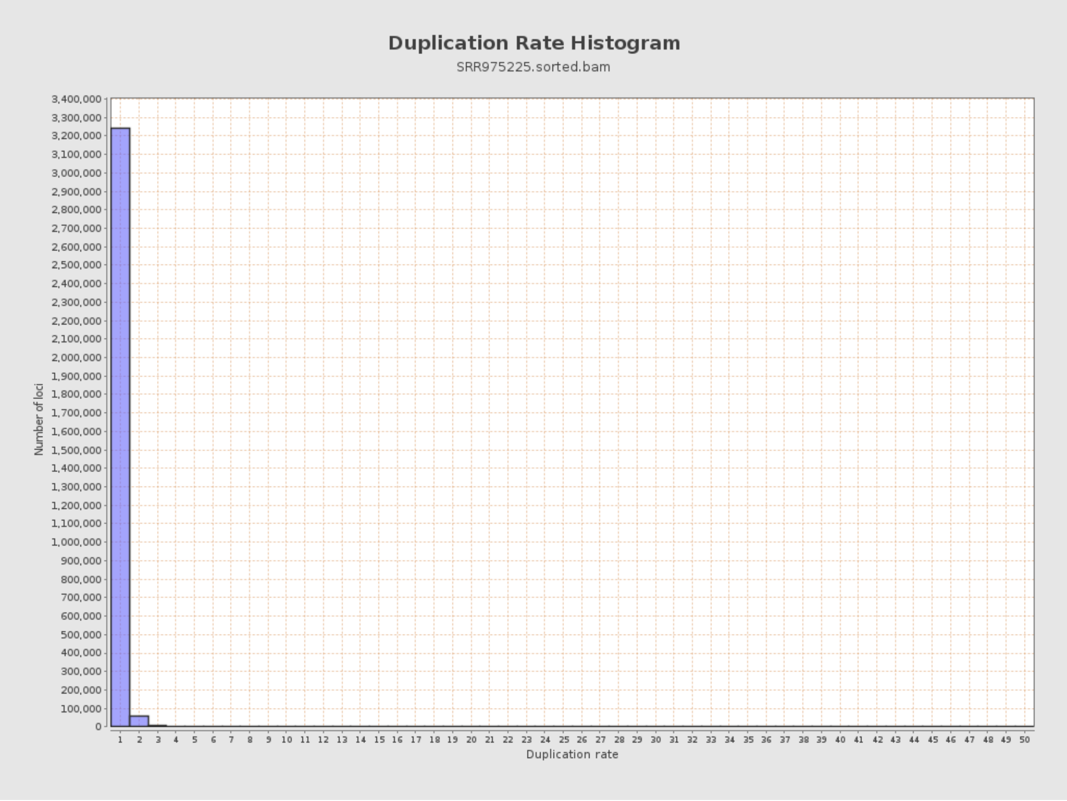
5. Results : Coverage Histogram (0-50X)



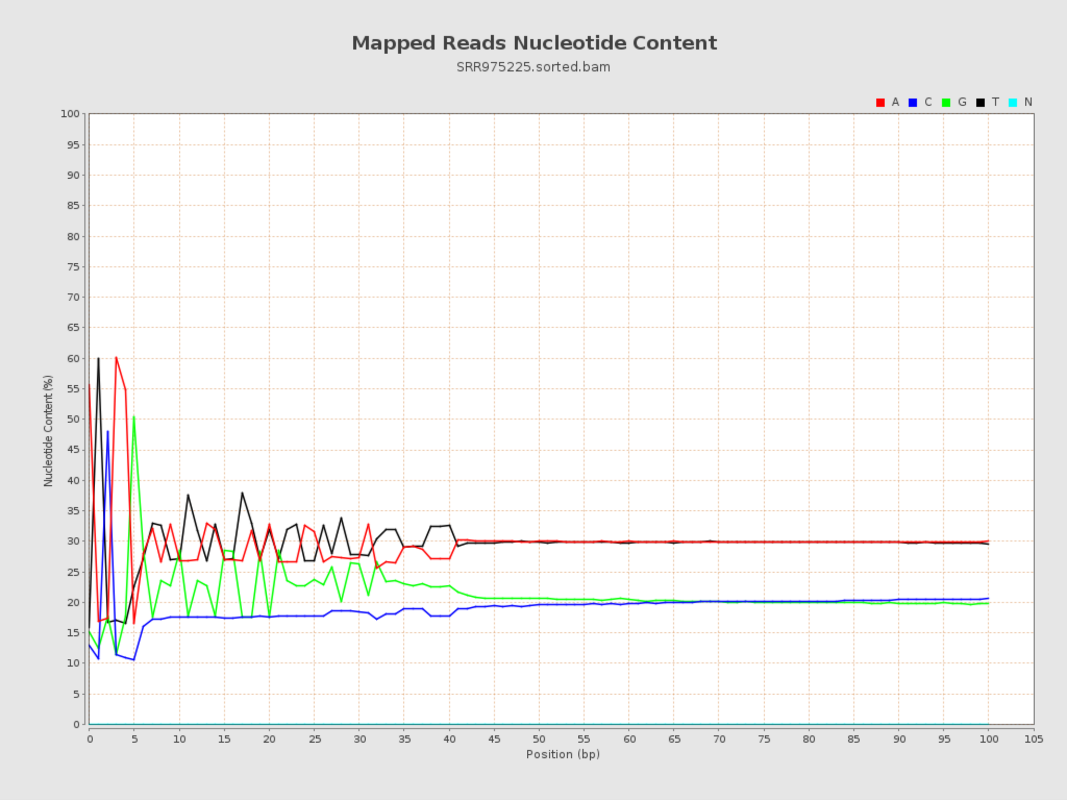
6. Results : Genome Fraction Coverage



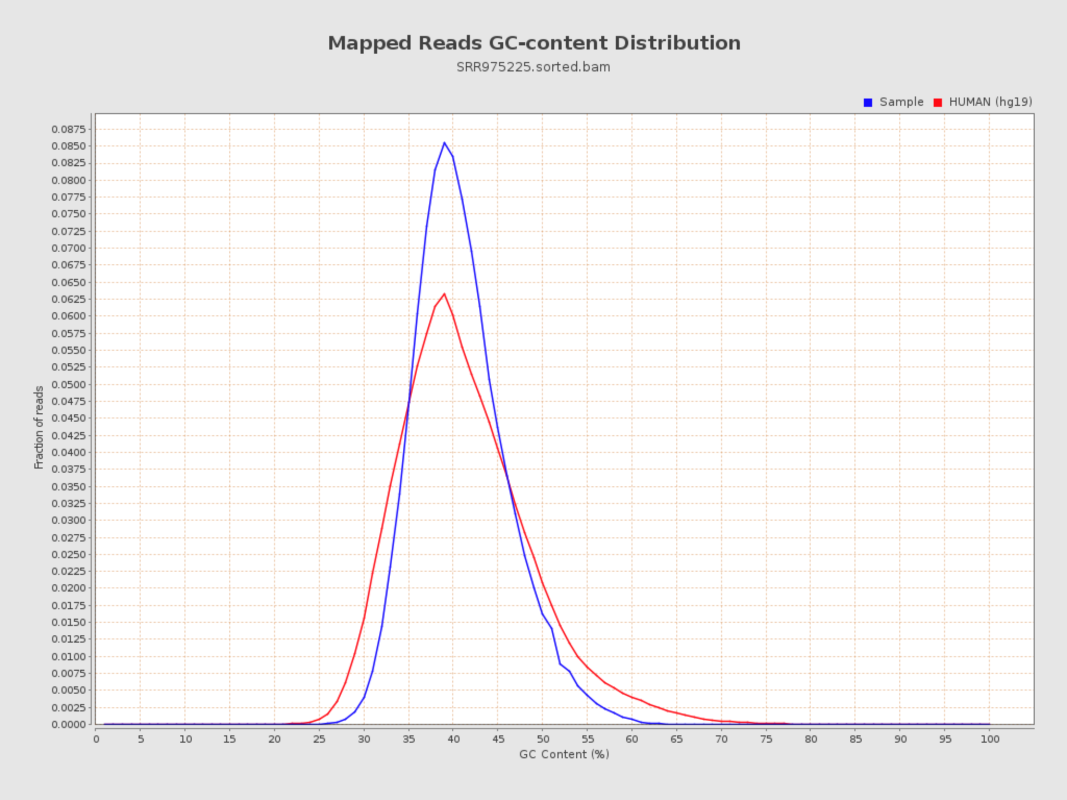
7. Results : Duplication Rate Histogram



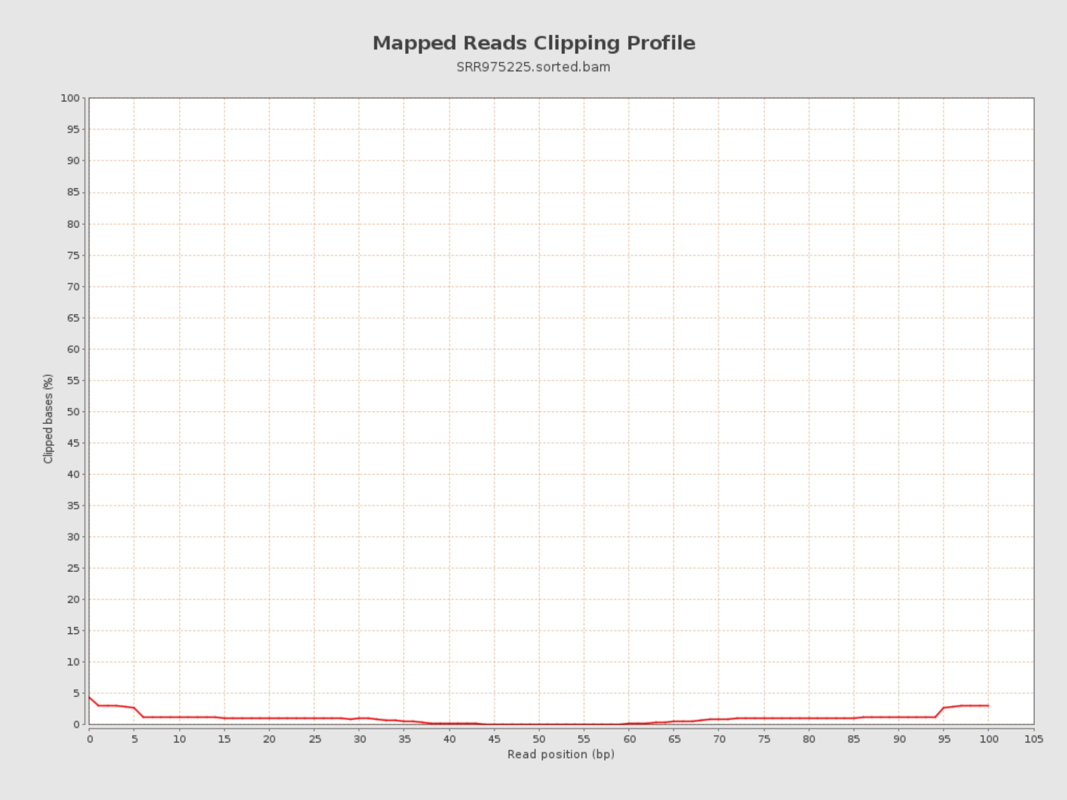
8. Results : Mapped Reads Nucleotide Content



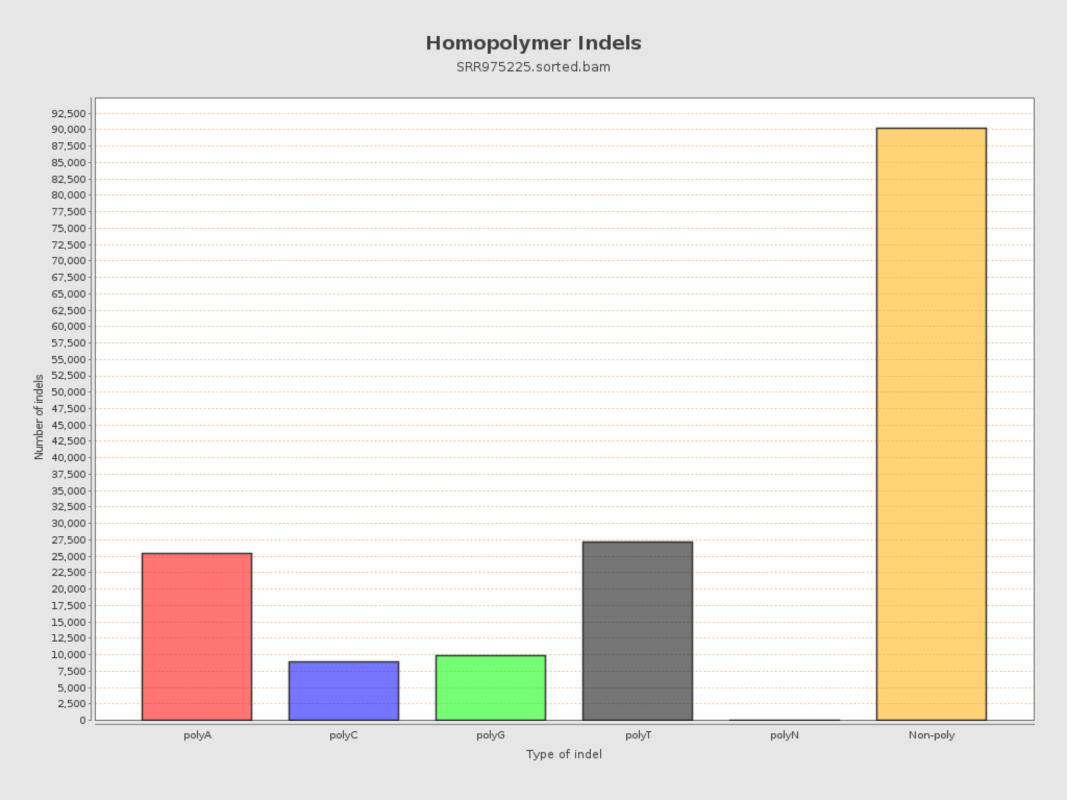
9. Results : Mapped Reads GC-content Distribution



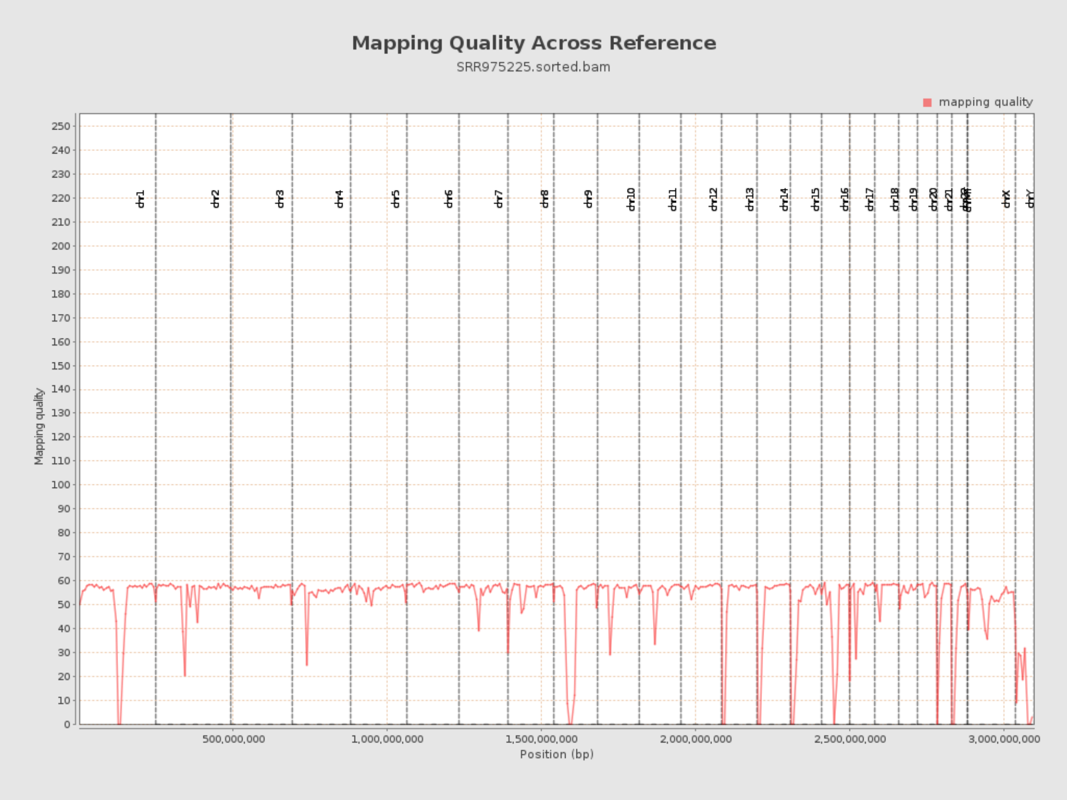
10. Results : Mapped Reads Clipping Profile



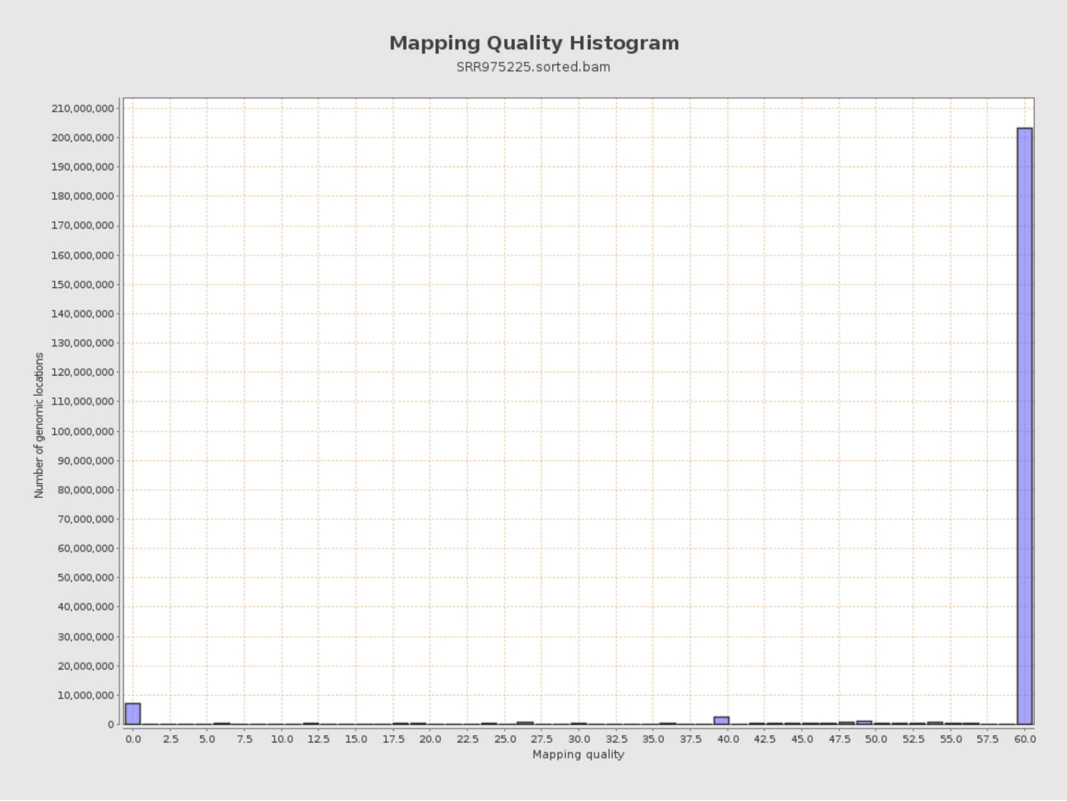
11. Results : Homopolymer Indels



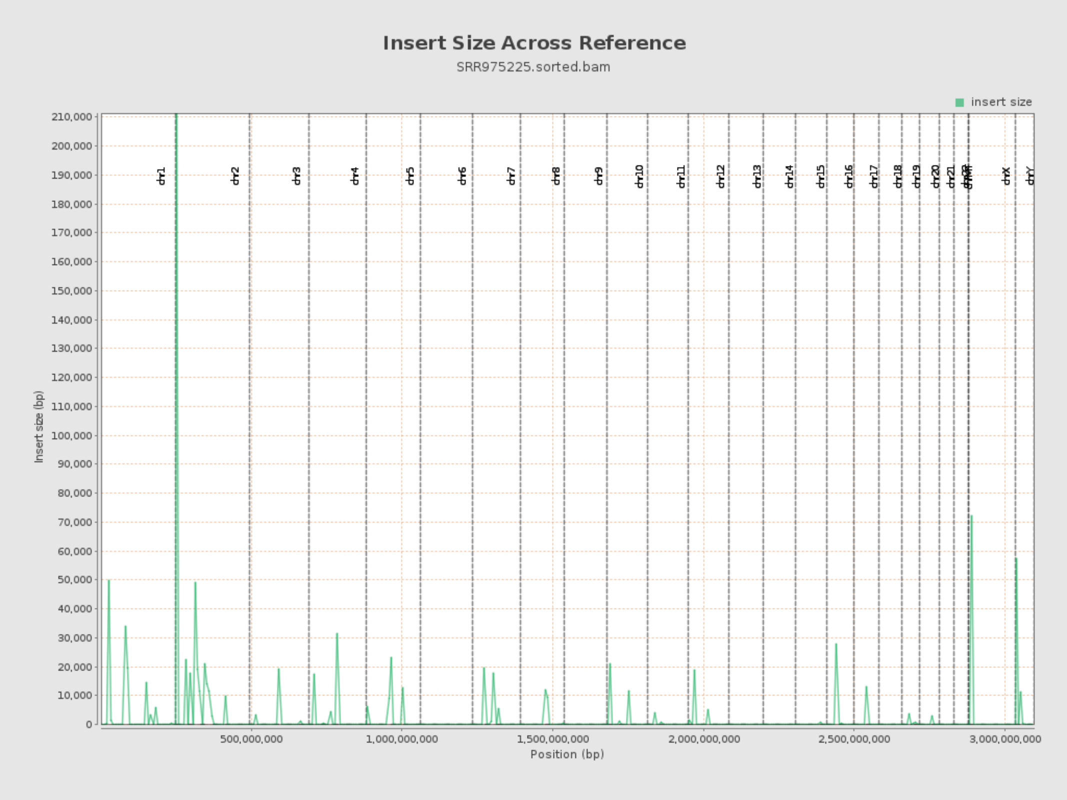
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram