Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/08 00:21:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961005.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_SRR961005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961005_1.fastq.gz SRR961005_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 08 00:21:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961005.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	386,104,440
Mapped reads	378,247,355 / 97.97%
Unmapped reads	7,857,085 / 2.03%
Mapped paired reads	378,247,355 / 97.97%
Mapped reads, first in pair	189,395,680 / 49.05%
Mapped reads, second in pair	188,851,675 / 48.91%
Mapped reads, both in pair	377,123,288 / 97.67%
Mapped reads, singletons	1,124,067 / 0.29%
Secondary alignments	0
Supplementary alignments	808,621 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	61,942,380 / 16.04%
Duplication rate	11.97%
Clipped reads	43,175,898 / 11.18%

2.2. ACGT Content

Number/percentage of A's	10,943,233,285 / 29.64%
Number/percentage of C's	7,499,191,622 / 20.31%
Number/percentage of T's	10,888,586,288 / 29.49%
Number/percentage of G's	7,573,140,703 / 20.51%
Number/percentage of N's	16,559,651 / 0.04%

GC Percentage	40.82%

2.3. Coverage

Mean	11.9302
Standard Deviation	140.8595

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	15,807.64
Standard Deviation	1,206,357.48
P25/Median/P75	113 / 124 / 134

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	204,161,071
Insertions	3,795,464
Mapped reads with at least one insertion	0.97%
Deletions	4,468,470
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.17%

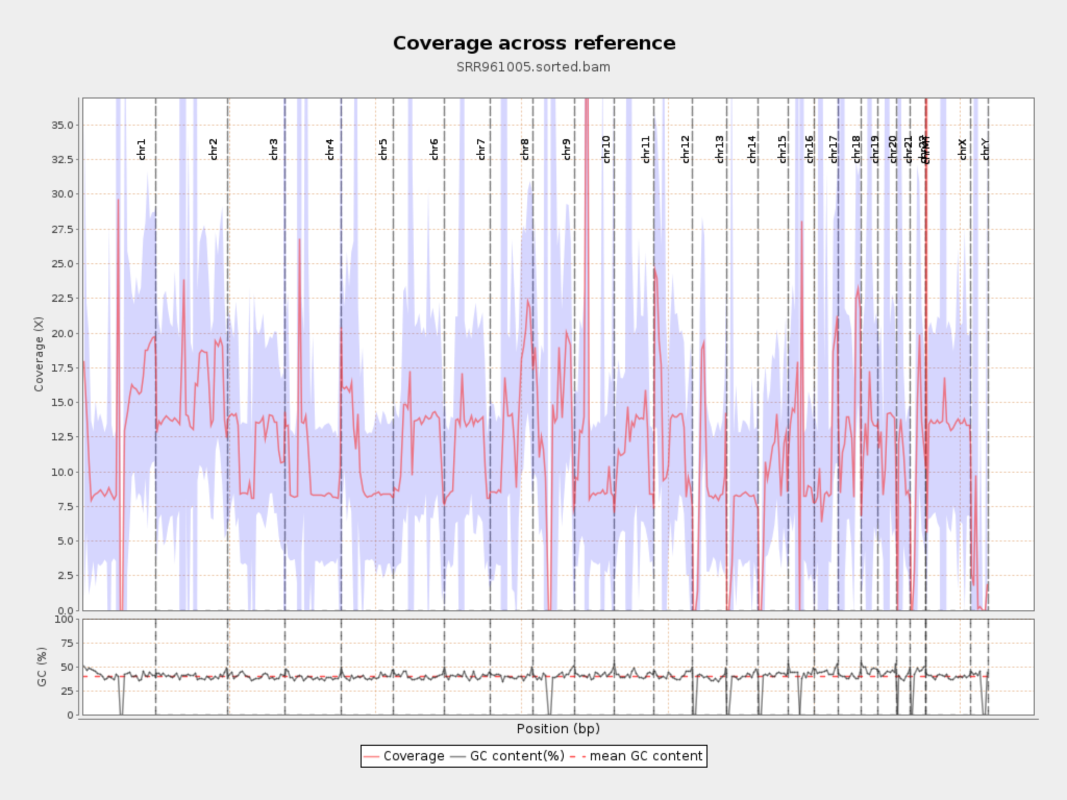
2.7. Chromosome stats

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

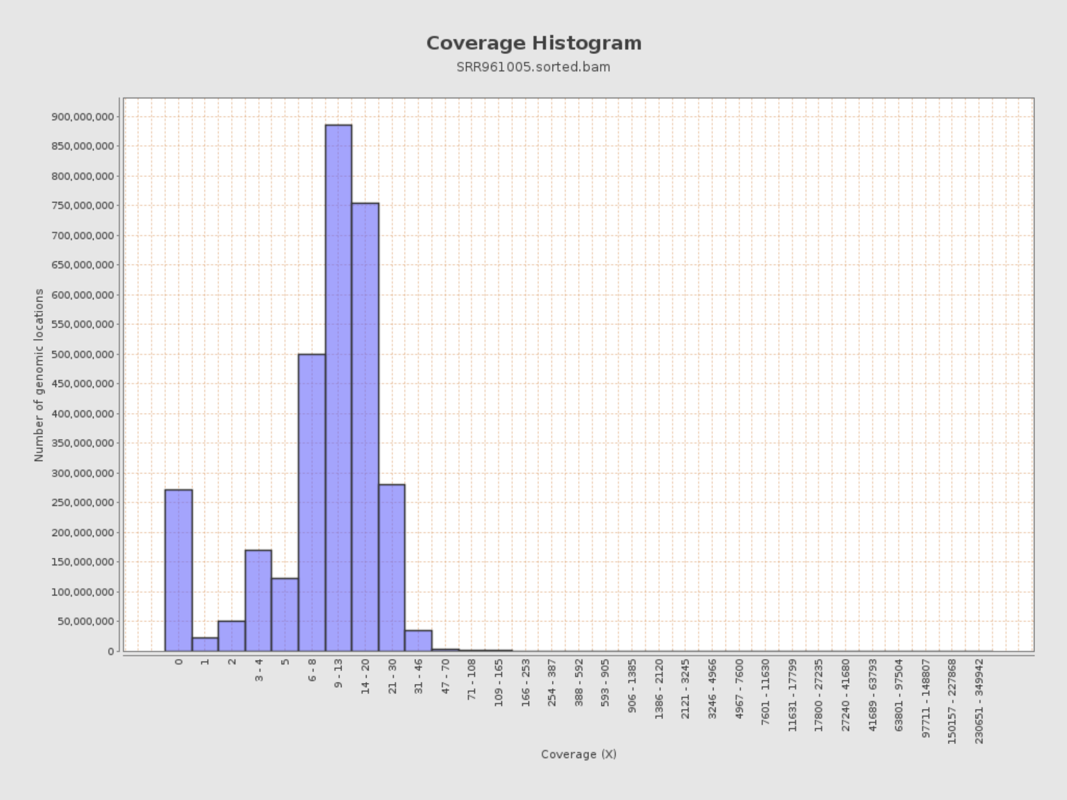
		bases	coverage	deviation
chr1	249250621	3188773859	12.7934	338.578
chr2	243199373	3815178305	15.6875	82.6028
chr3	198022430	2363027804	11.9331	41.9535
chr4	191154276	1966558880	10.2878	115.3172
chr5	180915260	1940604410	10.7266	13.1691
chr6	171115067	2193432978	12.8185	41.1288
chr7	159138663	1900476341	11.9423	87.0483
chr8	146364022	2067925330	14.1286	132.4457
chr9	141213431	1865278670	13.2089	94.2039
chr10	135534747	1629927463	12.0259	347.1619
chr11	135006516	1648752364	12.2124	54.0951
chr12	133851895	1856382434	13.8689	12.7415
chr13	115169878	1002669804	8.706	7.6503
chr14	107349540	736178559	6.8578	12.1873
chr15	102531392	933684232	9.1063	7.3035
chr16	90354753	1066937902	11.8083	132.929
chr17	81195210	896411852	11.0402	36.5582
chr18	78077248	1130091242	14.474	125.0591
chr19	59128983	769437706	13.0129	171.1255
chr20	63025520	781936672	12.4067	37.1816
chr21	48129895	455452462	9.463	63.0812
chr22	51304566	512549569	9.9903	11.2788
chrMT	16571	17326817	1,045.6108	177.9299
chrX	155270560	2072975149	13.3507	42.2883

chrY	59373566	120140039	2.0235	124.2185

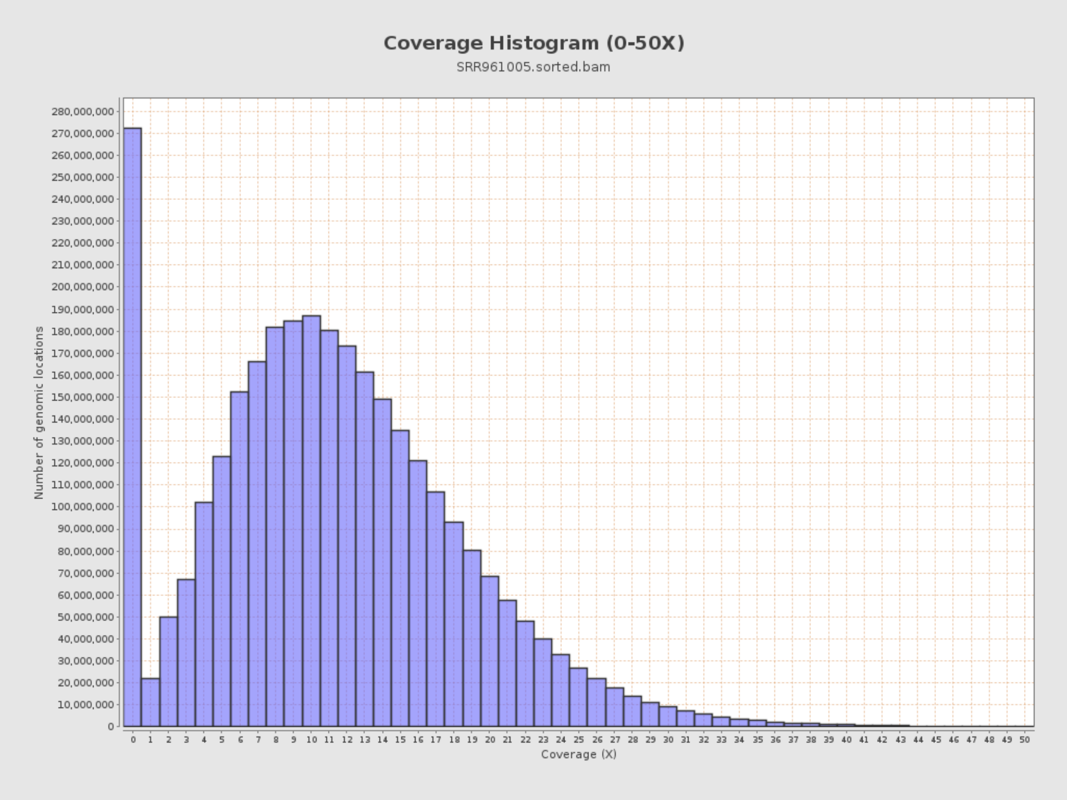
3. Results : Coverage across reference



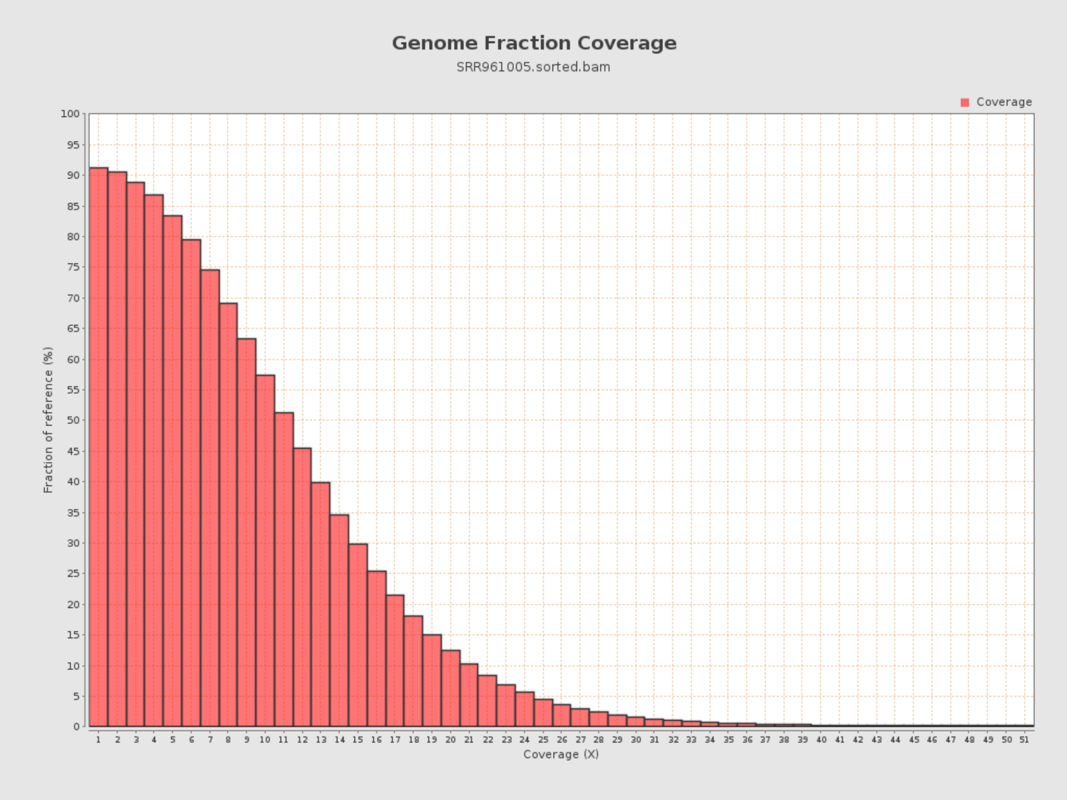
4. Results : Coverage Histogram



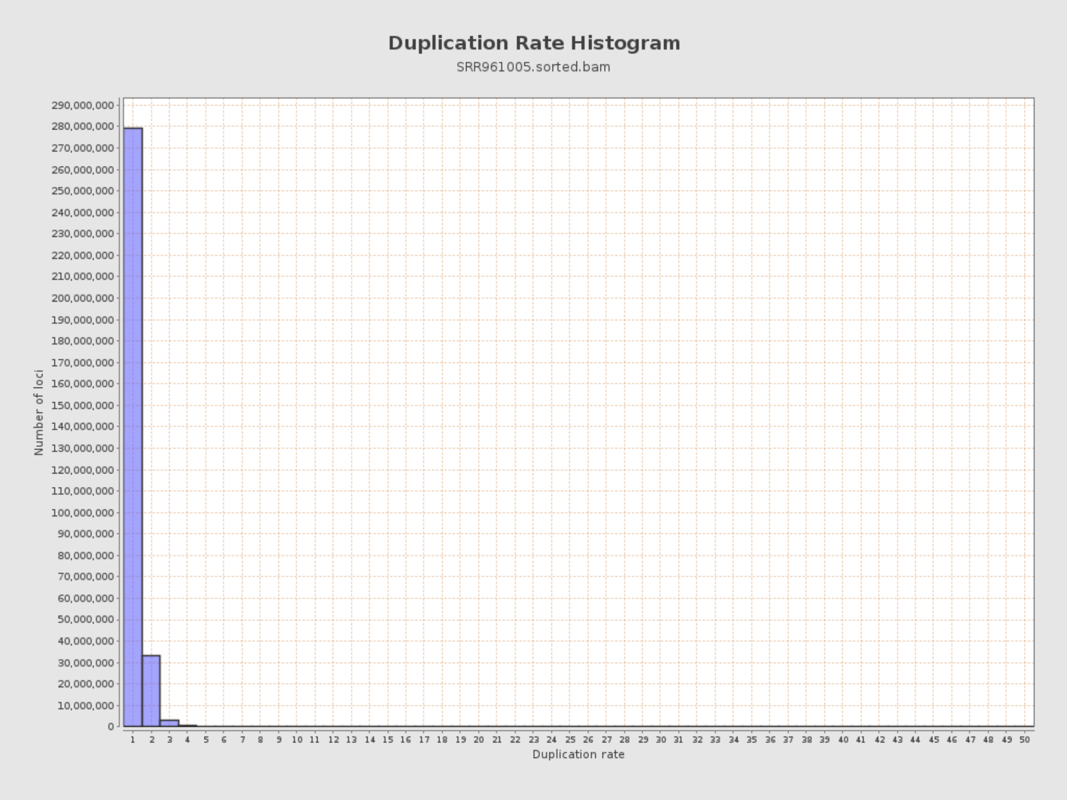
5. Results : Coverage Histogram (0-50X)



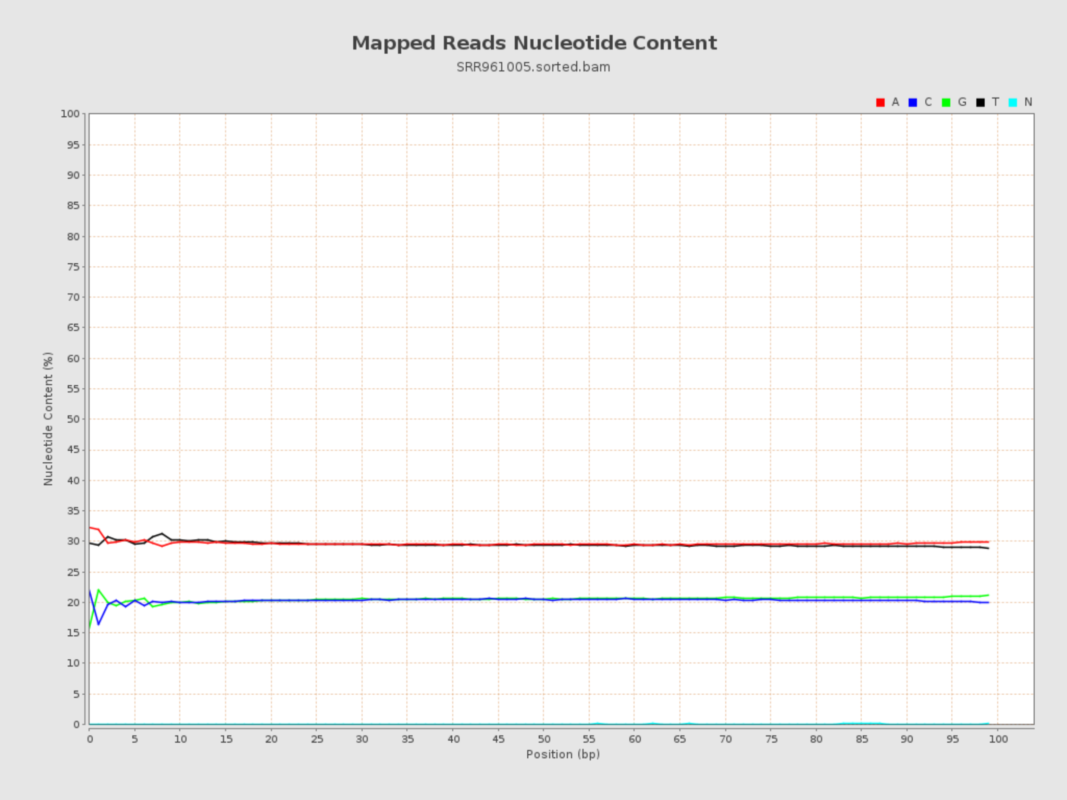
6. Results : Genome Fraction Coverage



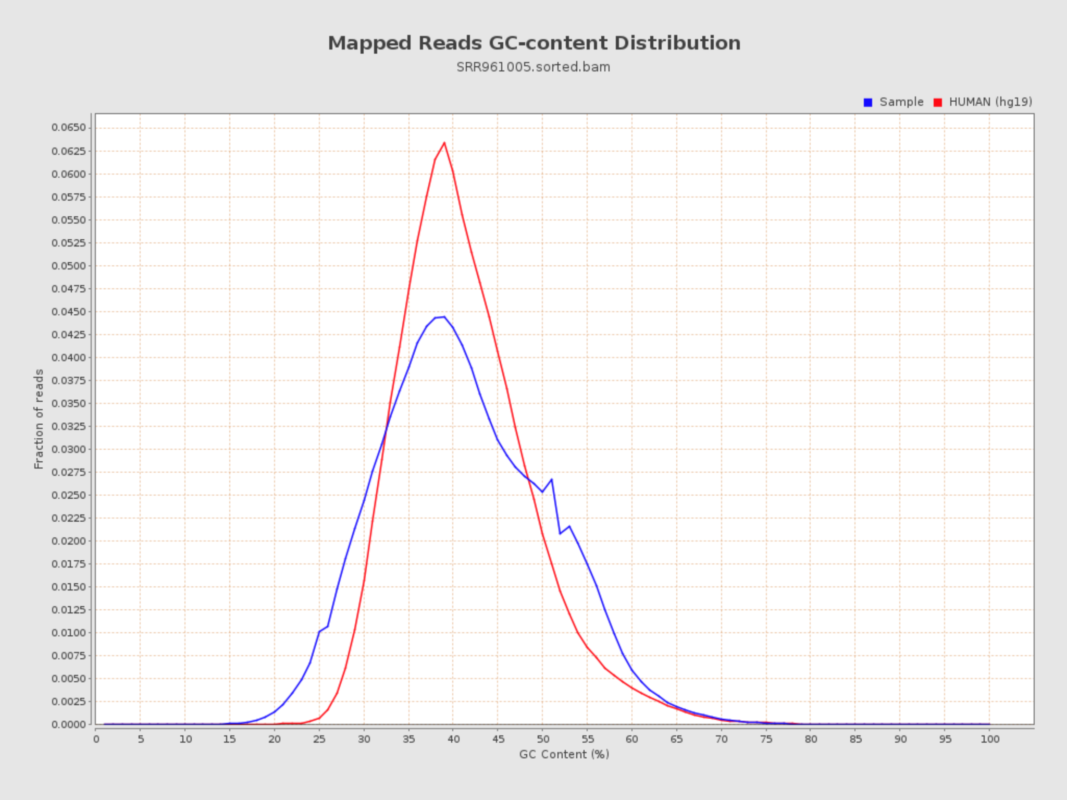
7. Results : Duplication Rate Histogram



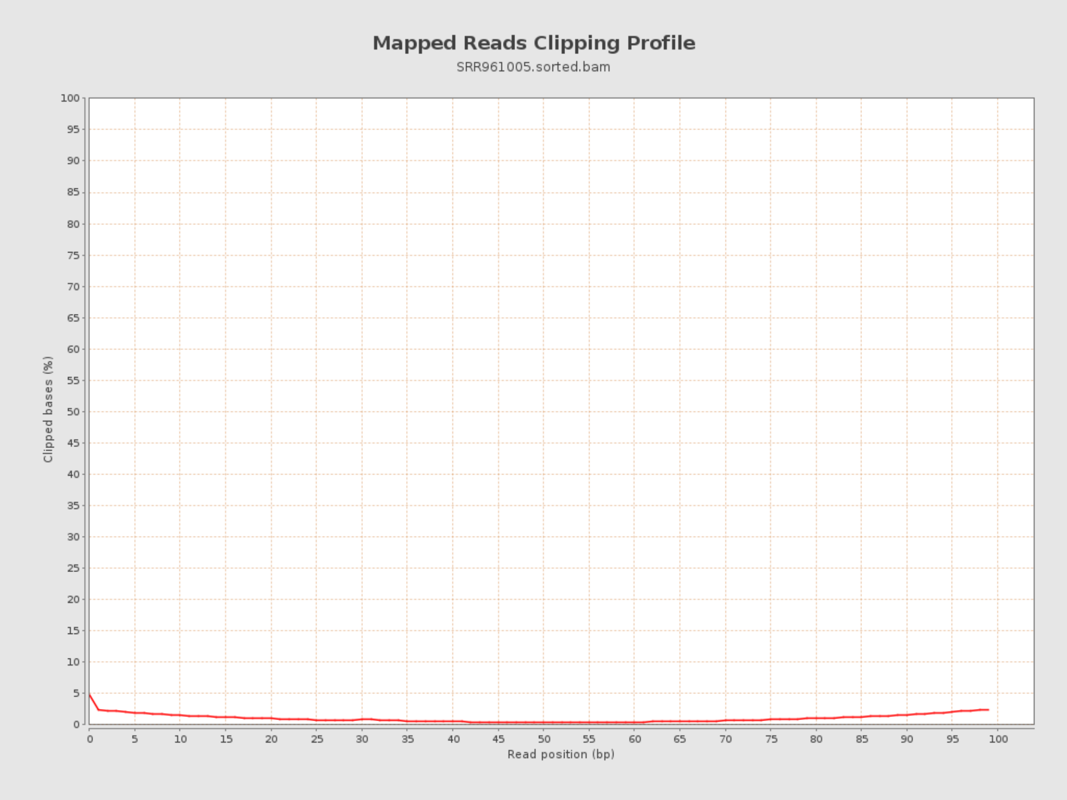
8. Results : Mapped Reads Nucleotide Content



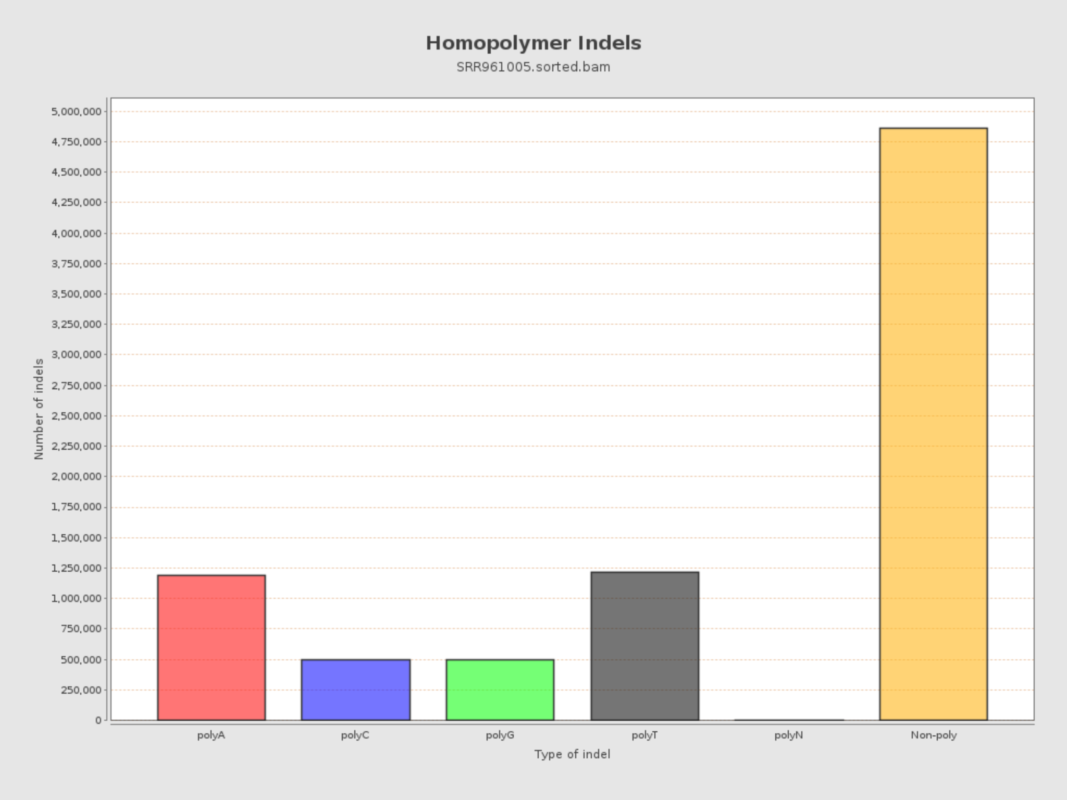
9. Results : Mapped Reads GC-content Distribution



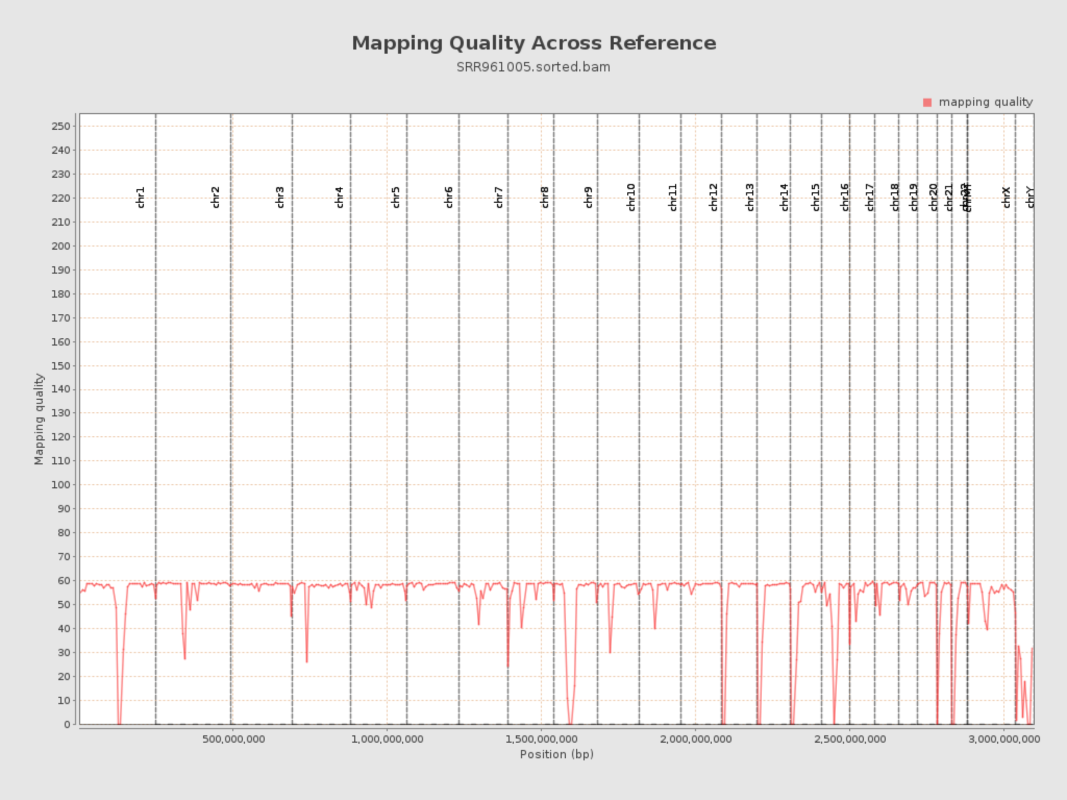
10. Results : Mapped Reads Clipping Profile



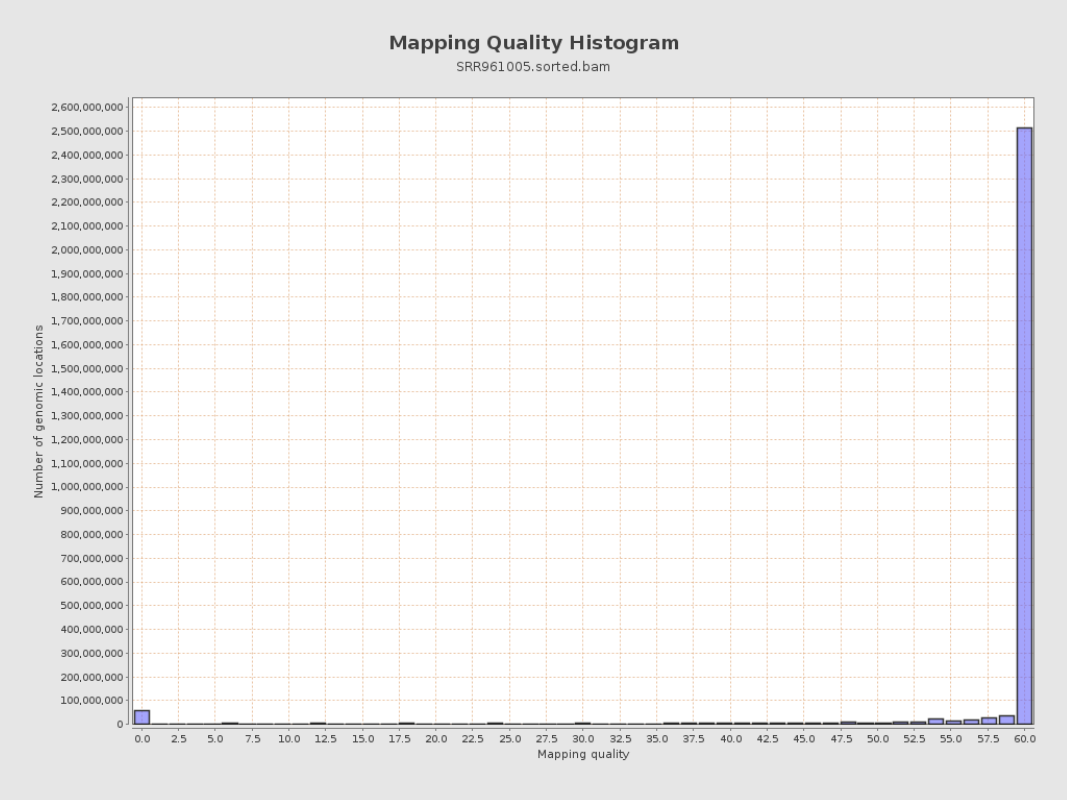
11. Results : Homopolymer Indels



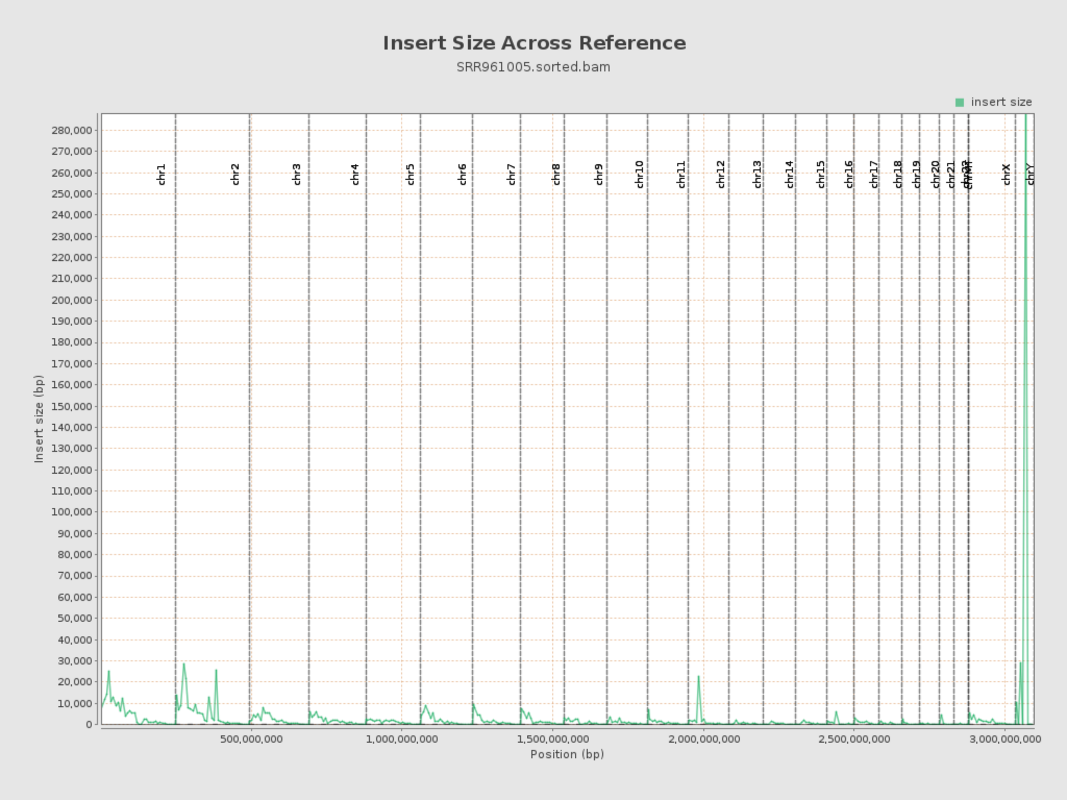
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram