Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/08 06:00:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961006.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_SRR961006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961006_1.fastq.gz SRR961006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 08 06:00:56 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	388,865,150
Mapped reads	381,088,636 / 98%
Unmapped reads	7,776,514 / 2%
Mapped paired reads	381,088,636 / 98%
Mapped reads, first in pair	190,789,602 / 49.06%
Mapped reads, second in pair	190,299,034 / 48.94%
Mapped reads, both in pair	380,022,508 / 97.73%
Mapped reads, singletons	1,066,128 / 0.27%
Secondary alignments	0
Supplementary alignments	814,622 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	62,720,252 / 16.13%
Duplication rate	12.05%
Clipped reads	43,876,569 / 11.28%

2.2. ACGT Content

Number/percentage of A's	11,021,678,386 / 29.64%
Number/percentage of C's	7,553,274,482 / 20.31%
Number/percentage of T's	10,966,867,722 / 29.49%
Number/percentage of G's	7,627,577,188 / 20.51%
Number/percentage of N's	18,602,267 / 0.05%

GC Percentage	40.82%

2.3. Coverage

Mean	12.0165
Standard Deviation	142.0789

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	15,704.1
Standard Deviation	1,198,544.44
P25/Median/P75	113 / 124 / 134

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	199,675,044
Insertions	3,824,873
Mapped reads with at least one insertion	0.97%
Deletions	4,498,641
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.16%

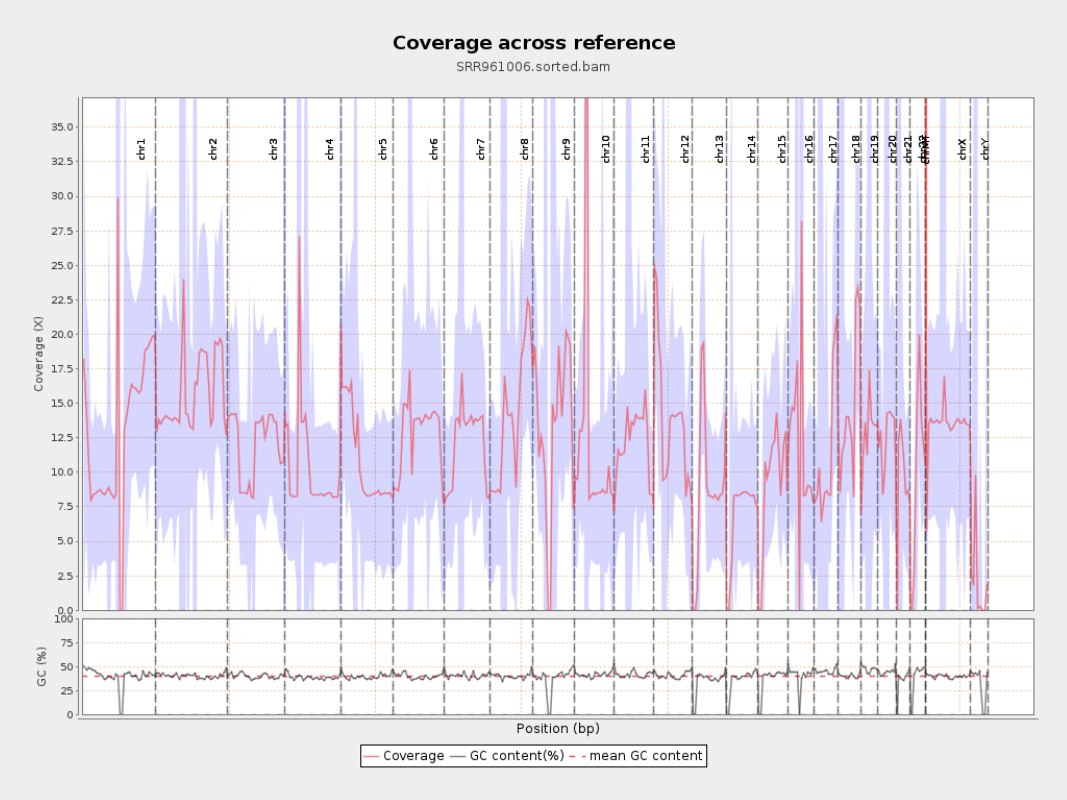
2.7. Chromosome stats

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

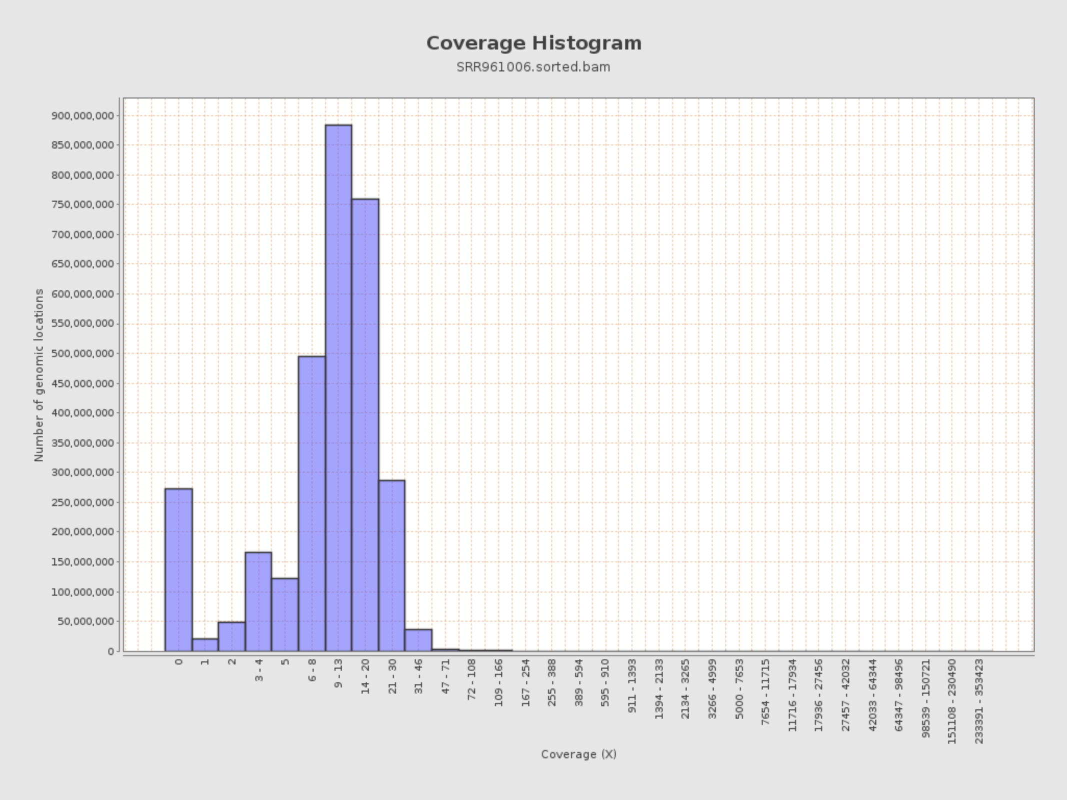
		bases	coverage	deviation
chr1	249250621	3212051466	12.8868	341.5524
chr2	243199373	3842209536	15.7986	82.9792
chr3	198022430	2378736507	12.0125	41.7396
chr4	191154276	1982051281	10.3689	116.8651
chr5	180915260	1954108192	10.8012	13.1753
chr6	171115067	2209175469	12.9105	41.4448
chr7	159138663	1914654431	12.0314	87.9436
chr8	146364022	2084322030	14.2407	133.1652
chr9	141213431	1879575374	13.3102	95.2279
chr10	135534747	1641735427	12.113	350.3576
chr11	135006516	1659514728	12.2921	54.4941
chr12	133851895	1871127050	13.9791	12.831
chr13	115169878	1009388712	8.7643	7.6833
chr14	107349540	741619904	6.9085	12.385
chr15	102531392	940919596	9.1769	7.3416
chr16	90354753	1074406602	11.891	133.8916
chr17	81195210	902915923	11.1203	36.9465
chr18	78077248	1137650565	14.5708	126.1271
chr19	59128983	775560344	13.1164	172.123
chr20	63025520	786957266	12.4863	37.7549
chr21	48129895	458038089	9.5167	64.3725
chr22	51304566	516156463	10.0606	11.2984
chrMT	16571	17564423	1,059.9495	183.1922
chrX	155270560	2088120532	13.4483	42.642

chrY	59373566	120916466	2.0365	124.6899

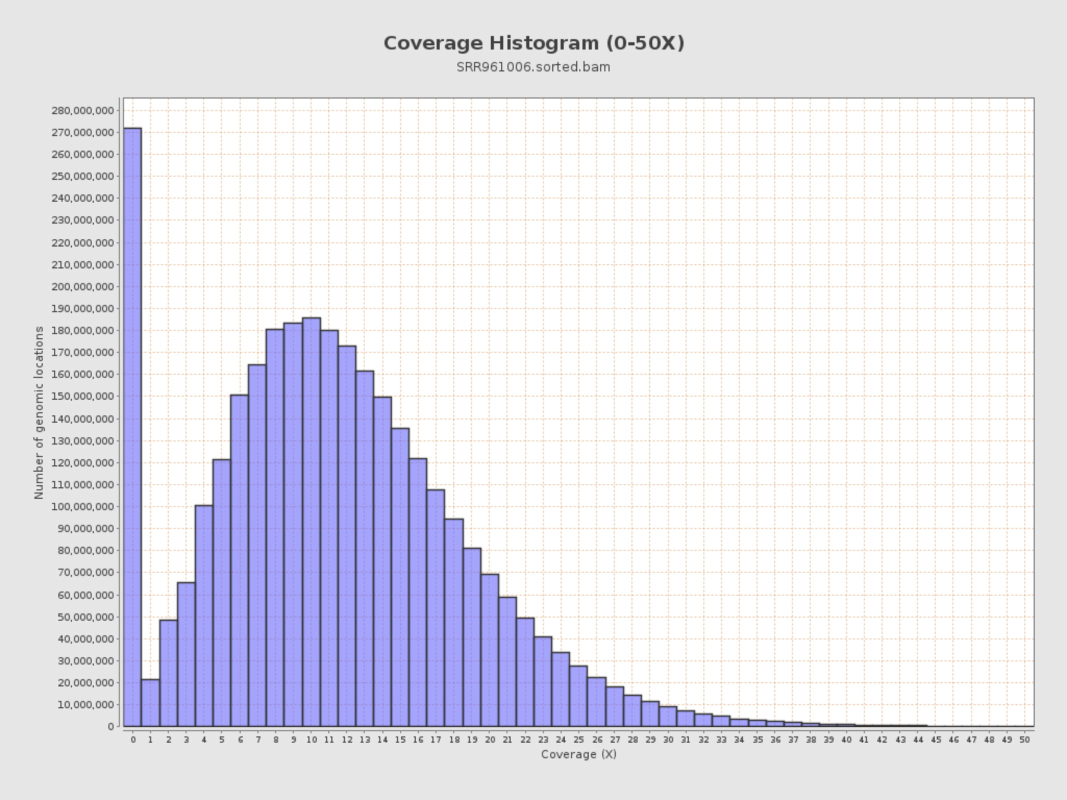
3. Results : Coverage across reference



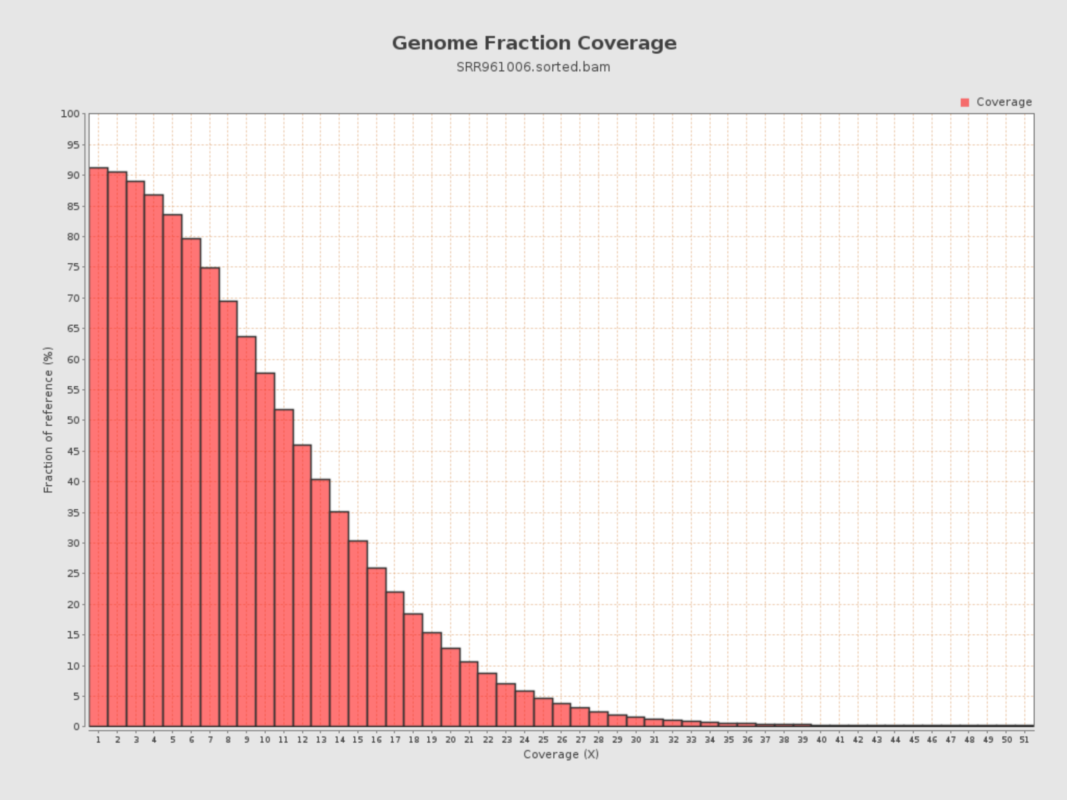
4. Results : Coverage Histogram



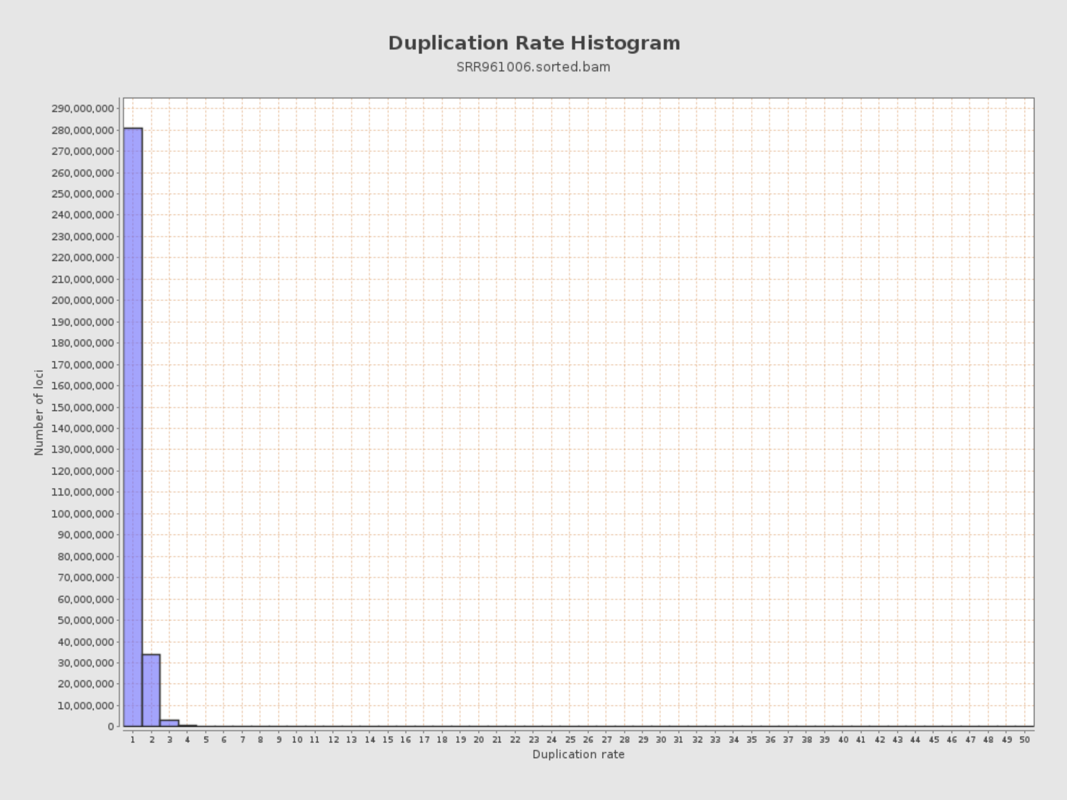
5. Results : Coverage Histogram (0-50X)



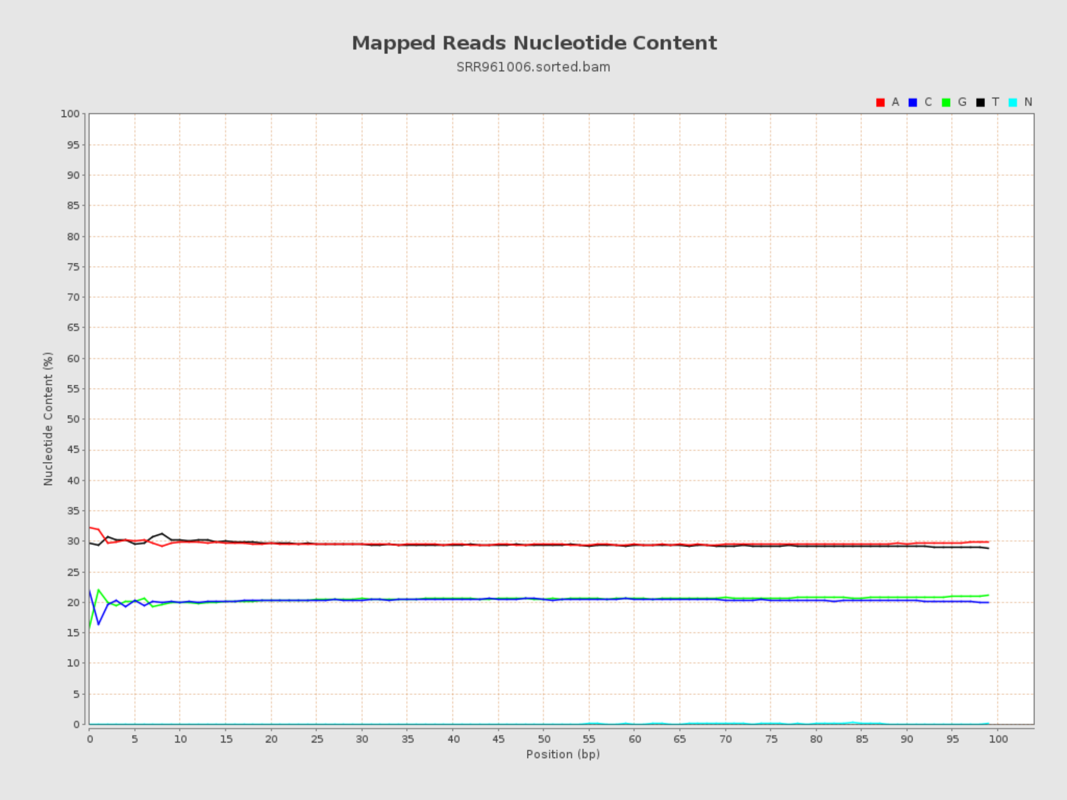
6. Results : Genome Fraction Coverage



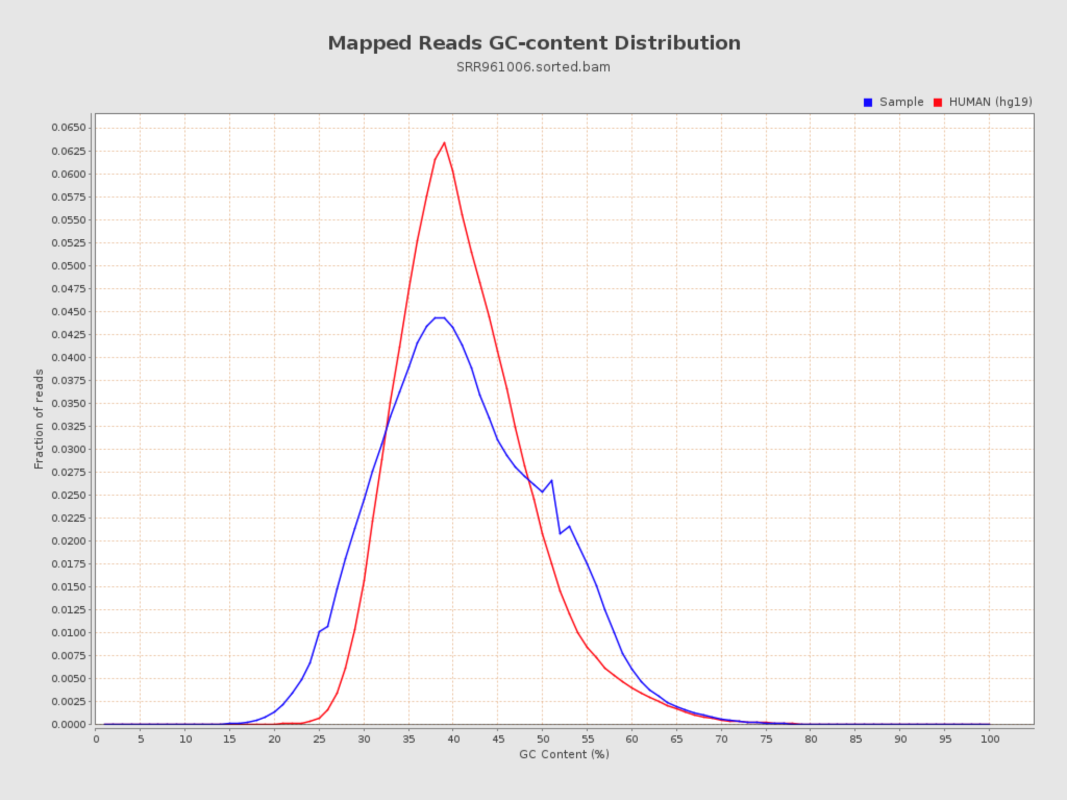
7. Results : Duplication Rate Histogram



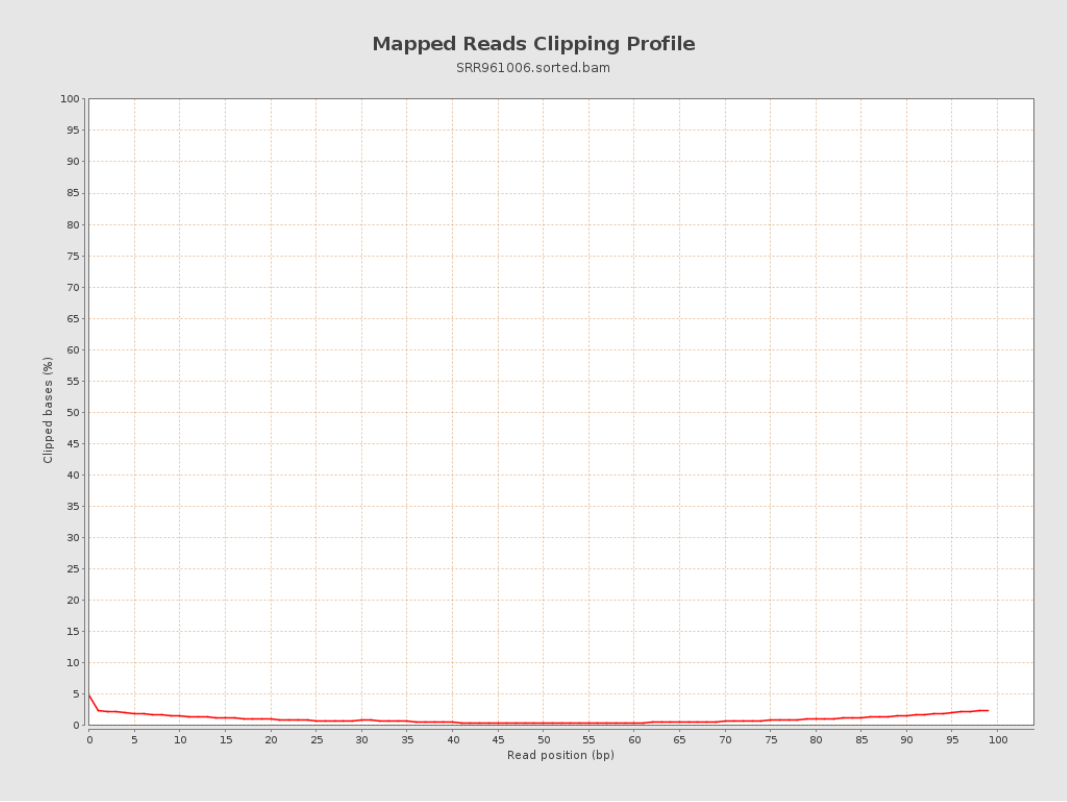
8. Results : Mapped Reads Nucleotide Content



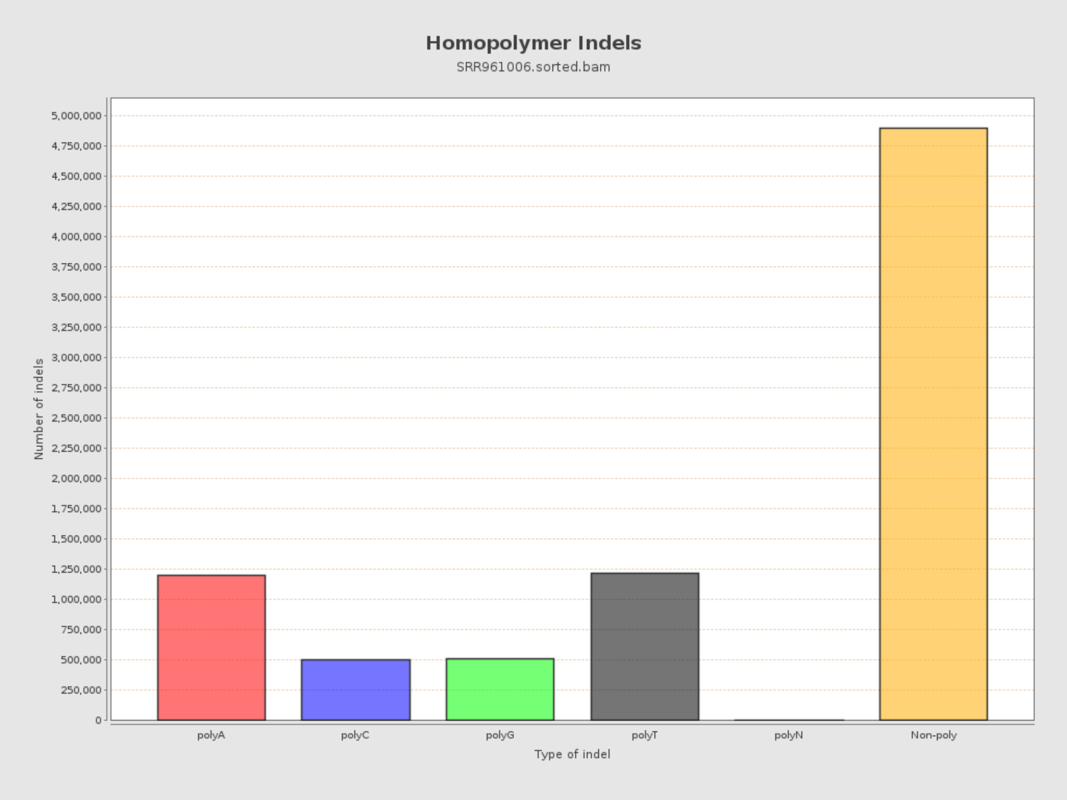
9. Results : Mapped Reads GC-content Distribution



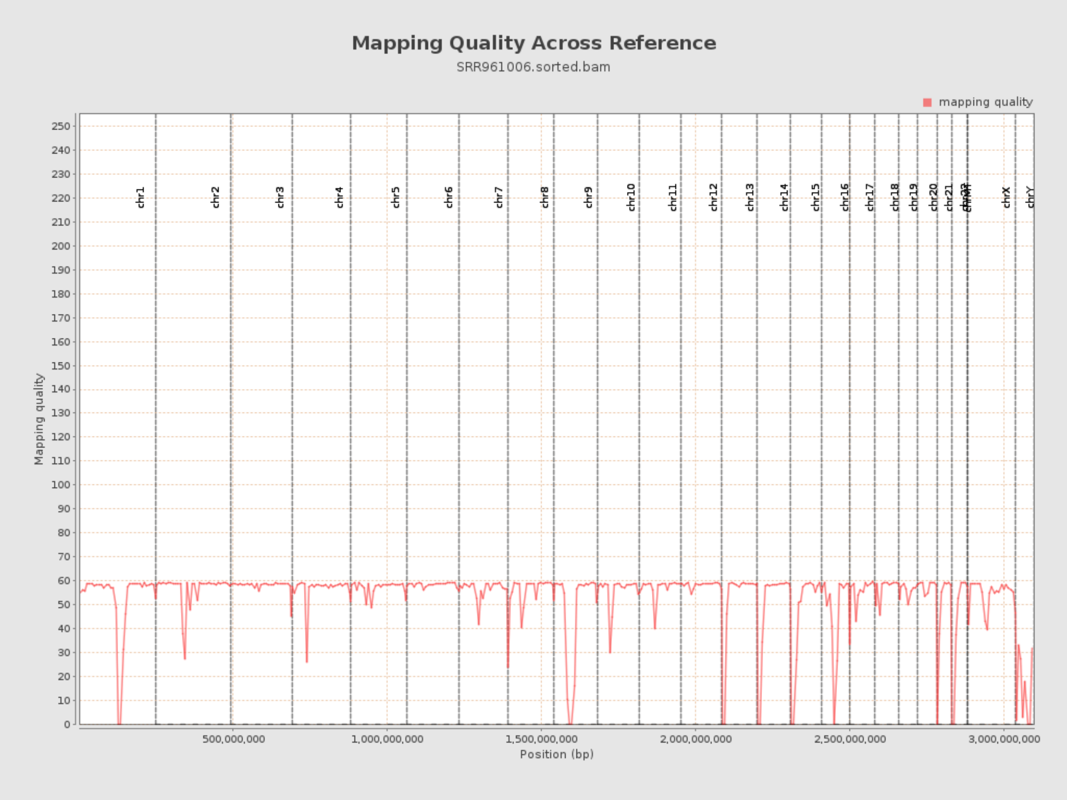
10. Results : Mapped Reads Clipping Profile



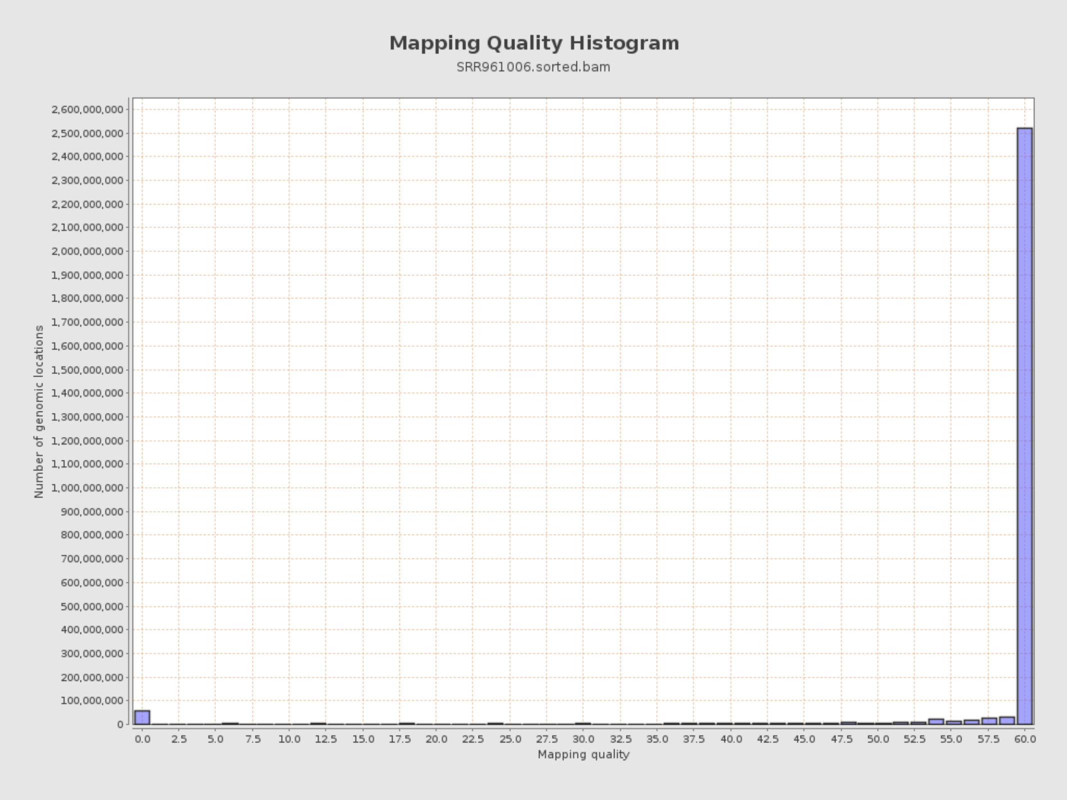
11. Results : Homopolymer Indels



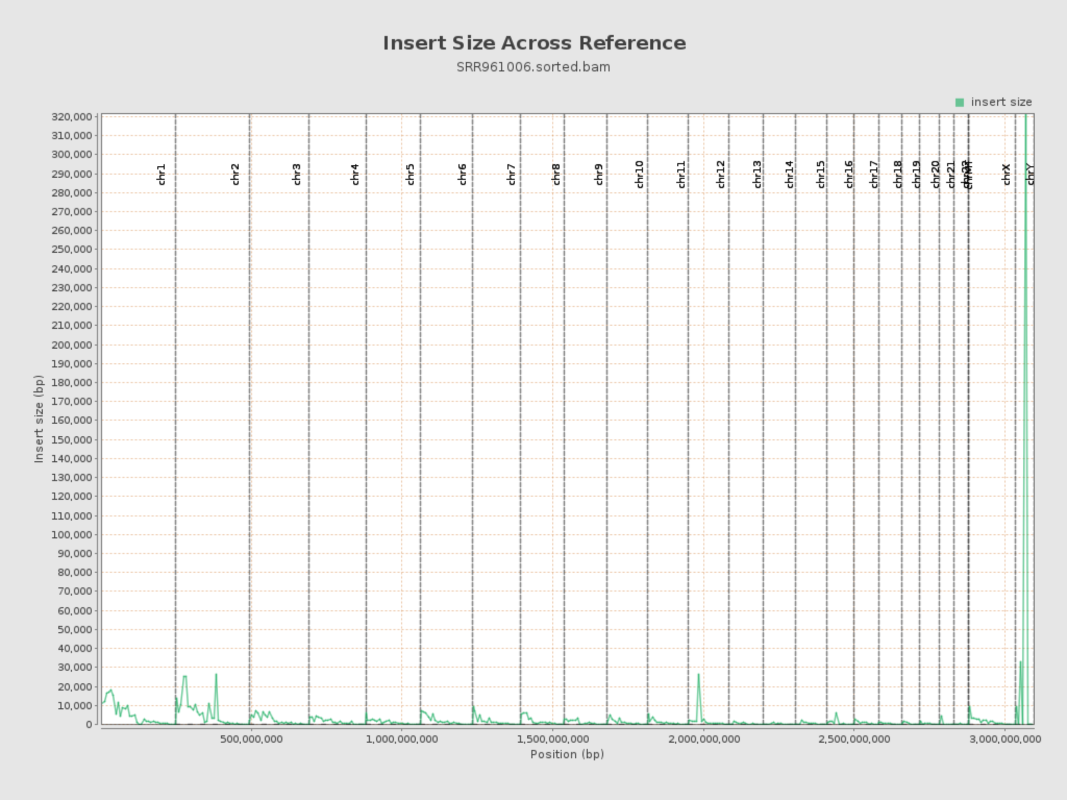
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram