Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/08 17:22:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961008.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_SRR961008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961008_1.fastq.gz SRR961008_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 08 17:22:56 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	391,567,662
Mapped reads	383,724,637 / 98%
Unmapped reads	7,843,025 / 2%
Mapped paired reads	383,724,637 / 98%
Mapped reads, first in pair	192,107,293 / 49.06%
Mapped reads, second in pair	191,617,344 / 48.94%
Mapped reads, both in pair	382,649,306 / 97.72%
Mapped reads, singletons	1,075,331 / 0.27%
Secondary alignments	0
Supplementary alignments	825,645 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	63,396,304 / 16.19%
Duplication rate	12.11%
Clipped reads	44,266,167 / 11.3%

2.2. ACGT Content

Number/percentage of A's	11,094,520,793 / 29.63%
Number/percentage of C's	7,604,695,418 / 20.31%
Number/percentage of T's	11,039,907,373 / 29.48%
Number/percentage of G's	7,682,625,477 / 20.52%
Number/percentage of N's	20,822,081 / 0.06%

GC Percentage	40.83%

2.3. Coverage

Mean	12.0988
Standard Deviation	142.9665

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	16,085.97
Standard Deviation	1,222,395.89
P25/Median/P75	113 / 124 / 134

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	206,852,992
Insertions	3,845,604
Mapped reads with at least one insertion	0.97%
Deletions	4,520,440
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.1%

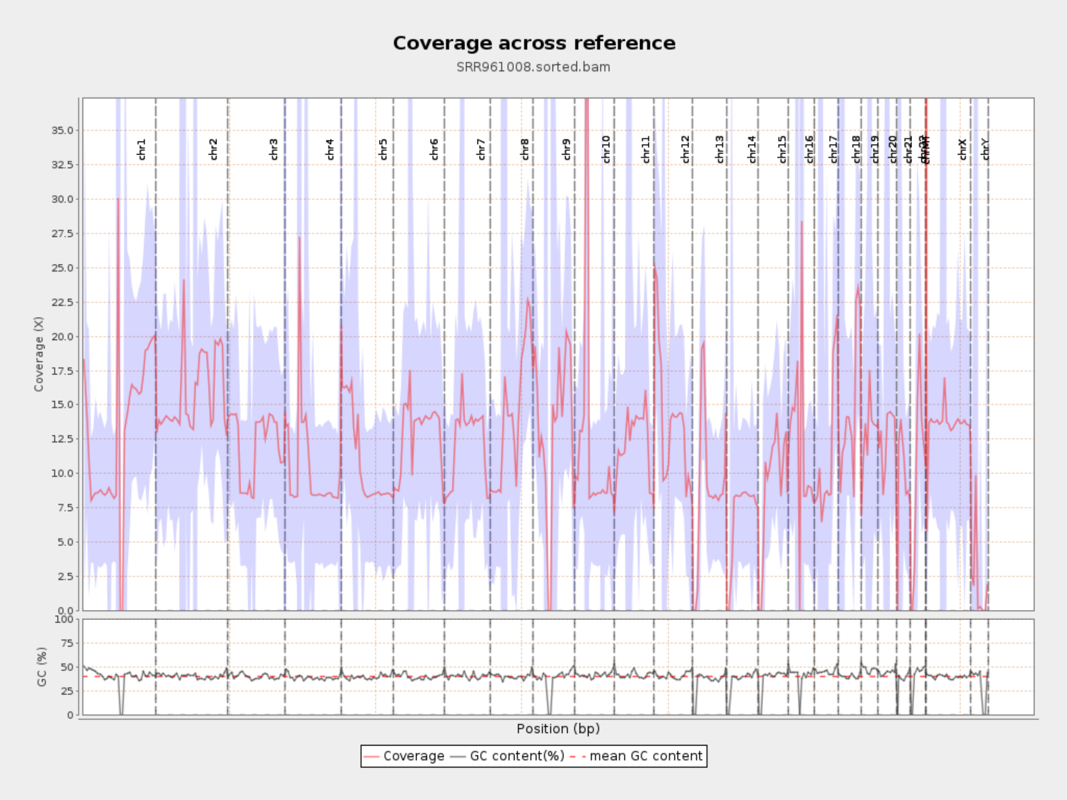
2.7. Chromosome stats

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

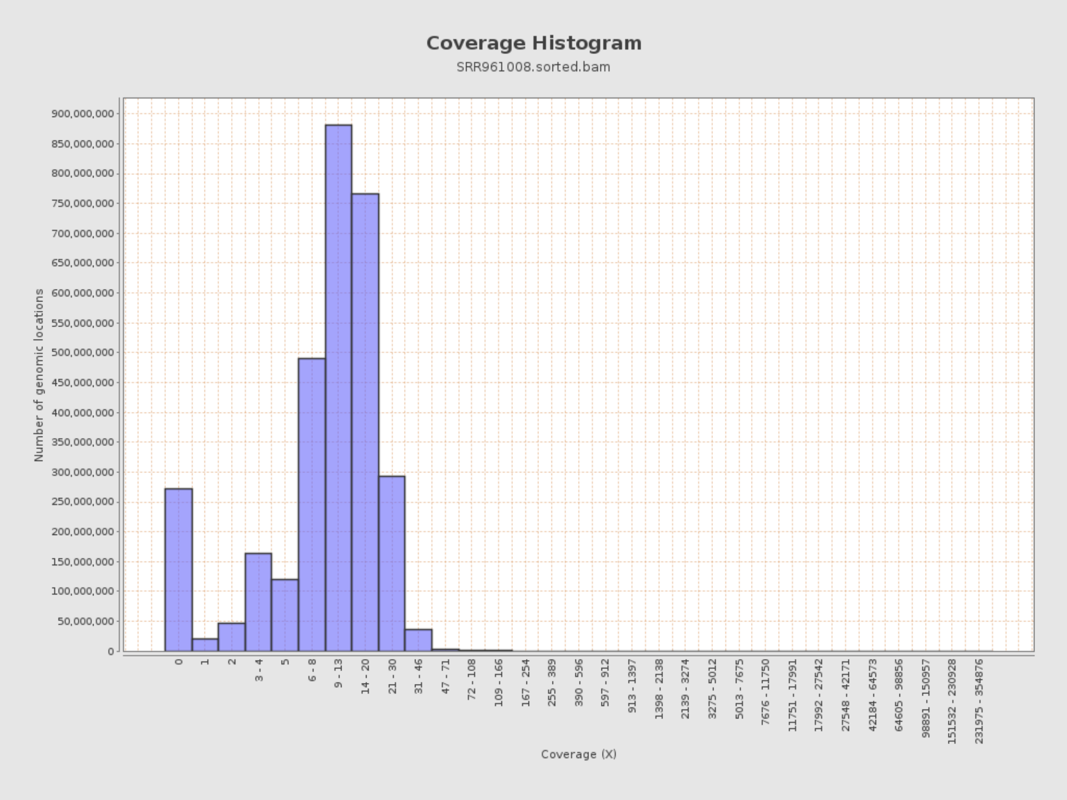
		bases	coverage	deviation
chr1	249250621	3233618237	12.9734	343.7739
chr2	243199373	3868180633	15.9054	83.6332
chr3	198022430	2395831652	12.0988	42.0499
chr4	191154276	1995290623	10.4381	117.7277
chr5	180915260	1966856524	10.8717	13.2637
chr6	171115067	2223569296	12.9946	41.6667
chr7	159138663	1927921351	12.1147	88.4775
chr8	146364022	2099092300	14.3416	134.5321
chr9	141213431	1891895102	13.3974	95.5607
chr10	135534747	1653617277	12.2007	352.0115
chr11	135006516	1671626050	12.3818	54.822
chr12	133851895	1883436395	14.071	13.0688
chr13	115169878	1016357036	8.8249	7.7313
chr14	107349540	745619672	6.9457	12.4039
chr15	102531392	947194928	9.2381	7.3866
chr16	90354753	1081934355	11.9743	134.7573
chr17	81195210	909546922	11.202	37
chr18	78077248	1145654840	14.6734	127.3037
chr19	59128983	780938013	13.2074	173.2044
chr20	63025520	793026683	12.5826	37.7133
chr21	48129895	461651318	9.5918	64.7778
chr22	51304566	520170024	10.1389	11.4575
chrMT	16571	17623348	1,063.5054	182.4556
chrX	155270560	2101385806	13.5337	42.7005

chrY	59373566	122064264	2.0559	125.9457

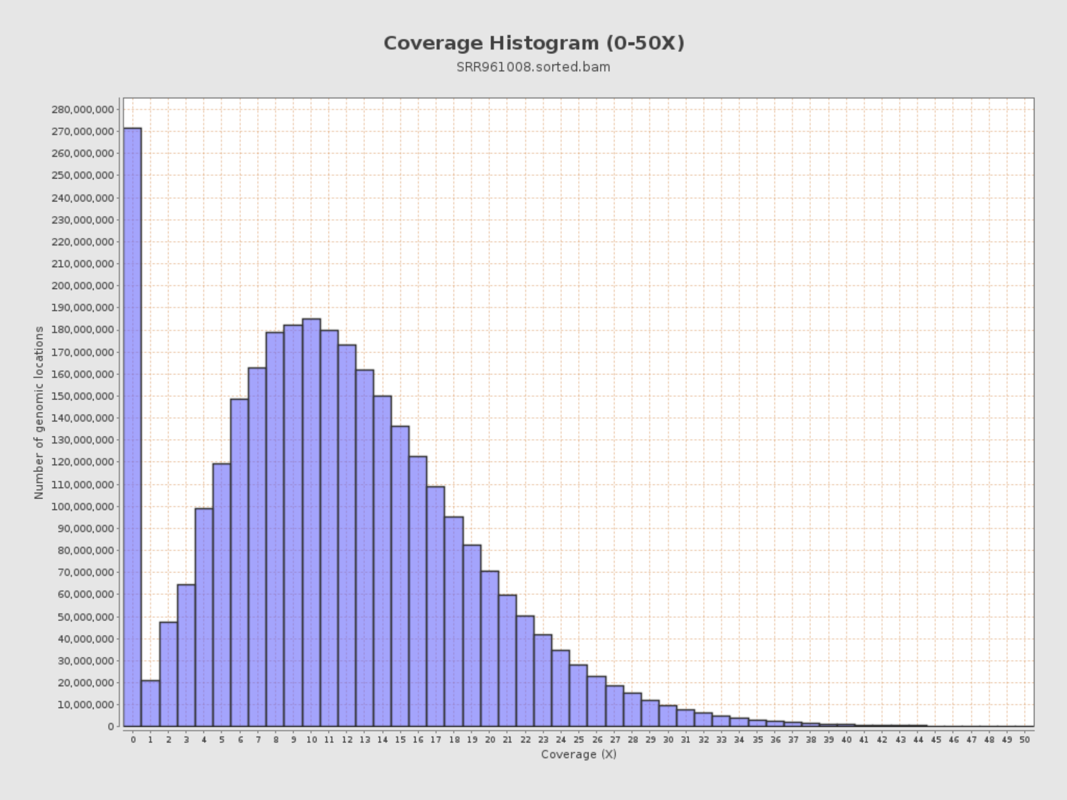
3. Results : Coverage across reference



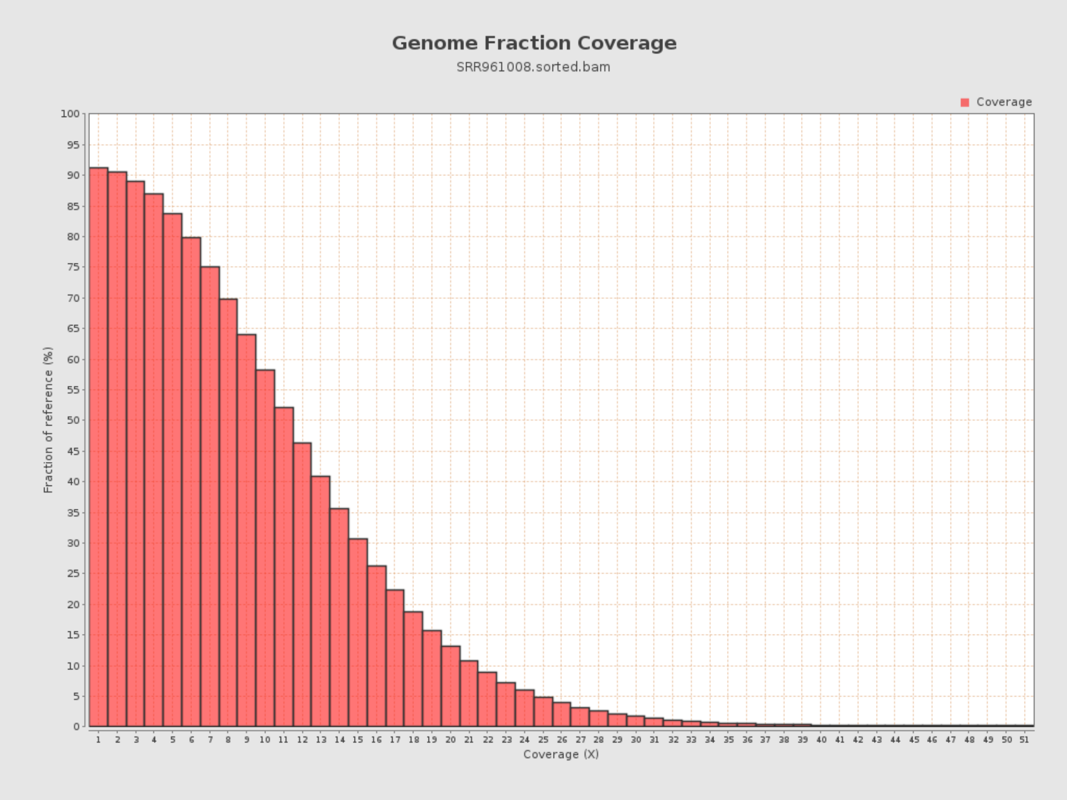
4. Results : Coverage Histogram



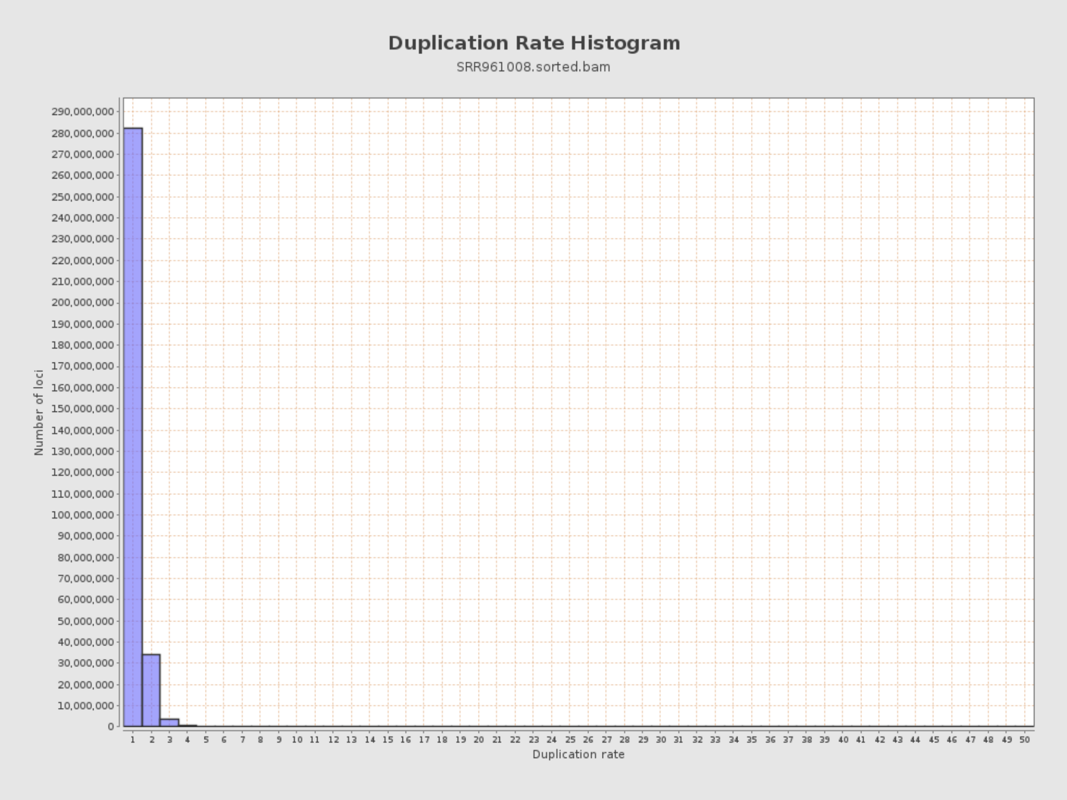
5. Results : Coverage Histogram (0-50X)



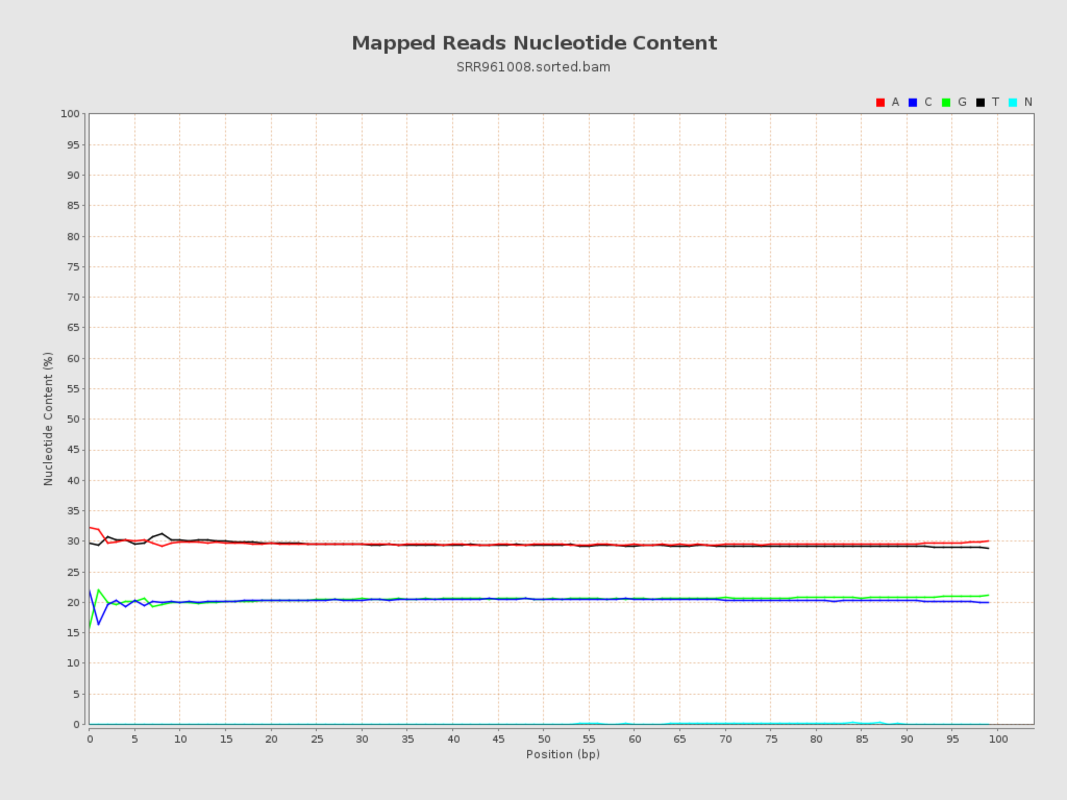
6. Results : Genome Fraction Coverage



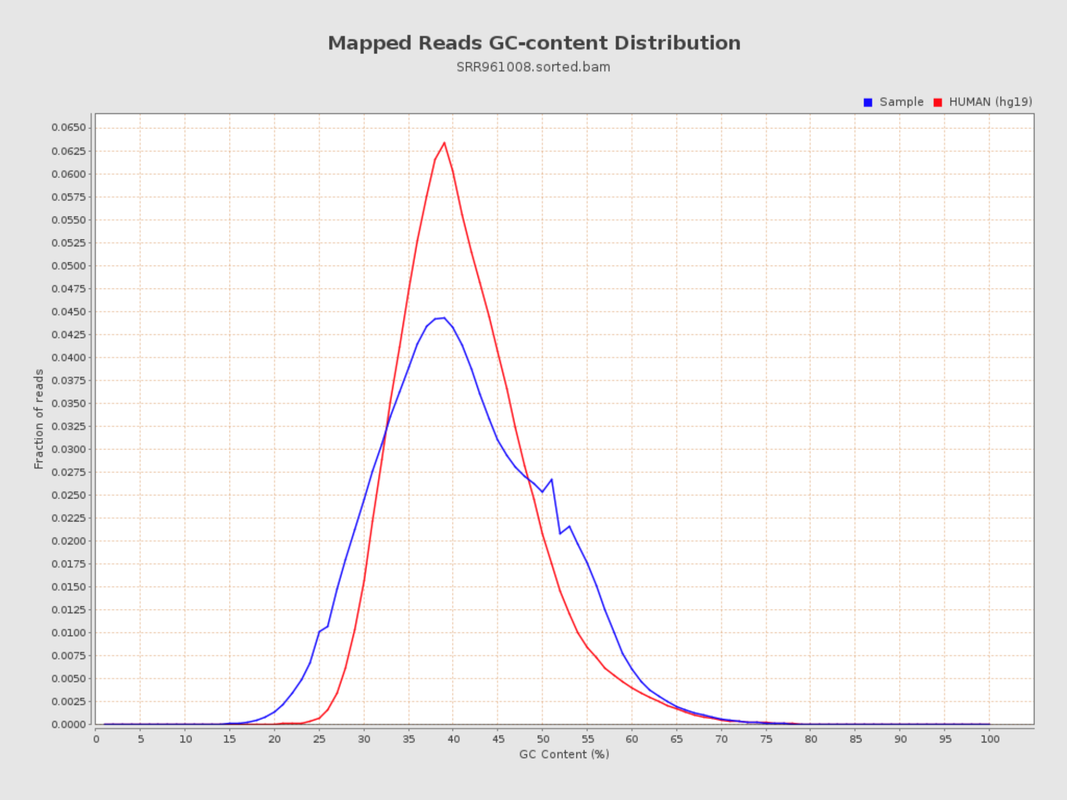
7. Results : Duplication Rate Histogram



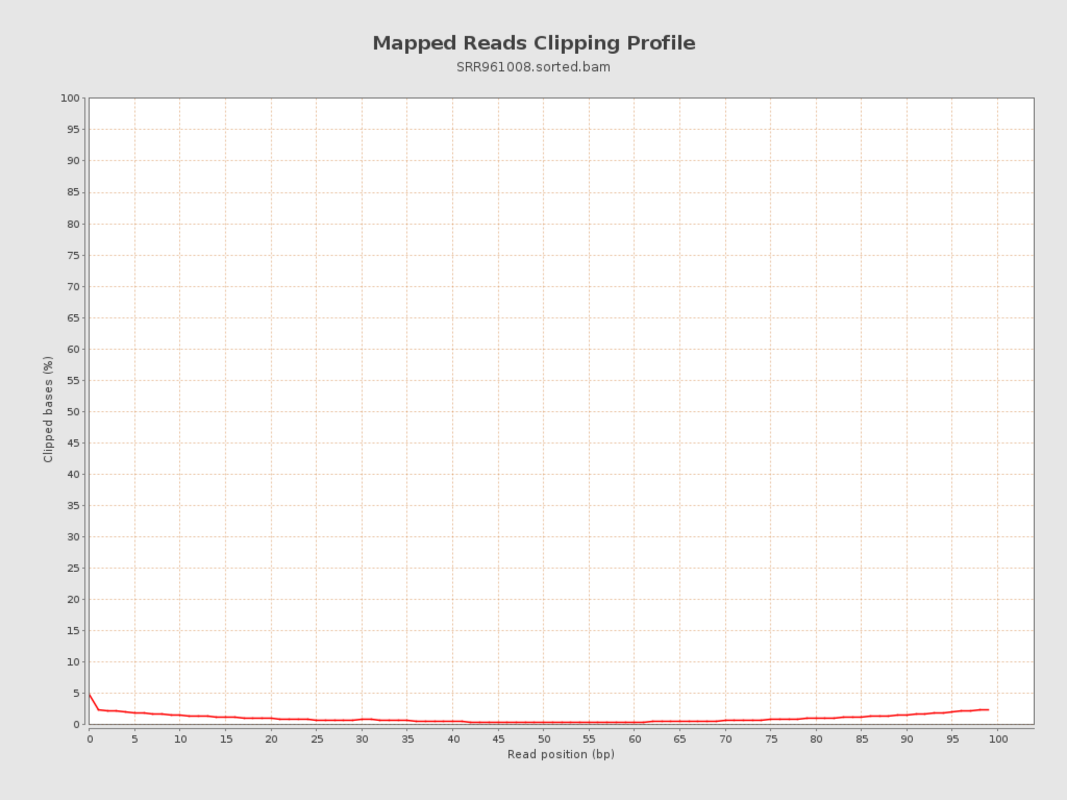
8. Results : Mapped Reads Nucleotide Content



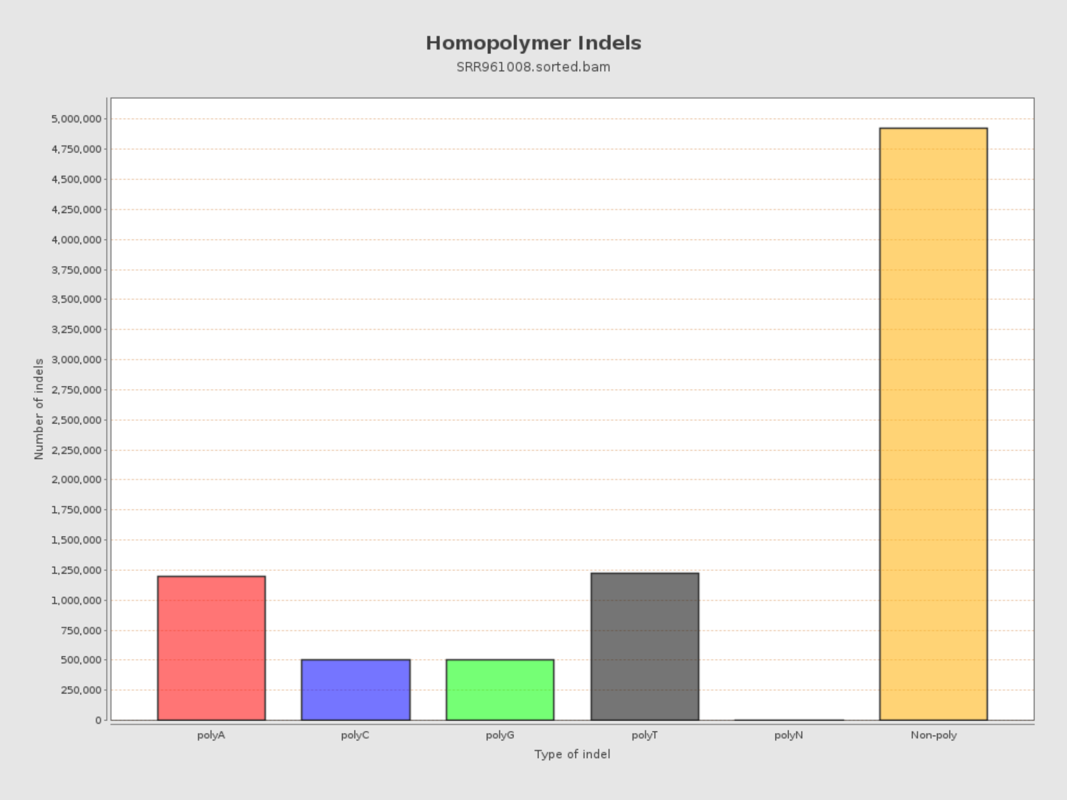
9. Results : Mapped Reads GC-content Distribution



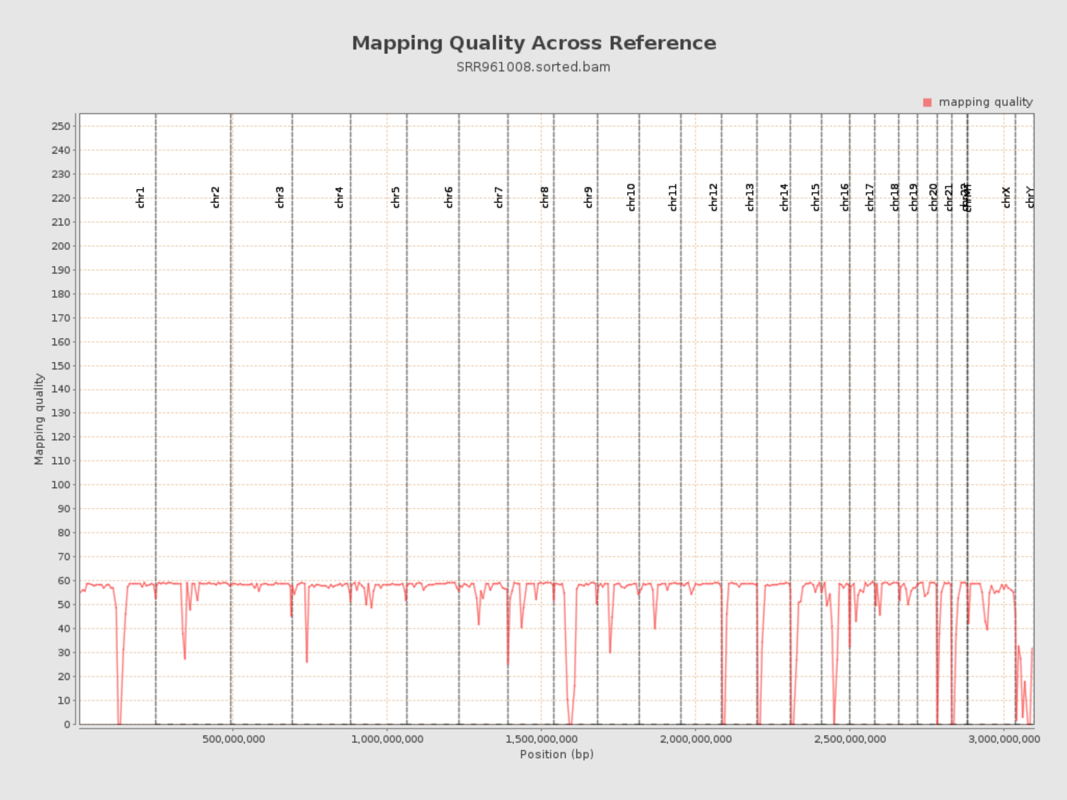
10. Results : Mapped Reads Clipping Profile



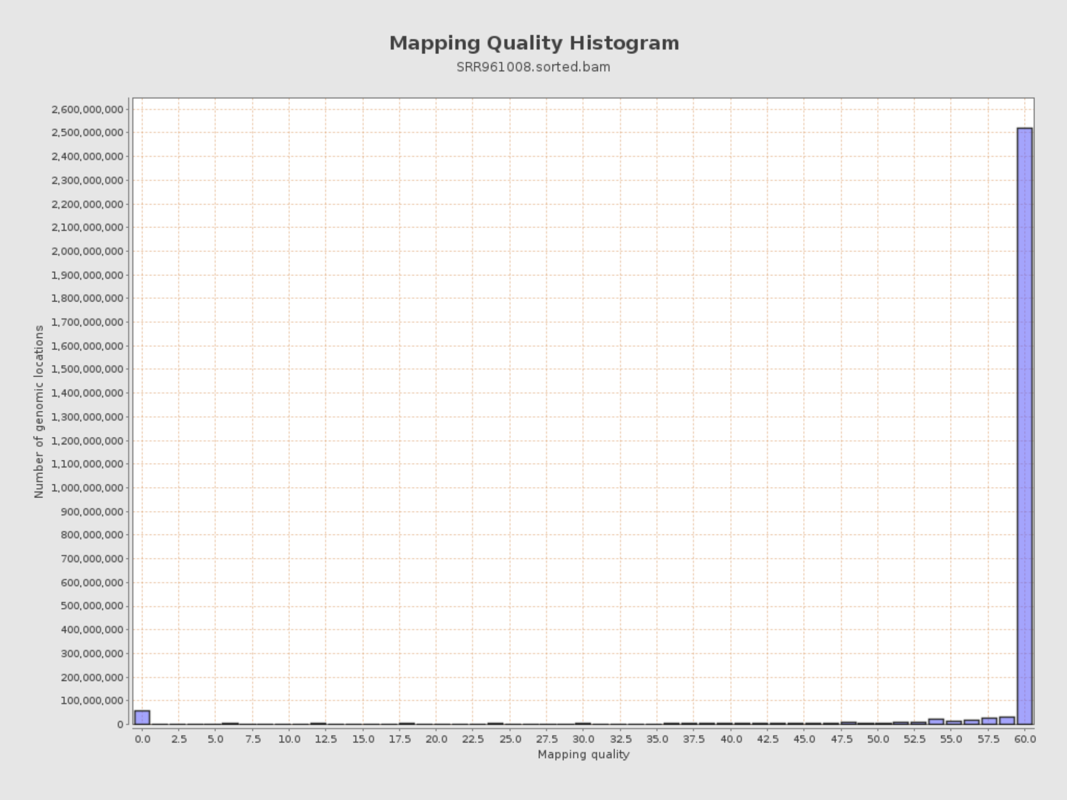
11. Results : Homopolymer Indels



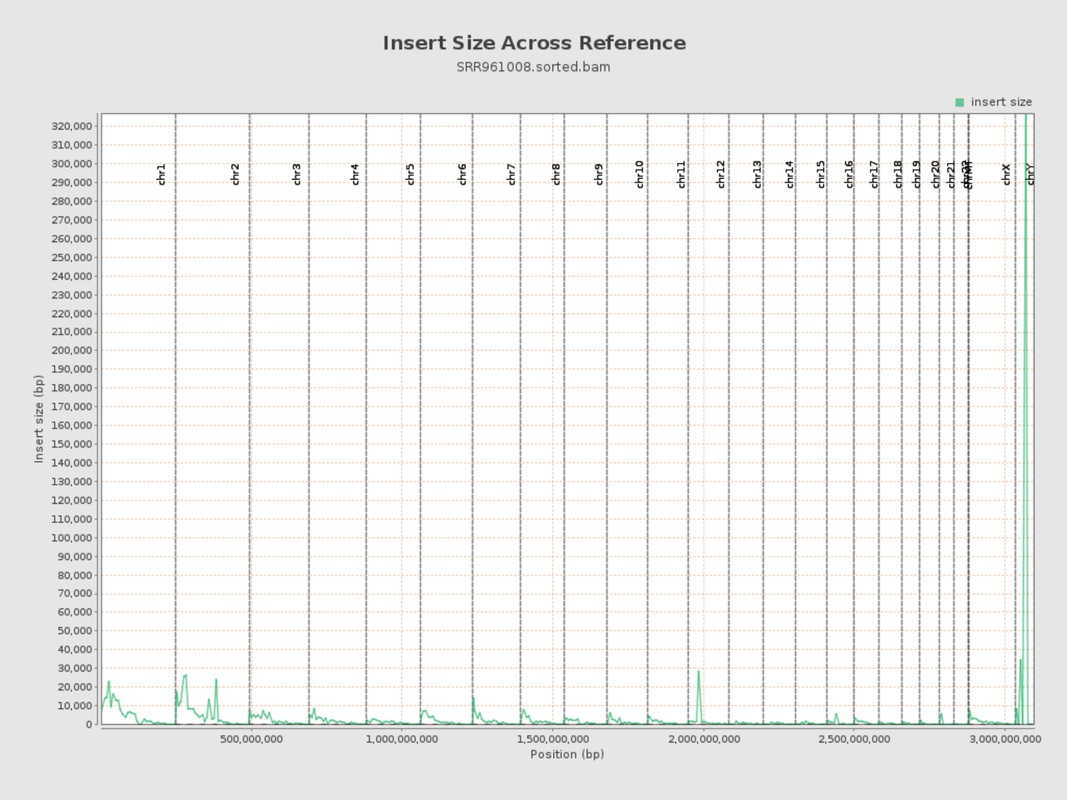
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram