Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/09 05:01:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961010.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_SRR961010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961010_1.fastq.gz SRR961010_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 09 05:01:18 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	369,392,790
Mapped reads	349,640,451 / 94.65%
Unmapped reads	19,752,339 / 5.35%
Mapped paired reads	349,640,451 / 94.65%
Mapped reads, first in pair	182,486,325 / 49.4%
Mapped reads, second in pair	167,154,126 / 45.25%
Mapped reads, both in pair	333,456,374 / 90.27%
Mapped reads, singletons	16,184,077 / 4.38%
Secondary alignments	0
Supplementary alignments	5,985,123 / 1.62%
Read min/max/mean length	30 / 100 / 100.68
Duplicated reads (estimated)	54,777,515 / 14.83%
Duplication rate	10.65%
Clipped reads	44,931,868 / 12.16%

2.2. ACGT Content

Number/percentage of A's	9,986,409,907 / 29.15%
Number/percentage of C's	7,105,123,285 / 20.74%
Number/percentage of T's	9,936,963,786 / 29.01%
Number/percentage of G's	7,158,343,326 / 20.9%
Number/percentage of N's	68,530,061 / 0.2%

GC Percentage	41.64%

2.3. Coverage

Mean	11.0687
Standard Deviation	137.4503

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	86,906.51
Standard Deviation	2,840,282.09
P25/Median/P75	127 / 142 / 155

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	371,977,684
Insertions	3,462,074
Mapped reads with at least one insertion	0.96%
Deletions	4,072,076
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.62%

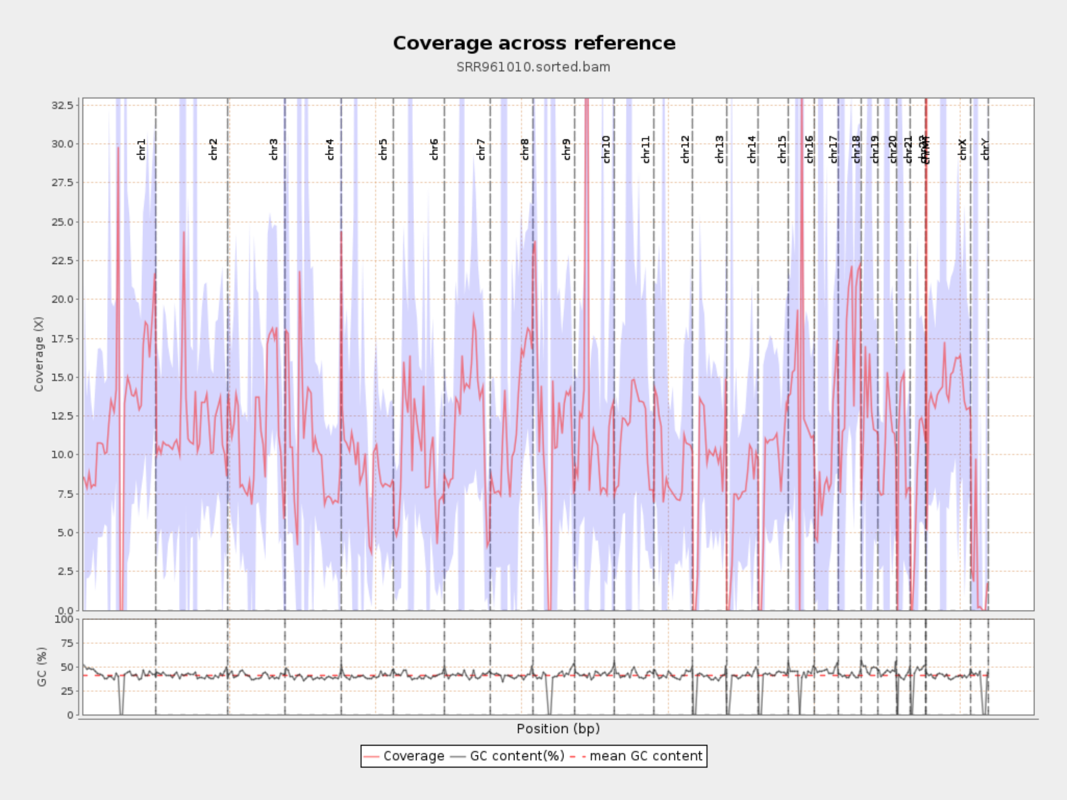
2.7. Chromosome stats

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

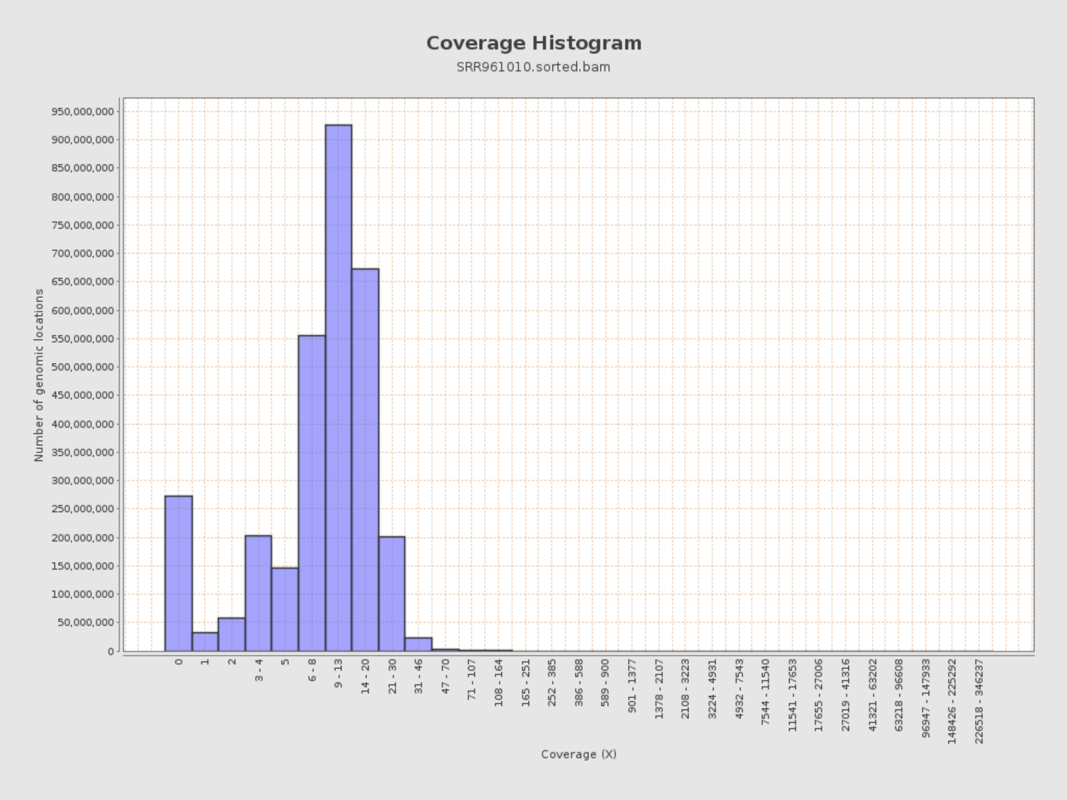
		bases	coverage	deviation
chr1	249250621	3169650987	12.7167	348.6856
chr2	243199373	2892921035	11.8953	81.8826
chr3	198022430	2316559666	11.6985	30.7326
chr4	191154276	2048738775	10.7177	95.1502
chr5	180915260	1644983090	9.0926	13.656
chr6	171115067	1680124163	9.8187	42.4321
chr7	159138663	1932816528	12.1455	86.6474
chr8	146364022	1761335896	12.0339	118.0539
chr9	141213431	1629741544	11.541	107.0669
chr10	135534747	1703689557	12.5701	304.9875
chr11	135006516	1554281118	11.5126	58.3752
chr12	133851895	1286362713	9.6103	11.6917
chr13	115169878	1046629570	9.0877	6.8601
chr14	107349540	753300751	7.0173	11.335
chr15	102531392	905928591	8.8356	6.9134
chr16	90354753	1280288284	14.1696	143.0943
chr17	81195210	733629986	9.0354	34.9591
chr18	78077248	1303700366	16.6976	134.2131
chr19	59128983	761056137	12.8711	171.7003
chr20	63025520	669984995	10.6304	33.9121
chr21	48129895	479510078	9.9628	51.5517
chr22	51304566	396533877	7.729	9.1613
chrMT	16571	7784684	469.7776	87.0645
chrX	155270560	2185769045	14.0772	45.1156

chrY	59373566	120015790	2.0214	107.7019

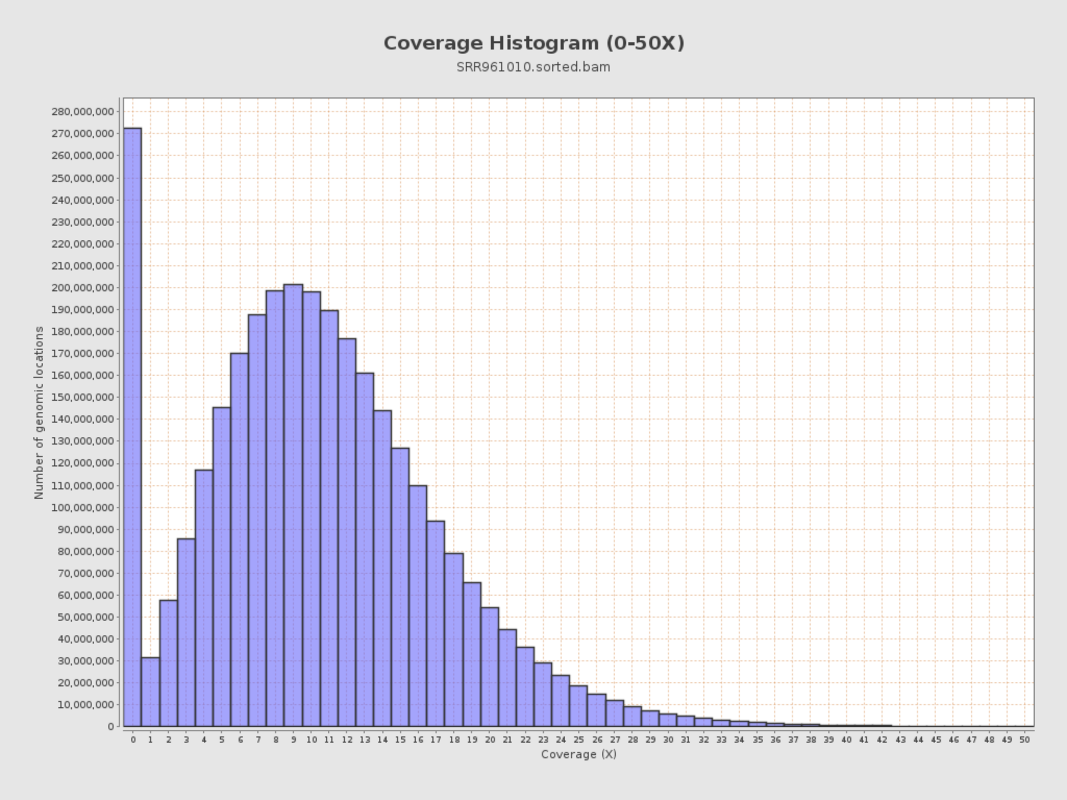
3. Results : Coverage across reference



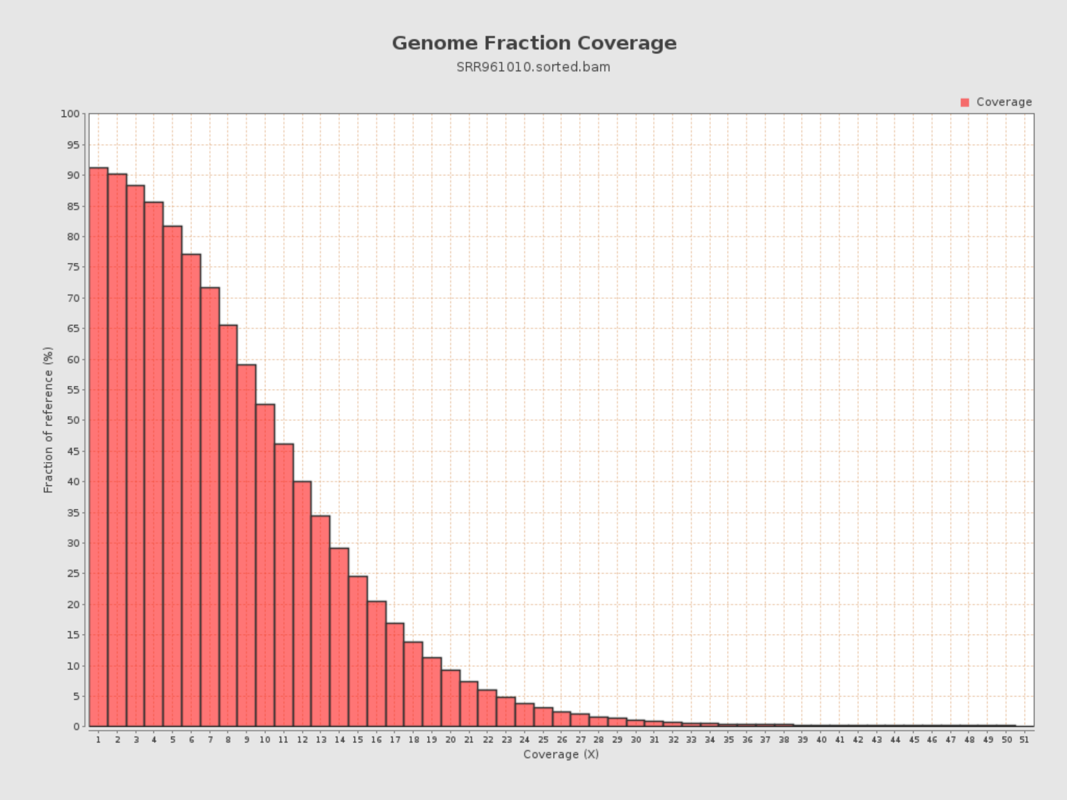
4. Results : Coverage Histogram



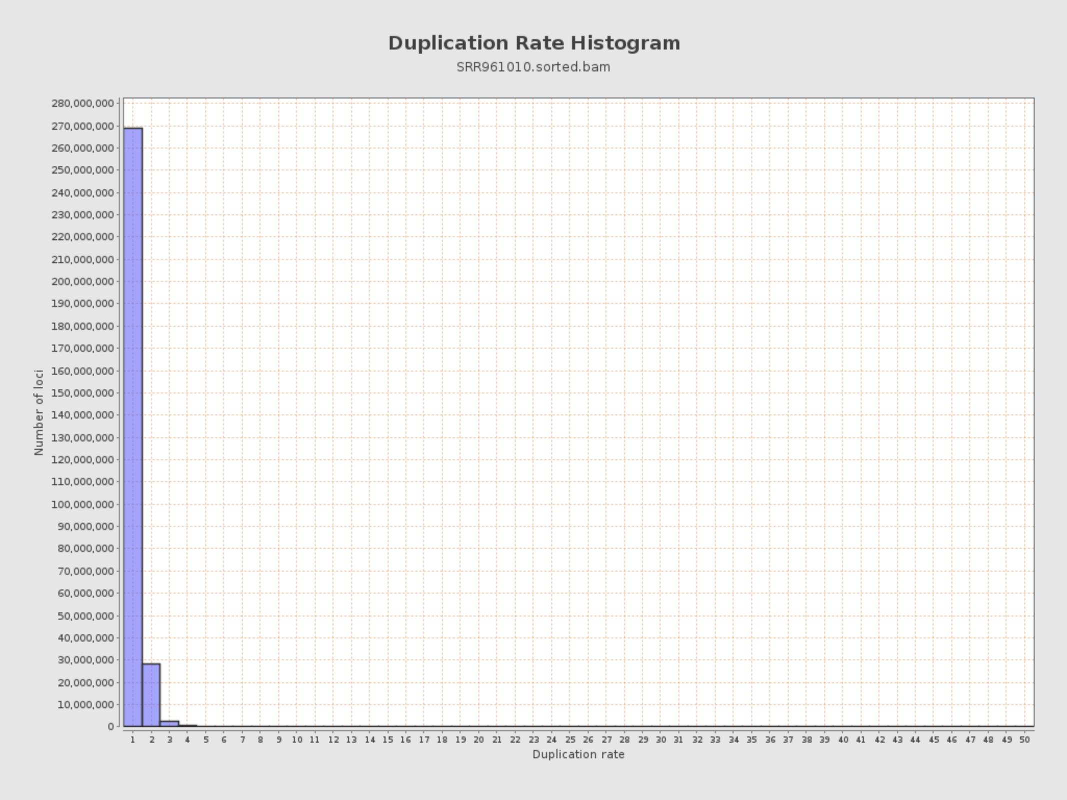
5. Results : Coverage Histogram (0-50X)



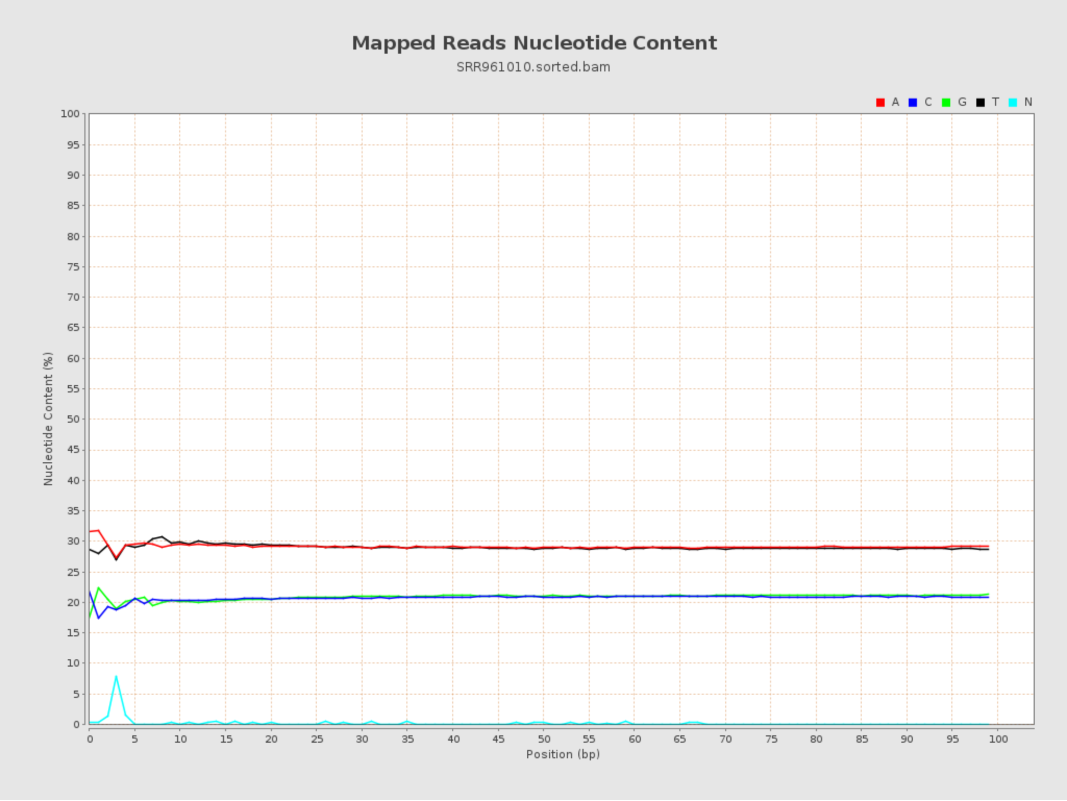
6. Results : Genome Fraction Coverage



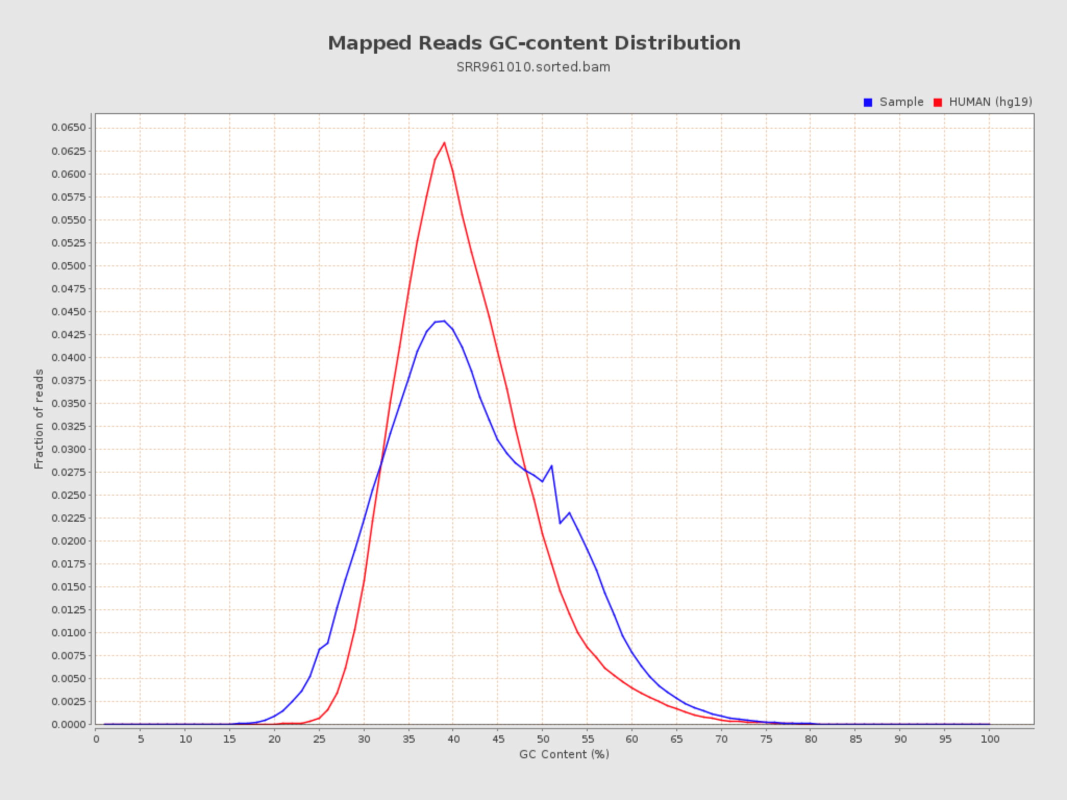
7. Results : Duplication Rate Histogram



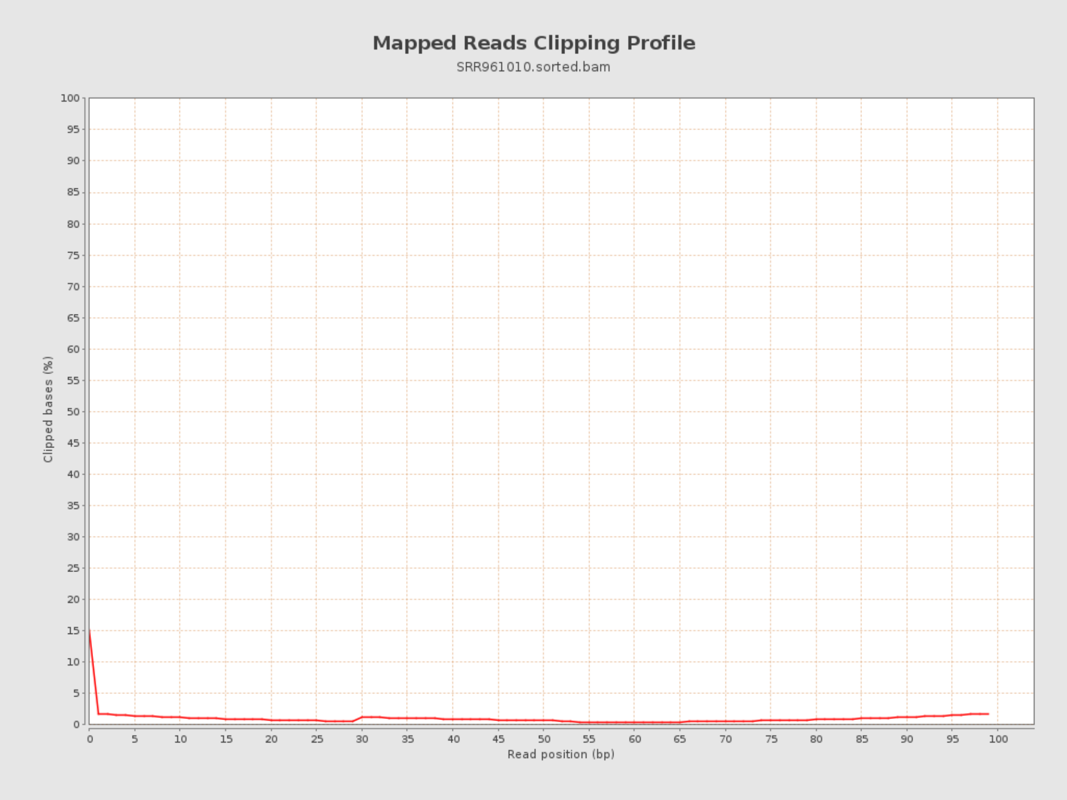
8. Results : Mapped Reads Nucleotide Content



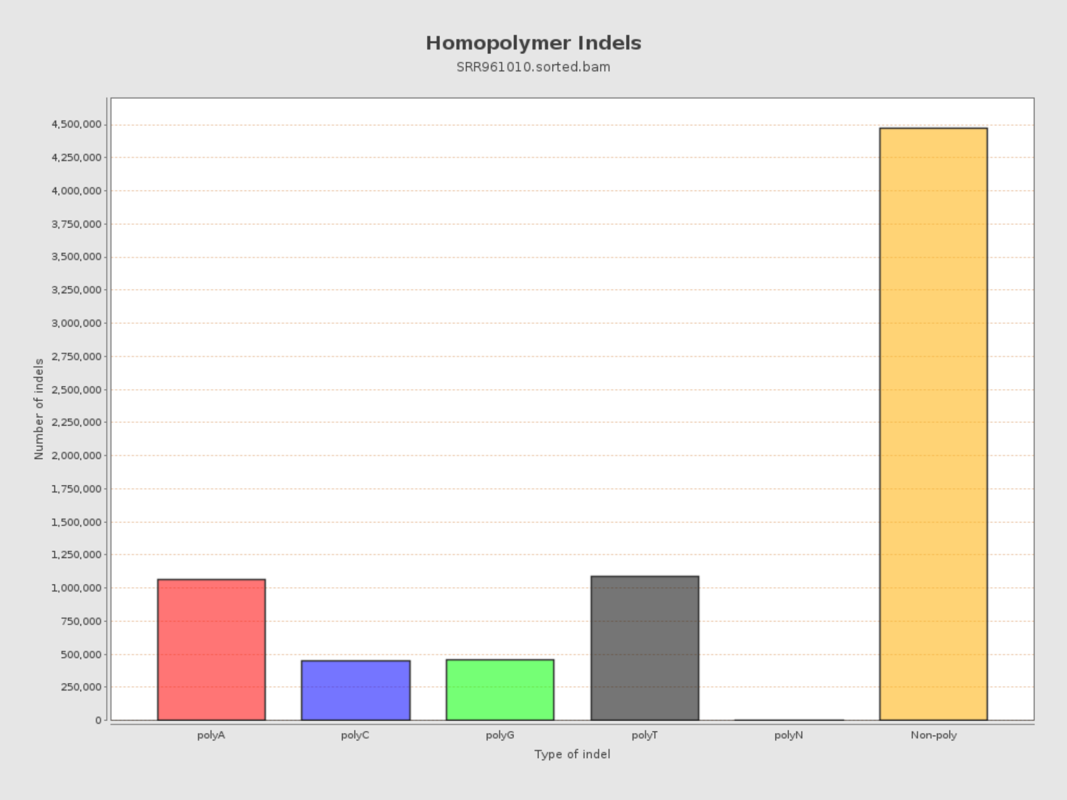
9. Results : Mapped Reads GC-content Distribution



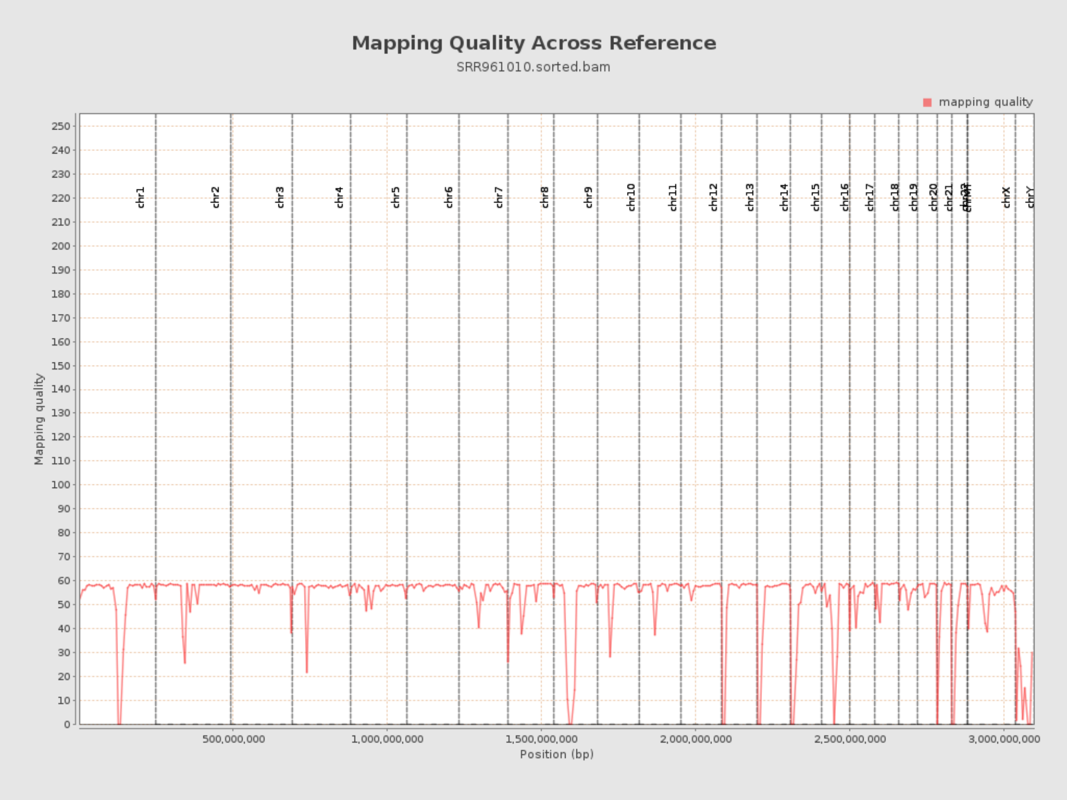
10. Results : Mapped Reads Clipping Profile



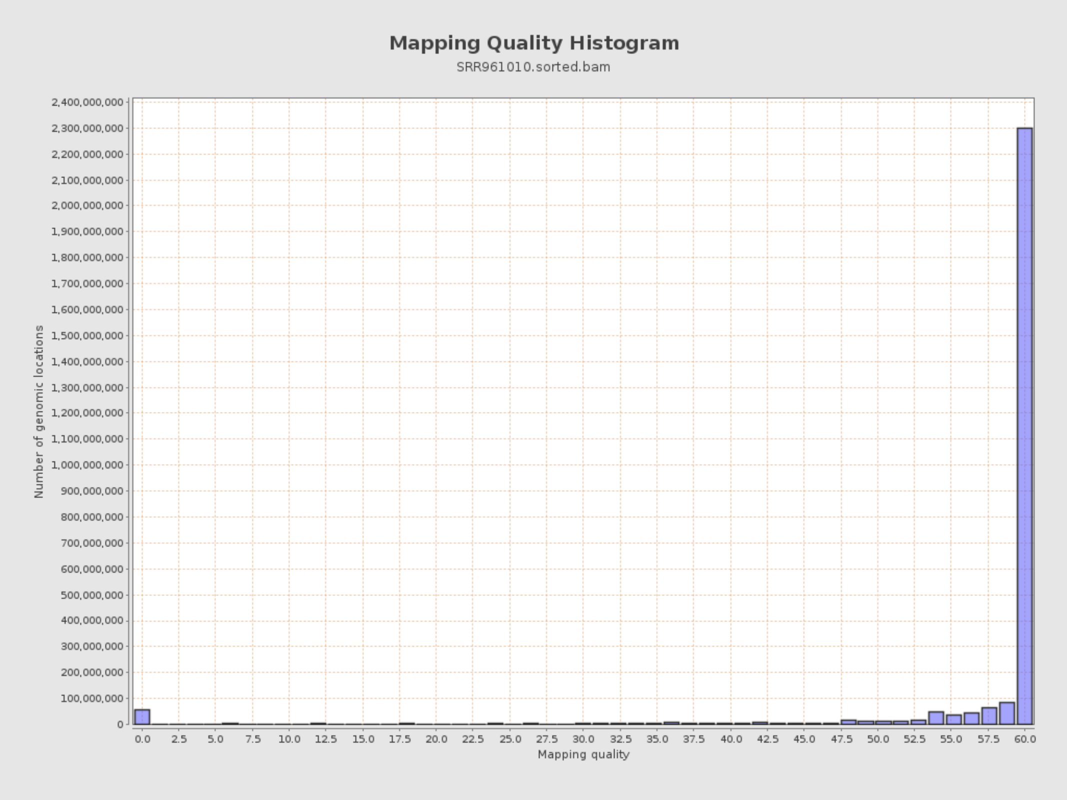
11. Results : Homopolymer Indels



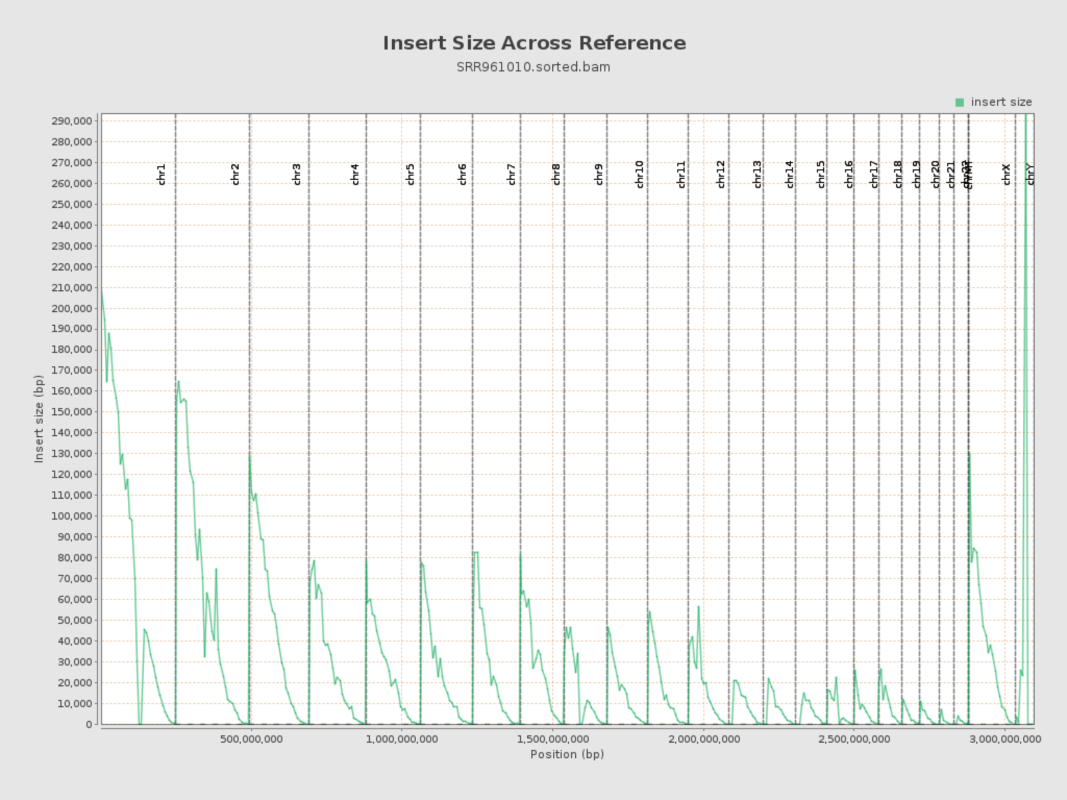
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram