Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/08 11:26:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961007.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_SRR961007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961007_1.fastq.gz SRR961007_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 08 11:26:35 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	387,313,726
Mapped reads	379,602,631 / 98.01%
Unmapped reads	7,711,095 / 1.99%
Mapped paired reads	379,602,631 / 98.01%
Mapped reads, first in pair	190,049,956 / 49.07%
Mapped reads, second in pair	189,552,675 / 48.94%
Mapped reads, both in pair	378,530,632 / 97.73%
Mapped reads, singletons	1,071,999 / 0.28%
Secondary alignments	0
Supplementary alignments	814,439 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	62,388,113 / 16.11%
Duplication rate	12.02%
Clipped reads	43,599,356 / 11.26%

2.2. ACGT Content

Number/percentage of A's	10,980,845,272 / 29.64%
Number/percentage of C's	7,523,542,181 / 20.31%
Number/percentage of T's	10,926,214,926 / 29.49%
Number/percentage of G's	7,600,541,736 / 20.52%
Number/percentage of N's	17,519,586 / 0.05%

GC Percentage	40.82%

2.3. Coverage

Mean	11.9715
Standard Deviation	141.5356

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	15,835.53
Standard Deviation	1,210,830.06
P25/Median/P75	113 / 124 / 134

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	204,762,112
Insertions	3,804,882
Mapped reads with at least one insertion	0.97%
Deletions	4,472,659
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.14%

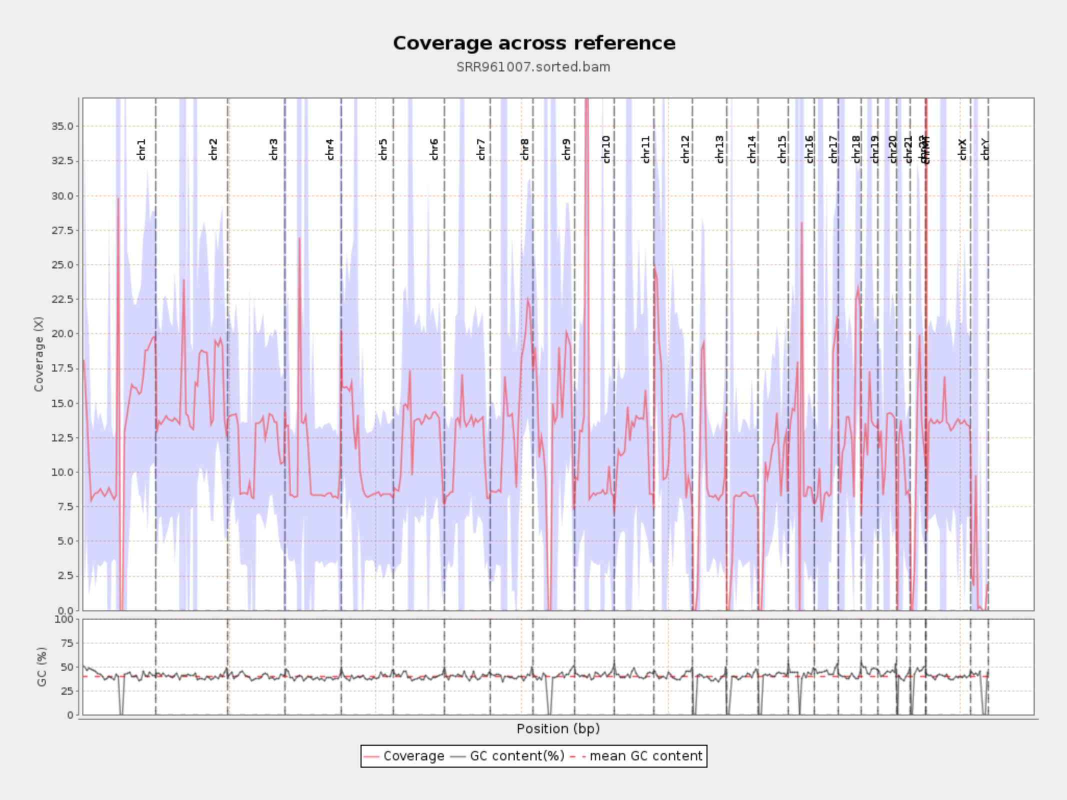
2.7. Chromosome stats

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

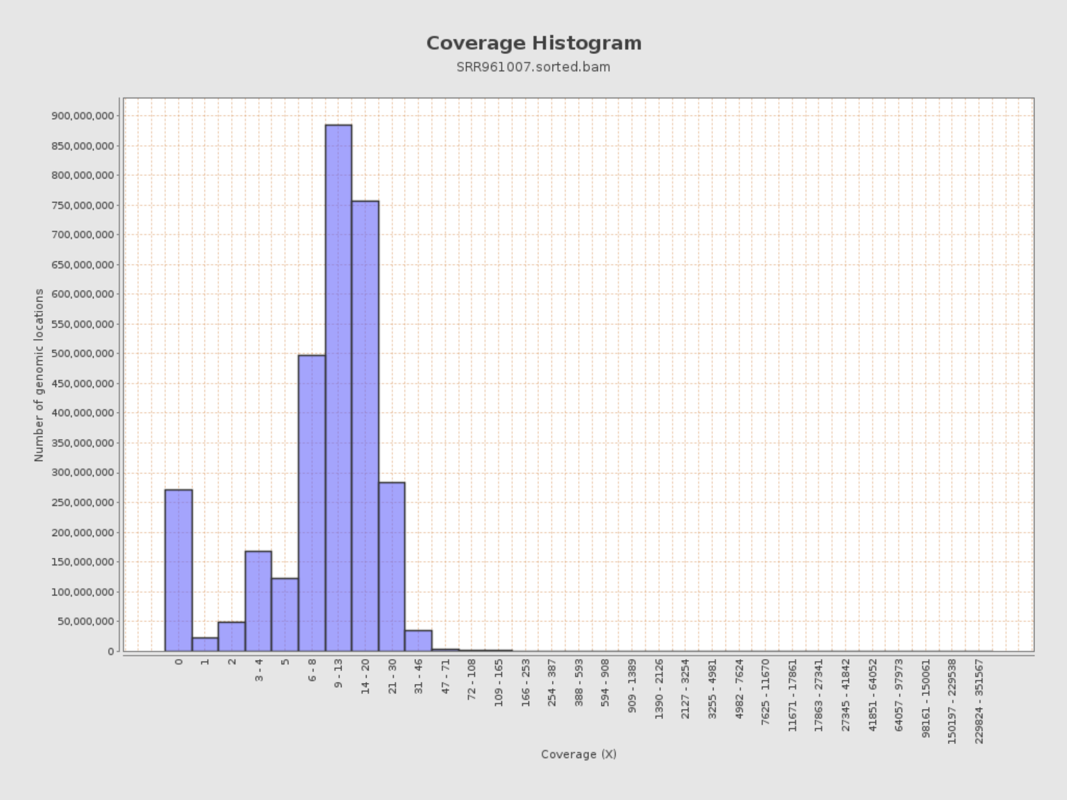
		bases	coverage	deviation
chr1	249250621	3197494830	12.8284	340.1459
chr2	243199373	3828177901	15.7409	82.8543
chr3	198022430	2369642204	11.9665	42.0725
chr4	191154276	1975080126	10.3324	116.6066
chr5	180915260	1946587588	10.7597	13.0669
chr6	171115067	2200970310	12.8625	41.3453
chr7	159138663	1906652480	11.9811	87.1622
chr8	146364022	2077395710	14.1933	133.0813
chr9	141213431	1872208828	13.258	94.7258
chr10	135534747	1635688184	12.0684	348.936
chr11	135006516	1654856657	12.2576	54.2434
chr12	133851895	1864274190	13.9279	12.7837
chr13	115169878	1005647996	8.7319	7.6108
chr14	107349540	738645629	6.8808	12.1646
chr15	102531392	937387495	9.1424	7.3275
chr16	90354753	1070227684	11.8447	133.2238
chr17	81195210	898837770	11.0701	36.6199
chr18	78077248	1133871523	14.5224	125.5503
chr19	59128983	771759876	13.0521	171.5213
chr20	63025520	784720931	12.4508	37.3362
chr21	48129895	456409752	9.4829	64.0745
chr22	51304566	514094118	10.0204	11.3264
chrMT	16571	17432739	1,052.0028	178.45
chrX	155270560	2081167870	13.4035	42.3497

chrY	59373566	120837831	2.0352	124.8571

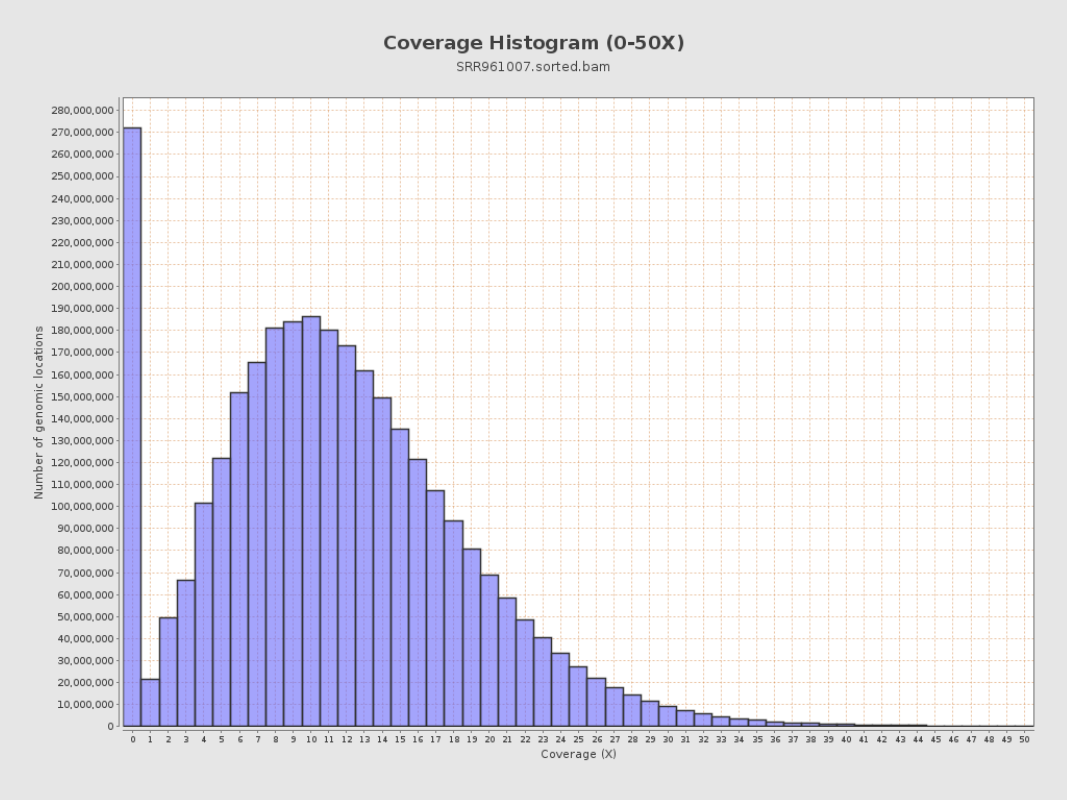
3. Results : Coverage across reference



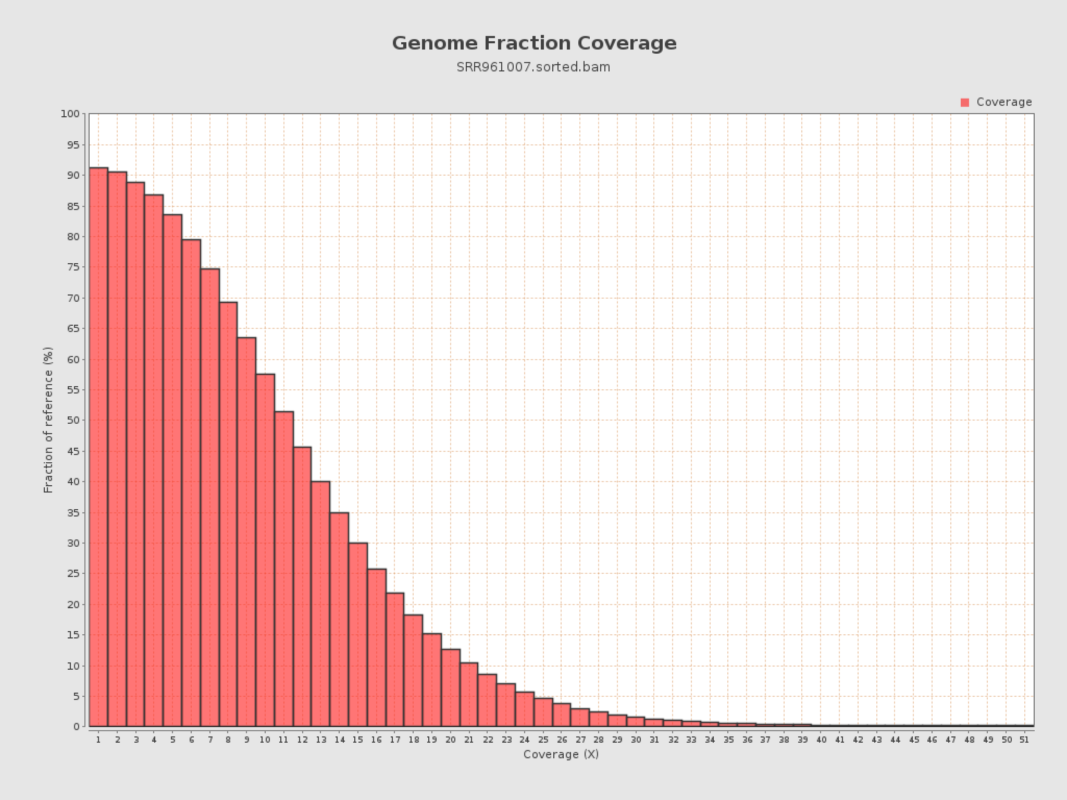
4. Results : Coverage Histogram



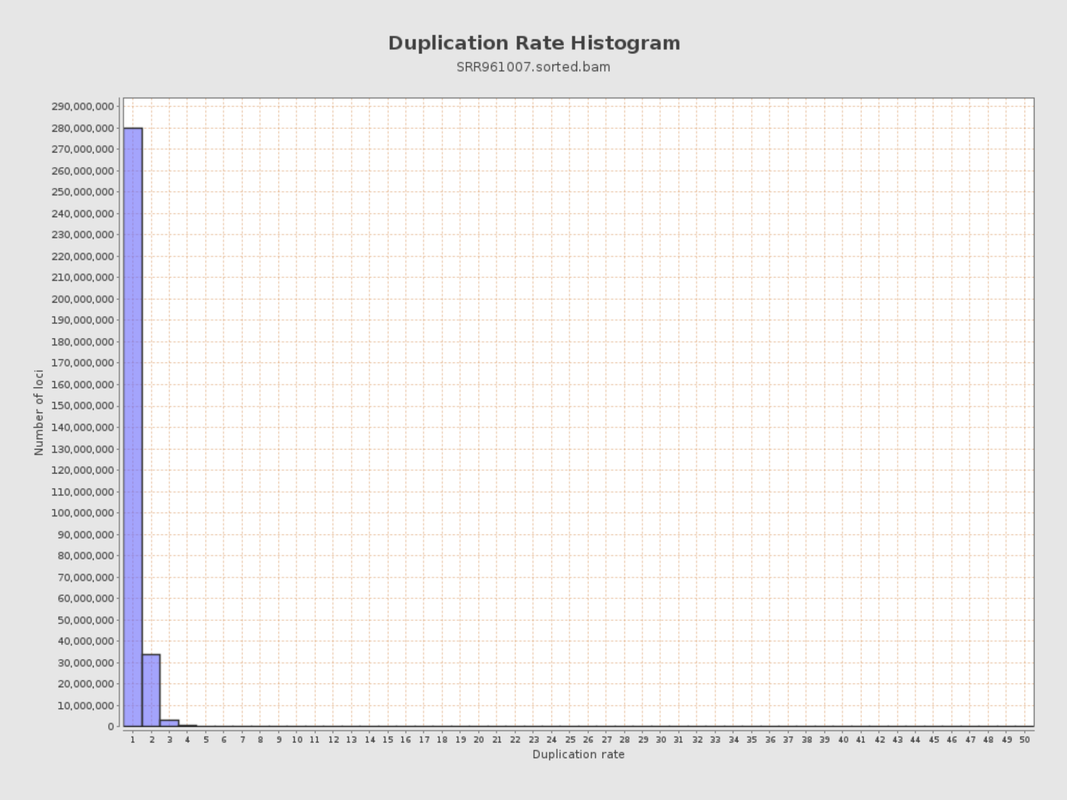
5. Results : Coverage Histogram (0-50X)



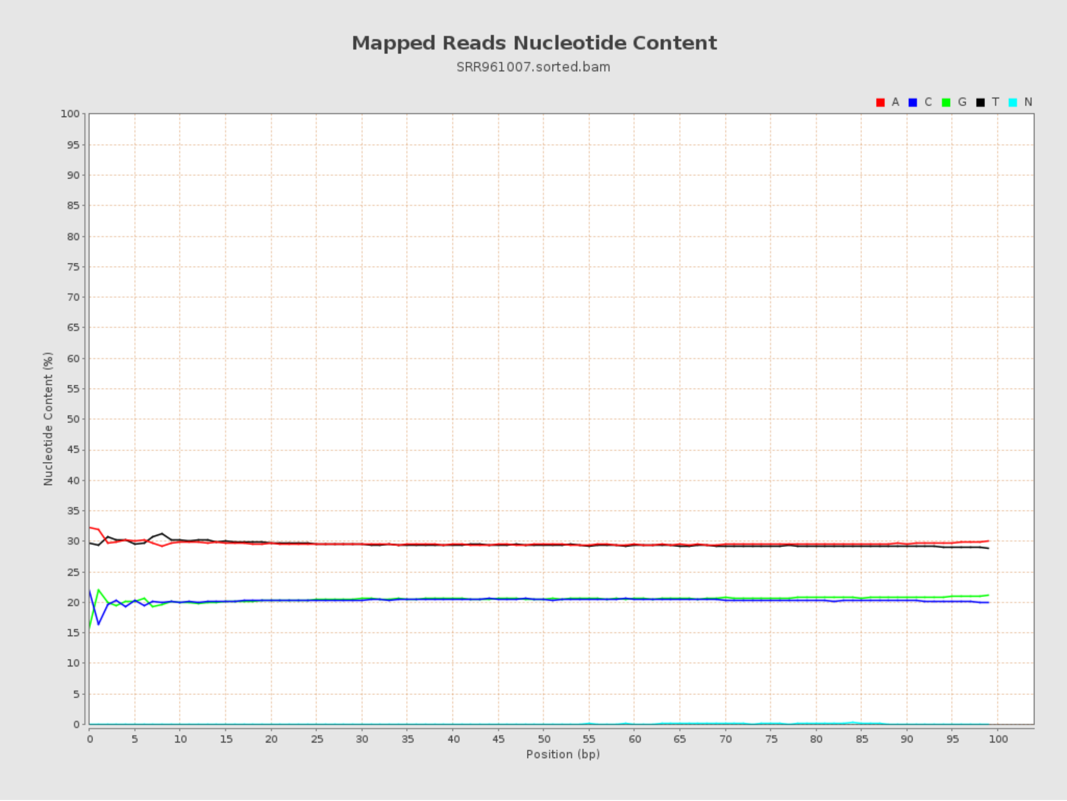
6. Results : Genome Fraction Coverage



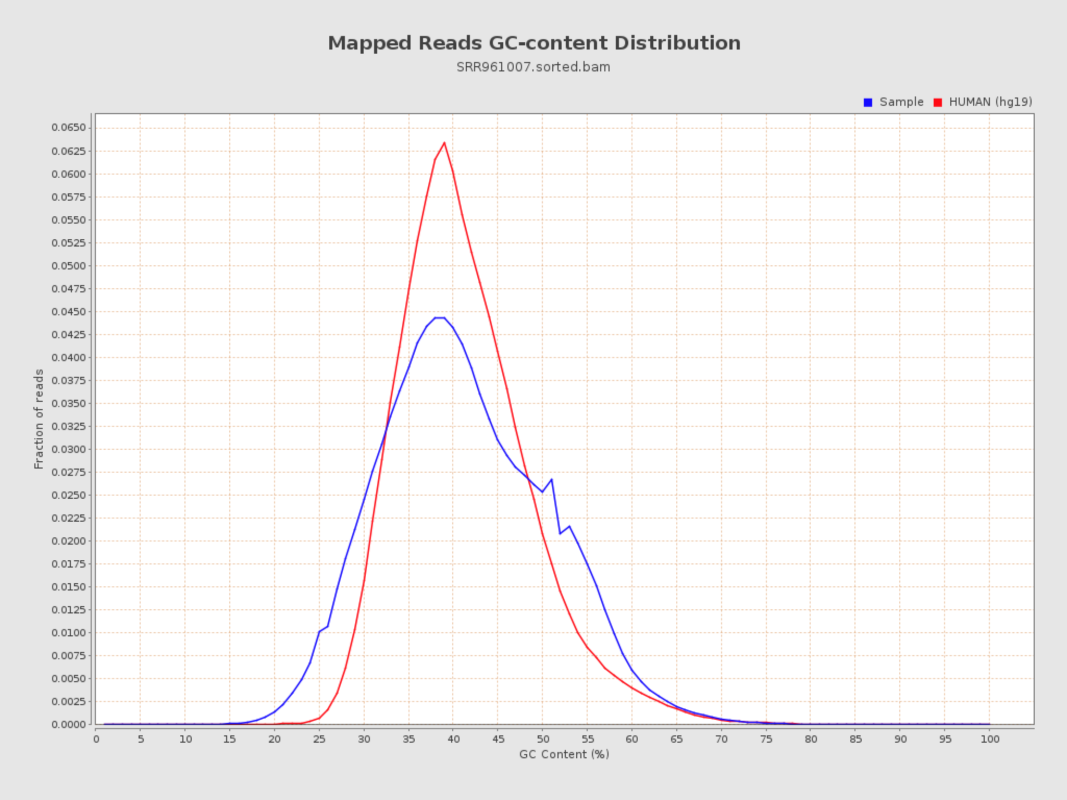
7. Results : Duplication Rate Histogram



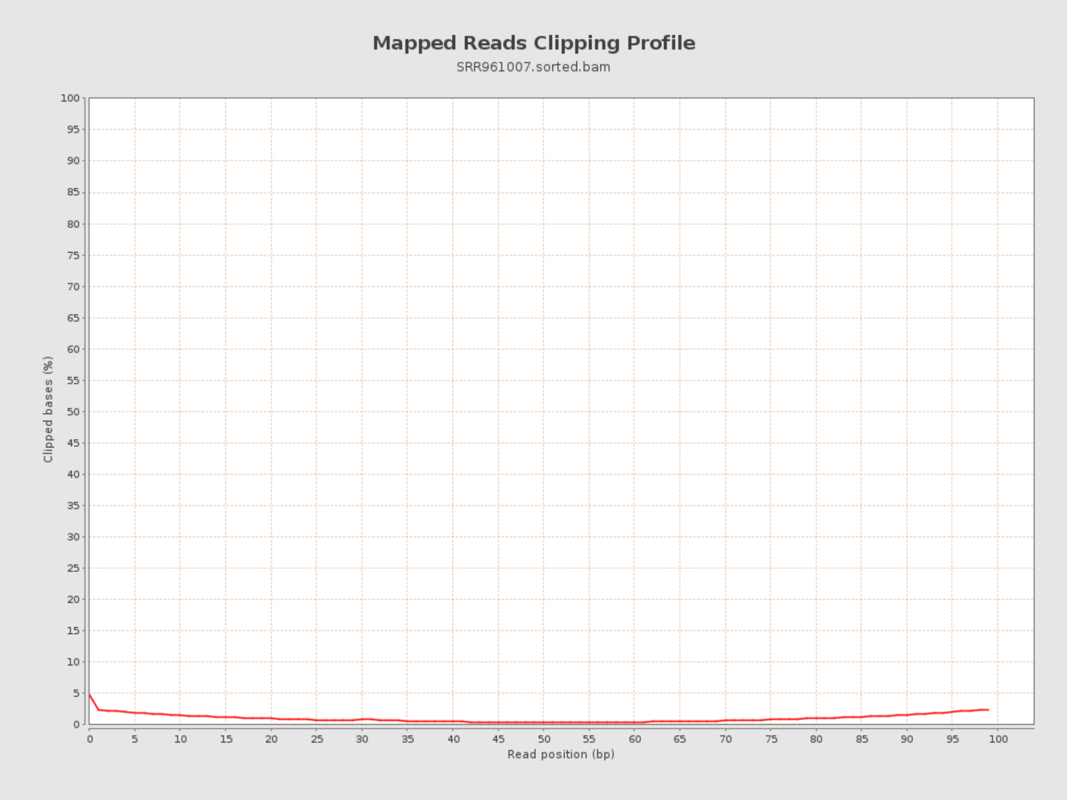
8. Results : Mapped Reads Nucleotide Content



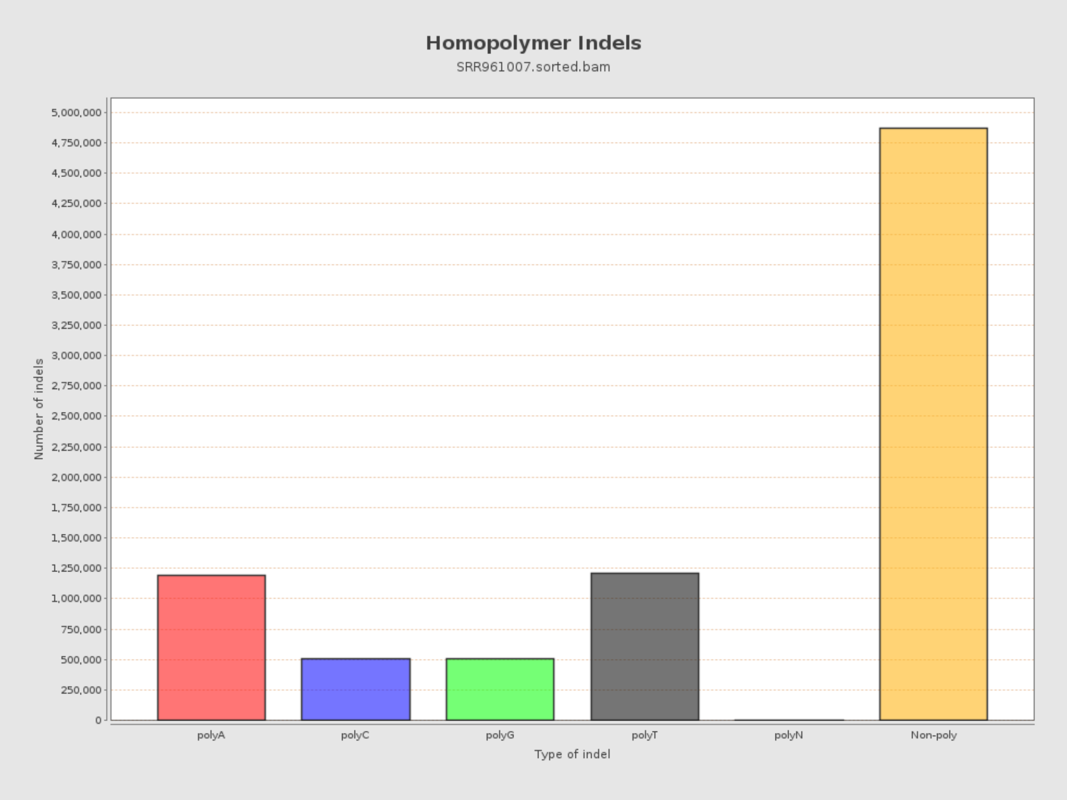
9. Results : Mapped Reads GC-content Distribution



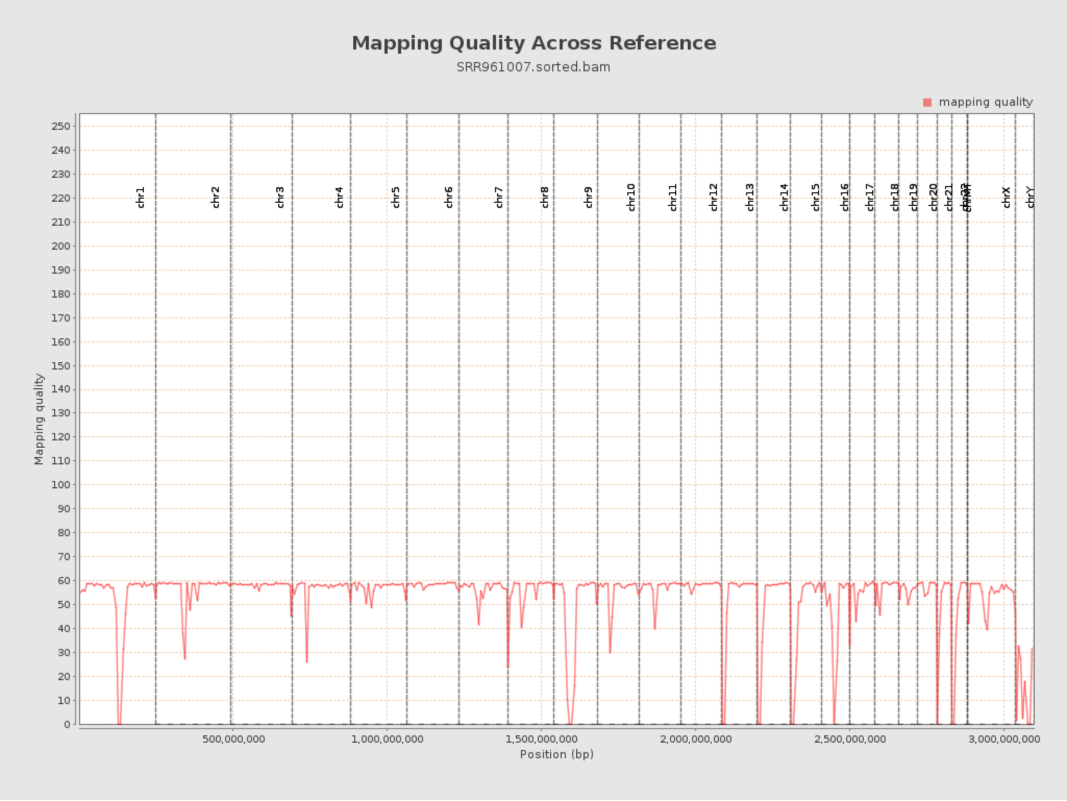
10. Results : Mapped Reads Clipping Profile



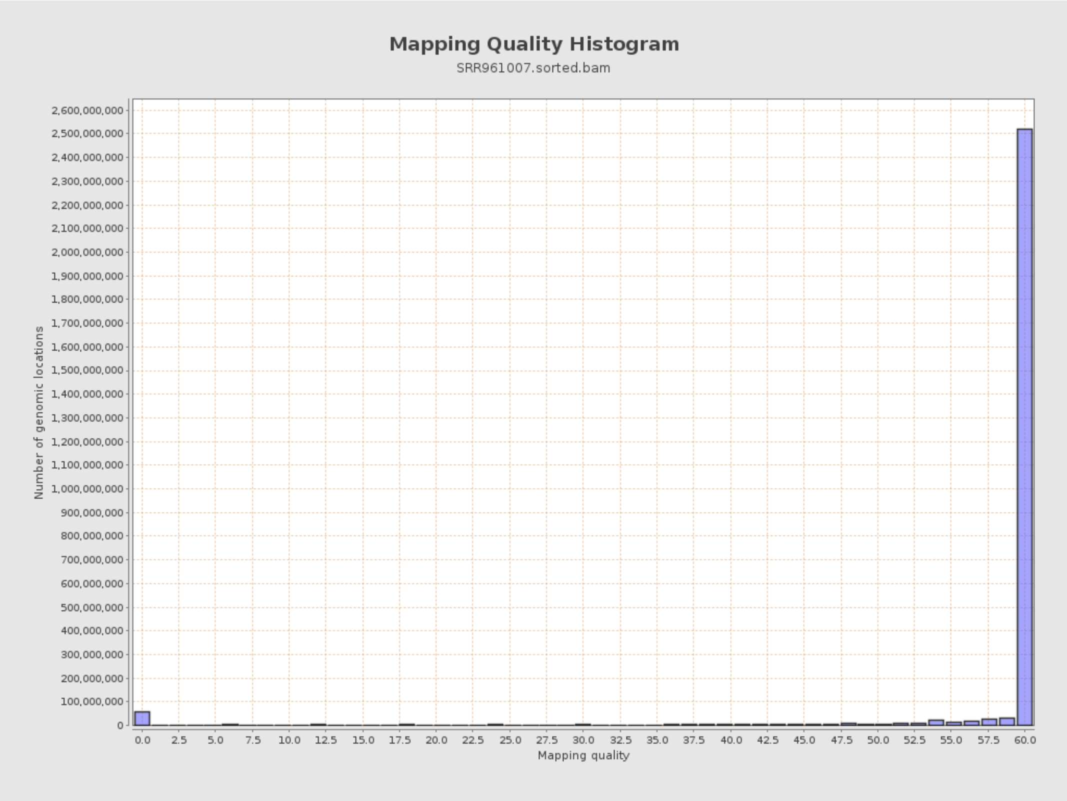
11. Results : Homopolymer Indels



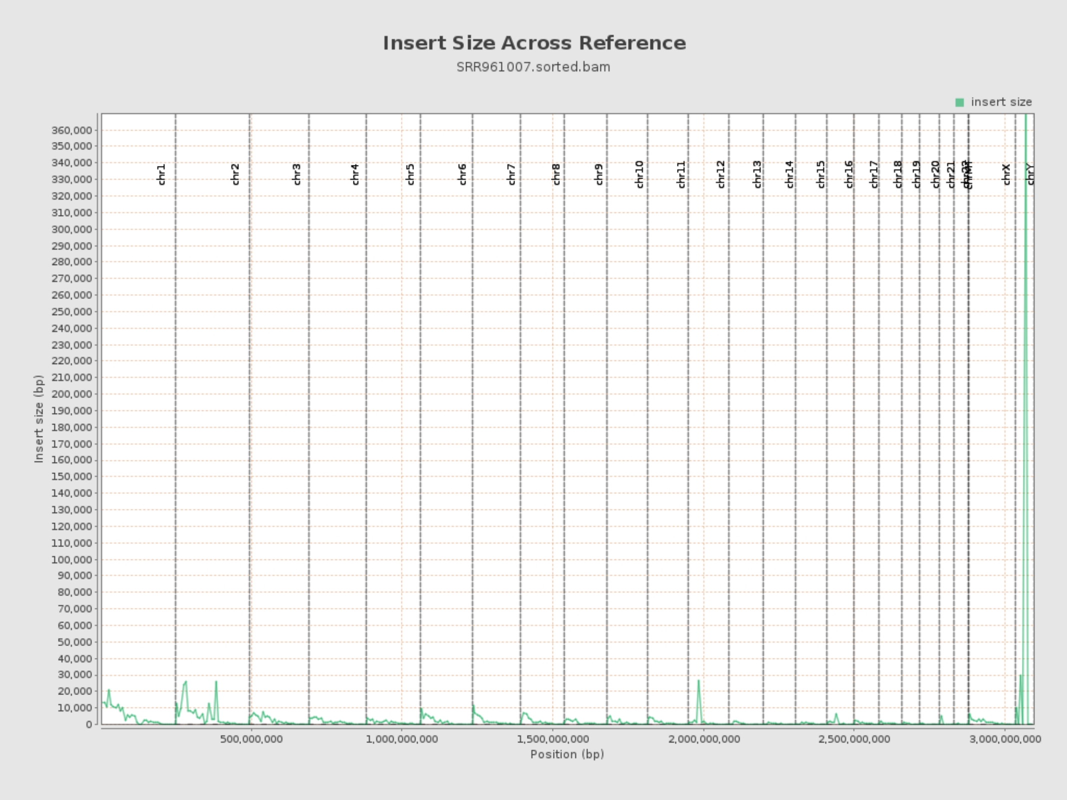
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram