Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:36:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124961.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_SRR3124961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124961_1.fastq.gz SRR3124961_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:36:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,023,576
Mapped reads	5,895,276 / 97.87%
Unmapped reads	128,300 / 2.13%
Mapped paired reads	5,895,276 / 97.87%
Mapped reads, first in pair	2,954,393 / 49.05%
Mapped reads, second in pair	2,940,883 / 48.82%
Mapped reads, both in pair	5,865,616 / 97.38%
Mapped reads, singletons	29,660 / 0.49%
Secondary alignments	0
Supplementary alignments	58,937 / 0.98%
Read min/max/mean length	30 / 101 / 101.39
Duplicated reads (estimated)	820,514 / 13.62%
Duplication rate	9.53%
Clipped reads	3,363,652 / 55.84%

2.2. ACGT Content

Number/percentage of A's	144,379,065 / 28.87%
Number/percentage of C's	91,303,960 / 18.26%
Number/percentage of T's	151,600,297 / 30.32%
Number/percentage of G's	112,764,999 / 22.55%
Number/percentage of N's	5,300 / 0%

GC Percentage	40.81%

2.3. Coverage

Mean	0.1616
Standard Deviation	2.491

2.4. Mapping Quality

Mean Mapping Quality	52.34

2.5. Insert size

Mean	83,450.31
Standard Deviation	2,719,350.4
P25/Median/P75	120 / 164 / 228

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	3,894,798
Insertions	81,801
Mapped reads with at least one insertion	1.34%
Deletions	163,746
Mapped reads with at least one deletion	2.72%
Homopolymer indels	45.76%

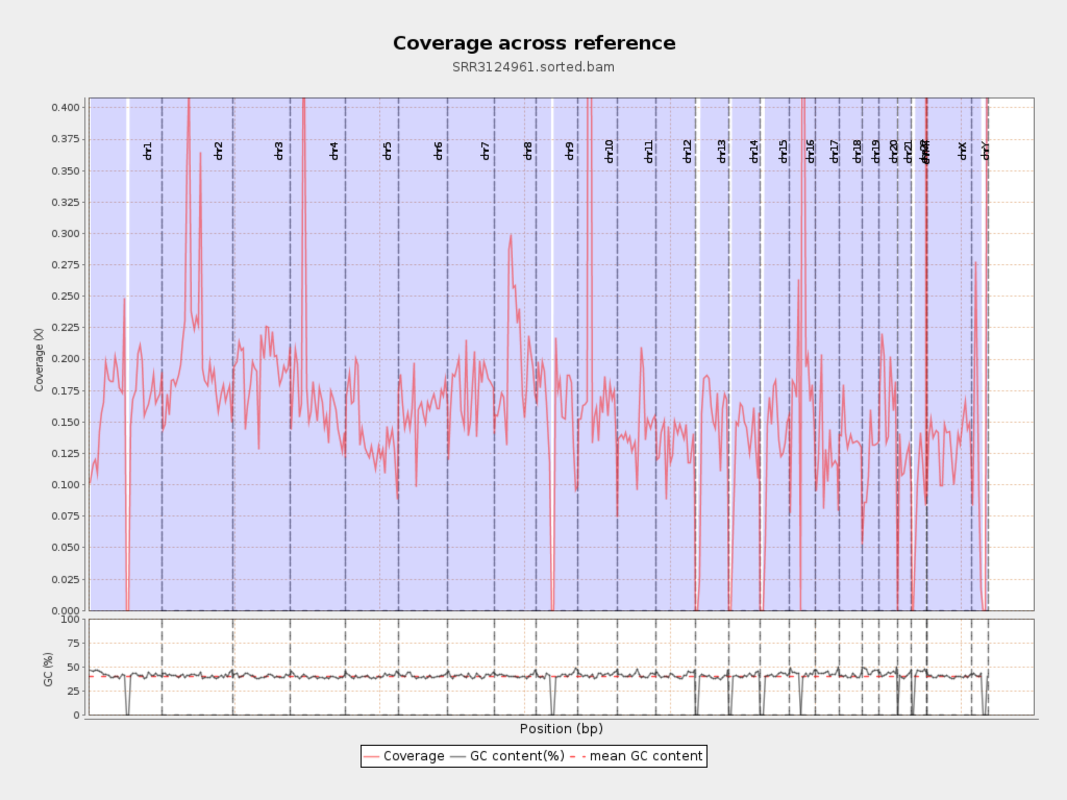
2.7. Chromosome stats

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

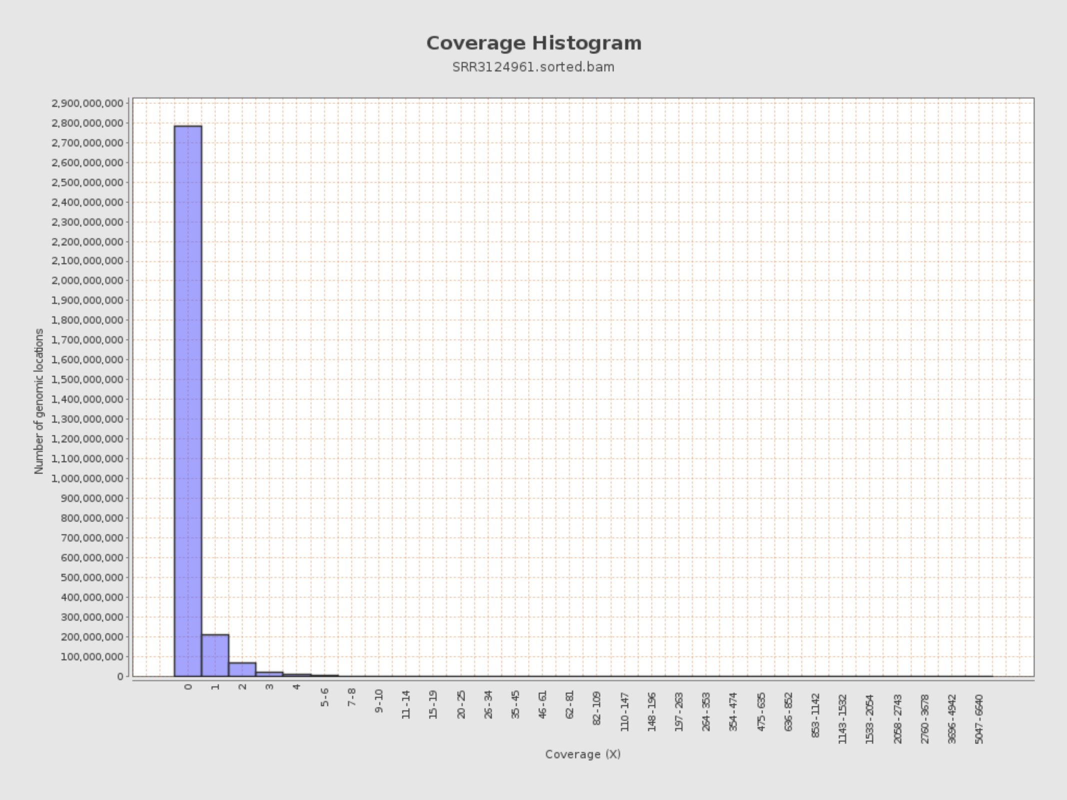
		bases	coverage	deviation
chr1	249250621	39835082	0.1598	1.428
chr2	243199373	49916116	0.2052	2.5345
chr3	198022430	38446247	0.1942	0.7411
chr4	191154276	33490930	0.1752	2.031
chr5	180915260	25394176	0.1404	0.5556
chr6	171115067	27792628	0.1624	0.7733
chr7	159138663	28188981	0.1771	1.1913
chr8	146364022	29351870	0.2005	0.8148
chr9	141213431	21224523	0.1503	1.8196
chr10	135534747	29491074	0.2176	9.1768
chr11	135006516	19526498	0.1446	0.8633
chr12	133851895	17652990	0.1319	0.5121
chr13	115169878	15541542	0.1349	0.5248
chr14	107349540	12841996	0.1196	0.5965
chr15	102531392	12429038	0.1212	0.5119
chr16	90354753	18932342	0.2095	3.8406
chr17	81195210	9784948	0.1205	1.5401
chr18	78077248	10924092	0.1399	1.8638
chr19	59128983	6904178	0.1168	0.8879
chr20	63025520	10888352	0.1728	0.801
chr21	48129895	5239901	0.1089	1.0288
chr22	51304566	4084074	0.0796	0.4912
chrMT	16571	3258741	196.6532	114.6578
chrX	155270560	20750600	0.1336	0.6891

chrY	59373566	8473044	0.1427	3.59

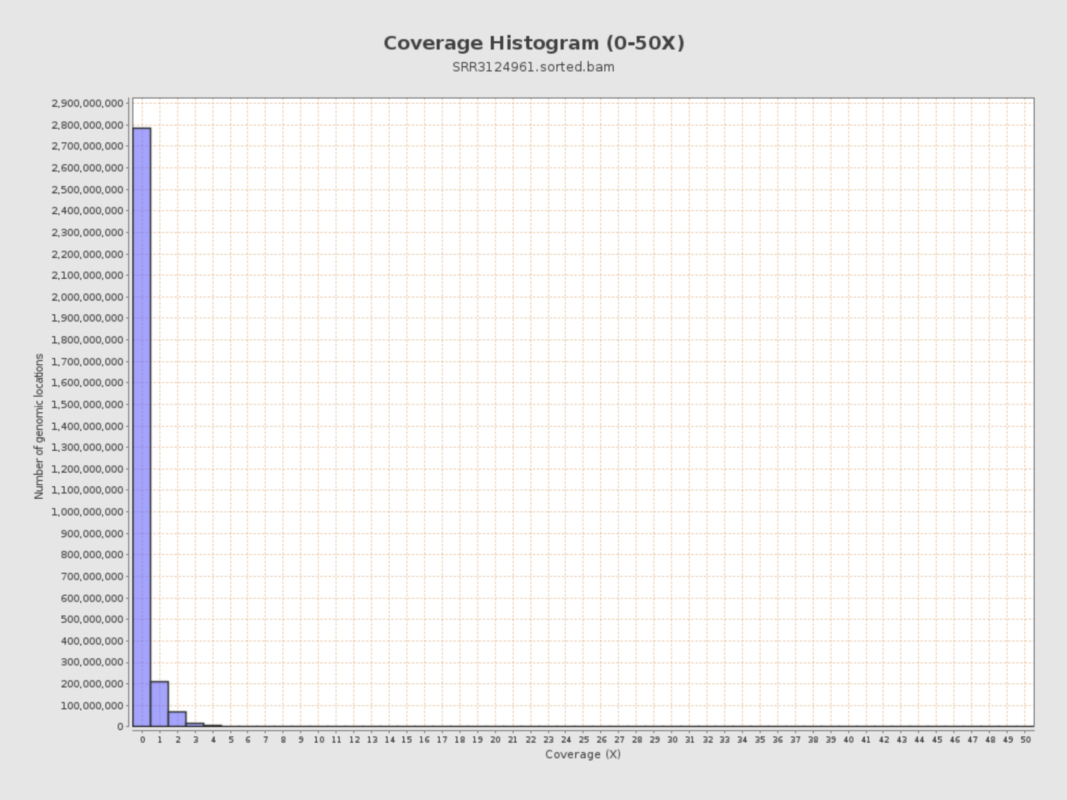
3. Results : Coverage across reference



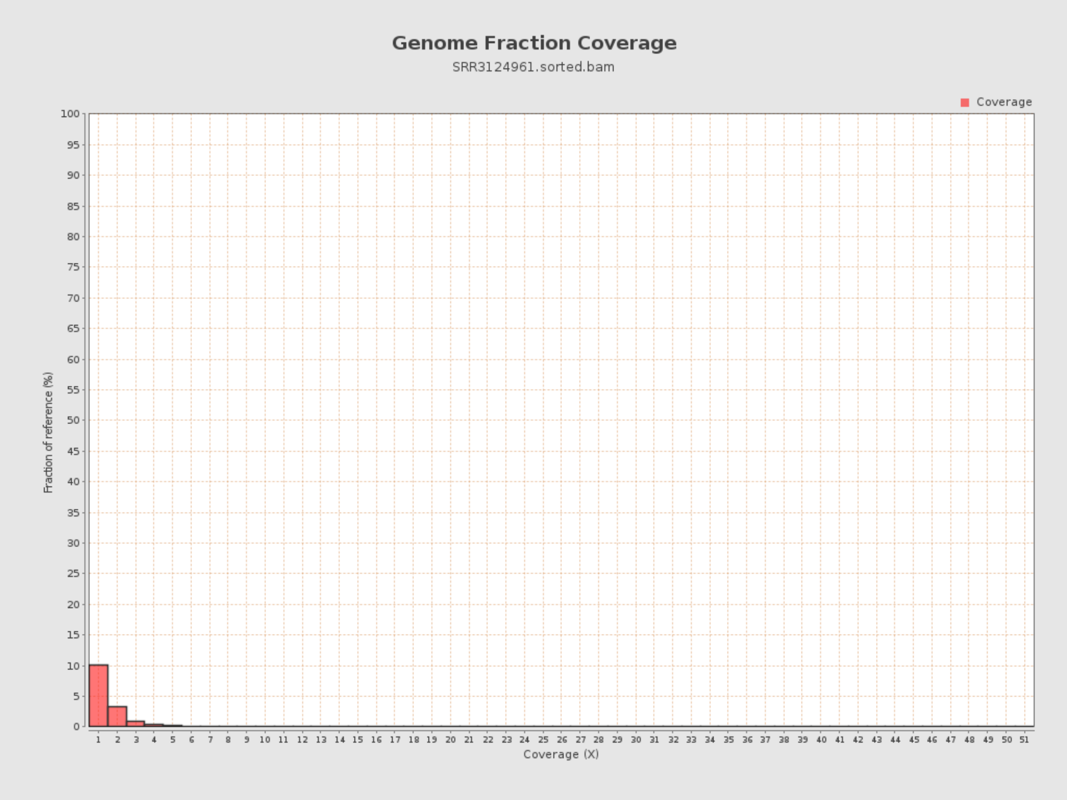
4. Results : Coverage Histogram



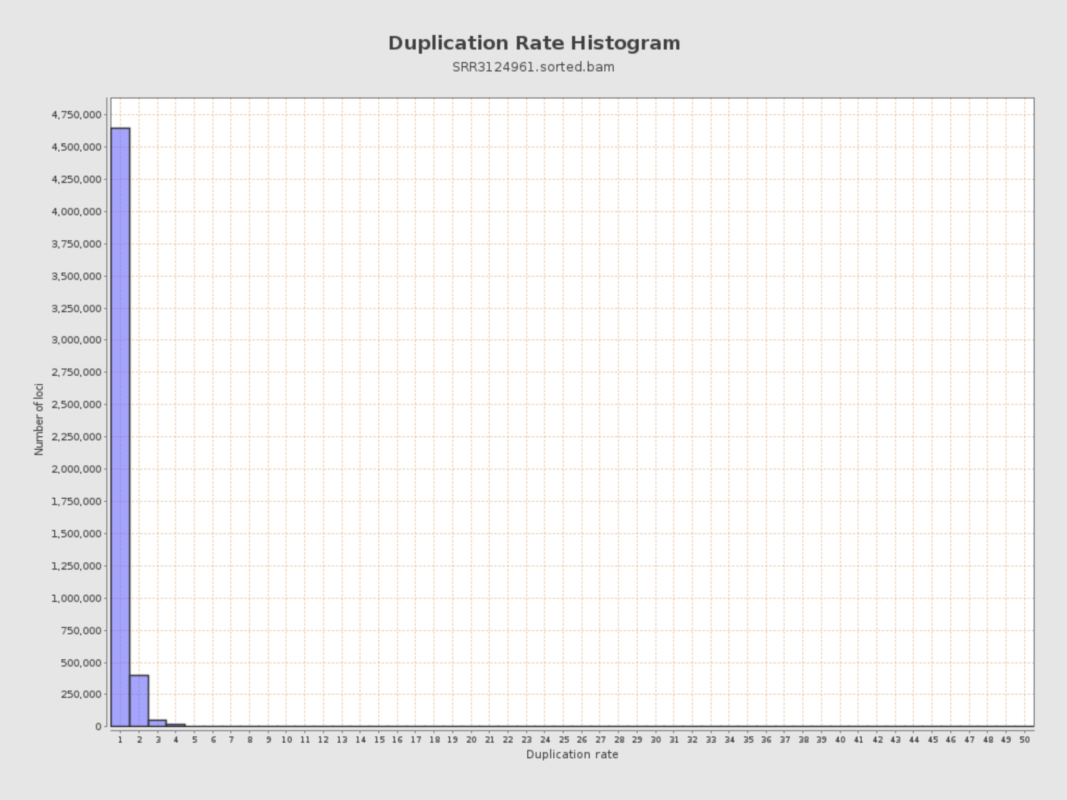
5. Results : Coverage Histogram (0-50X)



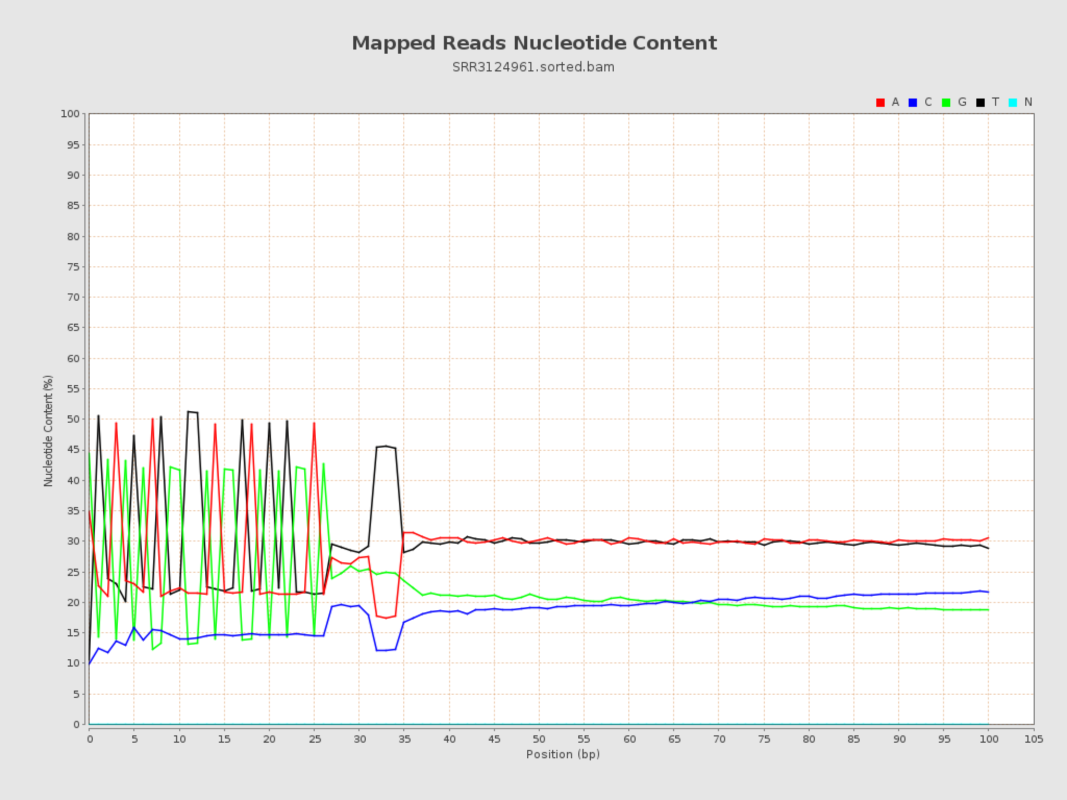
6. Results : Genome Fraction Coverage



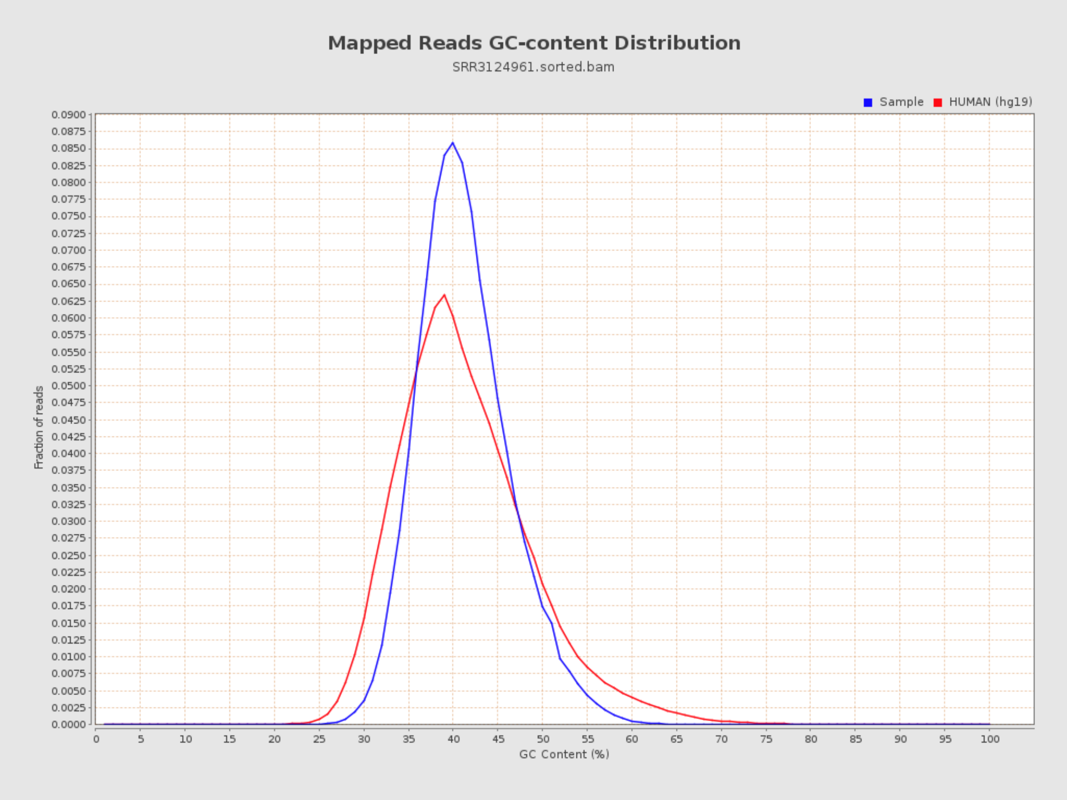
7. Results : Duplication Rate Histogram



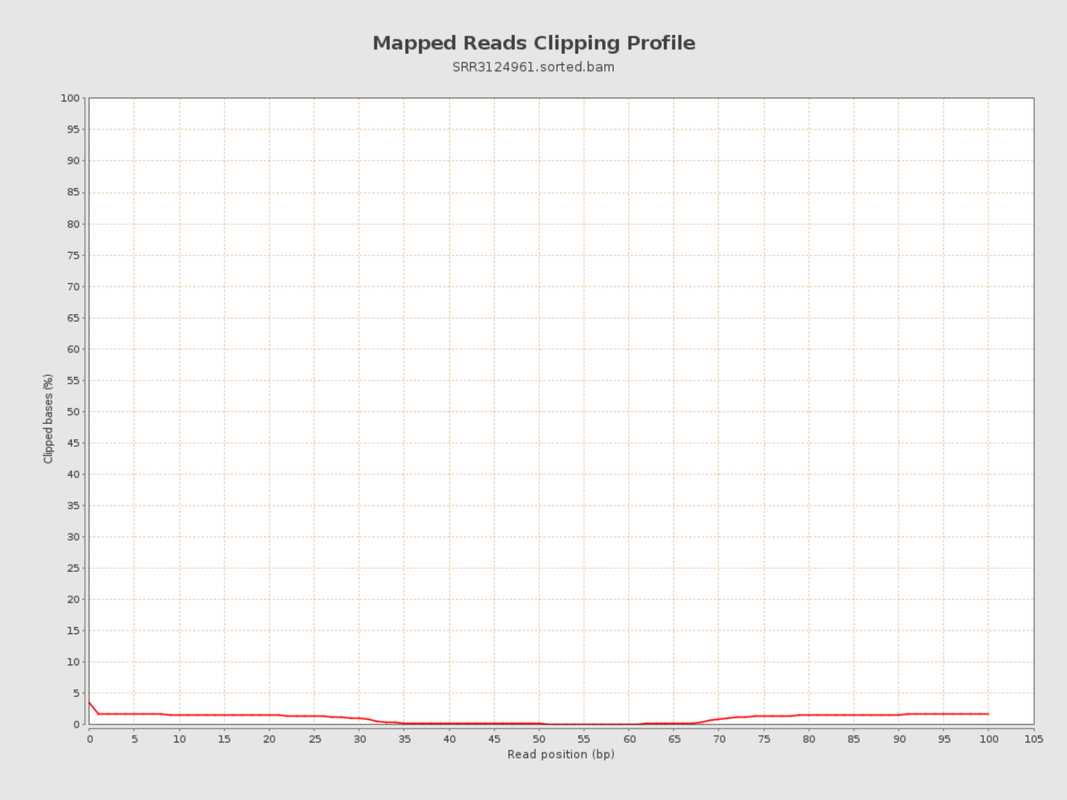
8. Results : Mapped Reads Nucleotide Content



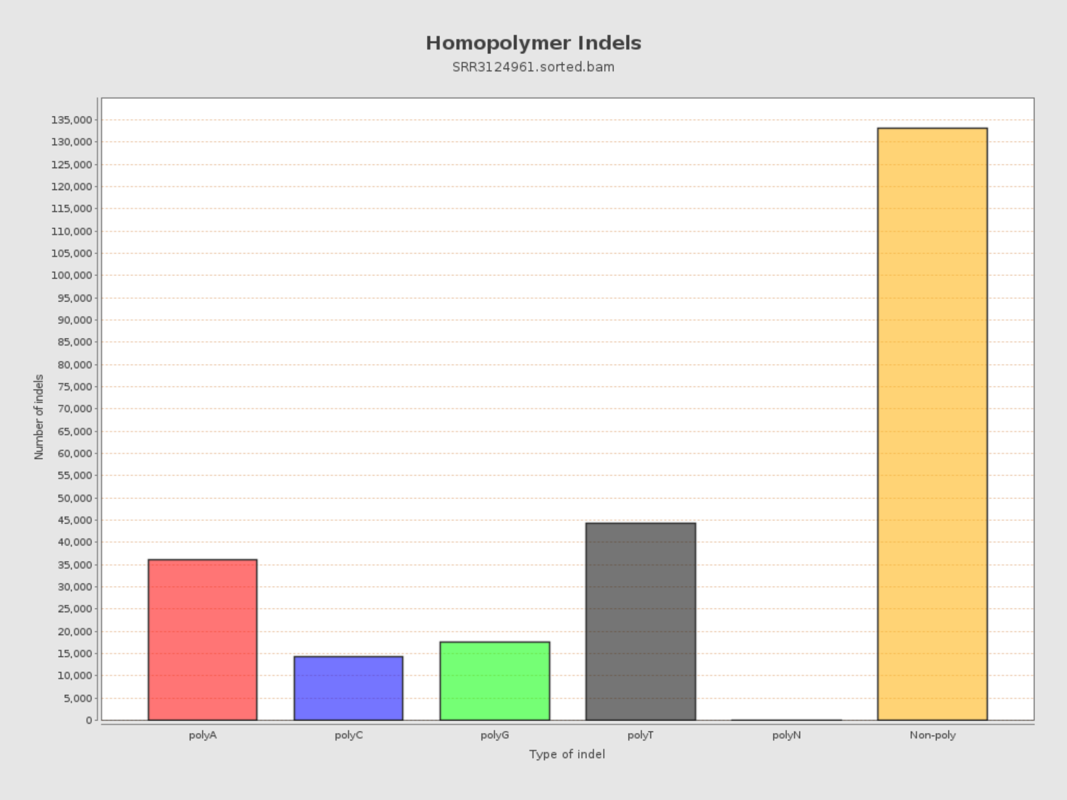
9. Results : Mapped Reads GC-content Distribution



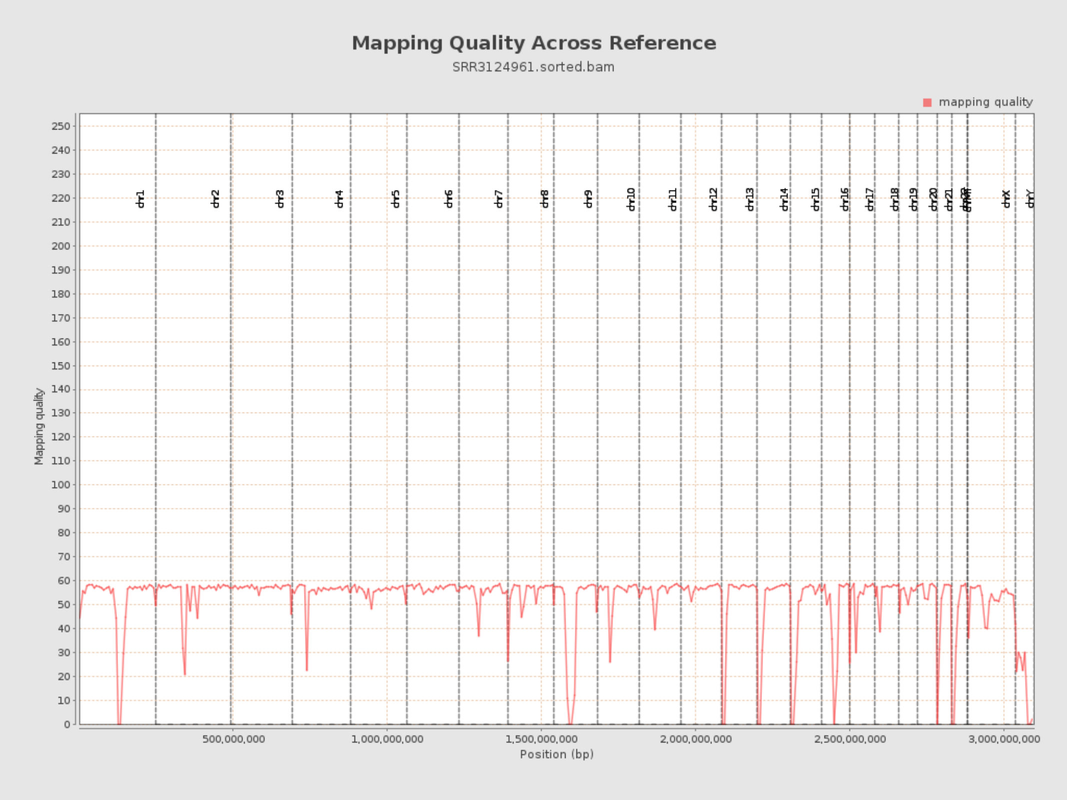
10. Results : Mapped Reads Clipping Profile



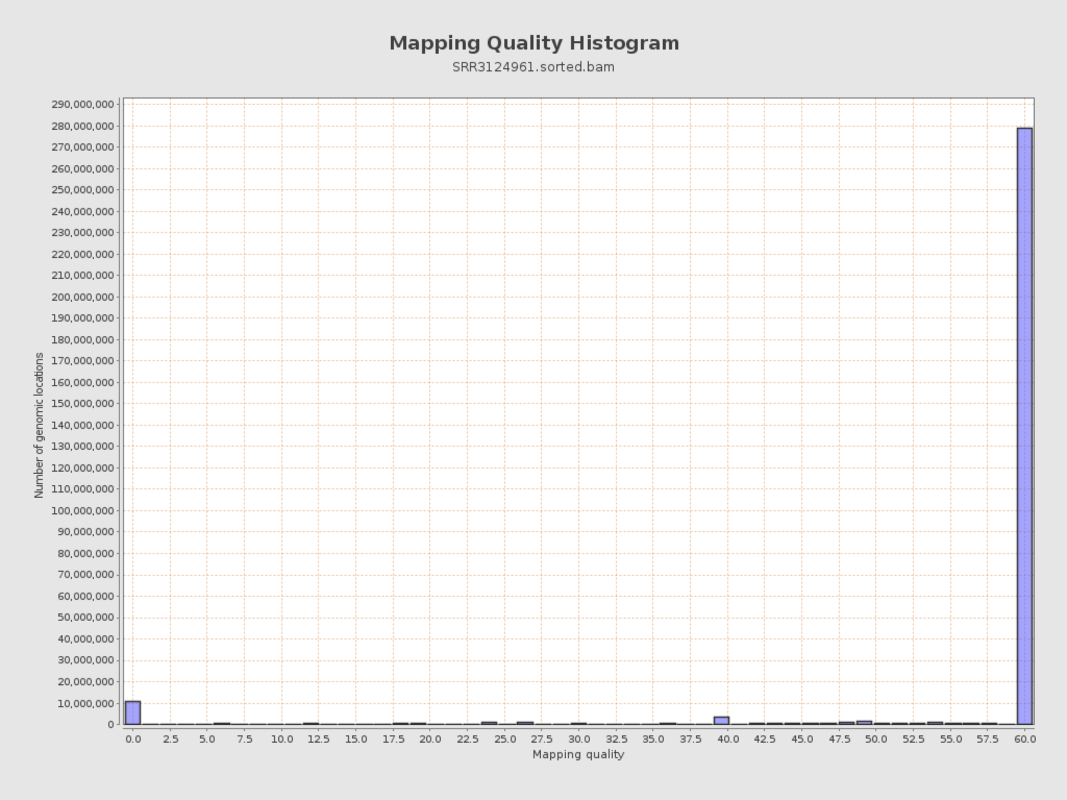
11. Results : Homopolymer Indels



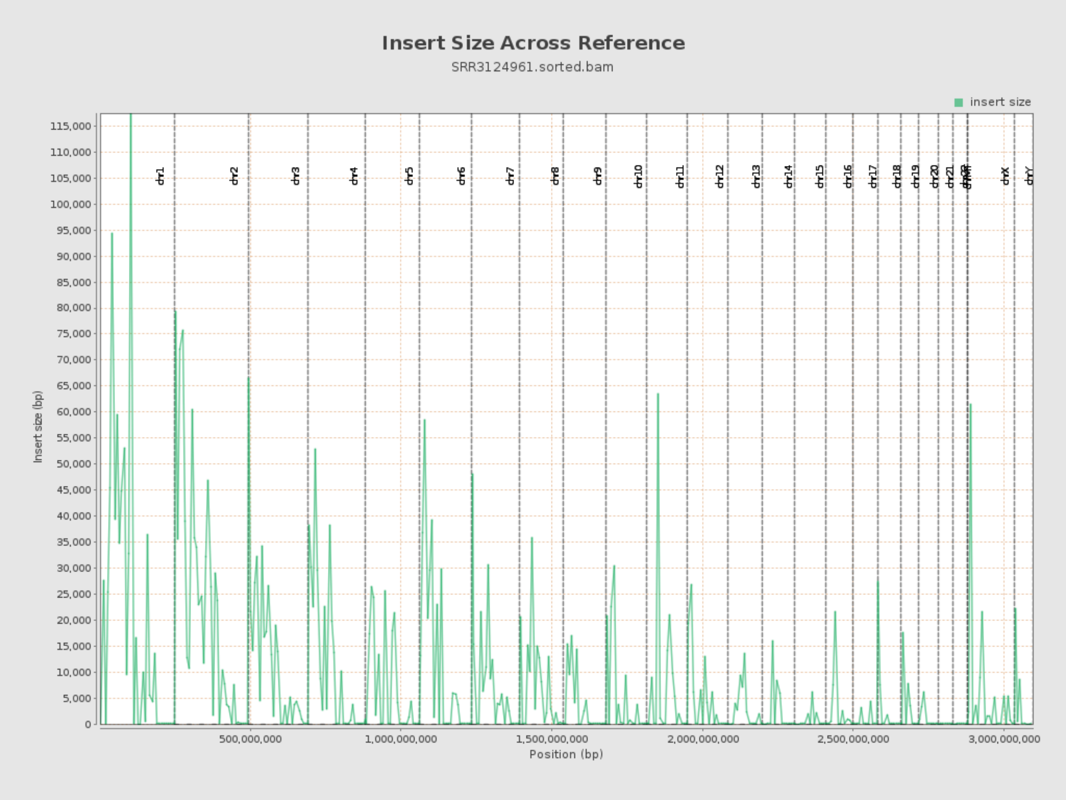
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram