Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 09:57:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961014.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_SRR961014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961014_1.fastq.gz SRR961014_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 09:57:19 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	392,604,452
Mapped reads	379,708,747 / 96.72%
Unmapped reads	12,895,705 / 3.28%
Mapped paired reads	379,708,747 / 96.72%
Mapped reads, first in pair	193,874,601 / 49.38%
Mapped reads, second in pair	185,834,146 / 47.33%
Mapped reads, both in pair	370,736,568 / 94.43%
Mapped reads, singletons	8,972,179 / 2.29%
Secondary alignments	0
Supplementary alignments	6,441,337 / 1.64%
Read min/max/mean length	30 / 100 / 100.68
Duplicated reads (estimated)	61,908,043 / 15.77%
Duplication rate	11.31%
Clipped reads	49,102,834 / 12.51%

2.2. ACGT Content

Number/percentage of A's	10,867,428,938 / 29.22%
Number/percentage of C's	7,685,762,191 / 20.66%
Number/percentage of T's	10,804,561,837 / 29.05%
Number/percentage of G's	7,749,483,380 / 20.83%
Number/percentage of N's	88,832,703 / 0.24%

GC Percentage	41.5%

2.3. Coverage

Mean	12.0189
Standard Deviation	149.5041

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	85,806.05
Standard Deviation	2,817,499.57
P25/Median/P75	127 / 142 / 155

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	430,395,749
Insertions	3,761,225
Mapped reads with at least one insertion	0.96%
Deletions	4,421,602
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.63%

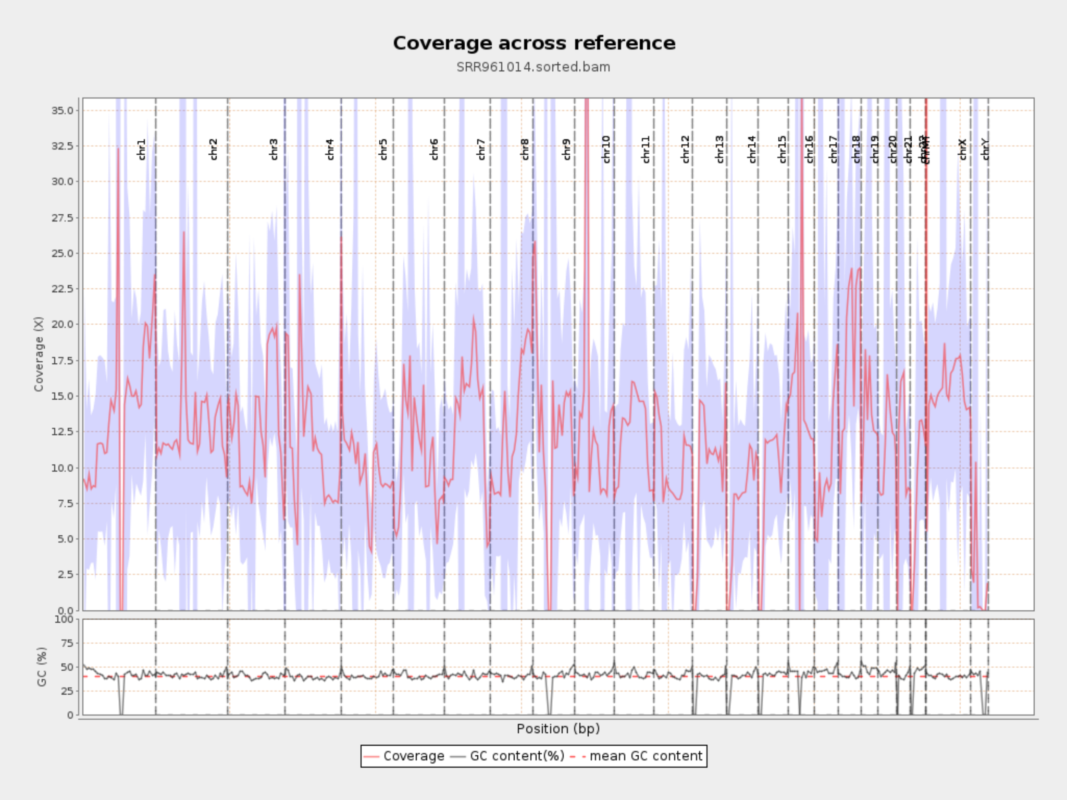
2.7. Chromosome stats

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

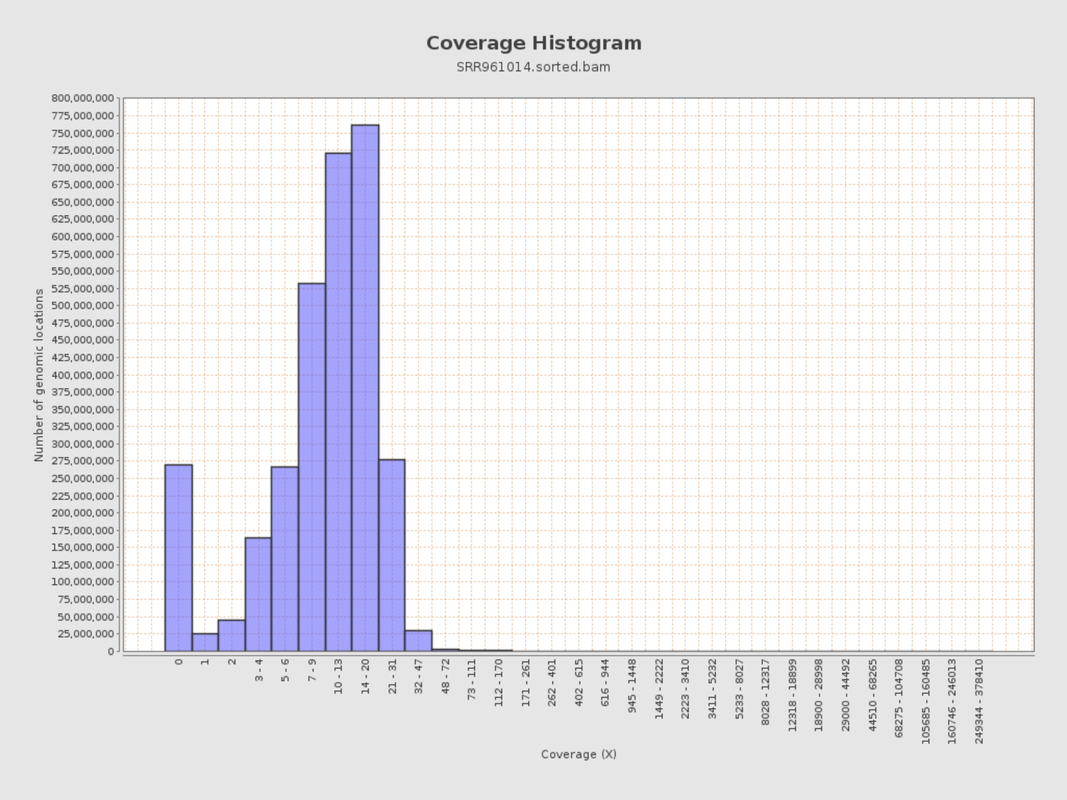
		bases	coverage	deviation
chr1	249250621	3440501137	13.8034	380.0876
chr2	243199373	3146377419	12.9374	88.9096
chr3	198022430	2521963938	12.7357	32.8636
chr4	191154276	2228525896	11.6583	101.9114
chr5	180915260	1789351058	9.8905	14.8165
chr6	171115067	1827909490	10.6823	46.1527
chr7	159138663	2100303053	13.1979	94.22
chr8	146364022	1914435937	13.08	132.4486
chr9	141213431	1770710791	12.5393	116.4355
chr10	135534747	1847045575	13.6278	330.2325
chr11	135006516	1686001789	12.4883	63.5979
chr12	133851895	1395235100	10.4237	12.6776
chr13	115169878	1139212384	9.8916	7.3459
chr14	107349540	818113643	7.621	12.0185
chr15	102531392	981662691	9.5743	7.4112
chr16	90354753	1383328641	15.31	155.1826
chr17	81195210	791878161	9.7528	37.7461
chr18	78077248	1416743603	18.1454	145.3556
chr19	59128983	819647202	13.862	185.4403
chr20	63025520	724408429	11.4939	36.744
chr21	48129895	521170395	10.8284	55.0772
chr22	51304566	426969900	8.3223	9.8053
chrMT	16571	8326759	502.4898	88.3187
chrX	155270560	2378479144	15.3183	48.8943

chrY	59373566	128560477	2.1653	114.8796

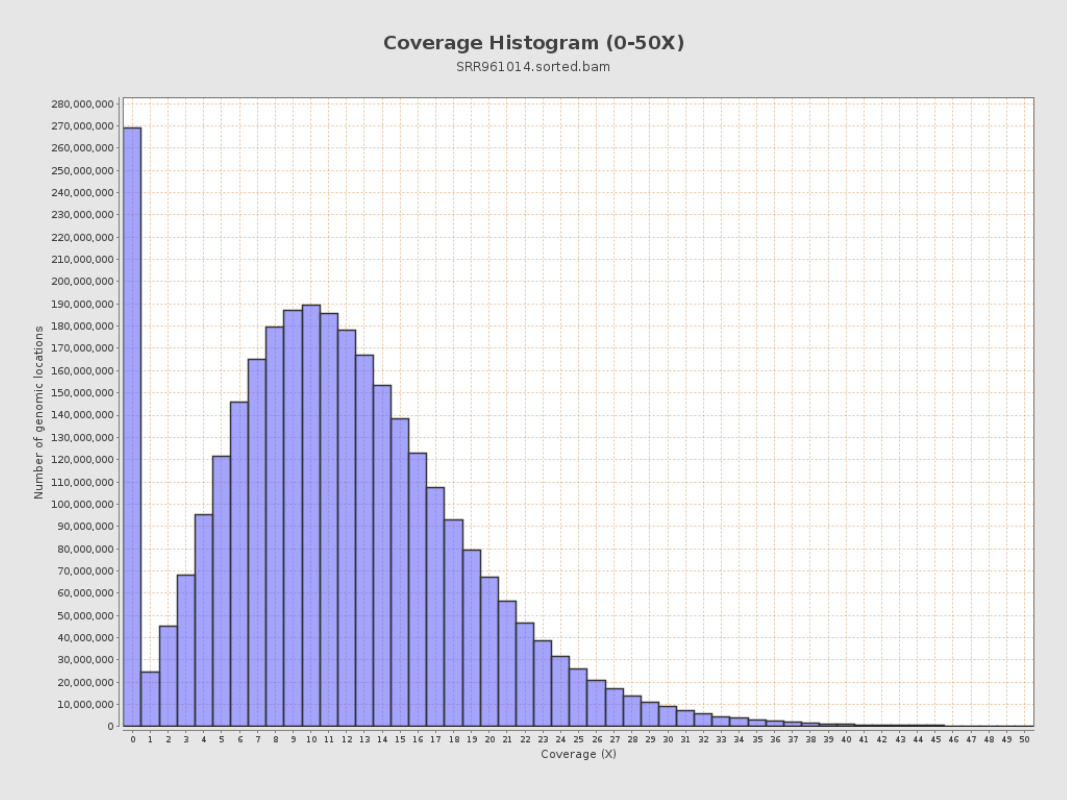
3. Results : Coverage across reference



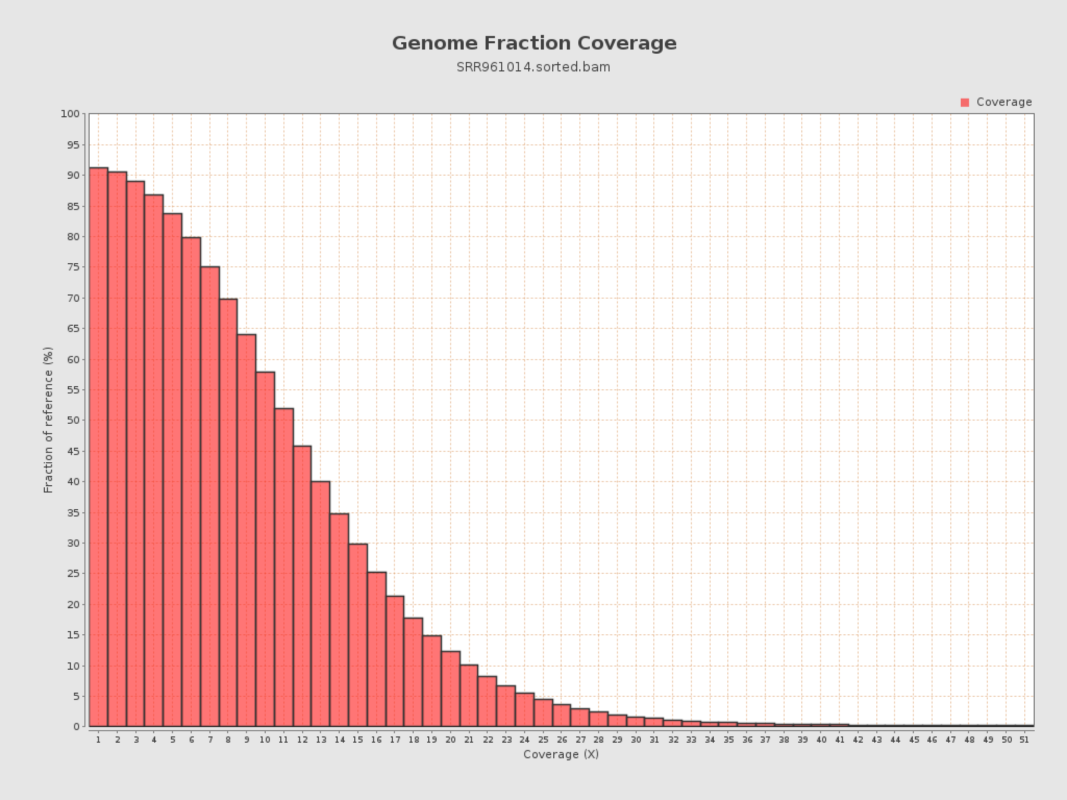
4. Results : Coverage Histogram



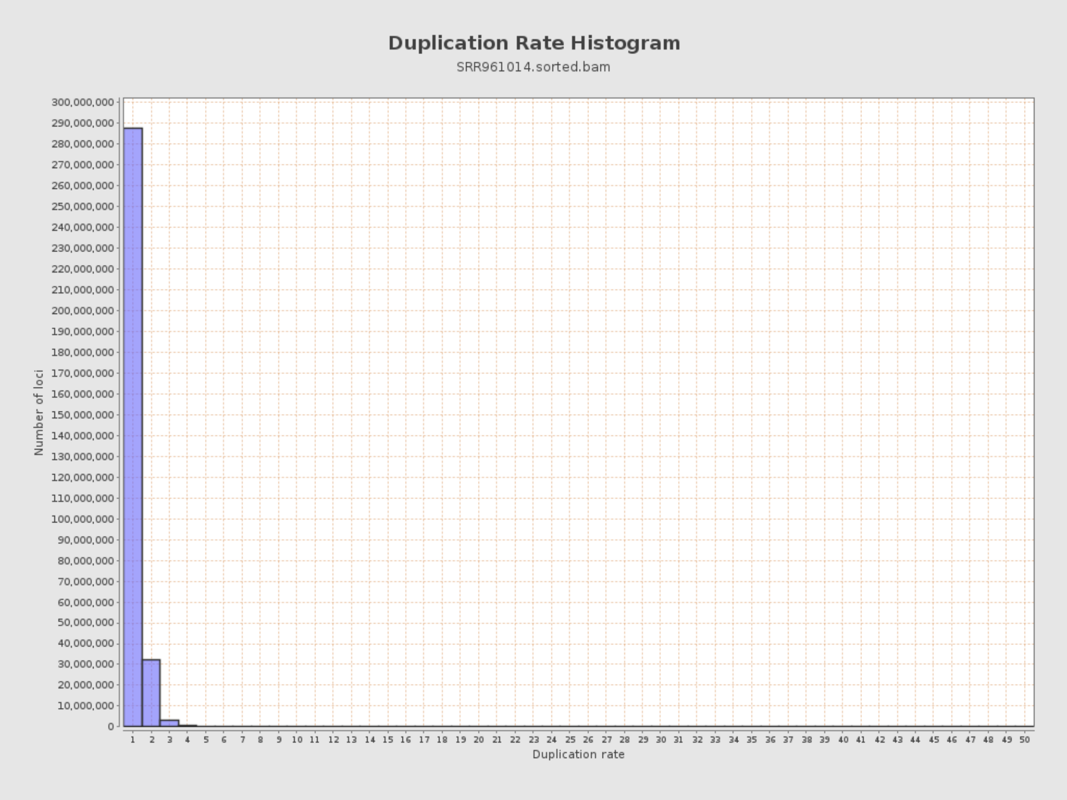
5. Results : Coverage Histogram (0-50X)



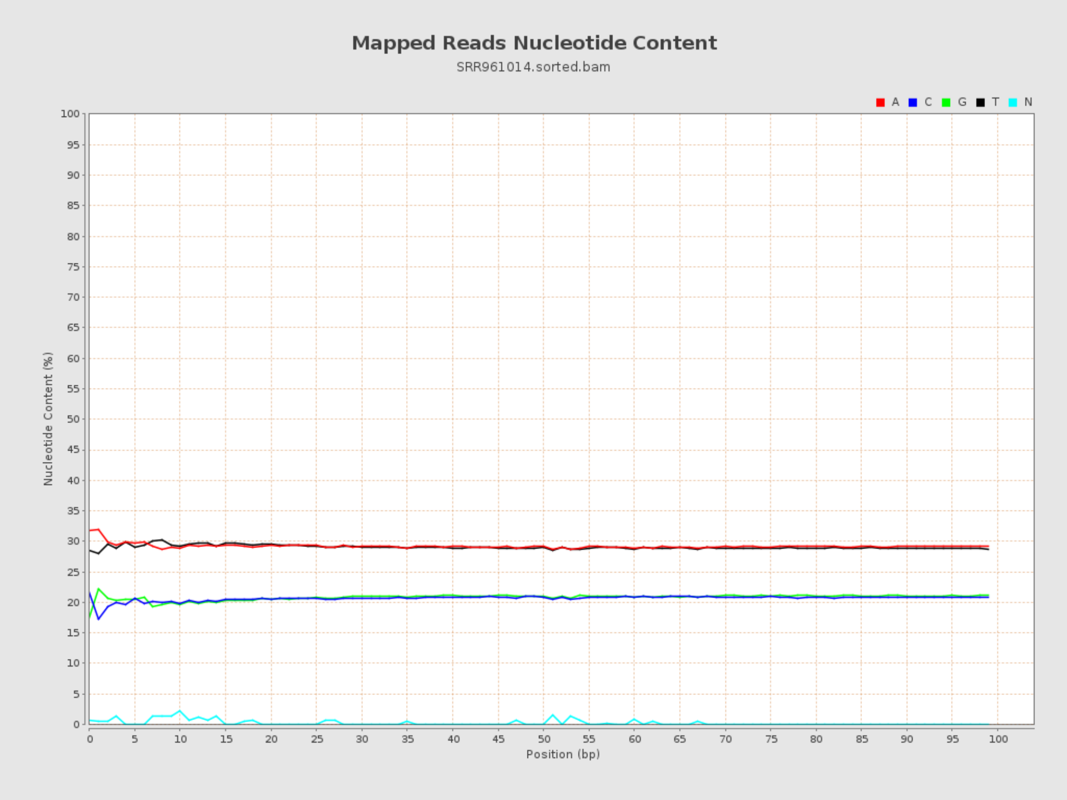
6. Results : Genome Fraction Coverage



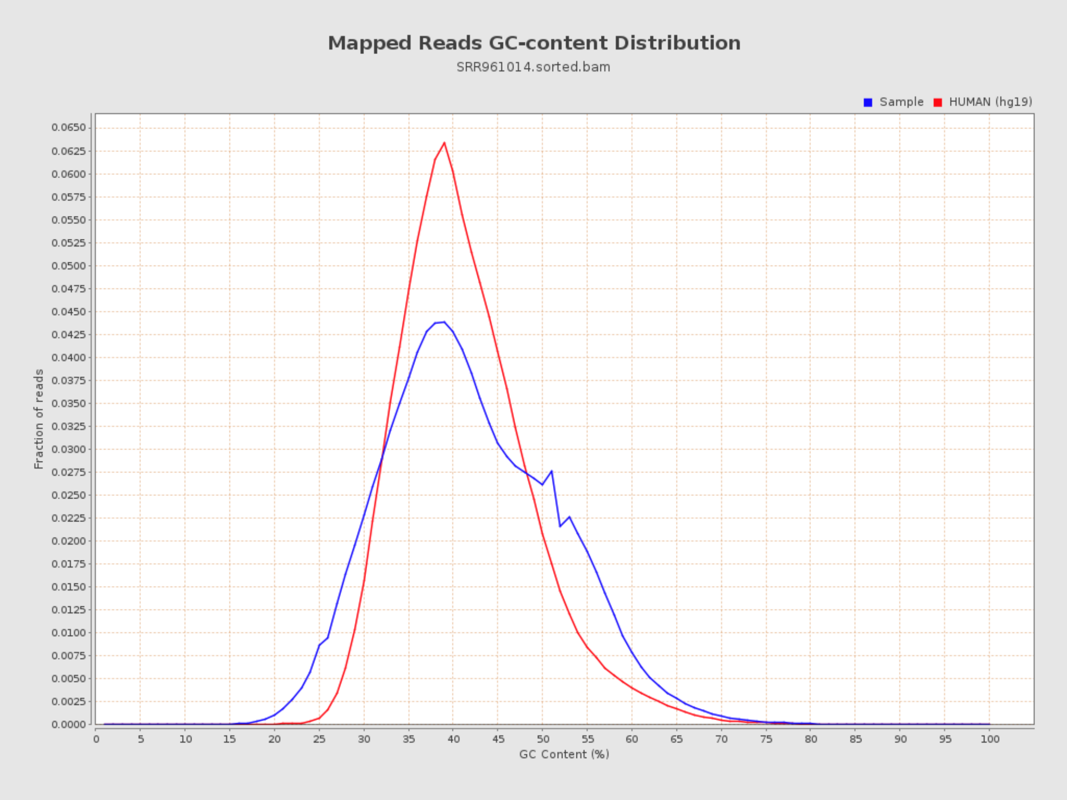
7. Results : Duplication Rate Histogram



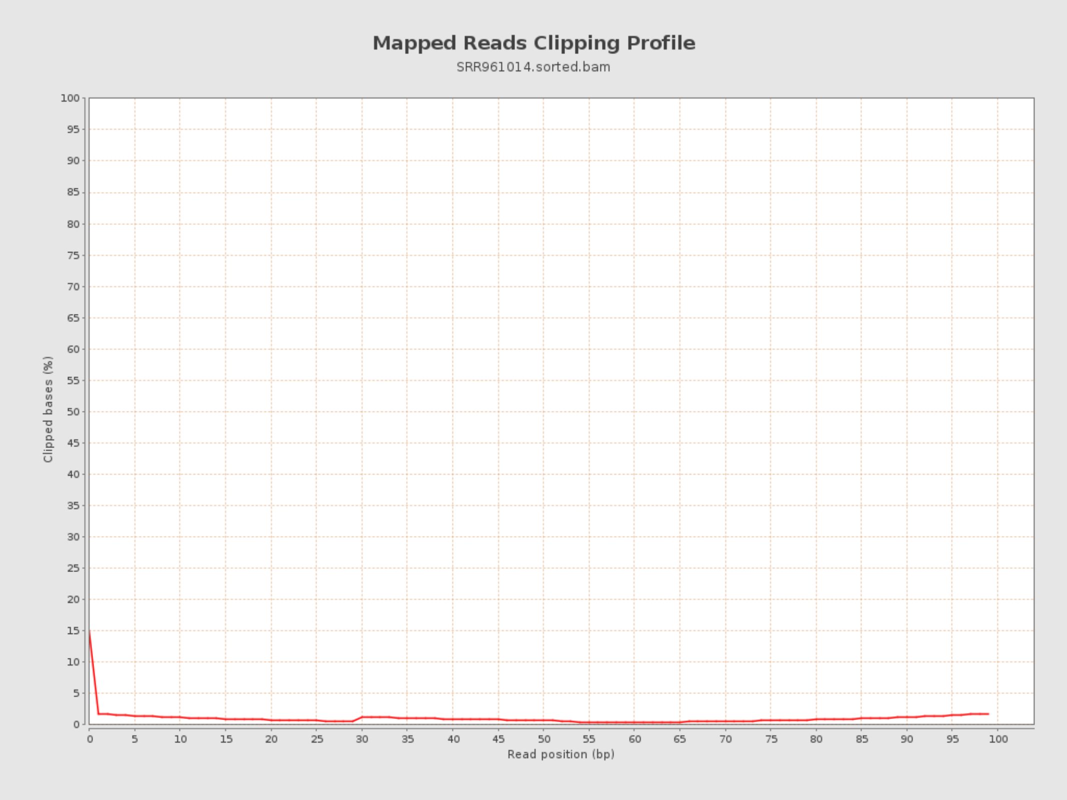
8. Results : Mapped Reads Nucleotide Content



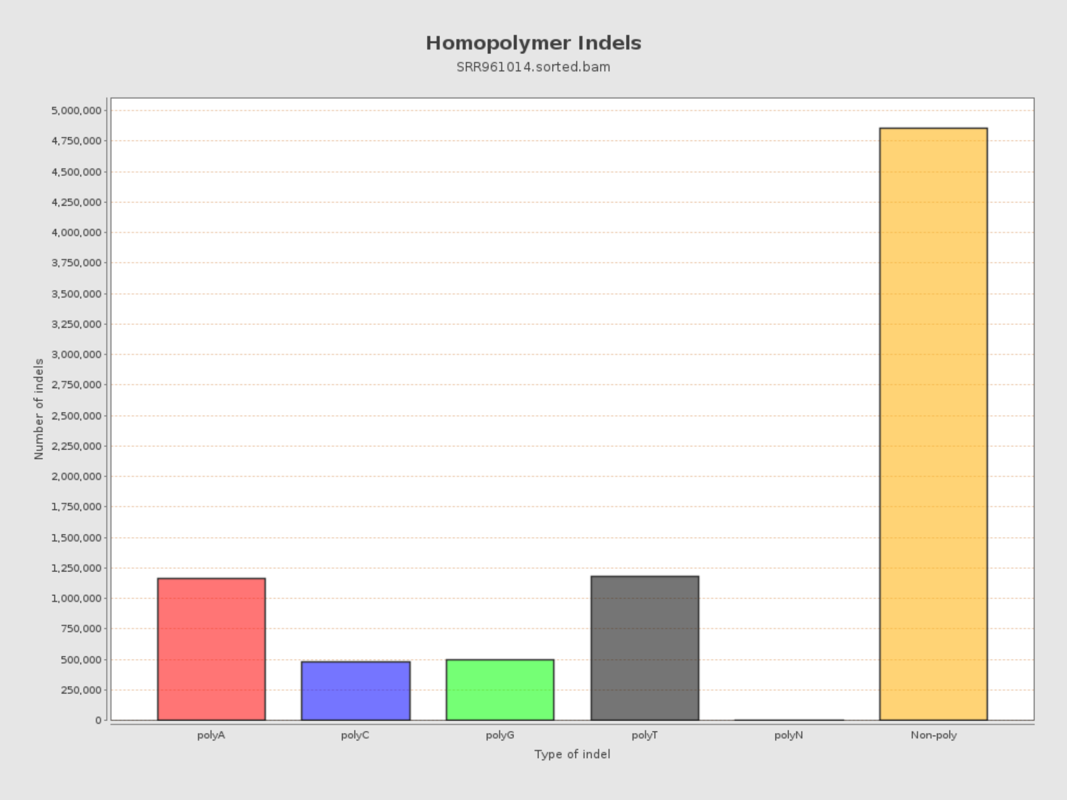
9. Results : Mapped Reads GC-content Distribution



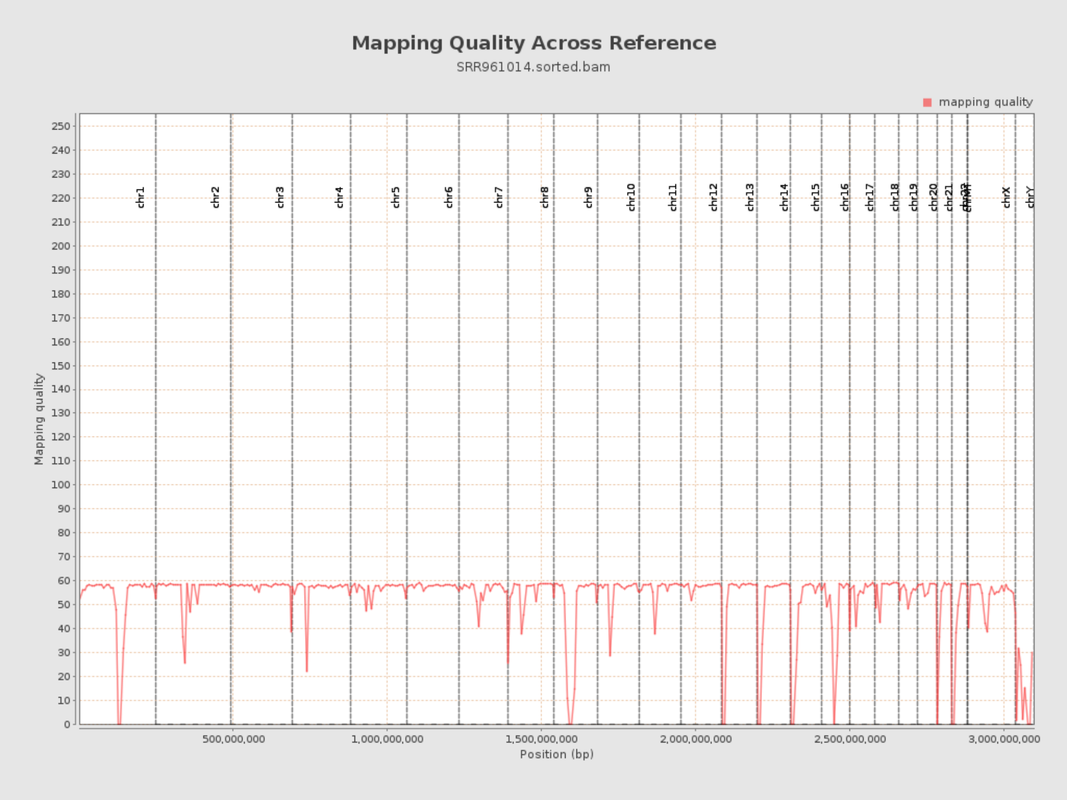
10. Results : Mapped Reads Clipping Profile



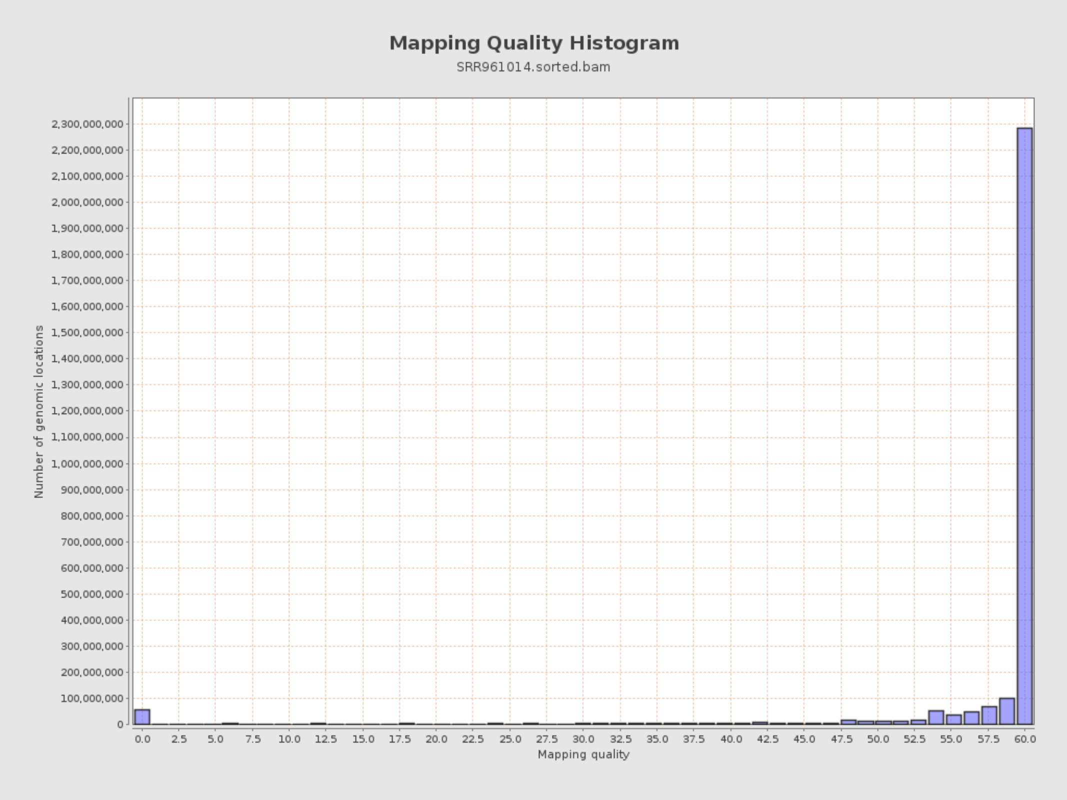
11. Results : Homopolymer Indels



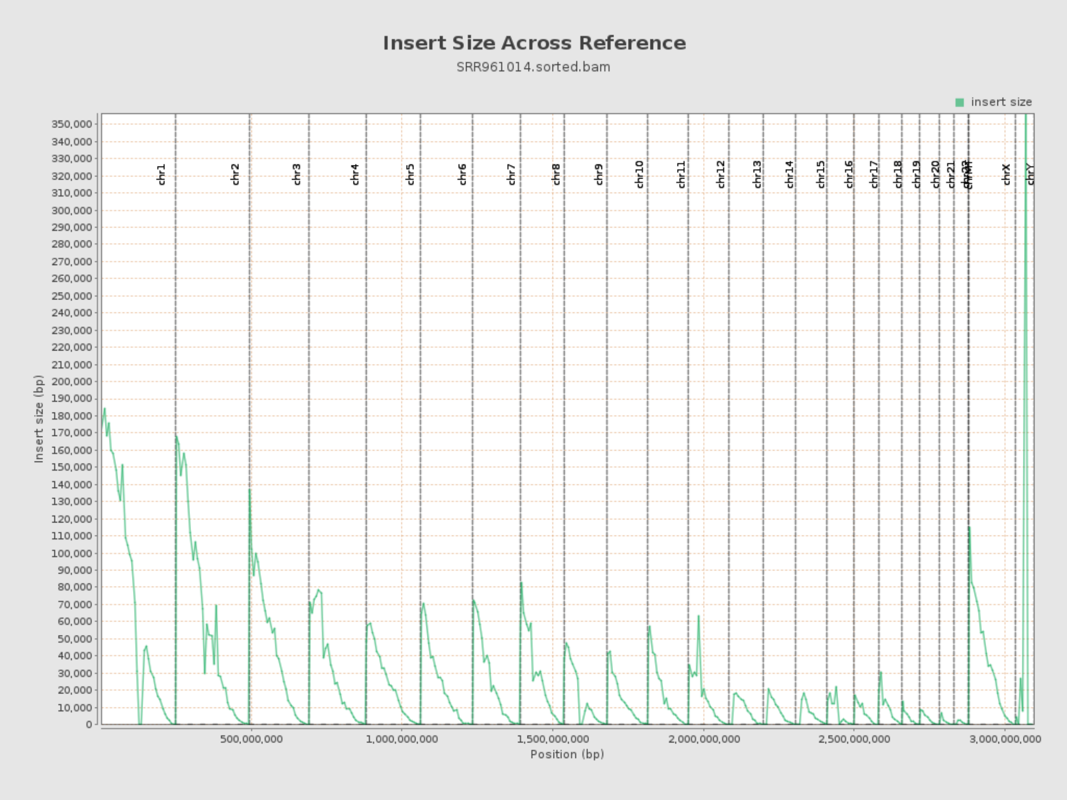
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram