Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/16 19:54:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961012.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_SRR961012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961012_1.fastq.gz SRR961012_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 16 19:54:08 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	388,735,092
Mapped reads	370,886,089 / 95.41%
Unmapped reads	17,849,003 / 4.59%
Mapped paired reads	370,886,089 / 95.41%
Mapped reads, first in pair	192,072,014 / 49.41%
Mapped reads, second in pair	178,814,075 / 46%
Mapped reads, both in pair	356,732,772 / 91.77%
Mapped reads, singletons	14,153,317 / 3.64%
Secondary alignments	0
Supplementary alignments	6,296,520 / 1.62%
Read min/max/mean length	30 / 100 / 100.67
Duplicated reads (estimated)	59,613,810 / 15.34%
Duplication rate	11.08%
Clipped reads	49,272,057 / 12.67%

2.2. ACGT Content

Number/percentage of A's	10,604,384,777 / 29.23%
Number/percentage of C's	7,505,668,615 / 20.69%
Number/percentage of T's	10,557,492,170 / 29.1%
Number/percentage of G's	7,567,246,159 / 20.86%
Number/percentage of N's	40,824,703 / 0.11%

GC Percentage	41.55%

2.3. Coverage

Mean	11.7215
Standard Deviation	145.2783

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	86,318.04
Standard Deviation	2,825,874.42
P25/Median/P75	127 / 142 / 155

2.6. Mismatches and indels

General error rate	1.13%
Mismatches	399,077,309
Insertions	3,735,803
Mapped reads with at least one insertion	0.97%
Deletions	4,373,621
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.55%

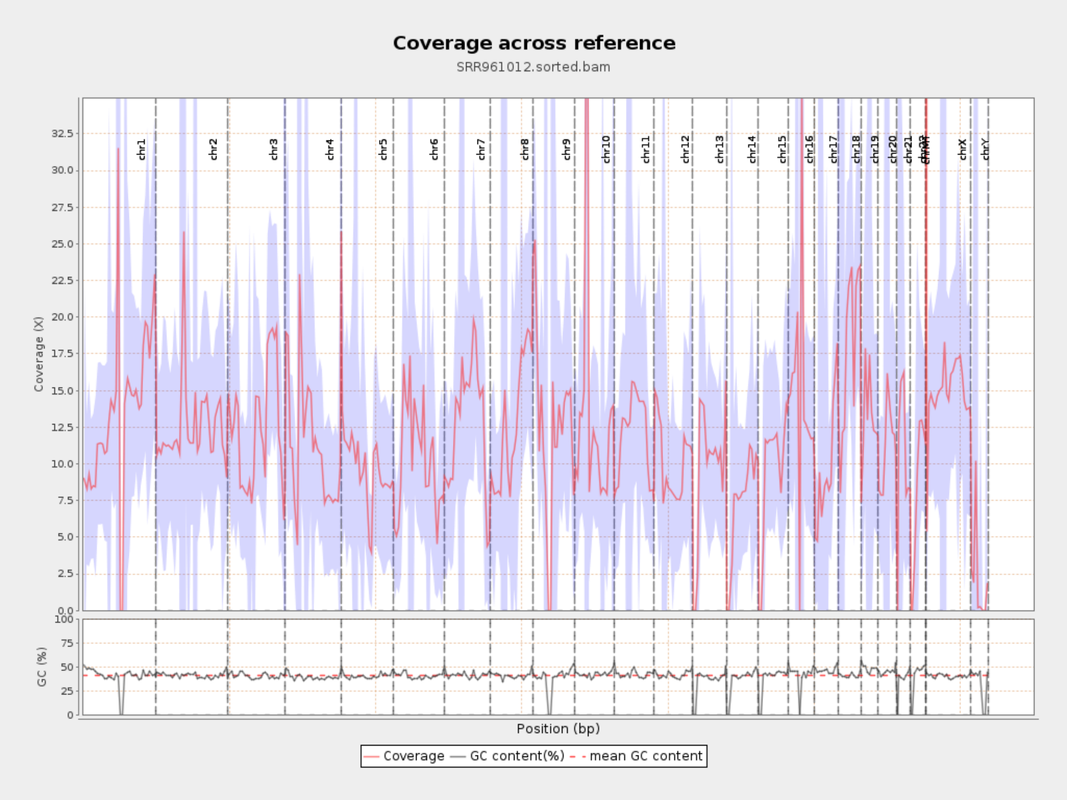
2.7. Chromosome stats

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

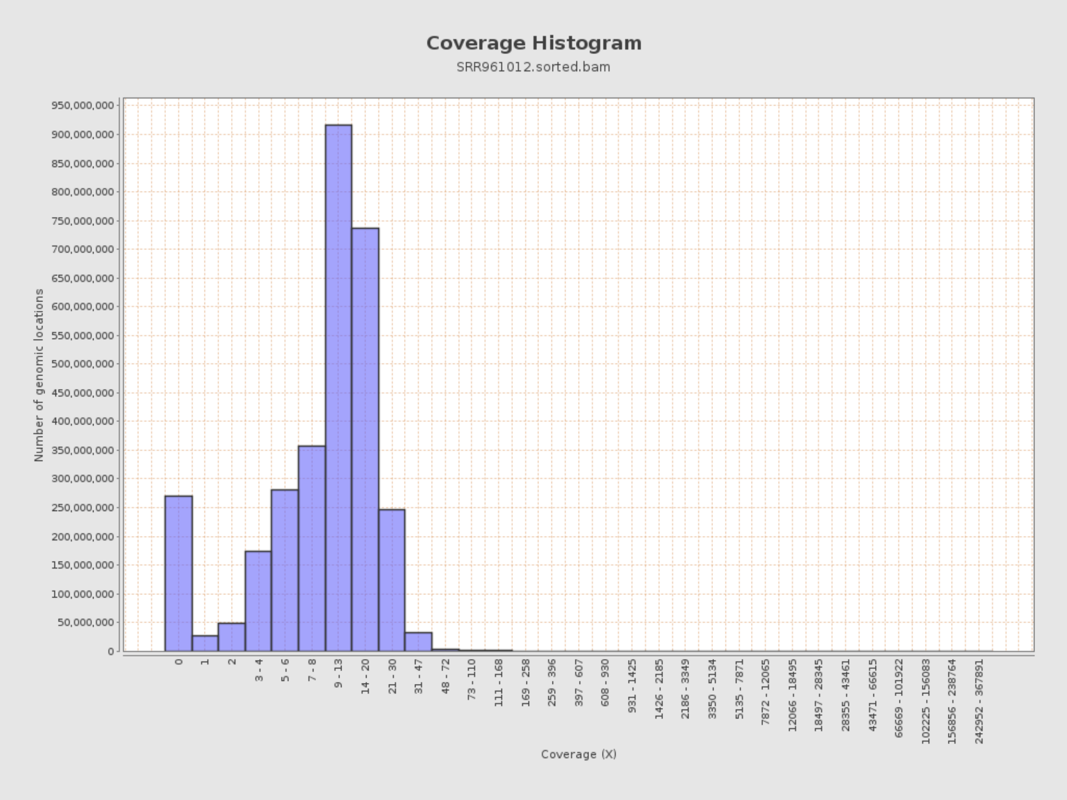
		bases	coverage	deviation
chr1	249250621	3355809748	13.4636	369.1041
chr2	243199373	3066789254	12.6102	86.4304
chr3	198022430	2457772961	12.4116	32.1618
chr4	191154276	2172985483	11.3677	98.7051
chr5	180915260	1744683438	9.6436	14.4771
chr6	171115067	1781745715	10.4126	45.0015
chr7	159138663	2048881235	12.8748	91.8382
chr8	146364022	1866121439	12.7499	128.3787
chr9	141213431	1727804704	12.2354	112.7152
chr10	135534747	1801454171	13.2915	321.1414
chr11	135006516	1644537687	12.1812	61.7255
chr12	133851895	1361473111	10.1715	12.2954
chr13	115169878	1110639016	9.6435	7.1575
chr14	107349540	797653654	7.4304	11.8316
chr15	102531392	957315836	9.3368	7.2165
chr16	90354753	1351048862	14.9527	150.998
chr17	81195210	772530544	9.5145	37.0441
chr18	78077248	1381446013	17.6933	141.7252
chr19	59128983	800858701	13.5443	180.5426
chr20	63025520	706375173	11.2078	35.7318
chr21	48129895	508908678	10.5737	53.9333
chr22	51304566	417265282	8.1331	9.5247
chrMT	16571	8163943	492.6645	88.5445
chrX	155270560	2318030265	14.929	47.592

chrY	59373566	125980230	2.1218	112.9564

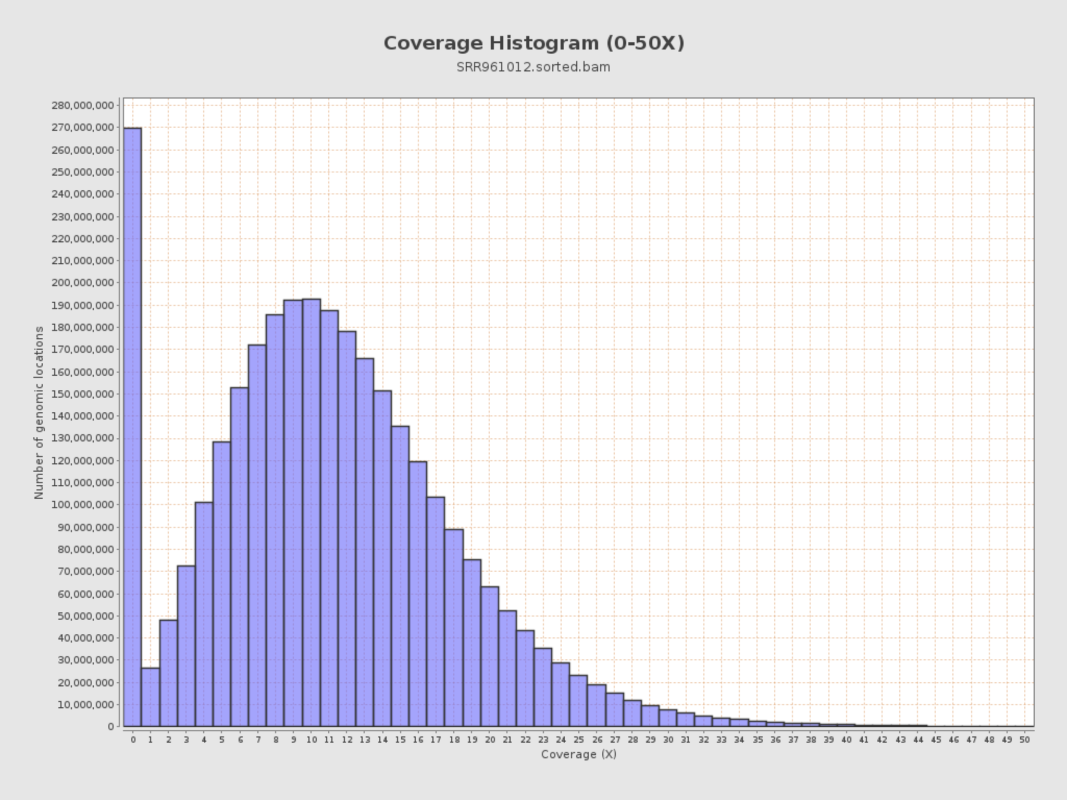
3. Results : Coverage across reference



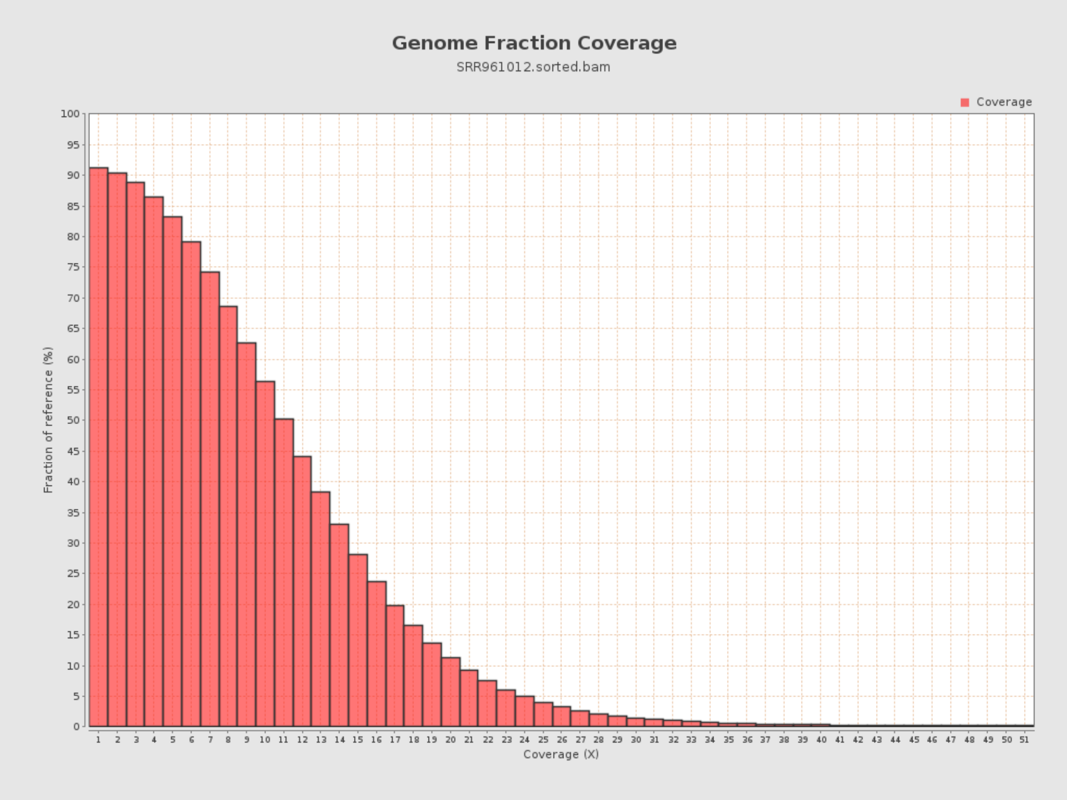
4. Results : Coverage Histogram



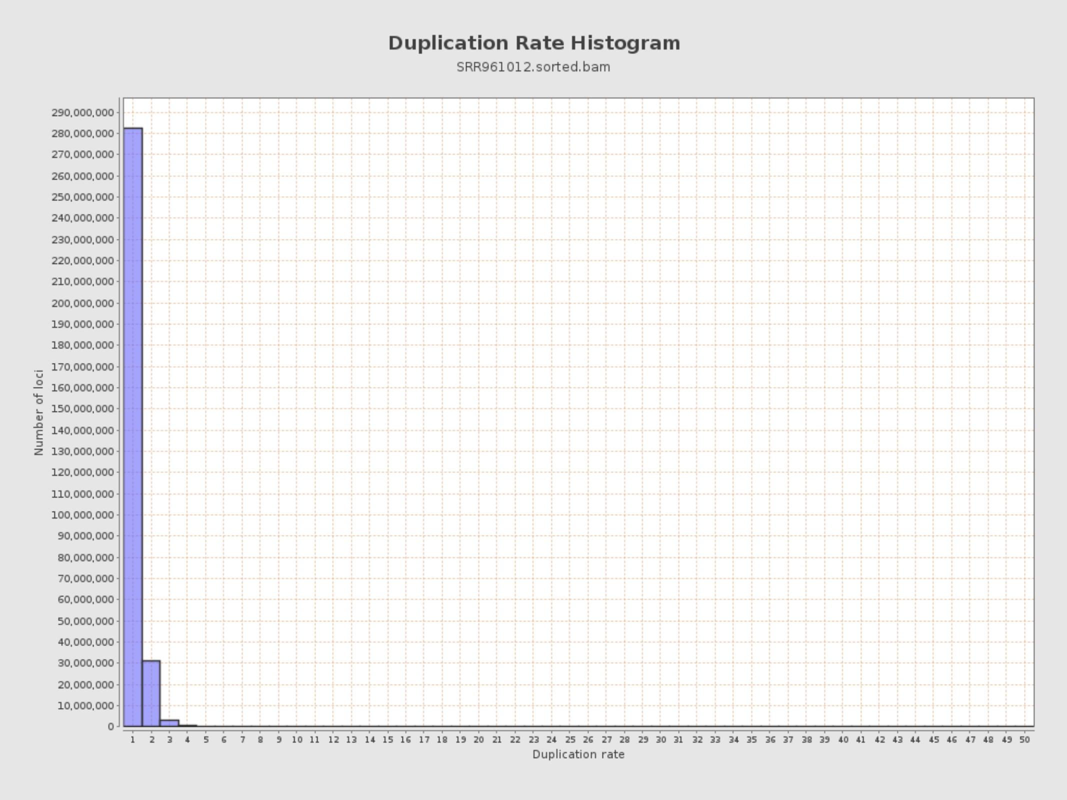
5. Results : Coverage Histogram (0-50X)



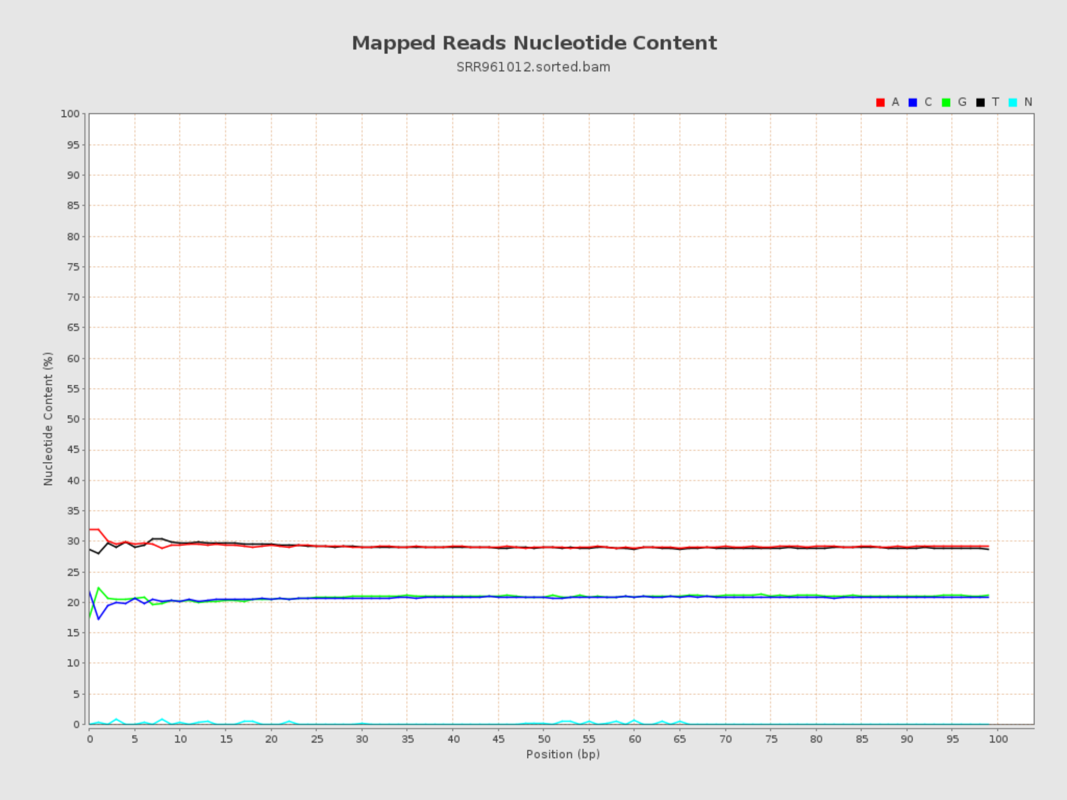
6. Results : Genome Fraction Coverage



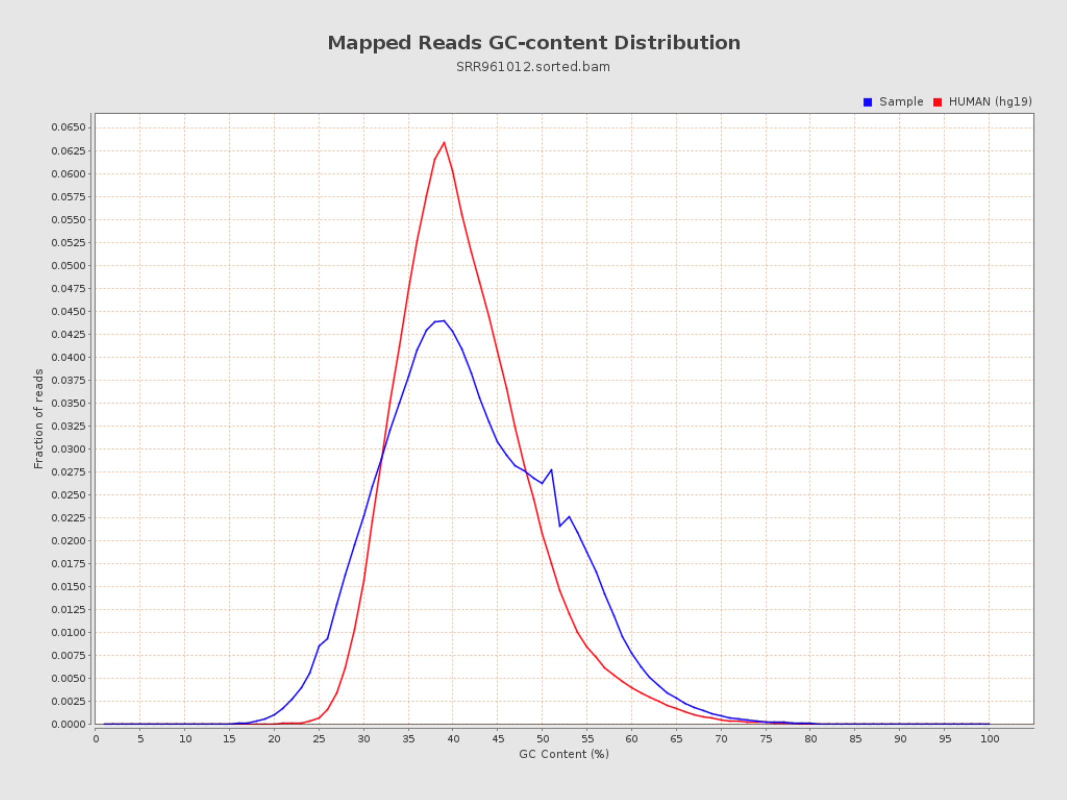
7. Results : Duplication Rate Histogram



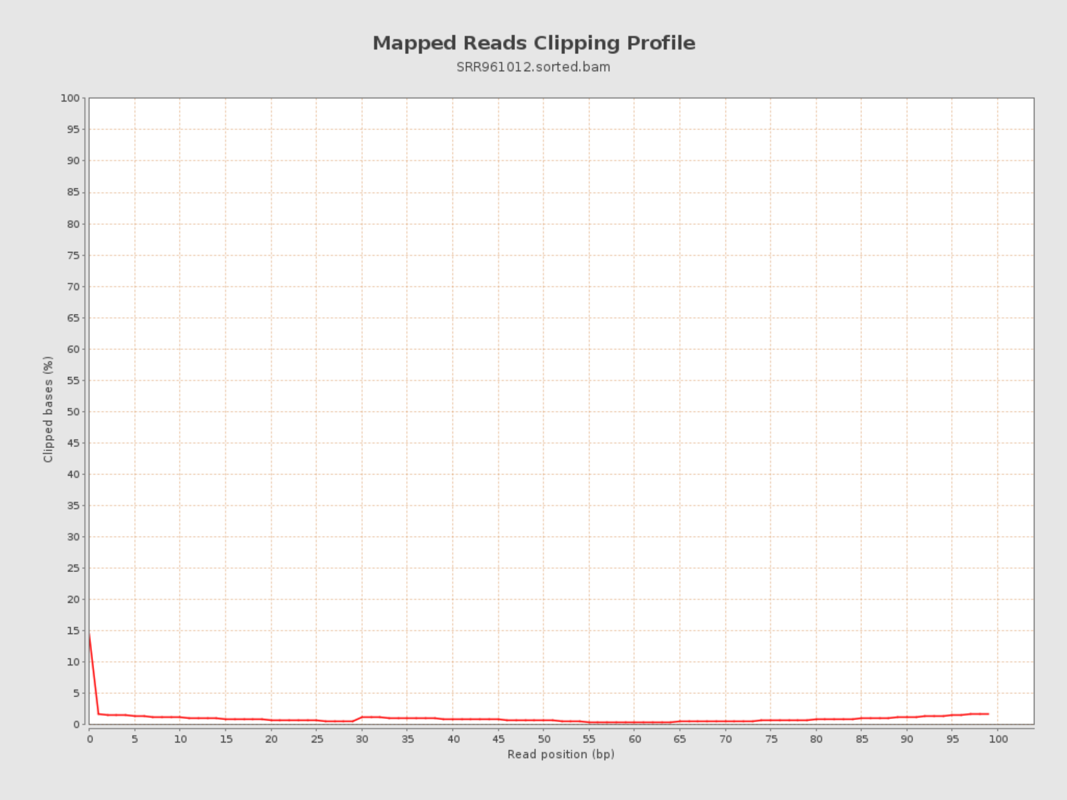
8. Results : Mapped Reads Nucleotide Content



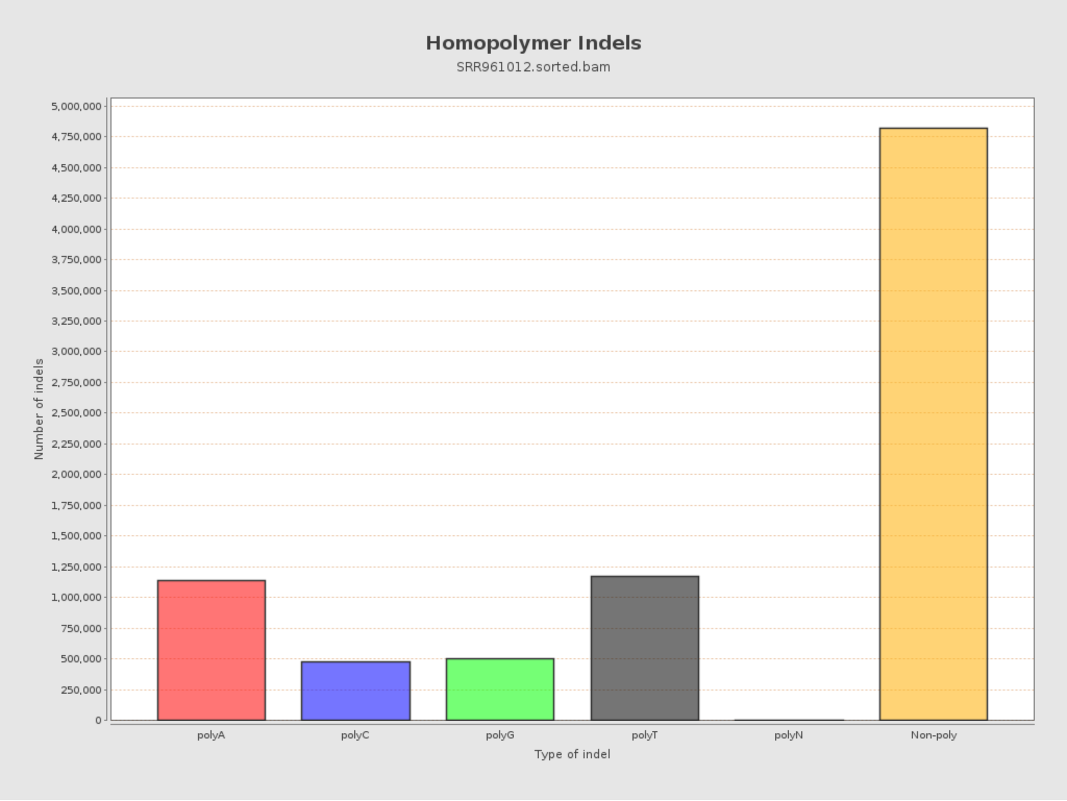
9. Results : Mapped Reads GC-content Distribution



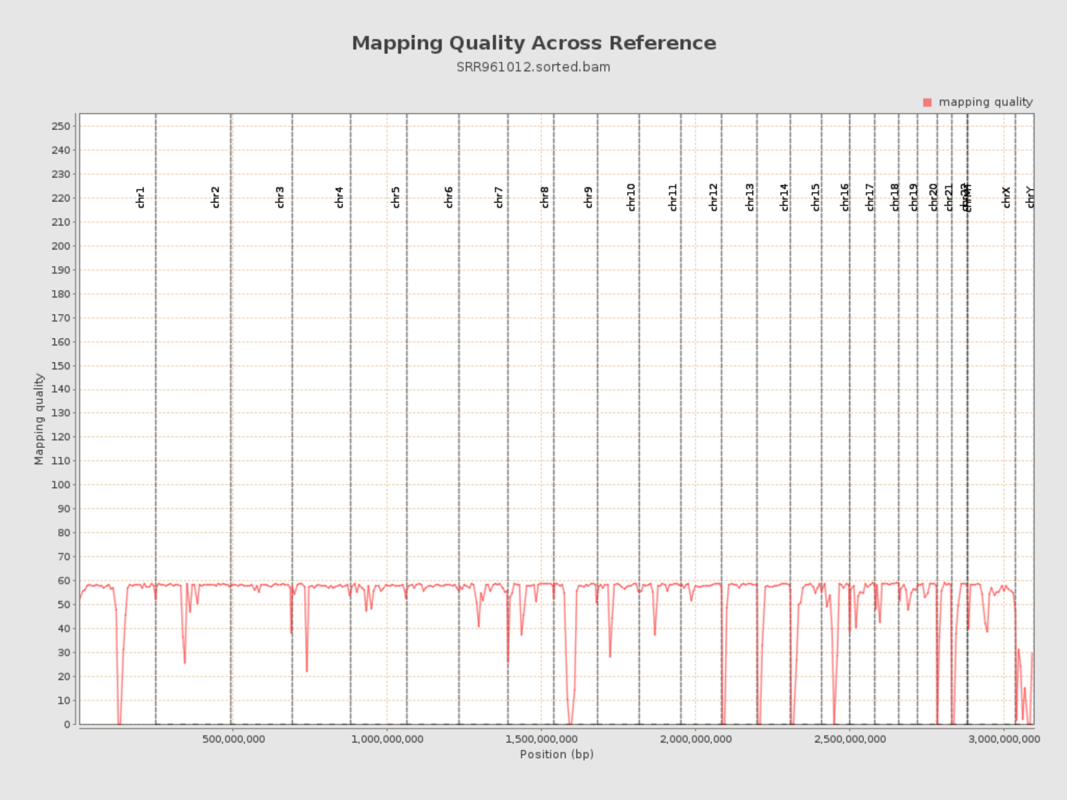
10. Results : Mapped Reads Clipping Profile



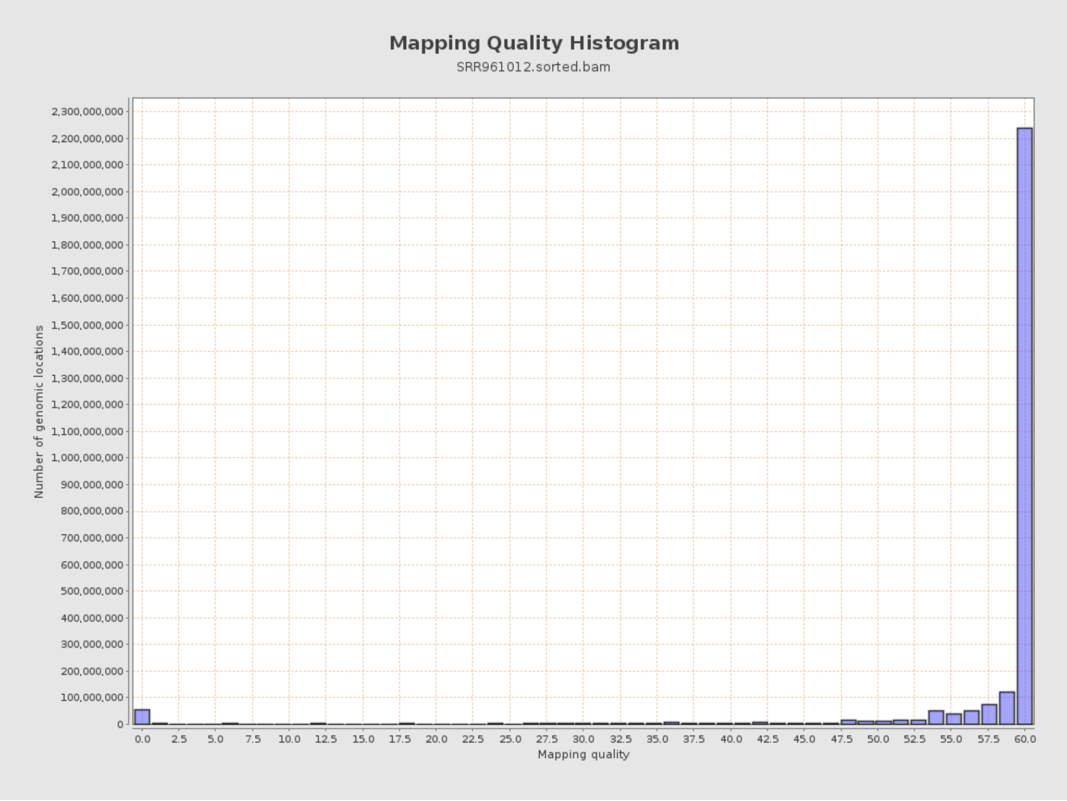
11. Results : Homopolymer Indels



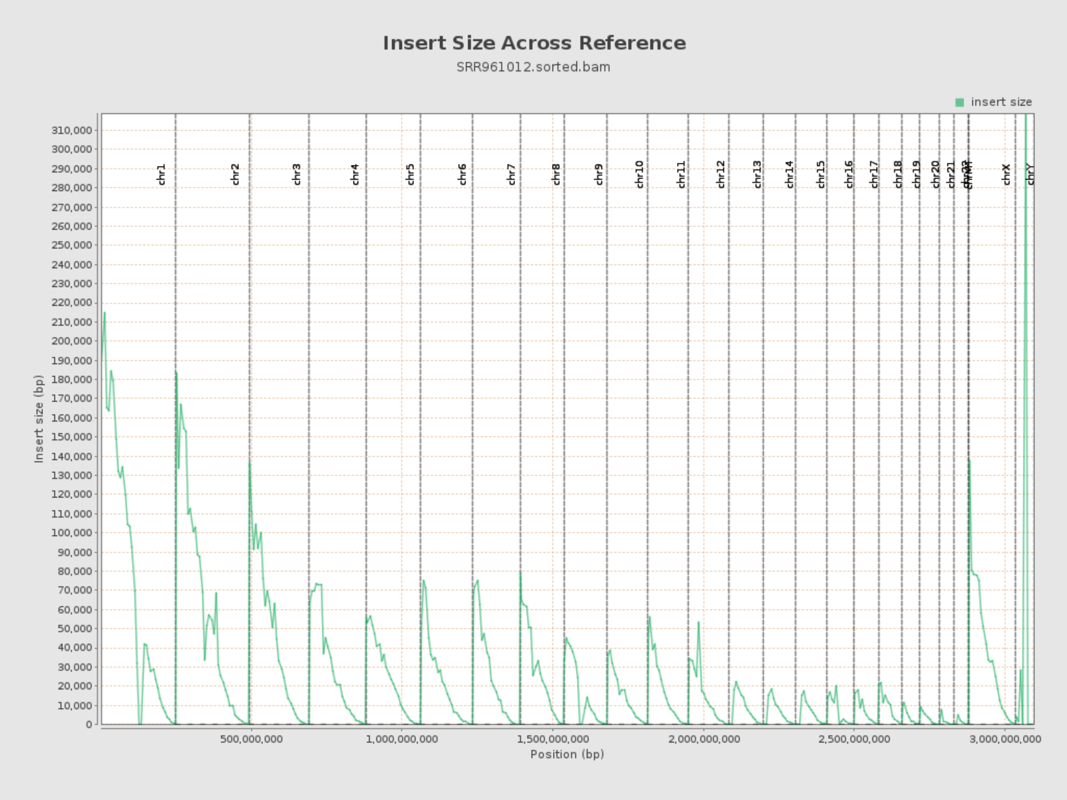
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram