Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/08 23:08:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961009.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_SRR961009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961009_1.fastq.gz SRR961009_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 08 23:08:39 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	385,985,368
Mapped reads	368,532,445 / 95.48%
Unmapped reads	17,452,923 / 4.52%
Mapped paired reads	368,532,445 / 95.48%
Mapped reads, first in pair	189,822,048 / 49.18%
Mapped reads, second in pair	178,710,397 / 46.3%
Mapped reads, both in pair	356,481,622 / 92.36%
Mapped reads, singletons	12,050,823 / 3.12%
Secondary alignments	0
Supplementary alignments	6,181,617 / 1.6%
Read min/max/mean length	30 / 100 / 100.67
Duplicated reads (estimated)	58,881,179 / 15.25%
Duplication rate	11.01%
Clipped reads	49,645,239 / 12.86%

2.2. ACGT Content

Number/percentage of A's	10,555,299,228 / 29.27%
Number/percentage of C's	7,463,576,382 / 20.7%
Number/percentage of T's	10,506,863,308 / 29.14%
Number/percentage of G's	7,522,721,785 / 20.86%
Number/percentage of N's	9,792,448 / 0.03%

GC Percentage	41.56%

2.3. Coverage

Mean	11.6513
Standard Deviation	144.0947

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	86,098.09
Standard Deviation	2,822,778.89
P25/Median/P75	127 / 142 / 155

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	406,623,002
Insertions	3,673,760
Mapped reads with at least one insertion	0.96%
Deletions	4,307,653
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.63%

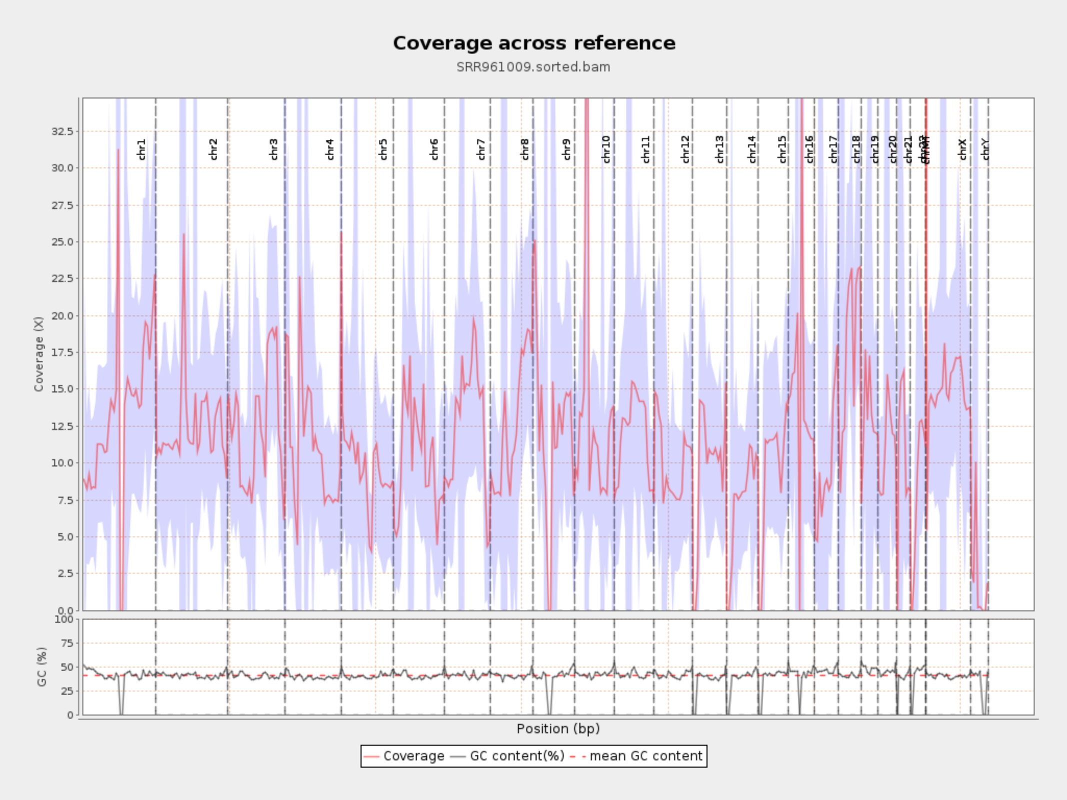
2.7. Chromosome stats

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

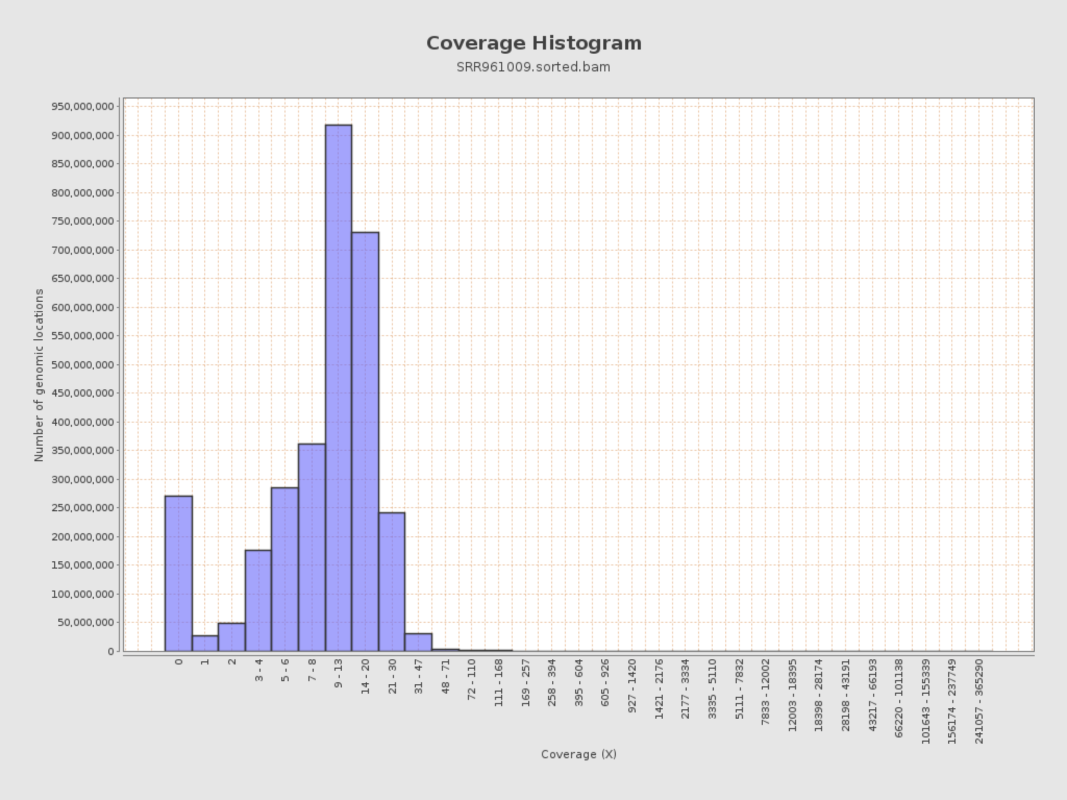
		bases	coverage	deviation
chr1	249250621	3334839614	13.3795	366.999
chr2	243199373	3049148022	12.5376	85.1611
chr3	198022430	2446081064	12.3525	31.913
chr4	191154276	2161385143	11.307	97.0524
chr5	180915260	1735938081	9.5953	14.2366
chr6	171115067	1773393229	10.3637	44.7861
chr7	159138663	2036492978	12.797	91.1514
chr8	146364022	1854923442	12.6734	127.5598
chr9	141213431	1715381800	12.1474	111.2331
chr10	135534747	1788787461	13.198	317.7594
chr11	135006516	1635063524	12.111	60.8386
chr12	133851895	1353015592	10.1083	12.1083
chr13	115169878	1105175273	9.596	7.0832
chr14	107349540	792826580	7.3855	11.806
chr15	102531392	951501601	9.2801	7.166
chr16	90354753	1340340199	14.8342	150.644
chr17	81195210	767401153	9.4513	36.7388
chr18	78077248	1374157440	17.6	139.5826
chr19	59128983	793573470	13.4211	179.0757
chr20	63025520	701201459	11.1257	34.8545
chr21	48129895	505887384	10.5109	53.2633
chr22	51304566	413850042	8.0665	9.4559
chrMT	16571	8061690	486.4939	83.906
chrX	155270560	2305949562	14.8512	46.8638

chrY	59373566	124364387	2.0946	110.135

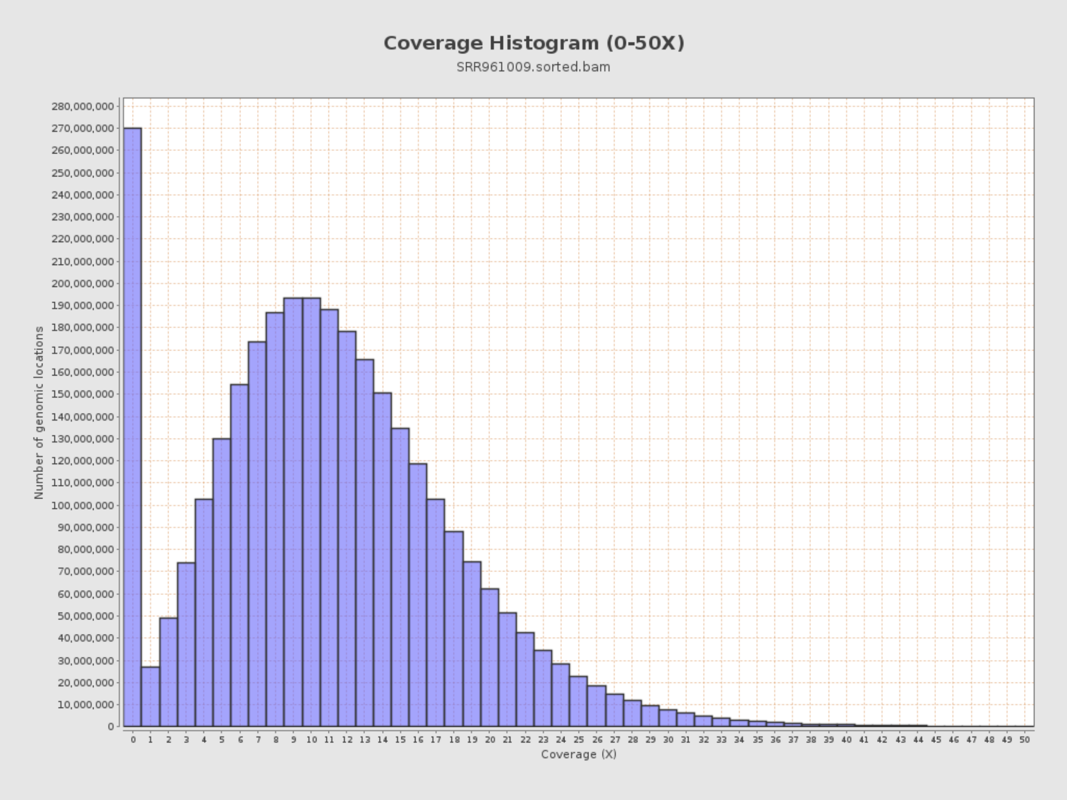
3. Results : Coverage across reference



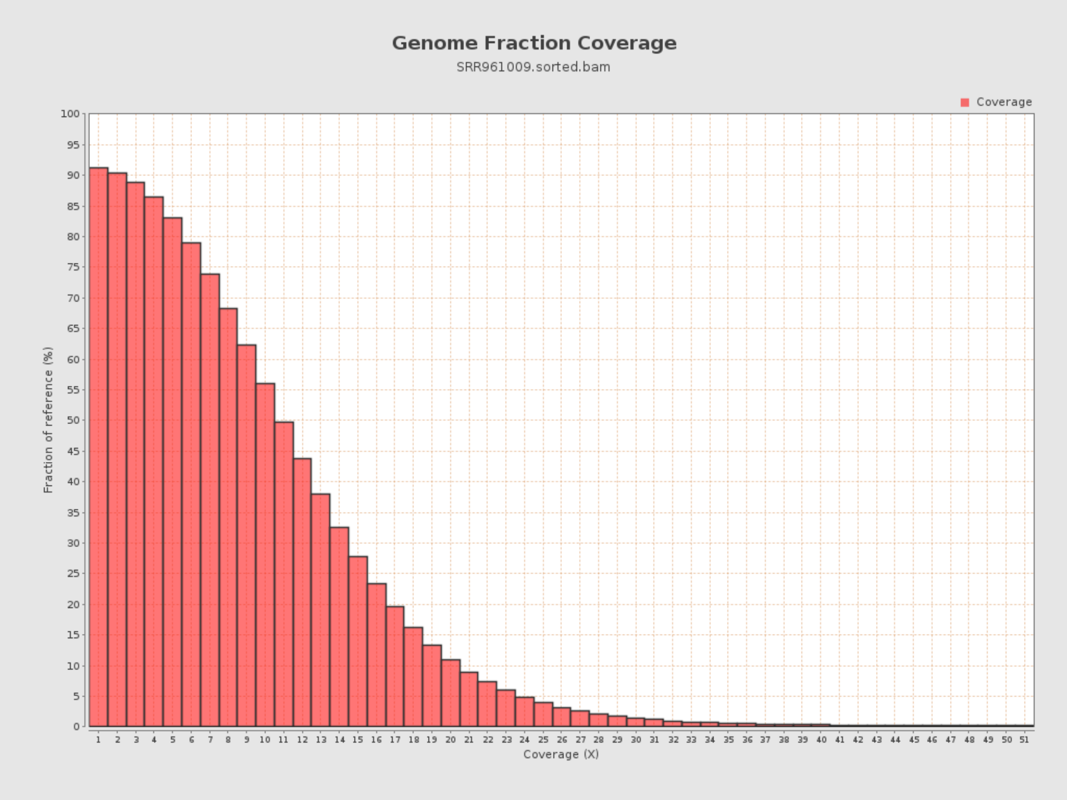
4. Results : Coverage Histogram



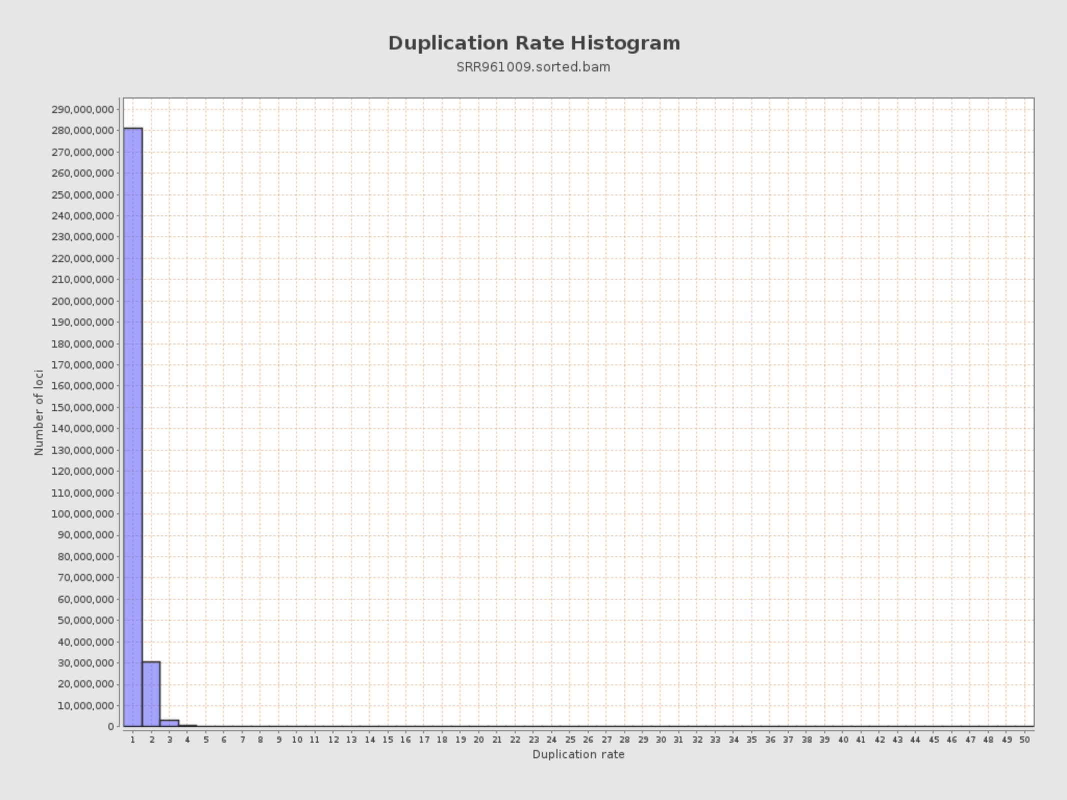
5. Results : Coverage Histogram (0-50X)



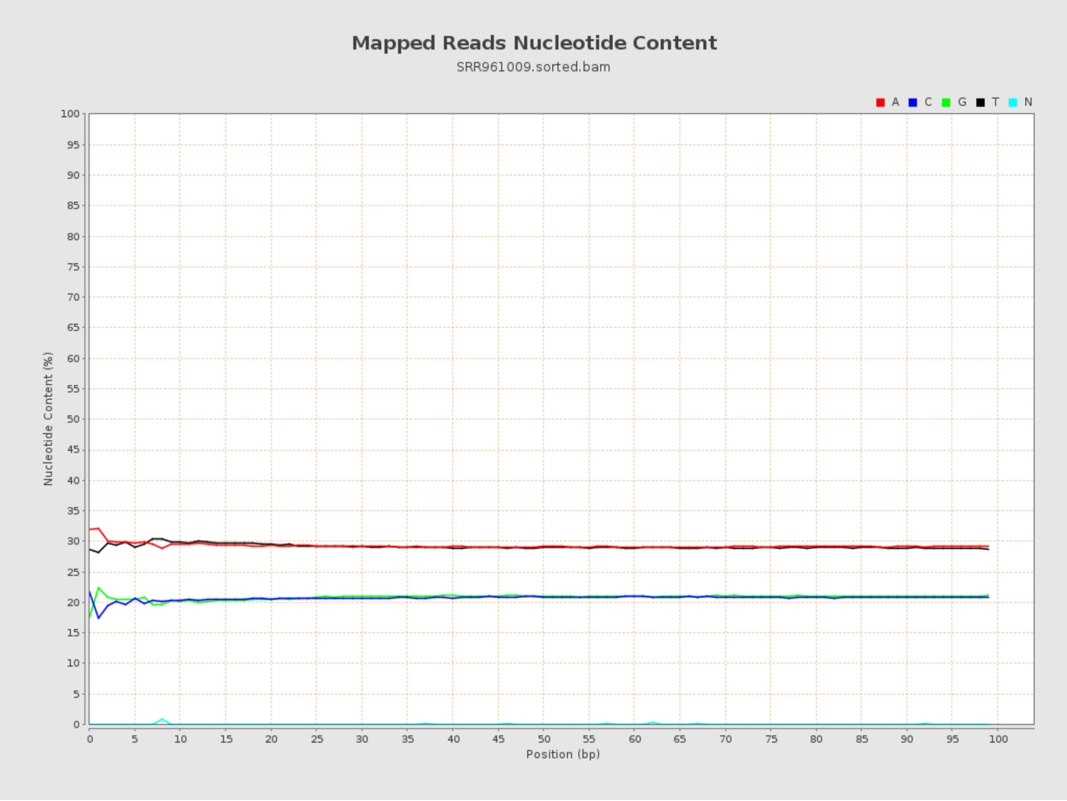
6. Results : Genome Fraction Coverage



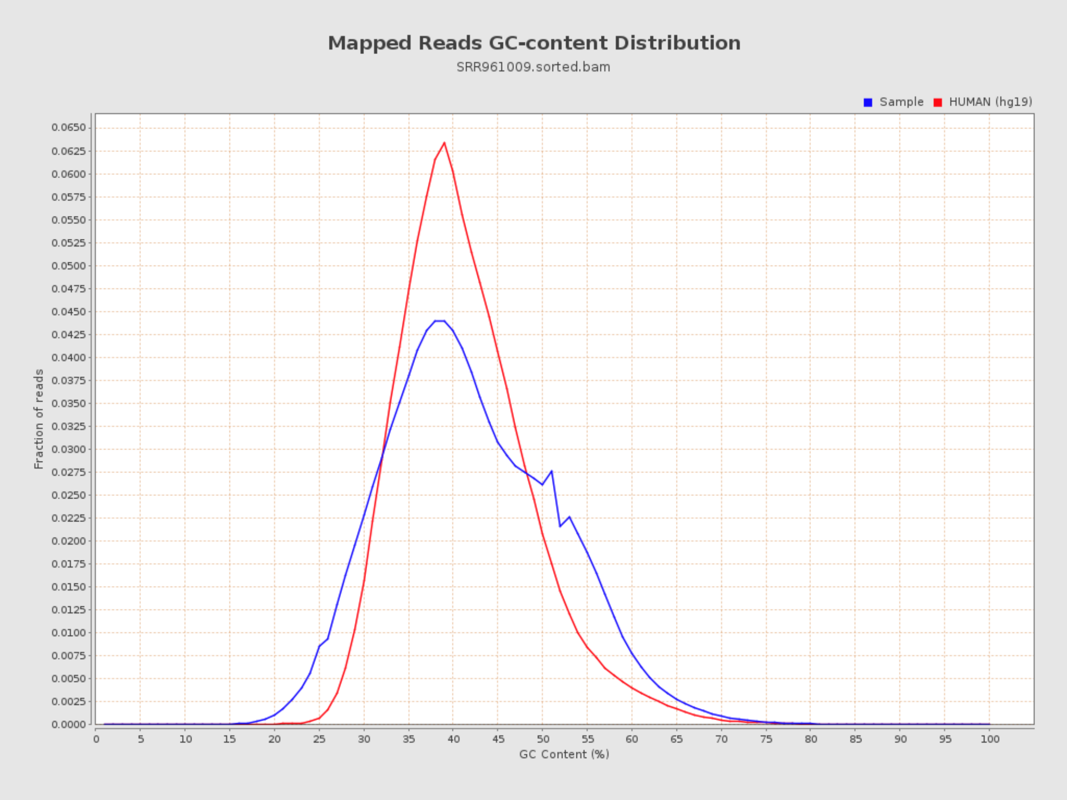
7. Results : Duplication Rate Histogram



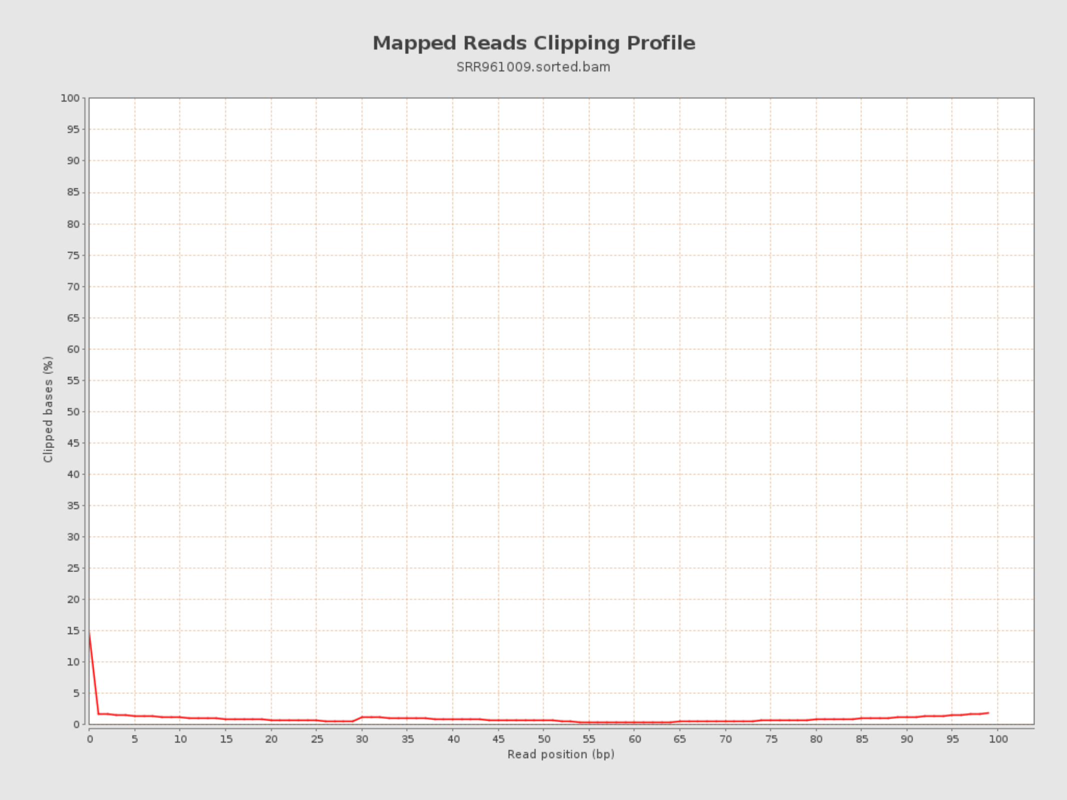
8. Results : Mapped Reads Nucleotide Content



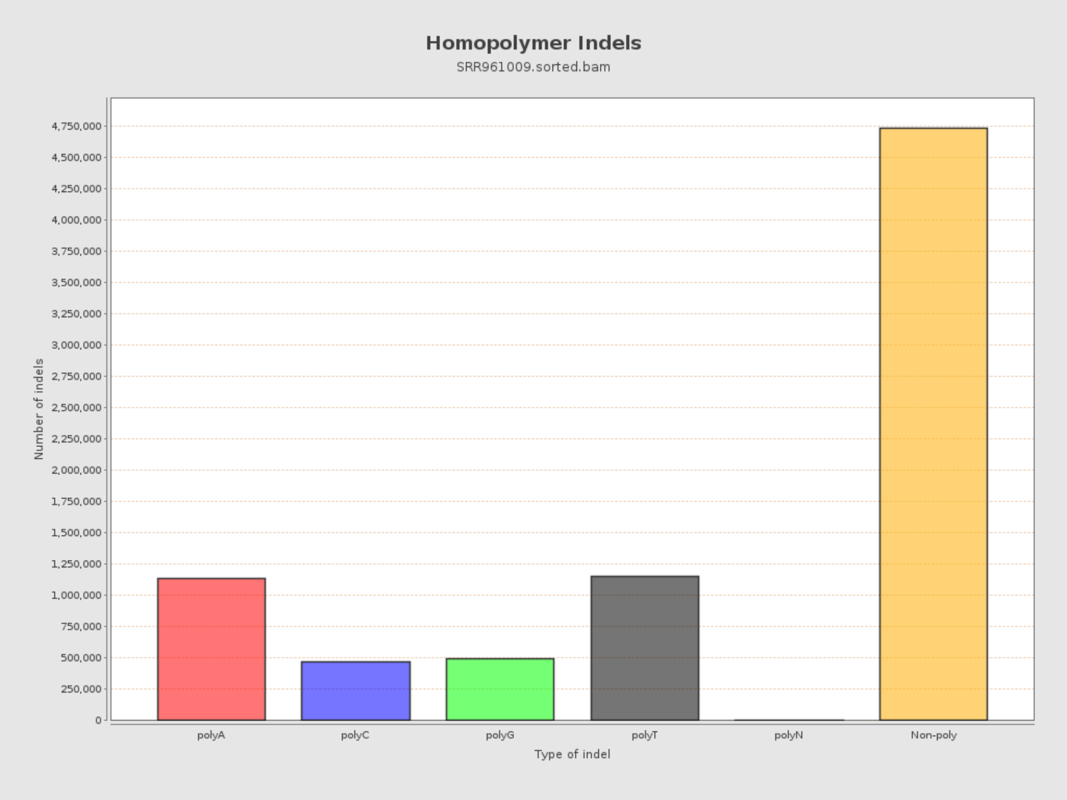
9. Results : Mapped Reads GC-content Distribution



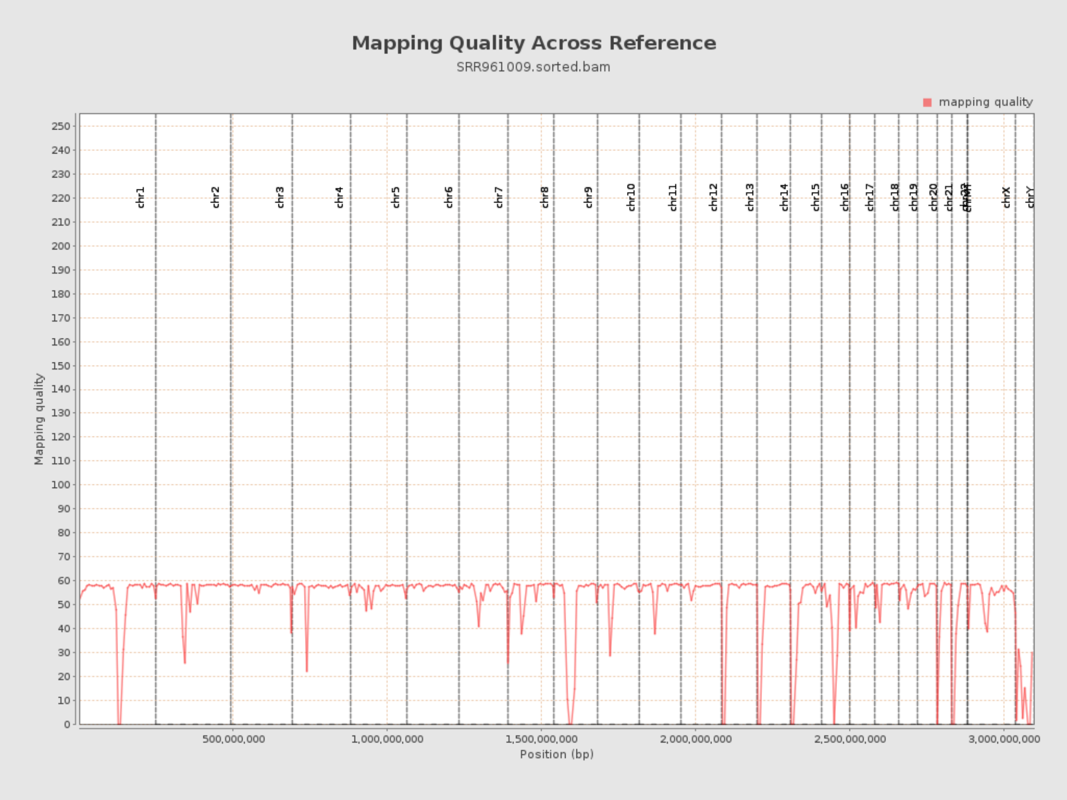
10. Results : Mapped Reads Clipping Profile



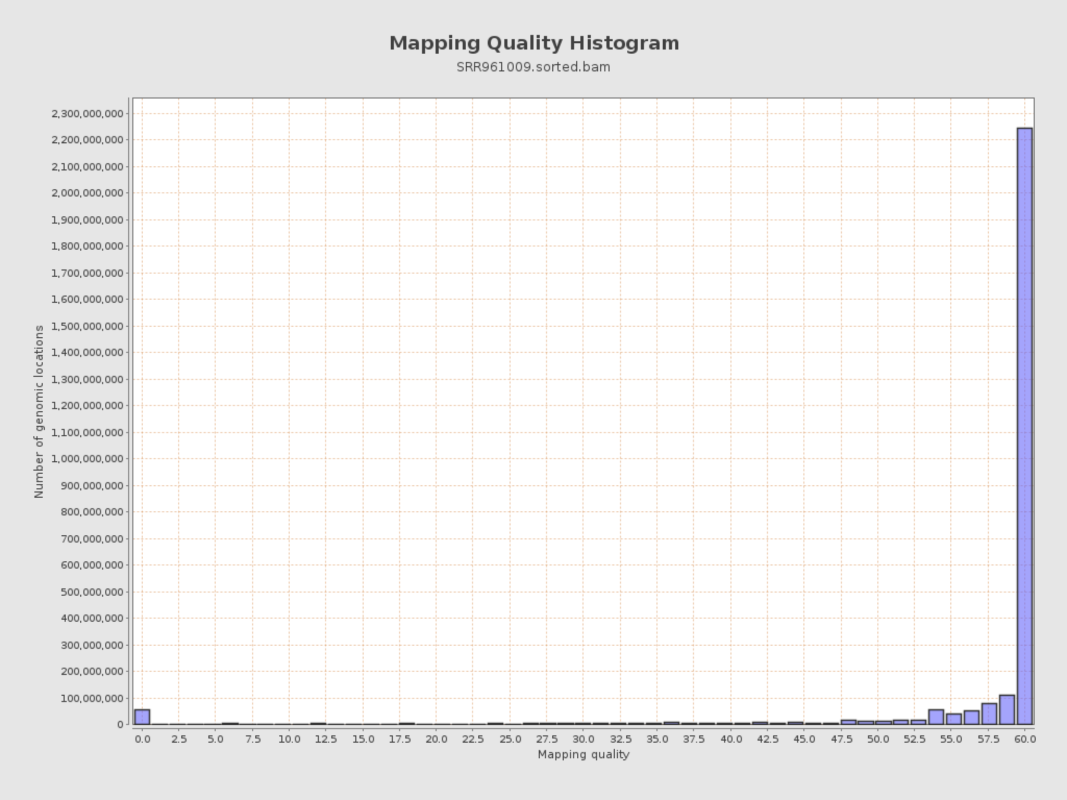
11. Results : Homopolymer Indels



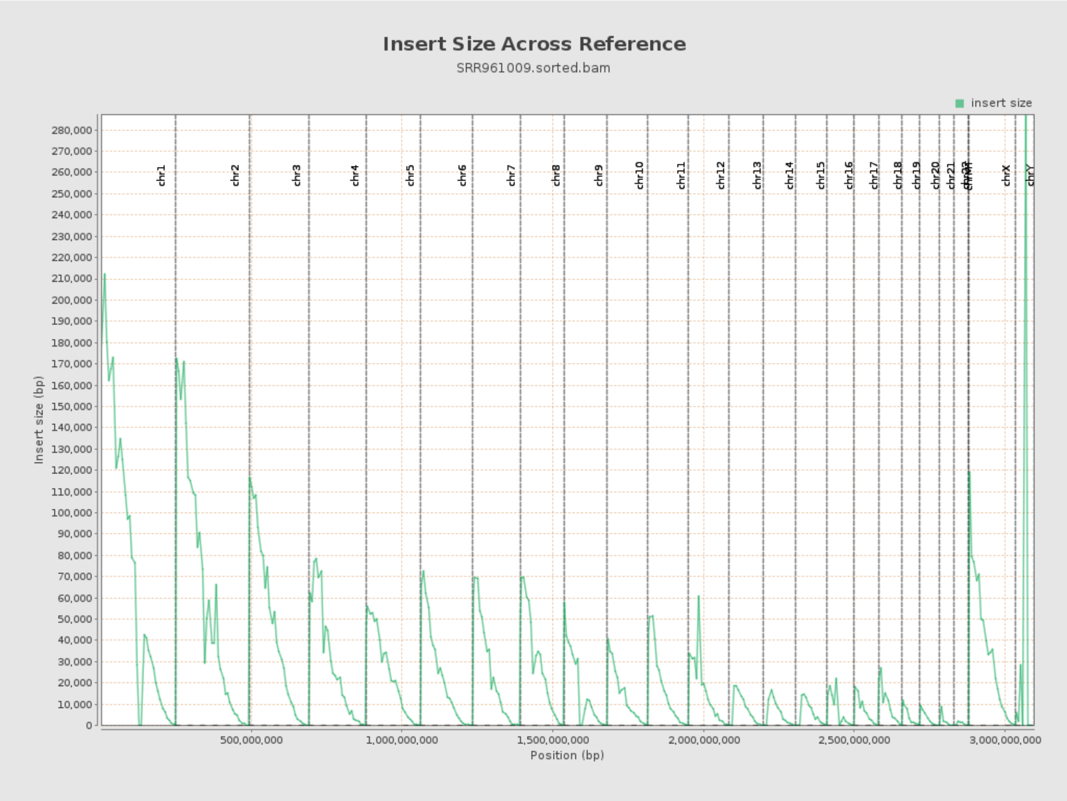
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram