Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 21:21:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960893.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_SRR960893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960893_1.fastq.gz SRR960893_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 21:21:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	223,815,558
Mapped reads	220,235,827 / 98.4%
Unmapped reads	3,579,731 / 1.6%
Mapped paired reads	220,235,827 / 98.4%
Mapped reads, first in pair	110,340,527 / 49.3%
Mapped reads, second in pair	109,895,300 / 49.1%
Mapped reads, both in pair	219,055,414 / 97.87%
Mapped reads, singletons	1,180,413 / 0.53%
Secondary alignments	0
Supplementary alignments	391,831 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	31,847,738 / 14.23%
Duplication rate	9.78%
Clipped reads	30,429,957 / 13.6%

2.2. ACGT Content

Number/percentage of A's	6,616,268,600 / 30.54%
Number/percentage of C's	4,220,641,142 / 19.48%
Number/percentage of T's	6,603,872,150 / 30.49%
Number/percentage of G's	4,220,217,939 / 19.48%
Number/percentage of N's	779,312 / 0%

GC Percentage	38.97%

2.3. Coverage

Mean	6.9994
Standard Deviation	94.875

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	15,557.19
Standard Deviation	1,176,638.52
P25/Median/P75	136 / 163 / 192

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	253,286,904
Insertions	2,586,551
Mapped reads with at least one insertion	1.14%
Deletions	2,722,929
Mapped reads with at least one deletion	1.2%
Homopolymer indels	40.78%

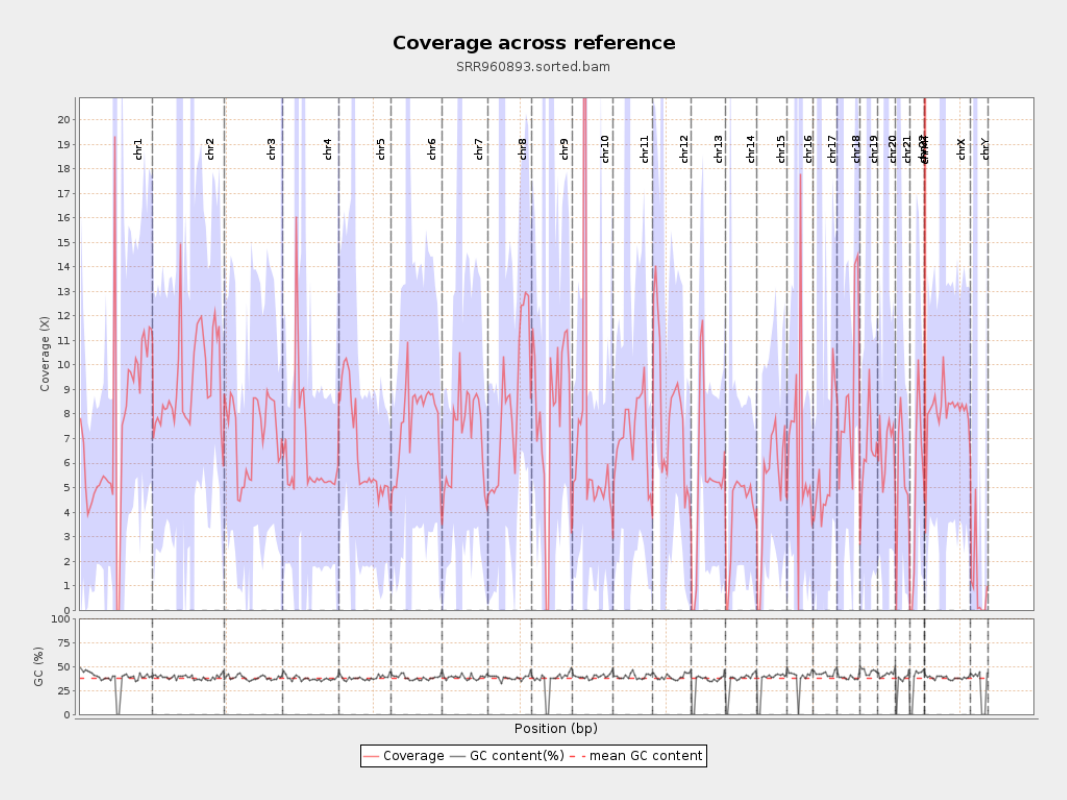
2.7. Chromosome stats

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

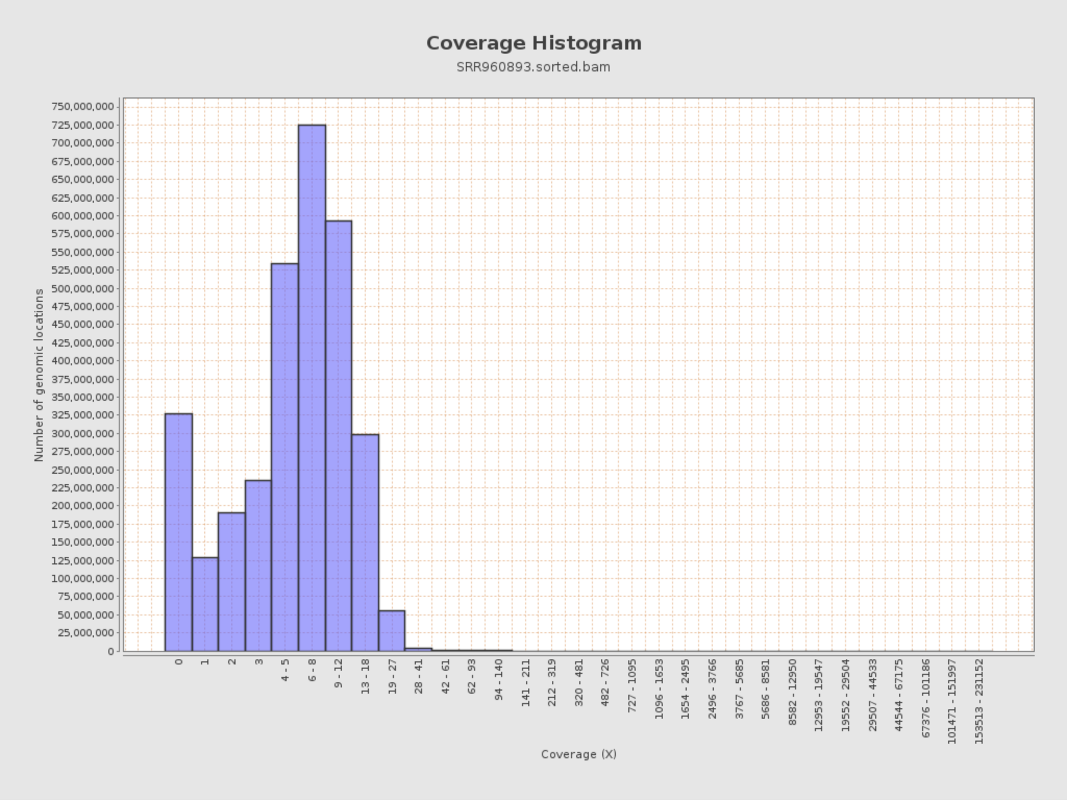
		bases	**coverage**	**deviation**
chr1	249250621	1837500675	7.3721	236.1391
chr2	243199373	2275828572	9.3579	50.8233
chr3	198022430	1423320425	7.1877	14.0853
chr4	191154276	1206407987	6.3112	77.2128
chr5	180915260	1170084087	6.4676	8.2698
chr6	171115067	1326134735	7.75	27.6534
chr7	159138663	1123669036	7.0609	59.6533
chr8	146364022	1237695473	8.4563	96.5982
chr9	141213431	1097347461	7.7708	77.5622
chr10	135534747	962344223	7.1004	222.441
chr11	135006516	960587874	7.1151	36.8907
chr12	133851895	1094651932	8.1781	7.9452
chr13	115169878	608784284	5.286	4.7271
chr14	107349540	430636482	4.0115	6.8311
chr15	102531392	530094648	5.1701	4.6427
chr16	90354753	587990630	6.5076	85.8786
chr17	81195210	463560914	5.7092	24.6608
chr18	78077248	683179428	8.75	80.9461
chr19	59128983	378786720	6.4061	103.6054
chr20	63025520	420345895	6.6695	22.6809
chr21	48129895	271122634	5.6331	31.2069
chr22	51304566	250160774	4.876	6.3023
chrMT	16571	8641152	521.4623	109.6017
chrX	155270560	1258614881	8.1059	25.9694

chrY	59373566	60623103	1.021	67.033

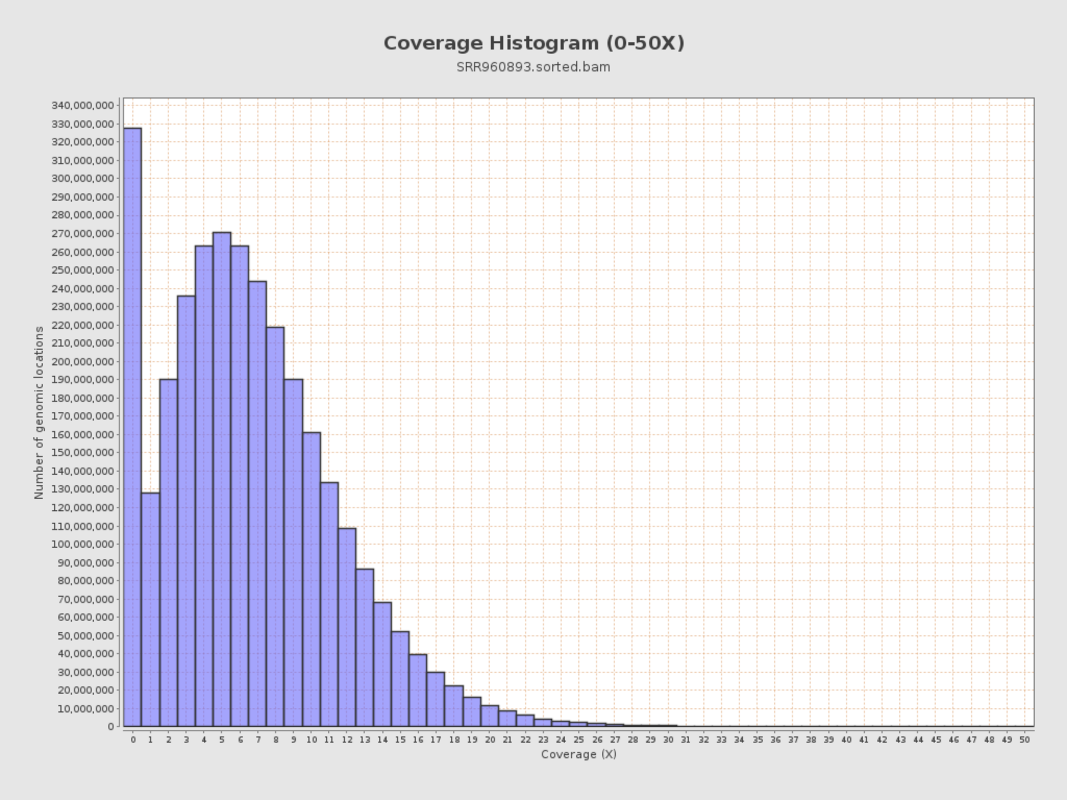
3. Results : Coverage across reference



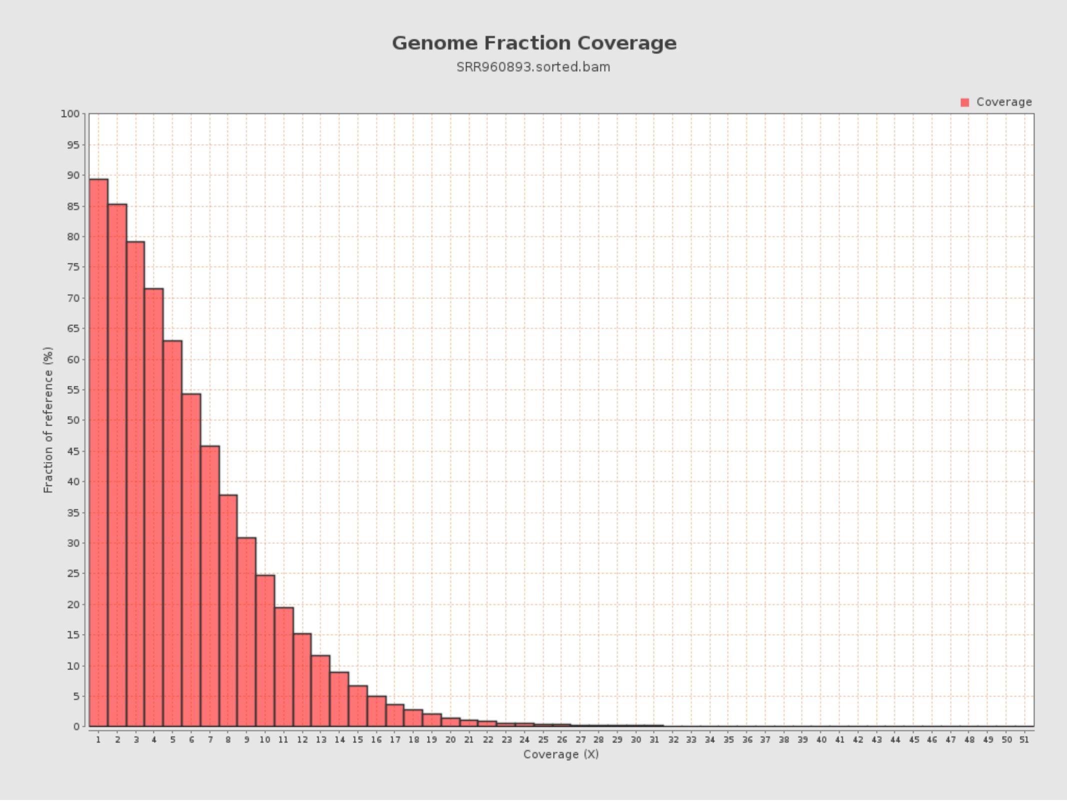
4. Results : Coverage Histogram



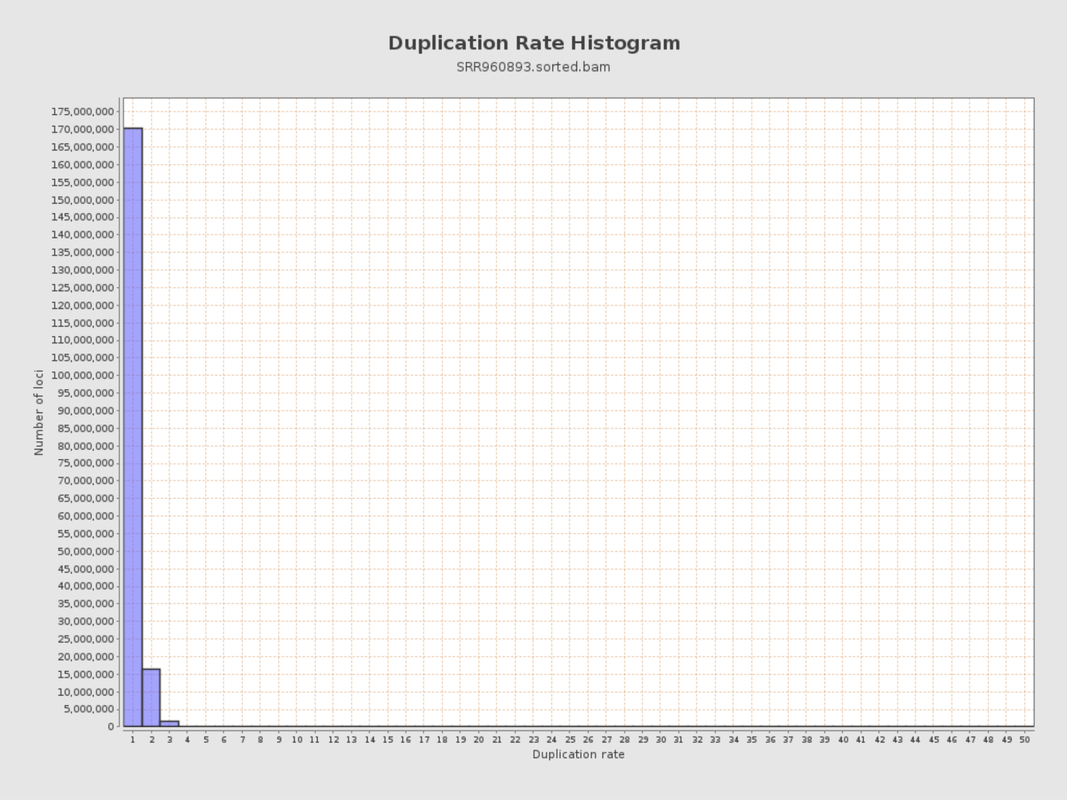
5. Results : Coverage Histogram (0-50X)



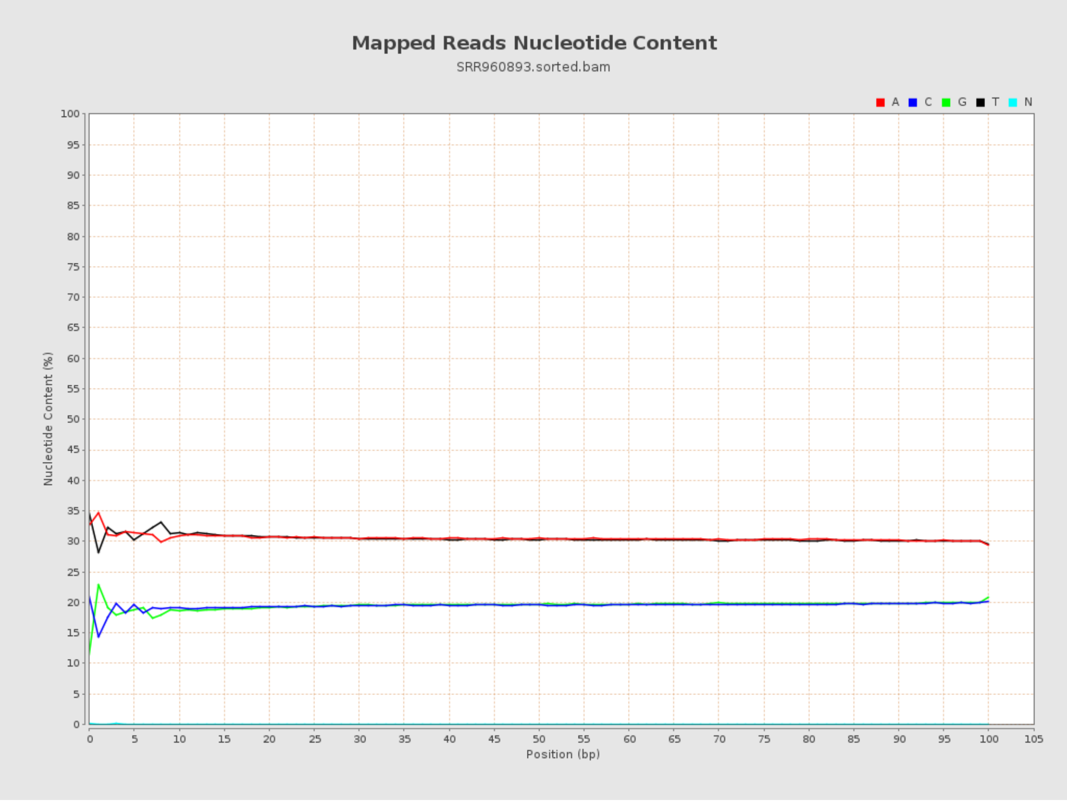
6. Results : Genome Fraction Coverage



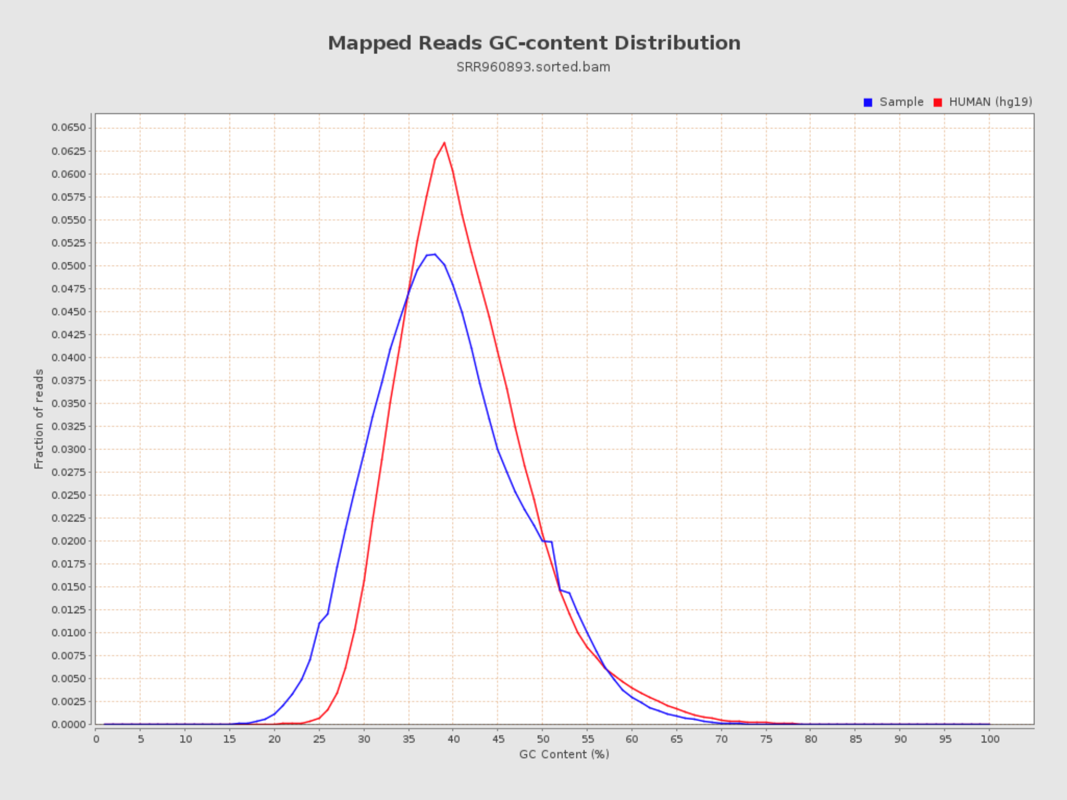
7. Results : Duplication Rate Histogram



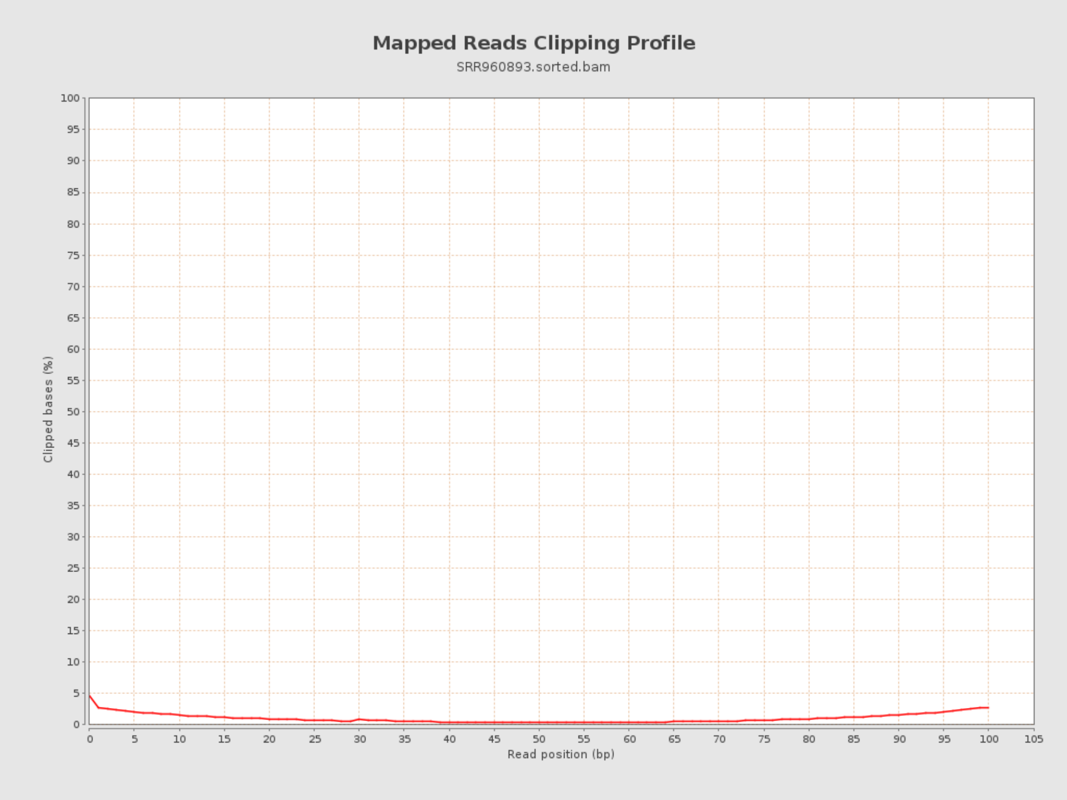
8. Results : Mapped Reads Nucleotide Content



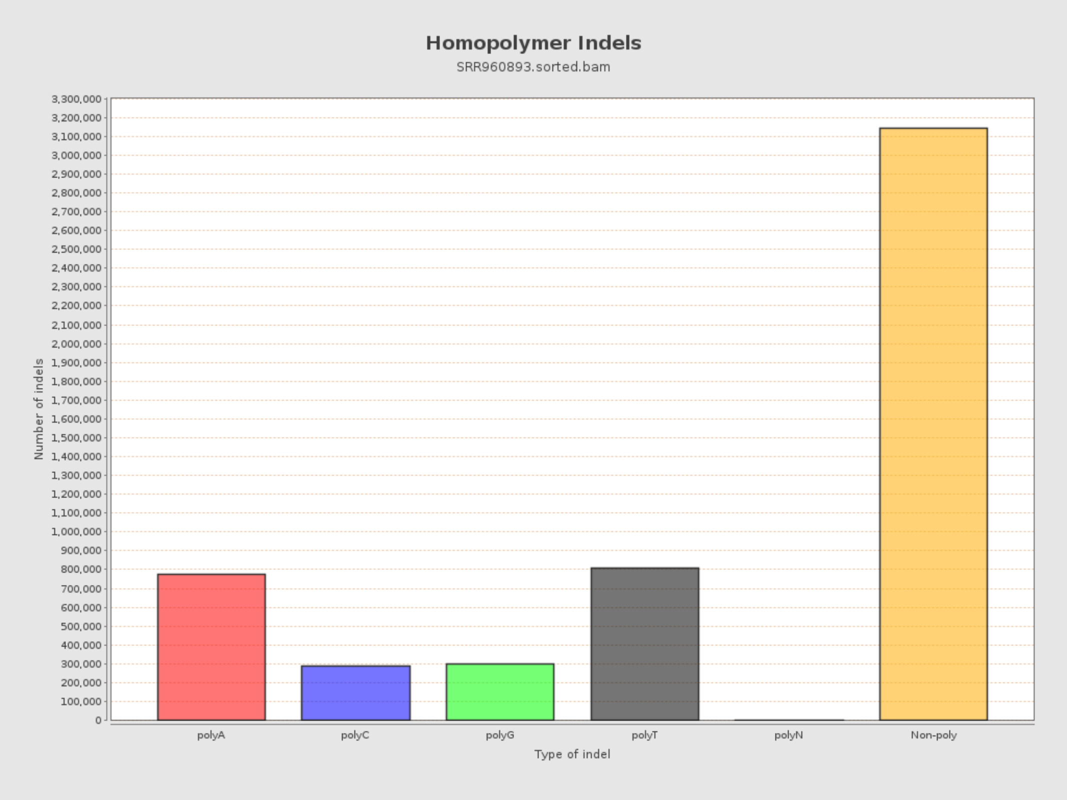
9. Results : Mapped Reads GC-content Distribution



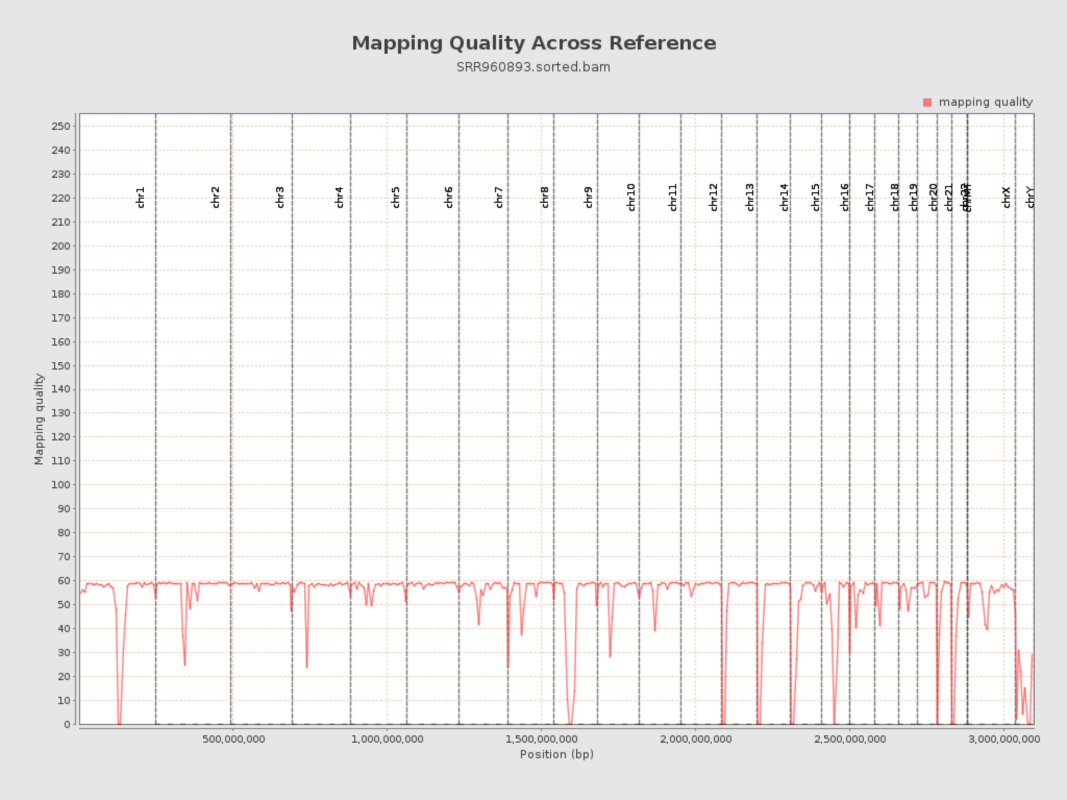
10. Results : Mapped Reads Clipping Profile



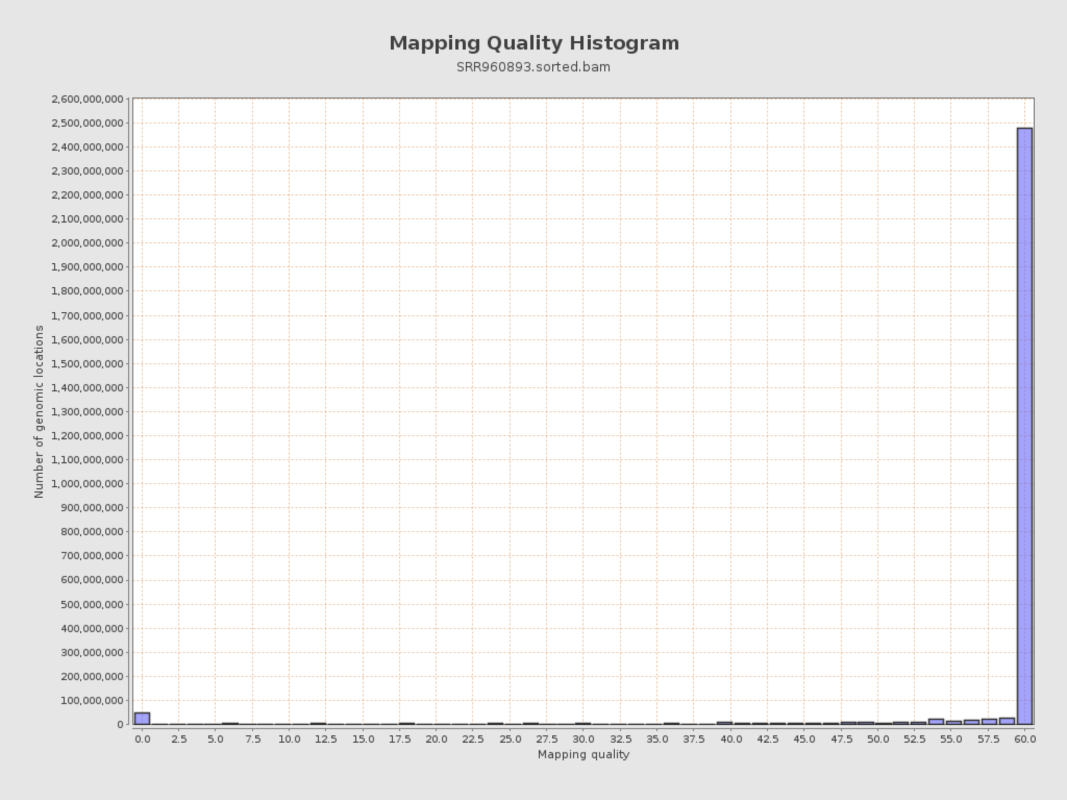
11. Results : Homopolymer Indels



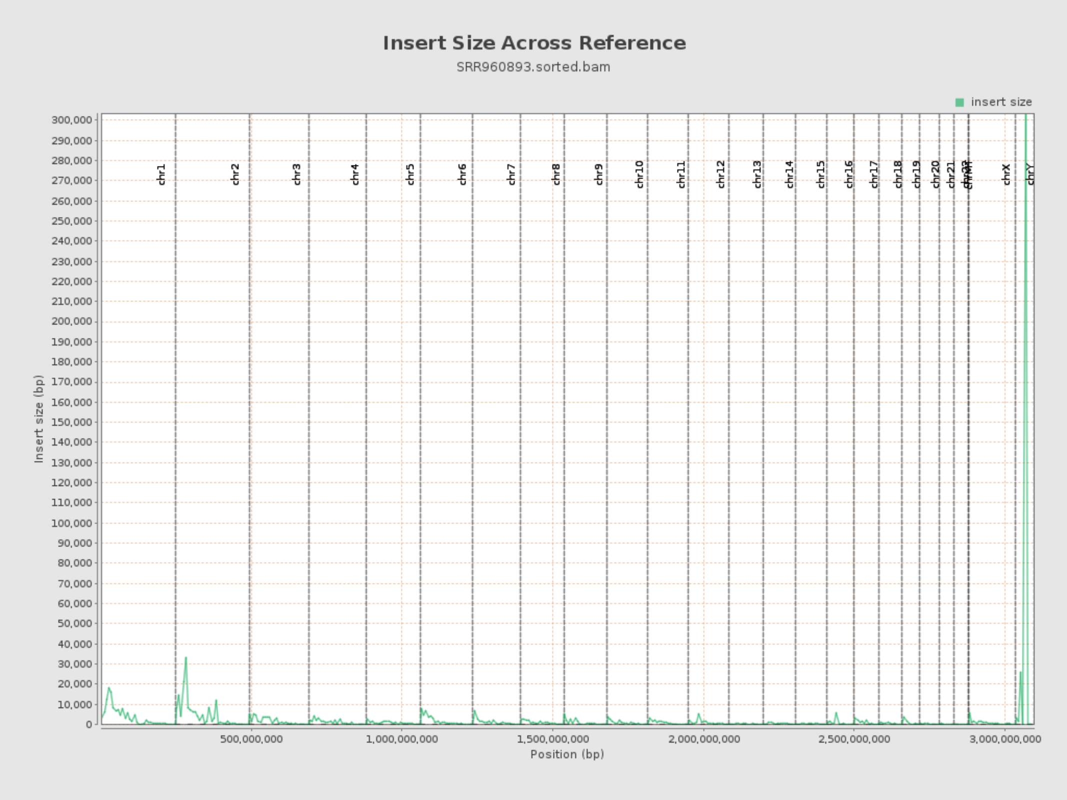
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram