Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/02 21:40:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504700.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_SRR504700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504700_1.fastq.gz SRR504700_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 02 21:40:04 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	346,652,634
Mapped reads	311,148,119 / 89.76%
Unmapped reads	35,504,515 / 10.24%
Mapped paired reads	311,148,119 / 89.76%
Mapped reads, first in pair	156,583,709 / 45.17%
Mapped reads, second in pair	154,564,410 / 44.59%
Mapped reads, both in pair	306,789,720 / 88.5%
Mapped reads, singletons	4,358,399 / 1.26%
Secondary alignments	0
Supplementary alignments	1,607,148 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	59,264,471 / 17.1%
Duplication rate	17.47%
Clipped reads	39,517,469 / 11.4%

2.2. ACGT Content

Number/percentage of A's	8,027,316,893 / 26.55%
Number/percentage of C's	7,010,118,632 / 23.18%
Number/percentage of T's	8,001,758,807 / 26.46%
Number/percentage of G's	7,189,555,558 / 23.78%
Number/percentage of N's	11,163,460 / 0.04%

GC Percentage	46.96%

2.3. Coverage

Mean	9.7705
Standard Deviation	19.9716

2.4. Mapping Quality

Mean Mapping Quality	53.97

2.5. Insert size

Mean	29,889.99
Standard Deviation	1,642,404.36
P25/Median/P75	207 / 436 / 484

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	215,475,815
Insertions	2,090,597
Mapped reads with at least one insertion	0.66%
Deletions	2,604,679
Mapped reads with at least one deletion	0.81%
Homopolymer indels	40.31%

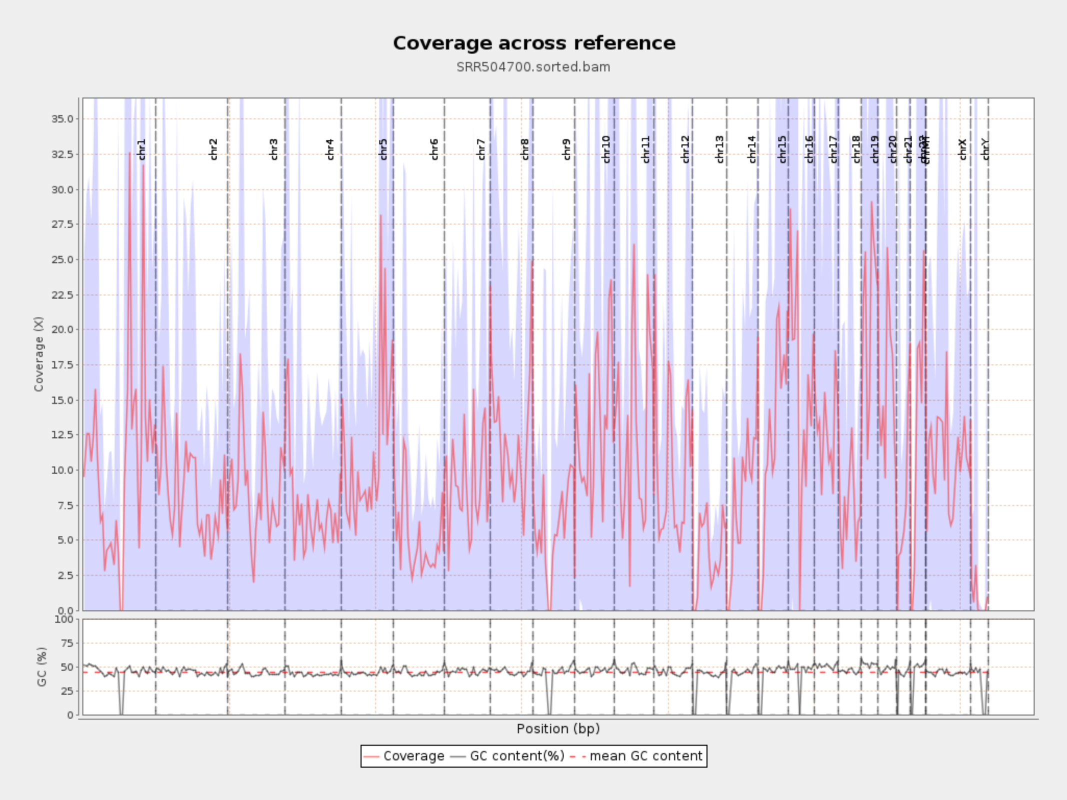
2.7. Chromosome stats

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

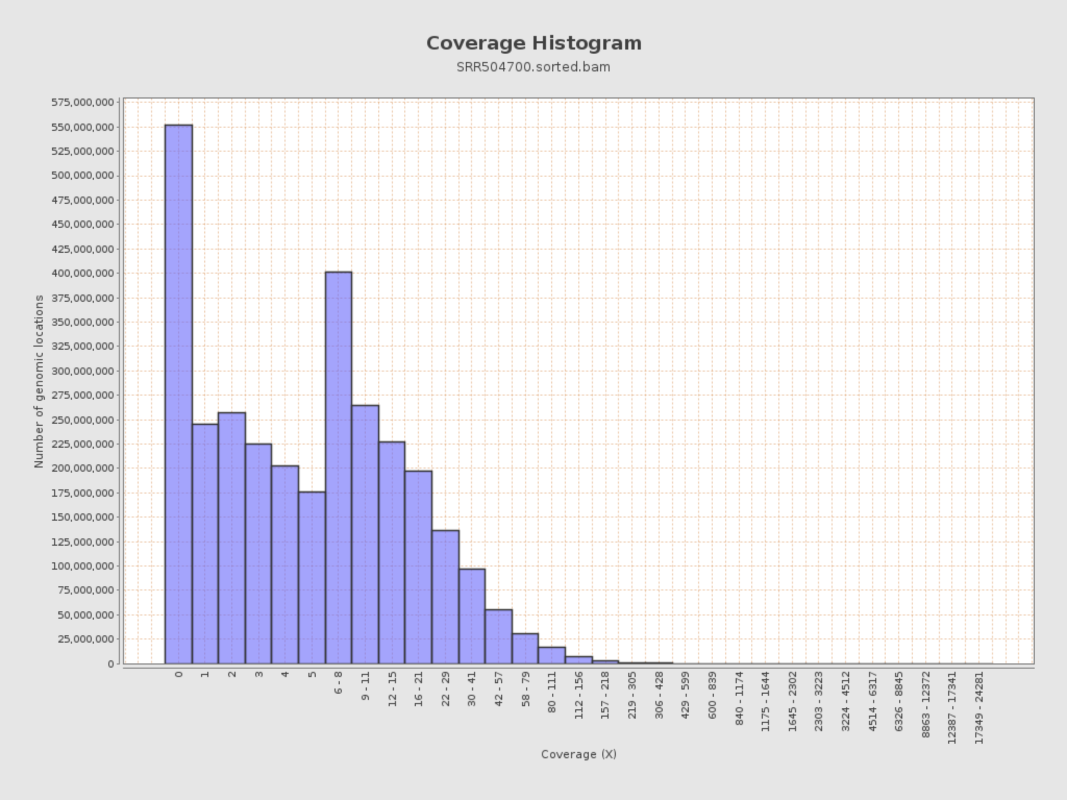
		bases	**coverage**	**deviation**
chr1	249250621	2651555546	10.6381	21.3793
chr2	243199373	2009464742	8.2626	13.222
chr3	198022430	1709529244	8.633	13.069
chr4	191154276	1398886600	7.3181	12.5697
chr5	180915260	2076737914	11.4791	17.5207
chr6	171115067	866626255	5.0646	9.0175
chr7	159138663	1429472731	8.9826	13.5364
chr8	146364022	1770504494	12.0966	21.5446
chr9	141213431	824033870	5.8354	12.3576
chr10	135534747	1795983401	13.2511	19.7719
chr11	135006516	1733061788	12.8369	21.6225
chr12	133851895	1366386512	10.2082	17.3335
chr13	115169878	465355242	4.0406	6.8168
chr14	107349540	851382708	7.9309	12.2932
chr15	102531392	1224302569	11.9408	19.2184
chr16	90354753	1452155414	16.0717	24.6191
chr17	81195210	1040156946	12.8106	20.631
chr18	78077248	558790564	7.1569	58.2805
chr19	59128983	1264569599	21.3866	31.7514
chr20	63025520	976611190	15.4955	21.4129
chr21	48129895	380063889	7.8966	18.5221
chr22	51304566	663444884	12.9315	23.9476
chrMT	16571	228437	13.7853	5.9996
chrX	155270560	1689515877	10.8811	15.6925

chrY	59373566	47522175	0.8004	27.7018

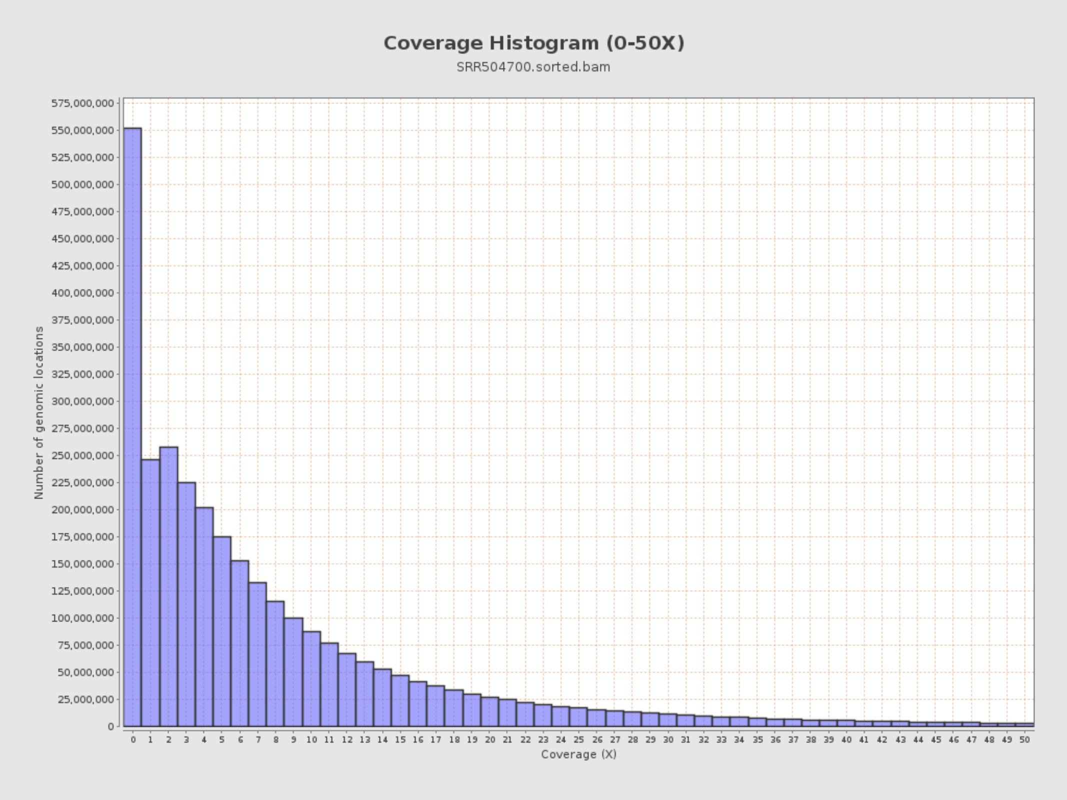
3. Results : Coverage across reference



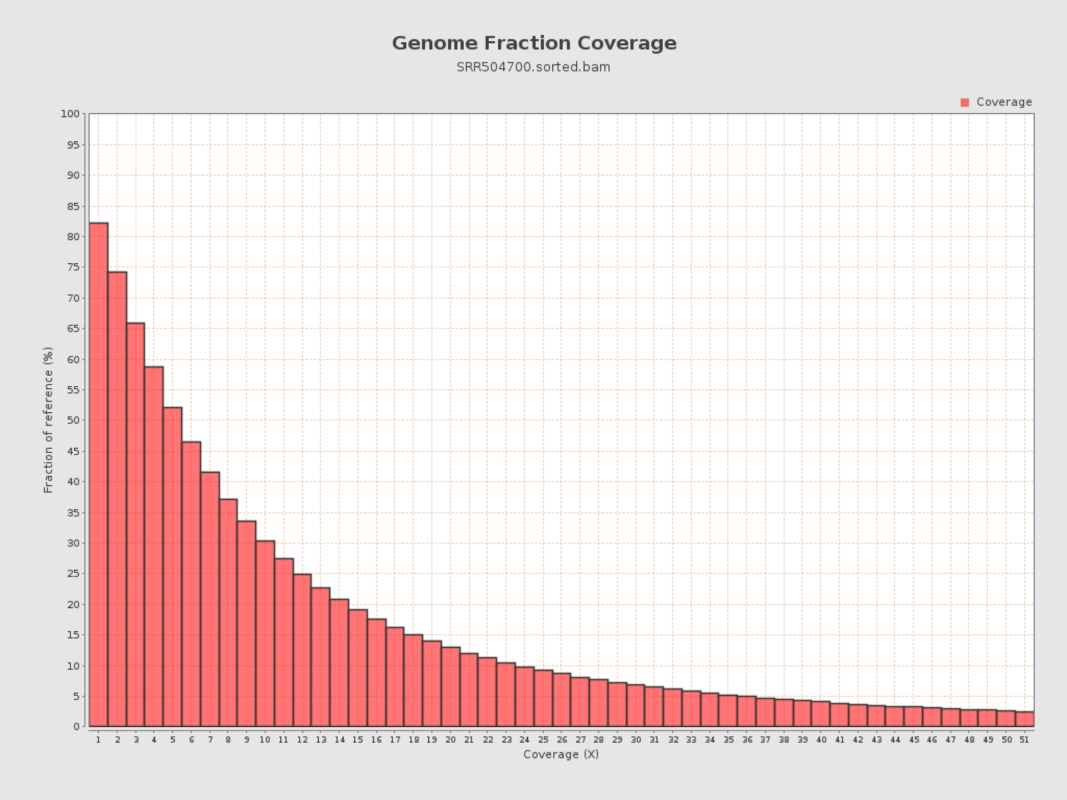
4. Results : Coverage Histogram



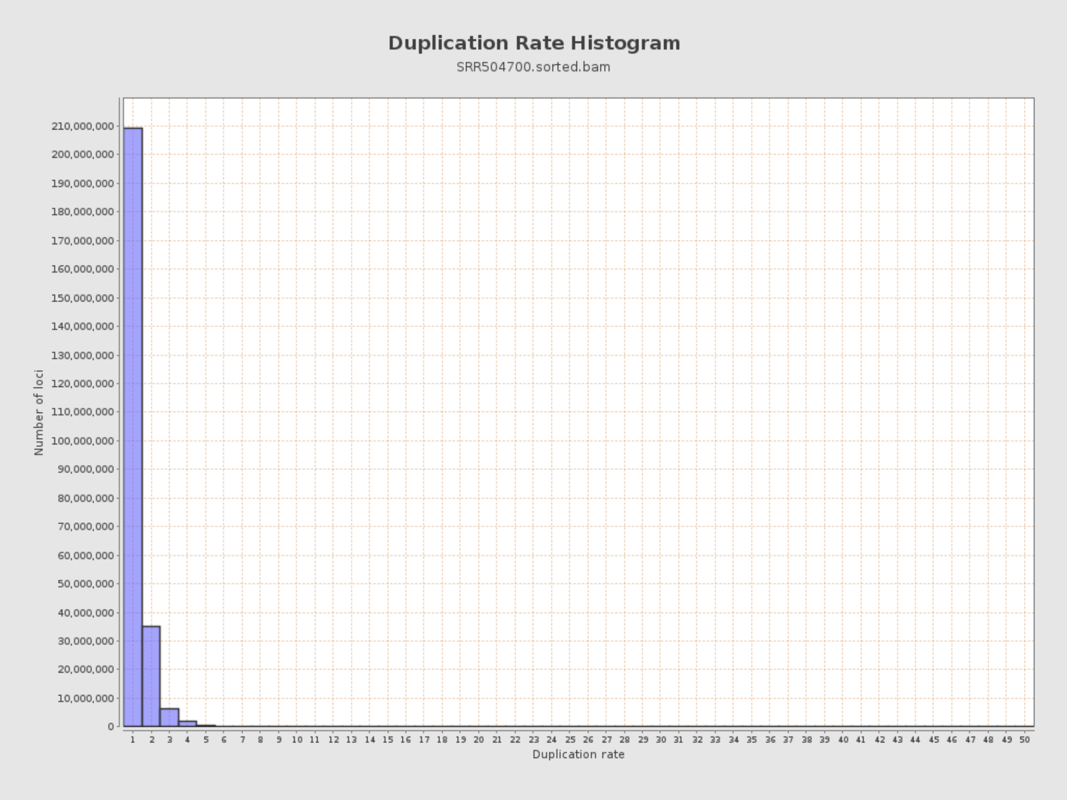
5. Results : Coverage Histogram (0-50X)



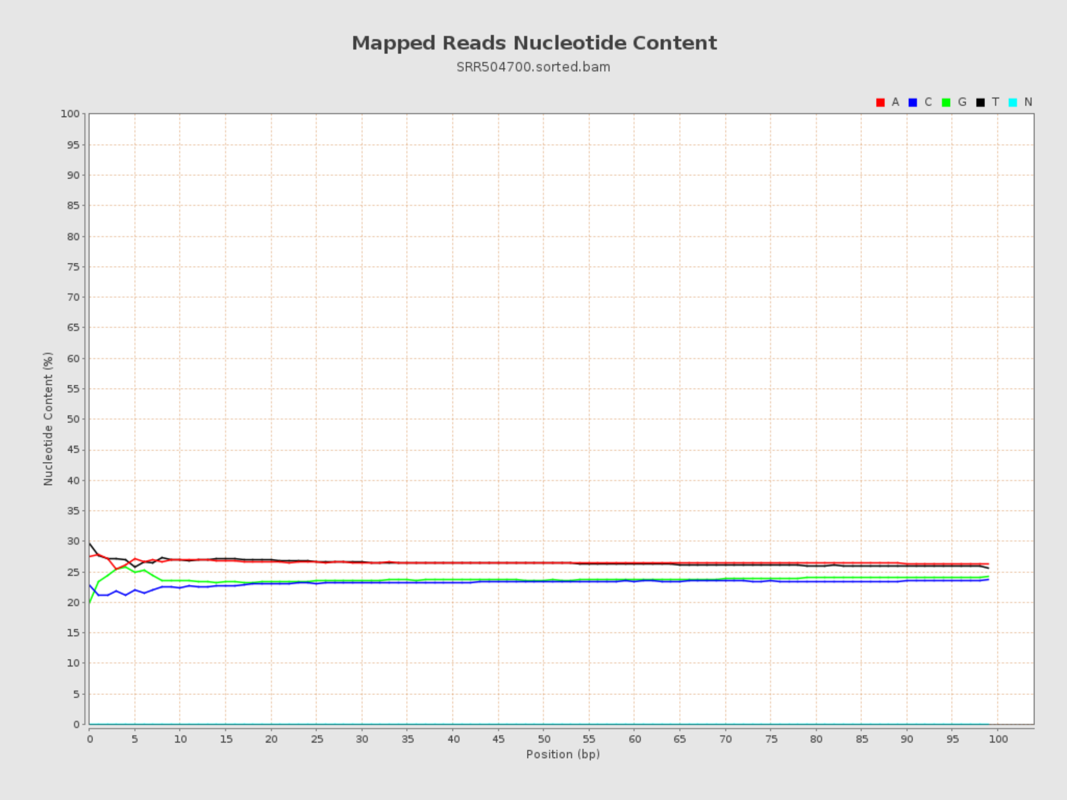
6. Results : Genome Fraction Coverage



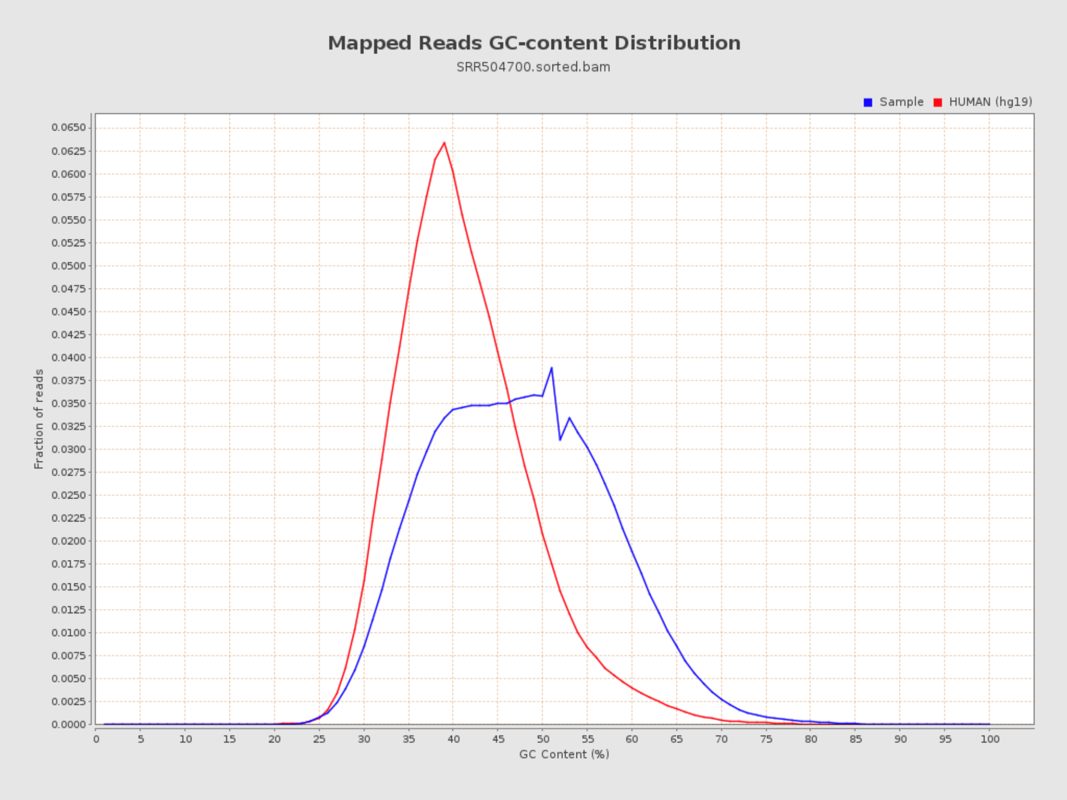
7. Results : Duplication Rate Histogram



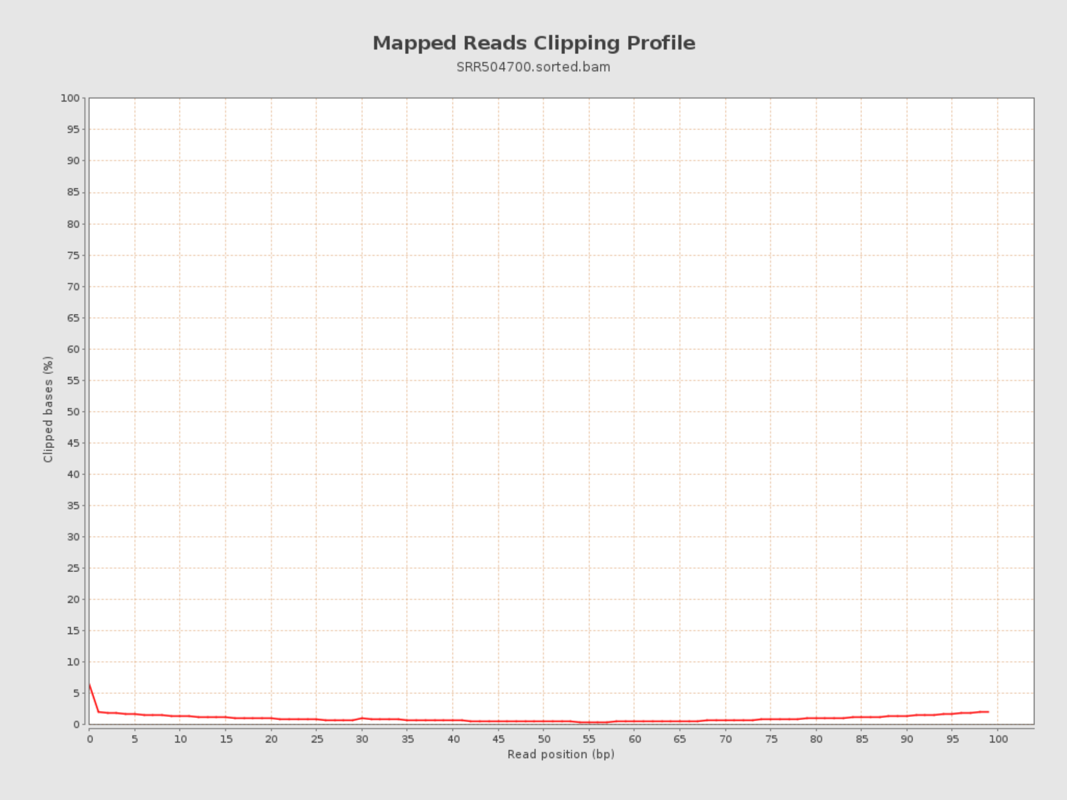
8. Results : Mapped Reads Nucleotide Content



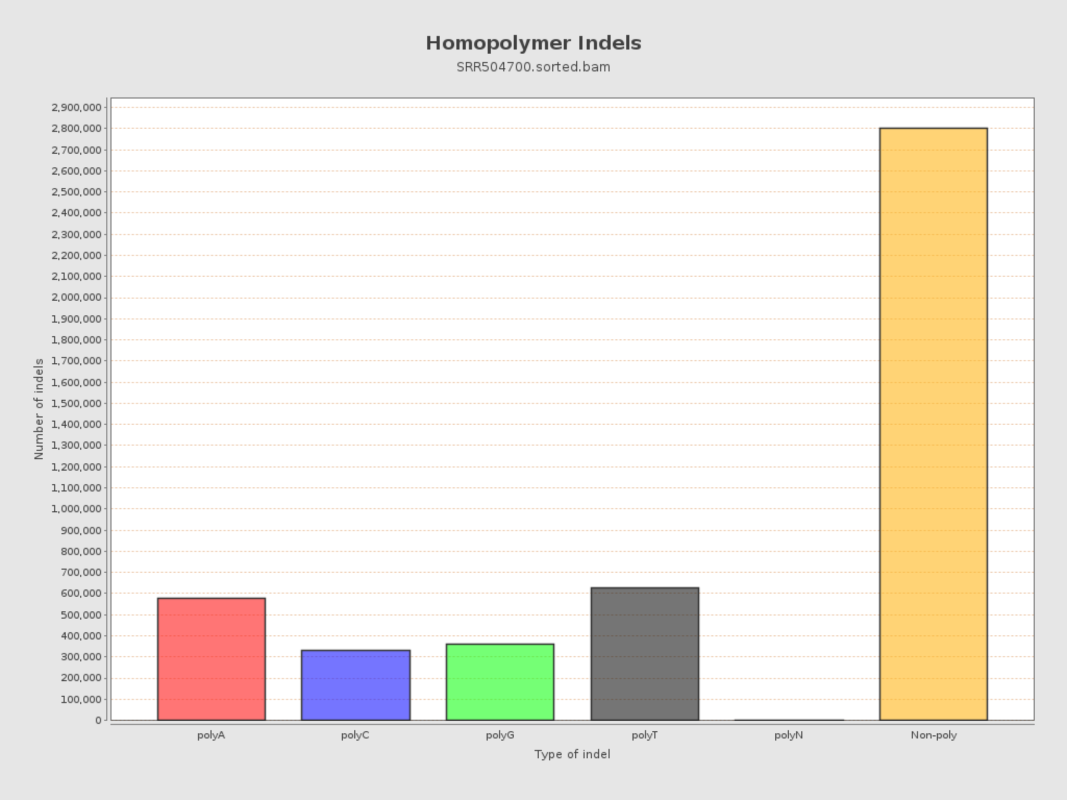
9. Results : Mapped Reads GC-content Distribution



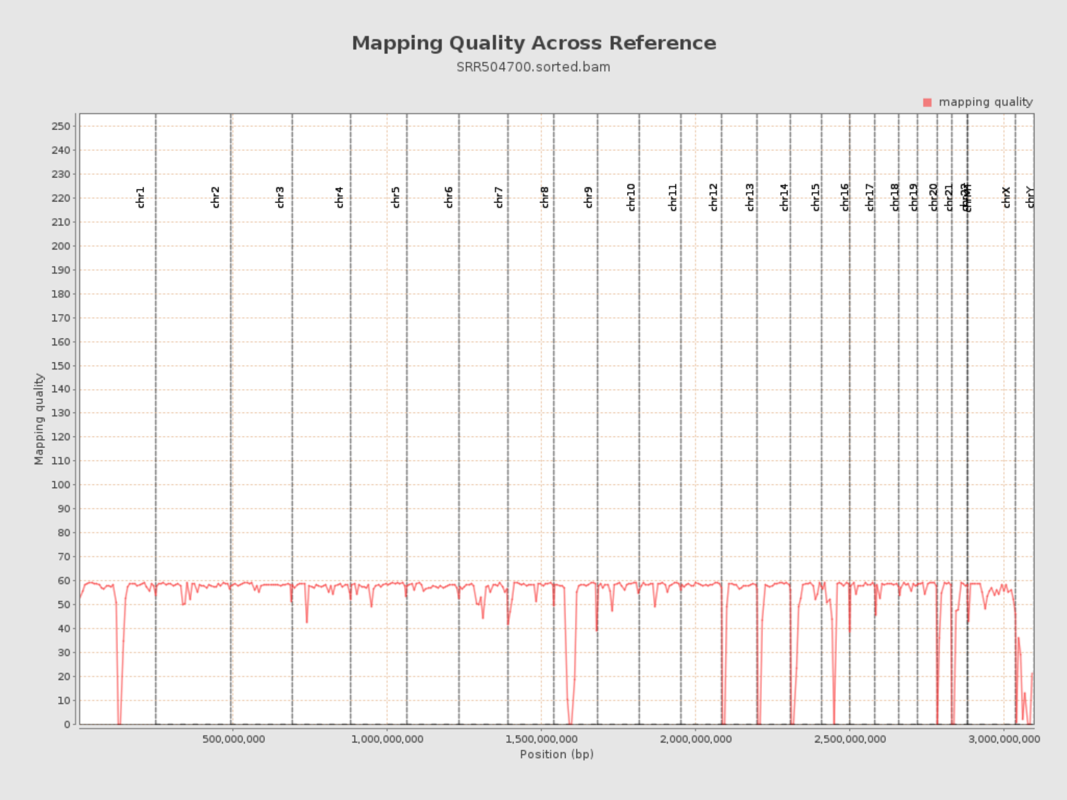
10. Results : Mapped Reads Clipping Profile



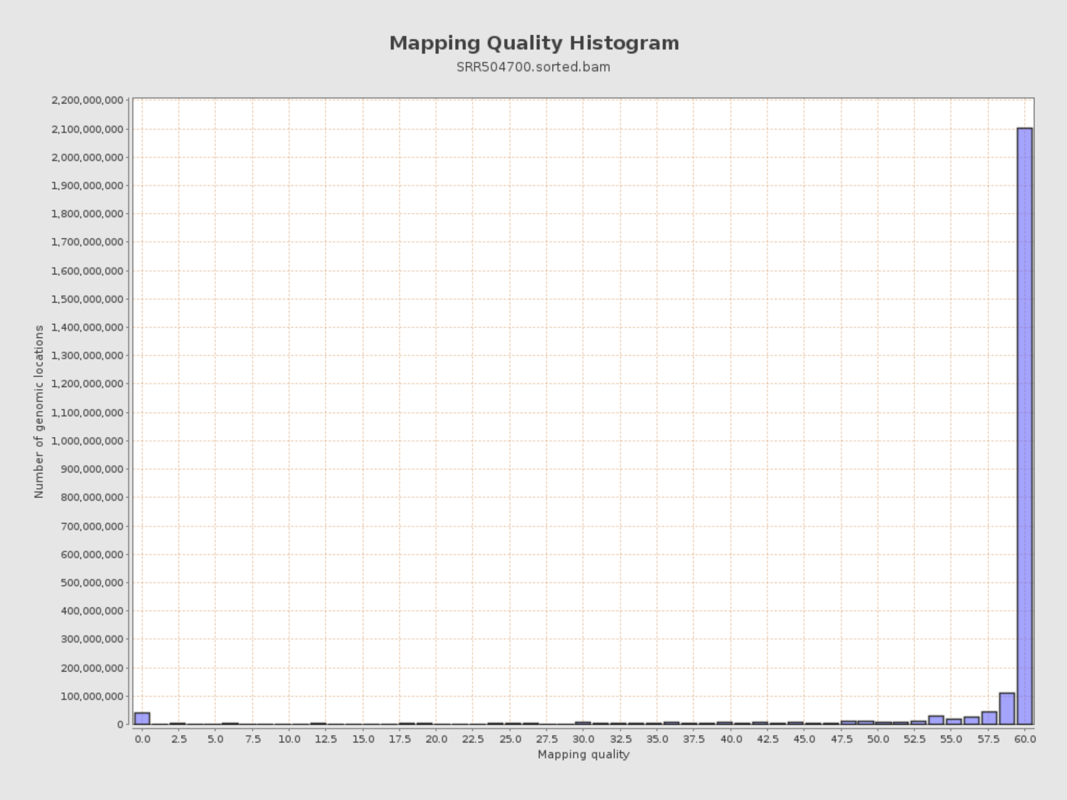
11. Results : Homopolymer Indels



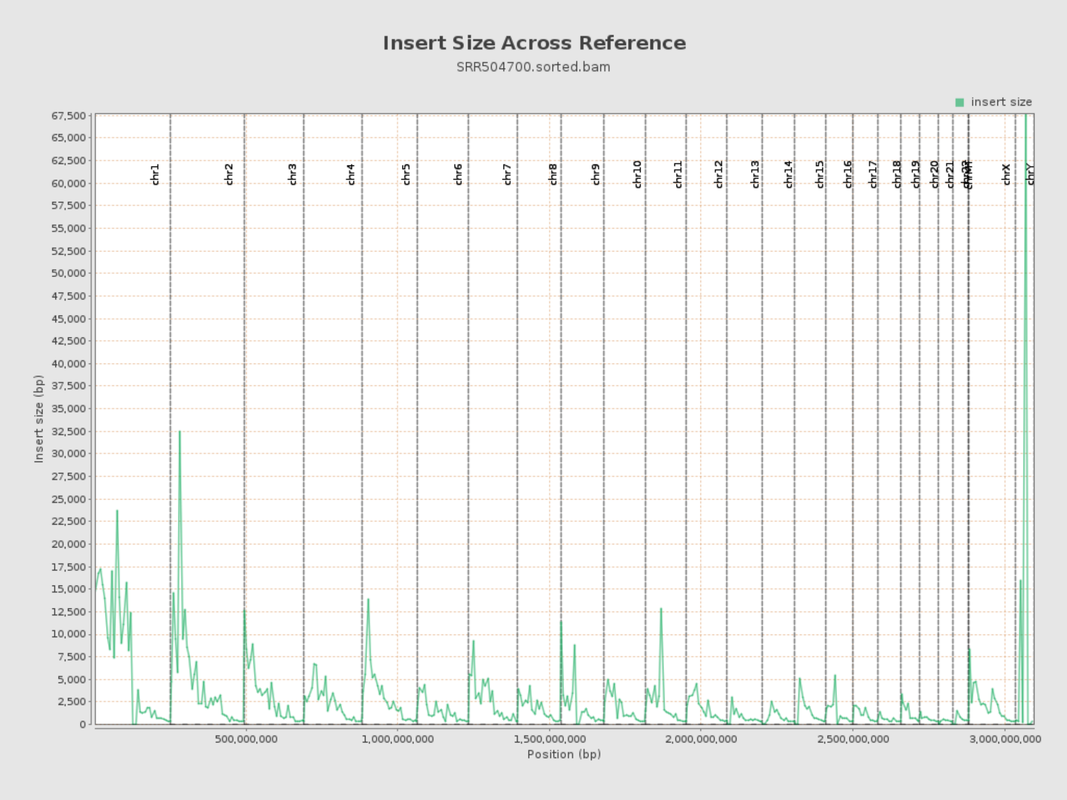
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram