Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 11:13:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504706.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_SRR504706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504706_1.fastq.gz SRR504706_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 11:13:03 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	488,572,822
Mapped reads	442,647,689 / 90.6%
Unmapped reads	45,925,133 / 9.4%
Mapped paired reads	442,647,689 / 90.6%
Mapped reads, first in pair	222,450,629 / 45.53%
Mapped reads, second in pair	220,197,060 / 45.07%
Mapped reads, both in pair	436,945,212 / 89.43%
Mapped reads, singletons	5,702,477 / 1.17%
Secondary alignments	0
Supplementary alignments	2,255,302 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	116,163,932 / 23.78%
Duplication rate	23.09%
Clipped reads	38,113,590 / 7.8%

2.2. ACGT Content

Number/percentage of A's	11,519,344,087 / 26.5%
Number/percentage of C's	10,118,989,125 / 23.27%
Number/percentage of T's	11,537,828,693 / 26.54%
Number/percentage of G's	10,287,129,128 / 23.66%
Number/percentage of N's	12,800,443 / 0.03%

GC Percentage	46.94%

2.3. Coverage

Mean	14.047
Standard Deviation	33.4483

2.4. Mapping Quality

Mean Mapping Quality	53.8

2.5. Insert size

Mean	43,207.76
Standard Deviation	1,936,494.37
P25/Median/P75	375 / 410 / 449

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	302,583,304
Insertions	3,404,908
Mapped reads with at least one insertion	0.75%
Deletions	3,756,504
Mapped reads with at least one deletion	0.83%
Homopolymer indels	40.5%

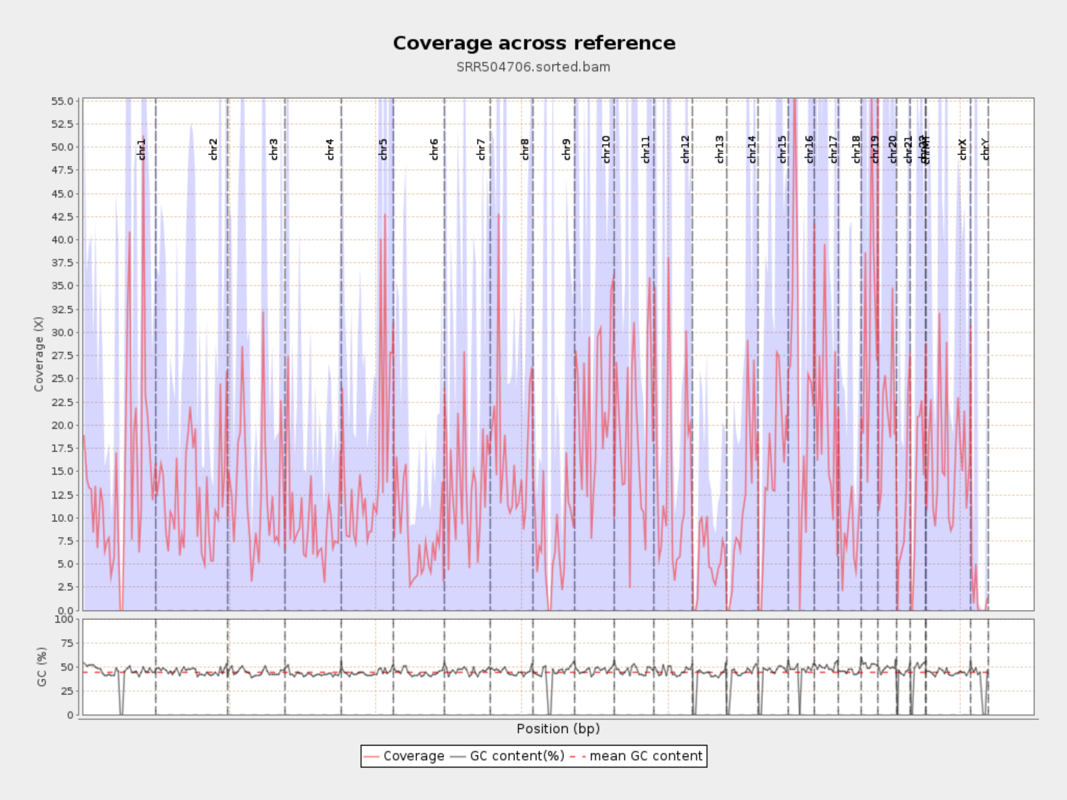
2.7. Chromosome stats

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

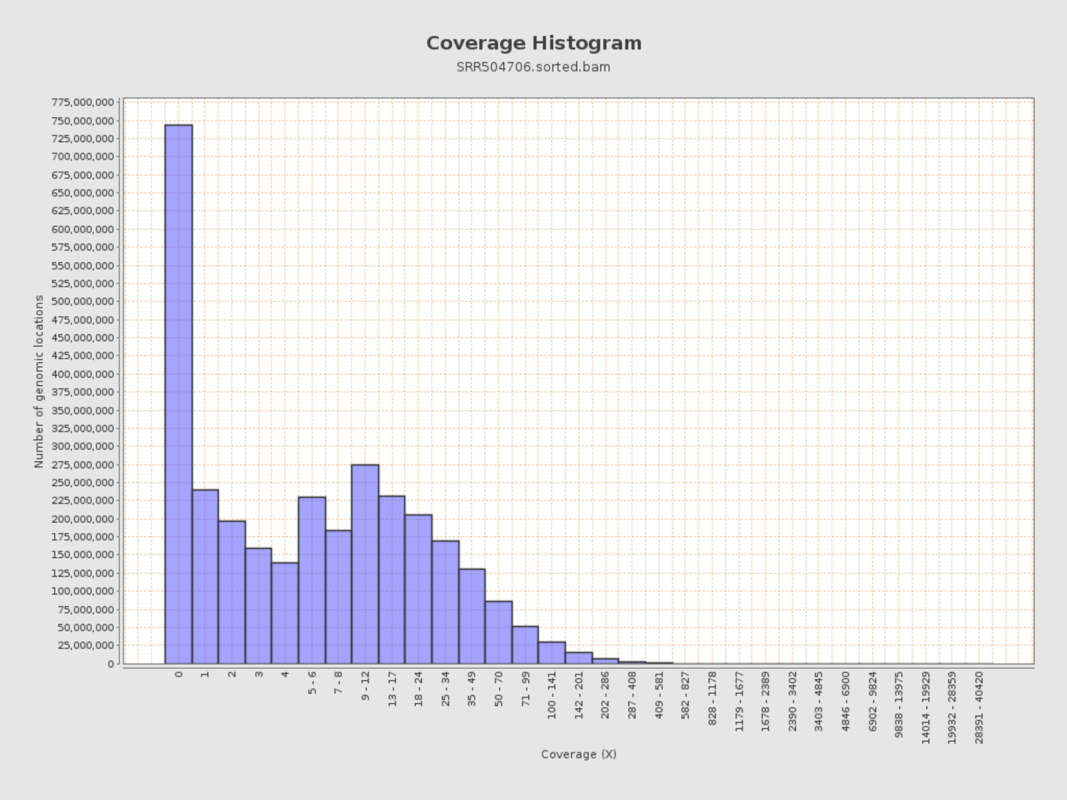
		bases	coverage	deviation
chr1	249250621	3581999284	14.3711	30.5768
chr2	243199373	2972223482	12.2213	23.0931
chr3	198022430	2534161748	12.7973	24.3129
chr4	191154276	1867316913	9.7686	17.4731
chr5	180915260	2842141739	15.7098	30.3264
chr6	171115067	1314065645	7.6794	15.3182
chr7	159138663	2227463300	13.997	24.1131
chr8	146364022	2445096845	16.7056	32.9322
chr9	141213431	1042335066	7.3813	27.3602
chr10	135534747	2955750556	21.8081	34.9047
chr11	135006516	2605574920	19.2996	35.2923
chr12	133851895	1978513308	14.7814	34.827
chr13	115169878	607763633	5.2771	10.6893
chr14	107349540	1255819065	11.6984	23.0749
chr15	102531392	1543398217	15.0529	29.3751
chr16	90354753	2184189478	24.1735	40.7401
chr17	81195210	1699252960	20.928	39.7608
chr18	78077248	677786919	8.681	96.696
chr19	59128983	1870253157	31.6301	59.0425
chr20	63025520	1339282115	21.2498	34.6564
chr21	48129895	555680697	11.5454	24.8825
chr22	51304566	715945058	13.9548	28.9356
chrMT	16571	189369	11.4277	16.7717
chrX	155270560	2587390193	16.6638	27.8054

chrY	59373566	81696726	1.376	47.8019

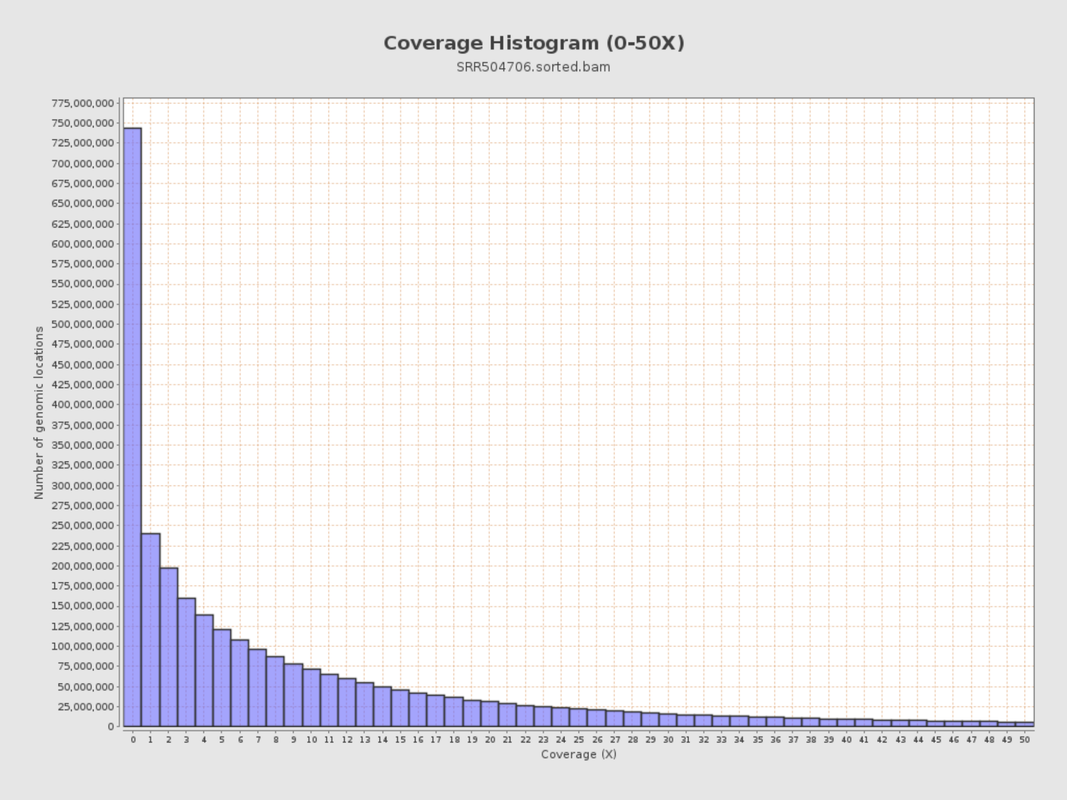
3. Results : Coverage across reference



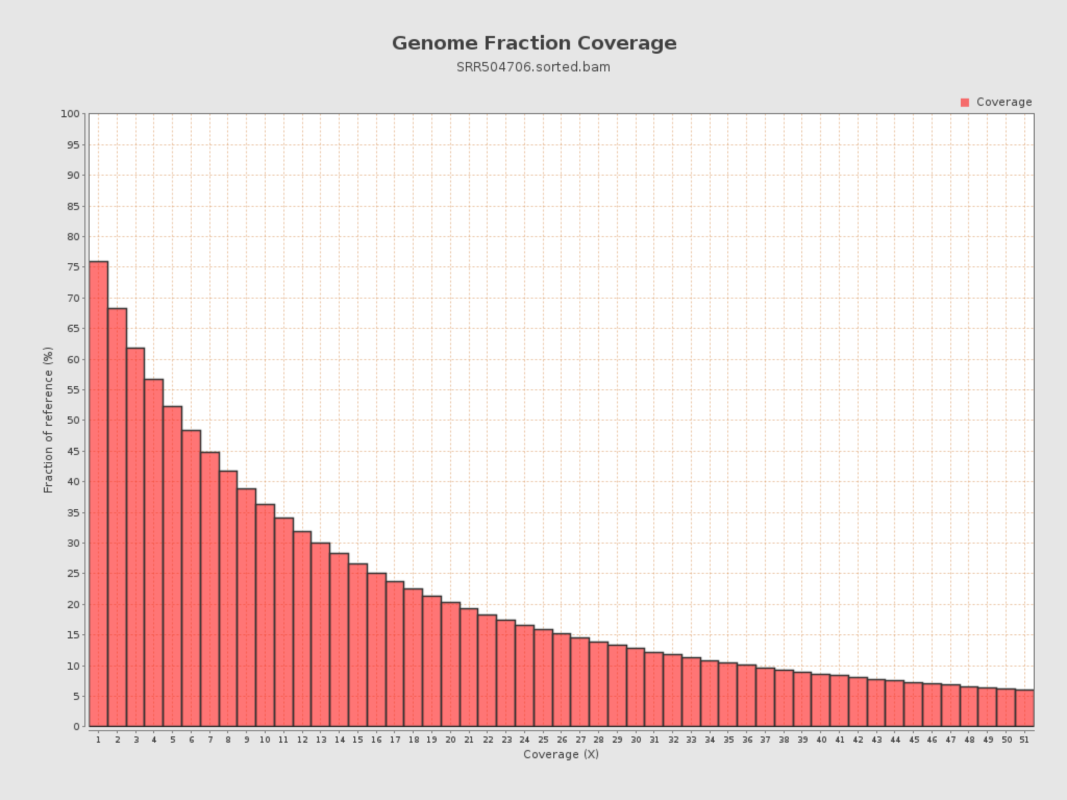
4. Results : Coverage Histogram



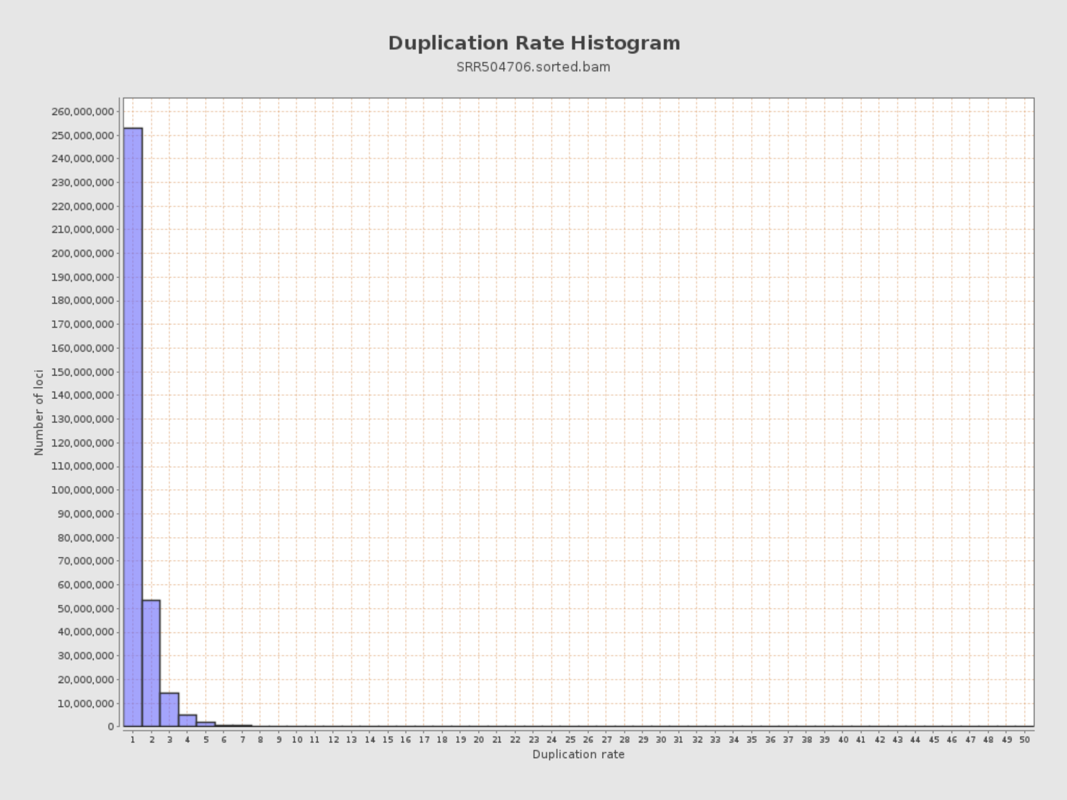
5. Results : Coverage Histogram (0-50X)



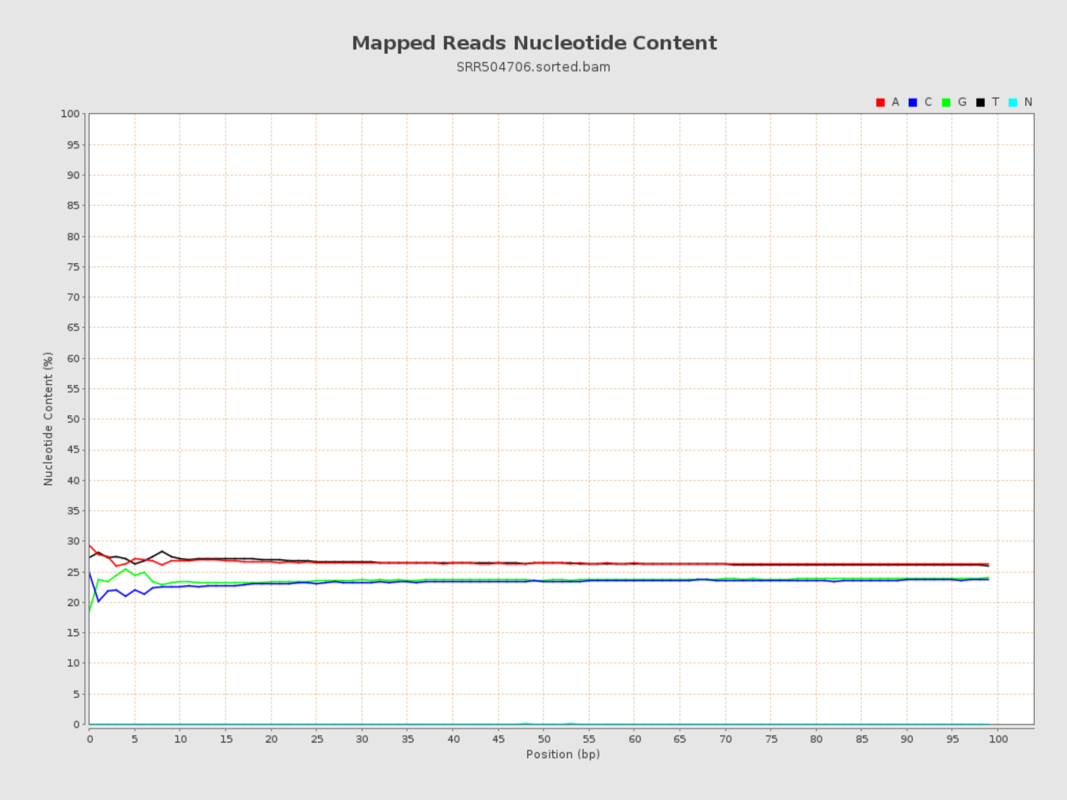
6. Results : Genome Fraction Coverage



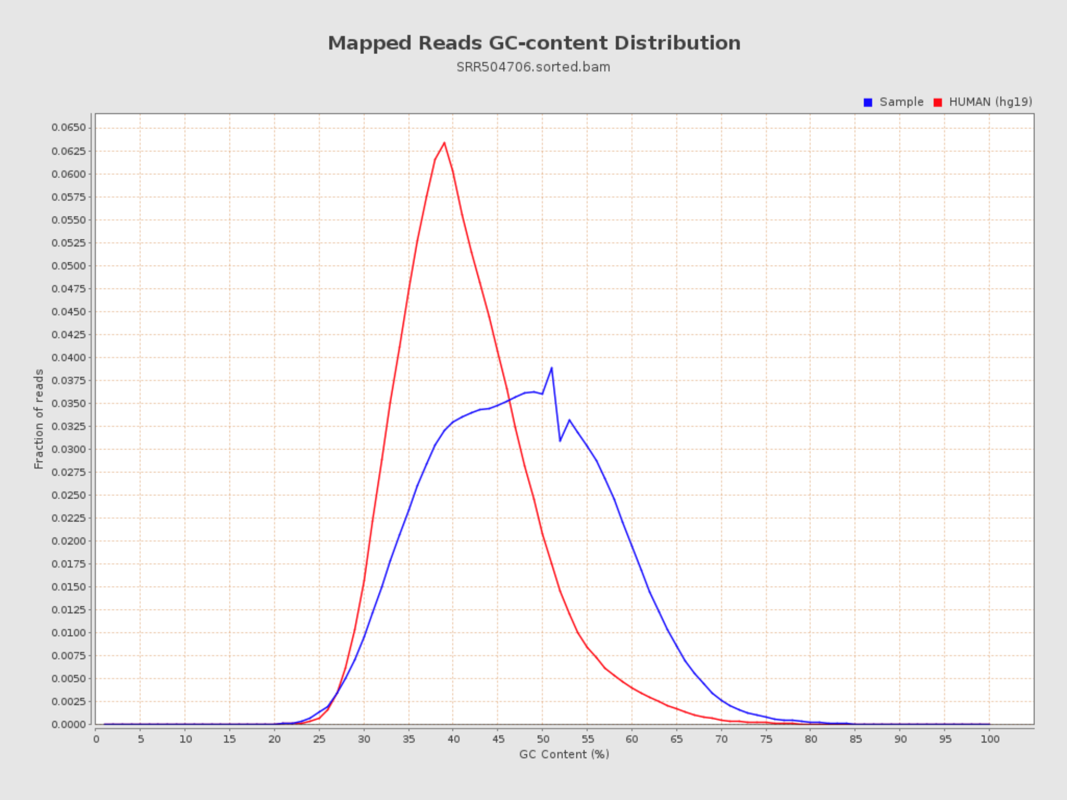
7. Results : Duplication Rate Histogram



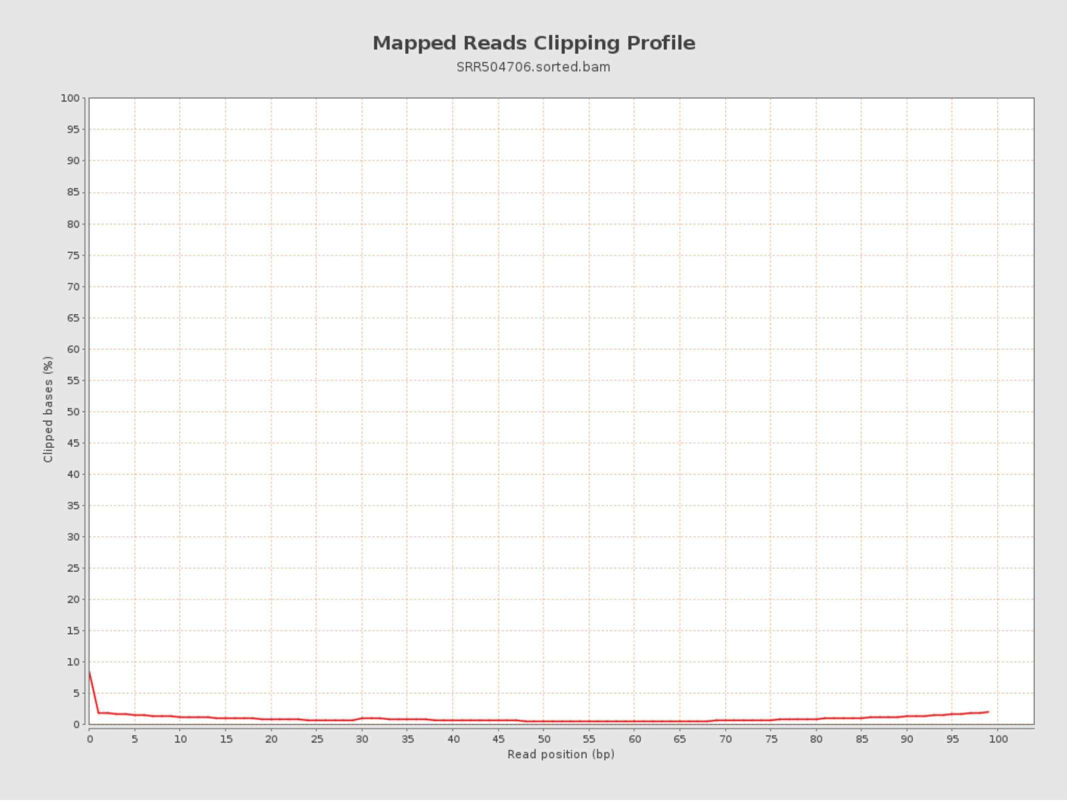
8. Results : Mapped Reads Nucleotide Content



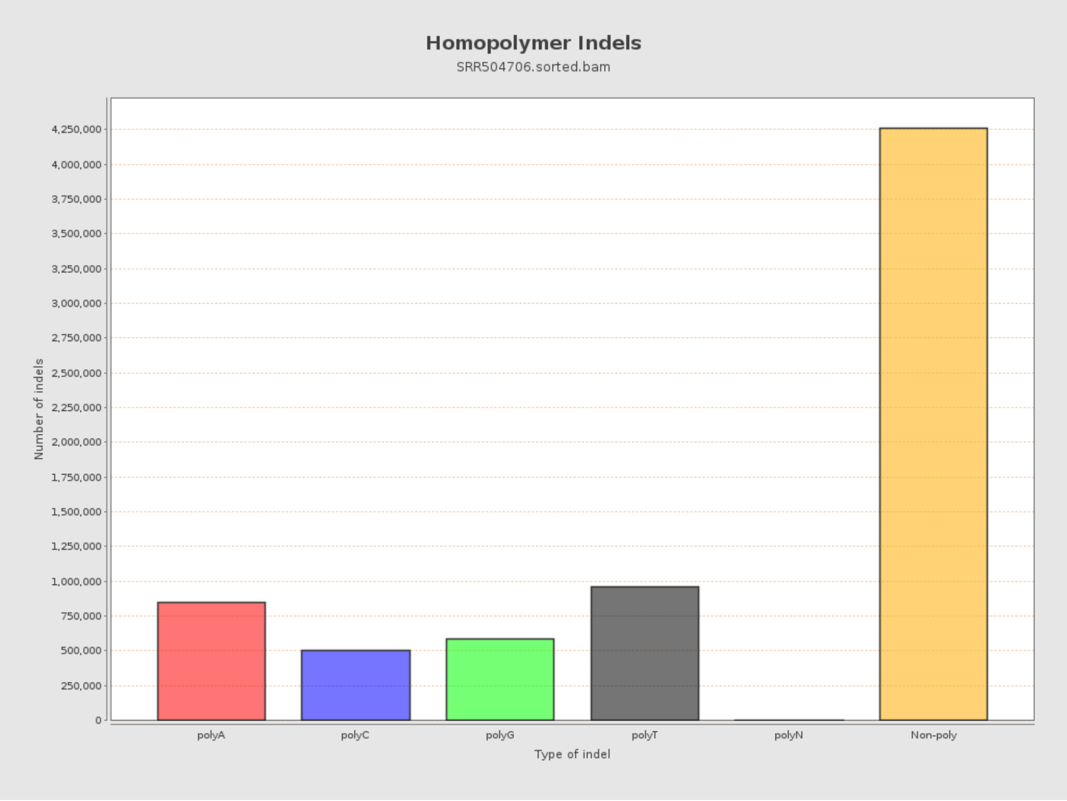
9. Results : Mapped Reads GC-content Distribution



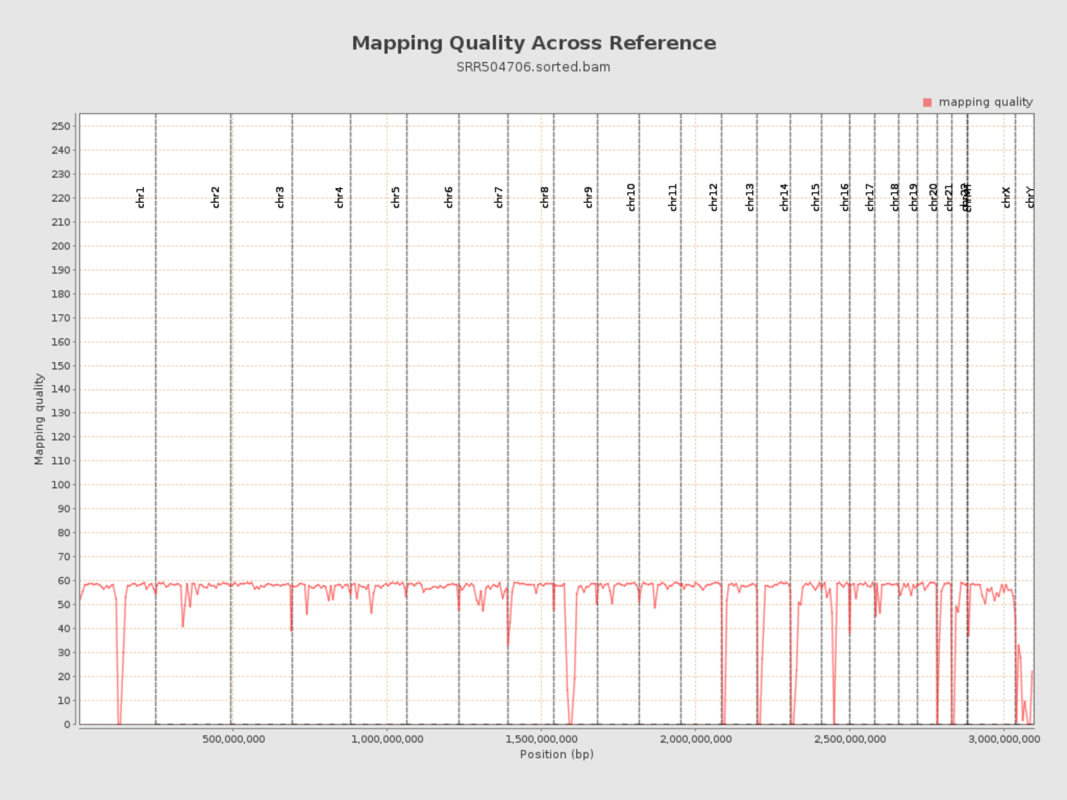
10. Results : Mapped Reads Clipping Profile



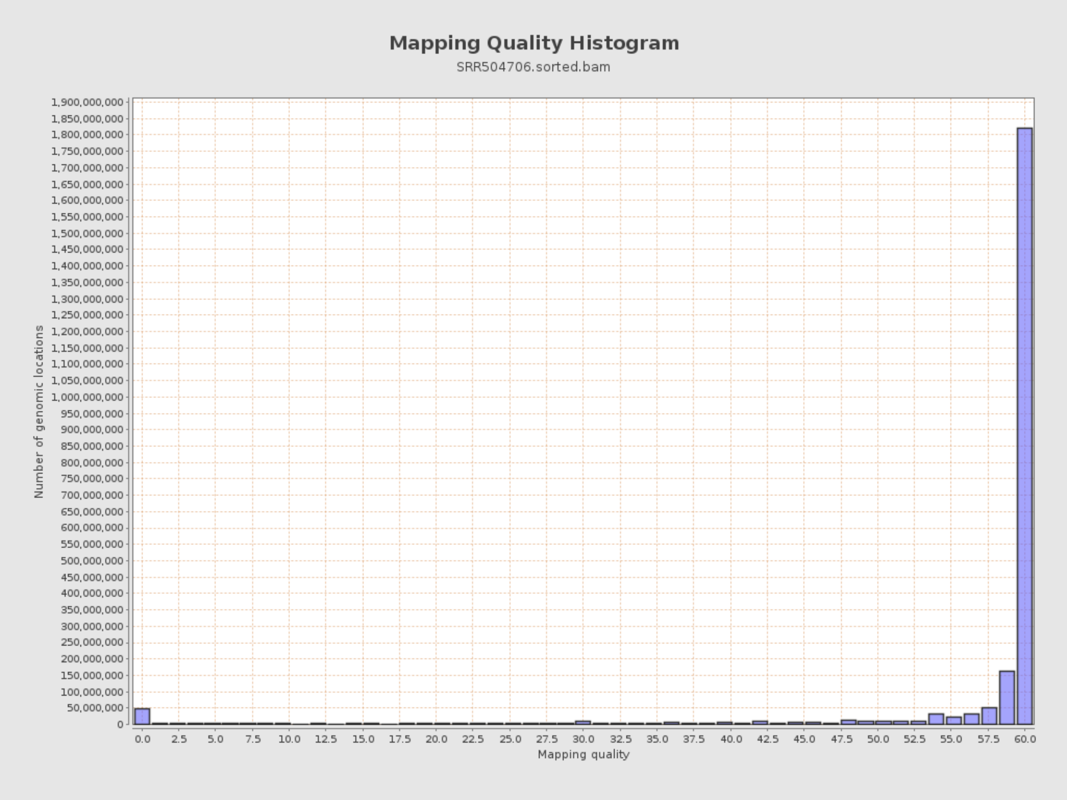
11. Results : Homopolymer Indels



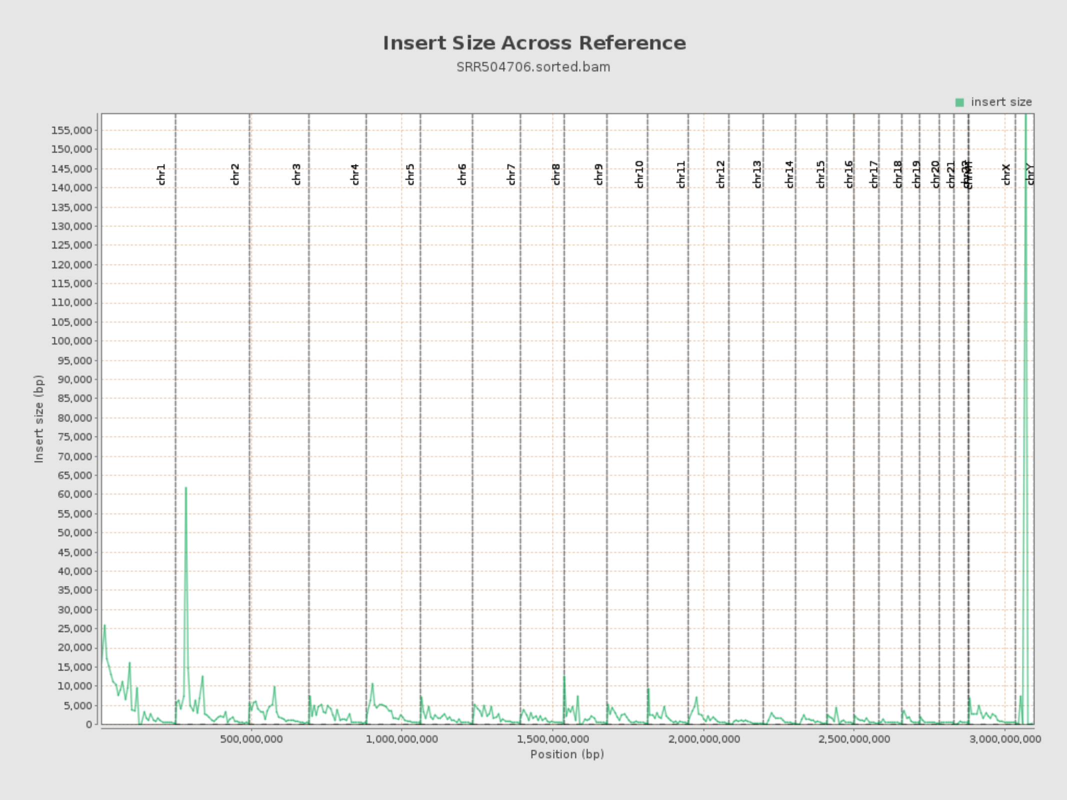
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram