Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 13:16:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617395.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_SRR617395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617395_1.fastq.gz SRR617395_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 13:16:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,603,877 / 92.51%
Unmapped reads	2,396,123 / 7.49%
Mapped paired reads	29,603,877 / 92.51%
Mapped reads, first in pair	14,879,397 / 46.5%
Mapped reads, second in pair	14,724,480 / 46.01%
Mapped reads, both in pair	29,044,098 / 90.76%
Mapped reads, singletons	559,779 / 1.75%
Secondary alignments	0
Supplementary alignments	437,222 / 1.37%
Read min/max/mean length	30 / 100 / 100.57
Duplicated reads (estimated)	1,329,603 / 4.16%
Duplication rate	4.1%
Clipped reads	3,432,732 / 10.73%

2.2. ACGT Content

Number/percentage of A's	869,076,352 / 29.89%
Number/percentage of C's	583,085,103 / 20.05%
Number/percentage of T's	858,509,554 / 29.53%
Number/percentage of G's	594,918,854 / 20.46%
Number/percentage of N's	2,088,678 / 0.07%

GC Percentage	40.51%

2.3. Coverage

Mean	0.9395
Standard Deviation	2.874

2.4. Mapping Quality

Mean Mapping Quality	53.86

2.5. Insert size

Mean	47,574.24
Standard Deviation	2,080,619.67
P25/Median/P75	169 / 207 / 266

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	35,220,238
Insertions	829,071
Mapped reads with at least one insertion	2.78%
Deletions	278,550
Mapped reads with at least one deletion	0.92%
Homopolymer indels	35.09%

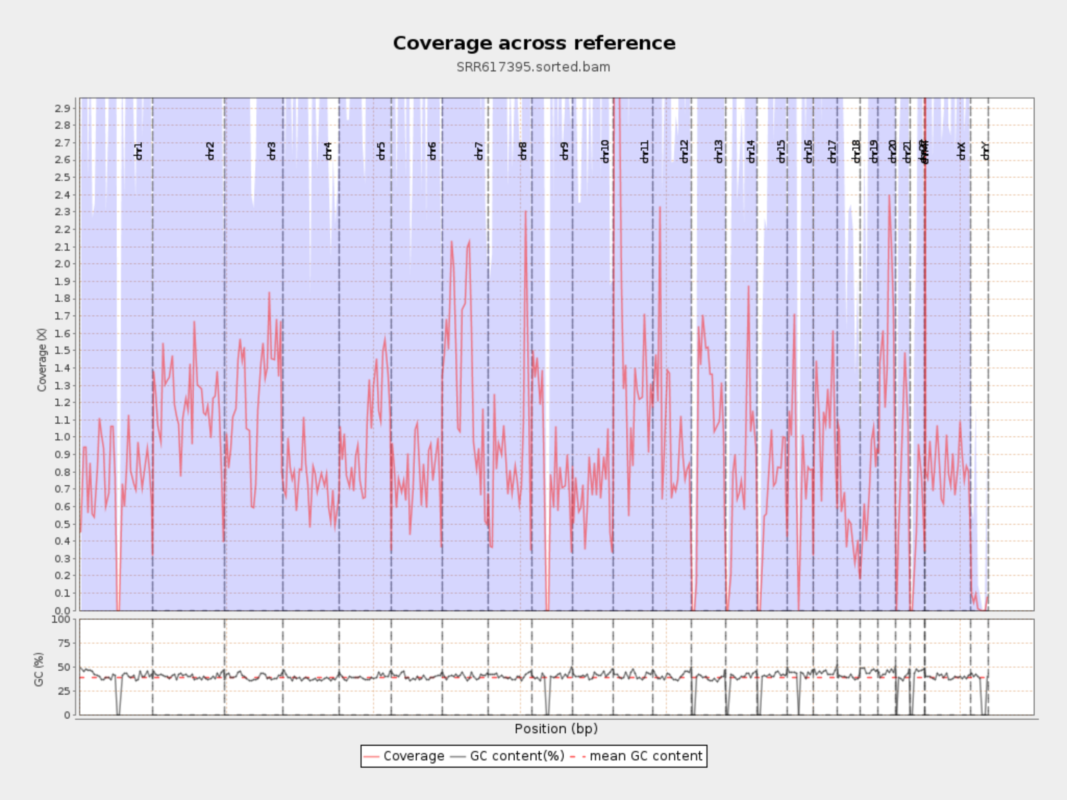
2.7. Chromosome stats

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

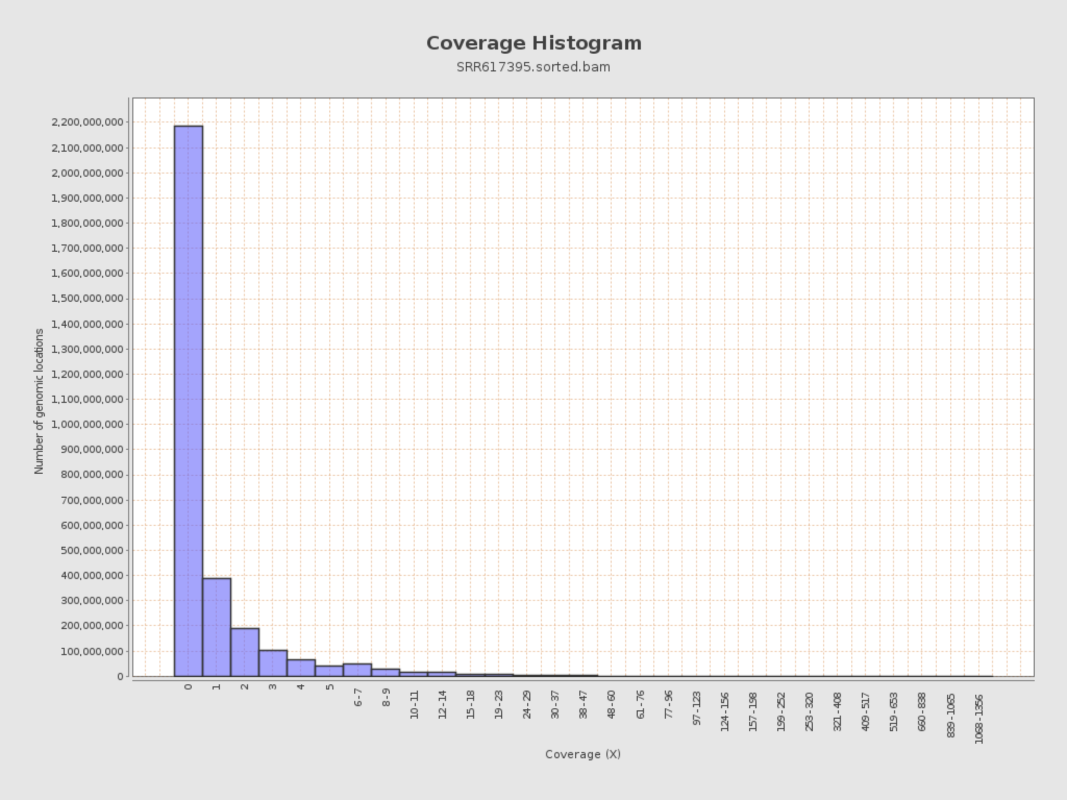
		bases	coverage	deviation
chr1	249250621	187074451	0.7505	2.717
chr2	243199373	290270560	1.1935	3.026
chr3	198022430	245958106	1.2421	3.3491
chr4	191154276	140558671	0.7353	2.2486
chr5	180915260	186248488	1.0295	2.8277
chr6	171115067	133654996	0.7811	2.5675
chr7	159138663	217919944	1.3694	3.181
chr8	146364022	128994949	0.8813	3.2121
chr9	141213431	116336033	0.8238	2.5709
chr10	135534747	93160146	0.6874	2.3631
chr11	135006516	215661651	1.5974	3.7602
chr12	133851895	138549045	1.0351	2.7204
chr13	115169878	126625974	1.0995	2.7224
chr14	107349540	84195854	0.7843	2.8354
chr15	102531392	66578112	0.6493	2.305
chr16	90354753	72859136	0.8064	3.2309
chr17	81195210	88932007	1.0953	3.6343
chr18	78077248	41780086	0.5351	1.9644
chr19	59128983	40961524	0.6927	2.2699
chr20	63025520	98591698	1.5643	4.6253
chr21	48129895	39909215	0.8292	2.5002
chr22	51304566	23120015	0.4506	2.0267
chrMT	16571	177995	10.7414	4.7905
chrX	155270560	127879220	0.8236	2.5242

chrY	59373566	2301110	0.0388	0.5506

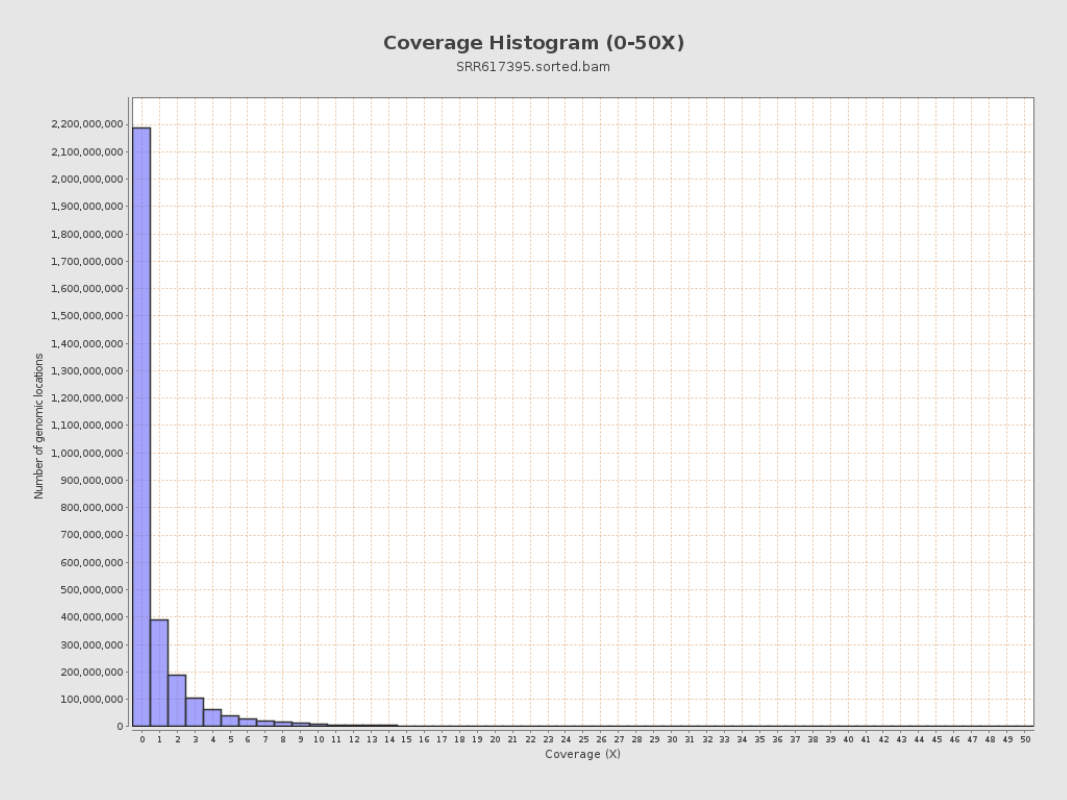
3. Results : Coverage across reference



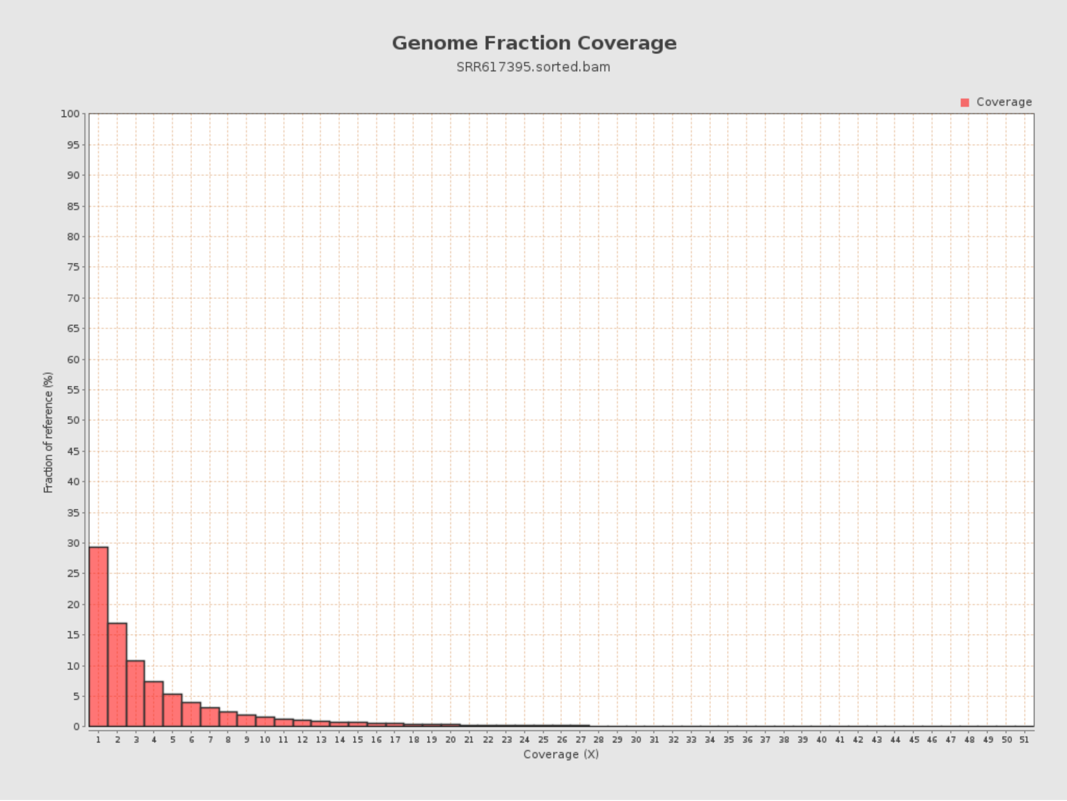
4. Results : Coverage Histogram



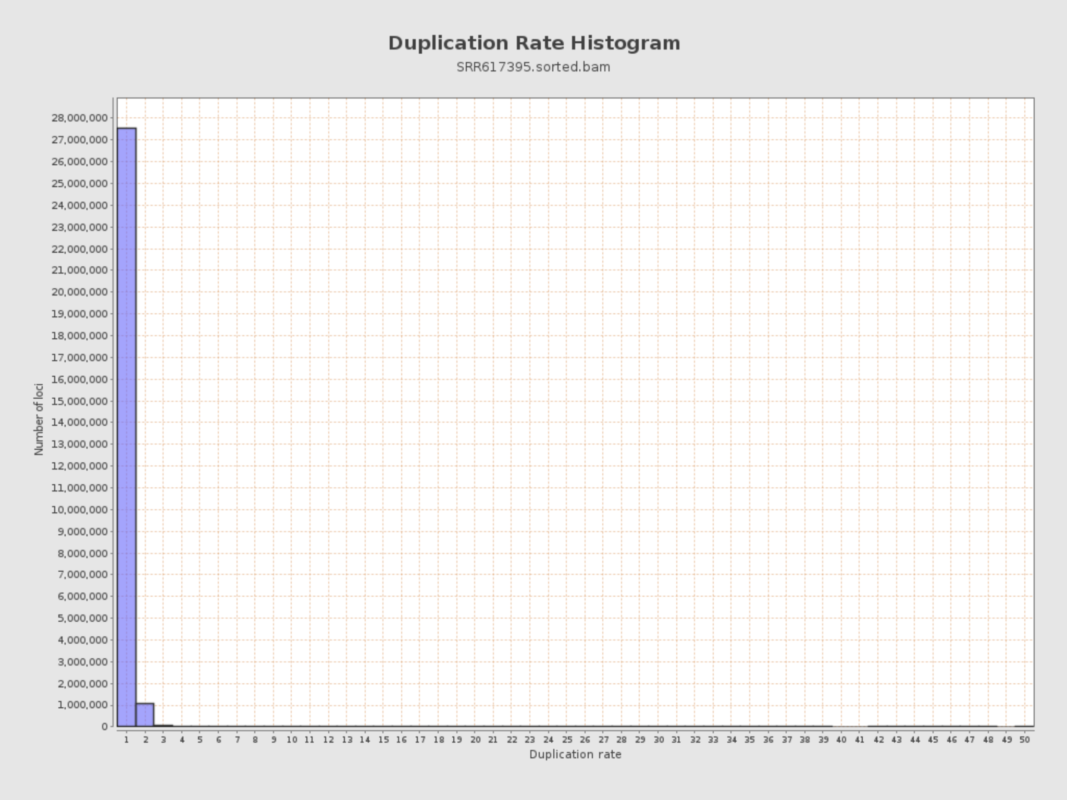
5. Results : Coverage Histogram (0-50X)



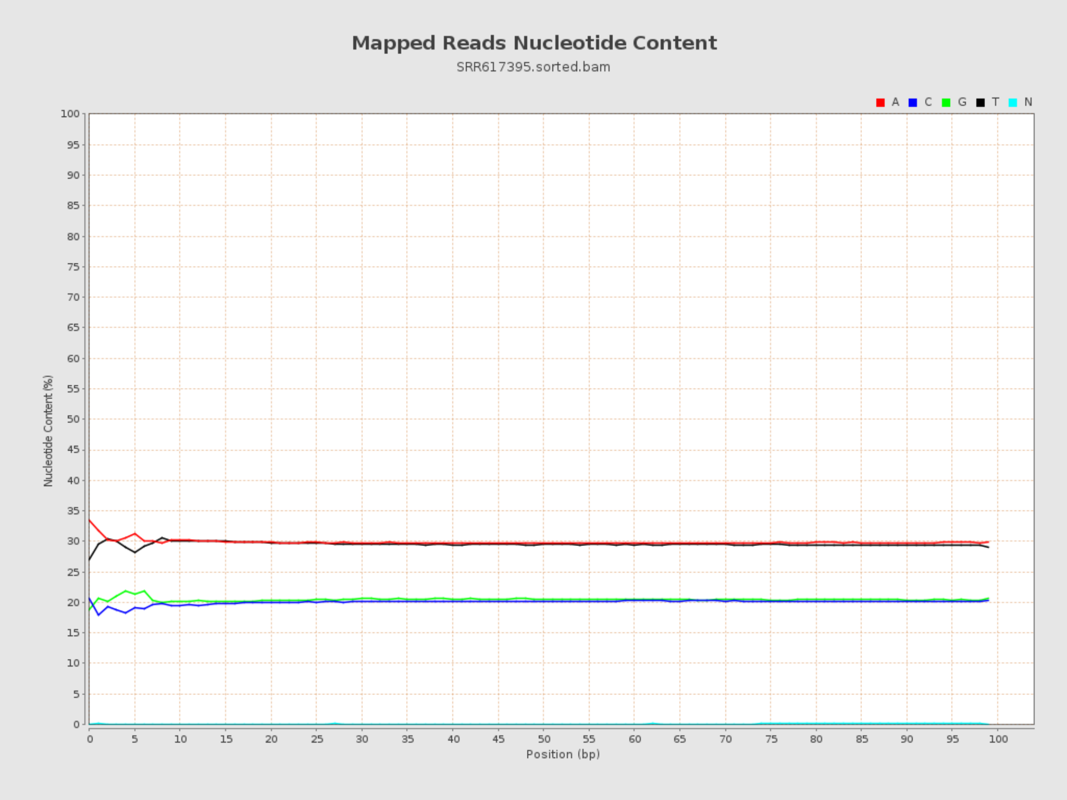
6. Results : Genome Fraction Coverage



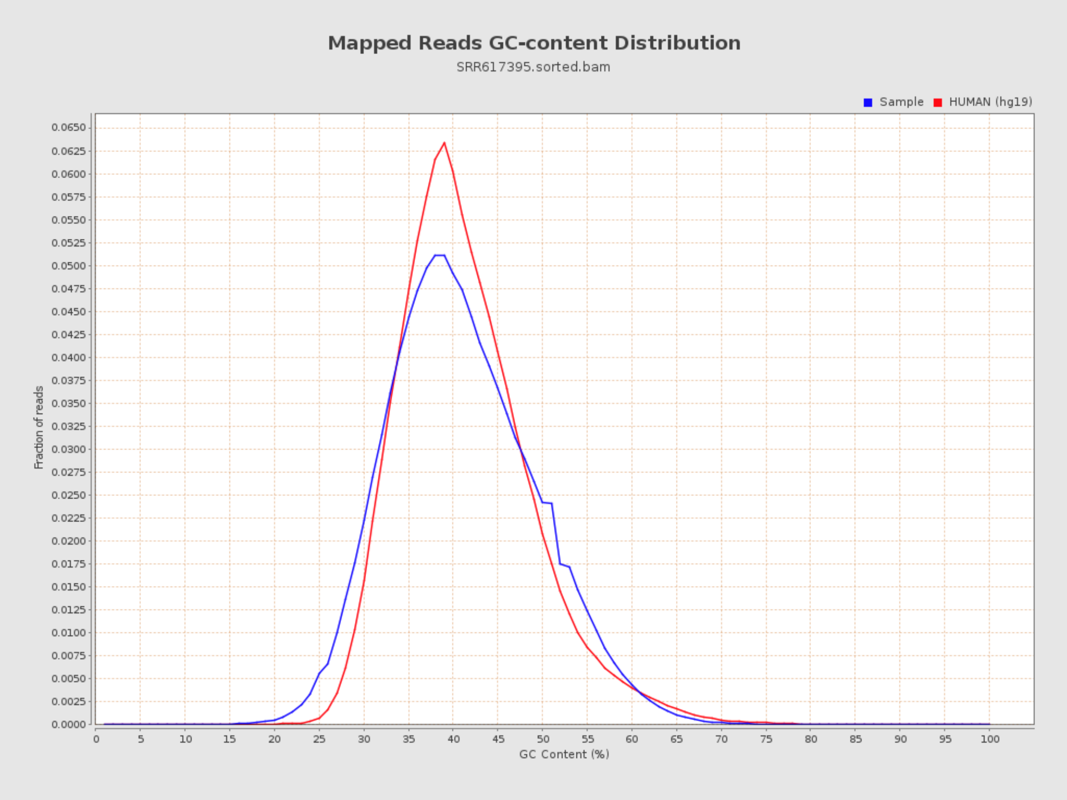
7. Results : Duplication Rate Histogram



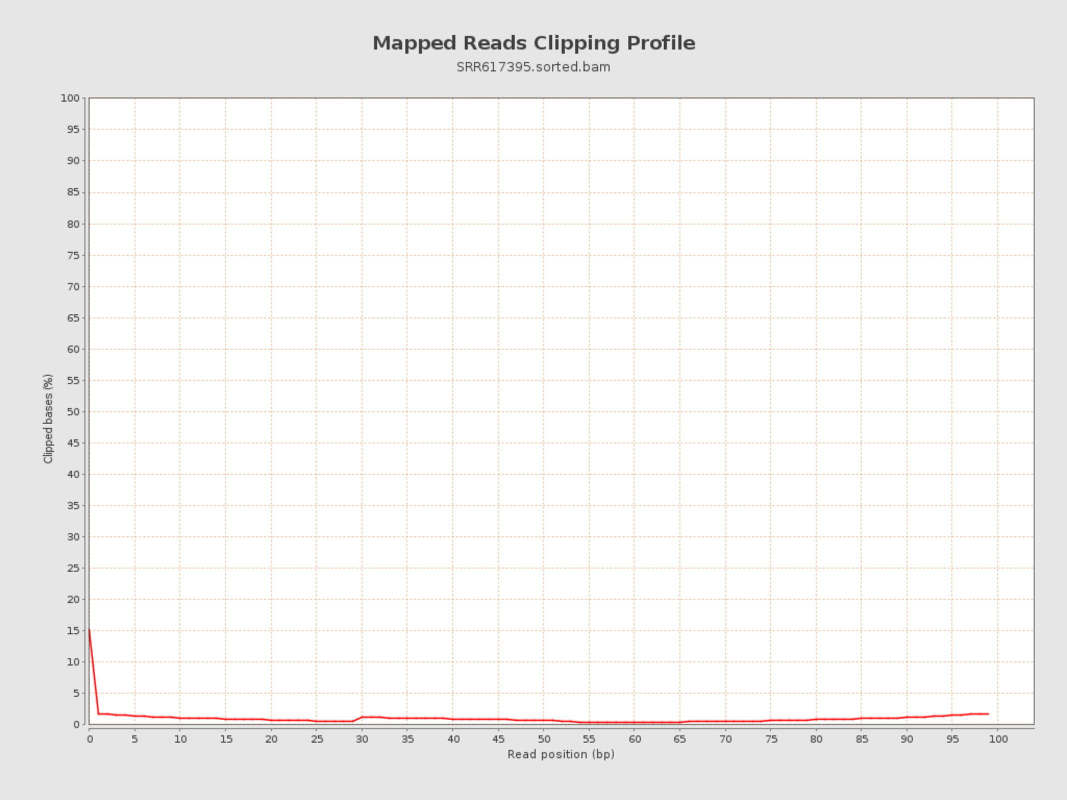
8. Results : Mapped Reads Nucleotide Content



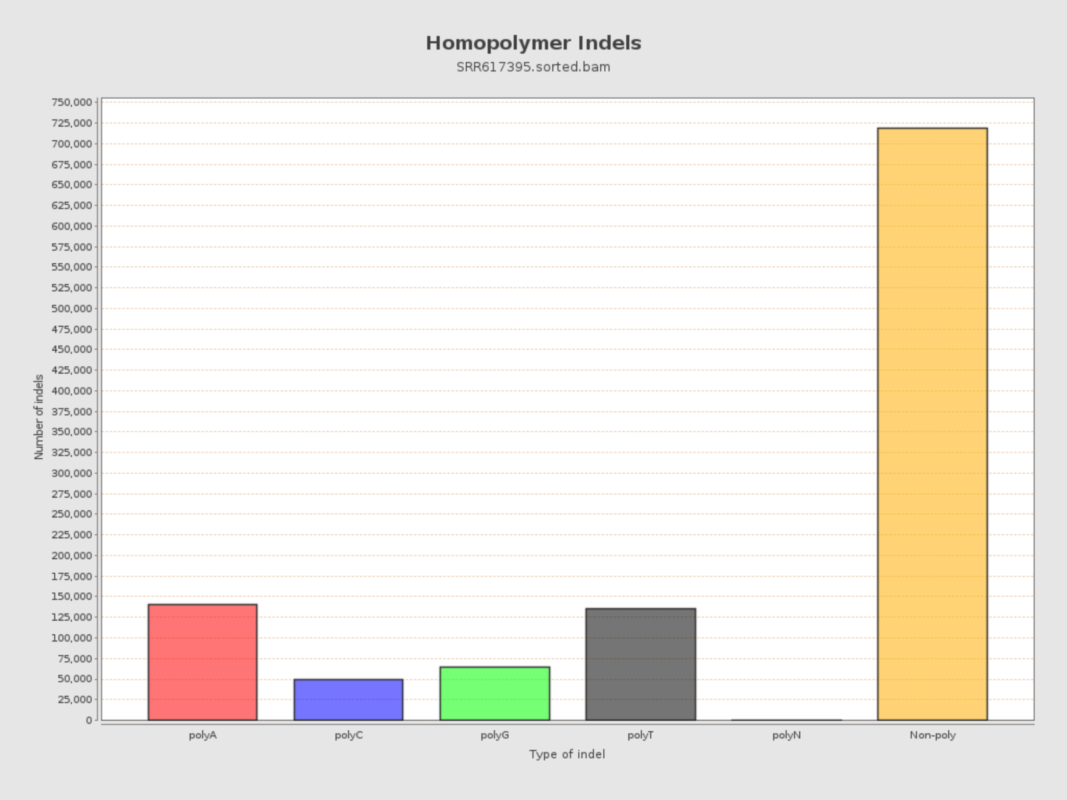
9. Results : Mapped Reads GC-content Distribution



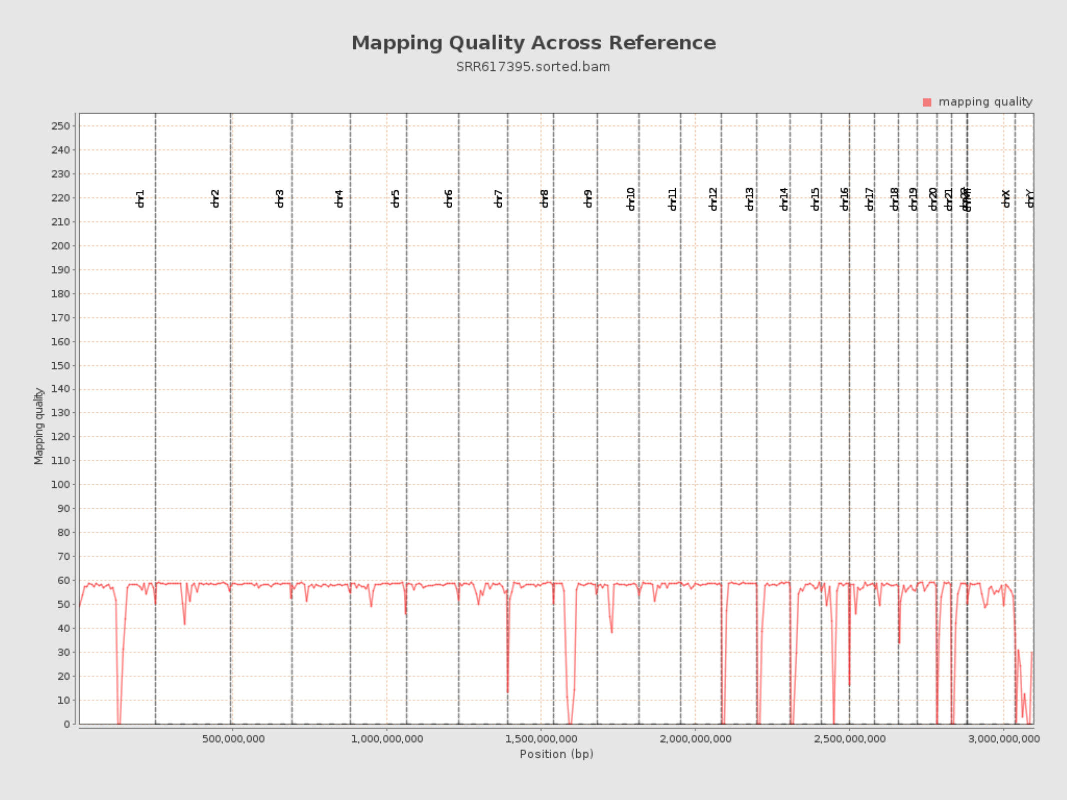
10. Results : Mapped Reads Clipping Profile



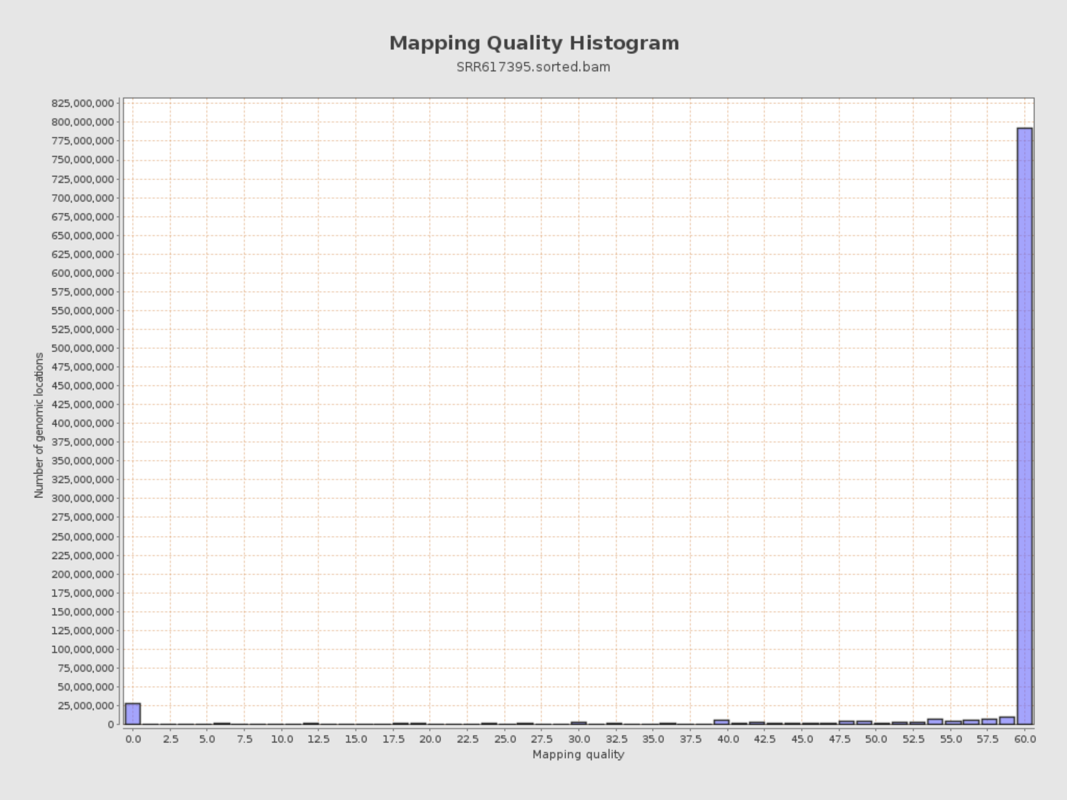
11. Results : Homopolymer Indels



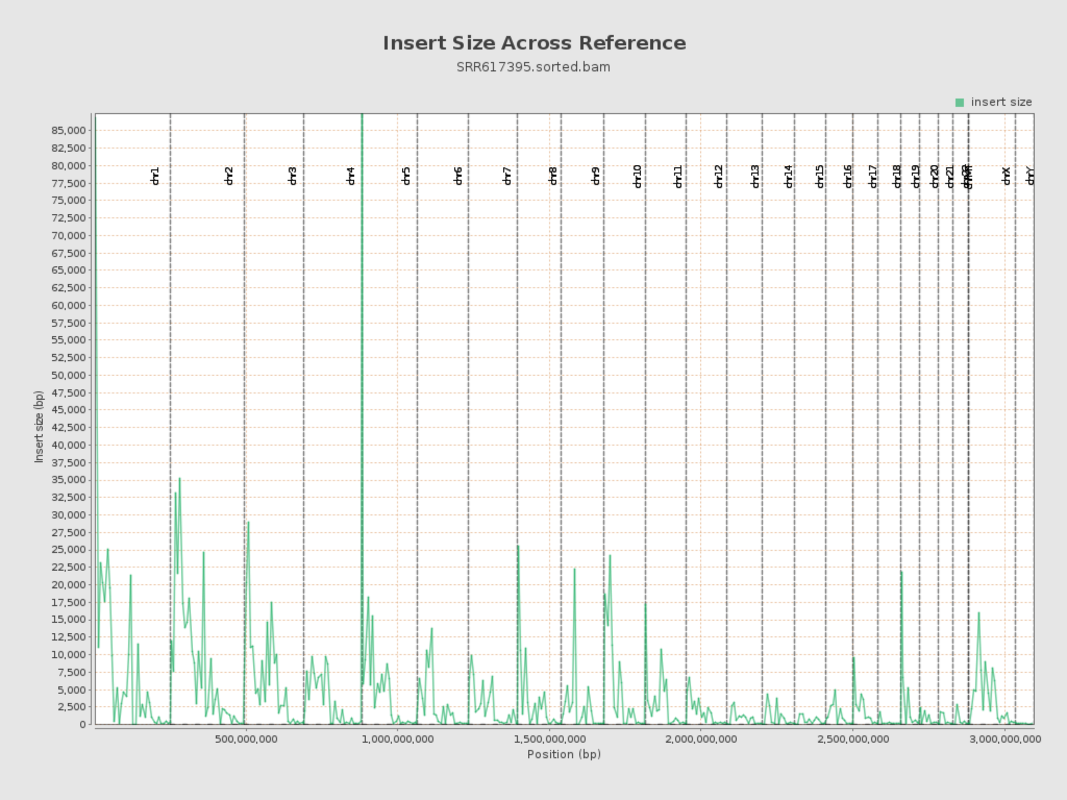
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram