Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 12:41:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038395.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_SRR5038395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038395_1.fastq.gz SRR5038395_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 12:41:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,873,080
Mapped reads	12,592,388 / 97.82%
Unmapped reads	280,692 / 2.18%
Mapped paired reads	12,592,388 / 97.82%
Mapped reads, first in pair	6,348,643 / 49.32%
Mapped reads, second in pair	6,243,745 / 48.5%
Mapped reads, both in pair	12,468,872 / 96.86%
Mapped reads, singletons	123,516 / 0.96%
Secondary alignments	0
Supplementary alignments	255,525 / 1.98%
Read min/max/mean length	30 / 150 / 151.03
Duplicated reads (estimated)	2,180,550 / 16.94%
Duplication rate	9.61%
Clipped reads	2,854,261 / 22.17%

2.2. ACGT Content

Number/percentage of A's	544,078,927 / 30.12%
Number/percentage of C's	354,045,871 / 19.6%
Number/percentage of T's	544,347,030 / 30.14%
Number/percentage of G's	363,818,813 / 20.14%
Number/percentage of N's	37,812 / 0%

GC Percentage	39.74%

2.3. Coverage

Mean	0.584
Standard Deviation	11.2618

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	76,243.88
Standard Deviation	2,518,233.89
P25/Median/P75	212 / 260 / 320

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	26,050,732
Insertions	374,880
Mapped reads with at least one insertion	2.79%
Deletions	670,719
Mapped reads with at least one deletion	5.11%
Homopolymer indels	46.83%

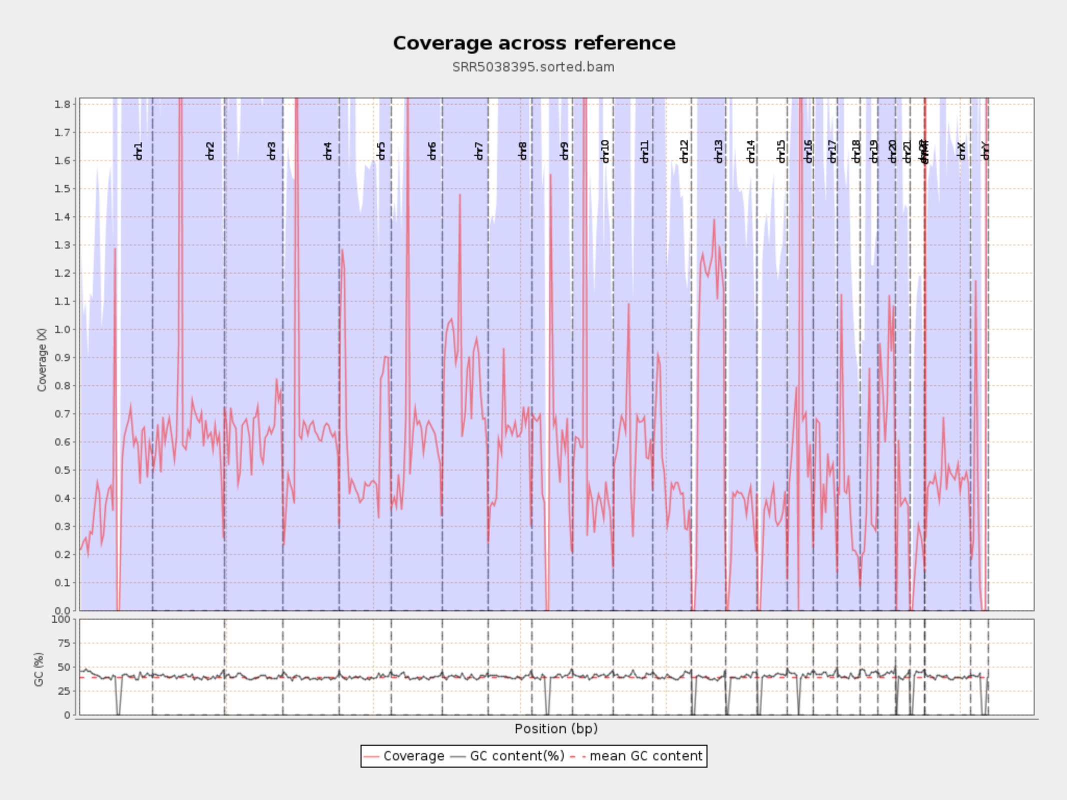
2.7. Chromosome stats

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

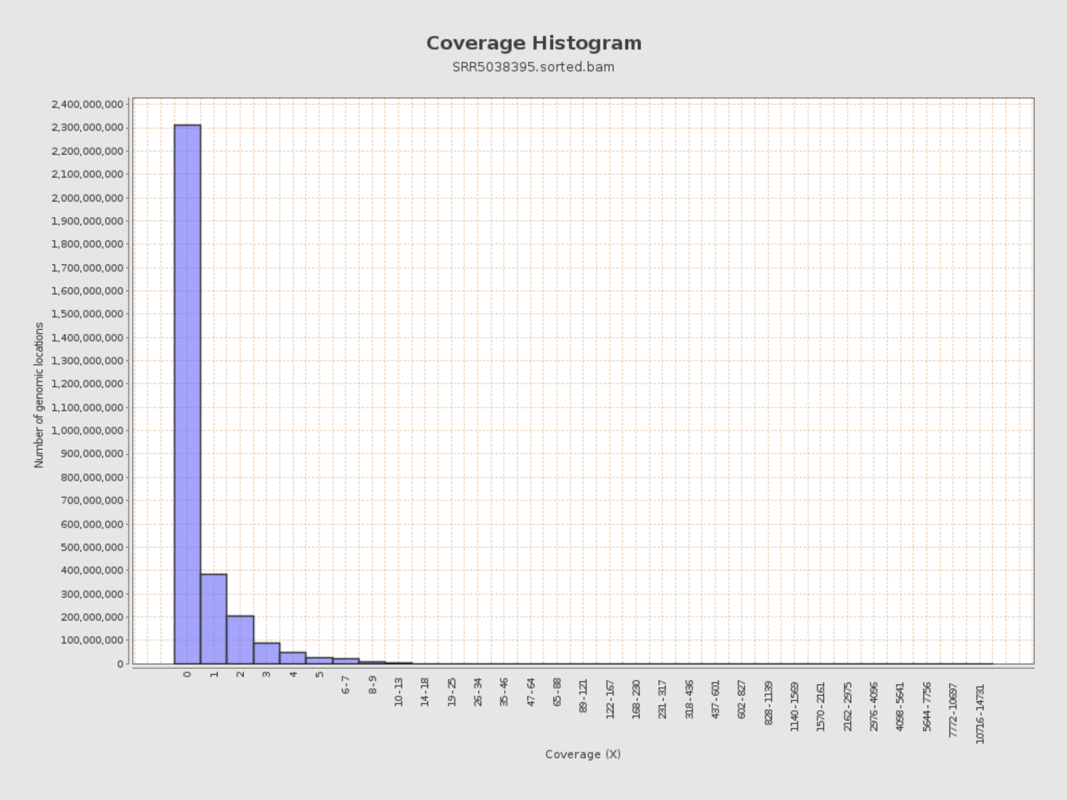
		bases	coverage	deviation
chr1	249250621	113160167	0.454	15.1347
chr2	243199373	170772231	0.7022	13.7471
chr3	198022430	126663030	0.6396	1.4294
chr4	191154276	124345561	0.6505	13.1758
chr5	180915260	110937006	0.6132	1.4847
chr6	171115067	106485191	0.6223	13.2075
chr7	159138663	137255026	0.8625	11.9521
chr8	146364022	86200946	0.5889	3.0795
chr9	141213431	77398069	0.5481	19.1392
chr10	135534747	82890756	0.6116	22.8864
chr11	135006516	81538340	0.604	7.0169
chr12	133851895	64745181	0.4837	1.2275
chr13	115169878	114235609	0.9919	1.8021
chr14	107349540	34462035	0.321	1.1347
chr15	102531392	30558427	0.298	0.8764
chr16	90354753	66014572	0.7306	15.5807
chr17	81195210	37251311	0.4588	5.6243
chr18	78077248	31666812	0.4056	14.2028
chr19	59128983	20390983	0.3449	8.4708
chr20	63025520	52132729	0.8272	4.0332
chr21	48129895	17273353	0.3589	5.7294
chr22	51304566	8420269	0.1641	0.7282
chrMT	16571	2417062	145.861	88.5249
chrX	155270560	72087197	0.4643	2.1321

chrY	59373566	38440237	0.6474	19.7047

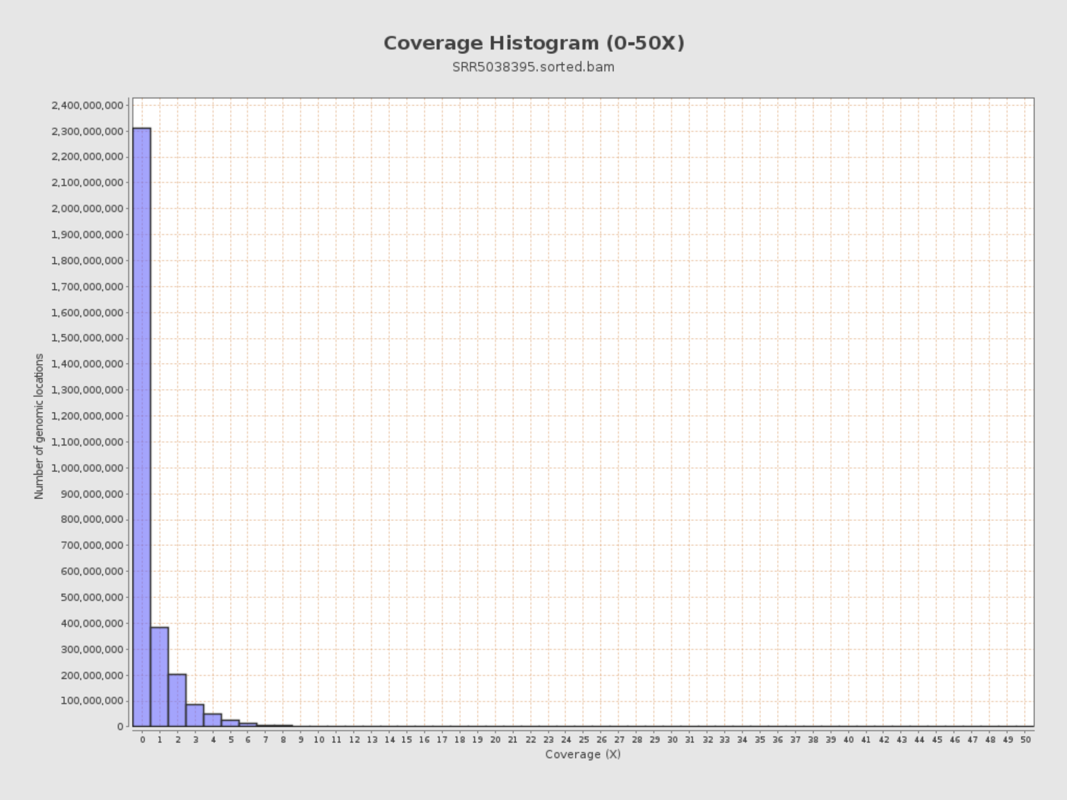
3. Results : Coverage across reference



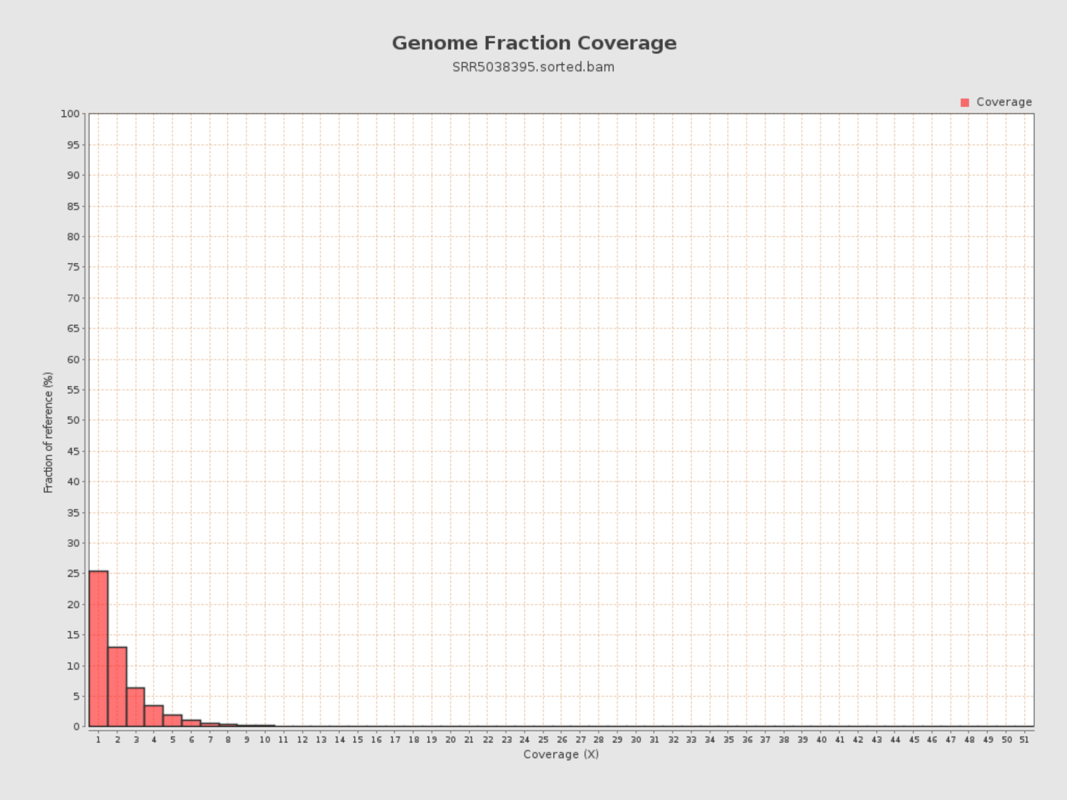
4. Results : Coverage Histogram



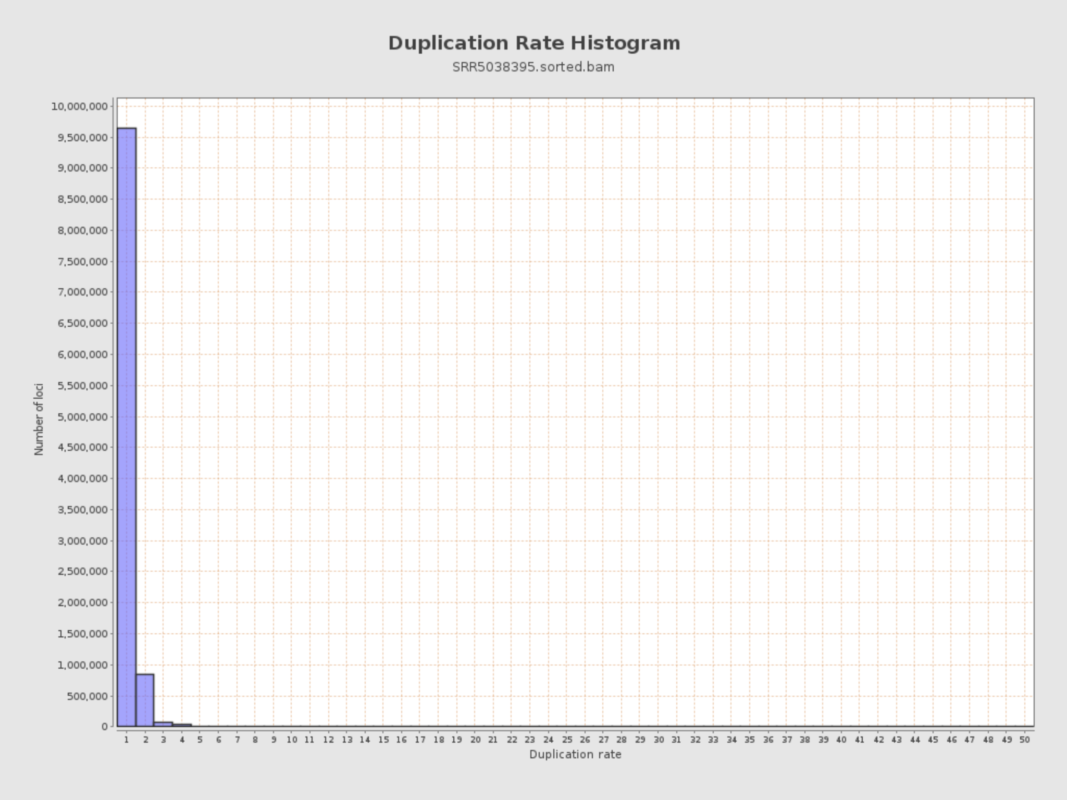
5. Results : Coverage Histogram (0-50X)



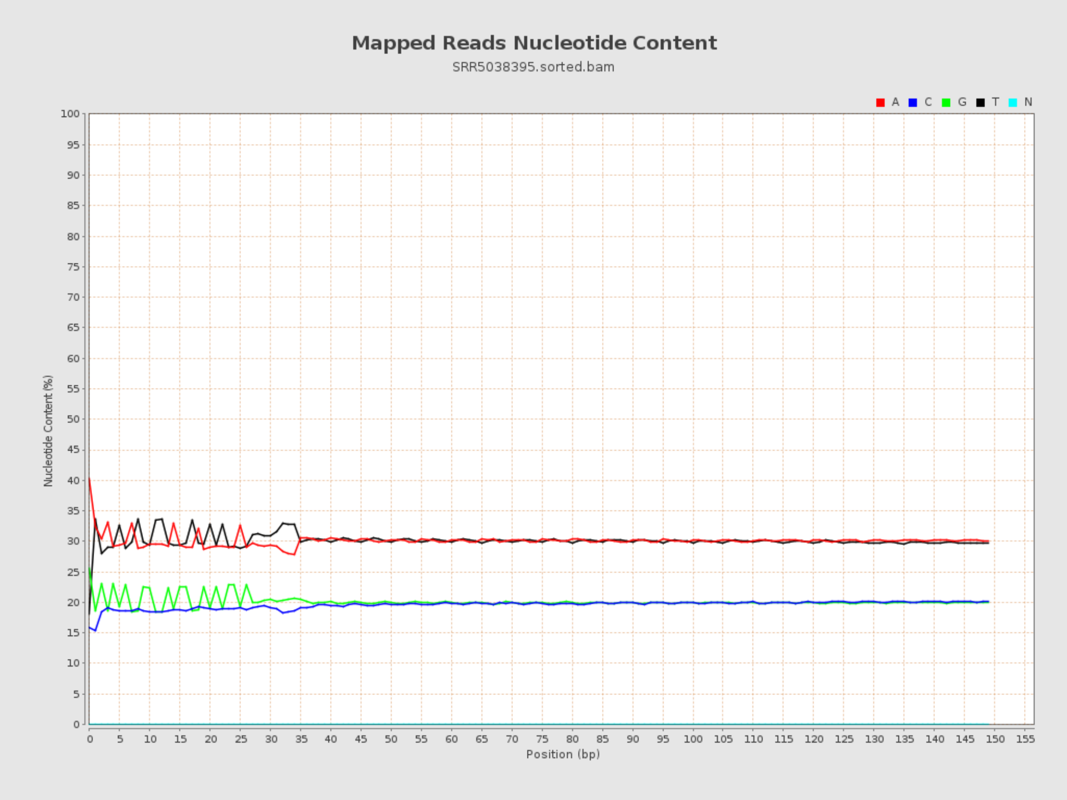
6. Results : Genome Fraction Coverage



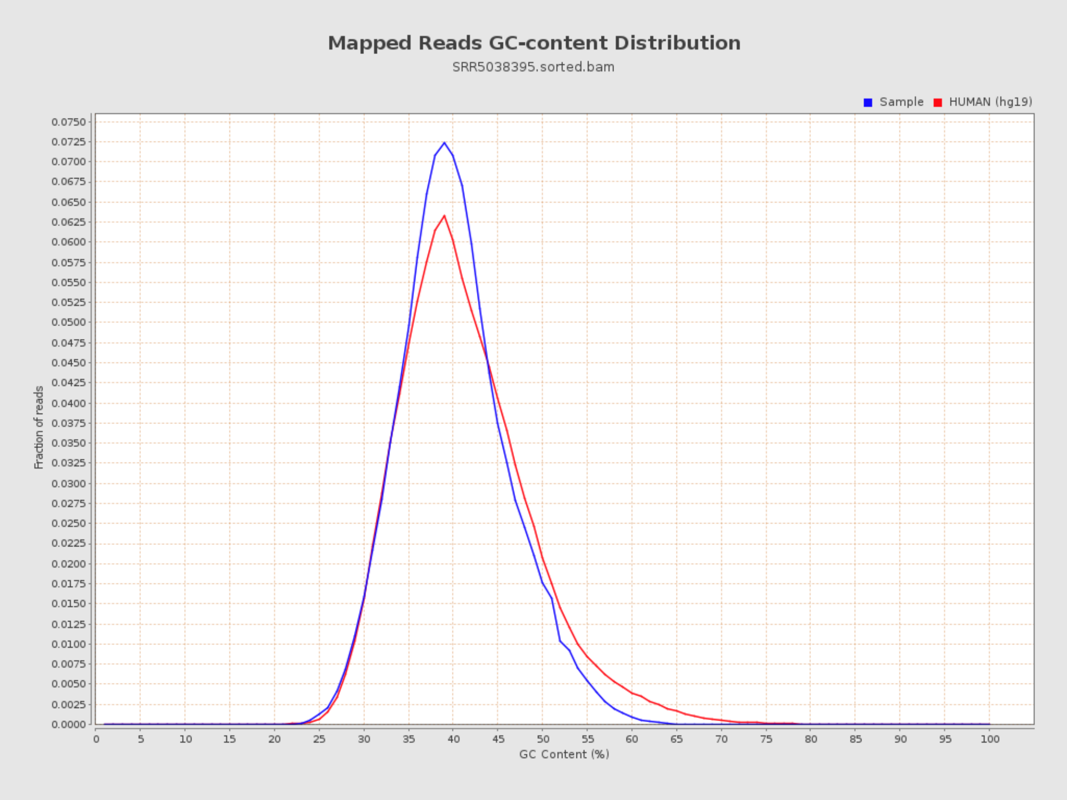
7. Results : Duplication Rate Histogram



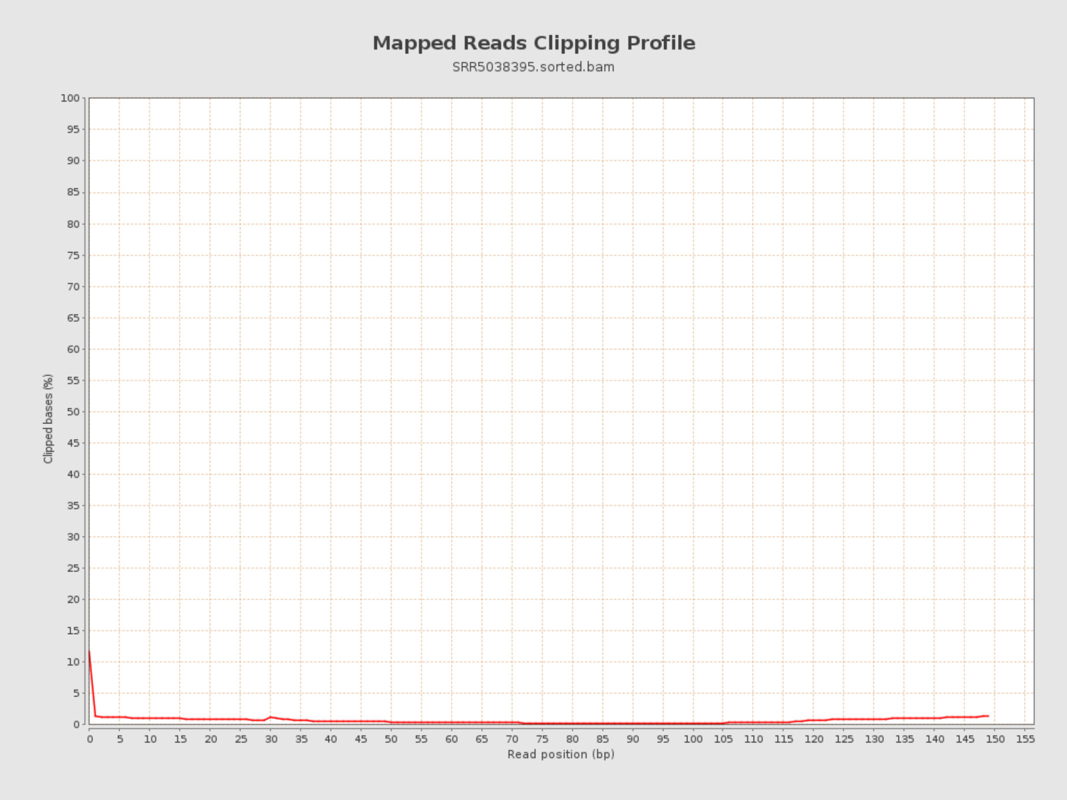
8. Results : Mapped Reads Nucleotide Content



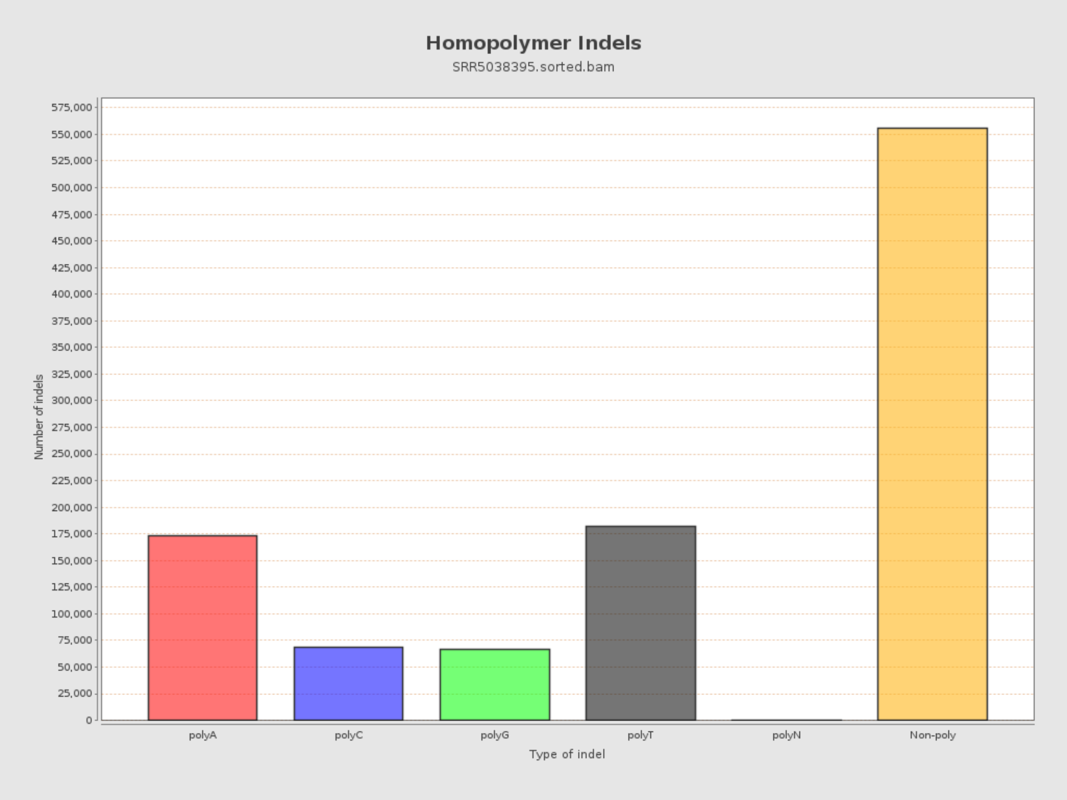
9. Results : Mapped Reads GC-content Distribution



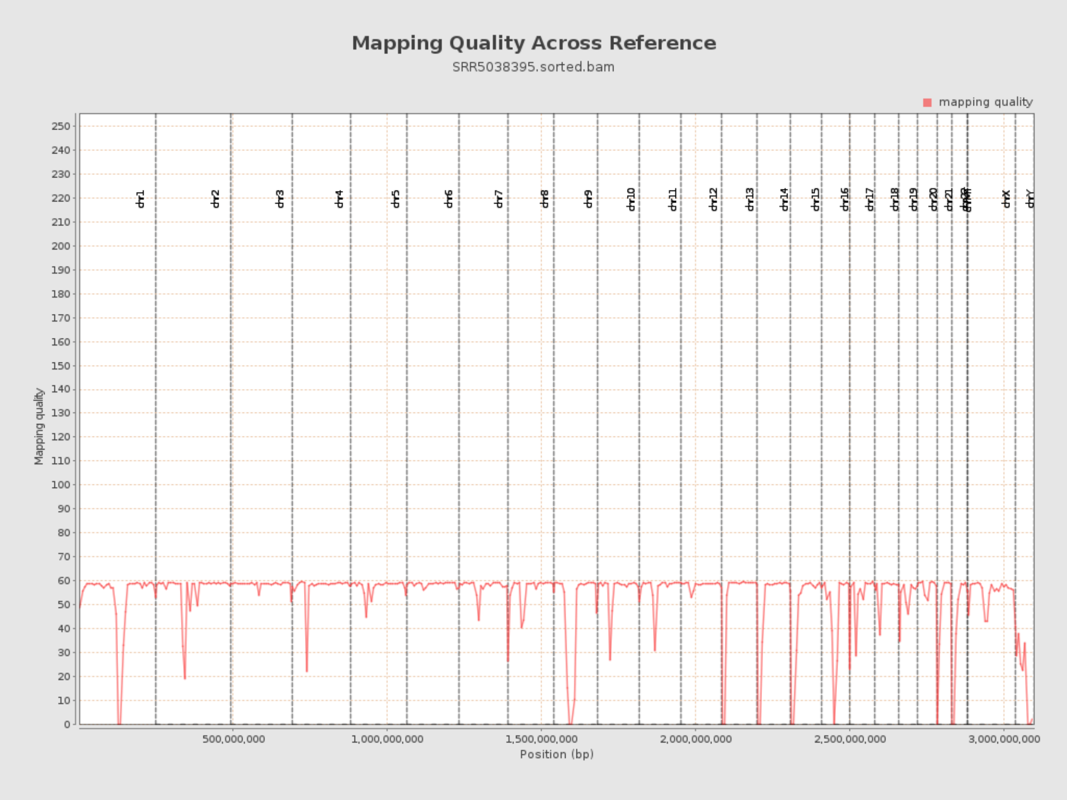
10. Results : Mapped Reads Clipping Profile



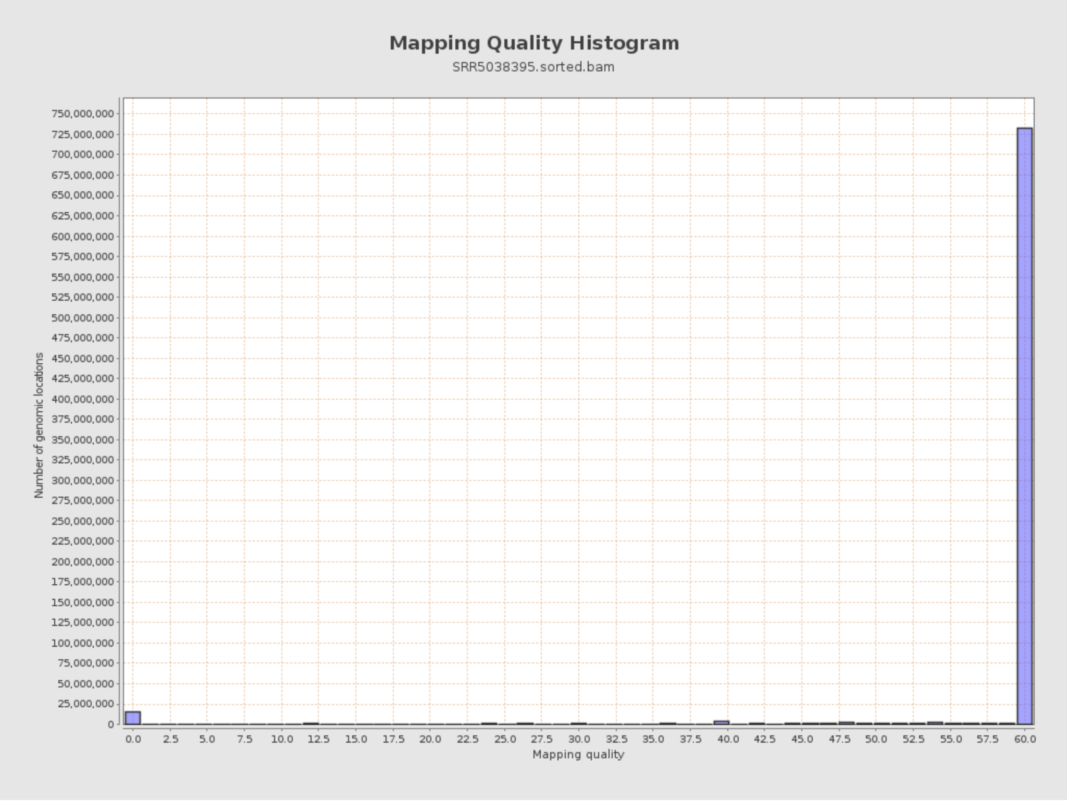
11. Results : Homopolymer Indels



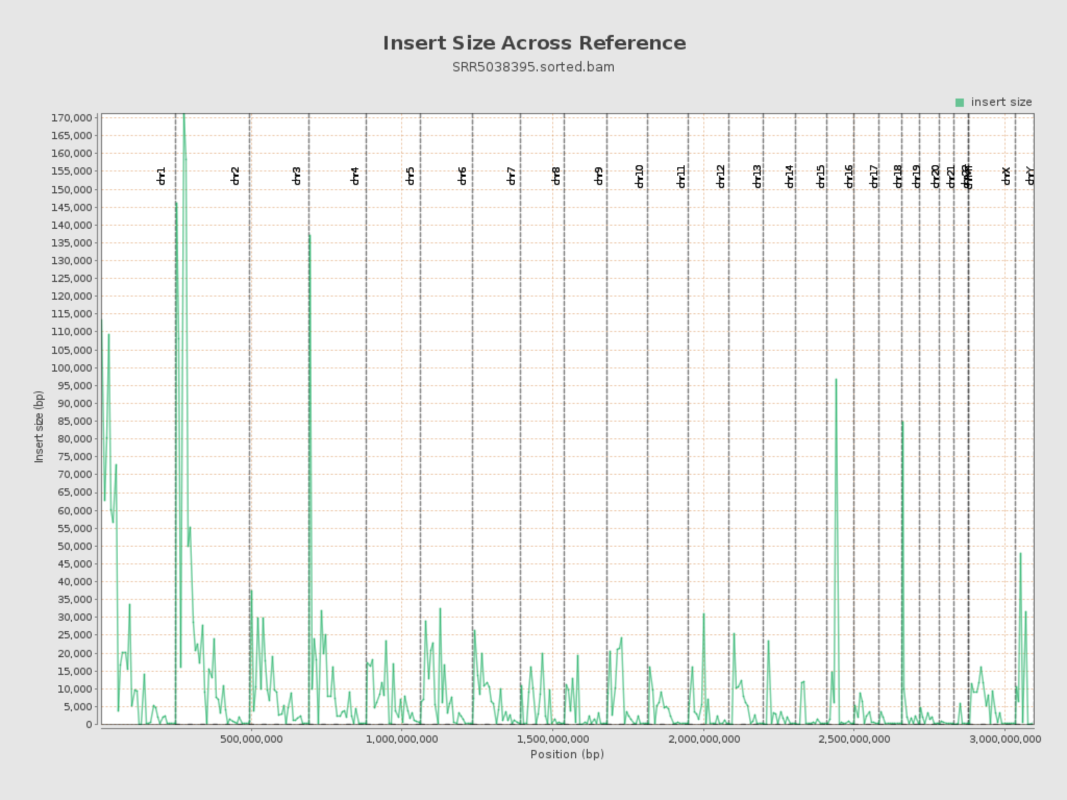
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram