Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 11:59:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038393.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_SRR5038393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038393_1.fastq.gz SRR5038393_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 11:59:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,514,274
Mapped reads	14,996,746 / 96.66%
Unmapped reads	517,528 / 3.34%
Mapped paired reads	14,996,746 / 96.66%
Mapped reads, first in pair	7,554,908 / 48.7%
Mapped reads, second in pair	7,441,838 / 47.97%
Mapped reads, both in pair	14,863,038 / 95.8%
Mapped reads, singletons	133,708 / 0.86%
Secondary alignments	0
Supplementary alignments	294,095 / 1.9%
Read min/max/mean length	30 / 150 / 150.99
Duplicated reads (estimated)	2,592,445 / 16.71%
Duplication rate	10.46%
Clipped reads	3,422,461 / 22.06%

2.2. ACGT Content

Number/percentage of A's	633,488,470 / 29.4%
Number/percentage of C's	439,626,954 / 20.4%
Number/percentage of T's	630,088,050 / 29.24%
Number/percentage of G's	451,393,366 / 20.95%
Number/percentage of N's	47,491 / 0%

GC Percentage	41.35%

2.3. Coverage

Mean	0.6965
Standard Deviation	12.7564

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	73,625.71
Standard Deviation	2,516,867.59
P25/Median/P75	196 / 240 / 296

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	29,422,480
Insertions	407,547
Mapped reads with at least one insertion	2.56%
Deletions	759,592
Mapped reads with at least one deletion	4.87%
Homopolymer indels	46.85%

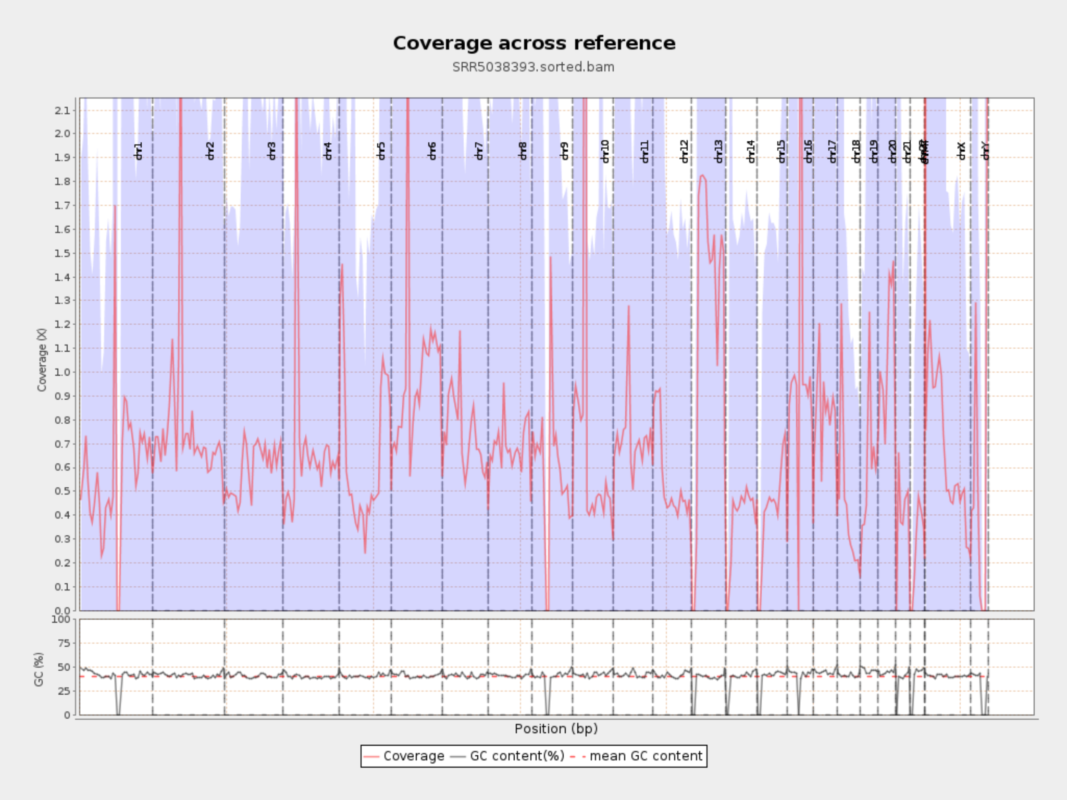
2.7. Chromosome stats

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

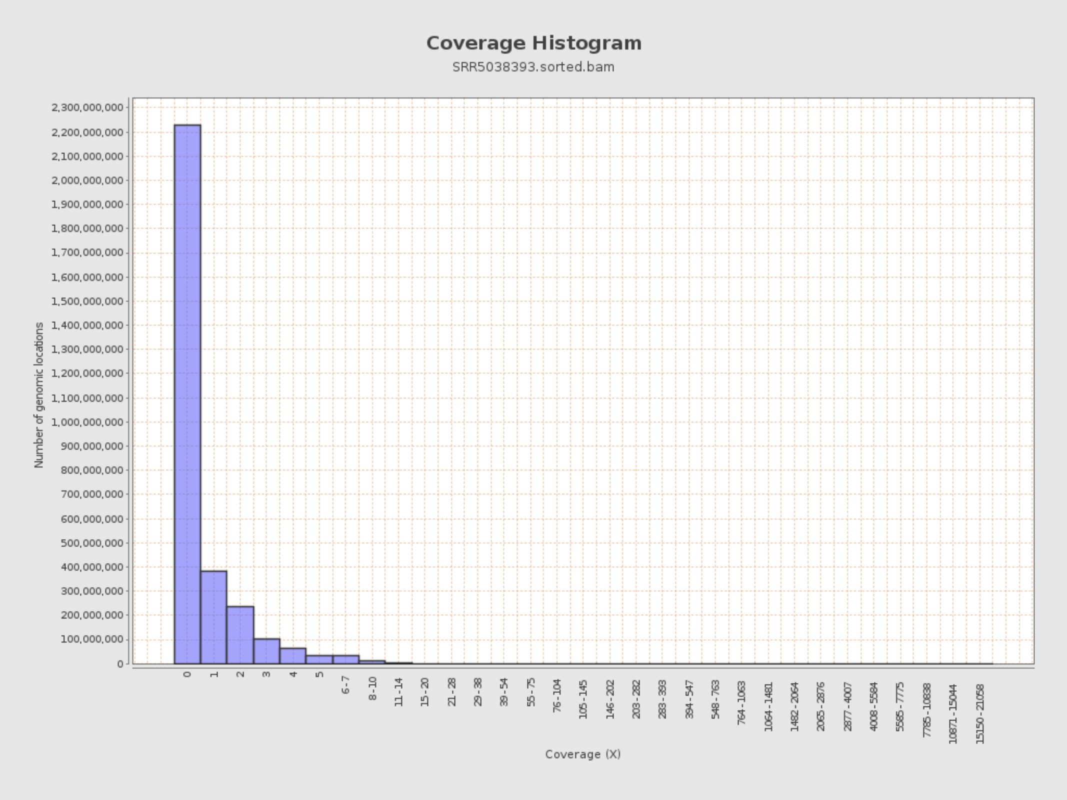
		bases	**coverage**	**deviation**
chr1	249250621	144716672	0.5806	21.0914
chr2	243199373	189091991	0.7775	11.2586
chr3	198022430	118568533	0.5988	1.4815
chr4	191154276	126776937	0.6632	11.8895
chr5	180915260	119273103	0.6593	1.5514
chr6	171115067	172515809	1.0082	19.9708
chr7	159138663	118455773	0.7444	8.8943
chr8	146364022	100738738	0.6883	2.9149
chr9	141213431	81810920	0.5793	17.3089
chr10	135534747	107064415	0.7899	28.331
chr11	135006516	96390112	0.714	9.8493
chr12	133851895	74571811	0.5571	1.3431
chr13	115169878	149032095	1.294	2.2427
chr14	107349540	40465136	0.3769	1.3664
chr15	102531392	43018343	0.4196	1.0802
chr16	90354753	93237959	1.0319	16.883
chr17	81195210	66911619	0.8241	11.714
chr18	78077248	33590408	0.4302	16.4721
chr19	59128983	34939575	0.5909	11.2179
chr20	63025520	67634134	1.0731	4.1873
chr21	48129895	19655443	0.4084	5.0976
chr22	51304566	13564651	0.2644	0.9051
chrMT	16571	1895741	114.4011	80.9253
chrX	155270560	104816320	0.6751	2.8097

chrY	59373566	37504473	0.6317	16.9938

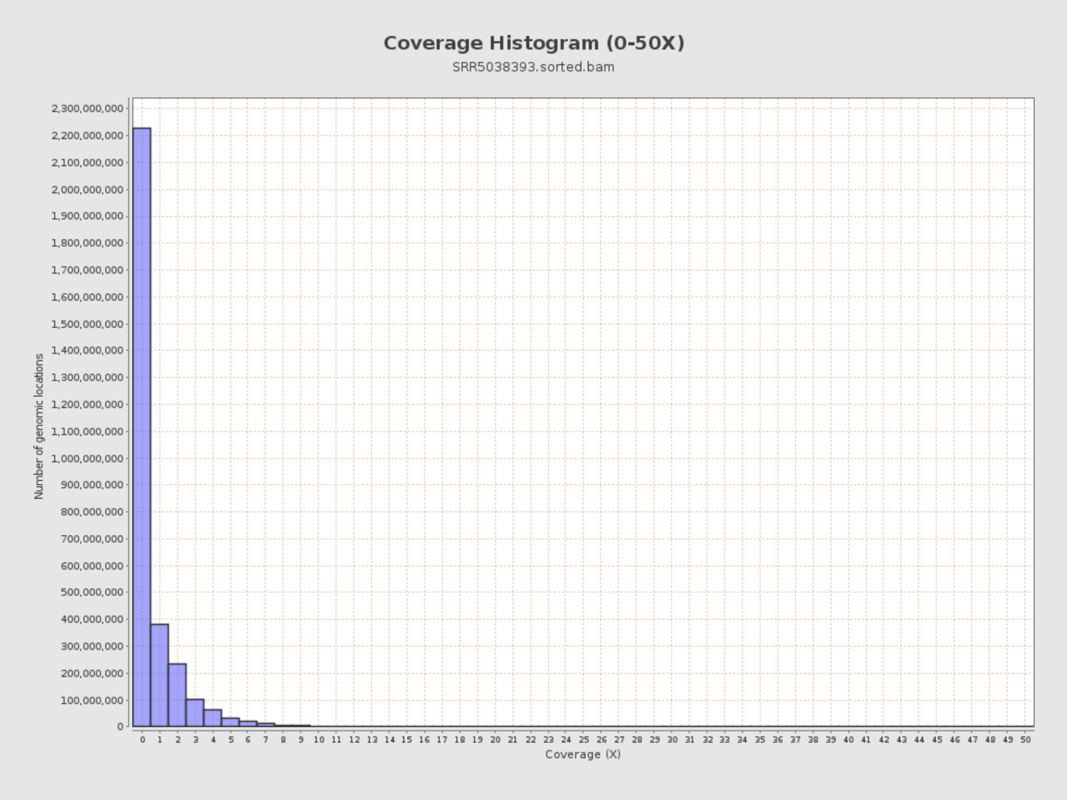
3. Results : Coverage across reference



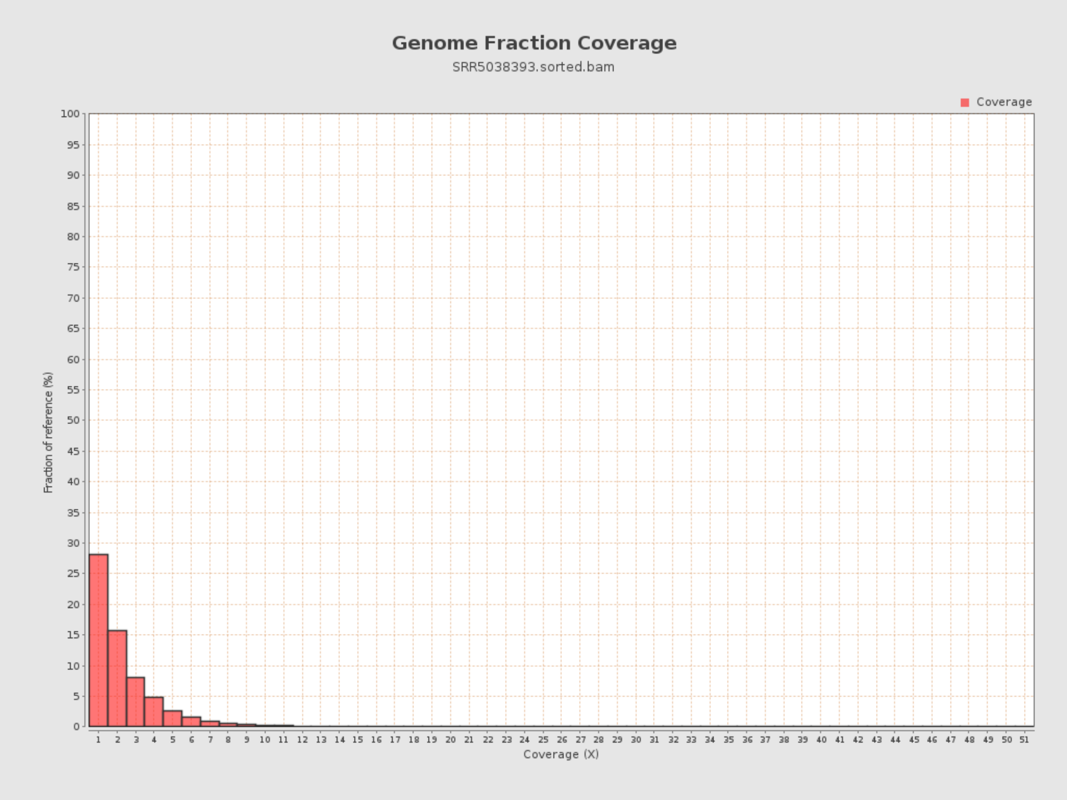
4. Results : Coverage Histogram



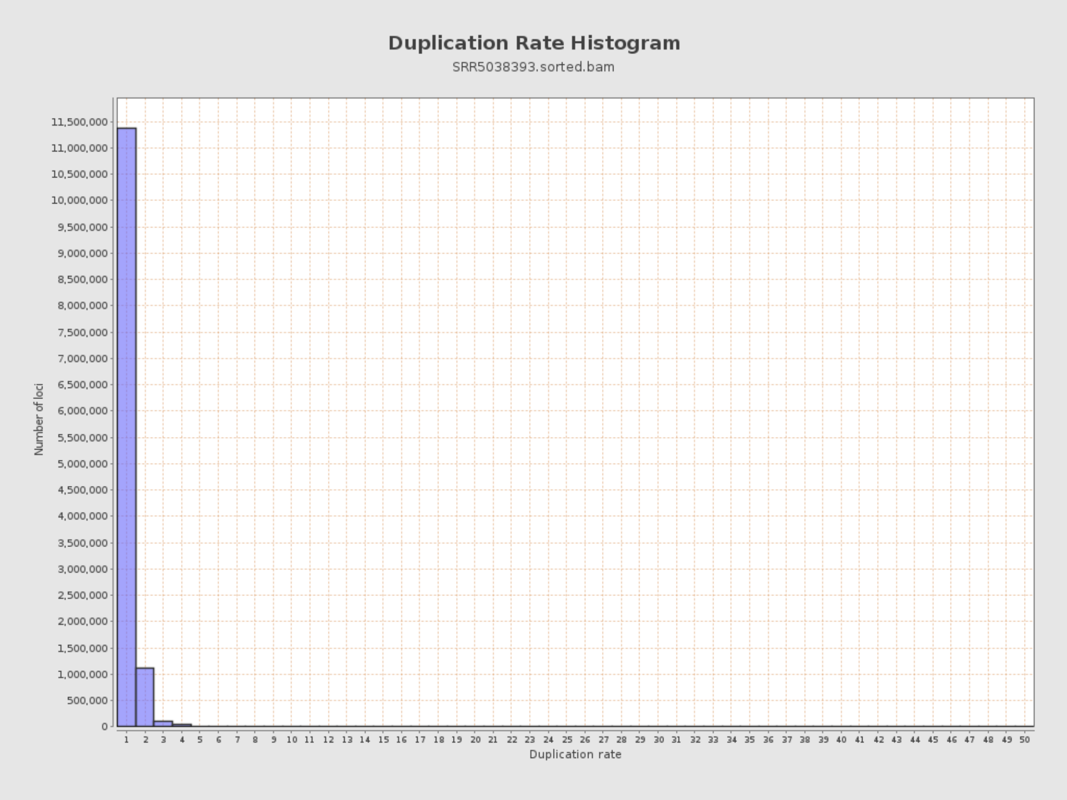
5. Results : Coverage Histogram (0-50X)



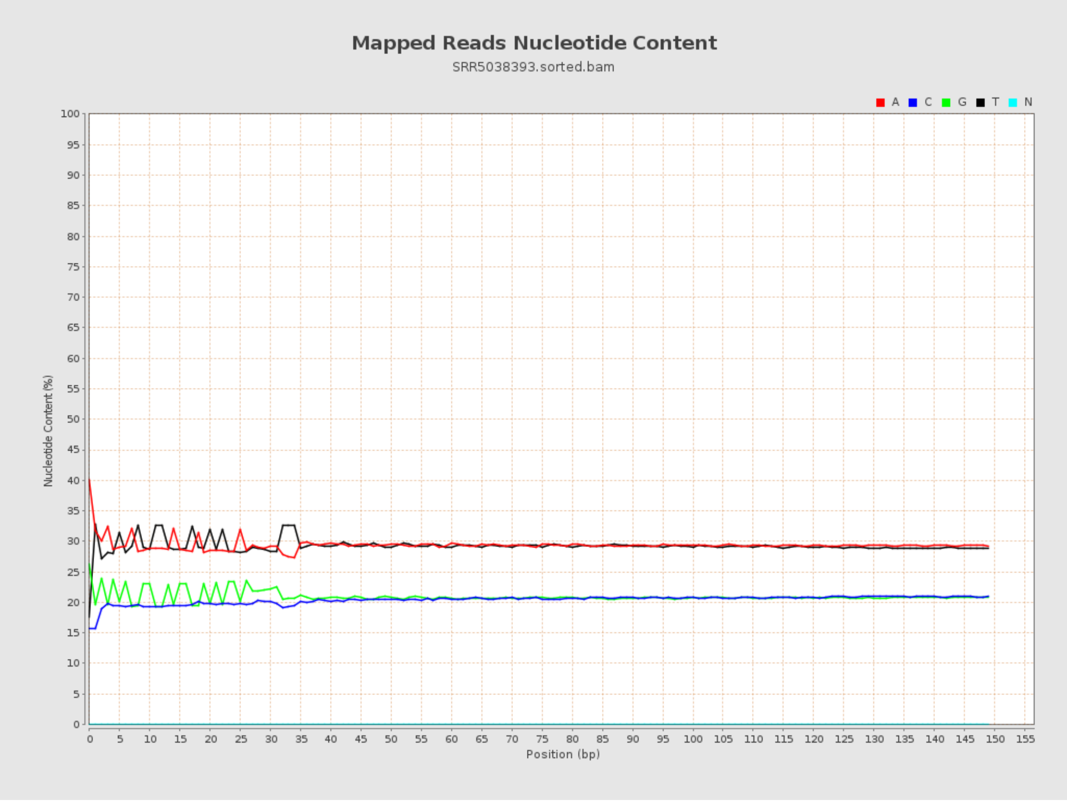
6. Results : Genome Fraction Coverage



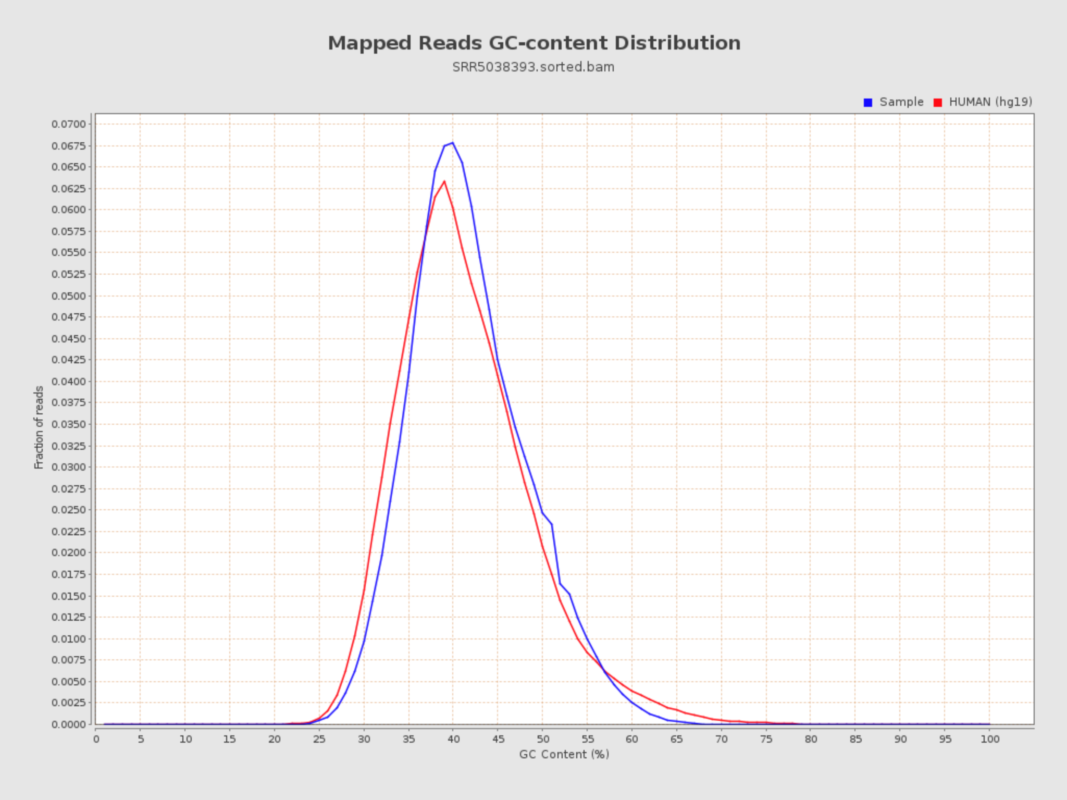
7. Results : Duplication Rate Histogram



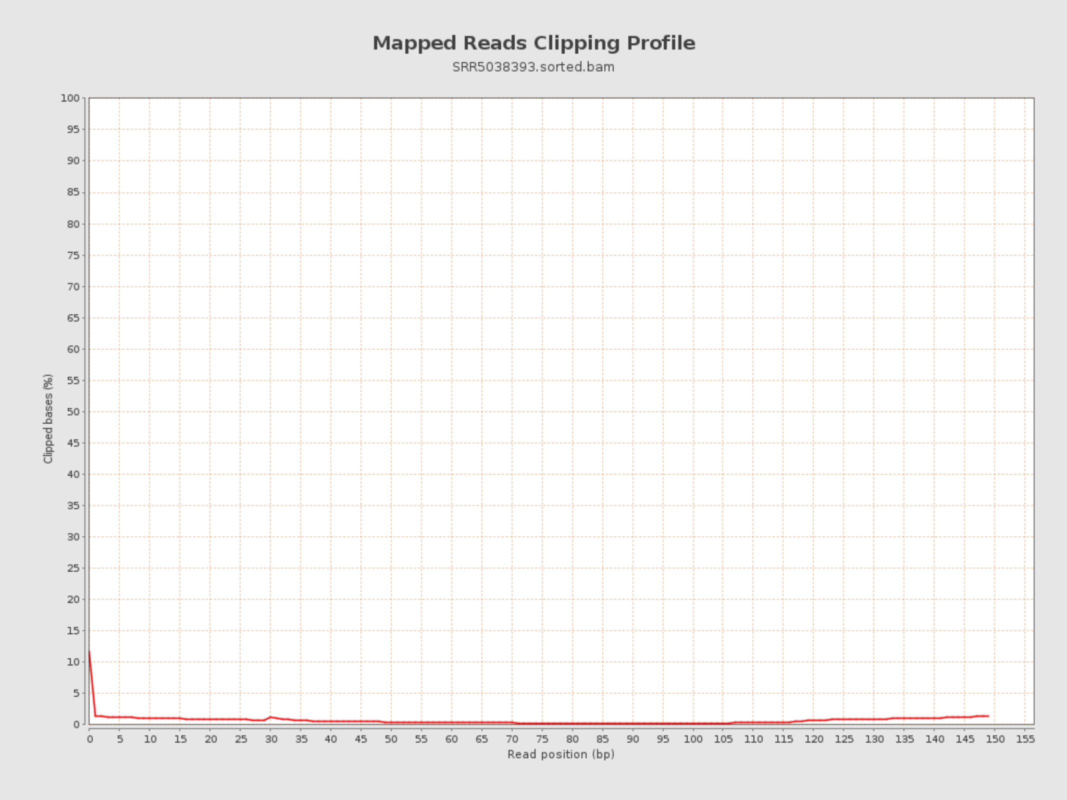
8. Results : Mapped Reads Nucleotide Content



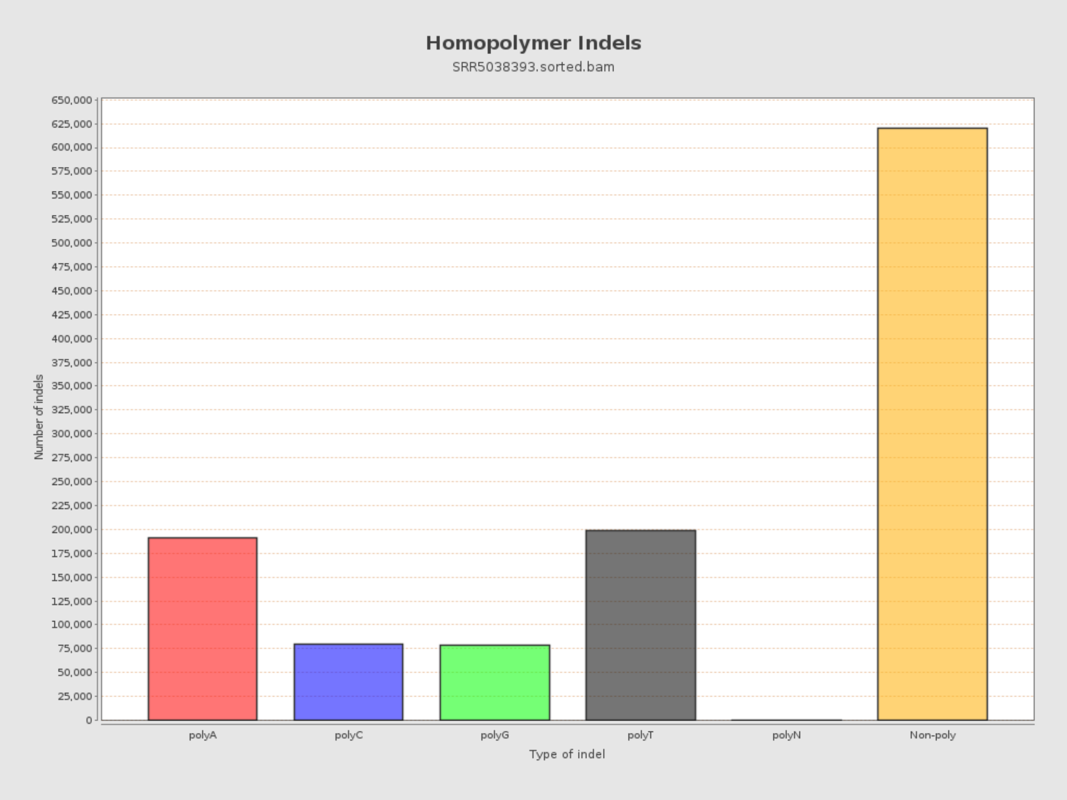
9. Results : Mapped Reads GC-content Distribution



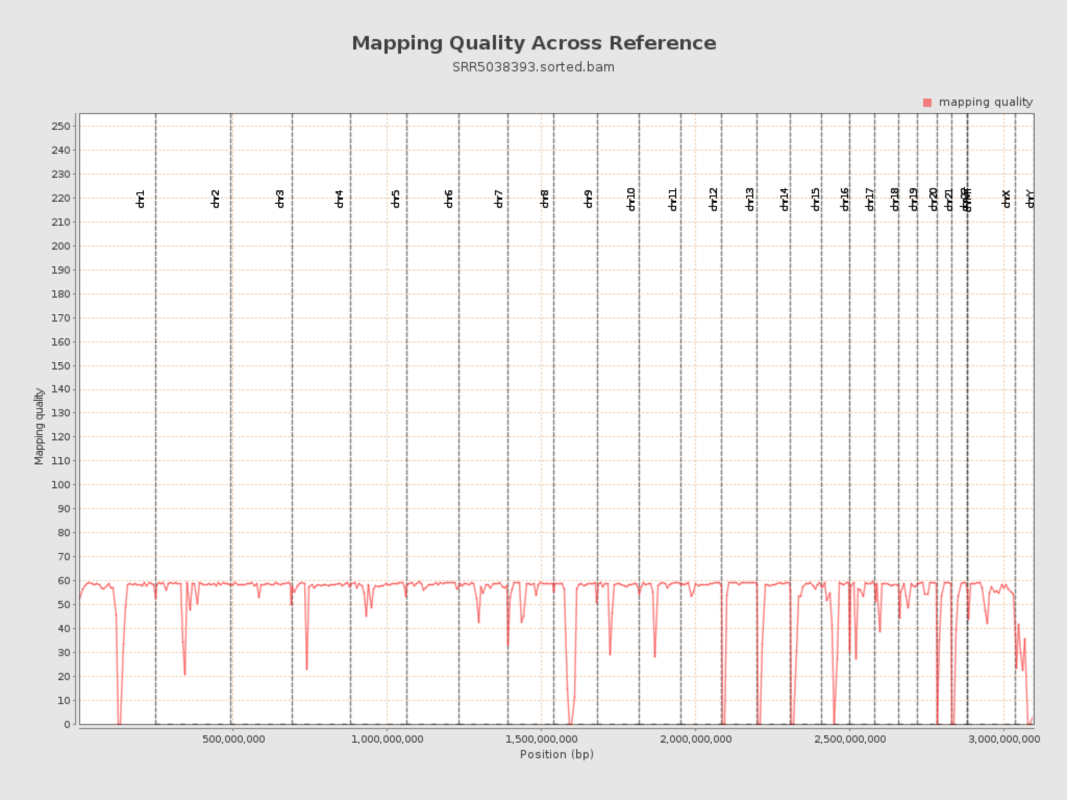
10. Results : Mapped Reads Clipping Profile



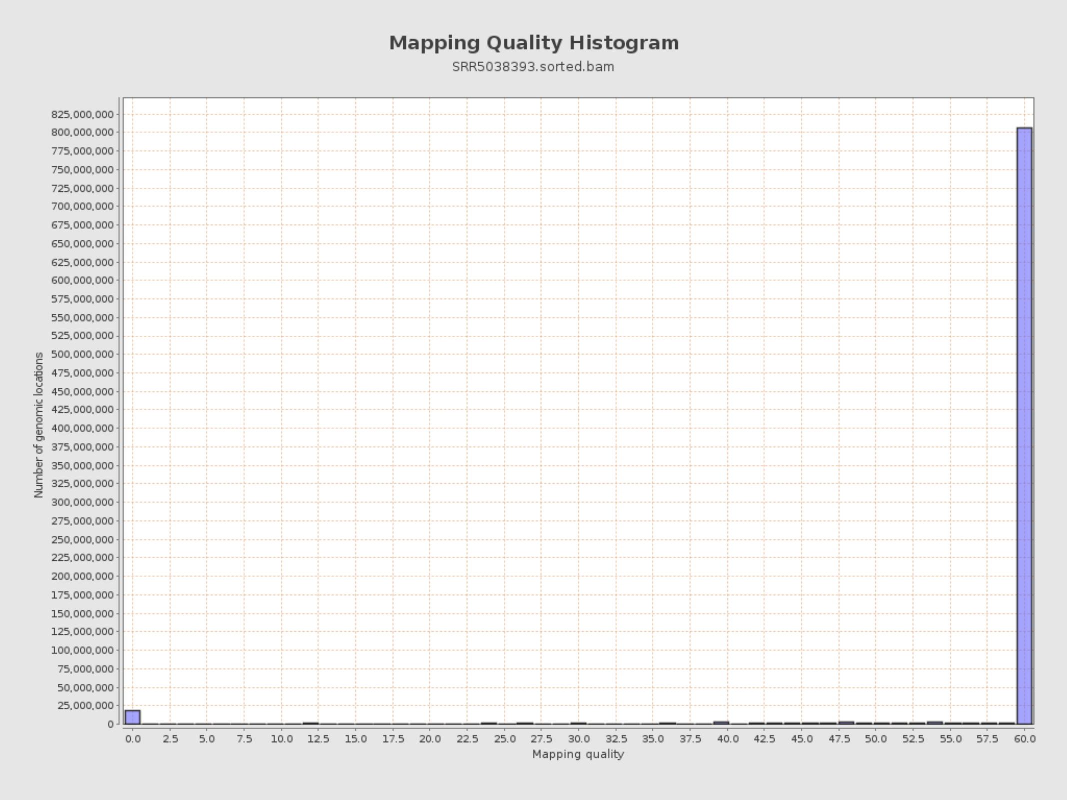
11. Results : Homopolymer Indels



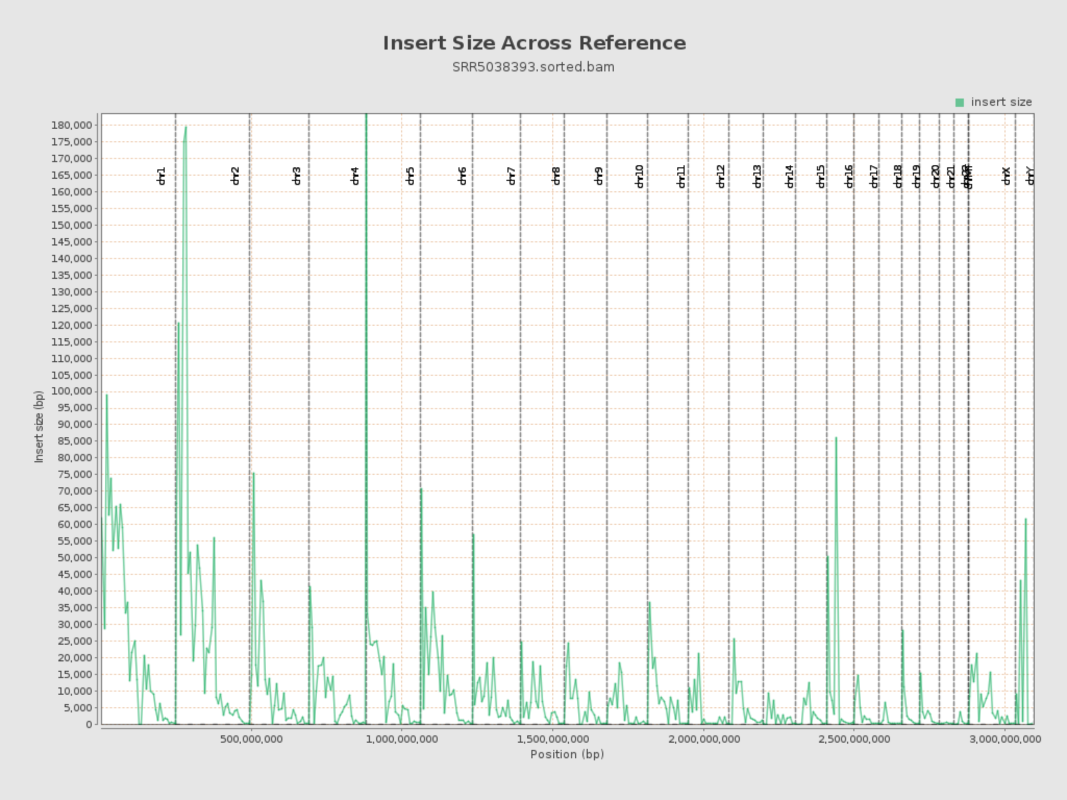
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram