Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 11:10:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038391.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_SRR5038391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038391_1.fastq.gz SRR5038391_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 11:10:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,020,924
Mapped reads	13,639,571 / 97.28%
Unmapped reads	381,353 / 2.72%
Mapped paired reads	13,639,571 / 97.28%
Mapped reads, first in pair	6,896,286 / 49.19%
Mapped reads, second in pair	6,743,285 / 48.09%
Mapped reads, both in pair	13,472,194 / 96.09%
Mapped reads, singletons	167,377 / 1.19%
Secondary alignments	0
Supplementary alignments	141,807 / 1.01%
Read min/max/mean length	30 / 150 / 150.52
Duplicated reads (estimated)	1,364,549 / 9.73%
Duplication rate	7.46%
Clipped reads	1,628,740 / 11.62%

2.2. ACGT Content

Number/percentage of A's	580,371,365 / 28.99%
Number/percentage of C's	424,357,430 / 21.2%
Number/percentage of T's	574,898,930 / 28.72%
Number/percentage of G's	422,160,828 / 21.09%
Number/percentage of N's	44,329 / 0%

GC Percentage	42.29%

2.3. Coverage

Mean	0.6469
Standard Deviation	6.203

2.4. Mapping Quality

Mean Mapping Quality	54.41

2.5. Insert size

Mean	93,133.35
Standard Deviation	3,014,112.67
P25/Median/P75	213 / 261 / 326

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	21,655,150
Insertions	241,492
Mapped reads with at least one insertion	1.67%
Deletions	257,360
Mapped reads with at least one deletion	1.81%
Homopolymer indels	44.4%

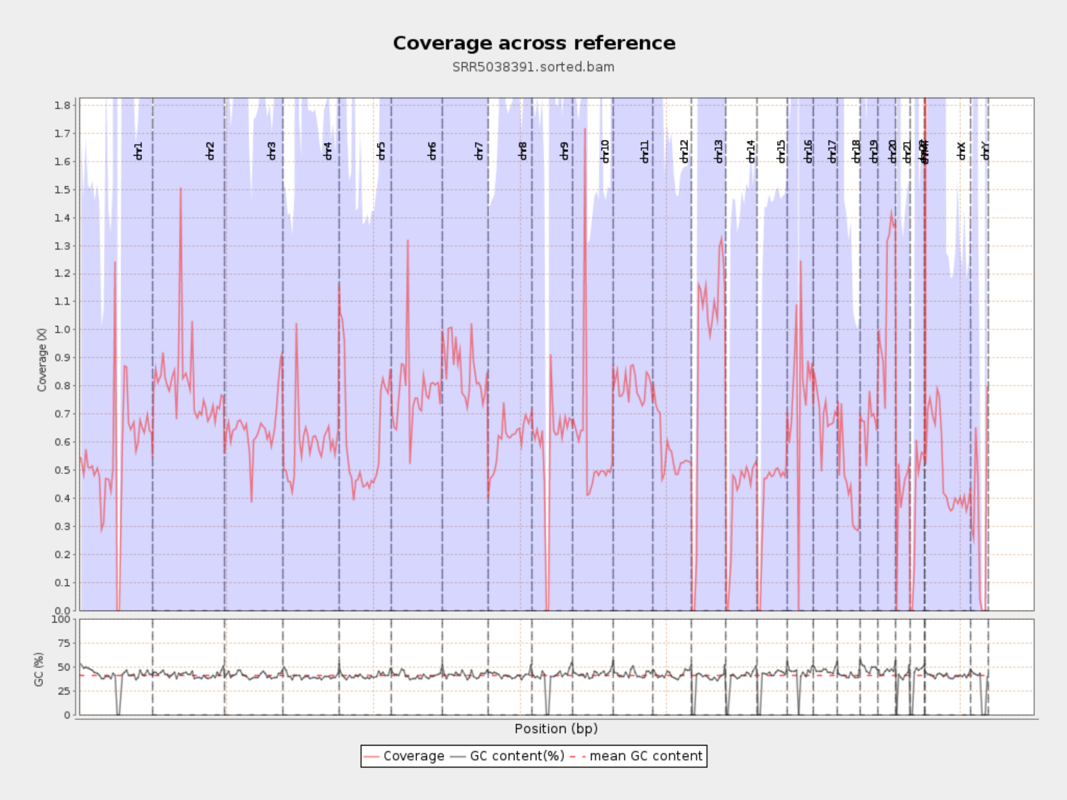
2.7. Chromosome stats

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

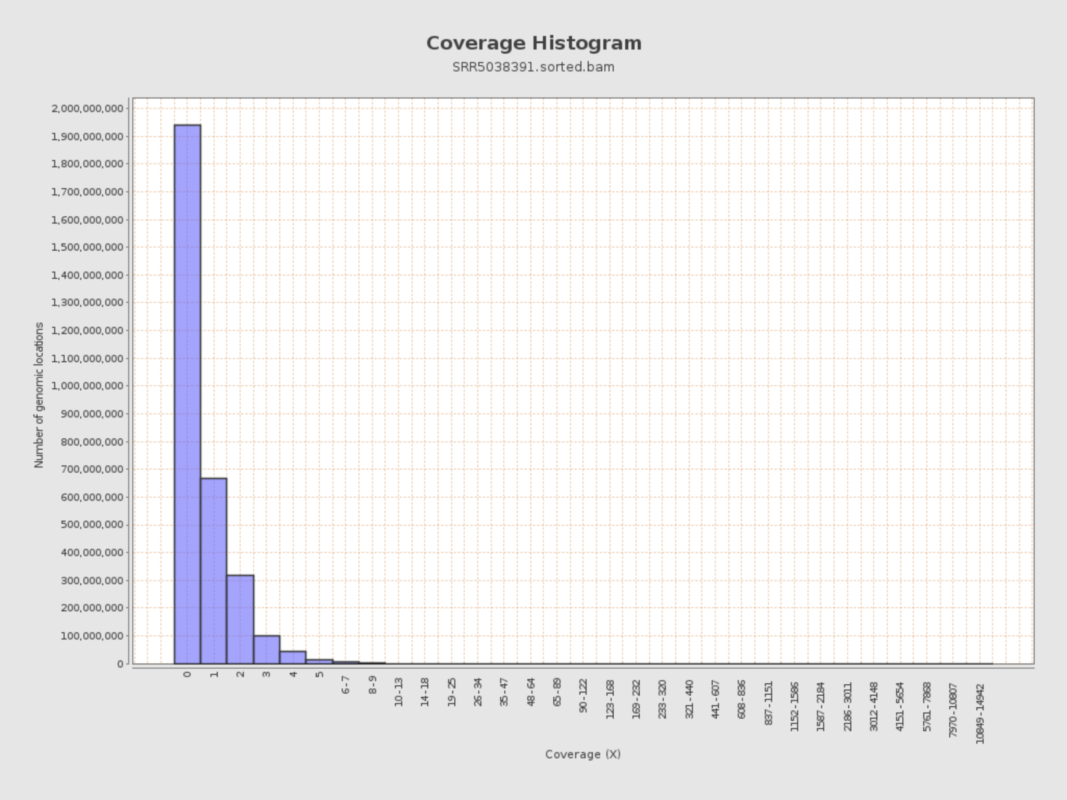
		bases	coverage	deviation
chr1	249250621	138074107	0.554	15.1803
chr2	243199373	195869046	0.8054	5.5106
chr3	198022430	128570015	0.6493	1.0382
chr4	191154276	112622279	0.5892	4.3893
chr5	180915260	112424121	0.6214	1.0846
chr6	171115067	133599983	0.7808	6.0073
chr7	159138663	137058441	0.8613	5.0577
chr8	146364022	89790719	0.6135	4.0563
chr9	141213431	81781767	0.5791	7.3466
chr10	135534747	80435340	0.5935	10.1051
chr11	135006516	108645070	0.8047	3.9104
chr12	133851895	76703903	0.5731	0.9959
chr13	115169878	108757847	0.9443	1.2938
chr14	107349540	42762763	0.3984	0.8805
chr15	102531392	41039258	0.4003	0.8185
chr16	90354753	70671036	0.7822	4.3123
chr17	81195210	56881902	0.7006	3.1204
chr18	78077248	34329135	0.4397	7.0703
chr19	59128983	39814085	0.6733	7.083
chr20	63025520	72070535	1.1435	1.9237
chr21	48129895	20169653	0.4191	2.8971
chr22	51304566	19481015	0.3797	2.6545
chrMT	16571	3490920	210.6644	25.8149
chrX	155270560	78659461	0.5066	1.3386

chrY	59373566	18836511	0.3173	5.9215

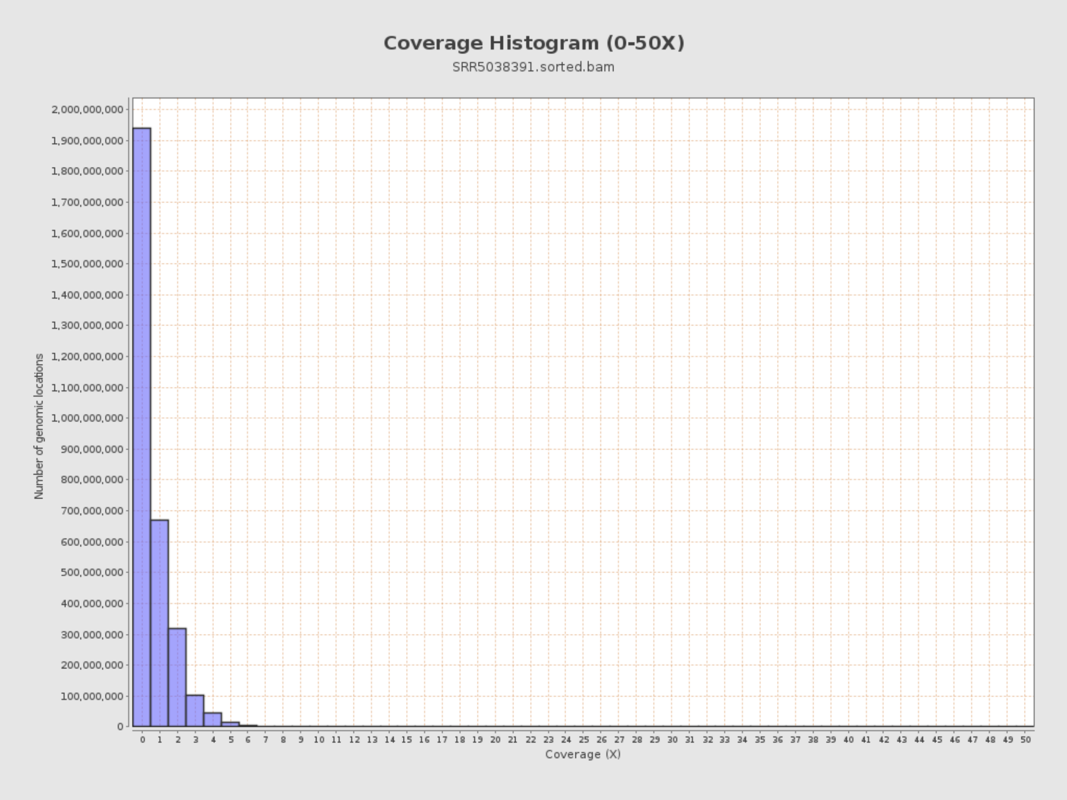
3. Results : Coverage across reference



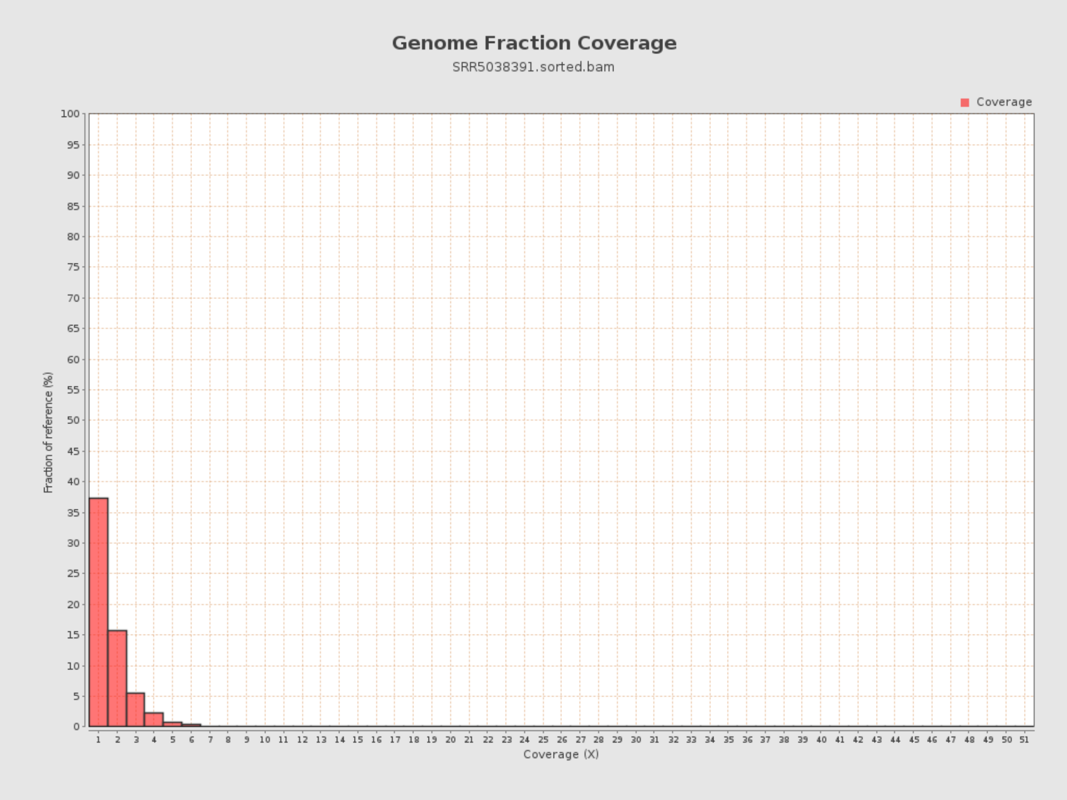
4. Results : Coverage Histogram



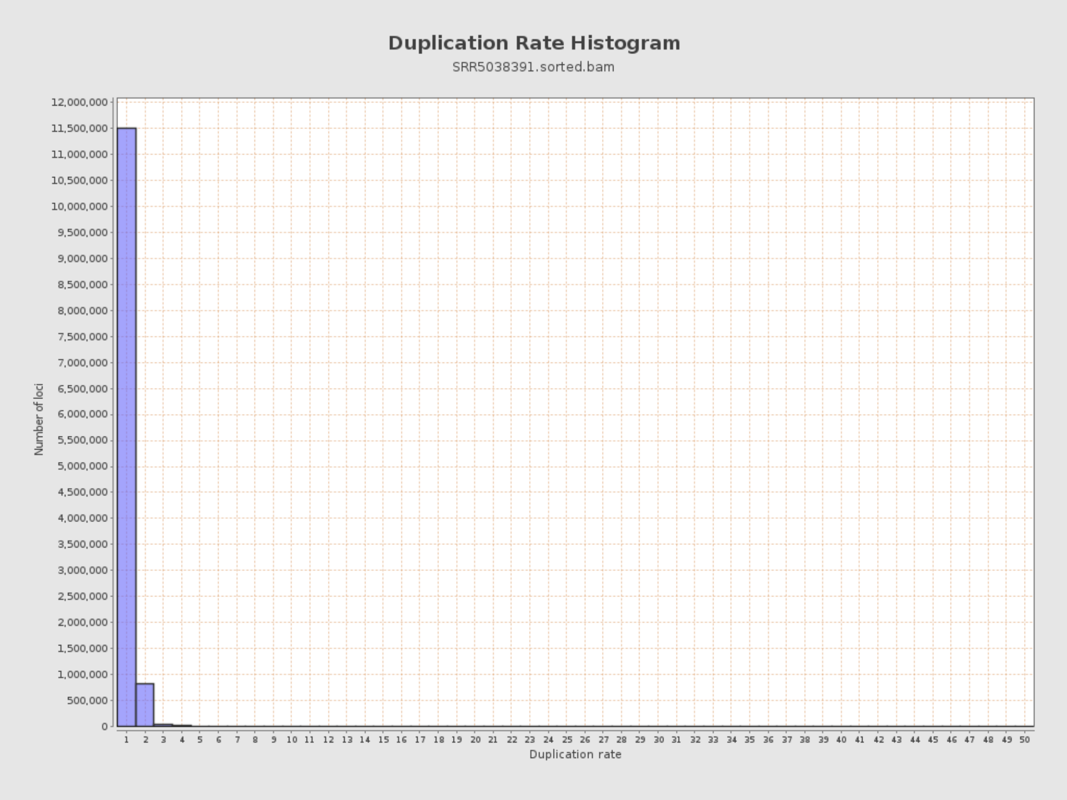
5. Results : Coverage Histogram (0-50X)



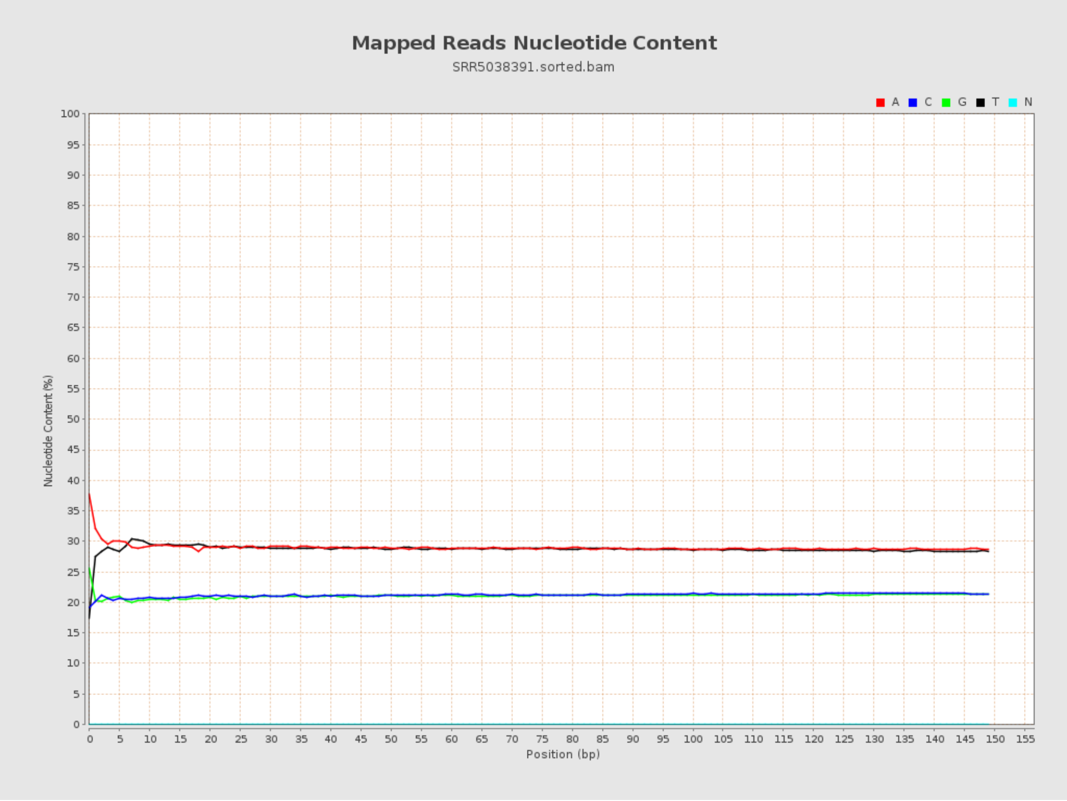
6. Results : Genome Fraction Coverage



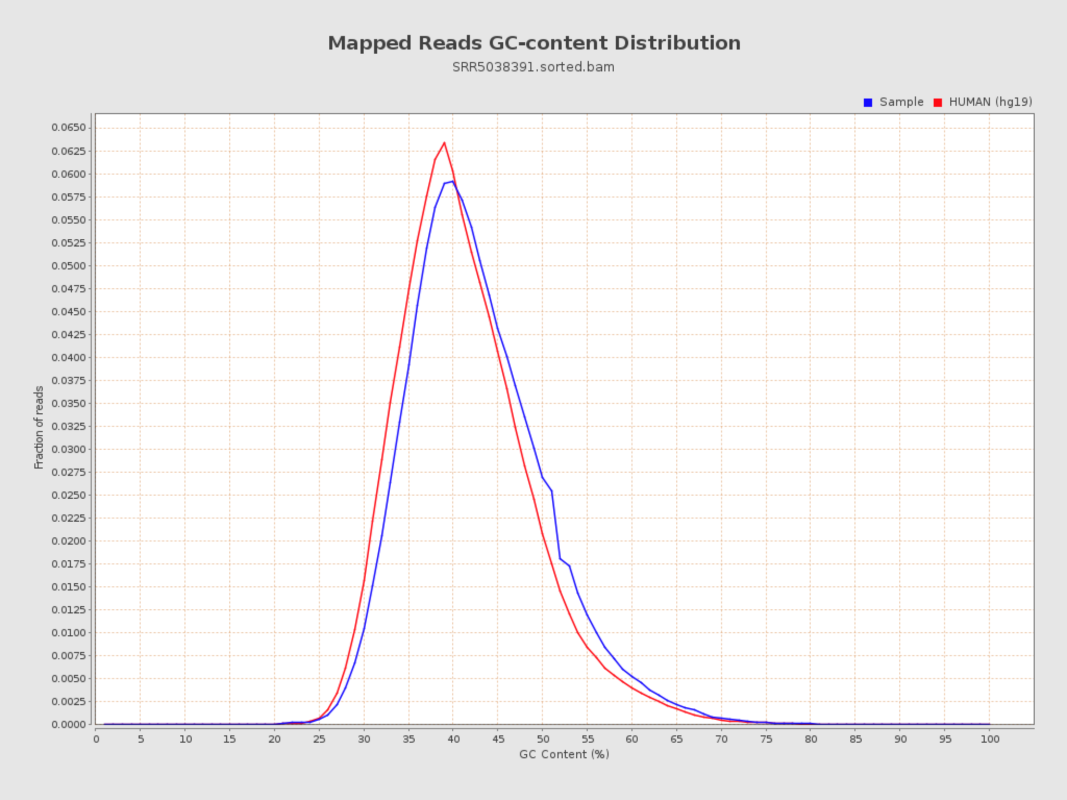
7. Results : Duplication Rate Histogram



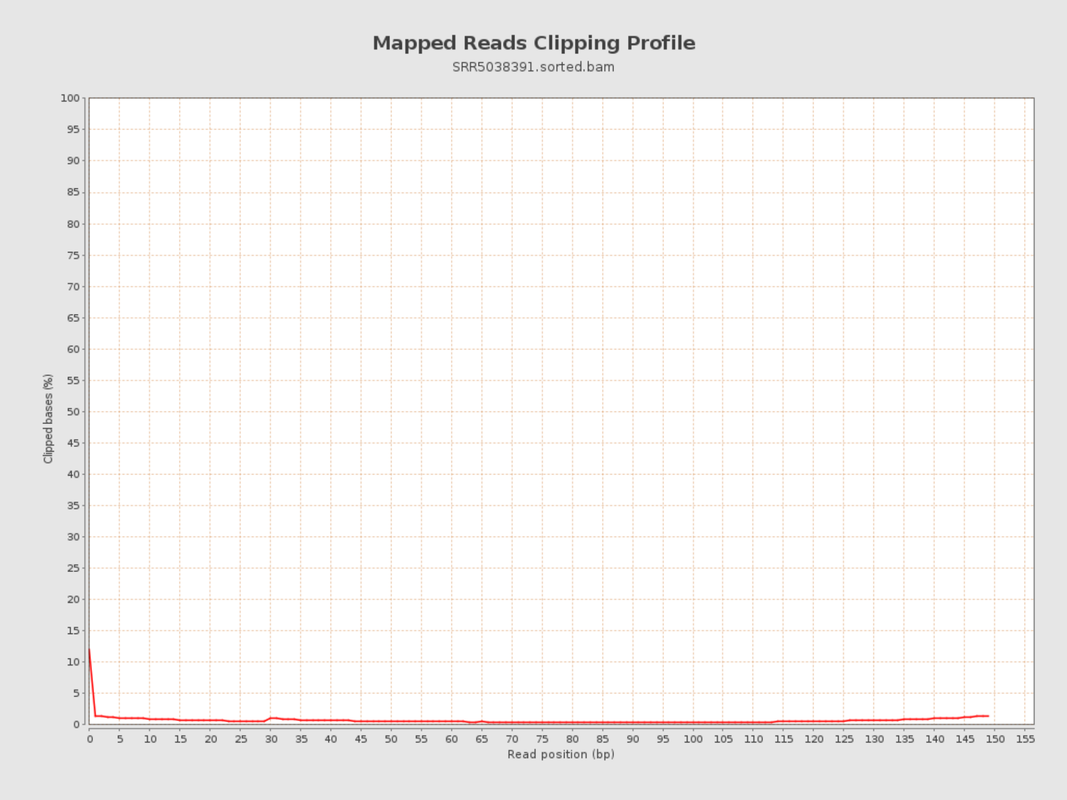
8. Results : Mapped Reads Nucleotide Content



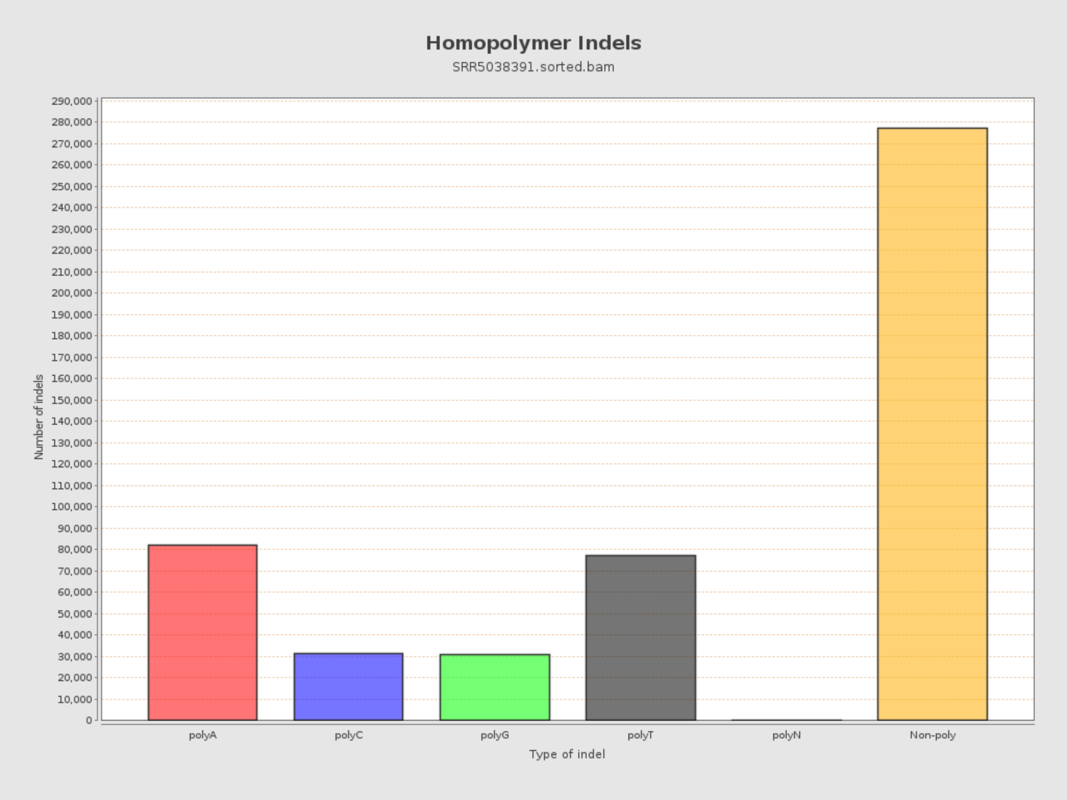
9. Results : Mapped Reads GC-content Distribution



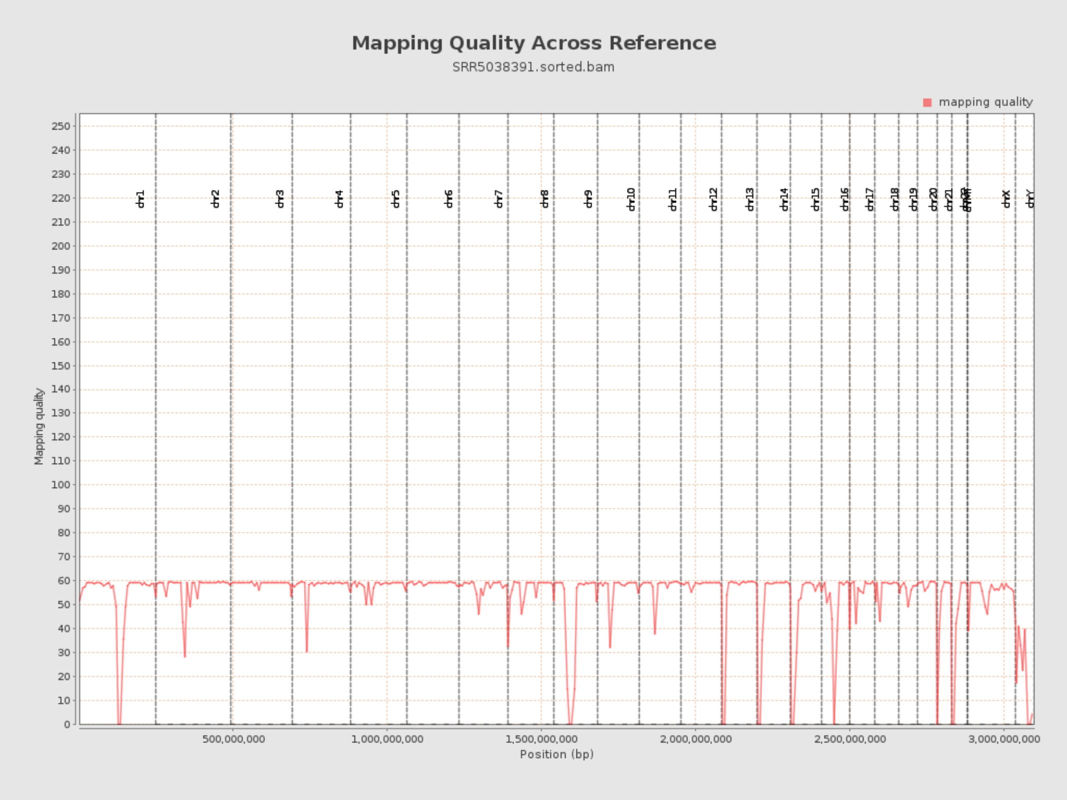
10. Results : Mapped Reads Clipping Profile



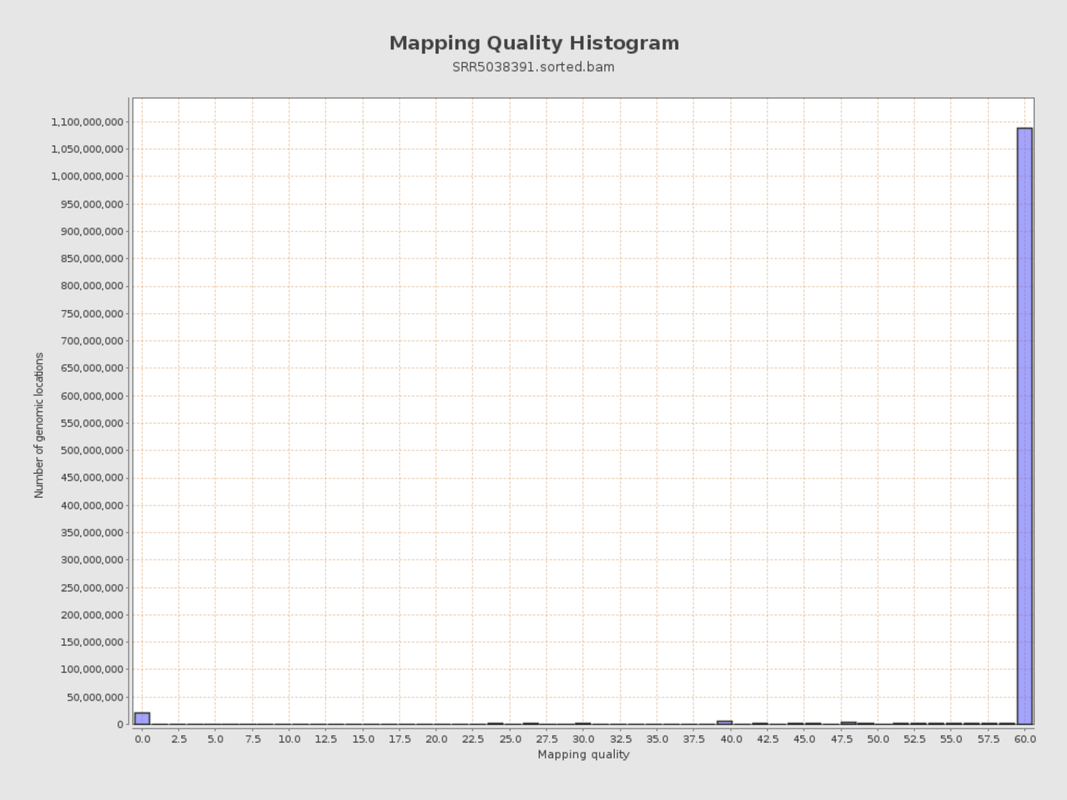
11. Results : Homopolymer Indels



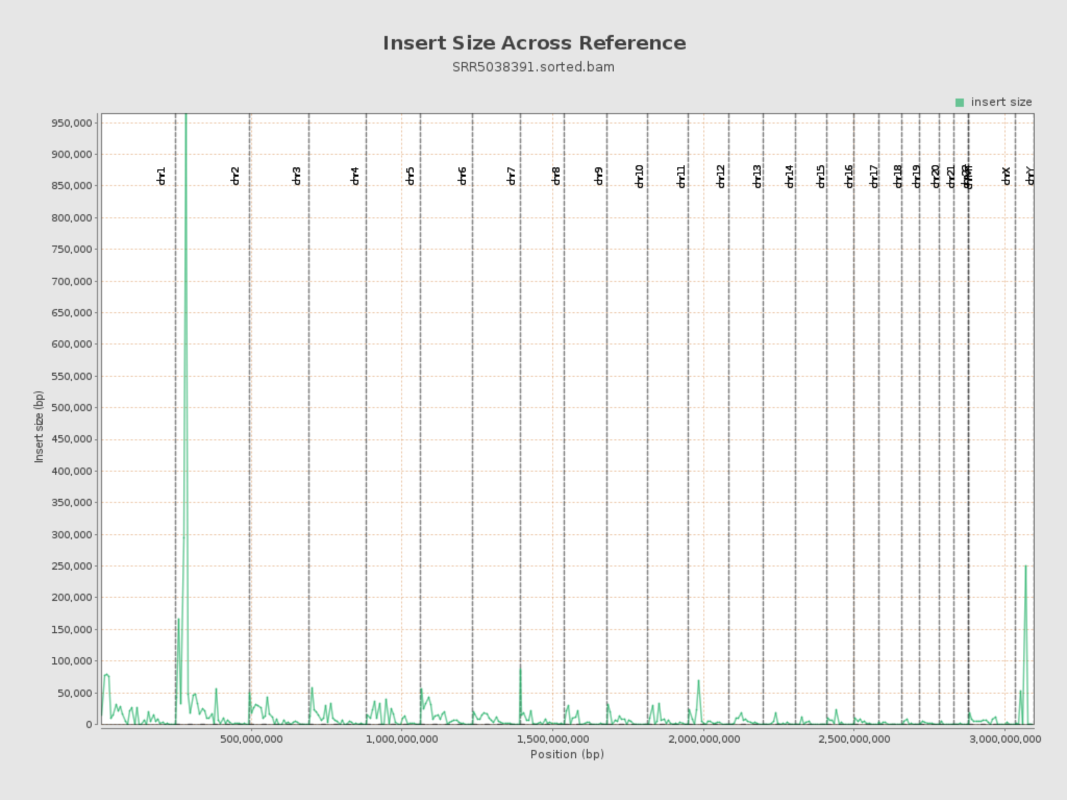
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram