Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 12:36:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927031.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_SRR927031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927031_1.fastq.gz SRR927031_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 12:36:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,892,094
Mapped reads	31,195,088 / 97.81%
Unmapped reads	697,006 / 2.19%
Mapped paired reads	31,195,088 / 97.81%
Mapped reads, first in pair	15,673,242 / 49.14%
Mapped reads, second in pair	15,521,846 / 48.67%
Mapped reads, both in pair	30,774,930 / 96.5%
Mapped reads, singletons	420,158 / 1.32%
Secondary alignments	0
Supplementary alignments	493,357 / 1.55%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	2,943,912 / 9.23%
Duplication rate	7.08%
Clipped reads	10,857,987 / 34.05%

2.2. ACGT Content

Number/percentage of A's	816,480,483 / 28.4%
Number/percentage of C's	568,068,948 / 19.76%
Number/percentage of T's	833,940,889 / 29.01%
Number/percentage of G's	656,087,624 / 22.82%
Number/percentage of N's	393,129 / 0.01%

GC Percentage	42.58%

2.3. Coverage

Mean	0.9294
Standard Deviation	4.0972

2.4. Mapping Quality

Mean Mapping Quality	53.32

2.5. Insert size

Mean	157,951.55
Standard Deviation	3,878,632.22
P25/Median/P75	146 / 190 / 254

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	30,610,118
Insertions	468,223
Mapped reads with at least one insertion	1.48%
Deletions	1,512,951
Mapped reads with at least one deletion	4.72%
Homopolymer indels	52.56%

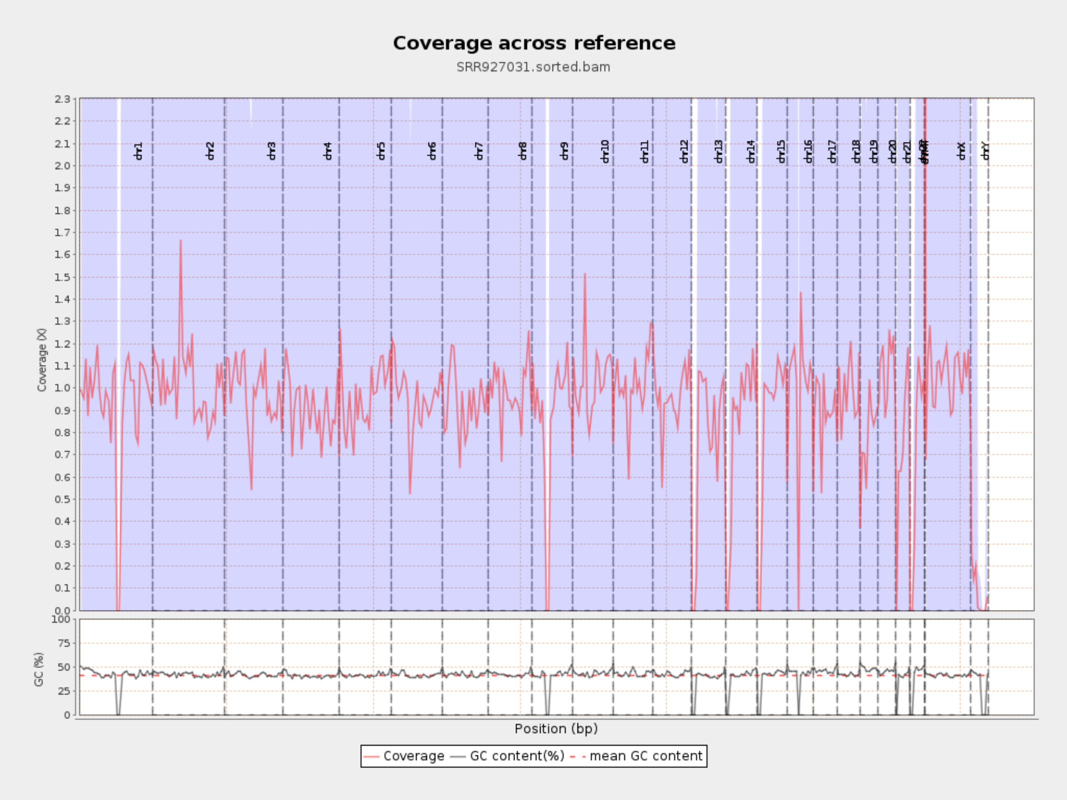
2.7. Chromosome stats

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

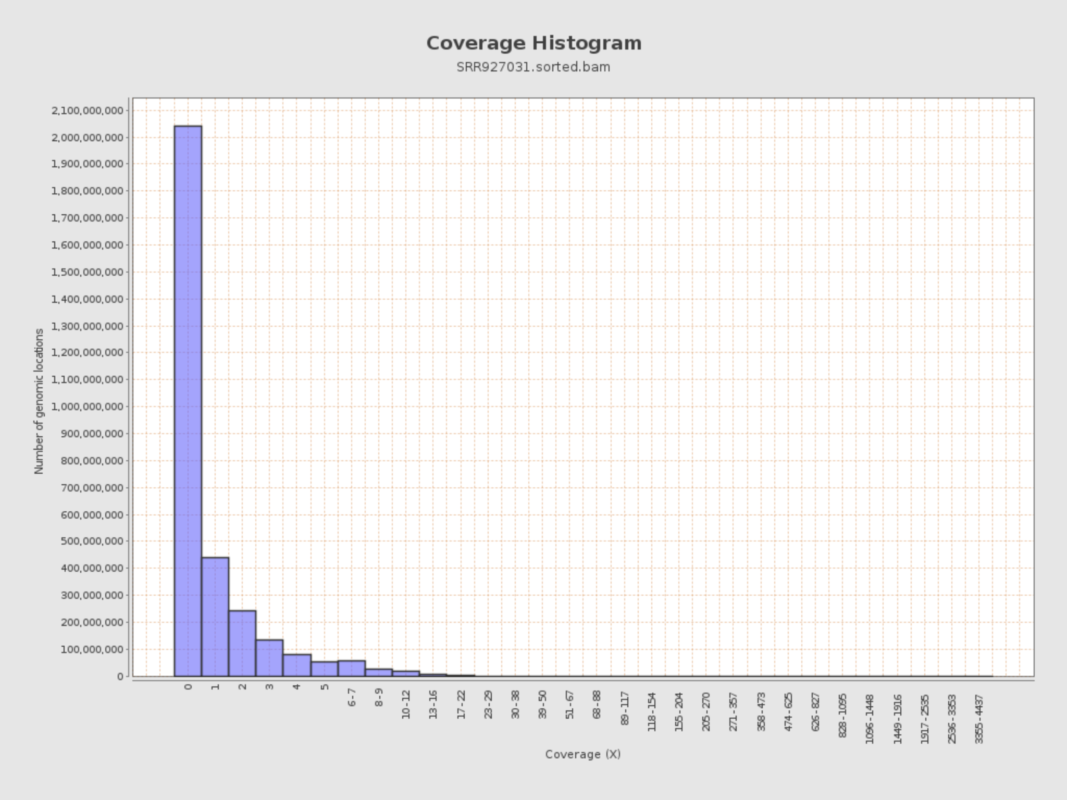
		bases	coverage	deviation
chr1	249250621	232400437	0.9324	4.6338
chr2	243199373	248822434	1.0231	5.6152
chr3	198022430	194274646	0.9811	1.9956
chr4	191154276	174335664	0.912	2.7815
chr5	180915260	174840015	0.9664	1.9465
chr6	171115067	163526189	0.9557	1.9881
chr7	159138663	148296569	0.9319	2.4799
chr8	146364022	144506733	0.9873	2.3138
chr9	141213431	120944643	0.8565	4.1931
chr10	135534747	141732638	1.0457	7.171
chr11	135006516	136888949	1.0139	2.8418
chr12	133851895	128964895	0.9635	1.9753
chr13	115169878	87882685	0.7631	1.7442
chr14	107349540	87525523	0.8153	1.9032
chr15	102531392	85819811	0.837	1.913
chr16	90354753	89408184	0.9895	4.982
chr17	81195210	72696089	0.8953	2.7678
chr18	78077248	78391847	1.004	4.4108
chr19	59128983	46269374	0.7825	2.7103
chr20	63025520	68230488	1.0826	2.2631
chr21	48129895	36206130	0.7523	2.4564
chr22	51304566	35087269	0.6839	1.8132
chrMT	16571	12326999	743.8899	571.1602
chrX	155270560	163194691	1.051	2.3961

chrY	59373566	4546530	0.0766	2.1448

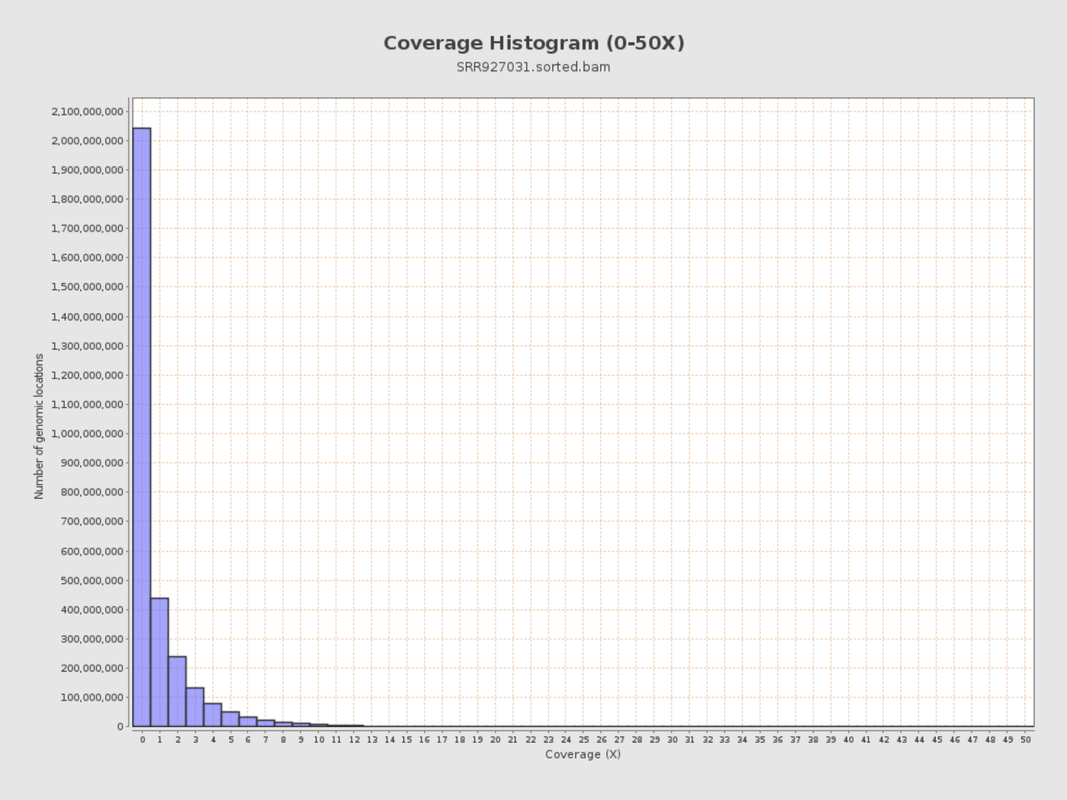
3. Results : Coverage across reference



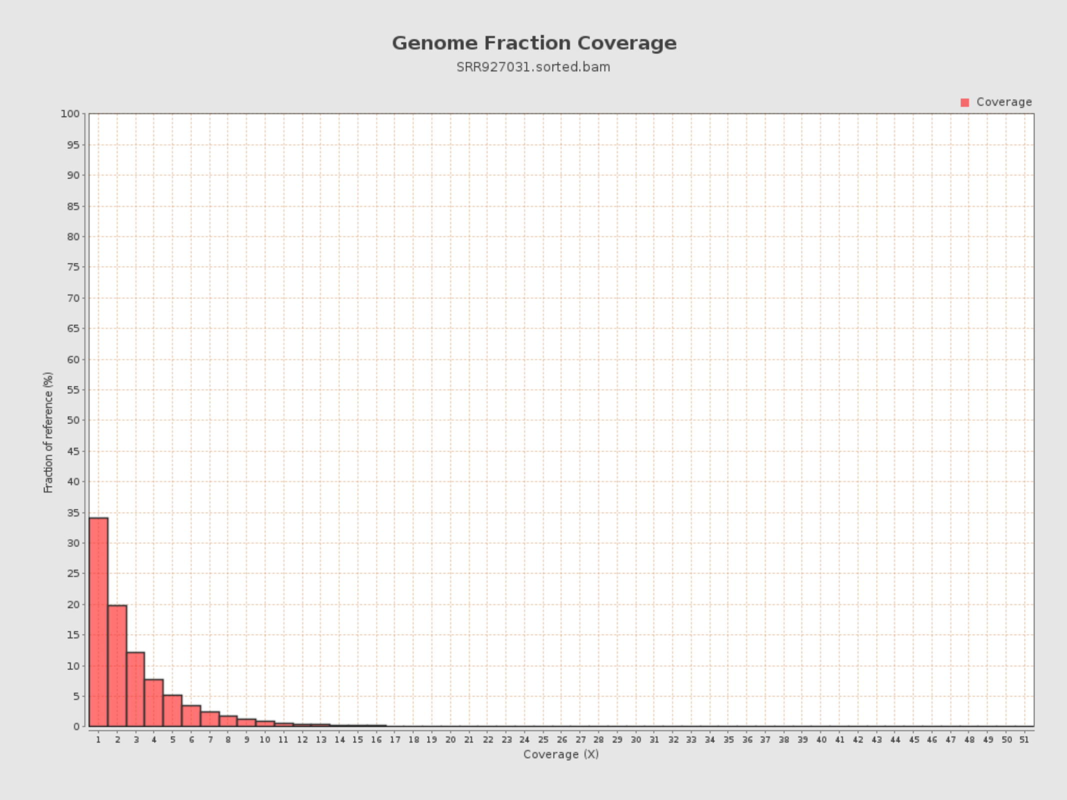
4. Results : Coverage Histogram



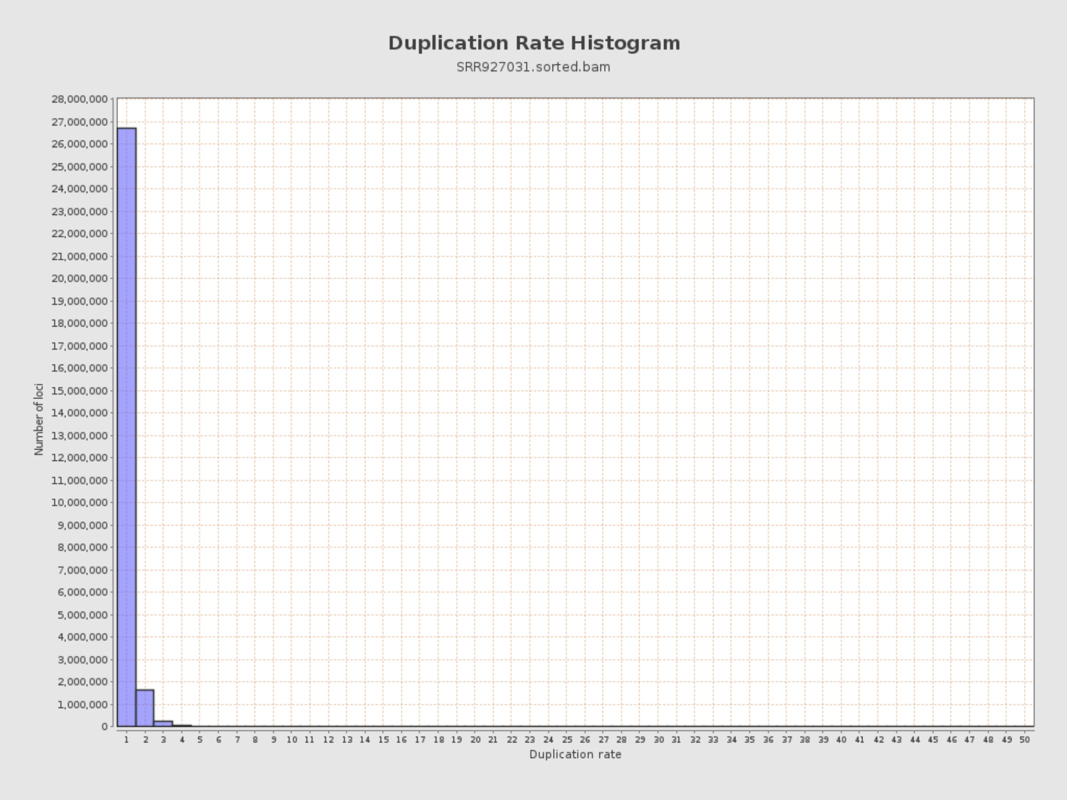
5. Results : Coverage Histogram (0-50X)



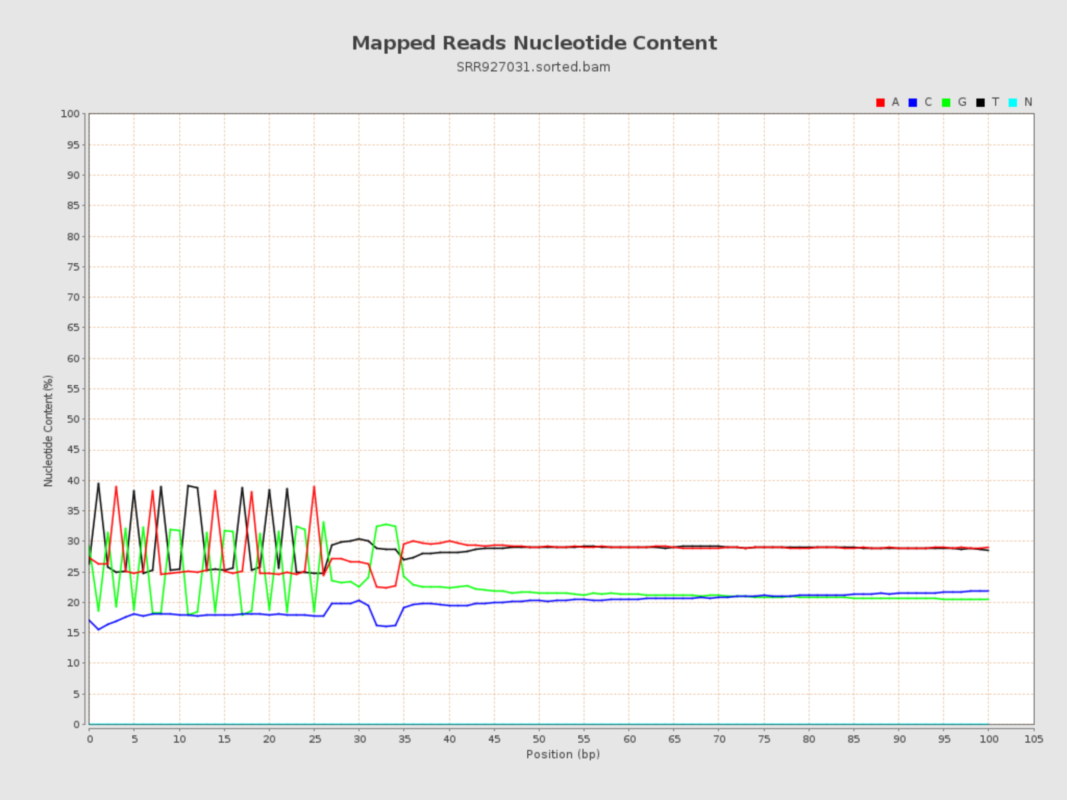
6. Results : Genome Fraction Coverage



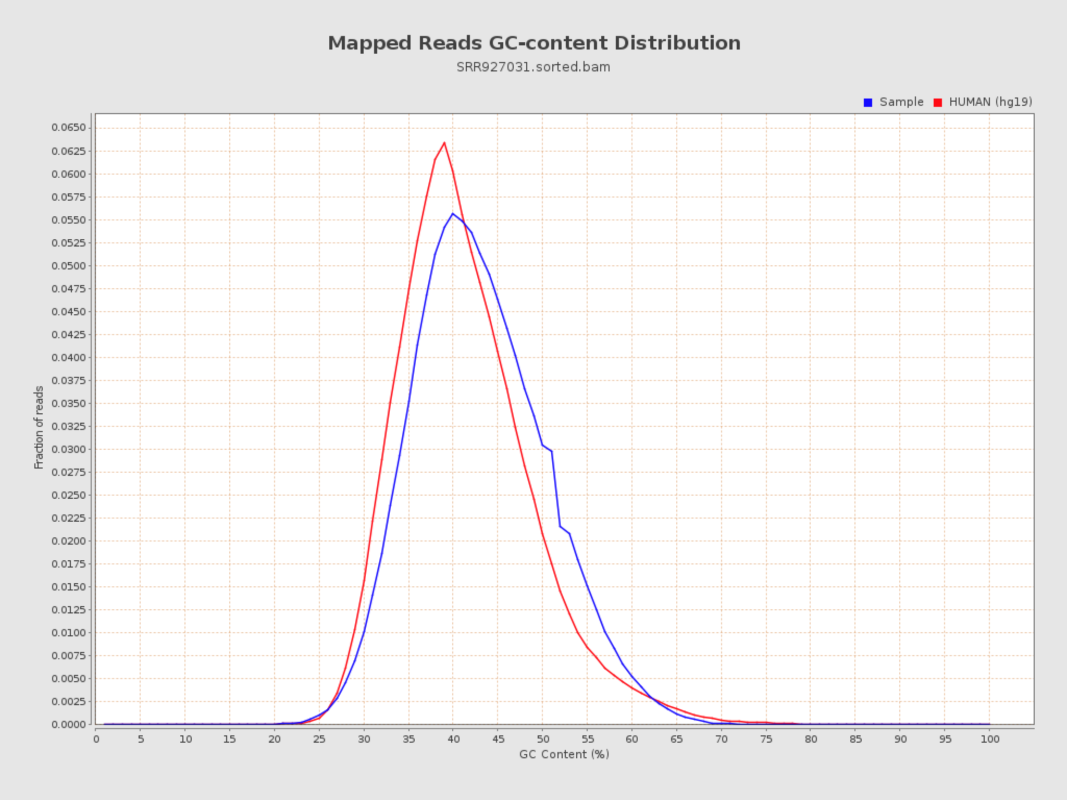
7. Results : Duplication Rate Histogram



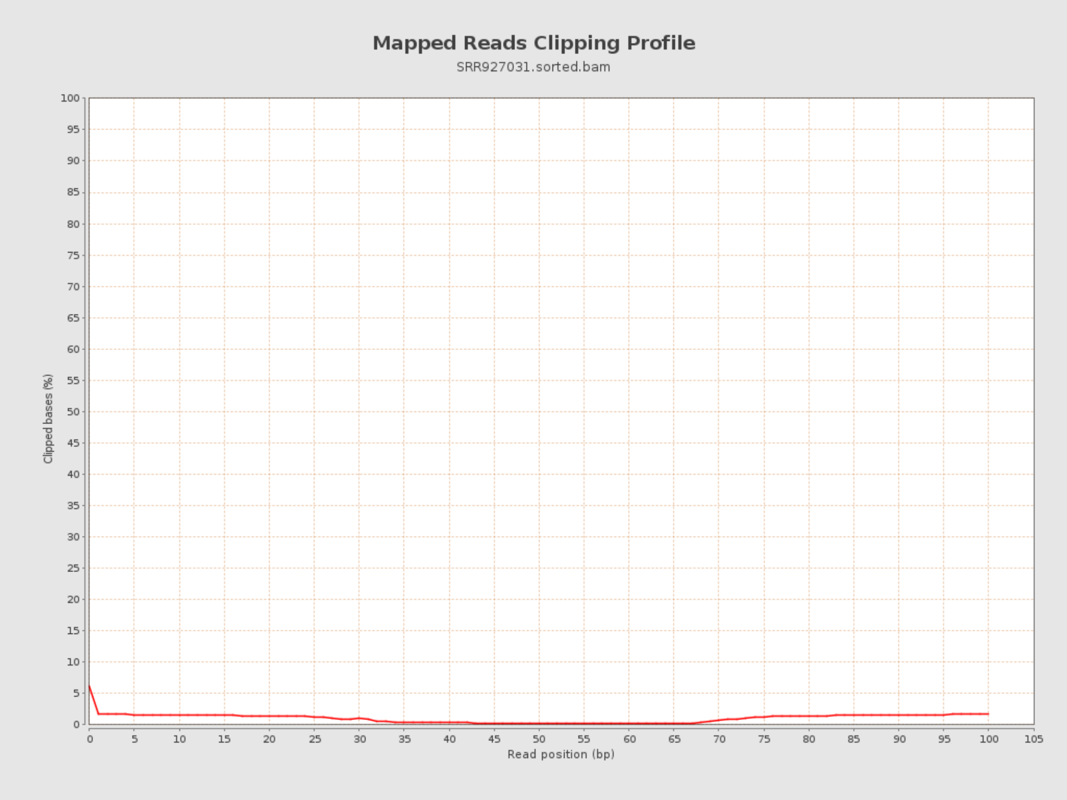
8. Results : Mapped Reads Nucleotide Content



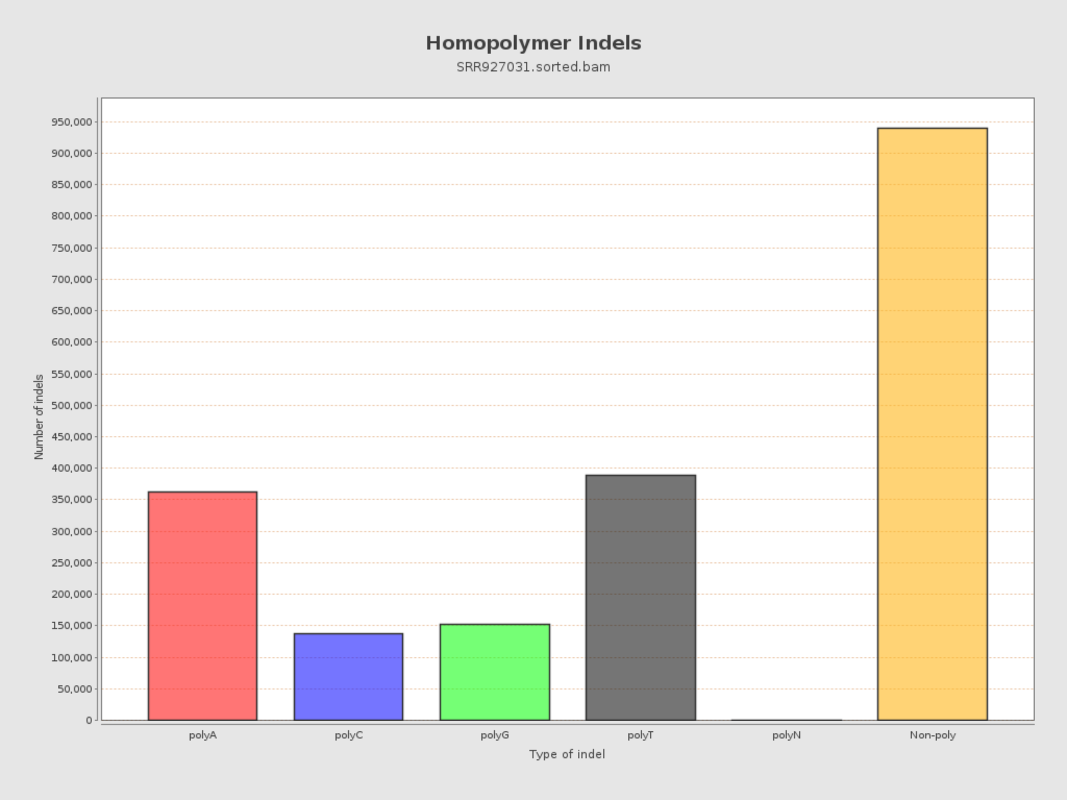
9. Results : Mapped Reads GC-content Distribution



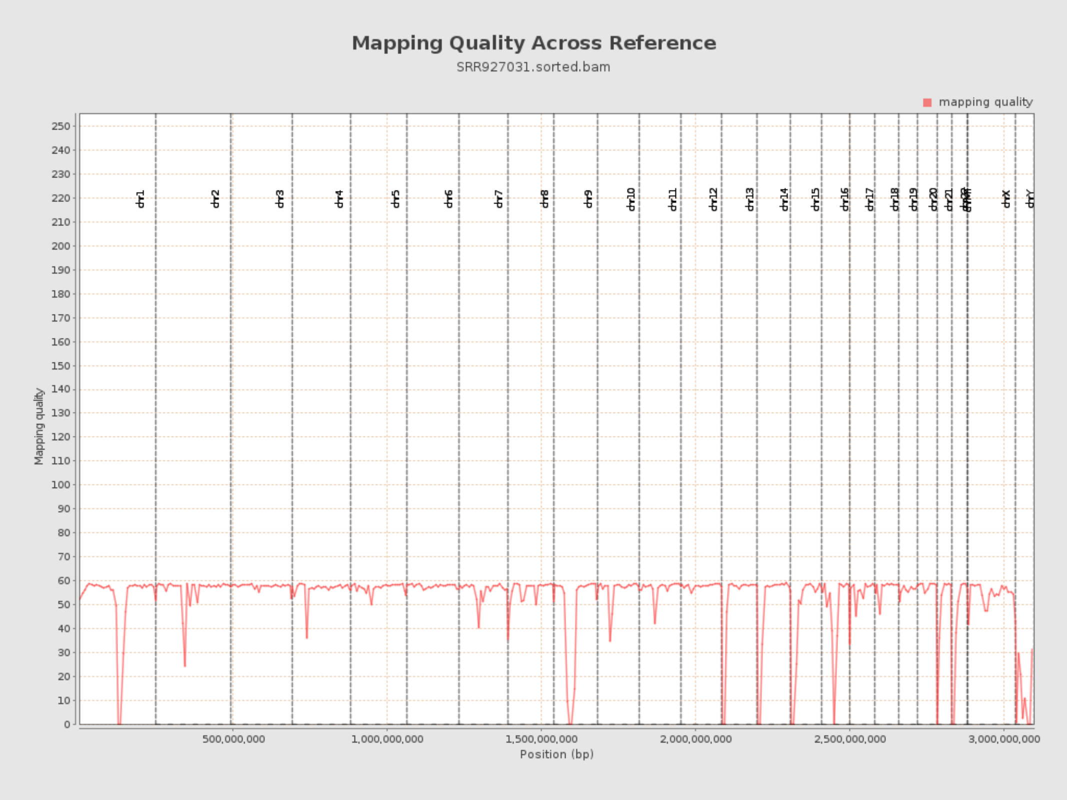
10. Results : Mapped Reads Clipping Profile



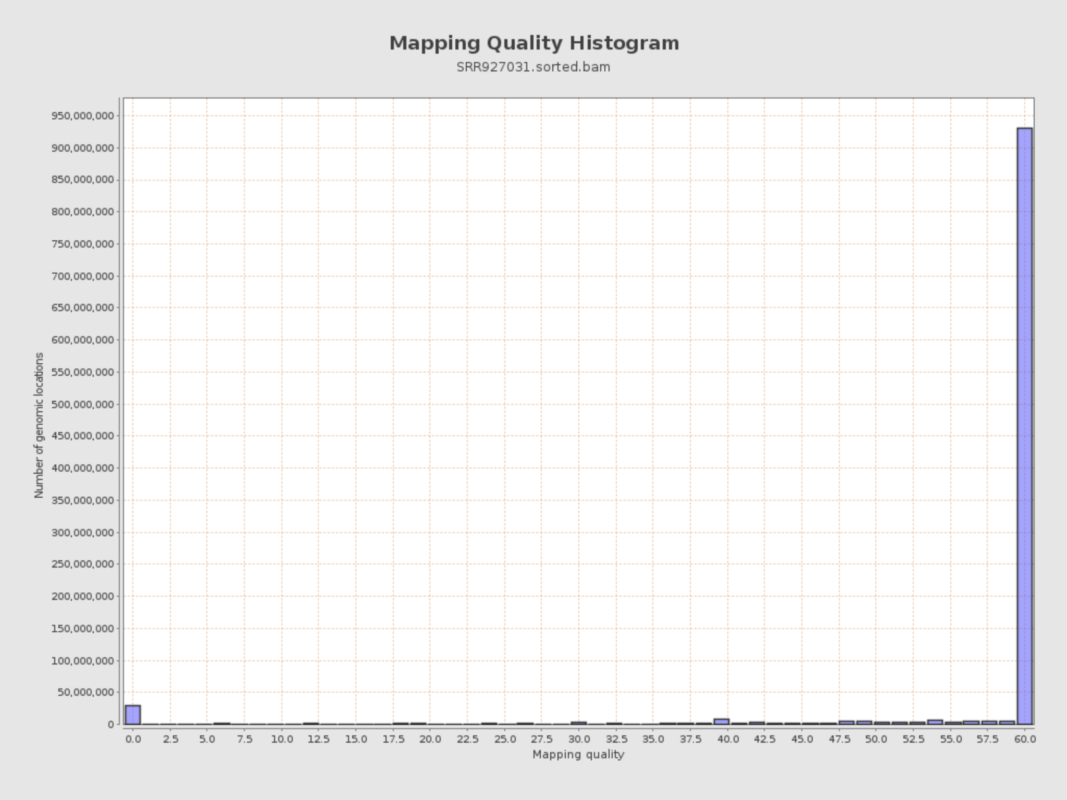
11. Results : Homopolymer Indels



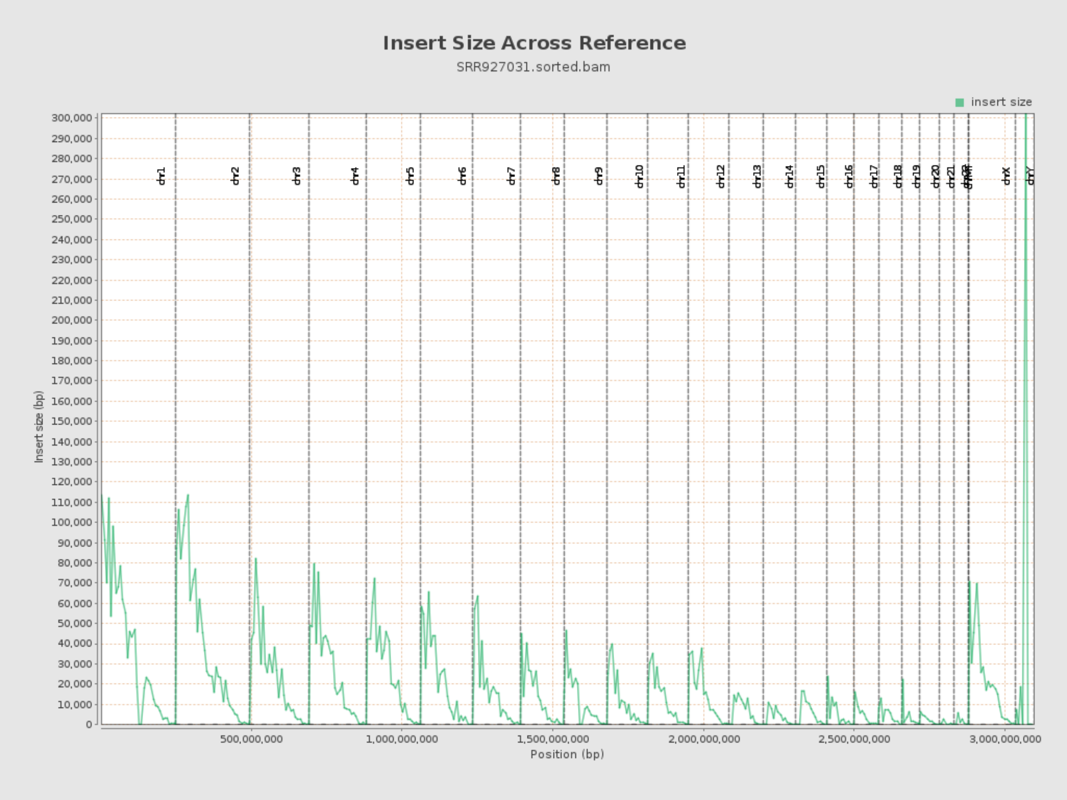
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram