

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:13:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975193.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_SRR975193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975193_1.fastq.gz SRR975193_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:13:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,164,196
Mapped reads	3,125,975 / 98.79%
Unmapped reads	38,221 / 1.21%
Mapped paired reads	3,125,975 / 98.79%
Mapped reads, first in pair	1,564,919 / 49.46%
Mapped reads, second in pair	1,561,056 / 49.33%
Mapped reads, both in pair	3,114,022 / 98.41%
Mapped reads, singletons	11,953 / 0.38%
Secondary alignments	0
Supplementary alignments	49,093 / 1.55%
Read min/max/mean length	30 / 151 / 151.78
Duplicated reads (estimated)	568,940 / 17.98%
Duplication rate	14.9%
Clipped reads	2,275,933 / 71.93%

2.2. ACGT Content

Number/percentage of A's	125,508,769 / 29.5%
Number/percentage of C's	84,847,570 / 19.94%
Number/percentage of T's	126,718,317 / 29.79%
Number/percentage of G's	88,321,972 / 20.76%
Number/percentage of N's	24,441 / 0.01%

GC Percentage	40.71%
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2.3. Coverage

Mean	0.1375
Standard Deviation	3.3953

2.4. Mapping Quality

Mean Mapping Quality	53.45
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2.5. Insert size

Mean	90,500.05
Standard Deviation	2,884,940.04
P25/Median/P75	140 / 174 / 222

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	5,405,429
Insertions	89,650
Mapped reads with at least one insertion	2.72%
Deletions	165,751
Mapped reads with at least one deletion	5.11%
Homopolymer indels	46.18%

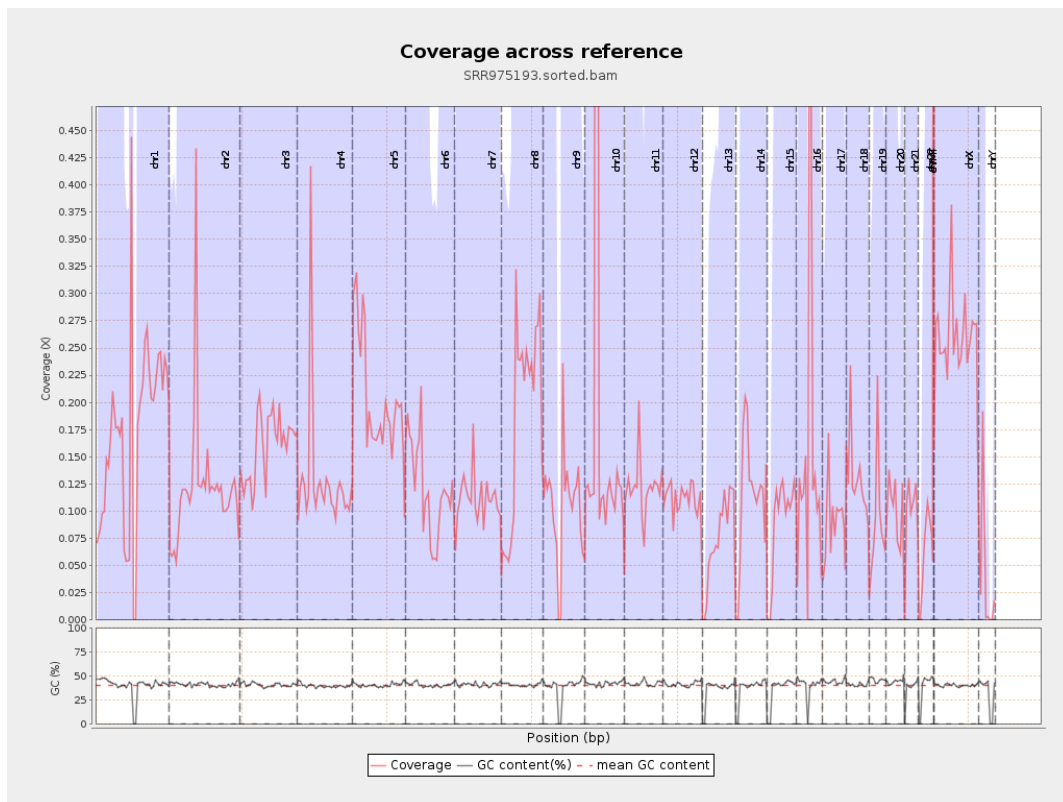
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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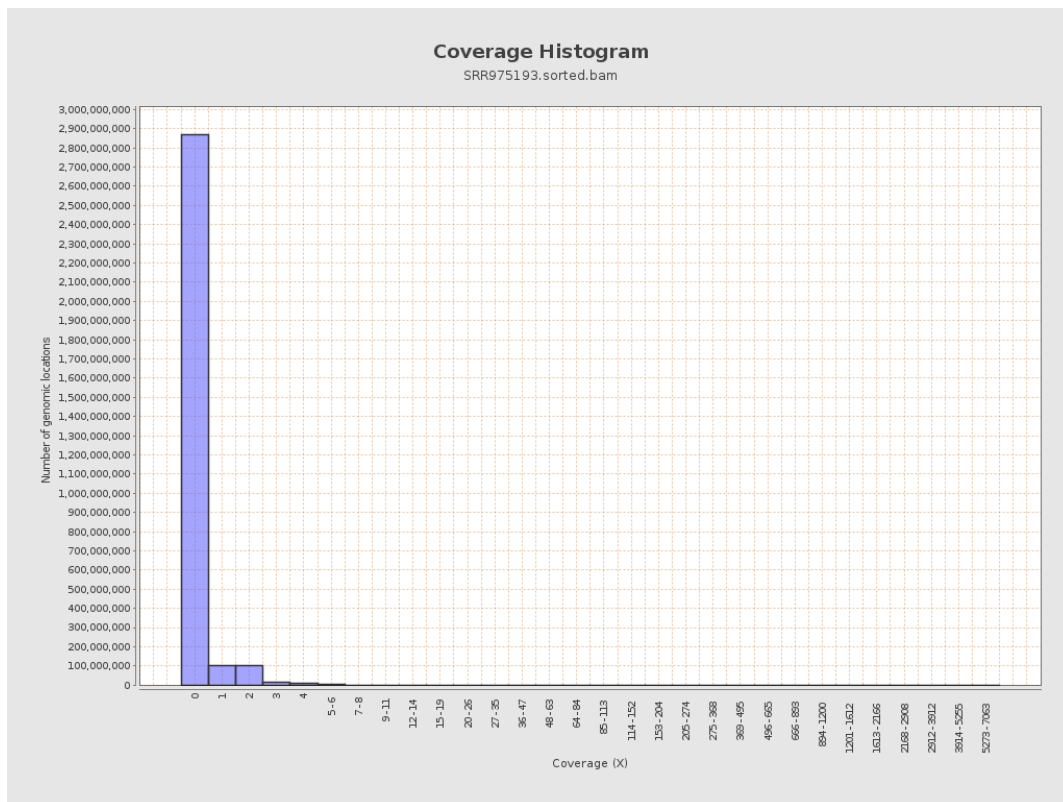
		bases	coverage	deviation
chr1	249250621	42805399	0.1717	4.314
chr2	243199373	29534866	0.1214	1.9516
chr3	198022430	31573991	0.1594	0.8103
chr4	191154276	24045055	0.1258	1.8609
chr5	180915260	36724521	0.203	0.6643
chr6	171115067	20430294	0.1194	1.1333
chr7	159138663	17868927	0.1123	1.3026
chr8	146364022	27499493	0.1879	0.9848
chr9	141213431	14826253	0.105	2.8011
chr10	135534747	26031027	0.1921	13.2025
chr11	135006516	16098477	0.1192	1.6916
chr12	133851895	14842629	0.1109	0.4718
chr13	115169878	8485894	0.0737	0.3792
chr14	107349540	12096898	0.1127	0.498
chr15	102531392	9189728	0.0896	0.4212
chr16	90354753	13930153	0.1542	3.9547
chr17	81195210	7123379	0.0877	1.7346
chr18	78077248	10259760	0.1314	2.8567
chr19	59128983	5428406	0.0918	1.9687
chr20	63025520	6469380	0.1026	0.8009
chr21	48129895	4736429	0.0984	1.0529
chr22	51304566	3089892	0.0602	0.3521
chrMT	16571	61677	3.722	3.1813
chrX	155270560	40516371	0.2609	1.24

chrY	59373566	2084353	0.0351	3.0142
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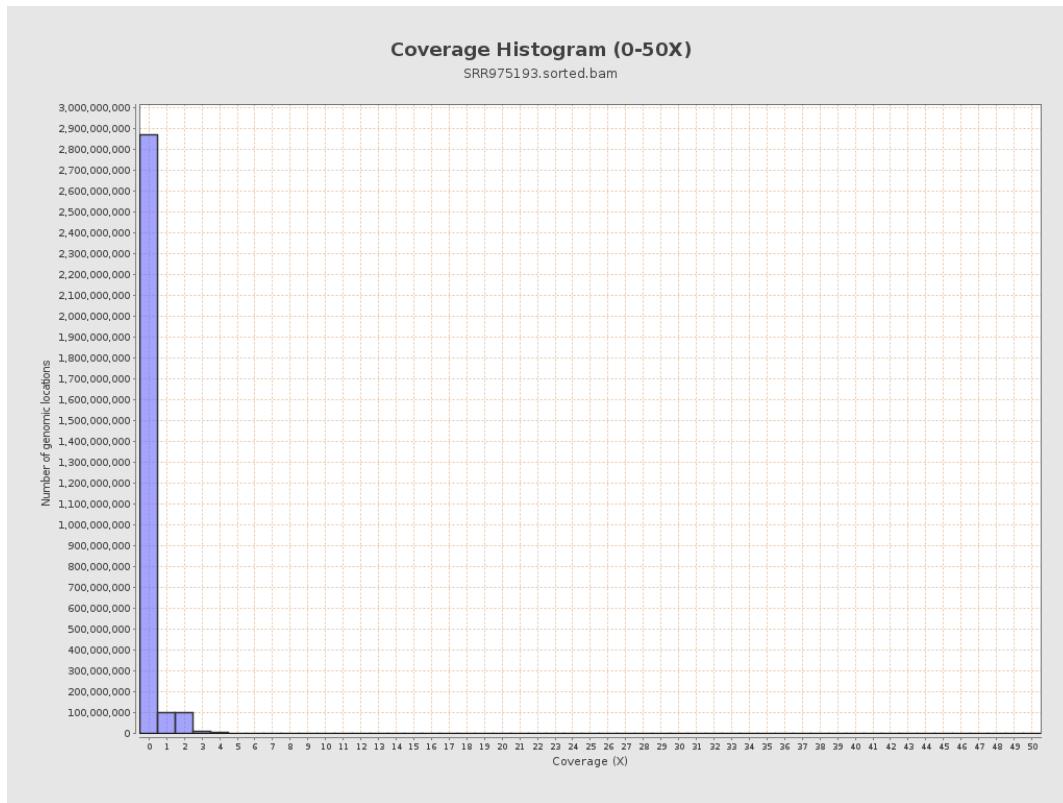
3. Results : Coverage across reference



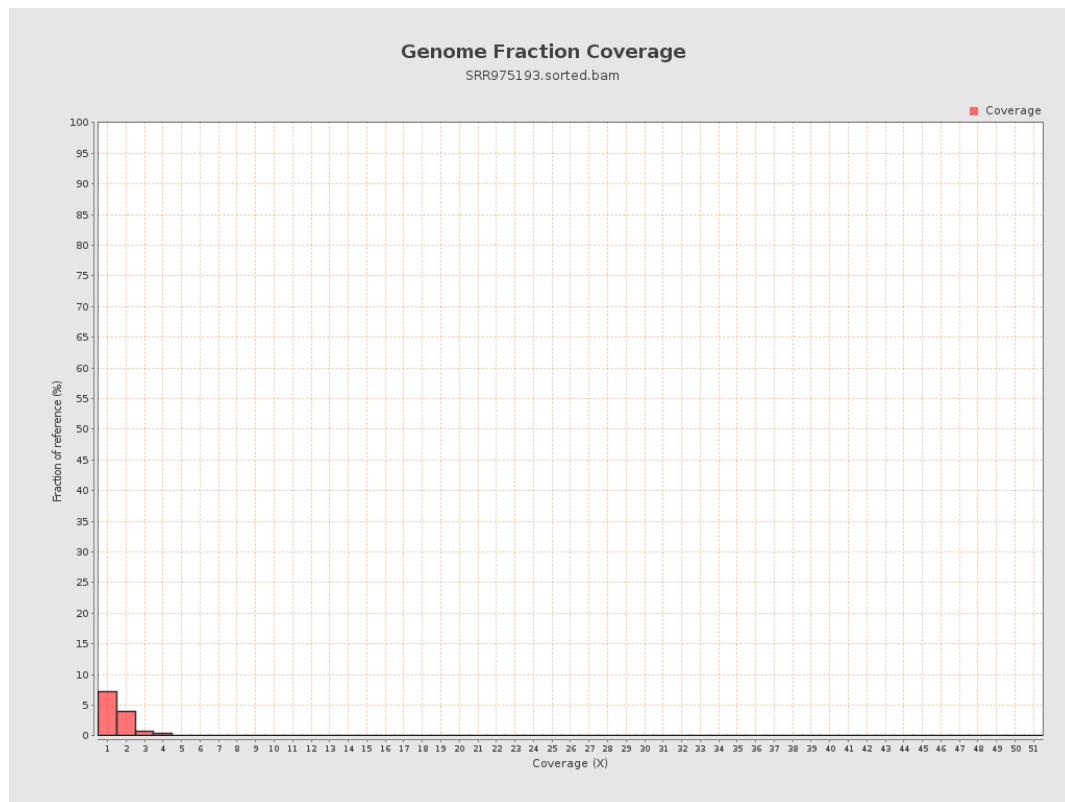
4. Results : Coverage Histogram



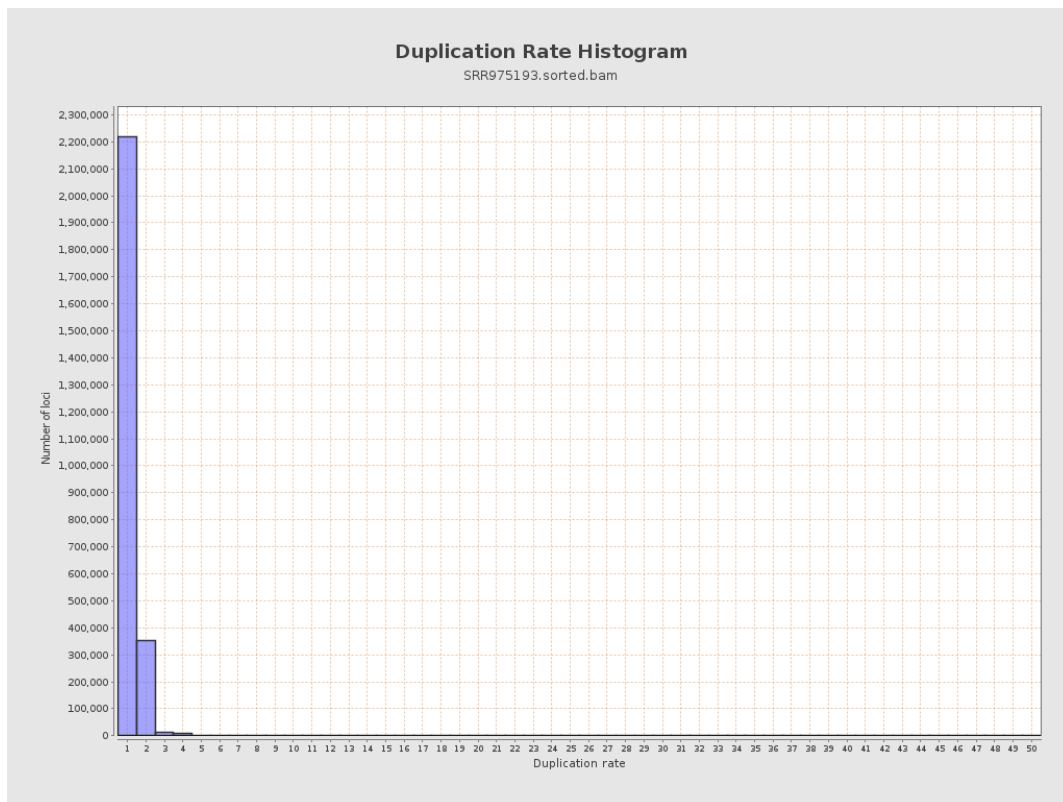
5. Results : Coverage Histogram (0-50X)



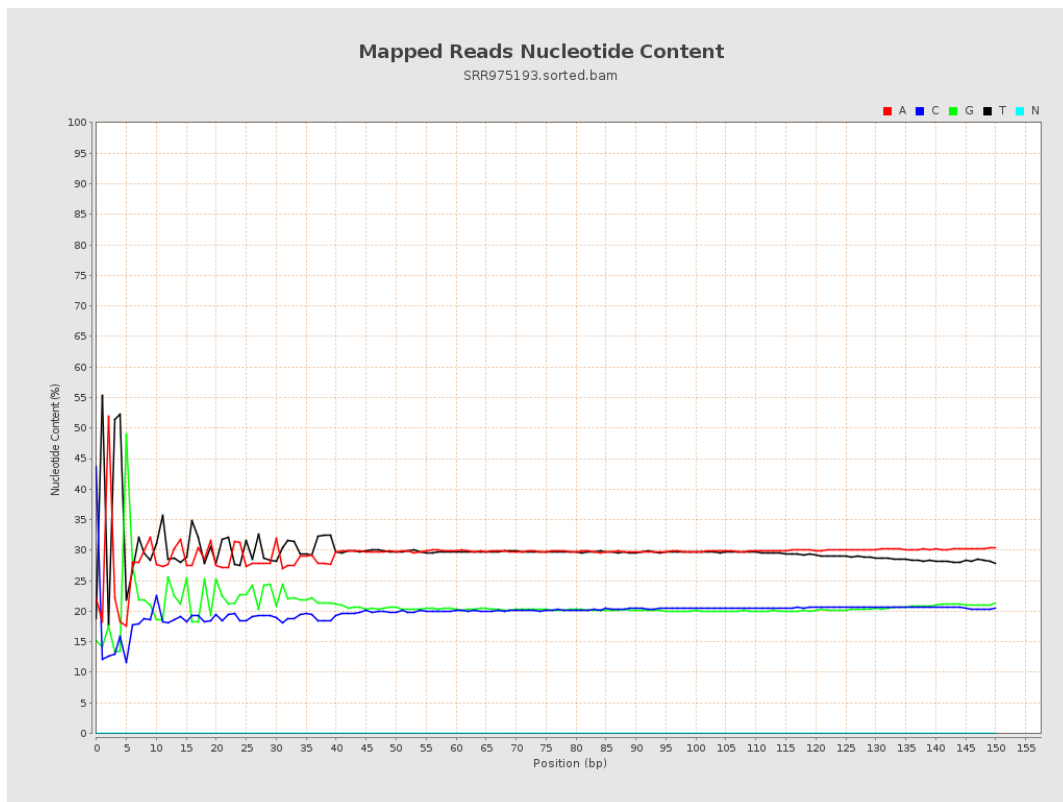
6. Results : Genome Fraction Coverage



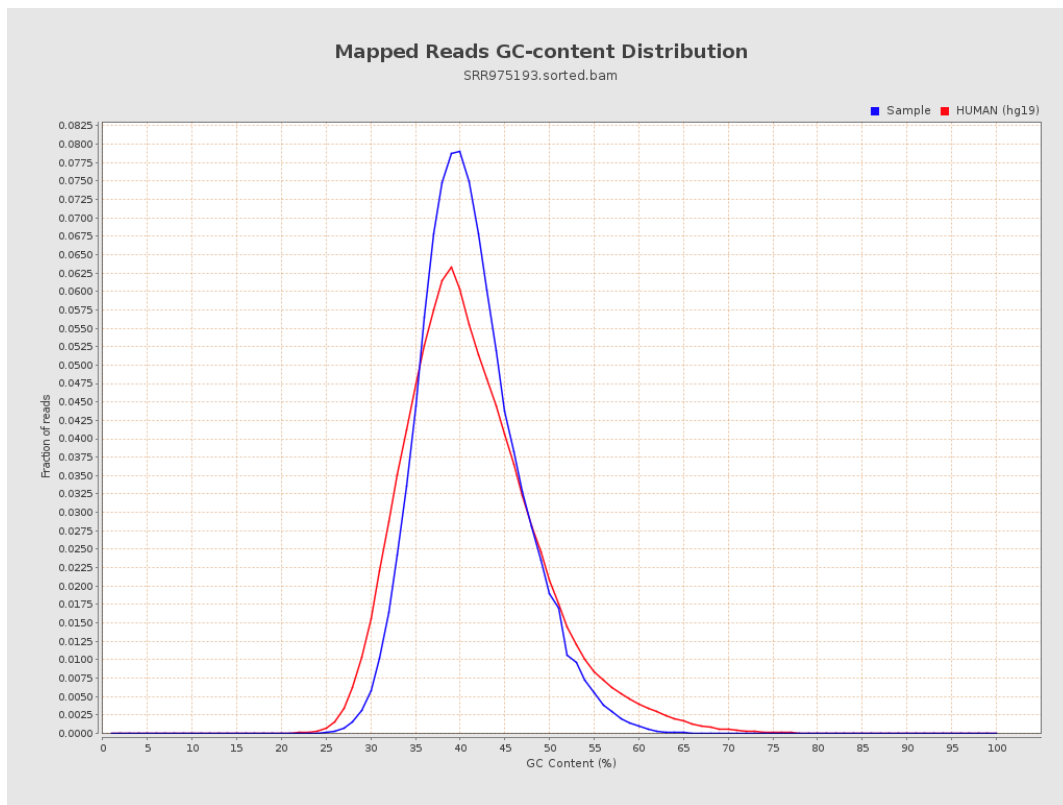
7. Results : Duplication Rate Histogram



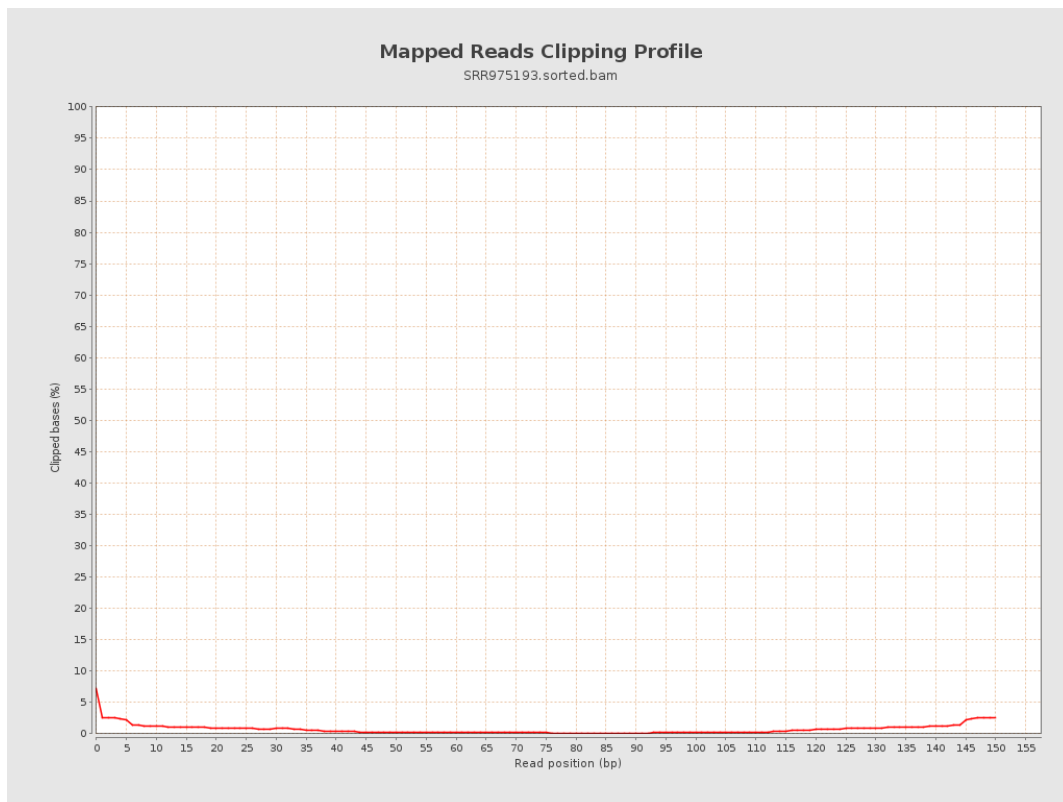
8. Results : Mapped Reads Nucleotide Content



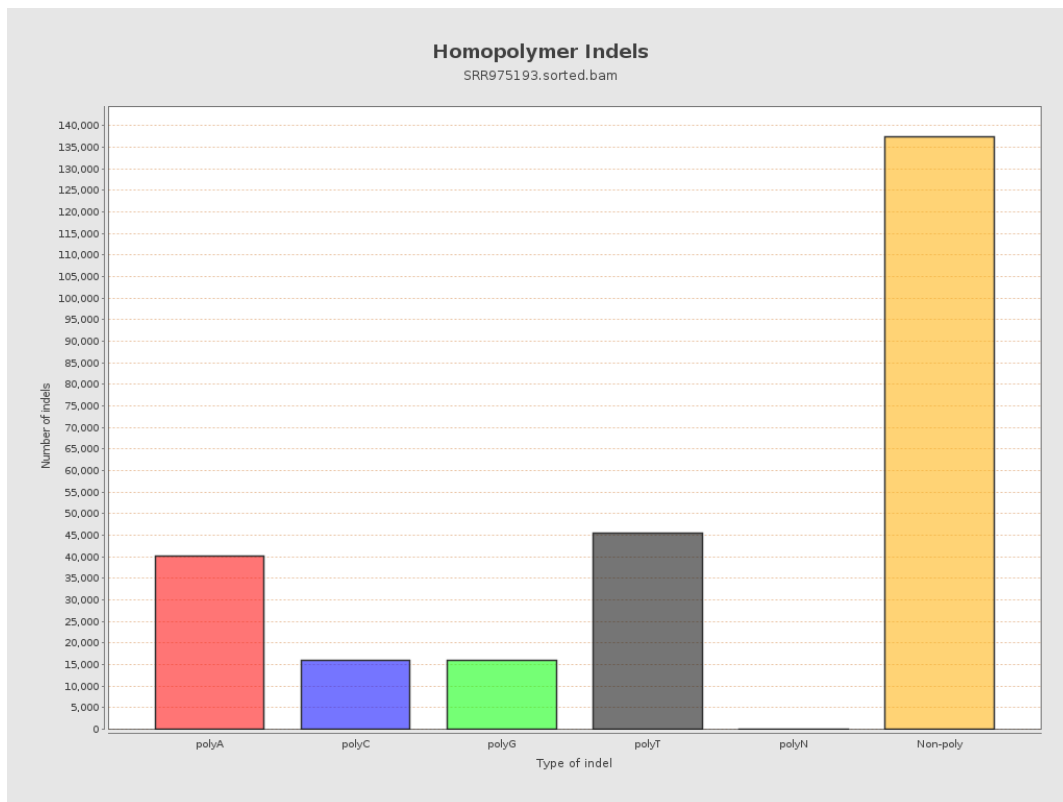
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



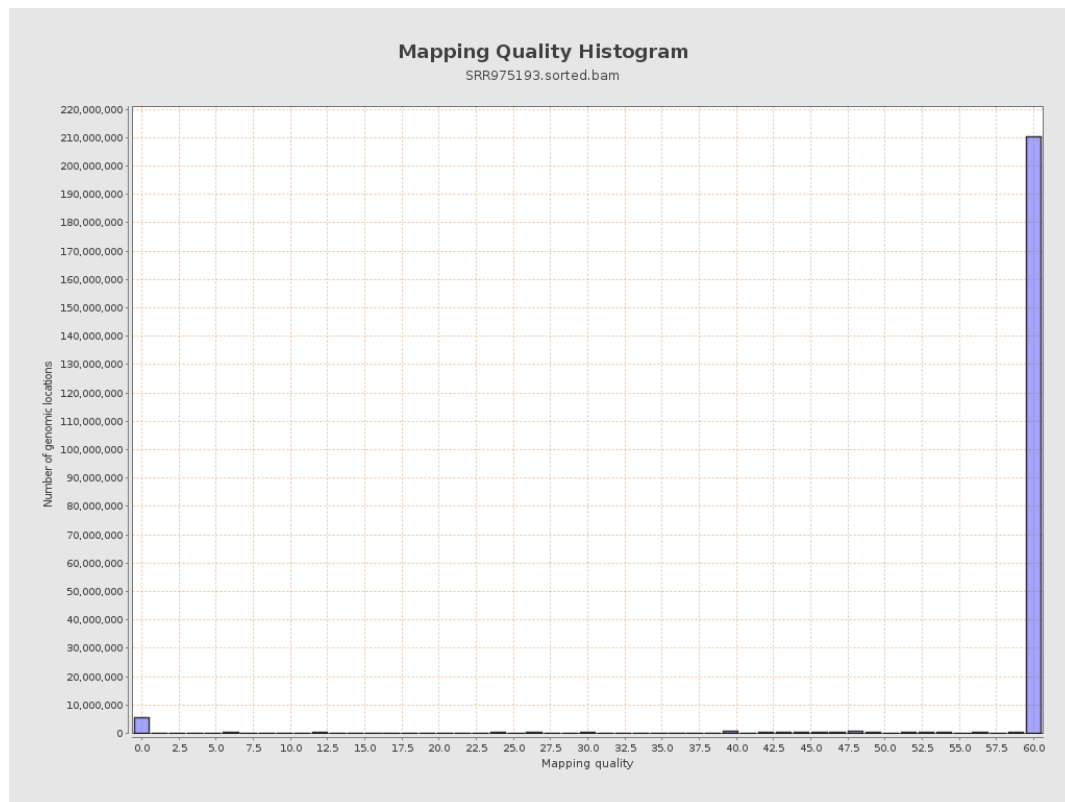
11. Results : Homopolymer Indels



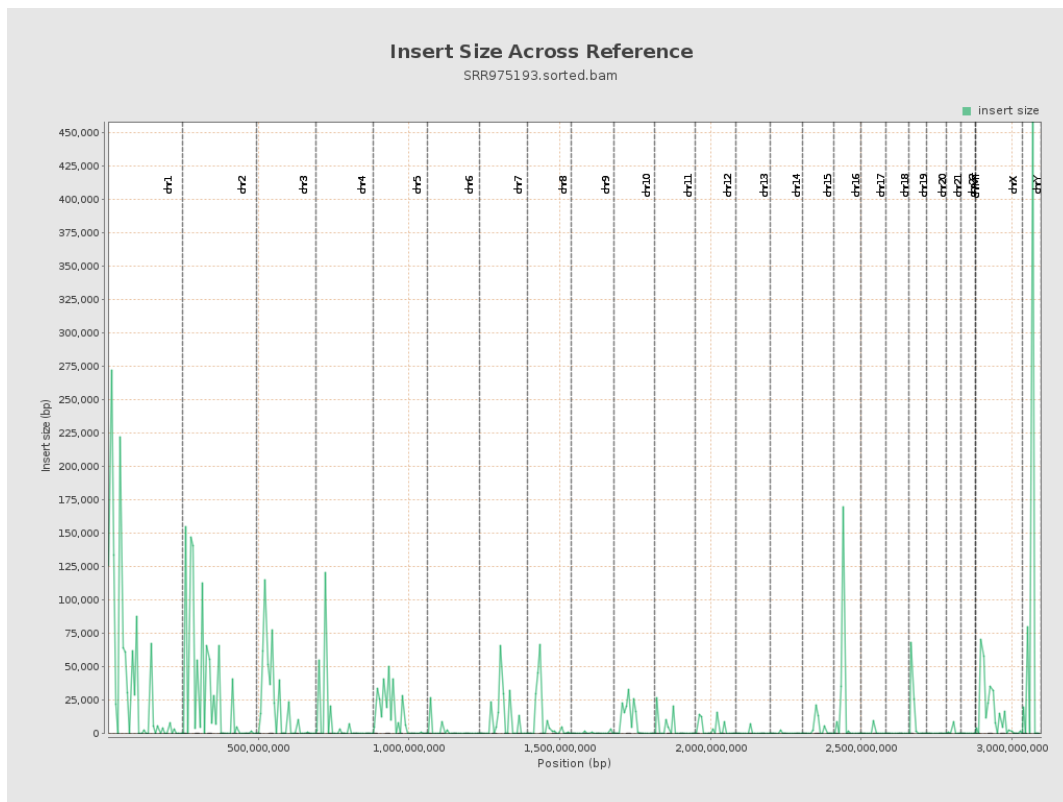
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

