Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 01:26:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927055.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_SRR927055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927055_1.fastq.gz SRR927055_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 01:26:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,500,126
Mapped reads	27,078,584 / 98.47%
Unmapped reads	421,542 / 1.53%
Mapped paired reads	27,078,584 / 98.47%
Mapped reads, first in pair	13,590,537 / 49.42%
Mapped reads, second in pair	13,488,047 / 49.05%
Mapped reads, both in pair	26,840,540 / 97.6%
Mapped reads, singletons	238,044 / 0.87%
Secondary alignments	0
Supplementary alignments	171,407 / 0.62%
Read min/max/mean length	30 / 101 / 101.26
Duplicated reads (estimated)	1,706,952 / 6.21%
Duplication rate	5.02%
Clipped reads	5,997,161 / 21.81%

2.2. ACGT Content

Number/percentage of A's	742,862,259 / 28.82%
Number/percentage of C's	516,265,483 / 20.03%
Number/percentage of T's	751,316,480 / 29.14%
Number/percentage of G's	566,988,728 / 21.99%
Number/percentage of N's	438,841 / 0.02%

GC Percentage	42.02%

2.3. Coverage

Mean	0.8334
Standard Deviation	3.0741

2.4. Mapping Quality

Mean Mapping Quality	53.82

2.5. Insert size

Mean	57,326.94
Standard Deviation	2,346,019.4
P25/Median/P75	149 / 191 / 254

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	26,037,726
Insertions	413,837
Mapped reads with at least one insertion	1.5%
Deletions	1,381,096
Mapped reads with at least one deletion	4.97%
Homopolymer indels	53.28%

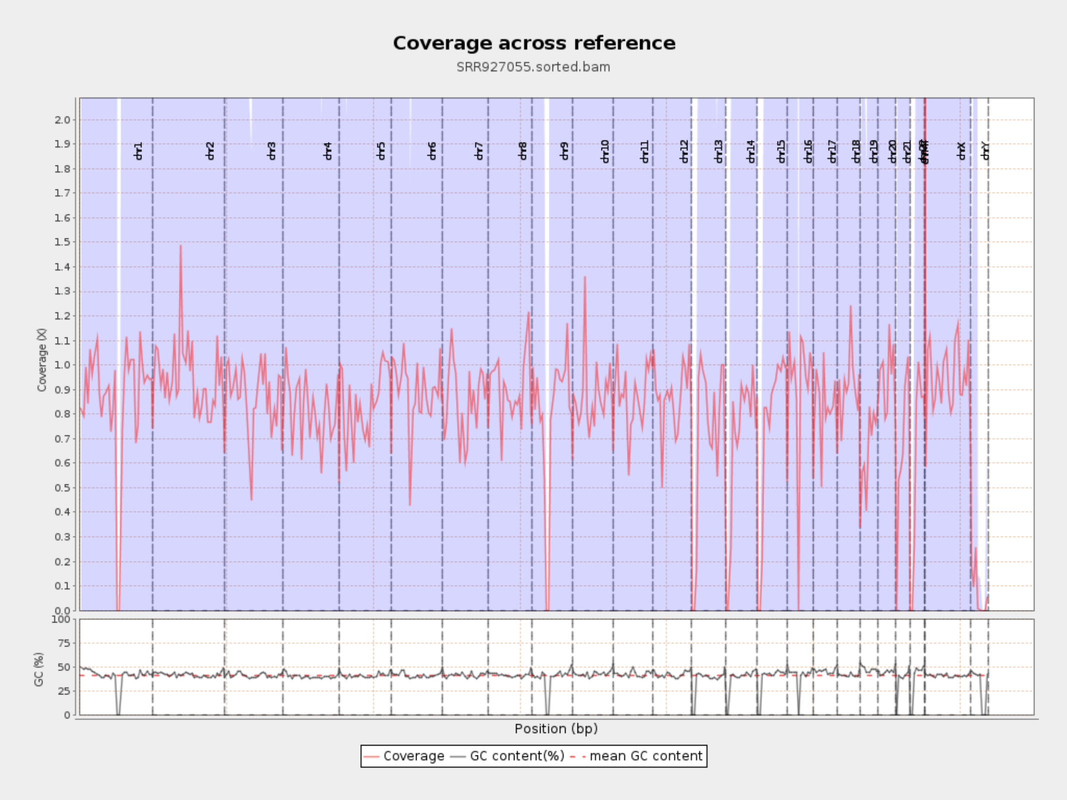
2.7. Chromosome stats

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

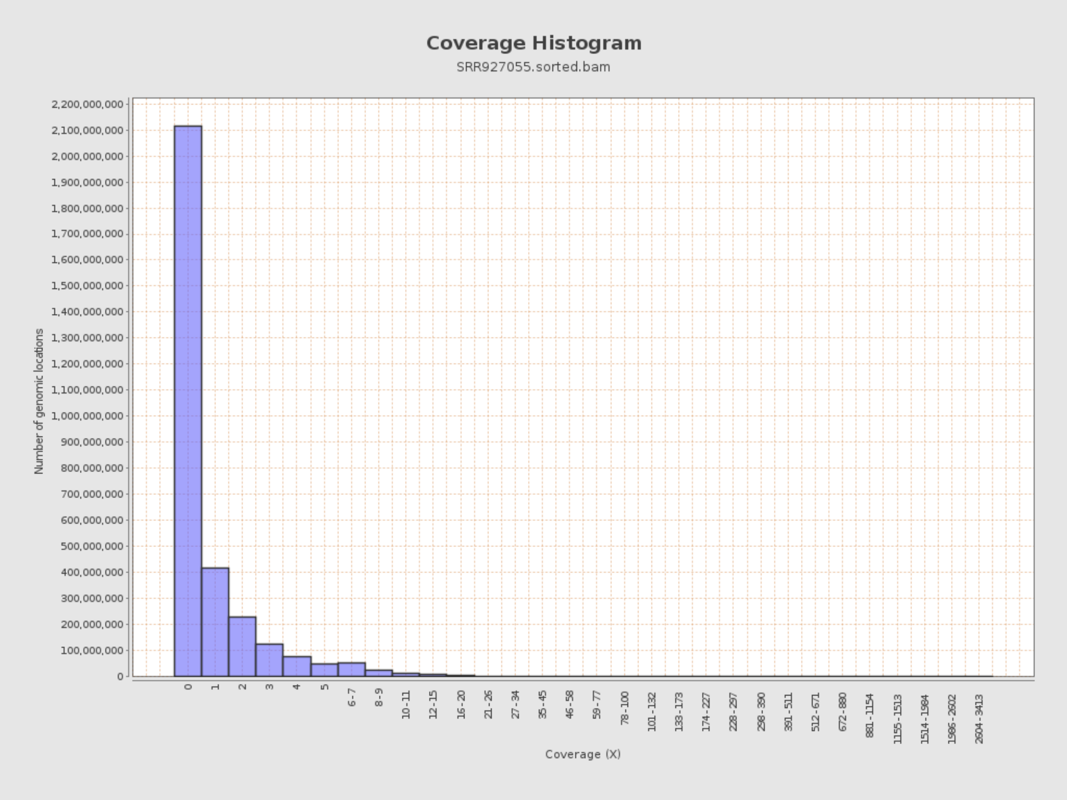
		bases	coverage	deviation
chr1	249250621	215488103	0.8645	4.0783
chr2	243199373	231737236	0.9529	4.8947
chr3	198022430	172459565	0.8709	1.824
chr4	191154276	156461102	0.8185	2.6784
chr5	180915260	151900314	0.8396	1.7647
chr6	171115067	153463583	0.8968	1.8811
chr7	159138663	136238484	0.8561	2.3989
chr8	146364022	133251790	0.9104	2.1592
chr9	141213431	110803656	0.7847	3.8261
chr10	135534747	119689095	0.8831	6.0241
chr11	135006516	117679814	0.8717	2.3324
chr12	133851895	116632776	0.8714	1.84
chr13	115169878	82056852	0.7125	1.6451
chr14	107349540	73066998	0.6806	1.6738
chr15	102531392	75154486	0.733	1.7307
chr16	90354753	80531927	0.8913	3.7306
chr17	81195210	67135115	0.8268	2.3761
chr18	78077248	72321449	0.9263	4.0062
chr19	59128983	38786469	0.656	2.4688
chr20	63025520	60056714	0.9529	2.0896
chr21	48129895	32687642	0.6792	2.2814
chr22	51304566	31537748	0.6147	1.653
chrMT	16571	118678	7.1618	6.2236
chrX	155270560	146365449	0.9426	2.158

chrY	59373566	4171894	0.0703	3.2229

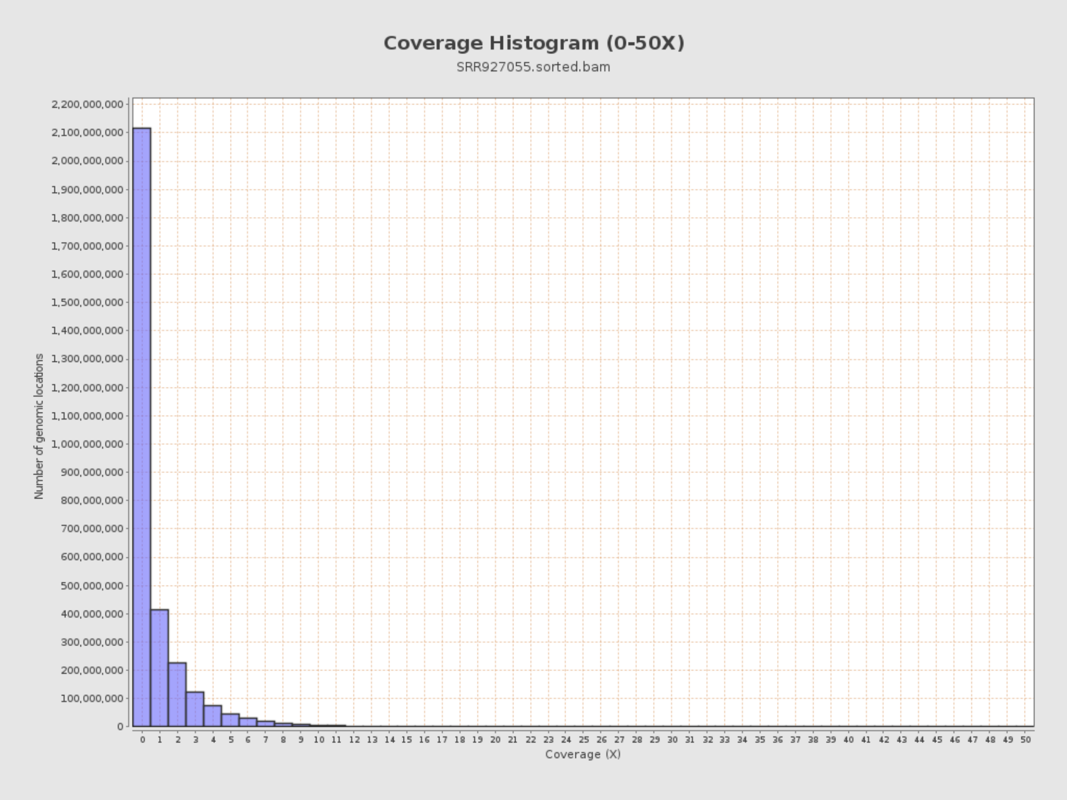
3. Results : Coverage across reference



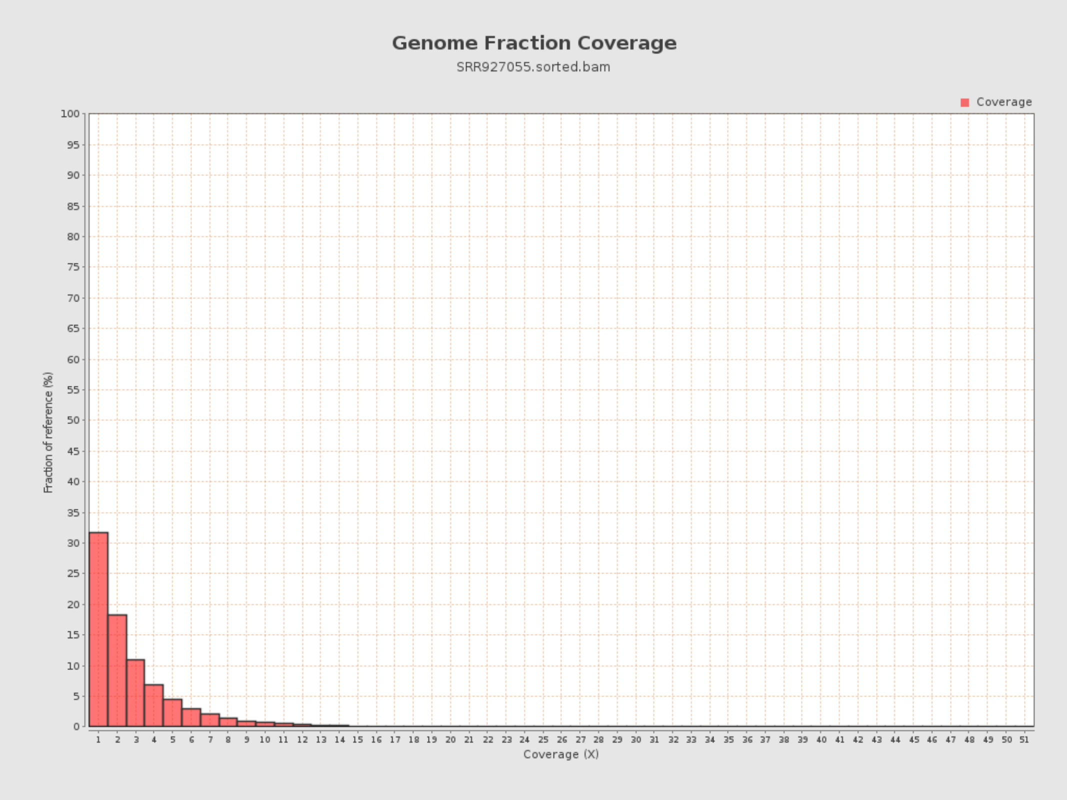
4. Results : Coverage Histogram



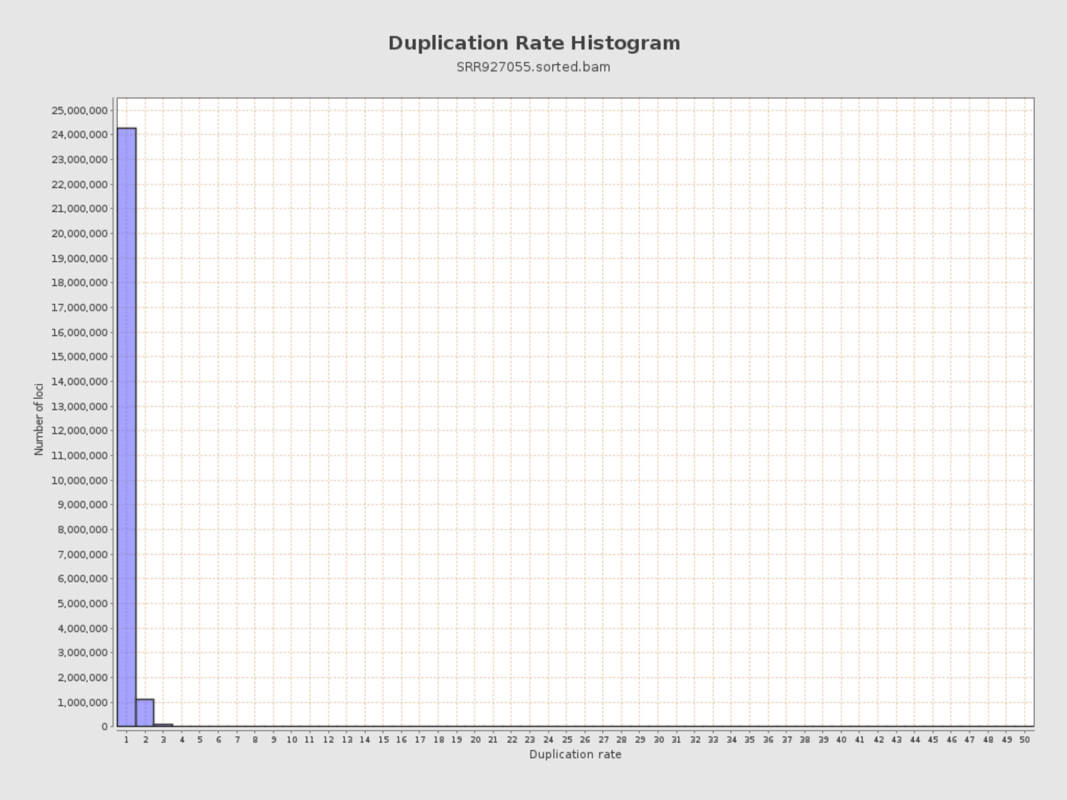
5. Results : Coverage Histogram (0-50X)



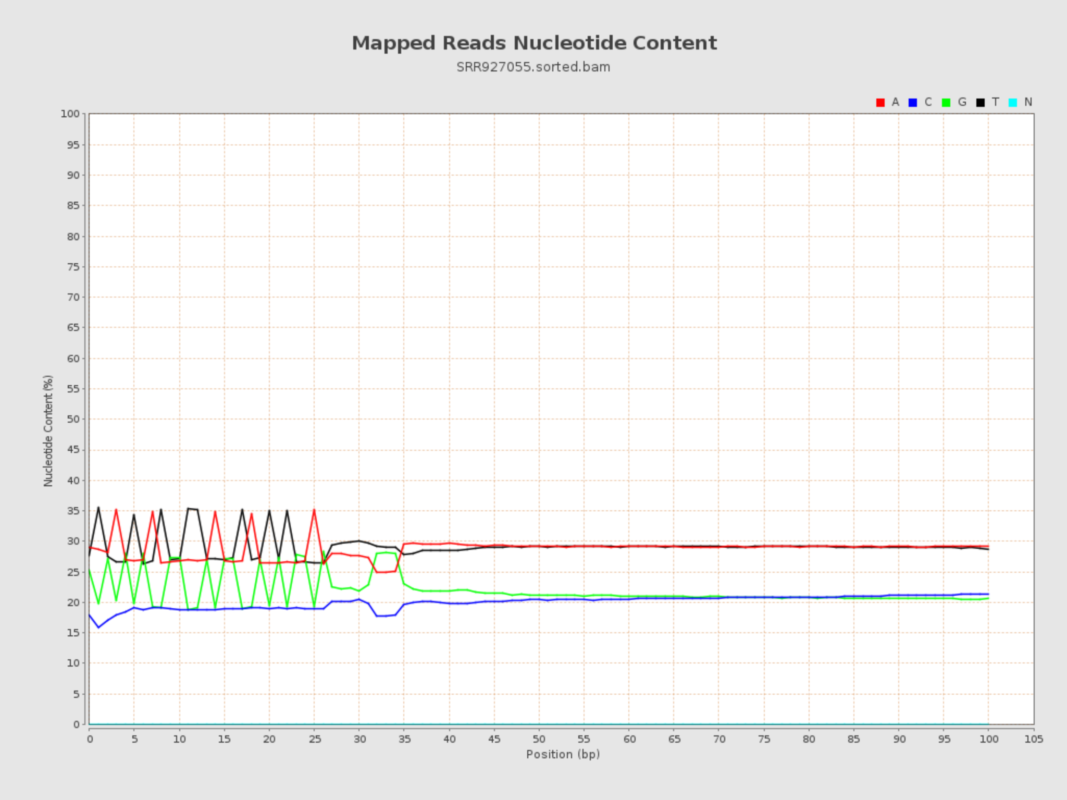
6. Results : Genome Fraction Coverage



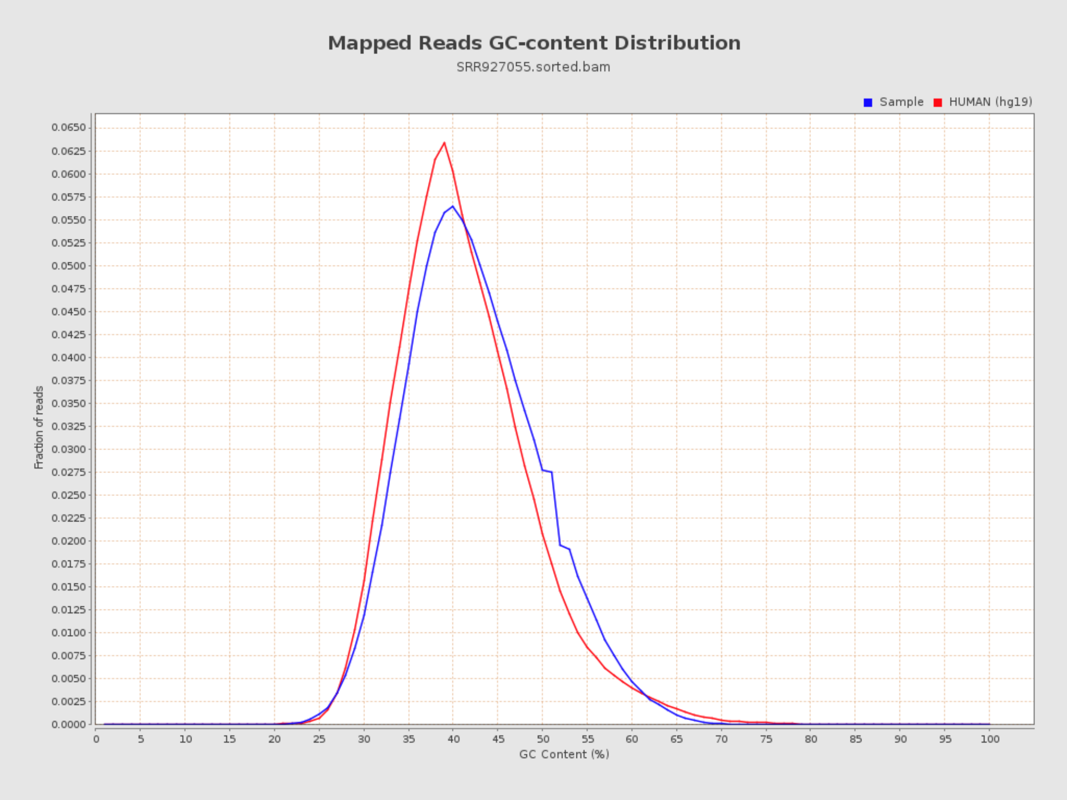
7. Results : Duplication Rate Histogram



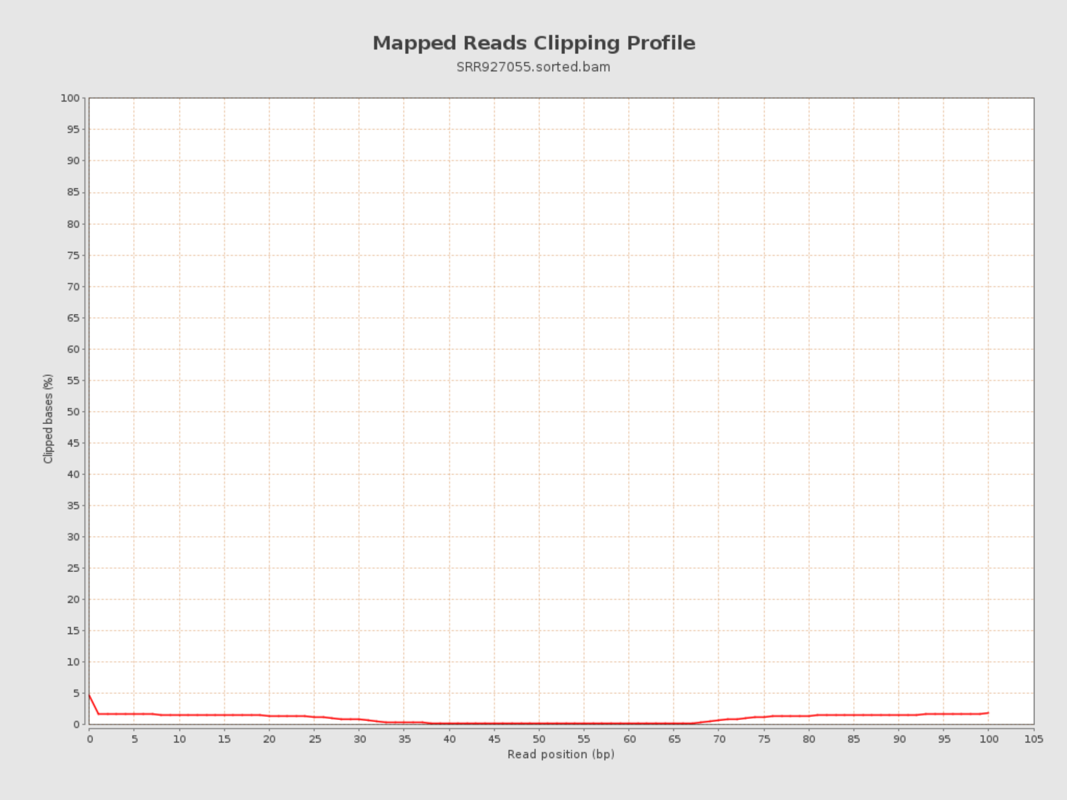
8. Results : Mapped Reads Nucleotide Content



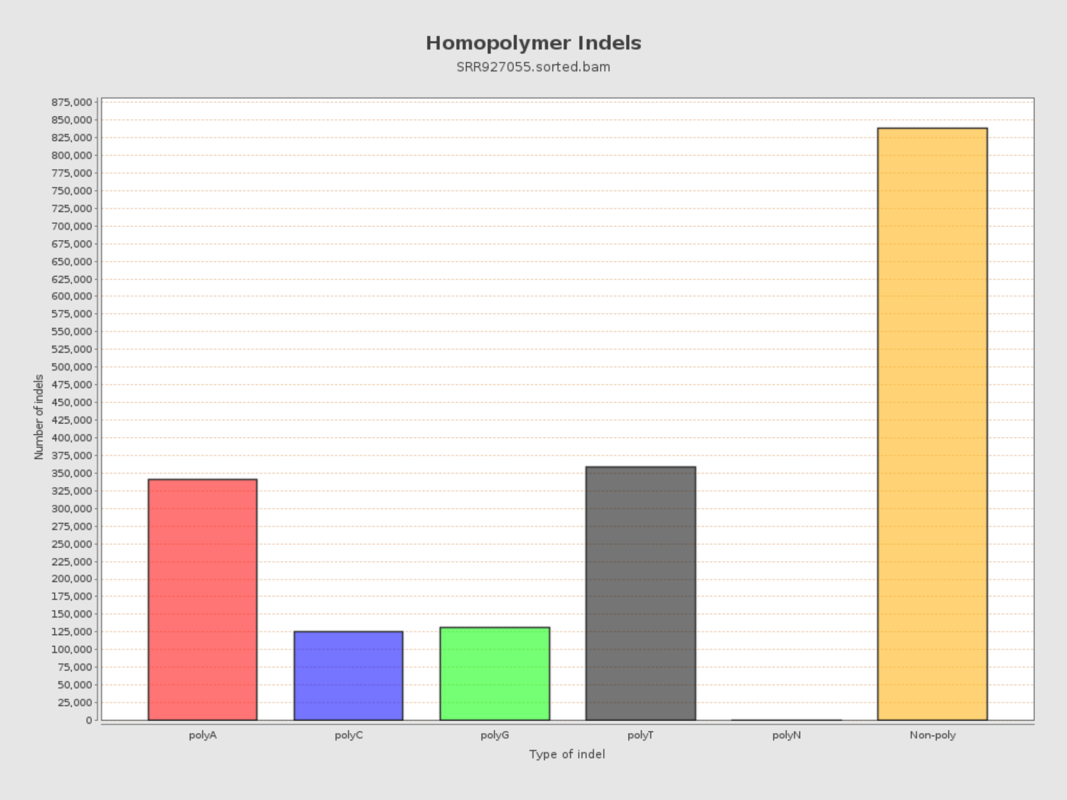
9. Results : Mapped Reads GC-content Distribution



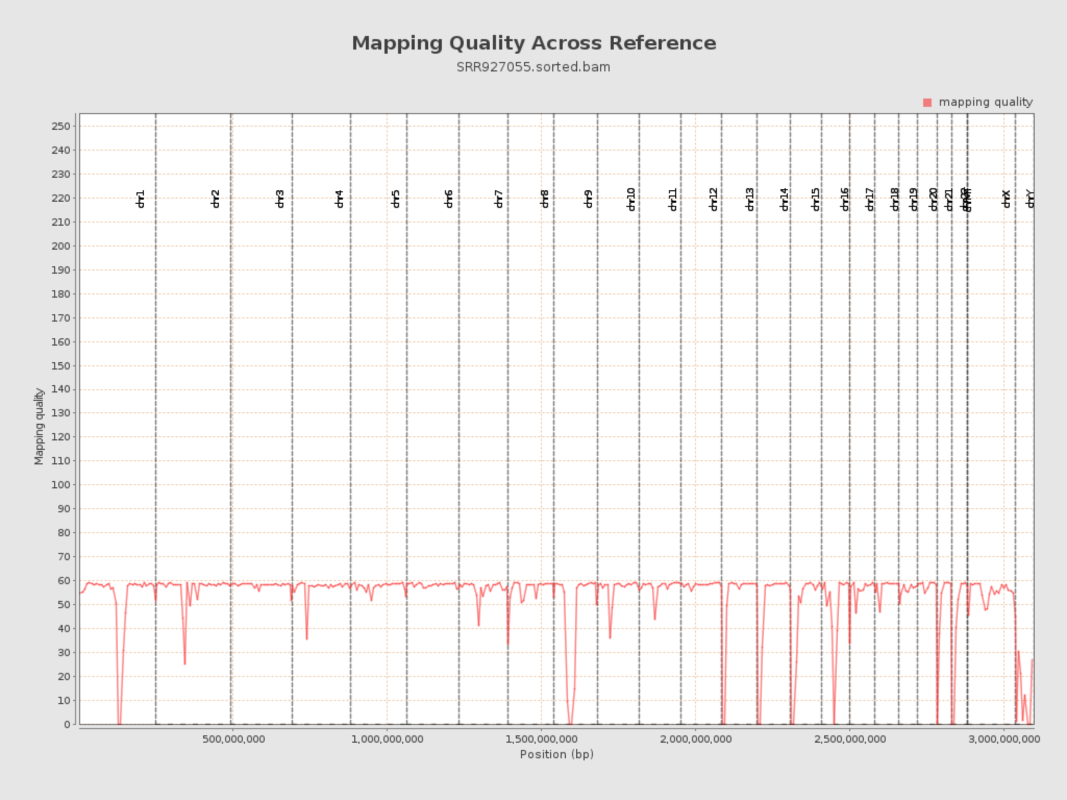
10. Results : Mapped Reads Clipping Profile



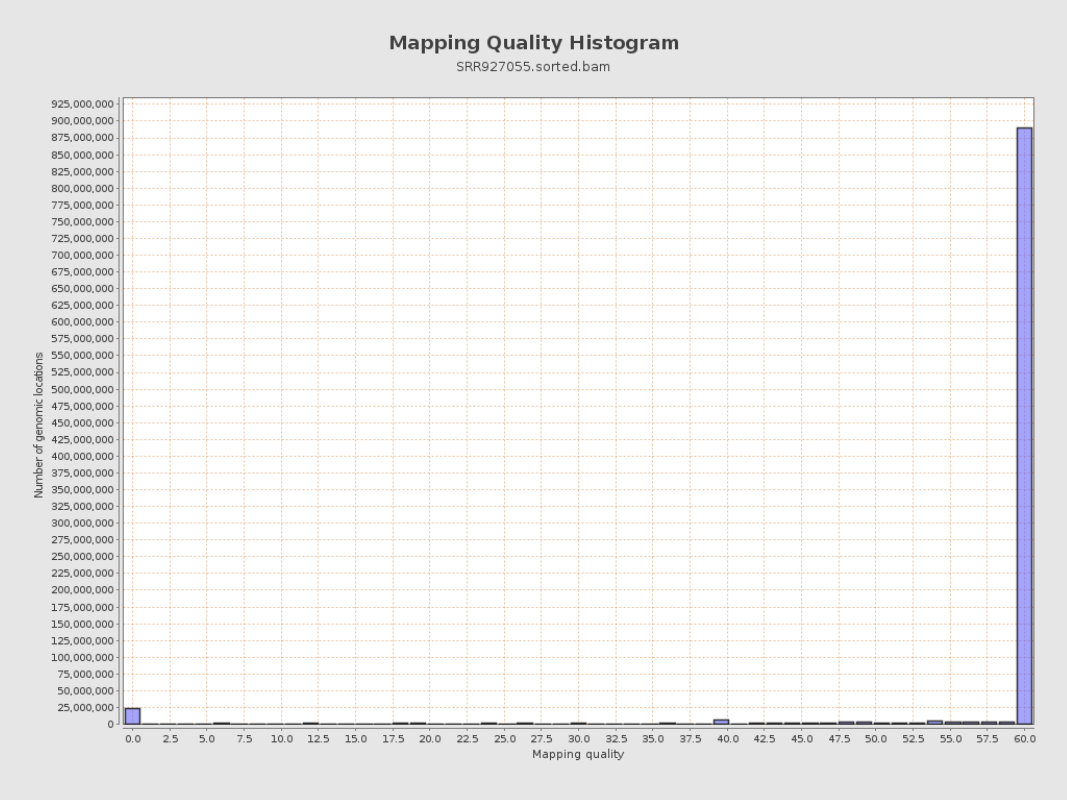
11. Results : Homopolymer Indels



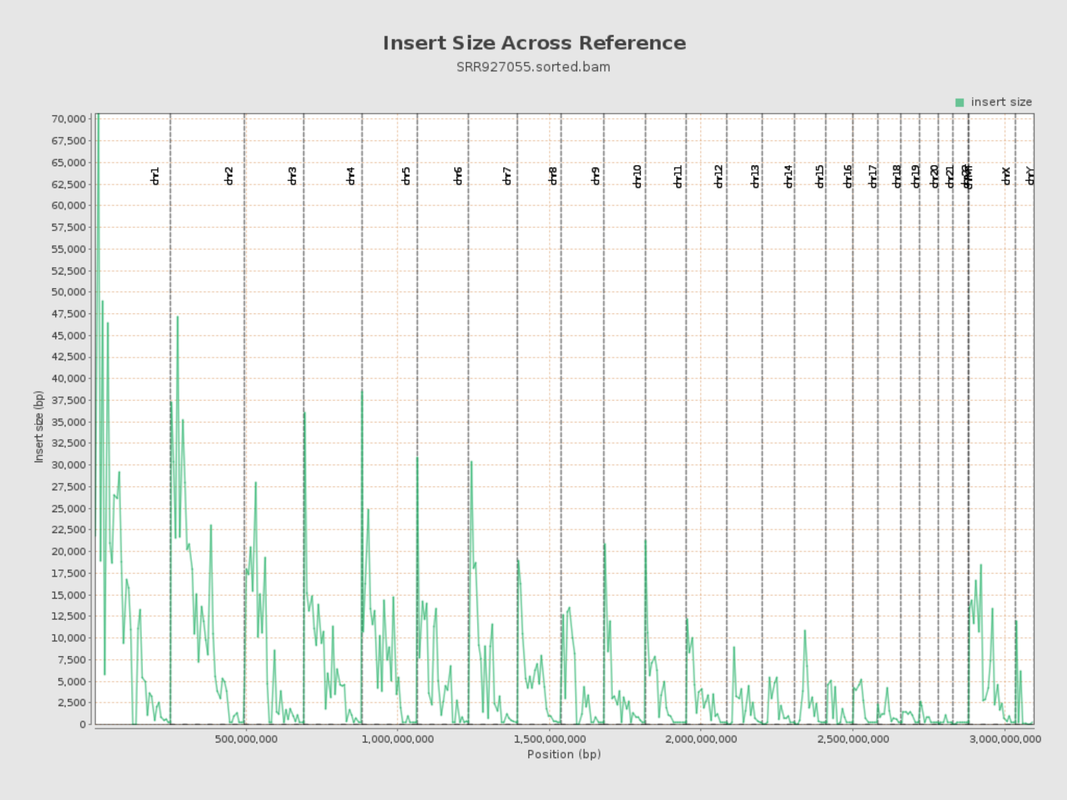
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram