Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 06:03:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927064.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_SRR927064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927064_1.fastq.gz SRR927064_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 06:03:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,137,772
Mapped reads	31,660,072 / 98.51%
Unmapped reads	477,700 / 1.49%
Mapped paired reads	31,660,072 / 98.51%
Mapped reads, first in pair	15,893,624 / 49.45%
Mapped reads, second in pair	15,766,448 / 49.06%
Mapped reads, both in pair	31,372,028 / 97.62%
Mapped reads, singletons	288,044 / 0.9%
Secondary alignments	0
Supplementary alignments	361,630 / 1.13%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	2,082,023 / 6.48%
Duplication rate	5.19%
Clipped reads	7,504,866 / 23.35%

2.2. ACGT Content

Number/percentage of A's	872,018,985 / 28.95%
Number/percentage of C's	599,570,472 / 19.9%
Number/percentage of T's	882,038,270 / 29.28%
Number/percentage of G's	658,382,162 / 21.85%
Number/percentage of N's	516,508 / 0.02%

GC Percentage	41.76%

2.3. Coverage

Mean	0.9739
Standard Deviation	3.5989

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	117,760.85
Standard Deviation	3,354,700.78
P25/Median/P75	149 / 191 / 256

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	30,845,861
Insertions	487,015
Mapped reads with at least one insertion	1.51%
Deletions	1,603,255
Mapped reads with at least one deletion	4.93%
Homopolymer indels	53.06%

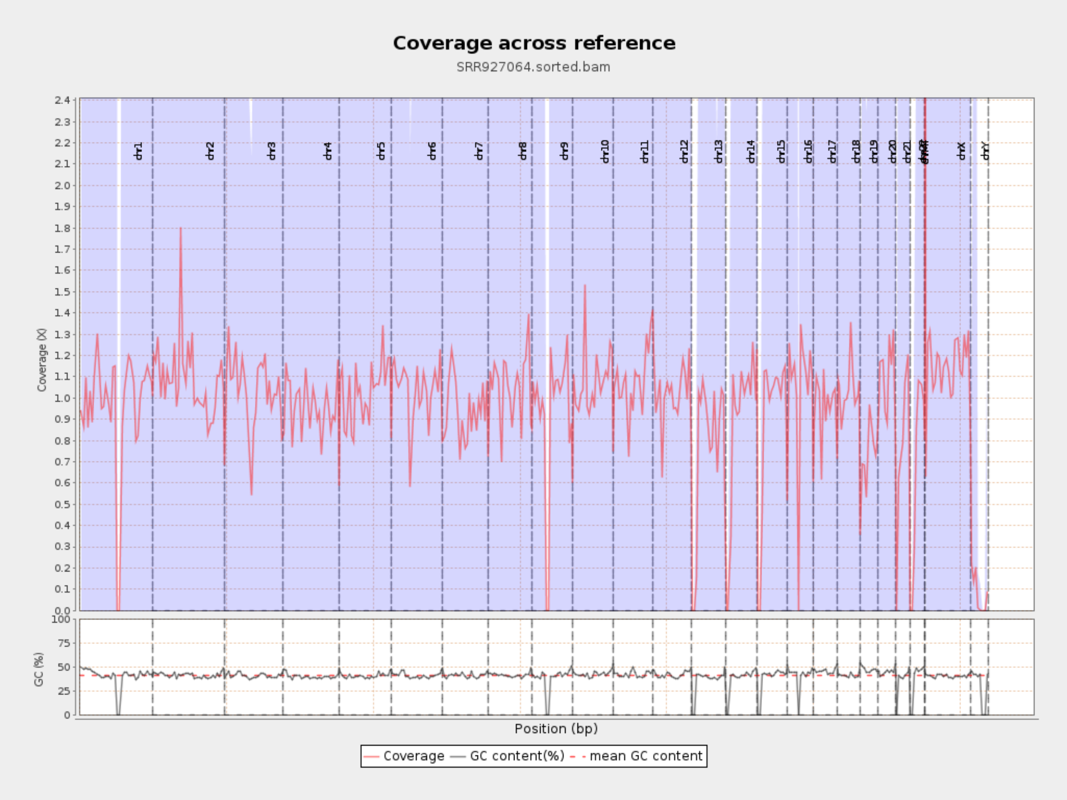
2.7. Chromosome stats

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

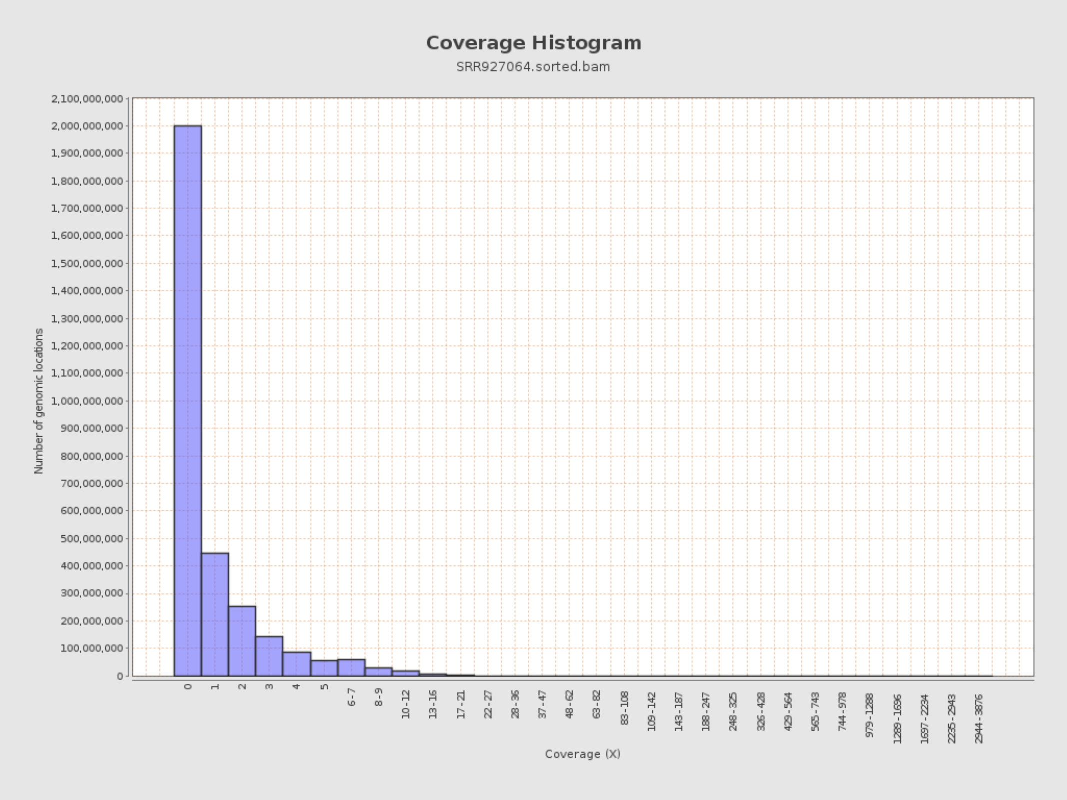
		bases	coverage	deviation
chr1	249250621	240982388	0.9668	4.5922
chr2	243199373	265840502	1.0931	5.9848
chr3	198022430	205327474	1.0369	2.0317
chr4	191154276	184207273	0.9637	2.7268
chr5	180915260	186238958	1.0294	1.998
chr6	171115067	178263110	1.0418	2.0325
chr7	159138663	149948250	0.9422	2.6838
chr8	146364022	155355728	1.0614	2.4722
chr9	141213431	129836463	0.9194	5.0654
chr10	135534747	147260550	1.0865	6.7752
chr11	135006516	144559375	1.0708	3.6599
chr12	133851895	136624924	1.0207	2.0188
chr13	115169878	88222156	0.766	1.7142
chr14	107349540	93106717	0.8673	1.927
chr15	102531392	89864110	0.8765	1.9536
chr16	90354753	92177233	1.0202	4.3263
chr17	81195210	77654416	0.9564	3.0305
chr18	78077248	81915475	1.0492	5.2418
chr19	59128983	43356740	0.7333	2.8927
chr20	63025520	69301349	1.0996	2.2965
chr21	48129895	38010301	0.7897	2.3402
chr22	51304566	34692560	0.6762	1.776
chrMT	16571	225038	13.5802	10.4638
chrX	155270560	177247729	1.1415	2.4643

chrY	59373566	4556782	0.0767	1.9718

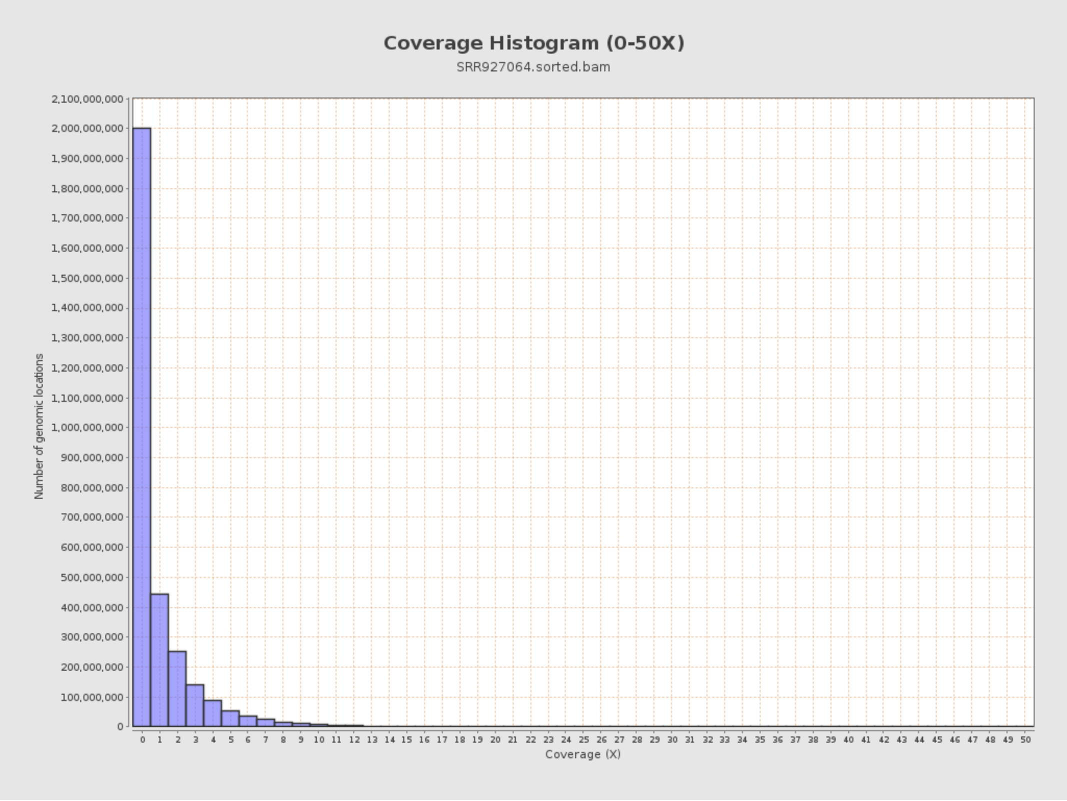
3. Results : Coverage across reference



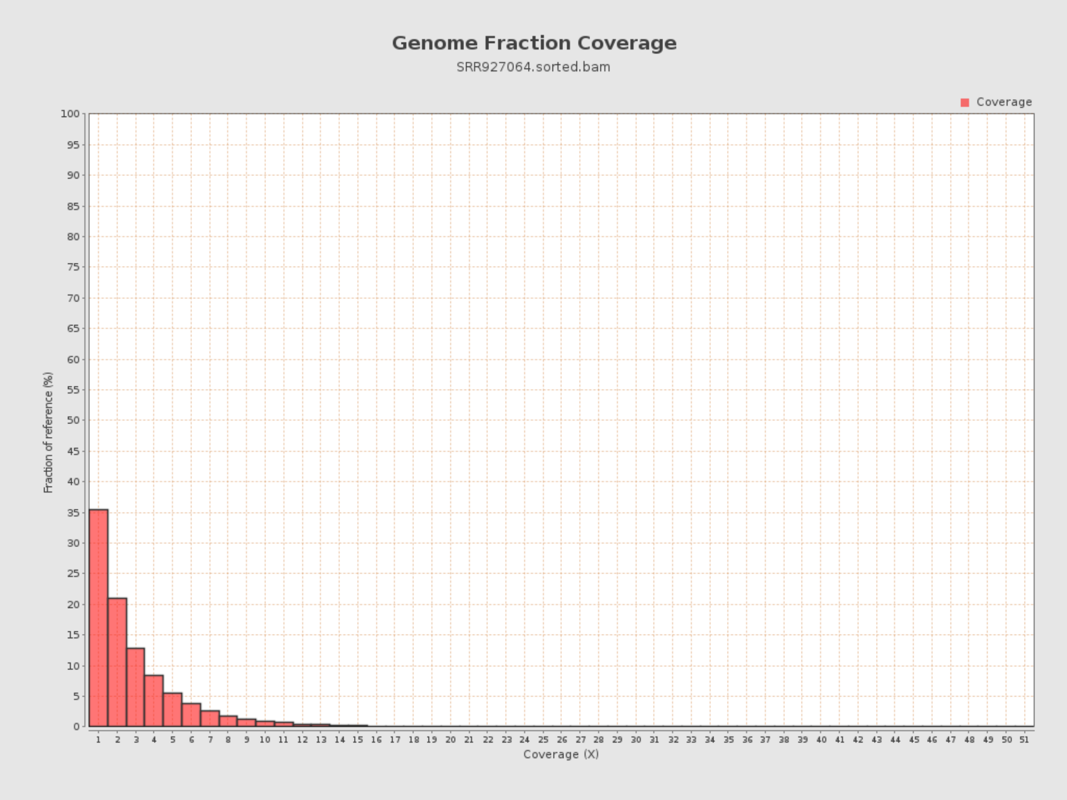
4. Results : Coverage Histogram



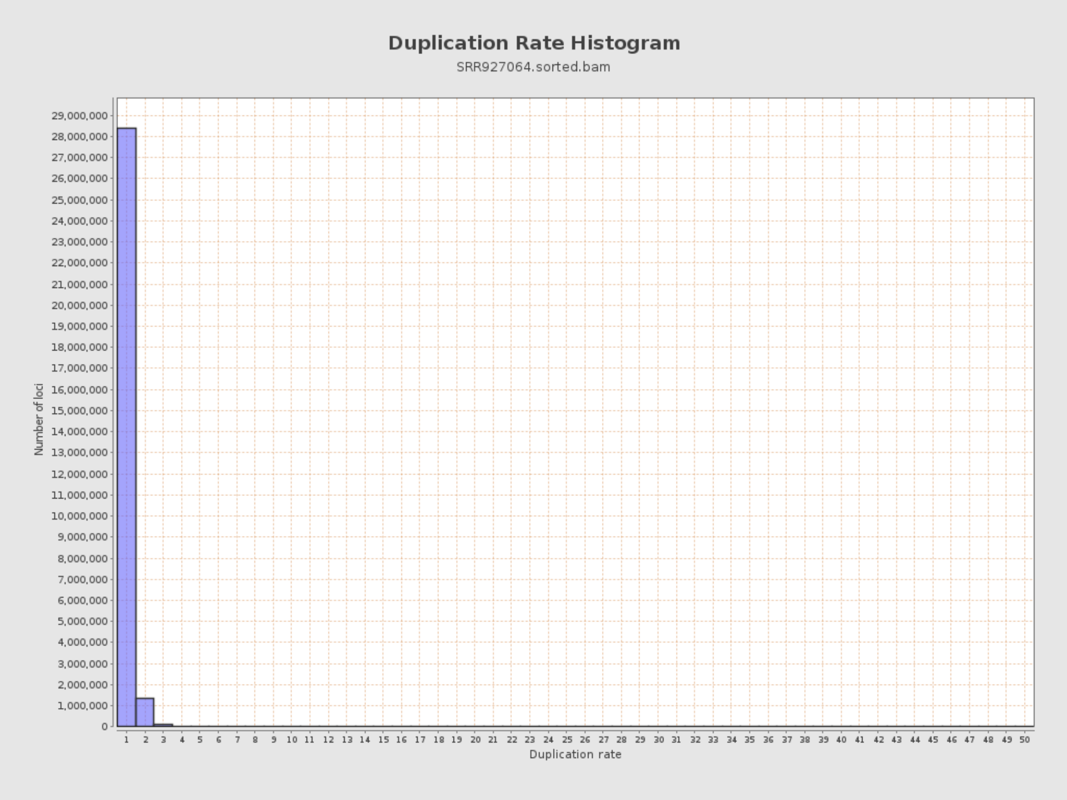
5. Results : Coverage Histogram (0-50X)



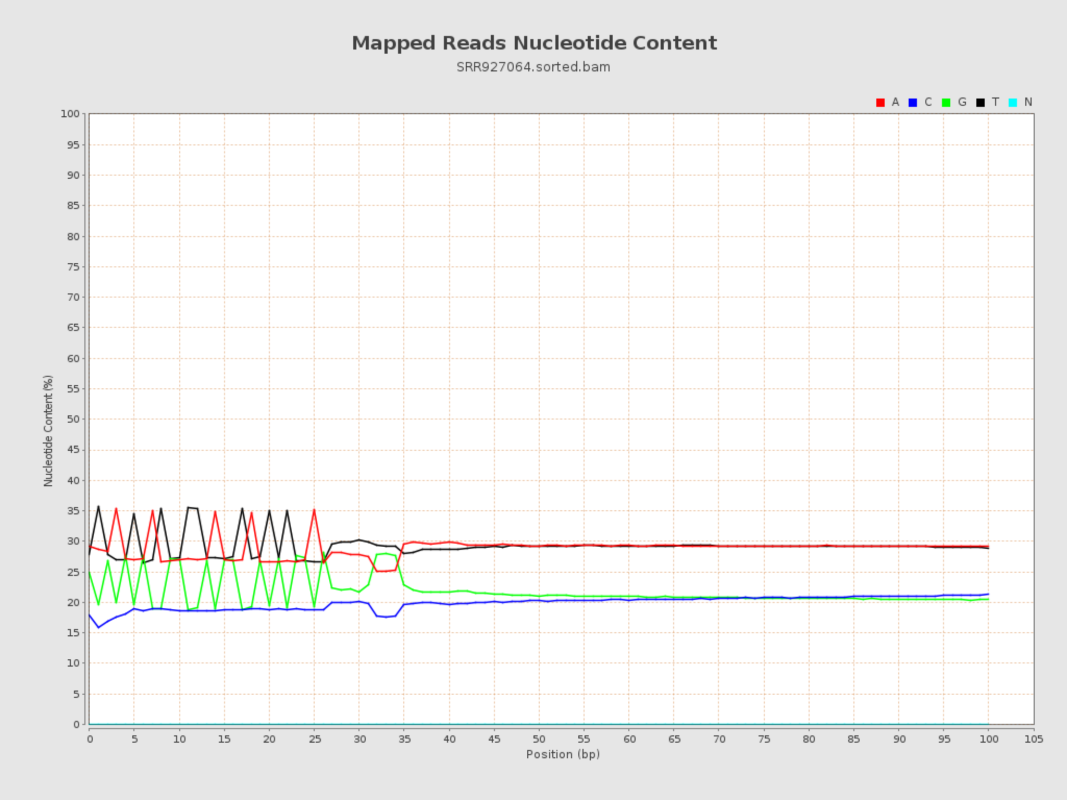
6. Results : Genome Fraction Coverage



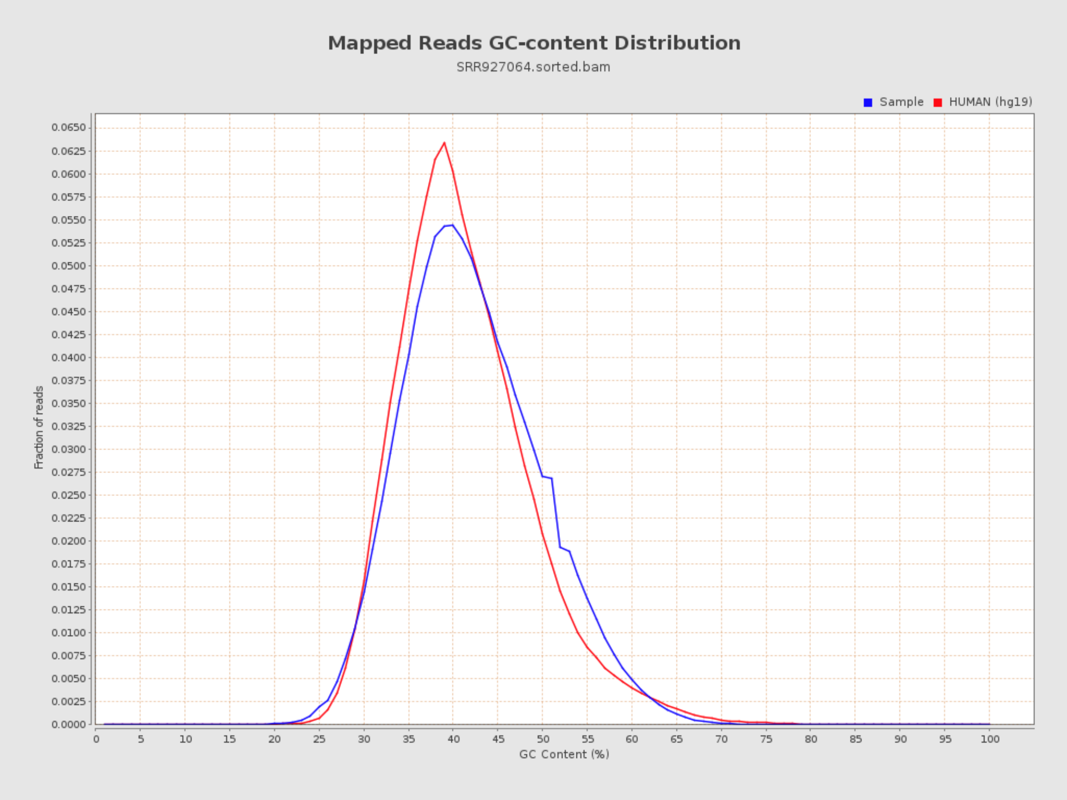
7. Results : Duplication Rate Histogram



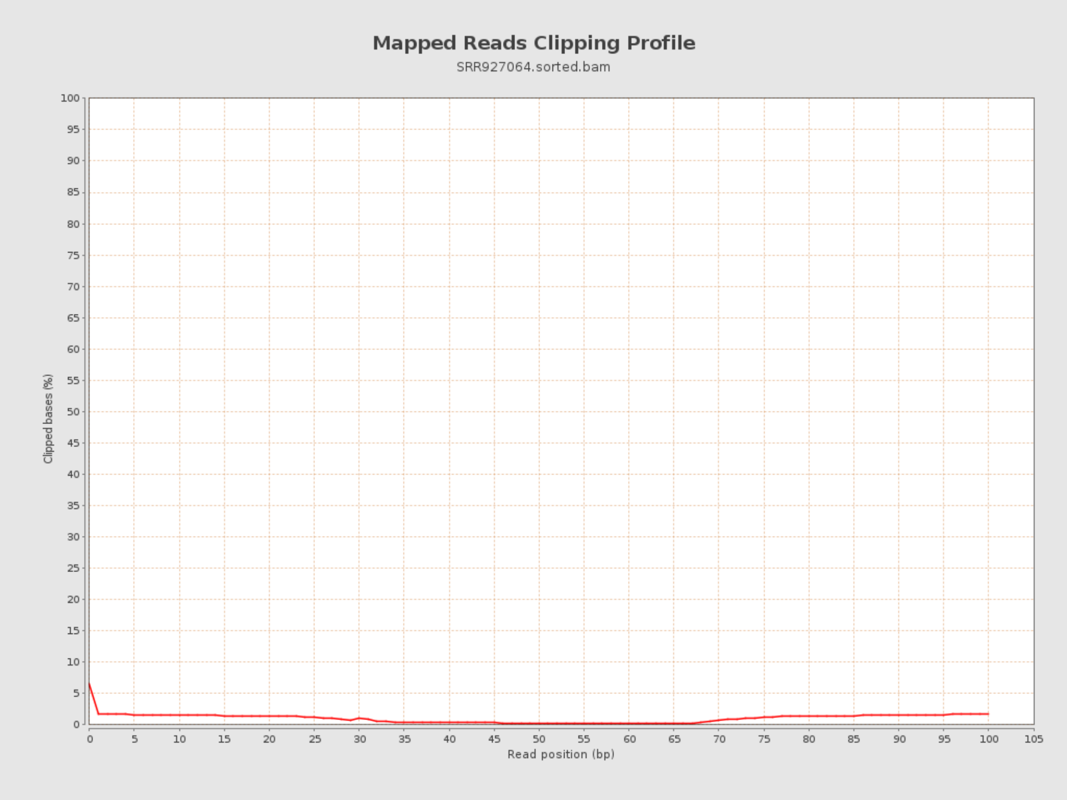
8. Results : Mapped Reads Nucleotide Content



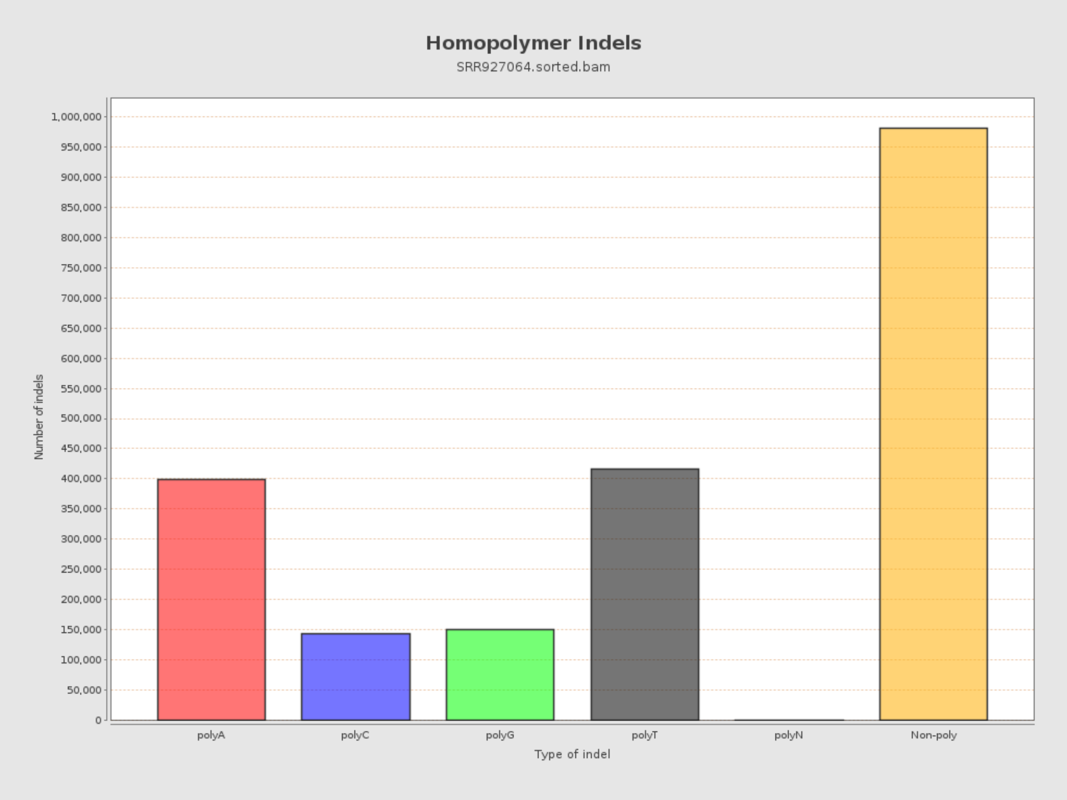
9. Results : Mapped Reads GC-content Distribution



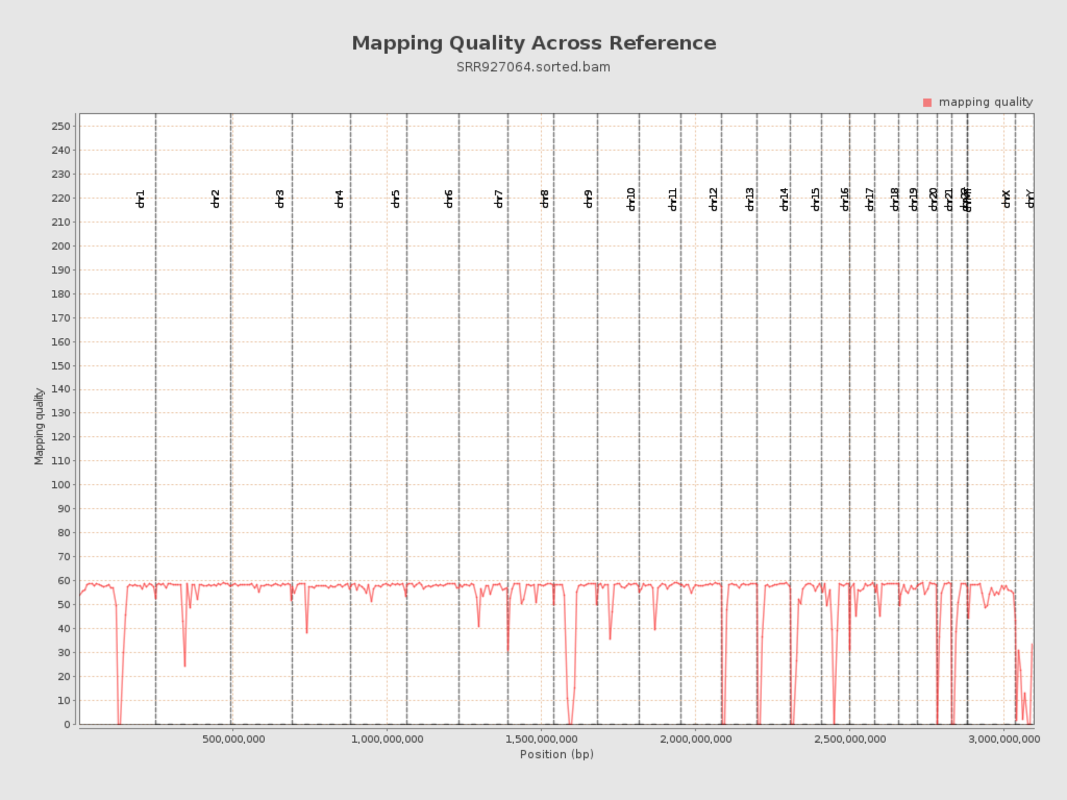
10. Results : Mapped Reads Clipping Profile



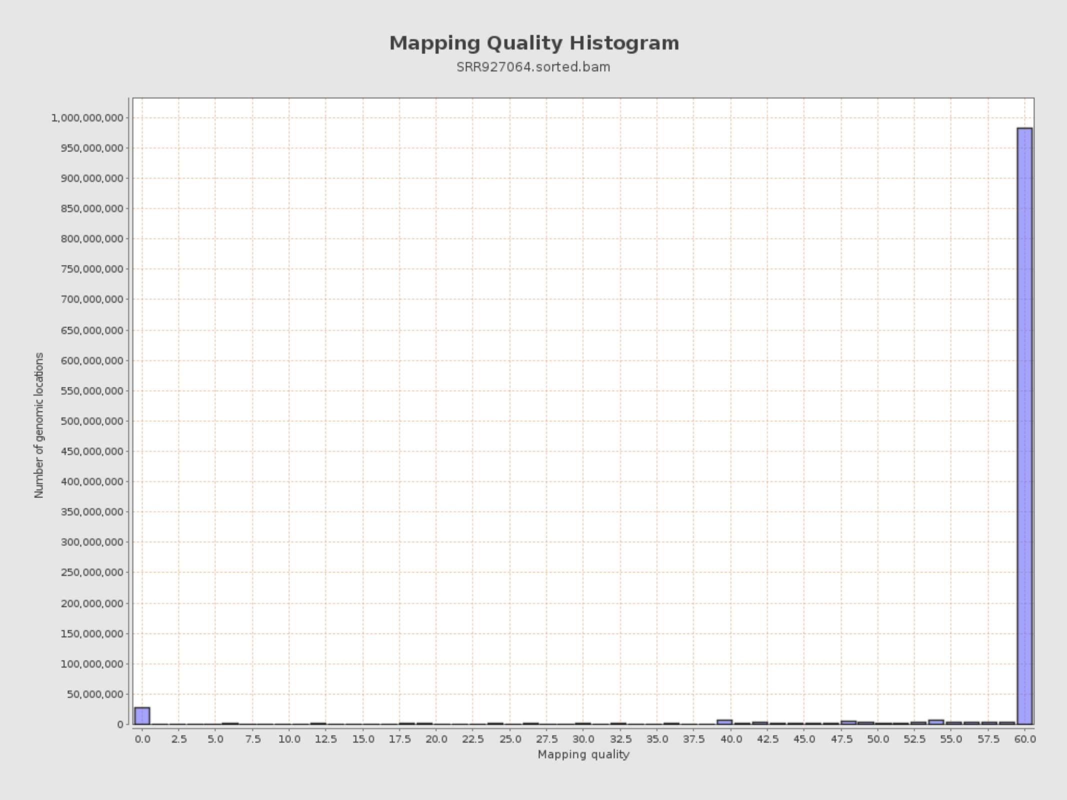
11. Results : Homopolymer Indels



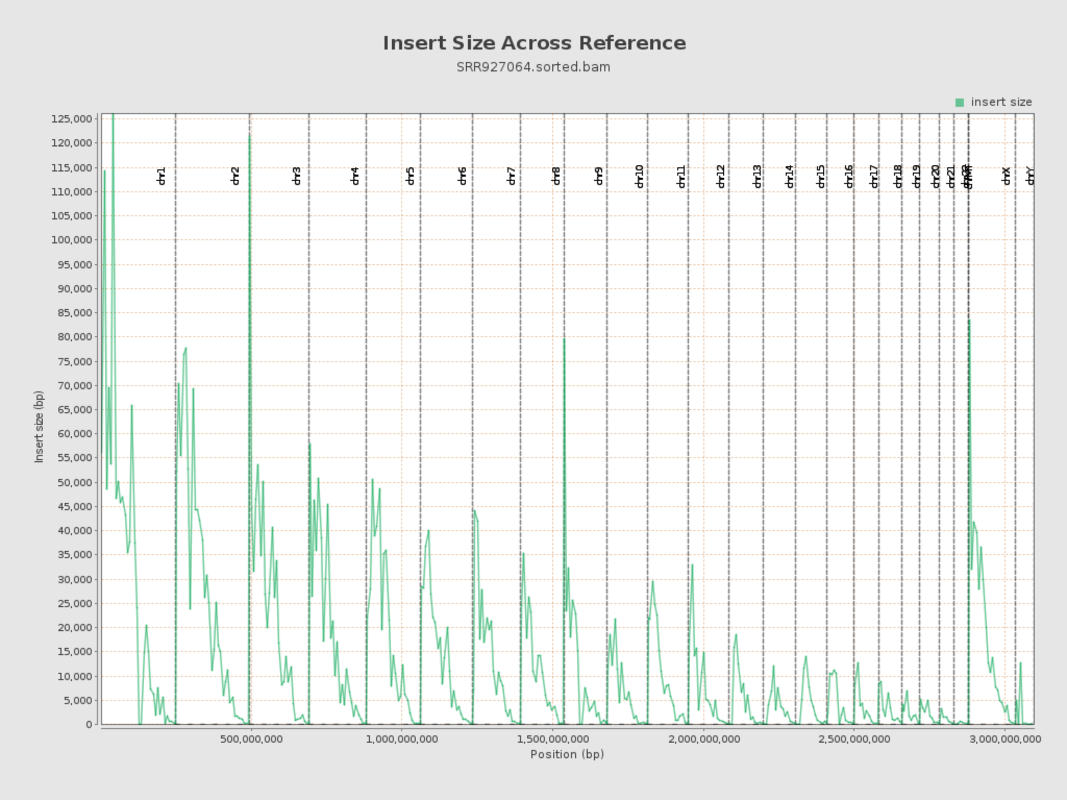
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram