Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 02:58:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927058.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_SRR927058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927058_1.fastq.gz SRR927058_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 02:58:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,828,920
Mapped reads	28,459,657 / 98.72%
Unmapped reads	369,263 / 1.28%
Mapped paired reads	28,459,657 / 98.72%
Mapped reads, first in pair	14,274,365 / 49.51%
Mapped reads, second in pair	14,185,292 / 49.21%
Mapped reads, both in pair	28,271,082 / 98.07%
Mapped reads, singletons	188,575 / 0.65%
Secondary alignments	0
Supplementary alignments	223,268 / 0.77%
Read min/max/mean length	30 / 101 / 101.32
Duplicated reads (estimated)	1,736,086 / 6.02%
Duplication rate	4.78%
Clipped reads	5,308,607 / 18.41%

2.2. ACGT Content

Number/percentage of A's	805,143,656 / 29.37%
Number/percentage of C's	540,762,856 / 19.73%
Number/percentage of T's	811,273,384 / 29.59%
Number/percentage of G's	583,922,045 / 21.3%
Number/percentage of N's	248,749 / 0.01%

GC Percentage	41.03%

2.3. Coverage

Mean	0.8862
Standard Deviation	3.4044

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	80,099.52
Standard Deviation	2,763,721.14
P25/Median/P75	147 / 186 / 247

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	25,279,216
Insertions	463,222
Mapped reads with at least one insertion	1.6%
Deletions	1,521,539
Mapped reads with at least one deletion	5.2%
Homopolymer indels	53.48%

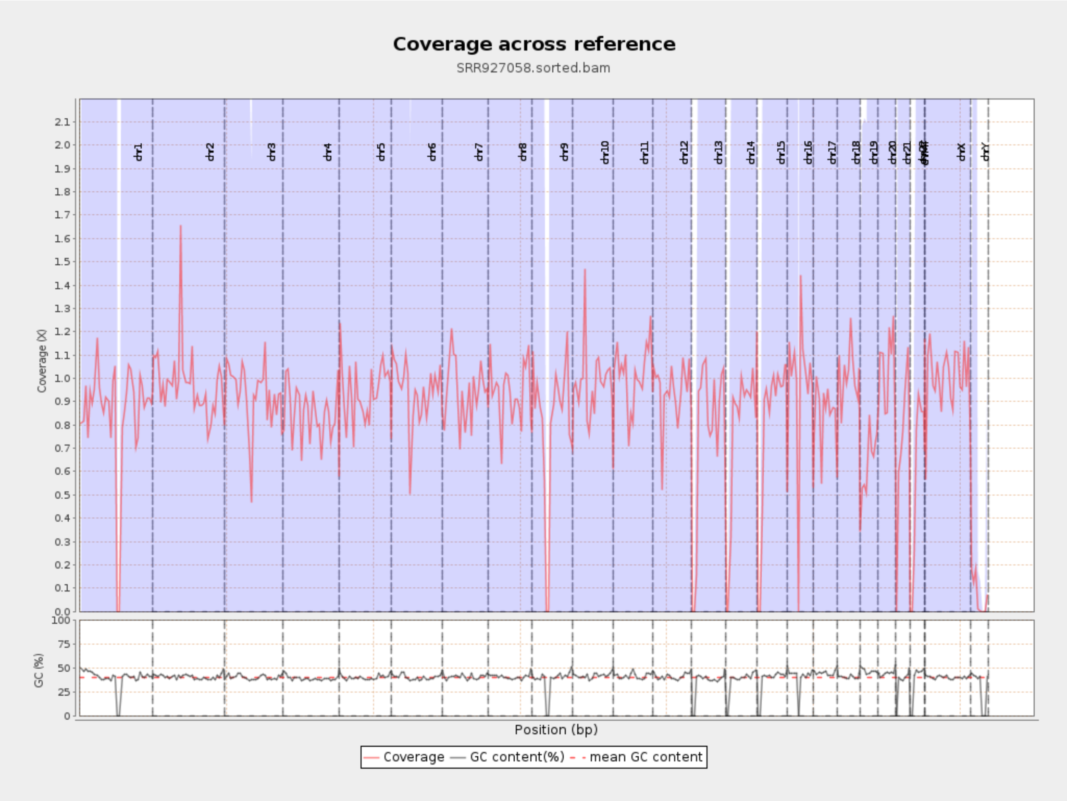
2.7. Chromosome stats

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

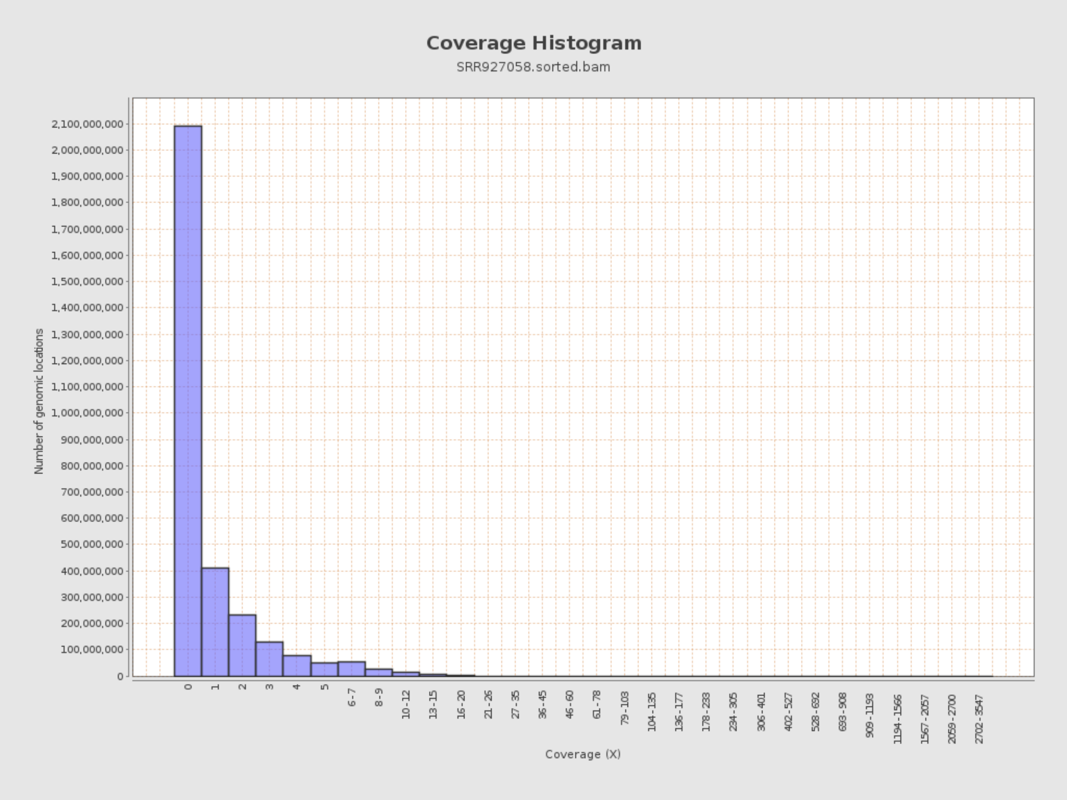
		bases	coverage	deviation
chr1	249250621	212550655	0.8528	4.2528
chr2	243199373	238243486	0.9796	5.7165
chr3	198022430	184287817	0.9306	1.9464
chr4	191154276	162691594	0.8511	2.7996
chr5	180915260	170684734	0.9435	1.9342
chr6	171115067	162193086	0.9479	2.0483
chr7	159138663	149720732	0.9408	2.8067
chr8	146364022	138143046	0.9438	2.2804
chr9	141213431	113082579	0.8008	4.0607
chr10	135534747	134297013	0.9909	6.4448
chr11	135006516	136528054	1.0113	3.4923
chr12	133851895	126623340	0.946	2.2528
chr13	115169878	87959033	0.7637	1.8352
chr14	107349540	82112393	0.7649	1.809
chr15	102531392	80636902	0.7865	1.9053
chr16	90354753	86535213	0.9577	4.852
chr17	81195210	68524897	0.844	2.627
chr18	78077248	79908230	1.0235	4.2828
chr19	59128983	37515941	0.6345	2.4897
chr20	63025520	65389764	1.0375	2.2693
chr21	48129895	36121061	0.7505	2.2503
chr22	51304566	29852889	0.5819	1.6718
chrMT	16571	19370	1.1689	1.5818
chrX	155270560	155910517	1.0041	2.3326

chrY	59373566	3963002	0.0667	2.0884

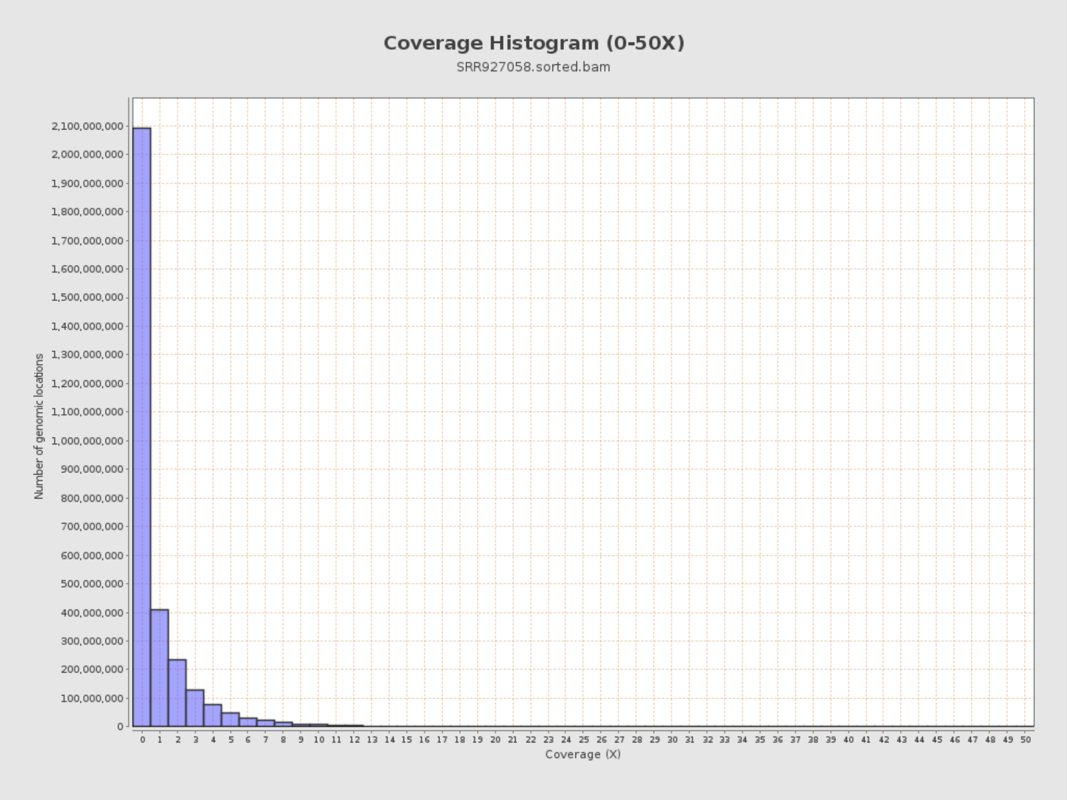
3. Results : Coverage across reference



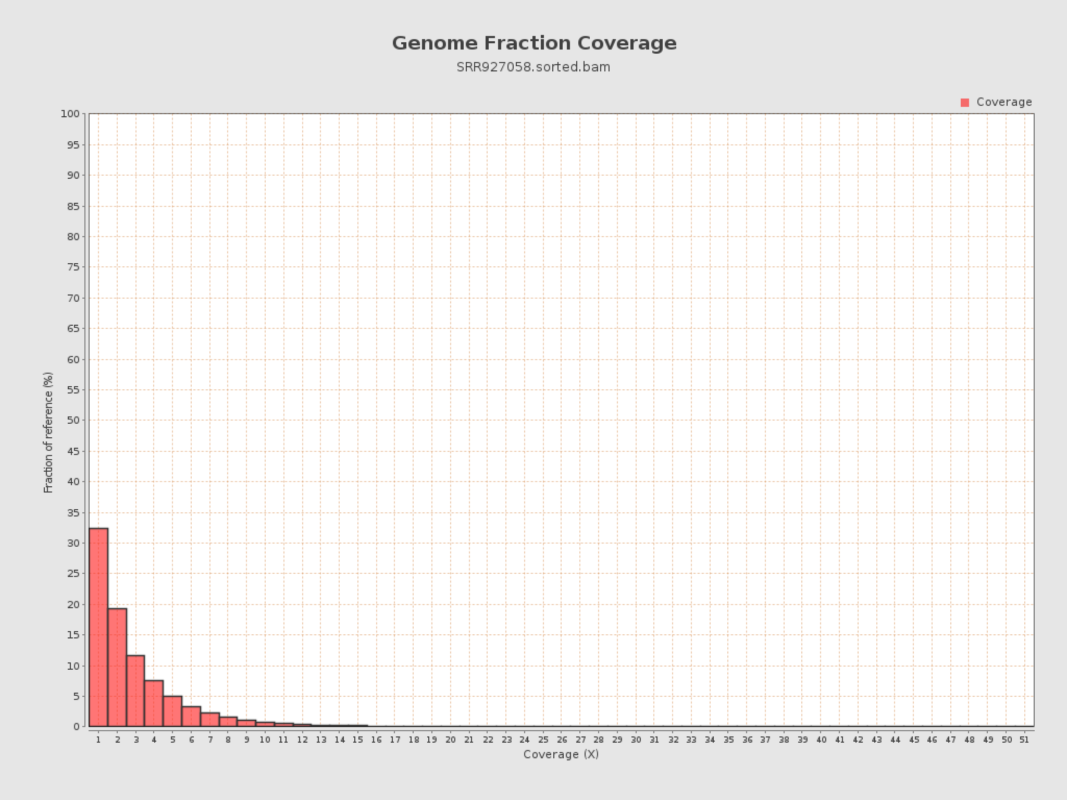
4. Results : Coverage Histogram



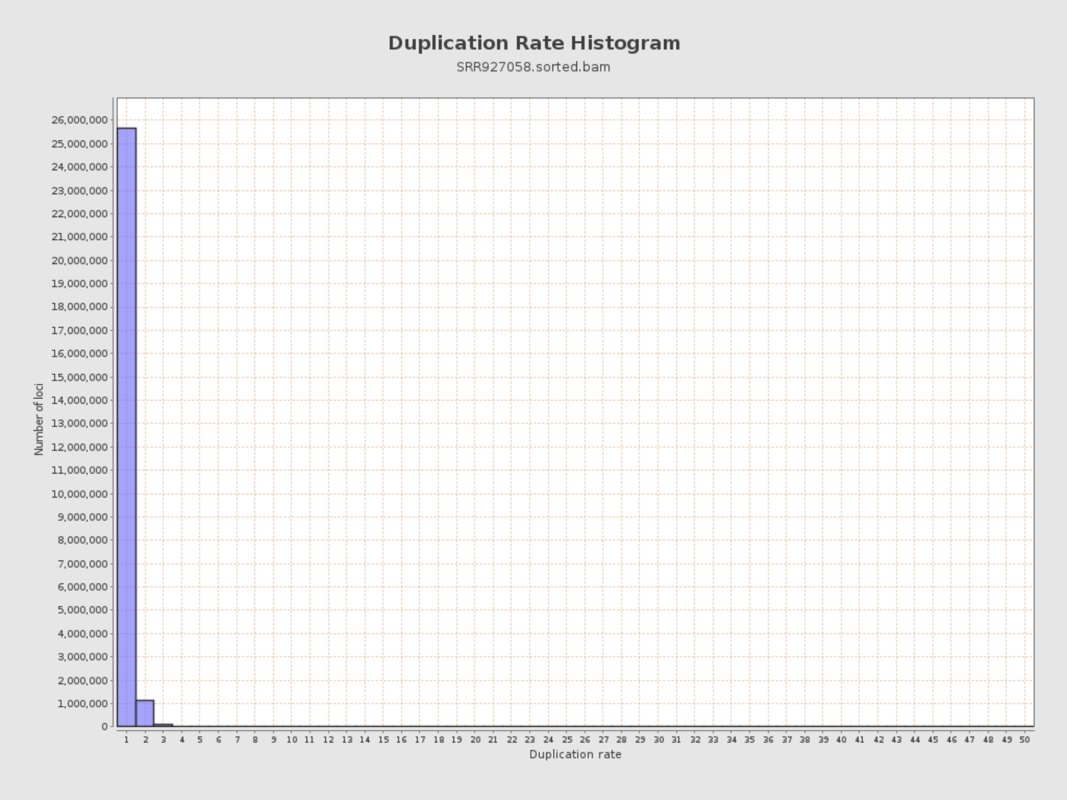
5. Results : Coverage Histogram (0-50X)



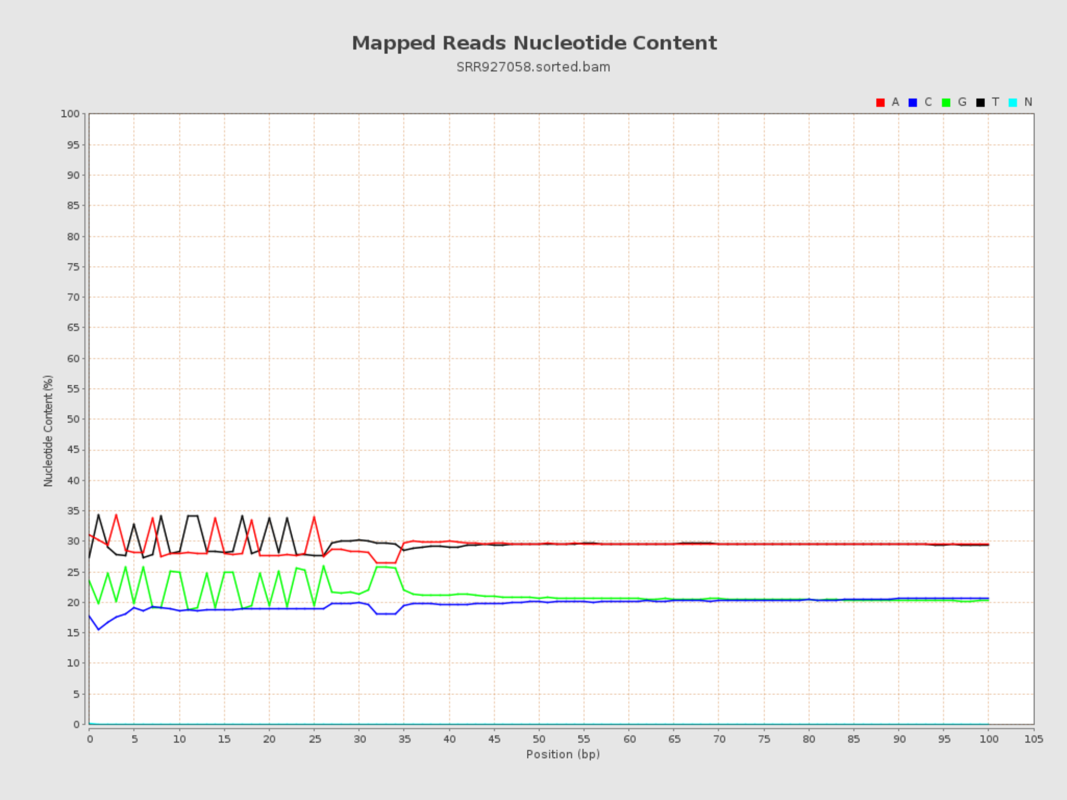
6. Results : Genome Fraction Coverage



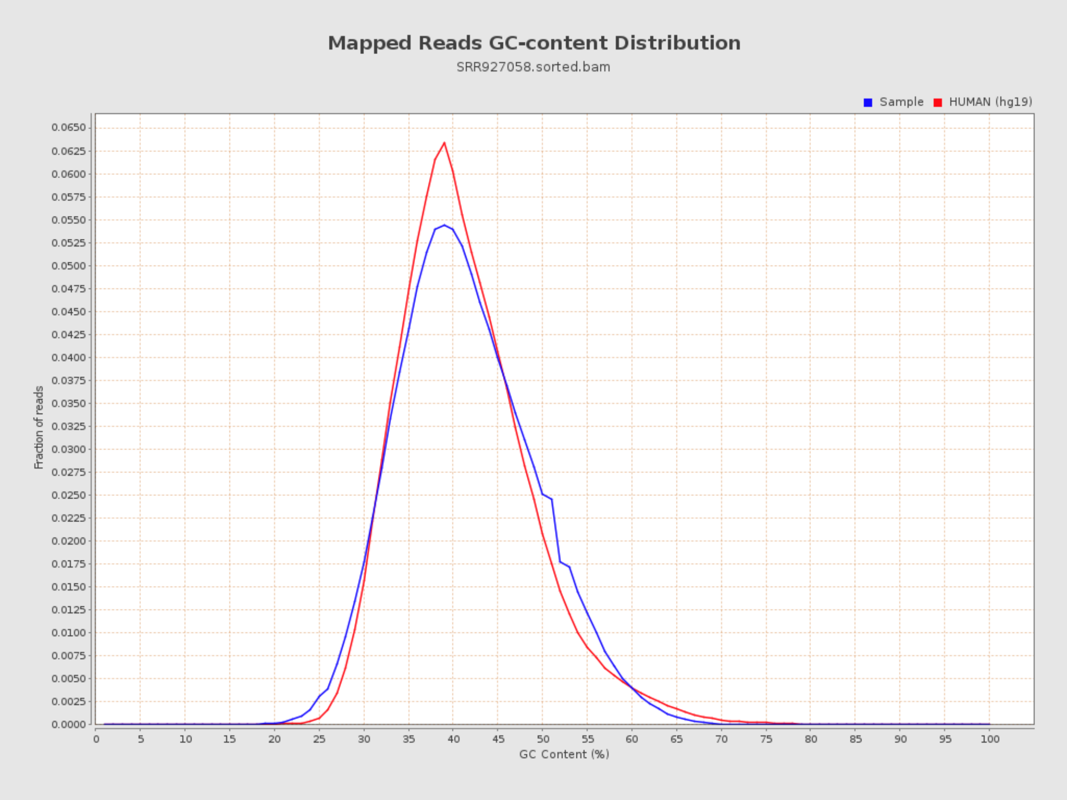
7. Results : Duplication Rate Histogram



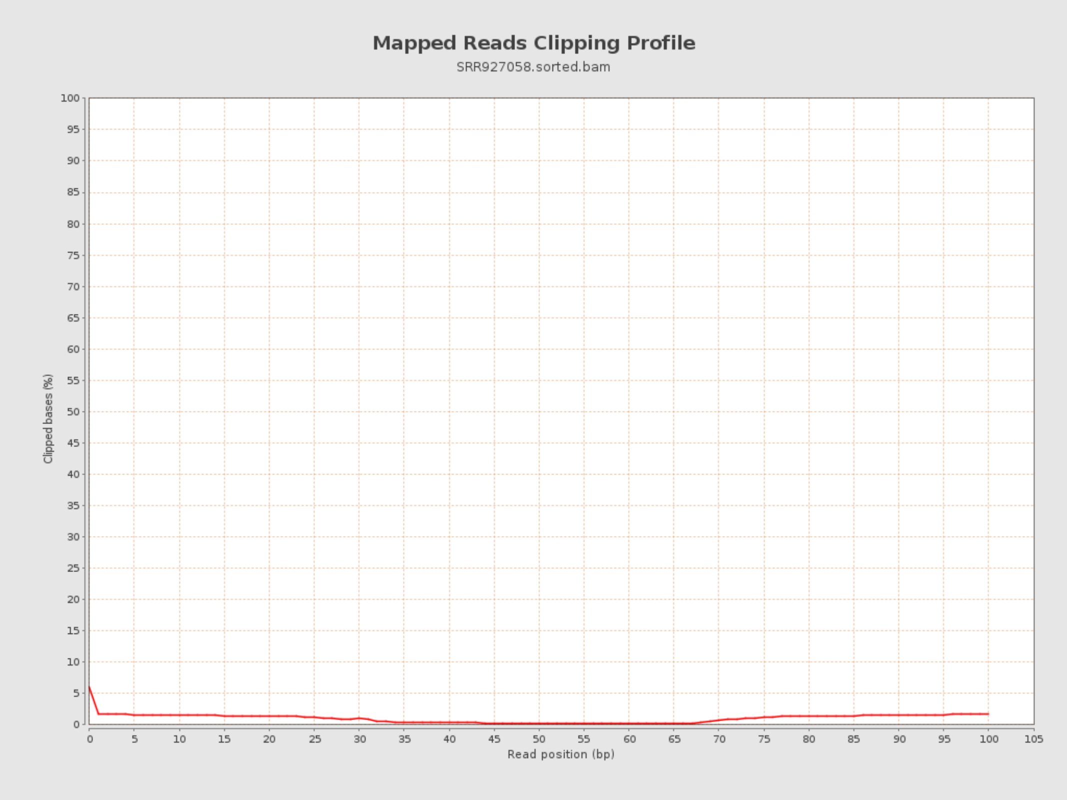
8. Results : Mapped Reads Nucleotide Content



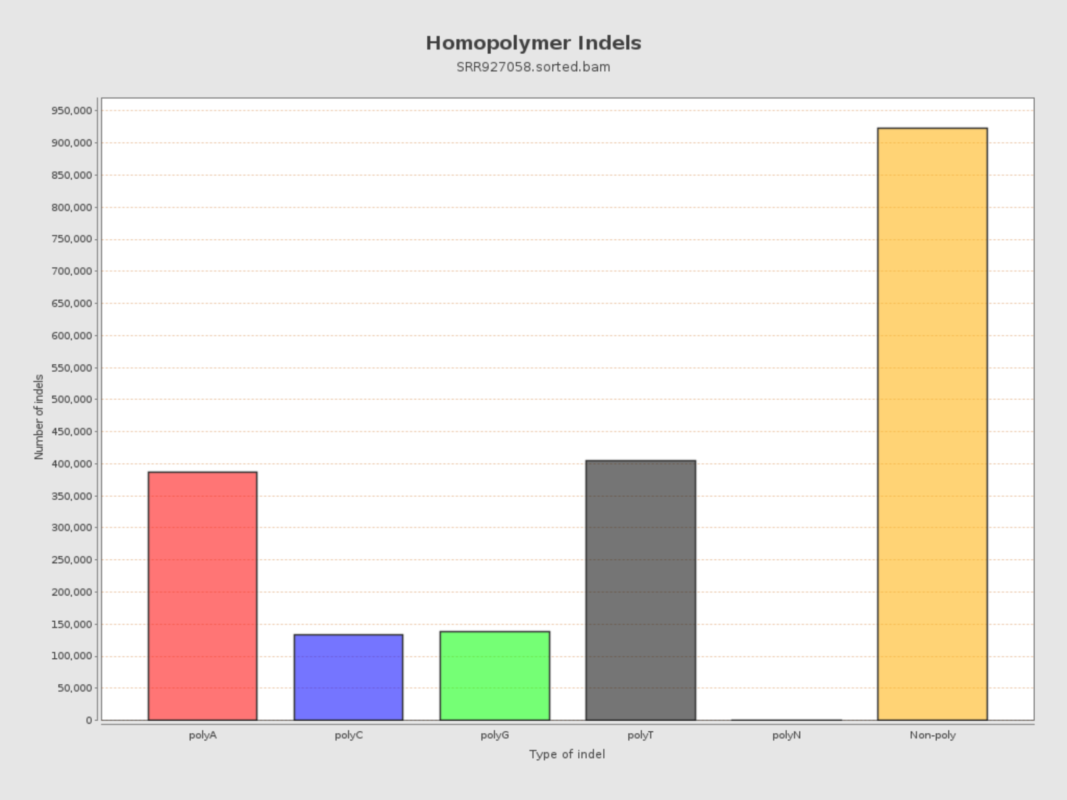
9. Results : Mapped Reads GC-content Distribution



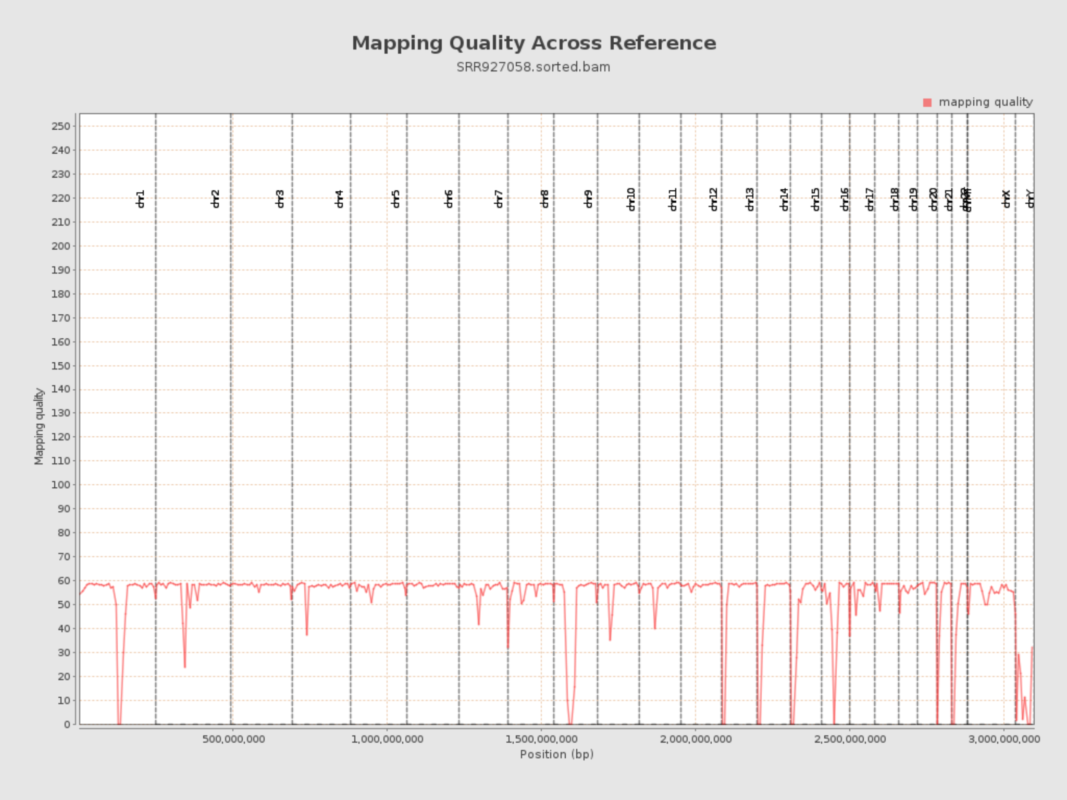
10. Results : Mapped Reads Clipping Profile



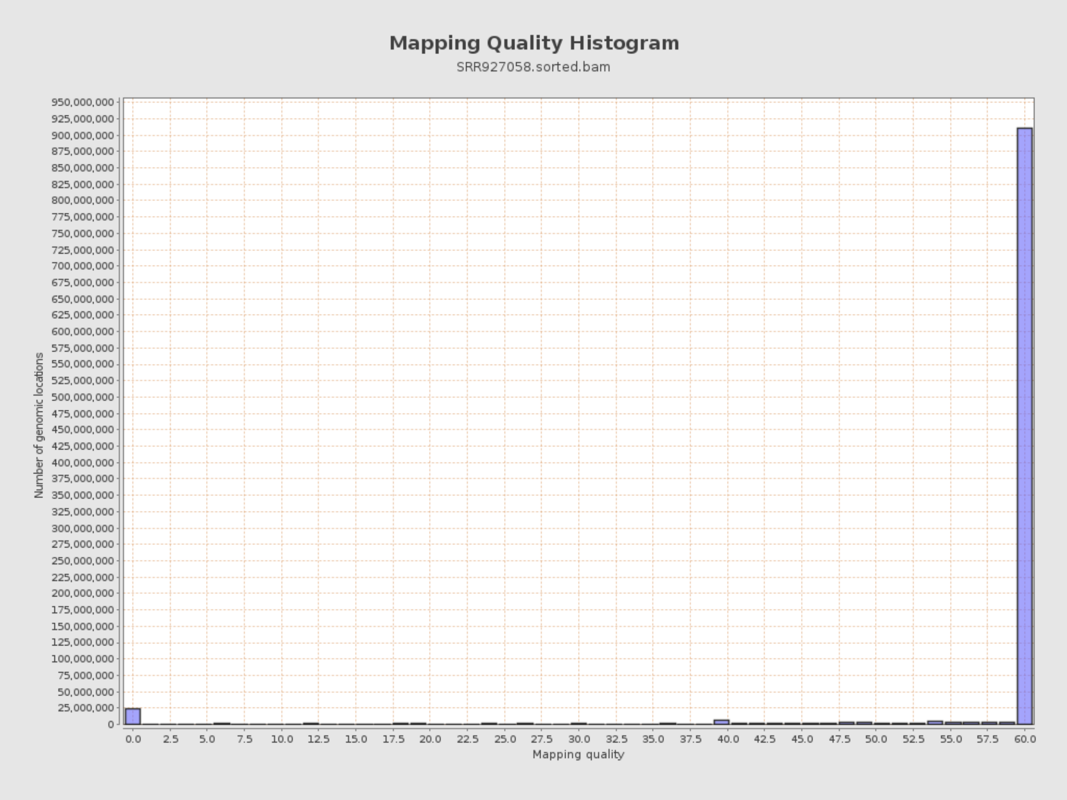
11. Results : Homopolymer Indels



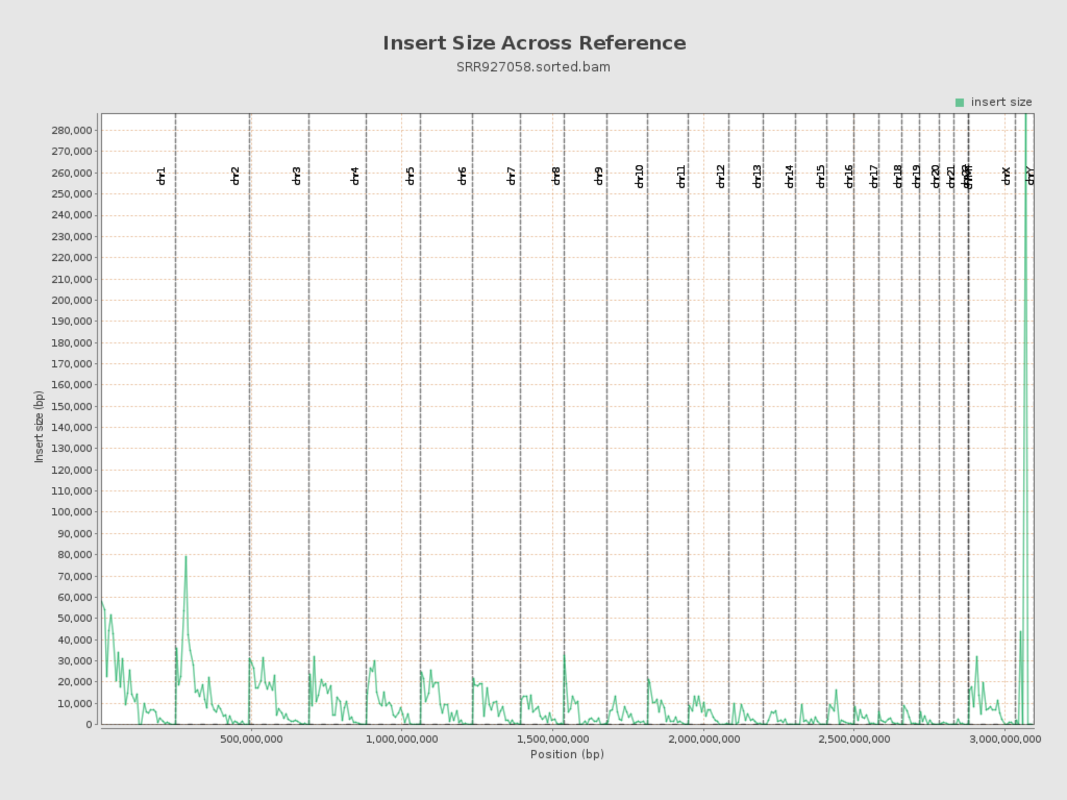
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram