Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 04:45:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926895.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_SRR926895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926895_1.fastq.gz SRR926895_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 04:45:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,307,972
Mapped reads	23,075,028 / 69.28%
Unmapped reads	10,232,944 / 30.72%
Mapped paired reads	23,075,028 / 69.28%
Mapped reads, first in pair	11,535,818 / 34.63%
Mapped reads, second in pair	11,539,210 / 34.64%
Mapped reads, both in pair	22,316,122 / 67%
Mapped reads, singletons	758,906 / 2.28%
Secondary alignments	0
Supplementary alignments	553,861 / 1.66%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	2,809,947 / 8.44%
Duplication rate	9.74%
Clipped reads	12,474,199 / 37.45%

2.2. ACGT Content

Number/percentage of A's	563,775,494 / 28.15%
Number/percentage of C's	379,148,902 / 18.93%
Number/percentage of T's	581,536,413 / 29.04%
Number/percentage of G's	477,771,026 / 23.86%
Number/percentage of N's	227,442 / 0.01%

GC Percentage	42.79%

2.3. Coverage

Mean	0.6474
Standard Deviation	2.6871

2.4. Mapping Quality

Mean Mapping Quality	52.51

2.5. Insert size

Mean	250,839.2
Standard Deviation	4,973,522.55
P25/Median/P75	134 / 179 / 245

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	19,896,518
Insertions	337,023
Mapped reads with at least one insertion	1.44%
Deletions	1,072,348
Mapped reads with at least one deletion	4.53%
Homopolymer indels	51.72%

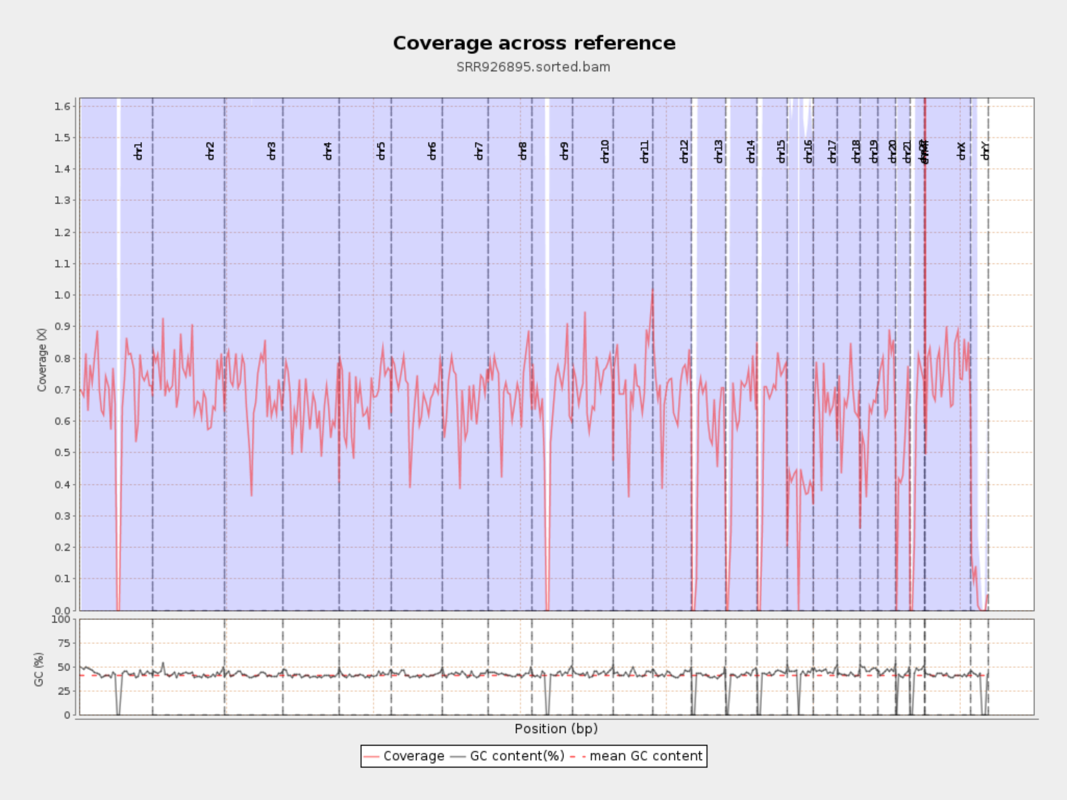
2.7. Chromosome stats

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

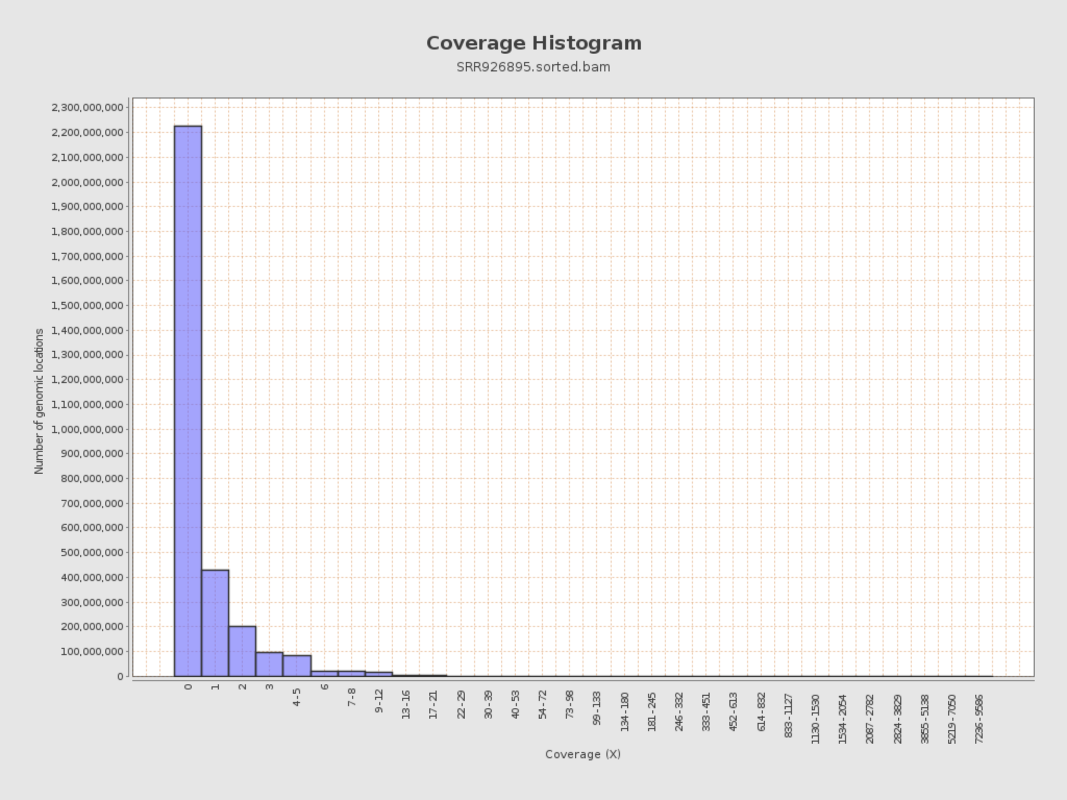
		bases	coverage	deviation
chr1	249250621	168632571	0.6766	2.0717
chr2	243199373	176788055	0.7269	6.7198
chr3	198022430	138771089	0.7008	1.6402
chr4	191154276	122641652	0.6416	1.7548
chr5	180915260	122974521	0.6797	1.593
chr6	171115067	117915229	0.6891	1.7332
chr7	159138663	105206720	0.6611	1.8285
chr8	146364022	103667235	0.7083	1.6987
chr9	141213431	86070261	0.6095	2.0779
chr10	135534747	98824928	0.7291	4.4576
chr11	135006516	97312181	0.7208	1.8371
chr12	133851895	93117791	0.6957	1.735
chr13	115169878	61207622	0.5315	1.4253
chr14	107349540	61365657	0.5716	1.5557
chr15	102531392	60730127	0.5923	1.5821
chr16	90354753	33079527	0.3661	2.264
chr17	81195210	52398771	0.6453	1.6818
chr18	78077248	52230179	0.669	2.0143
chr19	59128983	33511178	0.5667	1.6191
chr20	63025520	47546323	0.7544	1.8007
chr21	48129895	23000186	0.4779	1.897
chr22	51304566	25637707	0.4997	1.508
chrMT	16571	57990	3.4995	3.4562
chrX	155270560	118098225	0.7606	1.7768

chrY	59373566	3260244	0.0549	1.5834

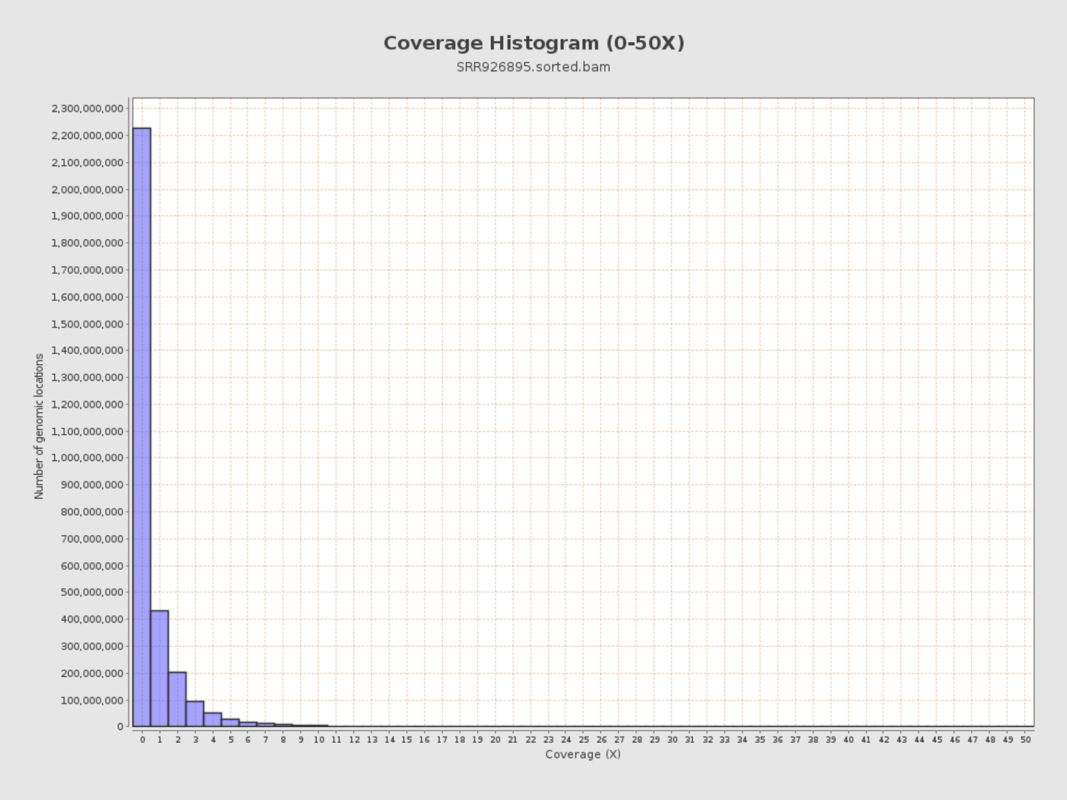
3. Results : Coverage across reference



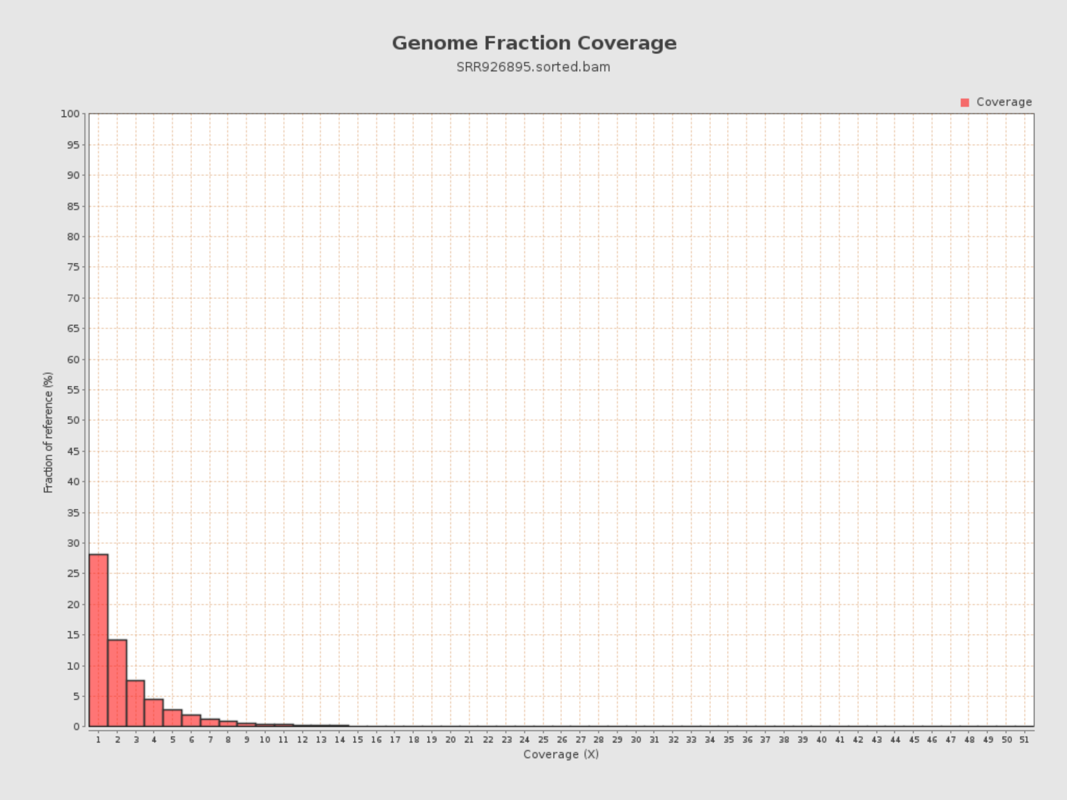
4. Results : Coverage Histogram



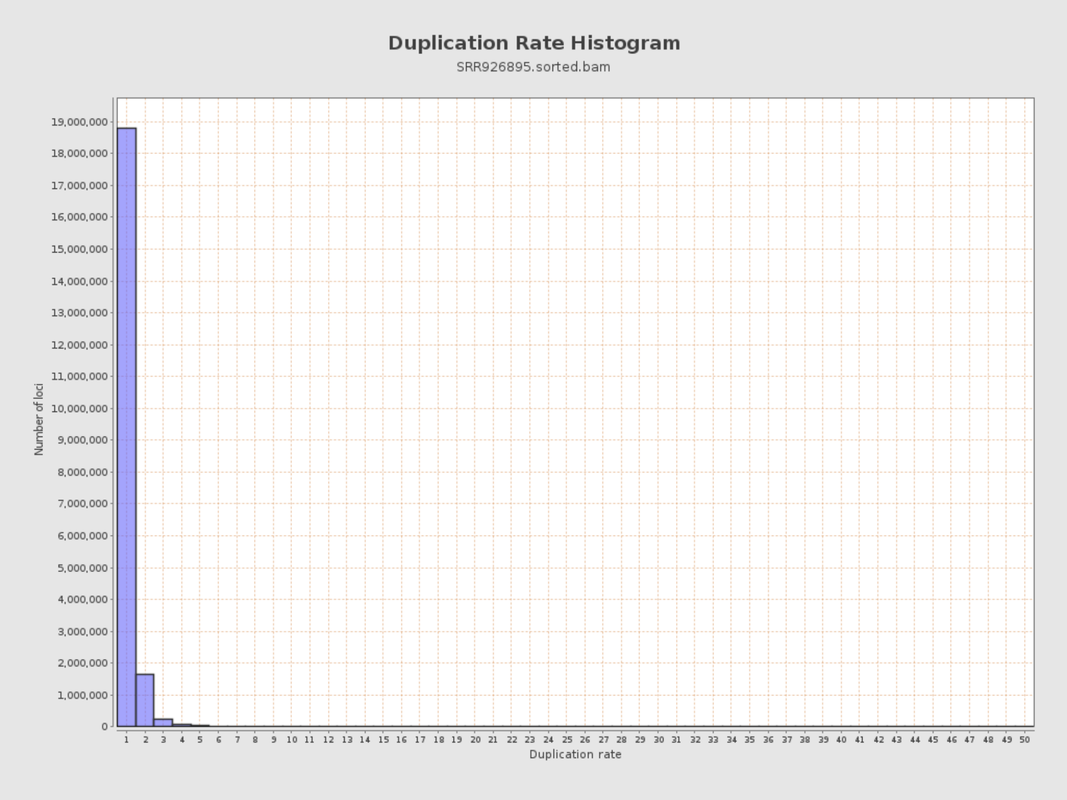
5. Results : Coverage Histogram (0-50X)



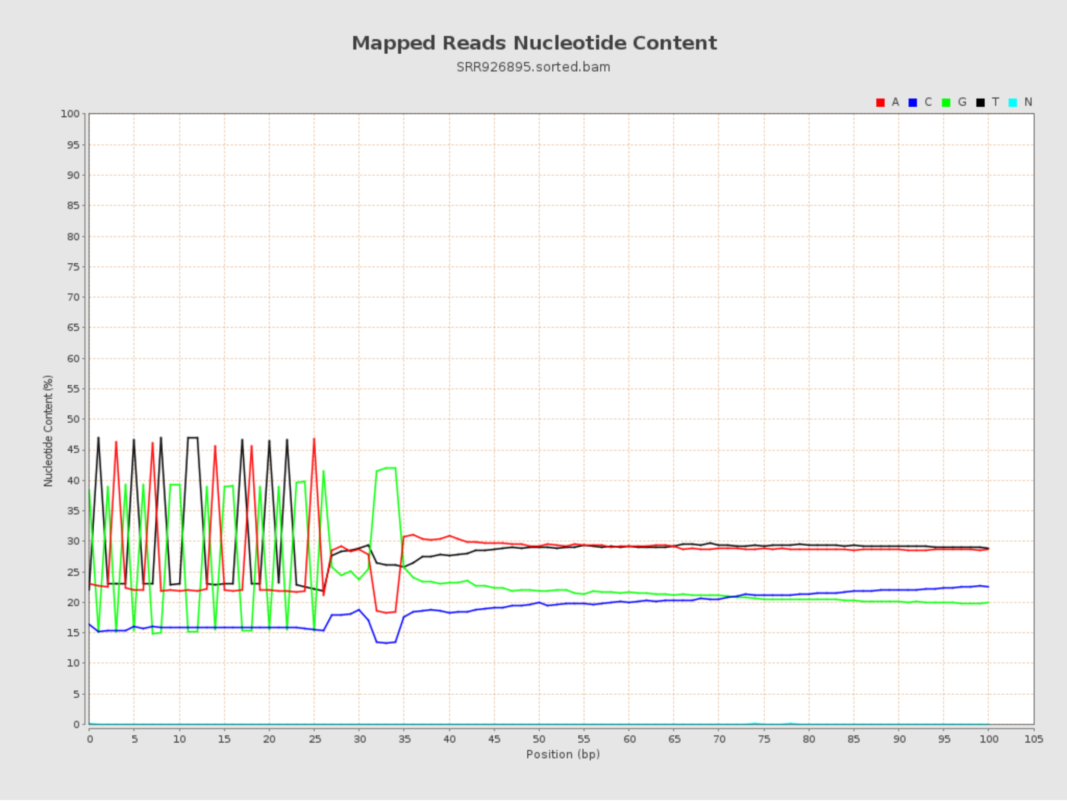
6. Results : Genome Fraction Coverage



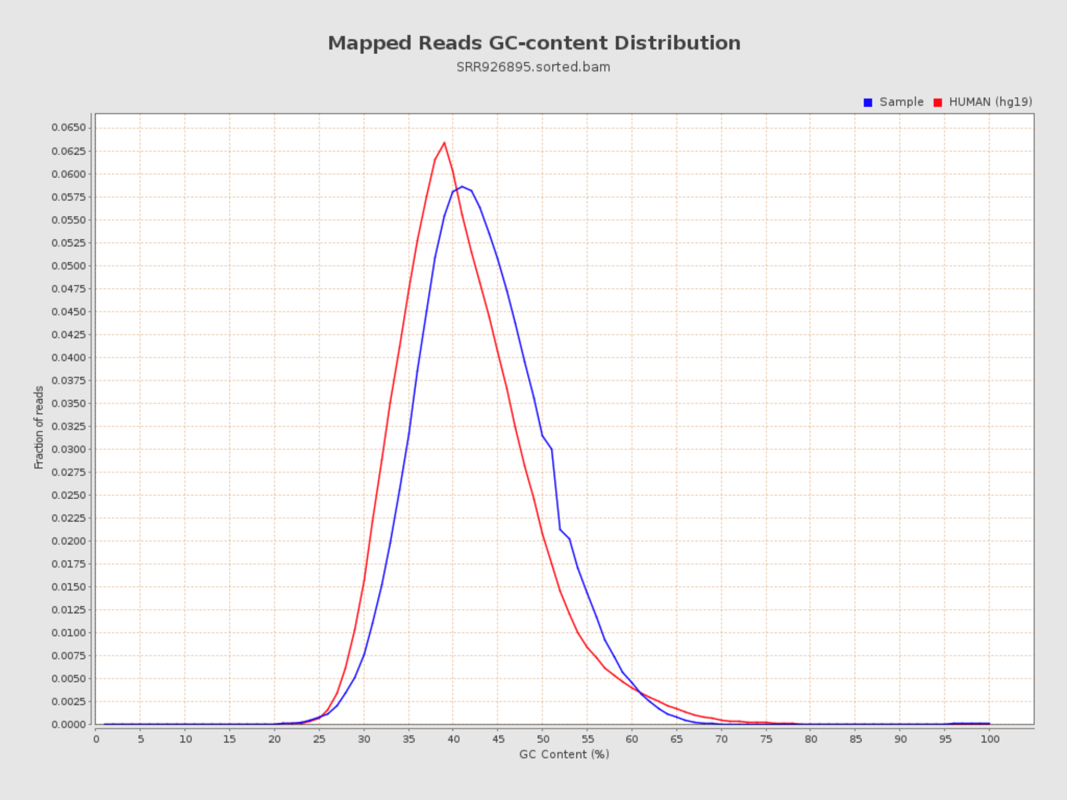
7. Results : Duplication Rate Histogram



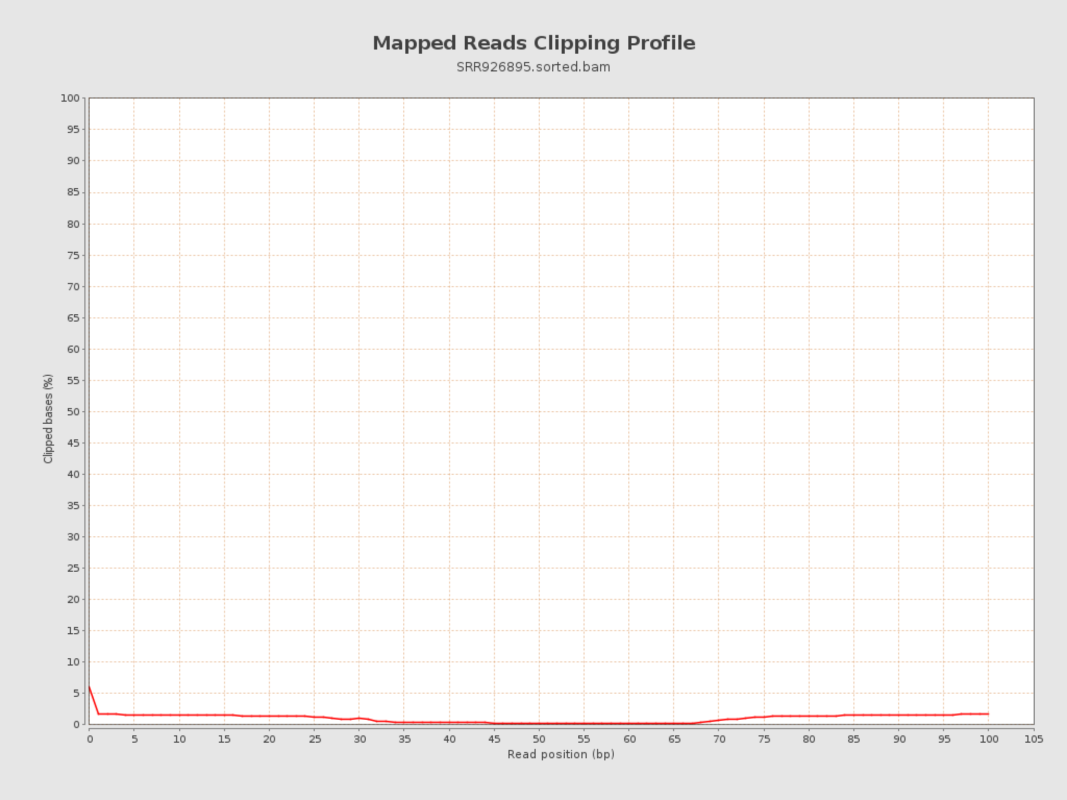
8. Results : Mapped Reads Nucleotide Content



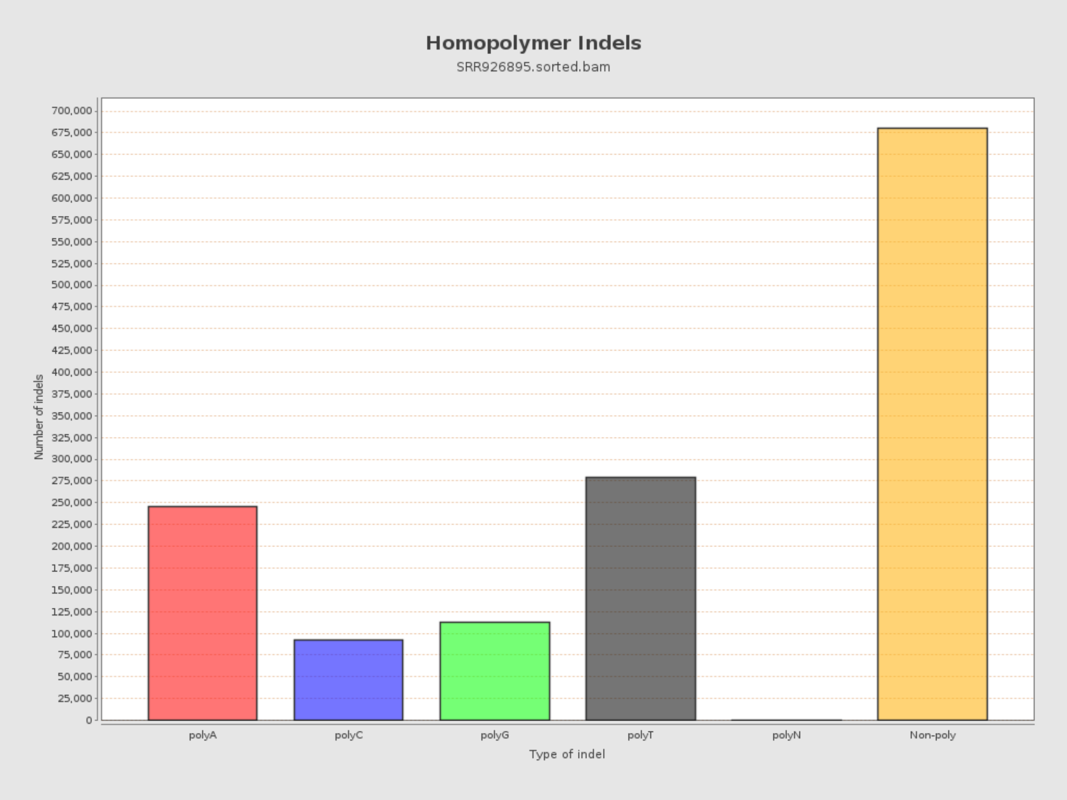
9. Results : Mapped Reads GC-content Distribution



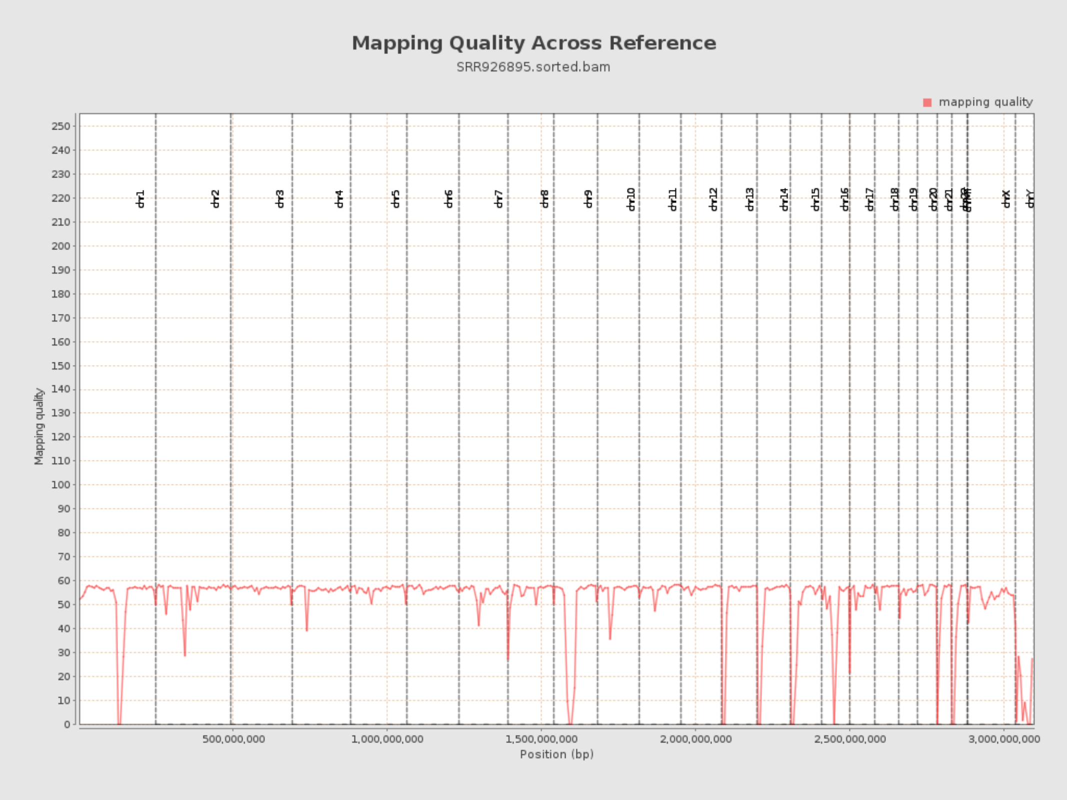
10. Results : Mapped Reads Clipping Profile



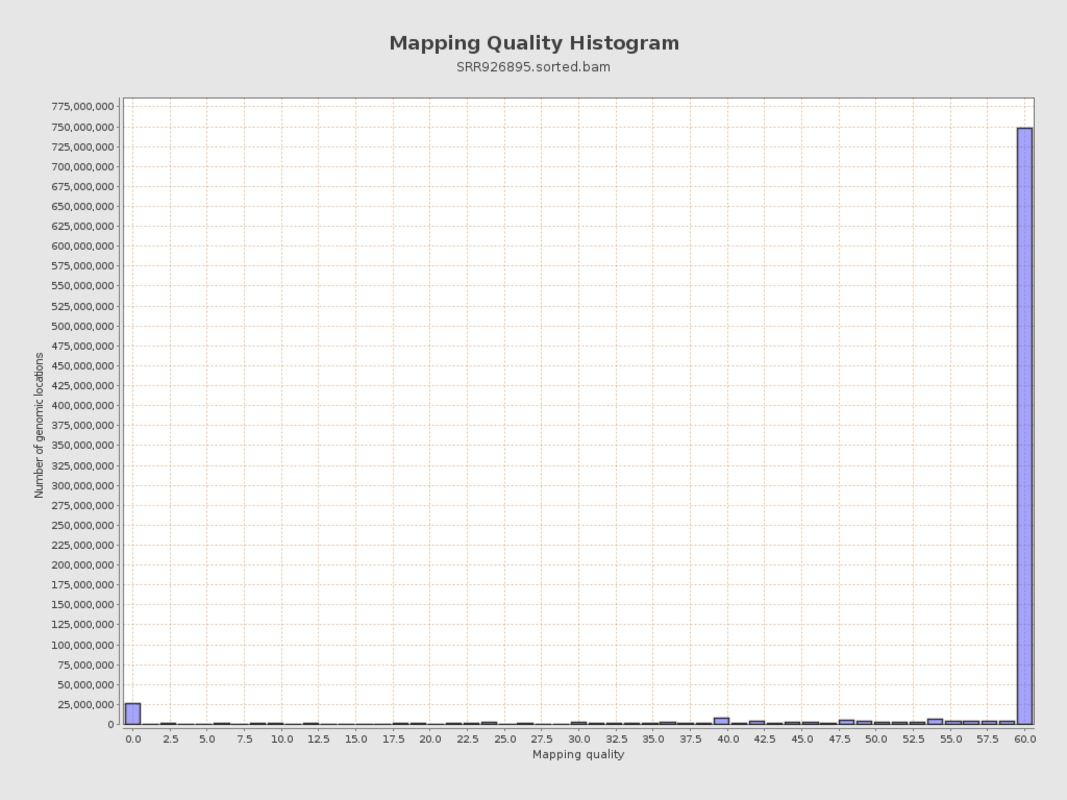
11. Results : Homopolymer Indels



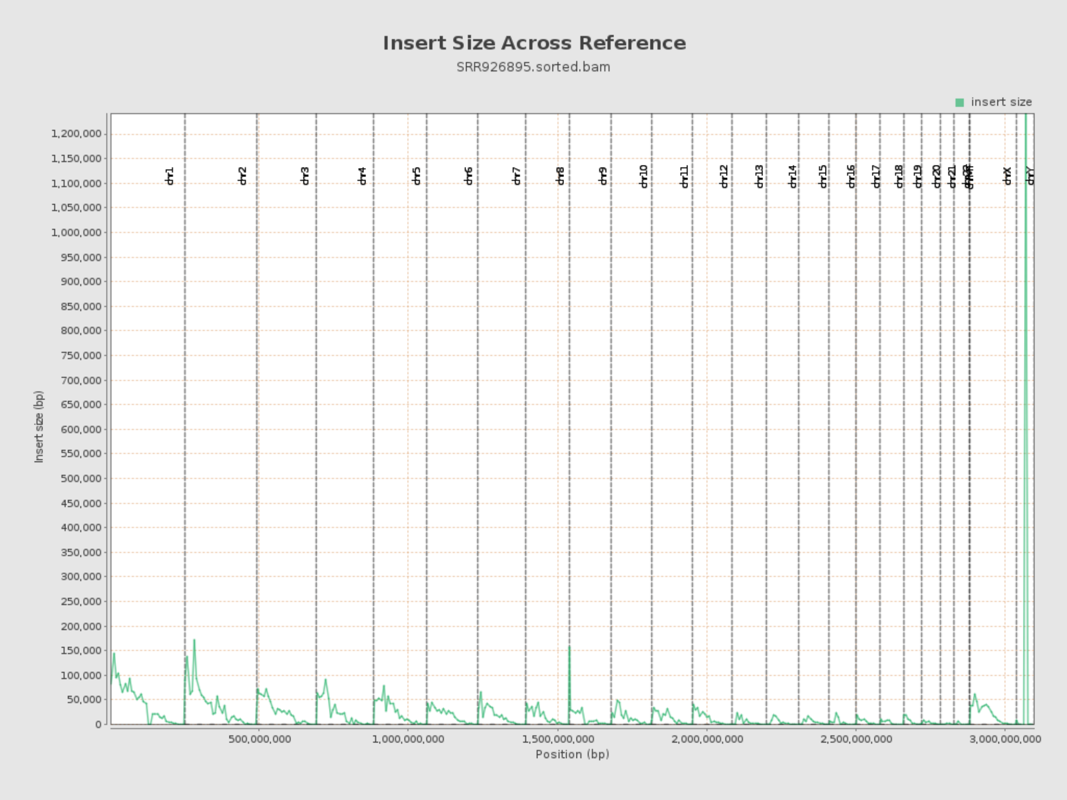
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram