Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 03:17:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927010.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_SRR927010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927010_1.fastq.gz SRR927010_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 03:17:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,366,694
Mapped reads	27,576,626 / 97.21%
Unmapped reads	790,068 / 2.79%
Mapped paired reads	27,576,626 / 97.21%
Mapped reads, first in pair	13,836,666 / 48.78%
Mapped reads, second in pair	13,739,960 / 48.44%
Mapped reads, both in pair	27,138,916 / 95.67%
Mapped reads, singletons	437,710 / 1.54%
Secondary alignments	0
Supplementary alignments	567,632 / 2%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	3,082,472 / 10.87%
Duplication rate	8.08%
Clipped reads	10,659,180 / 37.58%

2.2. ACGT Content

Number/percentage of A's	721,119,661 / 28.63%
Number/percentage of C's	487,321,062 / 19.34%
Number/percentage of T's	737,235,215 / 29.27%
Number/percentage of G's	572,979,679 / 22.75%
Number/percentage of N's	465,254 / 0.02%

GC Percentage	42.09%

2.3. Coverage

Mean	0.8144
Standard Deviation	5.0225

2.4. Mapping Quality

Mean Mapping Quality	48.91

2.5. Insert size

Mean	232,921.63
Standard Deviation	4,833,025.77
P25/Median/P75	146 / 193 / 263

2.6. Mismatches and indels

General error rate	1%
Mismatches	24,434,893
Insertions	434,156
Mapped reads with at least one insertion	1.54%
Deletions	1,371,761
Mapped reads with at least one deletion	4.84%
Homopolymer indels	52.08%

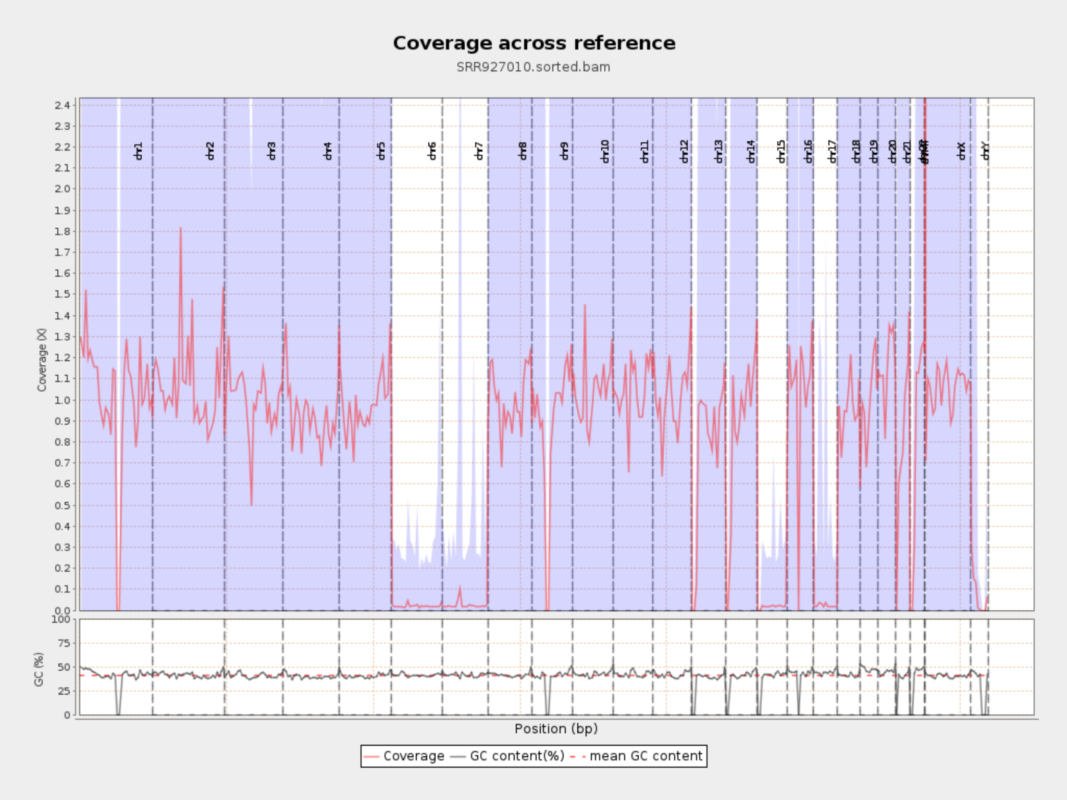
2.7. Chromosome stats

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

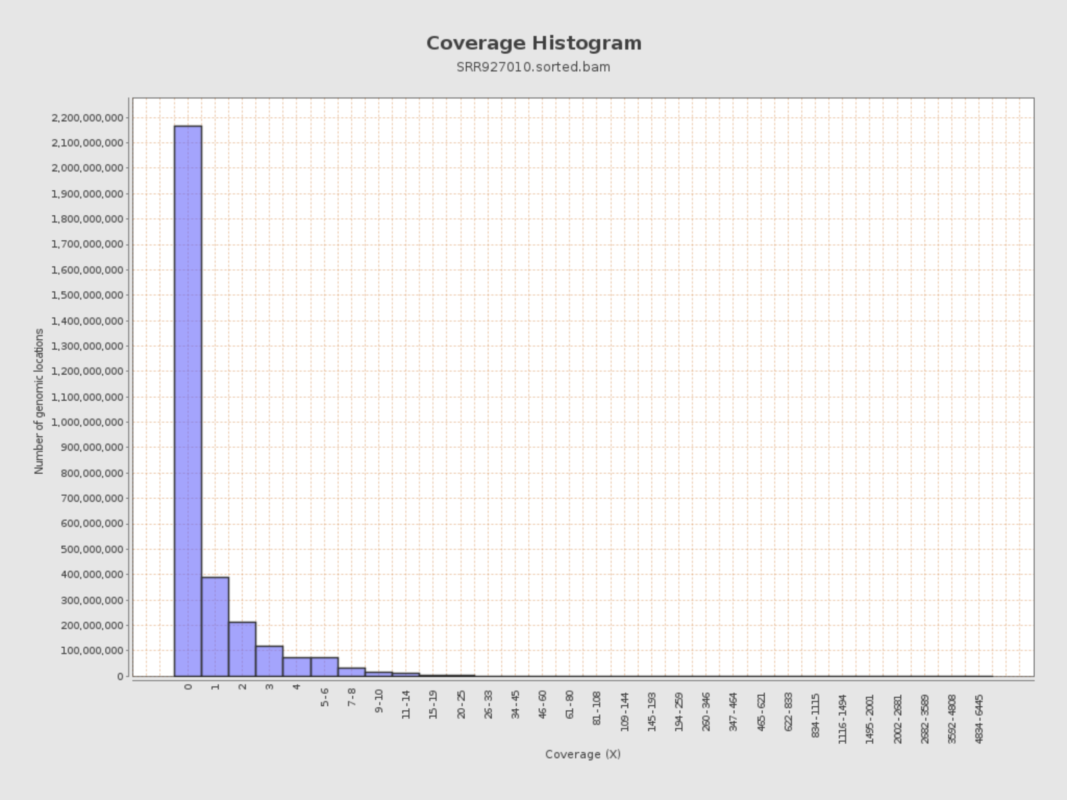
		bases	coverage	deviation
chr1	249250621	252072339	1.0113	4.8759
chr2	243199373	262318509	1.0786	7.0515
chr3	198022430	198126926	1.0005	1.9795
chr4	191154276	176988111	0.9259	2.6755
chr5	180915260	177948306	0.9836	1.9822
chr6	171115067	3712284	0.0217	0.4336
chr7	159138663	4187811	0.0263	0.8686
chr8	146364022	147119158	1.0052	2.3885
chr9	141213431	125141860	0.8862	3.9603
chr10	135534747	141690317	1.0454	7.4501
chr11	135006516	141721779	1.0497	3.1953
chr12	133851895	136533863	1.02	2.09
chr13	115169878	88619618	0.7695	1.7203
chr14	107349540	90503879	0.8431	1.9447
chr15	102531392	1841383	0.018	0.3325
chr16	90354753	93800630	1.0381	5.2101
chr17	81195210	1881560	0.0232	0.8104
chr18	78077248	75992783	0.9733	3.4439
chr19	59128983	59555977	1.0072	3.4262
chr20	63025520	73362119	1.164	2.3544
chr21	48129895	39736709	0.8256	3.7251
chr22	51304566	41796031	0.8147	2.0926
chrMT	16571	18786000	1,133.6673	963.1362
chrX	155270560	163315151	1.0518	2.4184

chrY	59373566	4359466	0.0734	2.7285

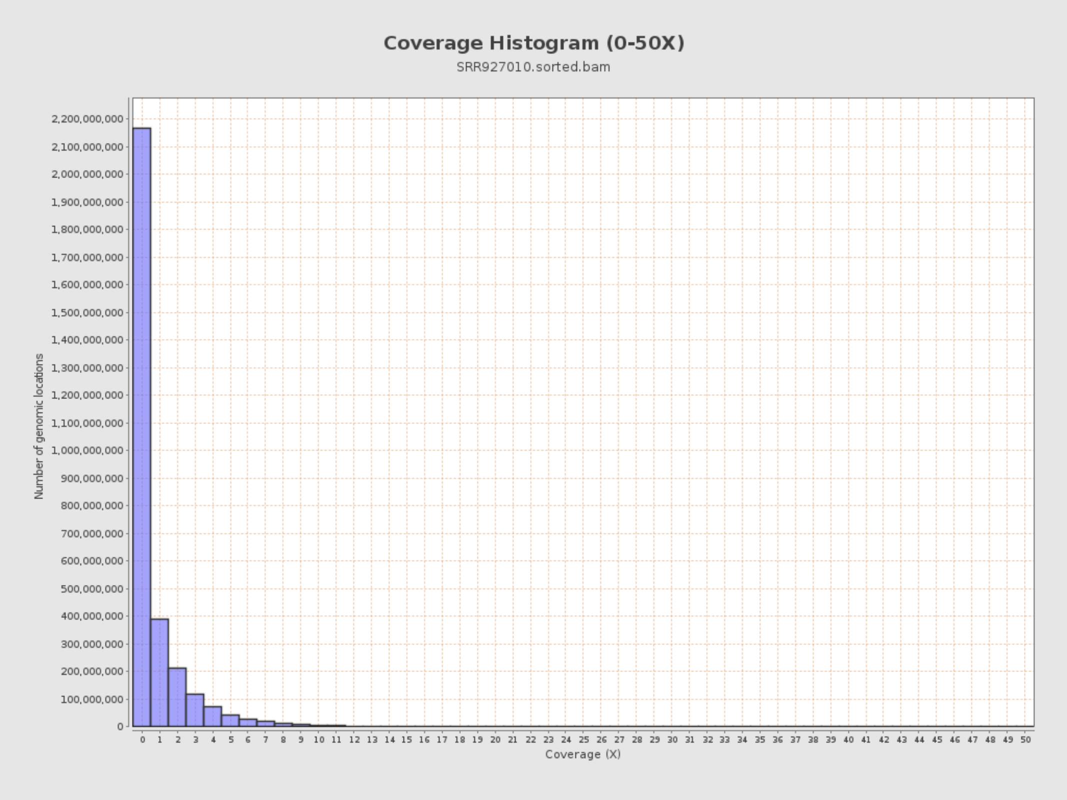
3. Results : Coverage across reference



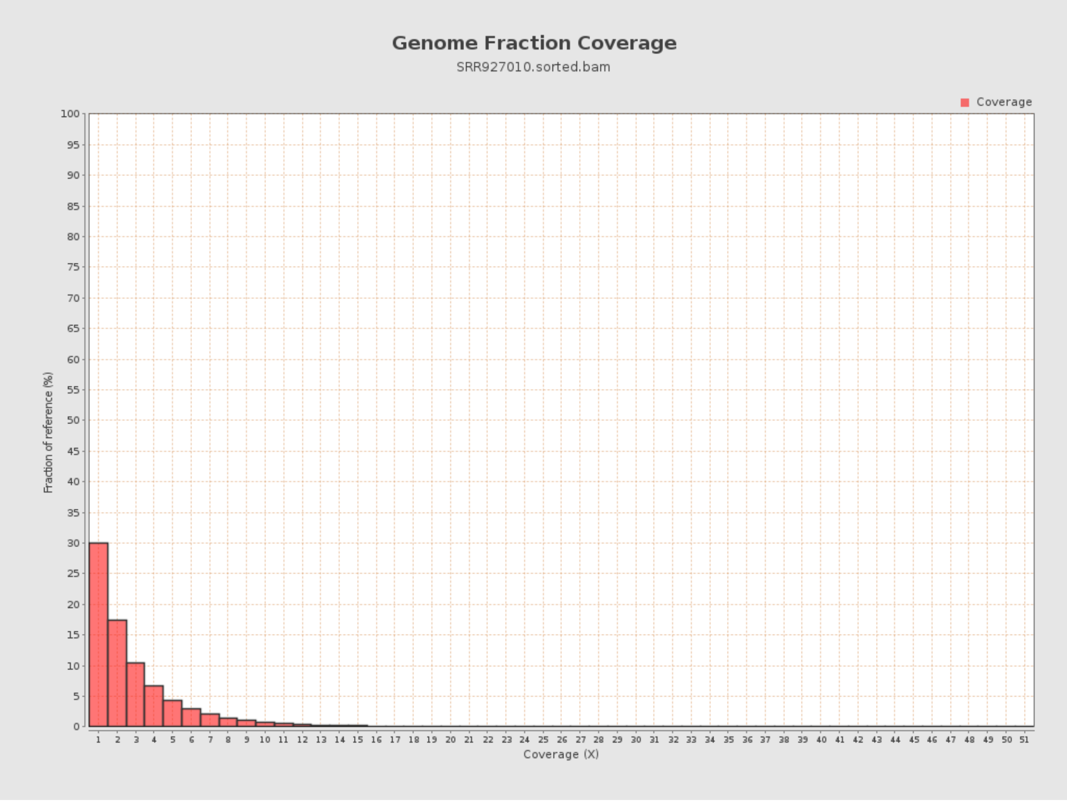
4. Results : Coverage Histogram



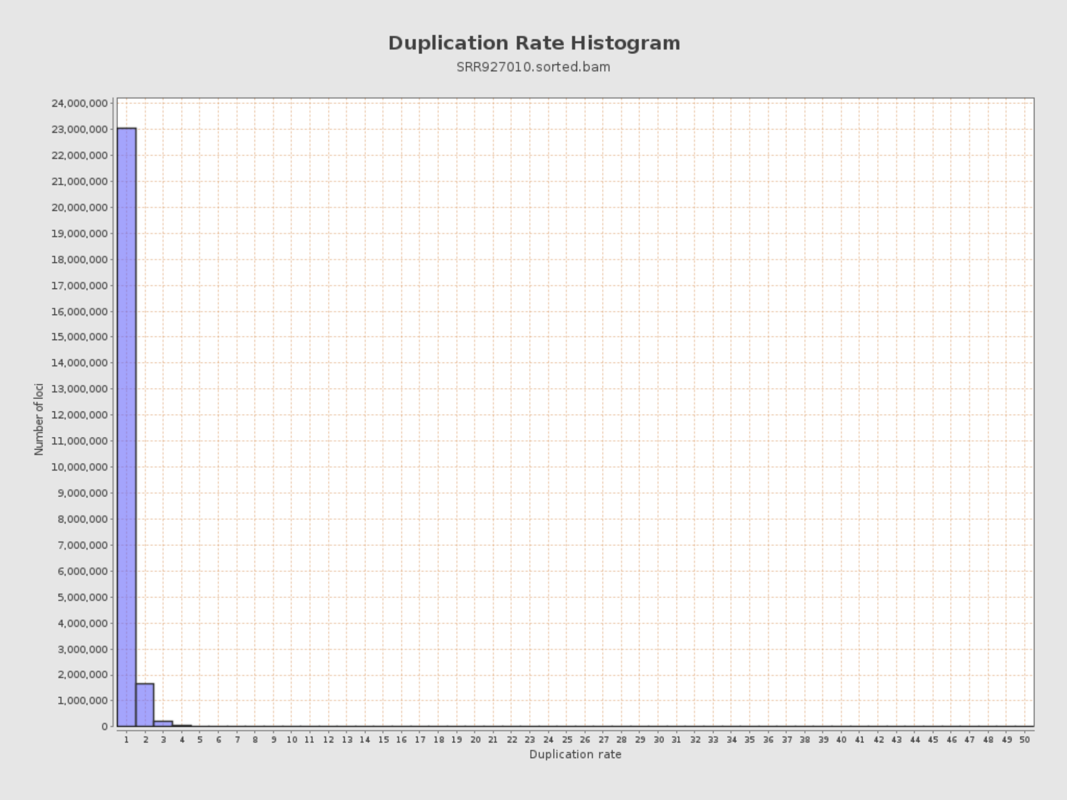
5. Results : Coverage Histogram (0-50X)



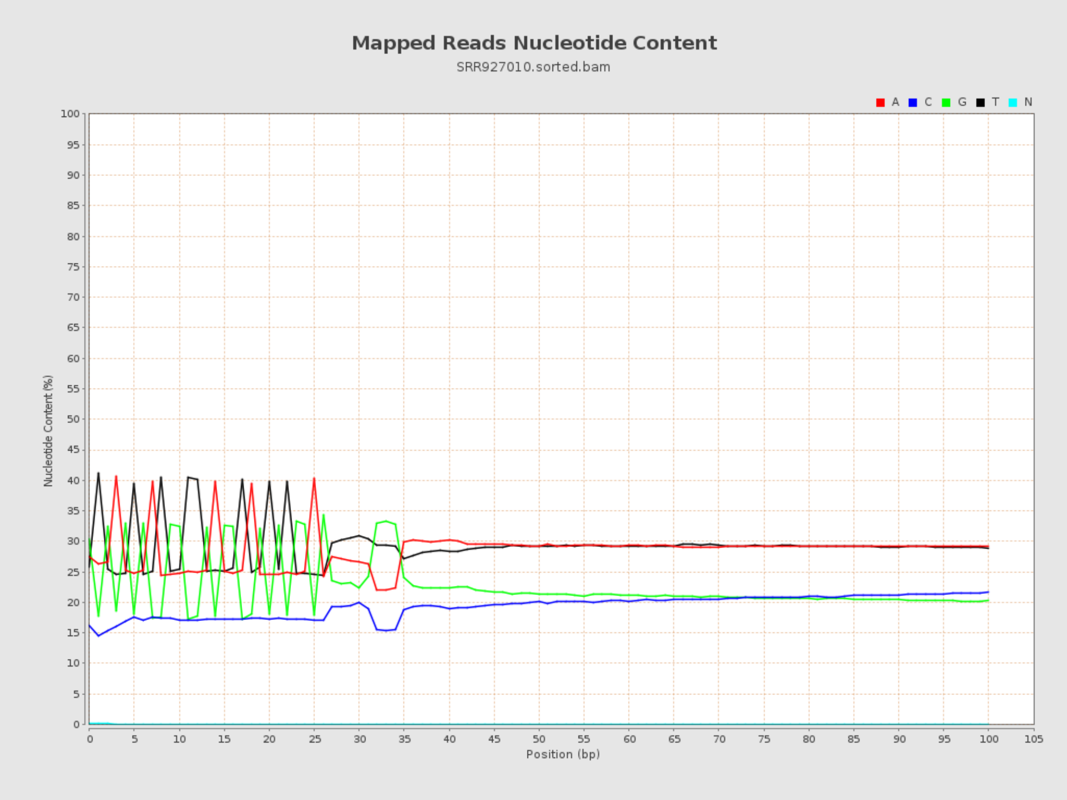
6. Results : Genome Fraction Coverage



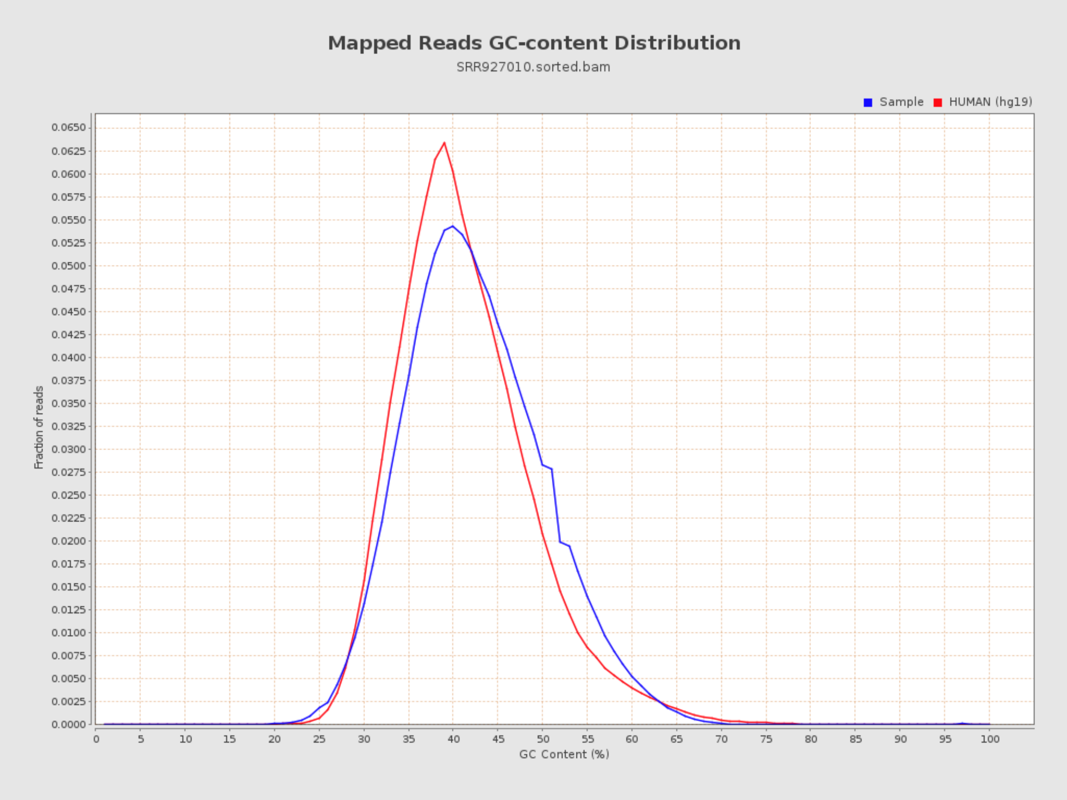
7. Results : Duplication Rate Histogram



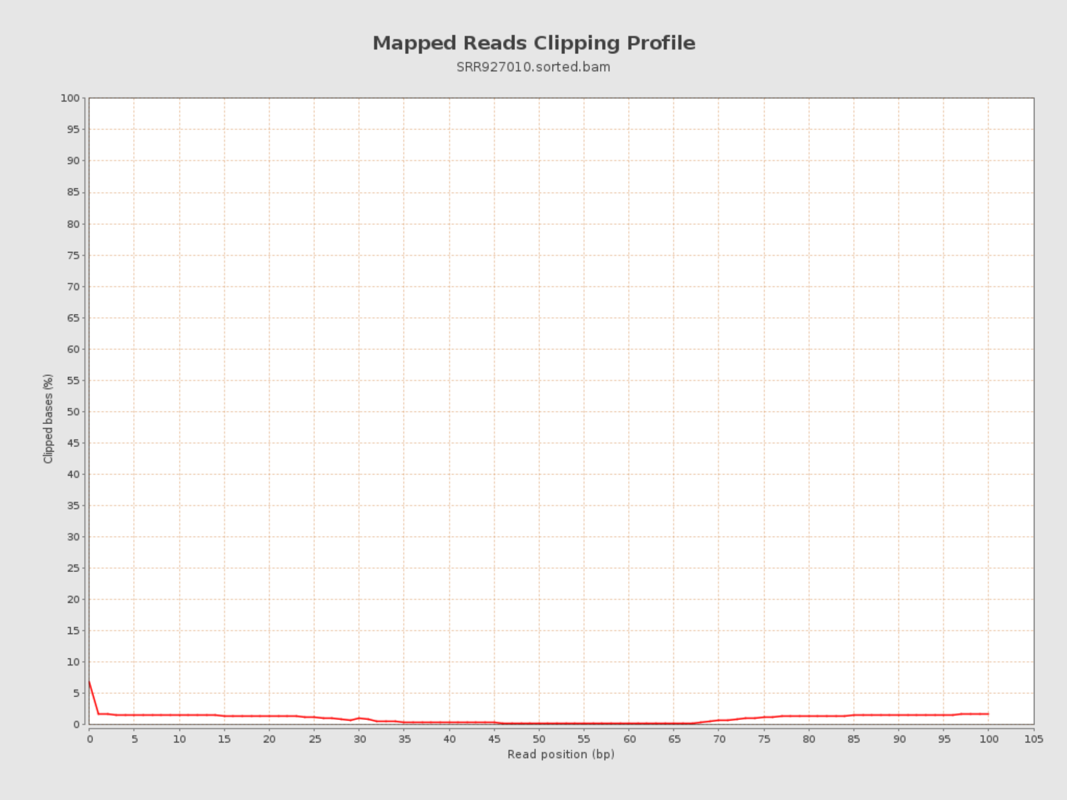
8. Results : Mapped Reads Nucleotide Content



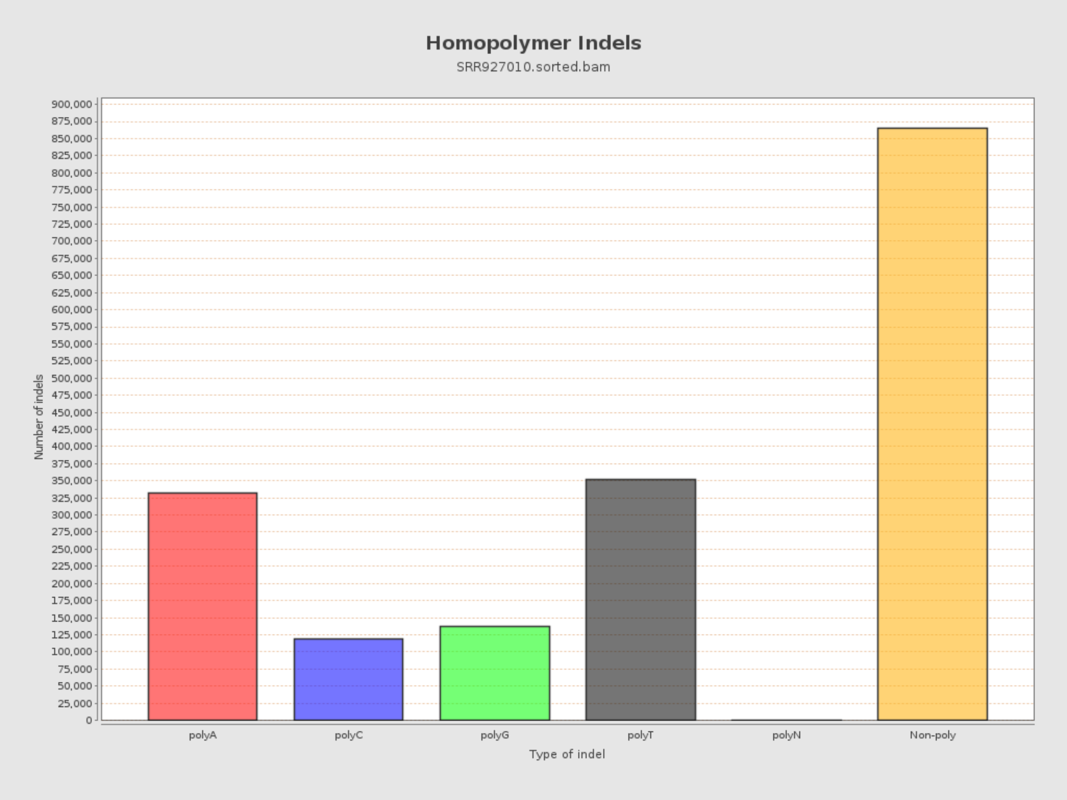
9. Results : Mapped Reads GC-content Distribution



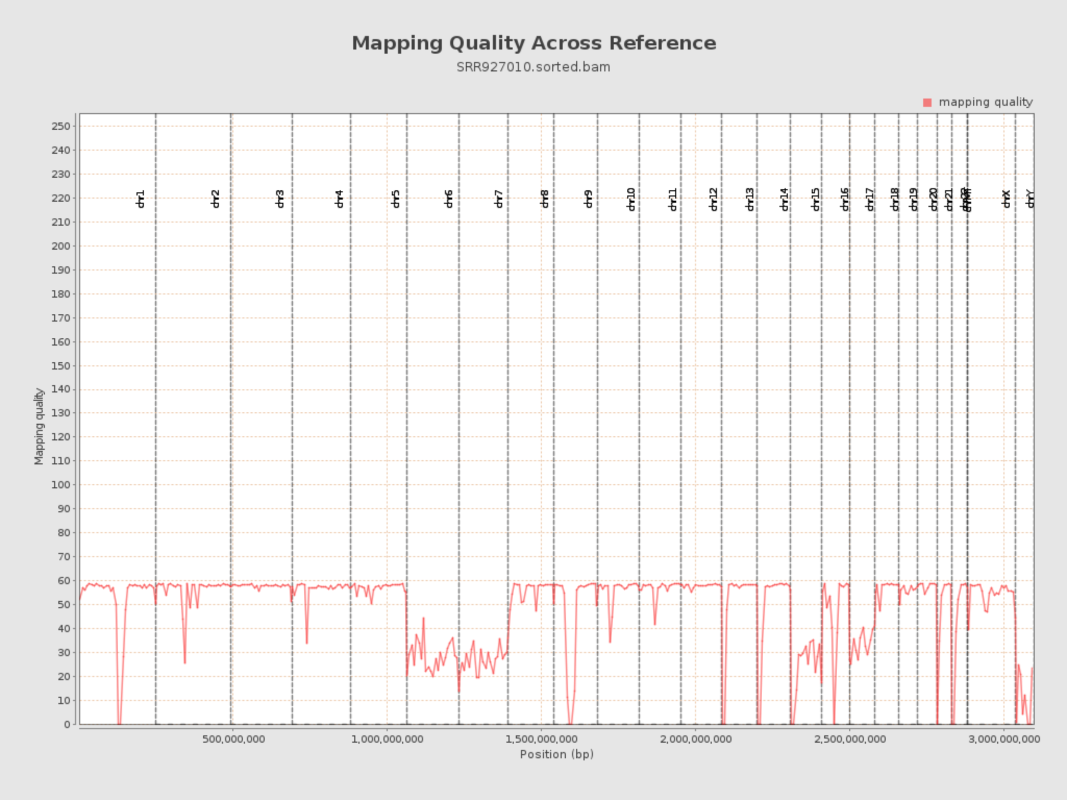
10. Results : Mapped Reads Clipping Profile



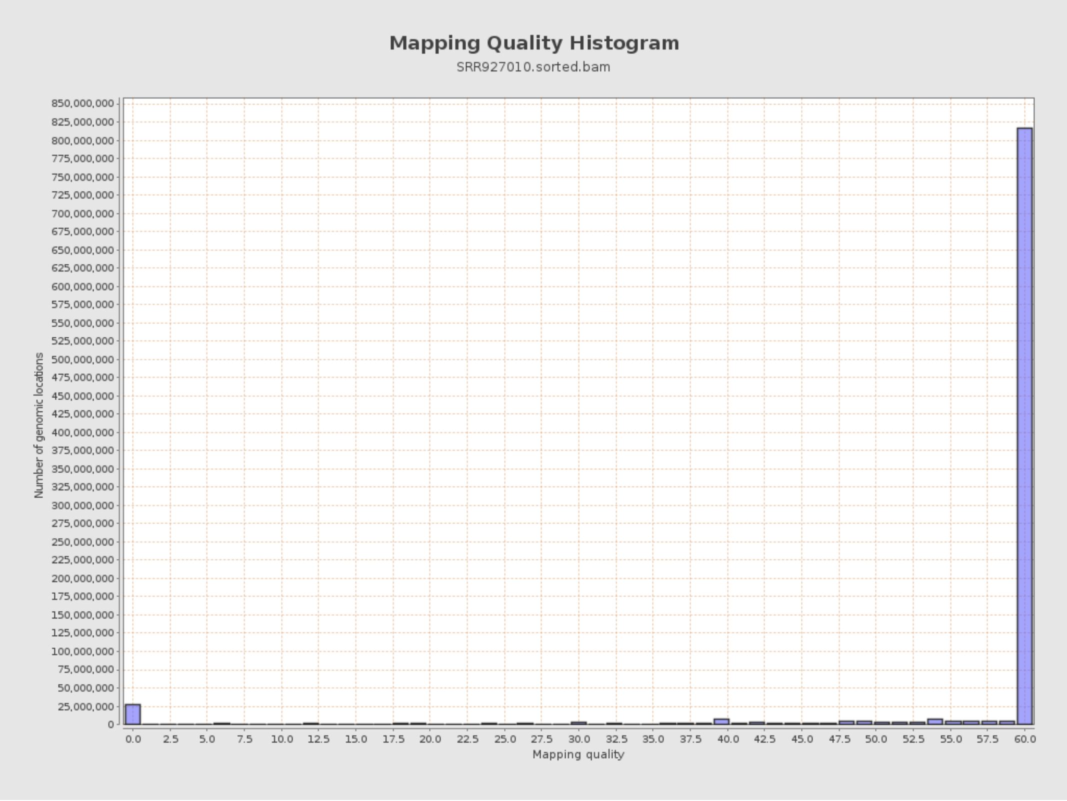
11. Results : Homopolymer Indels



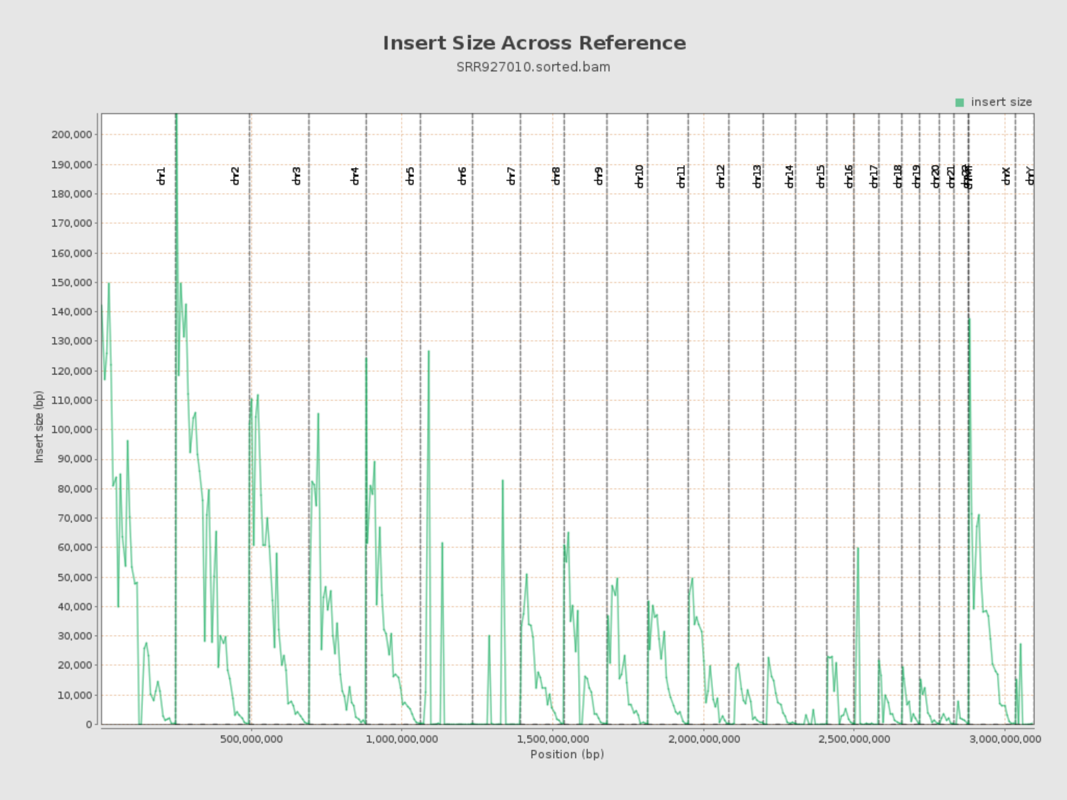
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram