Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 07:32:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926967.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_SRR926967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926967_1.fastq.gz SRR926967_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 07:32:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,496,372
Mapped reads	32,472,733 / 96.94%
Unmapped reads	1,023,639 / 3.06%
Mapped paired reads	32,472,733 / 96.94%
Mapped reads, first in pair	16,234,410 / 48.47%
Mapped reads, second in pair	16,238,323 / 48.48%
Mapped reads, both in pair	31,865,762 / 95.13%
Mapped reads, singletons	606,971 / 1.81%
Secondary alignments	0
Supplementary alignments	1,110,898 / 3.32%
Read min/max/mean length	30 / 101 / 102.37
Duplicated reads (estimated)	4,434,106 / 13.24%
Duplication rate	10.81%
Clipped reads	17,203,402 / 51.36%

2.2. ACGT Content

Number/percentage of A's	814,594,647 / 28.45%
Number/percentage of C's	547,945,453 / 19.14%
Number/percentage of T's	846,388,794 / 29.56%
Number/percentage of G's	653,578,244 / 22.83%
Number/percentage of N's	323,541 / 0.01%

GC Percentage	41.97%

2.3. Coverage

Mean	0.9255
Standard Deviation	3.5231

2.4. Mapping Quality

Mean Mapping Quality	52.51

2.5. Insert size

Mean	336,323.73
Standard Deviation	5,699,448.16
P25/Median/P75	123 / 163 / 221

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	29,557,898
Insertions	507,718
Mapped reads with at least one insertion	1.54%
Deletions	1,557,250
Mapped reads with at least one deletion	4.67%
Homopolymer indels	51.66%

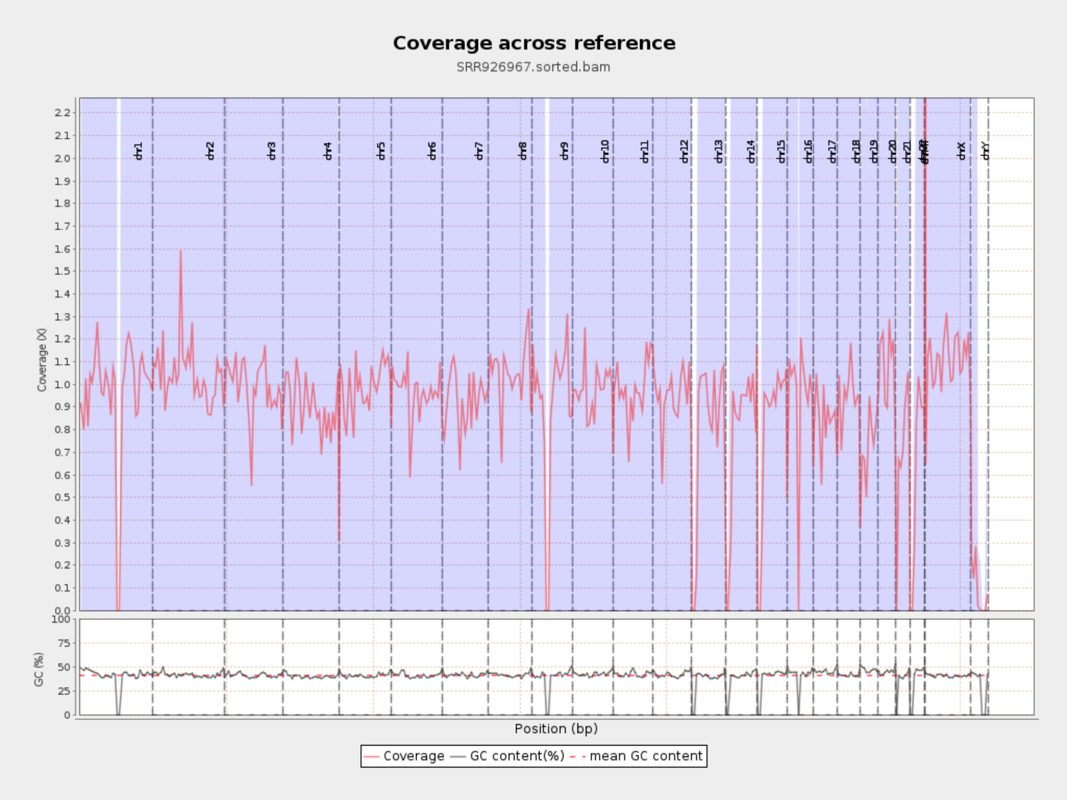
2.7. Chromosome stats

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

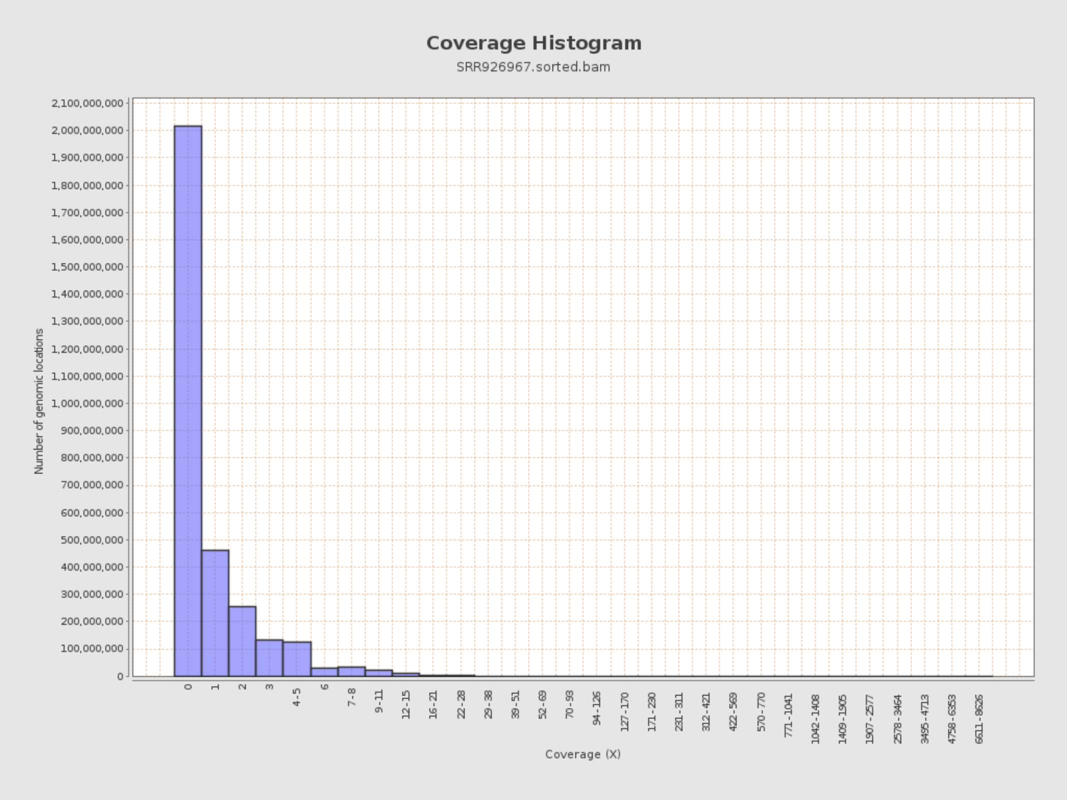
		bases	coverage	deviation
chr1	249250621	239287420	0.96	3.4671
chr2	243199373	255638895	1.0511	7.6835
chr3	198022430	196240613	0.991	2.0555
chr4	191154276	172877156	0.9044	2.8914
chr5	180915260	179010696	0.9895	2.032
chr6	171115067	165471450	0.967	2.79
chr7	159138663	147082890	0.9242	2.5329
chr8	146364022	154298162	1.0542	2.4554
chr9	141213431	126674831	0.897	3.5497
chr10	135534747	133345289	0.9838	4.7624
chr11	135006516	131640461	0.9751	3.9129
chr12	133851895	127050602	0.9492	2.1882
chr13	115169878	91280971	0.7926	1.8529
chr14	107349540	82492304	0.7684	1.8789
chr15	102531392	80695237	0.787	1.8969
chr16	90354753	83245847	0.9213	4.2853
chr17	81195210	68348050	0.8418	2.2792
chr18	78077248	75545867	0.9676	3.6978
chr19	59128983	42965408	0.7266	2.4126
chr20	63025520	68500216	1.0869	2.3641
chr21	48129895	34502796	0.7169	2.6231
chr22	51304566	31883074	0.6214	1.7819
chrMT	16571	614104	37.059	34.7487
chrX	155270560	171225226	1.1028	2.4682

chrY	59373566	5213955	0.0878	3.0405

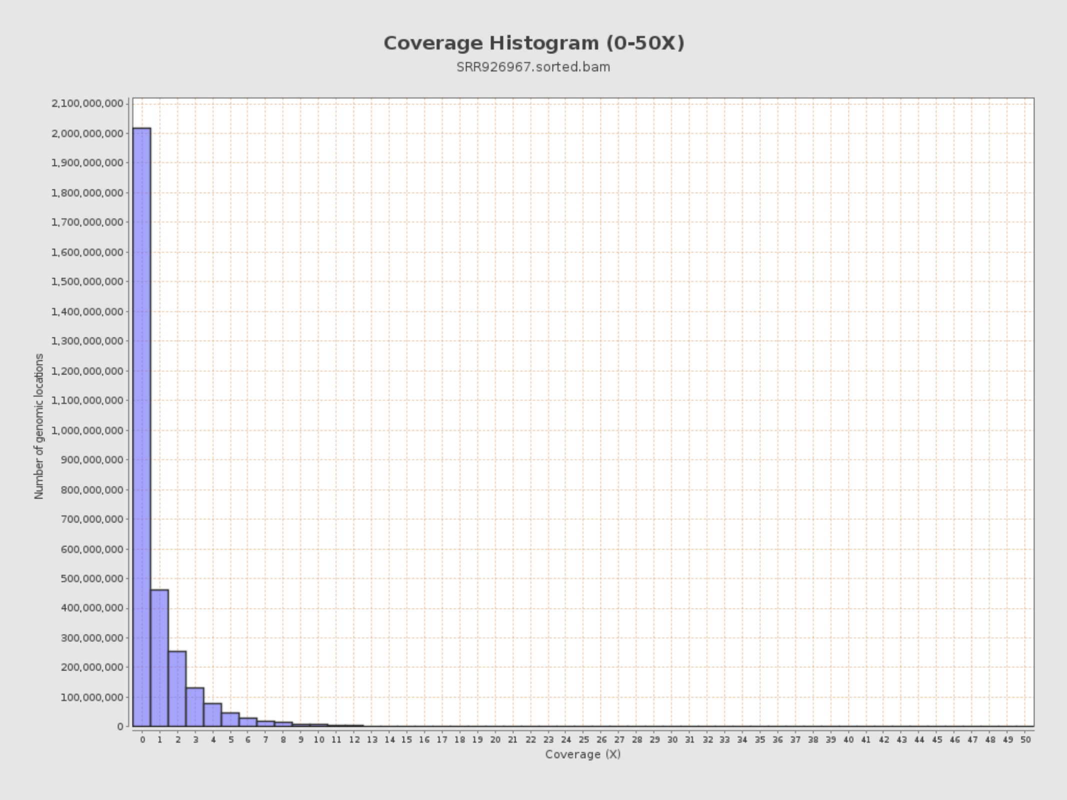
3. Results : Coverage across reference



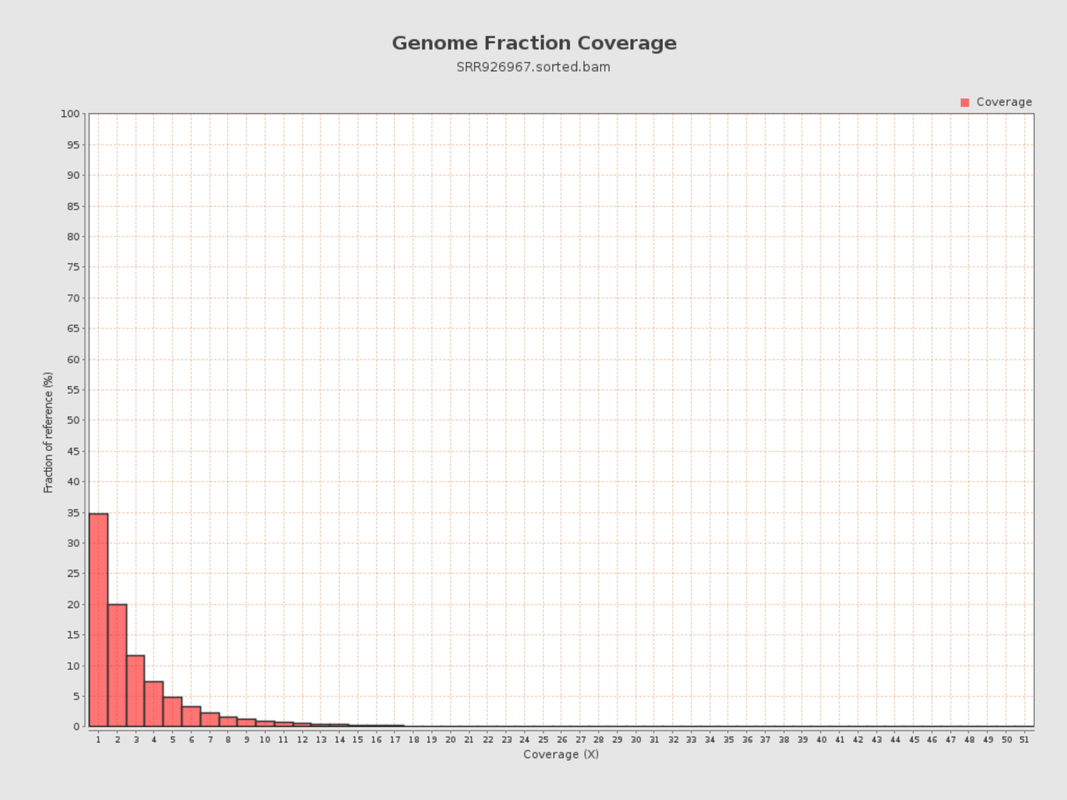
4. Results : Coverage Histogram



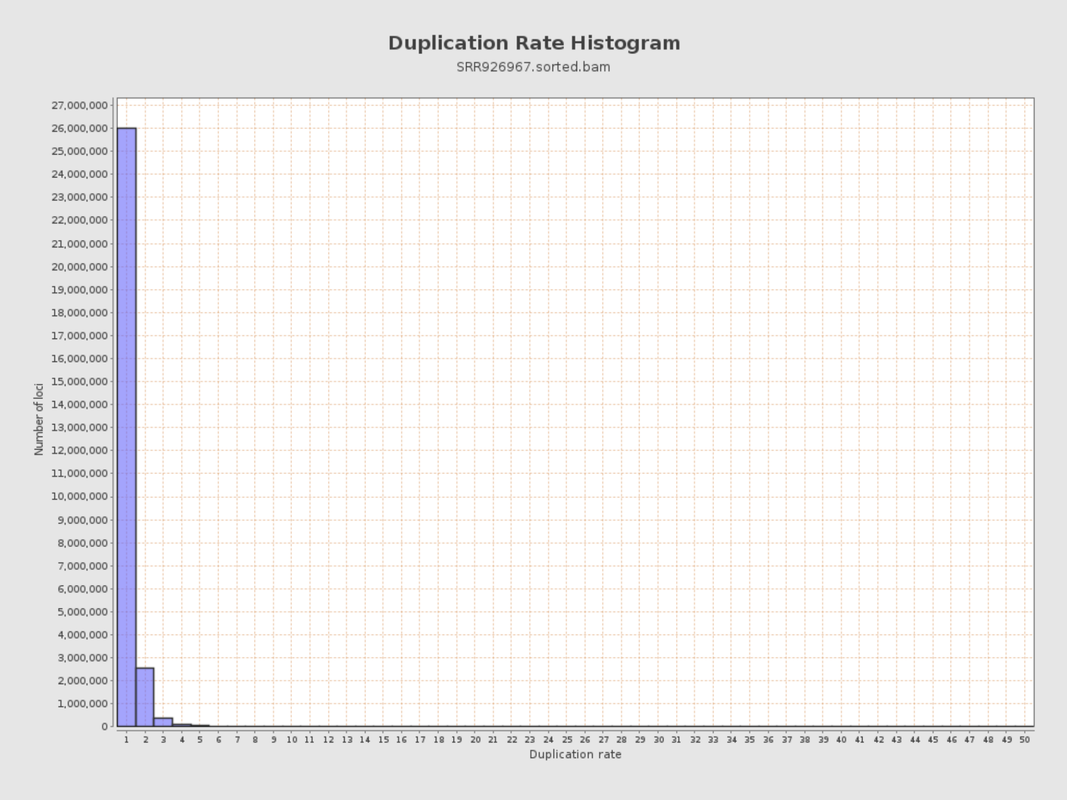
5. Results : Coverage Histogram (0-50X)



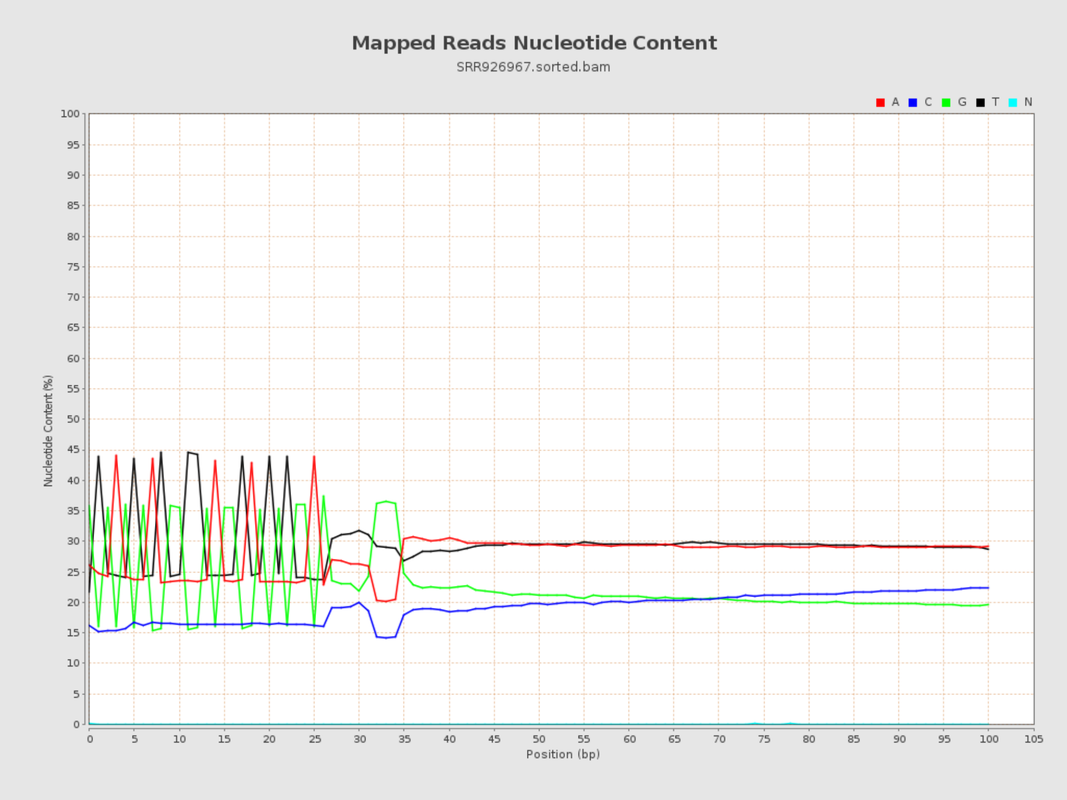
6. Results : Genome Fraction Coverage



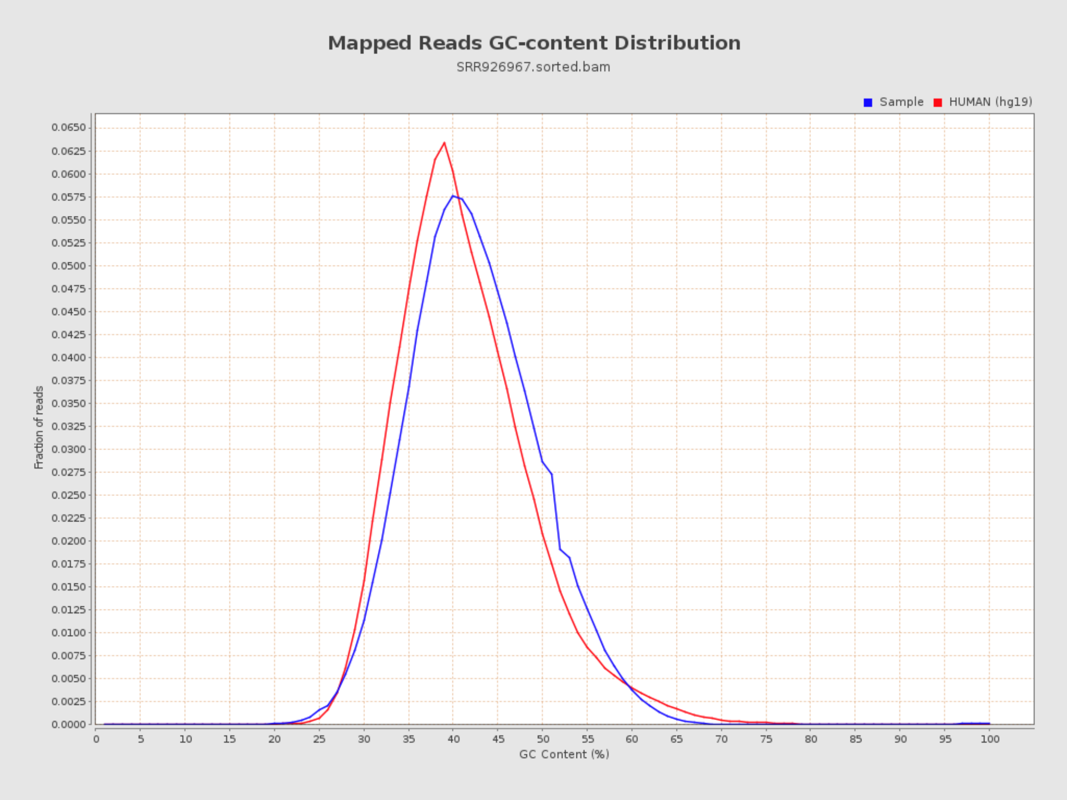
7. Results : Duplication Rate Histogram



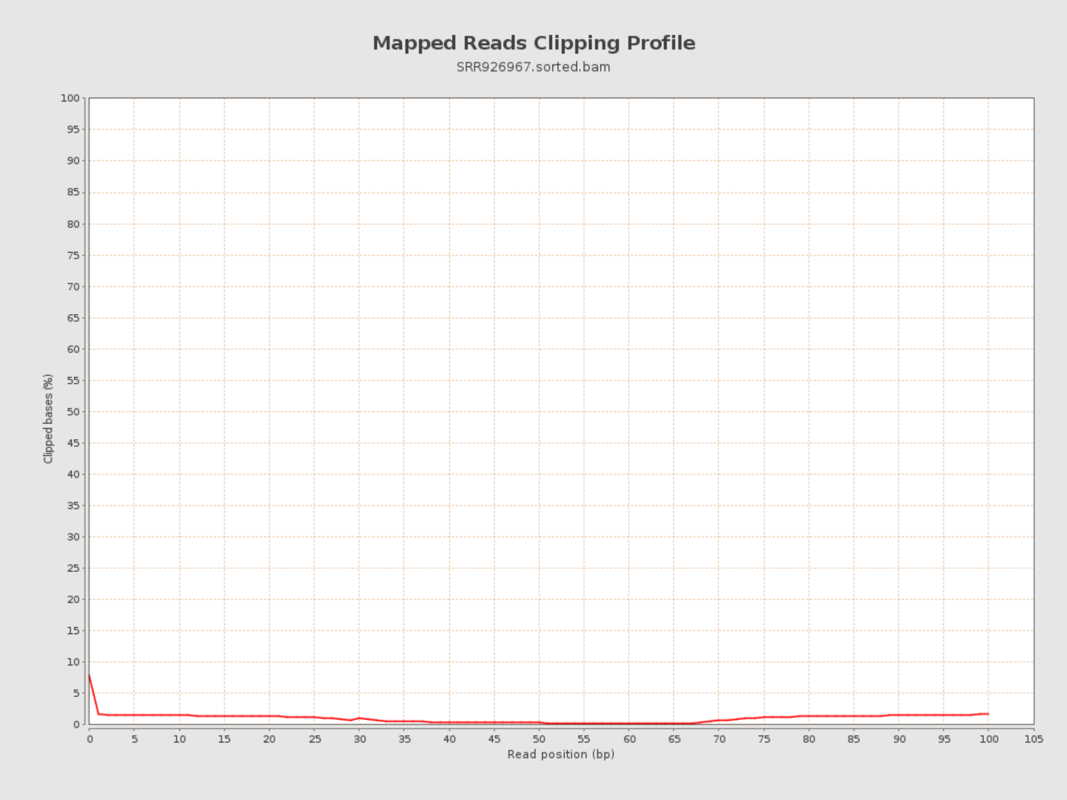
8. Results : Mapped Reads Nucleotide Content



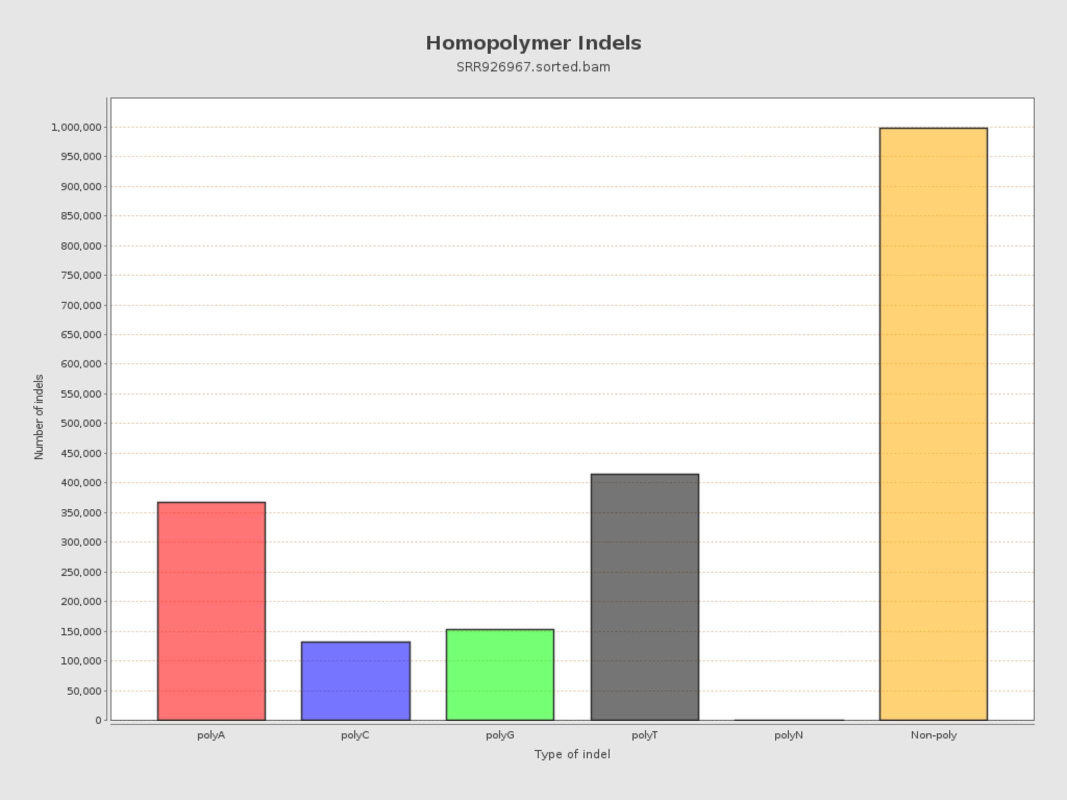
9. Results : Mapped Reads GC-content Distribution



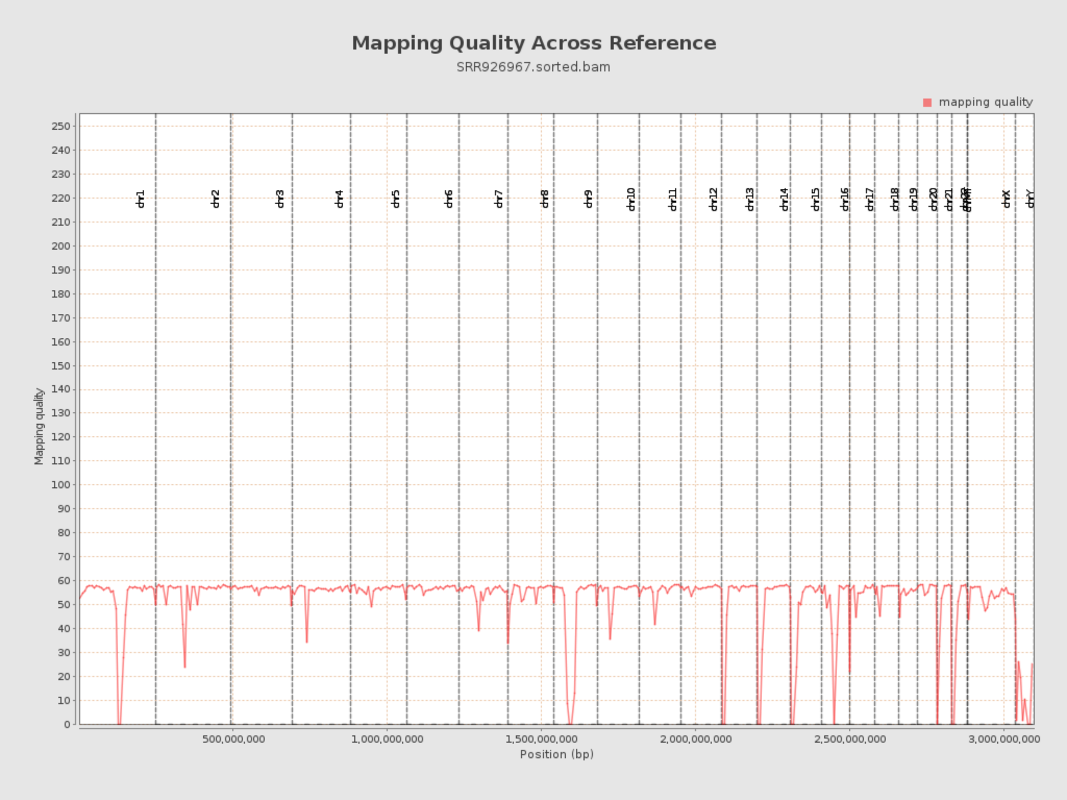
10. Results : Mapped Reads Clipping Profile



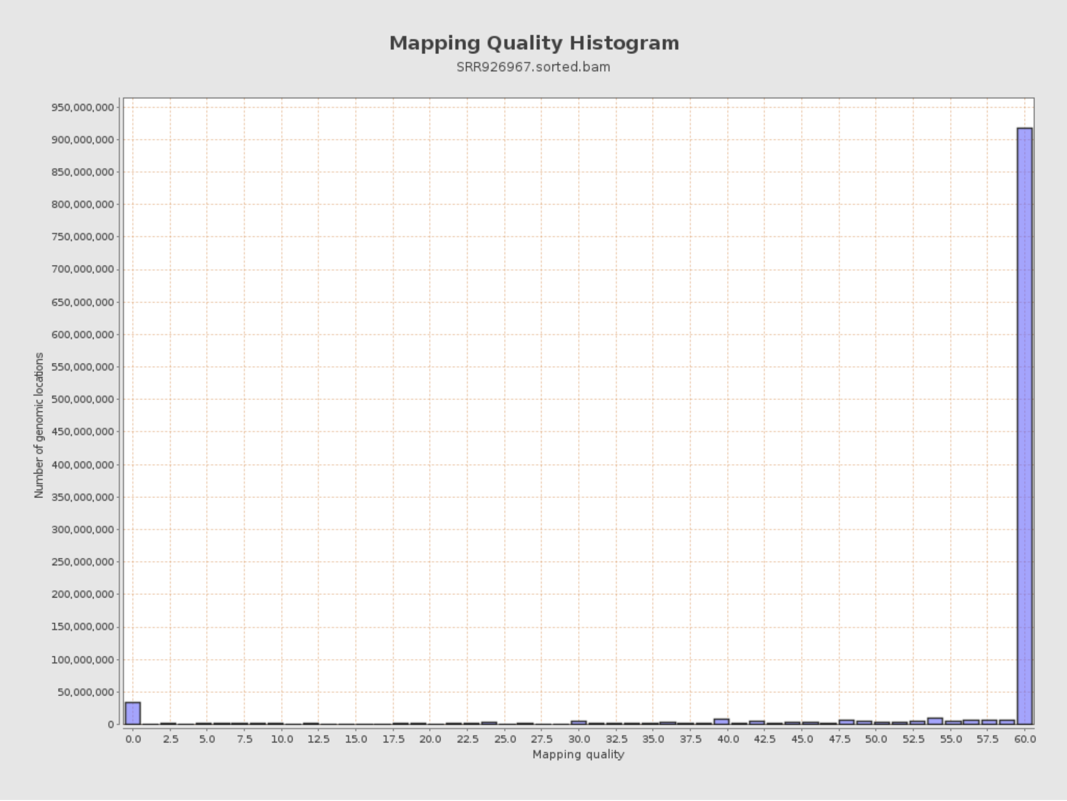
11. Results : Homopolymer Indels



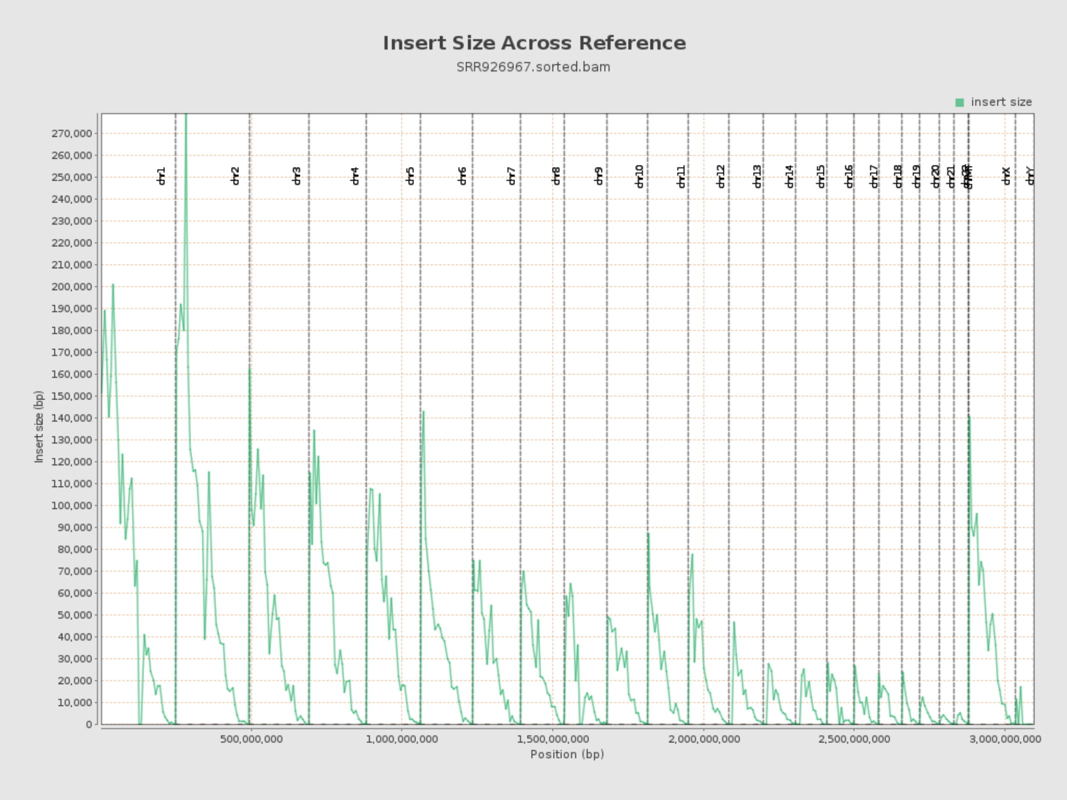
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram