Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 01:07:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926947.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_SRR926947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926947_1.fastq.gz SRR926947_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 01:07:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,473,910
Mapped reads	14,197,289 / 98.09%
Unmapped reads	276,621 / 1.91%
Mapped paired reads	14,197,289 / 98.09%
Mapped reads, first in pair	7,104,445 / 49.08%
Mapped reads, second in pair	7,092,844 / 49%
Mapped reads, both in pair	14,030,220 / 96.93%
Mapped reads, singletons	167,069 / 1.15%
Secondary alignments	0
Supplementary alignments	229,334 / 1.58%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	767,543 / 5.3%
Duplication rate	4.26%
Clipped reads	5,437,968 / 37.57%

2.2. ACGT Content

Number/percentage of A's	375,492,865 / 28.28%
Number/percentage of C's	270,743,472 / 20.39%
Number/percentage of T's	380,771,963 / 28.67%
Number/percentage of G's	300,865,291 / 22.66%
Number/percentage of N's	53,099 / 0%

GC Percentage	43.05%

2.3. Coverage

Mean	0.4293
Standard Deviation	1.9146

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	166,280.04
Standard Deviation	4,079,014.98
P25/Median/P75	145 / 185 / 244

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	11,881,178
Insertions	215,760
Mapped reads with at least one insertion	1.49%
Deletions	644,795
Mapped reads with at least one deletion	4.43%
Homopolymer indels	51.83%

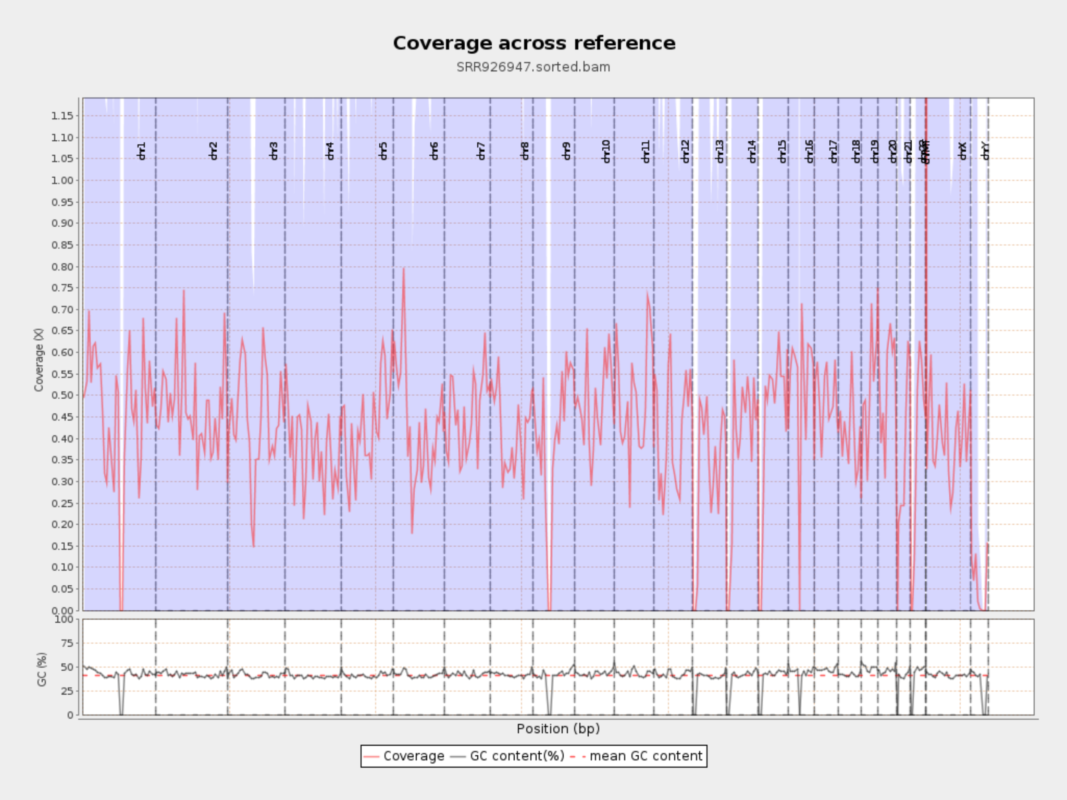
2.7. Chromosome stats

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

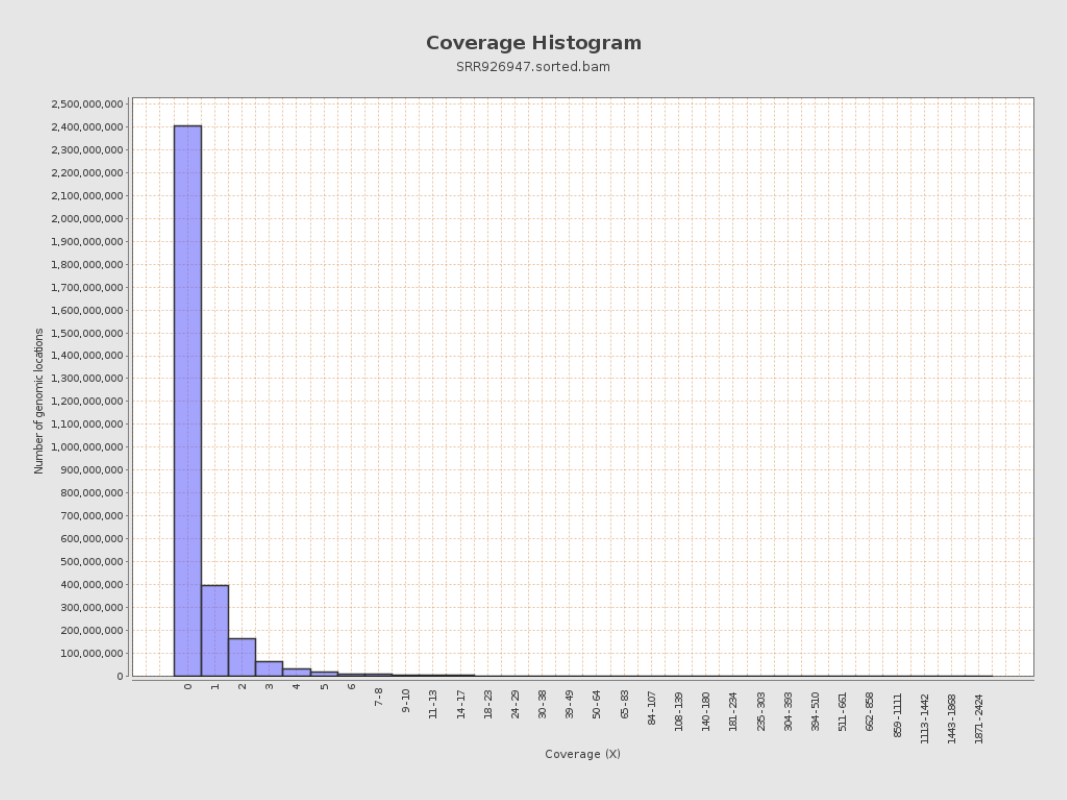
		bases	**coverage**	**deviation**
chr1	249250621	114168948	0.458	2.3803
chr2	243199373	114479220	0.4707	3.0892
chr3	198022430	87480135	0.4418	1.1806
chr4	191154276	71777112	0.3755	1.5969
chr5	180915260	78520833	0.434	1.1395
chr6	171115067	73450518	0.4292	1.3647
chr7	159138663	72736730	0.4571	1.5164
chr8	146364022	60503128	0.4134	1.1688
chr9	141213431	56275373	0.3985	1.9716
chr10	135534747	65379609	0.4824	3.3488
chr11	135006516	66812813	0.4949	1.6132
chr12	133851895	56454530	0.4218	1.2695
chr13	115169878	37191770	0.3229	0.9559
chr14	107349540	41124590	0.3831	1.0905
chr15	102531392	44507165	0.4341	1.2179
chr16	90354753	47008860	0.5203	2.7165
chr17	81195210	40692456	0.5012	1.5472
chr18	78077248	31863591	0.4081	1.9412
chr19	59128983	30337935	0.5131	1.9087
chr20	63025520	33372708	0.5295	1.6155
chr21	48129895	16672095	0.3464	1.3337
chr22	51304566	18961406	0.3696	1.121
chrMT	16571	2545775	153.6283	123.2266
chrX	155270560	62950849	0.4054	1.2208

chrY	59373566	3603622	0.0607	1.5355

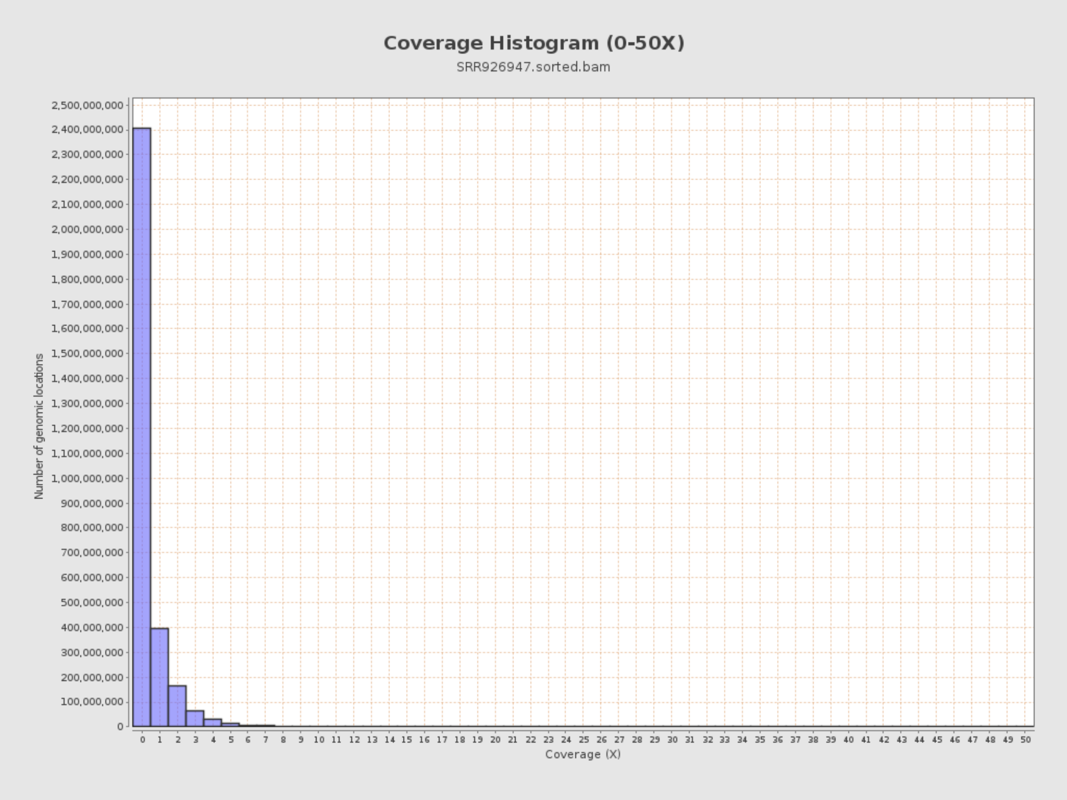
3. Results : Coverage across reference



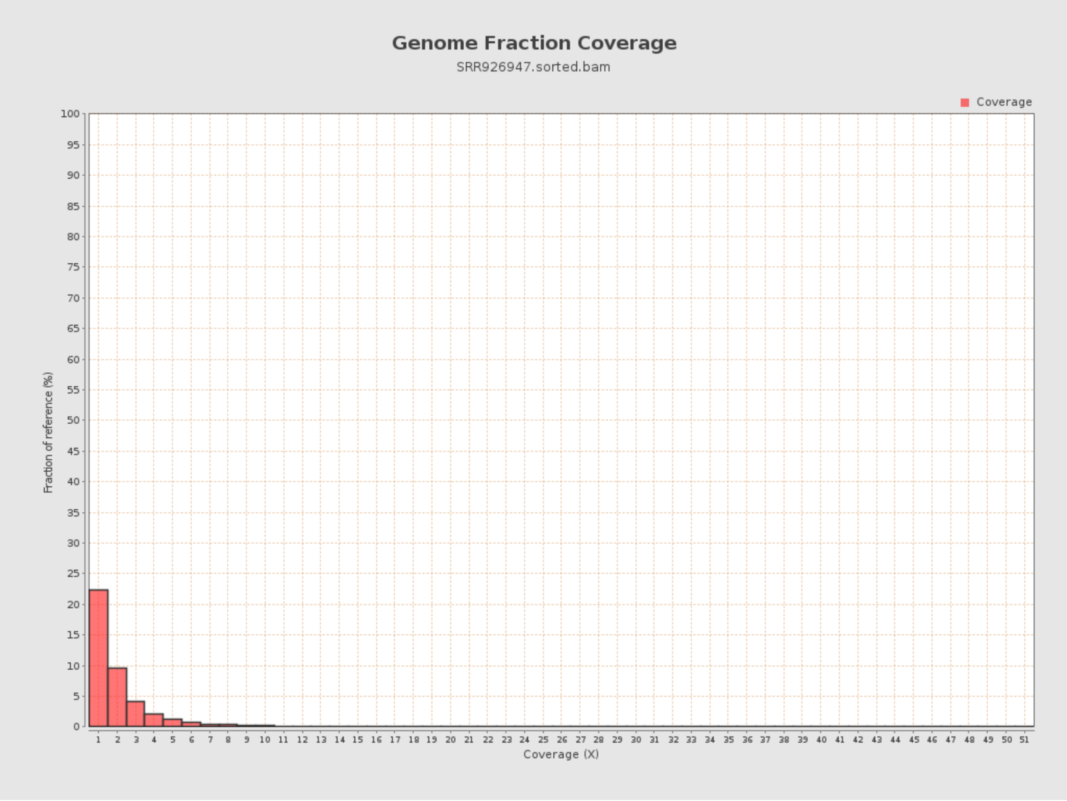
4. Results : Coverage Histogram



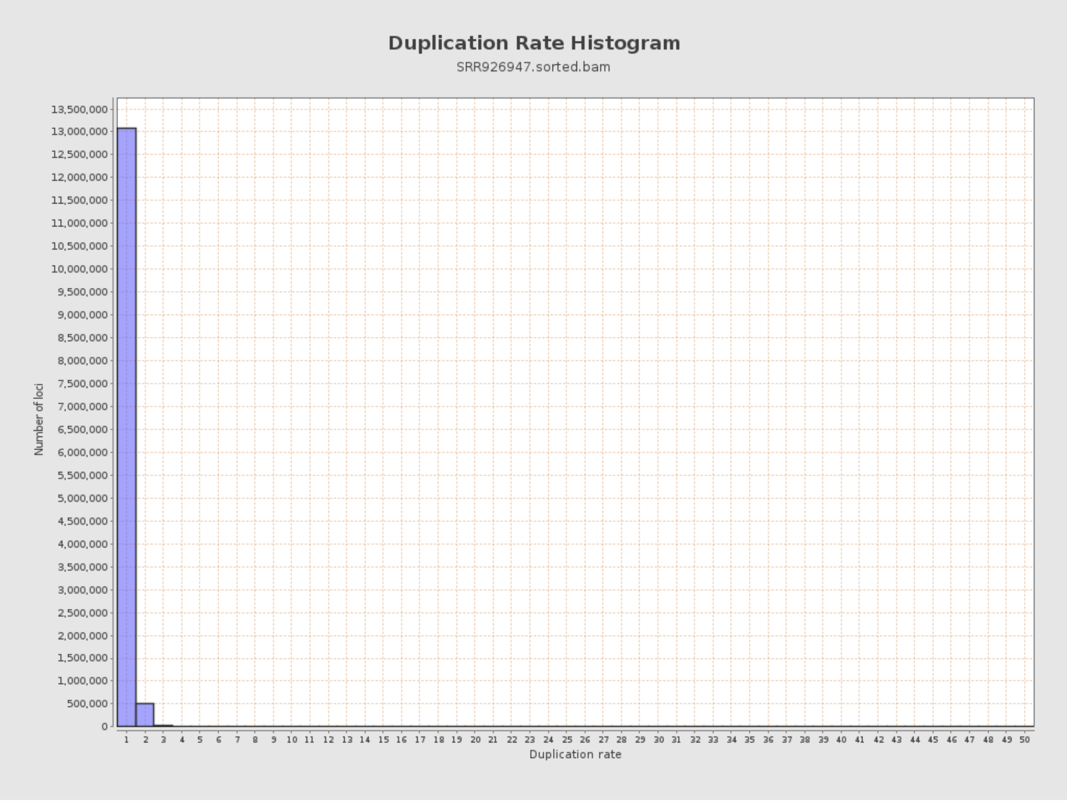
5. Results : Coverage Histogram (0-50X)



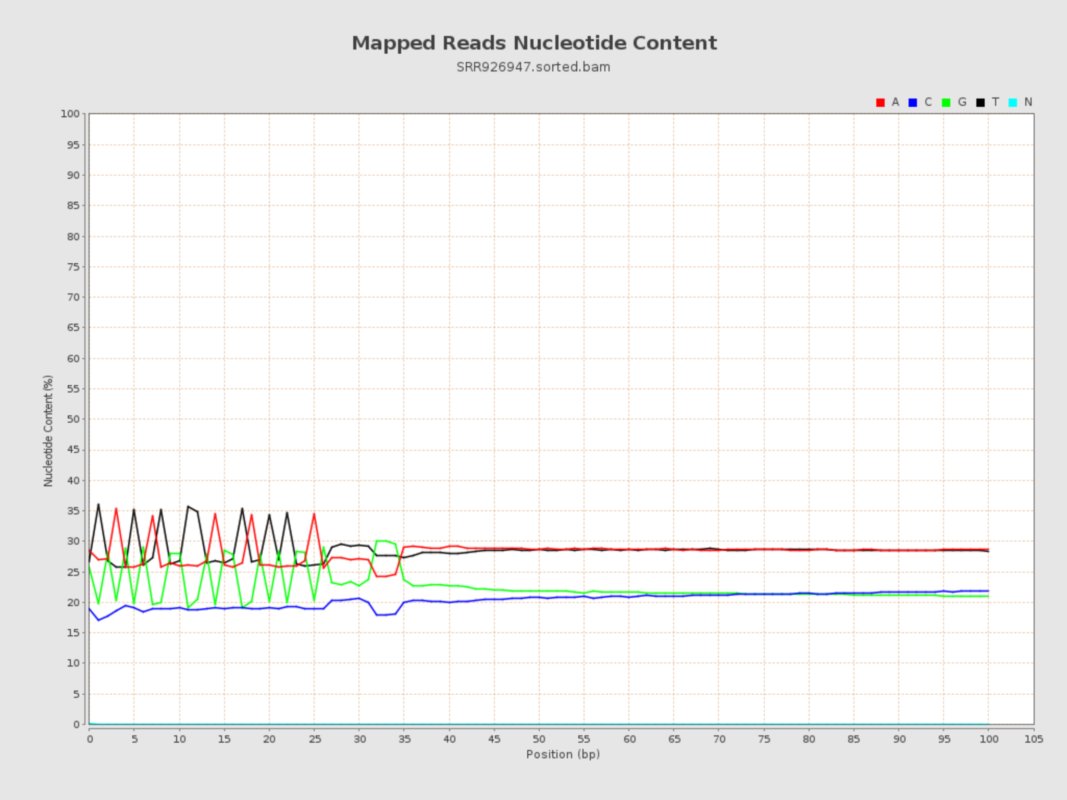
6. Results : Genome Fraction Coverage



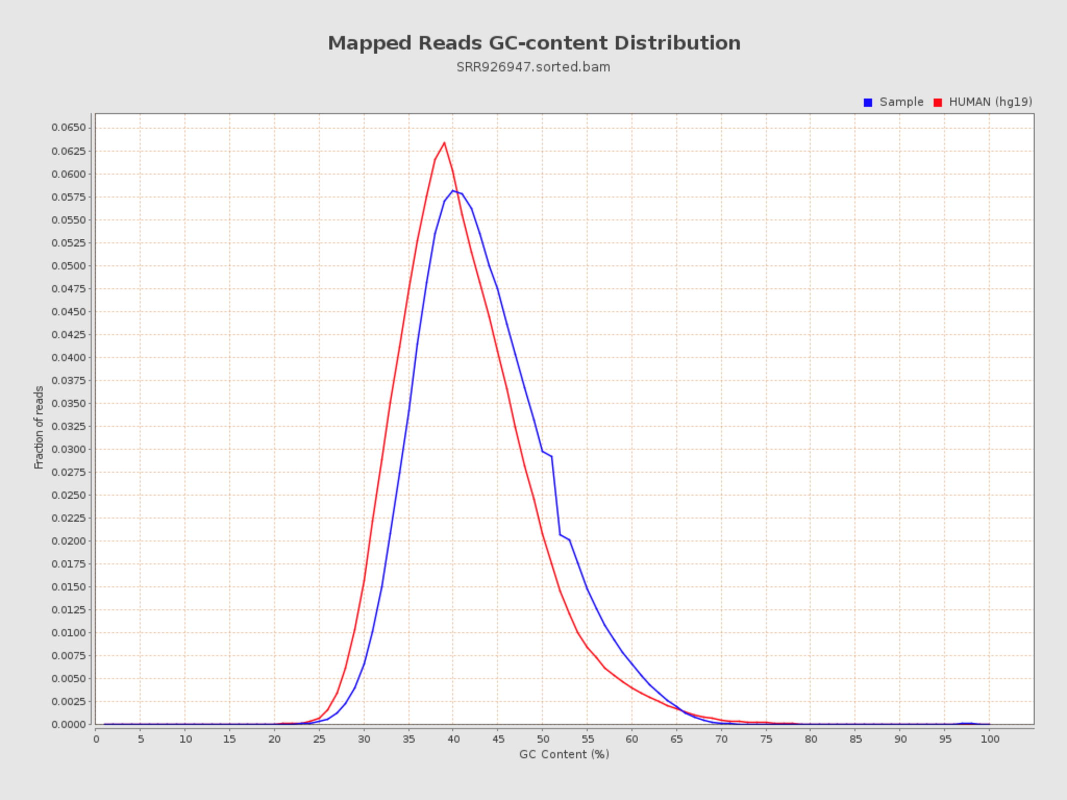
7. Results : Duplication Rate Histogram



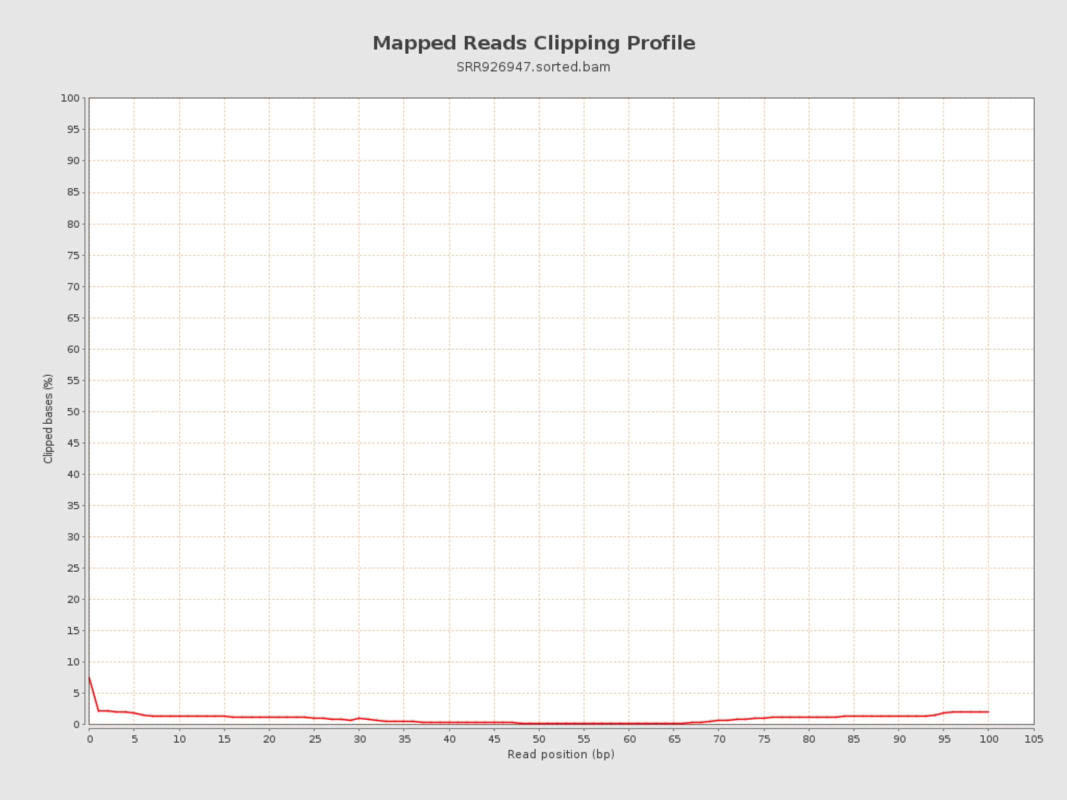
8. Results : Mapped Reads Nucleotide Content



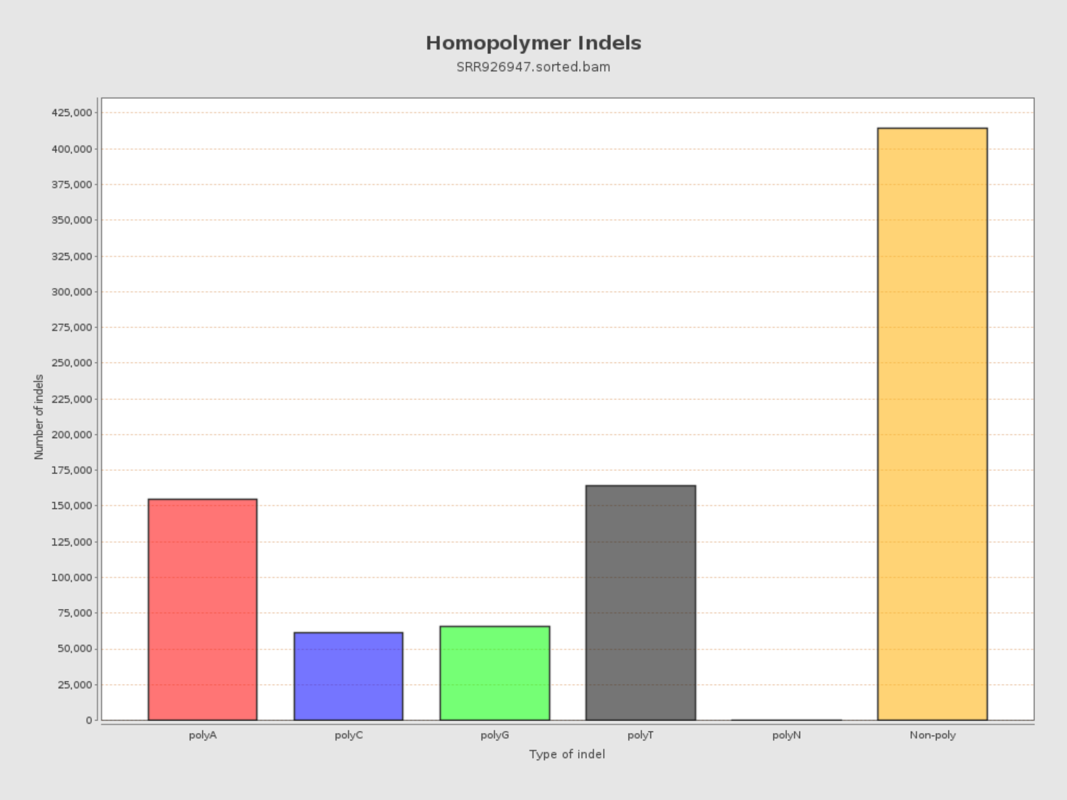
9. Results : Mapped Reads GC-content Distribution



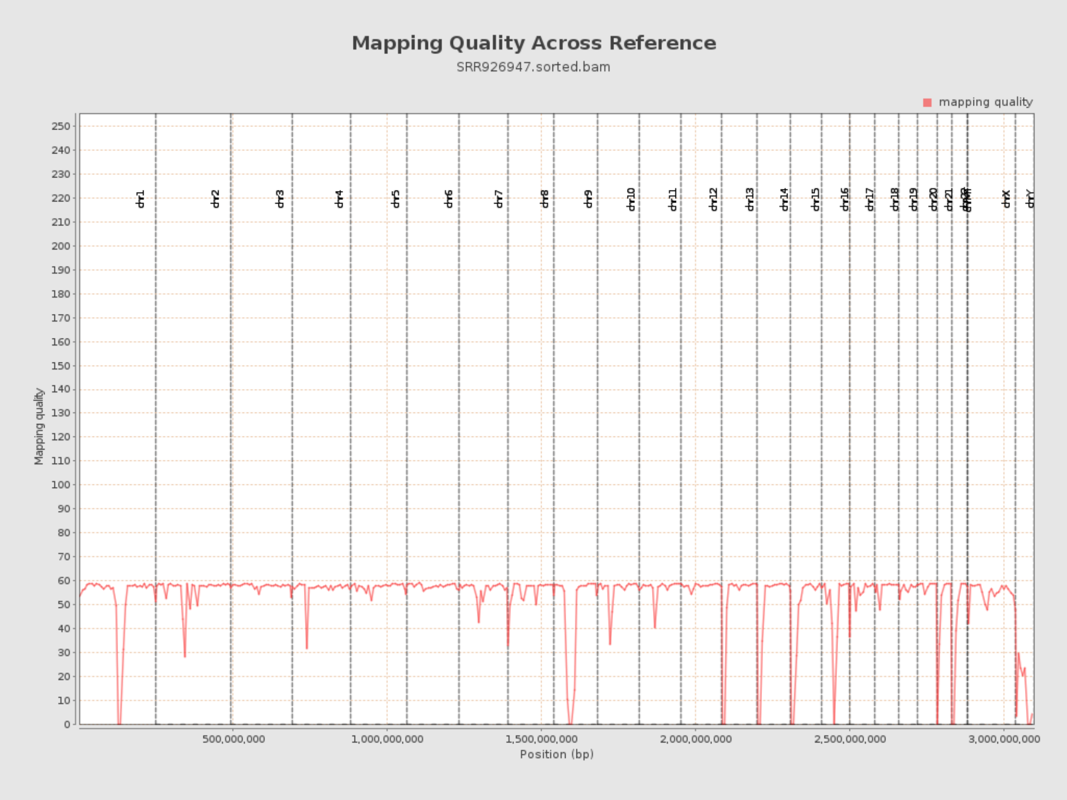
10. Results : Mapped Reads Clipping Profile



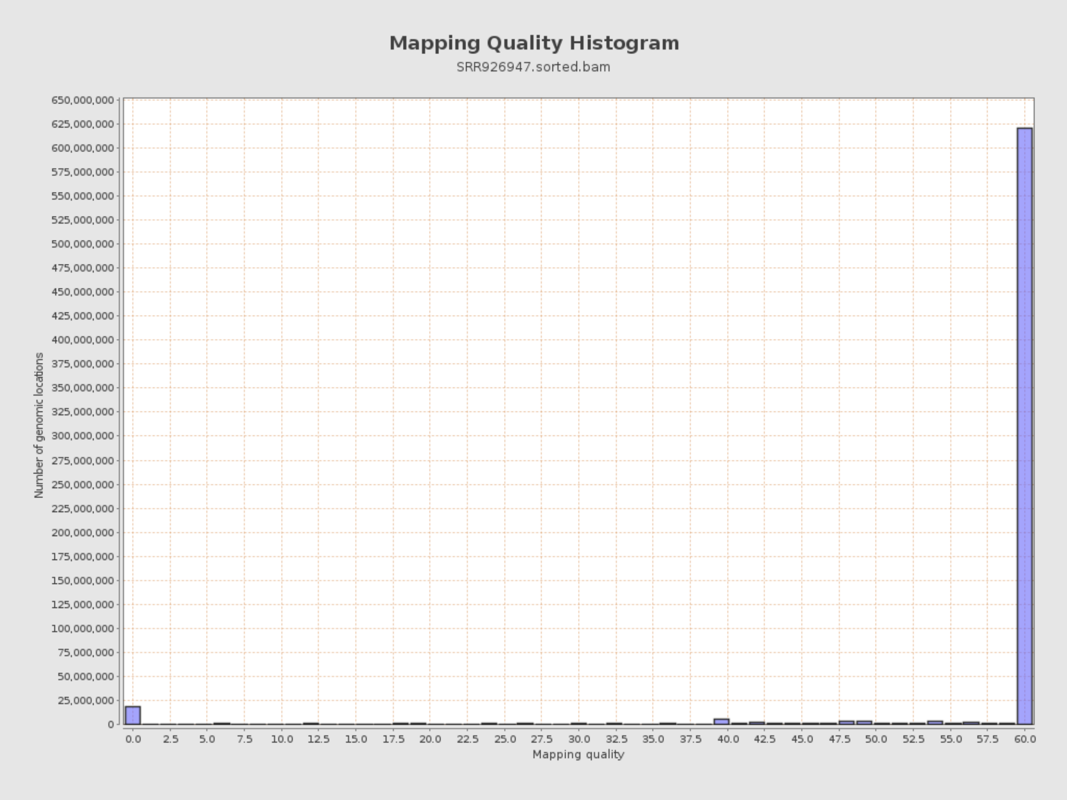
11. Results : Homopolymer Indels



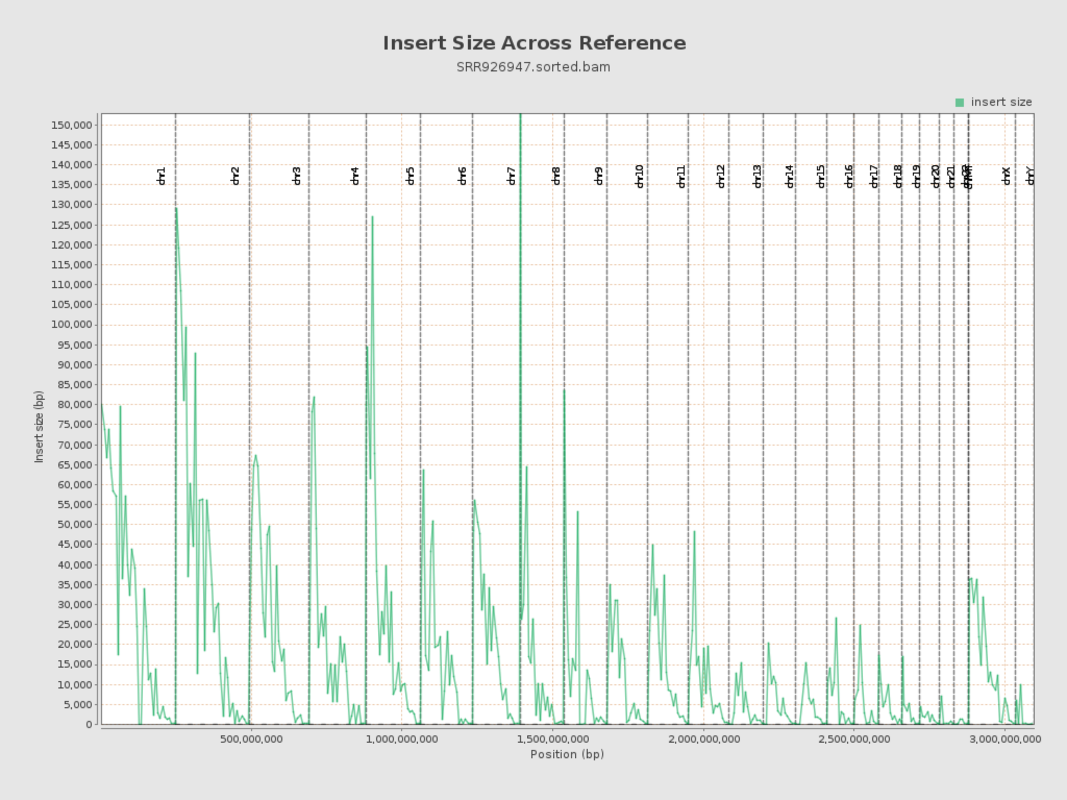
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram