Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 07:25:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927020.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_SRR927020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927020_1.fastq.gz SRR927020_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 07:25:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,027,056
Mapped reads	34,530,215 / 98.58%
Unmapped reads	496,841 / 1.42%
Mapped paired reads	34,530,215 / 98.58%
Mapped reads, first in pair	17,306,190 / 49.41%
Mapped reads, second in pair	17,224,025 / 49.17%
Mapped reads, both in pair	34,240,960 / 97.76%
Mapped reads, singletons	289,255 / 0.83%
Secondary alignments	0
Supplementary alignments	329,327 / 0.94%
Read min/max/mean length	30 / 101 / 101.39
Duplicated reads (estimated)	2,613,664 / 7.46%
Duplication rate	5.77%
Clipped reads	8,794,053 / 25.11%

2.2. ACGT Content

Number/percentage of A's	939,837,076 / 28.81%
Number/percentage of C's	648,434,228 / 19.88%
Number/percentage of T's	949,247,588 / 29.1%
Number/percentage of G's	724,088,580 / 22.2%
Number/percentage of N's	702,672 / 0.02%

GC Percentage	42.07%

2.3. Coverage

Mean	1.0546
Standard Deviation	4.6952

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	92,428
Standard Deviation	2,979,431.65
P25/Median/P75	149 / 192 / 256

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	29,858,075
Insertions	520,488
Mapped reads with at least one insertion	1.48%
Deletions	1,707,111
Mapped reads with at least one deletion	4.82%
Homopolymer indels	53.09%

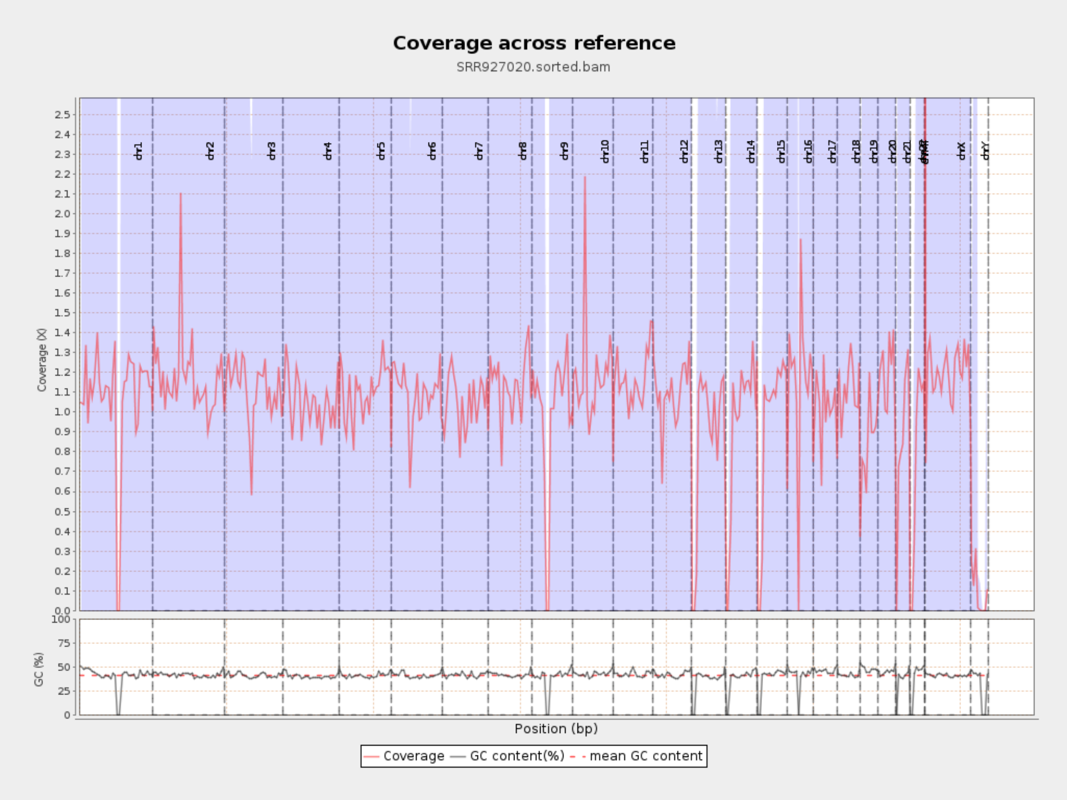
2.7. Chromosome stats

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

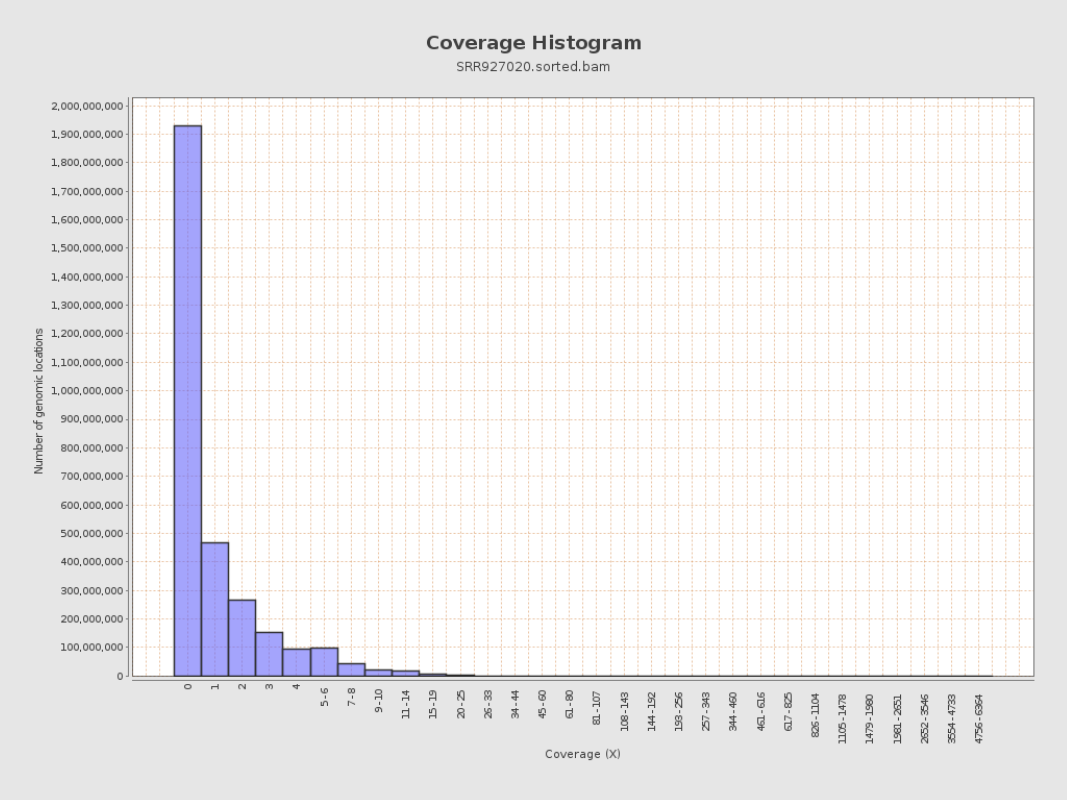
		bases	coverage	deviation
chr1	249250621	267075805	1.0715	6.9304
chr2	243199373	286477017	1.178	6.7924
chr3	198022430	220975582	1.1159	2.1577
chr4	191154276	200194281	1.0473	3.184
chr5	180915260	200188335	1.1065	2.0763
chr6	171115067	187639516	1.0966	2.1646
chr7	159138663	167118761	1.0501	3.1473
chr8	146364022	166822548	1.1398	2.5502
chr9	141213431	137856228	0.9762	4.9673
chr10	135534747	162574587	1.1995	11.6991
chr11	135006516	155877826	1.1546	5.3375
chr12	133851895	146360566	1.0935	2.0998
chr13	115169878	100217794	0.8702	1.8367
chr14	107349540	99192669	0.924	1.9806
chr15	102531392	93801008	0.9149	1.9572
chr16	90354753	103418979	1.1446	6.7116
chr17	81195210	82608758	1.0174	2.5795
chr18	78077248	88636761	1.1352	5.2103
chr19	59128983	49617489	0.8391	3.8344
chr20	63025520	75471399	1.1975	2.4436
chr21	48129895	42577065	0.8846	3.0658
chr22	51304566	39004185	0.7602	1.8916
chrMT	16571	208125	12.5596	10.6806
chrX	155270560	185203576	1.1928	2.8362

chrY	59373566	5607221	0.0944	2.7767

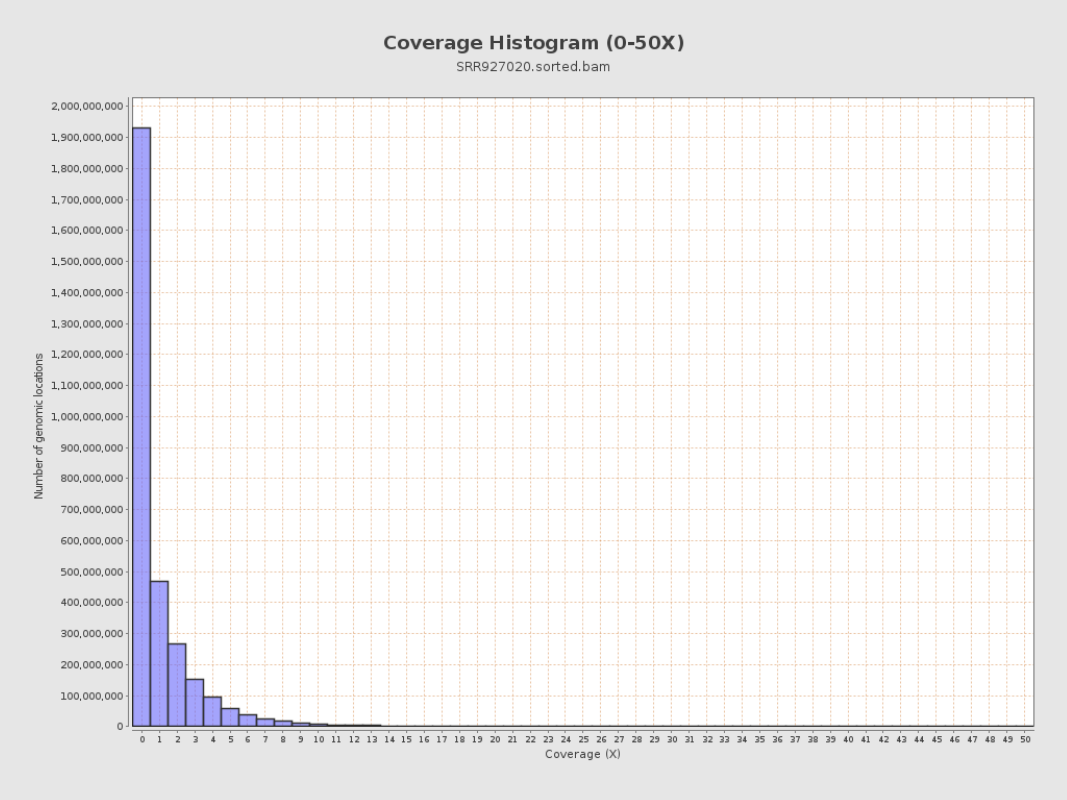
3. Results : Coverage across reference



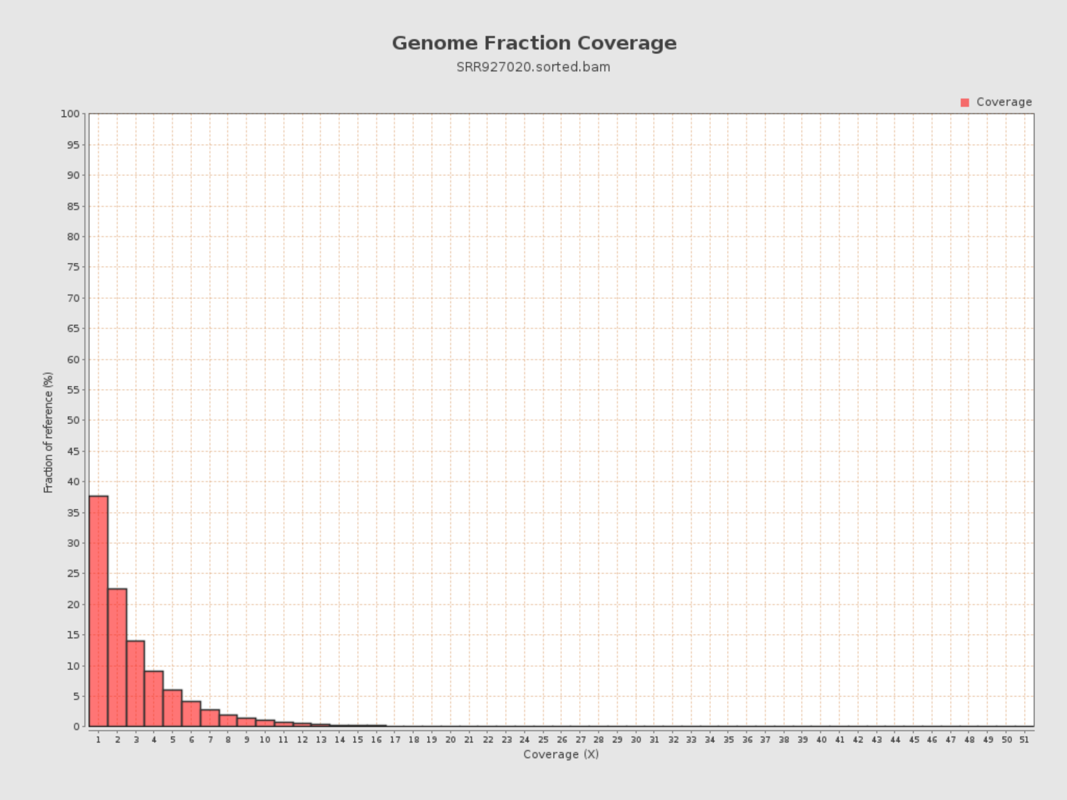
4. Results : Coverage Histogram



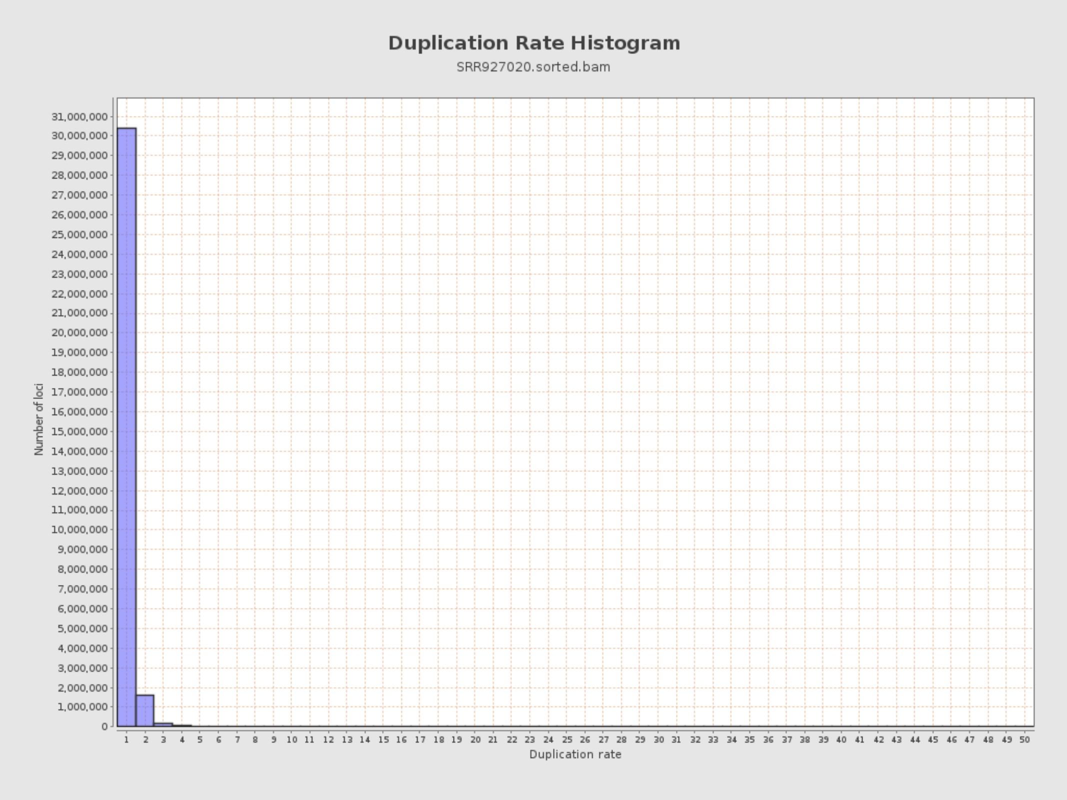
5. Results : Coverage Histogram (0-50X)



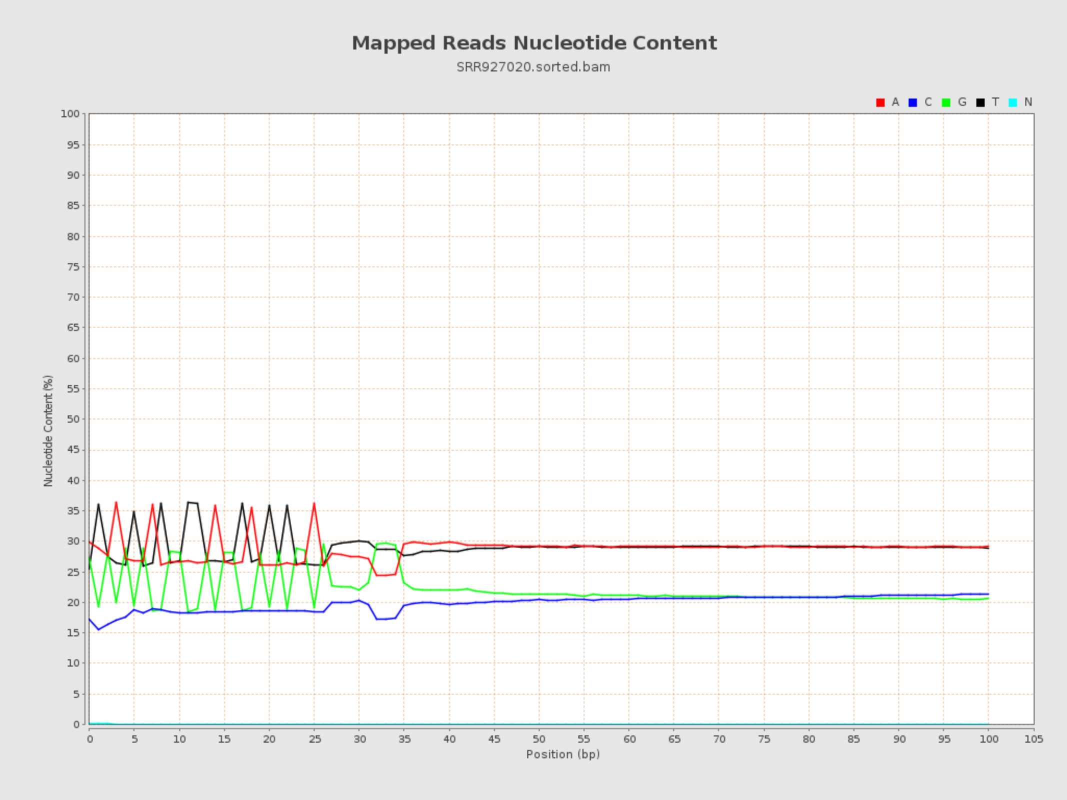
6. Results : Genome Fraction Coverage



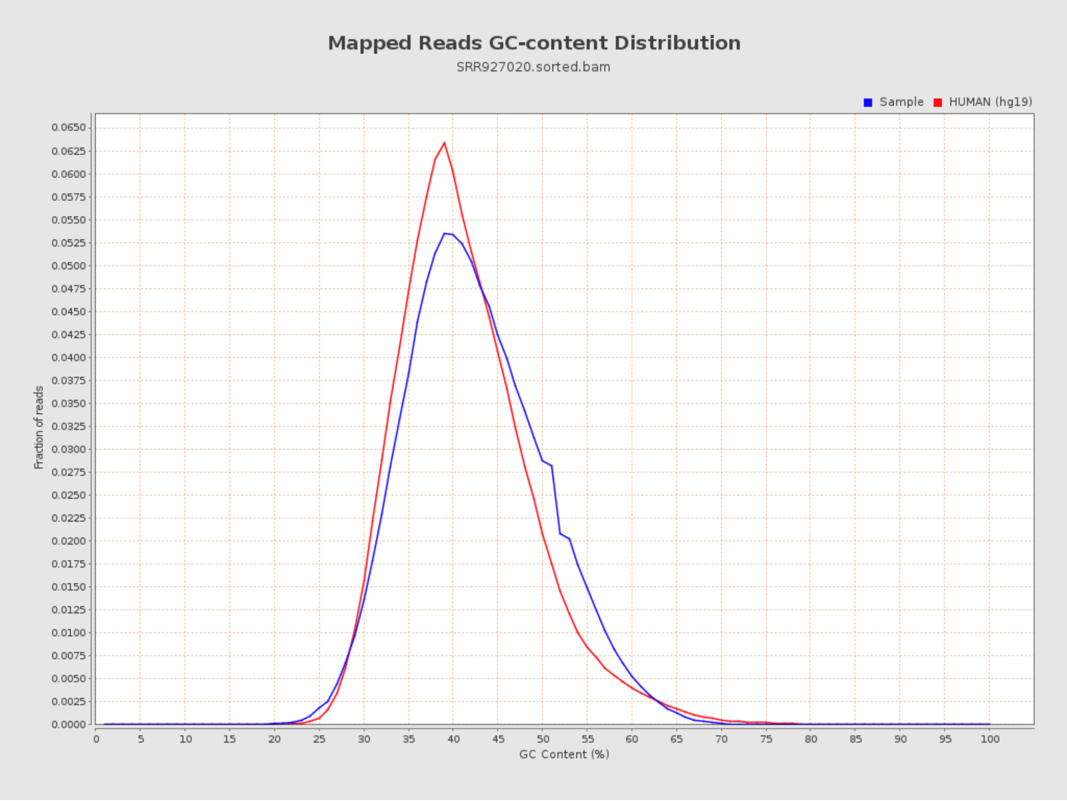
7. Results : Duplication Rate Histogram



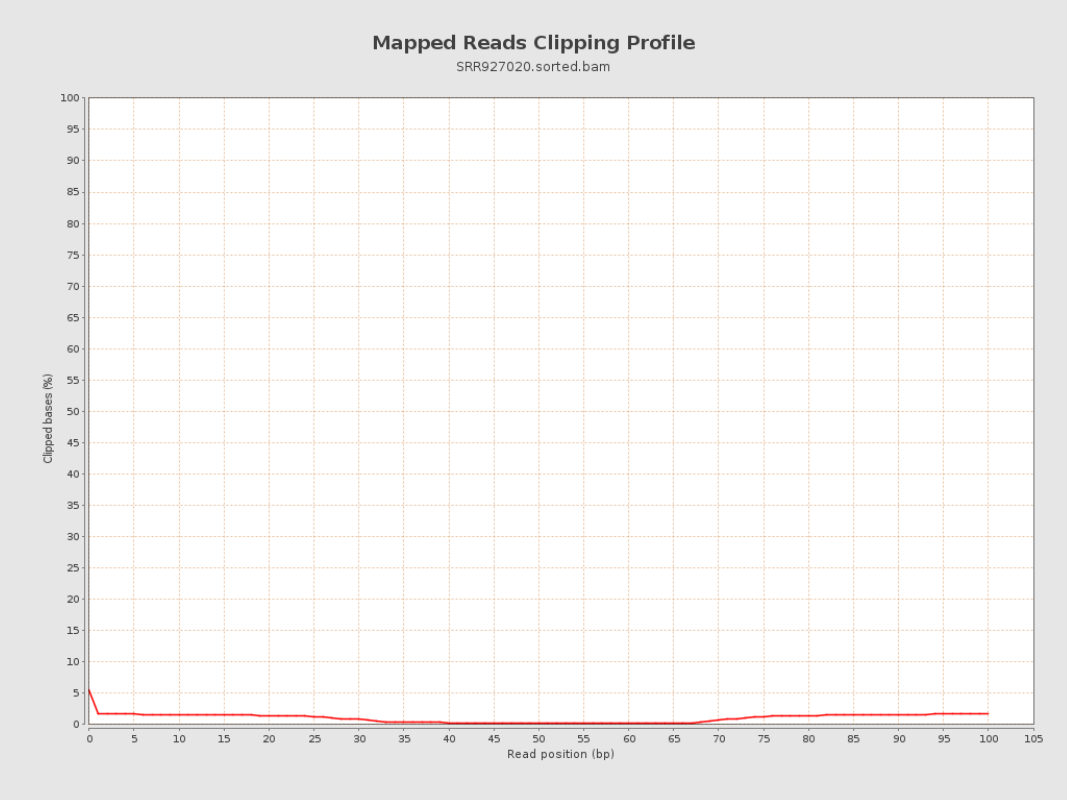
8. Results : Mapped Reads Nucleotide Content



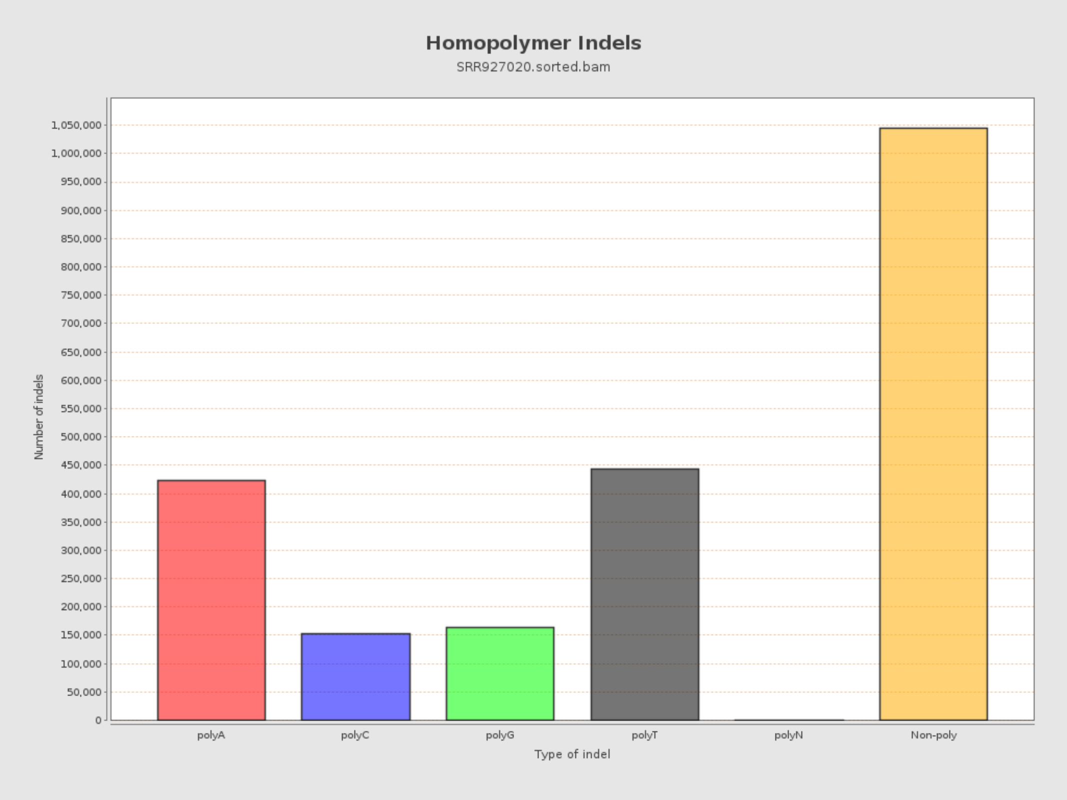
9. Results : Mapped Reads GC-content Distribution



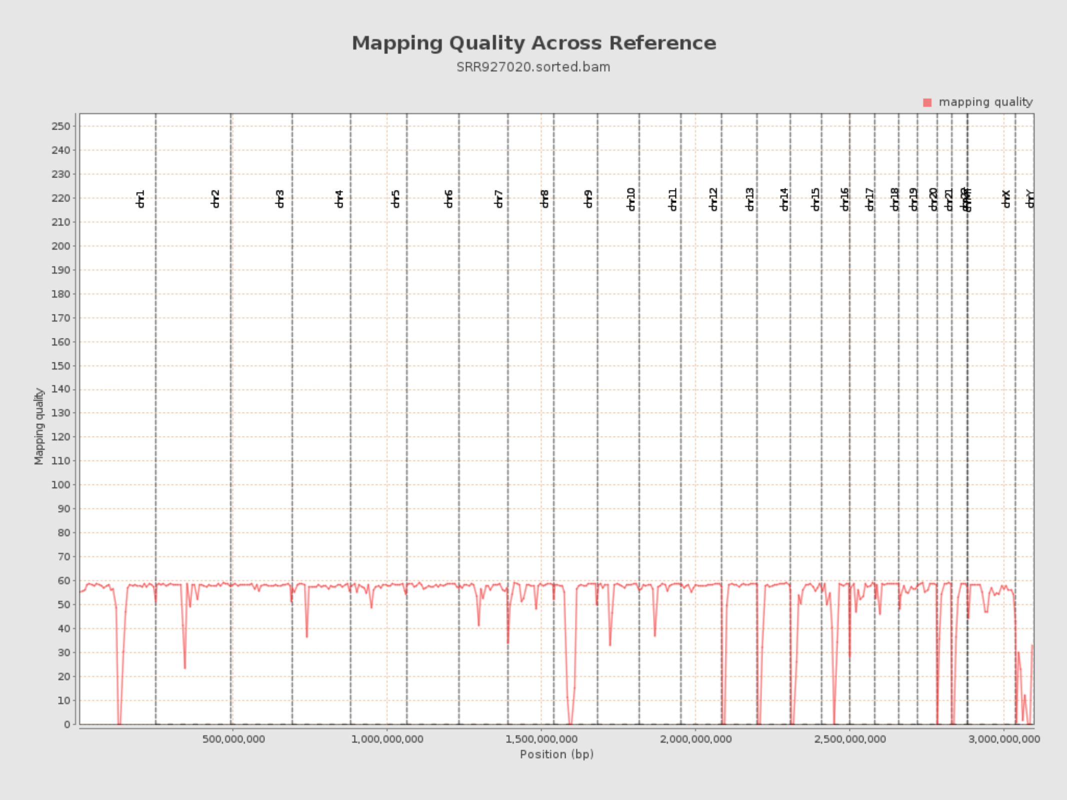
10. Results : Mapped Reads Clipping Profile



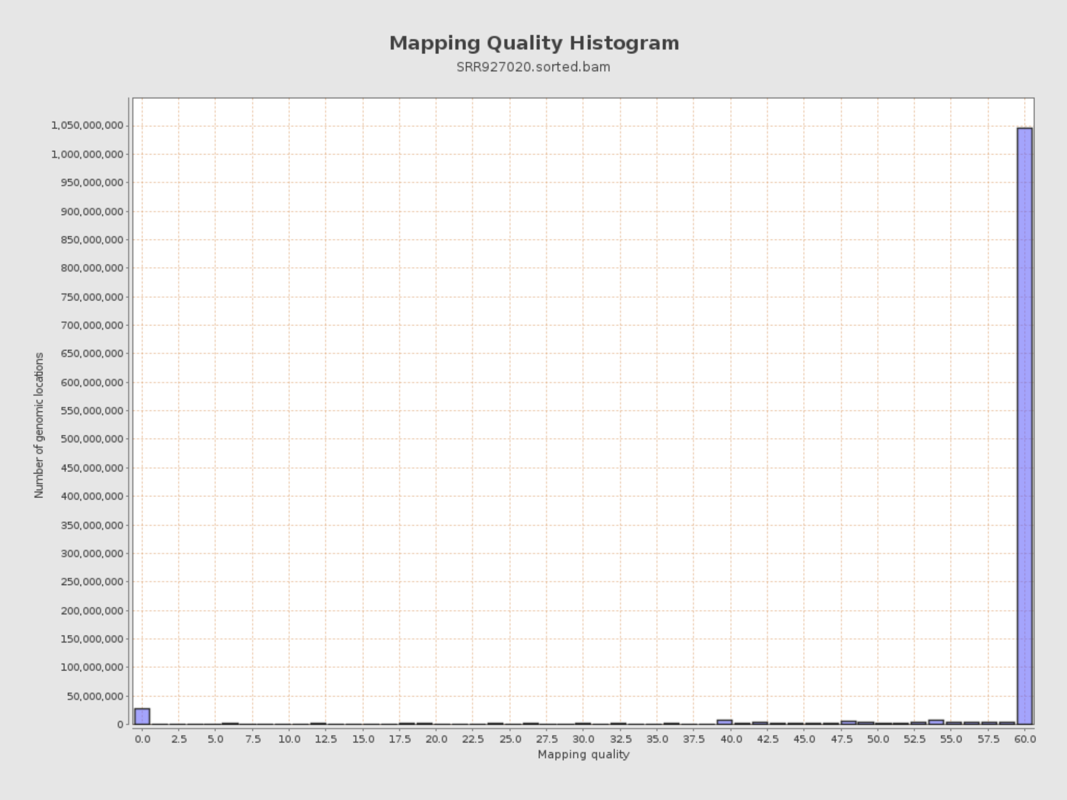
11. Results : Homopolymer Indels



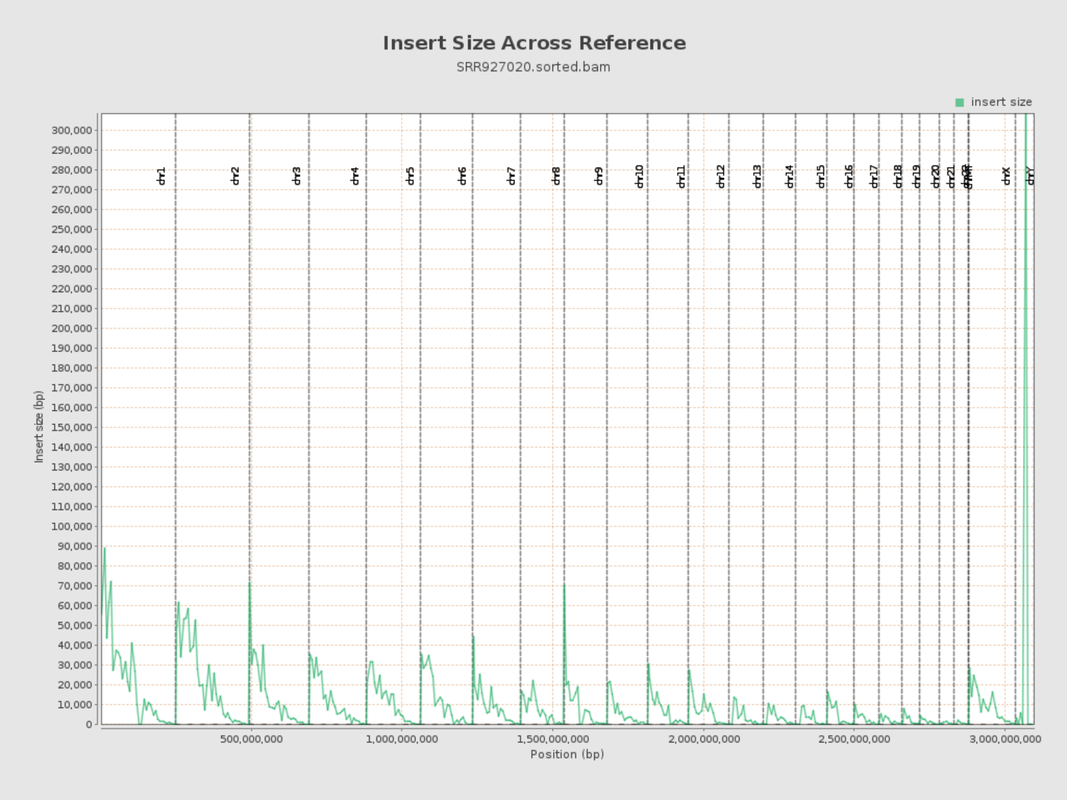
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram