Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 17:09:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927039.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_SRR927039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927039_1.fastq.gz SRR927039_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 17:09:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,375,858
Mapped reads	31,594,902 / 97.59%
Unmapped reads	780,956 / 2.41%
Mapped paired reads	31,594,902 / 97.59%
Mapped reads, first in pair	15,879,791 / 49.05%
Mapped reads, second in pair	15,715,111 / 48.54%
Mapped reads, both in pair	31,142,772 / 96.19%
Mapped reads, singletons	452,130 / 1.4%
Secondary alignments	0
Supplementary alignments	637,274 / 1.97%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	2,985,492 / 9.22%
Duplication rate	7.19%
Clipped reads	12,518,449 / 38.67%

2.2. ACGT Content

Number/percentage of A's	824,299,562 / 28.59%
Number/percentage of C's	564,124,415 / 19.56%
Number/percentage of T's	838,148,611 / 29.07%
Number/percentage of G's	656,498,277 / 22.77%
Number/percentage of N's	391,200 / 0.01%

GC Percentage	42.33%

2.3. Coverage

Mean	0.9321
Standard Deviation	3.7192

2.4. Mapping Quality

Mean Mapping Quality	52.64

2.5. Insert size

Mean	233,013.88
Standard Deviation	4,713,082.33
P25/Median/P75	138 / 184 / 252

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	30,927,659
Insertions	495,004
Mapped reads with at least one insertion	1.53%
Deletions	1,481,945
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.58%

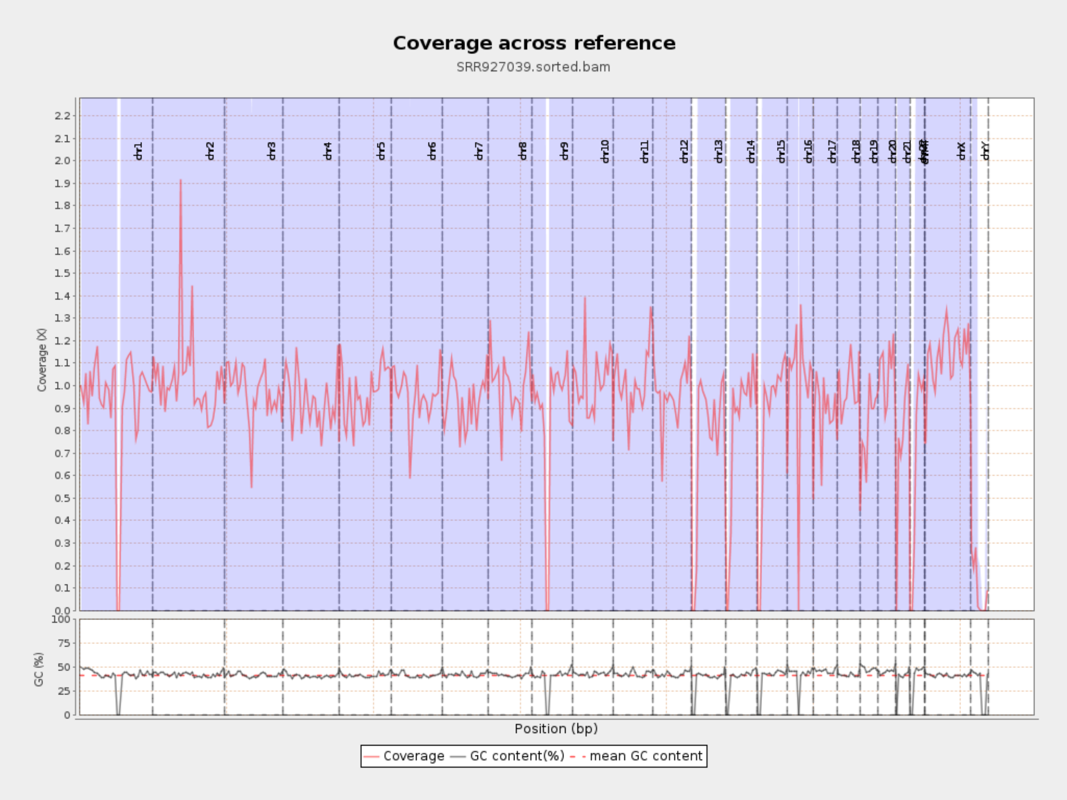
2.7. Chromosome stats

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

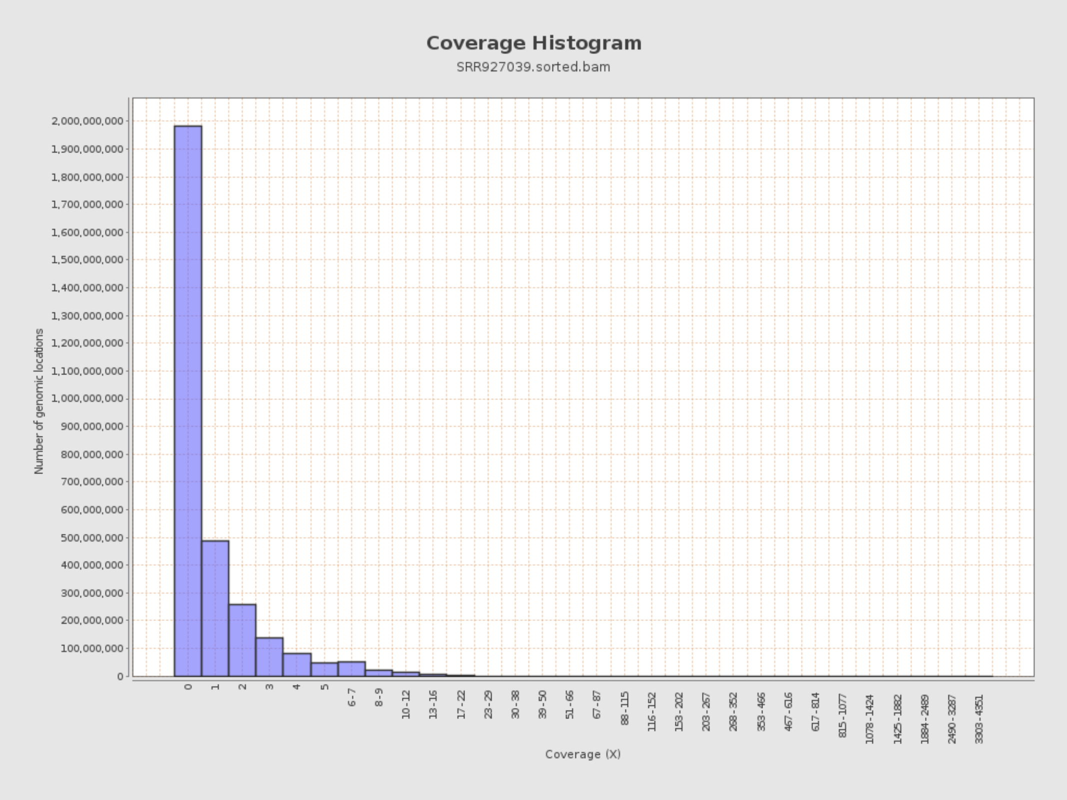
		bases	coverage	deviation
chr1	249250621	232306032	0.932	4.9366
chr2	243199373	251583235	1.0345	7.0201
chr3	198022430	192336541	0.9713	1.9376
chr4	191154276	178411713	0.9333	3.2649
chr5	180915260	175475625	0.9699	1.9459
chr6	171115067	164605528	0.962	1.9596
chr7	159138663	148650734	0.9341	2.7505
chr8	146364022	147508888	1.0078	2.4137
chr9	141213431	122161096	0.8651	4.9824
chr10	135534747	139144965	1.0266	5.3318
chr11	135006516	136444924	1.0107	3.0038
chr12	133851895	129489450	0.9674	2.0072
chr13	115169878	87147312	0.7567	1.6929
chr14	107349540	85907119	0.8003	1.8474
chr15	102531392	84942212	0.8285	1.8607
chr16	90354753	89865479	0.9946	5.4828
chr17	81195210	72111074	0.8881	2.6404
chr18	78077248	78330532	1.0032	4.9903
chr19	59128983	48400455	0.8186	3.0467
chr20	63025520	66752998	1.0591	2.2959
chr21	48129895	37579166	0.7808	2.9869
chr22	51304566	34440541	0.6713	1.8388
chrMT	16571	12351	0.7453	1.1622
chrX	155270560	176128105	1.1343	2.4353

chrY	59373566	5908246	0.0995	3.4704

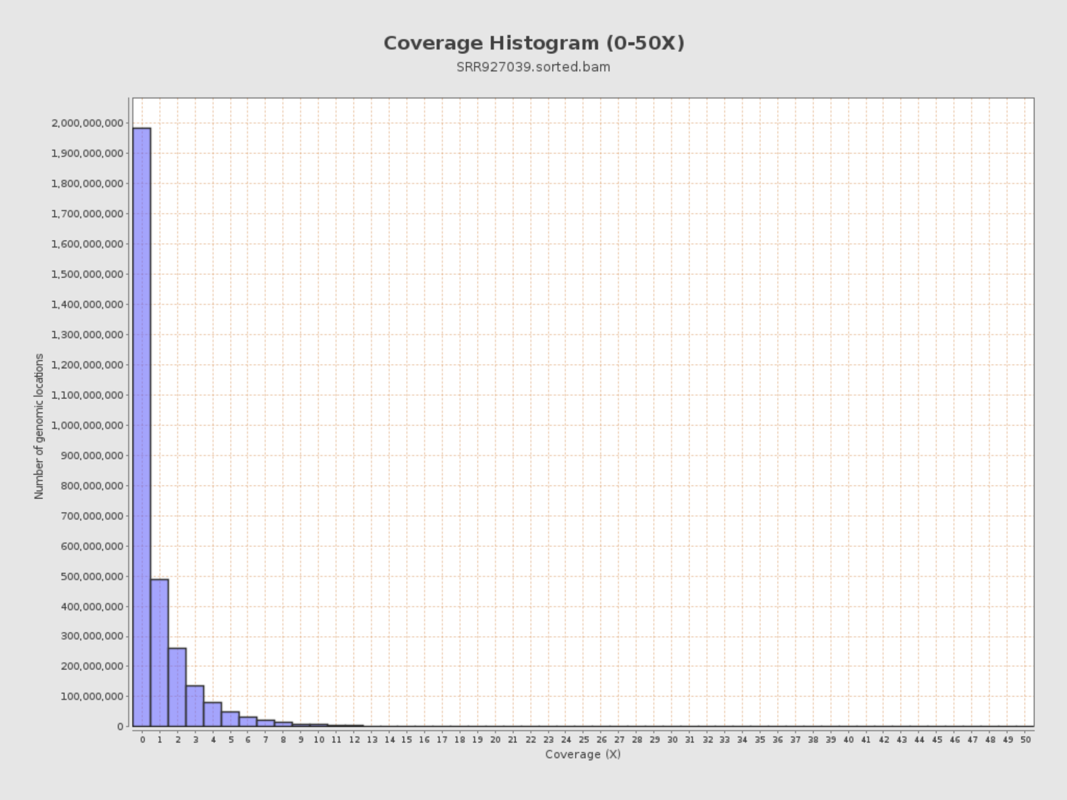
3. Results : Coverage across reference



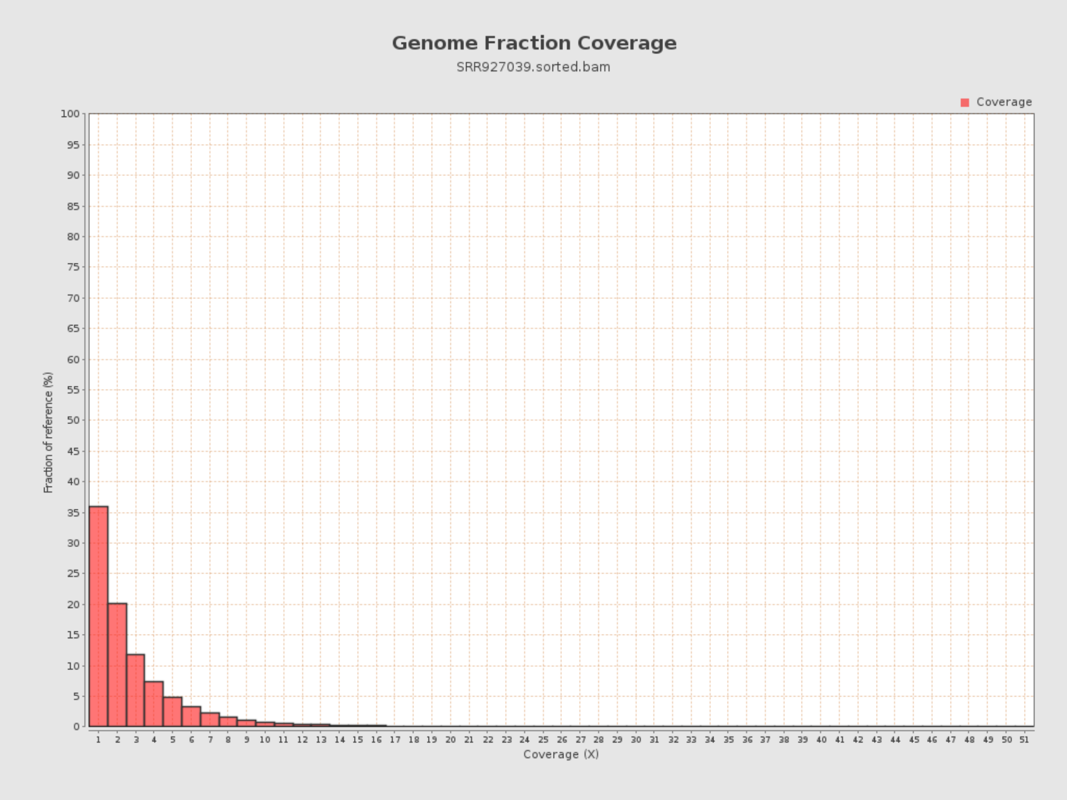
4. Results : Coverage Histogram



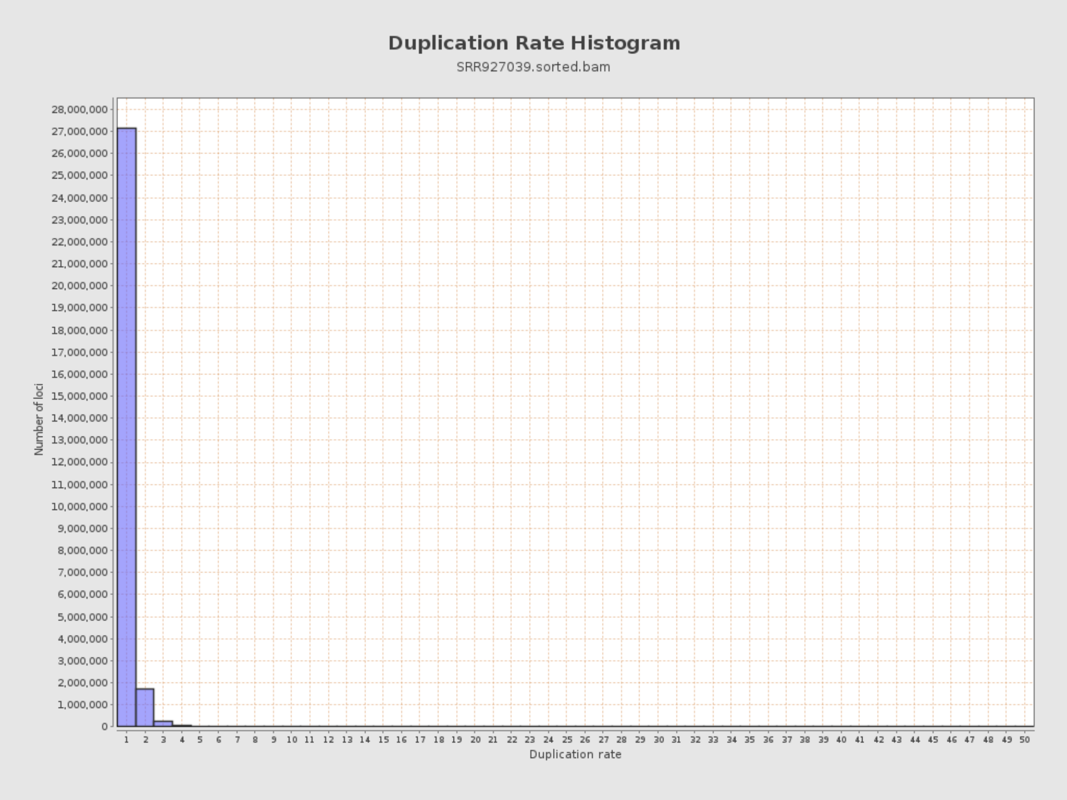
5. Results : Coverage Histogram (0-50X)



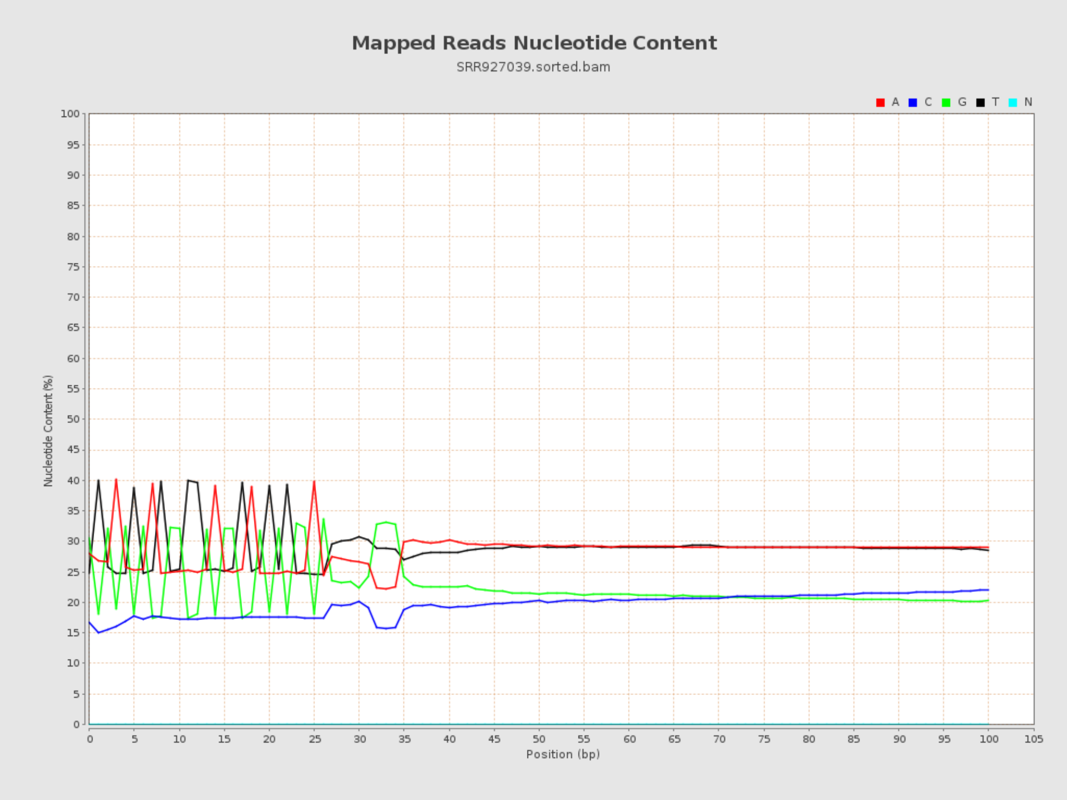
6. Results : Genome Fraction Coverage



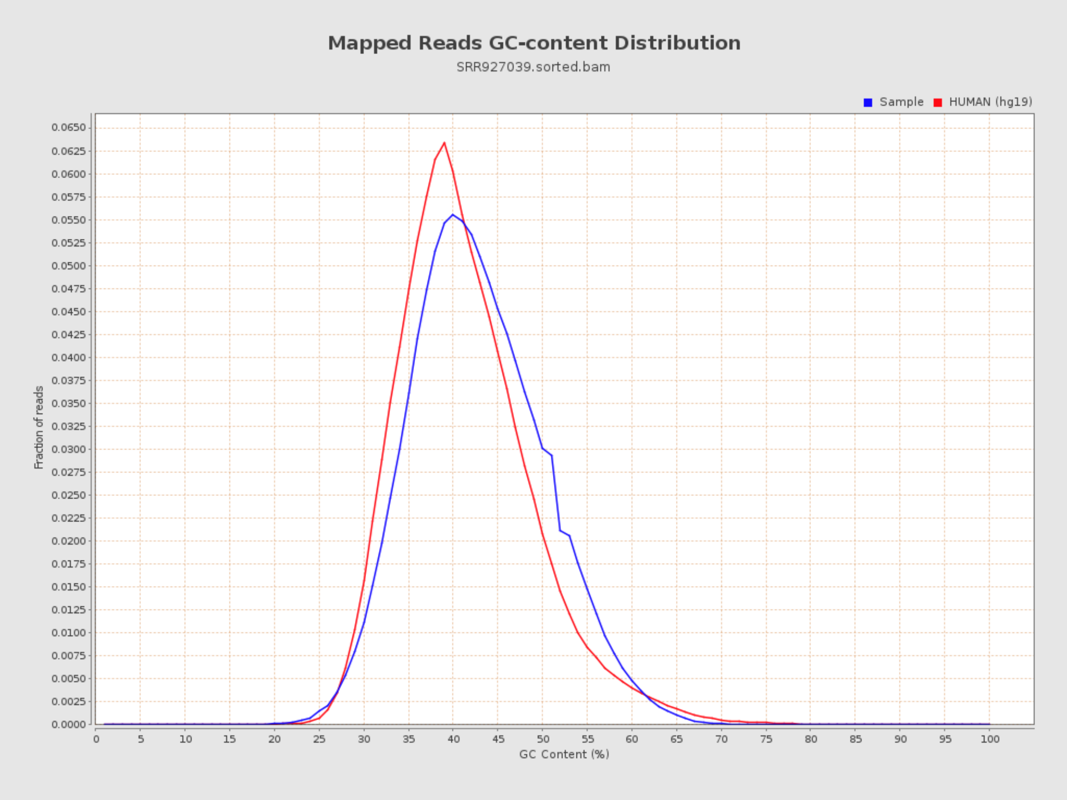
7. Results : Duplication Rate Histogram



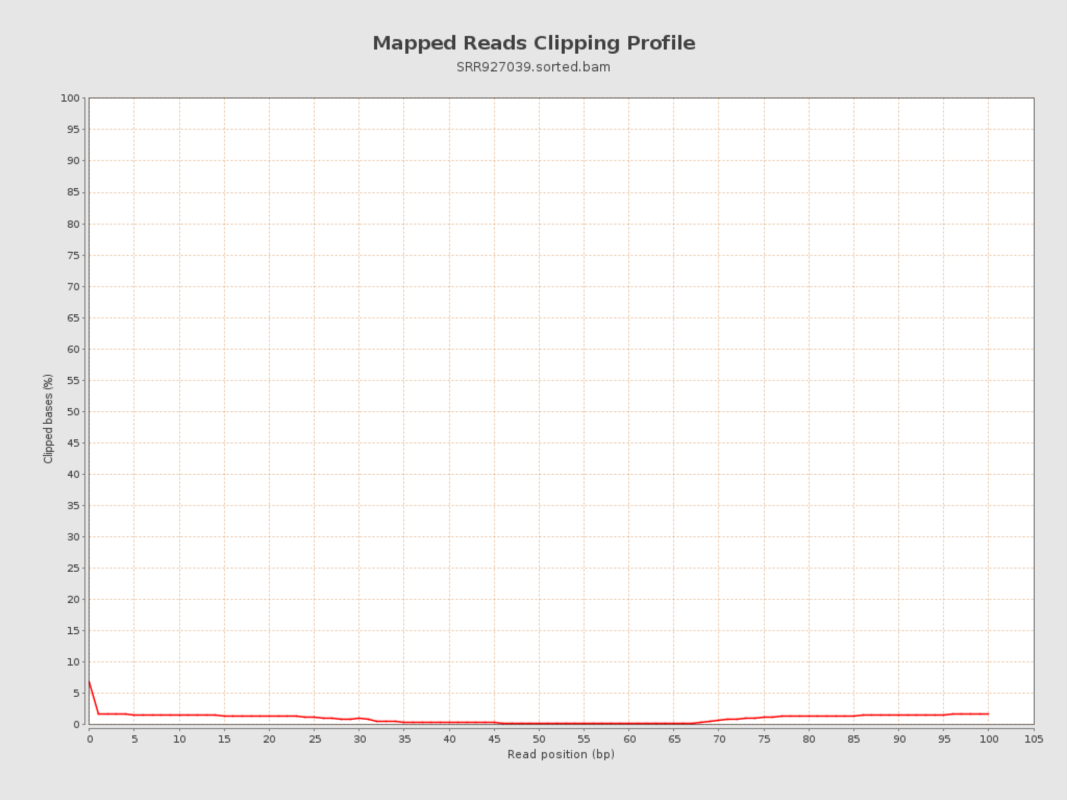
8. Results : Mapped Reads Nucleotide Content



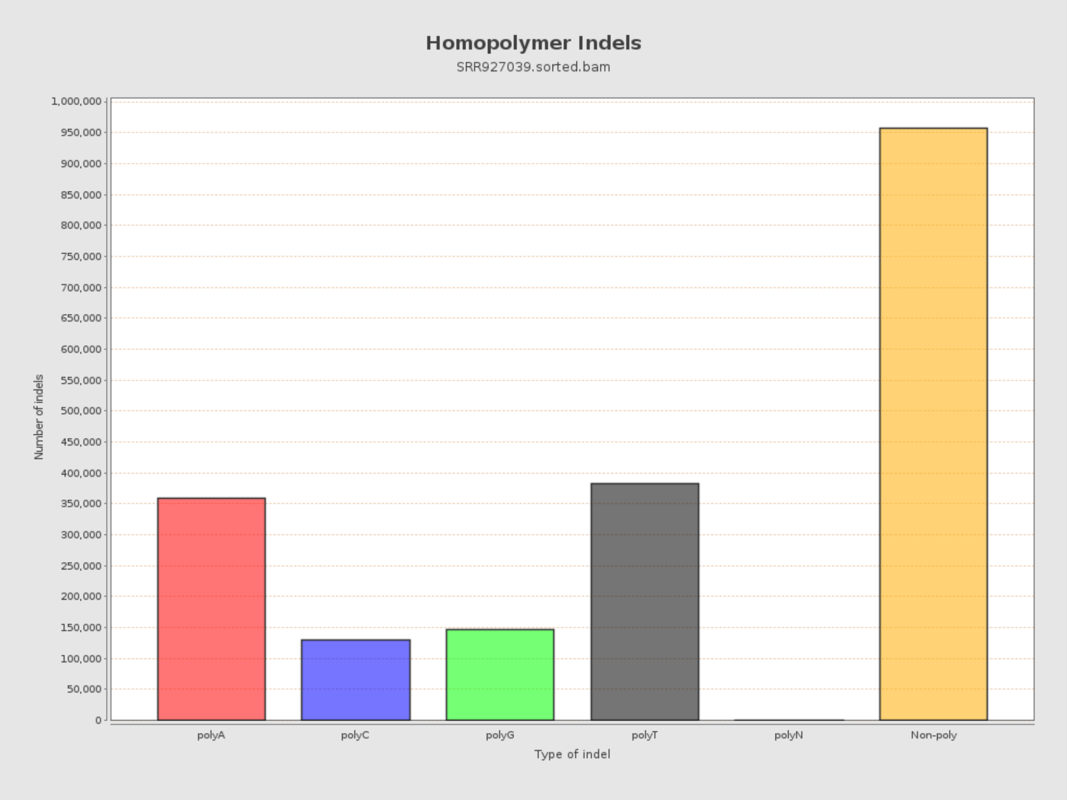
9. Results : Mapped Reads GC-content Distribution



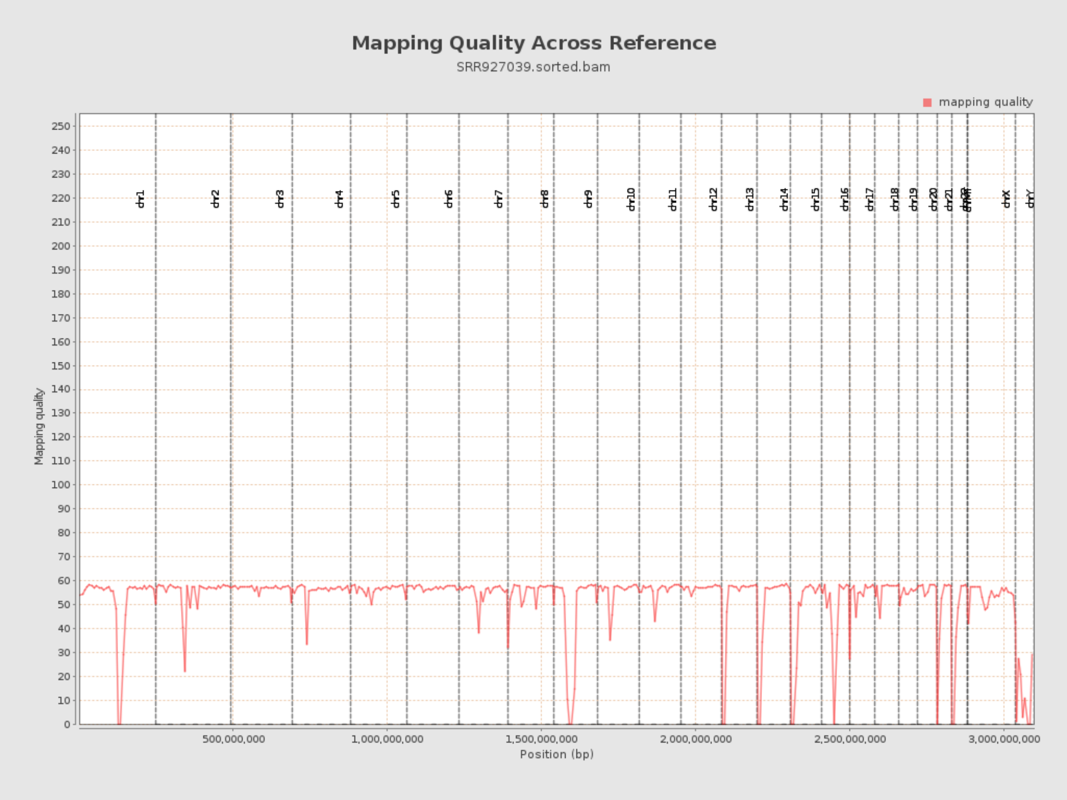
10. Results : Mapped Reads Clipping Profile



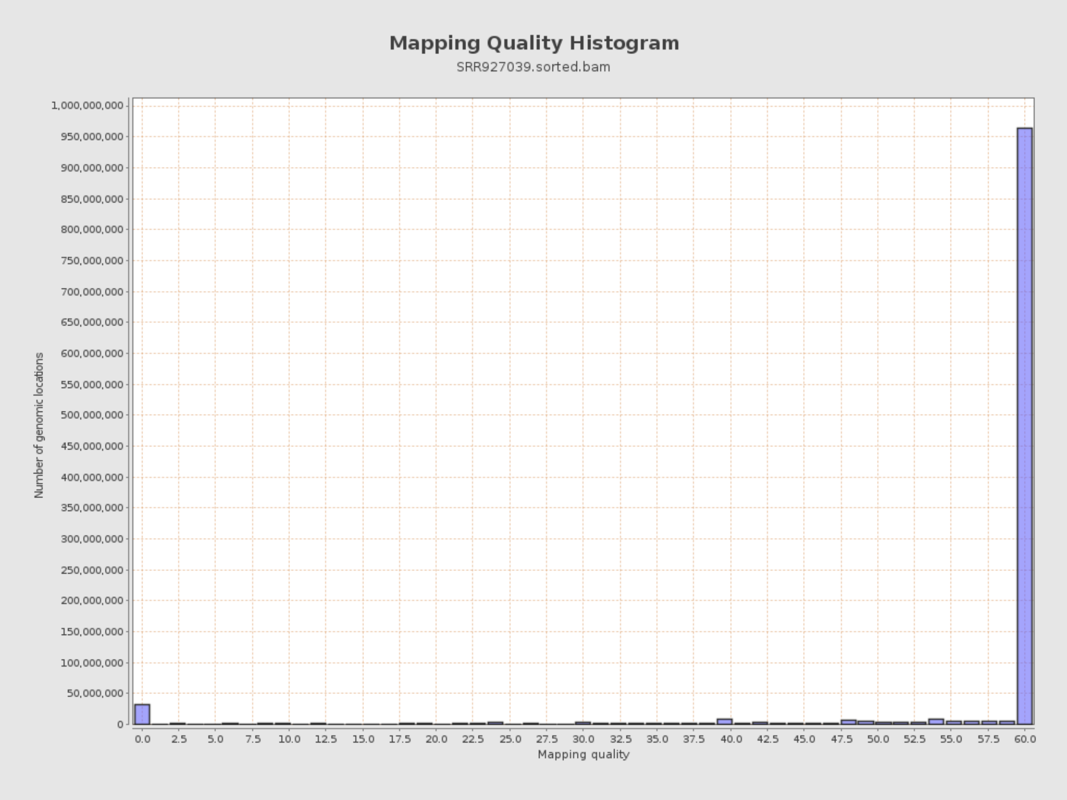
11. Results : Homopolymer Indels



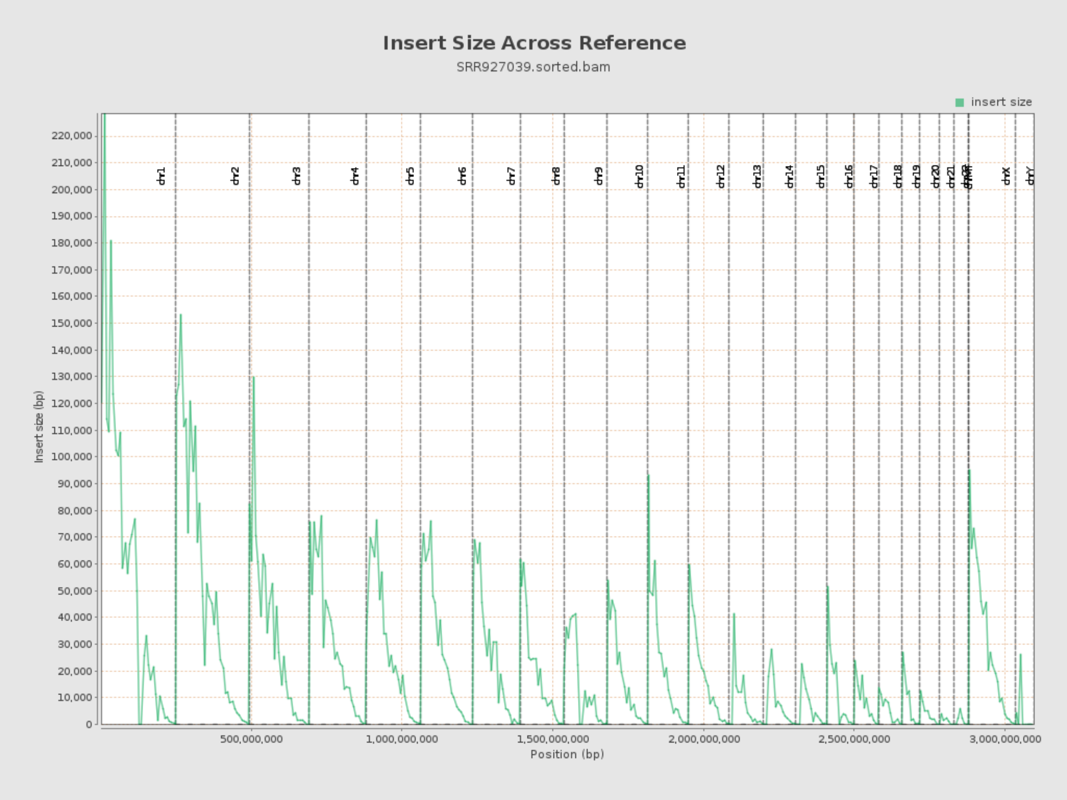
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram