Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 16:35:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927038.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_SRR927038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927038_1.fastq.gz SRR927038_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 16:35:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,242,730
Mapped reads	22,499,318 / 96.8%
Unmapped reads	743,412 / 3.2%
Mapped paired reads	22,499,318 / 96.8%
Mapped reads, first in pair	11,308,871 / 48.66%
Mapped reads, second in pair	11,190,447 / 48.15%
Mapped reads, both in pair	22,057,582 / 94.9%
Mapped reads, singletons	441,736 / 1.9%
Secondary alignments	0
Supplementary alignments	931,783 / 4.01%
Read min/max/mean length	30 / 101 / 102.67
Duplicated reads (estimated)	2,119,239 / 9.12%
Duplication rate	7.39%
Clipped reads	11,518,359 / 49.56%

2.2. ACGT Content

Number/percentage of A's	576,757,246 / 28.71%
Number/percentage of C's	382,095,675 / 19.02%
Number/percentage of T's	593,056,198 / 29.53%
Number/percentage of G's	456,511,130 / 22.73%
Number/percentage of N's	208,688 / 0.01%

GC Percentage	41.75%

2.3. Coverage

Mean	0.6493
Standard Deviation	2.489

2.4. Mapping Quality

Mean Mapping Quality	52.33

2.5. Insert size

Mean	446,431.43
Standard Deviation	6,510,384.15
P25/Median/P75	133 / 176 / 241

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	21,891,605
Insertions	352,996
Mapped reads with at least one insertion	1.54%
Deletions	1,054,710
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.69%

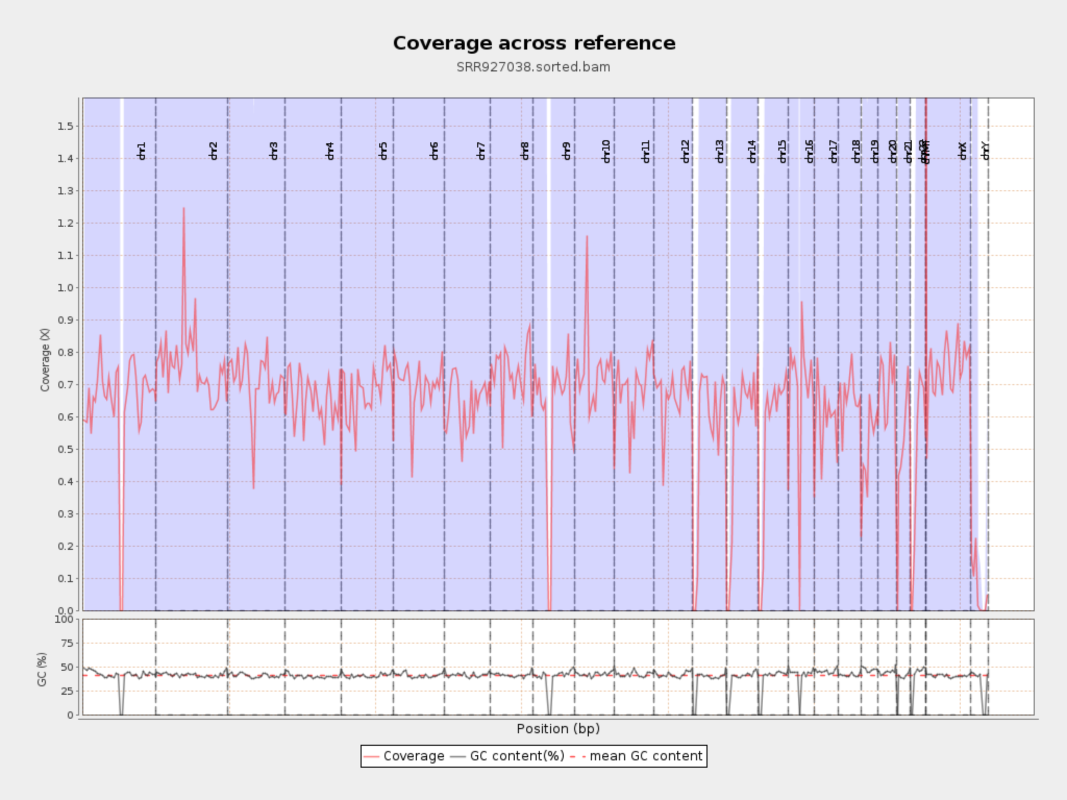
2.7. Chromosome stats

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

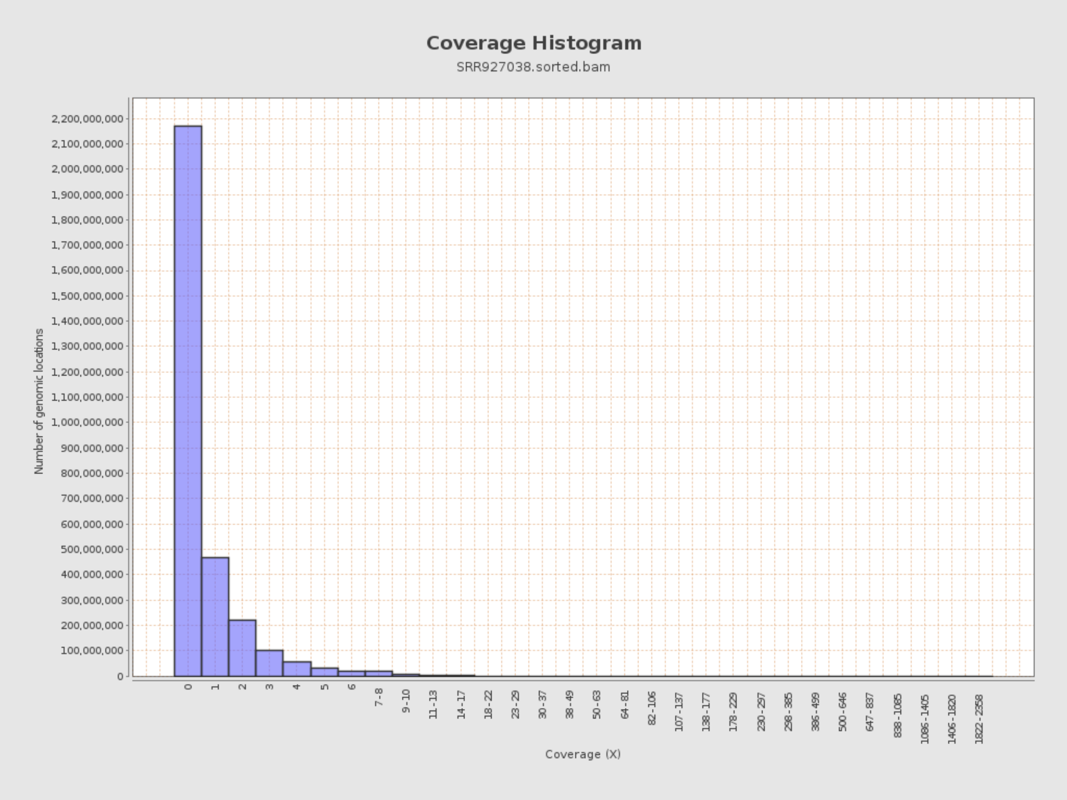
		bases	coverage	deviation
chr1	249250621	159619531	0.6404	2.678
chr2	243199373	185880268	0.7643	4.4367
chr3	198022430	140251382	0.7083	1.5025
chr4	191154276	125159218	0.6548	2.0873
chr5	180915260	122818678	0.6789	1.4332
chr6	171115067	119577128	0.6988	1.4941
chr7	159138663	102047348	0.6412	1.777
chr8	146364022	107768850	0.7363	1.7735
chr9	141213431	86144295	0.61	2.6911
chr10	135534747	99709376	0.7357	5.1289
chr11	135006516	92682921	0.6865	2.079
chr12	133851895	89943372	0.672	1.4538
chr13	115169878	62193159	0.54	1.2756
chr14	107349540	58111850	0.5413	1.3728
chr15	102531392	54311697	0.5297	1.2836
chr16	90354753	60748753	0.6723	3.5002
chr17	81195210	49063434	0.6043	1.8148
chr18	78077248	51700797	0.6622	2.733
chr19	59128983	30216245	0.511	1.7792
chr20	63025520	44094469	0.6996	1.5832
chr21	48129895	24237303	0.5036	1.7919
chr22	51304566	23653808	0.461	1.3196
chrMT	16571	52142	3.1466	3.0992
chrX	155270560	116300140	0.749	1.6958

chrY	59373566	3887329	0.0655	3.0817

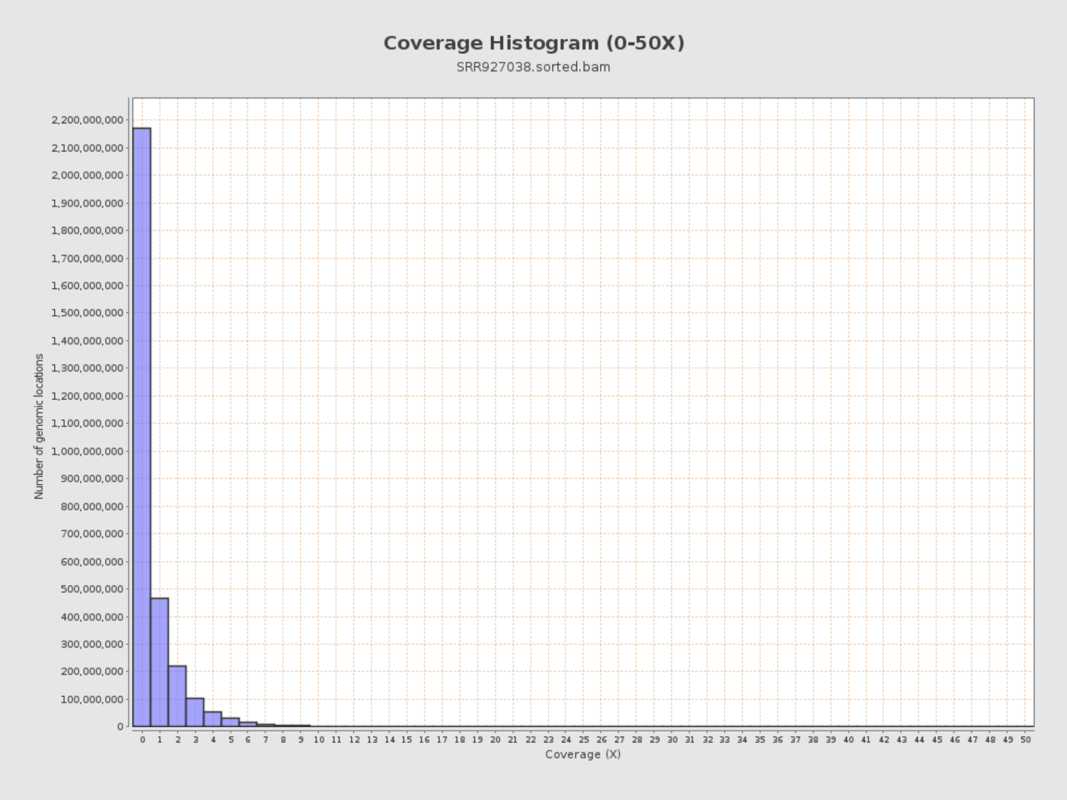
3. Results : Coverage across reference



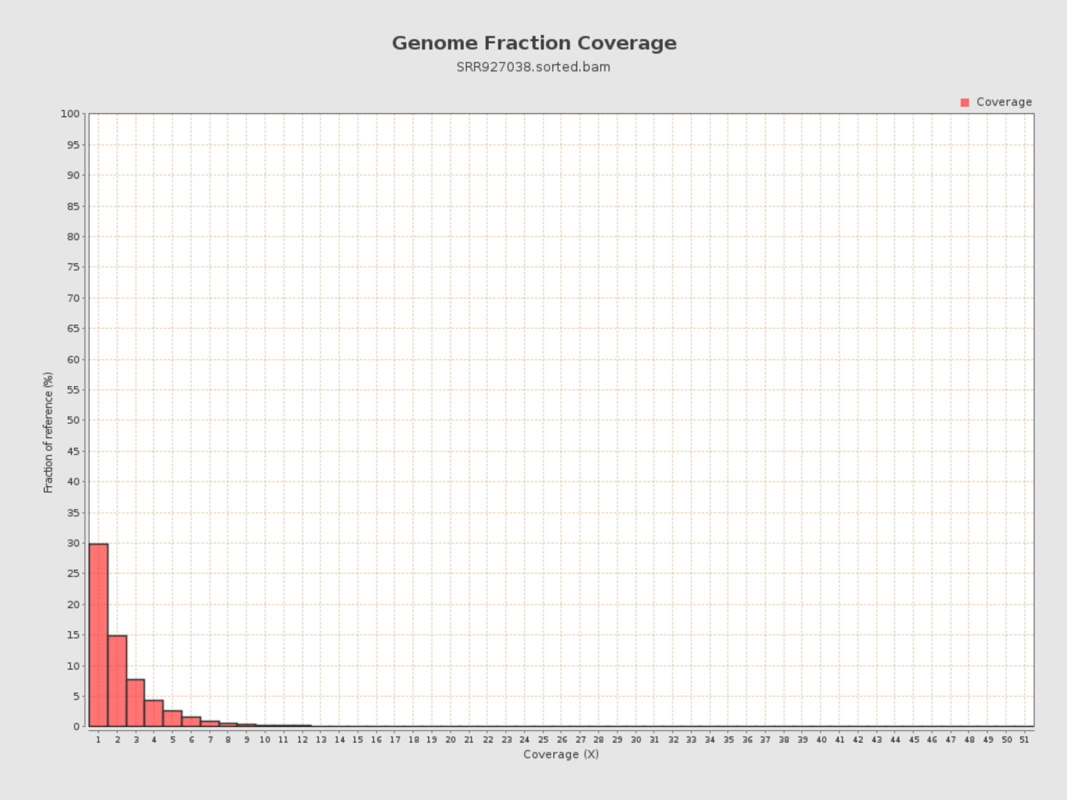
4. Results : Coverage Histogram



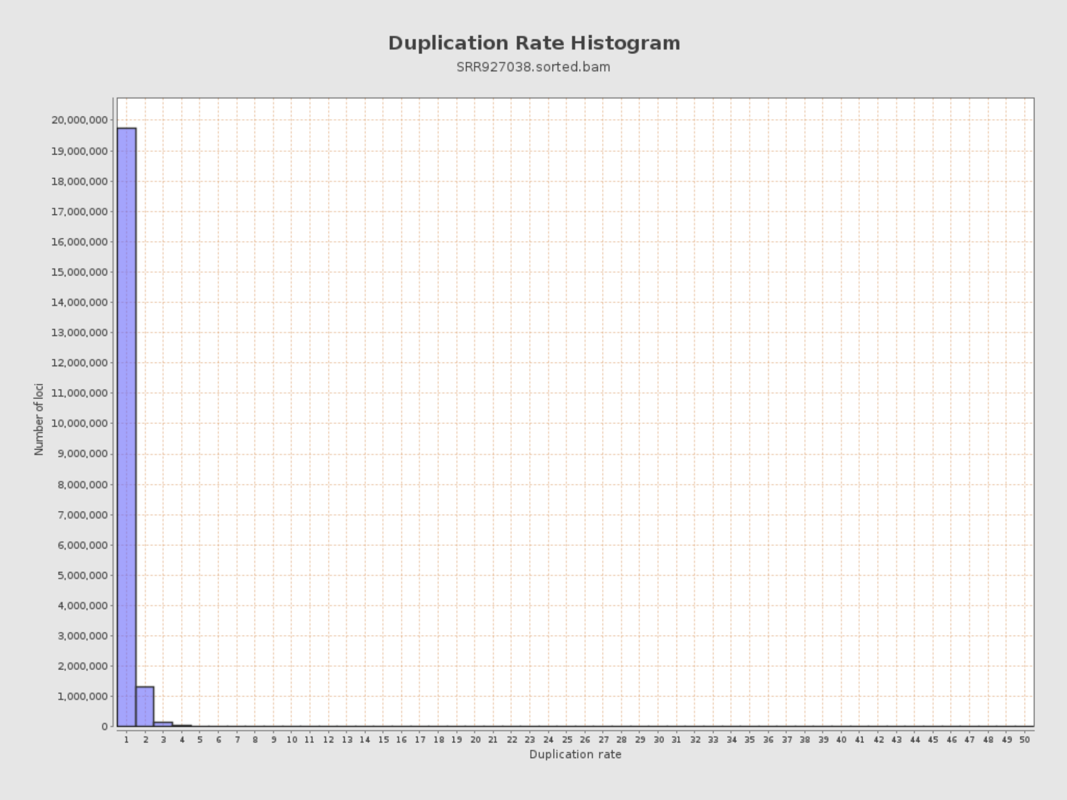
5. Results : Coverage Histogram (0-50X)



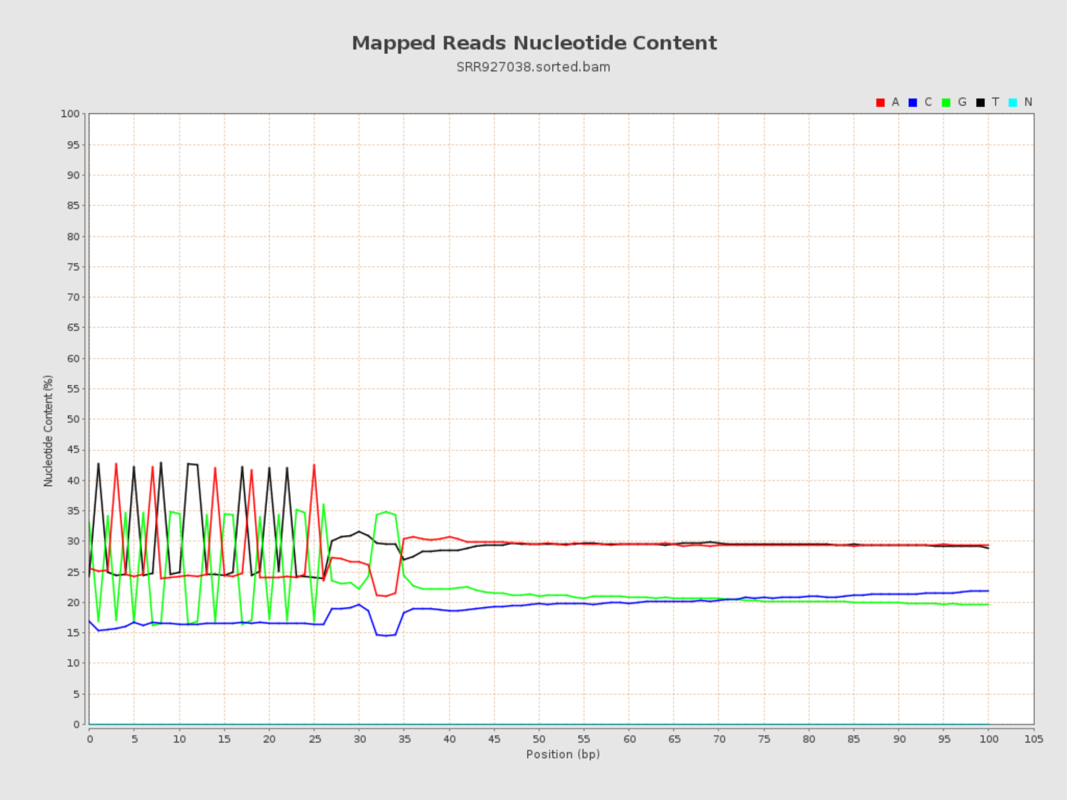
6. Results : Genome Fraction Coverage



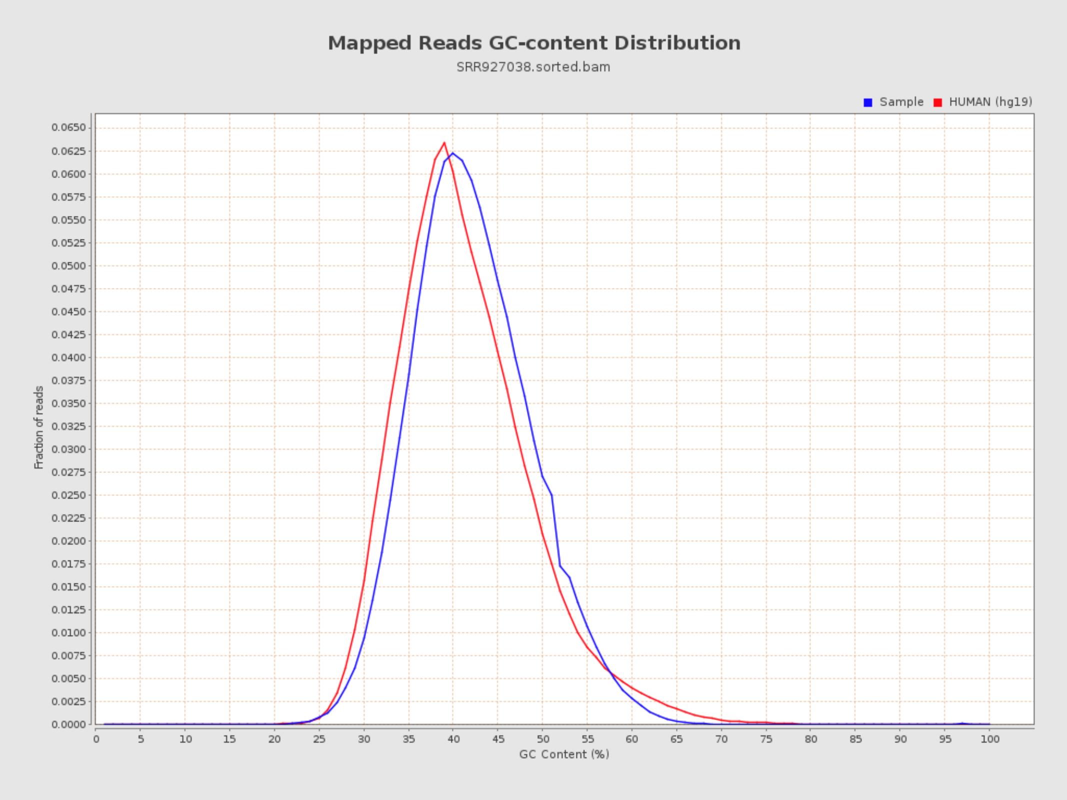
7. Results : Duplication Rate Histogram



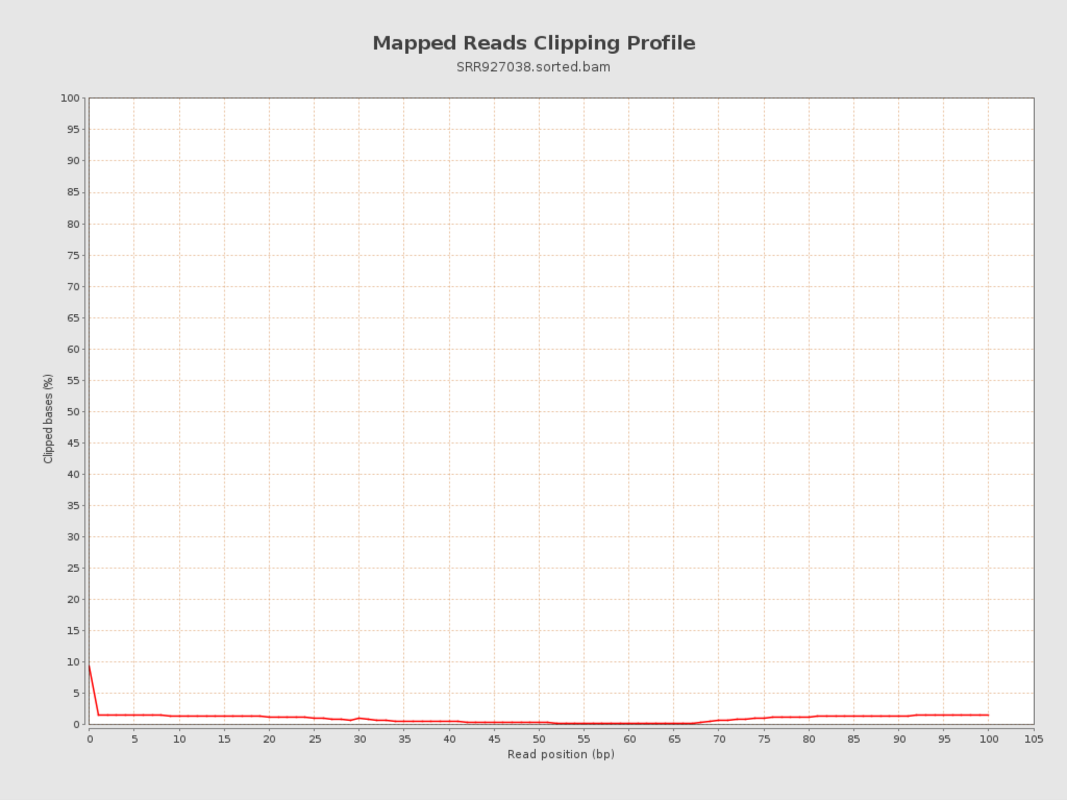
8. Results : Mapped Reads Nucleotide Content



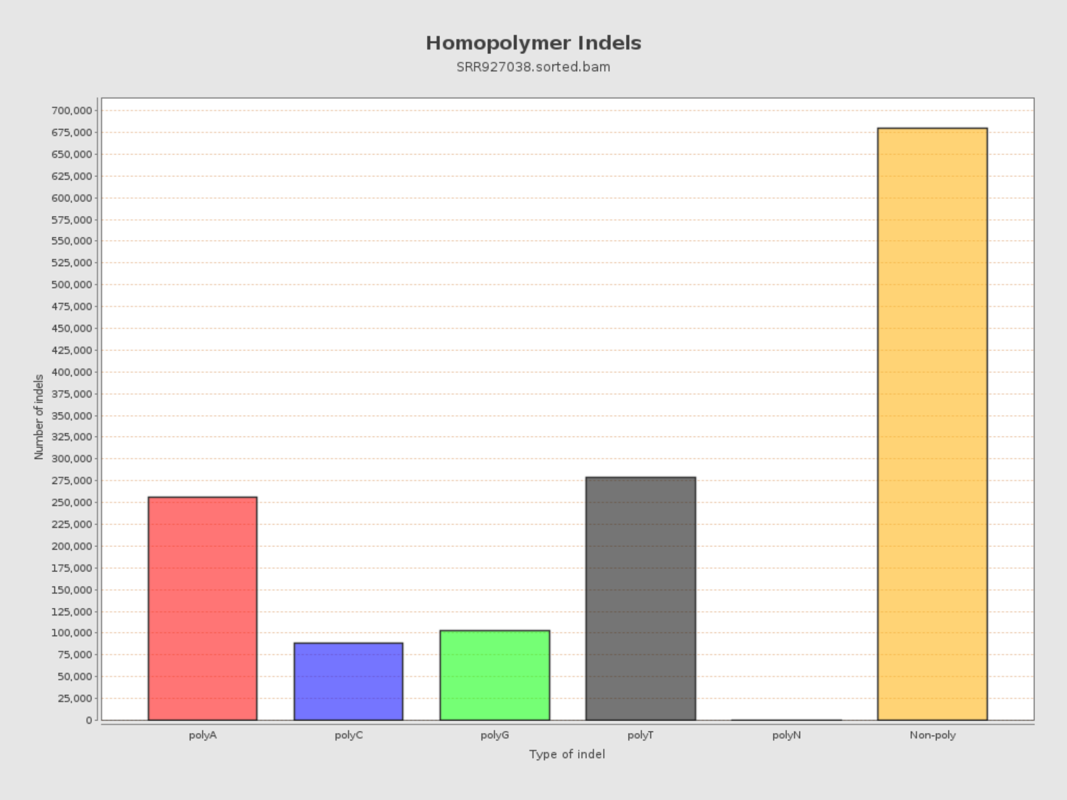
9. Results : Mapped Reads GC-content Distribution



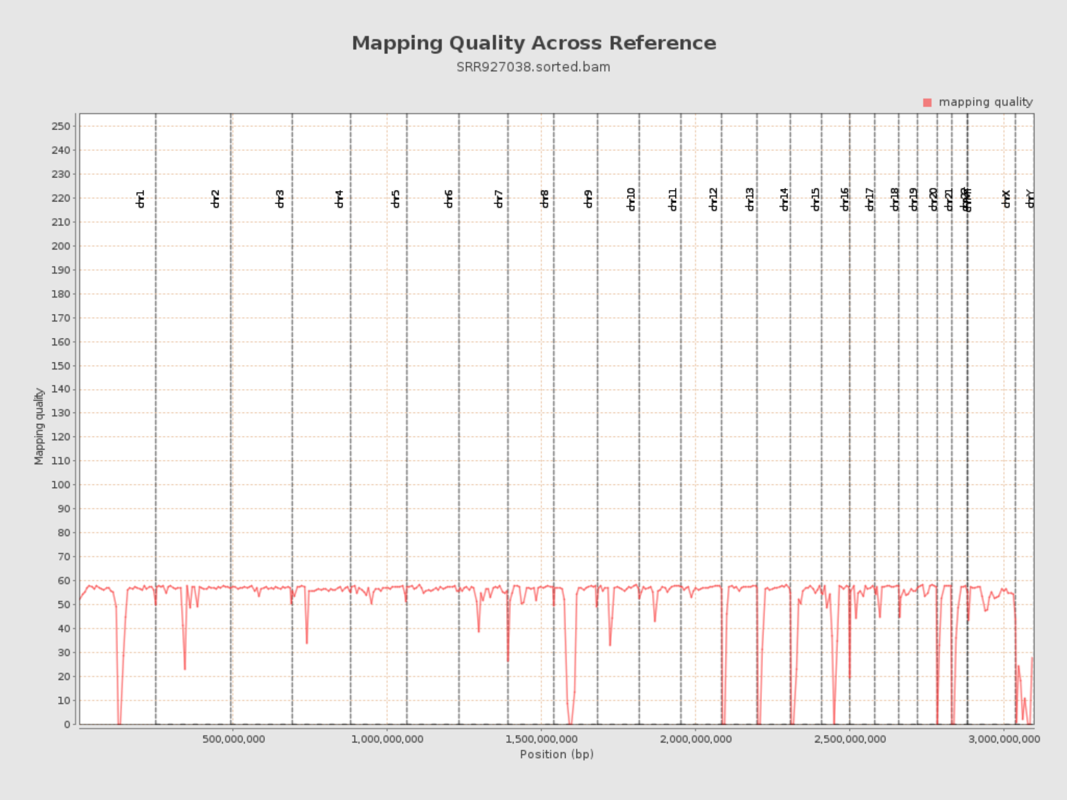
10. Results : Mapped Reads Clipping Profile



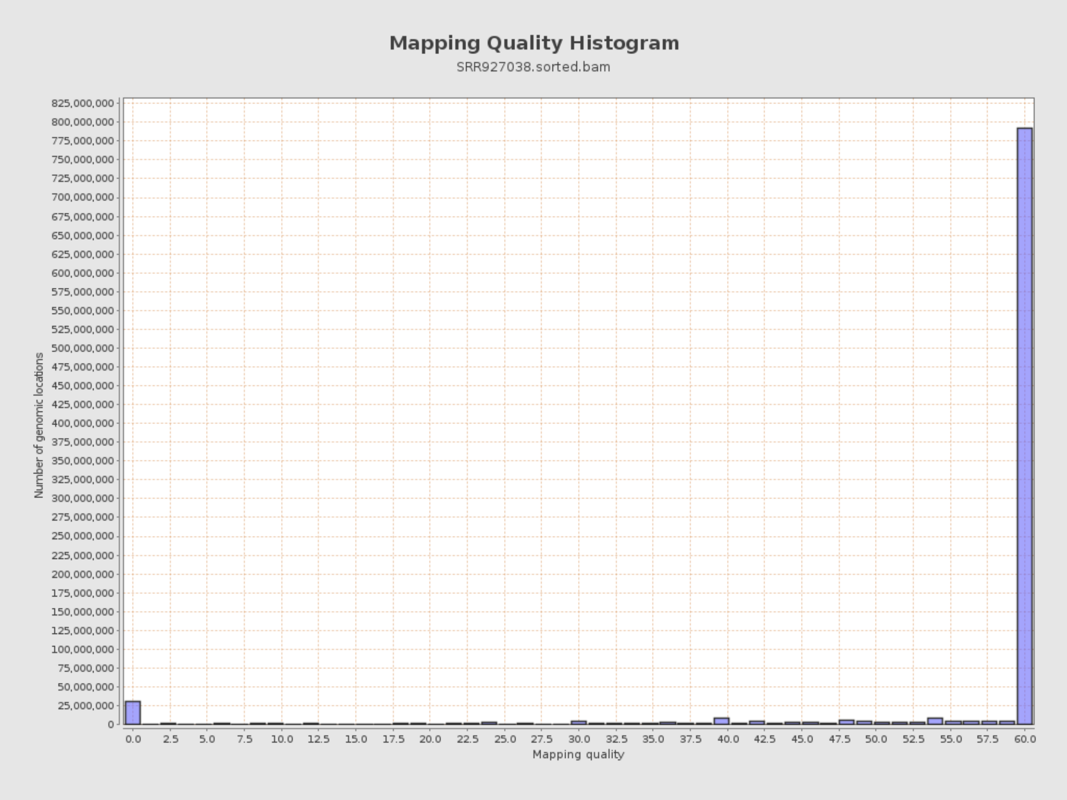
11. Results : Homopolymer Indels



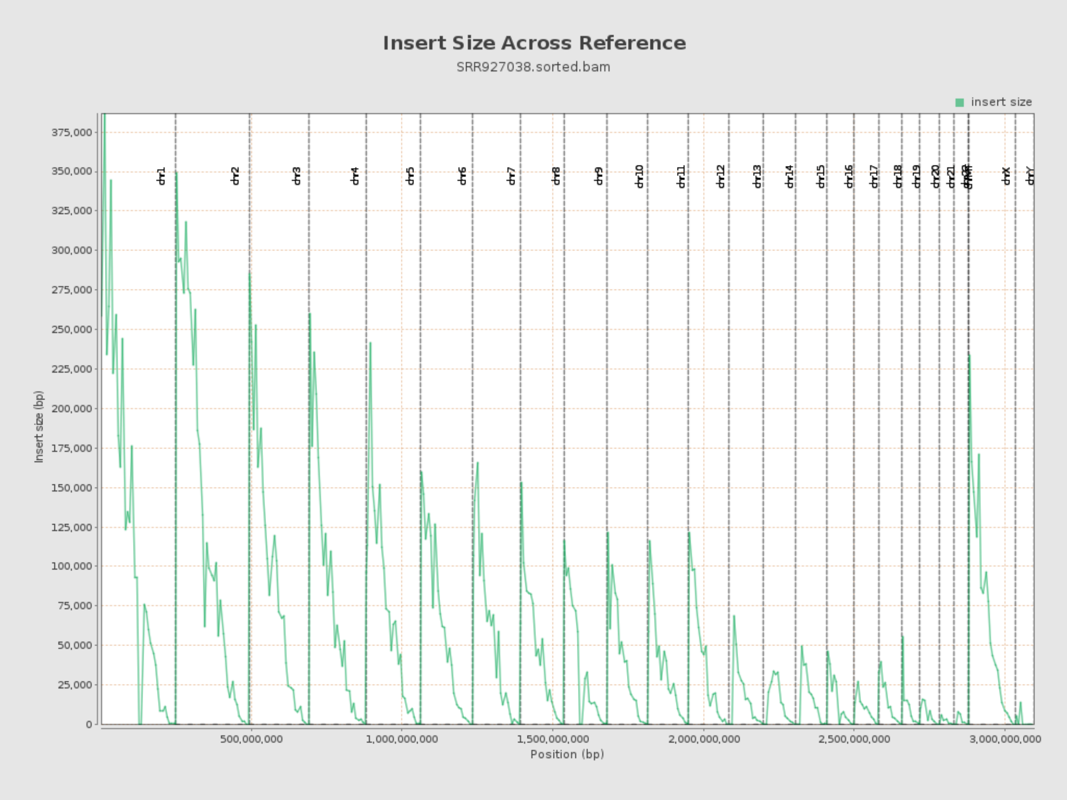
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram