Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 23:14:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926938.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_SRR926938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926938_1.fastq.gz SRR926938_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 23:14:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,291,528
Mapped reads	12,028,689 / 97.86%
Unmapped reads	262,839 / 2.14%
Mapped paired reads	12,028,689 / 97.86%
Mapped reads, first in pair	6,030,141 / 49.06%
Mapped reads, second in pair	5,998,548 / 48.8%
Mapped reads, both in pair	11,870,002 / 96.57%
Mapped reads, singletons	158,687 / 1.29%
Secondary alignments	0
Supplementary alignments	398,584 / 3.24%
Read min/max/mean length	30 / 101 / 102.34
Duplicated reads (estimated)	687,710 / 5.59%
Duplication rate	4.53%
Clipped reads	4,919,084 / 40.02%

2.2. ACGT Content

Number/percentage of A's	313,602,513 / 28.45%
Number/percentage of C's	216,932,579 / 19.68%
Number/percentage of T's	318,759,393 / 28.92%
Number/percentage of G's	252,718,254 / 22.93%
Number/percentage of N's	224,018 / 0.02%

GC Percentage	42.61%

2.3. Coverage

Mean	0.3563
Standard Deviation	1.5616

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	353,865.6
Standard Deviation	5,849,741.67
P25/Median/P75	142 / 184 / 246

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	10,023,940
Insertions	184,509
Mapped reads with at least one insertion	1.51%
Deletions	568,344
Mapped reads with at least one deletion	4.61%
Homopolymer indels	52.19%

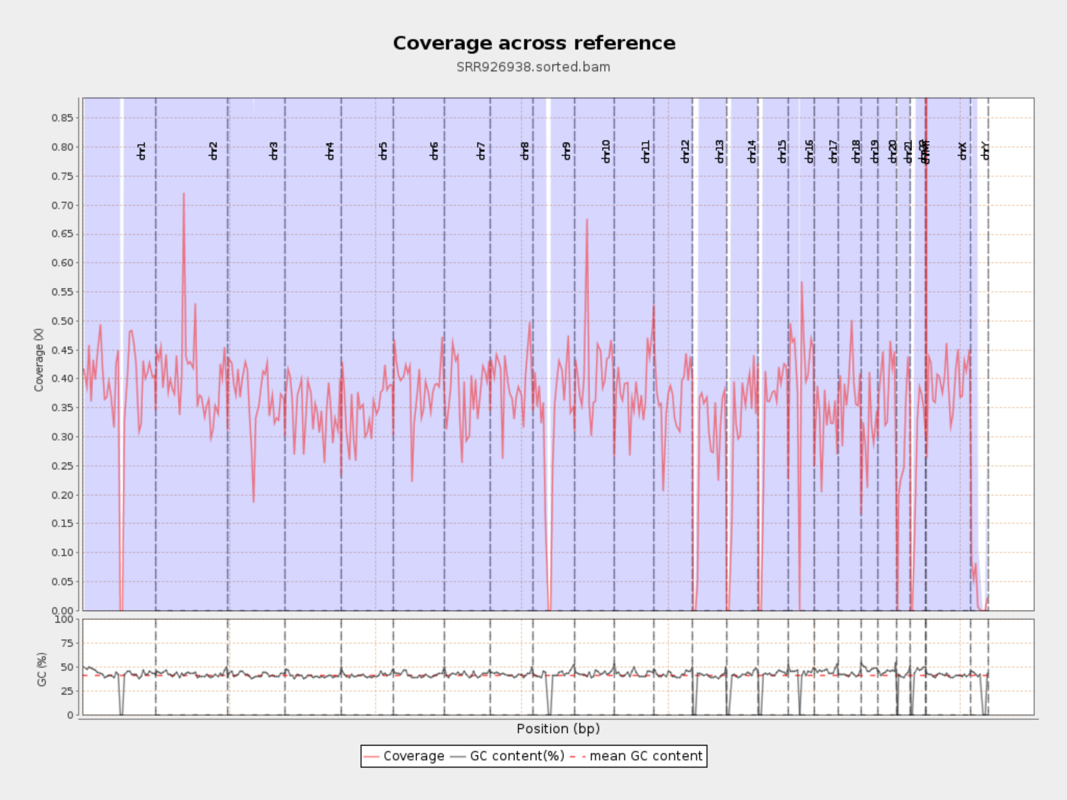
2.7. Chromosome stats

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

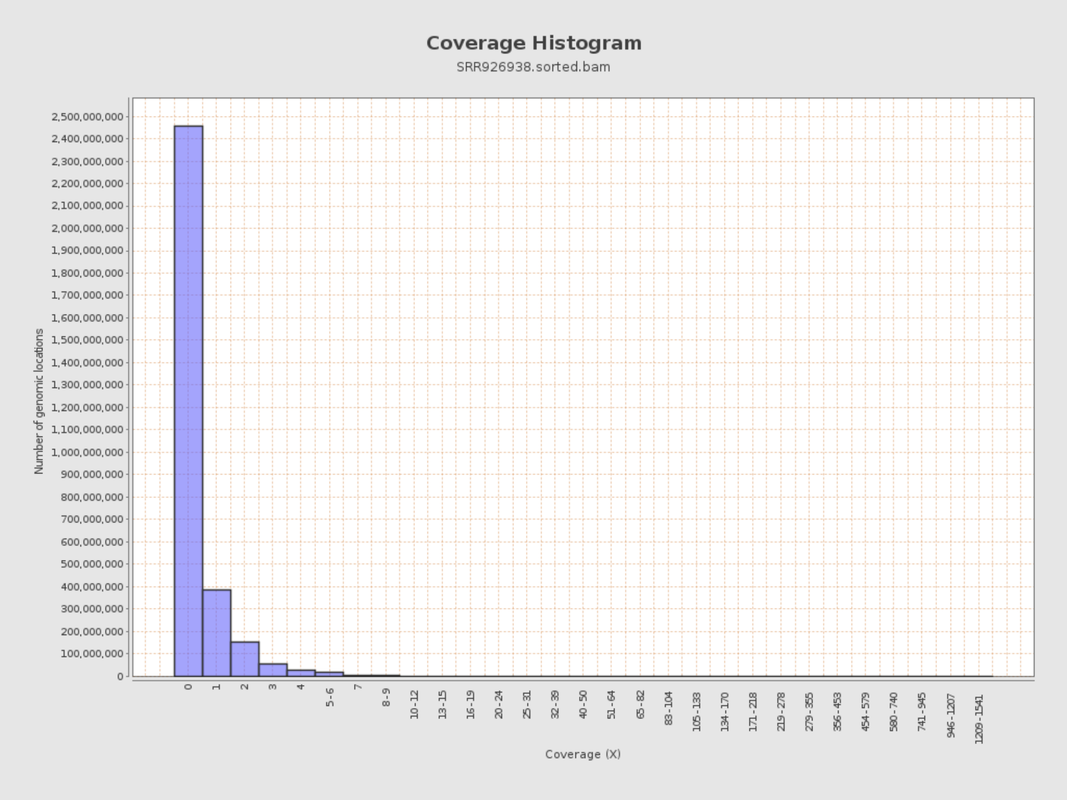
		bases	coverage	deviation
chr1	249250621	95026329	0.3812	1.8615
chr2	243199373	98499426	0.405	2.7435
chr3	198022430	72655328	0.3669	0.8954
chr4	191154276	66405505	0.3474	1.1506
chr5	180915260	62835362	0.3473	0.8521
chr6	171115067	66086293	0.3862	1.0463
chr7	159138663	59338487	0.3729	1.1593
chr8	146364022	57762654	0.3947	1.0666
chr9	141213431	45478793	0.3221	1.5768
chr10	135534747	56213003	0.4147	3.3692
chr11	135006516	51397619	0.3807	1.5761
chr12	133851895	49287057	0.3682	0.9129
chr13	115169878	31748353	0.2757	0.7595
chr14	107349540	32487114	0.3026	0.8354
chr15	102531392	32892604	0.3208	0.8703
chr16	90354753	36506048	0.404	2.1205
chr17	81195210	26649066	0.3282	1.0874
chr18	78077248	29903633	0.383	1.5639
chr19	59128983	18045554	0.3052	1.443
chr20	63025520	25048898	0.3974	0.9643
chr21	48129895	13245265	0.2752	1.0191
chr22	51304566	12601725	0.2456	0.7727
chrMT	16571	203231	12.2643	10.8459
chrX	155270560	61020906	0.393	1.0215

chrY	59373566	1727376	0.0291	0.9671

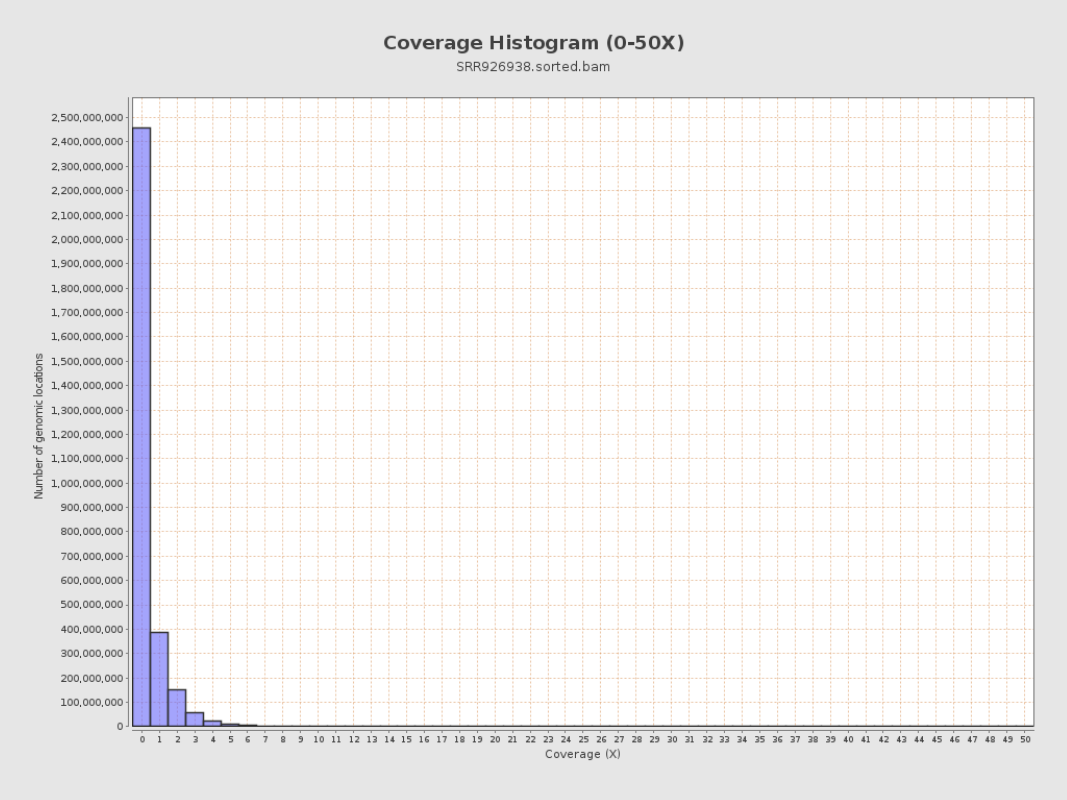
3. Results : Coverage across reference



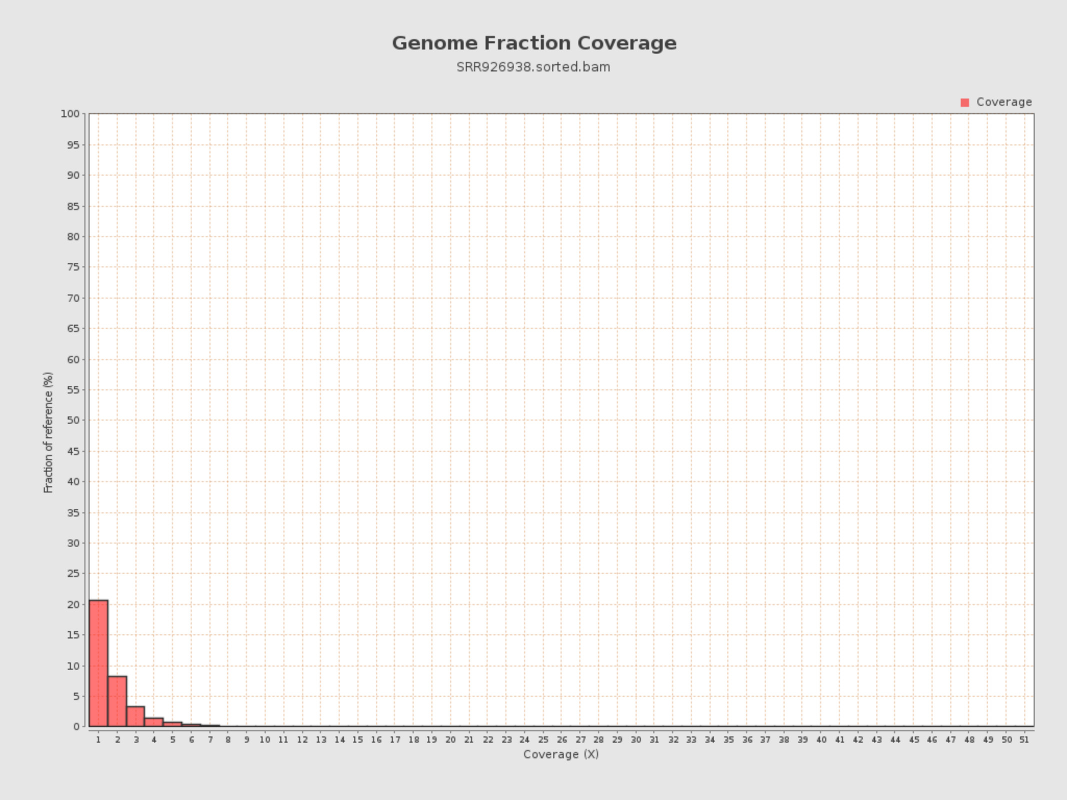
4. Results : Coverage Histogram



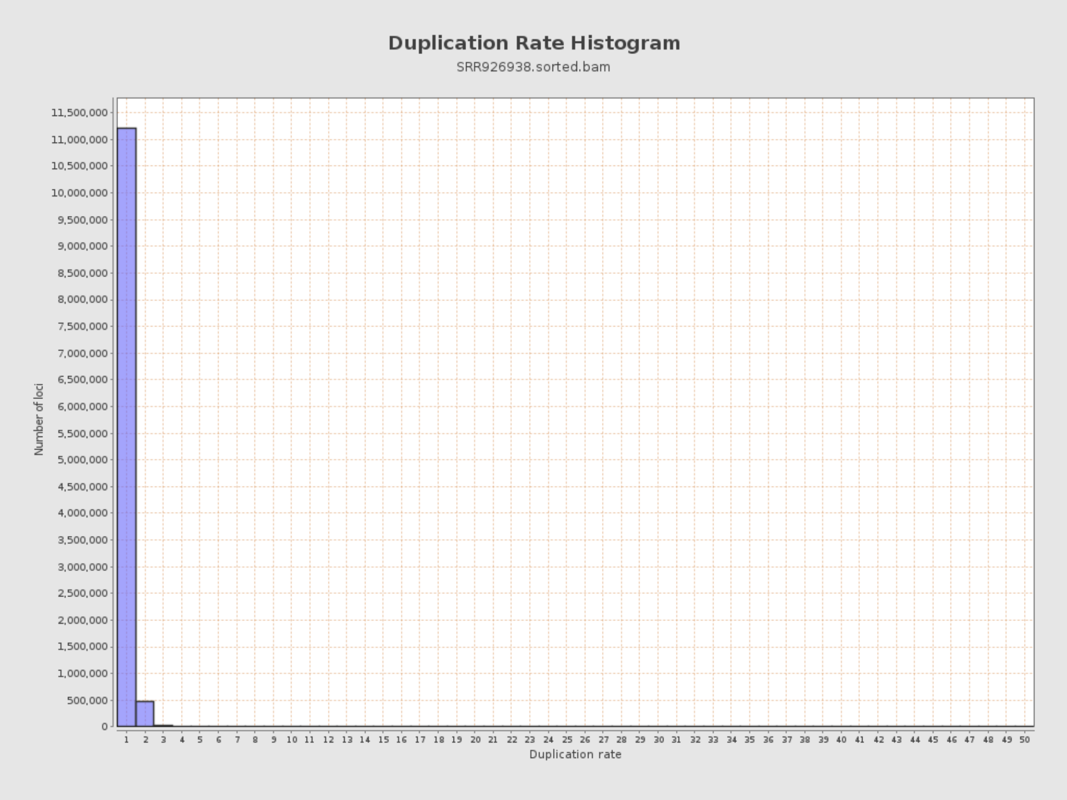
5. Results : Coverage Histogram (0-50X)



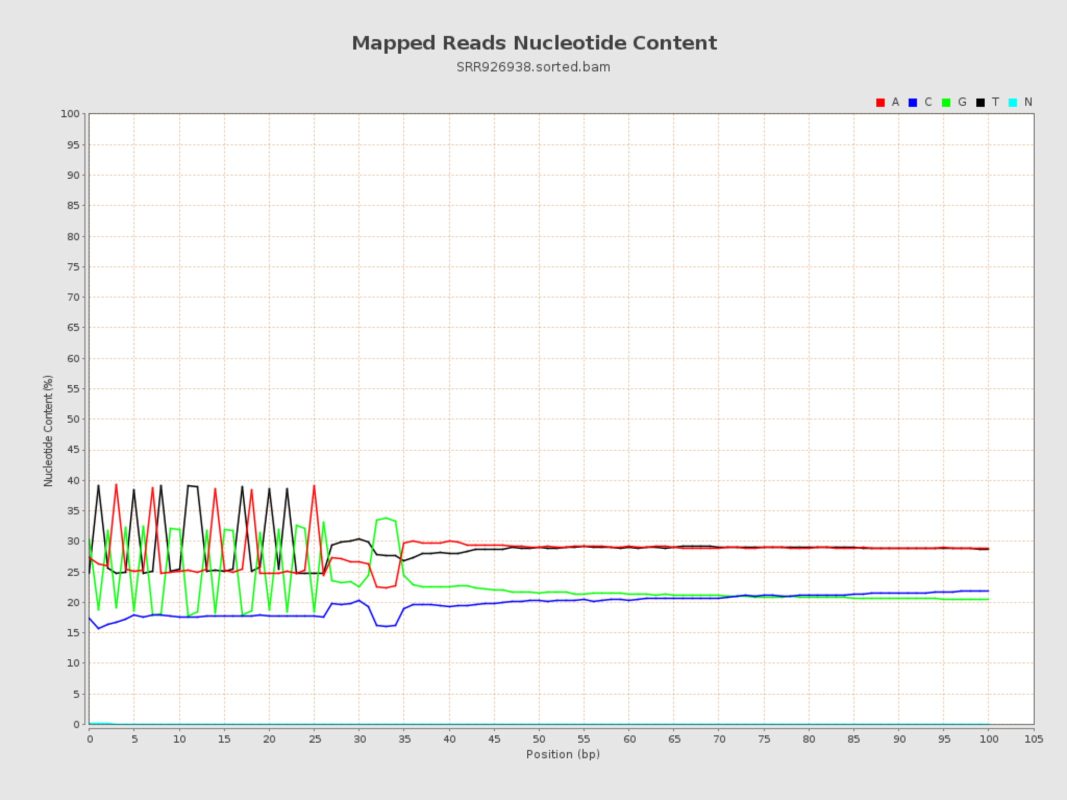
6. Results : Genome Fraction Coverage



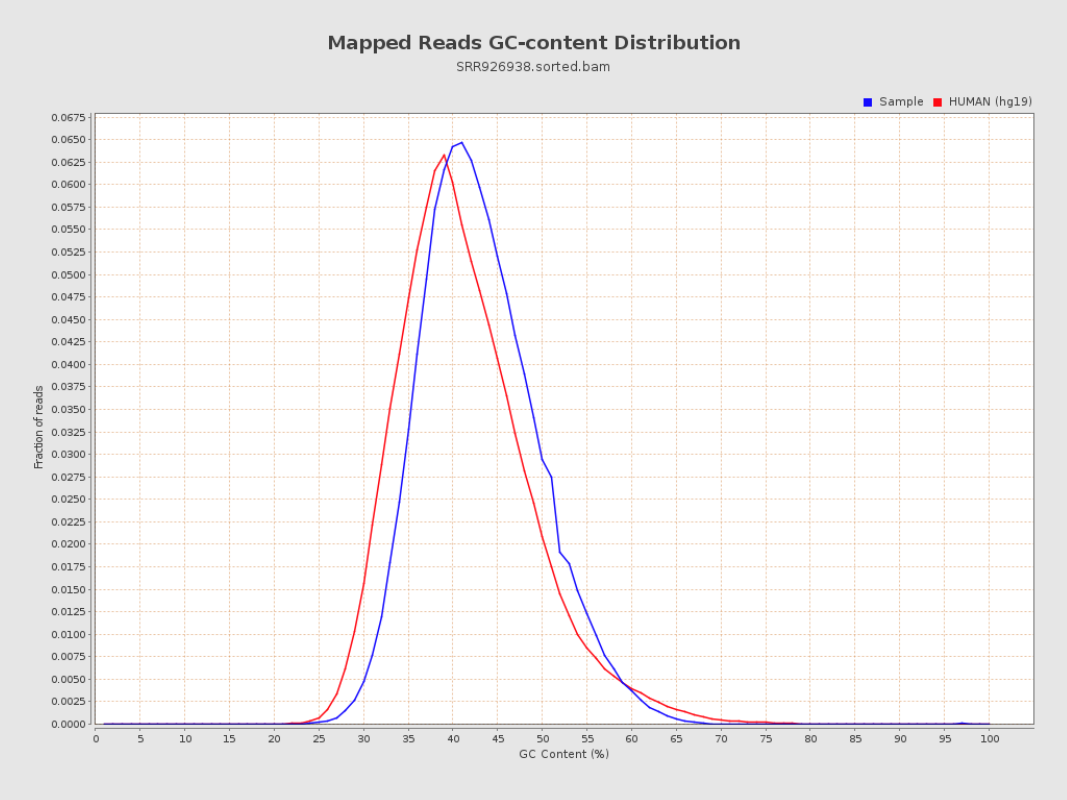
7. Results : Duplication Rate Histogram



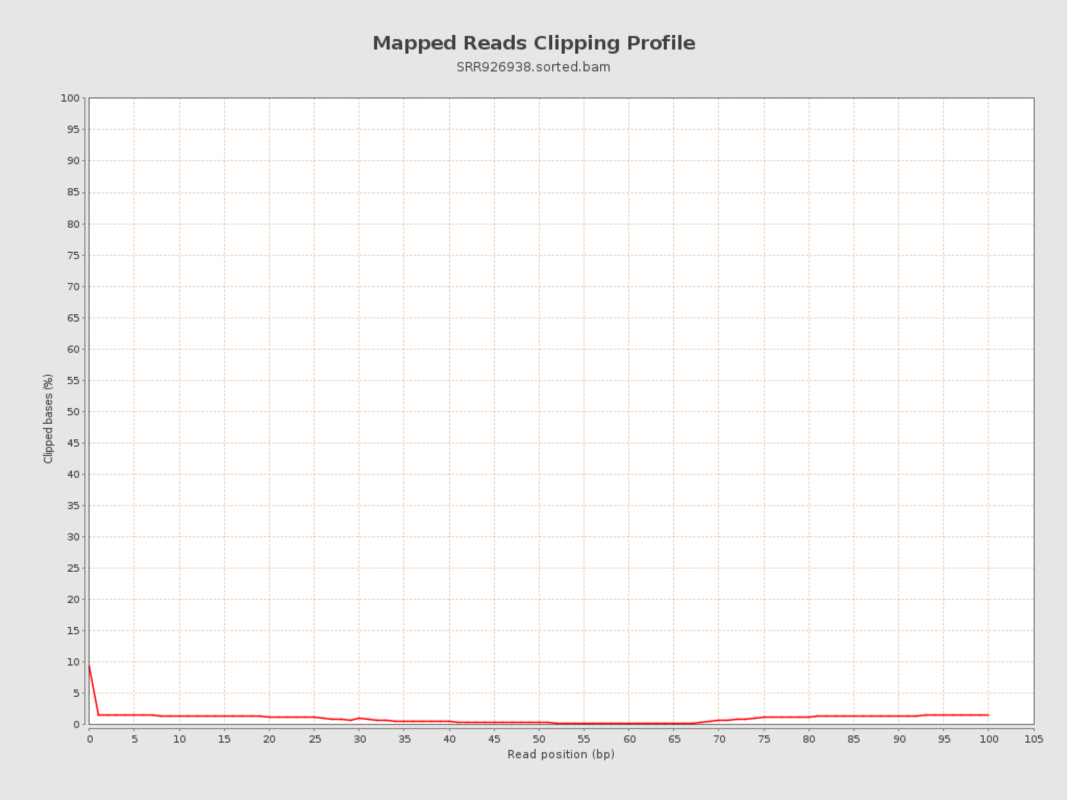
8. Results : Mapped Reads Nucleotide Content



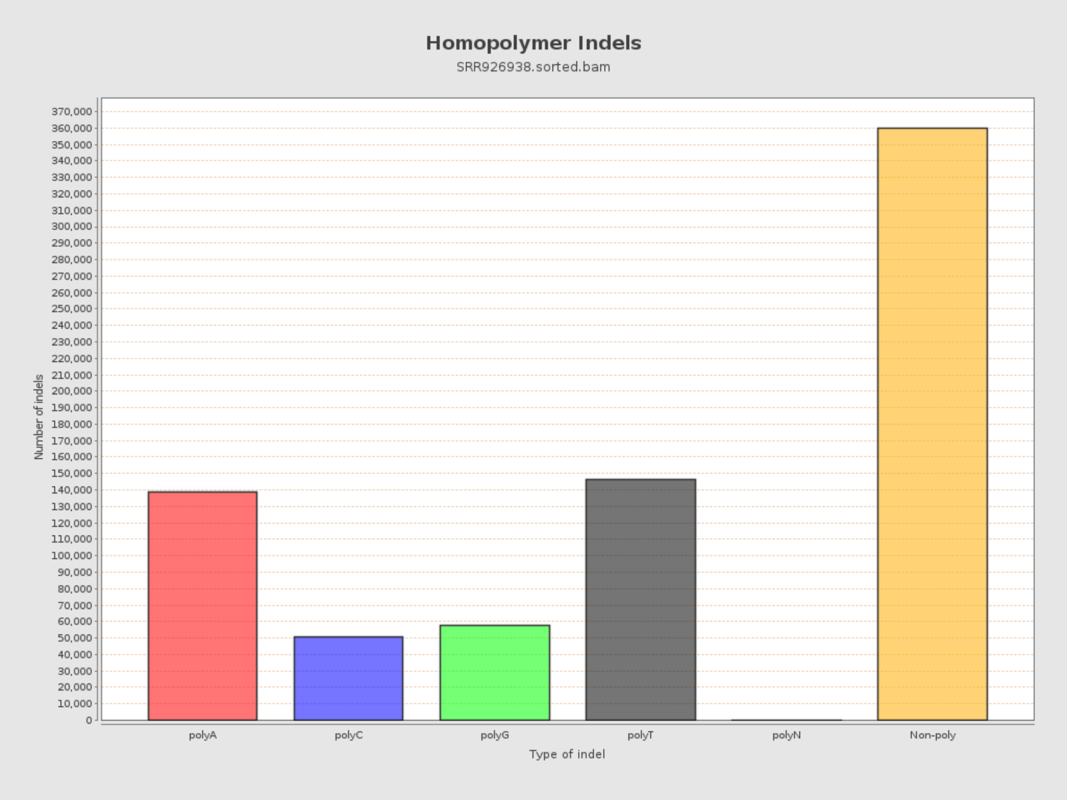
9. Results : Mapped Reads GC-content Distribution



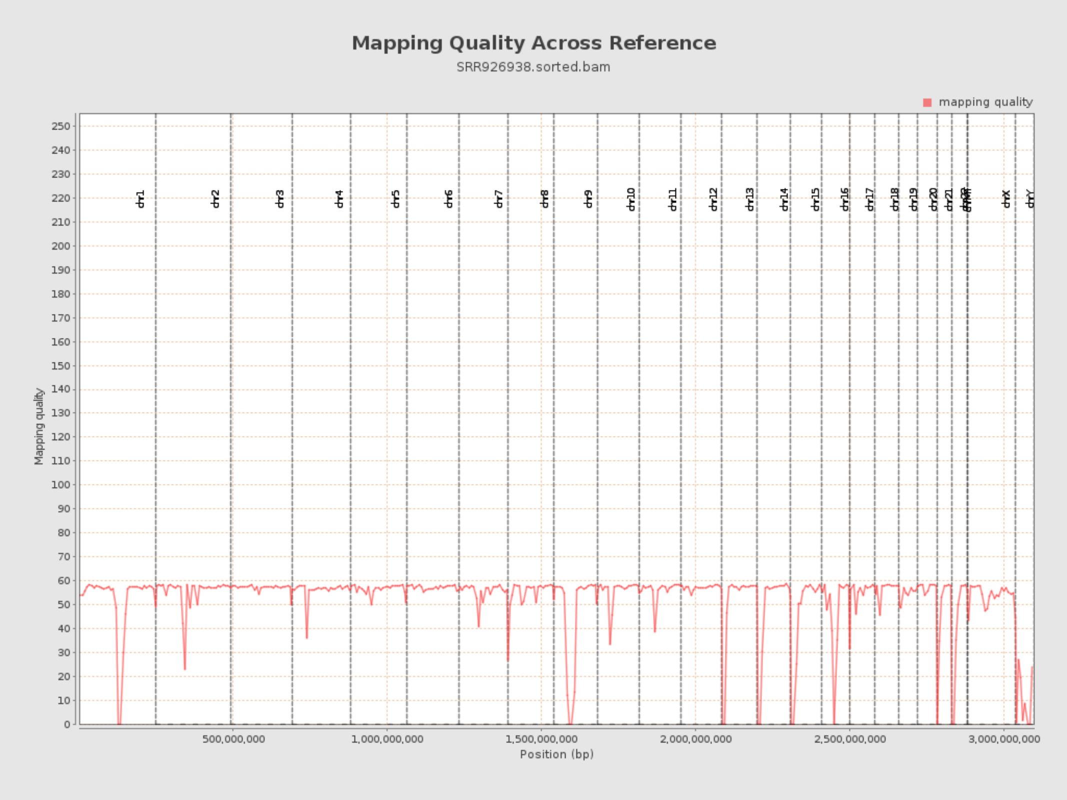
10. Results : Mapped Reads Clipping Profile



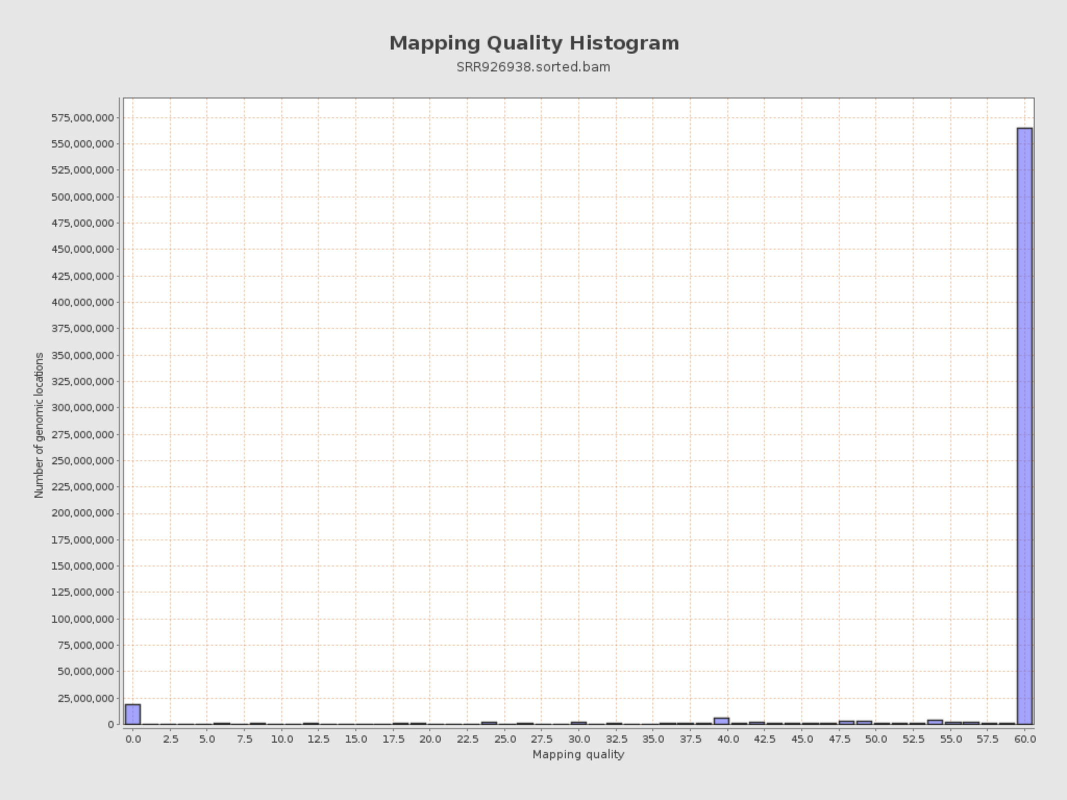
11. Results : Homopolymer Indels



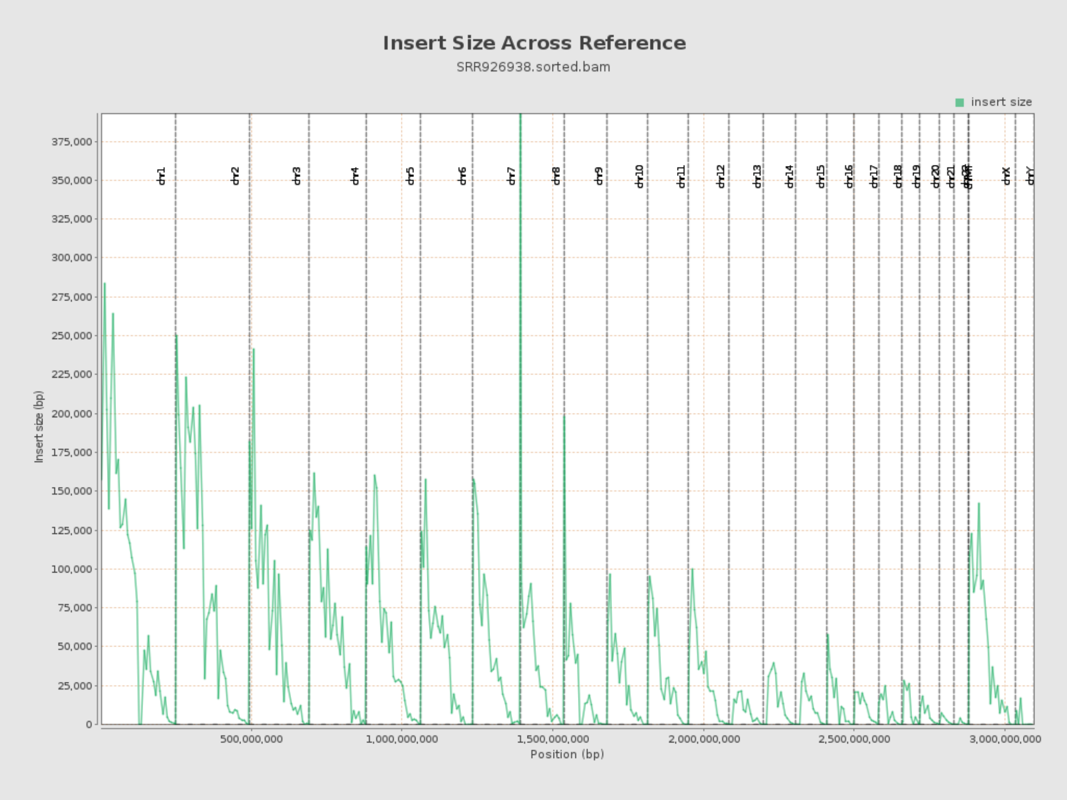
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram