Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 06:37:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927018.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_SRR927018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927018_1.fastq.gz SRR927018_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 06:37:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,836,442
Mapped reads	31,237,002 / 98.12%
Unmapped reads	599,440 / 1.88%
Mapped paired reads	31,237,002 / 98.12%
Mapped reads, first in pair	15,676,016 / 49.24%
Mapped reads, second in pair	15,560,986 / 48.88%
Mapped reads, both in pair	30,900,382 / 97.06%
Mapped reads, singletons	336,620 / 1.06%
Secondary alignments	0
Supplementary alignments	356,509 / 1.12%
Read min/max/mean length	30 / 101 / 101.46
Duplicated reads (estimated)	2,269,094 / 7.13%
Duplication rate	5.4%
Clipped reads	7,968,145 / 25.03%

2.2. ACGT Content

Number/percentage of A's	855,405,583 / 28.97%
Number/percentage of C's	582,047,824 / 19.72%
Number/percentage of T's	863,039,539 / 29.23%
Number/percentage of G's	651,629,561 / 22.07%
Number/percentage of N's	157,973 / 0.01%

GC Percentage	41.79%

2.3. Coverage

Mean	0.9544
Standard Deviation	4.4004

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	120,653.03
Standard Deviation	3,416,780.24
P25/Median/P75	158 / 202 / 269

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	27,220,327
Insertions	490,545
Mapped reads with at least one insertion	1.54%
Deletions	1,576,590
Mapped reads with at least one deletion	4.92%
Homopolymer indels	53.04%

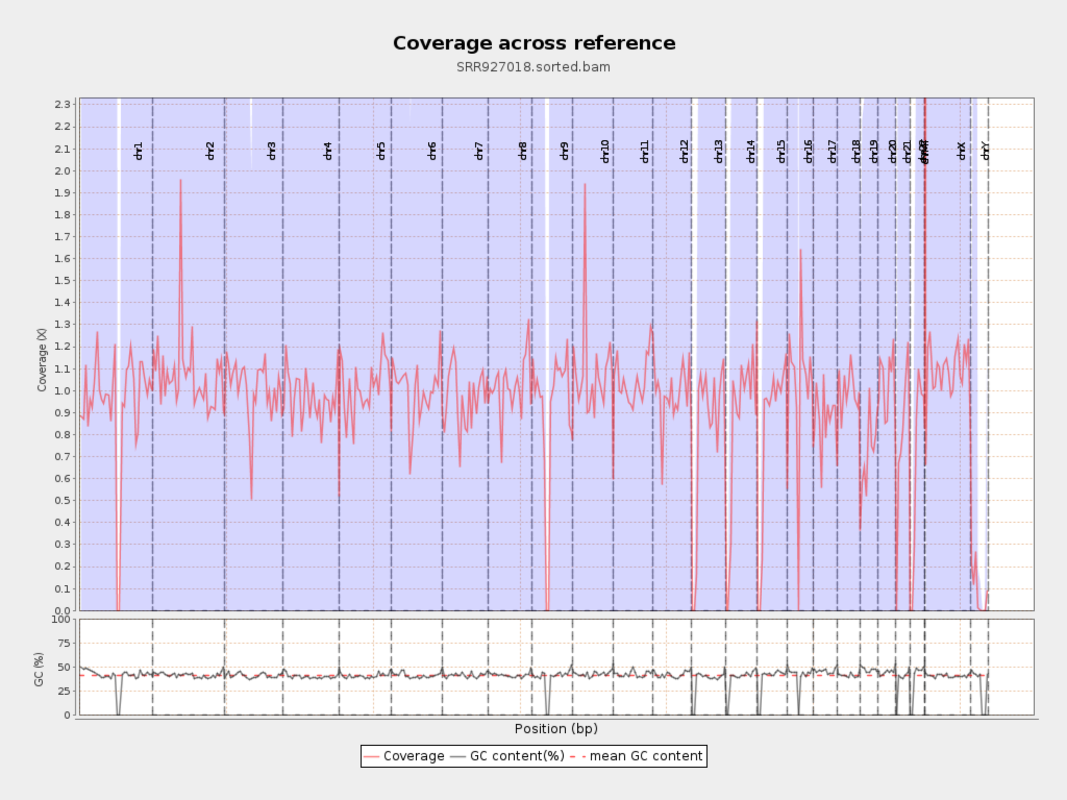
2.7. Chromosome stats

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

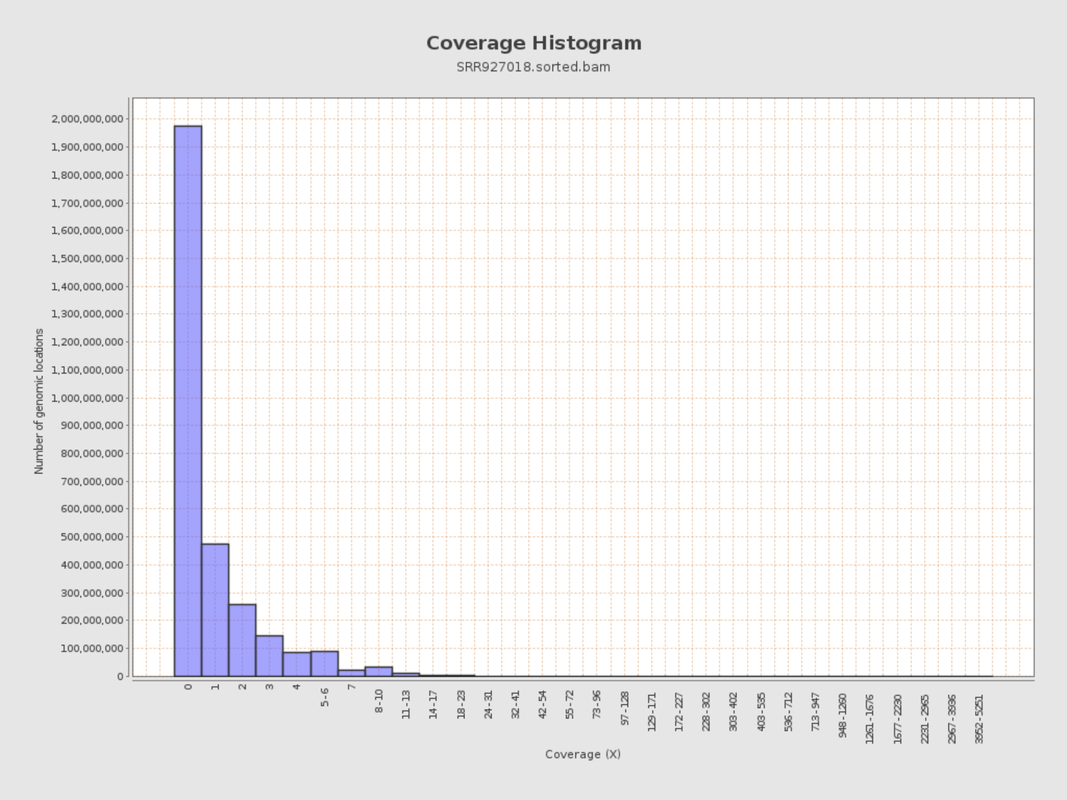
		bases	coverage	deviation
chr1	249250621	234894241	0.9424	5.9315
chr2	243199373	261434798	1.075	7.0429
chr3	198022430	199417531	1.007	2.2883
chr4	191154276	184981430	0.9677	2.9082
chr5	180915260	183818672	1.016	1.9194
chr6	171115067	172211259	1.0064	1.9933
chr7	159138663	153907981	0.9671	2.7042
chr8	146364022	149612363	1.0222	2.262
chr9	141213431	126929311	0.8988	4.8988
chr10	135534747	148428246	1.0951	9.9777
chr11	135006516	140076696	1.0376	5.4793
chr12	133851895	131825853	0.9849	1.9425
chr13	115169878	93714706	0.8137	1.7311
chr14	107349540	90159137	0.8399	1.8388
chr15	102531392	83141724	0.8109	1.7797
chr16	90354753	91426427	1.0119	5.8491
chr17	81195210	70404403	0.8671	2.3976
chr18	78077248	78848167	1.0099	5.1415
chr19	59128983	41909638	0.7088	3.4243
chr20	63025520	65344420	1.0368	2.1513
chr21	48129895	38785204	0.8058	2.3156
chr22	51304566	34282720	0.6682	1.7126
chrMT	16571	4902953	295.8755	217.4428
chrX	155270560	169178975	1.0896	2.5937

chrY	59373566	4898556	0.0825	2.4912

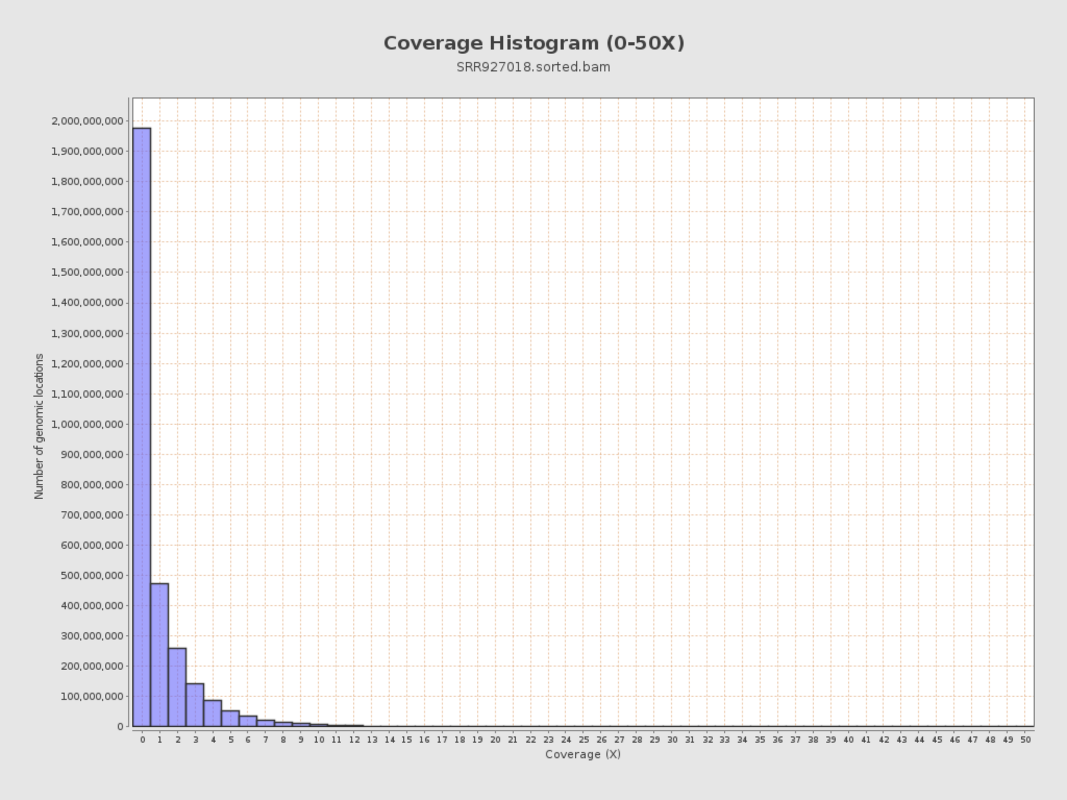
3. Results : Coverage across reference



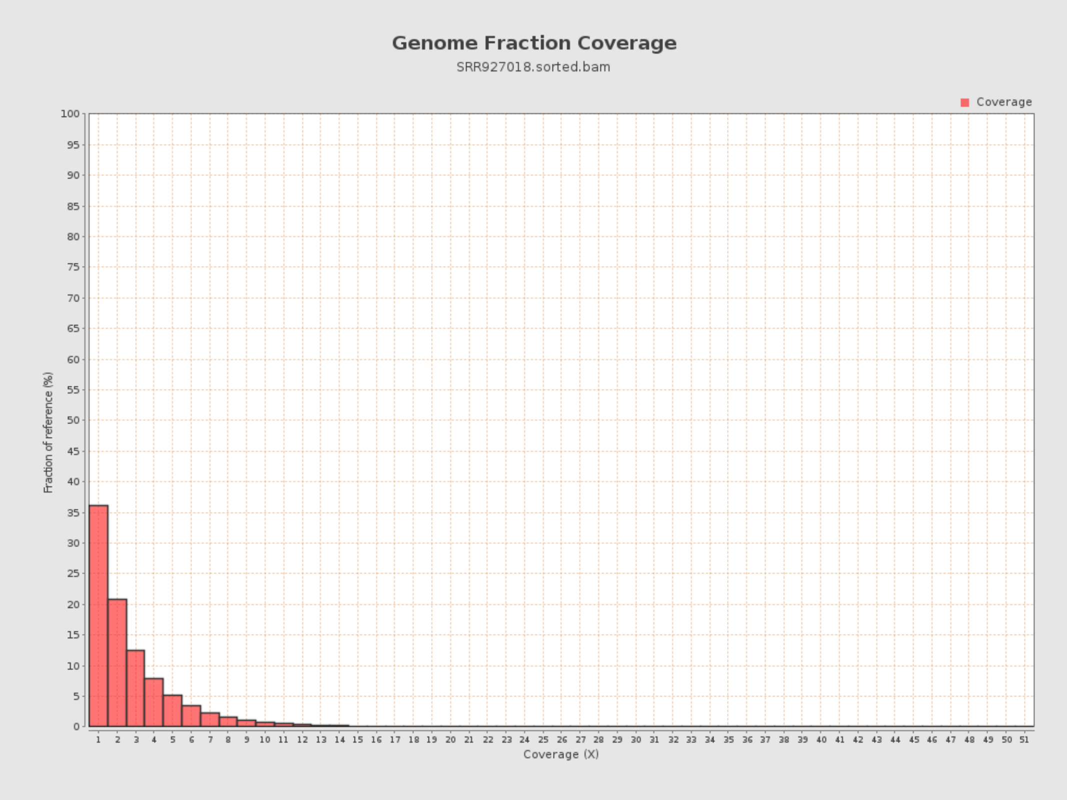
4. Results : Coverage Histogram



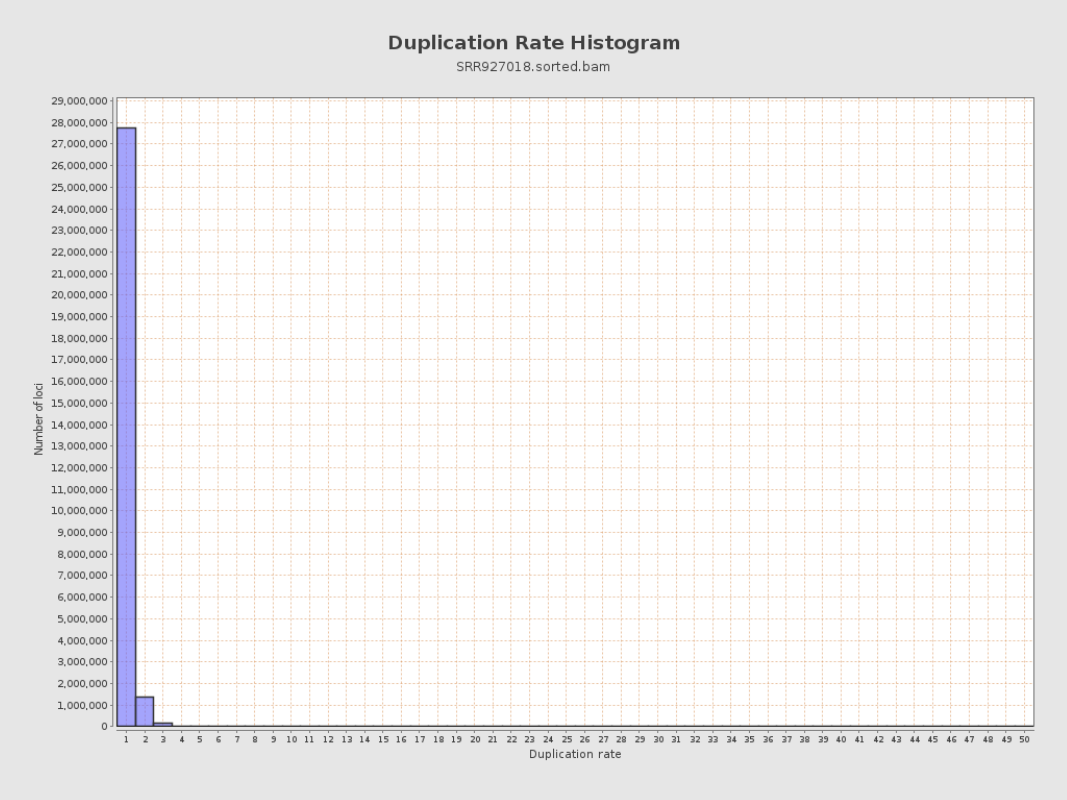
5. Results : Coverage Histogram (0-50X)



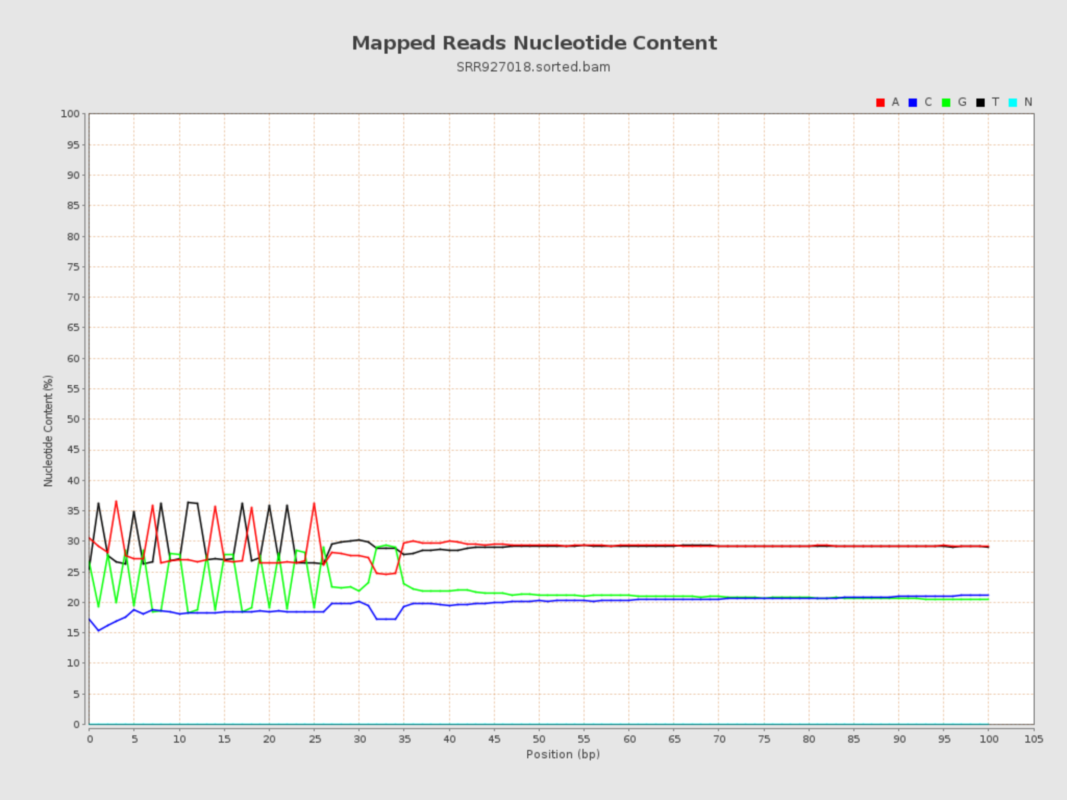
6. Results : Genome Fraction Coverage



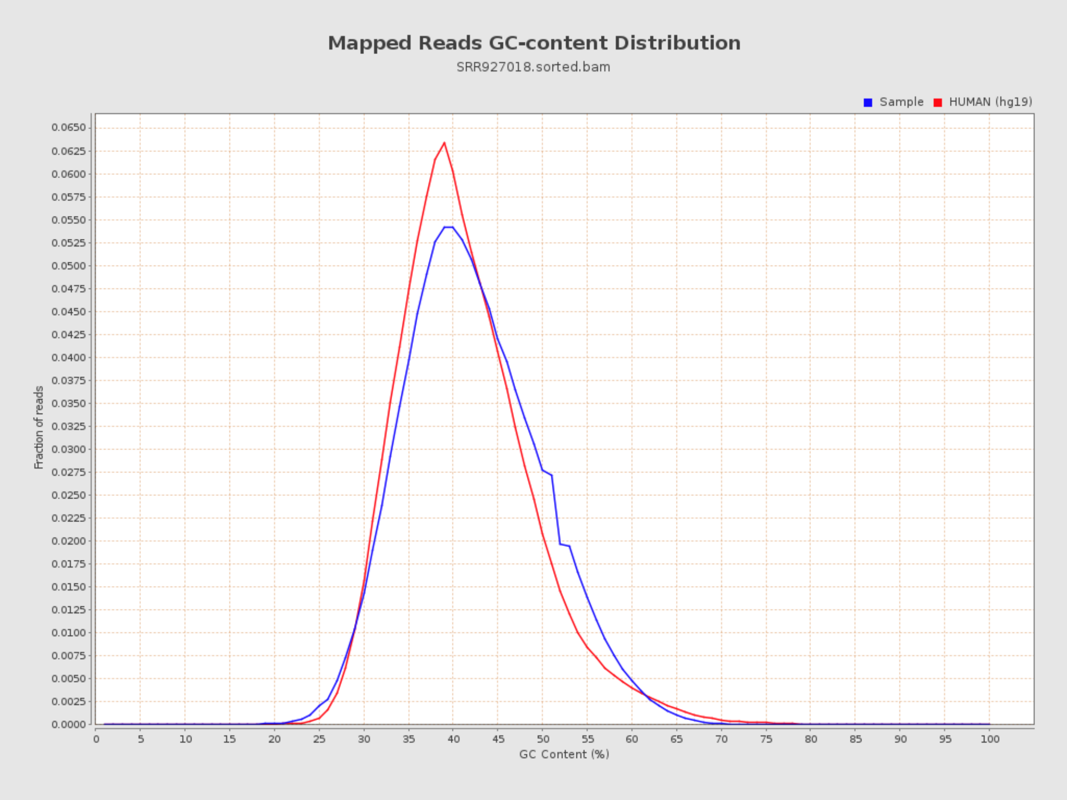
7. Results : Duplication Rate Histogram



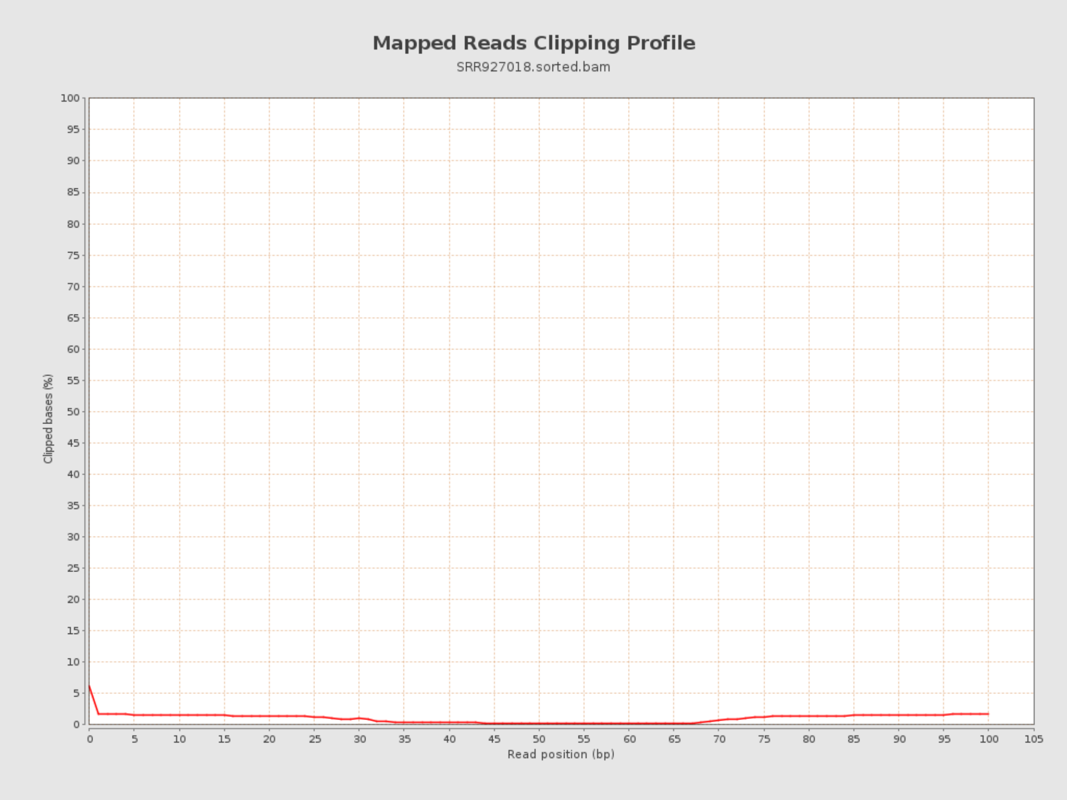
8. Results : Mapped Reads Nucleotide Content



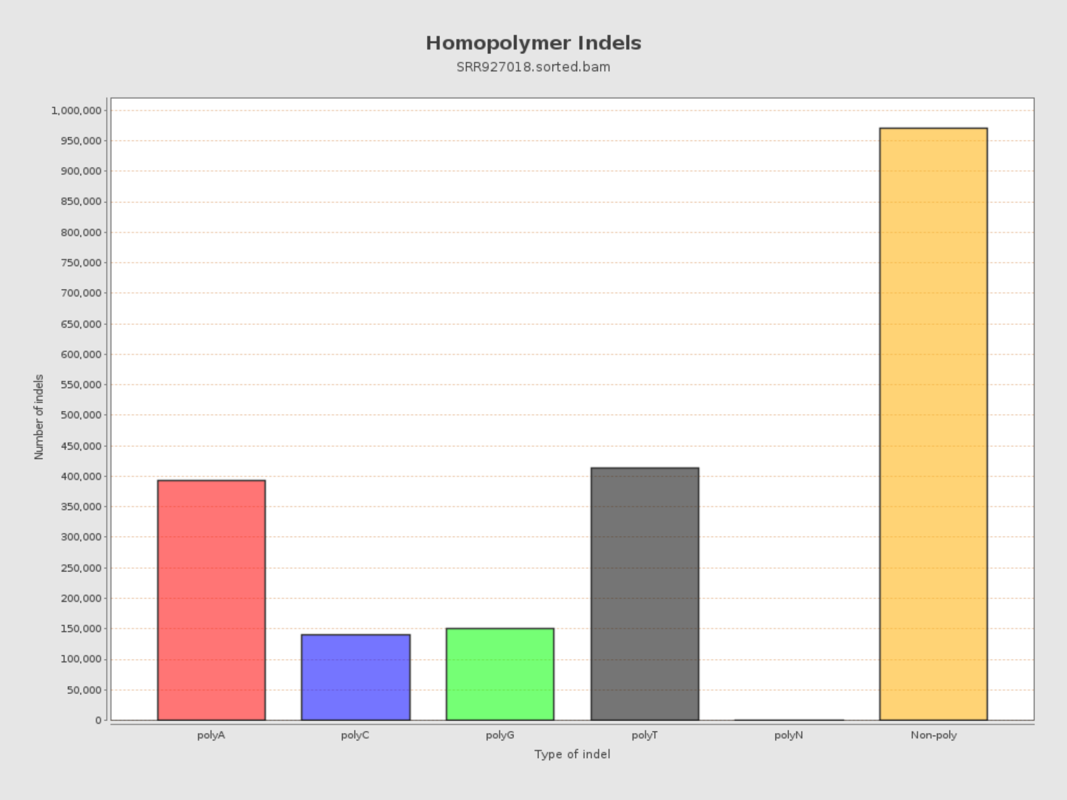
9. Results : Mapped Reads GC-content Distribution



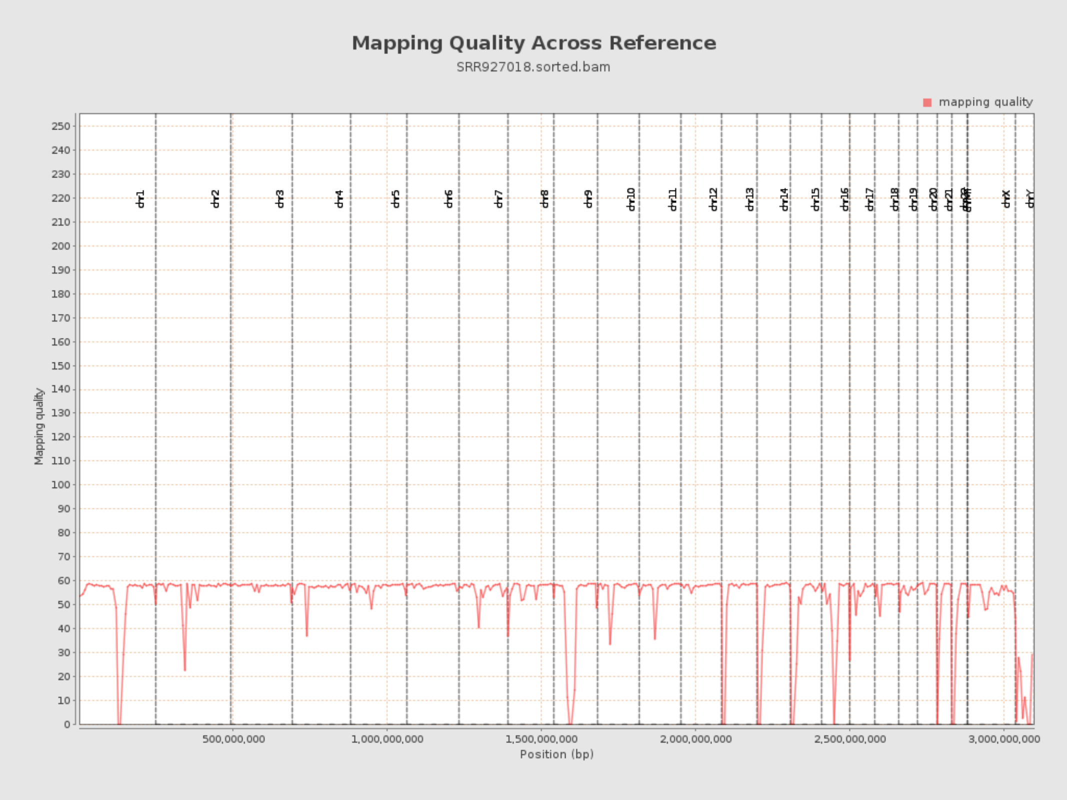
10. Results : Mapped Reads Clipping Profile



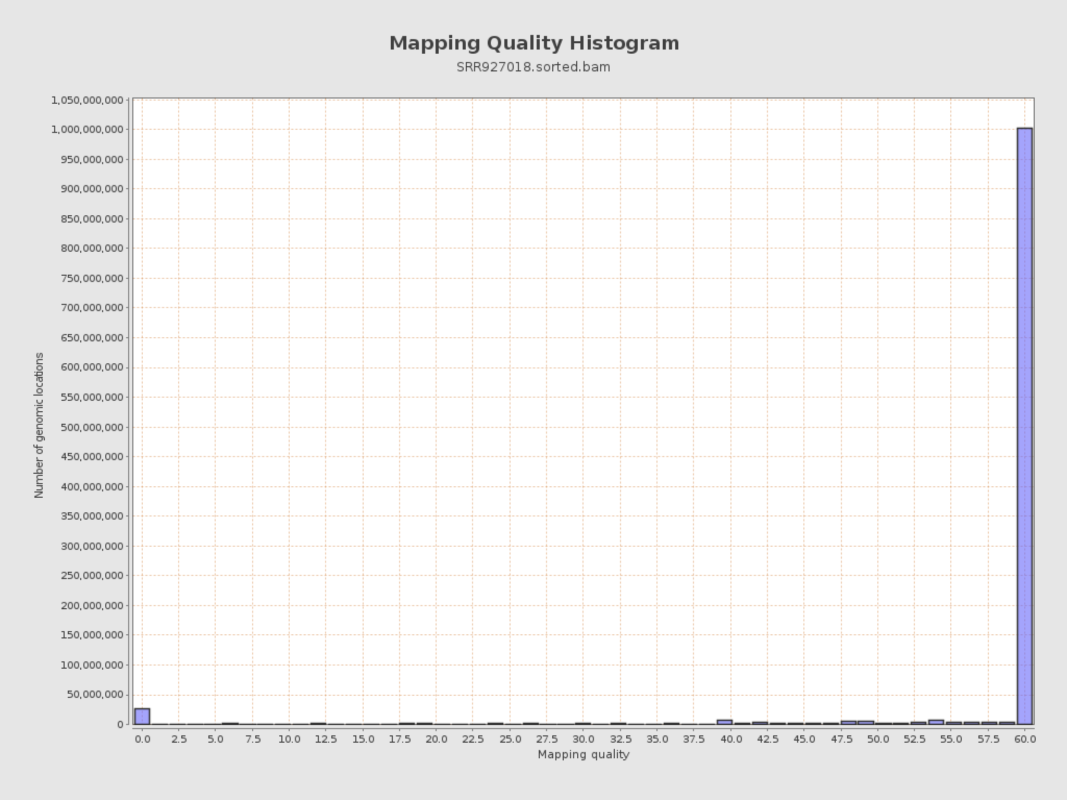
11. Results : Homopolymer Indels



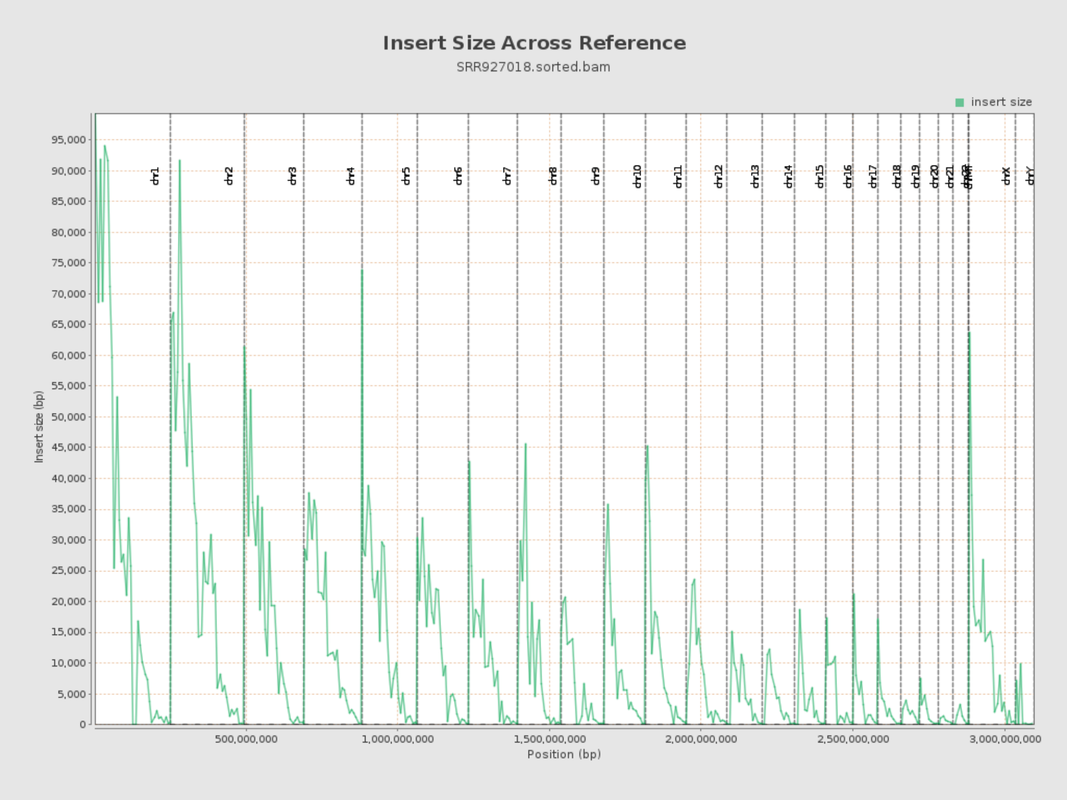
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram