Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 10:52:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926974.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_SRR926974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926974_1.fastq.gz SRR926974_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 10:52:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,605,450
Mapped reads	20,327,915 / 98.65%
Unmapped reads	277,535 / 1.35%
Mapped paired reads	20,327,915 / 98.65%
Mapped reads, first in pair	10,205,251 / 49.53%
Mapped reads, second in pair	10,122,664 / 49.13%
Mapped reads, both in pair	20,171,116 / 97.89%
Mapped reads, singletons	156,799 / 0.76%
Secondary alignments	0
Supplementary alignments	155,289 / 0.75%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	1,058,661 / 5.14%
Duplication rate	3.9%
Clipped reads	3,952,054 / 19.18%

2.2. ACGT Content

Number/percentage of A's	561,376,467 / 28.77%
Number/percentage of C's	394,308,775 / 20.21%
Number/percentage of T's	567,225,806 / 29.07%
Number/percentage of G's	427,889,401 / 21.93%
Number/percentage of N's	158,968 / 0.01%

GC Percentage	42.14%

2.3. Coverage

Mean	0.6307
Standard Deviation	2.6626

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	80,731.42
Standard Deviation	2,803,144.99
P25/Median/P75	147 / 182 / 235

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	18,535,168
Insertions	315,380
Mapped reads with at least one insertion	1.53%
Deletions	1,043,801
Mapped reads with at least one deletion	5%
Homopolymer indels	53.15%

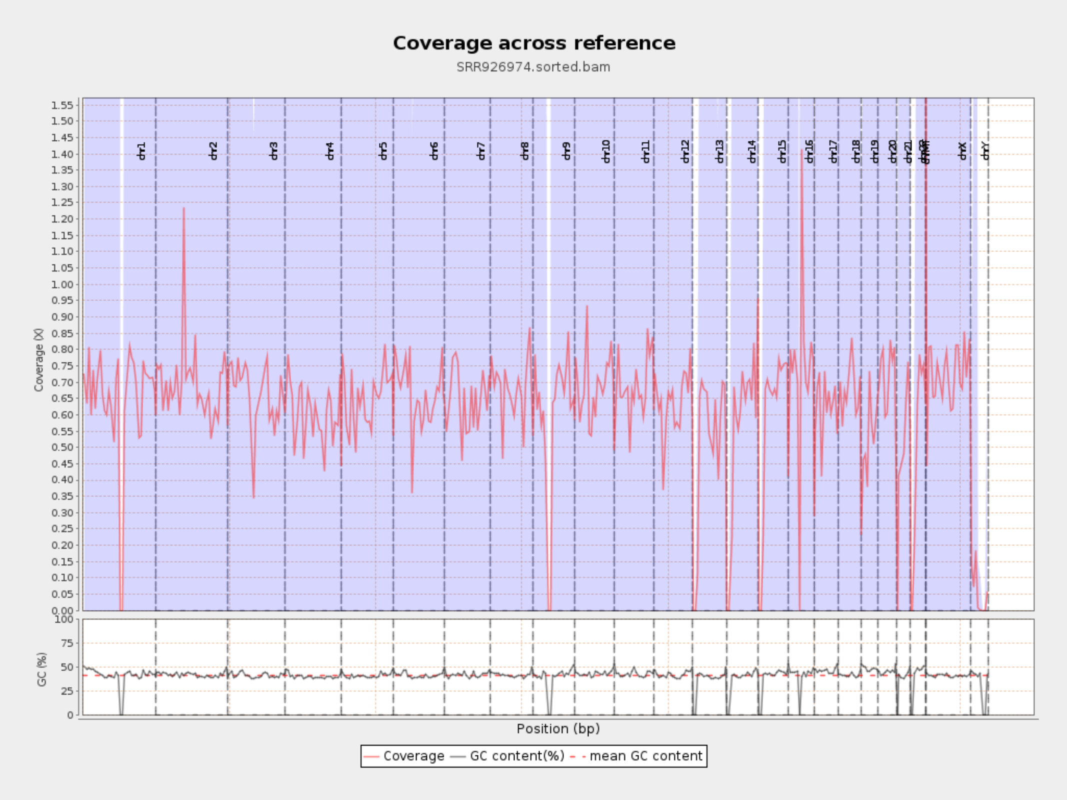
2.7. Chromosome stats

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

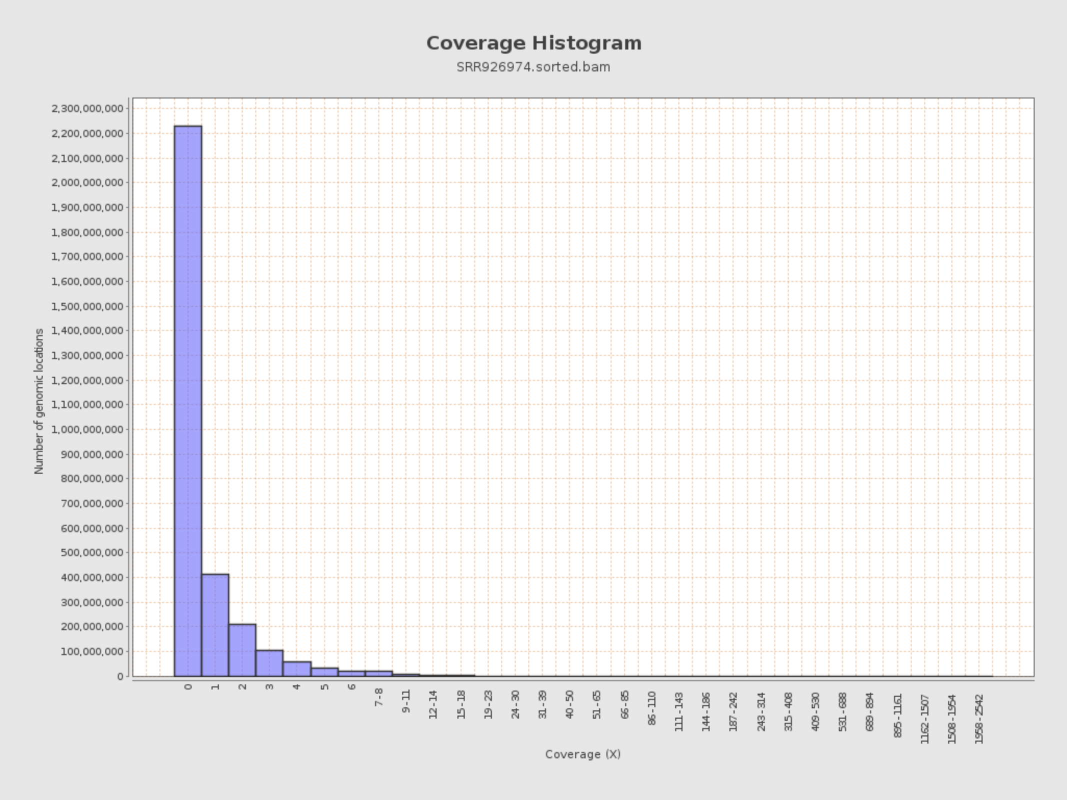
		bases	coverage	deviation
chr1	249250621	160283813	0.6431	3.2053
chr2	243199373	169653354	0.6976	4.1322
chr3	198022430	130442819	0.6587	1.436
chr4	191154276	115900255	0.6063	1.9584
chr5	180915260	118004880	0.6523	1.4064
chr6	171115067	113339772	0.6624	2.4268
chr7	159138663	102381410	0.6433	2.0198
chr8	146364022	99622555	0.6806	1.7062
chr9	141213431	84083719	0.5954	3.6447
chr10	135534747	93372313	0.6889	3.9634
chr11	135006516	92593856	0.6858	2.4733
chr12	133851895	85871645	0.6415	1.6579
chr13	115169878	58330160	0.5065	1.3197
chr14	107349540	59042030	0.55	1.3629
chr15	102531392	58773196	0.5732	1.4302
chr16	90354753	65759512	0.7278	5.5705
chr17	81195210	51064191	0.6289	2.4666
chr18	78077248	52748410	0.6756	3.8694
chr19	59128983	31181053	0.5273	2.154
chr20	63025520	45751492	0.7259	1.6192
chr21	48129895	23998287	0.4986	1.8936
chr22	51304566	25163258	0.4905	1.337
chrMT	16571	30406	1.8349	2.01
chrX	155270560	111814038	0.7201	1.7487

chrY	59373566	3227672	0.0544	1.6768

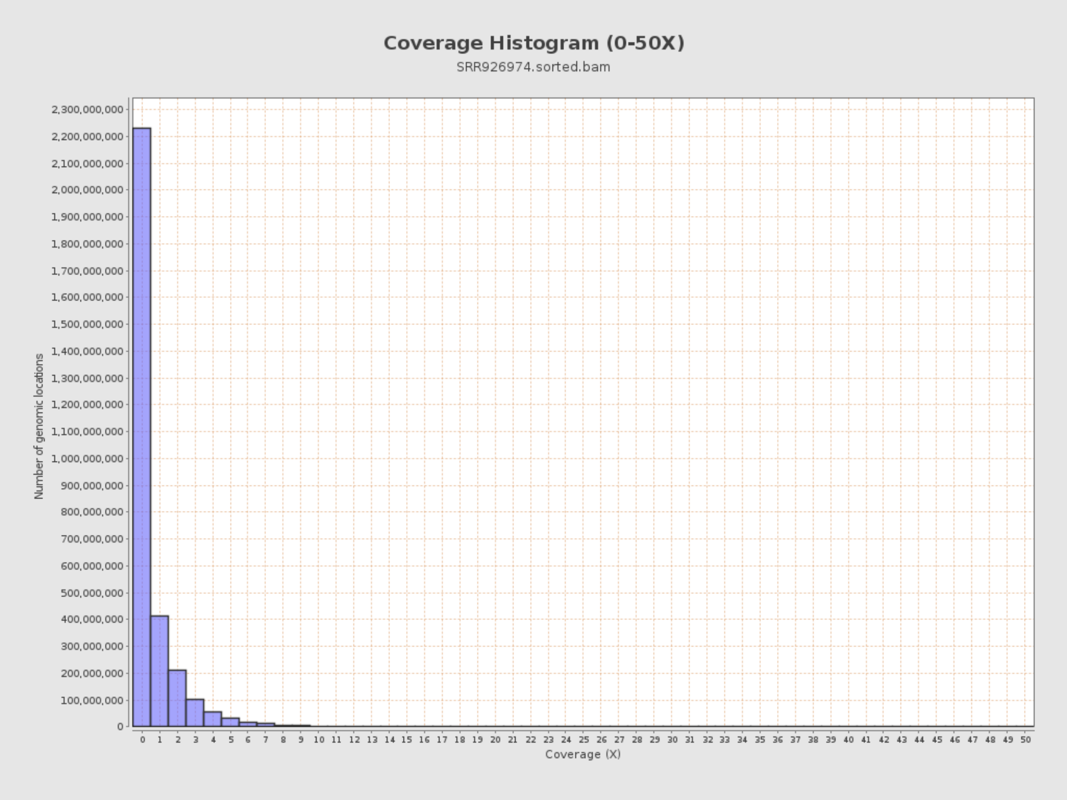
3. Results : Coverage across reference



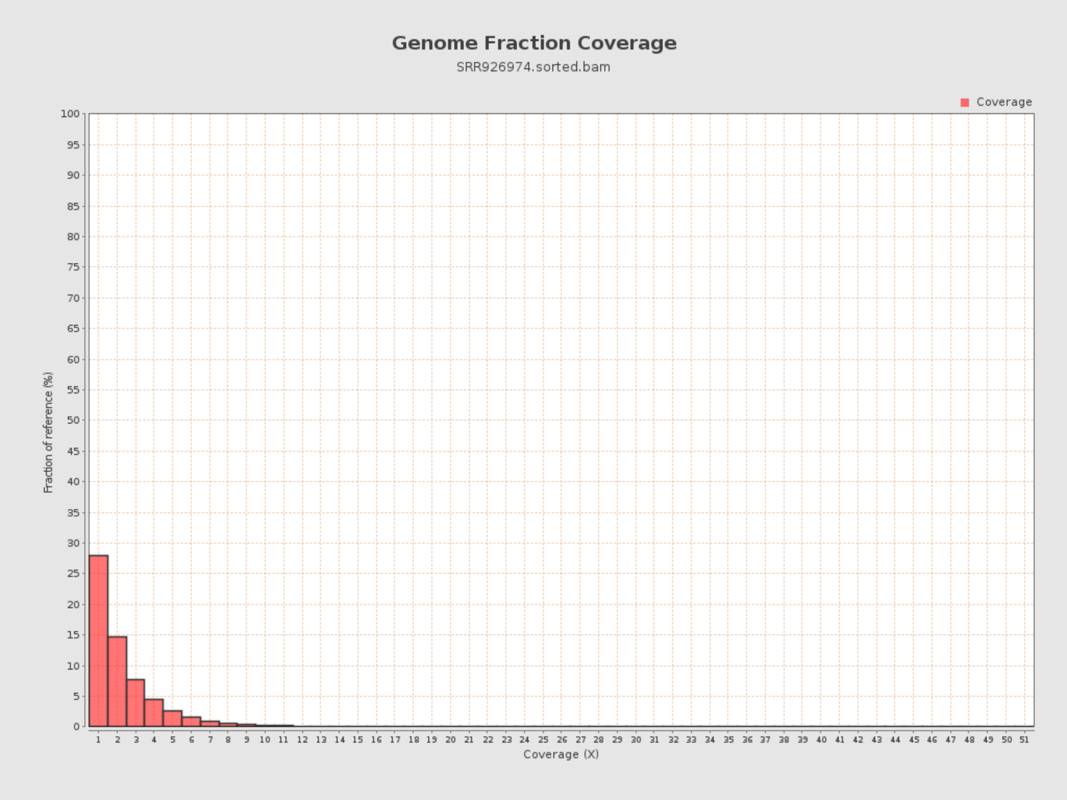
4. Results : Coverage Histogram



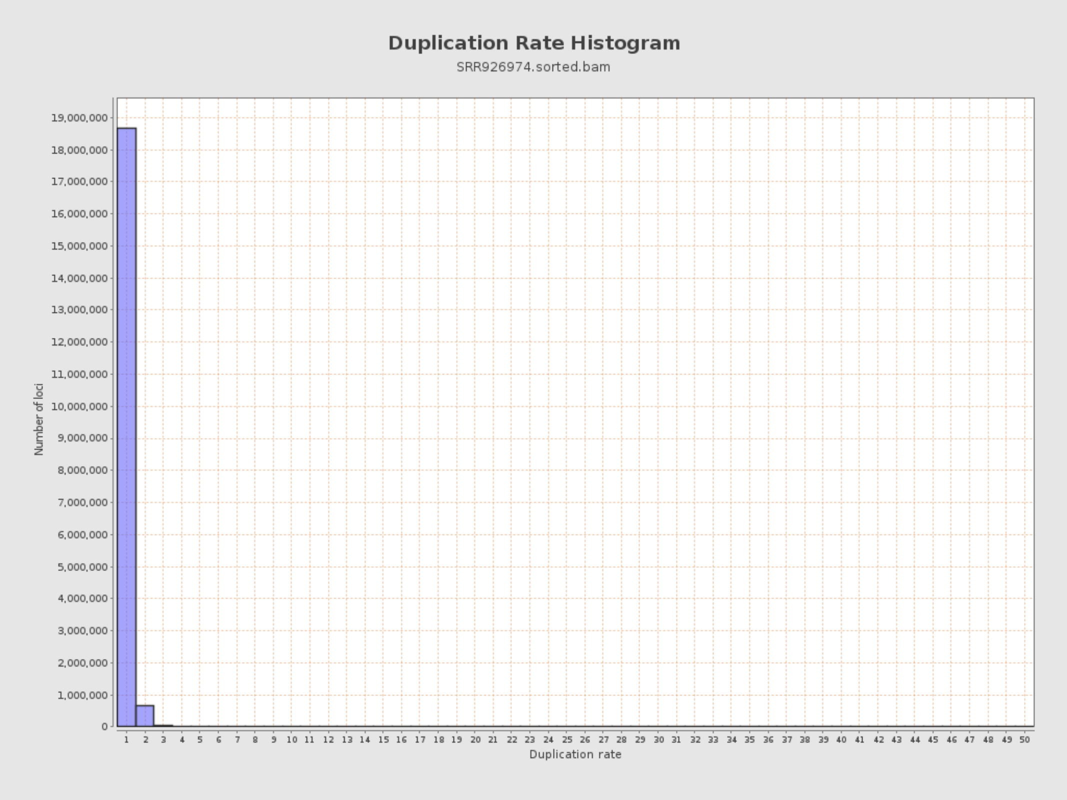
5. Results : Coverage Histogram (0-50X)



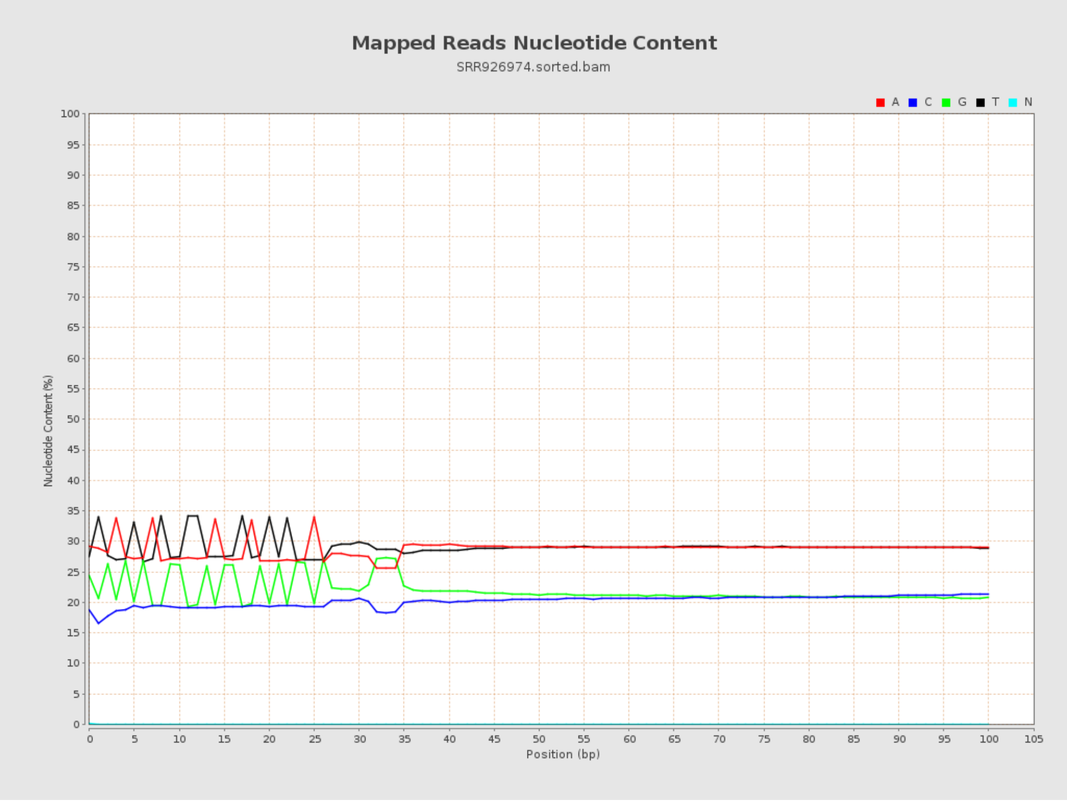
6. Results : Genome Fraction Coverage



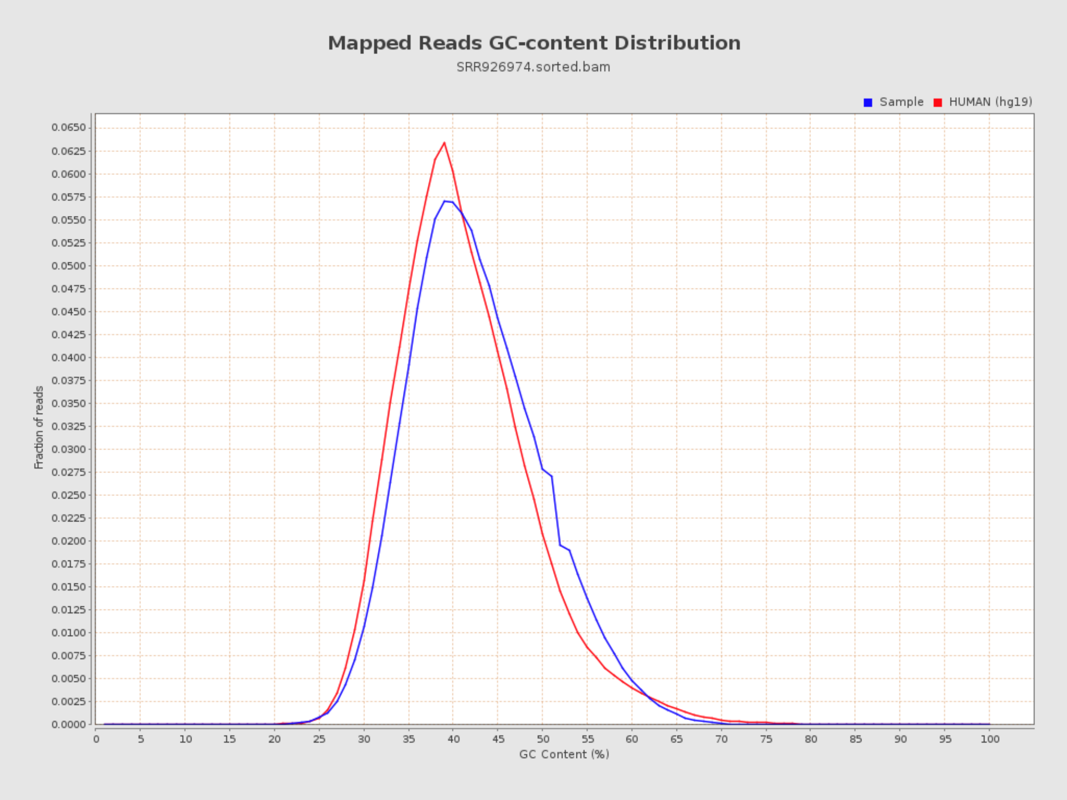
7. Results : Duplication Rate Histogram



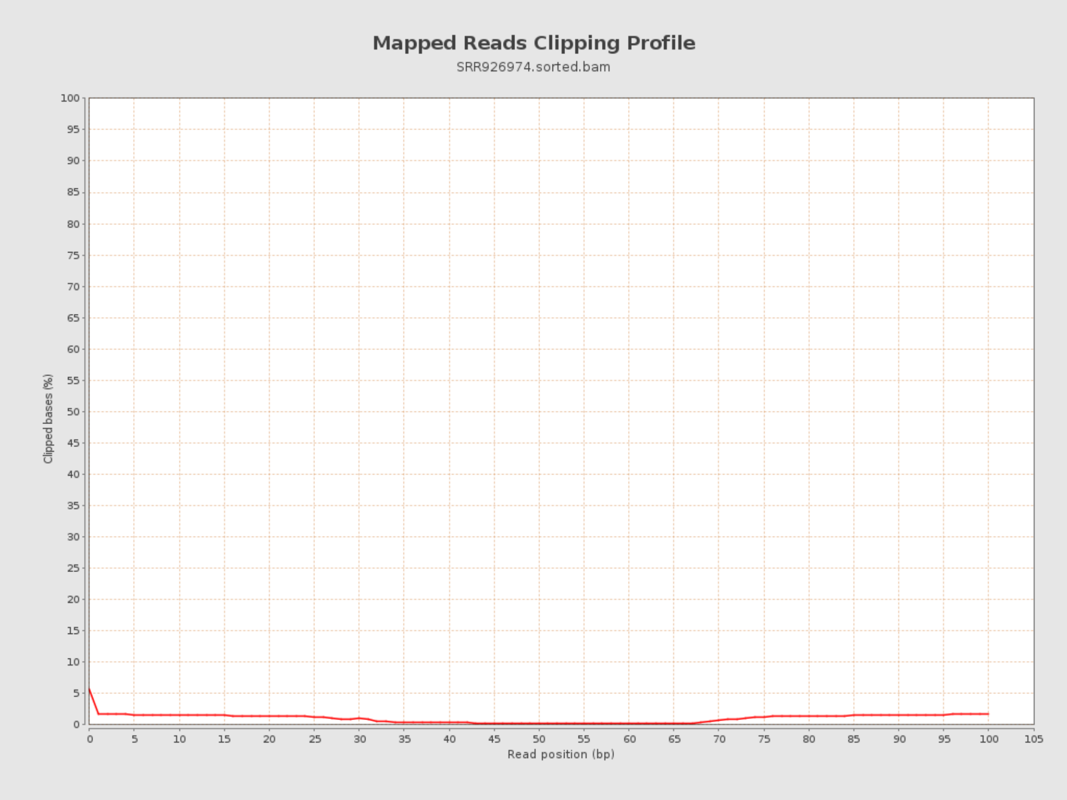
8. Results : Mapped Reads Nucleotide Content



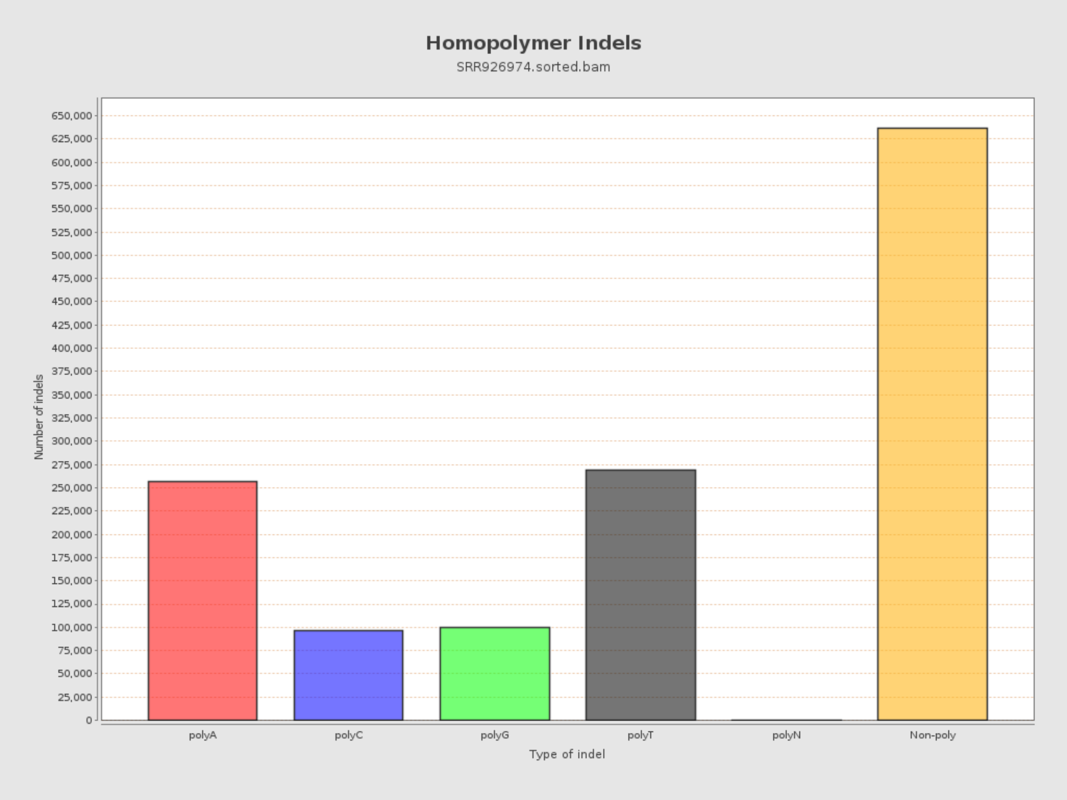
9. Results : Mapped Reads GC-content Distribution



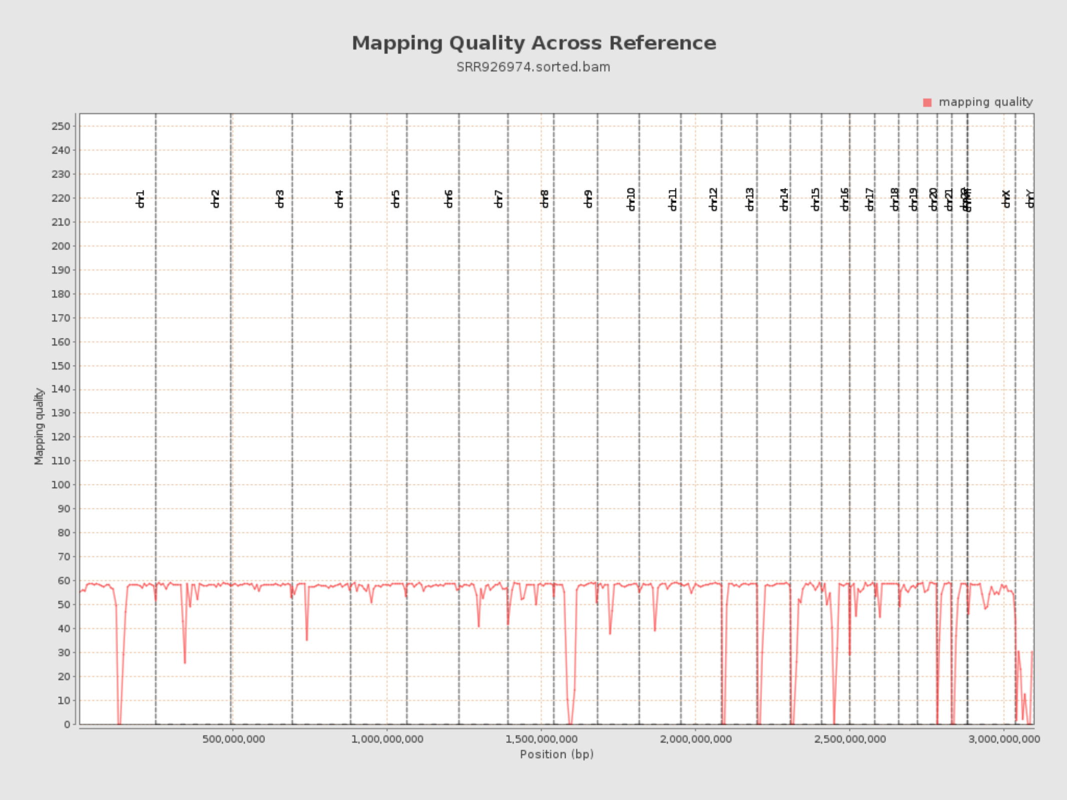
10. Results : Mapped Reads Clipping Profile



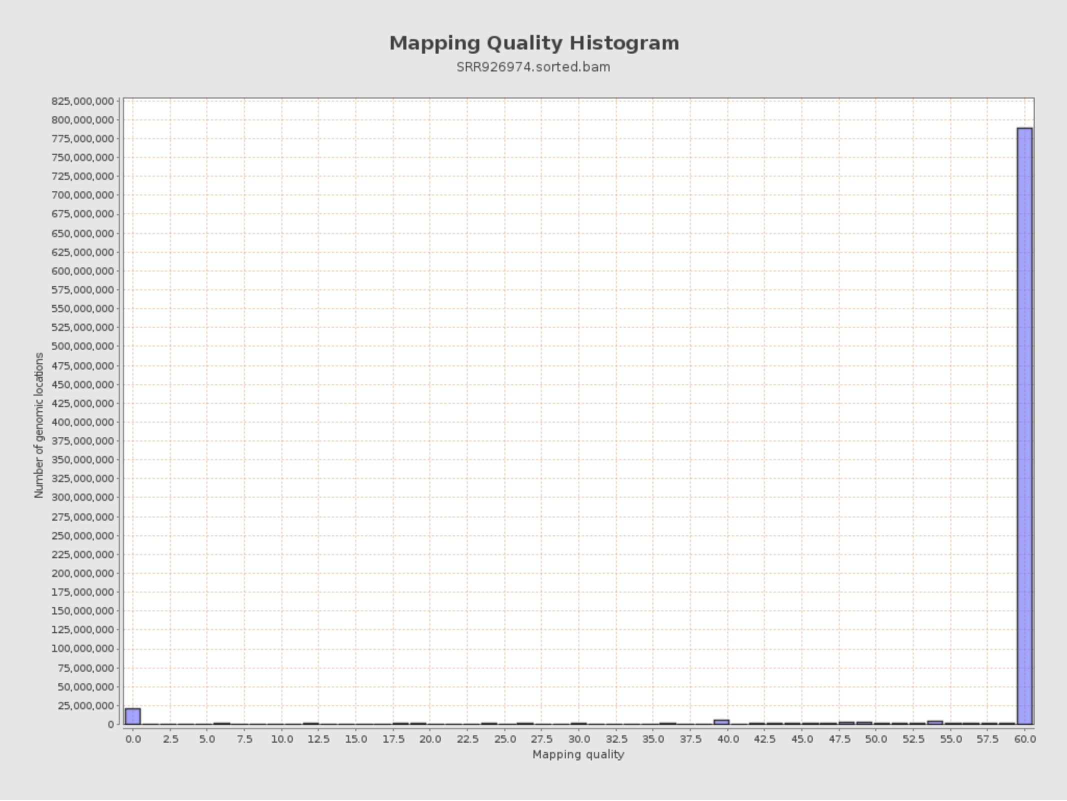
11. Results : Homopolymer Indels



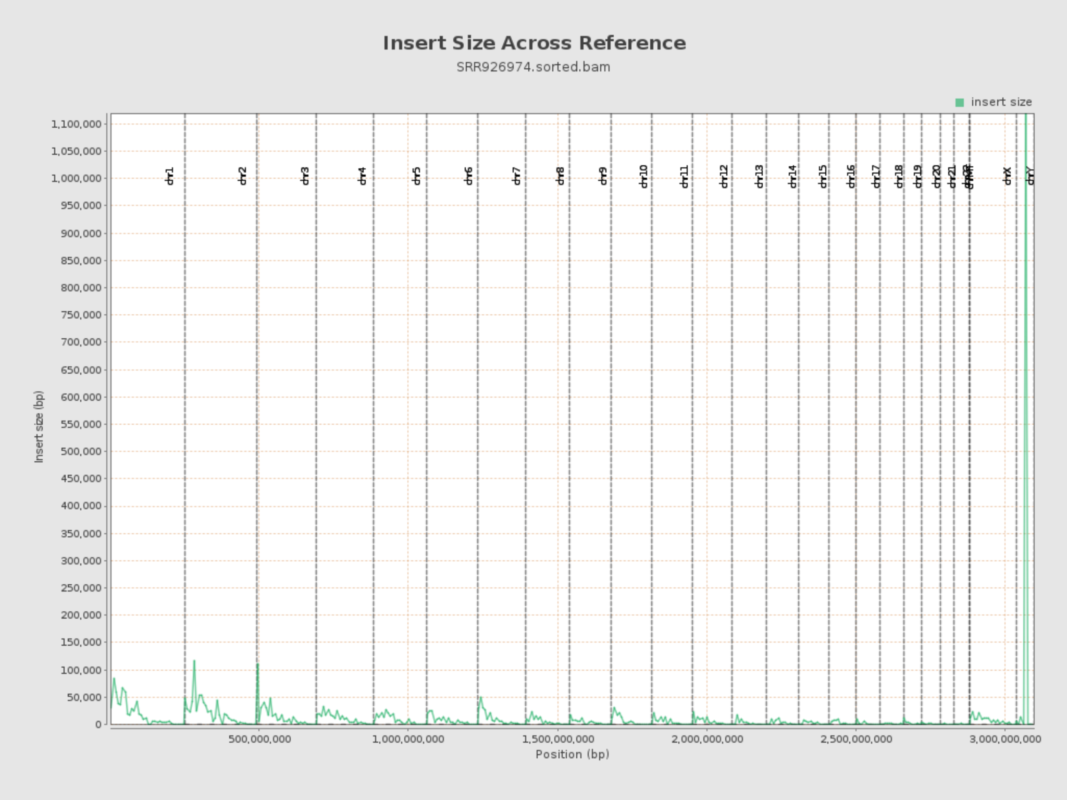
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram