Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 09:06:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926970.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_SRR926970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926970_1.fastq.gz SRR926970_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 09:06:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,928,510
Mapped reads	30,084,173 / 97.27%
Unmapped reads	844,337 / 2.73%
Mapped paired reads	30,084,173 / 97.27%
Mapped reads, first in pair	15,002,832 / 48.51%
Mapped reads, second in pair	15,081,341 / 48.76%
Mapped reads, both in pair	29,574,224 / 95.62%
Mapped reads, singletons	509,949 / 1.65%
Secondary alignments	0
Supplementary alignments	1,170,492 / 3.78%
Read min/max/mean length	30 / 101 / 102.57
Duplicated reads (estimated)	3,436,957 / 11.11%
Duplication rate	8.93%
Clipped reads	15,107,376 / 48.85%

2.2. ACGT Content

Number/percentage of A's	769,778,040 / 28.63%
Number/percentage of C's	513,939,466 / 19.11%
Number/percentage of T's	790,635,969 / 29.41%
Number/percentage of G's	614,085,871 / 22.84%
Number/percentage of N's	301,765 / 0.01%

GC Percentage	41.95%

2.3. Coverage

Mean	0.8692
Standard Deviation	3.2276

2.4. Mapping Quality

Mean Mapping Quality	52.47

2.5. Insert size

Mean	370,089.65
Standard Deviation	5,942,338.02
P25/Median/P75	128 / 166 / 224

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	26,924,036
Insertions	479,347
Mapped reads with at least one insertion	1.56%
Deletions	1,414,170
Mapped reads with at least one deletion	4.58%
Homopolymer indels	51.7%

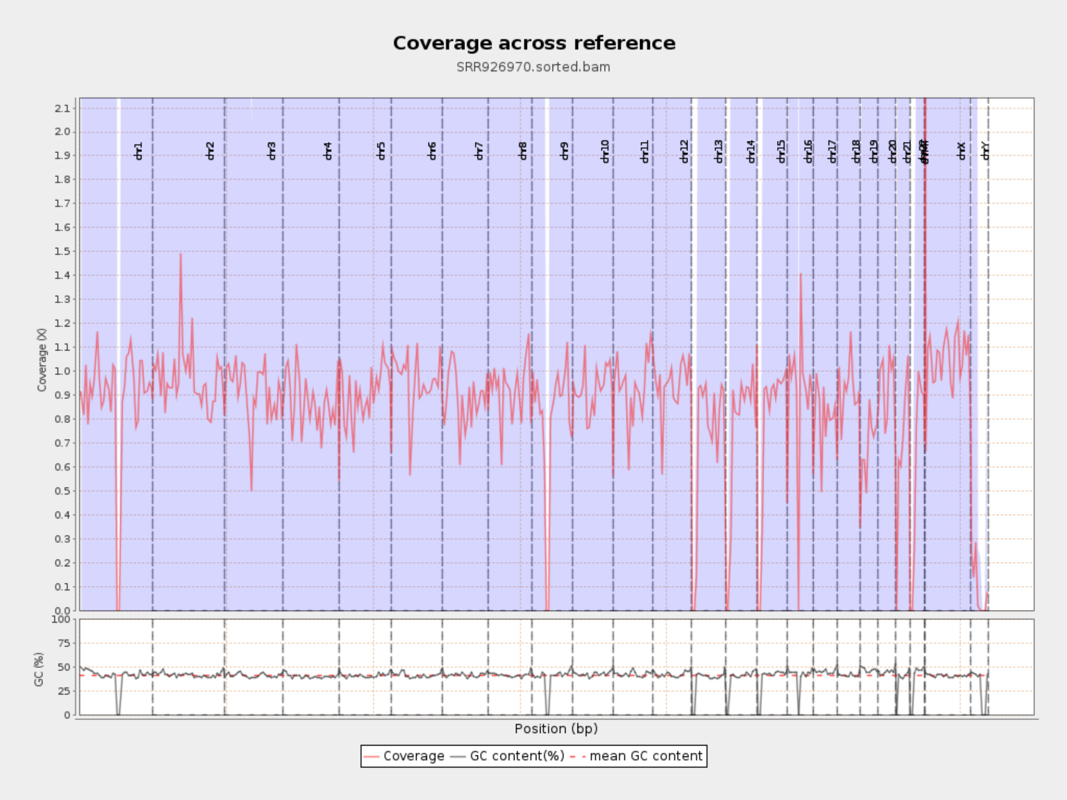
2.7. Chromosome stats

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

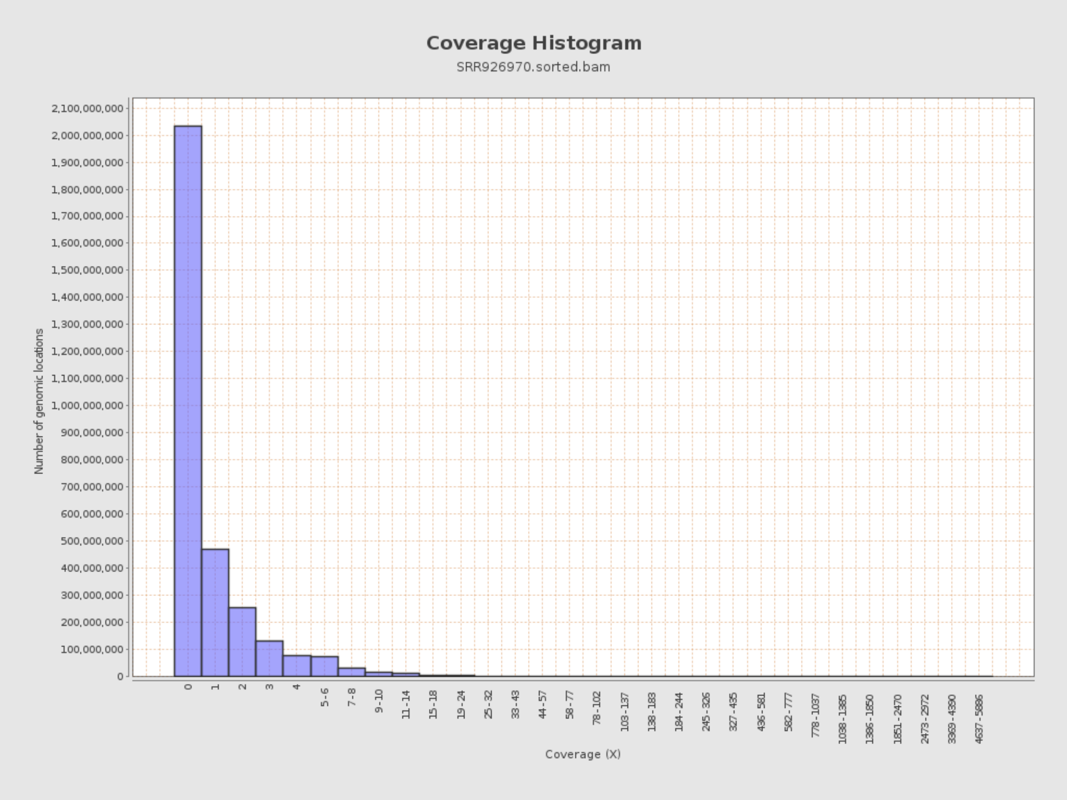
		bases	coverage	deviation
chr1	249250621	220939085	0.8864	3.2465
chr2	243199373	237463550	0.9764	6.2553
chr3	198022430	180994174	0.914	1.87
chr4	191154276	166937616	0.8733	3.0032
chr5	180915260	163685969	0.9048	1.8509
chr6	171115067	165390208	0.9665	2.8593
chr7	159138663	141109498	0.8867	2.4874
chr8	146364022	135853598	0.9282	2.1944
chr9	141213431	111041513	0.7863	3.6515
chr10	135534747	126312138	0.932	4.2013
chr11	135006516	125418265	0.929	2.8664
chr12	133851895	126471103	0.9449	2.0665
chr13	115169878	81177322	0.7048	1.6391
chr14	107349540	78986085	0.7358	1.7651
chr15	102531392	77538670	0.7562	1.775
chr16	90354753	80434760	0.8902	5.4444
chr17	81195210	65048765	0.8011	2.7765
chr18	78077248	73273957	0.9385	3.9442
chr19	59128983	40411236	0.6834	2.263
chr20	63025520	59365900	0.9419	2.1215
chr21	48129895	33897789	0.7043	2.5928
chr22	51304566	31130112	0.6068	1.6899
chrMT	16571	279509	16.8674	14.9399
chrX	155270560	162374059	1.0457	2.2631

chrY	59373566	5301246	0.0893	3.2184

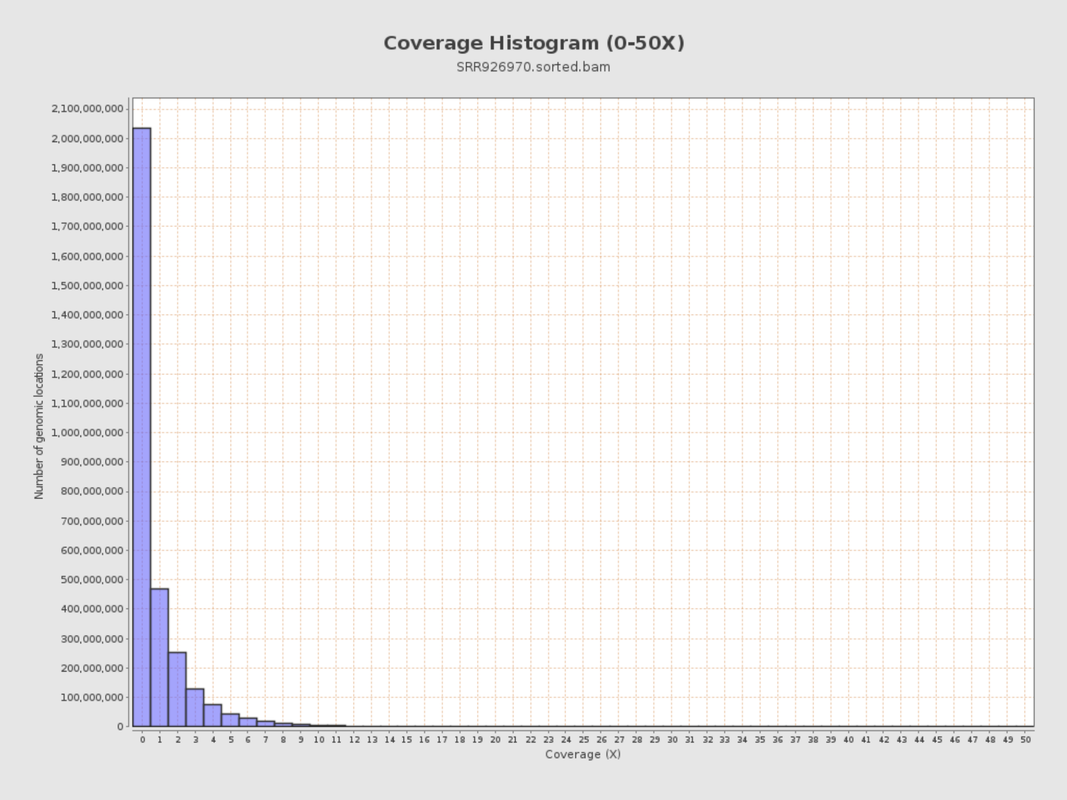
3. Results : Coverage across reference



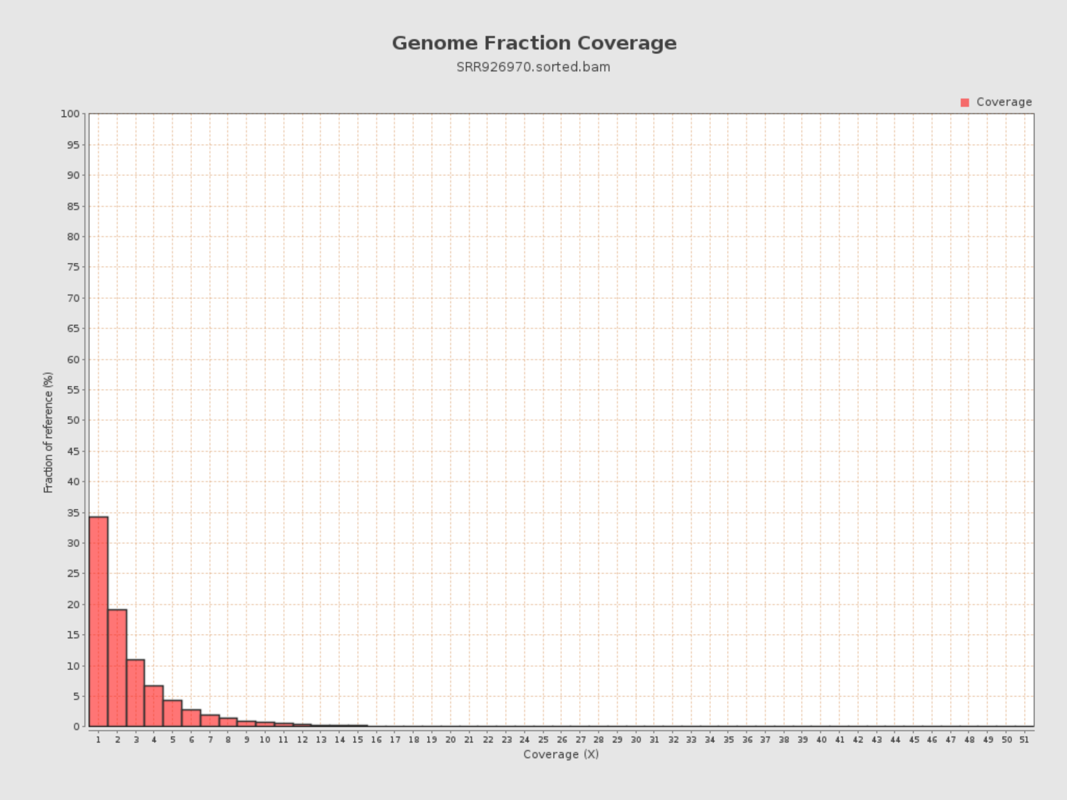
4. Results : Coverage Histogram



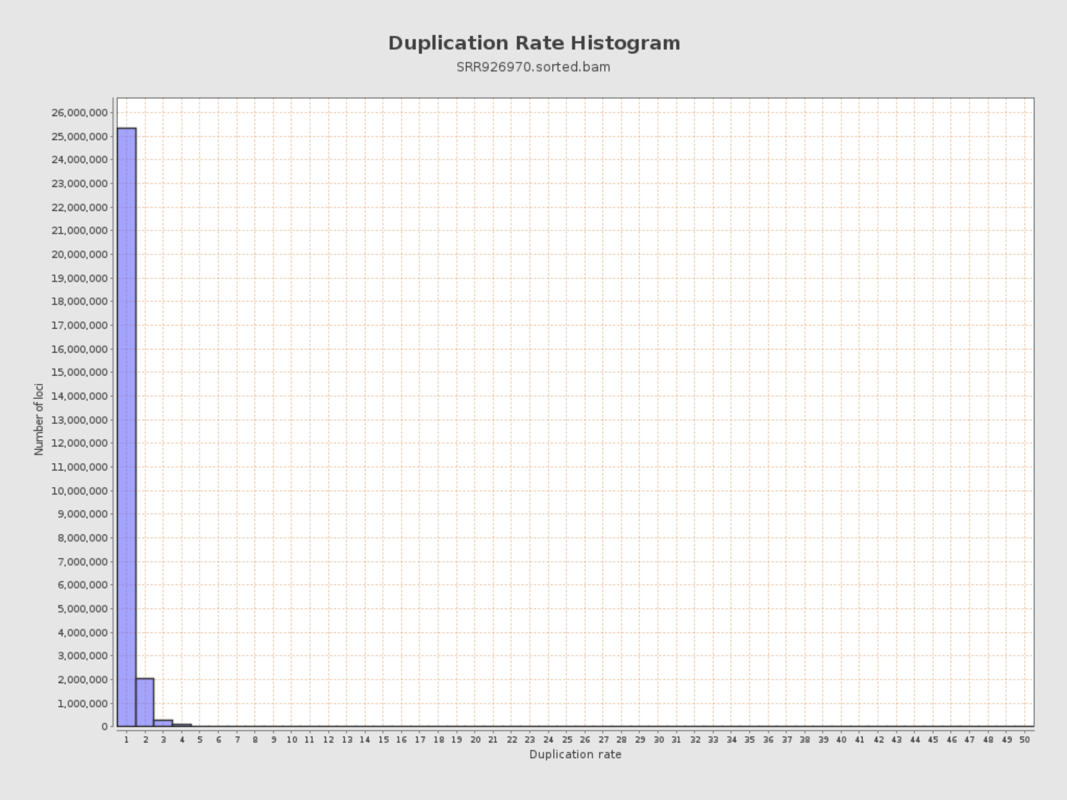
5. Results : Coverage Histogram (0-50X)



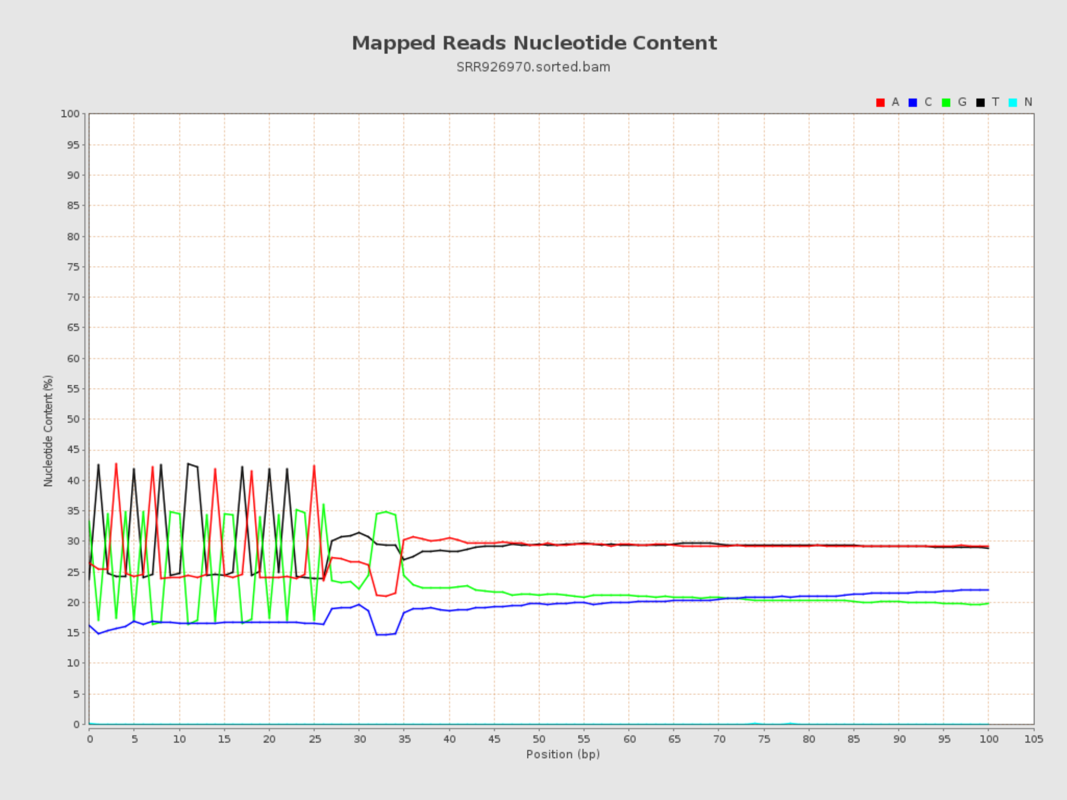
6. Results : Genome Fraction Coverage



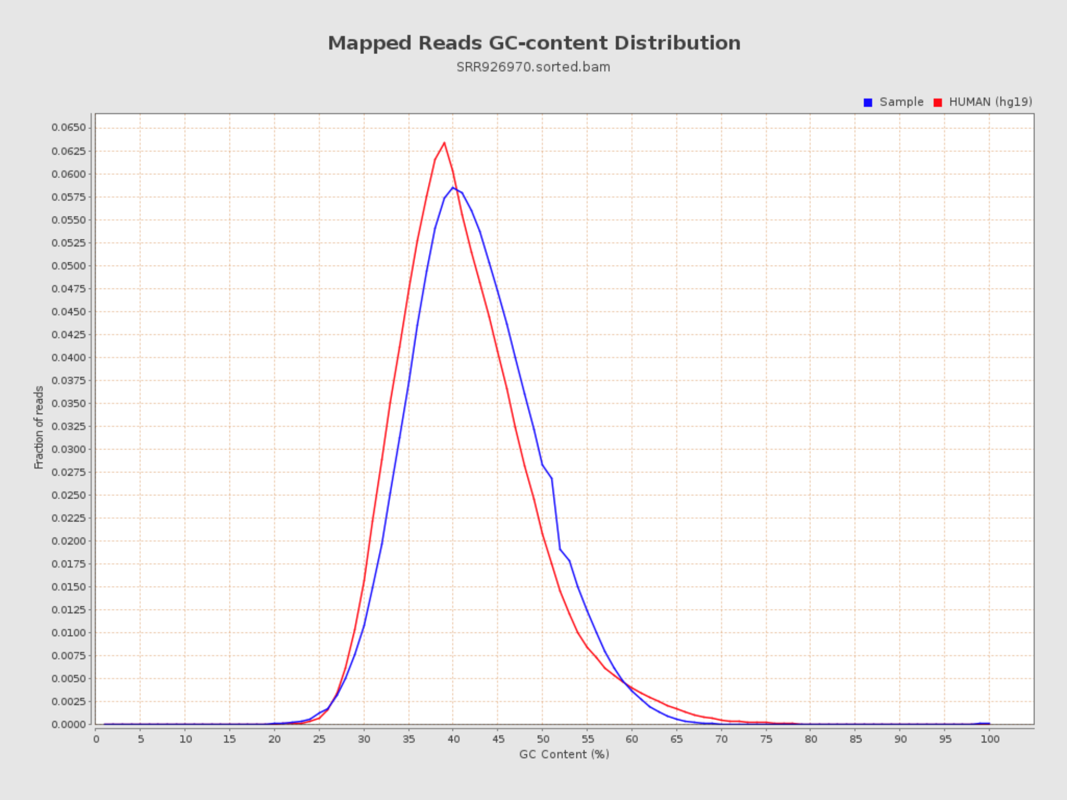
7. Results : Duplication Rate Histogram



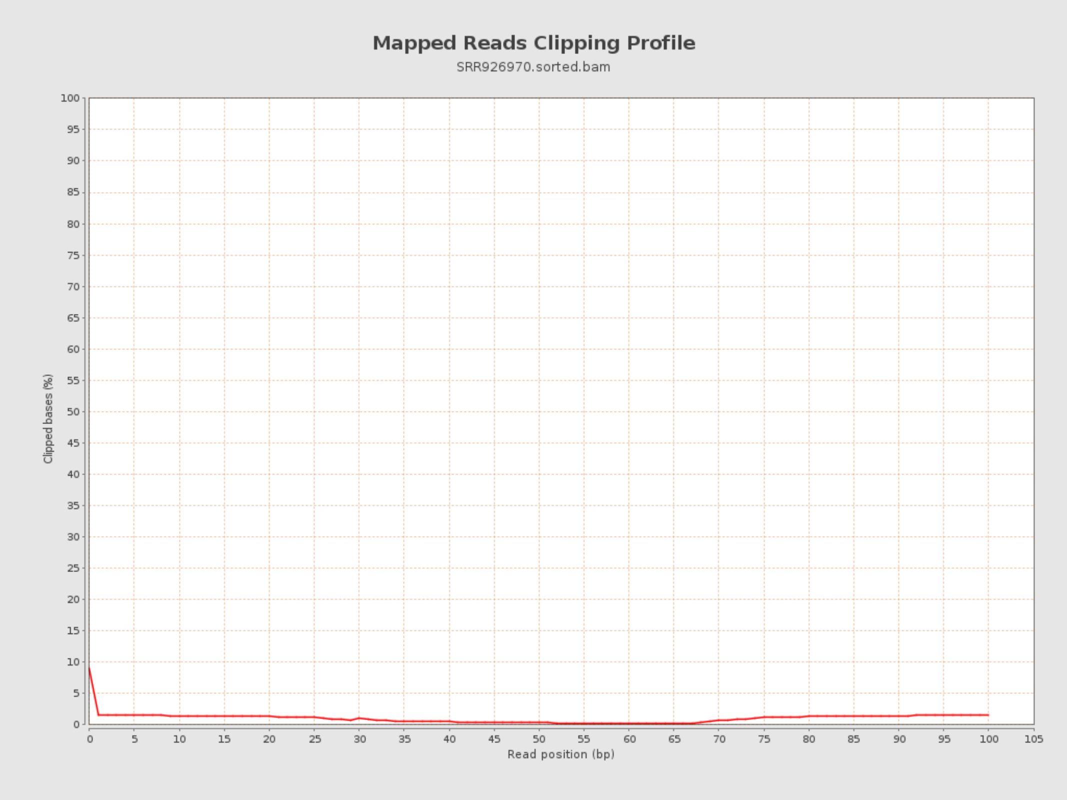
8. Results : Mapped Reads Nucleotide Content



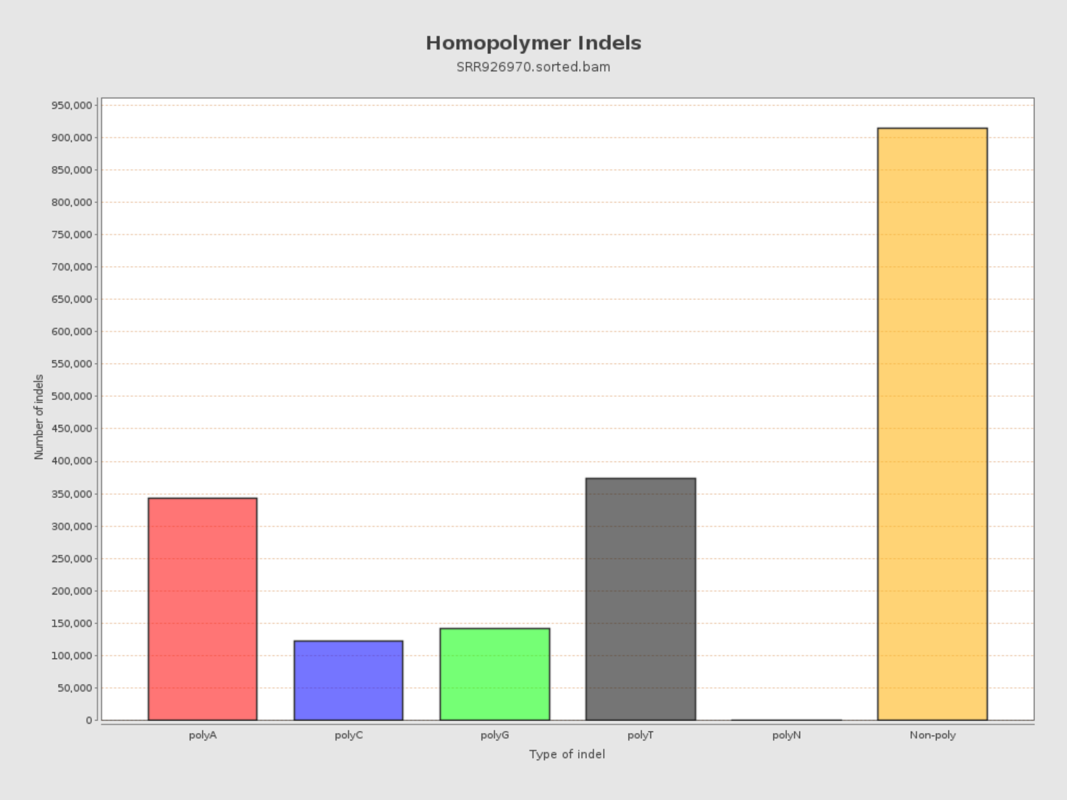
9. Results : Mapped Reads GC-content Distribution



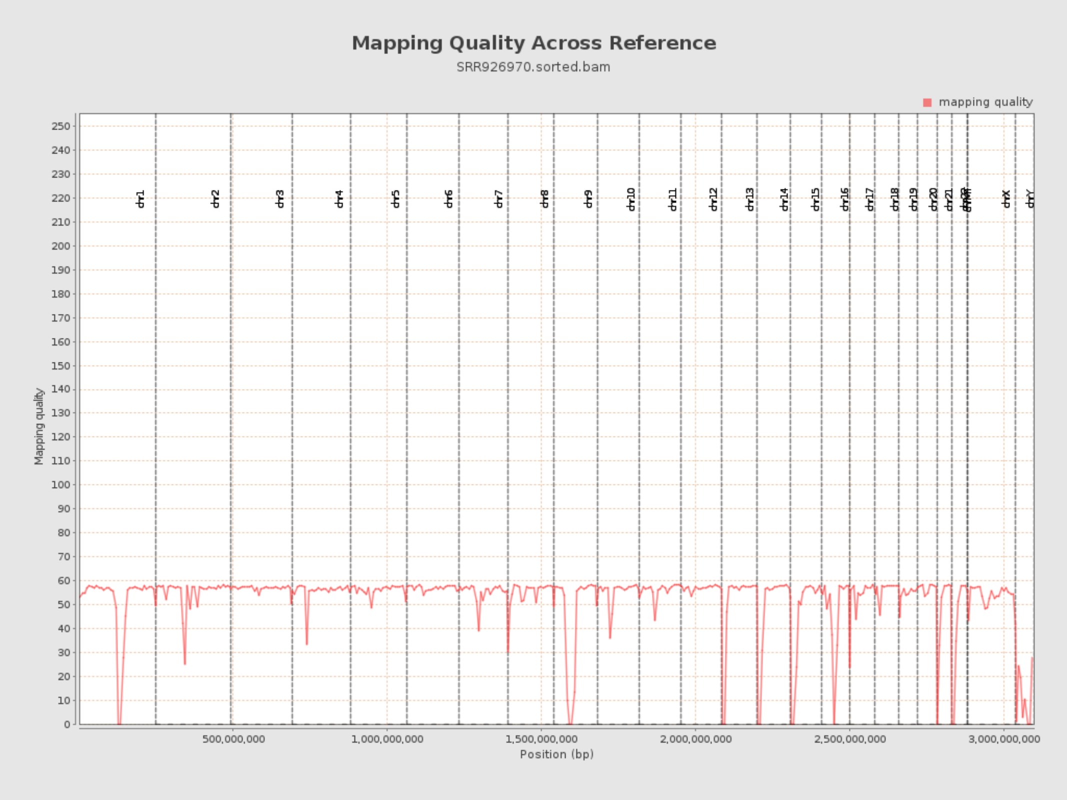
10. Results : Mapped Reads Clipping Profile



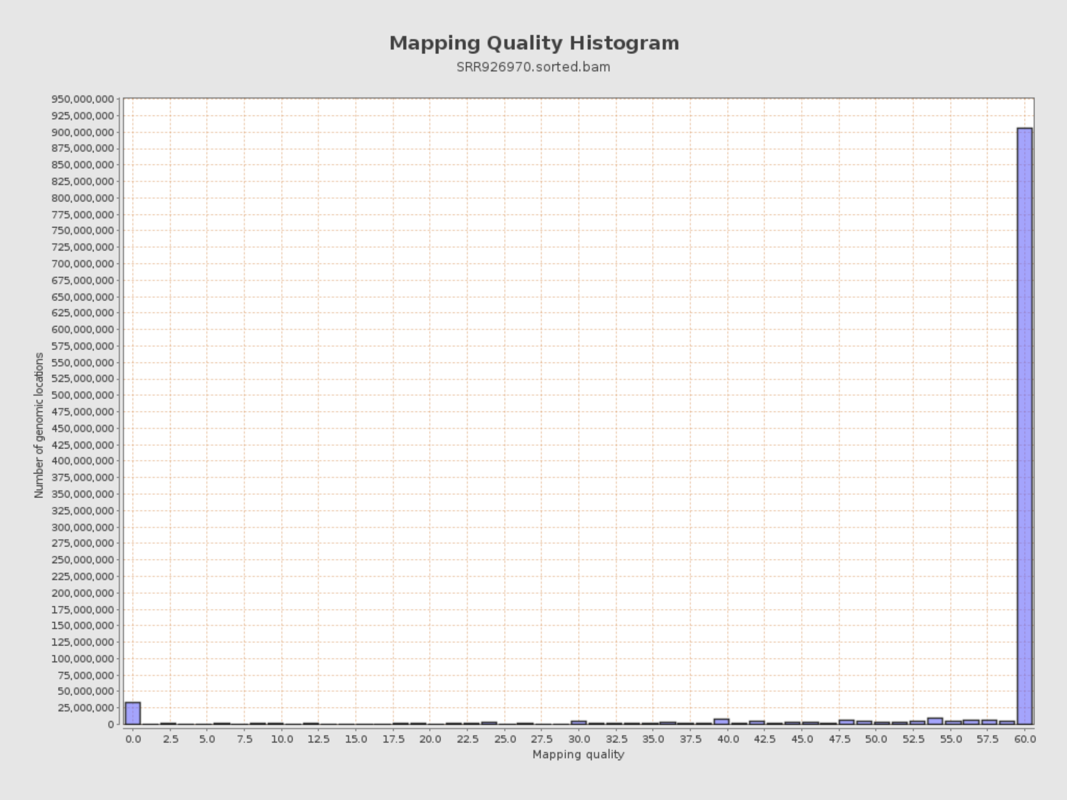
11. Results : Homopolymer Indels



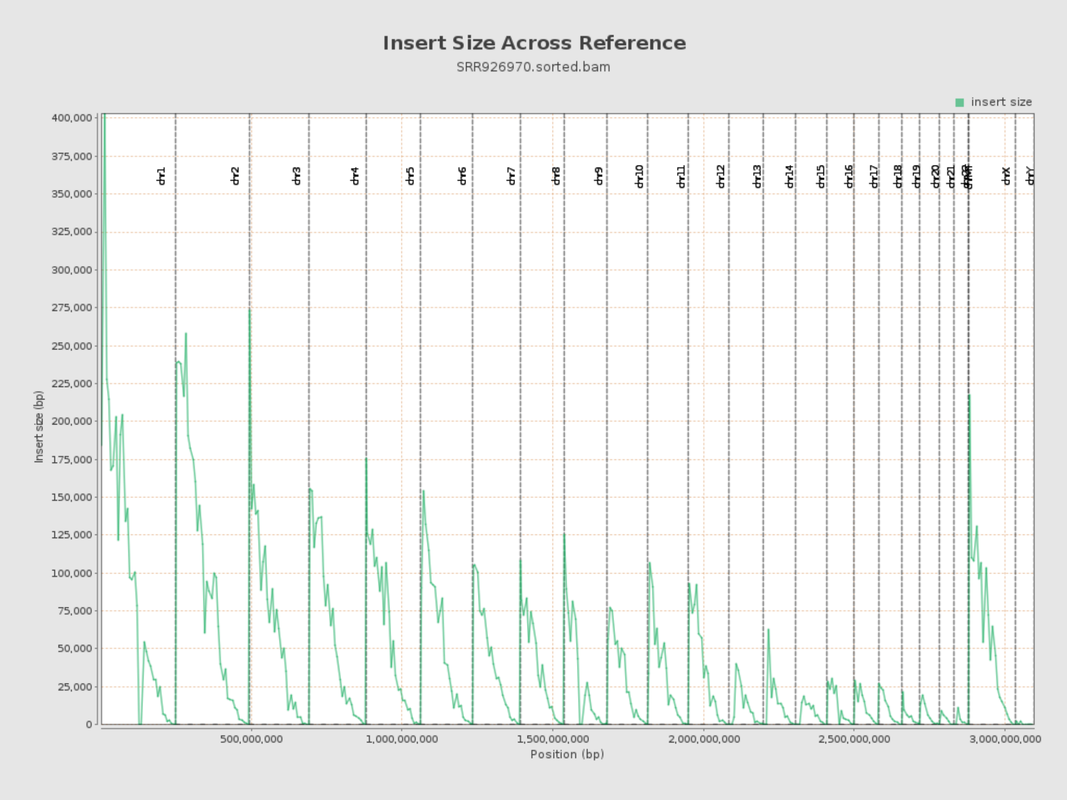
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram