Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 03:40:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926958.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_SRR926958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926958_1.fastq.gz SRR926958_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 03:40:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,796,144
Mapped reads	9,467,647 / 96.65%
Unmapped reads	328,497 / 3.35%
Mapped paired reads	9,467,647 / 96.65%
Mapped reads, first in pair	4,747,866 / 48.47%
Mapped reads, second in pair	4,719,781 / 48.18%
Mapped reads, both in pair	9,309,660 / 95.03%
Mapped reads, singletons	157,987 / 1.61%
Secondary alignments	0
Supplementary alignments	206,377 / 2.11%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	548,541 / 5.6%
Duplication rate	4.82%
Clipped reads	3,507,065 / 35.8%

2.2. ACGT Content

Number/percentage of A's	247,505,798 / 28.41%
Number/percentage of C's	172,783,956 / 19.83%
Number/percentage of T's	249,665,271 / 28.66%
Number/percentage of G's	201,232,931 / 23.1%
Number/percentage of N's	47,328 / 0.01%

GC Percentage	42.93%

2.3. Coverage

Mean	0.2817
Standard Deviation	1.2627

2.4. Mapping Quality

Mean Mapping Quality	52.58

2.5. Insert size

Mean	235,080.11
Standard Deviation	4,822,102.76
P25/Median/P75	149 / 197 / 269

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	8,655,519
Insertions	148,536
Mapped reads with at least one insertion	1.54%
Deletions	457,537
Mapped reads with at least one deletion	4.71%
Homopolymer indels	52.81%

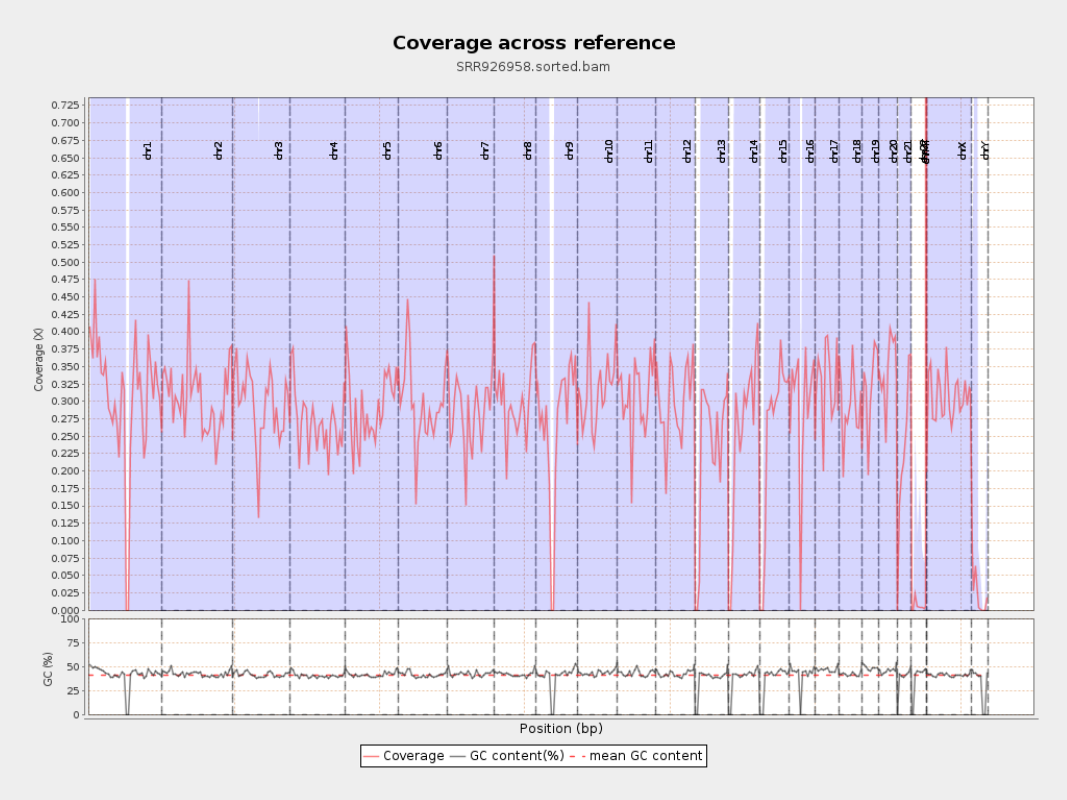
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

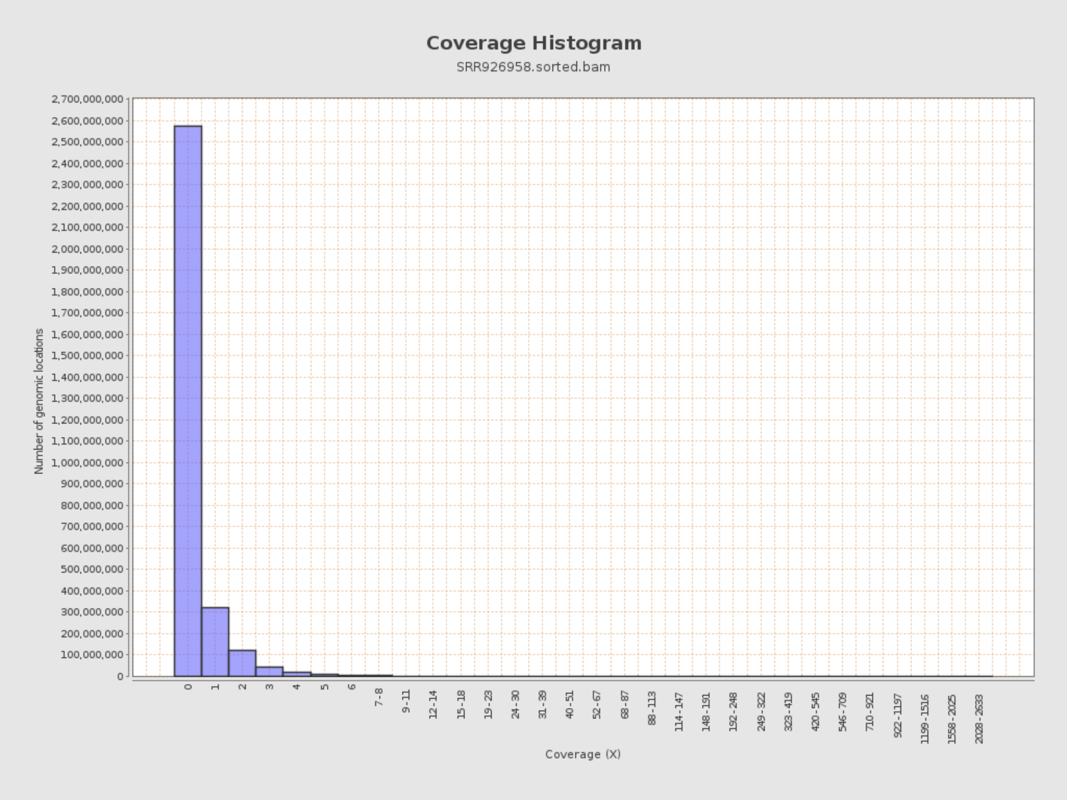
		bases	**coverage**	**deviation**
chr1	249250621	75705026	0.3037	1.5365
chr2	243199373	74578144	0.3067	2.4237
chr3	198022430	58224397	0.294	0.7914
chr4	191154276	51368573	0.2687	1.1041
chr5	180915260	52355245	0.2894	0.7768
chr6	171115067	50879288	0.2973	0.8132
chr7	159138663	45070356	0.2832	0.7909
chr8	146364022	43686791	0.2985	0.828
chr9	141213431	37158780	0.2631	0.8849
chr10	135534747	42616833	0.3144	2.3067
chr11	135006516	41829310	0.3098	0.9078
chr12	133851895	40261313	0.3008	0.9254
chr13	115169878	26255880	0.228	0.6862
chr14	107349540	27299852	0.2543	0.7497
chr15	102531392	26135162	0.2549	0.7463
chr16	90354753	26499638	0.2933	0.9784
chr17	81195210	26743536	0.3294	0.899
chr18	78077248	22852854	0.2927	0.9749
chr19	59128983	18805773	0.318	1.1031
chr20	63025520	21783446	0.3456	0.914
chr21	48129895	11072779	0.2301	0.9395
chr22	51304566	327317	0.0064	0.1275
chrMT	16571	1713373	103.3959	107.8198
chrX	155270560	47369780	0.3051	0.8093

chrY	59373566	1308914	0.022	0.7793

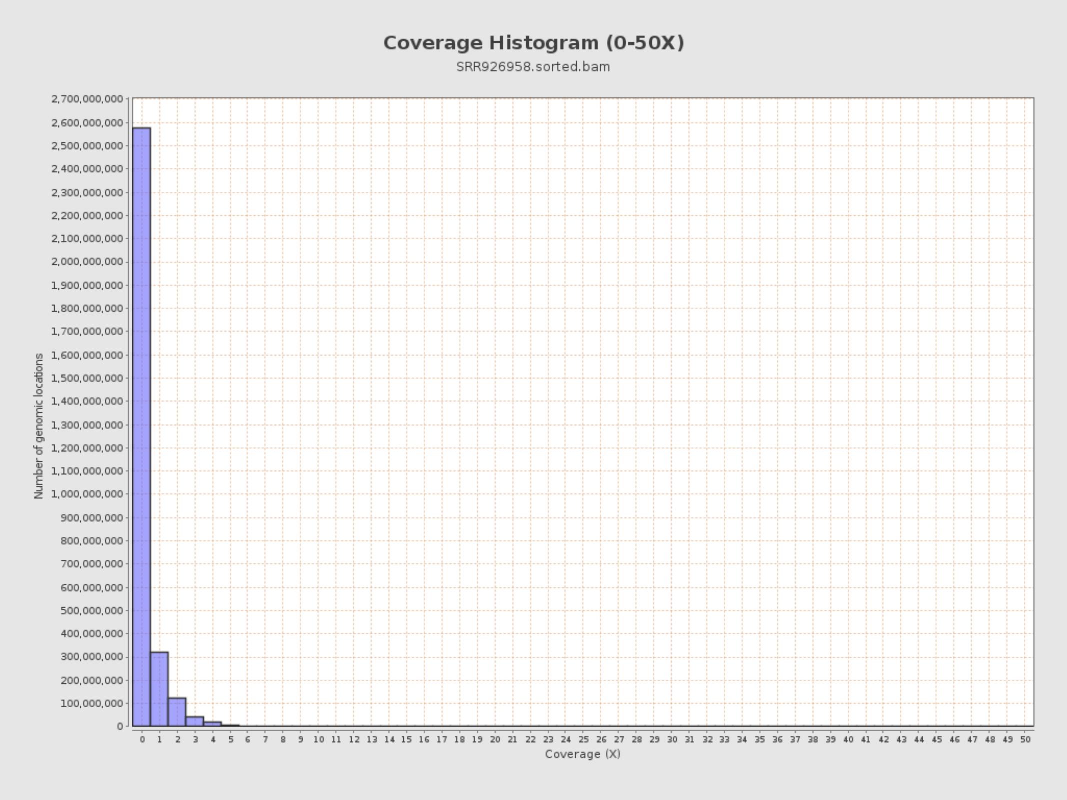
3. Results : Coverage across reference



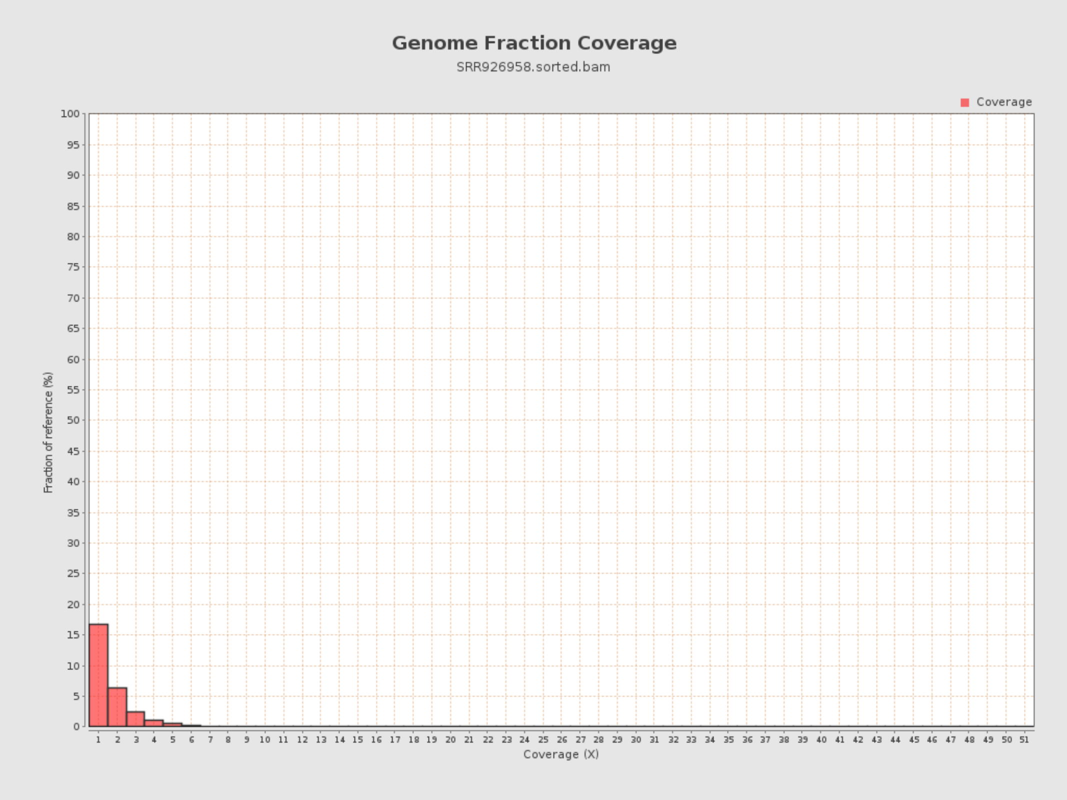
4. Results : Coverage Histogram



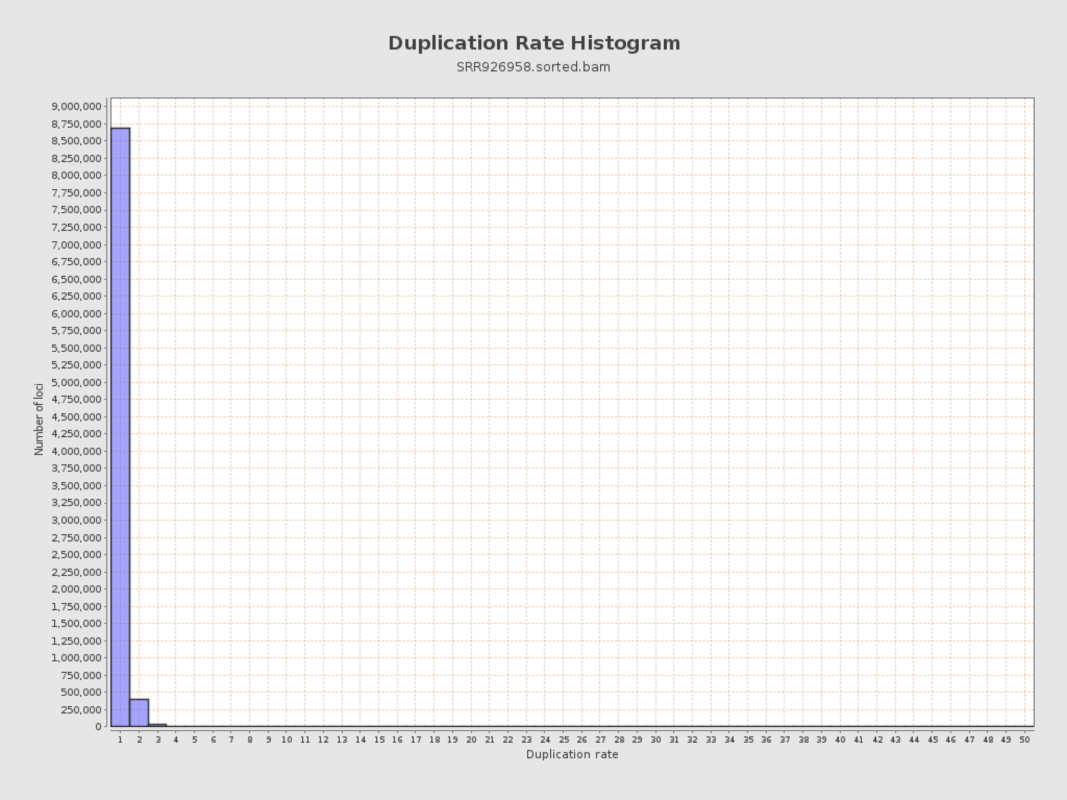
5. Results : Coverage Histogram (0-50X)



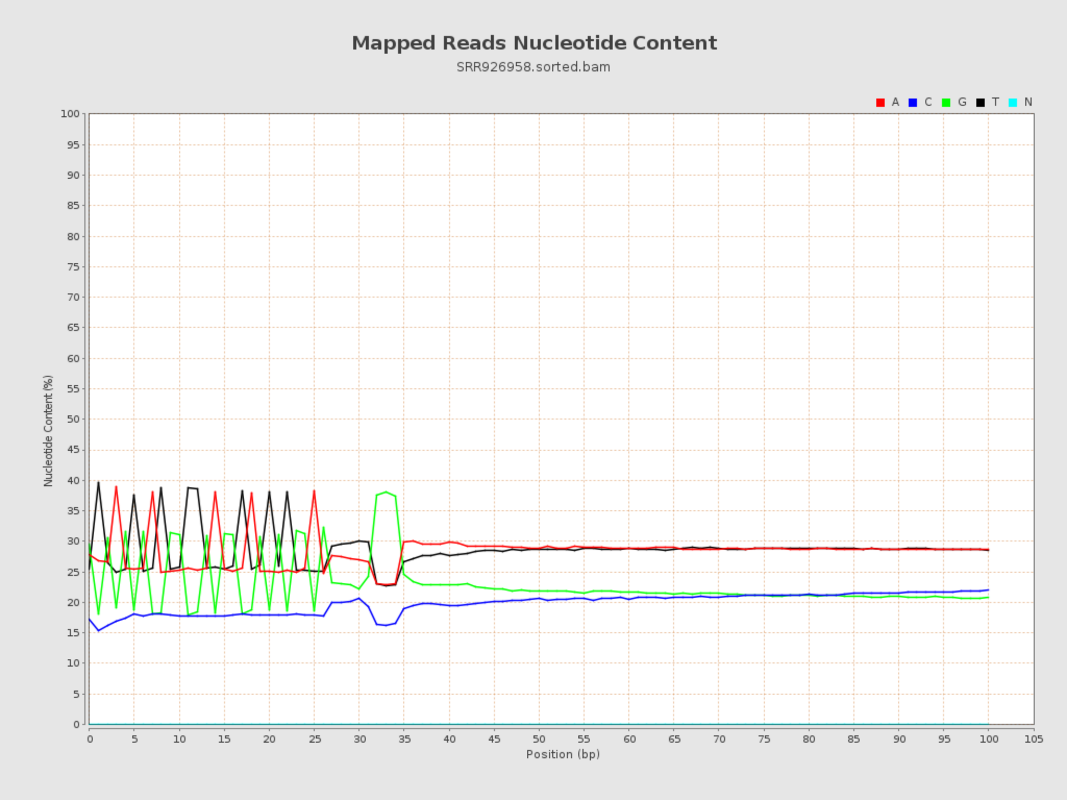
6. Results : Genome Fraction Coverage



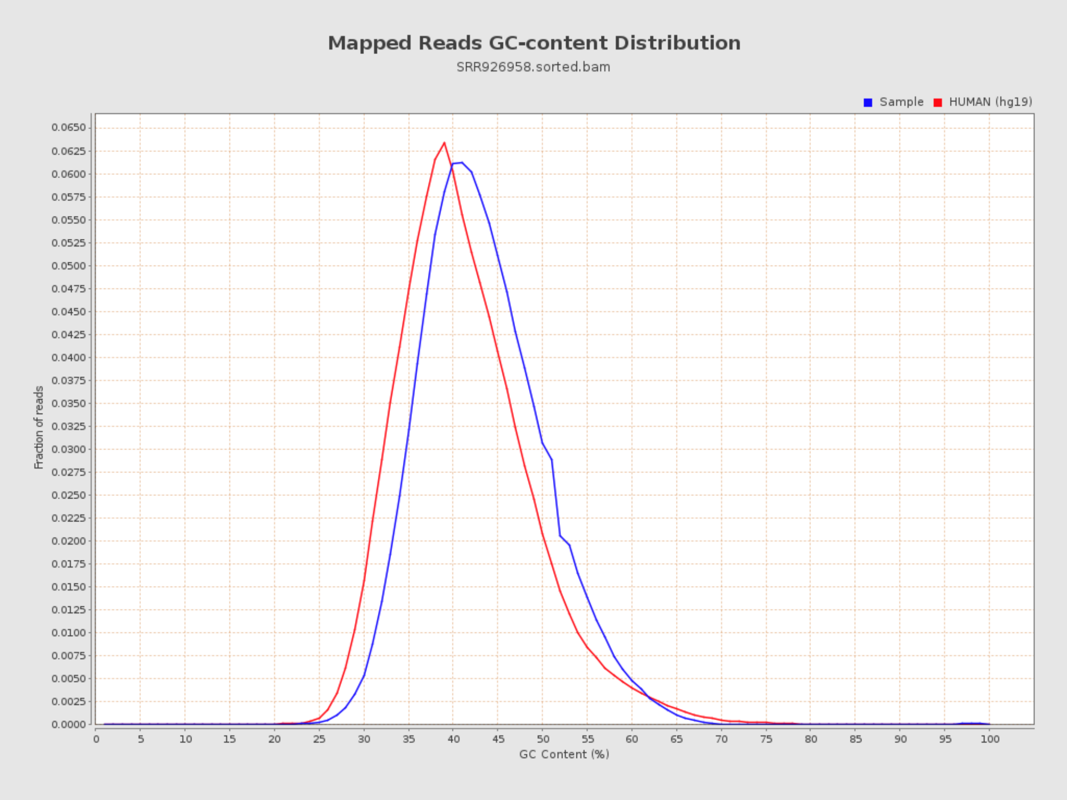
7. Results : Duplication Rate Histogram



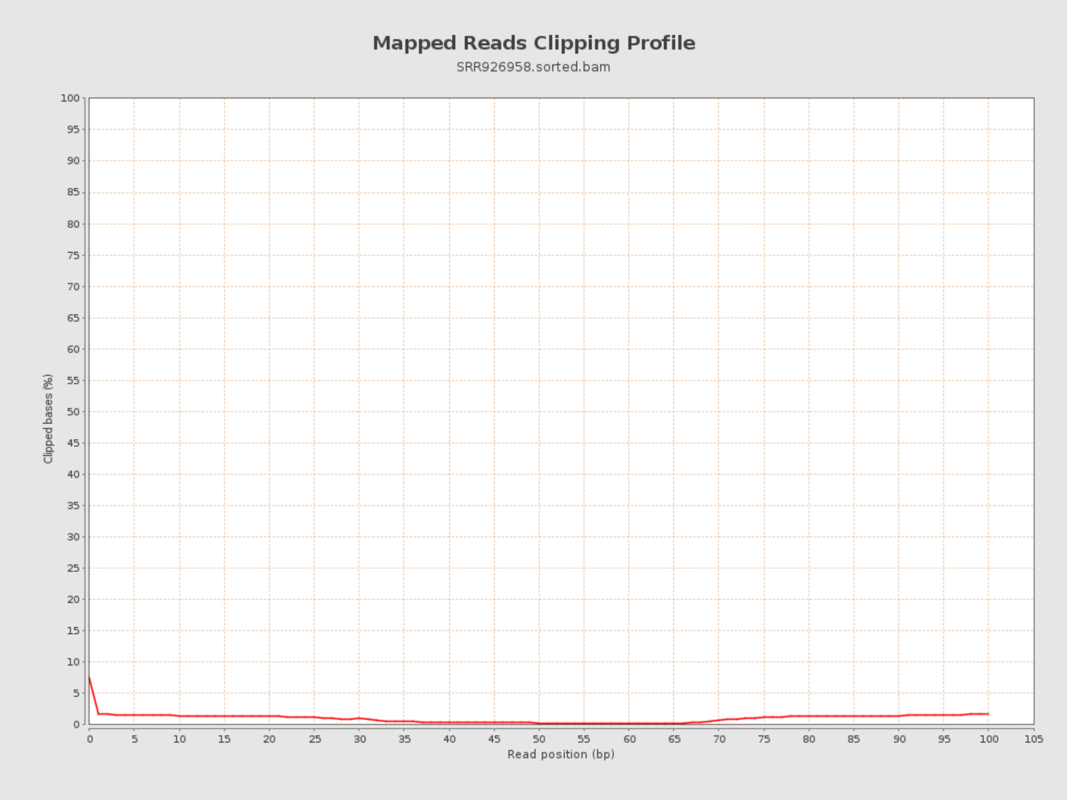
8. Results : Mapped Reads Nucleotide Content



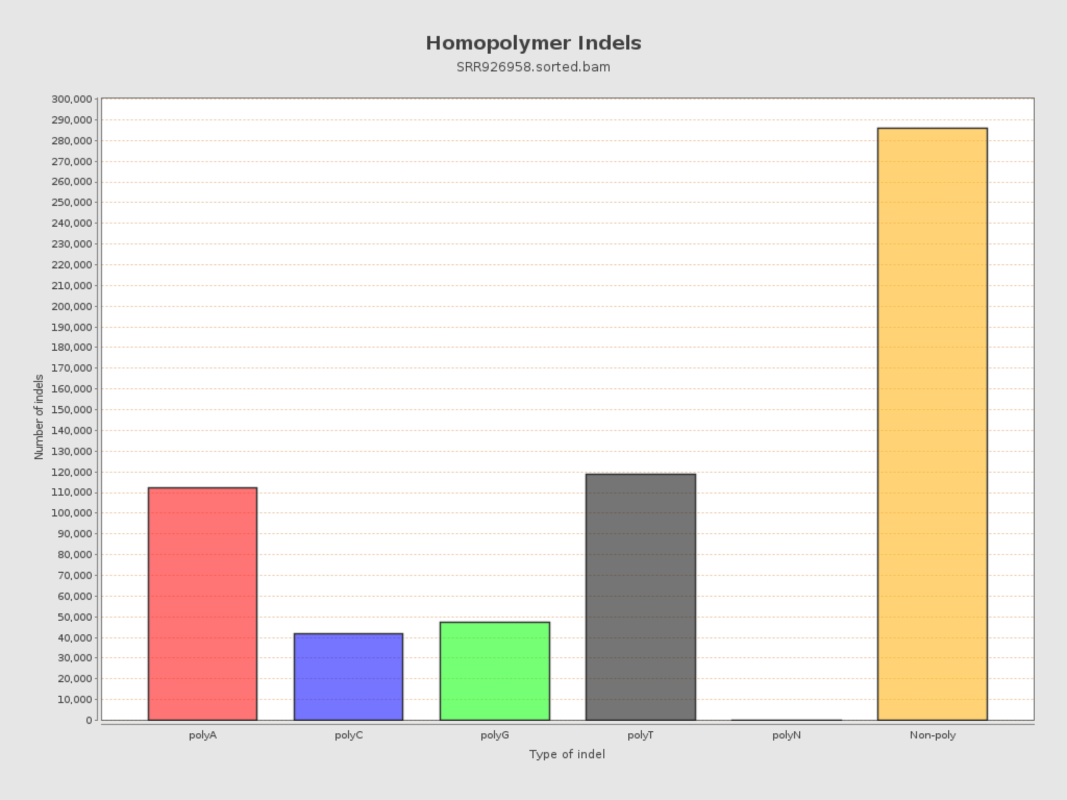
9. Results : Mapped Reads GC-content Distribution



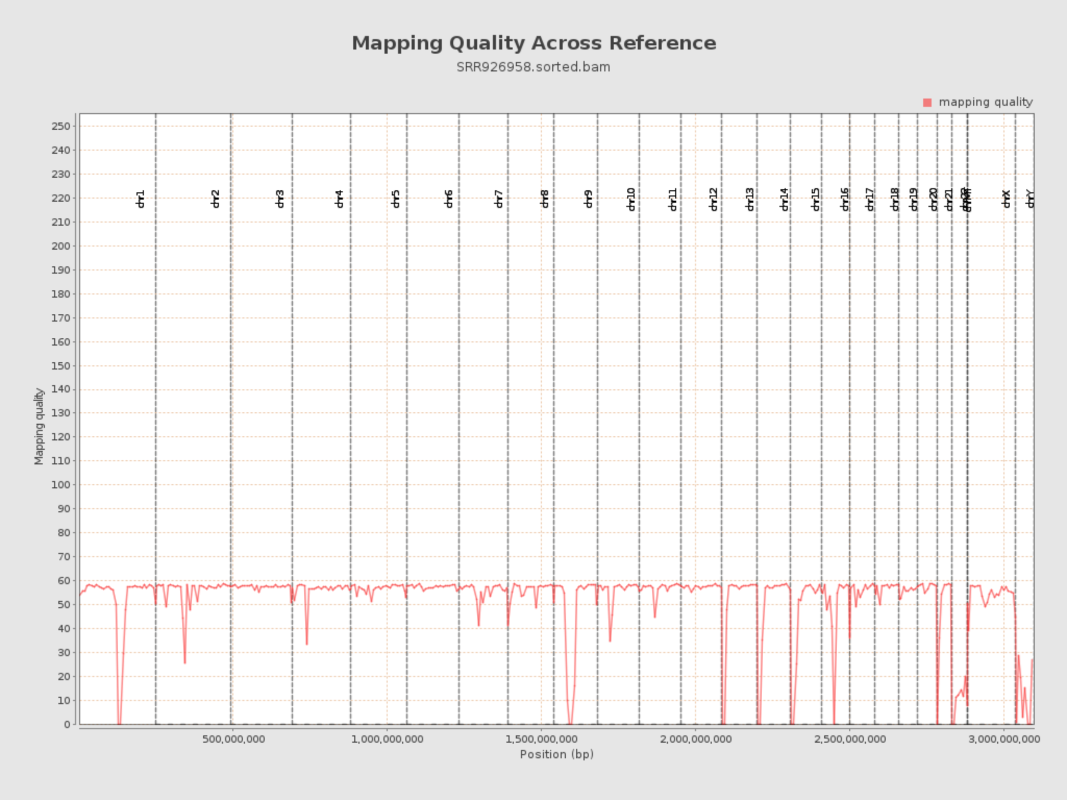
10. Results : Mapped Reads Clipping Profile



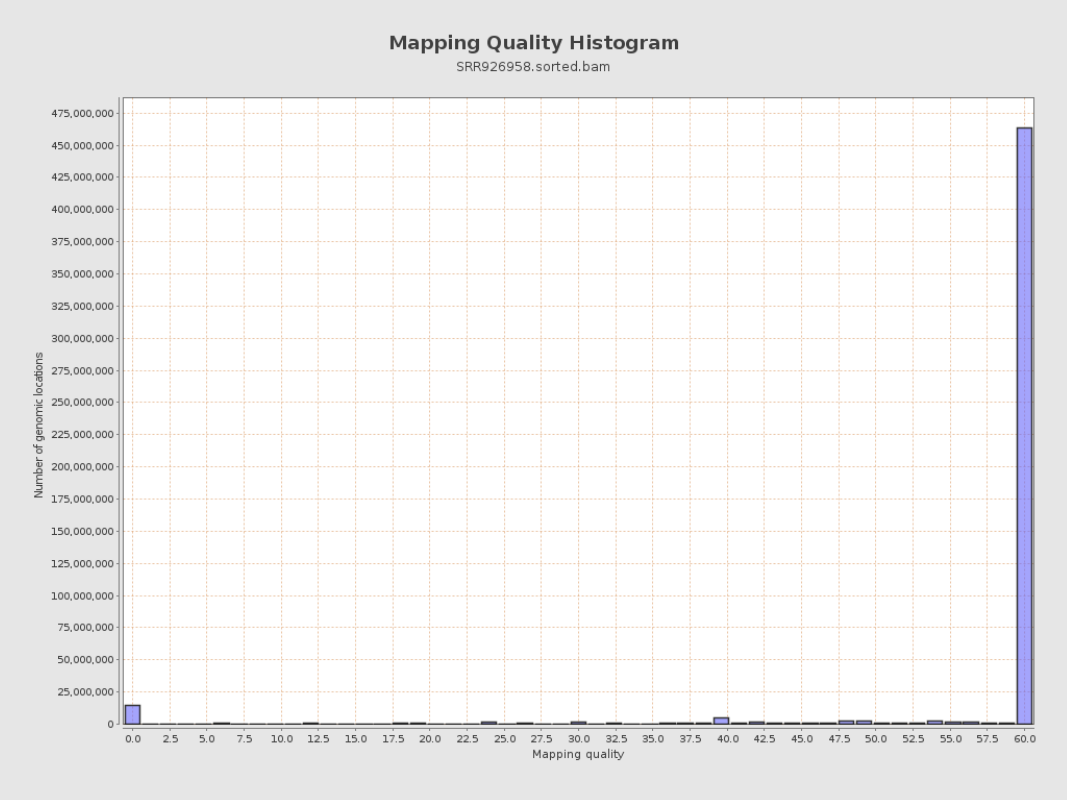
11. Results : Homopolymer Indels



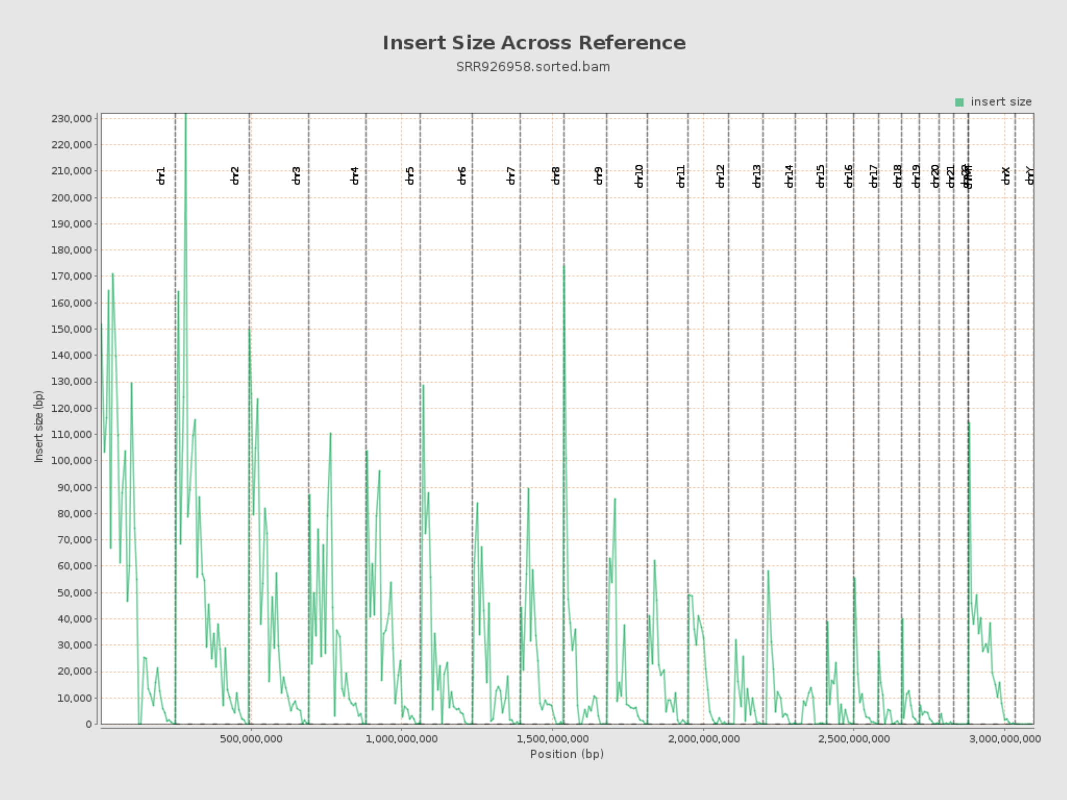
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram