Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 20:22:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926994.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_SRR926994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926994_1.fastq.gz SRR926994_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 20:22:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,517,494
Mapped reads	28,799,700 / 97.57%
Unmapped reads	717,794 / 2.43%
Mapped paired reads	28,799,700 / 97.57%
Mapped reads, first in pair	14,432,108 / 48.89%
Mapped reads, second in pair	14,367,592 / 48.67%
Mapped reads, both in pair	28,379,364 / 96.14%
Mapped reads, singletons	420,336 / 1.42%
Secondary alignments	0
Supplementary alignments	673,827 / 2.28%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	3,107,764 / 10.53%
Duplication rate	8.16%
Clipped reads	11,690,248 / 39.6%

2.2. ACGT Content

Number/percentage of A's	753,788,448 / 28.78%
Number/percentage of C's	498,414,068 / 19.03%
Number/percentage of T's	772,324,096 / 29.49%
Number/percentage of G's	593,848,578 / 22.68%
Number/percentage of N's	484,233 / 0.02%

GC Percentage	41.71%

2.3. Coverage

Mean	0.8466
Standard Deviation	3.5727

2.4. Mapping Quality

Mean Mapping Quality	53.06

2.5. Insert size

Mean	240,291.19
Standard Deviation	4,770,806.3
P25/Median/P75	149 / 195 / 262

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	25,252,051
Insertions	452,479
Mapped reads with at least one insertion	1.54%
Deletions	1,426,930
Mapped reads with at least one deletion	4.82%
Homopolymer indels	52.47%

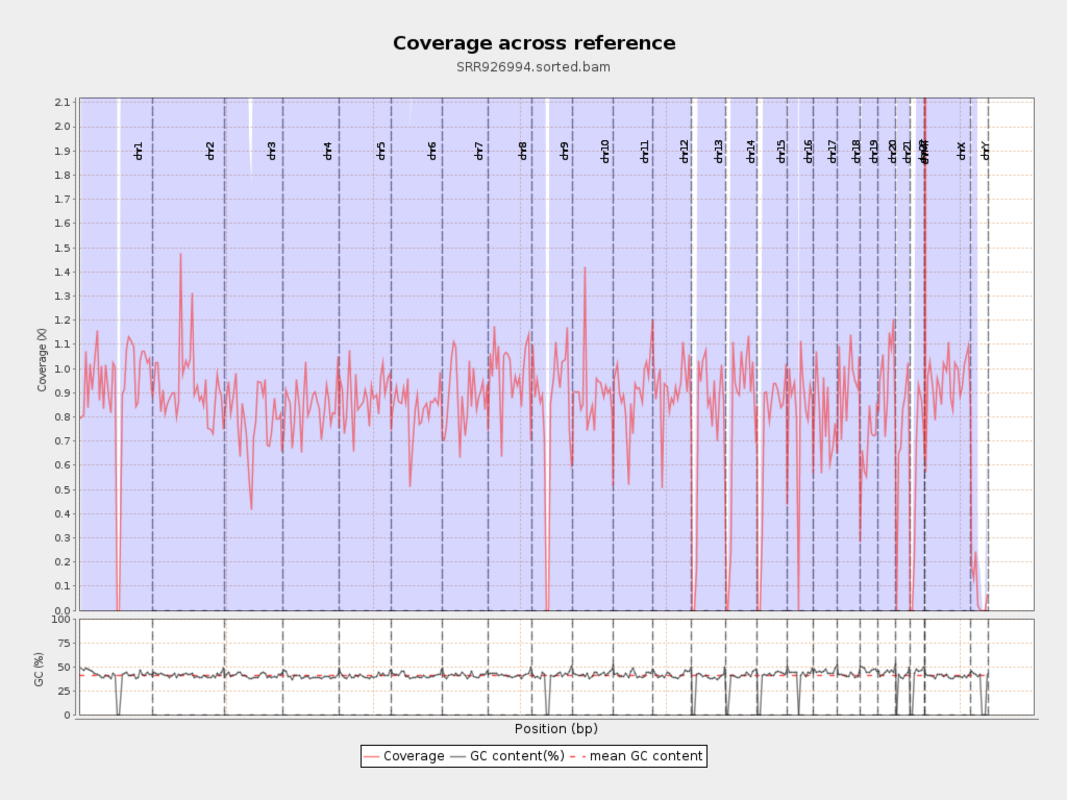
2.7. Chromosome stats

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

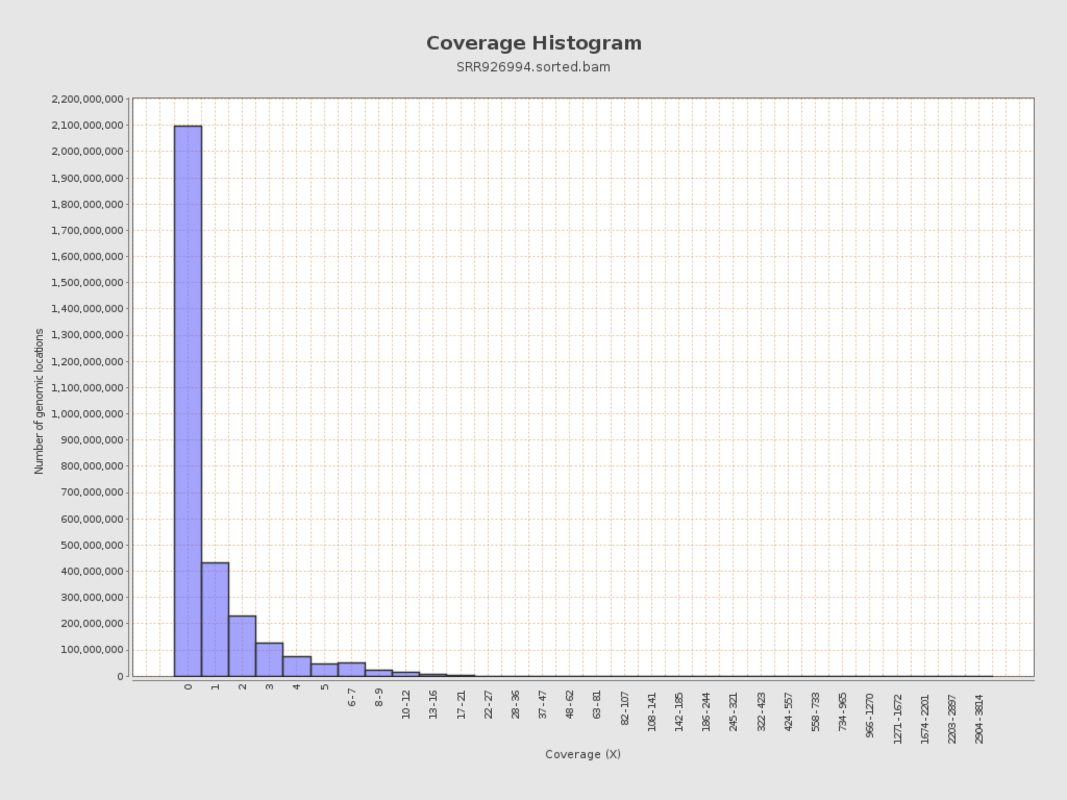
		bases	coverage	deviation
chr1	249250621	227190077	0.9115	4.3457
chr2	243199373	225023300	0.9253	5.2386
chr3	198022430	156648969	0.7911	1.7807
chr4	191154276	161343633	0.844	2.5103
chr5	180915260	160001353	0.8844	1.8374
chr6	171115067	143954446	0.8413	2.6059
chr7	159138663	140186957	0.8809	2.7794
chr8	146364022	144010086	0.9839	2.3759
chr9	141213431	116302649	0.8236	4.0483
chr10	135534747	122465018	0.9036	7.0291
chr11	135006516	120466262	0.8923	2.4121
chr12	133851895	122188334	0.9129	1.9443
chr13	115169878	87685895	0.7614	1.7243
chr14	107349540	85153843	0.7932	1.8428
chr15	102531392	74128577	0.723	1.7377
chr16	90354753	72990896	0.8078	3.9724
chr17	81195210	63878926	0.7867	2.3663
chr18	78077248	74668366	0.9563	3.8124
chr19	59128983	39911596	0.675	2.8808
chr20	63025520	61310538	0.9728	2.1022
chr21	48129895	34836431	0.7238	2.9351
chr22	51304566	27959247	0.545	1.565
chrMT	16571	7442344	449.1186	372.2427
chrX	155270560	146621319	0.9443	2.1759

chrY	59373566	4534302	0.0764	2.6474

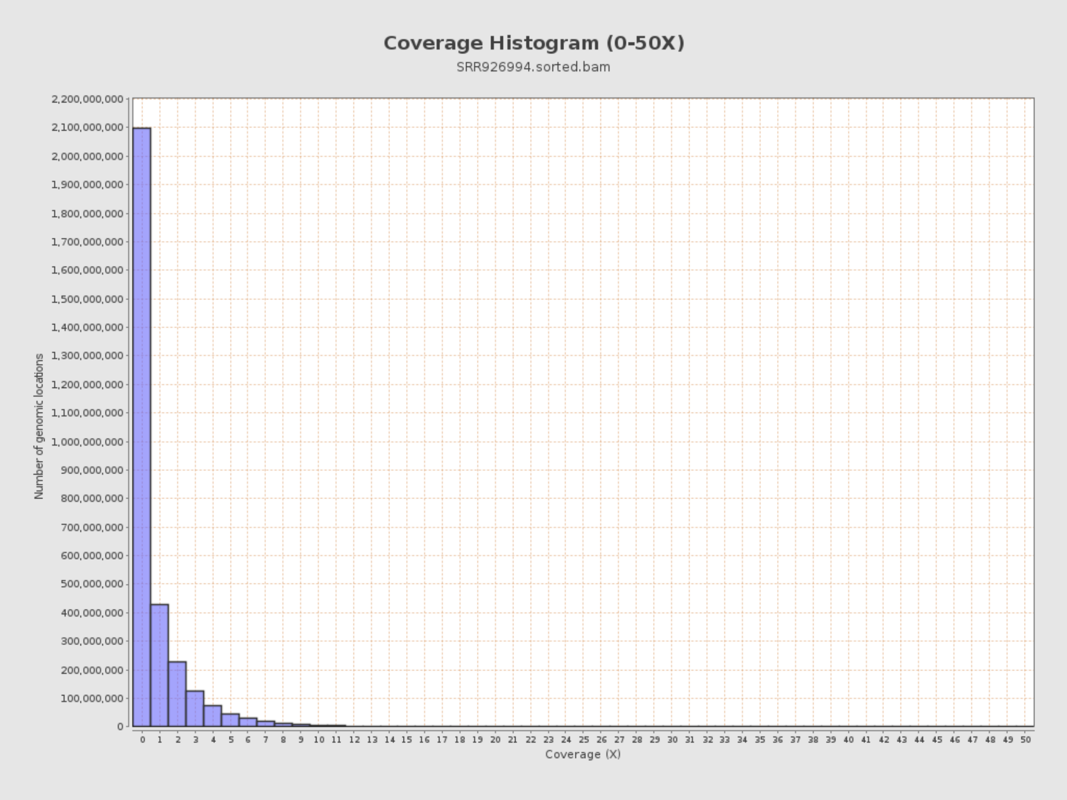
3. Results : Coverage across reference



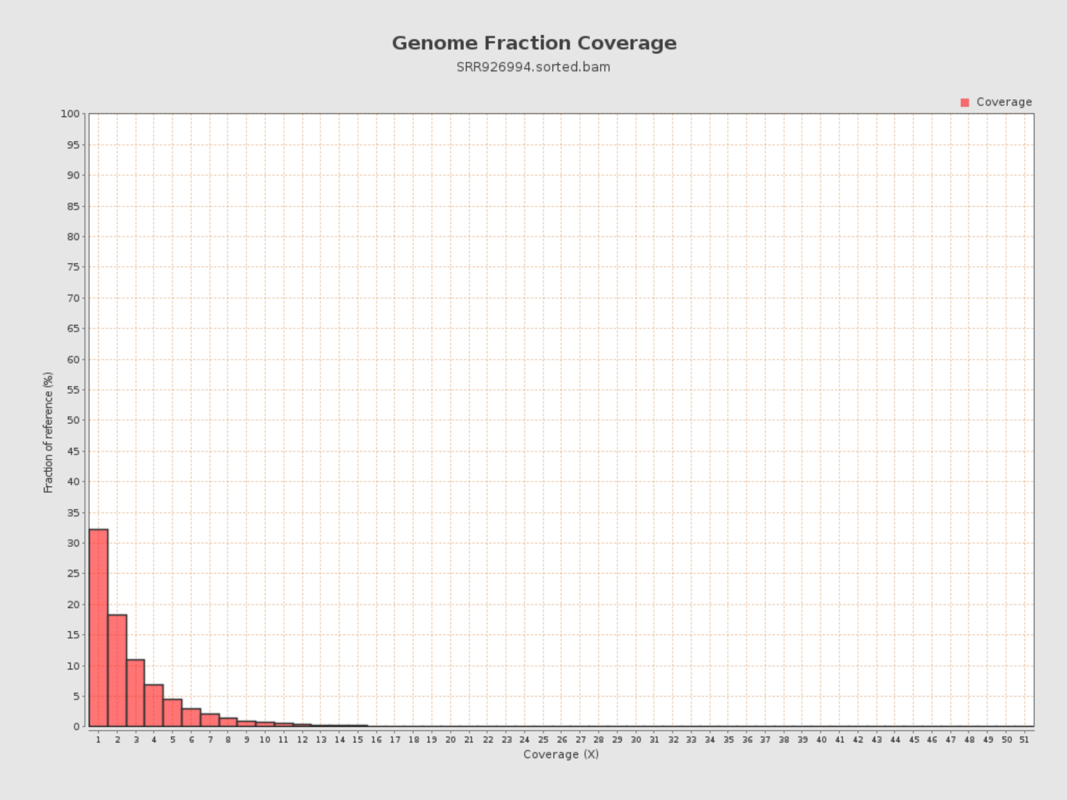
4. Results : Coverage Histogram



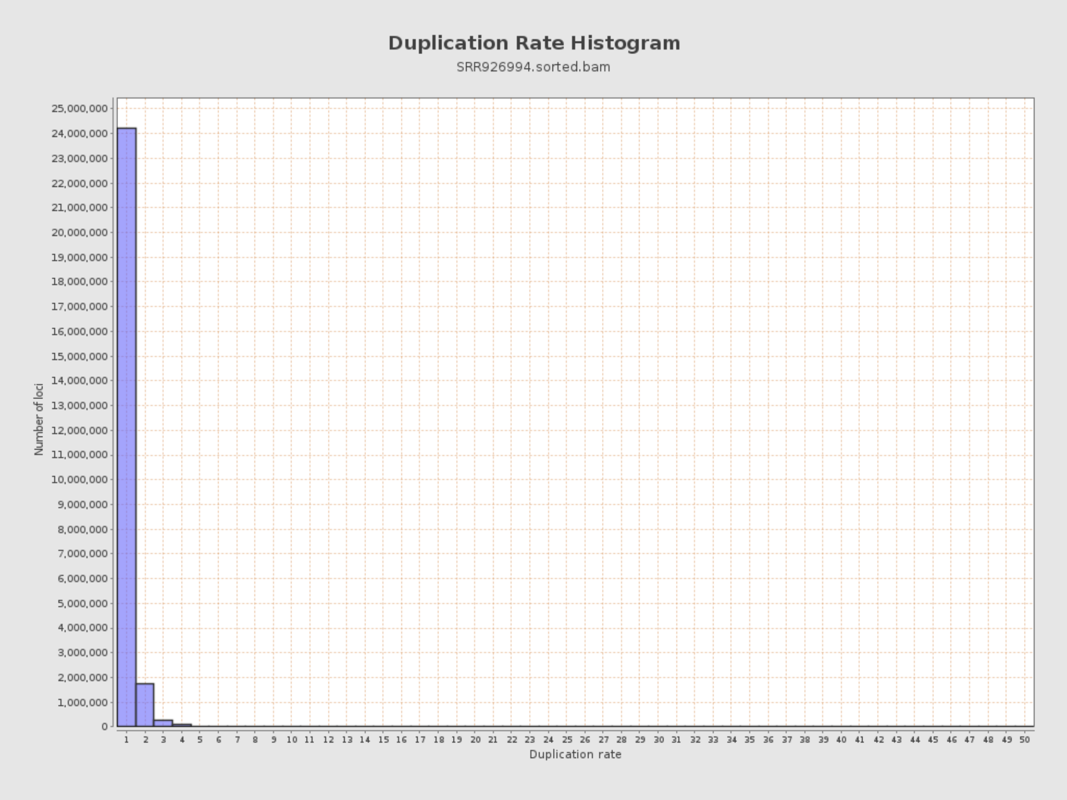
5. Results : Coverage Histogram (0-50X)



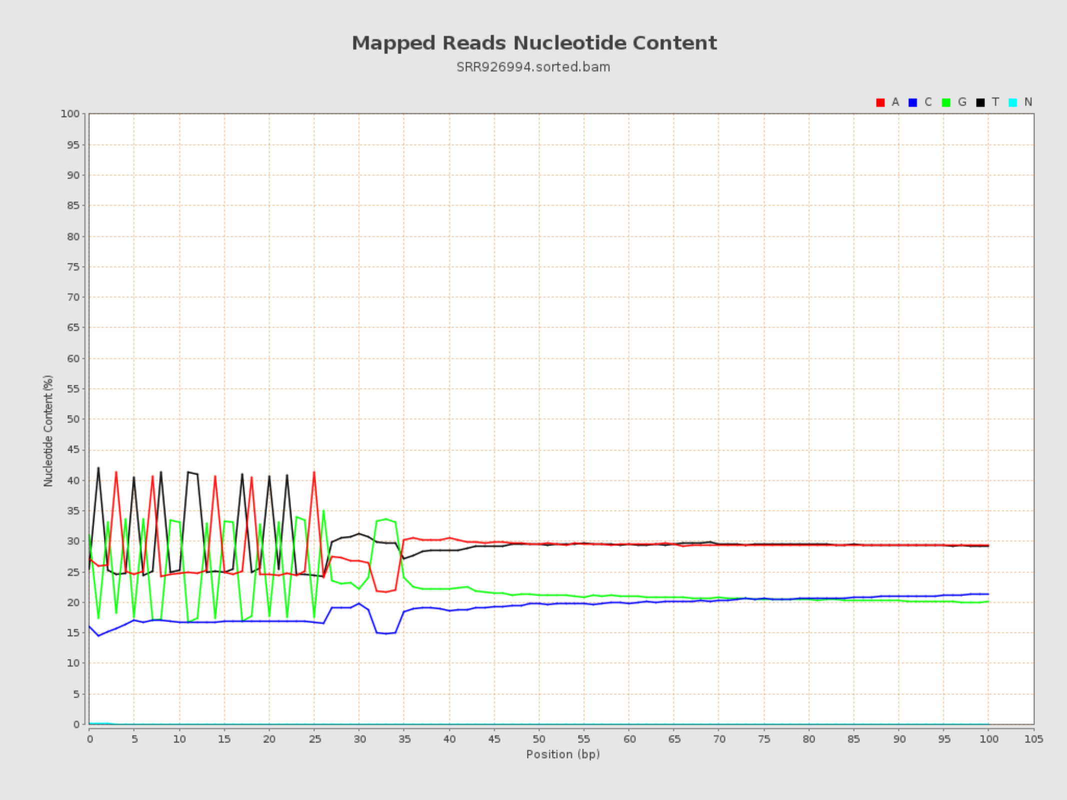
6. Results : Genome Fraction Coverage



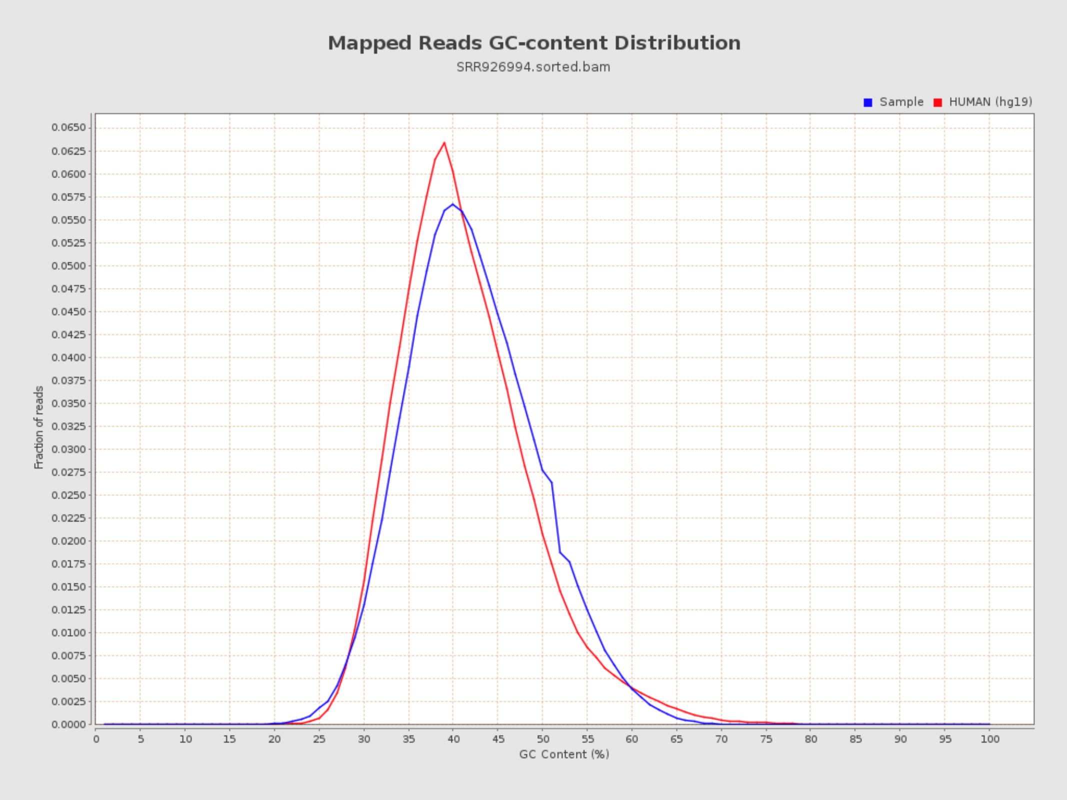
7. Results : Duplication Rate Histogram



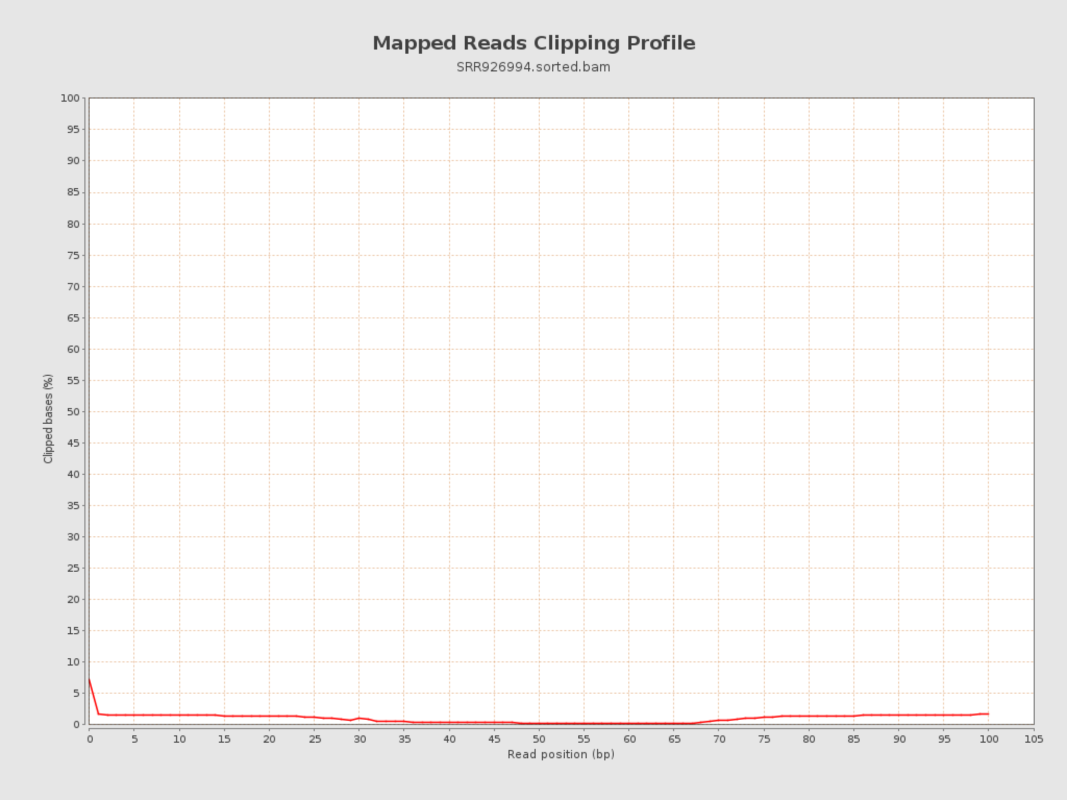
8. Results : Mapped Reads Nucleotide Content



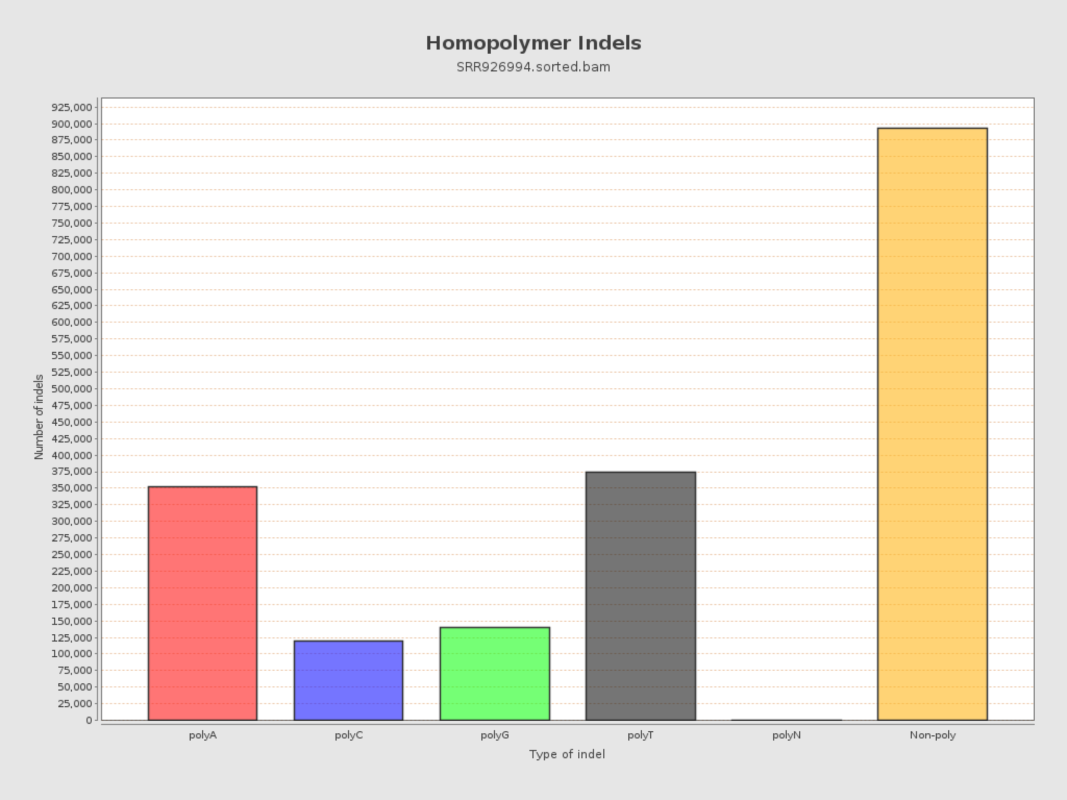
9. Results : Mapped Reads GC-content Distribution



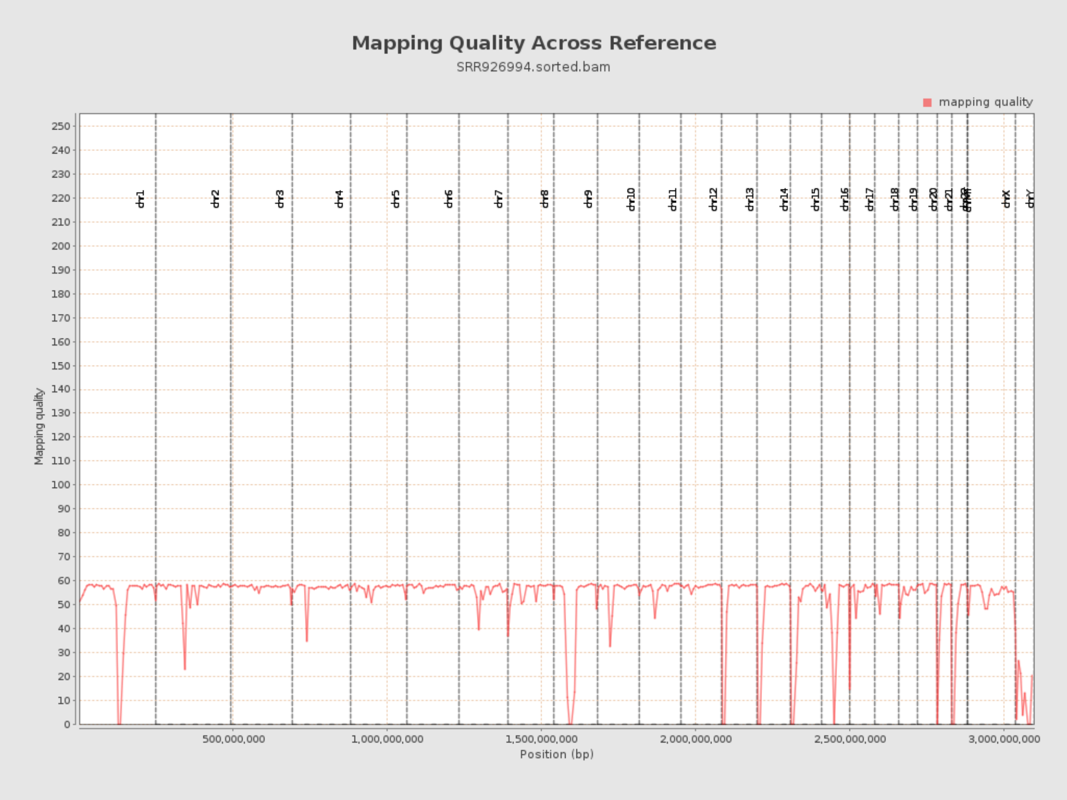
10. Results : Mapped Reads Clipping Profile



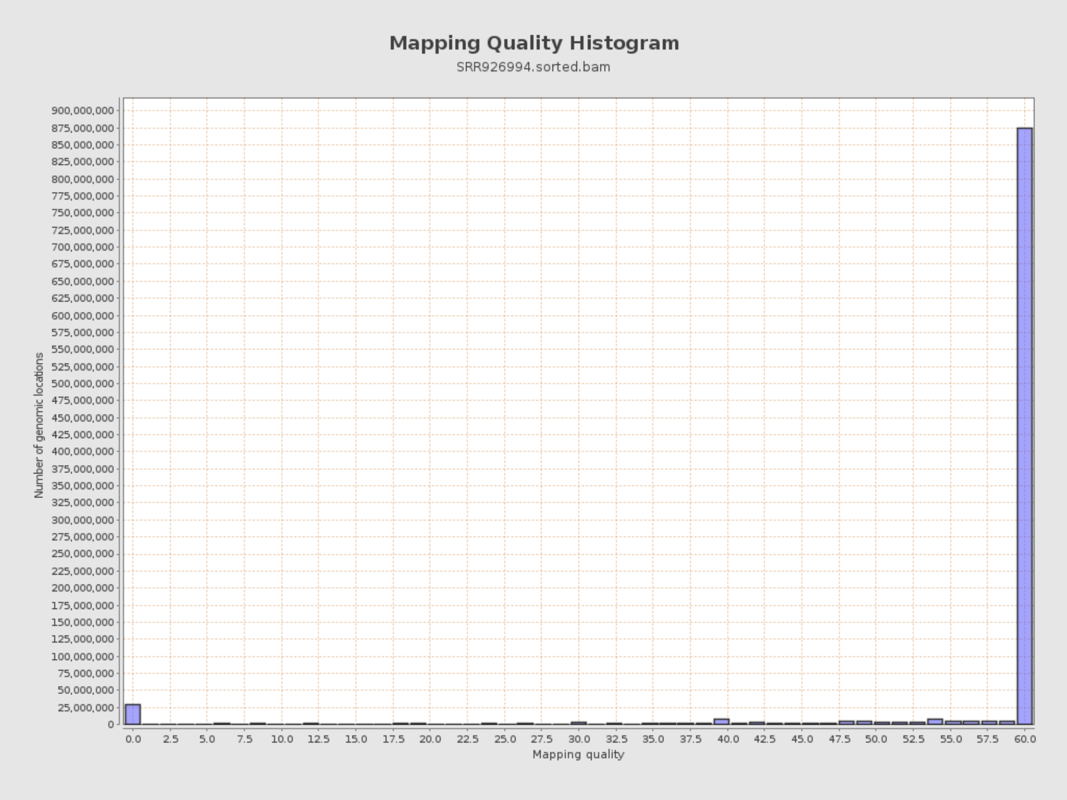
11. Results : Homopolymer Indels



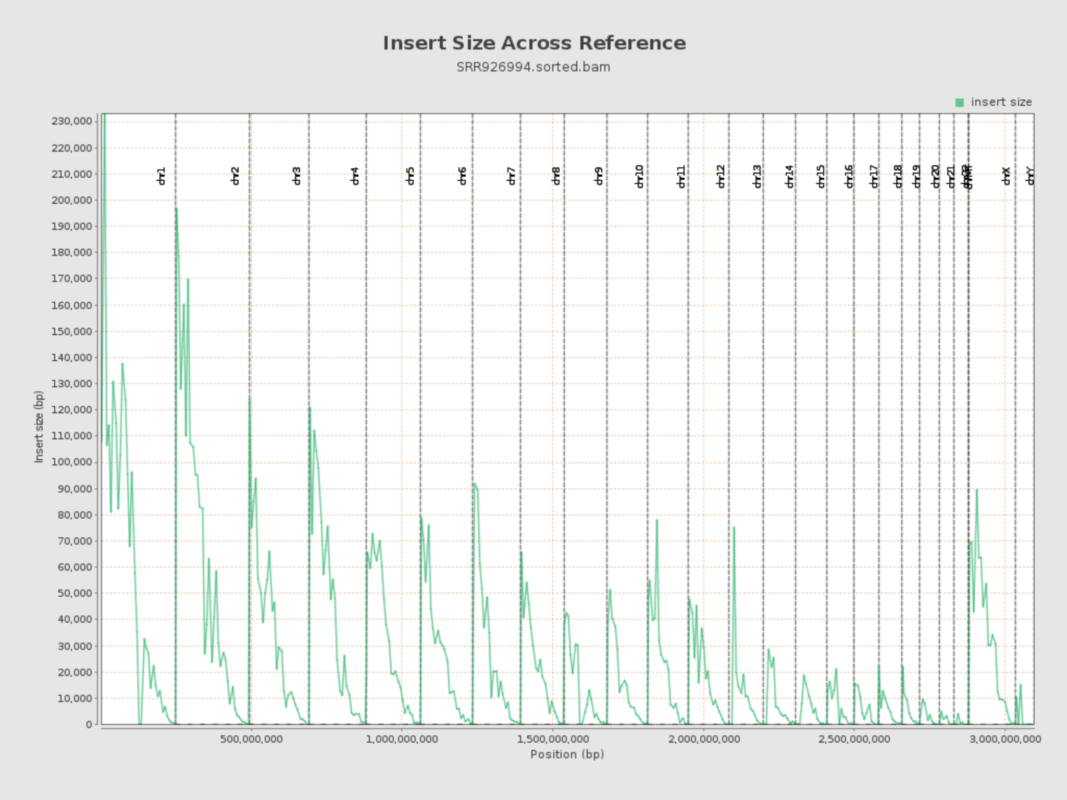
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram