Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:34:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975194.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_SRR975194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975194_1.fastq.gz SRR975194_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:34:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,279,236
Mapped reads	39,894,818 / 99.05%
Unmapped reads	384,418 / 0.95%
Mapped paired reads	39,894,818 / 99.05%
Mapped reads, first in pair	19,914,753 / 49.44%
Mapped reads, second in pair	19,980,065 / 49.6%
Mapped reads, both in pair	39,595,170 / 98.3%
Mapped reads, singletons	299,648 / 0.74%
Secondary alignments	0
Supplementary alignments	96,326 / 0.24%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	22,313,896 / 55.4%
Duplication rate	41.79%
Clipped reads	23,008,348 / 57.12%

2.2. ACGT Content

Number/percentage of A's	1,007,112,093 / 27.12%
Number/percentage of C's	809,931,215 / 21.81%
Number/percentage of T's	1,014,568,192 / 27.32%
Number/percentage of G's	882,263,693 / 23.75%
Number/percentage of N's	247,508 / 0.01%

GC Percentage	45.56%

2.3. Coverage

Mean	1.2002
Standard Deviation	17.2892

2.4. Mapping Quality

Mean Mapping Quality	55.64

2.5. Insert size

Mean	184,746.24
Standard Deviation	4,262,327.92
P25/Median/P75	189 / 234 / 286

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	22,255,389
Insertions	413,201
Mapped reads with at least one insertion	1.02%
Deletions	942,276
Mapped reads with at least one deletion	2.32%
Homopolymer indels	46.63%

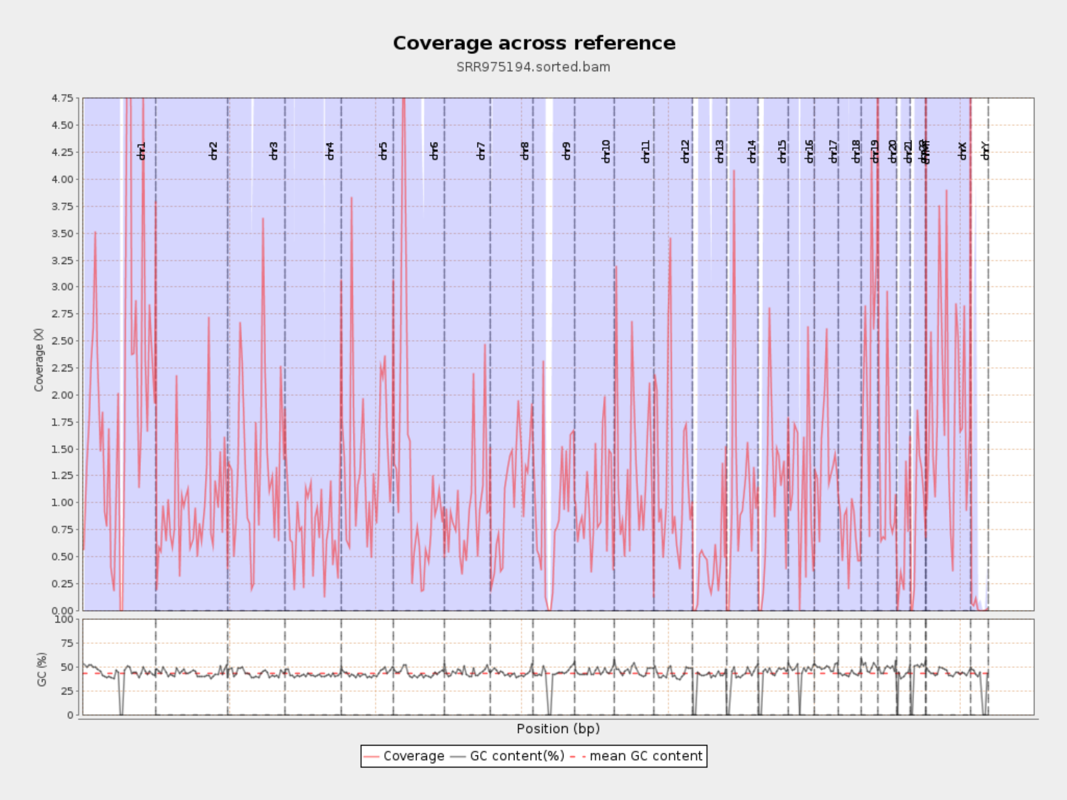
2.7. Chromosome stats

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

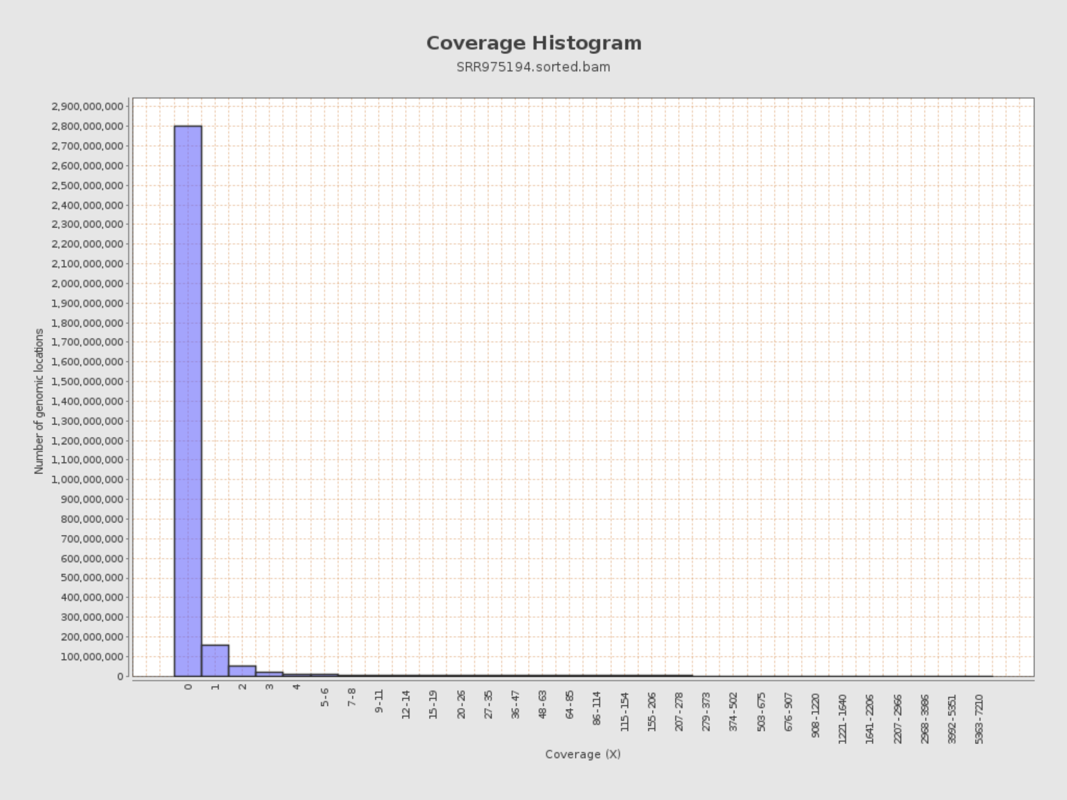
		bases	coverage	deviation
chr1	249250621	517678322	2.0769	26.2323
chr2	243199373	231107278	0.9503	13.2198
chr3	198022430	266429396	1.3455	17.8676
chr4	191154276	147997543	0.7742	12.7694
chr5	180915260	263609445	1.4571	19.4096
chr6	171115067	213742365	1.2491	18.4147
chr7	159138663	150111146	0.9433	14.712
chr8	146364022	160372875	1.0957	16.3724
chr9	141213431	123180686	0.8723	12.6027
chr10	135534747	137346999	1.0134	14.4559
chr11	135006516	175582292	1.3005	15.9124
chr12	133851895	175866593	1.3139	17.1141
chr13	115169878	48735442	0.4232	9.6484
chr14	107349540	122117092	1.1376	16.6969
chr15	102531392	105162515	1.0257	13.6256
chr16	90354753	101945039	1.1283	14.9002
chr17	81195210	118038187	1.4538	15.6945
chr18	78077248	56084693	0.7183	11.5131
chr19	59128983	150487724	2.5451	28.6872
chr20	63025520	71037460	1.1271	16.4492
chr21	48129895	29646668	0.616	9.807
chr22	51304566	46986534	0.9158	12.6288
chrMT	16571	89492	5.4005	10.4846
chrX	155270560	300386300	1.9346	25.8138

chrY	59373566	1773153	0.0299	1.7506

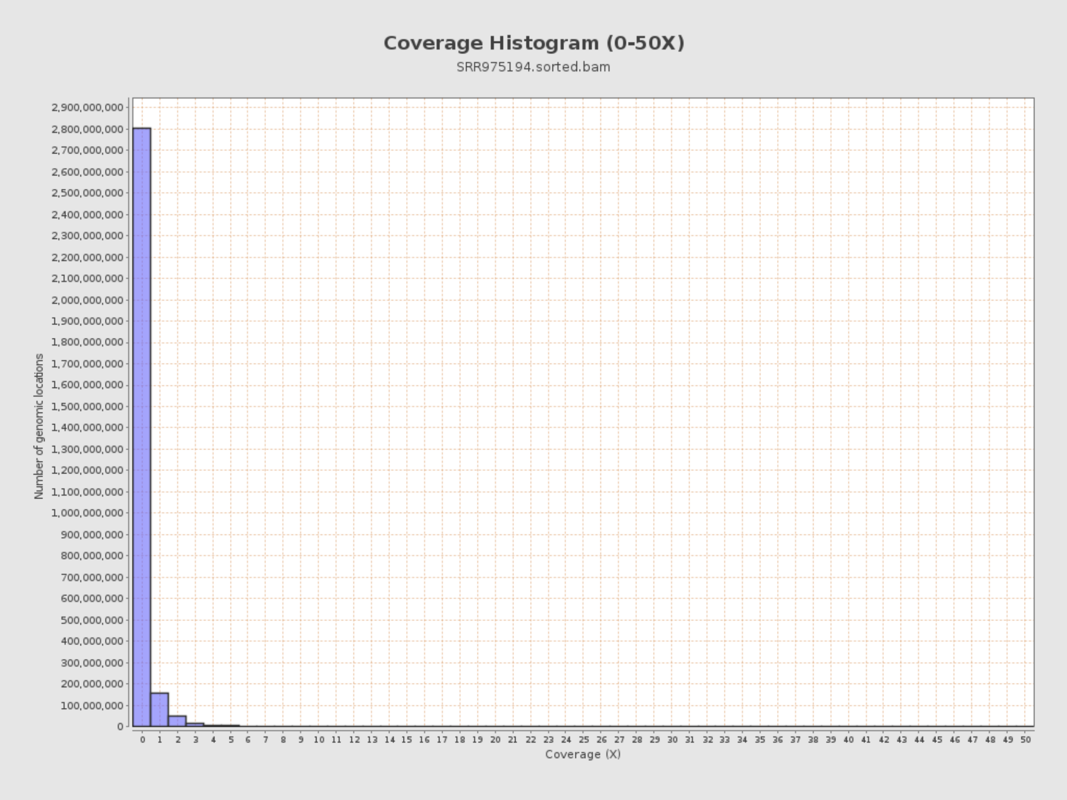
3. Results : Coverage across reference



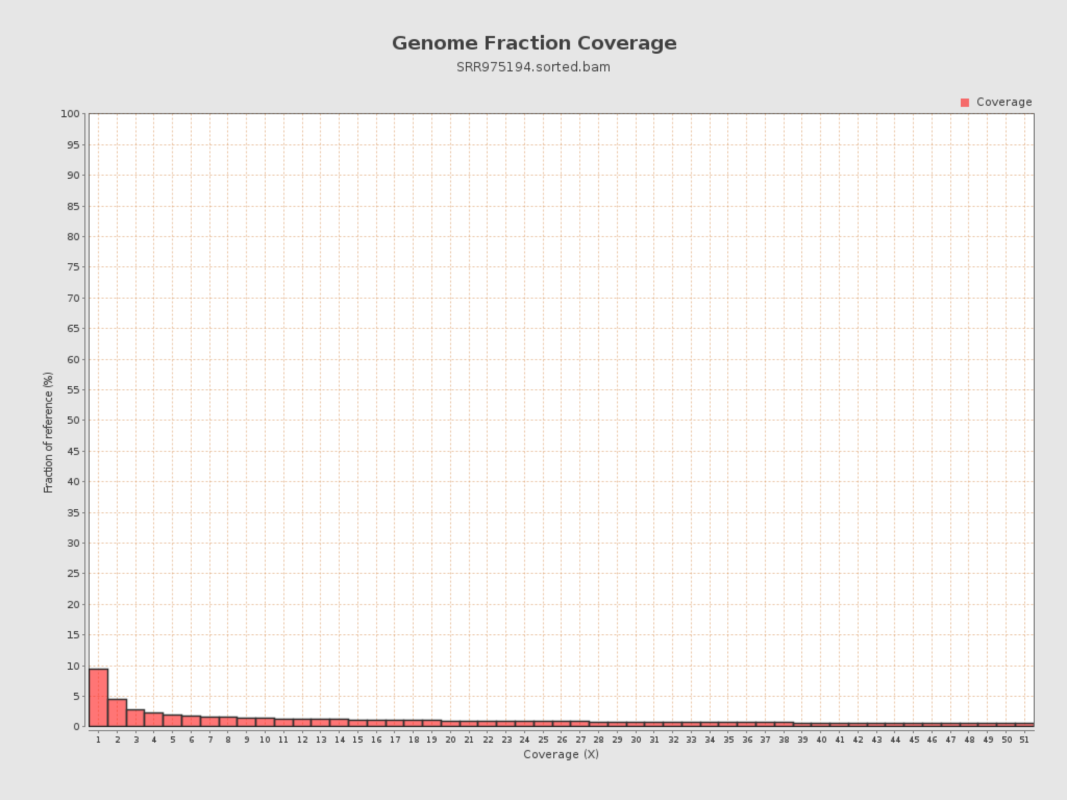
4. Results : Coverage Histogram



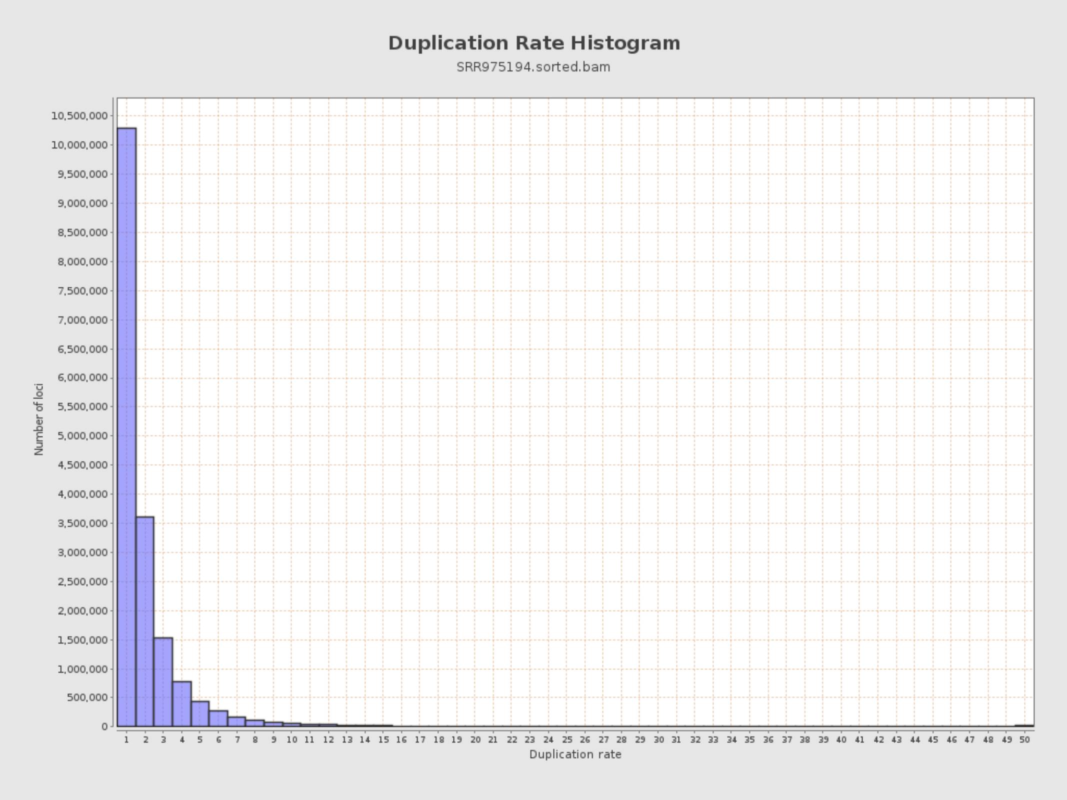
5. Results : Coverage Histogram (0-50X)



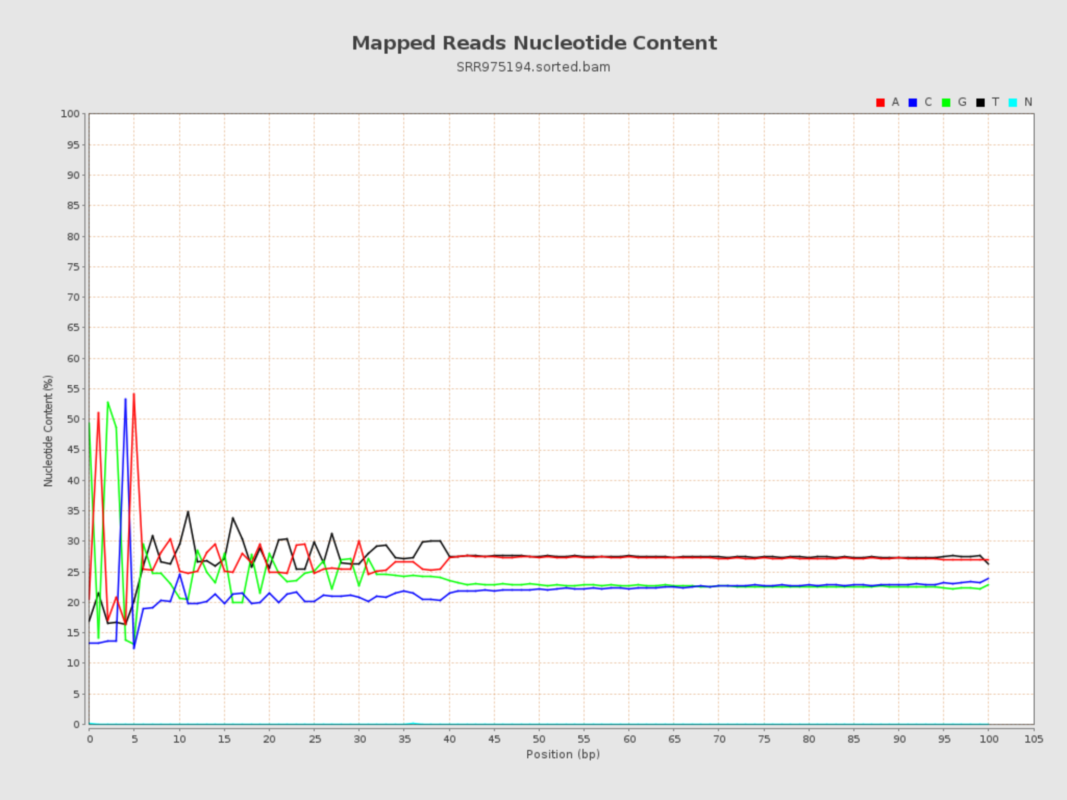
6. Results : Genome Fraction Coverage



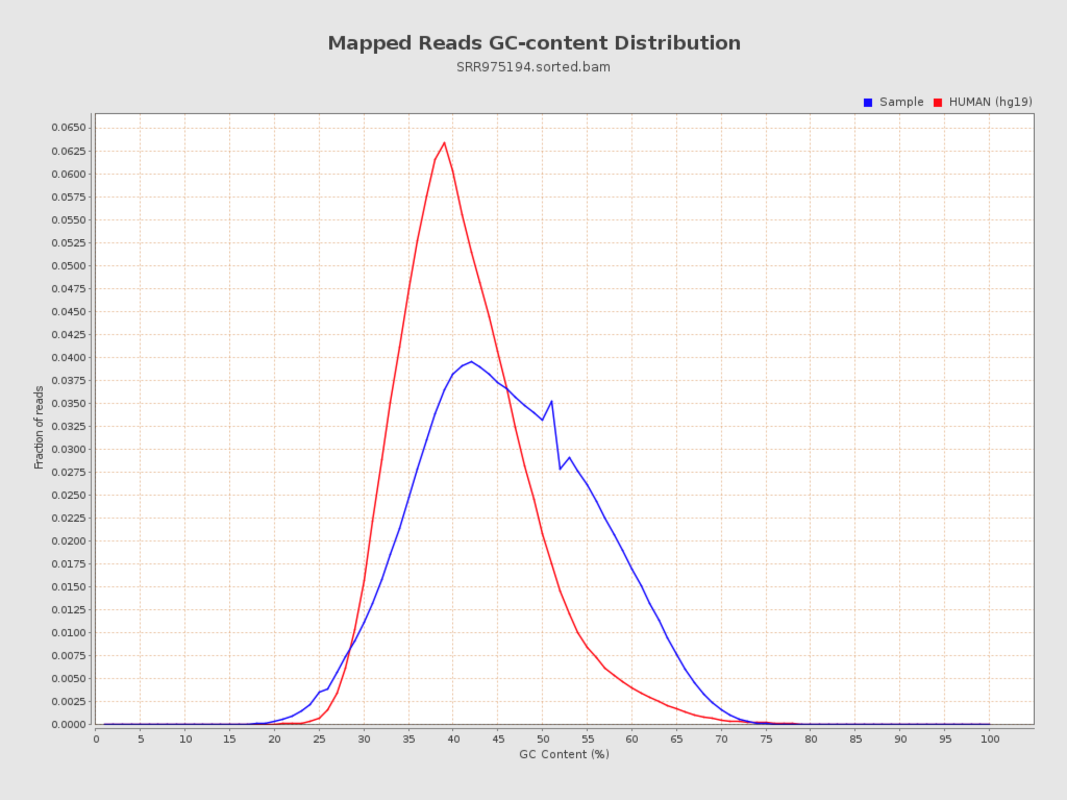
7. Results : Duplication Rate Histogram



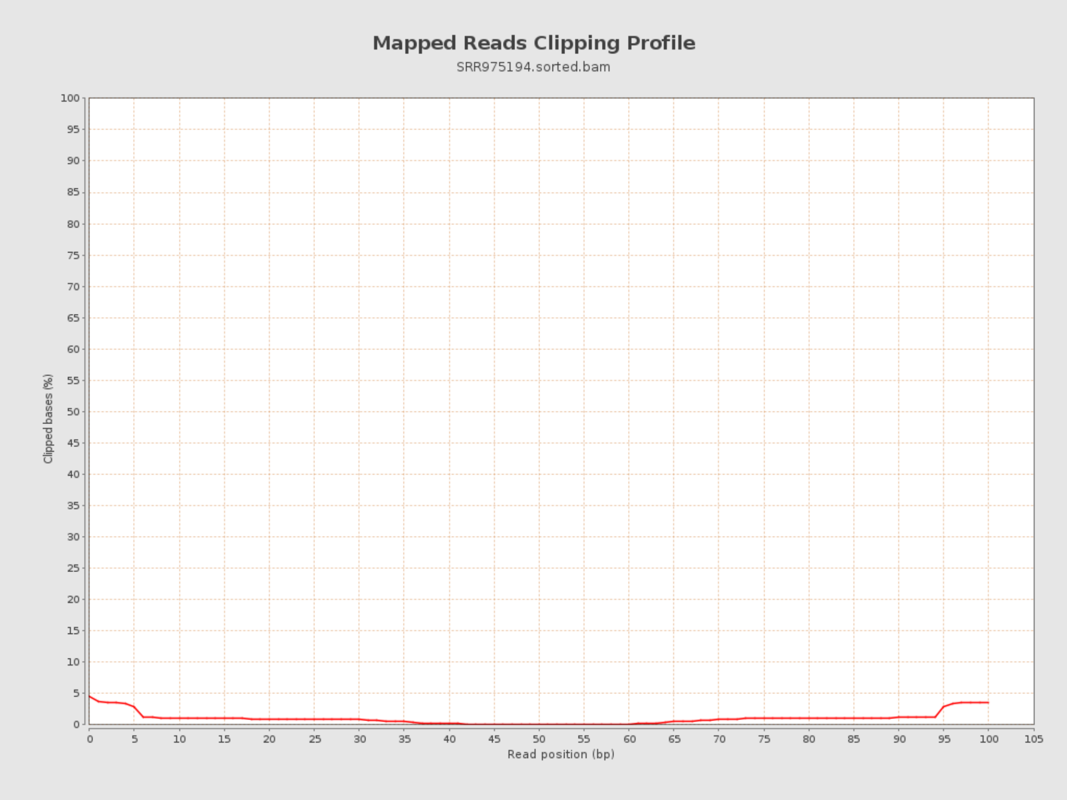
8. Results : Mapped Reads Nucleotide Content



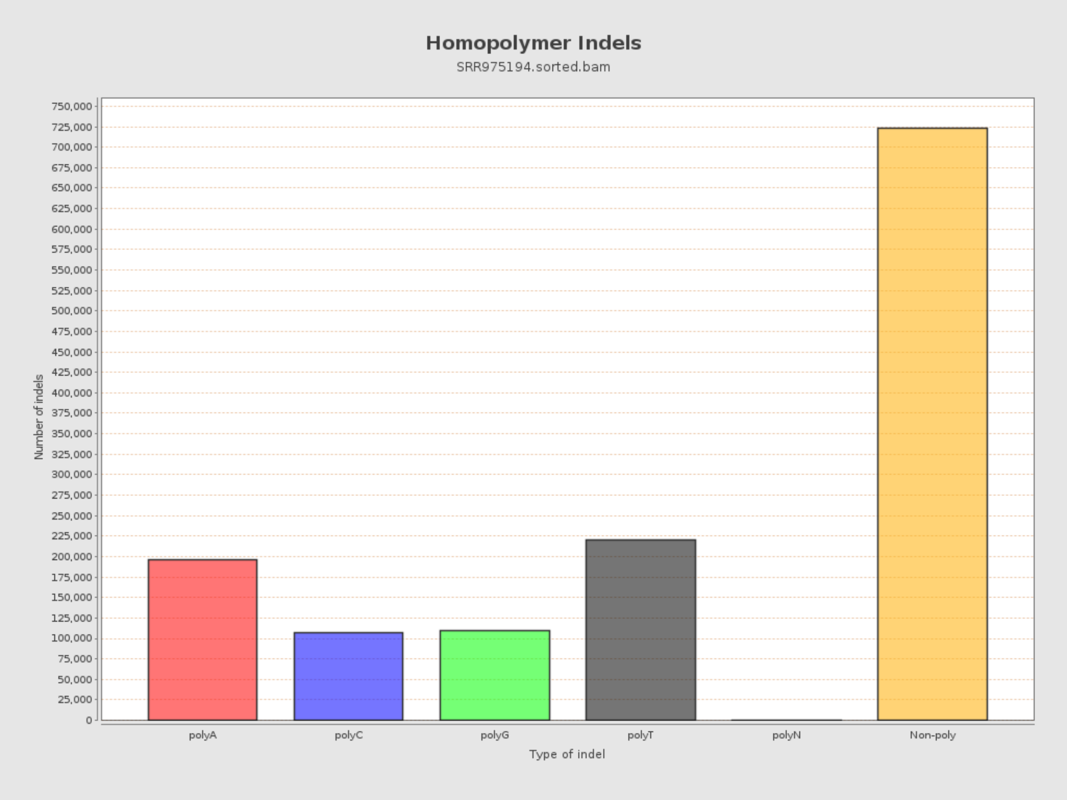
9. Results : Mapped Reads GC-content Distribution



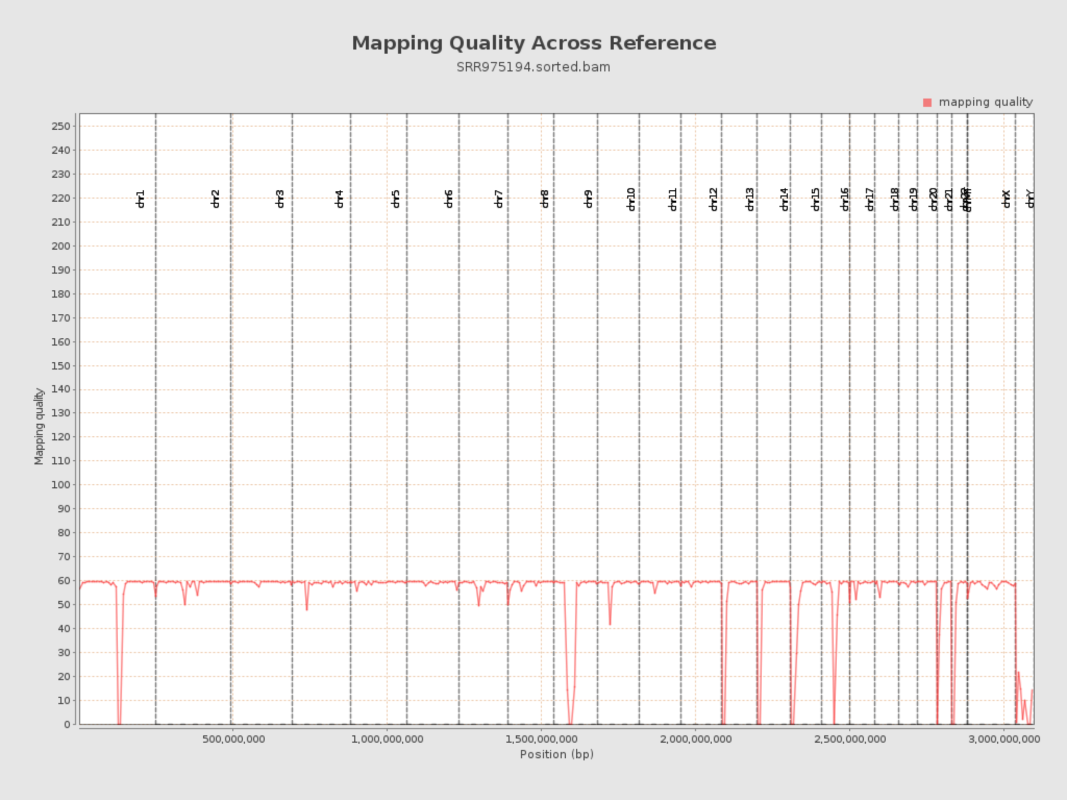
10. Results : Mapped Reads Clipping Profile



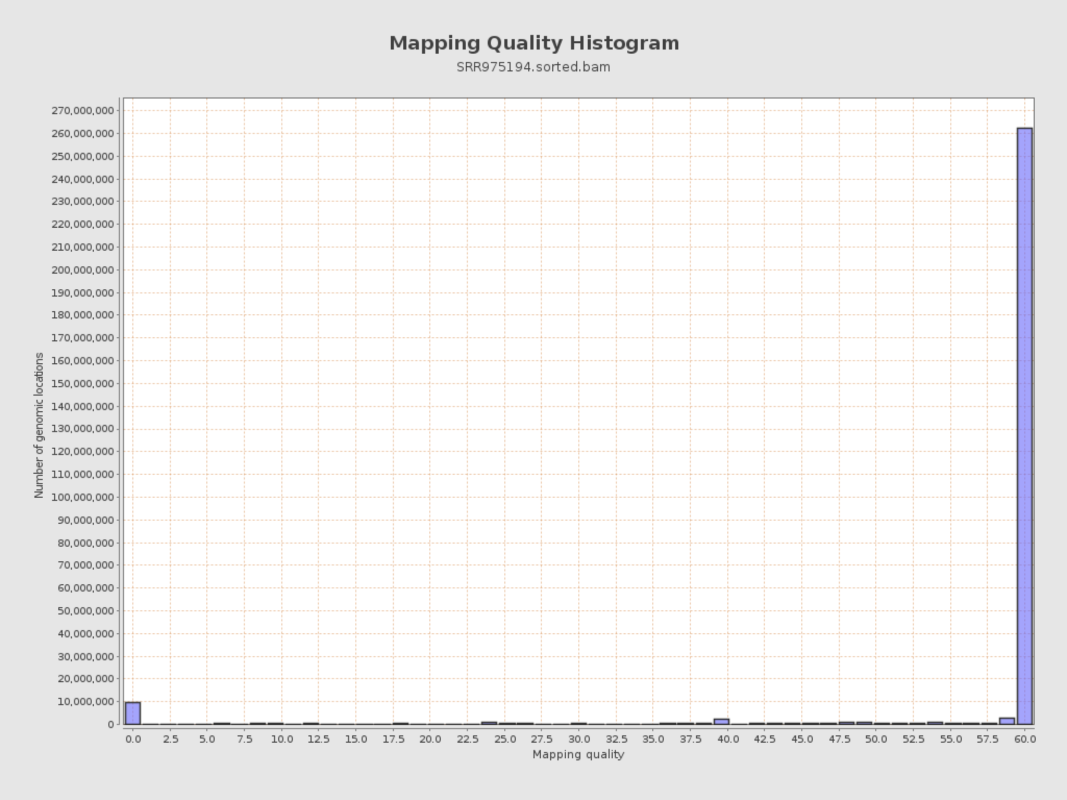
11. Results : Homopolymer Indels



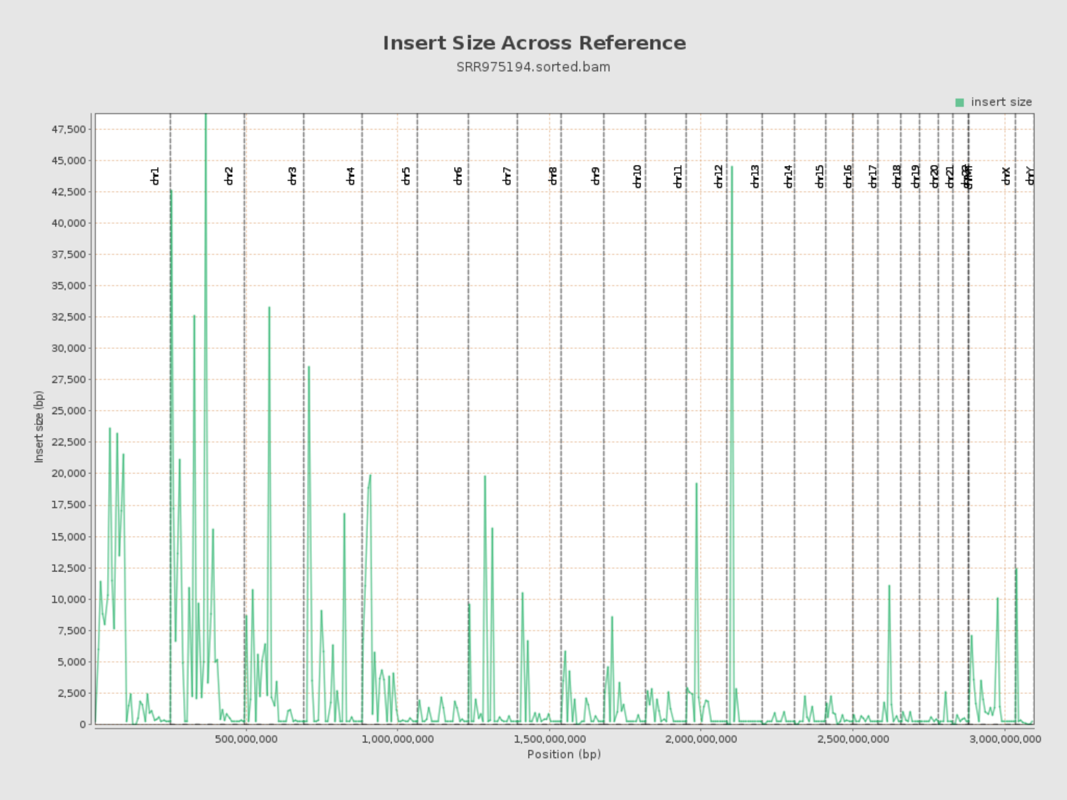
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram