Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 20:31:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779092.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_SRR1779092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779092_1.fastq.gz SRR1779092_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 20:31:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,873,340
Mapped reads	49,083,838 / 96.48%
Unmapped reads	1,789,502 / 3.52%
Mapped paired reads	49,083,838 / 96.48%
Mapped reads, first in pair	24,864,429 / 48.88%
Mapped reads, second in pair	24,219,409 / 47.61%
Mapped reads, both in pair	48,277,766 / 94.9%
Mapped reads, singletons	806,072 / 1.58%
Secondary alignments	0
Supplementary alignments	236,842 / 0.47%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	2,441,341 / 4.8%
Duplication rate	4.39%
Clipped reads	2,621,816 / 5.15%

2.2. ACGT Content

Number/percentage of A's	1,506,579,803 / 30.71%
Number/percentage of C's	940,077,854 / 19.17%
Number/percentage of T's	1,500,038,676 / 30.58%
Number/percentage of G's	956,833,085 / 19.51%
Number/percentage of N's	1,620,471 / 0.03%

GC Percentage	38.67%

2.3. Coverage

Mean	1.5849
Standard Deviation	3.9757

2.4. Mapping Quality

Mean Mapping Quality	53.42

2.5. Insert size

Mean	61,122.37
Standard Deviation	2,406,685.99
P25/Median/P75	220 / 290 / 367

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	24,030,906
Insertions	420,031
Mapped reads with at least one insertion	0.84%
Deletions	513,956
Mapped reads with at least one deletion	1.03%
Homopolymer indels	47.41%

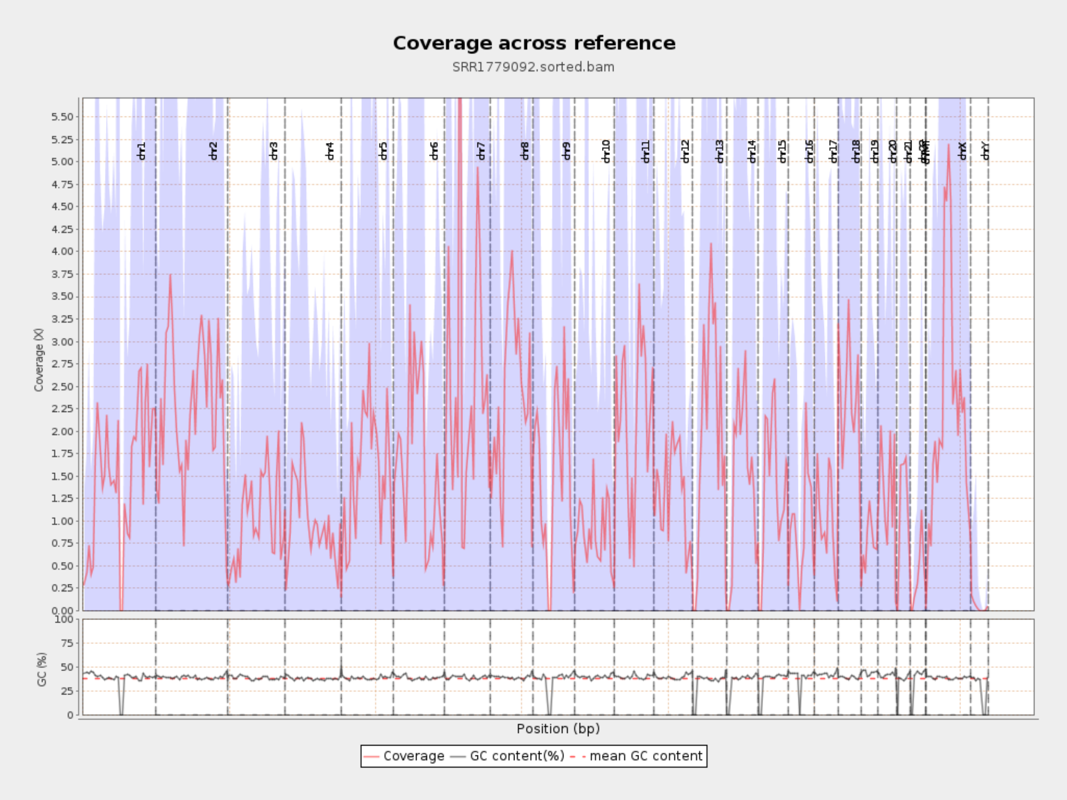
2.7. Chromosome stats

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

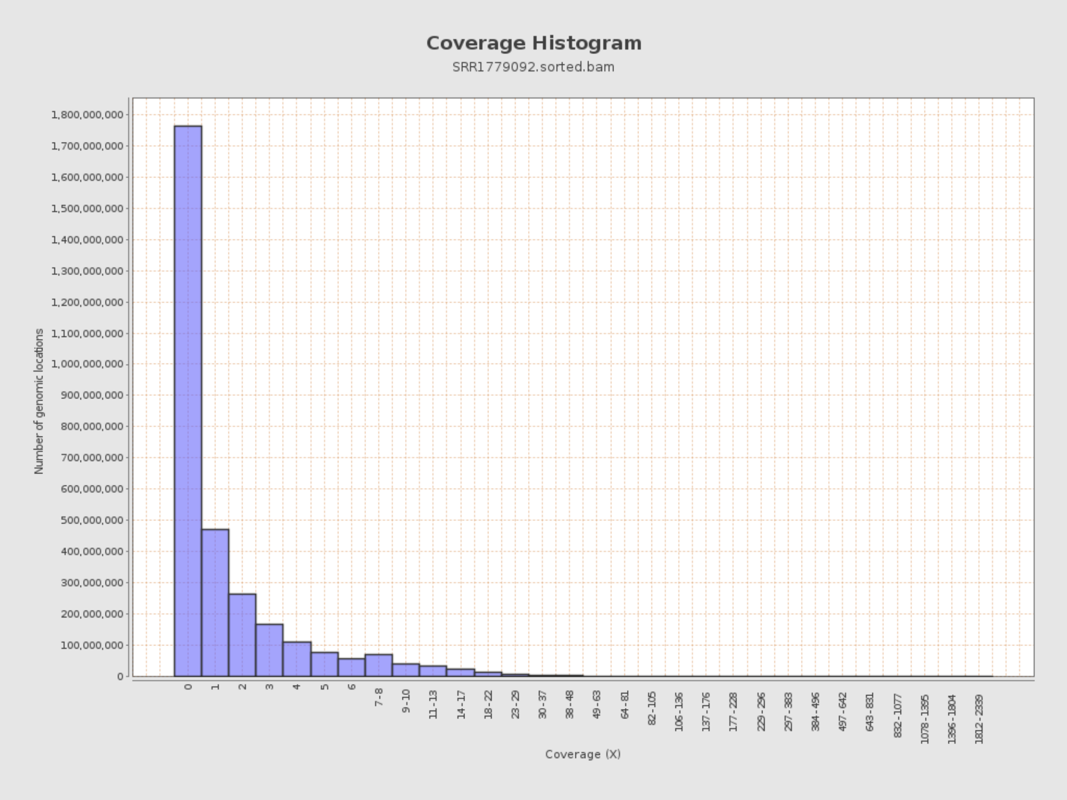
		bases	coverage	deviation
chr1	249250621	369901773	1.4841	4.0321
chr2	243199373	556637271	2.2888	4.3385
chr3	198022430	203747070	1.0289	2.4754
chr4	191154276	191058739	0.9995	2.3607
chr5	180915260	277303257	1.5328	3.0926
chr6	171115067	287873029	1.6823	3.4119
chr7	159138663	412986039	2.5951	8.79
chr8	146364022	349820209	2.3901	4.1007
chr9	141213431	216379867	1.5323	3.414
chr10	135534747	121613864	0.8973	4.0692
chr11	135006516	289788055	2.1465	3.9745
chr12	133851895	175095710	1.3081	3.062
chr13	115169878	236898366	2.0569	3.7849
chr14	107349540	160893228	1.4988	3.5105
chr15	102531392	139049434	1.3562	3.3511
chr16	90354753	83387351	0.9229	2.2107
chr17	81195210	81253853	1.0007	2.5831
chr18	78077248	184978494	2.3692	3.772
chr19	59128983	45843870	0.7753	2.3363
chr20	63025520	86411240	1.3711	3.0868
chr21	48129895	51785065	1.0759	2.4643
chr22	51304566	21413072	0.4174	1.4331
chrMT	16571	303	0.0183	0.1583
chrX	155270560	359621870	2.3161	4.7982

chrY	59373566	2561630	0.0431	0.7021

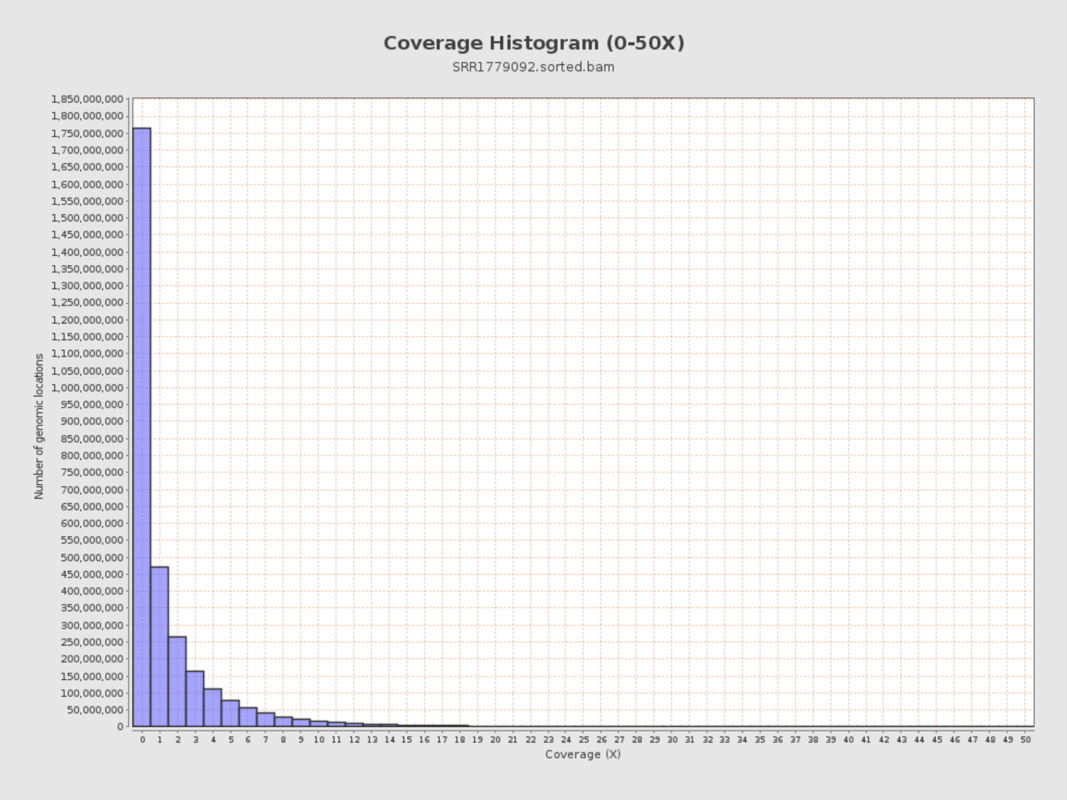
3. Results : Coverage across reference



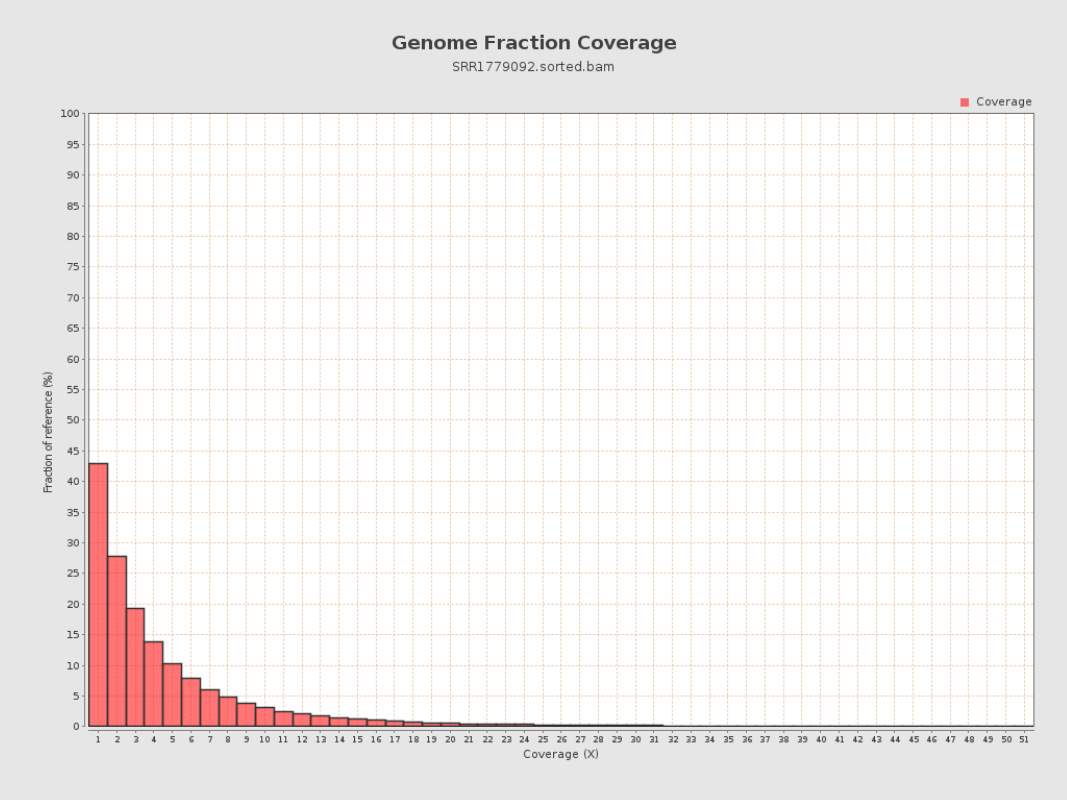
4. Results : Coverage Histogram



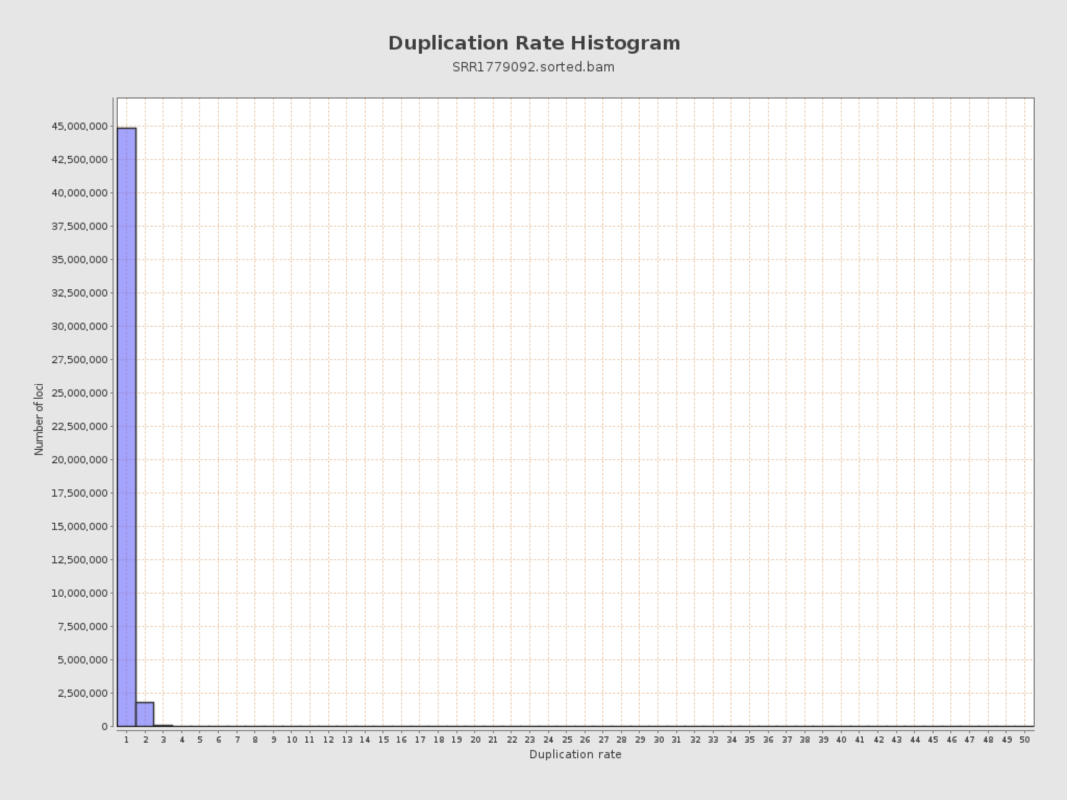
5. Results : Coverage Histogram (0-50X)



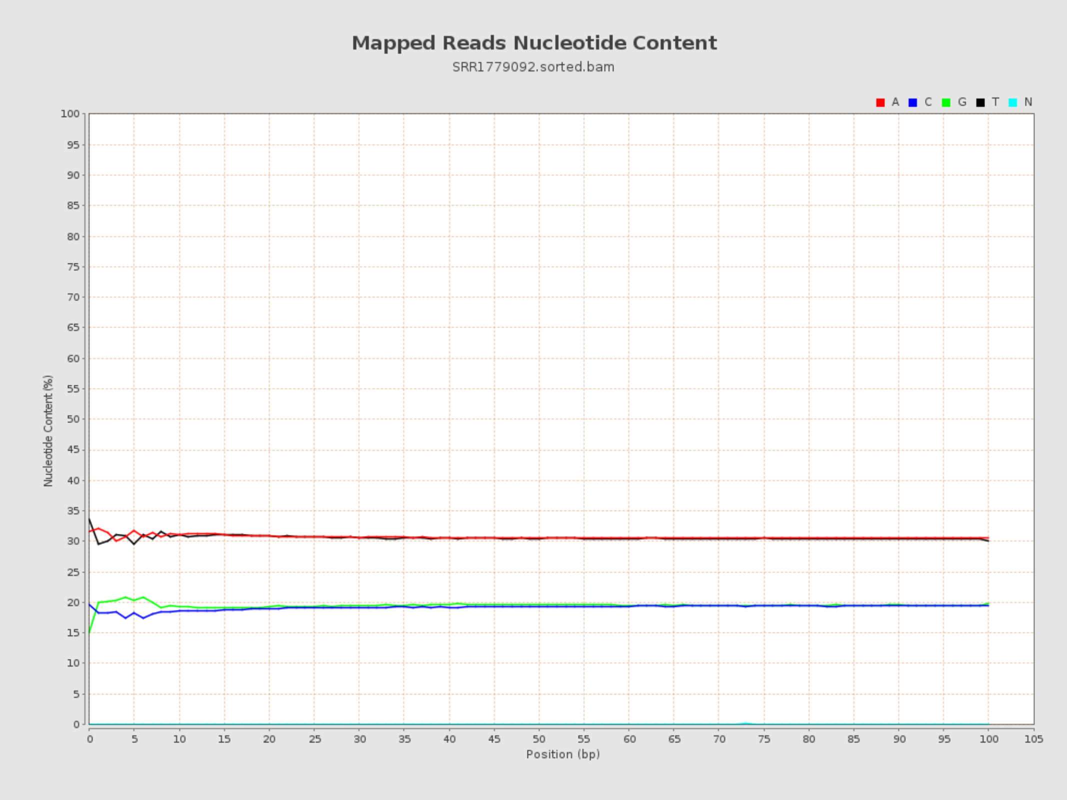
6. Results : Genome Fraction Coverage



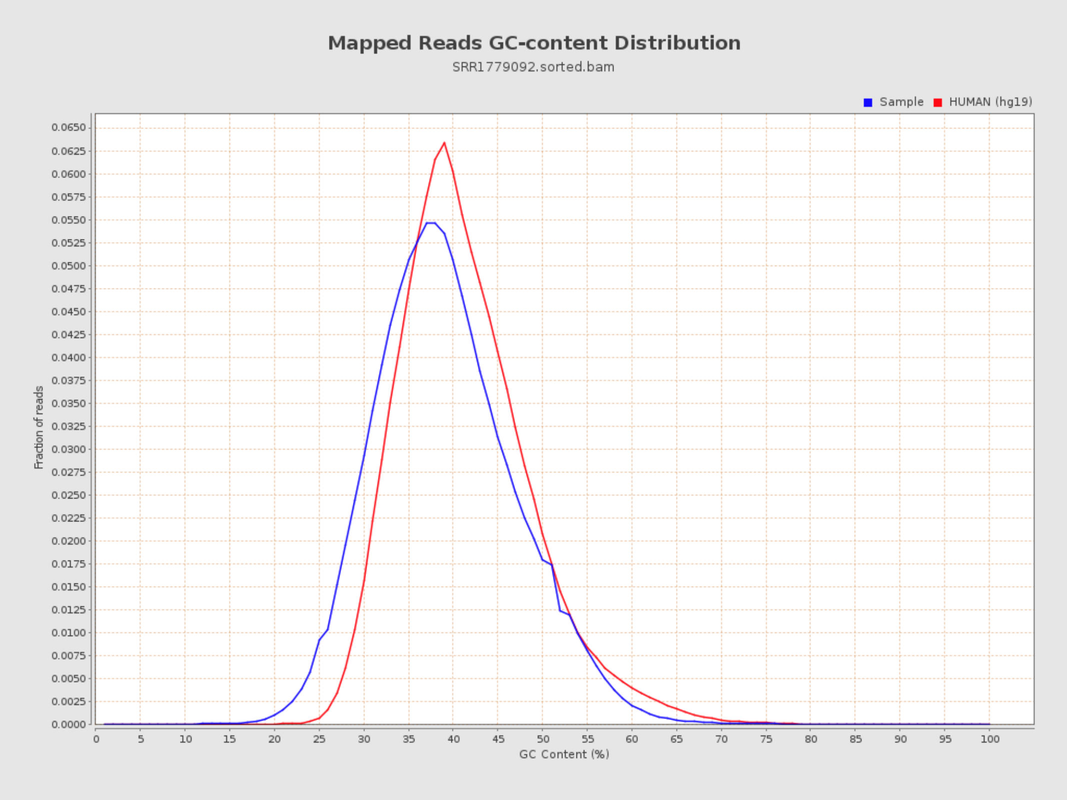
7. Results : Duplication Rate Histogram



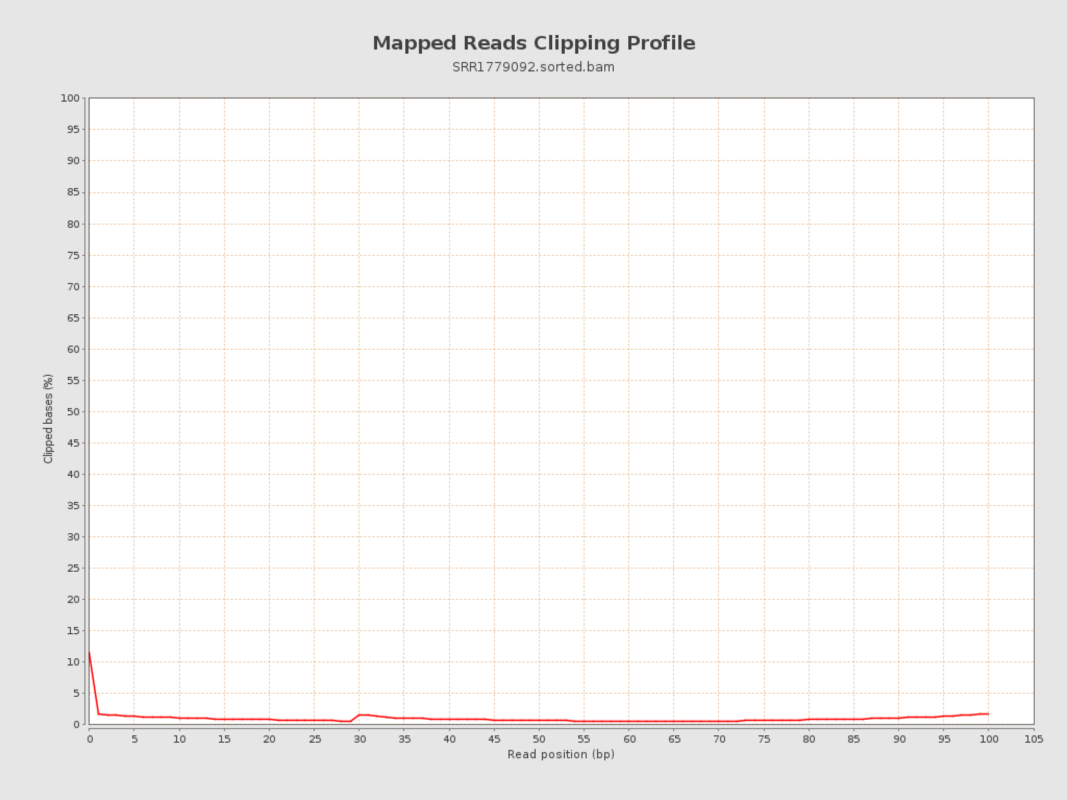
8. Results : Mapped Reads Nucleotide Content



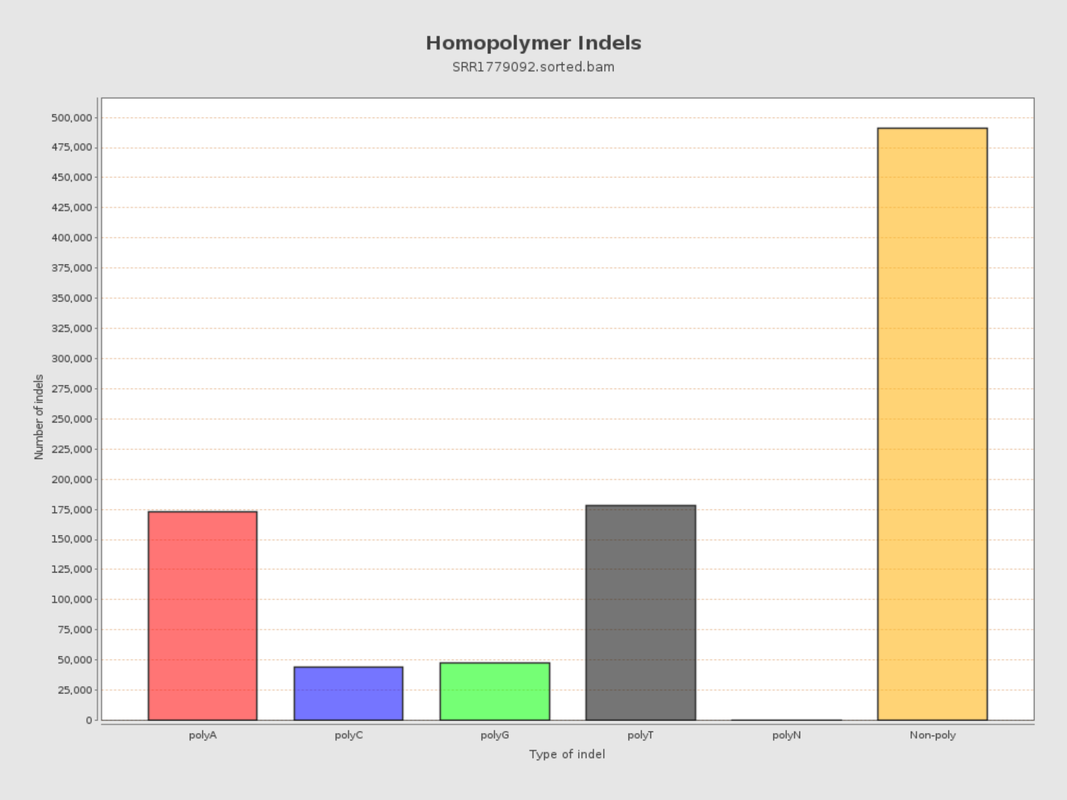
9. Results : Mapped Reads GC-content Distribution



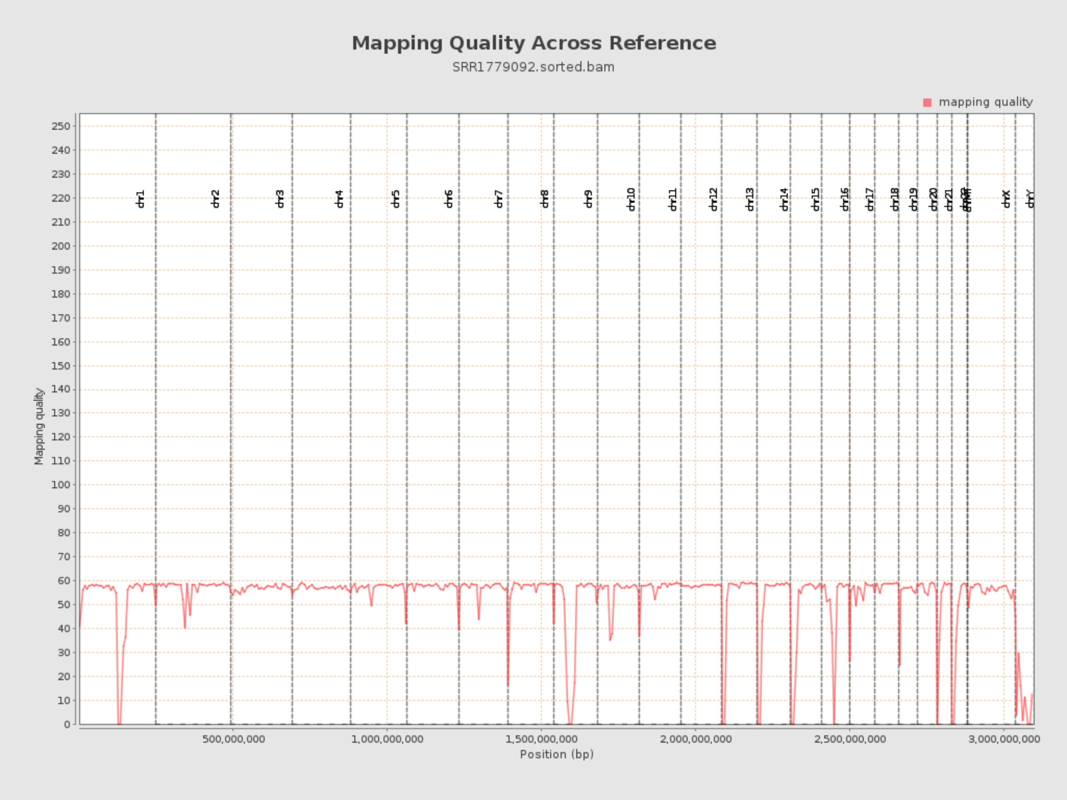
10. Results : Mapped Reads Clipping Profile



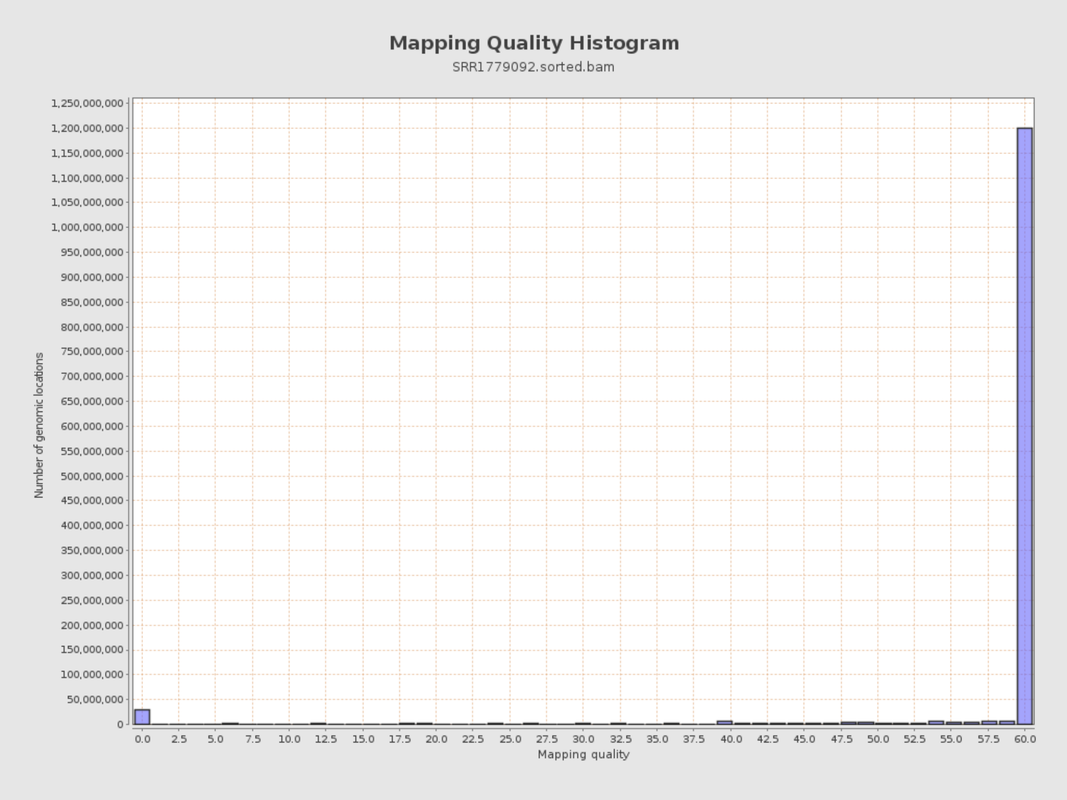
11. Results : Homopolymer Indels



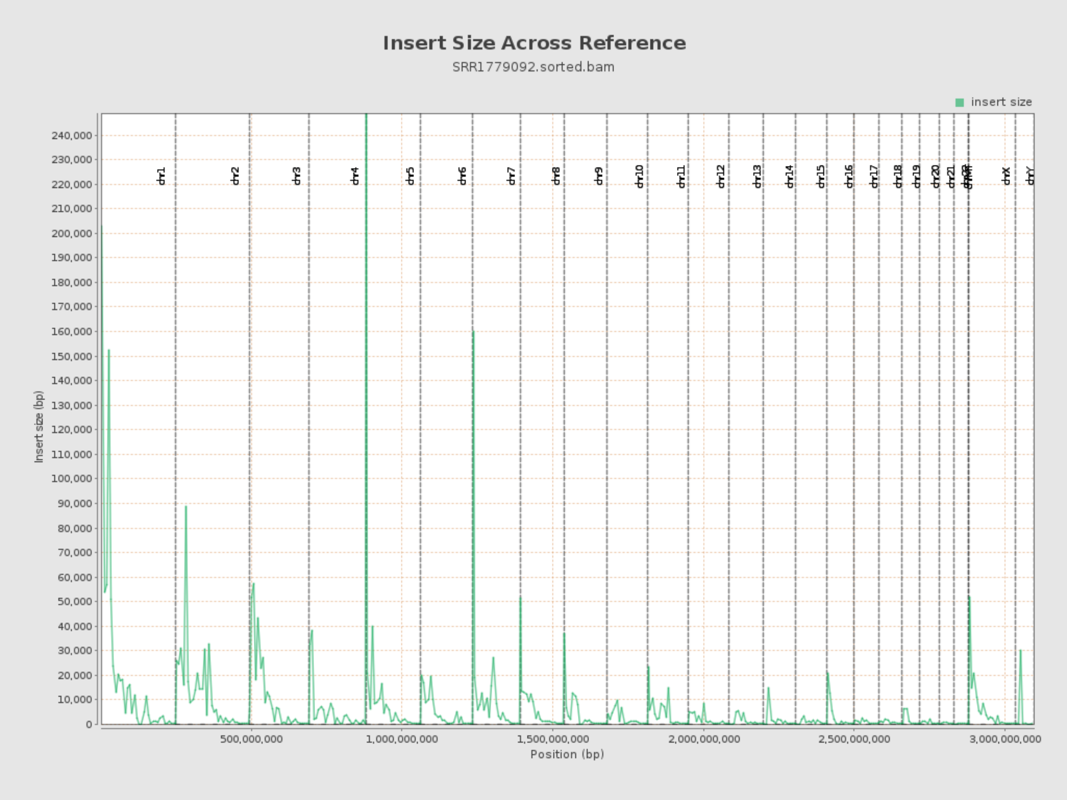
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram