Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 11:59:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472770.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_SRR3472770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472770_1.fastq.gz SRR3472770_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 11:59:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,030,188
Mapped reads	16,829,339 / 98.82%
Unmapped reads	200,849 / 1.18%
Mapped paired reads	16,829,339 / 98.82%
Mapped reads, first in pair	8,443,239 / 49.58%
Mapped reads, second in pair	8,386,100 / 49.24%
Mapped reads, both in pair	16,732,258 / 98.25%
Mapped reads, singletons	97,081 / 0.57%
Secondary alignments	0
Supplementary alignments	103,775 / 0.61%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	10,551,633 / 61.96%
Duplication rate	47.24%
Clipped reads	1,395,344 / 8.19%

2.2. ACGT Content

Number/percentage of A's	451,976,476 / 27.25%
Number/percentage of C's	380,512,491 / 22.94%
Number/percentage of T's	449,557,591 / 27.1%
Number/percentage of G's	376,276,058 / 22.69%
Number/percentage of N's	319,361 / 0.02%

GC Percentage	45.63%

2.3. Coverage

Mean	0.5359
Standard Deviation	17.2219

2.4. Mapping Quality

Mean Mapping Quality	55.12

2.5. Insert size

Mean	47,683
Standard Deviation	2,141,776.84
P25/Median/P75	177 / 245 / 327

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,411,585
Insertions	94,326
Mapped reads with at least one insertion	0.56%
Deletions	89,042
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.71%

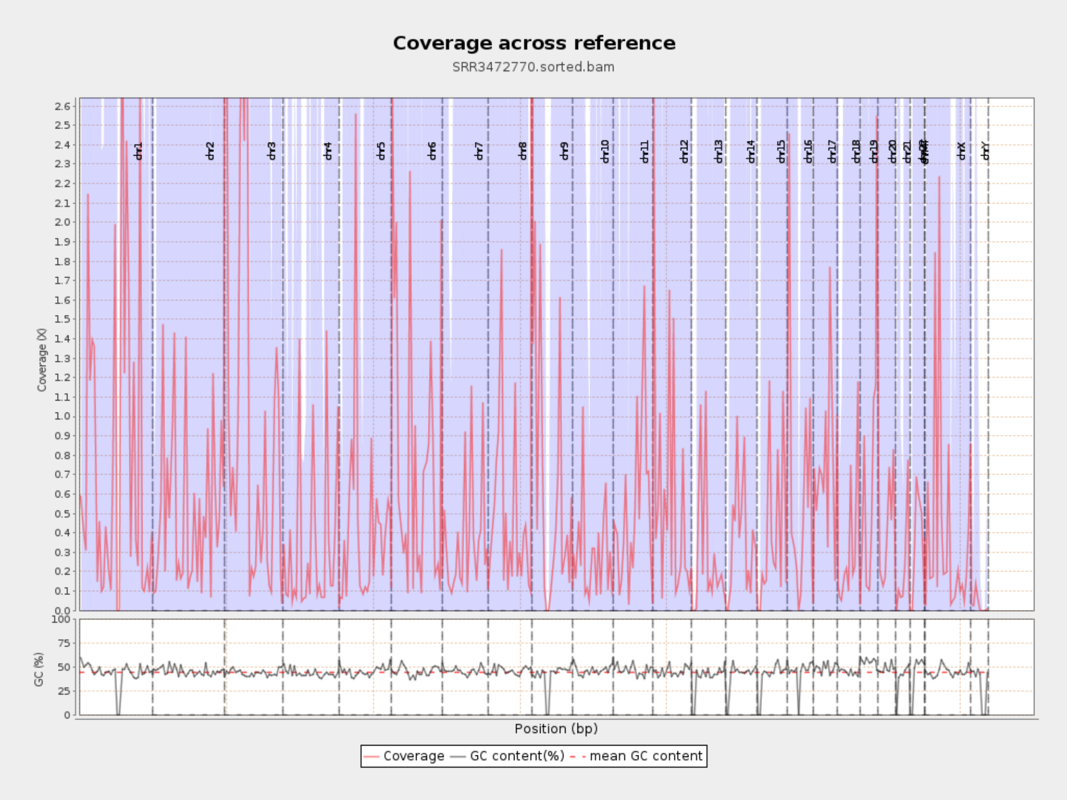
2.7. Chromosome stats

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

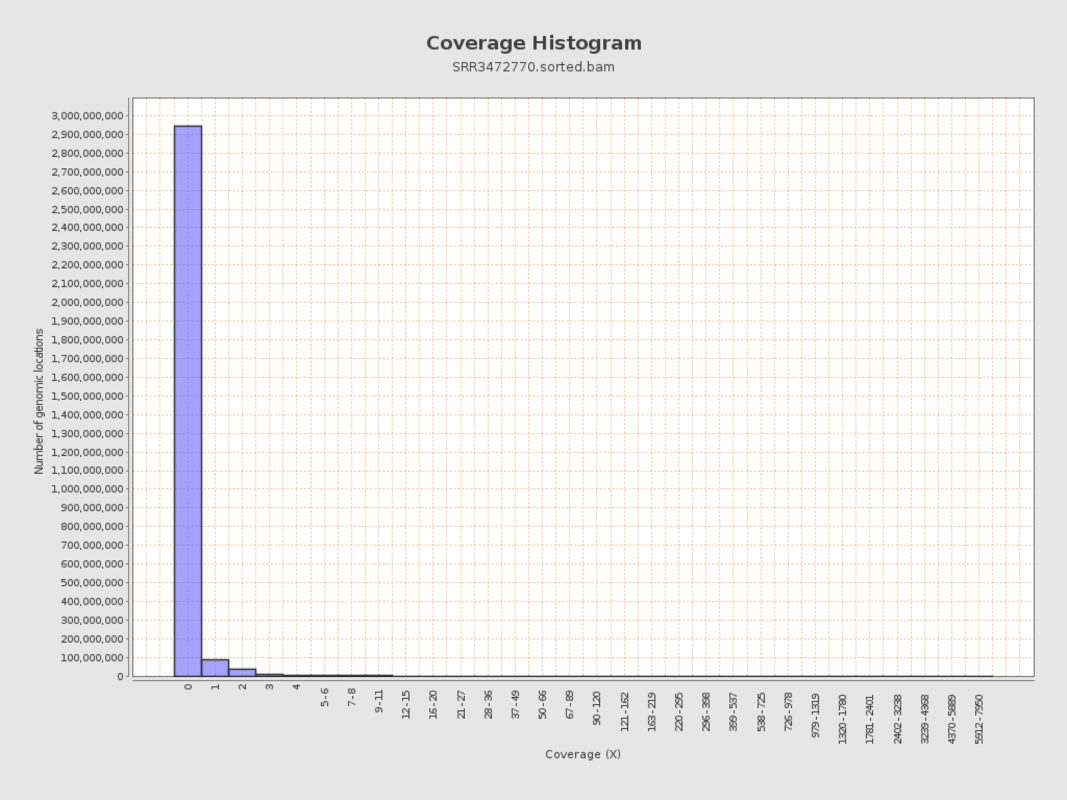
		bases	coverage	deviation
chr1	249250621	204386940	0.82	25.44
chr2	243199373	125866182	0.5175	17.1813
chr3	198022430	212672497	1.074	23.3527
chr4	191154276	63838191	0.334	14.0101
chr5	180915260	81399487	0.4499	13.074
chr6	171115067	133310755	0.7791	25.957
chr7	159138663	59538212	0.3741	10.185
chr8	146364022	69305205	0.4735	15.023
chr9	141213431	98658931	0.6987	18.364
chr10	135534747	40587750	0.2995	10.7979
chr11	135006516	72942535	0.5403	14.4019
chr12	133851895	82978900	0.6199	17.9394
chr13	115169878	32564168	0.2827	11.307
chr14	107349540	39054356	0.3638	13.3052
chr15	102531392	40574428	0.3957	13.1376
chr16	90354753	55863104	0.6183	18.0196
chr17	81195210	60932788	0.7504	15.5142
chr18	78077248	24910326	0.319	12.6787
chr19	59128983	37653403	0.6368	17.29
chr20	63025520	26518275	0.4208	10.4839
chr21	48129895	10154243	0.211	10.2198
chr22	51304566	17481002	0.3407	11.4061
chrMT	16571	6197	0.374	1.2368
chrX	155270560	65701795	0.4231	19.6357

chrY	59373566	1967416	0.0331	1.2579

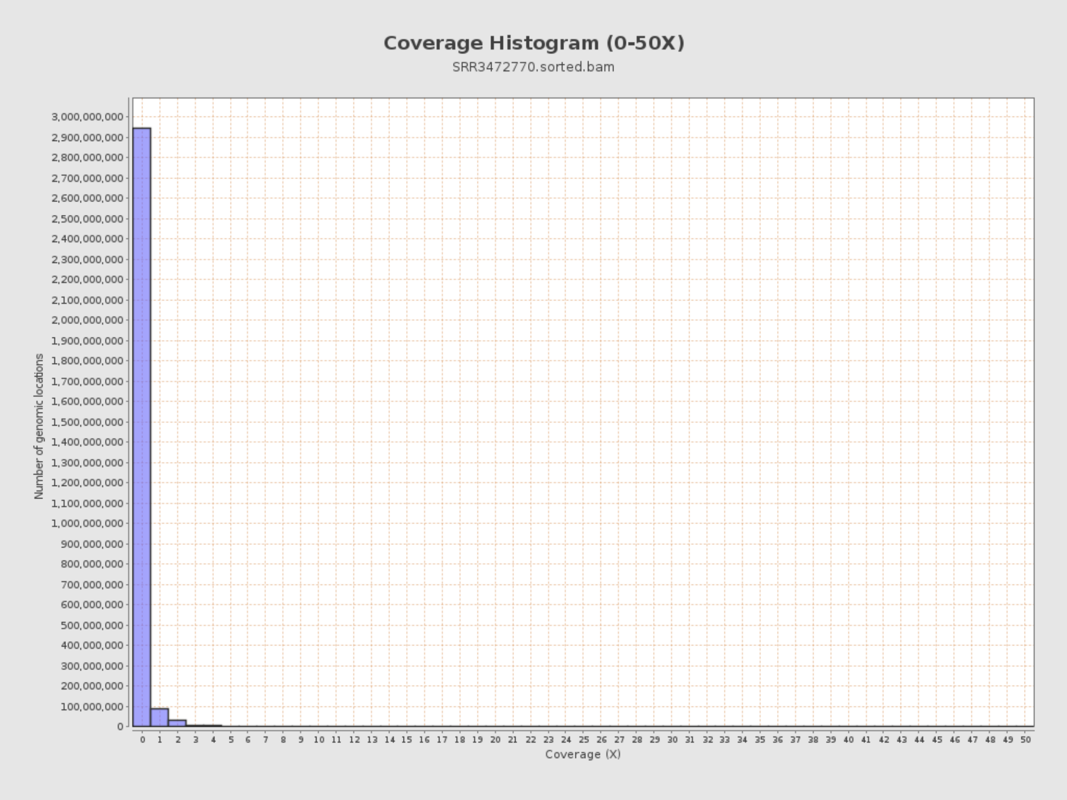
3. Results : Coverage across reference



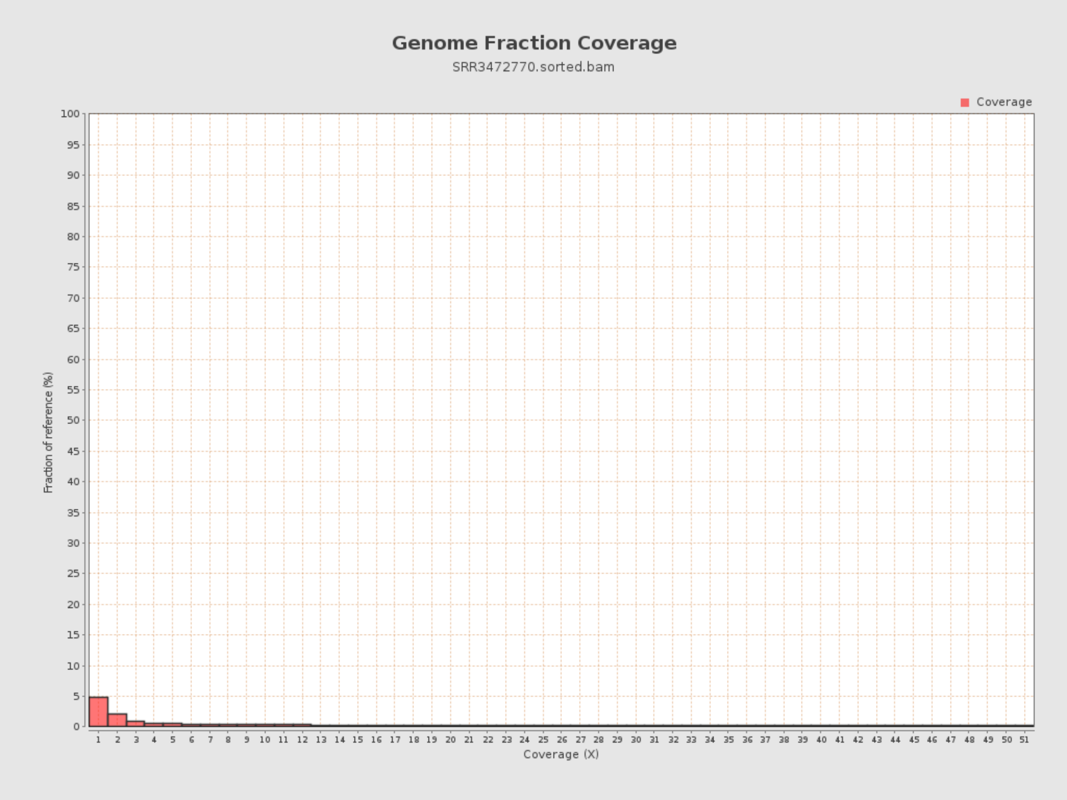
4. Results : Coverage Histogram



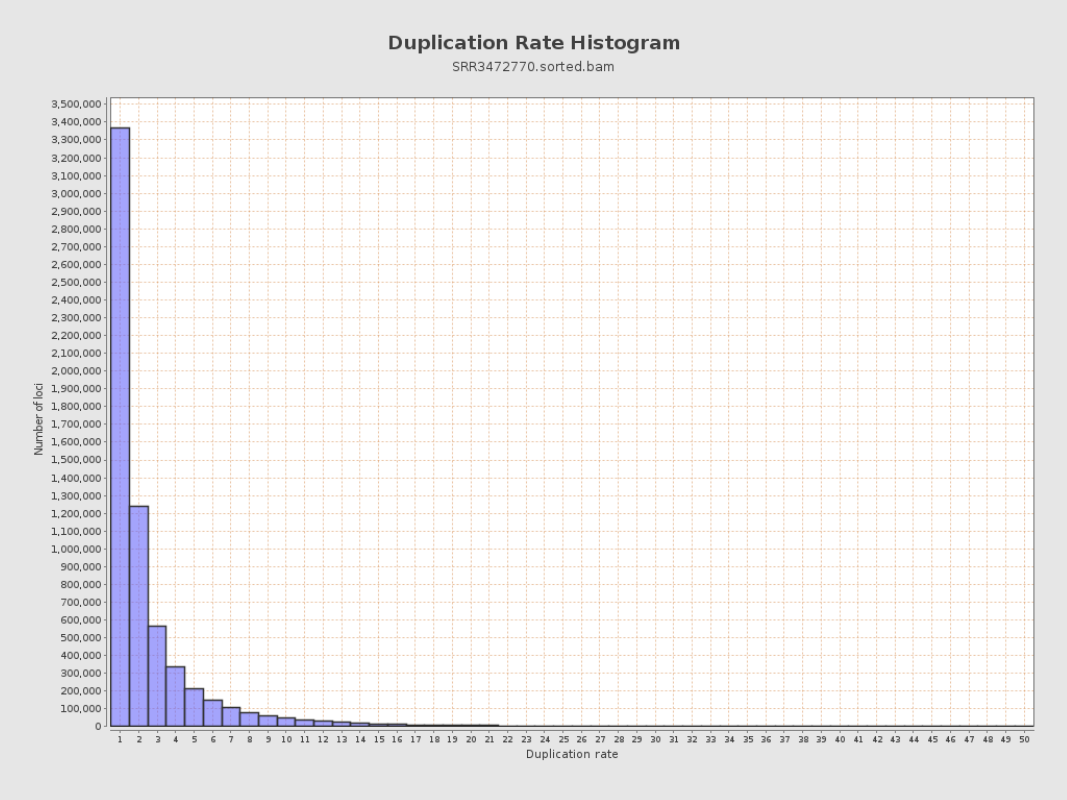
5. Results : Coverage Histogram (0-50X)



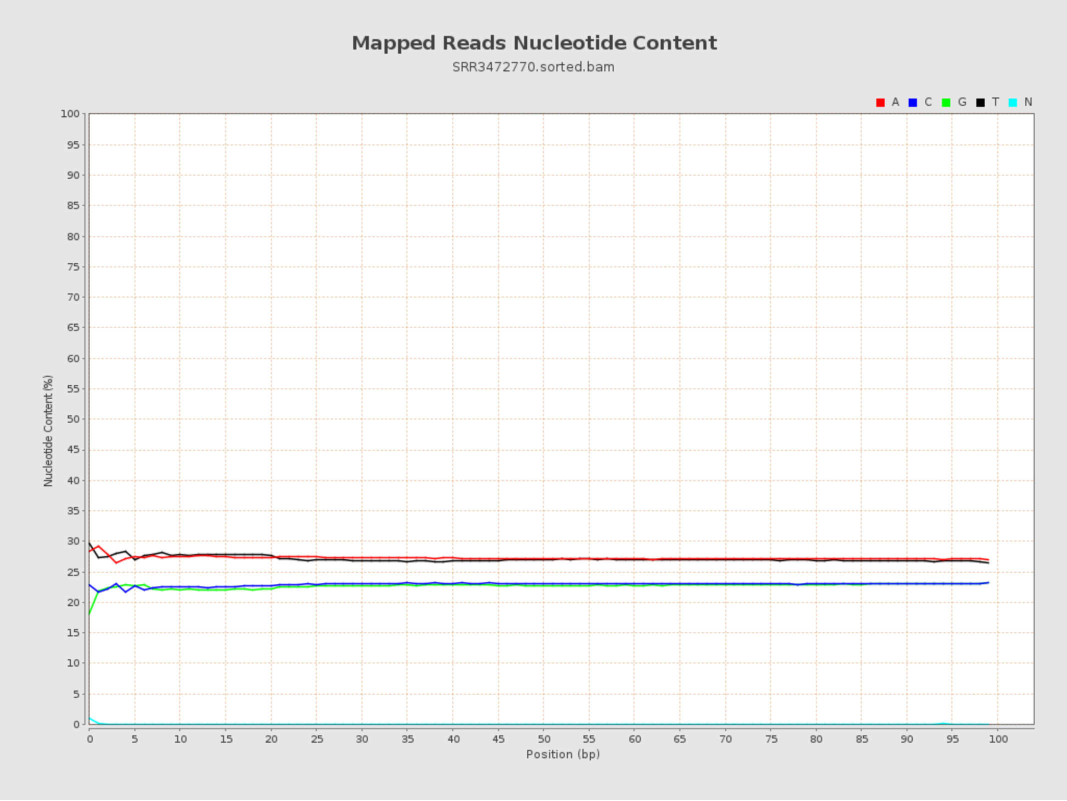
6. Results : Genome Fraction Coverage



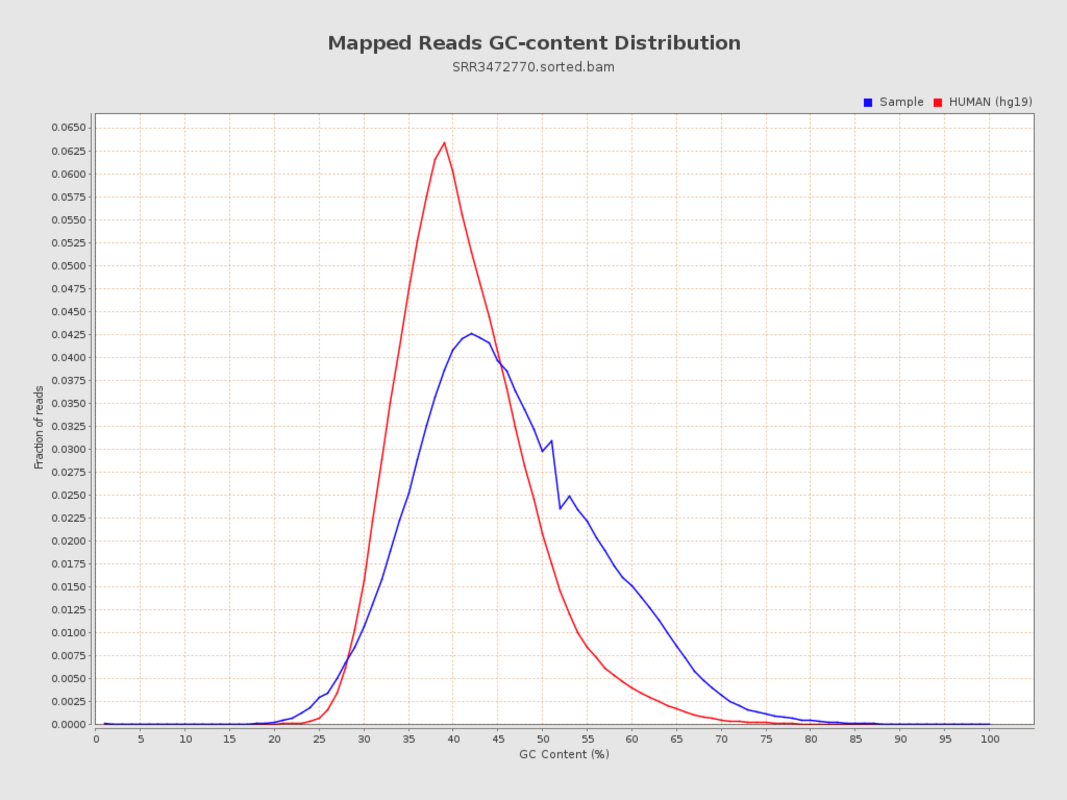
7. Results : Duplication Rate Histogram



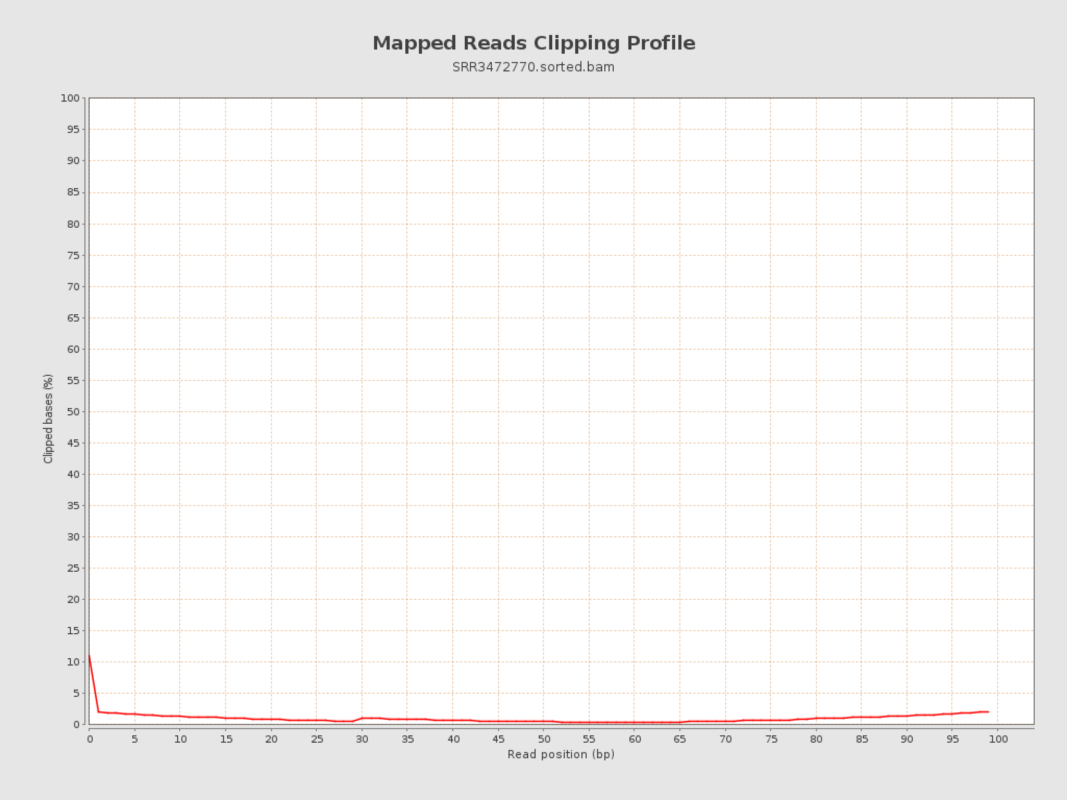
8. Results : Mapped Reads Nucleotide Content



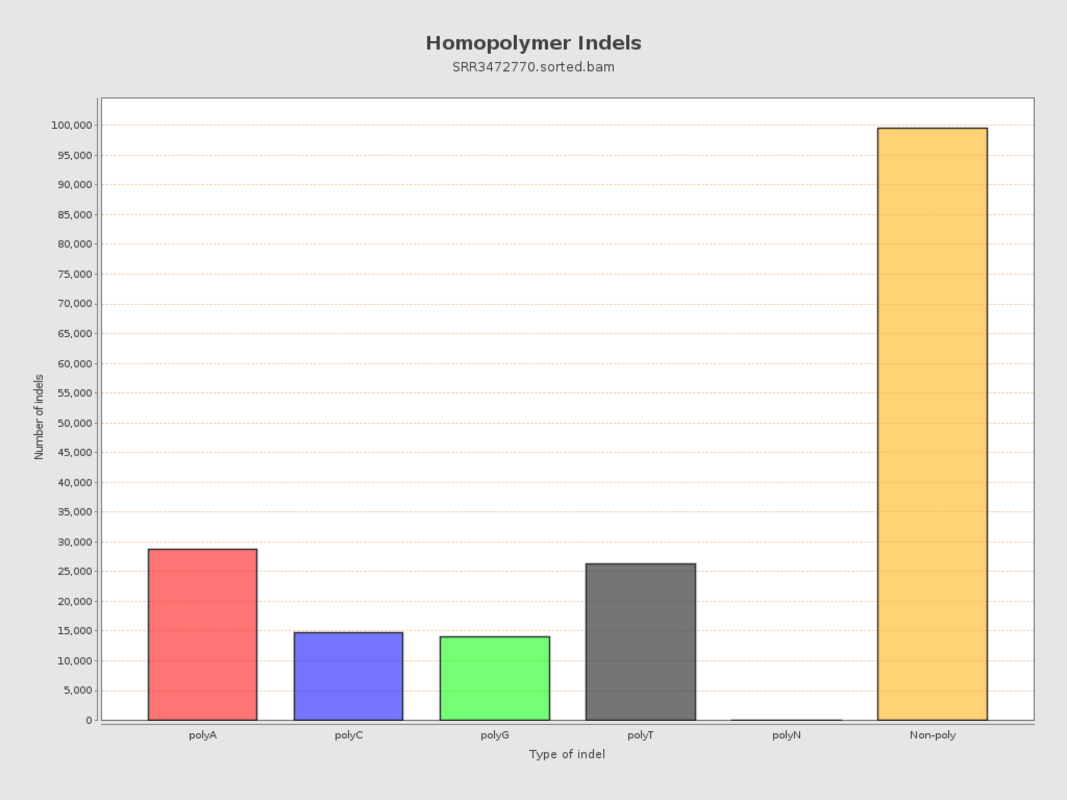
9. Results : Mapped Reads GC-content Distribution



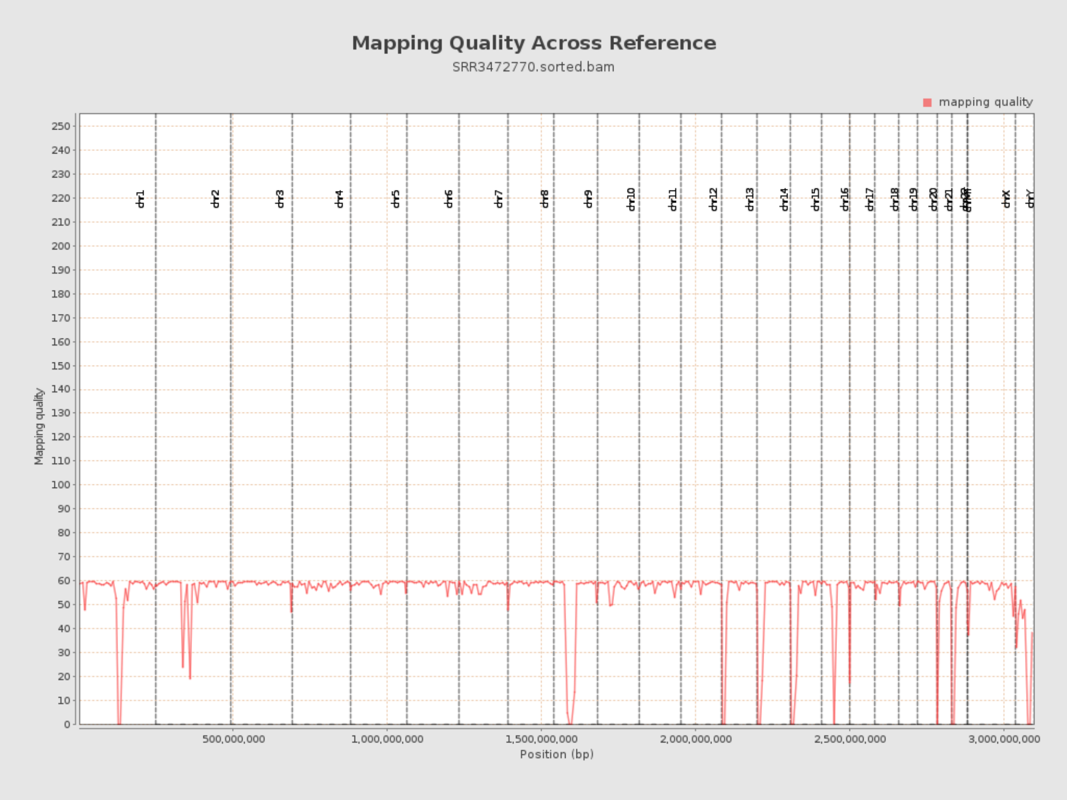
10. Results : Mapped Reads Clipping Profile



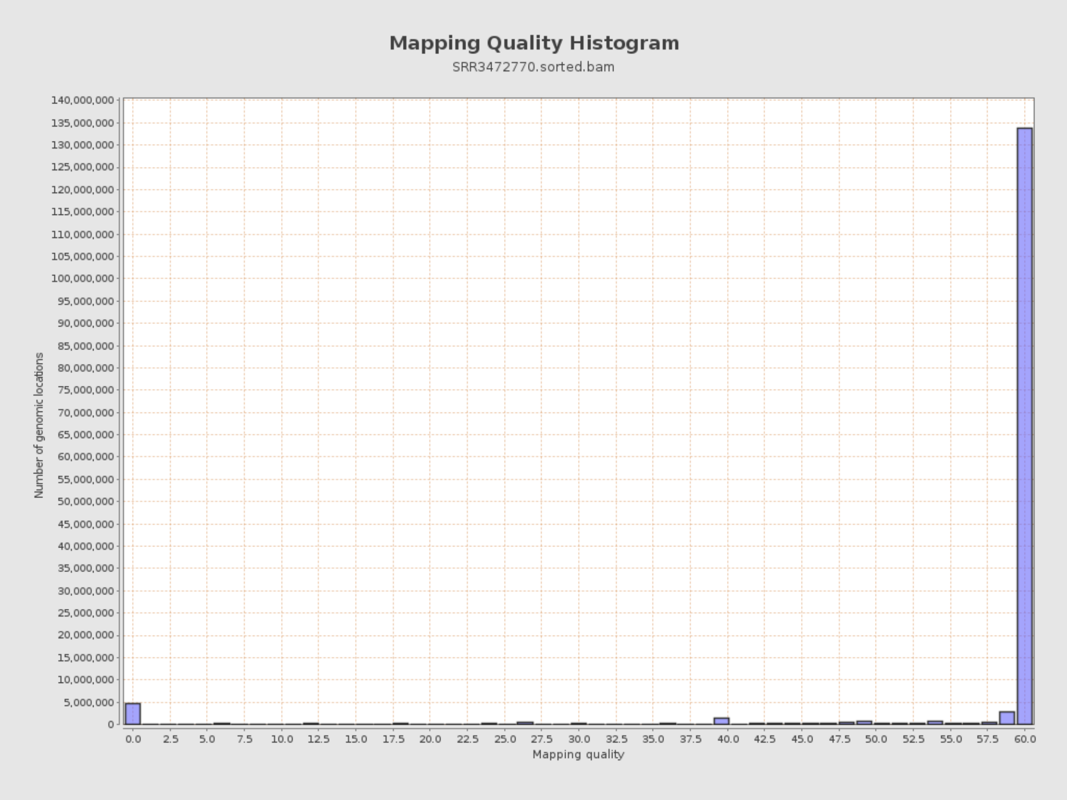
11. Results : Homopolymer Indels



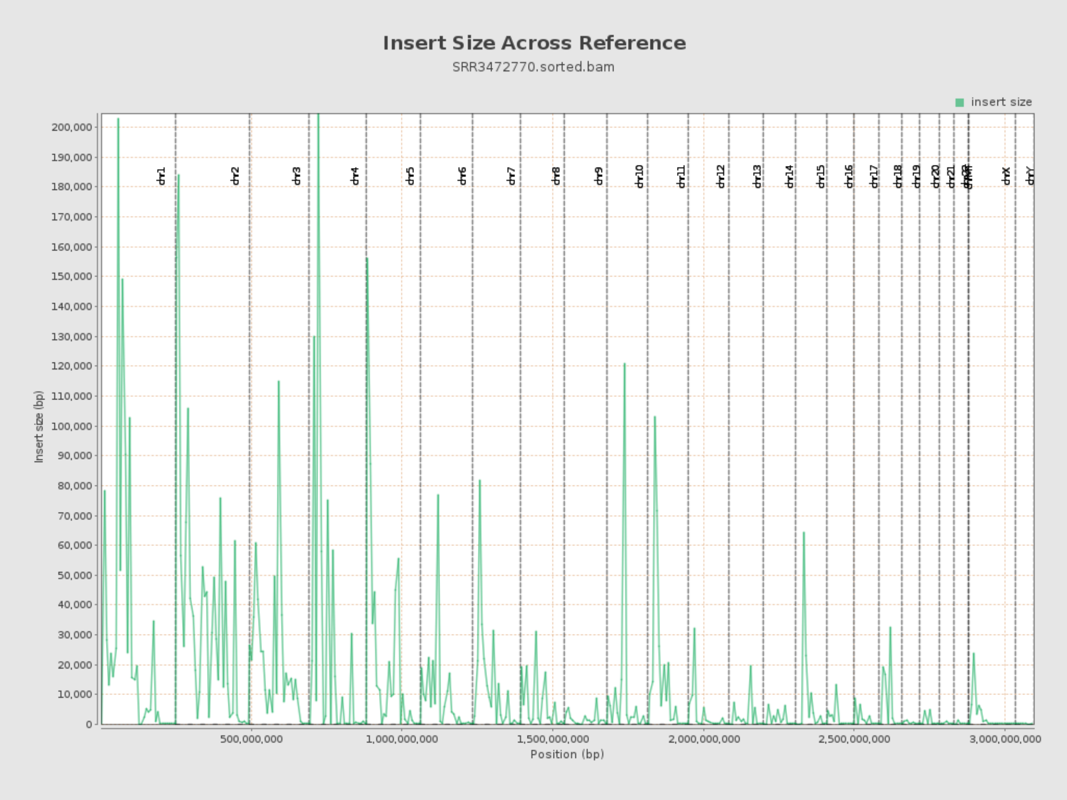
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram