Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 08:22:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472759.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_SRR3472759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472759_1.fastq.gz SRR3472759_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 08:22:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,859,802
Mapped reads	13,732,880 / 99.08%
Unmapped reads	126,922 / 0.92%
Mapped paired reads	13,732,880 / 99.08%
Mapped reads, first in pair	6,891,264 / 49.72%
Mapped reads, second in pair	6,841,616 / 49.36%
Mapped reads, both in pair	13,655,040 / 98.52%
Mapped reads, singletons	77,840 / 0.56%
Secondary alignments	0
Supplementary alignments	93,215 / 0.67%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	8,319,669 / 60.03%
Duplication rate	46.09%
Clipped reads	1,126,436 / 8.13%

2.2. ACGT Content

Number/percentage of A's	377,101,802 / 27.84%
Number/percentage of C's	302,156,056 / 22.3%
Number/percentage of T's	375,562,890 / 27.72%
Number/percentage of G's	299,633,151 / 22.12%
Number/percentage of N's	261,113 / 0.02%

GC Percentage	44.42%

2.3. Coverage

Mean	0.4377
Standard Deviation	14.3297

2.4. Mapping Quality

Mean Mapping Quality	55

2.5. Insert size

Mean	49,743.23
Standard Deviation	2,161,106.31
P25/Median/P75	173 / 241 / 326

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	8,366,359
Insertions	76,507
Mapped reads with at least one insertion	0.55%
Deletions	78,034
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.25%

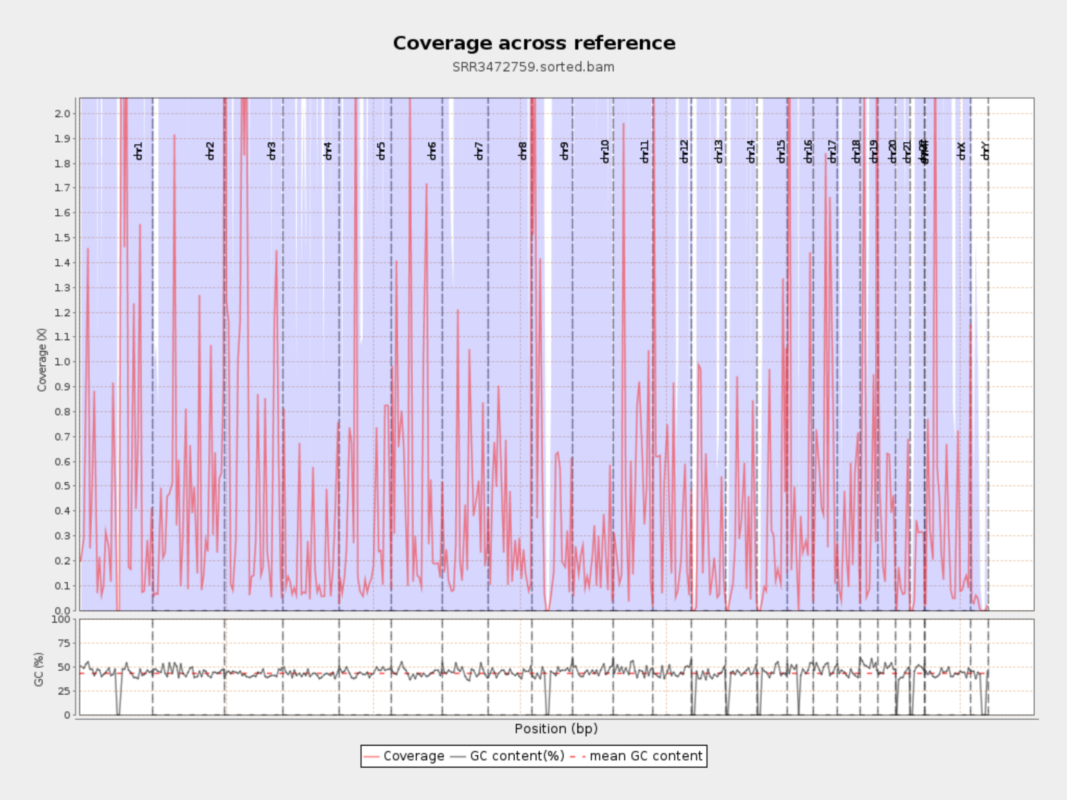
2.7. Chromosome stats

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

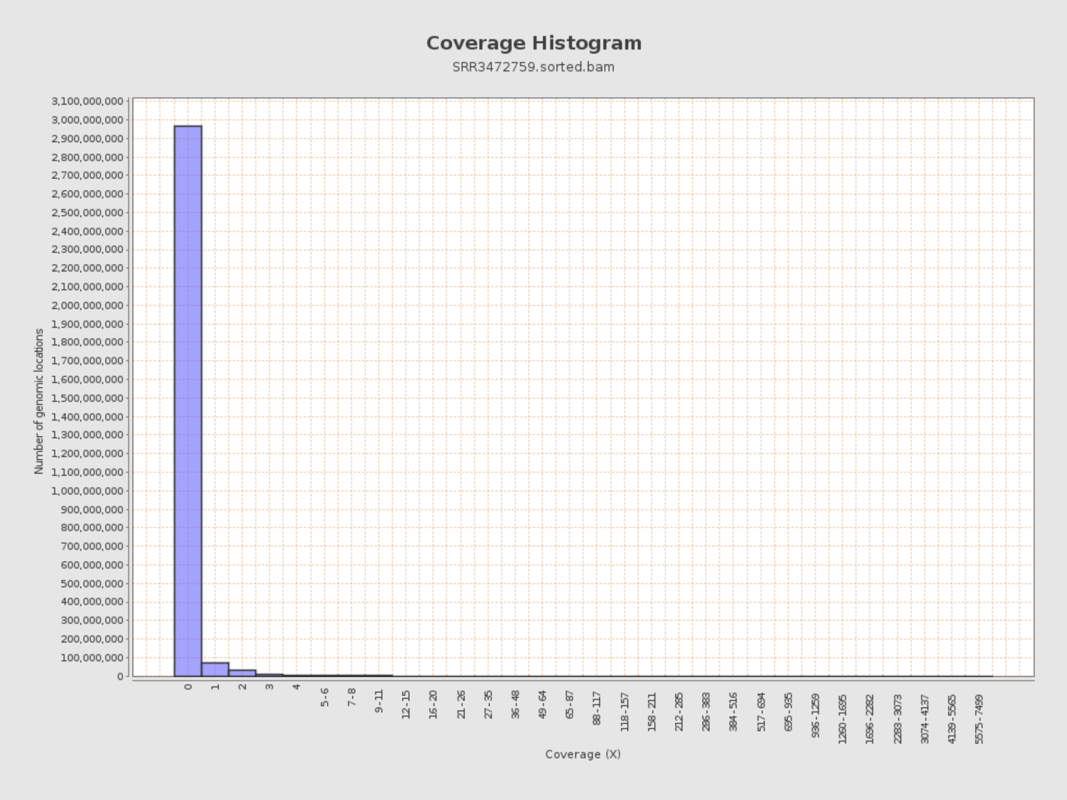
		bases	coverage	deviation
chr1	249250621	154063517	0.6181	22.309
chr2	243199373	110969542	0.4563	15.8681
chr3	198022430	151431473	0.7647	19.5594
chr4	191154276	42028759	0.2199	7.721
chr5	180915260	69099742	0.3819	12.1418
chr6	171115067	95056490	0.5555	15.1008
chr7	159138663	61641889	0.3873	12.6457
chr8	146364022	48394332	0.3306	10.0582
chr9	141213431	78484690	0.5558	13.9503
chr10	135534747	28053069	0.207	6.4587
chr11	135006516	68385869	0.5065	19.5093
chr12	133851895	64476296	0.4817	13.7955
chr13	115169878	33396430	0.29	10.9258
chr14	107349540	32193573	0.2999	10.417
chr15	102531392	34258305	0.3341	10.8503
chr16	90354753	50346675	0.5572	14.5721
chr17	81195210	55988577	0.6896	15.9094
chr18	78077248	24404273	0.3126	10.5895
chr19	59128983	42495258	0.7187	19.7256
chr20	63025520	27214050	0.4318	11.2404
chr21	48129895	8910301	0.1851	9.3643
chr22	51304566	10415110	0.203	6.4206
chrMT	16571	3151	0.1902	0.5873
chrX	155270560	61741387	0.3976	12.4013

chrY	59373566	1457190	0.0245	0.9528

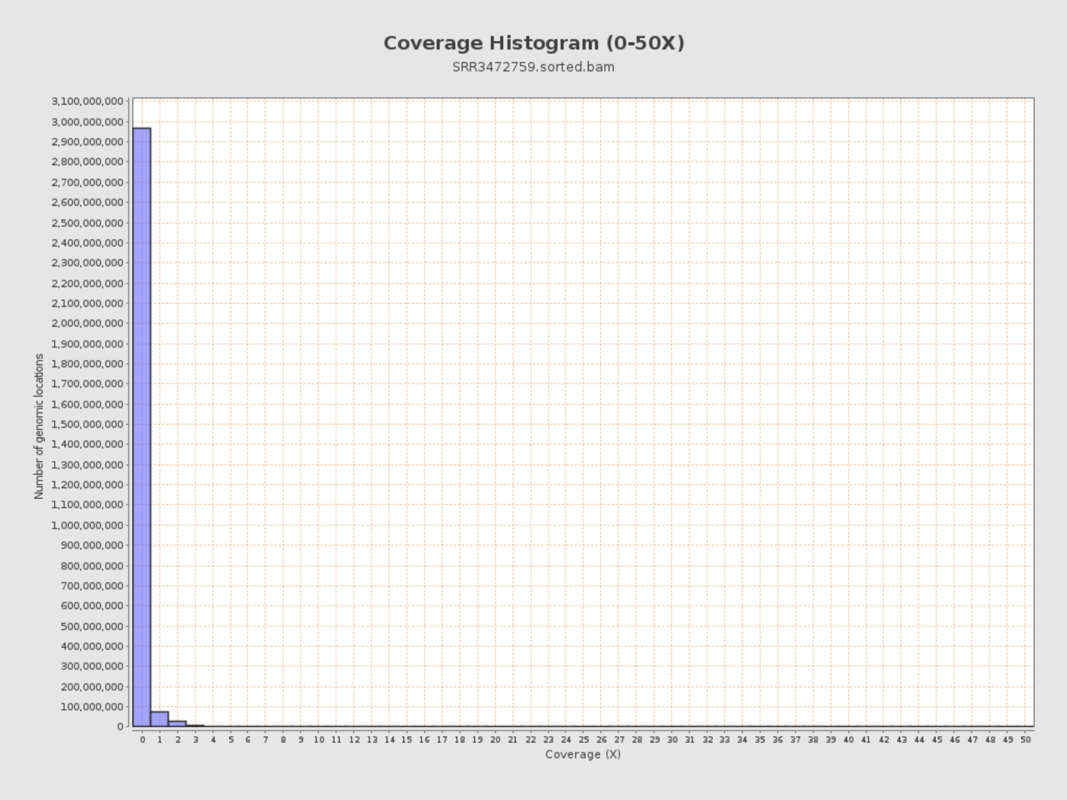
3. Results : Coverage across reference



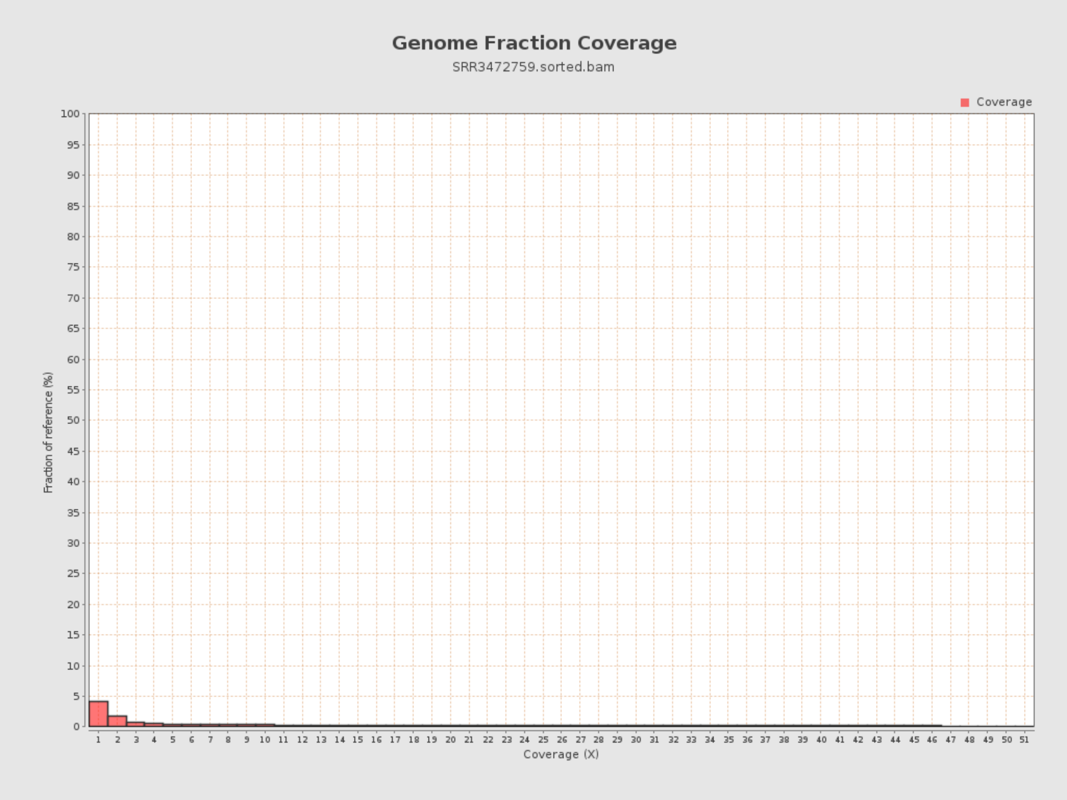
4. Results : Coverage Histogram



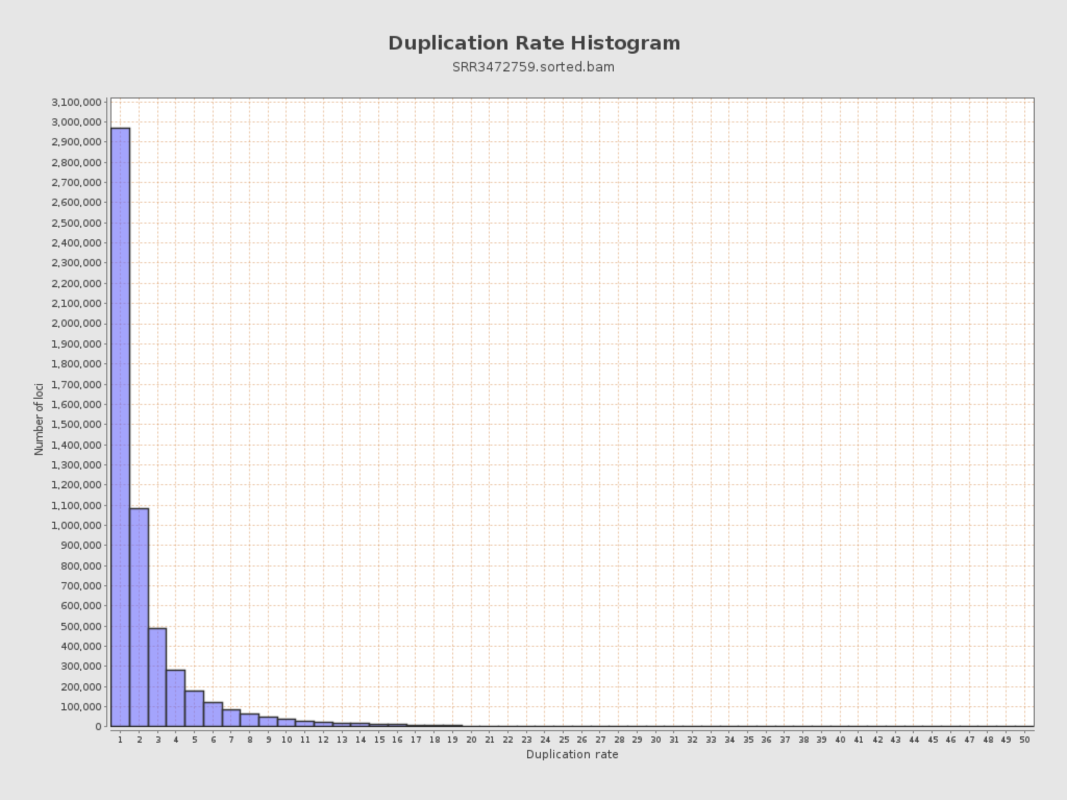
5. Results : Coverage Histogram (0-50X)



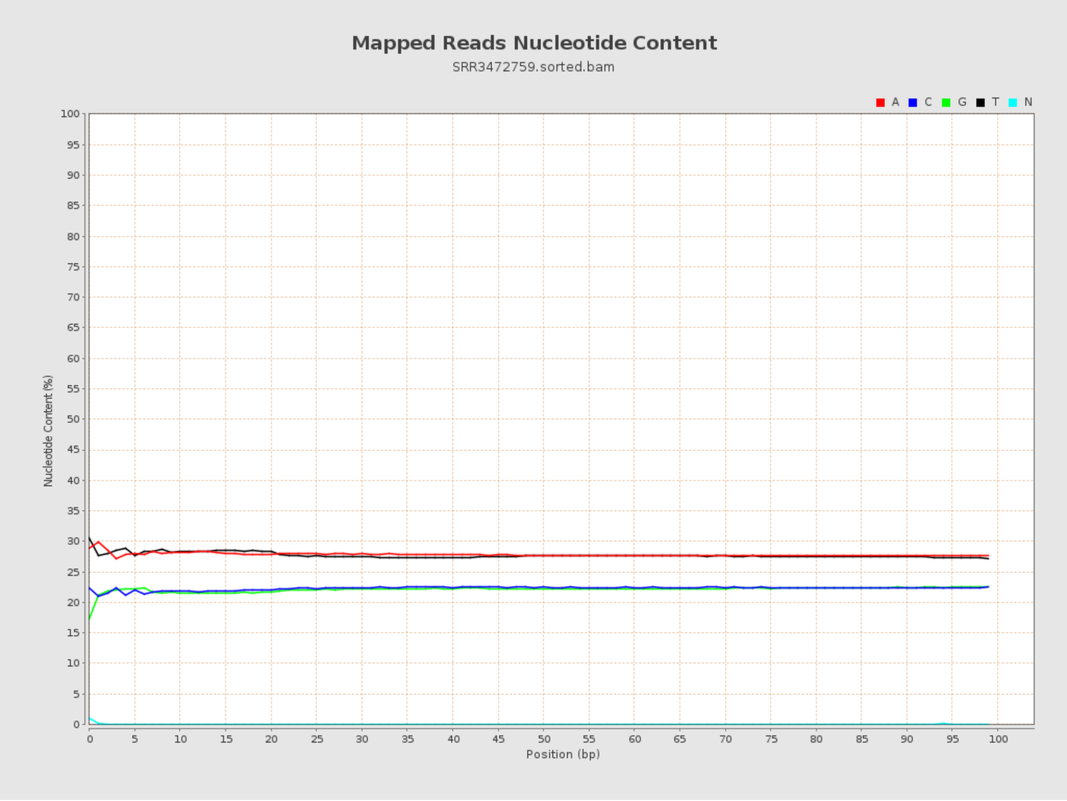
6. Results : Genome Fraction Coverage



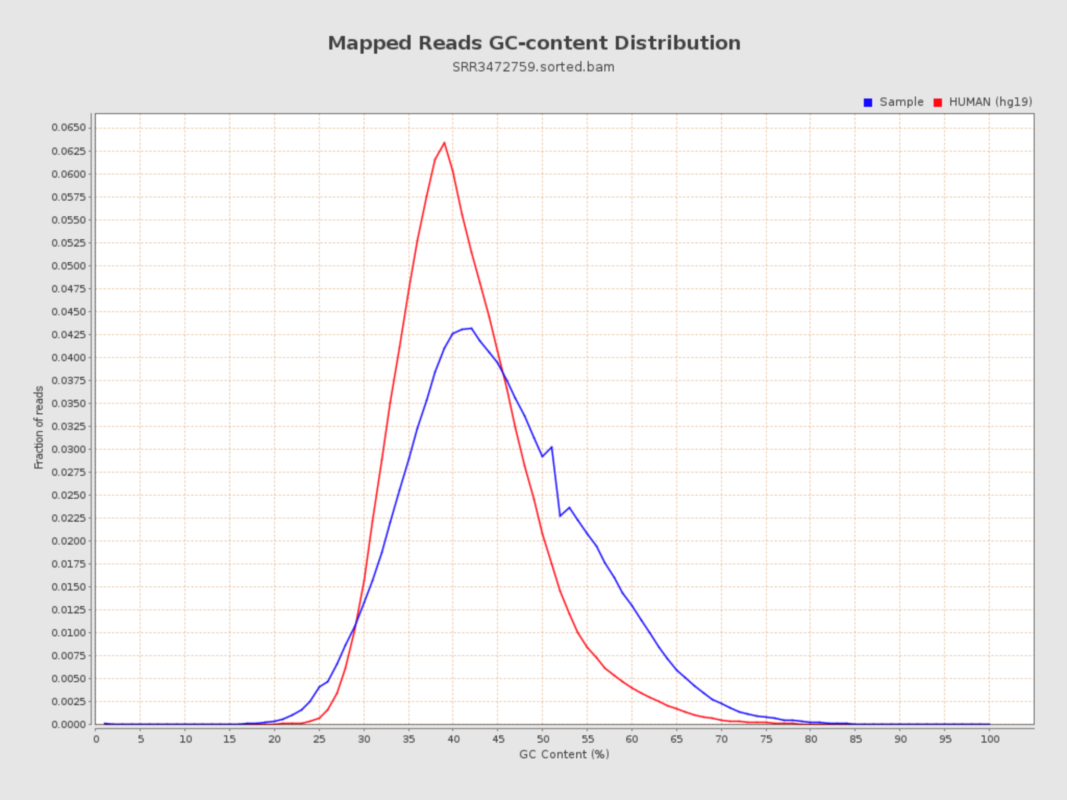
7. Results : Duplication Rate Histogram



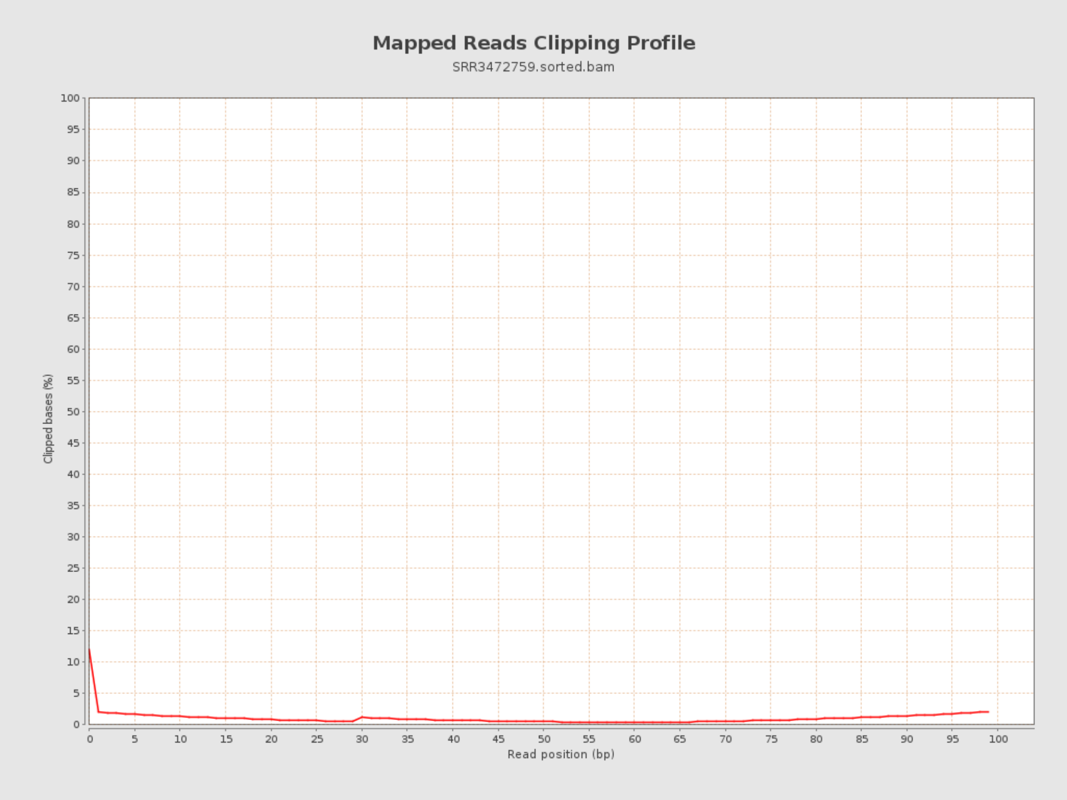
8. Results : Mapped Reads Nucleotide Content



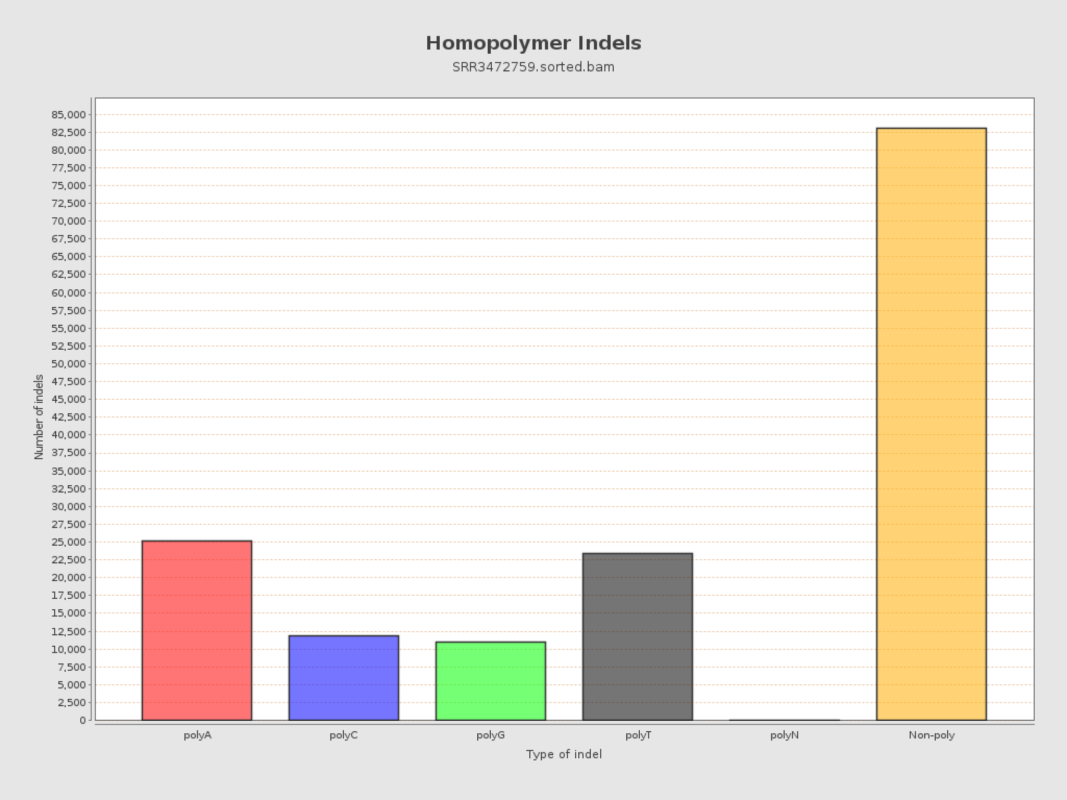
9. Results : Mapped Reads GC-content Distribution



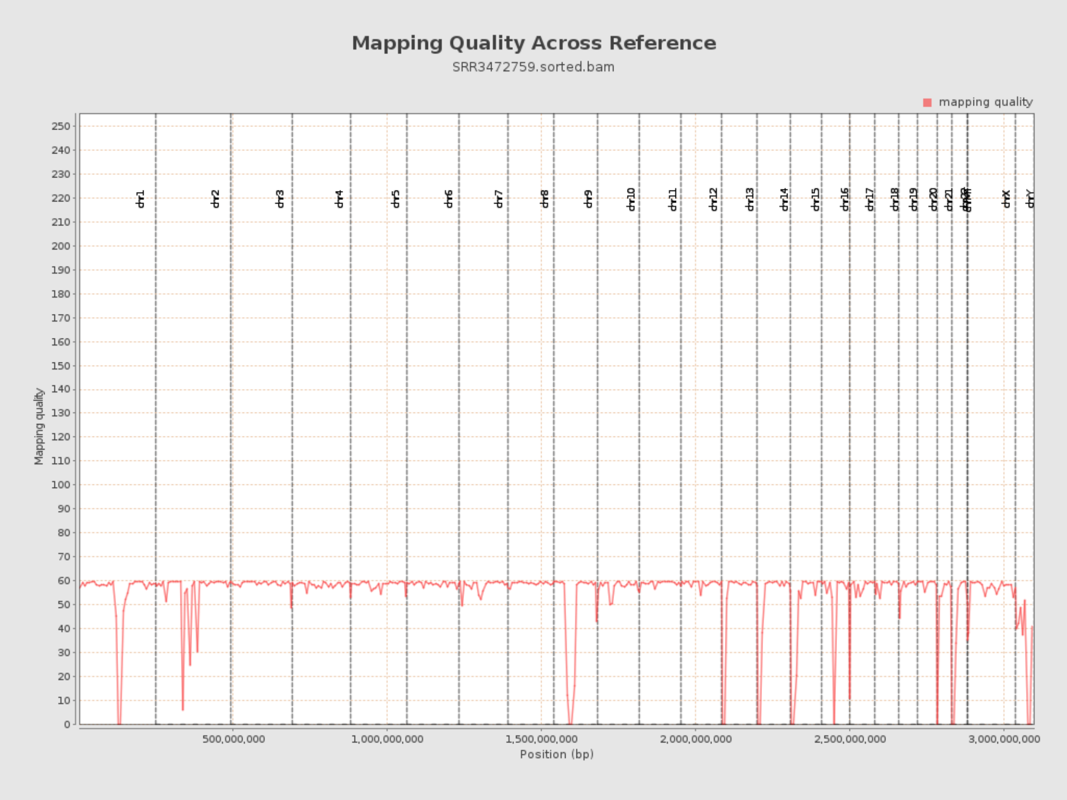
10. Results : Mapped Reads Clipping Profile



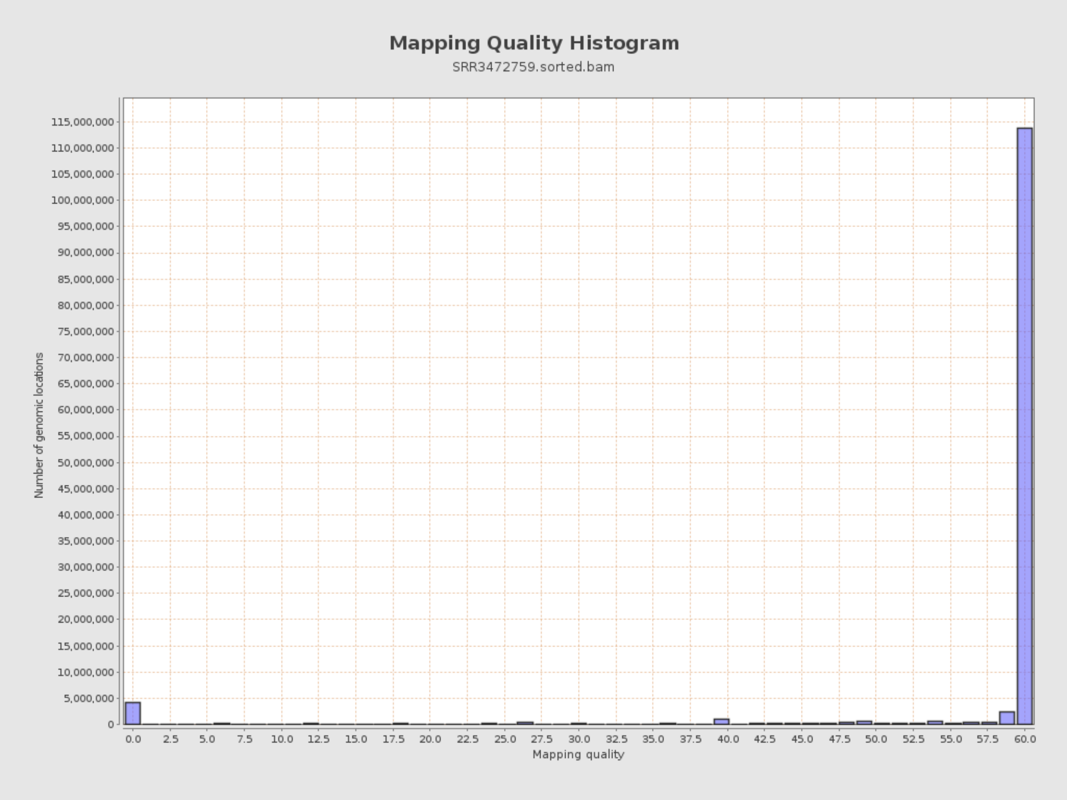
11. Results : Homopolymer Indels



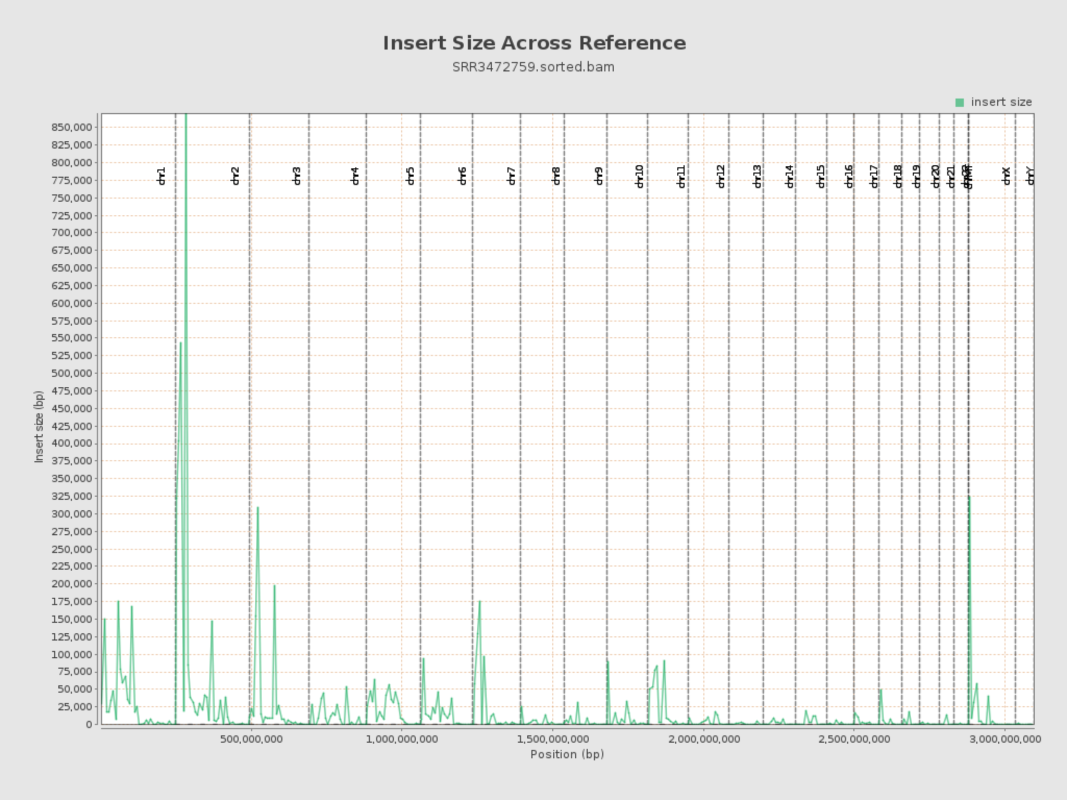
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram