Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 14:13:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472776.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_SRR3472776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472776_1.fastq.gz SRR3472776_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 14:13:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,125,804
Mapped reads	15,992,746 / 99.17%
Unmapped reads	133,058 / 0.83%
Mapped paired reads	15,992,746 / 99.17%
Mapped reads, first in pair	8,018,232 / 49.72%
Mapped reads, second in pair	7,974,514 / 49.45%
Mapped reads, both in pair	15,914,812 / 98.69%
Mapped reads, singletons	77,934 / 0.48%
Secondary alignments	0
Supplementary alignments	53,253 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	9,764,816 / 60.55%
Duplication rate	45.57%
Clipped reads	1,409,609 / 8.74%

2.2. ACGT Content

Number/percentage of A's	421,493,217 / 26.8%
Number/percentage of C's	367,566,088 / 23.38%
Number/percentage of T's	418,818,453 / 26.63%
Number/percentage of G's	364,276,419 / 23.17%
Number/percentage of N's	305,288 / 0.02%

GC Percentage	46.54%

2.3. Coverage

Mean	0.508
Standard Deviation	16.4268

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	22,880.46
Standard Deviation	1,502,606.62
P25/Median/P75	162 / 226 / 304

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	9,268,647
Insertions	93,285
Mapped reads with at least one insertion	0.58%
Deletions	81,382
Mapped reads with at least one deletion	0.5%
Homopolymer indels	43.7%

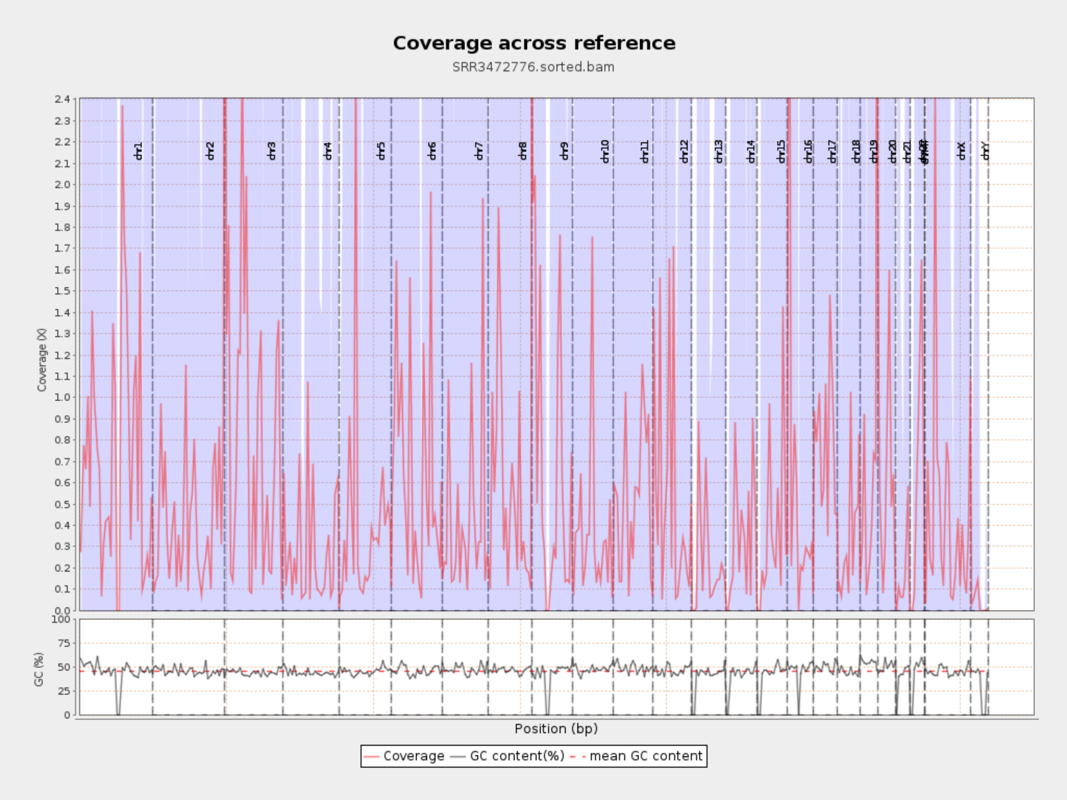
2.7. Chromosome stats

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

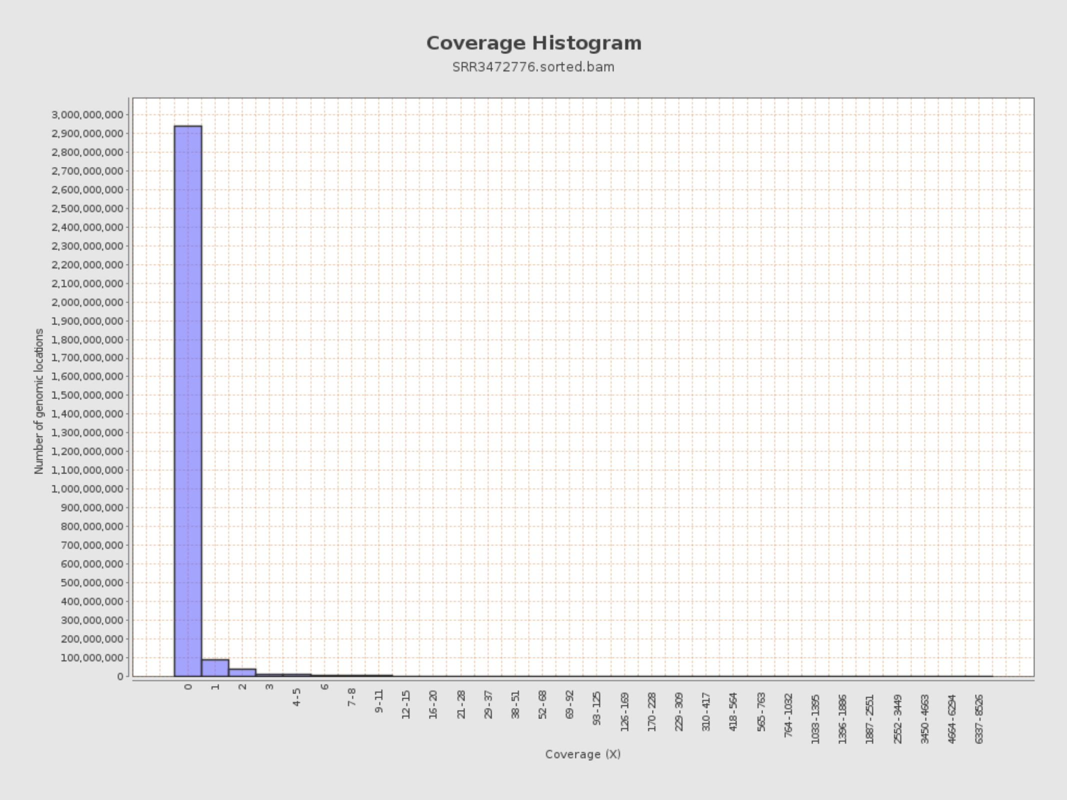
		bases	coverage	deviation
chr1	249250621	181911598	0.7298	21.7856
chr2	243199373	99487947	0.4091	13.2025
chr3	198022430	173320752	0.8753	20.555
chr4	191154276	53161826	0.2781	10.014
chr5	180915260	75149837	0.4154	12.2526
chr6	171115067	110523322	0.6459	22.4179
chr7	159138663	68934018	0.4332	13.9724
chr8	146364022	78738260	0.538	16.4105
chr9	141213431	97764663	0.6923	20.0396
chr10	135534747	49156326	0.3627	21.3974
chr11	135006516	73182170	0.5421	16.6997
chr12	133851895	76343446	0.5704	16.3387
chr13	115169878	26865641	0.2333	7.8032
chr14	107349540	36258144	0.3378	11.6117
chr15	102531392	39164910	0.382	10.5668
chr16	90354753	56789323	0.6285	17.7286
chr17	81195210	64494319	0.7943	20.0562
chr18	78077248	26741443	0.3425	12.0032
chr19	59128983	33108248	0.5599	14.0092
chr20	63025520	41114065	0.6523	18.3039
chr21	48129895	8038921	0.167	6.119
chr22	51304566	30282442	0.5902	19.8284
chrMT	16571	4616	0.2786	0.7907
chrX	155270560	69552801	0.4479	15.1977

chrY	59373566	2581473	0.0435	1.4461

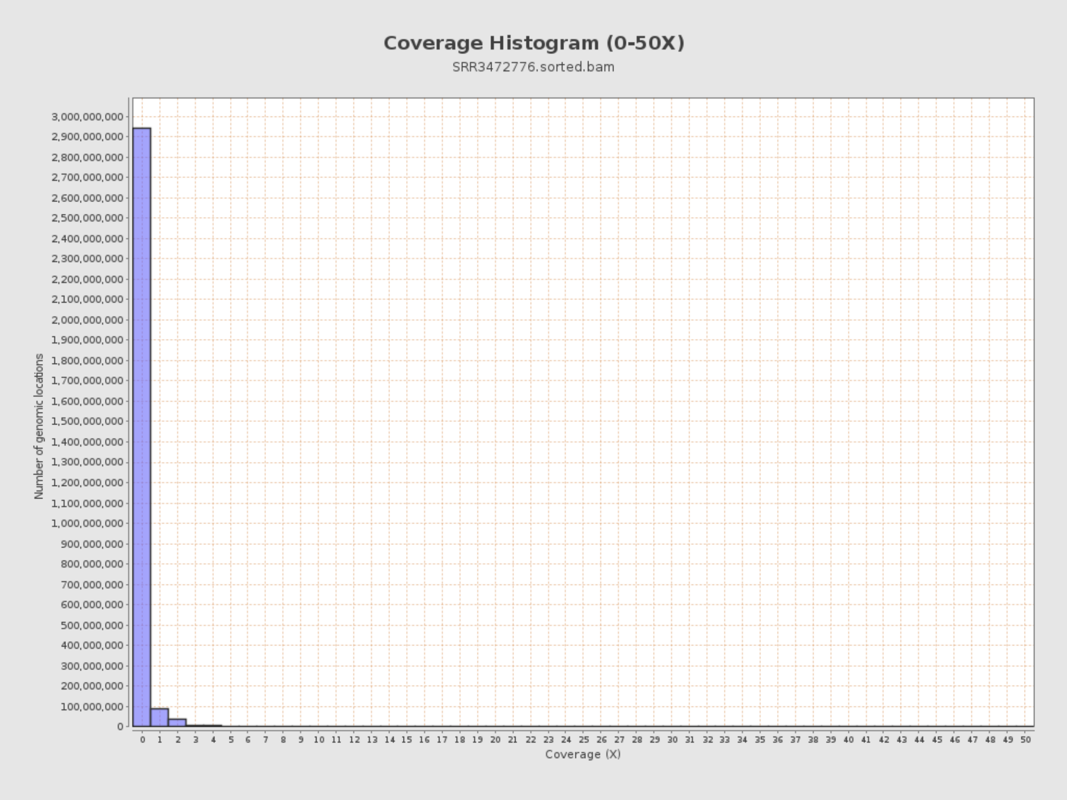
3. Results : Coverage across reference



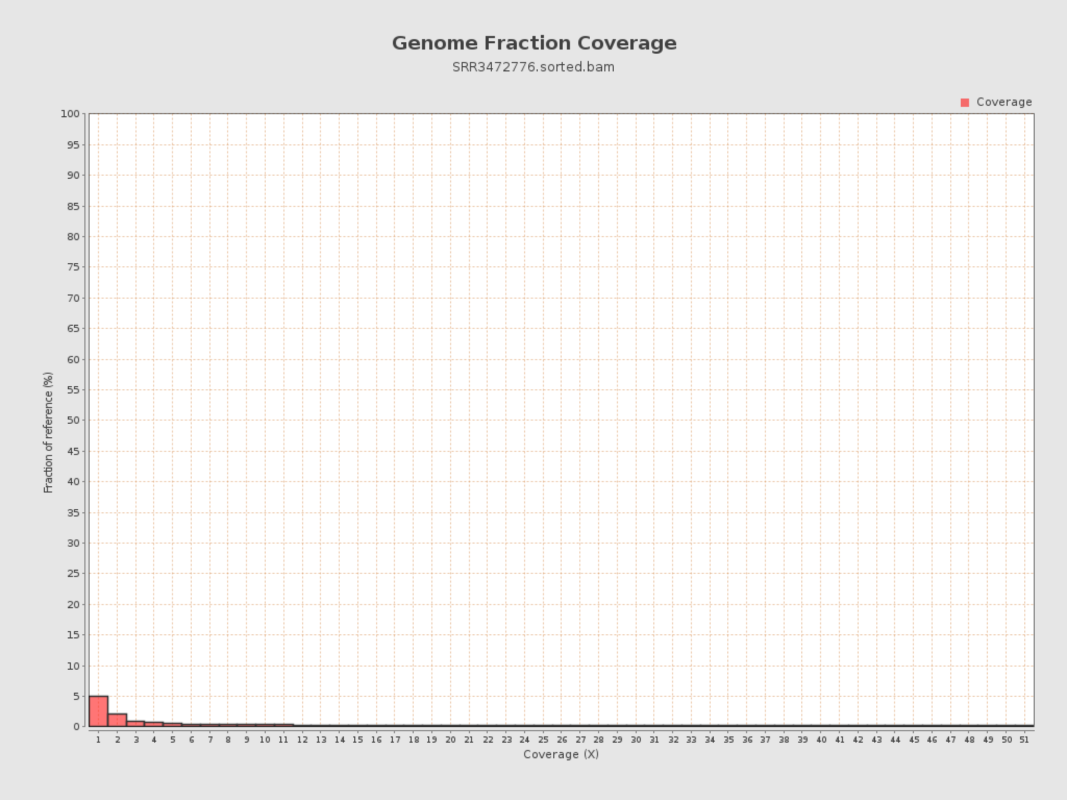
4. Results : Coverage Histogram



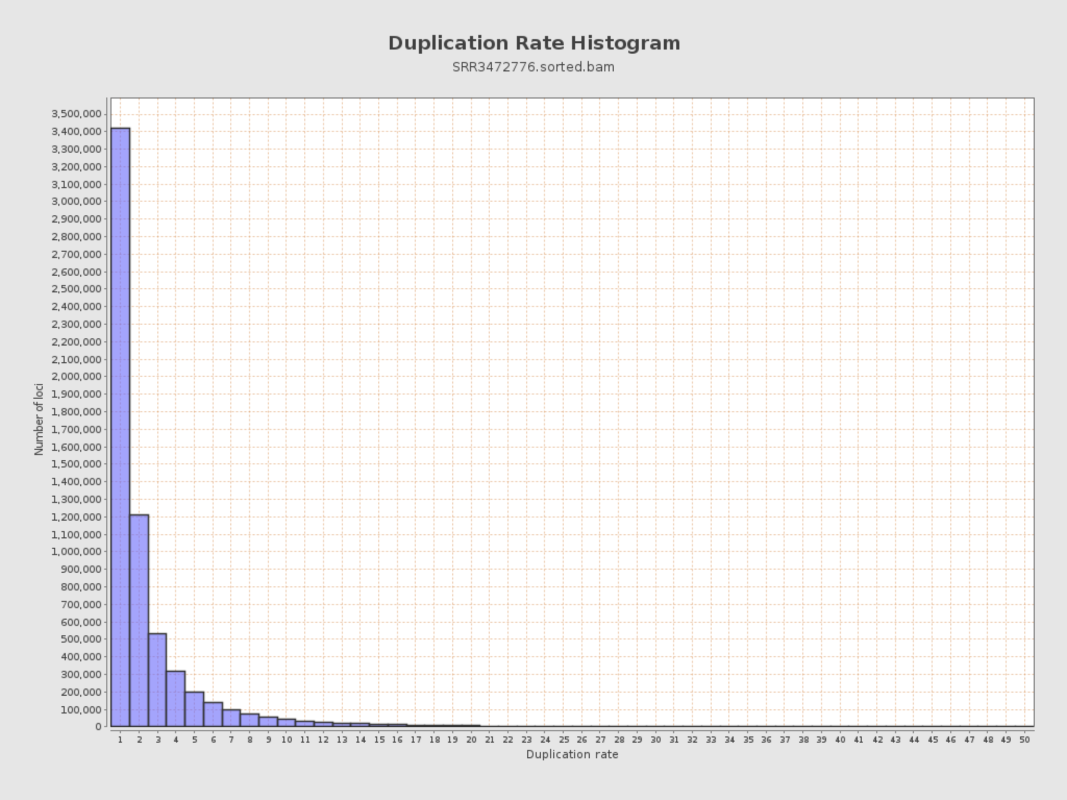
5. Results : Coverage Histogram (0-50X)



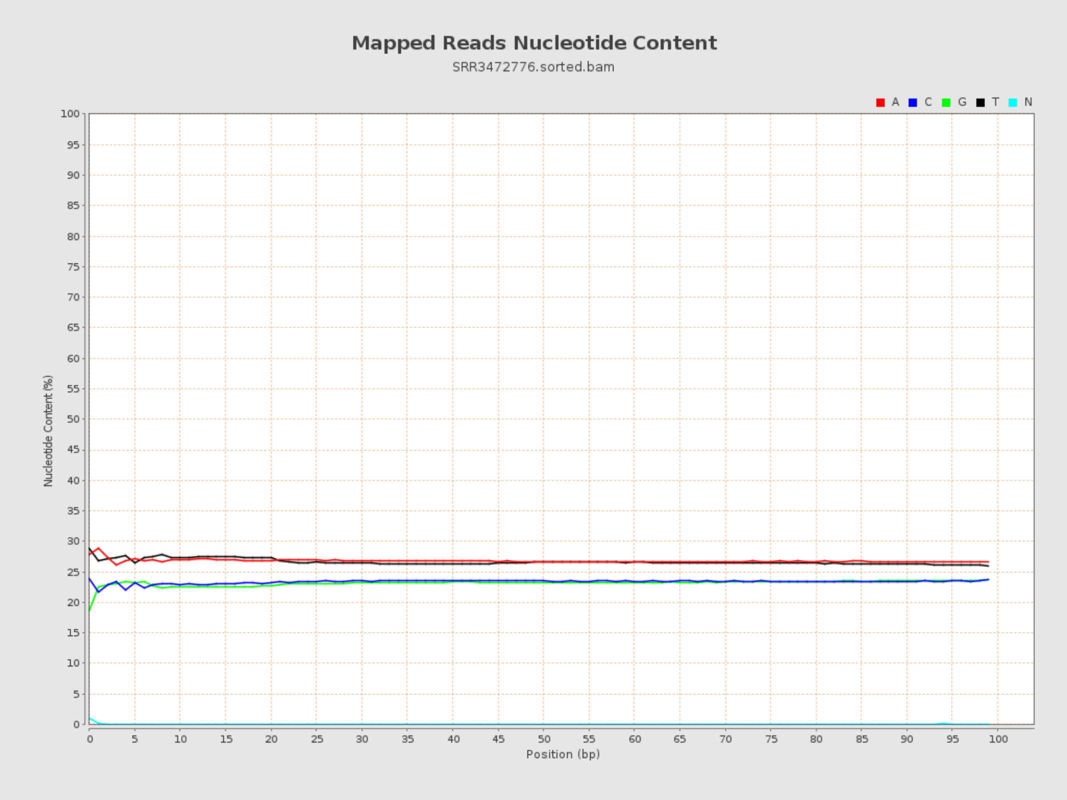
6. Results : Genome Fraction Coverage



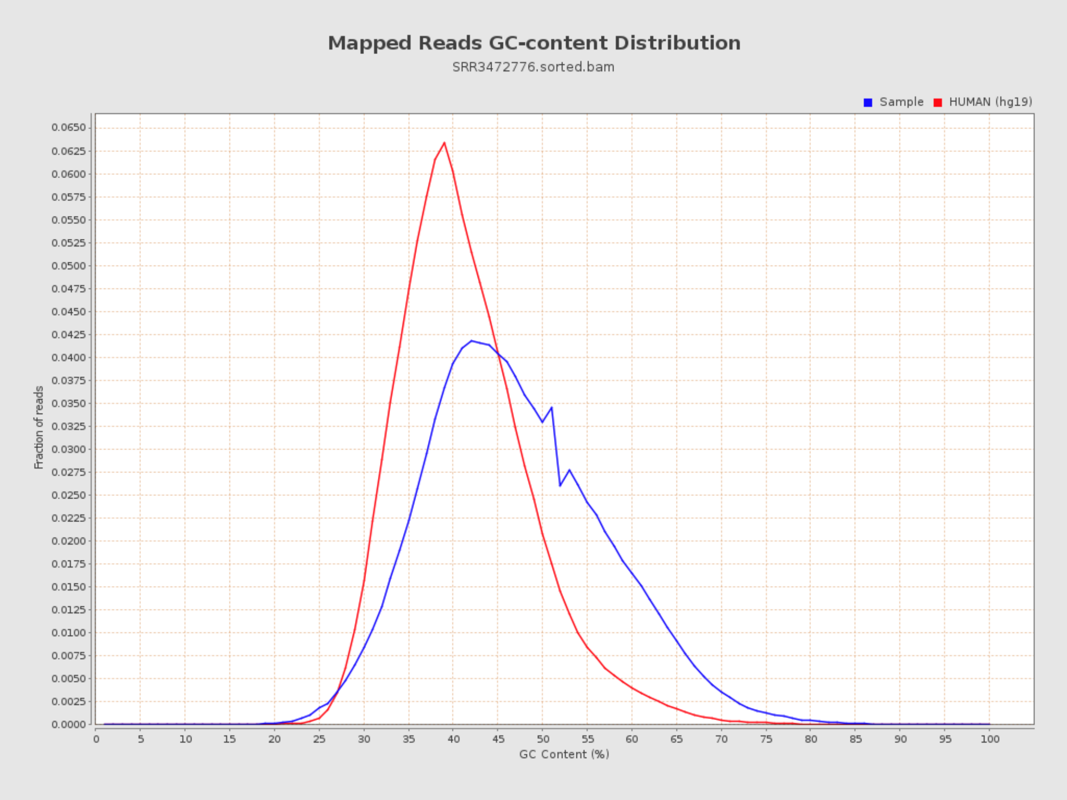
7. Results : Duplication Rate Histogram



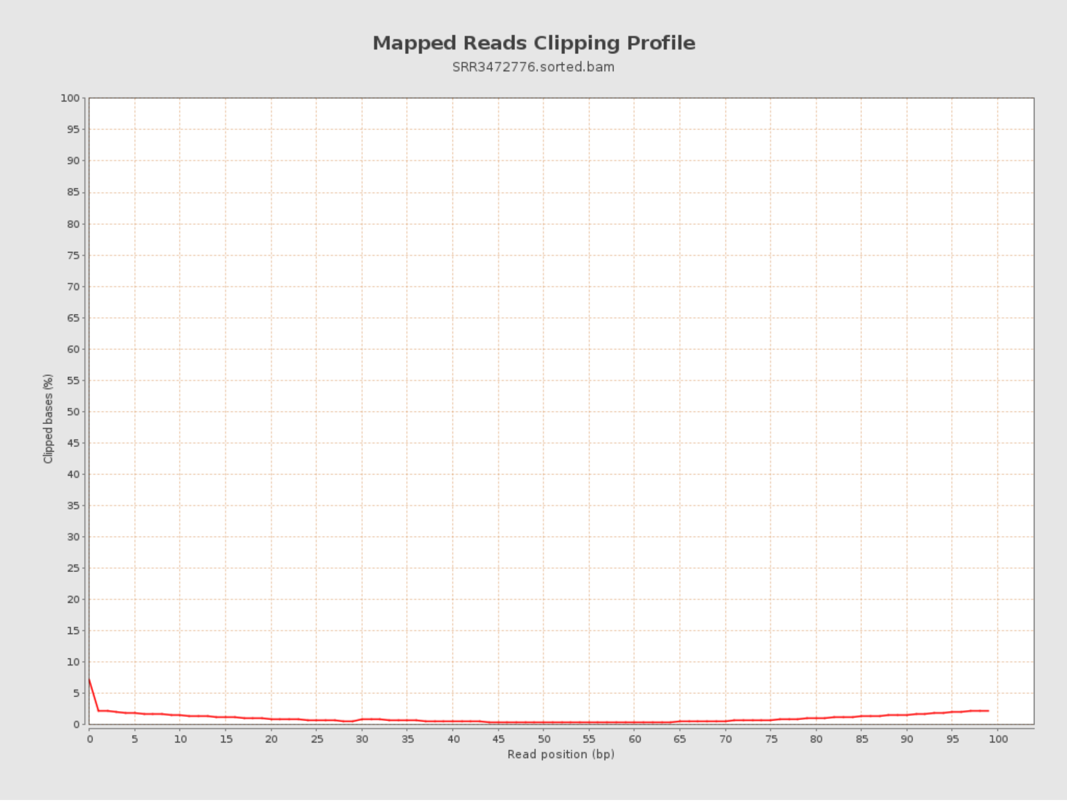
8. Results : Mapped Reads Nucleotide Content



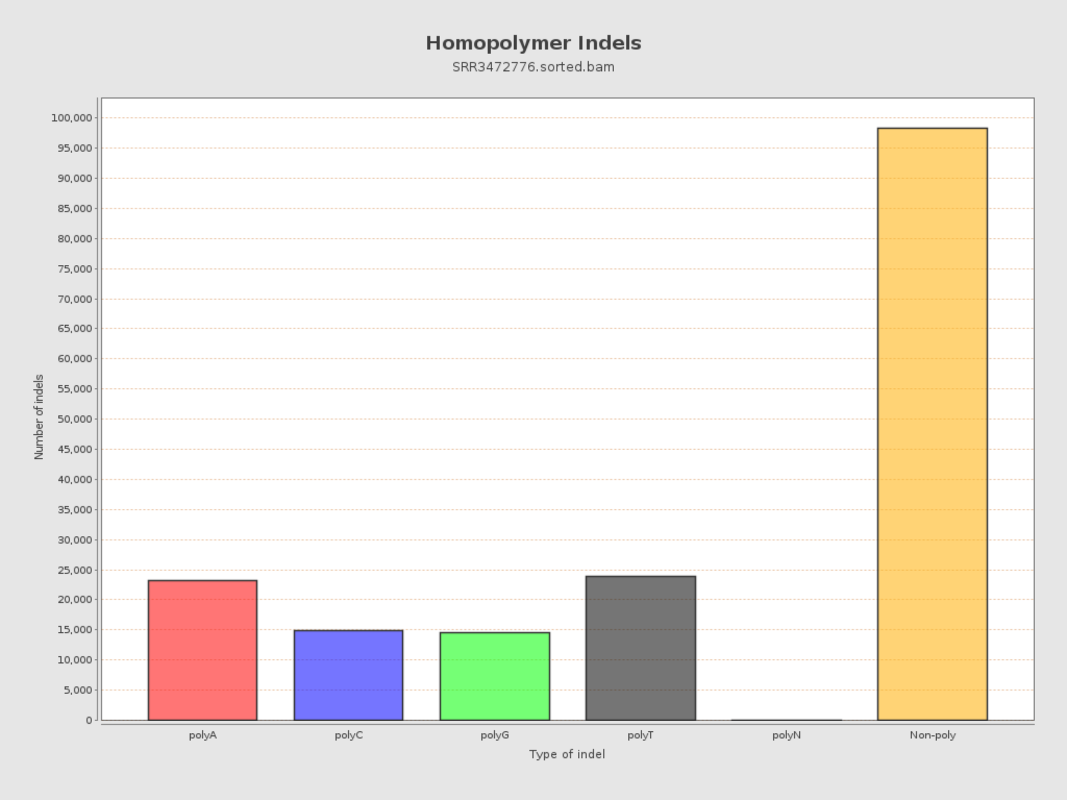
9. Results : Mapped Reads GC-content Distribution



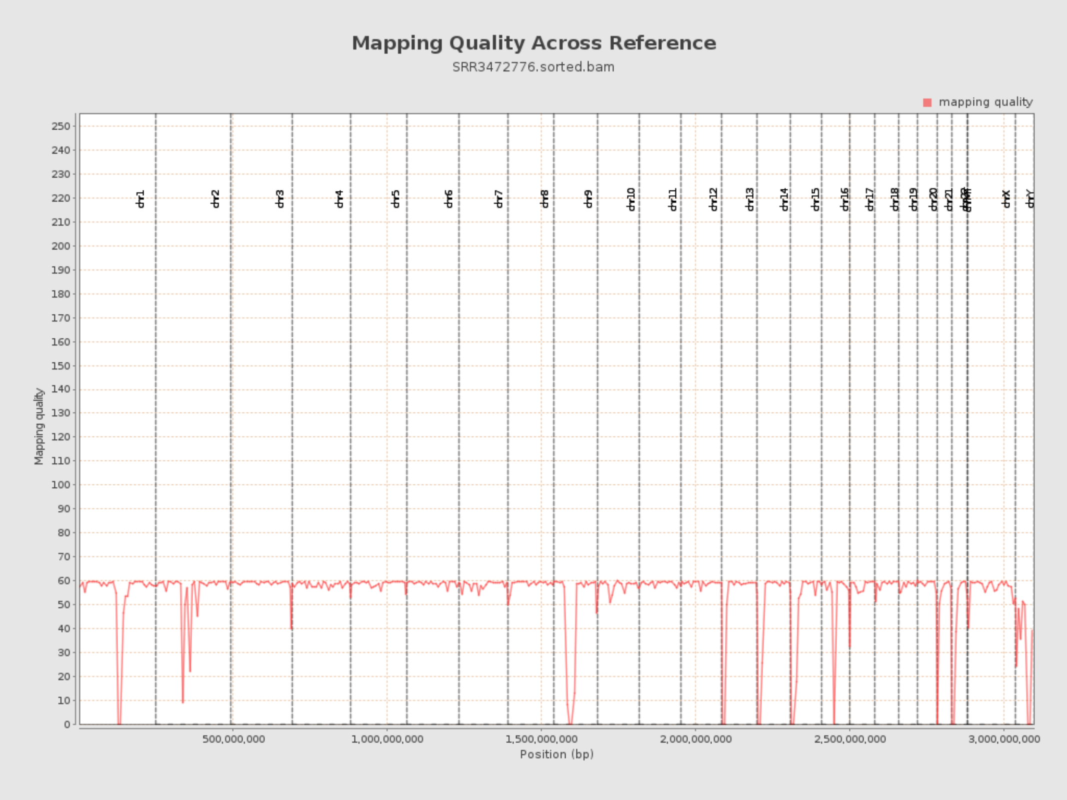
10. Results : Mapped Reads Clipping Profile



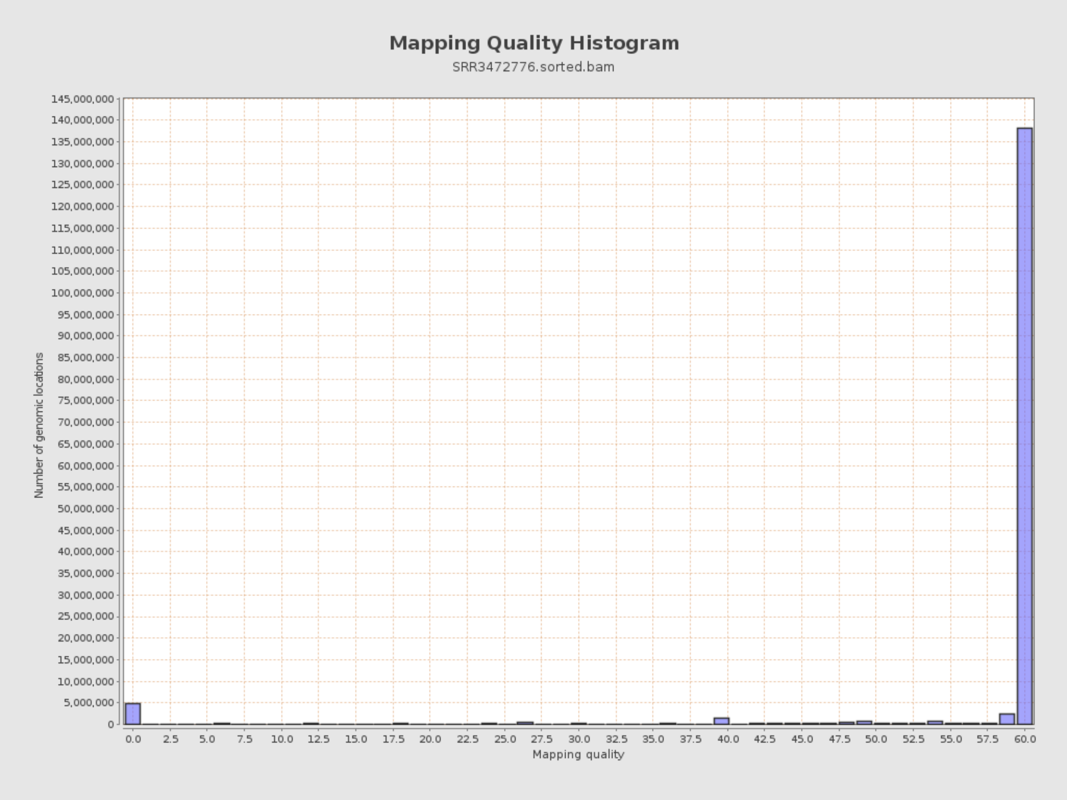
11. Results : Homopolymer Indels



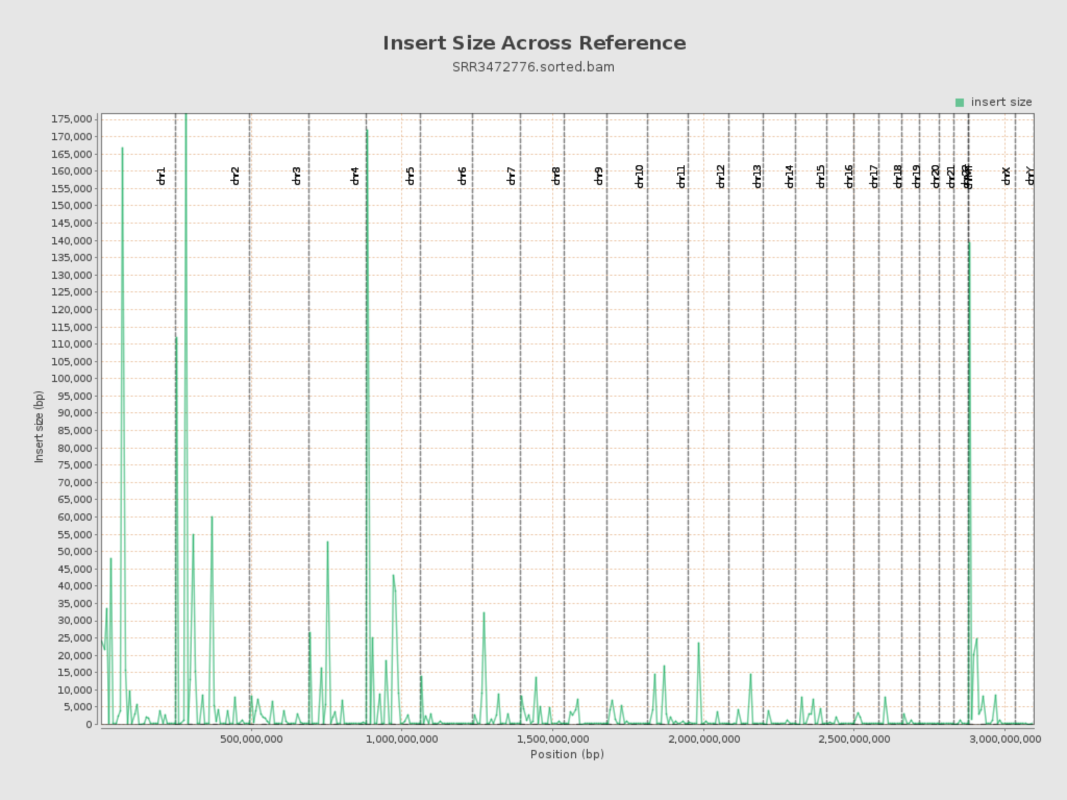
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram