Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 00:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472573.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_SRR3472573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472573_1.fastq.gz SRR3472573_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 00:26:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,606,918
Mapped reads	6,972,320 / 91.66%
Unmapped reads	634,598 / 8.34%
Mapped paired reads	6,972,320 / 91.66%
Mapped reads, first in pair	3,513,495 / 46.19%
Mapped reads, second in pair	3,458,825 / 45.47%
Mapped reads, both in pair	6,811,314 / 89.54%
Mapped reads, singletons	161,006 / 2.12%
Secondary alignments	0
Supplementary alignments	210,320 / 2.76%
Read min/max/mean length	30 / 100 / 101.08
Duplicated reads (estimated)	1,067,978 / 14.04%
Duplication rate	13.59%
Clipped reads	5,476,804 / 72%

2.2. ACGT Content

Number/percentage of A's	143,468,804 / 25.58%
Number/percentage of C's	112,581,677 / 20.07%
Number/percentage of T's	166,490,530 / 29.68%
Number/percentage of G's	137,987,486 / 24.6%
Number/percentage of N's	369,253 / 0.07%

GC Percentage	44.67%

2.3. Coverage

Mean	0.1813
Standard Deviation	1.7404

2.4. Mapping Quality

Mean Mapping Quality	50.35

2.5. Insert size

Mean	231,221.84
Standard Deviation	4,649,341.22
P25/Median/P75	87 / 125 / 174

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	6,671,491
Insertions	55,279
Mapped reads with at least one insertion	0.78%
Deletions	125,674
Mapped reads with at least one deletion	1.77%
Homopolymer indels	42.55%

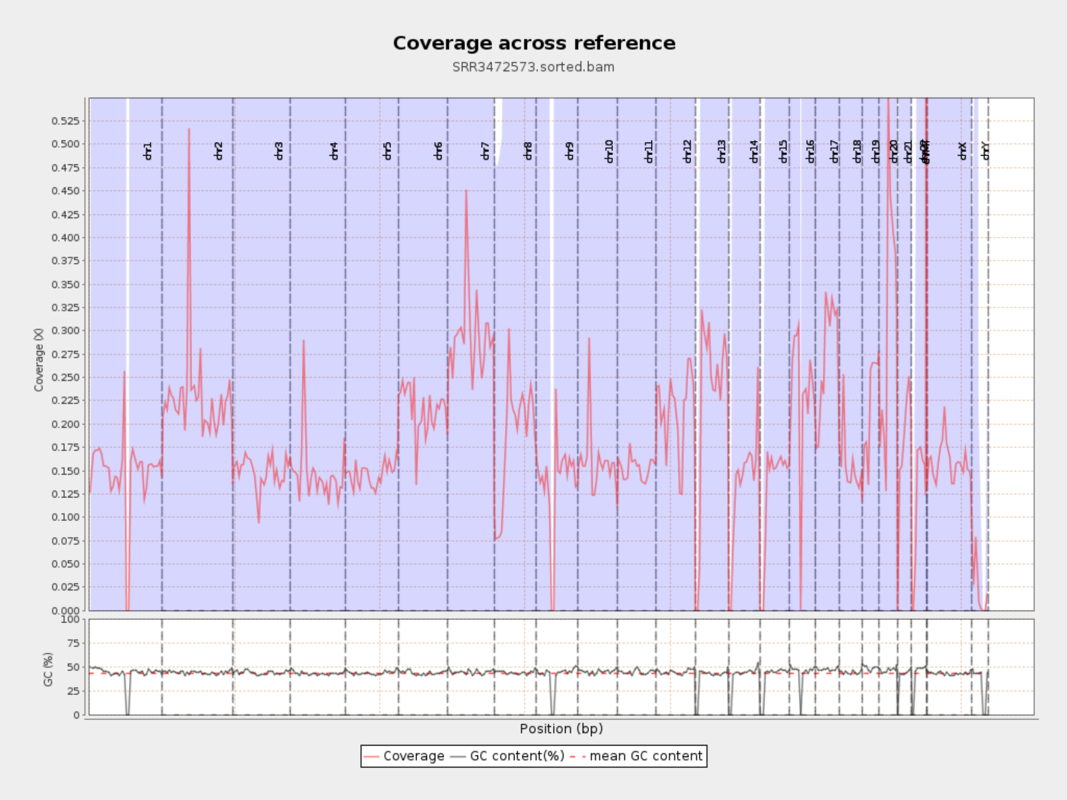
2.7. Chromosome stats

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

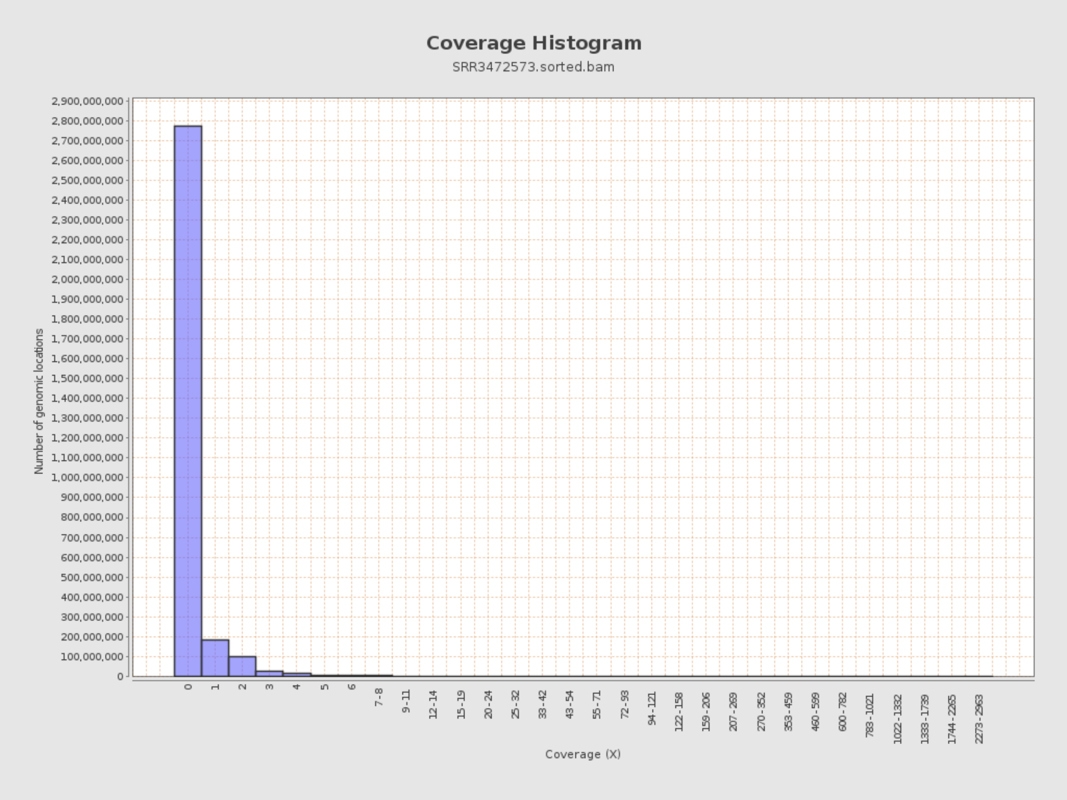
		bases	coverage	deviation
chr1	249250621	36527483	0.1465	2.0467
chr2	243199373	55963925	0.2301	2.4585
chr3	198022430	29394338	0.1484	0.5658
chr4	191154276	27995425	0.1465	0.9728
chr5	180915260	26484610	0.1464	0.5927
chr6	171115067	36970642	0.2161	1.0004
chr7	159138663	47375394	0.2977	3.2578
chr8	146364022	27239889	0.1861	1.4719
chr9	141213431	19240820	0.1363	1.7609
chr10	135534747	21707930	0.1602	1.5356
chr11	135006516	20472733	0.1516	1.2962
chr12	133851895	28693770	0.2144	0.7085
chr13	115169878	26107341	0.2267	0.7318
chr14	107349540	14558173	0.1356	4.1793
chr15	102531392	13251295	0.1292	0.5341
chr16	90354753	21057297	0.2331	1.0708
chr17	81195210	22447118	0.2765	1.4773
chr18	78077248	12260840	0.157	2.9419
chr19	59128983	12902744	0.2182	1.4868
chr20	63025520	19961423	0.3167	1.0934
chr21	48129895	8555841	0.1778	0.8067
chr22	51304566	5805897	0.1132	0.5085
chrMT	16571	63852	3.8532	3.7676
chrX	155270560	24759643	0.1595	0.8238

chrY	59373566	1335341	0.0225	0.7952

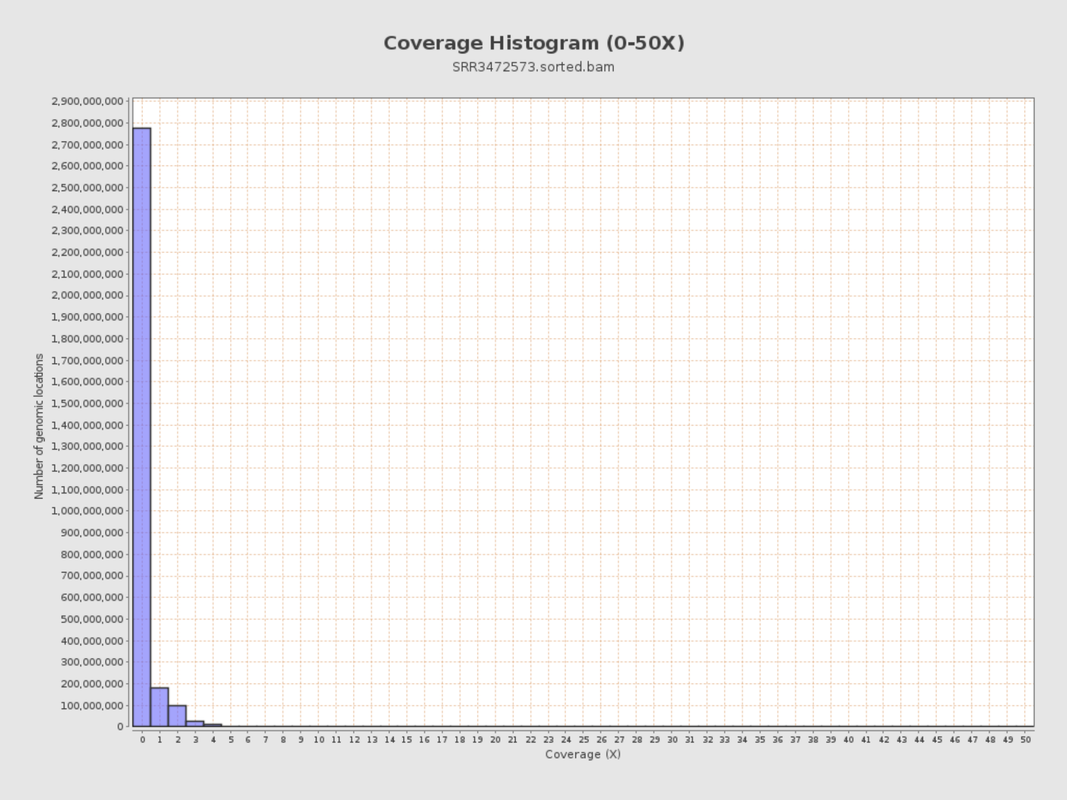
3. Results : Coverage across reference



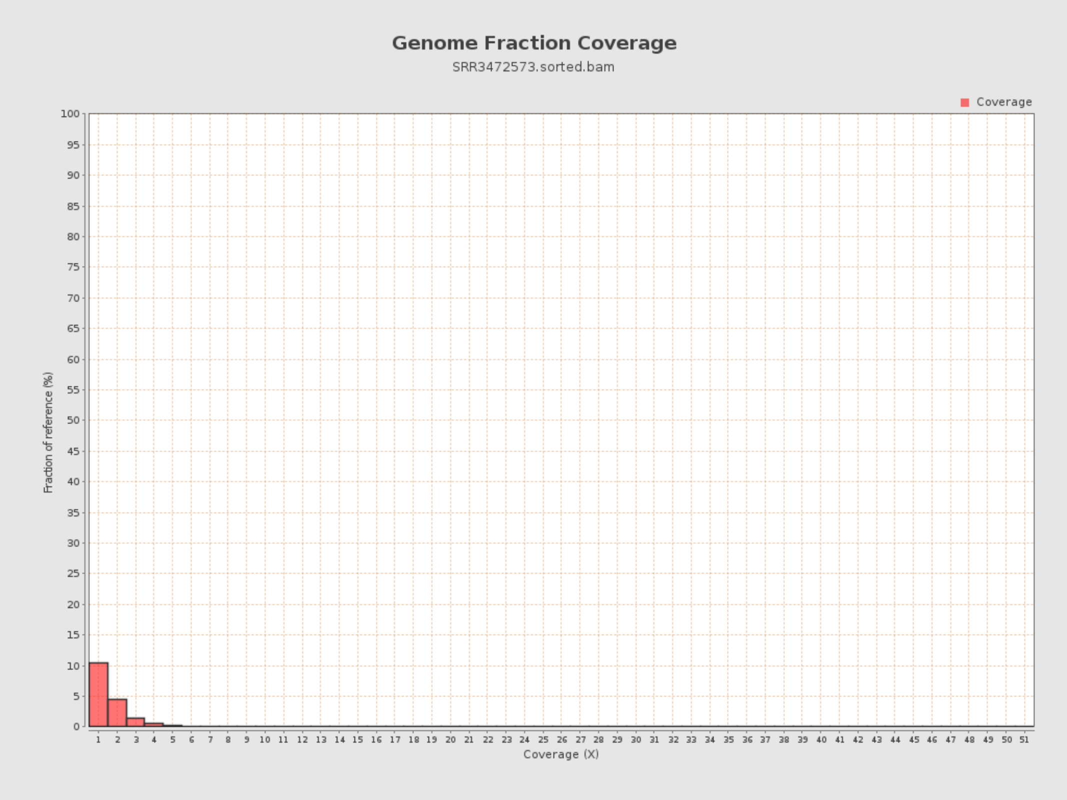
4. Results : Coverage Histogram



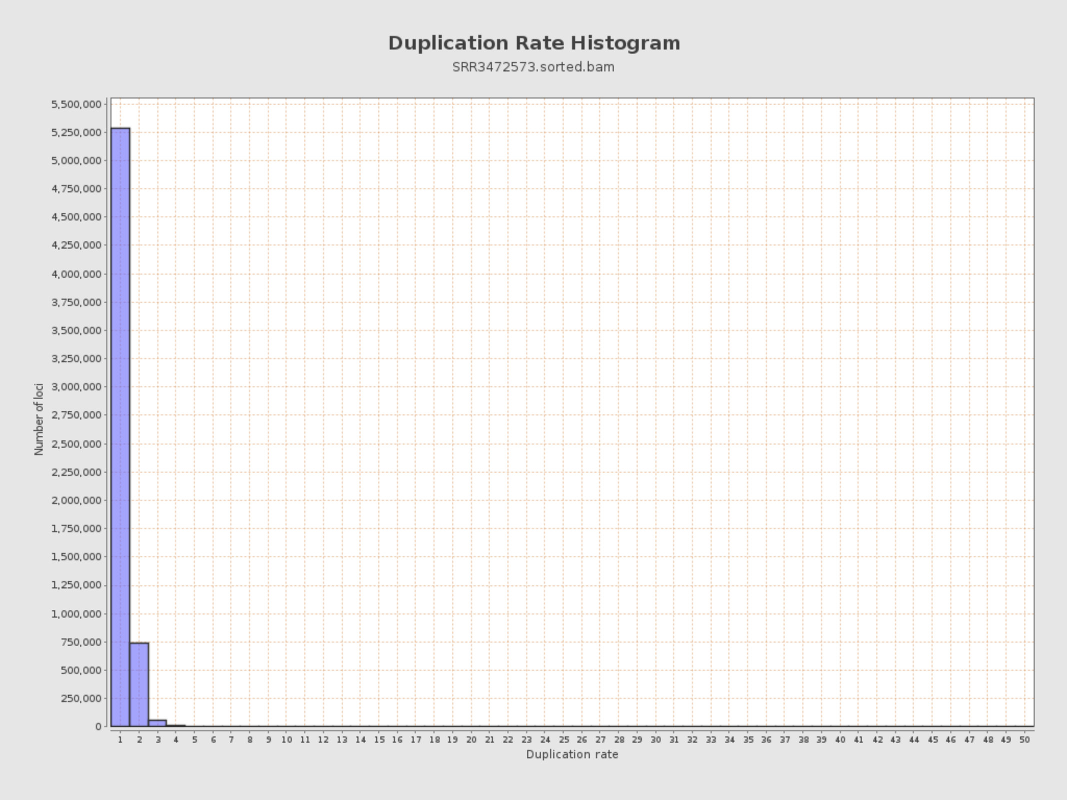
5. Results : Coverage Histogram (0-50X)



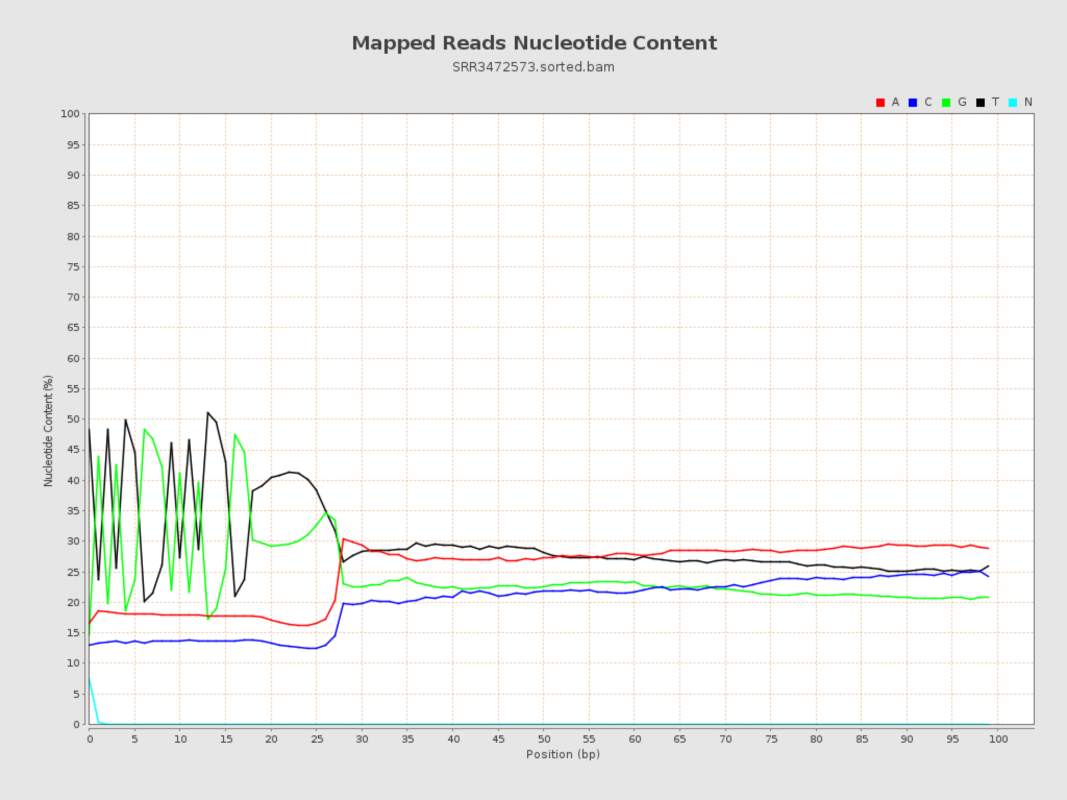
6. Results : Genome Fraction Coverage



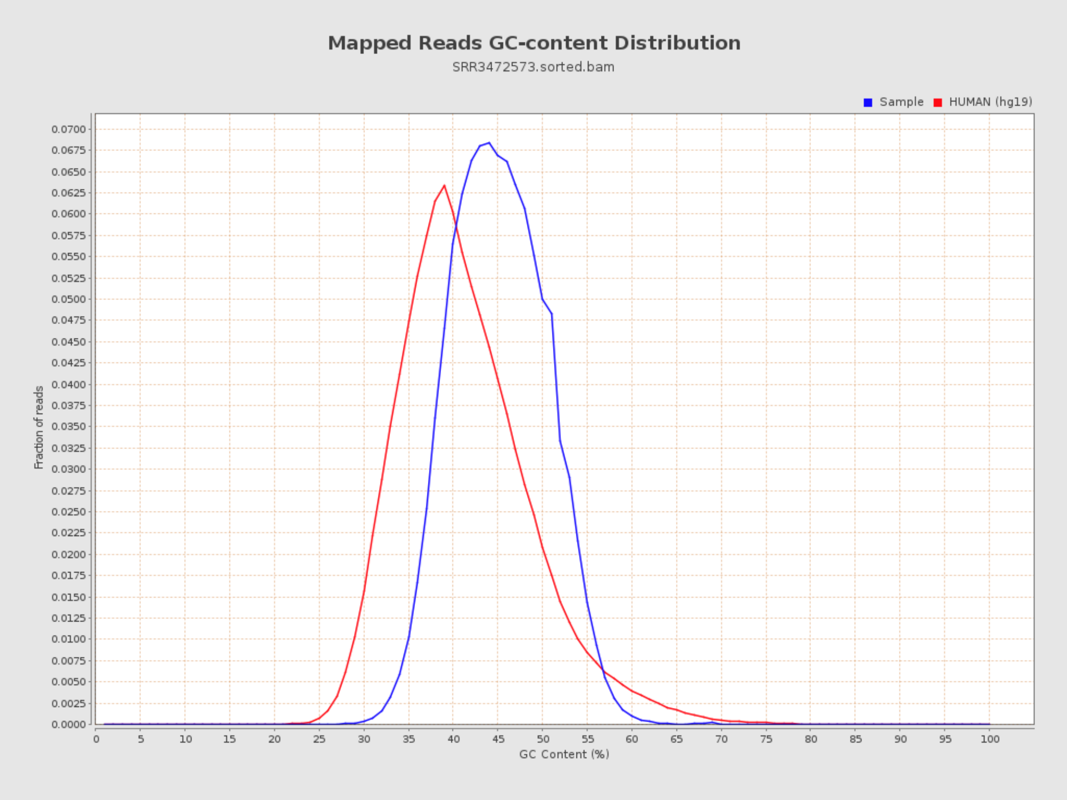
7. Results : Duplication Rate Histogram



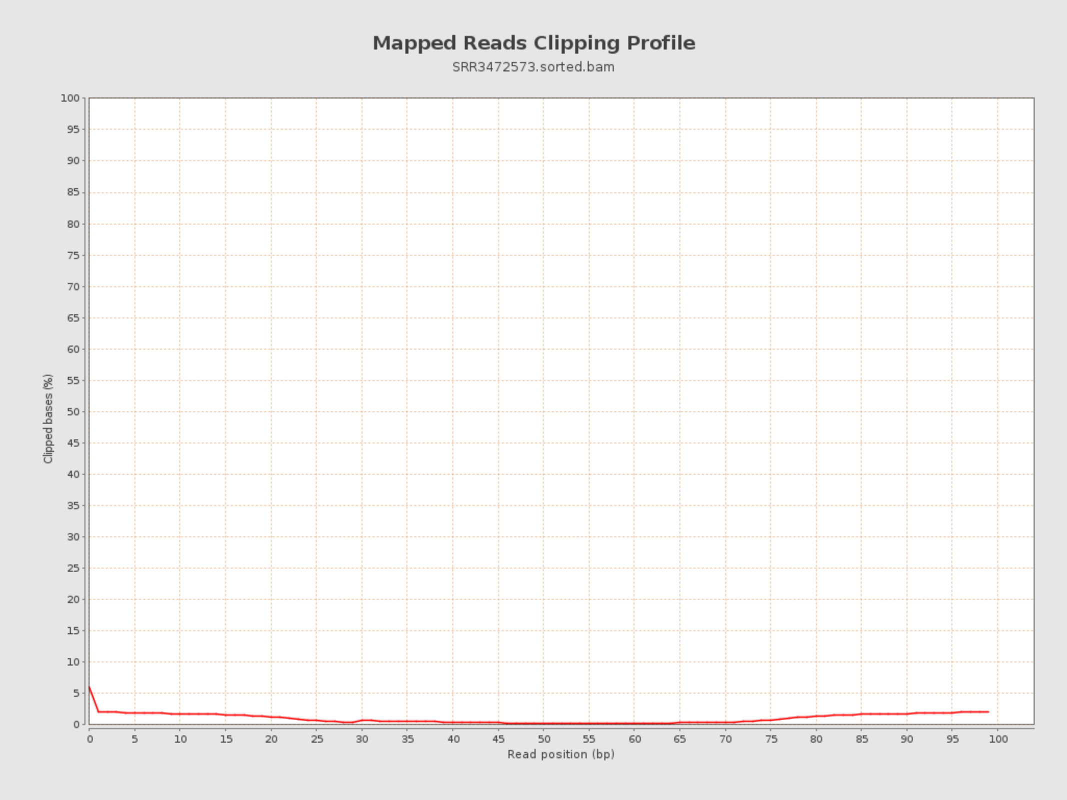
8. Results : Mapped Reads Nucleotide Content



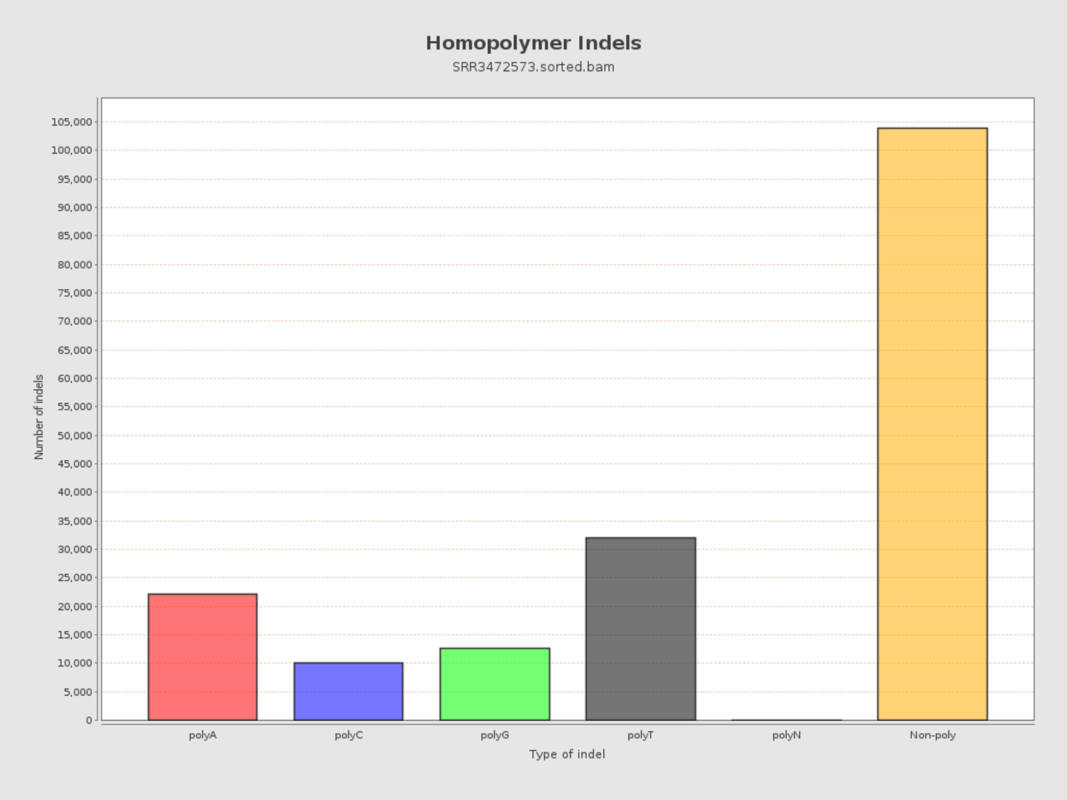
9. Results : Mapped Reads GC-content Distribution



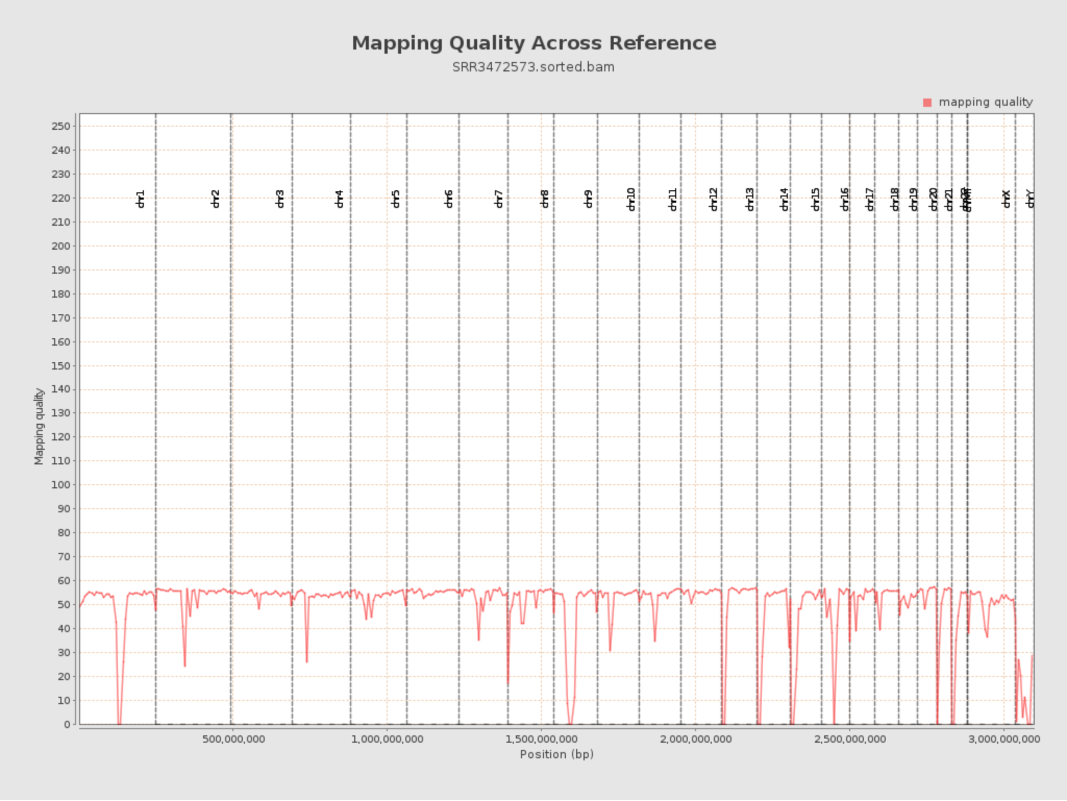
10. Results : Mapped Reads Clipping Profile



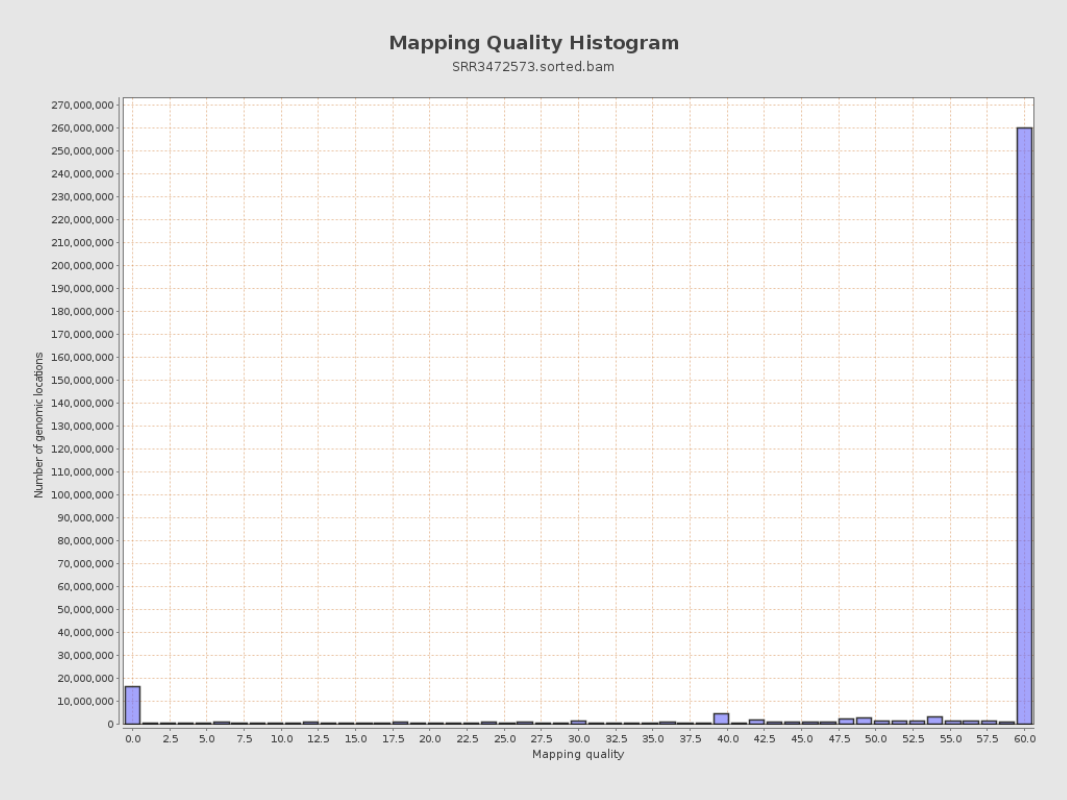
11. Results : Homopolymer Indels



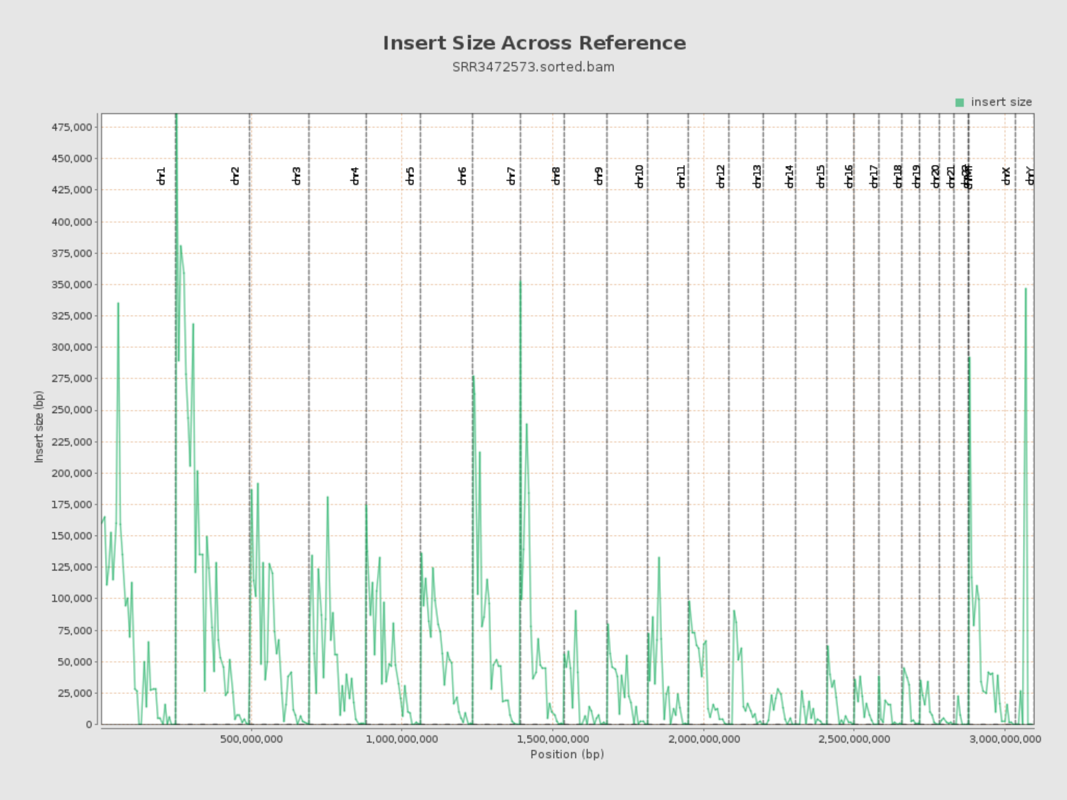
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram