Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:13:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472465.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_SRR3472465 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472465_1.fastq.gz SRR3472465_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:13:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472465.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,740,070
Mapped reads	31,392,576 / 98.91%
Unmapped reads	347,494 / 1.09%
Mapped paired reads	31,392,576 / 98.91%
Mapped reads, first in pair	15,731,154 / 49.56%
Mapped reads, second in pair	15,661,422 / 49.34%
Mapped reads, both in pair	31,228,948 / 98.39%
Mapped reads, singletons	163,628 / 0.52%
Secondary alignments	0
Supplementary alignments	112,767 / 0.36%
Read min/max/mean length	30 / 100 / 99.12
Duplicated reads (estimated)	22,310,250 / 70.29%
Duplication rate	47.79%
Clipped reads	2,806,178 / 8.84%

2.2. ACGT Content

Number/percentage of A's	809,600,469 / 26.48%
Number/percentage of C's	722,870,135 / 23.64%
Number/percentage of T's	806,807,722 / 26.39%
Number/percentage of G's	717,883,166 / 23.48%
Number/percentage of N's	394,427 / 0.01%

GC Percentage	47.12%

2.3. Coverage

Mean	0.9878
Standard Deviation	34.0052

2.4. Mapping Quality

Mean Mapping Quality	55.09

2.5. Insert size

Mean	17,658.84
Standard Deviation	1,369,379.26
P25/Median/P75	138 / 192 / 259

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	16,620,249
Insertions	181,456
Mapped reads with at least one insertion	0.57%
Deletions	143,136
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.13%

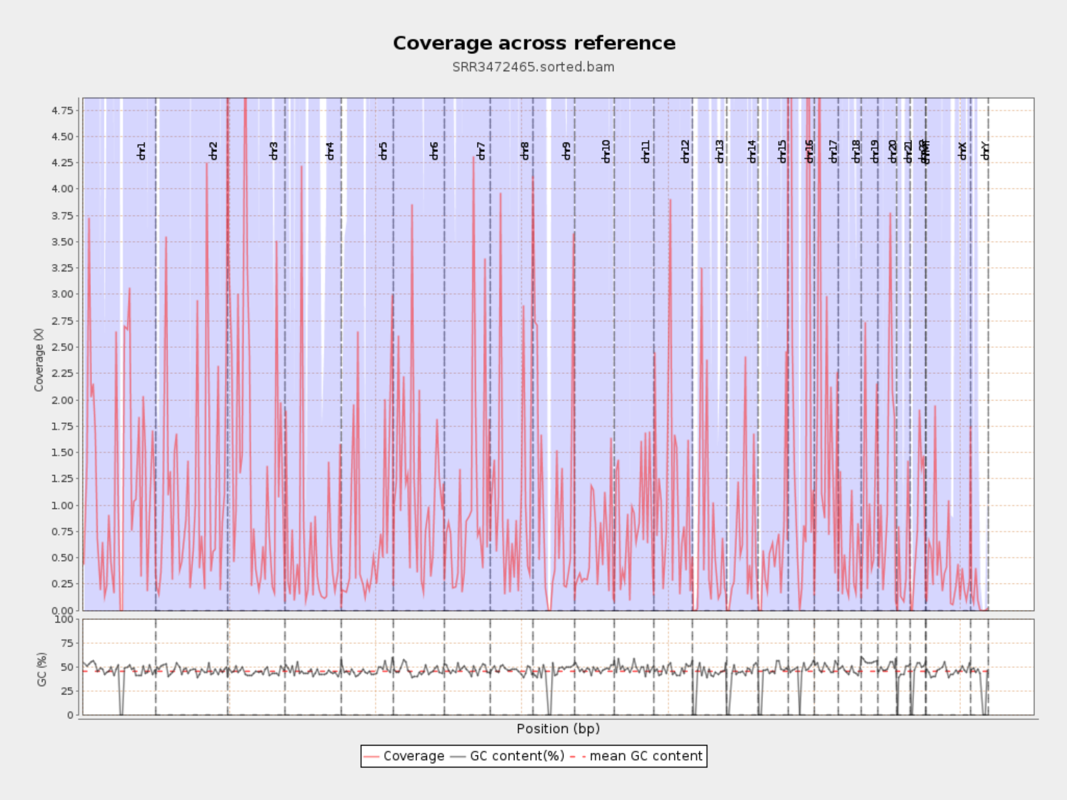
2.7. Chromosome stats

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

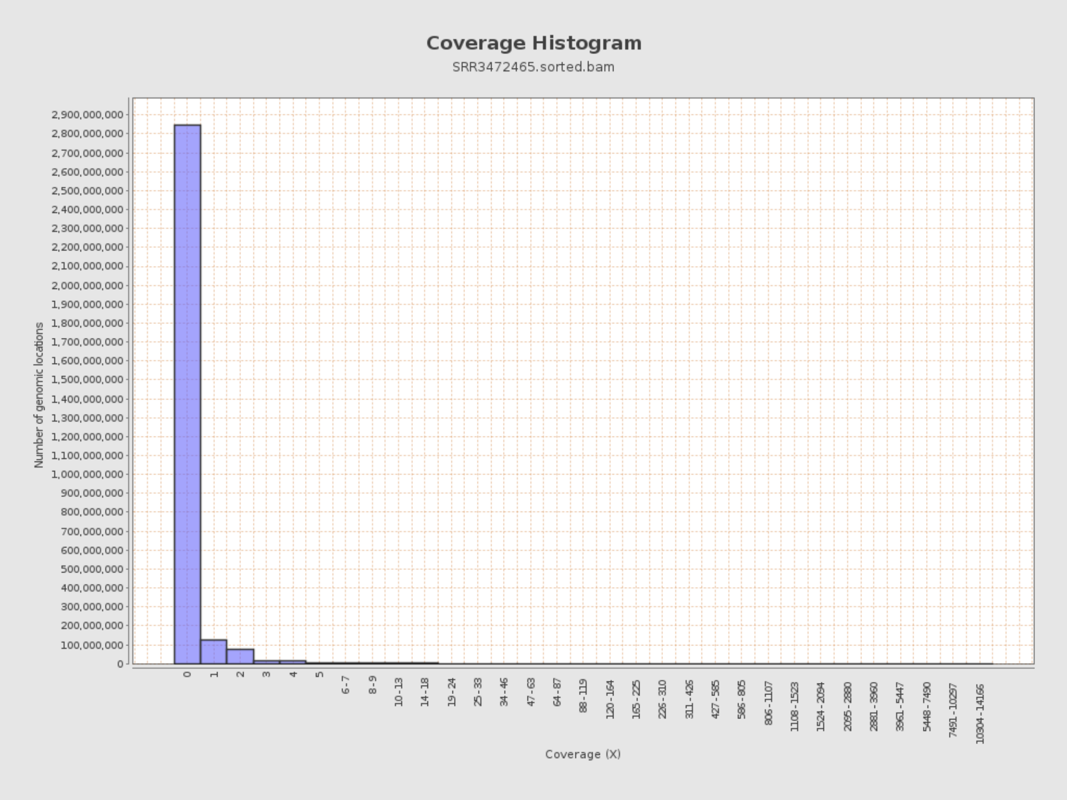
		bases	coverage	deviation
chr1	249250621	305843976	1.2271	36.1961
chr2	243199373	271730234	1.1173	39.5177
chr3	198022430	299790482	1.5139	39.3447
chr4	191154276	122908102	0.643	27.994
chr5	180915260	144518238	0.7988	31.2028
chr6	171115067	208687846	1.2196	33.2908
chr7	159138663	167337934	1.0515	35.1664
chr8	146364022	157947080	1.0791	36.3425
chr9	141213431	140666671	0.9961	31.0167
chr10	135534747	81856455	0.604	20.0671
chr11	135006516	114018332	0.8445	27.235
chr12	133851895	153556927	1.1472	31.1388
chr13	115169878	82044294	0.7124	27.5565
chr14	107349540	68169616	0.635	27.4718
chr15	102531392	59523396	0.5805	22.335
chr16	90354753	205313657	2.2723	70.072
chr17	81195210	146413194	1.8032	55.4612
chr18	78077248	39531971	0.5063	18.9873
chr19	59128983	63170110	1.0683	29.252
chr20	63025520	82466893	1.3085	47.3299
chr21	48129895	22422936	0.4659	22.431
chr22	51304566	45234996	0.8817	32.3952
chrMT	16571	3683	0.2223	0.5676
chrX	155270560	69312230	0.4464	13.4247

chrY	59373566	5440722	0.0916	4.5936

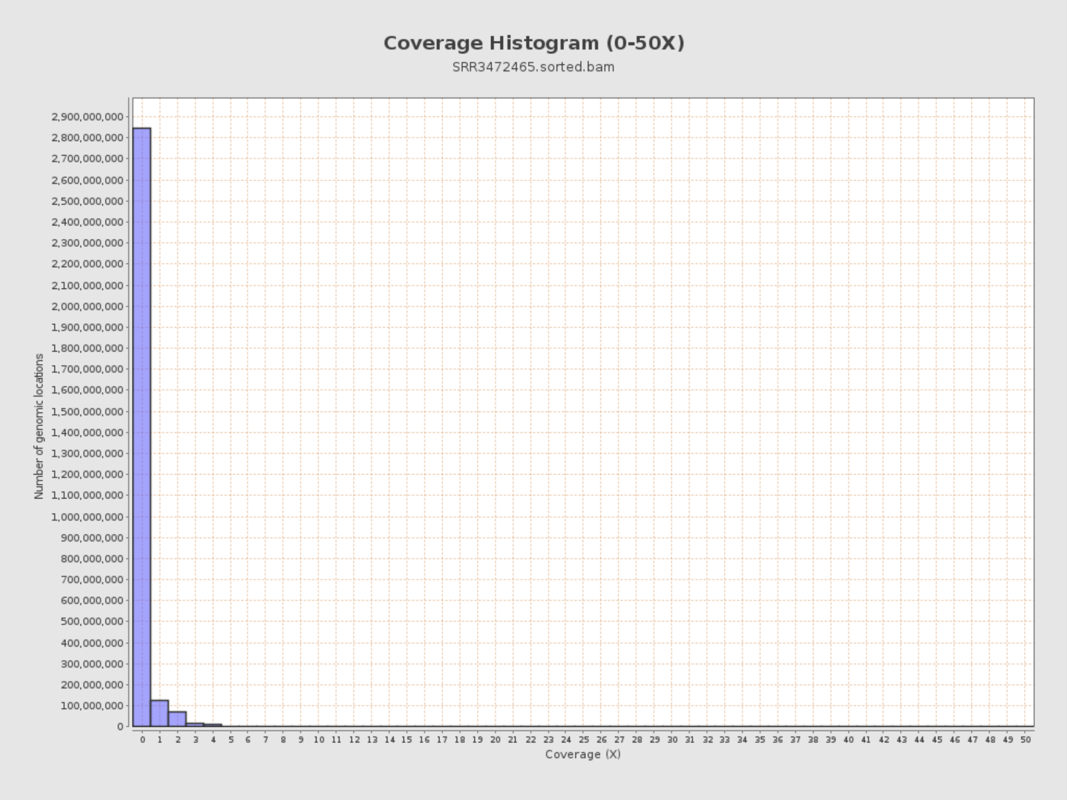
3. Results : Coverage across reference



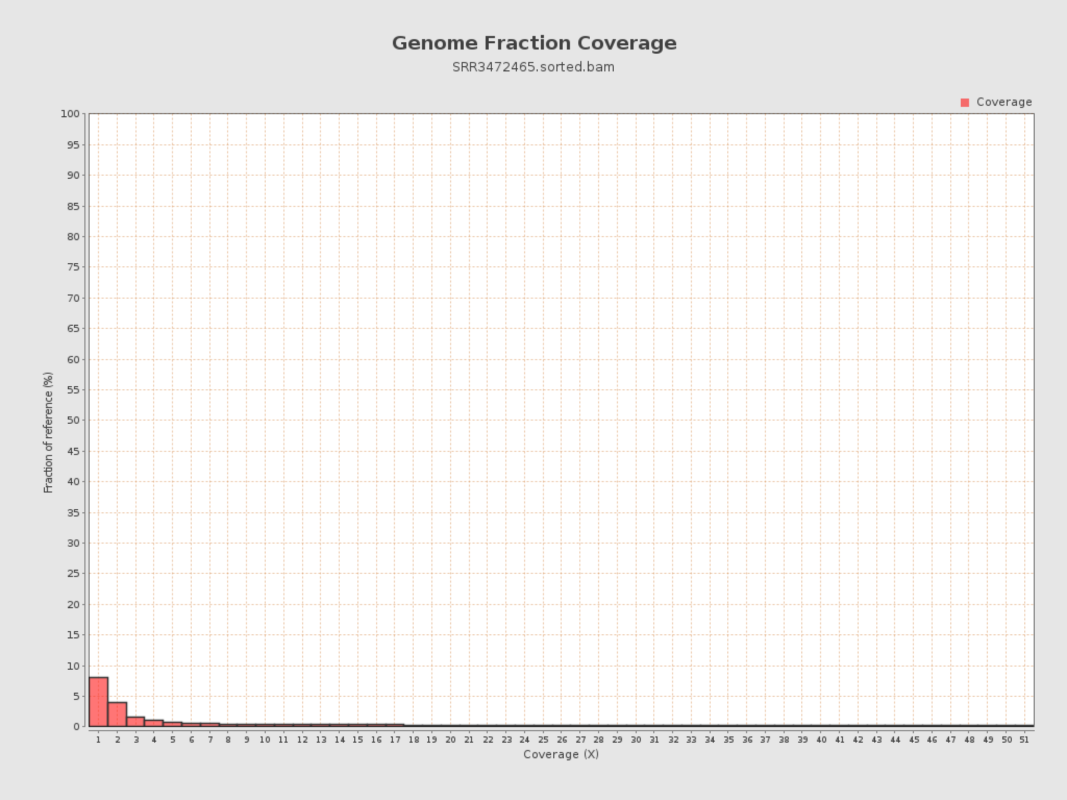
4. Results : Coverage Histogram



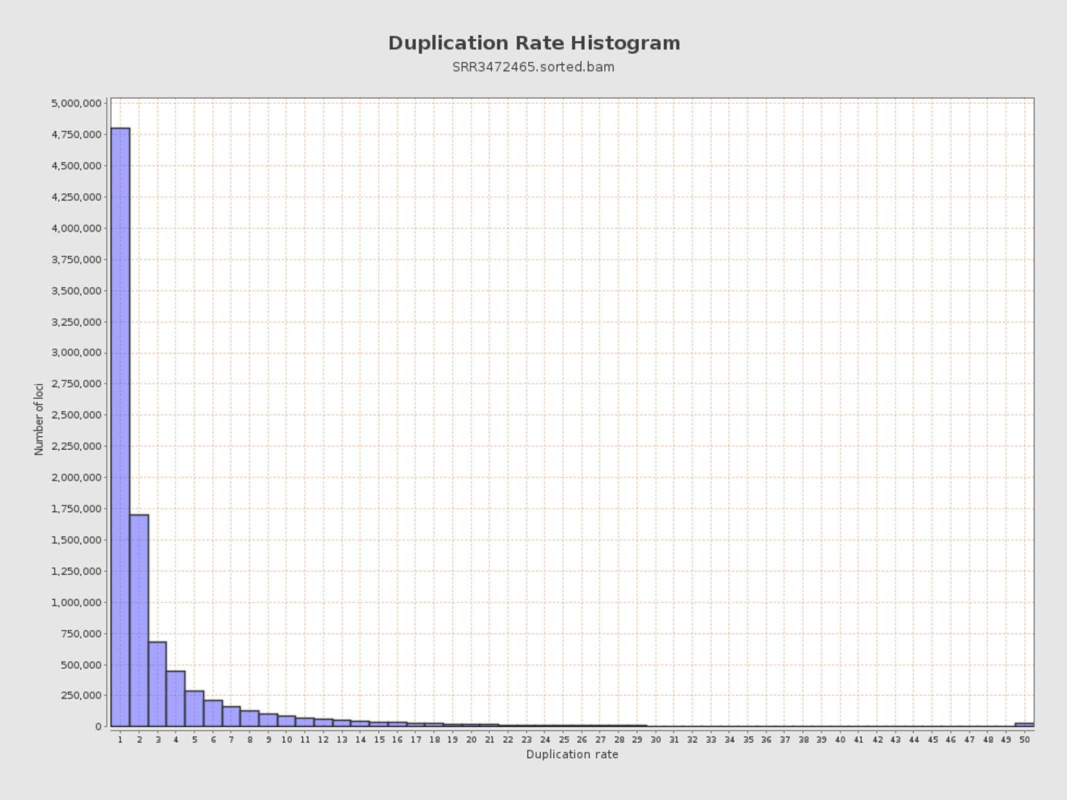
5. Results : Coverage Histogram (0-50X)



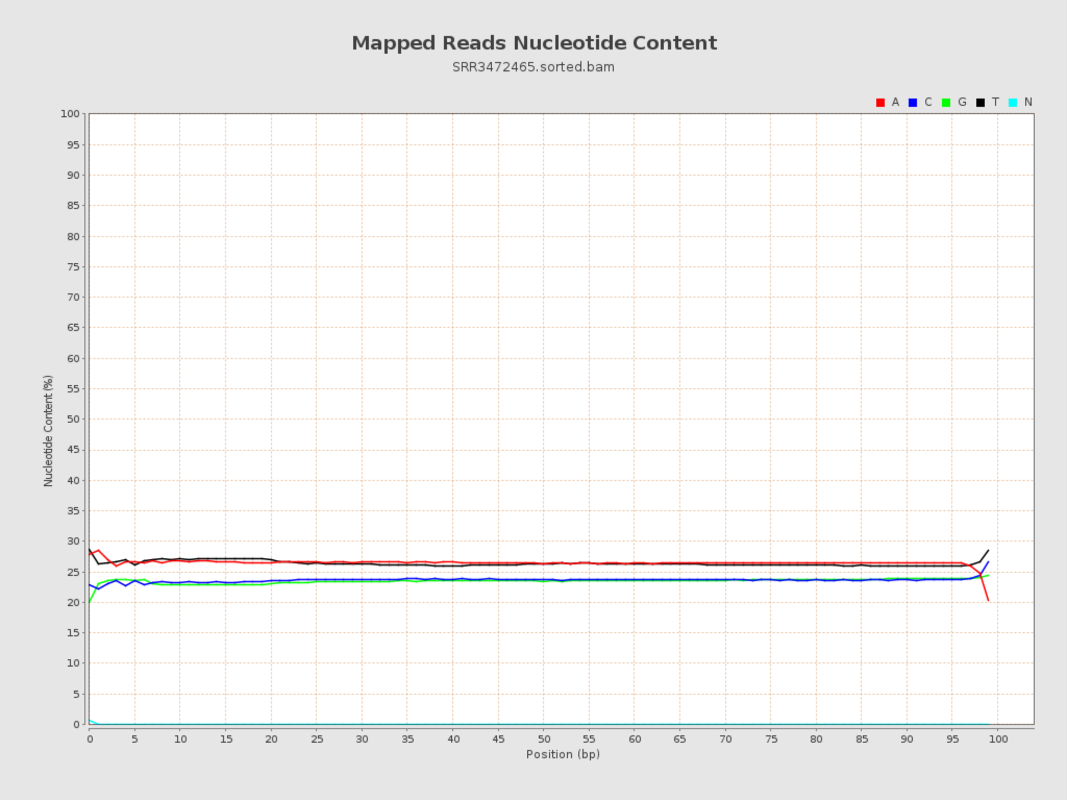
6. Results : Genome Fraction Coverage



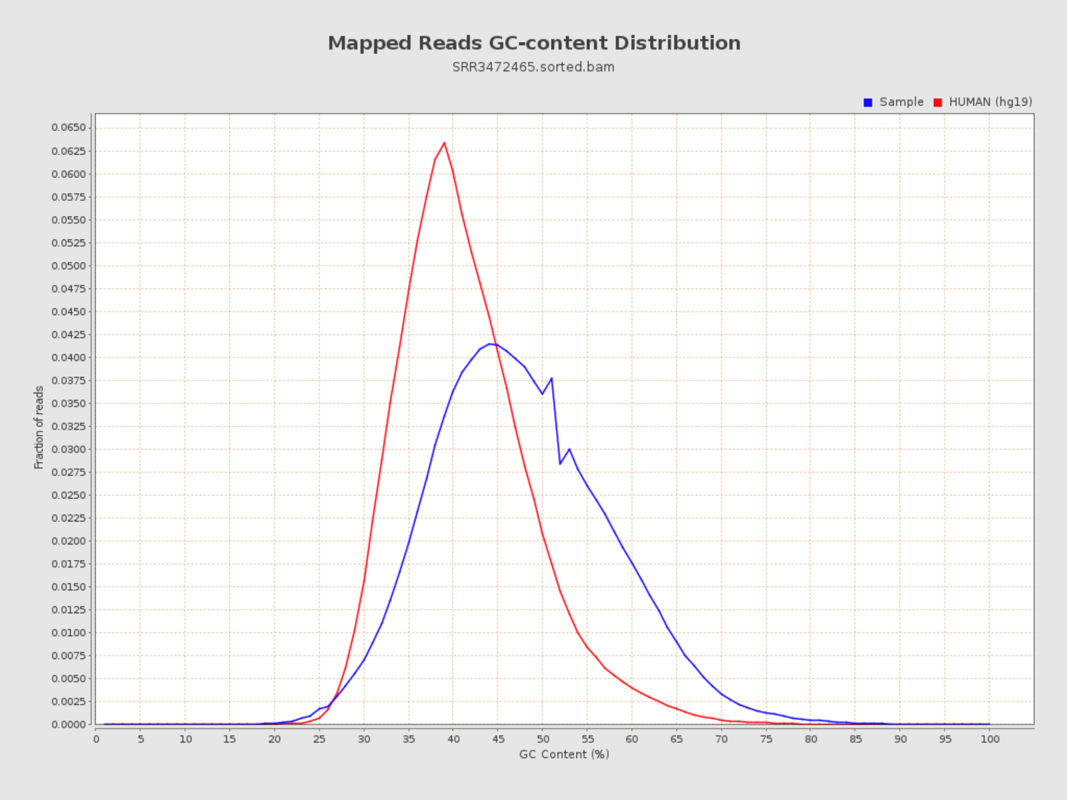
7. Results : Duplication Rate Histogram



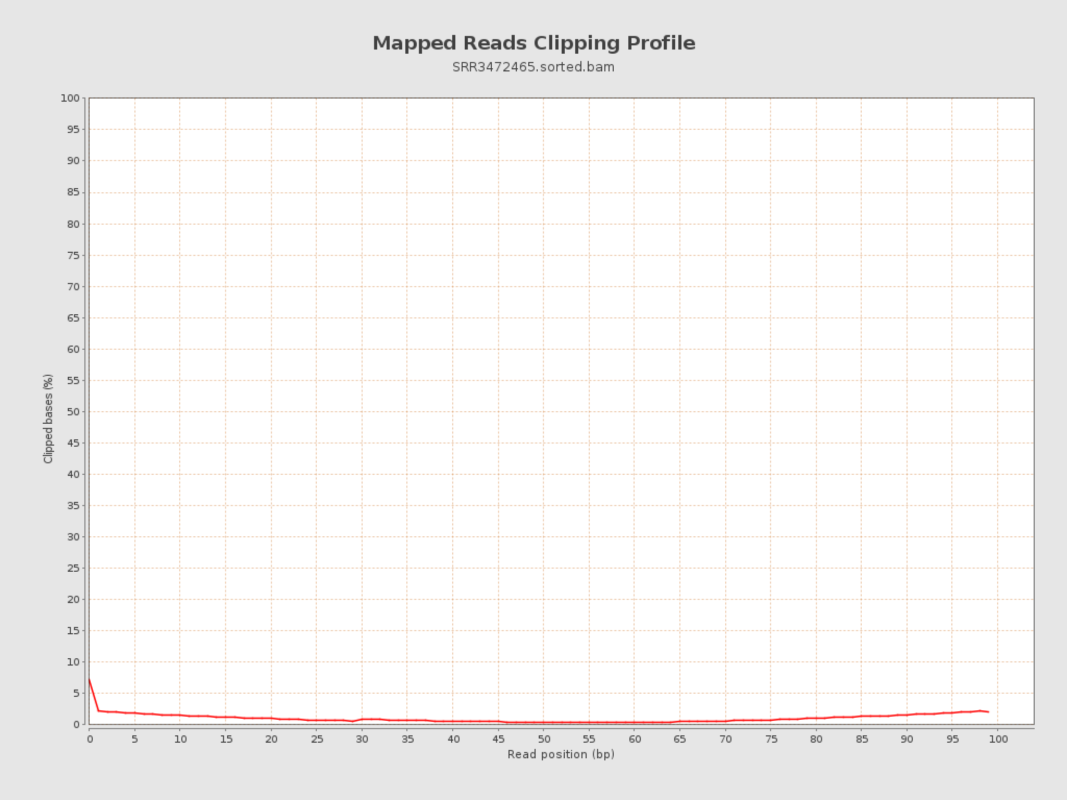
8. Results : Mapped Reads Nucleotide Content



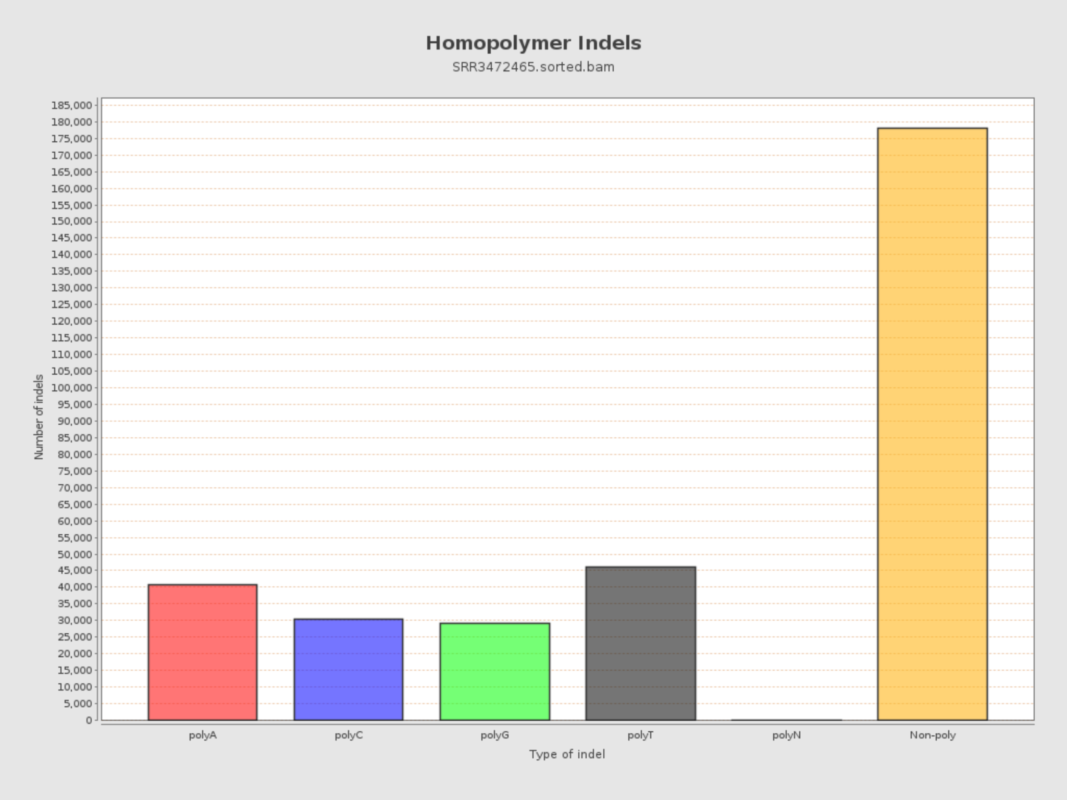
9. Results : Mapped Reads GC-content Distribution



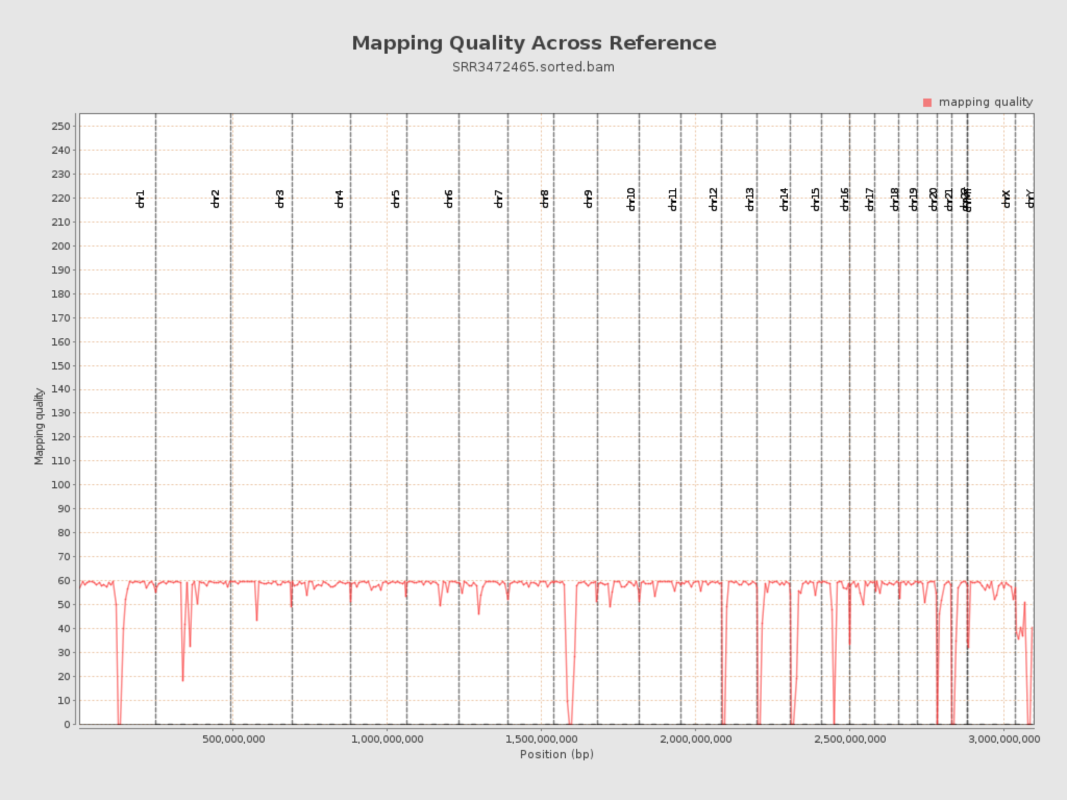
10. Results : Mapped Reads Clipping Profile



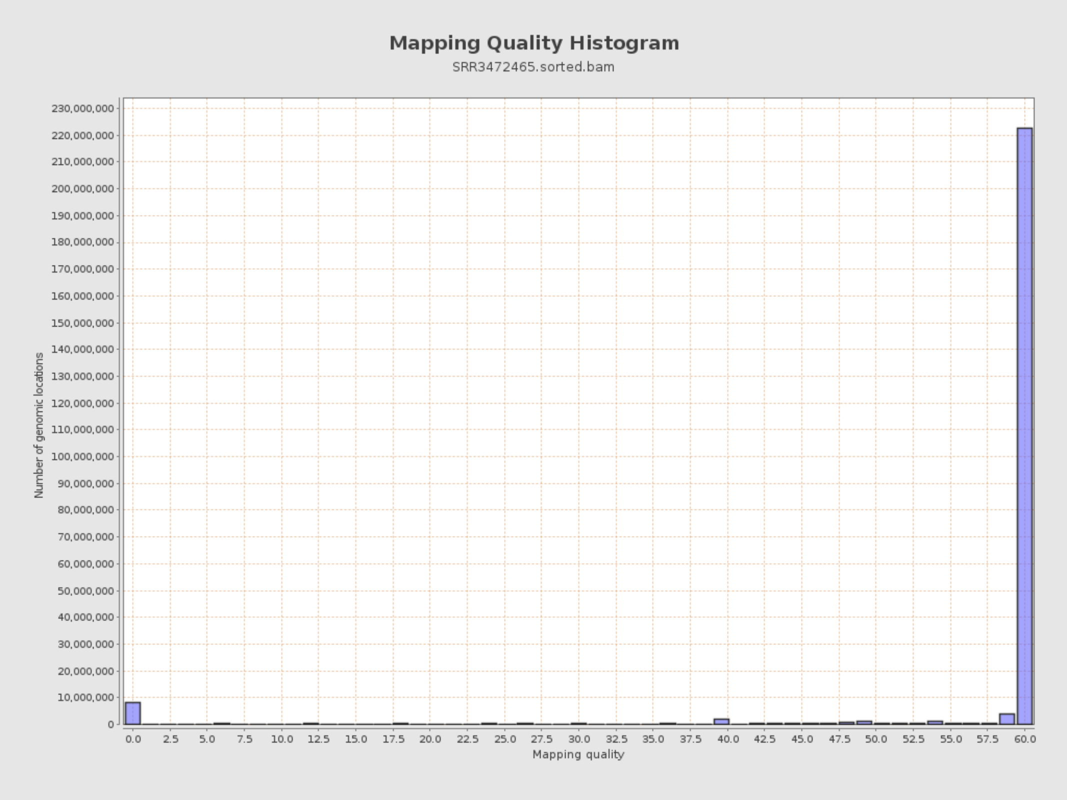
11. Results : Homopolymer Indels



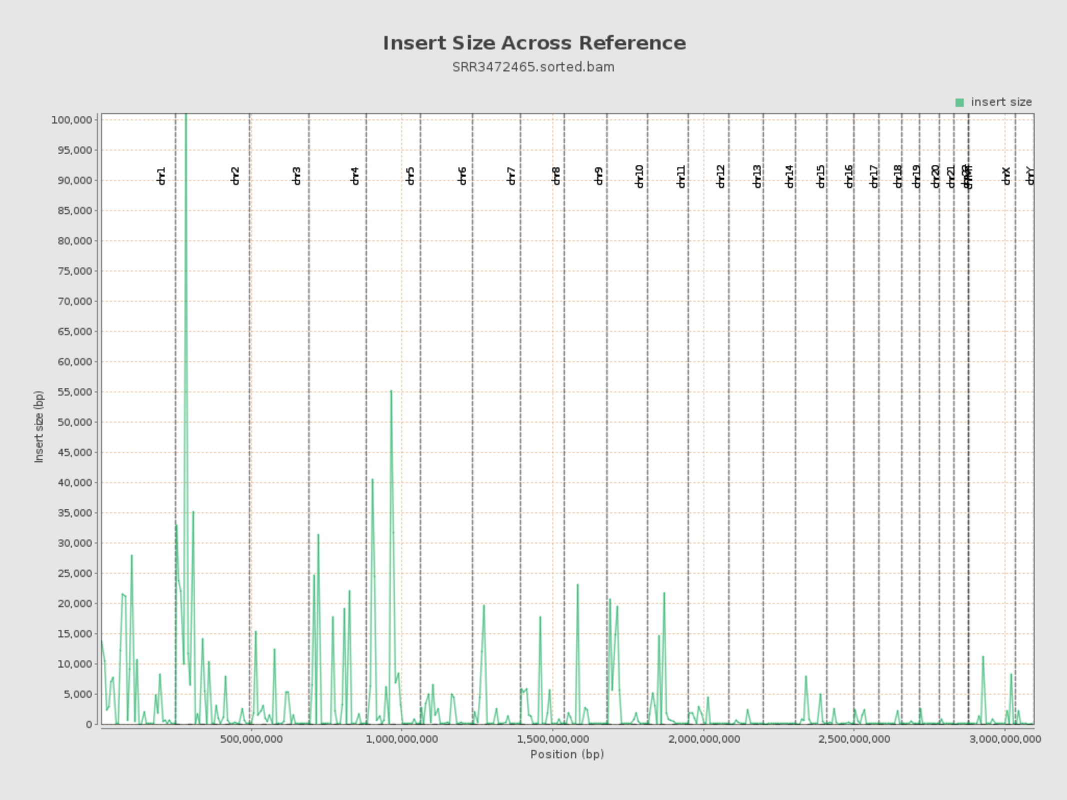
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram