Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 01:39:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472739.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_SRR3472739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472739_1.fastq.gz SRR3472739_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 01:39:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,411,618
Mapped reads	17,256,417 / 99.11%
Unmapped reads	155,201 / 0.89%
Mapped paired reads	17,256,417 / 99.11%
Mapped reads, first in pair	8,657,182 / 49.72%
Mapped reads, second in pair	8,599,235 / 49.39%
Mapped reads, both in pair	17,162,072 / 98.57%
Mapped reads, singletons	94,345 / 0.54%
Secondary alignments	0
Supplementary alignments	57,088 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	10,749,304 / 61.74%
Duplication rate	46.11%
Clipped reads	1,317,933 / 7.57%

2.2. ACGT Content

Number/percentage of A's	469,168,410 / 27.59%
Number/percentage of C's	383,726,291 / 22.56%
Number/percentage of T's	465,659,989 / 27.38%
Number/percentage of G's	381,720,200 / 22.45%
Number/percentage of N's	329,527 / 0.02%

GC Percentage	45.01%

2.3. Coverage

Mean	0.5494
Standard Deviation	18.1163

2.4. Mapping Quality

Mean Mapping Quality	55.15

2.5. Insert size

Mean	22,204.74
Standard Deviation	1,501,402.52
P25/Median/P75	177 / 248 / 333

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	10,565,992
Insertions	100,013
Mapped reads with at least one insertion	0.57%
Deletions	94,812
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.42%

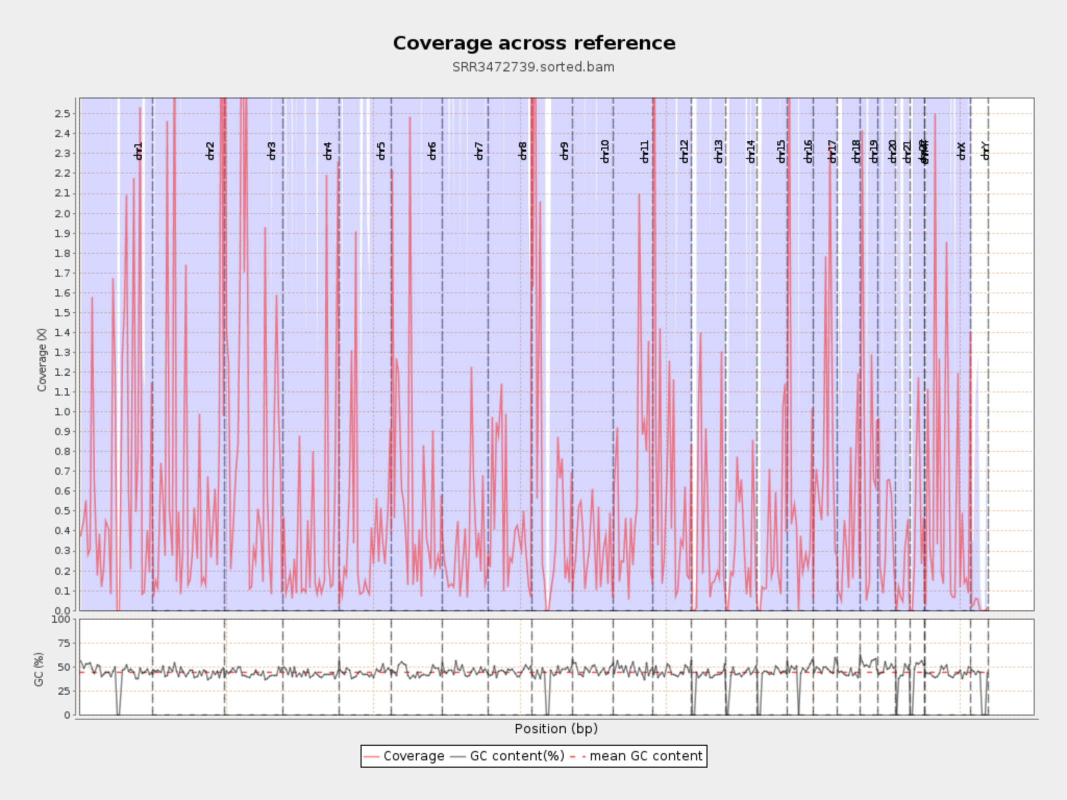
2.7. Chromosome stats

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

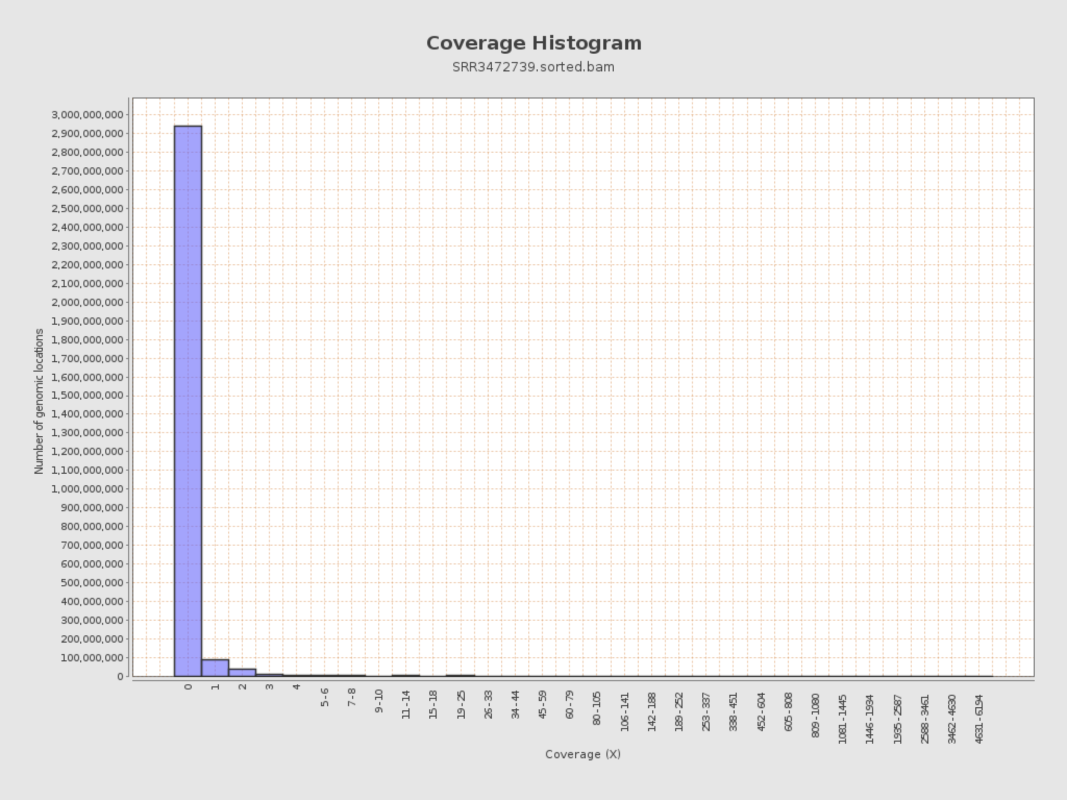
		bases	coverage	deviation
chr1	249250621	174769290	0.7012	22.9818
chr2	243199373	162690913	0.669	26.8907
chr3	198022430	195786929	0.9887	21.2354
chr4	191154276	75082433	0.3928	17.0561
chr5	180915260	74322103	0.4108	13.57
chr6	171115067	102680974	0.6001	17.8832
chr7	159138663	51295533	0.3223	8.9069
chr8	146364022	68164368	0.4657	13.5248
chr9	141213431	102268725	0.7242	17.1416
chr10	135534747	43513971	0.3211	10.0731
chr11	135006516	82719084	0.6127	18.5129
chr12	133851895	96810645	0.7233	22.6323
chr13	115169878	48488289	0.421	18.5896
chr14	107349540	33504709	0.3121	10.0512
chr15	102531392	36045004	0.3516	11.944
chr16	90354753	54966622	0.6083	16.1422
chr17	81195210	67927390	0.8366	22.1659
chr18	78077248	31044415	0.3976	13.6095
chr19	59128983	49651577	0.8397	29.2899
chr20	63025520	26769544	0.4247	13.6902
chr21	48129895	8093138	0.1682	8.3221
chr22	51304566	22541673	0.4394	13.3254
chrMT	16571	1182	0.0713	0.3505
chrX	155270560	90318835	0.5817	17.5407

chrY	59373566	1386226	0.0233	0.7253

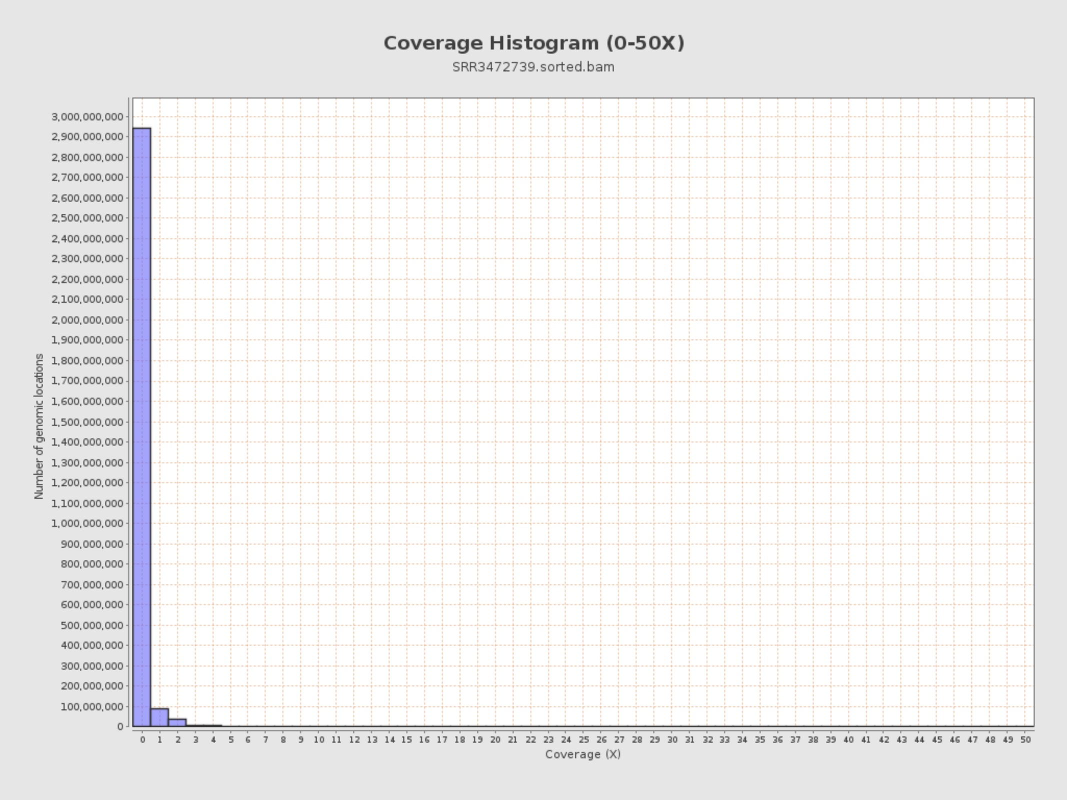
3. Results : Coverage across reference



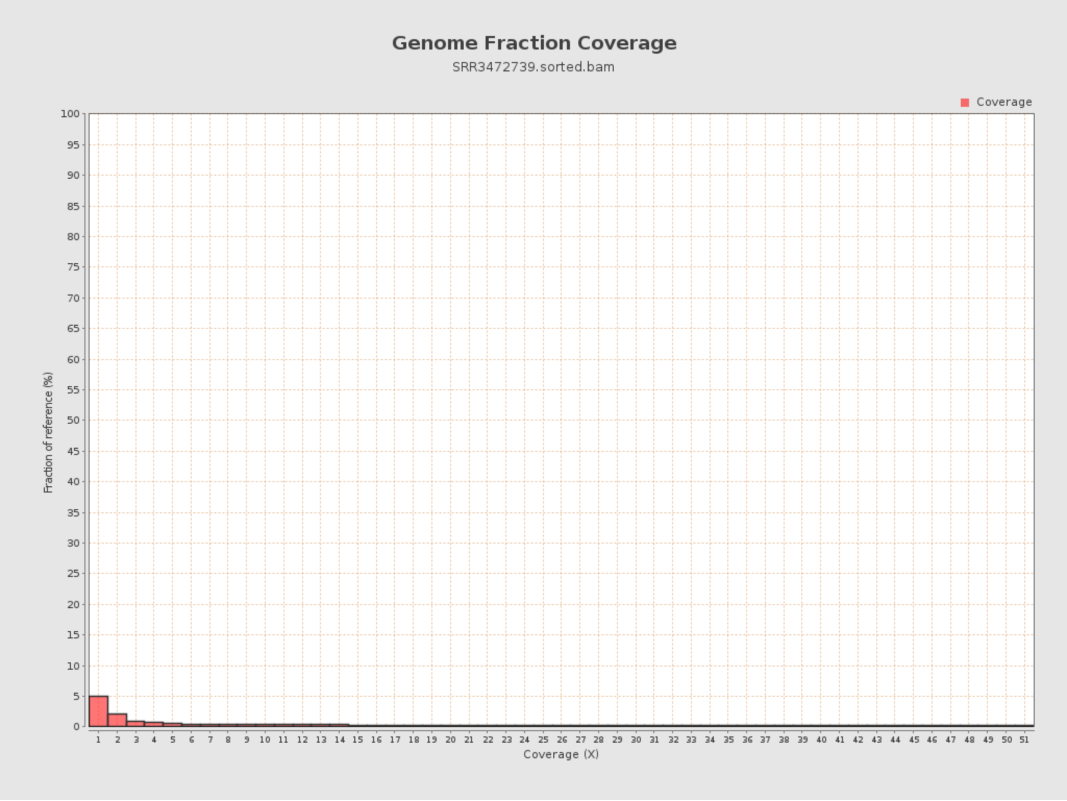
4. Results : Coverage Histogram



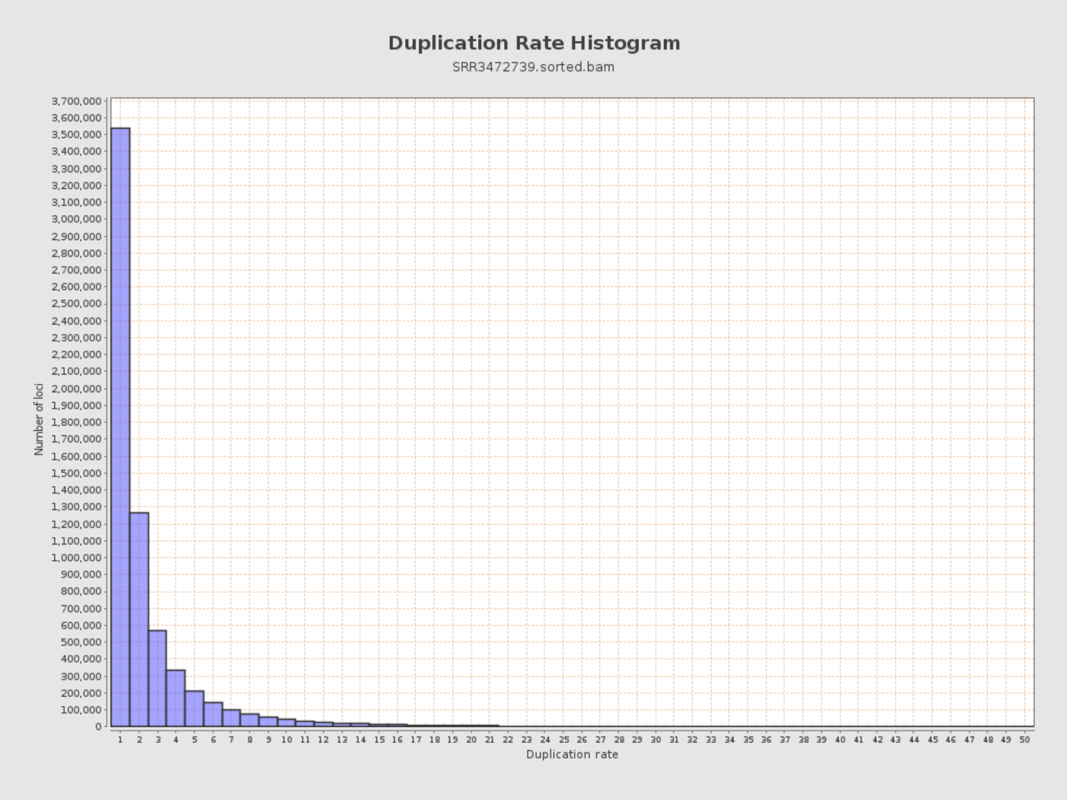
5. Results : Coverage Histogram (0-50X)



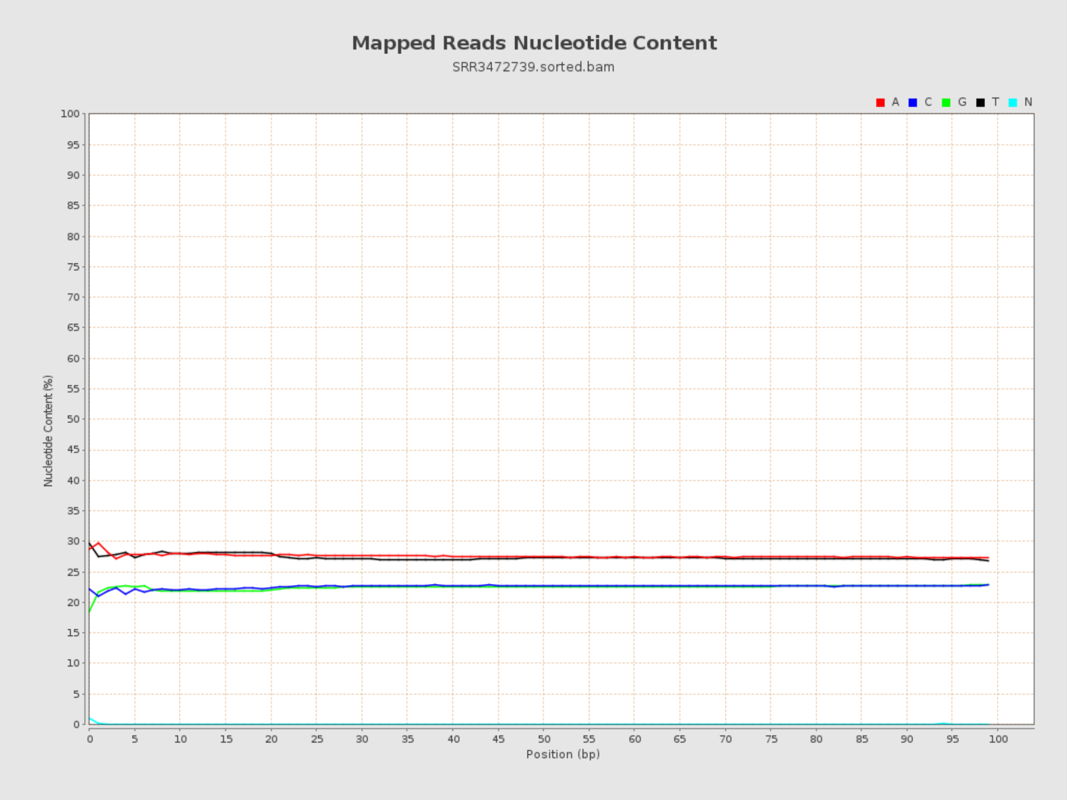
6. Results : Genome Fraction Coverage



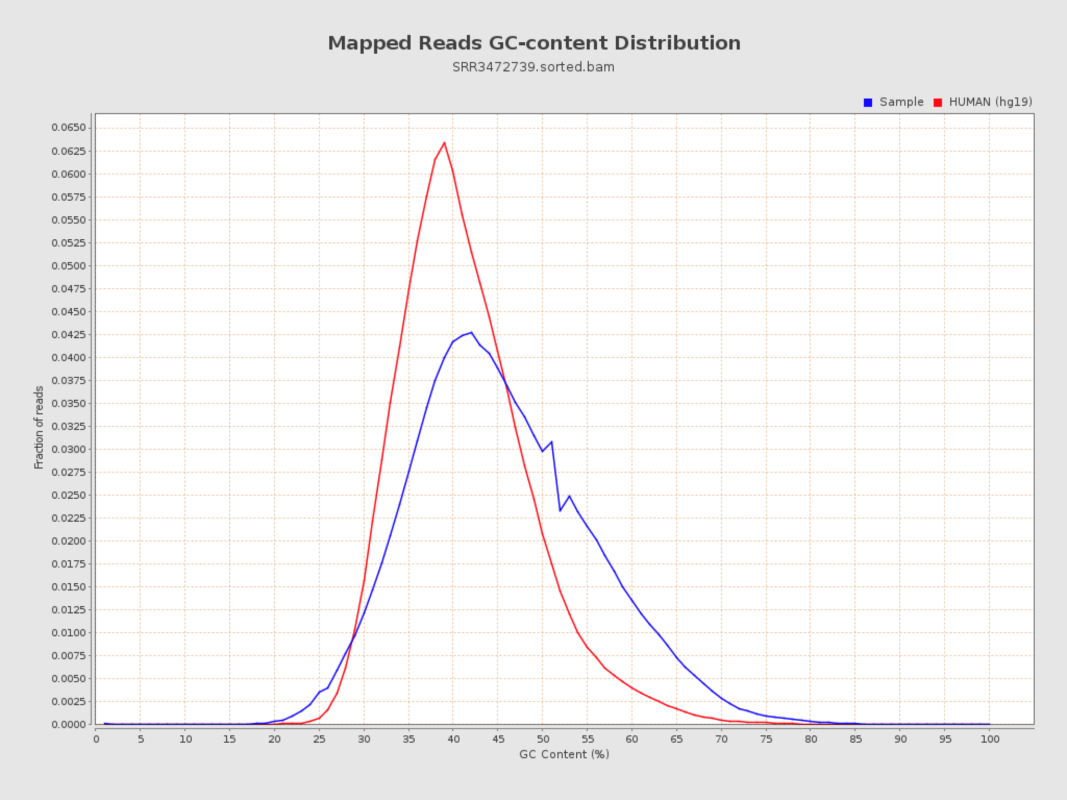
7. Results : Duplication Rate Histogram



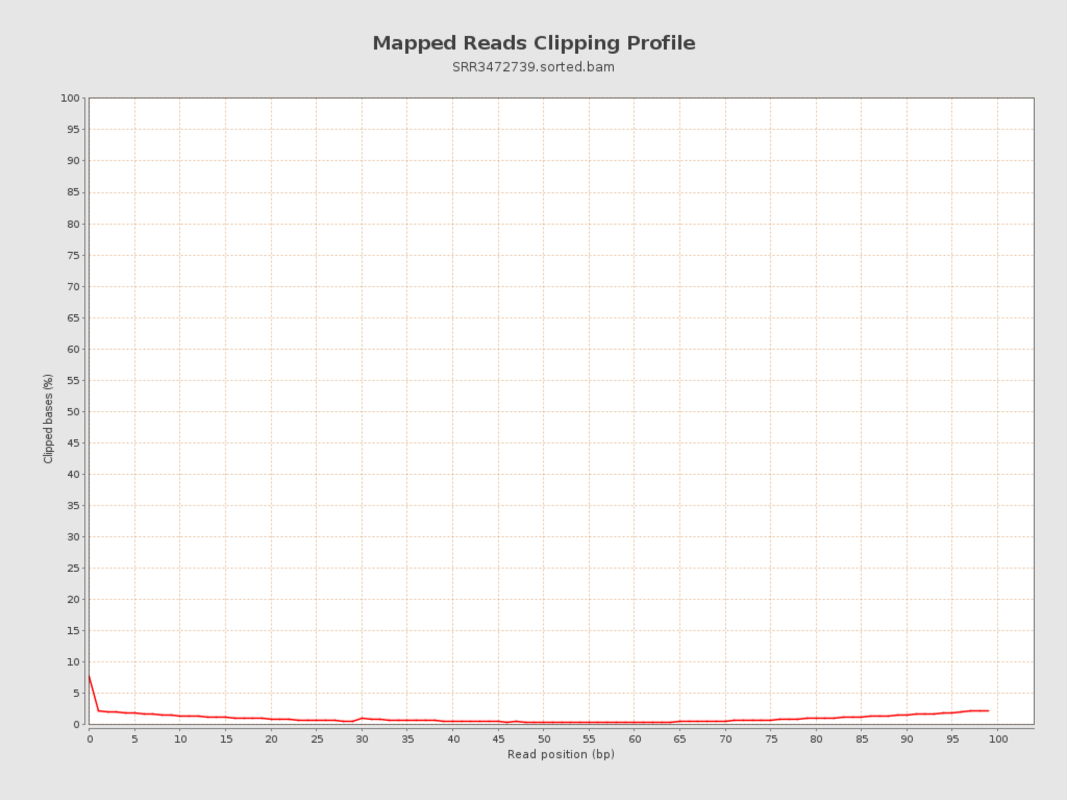
8. Results : Mapped Reads Nucleotide Content



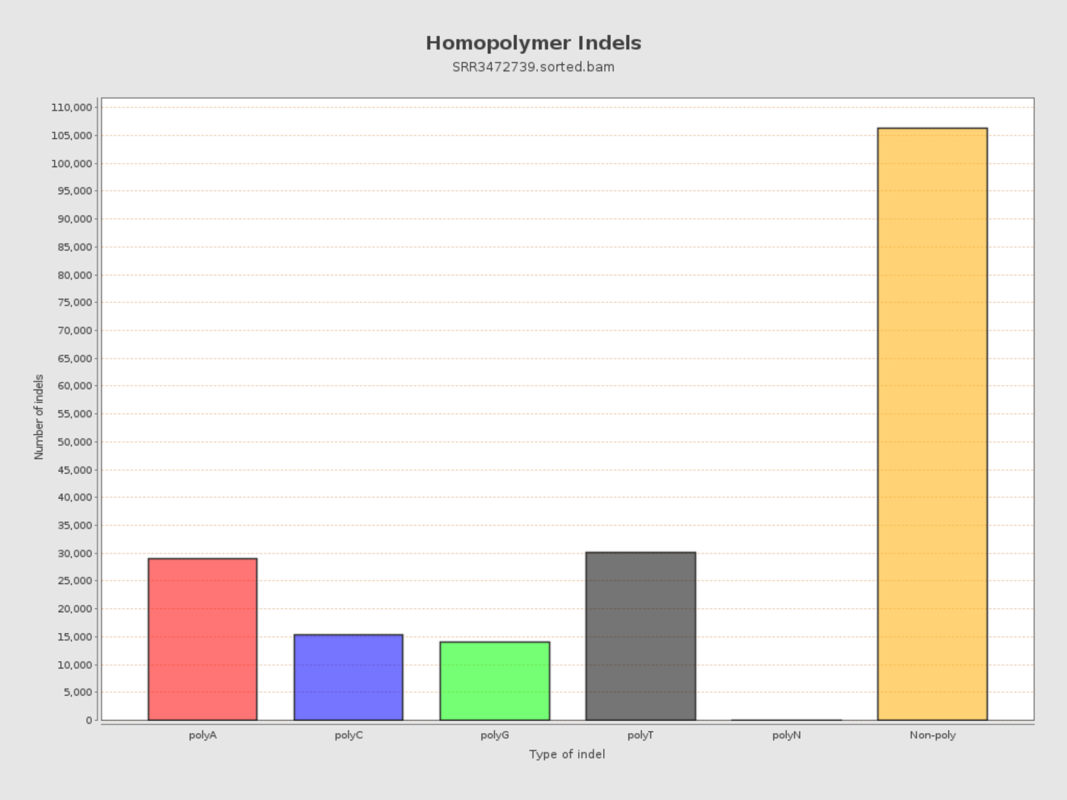
9. Results : Mapped Reads GC-content Distribution



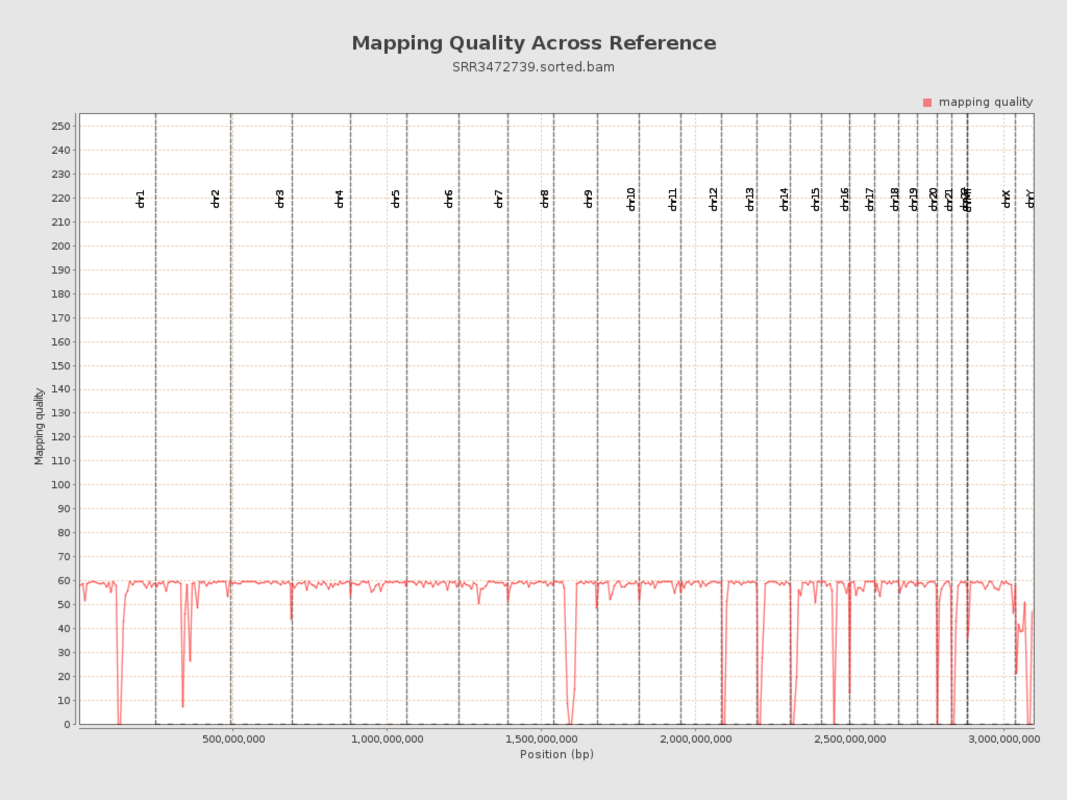
10. Results : Mapped Reads Clipping Profile



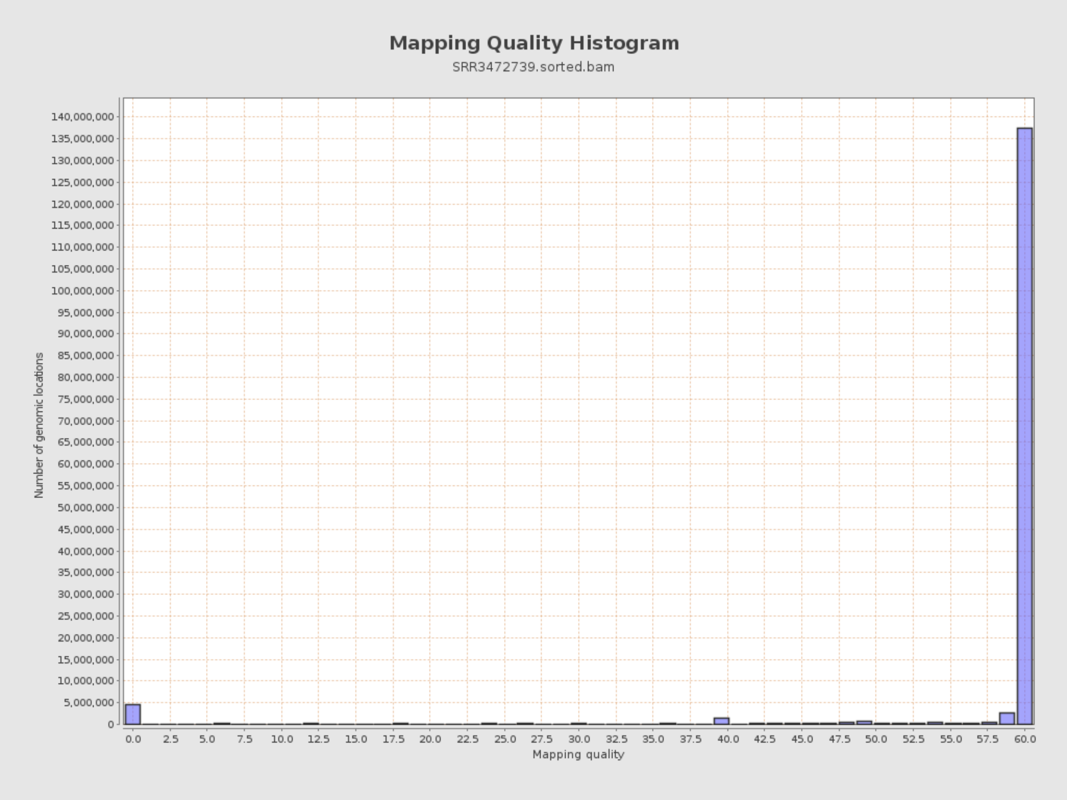
11. Results : Homopolymer Indels



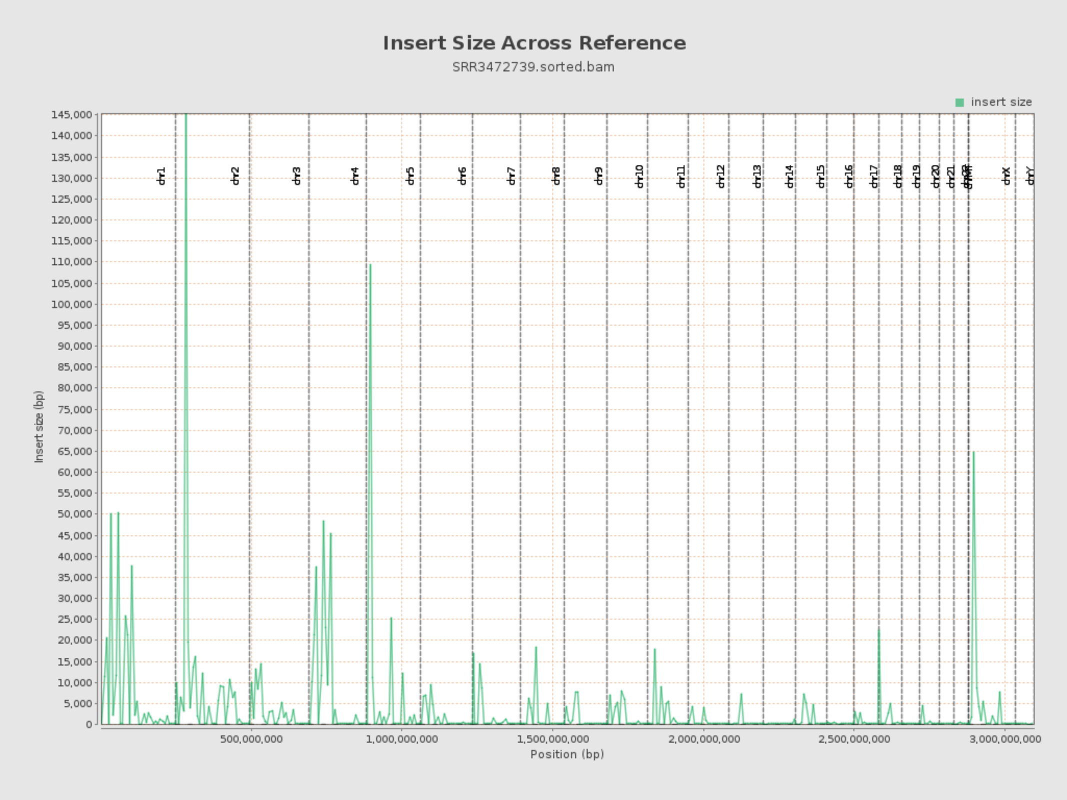
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram