Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 04:25:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472746.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_SRR3472746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472746_1.fastq.gz SRR3472746_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 04:25:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,425,874
Mapped reads	19,221,695 / 98.95%
Unmapped reads	204,179 / 1.05%
Mapped paired reads	19,221,695 / 98.95%
Mapped reads, first in pair	9,653,502 / 49.69%
Mapped reads, second in pair	9,568,193 / 49.25%
Mapped reads, both in pair	19,095,084 / 98.3%
Mapped reads, singletons	126,611 / 0.65%
Secondary alignments	0
Supplementary alignments	89,895 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	12,678,188 / 65.26%
Duplication rate	47.61%
Clipped reads	1,426,717 / 7.34%

2.2. ACGT Content

Number/percentage of A's	521,189,284 / 27.47%
Number/percentage of C's	430,366,540 / 22.68%
Number/percentage of T's	518,674,011 / 27.34%
Number/percentage of G's	426,608,946 / 22.49%
Number/percentage of N's	364,219 / 0.02%

GC Percentage	45.17%

2.3. Coverage

Mean	0.6129
Standard Deviation	22.1326

2.4. Mapping Quality

Mean Mapping Quality	55.4

2.5. Insert size

Mean	27,110.33
Standard Deviation	1,616,196.06
P25/Median/P75	186 / 260 / 349

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	12,700,433
Insertions	117,103
Mapped reads with at least one insertion	0.6%
Deletions	105,445
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.32%

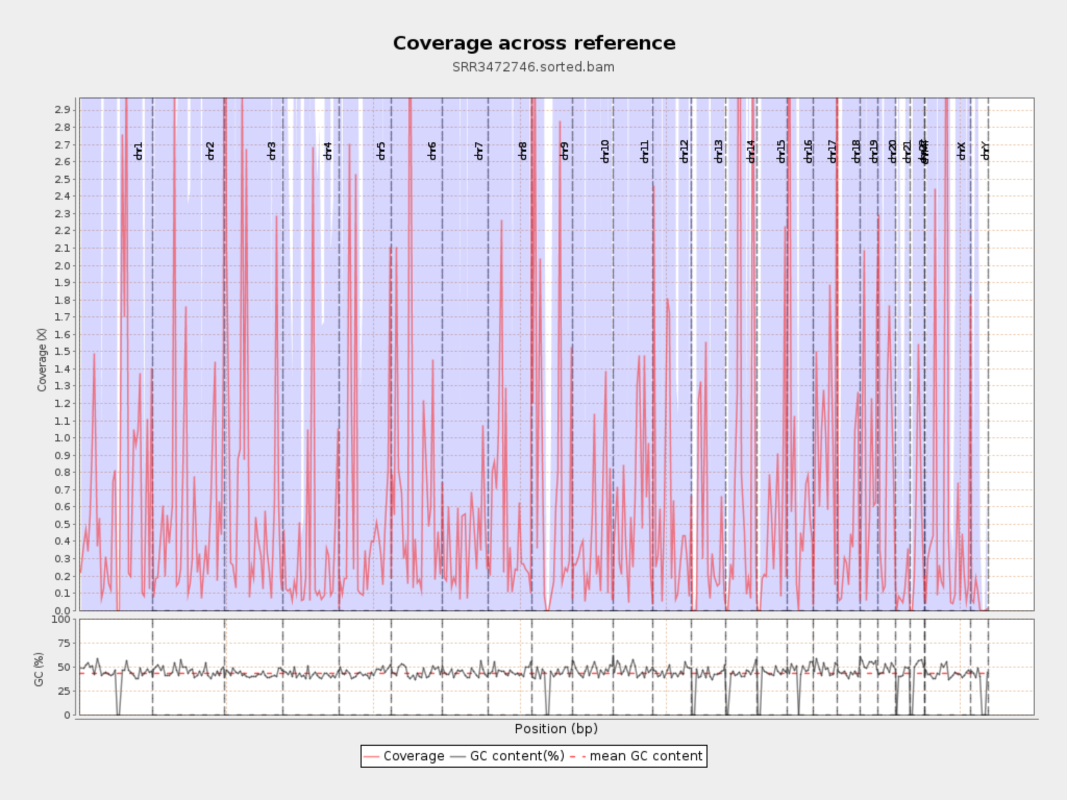
2.7. Chromosome stats

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

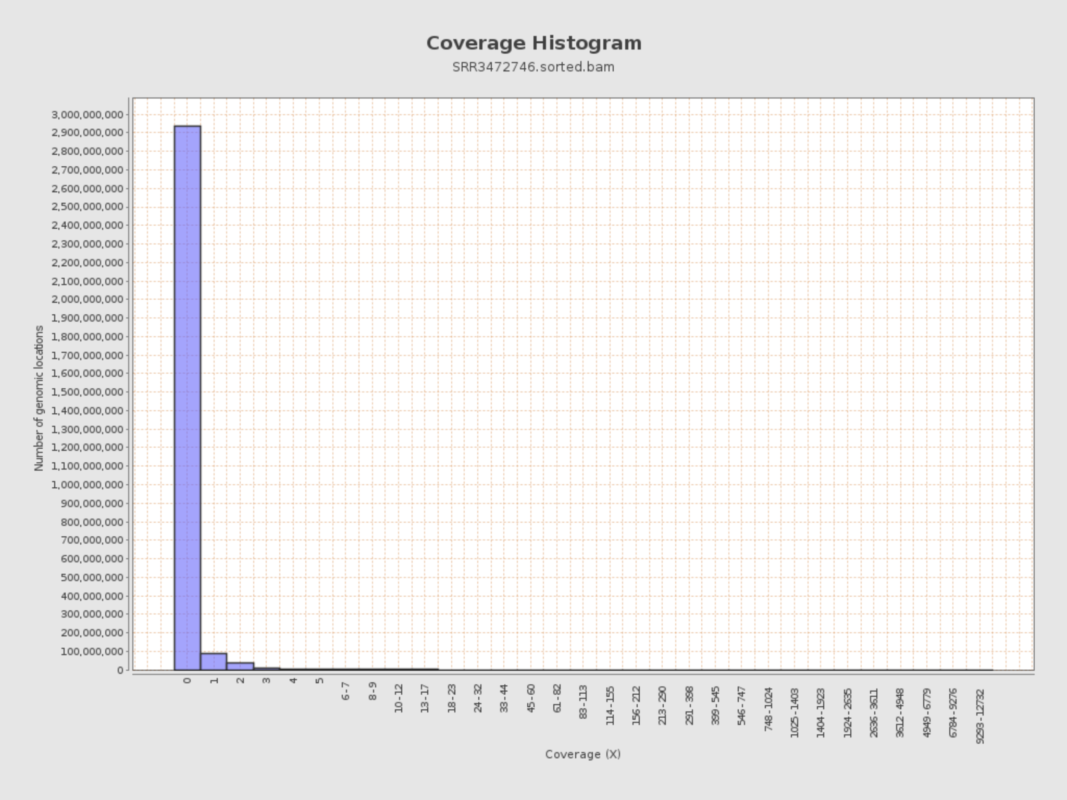
		bases	coverage	deviation
chr1	249250621	179724853	0.7211	24.9666
chr2	243199373	134606350	0.5535	20.0457
chr3	198022430	165859937	0.8376	19.8419
chr4	191154276	65240159	0.3413	16.184
chr5	180915260	108401777	0.5992	19.7825
chr6	171115067	126772014	0.7409	25.1166
chr7	159138663	64575716	0.4058	13.0774
chr8	146364022	78725058	0.5379	16.0026
chr9	141213431	117956335	0.8353	25.9089
chr10	135534747	58802483	0.4339	17.4474
chr11	135006516	84621569	0.6268	20.336
chr12	133851895	79947439	0.5973	20.1125
chr13	115169878	49292755	0.428	19.6278
chr14	107349540	101382533	0.9444	48.419
chr15	102531392	52935973	0.5163	17.6185
chr16	90354753	75964135	0.8407	24.2995
chr17	81195210	89225240	1.0989	25.9606
chr18	78077248	32878715	0.4211	16.8957
chr19	59128983	51675849	0.874	25.1389
chr20	63025520	57580858	0.9136	25.6868
chr21	48129895	5701087	0.1185	3.5593
chr22	51304566	25311833	0.4934	16.5935
chrMT	16571	3335	0.2013	0.6949
chrX	155270560	87137853	0.5612	24.5477

chrY	59373566	3142582	0.0529	1.9276

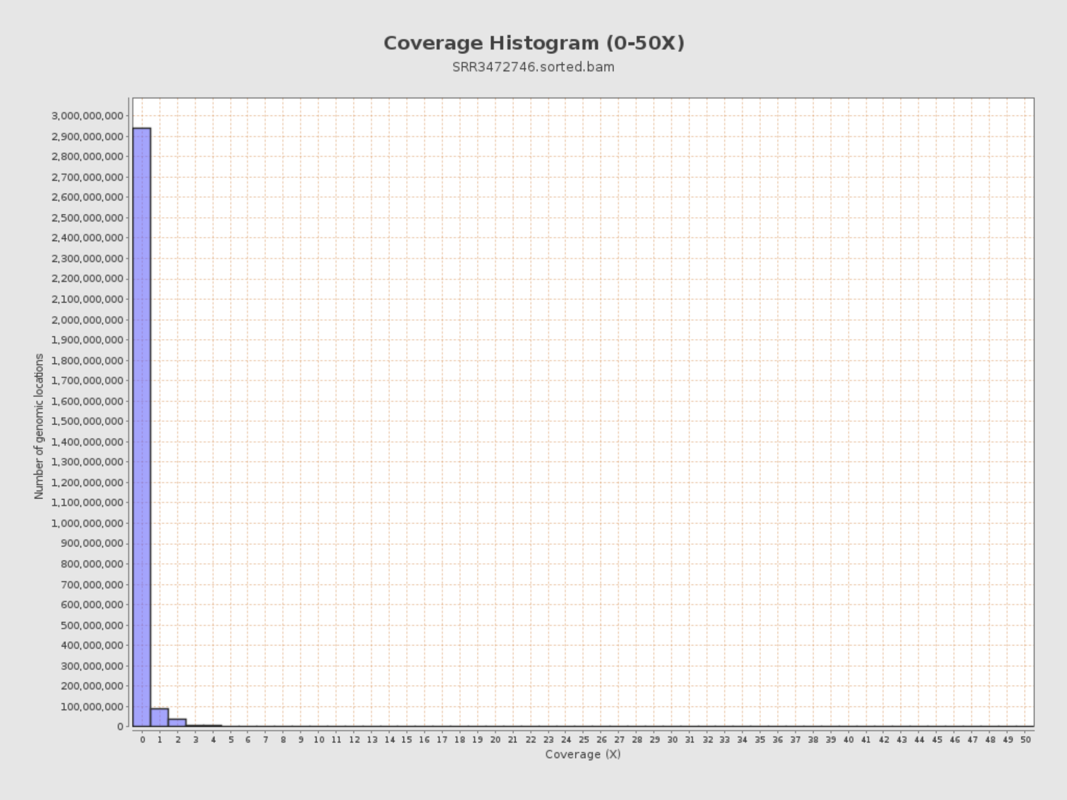
3. Results : Coverage across reference



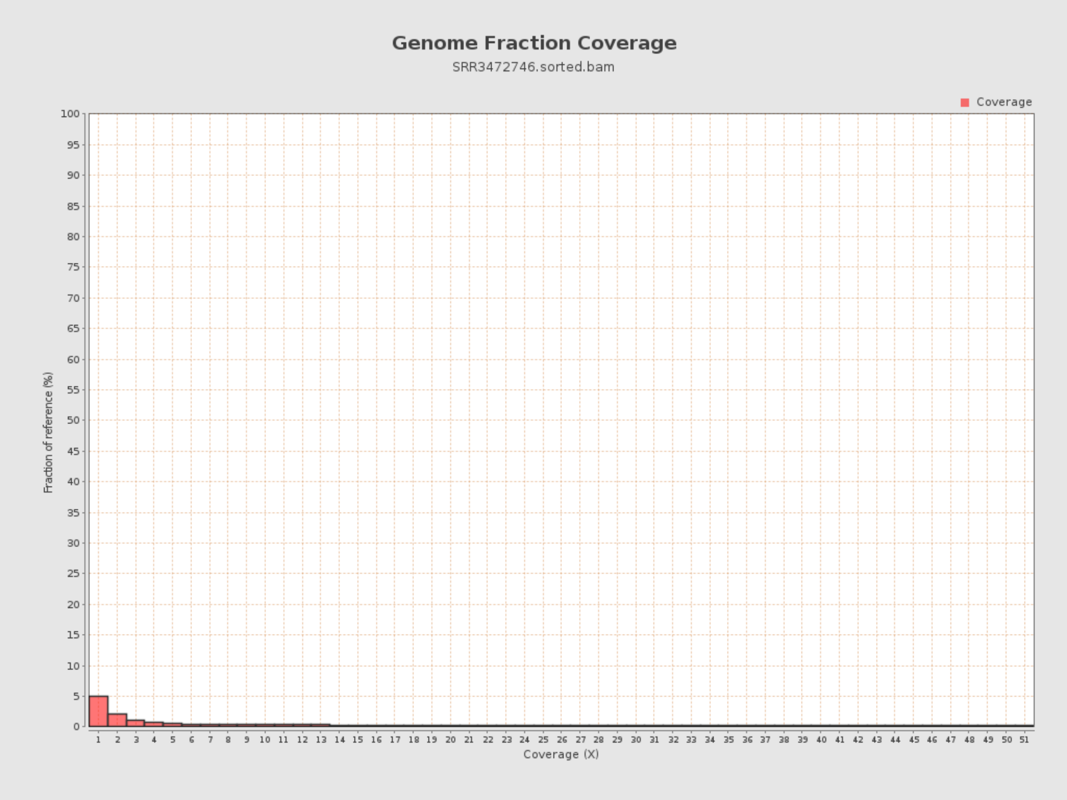
4. Results : Coverage Histogram



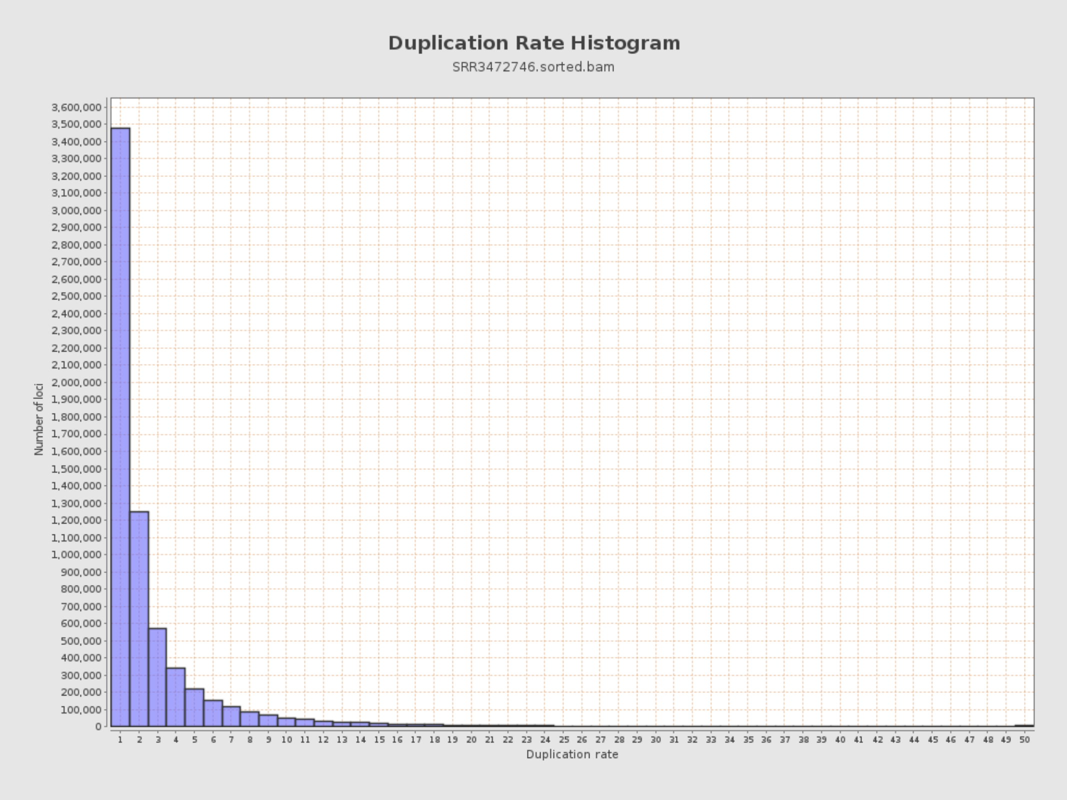
5. Results : Coverage Histogram (0-50X)



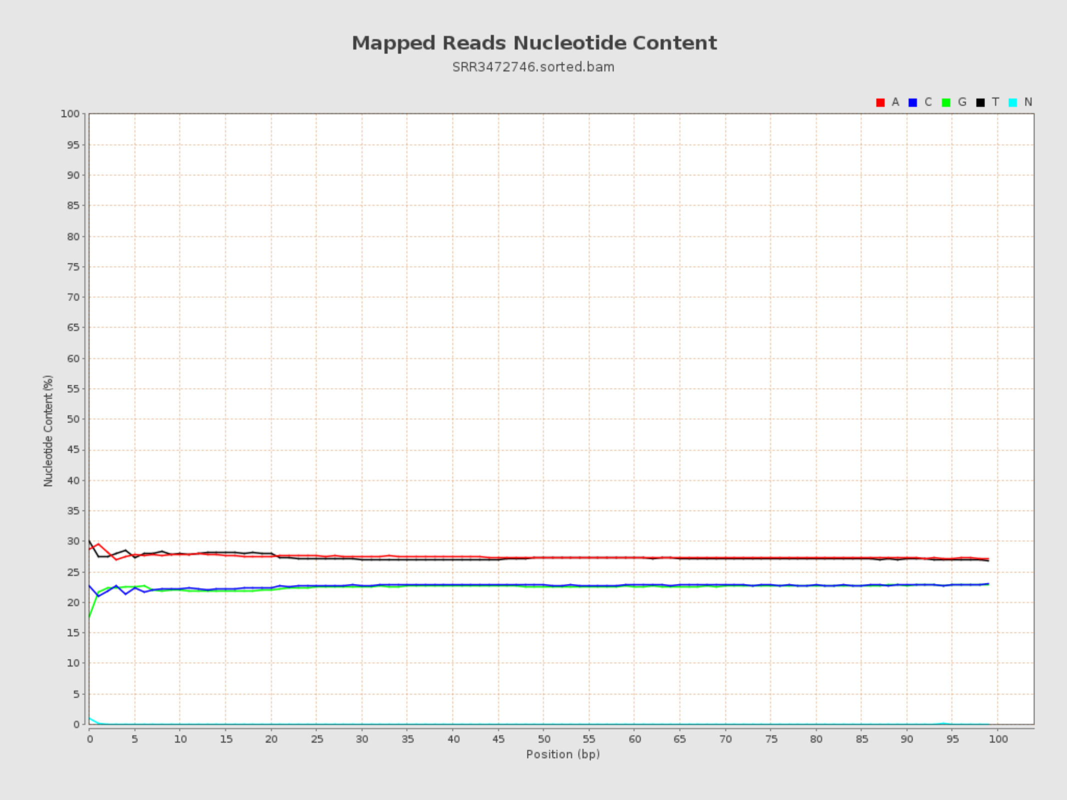
6. Results : Genome Fraction Coverage



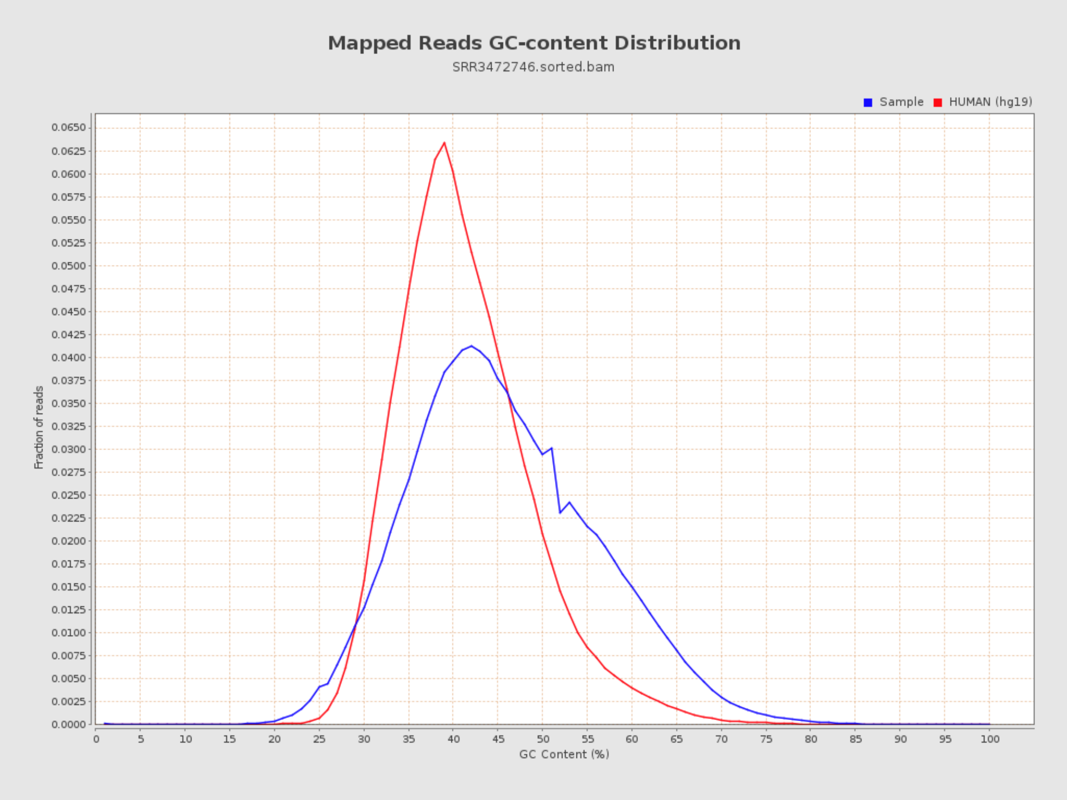
7. Results : Duplication Rate Histogram



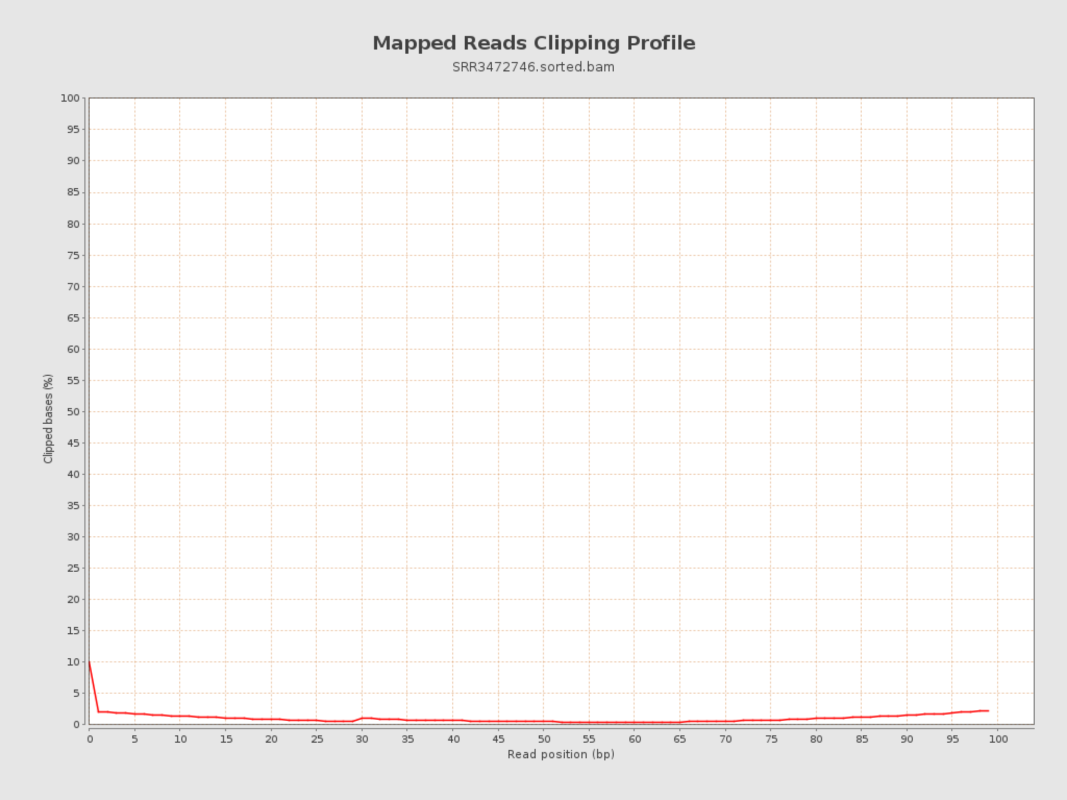
8. Results : Mapped Reads Nucleotide Content



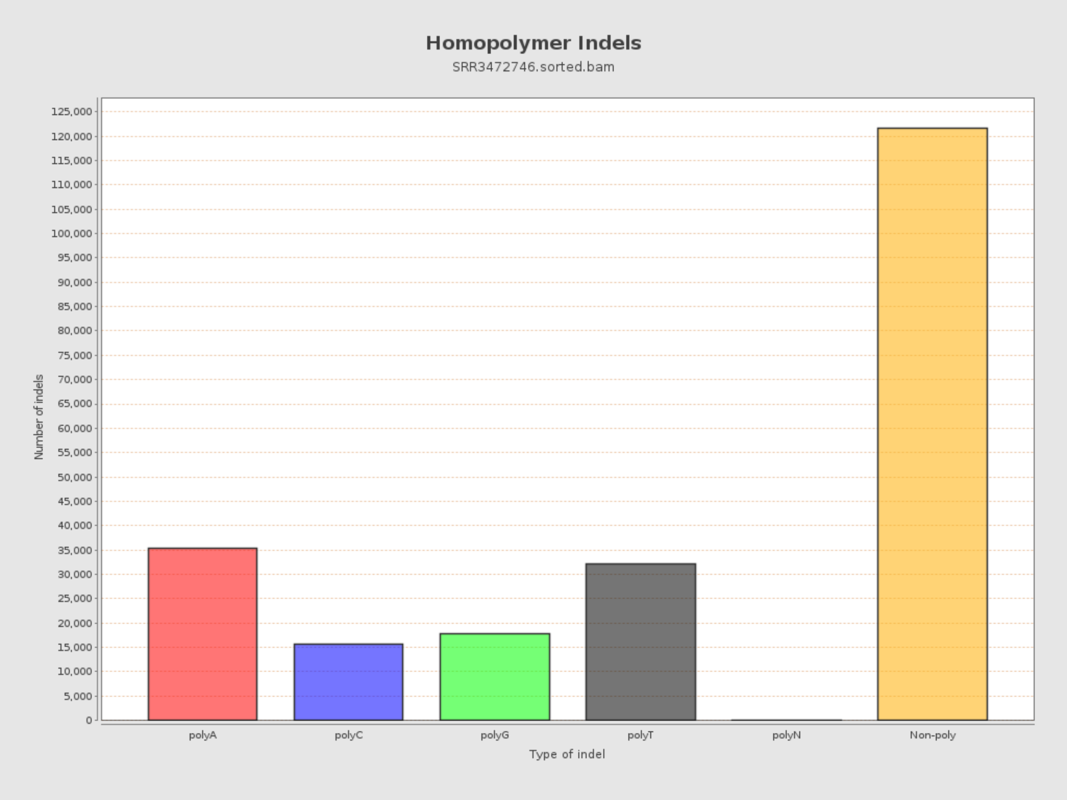
9. Results : Mapped Reads GC-content Distribution



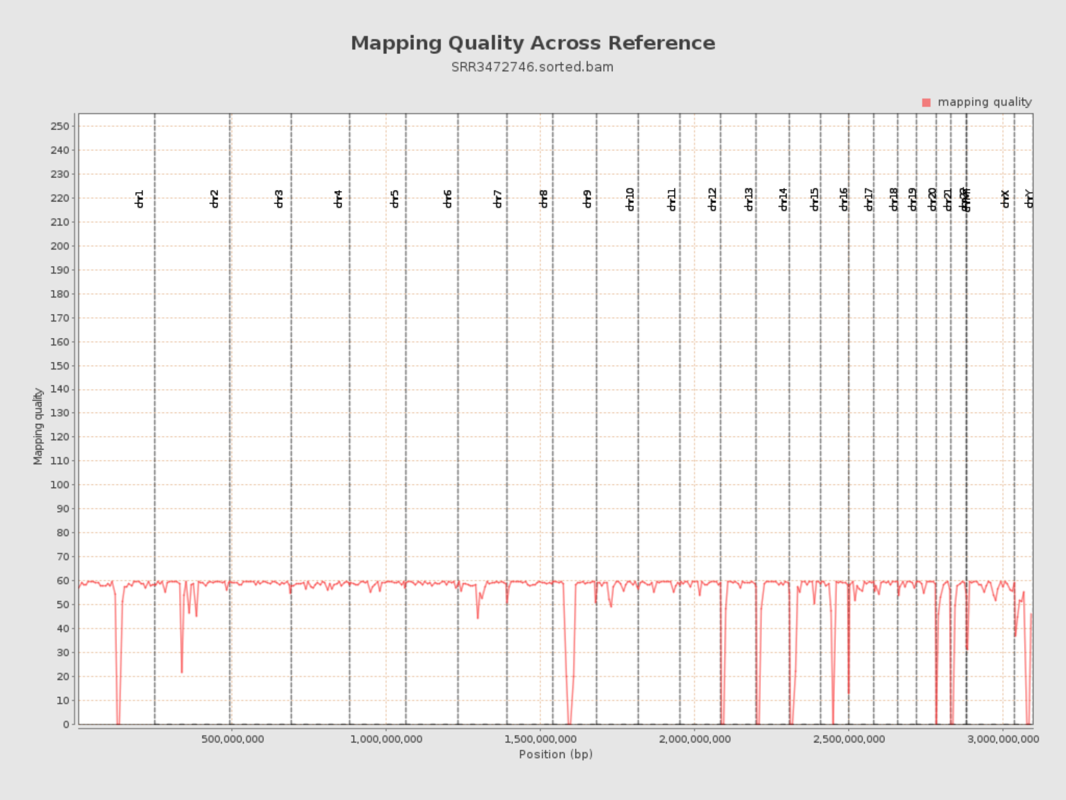
10. Results : Mapped Reads Clipping Profile



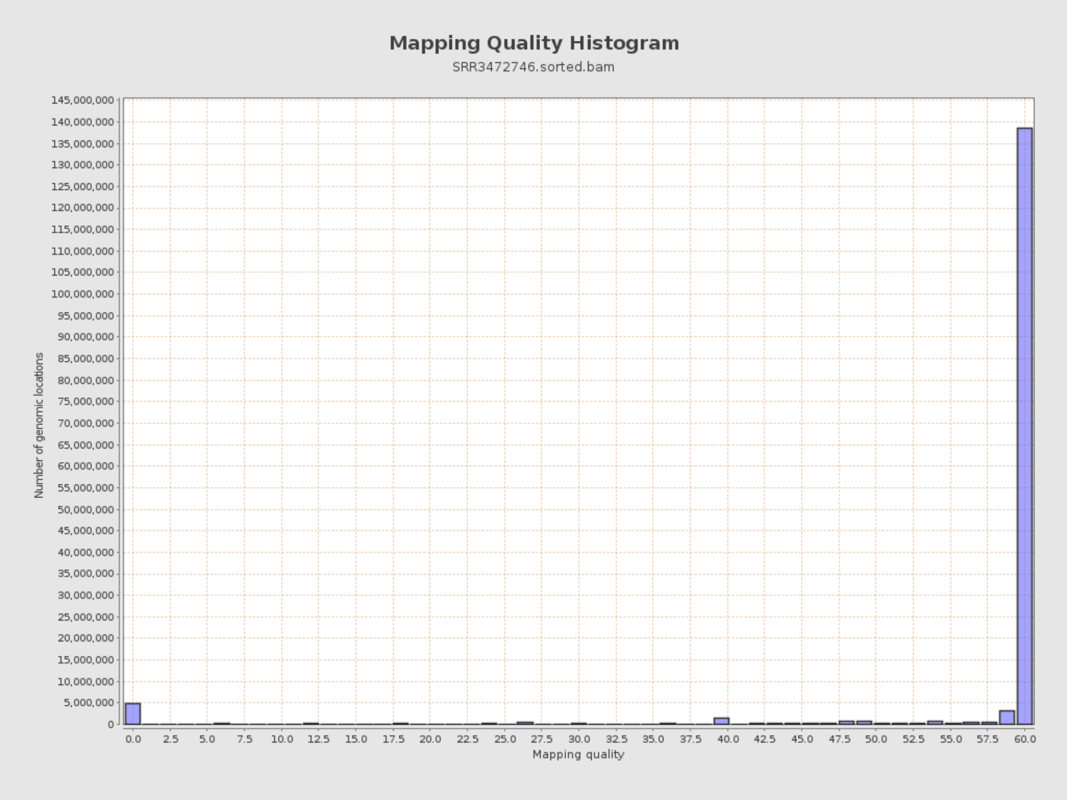
11. Results : Homopolymer Indels



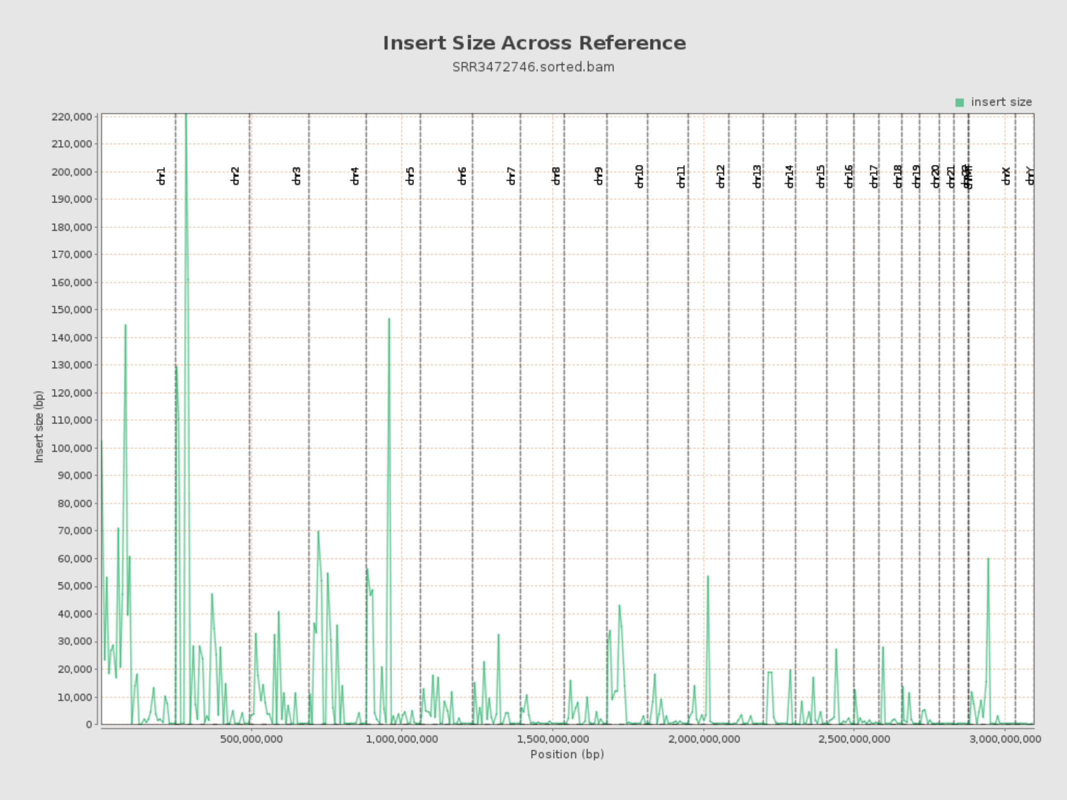
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram