Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:51:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472431.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_SRR3472431 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472431_1.fastq.gz SRR3472431_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:50:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472431.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,863,672
Mapped reads	13,709,066 / 98.88%
Unmapped reads	154,606 / 1.12%
Mapped paired reads	13,709,066 / 98.88%
Mapped reads, first in pair	6,883,273 / 49.65%
Mapped reads, second in pair	6,825,793 / 49.24%
Mapped reads, both in pair	13,621,140 / 98.25%
Mapped reads, singletons	87,926 / 0.63%
Secondary alignments	0
Supplementary alignments	49,568 / 0.36%
Read min/max/mean length	30 / 100 / 99.19
Duplicated reads (estimated)	8,191,460 / 59.09%
Duplication rate	47.08%
Clipped reads	1,017,608 / 7.34%

2.2. ACGT Content

Number/percentage of A's	364,210,889 / 27.15%
Number/percentage of C's	307,476,226 / 22.92%
Number/percentage of T's	365,450,737 / 27.25%
Number/percentage of G's	303,950,313 / 22.66%
Number/percentage of N's	165,779 / 0.01%

GC Percentage	45.59%

2.3. Coverage

Mean	0.4333
Standard Deviation	13.4196

2.4. Mapping Quality

Mean Mapping Quality	55

2.5. Insert size

Mean	17,734.24
Standard Deviation	1,312,966.67
P25/Median/P75	150 / 209 / 282

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	7,110,598
Insertions	74,952
Mapped reads with at least one insertion	0.54%
Deletions	61,736
Mapped reads with at least one deletion	0.45%
Homopolymer indels	46.67%

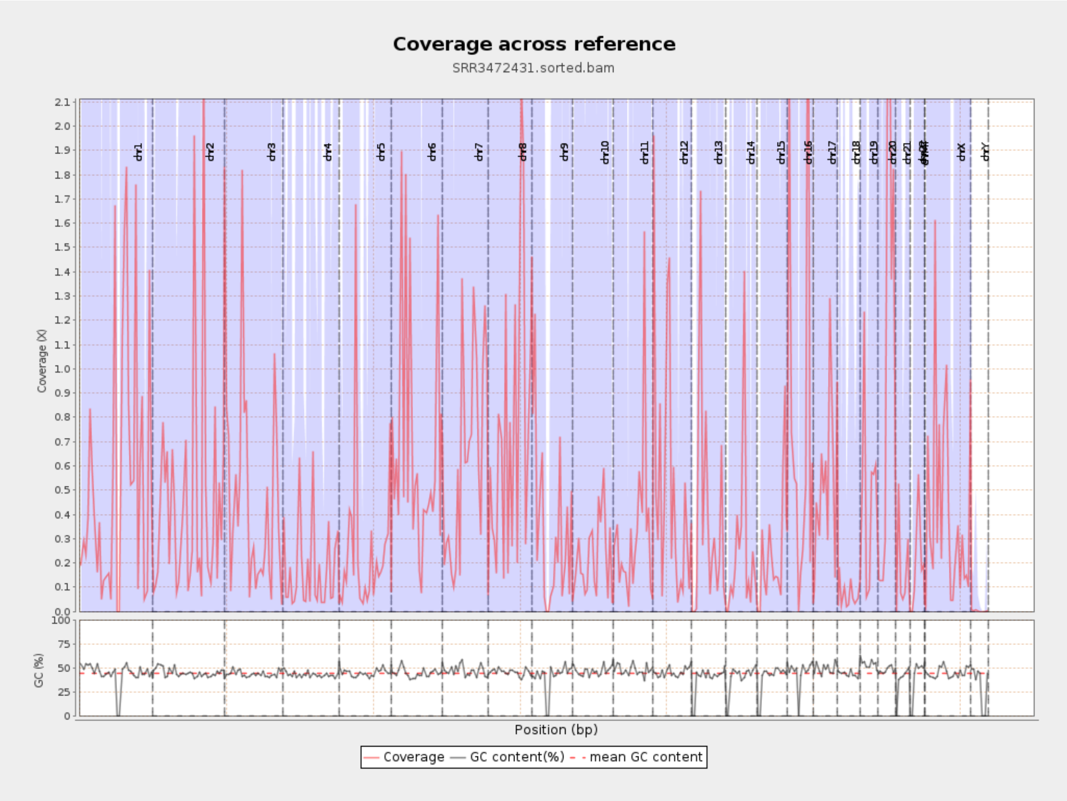
2.7. Chromosome stats

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

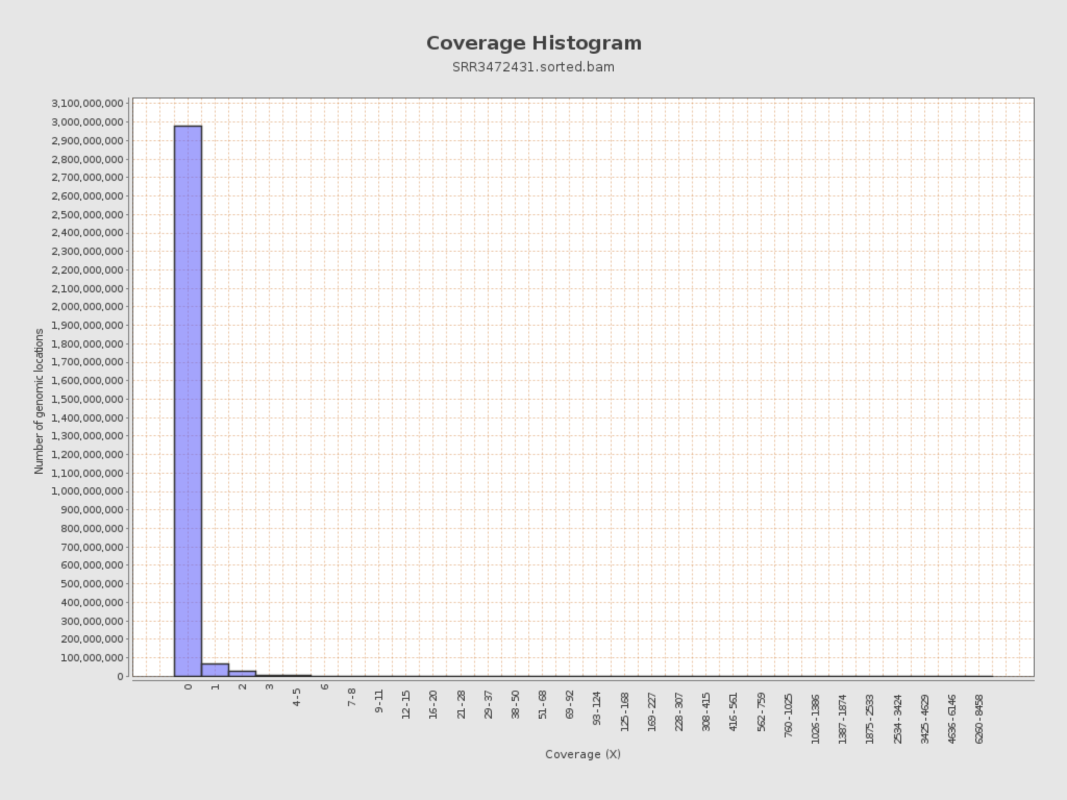
		bases	coverage	deviation
chr1	249250621	139982199	0.5616	15.5312
chr2	243199373	110707364	0.4552	13.0443
chr3	198022430	93358247	0.4715	10.9
chr4	191154276	32877360	0.172	6.048
chr5	180915260	46690608	0.2581	9.2316
chr6	171115067	115004047	0.6721	15.6897
chr7	159138663	100145795	0.6293	20.5242
chr8	146364022	111694142	0.7631	21.5545
chr9	141213431	48941390	0.3466	9.5189
chr10	135534747	30402172	0.2243	7.2106
chr11	135006516	44352101	0.3285	10.203
chr12	133851895	70272449	0.525	14.4891
chr13	115169878	45128388	0.3918	12.0505
chr14	107349540	25664587	0.2391	8.2503
chr15	102531392	25536616	0.2491	7.2236
chr16	90354753	71741219	0.794	19.8342
chr17	81195210	42606335	0.5247	10.5917
chr18	78077248	5458214	0.0699	1.9828
chr19	59128983	29513642	0.4991	10.3122
chr20	63025520	70223461	1.1142	31.3019
chr21	48129895	8353061	0.1736	7.9226
chr22	51304566	10318074	0.2011	5.5256
chrMT	16571	626	0.0378	0.2119
chrX	155270560	62231695	0.4008	12.3754

chrY	59373566	203180	0.0034	0.231

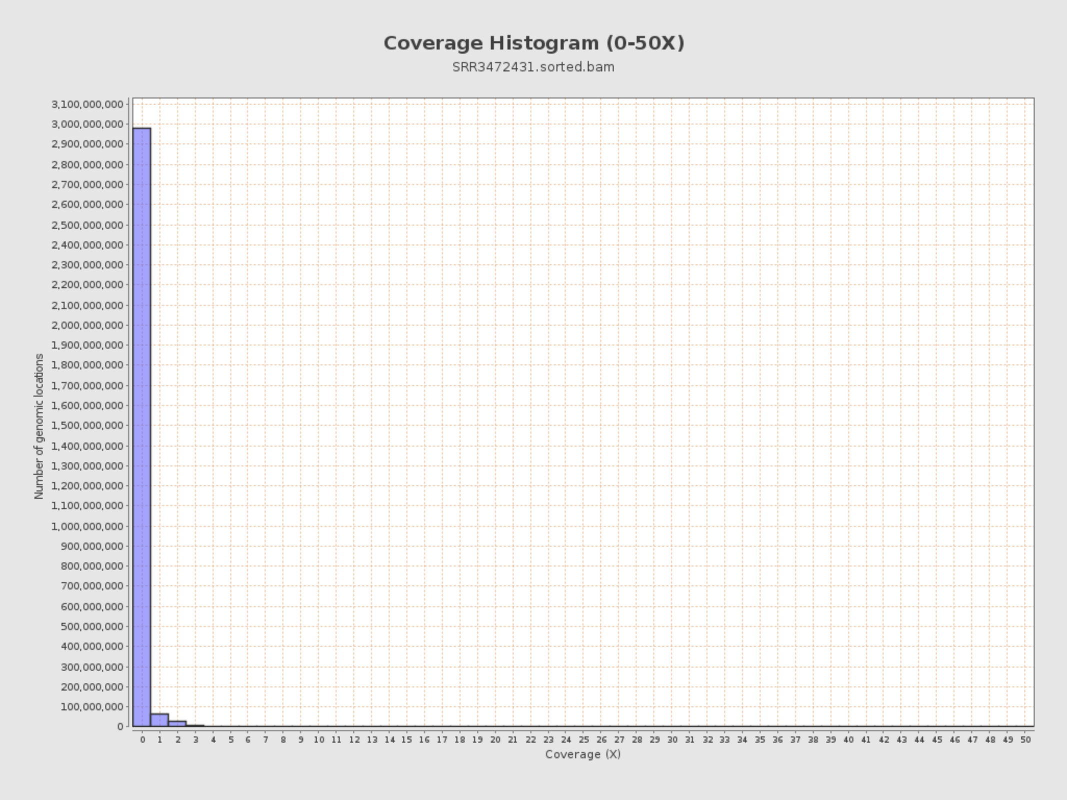
3. Results : Coverage across reference



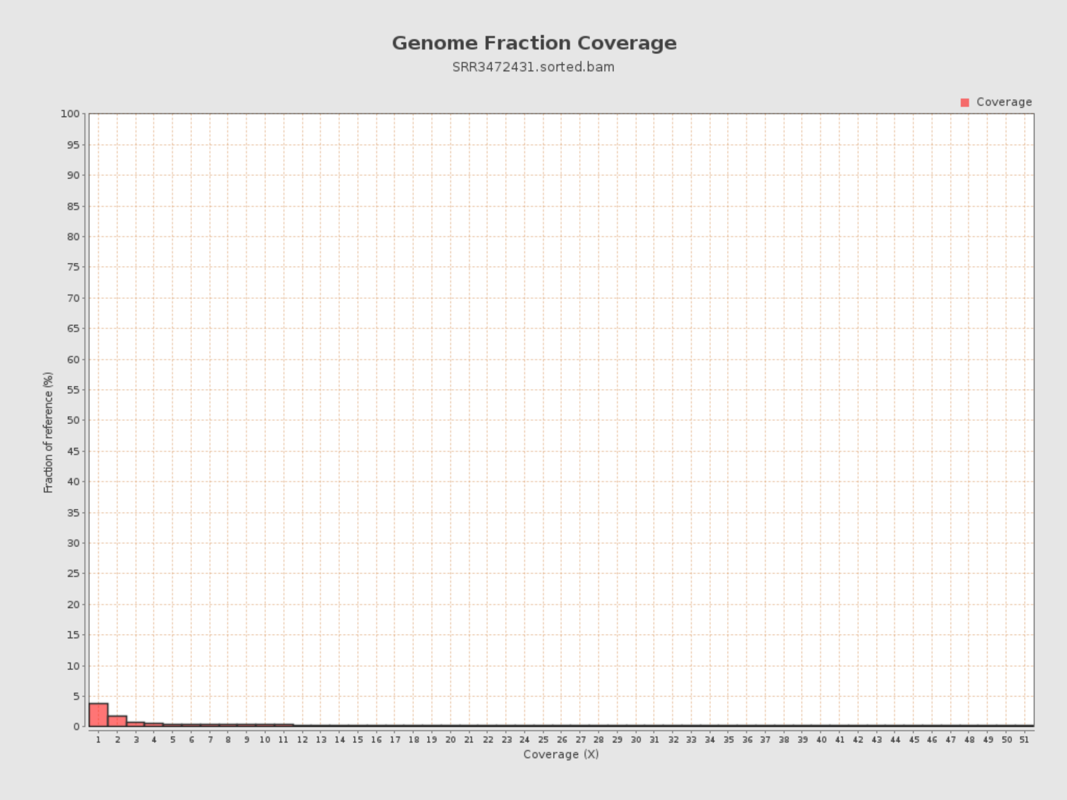
4. Results : Coverage Histogram



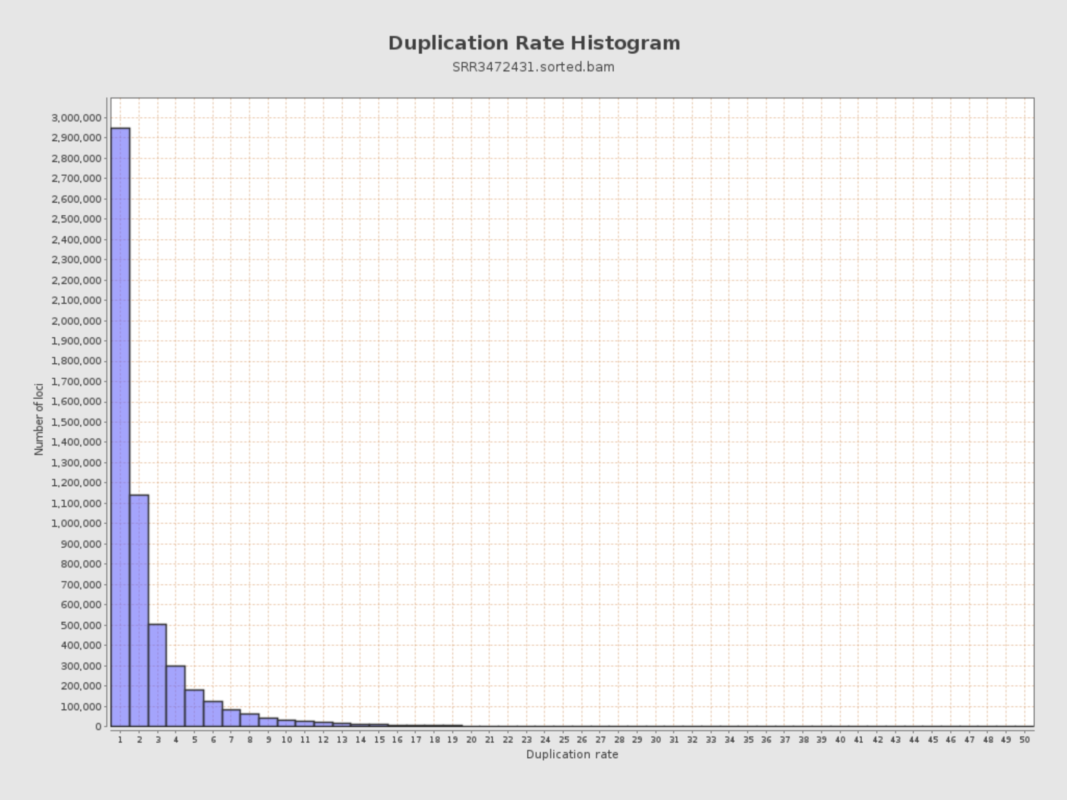
5. Results : Coverage Histogram (0-50X)



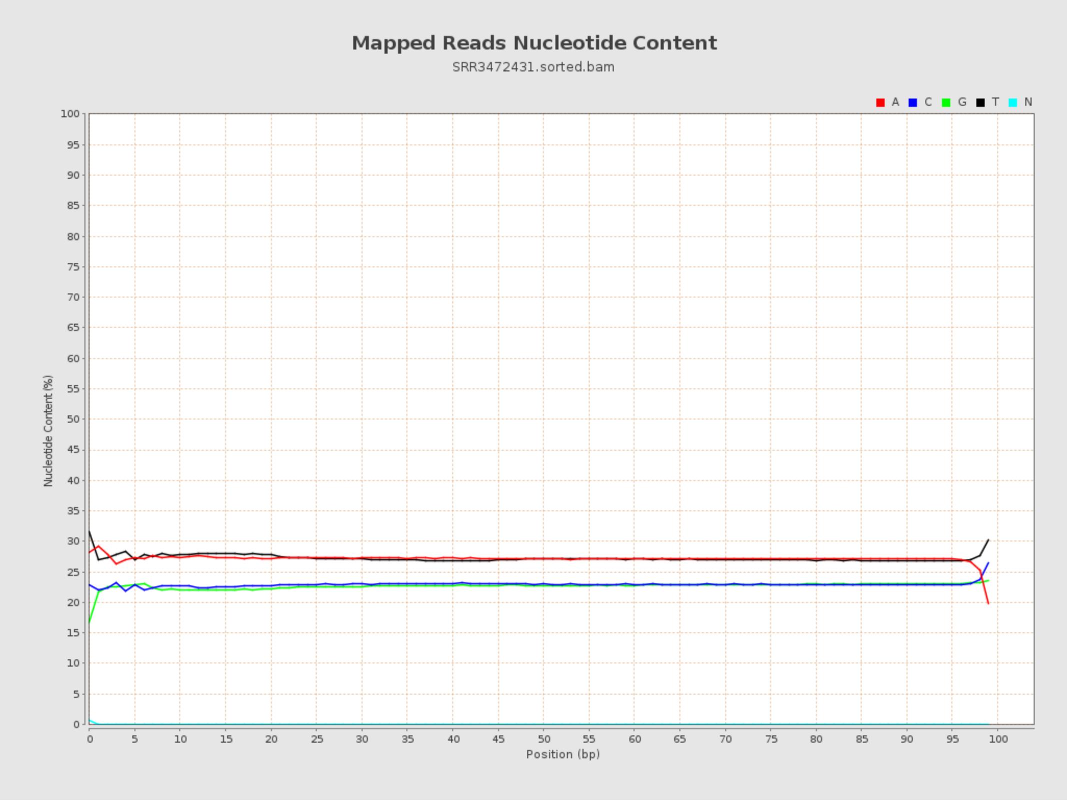
6. Results : Genome Fraction Coverage



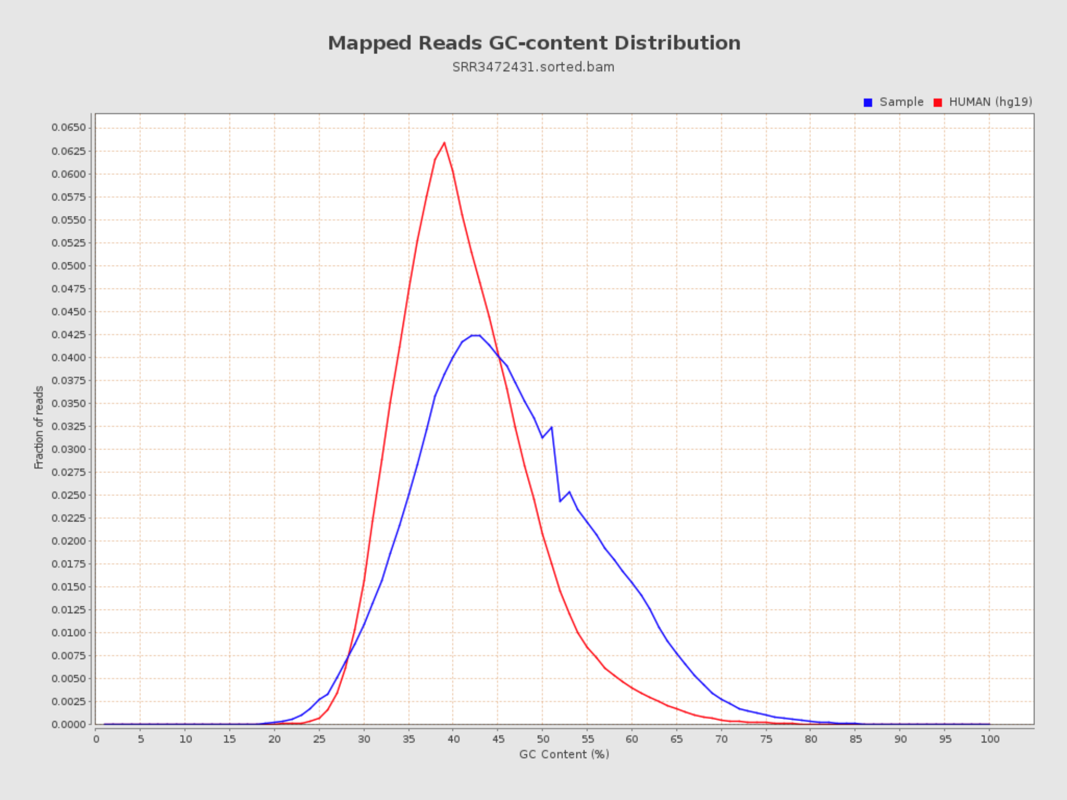
7. Results : Duplication Rate Histogram



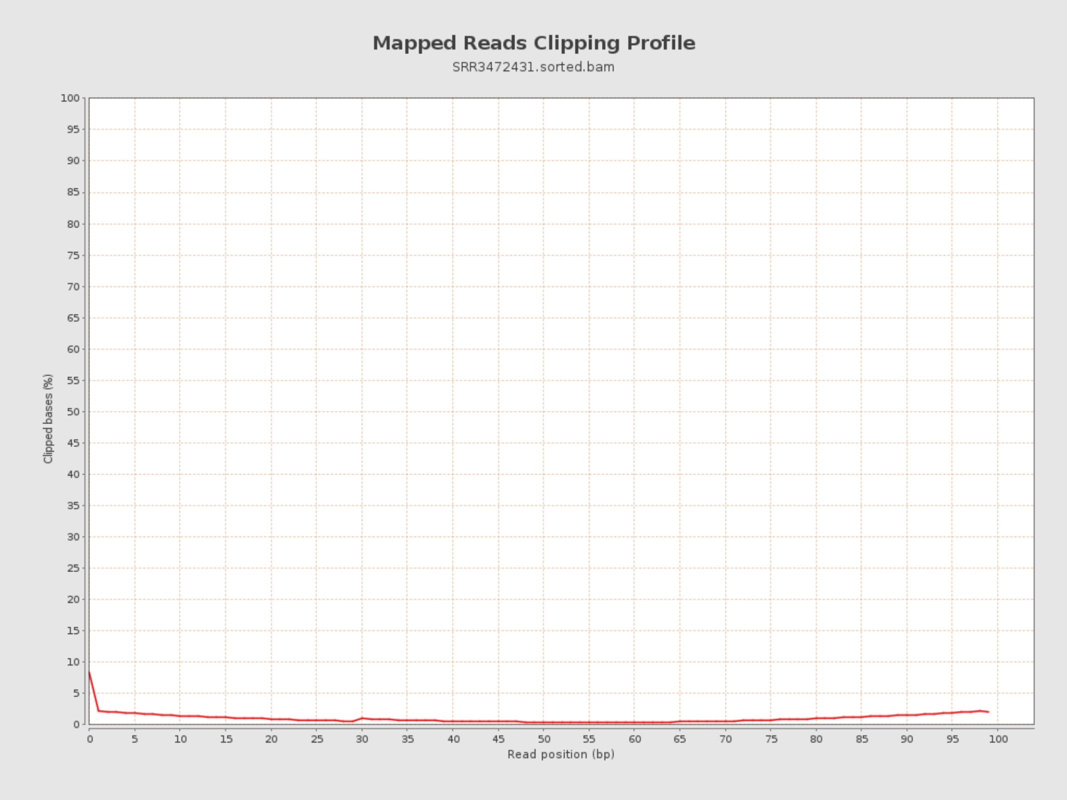
8. Results : Mapped Reads Nucleotide Content



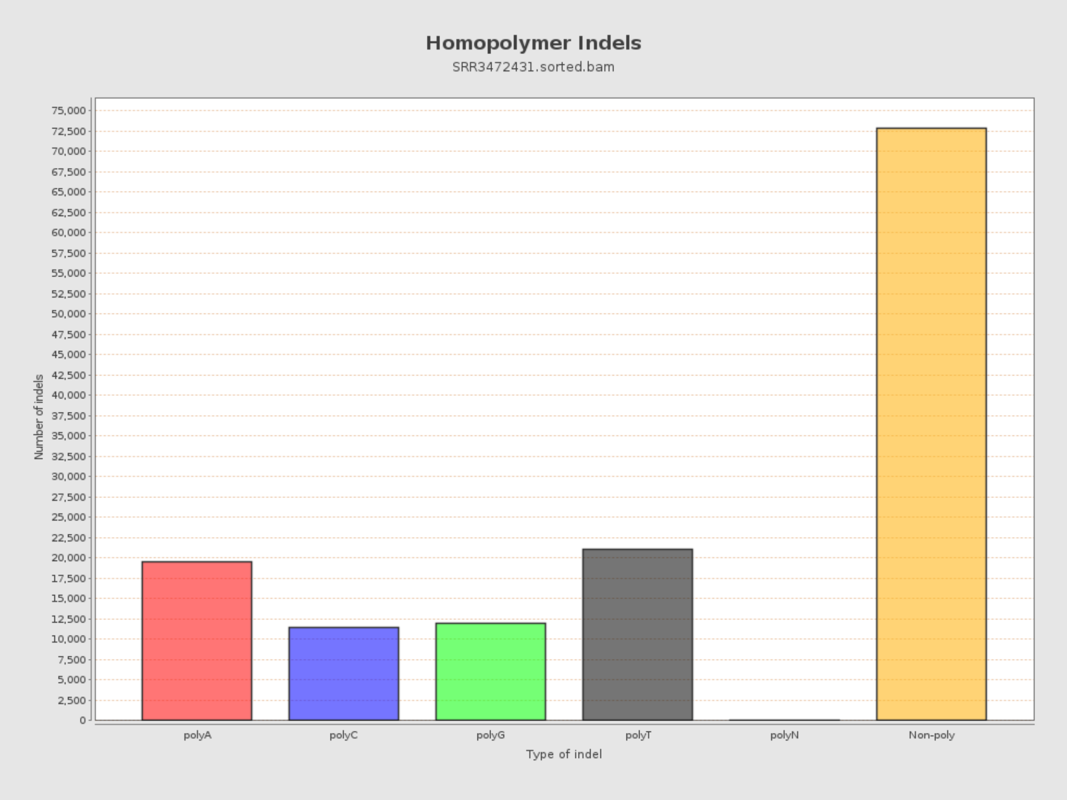
9. Results : Mapped Reads GC-content Distribution



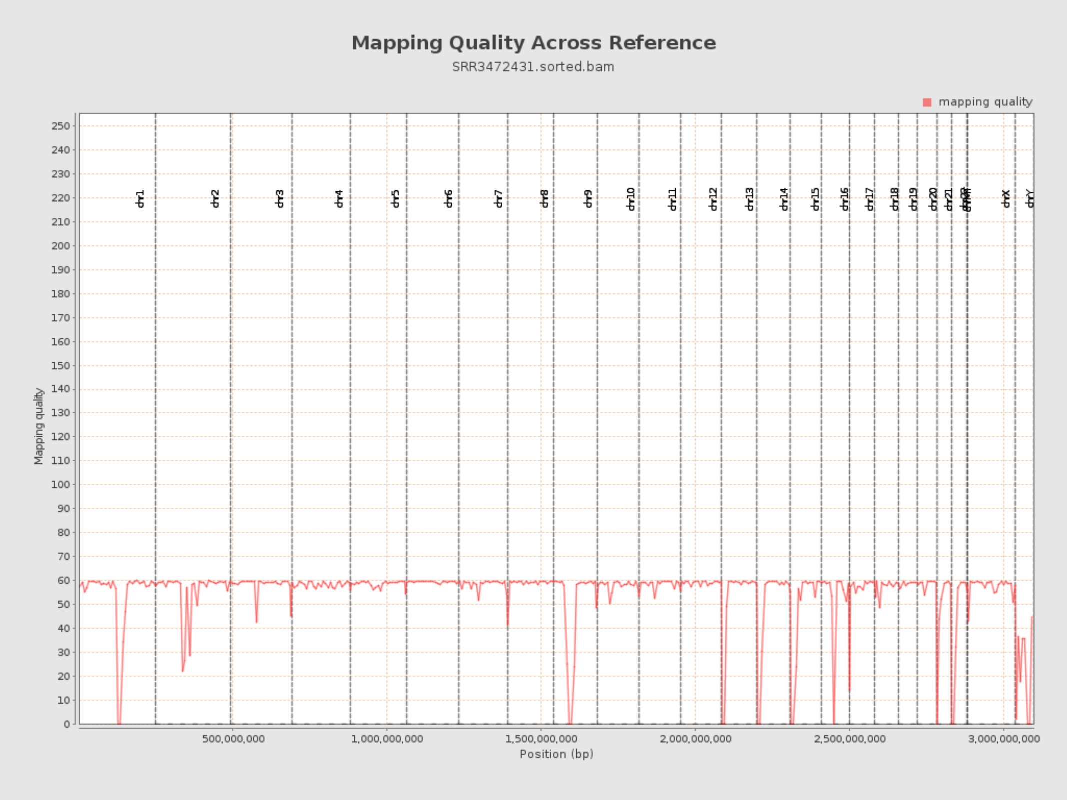
10. Results : Mapped Reads Clipping Profile



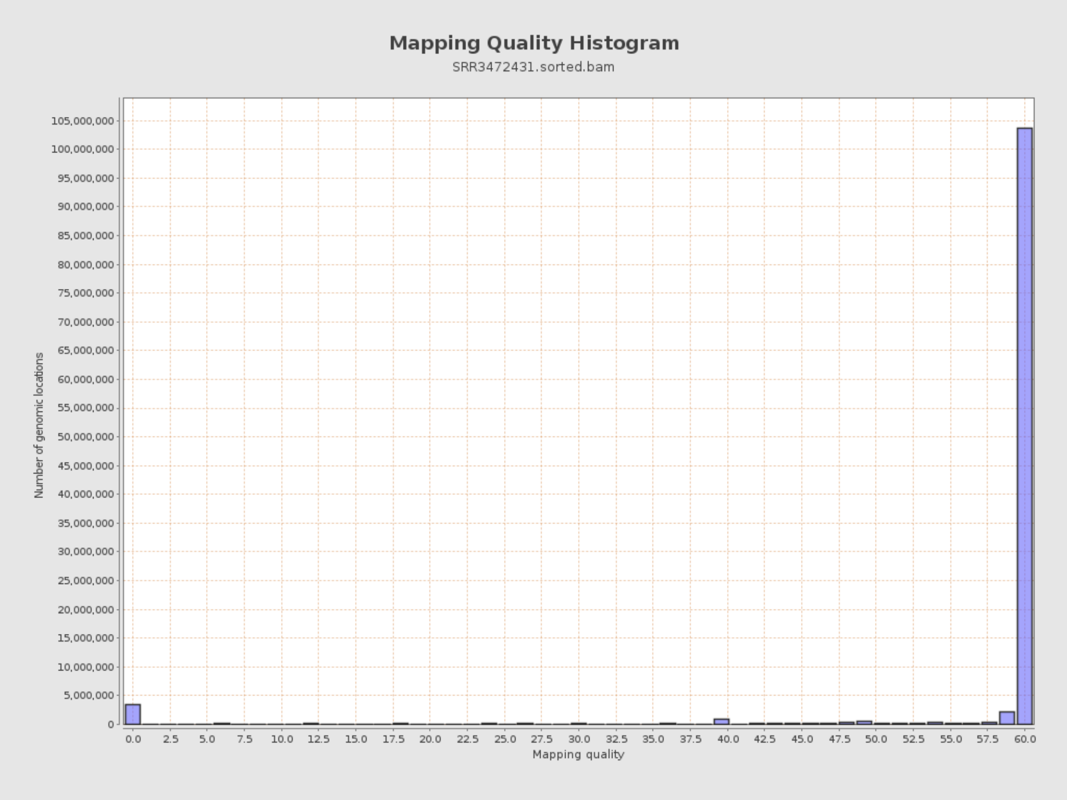
11. Results : Homopolymer Indels



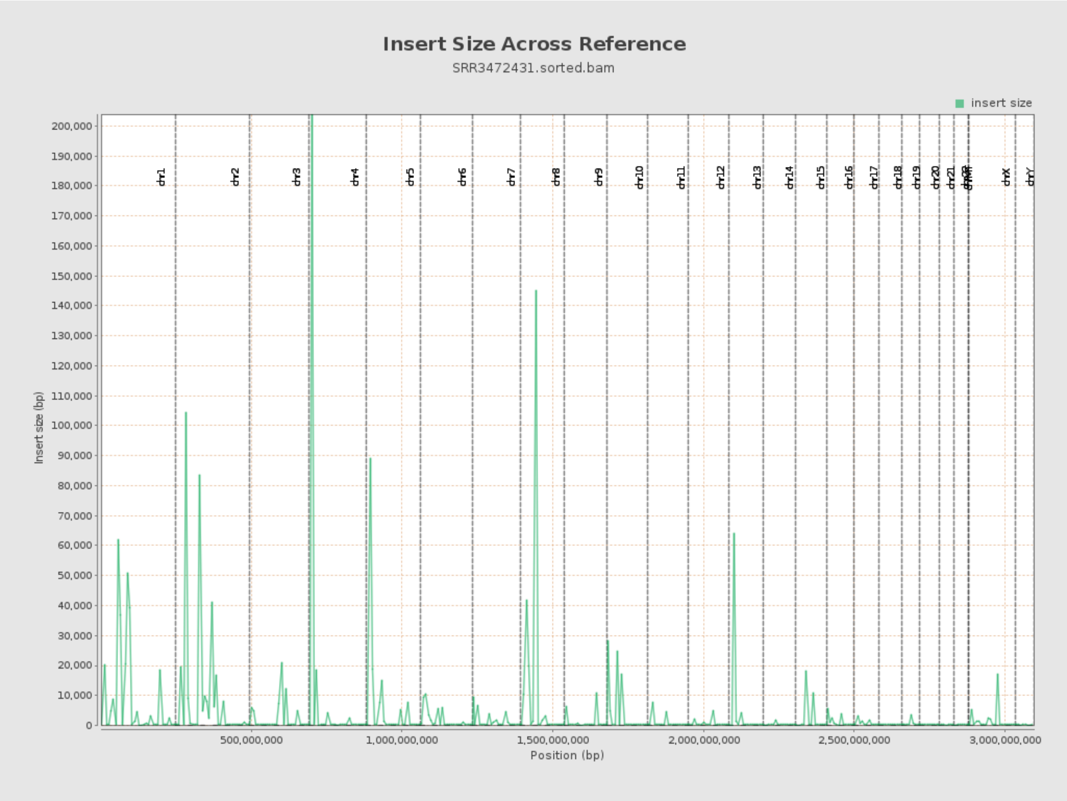
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram