Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:11:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472490.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_SRR3472490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472490_1.fastq.gz SRR3472490_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:11:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	185,840
Mapped reads	183,386 / 98.68%
Unmapped reads	2,454 / 1.32%
Mapped paired reads	183,386 / 98.68%
Mapped reads, first in pair	92,146 / 49.58%
Mapped reads, second in pair	91,240 / 49.1%
Mapped reads, both in pair	182,022 / 97.95%
Mapped reads, singletons	1,364 / 0.73%
Secondary alignments	0
Supplementary alignments	743 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	27,755 / 14.93%
Duplication rate	15%
Clipped reads	15,313 / 8.24%

2.2. ACGT Content

Number/percentage of A's	4,999,099 / 27.7%
Number/percentage of C's	4,047,291 / 22.42%
Number/percentage of T's	4,976,863 / 27.57%
Number/percentage of G's	4,022,867 / 22.29%
Number/percentage of N's	2,697 / 0.01%

GC Percentage	44.71%

2.3. Coverage

Mean	0.0058
Standard Deviation	0.1569

2.4. Mapping Quality

Mean Mapping Quality	55.07

2.5. Insert size

Mean	32,044.09
Standard Deviation	1,860,945.97
P25/Median/P75	169 / 235 / 318

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	108,636
Insertions	1,010
Mapped reads with at least one insertion	0.55%
Deletions	923
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.85%

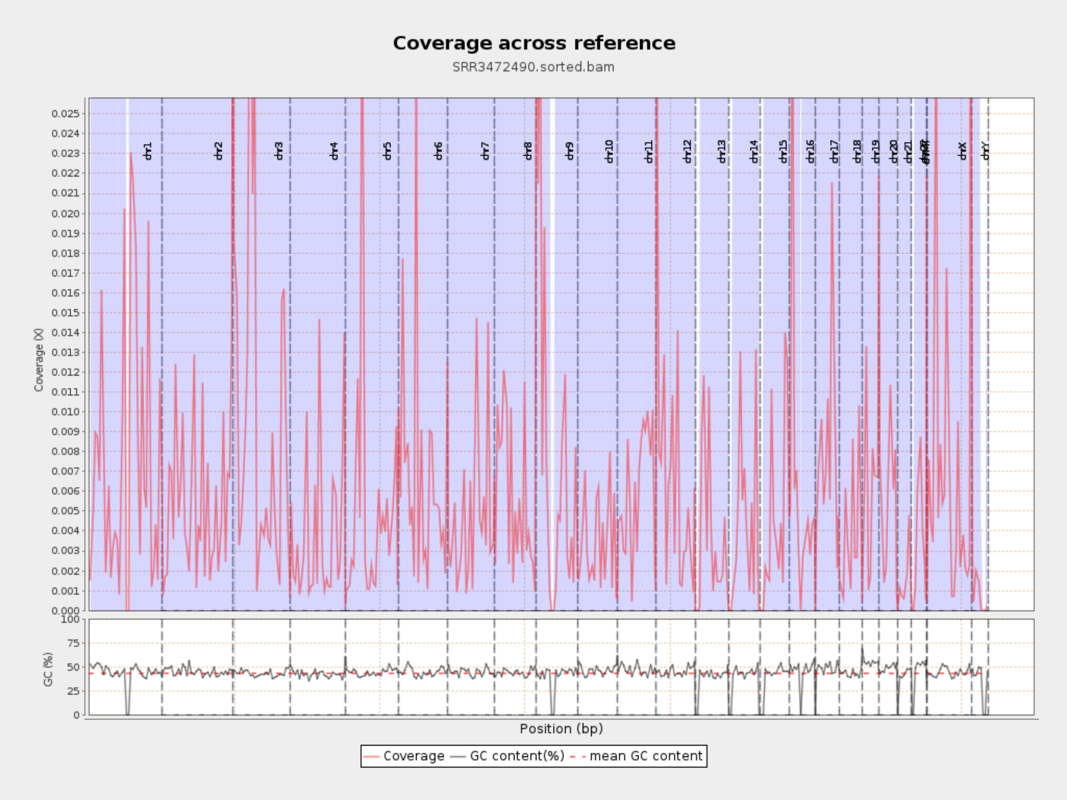
2.7. Chromosome stats

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

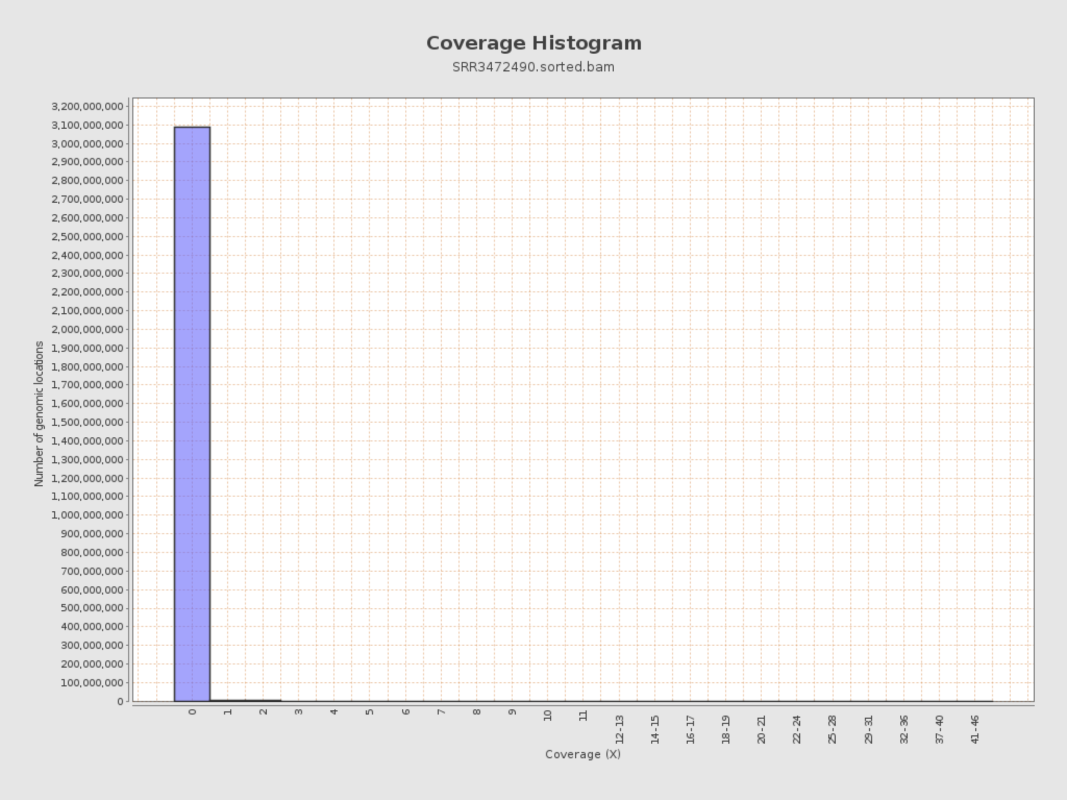
		bases	coverage	deviation
chr1	249250621	1918965	0.0077	0.2059
chr2	243199373	1301349	0.0054	0.1545
chr3	198022430	2071295	0.0105	0.2006
chr4	191154276	738362	0.0039	0.1241
chr5	180915260	949046	0.0052	0.1483
chr6	171115067	1177887	0.0069	0.1629
chr7	159138663	749353	0.0047	0.1316
chr8	146364022	824064	0.0056	0.1509
chr9	141213431	1104796	0.0078	0.1749
chr10	135534747	490309	0.0036	0.1261
chr11	135006516	807351	0.006	0.1618
chr12	133851895	918308	0.0069	0.1762
chr13	115169878	423726	0.0037	0.1188
chr14	107349540	475580	0.0044	0.1535
chr15	102531392	471542	0.0046	0.1397
chr16	90354753	594678	0.0066	0.1642
chr17	81195210	658183	0.0081	0.1731
chr18	78077248	310173	0.004	0.1298
chr19	59128983	384320	0.0065	0.1678
chr20	63025520	361020	0.0057	0.1454
chr21	48129895	75225	0.0016	0.0649
chr22	51304566	173477	0.0034	0.1005
chrMT	16571	362	0.0218	0.173
chrX	155270560	1036642	0.0067	0.16

chrY	59373566	35211	0.0006	0.0361

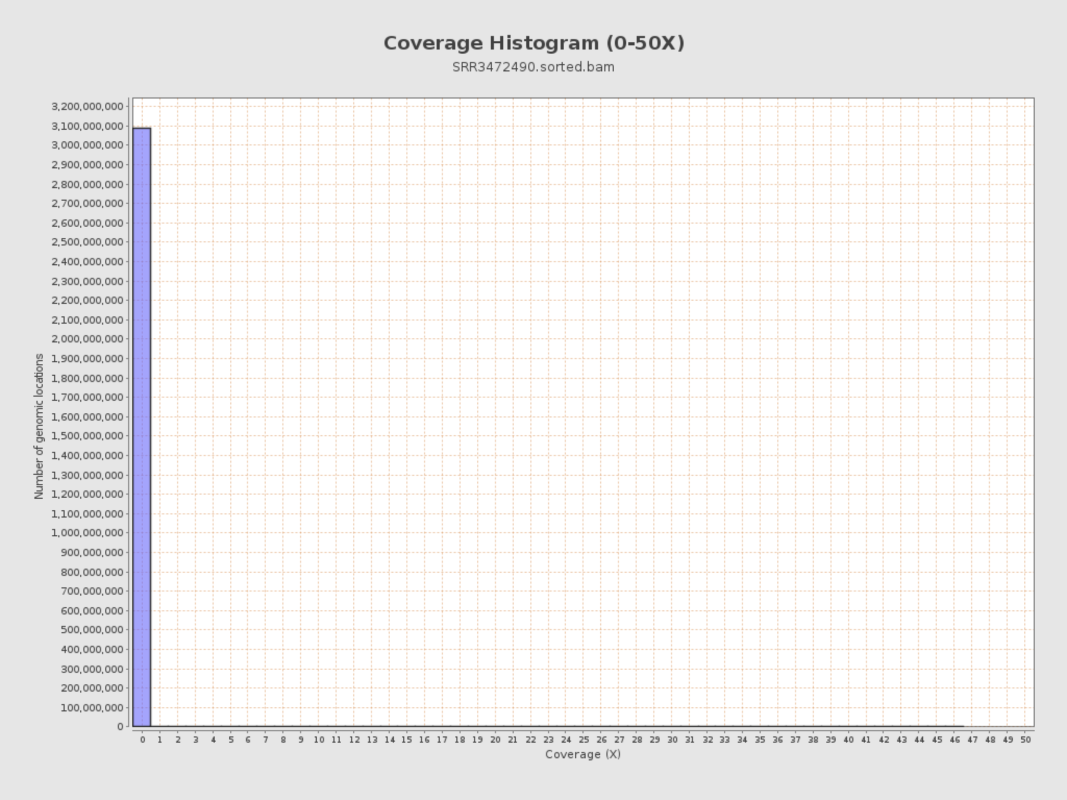
3. Results : Coverage across reference



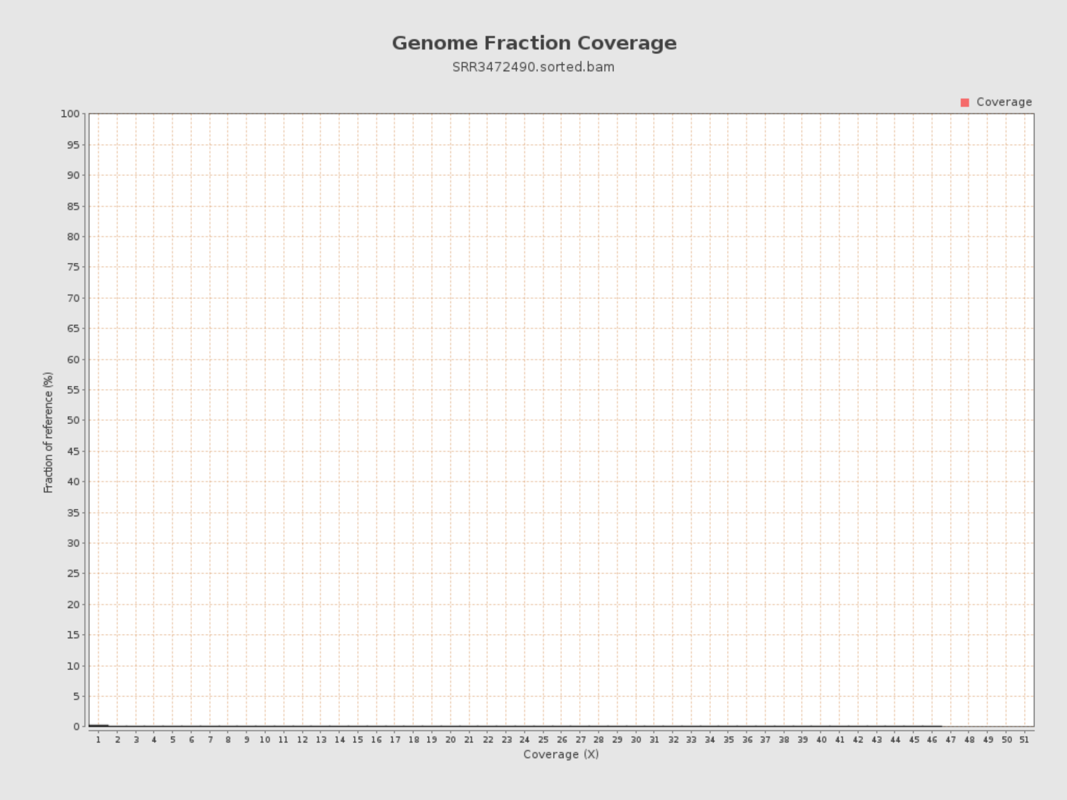
4. Results : Coverage Histogram



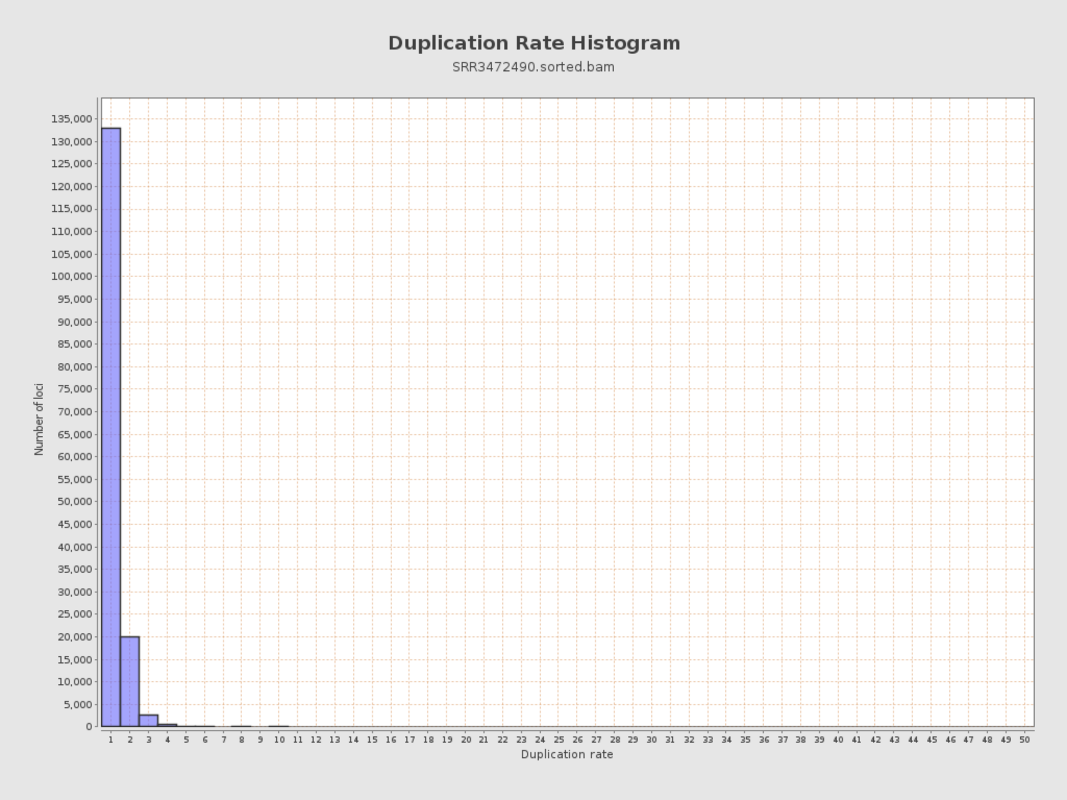
5. Results : Coverage Histogram (0-50X)



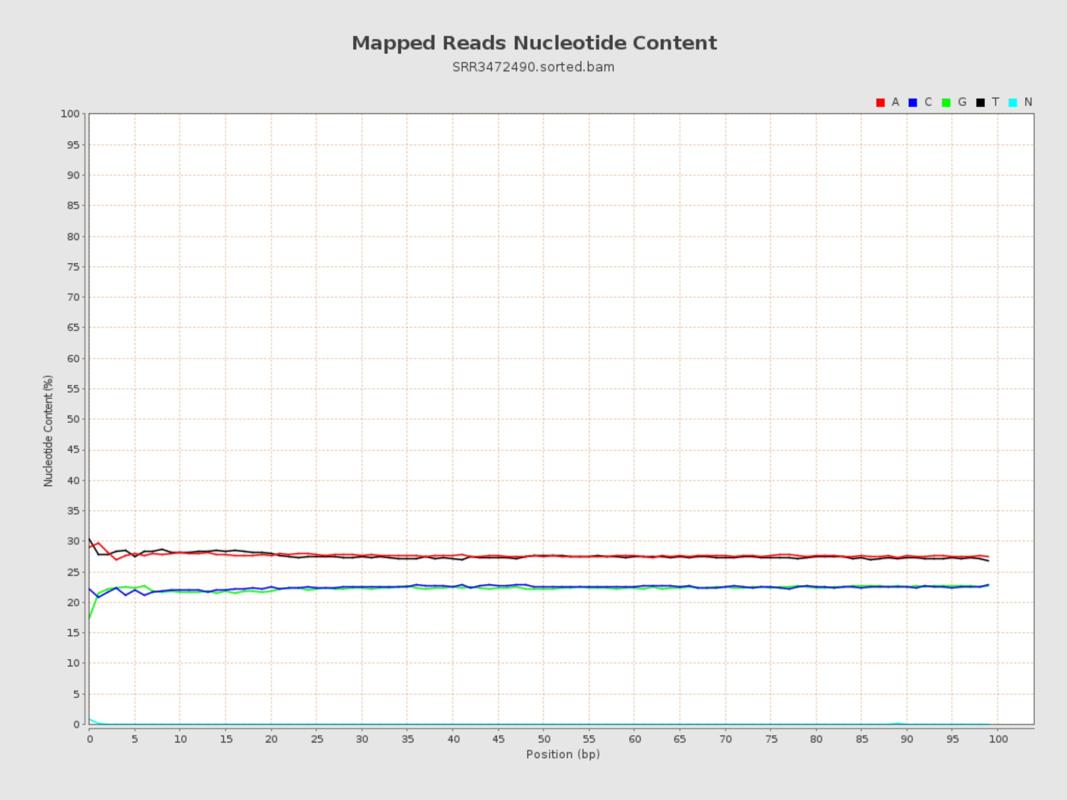
6. Results : Genome Fraction Coverage



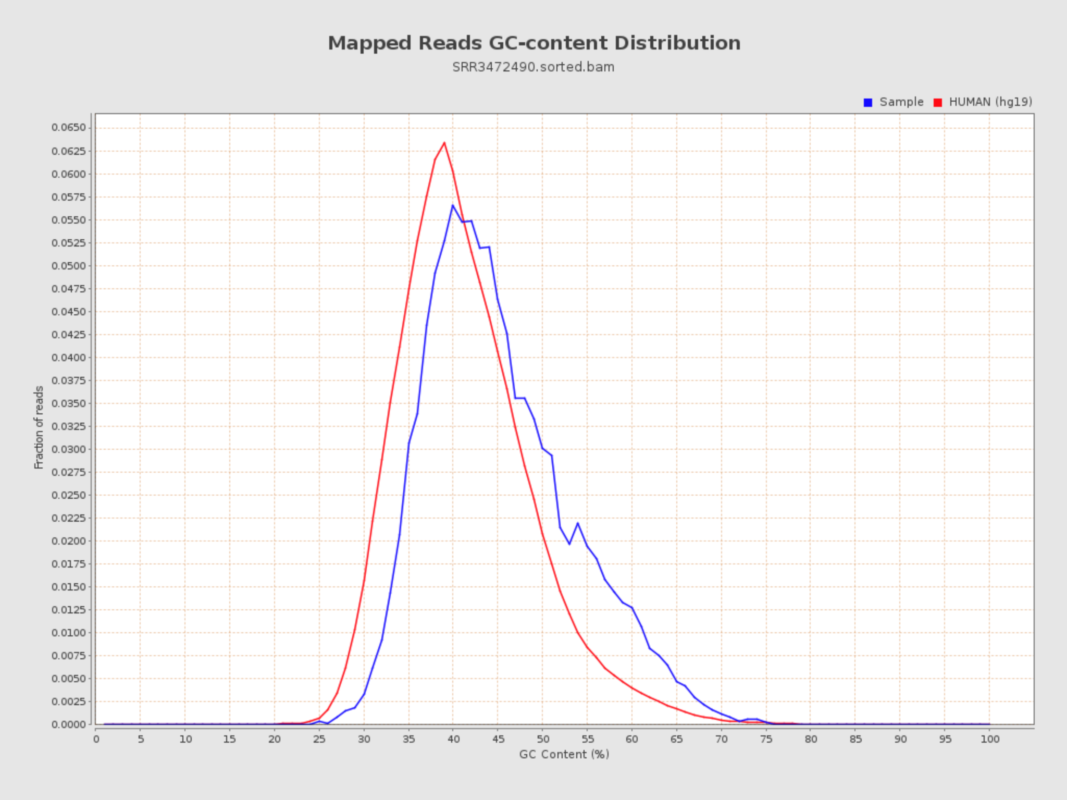
7. Results : Duplication Rate Histogram



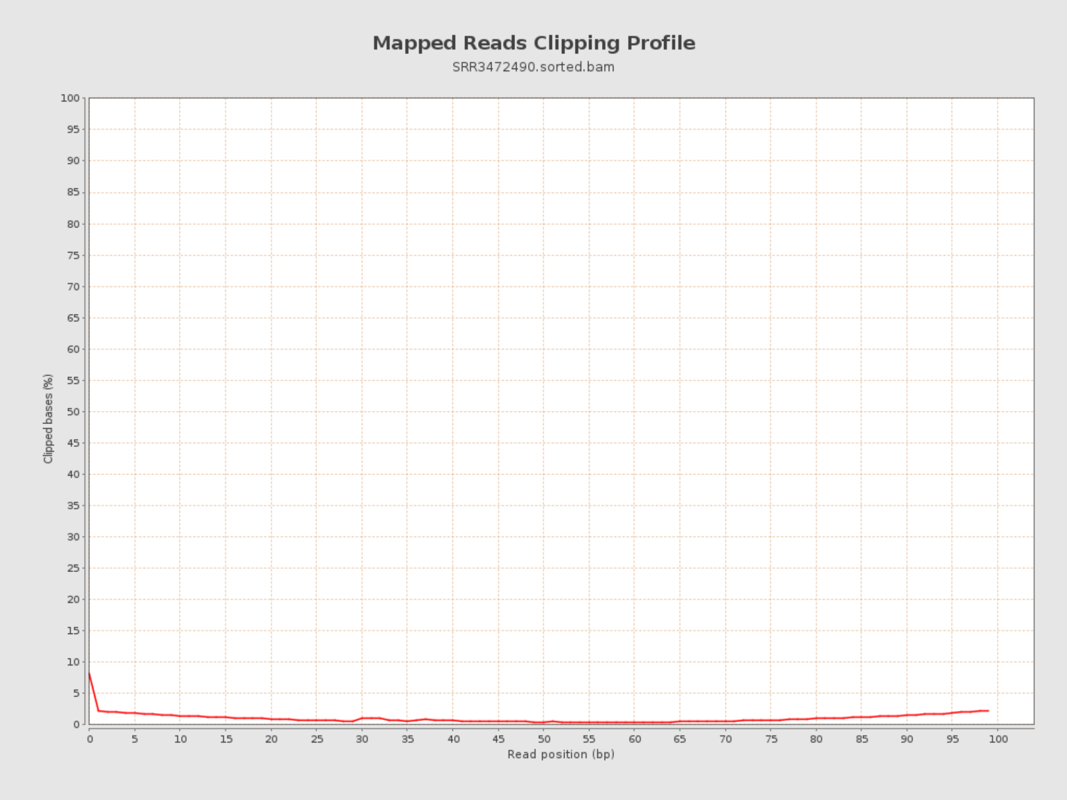
8. Results : Mapped Reads Nucleotide Content



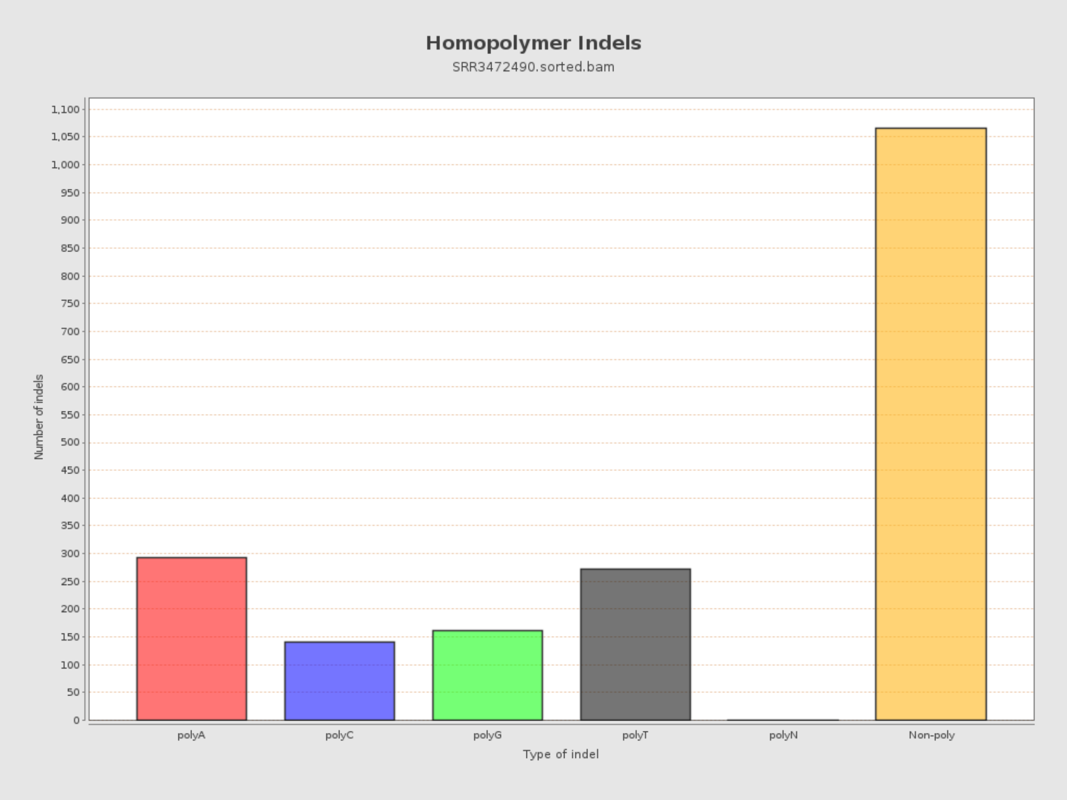
9. Results : Mapped Reads GC-content Distribution



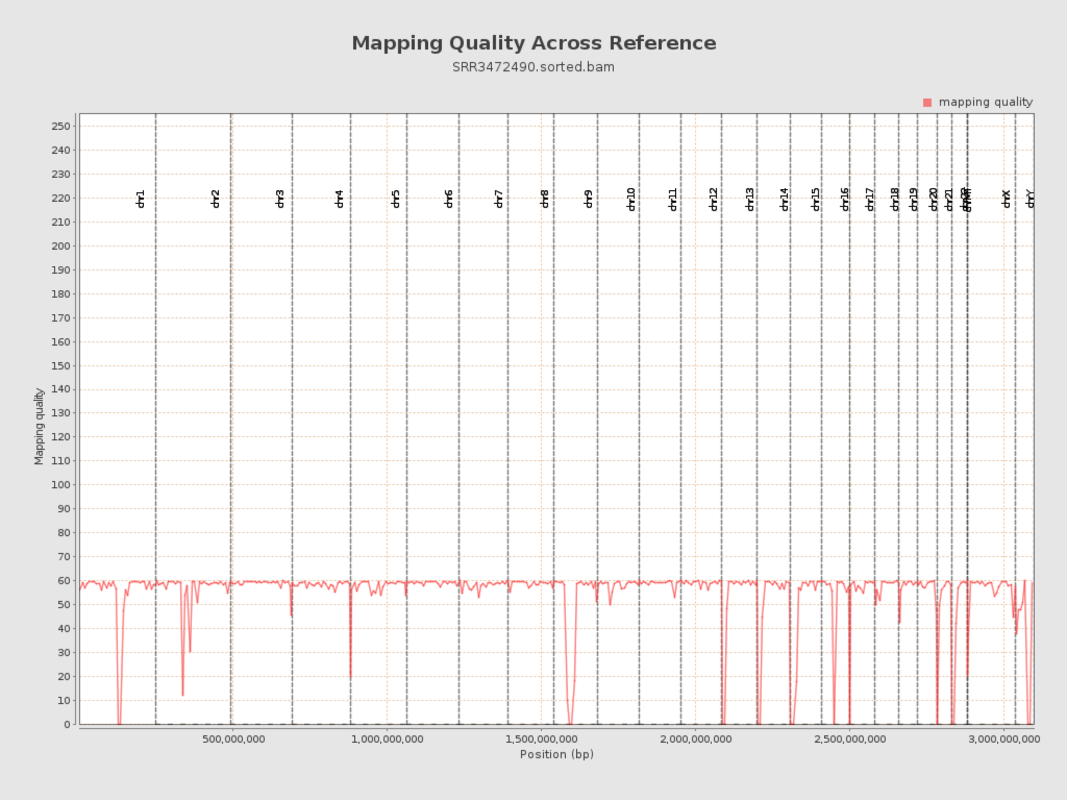
10. Results : Mapped Reads Clipping Profile



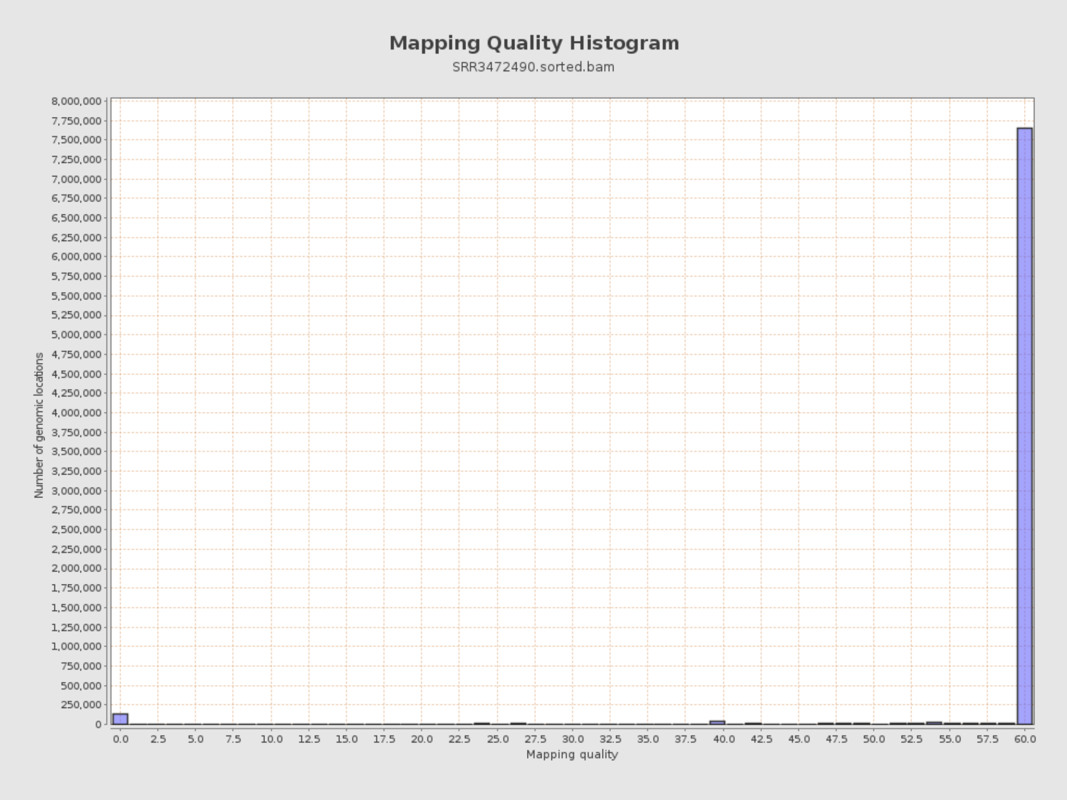
11. Results : Homopolymer Indels



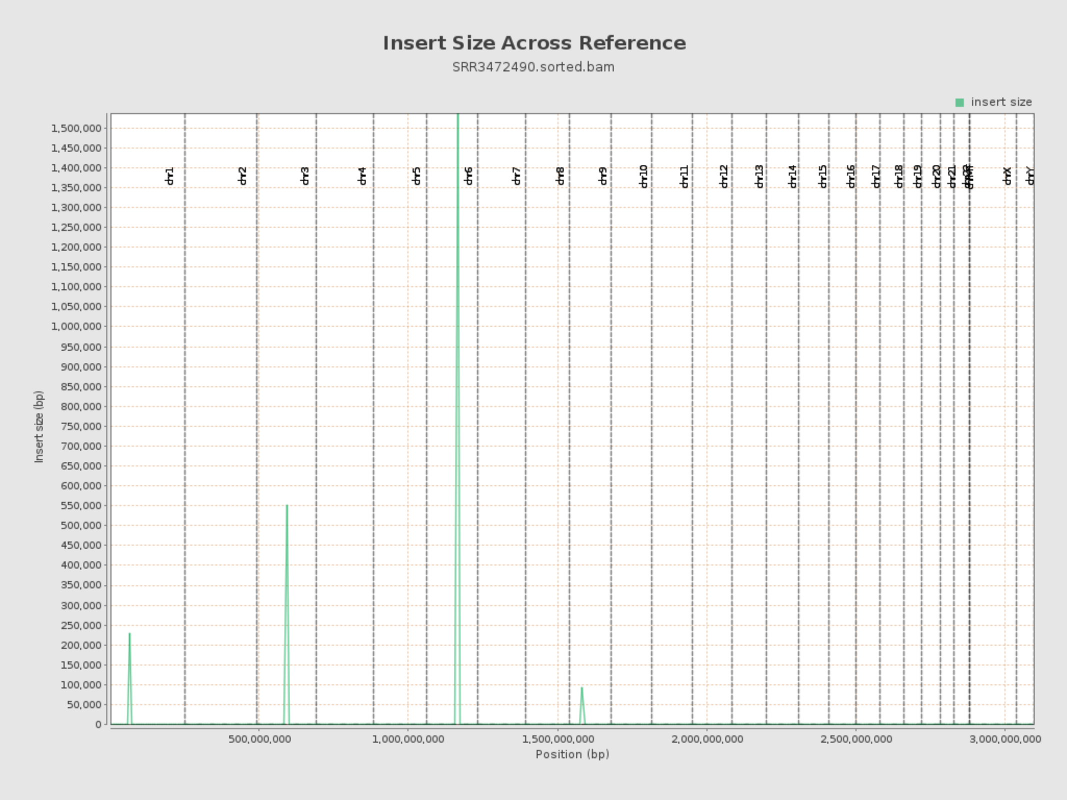
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram