Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 01:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472799.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_SRR3472799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472799_1.fastq.gz SRR3472799_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 01:51:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	95,480,976
Mapped reads	95,099,765 / 99.6%
Unmapped reads	381,211 / 0.4%
Mapped paired reads	95,099,765 / 99.6%
Mapped reads, first in pair	47,684,160 / 49.94%
Mapped reads, second in pair	47,415,605 / 49.66%
Mapped reads, both in pair	94,803,300 / 99.29%
Mapped reads, singletons	296,465 / 0.31%
Secondary alignments	0
Supplementary alignments	70,453 / 0.07%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	46,604,050 / 48.81%
Duplication rate	45.07%
Clipped reads	5,683,426 / 5.95%

2.2. ACGT Content

Number/percentage of A's	2,667,743,345 / 28.37%
Number/percentage of C's	2,032,955,741 / 21.62%
Number/percentage of T's	2,699,651,227 / 28.71%
Number/percentage of G's	2,002,797,295 / 21.3%
Number/percentage of N's	969,309 / 0.01%

GC Percentage	42.91%

2.3. Coverage

Mean	3.0382
Standard Deviation	23.165

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	13,405.2
Standard Deviation	1,146,767.77
P25/Median/P75	169 / 229 / 302

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	38,340,989
Insertions	388,916
Mapped reads with at least one insertion	0.4%
Deletions	463,083
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.59%

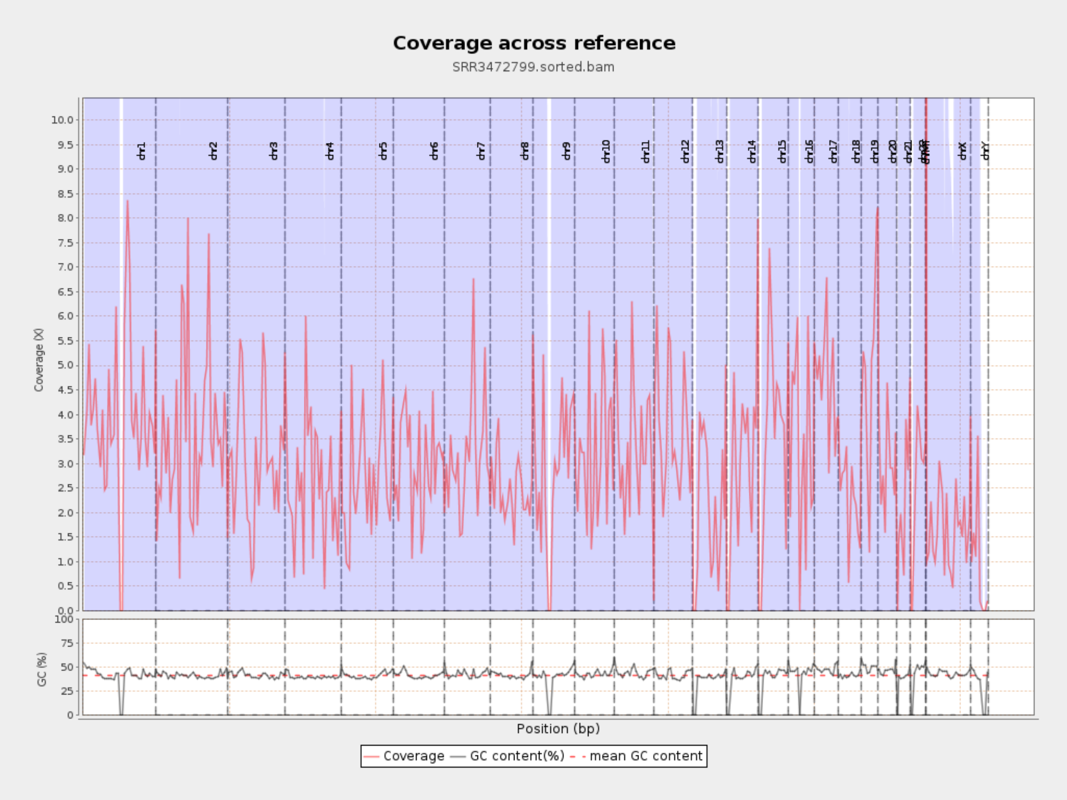
2.7. Chromosome stats

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

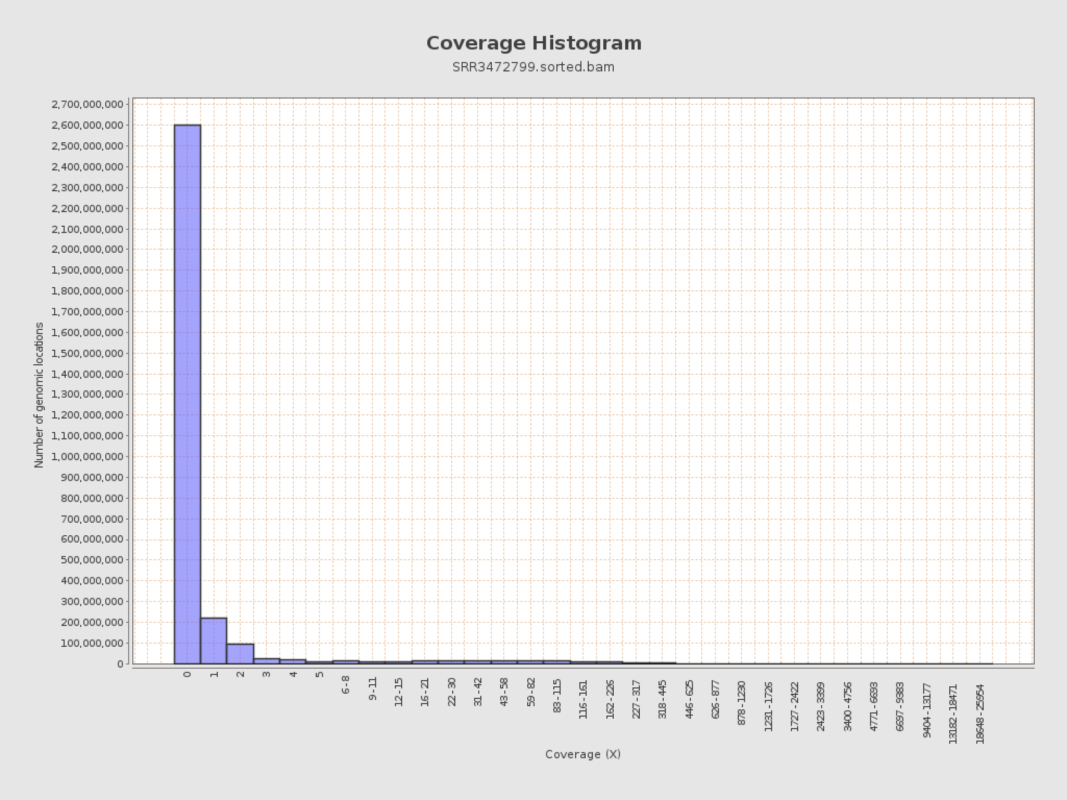
		bases	coverage	deviation
chr1	249250621	973768443	3.9068	28.2832
chr2	243199373	885749103	3.6421	26.7984
chr3	198022430	599757670	3.0287	21.2791
chr4	191154276	494276725	2.5857	20.8542
chr5	180915260	497391760	2.7493	20.616
chr6	171115067	508007297	2.9688	21.5466
chr7	159138663	503042228	3.161	22.6771
chr8	146364022	359474206	2.456	19.4624
chr9	141213431	398898857	2.8248	21.5402
chr10	135534747	438814084	3.2377	23.7823
chr11	135006516	462596028	3.4265	21.5035
chr12	133851895	502899194	3.7571	23.341
chr13	115169878	232840241	2.0217	18.1119
chr14	107349540	307412898	2.8637	21.5054
chr15	102531392	346062726	3.3752	22.4041
chr16	90354753	296743961	3.2842	21.8815
chr17	81195210	385364873	4.7462	23.5934
chr18	78077248	183068264	2.3447	19.2316
chr19	59128983	283623072	4.7967	22.589
chr20	63025520	183531170	2.912	19.1358
chr21	48129895	107121849	2.2257	20.7464
chr22	51304566	127954124	2.494	17.6043
chrMT	16571	16405835	990.0329	2,874.1661
chrX	155270560	254114471	1.6366	13.3635

chrY	59373566	56265448	0.9477	15.7252

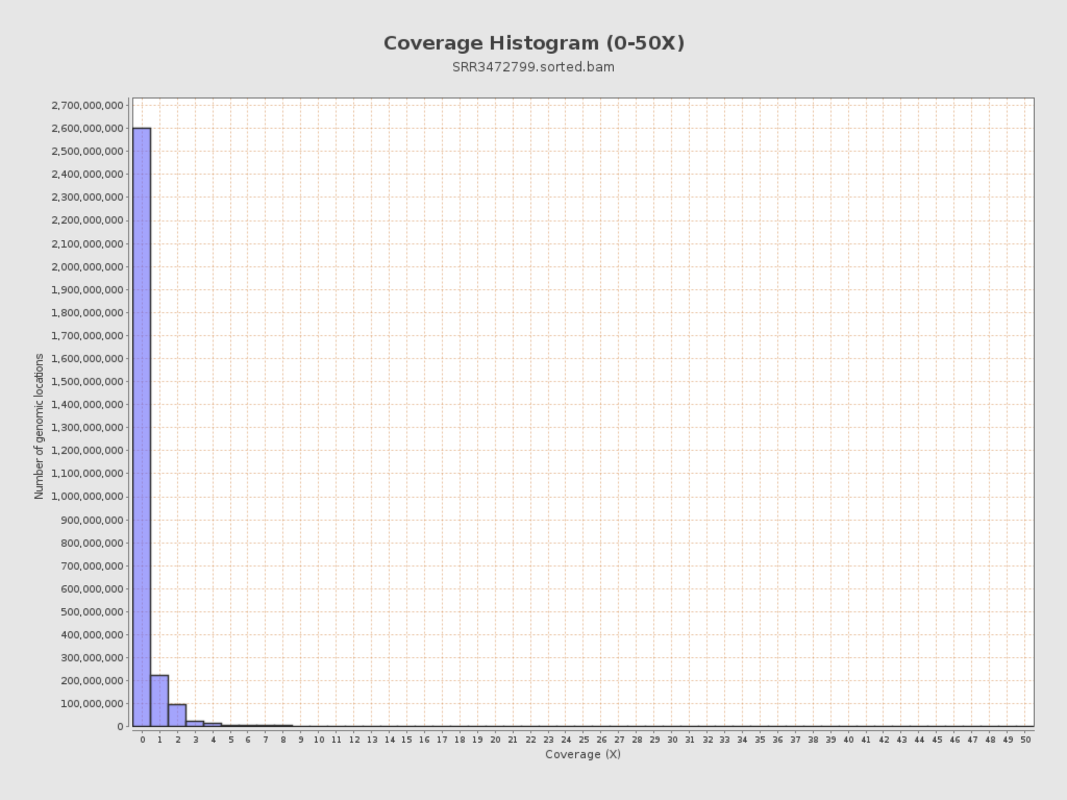
3. Results : Coverage across reference



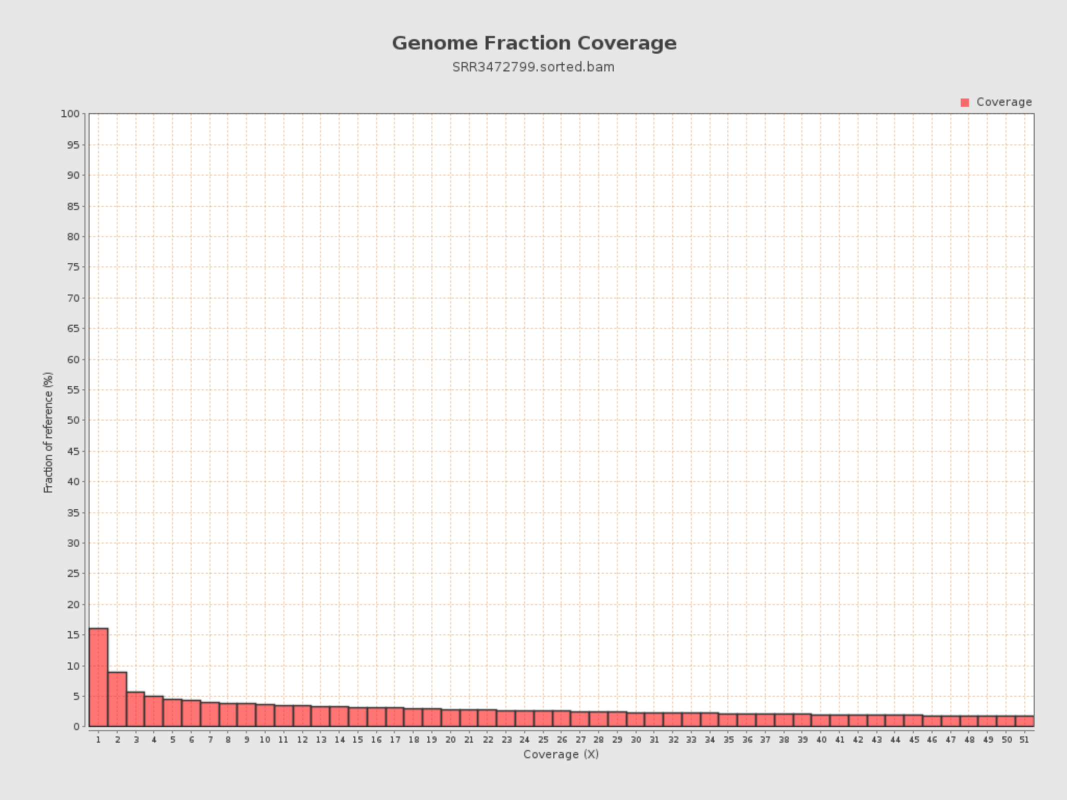
4. Results : Coverage Histogram



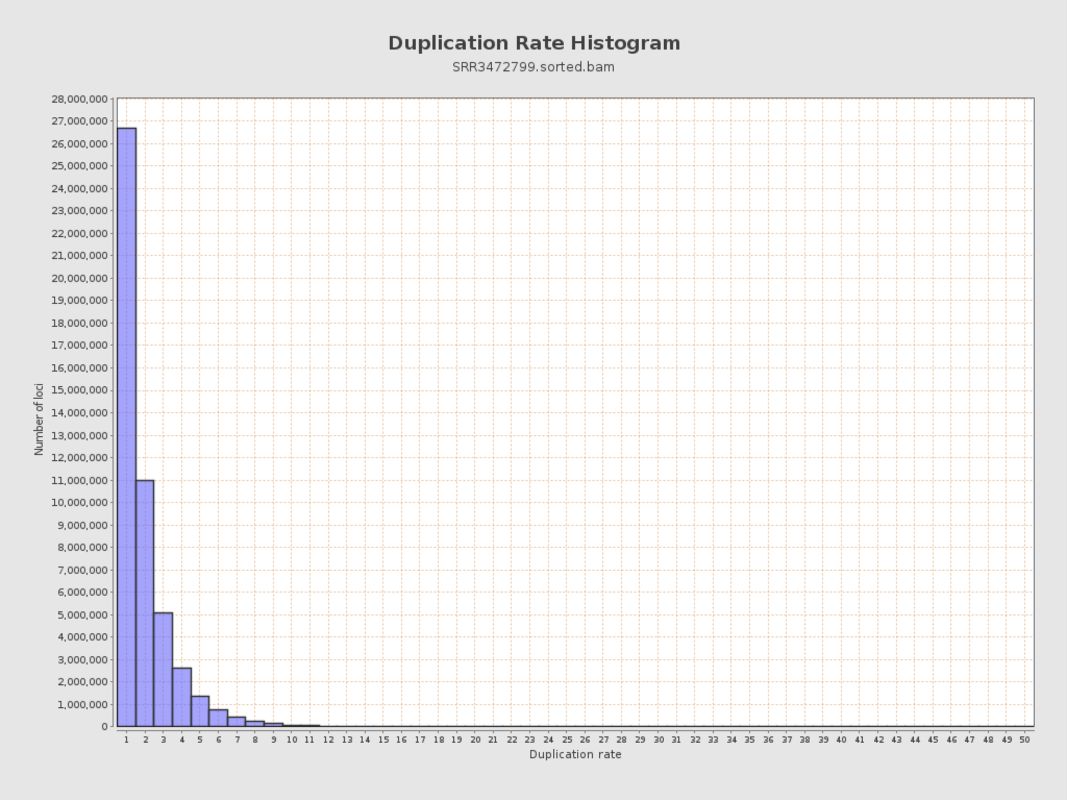
5. Results : Coverage Histogram (0-50X)



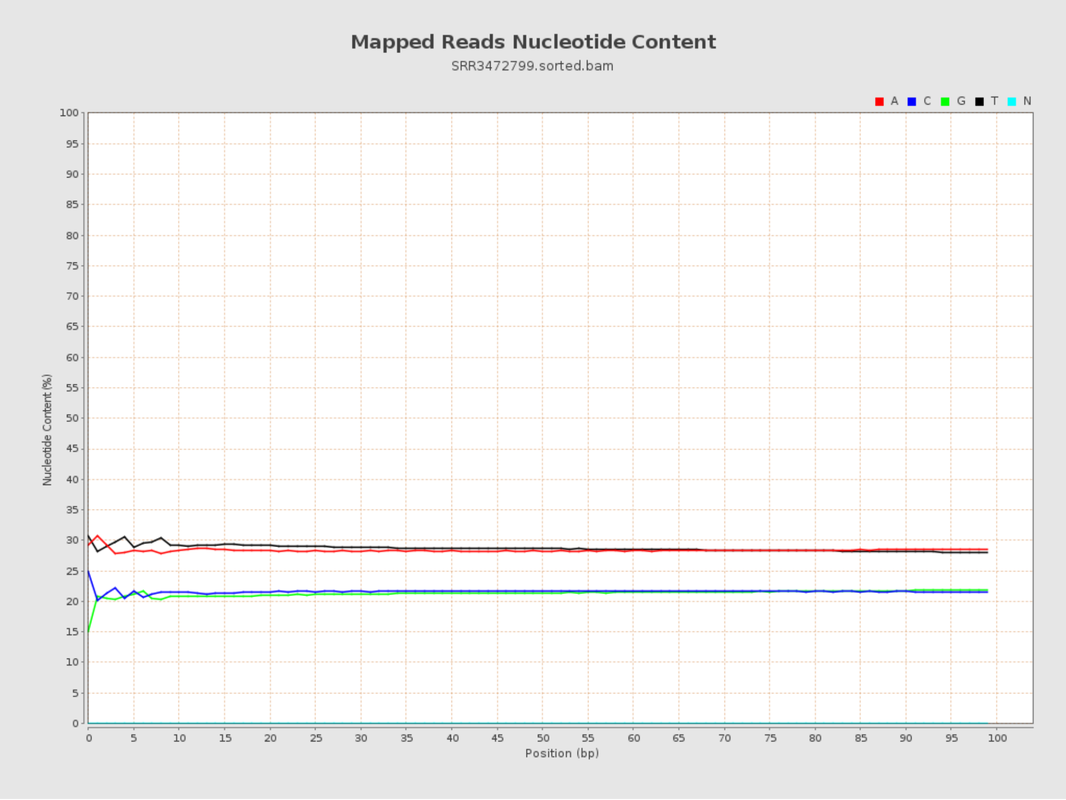
6. Results : Genome Fraction Coverage



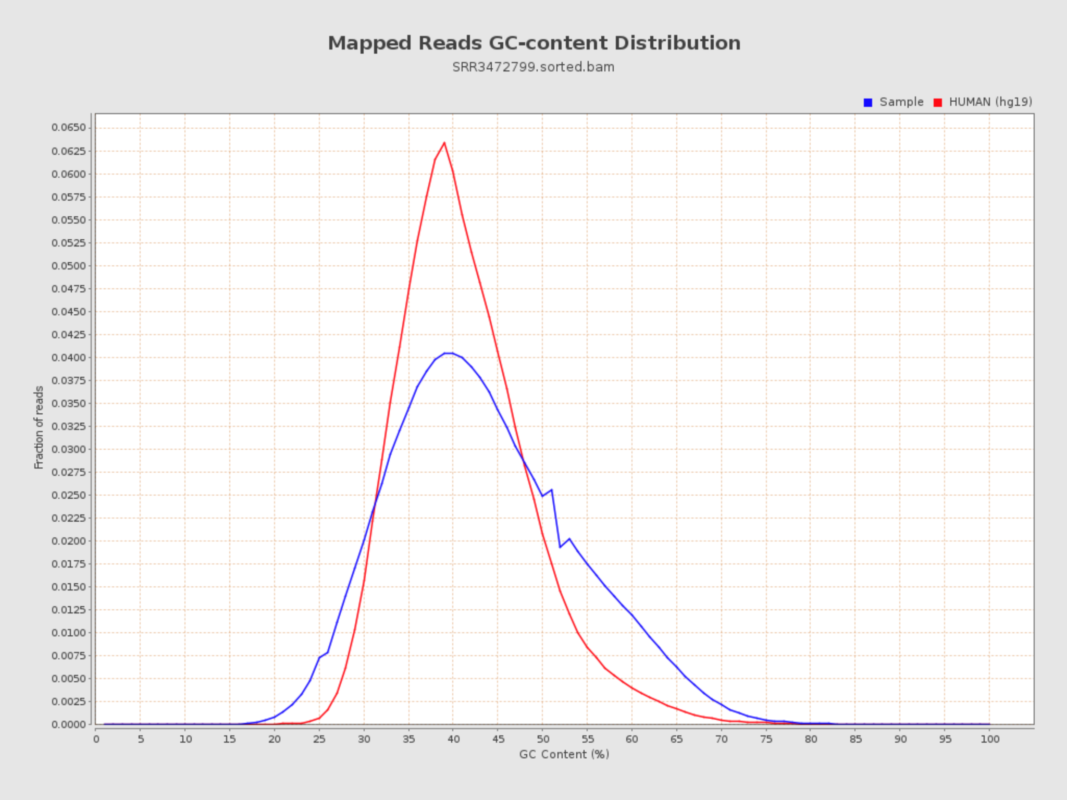
7. Results : Duplication Rate Histogram



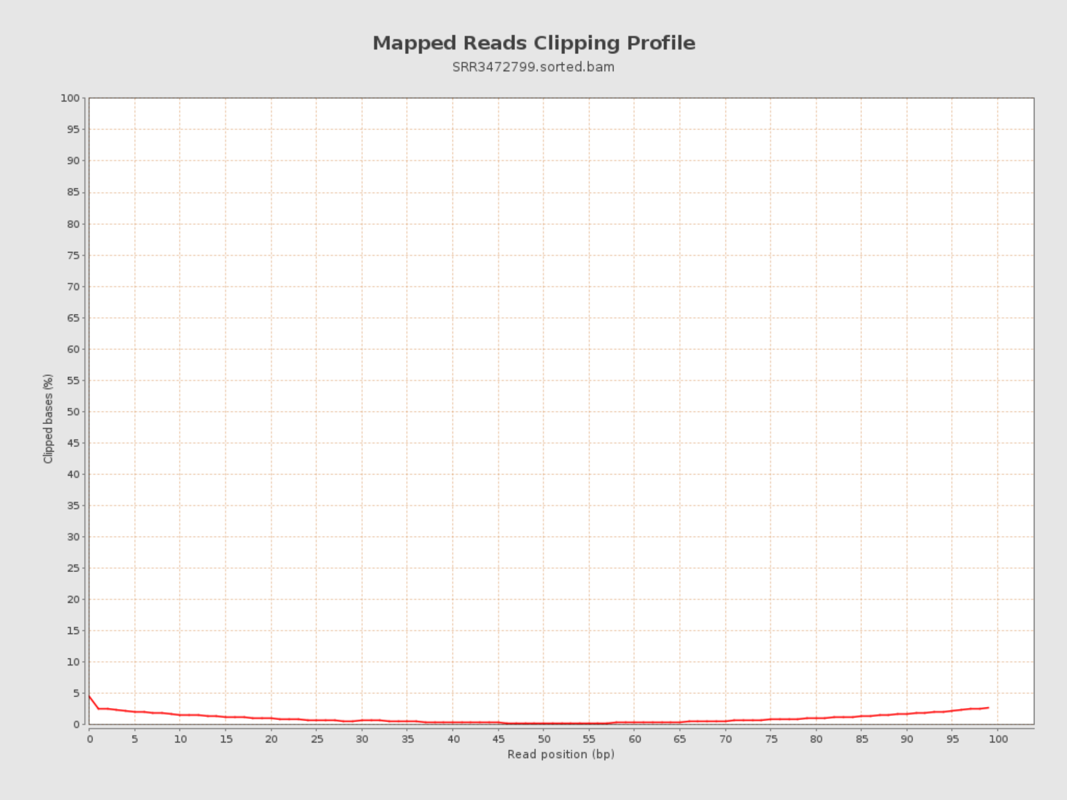
8. Results : Mapped Reads Nucleotide Content



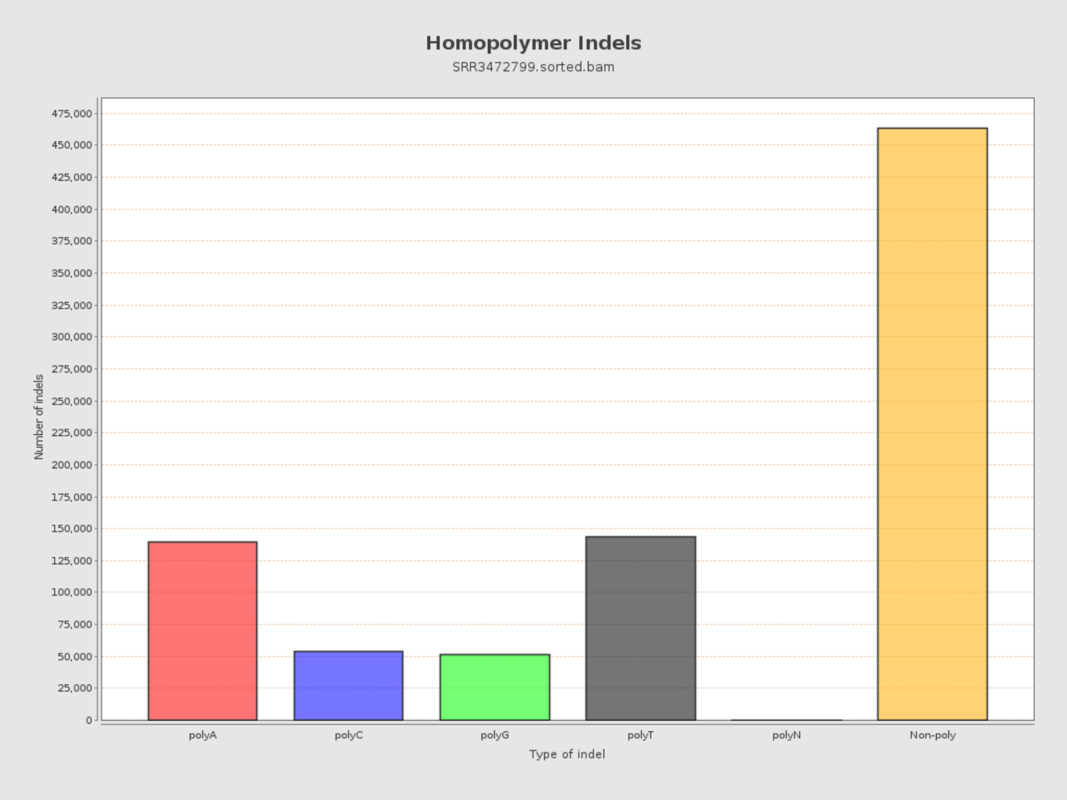
9. Results : Mapped Reads GC-content Distribution



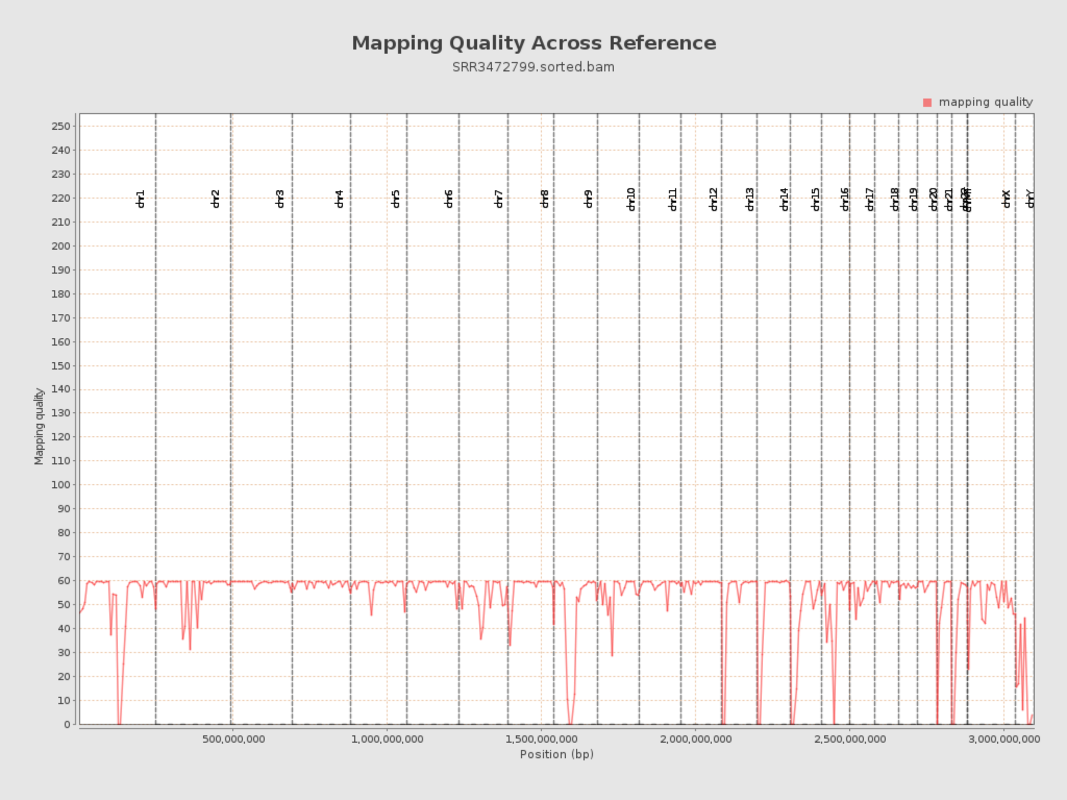
10. Results : Mapped Reads Clipping Profile



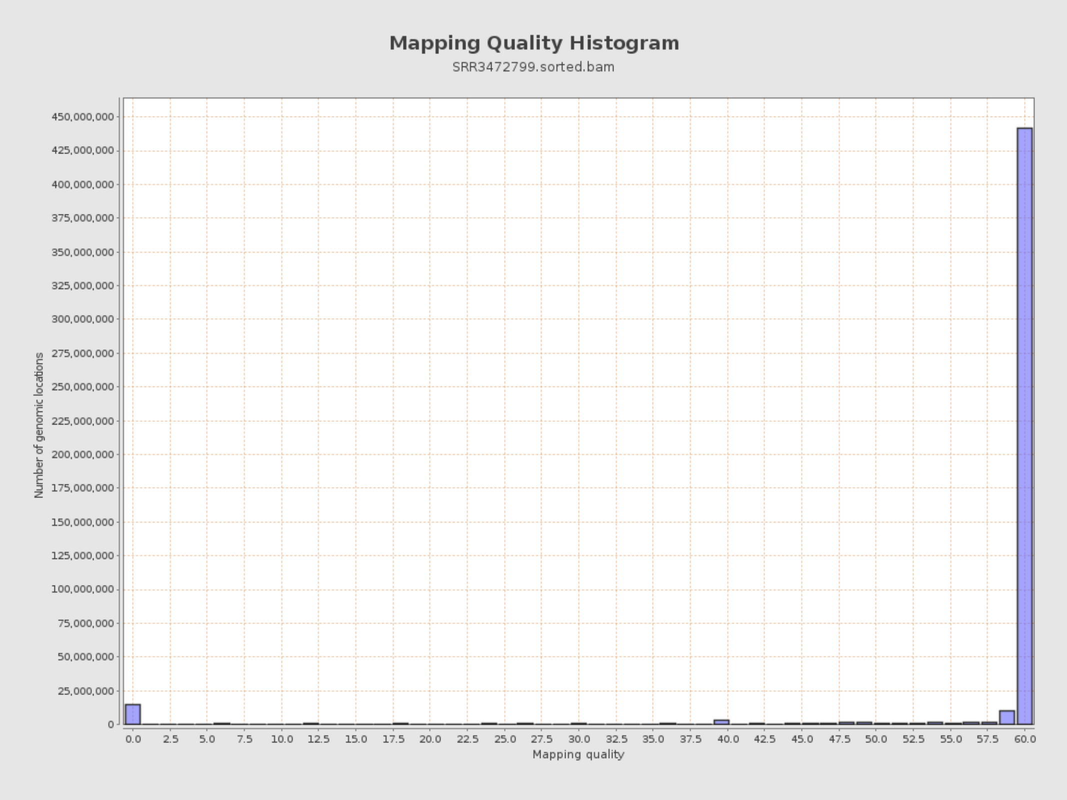
11. Results : Homopolymer Indels



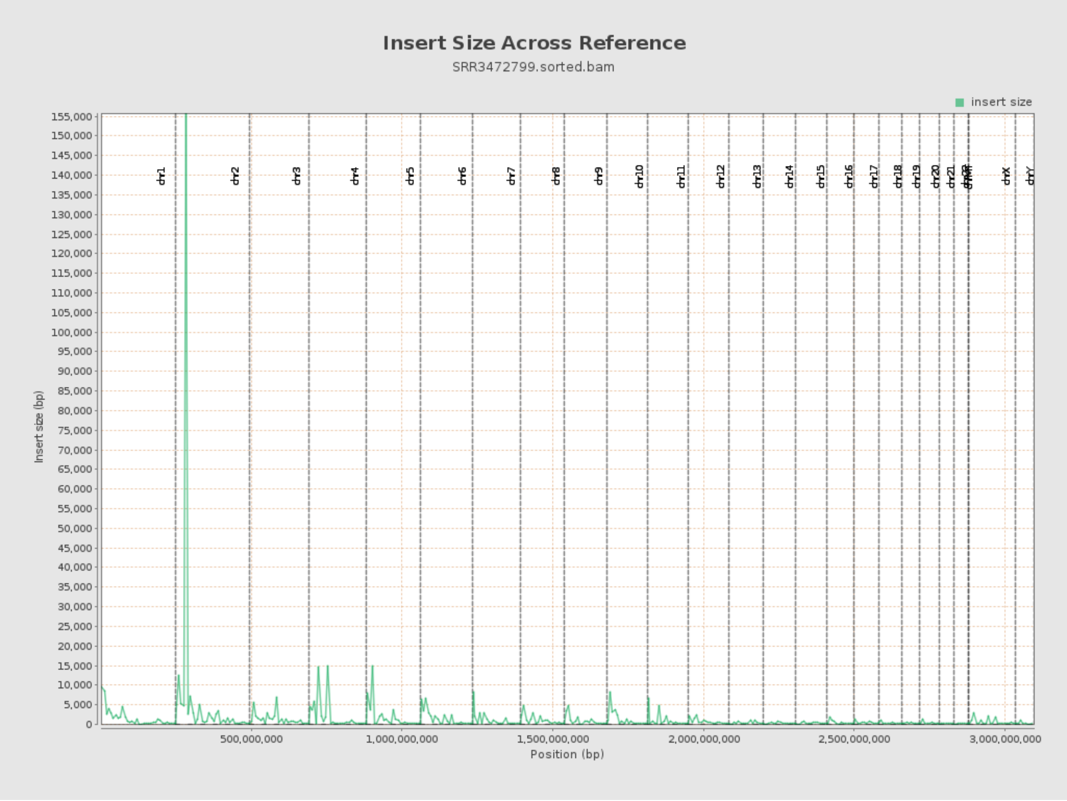
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram