Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 23:44:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472798.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_SRR3472798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472798_1.fastq.gz SRR3472798_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 23:44:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	132,786,076
Mapped reads	132,301,584 / 99.64%
Unmapped reads	484,492 / 0.36%
Mapped paired reads	132,301,584 / 99.64%
Mapped reads, first in pair	66,304,020 / 49.93%
Mapped reads, second in pair	65,997,564 / 49.7%
Mapped reads, both in pair	131,952,810 / 99.37%
Mapped reads, singletons	348,774 / 0.26%
Secondary alignments	0
Supplementary alignments	90,094 / 0.07%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	74,187,379 / 55.87%
Duplication rate	51.56%
Clipped reads	6,628,165 / 4.99%

2.2. ACGT Content

Number/percentage of A's	3,685,284,112 / 28.12%
Number/percentage of C's	2,863,578,097 / 21.85%
Number/percentage of T's	3,744,346,199 / 28.57%
Number/percentage of G's	2,811,243,979 / 21.45%
Number/percentage of N's	1,315,116 / 0.01%

GC Percentage	43.3%

2.3. Coverage

Mean	4.234
Standard Deviation	30.2779

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	11,672.7
Standard Deviation	1,073,804.49
P25/Median/P75	170 / 226 / 297

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	50,111,099
Insertions	561,787
Mapped reads with at least one insertion	0.42%
Deletions	666,812
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.97%

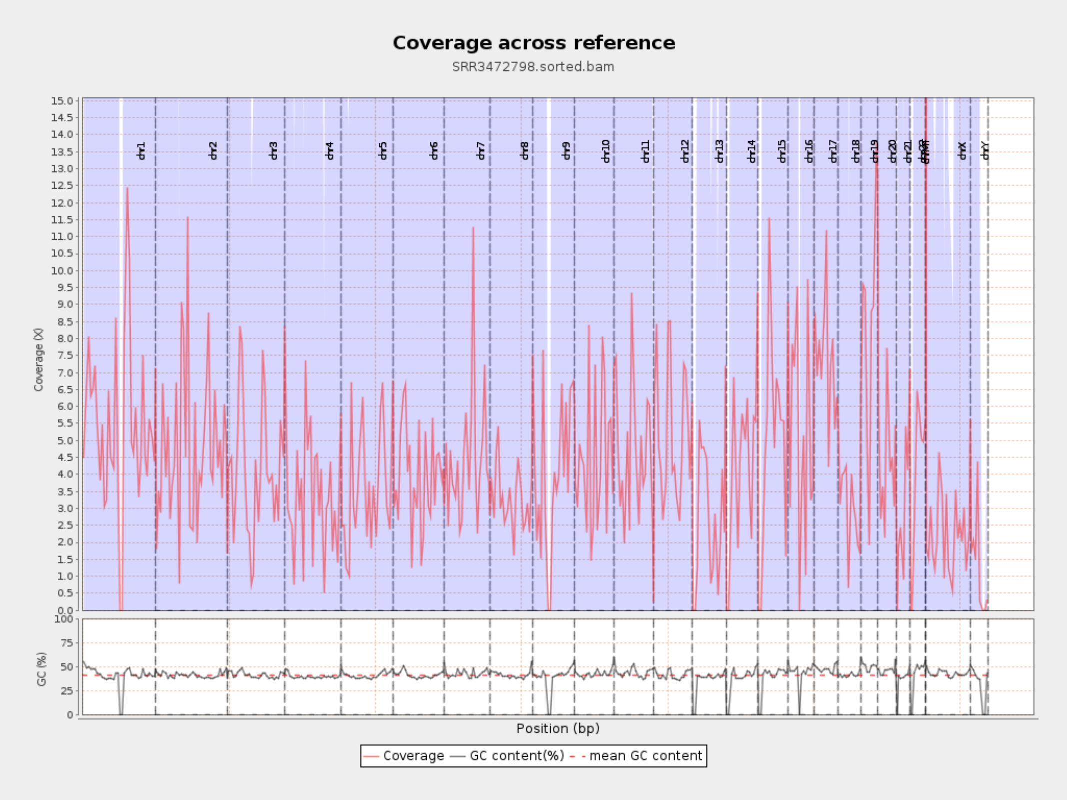
2.7. Chromosome stats

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

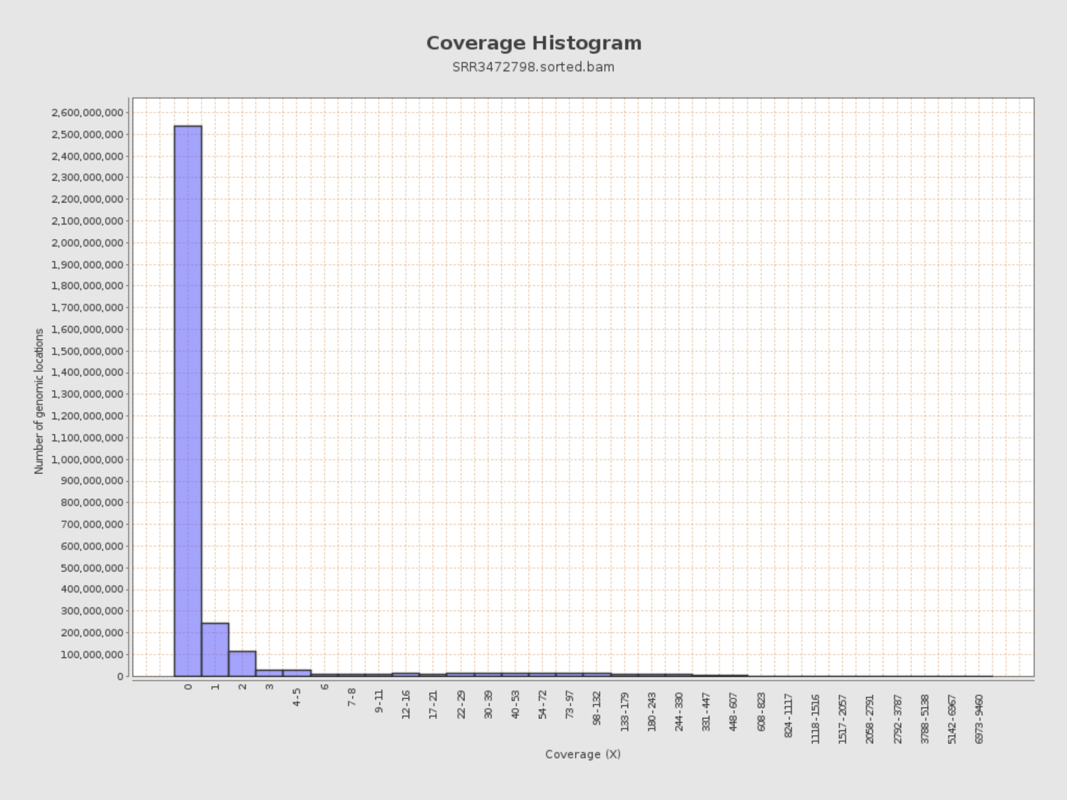
		bases	coverage	deviation
chr1	249250621	1354088889	5.4326	36.4102
chr2	243199373	1187717040	4.8837	36.2776
chr3	198022430	810329022	4.0921	28.5719
chr4	191154276	640822317	3.3524	26.9649
chr5	180915260	666792249	3.6857	27.675
chr6	171115067	673447785	3.9356	28.3337
chr7	159138663	711038651	4.468	32.3079
chr8	146364022	481298163	3.2884	25.8969
chr9	141213431	550242509	3.8965	29.2488
chr10	135534747	610239320	4.5025	32.5107
chr11	135006516	638358033	4.7283	29.3782
chr12	133851895	708243378	5.2912	32.1833
chr13	115169878	302852543	2.6296	23.7261
chr14	107349540	435678193	4.0585	29.9259
chr15	102531392	492361706	4.8021	31.6262
chr16	90354753	463219253	5.1267	33.4961
chr17	81195210	604280405	7.4423	36.3636
chr18	78077248	243917215	3.124	25.688
chr19	59128983	488855134	8.2676	36.701
chr20	63025520	266268280	4.2248	27.3566
chr21	48129895	149228669	3.1005	28.2852
chr22	51304566	201820835	3.9338	26.4682
chrMT	16571	6073415	366.5087	1,061.5686
chrX	155270560	345119944	2.2227	18.4601

chrY	59373566	75019808	1.2635	20.1294

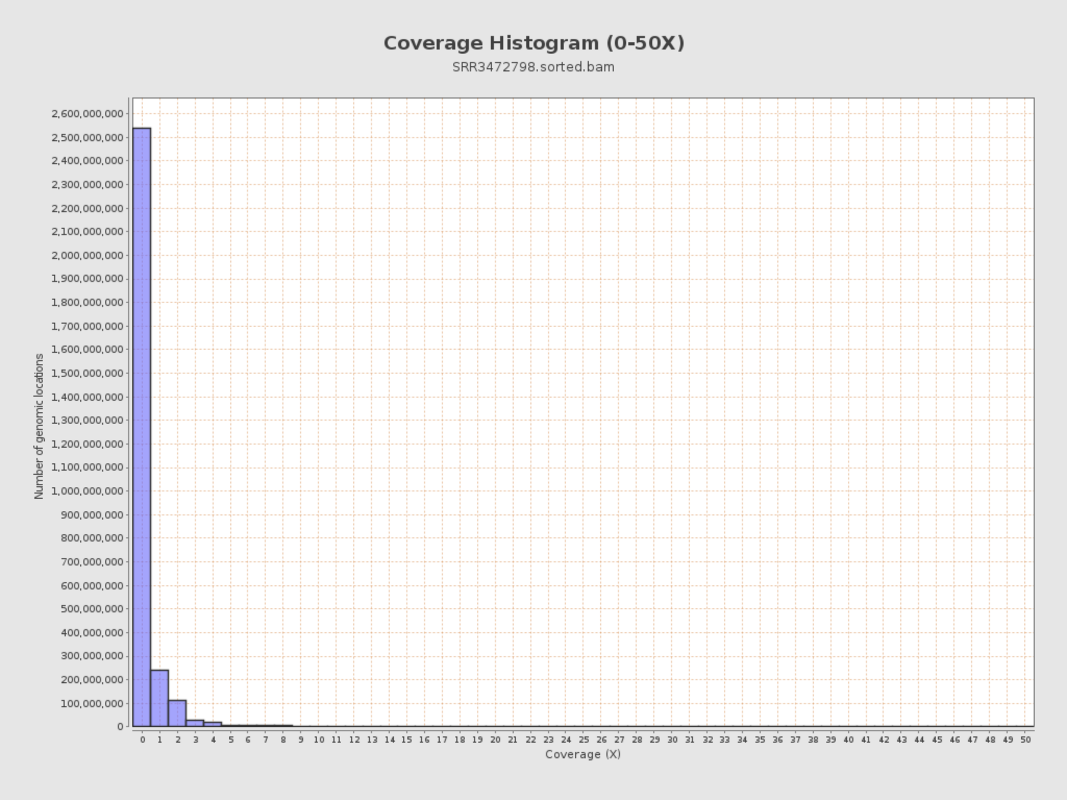
3. Results : Coverage across reference



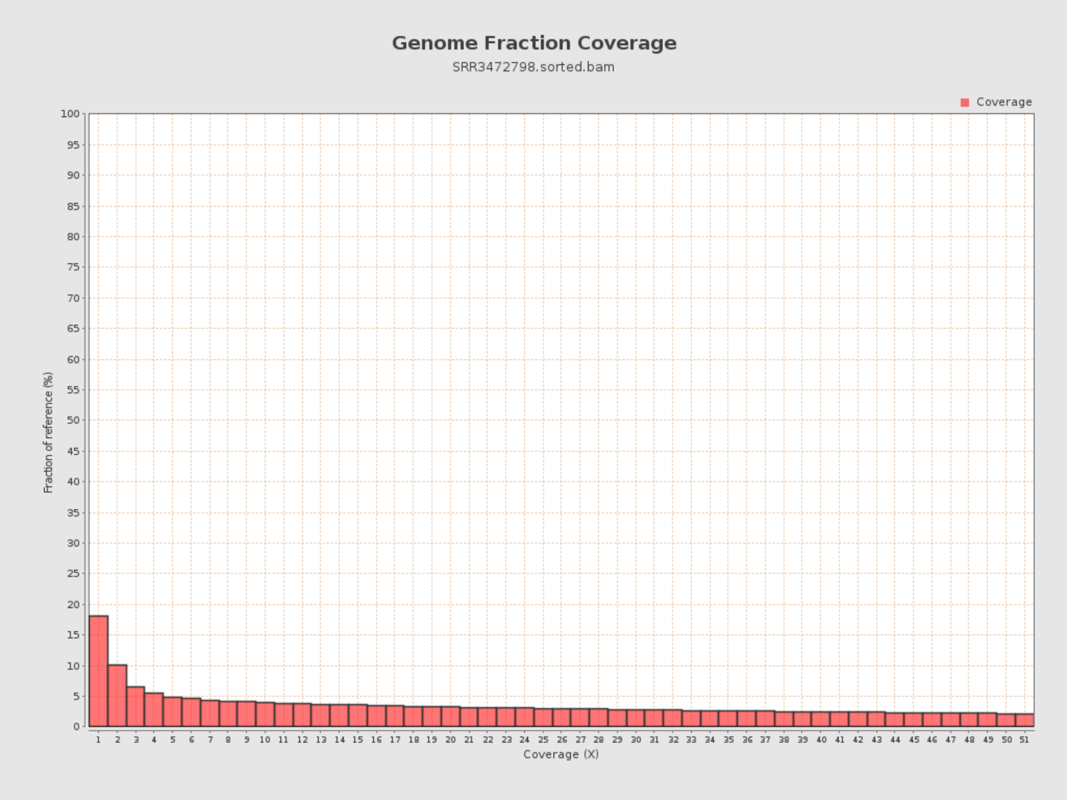
4. Results : Coverage Histogram



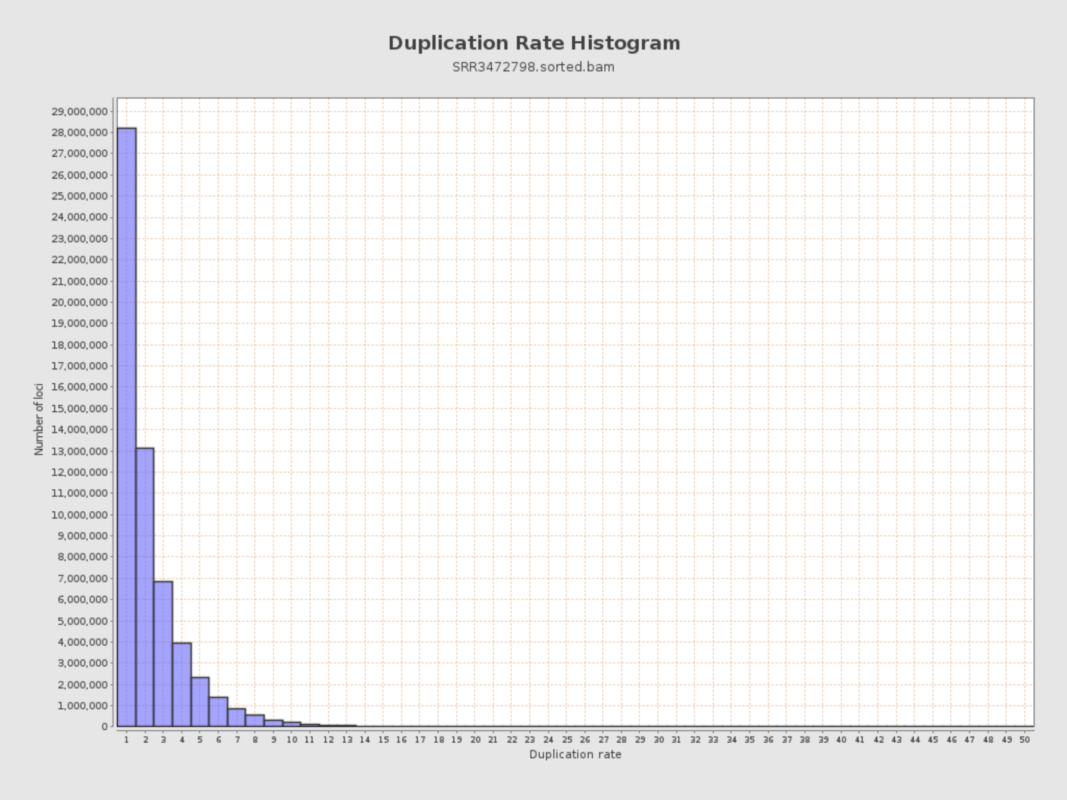
5. Results : Coverage Histogram (0-50X)



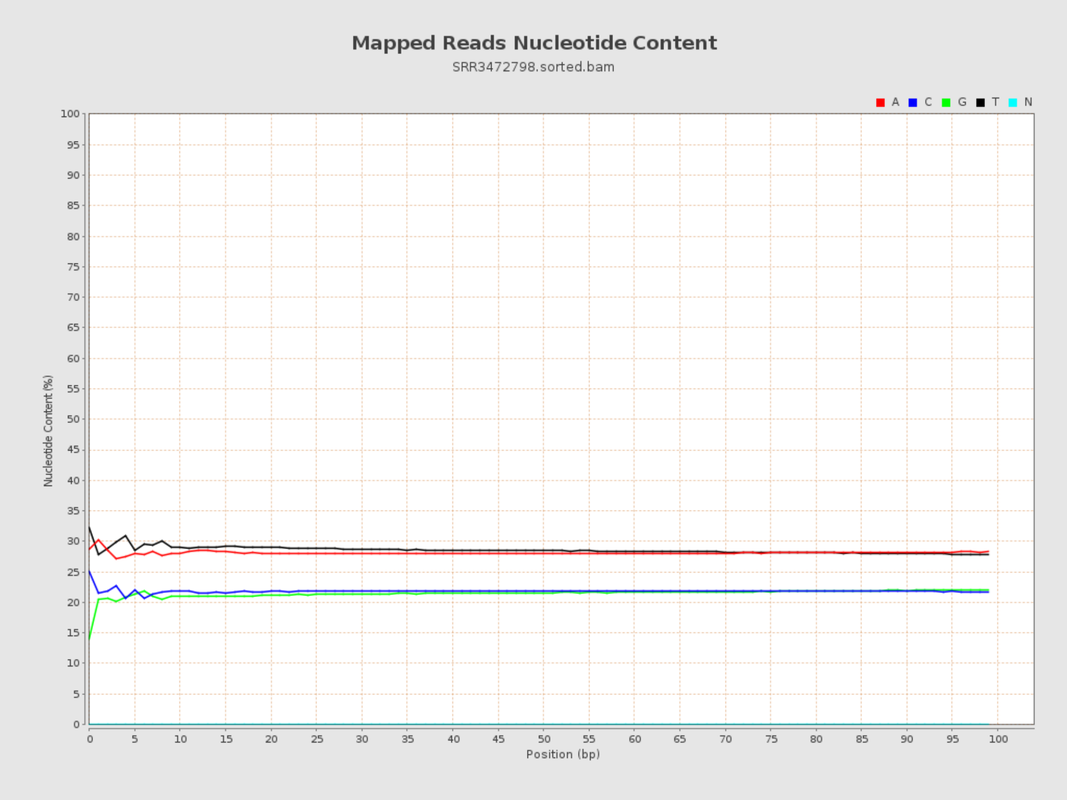
6. Results : Genome Fraction Coverage



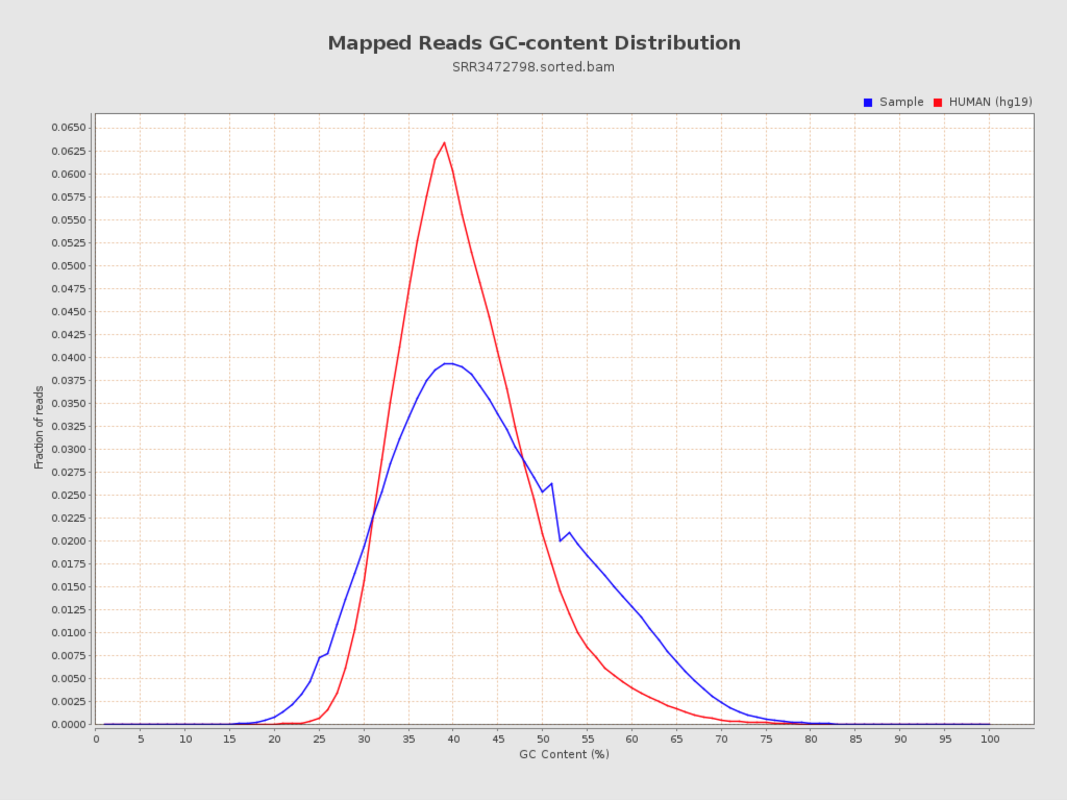
7. Results : Duplication Rate Histogram



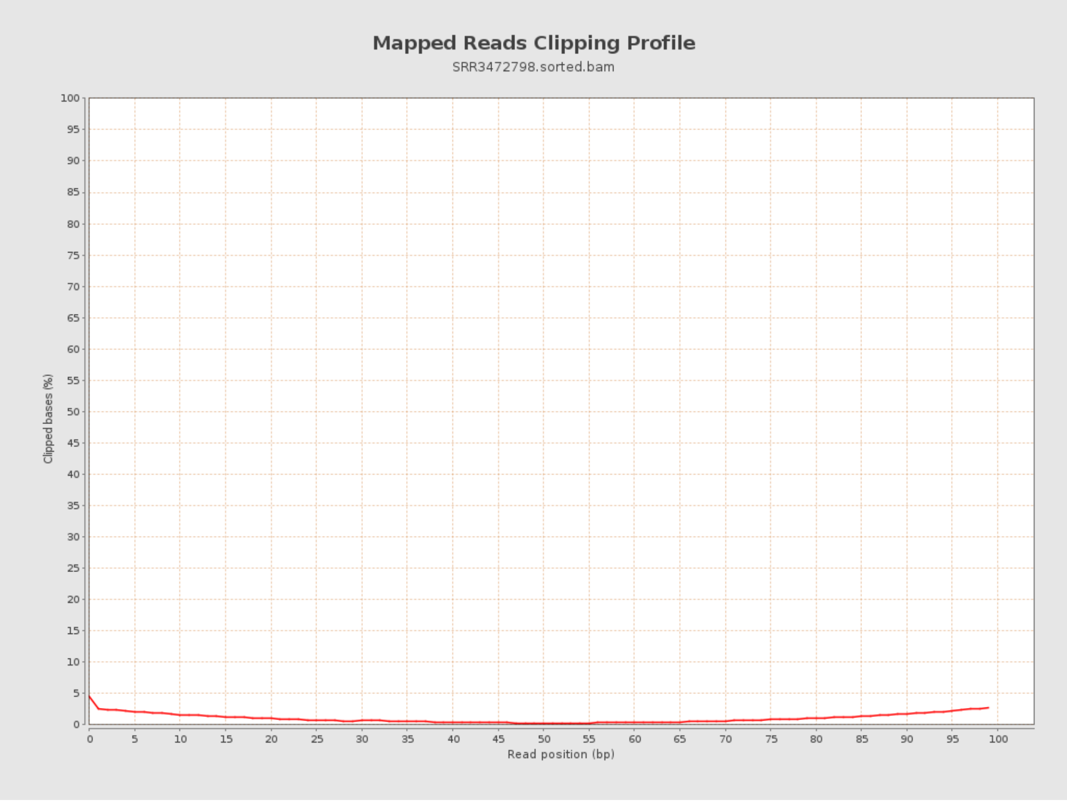
8. Results : Mapped Reads Nucleotide Content



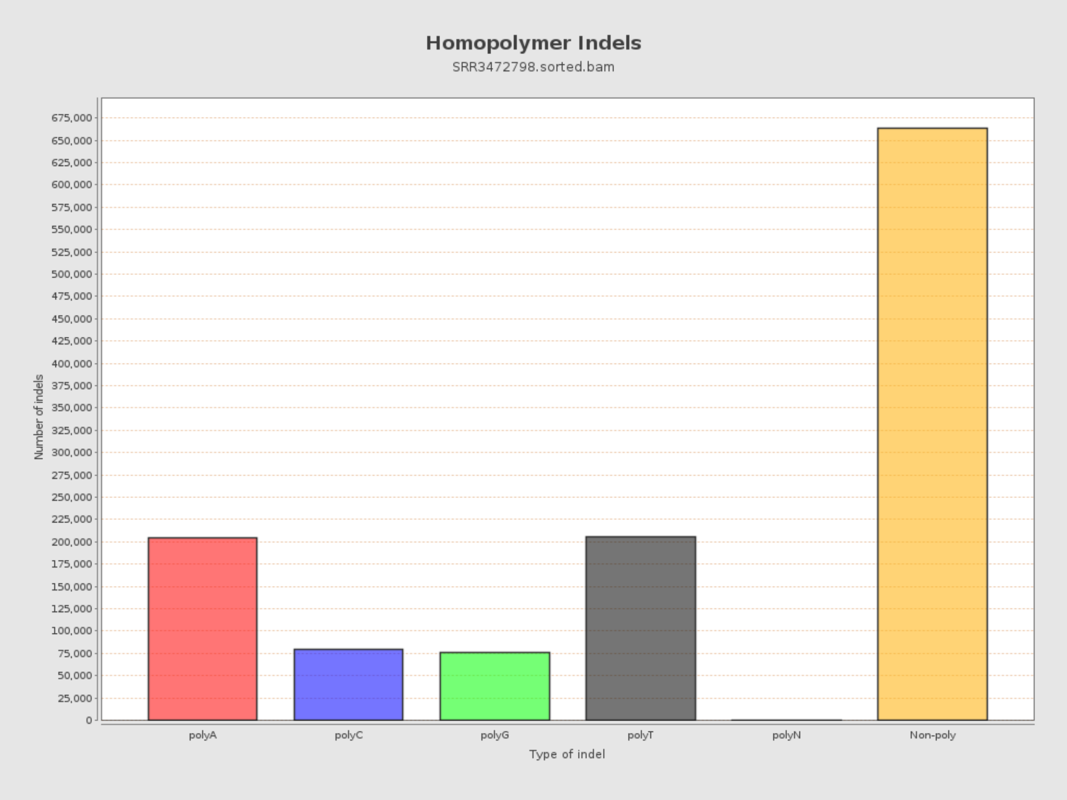
9. Results : Mapped Reads GC-content Distribution



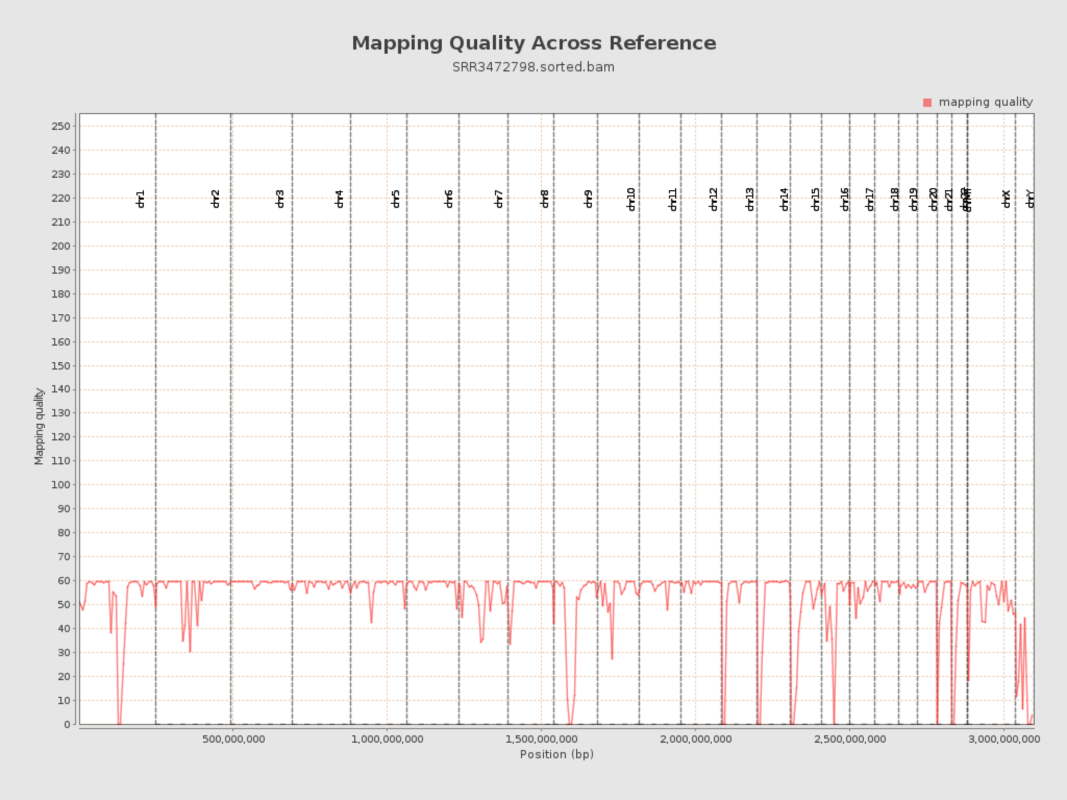
10. Results : Mapped Reads Clipping Profile



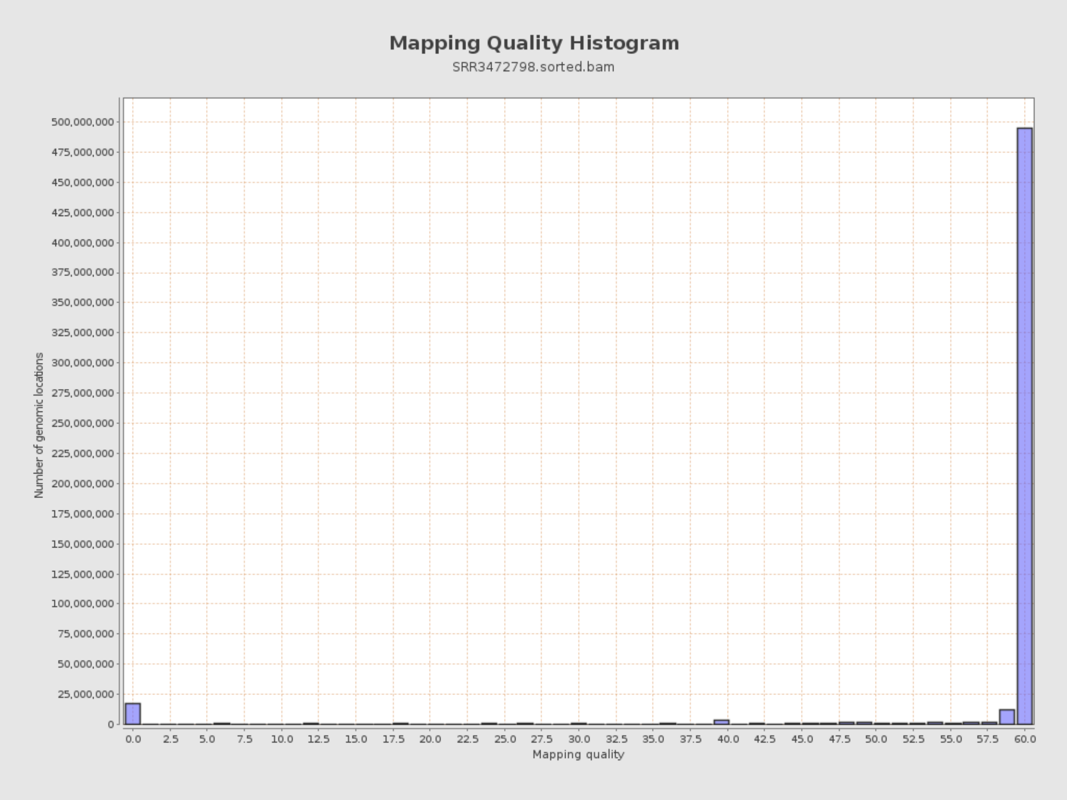
11. Results : Homopolymer Indels



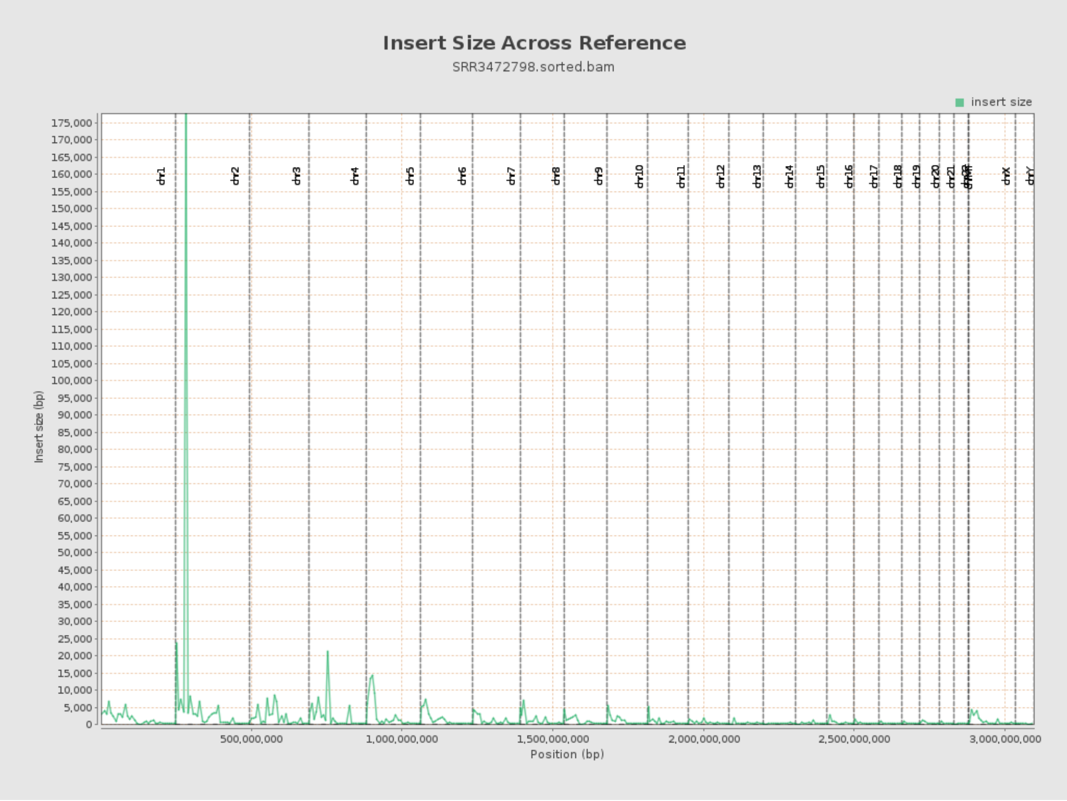
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram