Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 07:12:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472755.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_SRR3472755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472755_1.fastq.gz SRR3472755_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 07:12:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,933,142
Mapped reads	3,674,719 / 93.43%
Unmapped reads	258,423 / 6.57%
Mapped paired reads	3,674,719 / 93.43%
Mapped reads, first in pair	1,928,409 / 49.03%
Mapped reads, second in pair	1,746,310 / 44.4%
Mapped reads, both in pair	3,468,000 / 88.17%
Mapped reads, singletons	206,719 / 5.26%
Secondary alignments	0
Supplementary alignments	126,840 / 3.22%
Read min/max/mean length	30 / 100 / 101.21
Duplicated reads (estimated)	1,899,388 / 48.29%
Duplication rate	34.16%
Clipped reads	1,196,789 / 30.43%

2.2. ACGT Content

Number/percentage of A's	85,599,749 / 25.95%
Number/percentage of C's	63,131,174 / 19.14%
Number/percentage of T's	117,932,502 / 35.75%
Number/percentage of G's	63,200,992 / 19.16%
Number/percentage of N's	46,602 / 0.01%

GC Percentage	38.29%

2.3. Coverage

Mean	0.1066
Standard Deviation	11.0661

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Insert size

Mean	1,302,748.75
Standard Deviation	11,298,155.14
P25/Median/P75	208 / 297 / 408

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	3,327,378
Insertions	61,068
Mapped reads with at least one insertion	1.63%
Deletions	30,248
Mapped reads with at least one deletion	0.81%
Homopolymer indels	39.59%

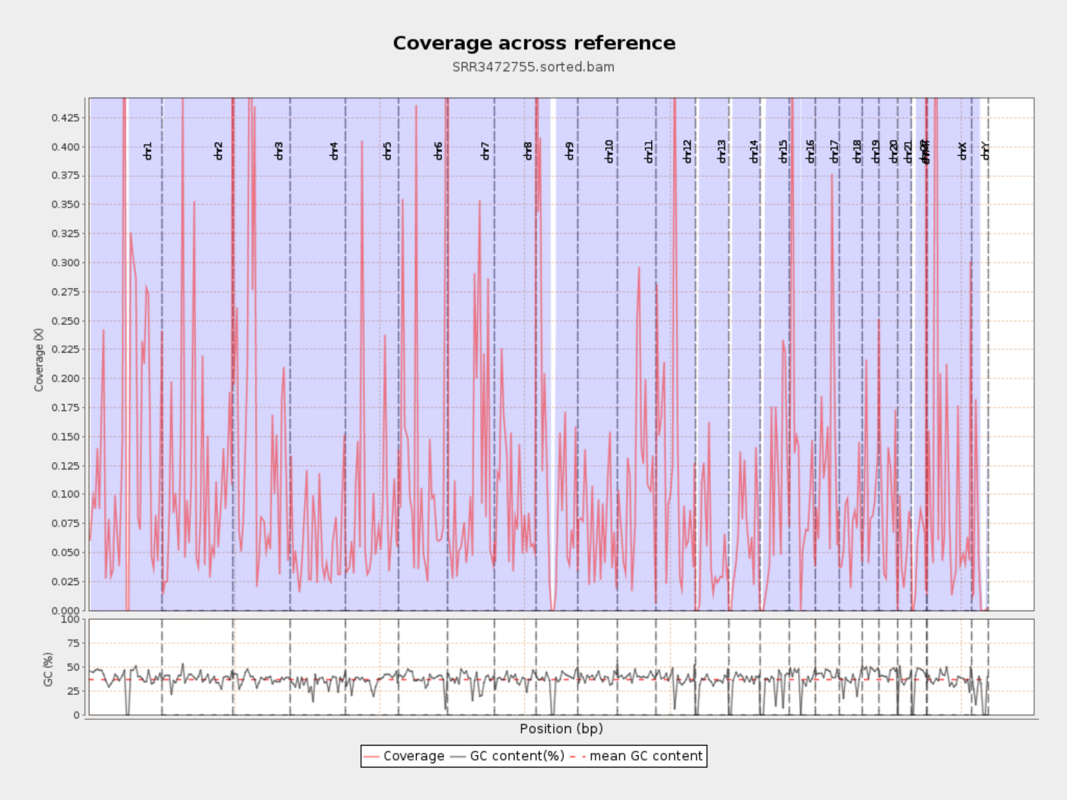
2.7. Chromosome stats

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

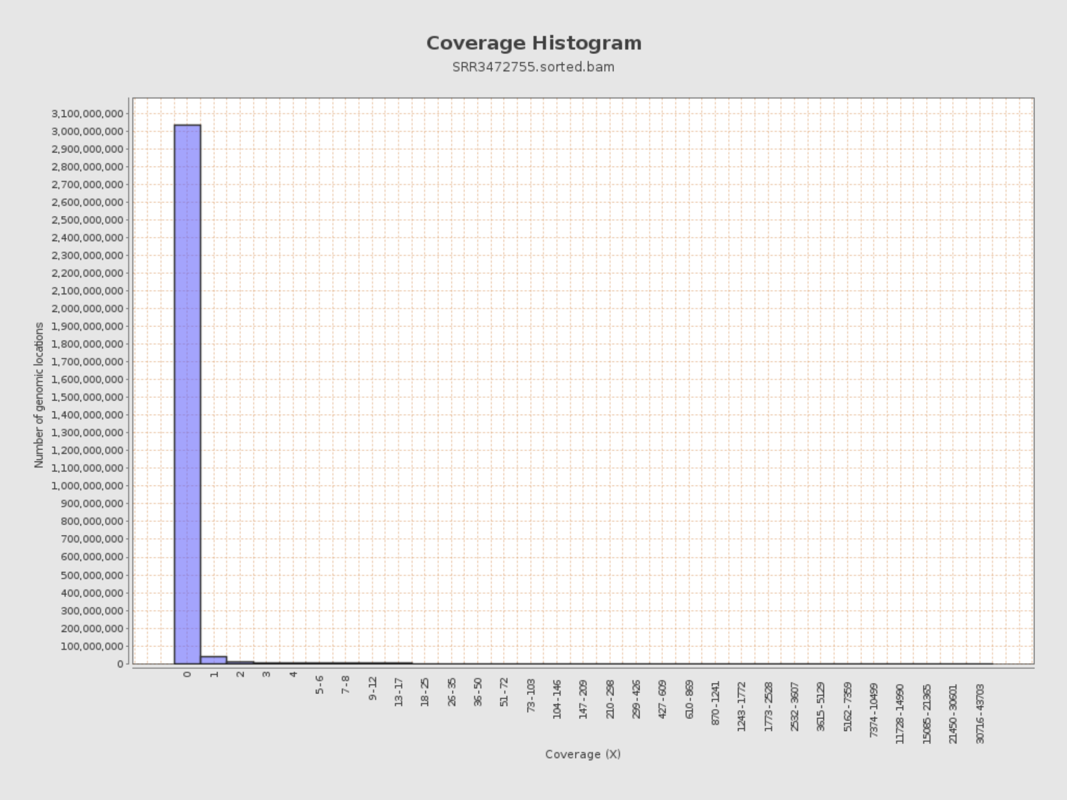
		bases	coverage	deviation
chr1	249250621	35149836	0.141	3.5955
chr2	243199373	26356902	0.1084	6.2662
chr3	198022430	32667350	0.165	3.8021
chr4	191154276	11151387	0.0583	5.2968
chr5	180915260	15940443	0.0881	5.2439
chr6	171115067	24507076	0.1432	21.0755
chr7	159138663	17814217	0.1119	15.7269
chr8	146364022	13551072	0.0926	3.4862
chr9	141213431	17193159	0.1218	3.0878
chr10	135534747	10118028	0.0747	3.7852
chr11	135006516	15517743	0.1149	4.2852
chr12	133851895	17082542	0.1276	32.3329
chr13	115169878	5629383	0.0489	1.4853
chr14	107349540	7086934	0.066	1.9375
chr15	102531392	9608006	0.0937	22.1903
chr16	90354753	11866456	0.1313	6.6312
chr17	81195210	10981447	0.1352	2.8333
chr18	78077248	5693214	0.0729	5.5692
chr19	59128983	6391374	0.1081	2.2013
chr20	63025520	6075840	0.0964	3.969
chr21	48129895	2589820	0.0538	4.8625
chr22	51304566	2383828	0.0465	0.9096
chrMT	16571	5437430	328.1293	1,000.2406
chrX	155270560	17289639	0.1114	3.6931

chrY	59373566	1902604	0.032	12.4093

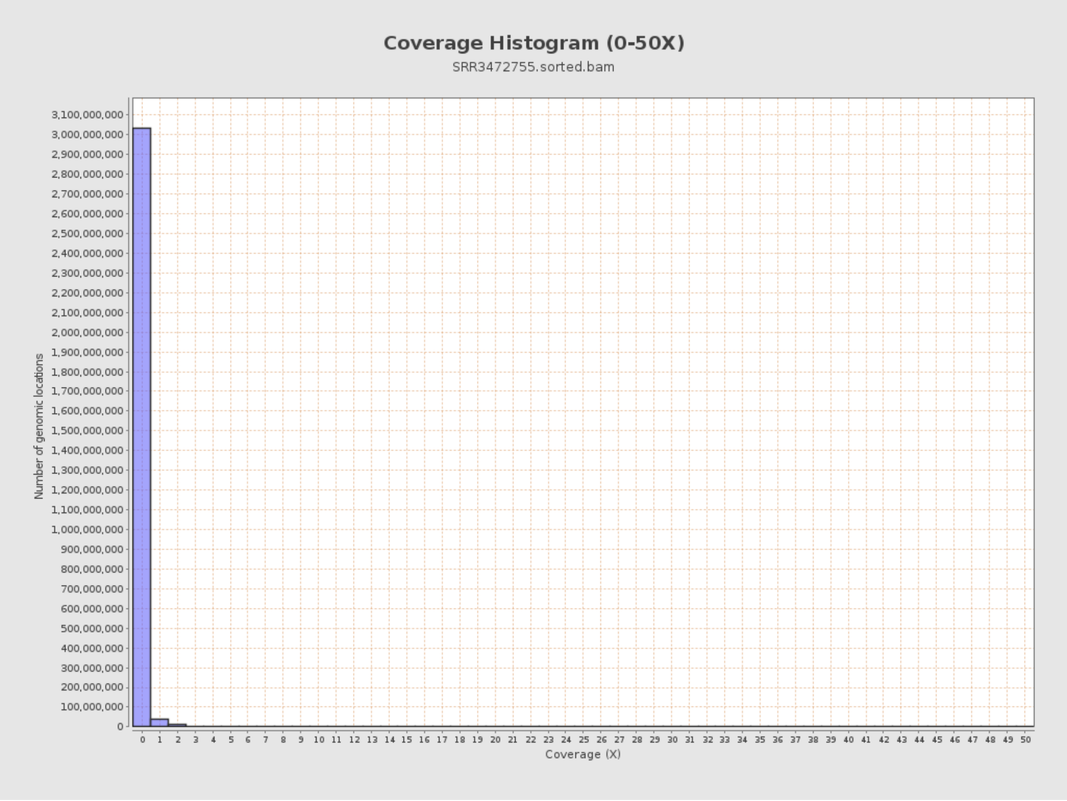
3. Results : Coverage across reference



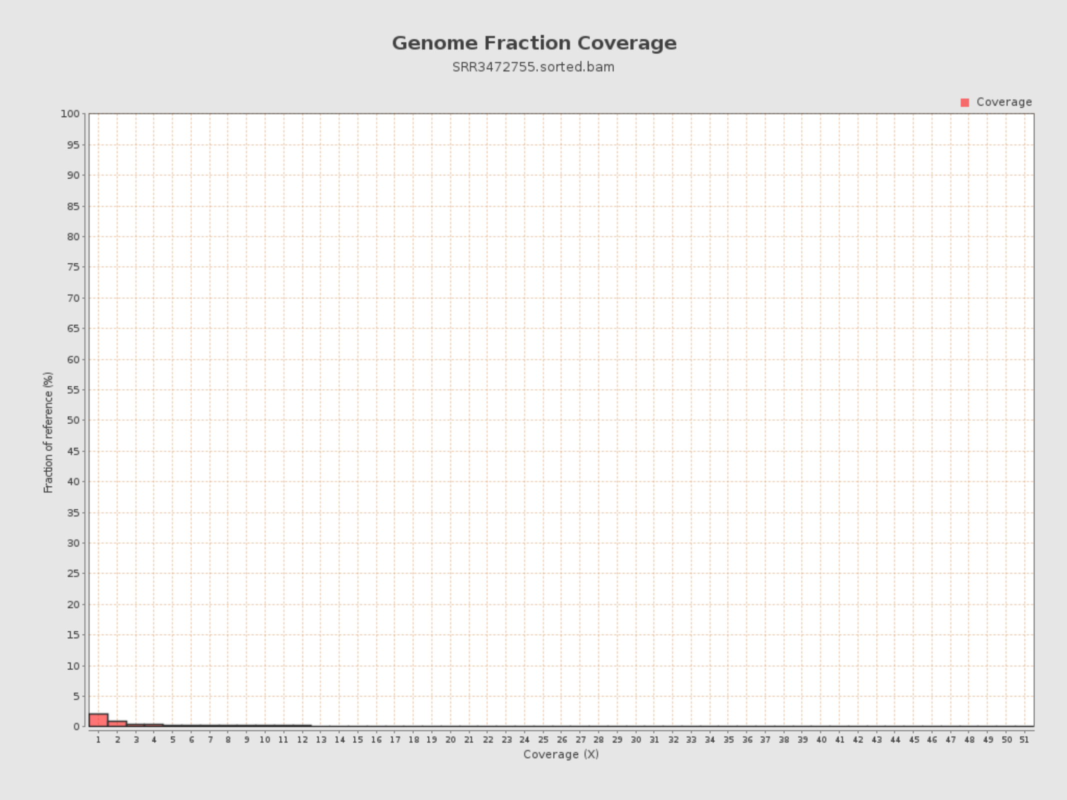
4. Results : Coverage Histogram



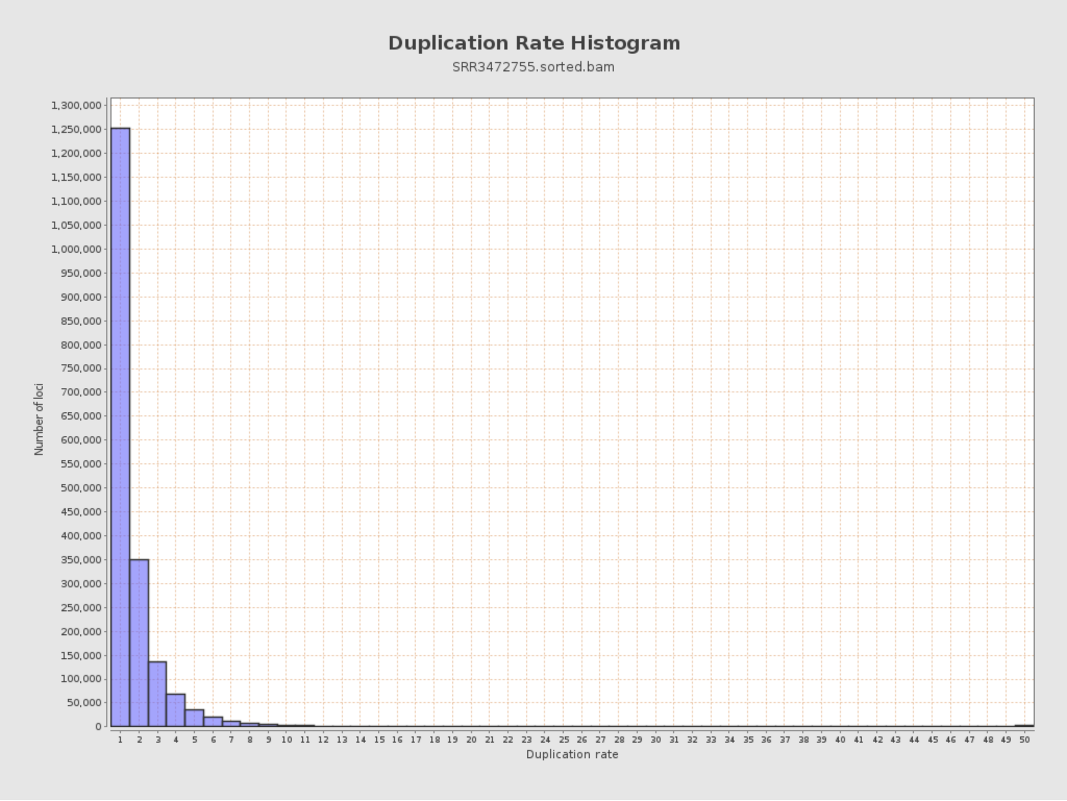
5. Results : Coverage Histogram (0-50X)



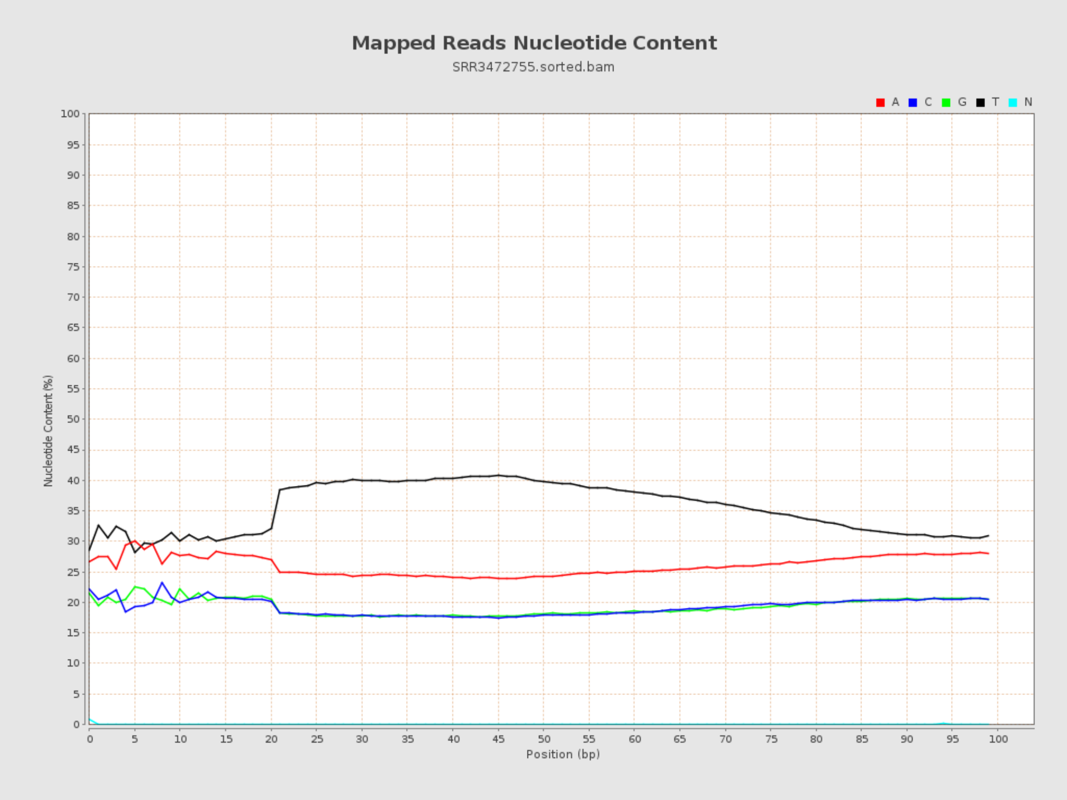
6. Results : Genome Fraction Coverage



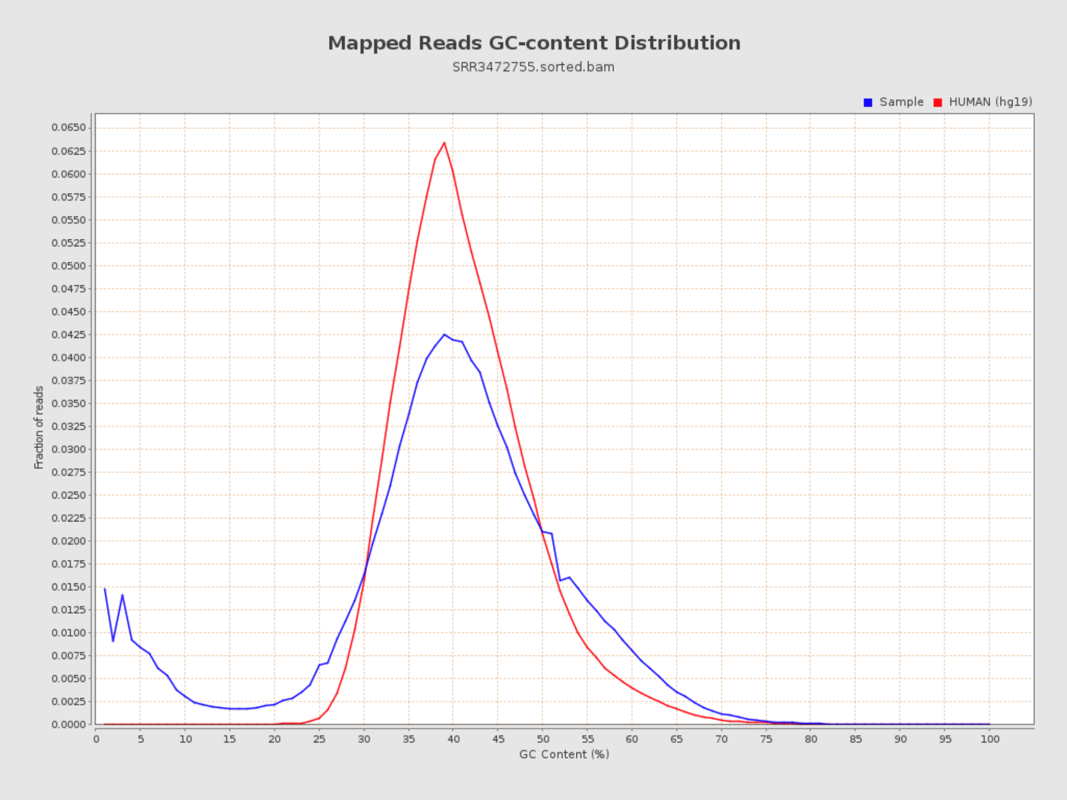
7. Results : Duplication Rate Histogram



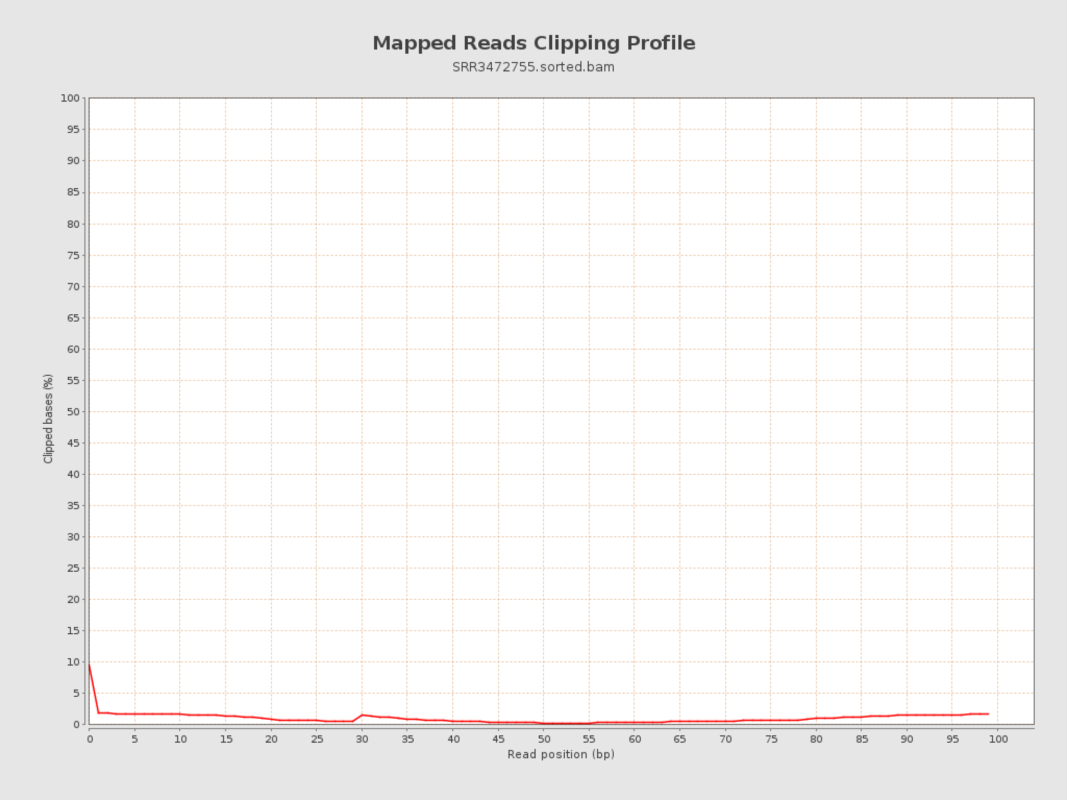
8. Results : Mapped Reads Nucleotide Content



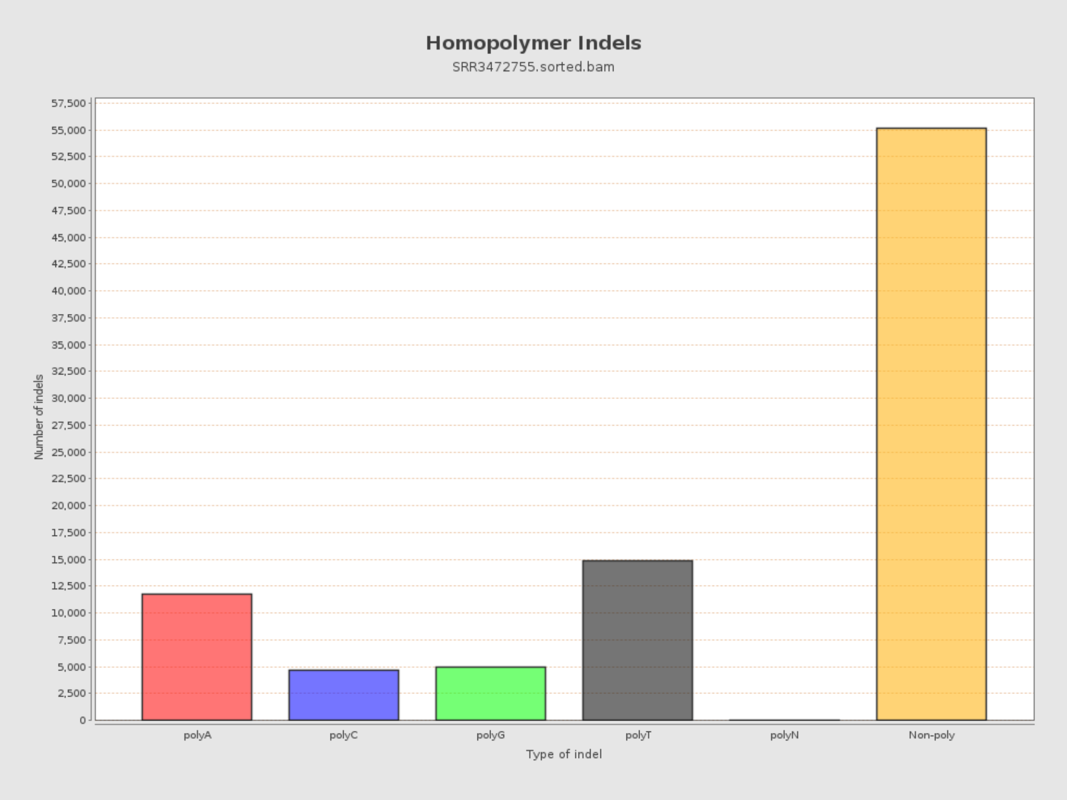
9. Results : Mapped Reads GC-content Distribution



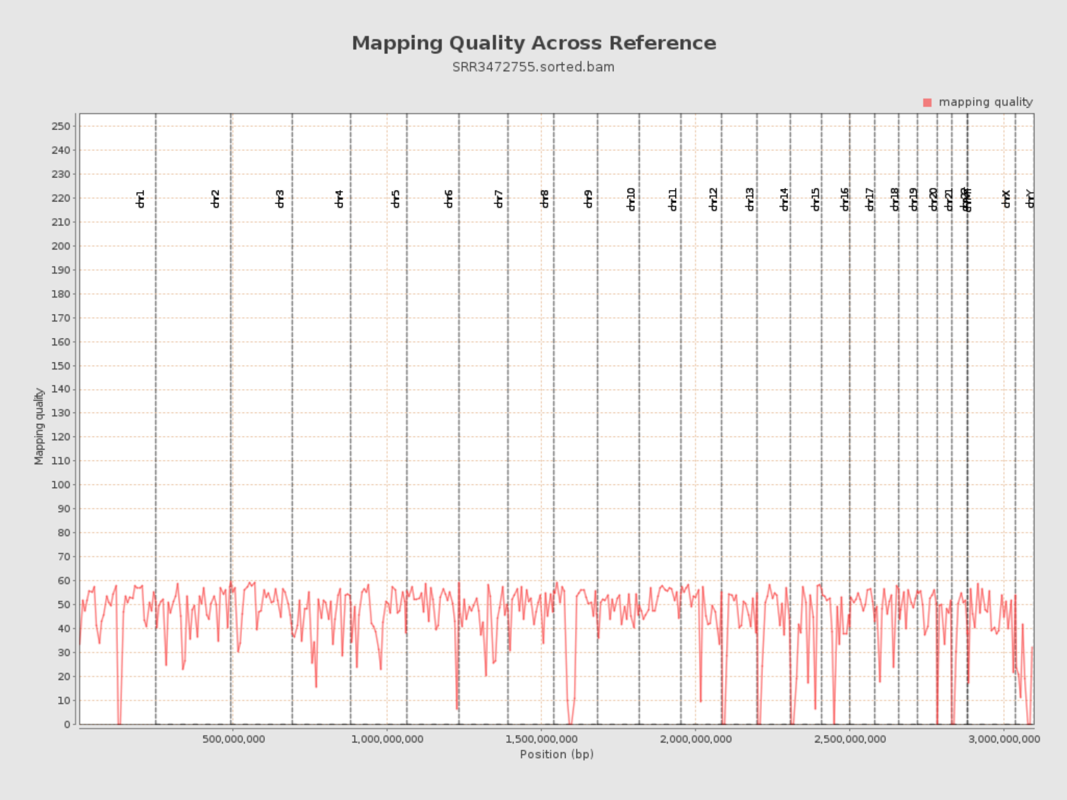
10. Results : Mapped Reads Clipping Profile



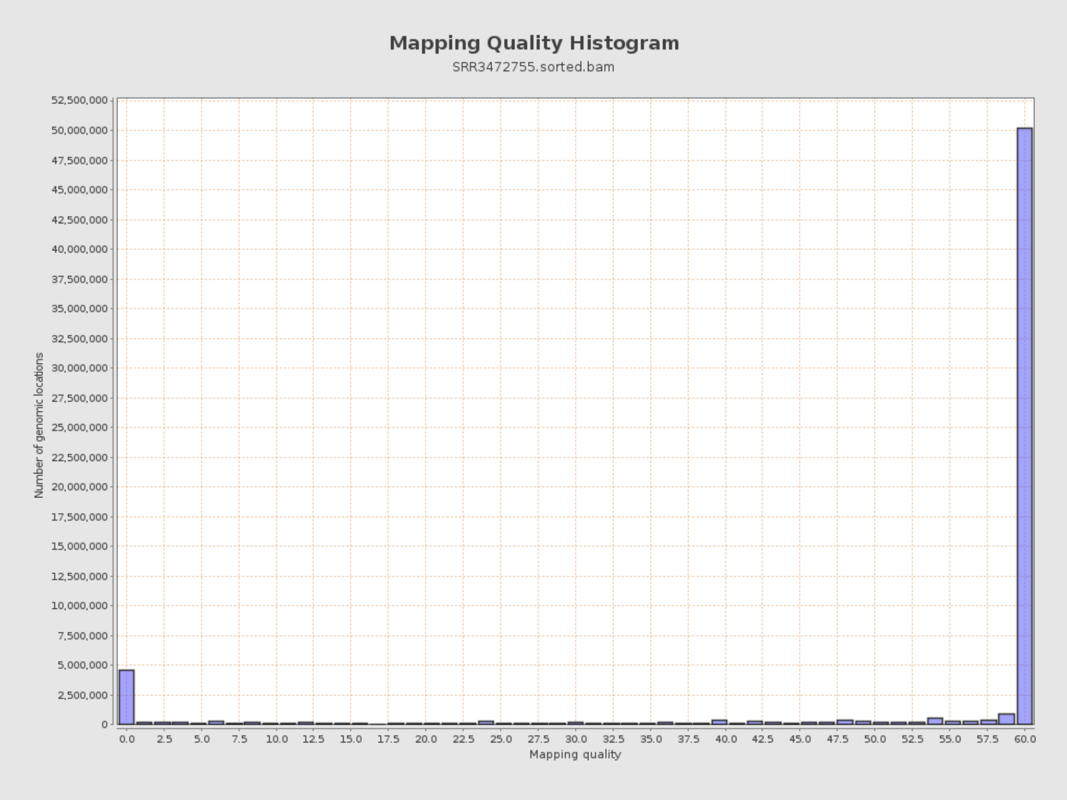
11. Results : Homopolymer Indels



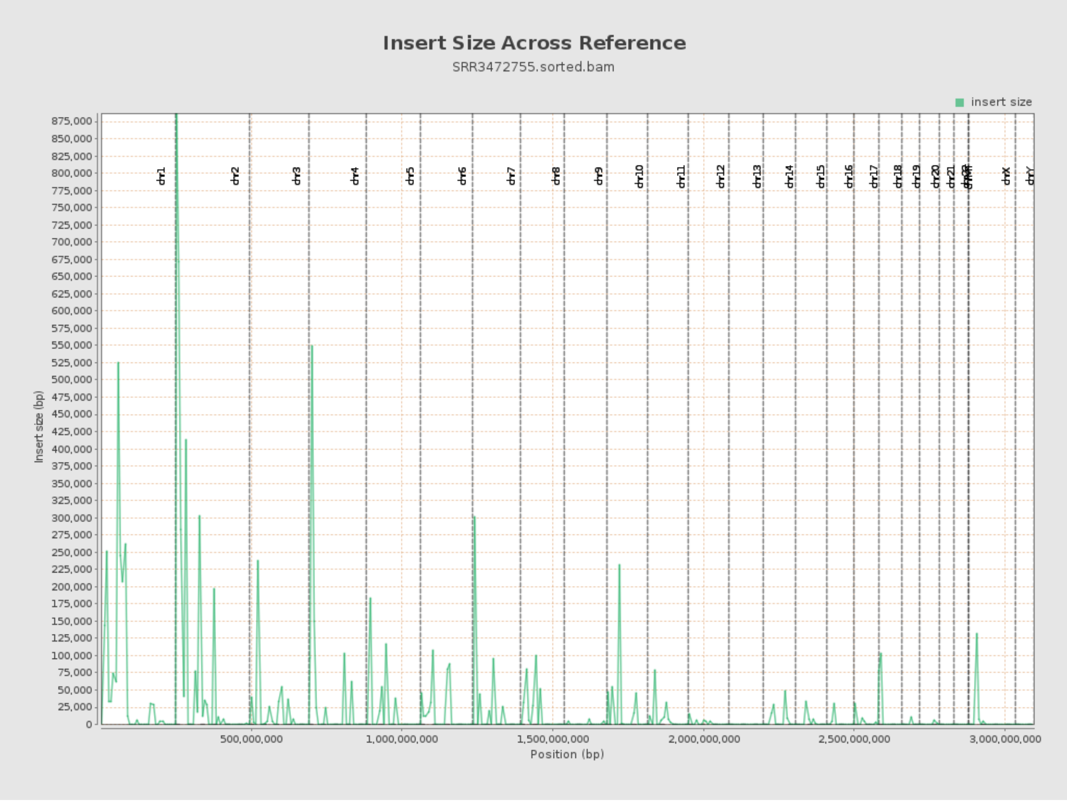
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram