Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 07:25:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472756.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_SRR3472756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472756_1.fastq.gz SRR3472756_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 07:25:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,847,526
Mapped reads	14,707,888 / 99.06%
Unmapped reads	139,638 / 0.94%
Mapped paired reads	14,707,888 / 99.06%
Mapped reads, first in pair	7,379,794 / 49.7%
Mapped reads, second in pair	7,328,094 / 49.36%
Mapped reads, both in pair	14,623,766 / 98.49%
Mapped reads, singletons	84,122 / 0.57%
Secondary alignments	0
Supplementary alignments	82,666 / 0.56%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	9,090,235 / 61.22%
Duplication rate	45.91%
Clipped reads	1,337,970 / 9.01%

2.2. ACGT Content

Number/percentage of A's	397,904,297 / 27.49%
Number/percentage of C's	327,718,223 / 22.64%
Number/percentage of T's	395,771,227 / 27.35%
Number/percentage of G's	325,645,981 / 22.5%
Number/percentage of N's	281,452 / 0.02%

GC Percentage	45.14%

2.3. Coverage

Mean	0.4676
Standard Deviation	16.0082

2.4. Mapping Quality

Mean Mapping Quality	55.01

2.5. Insert size

Mean	35,689.27
Standard Deviation	1,856,922.1
P25/Median/P75	162 / 227 / 312

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	8,610,639
Insertions	84,723
Mapped reads with at least one insertion	0.57%
Deletions	80,932
Mapped reads with at least one deletion	0.54%
Homopolymer indels	43.83%

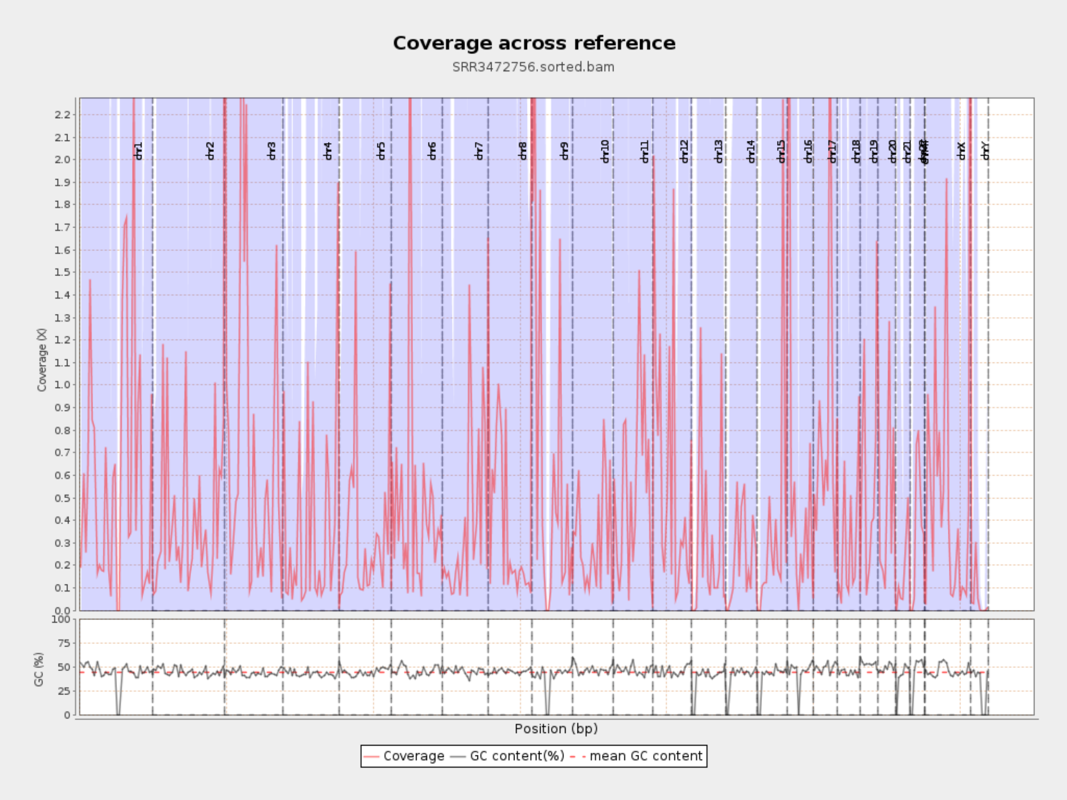
2.7. Chromosome stats

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

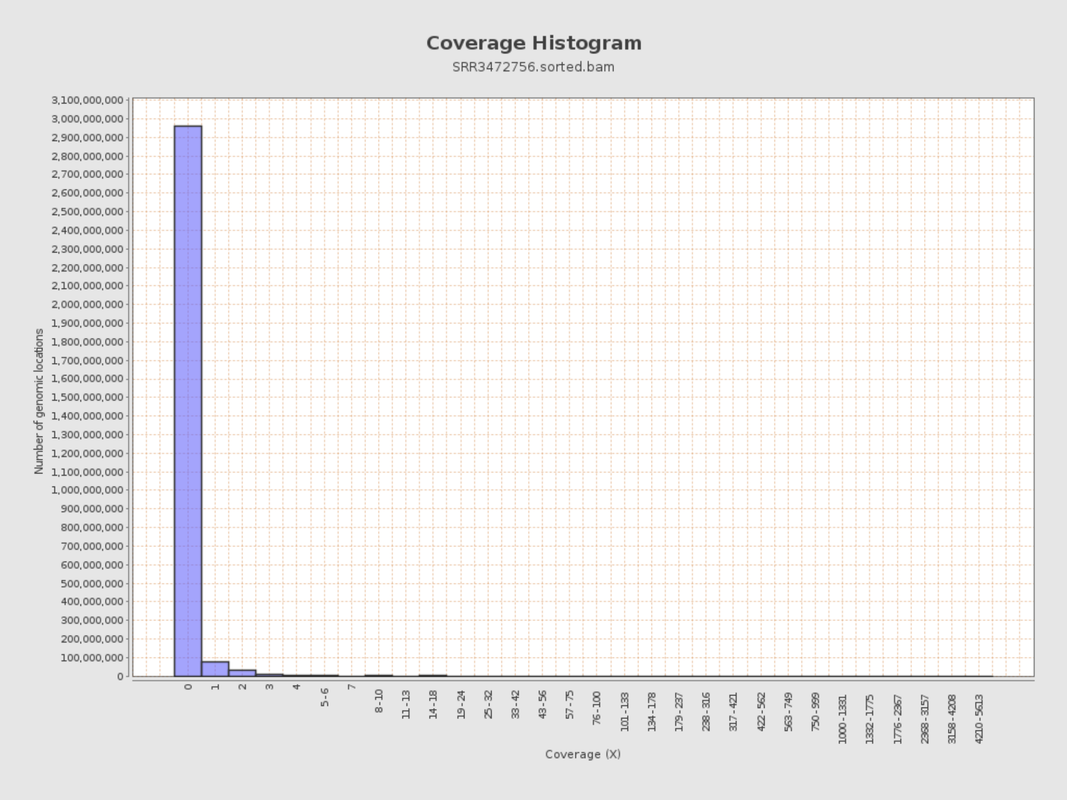
		bases	coverage	deviation
chr1	249250621	151294832	0.607	22.2223
chr2	243199373	96565579	0.3971	15.5096
chr3	198022430	159849853	0.8072	18.2931
chr4	191154276	69544486	0.3638	13.7901
chr5	180915260	64492513	0.3565	12.6485
chr6	171115067	81746388	0.4777	13.6619
chr7	159138663	61467726	0.3863	14.4773
chr8	146364022	50607428	0.3458	11.2452
chr9	141213431	95256785	0.6746	18.212
chr10	135534747	43270040	0.3193	12.7696
chr11	135006516	74564756	0.5523	20.8002
chr12	133851895	83635762	0.6248	19.4248
chr13	115169878	36660838	0.3183	13.2756
chr14	107349540	25222602	0.235	11.7733
chr15	102531392	38051703	0.3711	14.1614
chr16	90354753	52592365	0.5821	15.9338
chr17	81195210	63960385	0.7877	20.279
chr18	78077248	23984301	0.3072	11.4672
chr19	59128983	32902219	0.5564	13.5021
chr20	63025520	31117267	0.4937	17.3884
chr21	48129895	8789818	0.1826	7.9723
chr22	51304566	17928846	0.3495	14.1931
chrMT	16571	2591	0.1564	0.5022
chrX	155270560	80689060	0.5197	18.377

chrY	59373566	3316984	0.0559	2.6679

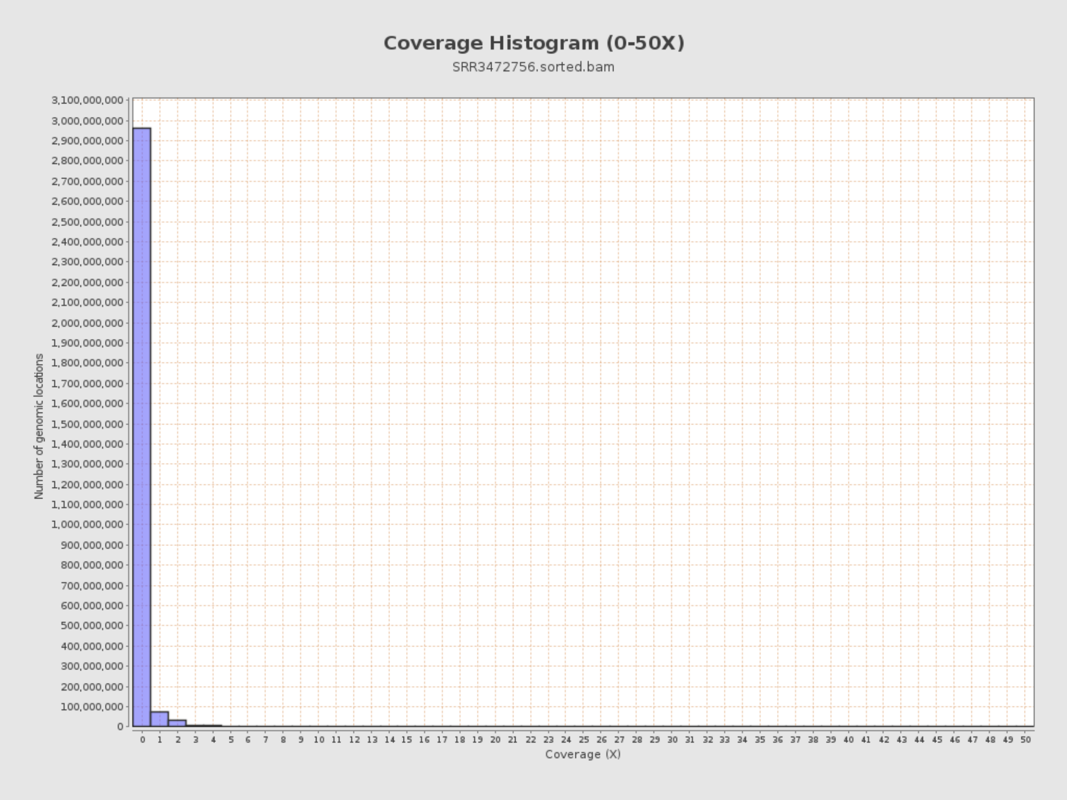
3. Results : Coverage across reference



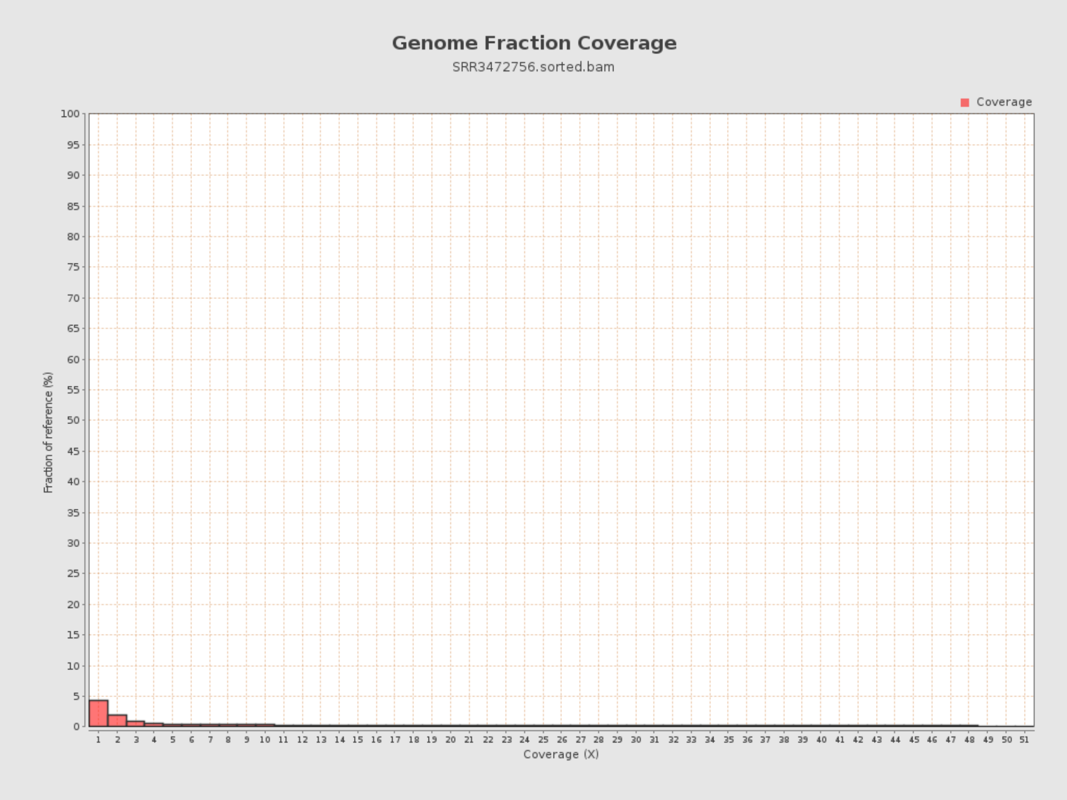
4. Results : Coverage Histogram



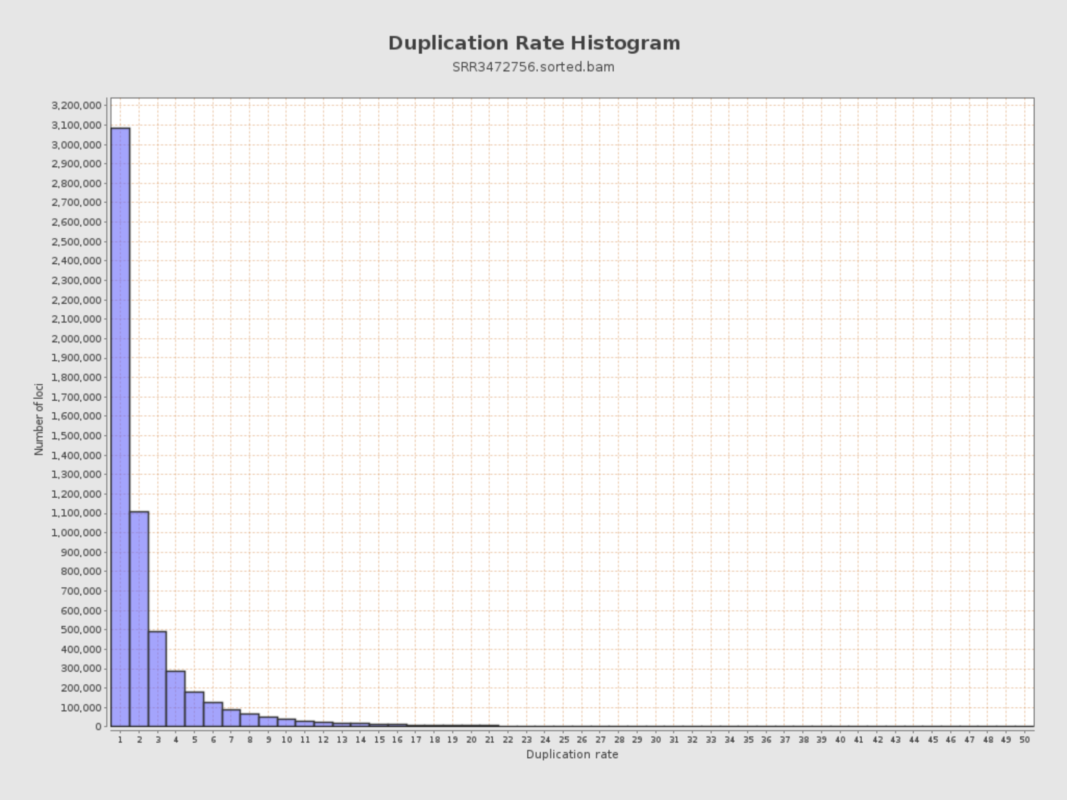
5. Results : Coverage Histogram (0-50X)



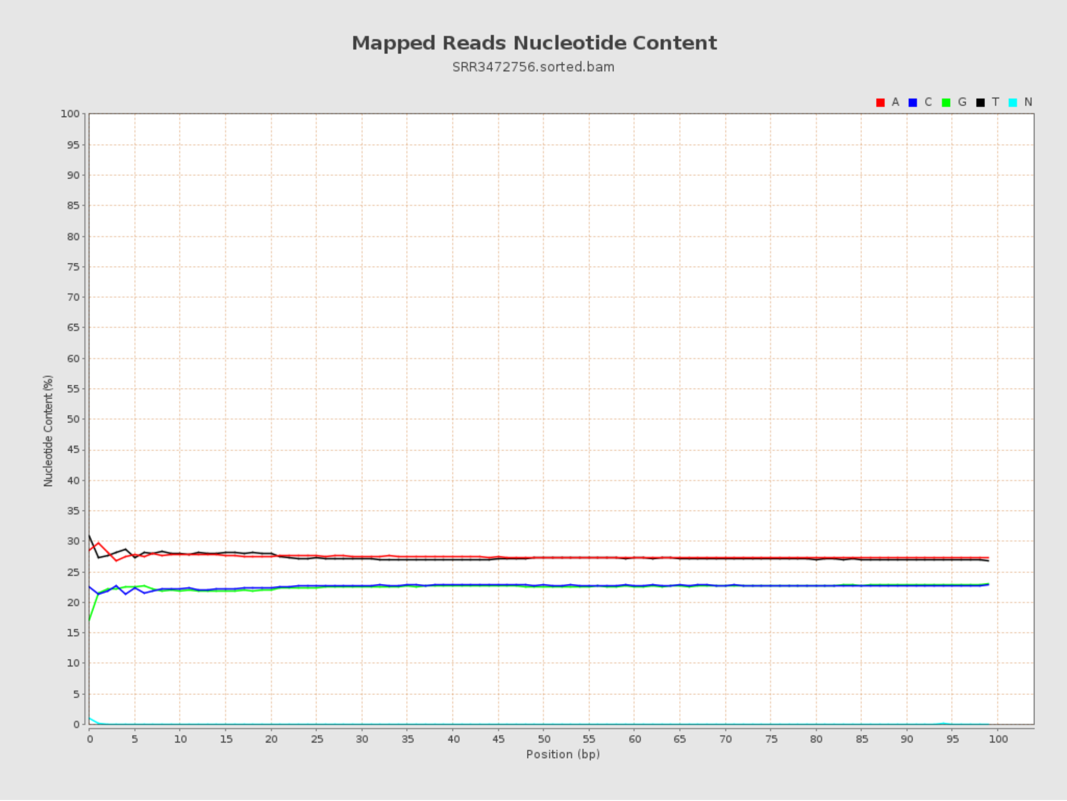
6. Results : Genome Fraction Coverage



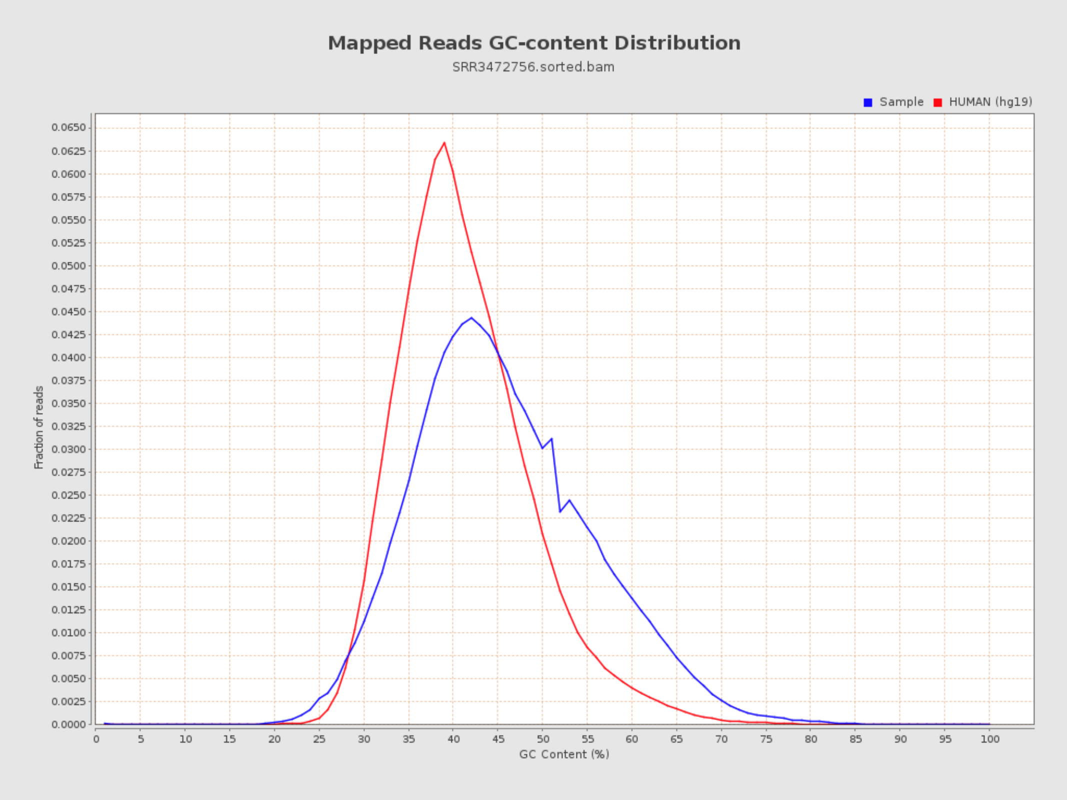
7. Results : Duplication Rate Histogram



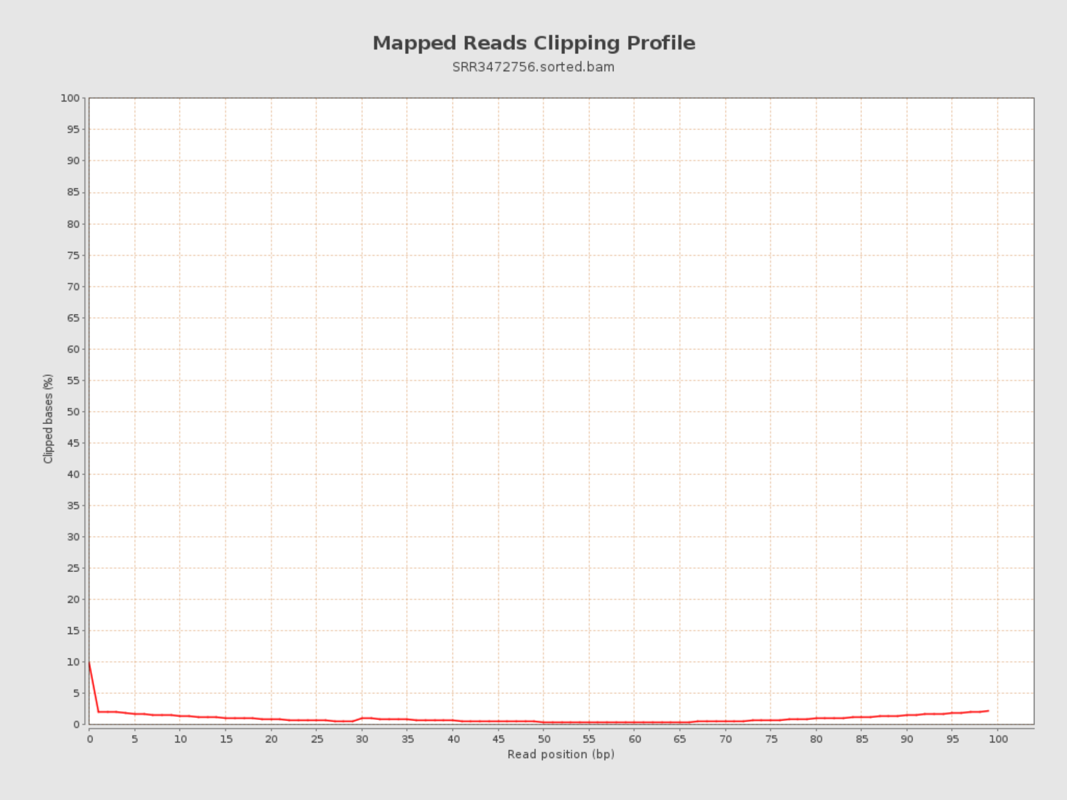
8. Results : Mapped Reads Nucleotide Content



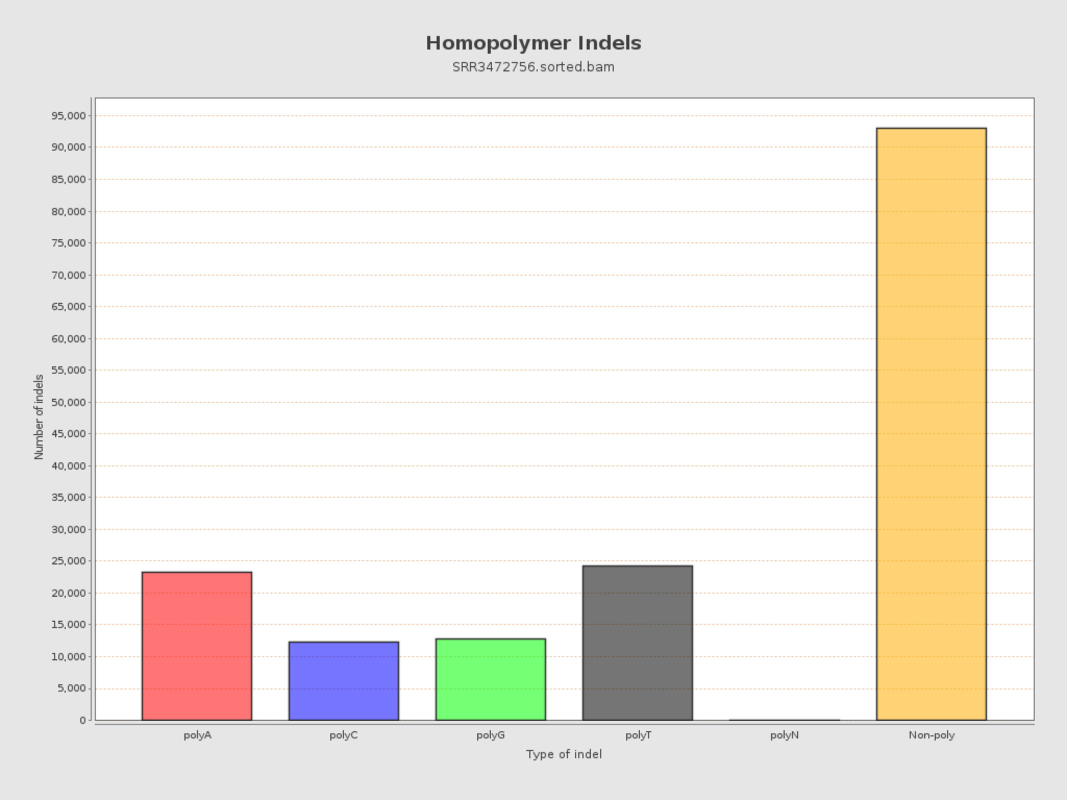
9. Results : Mapped Reads GC-content Distribution



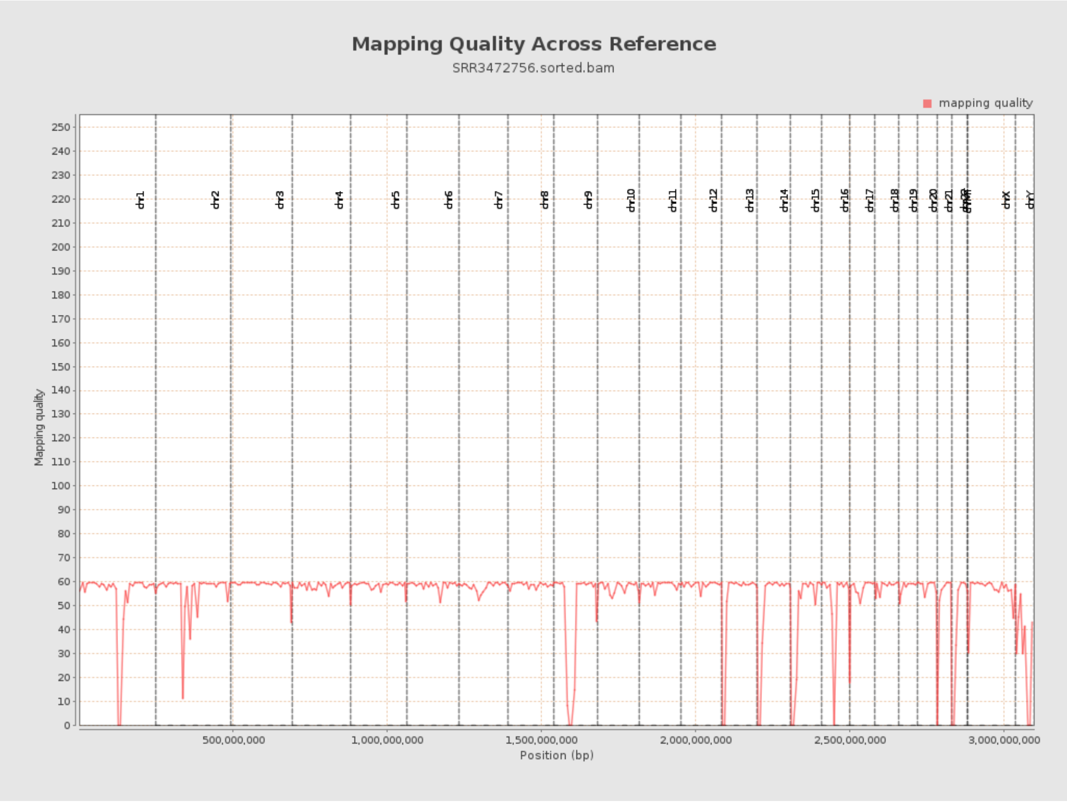
10. Results : Mapped Reads Clipping Profile



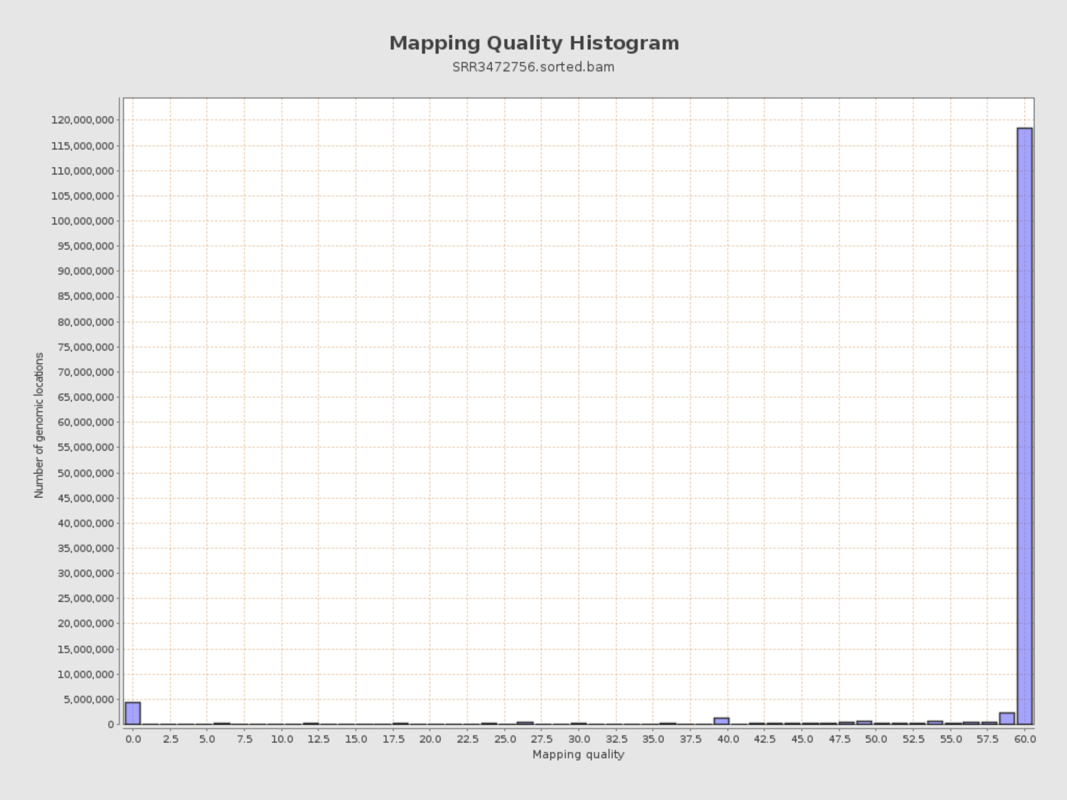
11. Results : Homopolymer Indels



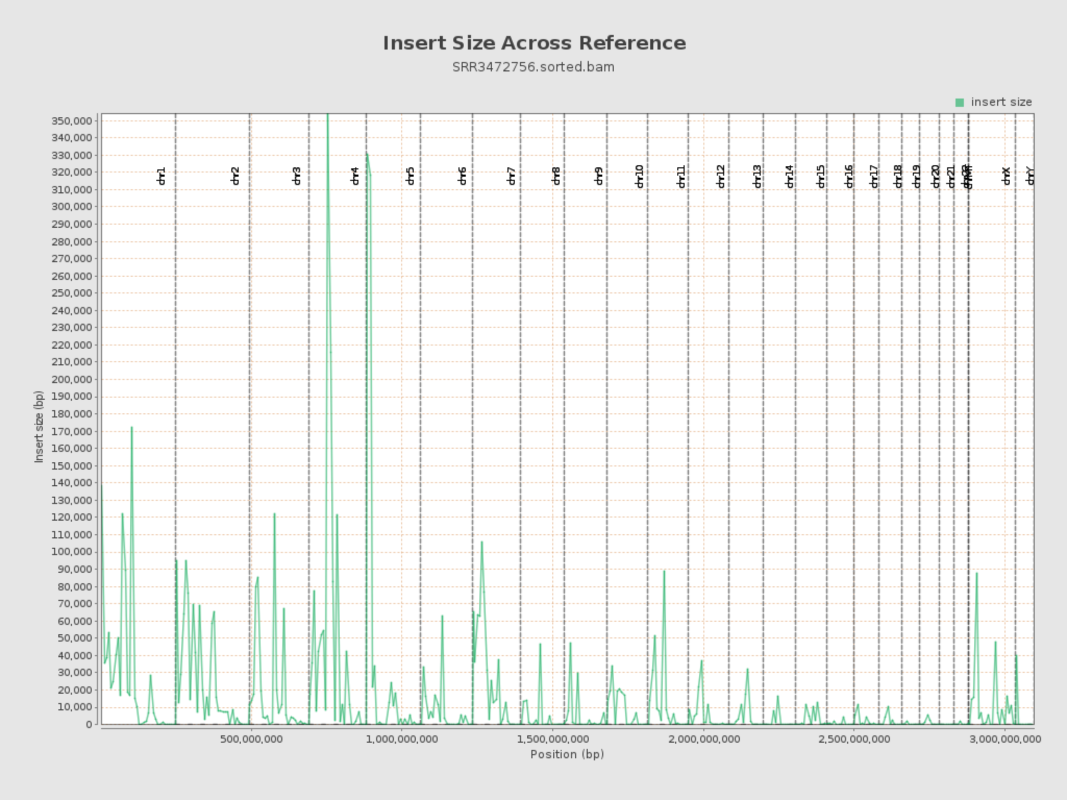
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram