Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 06:14:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472752.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_SRR3472752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472752_1.fastq.gz SRR3472752_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 06:14:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,706,000
Mapped reads	18,536,827 / 99.1%
Unmapped reads	169,173 / 0.9%
Mapped paired reads	18,536,827 / 99.1%
Mapped reads, first in pair	9,301,288 / 49.72%
Mapped reads, second in pair	9,235,539 / 49.37%
Mapped reads, both in pair	18,433,044 / 98.54%
Mapped reads, singletons	103,783 / 0.55%
Secondary alignments	0
Supplementary alignments	64,080 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,720,875 / 62.66%
Duplication rate	46.92%
Clipped reads	1,406,158 / 7.52%

2.2. ACGT Content

Number/percentage of A's	504,793,160 / 27.63%
Number/percentage of C's	411,807,611 / 22.54%
Number/percentage of T's	501,088,758 / 27.42%
Number/percentage of G's	409,141,742 / 22.39%
Number/percentage of N's	351,267 / 0.02%

GC Percentage	44.93%

2.3. Coverage

Mean	0.5903
Standard Deviation	19.5819

2.4. Mapping Quality

Mean Mapping Quality	55.37

2.5. Insert size

Mean	23,292.7
Standard Deviation	1,490,002.82
P25/Median/P75	181 / 255 / 343

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	11,572,419
Insertions	110,524
Mapped reads with at least one insertion	0.59%
Deletions	107,026
Mapped reads with at least one deletion	0.57%
Homopolymer indels	44.66%

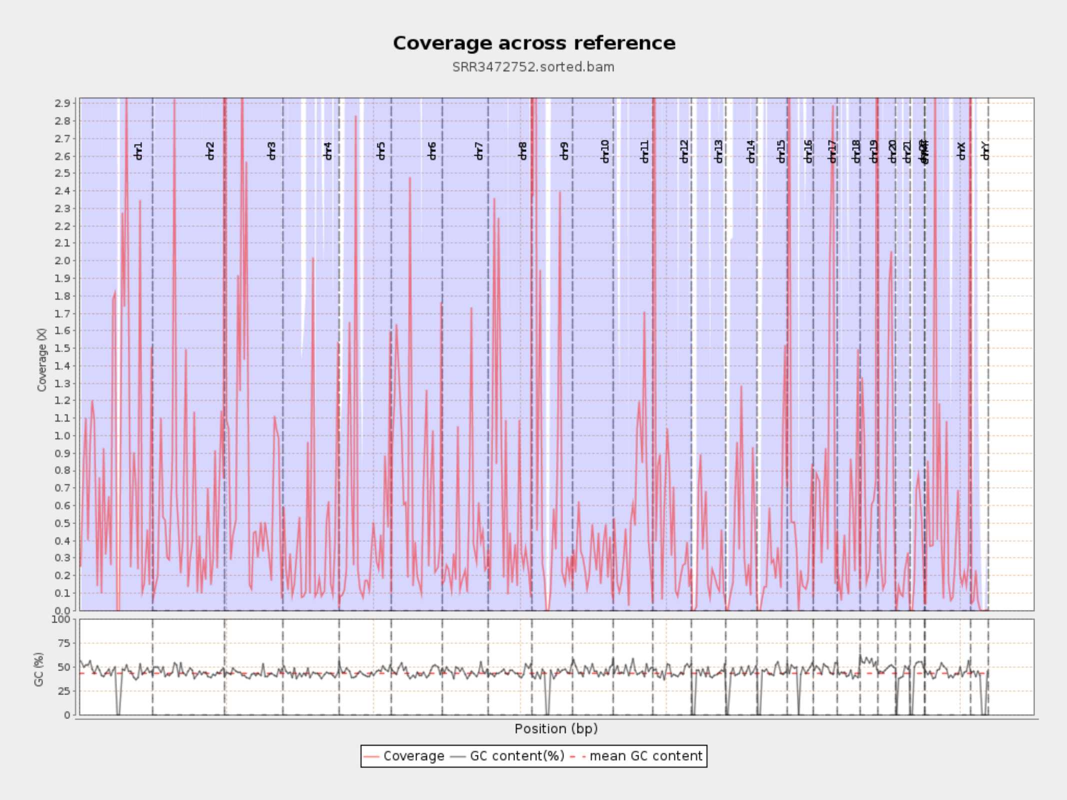
2.7. Chromosome stats

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

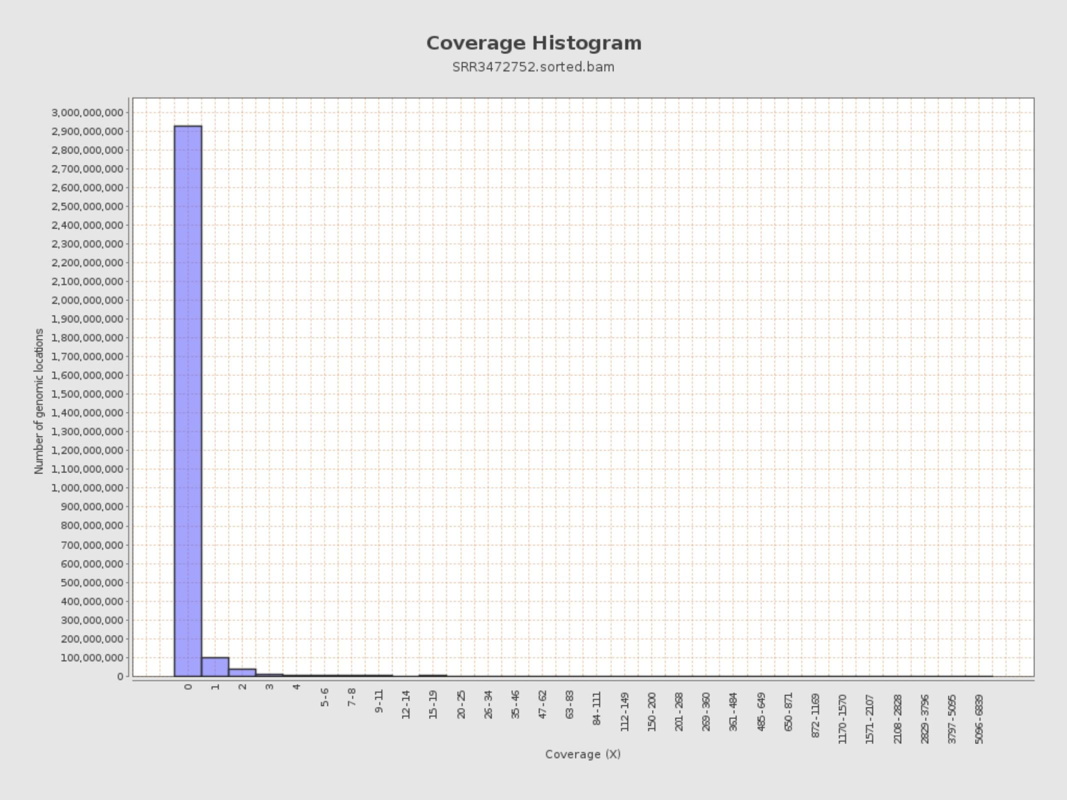
		bases	**coverage**	**deviation**
chr1	249250621	219667445	0.8813	28.7408
chr2	243199373	138415156	0.5691	19.4692
chr3	198022430	178475208	0.9013	19.4893
chr4	191154276	72041608	0.3769	19.8262
chr5	180915260	91504685	0.5058	15.7604
chr6	171115067	126576896	0.7397	19.4426
chr7	159138663	62364110	0.3919	10.9491
chr8	146364022	95149502	0.6501	20.0766
chr9	141213431	134896512	0.9553	25.7926
chr10	135534747	43002329	0.3173	9.9775
chr11	135006516	74780642	0.5539	17.1126
chr12	133851895	96455783	0.7206	25.1212
chr13	115169878	32231478	0.2799	9.7616
chr14	107349540	43147085	0.4019	19.3593
chr15	102531392	39159198	0.3819	12.2985
chr16	90354753	55783609	0.6174	16.8772
chr17	81195210	72001782	0.8868	23.9798
chr18	78077248	34214356	0.4382	15.3526
chr19	59128983	46839887	0.7922	25.9772
chr20	63025520	53217904	0.8444	33.9683
chr21	48129895	7298107	0.1516	5.9805
chr22	51304566	18375405	0.3582	9.5365
chrMT	16571	2342	0.1413	0.4746
chrX	155270560	88923810	0.5727	16.5698

chrY	59373566	2922078	0.0492	1.5157

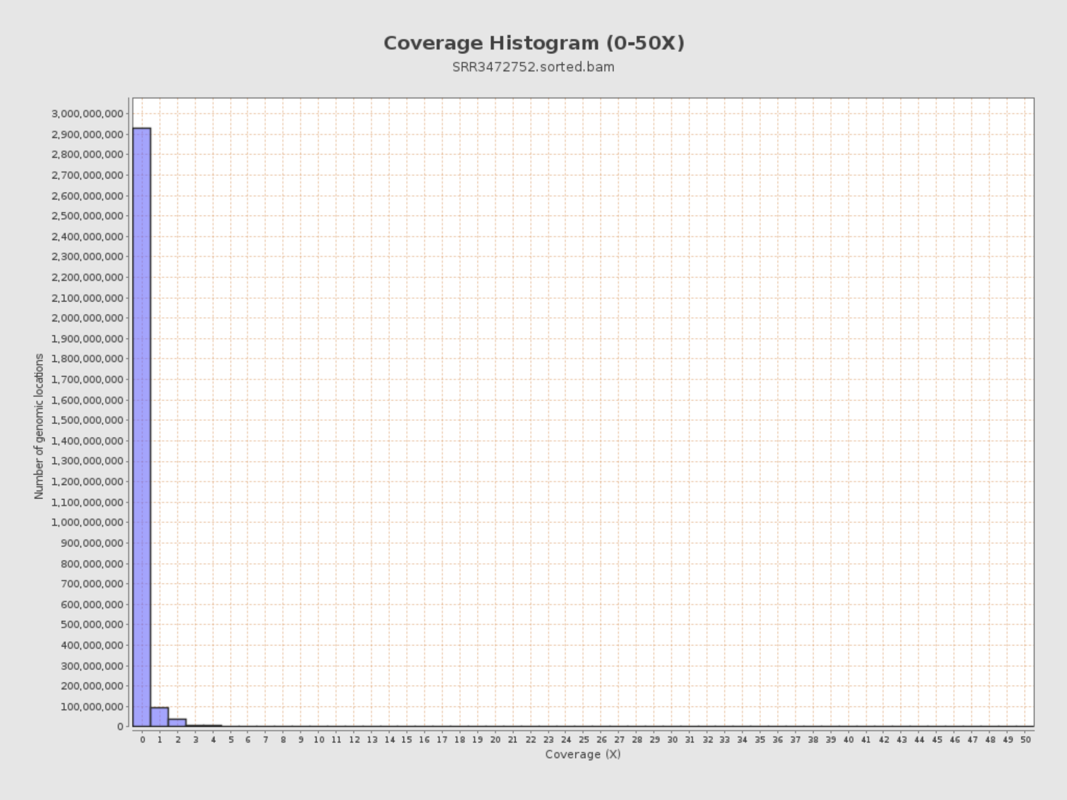
3. Results : Coverage across reference



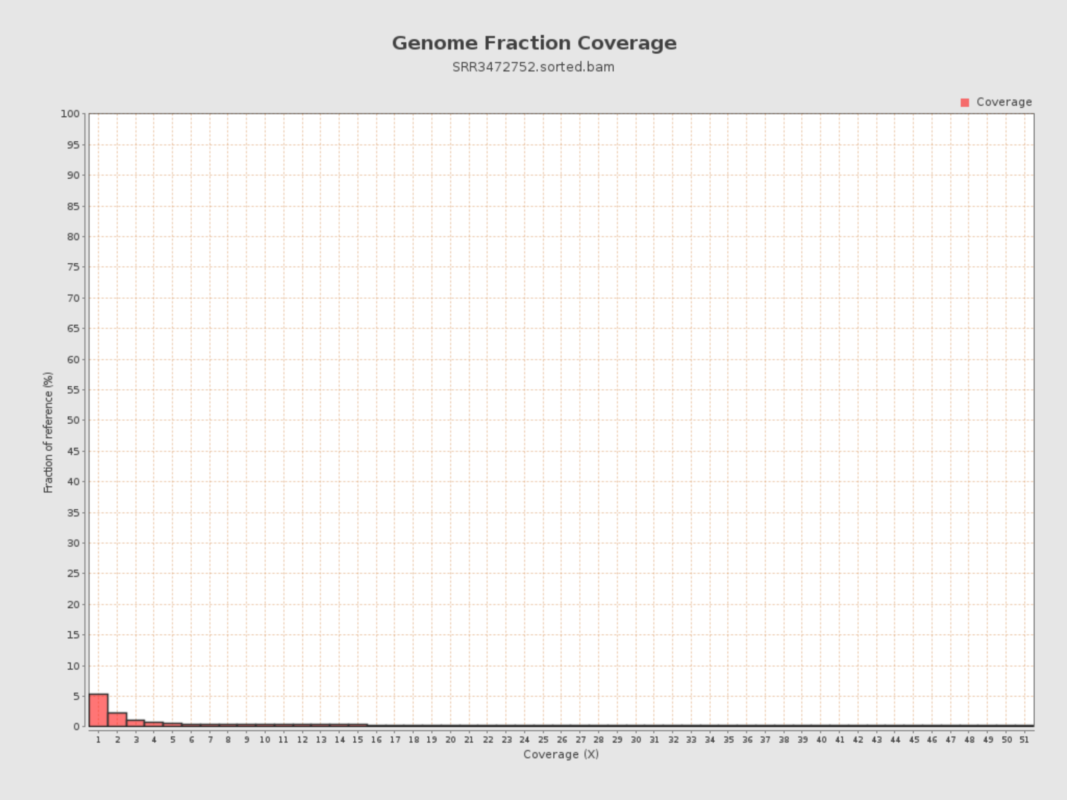
4. Results : Coverage Histogram



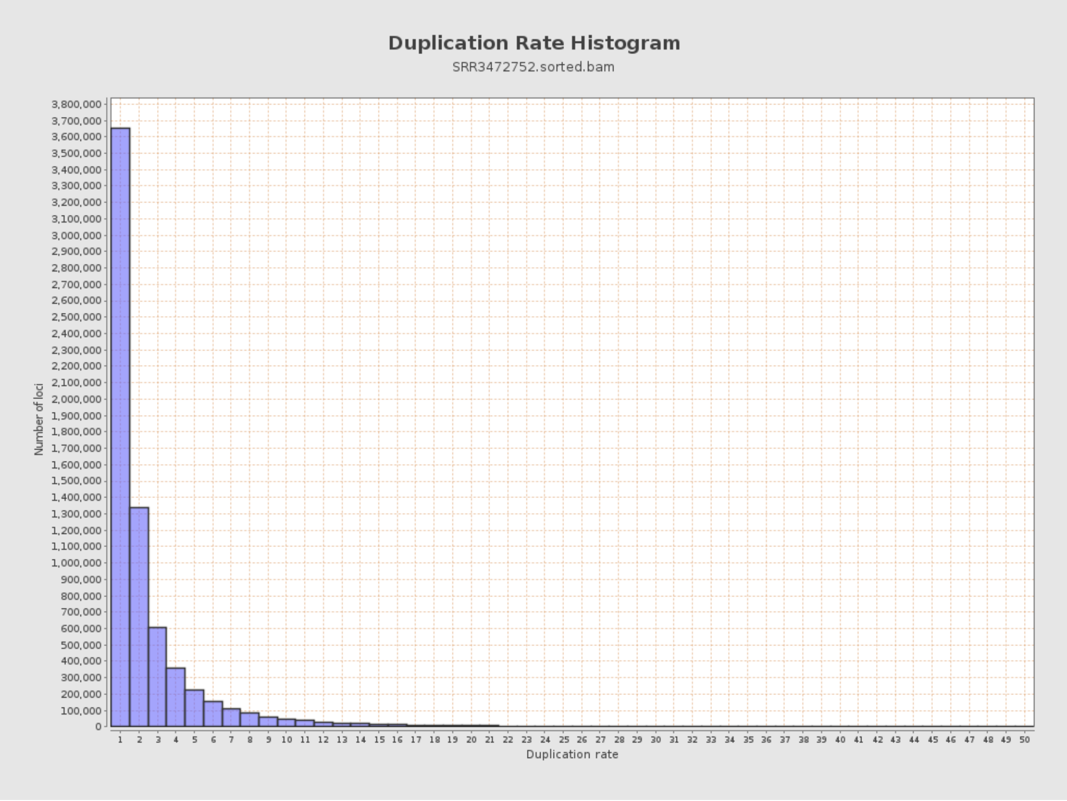
5. Results : Coverage Histogram (0-50X)



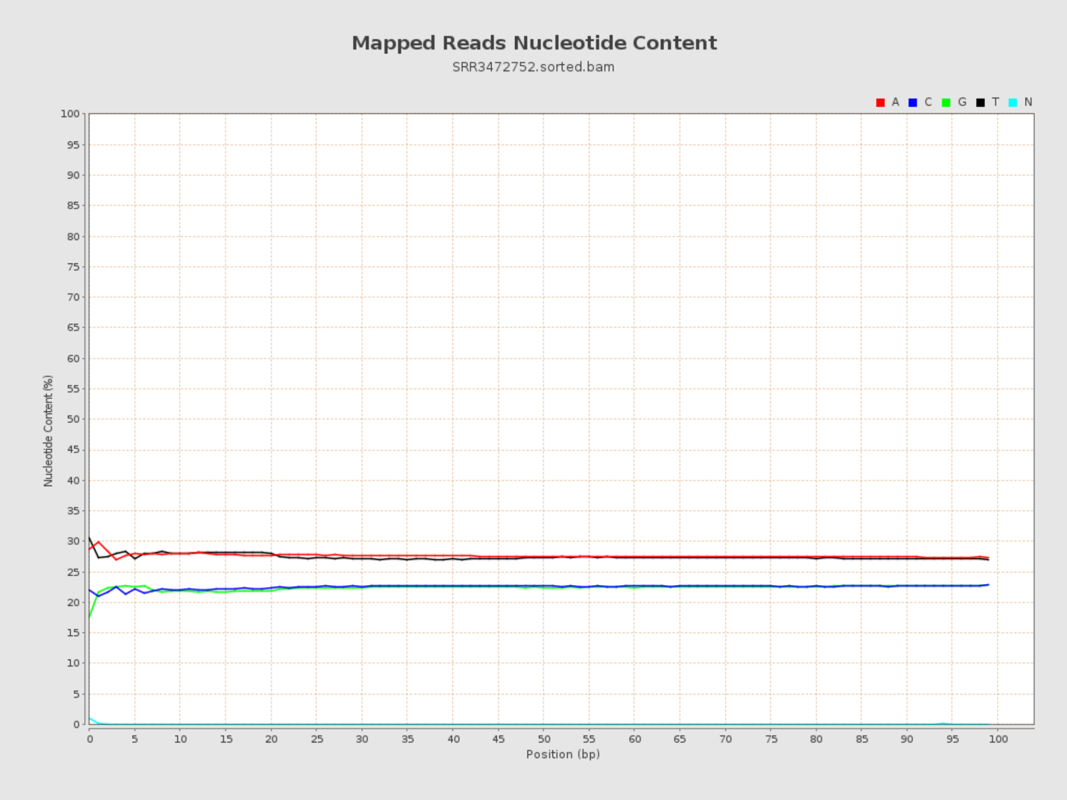
6. Results : Genome Fraction Coverage



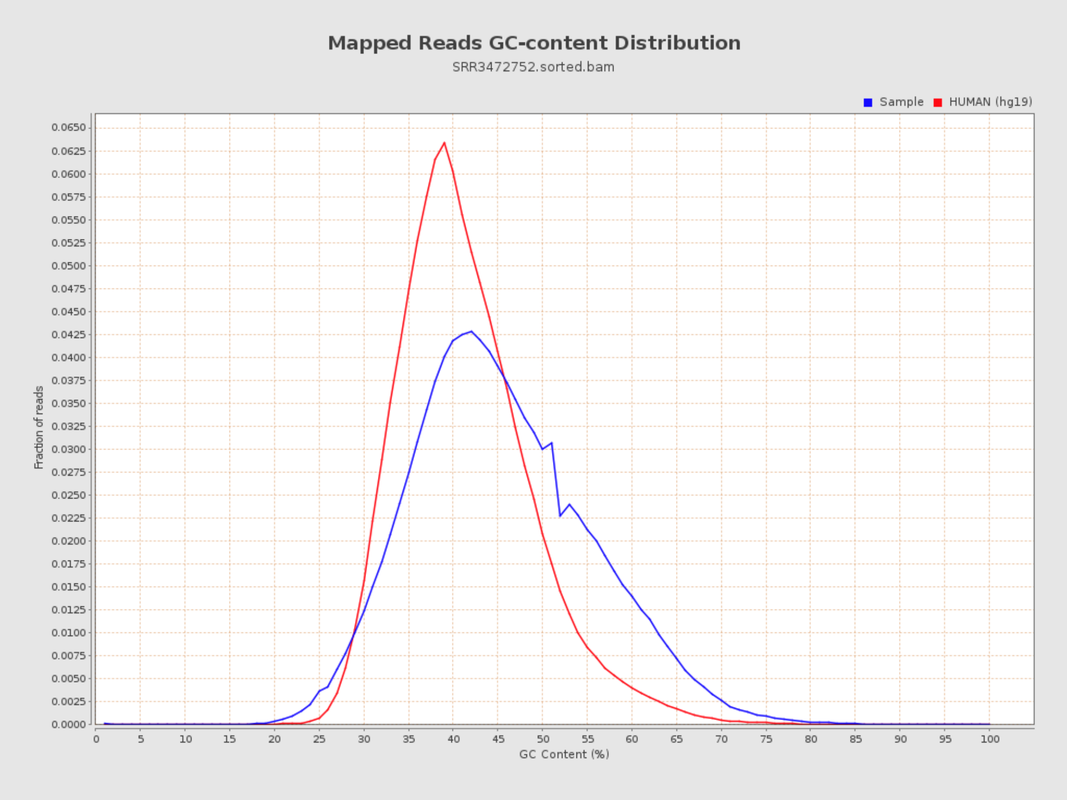
7. Results : Duplication Rate Histogram



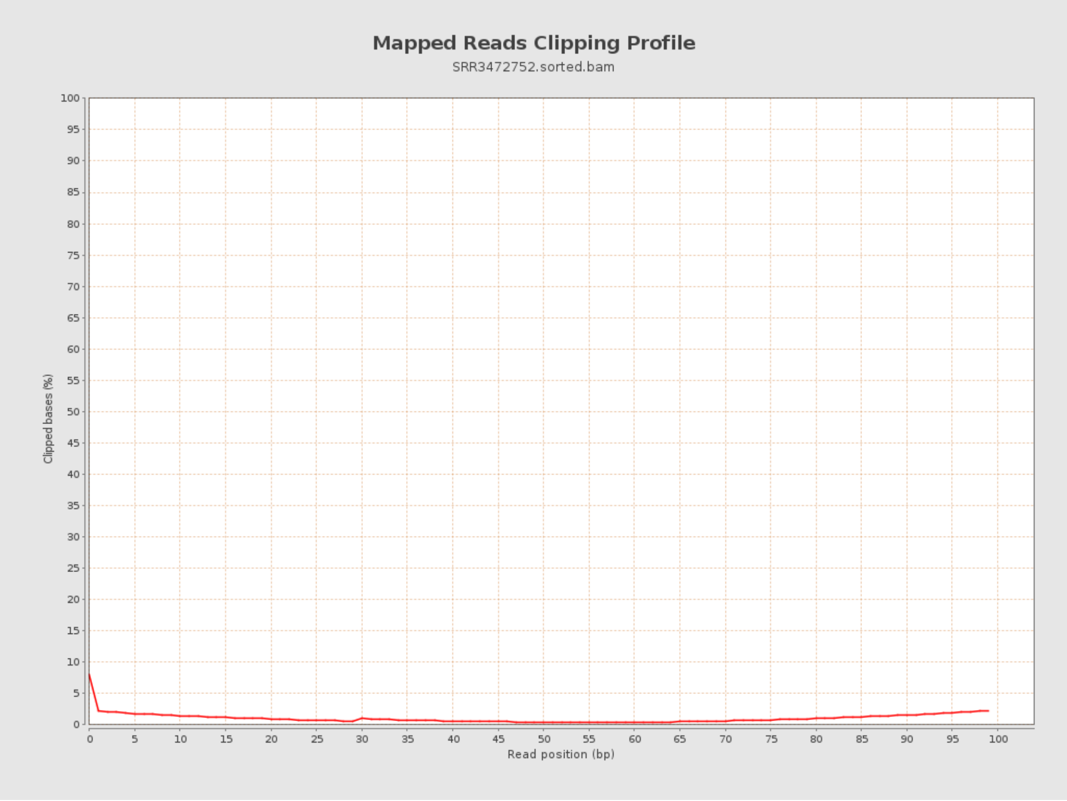
8. Results : Mapped Reads Nucleotide Content



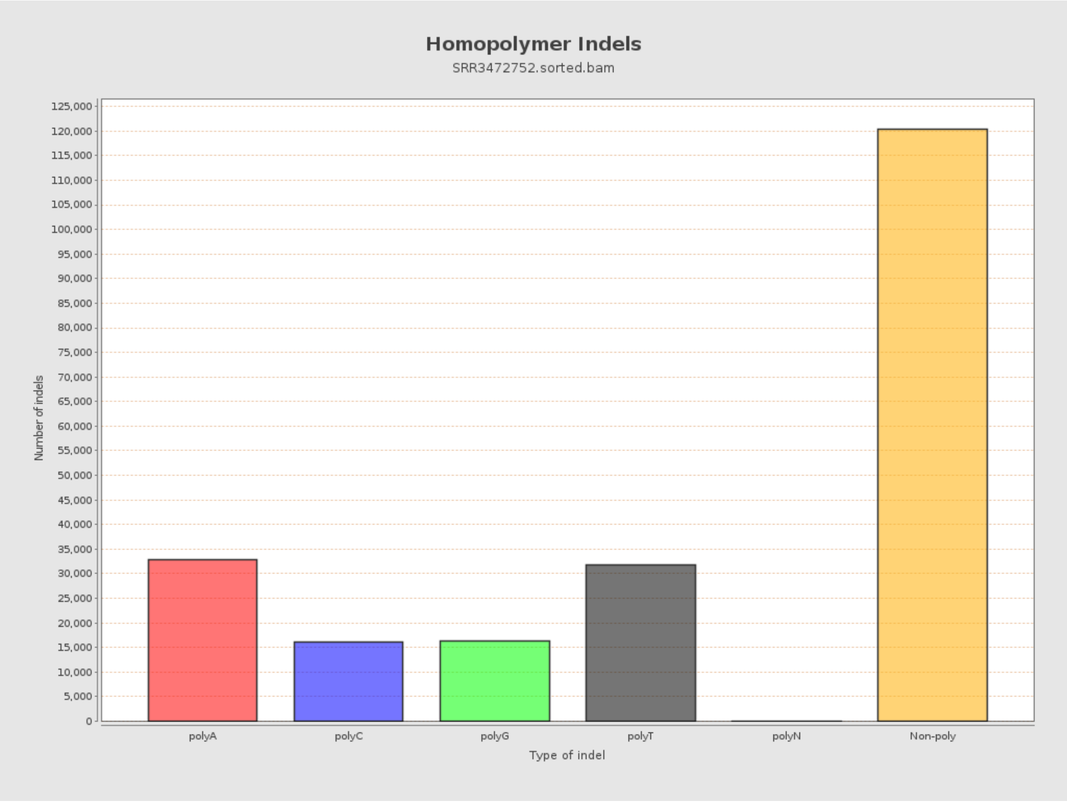
9. Results : Mapped Reads GC-content Distribution



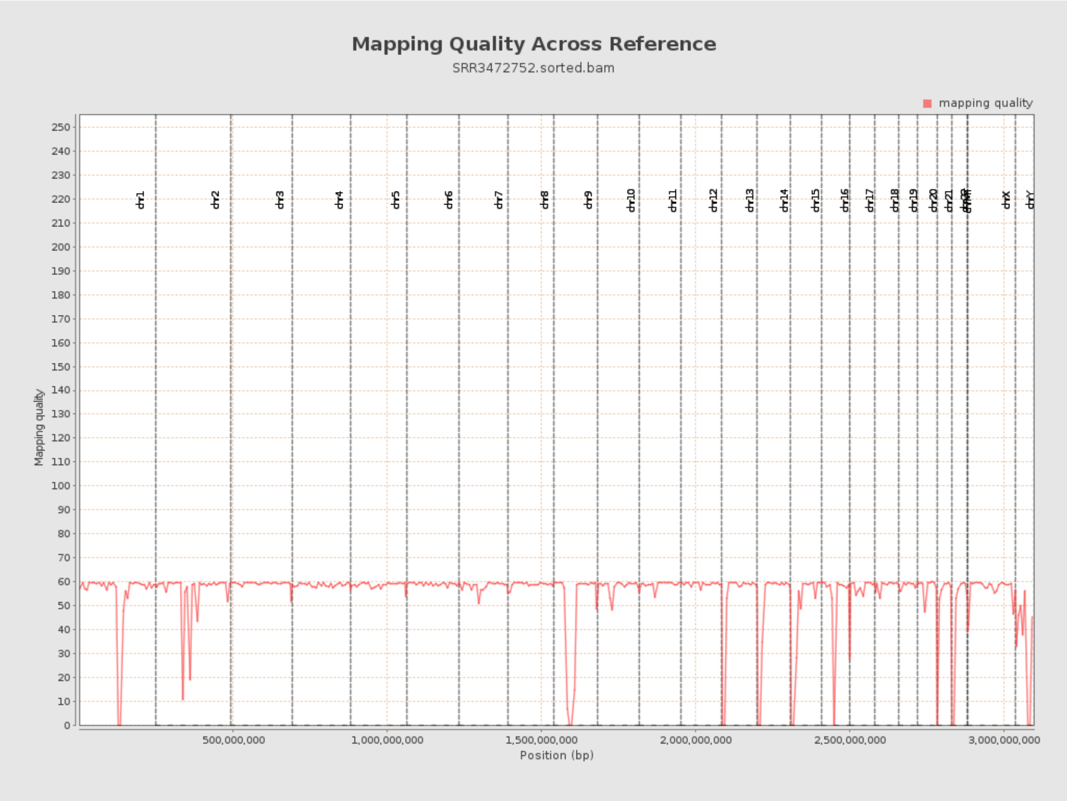
10. Results : Mapped Reads Clipping Profile



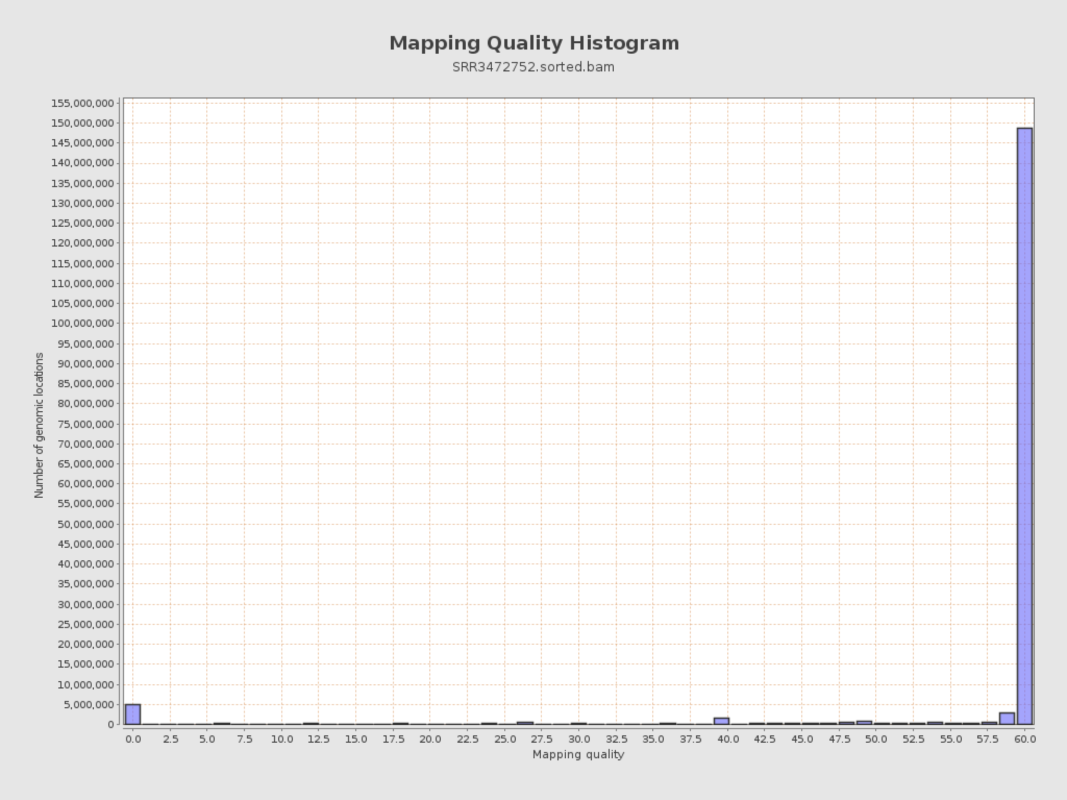
11. Results : Homopolymer Indels



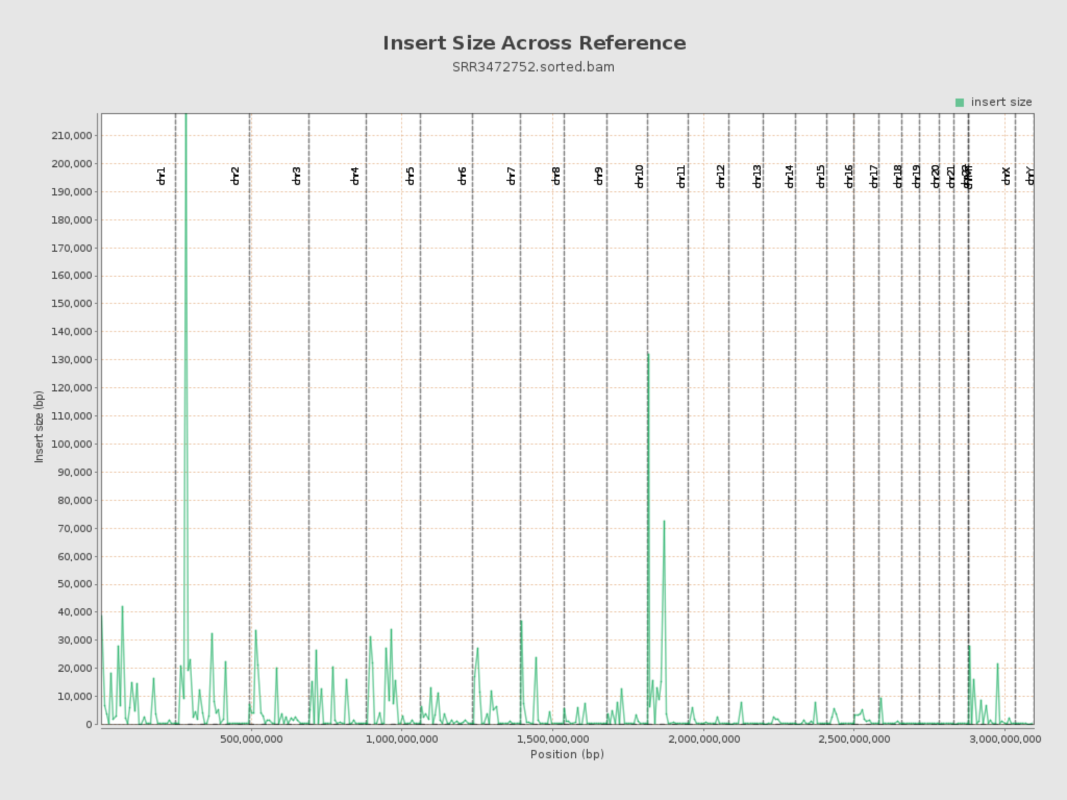
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram