Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:41:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472555.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_SRR3472555 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472555_1.fastq.gz SRR3472555_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:41:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472555.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,163,144
Mapped reads	12,947,727 / 98.36%
Unmapped reads	215,417 / 1.64%
Mapped paired reads	12,947,727 / 98.36%
Mapped reads, first in pair	6,494,989 / 49.34%
Mapped reads, second in pair	6,452,738 / 49.02%
Mapped reads, both in pair	12,849,398 / 97.62%
Mapped reads, singletons	98,329 / 0.75%
Secondary alignments	0
Supplementary alignments	58,396 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	8,005,665 / 60.82%
Duplication rate	45%
Clipped reads	1,209,362 / 9.19%

2.2. ACGT Content

Number/percentage of A's	351,223,052 / 27.66%
Number/percentage of C's	285,664,461 / 22.49%
Number/percentage of T's	348,636,953 / 27.45%
Number/percentage of G's	284,196,922 / 22.38%
Number/percentage of N's	195,922 / 0.02%

GC Percentage	44.87%

2.3. Coverage

Mean	0.4103
Standard Deviation	18.6128

2.4. Mapping Quality

Mean Mapping Quality	54.88

2.5. Insert size

Mean	32,934.13
Standard Deviation	1,759,234.53
P25/Median/P75	171 / 243 / 331

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	7,992,872
Insertions	71,902
Mapped reads with at least one insertion	0.55%
Deletions	65,449
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.6%

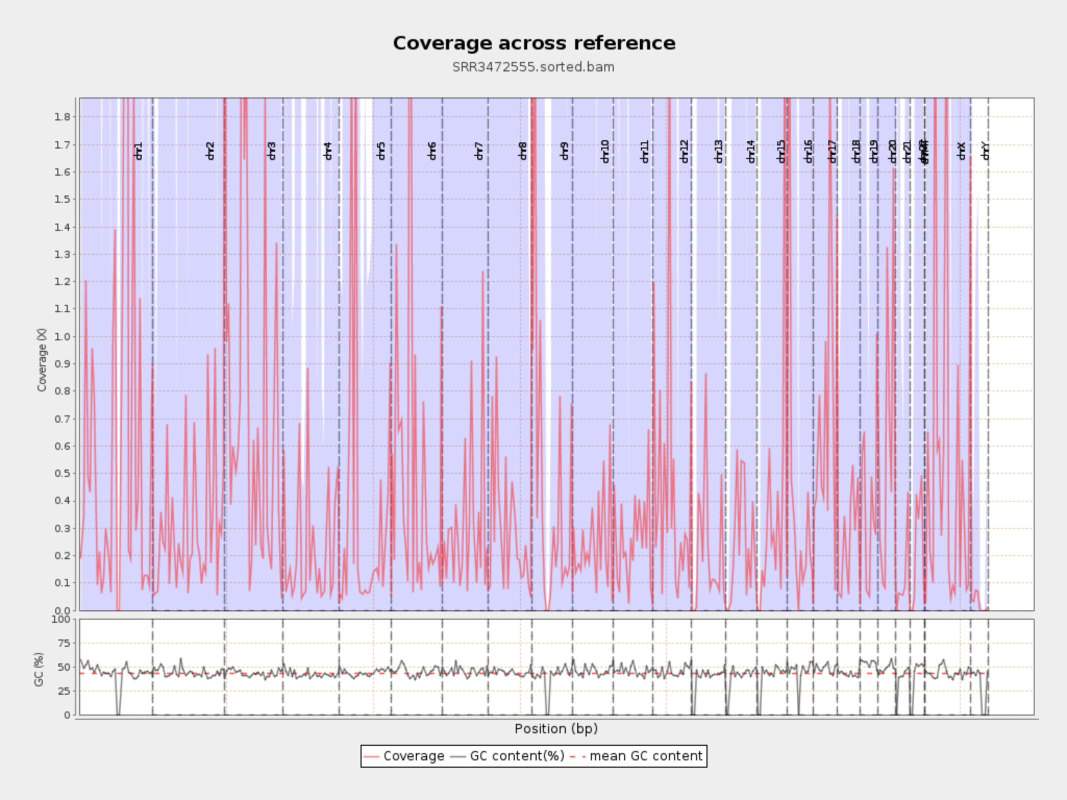
2.7. Chromosome stats

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

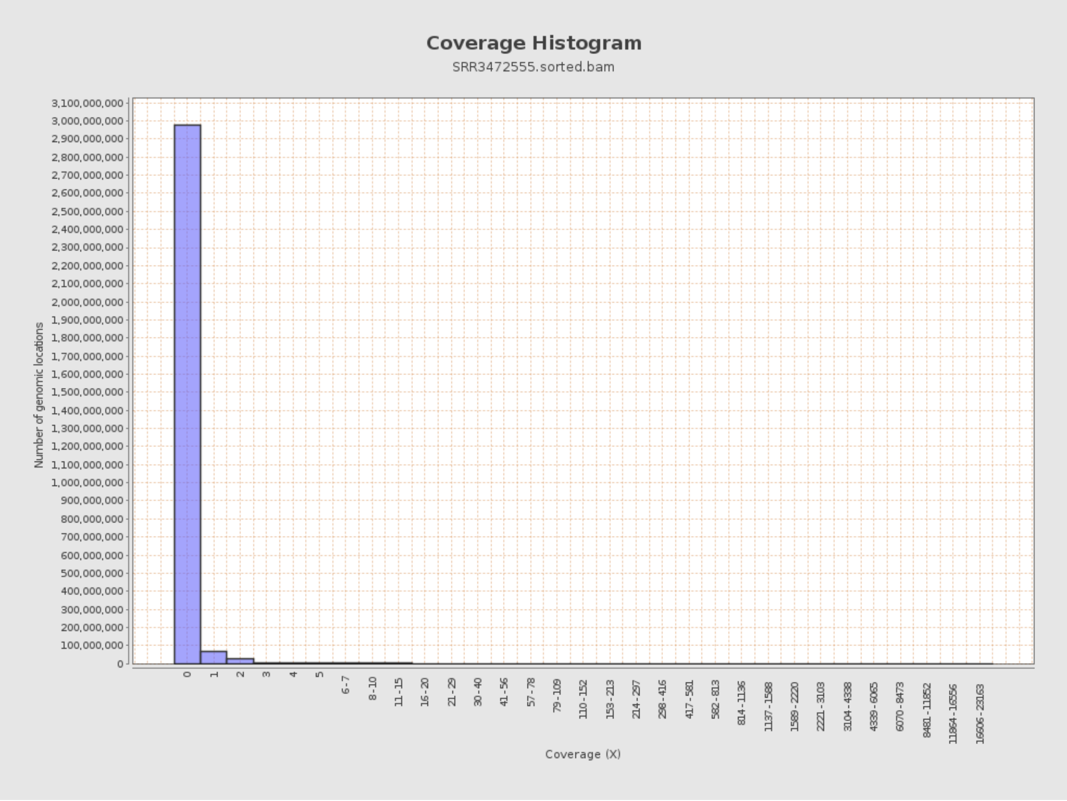
		bases	coverage	deviation
chr1	249250621	182593394	0.7326	44.7938
chr2	243199373	71870601	0.2955	10.639
chr3	198022430	158509372	0.8005	21.4979
chr4	191154276	43773411	0.229	10.5775
chr5	180915260	69320055	0.3832	16.0715
chr6	171115067	85844483	0.5017	16.7677
chr7	159138663	49874018	0.3134	14.0791
chr8	146364022	42935394	0.2933	9.8654
chr9	141213431	63943891	0.4528	12.9173
chr10	135534747	33522252	0.2473	10.0341
chr11	135006516	35654217	0.2641	10.0643
chr12	133851895	61814156	0.4618	14.9791
chr13	115169878	24285848	0.2109	7.914
chr14	107349540	25152599	0.2343	9.5247
chr15	102531392	42358259	0.4131	20.9441
chr16	90354753	37902988	0.4195	11.493
chr17	81195210	57709962	0.7108	17.8913
chr18	78077248	20016146	0.2564	10.8346
chr19	59128983	21099171	0.3568	10.431
chr20	63025520	38654623	0.6133	18.768
chr21	48129895	5703145	0.1185	4.3355
chr22	51304566	10824914	0.211	9.7097
chrMT	16571	2109	0.1273	0.436
chrX	155270560	85057244	0.5478	20.7448

chrY	59373566	1650681	0.0278	0.7484

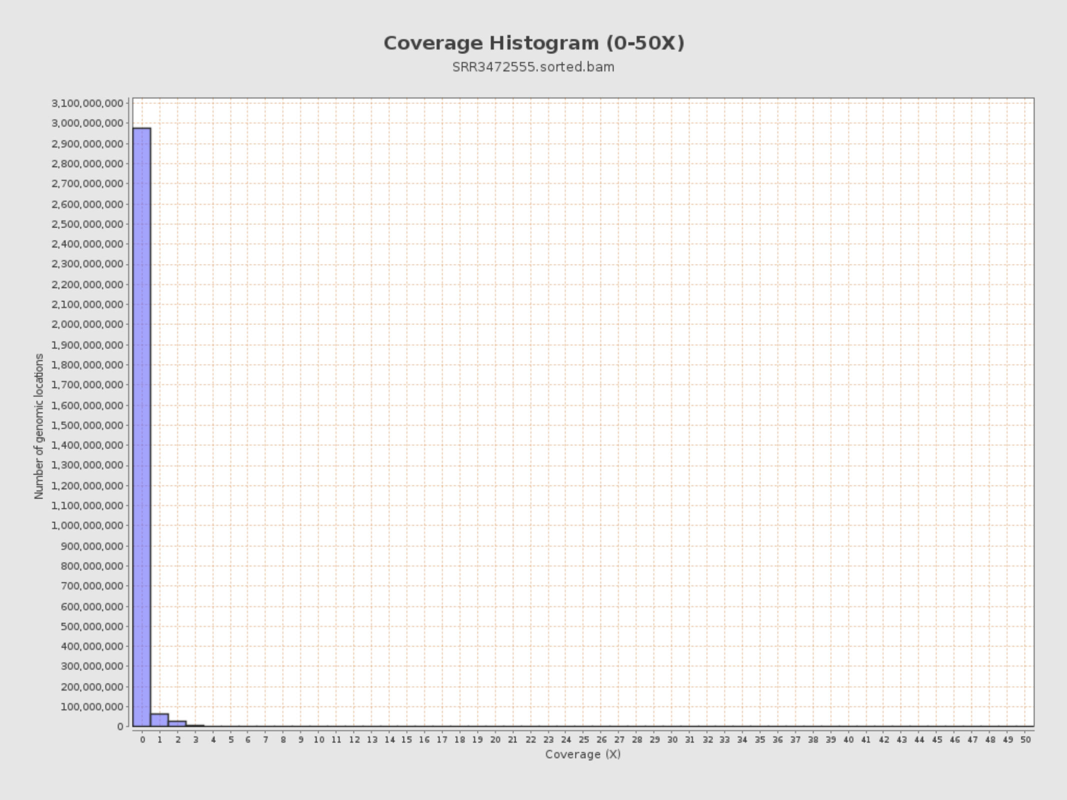
3. Results : Coverage across reference



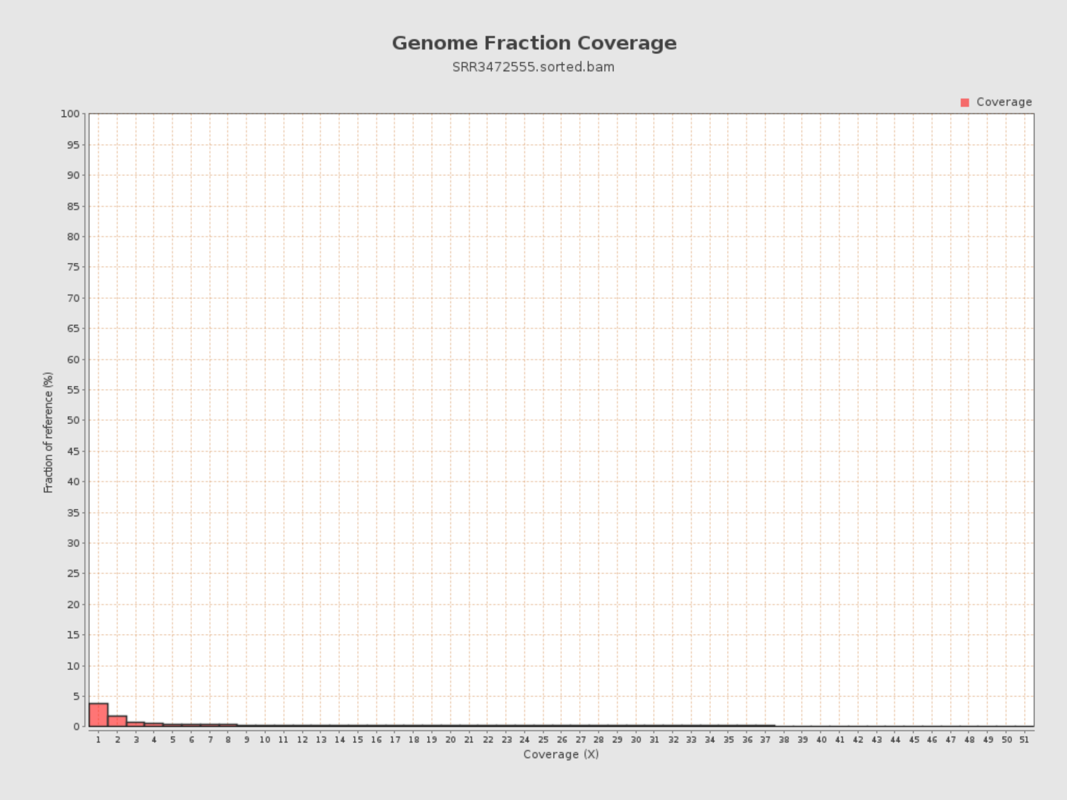
4. Results : Coverage Histogram



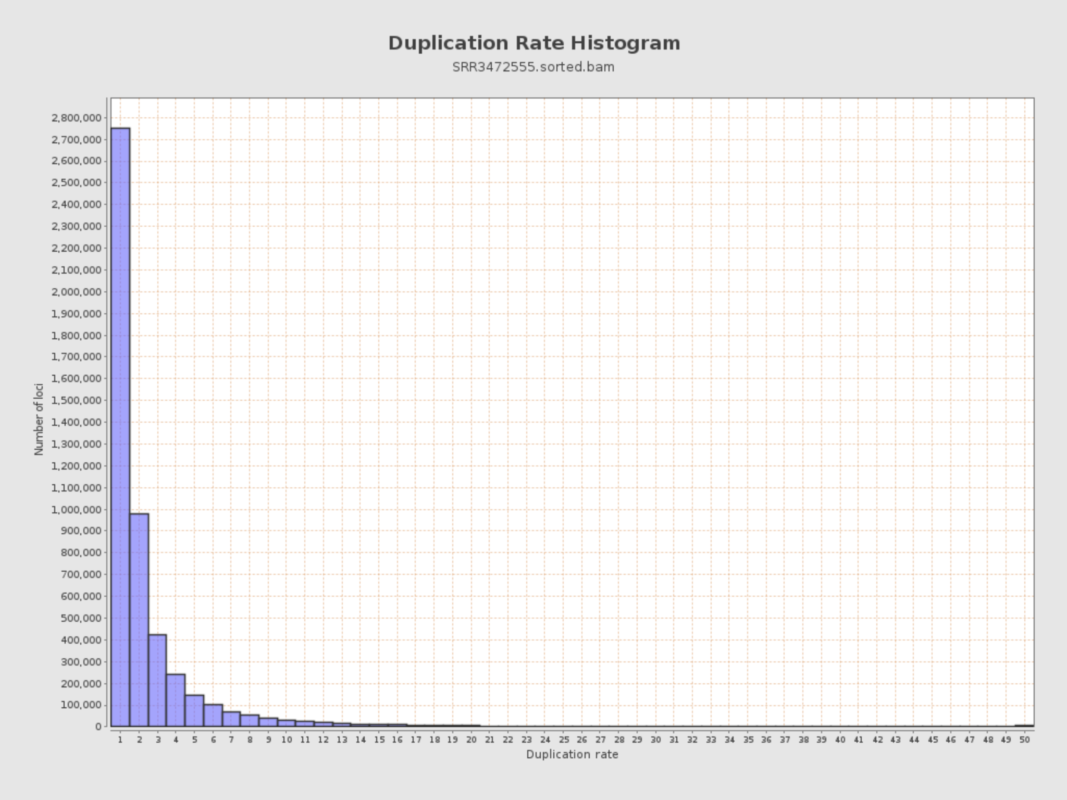
5. Results : Coverage Histogram (0-50X)



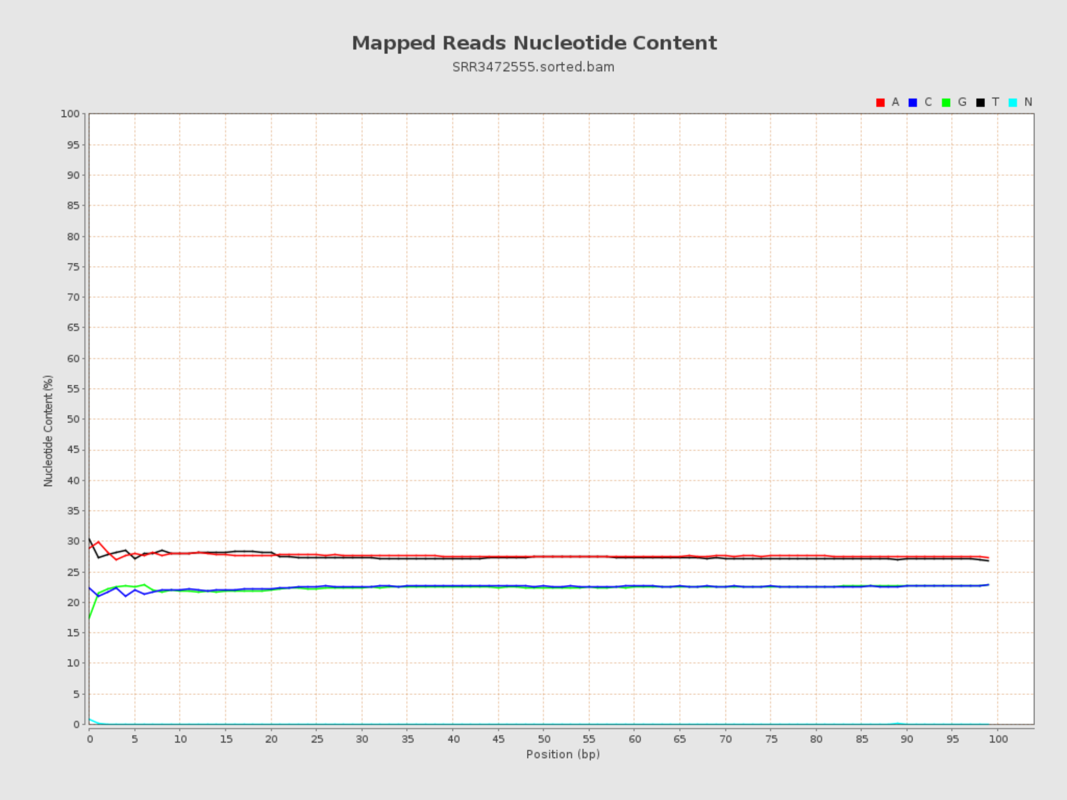
6. Results : Genome Fraction Coverage



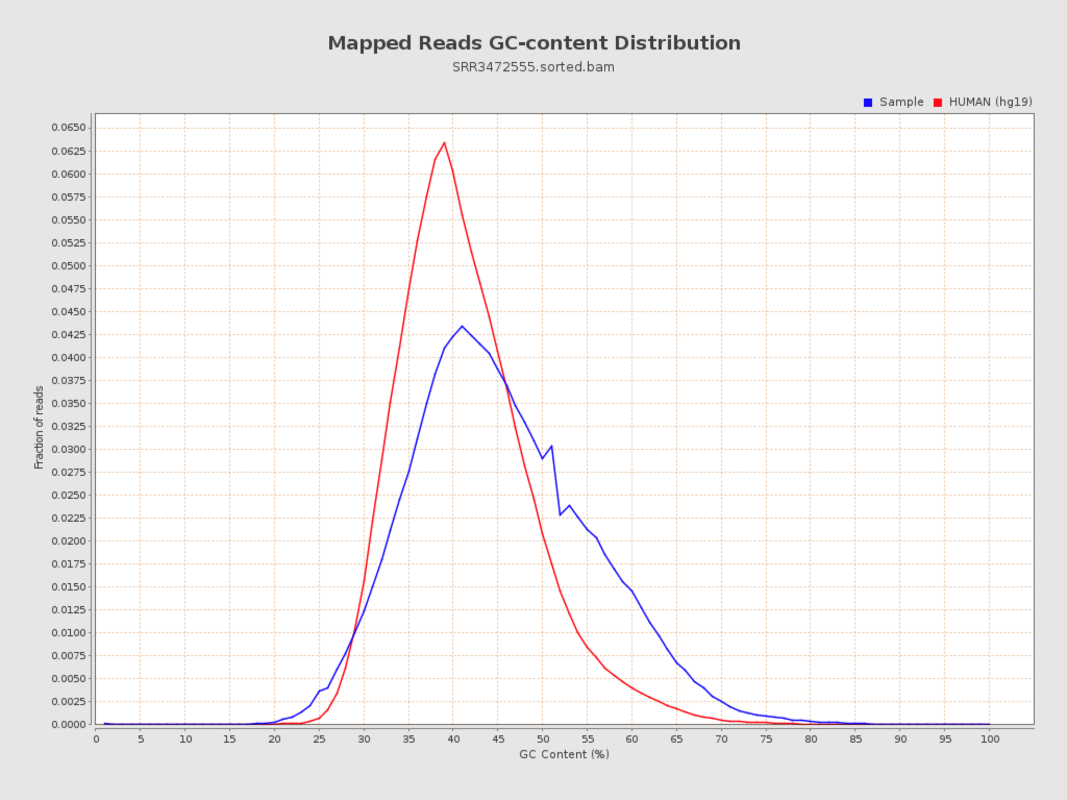
7. Results : Duplication Rate Histogram



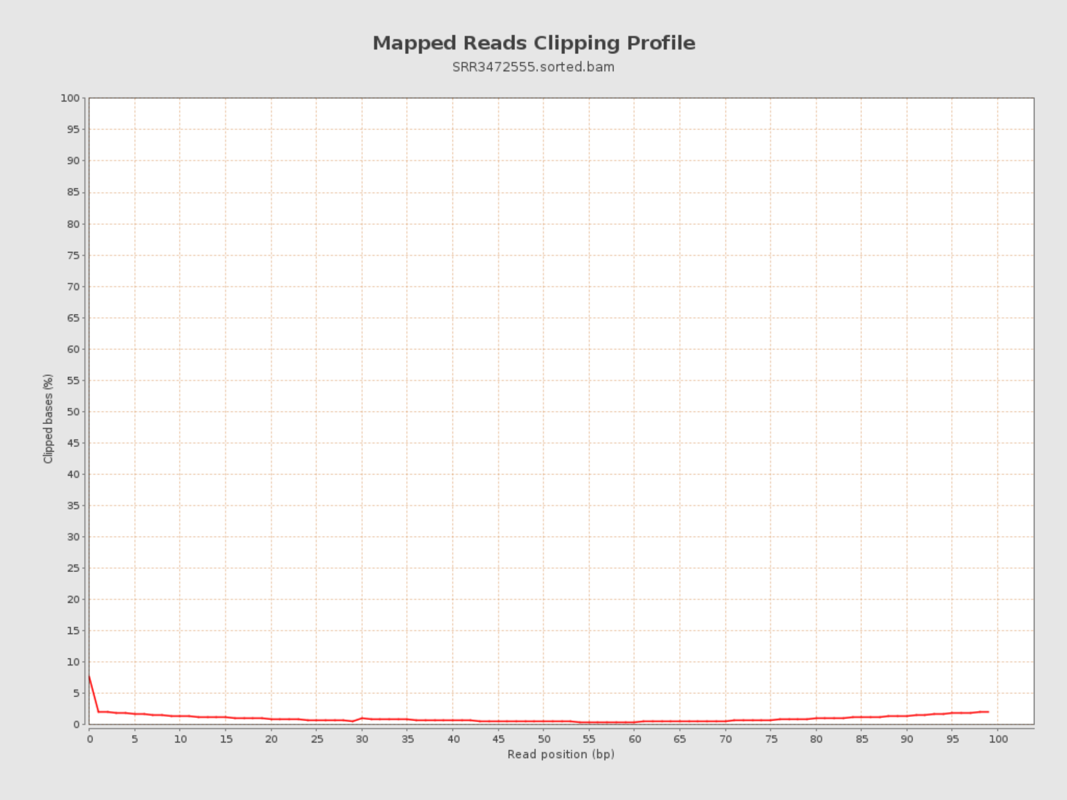
8. Results : Mapped Reads Nucleotide Content



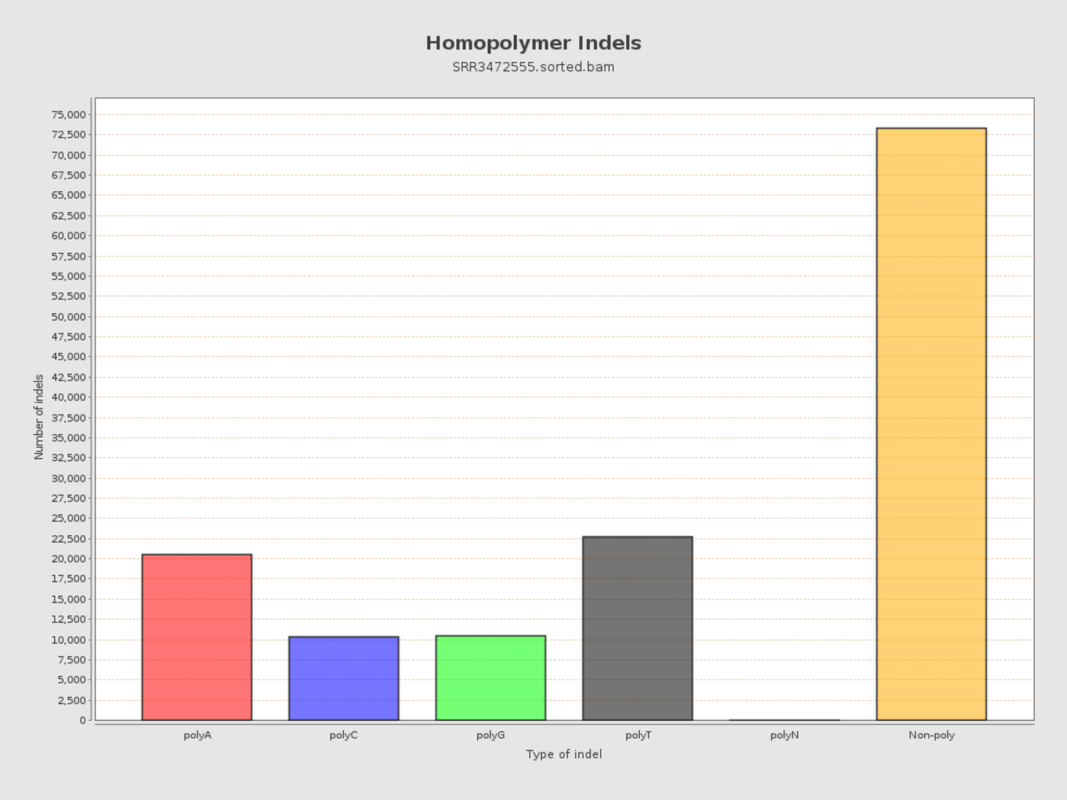
9. Results : Mapped Reads GC-content Distribution



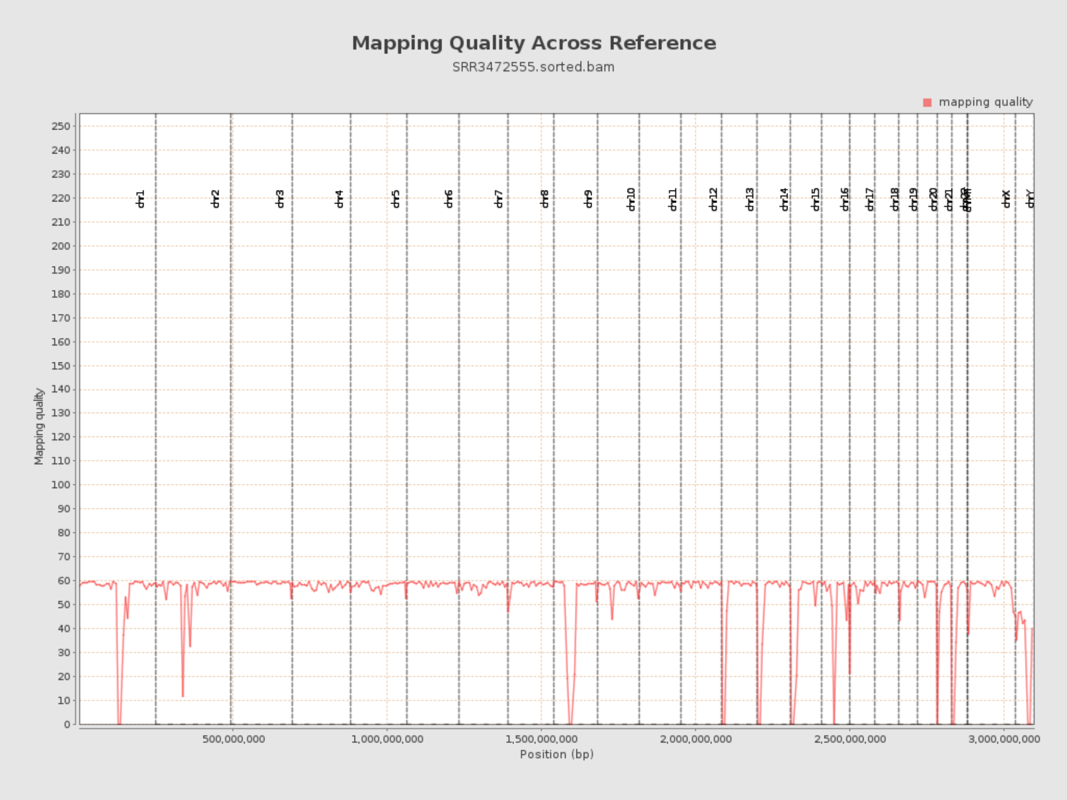
10. Results : Mapped Reads Clipping Profile



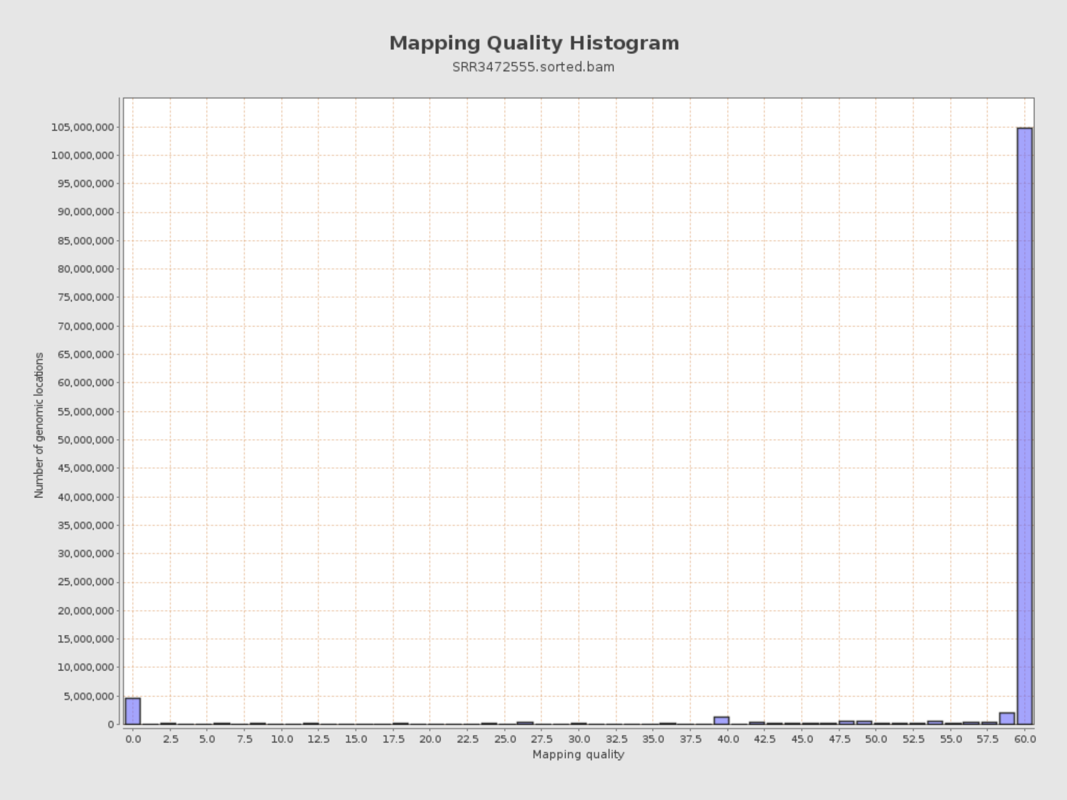
11. Results : Homopolymer Indels



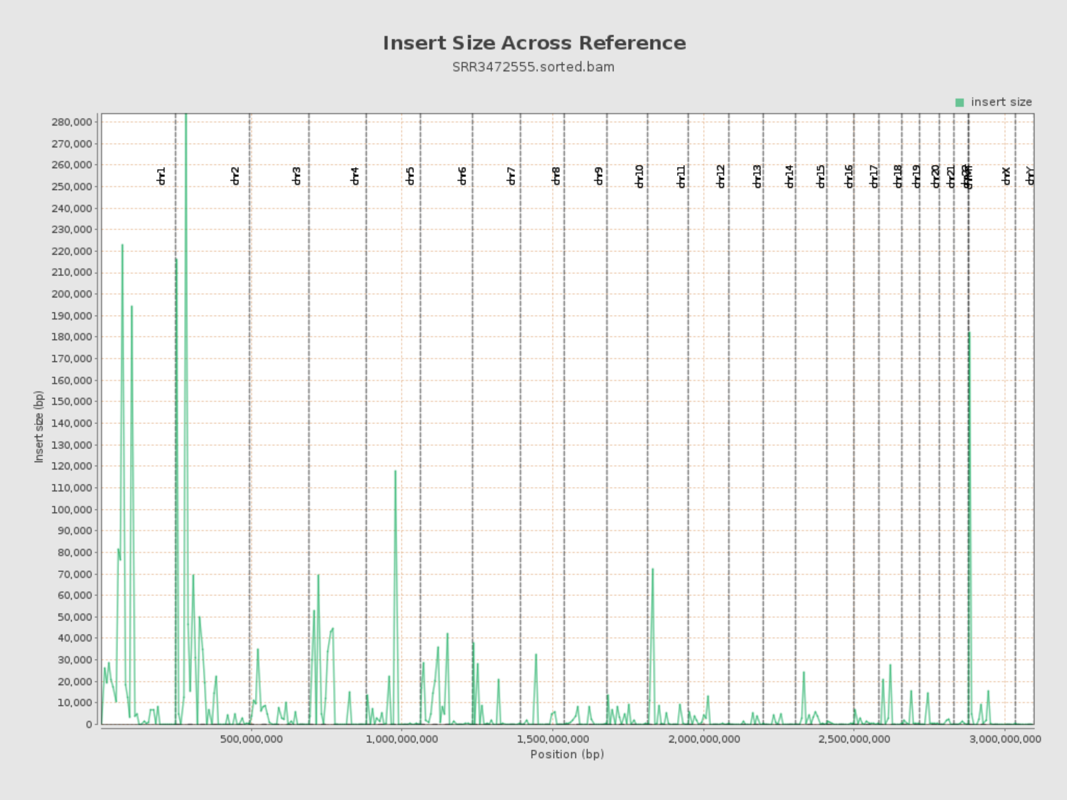
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram