Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:31:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472535.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_SRR3472535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472535_1.fastq.gz SRR3472535_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:31:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,818,502
Mapped reads	19,621,576 / 99.01%
Unmapped reads	196,926 / 0.99%
Mapped paired reads	19,621,576 / 99.01%
Mapped reads, first in pair	9,842,595 / 49.66%
Mapped reads, second in pair	9,778,981 / 49.34%
Mapped reads, both in pair	19,510,384 / 98.45%
Mapped reads, singletons	111,192 / 0.56%
Secondary alignments	0
Supplementary alignments	101,866 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	13,150,906 / 66.36%
Duplication rate	45.22%
Clipped reads	1,747,087 / 8.82%

2.2. ACGT Content

Number/percentage of A's	548,375,567 / 28.41%
Number/percentage of C's	420,247,769 / 21.77%
Number/percentage of T's	543,599,582 / 28.16%
Number/percentage of G's	417,813,618 / 21.64%
Number/percentage of N's	296,683 / 0.02%

GC Percentage	43.42%

2.3. Coverage

Mean	0.6236
Standard Deviation	24.5252

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	40,727.25
Standard Deviation	1,977,542.13
P25/Median/P75	169 / 238 / 322

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	11,889,885
Insertions	120,614
Mapped reads with at least one insertion	0.61%
Deletions	117,545
Mapped reads with at least one deletion	0.59%
Homopolymer indels	46.61%

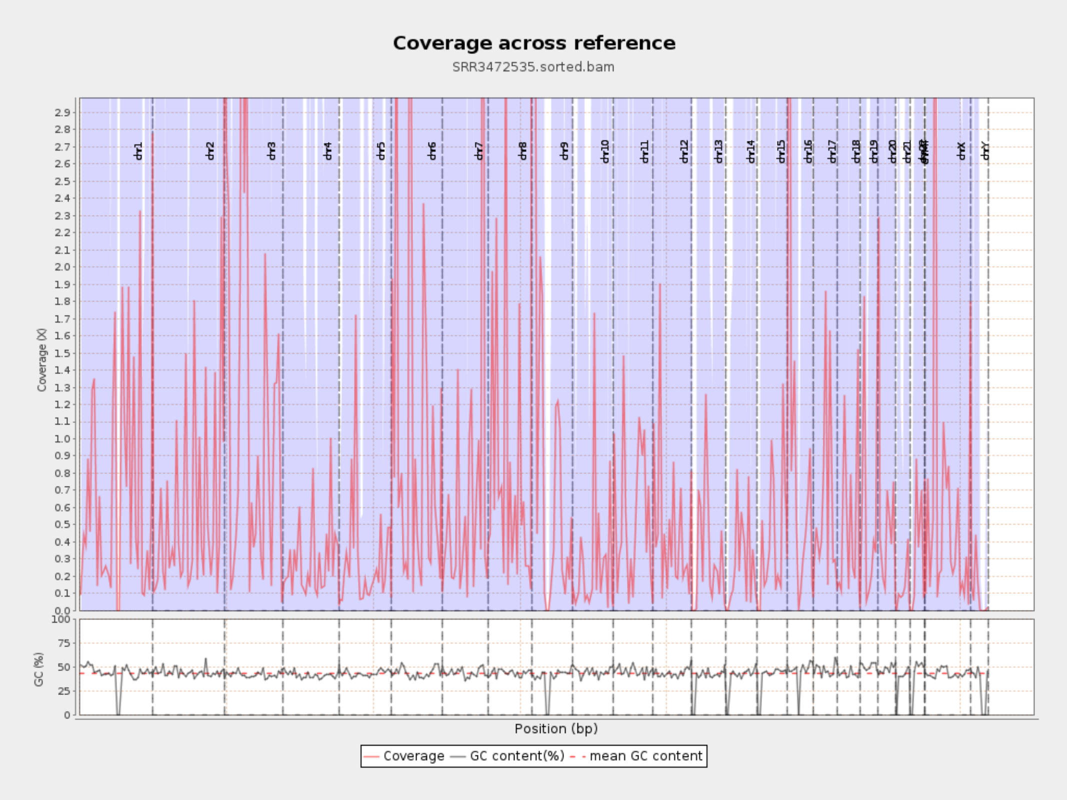
2.7. Chromosome stats

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

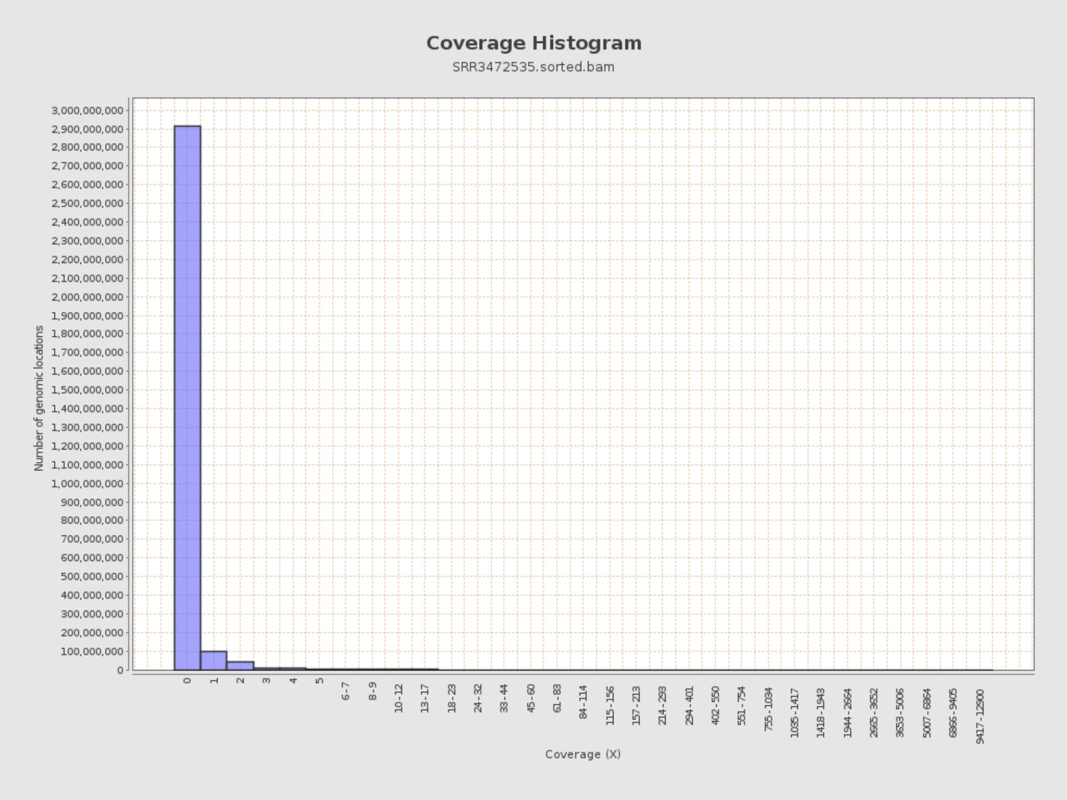
		bases	coverage	deviation
chr1	249250621	169835739	0.6814	25.31
chr2	243199373	138934038	0.5713	25.6454
chr3	198022430	264978077	1.3381	35.9465
chr4	191154276	55771799	0.2918	12.9874
chr5	180915260	56008899	0.3096	10.6463
chr6	171115067	177187148	1.0355	38.0996
chr7	159138663	116968973	0.735	30.0842
chr8	146364022	126902837	0.867	34.2765
chr9	141213431	155707641	1.1026	36.1946
chr10	135534747	41753904	0.3081	20.6676
chr11	135006516	76601156	0.5674	20.1439
chr12	133851895	63595372	0.4751	17.1256
chr13	115169878	37865338	0.3288	11.6613
chr14	107349540	29539242	0.2752	13.4839
chr15	102531392	43872713	0.4279	15.3966
chr16	90354753	87189664	0.965	29.3456
chr17	81195210	51121304	0.6296	18.3451
chr18	78077248	39987310	0.5122	21.3818
chr19	59128983	30657281	0.5185	18.0965
chr20	63025520	37360200	0.5928	21.9432
chr21	48129895	6590353	0.1369	3.7861
chr22	51304566	16558929	0.3228	14.092
chrMT	16571	12758	0.7699	1.3582
chrX	155270560	99538814	0.6411	21.2388

chrY	59373566	6066652	0.1022	4.5175

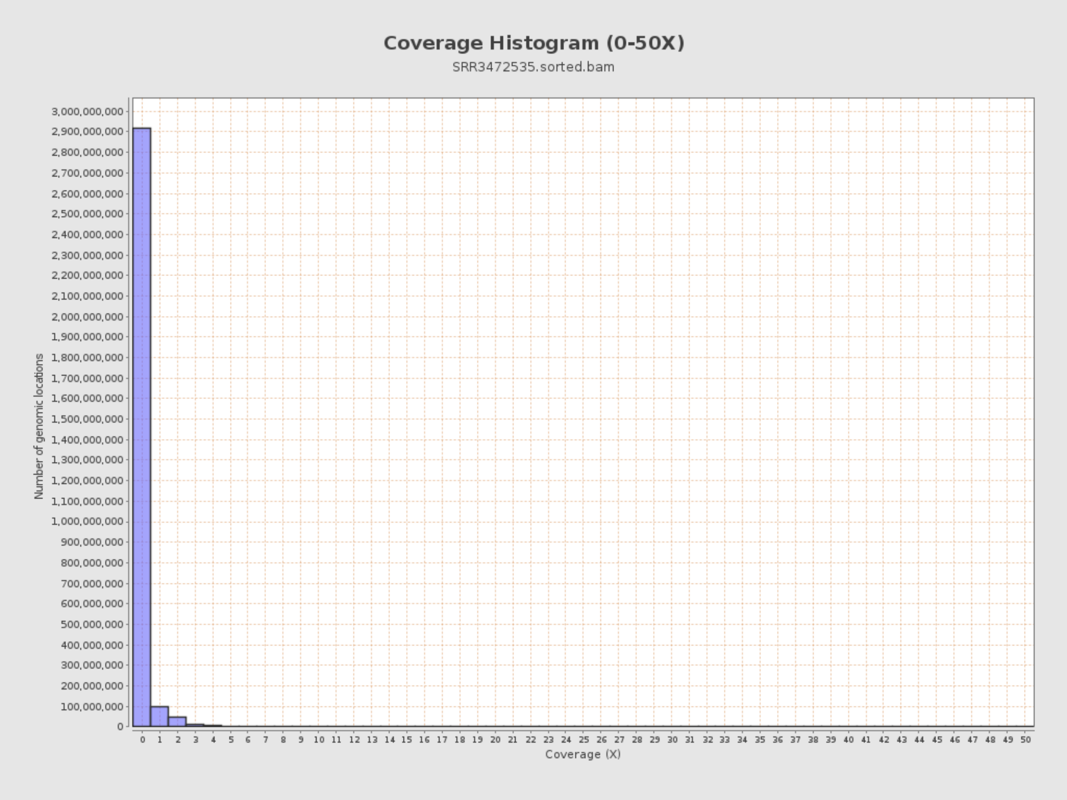
3. Results : Coverage across reference



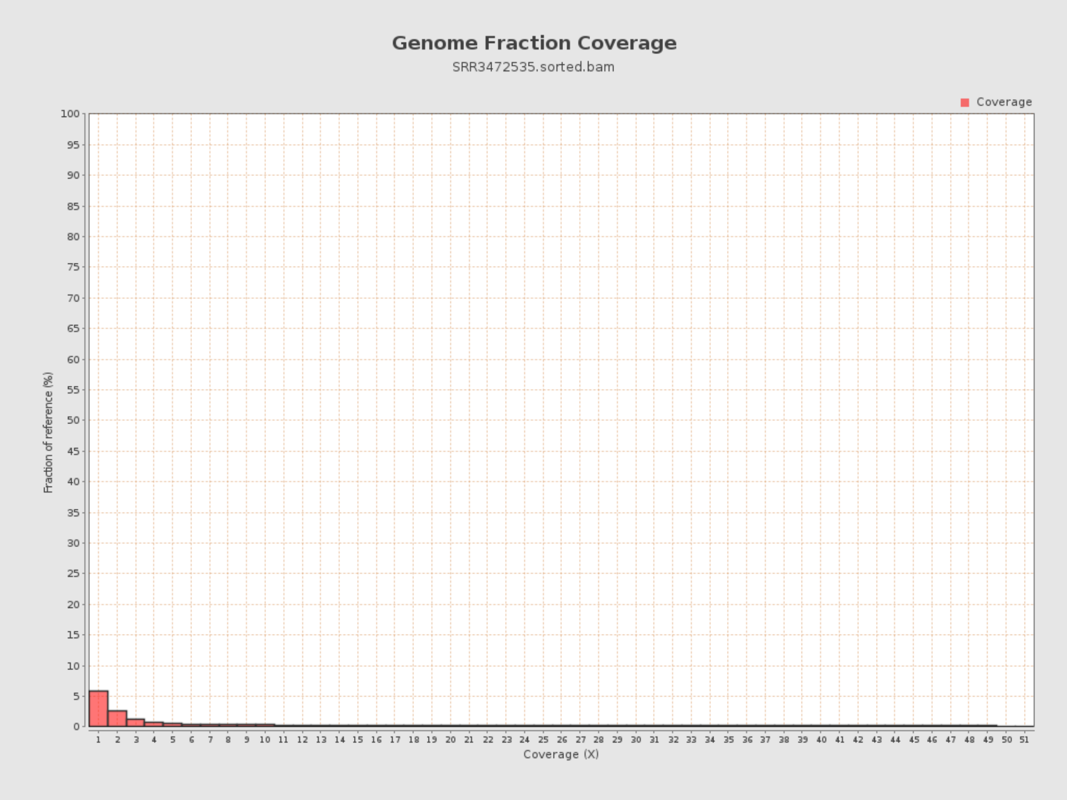
4. Results : Coverage Histogram



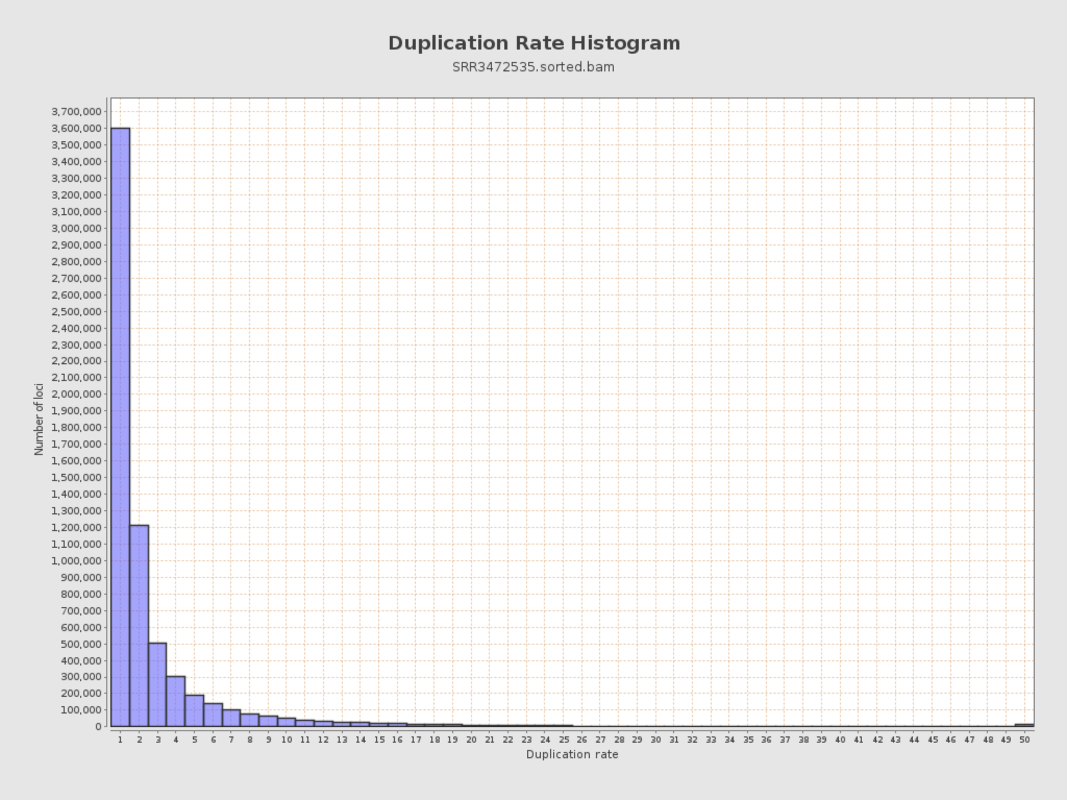
5. Results : Coverage Histogram (0-50X)



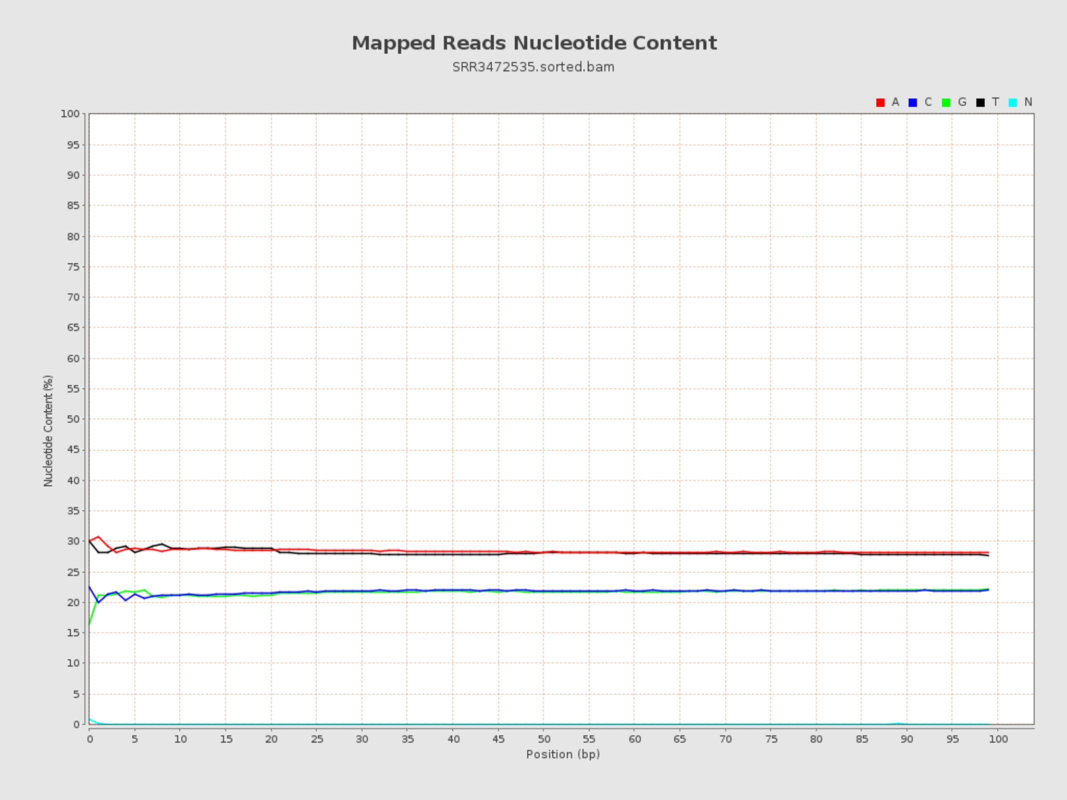
6. Results : Genome Fraction Coverage



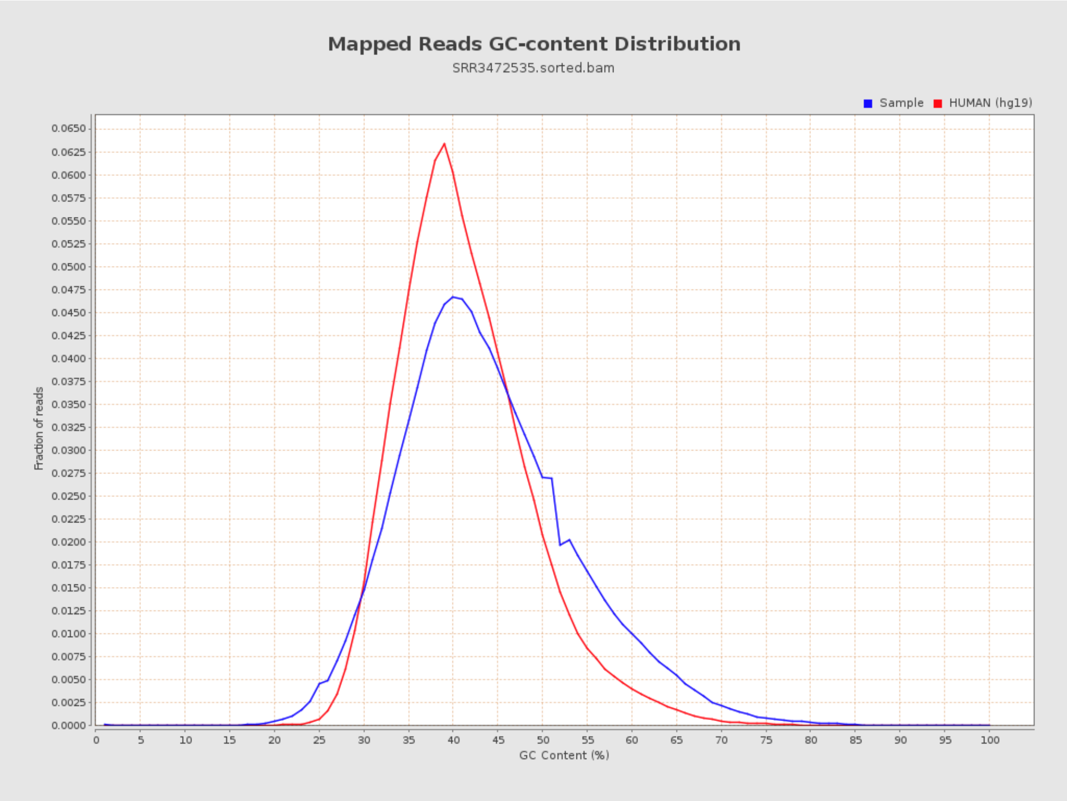
7. Results : Duplication Rate Histogram



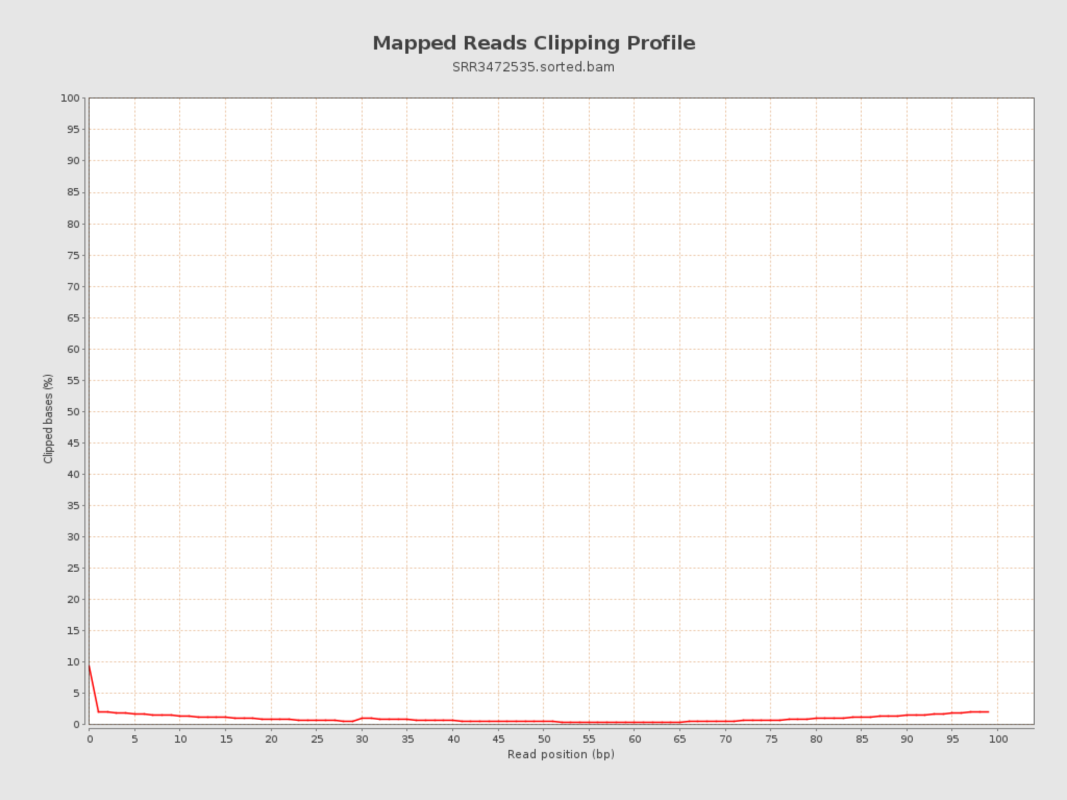
8. Results : Mapped Reads Nucleotide Content



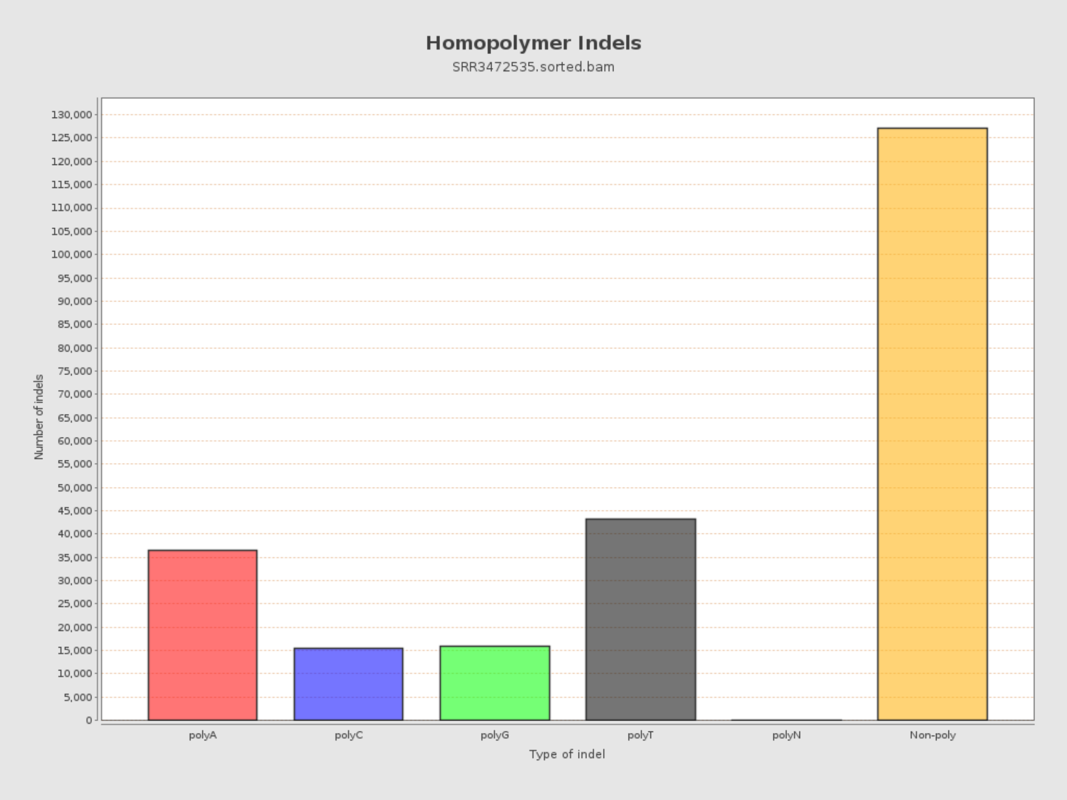
9. Results : Mapped Reads GC-content Distribution



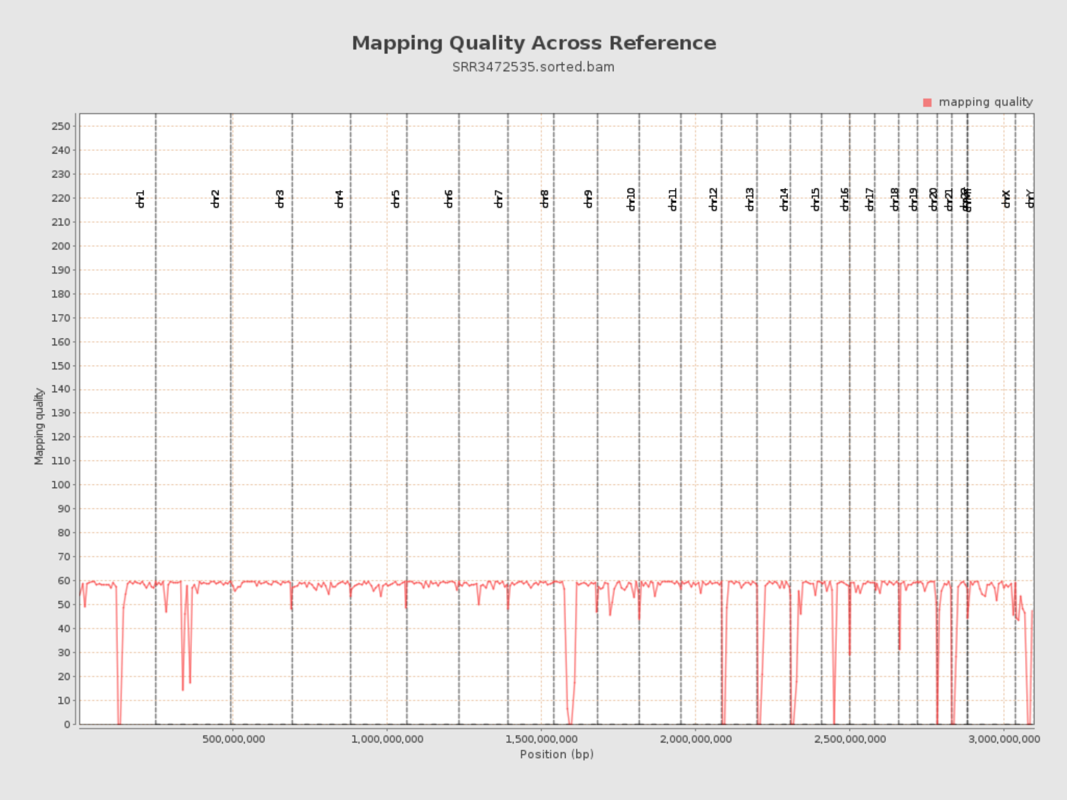
10. Results : Mapped Reads Clipping Profile



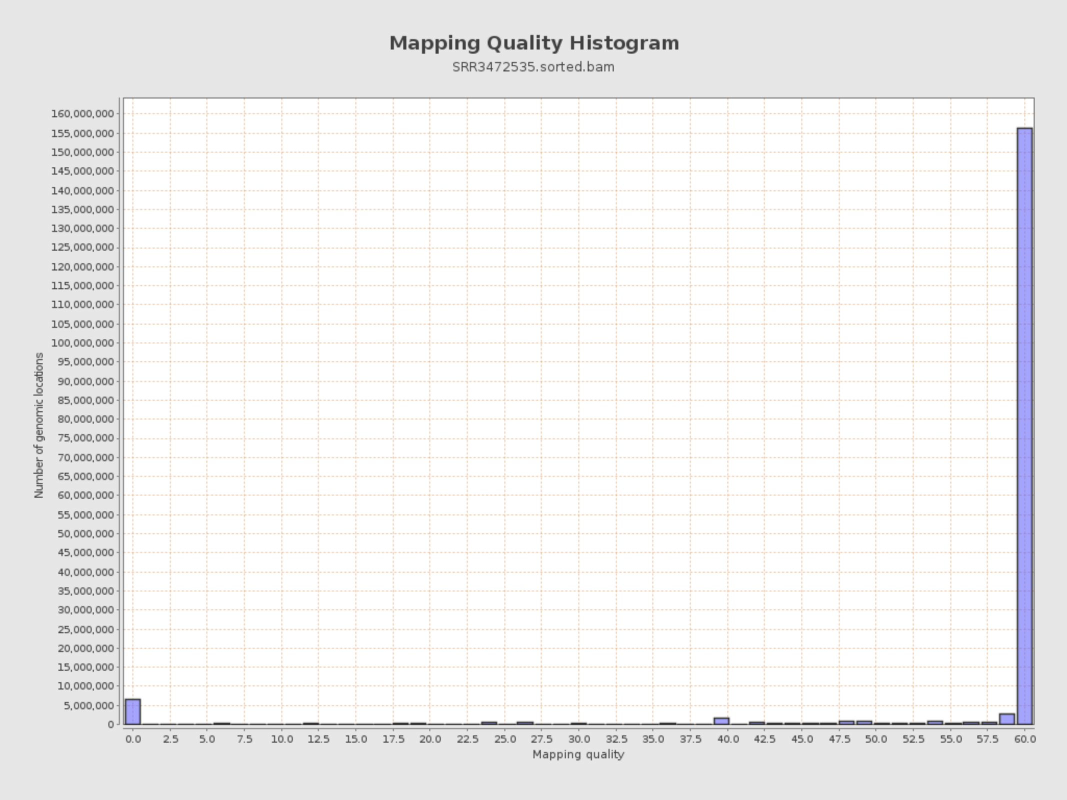
11. Results : Homopolymer Indels



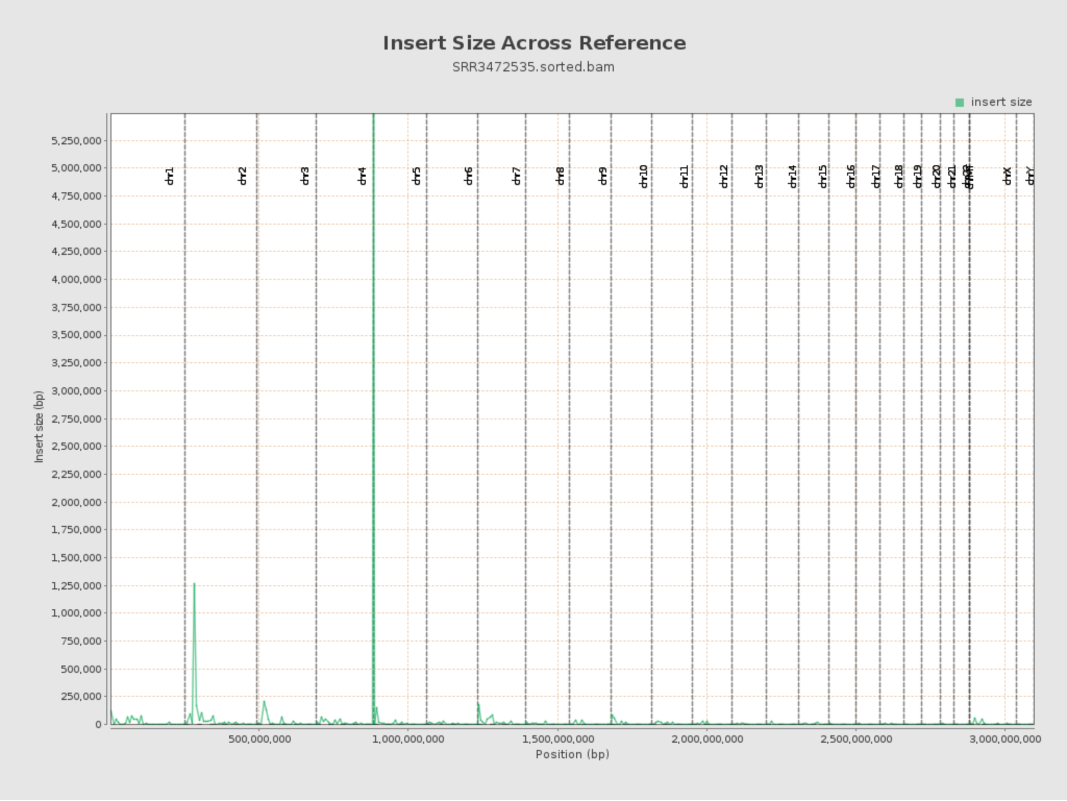
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram