Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:00:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472449.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_SRR3472449 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472449_1.fastq.gz SRR3472449_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:00:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472449.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,164,478
Mapped reads	17,010,403 / 99.1%
Unmapped reads	154,075 / 0.9%
Mapped paired reads	17,010,403 / 99.1%
Mapped reads, first in pair	8,528,150 / 49.68%
Mapped reads, second in pair	8,482,253 / 49.42%
Mapped reads, both in pair	16,922,726 / 98.59%
Mapped reads, singletons	87,677 / 0.51%
Secondary alignments	0
Supplementary alignments	66,483 / 0.39%
Read min/max/mean length	30 / 100 / 99.3
Duplicated reads (estimated)	10,559,620 / 61.52%
Duplication rate	47.09%
Clipped reads	1,281,140 / 7.46%

2.2. ACGT Content

Number/percentage of A's	457,485,480 / 27.49%
Number/percentage of C's	375,969,034 / 22.59%
Number/percentage of T's	458,251,508 / 27.54%
Number/percentage of G's	372,304,041 / 22.37%
Number/percentage of N's	206,708 / 0.01%

GC Percentage	44.96%

2.3. Coverage

Mean	0.5377
Standard Deviation	16.6456

2.4. Mapping Quality

Mean Mapping Quality	54.87

2.5. Insert size

Mean	18,664.87
Standard Deviation	1,357,234.41
P25/Median/P75	149 / 208 / 282

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	8,951,295
Insertions	102,492
Mapped reads with at least one insertion	0.6%
Deletions	80,482
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46.99%

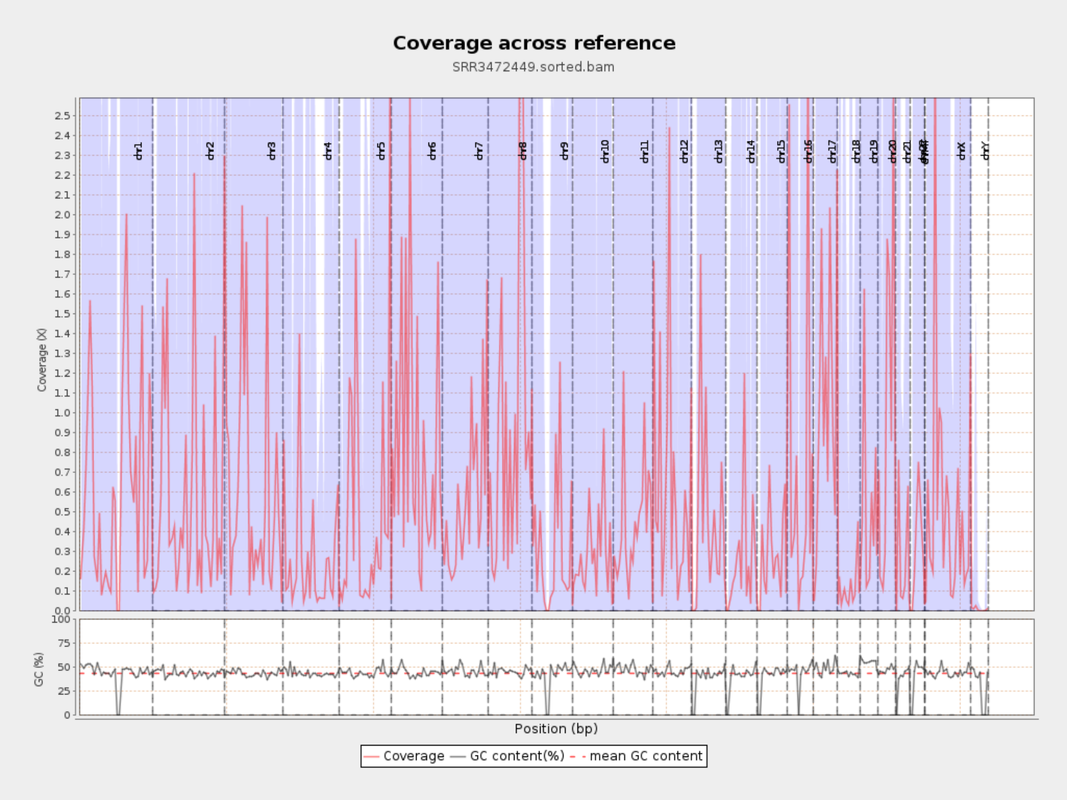
2.7. Chromosome stats

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

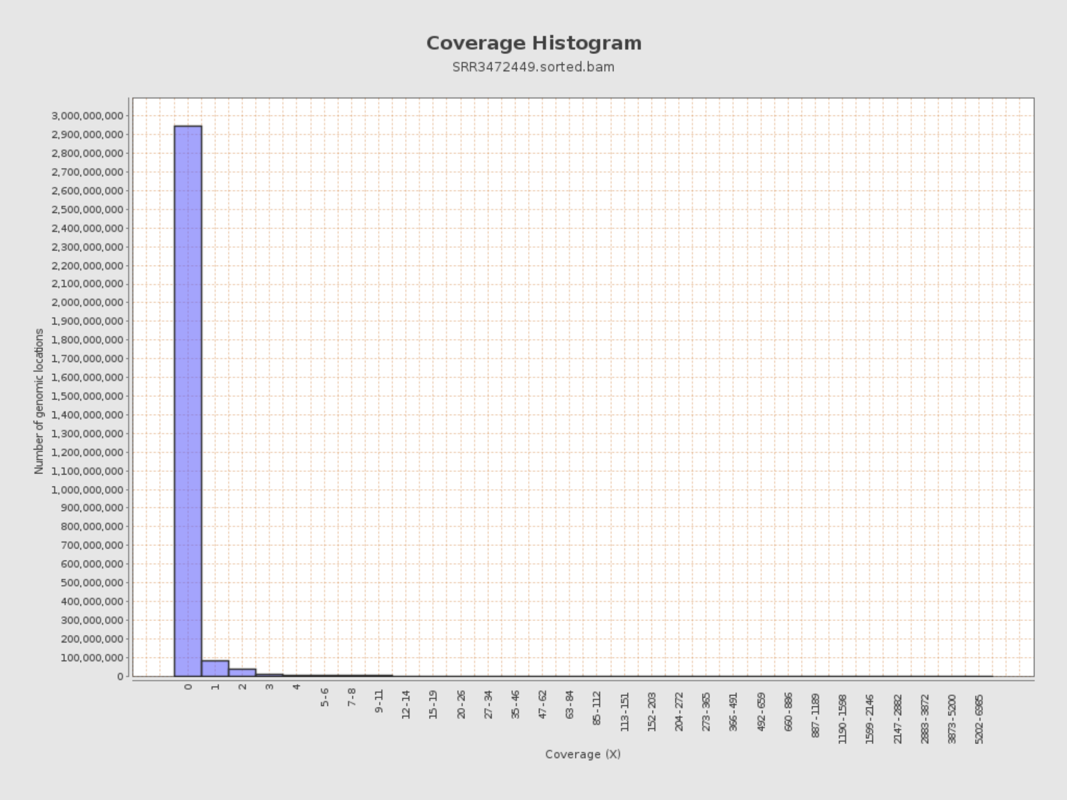
		bases	coverage	deviation
chr1	249250621	161197685	0.6467	18.5578
chr2	243199373	133393759	0.5485	18.4601
chr3	198022430	129295035	0.6529	16.1235
chr4	191154276	48065075	0.2514	9.8199
chr5	180915260	94563261	0.5227	24.7293
chr6	171115067	142418343	0.8323	18.8407
chr7	159138663	91190958	0.573	15.386
chr8	146364022	150317081	1.027	25.6399
chr9	141213431	44222596	0.3132	10.7849
chr10	135534747	39752086	0.2933	10.9212
chr11	135006516	60531986	0.4484	14.3687
chr12	133851895	87334253	0.6525	15.8996
chr13	115169878	54199724	0.4706	13.7231
chr14	107349540	26954069	0.2511	8.0203
chr15	102531392	28677881	0.2797	8.3194
chr16	90354753	72063643	0.7976	19.6972
chr17	81195210	82477188	1.0158	23.0484
chr18	78077248	9301078	0.1191	4.1758
chr19	59128983	32721035	0.5534	12.4736
chr20	63025520	63983179	1.0152	29.8545
chr21	48129895	13091581	0.272	13.4225
chr22	51304566	15885115	0.3096	9.5345
chrMT	16571	3406	0.2055	0.5522
chrX	155270560	82392783	0.5306	12.7863

chrY	59373566	372593	0.0063	0.6177

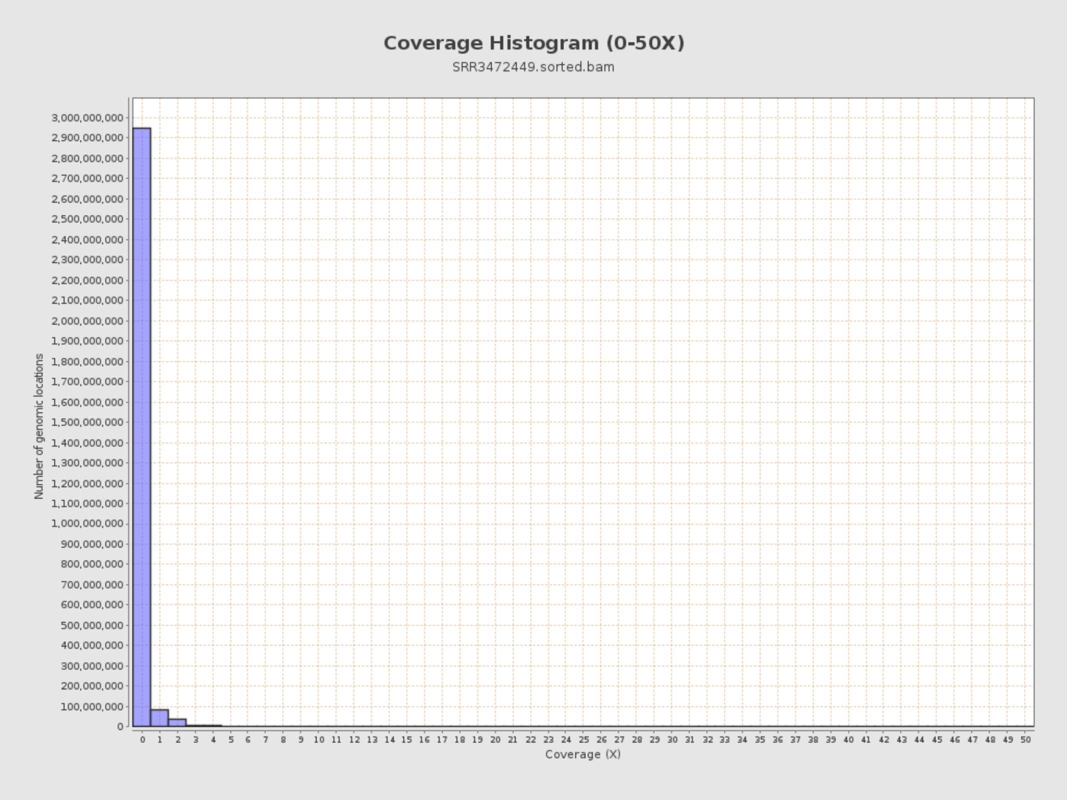
3. Results : Coverage across reference



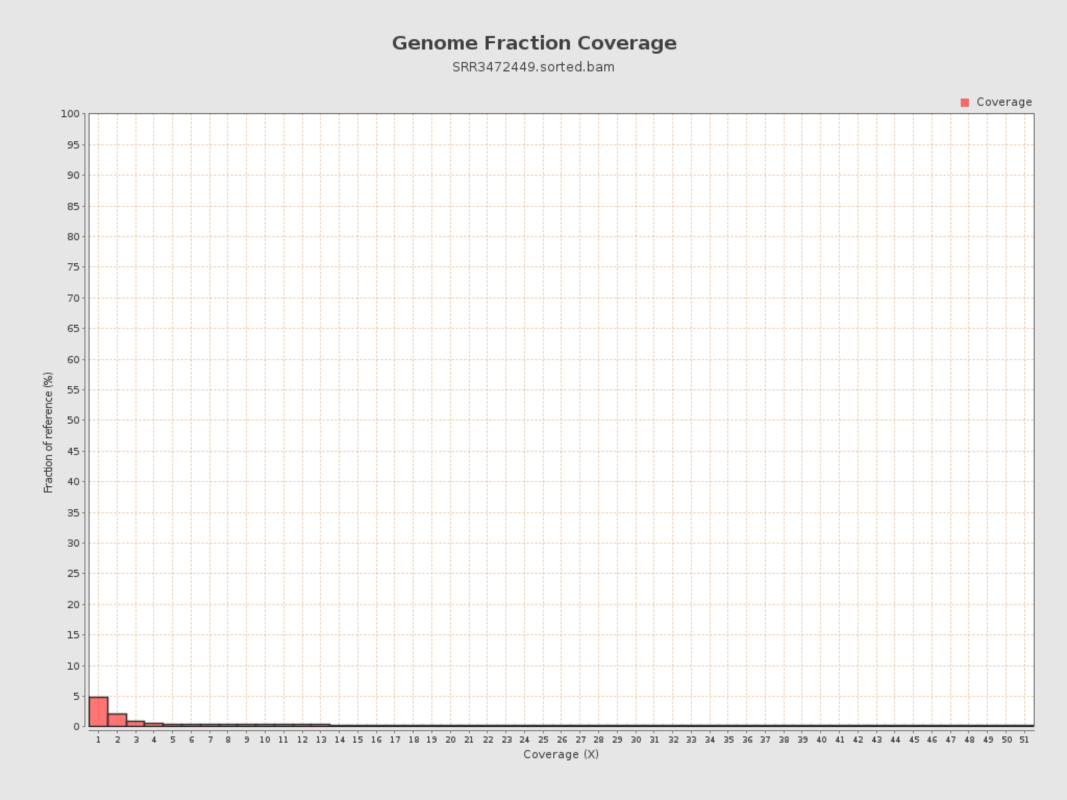
4. Results : Coverage Histogram



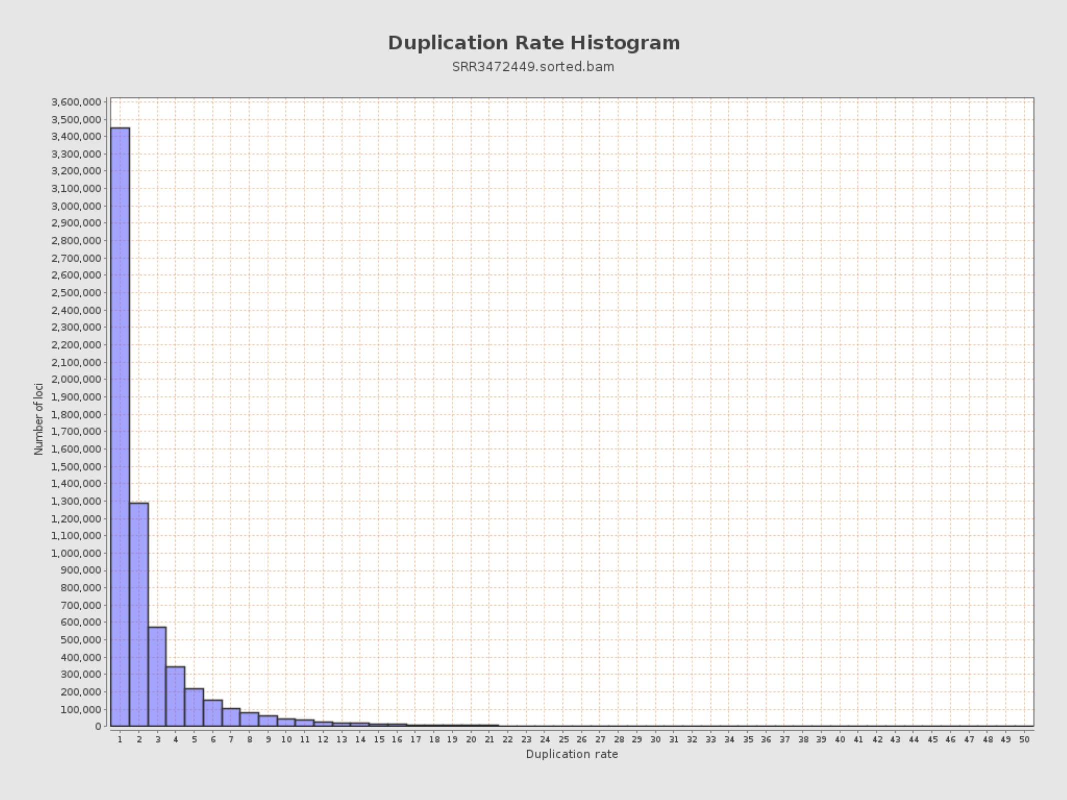
5. Results : Coverage Histogram (0-50X)



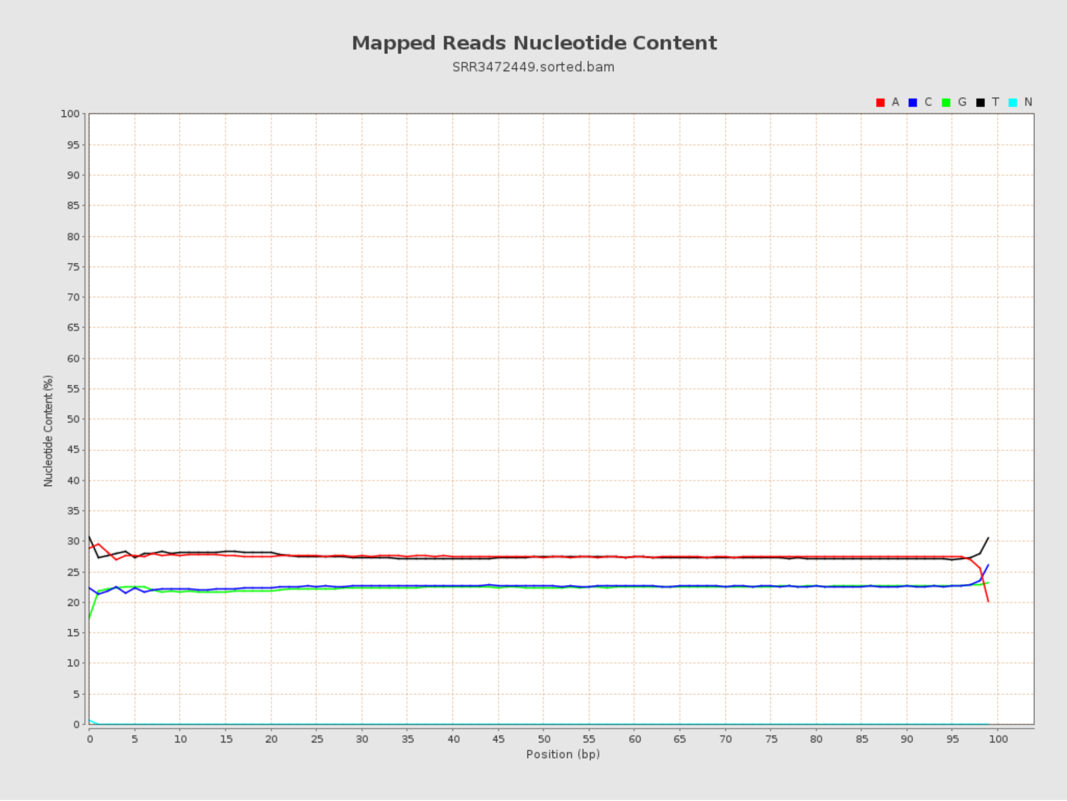
6. Results : Genome Fraction Coverage



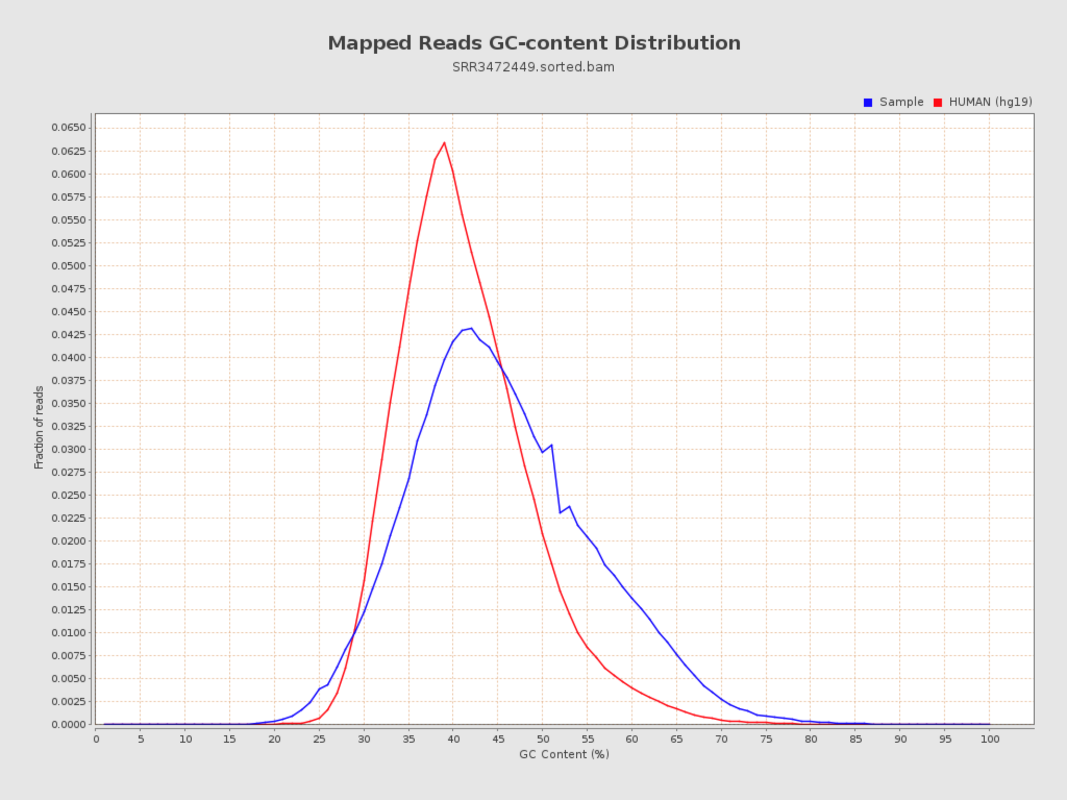
7. Results : Duplication Rate Histogram



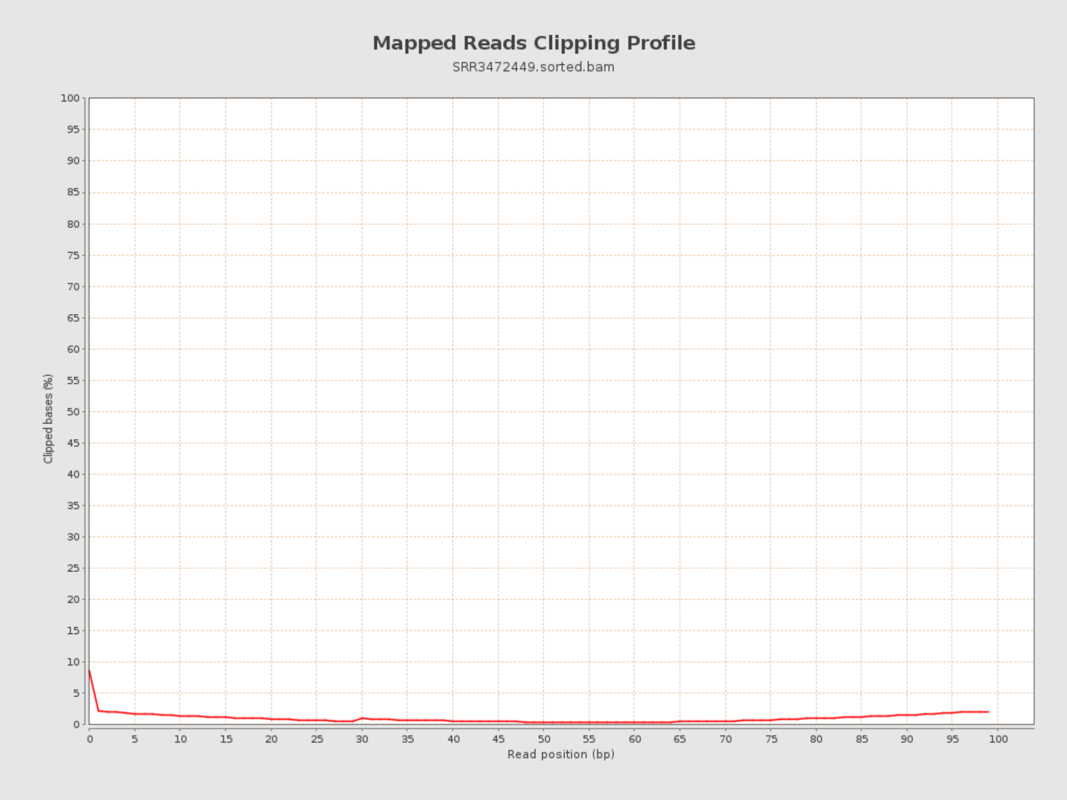
8. Results : Mapped Reads Nucleotide Content



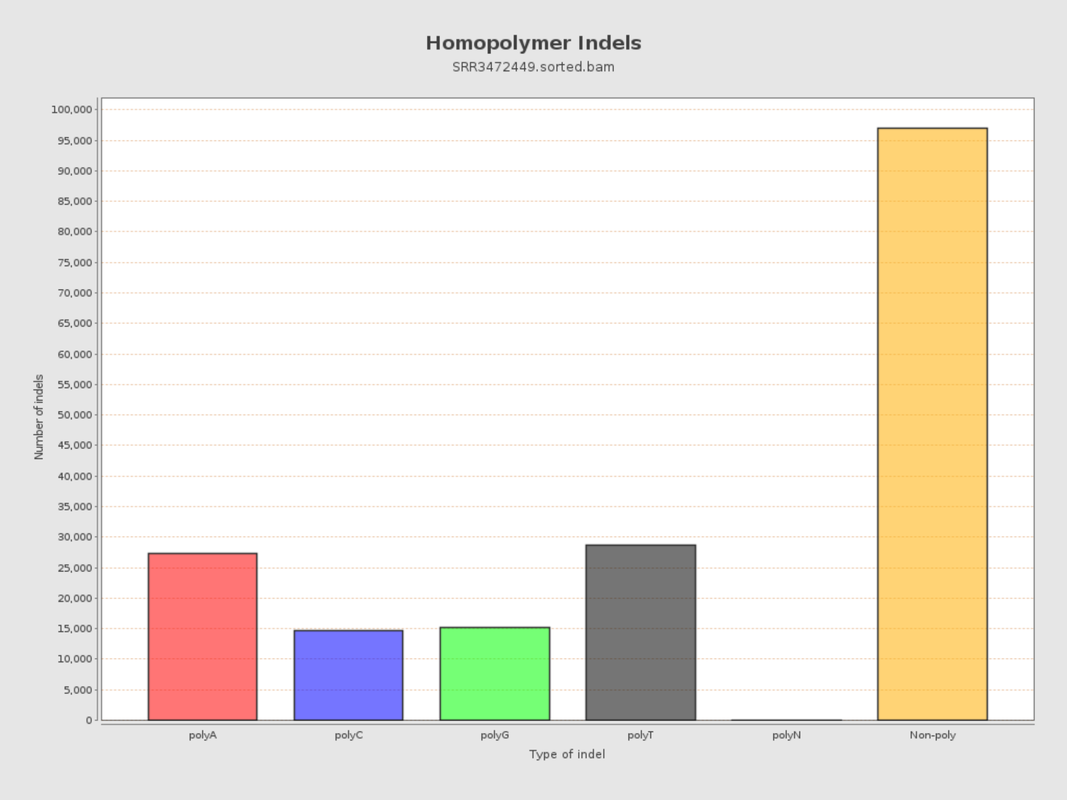
9. Results : Mapped Reads GC-content Distribution



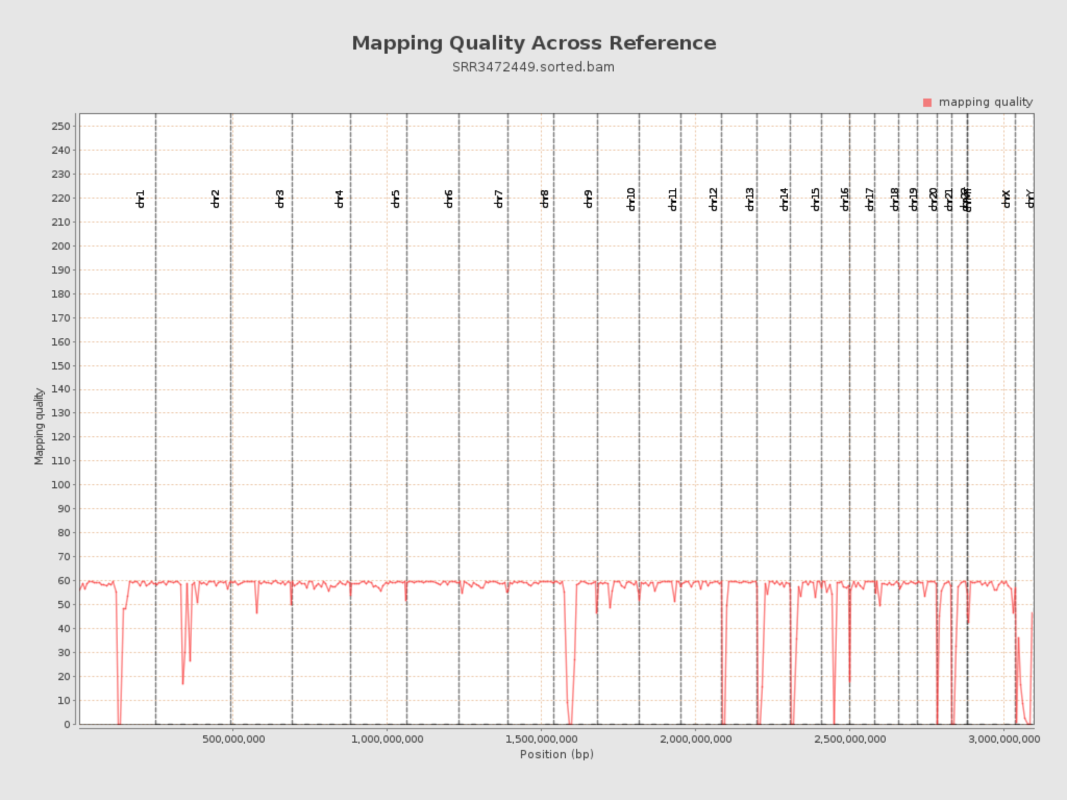
10. Results : Mapped Reads Clipping Profile



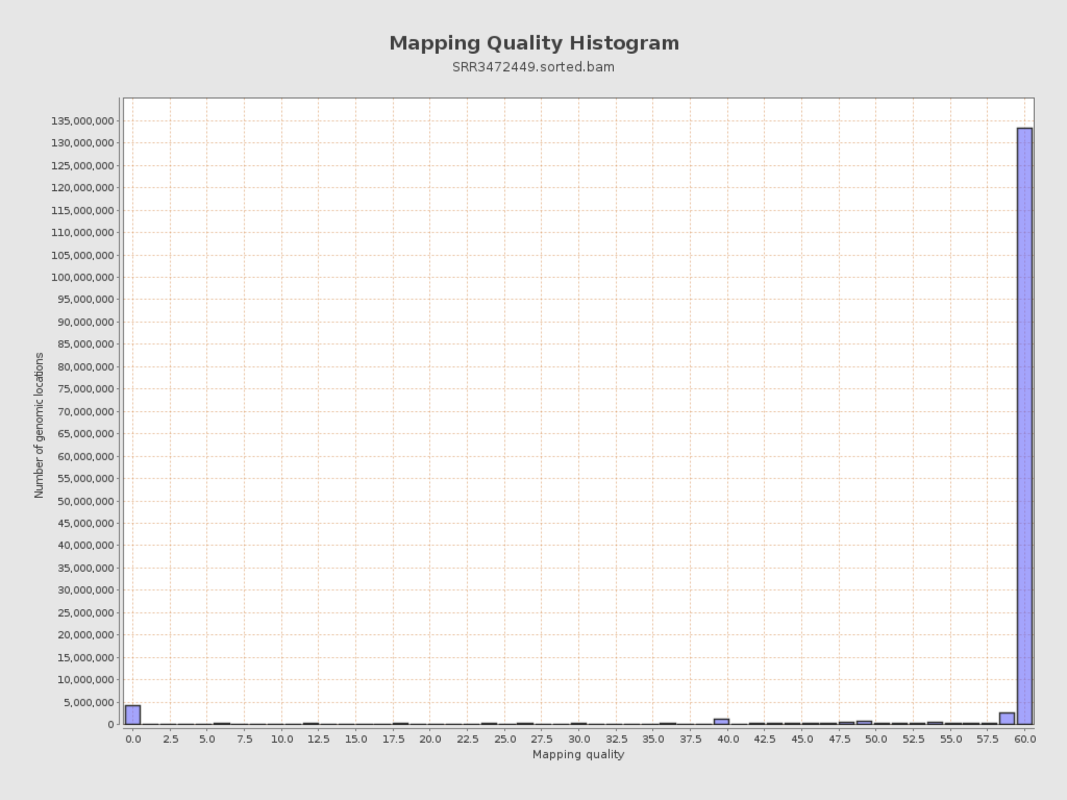
11. Results : Homopolymer Indels



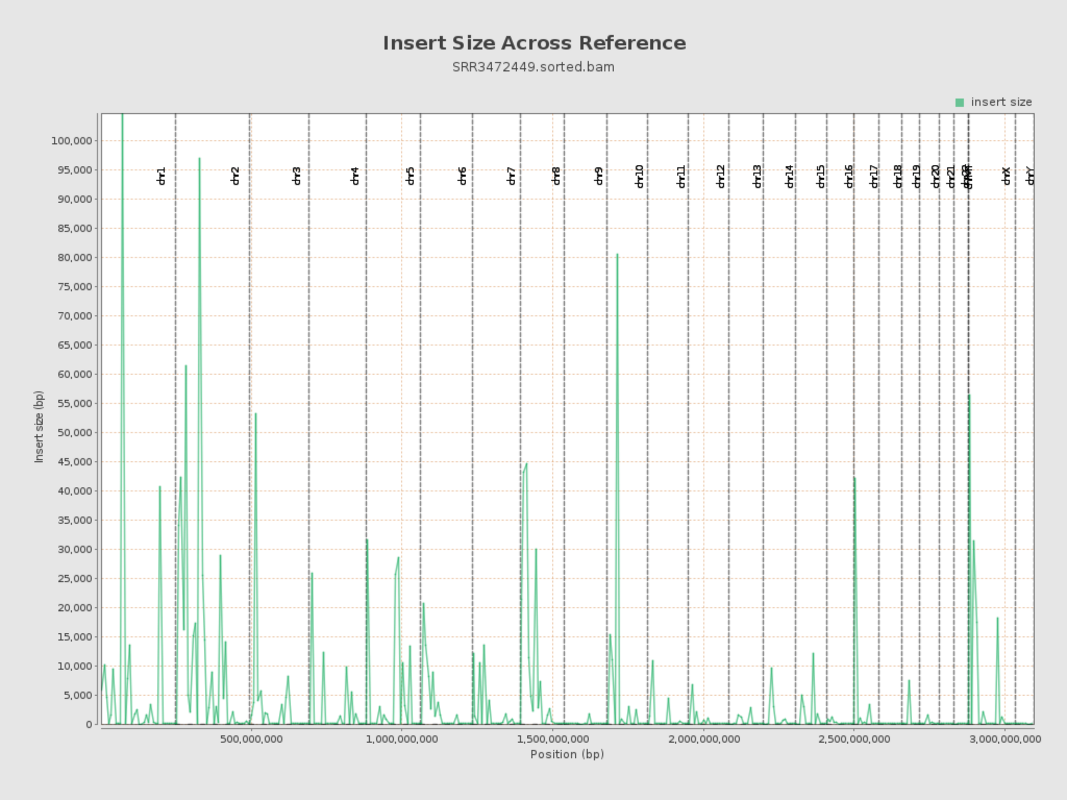
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram