Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:14:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472397.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_SRR3472397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472397_1.fastq.gz SRR3472397_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:14:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,121,624
Mapped reads	19,947,393 / 99.13%
Unmapped reads	174,231 / 0.87%
Mapped paired reads	19,947,393 / 99.13%
Mapped reads, first in pair	10,010,420 / 49.75%
Mapped reads, second in pair	9,936,973 / 49.38%
Mapped reads, both in pair	19,835,698 / 98.58%
Mapped reads, singletons	111,695 / 0.56%
Secondary alignments	0
Supplementary alignments	93,056 / 0.46%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	12,715,102 / 63.19%
Duplication rate	46.75%
Clipped reads	1,368,616 / 6.8%

2.2. ACGT Content

Number/percentage of A's	534,843,356 / 27.32%
Number/percentage of C's	445,326,311 / 22.75%
Number/percentage of T's	536,610,106 / 27.41%
Number/percentage of G's	440,617,682 / 22.51%
Number/percentage of N's	234,433 / 0.01%

GC Percentage	45.26%

2.3. Coverage

Mean	0.6324
Standard Deviation	19.8508

2.4. Mapping Quality

Mean Mapping Quality	54.82

2.5. Insert size

Mean	26,376.99
Standard Deviation	1,601,703.59
P25/Median/P75	163 / 231 / 314

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	10,844,142
Insertions	116,751
Mapped reads with at least one insertion	0.58%
Deletions	95,181
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46.58%

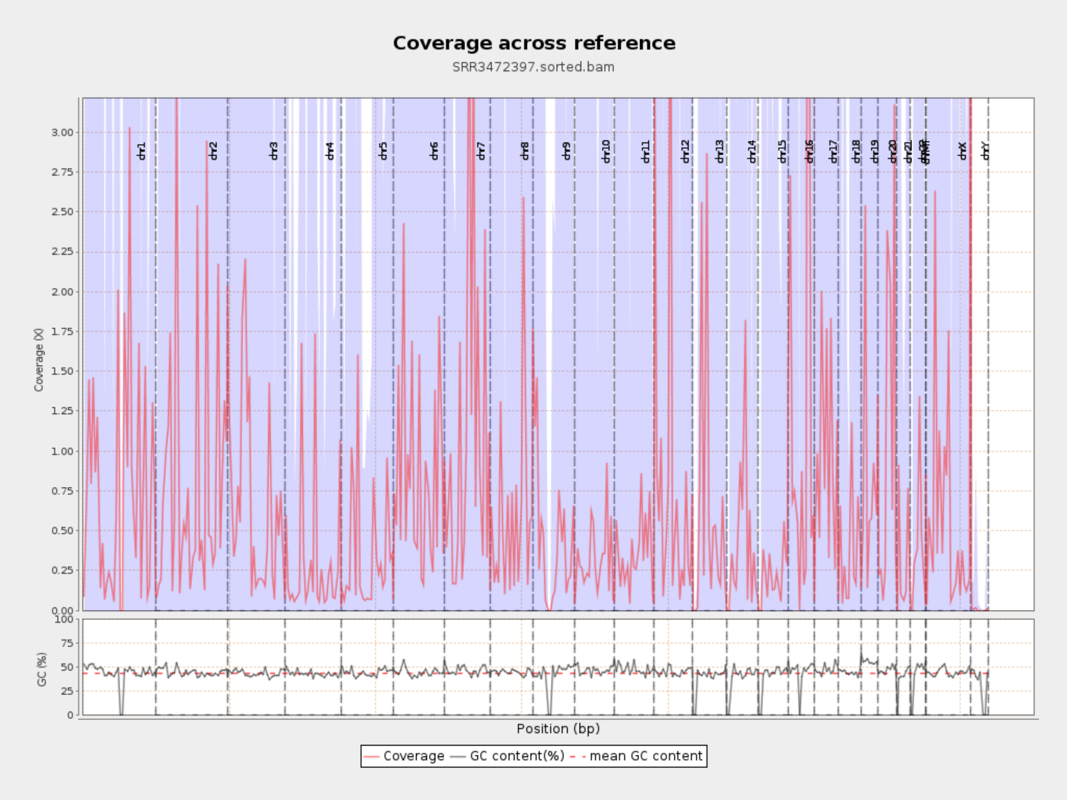
2.7. Chromosome stats

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

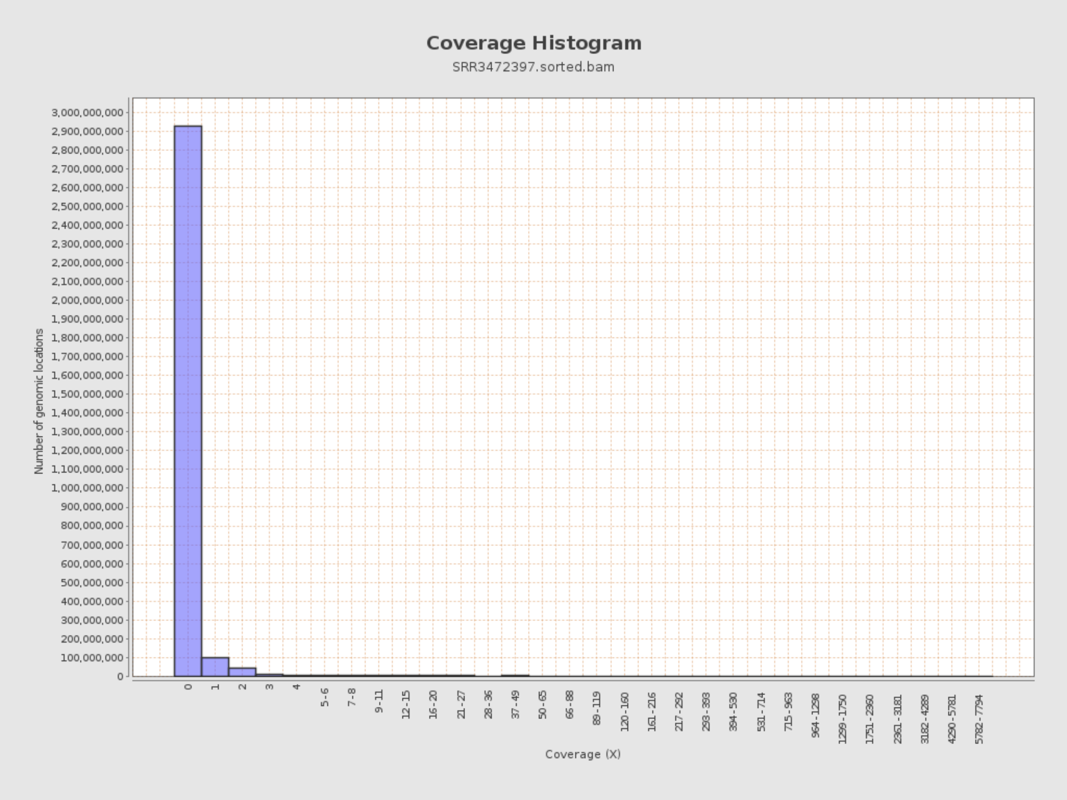
		bases	coverage	deviation
chr1	249250621	189412760	0.7599	20.6136
chr2	243199373	197701428	0.8129	24.0133
chr3	198022430	134000693	0.6767	15.3318
chr4	191154276	60855836	0.3184	15.6652
chr5	180915260	63103359	0.3488	9.9851
chr6	171115067	148120758	0.8656	19.2925
chr7	159138663	182546566	1.1471	34.9882
chr8	146364022	90454390	0.618	16.3751
chr9	141213431	59929639	0.4244	12.1399
chr10	135534747	45736437	0.3375	9.957
chr11	135006516	48581798	0.3598	10.7332
chr12	133851895	115598049	0.8636	29.5973
chr13	115169878	73362369	0.637	19.5328
chr14	107349540	45317190	0.4221	14.2352
chr15	102531392	21488346	0.2096	6.4545
chr16	90354753	112846332	1.2489	36.8939
chr17	81195210	79948784	0.9846	21.3572
chr18	78077248	28894117	0.3701	11.8319
chr19	59128983	48920472	0.8274	15.6105
chr20	63025520	70579978	1.1199	32.9664
chr21	48129895	15752230	0.3273	15.6388
chr22	51304566	21251746	0.4142	14.0818
chrMT	16571	14111	0.8515	1.1039
chrX	155270560	103097864	0.664	18.1923

chrY	59373566	335716	0.0057	0.3917

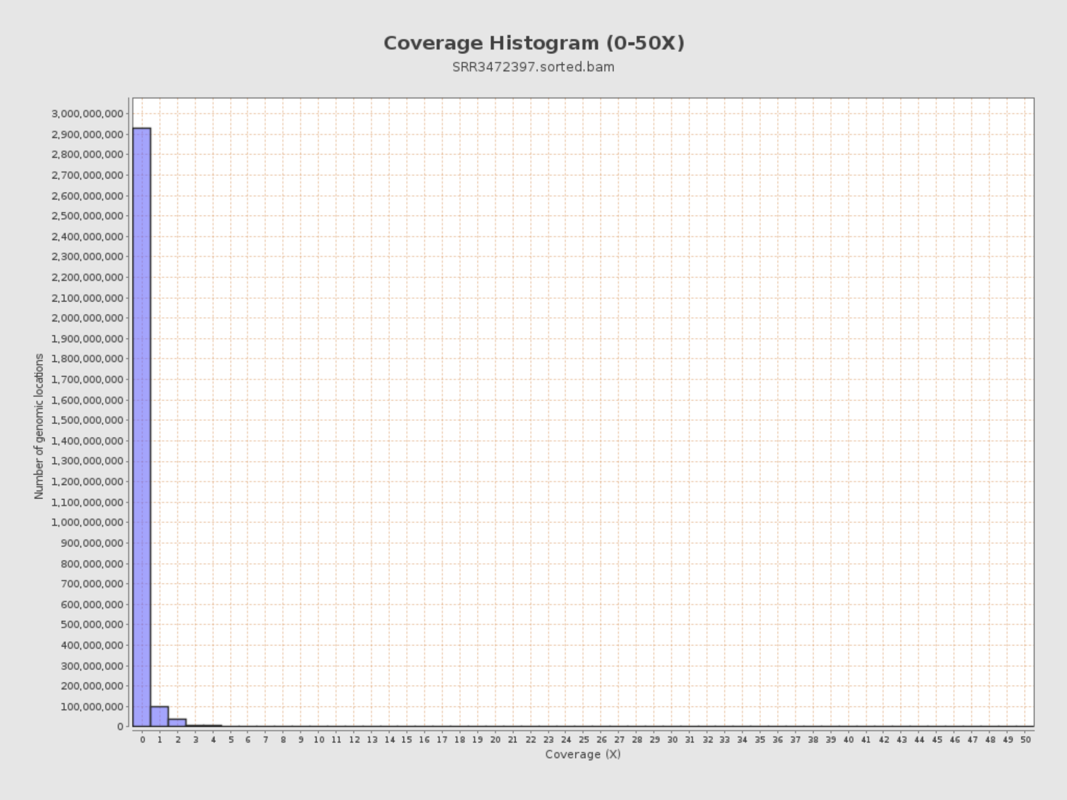
3. Results : Coverage across reference



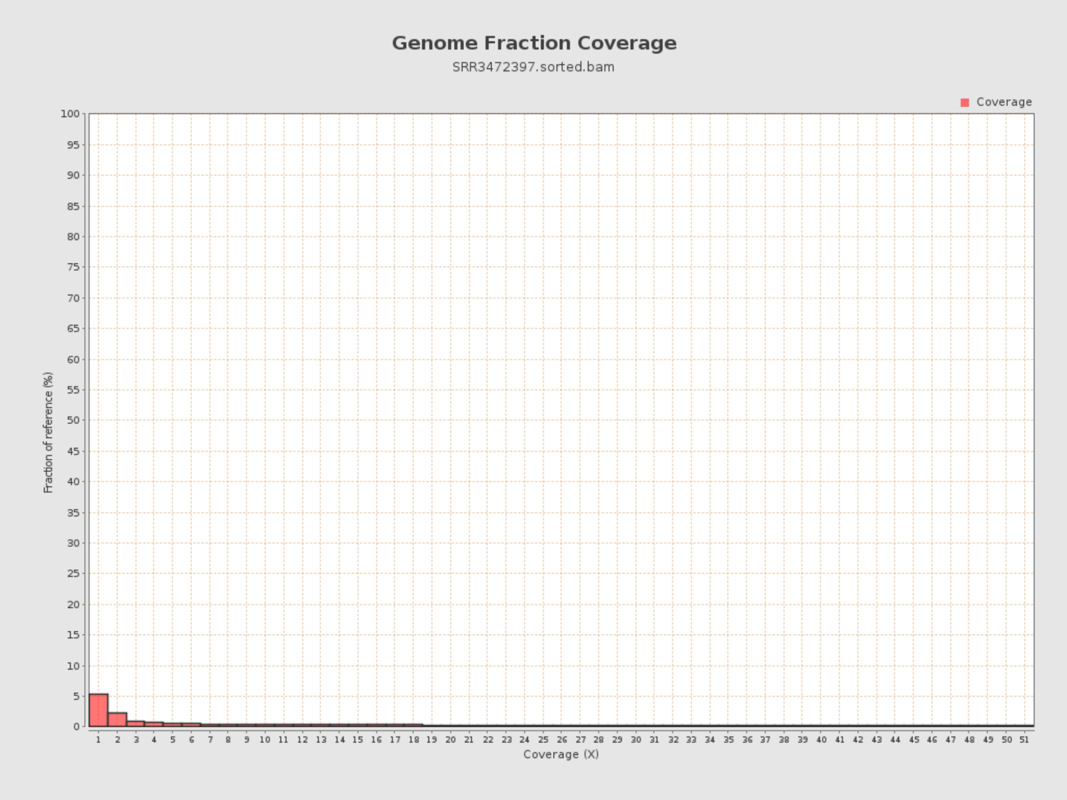
4. Results : Coverage Histogram



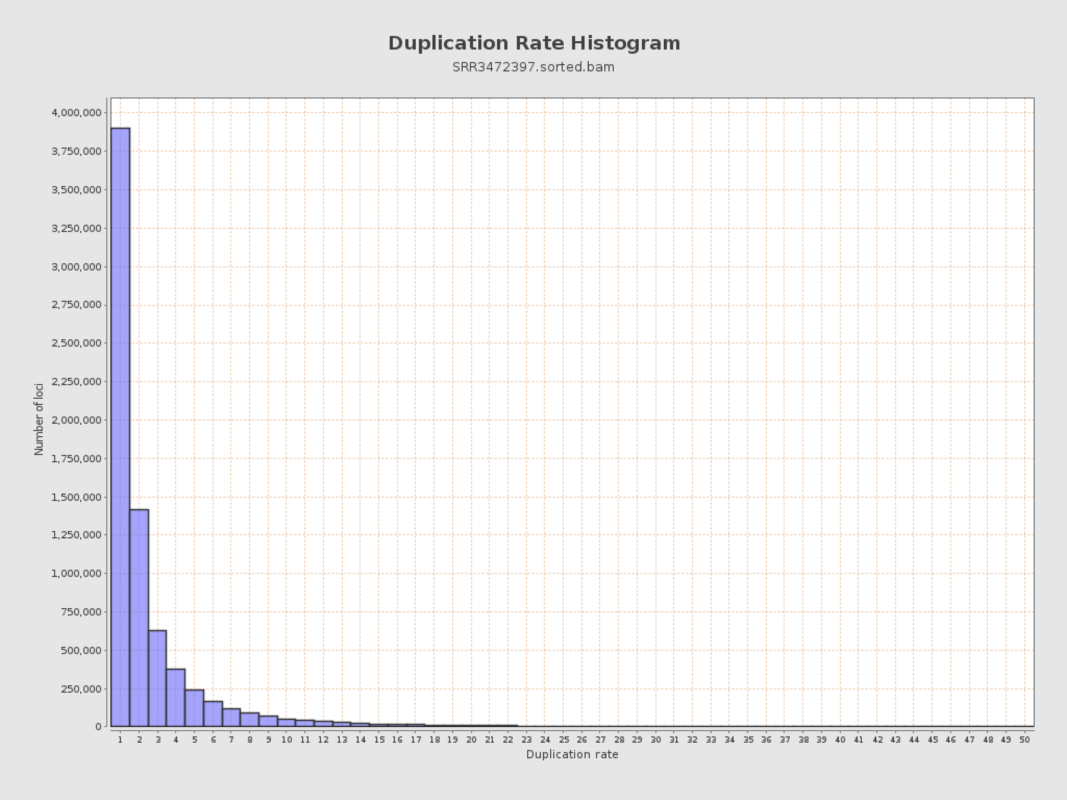
5. Results : Coverage Histogram (0-50X)



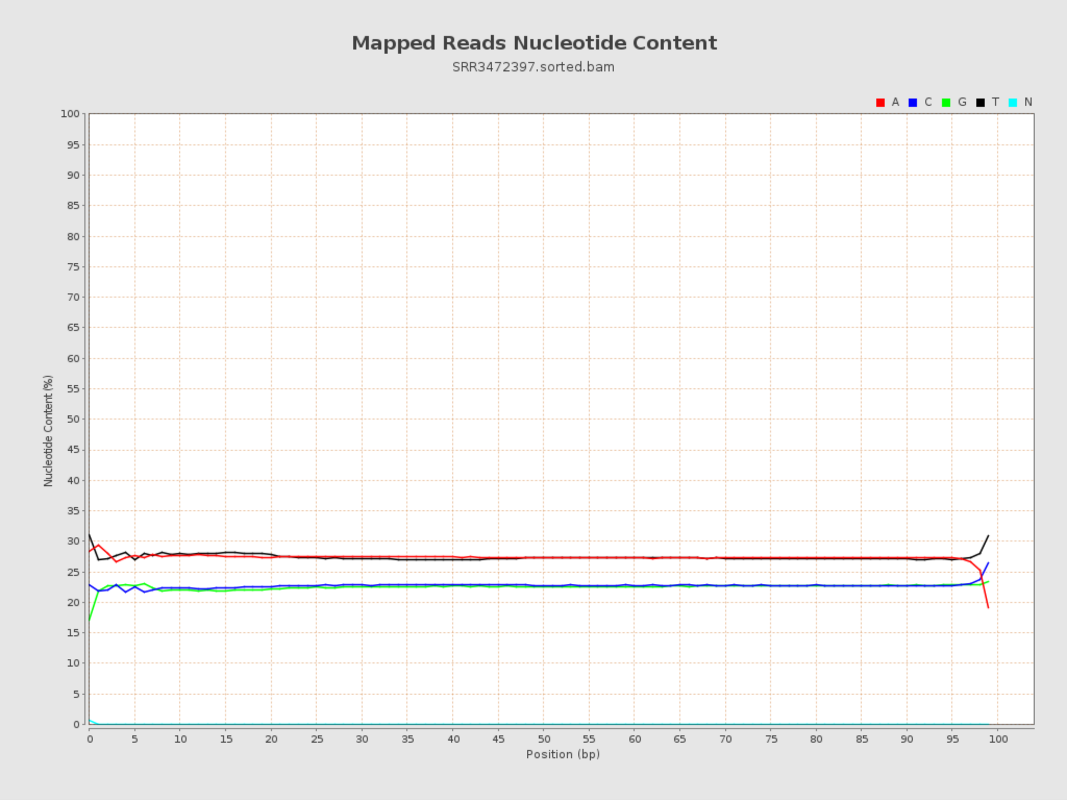
6. Results : Genome Fraction Coverage



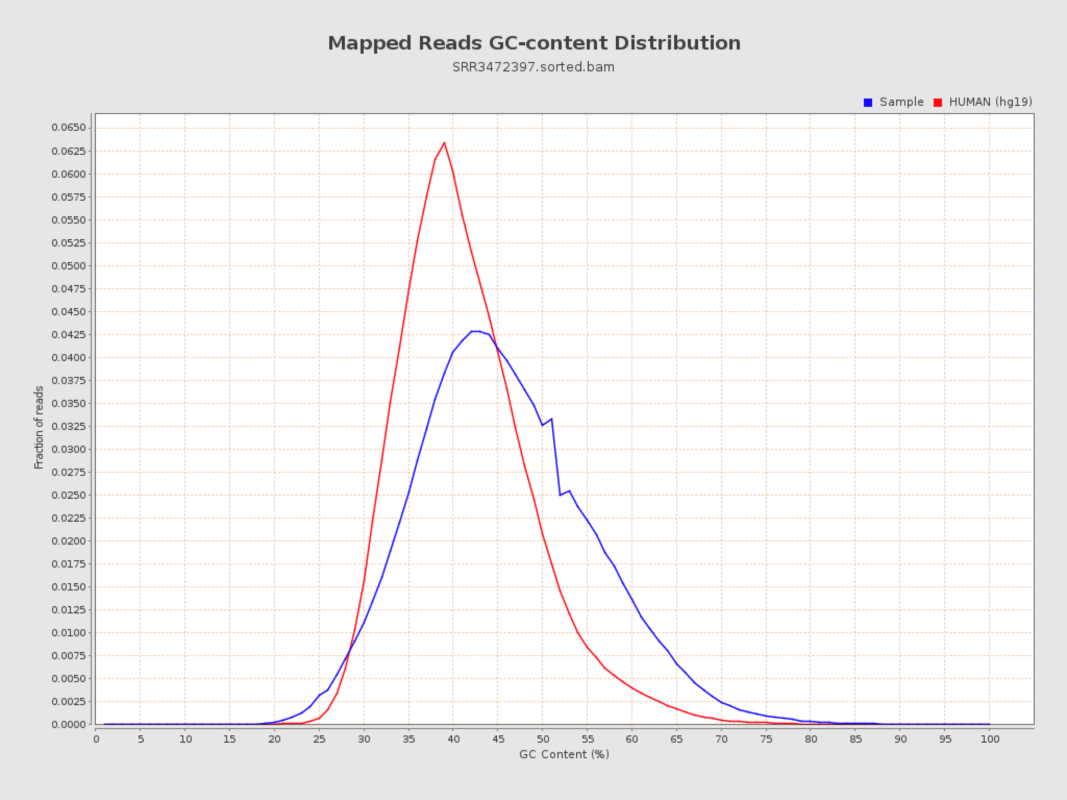
7. Results : Duplication Rate Histogram



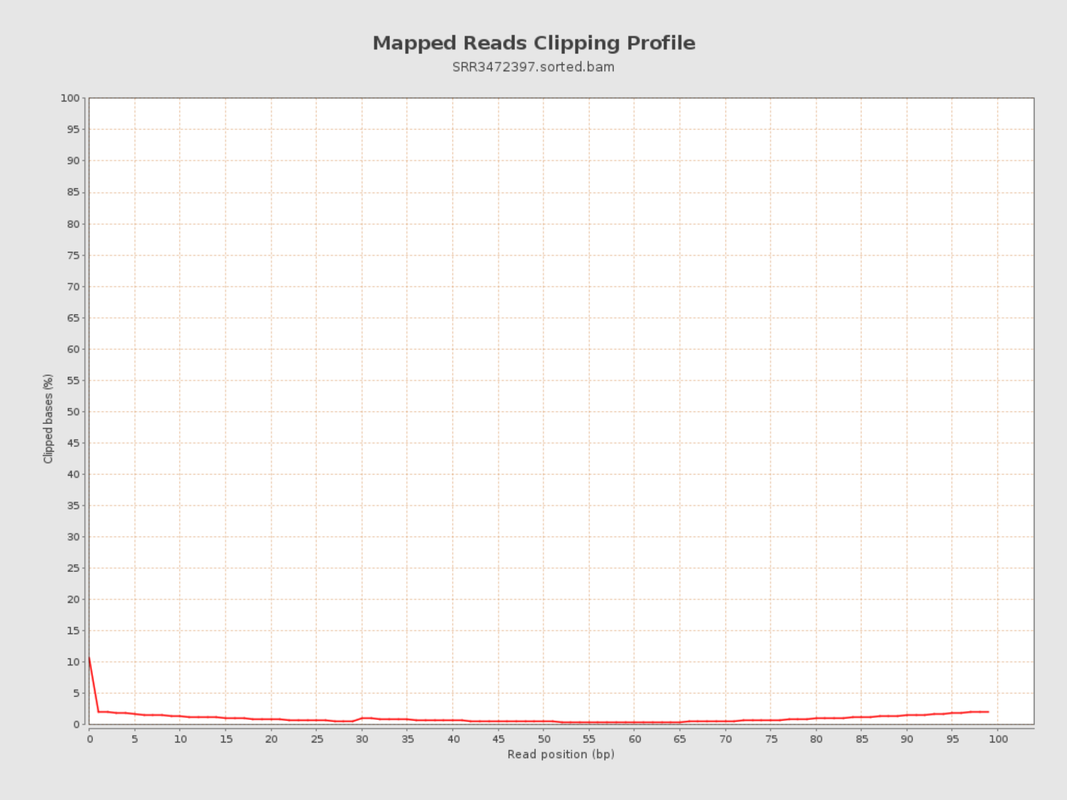
8. Results : Mapped Reads Nucleotide Content



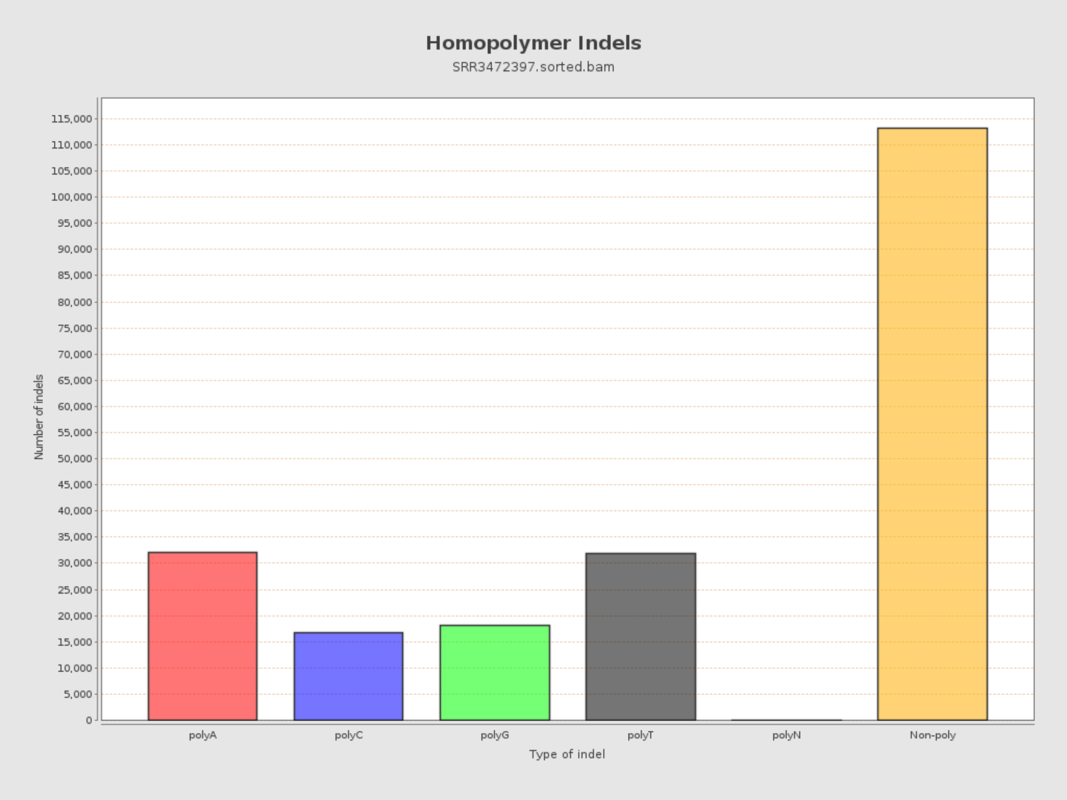
9. Results : Mapped Reads GC-content Distribution



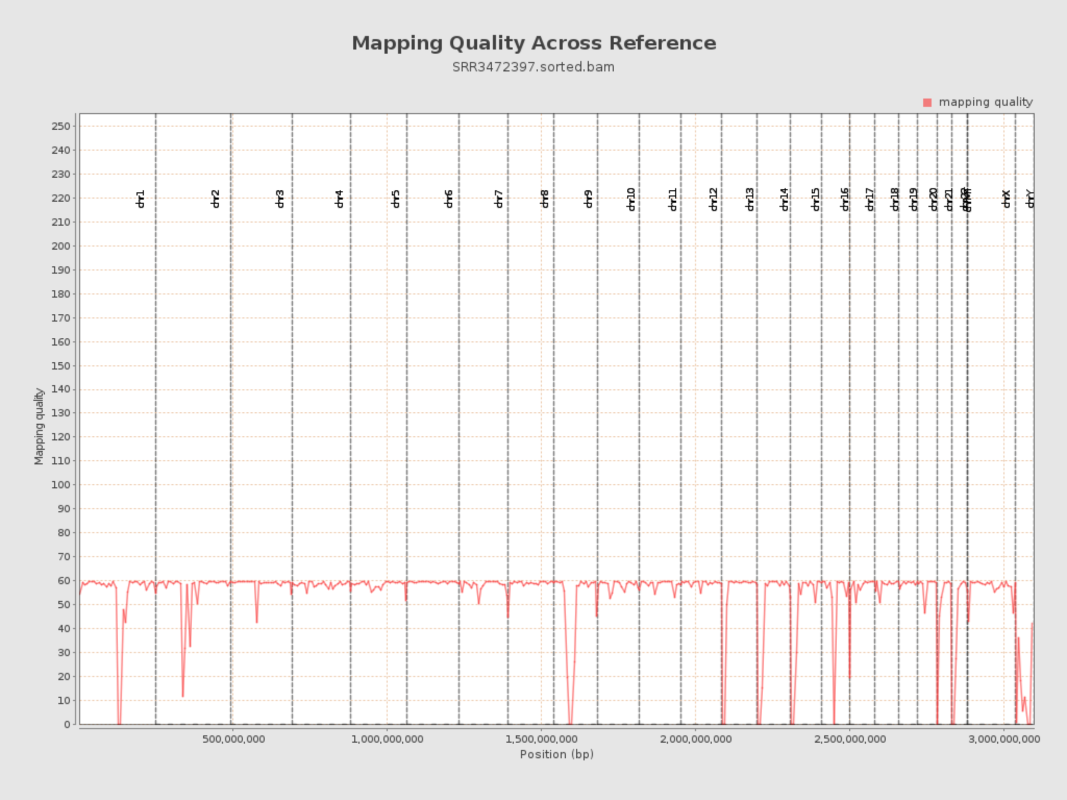
10. Results : Mapped Reads Clipping Profile



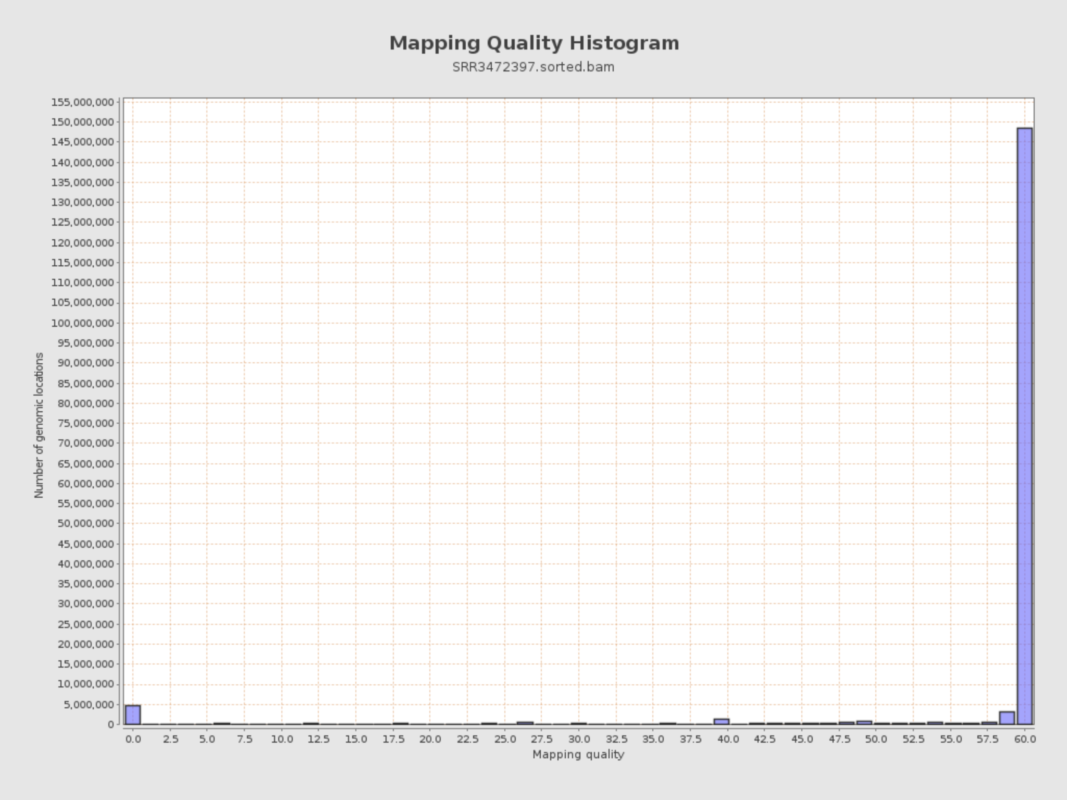
11. Results : Homopolymer Indels



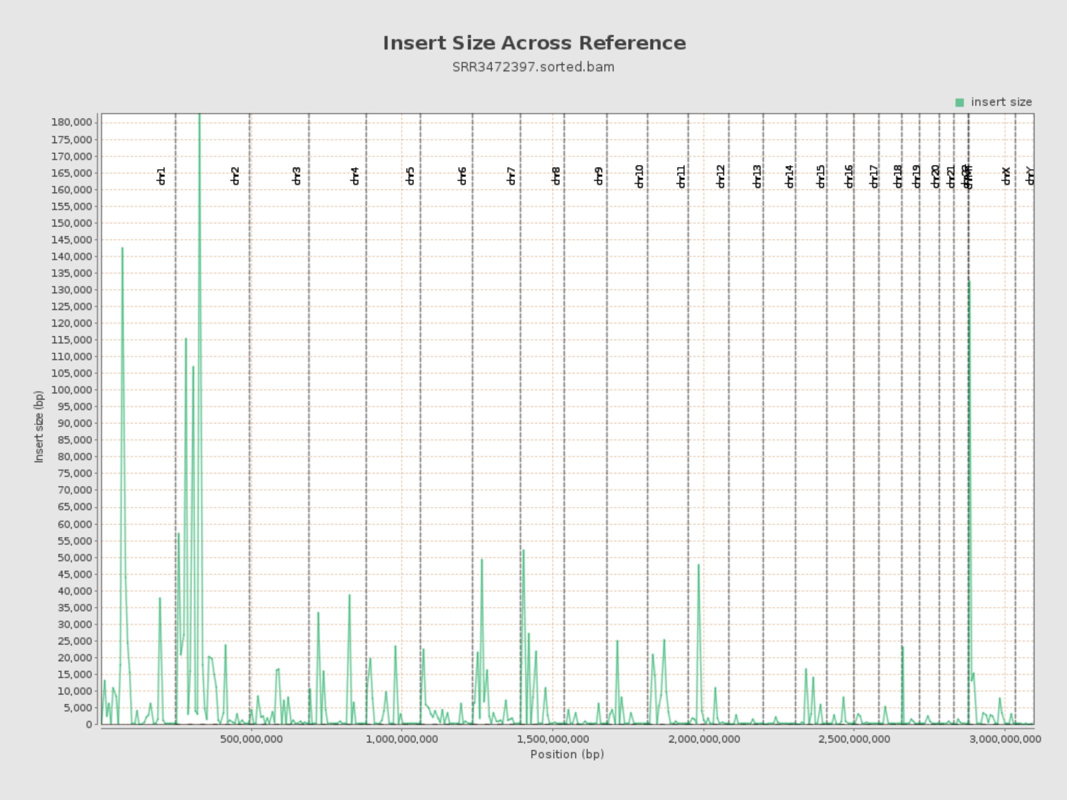
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram