Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:53:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472389.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_SRR3472389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472389_1.fastq.gz SRR3472389_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:53:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,594,778
Mapped reads	20,402,363 / 99.07%
Unmapped reads	192,415 / 0.93%
Mapped paired reads	20,402,363 / 99.07%
Mapped reads, first in pair	10,234,791 / 49.7%
Mapped reads, second in pair	10,167,572 / 49.37%
Mapped reads, both in pair	20,288,650 / 98.51%
Mapped reads, singletons	113,713 / 0.55%
Secondary alignments	0
Supplementary alignments	99,617 / 0.48%
Read min/max/mean length	30 / 100 / 99.58
Duplicated reads (estimated)	13,297,374 / 64.57%
Duplication rate	47.47%
Clipped reads	1,494,337 / 7.26%

2.2. ACGT Content

Number/percentage of A's	541,342,729 / 27.01%
Number/percentage of C's	461,514,202 / 23.03%
Number/percentage of T's	541,742,528 / 27.03%
Number/percentage of G's	459,168,273 / 22.91%
Number/percentage of N's	256,449 / 0.01%

GC Percentage	45.94%

2.3. Coverage

Mean	0.6474
Standard Deviation	21.0368

2.4. Mapping Quality

Mean Mapping Quality	54.73

2.5. Insert size

Mean	24,449.29
Standard Deviation	1,544,023.89
P25/Median/P75	162 / 227 / 306

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	11,464,400
Insertions	123,455
Mapped reads with at least one insertion	0.6%
Deletions	97,359
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.86%

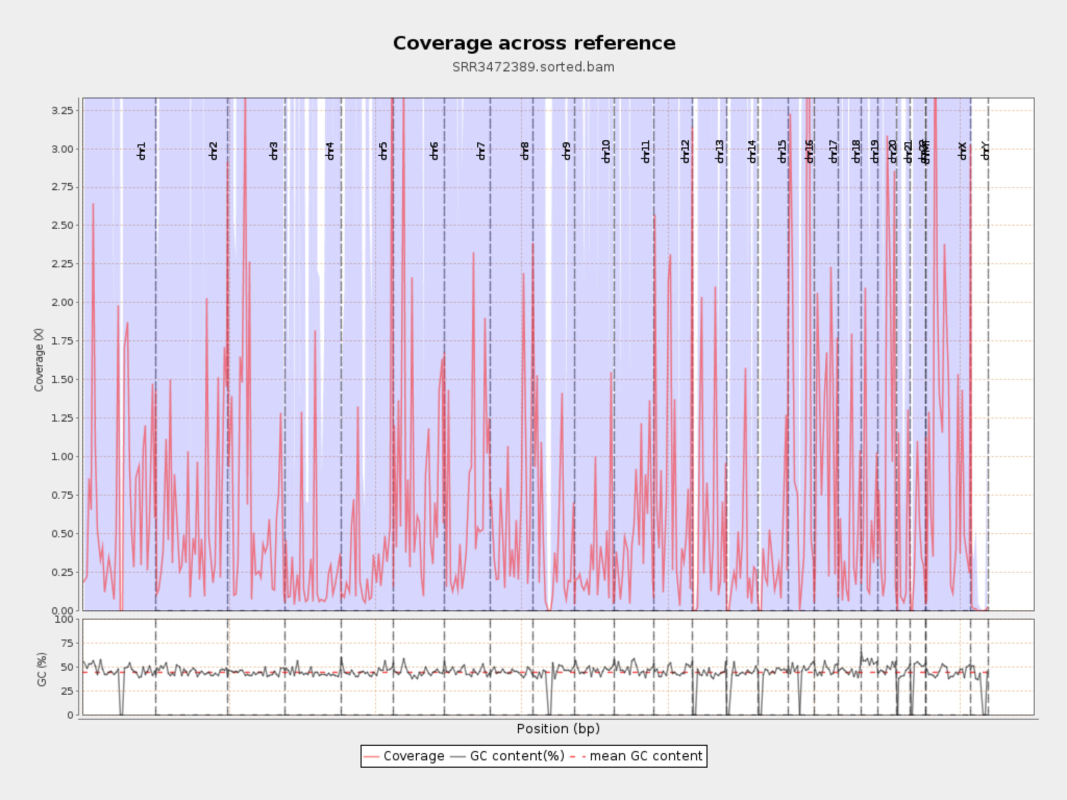
2.7. Chromosome stats

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

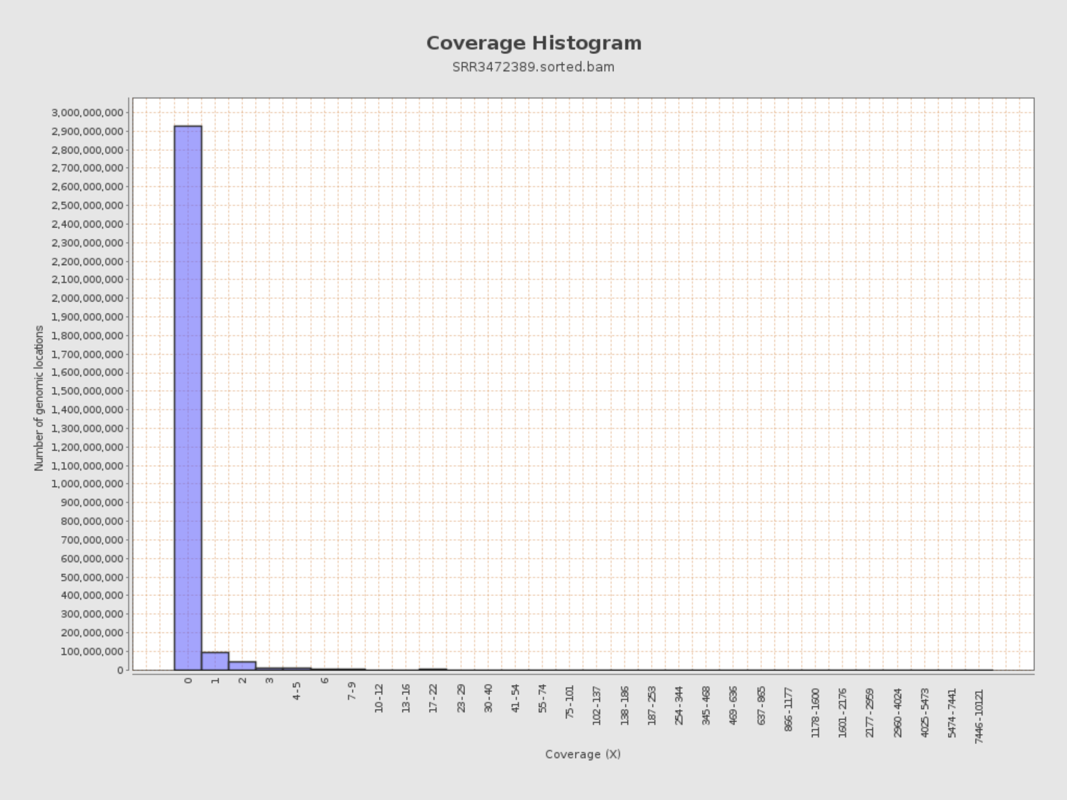
		bases	coverage	deviation
chr1	249250621	179984933	0.7221	20.5556
chr2	243199373	149630855	0.6153	17.8927
chr3	198022430	151657879	0.7659	20.657
chr4	191154276	52753312	0.276	12.4361
chr5	180915260	85117147	0.4705	22.9992
chr6	171115067	150866424	0.8817	21.9379
chr7	159138663	113874048	0.7156	23.9395
chr8	146364022	90405847	0.6177	18.8211
chr9	141213431	65913128	0.4668	12.3451
chr10	135534747	47179514	0.3481	14.8358
chr11	135006516	67954734	0.5033	16.0773
chr12	133851895	114851785	0.8581	22.4725
chr13	115169878	68903832	0.5983	21.417
chr14	107349540	32712422	0.3047	9.7013
chr15	102531392	34860952	0.34	11.5296
chr16	90354753	125900042	1.3934	36.5198
chr17	81195210	98449075	1.2125	35.199
chr18	78077248	35898429	0.4598	19.487
chr19	59128983	37978971	0.6423	18.4863
chr20	63025520	79309209	1.2584	35.7849
chr21	48129895	21741860	0.4517	22.7124
chr22	51304566	19772699	0.3854	12.7893
chrMT	16571	18670	1.1267	1.3414
chrX	155270560	178060323	1.1468	29.6033

chrY	59373566	471618	0.0079	0.5171

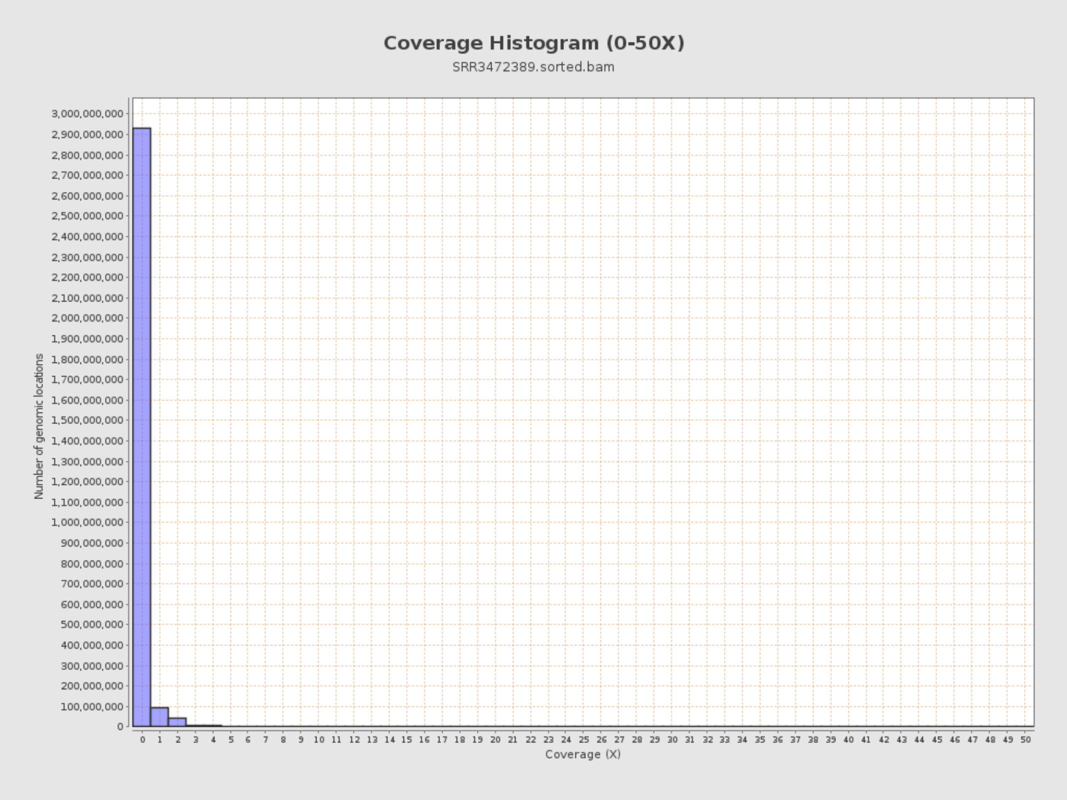
3. Results : Coverage across reference



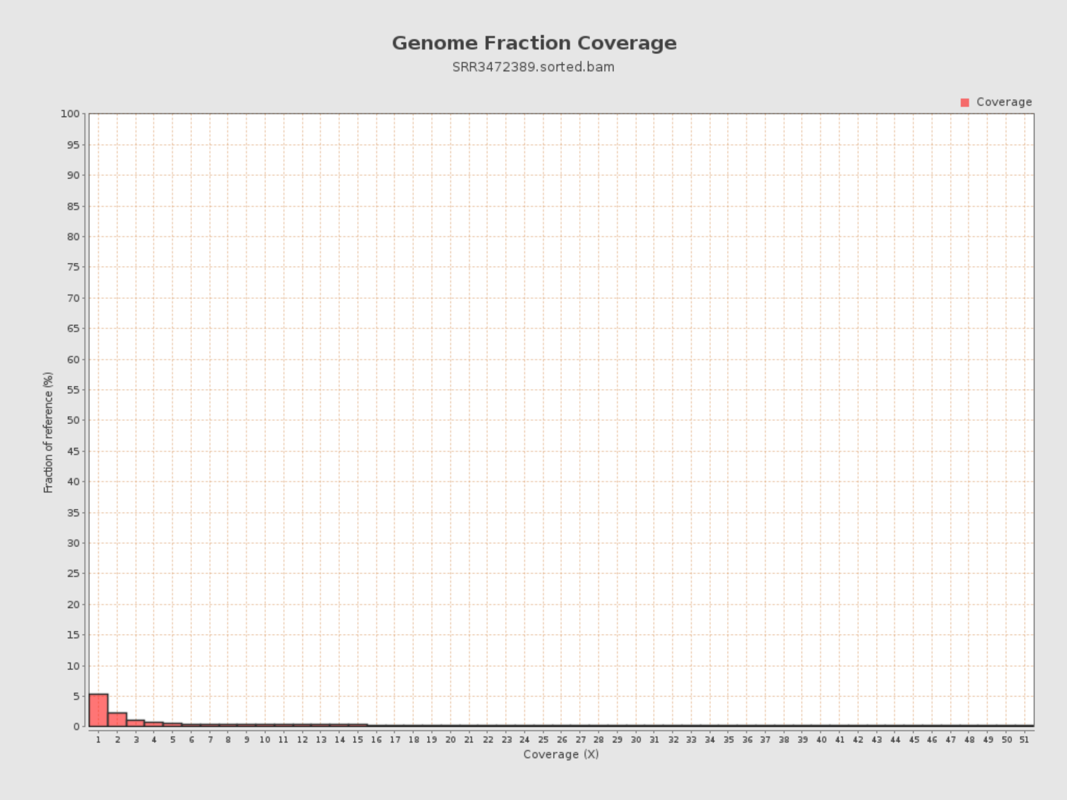
4. Results : Coverage Histogram



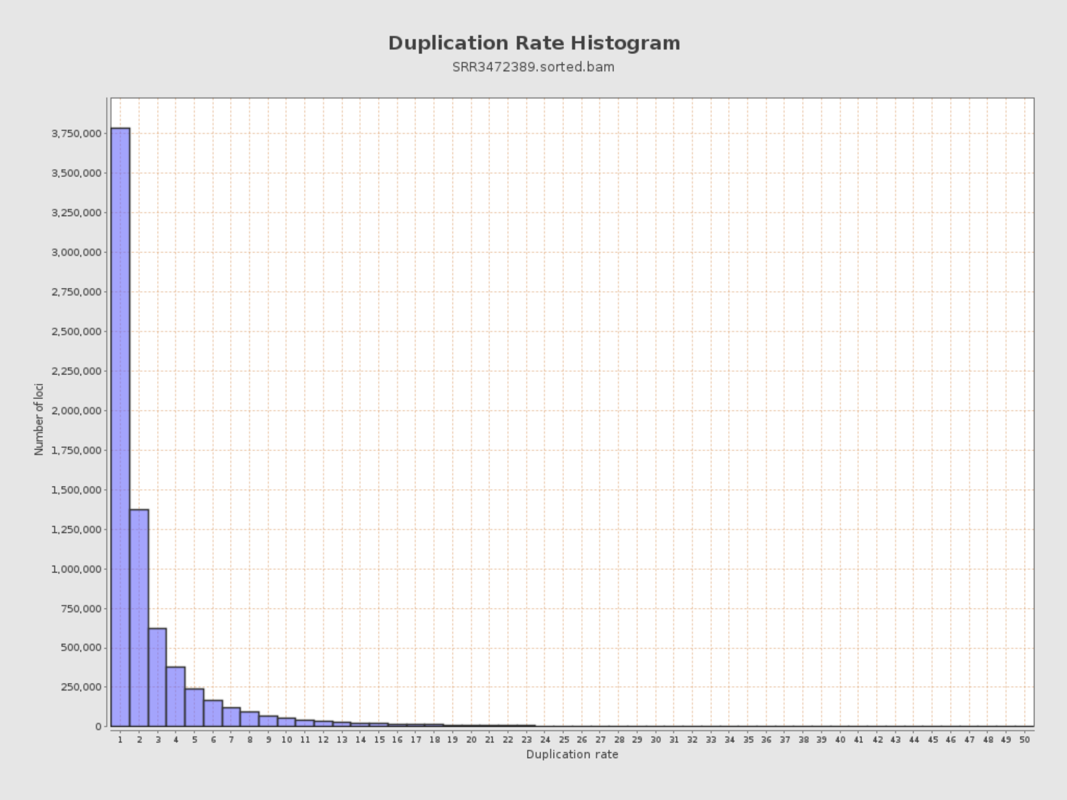
5. Results : Coverage Histogram (0-50X)



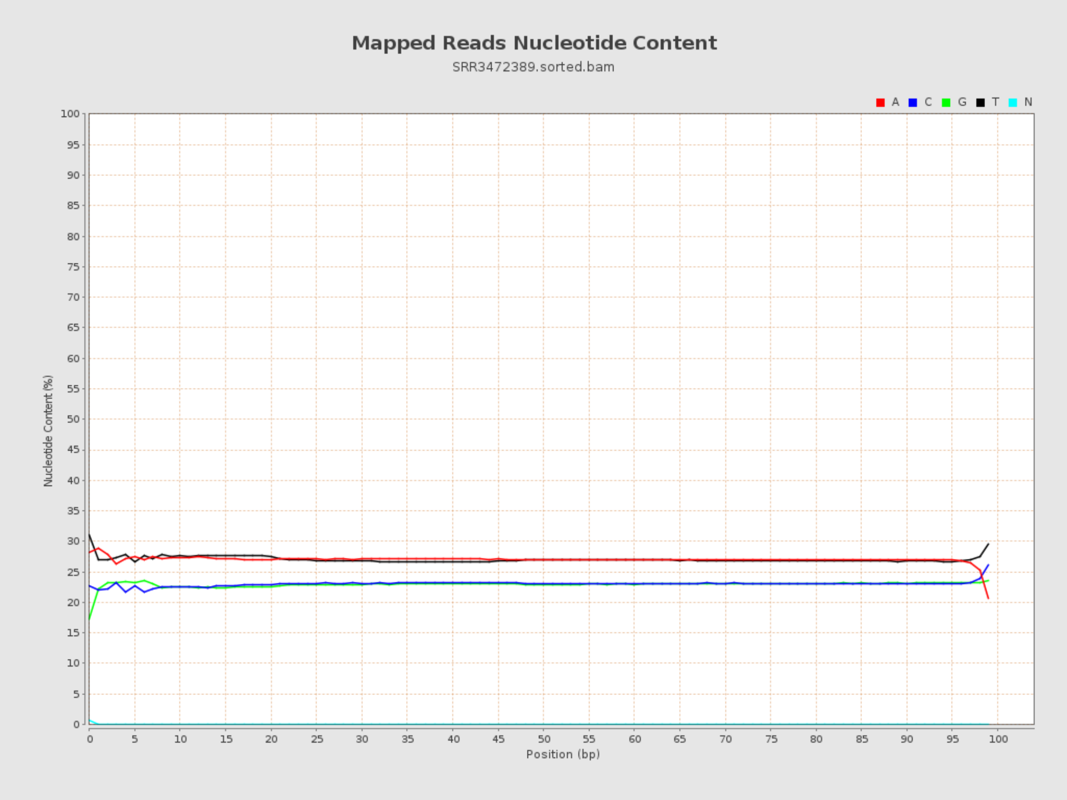
6. Results : Genome Fraction Coverage



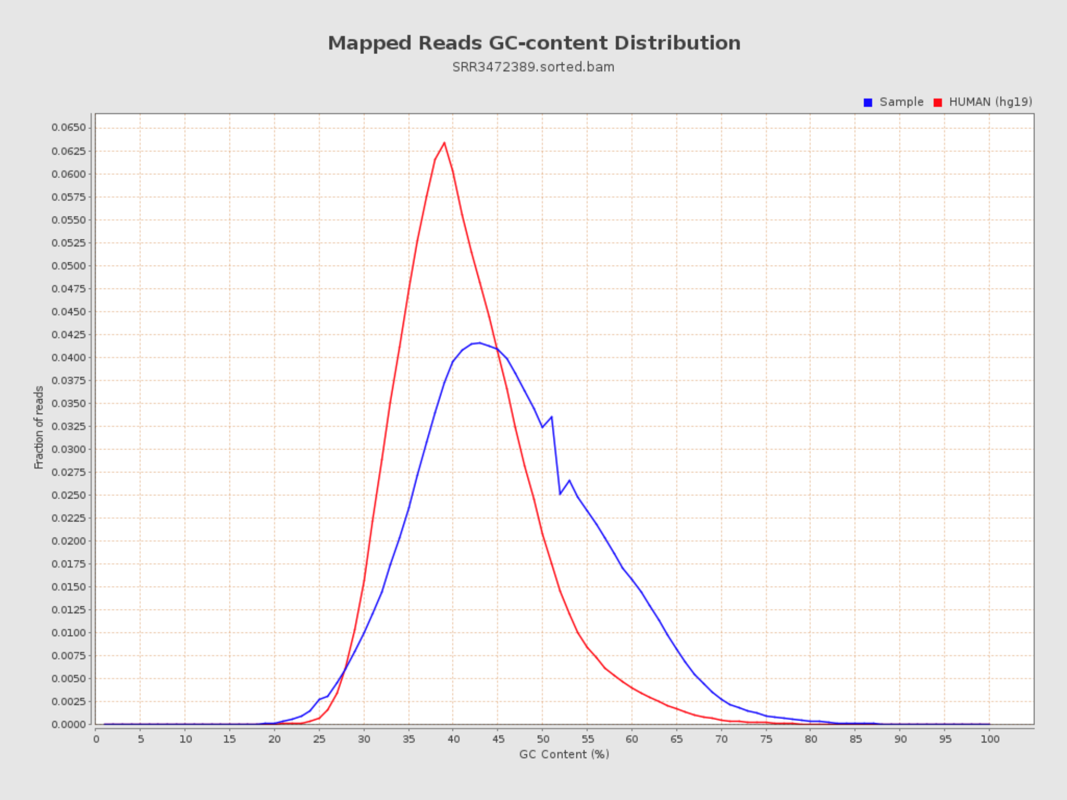
7. Results : Duplication Rate Histogram



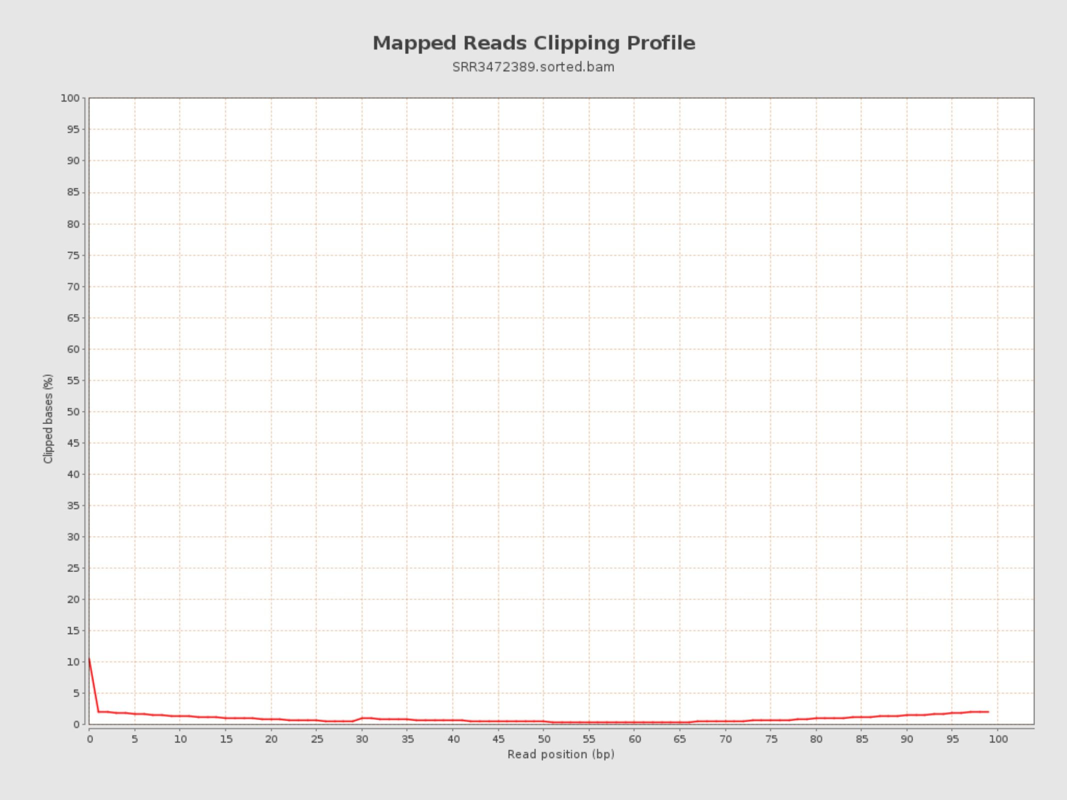
8. Results : Mapped Reads Nucleotide Content



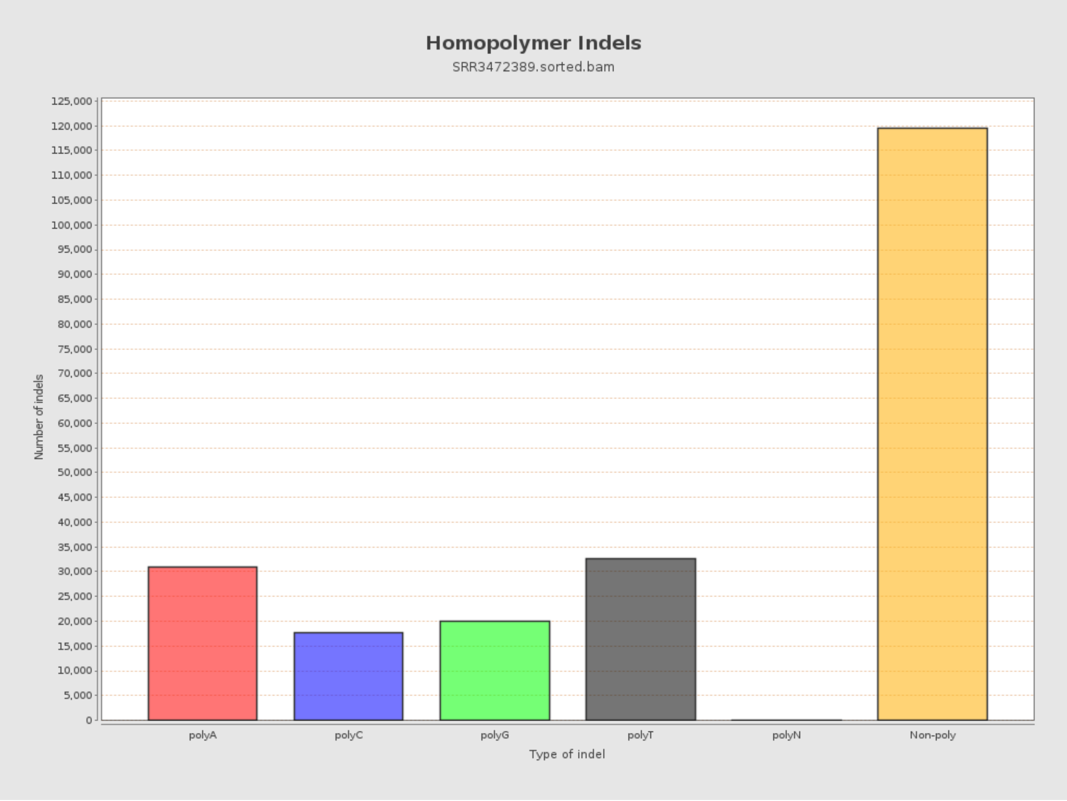
9. Results : Mapped Reads GC-content Distribution



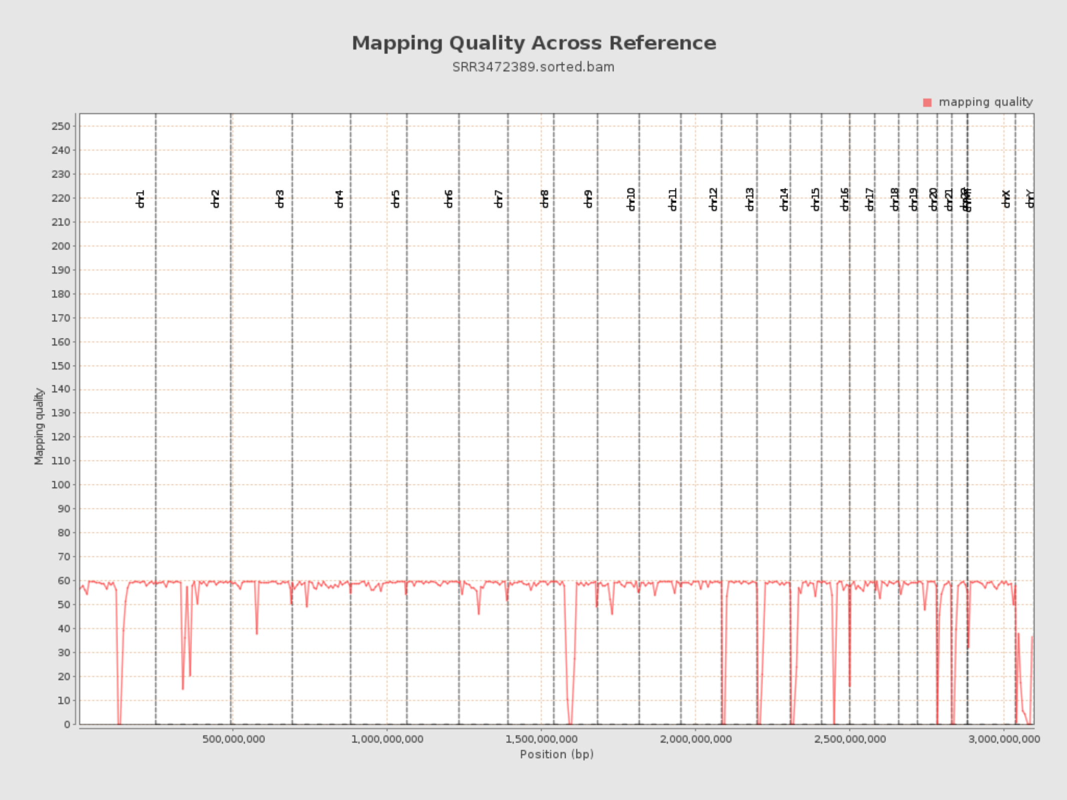
10. Results : Mapped Reads Clipping Profile



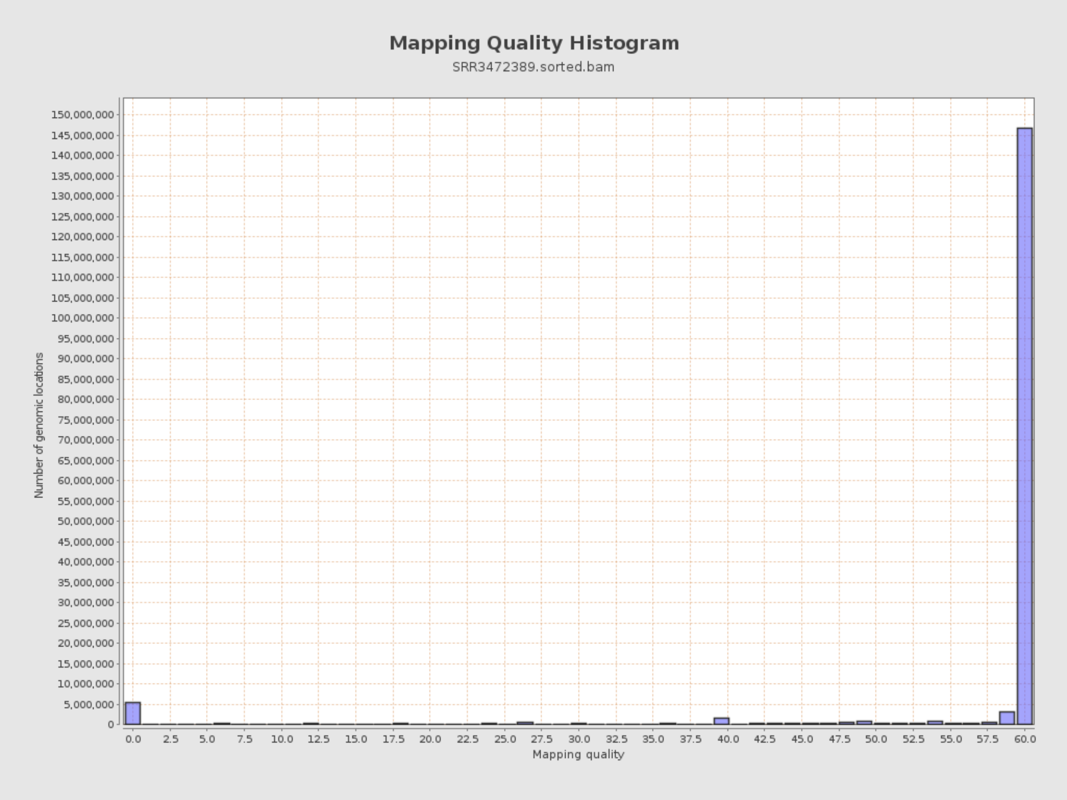
11. Results : Homopolymer Indels



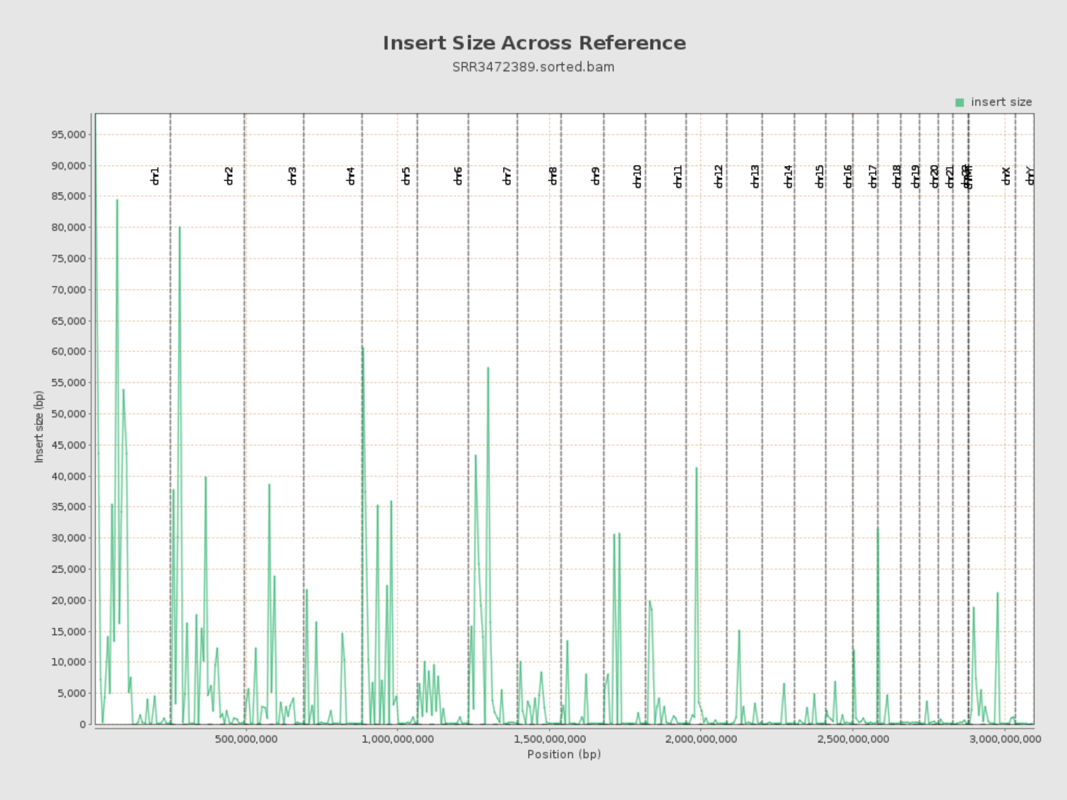
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram