

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

calN50

RRID:SCR_022015

Type: Tool

Proper Citation

calN50 (RRID:SCR_022015)

Resource Information

URL: <https://github.com/lh3/calN50/>

Proper Citation: calN50 (RRID:SCR_022015)

Description: Software tool as simple script to calculate N50/NG50 and auN/auNG.

Resource Type: software application, software resource, data analytics software

Keywords: calculate N50/NG50, calculate auN/auNG

Availability: Free, Available for download, Freely available

Resource Name: calN50

Resource ID: SCR_022015

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260812T044416+0000

Ratings and Alerts

No rating or validation information has been found for calN50.

No alerts have been found for calN50.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Mencius J, et al. (2025) Restoring flowcell type and basecaller configuration from FASTQ files of nanopore sequencing data. *Nature communications*, 16(1), 4102.

Sohn MH, et al. (2025) A telomere-to-telomere map of somatic mutation burden and functional impact in cancer. *bioRxiv : the preprint server for biology*.

Bortoluzzi C, et al. (2024) Genome assembly of wisent (*Bison bonasus*) uncovers a deletion that likely inactivates the THRSP gene. *Communications biology*, 7(1), 1580.

van Lopik J, et al. (2023) Unistrand piRNA clusters are an evolutionarily conserved mechanism to suppress endogenous retroviruses across the *Drosophila* genus. *Nature communications*, 14(1), 7337.

Payne ZL, et al. (2023) A gap-free genome assembly of *Chlamydomonas reinhardtii* and detection of translocations induced by CRISPR-mediated mutagenesis. *Plant communications*, 4(2), 100493.

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (*Albula glossodonta*), a vulnerable circumtropical sportfish. *GigaByte (Hong Kong, China)*, 2022, gigabyte44.

Leonard AS, et al. (2022) Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. *Nature communications*, 13(1), 3012.

Pickett BD, et al. (2022) The genome of a giant (trevally): *Caranx ignobilis*. *GigaByte (Hong Kong, China)*, 2022, gigabyte67.