

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

duphold

RRID:SCR_016938

Type: Tool

Proper Citation

duphold (RRID:SCR_016938)

Resource Information

URL: <https://github.com/brentp/duphold>

Proper Citation: duphold (RRID:SCR_016938)

Description: Software tool to annotate structural variant calls with sequence depth information that can add or remove confidence to SV predicted to affect copy number. Indicates the presence of a rapid change in depth relative to the regions surrounding the breakpoints. Allows the run time to be nearly independent of the number of variants important for large, jointly called projects with many samples. Annotates structural variant predictions made from both short read and long read data.

Resource Type: software resource, software application, data analysis software, data processing software

Keywords: annotate, structural, variation, call, sequence, depth, confidence, predict, copy, number, short, long, read, data

Availability: Free, Available for download, Freely available

Resource Name: duphold

Resource ID: SCR_016938

License: MIT License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260808T190236+0000

Ratings and Alerts

No rating or validation information has been found for duphold.

No alerts have been found for duphold.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Duan RV, et al. (2026) Widespread distribution of Alu/Alu-mediated genomic rearrangement predisposing to a broad range of Mendelian disease and cancer in human populations. *Genome medicine*, 18(1).

Cai Z, et al. (2024) Meta-analysis of six dairy cattle breeds reveals biologically relevant candidate genes for mastitis resistance. *Genetics, selection, evolution : GSE*, 56(1), 54.

Pedersen BS, et al. (2019) Duphold: scalable, depth-based annotation and curation of high-confidence structural variant calls. *GigaScience*, 8(4).