Resource Summary Report

Generated by dkNET on Apr 29, 2025

duphold

RRID:SCR_016938
Type: Tool

Proper Citation

duphold (RRID:SCR_016938)

Resource Information

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

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

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

Funding:

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: 20250429T055858+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 2 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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).