Resource Summary Report

Generated by NIF on Apr 9, 2025

Ricopili

RRID:SCR_004496
Type: Tool

Proper Citation

Ricopili (RRID:SCR_004496)

Resource Information

URL: http://www.broadinstitute.org/mpg/ricopili/

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Description: Ricopili is a tool for visualizing regions of interest in select GWAS data sets. How it works Choose a data set and enter a genomic location or a gene name in the form below. A .pdf plot will be generated, as well as a text file with single SNP results. You can also specify the following options: * Clumping: Independent regions will be colored differently, to highlight LD. If you request more than one clump, be sure to have at least one SNP passing the specified p-value-threshold (for performance reasons.) * SNP: SNPs in the region are colored by LD to this index SNP. * Anonymity: Frequency information is from HapMap to protect anonymity. * NHGRI results: Results from the NHGRI GWAS catalog will be included in the plot. Finally, please note that this tool is in development (it was released on September 19th, 2011) and should be considered beta. In particular, our development server is not equipped for high traffic. If the server fails to respond to your request, please try again at a later time.

Abbreviations: Ricopili

Resource Type: analysis service resource, data analysis service, service resource, production service resource

Keywords: gwas

Funding:

Resource Name: Ricopili

Resource ID: SCR_004496

Alternate IDs: nlx_143770

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250409T060404+0000

Ratings and Alerts

No rating or validation information has been found for Ricopili.

No alerts have been found for Ricopili.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Dahl A, et al. (2024) Genetic and brain similarity independently predict childhood anthropometrics and neighborhood socioeconomic conditions. Developmental cognitive neuroscience, 65, 101339.

Shi Y, et al. (2024) Multi-polygenic scores in psychiatry: From disorder specific to transdiagnostic perspectives. American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics, 195(1), e32951.

Strom NI, et al. (2024) Genome-wide association study identifies new loci associated with OCD. medRxiv : the preprint server for health sciences.

Gong T, et al. (2024) The genetic architecture of dog ownership: large-scale genome-wide association study in 97,552 European-ancestry individuals. G3 (Bethesda, Md.), 14(8).

Tubbs JD, et al. (2024) Real-time dynamic polygenic prediction for streaming data. medRxiv : the preprint server for health sciences.

Casazza W, et al. (2024) Sex-dependent placental methylation quantitative trait loci provide insight into the prenatal origins of childhood onset traits and conditions. iScience, 27(2), 109047.

Strom NI, et al. (2024) Genome-Wide Association Study of Obsessive-Compulsive Symptoms including 33,943 individuals from the general population. Molecular psychiatry,

29(9), 2714.

Norton SA, et al. (2024) A Phenome-Wide Association Study (PheWAS) of Genetic Risk for C-Reactive Protein in Children of European Ancestry: Results From the ABCD Study. medRxiv : the preprint server for health sciences.

Zhang X, et al. (2024) An axis of genetic heterogeneity in autism is indexed by age at diagnosis and is associated with varying developmental and mental health profiles. medRxiv : the preprint server for health sciences.

Song J, et al. (2024) Key subphenotypes of bipolar disorder are differentially associated with polygenic liabilities for bipolar disorder, schizophrenia, and major depressive disorder. Molecular psychiatry, 29(7), 1941.

Albiñana C, et al. (2023) Multi-PGS enhances polygenic prediction by combining 937 polygenic scores. Nature communications, 14(1), 4702.

Pan M, et al. (2023) Circulating S100B levels at birth and risk of six major neuropsychiatric or neurological disorders: a two-sample Mendelian Randomization Study. Translational psychiatry, 13(1), 174.

Baldwin JR, et al. (2023) A genetically informed Registered Report on adverse childhood experiences and mental health. Nature human behaviour, 7(2), 269.

Zhou H, et al. (2023) Multi-ancestry study of the genetics of problematic alcohol use in >1 million individuals. medRxiv : the preprint server for health sciences.

Baranger DA, et al. (2023) Prenatal cannabis exposure is associated with localized brain differences that partially mediate associations with increased adolescent psychopathology. medRxiv : the preprint server for health sciences.

Bulik CM, et al. (2023) Arfid Genes and Environment (ARFID-GEN): Study Protocol. Research square.

Li QS, et al. (2023) Genome-wide association study meta-analysis of suicide death and suicidal behavior. Molecular psychiatry, 28(2), 891.

Li Y, et al. (2023) A regulatory variant at 19p13.3 is associated with primary biliary cholangitis risk and ARID3A expression. Nature communications, 14(1), 1732.

Gonzales S, et al. (2023) SOX7: Novel Autistic Gene Identified by Analysis of Multi-Omics Data. bioRxiv : the preprint server for biology.

Zhou H, et al. (2023) Multi-ancestry study of the genetics of problematic alcohol use in over 1 million individuals. Nature medicine, 29(12), 3184.