Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

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, production service resource, service resource

Keywords: gwas

Resource Name: Ricopili

Resource ID: SCR_004496

Alternate IDs: nlx_143770

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260912T200132+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 100 mentions in open access literature.

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

Prachason T, et al. (2026) Sex differences in the independent and combined effects of genomic and exposomic risks for schizophrenia on distressing psychotic experiences: insights from the ABCD study. Archives of women's mental health, 29(1), 7.

Wang M, et al. (2026) Household cannabis cessation and adolescent mental health outcomes in a prospective cohort study. BMC medicine, 24(1).

Jin Y, et al. (2026) Risk factors underlying brain structure change rate in cognitive decline: Results from genomewide and phenomewide investigations. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(4), e71411.

Auning J, et al. (2026) Mapping the heritability of disease: a nationwide study. Nature communications, 17(1).

Kratzer L, et al. (2026) Disorganized attachment and identity dissociation: FKBP5 CATT as a molecular moderator. Psychiatry research, 360, 117079.

Monaghan A, et al. (2025) Brain wiring economics, network organisation and population-level genomics. Imaging neuroscience (Cambridge, Mass.), 3.

Streit F, et al. (2025) Genome-wide association study of borderline personality disorder identifies 11 loci and highlights shared risk with mental and somatic disorders. medRxiv : the preprint server for health sciences.

Wang Y, et al. (2025) Relationship between cognitive abilities and mental health as represented by cognitive abilities at the neural and genetic levels of analysis. eLife, 14.

Zhang X, et al. (2025) Polygenic and developmental profiles of autism differ by age at diagnosis. Nature, 646(8087), 1146.

Zhang Y, et al. (2025) Prematurity and genetic liability for autism spectrum disorder. Genome medicine, 17(1), 108.

Norbom LB, et al. (2025) Socioeconomic context influences the heritability of child cortical structure. Communications biology, 8(1), 1607.

Romero Villela PN, et al. (2025) Multi-ancestral genome-wide study of chronic pain reveals widespread genetic correlations with mental and physical health traits. medRxiv : the preprint server for health sciences.

Panagiotaropoulou G, et al. (2025) Identifying genetic differences between bipolar disorder and major depression through multiple genome-wide association analyses. The British journal of psychiatry : the journal of mental science, 226(2), 79.

Kraft J, et al. (2025) Polygenic contributions to lithium augmentation outcomes in antidepressant non-responders with unipolar depression. medRxiv : the preprint server for health sciences.

B??ckman J, et al. (2025) Polygenic scores and symptom severity change after internet-delivered cognitive behaviour therapy for depression and anxiety. Discover mental health, 5(1), 82.

Hog L, et al. (2025) ARFID InitiativE Sweden (ARIES): study protocol for a large-scale genetic and registry-linked cohort study on avoidant/restrictive food intake disorder. BMJ open, 15(4), e095559.

, et al. (2025) Trans-ancestry genome-wide study of depression identifies 697 associations implicating cell types and pharmacotherapies. Cell, 188(3), 640.

Norbom LB, et al. (2025) Socioeconomic context influences the heritability of child cortical structure. medRxiv : the preprint server for health sciences.

Hyat M, et al. (2025) Independent versus joint effects of polygenic or family-based schizophrenia risk in diverse ancestry youth in the ABCD study. Psychological medicine, 55, e327.

Gonzales S, et al. (2025) SOX7: Autism associated gene identified by analysis of multi-Omics data. PloS one, 20(5), e0320096.