

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 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, service resource, data analysis service, production service resource

Keywords: gwas

Resource Name: Ricopili

Resource ID: SCR_004496

Alternate IDs: nlx_143770

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260728T043202+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 93 mentions in open access literature.

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

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.

Buckman 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.

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

Hog L, et al. (2025) ARFID InitiativeE 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.

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.

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.