Resource Summary Report

Generated by RRID on Sep 10, 2026

GERMLINE

RRID:SCR_001720
Type: Tool

Proper Citation

GERMLINE (RRID:SCR_001720)

Resource Information

URL: http://gusevlab.org/projects/germline/

Proper Citation: GERMLINE (RRID:SCR_001720)

Description: Software application for discovering long shared segments of Identity by Descent (IBD) between pairs of individuals in a large population. It takes as input genotype or haplotype marker data for individuals (as well as an optional known pedigree) and generates a list of all pairwise segmental sharing., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GERMLINE

Resource Type: software application, software resource

Defining Citation: PMID:18971310

Keywords: gene, genetic, genomic, c++, linux, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GERMLINE

Resource ID: SCR_001720

Alternate IDs: biotools:germline, OMICS_00202, nlx_154080

Alternate URLs: https://bio.tools/germline

Old URLs: http://www1.cs.columbia.edu/~gusev/germline/

License: GNU General Public License

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260905T133225+0000

Ratings and Alerts

No rating or validation information has been found for GERMLINE.

No alerts have been found for GERMLINE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 451 mentions in open access literature.

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

Stowers RS, et al. (2025) Multimerized epitope tags for high-sensitivity protein detection. G3 (Bethesda, Md.), 15(6).

Merdler-Rabinowicz R, et al. (2025) A systematic evaluation of the therapeutic potential of endogenous-ADAR editors in cancer prevention and treatment. NAR cancer, 7(2), zcaf016.

Lawson-Michod KA, et al. (2025) Homologous recombination deficiency in ovarian high-grade serous carcinoma by self-reported race. medRxiv : the preprint server for health sciences.

Robinson K, et al. (2025) Rare variants in PRKCI cause Van der Woude syndrome and other features of peridermopathy. medRxiv : the preprint server for health sciences.

Tozawa S, et al. (2025) Novel function of Hox13 in regulating outgrowth of the newt hindlimb bud through interaction with Fgf10 and Tbx4. Development, growth & differentiation, 67(1), 10.

Kamdee K, et al. (2025) Comprehensive germline and somatic profiling of high-risk Thai breast cancer via next-generation sequencing. Scientific reports, 15(1), 11427.

Ul Haq S, et al. (2025) Pathogenic germline variants in small cell lung cancer: A systematic review and meta-analysis. HGG advances, 6(3), 100445.

Sweet-Jones J, et al. (2025) An antibody developability triaging pipeline exploiting protein language models. mAbs, 17(1), 2472009.

Broz AK, et al. (2025) Flipping the switch on some of the slowest mutating genomes: Direct measurements of plant mitochondrial and plastid mutation rates in msh1 mutants. PLoS genetics, 21(6), e1011764.

Treger TD, et al. (2025) Predisposition Footprints in the Somatic Genome of Wilms Tumors. Cancer discovery, 15(2), 286.

Helderman NC, et al. (2025) Clinical syndromes linked to biallelic germline variants in MCM8 and MCM9. HGG advances, 6(4), 100480.

Li L, et al. (2025) Multigene germline and somatic testing for epithelial ovarian cancer in China. NPJ precision oncology, 9(1), 281.

Lin D, et al. (2025) Dynamic circulating tumor DNA indicates pathological benefits of additional neoadjuvant chemoimmunotherapy courses for locally advanced non-small-cell lung cancer patients. Frontiers in oncology, 15, 1563315.

Mathur S, et al. (2025) Genomic Evaluation of Assisted Gene Flow Options in an Endangered Rattlesnake. Molecular ecology, 34(16), e70014.

Broz AK, et al. (2025) Flipping the switch on some of the slowest mutating genomes: Direct measurements of plant mitochondrial and plastid mutation rates in msh1 mutants. bioRxiv : the preprint server for biology.

Huang Y, et al. (2025) RMVar 2.0: an updated database of functional variants in RNA modifications. Nucleic acids research, 53(D1), D275.

Yeh YM, et al. (2025) The RASAL2 variant promotes aberrant RAS signaling and resistance to anti-EGFR therapy in colorectal cancer. Scientific reports, 15(1), 31076.

Selenica P, et al. (2025) Genomic landscape of breast cancer in elderly patients. NPJ breast cancer, 11(1), 70.

Liu R, et al. (2025) DirectHRD enables sensitive scar-based classification of homologous recombination deficiency. Nucleic acids research, 53(8).

Abbasi A, et al. (2025) HRProfiler Detects Homologous Recombination Deficiency in Breast and Ovarian Cancers Using Whole-Genome and Whole-Exome Sequencing Data. Cancer research, 85(13), 2504.