Resource Summary Report

Generated by NIF on Apr 17, 2025

GERMLINE

RRID:SCR_001720
Type: Tool

Proper Citation

GERMLINE (RRID:SCR_001720)

Resource Information

URL: http://www1.cs.columbia.edu/~gusev/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.

Abbreviations: GERMLINE

Resource Type: software resource, software application

Defining Citation: PMID:18971310

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

Funding:

Availability: GNU General Public License, Acknowledgement requested

Resource Name: GERMLINE

Resource ID: SCR_001720

Alternate IDs: biotools:germline, OMICS_00202, nlx_154080

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

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250416T063243+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 414 mentions in open access literature.

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

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.

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.

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Sanabria-Salas MC, et al. (2025) Clinical integration of germline findings from a tumor testing precision medicine program. BMC cancer, 25(1), 176.

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.

Meng Q, et al. (2025) Therapeutic Potential of Lappula patula Extracts on Germline Development and DNA Damage Responses in C. elegans. Pharmaceuticals (Basel, Switzerland), 18(1).

Contreras E, et al. (2024) Flp-recombinase mouse line for genetic manipulation of ipRGCs. bioRxiv : the preprint server for biology.

Li H, et al. (2024) Exploratory biomarker analysis in the phase III L-MOCA study of olaparib

maintenance therapy in patients with platinum-sensitive relapsed ovarian cancer. BMC medicine, 22(1), 199.

Telli ML, et al. (2024) Neoadjuvant talazoparib in patients with germline BRCA1/2 mutation-positive, early-stage triple-negative breast cancer: exploration of tumor BRCA mutational status. Breast cancer (Tokyo, Japan), 31(5), 886.

Liu Y, et al. (2024) MAGPIE: accurate pathogenic prediction for multiple variant types using machine learning approach. Genome medicine, 16(1), 3.

Chao AS, et al. (2024) Comparison of immediate germline sequencing and multi-step screening for Lynch syndrome detection in high-risk endometrial and colorectal cancer patients. Journal of gynecologic oncology, 35(1), e5.

Ruiz de Sabando A, et al. (2024) Somatic CAG repeat instability in intermediate alleles of the HTT gene and its potential association with a clinical phenotype. European journal of human genetics : EJHG, 32(7), 770.

Sat?awa T, et al. (2024) LAP: Liability Antibody Profiler by sequence & structural mapping of natural and therapeutic antibodies. PLoS computational biology, 20(3), e1011881.

Kvapilova K, et al. (2024) Validated WGS and WES protocols proved saliva-derived gDNA as an equivalent to blood-derived gDNA for clinical and population genomic analyses. BMC genomics, 25(1), 187.

Xu W, et al. (2024) Multiple-Wave Admixture and Adaptive Evolution of the Pamirian Wakhi People. Molecular biology and evolution, 41(12).

Sanders MWCB, et al. (2024) Somatic variant analysis of resected brain tissue in epilepsy surgery patients. Epilepsia, 65(12), e209.

Iglesia MD, et al. (2024) Differential chromatin accessibility and transcriptional dynamics define breast cancer subtypes and their lineages. Nature cancer, 5(11), 1713.

Joseph J, et al. (2024) High prevalence of PRDM9-independent recombination hotspots in placental mammals. Proceedings of the National Academy of Sciences of the United States of America, 121(23), e2401973121.

Frank S, et al. (2024) Molecular consequences of acute versus chronic CDK12 loss in prostate carcinoma nominates distinct therapeutic strategies. bioRxiv : the preprint server for biology.