

Resource Summary Report

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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 [dkNET](#).

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.

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

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*.

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*.