

Resource Summary Report

Generated by T1D on Jul 31, 2026

FAMHAP

RRID:SCR_009070

Type: Tool

Proper Citation

FAMHAP (RRID:SCR_009070)

Resource Information

URL: <http://www.uni-bonn.de/~umt70e/becker.html>

Proper Citation: FAMHAP (RRID:SCR_009070)

Description: Software application for haplotype association analysis of unphased genotype data. It can be used both for population data (case-control) and nuclear family data. The program is optimized for haplotype frequency estimation with the EM-algorithm for many markers. FAMHAP provides a method which searches for potential genotyping errors and several tests for haplotype-based association analysis. Particular emphasis is on Monte-Carlo simulations, which are necessary in the context of haplotype association, where asymptotic theory often fails, and in the context of multiple testing problems. (entry from Genetic Analysis Software)

Abbreviations: FAMHAP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, ms-windows, macos

Resource Name: FAMHAP

Resource ID: SCR_009070

Alternate IDs: nlx_154064

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260731T042759+0000

Ratings and Alerts

No rating or validation information has been found for FAMHAP.

No alerts have been found for FAMHAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Uden A, et al. (2025) Genotype and transcript processing of the tumour necrosis factor receptor TNFRSF1A in epithelial cells: implications for survival in cystic fibrosis. EBioMedicine, 118, 105848.

Stanke F, et al. (2021) Consistent Assignment of Risk and Benign Allele at rs2303153 in the CF Modifier Gene SCNN1B in Three Independent F508del-CFTR Homozygous Patient Populations. Genes, 12(10).

Pandey N, et al. (2021) Influence of TLR4 and TLR9 polymorphisms and haplotypes on multiple hrHPV infections and HPV16 copy number in cervical cancer and cervicitis. Microbial pathogenesis, 159, 105149.

Pandey NO, et al. (2019) Association of TLR4 and TLR9 polymorphisms and haplotypes with cervical cancer susceptibility. Scientific reports, 9(1), 9729.

Nowak I, et al. (2019) Association of Soluble HLA-G Plasma Level and HLA-G Genetic Polymorphism With Pregnancy Outcome of Patients Undergoing in vitro Fertilization Embryo Transfer. Frontiers in immunology, 10, 2982.

Debrah LB, et al. (2017) Single nucleotide polymorphisms in the angiogenic and lymphangiogenic pathways are associated with lymphedema caused by Wuchereria bancrofti. Human genomics, 11(1), 26.

Choi JH, et al. (2017) Variations in the bitterness perception-related genes TAS2R38 and CA6 modify the risk for colorectal cancer in Koreans. Oncotarget, 8(13), 21253.

Nowak I, et al. (2017) The methylenetetrahydrofolate reductase c.c.677 C>T and c.c.1298 A>C polymorphisms in reproductive failures: Experience from an RSA and RIF study on a Polish population. PloS one, 12(10), e0186022.

Esparza-Gordillo J, et al. (2015) Maternal filaggrin mutations increase the risk of atopic dermatitis in children: an effect independent of mutation inheritance. PLoS genetics, 11(3), e1005076.

Fiebig A, et al. (2008) Polymorphisms in the interleukin-1 (IL1) gene cluster are not associated with aggressive periodontitis in a large Caucasian population. Genomics, 92(5), 309.

Matesanz F, et al. (2008) The high producer variant of the Fc-receptor like-3 (FCRL3) gene is involved in protection against multiple sclerosis. Journal of neuroimmunology, 195(1-2), 146.

Knapp M, et al. (2004) Impact of genotyping errors on type I error rate of the haplotype-sharing transmission/disequilibrium test (HS-TDT). American journal of human genetics, 74(3), 589.