Resource Summary Report

Generated by RRID on Aug 7, 2026

Extended Haplotype Homozygosity

RRID:SCR_008491
Type: Tool

Proper Citation

Extended Haplotype Homozygosity (RRID:SCR_008491)

Resource Information

URL: http://ihg2.helmholtz-muenchen.de/cgi-bin/mueller/webehh.pl

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on March 11, 2013. Web-based tool to explore the relationship between population frequency and extended linkage disequilibrium measured as haplotype homozygosity of observed haplotypes within a specified candidate region. Haplotype homozygosity (HH) is an effective measure of linkage disequilibrium (LD) for more than 2 markers. If we want to see, how LD breaks down with increasing distance to a specified core region, we can calculate HH in a stepwise manner as extended HH (EHH, Sabeti et al. 2002). EHH is calculated between a distance x and the specified core region for a chromosome population carrying a single core haplotype. Distance x increases stepwise to the most outlying marker. The procedure is repeated for each core haplotype. HH is evaluated as HH = sum(pi2) - 1/n / 1 - 1/n with pi being the relative haplotype frequency and n the sample size. It corrects for sampling effects (Sabatti & Risch 2002). The variance of HH is estimated according to Nei (1975). EHH estimates the level of haplotype splitting due to recombination and mutation at extended regions on both sides of a specified core region. It may be used to explore haplotype-specific LD patterns, e.g. for disease associated haplotypes. In combination with the core haplotype frequency it may also serve as an indicator of recent positive selection. Frequent core haplotypes with an unusually high long-range LD are supposed to be positively selected. The various core haplotypes can serve as internal controls. Input file: A text file consisting of a haplotype (chromosome) population

Abbreviations: Extended Haplotype Homozygosity

Resource Type: software resource

Defining Citation: PMID:14764566

Keywords: haplotype, population frequency, linkage disequilibrium, homozygosity, candidate region, haplotype homozygosity

Funding: BFAM 031U112C

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Extended Haplotype Homozygosity

Resource ID: SCR_008491

Alternate IDs: nif-0000-30484

Old URLs: http://ihg.gsf.de/cgi-bin/mueller/webehh.pl

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260801T190355+0000

Ratings and Alerts

No rating or validation information has been found for Extended Haplotype Homozygosity.

No alerts have been found for Extended Haplotype Homozygosity.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Fry AE, et al. (2009) Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. Human molecular genetics, 18(14), 2683.