Resource Summary Report

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HAPLOTTER

RRID:SCR_009229
Type: Tool

Proper Citation

HAPLOTTER (RRID:SCR_009229)

Resource Information

URL: http://hg-wen.uchicago.edu/selection/haplotter.htm

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Description: A web application that has been developed to display the results of a scan for positive selection in the human genome using the HapMap data. It can be used as a resource to examine various population genetic measures in a genomic region. Measures that are currently displayed include iHS (a statistic developed to detect recent positive selection), Fay and Wu"s H, Tajima"s D and Fst. (entry from Genetic Analysis Software)

Abbreviations: HAPLOTTER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, web-based

Funding:

Resource Name: HAPLOTTER

Resource ID: SCR_009229

Alternate IDs: nlx_154386

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063540+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOTTER.

No alerts have been found for HAPLOTTER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Ji L, et al. (2020) Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. Genomics, proteomics & bioinformatics, 18(5), 489.

Jallow MW, et al. (2020) Differences in the frequency of genetic variants associated with iron imbalance among global populations. PloS one, 15(7), e0235141.

Liang J, et al. (2017) Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS genetics, 13(5), e1006728.

Thomsen H, et al. (2016) Runs of homozygosity and inbreeding in thyroid cancer. BMC cancer, 16, 227.

Thomsen H, et al. (2016) Evidence of Inbreeding in Hodgkin Lymphoma. PloS one, 11(4), e0154259.

North TL, et al. (2016) A study of common Mendelian disease carriers across ageing British cohorts: meta-analyses reveal heterozygosity for alpha 1-antitrypsin deficiency increases respiratory capacity and height. Journal of medical genetics, 53(4), 280.

Sun C, et al. (2016) High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. Nature genetics, 48(3), 323.

Polimanti R, et al. (2016) Evidence of Polygenic Adaptation in the Systems Genetics of Anthropometric Traits. PloS one, 11(8), e0160654.

Ye K, et al. (2015) Natural selection on HFE in Asian populations contributes to enhanced non-heme iron absorption. BMC genetics, 16, 61.

Liu X, et al. (2015) Signatures of natural selection at the FTO (fat mass and obesity associated) locus in human populations. PloS one, 10(2), e0117093.

Thomsen H, et al. (2015) Inbreeding and homozygosity in breast cancer survival. Scientific

reports, 5, 16467.

Seixas S, et al. (2012) Loss and gain of function in SERPINB11: an example of a gene under selection on standing variation, with implications for host-pathogen interactions. PloS one, 7(2), e32518.

Schleinitz D, et al. (2011) Genetic and evolutionary analyses of the human bone morphogenetic protein receptor 2 (BMPR2) in the pathophysiology of obesity. PloS one, 6(2), e16155.

Engel KM, et al. (2011) Reduced food intake and body weight in mice deficient for the G protein-coupled receptor GPR82. PloS one, 6(12), e29400.

Zhernakova A, et al. (2010) Evolutionary and functional analysis of celiac risk loci reveals SH2B3 as a protective factor against bacterial infection. American journal of human genetics, 86(6), 970.

Crespi B, et al. (2010) Evolutionary genomics of human intellectual disability. Evolutionary applications, 3(1), 52.

Southam L, et al. (2009) Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants? Diabetologia, 52(9), 1846.

Hariharan M, et al. (2009) dbSMR: a novel resource of genome-wide SNPs affecting microRNA mediated regulation. BMC bioinformatics, 10, 108.

Quach H, et al. (2009) Signatures of purifying and local positive selection in human miRNAs. American journal of human genetics, 84(3), 316.

Weedon MN, et al. (2006) A common haplotype of the glucokinase gene alters fasting glucose and birth weight: association in six studies and population-genetics analyses. American journal of human genetics, 79(6), 991.