Resource Summary Report

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CHECKMATRIX

RRID:SCR_009149
Type: Tool

Proper Citation

CHECKMATRIX (RRID:SCR_009149)

Resource Information

URL: http://www.atgc.org/XLinkage/

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Description: Software application that serves as a visualization tool to validate constructed genetic maps. CheckMatrix generates graphical genotypes and two-dimensional heat plots of pairwise scores. Visualization of regions with positive and negative linkage as well as of allele fraction per marker simplifies genetic map validation without applying statistical approaches. CheckMatrix works in conjunction with MadMapper and freely available at http://www.atgc.org/XLinkage/MadMapper/ (entry from Genetic Analysis Software)

Abbreviations: CHECKMATRIX

Synonyms: PY_MATRIX_D

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, python

Funding:

Resource Name: CHECKMATRIX

Resource ID: SCR_009149

Alternate IDs: nlx_154268

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250412T055348+0000

Ratings and Alerts

No rating or validation information has been found for CHECKMATRIX.

No alerts have been found for CHECKMATRIX.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Shen C, et al. (2021) Gossypium tomentosum genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. Genomics, 113(4), 1999.

Bhadauria V, et al. (2017) QTL mapping reveals genetic determinants of fungal disease resistance in the wild lentil species Lens ervoides. Scientific reports, 7(1), 3231.

Ellison S, et al. (2017) Fine Mapping, Transcriptome Analysis, and Marker Development for Y2 , the Gene That Conditions ?-Carotene Accumulation in Carrot (Daucus carota L.). G3 (Bethesda, Md.), 7(8), 2665.

Hulse-Kemp AM, et al. (2016) A HapMap leads to a Capsicum annuum SNP infinium array: a new tool for pepper breeding. Horticulture research, 3, 16036.

Duki? M, et al. (2016) A high-density genetic map reveals variation in recombination rate across the genome of Daphnia magna. BMC genetics, 17(1), 137.

Hulse-Kemp AM, et al. (2015) Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of Gossypium spp. G3 (Bethesda, Md.), 5(6), 1187.

Cavagnaro PF, et al. (2014) A gene-derived SNP-based high resolution linkage map of carrot including the location of QTL conditioning root and leaf anthocyanin pigmentation. BMC genomics, 15(1), 1118.

Truco MJ, et al. (2013) An Ultra-High-Density, Transcript-Based, Genetic Map of Lettuce. G3 (Bethesda, Md.), 3(4), 617.

Ma XF, et al. (2012) High resolution genetic mapping by genome sequencing reveals genome duplication and tetraploid genetic structure of the diploid Miscanthus sinensis. PloS one, 7(3), e33821.