

Resource Summary Report

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realSFS

RRID:SCR_002493

Type: Tool

Proper Citation

realSFS (RRID:SCR_002493)

Resource Information

URL: <http://128.32.118.212/thorfinn/realSFS/>

Proper Citation: realSFS (RRID:SCR_002493)

Description: Software program used to estimate allele frequency and SNP calling.

Resource Type: data analysis software, software application, data processing software, software resource

Keywords: allele frequency estimation, snp calling

Funding:

Availability: Open source

Resource Name: realSFS

Resource ID: SCR_002493

Alternate IDs: OMICS_00071

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250411T054739+0000

Ratings and Alerts

No rating or validation information has been found for realSFS.

No alerts have been found for realSFS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Nebenführ M, et al. (2024) High-speed whole-genome sequencing of a Whippet: Rapid chromosome-level assembly and annotation of an extremely fast dog's genome. GigaByte (Hong Kong, China), 2024, gigabyte134.

Rahman SR, et al. (2023) Genome-wide DNA methylation patterns in bumble bee (*Bombus vosnesenskii*) populations from spatial-environmental range extremes. Scientific reports, 13(1), 14901.

Sánchez-Barreiro F, et al. (2023) Historic Sampling of a Vanishing Beast: Population Structure and Diversity in the Black Rhinoceros. Molecular biology and evolution, 40(9).

Wooldridge TB, et al. (2022) An enhancer of Agouti contributes to parallel evolution of cryptically colored beach mice. Proceedings of the National Academy of Sciences of the United States of America, 119(27), e2202862119.

Giska I, et al. (2022) The evolutionary pathways for local adaptation in mountain hares. Molecular ecology, 31(5), 1487.

Imai R, et al. (2021) Mating system evolution and genetic structure of diploid sexual populations of *Cyrtomium falcatum* in Japan. Scientific reports, 11(1), 3124.

Jin T, et al. (2021) Natural variation in the promoter of GsERD15B affects salt tolerance in soybean. Plant biotechnology journal, 19(6), 1155.

Lewald KM, et al. (2021) Population genomics of *Drosophila suzukii* reveal longitudinal population structure and signals of migrations in and out of the continental United States. G3 (Bethesda, Md.), 11(12).

Sarfraz Z, et al. (2021) GWAS Mediated Elucidation of Heterosis for Metric Traits in Cotton (*Gossypium hirsutum* L.) Across Multiple Environments. Frontiers in plant science, 12, 565552.

Yan W, et al. (2021) Genome-Wide Association Study to Map Genomic Regions Related to the Initiation Time of Four Growth Stage Traits in Soybean. Frontiers in genetics, 12, 715529.

- Choi JY, et al. (2020) Divergent Selection and Primary Gene Flow Shape Incipient Speciation of a Riparian Tree on Hawaii Island. *Molecular biology and evolution*, 37(3), 695.
- Karikari B, et al. (2020) Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. *BMC plant biology*, 20(1), 404.
- Wang W, et al. (2020) Comprehensive Identification of Drought Tolerance QTL-Allele and Candidate Gene Systems in Chinese Cultivated Soybean Population. *International journal of molecular sciences*, 21(14).
- Yu Z, et al. (2019) Identification of QTN and Candidate Gene for Seed-flooding Tolerance in Soybean [*Glycine max* (L.) Merr.] using Genome-Wide Association Study (GWAS). *Genes*, 10(12).
- Wang X, et al. (2019) QTL mapping for aluminum tolerance in RIL population of soybean (*Glycine max* L.) by RAD sequencing. *PLoS one*, 14(10), e0223674.
- Wang L, et al. (2019) QTL fine-mapping of soybean (*Glycine max* L.) leaf type associated traits in two RILs populations. *BMC genomics*, 20(1), 260.
- Li S, et al. (2019) Dissecting the Genetic Architecture of Seed Protein and Oil Content in Soybean from the Yangtze and Huaihe River Valleys Using Multi-Locus Genome-Wide Association Studies. *International journal of molecular sciences*, 20(12).
- Du X, et al. (2018) Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. *BMC genomics*, 19(1), 451.
- Ni X, et al. (2017) Updated foxtail millet genome assembly and gene mapping of nine key agronomic traits by resequencing a RIL population. *GigaScience*, 6(2), 1.
- Crawford JE, et al. (2017) Population genomics reveals that an anthropophilic population of *Aedes aegypti* mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. *BMC biology*, 15(1), 16.