

Resource Summary Report

Generated by [dkNET](#) on Sep 9, 2026

[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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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

Keywords: allele frequency estimation, snp calling

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: realSFS

Resource ID: SCR_002493

Alternate IDs: OMICS_00071

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260905T132449+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 27 mentions in open access literature.

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

Zong C, et al. (2024) Identification of Gene-Allele System Conferring Alkali-Tolerance at Seedling Stage in Northeast China Soybean Germplasm. *International journal of molecular sciences*, 25(5).

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).

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.

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.

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.

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.