

Resource Summary Report

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VCF2Dis

RRID:SCR_022513

Type: Tool

Proper Citation

VCF2Dis (RRID:SCR_022513)

Resource Information

URL: <https://github.com/BGI-shenzhen/VCF2Dis>

Proper Citation: VCF2Dis (RRID:SCR_022513)

Description: Software to calculate p-distance matrix based Variant Call Format.

Resource Type: software application, software resource, data analytics software

Keywords: calculate p-distance matrix based Variant Call Format

Availability: Free, Available for download, Freely available

Resource Name: VCF2Dis

Resource ID: SCR_022513

License: MIT License

Record Creation Time: 20220623T050145+0000

Record Last Update: 20260812T044422+0000

Ratings and Alerts

No rating or validation information has been found for VCF2Dis.

No alerts have been found for VCF2Dis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Wang D, et al. (2026) Natural variation in PtoCPK3 governs drought tolerance by orchestrating xylem remodeling and lignin metabolism in *Populus*. *Science advances*, 12(23), eade2172.

Zhang JY, et al. (2026) Demographic history and identification of threats under climate and anthropogenic activity provide insights into conservation for *Cypripedium palangshanense*. *BMC plant biology*, 26(1), 213.

Xu L, et al. (2025) VCF2Dis: an ultra-fast and efficient tool to calculate pairwise genetic distance and construct population phylogeny from VCF files. *GigaScience*, 14.

Huang W, et al. (2024) De novo genome assembly and population genomics of a shrub tree *Barthea barthei* (Hance) Krass provide insights into the adaptive color variations. *Frontiers in plant science*, 15, 1365686.

Shao L, et al. (2024) High-quality genomes of *Bombax ceiba* and *Ceiba pentandra* provide insights into the evolution of Malvaceae species and differences in their natural fiber development. *Plant communications*, 5(5), 100832.

Shivute FN, et al. (2024) Genome-wide and pan-genomic analysis reveals rich variants of NBS-LRR genes in a newly developed wild rice line from *Oryza alta* Swallen. *Frontiers in plant science*, 15, 1345708.

Xu Y, et al. (2024) Kinship analysis and pedigree reconstruction by RAD sequencing in cattle. *GigaByte (Hong Kong, China)*, 2024, 1.

Zhou W, et al. (2024) Divergent Selection in Low Recombination Regions Shapes the Genomic Islands in Two Incipient Shorebird Species. *Molecular biology and evolution*, 41(2).

Sar P, et al. (2024) Exploring Genetic Diversity within aus Rice Germplasm: Insights into the Variations in Agro-morphological Traits. *Rice (New York, N.Y.)*, 17(1), 20.

Shen C, et al. (2023) *E. urophylla* × *E. grandis* high-quality genome and comparative genomics provide insights on evolution and diversification of eucalyptus. *BMC genomics*, 24(1), 223.

Srivastava R, et al. (2023) Genealogical Analyses of 3 Cultivated and 1 Wild Specimen of *Vitis vinifera* from Greece. *Genome biology and evolution*, 15(12).

Shahmohamadloo RS, et al. (2023) Intraspecific genetic variation is critical to robust toxicological predictions of aquatic contaminants. *bioRxiv : the preprint server for biology*.

Hang Y, et al. (2023) Genetic Diversity and Breeding Signatures for Regional Indica Rice Improvement in Guangdong of Southern China. *Rice (New York, N.Y.)*, 16(1), 25.

Njaci I, et al. (2023) Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. *Nature communications*, 14(1), 1915.

Wu XL, et al. (2023) Comparative genomics of widespread and narrow-range white-bellied rats in the *Niviventer niviventer* species complex sheds light on invasive rodent success. *Zoological research*, 44(6), 1052.

Li D, et al. (2023) Genome and whole-genome resequencing of *Cinnamomum camphora* elucidate its dominance in subtropical urban landscapes. *BMC biology*, 21(1), 192.

Everitt T, et al. (2023) The Genomic Basis of Adaptation to High Elevations in Africanized Honey Bees. *Genome biology and evolution*, 15(9).

Zhang Q, et al. (2023) Re-sequencing and morphological data revealed the genetics of stone shell and kernel traits in apricot. *Frontiers in plant science*, 14, 1196754.

Yang Y, et al. (2023) Genome sequencing of *Sitopsis* species provides insights into their contribution to the B subgenome of bread wheat. *Plant communications*, 4(4), 100567.

Dai F, et al. (2023) Genomic Resequencing Unravels the Genetic Basis of Domestication, Expansion, and Trait Improvement in *Morus Atropurpurea*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 10(24), e2300039.