

Resource Summary Report

Generated by [kravitz2](#) on Aug 23, 2026

XP-CLR

RRID:SCR_004961

Type: Tool

Proper Citation

XP-CLR (RRID:SCR_004961)

Resource Information

URL: <https://reich.hms.harvard.edu/software>

Proper Citation: XP-CLR (RRID:SCR_004961)

Description: XP-CLR (Chen et al. 2010) uses allele frequency differentiation at linked loci to detect selective sweeps. Source code and documentation are available.

Synonyms: XP-CLR Software

Resource Type: software resource, source code

Availability: Restricted

Resource Name: XP-CLR

Resource ID: SCR_004961

Alternate IDs: nlx_94751

Alternate URLs: <https://reich.hms.harvard.edu/software>

Old URLs: http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260821T193729+0000

Ratings and Alerts

No rating or validation information has been found for XP-CLR.

No alerts have been found for XP-CLR.

Data and Source Information

Usage and Citation Metrics

We found 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Zhang H, et al. (2026) Allelic variation at a single locus distinguishes spring and winter faba beans. *Nature genetics*, 58(3), 655.

Zhu Z, et al. (2026) Protocol for the identification of selected genes and haplotype analysis in soybean using next-generation sequencing. *STAR protocols*, 7(1), 104290.

Zhao C, et al. (2026) Genome-wide variation landscape reveals temperature adaptation in Chinese indigenous cattle. *Journal of animal science and biotechnology*, 17(1).

Wang L, et al. (2026) Integrated whole-genome resequencing and mRNA-miRNA analysis reveals selection signals and regulatory networks of antipyretic effect variation in *Morus alba* var. *multicaulis*. *BMC biotechnology*, 26(1).

Zhou Z, et al. (2026) Integrative multi-omics analysis reveals the domestication mechanism of black rice. *National science review*, 13(10), nwaf497.

Peng W, et al. (2025) Investigation of selection signatures of dairy goats using whole-genome sequencing data. *BMC genomics*, 26(1), 234.

Zhao Y, et al. (2025) Genomic selection and genetic architecture of agronomic traits during modern flowering Chinese cabbage breeding. *Horticulture research*, 12(2), uhae299.

Lv G, et al. (2025) Integrating parental genomes to reduce reference bias and identify intramuscular fat genes in Qinchuan Black pigs. *Journal of animal science and biotechnology*, 16(1), 104.

Xu Y, et al. (2025) The PeachSNP170K array facilitates insights into a large-scale population relatedness and genetic impacts on citrate content and flowering time. *Communications biology*, 8(1), 854.

Baek J, et al. (2025) Genomic insights into Yanbian cattle: Breed-specific selective sweeps identified by whole-genome sequencing. *PloS one*, 20(9), e0331448.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Yang M, et al. (2025) Genomic insights into the domestication and genetic basis of yield in papaya. *Horticulture research*, 12(5), uhaf045.

Wang Y, et al. (2025) Latitude-driven adaptive evolution of body length in diverse pig breeds across China. *BMC biology*, 23(1), 150.

Wang W, et al. (2025) Multi-omics integrated analysis reveals the molecular mechanism of tail fat deposition differences in sheep with different tail types. *BMC genomics*, 26(1), 465.

Long Z, et al. (2025) Evolutionary Genomics Unravels the Responses and Adaptation to Climate Change in a Key Alpine Forest Tree Species. *Molecular biology and evolution*, 42(7).

Guo N, et al. (2024) A graph-based pan-genome of *Brassica oleracea* provides new insights into its domestication and morphotype diversification. *Plant communications*, 5(2), 100791.

Li B, et al. (2024) Natural selection and genetic diversity maintenance in a parasitic wasp during continuous biological control application. *Nature communications*, 15(1), 1379.

Lin R, et al. (2024) Whole-genome selection signature differences between Chaohu and Ji'an red ducks. *BMC genomics*, 25(1), 522.

He Y, et al. (2024) Genomic insight into the origin, domestication, dispersal, diversification and human selection of Tartary buckwheat. *Genome biology*, 25(1), 61.

Qi L, et al. (2024) Genetic characteristics and selection signatures between Southern Chinese local and commercial chickens. *Poultry science*, 103(7), 103863.