Resource Summary Report

Generated by NIF on May 20, 2025

liftOver

RRID:SCR_018160
Type: Tool

Proper Citation

liftOver (RRID:SCR_018160)

Resource Information

URL: https://genome.ucsc.edu/cgi-bin/hgLiftOver

Proper Citation: liftOver (RRID:SCR_018160)

Description: Web tool to convert genome coordinates and genome annotation files between assemblies. Used to translate genomic coordinates from one assembly version into another and retrieves putative orthologous regions in other species using UCSC chained and netted alignments.

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

Defining Citation: DOI:10.1093/nar/gkj144

Keywords: Convert genome coordinate, genome annotation file, translate genomic coordinate, assembly version, retrieve orthologous region

Funding: NHGRI ;
Howard Hughes Medical Institute ;
NCI

Availability: Free, Available for download, Freely available

Resource Name: liftOver

Resource ID: SCR_018160

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250519T204539+0000

Ratings and Alerts

No rating or validation information has been found for liftOver.

No alerts have been found for liftOver.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 654 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Weng LC, et al. (2025) The impact of common and rare genetic variants on bradyarrhythmia development. Nature genetics, 57(1), 53.

Eulalio T, et al. (2025) regionalpcs improve discovery of DNA methylation associations with complex traits. Nature communications, 16(1), 368.

Mai J, et al. (2025) scTWAS Atlas: an integrative knowledgebase of single-cell transcriptome-wide association studies. Nucleic acids research, 53(D1), D1195.

Bá?ová A, et al. (2025) Genomic Rewilding of Domestic Animals: The Role of Hybridization and Selection in Wolfdog Breeds. Genes, 16(1).

Jung S, et al. (2025) Rare Variant Analyses in Ancestrally Diverse Cohorts Reveal Novel ADHD Risk Genes. medRxiv : the preprint server for health sciences.

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Tomczak K, et al. (2025) Plasma DNA Methylation-Based Biomarkers for MPNST Detection in Patients With Neurofibromatosis Type 1. Molecular carcinogenesis, 64(1), 44.

Nakatochi M, et al. (2025) Copy number variations in RNF216 and postsynaptic membrane-associated genes are associated with bipolar disorder: a case-control study in the Japanese population. Psychiatry and clinical neurosciences, 79(1), 12.

Cao C, et al. (2025) GWAShug: a comprehensive platform for decoding the shared genetic basis between complex traits based on summary statistics. Nucleic acids research, 53(D1), D1006.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. Molecular cell, 85(1), 24.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the Saudi Arabian population. bioRxiv : the preprint server for biology.

Wu LY, et al. (2024) Investigation of the genetic aetiology of Lewy body diseases with and without dementia. Brain communications, 6(4), fcae190.

Tan MMX, et al. (2024) Genome-wide determinants of mortality and motor progression in Parkinson's disease. NPJ Parkinson's disease, 10(1), 113.

Recinos Y, et al. (2024) Lineage-specific splicing regulation of MAPT gene in the primate brain. Cell genomics, 4(6), 100563.

Xu C, et al. (2024) Reference-informed prediction of alternative splicing and splicing-altering mutations from sequences. bioRxiv : the preprint server for biology.

Kerdoncuff E, et al. (2024) 50,000 years of Evolutionary History of India: Insights from ~2,700 Whole Genome Sequences. bioRxiv : the preprint server for biology.

Burnham KL, et al. (2024) eQTLs identify regulatory networks and drivers of variation in the individual response to sepsis. Cell genomics, 4(7), 100587.

Deguchi Y, et al. (2024) Subtype-specific alternative splicing events in breast cancer identified by large-scale data analysis. Scientific reports, 14(1), 14158.

Lochs SJA, et al. (2024) Combinatorial single-cell profiling of major chromatin types with MAbID. Nature methods, 21(1), 72.

Yang L, et al. (2024) Evolutionary insights from profiling LINE-1 activity at allelic resolution in a single human genome. The EMBO journal, 43(1), 112.