Resource Summary Report

Generated by T1D on Aug 2, 2026

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: 20260801T190849+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 762 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Park J, et al. (2026) A robust pleiotropy method with applications to lipid traits and to inflammatory bowel disease subtypes with sample overlap. HGG advances, 7(1), 100501.

Rraku E, et al. (2026) Developing Del2Phen: A Novel Phenotype Description Tool for Chromosome Deletions. Human mutation, 2026, 5239482.

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. Nature, 649(8095), 152.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. medRxiv : the preprint server for health sciences.

Diamond B, et al. (2025) Mutagenic Impact and Evolutionary Influence of Chemoradiotherapy in Hematologic Malignancies. Blood cancer discovery, 6(5), 450.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. Cell reports. Medicine, 6(8), 102278.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Jiang Q, et al. (2025) HIF regulates multiple translated endogenous retroviruses: Implications for cancer immunotherapy. Cell, 188(7), 1807.

Lobo D, et al. (2025) Ancient dog introgression into the Iberian wolf genome may have facilitated adaptation to human-dominated landscapes. Genome research, 35(3), 432.

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. Cell genomics, 5(3), 100775.

Jönsson J, et al. (2025) Impact of excess sugar on the whole genome DNA methylation pattern in human sperm. Epigenomics, 17(2), 89.

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

Torres-Oliva M, et al. (2025) Heterochrony in orthodenticle expression is associated with ommatidial size variation between Drosophila species. BMC biology, 23(1), 34.

Mandla R, et al. (2025) Large-scale admixture mapping in the All of Us Research Program improves the characterization of cross-population phenotypic differences. medRxiv : the preprint server for health sciences.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. Cancer discovery, 15(4), 717.

Cai W, et al. (2025) Mammary gland multi-omics data reveals new genetic insights into milk production traits in dairy cattle. PLoS genetics, 21(4), e1011675.

Gotoh-Saito S, et al. (2025) Drug-induced cis-regulatory elements in human hepatocytes affect molecular phenotypes associated with adverse reactions. Nature communications, 16(1), 3851.

Khodursky S, et al. (2025) Plasma proteome-wide Mendelian randomization reveals the association of extracellular matrix proteins with abdominal aortic aneurysm. JVS-vascular science, 6, 100290.

Pérez-Jeldres T, et al. (2025) Prediction of Extraintestinal Manifestations in Inflammatory Bowel Disease Using Clinical and Genetic Variables with Machine Learning in a Latin IBD Group. International journal of molecular sciences, 26(12).

Sagulkoo P, et al. (2025) Integrative bioinformatics frameworks for abdominal aortic aneurysm using GWAS meta-analysis, biological network construction, and structural modeling. Scientific reports, 15(1), 22331.