Resource Summary Report

Generated by kravitz2 on Aug 3, 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, service resource, data processing software, software application

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: 20260803T040754+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 kravitz2 .

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.

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.

Hinken J, et al. (2025) Translocations associated with colour-sidedness are common in northern Swedish cattle breeds. Hereditas, 162(1), 122.

Kosugi S, et al. (2025) TRsv: simultaneous detection of tandem repeat variations, structural variations, and short indels using long read sequencing data. Genome biology, 26(1), 246.

Liu Z, et al. (2025) Single-cell multiregion epigenomic rewiring in Alzheimer's disease progression and cognitive resilience. Cell, 188(18), 4980.

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

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.

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.

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

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

Mills JV, et al. (2025) Detection of Genome-Wide IGF-1R Recruitment to Enhancer and Promoter Regions of Chromatin in Clinical Prostate Cancers. Cancer medicine, 14(19), e71257.

Mouillet JF, et al. (2025) The Chromosome 19 miRNA cluster guards trophoblasts against overacting innate immunity. Communications biology, 8(1), 1511.

Chakraborty S, et al. (2025) Noncoding and coding mechanisms of aging-related heart failure with preserved ejection fraction associated with thyroid dysfunction. Disease models & mechanisms, 18(11).

Baniulyte G, et al. (2025) p53motifDB: integration of genomic information and tumour suppressor p53 binding motifs. Database : the journal of biological databases and curation, 2025.