

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 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: data processing software, service resource, software application, software resource

Defining Citation: [DOI:10.1093/nar/gkj144](https://doi.org/10.1093/nar/gkj144)

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

Funding: Howard Hughes Medical Institute ;
NCI ;
NHGRI

Availability: Free, Available for download, Freely available

Resource Name: liftOver

Resource ID: SCR_018160

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260905T133054+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 885 mentions in open access literature.

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

Payne E, et al. (2026) Behavioral Features in Phelan-McDermid Syndrome: Characteristics and Genetic and Metabolic Contributions in a Cohort of 56 Individuals. *Genes*, 17(2).

Li M, et al. (2026) Genome-wide association study reveals candidate genes for body size and reproductive traits in Hu sheep. *Animal bioscience*, 39(5), 250716.

Zheng Y, et al. (2026) Classification of SINE Tails in the Porcine Genome and Its Potential Impact on VWA8 Gene. *Genes*, 17(2).

Tian W, et al. (2026) Genetic alternative splicing regulation mapping of cartilage and synovium reveals tissue-specific mechanisms of joint-related traits. *Nature communications*, 17(1).

Ma X, et al. (2026) Development and application of a 10 K low-density whole-genome SNP array for chickens. *Poultry science*, 105(6), 106707.

Moreno E, et al. (2026) Genome-wide association meta-analyses over one million individuals identify 54 loci associated with urinary incontinence and its subtypes. *medRxiv* : the preprint server for health sciences.

Li S, et al. (2026) MYC-bound enhancer RNAs in cis regulate gene transcription and tumorigenesis. *Science advances*, 12(17), eaeb5147.

Ren W, et al. (2026) A Murine Database of Structural Variants Identifies A Candidate Gene for a Spontaneous Murine Lymphoma Model. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(17), e22890.

Rojat V, et al. (2026) Automated mapping of DNA replication fork progression in human cells with ForkML. *Nature communications*, 17(1).

Liu J, et al. (2026) Mendelian randomization study of GLP-1R effects on ovarian cancer subtypes mediated by metabolic factors. *Communications medicine*, 6(1), 113.

Citu C, et al. (2026) VISDB 2.0: A manually curated resource of viral integration sites and their regulatory maps in human diseases. *Scientific data*, 13(1).

Vallée Marcotte B, et al. (2026) Agnostic polygenic prediction of weight loss after bariatric surgery. JCI insight, 11(9).

Zhang W, et al. (2026) An atlas of genetic effects on the monocyte methylome across European and African populations. Genome medicine, 18(1).

He LS, et al. (2026) Multi-omic profiling of human and mouse dorsal root ganglia enables targeted gene delivery to nociceptors. bioRxiv : the preprint server for biology.

Singh N, et al. (2026) Chromatin dynamics identifies 78 genes at loci associated with elevated intraocular pressure and primary open-angle glaucoma. bioRxiv : the preprint server for biology.

Ding W, et al. (2026) Accurate and efficient HiChIP interaction detection by modeling restriction enzyme cut site density as biological signal. Briefings in bioinformatics, 27(3).

Fu B, et al. (2026) The molecular asynchrony of single cells. bioRxiv : the preprint server for biology.

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

Pielies Avellí M, et al. (2026) Modeling nascent transcription from chromatin landscape and structure with CLASTER. Genome biology, 27(1).

Dekkers KF, et al. (2026) Genome-wide association analyses highlight the role of the intestinal molecular environment in human gut microbiota variation. Nature genetics, 58(3), 540.