



Lift Genome Annotations

This tool converts genome coordinates and genome annotation files between assemblies. The input data can be pasted into the text box, or uploaded from a file. If a pair of assemblies cannot be selected from the pull-down menus, a direct lift between them is unavailable. However, a sequential lift may be possible. Example: lift from Mouse, May 2004, to Mouse, Feb. 2006, and then from Mouse, Feb. 2006 to Mouse, July 2007 to achieve a lift from mm5 to mm9.

Original Genome:

Original Assembly:

New Genome:

New Assembly:

D. melanogaster

Aug. 2014 (BDGP Release 6 + ISO1 MT/dm6)

D. melanogaster

Apr. 2006 (BDGP R5/dm3)

Minimum ratio of bases that must remap:

0.95

BED 4 to BED 6 Options

Allow multiple output regions:

Minimum hit size in query:

Minimum chain size in target:

BED 12 Options

Min ratio of alignment blocks or exons that must map:

If thickStart/thickEnd is not mapped, use the closest mapped base:

Paste in data ([BED](#) or chrN:start-end formats):