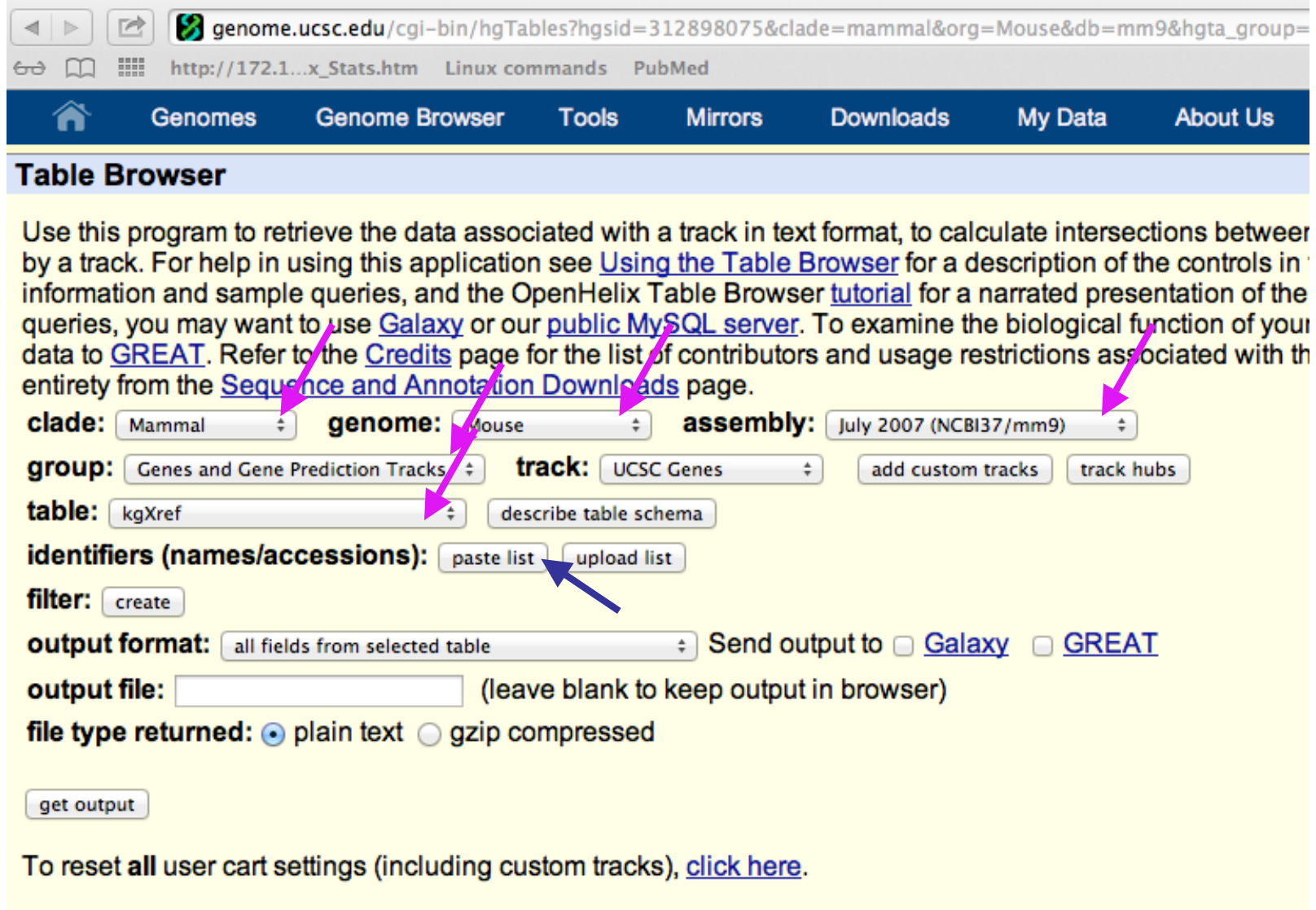


UCSC Table Browser upload



The screenshot shows the UCSC Table Browser interface. The browser's address bar contains the URL: `genome.ucsc.edu/cgi-bin/hgTables?hgsid=312898075&clade=mammal&org=Mouse&db=mm9&hgta_group=`. The navigation menu includes: Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, and About Us. The main heading is "Table Browser".

Below the heading is a descriptive paragraph: "Use this program to retrieve the data associated with a track in text format, to calculate intersections between by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with the entirety from the [Sequence and Annotation Downloads](#) page."

Form fields and controls include:

- clade:** Mammal
- genome:** Mouse
- assembly:** July 2007 (NCBI37/mm9)
- group:** Genes and Gene Prediction Tracks
- track:** UCSC Genes
- Buttons: add custom tracks, track hubs
- table:** kgXref
- Button: describe table schema
- identifiers (names/accessions):** paste list, upload list
- filter:** create
- output format:** all fields from selected table
- Send output to: Galaxy GREAT
- output file:** (leave blank to keep output in browser)
- file type returned:** plain text gzip compressed
- Button: get output

At the bottom, a note states: "To reset **all** user cart settings (including custom tracks), [click here](#)."

Annotations: Three pink arrows point to the "clade", "genome", and "assembly" dropdown menus. A blue arrow points to the "upload list" button.