

Table Browser

Use this program to get the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. See [Using the Table Browser](#) for a description of the controls in this form.

clade: Vertebrate **genome:** Human **assembly:** Mar. 2006

group: Genes and Gene Prediction Tracks **track:** Conservation

table: multiz17way [describe table schema](#)

region: genome position chr11:93103000-93108000

filter: [create](#)

intersection: [create](#)

correlation: [create](#)

output format: MAF - multiple alignment format

output file: region.maf (leave blank to keep output in browser)

file type returned: plain text gzip compressed

[get output](#) [summary/statistics](#)

To reset **all** user cart settings (including custom tracks), [click here](#).