

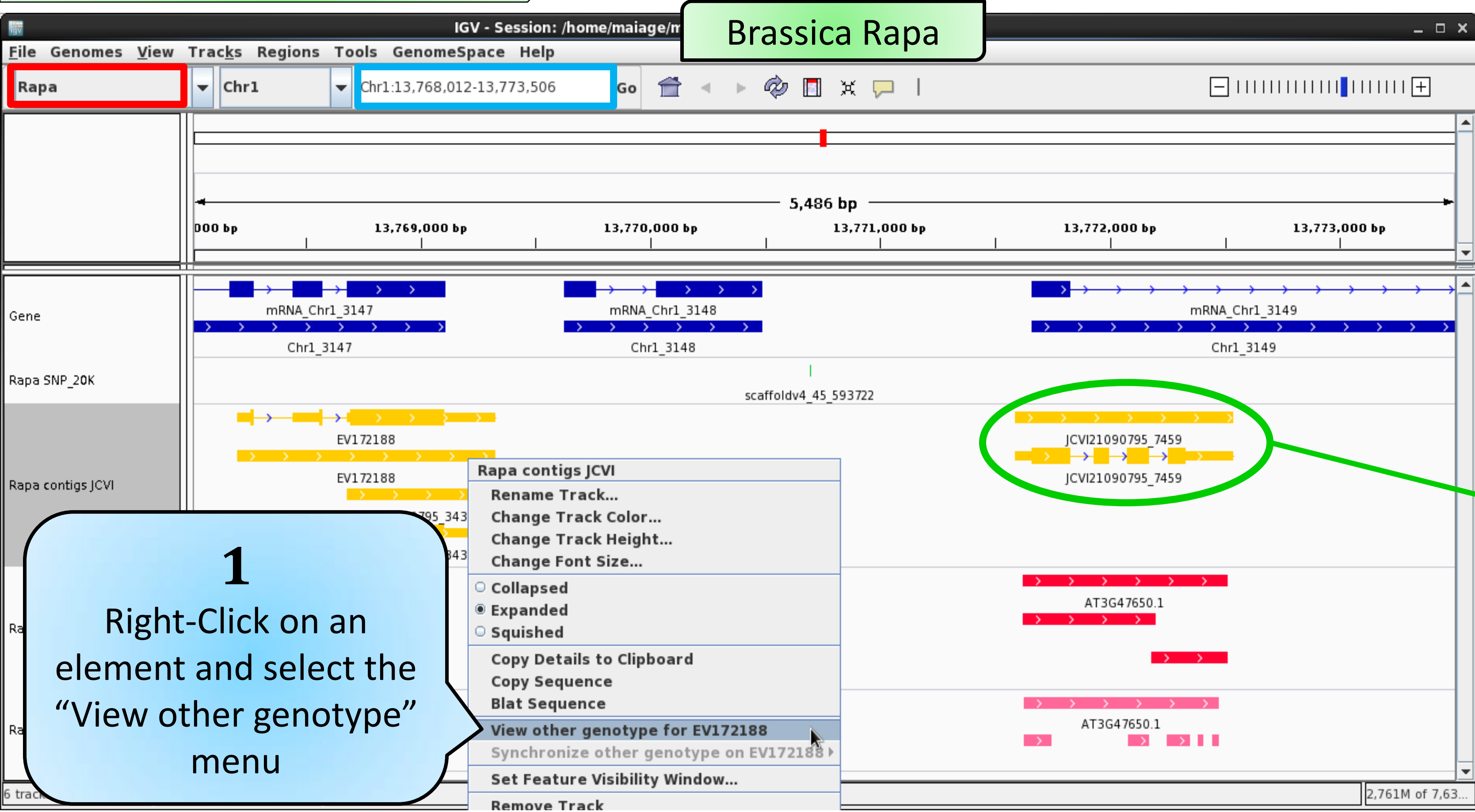
Abstract

IGV (Integrative Genomics Viewer) is a very efficient genome browser written in Java, allowing users to visualize and explore a large variety of genomic data types, but limited to a single genome. However, to perform comparative genomic studies, it is very useful to be able to observe different types of data simultaneously on several genotypes. As part of the BioDataCloud project, which received funding from the call for proposals "Cloud computing 3 - Big data" of Investments for the Future Initiative program, a collaboration between the INRA Migale platform and the Biogemma company was established to tackle this issue. According to the technical specifications set by Biogemma, a new feature has been added to IGV that allows users to jump to a new genotype from different types of data (genes, regions in genomic sequence, genetic markers) selected by the user on the reference genome. This jump results in the opening of a new IGV window on these data, if they are available for the new genotype. This window retains all IGV features and synchronizes simultaneously with the main window. The number of jumps achievable and therefore the number of simultaneously observable genotypes is unlimited and depends only upon the available hardware capabilities and the availability of the corresponding data. All jumps can be saved in an IGV session file allowing users to quickly restore already used genotypes and data or to share them with other.

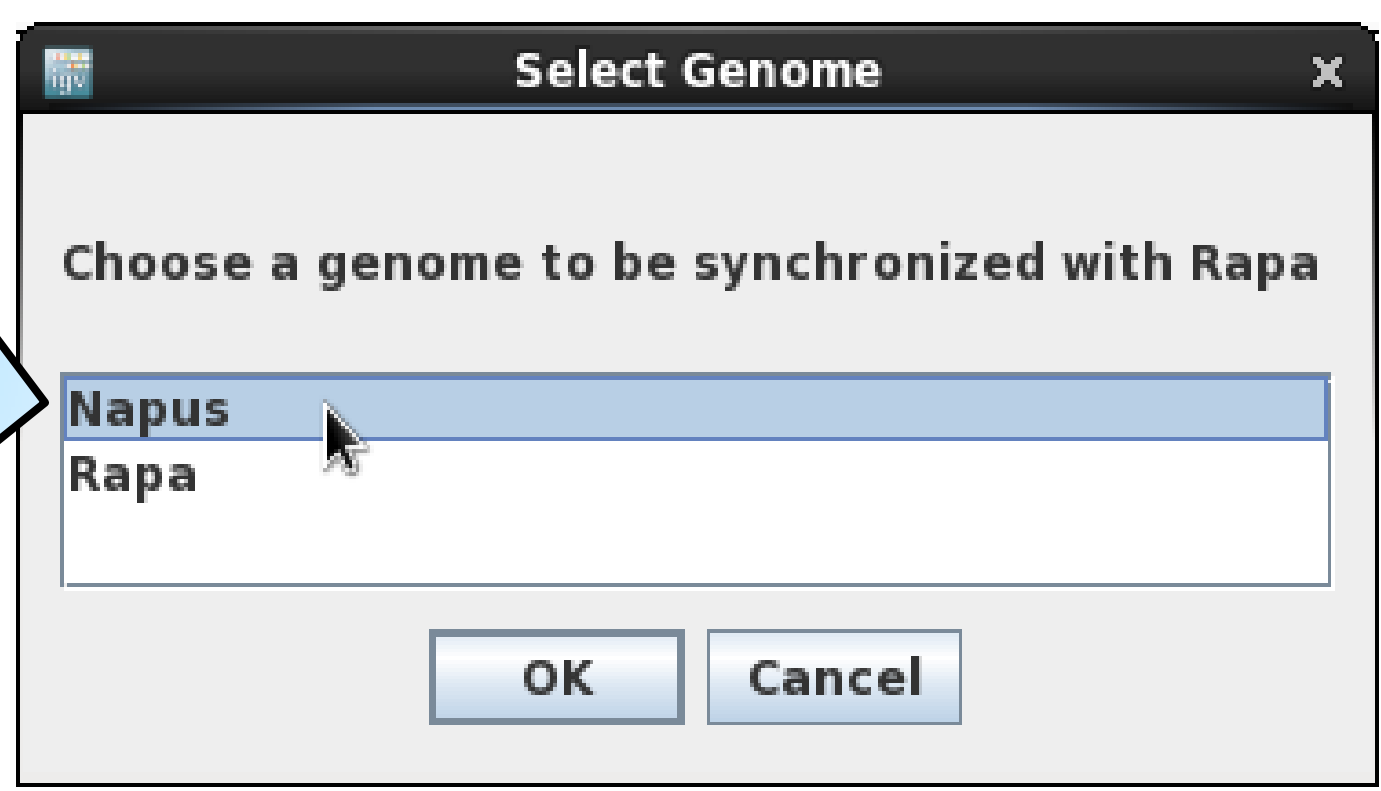
With this new feature, the user can now compare different genotypes with the reference genome and navigate between them synchronously while keeping the IGV performance.

Reference: Helga Thorvaldsdóttir, James T. Robinson, Jill P. Mesirov. **Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. Briefings in Bioinformatics 14, 178-192 (2013)**

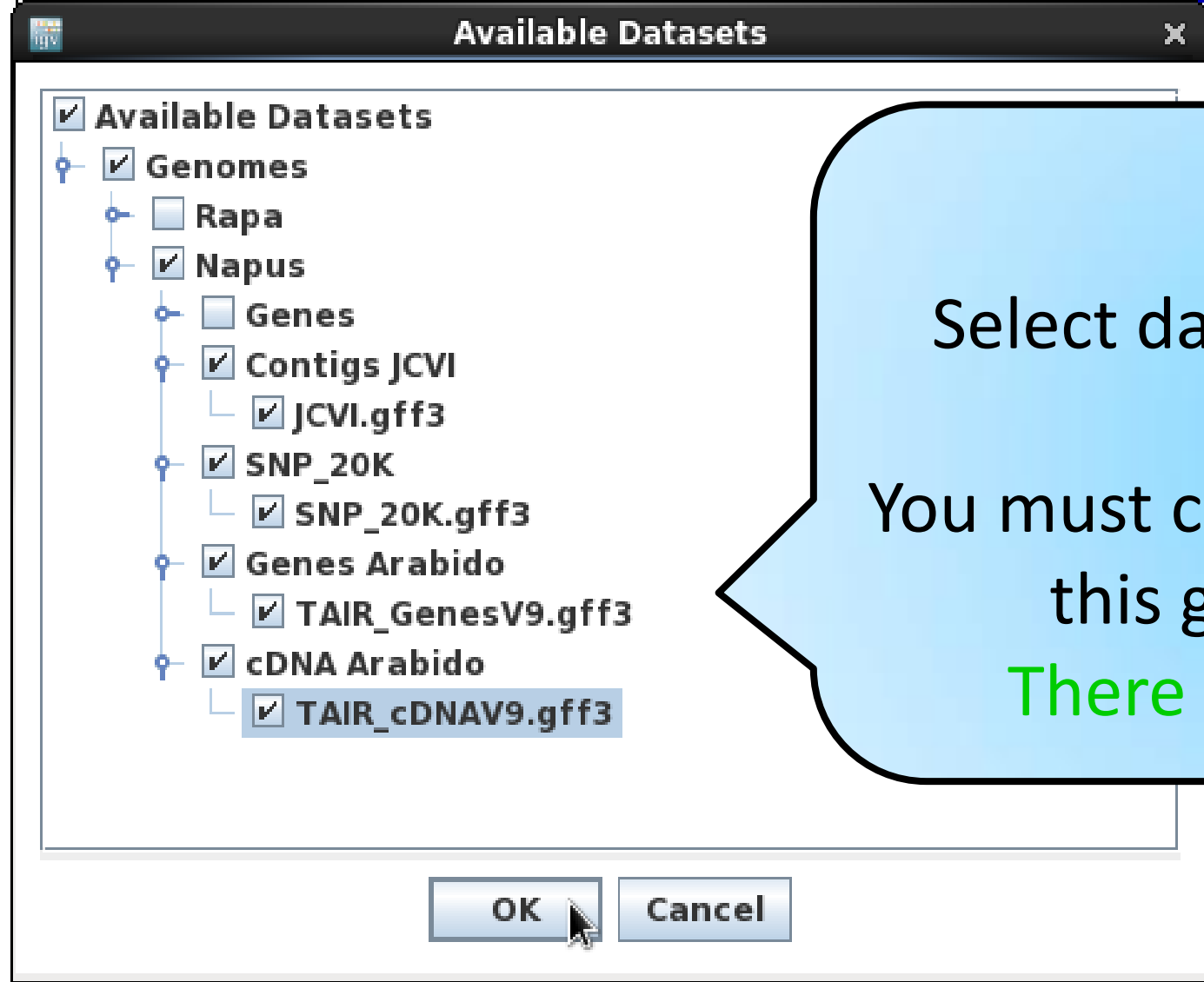
Jump, view and compare



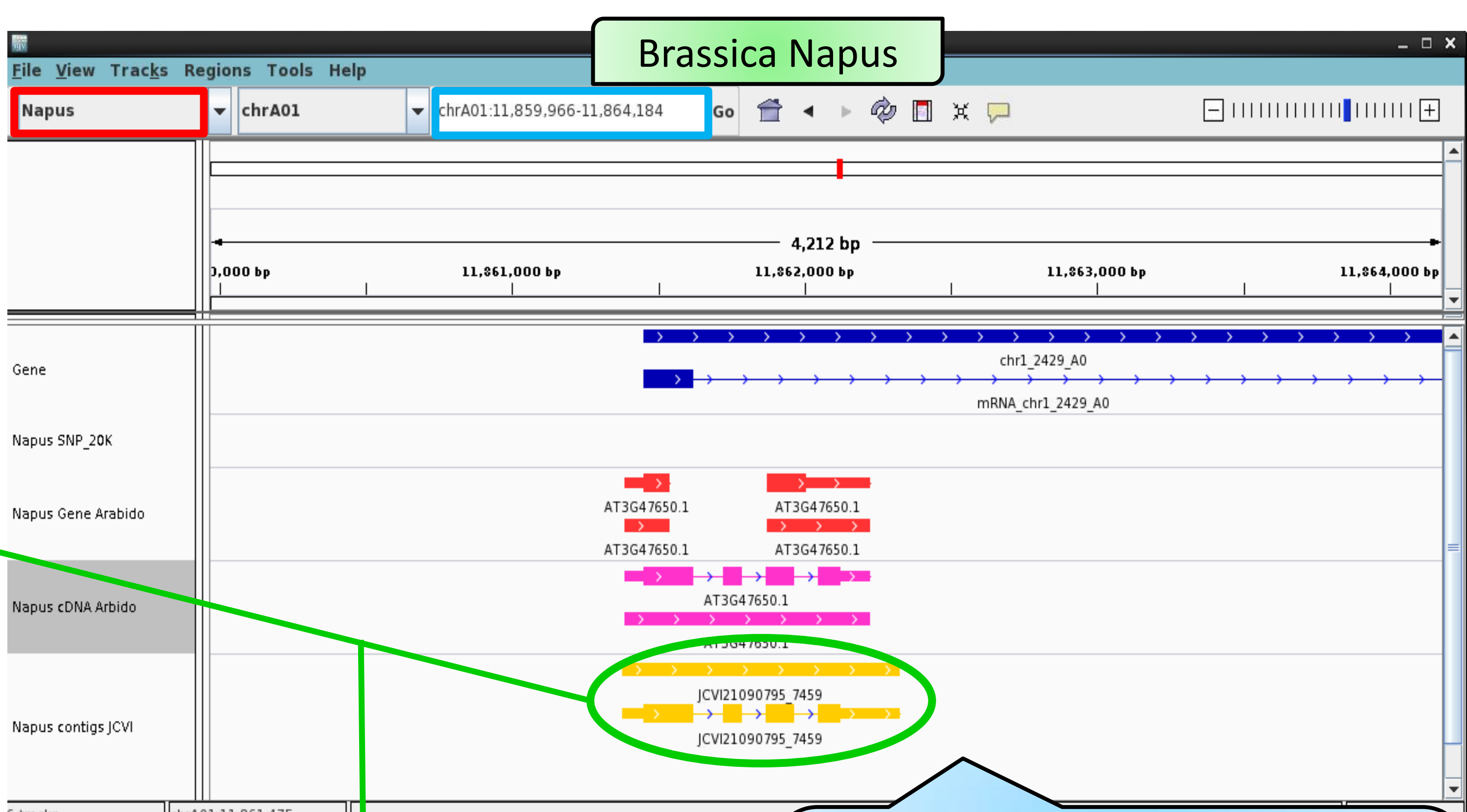
1
Right-Click on an element and select the "View other genotype" menu



2
Select the new genome to be viewed



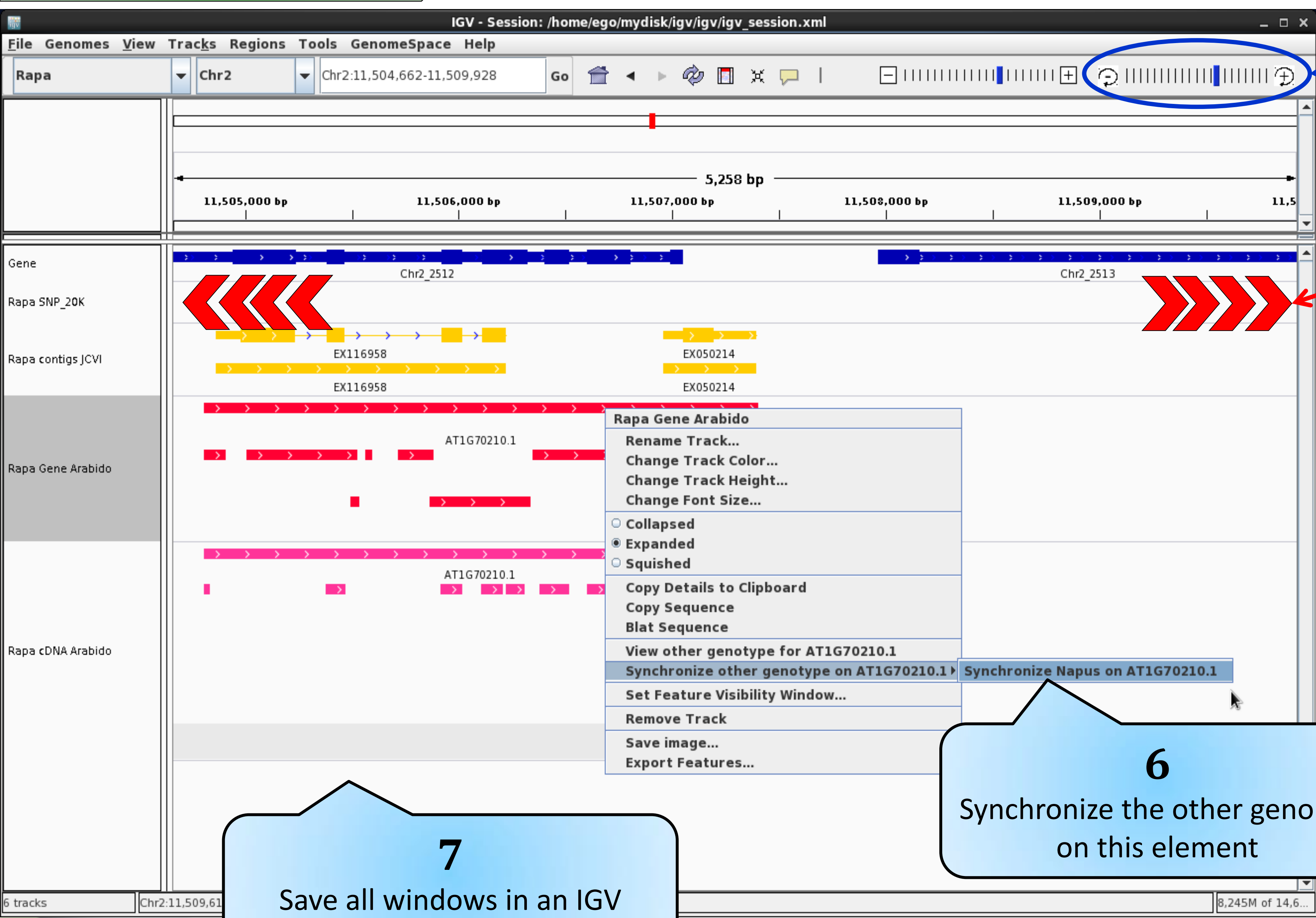
3
Select data to be viewed on the new genome. You must choose data to jump from this genome to another. There needs to be a match



4
A new IGV window opens on the selected genome. This window keeps all IGV features

Available on the IFB cloud

Explore and synchronize



5
Explore, move and zoom simultaneously in all genomes from the main window

6
Synchronize the other genome on this element

7
Save all windows in an IGV session file

