

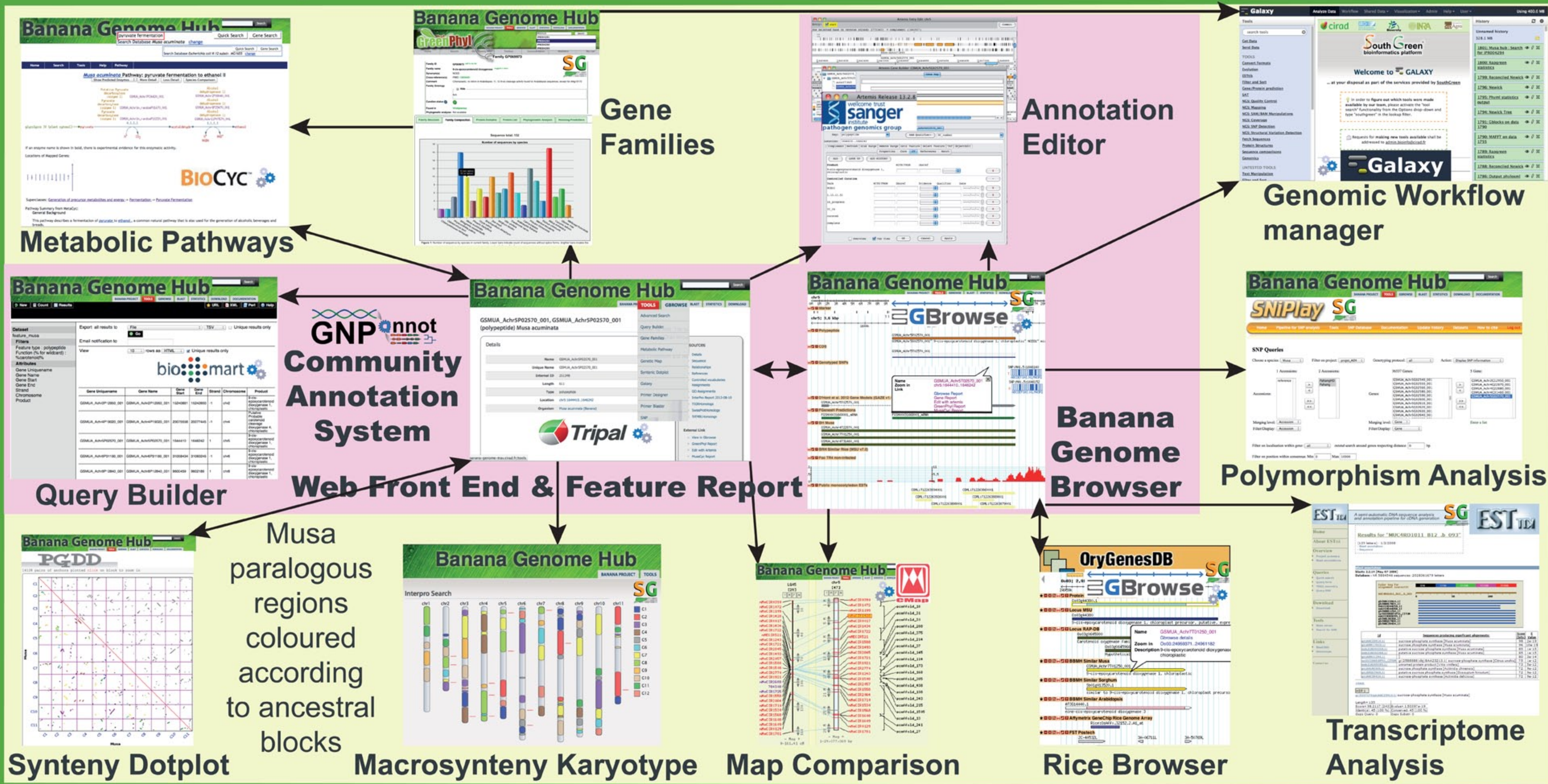
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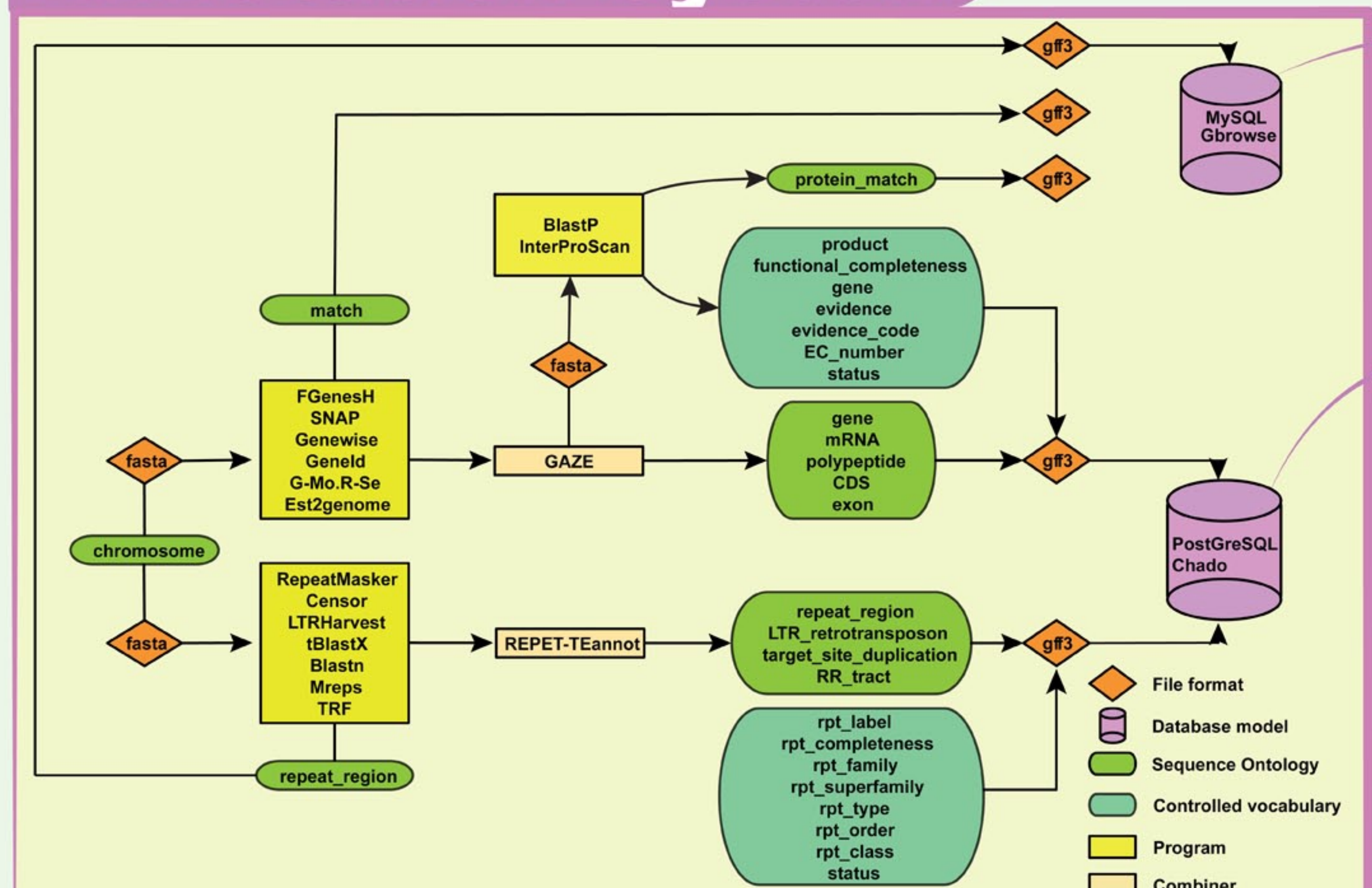


Banana is one of the world's favorite fruits and one of the most important crops for developing countries. The banana reference genome sequence (*Musa acuminata*) was recently released (1). To support genome studies, we developed a hub (2) that enhances interoperability between information systems containing genomics data on banana. Such hub is generic and is being extended to other species (Cacao, Coffee).

Hub Components

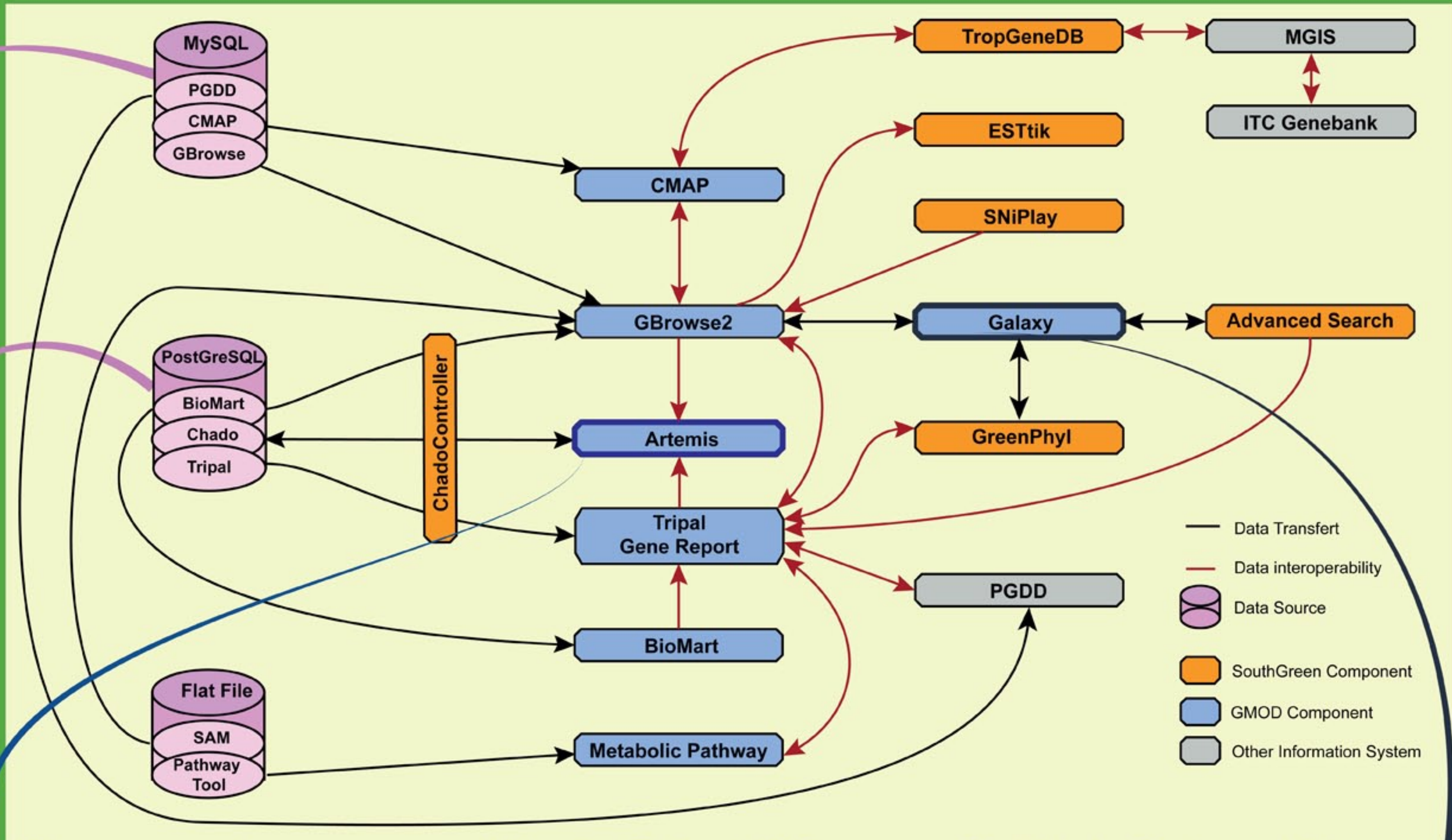


Annotation System



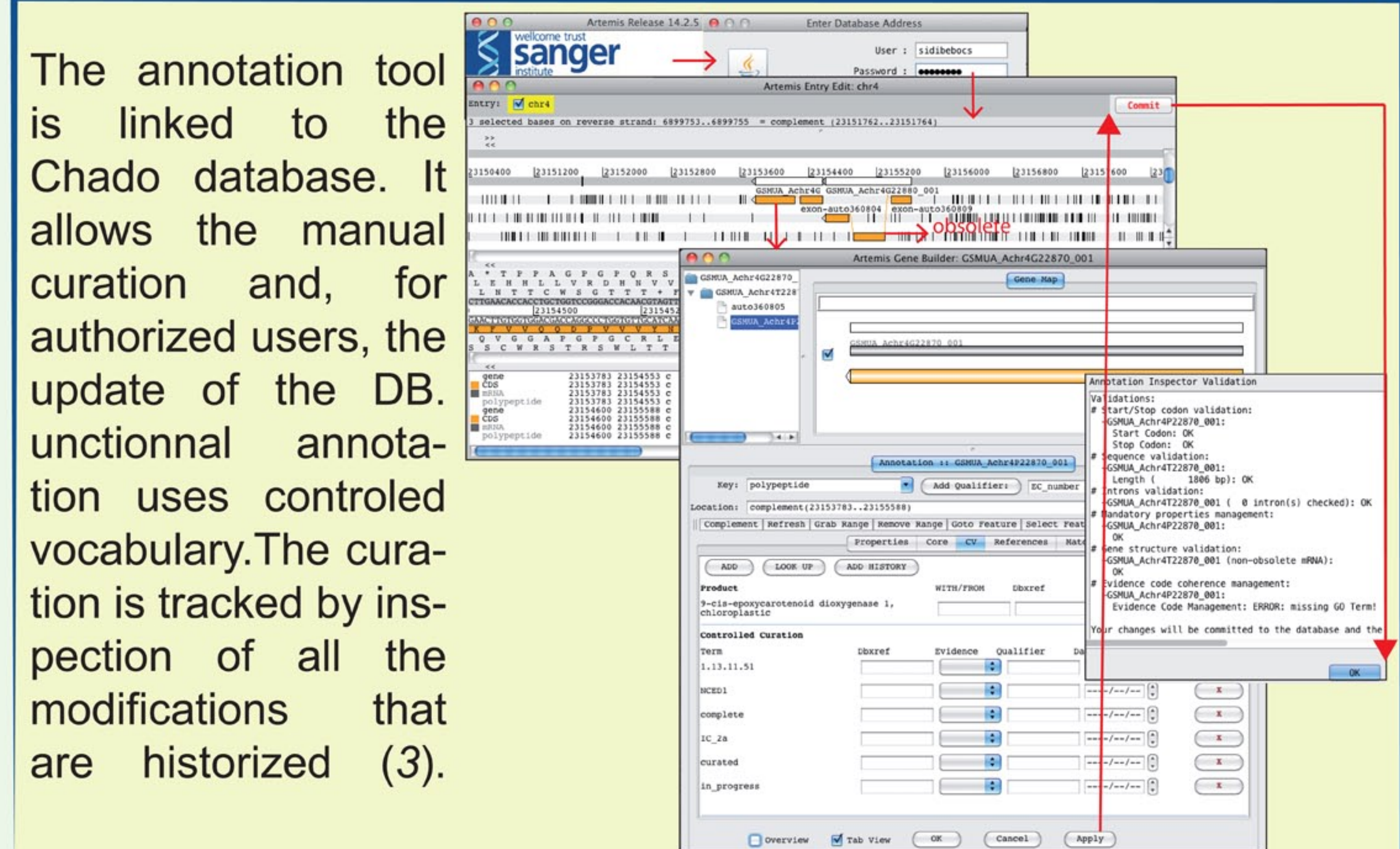
The sequence is analysed with pipelines predicting genes & repetitive elements. Results are structured with the Sequence Ontology & controlled vocabularies & formatted in GFF3 before insertion into Chado and GBrowse databases using Perl loaders.

Hub Architecture



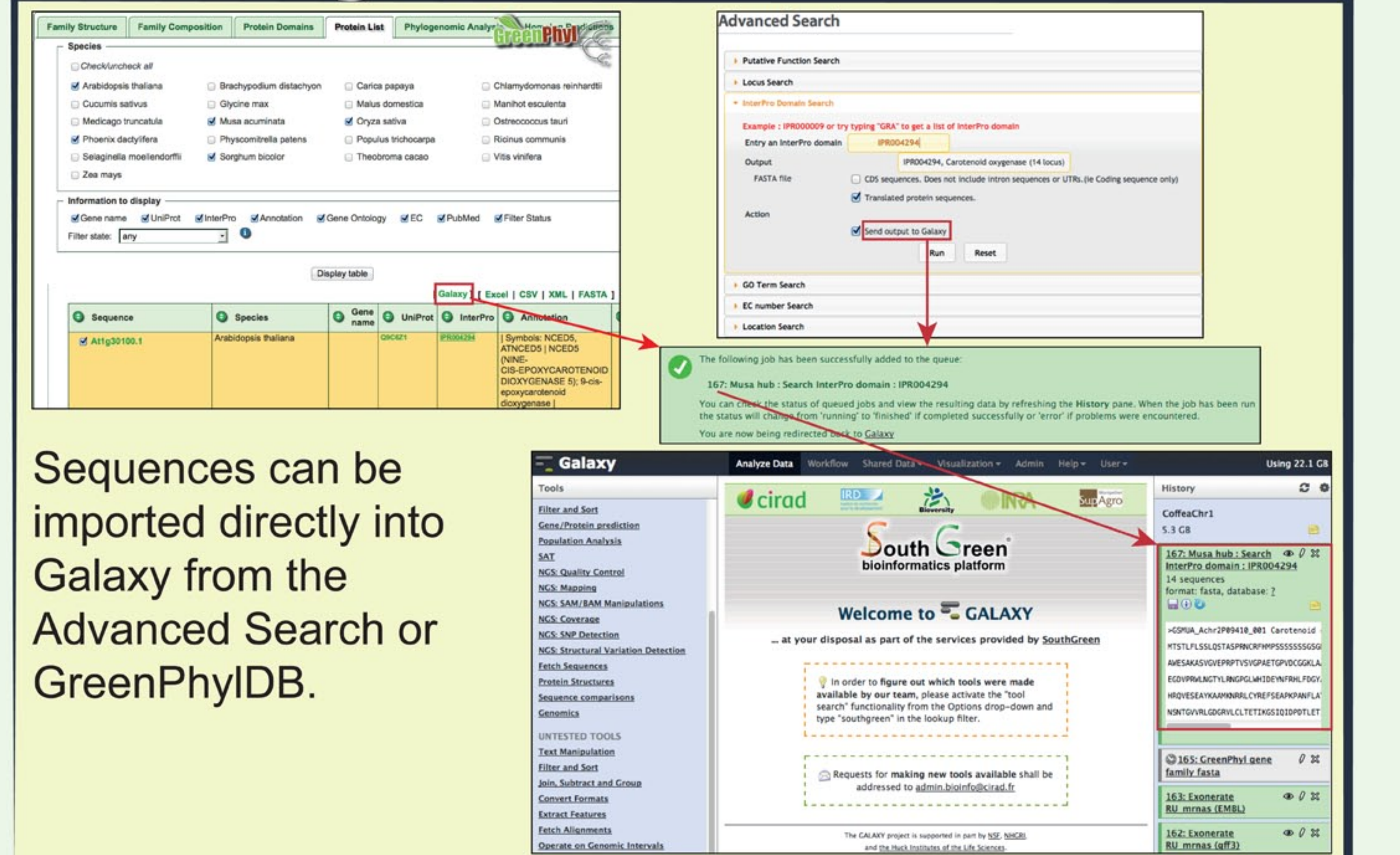
Gene reports are accessible via Tripal, GBrowse, BioMart. Polypeptides are analyzed with GreenPhylDB, Galaxy, MusaCyc, OryGenesDB. Genetic markers with CMAP & TropGeneDB linked to the Musa Germplasm Information System (MGIS). SNIPlay is dedicated to SNPs.

Artemis



(1) A. D'Hont et al., The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature*, 488:213, 2012.
 (2) G. Droc et al., The Banana Genome Hub. *Database: the journal of biological databases and curation*, 2013, Submitted revision (manuscript ID DATABASE-2012-0102.R1). BGH is supported by South Green Bioinformatics Platform <http://southgreen.cirad.fr/>

Galaxy



(3) V. Guignon et al., Chado Controller: advanced annotation management with a community annotation system. *Bioinformatics*, 28:1054, 2012.