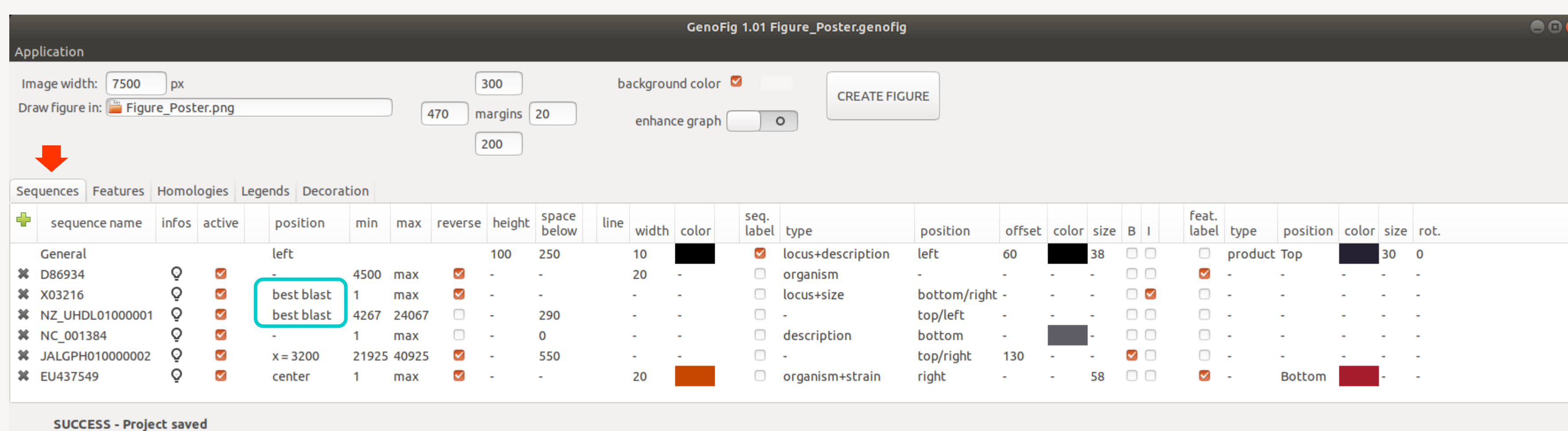


Visual comparison of genomic regions from related species or strains is crucial to understand the molecular evolutionary history of species, particularly in complex mobile regions [1]. **GenoFig** is a stand-alone graphical application dedicated to the generation of high quality figures for comparative genomics. It is intended to be as easy to use as possible and flexible enough to adapt to a variety of needs. The application works on Linux, MacOS and Windows platforms.

GenoFig is freely available under a GPL3 license at : <https://forgemia.inra.fr/public-pgba/genofig>

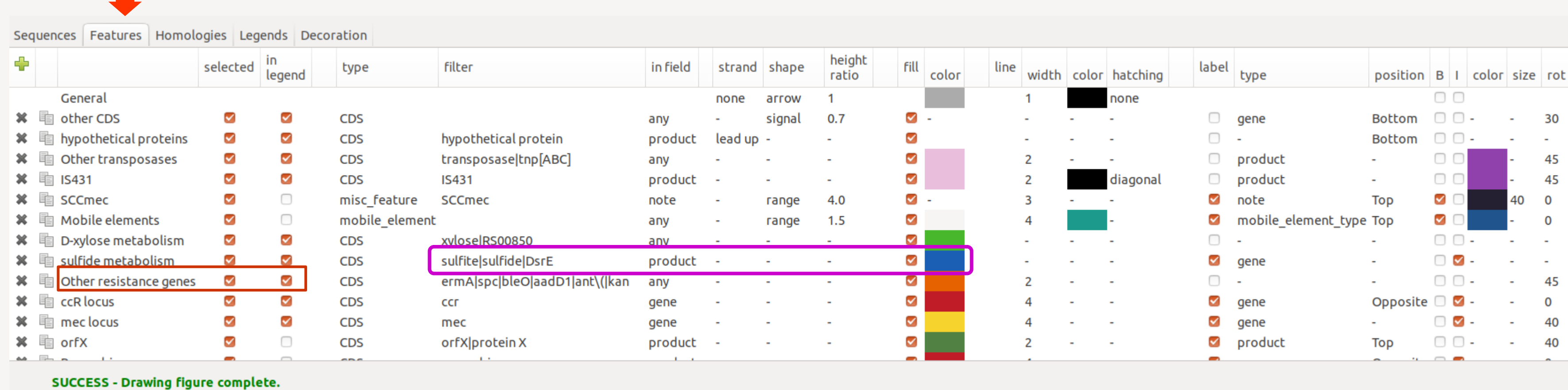
How to simply produce a figure with GenoFig?

1. Add sequences



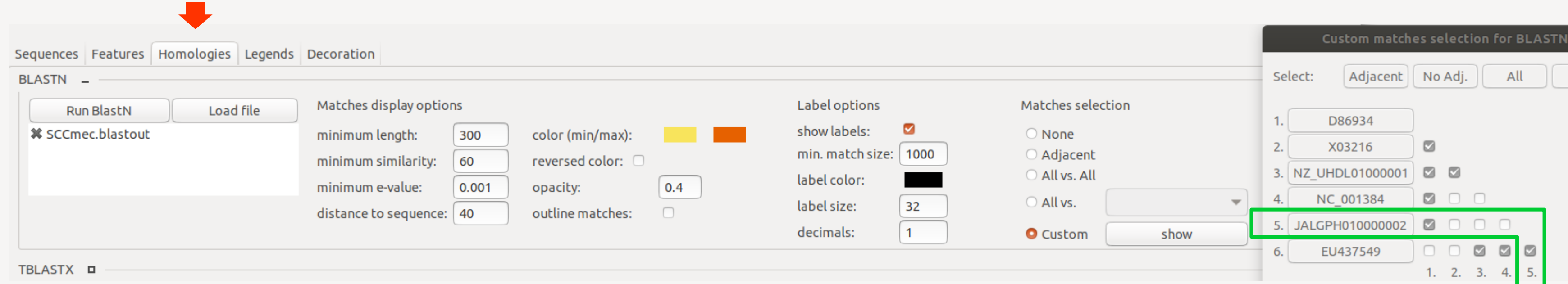
- (multi-)GenBank/FASTA accepted
- possibility to set up multiple parameters sequence by sequence or globally (General)
- a **'best blast'** option for sequence positioning, for optimal alignment of homologous regions.
- various information about sequences can be displayed as sequence labels

2. Add features



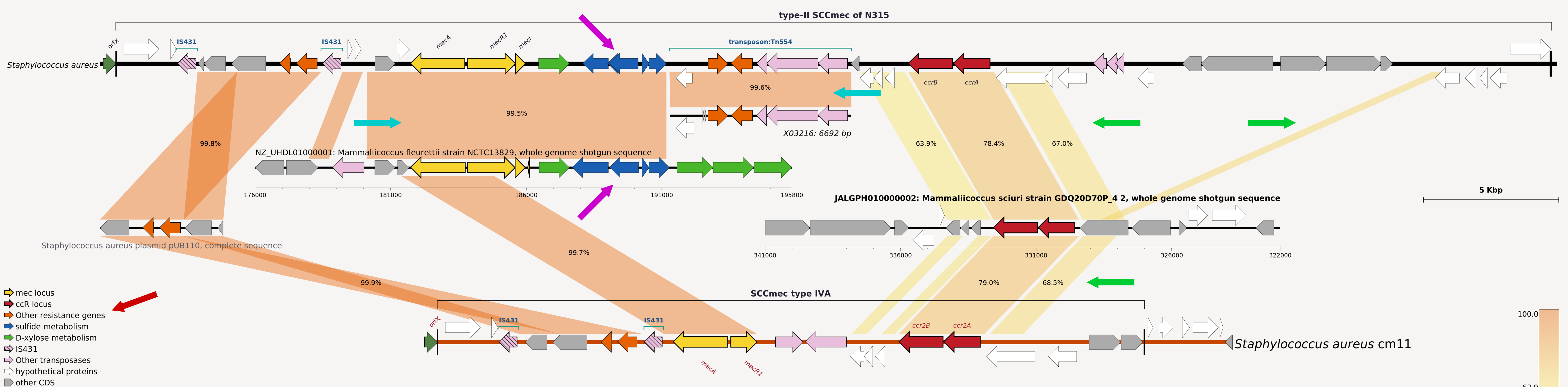
- displayed features are selected according to the detection of regular expressions ('filter' column) in user-defined fields of GenBank annotations.
- bottom-to-top priority: features will be displayed with parameters of the last matching filter (*i.e.* **transposases** of the **IS431** family will be displayed with hatching)
- feature names are user-defined and can be displayed in the legend.

3. Add homologies



- homologies are based on blastN or tblastX. Blast hits (matches) are stored in a file and are not computed every time.
- define which and how matches will be displayed
- select between which pair of sequences to display homologies with the **'Custom'** matches selection.

4. Create the figure



Technical implementation

GenoFig is developed in python3, using biopython and cairosvg modules. The GUI (graphical user interface) is implemented with the GTK3+ API. The drawing engine is based on the open-source code of **Easyfig 2** [2], with some major reimplementations.