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BioMercator: A complete framework to integrate QTL, meta-QTL, genome annotation and genome-wide association studies

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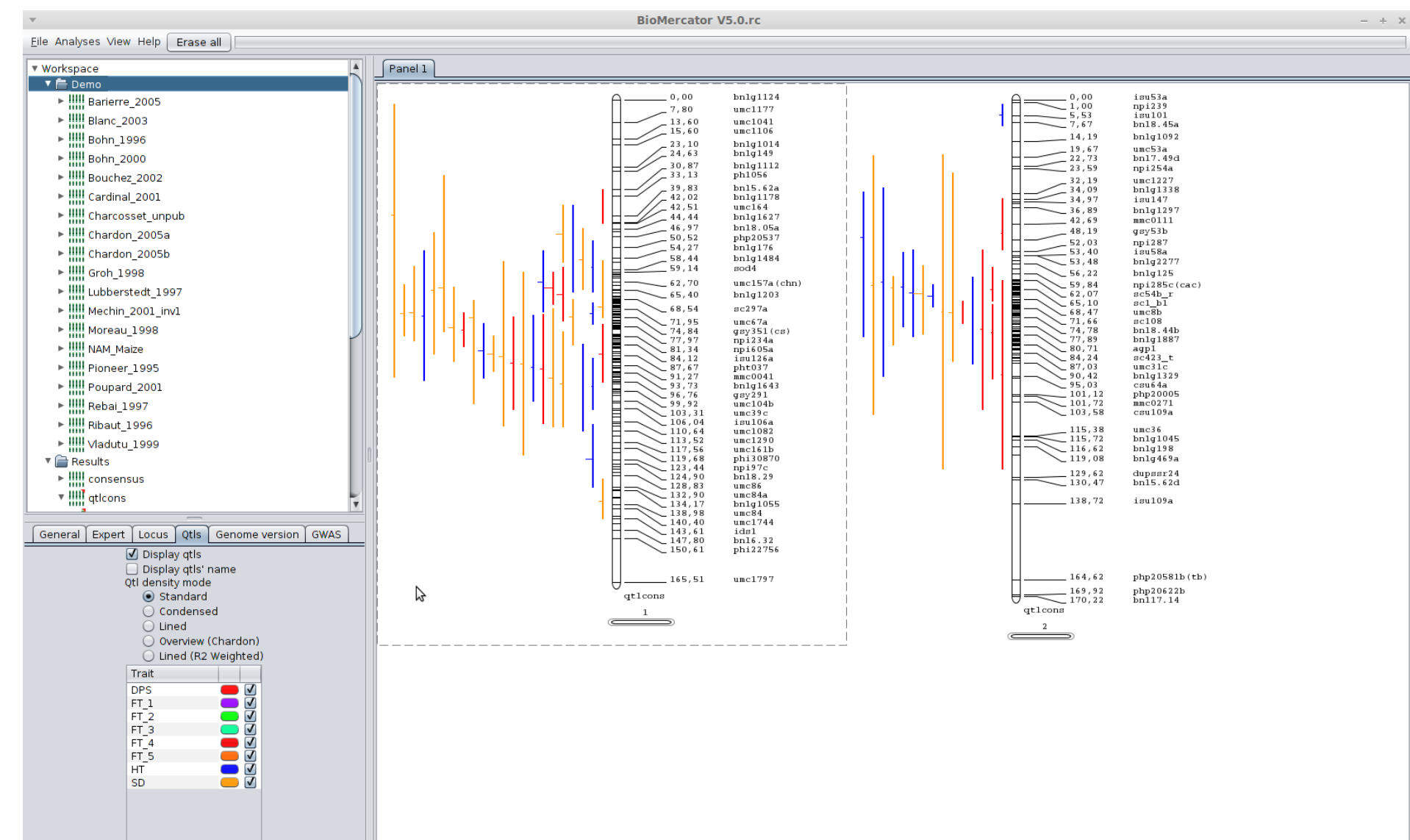
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BioMercator : A complete framework to integrate QTL, meta-QTL, genome annotation and genome-wide association studies

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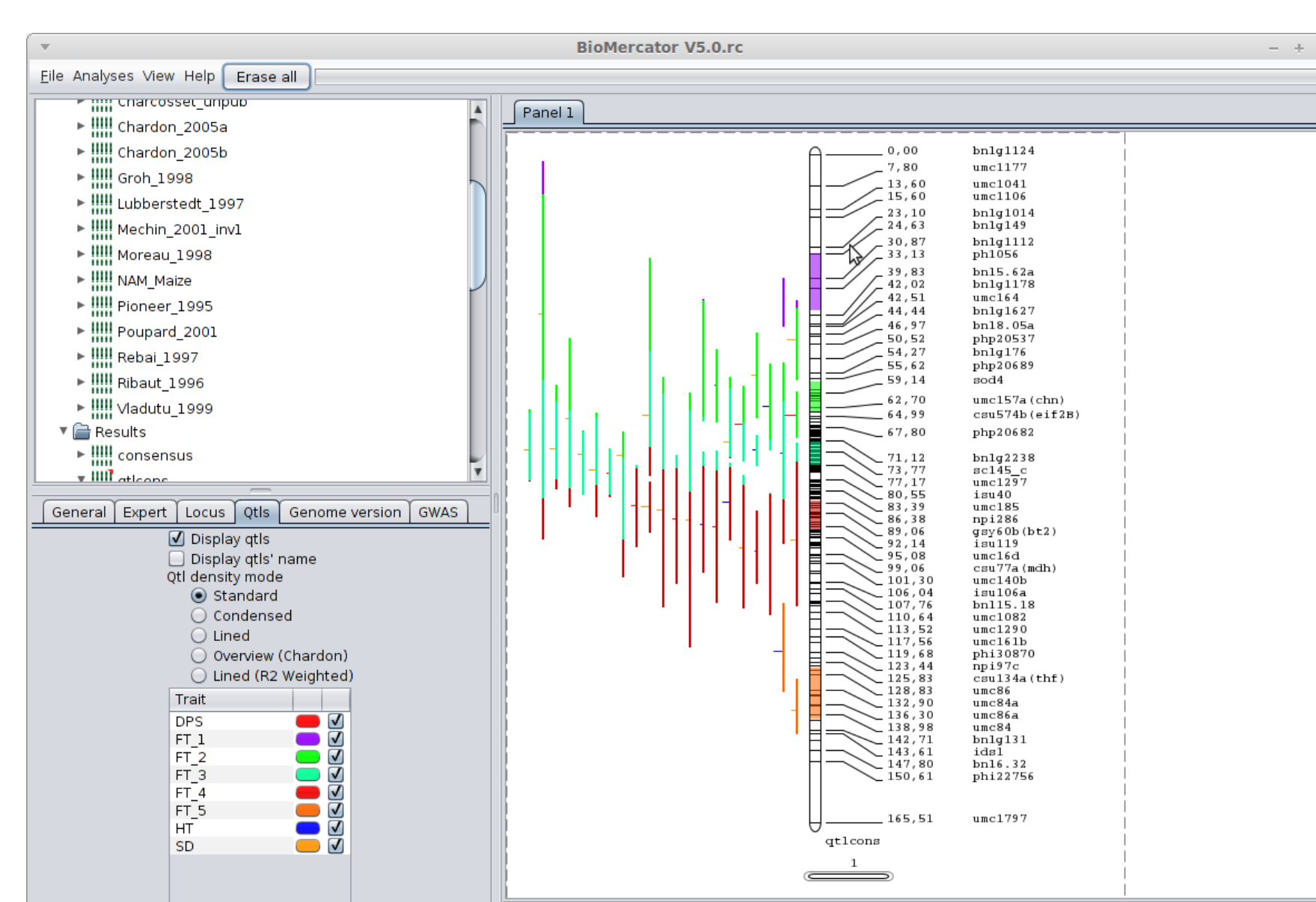
Genetic maps compilation & QTL meta-analysis



Genetic map compiled. This map is the result of the compilation of the « Demo » folder. QTLs have been projected on the result map.

Compilation of genetic maps combined to QTL meta-analysis has proven to be a powerful approach contributing to the identification of candidate genes underlying quantitative traits. One of the most interesting properties of meta-QTL (or consensus QTL) is its confidence interval (IC) often shorter than IC of corresponding QTLs, decreasing the number of candidate gene to consider. BioMercator enables compilation and visualization of a large number of genetic maps, from different sources (literature, database, own experiment etc.). BioMercator enables also QTL meta-analysis using Veyrieras methods^[1]. Meta-analysis are run at the chromosome level and QTLs from related traits can be jointly subjected to a single meta-analysis by grouping corresponding traits into meta-traits.

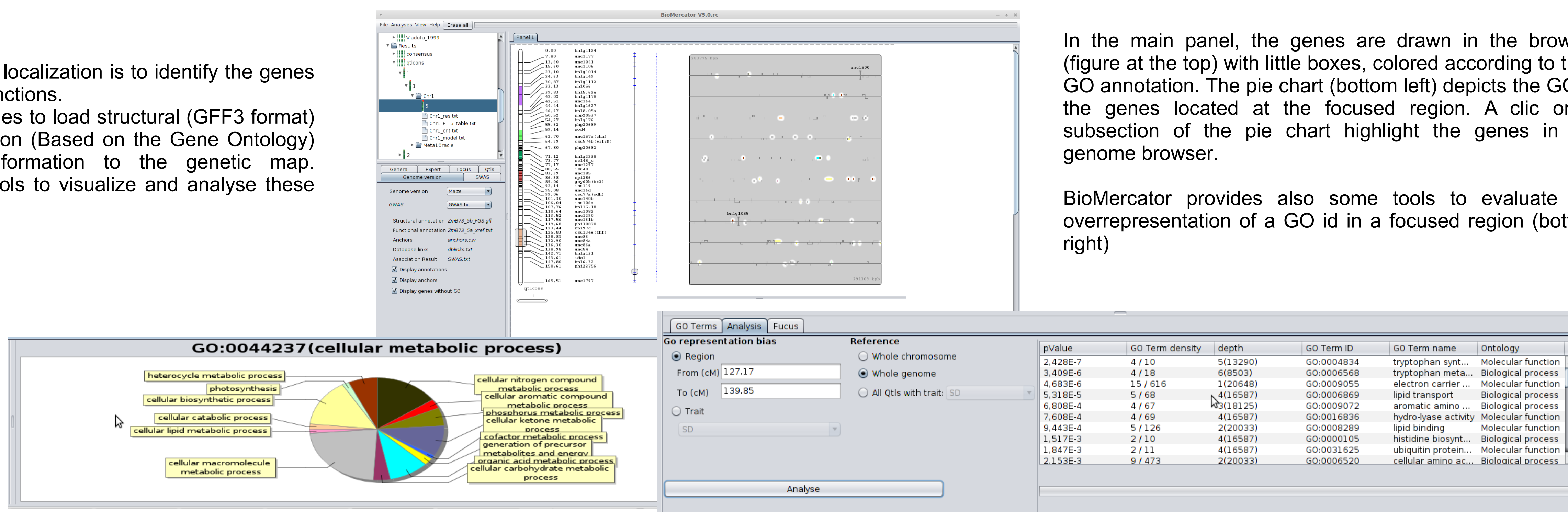
[1] Jean-Baptiste Veyrieras, Bruno Goffinet and Alain Charcosset. MetaQTL: a package of new computational methods for the meta-analysis of QTL mapping experiments. BMC Bioinformatics (2007), 8:49



QTLs meta-analysis. Meta-QTLs are represented by colored section on the chromosome. The former QTLs are colored according to the clustering result of the meta-analysis.

Structural and functional annotation view

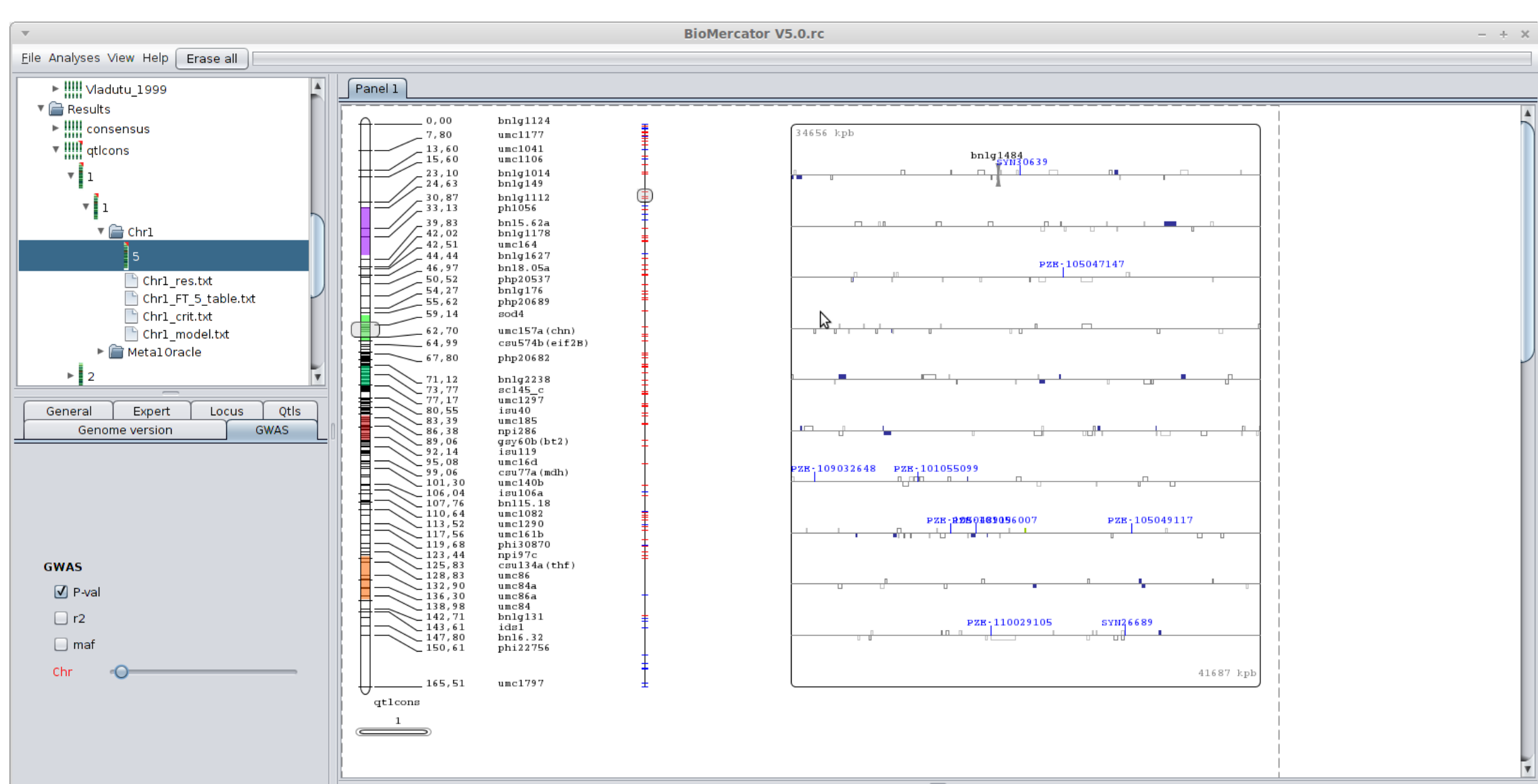
The next step after QTL localization is to identify the genes at this locus and their functions. Thus, BioMercator enables to load structural (GFF3 format) and functional annotation (Based on the Gene Ontology) and to link these information to the genetic map. BioMercator provides tools to visualize and analyse these information.



In the main panel, the genes are drawn in the browser (figure at the top) with little boxes, colored according to their GO annotation. The pie chart (bottom left) depicts the GO of the genes located at the focused region. A clic on a subsection of the pie chart highlight the genes in the genome browser.

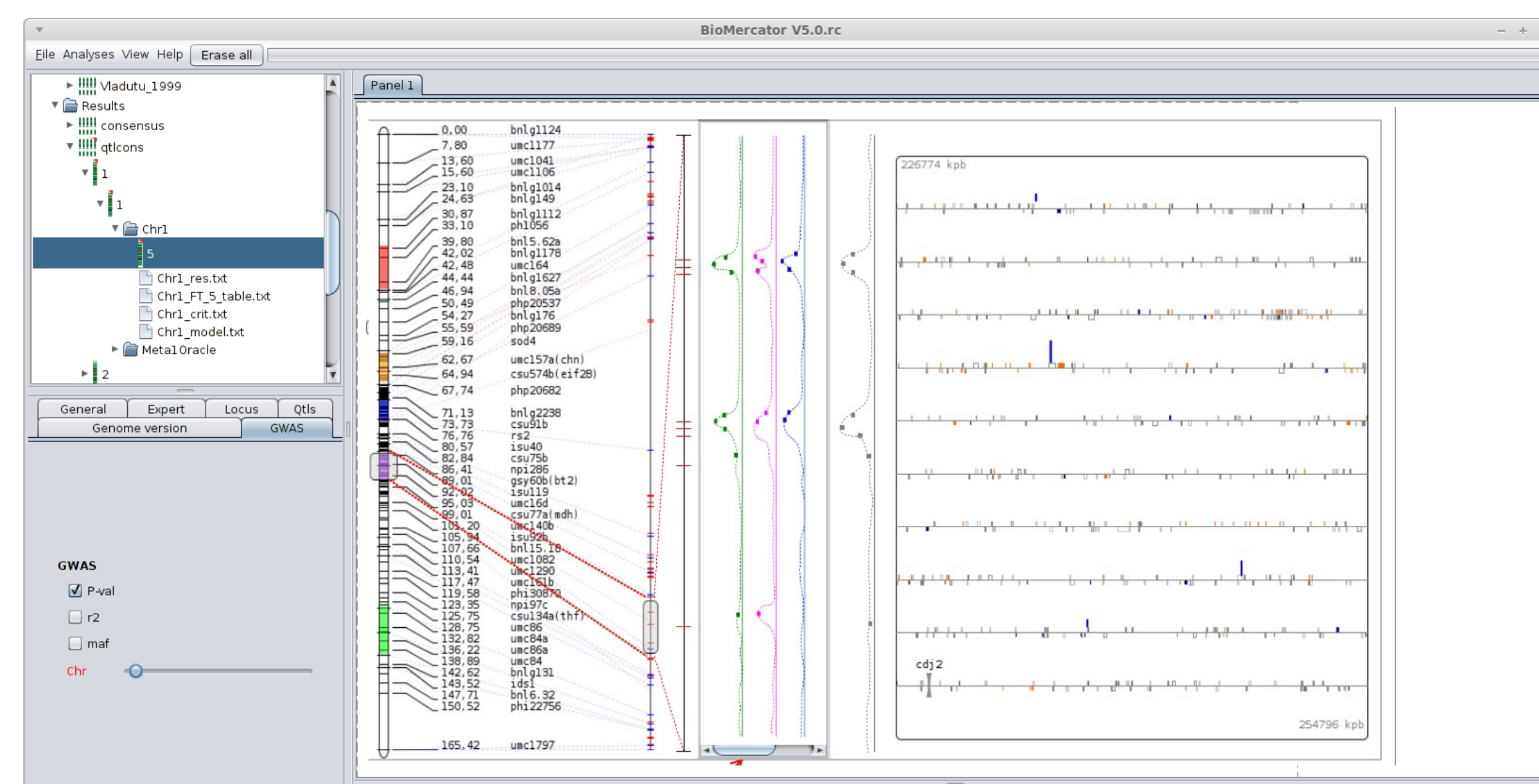
BioMercator provides also some tools to evaluate the overrepresentation of a GO id in a focused region (bottom right)

GWAS view & GWAS meta-analysis



In order to improve candidate genes detection we aim to provide new methods like genome wide association studies (GWAS). BioMercator enables GWAS results loading in BioMercator (GnpAsso format^[2]). Currently, one GWAS can be loaded in BioMercator and results can be filtered according to the p-value or the R2. In the left figure, the relevant markers are depicted with a little blue stick. The left picture shows a template of what we aim to develop next year for BioMercator.

[2] <https://urgi.versailles.inra.fr/Projects/GnpAsso>



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