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A Web-based Visual Analytics Application for Biological Networks

Motivation: Research in a clinical environment today is confronted with large amounts of multi-level high-throughput omics data. In our work, we focus on transcriptomics, i.e., the over- or under-expression of genes. Each gene can be part of one or more biological pathways. A pathway models the molecular interactions in an organism that lead to a specific chemical change.

App Design & User Requirements: We present a web-based visual analytics app written in JavaScript using *D3* [1] and *node.js* that facilitates exploring the network of biological pathways corresponding to a given input set of genes. The network is constructed from pathways derived from the KEGG database [2]. Users can interactively zoom and filter the network and get details on demand. The main user requirements for our application are the following:

1. Visualize all pathways affected by regulated genes
2. Preserve the known KEGG layout of the pathway
3. Support the comparison of different measurements

Outlook: Our application is currently work in progress. In subsequent steps, we will add more features, such as the ability to compare data from different individuals or to visualize time series data. Furthermore, we want to improve the network visualization [3] and extend our application to visualize multi-omics data.
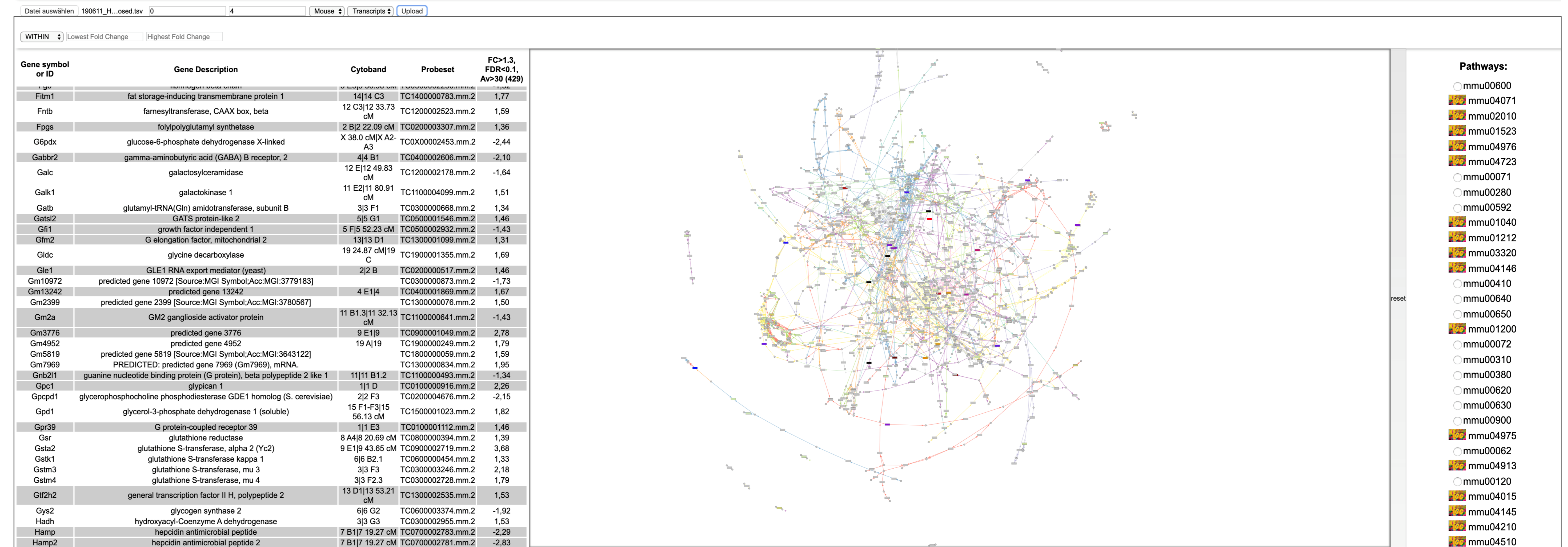
▲ Our visual analytics web-app for biological pathways. The table to the left lists information about all genes in the data set. The list to the right shows all pathways from the KEGG database containing at least one of the genes. The central graph view shows an overview of the network of these pathways. Our application supports the exploration of the data by visualizing details on demand.
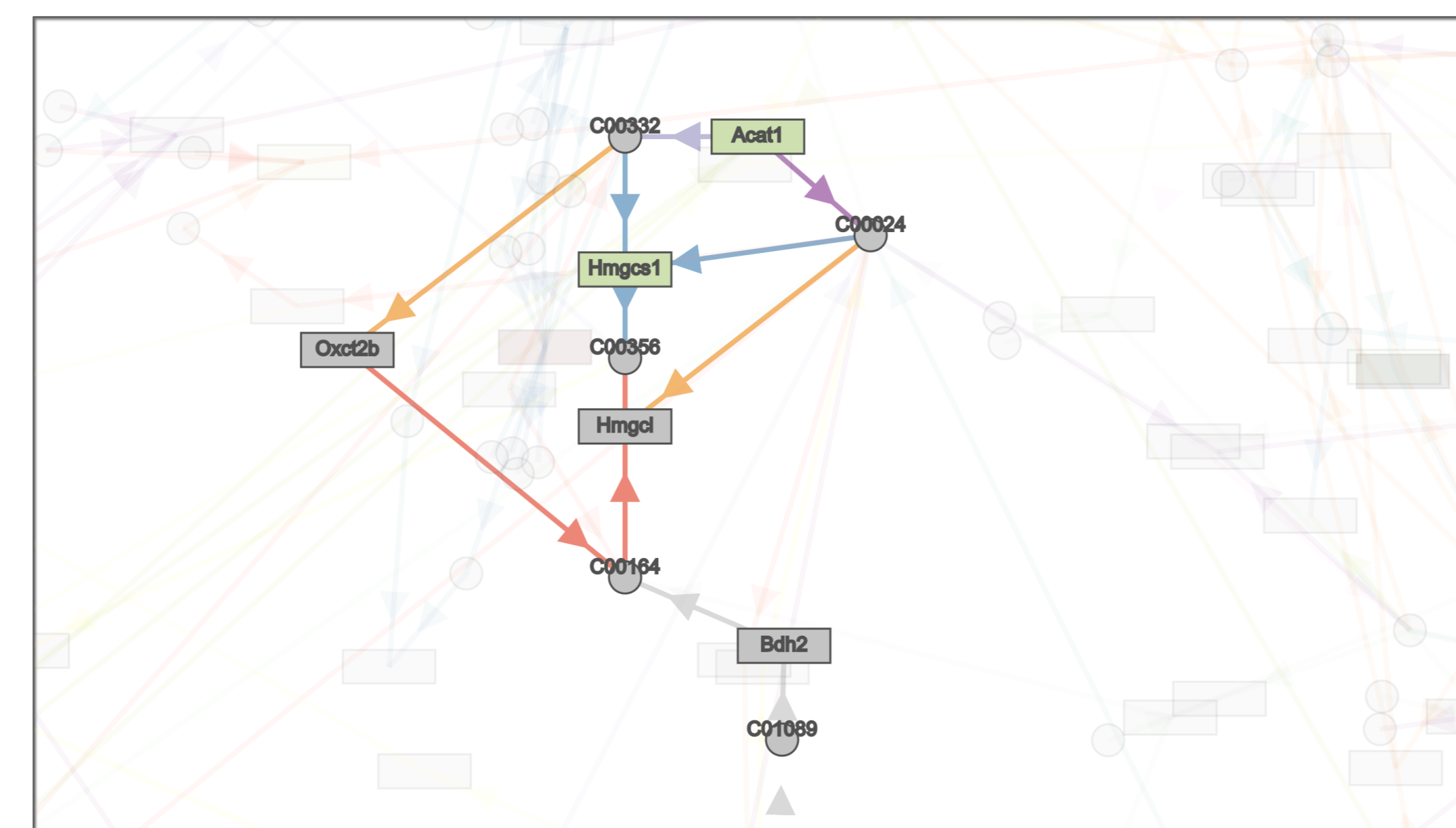
◀ Detailed view of a selected pathway. All other pathways are de-emphasized using transparency. The selected pathway has been newly laid out to match the layout provided by KEGG (shown to the right). White nodes in the KEGG image are genes that are not present in the selected organism, thus, we remove them.
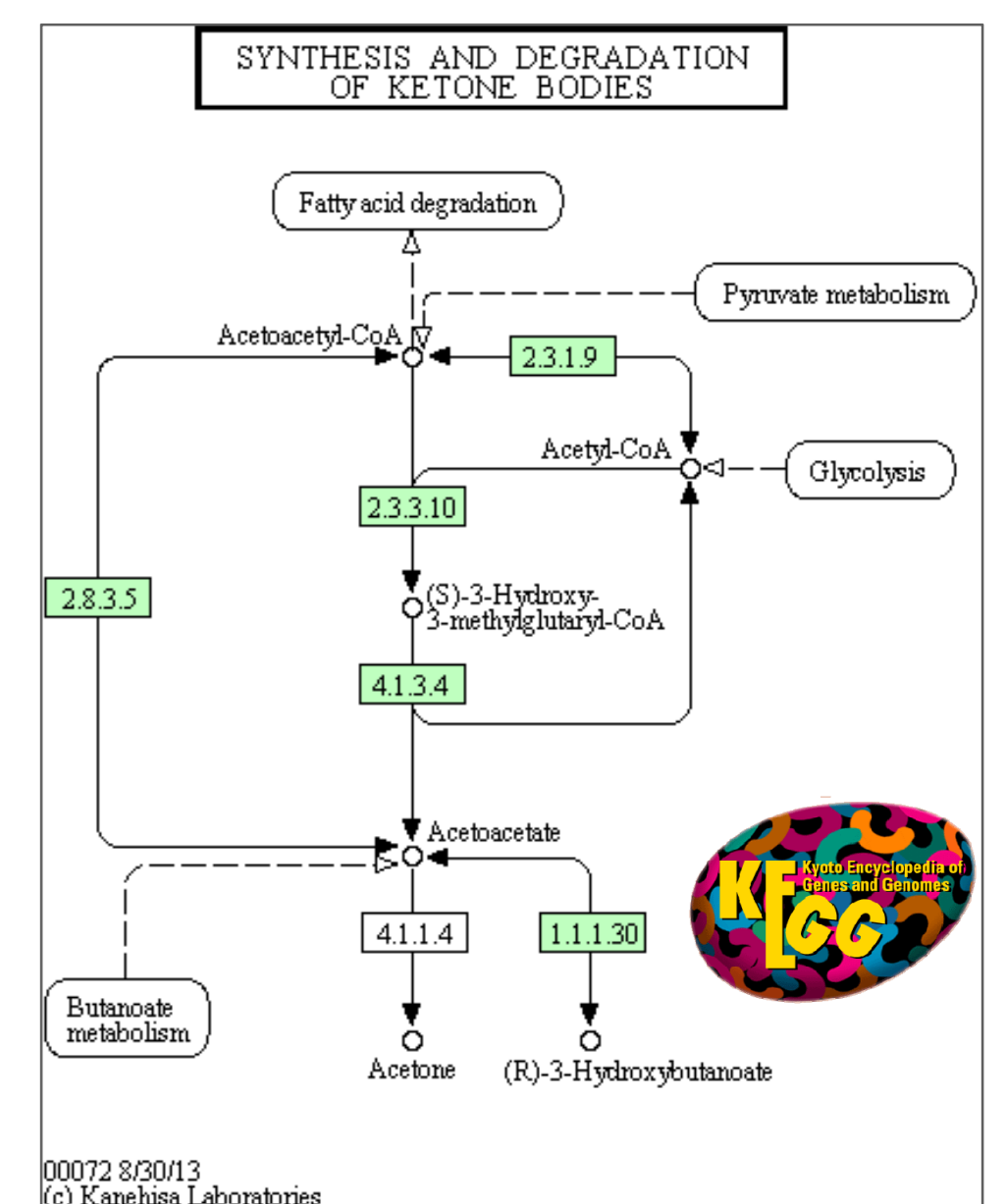
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References:
[1] Bostock, Ogievetsky, Heer: D3 Data-Driven Documents. IEEE TVCG 17(12), 2011.
[2] Kanehisa, Goto: KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Res. 28(1), 2000.
[3] Marai, Pinaud, Bühler, Lex, Morris: Ten simple rules to create biological network figures for communication. PLOS Comput. Biol. 15(9), 2019.

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