

Draft Genome of the Liver Fluke *Fasciola gigantica*

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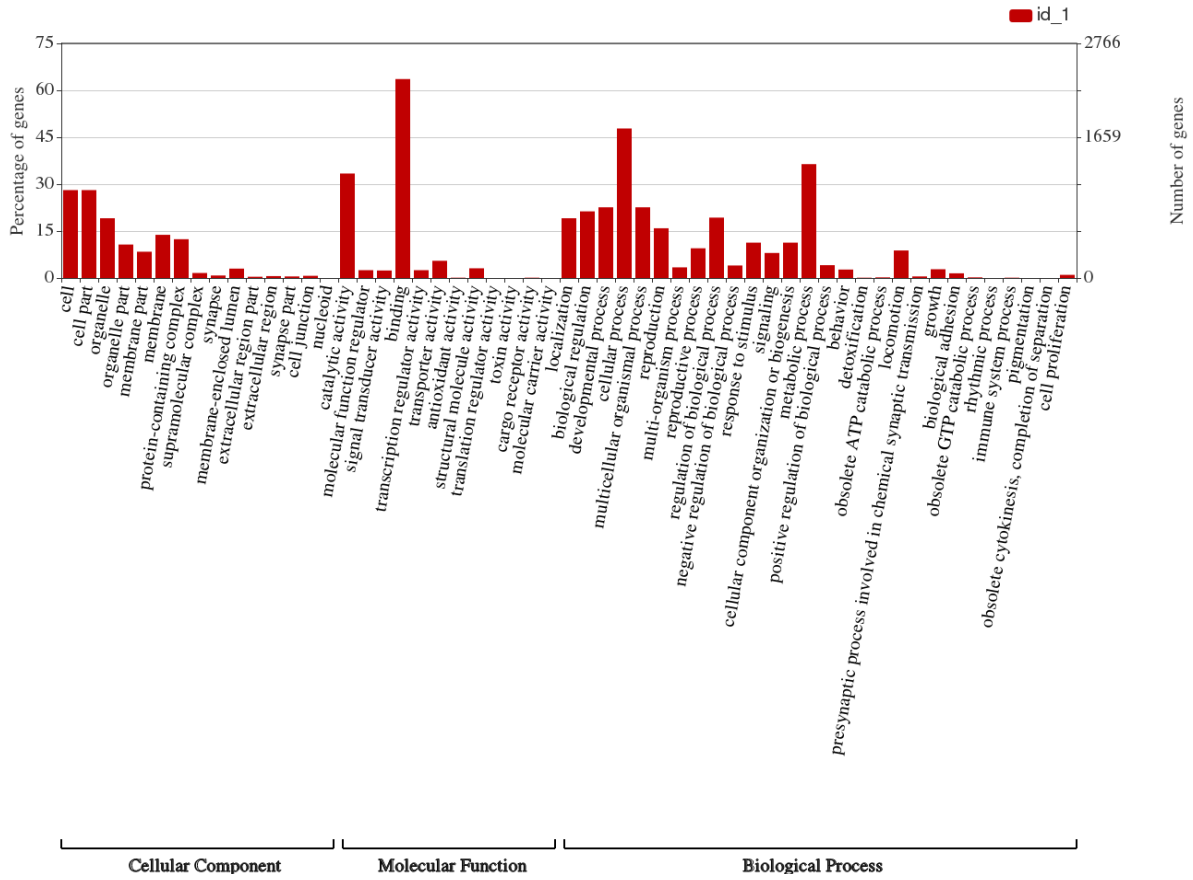
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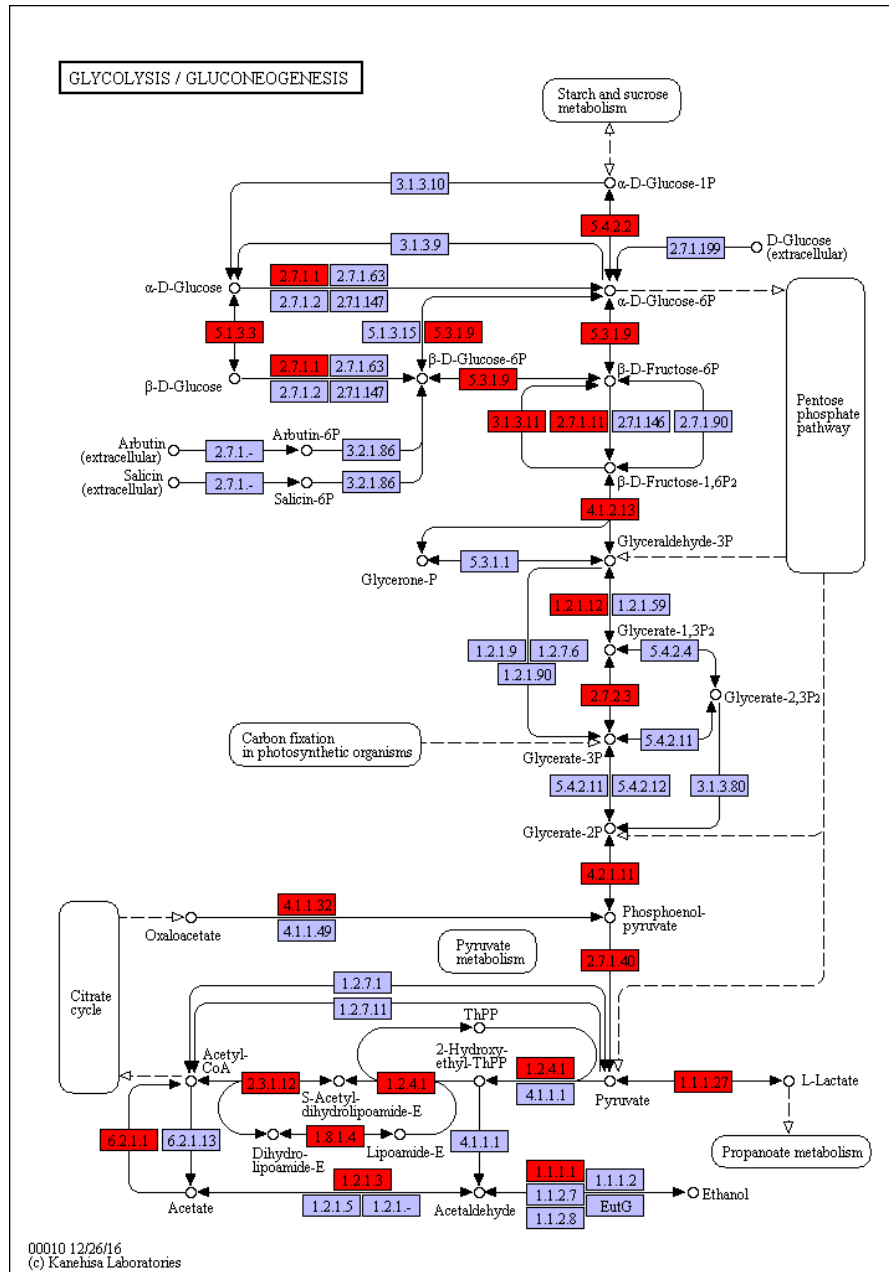
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#Both authors contributed equally to the work

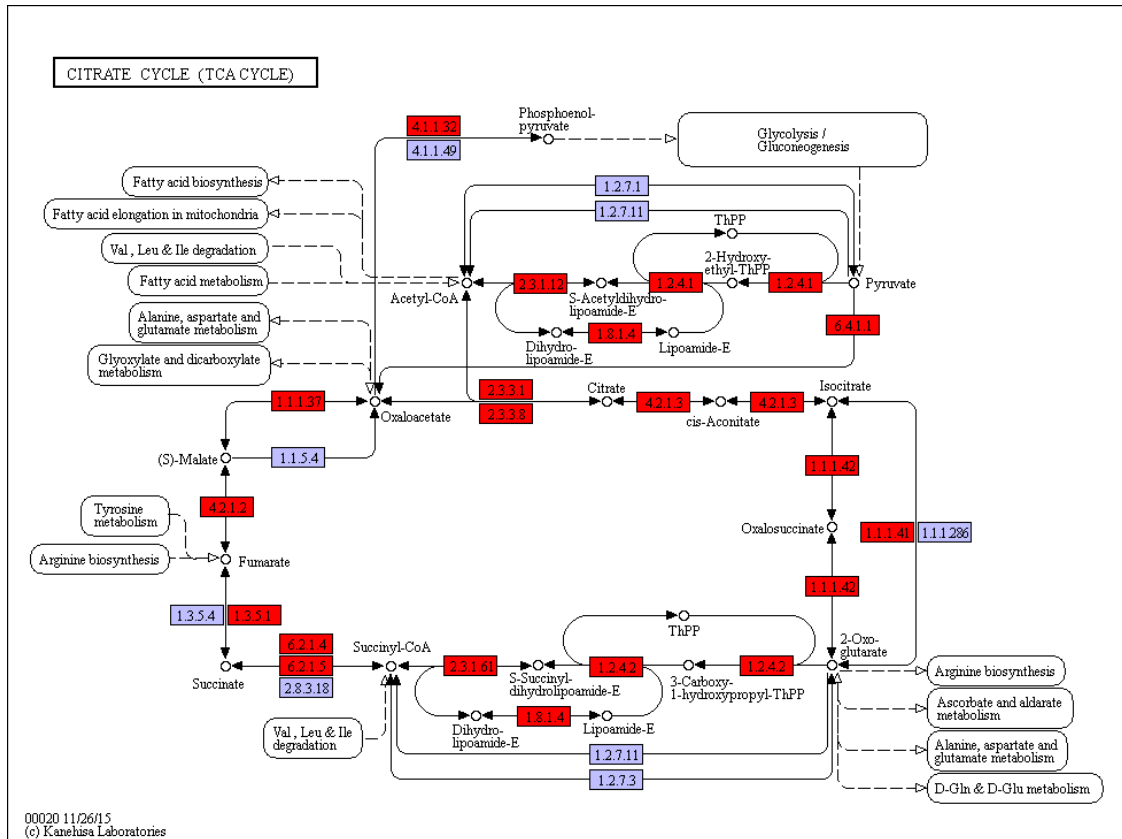
Supplementary Figure S1. GO classification of genes similar in *F. hepatica* and *F. gigantica*.



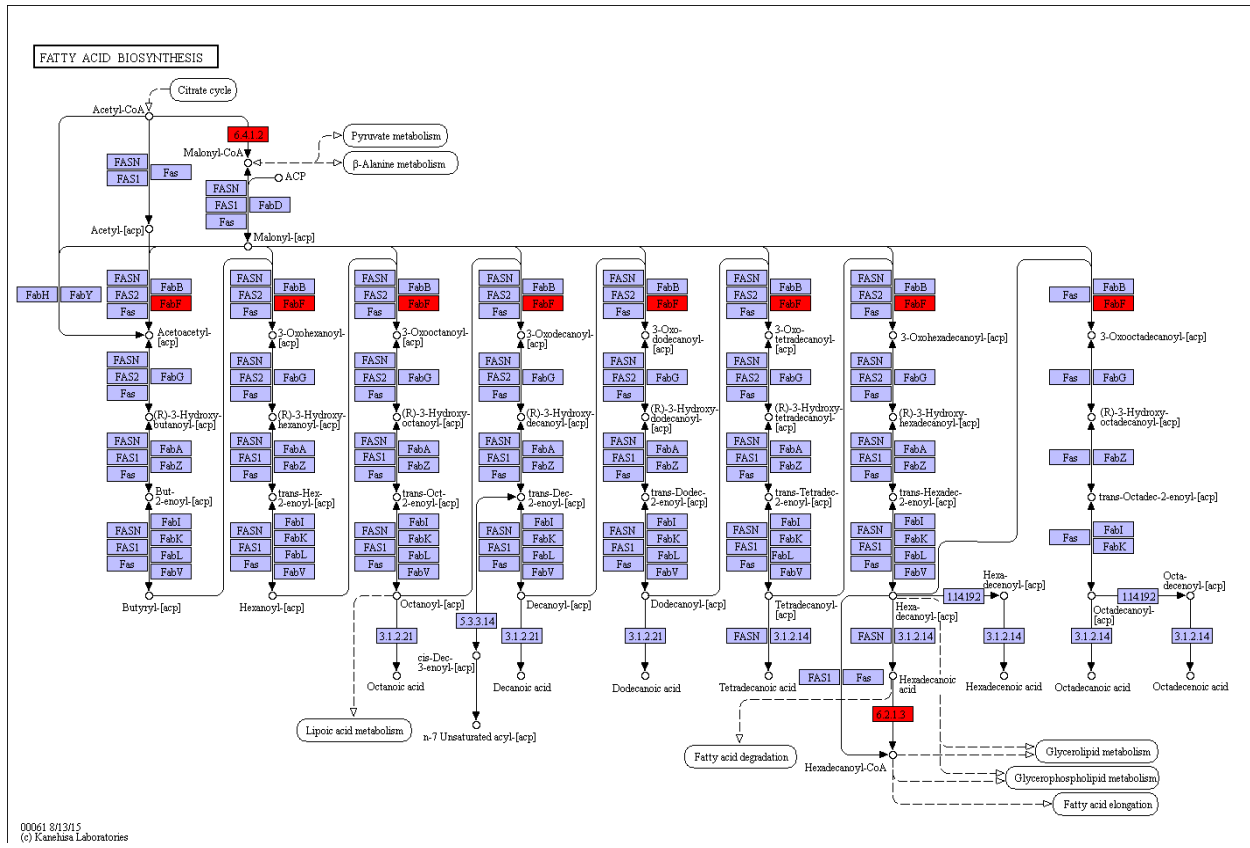
Supplementary Figure S2. Schematic pathway of glycolysis ¹⁻³.



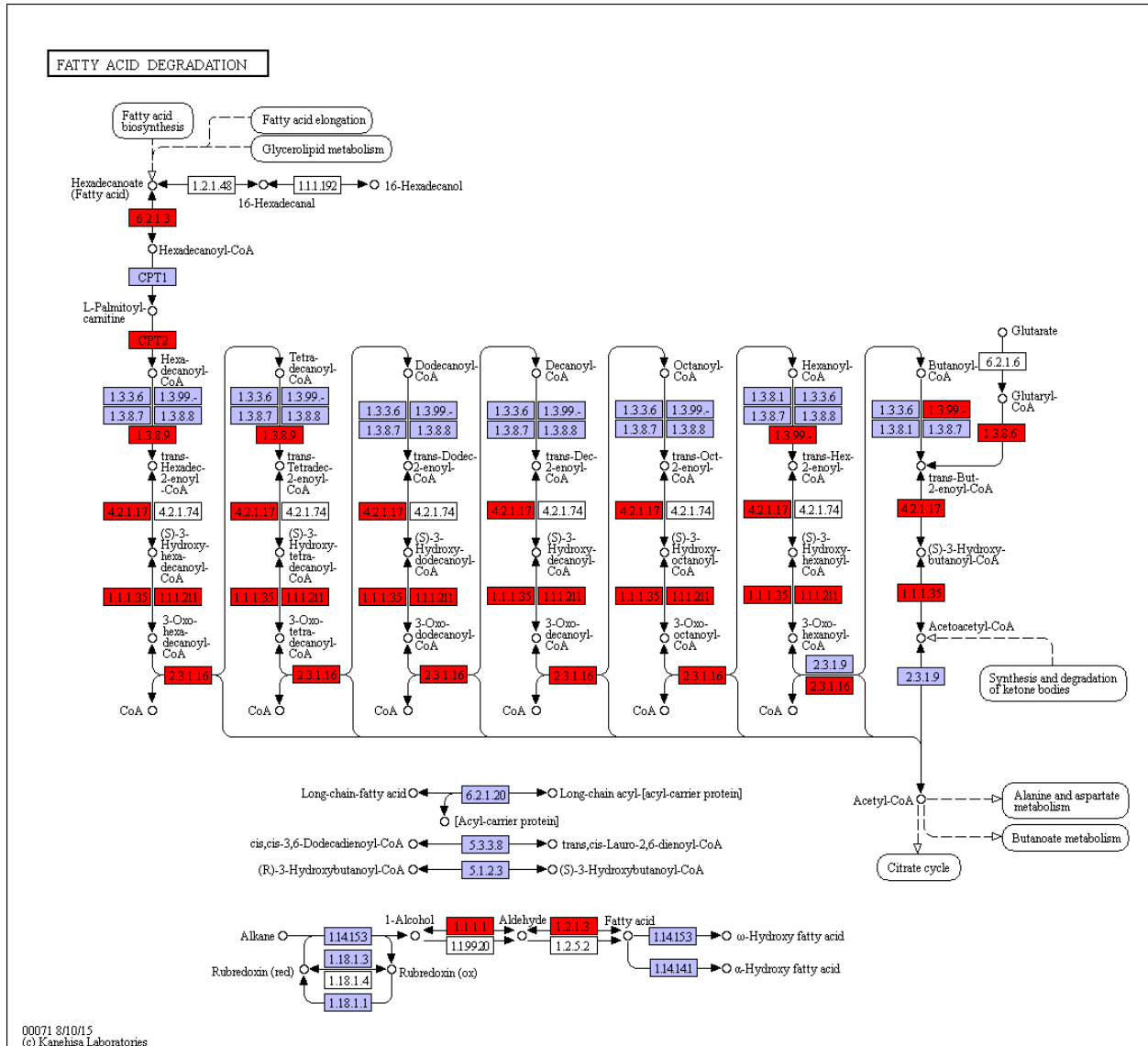
Supplementary Figure S3. Schematic pathway of TCA cycle ¹⁻³.



Supplementary Figure S4. Schematic pathway of fatty acid biosynthesis ¹⁻³.



Supplementary Figure S5. Schematic pathway of fatty acid degradation ¹⁻³.



Note:

The Supplementary Figure S2-S5 are taken from the KEGG website (<https://www.genome.jp/kegg/>) and are cited at places used, and reference are provided below:

References for KEGG pathways:

- 1 Kanehisa, M., Furumichi, M., Tanabe, M., Sato, Y. & Morishima, K. KEGG: new perspectives on genomes, pathways, diseases and drugs. *Nucleic Acids Res* **45**, D353-361, (2017).
- 2 Kanehisa, M. & Goto, S. KEGG: Kyoto encyclopedia of genes and genomes. *Nucleic Acids Res* **28**, 27-30 (2000).
- 3 Kanehisa, M., Sato, Y., Kawashima, M., Furumichi, M. & Tanabe, M. KEGG as a reference resource for gene and protein annotation. *Nucleic Acids Res* **44**, D457-462 (2016).