A comprehensive analysis of the *Lactuca sativa*, L. transcriptome during different stages of the compatible interaction with *Rhizoctonia solani*

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[3]Current address, department of Computational Biology, Bielefeld University, Bielefeld, Germany

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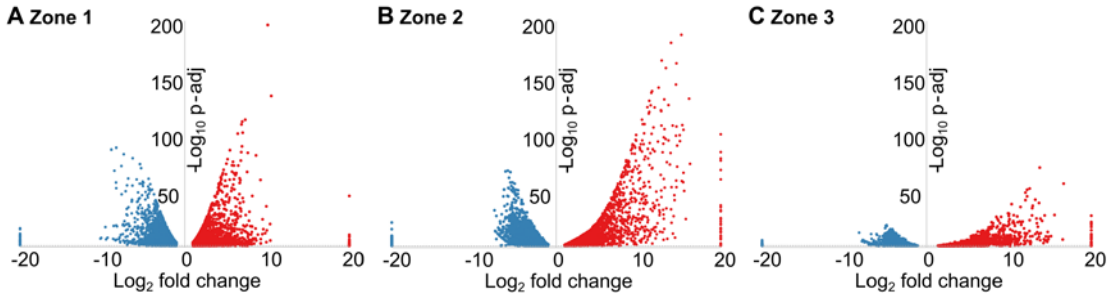
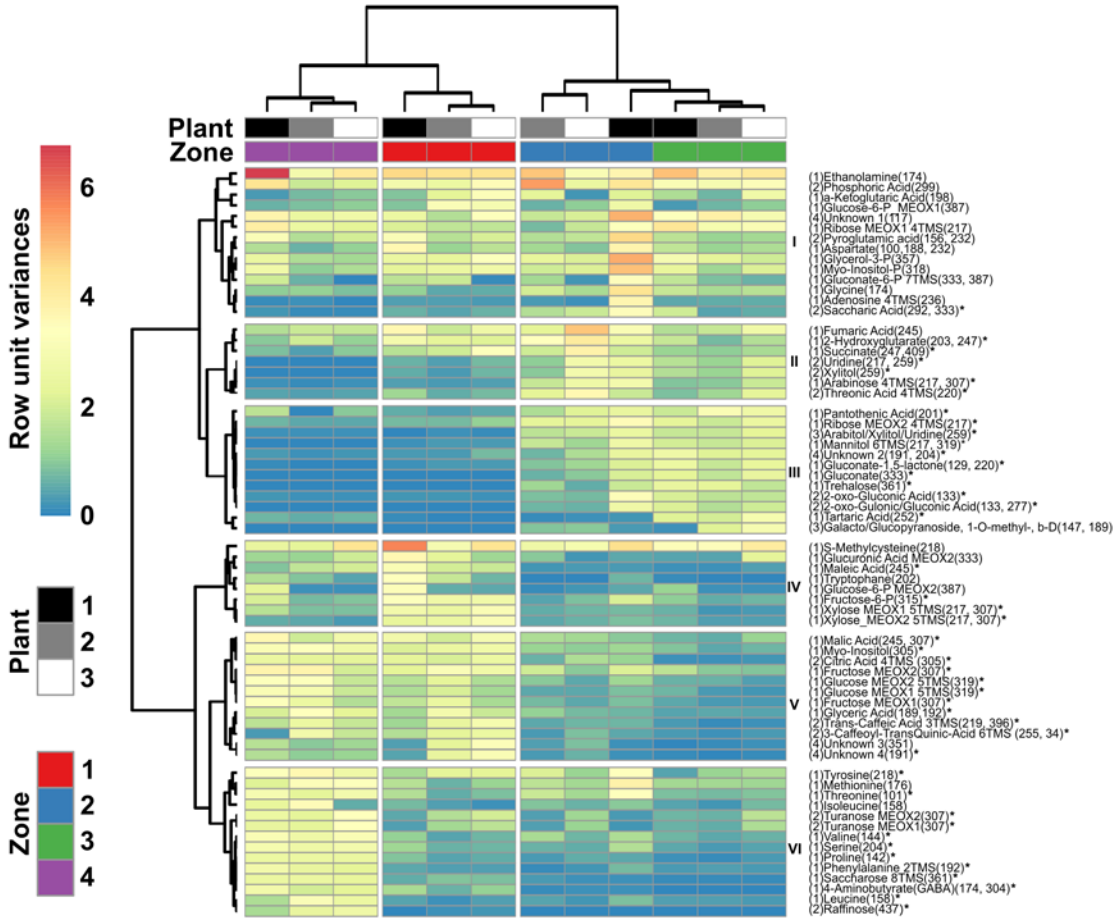


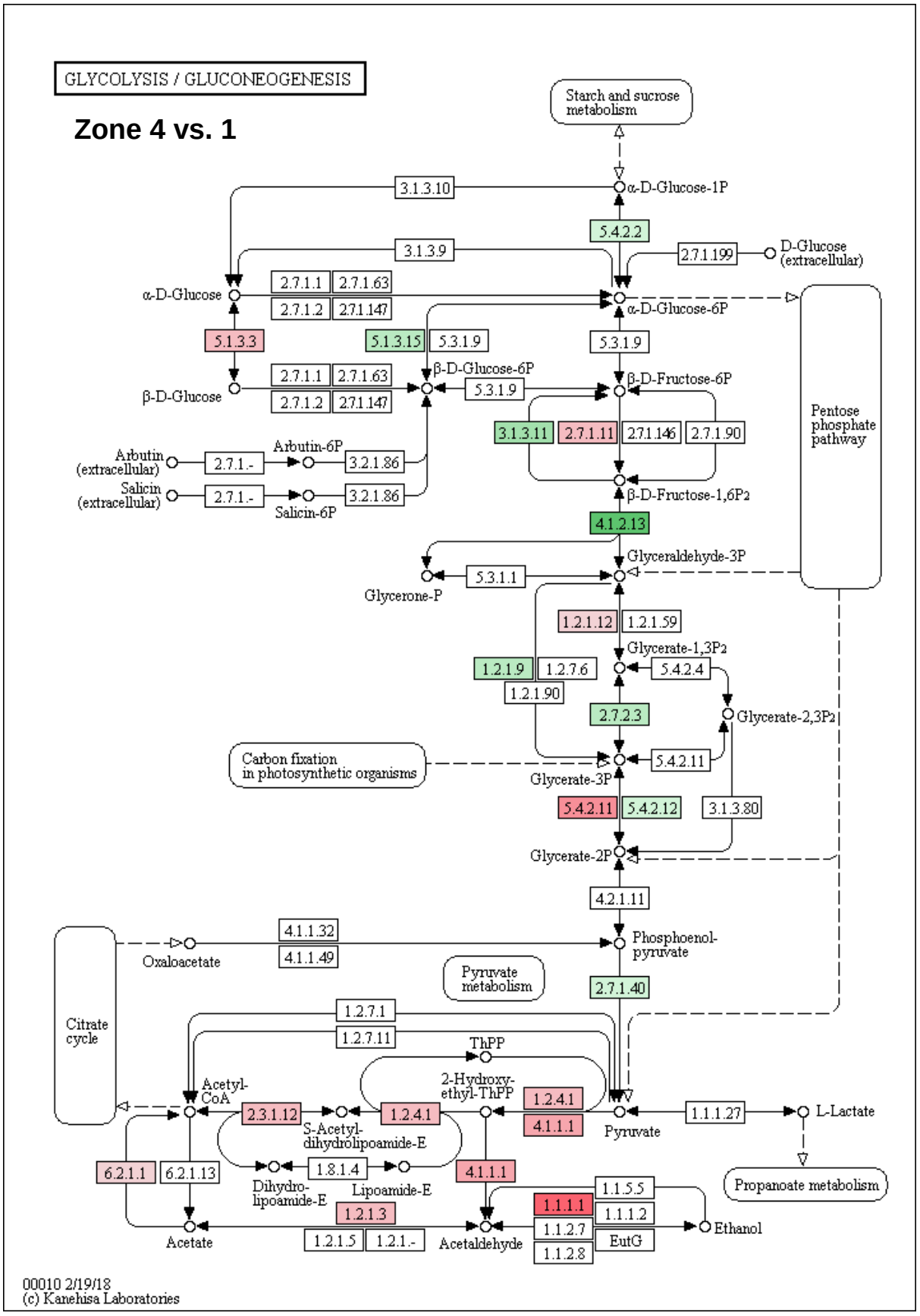
Supplementary Figure S1: DESeq based volcano plots depicting the differentially expressed genes of *L. sativa* between the interaction zones 1, 2 and 3 in comparison to the control (zone 4).



Supplementary Figure S2: Enlarged depiction of Figure 6B. Metabolite based heat map; unite variance scaling was applied on rows and Ward clustering was used for rows and columns[31]. The designations of single metabolites include the indicator of the level of identification within the first brackets, according to the reporting standards as proposed by the Metabolomics Standards Initiative [41] ranging from (1): identified by the measurement of the chemical reference standard, (2): putatively identified by significant database hit, (3) putatively characterized by database hit as compound of a certain chemical class, (4): unknown compound. The chemical name of the compound is accompanied in relevant cases by the information concerning the derivatization status (MEOX,TMS). The last brackets indicate the m/z values, which have been used for the identification and the integration of the signals corresponding to the given metabolite. The asterisks indicate significance as tested with ANOVA.

KAAS Kegg mapping of *L. sativa* cv. Tizian DEG's

Only DEG's with p-adjusted values of 0.05 or smaller and absolute fold changes of 2 or higher are depicted



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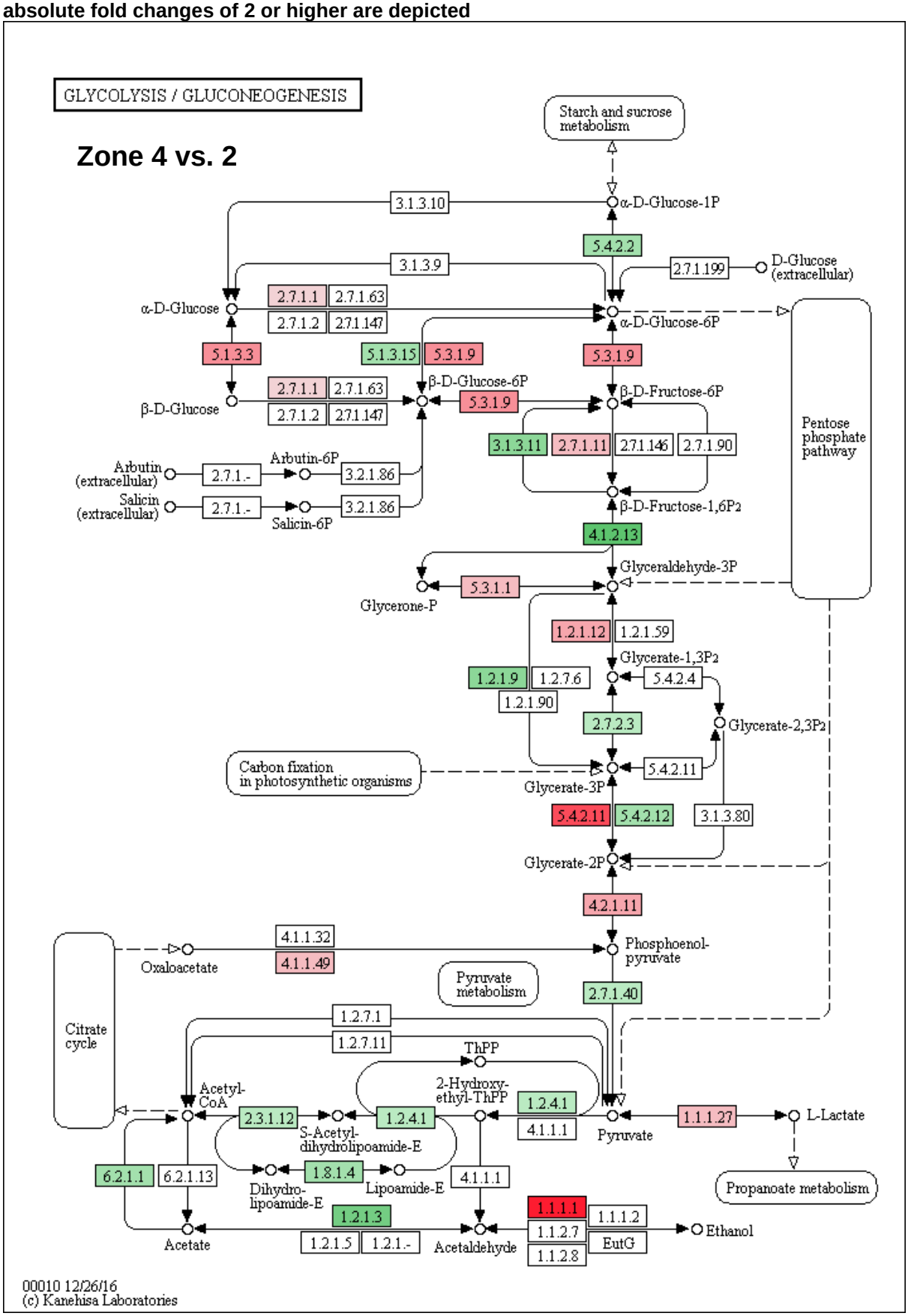

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(c) Kanehisa Laboratories

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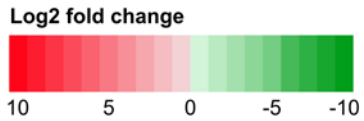

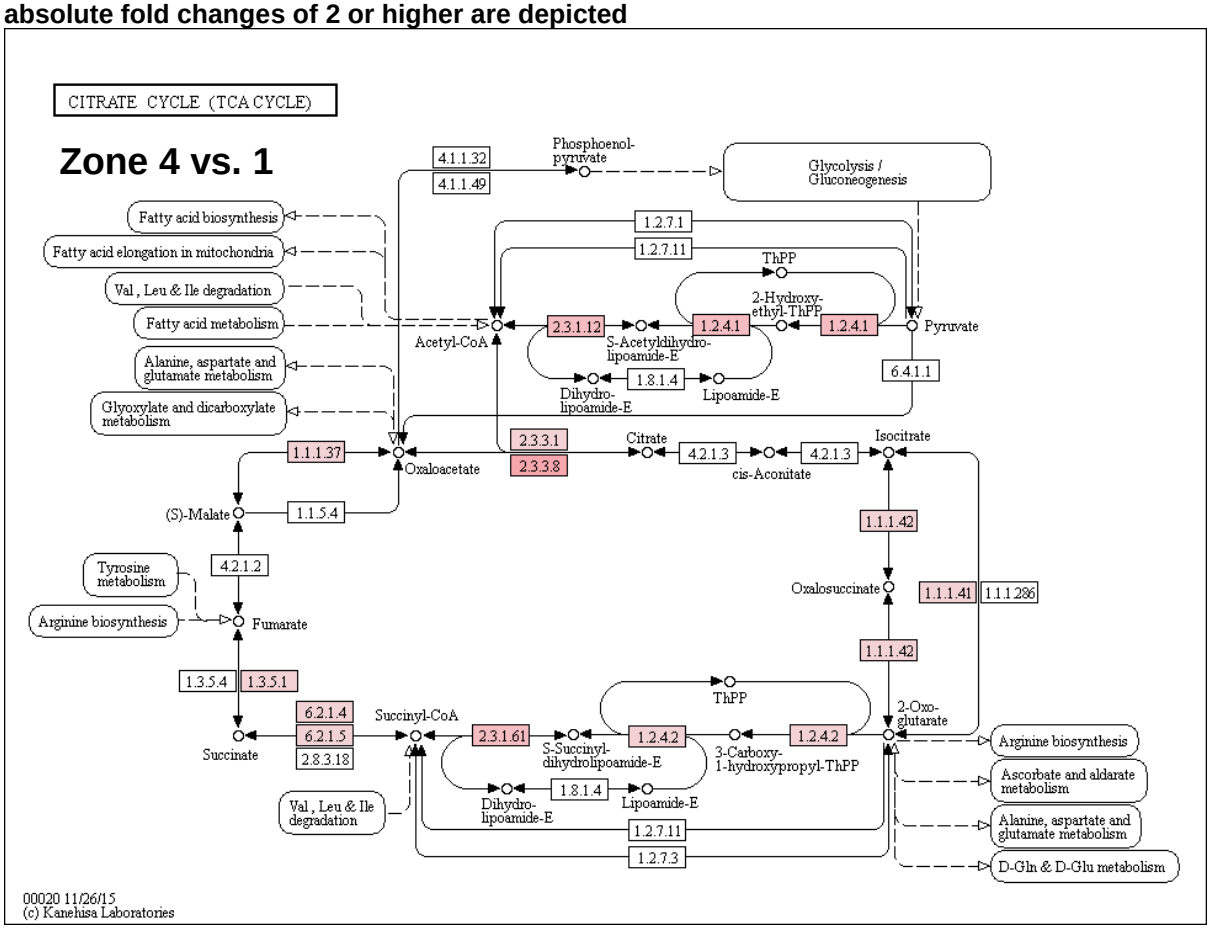

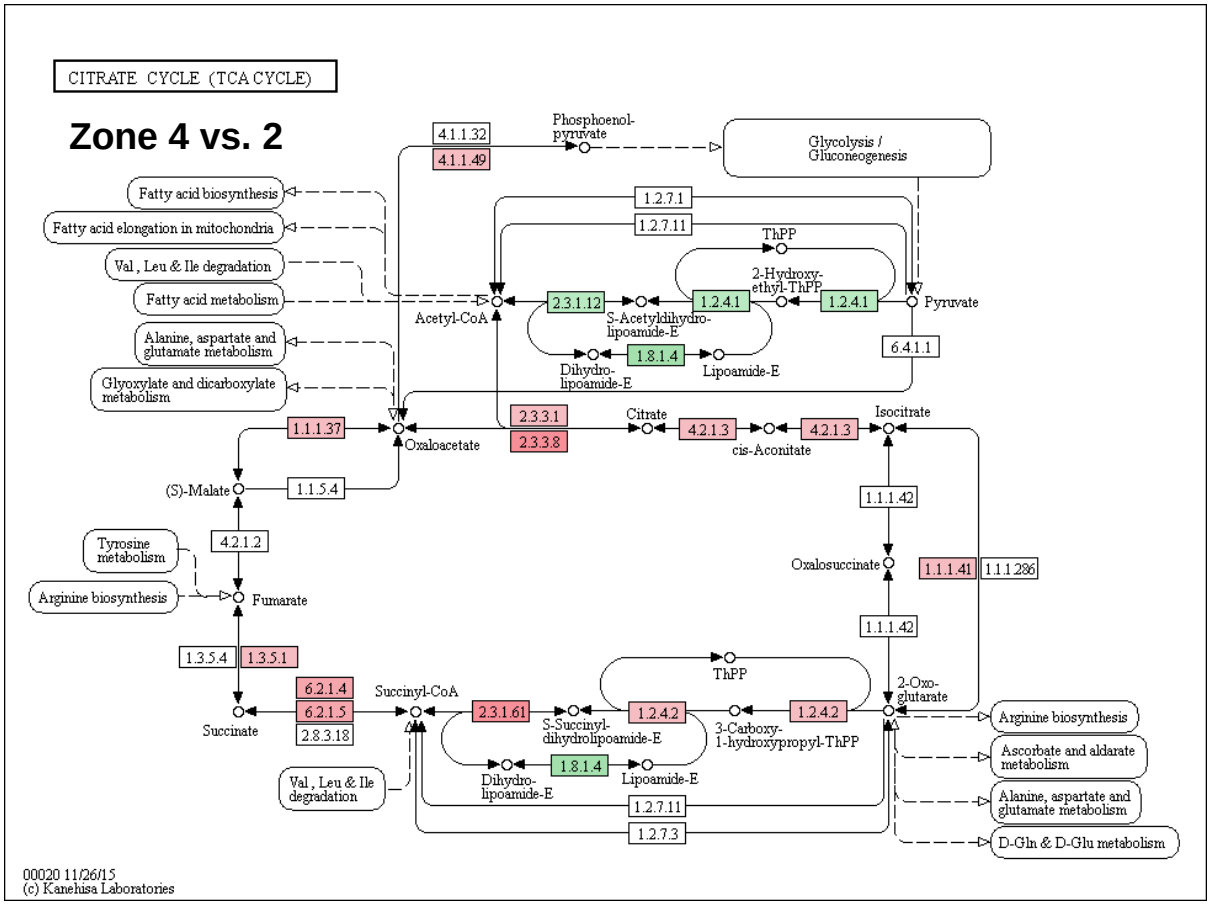

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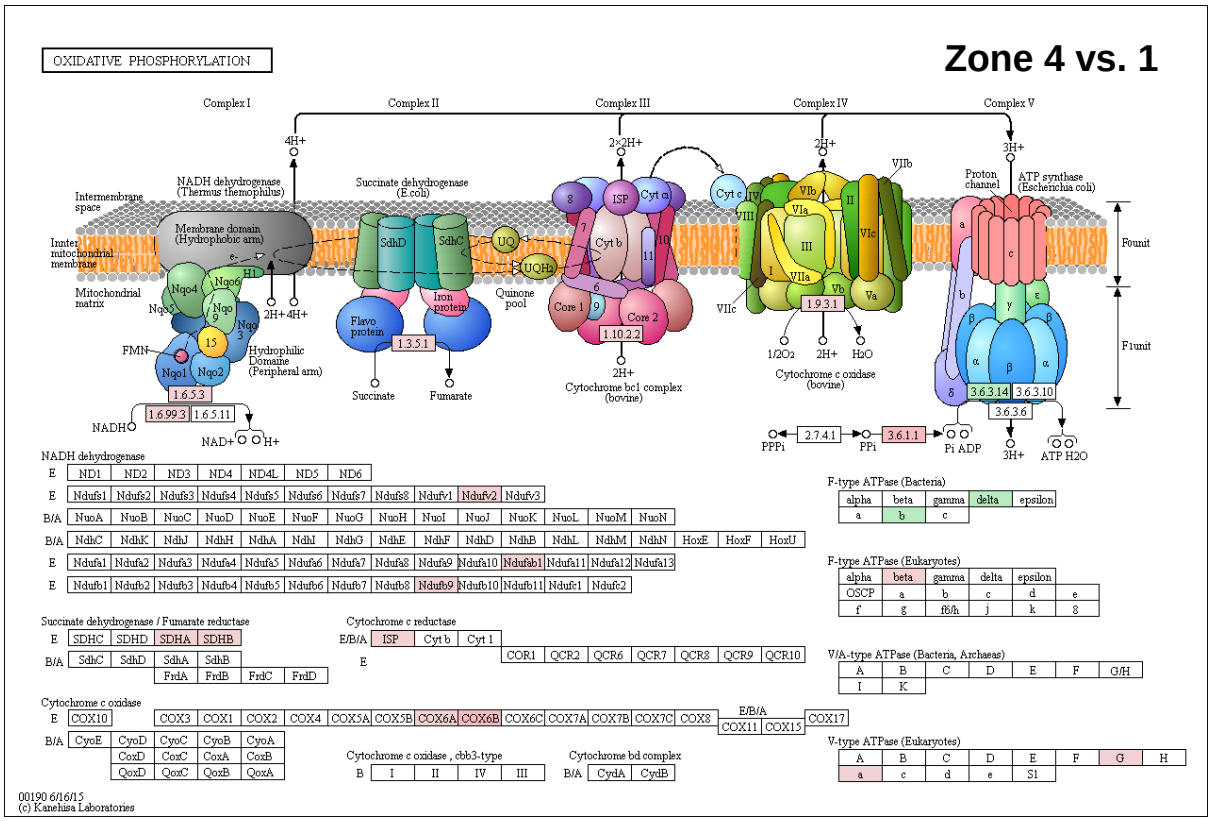
Log2 fold change

10 5 0 -5 -10



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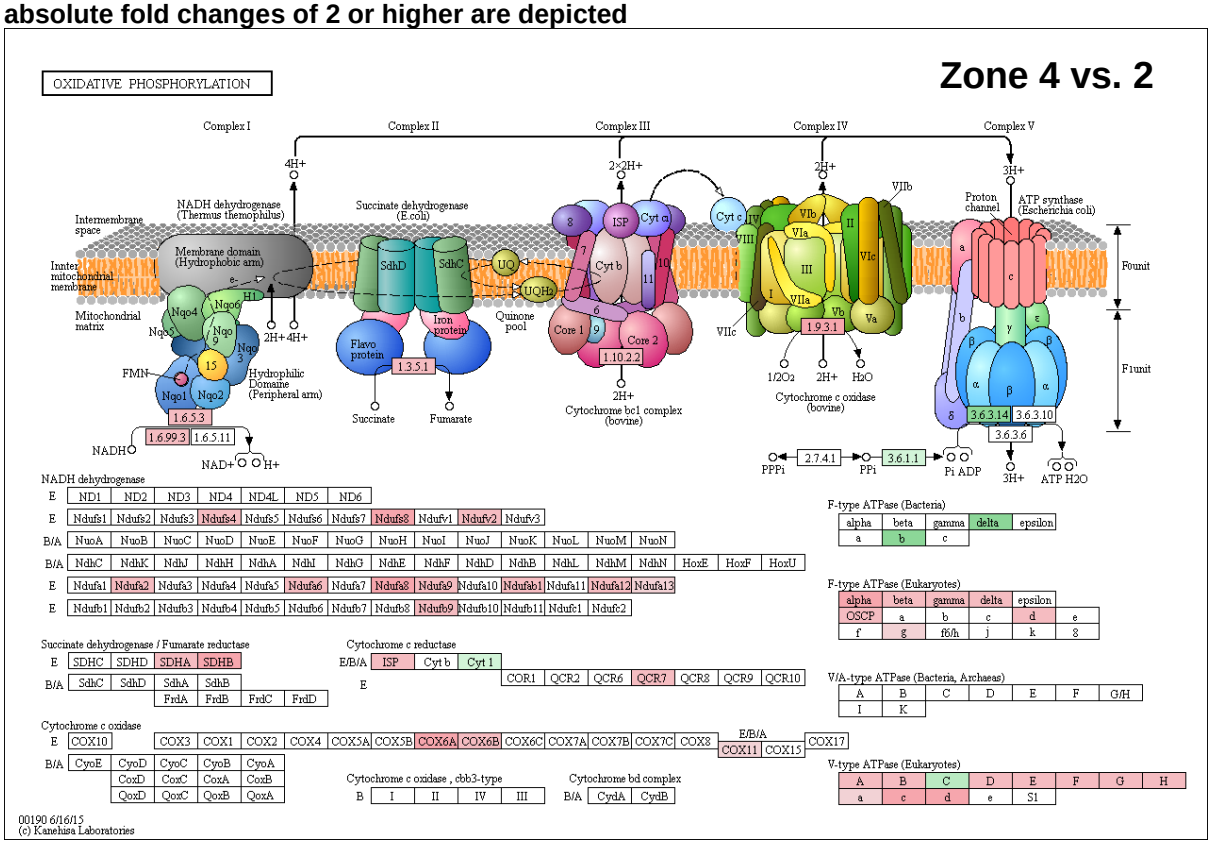
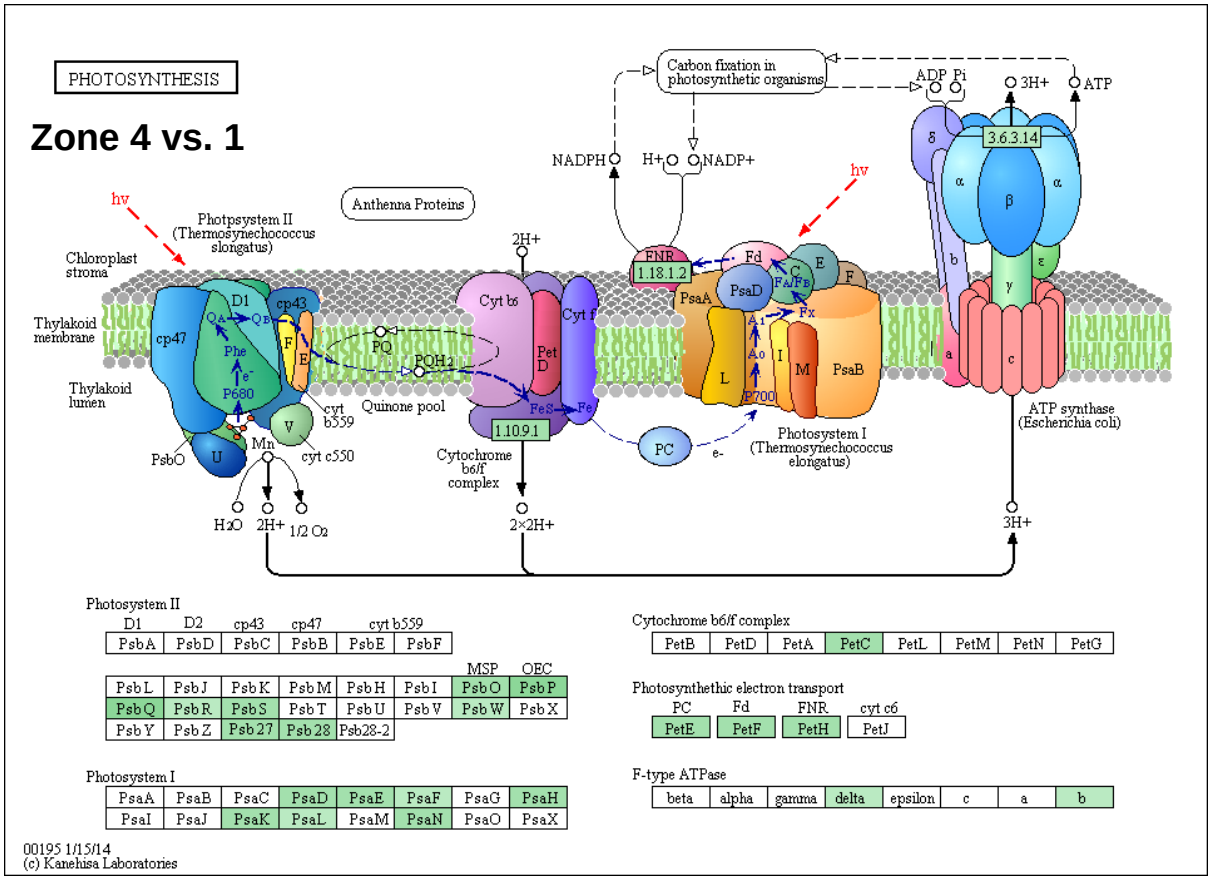
Zone 4 vs. 2



Zone 4 vs. 1



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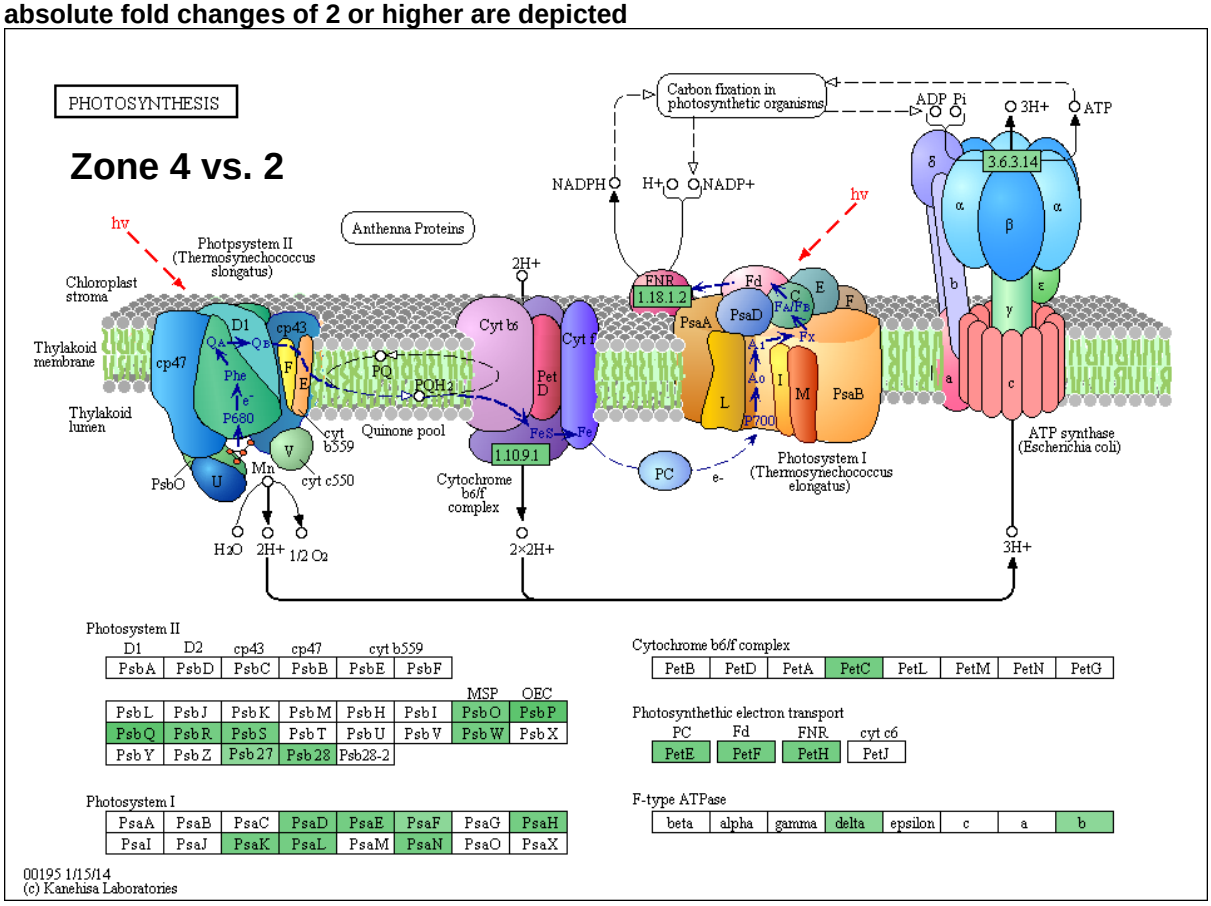

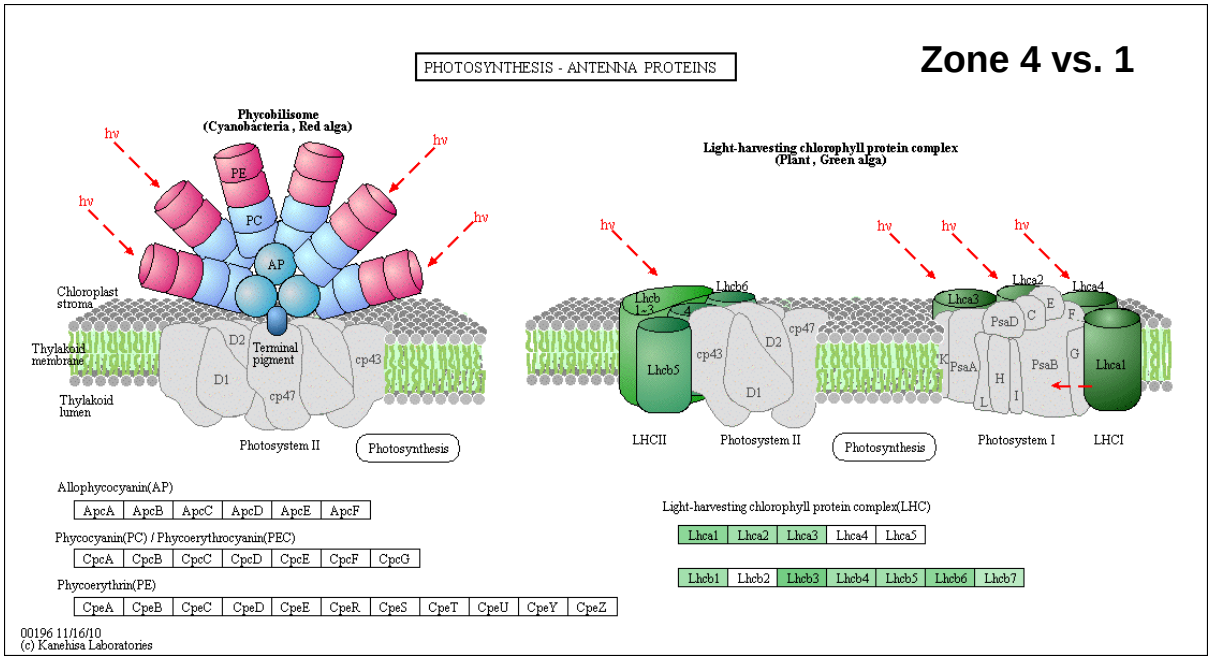

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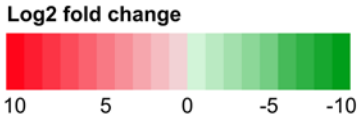

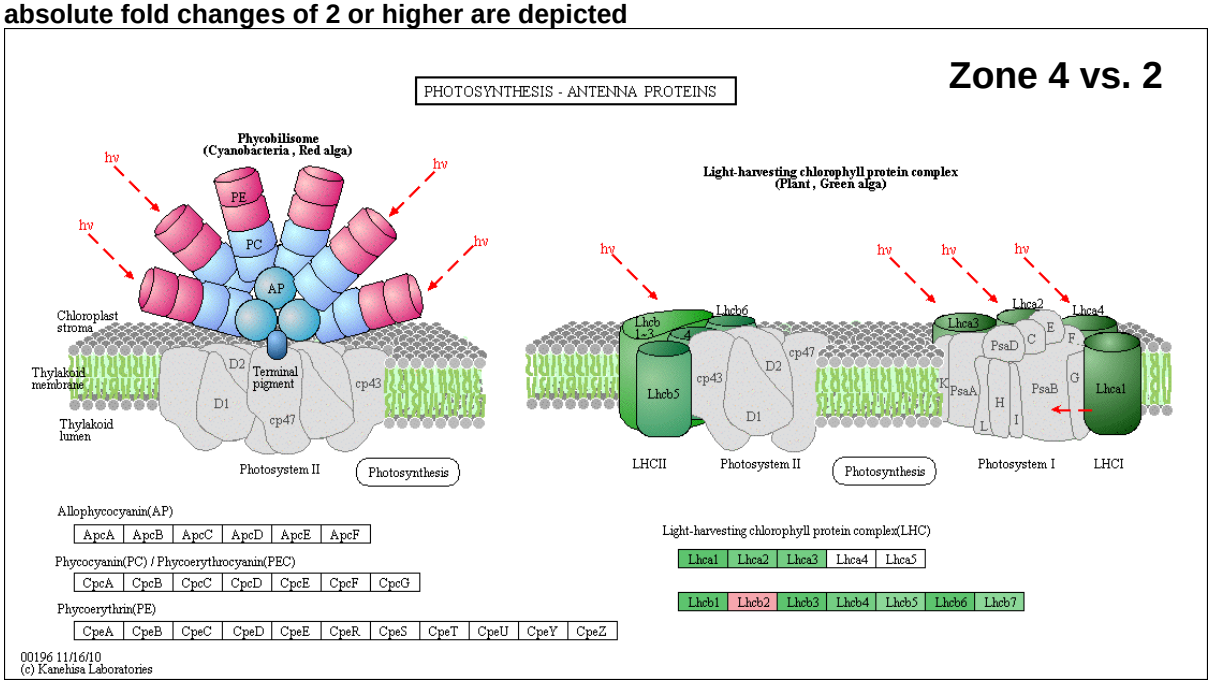

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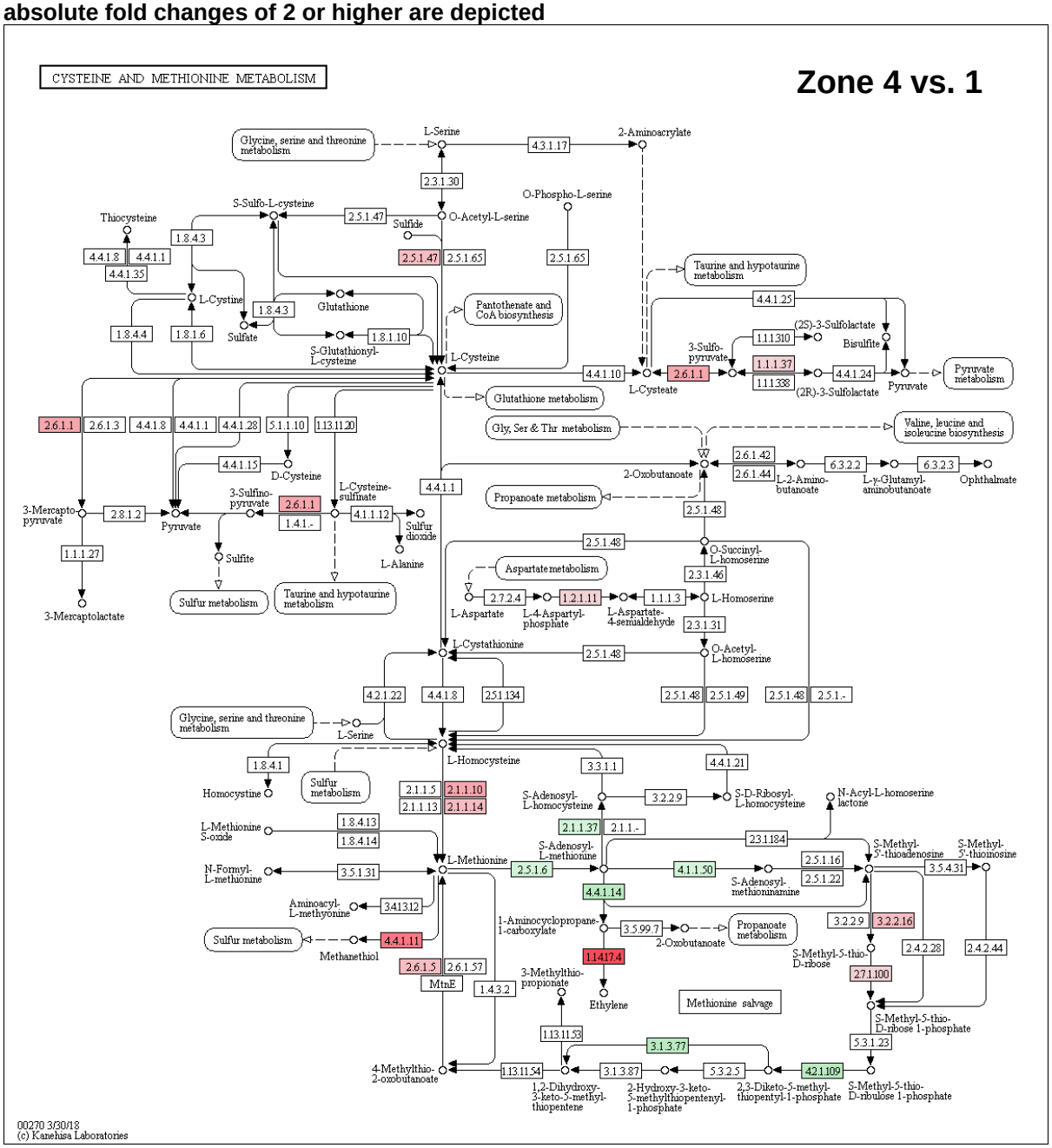

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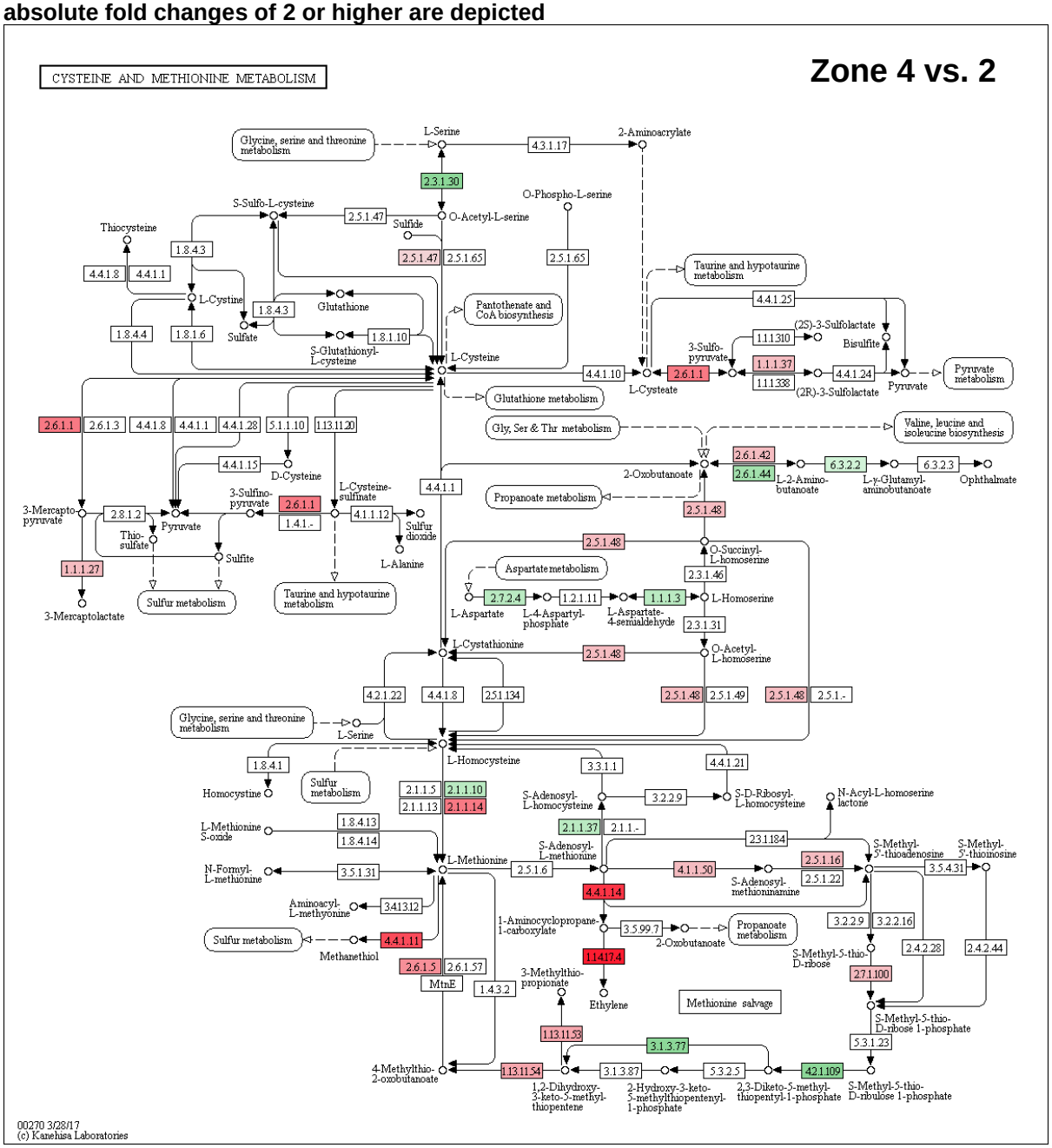
Zone 4 vs. 2



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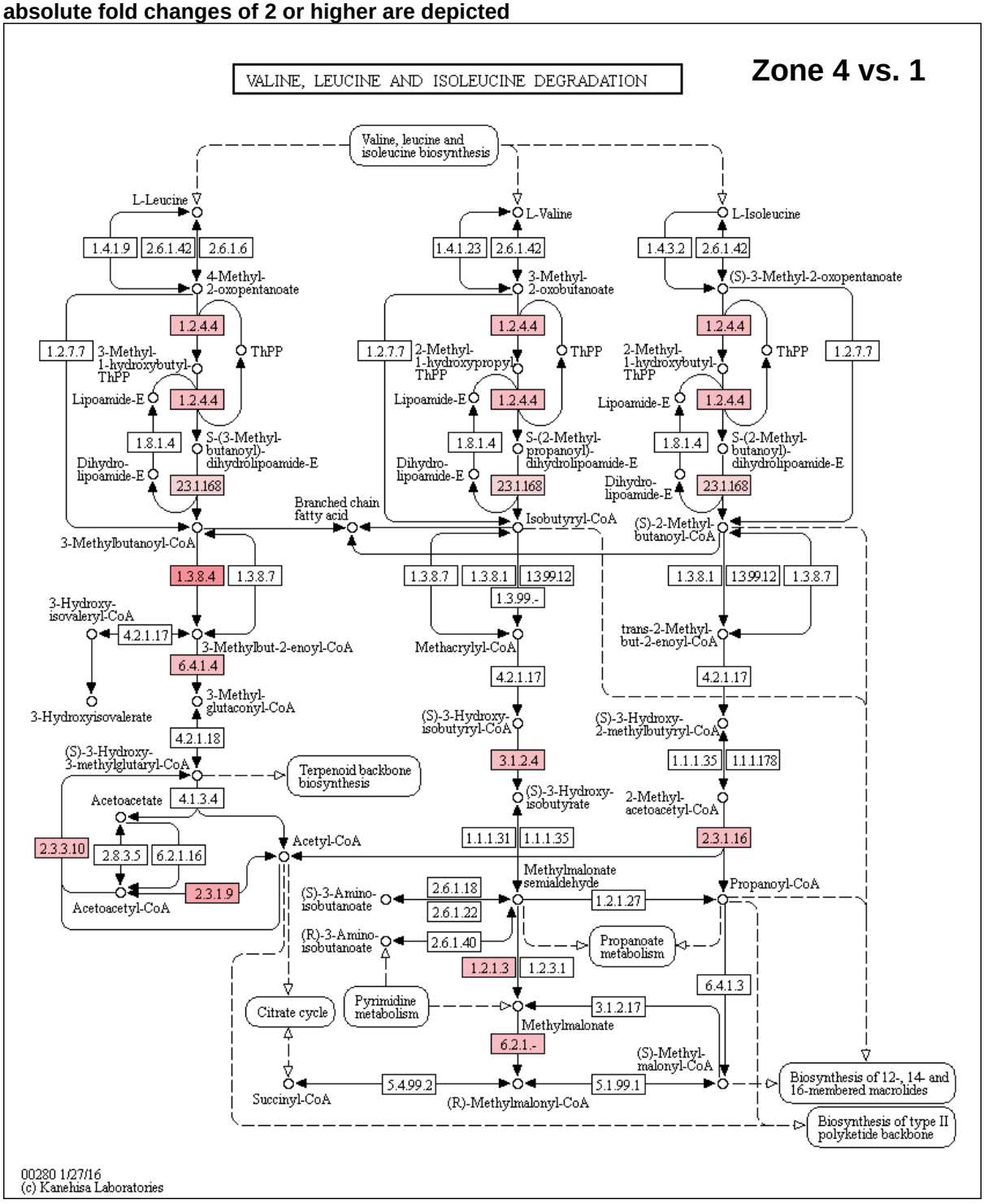

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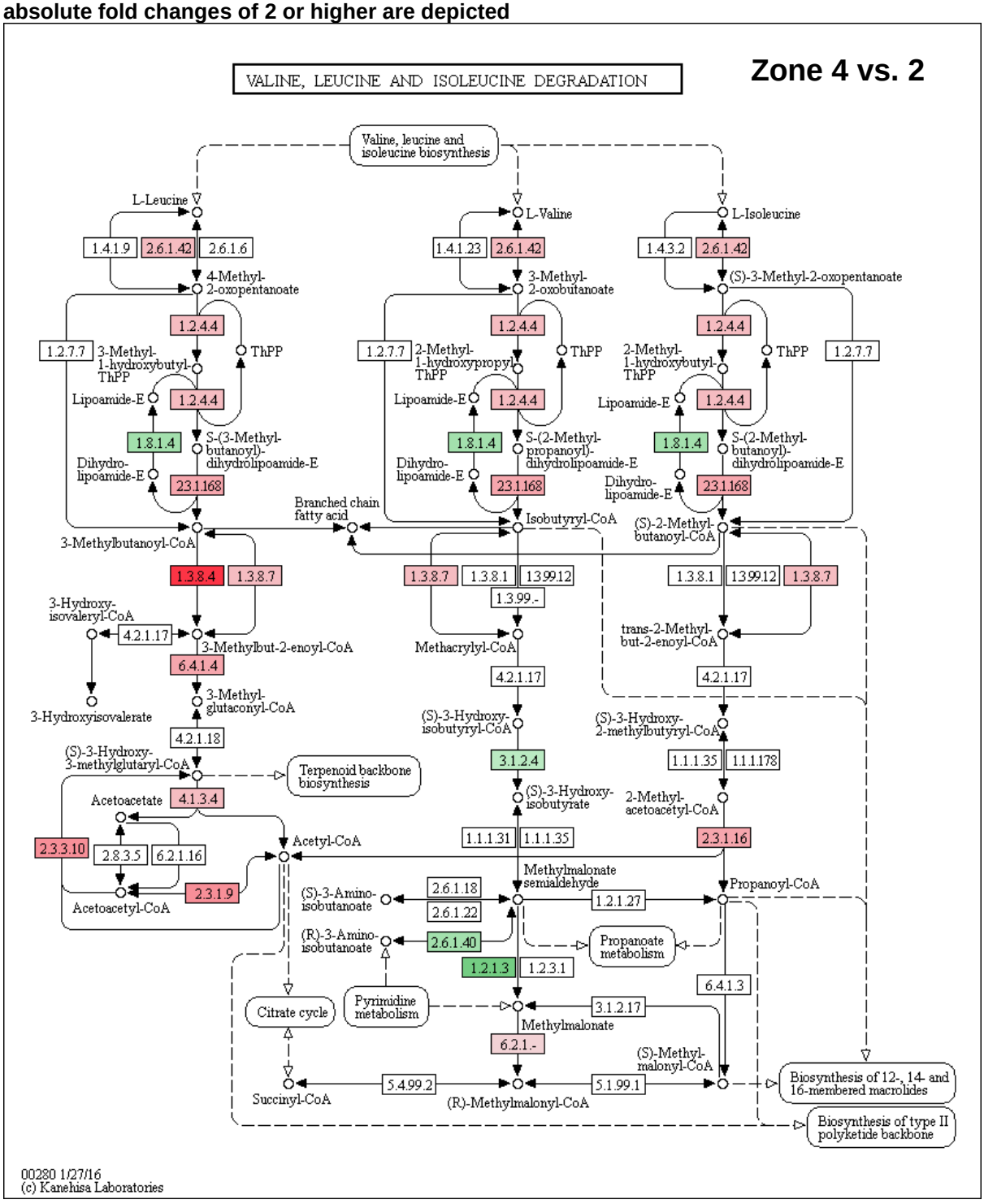

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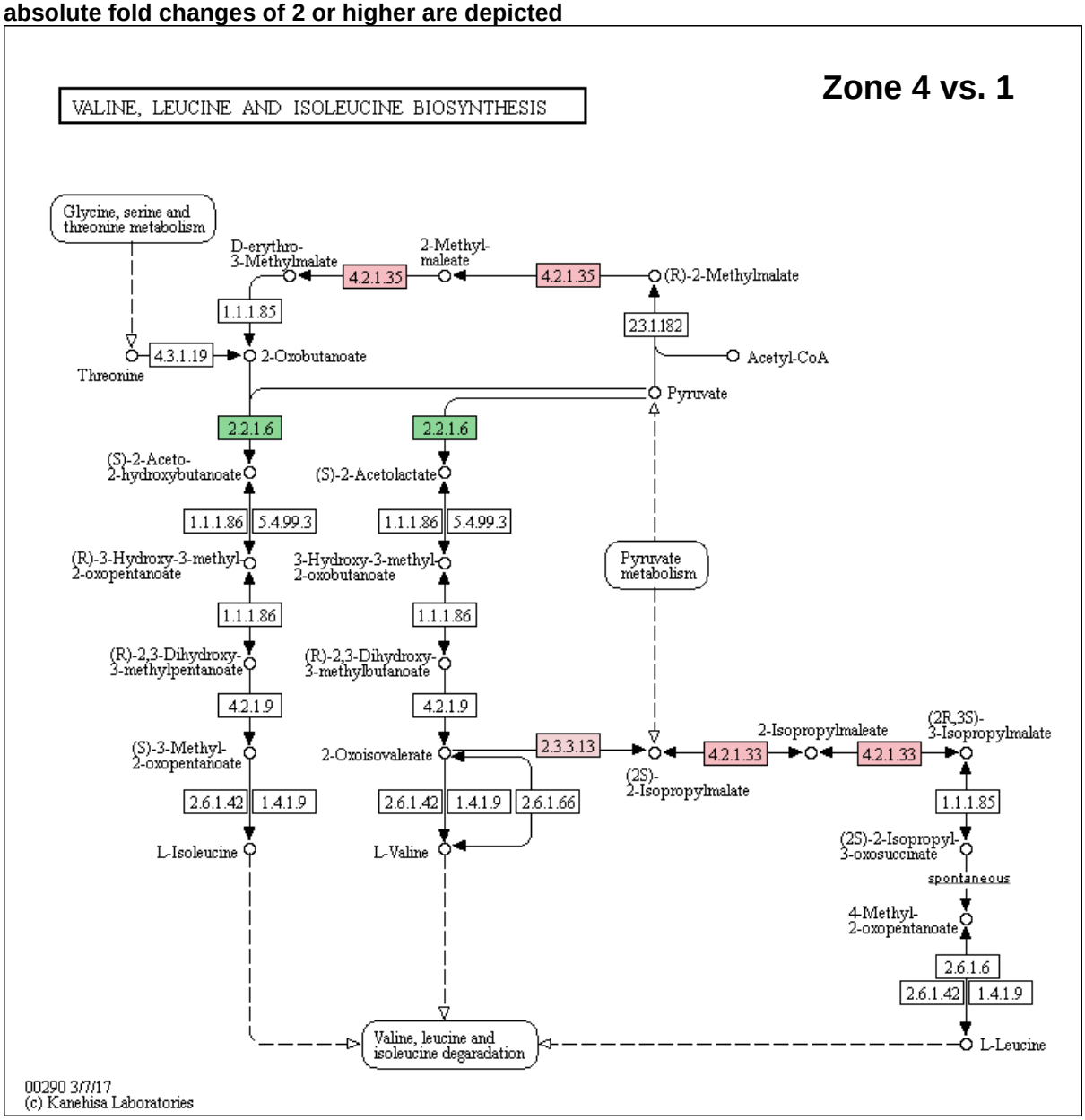

Log2 fold change

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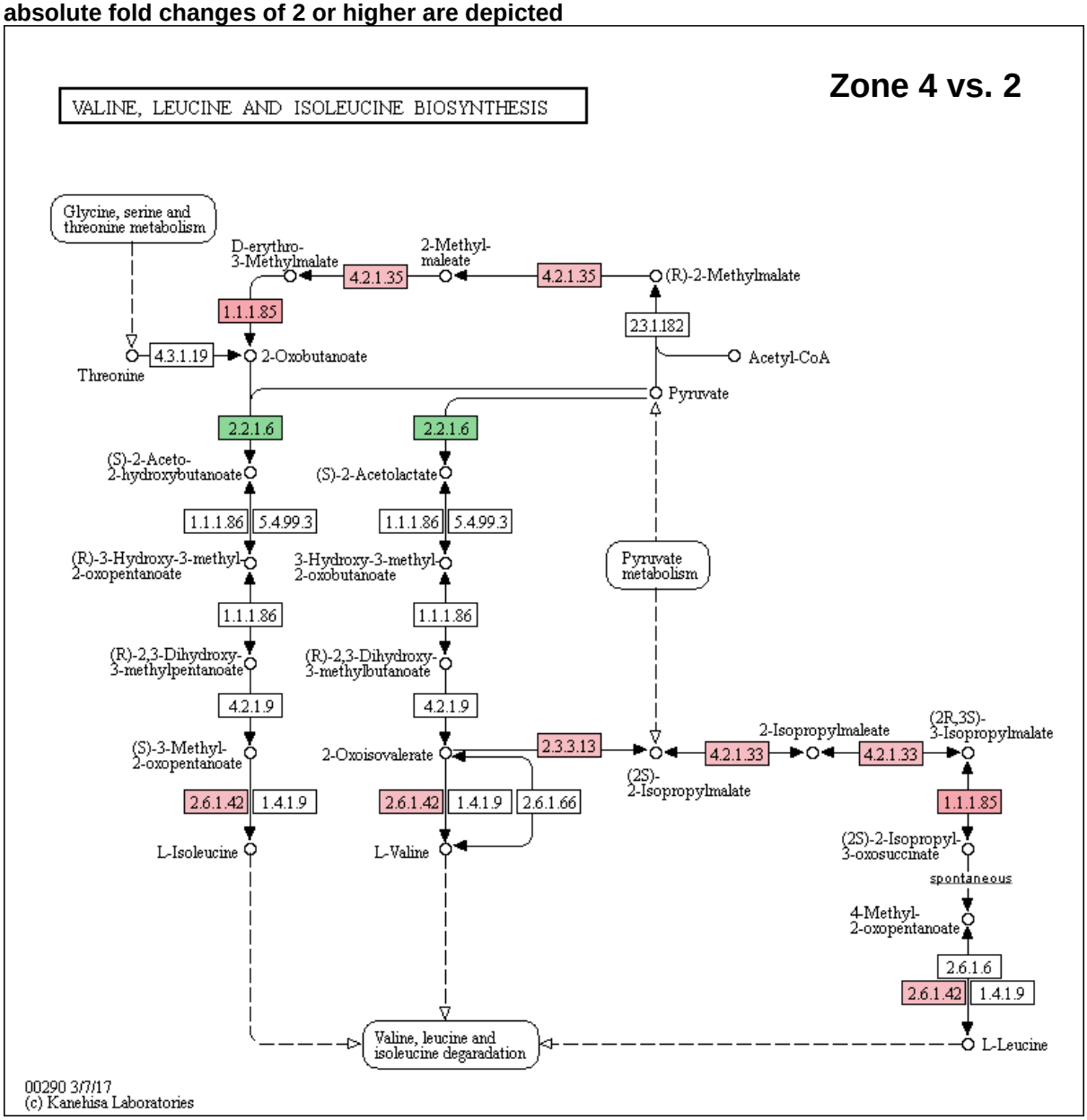

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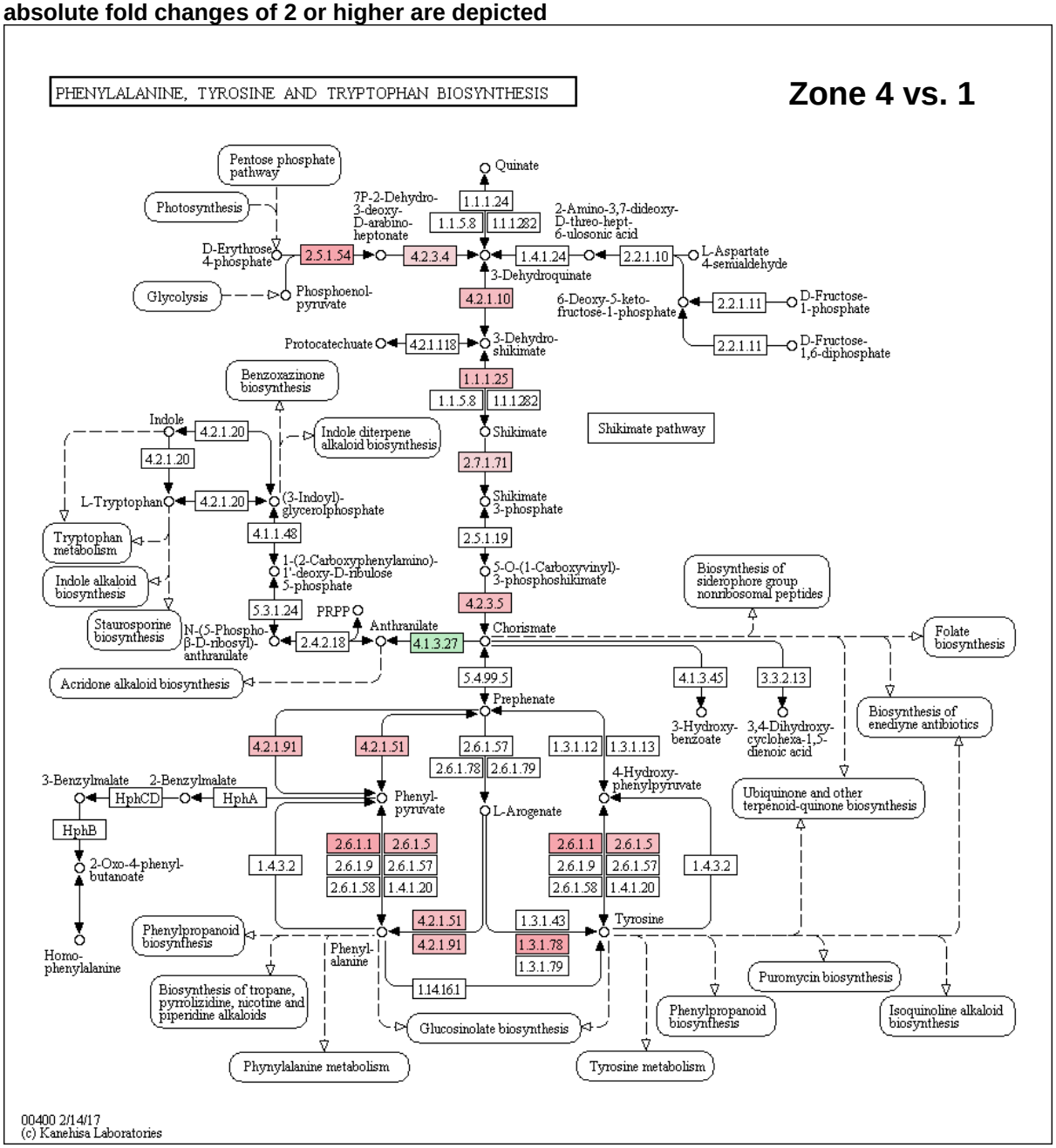

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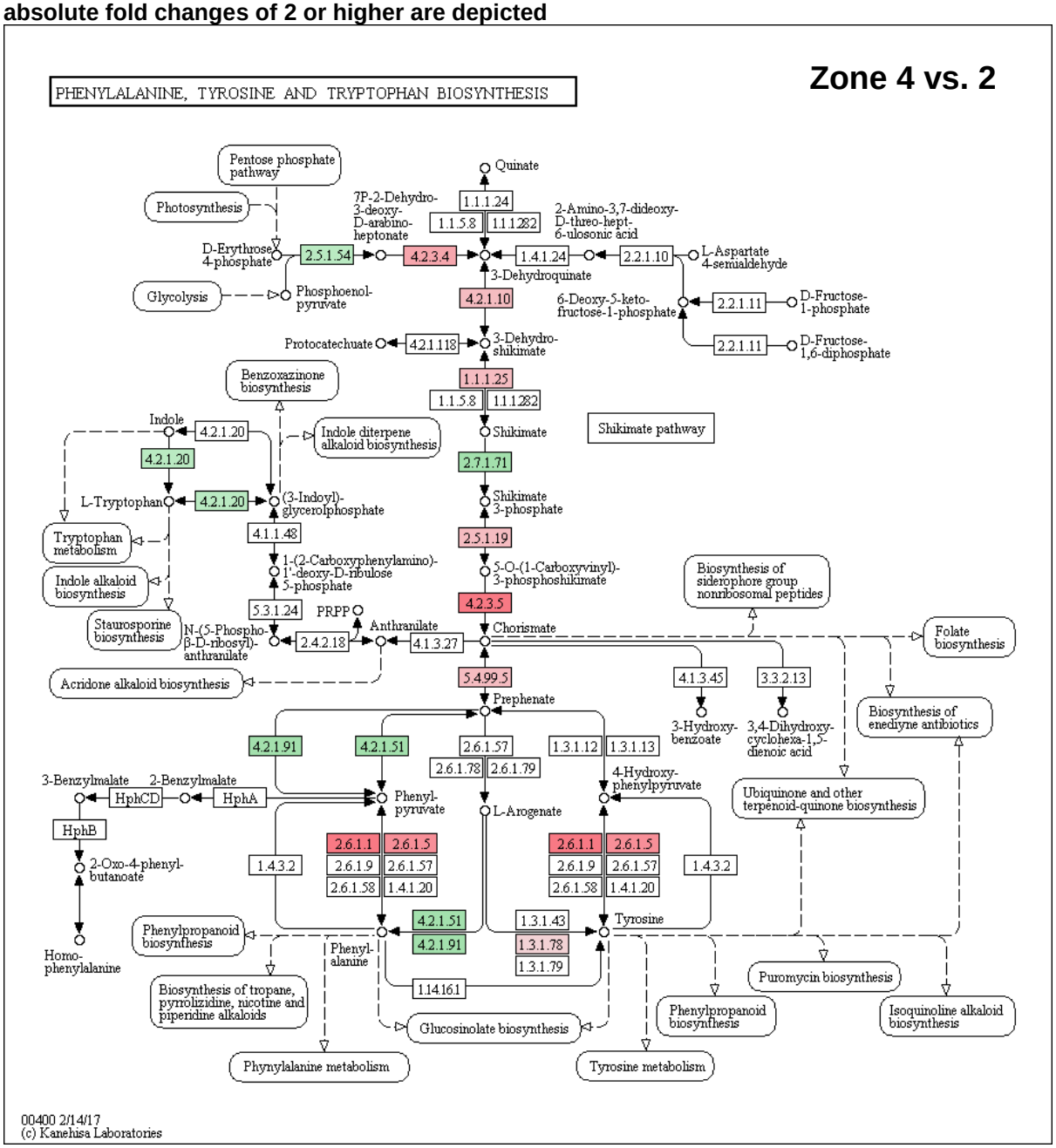

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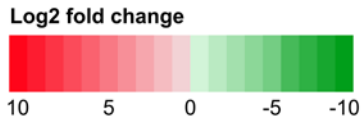

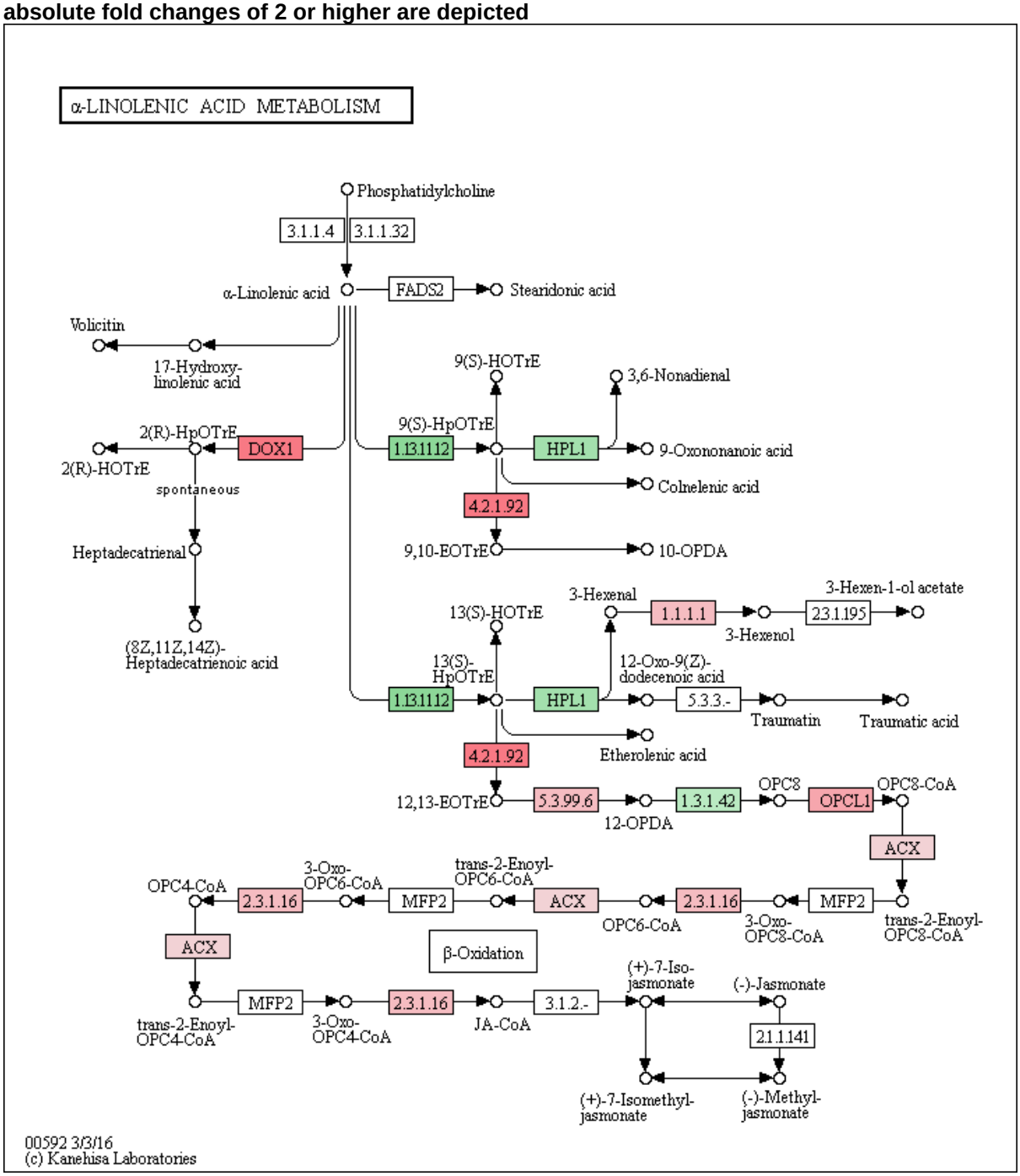

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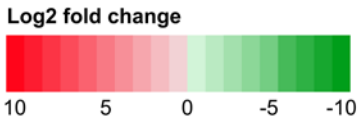
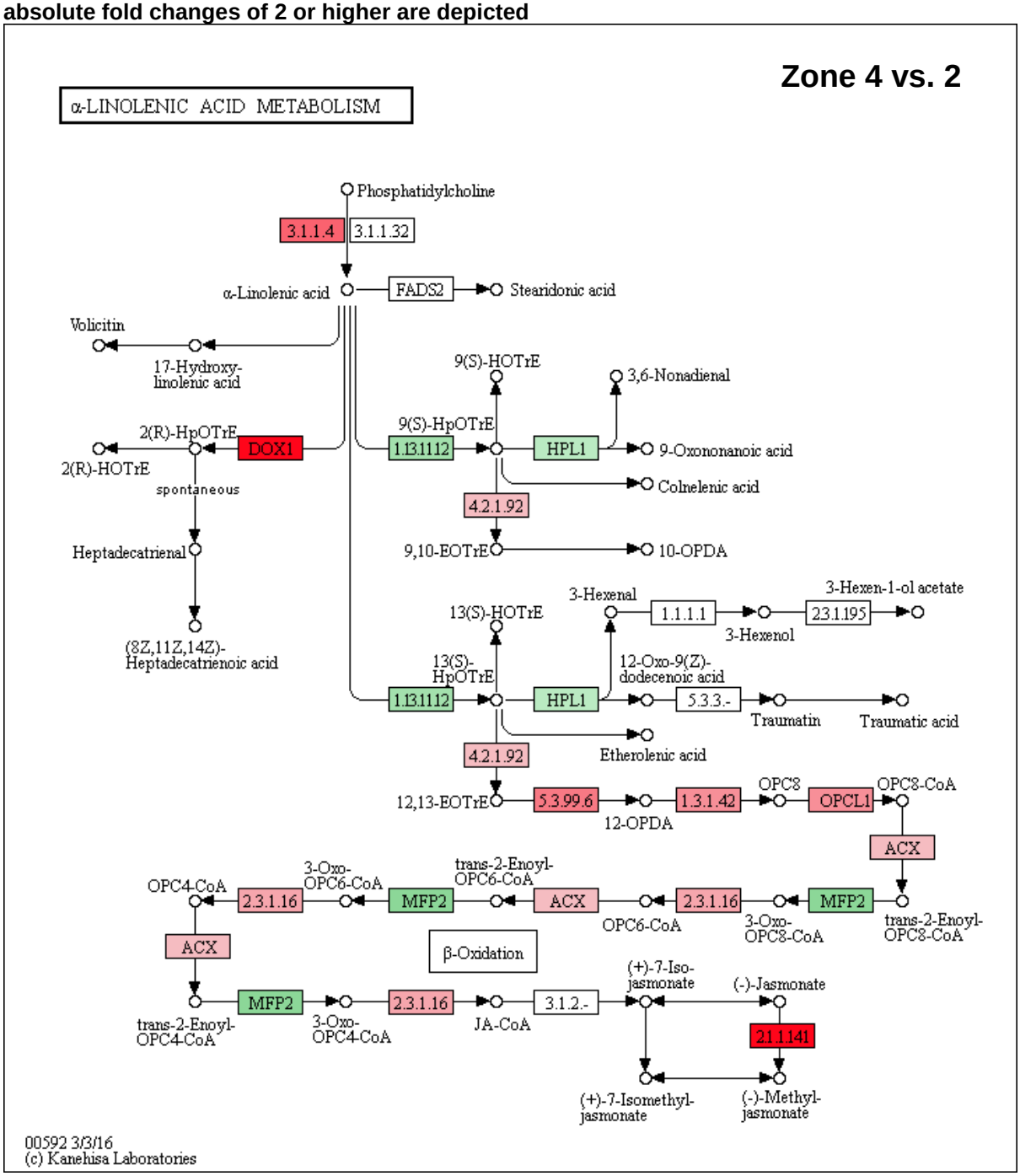


Zone 4 vs. 2



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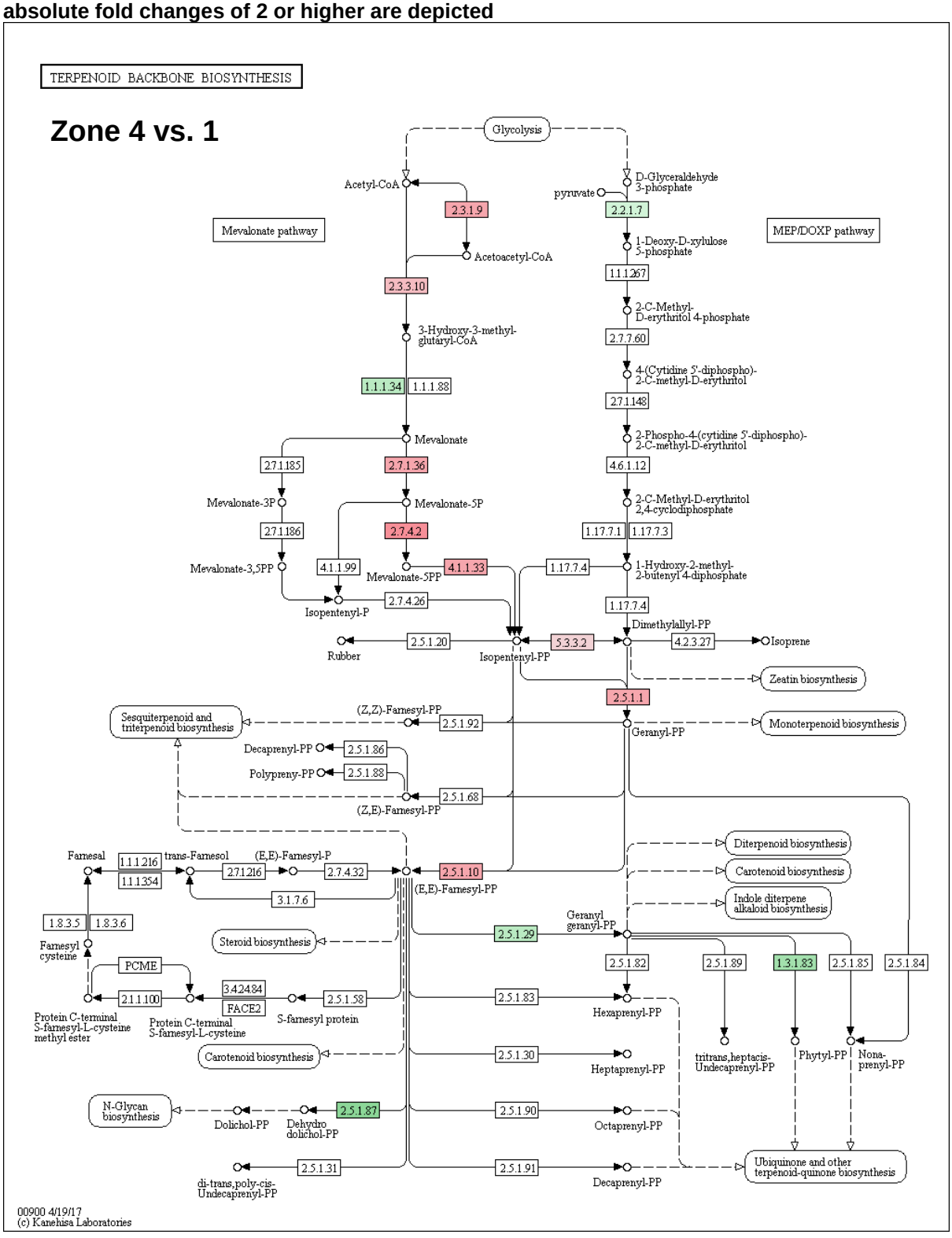

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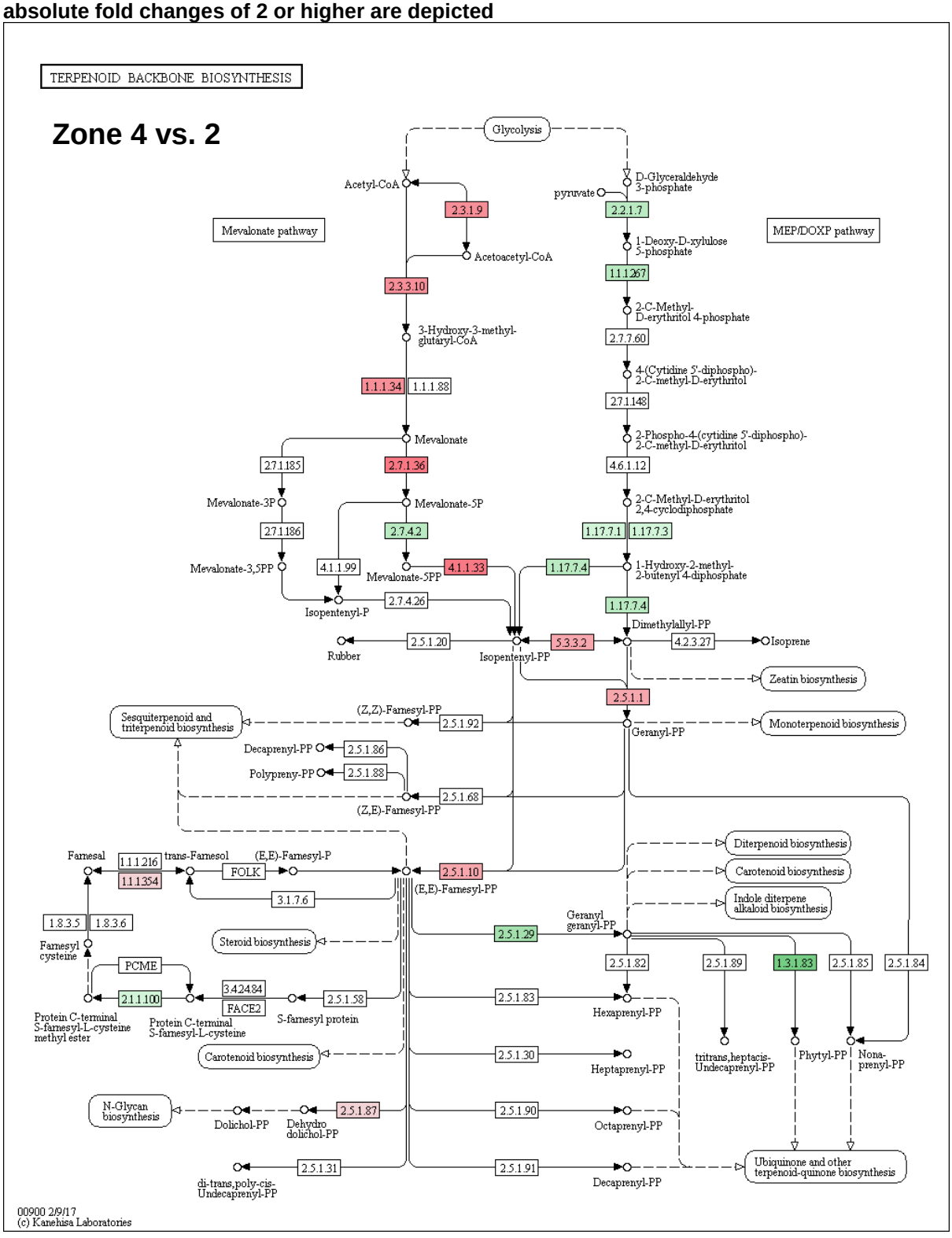

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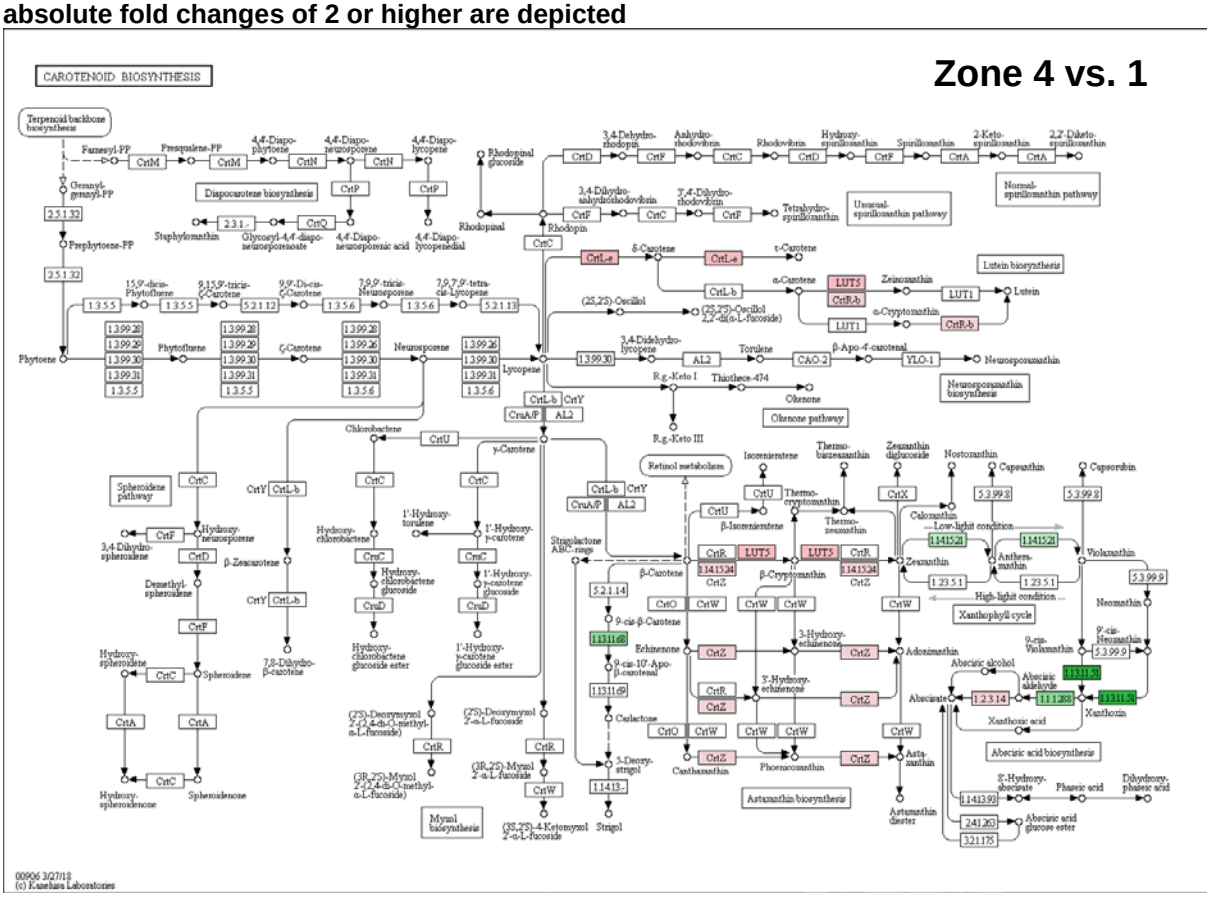
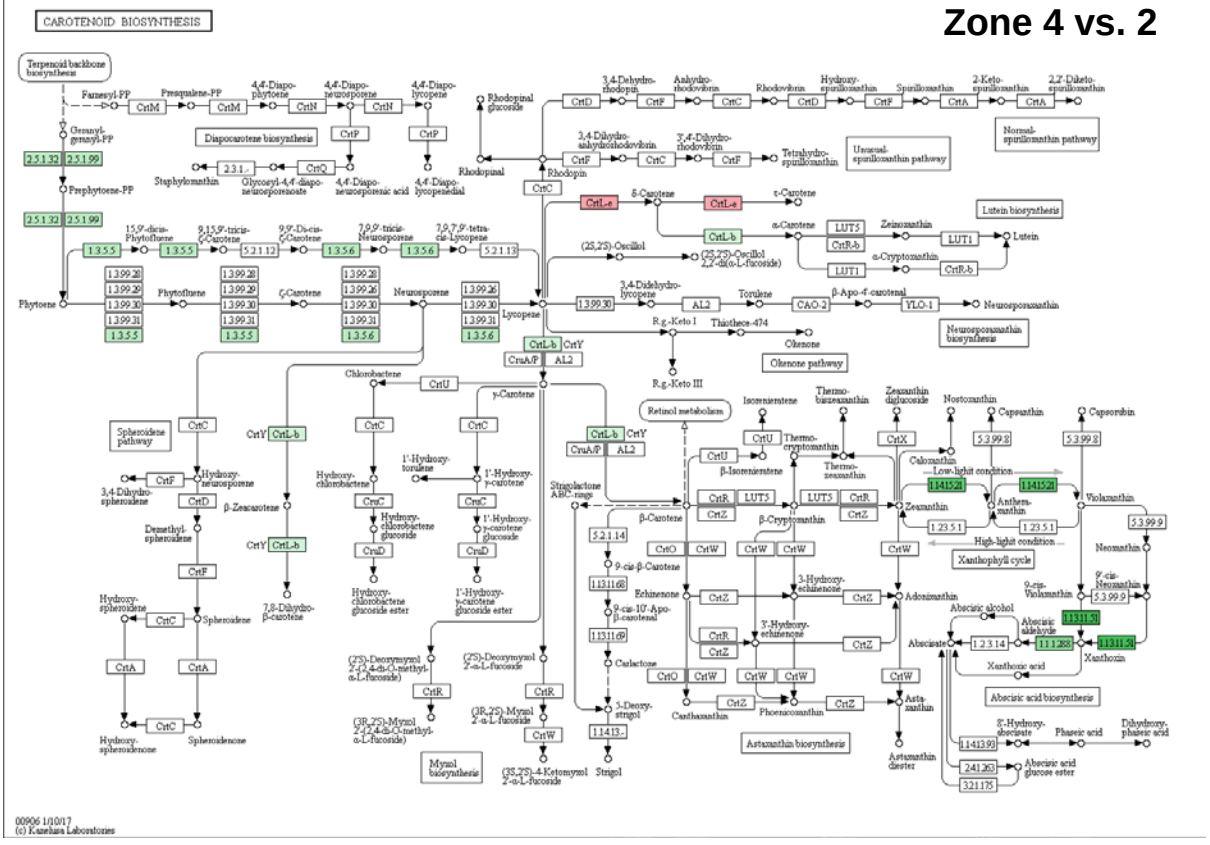
Log2 fold change

10 5 0 -5 -10

Zone 4 vs. 1



Zone 4 vs. 2



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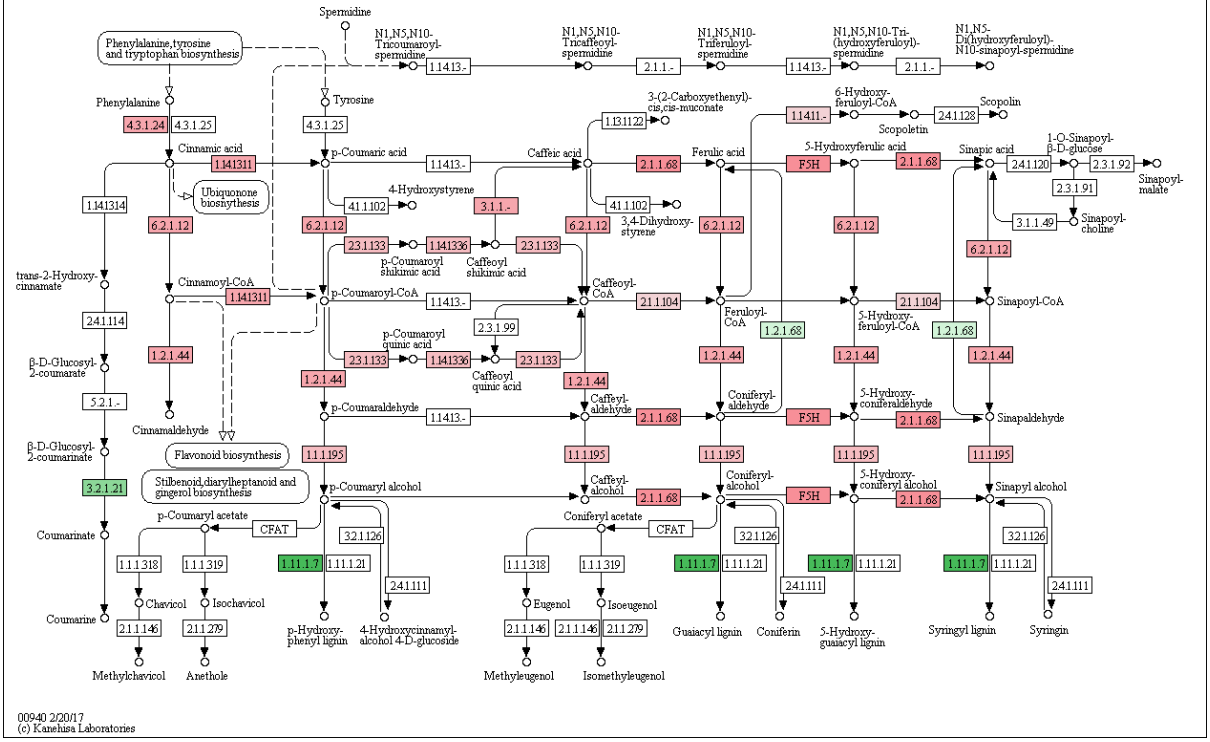

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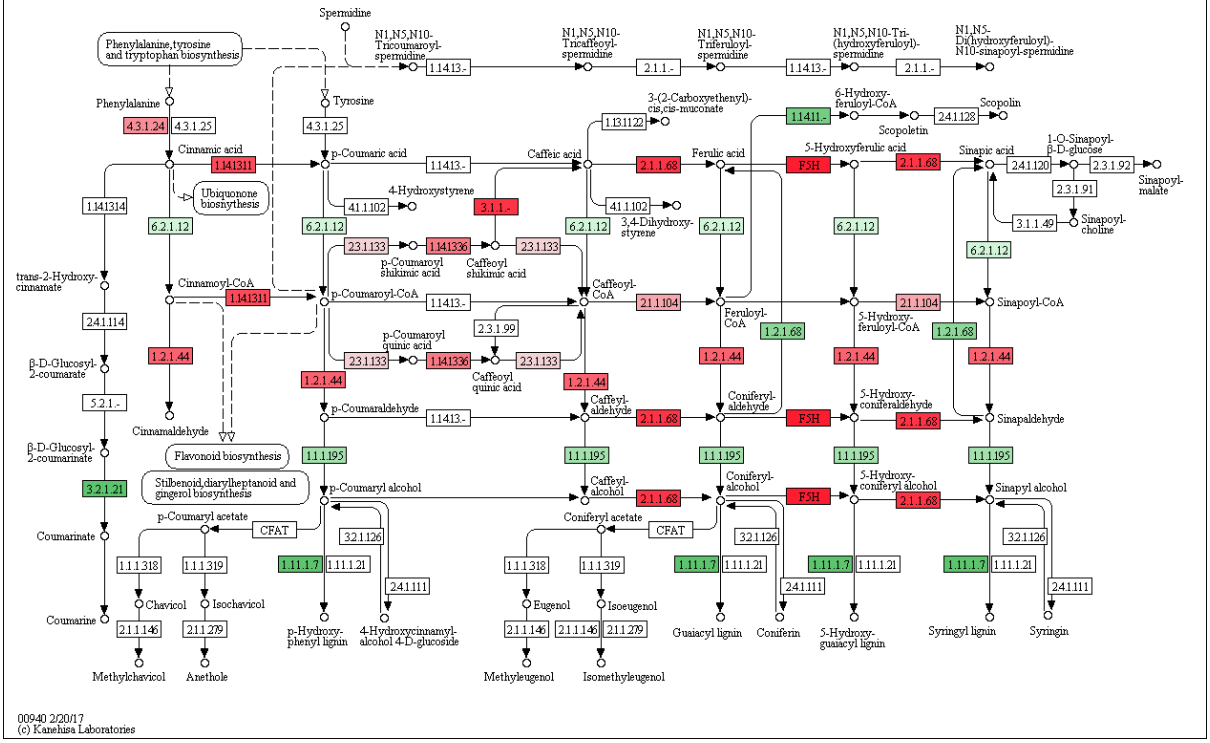

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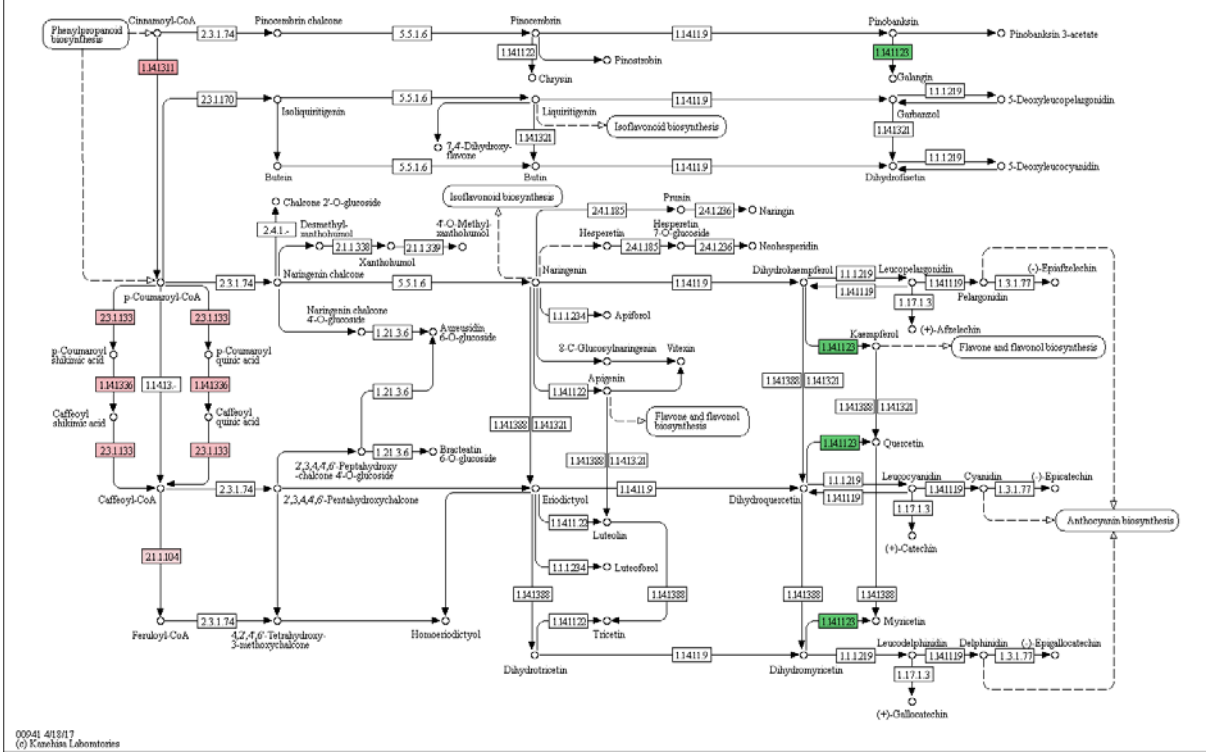
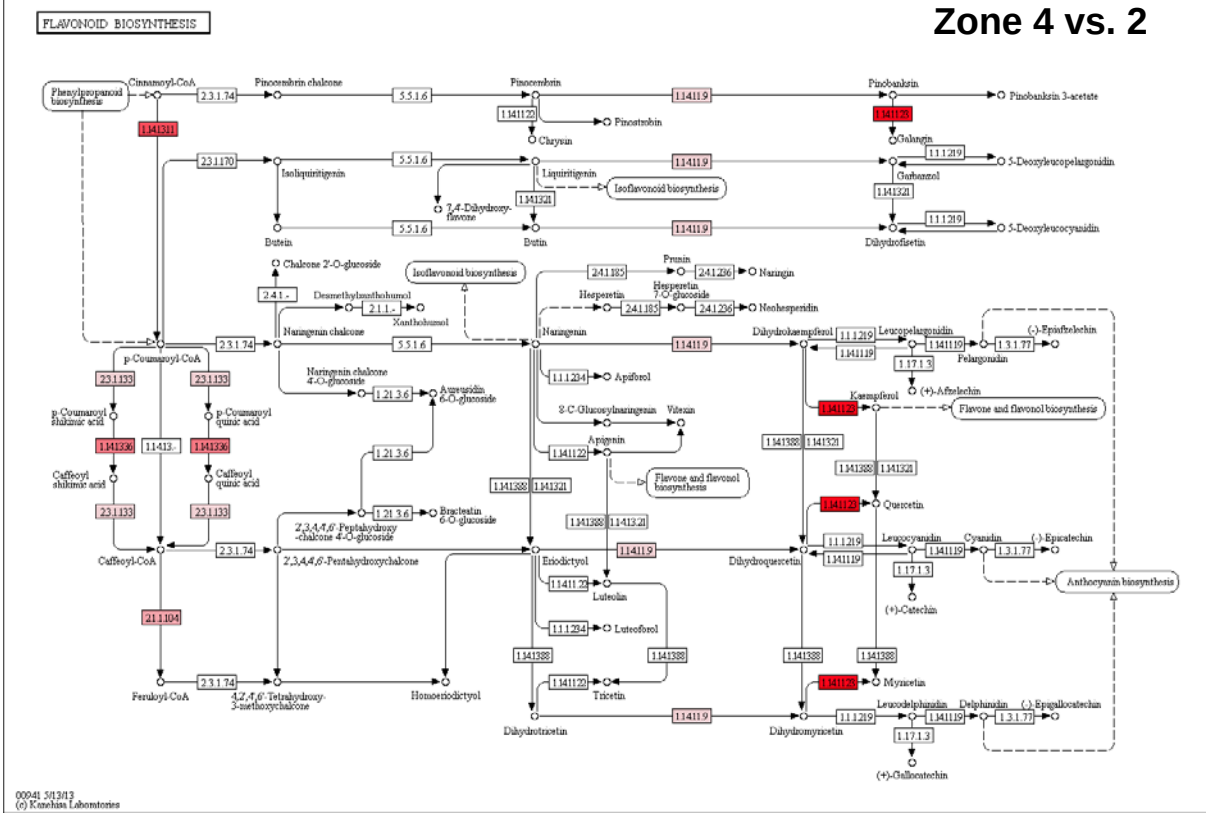


Zone 4 vs. 2



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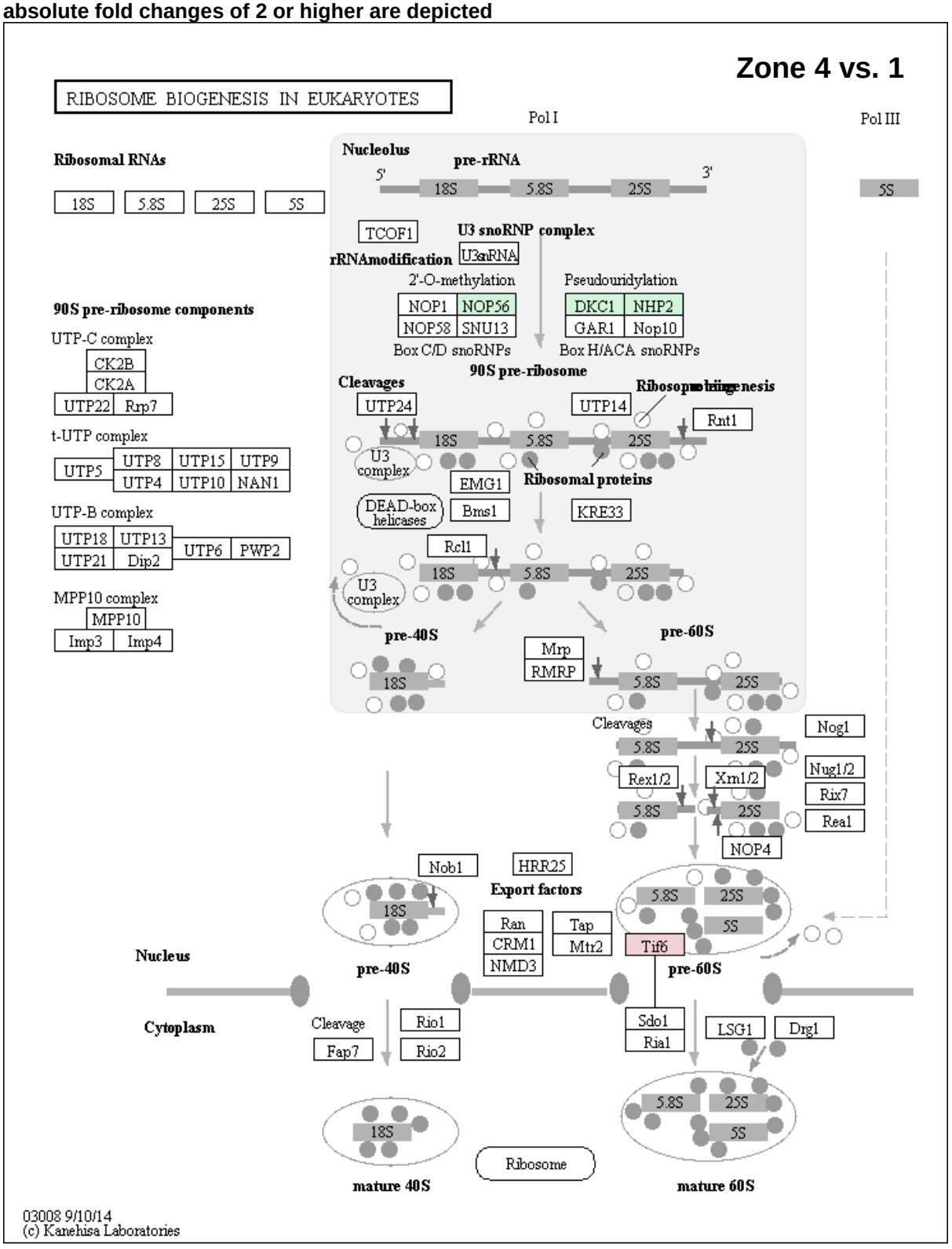

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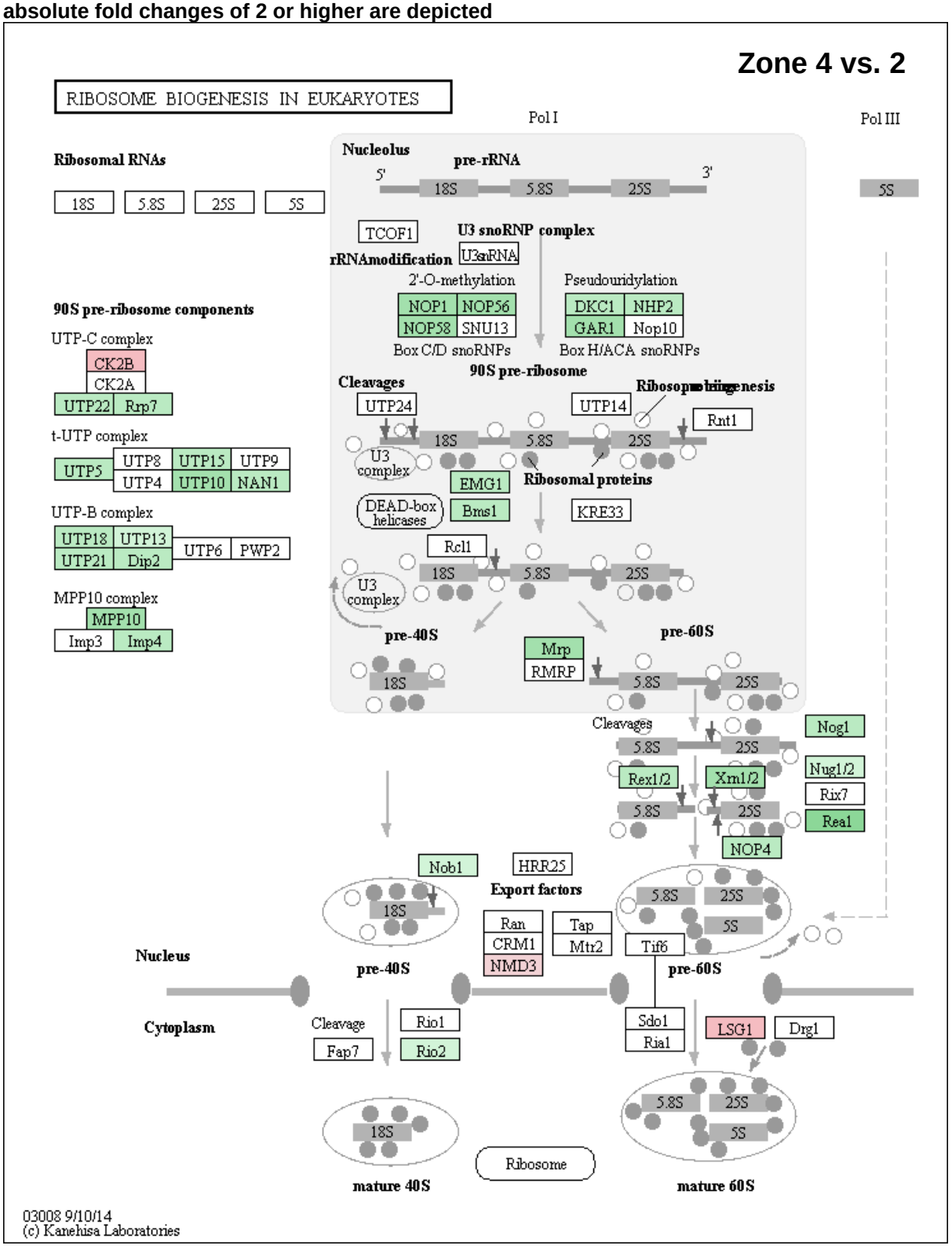

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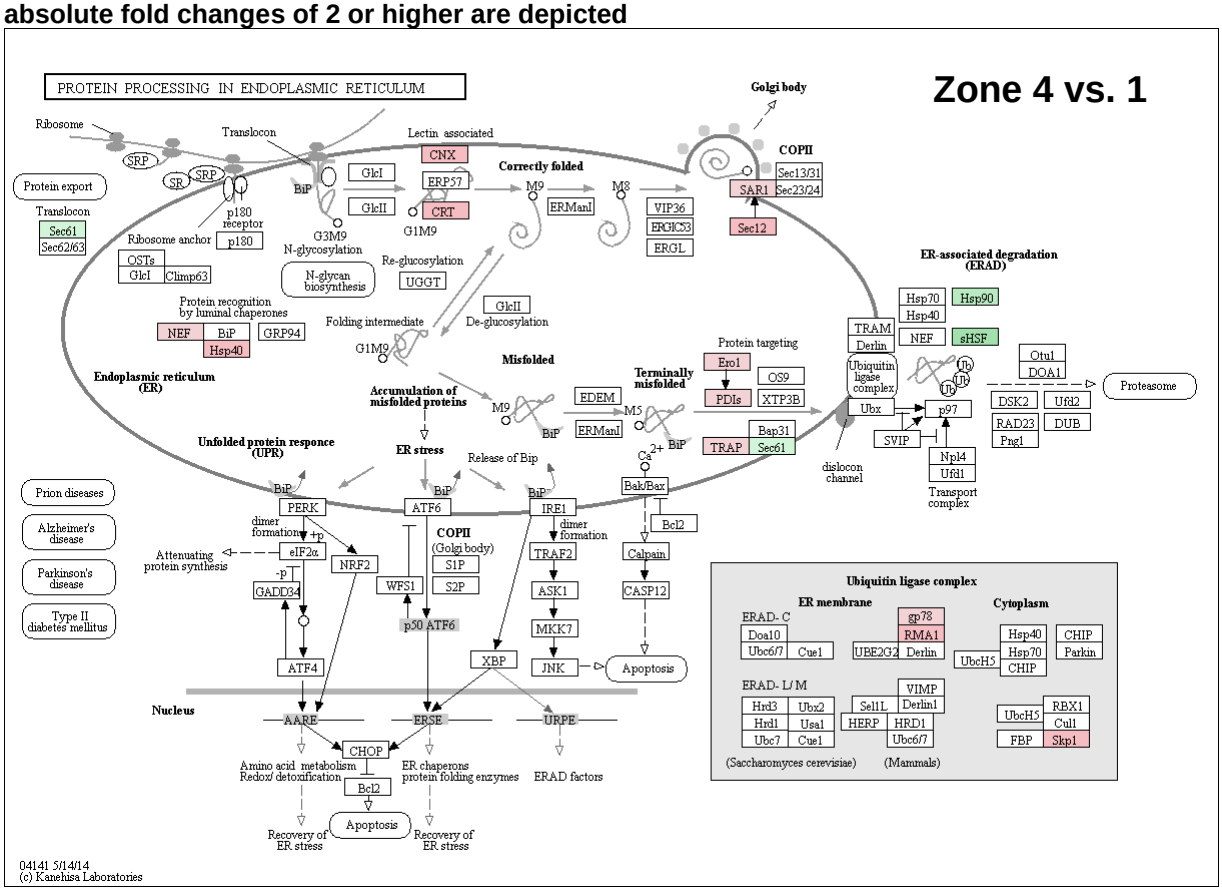

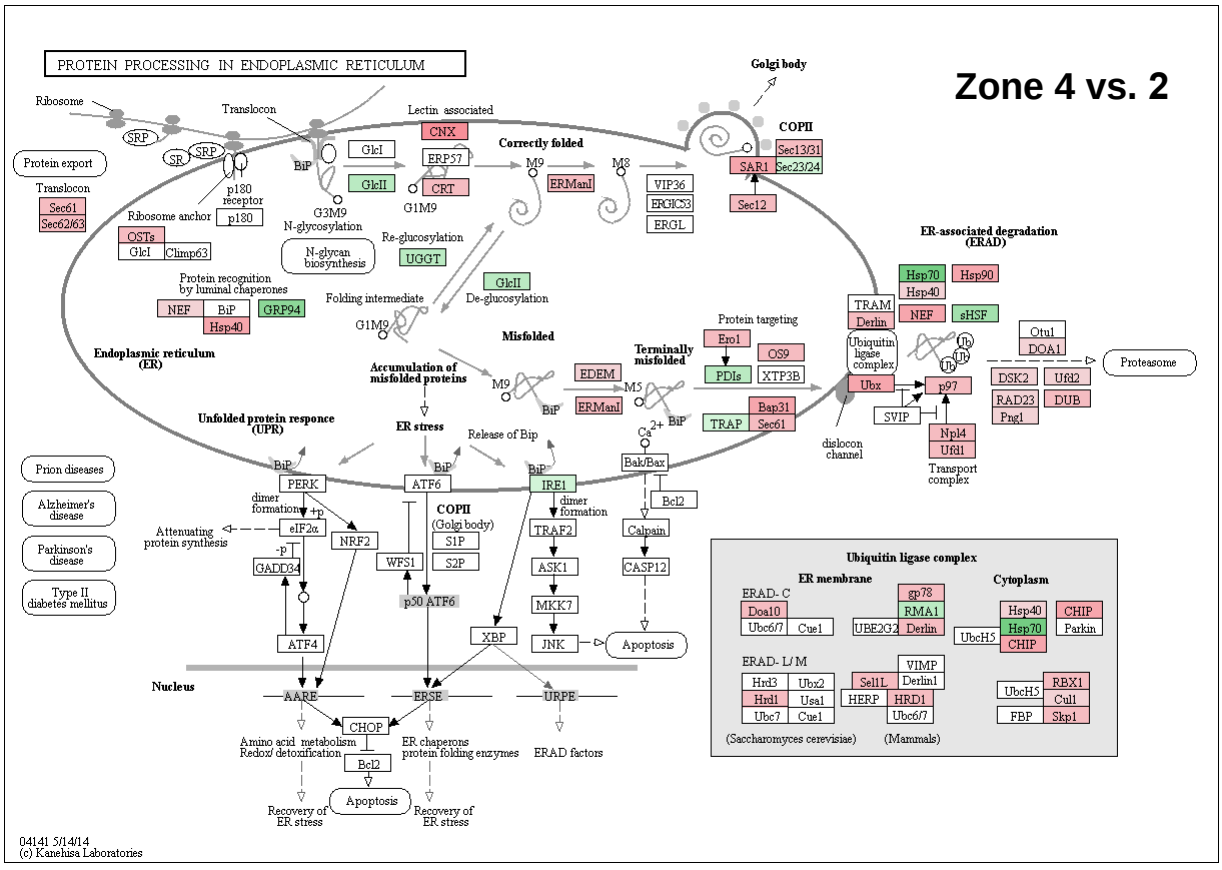

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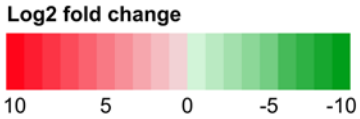

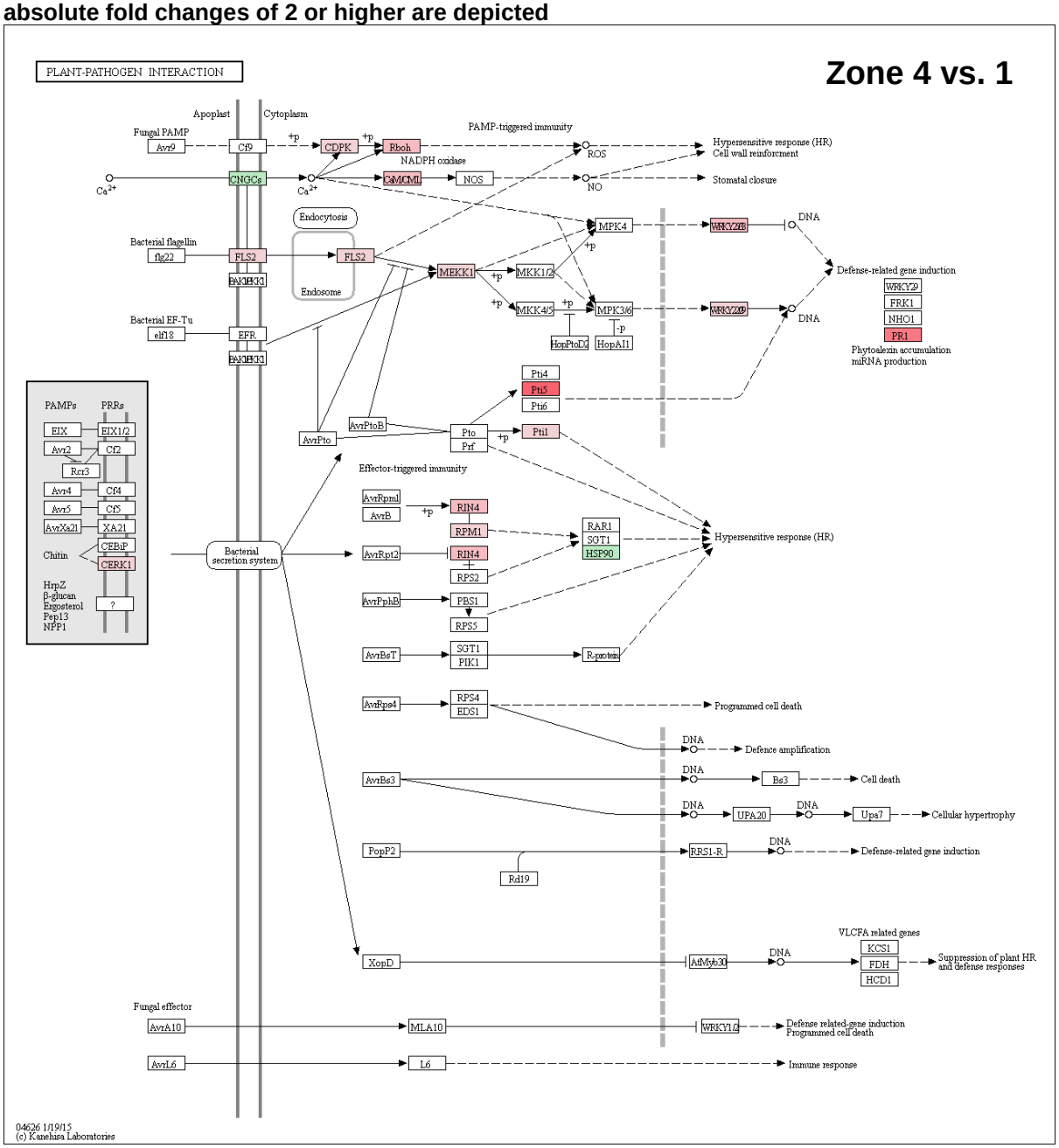

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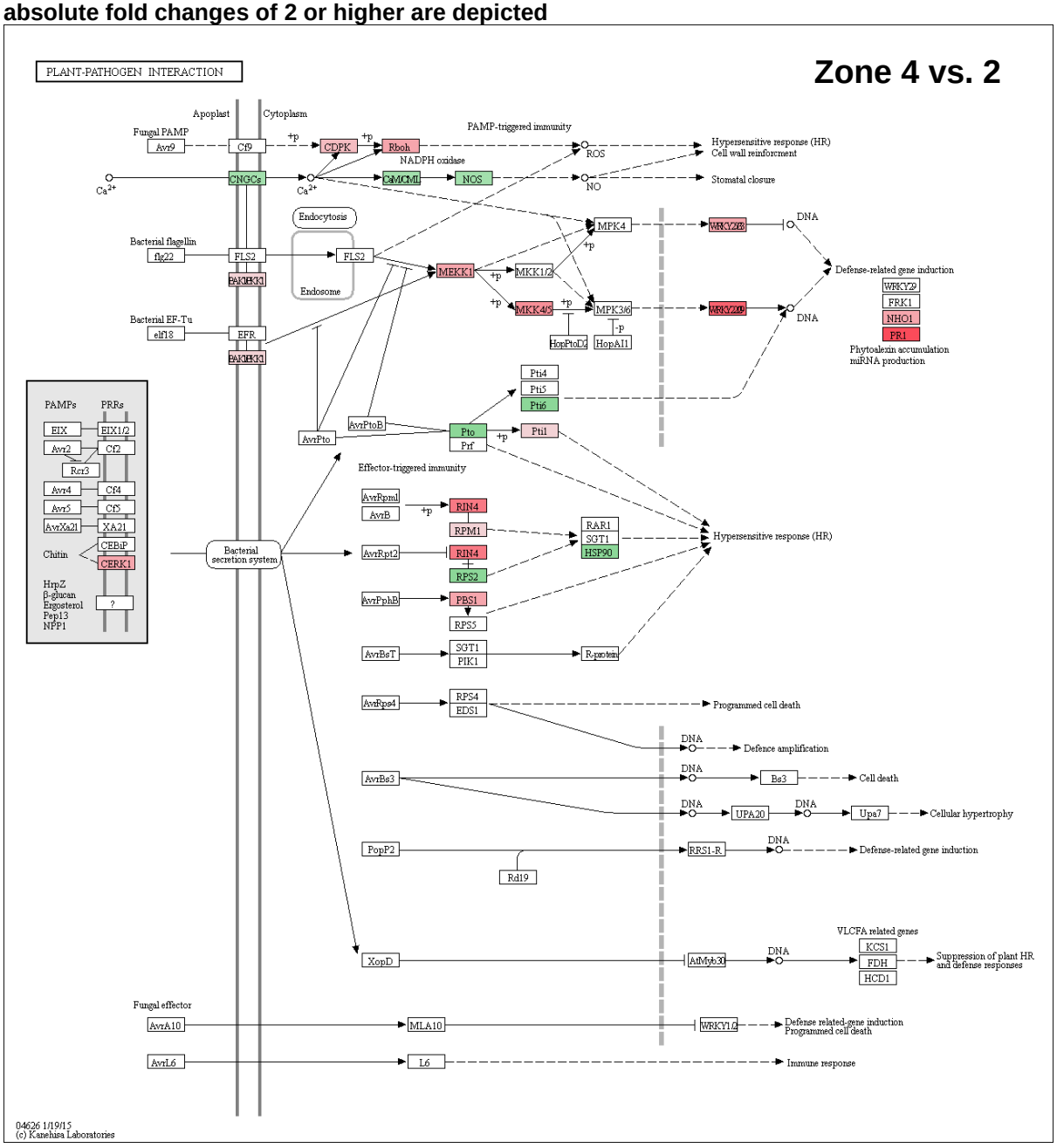

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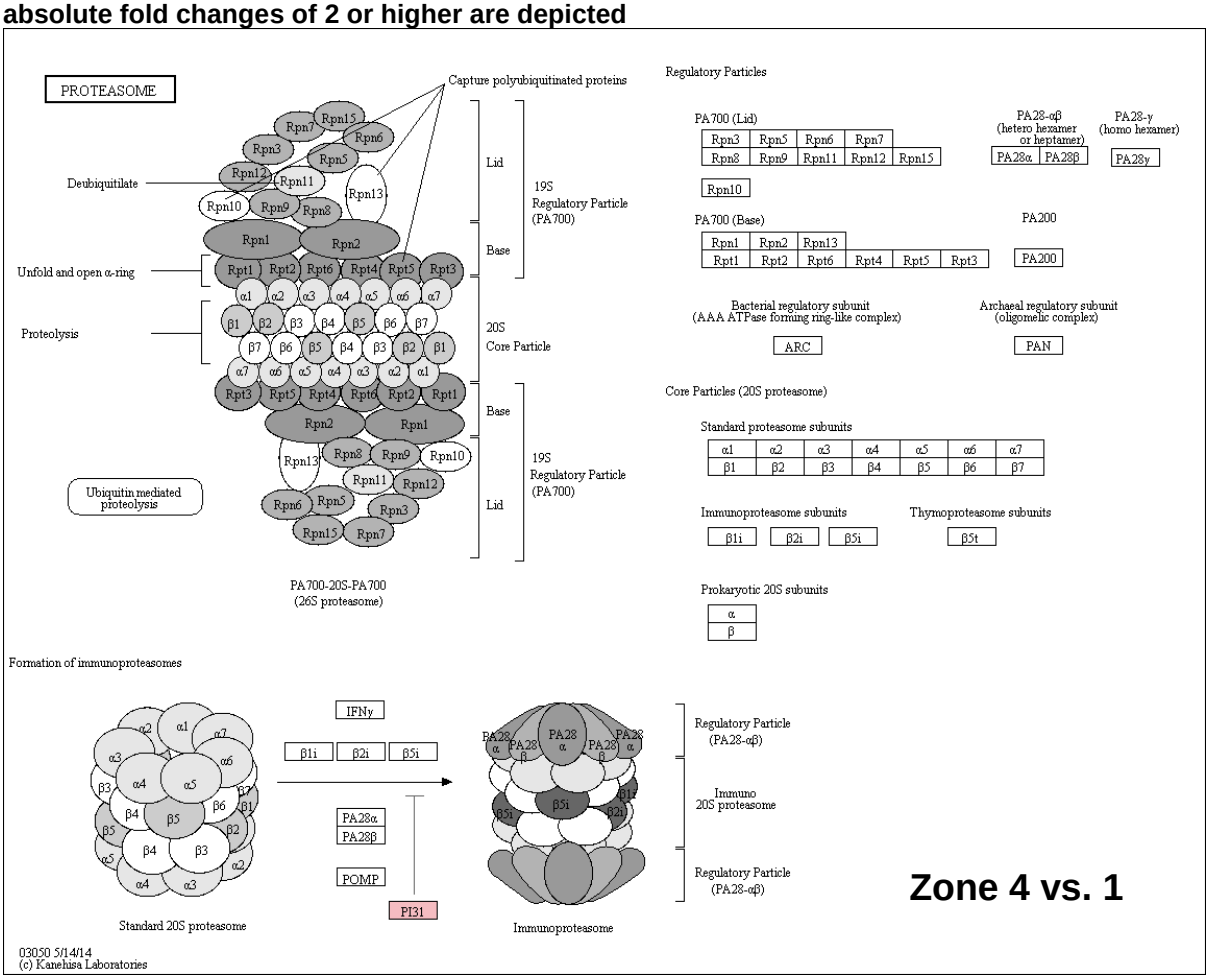

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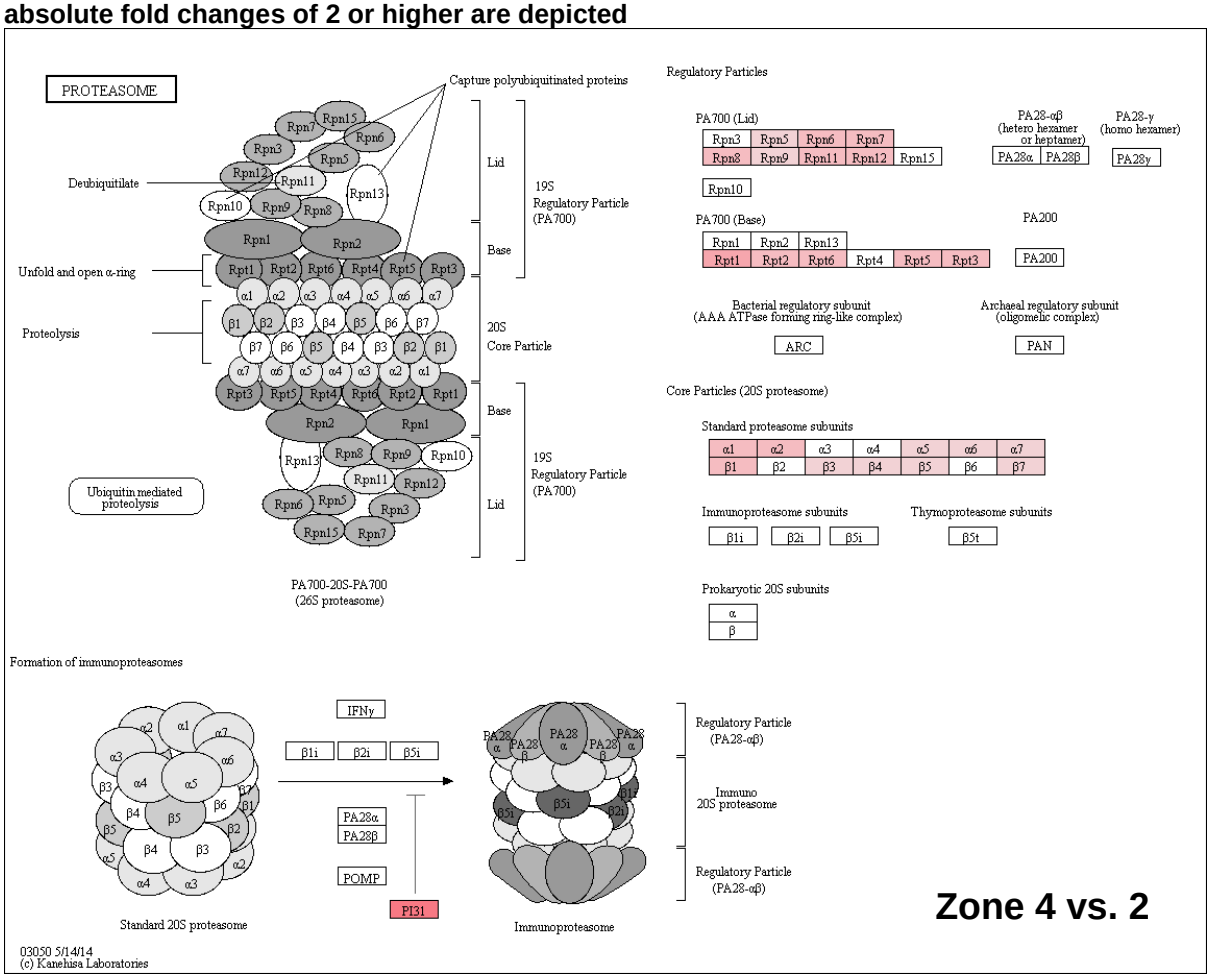

Supplementary Figure S3: KEGG Transcriptome mappings of DEGs based on fold changes. Only DEGs with log2 fold changes of 1 or more and p-adj values of 0.05 or less are depicted. KEGG maps were obtained from www.kegg.jp[40-43]