**Transcriptome analysis reveals reduced immunity and metabolic level under cold stress in *Mauremys mutica***

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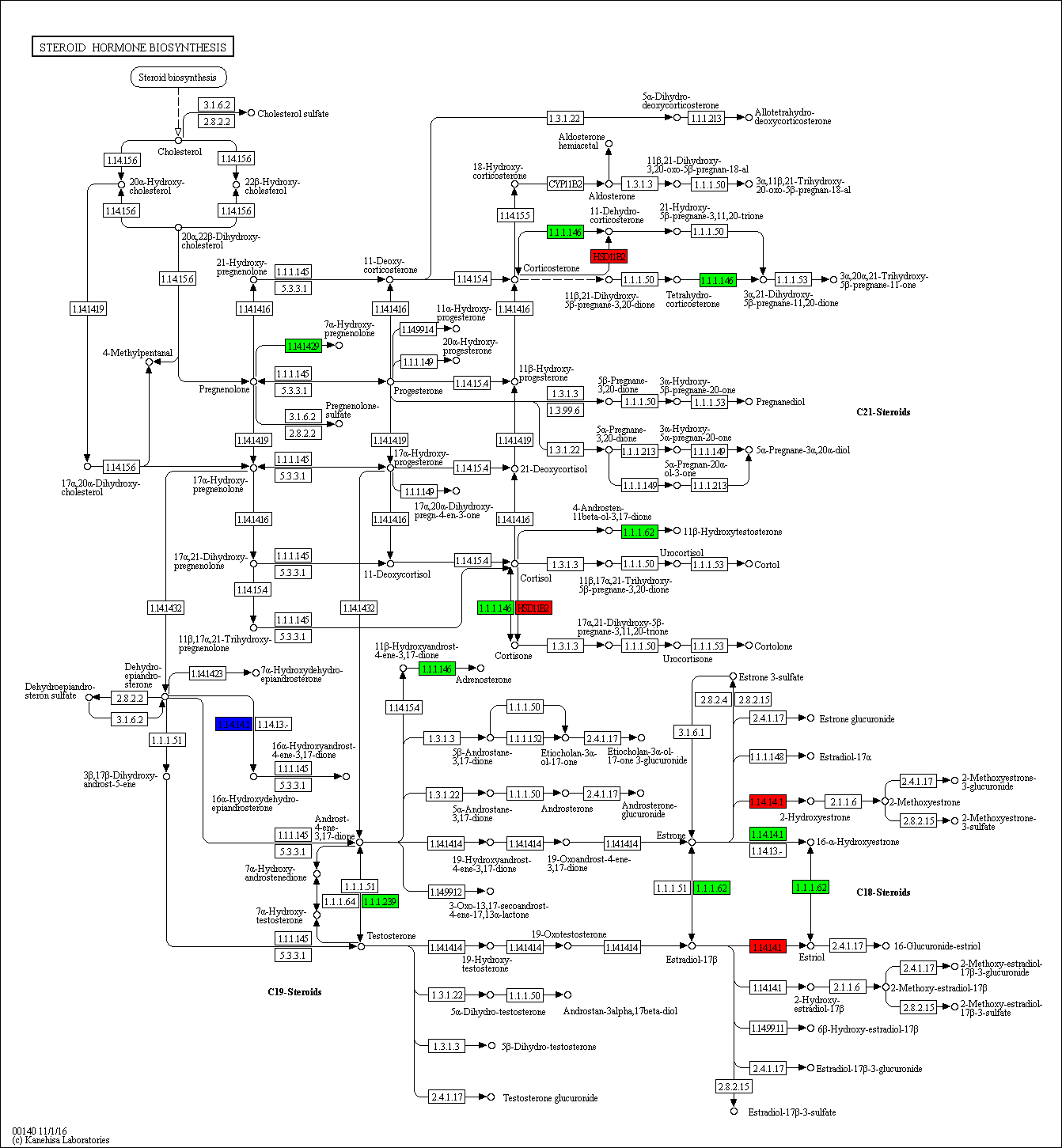
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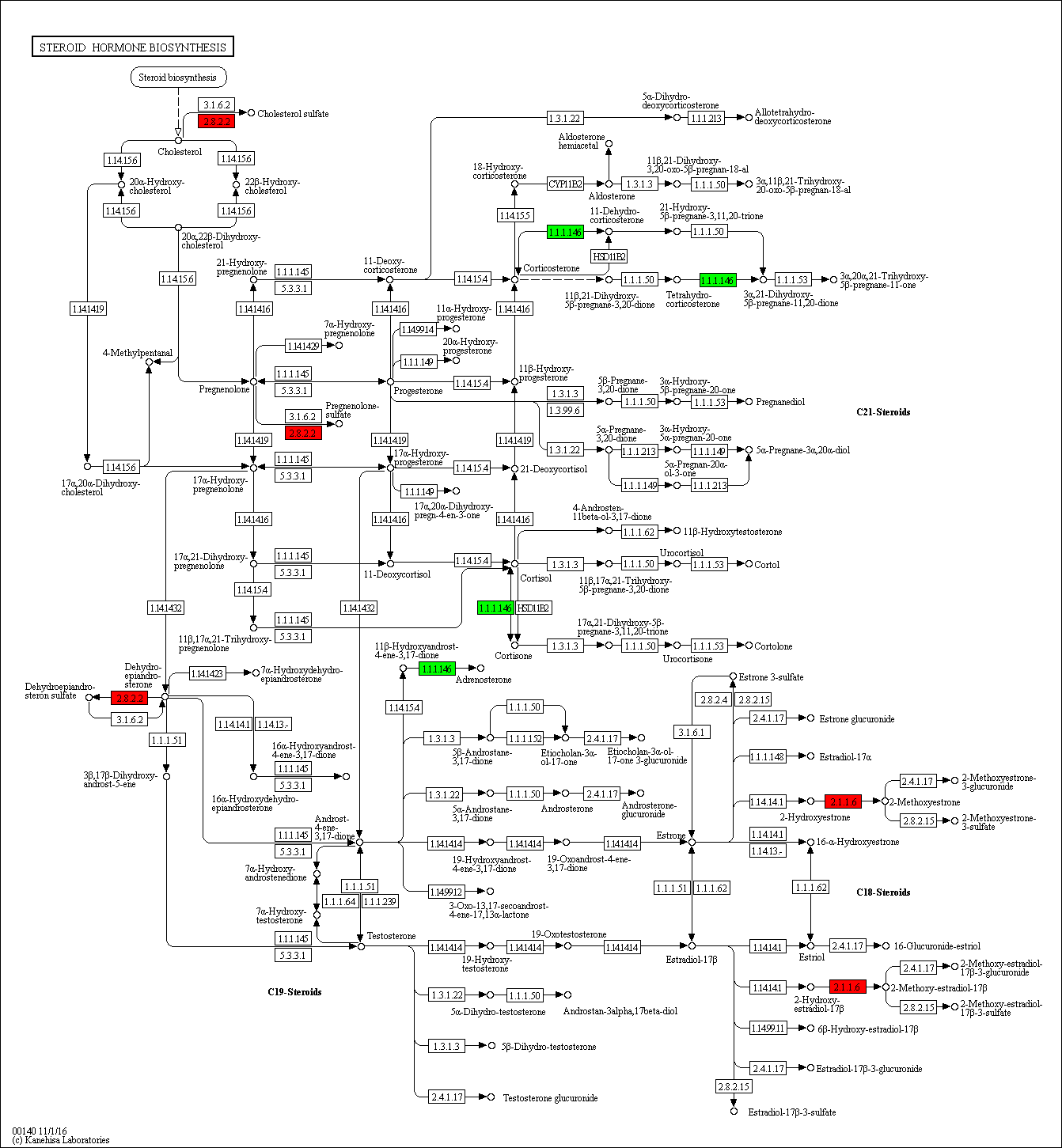
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Figure S1. KEGG pathway enrichment maps for each time point. The green, red and blue background colours in the pathway represent down-regulated, up-regulated and up-down-regulated genes respectively. ( Steroid hormone biosynthesis in 48h (A) and R (B). Glycine, serine and threonine metabolism in 48h (C) and R (D). Unsaturated fatty acid biosynthetic pathways in 48h (E) and R (F). NOD-like receptor signalling pathways in 48h (G) and 24h (H). Neuroactive ligand receptor interactions in 48h (I) and 24h(J). Cytokine-cytokine receptor interactions in 48h (K) and 24h (L). Ether lipid metabolism in 24h (M) and R (N).)

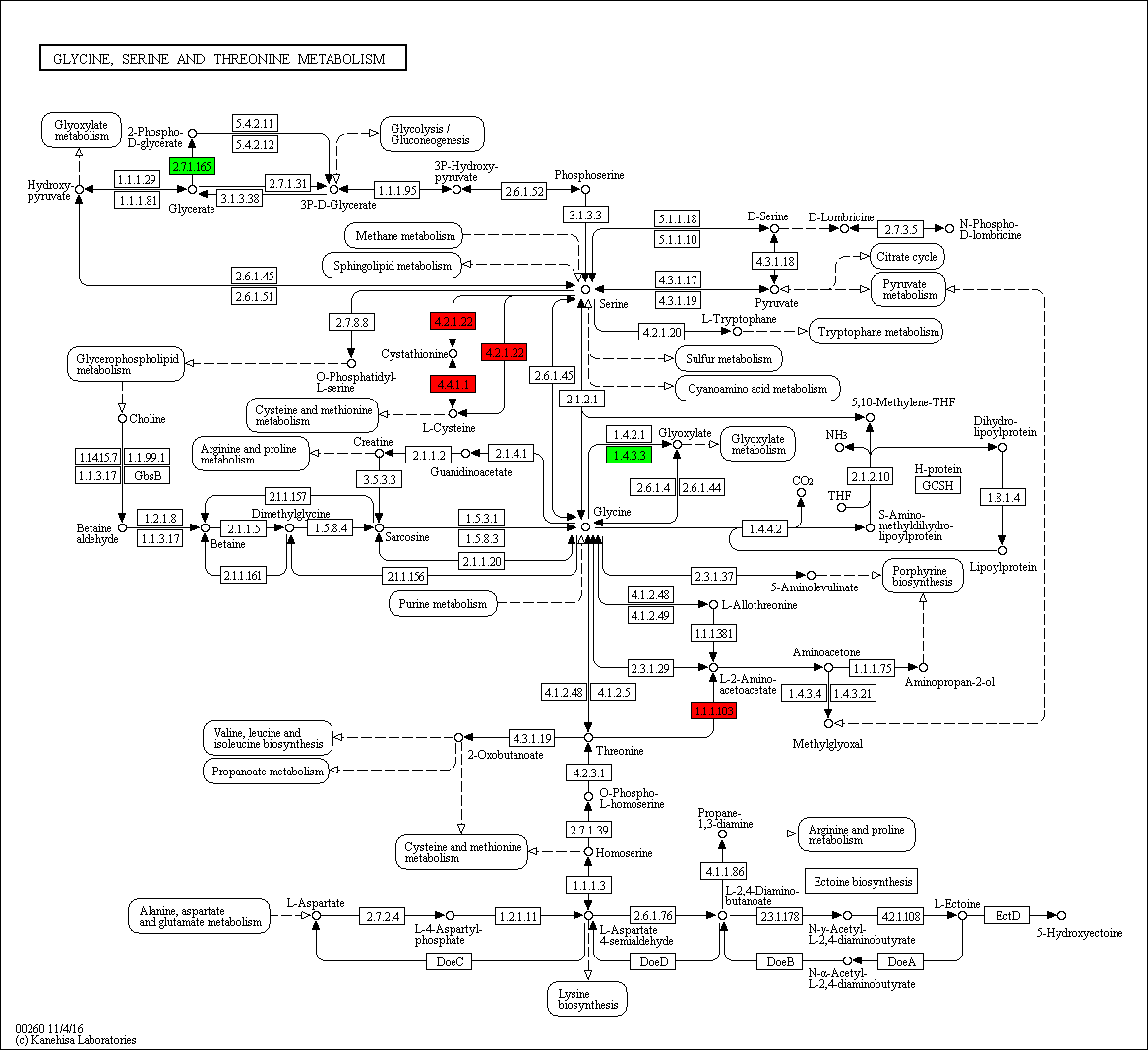
A



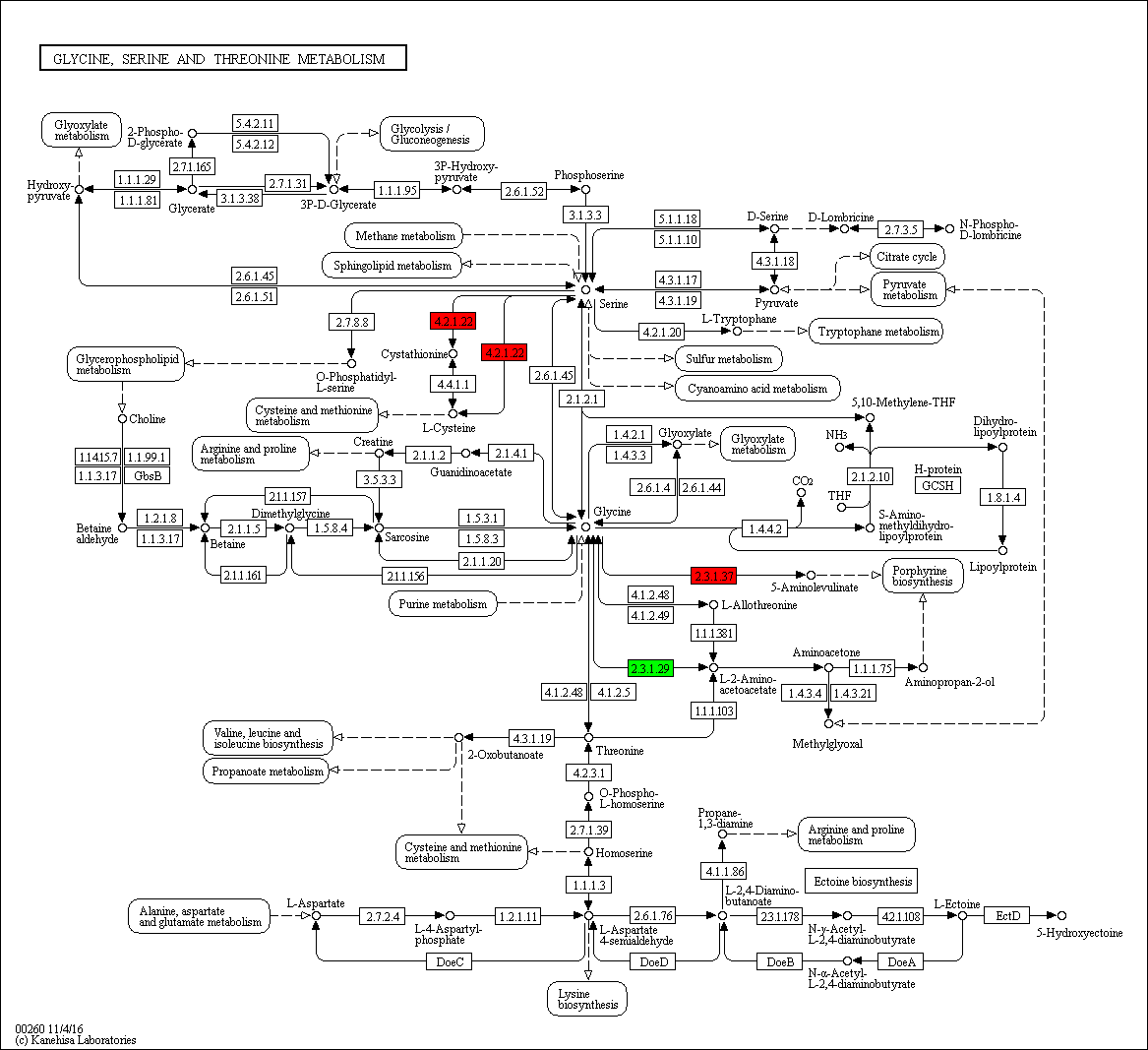
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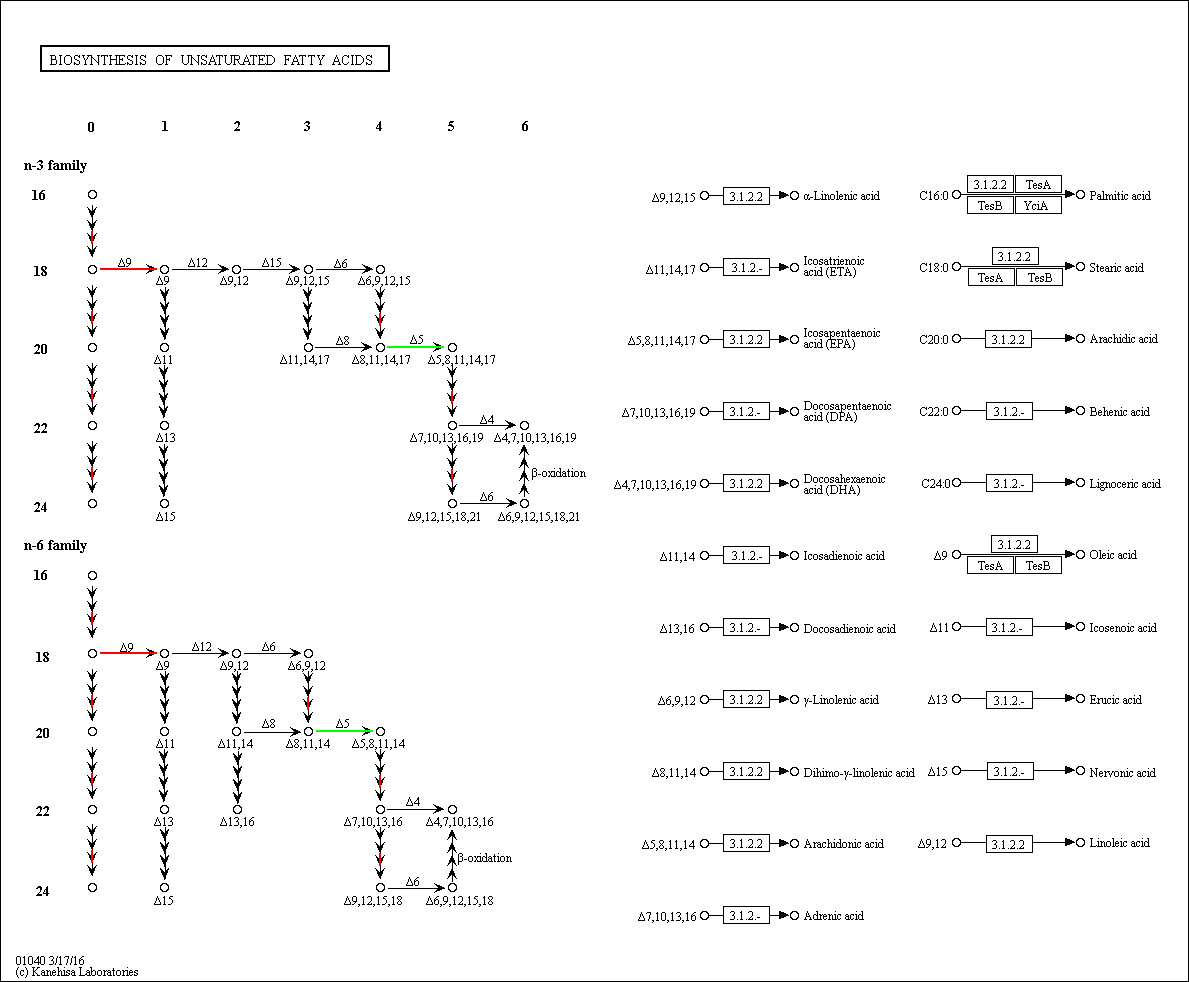
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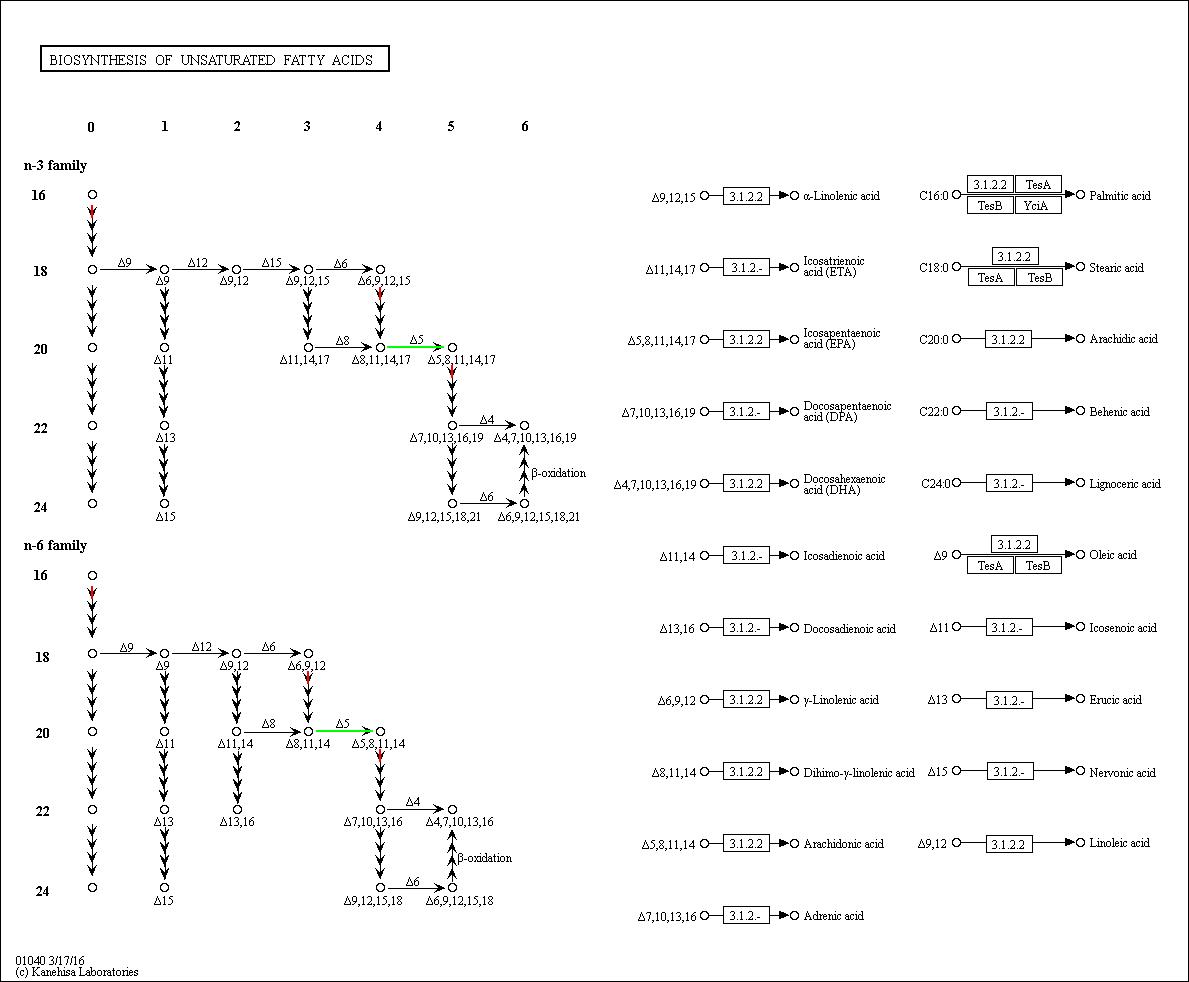
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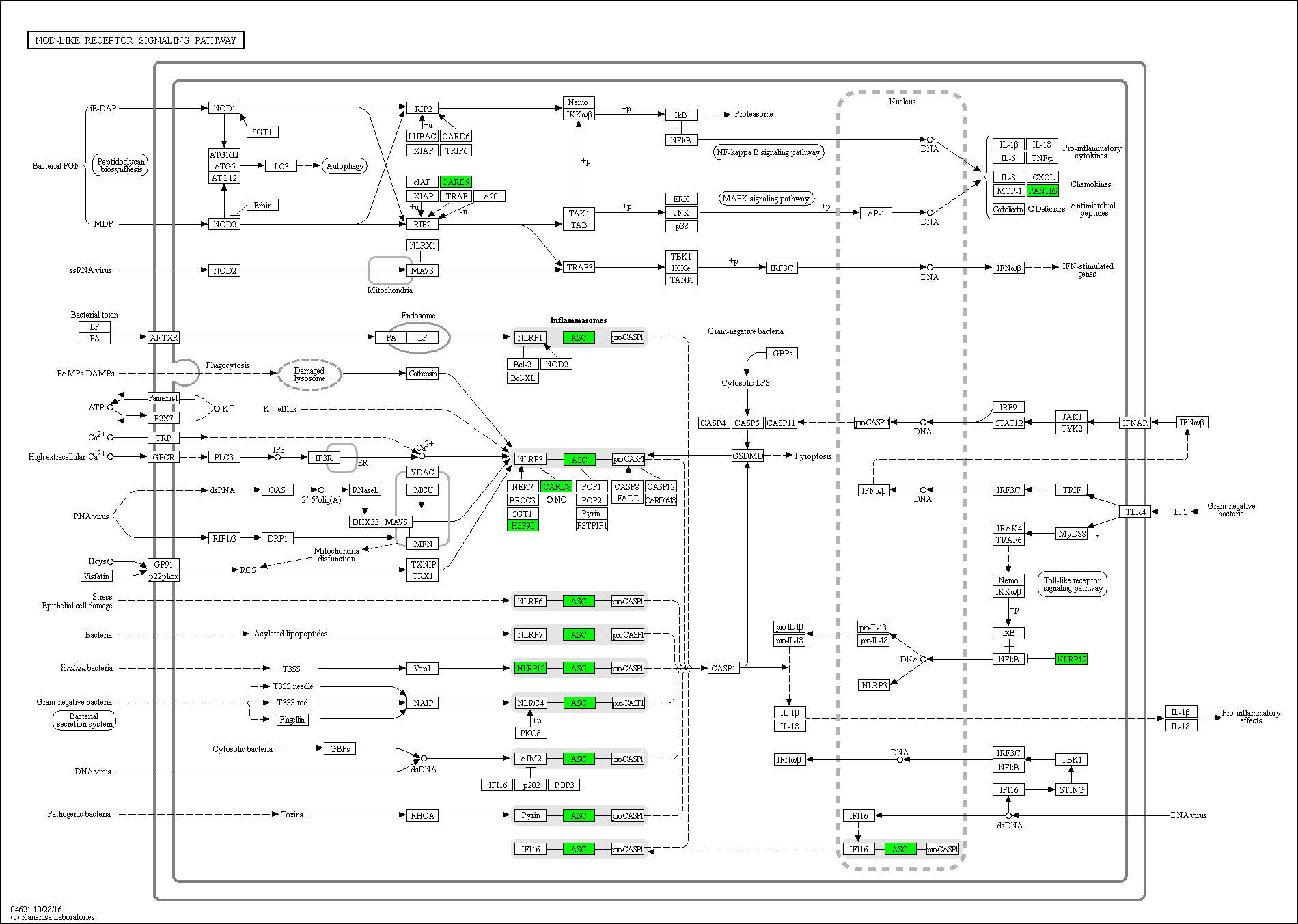
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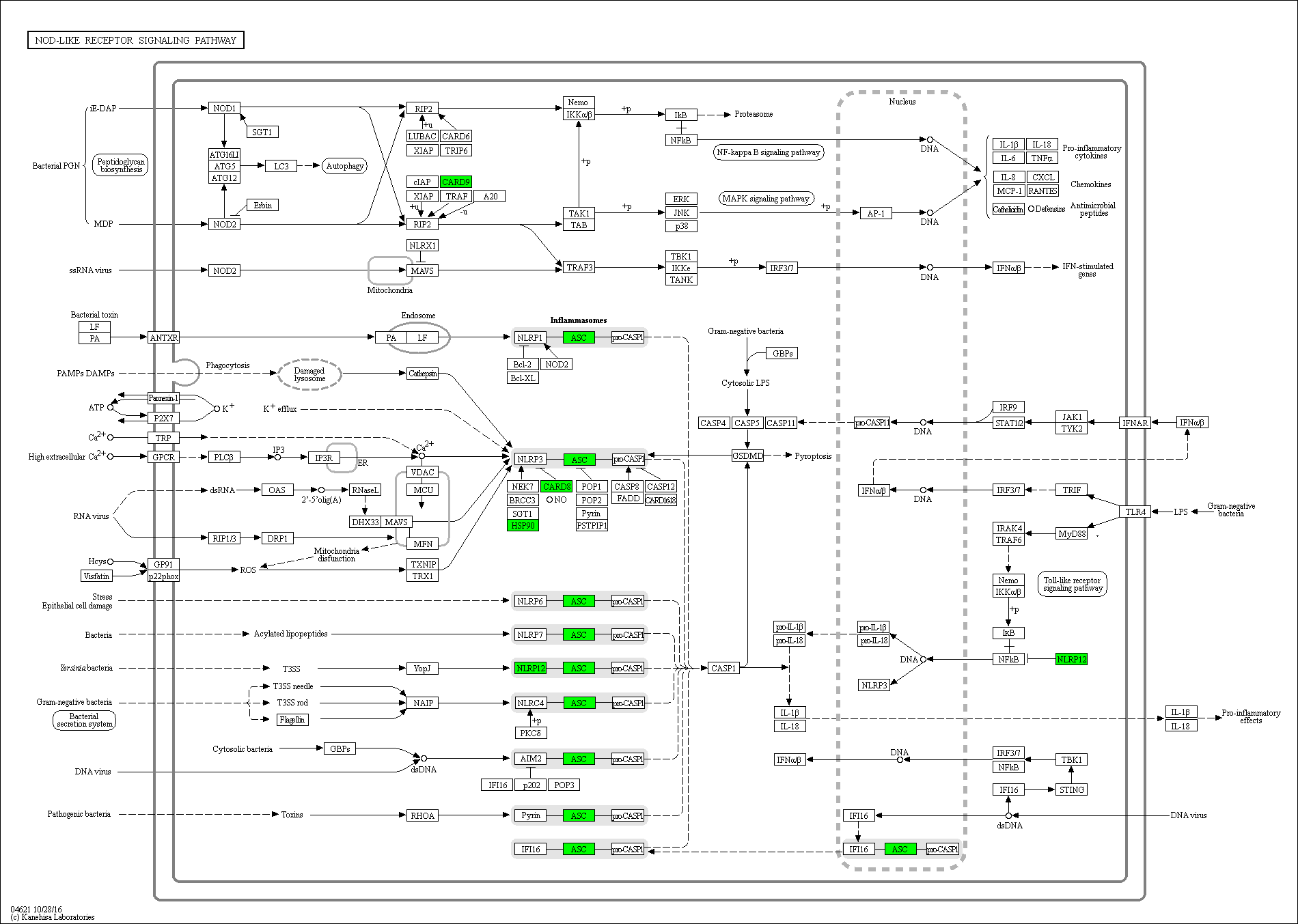
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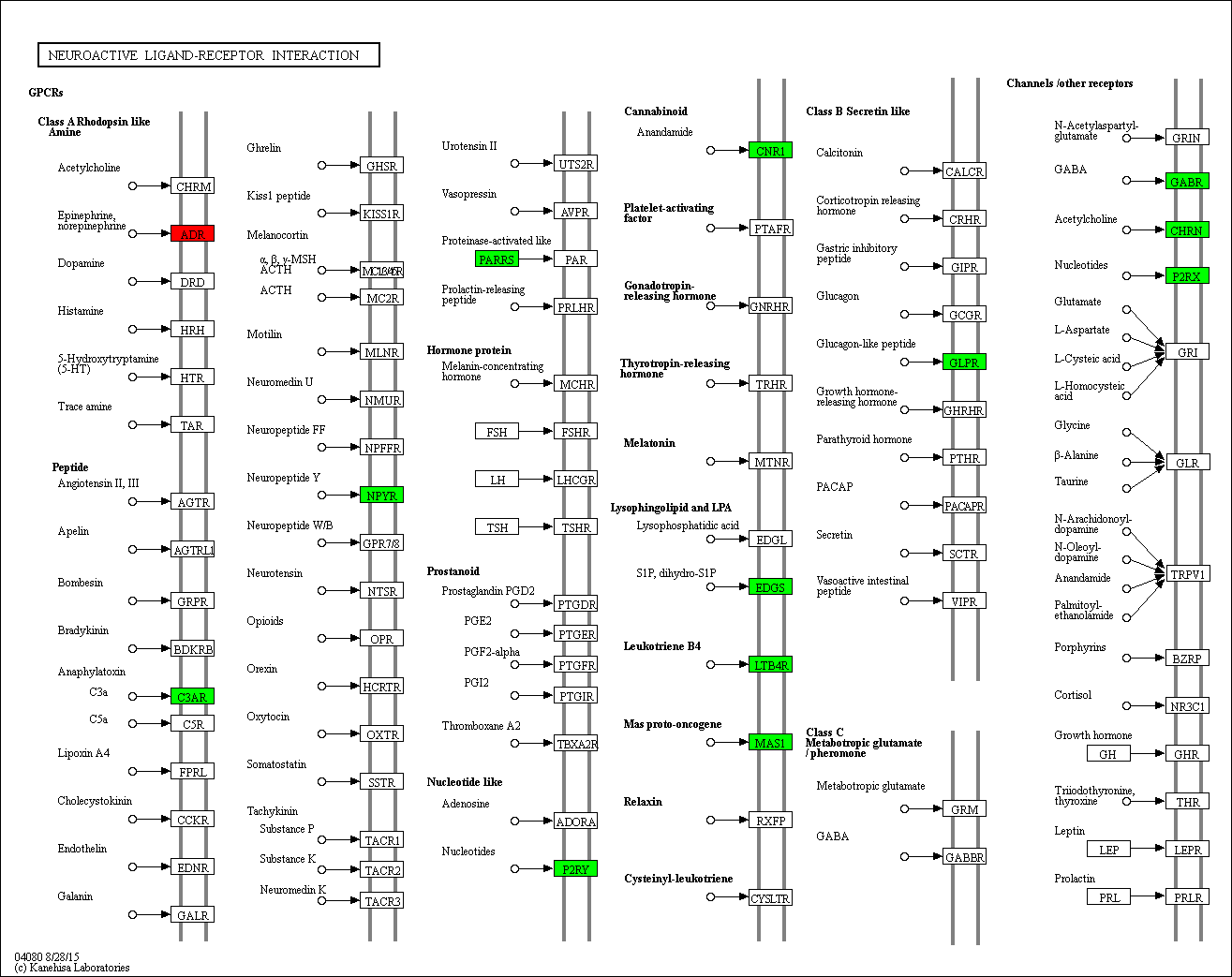
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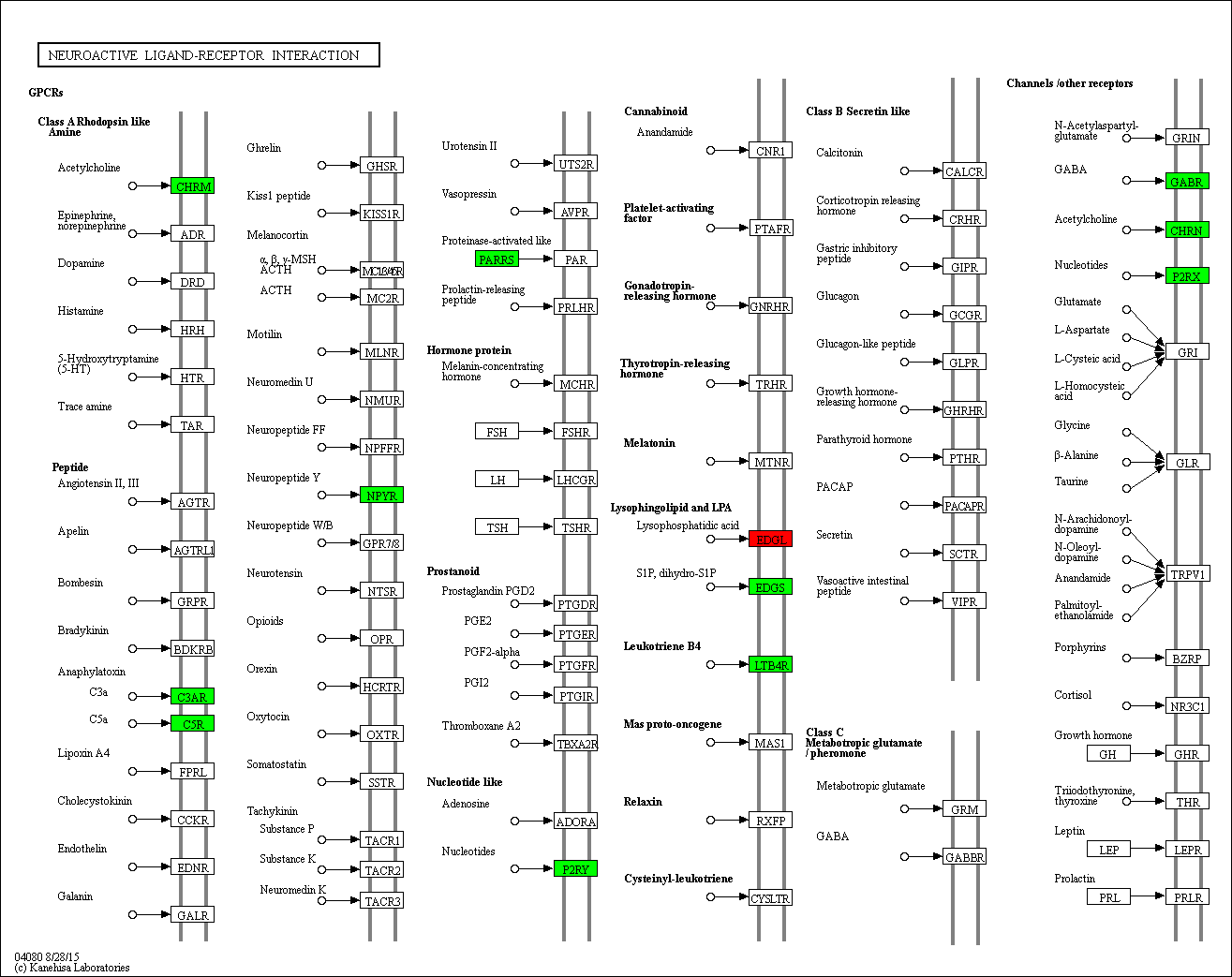
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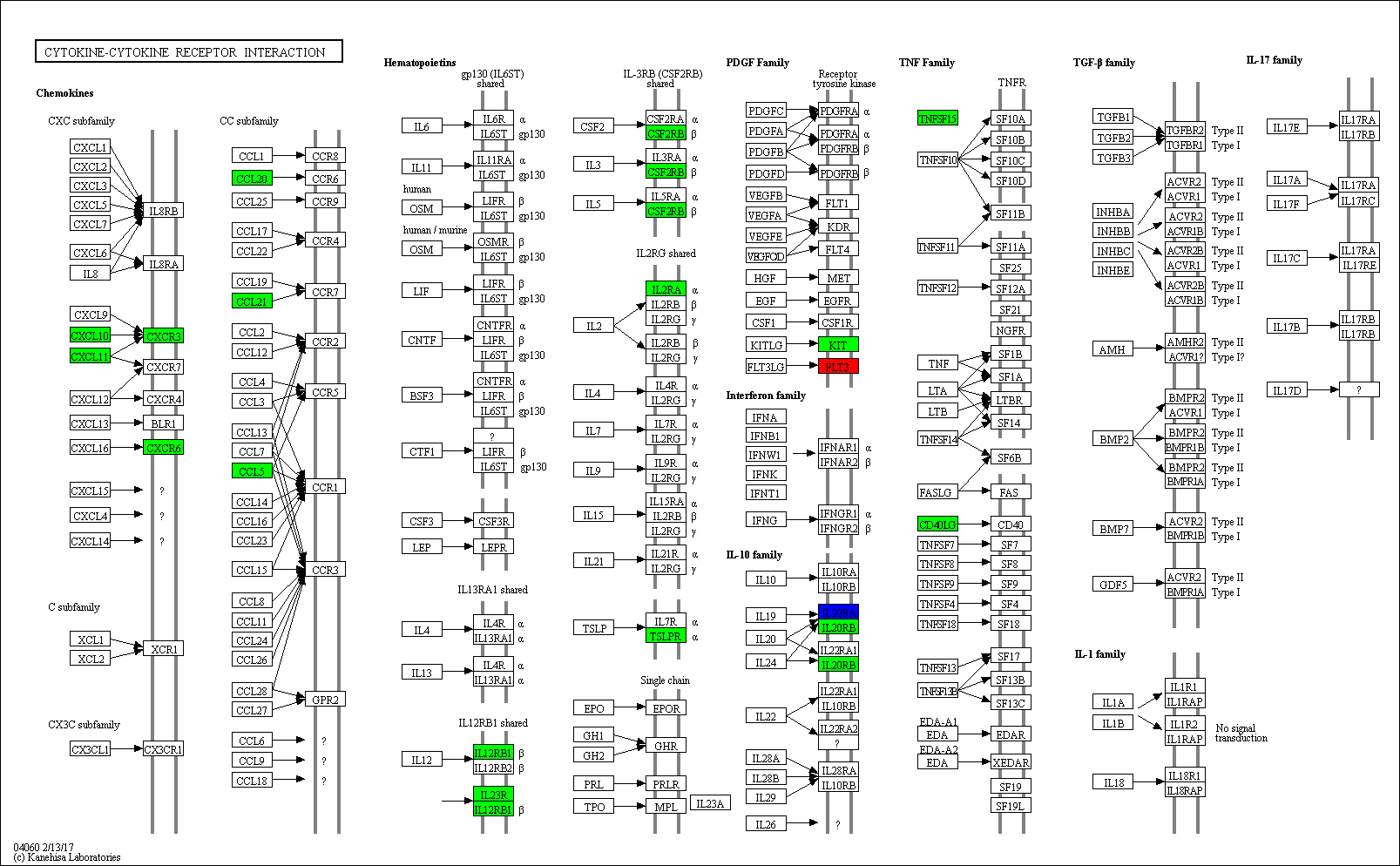
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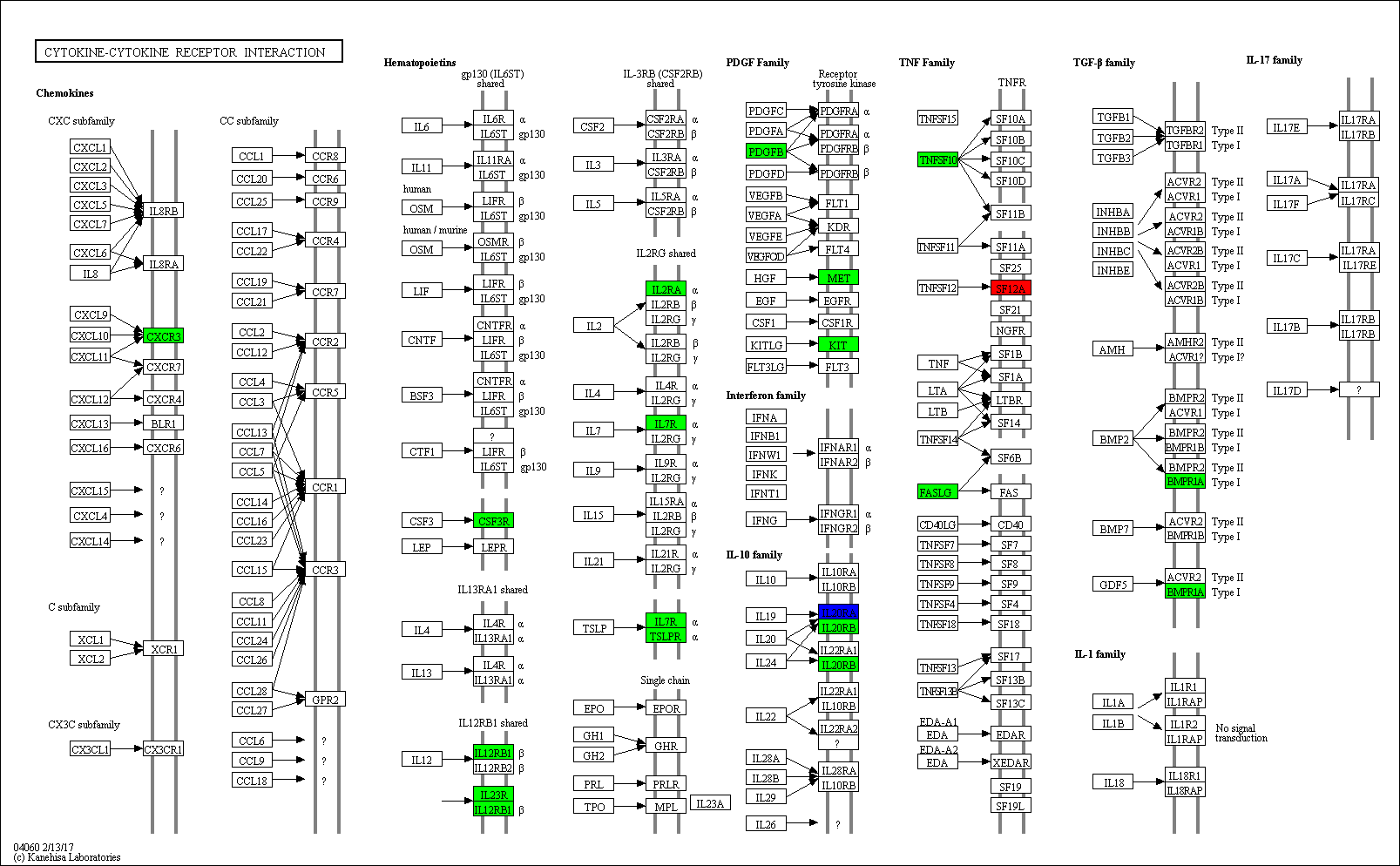
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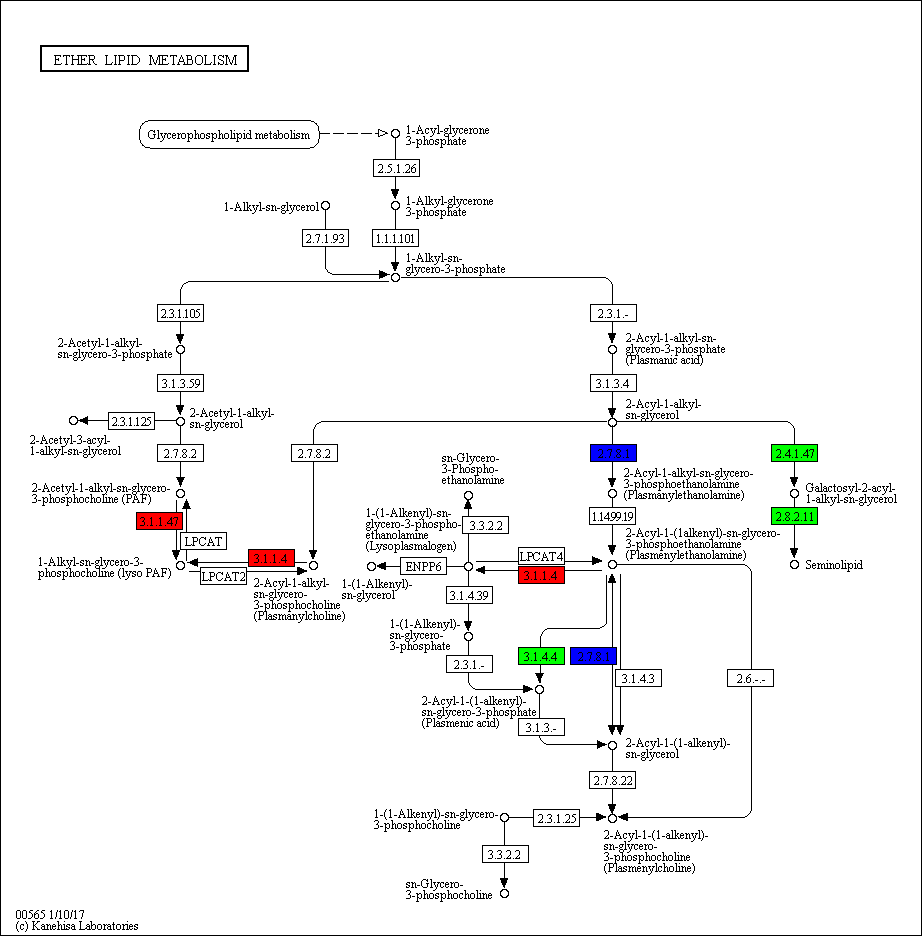
K



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M



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