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Supplementary

Streptozotocin-induced Type 1 and 2 Diabetes Mellitus Mouse Models Show Different Functional, Cellular and Molecular Patterns of Diabetic Cardiomyopathy

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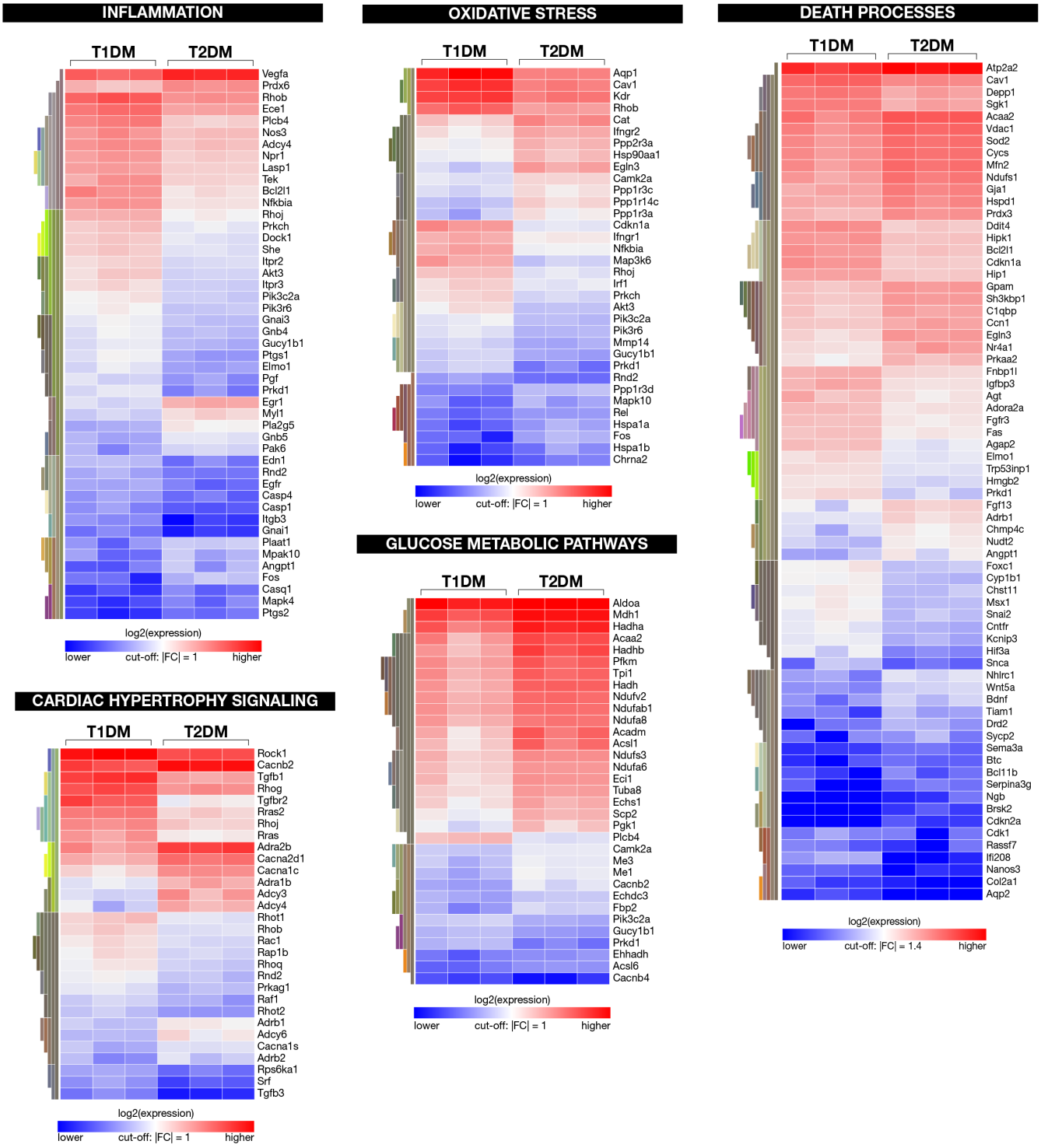

Supplementary Figure S1. RNA-seq analysis from STZ-based DMT1 and DMT2 mouse models displays a modulation in genes involved in selected biological processes. Heatmaps showing differentially expressed genes involved in inflammation, oxidative stress, death processes (Apoptosis, Autophagy and Necrosis), cardiac hypertrophy signaling and glucose metabolic pathways in T1DM vs. T2DM.