Supplementary Materials: Microarray Study of Pathway Analysis Expression Profile Associated with MicroRNA-29a with Regard to Murine Cholestatic Liver Injuries

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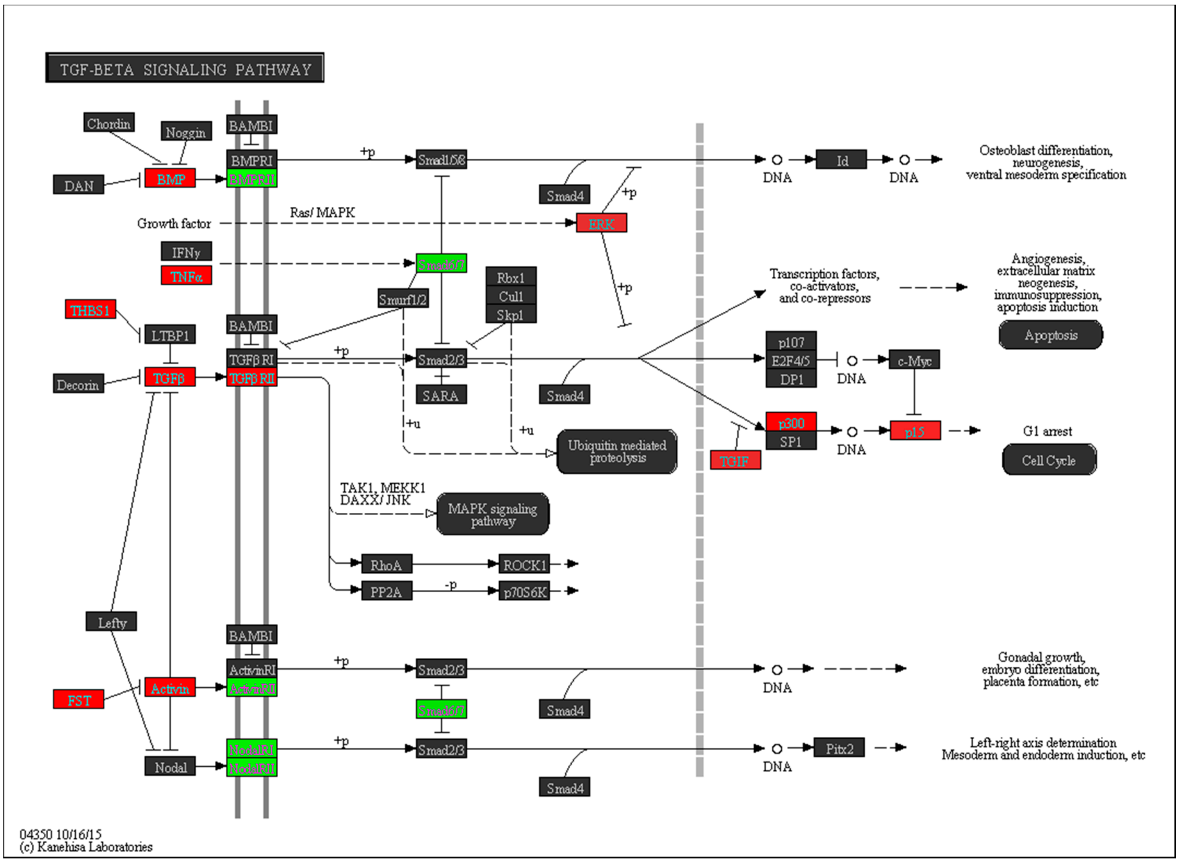

Figure S1. TGF-β signaling pathway. We mapped the differentially expressed genes back to KEGG pathways to determine if they were significantly enriched in several pathways. The TGF-beta signaling pathway was significantly enriched (*p* = 0.009331) by 2173 differentially expressed genes within the WT-BDL *vs.* WT-sham comparison. The genes that underwent upregulation, downregulation, and non-alteration in the BDL samples are highlighted in the red, green, and gray boxes, respectively.