

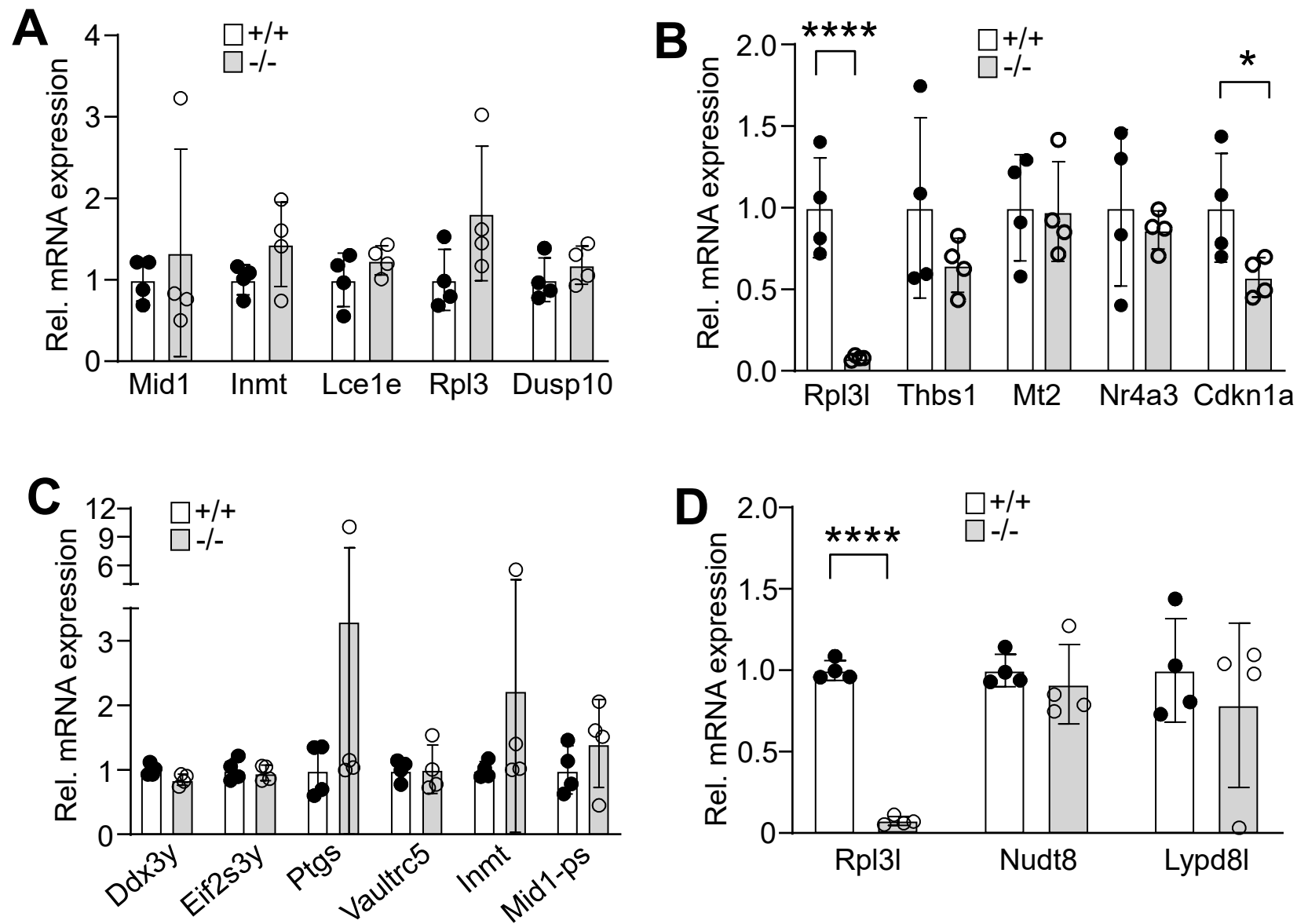


Figure S1: Quantitative PCR from cardiac mRNA to examine reproducibility of results from the microarray and ribosome sequencing results generated in wildtype versus *Rpl3l*^{-/-} mice at 2-3 months of age. A) qPCR for the indicated genes that represent the 5 most upregulated and, B) the 5 most downregulated transcripts from the microarray dataset (**** = $p < 0.0001$, * = $p < 0.05$). Only *Rpl3l* and *Cdkn1a* validated, while the remaining transcripts were not altered and represent false positives in the Affymetrix array data. C) All upregulated and D) downregulated mRNAs from the ribosome sequencing dataset (**** = $p < 0.0001$). Data are mean $\pm$ SEM. Only *Rpl3l* validated as significantly changed, and all others were false positives from the ribosome sequencing procedure.