

Supplementary figures

Figure S1. Genes in the same protein complexes show higher co-expression than genes that are not.

Figure S2. Expression heatmap of the adaptive and innate immune response genes.

Figure S3. Volcano plots that compares the distribution of the innate and adaptive immune response genes (red) against all genes (black), showing no obvious deviation.

Figure S4. Z-scores of the network measures presented in Figure 4. Solid lines: innate network; dashed lines: adaptive network.

Figure S5. The intranet of the innate and adaptive immunity genes exhibit good scale-free behavior.

Figure S6. Top 3 KEGG pathways (see Table 2) that are different in co-expression network structure between RO-T1D and uHC, as identified by CoGA. Color of a node indicates the expression $\log_2FC$ of the corresponding gene between RO-T1D and uHC.

Figure S1

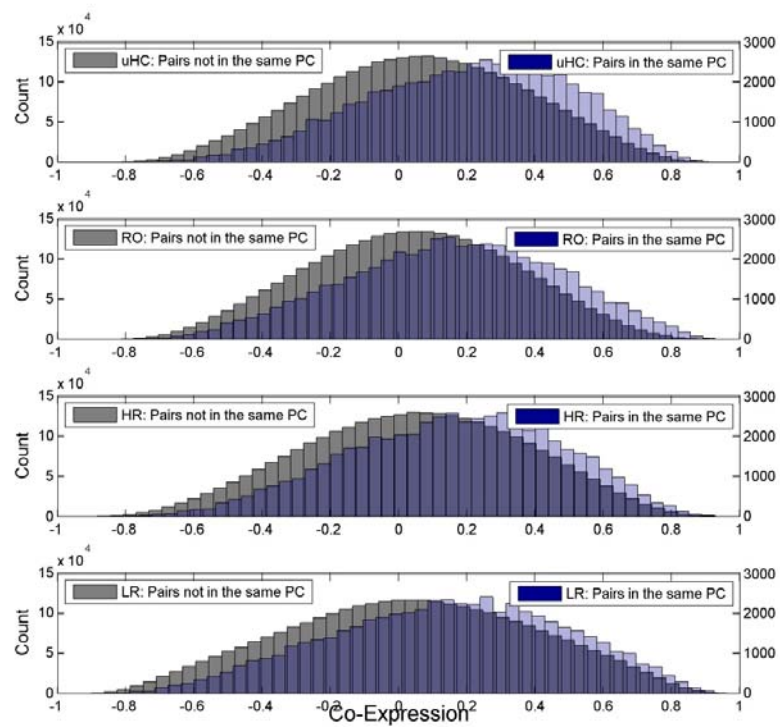


Figure S2

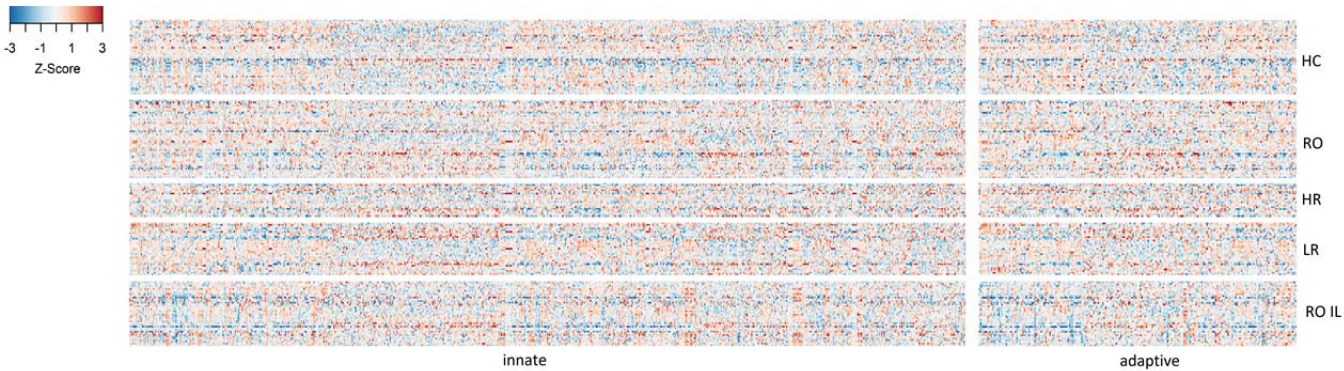


Figure S3

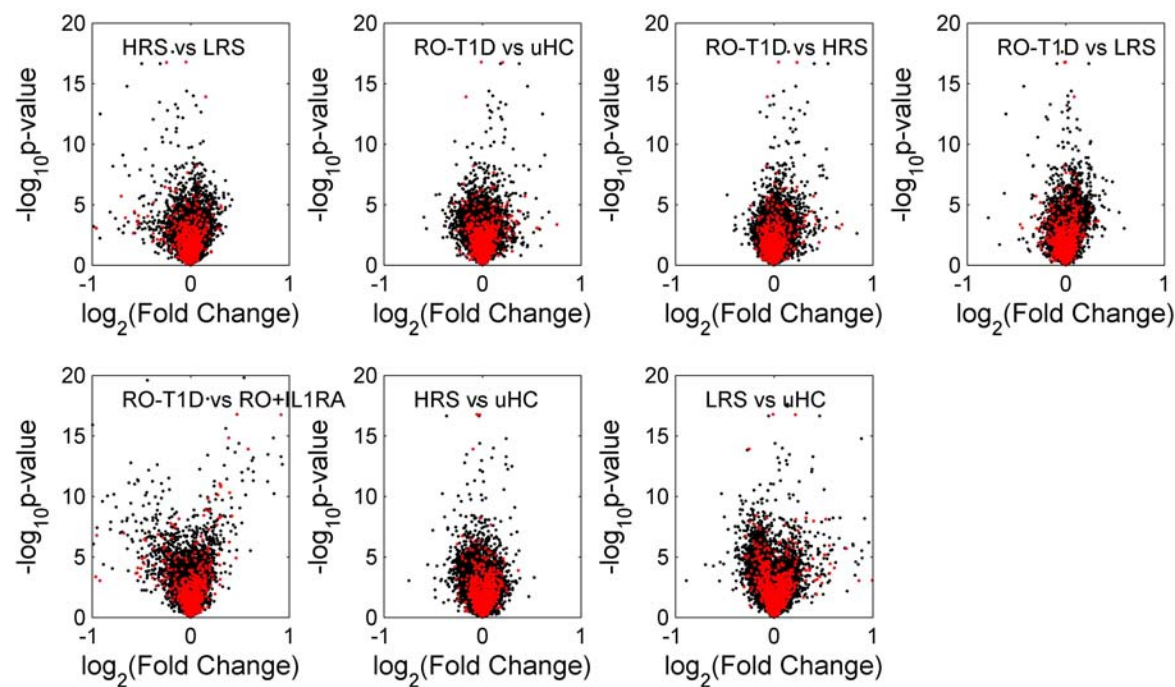


Figure S4

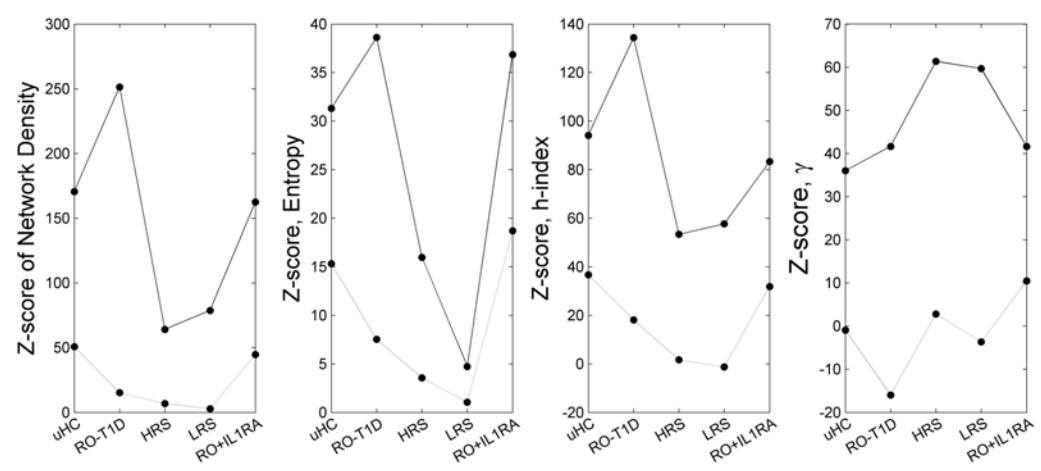


Figure S5

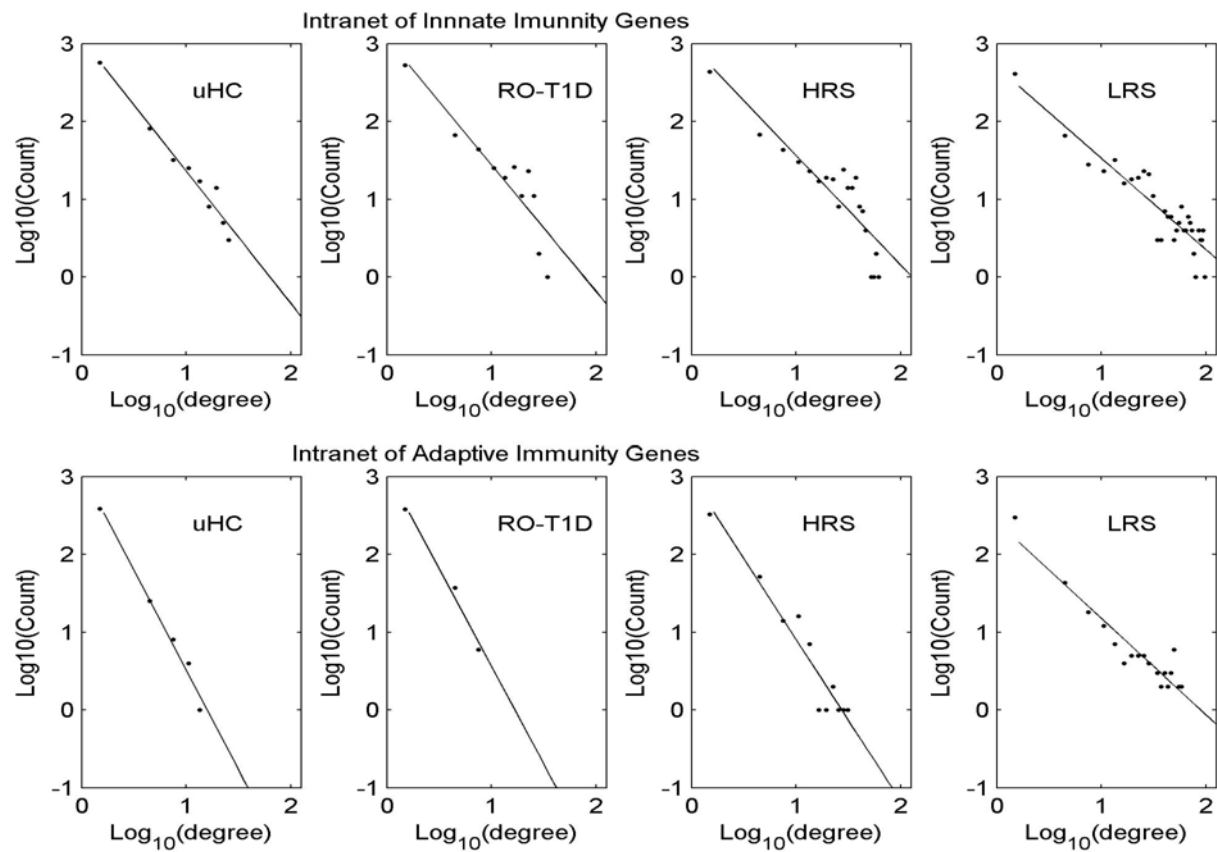
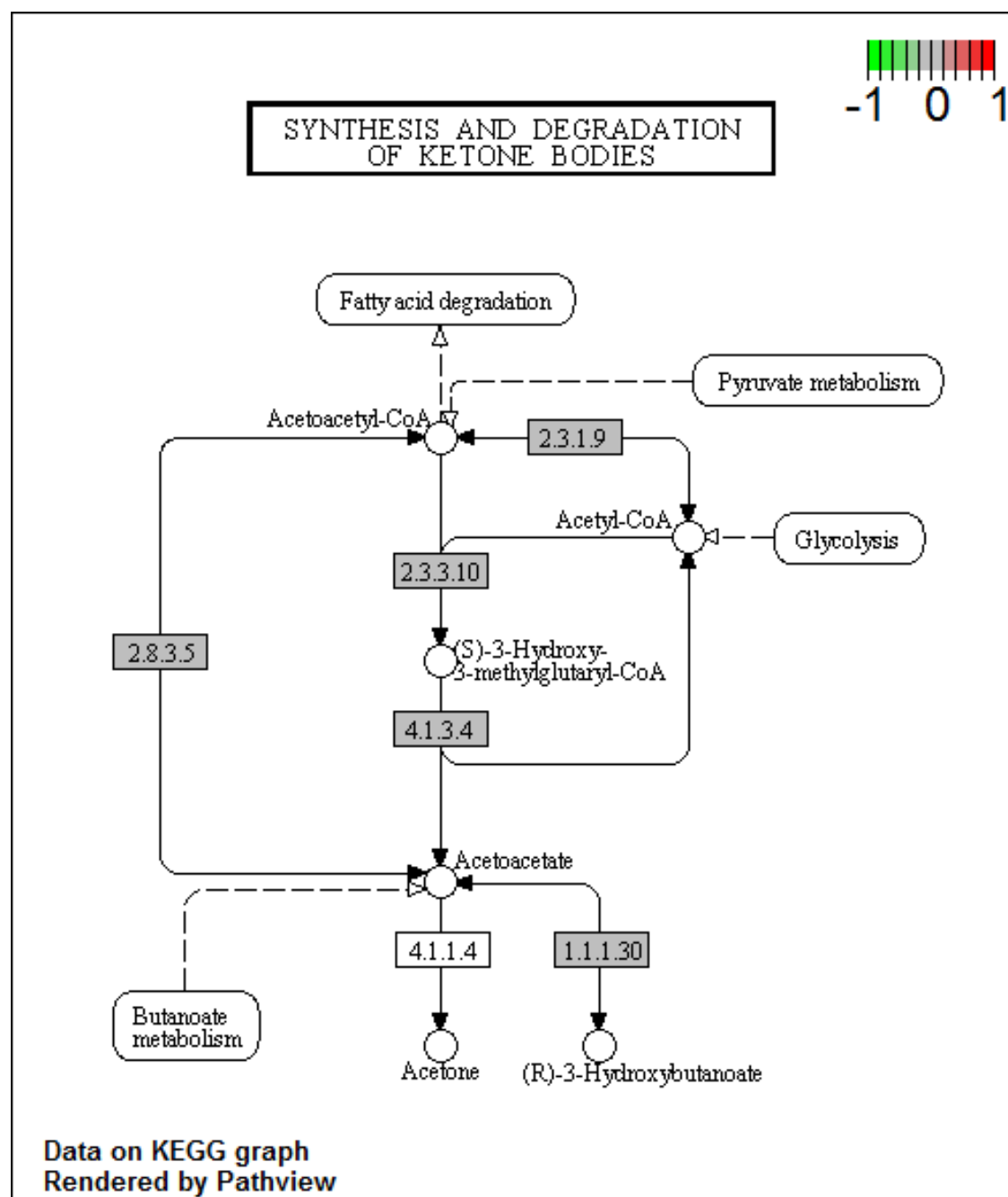
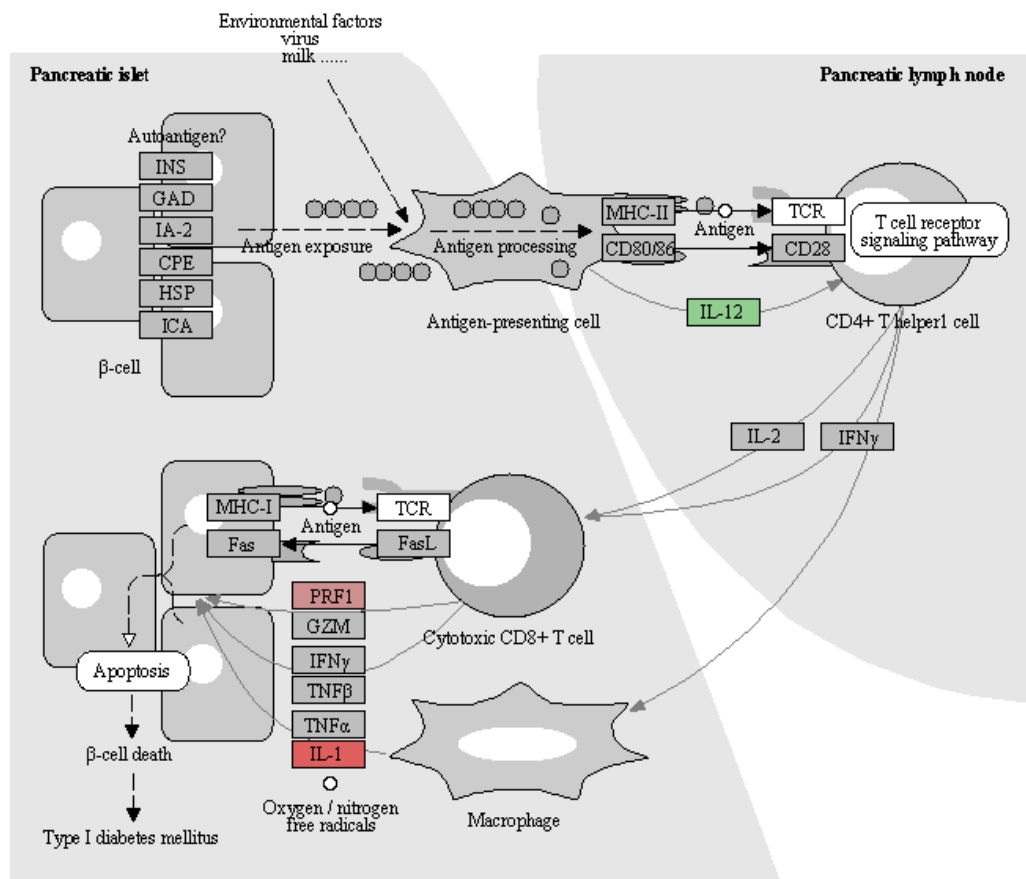
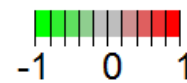


Figure S6



TYPE I DIABETES MELLITUS



Data on KEGG graph
Rendered by Pathview

